

Universidade do Minho Escola de Ciências da Saúde

Andreia Alexandra Neves de Carvalho

When gaining is loosing: insights into the function of ataxin-3 and its perturbation in the context of Machado-Joseph disease

Quando ganhar é perder: estudo da função da ataxina-3 e da sua perturbação no contexto da Doença de Machado-Joseph



Universidade do Minho Escola de Ciências da Saúde

Andreia Alexandra Neves de Carvalho

When gaining is loosing: insights into the function of ataxin-3 and its perturbation in the context of Machado-Joseph disease

Quando ganhar é perder: estudo da função da ataxina-3 e da sua perturbação no contexto da Doença de Machado-Joseph

Tese de Doutoramento em Ciências da Saúde

Trabalho realizado sob a orientação da **Professora Doutora Patrícia Espinheira de Sá Maciel**

DECLARAÇÃO DE INTEGRIDADE

Declaro ter atuado com integridade na elaboração da presente tese. Confirmo que em todo o trabalho conduncente à sua elaboração não recorri à pratica de plágio ou a qualquer forma de falsificação de resultados.

Mais declaro que tomei conhecimento integral do Código de Conduta Ética da Universidade do Minho.

Universidade do Minho, _____ de _____ de _____

Nome completo: _____

Assinatura: _____

Agradecimentos/ Acknowledgments

As últimas palavras de uma tese são provavelmente as de maior importância e certamente as mais difíceis de escrever. Ao finalizar este trabalho, gostaria de expressar o meu profundo agradecimento e reconhecimento a todos os que de alguma forma contribuíram para a sua realização. Mais do que uma experiência desafiante no laboratório, este trabalho proporcionou-me um ambiente enriquecedor de crescimento pessoal.

Com o apoio de todos os que humildemente homenageio aqui, os meus olhos abriram-se para um mundo novo!

With the support of those who I acknowledge herein, my eyes were opened to different "funny" things.

Obrigada! Thank you! Dank U Wel!

ICVS

À Professora Doutora Patrícia Maciel pela oportunidade de integrar o seu grupo de investigação e pela orientação, apoio, energia e acompanhamento ao longo destes [8] anos com o devido grau de exigência e rigor. Obrigada pelas oportunidades de formação. Obrigada por querer *sempre mais*.

À Professora Doutora Cecília Leão e restantes membros do Concelho Científico, em particular ao Professor Doutor Jorge Pedrosa presidente do Instituto de Investigação em Ciências da Vida e da Saúde (ICVS) e ao Professor Doutor Nuno Sousa presidente do Domínio de Investigação em Neurociências (NeRD), por me terem aceitado como aluna de doutoramento da Escola de Ciências da Saúde (ECS) e do seu Instituto de Investigação e por terem reunido todas as condições necessárias à realização deste trabalho.

À Fundação para a Ciência e Tecnologia (FCT) pelo financiamento.

VU, Amsterdam, Holland

I would like to thank Professor Peter Heutink for allowing me to work in his lab, for the energy and scientific input. For his avaibility and encouragement words. For the Thursdays afternoon beers at the *Basket*!

Shoey: for his help with *Sushi* cells, for being always available to answer all my emails. For the scientifical ideas and sharing of information. For teaching me that in the Netherlands people greet each other with three kisses.

Sasja: for the wonderful smile, for the avaibility and help. For introducing me to the "tau word".

Francesca: for hosting me since the very first moment and introduce me to everyone. For sharing with me the experience of being an *expat at Adam*.

Ashu and Sjirk for the *VERY* spicy indian food. For making fun of my height and microscopic handwriting. Thanks for the help.

IBMC

À Professora Doutora Elsa Logarinho pelo sorriso, pela calma e pela *confiança* no meu trabalho. Porque sempre arranjou um tempinho para adquirir as minhas imagens.

Ao Professor Doutor João Relvas pelas *ideias* e discussões científicas.

À Professora Doutora Sandra Macedo Ribeiro por me abrir as portas do seu *laboratório* sempre que precisei.

Ao Bruno Almeida, por todos os *"favorzinhos"* e por todas as dicas e por partilhares o teu conhecimento sobre proteínas.

University of Michigan, USA

I would like to thank Professor Henry Paulson for the scientific input.

Carmo (aka Maria do charme): pela ajuda e pela partilha de conhecimento sobre integrinas. Pelas *críticas* duras mas sempre relevantes. Por acreditares no meu trabalho. Por todos os "coisos" e por me fazeres rir.

Neurociências

A todos os NeRDs pelo sentido de crítica, exigência, ajuda e partilha. Pelas boas memórias do ICVS amarelo. Pelo bom ambiente no laboratório, pelos momentos divertidos de descontração e pelo esforço de sermos um grupo e aprendermos a trabalhar num *open space*!

Em especial...

Joana Silva (aka Joaninha): pela ajuda, pelas risadas e pelos desabafos. Pelos infinitos Western blots. Pelos jantares temáticos em tua casa. Por me chamares *Andreiinha* com tanto carinho. Por seres minha amiga.

Carina Cunha: pela companhia nos almoços, lanches e intervalos. Por me compreenderes e ouvires. Pela tua má disposição e pessimismo (*sempre com resolução*) que me fazem rir. Pela ajuda. Por seres minha amiga.

Bárbara: por nunca te *zangares* comigo quando brinco contigo. Pela tua calma e boa disposição e por me ajudares sempre com o MAC. Por seres minha amiga.

John (aka Jonecas): já devias saber português! Anyway, thanks for all the "*relp*" and all the "*portant*" and important scientific discussions. For all the advices and for believing in me. For understanding me with no need of words. Thanks also for the craziness and for making me laugh. For teaching me the greek. For being my friend.

Ana João (aka Ani Joni): por acreditares em mim mais do que eu própria. Pelos desabafos e incentivos sempre com a certeza de que vou conseguir. Pela ajuda, pela cumplicidade, por me defenderes e pelos *panikes* gordurosos. Por teres sido a minha primeira inspiração na vida científica. Por continuar a ser *a tua menina* e o teu *monstrinho*. Por seres minha amiga.

Fábio (aka Fabinho): pela ajuda e por estares *sempre* lá. Por me fazeres ri. Por seres meu amigo. O pastel de nata não está esquecido!

Miguel Carvalho (aka Migas): por seres o meu *coleguinha* de sempre. Por partilhares angústias e desafios. Por não me teres deixado desistir. Por seres meu amigo.

André Lopes, Belém, Sofia Serra, Eduardo, Ana Pires, Ana Freitas, Margarida, Nuno Silva, Tó, Ana Inês Silva, Ana Oliveira: pela ajuda técnica, pela partilha de conhecimentos e por me deixarem *"cravar"* coisas. Pelos bons e maus momentos na cultura de células e por haver sempre um *cantinho* na câmara!

Macielitas

Sara Silva (aka Sarinha): pelas discussões no telhado, no laboratório, no biotério..intermináveis! Por te entusiasmares com o meu trabalho, pela ajuda e generosidade. Pelas 8:45 no baroque. Por falares sempre que tive vergonha. Por contarmos as mesmas histórias vezes sem conta, pelas gargalhadas e por nunca te zangares comigo (mas por me ralhares de vez em quando). Por não precisarmos de palavras. Pelo amor, carinho e cumplicidade. Por me conheceres. Por seres o meu *Tico* ou o meu *Teco*. Por estares (sempre), lá!

Anabela (aka Belita): pela ajuda com as culturas primárias, a estatística e o Photoshop e por me explicares com paciência as tuas "ratices". Pelos breaks no telhado, pela cumplicidade e amizade sincera. Por sentires falta do meu "barulho" quando não estou, pelas ideias *brilhantes* de negócio, as sangrias e as *bubbles*; um dia ainda vamos ter a nossa *roulotte* de genotipagem no S. Pedro!

Ana Jalles (aka Mary Jalles): por teres esse jeito especial de me *"tratar mal"* que me faz rir. Por partilhares os teus resultados e as fotos dos teus sobrinhos.

Andreia Castro (aka De Castro): pelos "Maria", "ouvi dizer que me ias fazer isto", "asap"..pela tua atitude sempre crítica, pela ajuda e por teres sempre *"2 minutinhos".* Pelo teu mau humor de Segunda-feira e pelas tuas gargalhadas. Pelo tour por Chicago. Falhaste o ano do teu casamento!

Sofia (aka Sofs): pelas *"bananas",* pelas horas partilhadas no biotério e pelas patetices para passar o tempo. Por ter aprendido contigo que nem tudo o que parece é. Liliana Santos (aka Li): pelas conversas sociais e científicas e por desenvolveres *novas ideias* no grupo. Por ter aprendido contigo a ver o que não está à mostra.

Dulce, Marta e Stephanie: pela paciência na descrição das infinitas estirpes de *C. elegans* e dos cruzamentos on going. Por me fazerem relembrar o tempo em que também fui *"elegante"*!

Fátima Lopes: por me ensinares o dialecto fafense, pelos teus comentários cómicos e pela "mãozinha" no projeto do *splicing*.

Gang do neurodesenvolvimento (Filipe, Marina e Carlos Bessa): pela partilha de conhecimento e pela *boa vizinhança*!

Alguns amigos/ Some friends

Àqueles que sabem quem são...por serem verdadeiros comigo e por gostarem de mim como eu sou. Por não me cobrarem nada e por me levarem ao colo quando mais precisei. Por fazerem com que a vida valha a pena ser vivida. Por fazerem caminho comigo. Pelas grandes e pelas pequenas coisas. Por serem *quem são e como são*.

Em especial..

Loirinha (e Zé): pela tua maneira particular e tão especial de ser! Porque nunca te esqueces da Biologia do 12° ano para tentares perceber o que eu faço. Por nunca teres desistido da nossa amizade e por compreenderes que "ainda" continuo a estudar. Pelas mensagens de apoio, pelos beijinhos e pelo *carinho*. Espero estar à altura de retribuir!

Liliana (aka Jimi): mesmo à distância *continuas* presente! Obrigada por te preocupares comigo, por partilhares sucessos e fracassos e por seres minha amiga e minha "prima".

Óscar: por muito que os nossos caminhos se cruzem e descruzem, estiveste *sempre lá*... e ainda estás! Obrigada pela paciência, pela compreensão, pelo carinho, por me fazeres rir e por te rires comigo.

Hugo Almeida (aka Huguito), Magda (aka Maguxa) e Pedro Leão (aka Peter Lion): por todas as conversas loucas, pelos momentos divertidos, pelos jantares em que se *ria mais do que se comia*. Por me terem apoiado sempre ao longo do caminho. Por partilharem stress, angustias e vitórias. Por serem meus amigos mais do que meus colegas de trabalho.

Emiel: my first real dutch friend! Thank you for inviting me to party, for the music at the lab, for making fun of me and making me laugh. *I still laugh*! For introducing me to the chameleons! Miss you! Dank U Wel!

Margherita (aka Magui): *menina*...obrigada pela companhia ao jantar (pela *pasta*), pelas longas e divertidas conversas, pela amizade, pelo otimismo científico, pela partilha de experiências. Por me fazeres rir com os "combolhos". Por guardares sempre a minha bicicleta e por me arranjares sempre um *espacinho* na tua casa (I'm sure you can follow this!) Miss you!

Mohit: for upsetting me all the time (in a good way), for all the chatting, for worrying about me. For the good moments and for cooking for me. For the *Bollywood* parties. For being the party animal and for loving Porto wine! Well.. I also miss you!

Nikhil: for being my buddy, for all the meetings at the ping pong table. For all the late in night chatting. For lending me your *[small]* lab coat! I am sure you are going to be a brilliant scientist! Miss you!

Stella: my first and favorite roommate! Thank you for ALL the good and funny moments. For the Bulgarian food and other "*stuff*". Still have your t-shirt with me and will keep it forever! Hope we can catch up soon...miss you girl! Dimitri thanks for the *contagious* laugh!

À minha segunda família

D. Luzia, Sr. Belmiro, Bruno (O meu *chatinho* preferido! Obrigada pelo carinho, pelo apoio e pelas nossas brincadeiras..parece que vou ter de te aturar por muito tempo!), Avó Cândida, tia Adélia, tia Lurdes, tio Lúcio, Luciano, Luiz Carlos, Bibiana, Filipe, D. Helena, Sr. João e restante

família...obrigada pelo vosso carinho, pelo apoio, por se preocuparem comigo, pelo *mimooooo* e por me fazerem sentir "da casa".

Ao André

Talvez as palavras mais difíceis de escrever...porque entre nós não é preciso dizer muito; conhecesme de cor! Obrigada pela partilha incondicional, pela compreensão, pelo apoio desmedido. Por conseguires pôr sempre tudo em perspectiva. Por teres orgulho em mim e nunca duvidares que seria capaz. Por me fazeres rir. Pelo amor. E por tudo aquilo que nunca ninguém entenderá..."Para lá do infinito". *Oscar Bravo*!

À minha família

Avô Lourenço, avó Rosa e avô Manel: simplesmente por terem feito parte da minha vida e continuarem a ser as *estrelas mais brilhantes* todas as noites!

Família Coelhoso e Zulmirinha: não são do meu sangue, mas *são família!* Obrigada pelo apoio e por partilharem sempre as minhas alegrias.

Mãe, pai, mano e cunhada: porque *os últimos são sempre os primeiros*. Mas vocês são os primeiros e os últimos, as minhas lágrimas e o meu riso, o meu medo e a minha coragem, o meu sossego e a minha inquietude, a minha partida e a minha chegada. Obrigada pelo apoio incondicional, pelo amor, pelo mimo, por compreenderem que nunca tenho tempo nem horários, por terem aprendido a usar o Skype e o Facebook.. Obrigada, obrigada, obrigada, obrigada, obrigada...

Esta tese também é vossa! This thesis is also yours! Deze thesis is ook van jou!

"Science...never solves a problem without creating ten more!"

George Bernard Shaw

"When gaining is loosing: insights into the function of ataxin-3 in neurons and its perturbation in the context of Machado-Joseph Disease"

Ataxin-3 (ATXN3) is the protein involved in Machado-Joseph Disease (MJD), one of the nine neurodegenerative disorders known to be caused by a polyglutamine (polyQ) expansion. This polyQ tract causes the appearance of misfolded protein species, protein aggregates, neuronal dysfunction and cell death. ATXN3 is known to interact with polyubiquitin chains and to have deubiquitylating (DUB) activity *in vitro*, but its substrates and its cellular and physiological role(s) remain unknown, specially in neurons. Since the leading hypothesis concerning the pathogenesis of MJD is that the expanded polyQ tract confers a toxic gain of function of ATXN3, not much attention has been dedicated to its normal function. However, it is believed that a partial loss of the normal function of ATXN3 may also contribute to and modulate disease progression.

This study was based on the idea that understanding the normal physiological role of ATXN3 will be of relevance for our understanding of the pathogenesis of MJD.

In this work, we explored the function of ATXN3 in neuronal cells and its perturbation in the context of MJD. We found that ATXN3 is required for neuronal differentiation and for normal cellular morphology, cytoskeleton organization, proliferation and survival. This phenotype is associated with increased proteasomal degradation of alpha5-integrin subunit (ITGA5) and reduced activation of integrin signaling. Interestingly, we show that silencing of ATXN3, overexpression of a catalytically inert version of the protein or a mutant protein bearing an expanded polyQ tract led to partially overlapping phenotypes, suggesting that a loss of the neuronal function of ATXN3 may be contributing to neurodegeneration.

Consistent with a wider role of ATXN3 in the regulation of the cytoskeleton network, we found that loss of function of ATXN3 also leads to a deregulation of tau expression, namely a deregulation of tau exon 10 splicing. This event has a negative impact in neuronal morphology and differentiation. Additionally, we found that ATXN3 interacts with SFRS7, a regulator of tau splicing, and regulates its ubiquitylation levels. As similar alterations were found in the brain of a mouse model of MJD, it is likely that this mechanism is contributing to pathogenesis of this disorder. Hence, this work establishes for the first time a functional link between two key proteins involved in different neurodegenerative diseases.

Lastly, we characterized the ubiquitome of neuronal cells lacking ATXN3 in an attempt to identify potential substrates of its DUB activity. We found that a large proportion of these proteins were involved in RNA post-transcriptional modification. Considering this, we analyzed by transcriptomic analysis and using reporter minigenes the global splicing pattern in neuronal cells upon silencing of ATXN3 and found that splicing was globally altered in these cells. These findings lead us to propose for the first time that ATXN3 plays a role in splicing regulation in neurons, a novel function for this protein.

In summary, this work adds new knowledge about the relevance for neurons of one specific DUB, ataxin-3, and provides new clues about its biological functions and the pathways in which it is involved. It reinforces ATXN3's involvement with the UPP and it also raises new hypotheses for its role in cytoskeleton organization and in splicing regulation. Additionally, it provides evidence for perturbation of the normal function of ATXN3 in the context of disease, through a dominant negative effect, which may have relevance for the development of future therapeutical strategies.

"Quando ganhar é perder: estudo da função da ataxina-3 e a sua perturbação no contexto da Doença de Machado-Joseph"

A Ataxina-3 (ATXN3) é a proteína envolvida na Doença de Machado-Joseph (DMJ), uma das nove doenças neurodegenerativas que se sabe serem causadas por uma expansão de poliglutaminas (poliQ). Este trato de poliQ causa o aparecimento de espécies proteicas com uma conformação anormal, agregados proteicos, disfunção neuronal e morte celular. A ATXN3 interage com cadeias de poliubiquitina e tem atividade de ubiquitina hidrolase (DUB) *in vitro*, mas os seus substratos e a(s) sua(s) função(ões) fisiológica(s) permanecem desconhecidos, especialmente em neurónios. Dado que a hipótese actualmente mais aceite relativa ao mecanismo patogénico da DMJ considera que o trato de poliQ expandido confere um ganho tóxico de função à ATXN3, não tem sido dedicada muita atenção à sua função normal. Contudo, acredita-se que a perda parcial da função normal da ATXN3 também pode contribuir e modular a progressão da doença.

Este estudo baseou-se na ideia de que conhecer a função fisiológica normal da ATXN3 será relevante para conseguirmos compreender a patogénese da doença.

Neste estudo, explorámos a função da ATXN3 em neurónios e a sua perturbação pela expansão poliQ em DMJ. Descobrimos que a ATXN3 é necessária para a diferenciação neuronal e para a normal morfologia celular, organização do citosqueleto, proliferação e sobrevivência. Este fenótipo está associado a um aumento da degradação da subunidade 5-alpha da integrina (ITGA5) pelo proteossoma e uma ativação diminuída da sinalização pela via das integrinas. Curiosamente, demonstrámos que o silenciamento da ATXN3, a sobre-expressão de uma versão cataliticamente inerte da proteína ou de uma proteína mutante contendo um trato de poliQ expandido conduzem a fenótipos parcialmente sobreponíveis, sugerindo que a perda da função neuronal da ATXN3 pode contribuir para a neurodegeneração.

De forma consistente com um papel mais abrangente da ATXN3 na regulação da organização do citosqueleto, descobrimos que a perda de função da ATXN3 também origina uma desregulação da expressão da tau, nomeadamente uma desregulação do splicing do exão 10 da tau em células neuronais. Este evento tem um impacto negativo na sua morfologia e diferenciação. Além disso, descobrimos que a ATXN3 interage com o SFRS7, um factor regulador do splicing da tau, e regula os seus níveis de ubiquitilação. Considerando que alterações semelhantes foram

encontradas no cérebro do modelo de DMJ em ratinho, este mecanismo parece contribuir para a patogénese. Este trabalho estabelece assim, pela primeira vez, uma ligação funcional entre duas proteínas chave envolvidas em diferentes doenças neurodegenerativas.

Por fim, caracterizámos o ubiquitoma de células neuronais silenciadas para a ATXN3, com o objectivo de identificar potenciais candidatos para a sua atividade DUB. Concluímos que uma grande proporção destas proteínas estão envolvidas na modificação pós-transcripcional do RNA. Tendo este dado em consideração, analisámos o padrão global do splicing por análises de transcriptómica e usando minigenes repórteres, e descobrimos que o splicing estava globalmente afetado nestas células. Estes achados levaram-nos a propor pela primeira vez que a ATXN3 desempenha um papel na regulação do splicing em neurónios, uma nova função para esta proteína.

Em sumário, este trabalho amplia o conhecimento acerca da relevância para os neurónios de uma DUB específica, a ataxina-3, e fornece indicativos sobre as suas funções biológicas e as vias celulares onde está envolvida. Além disso, reforça o envolvimento da ATXN3 com a UPP, levantando também novas hipóteses para o seu papel na regulação do citosqueleto e na regulação do splicing. Adicionalmente, são apresentadas evidências para a perturbação da função normal da ATXN3 no contexto da doença através de um efeito dominante negativo, facto que poderá ser relevante para o desenvolvimento de futuras estratégias terapêuticas.

Table of contents

Declaração	i
Agradecimentos/ Acknowledgments	iii
Abstract	xiii
Resumo	XV
Table of contents	xvii
Abbreviations	xxi
Thesis planning	xxiii
Chapter 1. General Introduction	1
1.1 The Ubiquitin-proteasome system	3
1.1.1 Roles of the ubiquitin signaling	3
1.1.2 (Poly)Ubiquitylation	4
1.1.3 Ubiquitin-conjugating enzymes: E1, E2, E3 and E4	5
1.1.4 Deubiquitylating enzymes (DUBs)	6
1.1.1.4 Non-catalytic activity of DUBs	8
1.1.5 Adaptor proteins and Ub-like proteins	8
1.2 Role of Ubiquitin signalling in neuronal function	9
1.2.1 Transport of Ubiquitin in neurons	10
1.2.2 Neuronal migration	10
1.2.3 Axonal growth, guidance and morphogenesis	10
1.2.4 Pre-synaptic function	11
1.2.5 Postsynaptic plasticity	11
1.2.6 Nonproteolytic functions of Ubiquitin signaling	12
1.3 The UPS and Ub in neurodegenerative disorders	13
1.3.1 Ub deposition in protein aggregates	13
1.3.2 The UPS in Parkinson's disease (PD)	13
1.3.3 The UPS in Alzheimer's disease (AD)	14
1.3.4 The UPS in Huntington's disease (HD)	15

1.3.5 The UPS in Ataxias	16
1.3.6 Connection between UPS and neurodegeneration through autophagy	16
1.3.7 The UPS as a therapeutic target	17
1.4 Machado-Joseph disease	18
1.4.1 Clinical and pathological features	19
1.4.2 MJD genetics	20
1.4.3 Therapeutic approaches	20
1.4.4 MJD protein: Ataxin-3 (ATXN3)	24
1.4.4.1 Function, biological function and molecular partners	26
1.4.4.2 Regulation of Ataxin-3 DUB activity	30
Bibliography	31
Objectives	47
Chapter 2. Dominant negative effect of polyglutamine expansion perturbs normal functi	on
of ataxin-3 in neuronal cells	49
Supplementary Material	69
Chapter 3. Perturbation of ATXN3 function leads to Tau splicing deregulation and	
contributes to Machado-Joseph disease	68
Bibliography	96
Chapter 4. Loss of function of ATXN3 alters the ubiquitome of neuronal cells, negatively	,
impacting on the splicing process	99
Bibliography	123
Chapter 5. General Discussion and Future Perspectives	125
5.1 The neuronal function(s) of ATXN3	127
5.1.1 Defining the ubiquitome of SH-SY5Y ATXN3 KD cells	127
5.1.2 The balance of ubiquitylation and ATXN3	128
5.1.3 Splicing and ATXN3	130
5.1.4 Cell structure, cytoskeleton and ATXN3	133
5.1.5 Cell signaling and ATXN3	136

Appendices	153
Bibliography	146
5.3.1 Ataxin-3 in the disease context: gain or loss of function?	144
5.3 Relevance of the novel findings and main conclusions of the work	142
5.2 Effects of absence of ATXN3 in cells and organisms: discrepancies and communalities	140
5.1.8 Other functions of ATXN3 – DNA repair	140
5.1.7 Neuronal differentiation and ATXN3	139
5.1.6 Transcription and ATXN3	137

Abbreviations

3R-tau: 3 repeat tau isoform	GABA: Gamma-aminobutyric acid
4R-tau: 4 repeat tau isoform	GO: Gene ontology
17-AAG: 17-N-Allylamino-17-	HD: Huntington's disease
demethoxygeldanamycin	HDL2: Huntington disease-like 2
17-DMAG: 17-dimethylaminoethylamino-17-	hnRNP: Heterogeneous nuclear
demethoxygeldanamycin	ribonucleoproteins)
AD: Alzheimer's disease	HS: Horse serum
ALS: Amyotrophic lateral sclerosis	HSP: Heat shock protein
AMPA: α-Amino-3-hydroxy-5-methyl-4-	HSR: Heat shock response
isoxazolepropionic acid	JD: Josephin domain
C14: Cysteine 14	JOSD: Josephin-domain proteins
C. elegans. Caenorhabditis elegans	K: Lysine
CHIP-seq: Chromatin immunoprecipitation	Kb: Kilobase
sequencing	KD: Knockdown
CLIP-seq: Cross-linking immunoprecipitation	kDa: Kilodalton
sequencing	KEGG: Kyoto encyclopedia of genes and
CNS: Central nervous system	genomes
DAPI: 4',6-diamidino-2-phenylindole	KO: Knockout
DMEM/F-12: Dulbecco's Modified Eagle	LB: Luria-Bertani
Medium/Nutrient Mixture F-12	LC-MS/MS: Liquid chromatography-tandem
DRG: Dorsal root ganglia	mass spectrometry
DRPLA: Dentatorubral-pallidoluysan atrophy	LNA: Locked nucleic acid
DUB: Deubiquitylting enzyme/deubiquitylase	MAP: Microtubule-associated protein
ECM: Extracellular matrix	MG132: Carbobenzoxy-Leu-Leu-leucinal
EGFP: Enhanced green fluorescent protein	Min: Minute
EYFP: Enhanced yellow fluorescent protein	MJD: Machado-Joseph disease
FBS: Fetal bovine serum	MRI: Magnetic resonance imaging
FCS: Fetal calf serum	mRNA: Messenger RNA
FTD: Frontotemporal dementias	MTOC: Microtubule-organizing center
FTDP-17: Parkinsonism linked to chromosome	NES: Nuclear export signals
17	NLS: Nuclear localization signal

NMDA: N-methyl-aspartic acid	SDS: Sodium dodecyl sulphate
Opti-MEM: Reduced serum medium	SDS-PAGE: Sodium dodecyl sulphate –
O/N: Overnight	polyacrylamide gel electrophoresis
P4: Postnatal day 4	SMA: Spinal muscular atrophy
PBS: Phosphate-buffered saline	SMBA: Spinobulbar muscular atrophy
PD: Parkinson's disease	SMN: Survival motor neuron
PD: Pick's disease	SN: <i>Substantia nigra</i>
PI: Propidium iodide	snRNP: Small nuclear ribonucleoprotein
PNA: Peptide nucleic acid	t-test: Student's t test
PolyQ: Polyglutamine	TUBEs: Tandem ubiquitin binding entities
PolyUb: Polyubiquitin	UBA: Ubiquitin-associated domains
PROTACS: Proteolysis targeting chimera	UBB ⁺¹ : Ubiquitin mutant
molecules	UBL: Ubiquitin-binding domain
PTM: Post-translational modifications	UCH: Ubiquitin C-terminal hydrolases
RA: Retinoic acid	UDP: Ubiquitin-domain protein
RNAi: RNA interference	UIM: Ubiquitin-interacting motifs
RNA-seq: RNA sequencing	UPP: Ubiquitin-proteasome pathway
RT_qPCR: quantitative real time polymerase	UPS: Ubiquitin proteasome system
chain reaction	USP: Ubiquitin specific proteases
SCA: Spinocerebellar ataxias	UTR: Untranslated regions
SCA3: Spinocerebellar ataxia type 3	WT: Wild type
SCR: Scrambled	

Thesis planning

The present dissertation is organized in five different chapters. Chapter 1 is the General Introduction, the experimental work is presented in Chapter 2 to 4 in the shape of research articles (published and in preparation) and Chapter 5 is the General Discussion of the work.

In **chapter 1**, a general introduction to the theme of this dissertation is provided. An overview of the Ubiquitin proteasome system (UPS) and its components is given, concerning its role in the neuronal function. Some considerations about the involvement of the UPS in neurodegenerative disorders are also made. Then, an extensive presentation is provided about Machado-Joseph disease (MJD) and ataxin-3 (ATXN3), the protein involved in this disorder. At the end, there is a compilation of the available evidence concerning the function of ATXN3 in cells, ranging from *in vitro* studies to known protein interactors. A brief description of pathways in which ATXN3 is thought to be involved is also provided.

In **chapter 2**, the work "*Dominant negative effect of polyglutamine expansion perturbs normal function of ataxin-3 in neuronal cells*" shows that loss of function of ATXN3 has a negative impact on neuronal differentiation and deregulates proteasome degradation of alpha-5 integrin subunit, leading to decreased cell adhesion and disorganization of neuronal cytoskeleton. In this study we also present evidence suggesting a partial loss of this function of ataxin-3 in the context of MJD.

Chapter 3, "*Perturbation of ATXN3 function leads to Tau splicing deregulation and contributes to Machado-Joseph disease*" focuses on the role of ATXN3 in the regulation of the neuronal cytoskeleton network, extending our knowledge of ATXN3 function. We show that depletion of ATXN3 in SH-SY5Y cells leads to a deregulation of tau exon 10 splicing, perturbing the 3R/4R tau ratio, a mechanism that seems to contribute for MJD pathogenesis.

Chapter 4, "Loss of function of ATXN3 alters the ubiquitome of neuronal cells, negatively impacting on the splicing process" presents an exploratory work regarding the identification of candidate targets of ATXN3's DUB activity. These potential substrates were searched using the

Tandem ubiquitin binding entities (TUBEs) system combined with mass spectrometry. We present data indicating that ATXN3 might be regulating RNA transport and processing in neurons, a hypothesis that we validated using reporter minigenes and transcriptomic analysis.

The **General Discussion** of the dissertation, as well as the Future Perspectives, are presented in Chapter 5.

Two **appendices** are included in this thesis; appendix 1 corresponds to the list of primers used in this work. Appendix 2 shows a list of the splicing factors with altered expression in ATXN3 knockdwn cells and the predicted upstream regulators of these factors.

Chapter 1

General Introduction

1.1 The Ubiquitin-proteasome system

The UPS is a highly conserved intracellular pathway for degradation of proteins [1]. The 26S proteasomes, localized both in the cytoplasm and in the nucleus [1, 2], are essential for cell quality control by eliminating defective proteins, and for regulation of fundamental cellular processes by rapid destruction of key proteins (Reviewed in [3]). More recently, the UPS has also emerged as a crucial mechanism in the regulation of many physiological functions of the nervous system (Reviewed in [4, 5]).

Proteolysis by the UPS is highly regulated and precise: only selectively polyubiquitylated proteins are degraded by the proteasome, at the expense of ATP [6]. However, ubiquitylation of a substrate fated to be degraded can be reversed by deubiquitylating enzymes (DUBs).

1.1.1 Roles of the ubiquitin signaling

In all tissues, the UPS and the ubiquitin signaling play crucial roles in regulating the levels and/or the fate or localization of proteins acting in several basal processes: i) rapid degradation of proteins – termination of cellular processes and adaptation to new physiological conditions [7], ii) transcriptional regulation – degradation of transcriptional factors or alteration of their localization [8], iii) quality control mechanism – elimination of misfolded or damaged proteins that have arisen by biosynthesis errors, by mutations or damage by oxygen radicals and/or denaturation (protein aging) [9, 10], iv) source of amino acids – maintenance of cellular homeostasis at low energy costs by recycling of amino acids, v) non-proteolytic functions – monoubiquitylation tagging triggers internalization of cell surface proteins into the endocytic pathway [11].

More recently, an increasing amount of data has suggested that several UPS-related genes are causally linked to neurodegenerative diseases, such as Alzheimer's disease (AD), Parkinson's disease (PD), Amyotrophic lateral sclerosis (ALS), Frontotemporal dementias (FTD), Huntington's disease (HD), and other polyglutamine (polyQ) diseases (Reviewed in [12]). Although not clearly sustained yet by experimental data, some authors additionally suggest that dysfunction of the UPS may also be a consequence of the neurodegeneration observed in these disorders [12]. Moreover, a better understanding and identification of the components involved in the UPS-mediated proteolysis have also implicated this mechanism in other disease conditions, as for example cardiac dysfunction, cancer, viral infections, inflammation, and autoimmune diseases [13]. Additionally, multiple lines of evidence support the concept that UPS components are promising drug target candidates for therapeutic intervention in many of these disorders (Reviewed in [14-18]).

1.1.2 (Poly)Ubiquitylation

Ubiquitin (Ub) is a small 76 amino acid regulatory protein, highly conserved among eukaryotes. Ub first captured the interest of neuroscientists due to its presence in protein aggregates that were observed in various neurodegenerative diseases (Reviewed in [19-22]). Conjugation of Ub to a substrate through a series of enzymatic reactions is called ubiquitylation. Ub molecules can also be attached to other Ubs via an isopeptide linkage between the lysine residue of the previous Ub and the C-terminal glycine residue of the subsequent Ub [23] (Figure 1). Therefore, a target protein can be modified by a single Ub molecule (monoubiquitylation) or by a poly-Ub chain (polyubiquitylation). There are seven different lysine (K) residues in Ub that can potentially be used *in vivo* for Ub-chain synthesis – K6, K11, K27, K29, K33, K48 and K63. Depending on the type of ubiquitylation, the length of the Ub chain and the nature of Ub-Ub linkage, the modified protein is subjected to different fates (Reviewed in [24-27]). For example, proteins conjugated with K48-linked poly-Ub chains are usually targeted for proteasomal degradation. Monoubiquitylation and polyubiquitylation using other lysines, such as K63, have been implicated in non-degradative pathways, including regulation of subcellular localization, vesicular trafficking, protein sorting and activation of DNA repair [23, 27].



Figure 1. Diversity and specificity of ubiquitin signaling. Protein substrates can be monoubiquitylated (A) or multiubiquitylated (B), or even polyubiquitylated (C, D and E). Ubiquitin chains can form extended or closed conformations for one or more linkage type (B and C) or even forked chains with multiple ubiquitin attached to a common moiety (D). Adapted from [28].

1.1.3 Ubiquitin-conjugating enzymes: E1, E2, E3 and E4

Ubiquitylation is a cascade of sequential reactions regulated by the action of three enzymes: E1 (Ub-activating enzyme), E2 (Ub-conjugating enzyme) and E3 (Ub-protein ligase) (Figure 2). The first reaction is the activation of Ub by the E1 enzyme in an ATP-dependent manner. The activated Ub is then transferred from the E1 to the active cysteine site of the E2 enzyme. Finally, the E3 enzyme catalyzes the transfer of the Ub moiety to a lysine residue in the substrate protein. There are two major classes of E3s: the HECT domain and the RING finger E3s. Typically, DUBs oppose the activity of the E3s by mediating the removal of Ub from target proteins. Additionally, the E3s can regulate their own stability by ubiquitylating themselves, and DUBs may also regulate their proteasomal degradation, either by preventing or promoting it [29-31]. Among the three classes of ubiquitin-conjugating enzymes, the E2s are the more selective and are thought to interact with specific E3s, which largely determine the substrate specificity (Reviewed in [32]). The number of E2s in humans is estimated to be around 39 while the diversity of E3s is even greater (estimated to be about 475) [33]. Although the substrate specificity of ubiquitylation is essentially determined by the E3s, the diversity of E2s and E3 adaptor proteins, and the combination of E2s and E3s also contribute to a high degree of specificity [34].

An additional component of the UPS is the E4 enzymes. E4s were initially shown to be involved in the elongation of short Ub chains [35], but, more recently, these enzymes were shown to edit polyubiquitin chains and it was suggested that they might be involved in the regulation of the activation of specific proteins, by acting on the switch between the mono and polyubiquitylated states of these target proteins (Reviewed in [36]). The number of E4 ligases encoded in eukaryotic genomes is still not knwon [33].



Figure 2. The ubiquitylation cycle. Ubiquitylation requires the involvement of a E1 ubiquitinactivating enzyme that transfers ubiquitin to the ubiquitin-conjugating enzyme (E2). Then, the E2 transfers the ubiquitin molecule to an ubiquitin-protein ligase (E3) which subsequently ubiquitylates the substrate. In the case of K48 ubiquitylation, the substrate is sent for proteasomal degradation and ubiquitin is recycled. Adapted from www.tebu-bio.com.

1.1.4 Deubiquitylating enzymes (DUBs)

The DUBs are key regulators in the two major degradation pathways, the proteasomal and lysosomal (autophagy) routes, where they play different catalytic roles: i) processing of the Ub percursors, ii) editing and/or rescue of Ub conjugates, iii) recycling of Ub from Ub targeted conjugates, and iv) disassembly of anchored ubiquitin oligomers. Autophagy is an alternative pathway to the UPS, that can degrade long-lived proteins and protein aggregates which cannot be degraded by the proteasome [37, 38]. The fact that DUBs (and probably other UPS components) act on these two pathways is consistent with the observations that severe impairment of the proteasome also impairs autophagy and vice-versa [39]. The human genome encodes 80-90 DUBs, categorized into five classes based on the architecture of their catalytic domains: the USP family (ubiquitin specific proteases), the UCH family (ubiquitin C-terminal hydrolases), the OUT family (otubain protease), the Josephin/MJD family (genes containing the Josephin domain and ataxin-3), and the JAMM family (JAB1/MPN/MOV34 metaloenzyme).

USP family

The USPs are the largest family of DUBs and are thought to specifically recognize the free carboxy-terminus Gly-Gly motif of Ub [40-43]. Several USPs have been associated with DNA repair pathways [44-47], control of differentiation and maintenance of stem cell characteristics in osteosarcoma cells [48], and regulation of tumor suppression proteins [49].

UCH family

The UCH family comprises DUBs that preferentially cleave Ub from small substrates [50] and other enzymes that can accommodate larger substrates in their catalytic site [51]. One of the most studied UCHs is the ubiquitin carboxyl-terminal hydrolase L1 (UCHL1). UCHL1 is a highly abundant neuronal enzyme involved in the stabilization and recycling of mono-Ub, and is known to be genetically linked to PD (Reviewed in [52, 53]) and a major target of oxidative damage in AD [54]. Additionally, aberrant expression of UCHL1 is observed in a variety of cancer types and has been associated with the determination of cellular invasiveness [55].

OTU family

Despite the structural conservation within the catalytic domain, OUT proteins show diverse specificity for Ub chain linkages. These enzymes have been linked to regulation of the proinflamatory NFkB pathway (OUT protein A20) (Reviewed in [56-58]), to suppression of K63-linked polyubiquitylation of histones (that likely include H2A and H2AX) at DNA double-strand breaks (OTUB1) [59], and to the inhibition of the activity of associated E2 enzymes [59-61].

JAMM family

JAMMs are generally part of large multimeric complexes such as the proteasome lid complex and the endocytic ESCRT machinery (Reviewed in [62, 63]). While several members of this family show a strong preference for K63 polyUb chains, others preferably cleave Ub proximal to a substrate protein [64-66].

Josephin/MJD family

Josephin/MJD DUBs seem to represent a relatively late addition to the Ub system, since no homologues were found in yeast [67]. So far, the substrates for these DUBs remain mostly unknown. The most well studied protein from this family is ataxin-3 (ATXN3). Although it has been

shown that ATXN3 is involved in Machado-Joseph disease (MJD) [68], its biological function remains poorly characterized. It was recently demonstrated that ATXN3 directly ubiquitylates Parkin [69] and most likely regulates the degradation of α 5-integrin [70]. This will be further discussed in the next chapters.

1.1.1.4 Non-catalytic activity of DUBs

Not all DUB functions require catalytic activity. Many DUBs contain additional non-catalytic functions that mediate their function in membrane trafficking, cellular signaling, transcriptional regulation and DNA repair (Reviewe in [71]). Several DUBs, referred as housekeeping enzymes, such as Ubiquitin-specific protease 14 (USP14), the Ubiquitin-carboxy-terminal hydrolases UCH37/UCH-L5 and RPN11/POH1, protect Ub from degradation thus maintaining sufficient levels of free Ub that can be used for chain assembly [63]. Other DUBs regulate proteasome activity noncatalytically. For example, it was reported that Ubp6, the yeast homologue of human USP14, uses catalytic and noncatalytic mechanisms to modulate proteasome function; besides cleaving the Ub chains regulating proteasomal degradation of a specific substrate, Ubp6 appears to inhibit the proteasome directly, reducing the flux of some specific substrates through the proteasome [72]. Also, USP14 was shown to regulate synaptic function through a DUB-independent mechanism [73].

1.1.5 Adaptor proteins and Ub-like proteins

As mentioned above, ubiquitylation generates a broad repertoire of signals that are not strictly related to the proteasomal degradation. Several adaptor proteins associated with the ubiquitin signalling have been recognized to contain protein domains that bind Ub. Such domains include the Ub-binding domains (UBLs), the Ub-associated domains (UBAs) and the Ub-interacting motifs (UIMs) (Reviewed in [74]).

In addition, several other proteins with structural and biochemical similarity with Ub have been identified as modulating protein degradation. These proteins can be divided into two classes: proteins containing an Ub-domain (UDPs) and Ub-like proteins (UBLs). The UDPs are highly homologous to Ub but instead of conjugating with substrates, they function as adaptors, binding to Ub or Ubl proteins, and are able to bind to proteasome subunits [75]. UDP proteins include Rad23, Parkin and PLIC (protein linking IAP to the cytoskeleton) (Reviewed in [76, 77]). The UBLs can either freely or covalently form conjugates with proteins. Two examples of UBL proteins are NEDD8

8

(neuronal-precursor cell expressed developmentally downregulated 8) and SUMO (small ubiquitinlike modifier) (Reviewed in [78]).

The functions of these adaptor and Ub-like proteins are still poorly characterized, but it is thought that they can be identified by downstream receptors/interactors and can be used to regulate a large variety of cellular processes including cytoskeleton regulation, cell cycle control, mRNA processing, signal transduction, homeostasis, stress response, and metabolism (Reviewed in [76]).

1.2 Role of Ubiquitin signalling in neuronal function

The function of the nervous system relies on the precise formation of highly dynamic networks of synaptic connections. The UPS has emerged as a critical mechanism used by neurons to control the free pool of Ub and the renewal of internal components, both necessary for the normal nervous system development and function (Reviewed in [4]). During neuronal development, synapse formation and pruning [79, 80], axon pathfinding [81, 82] and neuronal migration [83, 84] are regulated by the UPS, as are inhibitory [85] and excitatory neurotransmission [85, 86] in the mature brain (Figure 3).



Figure 3. Roles for ubiquitin and protein degradation in neuronal function. The UPS regulates several aspects of synaptic biology, playing a role on neuronal function. Adapted from [87].

1.2.1 Transport of Ubiquitin in neurons

Two classes of genes encode for Ub in mammalian genome: the genes encoding ribosomal fusion proteins Rsp27a and Uba52, and the polyubiquitin genes *Ubb* and *Ubc*. The levels of free Ub in a cell are determined by Ub synthesis and degradation, and by polyubiquitin chain assembly and disassembly. Nevertheless, both *Ubb* and *Ubc* genes are transcribed at increased rates in response to cell stress, as Ub is a component of the cellular response to heat shock and other stressors [88]. Following the *de novo* synthesis of Ub in the soma of the neuron, Ub is transported via axonal transport to axons and dendrites [89], a process that may take days or even months in certain neurons [90]. For this reason, although the levels of free Ub are maintained high in neurons, as a reservoir to allow for rapid responses to cell stimulation or stress, distal axons and dendrites are particularly vulnerable to stress and may be particularly sensitive to local fluctuations in Ub levels [91].

1.2.2 Neuronal migration

Nervous system development requires proper migration of neuronal cells. Neuronal migration is regulated by a wide range of extracellular cues and intracellular signaling cascades, and dependent on cell adhesion proteins and various cell surface receptors, which, in turn, are regulated by the UPS and related components (Reviewed in [4]). Many studies have shown that the neuronal migration is dependent, directly or indirectly, on the activity of E3 ligases, making ubiquitylation one of the intracellular signaling pathways regulating neuronal migration [92-94]. For example, it was recently described that the FBXO31-SCF centrosomal E3 ligase is required for an efficient migration of neurons in the developing cerebellum [94].

1.2.3 Axonal growth, guidance and morphogenesis

Growth and guidance of axons are vital steps in the establishment of neuronal circuits. The UPS has been shown to regulate these processes through ubiquitylation and/or proteasomal degradation of proteins involved in the axonal cytoskeleton, transcription factors and small GTPases (Reviewed in [95]). The most well studied UPS-dependent regulators of axon growth and guidance are the PHR proteins, Nedd4, cdc20 and cdh1 E3 ligases. Cdh1, for example, was shown to bind to the anaphase-promoting complex (APC) [96], regulating the degradation/stability of specific transcription factors (such as Id2 and SnoN), impacting on axon growth [97-99]. Other E3 ligases, such as smurf-1, also have identified roles: smurf-1 was shown to directly target RhoA, a small

10
GTPase associated with the actin filaments network, for ubiquitylation and proteasomal degradation [100], thus enhancing axonal outgrowth [101].

Notably, many E3 ligases that are important for axonal growth and guidance also regulate axonal morphogenesis. For example, PAM (an E3 ligase, member of the PHR family) primarily regulates axon growth and guidance, but it also plays a role in axon morphology [79, 102, 103].

1.2.4 Pre-synaptic function

Growing evidence supports a contribution of the UPS to the regulation of synaptic physiology and transmission, by regulating the proteolysis of key presynaptic elements at the synaptic terminals (Reviewed in [74, 104-106]). Several regulatory molecules controlling long-term synaptic plasticity as well as synaptic transmission and short-term synaptic plasticity have been shown to be substrates for UPS-mediated degradation. For example, the protein Duc-13, which is critical in priming synaptic vesicles, accumulates in presynaptic terminals upon proteasome inhibition [107]. Also, specific Ub ligases interacting with syntaxin 1 – a presynaptic protein involved in synaptic vesicle exocytosis – and RIM1 α (Rab3-interactig molecule 1 α) – which acts as a presynaptic scaffold – have been identified [108, 109]. Additionally, it appears that the UPS also functions in recycling of synaptic vesicles and maintaining vesicle homeostasis [110]. Recently, Waith and colleagues described that presynaptic Ca_v2 channels are targets of the UPS, adding further to the relevance of UPS function in neurons [111].

1.2.5 Postsynaptic plasticity

The discovery of UPS components and target proteins at synapses gave indirect evidence for a postsynaptic role of this system (Reviewed in [74, 112-114]). Subsequent studies indicated that the UPS modulates regulatory molecules, structural proteins and neurotransmitter receptors in the postsynaptic compartment [106]. Studies in *Caenorhabditis elegans* and mammalian neurons showed a role for ubiquitin in trafficking and endocytosis of neurotransmitter receptors such as AMPA [85], GABA [115], NMDA [116] and glycine receptors [117]. Also, Colledge and collaborators showed that the postsynaptic density protein PSD-95 is regulated by UPS-mediated degradation, which in turn modulates AMPA receptors [85]. In addition to PSD-95, the UPS seems to regulate several other proteins, namely structural proteins such as Shank, GKAP and AKAP97/150 [118]. Finally, there is also evidence that the UPS contributes for the regulation of spine shape by

modulating the degradation of SPAR, a protein that acts on the reorganization of the actin cytoskeleton at the spine [119].

1.2.6 Nonproteolytic functions of Ubiquitin signaling

In recent years, mounting evidence suggests that Ub has also nonproteolytic functions; Ub or polyUb chains serve as a signal to recruit proteins harboring UBD, bringing together ubiquitylated substrates and Ub receptors to perform specific biological functions. These functions include membrane trafficking, protein kinase activation, transcriptional regulation and DNA repair (Reviewed in [120]).

Membrane trafficking

Monoubiquitylation and the attachment of K63-linked Ub dimers have been shown to maintain the balance between degradation, recycling and trafficking of cargo molecules and cell surface receptors [11, 62]. For example, depletion of the DUB AMSH accelerates epidermal growth factor receptor (EGFR) trafficking to lysosomes [121, 122].

Protein kinase activation

K63 polyubiquitylation is an important post-transcriptional modification of signaling cascades, such as NF-kB and the Wnt pathway, playing a key role in the activation of protein kinases [123, 124]. For example, the DUB USP4 was shown to be required for the regulation of the Wnt signaling activation [125].

Transcriptional regulation and DNA repair

DUBs can directly influence the structure of chromatin and coordinate DNA repair mechanisms or contribute to gene transcriptional regulation through reversible ubiquitylation of specific transcription factors and histones (Reviewed in [126]). It has been shown that certain DUBs can reverse monoubiquitylation of both H2A and H2B [127-130], impacting on multiple nuclear processes including mitosis, transcriptional initiation and elongation, mRNA export [127, 131-133] and gene silencing [46, 134].

1.3 The UPS and Ub in neurodegenerative disorders

Components of the UPS have been linked to several diseases of the nervous system, including neurodevelopmental and neurodegenerative diseases (Reviewed in [5, 32, 135]). In some cases, mutations in specific UPS genes have been linked to the etiology of the disease while in other events, impairment of the UPS seems to be a late event in the pathogenesis (Reviewed in [136]). It is believed that one of the first effects of perturbations in UPS-mediated proteolysis is synaptic malfunction that is followed later in disease progression by cell death and/or degeneration (Reviewed in [137]). Nevertheless, it is still poorly understood whether UPS impairment is a cause or a consequence of the disease - or both.

1.3.1 Ub deposition in protein aggregates

Misfolded or aberrant proteins are targeted for degradation through the UPS [138]. Failure to remove misfolded proteins may lead to their sequestration in aggregates, a shared hallmark of many neurodegenerative disorders, including PD, AD, HD and other polyQ disorders (Reviewed in [139-144]). These aggregates are immunoreactive for Ub and UPS-associated components [21, 136, 145]. However, the significance of these aggregates in the etiology of neurodegenerative disorders remains highly controversial. Several findings suggest that the visible aggregates do not fully correlate with neuronal death [146-149]. In contrast, several studies indicate that these Ub-rich aggregates contain the pathogenic protein (and in some cases the normal protein as well), UPS components, chaperones and transcription factors [150-155], which has been interpreted as evidence that sequestration of these key cellular proteins may lead to neuronal dysfunction and death. Additionally, a recent study showed a polyQ-induced global UPS impairment *in vivo* in an HD mouse model [156], while others exclude such an effect [157, 158]. Despite this discrepancy, the fact that mutations in UPS genes are linked to inherited neurological diseases supports the concept that UPS dysfunction might contribute to a wide range of nervous system diseases (Reviewed in [12, 159]).

1.3.2 The UPS in Parkinson's disease (PD)

PD is an age-related progressive neurodegenerative disorder affecting, among others, dopaminergic neurons of the *substantia nigra* (SN).

The first evidence implicating a role for the UPS in PD came from the finding of diseasecausing mutations in the E3 ligase parkin, which is now known to be involved in proteasomal degradation of several important neuronal substrates, including α -synuclein and synaptotagmin XI [160-164]. Ubiquitylated α -synuclein was shown to accumulate contributing to the formation of Lewy-like inclusions, providing more evidence for a role of the UPS in PD [165].

A link between proteasome dysfunction and PD has also been demonstrated in a mouse model using conditional depletion of the 26S proteasome through inactivation of a 19S proteasome subunit, Psmc1. Upon 26S proteasome depletion, these mice displayed neurodegeneration and Lewy-like inclusions containing Ub and α -synuclein in neurons of nigrostriatal pathway and forebrain, similar to the ones found in the brains of human PD patients [165, 166].

Consistent with a role for the UPS in PD, other components of this pathway also seem to play a role in PD pathology. For example, a missense mutation (I93M) in the UCHL1 was found in a pair of German siblings with inherited PD. Notably, this mutation markedly reduces UCHL1 DUB activity *in vitro* [52]. Mutations in the 26S ATPase of the regulatory subunit of the proteasome (PSMD4/RPN10) have also been described as increasing the risk for PD [166]. Furthermore, *in vitro* analyses of SN extracts from PD brains revealed a marked decrease in the activity of the 20S proteasome and in the levels of proteasomal core subunits [167, 168].

1.3.3 The UPS in Alzheimer's disease (AD)

AD is the most common neurodegenerative disorder, clinically characterized by progressive loss of memory and other cognitive skills, resulting in severe dementia. In the brain, the pathological include the presence of both intracellular neurofibrillary tangles containing signs hyperphosphorylated microtubule associated protein (MAPT) and extracellular amyloid- β plaques (Reviewed in [169]). The fact that these protein aggregates are ubiquitylated, strongly suggest that a malfunctioning or overloaded UPS may contribute for AD pathology [170-172]. In addition, several studies have implicated the UPS and proteolytic defects in AD. An ubiquitin mutant (UBB⁺¹) was identified as a potent inhibitor of the proteasome in AD brains, and shown to accumulate and colocalize with the amyloid plaques and neurofibrillary tangles [171]. Interestingly, ubiquitylation of UBB⁺¹ was shown to be mediated by the ubiquitin-conjugating enzyme, E2-25K/HIP-2, found to be critical for AB toxicity in AD animal models [173]. Additionally, *in vitro* experiments showed that AB could bind and inhibit the proteasome, thus blocking degradation of ubiquitylated substrates [174, 175]. The neuronally expressed DUB enzyme UCHL1 (linked to PD, as described above) was shown to have a highly reduced activity in AD brains due to its increased oxidation [176]. Also, both expression of the 26S protease regulatory subunit 6B (PSMC4, RTP3) [177] as well as the

proteasome function were shown to be reduced in several brain regions of AD patients (reviewed in [178]).

1.3.4 The UPS in Huntington's disease (HD)

HD is one of the nine polyQ disorders known to date, which is caused by an expansion in the CAG repeat in the huntingtin (*Htt*) gene. The polyQ tract renders a mutant protein prone to aggregate, causing cellular toxicity [179-181]. The neuropathological changes in HD lead to a progressive cognitive decline ending in severe dementia, motor dysfunction and psychiatric disturbances, namely depression and psychosis [182]. Various studies suggested that the UPS is involved in the processing of mutant Htt, since intranuclear aggregates containing the mutant protein are positively stained for Ub and proteasome subunits in cell cultures, HD transgenic mouse models and human HD brains [152, 183, 184]. When present in the nucleus, Htt is degraded by the UPS [185]. However, experiments with purified 26S proteasomes showed that proteasomes may be unable to degrade the protein bearing a polyQ expansion. Thus, long polyQ sequences have been proposed to cause the clogging of the proteasome impairing UPS function [186].

Indeed, several studies in cell models and in patient's material have reported an impairment of the UPS and its components in HD. For example, a change in the activity of the 20S proteasome was shown in HD patient's brains, causing an increase in the half-life of a polyubiquitylated reporter [187]. Furthermore, co-expression of mutant Htt with proteasomal subunits in cells revealed irreversible recruitment of proteasomes into HD aggregates [188]. Also, global proteasome impairment was reported when mutant aggregates were present both in the nucleus and in the cytoplasm of HEK293 cells [189].

Interestingly, experiments using a model for polyQ disorders showed that the E2-25K/HIP-2 enzyme increases aggregation of polyQ proteins, in addition to its role in mediating the toxicity of A β and UBB¹⁺ [190]. This suggests that the impairment of the UPS may be a common mechanism among several neurodegenerative disorders, irrespective of the toxic protein species.

However, there are also contradictory reports regarding the relevance of the proteasome impairment for HD pathogenesis. For example, a recent study suggested that toxic forms of Htt do not impair proteasome function [191]. Also, no global impairment of UPS activities was found in an HD mouse model characterized by Mangiarini et al [184, 192]. These apparently opposing results may be in part explained by the discrepancy between results obtained from cell and mouse models [193, 194]. However, more recently, Ortega and collaborators proposed a possible explanation that

reconciles the data from cell models supporting the polyQ-induced UPS impairment with the contradictory findings of no impairment in mouse models – their results demonstrate that mutant Htt can indeed impair UPS function *in vivo* but that this is only a transient event due to the protective effect on mutant Htt aggregation [157].

1.3.5 The UPS in Ataxias

Ataxia is a neurological symptom present in a group of disorders, generally caused by degeneration of neurons in the cerebellum, brain stem and spinocerebellar tracts, which is related with the patients' loss of control of body movements. Several inherited ataxias are caused by an abnormal polyQ expansion within a variety of mutant proteins (Reviewed in [195]). As in HD, expanded polyQ bearing proteins tend to aggregate and form intranuclear inclusions. These inclusions contain several cellular components, including Ub and subunits of the proteasome, therefore suggesting a relationship between spinopontocerebellar neurodegeneration and the UPS [153-155]. In addition, some disease-causing proteins such as ataxin 1, 3 and 7, are known to be ubiquitylated and targeted for proteasomal degradation [196-198]. Several evidence suggest that the misfolding of the polyQ proteins might lead to difficulties in the recognition and degradation process by the proteasome, resulting in impaired clearance of mutant proteins (Reviewed in [199]).

Besides the proteasome, other components of the UPS have been implicated in the development of ataxia. For example, the loss of DUB activity of the Ups14 enzyme, that regulates important cellular processes such as inhibition of proteasome and protein turnover [200], causes ataxia in a mouse model, which is associated with synaptic transmission defects [201].

1.3.6 Connection between UPS and neurodegeneration through autophagy

Autophagy is a lysosomal-dependent degradation pathway that can be divided into macroautophagy (bulk degradation of the cytosol), chaperone-mediated autophagy (CMA) and mitophagy (selective degradation of mitochondria) (Reviewed in [202]). Protein aggregates that cannot be transported to and degraded by the proteasome are usually degraded by autophagy [203]. Therefore, it has been proposed that autophagy could serve as an alternative degradation pathway when the proteasome capacity is insufficient or its function is impaired (Reviewed in [204]). Clearance by autophagy has been shown for several disease proteins such as tau [205], α -synuclein

[206] and a range of polyQ expanded proteins [37, 205, 207, 208]. Interestingly, Wild type proteins show a much lower dependence on autophagy for their clearance, compared with their mutant counterparts, and can be rapidly degraded by the proteasome [206, 209].

Nevertheless, recent findings showing that impairment of the proteasome also impairs autophagy and vice versa, suggested an interdependence of UPS and autophagy [39]. Indeed, it is known that ubiquitylation, mainly through K63 polyUb chains, can lead to autophagic degradation of the ubiquitylated targets [210]. In addition, several Ubl proteins, such as Atg5, 7, 8 and 12, are critical for autophagy; it was shown that mice lacking either Atg5 and Atg7 in the central nervous system (CNS) presented ubiquitylated aggregates, which were associated with neurodegeneration and motor deficits [211]. Also, mutations in proteasome subunits caused neurodegeneration in a *Drosophila* model, which was rescued by overexpression of the histone deacetylase 6 (HDAC6) in an autophagy-dependent manner [212]. Defects in autophagy have been linked to the pathology of several neurodegenerative diseases, such as AD, PD and HD (Reviewed in [213, 214]). It is believed that an abnormal autophagic activity leads to accumulation of intracellular protein aggregates in axons, dendrites and/or synapses, affecting the intercellular communication of selective neuronal populations [215].

Opposing results, however, suggest that proteasome inactivation induces autophagy [204, 216-218]. For example, Ding and co-workers showed that proteasome inhibition activates autophagy and, conversely, blockage of autophagy leads to the formation of polyubiquitylated aggregates [218]. Also, proteasome inactivation induced autophagy via the hypoxia signaling in *Drosophila* [216]. These results suggest that a compensatory autophagy may be induced when the proteasome fails to efficiently remove aggregate-prone proteins. However, the fact that several substrates of autophagy and UPS overlap (Reviewed in [204, 217, 219]), may potentially explain why in some cases impairment of one of these pathways leads to impairment of the other.

1.3.7 The UPS as a therapeutic target

As described above, it is now widely accepted that the UPS contributes for the pathology of several neurodegenerative disorders. Therefore, targeting the proteasome or UPP components has emerged as an attractive therapeutic approach for these disorders (Reviewed in [17, 220-222]).

One of the most appealing targets for therapeutic intervention is the proteasome itself. Since abnormal protein aggregates and inhibition of the proteasome are common features of neurodegenerative diseases, enhancement of proteasome activity might be an efficient way to

remove aggregates that accumulate in the brain (Reviewed in [223]). This may be achieved by employing the following strategies: i) increasing proteasome activity by promoting assembly of 19S and 20S complex of proteasome [224], ii) overexpressing the β 5, the proteasome maturation protein (POMP) [225] or the arsenite-inducible RNA-associated protein (AIRAP) [226], all resulting in enhanced proteasome activity, iii) stimulating proteasome activity using natural and/or synthetic activators such as olive oil, fatty acids and SDS [227-229], iv) enhancing ubiquitylation of a substrate using proteolysis targeting chimera molecules (PROTACS), molecules comprising a ligand for the target protein, a linker moiety, and a ligand for an E3 Ub ligase [230], v) promoting SUMOylation of proteins implicated in neurodegenerative disorders such as tau, α -synuclein and huntingtin [231], vi) facilitating substrate proteasomal degradation through overexpression or modulation of heat shock proteins [232-234].

Besides the proteasome, other UPS components are now been envisaged as "druggable" targets to treat neurodegenerative diseases. As substrate specificity is mainly determined by E3s, they have been proposed as the best potential therapeutic targets [5, 32]. Therefore, modification of the active site of E3s either to increase or to decrease the affinity towards specific substrates, could be one strategy to selectively control the accumulation of ubiquitylated proteins [223]. However, interfering with E3s is not easy to devise due to the lack of knowledge about their mechanisms of catalysis (Reviewed in [235]). DUBs have also been attractive molecular targets for the development of therapeutic approaches. Perhaps the best example of the use of DUBs for therapy is USP14. Lee and colleagues showed that specific inhibition of the USP14 E3 ligase might improve clearance of misfolded proteins in neurodegenerative diseases [200]. However, one shall be mindful of the potential side effects from inhibiting/activating this DUB's activity. Indeed, it was shown that mutations or silencing of several DUBs in mice, including USP14, negatively impacted on the entire organism or on specific organ systems. Also, KD of most DUBs in a *Drosophila* model had negative physiological consequences during development and in adult animals [236].

1.4 Machado-Joseph disease

In the early 1990's, converging lines of investigation identified a new type of mutation: the dynamic expansion of a trinucleotide repeat sequence within the coding region of a given gene, translated into a repetitive aminoacid sequence in the corresponding protein. Among them, the polyQ diseases, caused by CAG repeat expansions are the most common. To date, ten polyQ diseases have been characterized: Kennedy's disease or spinobulbar muscular atrophy (SMBA)

[237], spinocerebellar ataxias (SCA) type 1 [238], 2, 3 [68], 6 [239], 7 [240], and 17 [241, 242], dentatorubral-pallidoluysan atrophy (DRPLA) [243, 244], HD and Huntington disease-like 2 (HDL2) [245]. These group of diseases share several features that suggest a common toxic mechanism, not yet fully understood: i) the CAG expansion is translated into an abnormally long tract of glutamines, ii) there is a negative correlation between the age of onset and the number of CAG repeats, i.e., the age of onset of symptoms decrease with increased polyQ length [241, 246-248], iii) the CAG repeats present an intergenerational instability, with a tendency for disease to worsen in successive generations (anticipation) [246, 249], iv) formation of protein aggregates or inclusion bodies in the nucleus and/or cytoplasm of neuronal cells [241].

Machado-Joseph disease (MJD), also known as spinocerebellar ataxia type 3 (SCA3), is now known to exist worldwide [250], representing the most common dominantly inherited ataxia (Reviewed in [250-252]) and the second most common polyQ disease [253]. Despite the increasing number of therapeutic strategies assessed in mouse models of polyQ diseases (around 250 preclinical therapeutic trials have already been described [254]), there are no effective treatments for these disorders, including MJD, and current therapeutic approaches are only able to provide limited symptomatic relief (Reviewed in [255]).

1.4.1 Clinical and pathological features

The core clinical feature in MJD is a slowly progressive ataxia, being the average age at onset 40 years and the mean survival time of 21 years (Reviewed in [256]). Numerous other clinical symptoms, including weight loss, dystonia, dysarthria, spasticity, rigidity, fasciculations, postural instability, proprioceptive loss, visual, speech and sleep disorders, dysphagia, amyotrophy, corticospinal and autonomic nervous system dysfunctions and neuopathy, are also frequently observed in MJD patients [257-261].

Neuropathologically, MJD is characterized by neuronal loss in the cerebellum, substantia nigra, striatum, thalamus, pontine nuclei, spinal cord and cranial nerves, precerebelar brainstem, cholinergic and dopaminergic midbrain, as well as visual, auditory, vestibular, somatosensory, and ingestion and urination-related systems. Retained integrity of the cortical and subcortical regions of the limbic system and mild degeneration of cerebral and cerebellar cortexes, white matter of cerebellum, inferior olive and Purkinje cells, are also characteristic of MJD [248, 258, 260, 262-266]. Magnetic resonance imaging (MRI) and neuroimaging studies have revealed an enlargement

of the fourth ventricule, atrophy of the pons, cerebellar vermis and hemispheres, basal ganglia, midbrain and medulla oblongata [267-271]. Regarding brain functionality, magnetic spectroscopy analysis has shown decreased metabolism in the cerebellum, brainstem, cerebral cortex, thalamus and putamen, suggestive of axonal dysfunction, at symptomatic ages [257, 259, 272-274].

1.4.2 MJD genetics

The MJD causative gene – ATXN3 gene – was mapped to the long arm of chromosome 14 (14q32.1) [68]. The gene spans 48 kb and contains 13 exons (two of them recently described), with the (CAG), tract located at exon 10 [275, 276]. In the healthy population, the number of CAG repeats ranges from 12 to 44 CAG, while expanded alleles usually comprise from 61 to 87 repeat units (Reviewed in [277, 278]). Four different *ATXN3* transcripts of approximately 1.4, 1.8, 4.5 and 7.5 kb were described to be ubiquitously expressed in neuronal and non-neuronal human tissues [276, 279]. These different mRNA species may result from differential splicing of exons 2, 10 and 11 of *ATXN3* gene, and alternative polyadenylation of exon 10 [68, 276, 280]. A recent study proposed the existence of 50 potential new splice variants of *ATXN3* gene, generated by different types of splicing events (exon skipping, new exons and usage of alternative 5' or 3' splice sites) [275]. This suggests that alternative splicing may be an important mechanism regulating *ATXN3* expression. Additionally, the existence of *ATXN3* transcripts carrying different 3' untranslated regions (UTRs), suggest another potential level of regulation of *ATXN3* expression [276], which remains unexplored.

1.4.3 Therapeutic approaches

To date, no effective treatment for MJD and other polyQ diseases have been developed. However, some symptoms of disease can be treated using pharmacological approaches. Importantly, efforts have been made to generate animal models of the disease that will facilitate the understanding of MJD pathogenic mechanisms and subsequent therapeutic testing (Reviewed in [281]).

Silencing of ATXN3 gene

Because the detailed pathogenic mechanism remains unclear in MJD, silencing strategies targeting the causative gene have shown to be the most promising. Indeed, Boy and collaborators showed that switching off the expression of the pathogenic protein reverted the disease phenotype (including motor deficits, inclusion formation and neuronal degeneration) in a conditional mouse

model of MJD [282]. Silencing of *ATXW3* gene by RNA interference (RNAi) in a non-allele-specific manner has also been shown to mitigate degeneration in a rat model of MJD, indicating that silencing of Wild type ATXN3 together with the mutant protein appears not to be deleterious [283, 284]. In fact, *Atxn3* knockout mice do not show any signs of neurodegeneration [285]. Accordingly, Rodríguez-Lebrón and colleagues also showed that short term silencing of mutant ATXN3 in the cerebellum of an MJD mouse model, using RNAi sequences targeting 3'UTR of ATXN3, cleared abnormal nuclear accumulation of the disease protein [286]. However, and unexpectally, chronic RNAi treatment did not improve survival or motor function in treated transgenic mice. One possible explanation is that the RNAi-mediated suppression of Atxn3 expression was relatively low (roughly 50%) and confined to the cerebellum, and the delivery of the virus occurred in lower extents to other CNS regions also affected in disease. The failure of the treatment to improve the motor dysfunction of the MJD mice suggests that the phenotype is not solely due to cerebellar dysfunction, as it likely happens in MJD patients. This illustrates the need of silencing strategies enabling broader delivery approaches, in order to target different brain regions/nuclei affected in the disease context.

Other types of molecules targeting RNA, such as peptide nucleic acids (PNAs) and locked nucleic acids (LNAs) have also been shown to be effective in silencing *ATXN3* in fibroblasts from MJD patients [287], supporting the idea that this strategy may constitute a potential route to MJD therapy.

However, a major problem of ataxin-3 silencing may be the lack of knowledge about its function, specially in neurons. It is still unclear to what extent ataxin-3 is an essential protein for normal cellular function. Although studies using knockout (KO) animal models suggest that depletion of ataxin-3 is not detrimental [285, 288], we cannot exclude the existence of compensatory mechanisms masking the effects of the absence of the protein in these models. Of note, ataxin-3 contains several highly evolutionarily conserved domains [289], which may indicate that the protein is not completely dispensable. Also, silencing of ataxin-3 in non-neuronal cultured cells [70, 290] resulted in cytoskeletal disruption, loss of cell adhesion, increased ubiquitylation and increased cell death, further suggesting that prolonged full knockdown of the normal protein could be harmful. Therefore, understanding the exact physiological(s) role(s) of ataxin-3 is of relevance for the development of efficient and safe therapeutic strategies.

An alternative oligonucleotide therapy proposes the removal of the polyQ tract from the ATXN3 protein by exon skipping, maintaining the expression levels and the main functional domains and Ub binding capacity of the protein [291]. However, it is still necessary to assess whether the resulting modified ataxin-3 protein is not toxic and to evaluate whether its localization and function are not affected. Furthermore, future studies are required to evaluate whether polyQ skipping ameliorates the phenotype of MJD animal models.

Prevention of aggregation

As previously described, ATXN3 protein aggregates are a hallmark of MJD, and probably play a central role in the disease mechanism. Therefore, preventing aggregation may have therapeutic potential. The finding that heat shock proteins (HSPs) co-localize with aggregates of mutant ataxin-3 [292-294], suggested that these chaperones act (or attempt to act) in promoting the correct refolding of the pathogenic proteins in order to reduce the formation of toxic aggregated forms. Therefore, it has been proposed that the use of compounds that induce expression of HSPs, might have a beneficial effect in the clearance of the mutant protein (Reviewed in [295, 296]). Indeed, increased activity of molecular chaperones such as heat shock protein 70 (HSP70) and heat shock protein 40 (HSP40) was shown to reduce both aggregation and toxicity of expanded polyQ tracts in cell and mouse models, resulting in improved phenotypes [297, 298]. It was proposed that these molecular chaperones increase the solubility of expanded polyQ tracts and subsequently, the degradation of the protein by the proteasome [299-302]. Pharmacologic inactivation of the heat shock protein 90 (HSP90) triggers overexpression of several molecular chaperones, activating the heat shock response (HSR), through the persistence of the heat shock factor 1 (HSF-1) action [303, 304] and thus was thought to be a promising therapeutic strategy, warnessing the cell's protective potential. Indeed, HSP90 inhibitors (such as 17-AAG and 17-DMAG) have been shown to reduce aggregate load and toxicity in cell, fly, nematode and mouse models of several neurodegenerative diseases, including Huntington and MJD [305-310]. For example, it was shown that exposure of ataxin-3 mutant C. elegans or mice expressing mutant ATXN3 to 17-DMAG improved the motility defects of these transgenic animals when compared to untreated controls [308, 311].

Activation of autophagy

Enhancing degradation of ATXN3 by stimulating cellular degradative systems that regulate its turnover may be an alternative therapeutic strategy for MJD. Indeed, pharmacological induction of autophagy using tensirolimus (a rapamycin analogue already used in patients for treatment of renal cell carcinoma) resulted in increased degradation of mutant ATXN3, a reduction in the number of aggregates, and improved the motor phenotype (with some limitations) in a mouse model of MJD [312]. Additionally, overexpression of the autophagic protein beclin-1 was shown to increase clearance of the mutant protein and to prevented neurodegeneration in a rat model of localized ATXN3 over-expression [313].

Other studies showed that treatment of *Drosophila*, *C. elegans* and mouse models of MJD with inhibitors of HSP90 decreased mutant ATXN3 aggregation and improved motor phenotype in MJD transgenic *C. elegans* and mouse models [308, 311, 314]. Although these compounds were expected to act by inducing chaperone expression and thus promoting refolding of the mutant protein, as described above, it has also been shown that these compounds are able to activate autophagy in different model systems [315-317].

Finally, lithium chloride was also shown to have therapeutic potential in a *Drosophila* MJD model through upregulation of autophagy [318]. While this was not confirmed in a mouse model of MJD [319], a recent phase II/III clinical trial with this compound, although not effective considering its major endpoint, showed a significant reduction in the progression of gait ataxia severity [320].

Proteolytic cleavage inhibition

Proteolytic cleavage of ATXN3 may also be relevant for polyQ-expanded ATXN3 toxicity. There is indeed evidence supporting the proteolysis of ATXN3 in mammalian cells, transgenic animals and MJD brain tissue [321-324], and it has been proposed that this event is required for inclusion formation, because truncated ATXN3 is detected in neuronal inclusions in human brain [321, 325]. In line with this, inhibition of ATXN3 proteolysis, by mutating its putative cleavage sites, was shown to reduce toxicity in a *Drosophila* model of MJD [326, 327]. Also, inhibition of the calpains showed a good potential in reducing mutant ATXN3 toxicity in several cellular and animal models [324, 328-330].

Antioxidants

There is some evidence that impairment in the cellular defense mechanism against oxidative stress could play a role in MJD pathogenesis [331, 332]. Yu and colleagues showed that certain antioxidant enzymes such as glutathione reductase, catalase and superoxide dismutase (SOD) exhibit decreased activity in a mutant MJD cell line as compared to Wild type cells [331].

Therefore, antioxidants might have a beneficial effect for neuronal dysfunction and neurodegeneration in MJD. Although antioxidants have been demonstrated to have beneficial effects for other polyQ diseases such as HD [333-338], nothing is known about their effects in MJD. Furthermore, creatine, a bioenergetic supplier for the cell, was also demonstrated to have antioxidant properties, which could have beneficial effects in these diseases [339-341]. Indeed, food supplementation with creatine was shown to improve muscle strength and motor coordination deficits in a MJD mouse model (Duarte-Silva, S. et al, *in preparation*).

1.4.4 MJD protein: Ataxin-3 (ATXN3)

Ataxin-3 (ATXN3) is an evolutionarily conserved protein, with orthologs in a wide range of eukaryotic organisms, from protozoans to vertebrates [279, 288, 342, 343]. Wild type human ATXN3 has a molecular weight of 42 kDa, the size slightly varying according to the length of the polymorphic glutamine tract. Despite the localized neuronal degeneration observed in MJD patients, ATXN3 is ubiquitously expressed among different body tissues and cell types, being widely expressed throughout the brain [20, 276, 325, 342, 344]. Also in terms of subcellular localization, ATXN3 is ubiquitously found and is able to translocate from the cytoplasm to the nucleus and viceversa [20, 153, 325, 344-346]. This ability was shown to be associated with the existence of a nuclear localization signal (NLS) and 6 potential nuclear export signals (NES) in the ATXN3 protein sequence [289, 346-348]. Furthermore, the first 27 amino acids of ATXN3 were shown to have a role in the regulation of ATXN3 nuclear localization [345]. Nuclear localization was also shown to be modulated by phosphorylation events. These phosphorylation sites were shown to be targets for the serine-threonine kinase 2 (CK2) and for the glycogen synthase kinase 3β (GSK 3β) [349, 350]. While likely important for pathogenesis [351], the biological relevance of this regulated subcellular distribution of ATXN3 remains to be clarified.

Structure and domains

ATXN3 belongs to the family of cysteine proteases. Structurally, it is essentially composed by a structured globular N-terminal – the catalytic Josephin domain (JD) – followed by a flexible Cterminal tail that contains 2 or 3 ubiquitin interacting motifs (UIMs) and the polyQ tract [280, 289, 352-355] (Figure 4). Comparative analysis of the JD showed that ATXN3 belongs to the papain-like cysteine protease family and contains two binding sites for Ub [355-357]. The Ub protease activity resides in the catalytic pocket, which comprises that catalytic triad, C14, H119 and N134, strictly conserved among different classes of DUBs (Figure 4). The Q9 residue was also shown to be important for the catalytic activity of ATXN3 [355, 357]. Biochemical evidence confirmed that the DUB activity of this protein requires the active site cysteine 14 (Reviewed in [198, 354, 358]). The UIMs may help to recruit and position the polyubiquitylated substrates relative to the catalytic site, determining ATXN3 preference for specific topologies of polyUb chains and allowing for a sequential editing [357, 359]. However, despite this important role in the regulation of the type of chains that can be cleaved by ATXN3, UIMs seem to be dispensable for its activation [360]. Although several potential ATXN3 isoforms might be translated, only two have been studied in detail; both of these isoforms contain the polyQ tract and UIMs 1 and 2, but only one contains UIM3. The 3 UIMs protein was proposed to be the predominant isoform in the brain [325, 344, 361]. However, some important limitations may have affected this conclusion: the 2UIM ataxin-3 isoform is a less stable protein than the 3UIM ataxin-3 and is subjected to rapid proteasomal degradation, ii) the 2UIM ataxin-3 is more prone to aggregate than the 3 UIM protein, and iii) the YACs used for the generation of the mouse model possesses a slightly longer 2 UIM isoform with a predicted molecular weight very closed to the molecular weight of the 3 UIM ataxin-3. Therefore, further analyses are needed to conclude about the relative abundance of ATXN3 isoforms in the brain.



Figure 4. Domain architecture, structure and post-translational modifications of ataxin-3. (A) ATXN3 is mainly composed by a N-terminal catalytic domain, the Josephin domain with DUB activity, followed by a C-terminal tail containing 2 or 3 UIMs and a polyQ sequence of variable length. Five serine residues present in the UIMs (S236, S259, S260/S261, S340 and S352) have been identified as phosphorylation sites and an ubiquitylatable lysine residue was mapped to aminoacid 117 in the JD. One functional NLS and two NES are also present in the JD. Adapted from [362]. (B) Solution structure of the JD (PBD code: 1YZB). The active site amino acid (Q9, C14, H119 and N134) localize in a cleft formed by the globular catalytic and the helical hairpin subdomains of the JD. Reproduced from [362].

1.4.4.1 Function, biological function and molecular partners

Deubiquitylating (DUB) activity and regulation of protein degradation: involvement in the UPS

As for most DUBS, the precise physiological role of ATXN3 remains undetermined. However, multiple lines of evidence implicate ATXN3 in the UPS, playing a role in the cellular protein quality control. Supporting this idea, it is now widely accepted that ATXN3 has DUB activity *in vitro* mediated by the JD, being able to bind and cleave both K48 and K63-linked chains, in a UIM-dependent manner [198, 354, 359, 363-365]. Curiously, Winborn and colleagues found that ATXN3 preferentially cleaves K63-linked chains and chains of mixed K48 and K63 linkage, suggesting that it may function as a regulator of polyubiquitin chains with complex topology [359]. Additionally, ATXN3 also interacts with polyubiquitylated proteins and subunits of the proteasome [198, 354, 363, 366], with the ubiquitin-like protein NEDD8 [367], with proteins known to be involved in the shuttling of substrates for proteasomal degradation, such as VCP/p97, Ubiquilin/PLIC1 and Rad23 homologues [363, 368-372], and with UBXN-5, an adaptor of substrate binding of VCP/p97 [373]. ATXN3 was also shown to bind polyUb chains in neuronal cells in a UIM-dependent manner [364].

Although when assessed using artificial substrates such as polyUb chains, Ub aldehyde and Ub-AMC, the DUB activity of ATXN3 *in vitro* appears to be very low, it was possible to determine that it has a preference for chains of no less than 4 Ub moieties, which notably corresponds to the smallest Ub stretch involved in the targeting of proteins for proteasomal degradation [285, 353, 354, 357, 359]. In addition to facilitating protein degradation through the UPS, it has been proposed that ATXN3 partially deubiquitylates targeted proteins, preventing their degradation by binding through the UIMs. Indeed, it was shown that ATXN3 is able to block proteasome-dependent degradation of an artificial substrate *in vitro*, by editing K48-linked polyUb chains [374]. The low proteolytic activity of ATXN3 *in vitro* may be explained by the absence of an endogenous substrates and other external factor(s) that may be required for optimal proteolysis such as co-factors or activating molecular partners [375, 376]. In agreement with this idea, Reyes-Turcu and collaborators propose that as many DUBs, ATXN3 might require association with proper substrate(s) to acquire an optimal catalytsis-competent conformation.

Studies using *Atxn3* KO mice provided the first *in vivo* (albeit indirect) evidence that ATXN3 may function as a DUB: these mice had increased levels of total ubiquitylated proteins, suggesting that ATXN3 may regulate the (de)ubiquitylation of target proteins [285, 288]. More recently, it was

also shown that the worm and mouse ATXN3 orthologues are involved in the turnover of a model substrate *in vitro* [288, 370].

The fact that mouse and nematode KOs for ATXN3 do not show an overt phenotype (other than a temperature sensitive movement impairment and an altered stress response in the worm [373, 377]) suggested the existence of redundancy among DUBS and/or compensatory mechanism in these organisms [70, 285, 288]. In contrast, the absence of ATXN3 in cell lines did lead to relevant cellular phenotypes, as described below, maybe because less compensation mechanisms take place.

Transcriptional regulation

Besides its role in protein degradation, ATXN3 has been involved in transcriptional regulation. The binding of ATXN3 to DNA together with *in vitro* and *in situ* molecular interaction studies, support a function of ATXN3 as a transcription regulator, through diverse mechanisms [378]. ATXN3 is known to interact with numerous transcriptional regulators (both activators and repressors): TATA box binding protein (TBP) associated factor 4 (TAF4) [379], cAMP response element-binding protein binding protein (CBP) [155, 378, 380], p300, p300/CBP associated factor (PCAF) [378], nuclear receptor co-repressor (NCoR1), HDAC 3 and 6 [374, 381], and forkhead box 0 (FOXO) transcription factor FOXO4 [382]. Moreover, through its interaction with HDAC3 and NCoR1, ATXN3 has been shown to decrease histone acetylation and consequent transcription, by inhibition of p300-mediated histone acetylation [378, 381].

Interestingly, it has been proposed that the UPS may also be associated with transcriptional regulation. It has been hypothesized that ATXN3, through its DUB activity, may interfere with the turnover or the activation of transcription machinery components with which it interacts. Additionally, the structure of chromatin, which in turn regulates transcription, is also modulated by ubiquitylation [381].

Aggresome formation, cytoskeleton organization and myogenesis

Another circumstance where ATXN3 has been associated with protein quality control systems is its proposed role in aggresome formation. Aggresomes are aggregates of misfolded/toxic proteins, found near the microtubule-organizing center (MTOC), when the UPS is compromised or overwhelmed. This protective process is dependent on microtubule-based transport [374]. Thus, the fact that ATXN3 interacts with dynein, HDAC6, PLIC1, microtubules, tubulin, and microtubule-

associated protein 2 (MAP2), further supports the involvement of ATXN3 in aggresome formation. In agreement, ATXN3 was shown to co-localize with aggresomes and preaggresomes [290, 372, 374, 383]. Indeed, a recent study showed that ATXN3 promotes the recruitment of a mutant version of superoxide dismutase 1 (SOD1, involved in ALS) to the aggresome, a process that was found to be dependent on the DUB activity of ATXN3 [384].

Besides its involvement in aggresome formation, ATXN3 has also been shown to be important for the organization of the cytoskeleton itself. Absence of ATXN3 was shown to cause disorganization of cytoskeleton components (microtubules, filaments and intermediate filaments), loss of cell adhesion and morphological alterations in different cell types (namely HeLa and C2C12 cell lines) [70, 290]. ATXN3 was also shown to be critical for the initial myoblast differentiation steps in C2C12 cells, for organization of the cytoskeleton of myoblasts, and for regulation of the levels of integrin subunits [70], which are key participants in muscle differentiation (Reviewed in [385]). ATXN3 was shown to interact with the alpha-5 subunit of integrin (ITGA5) and to repress its degradation, with impact on myogenesis.

Heat shock and oxidative stress response

Several studies have proposed that ATXN3 may participate in the cellular stress response. It was shown that heat shock and oxidative stress increase the nuclear localization of ATXN3, most likely by regulating expression of genes that encode components of the cellular stress response [386]. Indeed, another study showed that upon oxidative stress, ATXN3 is translocated to the nucleus together with its molecular partner FOXO4, activating the transcription of manganese superoxide dismutase (SOD2), which in turn protects cells from oxidative damage [382]. Additionally, Reina and colleagues found that ATXN3 KO fibroblasts were more sensitive to heat stress than controls [386].

Interestingly, *C. elegans atx-3* KOs display a temperature-dependent phenotype: when subjected to a noxious heat shock stimulus, ATXN-3 mutants have an exarcebated stress response and survive significantly better than Wild type animals, as a result of activation of DAF-16 pathway and a consequent overexpression of molecular chaperones [377]. These results support the involvement of ATXN3 in stress response, in this case a negative regulatory role [373].

Role in longevity

Recent work provided the first indications for a role of ataxin-3 in the regulation of longevity. Through a synergistic interaction with the AAA ATPase valosin-containing protein (VCP/p97), ataxin-3 was shown to be important in longevity, as double KOs in *C. elegans* have a longer lifespan than Wild type (WT) worms. Additionally, ataxin-3 also seems to regulate the ubiquitylation and degradation of components of the insulin/insulin-like growth factor 1 (IGF1) signaling pathway implicated in lifespan regulation, further suggesting a role for ataxin-3 in longevity [370]. Interestingly, the IGF1 pathway has been proposed as a link between aging, proteotoxicity and neurodegenerative diseases [387-389], as is a strong modifier of MJD pathogenesis [308].

Regulation of E3s function

Typically, DUBs oppose E3's activity by mediating the removal of Ub from target proteins. However, and because they are often regulated by monoubiquitylation, DUBs can also modulate the activity of these enzymes. ATXN3 was demonstrated to deubiquitylate the Hsc70 interacting protein (CHIP), which in turn enhances the overall DUB activity of ATXN3 [390]. ATXN3 is recruited to the ubiquitylation complex by monoubiquitylated CHIP, where it limits the length of polyUb chains of substrates and terminates the ubiquitylation cycle by removing monoUb from CHIP [391]. The fact that changes in ATXN3 levels do not affect CHIP levels, makes it likely that ATXN3 regulates the E3 ligase activity of CHIP rather than its degradation.

ATXN3 also interacts with Parkin, the Parkinson Disease-associated E3. Through this interaction, ATXN3 regulates the ability of Parkin to ubiquitylate itself [392, 393] but does not affect its stability [69]. It is possible that ATXN3 controls the levels and edits the architecture of Ub chains linked to Parkin, thus targeting this protein for specific cellular pathways or affecting its activation state [69].

Neuroprotection

ATXN3 has also been proposed to act as a neuroprotectant. Studies conducted in *Drosophila* showed that overexpression of ATXN3 alleviated neurodegeneration caused by several polyQ disease proteins, including ATXN3 itself, huntingtin and ataxin-1 [394]. Also, Tsou and collaborators recently demonstrated that catalytically active ATXN3 protects against polyQ-dependent degeneration in flies. This neuroprotective process seems to be dependent on ATXN3 ubiquitylation [395]. Of notice, Drosophila does not possess an orthologue of ATXN3. This may explain the contradictory evidence, showing that ATXN3 does not serve as a neuroprotectant in other species.

Hubener and colleagues showed that co-expression of normal ATXN3 with the pathogenic version did not have a beneficial effect in a mouse model of MJD [396]. Also, overexpression of Wild type ATXN3 did not protect against MJD pathology in a rat model of MJD [284] nor in a *C. elegans* model of the disease [397].

DNA repair

A role for ATXN3 in DNA repair has also been suggested. Wang and collaborators found that ATXN3 interacts binds to important participants of the DNA repair pathway, the two human homologues of the yeast DNA repair protein RAD23, HHR23A and HHR23B [371].

1.4.4.2 Regulation of Ataxin-3 DUB activity

Due to its critical cellular function, DUBs are precisely regulated through diverse mechanisms. The cellular localization of ATXN3 is one of the mechanisms that might be influencing its function [376]. On the other hand, regulation of ATXN3 localization seems to be determined by post-translational modifications (PTMs) (Figure 4). Additionally, PTMs can enhance ATXN3 activity, as *in vitro* experiments reported low activity of ATXN3 in the absence of PTMS [355, 375].

Another factor influencing ATXN3 DUB activity is its interaction with other proteins (scaffolds or adaptors), important for DUB activation and the correct placement of substrate molecules relative to the catalytic site, thus compensating for the possible low affinity with certain substrates [376]. PTMs may also be important in regulating these interactions and thus, interfering with ATXN3 DUB activity.

Todi and co-workers demonstrated that ATXN3 monoubiquitylation increases its DUB activity [360]. Indeed, ubiquitylation of the residue K117 of the JD was sufficient to enhance ATXN3 DUB activity both *in vitro* and in cells [390] (Figure 4).

Several E3 ligases and proteasome shuttle proteins were reported to be involved in ATXN3 proteasome-mediated degradation, such as E4B/VCP, HIP/HSP70, E6-AP/HSP70 and Gp78 [398-401]. Direct binding to the 19S proteasome also seems to control ATXN3 degradation [402]. More recently, it was shown that this ubiquitination-independent degradation of ATXN3 is also regulated by protein interactions with the proteasome-associated proteins Rad23A/B, through an ubiquitin-binding site 2 (UbS2) located in the N terminal domain of ATXN3 [403]. However, it remains unclear whether other protein quality control pathways may also be involved in the regulation of ATXN3 turnover. Interestingly, ATXN3 turnover may also be regulated by its own DUB activity [404].

Bibliography

- 1. Hershko, A. and A. Ciechanover, *The ubiquitin system.* Annu Rev Biochem, 1998. **67**: p. 425-79.
- 2. von Mikecz, A., The nuclear ubiquitin-proteasome system. J Cell Sci, 2006. 119(Pt 10): p. 1977-84.
- 3. Navon, A. and A. Ciechanover, *The 26 S proteasome: from basic mechanisms to drug targeting.* J Biol Chem, 2009. **284**(49): p. 33713-8.
- 4. Kawabe, H. and N. Brose, *The role of ubiquitylation in nerve cell development.* Nat Rev Neurosci, 2011. **12**(5): p. 251-68.
- 5. Baptista, M.S., C.B. Duarte, and P. Maciel, *Role of the ubiquitin-proteasome system in nervous system function and disease: using C. elegans as a dissecting tool.* Cell Mol Life Sci, 2012. **69**(16): p. 2691-715.
- 6. Hartmann-Petersen, R., M. Seeger, and C. Gordon, *Transferring substrates to the 26S proteasome.* Trends Biochem Sci, 2003. **28**(1): p. 26-31.
- 7. Lecker, S.H., A.L. Goldberg, and W.E. Mitch, *Protein degradation by the ubiquitin-proteasome pathway in normal and disease states.* J Am Soc Nephrol, 2006. **17**(7): p. 1807-19.
- Lipford, J.R., et al., *A putative stimulatory role for activator turnover in gene expression*. Nature, 2005. 438(7064): p. 113-6.
- 9. Jensen, T.J., et al., *Multiple proteolytic systems, including the proteasome, contribute to CFTR processing.* Cell, 1995. **83**(1): p. 129-35.
- Ward, C.L., S. Omura, and R.R. Kopito, *Degradation of CFTR by the ubiquitin-proteasome pathway.* Cell, 1995.
 83(1): p. 121-7.
- 11. Hicke, L. and R. Dunn, *Regulation of membrane protein transport by ubiquitin and ubiquitin-binding proteins.* Annu Rev Cell Dev Biol, 2003. **19**: p. 141-72.
- 12. Dennissen, F.J., N. Kholod, and F.W. van Leeuwen, *The ubiquitin proteasome system in neurodegenerative diseases: culprit, accomplice or victim?* Prog Neurobiol, 2012. **96**(2): p. 190-207.
- 13. Paul, S., *Dysfunction of the ubiquitin-proteasome system in multiple disease conditions: therapeutic approaches.* Bioessays, 2008. **30**(11-12): p. 1172-84.
- 14. Shen, M., et al., *Targeting the ubiquitin-proteasome system for cancer therapy.* Expert Opin Ther Targets, 2013. **17**(9): p. 1091-108.
- 15. Lim, K.H. and K.H. Baek, *Deubiquitinating enzymes as therapeutic targets in cancer.* Current Pharmaceutical Design, 2013. **19**(22): p. 4039-52.
- 16. Dantuma, N.P. and L.C. Bott, *The ubiquitin-proteasome system in neurodegenerative diseases: precipitating factor, yet part of the solution.* Front Mol Neurosci, 2014. **7**: p. 70.
- 17. Hol, E.M., et al., *Ubiquitin proteasome system as a pharmacological target in neurodegeneration.* Expert Rev Neurother, 2006. **6**(9): p. 1337-47.
- 18. Ying, Z., H. Wang, and G. Wang, *The ubiquitin proteasome system as a potential target for the treatment of neurodegenerative diseases.* Current Pharmaceutical Design, 2013. **19**(18): p. 3305-14.
- 19. Lennox, G., et al., *Ubiquitin is a component of neurofibrillary tangles in a variety of neurodegenerative diseases.* Neurosci Lett, 1988. **94**(1-2): p. 211-7.
- 20. Paulson, H.L., et al., *Machado-Joseph disease gene product is a cytoplasmic protein widely expressed in brain.* Ann Neurol, 1997. **41**(4): p. 453-62.
- 21. Lowe, J., et al., *Ubiquitin is a common factor in intermediate filament inclusion bodies of diverse type in man, including those of Parkinson's disease, Pick's disease, and Alzheimer's disease, as well as Rosenthal fibres in cerebellar astrocytomas, cytoplasmic bodies in muscle, and mallory bodies in alcoholic liver disease.* J Pathol, 1988. **155**(1): p. 9-15.
- 22. Mori, H., J. Kondo, and Y. Ihara, *Ubiquitin is a component of paired helical filaments in Alzheimer's disease.* Science, 1987. **235**(4796): p. 1641-4.
- Glickman, M.H. and A. Ciechanover, *The ubiquitin-proteasome proteolytic pathway: destruction for the sake of construction.* Physiol Rev, 2002. 82(2): p. 373-428.
- 24. Pickart, C.M. and D. Fushman, *Polyubiquitin chains: polymeric protein signals.* Curr Opin Chem Biol, 2004. **8**(6): p. 610-6.
- 25. Haglund, K. and I. Dikic, Ubiquitylation and cell signaling. EMBO J, 2005. 24(19): p. 3353-9.
- 26. Kim, I. and H. Rao, *What's Ub chain linkage got to do with it?* Sci STKE, 2006. **2006**(330): p. pe18.
- 27. Woelk, T., et al., *The ubiquitination code: a signalling problem.* Cell Div, 2007. **2**: p. 11.
- 28. Ye, Y. and M. Rape, *Building ubiquitin chains: E2 enzymes at work.* Nat Rev Mol Cell Biol, 2009. **10**(11): p. 755-64.

- 29. Kao, W.H., et al., *Human papillomavirus type 16 E6 induces self-ubiquitination of the E6AP ubiquitin-protein ligase.* J Virol, 2000. **74**(14): p. 6408-17.
- 30. de Bie, P., D. Zaaroor-Regev, and A. Ciechanover, *Regulation of the Polycomb protein RING1B ubiquitination by USP7.* Biochem Biophys Res Commun, 2010. **400**(3): p. 389-95.
- 31. Nathan, J.A., et al., *The ubiquitin E3 ligase MARCH7 is differentially regulated by the deubiquitylating enzymes USP7 and USP9X.* Traffic, 2008. **9**(7): p. 1130-45.
- 32. Hegde, A.N. and S.C. Upadhya, *Role of ubiquitin-proteasome-mediated proteolysis in nervous system disease.* Biochim Biophys Acta, 2011. **1809**(2): p. 128-40.
- Gao, T., et al., UUCD: a family-based database of ubiquitin and ubiquitin-like conjugation. Nucleic Acids Res, 2013. 41(Database issue): p. D445-51.
- 34. Nagy, V. and I. Dikic, *Ubiquitin ligase complexes: from substrate selectivity to conjugational specificity.* Biol Chem, 2010. **391**(2-3): p. 163-9.
- 35. Koegl, M., et al., *A novel ubiquitination factor, E4, is involved in multiubiquitin chain assembly.* Cell, 1999. **96**(5): p. 635-44.
- Hoppe, T., *Multiubiquitylation by E4 enzymes: 'one size' doesn't fit all.* Trends Biochem Sci, 2005. **30**(4): p. 183-7.
- 37. Ravikumar, B., R. Duden, and D.C. Rubinsztein, *Aggregate-prone proteins with polyglutamine and polyalanine expansions are degraded by autophagy.* Hum Mol Genet, 2002. **11**(9): p. 1107-17.
- 38. Qin, Z.H., et al., *Autophagy regulates the processing of amino terminal huntingtin fragments.* Hum Mol Genet, 2003. **12**(24): p. 3231-44.
- 39. Dammer, E.B., et al., *Polyubiquitin linkage profiles in three models of proteolytic stress suggest the etiology of Alzheimer disease*. J Biol Chem, 2011. **286**(12): p. 10457-65.
- 40. Bonnet, J., et al., *Zinc-finger UBPs: regulators of deubiquitylation.* Trends Biochem Sci, 2008. **33**(8): p. 369-75.
- 41. Nicassio, F., et al., *Human USP3 is a chromatin modifier required for S phase progression and genome stability.* Curr Biol, 2007. **17**(22): p. 1972-7.
- 42. Pai, M.T., et al., *Solution structure of the Ubp-M BUZ domain, a highly specific protein module that recognizes the C-terminal tail of free ubiquitin.* J Mol Biol, 2007. **370**(2): p. 290-302.
- 43. Reyes-Turcu, F.E., et al., *The ubiquitin binding domain ZnF UBP recognizes the C-terminal diglycine motif of unanchored ubiquitin.* Cell, 2006. **124**(6): p. 1197-208.
- 44. Cohn, M.A., et al., *A UAF1-containing multisubunit protein complex regulates the Fanconi anemia pathway.* Mol Cell, 2007. **28**(5): p. 786-97.
- 45. Huang, T.T., et al., *Regulation of monoubiquitinated PCNA by DUB autocleavage.* Nat Cell Biol, 2006. **8**(4): p. 339-47.
- 46. Lee, K.Y., et al., *Human ELG1 regulates the level of ubiquitinated proliferating cell nuclear antigen (PCNA) through Its interactions with PCNA and USP1.* J Biol Chem, 2010. **285**(14): p. 10362-9.
- 47. Nijman, S.M., et al., *The deubiquitinating enzyme USP1 regulates the Fanconi anemia pathway.* Mol Cell, 2005. **17**(3): p. 331-9.
- 48. Williams, S.A., et al., *USP1 deubiquitinates ID proteins to preserve a mesenchymal stem cell program in osteosarcoma.* Cell, 2011. **146**(6): p. 918-30.
- 49. Kon, N., et al., *Inactivation of HAUSP in vivo modulates p53 function.* Oncogene, 2010. **29**(9): p. 1270-9.
- 50. Amerik, A.Y. and M. Hochstrasser, *Mechanism and function of deubiquitinating enzymes.* Biochim Biophys Acta, 2004. **1695**(1-3): p. 189-207.
- 51. Misaghi, S., et al., *Structure of the ubiquitin hydrolase UCH-L3 complexed with a suicide substrate.* J Biol Chem, 2005. **280**(2): p. 1512-20.
- 52. Leroy, E., et al., *The ubiquitin pathway in Parkinson's disease.* Nature, 1998. **395**(6701): p. 451-2.
- 53. Wilkinson, K.D., S. Deshpande, and C.N. Larsen, *Comparisons of neuronal (PGP 9.5) and non-neuronal ubiquitin C-terminal hydrolases.* Biochem Soc Trans, 1992. **20**(3): p. 631-7.
- 54. Choi, J., et al., *Oxidative modifications and down-regulation of ubiquitin carboxyl-terminal hydrolase L1 associated with idiopathic Parkinson's and Alzheimer's diseases.* J Biol Chem, 2004. **279**(13): p. 13256-64.
- 55. Kim, H.J., et al., *Ubiquitin C-terminal hydrolase-L1 is a key regulator of tumor cell invasion and metastasis.* Oncogene, 2009. **28**(1): p. 117-27.
- 56. Hard, R.L., et al., *HDAC6 and Ubp-M BUZ domains recognize specific C-terminal sequences of proteins.* Biochemistry, 2010. **49**(50): p. 10737-46.
- 57. Ma, A. and B.A. Malynn, *A20: linking a complex regulator of ubiquitylation to immunity and human disease.* Nat Rev Immunol, 2012. **12**(11): p. 774-85.

- 58. Shembade, N. and E.W. Harhaj, *Regulation of NF-kappaB signaling by the A20 deubiquitinase.* Cell Mol Immunol, 2012. **9**(2): p. 123-30.
- 59. Juang, Y.C., et al., *OTUB1 co-opts Lys48-linked ubiquitin recognition to suppress E2 enzyme function.* Mol Cell, 2012. **45**(3): p. 384-97.
- 60. Sato, Y., et al., *Molecular basis of Lys-63-linked polyubiquitination inhibition by the interaction between human deubiquitinating enzyme OTUB1 and ubiquitin-conjugating enzyme UBC13.* J Biol Chem, 2012. **287**(31): p. 25860-8.
- 61. Wiener, R., et al., *The mechanism of OTUB1-mediated inhibition of ubiquitination.* Nature, 2012. **483**(7391): p. 618-22.
- 62. Clague, M.J. and S. Urbe, *Endocytosis: the DUB version.* Trends Cell Biol, 2006. 16(11): p. 551-9.
- 63. Finley, D., *Recognition and processing of ubiquitin-protein conjugates by the proteasome.* Annu Rev Biochem, 2009. **78**: p. 477-513.
- 64. Cooper, E.M., et al., *K63-specific deubiquitination by two JAMM/MPN+ complexes: BRISC-associated Brcc36 and proteasomal Poh1.* EMBO J, 2009. **28**(6): p. 621-31.
- 65. Sato, Y., et al., *Structural basis for specific cleavage of Lys 63-linked polyubiquitin chains.* Nature, 2008. **455**(7211): p. 358-62.
- 66. Yao, T. and R.E. Cohen, *A cryptic protease couples deubiquitination and degradation by the proteasome.* Nature, 2002. **419**(6905): p. 403-7.
- 67. Nijman, S.M., et al., *A genomic and functional inventory of deubiquitinating enzymes.* Cell, 2005. **123**(5): p. 773-86.
- 68. Kawaguchi, Y., et al., *CAG expansions in a novel gene for Machado-Joseph disease at chromosome 14q32.1.* Nat Genet, 1994. **8**(3): p. 221-8.
- 69. Durcan, T.M., et al., *The Machado-Joseph disease-associated mutant form of ataxin-3 regulates parkin ubiquitination and stability.* Hum Mol Genet, 2011. **20**(1): p. 141-54.
- 70. do Carmo Costa, M., et al., *Ataxin-3 plays a role in mouse myogenic differentiation through regulation of integrin subunit levels.* PLoS One, 2010. **5**(7): p. e11728.
- 71. Ventii, K.H. and K.D. Wilkinson, *Protein partners of deubiquitinating enzymes.* Biochem J, 2008. **414**(2): p. 161-75.
- 72. Hanna, J., et al., *Deubiquitinating enzyme Ubp6 functions noncatalytically to delay proteasomal degradation.* Cell, 2006. **127**(1): p. 99-111.
- 73. Walters, B.J., et al., *A catalytic independent function of the deubiquitinating enzyme USP14 regulates hippocampal short-term synaptic plasticity and vesicle number.* J Physiol, 2013.
- 74. Yi, J.J. and M.D. Ehlers, *Emerging roles for ubiquitin and protein degradation in neuronal function.* Pharmacol Rev, 2007. **59**(1): p. 14-39.
- 75. Welchman, R.L., C. Gordon, and R.J. Mayer, *Ubiquitin and ubiquitin-like proteins as multifunctional signals.* Nat Rev Mol Cell Biol, 2005. **6**(8): p. 599-609.
- 76. Lilienbaum, A., *Relationship between the proteasomal system and autophagy.* Int J Biochem Mol Biol, 2013. **4**(1): p. 1-26.
- 77. Hicke, L., H.L. Schubert, and C.P. Hill, *Ubiquitin-binding domains.* Nat Rev Mol Cell Biol, 2005. **6**(8): p. 610-21.
- 78. Hochstrasser, M., *There's the rub: a novel ubiquitin-like modification linked to cell cycle regulation.* Genes Dev, 1998. **12**(7): p. 901-7.
- 79. DiAntonio, A., et al., *Ubiquitination-dependent mechanisms regulate synaptic growth and function.* Nature, 2001. **412**(6845): p. 449-52.
- 80. Ding, M., et al., *Spatial regulation of an E3 ubiquitin ligase directs selective synapse elimination.* Science, 2007. **317**(5840): p. 947-51.
- 81. Chilton, J.K., *Molecular mechanisms of axon guidance.* Dev Biol, 2006. 292(1): p. 13-24.
- 82. Dickson, B.J., *Molecular mechanisms of axon guidance.* Science, 2002. **298**(5600): p. 1959-64.
- 83. Feng, L., et al., *Cullin 5 regulates Dab1 protein levels and neuron positioning during cortical development.* Genes Dev, 2007. **21**(21): p. 2717-30.
- 84. Simo, S., Y. Jossin, and J.A. Cooper, *Cullin 5 regulates cortical layering by modulating the speed and duration of Dab1-dependent neuronal migration.* J Neurosci, 2010. **30**(16): p. 5668-76.
- 85. Colledge, M., et al., *Ubiquitination regulates PSD-95 degradation and AMPA receptor surface expression.* Neuron, 2003. **40**(3): p. 595-607.
- 86. Burbea, M., et al., *Ubiquitin and AP180 regulate the abundance of GLR-1 glutamate receptors at postsynaptic elements in C. elegans.* Neuron, 2002. **35**(1): p. 107-20.

- 87. Yi, J.J. and M.D. Ehlers, *Emerging roles for ubiquitin and protein degradation in neuronal function.* Pharmacological Reviews, 2007. **59**(1): p. 14-39.
- 88. Fornace, A.J., Jr., et al., *Ubiquitin mRNA is a major stress-induced transcript in mammalian cells.* Nucleic Acids Res, 1989. **17**(3): p. 1215-30.
- 89. Bizzi, A., et al., *Axonal transport of two major components of the ubiquitin system: free ubiquitin and ubiquitin carboxyl-terminal hydrolase PGP 9.5.* Brain Res, 1991. **548**(1-2): p. 292-9.
- 90. Hallengren, J., P.C. Chen, and S.M. Wilson, *Neuronal ubiquitin homeostasis.* Cell Biochem Biophys, 2013. **67**(1): p. 67-73.
- 91. Chen, P.C., et al., *Ubiquitin homeostasis is critical for synaptic development and function.* J Neurosci, 2011. **31**(48): p. 17505-13.
- 92. Saiga, T., et al., *Fbxo45 forms a novel ubiquitin ligase complex and is required for neuronal development.* Mol Cell Biol, 2009. **29**(13): p. 3529-43.
- 93. D'Arca, D., et al., *Huwe1 ubiquitin ligase is essential to synchronize neuronal and glial differentiation in the developing cerebellum.* Proc Natl Acad Sci U S A, 2010. **107**(13): p. 5875-80.
- 94. Vadhvani, M., et al., *The centrosomal E3 ubiquitin ligase FBXO31-SCF regulates neuronal morphogenesis and migration.* PLoS One, 2013. **8**(2): p. e57530.
- 95. Hamilton, A.M. and K. Zito, *Breaking it down: the ubiquitin proteasome system in neuronal morphogenesis.* Neural Plast, 2013. **2013**: p. 196848.
- 96. Puram, S.V. and A. Bonni, *Novel functions for the anaphase-promoting complex in neurobiology.* Semin Cell Dev Biol, 2011. **22**(6): p. 586-94.
- 97. Ikeuchi, Y., et al., *A SnoN-Ccd1 pathway promotes axonal morphogenesis in the mammalian brain.* J Neurosci, 2009. **29**(13): p. 4312-21.
- 98. Lasorella, A., et al., *Degradation of Id2 by the anaphase-promoting complex couples cell cycle exit and axonal growth*. Nature, 2006. **442**(7101): p. 471-4.
- 99. Stegmuller, J., et al., *Cell-intrinsic regulation of axonal morphogenesis by the Cdh1-APC target SnoN.* Neuron, 2006. **50**(3): p. 389-400.
- 100. Wang, H.R., et al., *Regulation of cell polarity and protrusion formation by targeting RhoA for degradation.* Science, 2003. **302**(5651): p. 1775-9.
- 101. Cheng, P.L., et al., *Phosphorylation of E3 ligase Smurf1 switches its substrate preference in support of axon development.* Neuron, 2011. **69**(2): p. 231-43.
- 102. Schaefer, A.M., G.D. Hadwiger, and M.L. Nonet, *rpm-1, a conserved neuronal gene that regulates targeting and synaptogenesis in C. elegans.* Neuron, 2000. **26**(2): p. 345-56.
- 103. Zhen, M., et al., *Regulation of presynaptic terminal organization by C. elegans RPM-1, a putative guanine nucleotide exchanger with a RING-H2 finger domain.* Neuron, 2000. **26**(2): p. 331-43.
- 104. Bingol, B. and E.M. Schuman, *A proteasome-sensitive connection between PSD-95 and GluR1 endocytosis.* Neuropharmacology, 2004. **47**(5): p. 755-63.
- 105. Haas, K.F. and K. Broadie, *Roles of ubiquitination at the synapse.* Biochim Biophys Acta, 2008. **1779**(8): p. 495-506.
- 106. Hegde, A.N., *The ubiquitin-proteasome pathway and synaptic plasticity.* Learn Mem, 2010. **17**(7): p. 314-27.
- 107. Speese, S.D., et al., *The ubiquitin proteasome system acutely regulates presynaptic protein turnover and synaptic efficacy.* Curr Biol, 2003. **13**(11): p. 899-910.
- 108. Chin, L.S., J.P. Vavalle, and L. Li, *Staring, a novel E3 ubiquitin-protein ligase that targets syntaxin 1 for degradation.* J Biol Chem, 2002. **277**(38): p. 35071-9.
- 109. Yao, I., et al., *SCRAPPER-dependent ubiquitination of active zone protein RIM1 regulates synaptic vesicle release.* Cell, 2007. **130**(5): p. 943-57.
- Willeumier, K., S.M. Pulst, and F.E. Schweizer, *Proteasome inhibition triggers activity-dependent increase in the size of the recycling vesicle pool in cultured hippocampal neurons.* J Neurosci, 2006. **26**(44): p. 11333-41.
- 111. Waithe, D., et al., *Beta-subunits promote the expression of Ca(V)2.2 channels by reducing their proteasomal degradation.* J Biol Chem, 2011. **286**(11): p. 9598-611.
- 112. DiAntonio, A. and L. Hicke, *Ubiquitin-dependent regulation of the synapse.* Annu Rev Neurosci, 2004. **27**: p. 223-46.
- 113. Tai, H.C. and E.M. Schuman, *Ubiquitin, the proteasome and protein degradation in neuronal function and dysfunction.* Nat Rev Neurosci, 2008. **9**(11): p. 826-38.
- 114. Ding, M. and K. Shen, *The role of the ubiquitin proteasome system in synapse remodeling and neurodegenerative diseases.* Bioessays, 2008. **30**(11-12): p. 1075-83.

- 115. Saliba, R.S., et al., *Activity-dependent ubiquitination of GABA(A) receptors regulates their accumulation at synaptic sites.* J Neurosci, 2007. **27**(48): p. 13341-51.
- 116. Kato, A., et al., *Activity-dependent NMDA receptor degradation mediated by retrotranslocation and ubiquitination.* Proc Natl Acad Sci U S A, 2005. **102**(15): p. 5600-5.
- 117. Buttner, C., et al., *Ubiquitination precedes internalization and proteolytic cleavage of plasma membrane-bound glycine receptors.* J Biol Chem, 2001. **276**(46): p. 42978-85.
- 118. Ehlers, M.D., *Activity level controls postsynaptic composition and signaling via the ubiquitin-proteasome system.* Nat Neurosci, 2003. **6**(3): p. 231-42.
- 119. Park, E.C., D.R. Glodowski, and C. Rongo, *The ubiquitin ligase RPM-1 and the p38 MAPK PMK-3 regulate AMPA receptor trafficking.* PLoS One, 2009. **4**(1): p. e4284.
- Chen, Z.J. and L.J. Sun, *Nonproteolytic functions of ubiquitin in cell signaling.* Mol Cell, 2009. **33**(3): p. 275-86.
- 121. Bowers, K., et al., *Degradation of endocytosed epidermal growth factor and virally ubiquitinated major histocompatibility complex class I is independent of mammalian ESCRTII.* J Biol Chem, 2006. **281**(8): p. 5094-105.
- 122. McCullough, J., M.J. Clague, and S. Urbe, *AMSH is an endosome-associated ubiquitin isopeptidase.* J Cell Biol, 2004. **166**(4): p. 487-92.
- 123. Harhaj, E.W. and V.M. Dixit, *Deubiquitinases in the regulation of NF-kappaB signaling.* Cell Res, 2011. **21**(1): p. 22-39.
- 124. Mukai, A., et al., *Balanced ubiquitylation and deubiquitylation of Frizzled regulate cellular responsiveness to Wg/Wnt*. EMBO J, 2010. **29**(13): p. 2114-25.
- 125. Zhao, B., et al., *The ubiquitin specific protease 4 (USP4) is a new player in the Wnt signalling pathway.* J Cell Mol Med, 2009. **13**(8B): p. 1886-95.
- 126. Clague, M.J., J.M. Coulson, and S. Urbe, *Cellular functions of the DUBs.* J Cell Sci, 2012. **125**(Pt 2): p. 277-86.
- 127. Dai, M.S. and H. Lu, *Inhibition of MDM2-mediated p53 ubiquitination and degradation by ribosomal protein L5.* J Biol Chem, 2004. **279**(43): p. 44475-82.
- 128. Dornan, D., et al., *The ubiquitin ligase COP1 is a critical negative regulator of p53.* Nature, 2004. **429**(6987): p. 86-92.
- 129. Dornan, D., et al., *ATM engages autodegradation of the E3 ubiquitin ligase COP1 after DNA damage.* Science, 2006. **313**(5790): p. 1122-6.
- 130. Chen, D., et al., *ARF-BP1/Mule is a critical mediator of the ARF tumor suppressor.* Cell, 2005. **121**(7): p. 1071-83.
- 131. Dai, M.S., et al., *Ribosomal protein L23 activates p53 by inhibiting MDM2 function in response to ribosomal perturbation but not to translation inhibition.* Mol Cell Biol, 2004. **24**(17): p. 7654-68.
- 132. Fu, X., et al., *RFWD3-Mdm2 ubiquitin ligase complex positively regulates p53 stability in response to DNA damage.* Proc Natl Acad Sci U S A, 2010. **107**(10): p. 4579-84.
- Leng, R.P., et al., *Pirh2, a p53-induced ubiquitin-protein ligase, promotes p53 degradation.* Cell, 2003. 112(6): p. 779-91.
- 134. Weger, S., E. Hammer, and R. Heilbronn, *Topors acts as a SUMO-1 E3 ligase for p53 in vitro and in vivo.* FEBS Lett, 2005. **579**(22): p. 5007-12.
- 135. Ciechanover, A. and P. Brundin, *The ubiquitin proteasome system in neurodegenerative diseases: sometimes the chicken, sometimes the egg.* Neuron, 2003. **40**(2): p. 427-46.
- 136. Layfield, R., J.R. Cavey, and J. Lowe, *Role of ubiquitin-mediated proteolysis in the pathogenesis of neurodegenerative disorders.* Ageing Res Rev, 2003. **2**(4): p. 343-56.
- 137. Selkoe, D.J., *Alzheimer's disease is a synaptic failure.* Science, 2002. **298**(5594): p. 789-91.
- 138. Sherman, M.Y. and A.L. Goldberg, *Cellular defenses against unfolded proteins: a cell biologist thinks about neurodegenerative diseases.* Neuron, 2001. **29**(1): p. 15-32.
- 139. Dohm, C.P., P. Kermer, and M. Bahr, *Aggregopathy in neurodegenerative diseases: mechanisms and therapeutic implication.* Neurodegener Dis, 2008. **5**(6): p. 321-38.
- 140. Taylor, J.P., J. Hardy, and K.H. Fischbeck, *Toxic proteins in neurodegenerative disease.* Science, 2002. **296**(5575): p. 1991-5.
- 141. Fink, A.L., *The aggregation and fibrillation of alpha-synuclein.* Acc Chem Res, 2006. **39**(9): p. 628-34.
- 142. Bruijn, L.I., et al., *ALS-linked SOD1 mutant G85R mediates damage to astrocytes and promotes rapidly progressive disease with SOD1-containing inclusions.* Neuron, 1997. **18**(2): p. 327-38.
- 143. Chen, S., F.A. Ferrone, and R. Wetzel, *Huntington's disease age-of-onset linked to polyglutamine aggregation nucleation.* Proc Natl Acad Sci U S A, 2002. **99**(18): p. 11884-9.

- 144. Thorpe, J.R., et al., *Fine structural analysis of the neuronal inclusions of frontotemporal lobar degeneration with TDP-43 proteinopathy.* J Neural Transm, 2008. **115**(12): p. 1661-71.
- 145. Mayer, R.J., et al., *Intermediate filaments and ubiquitin: a new thread in the understanding of chronic neurodegenerative diseases.* Prog Clin Biol Res, 1989. **317**: p. 809-18.
- 146. Rub, U., et al., *Spinocerebellar ataxia type 3 (SCA3): thalamic neurodegeneration occurs independently from thalamic ataxin-3 immunopositive neuronal intranuclear inclusions.* Brain Pathol, 2006. **16**(3): p. 218-27.
- 147. Davies, S.W., et al., *Formation of neuronal intranuclear inclusions underlies the neurological dysfunction in mice transgenic for the HD mutation.* Cell, 1997. **90**(3): p. 537-48.
- 148. Klement, I.A., et al., *Ataxin-1 nuclear localization and aggregation: role in polyglutamine-induced disease in SCA1 transgenic mice.* Cell, 1998. **95**(1): p. 41-53.
- Reddy, P.H., et al., *Transgenic mice expressing mutated full-length HD cDNA: a paradigm for locomotor changes and selective neuronal loss in Huntington's disease.* Philos Trans R Soc Lond B Biol Sci, 1999.
 354(1386): p. 1035-45.
- 150. Perez, M.K., et al., *Recruitment and the role of nuclear localization in polyglutamine-mediated aggregation.* J Cell Biol, 1998. **143**(6): p. 1457-70.
- Chai, Y., et al., *Evidence for proteasome involvement in polyglutamine disease: localization to nuclear inclusions in SCA3/MJD and suppression of polyglutamine aggregation in vitro.* Hum Mol Genet, 1999. 8(4): p. 673-82.
- 152. Waelter, S., et al., *Accumulation of mutant huntingtin fragments in aggresome-like inclusion bodies as a result of insufficient protein degradation.* Mol Biol Cell, 2001. **12**(5): p. 1393-407.
- 153. Cummings, C.J., et al., *Chaperone suppression of aggregation and altered subcellular proteasome localization imply protein misfolding in SCA1.* Nat Genet, 1998. **19**(2): p. 148-54.
- 154. Schmidt, T., et al., *Protein surveillance machinery in brains with spinocerebellar ataxia type 3: redistribution and differential recruitment of 26S proteasome subunits and chaperones to neuronal intranuclear inclusions.* Ann Neurol, 2002. **51**(3): p. 302-10.
- 155. McCampbell, A., et al., *CREB-binding protein sequestration by expanded polyglutamine.* Hum Mol Genet, 2000. **9**(14): p. 2197-202.
- 156. Ortega, Z., et al., *Acute polyglutamine expression in inducible mouse model unravels ubiquitin/proteasome system impairment and permanent recovery attributable to aggregate formation.* J Neurosci, 2010. **30**(10): p. 3675-88.
- 157. Ortega, Z., et al., *Acute polyglutamine expression in inducible mouse model unravels ubiquitin/proteasome system impairment and permanent recovery attributable to aggregate formation.* Journal of Neuroscience, 2010. **30**(10): p. 3675-88.
- 158. Schipper-Krom, S., K. Juenemann, and E.A. Reits, *The Ubiquitin-Proteasome System in Huntington's Disease: Are Proteasomes Impaired, Initiators of Disease, or Coming to the Rescue?* Biochem Res Int, 2012. **2012**: p. 837015.
- Li, Q., J.A. Lee, and D.L. Black, *Neuronal regulation of alternative pre-mRNA splicing*. Nat Rev Neurosci, 2007.
 8(11): p. 819-31.
- 160. Imai, Y., M. Soda, and R. Takahashi, *Parkin suppresses unfolded protein stress-induced cell death through its E3 ubiquitin-protein ligase activity.* J Biol Chem, 2000. **275**(46): p. 35661-4.
- 161. Shimura, H., et al., *Familial Parkinson disease gene product, parkin, is a ubiquitin-protein ligase.* Nat Genet, 2000. **25**(3): p. 302-5.
- 162. Zhang, Y., et al., *Parkin functions as an E2-dependent ubiquitin- protein ligase and promotes the degradation of the synaptic vesicle-associated protein, CDCrel-1.* Proc Natl Acad Sci U S A, 2000. **97**(24): p. 13354-9.
- 163. Huynh, D.P., et al., *The autosomal recessive juvenile Parkinson disease gene product, parkin, interacts with and ubiquitinates synaptotagmin XI.* Hum Mol Genet, 2003. **12**(20): p. 2587-97.
- 164. Ebrahimi-Fakhari, D., et al., *Distinct roles in vivo for the ubiquitin-proteasome system and the autophagylysosomal pathway in the degradation of alpha-synuclein.* J Neurosci, 2011. **31**(41): p. 14508-20.
- 165. Bedford, L., et al., *Depletion of 26S proteasomes in mouse brain neurons causes neurodegeneration and Lewy-like inclusions resembling human pale bodies.* J Neurosci, 2008. **28**(33): p. 8189-98.
- 166. Wahl, C., et al., *A comprehensive genetic study of the proteasomal subunit S6 ATPase in German Parkinson's disease patients.* J Neural Transm, 2008. **115**(8): p. 1141-8.
- McNaught, K.S., et al., *Altered proteasomal function in sporadic Parkinson's disease.* Exp Neurol, 2003.
 179(1): p. 38-46.
- 168. Furukawa, Y., et al., *Brain proteasomal function in sporadic Parkinson's disease and related disorders.* Ann Neurol, 2002. **51**(6): p. 779-82.

- 169. Hardy, J. and D.J. Selkoe, *The amyloid hypothesis of Alzheimer's disease: progress and problems on the road to therapeutics.* Science, 2002. **297**(5580): p. 353-6.
- 170. Forman, M.S., et al., *Frontotemporal dementia: clinicopathological correlations.* Ann Neurol, 2006. **59**(6): p. 952-62.
- 171. van Leeuwen, F.W., et al., *Frameshift mutants of beta amyloid precursor protein and ubiquitin-B in Alzheimer's and Down patients.* Science, 1998. **279**(5348): p. 242-7.
- 172. Wang, L.N., et al., *[An analysis of the causes of dementia in 383 elderly autopsied cases].* Zhonghua Nei Ke Za Zhi, 2003. **42**(11): p. 789-92.
- 173. Ko, S., et al., *Structural basis of E2-25K/UBB+1 interaction leading to proteasome inhibition and neurotoxicity.* J Biol Chem, 2010. **285**(46): p. 36070-80.
- 174. Shringarpure, R., et al., 4-Hydroxynonenal-modified amyloid-beta peptide inhibits the proteasome: possible importance in Alzheimer's disease. Cell Mol Life Sci, 2000. **57**(12): p. 1802-9.
- 175. Gregori, L., et al., *Binding of amyloid beta protein to the 20 S proteasome.* J Biol Chem, 1997. **272**(1): p. 58-62.
- 176. Sultana, R., et al., *Redox proteomics identification of oxidized proteins in Alzheimer's disease hippocampus and cerebellum: an approach to understand pathological and biochemical alterations in AD.* Neurobiol Aging, 2006. **27**(11): p. 1564-76.
- 177. Zouambia, M., et al., *Proteasome subunit proteins and neuropathology in tauopathies and synucleinopathies: Consequences for proteomic analyses.* Proteomics, 2008. **8**(6): p. 1221-36.
- 178. Keller, J.N., K.B. Hanni, and W.R. Markesbery, *Impaired proteasome function in Alzheimer's disease.* J Neurochem, 2000. **75**(1): p. 436-9.
- 179. Ross, C.A. and M.A. Poirier, *Opinion: What is the role of protein aggregation in neurodegeneration?* Nat Rev Mol Cell Biol, 2005. **6**(11): p. 891-8.
- 180. Sanchez, I., C. Mahlke, and J. Yuan, *Pivotal role of oligomerization in expanded polyglutamine neurodegenerative disorders.* Nature, 2003. **421**(6921): p. 373-9.
- 181. Arrasate, M., et al., *Inclusion body formation reduces levels of mutant huntingtin and the risk of neuronal death.* Nature, 2004. **431**(7010): p. 805-10.
- 182. Walker, F.O., *Huntington's disease.* Lancet, 2007. **369**(9557): p. 218-28.
- DiFiglia, M., et al., Aggregation of huntingtin in neuronal intranuclear inclusions and dystrophic neurites in brain. Science, 1997. 277(5334): p. 1990-3.
- 184. Mangiarini, L., et al., *Exon 1 of the HD gene with an expanded CAG repeat is sufficient to cause a progressive neurological phenotype in transgenic mice.* Cell, 1996. **87**(3): p. 493-506.
- 185. Iwata, A., et al., *Intranuclear degradation of polyglutamine aggregates by the ubiquitin-proteasome system.* J Biol Chem, 2009. **284**(15): p. 9796-803.
- 186. Venkatraman, P., et al., *Eukaryotic proteasomes cannot digest polyglutamine sequences and release them during degradation of polyglutamine-containing proteins.* Mol Cell, 2004. **14**(1): p. 95-104.
- 187. Seo, H., K.C. Sonntag, and O. Isacson, *Generalized brain and skin proteasome inhibition in Huntington's disease.* Ann Neurol, 2004. **56**(3): p. 319-28.
- 188. Holmberg, C.I., et al., *Inefficient degradation of truncated polyglutamine proteins by the proteasome.* EMBO J, 2004. **23**(21): p. 4307-18.
- 189. Bennett, E.J., et al., *Global impairment of the ubiquitin-proteasome system by nuclear or cytoplasmic protein aggregates precedes inclusion body formation.* Mol Cell, 2005. **17**(3): p. 351-65.
- 190. de Pril, R., et al., *Ubiquitin-conjugating enzyme E2-25K increases aggregate formation and cell death in polyglutamine diseases.* Mol Cell Neurosci, 2007. **34**(1): p. 10-9.
- 191. Li, X., et al., *Inhibiting the ubiquitin-proteasome system leads to preferential accumulation of toxic N-terminal mutant huntingtin fragments.* Hum Mol Genet, 2010. **19**(12): p. 2445-55.
- 192. Maynard, C.J., et al., *Accumulation of ubiquitin conjugates in a polyglutamine disease model occurs without global ubiquitin/proteasome system impairment.* Proc Natl Acad Sci U S A, 2009. **106**(33): p. 13986-91.
- 193. Ortega, Z., M. Diaz-Hernandez, and J.J. Lucas, *Is the ubiquitin-proteasome system impaired in Huntington's disease?* Cellular and Molecular Life Sciences, 2007. **64**(17): p. 2245-57.
- 194. Davies, J.E., S. Sarkar, and D.C. Rubinsztein, *The ubiquitin proteasome system in Huntington's disease and the spinocerebellar ataxias.* BMC Biochem, 2007. **8 Suppl 1**: p. S2.
- 195. Orr, H.T., Cell biology of spinocerebellar ataxia. J Cell Biol, 2012. 197(2): p. 167-77.
- 196. Cummings, C.J., et al., *Mutation of the E6-AP ubiquitin ligase reduces nuclear inclusion frequency while accelerating polyglutamine-induced pathology in SCA1 mice.* Neuron, 1999. **24**(4): p. 879-92.
- 197. Matilla, A., et al., *Association of ataxin-7 with the proteasome subunit S4 of the 19S regulatory complex.* Hum Mol Genet, 2001. **10**(24): p. 2821-31.

- 198. Chai, Y., et al., *Poly-ubiquitin binding by the polyglutamine disease protein ataxin-3 links its normal function to protein surveillance pathways.* J Biol Chem, 2004. **279**(5): p. 3605-11.
- 199. Duenas, A.M., R. Goold, and P. Giunti, *Molecular pathogenesis of spinocerebellar ataxias.* Brain, 2006. **129**(Pt 6): p. 1357-70.
- 200. Lee, B.H., et al., *Enhancement of proteasome activity by a small-molecule inhibitor of USP14.* Nature, 2010. **467**(7312): p. 179-84.
- 201. Wilson, S.M., et al., *Synaptic defects in ataxia mice result from a mutation in Usp14, encoding a ubiquitinspecific protease.* Nat Genet, 2002. **32**(3): p. 420-5.
- 202. Martinez-Vicente, M. and A.M. Cuervo, *Autophagy and neurodegeneration: when the cleaning crew goes on strike.* Lancet Neurol, 2007. **6**(4): p. 352-61.
- 203. Ravikumar, B., et al., *Regulation of mammalian autophagy in physiology and pathophysiology.* Physiol Rev, 2010. **90**(4): p. 1383-435.
- 204. Korolchuk, V.I., F.M. Menzies, and D.C. Rubinsztein, *Mechanisms of cross-talk between the ubiquitin*proteasome and autophagy-lysosome systems. FEBS Lett, 2010. **584**(7): p. 1393-8.
- 205. Berger, Z., et al., *Rapamycin alleviates toxicity of different aggregate-prone proteins.* Hum Mol Genet, 2006. **15**(3): p. 433-42.
- 206. Webb, J.L., et al., *Alpha-Synuclein is degraded by both autophagy and the proteasome.* J Biol Chem, 2003. **278**(27): p. 25009-13.
- 207. Ravikumar, B., et al., *Inhibition of mTOR induces autophagy and reduces toxicity of polyglutamine expansions in fly and mouse models of Huntington disease.* Nat Genet, 2004. **36**(6): p. 585-95.
- 208. Montie, H.L., et al., *Cytoplasmic retention of polyglutamine-expanded androgen receptor ameliorates disease via autophagy in a mouse model of spinal and bulbar muscular atrophy.* Hum Mol Genet, 2009. **18**(11): p. 1937-50.
- 209. Sarkar, S., et al., *Trehalose, a novel mTOR-independent autophagy enhancer, accelerates the clearance of mutant huntingtin and alpha-synuclein.* J Biol Chem, 2007. **282**(8): p. 5641-52.
- 210. Kirkin, V., et al., *A role for ubiquitin in selective autophagy.* Mol Cell, 2009. **34**(3): p. 259-69.
- 211. Komatsu, M., et al., *Loss of autophagy in the central nervous system causes neurodegeneration in mice.* Nature, 2006. **441**(7095): p. 880-4.
- 212. Pandey, U.B., et al., *HDAC6 rescues neurodegeneration and provides an essential link between autophagy and the UPS.* Nature, 2007. **447**(7146): p. 859-63.
- 213. Cheung, Z.H. and N.Y. Ip, *Autophagy deregulation in neurodegenerative diseases recent advances and future perspectives.* J Neurochem, 2011. **118**(3): p. 317-25.
- 214. Lee, J.A., *Neuronal autophagy: a housekeeper or a fighter in neuronal cell survival?* Exp Neurobiol, 2012. **21**(1): p. 1-8.
- 215. Son, J.H., et al., Neuronal autophagy and neurodegenerative diseases. Exp Mol Med, 2012. 44(2): p. 89-98.
- 216. Low, P., et al., *Impaired proteasomal degradation enhances autophagy via hypoxia signaling in Drosophila.* BMC Cell Biol, 2013. **14**: p. 29.
- 217. Lamark, T. and T. Johansen, *Autophagy: links with the proteasome.* Curr Opin Cell Biol, 2010. 22(2): p. 1928.
- 218. Ding, W.X., et al., *Linking of autophagy to ubiquitin-proteasome system is important for the regulation of endoplasmic reticulum stress and cell viability.* Am J Pathol, 2007. **171**(2): p. 513-24.
- 219. Wong, E. and A.M. Cuervo, *Integration of clearance mechanisms: the proteasome and autophagy.* Cold Spring Harb Perspect Biol, 2010. **2**(12): p. a006734.
- Nalepa, G., M. Rolfe, and J.W. Harper, *Drug discovery in the ubiquitin-proteasome system*. Nat Rev Drug Discov, 2006. 5(7): p. 596-613.
- 221. Bedford, L., et al., *Ubiquitin-like protein conjugation and the ubiquitin-proteasome system as drug targets.* Nat Rev Drug Discov, 2011. **10**(1): p. 29-46.
- Edelmann, M.J., B. Nicholson, and B.M. Kessler, *Pharmacological targets in the ubiquitin system offer new ways of treating cancer, neurodegenerative disorders and infectious diseases.* Expert Rev Mol Med, 2011. 13: p. e35.
- 223. Upadhya, S.C. and A.N. Hegde, *Ubiquitin-proteasome pathway components as therapeutic targets for CNS maladies.* Curr Pharm Des, 2005. **11**(29): p. 3807-28.
- 224. Chondrogianni, N., et al., *Overexpression of proteasome beta5 assembled subunit increases the amount of proteasome and confers ameliorated response to oxidative stress and higher survival rates.* J Biol Chem, 2005. **280**(12): p. 11840-50.
- 225. Chondrogianni, N. and E.S. Gonos, *Overexpression of hUMP1/POMP proteasome accessory protein enhances proteasome-mediated antioxidant defence.* Exp Gerontol, 2007. **42**(9): p. 899-903.

- 226. Stanhill, A., et al., *An arsenite-inducible 19S regulatory particle-associated protein adapts proteasomes to proteotoxicity.* Mol Cell, 2006. **23**(6): p. 875-85.
- 227. Dahlmann, B., et al., *Activation of the multicatalytic proteinase from rat skeletal muscle by fatty acids or sodium dodecyl sulphate.* Biochem J, 1985. **228**(1): p. 171-7.
- 228. Watanabe, N. and S. Yamada, *Activation of 20S proteasomes from spinach leaves by fatty acids.* Plant Cell Physiol, 1996. **37**(2): p. 147-51.
- 229. Kisselev, A.F., D. Kaganovich, and A.L. Goldberg, *Binding of hydrophobic peptides to several non-catalytic sites* promotes peptide hydrolysis by all active sites of 20 S proteasomes. Evidence for peptide-induced channel opening in the alpha-rings. J Biol Chem, 2002. **277**(25): p. 22260-70.
- 230. Sakamoto, K.M., et al., *Protacs: chimeric molecules that target proteins to the Skp1-Cullin-F box complex for ubiquitination and degradation.* Proc Natl Acad Sci U S A, 2001. **98**(15): p. 8554-9.
- 231. Dorval, V. and P.E. Fraser, *SUMO on the road to neurodegeneration.* Biochim Biophys Acta, 2007. **1773**(6): p. 694-706.
- 232. Katsuno, M., et al., *Pharmacological induction of heat-shock proteins alleviates polyglutamine-mediated motor neuron disease.* Proc Natl Acad Sci U S A, 2005. **102**(46): p. 16801-6.
- Yasuda, H., et al., Neuroprotective effect of a heat shock protein inducer, geranylgeranylacetone in permanent focal cerebral ischemia. Brain Res, 2005. 1032(1-2): p. 176-82.
- 234. Herbst, M. and E.E. Wanker, *Small molecule inducers of heat-shock response reduce polyQ-mediated huntingtin aggregation. A possible therapeutic strategy.* Neurodegener Dis, 2007. **4**(2-3): p. 254-60.
- 235. Eldridge, A.G. and T. O'Brien, *Therapeutic strategies within the ubiquitin proteasome system.* Cell Death Differ, 2010. **17**(1): p. 4-13.
- 236. Tsou, W.L., et al., *Systematic analysis of the physiological importance of deubiquitinating enzymes.* PLoS One, 2012. **7**(8): p. e43112.
- 237. La Spada, A.R., et al., *Androgen receptor gene mutations in X-linked spinal and bulbar muscular atrophy.* Nature, 1991. **352**(6330): p. 77-9.
- 238. Orr, H.T., et al., *Expansion of an unstable trinucleotide CAG repeat in spinocerebellar ataxia type 1.* Nat Genet, 1993. **4**(3): p. 221-6.
- 239. Zhuchenko, O., et al., *Autosomal dominant cerebellar ataxia (SCA6) associated with small polyglutamine expansions in the alpha 1A-voltage-dependent calcium channel.* Nat Genet, 1997. **15**(1): p. 62-9.
- 240. David, G., et al., *Cloning of the SCA7 gene reveals a highly unstable CAG repeat expansion.* Nat Genet, 1997. **17**(1): p. 65-70.
- Zoghbi, H.Y. and H.T. Orr, *Glutamine repeats and neurodegeneration.* Annu Rev Neurosci, 2000. 23: p. 217-47.
- 242. Nakamura, K., et al., *SCA17, a novel autosomal dominant cerebellar ataxia caused by an expanded polyglutamine in TATA-binding protein.* Hum Mol Genet, 2001. **10**(14): p. 1441-8.
- 243. Li, S.H., et al., *Novel triplet repeat containing genes in human brain: cloning, expression, and length polymorphisms.* Genomics, 1993. **16**(3): p. 572-9.
- 244. Nagafuchi, S., et al., *Dentatorubral and pallidoluysian atrophy expansion of an unstable CAG trinucleotide on chromosome 12p.* Nat Genet, 1994. **6**(1): p. 14-8.
- 245. Holmes, S.E., et al., *A repeat expansion in the gene encoding junctophilin-3 is associated with Huntington disease-like 2.* Nat Genet, 2001. **29**(4): p. 377-8.
- 246. Maciel, P., et al., *Correlation between CAG repeat length and clinical features in Machado-Joseph disease.* Am J Hum Genet, 1995. **57**(1): p. 54-61.
- 247. Ranum, L.P., et al., *Spinocerebellar ataxia type 1 and Machado-Joseph disease: incidence of CAG expansions among adult-onset ataxia patients from 311 families with dominant, recessive, or sporadic ataxia.* Am J Hum Genet, 1995. **57**(3): p. 603-8.
- 248. Durr, A., et al., *Spinocerebellar ataxia 3 and Machado-Joseph disease: clinical, molecular, and neuropathological features.* Ann Neurol, 1996. **39**(4): p. 490-9.
- 249. Rubinsztein, D.C., et al., *Phenotypic characterization of individuals with 30-40 CAG repeats in the Huntington disease (HD) gene reveals HD cases with 36 repeats and apparently normal elderly individuals with 36-39 repeats.* Am J Hum Genet, 1996. **59**(1): p. 16-22.
- Paulson, H., *Machado-Joseph disease/spinocerebellar ataxia type 3.* Handb Clin Neurol, 2012. **103**: p. 437-49.
- 251. Bettencourt, C. and M. Lima, *Machado-Joseph Disease: from first descriptions to new perspectives.* Orphanet J Rare Dis, 2011. **6**: p. 35.
- 252. Matos, C.A., S. de Macedo-Ribeiro, and A.L. Carvalho, *Polyglutamine diseases: the special case of ataxin-3 and Machado-Joseph disease.* Prog Neurobiol, 2011. **95**(1): p. 26-48.

- Schols, L., et al., Autosomal dominant cerebellar ataxias: clinical features, genetics, and pathogenesis. Lancet Neurol, 2004. 3(5): p. 291-304.
- 254. Switonski, P.M., et al., *Mouse models of polyglutamine diseases in therapeutic approaches: review and data table. Part II.* Mol Neurobiol, 2012. **46**(2): p. 430-66.
- 255. Bauer, P.O. and N. Nukina, *The pathogenic mechanisms of polyglutamine diseases and current therapeutic strategies.* J Neurochem, 2009. **110**(6): p. 1737-65.
- 256. Coutinho, P. and J. Sequeiros, *[Clinical, genetic and pathological aspects of Machado-Joseph disease].* J Genet Hum, 1981. **29**(3): p. 203-9.
- 257. Riess, O., et al., *SCA3: neurological features, pathogenesis and animal models.* Cerebellum, 2008. **7**(2): p. 125-37.
- 258. Rosenberg, R.N., *Machado-Joseph disease: an autosomal dominant motor system degeneration.* Mov Disord, 1992. **7**(3): p. 193-203.
- 259. Soong, B., et al., *Machado-Joseph disease: clinical, molecular, and metabolic characterization in Chinese kindreds.* Ann Neurol, 1997. **41**(4): p. 446-52.
- 260. Sudarsky, L. and P. Coutinho, *Machado-Joseph disease*. Clin Neurosci, 1995. 3(1): p. 17-22.
- 261. Schols, L., et al., *Sleep disturbance in spinocerebellar ataxias: is the SCA3 mutation a cause of restless legs syndrome?* Neurology, 1998. **51**(6): p. 1603-7.
- 262. Alves, S., et al., *Striatal and nigral pathology in a lentiviral rat model of Machado-Joseph disease.* Hum Mol Genet, 2008. **17**(14): p. 2071-83.
- 263. Coutinho, P. and C. Andrade, *Autosomal dominant system degeneration in Portuguese families of the Azores Islands. A new genetic disorder involving cerebellar, pyramidal, extrapyramidal and spinal cord motor functions.* Neurology, 1978. **28**(7): p. 703-9.
- 264. Kanda, T., et al., *Type III Machado-Joseph disease in a Japanese family: a clinicopathological study with special reference to the peripheral nervous system.* Clin Neuropathol, 1989. **8**(3): p. 134-41.
- 265. Rub, U., E.R. Brunt, and T. Deller, *New insights into the pathoanatomy of spinocerebellar ataxia type 3 (Machado-Joseph disease).* Curr Opin Neurol, 2008. **21**(2): p. 111-6.
- 266. Shimizu, H., et al., *Involvement of Onuf's nucleus in Machado-Joseph disease: a morphometric and immunohistochemical study.* Acta Neuropathol, 2010. **120**(4): p. 439-48.
- 267. Etchebehere, E.C., et al., *Brain single-photon emission computed tomography and magnetic resonance imaging in Machado-Joseph disease.* Arch Neurol, 2001. **58**(8): p. 1257-63.
- Klockgether, T., et al., Autosomal dominant cerebellar ataxia type I. MRI-based volumetry of posterior fossa structures and basal ganglia in spinocerebellar ataxia types 1, 2 and 3. Brain, 1998. 121 (Pt 9): p. 1687-93.
- 269. Murata, Y., et al., *Characteristic magnetic resonance imaging findings in spinocerebellar ataxia 6.* Arch Neurol, 1998. **55**(10): p. 1348-52.
- Taniwaki, T., et al., *Positron emission tomography (PET) in Machado-Joseph disease.* J Neurol Sci, 1997.
 145(1): p. 63-7.
- 271. Yoshizawa, T., et al., *Magnetic resonance imaging demonstrates differential atrophy of pontine base and tegmentum in Machado-Joseph disease.* J Neurol Sci, 2003. **215**(1-2): p. 45-50.
- 272. Wullner, U., et al., *Dopamine transporter positron emission tomography in spinocerebellar ataxias type 1, 2, 3, and 6.* Arch Neurol, 2005. **62**(8): p. 1280-5.
- 273. D'Abreu, A., et al., *Axonal dysfunction in the deep white matter in Machado-Joseph disease.* J Neuroimaging, 2009. **19**(1): p. 9-12.
- 274. Soong, B.W. and R.S. Liu, *Positron emission tomography in asymptomatic gene carriers of Machado-Joseph disease.* J Neurol Neurosurg Psychiatry, 1998. **64**(4): p. 499-504.
- 275. Bettencourt, C., et al., *Increased transcript diversity: novel splicing variants of Machado-Joseph disease gene (ATXN3).* Neurogenetics, 2010. **11**(2): p. 193-202.
- 276. Ichikawa, Y., et al., *The genomic structure and expression of MJD, the Machado-Joseph disease gene.* J Hum Genet, 2001. **46**(7): p. 413-22.
- 277. Maciel, P., et al., *Improvement in the molecular diagnosis of Machado-Joseph disease.* Arch Neurol, 2001.
 58(11): p. 1821-7.
- 278. Cummings, C.J. and H.Y. Zoghbi, *Fourteen and counting: unraveling trinucleotide repeat diseases.* Hum Mol Genet, 2000. **9**(6): p. 909-16.
- 279. Schmitt, I., et al., *Characterization of the rat spinocerebellar ataxia type 3 gene.* Neurogenetics, 1997. **1**(2): p. 103-12.
- 280. Goto, J., et al., *Machado-Joseph disease gene products carrying different carboxyl termini.* Neurosci Res, 1997. **28**(4): p. 373-7.

- Costa Mdo, C. and H.L. Paulson, *Toward understanding Machado-Joseph disease*. Prog Neurobiol, 2012.
 97(2): p. 239-57.
- 282. Boy, J., et al., *Reversibility of symptoms in a conditional mouse model of spinocerebellar ataxia type 3.* Hum Mol Genet, 2009. **18**(22): p. 4282-95.
- Alves, S., et al., Allele-specific RNA silencing of mutant ataxin-3 mediates neuroprotection in a rat model of Machado-Joseph disease. PLoS One, 2008. 3(10): p. e3341.
- 284. Alves, S., et al., *Silencing ataxin-3 mitigates degeneration in a rat model of Machado-Joseph disease: no role for wild-type ataxin-3?* Hum Mol Genet, 2010. **19**(12): p. 2380-94.
- 285. Schmitt, I., et al., *Inactivation of the mouse Atxn3 (ataxin-3) gene increases protein ubiquitination.* Biochem Biophys Res Commun, 2007. **362**(3): p. 734-9.
- 286. Costa Mdo, C., et al., *Toward RNAi therapy for the polyglutamine disease Machado-Joseph disease.* Mol Ther, 2013. **21**(10): p. 1898-908.
- 287. Hu, J., et al., *Allele-specific silencing of mutant huntingtin and ataxin-3 genes by targeting expanded CAG repeats in mRNAs.* Nat Biotechnol, 2009. **27**(5): p. 478-84.
- 288. Rodrigues, A.J., et al., *Functional genomics and biochemical characterization of the C. elegans orthologue of the Machado-Joseph disease protein ataxin-3.* FASEB J, 2007. **21**(4): p. 1126-36.
- Albrecht, M., et al., *Structural and functional analysis of ataxin-2 and ataxin-3*. Eur J Biochem, 2004. **271**(15):
 p. 3155-70.
- 290. Rodrigues, A.J., et al., *Absence of ataxin-3 leads to cytoskeletal disorganization and increased cell death.* Biochim Biophys Acta, 2010. **1803**(10): p. 1154-63.
- 291. Evers, M.M., et al., *Ataxin-3 protein modification as a treatment strategy for spinocerebellar ataxia type 3: removal of the CAG containing exon.* Neurobiol Dis, 2013. **58**: p. 49-56.
- 292. Chai, Y., et al., *Analysis of the role of heat shock protein (Hsp) molecular chaperones in polyglutamine disease.* J Neurosci, 1999. **19**(23): p. 10338-47.
- 293. Williams, A.J., et al., *In vivo suppression of polyglutamine neurotoxicity by C-terminus of Hsp70-interacting protein (CHIP) supports an aggregation model of pathogenesis.* Neurobiol Dis, 2009. **33**(3): p. 342-53.
- 294. Yoshida, H., et al., *Chemical chaperones reduce aggregate formation and cell death caused by the truncated Machado-Joseph disease gene product with an expanded polyglutamine stretch.* Neurobiol Dis, 2002. **10**(2): p. 88-99.
- 295. Kaushik, S. and A.M. Cuervo, *Chaperones in autophagy.* Pharmacol Res, 2012. 66(6): p. 484-93.
- 296. Lamark, T. and T. Johansen, *Aggrephagy: selective disposal of protein aggregates by macroautophagy.* Int J Cell Biol, 2012. **2012**: p. 736905.
- 297. Adachi, H., et al., *Heat shock protein 70 chaperone overexpression ameliorates phenotypes of the spinal and bulbar muscular atrophy transgenic mouse model by reducing nuclear-localized mutant androgen receptor protein.* J Neurosci, 2003. **23**(6): p. 2203-11.
- 298. Cummings, C.J., et al., *Over-expression of inducible HSP70 chaperone suppresses neuropathology and improves motor function in SCA1 mice.* Hum Mol Genet, 2001. **10**(14): p. 1511-8.
- 299. Chan, H.Y., et al., *Mechanisms of chaperone suppression of polyglutamine disease: selectivity, synergy and modulation of protein solubility in Drosophila.* Hum Mol Genet, 2000. **9**(19): p. 2811-20.
- 300. Muchowski, P.J., et al., *Hsp70 and hsp40 chaperones can inhibit self-assembly of polyglutamine proteins into amyloid-like fibrils.* Proc Natl Acad Sci U S A, 2000. **97**(14): p. 7841-6.
- 301. Bailey, C.K., et al., *Molecular chaperones enhance the degradation of expanded polyglutamine repeat androgen receptor in a cellular model of spinal and bulbar muscular atrophy.* Hum Mol Genet, 2002. **11**(5): p. 515-23.
- 302. Verhoef, L.G., et al., *Aggregate formation inhibits proteasomal degradation of polyglutamine proteins.* Hum Mol Genet, 2002. **11**(22): p. 2689-700.
- 303. Zou, J., et al., Repression of heat shock transcription factor HSF1 activation by HSP90 (HSP90 complex) that forms a stress-sensitive complex with HSF1. Cell, 1998. 94(4): p. 471-80.
- 304. Kim, H.R., H.S. Kang, and H.D. Kim, *Geldanamycin induces heat shock protein expression through activation of HSF1 in K562 erythroleukemic cells.* IUBMB Life, 1999. **48**(4): p. 429-33.
- 305. Hay, D.G., et al., *Progressive decrease in chaperone protein levels in a mouse model of Huntington's disease and induction of stress proteins as a therapeutic approach.* Hum Mol Genet, 2004. **13**(13): p. 1389-405.
- 306. Sittler, A., et al., *Geldanamycin activates a heat shock response and inhibits huntingtin aggregation in a cell culture model of Huntington's disease.* Hum Mol Genet, 2001. **10**(12): p. 1307-15.
- 307. Auluck, P.K., M.C. Meulener, and N.M. Bonini, *Mechanisms of Suppression of {alpha}-Synuclein Neurotoxicity by Geldanamycin in Drosophila.* J Biol Chem, 2005. **280**(4): p. 2873-8.

- 308. Teixeira-Castro, A., et al., *Neuron-specific proteotoxicity of mutant ataxin-3 in C. elegans: rescue by the DAF-16 and HSF-1 pathways.* Hum Mol Genet, 2011. **20**(15): p. 2996-3009.
- 309. Waza, M., et al., *17-AAG, an Hsp90 inhibitor, ameliorates polyglutamine-mediated motor neuron degeneration.* Nat Med, 2005. **11**(10): p. 1088-95.
- 310. Tokui, K., et al., *17-DMAG ameliorates polyglutamine-mediated motor neuron degeneration through wellpreserved proteasome function in an SBMA model mouse.* Hum Mol Genet, 2009. **18**(5): p. 898-910.
- 311. Silva-Fernandes, A., et al., *Chronic Treatment with 17-DMAG Improves Balance and Coordination in A New Mouse Model of Machado-Joseph Disease.* Neurotherapeutics, 2014.
- 312. Menzies, F.M., et al., *Autophagy induction reduces mutant ataxin-3 levels and toxicity in a mouse model of spinocerebellar ataxia type 3.* Brain, 2010. **133**(Pt 1): p. 93-104.
- 313. Nascimento-Ferreira, I., et al., *Overexpression of the autophagic beclin-1 protein clears mutant ataxin-3 and alleviates Machado-Joseph disease*. Brain, 2011. **134**(Pt 5): p. 1400-15.
- 314. Fujikake, N., et al., *Heat shock transcription factor 1-activating compounds suppress polyglutamine-induced neurodegeneration through induction of multiple molecular chaperones.* J Biol Chem, 2008. **283**(38): p. 26188-97.
- 315. Riedel, M., et al., *17-AAG induces cytoplasmic alpha-synuclein aggregate clearance by induction of autophagy.* PLoS One, 2010. **5**(1): p. e8753.
- 316. Palacios, C., et al., *Autophagy inhibition sensitizes multiple myeloma cells to 17-dimethylaminoethylamino-17demethoxygeldanamycin-induced apoptosis.* Leuk Res, 2010. **34**(11): p. 1533-8.
- 317. Rusmini, P., et al., *17-AAG increases autophagic removal of mutant androgen receptor in spinal and bulbar muscular atrophy.* Neurobiol Dis, 2011. **41**(1): p. 83-95.
- 318. Jia, D.D., et al., *Lithium chloride alleviates neurodegeneration partly by inhibiting activity of GSK3beta in a SCA3 Drosophila model.* Cerebellum, 2013. **12**(6): p. 892-901.
- 319. Duarte-Silva, S., et al., *Lithium Chloride Therapy Fails to Improve Motor Function in a Transgenic Mouse Model of Machado-Joseph Disease.* Cerebellum, 2014.
- 320. Saute, J.A., et al., *A randomized, phase 2 clinical trial of lithium carbonate in Machado-Joseph disease.* Movement Disorders, 2014. **29**(4): p. 568-73.
- 321. Goti, D., et al., *A mutant ataxin-3 putative-cleavage fragment in brains of Machado-Joseph disease patients and transgenic mice is cytotoxic above a critical concentration.* J Neurosci, 2004. **24**(45): p. 10266-79.
- 322. Berke, S.J., et al., *Caspase-mediated proteolysis of the polyglutamine disease protein ataxin-3.* J Neurochem, 2004. **89**(4): p. 908-18.
- 323. Colomer Gould, V.F., et al., *A mutant ataxin-3 fragment results from processing at a site N-terminal to amino acid 190 in brain of Machado-Joseph disease-like transgenic mice.* Neurobiol Dis, 2007. **27**(3): p. 362-9.
- 324. Haacke, A., F.U. Hartl, and P. Breuer, *Calpain inhibition is sufficient to suppress aggregation of polyglutamineexpanded ataxin-3.* J Biol Chem, 2007. **282**(26): p. 18851-6.
- 325. Schmidt, T., et al., *An isoform of ataxin-3 accumulates in the nucleus of neuronal cells in affected brain regions of SCA3 patients.* Brain Pathol, 1998. **8**(4): p. 669-79.
- 326. Jung, J., et al., *Preventing Ataxin-3 protein cleavage mitigates degeneration in a Drosophila model of SCA3.* Hum Mol Genet, 2009. **18**(24): p. 4843-52.
- Tarlac, V. and E. Storey, *Role of proteolysis in polyglutamine disorders.* J Neurosci Res, 2003. **74**(3): p. 406-16.
- 328. Koch, P., et al., *Excitation-induced ataxin-3 aggregation in neurons from patients with Machado-Joseph disease.* Nature, 2011. **480**(7378): p. 543-6.
- 329. Hubener, J., et al., *Calpain-mediated ataxin-3 cleavage in the molecular pathogenesis of spinocerebellar ataxia type 3 (SCA3).* Hum Mol Genet, 2013. **22**(3): p. 508-18.
- 330. Simoes, A.T., et al., Calpastatin-mediated inhibition of calpains in the mouse brain prevents mutant ataxin 3 proteolysis, nuclear localization and aggregation, relieving Machado-Joseph disease. Brain, 2012. 135(Pt 8): p. 2428-39.
- 331. Yu, Y.C., et al., *Decreased antioxidant enzyme activity and increased mitochondrial DNA damage in cellular models of Machado-Joseph disease.* J Neurosci Res, 2009. **87**(8): p. 1884-91.
- Pacheco, L.S., et al., Association between Machado-Joseph disease and oxidative stress biomarkers. Mutat Res, 2013. 757(2): p. 99-103.
- 333. Dedeoglu, A., et al., *Creatine therapy provides neuroprotection after onset of clinical symptoms in Huntington's disease transgenic mice.* J Neurochem, 2003. **85**(6): p. 1359-67.
- 334. Beal, M.F., et al., *Coenzyme Q10 and nicotinamide block striatal lesions produced by the mitochondrial toxin malonate.* Ann Neurol, 1994. **36**(6): p. 882-8.

- 335. Jenkins, B.G., et al., *Non-invasive neurochemical analysis of focal excitotoxic lesions in models of neurodegenerative illness using spectroscopic imaging.* J Cereb Blood Flow Metab, 1996. **16**(3): p. 450-61.
- 336. Keene, C.D., et al., *Tauroursodeoxycholic acid, a bile acid, is neuroprotective in a transgenic animal model of Huntington's disease.* Proc Natl Acad Sci U S A, 2002. **99**(16): p. 10671-6.
- 337. Klivenyi, P., et al., *Increased survival and neuroprotective effects of BN82451 in a transgenic mouse model of Huntington's disease.* J Neurochem, 2003. **86**(1): p. 267-72.
- 338. Fontaine, M.A., et al., Effect of exogenous and endogenous antioxidants on 3-nitropionic acid-induced in vivo oxidative stress and striatal lesions: insights into Huntington's disease. J Neurochem, 2000. **75**(4): p. 1709-15.
- 339. Ferrante, R.J., et al., *Neuroprotective effects of creatine in a transgenic mouse model of Huntington's disease.* J Neurosci, 2000. **20**(12): p. 4389-97.
- 340. Hersch, S.M., et al., *Creatine in Huntington disease is safe, tolerable, bioavailable in brain and reduces serum* 80H2'dG. Neurology, 2006. **66**(2): p. 250-2.
- 341. Sestili, P., et al., *Creatine supplementation affords cytoprotection in oxidatively injured cultured mammalian cells via direct antioxidant activity.* Free Radic Biol Med, 2006. **40**(5): p. 837-49.
- 342. Costa, M.C., et al., *Genomic structure, promoter activity, and developmental expression of the mouse homologue of the Machado-Joseph disease (MJD) gene.* Genomics, 2004. **84**(2): p. 361-73.
- Linhartova, I., et al., Conserved domains and lack of evidence for polyglutamine length polymorphism in the chicken homolog of the Machado-Joseph disease gene product ataxin-3. Biochim Biophys Acta, 1999.
 1444(2): p. 299-305.
- 344. Trottier, Y., et al., *Heterogeneous intracellular localization and expression of ataxin-3.* Neurobiol Dis, 1998. **5**(5): p. 335-47.
- 345. Pozzi, C., et al., *Study of subcellular localization and proteolysis of ataxin-3.* Neurobiol Dis, 2008. **30**(2): p. 190-200.
- 346. Tait, D., et al., *Ataxin-3 is transported into the nucleus and associates with the nuclear matrix.* Hum Mol Genet, 1998. **7**(6): p. 991-7.
- 347. Antony, P.M., et al., *Identification and functional dissection of localization signals within ataxin-3.* Neurobiol Dis, 2009. **36**(2): p. 280-92.
- 348. Macedo-Ribeiro, S., et al., *Nucleocytoplasmic shuttling activity of ataxin-3.* PLoS One, 2009. **4**(6): p. e5834.
- 349. Mueller, T., et al., *CK2-dependent phosphorylation determines cellular localization and stability of ataxin-3.* Hum Mol Genet, 2009. **18**(17): p. 3334-43.
- 350. Fei, E., et al., *Phosphorylation of ataxin-3 by glycogen synthase kinase 3beta at serine 256 regulates the aggregation of ataxin-3.* Biochem Biophys Res Commun, 2007. **357**(2): p. 487-92.
- 351. Bichelmeier, U., et al., *Nuclear localization of ataxin-3 is required for the manifestation of symptoms in SCA3: in vivo evidence.* Journal of Neuroscience, 2007. **27**(28): p. 7418-28.
- 352. Masino, L., et al., *Domain architecture of the polyglutamine protein ataxin-3: a globular domain followed by a flexible tail.* FEBS Lett, 2003. **549**(1-3): p. 21-5.
- 353. Tzvetkov, N. and P. Breuer, *Josephin domain-containing proteins from a variety of species are active deubiquitination enzymes.* Biol Chem, 2007. **388**(9): p. 973-8.
- 354. Burnett, B., F. Li, and R.N. Pittman, *The polyglutamine neurodegenerative protein ataxin-3 binds polyubiquitylated proteins and has ubiquitin protease activity.* Hum Mol Genet, 2003. **12**(23): p. 3195-205.
- 355. Nicastro, G., et al., *The solution structure of the Josephin domain of ataxin-3: structural determinants for molecular recognition.* Proc Natl Acad Sci U S A, 2005. **102**(30): p. 10493-8.
- 356. Nicastro, G., et al., *Josephin domain of ataxin-3 contains two distinct ubiquitin-binding sites.* Biopolymers, 2009. **91**(12): p. 1203-14.
- 357. Mao, Y., et al., *Deubiquitinating function of ataxin-3: insights from the solution structure of the Josephin domain.* Proc Natl Acad Sci U S A, 2005. **102**(36): p. 12700-5.
- 358. Berke, S.J. and H.L. Paulson, *Protein aggregation and the ubiquitin proteasome pathway: gaining the UPPer hand on neurodegeneration.* Curr Opin Genet Dev, 2003. **13**(3): p. 253-61.
- 359. Winborn, B.J., et al., *The deubiquitinating enzyme ataxin-3, a polyglutamine disease protein, edits Lys63 linkages in mixed linkage ubiquitin chains.* J Biol Chem, 2008. **283**(39): p. 26436-43.
- 360. Todi, S.V., et al., *Ubiquitination directly enhances activity of the deubiquitinating enzyme ataxin-3.* EMBO J, 2009. **28**(4): p. 372-82.
- 361. Harris, G.M., et al., *Splice isoforms of the polyglutamine disease protein ataxin-3 exhibit similar enzymatic yet different aggregation properties.* PLoS One, 2010. **5**(10): p. e13695.
- 362. Matos, C.A., S. de Macedo-Ribeiro, and A.L. Carvalho, *Polyglutamine diseases: the special case of ataxin-3 and Machado-Joseph disease.* Progress in Neurobiology, 2011. **95**(1): p. 26-48.

- 363. Doss-Pepe, E.W., et al., *Ataxin-3 interactions with rad23 and valosin-containing protein and its associations with ubiquitin chains and the proteasome are consistent with a role in ubiquitin-mediated proteolysis.* Mol Cell Biol, 2003. **23**(18): p. 6469-83.
- 364. Berke, S.J., et al., *Defining the role of ubiquitin-interacting motifs in the polyglutamine disease protein, ataxin-3.* J Biol Chem, 2005. **280**(36): p. 32026-34.
- 365. Donaldson, K.M., et al., *Ubiquitin-mediated sequestration of normal cellular proteins into polyglutamine aggregates.* Proc Natl Acad Sci U S A, 2003. **100**(15): p. 8892-7.
- 366. Tsai, Y.C., et al., *Parkin facilitates the elimination of expanded polyglutamine proteins and leads to preservation of proteasome function.* J Biol Chem, 2003. **278**(24): p. 22044-55.
- 367. Ferro, A., et al., *NEDD8: a new ataxin-3 interactor.* Biochim Biophys Acta, 2007. **1773**(11): p. 1619-27.
- 368. Zhong, X. and R.N. Pittman, *Ataxin-3 binds VCP/p97 and regulates retrotranslocation of ERAD substrates.* Hum Mol Genet, 2006. **15**(16): p. 2409-20.
- 369. Wang, Q., L. Li, and Y. Ye, *Regulation of retrotranslocation by p97-associated deubiquitinating enzyme ataxin-3.* J Cell Biol, 2006. **174**(7): p. 963-71.
- 370. Kuhlbrodt, K., et al., *The Machado-Joseph disease deubiquitylase ATX-3 couples longevity and proteostasis.* Nat Cell Biol, 2011. **13**(3): p. 273-81.
- 371. Wang, G., et al., *Ataxin-3, the MJD1 gene product, interacts with the two human homologs of yeast DNA repair protein RAD23, HHR23A and HHR23B.* Hum Mol Genet, 2000. **9**(12): p. 1795-803.
- Heir, R., et al., *The UBL domain of PLIC-1 regulates aggresome formation.* EMBO Rep, 2006. 7(12): p. 1252-8.
- 373. Rodrigues, A.J., et al., *ATX-3, CDC-48 and UBXN-5: a new trimolecular complex in Caenorhabditis elegans.* Biochem Biophys Res Commun, 2009. **386**(4): p. 575-81.
- 374. Burnett, B.G. and R.N. Pittman, *The polyglutamine neurodegenerative protein ataxin 3 regulates aggresome formation.* Proc Natl Acad Sci U S A, 2005. **102**(12): p. 4330-5.
- 375. Chow, M.K., et al., *Structural and functional analysis of the Josephin domain of the polyglutamine protein ataxin-3.* Biochem Biophys Res Commun, 2004. **322**(2): p. 387-94.
- 376. Reyes-Turcu, F.E., K.H. Ventii, and K.D. Wilkinson, *Regulation and cellular roles of ubiquitin-specific deubiquitinating enzymes.* Annu Rev Biochem, 2009. **78**: p. 363-97.
- Rodrigues, A.J., et al., *Absence of ataxin-3 leads to enhanced stress response in C. elegans.* PLoS One, 2011.
 6(4): p. e18512.
- 378. Li, F., et al., *Ataxin-3 is a histone-binding protein with two independent transcriptional corepressor activities.* J Biol Chem, 2002. **277**(47): p. 45004-12.
- 379. Shimohata, T., et al., *Expanded polyglutamine stretches interact with TAFII130, interfering with CREBdependent transcription.* Nat Genet, 2000. **26**(1): p. 29-36.
- 380. Chai, Y., et al., *Live-cell imaging reveals divergent intracellular dynamics of polyglutamine disease proteins and supports a sequestration model of pathogenesis.* Proc Natl Acad Sci U S A, 2002. **99**(14): p. 9310-5.
- 381. Evert, B.O., et al., *Ataxin-3 represses transcription via chromatin binding, interaction with histone deacetylase 3, and histone deacetylation.* J Neurosci, 2006. **26**(44): p. 11474-86.
- 382. Araujo, J., et al., *FOXO4-dependent upregulation of superoxide dismutase-2 in response to oxidative stress is impaired in spinocerebellar ataxia type 3.* Hum Mol Genet, 2011. **20**(15): p. 2928-41.
- 383. Mazzucchelli, S., et al., Proteomic and biochemical analyses unveil tight interaction of ataxin-3 with tubulin. Int J Biochem Cell Biol, 2009. 41(12): p. 2485-92.
- 384. Wang, H., Z. Ying, and G. Wang, *Ataxin-3 regulates aggresome formation of copper-zinc superoxide dismutase* (*SOD1*) by editing K63-linked polyubiquitin chains. J Biol Chem, 2012. **287**(34): p. 28576-85.
- 385. Mayer, U., *Integrins: redundant or important players in skeletal muscle?* J Biol Chem, 2003. **278**(17): p. 14587-90.
- 386. Reina, C.P., X. Zhong, and R.N. Pittman, *Proteotoxic stress increases nuclear localization of ataxin-3.* Hum Mol Genet, 2010. **19**(2): p. 235-49.
- 387. Hsu, A.L., C.T. Murphy, and C. Kenyon, *Regulation of aging and age-related disease by DAF-16 and heat-shock factor.* Science, 2003. **300**(5622): p. 1142-5.
- 388. Morley, J.F. and R.I. Morimoto, *Regulation of longevity in Caenorhabditis elegans by heat shock factor and molecular chaperones.* Mol Biol Cell, 2004. **15**(2): p. 657-64.
- 389. Cohen, E., et al., *Opposing activities protect against age-onset proteotoxicity.* Science, 2006. **313**(5793): p. 1604-10.
- 390. Todi, S.V., et al., *Activity and cellular functions of the deubiquitinating enzyme and polyglutamine disease protein ataxin-3 are regulated by ubiquitination at lysine 117.* J Biol Chem, 2010. **285**(50): p. 39303-13.

- 391. Scaglione, K.M., et al., *Ube2w and ataxin-3 coordinately regulate the ubiquitin ligase CHIP.* Mol Cell, 2011.
 43(4): p. 599-612.
- 392. Durcan, T.M. and E.A. Fon, *Mutant ataxin-3 promotes the autophagic degradation of parkin.* Autophagy, 2011. **7**(2): p. 233-4.
- 393. Durcan, T.M., et al., *Ataxin-3 deubiquitination is coupled to Parkin ubiquitination via E2 ubiquitin-conjugating enzyme.* J Biol Chem, 2012. **287**(1): p. 531-41.
- 394. Warrick, J.M., et al., *Ataxin-3 suppresses polyglutamine neurodegeneration in Drosophila by a ubiquitinassociated mechanism.* Mol Cell, 2005. **18**(1): p. 37-48.
- 395. Tsou, W.L., et al., *Ubiquitination regulates the neuroprotective function of the deubiquitinase ataxin-3 in vivo.* J Biol Chem, 2013. **288**(48): p. 34460-9.
- 396. Hubener, J. and O. Riess, *Polyglutamine-induced neurodegeneration in SCA3 is not mitigated by non-expanded ataxin-3: conclusions from double-transgenic mouse models.* Neurobiol Dis, 2010. **38**(1): p. 116-24.
- 397. Teixeira-Castro, A., *Identification of modulators of ataxin-3 proteotoxicity in animals models of Machado-Joseph disease*, 2011, University of Minho.
- 398. Jana, N.R., et al., *Co-chaperone CHIP associates with expanded polyglutamine protein and promotes their degradation by proteasomes.* J Biol Chem, 2005. **280**(12): p. 11635-40.
- 399. Matsumoto, M., et al., *Molecular clearance of ataxin-3 is regulated by a mammalian E4.* EMBO J, 2004. **23**(3): p. 659-69.
- 400. Mishra, A., et al., *E6-AP promotes misfolded polyglutamine proteins for proteasomal degradation and suppresses polyglutamine protein aggregation and toxicity.* J Biol Chem, 2008. **283**(12): p. 7648-56.
- 401. Ying, Z., et al., *Gp78, an ER associated E3, promotes SOD1 and ataxin-3 degradation.* Hum Mol Genet, 2009. **18**(22): p. 4268-81.
- 402. Wang, H., et al., *p45, an ATPase subunit of the 19S proteasome, targets the polyglutamine disease protein ataxin-3 to the proteasome.* J Neurochem, 2007. **101**(6): p. 1651-61.
- 403. Blount, J.R., et al., *Ubiquitin-binding site 2 of ataxin-3 prevents its proteasomal degradation by interacting with Rad23*. Nat Commun, 2014. **5**: p. 4638.
- 404. Todi, S.V., et al., *Cellular turnover of the polyglutamine disease protein ataxin-3 is regulated by its catalytic activity.* J Biol Chem, 2007. **282**(40): p. 29348-58.
Objectives

In the last years several published works have contributed for our understanding of ATXN3 biochemical activity *in vitro* and in cells. Although the enzymatic activities described for this protein as a DUB suggest a role for ATXN3 in the UPS, the physiologic and cellular relevance of this activity has not been extensively characterized, specially in neurons, and the substrates of its action remain mostly unidentified.

The goal of this work was to define the functional relevance of ATXN3 and to identify new substrates of its DUB activity in neurons. We also explored the potential perturbation (gain or loss) of ATXN3 function by expansion of the polyQ tract at its C-terminus, and its contribution to human disease.

The specific aims of this work were:

To characterize the phenotypic effects caused by absence of ATXN3 or overexpression of a catalytically inactive version of the protein: morphology, proliferation, migration, cell death, differentiation, signaling pathways and gene expression (Chapter 2)

To study the effects of ATXN3 absence on alternative splicing: splicing of microtubule associated protein tau, global splicing patterns (Chapters 3, 4)

To identify potential substrates of ATXN3 DUB activity in neurons: characterization of the ubiquitome of neuronal cells lacking ATXN3 (Chapter 4)

To define the relevance of candidate ATXN3 substrates for the disease process in cellular and mouse models of MJD: cellular consequences of overexpression of mutant ATXN3 and link to MJD pathogenesis (Chapters 2, 3, 4)

Chapter 2

Dominant negative effect of polyglutamine expansion perturbs

normal function of ataxin-3 in neuronal cells

Dominant negative effect of polyglutamine expansion perturbs normal function of ataxin-3 in neuronal cells

Andreia Neves-Carvalho^{1,2}, Elsa Logarinho³, Ana Freitas^{1,2}, Sara Duarte-Silva^{1,2}, Maria do Carmo Costa⁴, Anabela Silva-Fernandes^{1,2}, Margarida Martins^{1,2}, Sofia Cravino Serra^{1,2}, André T. Lopes^{1,2}, Henry L. Paulson⁴, Peter Heutink⁵, João B. Relvas³ and Patrícia Maciel^{1,2,*}

¹Life and Health Sciences Research Institute (ICVS), School of Health Sciences, University of Minho, 4710-057 Braga, ²ICVS/3B's—PT Government Associate Laboratory, Braga/Guimarães and ³Institute for Molecular and Cell Biology, University of Porto, Porto, Portugal, ⁴Department of Neurology, University of Michigan, Ann Arbor, MI, USA and ⁵German Center for Neurodegenerative Diseases (DZNE), Tübingen, Germany

Received July 1, 2014; Revised August 7, 2014; Accepted August 14, 2014

The physiological function of Ataxin-3 (ATXN3), a deubiquitylase (DUB) involved in Machado–Joseph Disease (MJD), remains elusive. In this study, we demonstrate that ATXN3 is required for neuronal differentiation and for normal cell morphology, cytoskeletal organization, proliferation and survival of SH-SY5Y and PC12 cells. This cellular phenotype is associated with increased proteasomal degradation of α 5 integrin subunit (ITGA5) and reduced activation of integrin signalling and is rescued by ITGA5 overexpression. Interestingly, silencing of ATXN3, overexpression of mutant versions of ATXN3 lacking catalytic activity or bearing an expanded polyglutamine (polyQ) tract led to partially overlapping phenotypes. *In vivo* analysis showed that both Atxn3 knockout and MJD transgenic mice had decreased levels of ITGA5 in the brain. Furthermore, abnormal morphology and reduced branching were observed both in cultured neurons expressing shRNA for ATXN3 and in those obtained from MJD mice. Our results show that ATXN3 rescues ITGA5 from proteasomal degradation in neurons and that polyQ expansion causes a partial loss of this cellular function, resulting in reduced integrin signalling and neuronal cytoskeleton modifications, which may be contributing to neurodegeneration.

INTRODUCTION

The importance of ubiquitin signalling in the nervous system is becoming increasingly recognized (1-3). Impairment of the ubiquitin-proteasome pathway (UPP) and mutations in some of its components have been linked to both neurodevelopmental and neurodegenerative disorders, the later including Alzheimer's, Parkinson's and Huntington's diseases (4-6). In the context of the nervous system, deubiquitylases (DUBs) are central players in the regulation of protein ubiquitylation in processes, such as (i) axon guidance and establishment of neuronal connectivity (7), (ii) dendritic and axon pruning (8,9), (iii) regulation of synaptic number and size (10,11), (iv) regulation of synaptic plasticity (11) and (v) modulation of the postsynaptic structure (7,12).

Ataxin-3 (ATXN3) is a protein with DUB activity known to be mutated in Machado–Joseph Disease (MJD), an autosomal dominant neurodegenerative disorder caused by a polyglutamine (polyQ) tract expansion within the C-terminus of this protein (13). PolyQ expansions are thought to cause deleterious effects in neurons by conferring toxic properties to the proteins into which they are inserted (gain of function model) and by perturbing some of the biological activities of these proteins (partial loss of function model) (14–16).

Although the physiological role and substrates of ATXN3 are mostly unknown, functional analyses in different cell and animal

© The Author 2014. Published by Oxford University Press. All rights reserved. For Permissions, please email: journals.permissions@oup.com

^{*}To whom correspondence should be addressed at: Life and Health Sciences Research Institute (ICVS), School of Health Sciences, University of Minho, 4710-057 Braga, Portugal; ICVS/3B's—PT Government Associated Laboratory, Braga/Guimarães, Portugal. Tel: +351 253 604824; Fax: +351 253 604820; Email: pmaciel@ecsaude.uminho.pt

models have shed some light on its biological functions. Evidence supports ATXN3 involvement in protein quality control pathways: (i) DUB activity conferred by cysteine 14 (C14) within the N-terminal Josephin-domain, which is essential for its protease activity (17-19); (ii) interaction with ubiquitin, polyubiquitin chains, ubiquitylated proteins (20-22) and proteasome subunits (21,23); (iii) interaction with the ubiquitin-like protein NEDD8 and deneddylase activity (24) and (iv) binding to and regulating the activity of VCP/p97, which is involved in shuttling substrates for proteasomal degradation (25,26) and binding to UBXN-5, an adaptor of substrate binding to VCP (27). In addition to its involvement in the regulation of protein degradation, the numerous molecular partners of ATXN3 known to date suggest that it is involved in other cellular processes (28-31). Although mouse and nematode knockouts (KO) for this gene are viable and show no gross phenotype, our previous results showed that the absence of ataxin-3 in Caenorhabditis elegans affects the expression of several transcripts related to cell structure/motility (32) and that ataxin-3 regulates the degradation of integrin subunits such as $\alpha 5$ integrin subunit (ITGA5), a molecular partner of ATXN3 (33). These regulatory functions were shown to be important for the cytoskeleton organization of different cell types (31,33).

Integrins are the major family of transmembrane cell surface receptors that mediate cell-to-cell and cell-to-extracellular matrix (ECM) interactions, regulating many cellular functions (34,35). Integrins are implicated in many aspects of neuronal development and function, such as proliferation, survival, adhesion, cytoskeletal organization, process outgrowth and synaptic function (36–40). Furthermore, cumulative evidence suggests that a disruption of the neuronal cytoskeleton network may be a common feature contributing to several neurodegenerative diseases (41,42). Data suggest that cytoskeletal deregulation initiates a cascade of intracellular events that may underlie the loss of synaptic connectivity, the decreased ability to transmit incoming axonal information and the cell death that is observed in these disorders (43–47).

In this work, we demonstrate that ATXN3 depletion deregulates ITGA5 levels through increased proteasomal degradation, which leads to decreased cell adhesion and disorganization of the neuronal cytoskeleton. Loss of function of ATXN3 also has a negative impact on neuronal differentiation and on the associated exit from the cell cycle, promoting continued proliferation. Our data also indicate that an expanded polyQ tract leads to a partial loss of the cellular function of ATXN3 that may be relevant to neurodegeneration.

RESULTS

ATXN3 knock down results in altered morphology, proliferation, migration and cell death in differentiating SH-SY5Y cells

We evaluated the effects of ataxin-3 silencing in SH-SY5Y human neuroblastoma cells, widely used as a model for neuronal function and differentiation (1). After lentiviral infection and puromycin selection, we obtained monoclonal stable SH-SY5Y cell lines containing a shRNA sequence targeting *ATXN3* (ATXN3^{shRNA}), the empty vector pLKO.1 (SH-SY5Y-pLKO.1) or a scrambled shRNA (SCR^{shRNA}) sequence. A western blot analysis

of protein extracts confirmed that ATXN3 expression was markedly suppressed and almost undetectable in $\mathrm{ATXN3}^{\mathrm{shRNA}}$ clones when compared with SH-SY5Y-pLKO.1 and SCR^{shRNA} controls (Supplementary Material, Fig. S1A and B). We confirmed by real-time quantitative reverse transcription polymerase chain reaction (gRT-PCR) that the shRNA sequence used for silencing ATXN3 did not interfere with similar mRNAs, as the expression levels of the transcripts encoding the ATXN3-like (ATXN3L) and Josephin-domain proteins (JOSD1 and JOSD2) were not significantly different between ATXN3^{shRNA} and SCR^{shRNA} cells (Supplementary Material, Fig. S1C). ATXN3 depletion in non-differentiated SH-SY5Y cells had a mild impact on cell morphology (Supplementary Material, Fig. S2A) and statistically significant effect in migration (Supplementary Material, Fig. S2B); however, it did not affect cell cycle progression (Supplementary Material, Fig. S2C) or survival (Supplementary Material, Fig. S2E). Subsequently, we sought to analyze the effect of ATXN3 depletion on retinoic acid (RA)-differentiated SH-SY5Y cells. RA has previously been shown to induce differentiation and inhibit the cellular growth of cultured human SH-SY5Y cells (48). As shown in Figure 1A, after 7 days of RA-induced differentiation, SCR^{shRNA} control cells exhibited branching neuritic networks with small rounded bodies and an inhibition of cell proliferation, whereas cells in which ATXN3 had been silenced displayed large, flat cell bodies with very few extensions. These striking morphological changes were observed in the different clonal cell lines and were evident in cells with only a few passages after silencing (fATXN3^{shRNA}) as well as cells with long-term silencing of ATXN3, albeit in a more attenuated way in the latter. Such partial recovery in cell morphology might be explained by compensatory mechanisms, as has been observed in different ATXN3 KO animal models (32,49).

After RA treatment, there were significantly more ATXN3^{shRNA} cells when compared with SCR^{shRNA} control cultures (P =0.0019) (Fig. 1B). Consistent with a higher proliferation rate, ATXN3^{shRNA} cultures showed an increased number of Ki-67-positive cells (61.57% versus 24.24% in control cells; $P = 9.46 \times 10^{-6}$) (Fig. 1C and D). Accordingly, in comparison to the control SCR^{shRNA} cells, the ATXN3^{shRNA} cell population had a greater number of cells in S phase (24.4% compared with 14.5%; P = 0.0018) (Fig. 1E and F). This higher cell proliferation was accompanied by an increased cell death in RA-treated ATXN3^{shRNA} cultures as determined by flow cytometry analysis (22.8% versus 8.02% of PI-positive cells; P = 0.0001) that was even higher in fATXN3^{shRNA} cultures (40.1%; $P = 5.60 \times$ 10^{-5}) (Fig. 1G). Because it has previously been demonstrated that ataxin-3 interacts with and regulates the levels of integrins (33) and because adhesion to the substrate is key for cell migration, we analyzed collective cell movement using a wound healing assay (50). Cells were monitored for 24 h starting immediately after the initial wound. As shown in Figure 1H and I, ATXN3^{shRNA} cells had partially recolonized the scratched area and exhibited a 50% increase in the cell migration rate when compared with SCR^{shRNA} cells ($P = 4.42 \times 10^{-7}$), which suggests that ATXN3^{shRNA} cells did not adhere as well to the substrate. The same was observed in two other clonal cell lines with similar degrees of ATXN3 silencing. Interestingly, these effects of ATXN3 absence seem to be generalized to different neuronal cell types, as similar phenotypes were observed in









Figure 1. Characterization of a SH-SY5Y neuronal cell line stably silenced for ATXN3. (**A**) ATXN3^{shRNA} cells were less elongated and showed thin cell extensions as compared with the SCR^{shRNA} controls after RA treatment. This phenotype was more pronounced in fATXN3^{shRNA} cells. Scale bar: 100 μ m. (**B**) RA treatment did not inhibit proliferation of ATXN3^{shRNA} cells. (**C** and **D**) Ki-67 staining (red) showed that RA did not inhibit proliferation of ATXN3^{shRNA} cells. Nuclei were counterstained with DAPI (blue). Scale bar: 200 μ m. (**E** and **F**) Flow cytometry analysis of the cell cycle showed an increase in the percentage of cells in S phase in ATXN3^{shRNA} cultures. (**G**) Flow cytometry analysis using PI showed an increased cell death in ATXN3^{shRNA} cultures, which was even higher in fATXN3^{shRNA} cultures. (**H** and **I**) ATXN3 knockdown increased SH-SY5Y cell migration in a wound scratch assay. Bars represent migration rate expressed as a percentage of control and calculated as the proportion of the distance between the borderlines caused by scratching, to the distance that remained cell-free after 24 h. $n \ge 3$ independent biological replicates in all experiments. **P < 0.001; ***P < 0.001.

PC12 cells upon ATXN3 silencing (PC12_ATXN3^{shRNA}), in the context of nerve growth factor (NGF)-induced differentiation (Supplementary Material, Figs S1D–F and S6).

ATXN3^{shRNA} cells fail to progress towards a mature neuronal phenotype

RA treatment increases the synthesis of neuron-specific enzymes, neurotransmitters, neuropeptide hormones, growth factors and cell surface receptors and induces changes in cytoskeleton markers in SH-SY5Y cells (51). Because we observed that neuronal differentiation was impaired in ATXN3^{shRNA} cells, we wanted to further characterize the differentiation status of these cells. For this, we evaluated several neuronal markers associated with RA-induced differentiation (52).

As expected, we observed increased mRNA levels for most of the neuronal markers in the SCR^{shRNA} cells after RA treatment and decreased expression of nestin, a marker of undifferentiated cells (Fig. 2A). In contrast, the mRNA expression pattern in RA-treated ATXN3^{shRNA} cells was consistent with immature stages of neuronal differentiation, with increased expression of nestin (P = 0.02) and decreased expression of β III-tubulin (P = 0.0002), laminin (P = 0.02), synaptophysin (P = 0.01), neurogenin (P = 0.03), neuroD1 ($P = 7.63 \times 10^{-5}$) and dopamine transporter (DAT) (P = 0.04) (Fig. 2A). Consistently, decreased expression of some neuronal differentiation markers, including β III-tubulin (P = 0.01), was also observed in NGF-treated PC12_ATXN3^{shRNA} cells (Supplementary Material, Fig. S6F). Immunocytochemistry confirmed that the percentage of β III-tubulin positive cells, a marker for mature neurons, was lower in ATXN3^{shRNA} cultures (86.26% versus 97.26%) upon RA treatment and more significantly so in fATXN3^{shRNA} cells (41.96%; $P = 4.12 \times 10^{-8}$) (Fig. 2B and C). Additionally, the average neurite length was significantly reduced in RA-treated fATXN3^{shRNA} cells ($P = 1.18 \times 10^{-15}$) when compared with control cells (Fig. 2D), which is compatible with the immature filopodia phenotype observed in the absence of ATXN3.

These results indicate that ATXN3-deficient cells fail to progress towards a mature neural phenotype upon RA treatment. Nevertheless, we verified that these cells are able to respond to RA, as demonstrated by the induction of the RA-responsive tissue transglutaminase (tTG) gene (53) (Supplementary Material, Fig. S3A).

ATXN3 depletion disrupts the actin cytoskeleton network in SH-SY5Y cells

Neuronal development is highly dependent on controlled cytoskeleton dynamics and reorganization, and it has been shown that in several neurodegenerative diseases, this reorganization is defective (41,42). Phalloidin staining of actin polymers revealed the presence of disarrayed actin filaments and aggregates in ATXN3^{shRNA} and fATXN3^{shRNA} cells (Fig. 3A) as well as in PC12_ATXN3^{shRNA} cells (Supplementary Material, Fig. S6G). Additionally, the ATXN3^{shRNA} cells exhibited a higher number of small filopodia (microspikes) and the PC12_ATXN3^{shRNA} cells grew mostly in multilayers, which were not observed in the control cultures. These cytoplasmic projections are normally present in migrating cells and at initial stages of neurogenesis (54). This finding further supports the hypothesis that in the absence of ATXN3, cells fail to properly complete differentiation and to establish mature neuronal processes. Very importantly, primary neurons with silenced ATXN3 expression also show a highly disrupted cytoskeleton network as compared with the scrambled controls, providing further evidence for the role of ataxin-3 in the regulation of the cytoskeleton (Fig. 3B).

Absence of ATXN3 leads to downregulation of α 5 integrin signalling

Integrins play an important role in mediating cell adhesion to the ECM proteins and activating signalling cascades that control cytoskeletal organization and cell motility (55,56). We have previously reported that ataxin-3 regulates the degradation of integrin subunits such as the ITGA5 (33). Accordingly, we observed that depletion of ATXN3 downregulates ITGA5 protein levels in SH-SY5Y (P = 0.001) and PC12 (P = 0.0047) cells induced to differentiate (with RA and NGF treatment, respectively) (Fig. 4A and B, Supplementary Material, Fig. S6H-J, respectively), but does not affect those of other integrin subunits, such as the α 1 integrin subunit (Supplementary Material, Fig. S4A). Because $\alpha 5\beta 1$ is the receptor for fibronectin (FN), which has been implicated in neuronal cell migration, adhesion, proliferation and differentiation both *in vitro* and *in vivo* (36), we next assessed the FN-binding capacity of $ATXN3^{shRNA}$ cells using a CultreCoat®Fibronectin 96 well adhesion assay (Ambsio). As expected, the adhesion of ATXN3^{shRNA} cells to FN was sig-nificantly reduced (89.5%; P = 0.004) in relation to SCR^{shRNA} controls (Fig. 4C). We subsequently assessed cell migration on an FN substrate. For this, we coated the plates with FN and performed the wound healing assay as described above. As shown in Figure 4D, RA-treated ATXN3^{shRNA} cells had almost fully recolonized the scratched area with an 89% increase in the woundhealing rate when compared with the RA-treated SCR^{shRNA} control cells (P = 0.0009). Interestingly, this phenotype was specific for FN, because on laminin or poly-D-lysine substrates, no significant differences between cells with or without ATXN3 were observed (Supplementary Material, Fig. S4B). Additionally, it has been suggested that integrins modulate CDK5 activity, which in turn modulates the activity of the ERK and PI3K/AKT pathways (57) affecting neuronal development and survival (58). Immunoblotting analysis of RA-treated ATXN3^{shRNA} cells showed a decreased expression of p35 ($P = 5.94 \times$ 10^{-5}), which is known to be associated with a decrease in CDK5 activity (Fig. 4E and F). The decrease in CDK5/p35 complex activity is associated with reduced phosphorylationmediated activation of ERK1/2 (P = 0.001), AKT (P = 0.005) and PI3K (P = 0.012) in ATXN3^{shRNA} cells, with no alteration in the total levels of these proteins, and, with a downregulation of BCL2 (P = 0.007) (Fig. 4E and F). BCL2 inhibits BAX and BAK apoptotic functions (59); therefore, decreased levels of BCL2 may contribute to the increased neuronal death observed in ATXN3^{shRNA} cultures (Fig. 1G). Interestingly, the levels of nuclear CDK5 were also significantly reduced in ATXN3^{shRNA} cells (Fig. 4E and F), which correlates well with the increased proliferation (Fig. 1C and D) observed upon RA treatment (60). Knowing that integrin cell signalling can modulate the activity of Rho and Rac1 GTPases (61), we next investigated if the



Figure 2. Impairment of the differentiation process in ATXN3^{shRNA} cultures. (**A**) qRT-PCR analysis of the variation of neuronal markers after RA treatment showed that the mRNA level was not altered for *TH* and *DRD2*, was increased for nestin and decreased for the other markers analyzed in ATXN3^{shRNA} cultures. Transcript levels were normalized to levels in undifferentiated cells and to the *HBMS* gene. (**B** and **C**) ATXN3^{shRNA} cultures presented a decreased number of β III-tubulin positive cells. (**D**) The average length of the neurites was reduced in fATXN3^{shRNA} cells. This morphological alteration was attenuated after long-term silencing of ATXN3. **P* < 0.05; *n* ≥ 3 independent biological replicates in all experiments. ***P* < 0.001; ****P* < 0.001.

decreased levels of ITGA5 affected the activity of these regulatory proteins in neuronal cells lacking ATXN3. We found that the activities of both Rho and Rac1 proteins were significantly reduced in RA-treated ATXN3^{shRNA} cells (Fig. 4G). To verify the relevance of our findings *in vivo*, we assessed the levels of Itga5 in the cerebellum of *Atxn3* KO mice (62), confirming that they were reduced as observed in the ATXN3 knockdown neuronal cell cultures (Fig. 4H and I).

Based on previous observations in non-neuronal cells (33) and considering that ATXN3 is a DUB enzyme, we hypothesized

that ATXN3 could modify ubiquitylation and regulate the degradation of ITGA5 through the UPP. To test this hypothesis, we assessed the levels of ITGA5 upon proteasome inhibition with 5 μ M MG132 for 24 h in cultures treated with RA and found them to be significantly increased in ATXN3^{shRNA} cells (Fig. 4J). Additionally, inhibition of protein synthesis by cycloheximide (CHX) treatment showed a decrease in ITGA5 halflife in these cells (Fig. 4K); this suggests that ATXN3 normally acts to inhibit ITGA5 degradation also in neurons. We found that inhibition of the proteasome with MG132 increased the levels of



Figure 3. ATXN3 depletion affects the actin cytoskeleton network in neuronal cells. (A) Phalloidin staining (green) showed unparallel actin filaments and abnormal filopodia in ATXN3^{shRNA} cells. The right panel shows a detailed view of isolated cells. (B) Primary neurons silenced for ATXN3 (GFP positive cells) showed a disrupted network of actin filaments as assessed by phalloidin staining (green). The lower panel shows a detailed view of isolated cells. Nuclei were counterstained with DAPI (purple). $n \ge 3$ independent biological replicates in all experiments. Scale bar is 5 µm.



Figure 4. Decrease in adhesion proteins and decreased activation of regulatory molecules in ATXN3^{shRNA} cells. (**A** and **B**) Western blot analysis showed a decrease of ITGA5 levels in ATXN3^{shRNA} cells. (**C**) Depletion of ATXN3 leads to decreased FN responsiveness in SH-SY5Y cells. (**D**) ATXN3^{shRNA} cells showed increased cell migration on a FN substrate. Bars represent migration rate relative to control cells and expressed as the proportion of the mean distance that remained cell free after 24 h. (**E** and **F**) Deregulation of the ERK and PI3K/AKT pathways, with decreased levels of p35, pERK1/2, pAKT and PI3K, and decreased levels of nuclear CDK5 in ATXN3^{shRNA} cells. The results were normalized for H3 levels. (**G**) ATXN3^{shRNA} cells showed significantly decreased levels of active Rac1 and Rho proteins. (**H** and **I**) Western blot analysis showed decreased levels of Itga5 in the cerebellum of Atxn3 KO mice. The results were normalized for *a*-tubulin levels. (**J**) Levels of ITGA5 were increased upon treatment with 5 μ M MG132 for 24 h after induction of differentiation with RA for 7 days in ATXN3^{shRNA} cells. (**K**) Relative amounts of ITGA5 in SCR^{shRNA} and ATXN3^{shRNA} cells. The results were normalized for H3 results were normalized for H3 or CD147 levels. $n \ge 3$ independent biological replicates in all experiments. *P < 0.05, **P < 0.01, ***P < 0.001.

ubiquitylated ITGA5 in ATXN3^{shRNA} cells (P = 0.02) (Fig. 4L). We confirmed that ATXN3 affects the steady-state levels of ITGA5 by acting at the protein level, as qRT-PCR analysis revealed no significant differences in *ITGA5* transcript levels between ATXN3^{shRNA} and SCR^{shRNA} cells (Supplementary Material, Fig. S3B). Together, these results suggest that excessive degradation of ITGA5 in ATXN3^{shRNA} cells induced to differentiate caused defects in adhesion to FN substrates, deregulation of the ERK and PI3K/AKT pathways and a decrease in the activity of small GTPases Rho and Rac1, leading to abnormal cell morphology, motility, proliferation and differentiation.

Restoring the levels of ITGA5 ameliorates the phenotype of ATXN3 $^{\rm shRNA}$ cells

To test if the ATXN3 depletion phenotype could be reverted by the normalization of ITGA5 levels, we overexpressed *ITGA5* in ATXN3^{shRNA} cells (ATXN3^{shRNA}_ α 5) and evaluated their phenotype upon RA treatment. We found that not only were the cellular morphology (Fig. 5A) and cytoskeletal organization (Fig. 5B) significantly restored but also the ATXN3^{shRNA}_ α 5 cells expressed normal levels of the majority of the neuronal markers tested (Fig. 5C). In addition, the migration rate (Fig. 5D) and cell cycle progression (Fig. 5E and F) were comparable to the SCR^{shRNA}_ α 5 control cells. Therefore, we conclude that most aspects of the phenotype observed in ATXN3-deficient cells were caused by the reduction in the ITGA5 levels.

Interference with the DUB activity of ATXN3 leads to an abnormal neuronal phenotype that parallels the loss of expression of this protein

To clarify whether the regulation of ITGA5 levels by ATXN3 was dependent on its DUB activity, we generated a SH-SY5Y cell line that stably overexpressed a catalytically inert version of ATXN3 (Supplementary Material, Fig. S5A), obtained by mutating the catalytic cysteine residue (C14) (ATXN3 C14A). Interestingly, cells expressing ATXN3_C14A recapitulated many characteristics of ATXN3-deficient neurons: (i) a round, flat shape with very few and short extensions in comparison to the controls (Supplementary Material, Fig. S5B); (ii) a lack of proliferative inhibition after RA treatment as assessed by Ki-67 staining (62.97% Ki-67-positive cells in ATXN3_C14A cultures versus 25.03% for the pEGFP controls; $P = 1.10 \times 10^{-14}$) (Fig. 6A and B) and cell cycle analysis (74.9% in S phase versus 17.5%; P = 0.0018) (Fig. 6C and D); (iii) an increased cell death (32.1% versus 10.9%; P = 0.002) (Fig. 6E); (iv) a significant decrease in mRNA levels for several neuronal markers, indicating an immature differentiation status (Fig. 6F) and (v) misaligned actin with randomly distributed filaments (Fig. 6G). ATXN3_C14A cells also showed decreased levels of ITGA5 (P = 0.0017) and downstream targets of CDK5 (the expression of p35 protein was not detectable) (Fig. 6H and I). These results suggest that ATXN3 with the C14A mutation interferes with the function of normal (endogenous) ATXN3 through a dominant negative effect, provoking a more severe phenotype as compared with the silencing, probably due to the lack of the compensatory mechanisms. Importantly, as found in ATXN3^{shRNA} cells (Fig. 4J), 5 μ M

MG132 treatment for 24 h increased the levels of polyubiquitylated ITGA5 in ATXN3_C14A cultures treated with RA (Fig. 6H and I), supporting the hypothesis that ITGA5 is a substrate of the DUB activity of ATXN3 in neurons.

PolyQ expansion in ATXN3 causes a similar but milder neuronal phenotype than the absence of this protein

To determine whether the presence of an expanded polyQ tract within ATXN3 would lead to a gain or loss of function, we generated a SH-SY5Y cell line expressing an ATXN3 protein bearing 83 glutamines (ATXN3_83Q) (Supplementary Material, Fig. S5A). We found that, although expression of the polyQ did not cause visible aggregation of the expanded ATXN3, it led to a similar but slightly milder neuronal phenotype than the one observed in cells lacking this protein. Upon RA treatment, the cells displayed: (i) an abnormal morphology without extensions (Supplementary Material, Fig. S5B); (ii) maintenance of their proliferative activity (64.39% Ki-67positive cells; $P = 1.03 \times 10^{-13}$) (Fig. 7A and B); an increased proportion of cells in the S phase (80.5% versus 17.5% for the pEGFP controls; P = 0.0008) (Fig. 7C and D); (iii) increased cell death (25.4% versus 18.4% for ATXN3_28Q; P = 0.009and 10.9% for the pEGFP controls; $P = 1.43 \times 10^{-5}$) (Fig. 7E); (iv) reduced expression of several neuronal differentiation markers (Fig. 7F) and (v) disorganization of the actin cytoskeleton (Fig. 7G). ATXN3_83Q cells also had reduced levels of ITGA5 (P = 0.01) and decreased activation of its downstream targets (Fig. 7H and I). While overexpression to similar levels, i.e. 2.5-fold, of wild-type (WT) ATXN3 (with 28 glutamines) also caused some degree of perturbation in differentiation and cytoskeleton organization, the effects were much milder than those of ATXN3 loss of function or polyO expansion (Fig. 7). Together, these results suggest that the dose of ATXN3 needs to be strictly balanced and that polyQ expansion perturbs the normal function of ATXN3 in neuronal cells.

In vivo evidence for downregulation of α 5 integrin signalling in the context of Machado–Joseph disease

To investigate whether the partial loss of function of expanded ATXN3 could contribute to the pathogenesis of MJD, we analyzed the levels of Itga5 in the nervous system of an MJD mouse model (CMVMJD135) generated in our lab, expressing an expanded human ATXN3 with 135 glutamines and mimicking the neurological and neuropathological phenotype of the human disease, as described elsewhere (63). As shown in Figure 8A and B, CMVMJD135 mice had significantly reduced levels of Itga5 in the brainstem (an affected brain region) (P = 0.04) and dorsal root ganglia (DRG) (P =0.0019). Considering the cytoskeletal disorganization and reduced branching phenotype observed in the absence of ATXN3, we analyzed neurons isolated from the DRGs of CMVMJD135 mice. We found a marked difference in the morphology of these neurons (Fig. 8C and D), with a drastic reduction in both the total $(P = 1.4 \times 10^{-7})$ and mean $(P = 1.6 \times 10^{-7})$ 10^{-12}) neurite length when compared with WT littermate controls (Fig. 8C and D). Additionally, the cell bodies of the DRGs from transgenic animals had a reduced diameter in comparison to those from WT controls ($P = 3.63 \times 10^{-10}$) (Fig. 8C



Figure 5. The phenotype observed in ATXN3^{shRNA} is dependent on α 5 integrin subunit levels. (A) Overexpression of ITGA5 in ATXN3^{shRNA} cells (ATXN3^{shRNA}_ α 5) restored their cellular morphology upon RA treatment. Scale bar: 100 µm. (B) ATXN3^{shRNA}_ α 5 cells no longer presented detectable actin filament disorganization, as shown by phalloidin staining (green). Nuclei were counterstained with DAPI (purple). Upper panel scale bar: 20 µm. Lower panel scale bar: 5 µm. (C) mRNA levels of the neuronal markers analyzed by qRT-PCR in ATXN3^{shRNA}_ α 5 cells were normal and comparable to the SCR^{shRNA}_ α 5 control cells. mRNA levels were normalized to undifferentiated cells and *HMBS* gene. (D) Normalized ITGA5 levels abolished their increased migration of ATXN3^{shRNA} cells in a wound scratch assay, 24 h after scratching. Bars represent migration rate expressed as a percentage of control and calculated calculated as the proportion of the distance between the borderlines caused by scratching, to the distance that remained cell-free after 24 h. (E and F) Normal cell cycle in ATXN3^{shRNA}_ α 5 cells. $n \ge 3$ independent biological replicates in all experiments. **P* < 0.05.



Figure 6. Effects of ATXN3 silencing is likely related to its DUB activity. (**A** and **B**) RA treatment did not inhibit proliferation of ATXN3_C14A cells, as assessed by Ki-67 labelling (red). Nuclei were counterstained with DAPI (blue). Scale bar: 200 μ m. (**C** and **D**) Flow cytometry analysis of the cell cycle showed an increase in S phase in ATXN3_C14A cultures. (**E**) ATXN3_C14A cultures presented high percentage of cell death as compared with the pEGFP controls, as assessed by PI staining followed by flow cytometry analysis. (**F**) ATXN3_C14A cells presented increased expression of nestin and decreased mRNA levels of neuronal markers. mRNA levels were normalized to undifferentiated cells and *HMBS* gene expression. (**G**) Phalloidin staining (green) showed that actin filaments were disorganized and not parallel in ATXN3_C14A cells. Nuclei were counterstained with DAPI (purple). Scale bar: 20 μ m. (**H** and **I**) Western blot analysis showed a decrease of ITGA5 levels and downstream targets of CDK5 in ATXN3_C14A cells. The results were normalized for H3 levels. $n \ge 3$ independent biological replicates in all experiments. *P < 0.05, **P < 0.01, ***P < 0.001.



Figure 7. Partial loss of function of expanded ATXN3. (**A** and **B**) Ki-67 staining (red) showed that ATXN3_83Q cells kept their proliferative activity upon RA treatment. Nuclei were counterstained with DAPI (blue). Scale bar: 200 μ m. (**C** and **D**) ATXN3_83Q cultures showed an increase in S phase of the cell cycle as assessed by flow cytometry analysis. (**E**) Increased cell death in ATXN3_83Q cultures as assessed by flow cytometry analysis. (**F**) mRNA level of nestin was increased and expression of neuronal differentiation markers was significantly decreased in ATXN3_83Q cells. mRNA levels were normalized to undifferentiated cells and *HMBS* gene expression. (**G**) Actin filaments network was severely affected in ATXN3_83Q cells with unparalleled actin polymers, as shown by phalloidin staining. Nuclei were counterstained with DAPI (purple). Scale bar: 20 μ m. (**H** and **I**) Western blot analysis showed a decrease of ITGA5 levels and its downstream targets in ATXN3_83Q cells. The results were normalized for H3 levels. $n \ge 3$ independent biological replicates in all experiments. *P < 0.05; **P < 0.01; ***P < 0.001.

and D). This supports the hypothesis that a partial loss of function of ATXN3 due to the expansion of the polyQ tract may contribute to neuronal dysfunction in MJD.

DISCUSSION

Given the significance of DUBs to nervous system function and homeostasis, we focussed here on characterization of the normal function of ATXN3 in neuronal cells. Stable depletion of ATXN3 in SH-SY5Y cells by lentiviral transduction of shRNA inhibited neuronal differentiation following exposure to RA. ATXN3-depleted cells displayed a markedly abnormal morphology, becoming flat and with very few extensions, and showing an altered structure of the actin cytoskeleton. Furthermore, the proliferative activity of these cells was not inhibited by RA treatment, their motility was increased and cell survival was significantly reduced.

Although ATXN3 KO animals do not show an overt phenotype, including any neuronal differentiation abnormalities, which is likely due to compensatory mechanisms (32,49,62), the current findings concur with previous studies showing abnormal differentiation, adhesion and morphology in other, nonneuronal, cellular models of ATXN3 loss of function (31,33).

This is interesting, as cumulative evidence suggests that disruption of the neuronal cytoskeleton network may be a common feature contributing to neurodegeneration in several diseases, including polyQ disorders (41,64-66). In addition, ATXN3^{shRNA} cultures showed reduced levels of many neuronal markers while maintaining expression of immature cell markers and a significantly decreased neurite length, which is compatible with an immature filopodia phenotype. Filopodia play an important role in cell migration, neurite outgrowth and wound healing, and their elongation depends on tightly regulated actin polymerization (54). Thus, disruption of the actin filament network impairs neurite elongation and ultimately cell differentiation, as we observed in ATXN3-deficient neuronal cells. Interestingly, when ATXN3^{shRNA} cells were kept in culture for long, we observed a partial recovery of several effects seen with silencing of ATXN3, which might be explained by compensatory mechanisms similar to those occurring in ATXN3 KO animal models. This recovery was less evident in cells expressing the catalytically silent version of the protein. In the disease model (ATXN3_83Q), the compensatory mechanisms also seem to be prevented by the presence of the expanded protein, which has a dominant negative effect.

Neuronal process outgrowth and maturation, as well as neuronal survival, are at least partially regulated by the integrin signalling pathway. We found that the phenotype observed in ATXN3^{shRNA} cells was due to a decrease in the expression of ITGA5, associated with a decrease in the CDK5/p35 complex activity and, consequently, to a deregulation of the PI3K/AKT and ERK pathways. This had a negative impact on neurite outgrowth, cytoskeleton regulation, cell adhesion and motility and survival. CDK5 plays an important role in neuronal differentiation (60), morphogenesis (67), proliferation (68,69), survival, axon guidance, synaptic transmission, neurocytoskeletal dynamics and neuronal degeneration (70-75). It has been shown that inhibition of CDK5 either pharmacologically (with roscovitine) or by expression of a dominant negative form, causes a dramatic decrease in RA-induced cell differentiation (73). Moreover, Cdk5-deficient neurons are significantly arrested or delayed in their developmental program, both in vitro and in vivo (60), and homozygous Cdk5 KO mice mutants die in utero with neuronal migration deficits throughout the brain (70). Additionally, we observed decreased activation of small GTPases, both Rac1 and the Rho family, which are key actin cytoskeleton regulators, further compromising actin dynamics. Interestingly, a recent large-scale huntingtin-protein interaction study revealed that Rho family GTPases and actin remodelling play an important role in huntingtin function and Huntington's disease pathogenesis (76).

The fact that cells expressing the catalytically inactive ATXN3 also show a reduction of ITGA5 protein levels and that inhibition of the proteasome leads to an accumulation of polyubiquitylated ITGA5 species in both ATXN3^{shRNA} and ATXN3_C14A cells suggests that ITGA5 protein levels are regulated through the DUB activity of ATXN3 that defines the extent of ITGA5 degradation by the proteasome. This proposed mechanism is compatible with the previous finding that the ITGA5 is a molecular partner of ataxin-3 (33). Confirming the relevance of ATXN3 for regulation of ITGA5 *in vivo*, the levels of this protein were significantly reduced in the nervous system of Atxn3 KO mice.

To date, the type(s) of ubiquitylation of ITGA5 and the amino acid position of this modification are not known. However, comparing the cytoplasmic tails of all human α integrins, Lobert and Stenmark observed that the first lysine residue was strictly conserved among human integrins and suggested that this might be the site at which ubiquitylation occurs (77). Although it has been described that ITGA5 may be degraded in lysosomes (78), there are also reports demonstrating that it is degraded by the proteasome through the action of the E3 ligase Cbl (33,79). Indeed, Kaabeche and colleagues showed that Cbl recruitment induced by FGFR2 activation triggers ITGA5 proteasomal degradation (79). These observations, together with the fact that FGFR2 expression is known to be upregulated by RA (80), lead us to propose a mechanism that may explain the phenotype of ATXN3^{shRNA} cells upon RA treatment (Fig. 9). In this model, ATXN3 prevents the degradation of ITGA5 triggered by the RA-induced activation of FGFR2 (Fig. 9A). When ATXN3 is silenced, RA treatment causes ITGA5 degradation to an extent that leads to a deregulation of the CDK5, PI3K/AKt and ERK pathways and affects neuronal morphology and cell adhesion, proliferation, differentiation and survival (Fig. 9B). In agreement with this model, overexpression of a catalytically inactive form of ATXN3 led to similar morphological and biochemical changes and the same differentiation impairment as the silencing of ATXN3, suggesting that the regulation of ITGA5 levels in neurons is dependent on the DUB activity of ATXN3. Furthermore, the fact that proteasomal inhibition prevents the decrease of ITGA5 in ATXN3^{shRNA} cells indicates that ATXN3 rescues ITGA5 from degradation by the proteasome. Importantly, restoring the levels of ITGA5 rescued most of the abnormal fea-tures of ATXN3^{shRNA} cells.

Given that this DUB is involved in the human neurodegenerative disease MJD, we conducted experiments to determine the relevance of this abnormal phenotype and impairment in neuronal differentiation to MJD pathogenesis. Interestingly, similar but milder alterations were found in cultures expressing expanded ATXN3, which suggests a partial loss of normal function of the protein in the presence of this type of mutation. Overexpression of the WT ATXN3 also caused some degree of toxicity, suggesting the importance of a tight regulation of ATXN3 expression levels, as has been described elsewhere (81–85).

Confirming the perturbation of ATXN3 normal function by polyQ expansion, we observed a downregulation of Itga5 in the brainstem and DRGs of CMVMJD135 transgenic mice. Cultures of DRG neurons from these animals showed that transgenic neurons were smaller and displayed a drastic decrease in the neurite length, as observed in neuronal cultures depleted for ATXN3. This finding suggests that the loss of this normal cellular function of ATXN3 might be relevant for the neurodegeneration caused by the polyQ tract. Although the in vitro assays performed so far suggest that the polyQ expansion does not significantly affect ATXN3 DUB activity (86), these assays were performed using artificial substrates that may not mirror the biological substrates of ATXN3, or the post-translational modifications, co-factors and key partners that may be lacking. Improved assays addressing DUB activity within a cellular environment based on specific substrates and/or addressing ATXN3 as part of multi-protein complexes would be important to adequately assess WT and mutant ATXN3 activity.



Figure 8. The polyQ expansion in ATXN3 affects the integrin signalling pathway. (**A** and **B**) Western blot analysis showed decreased levels of Itga5 in the nervous system of CMVMJD135 mice (n = 5 animals/genotype). The results were normalized for α -tubulin levels. (**C** and **D**) DRG neurons from CMVMJD135 mouse (two pools of three animals for each genotype) showed no differences in the number of neurites and decreased neurite length and soma diameter as compared with the WT controls. Neurite length was measured using NeuronJ software and Feret's diameter was used to measure the soma (n = 50 neurons/genotype). Scale bar: 200 μ m. $n \ge 3$ independent biological replicates in all experiments. *P < 0.05; ***P < 0.001.



Figure 9. Model of α 5 integrin subunit modulation of the PI3K/AKT and ERK cascades to insure neuronal differentiation and survival. (**A**) In normal functioning neurons, ATXN3 is preventing degradation of ITGA5 triggered by the RA induced activation of FGFR2. (**B**) When ATXN3 is silenced, RA treatment causes ITGA5 degradation to an extent that leads to a deregulation of the PI3K/AKt and ERK pathways affecting neuronal morphology and cell adhesion and survival.

Overall, our data support the importance of ATXN3 in neuronal cells and the link between its biological function and MJD. Loss of function of ATXN3 in neuronal cells affects degradation of ITGA5 through its DUB activity, which affects many processes that are important for neuronal development and function, such as cell adhesion, differentiation, cytoskeleton organization and neurite length. PolyQ expansion imparts loss of this cellular function of ATXN3 in neurons, with effects on neuronal morphology and process extension, which chronically may contribute to neurodegeneration.

MATERIALS AND METHODS

Cell culture

SH-SY5Y cell cultures: human neuroblastoma SH-SY5Y cell line (ATCC, CRL-2266) was cultured in Dulbecco's modified eagle medium: nutrient mixture (DMEM)/F-12 (Invitrogen) supplemented with 10% (v/v) fetal bovine serum (FBS) (Biochrom), 2 mM glutaMAX (Invitrogen), 100 U/ml penicillin, 100 µg/ml streptomycin and 25 ng/ml puromycin (Sigma Aldrich). Medium was changed every 2 days. Differentiation was induced by 0.1 µM all-trans-retinoic acid (Sigma Aldrich) in opti-MEM (Invitrogen) supplemented with 0.5% FBS. Medium was replaced every 2 days. PC12 cell cultures: rat PC12 cells were cultured in DMEM (Invitrogen) supplemented with 10% (v/v) FBS (Biochrom), 5% (v/v) horse serum (HS) (Biochrom), 2 mM GlutaMAX (Invitrogen), 100 U/ml penicillin, 100 µg/ml streptomycin and 25 ng/ml puromycin (Sigma Aldrich). Medium was changed every 2 days. Differentiation was induced by 1 µg/ml NGF (Invitrogen) in DMEM supplemented with 0.75% FBS and 0.75% HS. Medium was replaced every 2 days. Primary cultures of dorsal root ganglion neurons: for dorsal root ganglion (DRG) neuron culture, cells isolated from 8 weeks-old mice were plated in poly-D-lysine

(Sigma) and laminin (Sigma) pre-coated coverslips at a density of 5×10^3 cells/ml in DMEM/F12 supplemented with 10% (v/v) FBS, 100 U/ml penicillin, 100 µg/ml streptomycin, 50 ng/ml NGF (Millipore), $1 \times B27$ (Invitrogen) and 1.176 g/ L L-glutamine (Invitrogen) for 72 h. *Primary cultures of hipoc-campal neurons*: hippocampal neuron cultures were prepared from P4 Wister rats. Briefly, upon dissection, hippocampi were submitted to a trypsin-based enzymatic digestion followed by mechanical dissociation. Isolated cells were then plated on coverslips previously coated with poly-p-lysine (Sigma) at a density of 40 000 cells/cm² using Neurobasal A medium (Gibco) supplemented with 1 mM GlutaMAX (Gibco), 10 ng/ml bFGF (Gibco), 0.1 mg/ml kanamycin (Gibco) and 1 × B27 (Gibco) for 7 days. Cells were incubated in a humidified $37^{\circ}C/95\%$ air/5% CO₂ incubator.

Vectors and lentivirus packaging

HEK293T packaging cells were plated at a density of 3×10^5 cells/well in 6-well plates, cultured in opti-MEM supplemented with 10% FBS and transfected on the following day with the scrambled sequence vector (CAACAAGATGAAGAG CACCAA), the pLKO.1/shRNA-ATXN3 vector (CCGGGCAG GGCTATTCAGCTAAGTACTCGAGTACTTAGCTGAATA GCCCTGCTTTTT) or the empty vector pLKO-1 (TRC1; Open Biosystems) for virus production, following the RNAi Consortium High-Throughput Lentiviral production protocol (87). For overexpression the following plasmids were used: PPCB7/ ITGA5 (Addgene plasmid 16 041), pEGFP/ATXN3_28Q, pEGFP/ATXN3_83Q and pEGFP/ATNX3_C14A. Medium was changed in the next day and cells were cultured for 48 h. Conditioned medium was then collected and stored at -80° C.

Transduction of target cells

A total of 2.5×10^5 SH-SY5Y or PC12 cells were seeded on a 6-well plate in complete DMEM/F-12 medium and transduced by the lentiviral vectors. Medium was changed 24 h after, and cells were incubated for 72 h. For selection of clones with stable shRNA expression, fresh complete DMEM/F-12 or DMEM medium containing 25 µg/ml puromycin was added to the cells. During the selection period, medium was replaced by fresh medium containing puromycin every 2 days. After 5 days, cells that formed colonies were selected and sub-cultured in 96-well plates under puromycin selective pressure (2.5 µg/ml puromycin) for subsequent expansion, with passaging every 3-5 days. The percentage of silencing of each clone was monitored by immunoblotting.

High-throughput high-content functional imaging

SH-SY5Y cells were seeded at a density of 4×10^3 cells/well in flat bottom 96-well plates previously coated with Matrigel (BD, Biosciences), and 10 μ M all-trans-retinoic acid (Sigma Aldrich) was added the day after plating in DMEM/F-12 with 1% FBS. After 5 days, cells were washed with DMEM/F-12 and incubated with 50 ng/ml BDNF (Peprotech) in DMEM/F-12 without serum for 3 days. Cells were then labelled for β III-tubulin (1:1000, R&D Systems), scanned at different locations of each well and the quantitative analysis of total number of cells, number of β III-tubulin positive cells and neurite length were automatically done using the automatic imaging system Thermo Scientific Cellomics® ArrayScan® VTI.

Pulldown

RA-treated SH-SY5Y cells were washed in ice-cold PBS, incubated 5 min on ice in FISH buffer (50 mM Tris-HCl, pH 7.4, 2 mM MgCl₂, 10% glycerol, 1% NP-40, 100 mM NaCl and protease inhibitors cocktail) and centrifuged for 5 min, 21 000 g, at 4°C. Aliquots were taken from the supernatant to compare protein amounts. The supernatant was incubated with bacterially produced GST-PAK-CD or GST-RHOTEKIN-RBD fusion proteins bound to glutathione-coupled sepharose beads (GE Healthcare) at 4°C for 30 min. The beads and proteins bound to the fusion protein were washed three times in an excess of FISH buffer, eluted in Laemmli buffer and analyzed for bound Rho and Rac1 by immunoblotting. For the pulldown of polyubiquitylated proteins, RA-treated cells were lysed in lysis buffer (50 mm HEPES, pH 7.5, 0.15 M NaCl, 1 mM EDTA, 1% NP-40, 10% glycerol, 50 µM PR-619 and protease inhibitors cocktail) and centrifuged for 10 min, 14 000 g, at 4°C, or treated with 5 μ M MG132 (Calbiochem) for 24 h prior to lysis. One milligram of the supernatant were incubated with 100 µl of Agarose-TUBEs (Lifesensors) and incubated 1 h at 4°C. Beads were washed three times with TBS-T and bound proteins were eluted in Laemmli buffer.

Protein synthesis inhibition and proteasome inhibition

RA-treated SH-SY5Y cells were incubated with 5 μ M CHX (Merck) during 30, 60 or 180 min. For proteasome inhibition,

RA-treated cells were incubated with 5 μM MG132 (Calbiochem) for 24 h prior to lysis.

Immunoblotting

RA-treated SH-SY5Y cells or NGF-treated PC12 cells were pelleted and frozen in liquid nitrogen. For cellular and brain tissue extracts, 50 µg of total protein isolated in RIPA buffer [150 mM NaCl, 50 mM Tris-HCl, pH 7.6, 0.5% NP-40, 1 mM Phenylmethylsulfonyl fluoride, protease inhibitors (Roche)] were resolved in 10% SDS-PAGE gels and transferred to a nitrocellulose membrane (Bio-Rad). After incubation with the primary antibodies against ATXN3 (1H9, 1:2000, Millipore), α 5 integrin (1:5000, Millipore), CDK5 (1:1000, Millipore), p35 (1:1000, cell signalling), pERK1/2 (1:2000, cell signalling), ERK1/2 (1:1000, cell signalling), PI3K (1:1000, cell signalling), pAKT (1:1000, cell signalling), AKT (1:3000, cell signalling), BCL2 (1:100, Abcam), pan-Rho (1:1500, Millipore) and Rac1 (1:2000, Millipore), overnight at 4°C, membranes were incubated with secondary antibodies for 1 h at room temperature (anti-rabbit or anti-mouse, 1:10 000, Bio-Rad). Antibody affinity was detected by chemiluminescence (Clarity kit, Bio-Rad). Histone H3 (1:7500, Millipore), MCT4 (1:500, Santa Cruz), CD147 (1:500, Santa Cruz) and α -tubulin (1:500, DSHB) were assessed as loading controls.

Flow cytometry

For propidium iodide (PI) staining, RA-treated SH-SY5Y cells or NGF-treated PC12 cells were collected and fixed using ice-cold 70% ethanol for 1 h on ice. Pelleted cells were washed with PBS and incubated with staining solution (0.1% Triton-X100, 20 μ g/ml PI solution, 250 μ g/ml RNase in PBS) for 1 h at 50°C. For cell cycle analysis, cells were starved for 6 h before RA treatment. Samples were washed with PBS and analyzed using a FACSCaliber2 flow cytometer (BD-Biosciences) with a 568-nm excitation laser. Signals from 30 000 cells/sample were captured in FL3 (>670 nm) at a flow rate of 1000 cells/s. Offline data were processed with the FlowJo (Tree Star) software and quantified with WinList software.

Wound healing assay

SH-SY5Y cells were grown to confluent monolayers on 6-well plates. After RA treatment, monolayers were wounded by a pipette tip. This initial wounding and the movement of the cells in the scratch were photographically monitored using the Olympus IX-51 inverted microscope equipped with a TH4-200 camera for 24 h. This time window has been chosen because it is shorter than the doubling time reported for SH-SY5Y cell line (88). Eight different fields were considered for quantitative estimation of the distance between the borderlines and in each image five different equidistant points were measured. The migration rate was calculated as the distance between the borderlines caused by scratching (defined at 0 h) minus the width that remained cell-free after 24 h and expressed as a percentage of the control.

Real-time quantitative reverse transcription polymerase chain reaction

One microgram of total RNA purified from RA-treated SH-SY5Y cells or NGF-treated PC12 cells was reverse transcribed using the One-step SuperScript kit (Bio-Rad). qRT-PCR reaction was performed using the Quantitec SYBR Green kit (Qiagen) and the primers previously described (52), in a CFX96 real-time PCR detection system (Bio-Rad). Gene expression was normalized to *HMBS* levels. The results are presented as fold change.

Immunocytochemistry

Cells cultured on poly-D-lysine (Sigma Aldrich) and gelatin, Collagen (BD Biosciences) or Ply-D-lysine pre-coated glass coverslips (SH-SY5Y, PC12 or primary neurons, respectively) were fixed with 4% paraformaldehyde in PBS for 30 min at room temperature. Cells were permeabilized with 0.5% Triton X-100 in PBS for 5 min. Next, cells were incubated with 10% fetal calf serum blocking buffer for 1 h, followed by overnight incubation with primary antibody against Ki-67 (1:300, Millipore) or β IIItubulin (1:1000, R&D systems) at 4°C, or by incubation with phalloidin (1:500, Sigma Aldrich) for 45 min and counterstained with DAPI (1:2000, Sigma Aldrich) for 10 min at room temperature. Alexa Fluor 568 (A11004) conjugated antibody was used at 1:2000 (Molecular probes).

Animals

The MJD mouse model (CMVMJD135) was generated as described (63). Wister Rats used for the primary cultures were purchased from Charles River, Spain. For the mouse primary cultures, two pools of three male animals for each genotype at approximately 2 months of age were used. Animals were sacrificed by decapitation and the DRGs were removed along the spinal cord. For the rat primary cultures, six P4 rats per experiment were used. Animals were sacrificed by decapitation and brains were dissected. All animal procedures were conducted in accordance with European regulations (European Union Directive 86/609/EEC) and approved by the joint Animal Ethics Committee of the Life and Health Sciences Research Institute, University of Minho. Health monitoring was performed according to FELASA guidelines (89). All animals were housed and maintained in a controlled environment at 22-24°C and 55% humidity, on 12 h light/dark cycles and fed with regular rodent's chow and tap water ad libitum. Animal facilities and the people directly involved in animal experiments (A.N.-C., S.D.-S. and A.S.-F.) were certified by the Portuguese regulatory entity-Direcção Geral de Alimentação e Veterinária. Animals were sacrificed by decapitation at 8 weeks of age. Their brains were immediately dissected and stored at -80° C.

Microscopy

Image acquisition of fixed cells was carried out in a Zeiss Axio-Imager Z1 equipped with a Axiocam MR. Images represent maximum-intensity projections of all Z planes acquired with PLANAPO $\times 40$ or $\times 63$ objectives and following blind deconvolution with a AutoquantX (Media Cybernetics). Adobe photoshop CS5 (adobe Systems) was used for image processing.

Statistical analysis

Comparison between the different cell lines was performed using the *t*-test in the GraphPad prism version 5.0 software, assuming the homogeneity of the variances. For immunoblottings, the mean density and area of each band were measured using at least three experiments in TINA 2.0 software according to manufacturer's instructions. For qRT-PCR data, results were presented using the $\Delta\Delta$ Ct method, as described before (90). A critical value for significance of two-tailed P < 0.05 was used throughout the study.

SUPPLEMENTARY MATERIAL

Supplementary Material is available at HMG online.

ACKNOWLEDGEMENTS

We would like to thank Dr Shushant Jain for the help with generation of cell lines, Dr António Salgado for the help with the primary cultures and Dr Belém Marques for the support with the flow cytometry analysis.

Conflict of Interest statement. None declared.

FUNDING

This work was supported by Fundação para a Ciência e Tecnologia and COMPETE through the project '(PTDC/SAU-GMG/ 101572/2008)' and by National Institutes of Health (NIH) '(R01NS038712)'. A.N-C, S.D-S and A.S-F were supported by the FCT fellowships SFRH/BD/51059/2010, SFRH/BD/ 78388/2011 and SFRH/BPD/91562/2012, respectively.

REFERENCES

- Chen, P.C., Bhattacharyya, B.J., Hanna, J., Minkel, H., Wilson, J.A., Finley, D., Miller, R.J. and Wilson, S.M. (2011) Ubiquitin homeostasis is critical for synaptic development and function. *J. Neurosci.*, **31**, 17505–17513.
- Baptista, M.S., Duarte, C.B. and Maciel, P. (2012) Role of the ubiquitin-proteasome system in nervous system function and disease: using *C. elegans* as a dissecting tool. *Cell. Mol. Life Sci.*, 69, 2691–2715.
- Kowalski, J.R. and Juo, P. (2012) The role of deubiquitinating enzymes in synaptic function and nervous system diseases. *Neural Plast.*, 2012, 892749.
- de Vrij, F.M., Fischer, D.F., van Leeuwen, F.W. and Hol, E.M. (2004) Protein quality control in Alzheimer's disease by the ubiquitin proteasome system. *Progr. Neurobiol.*, 74, 249–270.
- Upadhya, S.C. and Hegde, A.N. (2005) Ubiquitin-proteasome pathway components as therapeutic targets for CNS maladies. *Curr. Pharm. Des.*, 11, 3807–3828.
- Rubinsztein, D.C. (2006) The roles of intracellular protein-degradation pathways in neurodegeneration. *Nature*, 443, 780–786.
- 7. Bingol, B. and Schuman, E.M. (2005) Synaptic protein degradation by the ubiquitin proteasome system. *Curr. Opin. Neurobiol.*, **15**, 536–541.
- Watts, R.J., Hoopfer, E.D. and Luo, L. (2003) Axon pruning during *Drosophila* metamorphosis: evidence for local degeneration and requirement of the ubiquitin-proteasome system. *Neuron*, 38, 871–885.

- Kuo, C.T., Zhu, S., Younger, S., Jan, L.Y. and Jan, Y.N. (2006) Identification of E2/E3 ubiquitinating enzymes and caspase activity regulating *Drosophila* sensory neuron dendrite pruning. *Neuron*, 51, 283–290.
- Hegde, A.N. and DiAntonio, A. (2002) Ubiquitin and the synapse. *Nat. Rev. Neurosci.*, 3, 854–861.
- Hegde, A.N. (2004) Ubiquitin-proteasome-mediated local protein degradation and synaptic plasticity. *Progr. Neurobiol.*, **73**, 311–357.
- Colledge, M., Snyder, E.M., Crozier, R.A., Soderling, J.A., Jin, Y., Langeberg, L.K., Lu, H., Bear, M.F. and Scott, J.D. (2003) Ubiquitination regulates PSD-95 degradation and AMPA receptor surface expression. *Neuron*, 40, 595–607.
- Kawaguchi, Y., Okamoto, T., Taniwaki, M., Aizawa, M., Inoue, M., Katayama, S., Kawakami, H., Nakamura, S., Nishimura, M., Akiguchi, I. *et al.* (1994) CAG expansions in a novel gene for Machado–Joseph disease at chromosome 14q32.1. *Nat. Genet.*, 8, 221–228.
- Cattaneo, E., Zuccato, C. and Tartari, M. (2005) Normal huntingtin function: an alternative approach to Huntington's disease. *Nat. Rev. Neurosci.*, 6, 919–930.
- Lim, J., Crespo-Barreto, J., Jafar-Nejad, P., Bowman, A.B., Richman, R., Hill, D.E., Orr, H.T. and Zoghbi, H.Y. (2008) Opposing effects of polyglutamine expansion on native protein complexes contribute to SCA1. *Nature*, 452, 713–718.
- Orr, H.T. (2012) Cell biology of spinocerebellar ataxia. J. Cell Biol., 197, 167–177.
- Chow, M.K., Mackay, J.P., Whisstock, J.C., Scanlon, M.J. and Bottomley, S.P. (2004) Structural and functional analysis of the Josephin domain of the polyglutamine protein ataxin-3. *Biochem. Biophys. Res. Commun.*, **322**, 387–394.
- Mao, Y., Senic-Matuglia, F., Di Fiore, P.P., Polo, S., Hodsdon, M.E. and De Camilli, P. (2005) Deubiquitinating function of ataxin-3: insights from the solution structure of the Josephin domain. *Proc. Natl. Acad. Sci. USA*, **102**, 12700–12705.
- Nicastro, G., Menon, R.P., Masino, L., Knowles, P.P., McDonald, N.Q. and Pastore, A. (2005) The solution structure of the Josephin domain of ataxin-3: structural determinants for molecular recognition. *Proc. Natl. Acad. Sci.* USA, 102, 10493–10498.
- Burnett, B., Li, F. and Pittman, R.N. (2003) The polyglutamine neurodegenerative protein ataxin-3 binds polyubiquitylated proteins and has ubiquitin protease activity. *Hum. Mol. Genet.*, 12, 3195–3205.
- Doss-Pepe, E.W., Stenroos, E.S., Johnson, W.G. and Madura, K. (2003) Ataxin-3 interactions with rad23 and valosin-containing protein and its associations with ubiquitin chains and the proteasome are consistent with a role in ubiquitin-mediated proteolysis. *Mol. Cell. Biol.*, 23, 6469–6483.
- Chai, Y., Berke, S.S., Cohen, R.E. and Paulson, H.L. (2004) Poly-ubiquitin binding by the polyglutamine disease protein ataxin-3 links its normal function to protein surveillance pathways. *J. Biol. Chem.*, **279**, 3605–3611.
- Tsai, Y.C., Fishman, P.S., Thakor, N.V. and Oyler, G.A. (2003) Parkin facilitates the elimination of expanded polyglutamine proteins and leads to preservation of proteasome function. *J. Biol. Chem.*, 278, 22044–22055.
- Ferro, A., Carvalho, A.L., Teixeira-Castro, A., Almeida, C., Tome, R.J., Cortes, L., Rodrigues, A.J., Logarinho, E., Sequeiros, J., Macedo-Ribeiro, S. *et al.* (2007) NEDD8: a new ataxin-3 interactor. *Biochim. Biophys. Acta*, 1773, 1619–1627.
- Wang, Q., Li, L. and Ye, Y. (2006) Regulation of retrotranslocation by p97-associated deubiquitinating enzyme ataxin-3. *J. Cell Biol.*, **174**, 963–971.
- Zhong, X. and Pittman, R.N. (2006) Ataxin-3 binds VCP/p97 and regulates retrotranslocation of ERAD substrates. *Hum. Mol. Genet.*, 15, 2409–2420.
- Rodrigues, A.J., Neves-Carvalho, A., Ferro, A., Rokka, A., Corthals, G., Logarinho, E. and Maciel, P. (2009) ATX-3, CDC-48 and UBXN-5: a new trimolecular complex in *Caenorhabditis elegans. Biochem. Biophys. Res. Comm.*, 386, 575–581.
- Li, F., Macfarlan, T., Pittman, R.N. and Chakravarti, D. (2002) Ataxin-3 is a histone-binding protein with two independent transcriptional corepressor activities. J. Biol. Chem., 277, 45004–45012.
- Evert, B.O., Araujo, J., Vieira-Saecker, A.M., de Vos, R.A., Harendza, S., Klockgether, T. and Wullner, U. (2006) Ataxin-3 represses transcription via chromatin binding, interaction with histone deacetylase 3, and histone deacetylation. J. Neurosci., 26, 11474–11486.
- Woelk, T., Sigismund, S., Penengo, L. and Polo, S. (2007) The ubiquitination code: a signalling problem. *Cell Div.*, 2, 11.
- Rodrigues, A.J., do Carmo Costa, M., Silva, T.L., Ferreira, D., Bajanca, F., Logarinho, E. and Maciel, P. (2010) Absence of ataxin-3 leads to

cytoskeletal disorganization and increased cell death. *Biochim. Biophys. Acta*, **1803**, 1154–1163.

- 32. Rodrigues, A.J., Coppola, G., Santos, C., Costa Mdo, C., Ailion, M., Sequeiros, J., Geschwind, D.H. and Maciel, P. (2007) Functional genomics and biochemical characterization of the *C. elegans* orthologue of the Machado–Joseph disease protein ataxin-3. *FASEB J.*, 21, 1126–1136.
- do Carmo Costa, M., Bajanca, F., Rodrigues, A.J., Tome, R.J., Corthals, G., Macedo-Ribeiro, S., Paulson, H.L., Logarinho, E. and Maciel, P. (2010) Ataxin-3 plays a role in mouse myogenic differentiation through regulation of integrin subunit levels. *PLoS One*, 5, e11728.
- Hynes, R.O. (1992) Integrins: versatility, modulation, and signaling in cell adhesion. *Cell*, 69, 11–25.
- Berrier, A.L. and Yamada, K.M. (2007) Cell-matrix adhesion. J. Cell. Physiol., 213, 565–573.
- George, E.L., Georges-Labouesse, E.N., Patel-King, R.S., Rayburn, H. and Hynes, R.O. (1993) Defects in mesoderm, neural tube and vascular development in mouse embryos lacking fibronectin. *Development*, 119, 1079–1091.
- Chun, D., Gall, C.M., Bi, X. and Lynch, G. (2001) Evidence that integrins contribute to multiple stages in the consolidation of long term potentiation in rat hippocampus. *Neuroscience*, **105**, 815–829.
- Chan, C.S., Weeber, E.J., Kurup, S., Sweatt, J.D. and Davis, R.L. (2003) Integrin requirement for hippocampal synaptic plasticity and spatial memory. *J. Neurosci.*, 23, 7107–7116.
- Sheng, L., Leshchyns'ka, I. and Sytnyk, V. (2013) Cell adhesion and intracellular calcium signaling in neurons. *Cell Commun. Signal.*, 11, 94.
- Denda, S. and Reichardt, L.F. (2007) Studies on integrins in the nervous system. *Methods Enzymol.*, 426, 203–221.
- Hoffner, G., Kahlem, P. and Djian, P. (2002) Perinuclear localization of huntingtin as a consequence of its binding to microtubules through an interaction with beta-tubulin: relevance to Huntington's disease. J. Cell Sci., 115, 941–948.
- Gunawardena, S. and Goldstein, L.S. (2005) Polyglutamine diseases and transport problems: deadly traffic jams on neuronal highways. *Arch. Neurol.*, 62, 46–51.
- McMurray, C.T. (2000) Neurodegeneration: diseases of the cytoskeleton? Cell Death Differ., 7, 861–865.
- Schafer, D.P., Jha, S., Liu, F., Akella, T., McCullough, L.D. and Rasband, M.N. (2009) Disruption of the axon initial segment cytoskeleton is a new mechanism for neuronal injury. *J. Neurosci.*, 29, 13242–13254.
- Balaratnasingam, C., Morgan, W.H., Bass, L., Kang, M., Cringle, S.J. and Yu, D.Y. (2011) Axotomy-induced cytoskeleton changes in unmyelinated mammalian central nervous system axons. *Neuroscience*, 177, 269–282.
- Duan, Y., Dong, S., Gu, F., Hu, Y. and Zhao, Z. (2012) Advances in the pathogenesis of Alzheimer's disease: focusing on tau-mediated neurodegeneration. *Transl. Neurodegener.*, 1, 24.
- Florenzano, F. (2012) Localization of axonal motor molecules machinery in neurodegenerative disorders. *Int. J. Mol. Sci.*, 13, 5195–5206.
- Pahlman, S., Ruusala, A.I., Abrahamsson, L., Mattsson, M.E. and Esscher, T. (1984) Retinoic acid-induced differentiation of cultured human neuroblastoma cells: a comparison with phorbolester-induced differentiation. *Cell Differ.*, 14, 135–144.
- Schmitt, I., Linden, M., Khazneh, H., Evert, B.O., Breuer, P., Klockgether, T. and Wuellner, U. (2007) Inactivation of the mouse Atxn3 (ataxin-3) gene increases protein ubiquitination. *Biochem. Biophys. Res. Commun.*, 362, 734–739.
- Liang, C.C., Park, A.Y. and Guan, J.L. (2007) In vitro scratch assay: a convenient and inexpensive method for analysis of cell migration in vitro. *Nat. Protoc.*, 2, 329–333.
- Melino, G., Thiele, C.J., Knight, R.A. and Piacentini, M. (1997) Retinoids and the control of growth/death decisions in human neuroblastoma cell lines. *J. Neuro-Oncol.*, **31**, 65–83.
- Constantinescu, R., Constantinescu, A.T., Reichmann, H. and Janetzky, B. (2007) Neuronal differentiation and long-term culture of the human neuroblastoma line SH-SY5Y. *J. Neural Transm. Suppl.*, 72, 17–28.
- Tucholski, J., Lesort, M. and Johnson, G.V. (2001) Tissue transglutaminase is essential for neurite outgrowth in human neuroblastoma SH-SY5Y cells. *Neuroscience*, **102**, 481–491.
- Mattila, P.K. and Lappalainen, P. (2008) Filopodia: molecular architecture and cellular functions. *Nat. Rev. Mol. Cell Biol.*, 9, 446–454.
- Legate, K.R., Wickstrom, S.A. and Fassler, R. (2009) Genetic and cell biological analysis of integrin outside-in signaling. *Genes Dev.*, 23, 397–418.
- Huttenlocher, A. and Horwitz, A.R. (2011) Integrins in cell migration. Cold Spring Harb. Perspect. Biol., 3, a005074.

- 57. Li, B.S., Ma, W., Jaffe, H., Zheng, Y., Takahashi, S., Zhang, L., Kulkarni, A.B. and Pant, H.C. (2003) Cyclin-dependent kinase-5 is involved in neuregulin-dependent activation of phosphatidylinositol 3-kinase and Akt activity mediating neuronal survival. J. Biol. Chem., 278, 35702–35709.
- Harada, T., Morooka, T., Ogawa, S. and Nishida, E. (2001) ERK induces p35, a neuron-specific activator of Cdk5, through induction of Egr1. *Nat. Cell Biol.*, 3, 453–459.
- Dlugosz, P.J., Billen, L.P., Annis, M.G., Zhu, W., Zhang, Z., Lin, J., Leber, B. and Andrews, D.W. (2006) Bcl-2 changes conformation to inhibit Bax oligomerization. *EMBO J.*, 25, 2287–2296.
- Cicero, S. and Herrup, K. (2005) Cyclin-dependent kinase 5 is essential for neuronal cell cycle arrest and differentiation. J. Neurosci., 25, 9658–9668.
- Schwartz, M.A. and Shattil, S.J. (2000) Signaling networks linking integrins and rho family GTPases. *Trend. Biochem. Sci.*, 25, 388–391.
- 62. Reina, C.P., Zhong, X. and Pittman, R.N. (2010) Proteotoxic stress increases nuclear localization of ataxin-3. *Hum. Mol. Genet.*, **19**, 235–249.
- Silva-Fernandes, A., Duarte-Silva, S., Neves-Carvalho, A., Amorim, M., Soares-Cunha, C., Oliveira, P., Thirstrup, K., Teixeira-Castro, A. and Maciel, P. (2014) Chronic treatment with 17-DMAG improves balance and coordination in a new mouse model of Machado–Joseph disease. *Neurotherapeutics*, 19, 235–249.
- Berke, S.J., Chai, Y., Marrs, G.L., Wen, H. and Paulson, H.L. (2005) Defining the role of ubiquitin-interacting motifs in the polyglutamine disease protein, ataxin-3. J. Biol. Chem., 280, 32026–32034.
- Vickers, J.C., King, A.E., Woodhouse, A., Kirkcaldie, M.T., Staal, J.A., McCormack, G.H., Blizzard, C.A., Musgrove, R.E., Mitew, S., Liu, Y. *et al.* (2009) Axonopathy and cytoskeletal disruption in degenerative diseases of the central nervous system. *Brain Res. Bull.*, 80, 217–223.
- Wu, C.H., Fallini, C., Ticozzi, N., Keagle, P.J., Sapp, P.C., Piotrowska, K., Lowe, P., Koppers, M., McKenna-Yasek, D., Baron, D.M. *et al.* (2012) Mutations in the profilin 1 gene cause familial amyotrophic lateral sclerosis. *Nature*, 488, 499–503.
- Nikolic, M., Dudek, H., Kwon, Y.T., Ramos, Y.F. and Tsai, L.H. (1996) The cdk5/p35 kinase is essential for neurite outgrowth during neuronal differentiation. *Genes Dev.*, **10**, 816–825.
- Kimura, T., Ishiguro, K. and Hisanaga, S. (2014) Physiological and pathological phosphorylation of tau by Cdk5. *Front. Mol. Neurosci.*, 7, 65.
- Niu, Y., Li, H., Herrup, K. and Zhang, J. (2012) Neuronal cell cycle regulation of Cdk5 in Alzheimer's disease. *Brain Disord. Ther.*, S1, 004.
- Gilmore, E.C., Ohshima, T., Goffinet, A.M., Kulkarni, A.B. and Herrup, K. (1998) Cyclin-dependent kinase 5-deficient mice demonstrate novel developmental arrest in cerebral cortex. *J. Neurosci.*, 18, 6370–6377.
- Tanaka, T., Veeranna, Ohshima, T., Rajan, P., Amin, N.D., Cho, A., Sreenath, T., Pant, H.C., Brady, R.O. and Kulkarni, A.B. (2001) Neuronal cyclin-dependent kinase 5 activity is critical for survival. *J. Neurosci.*, 21, 550–558.
- Li, B.S., Zhang, L., Takahashi, S., Ma, W., Jaffe, H., Kulkarni, A.B. and Pant, H.C. (2002) Cyclin-dependent kinase 5 prevents neuronal apoptosis by negative regulation of c-Jun N-terminal kinase 3. *EMBO J.*, 21, 324–333.
- Smith, D.S. and Tsai, L.H. (2002) Cdk5 behind the wheel: a role in trafficking and transport? *Trend. Cell Biol.*, 12, 28–36.
- Gupta, A. and Tsai, L.H. (2003) Cyclin-dependent kinase 5 and neuronal migration in the neocortex. *Neuro-Signals*, 12, 173–179.
- 75. Kesavapany, S., Li, B.S. and Pant, H.C. (2003) Cyclin-dependent kinase 5 in neurofilament function and regulation. *Neuro-Signals*, **12**, 252–264.

- Annweiler, C. and Beauchet, O. (2011) Vitamin D-mentia: randomized clinical trials should be the next step. *Neuroepidemiology*, 37, 249–258.
- 77. Lobert, V.H. and Stenmark, H. (2010) Ubiquitination of alpha-integrin cytoplasmic tails. *Commun. Integr. Biol.*, **3**, 583–585.
- Lobert, V.H., Brech, A., Pedersen, N.M., Wesche, J., Oppelt, A., Malerod, L. and Stenmark, H. (2010) Ubiquitination of alpha 5 beta 1 integrin controls fibroblast migration through lysosomal degradation of fibronectin-integrin complexes. *Dev. Cell*, **19**, 148–159.
- Kaabeche, K., Guenou, H., Bouvard, D., Didelot, N., Listrat, A. and Marie, P.J. (2005) Cbl-mediated ubiquitination of alpha5 integrin subunit mediates fibronectin-dependent osteoblast detachment and apoptosis induced by FGFR2 activation. J. Cell Sci., 118, 1223–1232.
- Johannesson, M., Stahlberg, A., Ameri, J., Sand, F.W., Norrman, K. and Semb, H. (2009) FGF4 and retinoic acid direct differentiation of hESCs into PDX1-expressing foregut endoderm in a time- and concentration-dependent manner. *PLoS One*, 4, e4794.
- Fujigasaki, H., Uchihara, T., Koyano, S., Iwabuchi, K., Yagishita, S., Makifuchi, T., Nakamura, A., Ishida, K., Toru, S., Hirai, S. *et al.* (2000) Ataxin-3 is translocated into the nucleus for the formation of intranuclear inclusions in normal and Machado–Joseph disease brains. *Exp. Neurol.*, 165, 248–256.
- Takahashi, J., Tanaka, J., Arai, K., Funata, N., Hattori, T., Fukuda, T., Fujigasaki, H. and Uchihara, T. (2001) Recruitment of nonexpanded polyglutamine proteins to intranuclear aggregates in neuronal intranuclear hyaline inclusion disease. *J. Neuropathol. Exp. Neurol.*, **60**, 369–376.
- Uchihara, T., Fujigasaki, H., Koyano, S., Nakamura, A., Yagishita, S. and Iwabuchi, K. (2001) Non-expanded polyglutamine proteins in intranuclear inclusions of hereditary ataxias—triple-labeling immunofluorescence study. *Acta Neuropathol.*, **102**, 149–152.
- Broderick, J., Wang, J. and Andreadis, A. (2004) Heterogeneous nuclear ribonucleoprotein E2 binds to tau exon 10 and moderately activates its splicing. *Gene*, 331, 107–114.
- Seilhean, D., Takahashi, J., El Hachimi, K.H., Fujigasaki, H., Lebre, A.S., Biancalana, V., Durr, A., Salachas, F., Hogenhuis, J., de The, H. *et al.* (2004) Amyotrophic lateral sclerosis with neuronal intranuclear protein inclusions. *Acta Neuropathol.*, **108**, 81–87.
- Winborn, B.J., Travis, S.M., Todi, S.V., Scaglione, K.M., Xu, P., Williams, A.J., Cohen, R.E., Peng, J. and Paulson, H.L. (2008) The deubiquitinating enzyme ataxin-3, a polyglutamine disease protein, edits Lys63 linkages in mixed linkage ubiquitin chains. *J. Biol. Chem.*, 283, 26436–26443.
- 87. Moffat, J., Grueneberg, D.A., Yang, X., Kim, S.Y., Kloepfer, A.M., Hinkle, G., Piqani, B., Eisenhaure, T.M., Luo, B., Grenier, J.K. *et al.* (2006) A lentiviral RNAi library for human and mouse genes applied to an arrayed viral high-content screen. *Cell*, **124**, 1283–1298.
- Aguirre, P., Valdes, P., Aracena-Parks, P., Tapia, V. and Nunez, M.T. (2007) Upregulation of gamma-glutamate-cysteine ligase as part of the long-term adaptation process to iron accumulation in neuronal SH-SY5Y cells. *Am. J. Phys. Cell Physiol.*, **292**, C2197–C2203.
- Nicklas, W., Baneux, P., Boot, R., Decelle, T., Deeny, A.A., Fumanelli, M. and Illgen-Wilcke, B. (2002) Recommendations for the health monitoring of rodent and rabbit colonies in breeding and experimental units. *Lab. Anim.*, 36, 20–42.
- 90. Pfaffl, M.W. (2001) A new mathematical model for relative quantification in real-time RT-PCR. *Nucleic Acids Res.*, **29**, e45.

Supplementary Material



Figure S1. Establishment of a neuronal cell line with stably silenced ATXN3. (A, B) ATXN3^{±hRMA} cells showed a high decrease in ATXN3 expression, as compared to SCR^{±hRMA} and empty vector (pLKO.1) control cells. The ATXN3 level in the pLKO.1 cells expressing the empty vector was considered as 100% and α-tubulin was used as a loading control. (C) qRT-PCR analysis showed that transcript levels of genes encoding ATXN3L and JOSD1 and JOSD2 proteins were similar between ATXN3^{±hRMA} and SCR^{±hRMA} cells. (D, E) PC12_ATXN3^{±hRMA} cells showed a high decrease in ATXN3 levels, as compared to PC12_SCR^{±hRMA} cells. The results were normalized for MCT4 levels. (F) Increased expression of *ITGA5* in both SCR^{±hRMA} and ATXN3^{±hRMA} cells overexpressing ITGA5. mRNA levels were normalized to *HBMS* gene. *p<0.05.



Figure S2. Survival and cell cycle progression are not altered in non-differentiated neuronal cells lacking ATXN3. (A) ATXN3^{dhRNA} cells were flattened as compared with the SCR^{dhRNA} cells. (B) ATXN3 knockdown increased SH-SY5Y cell migration in a wound scratch assay. Bars represent migration rate expressed as a percentage of control and calculated as the proportion of the mean distance that remained cell-free after 24 hours. (C, D) Flow cytometry analysis using PI showed no alterations of the cell cycle progression in ATXN3^{dhRNA} cells. (E) No effect on cell survival measured by propidium iodide (PI) incorporation caused by silencing of ATXN3. (F) Phalloidin staining (green) showed no major defects on the actin cytoskeleton in ATXN3^{dhRNA} cells as compared with the controls. Nuclei were counterstained with DAPI (purple). Scale bar: 20 μm. ***p<0.001.



Figure S3. ATXN3 silencing does not affect expression of RA-responsive genes and does not alter the mRNA levels of several integrin subunits (A) Transcript levels of *tTG*, a RA-responsive gene, were not altered in ATXN3⁺ cells suggesting that these cells respond to RA treatment. (B) ATXN3 did not regulate the amounts of *ITGA5* in SH-SY5Y cells as measured by qRT-PCR. mRNA levels are normalized to *HBMS* gene.



Figure S4. The phenotype of ATXN3^{thRNA} cells is ITGA5-related. (A) Western blot analysis showed no differences in alpha-1 integrin levels comparing ATXN3^{thRNA} and the SCR^{thRNA} control cells. (B) Wound scratch assay showed no differences on migration comparing ATXN3^{thRNA} and the SCR^{thRNA} control cells, when using Laminin or Poly-D-Lysine coatings, 24 h after scratching.



В



Figure S5. Overexpression of both catalytic and expanded mutant versions of ATXN3 results in an abnormal cell morphology. (A) Overexpression of Wild type (ATXN3_28Q), catalytic mutant (ATXN3_C14A) or expanded ATXN3 (ATXN3_83Q) in SH-SY5Y cells. mRNA levels were normalized to *HMBS* gene. (B) Cells overexpressing catalytic mutant (ATXN3_C14A) or expanded ATXN3 (ATXN3_83Q) cells failed to acquire a neuron-like morphology as compared with their counterpart controls, after RA treatment. Scale bar: 100 μ m. *p<0.05, ***p<0.001.



Figure S6. Characterization of a PC12 neuronal cell line with stably silenced ATXN3. (A) PC12_ATXN3^{thma} cells were less elongated and showed shorter extensions as compared with the PC12 SCR structure control cells after NGF treatment. Scale bar: 100 µm. NGF treatment did not inhibit proliferation of PC12_ATXN3^{thRMA} cells as seen by optical microscopy (B) and (C, D) Ki-67 staining (red). Nuclei were counterstained with DAPI (blue). Scale bar: 200 µm. (E) Flow cytometry analysis using propidium iodide (PI) showed increased cell death in PC12_ATXN3^{shma} cultures. (F) qRT-PCR analysis of the variation of neuronal markers after NGF treatment showed that mRNA levels were decreased for βIII-tubulin and Tau in PC12_ATXN3^{MMM} cultures. Transcript levels were normalized to levels in undifferentiated cells and to HMBS gene expression. (G) Phalloidin staining (green) showed that the actin cytoskeleton was less spread than in control cells, with less extensions, and that actin filaments were disorganized and not parallel in PC12_ATXN3 mere cells. Nuclei were counterstained with DAPI (purple). Arrows mark evidences for higher adhesion in control cells and asterisks mark microspikes in PC12_ATXN3^{shRNA} cells. Scale bar: 20 µm. (H, I) Western blot analysis showed a decrease of ITGA5 levels in PC12_ATXN3shrma cells. The results were normalized for MCT4 expression. (J) ATXN3 did not regulate the amounts of ITGA5 mRNA expression in PC12 cells, measured by qRT-PCR. mRNA levels were normalized to HMBS gene expression.

Chapter 3

Perturbation of ATXN3 function leads to tau splicing deregulation

and contributes to Machado-Joseph disease

Perturbation of ATXN3 function leads to Tau splicing deregulation and contributes to Machado-Joseph disease

Neves-Carvalho A^{1,2}, Silva J^{1,2}, Heetveld S³, Jain S³, Freitas A^{1,2}, Sotiropoulos I^{1,2}, Heutink H³ and Maciel P^{1,2}

¹ Life and Health Sciences Research Institute (ICVS), School of Health Sciences, University of Minho, 4710-057 Braga, Portugal, ² ICVS/3B's – PT Government Associate Laboratory, Braga/Guimarães, Portugal, ³ German Center for Neurodegenerative Diseases (DZNE), Tübingen, Germany

ABSTRACT

The microtubule-binding protein tau is important for normal neuronal function in the nervous system. Alternative splicing of tau exon 10 originates tau isoforms including 3 or 4 microtubulebinding repeats – 3R or 4R tau. Disruption of the 4R/3R tau ratio has been suggested to contribute to several neurodegenerative disorders. Ataxin-3 (ATXN3) is a protein with deubiquitylating (DUB) activity, known to bind microtubules and to regulate cytoskeletal organization. Expansion of a polyglutamine tract in the C-terminus of ATXN3 causes Machado-Joseph Disease (MJD) (also known as Spinocerebellar ataxia type 3 – SCA3). Here we show that loss of function of ATXN3 leads to a deregulation of tau exon 10 splicing resulting in a decreased 4R/3R tau ratio, negatively impacting in neuronal morphology and differentiation. Additionally, we found that SFRS7 (9G8), a regulator of tau exon 10 splicing, physically interacts with ATXN3 and shows altered polyubiquitylation patterns in neuronal cells lacking this protein. The fact that similar alterations were found in the brain of a mouse model of MJD expressing mutant human ATXN3 with an expanded polyglutamine tract, suggests that this mechanism might be contributing for the pathogenesis of MJD, and establishes a link between two key proteins involved in different neurodegenerative disorders.

INTRODUCTION

Tau proteins are microtubule-associated proteins (MAPs) predominantly expressed in neurons (Reviewed in [1]). Their major known biological function is the assembly and stabilization of microtubules, contributing to morphogenesis, cell division, axonal extension and axonal transport (Reviewed in [2]). Alternative splicing of the tau (*MAPT*) gene generates tau isoforms containing 3 or 4 microtubule binding repeats, 3R tau or 4R tau [3, 4], in a 1:1 ratio [5, 6]. Although approximately

77

equal levels of 3R tau and 4R tau are found in a normal human adult brain, their expression is developmentally controlled, suggesting that the regulation of tau isoforms is important during brain formation [5, 7]. Disruption of the 4R/3R tau isoform ratio has been associated with neurodegenerative diseases. For example, it was found that the splicing of tau exon 10 was disrupted in some individuals with Frototemporal dementia with Parkinsonism liked to chromosome 17 (FTDP-17) carrying silent and intronic mutation in *tau* gene (Reviewed in [8]). More recently, it was also demonstrated that the HTT mutation leads to an increase of the 4R/3R tau isoform ratio, which seems to contribut for Huntington Disease (HD) pathogenesis [9]. In addition to FTDP-17 and HD, altered 4R/3R tau ratio was also reported in Alzheimer's disease (AD) brains, but the observations from different reports are contradictory; while some show an increase in 4R tau isoform, others report lower 4R/3R tau ratio values [10-14]. One possible explanation is that this ratio is differentially regulated in the different pathological conditions. Furthermore, exon 10 splicing is controlled by a complex set of splicing factors whose activity might be differentially affected in different diseases and/or by the Thus, the maintenance of this delicate balance appears to be critical for neuronal function (Reviewed in [11, 15-18]), and dependent on multiple etiological factors. The mechanism by which the 4R/3R tau ratio is disrupted in neurological diseases is still not completely understood. Alternative splicing of the MAPT gene has been shown to be regulated by enhancers and silencers as well as by trans factors and their phosphorylation [19-24], mostly belonging to two superfamilies – the SR (serine/arginine-rich)/SR-like and hnRNP (heterogeneous nuclear ribonucleoproteins) proteins (Reviewed in [25, 26]). One such protein, the SFRS7 (serine/arginine splicing factor 7), also known as 9G8 [27], is believed to participate in the regulation of tau exon 10 alternative splicing [28, 29], usually acting as a splicing activator, leading to tau exon 10 inclusion [30-32]. Thus, an alteration of SFRS7 expression or function may be critical for both the splicing regulation and the disease-causing potential of the tau proteins. Deubiquitinating (DUB) enzymes modify ubiquitin (Ub) chains removing Ub units, and play an important role in the modulation of the degradation of proteins by the proteasome (Reviewed in [33-35]) and in ubiquitin signaling in general. Ataxin-3 (ATXN3) is a protein with DUB activity, known to cause neurodegeneration in Machado-Joseph disease (MJD) [36], Interestingly, in addition to being involved in the ubiquitin-proteasome pathway (UPP) [37, 38], ATXN3 appears to play a role in the organization of the cytoskeleton network [39-41] has the ability to bind to microtubules and dynein [39, 40, 42], and seems to be involved in transcriptional regulation and DNA repair [43]. Additionally, our previous data suggested that SH-SY5Y cells lacking ATXN3 show decreased levels of the adhesion protein α 5-integrin (ITGA5), resulting in abnormal differentiation and decreased expression of several neuronal markers, including tau. Interestingly, overexpression of ITGA5 ameliorated the neuronal phenotype of these cells and normalized the expression of most of the differentiation markers, but it did not rescue the levels of TAU, suggesting that complementary mechanisms are in place.

In this work, we studied the effect of loss of function of ATXN3 on tau expression in neurons. We show that depletion of ATXN3 in SH-SY5Y cells led to a deregulation of tau exon 10 splicing which perturbs the 3R/4R tau ratio, a mechanism that seems to contribute for MJD pathogenesis.

MATERIALS AND METHODS

Cell culture

Human neuroblastoma SH-SY5Y cells (ATCC, CRL-2266) were transfected with a shRNA sequence targeting *ATXN3* or with a scrambled shRNA sequence as described before [41]. Stably infected cells were cultured in DMEM/F-12 (Invitrogen) supplemented with 10% (v/v) Fetal Bovine Serum (Biochrom), 2mM glutaMAX (Invitrogen), 100 U/mL penicillin, 100 µg/mL streptomycin and 25 ng/mL puromycin (Sigma Aldrich). Cells were maintained in a humidified 37°C/95%-air/5%-CO₂ incubator. The medium was replaced every two days. Differentiation was induced by 0.1 µM all-trans-retinoic acid (RA) (Sigma Aldrich) in opti-MEM (Invitrogen) supplemented with 0.5% FBS for 7 days. The medium was changed every two days.

Vectors and lentivirus packaging

The packaging cell line (HEK293T) was plated at a density of 3x10⁵ cells per well in 6-well plates, cultured in opti-MEM supplemented with 10% FBS, and transfected on the following day with the pEYFP-N1_3R1N vector, the pEYFP-N1_4RN1 vector or the empty vector pEGFP for virus production, following the RNAi Consortium High-Throughput Lentiviral production protocol [44]. The medium was changed the next day and cells were cultured for 48 h. The conditioned medium, containing the viruses, was then collected and stored at -80°C.

Transduction of target cells

SH-SY5Y cells with stably silenced ATXN3 expression (ATXN3+hm) and the scrambled shRNA controls (SCR+hm) [41] were cultured at a density of 2.5x10⁵ on a 6-well plate with 2 mL of complete DMEM/F-12 medium and transduced with the lentiviral vectors. The medium was changed 24h after, and cells were incubated for 72h. Expression of the constructs was evaluated by fluorescence microscopy (GFP expression) and qRT-PCR. The transduced cell lines were cultured in complete DMEM/F-12 medium containing 2.5 µg/mL puromycin, passaging every 3-5 days.

RT² **PROFILER**[™] **PCR** array analysis of human cytoskeleton regulators

The mRNA expression level of 84 key genes related to the intracellular scaffolding's biogenesis, organization, polymerization and depolymerization, of 5 housekeeping genes and of controls for DNA contamination, reverse transcription and PCR efficiency, were determined simultaneously using Superarray technology (SABiosciences[™]). For this experiment, 5x10⁴ RA-treated SH-SY5Y cells were collected by trypsinization, immediately frozen in liquid nitrogen and stored a -80°C. The RNA extraction was done using the RNasy® micro kit (Qiagen) following the manufacturer's instructions. RNA samples were suspended in RNase-free water and RNA quality was monitored using the Experion[™] Automated electrophoresis System (BioRad). 1µg of total RNA was first converted into first-strand cDNA using the RT² First strand kit (SABiosciences[™]) and the RT-qPCR reaction was performed using the RT² SYBR Green Mastermix (SABiosciences[™]), following the manufacturer's guidelines. A total of 3 arrays per condition was hybridized.

Pulldown of polyubiquitylated proteins

RA-treated ATXN3^{±INMA} and SCR^{±INMA} cells were lysed by sonication on ice in lysis buffer (50 mM Tris-HCI pH 7.5, 0.15 M NaCI, 1mM EDTA, 1% NP-40, 10% Glycerol, protease inhibitors (Roche) and 50µM UB/UBI protease inhibitor PR-619 (LifeSensors)). After lysis, 2 mg of total protein extract were incubated with 50 µL of pre-equilibrated Agarose-TUBEs 2 (LifeSensors), overnight at 4°C on a rocking platform. Sedimented beads were washed 3 times with washing buffer (20 mM Tris pH 8.0, 0.15 M NaCl, 0.1% Tween-20) before being eluted with 1x Laemmli buffer (62,5mM Tris-HCl pH 6.8, 10% glycerol, 2% SDS, Bromophenol Blue). Eluted proteins were immediately boiled at 98°C for 15min and separated/analyzed in a 10% SDS-PAGE gel.

Cell fractionation

RA-treated pelleted cells were resuspended in iced cold RSB buffer (10 mM Tris-HCl pH 7.4, 10 M NaCl) and incubated on ice for 3 min. After centrifugation for 5 min, 4000 rpm at 4°C, the pellet was resuspended in RSBG40 buffer (10 mM Tris-HCl pH 7.4, 10 mM NaCl, 3 mM MgCl₂, 10% glycerol, 0,5% NP-40, 0,5 mM DTT) and centrifuged for 3 min, 7000 rpm at 4°C. The supernatant was collected as cytoplasmic fraction and stored at -80°C. The nuclear pellet was resuspended in 50 μ L B1 buffer (20 mM Tris-HCl pH 7.9, 75 mM NaCl, 5% glycerol, 0.5 mM EDTA, 0.85 mM DTT, 0.125 mM PMSF) and 450 μ L B2 buffer (20 mM HEPES pH 7.6, 300 mM NaCl, 0.2 mM EDTA, 1 mM DTT, 7,5 mM MgCl₂, 1 M Urea, 1% NP-40). Samples were vortexed for 5 sec, incubated on ice for 10 min and centrifuged for 5 min, 15000 rpm at 4°C. The supernatant was collected as nuclear fraction and stored at -80°C.

Immunoprecipitation

RA-treated cells were washed in ice-cold PBS and lysed by sonication on ice in NP-40 buffer. Aliquots were taken from protein extracts as 10% inputs. 1 mg of total protein were pre-cleared for 3 h at 4°C by incubation with glutathione-coupled sepharose beads (GE Healthcare) previously equilibrated in Wash buffer 1 (50 mM Tris-HCI pH 7.5, 150 nM NaCl, 1% NP-40, 1x protease inhibitors (Roche)) for 3 times, 10 min at 4°C. Beads were then centrifuged and the supernatant was incubated O/N at 4°C with 50 μ L equilibrated beads. After centrifugation, the supernatant was discarded and the beads were washed 2 times with Wash buffer 1 for 10 min at 4°C. Beads were then washed twice with Wash buffer 2 (50 mM Tris-HCl pH 7.5, 500 mM NaCl, 0.1% NP-40) for 10 min at 4°C, and once with Wash buffer 3 (50 mM Tris-HCL pH 7.5, 0.1% NP-40) for 20 min at 4°C. The supernatant was discarded and the bound proteins were eluted with 1x Laemmli buffer, boiled for 5 min at 98°C and run in a 10% SDS-PAGE gel.

Immunoblotting

RA-treated cells were pelleted and frozen in liquid nitrogen. For cellular extracts, 50µg of total protein isolated in NP-40 buffer (150 mM NaCl, 50 mM Tris-HCl pH 7.6, 0.5% NP-40, protease inhibitors (Roche)). For CMVMJD135 brain tissue extracts, brain tissue was homogenized in cold 0.1 M Tris-HCl pH 7.5, 0.1 M EDTA and protease inhibitors (Roche), and sonicated for 10s. Samples were resolved in 10% SDS-PAGE gels and then transferred to a nitrocellulose membrane. After incubation with the primary antibodies: TAU-5 (1:2000, Abcam), TAU-4R (1:1000, Millipore),

TAU-3R (1:2000, Millipore), TAU (E178) (1:1000, Abcam), Histone H3 (1:10000, Abcam), SFRS7 (9G8) (1:1000, kindly provided by Dr. James Stévine), actin (1:200, DSHB) overnight at 4°C, membranes were incubated with secondary antibodies for 1 hour at room temperature (anti-rabbit or anti-mouse, 1:10000, Bio-Rad, anti-goat, 1:5000, Santa-Cruz Biotecnhologies). Antibody binding was detected by chemiluminescence (Clarity kit, Bio-Rad).

High-throughput high-content functional imaging

Cells were seeded at an initial density of $4x10^3$ cells/well in flat bottom 96-well plates previously coated with Matrigel (BD, Biosciences), and 0.1 μ M RA was added the day after plating in DMEM/F-12 with 1% FBS. After 5 days, cells were washed with DMEM/F-12 and incubated with 50 ng/mL BDNF (Peprotech) in DMEM/F-12 without serum for 3 days. Cells were then labeled by immunocytochemistry for β III-tubulin (1:1000, R&D Systems) and scanned at different locations of each well. The quantitative analysis of total number of cells, number of β III-tubulin positive cells and neurite length was performed using the automatic imaging system Thermo Scientific Cellomics® ArrayScan® VTI.

qRT-PCR

1 μg of total RNA purified from differentiated cells was reversed transcribed using the Onestep SuperScript kit (Bio-Rad). The qRT-PCR reaction was performed in a CFX96 Real-time PCR detection system (Bio-Rad) using the Quantitec SYBR Green kit (Qiagen) and the primers listed on Table 1. Gene expression was normalized to *HMBS* levels within each sample. Results are presented as fold change, comparing ATXN3^{shRMA} with SCR^{shRMA} control cells.

Animals

The MJD mouse model (CMVMJD135) was generated as described [45]. All animal procedures were conducted in accordance with European regulations (European Union Directive 86/609/EEC) and approved by the joint Animal Ethics Committee of the Life and Health Sciences Research Institute, University of Minho. Health monitoring was performed according to FELASA guidelines [46]. Animal facilities and the people directly involved in animal experiments were certified by the Portuguese regulatory entity – Direcção Geral de Veterinária [46]. CMVMJD135 mice and control littermates were sacrificed at 45 weeks of age by decapitation, the brainstem (an affected area) was immediately removed and stored at -80°C.
Statistical analysis

For PCR arrays, data was analyzed using the SPSS software version 22.0. In order to identify differentially expressed genes having biological relevance, significantly altered genes identified by SPSS analysis (p<0.05) were further filtered using a 1.5 fold change cut-off. For all the other comparisons between the different cell lines were performed using t-test in the GraphPad prism version 5.0 software. For immunoblotings, the mean density and area of each band was measured using at least three experiments in TINA 2.0 software according to the manufacturer's instruction. For real-time quantitative PCR data, the same approach was used and results were presented using the $\Delta\Delta$ Ct method, as described before [47]. A critical value for significance of two-tailed p<0.05 was used throughout the study.

RESULTS

Silencing of ATXN3 leads to changes in gene expression of cytoskeleton regulators

Loss of function of ATXN3 was previously shown to cause a disruption of the cytoskeleton network [39, 40], loss of cell adhesion and perturbed differentiation [40], namely in neuronal cells [41]. Although increased degradation of alpha-5-integrin (ITGA5) - leading to loss of cell adhesion and altered signaling to the cytoskeleton - partially explains this cellular phenotype, the detailed mechanisms underlying the extensive modifications of the cytoskeleton remain mostly unknown. In the attempt to further define the pathways that are deregulated in the absence of ATXN3, specifically those affecting cytoskeletal organization, we quantified by qRT-PCR the expression of 84 genes controlling cytoskeleton biogenesis, fiber arrangement, polymerization and depolymerization, in Retinoic Acid (RA)-treated SH-SY5Y cells with stable silencing of ATXN3 (ATXN3 the cells). This analysis revealed a number of significant changes in expression, mostly corresponding to downregulation of cytoskeleton regulatory genes in ATXN3^{6/RNA} cells (Table 1). The 28 differentially expressed genes were distributed across different functional groups, related to cell projections (38%), kinases and phosphatases (38%), G-protein signaling (33.3%), actin filaments (28.6%), cell motility/migration (23.8%), cell cycle and division (9.5%), cytoskeleton adaptor activity (9.5%), calmodulin/calcineurin (9,5%), microtubules (4.8%), cell shape, size, polarity and morphogenesis (4.8%). This provided further evidence that ATXN3 is involved in the modulation of the cytoskeleton network and that its absence triggers changes in several important regulators.

Interestingly, we confirmed that the neurodegeneration-related gene *MAPT*, encoding the Tau protein, was among those with significantly reduced expression in ATXN3^{shRMA} cells and belonged to one of the most representative functional groups (cell projections). As mentioned above, our previous data suggested that the neuronal phenotype of ATXN3^{shRMA} cells was partial explained by the reduced levels of ITGA5 in these cells [41]. Interestingly, overexpression of ITGA5 in ATXN3^{shRMA} cells ameliorated their neuronal phenotype and normalized the expression levels of several neuronal markers, but did not rescue the levels of *TAU*. Hence, we focused our analysis on the role of this specific gene and protein in cells lacking ATXN3.

RefSeq	Gene name	Description	Group	p value	Fold change
NM_005910	MAPT	Microtubule-associated protein tau	Cell projections/ microtubules	0.000	-1.93
NM 002491	00010100	Protein phosphatase 1, regulatory	Cell prejections (kingson and pheepheteens	0.001	2.20
NW_002461	FFF1R12D	(inhibitor) subunit 12B	Cell projections/ kinases and prosphatases	0.001	-2.29
NM 002041	WASI	Wickott Aldrich syndroma lika	Actin filaments/ cell projections/ cell	0.001	2 70
NWI_003941	WASL	WISKOU-AIGHCH Syndrome-like	motility/migration/ G-protein signalling	0.001	-3.70
NM 00717/	CIT	Citron (rho-interacting, serine/threonine	Kinases and phosphatases/ cell cycle/	0.002	1 70
NM_007174	CIT	kinase 21)	division/ G-protein signalling	0.002	-1.75
NM_003914	CCNA1	Cyclin A1	Cell cycle and cell division	0.003	-2.95
NM 005719		Actin related protein 2/3 complex,	Actin filaments (cell motility/migration	0.004	1 66
NWI_003713	ANI CO	subunit 3, 21kDa		0.004	1.00
NM 000377	WAS	Wiskott-Aldrich syndrome (eczema-	Cell motility/migration/ G-protein signalling	0.004	-2 88
1111_000077	in lo	thrombocytopenia)		0.004	2.00
NM_001175	ARHGDIB	Rho GDP dissociation inhibitor (GDI) B	Actin filaments/cell motility/G-protein signalling	0.004	-15.29
NM 002754	MAPK13	Mitogen-activated protein kinase 13	Kinases and phosphatases/	0 007	-2 75
NW_002754 WAI N15			G-protein signalling	0.007	2.70
NM_033389	SSH2	Slingshot homolog 2 (Drosophila)	Actin filaments/ kinases and phosphatases	0.008	-2.04
NM_000381	MID1	Midline 1 (Opitz/BBB syndrome)	Microtubules	0.009	-2.41
			Actin filaments/ cell projection/ cell shape,		
NM_014376	CYFIP2	Cytoplasmic FMR1 interacting protein 2	size, polarity/ morphogenesis/ G-protein	0.009	-1.37
			signlling		
NM 003885		Cyclin-dependent kinase 5, regulatory	Cell projections/ cell motility/migration/	0.010	1 96
NM_0000000	ODIIGINI	subunit 1 (p35)	kinases and phosphatases	0.010	-1.50
NM_005219	DIAPH1	Diaphanous homolog 1 (Drosophila)	Actin filaments/ G-protein signalling	0.011	-5.41
NM 002480	PPP1R12A	Protein phosphatase 1, regulatory	Cell projections / kinases and phosphatases	0.012	-1 81
NM_002400		(inhibitor) subunit 12A		0.012	-1.01
NM 003253	TIAM1	T-cell lymphoma invasion and metastasis	G-protein signalling	0.013	-1 65
1111_000200	10,001	1		0.010	1.00
NM 053025	MYLK	Mvosin light chain kinase	Calmodulin/calcineurin/ kinases and	0.015	-1.71
			phosphatases		

Table 1. Changes in gene expression of cytoskeleton regulators. The fold change is the average of 3 biological replicates. A fold change of 1.5 was used as a cut-off.

NM_017737	FNBP1L	Formin binding protein 1-like	Actin filaments	0.018	-2.12
NM 003160	AURKC	Aurora kinase C	Cell cycle and cell division/ kinases and	0 020	-2 40
	, lotato		phospatases	0.020	2.10
NM_012418	FSCN2	Fascin homolog 2, actin-bundling protein,	Actin filaments	0.020	-6.94
		retinal			
NM 003688	CASK	Calcium/calmodulin-dependent serine	Actin filaments, calmodulin/ calcineurin/	0.024	-1.55
1111_000000	on on t	protein kinase	kinases and phosphatases	0.021	
NM 006340	RAIAD2	RALL accordated protain 2	Cell projections/ cytoskeleton	0.025	-2.73
1111_000340			adpator activity	0.025	
NM 002576		P21 protein (Cdc42/Rac)-activated	Cytoskeleton adaptor activity/ kinases and	0.020	-1.46
NWI_002570	FANI	kinase 1	phosphatases	0.029	
	200 נפט וווס	Pleckstrin homology-like domain, family	Migratubulas	0.025	-1 99
NM_145753 PHLDB2		B, member 2	Microtubules	0.055	-1.99
NM 004025	CDKE	DKE Ovelin dependent kingse 5	Cell projections/ cell motility/migration/	0.042	-1.52
14141_004955	CDNS	Cyclin-dependent kinase 5	kinases and phosphatases	0.045	
NM 004054	MADKO	MAP/microtubule affinity-regulating	Kinases and phosphatases/ cell shape,	0.044	0.00
NW_004904	MARKZ	kinase 2	size, polarity, morphogenesis	0.044	-2.33
			Calmodulin/calcineurin/ cell shape,		
NM_033118	MYLK2	Myosin light chain kinase 2	size, polarity, morphogenesis/ kinases and	0.047	-3.92
			phosphatases		
NM 002444	MON	Moosin	Cell projections/ cell motility/migartion/	0.052	1 66
11110_002444	NICIN	WOESIN	cytoskeleton adaptor activity	0.000	1.00

ATXN3 loss of function perturbs the 4R/3R tau ratio in SH-SY5Y cells

Tau is a neuronal microtubule-associated protein of known relevance for the morphology, differentiation and survival of neurons, and is involved in central pathways of several neurodegenerative disorders (Reviewed in [48-50]. Considering this and taking into account the importance of a balanced ratio of 4R/3R tau isoforms in neurons, we next analyzed mRNA levels of these isoforms in ATXN3^{chRNA} and SCR^{chRNA} cells. We found a significant decrease (4.7 fold decrease, p=7.4x10⁻¹¹) of the 4R tau isoform in ATXN3^{chRNA} cells (Figure 1A), but no alteration of the 3R tau isoform (p=0.270) as compared with SCR^{chRNA} control cells (Figure 1B), leading to an altered 4R/3R tau ratio (Figure 1C).

Interestingly, overexpression of a catalytically inert version of ATXN3 in SH-SY5Y cells (ATXN3_C14A) recapitulated the alterations on tau isoform expression seen in cells with silenced ATXN3, leading to decreased expression of total tau (5.7 fold decrease, $p=3.7x10^{\circ}$) (Figure 1D), decreased 4R tau expression (4.4 fold decrease, $p=1.1x10^{\circ}$) (Figure 1E) with no alterations on the 3R tau isoform (Figure 1F), and decreased 4R/3R tau ratio (p=0.0088) (Figure 1G).



Figure 1. Disruption of 4R/3R tau ratio in ATXN3^{thRNA} cells. (A) Depletion of ATXN3 lead to decreased transcripts levels of 4R tau and (B) no alterations in the mRNA levels of the 3R tau isoform. (C) ATXN3^{thRNA} cells showed a significant decrease of the 4R/3R tau ratio comparing with the SCR^{thRNA} controls. ATXN3_C14A cells present (D, E) decreased mRNA levels of tau and 4R tau isoform, (F) no alterations in 3R tau expression and (G) decreased 4R/3R tau ratio. 4R/3R tau ratio was obtained by dividing 4R and 3R tau mRNA levels. **p<0.01; ***p<0.001.

Normalizing the levels of 4R tau isoform partially rescues the neuronal phenotype of ATXN3^{shRMA} cells

Besides the cytoskeleton deregulation, depletion of ATXN3 seems to perturb the differentiation process in neuronal cells, as we have previously described [41]: after induction of differentiation by RA treatment, ATXN3^{anna} cells keep their proliferative activity (in spite of a parallel increase in cell death) and show decreased expression of several differentiation markers. Considering that the balance between tau isoforms is important for neuronal development (Reviewed in [51]) and that the 4R isoform suppresses proliferation and promotes neuronal differentiation [52],

we hypothesized that the deregulation of the 4R/3R tau ratio might be contributing to the neuronal phenotype observed in ATXN3 MARKA cells. In order to test this hypothesis, we overexpressed the 3R or 4R tau isoforms in ATXN3shrna cells (ATXN3shrna_3R and ATXN3shrna_4R, respectively) (Figure S1) and evaluated their ability to differentiate into neuronal cells upon RA treatment. Indeed, the expression levels of several neuronal differentiation markers (MAP2, β III-tubulin, neurogenin and DAT), which we had previously identified as reduced in cells lacking ATXN3 [41], were comparable between ATXN3shma_4R and SCRshma_4R cells and the increased expression of Nestin, a marker for proliferative cells [53] was also rescued by 4R tau isoform overexpression (Figure 2A). Accordingly, and in contrast with the observations in cells lacking ATXN3, the number of cells was similar between ATXN3shrwa_4R and SCRshrwa_4R (p=0.422) 7 days after induction of differentiation with RA (Figure 2B). Additionally, the number of *β*III-tubulin positive cells was not significantly different among the two cell lines (p=0.8727) and thus restored if we compare them with those of cells after ATXN3 silencing (fATXN3^{shrwa}) (Figure 2C). The average neurite length was also restored in ATXN3^{shRMA}_4R cells as compared with fATXN3^{shRMA} cells (p=1.7x10⁻¹⁰) (Figure 2D). Interestingly, although we observed that increasing the levels of the 3R isoform of tau also ameliorated the neuronal phenotype of ATXN3^{dema}cells in terms of expression of differentiation markers (Figure 2E), neuronal maturation (Figure 2F) and neurite length (Figure 2G), it did not abolish the proliferative activity of ATXN3shma_3R upon RA treatment, as shown by the increased number of cells (p=0.0083) (Figure 2H) and the increased expression of Nestin (p=0.0006) (Figure 2E).



Figure 2. Overexpression of 4R tau ameliorates the phenotype of ATXN3^{shRMA} cells. (A) mRNA levels of several neuronal markers analyzed in ATXN3^{shRMA} cells were normalized by overexpression of 4R tau. mRNA levels were normalized to *HMBS* gene (B) After RA treatment the number of ATXN3^{shRMA}_4R cells was similar to the number of SCR^{shRMA}_4R cells. (C) Overexpression of 4R tau rescued the expression of βIII-tubulin and (D) the average length of neurites in cells lacking ATXN3. (E) Overexpression of 3R tau had a milder effect on the expression of differentiation markers, (F)

neuronal maturation, and (G) neurite length, and (H) no effect on the proliferative activity of ATXN3^{thTMA} cells upon RA treatment. *p<0.05; **p<0.01; ***p<0.001. + corresponds to rescued expression.

Cells lacking ATXN3 show decreased levels of SFRS7 (9G8), a protein involved in the splicing of *tau* exon 10

Taking into account the altered 4R/3R tau ratio in ATXN3⁺ cells, and considering the involvement of ATXN3 in proteolytic pathways we assessed the levels of SFRS7, a splicing regulator of *tau*, in these cultures. ATXN3⁺ cells presented decreased levels of SFRS7 protein compared with the SCR⁺ controls (p=0.025) (Figure 3A), suggesting that in the absence of ATXN3, SFRS7 is being more degraded. Because SFRS7 normally presents a nuclear localization, we performed cell fractionation and analyzed the levels of SFRS7 in the nuclear fraction. As shown in Figure 3B, this assay confirmed the reduced levels of SFRS7 in ATXN3⁺ cells in comparison with the control cells (p=0.001). The expression of SFRS7 was undetectable in the cytoplasmic fraction (data not shown).

To define whether ATXN3 affects the expression of SFRS7 at the protein or mRNA level, we extracted total RNA from ATXN3^{thRMA} and SCR^{thRMA} cells and performed qRT-PCR to determine the levels of *SFRS7* transcripts. No significant differences (p=0.712) were observed between the two cell lines (Figure 3C), suggesting that the effect of ATXN3 depletion on SRSF7 levels occurs at the protein level.



Figure 3. ATXN3^{dema} cells show decreased SFRS7 protein levels. (A) Western-blot analysis showed a downregulation of both total and (B) nuclear SFRS7 levels in ATXN3^{dema} cells. The results were normalized for H3. Relative band density for each protein was analyzed. (C) No significant differences were observed in the mRNA levels of *SFRS7* between the ATXN3^{dema} cells and the SCR^{dema} controls. mRNA levels were normalized to the *HMBS* gene. *p<0.05; **p<0.01.

SFRS7 (9G8), a protein involved in the splicing of Tau exon 10, is a candidate substrate of ATXN3's DUB activity

Considering the decreased levels of SFRS7 associated with the loss of function of ATXN3, we next analyzed the ubiquitylation levels of this splicing factor. For this, we performed a pulldown of polyubiquitylated proteins using Agarose-TUBEs 2, followed by immunoblotting against the SFRS7 protein. As shown in Figure 4A, we detected decreased levels of ubiquitylated forms of SFRS7 in ATXN3^{shrma} cells as compared with the scrambled control cells (SCR^{shrma}) (p=0.02). Given these observations, we hypothesized that SFRS7 could be a substrate of the DUB activity of ATXN3. To test this hypothesis, we first verified whether these two proteins interact in the context of neuronal cells. Co-immunoprecipitation using protein extracts from differentiated Wild type SH-SY5Y cells confirmed the interaction between ATXN3 and SFRS7, which is compatible with the hypothesis of SFRS7 being a substrate of ATXN3 in neurons (Figure 4B). To further explore the relevance of this interaction in the regulation of SFRS7 stability, we measured the levels of SFRS7 upon proteasome inhibition. In this condition, however, we found a similar downregulation of SFRS7 in ATXN3**** and SCR-muccells (Figure 4C). Indeed, as proteasome inhibition leads to a heat shock response [54], a blockade of splicing and a global downregulation of splicing factors have been described in cells exposed to proteasome inhibition [55], and this may be hampering our analysis of the possible link between ATXN3 degradation of SFRS7 by the UPS.





Figure 4. Decreased levels of polyubiquitylated SFRS7 (9G8) in ATXN3^{chRNA} cells. (A) Western-blot analysis after capture of polyubiquitylated proteins confirmed the decrease in polyubiquitylated forms of SFRS7 in ATXN3^{chRNA} cells. (B) Human ATXN3 co-immunoprecipitates with SFRS7. (C) Western-blot analysis showed that the levels of SFRS7 decreased at similar levels both in ATXN3^{chRNA} and SCR^{chRNA} cells upon MG132 treatment. Relative band density for each protein was analyzed. The results were normalized for H3.

Pathogenic ATXN3 causes similar molecular alterations as silencing

In order to determine if the presence of an expanded polyglutamine (polyQ) tract within ATXN3 would lead to a modification of the activity of this protein in *MAPT* splicing regulation, altering the 4R/3R tau ratio, we analyzed a SH-SY5Y cell line expressing a version of ATXN3 bearing 83 glutamines (ATXN3_83Q). Interestingly, we found that expression of ATXN3_83Q leads to a similar alteration on the expression of tau isoforms as that observed in cells lacking ATXN3 or expressing a catalytic mutant version of this protein: i) decreased expression of tau (2.7 fold decrease, $p=7.5x10^{\circ}$) (Figure 5A), ii) decreased expression of 4R tau isoform (2.4 fold decrease, $p=8.1x10^{\circ}$) and no alterations on the 3R tau isoform (Figure 5B and 5C, respectively), and iii) a decrease of the 4R/3R tau ratio (p=0.0313) (Figure 5D).

However, it is important to mention that the overexpression of the Wild type ATXN3 (ATXN3_28Q) also caused some degree of perturbation (Figure 5), pointing to the importance of a tight regulation of ATXN3 dosage in neurons. These results suggest that the polyQ expansion caused a perturbation of the normal function of ATXN3 in neuronal cells.



Figure 5. PolyQ expansion in ATXN3 affects tau splicing in neuronal cells. (A, B) Expression of ATXN3_C14A led to decreased mRNA levels of tau and 4R tau isoform, (C) no alterations in 3R tau expression and (D) decreased 4R/3R tau ratio. mRNA levels were normalized to the *HMBS* gene. **p<0.05; ***p<0.001.

Deregulation of tau splicing in the context of Machado-Joseph disease

Considering that a partial loss of function of the expanded ATXN3 might be contributing to the pathogenesis of MJD, as has been suggested for other polyQ disorders [56-58]we analyzed the 4R/3R tau ratio in the brains of transgenic mice expressing human expanded ATXN3 with 135 glutamines (CMVMJD135) [45], a mouse model of MJD. Similarly to what we have observed in neuronal cells lacking ATXN3 or overexpressing the expanded protein, we found a significantly decreased expression of the 4R tau isoform in the brainstem (an affected brain area) of CMVMJD135 mice both at protein level (p=2.8x10⁻⁵) and mRNA level (3.7 fold decrease, p=7x10⁻⁵) comparing with the Wild type (WT) littermate controls (Figure 6A and 6B, respectively), but no alterations of the 3R tau isoform expression (Figure 6C and 6D). The decreased expression of 4R tau led to a decreased protein level of total Tau in CMVMJD135 mice (p=0.0049) comparing with the WT animals (Figure 6E) and an altered 4R/3R tau ratio (Figure 6F). Moreover, as seen in ATXN3^{-metran} cells, we found a downregulation of Sfrs7 protein level in CMVMJD135 mice as compared with the WT controls (p=0.0093) (Figure 6G), but no alterations at the mRNA level (Figure 6H).

All together, these results suggest that the interaction of ATXN3 with SFRS7 and its impact on molecular pathways regulating tau splicing may be relevant in the pathogenesis of MJD.



Figure 6. Deregulation of tau splicing in CMVMJD135 mice. (A, B) CMVMJD135 mice presented a decrease in the protein and mRNA levels of 4R tau but (C, D) no statistically significant differences in the protein and mRNA levels of 3R tau in CMVMJD135 mice comparing with WT controls. (E) Expression of mutant human ATXN3 led to statistically decreased levels of total tau and (F) a disruption of the 4R/3R tau ratio in the brainstem of transgenic mice. (G) CMVMJD135 mice showed decreased levels of Sfrs7 but (H) no alterations in the expression of *Sfrs7* at the mRNA level. mRNA levels were normalized to the *HPRT* gene. Relative band density for each protein was analyzed. The results were normalized for actin levels. **p<0.01; ***p<0.001.

DISCUSSION

Tau is an important microtubule-binding protein in neurons. Abnormalities in tau expression and a disruption of MAPT exon 10 splicing have been suggested to play an important role in several neurodegenerative disorders [15-18]. Considering our observation of tau expression deregulation in ATXN3:MMA cells, we hypothesized that the 4R/3R tau ratio could be disrupted. Indeed, while it has been described that the normal adult human brain expresses approximately equal levels of 4R and 3R tau isoforms [3, 5], we found that loss of function of ATXN3 disrupts this balance in SH-SY5Y cells exposed to a differentiation stimulus (RA), leading to a decreased 4R/3R tau ratio, that seems to be caused by decreased levels of SFRS7, a splicing regulator known to modulate inclusion of tau exon 10 [28, 29]. While this work was being done, an article was published showing an increased 4R/3R tau ratio in the brains of subjects with HD, which seemed to be related with alterations in SFRS6, another known modulator of tau exon 10 splicing [59], strengthening the idea that an imbalance of tau isoforms might be contributing for the pathology of several neurodegenerative diseases, including poliQ diseases. In addition to that, ATXN3^{LINIA} cells presented increased relative levels of the 3R tau isoform, which correlates with the immature phenotype of these cells that we previously described [41], since the 3R is the predominant tau isoform in undifferentiated SH-SY5Y cells [60, 61]. Importantly, normalizing the levels of 4R tau isoform partially ameliorates the neuronal phenotype of ATXN3 there cells in terms of expression of differentiation markers, neuronal maturation and neurite length. Taking into account that loss of function of ATXN3 deregulated the levels of SFRS7 at the protein level, we hypothesized that this splicing factor could be a substrate of the DUB activity of ATXN3, which could modulate its degradation. In line with that, we observed that ATXN3 co-immunoprecipitated with SFRS7, suggesting that these two proteins are molecular partners in neuronal cells. Moreover, the fact that SFRS7 was captured using the Agarose-TUBEs that have high affinity for polyubiquitin chains [62] suggests that this splicing factor is polyubiquitylated and thus might be degraded through the UPS. Trying to explore if this interaction could be indicative that ATXN3 is modulating the degradation of SFRS7 through the proteasome, we measured the levels of this protein upon proteasome inhibition; unexpectedly, we found similarly reduced levels of this splicing factor in ATXN3^{thRMA} and SCR^{thRMA} cells. Additionally, in the absence of proteasome inhibition, ATXN3^{GRWA} cells presented decreased amounts of polyubiquitylated forms of SFRS7. Although we found no data in the literature specifically relating SFRS7 expression and MG132 treatment, it is known that proteasome inhibition elicits a stress response, globally repressing transcription and mRNA processing, including splicing. This stress induction may explain

our unexpected result, since *SFRS7* is a heat shock suppressed gene [63-65]. Further experiments using conditions leading to milder proteasome inhibition may help overcome this technical limitation, which is hindering the clarification of the mechanism of SFSR7 reduction in cells lacking ATXN3.

As mentioned before, SFRS7 has been involved in the splicing of tau exon 10, playing an important role in the regulation of the 4R/3R tau ratio balance [28, 29]. The effect of SFRS7 on tau splicing initially appears to be controversial on the literature: while some authors refer that it acts as a tau exon 10 splicing enhancer [66], others state that it suppresses tau exon 10 inclusion [28, 29]. An unifying explanation is that the function of SFRS7 acting as a splicing silencer or enhancer is celltype dependent. In this perspective, Van Abel and co-workers reported that SFRS7 acts as a tau splicing enhancer in the same type of cells that we have used in this study [66]; they observed a decreased 4R/3R tau ratio upon downregulation of SFRS7 in these cells, both of which we also observed in cells lacking ATXN3. Interestingly, we also found a decreased 4R/3R tau ratio as well as decreased protein levels of Sfrs7 in affected brain regions of 45 weeks-old CMVMJD135 mice as compared with their littermate controls. At this age, the transgenic animals display an overt phenotype resembling behavioral and pathological characteristics present in human patients [45]. Thus, the observed deregulation of tau splicing suggests that this mechanism may be contributing to MJD pathogenesis, as it does to other neurodegenerative disorders albeit in the opposing sense concerning 4R relative abundance. However, it still remains to clarify whether this change occurs before symptoms or if it is a consequence of the disease progression. Considering that we observed a similar phenomenon using cells lacking ATXN3 and cells expressing a catalytic mutant of the protein, it is reasonable to think that the DUB activity of ATXN3 is important in this process and that the polyQ expansion might cause a partial loss of this normal function of the protein, contributing to MJD pathologenesis. Future work should allow us to verify the relevance of these findings and to unravel how the imbalance of 4R/3R tau isoforms ratio leads to neurodegeneration. One possible scenario is that it leads to altered microtubule dynamics, which causes multiple subsequent intracellular alterations such as pathogenic disruption of axonal transport, a hypothesis that we are currently assessing.

Bibliography

- Weingarten, M.D., et al., *A protein factor essential for microtubule assembly.* Proc Natl Acad Sci U S A, 1975. 72(5): p. 1858-62.
- 2. Drubin, D.G. and M.W. Kirschner, *Tau protein function in living cells.* J Cell Biol, 1986. **103**(6 Pt 2): p. 2739-46.
- 3. Goedert, M., et al., *Multiple isoforms of human microtubule-associated protein tau: sequences and localization in neurofibrillary tangles of Alzheimer's disease.* Neuron, 1989. **3**(4): p. 519-26.
- 4. Andreadis, A., W.M. Brown, and K.S. Kosik, *Structure and novel exons of the human tau gene.* Biochemistry, 1992. **31**(43): p. 10626-33.
- 5. Goedert, M. and R. Jakes, *Expression of separate isoforms of human tau protein: correlation with the tau pattern in brain and effects on tubulin polymerization.* EMBO J, 1990. **9**(13): p. 4225-30.
- 6. Kosik, K.S., et al., *Developmentally regulated expression of specific tau sequences.* Neuron, 1989. **2**(4): p. 1389-97.
- 7. Goedert, M., et al., *Cloning and sequencing of the cDNA encoding an isoform of microtubule-associated protein tau containing four tandem repeats: differential expression of tau protein mRNAs in human brain.* EMBO J, 1989. **8**(2): p. 393-9.
- 8. D'Souza, I. and G.D. Schellenberg, *Regulation of tau isoform expression and dementia.* Biochimica et Biophysica Acta, 2005. **1739**(2-3): p. 104-15.
- 9. Fernandez-Nogales, M., et al., *Huntington's disease is a four-repeat tauopathy with tau nuclear rods.* Nature Medicine, 2014. **20**(8): p. 881-5.
- 10. Connell, J.W., et al., *Quantitative analysis of tau isoform transcripts in sporadic tauopathies.* Brain Research. Molecular Brain Research, 2005. **137**(1-2): p. 104-9.
- 11. Glatz, D.C., et al., *The alternative splicing of tau exon 10 and its regulatory proteins CLK2 and TRA2-BETA1 changes in sporadic Alzheimer's disease.* Journal of Neurochemistry, 2006. **96**(3): p. 635-44.
- 12. Conrad, C., et al., *Single molecule profiling of tau gene expression in Alzheimer's disease.* Journal of Neurochemistry, 2007. **103**(3): p. 1228-36.
- 13. Ksiezak-Reding, H., B. Shafit-Zagardo, and S.H. Yen, *Differential expression of exons 10 and 11 in normal tau and tau associated with paired helical filaments.* Journal of Neuroscience Research, 1995. **41**(5): p. 583-93.
- 14. Yoshida, M., *Cellular tau pathology and immunohistochemical study of tau isoforms in sporadic tauopathies.* Neuropathology, 2006. **26**(5): p. 457-70.
- 15. D'Souza, I. and G.D. Schellenberg, *Regulation of tau isoform expression and dementia.* Biochim Biophys Acta, 2005. **1739**(2-3): p. 104-15.
- 16. Goedert, M. and R. Jakes, *Mutations causing neurodegenerative tauopathies.* Biochim Biophys Acta, 2005. **1739**(2-3): p. 240-50.
- 17. Sergeant, N., A. Delacourte, and L. Buee, *Tau protein as a differential biomarker of tauopathies.* Biochim Biophys Acta, 2005. **1739**(2-3): p. 179-97.
- Himmelstein, D.S., et al., *Tau as a therapeutic target in neurodegenerative disease.* Pharmacol Ther, 2012.
 136(1): p. 8-22.
- 19. Gao, Q.S., et al., *Complex regulation of tau exon 10, whose missplicing causes frontotemporal dementia.* J Neurochem, 2000. **74**(2): p. 490-500.
- 20. Hartmann, A.M., et al., *Regulation of alternative splicing of human tau exon 10 by phosphorylation of splicing factors*. Mol Cell Neurosci, 2001. **18**(1): p. 80-90.
- 21. Broderick, J., J. Wang, and A. Andreadis, *Heterogeneous nuclear ribonucleoprotein E2 binds to tau exon 10 and moderately activates its splicing.* Gene, 2004. **331**: p. 107-14.
- 22. Kondo, S., et al., *Tra2 beta, SF2/ASF and SRp30c modulate the function of an exonic splicing enhancer in exon 10 of tau pre-mRNA.* Genes Cells, 2004. **9**(2): p. 121-30.
- 23. Wang, J., et al., *Tau exon 10, whose missplicing causes frontotemporal dementia, is regulated by an intricate interplay of cis elements and trans factors.* J Neurochem, 2004. **88**(5): p. 1078-90.
- 24. Wang, Y., et al., *Tau exons 2 and 10, which are misregulated in neurodegenerative diseases, are partly regulated by silencers which bind a SRp30c.SRp55 complex that either recruits or antagonizes htra2beta1.* J Biol Chem, 2005. **280**(14): p. 14230-9.
- 25. Graveley, B.R., Sorting out the complexity of SR protein functions. RNA, 2000. 6(9): p. 1197-211.
- 26. Dreyfuss, G., V.N. Kim, and N. Kataoka, *Messenger-RNA-binding proteins and the messages they carry.* Nat Rev Mol Cell Biol, 2002. **3**(3): p. 195-205.

- 27. Cavaloc, Y., et al., *Characterization and cloning of the human splicing factor 9G8: a novel 35 kDa factor of the serine/arginine protein family.* EMBO J, 1994. **13**(11): p. 2639-49.
- 28. Gao, L., et al., *SR protein 9G8 modulates splicing of tau exon 10 via its proximal downstream intron, a clustering region for frontotemporal dementia mutations.* Mol Cell Neurosci, 2007. **34**(1): p. 48-58.
- Ding, S., et al., *Regulation of alternative splicing of tau exon 10 by 9G8 and Dyrk1A*. Neurobiol Aging, 2012.
 33(7): p. 1389-99.
- 30. Cramer, P., et al., *Coupling of transcription with alternative splicing: RNA pol II promoters modulate SF2/ASF and 9G8 effects on an exonic splicing enhancer.* Mol Cell, 1999. **4**(2): p. 251-8.
- 31. Li, X., et al., *SR proteins Asf/SF2 and 9G8 interact to activate enhancer-dependent intron D splicing of bovine growth hormone pre-mRNA in vitro.* RNA, 2000. **6**(12): p. 1847-58.
- 32. Galiana-Arnoux, D., et al., *The CD44 alternative v9 exon contains a splicing enhancer responsive to the SR proteins 9G8, ASF/SF2, and SRp20.* J Biol Chem, 2003. **278**(35): p. 32943-53.
- 33. Nijman, S.M., et al., *A genomic and functional inventory of deubiquitinating enzymes.* Cell, 2005. **123**(5): p. 773-86.
- 34. Komander, D., M.J. Clague, and S. Urbe, *Breaking the chains: structure and function of the deubiquitinases.* Nat Rev Mol Cell Biol, 2009. **10**(8): p. 550-63.
- Clague, M.J., J.M. Coulson, and S. Urbe, *Cellular functions of the DUBs.* J Cell Sci, 2012. **125**(Pt 2): p. 277-86.
- 36. Kawaguchi, Y., et al., *CAG expansions in a novel gene for Machado-Joseph disease at chromosome 14q32.1.* Nat Genet, 1994. **8**(3): p. 221-8.
- 37. Burnett, B., F. Li, and R.N. Pittman, *The polyglutamine neurodegenerative protein ataxin-3 binds polyubiquitylated proteins and has ubiquitin protease activity.* Hum Mol Genet, 2003. **12**(23): p. 3195-205.
- Doss-Pepe, E.W., et al., *Ataxin-3 interactions with rad23 and valosin-containing protein and its associations with ubiquitin chains and the proteasome are consistent with a role in ubiquitin-mediated proteolysis.* Mol Cell Biol, 2003. 23(18): p. 6469-83.
- 39. Rodrigues, A.J., et al., *Absence of ataxin-3 leads to cytoskeletal disorganization and increased cell death.* Biochim Biophys Acta, 2010. **1803**(10): p. 1154-63.
- 40. do Carmo Costa, M., et al., *Ataxin-3 plays a role in mouse myogenic differentiation through regulation of integrin subunit levels.* PLoS One, 2010. **5**(7): p. e11728.
- 41. Neves-Carvalho, A., Logarinho E., Freitas A., Duarte-Selva S., Costa M.C., Silva-Fernandes A., Martins M., Serra S.C., Lopes, A. T., Paulson, H.L., Heutink, P., Relvas, J.B. and Maciel P., *Dominant negative effect of polyglutamine expansion perturbs normal function of ataxin-3 in neuronal cells.* Human Molecular Genetics, 2014.
- 42. Zhong, X. and R.N. Pittman, *Ataxin-3 binds VCP/p97 and regulates retrotranslocation of ERAD substrates.* Hum Mol Genet, 2006. **15**(16): p. 2409-20.
- 43. Wang, G., et al., *Ataxin-3, the MJD1 gene product, interacts with the two human homologs of yeast DNA repair protein RAD23, HHR23A and HHR23B.* Hum Mol Genet, 2000. **9**(12): p. 1795-803.
- 44. Moffat, J., et al., *A lentiviral RNAi library for human and mouse genes applied to an arrayed viral high-content screen.* Cell, 2006. **124**(6): p. 1283-98.
- 45. Silva-Fernandes, A., et al., *Chronic Treatment with 17-DMAG Improves Balance and Coordination in A New Mouse Model of Machado-Joseph Disease.* Neurotherapeutics, 2014.
- 46. Nicklas, W., et al., *Recommendations for the health monitoring of rodent and rabbit colonies in breeding and experimental units.* Lab Anim, 2002. **36**(1): p. 20-42.
- 47. Pfaffl, M.W., *A new mathematical model for relative quantification in real-time RT-PCR.* Nucleic Acids Res, 2001. **29**(9): p. e45.
- 48. Lee, V.M., M. Goedert, and J.Q. Trojanowski, *Neurodegenerative tauopathies.* Annu Rev Neurosci, 2001. **24**: p. 1121-59.
- 49. Goedert, M. and M.G. Spillantini, *A century of Alzheimer's disease.* Science, 2006. **314**(5800): p. 777-81.
- 50. Ballatore, C., V.M. Lee, and J.Q. Trojanowski, *Tau-mediated neurodegeneration in Alzheimer's disease and related disorders.* Nat Rev Neurosci, 2007. **8**(9): p. 663-72.
- 51. Maccioni, R.B. and V. Cambiazo, *Role of microtubule-associated proteins in the control of microtubule assembly.* Physiol Rev, 1995. **75**(4): p. 835-64.
- 52. Sennvik, K., et al., *Tau-4R suppresses proliferation and promotes neuronal differentiation in the hippocampus of tau knockin/knockout mice.* FASEB J, 2007. **21**(9): p. 2149-61.
- 53. Duggal, N. and R.R. Hammond, *Nestin expression in ganglioglioma*. Exp Neurol, 2002. **174**(1): p. 89-95.

- 54. Bush, K.T., A.L. Goldberg, and S.K. Nigam, *Proteasome inhibition leads to a heat-shock response, induction of endoplasmic reticulum chaperones, and thermotolerance.* Journal of Biological Chemistry, 1997. **272**(14): p. 9086-92.
- 55. Yost, H.J. and S. Lindquist, *RNA splicing is interrupted by heat shock and is rescued by heat shock protein synthesis.* Cell, 1986. **45**(2): p. 185-93.
- 56. Dragatsis, I., M.S. Levine, and S. Zeitlin, *Inactivation of Hdh in the brain and testis results in progressive neurodegeneration and sterility in mice.* Nat Genet, 2000. **26**(3): p. 300-6.
- 57. Strand, A.D., et al., *Expression profiling of Huntington's disease models suggests that brain-derived neurotrophic factor depletion plays a major role in striatal degeneration.* J Neurosci, 2007. **27**(43): p. 11758-68.
- 58. Lim, J., et al., *Opposing effects of polyglutamine expansion on native protein complexes contribute to SCA1.* Nature, 2008. **452**(7188): p. 713-8.
- 59. Yin, X., et al., *Dual-specificity tyrosine phosphorylation-regulated kinase 1A (Dyrk1A) modulates serine/arginine-rich protein 55 (SRp55)-promoted Tau exon 10 inclusion.* Journal of Biological Chemistry, 2012. **287**(36): p. 30497-506.
- 60. Smith, C.J., et al., *Tau isoform expression and phosphorylation state during differentiation of cultured neuronal cells.* FEBS Lett, 1995. **375**(3): p. 243-8.
- 61. Uberti, D., et al., *Characterization of tau proteins in human neuroblastoma SH-SY5Y cell line.* Neurosci Lett, 1997. **235**(3): p. 149-53.
- 62. Hjerpe, R., et al., *Efficient protection and isolation of ubiquity/lated proteins using tandem ubiquitin-binding entities.* EMBO Rep, 2009. **10**(11): p. 1250-8.
- 63. Bush, K.T., A.L. Goldberg, and S.K. Nigam, *Proteasome inhibition leads to a heat-shock response, induction of endoplasmic reticulum chaperones, and thermotolerance.* J Biol Chem, 1997. **272**(14): p. 9086-92.
- 64. Lee, D.H. and A.L. Goldberg, *Proteasome inhibitors cause induction of heat shock proteins and trehalose, which together confer thermotolerance in Saccharomyces cerevisiae.* Mol Cell Biol, 1998. **18**(1): p. 30-8.
- 65. Lecomte, S., et al., *Roles of heat shock factor 1 and 2 in response to proteasome inhibition: consequence on p53 stability.* Oncogene, 2010. **29**(29): p. 4216-24.
- 66. van Abel, D., et al., *SFRS7-mediated splicing of tau exon 10 is directly regulated by STOX1A in glial cells.* PLoS One, 2011. **6**(7): p. e21994.

Chapter 4

Loss of function of ATXN3 alters the ubiquitome of neuronal

cells negatively impacting on the splicing process

Loss of function of ATXN3 alters the ubiquitome of neuronal cells, negatively impacting on the splicing process

Neves-Carvalho A^{1,2}, Fátima Lopes^{1,2}, Ka Wan Li³ and Maciel P^{1,2}

¹ Life and Health Sciences Research Institute (ICVS), School of Health Sciences, University of Minho, 4710-057 Braga, Portugal, ² ICVS/3B's – PT Government Associate Laboratory, Braga/Guimarães, Portugal, ³Vrije University Medisch Centrum (VUMC), Amsterdam, The Netherlands

ABSTRACT

Ubiquitylation is a tightly controlled process that has been shown not only to mediate protein degradation, but also to modulate protein function and subcellular localization, playing a crucial role in the function and development of the nervous system. Deubiquitylating (DUB) enzymes have been recognized as central players in the maintenance of the correct ubiquitylation/deubiquitylation balance in cells. Ataxin-3 (ATXN3) is a protein with DUB activity mutated in Machado-Joseph disease (MJD). To date, besides the involvement of ATXN3 in the Ubiquitin-proteasome pathway (UPP) and its potential involvement in transcription regulation and DNA repair, its normal cellular functions remain mostly unknown and few substrates of its DUB activity have been identified. In this work, in the attempt to identify potential targets of the DUB activity of this protein, we characterized the ubiquitome of neuronal cells lacking ATXN3 (ATXN3 farma cells) by mass spectrometry. We found that a large proportion of the proteins with altered polyubiquitylation in ATXN3^{shma} cells were known to be involved in RNA post-transcriptional modification, namely splicing factors. Using transcriptomic analysis and reporter minigenes we confirmed that splicing was globally altered in cells lacking ATXN3. Among the mRNA targets with altered splicing were those of genes encoding components of the spliceosome itself, involved in ubiquitin mediated proteolysis, in axon guidance and in the MAPK signaling pathway. These findings lead us to propose that ATXN3 plays a role in splicing regulation in neurons, a novel function for this protein.

INTRODUCTION

Ubiquitylation is a highly dynamic biochemical modification in which an Ubiquitin (Ub) moiety is attached to a protein. This process is catalyzed by the sequential actions of a Ub-activating enzyme (E1), Ub-conjugating enzymes (E2) and UB-protein ligases (E3) that bind Ub to different

lysine (K) residues in the substrate, resulting in mono or poly Ub chains (Reviewed in [1]). Ubiquitylated substrates are then recognized by proteins containing Ubiquitin binding domains and directed to different fates. Different types of polyubiquitin (polyUb) chains are thought to be functionally linked to different fates. For example, K48 usually targets proteins for proteasomal degradation, which is initiated when a minimum of four ubiquitins is reached [1], while K63-linked polyUb regulates protein activation, subcellular localization or degradation in lysosome (autophagy) and is known to be relevant for DNA repair (Reviewed in [2]). Ubiquitylation and proteolysis by the ubiquitin-proteasome pathway (UPP) are now recognized as important mechanisms in the nervous system as this proteolytic pathway is known to degrade misfolded or short-lived regulatory proteins (Reviewed in [3-5]). Impairment of the UPP has been connected to several neurodegenerative diseases such as Alzheimer's (Reviewed in [6]), Parkinson's (Reviewed in [7]) and Hungtington's (Reviewed in [8]) diseases. However, recent findings showing an accumulation of K63-linked polyubiquitin chains in neurodegenerative diseases suggest that the involvement of ubiquitylation in signaling pathways not related to protein control, such as autophagy, may also contribute to disease [9-11].

Ubiquitin signaling has also been recently implicated in the regulation of splicing, that plays key roles in many processes important for the development and function of the nervous system, such as synaptogenesis, neurite outgrowth, axon guidance, ion channel activity and long-term potentiation (Reviewed in [12-14]). Ubiquitin and Ub-like proteins have been shown to co-purify with splicing complexes [15, 16] and ubiquitylated splicing factors have been identified in a proteomic screen [17]. Like most post-transcriptional modifications, ubiquitylation is a reversible signal and is counterbalanced by deubiquitylating (DUB) enzymes that remove Ub from target proteins and recycle the free Ub pool. Thus, the action of DUBs has a major impact on the ubiquitylated proteome (also known as ubiquitome). Ataxin-3 (ATXN3) is a protein with DUB activity known to be involved in Machado-Joseph Disease (MJD), a neurodegenerative disorder of adult onset caused by the expansion of a polyglutamine (polyQ) tract in this protein. A crucial step towards the understanding of ATXN3 function was the discovery of its DUB activity in vitro [18]. ATXN3 is able to cleave Ub from polyubiquitylated substrates, both with K48, K63 or mixed linkages [18-20], to interact with the ubiquitin-like protein NEDD8 [21], with subunits of the proteasome [18, 22], with VCP/p97 [19, 20], with UBXN5 [23] and with the E3 ligases Parkin [24] and CHIP [25]. Although these enzymatic activities of ATXN3 strongly suggest a role for the protein in the UPP, the biological consequences of these functions have not been extensively characterized yet and the substrates of

102

its action are not known, namely in neurons. In this work, we used Tandem ubiquitin binding entities (TUBES) [26] to purify polyubiquitylated proteins from a neuronal cell line lacking ATXN3, with the goal of identifying candidate targets of its DUB activity. Among the proteins found to have altered polyubiquitylation patterns in cells lacking ATXN3, a large proportion were proteins involved in RNA transport and processing, indicating that ATXN3 might be regulating these processes in neurons, a hypothesis that we validated using reporter minigenes and transcriptomic analysis.

MATERIALS AND METHODS

Cell culture

The human neuroblastoma SH-SY5Y cell line (ATCC number CRL-2266) was transfected with a shRNA sequence targeting *ATXN3* or a scrambled shRNA sequence as described elsewhere [27]. Stably infected cell lines were cultured in a 1:1 mixture DMEM/F-12 nutrient (Invitrogen) supplemented with 10% (v/v) Fetal Bovine Serum (FBS) (Biochrom), 2mM glutaMAX (Invitrogen), 100 U/mL penicillin, 100 μ g/mL streptomycin and 25 ng/mL puromycin (Sigma Aldrich). The cells were maintained in a humidified 37°C/95%-air/5%-CO₂ incubator. The medium was changed every two days. Differentiation was induced by 0.1 μ M all-trans-retinoic acid (RA) (Sigma Aldrich) in opti-MEM (Invitrogen) supplemented with 0.5% FBS for 7 days. The medium was replaced every two days.

Pulldown of polyubiquitylated proteins

Cells treated with RA were lysed by sonication on ice in lysis buffer (50 mM Tris-HCl pH 7.5, 0.15 M NaCl, 1mM EDTA, 1% NP-40, 10% Glycerol, complete protease inhibitors (Roche) and 50µM UB/UBI protease inhibitor PR-619 (LifeSensors)). After lysis, 2 mg of total protein extract were incubated with 100 µL of pre-equilibrated Agarose-TUBEs (LifeSensors), overnight at 4°C on a rocking platform. Sedimented beads were washed 3 times with washing buffer (20 mM Tris pH 8.0, 0.15 M NaCl, 0.1% Tween-20) before being eluted with 1x SDS sample buffer (62.5mM Tris-HCl pH 6.8, 10% glycerol, 2% SDS, Bromophenol Blue). Eluted proteins were immediately boiled at 98°C for 15min and run in a 10% SDS-PAGE gel.

Immunoblotting

Cells treated with 0.1 µM RA for 7 days were pelleted and frozen in liquid nitrogen. Proteins eluted from TUBEs were resolved in 10% SDS-PAGE gels and then transferred to a nitrocellulose membrane. After incubation with the FK2 anti-ubiquitin primary antibody (1:2000, Millipore) overnight at 4°C, membranes were incubated with secondary antibody for 1 hour at room temperature (anti-mouse, 1:10000, Bio-Rad). Antibody binding was detected by chemiluminescence (Clarity kit, Bio-Rad).

Digestion of proteins from preparative 1D-PAGE gel

The 1D PAGE LC-MS/MS approach was used for protein identification as previously described [28]. Eluted proteins were separated using 1.5mm and 10% SDS-PAGE gels. The quality of purification was controlled by Coomassie Brilliant Blue g-250 (Sigma) staining before MS analysis. Gel image was acquired the Gel Doc[™] EZ system (Bio-rad). After Coomassie staining, all the visible blue-stained protein spots were manually excised from the gel. The gel pieces were destained overnight at room temperature using 50% acetonitrile in 25 mM ammonium bicarbonate buffer, pH 8.5, and then dehydrated with 100% acetonitrile. The shrunken pieces were then re-swollen in 50 mM ammonium bicarbonate buffer, dehydrated in 100% acetronitrile and dried in a speedvac® concentrator (Savant) for 30 min. The gel pieces were rehydrated in 60 µL of 20 µg/mL Trypsin (Promega) in 50 mM ammonium bicarbonate solution and incubated for 2h at 55°C. The gel pieces were then incubated with 0.1% trifluoroacetic acid in 50% acetonitrile for 20 min at room temperature in order to extract the remaining peptides from the gel. The tryptic peptides were dried in a speedvac for 2 h.

Liquid chromatography-tandem mass spectrometry (LC-MS/MS)

After re-dissolution in 17 µL 0.1% acetic acid, samples were separated on a capillary C18 column using a nano LC-ultra 1D plus HPLC system (Eksigent) and analyzed on-line with a electrospray LTQ-Orbitrap Discovery mass spectrometer (Thermo Fisher Scientific). MS/MS spectra were searched against a human database (uniprot_sprot, 2010_01) with the ProteinPilot[™] software (version 3.0; AB-sciex) using the Paragon[™] algorithm (version 3.0.0.0 [29]) as the search engine. The detected protein threshold (unused protscore (confidence)) in the software was set to 0.10 to achieve 20% confidence and the proteins identified were grouped to minimize redundancy.

Peptides with "unused" values < 2 have low confidence and were excluded from analysis. The "unused" value is defined in the handbook of ProteinPilot as a sum of peptide scores from all the non-redundant peptides matched to a protein. Peptides with confidence of \geq 99% would have a peptide score of 2. Tryptic peptides shared by multiple proteins were assigned to the winner protein.

RNA extraction and Array hybridization

Total RNA was isolated from ATXN3^{dente} and SCR^{dente} cells using an miRNeasy mini kit (Qiagen) and quality assessment was achieved using RNA 6000 Nano labchip (Bioanalyzer, Agilent) and by a Nanodrop spectrophotometer (Thermo). Total RNAs RIN values were between 8.7 and 9.3 (average: 9.17). Affymetrix Human Transcriptome Array 2.0 ST arrays were hybridized according Affymetrix recommendations using the Ambion WT protocol (Life technologies, France) and Affymetrix labelling and hybridization kits. Raw data, transcript data and exon data were controlled with Expression console (Affymetrix).

Microarray data analysis

Affymetrix Human Transcriptome Array 2.0 ST dataset analysis was performed using the GenoSplice technology (www.genosplice.com). Data were normalized using quantile normalization. Background corrections were made with antigenomic probes and probes were selected according to their %GC, cross-hybridization status and potential overlap with repeat region as previously described [PMID:23861464, PMID:23321315, PMID:23284676]. Only probes targeting exons and exon-exon junctions annotated from FAST DB® transcripts (release fastdb_2013_2) were selected [PMID:16052034, PMID:17547750]. Only probes with a DABG P value ≤0.05 in at least half of the arravs were considered for statistical analysis [PMID:23861464, PMID:23321315, PMID:23284676]. Only genes expressed in at least one compared condition were analyzed. To be considered to be expressed, the DABG P-value had to be ≤ 0.05 for at least half of the gene probes. We performed an unpaired Student's t-test to compare gene intensities between ATXN3^{thRMA} and SCR[™] cells. Genes were considered significantly regulated when fold-change was ≥1.5 and P-value ≤0.05 (unadjusted P-value). Analysis at the splicing level was first performed taking into account only exon probes ('EXON analysis) in order to potentially detect new alternative events that could be differentially regulated (i.e., without taking into account exon-exon junction probes). Analysis at the splicing level was also performed by taking into account exon-exon junction probes ('SPLICING PATTERN analysis) using the FAST DB® splicing pattern annotation (i.e., for each gene, all possible

splicing patterns were defined and analyzed. All types of alternative events can be analyzed: Alternative first exons, alternative terminal exons, cassette exon, mutually exclusive exons, alternative 5' donor splice site, alternative 3' acceptor splice sites and intron retention). EXON and SPLICING PATTERN analyses were performed using unpaired Student's t-test on the splicing-index as previously described [PMID:23861464, PMID:23321315, PMID:23284676]. Results were considered statistically significant for unadjusted P-values \leq 0.05 and fold-changes \geq 1.5 for SPLICING PATTERN analysis and unadjusted P-values \leq 0.05 and fold-changes \geq 2.0 for EXON analysis. Gene Ontology (GO), KEGG and REACTOME analyses of differentially regulated genes were performed using DAVID [PMID:19131956].

Plasmid purification

Hybrid minigene reporter plasmids pyPY, AdML and α-globulin [30, 31] were kindly provided by Prof. Juan Valcárcel (Centre de Regulació Genòmica (CRG), Barcelona). Top10 competent cells (Invitrogen) were transformed with 100 ng of plasmid DNA, according to the recommended protocol. Briefly, the cells were incubated with the constructs on ice for 30 min followed by heat shock at 42°C for 1 min. After incubation on ice for 2 min, 500 uL of LB medium was added to the cell vial and incubated at 150 rpm for 60 min at 37°C. Cultures were grown overnight at 37°C in LB/ampicillin plates. The next day, one colony was inoculated in LB/ampicilin (100 mg/mL) at 37°C overnight. Plasmid extraction was carried out using the ZR Plasmid Miniprep™ (Zymo Research) according with the manufacturer's protocol. DNA concentration was determined using Nanodrop (Alfagene) and integrity verified by running 200 ng in an agarose gel.

Cell transfection

4x10^s cells per well were plated in gelatin-coated 6 well plates and incubated 24 h. Before transfection, the culture medium was changed to DMEM/F-12-AA without antibiotics and supplemented with 5% FBS. Cell were transfected with 200ng of the reporter plasmids using Lipofectamine® 2000 Transfection Reagent (Invitrogen) according with the manufacturer's instructions. Briefly, reporter plasmid minigenes and the transfection reagents were appropriately diluted in Opti-MEM medium separately and incubated for 5 min at room temperature. The mixed reagents were then incubated at room temperature for 20 min allowing the formation of transfection complexes. The cells were then incubated for 24 h with the transfection mix.

Semi-quantitative PCR

PCR amplification of pyPY, AdML and α-globin reporter genes was carried out using Taq DNA Polymerase (Thermo Fisher Scientific) following the manufacturer's protocol. The cycling conditions were: 95°C for 5 min followed by 24 cycles of denaturing at 95°C for 1 min, annealing at 60°C for 45 sec, extension at 72°C for 1 min and final extension at 72°C for 5 minutes. The primers used are listed in Table A1. The PCR product was run in a 2% agarose gel. Gel analyses and splicing efficiency calculations were performed using Image Lab software (Bio-Rad).

Statistical analysis

Comparison between the different cell lines was performed using t-test in the GraphPad prism version 5.0 software. For real-time quantitative PCR data, the same approach was used and results were presented using the $\Delta\Delta$ Ct method, as described before [32]. A critical value for significance of two-tailed p<0.05 was used throughout the study.

RESULTS

Pulldown of the ubiquitome of ATXN3^{IMPA} cells using Tandem Ubiquitin Binding Entities (TUBEs) and identification of polyubiquitylated proteins by LC-MS/MS

In order to identify variations in the ubiquitome in neuronal cells lacking ATXN3 (ATXN3 Interval cells) [27], we used a recently developed methodology that combines Tandem Binding Ubiquitin Entities (TUBEs) with mass spectrometry (TUBEs-LC-MS/MS) [26]. Figure 1 summarizes the steps followed for the purification and identification of the polyubiquitylated proteins in ATXN3 Interval and SCR Interval cells. The integration of the data and the comparison between the proteins identified in ATXN3 Interval versus SCR Interval cells resulted in a list of proteins with altered polyubiquitylation in cells lacking ATXN3; among these are potential direct targets of the DUB activity of ATXN3, i.e., putative ATXN3 substrates.



Figure 1. Experimental design – purification of polyubiquitylated proteins using TUBEs. (A-I, B) RAtreated SH-SY5Y cells (with silenced ATXN3 or not) were lysed and protein extracts were incubated with TUBEs. (A-II) TUBEs-captured proteins were recovered with Laemmli buffer and analyzed by (C) comassie blue staining of the polyubiquitylated proteins purified using TUBEs run in a 1-D SDS-PAGE gel or (D) western blot with anti-ubiquitin FK2 antibody. (A-III) Polyubiquitylated proteins were trypsin digested and identified by LC-MS/MS. (E) After acquisition, data were processed and integrated in functional networks. Adapted from [33].

In each pulldown experiment, around 1200-1300 proteins were identified. When the results of all the independent experiments were merged, we observed that many of these proteins were sporadically detected across the different experiments. For the remaining analysis, these proteins were excluded, reducing the list to about 615 proteins. From these polyubiquitylated proteins,

around 193 proteins showed altered levels in ATXN3^{shRNA} cells comparing with the SCR^{shRNA} controls (p<0.05) (Table 1).

Curiously, the majority of these polyubiquitylated proteins were absent (44.04%) or showed decreased polyubiquitylation levels (24.35%) in ATXN3^{-INTMA} cells. The proteins found to have altered polyubiquitylation levels in ATXN3^{-INTMA} cells where analyzed (enrichment analysis) using Ingenuity Pathways Analysis software (IPA, Ingenuity systems®) and can be grouped in 10 functional networks, including: (i) Gene expression, DNA replication, recombination and repair (17.7%), (ii) RNA post-transcriptional modification (13.3%), (iii) Molecular transport, RNA trafficking (10.8%), (iv) Cell death and survival (8.9%), and (v) Organ morphology (8.9%) (Figure 1E). The fact that a significant proportion of the proteins with altered polyubiquitylation in ATXN3^{-INTMA} cells are involved in RNA post-transcriptional modification, around 8% of them being splicing factors (Table 1), suggested to us that ATXN3 could be playing a role in this cellular process.

Table 1. Differences in polyubiquitylated proteins identified by TUBEs-MS in SH-SY5Y cells lacking ATXN3. List of polyubiquitylated proteins with altered levels in RA-treated ATXN3^{shRMA} cells as compared with the SCR^{shRMA} controls (p<0.05). These proteins were detected in at least 3 independent experiments. The values are the average of "unused" values given by the Proteinpilot algorithm. The absent "unused" values indicate the (near) complete absence of the polyubiquitylated protein. In red and green are proteins with increased and decreased polyubiquitylated levels, respectively. \$ indicates splicing factors.

	Average unused values				
Name	SCR ^{shRNA}	ATXN3 ^{shrna}	p value		
Network 1 – Gene expression, DNA replication and repair					

PGRMC1 (Membrane-associated progesterone receptor)	2.01	Absent	1.12E-14
RANBP2 (E3 SUMO-protein ligase)	Absent	2.02	6.16E-06
NASP (Nuclear autoantigenic sperm protein)	2.01	Absent	6.21E-06
PURB (Transcriptional activator protein Pur-beta)	2.01	Absent	6.22E-06
EHMT2 (Uncharacterized protein)	2.01	Absent	6.22E-06
CAP1 (Adenylyl cyclase-associated protein 1)	2.02	Absent	5.54E-05
TNPO1 (Transportin-1)	2.02	Absent	9.80E-05
DR1 (Protein Dr1)	Absent	2.04	3.00E-04
TRIM28 (Transcription intermediary factor 1-beta)	6.94	3.16	2.00E-03
EIF6 (Eukaryotic translation initiation factor 6)	3.80	5.80	2.00E-03
PLEC (Plectin)	Absent	13.96	4.00E-03

SNRPN (Small nuclear ribonucleoprotein-associated protein N)	5.3	8.01	5.00E-03
SFRS9 (Serine/arginine-rich splicing factor 9)	7	11.51 \$	7.00E-03
HDAC2 (Histone deacetylase 2)	8.35	3.97	9.00E-03
POLR2E (DNA-directed RNA polymerases I, II, and III subunit)	4.01	2.29	1.00E-02
HSP90B1 (Endoplasmin)	12.18	5.2	1.00E-02
SMARCB1 (Integraseinteractor 1b protein)	3.02	Absent	2.00E-02
UBC (Ubiquitin C splice variant)	12.91	9.03	2.00E-02
SKIV2L2 (Superkillerviralicidic activity 2-like 2)	5.18	Absent \$	3.00E-02
FUS (RNA-binding protein)	11.88	6.9 \$	3.00E-02
HNRNPK (Heterogeneous nuclear ribonucleoprotein K)	7.21	12.73 \$	3.00E-02
FLOT1 (Flotillin-1)	3.27	Absent	4.00E-02
CBX5 (Uncharacterized protein)	3.51	Absent	4.00E-02
GNB2L1 (Guanine nucleotide-binding protein subunit beta-2)	6.26	Absent	4.00E-02
SMARCC2 (SWI/SNF complex subunit SMARCC2)	9.22	6.44	4.00E-02
TPM3 (Isoform 2 of Tropomyosin alpha-3 chain)	18.68	7.76	4.00E-02
C14orf166 (UPF0568 protein)	3.18	8.34	4.00E-02
ATRX (Transcriptional regulator)	5.31	13.08	4.00E-02
GAPDH (Glyceraldehyde-3-phosphate dehydrogenase)	17.00	11.55	5.00E-02

Newtwork 2 – RNA pot-transcriptional modification

RPS10 (RPS10-NUDT3 protein)	2.37	Absent	6.22E-06
C1QBP (Complement 1Q subcomponent-binding protein)	Absent	4.42	8.00E-04
BPTF (Nucleosome-remodeling factor subunit)	2.08	Absent	1.00E-03
PRPF8 (Pre-mRNA-processing-splicing factor 8)	44.08	73.98 \$	1.00E-03
SFRS5 (Serine/arginine-rich splicing factor 5)	4.18	9.73 \$	5.00E-03
EMD (Emerin)	Absent	3.47	9.00E-03
HMGB3 (Uncharacterized protein)	3.84	2.18	1.00E-02
NUP205 (Nuclear pore complex protein)	8.3	30.67	1.00E-02
PRKCA (Protein kinase C alpha type)	2.37	Absent	2.00E-02
HNRNPA1P10 (Heterogeneous nuclear ribonucleoprotein A1)	7.8	Absent	2.00E-02
LRPPRC (Leucine-rich PPR motif-containing protein)	4.5	2.08	2.00E-02
AQR (Intron-binding protein aquarius)	8.71	12.1	2.00E-02
CAPZA1 (F-actin-capping protein subunit alpha-1)	2.37	Absent	3.00E-02
EEF1B2 (Elongation factor 1-beta)	3	Absent	3.00E-02
RPL9 (60S ribosomal protein L9)	Absent	4.42	3.00E-02
RPL18 (Uncharacterized protein)	2.37	Absent	4.00E-02
SRRT (Serrate RNA effector molecule)	3.25	2.02	4.00E-02
RBMX (Heterogeneous nuclear ribonucleoprotein G)	18.01	12.08 \$	4.00E-02
CNTN1 (Contactin-1)	Absent	4.42	4.00E-02
			1

THOC2 (THO complex subunit)	2.78	5.21	6.00E-02
IARS (Uncharacterized protein)	Absent	4.42	8.00E-02
Network 3 – Molecular transport, RNA trafficking			
DBN1 (Uncharacterized protein)	2.01	Absent	6.22E-06
UQCRC2 (Cytochrome b-c1 complex subunit 2)	4.04	Absent	1.38E-05
CANX (Calnexin)	4.05	Absent	2.00E-04
SPTBN1 (Spectrin beta chain)	6.34	3.01	1.00E-03
CALR (Calreticulin)	3.32	Absent	2.00E-03
KIF5C (Kinesin heavy chain isoform 5C)	7.65	Absent	2.00E-03
PSMA4 (Proteasome subunit alpha type-4)	2.13	4.7	2.00E-03
RAE1 (Uncharacterized protein)	<2	5.77	2.00E-03
CAND1 (Cullin-associated NEDD8-dissociated protein 1)	3.52	Absent	3.00E-03
YWHAG (14-3-3 protein gamma)	6.61	2.71	5.00E-03
PDIA3 (Protein disulfide-isomerase A3)	14.60	6.66	1.00E-02
NUP107 (Nuclear pore complex protein)	2.48	5.51	1.00E-02
NUP160 (Nuclear pore complex protein)	2.63	7.87	1.00E-02
PTPLAD1 (Butyrate-induced transcript 1)	3	Absent	3.00E-02
PSMC5 (26S protease regulatory subunit 8)	2.82	Absent	4.00E-02
CTPS (CTP synthase 1)	5	Absent	4.00E-02

Network 4 - Cell death and survival

PSME2 (Uncharacterized protein)	2.01	Absent	1.78E-16
GPI (Glucose-6-phosphate isomerase)	4.84	Absent	1.54E-05
ASNS (Asparagine synthetase)	2.81	Absent	2.00E-04
ESYT1 (Uncharacterized protein)	2.04	Absent	2.00E-04
ATAD3A (ATPase family AAA domain-containing protein 3A)	3.61	Absent	8.00E-04
ANXA5 (Annexin A5)	2.08	Absent	1.00E-03
HSPH1 (Heat-shock protein 105 kDa)	2.09	Absent	2.00E-03
RCC1 (Regulator of chromosome condensation)	4.93	3.47	2.00E-03
HSPD1 (60 kDa heat shock protein)	20.74	9.12	2.00E-03
PRDX1 (Uncharacterized protein)	Absent	6.71	2.00E-02
VARS (ValyI-tRNAsynthetase)	2.73	Absent	4.00E-02
EIF4A1 (Eukaryotic initiation factor 4A-I)	7.52	3.45	4.00E-02
RARS (Isoform Monomeric of Arginyl-tRNAsynthetase)	3.21	Absent	5.00E-02
RPL21 (60S ribosomal protein L21)	Absent	7.91	5.00E-02
ESYT1 (Uncharacterized protein) ATAD3A (ATPase family AAA domain-containing protein 3A) ANXA5 (Annexin A5) HSPH1 (Heat-shock protein 105 kDa) RCC1 (Regulator of chromosome condensation) HSPD1 (60 kDa heat shock protein) PRDX1 (Uncharacterized protein) VARS (ValyI-tRNAsynthetase) EIF4A1 (Eukaryotic initiation factor 4A-I) RARS (Isoform Monomeric of ArginyI-tRNAsynthetase) RPL21 (60S ribosomal protein L21)	2.04 3.61 2.08 2.09 4.93 20.74 Absent 2.73 7.52 3.21 Absent	Absent Absent Absent 3.47 9.12 6.71 Absent 3.45 Absent 7.91	2.00E-04 2.00E-04 8.00E-04 1.00E-03 2.00E-03 2.00E-03 2.00E-02 4.00E-02 4.00E-02 5.00E-02 5.00E-02

Network 5 –Organ morphology

TBL2 (Uncharacterized protein)	Absent	2.01	7.59E-14

Chapter 4. Ataxin-3 and splicing

2.04	Absent	1.19E-13
2.01	Absent	6.22E-06
2.19	Absent \$	4.71E-05
3.84	Absent	3.00E-03
17.24	12.22	4.00E-03
15.76	10.35	7.00E-03
8.32	3.98	1.00E-02
4.00	Absent	3.00E-02
5.32	Absent	3.00E-02
8.38	4.57	3.00E-02
Absent	3.01	3.00E-02
11.14	5.87	4.00E-02
48.70	62.36	4.00E-02
	2.04 2.01 2.19 3.84 17.24 15.76 8.32 4.00 5.32 8.38 8.38 Absent 11.14 48.70	2.04 Absent 2.01 Absent 2.19 Absent \$ 3.84 Absent \$ 17.24 12.22 15.76 10.35 8.32 3.98 4.00 Absent 5.32 Absent 8.38 4.57 8.38 3.01 11.14 5.87 48.70 62.36

Network 6 - DNA replication, recombination and repair, cell death and Survival

ATXN10 (Ataxin-10)	2.01	Absent	1.78E-16
SNRPB2 (U2 small nuclear ribonucleoprotein B)	Absent	2.01	3.26E-11
SFRS2 (Splicing factor arginine/serine-rich 2)	Absent	2.16 \$	5.36E-11
RBM8A (RNA-binding protein 8A)	Absent	4.01	1.56E-06
MDC1 (Uncharacterized protein)	Absent	2.01	6.22E-06
SFRS7 (Serine/arginine-rich splicing factor 7)	7.45	5.29 \$	8.00E-04
NHP2 (Uncharacterized protein)	Absent	2.12	3.00E-03
TFAP2B (Isoform 2 of Transcription factor AP-2-beta)	7.60	3.37	2.00E-02
MAP1B (Microtubule-associated protein 1B)	11.14	6.12	2.00E-02
CRKL (Crk-like protein)	Absent	4.705	2.00E-02
CAD (Uncharacterized protein)	3.56	Absent	4.00E-02
VIM (Vimentin)	12.20	27.61	4.00E-02

Network 7 - Cell cycle, Cell death and survival

CS (Citrate synthase)	2.01	Absent	1.78E-16
UBXN1 (UBX domain-containing protein 1)	2.01	Absent	1.78E-16
TUBA4A (Tubulin alpha-4 chain)	4.05	Absent	3.00E-03
SAFB (Uncharacterized protein)	6.01	6.32	4.00E-03
ACLY (Uncharacterized protein)	2.2	Absent	8.00E-03
BRD1 (Bromodomain-containing protein 1)	2.65	Absent	1.00E-02
SON (Isoform C of Protein SON)	4.15	9.79	1.00E-02
PHB2 (Prohibitin-2)	22.15	6.71	2.00E-02
PRPF40A (Pre-mRNA-processing factor 40 homolog A)	7.17	10.6 \$	2.00E-02
PHB (Prohibitin)	13.05	4.96	3.00E-02
			•

HSP90AB1 (Heat shock protein HSP 90-beta)	28.70	18.89	3.00E-02
WDR3 (WD repeat-containing protein 3)	15.65	9.64	4.00E-02

Network 8 - Cellular compromise, Cell death and survival

MYL6 (Myosin light polypeptide 6)	Absent	2.01	7.60E-14
ENO2 (Enolase)	2.02	Absent	6.16E-06
ERLIN2 (Uncharacterized protein)	Absent	2.01	2.48E-05
RPL23A (60S ribosomal protein)	4.16	2.23	5.63E-05
CLIC1 (Chloride intracellular channel protein 1)	3.39	Absent	1.00E-03
ATAD2B (ATPase family AAA domain-containing protein 2B)	4.15	Absent	1.00E-03
ATP5B (ATP synthase subunit beta)	15.65	13.16	7.00E-03
CDK5 (Cyclin-dependent kinase 5)	4.25	2.67	9.00E-03
SPTAN1 (Spectrin alpha chain)	19.02	12.18	2.00E-02
SPIN1 (Spindlin-1)	Absent	2.85	2.00E-02
GNAO1 (Guanine nucleotide-binding protein G(o) subunit			
alpha)	Absent	4	4.00E-02

Network 9 - Cellular growth and proliferation, Gene expression, Cell cycle

GNAL (Guanine nucleotide-binding protein G(olf) subunit alpha)	Absent	2.07	2.05E-10
EIF3L (Eukaryotic translation initiation factor 3)	2.01	Absent	6.22E-06
EIF3B (Uncharacterized protein)	2.01	Absent	6.22E-06
TMEM33 (Transmembrane protein 33)	Absent	2.01	6.22E-06
RAB5C (Uncharacterized protein)	3.35	Absent	9.71E-05
SIX6 (Homeobox protein)	2.02	Absent	9.80E-05
RPA1 (Replication protein A 70 kDa)	4.73	Absent	2.00E-02
COPA (Coatomer subunit alpha)	5.69	Absent	2.00E-02
MAB21L1 (Protein mab-21-like 1)	6.16	Absent	2.00E-02
RAB1B (Ras-related protein)	Absent	3.17	2.00E-02
RBM12B (RNA-binding protein 12B)	6.09	7.91	2.00E-02

Network 10 . Cellular development, Cell death and survival, Cell cycle

RBM10 (RNA-binding protein 10)	Absent	2.02	4.78E-19
CCT8 (T-complex protein 1 subunit theta)	6.42	Absent	5.72E-08
TCP1 (T-complex protein 1 subunit alpha)	6.01	Absent	2.77E-06
PSMA1 (Proteasome subunit alpha type-1)	2.01	Absent	6.22E-06
MAP1S (BPY2 interacting protein 1)	Absent	2.04	5.43E-05
GLTSCR2 (Uncharacterized protein)	2.02	Absent	9.80E-05
CCT5 (T-complex protein 1 subunit epsilon)	2.04	Absent	2.16E-04
GDI1 (Rab GDP dissociation inhibitor alpha)	4.77	Absent	9.16E-04

Chapter 4. Ataxin-3 and splicing

TUBB2C (Tubulin beta-2C chain)	20.31	Absent	4.76E-02
CCT4 (T-complex protein 1 subunit delta)	5.16	2.46	4.78E-02
Other			
CUTA (Isoform A of Protein CutA)	Absent	2.01	7.59E-14
GNAI3 (Guanine nucleotide-binding protein G(k) subunit alpha)	Absent	2.01	7.59E-14
TRAP1 (Uncharacterized protein)	2.04	Absent	6.58E-13
ABT1 (Activator of basal transcription 1)	Absent	2.02	2.34E-12
PSMA8 (Proteasome subunit alpha type-7-like)	2.03	Absent	7.71E-12
POTEE (POTE ankyrin domain family member E)	Absent	2.02	7.49E-11
C9orf114 (Uncharacterized protein)	4.01	Absent	1.56E-06
SEPT7 (Uncharacterized protein)	2.01	Absent	6.21E-06
HMBOX1 (Uncharacterized protein)	2.01	Absent	6.21E-06
GLOD4 (CGI-150 protein)	2.01	Absent	6.22E-06
DDX41 (DEAD-box protein abstrakt variant)	2.01	Absent	6.22E-06
DDX56 (ATP-dependent RNA helicase)	2.05	Absent	2.38E-05
PSMA8 (Uncharacterized protein)	Absent	2.01	2.48E-05
TOMM22 (Mitochondrial import receptor subunit)	Absent	4.59	2.54E-05
HIST2H2BD (Histone H2B type 2-D)	Absent	2.77	9.17E-05
BLVRA (Biliverdinreductase A)	2.7	Absent	2.00E-04
ACTL6B (Actin-like protein 6B)	Absent	2.525	3.00E-04
LUC7L (Putative RNA-binding protein Luc7-like 1)	2.68	Absent	5.00E-04
CHMP5 (Charged multivesicular body protein 5)	3.02	Absent	6.00E-04
ISOC1 (Isochorismatase domain-containing protein 1)	3	Absent	7.00E-04
RPL24 (60S ribosomal protein L24)	5.97	2.32 \$	2.00E-03
ABCF1 (ATP-binding cassette sub-family F member 1)	2.75	Absent	3.00E-03
BMS1 (Ribosome biogenesis protein)	5.64	9.42	4.00E-03
PDS5B (Sister chromatid cohesion protein)	4.13	15.82	4.00E-03
PSMD1 (26S proteasome non-ATPase regulatory subunit 1)	3.80	Absent	5.00E-03
DIMT1 (Probable dimethyladenosinetransferase)	3.29	Absent	6.00E-03
WDR75 (WD repeat-containing protein 75)	10.98	8.46	7.00E-03
DDX10 (Probable ATP-dependent RNA helicase)	7.60	3	1.00E-02
DPM1 (Uncharacterized protein)	2.61	6.08	1.00E-02
SLC25A11 (Mitochondrial 2-oxoglutarate/malate carrier)	2.04	6.56	1.00E-02
FN3K (Fructosamine-3-kinase)	2.32	Absent	2.00E-02
ZNF828 (ZNF828 Zinc finger protein 828)	3.05	Absent	2.00E-02
DDX49 (Probable ATP-dependent RNA helicase)	4.32	2.06	2.00E-02
EIF5B (Eukaryotic translation initiation factor 5B)	3.97	10.36	2.00E-02
RTL1 (Retrotransposon-like protein 1)	3.51	Absent	3.00E-02

RANP1 (Uncharacterized protein)	8.63	4.17	3.00E-02
DHX8 (Uncharacterized protein)	Absent	3.01	3.00E-02
MYEF2 (Myelin expression factor 2)	5.58	2.89	4.00E-02
HMGA1 (High mobility group protein HMG-I/HMG-Y)	3.85	3.1	4.00E-02
PELP1 (Proline-, glutamic acid-, leucine-rich protein 1)	6.83	11.12	4.00E-02

Absence of DUB ATXN3 leads to a deregulation of the splicing machinery in neuronal cells

Given the altered ubiquitylation of splicing factors in ATXN3^{±MRMA} cells, we hypothesized that absence of ATXN3 could lead to a global deregulation of the pre-mRNA splicing process. To address this, we used three hybrid minigene reporter plasmids: the α-globin minigene for which the alternative splicing (exon skipping) is indicative of the performance of regulatory splicing factors such as hnRNP and SF proteins, the AdML minigene representing constitutive/strong splicing events, and the pyPY minigene, representing splicing events with alternative competing 3' acceptor sites/splice sites [30, 31] (Figure 2A). As shown in Figure 2B and C, knockdown of ATXN3 significantly altered the processing of the 3 splicing reporters, suggesting a general deregulation of the splicing machinery.



Figure 2. Efficacy of RNA processing assessed by splicing reporter minigenes in ATXN3^{+MMA} cells. (A) Schematic representation of the splicing reporter minigenes used for cell transfection. Exons are represented as colored boxes and introns by black lines. The AdML minigene contains one intron, giving rise to two bands: the upper band corresponds to the unspliced transcript, the lower band to the spliced product. The pyPY minigene contains two alternative splice sites originating three bands: an upper band corresponding to the unspliced transcript, a middle band corresponding to the splicing of the weak py tract and a lower band corresponding to the splicing product of the strong PY tract. The pyPY minigene contains two alternative 3' splice sites associated with polypirimidine (Py) tracts with different strengths. The weak Py tract (py) is represented by thin black lines and the strong Py tract (PY) by a thick black line. The α -globin minigene contains two introns and a set of G triplets in intron 2 that promote the recognition of the 5' splice site leading to skipping of exon 2. (B, C) Semi-quantitative analysis of minigene alternative splicing showed a decreased efficiency of splicing in ATXN3^{+MMA} cells. Schemes for the splicing products are indicated on the right. *p<0,05; **p<0,01; ***p<0,001.

Microarray analysis of alternative splicing in ATXN3shrma cells

To further explore the putative involvement of ATXN3 in splicing and in alternative splicing regulation in neuronal cells, we performed microarray analysis (Figure 3A) using specific arrays that contain additional probes for exon/exon junctions. In agreement with our hypothesis, a large proportion of the 7450 differentially expressed genes (43%) presented differentially regulated alternative splicing events (Table A2) in RA-treated ATXN3^{entrue} cells. The most prevalent alternative event types were related with exon cassettes (34%) and usage of alternative first exons (20%) (Figure 3B).





Figure 3. Experimental design – microarray analysis of alternative splicing. (A) Affymetrix Human Transcriptome Array 2.0 ST analysis were used to assess perturbation of global splicing patterns in RA-treated ATXN3^{thRMA} cells. (B) Distribution of the differentially regulated alternative splicing events in ATXN3^{thRMA} cells. Three independent biological replicates were used for analysis.

KEGG pathway analysis of the genes with differentially regulated alternative splicing events identified 22 significant pathways (Table 2).

Table 2. KEGG pathway analysis of genes with altered splicing in ATXN3^{thRNA} cells. The genes identified on the KEGG pathway analysis presented at least one differentially regulated exon/splicing pattern in ATXN3^{thRNA} cells.

Pathway description (KEGG)	Number of genes in the pathway	Number of altered genes	p value
Nucleotide excision repair	44	21	1.24E-04
Adherens junction	77	30	1.40E-04
Spliceosome	126	42	1.93E-04
Ubiquitin mediated proteolysis	137	43	3.16E-04
Endometrial cancer	52	21	5.37E-04
Neurotrophin signaling pathway	124	38	1.23E-03
Axon guidance	129	39	1.39E-03
Pathogenic Escherichia coli infection	57	22	2.03E-03
Endocytosis	184	52	3.36E-03
Prostate cancer	89	30	4.20E-03
RNA degradation	57	20	5.01E-03
Ribosome	87	28	6.12E-03
Pathways in cancer	328	79	7.35E-03
Focal adhesion	201	52	1.25E-02
MAPK signaling pathway	267	64	1.79E-02
Apoptosis	87	25	2.26E-02
VEGF signaling pathway	75	22	2.70E-02
Colorectal cancer	84	24	2.75E-02
Pancreatic cancer	72	21	3.30E-02
Type I diabetes mellitus	42	17	3.45E-02
Fc gamma R-mediated phagocytosis	95	27	3.53E-02
Selenoamino acid metabolism	26	10	3.71E-02
Alzheimer's disease	163	40	4.49E-02

Intriguingly, one of the top KEGG pathways was the spliceosome itself (p=0.000193) with 33% of the genes involved in the pathway presenting altered splicing events in ATXN3^{±HTMA} cells (Figure 4A). Some of these genes were also differentially expressed and had altered ubiquitylation in ATXN3^{±HTMA} cells (Table 1 and Figure 4A). Other relevant pathways were the ubiquitin mediated proteolysis, neurotrophin signaling, axon guidance, focal adhesion and MAPK signaling pathway, as well as the link to AD (Table 2). We next analyzed the candidate splicing factors related to the deregulated splicing events in ATXN3^{±HTMA} cells. Remarkably, around 6% of the proteins presenting altered polyubiquitylation levels in ATXN3^{±HTMA} cells while showing no alterations at the transcription level, were identified in the bioinformatic analysis of the microarray data as predicted regulators of genes with a differentially regulated exon/splicing pattern in these cells. Among these, four splicing factors did not present alterations in expression nor differentially regulated exons, but showed
decreased abundance in the polyubiquitylated protein fraction: SFRS2, SFRS5, SFRS7 and SFRS9 (Figure 4B). These proteins are good candidate substrates of ATXN3. While SFRS 2,7,and 9 were predicted to regulate splicing events of a large amount of genes (Table S2), SFRS5 was predicted to regulate only the *TRIM36* gene, which presents alternative first exon and exon cassette events differentially regulated in ATXN3+### cells. Together, these results support our hypothesis that ATXN3 may play a role in pre-mRNA splicing regulation through modulation of the ubiquitylation of splicing factors in neuronal cells.



В



Figure 4. Absence of ATXN3 alters expression, ubiquitylation and exon regulation of splicing components. (A) Scheme of the spliceosome assembly pathway, involving genes differentially

regulated in ATXN3™ at the alternative splicing (blue/black), total mRNA expression (white/red), both alternative splicing and total mRNA expression (blue/red) and ubiquitylation (green dot) level. (B) Venn diagram showing overlapping of splicing factors presenting globally altered expression, differentially regulated exons and altered polyubiquitylation levels in ATXN3™ cells. p≤0.05.

DISCUSSION

Ubiquitin signaling is now widely recognized as a fundamental molecular mechanism controlling a broad range of intracellular events in the nervous system (Reviewed in [5, 34, 35]). Taking into account the importance of DUB enzymes in maintaining the ubiquitylation balance, we focused on the characterization of the ubiquitome of neuronal cells lacking ATXN3 [27]. Using TUBEs, that enable the pulldown of polyubiquitylated proteins without further genetic manipulation or inhibition of the proteasome [26], in combination with LC-MS/MS, we were able to consistently identify around 615 proteins per condition, which seems to be a yield comparable to those described in other studies [33, 36]. Among the proteins identified, approximately one third presented altered levels of polyubiquitylation in ATXN3²⁰⁰⁰⁰ cells. Curiously, the majority of these proteins presented decreased levels of polyubiquitylation, suggesting that normally ATXN3 might be preventing their degradation for instance by editing the substrate's ubiquitylation and preventing its degradation. Therefore, when ATXN3 is silenced, the ubiquitin signaling is not removed, which may result in an increased degradation of the targeted protein. We have previously shown that absence of ATXN3 causes a decrease of the polyubiquitylated forms of α 5-integrin, a potential substrate of ATXN3 DUB activity, in parallel with a decrease of the total levels of this protein [27, 37].

The fact that a significant proportion of the proteins with altered polyubiquitylation levels in ATXN3^{LINTM} cells were splicing factors and proteins involved in RNA processing, led us to raise the hypothesis that ATXN3 could be playing a role in the pre-mRNA splicing process in neuronal cells. Indeed, the relative concentration of splicing factors and heterogeneous nuclear ribonucleoproteins (hnRNPs) have been shown to regulate alternative splicing (Reviewed in [38]). When we assessed general splicing effectiveness in cells depleted of ATXN3 using artificial reporter minigenes, we found a reduction in reporter splicing, further suggesting the involvement of ATXN3 in the regulation of the splicing machinery. Additionally, genome wide microarray analysis of splicing events revealed that absence of ATXN3 leads to an alteration in the pattern of alternative splicing events in a large number of genes in neuronal cells, including genes encoding spliceosome components, but also genes related with protein degradation, adhesion, axon guidance and signaling pathways. These findings are interesting, since we have previously described that absence of ATXN3 leads to

impairment in neuronal differentiation and adhesion, and deregulates the degradation of target proteins [27]. Significantly, a portion of predicted regulators of those genes were found to have altered levels of polyubiquitylation in our proteomic analysis, the majority of them being Serine/arginine (SR)-rich phosphoproteins. Proteins of the SR family are key players in the control of alternative splicing, regulating the selection of alternative sites (Reviewed in [39, 40]). Protein kinases such as AKT that are involved in the phosphorylation of SR and hnRNP, usually acting as antagonists of SR proteins in alternative splicing process, were also found to have altered ubiquitylation patterns in our study [41]. Interestingly, we have previously observed that the phosphatidylinositol 3-kinase (PI3K)/AKT signaling pathway was deregulated in ATXN3 me cells [27]. While the majority of the identified SR factors were predicted to regulate a large number of genes (Supplementary Table A2), the serine/arginine-rich splicing factor 2 (SFSR2) was predicted to regulate the Tripartite motif 36 (TRIM36) gene. TRIM36 is an E3 ubiquitin ligase [42, 43] that mediates ubiquitylation and subsequent proteasomal degradation of target proteins and was also reported to be associated with the microtubule cytoskeleton [44, 45] and to regulate cell cycle [45]. As we have previously observed that ATXN3. A cells showed a disruption of the cytoskeletal network and that they keep proliferating even after being induced to differentiate, it would be interesting to dissect the contribution of SFSR2 and TRIM36 to this phenotype.

Overall, our data suggest that ATXN3 is involved in splicing regulation probably through the modulation of the ubiquitylation of splicing factors. This regulatory role may be mediated through the DUB activity of ATXN3 by modulating activation, degradation and/or subcellular localization of splicing factor, or may be an indirect result of the modulation of E3 ligases specific for these targets. It remains to be seen whether this finding is also relevant for the neurodegeneration observed in MJD. Recently, several pieces of evidence have suggested an association between perturbation of alternative splicing and several neurodegenerative disorders, including AD, HD, PD, SMA and ALS (Reviewed in [46-48]). For example, it was described that several ataxia-causing proteins interact with splicing factors [49]. Also, the RNA-binding protein TDP-43 has been found to be the major component of the characteristic inclusions seen in a number of neurodegenerative diseases [50-52]. Sun and colleagues have shown that expression of mutant ATXN3 bearing an expanded polyQ tract in HeLa cells alters the ability of the subnuclear domains known as Cajal bodies to participate efficiently in small nuclear ribonucleoprotein (snRNP) biogenesis pathway and reduces the efficacy of splicing of reporter genes, and suggested that this was a consequence of the disruption of the normal function of ATXN3 in the UPS [53]. This possibility should be further explored in neuronal

cells and animal models expressing expanded ATXN3. This should contribute to our understanding whether the role of ATXN3 in splicing is important for MJD pathogenesis.

Bibliography

- 1. Hershko, A. and A. Ciechanover, *The ubiquitin system*. Annu Rev Biochem, 1998. **67**: p. 425-79.
- 2. Komander, D., *The emerging complexity of protein ubiquitination.* Biochem Soc Trans, 2009. **37**(Pt 5): p. 937-53.
- 3. Hegde, A.N., *Ubiquitin-proteasome-mediated local protein degradation and synaptic plasticity.* Prog Neurobiol, 2004. **73**(5): p. 311-57.
- 4. Tai, H.C. and E.M. Schuman, *Ubiquitin, the proteasome and protein degradation in neuronal function and dysfunction.* Nat Rev Neurosci, 2008. **9**(11): p. 826-38.
- 5. Hegde, A.N. and S.C. Upadhya, *Role of ubiquitin-proteasome-mediated proteolysis in nervous system disease.* Biochim Biophys Acta, 2011. **1809**(2): p. 128-40.
- 6. de Vrij, F.M., et al., *Protein quality control in Alzheimer's disease by the ubiquitin proteasome system.* Prog Neurobiol, 2004. **74**(5): p. 249-70.
- 7. Upadhya, S.C. and A.N. Hegde, *Ubiquitin-proteasome pathway components as therapeutic targets for CNS maladies.* Curr Pharm Des, 2005. **11**(29): p. 3807-28.
- Rubinsztein, D.C., *The roles of intracellular protein-degradation pathways in neurodegeneration.* Nature, 2006.
 443(7113): p. 780-6.
- 9. Tan, J.M., et al., *Lysine 63-linked ubiquitination promotes the formation and autophagic clearance of protein inclusions associated with neurodegenerative diseases.* Hum Mol Genet, 2008. **17**(3): p. 431-9.
- 10. Paine, S., et al., *Immunoreactivity to Lys63-linked polyubiquitin is a feature of neurodegeneration.* Neurosci Lett, 2009. **460**(3): p. 205-8.
- 11. Dennissen, F.J., N. Kholod, and F.W. van Leeuwen, *The ubiquitin proteasome system in neurodegenerative diseases: culprit, accomplice or victim?* Prog Neurobiol, 2012. **96**(2): p. 190-207.
- Li, Q., J.A. Lee, and D.L. Black, *Neuronal regulation of alternative pre-mRNA splicing.* Nat Rev Neurosci, 2007. 8(11): p. 819-31.
- 13. Ule, J. and R.B. Darnell, *RNA binding proteins and the regulation of neuronal synaptic plasticity.* Curr Opin Neurobiol, 2006. **16**(1): p. 102-10.
- 14. Norris, A.D. and J.A. Calarco, *Emerging Roles of Alternative Pre-mRNA Splicing Regulation in Neuronal Development and Function.* Front Neurosci, 2012. **6**: p. 122.
- 15. Makarov, E.M., et al., *Small nuclear ribonucleoprotein remodeling during catalytic activation of the spliceosome*. Science, 2002. **298**(5601): p. 2205-8.
- 16. Rappsilber, J., et al., *Large-scale proteomic analysis of the human spliceosome.* Genome Res, 2002. **12**(8): p. 1231-45.
- 17. Peng, J., et al., *A proteomics approach to understanding protein ubiquitination.* Nat Biotechnol, 2003. **21**(8): p. 921-6.
- Doss-Pepe, E.W., et al., *Ataxin-3 interactions with rad23 and valosin-containing protein and its associations with ubiquitin chains and the proteasome are consistent with a role in ubiquitin-mediated proteolysis.* Mol Cell Biol, 2003. 23(18): p. 6469-83.
- 19. Wang, Q., L. Li, and Y. Ye, *Regulation of retrotranslocation by p97-associated deubiquitinating enzyme ataxin-3.* J Cell Biol, 2006. **174**(7): p. 963-71.
- 20. Zhong, X. and R.N. Pittman, *Ataxin-3 binds VCP/p97 and regulates retrotranslocation of ERAD substrates.* Hum Mol Genet, 2006. **15**(16): p. 2409-20.
- 21. Ferro, A., et al., *NEDD8: a new ataxin-3 interactor.* Biochim Biophys Acta, 2007. **1773**(11): p. 1619-27.
- 22. Tsai, Y.C., et al., *Parkin facilitates the elimination of expanded polyglutamine proteins and leads to preservation of proteasome function.* J Biol Chem, 2003. **278**(24): p. 22044-55.
- 23. Rodrigues, A.J., et al., *ATX-3, CDC-48 and UBXN-5: a new trimolecular complex in Caenorhabditis elegans.* Biochem Biophys Res Commun, 2009. **386**(4): p. 575-81.
- 24. Durcan, T.M., et al., *The Machado-Joseph disease-associated mutant form of ataxin-3 regulates parkin ubiquitination and stability.* Hum Mol Genet, 2011. **20**(1): p. 141-54.
- 25. Jana, N.R., et al., *Co-chaperone CHIP associates with expanded polyglutamine protein and promotes their degradation by proteasomes.* J Biol Chem, 2005. **280**(12): p. 11635-40.
- 26. Hjerpe, R., et al., *Efficient protection and isolation of ubiquity/lated proteins using tandem ubiquitin-binding entities.* EMBO Rep, 2009. **10**(11): p. 1250-8.
- 27. Neves-Carvalho, A., Logarinho E., Freitas A., Duarte-Selva S., Costa M.C., Silva-Fernandes A., Martins M., Serra S.C., Lopes, A. T., Paulson, H.L., Heutink, P., Relvas, J.B. and Maciel P., *Dominant negative effect of*

polyglutamine expansion perturbs normal function of ataxin-3 in neuronal cells. Human Molecular Genetics, 2014.

- Colledge, M., et al., *Targeting of PKA to glutamate receptors through a MAGUK-AKAP complex.* Neuron, 2000.
 27(1): p. 107-19.
- Shilov, I.V., et al., *The Paragon Algorithm, a next generation search engine that uses sequence temperature values and feature probabilities to identify peptides from tandem mass spectra.* Mol Cell Proteomics, 2007. 6(9): p. 1638-55.
- 30. Guth, S., et al., *Evidence for substrate-specific requirement of the splicing factor U2AF(35) and for its function after polypyrimidine tract recognition by U2AF(65).* Mol Cell Biol, 1999. **19**(12): p. 8263-71.
- 31. Pacheco, T.R., et al., *In vivo requirement of the small subunit of U2AF for recognition of a weak 3' splice site.* Mol Cell Biol, 2006. **26**(21): p. 8183-90.
- 32. Pfaffl, M.W., *A new mathematical model for relative quantification in real-time RT-PCR*. Nucleic Acids Res, 2001. **29**(9): p. e45.
- 33. Lopitz-Otsoa, F., et al., *Integrative analysis of the ubiquitin proteome isolated using Tandem Ubiquitin Binding Entities (TUBEs).* J Proteomics, 2012. **75**(10): p. 2998-3014.
- 34. Yi, J.J. and M.D. Ehlers, *Emerging roles for ubiquitin and protein degradation in neuronal function.* Pharmacol Rev, 2007. **59**(1): p. 14-39.
- 35. Baptista, M.S., C.B. Duarte, and P. Maciel, *Role of the ubiquitin-proteasome system in nervous system function and disease: using C. elegans as a dissecting tool.* Cell Mol Life Sci, 2012. **69**(16): p. 2691-715.
- 36. Li, K.W., et al., *Identifying true protein complex constituents in interaction proteomics: the example of the DMXL2 protein complex.* Proteomics, 2012. **12**(15-16): p. 2428-32.
- 37. do Carmo Costa, M., et al., *Ataxin-3 plays a role in mouse myogenic differentiation through regulation of integrin subunit levels.* PLoS One, 2010. **5**(7): p. e11728.
- 38. Busch, A. and K.J. Hertel, *Evolution of SR protein and hnRNP splicing regulatory factors.* Wiley Interdiscip Rev RNA, 2012. **3**(1): p. 1-12.
- 39. Graveley, B.R., *Sorting out the complexity of SR protein functions.* RNA, 2000. **6**(9): p. 1197-211.
- 40. Fu, X.D., *The superfamily of arginine/serine-rich splicing factors.* RNA, 1995. **1**(7): p. 663-80.
- 41. Blaustein, M., et al., *Concerted regulation of nuclear and cytoplasmic activities of SR proteins by AKT.* Nat Struct Mol Biol, 2005. **12**(12): p. 1037-44.
- 42. Henry, J., et al., *B30.2-like domain proteins: update and new insights into a rapidly expanding family of proteins.* Mol Biol Evol, 1998. **15**(12): p. 1696-705.
- 43. Reymond, A., et al., *The tripartite motif family identifies cell compartments.* EMBO J, 2001. **20**(9): p. 2140-51.
- Short, K.M. and T.C. Cox, Subclassification of the RBCC/TRIM superfamily reveals a novel motif necessary for microtubule binding. J Biol Chem, 2006. 281(13): p. 8970-80.
- 45. Miyajima, N., et al., *TRIM36 interacts with the kinetochore protein CENP-H and delays cell cycle progression.* Biochem Biophys Res Commun, 2009. **381**(3): p. 383-7.
- 46. Singh, N.N. and R.N. Singh, *Alternative splicing in spinal muscular atrophy underscores the role of an intron definition model.* RNA Biol, 2011. **8**(4): p. 600-6.
- 47. Orozco, D. and D. Edbauer, *FUS-mediated alternative splicing in the nervous system: consequences for ALS and FTLD.* J Mol Med (Berl), 2013. **91**(12): p. 1343-54.
- 48. Mills, J.D. and M. Janitz, *Alternative splicing of mRNA in the molecular pathology of neurodegenerative diseases.* Neurobiol Aging, 2012. **33**(5): p. 1012 e11-24.
- 49. Ranum, L.P. and T.A. Cooper, *RNA-mediated neuromuscular disorders.* Annu Rev Neurosci, 2006. **29**: p. 259-77.
- 50. Arai, T., et al., *TDP-43 is a component of ubiquitin-positive tau-negative inclusions in frontotemporal lobar degeneration and amyotrophic lateral sclerosis.* Biochem Biophys Res Commun, 2006. **351**(3): p. 602-11.
- 51. Kwong, L.K., et al., *TDP-43 proteinopathies: neurodegenerative protein misfolding diseases without amyloidosis.* Neurosignals, 2008. **16**(1): p. 41-51.
- 52. Neumann, M., et al., *Ubiquitinated TDP-43 in frontotemporal lobar degeneration and amyotrophic lateral sclerosis.* Science, 2006. **314**(5796): p. 130-3.
- 53. Sun, J., et al., *Differential effects of polyglutamine proteins on nuclear organization and artificial reporter splicing.* J Neurosci Res, 2007. **85**(11): p. 2306-17.

Chapter 5

General Discussion and Future Perspectives

5.1 The neuronal function(s) of ATXN3

The precise physiological role(s) of ATXN3 are still poorly identified. This is particularly true when focusing on its biological function in neurons. However, the selective neuronal degeneration observed in MJD highlights the importance of determining what is ATXN3 doing in neurons, for our understanding of the pathogenic mechanism(s). We chose the SH-SY5Y human neuroblastoma cell line as a model to generate mutant cell lines of ATXN3 knockdown, to gain insight into the physiological function of ATXN3 in neuronal cells. Interestingly, ablation of ATXN3 function in these cells led to a clear phenotype, which will be discussed in the following sections.

5.1.1 Defining the ubiquitome of SH-SY5Y ATXN3 KD cells

As mentioned above, although it has been demonstrated that ataxin-3 is a DUB enzyme, its substrates remain mostly unidentified. To date, it was only demonstrated that ataxin-3 deubiquitylates CHIP [1] and parkin both *in vitro* and in cells [2], and it most likely regulates the ubiquitylation and degradation of α 5-integrin [3, 4]. However, the fact that Atxn3 KO mice present increased total levels of ubiquitylated proteins [5] suggests that ataxin-3 may regulate the ubiquitylation status of many proteins.

Typically, researchers study the fate of a single Ub substrate, characterize its mode of recognition and ubiquitylation, and study its regulation under variable pathophysiological conditions. In this study, taking into account the suggested diversity of substrates for ATXN3, we took an integrated approach based on mass spectrometry. There are at least three confounding factors that could limit this approach: (i) only a small percentage of a given protein is ubiquitylated in the steady state, (ii) the enzymatic action of DUBs decrease the levels of ubiquitylated proteins upon cell lysis, and (iii) the existence of ub-like proteins. To overcome these limitations, we used a recently described methodology based in Tandem Ubiquitin Binding Entities (TUBEs) to isolate

polyubiquitylated proteins from our cell lines depleted for ATXN3 and compare them to control cells. This strategy presents the following advantages over the classical approaches: TUBEs (i) protect polyubiquitylated proteins against DUBs and the proteasome, (ii) do not require the presence of chemical inhibitors, addition of tags, protein overexpression or genetic manipulations, (iii) reduce the effects on Ub chain architecture, and (iv) specifically recognize polyUB chains and no other Ub-like proteins [6, 7].

From this experiment, we have successfully identified 615 ubiquitylated proteins, from which 193 were present at altered levels in ATXN3 KD cells, some of which may constitute candidate substrates of ATXN3's DUB activity.

5.1.2 The balance of ubiquitylation and ATXN3

Because ubiquitylation has been shown to play a crucial role in the regulation of neuronal development, differentiation and function, it needs to be tightly controlled (Reviewed in [8]). Thus, loss of DUB enzymes and consequent disruption of the ubiquitylation homeostasis might disturb neuronal function, by altering the stability of individual proteins, leading to neuronal dysfunction. In agreement with this hypothesis, we found that silencing of ATXN3 in neuronal cells led to an alteration of the polyubiquitylation in 32% of the identified proteins in our TUBES-LC-MS/MS approach (Chapter 4). Curiously, the majority of these proteins showed decreased abundance in the polyubiquitylated protein fraction in ATXN3 KD cells, and we showed that proteasome inhibition leads to an accumulation of such proteins. One good example is ITGA5. We have shown that ATXN3 interacts with ITGA5 [3] and normally acts to inhibit ITGA5 degradation, affecting its steady-state levels; when ATXN3 is silenced, more ubiquitylated ITGA5 accumulates in the cell (detectable only upon proteasome inhibition), and ITGA5 is extensively degraded causing defects in cell

adhesion and deregulation of downstream cascades (Chapter 2). Interestingly, this regulatory mechanism seems to be important for different cellular types, since our team has shown before that rescue of Itga5 from proteasomal degradation by mouse Atxn3 is essential for muscle cell differentiation *in vitro* [3]. Another finding illustrating this concept is the decreased levels of SFRS7 that are observed in ATXN3 depleted cells (Chapter 3). In this case, technical limitations excluded the confirmation of SFRS7 as a target of direct regulation by ATXN3, as the inhibition of the proteasome leads to a general inhibition of splicing factors expression. Optimization of this assay is ongoing. However, the possibility remains that SFRS7 and other proteins can also be indirect targets of the DUB activity of ATXN3. It is possible that ATXN3 is modulating the activity of E3 ligases for these substrates and this way controlling their degradation. In line with that, ATXN3 was already shown to regulate the activity of some E3s, such as Parkin [2] and CHIP [9]. In the case of ITGA5, at least one E3 ligase was already identified that coordinates its degradation by the proteasome – Cbl [10]. To better understand the regulation of ITGA5 by ATXN3, it would be valuable to determine whether ATXN3 interacts directly with the intracellular domain of this protein and deubiquitylates it *in vitro*, or whether it interacts with and regulates Cbl activity.

Alternatively, many of these molecular alterations may also occur due to cellular compensatory mechanisms and/or be a consequence of other cellular changes due to the absence of ATXN3. In this case, overexpression of an ATXN3 version lacking the cysteine 14 residue (ATXN3_C14A), critical for its DUB activity [11] allows us to dissociate the ubiquitome changes induced by the absence of ATXN3 (and cellular compensations induced by this absence) from the ones associated with the abolishment/perturbation of its DUB activity.

Looking at the overall changes in the ubiquitome of neuronal cells lacking ATXN3, it seems evident that ATXN3 is contributing (either direct or indirectly) to the regulation of proteasomal

degradation of many diverse substrates and can be participating in different biological pathways. Grouping the proteins with altered levels of polyubiquitylation in ATXN3 mutant cells, we found that a significant number were involved in: i) gene expression, ii) RNA post-transcriptional modifications, iii) molecular transport and RNA trafficking, and iv) cell death and survival, classes that were in concordance with other findings, which supports the importance of the ubiquitylation balance for cellular homeostasis. This will be discussed in the next sections.

5.1.3 Splicing and ATXN3

The fact that a significant proportion of the proteins with altered polyubiquitylation levels in ATXN3 cells were splicing factors and proteins involved in RNA processing caught our attention. Recently, the use of new technologies such as exon arrays and RNA-seq to study the human transcriptome have revealed an association between alternative splicing and a number of neurodegenerative disorders, including AD, HD, PD, Spinal Muscular Atrophy (SMA), Amyotrophic lateral sclerosis (ALS) and Frontotemporal lobar degeneration (FTDP-17) (Reviewed in [12-15]). For example, mutations in presenilin 1 (PSEN1) and presenilin 2 (PSEN2), proteins involved in AD pathology, lead to the formation of aberrant transcripts bearing in frame insertions or lacking exon 4, resulting in increased β -amyloid levels, causally linked to AD [16-18]. Also, mutant Huntingtin (htt), the disease-protein involved in HD, was shown to affect alternative splicing of the BDNF gene, in a transgenic mouse model of HD [19]. Recently, it was shown that mutant HTT alters alternative splicing of tau exon 10 causing a deregulation of the 4R/3R tau isoform ratio and ttal tau content, a phenomenon that seems to be playing a role in HD pathogenesis [20]. The alteration of FUSregulated RNA processing has also been proposed as a key event in ALS (Reviewed in [21-23]). The skipping of exon 7 of survival motor neuron (SMN) gene leads to a truncated and highly unstable protein resulting in SMA [13]. The RNA-binding protein TDP-43 is a major component of inclusions characteristic of a number of neurodegenerative conditions [24-26]. Although not yet explored in detail, interaction of several ataxia-causing proteins with splicing factors have also been described, namely for proteins linked to SCA2, 8, 10 and 12 (Reviewed in [27]).

Indirect pieces of evidence suggest that ubiquitylation may regulate splicing: i) Ub and Ublike proteins co-purify with splicing complexes [28, 29], ii) ubiquitylated splicing factors have been identified in proteomic studies [30], iii) several protein domains related to the UPS were found in key spliceosome proteins [31-34], iv) essential splicing factors as Prp19 and Prp8 have Ub ligase activity *in vitro* [31, 35, 36], and v) Ub mutants (I44A) with diminished capacity for protein-protein interactions strongly inhibit splicing *in vitro* [37]. Additionally, the relative concentration of splicing factors and heretogeneous nuclear ribonucleoproteins (hnRNPs) have been shown to regulate alternative splicing (Reviewed in [38]). Considering that ATXN3 is an Ub hydrolase, we hypothesized that it could also be playing a role in the regulation of pre-mRNA processing.

Indeed, we have shown that ATXN3 interacts with the splicing factor SRSF7, a protein acting on the alternative splicing of tau mRNA. Additionally, we demonstrated that absence of ATXN3 leads to a deregulation of tau exon 10 alternative splicing, perturbing the 3R/4R tau isoform ratio (Chapter 3). We further demonstrated that this effect might be relevant for MJD pathogenesis, since we have observed similar events in cells overexpressing mutant ATXN3 and in the brain of a transgenic mouse model of MJD. Interestingly, overexpression of the 4R isoform in cells lacking ATXN3, rescued some of the phenotypic abnormalities of these cells, described in Chapter 2. This result prompted us to ask whether the potential role for ATXN3 in the pre-mRNA splicing process was specific for the *MAPT* gene or if absence of ATXN3 could have a global impact on splicing machinery. Interestingly, we found that knockdown of ATXN3 significantly reduced the efficacy of the processing of three hybrid minigene reporters, suggesting a global deregulation of the splicing process in the cell (Chapter 4). In addition to this, by performing microarray analysis of alternative splicing, we uncovered dramatic changes in alternative splicing (mostly exon cassettes and usage of alternative first exons) in neuronal cells lacking ATXN3. Remarkably, several proteins presenting altered polyubiquitylation levels in ATXN3 mutant cells were identified in the bioinformatic analysis of the microarray data as predicted regulators of splicing genes with an altered splicing pattern in these cells, namely SFRS2, 5, 7 and 9. Among them, SFRS2 caught our attention because it was predicted to regulate the tripartite motif 36 (*TRIM36*) gene. TRIM36 is an E3 Ub ligase reported to regulate cell cycle [39] and to be associated with the microtubule cytoskeleton [40]. As we have observed that absence of ATXN3 causes a disruption of the cytoskeleton network and that mutant cells have an abnormal proliferative activity (Chapter 2), it would be interesting to evaluate the contribution of TRIM36 to this phenotype. Furthermore, KEGG pathway analysis of the microarray data identified several genes with altered alternative splicing patterns belonging to Ub mediated proteolysis, neurotrophin signaling, axon guidance, focal adhesion and MAPK signaling pathways, as well as linked to AD, which would also be interesting to further explore.

In line with our observations, Sun and colleagues have shown that expression of mutant ATXN3 (bearing an expanded polyQ tract) disturbs the biogenesis of small nuclear ribonucleoproteins (snRNPs) and reduces the efficacy of splicing reporter genes in HeLa Cells [41]. It would be interesting to further explore if this novel role of ATXN3 is also relevant for the neurodegeneration observed in MJD, by analyzing this process in primary cultures of neuronal cells and in affected brain regions of animal models expressing expanded ATXN3. If this were the case, it would also be interesting to determine whether the splicing alterations were age-related (since MJD is a late onset disease) and if they could correlate with the symptoms and neurodegeneration present in MJD patients. Indeed, it was reported that age-related splicing changes occur in healthy individuals and that this event may constitute a link between aging and neurodegeneration in AD

[42]. The tissue-specific splicing patterns coud also provid a key to neurospecificity in MJD and other neurodegenerative diseases.

Other pathways enriched in our analysis were pathways related with cancer and nucleotide excision repair (NER). Indeed, several recent reports have been demonstrating a link between alteration of splicing profiles and cancer [43-45]. It is thought that altered activity, expression levels or even mutations of splicing regulators may be associated with tumor progression and to contribute to metastases formation [46]. Interestingly, in the last few years a tight connection between SRSFs and cancer has been demonstrated. Also, although some aspects of the relantionship between DNA repair mechanisms and alternative splicing have not been fully explained, a link between mRNA metabolism and genomic stability has been provided by the following observations: i) the mRNA splicing pattern of crucial genes is altered in DNA damage response [47], ii) the intracellular distribution of splicing factors changes following genotoxic damage (Reviewed in [48, 49]), iii) DNA damage inhibits transcription [48, 49], and iv) mRNa stability is affected by DNA damage (Reviewed in [50]).

Therefore, understanding how alternative splicing factors can contribute to disease and, in turn, the splicing pattern alterations in pathological conditions can be valuable for the discovery of novel targets for therapies of diverse diseases, including several types of cancer and neurodegenerative disorders.

5.1.4 Cell structure, cytoskeleton and ATXN3

Neurons are highly dependent on a well-structured dynamic cytoskeleton network. The neuronal cytoskeleton is essential for the maintenance of the structural integrity of the neuron, neurite outgrowth and axonal transport, as well as cell-cell interactions and cell connections with extracellular matrix (ECM) components. Therefore, although the initiators of neuronal dysfunction may differ, disruption of the neuronal cytoskeleton has been suggested to be a common feature contributing to neurodegeneration in several diseases, including polyQ diseases (Reviewed in [51-54]). For example, mutations in the cytoskeletal protein β -III spectrin were shown to cause SCA5. Also, abnormal aggregates of cytoskeletal components such as intermediate filament proteins and microtubule-associated proteins (MAPs) (e.g. tau) have been identified as neuropathological signatures of many neurodegenerative diseases. Although there was no data so far regarding cytoskeletal involvement in MJD, the demonstration that ATXN3 interacts with alpha-tubulin [55] suggested to us that this protein could play a role in cytoskeleton regulation. Indeed, subsequent studies from our lab and others further supported this hypothesis: i) large proportions of ataxin-3 molecular partners identified in Yeast-two hybrid and pull down screenings are cytoskeleton components [56, 57], ii) ataxin-3 interacts with HDAC6, which mediates post-transcriptional modifications of cytoskeleton proteins (Reviewed in [58]), iii) ATXN3 is a MAP [55], iv) ATX-3 KO C. elegans have a significant transcriptional deregulation of cytoskeleton proteins [59], and v) ATXN3 KD leads to obvious cytoskeleton defects and abnormal cell morphology in C2C12 and HeLa cells [3, 55]. But could this function be important also for the nervous system? Could ATXN3 be involved in cytoskeleton organization and cell structure maintenance also in neuronal cells? In this work, we showed that absence of ATXN3 lead to a deregulation of the cytoskeleton network of SH-SY5Y cells, which was associated with an abnormal morphology and reduced branching (Chapter 2). Although the increased degradation of ITGA5 and consequent alteration of the signaling to the cytoskeleton can partially explain this cellular phenotype, we believe that silencing of ATXN3 perturbs several different pathways that may contribute to this cellular phenotype. Indeed, we found that in the absence of ATXN3 many genes controlling cytoskeleton biogenesis and reorganization were differentially transcribed impacting, for example, on cell projections, G-protein signaling, cell motility/migration, cell cycle and division and cell shape. One of the genes that caught our attention was the MAPT gene, which was significantly downregulated in the mutant cells (Chapter 3). This

finding, together with the observations that i) ATXN3 interacts with SFSR7 in SH-SY5Y neuronal cells, ii) absence of ATXN3 disturbed tau splicing – ATXN3 mutant cells presenting reduced levels of the 4R tau isoform, iii) normalizing the levels of the 4R isoform partially rescued the phenotype of the KD cells, and iv) overexpression of ITGA5 did not rescue the levels of tau, suggest that deregulation of tau expression may also contribute for the abnormal morphology and cytoskeleton disorganization observed in ATXN3 KD cells. Furthermore, because ATXN3 is known to interact with dynein, a stabilizer of the microtubules [58], it would be valuable to determine whether the localization/function of this protein may be perturbed in the absence of ATXN3, originating a disorganization of the cytoskeleton. Recently, it has been proposed that some MAPs also function to decrease oxidative stress in neurons, for example by protecting the microtubules from degradation [60, 61]. Considering that ATXN3 is a MAP, it would be interesting to clarify if it has this particular function, and if it could have a neuroprotective role. But how is ATXN3 regulating the cytoskeleton network? We have previously shown that the levels of the major cytoskeletal components were not altered in absence of ATXN3, making it unlikely that they are direct substrates of ATXN3 DUB activity [55]. However, in this work we showed that ATXN3 is modulating the degradation or the expression of other proteins important for a correct cytoskeletal organization, such as ITGA5 and tau isoforms. Supporting the relevance of the DUB activity of ATXN3 for these cellular functions, we have shown that overexpression of a catalytic deficient version of ATXN3 (C14A) recapitulated the alterations both on ITGA5 degradation (Chapter 2) and tau expression (Chapter 3).

Finally, we asked whether the presence of the polyglutamine expansion within ATXN3 could also lead to similar alterations. Indeed, we found decreased levels of both ITGA5 and tau as well as decreased expression of 4R tau isoform both in neuronal cells overexpressing an expanded ATXN3 and in the nervous system of MJD mice (Chapters 2 and 3). In addition, neurons isolated from the DRG of the CMVMJD135 transgenic mice displayed a drastic reduction in neurite length, as we have

observed in the cells lacking ATXN3. Together, these findings not only suggest that a disruption of the cytoskeleton network may be contributing for the neurodegeneration observed in MJD, but also that a partial loss of the normal cellular function(s) of ATXN3 may contribute for MJD pathogenesis.

5.1.5 Cell signaling and ATXN3

As discussed above, ATXN3 is regulating the degradation of ITGA5, impacting on cytoskeleton organization. But it seems that not only the cytoskeleton is affected in the absence of ATXN3, since our work revealed that ATXN3 KD cells appear to have reduced adhesion to fibronectin, which may be explained by the lower levels of ITGA5 (Chapter 2). Interestingly, and in agreement with this finding, HeLa and C2C12 cells and neurons of Atxn3 KO mice also display low levels of integrin subunits in the absence of ataxin-3, in association with low cell-cell interconnectivity [3, 55] (Chapter 2). Besides participating in cell attachment to other cells and to the ECM, integrins also play a role in the transduction of signals from ECM components, the so-called "outside-in" signaling. This integrin-mediated signal transduction is achieved through a variety of intracellular protein kinases and adaptor molecules. We found that low expression of ITGA5 in ATXN3 KD cells was associated with a decrease in the CDK5/p35 complex activity and a change on its subcellular localization, and consequently, to a deregulation of the PI3K/AKT and ERK pathways. The inhibition of CDK5 activity has been shown to impair neuronal differentiation, function and survival (Reviewed in [62-69]). Interestingly, CDK5 has been proposed as a candidate for a therapeutic target for AD due to its role as a mediator of tau hyperphosphorylation [70]. As we observed a deregulation of tau expression in the absence of ATXN3, it would be interesting to assess tau phosphorylation in this situation. Additionally, we also found that silencing of ATXN3 leads to a decreased activation of the small GTPases Rac1 and Rho family, which compromised cell cycle and actin cytoskeleton regulation as well as increased motility.

In agreement with an involvement of ATXN3 in cell signaling pathways, is the deregulation of the ubiquitylation levels of a variety of substrates observed in the absence of ATXN3 (Chapter 4). It would be important now to determine which of these proteins are direct substrates of ATXN3. ATXN3 was shown to have DUB activity against K48, K63 and mixed polyUb linkages [1]. While usually K48-linked polyUb chains target protein for proteasomal degradation, K63 chains regulate, among other processes, protein activation and/or subcellular localization (Reviewed in [71, 72]). This may indicate that besides modulating protein degradation, ATXN3 may also regulate activation of specific substrates. Importantly, the UPS has emerged as a crucial mechanism for the normal nervous system development and function (Reviewed in [73, 74]). Therefore, it would be of interesting to i) determine whether ATXN3 is modulating the degradation of the proteins presenting altered levels of polyubiquitylation, by assessing their levels, or ii) to clarify whether this deregulation reflects an alteration of the subcellular localization and/or activity of these proteins. These experiments could also provide some additional clues about the specificity of the neuronal dysfunction observed in MJD. Nonetheless, we have already determined that cells expressing the expanded ATXN3 also presented decreased levels of ITGA5 and similar alterations on the integrinmediated signaling. Additionally, the levels of Itga5 in the brainstem and DRG of the transgenic mice were also downregulated, not only confirming the perturbation of ATXN3 normal function by polyQ expansion, but also suggesting that it may be relevant for the disease mechanism.

5.1.6 Transcription and ATXN3

In addition to its role in protein degradation, ataxin-3 has also been proposed to function in transcriptional regulation (see section 1.4.4.1). In order to understand which molecular changes were occurring in the ATXN3 KD cells, we performed a detailed transcriptomic analysis of these cells. Even though our bioinformatic analyses were more focused on the splicing events, we found that a large proportion of genes (7450 genes) were differentially expressed in the absence of ATXN3

(data not shown). Also, previous transcriptomic studies from our lab identified 290 genes altered in ATX-3 KO C. elegans [59]. Although a transcriptional repressor role has been attributed to ataxin-3, we found approximately the same proportion of genes up and downregulated in cells depleted of ATXN3. Although it is possible that many of these genes are ATXN3 direct transcriptional targets, these alterations may alternatively be a consequence of cellular compensatory mechanisms or changes in repressor complexes in which ATXN3 does not take part. As an example, it was recently described that the USP15 DUB enzyme regulates the proteasomal degradation of the transcriptional repressor RE1 silencing transcription factor (REST), which is critical both for neuronal differentiation and for activation of the mitotic exit [75]. Therefore, if absence of ATXN3 indirectly perturbs this mechanism of REST stability control by USP15, it will result in a change in transcription that ultimately may be related with an impairment in neuronal differentiation, that we actually observed in ATXN3 KD cells. A way of identifying ATXN3 direct transcriptional targets would be by performing: i) CHIP-seq analysis, ii) CLIP-seq (a method to purify protein-RNA complexes coupled with high throughput sequencing) [76], and/or iii) similar transcriptomic analysis in cells expressing C14A ATXN3. Another possibility is that the observed alterations are a consequence of changes in the levels of transcription factors downstream of ATXN3. Indeed, we found a proportion of transcription factors differentially expressed in ATXN3 KD cells. This observation suggests that these changes may occur at a transcriptomic stage. However, we cannot exclude the possibility that ATXN3 is modulating the degradation of transcription factors, thus impacting on transcription. Indeed, several of the proteins presenting altered polyubiquitylation levels and no alterations at the transcriptional level in ATXN3 KD cells in this study were previously identified as regulators of gene transcription (Chapter 4), which may indicate that ATXN3 is regulating their degradation and/or activity.

Another question that remains to elucidate is: are these transcriptomic changes relevant in the context of MJD? Trying to investigate this, we are already performing transcriptomic analysis in

pre and post symptomatic MJD mice (Silva-Fernandes A. et al., in preparation). Besides finding transcriptomic changes associated with disease progression, we also aim to look for overlapping changes between silencing of ATXN3 and overexpression of the expanded protein. This, in turn, may help to further elucidate how a partial loss of the normal function of ATXN3 on transcriptional regulation may contribute to disease.

5.1.7 Neuronal differentiation and ATXN3

One of the most striking effects of ATXN3 silencing in SH-SY5Y human cells was the impairment of the differentiation process. We found that mutant cells fail to progress toward a mature phenotype, as after RA treatment (normally a neuronal differentiation stimulus) they present: i) deficient inhibition of the proliferative activity, ii) increased expression of Nestin and decreased expression of several markers for mature neurons, iii) significantly reduced average neurite length, iv) increased number of small filopodia, v) large and flat cell bodies with reduced extensions, vi) severe disruption of the cytoskeleton network, and vii) increased cell migration (Chapter 2).

Interestingly, overexpression of mutant ATXN3 bearing an expanded polyQ tract led to a similar phenotype as the overexpression of a catalytic mutant or the absence of ATXN3. Additionally, neurons from our CMVMJD135 mouse model showed abnormal morphology and neuritic branching, which provides evidence supporting that the polyQ expansion causes a partial loss of the normal function of the protein *in vivo*.

But how does ATXN3 modulate neuronal differentiation? Regarding our results, we hypothesized that ATXN3 prevents the degradation of ITGA5 normally triggered by the activation of FGFR2 by RA [10]. This, in turn, activates the PI3K/AKT and ERK pathways, regulating neuronal morphology and cell adhesion and survival. However, we believe that this is not the only role of ATXN3 on neuronal differentiation. We also found that ATXN3 is involved in the regulation of tau isoform expression, which plays an important role in neuronal differentiation and axonal trafficking.

While we have already found that overexpression of 4R tau isoform partially rescues the neuronal differentiation phenotype of ATXN3 KD cells, it will now be interesting to evaluate whether silencing of ATXN3 or expression of the expanded protein causes an impairment of the axonal transport, which we are currently doing.

5.1.8 Other functions of ATXN3 – DNA repair

Recent data also support a role for ATXN3 in DNA repair. It was found that ATXN3 interacts and activates the Polynucleotide Kinase 3'-Phosphatase (PNKP) – a DNA strand break repair enzyme – suggesting a role for ATXN3 in PNKP-mediated DNA strand breaks repair (Chatterjee et al, 2014, PLoS Genetics, *submitted for publication*). Also, it has been found that the interaction of the DUB ataxin-3 bearing a disease-causing mutation with the polynucleotide kinase 3'-phosphatase (PNKP) – a DNA strand break repair enzyme – inactivates its activity, resulting in persistent accumulation of DNA strand breaks as well as chronic activation of DNA damage-response ataxia telangiectasia mutated (ATM) signaling, which may lead to cell death and neurodegeneration (Gao R, et al, 2014, *submitted for publication*).

5.2 Effects of absence of ATXN3 in cells and organisms: discrepancies and communalities

The fact that the *C. elegans* [59] and mouse ataxin-3 KO models [5, 77] are viable and exhibit no obvious phenotype at basal conditions was initially surprising. One possible explanation is the redundancy of function between ataxin-3 and other Josephin domain containing proteins. While in *C. elegans* another member of the Josephin family exists, Y71H2AR.3 (which, however, does not present a NLS or UIM and was not overexpressed in KO animals), in mouse at least two more, Josd1 and Josd2, and in humans three proteins were described, JOSD1, JOSD2 and ATXN3L. Because all these Josephin proteins are thought to be DUB enzymes [78, 79], it has been proposed

that they compensate for ataxin-3 absence. Additionally, a recent study showed that the DUB activity of JOSD1 is regulated by ubiquitylation through a conformational change at the catalytic site, similarly to ATXN3 [78, 80, 81]. The significance of this redundancy would be strengthened by experiments using double and triple mutants, i.e., mutants lacking ataxin-3 and the Josephin-like proteins, to evaluate their phenotype. To study this hypothesis, we have crossed a KO strain for the Josephin protein with *atx-3* mutants. However, we found no significant differences between atx-3 KO animals and the double mutants, suggesting that the absence of the Josephin protein does not aggravate the phenotype of *atx-3* mutants (unpublished data).

On the other hand, however, when ATX-3 KO *C. elegans* were challenged with a protein homeostasis stress (heat shock), they showed an enhanced stress response, which was correlated with increased expression of several molecular chaperones, probably an adaptative mechanism to deal with the absence of the DUB activity of ataxin-3 [82].

Contrary to the multicellular organisms, both mouse and human cells depleted of ataxin-3 show clear phenotypes, with severe cytoskeletal defects, increased ubiquitylated foci, increased sensitivity to heat shock [83] and oxidative stress [84]. Moreover, as we have shown in the present work that human neuronal cells depleted for ATXN3 display an abnormal cell morphology, cytoskeletal defects, and an impairment in the differentiation process.

This seems somehow incongruent, but a cellular model is indeed different from a multicellular system. Also, in most studies using cellular models, silencing of ataxin-3 was transiently performed and so, cells might not have time to adjust to this situation, while mouse and worm KO animals may undergo an adaptative process during development. In agreement, in our study, where we used cells stably silenced for ATXN3, we observed a partial recovery in cell morphology and

proliferation rate with multiple passages (Chapter 2). A conditional ataxin-3 KO model would be therefore valuable for a better understanding of these adaptative and compensatory mechanisms.

Nevertheless, we cannot exclude that both mouse and worms have yet undiscovered subtle defects. Indeed, although not yet studied in detail, we found a decreased expression of Itga5 in neurons of Atxn3 KO mice, which may be associated with a disruption of the cytoskeletal network and decreased process length as we observed in cells. In line with this, we previously found that ATX-3 KO *C. elegans* have a significant change in the transcriptomic profile [59], which may be indicative of subtle anomalies not found so far.

Finally, it was interesting that both ataxin-3 mutant cells and worms displayed signs of cellular stress, supporting that there probably exist some common features between cells and organisms.

5.3 Relevance of the novel findings and main conclusions of the work

As described in Chapter 1, Ub signaling is now widely known as a fundamental mechanism controlling a broad range of intracellular events in the nervous system. The reverse process, the removal of the Ub moieties, is carried out by DUBs. Although these enzymes have been recognized as central players in maintaining the correct ubiquitylation balance in cells, their mechanisms of regulation and substrate specificity are poorly understood.

This work added new knowledge about the relevance for neurons of one specific DUB, ataxin-3, and provided evidence for perturbation of this normal function in the context of disease, through a dominant negative effect.

We showed that ATXN3 function is important for neuronal differentiation, as silencing or DUB activity abrogation of this protein has a strong negative impact on cell morphology, leading to altered neurite extension, cytoskeletal disorganization, and altered proliferation and survival of SH-SY5Y cells. At the molecular level, this phenotype was shown to result from an excessive proteasome-dependent degradation of ITGA5 subunit levels in the absence of ATXN3 activity, which was observed both *in vitro* and *in vivo*. ITGA5 is the first ATXN3 substrate identified in neurons. This knowledge may be of relevance for the development of therapeutic strategies. In addition, we also showed that loss of function of ATXN3 leads to a deregulation of tau exon 10 splicing, resulting in a decreased 4R/3R tau ratio, which we demonstrated to be also contributing for the impairment in the differentiation process and the abnormal morphology of the mutant cells. Besides impacting on neuronal maintenance, these cytoskeletal changes can also have a negative impact on axonal transport.

The loss of ATXN3 transcriptional regulation role may also have caused significant changes in the transcriptomic profile in our cellular model, an aspected we did not dissect in detail in this work. Because neurons are a highly sensitive and specific cell type, and their function needs to be precisely regulated, these transcriptional changes can be extremely deleterious if they also occur in the context of human expanded polyQ-related disease.

Through its DUB activity, ATXN3 seems to function in regulating the ubiquitome in cells. We found that silencing of ATXN3 in SH-SY5Y cells causes a deregulation of the polyubiquitylation levels of a significant number of target proteins. These proteins are good candidates for being targets of the DUB activity of ATXN3 and, depending on their function and relevance for the cell, can also be

potential therapeutic targets. Among the proteins found to have altered polyubiquitylation patterns in the absence of ATXN3, a large proportion were proteins involved in RNA post-transcriptional modification. This data, together with the observation that absence of ATXN3 perturbs alternative splicing and specifically the splicing of tau, suggested to us that ATXN3 could be regulating this process in neurons, a hypothesis that we validated using reporter minigenes and transcriptomic analysis. These findings lead us to propose that ATXN3 plays a role in splicing regulation more globally in neurons, a novel function for this protein.

5.3.1 Ataxin-3 in the disease context: gain or loss of function?

This work was based on the idea that the study of the normal molecular and physiological function of ATXN3 is also important for the understanding of the pathogenic mechanism. Currently, studies in several polyQ diseases support the combinatory pathogenic model of gain and loss of function. In this way, for example, the identification of the ubiquitome in cells expressing expanded ataxin-3 may be an important contribution for the understanding of the pathogenic mechanism. This can also help to explore the proposed gain and loss of function model, given that ataxin-3's interactions with its substrates can either be gained or lost in the context of disease. The functional study of these interactions and the involvement of ataxin-3 in the suggested pathways can thus give important insights into the pathogenic mechanism and can also help to explain the selective neurodegeneration observed in MJD, which might be correlated with the stability and expression of the specific substrates, or with tissue-specific splicing patterns.

Indeed, our data supports this line of thought: the role of ATXN3 in regulating ITGA5 stability, here described, was shown not only to be relevant in physiological conditions for neuronal differentiation but also to be potentially involved in MJD pathogenesis. Interestingly, α 5-integrin subunit is known to be a key regulator of the actin cytoskeleton, and also to be implicated in the

regulation of spine morphogenesis, synapse formation and synaptic plasticity. According to this evidence, we may speculate that the reduced levels of α 5-integrin subunit and the reduced branching found in the presence of expanded ATXN3, both *in vitro* and *in vivo*, may be impairing synaptic plasticity thus contributing for MJD pathology.

Also consistent with this hypothesis, we found that both silencing of ATXN3 or expression of an expanded version led to a deregulation of tau exon 10 splicing, also with effect on neuronal morphology and differentiation. This is another evidence that partial loss of the normal function(s) of ataxin-3 might be contributing for MJD. In addition, these results also establish a link between two key proteins involved in different neurodegenerative diseases. Curiously, a relation between ataxin-3 and proteins associated with other neurodegenerative diseases, including Parkin [2], CHIP [81] and SOD1 [85], has already been observed, suggesting that there may exist common pathogenic mechanisms.

Altogether, these data support the idea that we should not look at MJD exclusively as a gain of function disease. Even tough it is well established that the polyQ expansion triggers the disease, a partial loss of the cellular DUB activity(ies) of ATXN3 through dominant-negative effects, may also modulate and contribute for disease progression and the specificity of neurodegeneration.

Bibliography

- 1. Winborn, B.J., et al., *The deubiquitinating enzyme ataxin-3, a polyglutamine disease protein, edits Lys63 linkages in mixed linkage ubiquitin chains.* J Biol Chem, 2008. **283**(39): p. 26436-43.
- 2. Durcan, T.M., et al., *The Machado-Joseph disease-associated mutant form of ataxin-3 regulates parkin ubiquitination and stability.* Hum Mol Genet, 2011. **20**(1): p. 141-54.
- 3. do Carmo Costa, M., et al., *Ataxin-3 plays a role in mouse myogenic differentiation through regulation of integrin subunit levels.* PLoS One, 2010. **5**(7): p. e11728.
- 4. Neves-Carvalho, A., Logarinho E., Freitas A., Duarte-Selva S., Costa M.C., Silva-Fernandes A., Martins M., Serra S.C., Lopes, A. T., Paulson, H.L., Heutink, P., Relvas, J.B. and Maciel P., *Dominant negative effect of polyglutamine expansion perturbs normal function of ataxin-3 in neuronal cells.* Human Molecular Genetics, 2014.
- 5. Schmitt, I., et al., *Inactivation of the mouse Atxn3 (ataxin-3) gene increases protein ubiquitination.* Biochem Biophys Res Commun, 2007. **362**(3): p. 734-9.
- 6. Lopitz-Otsoa, F., M.S. Rodriguez, and F. Aillet, *Properties of natural and artificial proteins displaying multiple ubiquitin-binding domains.* Biochem Soc Trans, 2010. **38**(Pt 1): p. 40-5.
- 7. Hjerpe, R., et al., *Efficient protection and isolation of ubiquity/lated proteins using tandem ubiquitin-binding entities.* EMBO Rep, 2009. **10**(11): p. 1250-8.
- Hallengren, J., P.C. Chen, and S.M. Wilson, *Neuronal ubiquitin homeostasis.* Cell Biochem Biophys, 2013.
 67(1): p. 67-73.
- 9. Jana, N.R., et al., *Co-chaperone CHIP associates with expanded polyglutamine protein and promotes their degradation by proteasomes.* J Biol Chem, 2005. **280**(12): p. 11635-40.
- 10. Kaabeche, K., et al., *Cbl-mediated ubiquitination of alpha5 integrin subunit mediates fibronectin-dependent osteoblast detachment and apoptosis induced by FGFR2 activation.* J Cell Sci, 2005. **118**(Pt 6): p. 1223-32.
- 11. Ichikawa, Y., et al., *The genomic structure and expression of MJD, the Machado-Joseph disease gene.* J Hum Genet, 2001. **46**(7): p. 413-22.
- 12. Mills, J.D. and M. Janitz, *Alternative splicing of mRNA in the molecular pathology of neurodegenerative diseases.* Neurobiol Aging, 2012. **33**(5): p. 1012 e11-24.
- 13. Singh, N.N. and R.N. Singh, *Alternative splicing in spinal muscular atrophy underscores the role of an intron definition model.* RNA Biol, 2011. **8**(4): p. 600-6.
- 14. Orozco, D. and D. Edbauer, *FUS-mediated alternative splicing in the nervous system: consequences for ALS and FTLD.* J Mol Med (Berl), 2013. **91**(12): p. 1343-54.
- 15. Gasparini, L., B. Terni, and M.G. Spillantini, *Frontotemporal dementia with tau pathology.* Neurodegener Dis, 2007. **4**(2-3): p. 236-53.
- 16. De Jonghe, C., et al., *Aberrant splicing in the presenilin-1 intron 4 mutation causes presenile Alzheimer's disease by increased Abeta42 secretion.* Hum Mol Genet, 1999. **8**(8): p. 1529-40.
- 17. Tysoe, C., et al., *A presenilin-1 truncating mutation is present in two cases with autopsy-confirmed early-onset Alzheimer disease.* Am J Hum Genet, 1998. **62**(1): p. 70-6.
- 18. Singleton, A.B., et al., *Pathology of early-onset Alzheimer's disease cases bearing the Thr113-114ins presenilin-1 mutation.* Brain, 2000. **123 Pt 12**: p. 2467-74.
- 19. Zuccato, C., et al., *Progressive loss of BDNF in a mouse model of Huntington's disease and rescue by BDNF delivery.* Pharmacol Res, 2005. **52**(2): p. 133-9.
- 20. Fernandez-Nogales, M., et al., *Huntington's disease is a four-repeat tauopathy with tau nuclear rods.* Nature Medicine, 2014. **20**(8): p. 881-5.
- 21. Kwiatkowski, T.J., Jr., et al., *Mutations in the FUS/TLS gene on chromosome 16 cause familial amyotrophic lateral sclerosis.* Science, 2009. **323**(5918): p. 1205-8.
- 22. Anthony, K. and J.M. Gallo, *Aberrant RNA processing events in neurological disorders.* Brain Res, 2010. **1338**: p. 67-77.
- 23. Rabin, S.J., et al., *Sporadic ALS has compartment-specific aberrant exon splicing and altered cell-matrix adhesion biology.* Hum Mol Genet, 2010. **19**(2): p. 313-28.
- 24. Arai, T., et al., *TDP-43 is a component of ubiquitin-positive tau-negative inclusions in frontotemporal lobar degeneration and amyotrophic lateral sclerosis.* Biochem Biophys Res Commun, 2006. **351**(3): p. 602-11.
- 25. Kwong, L.K., et al., *TDP-43 proteinopathies: neurodegenerative protein misfolding diseases without amyloidosis.* Neurosignals, 2008. **16**(1): p. 41-51.
- 26. Neumann, M., et al., *Ubiquitinated TDP-43 in frontotemporal lobar degeneration and amyotrophic lateral sclerosis.* Science, 2006. **314**(5796): p. 130-3.

- Ranum, L.P. and T.A. Cooper, *RNA-mediated neuromuscular disorders*. Annu Rev Neurosci, 2006. 29: p. 259-77.
- 28. Rappsilber, J., et al., *Large-scale proteomic analysis of the human spliceosome.* Genome Res, 2002. **12**(8): p. 1231-45.
- 29. Makarov, E.M., et al., *Small nuclear ribonucleoprotein remodeling during catalytic activation of the spliceosome*. Science, 2002. **298**(5601): p. 2205-8.
- 30. Peng, J., et al., *A proteomics approach to understanding protein ubiquitination.* Nat Biotechnol, 2003. **21**(8): p. 921-6.
- 31. Bellare, P., et al., *Ubiquitin binding by a variant Jab1/MPN domain in the essential pre-mRNA splicing factor Prp8p.* RNA, 2006. **12**(2): p. 292-302.
- Kramer, A., et al., Mammalian splicing factor SF3a120 represents a new member of the SURP family of proteins and is homologous to the essential splicing factor PRP21p of Saccharomyces cerevisiae. RNA, 1995.
 1(3): p. 260-72.
- 33. Manderson, E.N., M. Malleshaiah, and S.W. Michnick, *A novel genetic screen implicates Elm1 in the inactivation of the yeast transcription factor SBF.* PLoS One, 2008. **3**(1): p. e1500.
- 34. Makarova, O.V., E.M. Makarov, and R. Luhrmann, *The 65 and 110 kDa SR-related proteins of the U4/U6.U5 tri-snRNP are essential for the assembly of mature spliceosomes.* EMBO J, 2001. **20**(10): p. 2553-63.
- 35. Hatakeyama, S., et al., *U box proteins as a new family of ubiquitin-protein ligases.* J Biol Chem, 2001. **276**(35): p. 33111-20.
- 36. Ohi, M.D., et al., *Structural insights into the U-box, a domain associated with multi-ubiquitination.* Nat Struct Biol, 2003. **10**(4): p. 250-5.
- 37. Bellare, P., et al., *A role for ubiquitin in the spliceosome assembly pathway.* Nat Struct Mol Biol, 2008. **15**(5): p. 444-51.
- 38. Busch, A. and K.J. Hertel, *Evolution of SR protein and hnRNP splicing regulatory factors.* Wiley Interdiscip Rev RNA, 2012. **3**(1): p. 1-12.
- 39. Miyajima, N., et al., *TRIM36 interacts with the kinetochore protein CENP-H and delays cell cycle progression.* Biochem Biophys Res Commun, 2009. **381**(3): p. 383-7.
- 40. Short, K.M. and T.C. Cox, *Subclassification of the RBCC/TRIM superfamily reveals a novel motif necessary for microtubule binding.* J Biol Chem, 2006. **281**(13): p. 8970-80.
- 41. Sun, J., et al., *Differential effects of polyglutamine proteins on nuclear organization and artificial reporter splicing.* J Neurosci Res, 2007. **85**(11): p. 2306-17.
- 42. Tollervey, J.R., et al., *Analysis of alternative splicing associated with aging and neurodegeneration in the human brain.* Genome Res, 2011. **21**(10): p. 1572-82.
- Biamonti, G., et al., *The alternative splicing side of cancer.* Seminars in Cell and Developmental Biology, 2014.
 32: p. 30-6.
- 44. Lenzken, S.C., A. Loffreda, and S.M. Barabino, *RNA splicing: a new player in the DNA damage response.* Int J Cell Biol, 2013. **2013**: p. 153634.
- 45. Zhang, J. and J.L. Manley, *Misregulation of pre-mRNA alternative splicing in cancer.* Cancer Discov, 2013. **3**(11): p. 1228-37.
- 46. Hagen, R.M. and M.R. Ladomery, *Role of splice variants in the metastatic progression of prostate cancer.* Biochemical Society Transactions, 2012. **40**(4): p. 870-4.
- Rockx, D.A., et al., UV-induced inhibition of transcription involves repression of transcription initiation and phosphorylation of RNA polymerase II. Proceedings of the National Academy of Sciences of the United States of America, 2000. 97(19): p. 10503-8.
- 48. Shanbhag, N.M., et al., *ATM-dependent chromatin changes silence transcription in cis to DNA double-strand breaks.* Cell, 2010. **141**(6): p. 970-81.
- 49. Dutertre, M., et al., *The emerging role of pre-messenger RNA splicing in stress responses: sending alternative messages and silent messengers.* RNA Biol, 2011. **8**(5): p. 740-7.
- 50. Montecucco, A. and G. Biamonti, *Pre-mRNA processing factors meet the DNA damage response.* Front Genet, 2013. **4**: p. 102.
- Hoffner, G., P. Kahlem, and P. Djian, *Perinuclear localization of huntingtin as a consequence of its binding to microtubules through an interaction with beta-tubulin: relevance to Huntington's disease.* J Cell Sci, 2002. 115(Pt 5): p. 941-8.
- 52. Berke, S.J., et al., *Defining the role of ubiquitin-interacting motifs in the polyglutamine disease protein, ataxin-3.* J Biol Chem, 2005. **280**(36): p. 32026-34.
- 53. Wu, C.H., et al., *Mutations in the profilin 1 gene cause familial amyotrophic lateral sclerosis.* Nature, 2012. **488**(7412): p. 499-503.

- 54. Vickers, J.C., et al., *Axonopathy and cytoskeletal disruption in degenerative diseases of the central nervous system.* Brain Res Bull, 2009. **80**(4-5): p. 217-23.
- 55. Rodrigues, A.J., et al., *Absence of ataxin-3 leads to cytoskeletal disorganization and increased cell death.* Biochim Biophys Acta, 2010. **1803**(10): p. 1154-63.
- 56. do Carmo Costa, M., *Study of the homologue of the Machado-Joseph disease gene in Mus musculus*, 2008, University of Minho.
- 57. Rodrigues, A.J., *C. elegans ataxin-3: function, loss of function and molecular partners*, 2008, University of Minho.
- 58. Burnett, B.G. and R.N. Pittman, *The polyglutamine neurodegenerative protein ataxin 3 regulates aggresome formation.* Proc Natl Acad Sci U S A, 2005. **102**(12): p. 4330-5.
- 59. Rodrigues, A.J., et al., *Functional genomics and biochemical characterization of the C. elegans orthologue of the Machado-Joseph disease protein ataxin-3.* FASEB J, 2007. **21**(4): p. 1126-36.
- 60. Yang, Z., et al., *Protective effects of tetramethylpyrazine on rat retinal cell cultures.* Neurochem Int, 2008. **52**(6): p. 1176-87.
- 61. Zemlyak, I., R. Sapolsky, and I. Gozes, *NAP protects against cytochrome c release: inhibition of the initiation of apoptosis.* Eur J Pharmacol, 2009. **618**(1-3): p. 9-14.
- 62. Cicero, S. and K. Herrup, *Cyclin-dependent kinase 5 is essential for neuronal cell cycle arrest and differentiation.* J Neurosci, 2005. **25**(42): p. 9658-68.
- 63. Nikolic, M., et al., *The cdk5/p35 kinase is essential for neurite outgrowth during neuronal differentiation.* Genes Dev, 1996. **10**(7): p. 816-25.
- 64. Gilmore, E.C., et al., *Cyclin-dependent kinase 5-deficient mice demonstrate novel developmental arrest in cerebral cortex.* J Neurosci, 1998. **18**(16): p. 6370-7.
- 65. Tanaka, T., et al., *Neuronal cyclin-dependent kinase 5 activity is critical for survival.* J Neurosci, 2001. **21**(2): p. 550-8.
- 66. Li, B.S., et al., *Cyclin-dependent kinase 5 prevents neuronal apoptosis by negative regulation of c-Jun Nterminal kinase 3.* EMBO J, 2002. **21**(3): p. 324-33.
- 67. Smith, D.S. and L.H. Tsai, *Cdk5 behind the wheel: a role in trafficking and transport?* Trends Cell Biol, 2002. **12**(1): p. 28-36.
- 68. Gupta, A. and L.H. Tsai, *Cyclin-dependent kinase 5 and neuronal migration in the neocortex.* Neurosignals, 2003. **12**(4-5): p. 173-9.
- 69. Kesavapany, S., B.S. Li, and H.C. Pant, *Cyclin-dependent kinase 5 in neurofilament function and regulation.* Neurosignals, 2003. **12**(4-5): p. 252-64.
- 70. Lopez-Tobon, A., et al., *Silencing of CDK5 as potential therapy for Alzheimer's disease.* Rev Neurosci, 2011. **22**(2): p. 143-52.
- 71. Glickman, M.H. and A. Ciechanover, *The ubiquitin-proteasome proteolytic pathway: destruction for the sake of construction.* Physiol Rev, 2002. **82**(2): p. 373-428.
- 72. Woelk, T., et al., *The ubiquitination code: a signalling problem.* Cell Div, 2007. **2**: p. 11.
- 73. Baptista, M.S., C.B. Duarte, and P. Maciel, *Role of the ubiquitin-proteasome system in nervous system function and disease: using C. elegans as a dissecting tool.* Cell Mol Life Sci, 2012. **69**(16): p. 2691-715.
- 74. Kawabe, H. and N. Brose, *The role of ubiquitylation in nerve cell development.* Nat Rev Neurosci, 2011. **12**(5): p. 251-68.
- 75. Faronato, M., et al., *The deubiquitylase USP15 stabilizes newly synthesized REST and rescues its expression at mitotic exit.* Cell Cycle, 2013. **12**(12): p. 1964-77.
- Murigneux, V., et al., *Transcriptome-wide identification of RNA binding sites by CLIP-seq.* Methods, 2013.
 63(1): p. 32-40.
- 77. Switonski, P.M., et al., *Mouse ataxin-3 functional knock-out model.* Neuromolecular Med, 2011. **13**(1): p. 54-65.
- 78. Seki, T., et al., *JosD1, a membrane-targeted deubiquitinating enzyme, is activated by ubiquitination and regulates membrane dynamics, cell motility, and endocytosis.* J Biol Chem, 2013. **288**(24): p. 17145-55.
- 79. Tzvetkov, N. and P. Breuer, *Josephin domain-containing proteins from a variety of species are active deubiquitination enzymes.* Biol Chem, 2007. **388**(9): p. 973-8.
- 80. Todi, S.V., et al., *Ubiquitination directly enhances activity of the deubiquitinating enzyme ataxin-3.* EMBO J, 2009. **28**(4): p. 372-82.
- 81. Todi, S.V., et al., *Activity and cellular functions of the deubiquitinating enzyme and polyglutamine disease protein ataxin-3 are regulated by ubiquitination at lysine 117.* J Biol Chem, 2010. **285**(50): p. 39303-13.
- Rodrigues, A.J., et al., *Absence of ataxin-3 leads to enhanced stress response in C. elegans.* PLoS One, 2011.
 6(4): p. e18512.

- 83. Reina, C.P., X. Zhong, and R.N. Pittman, *Proteotoxic stress increases nuclear localization of ataxin-3.* Hum Mol Genet, 2010. **19**(2): p. 235-49.
- 84. Zhou, L., et al., *Ataxin-3 protects cells against H2O2-induced oxidative stress by enhancing the interaction between Bcl-X(L) and Bax.* Neuroscience, 2013. **243**: p. 14-21.
- 85. Wang, H., Z. Ying, and G. Wang, *Ataxin-3 regulates aggresome formation of copper-zinc superoxide dismutase* (*SOD1*) by editing K63-linked polyubiquitin chains. J Biol Chem, 2012. **287**(34): p. 28576-85.

Appendices

Name	Forward (5'-3')	Reverse (5'-3')
руРҮ	TGAGGGGAGGTGAATGAGGAG	TCCACTGGAAAACCGCGAAG
ру	AGGCTTTGAGAACCTGTGGA	AACCGCGAGCTTGAACAG
PY	AGGCTTTGAGAACCTGTGGA	TGAGAGTCATTTCACCTTGAACA
AdML	GTCGACGACACTTGCTCAAC	AAGCTTGCATGCAATCAGTAG
lpha-globulin	GTCGACGACACTTGCTCAAC	AAGCTTGCATGCAATCAGTAG

Table /	A1. Li:	st of	primers	used	in	this	study.
---------	----------------	-------	---------	------	----	------	--------

Appendices

Table A2. Genes with altered splicing in ATXN3^{thRMA} cells. List of genes with altered splicing in RA-treated ATXN3^{thRMA} cells as compared with the SCR^{thRMA} controls. Genes were considered significantly regulated when fold-change was \geq 1.5 and p \leq 0.05. The predicted upstream regulators of the splicing events are listed (based on SpliceAid-F database).

				Prediction of upstream regulator			
Gene Symbol	Alter. Event Type	Fold change	p-value	Splicing Factor Symbol(s)			
FAM213B	Intron Retention	2.26	3.80E-05	ETR-3, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP P (TLS), KSRP, SC35, YB-1, ZRANB2			
Alter. Acceptor Site		1.89	7.42E-04				
DFFB	Complex (e3-4)	1.62	6.48E-03	Encortex, ruska, mixta A, mixta A, mixta A, mixta A, mixta E, mixta E, mixta F, mixta F, mixta F, FD, mixta F, FD, mixta F, FD, FD, FD, FD, FD, FD, FD, FD, FD,			
	Exon Cassette	1.62	6.48E-03				
UBE4B	Exon Cassette	1.76	5.84E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2			
KIF1B	Alter. First Exon (e1-11,e14- 16,e18-25,e27-30)	3.09	5.15E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP D1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS),			
	Alter. Terminal Exon (e26)	3.35	1.24E-04				
CLCN6 // NPPA-	Alter. Terminal Exon (e4)	1.64	4.79E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP H, hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha,			
AS1	Exon Cassette	1.58	1.44E-03	HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20c, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2			
DDI2 // RSC1A1	Alter. Terminal Exon (e5)	1.96	1.46E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2			
MST1P2	Alter. Acceptor Site	1.82	9.58E-03	hnRNP I (PTB), hnRNP P (TLS), KSRP, Nova-1, Nova-2, SC35, YB-1			
CDC42	Exon Cassette	1.92	9.06E-03	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, RBM5, Sam68, SC35, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2			
ZBTB40	Intron Retention	2.60	1.22E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HuB, KSRP, Nova-1, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1			
	Exon Cassette	2.05	9.02E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1,			
SRRM1	Exon Cassette	1.53	3.54E-06	Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2			
WDTC1	Intron Retention	1.66	1.84E-03	ETR-3, Fox-1, Fox-2, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Sam68, SC35, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2			
PHACTR4	Exon Cassette	2.14	1.16E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SF2/ASF, SRp30c, TIA-1, TIAL1, YB-1			
YTHDF2	Intron Retention	1.70	3.06E-03	ETR-3, hnRNP E1, hnRNP E2, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, RBM5, SC35, TIA-1, TIAL1, YB-1			
EDD/1	Alter. Terminal Exon (e14)	1.90	4.36E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-2,			
EPB41	Exon Cassette	3.84	3.93E-05	Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2			
ZCCHC17	Exon Cassette	1.58	5.62E-03	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2			
	Alter. Terminal Exon (e6)	1.58	5.06E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1,			
HDACI	Exon Cassette	1.61	1.10E-03	HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2			
S100PBP	Exon Cassette	2.10	2.04E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP I (PTB), hnRNP F, hnRNP P (TLS), HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2			
AGO3	Alter. Terminal Exon (e7-8) 1.67 3.67E-05 HT		3.67E-05	CUG-BP1, ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2			
	Exon Cassette	5.99	5.80E-05				
	Alter. Donor Site	2.28	1.79E-04				
PPIE	Exon Cassette	1.93	4.10E-03	UUG-071, ELK-5, IIIINKY AL, IIIINKY CJ, IIINKY			
	Intron Retention	2.01	1.04E-04	אוויזיב, וושיע בין הטיוע בין הטווע בין הטוויגי, שווויטע שוויטע אוויע בין הטווע בין הטווע בין הטווע בין הטווע בי			
CCDC30	Mutualy Exclusive Exons (e9- 11,e13-15)	2.06	6.60E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2			
ZNF691	Intron Retention	1.66	1.36E-02	ETR-3, hnRNP A1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), HuB, KSRP, Nova-1, Sam68, SC35, SRp20, TIA-1, TIAL1, YB-1			
	Exon Cassette	1.54	6.03E-05	CUG-BP1. ETR-3. Fox-1. Fox-2. hnRNP A1. hnRNP A2/B1. hnRNP C1. hnRNP D. hnRNP E1. hnRNP E2. hnRNP F. hnRNP H1. hnRNP H2. hnRNP I (PTB). hnRNP K. hnRNP P (TLS). HTra2beta1. HuB. HuD. HuR. KSRP.			
------------------------------	------------------------------	------	----------	--			
AKR1A1	Intron Retention	1.66	2.56E-04	MBNL1, Nova-1, Nova-2, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2			
RAD54L	Complex	1.58	9.76E-03	ETR-3, hnRNP A1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F2, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Sam68, SC35, SRp30c, TIA-1, TIAL1, YB-1			
ZYG11B	Exon Cassette	2.08	3.90E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP K, hnRNP P (TLS), HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2			
SGIP1	Exon Cassette	8.34	2.00E-05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2			
FPGT//FPGTTNN I3K//TNNI3K	Alter. Terminal Exon (e22)	1.77	8.94E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2			
ACADM	Exon Cassette	1.52	1.76E-02	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2			
FNBP1L	Intron Retention	2.18	2.42E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, KSRP, MBNL1, Nova-1, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1			
AMY2B // RNPC3	Alter. First Exon (e17-18)	1.81	4.77E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2			
PRPE38B	Alter. Terminal Exon (e5-6)	1.67	2.24E-05	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1,			
1111305	Exon Cassette	1.59	2.98E-04	Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2			
AHCYL1	Alter. Acceptor Site	1.54	1.46E-03	ETR-3, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HuB, Nova-1, RBM5, Sam68, SC35, SRp30c, TIA-1, TIAL1, YB-1			
STRIP1	Intron Retention	1.56	5.30E-03	ETR3, Fox1, Fox2, hnRNP C1, hnRNP P (PTB), hnRNP P (TLS), HuD, Nova-1, SRp20, TIA-1, TIAL1, YB-1			
RAP1A	Exon Cassette	1.61	1.46E-03	CUG-BP1, E1R-3, Fox-1, Fox-2, hnRNP F1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP F2, hnRNP F2, hnRNP F1, hnRNP F1, hnRNP F3, hnRNP F1(P1B), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2			
DDX20	Intron Retention	1.69	1.08E-02	ETR.3, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, KSRP, Nova-1, SRp20, TIA-1, TIAL1, YB-1			
RBM8A	Intron Retention	2.55	2.30E-03				
PIAS3	Intron Retention	1.67	2.12E-03	EIR3, bnRNP CL, bnRNP D, bnRNP EZ, bnRNP FZ, bnRNP HL, bnRNP HZ, bnRNP (PLB), bnRNP K, bnRNP P (LS), MBNLL, Nova-I, SC35, SRp20, 11A-I, 1IALI, YB-I			
VPS45	Intron Retention	2.05	8.84E-03	EIK3, INKIV AL, INKIV F (L, INKIV F (LS), HI7226431, HUB, KSKP, NOV3-1, NOV3-2, SAMOS, SC35, HA-1, HALL, YB-1 TTO 2, HOND AL HOND AC AD HOND CALMOND CATE ON LOTAL HOND K. HOND AD LIST LITER 20 HOND AL HOND AL HOND CALMOND CALMOND AT HOND AD HOND CALMOND AT HOND AD HOND CALMOND AD HOND			
PIP5K1A	Exon Cassette	1.96	1.28E-03	ETR-3, flixter A2, hirkiter A2/B1, hirkiter C1, hirkiter			
PSMB4	Intron Retention	1.89	9.24F-04	FIR3. INRVP (/TB). INRVP TI S). Nova-1. Sc.35. YB-1			
RIIAD1	Alter. First Exon (e1-5)	6.53	5.60E-05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP D1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MRN1 1, Nova-1, Nova-2, PSE, RBM5, Sam68, SC35, SF1, SRn20, SRn30, TIA-1, TIA1 1, YB-1, ZRANB2			
CHTOP	Alter. Terminal Exon (e3)	1.72	7.62E-04				
INTS3	Intron Retention	1.52	1.61E-02	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, KSRP, MBNL1, Nova-1, RBM5, SC35, SF2/ASF, SRp30c, TIA-1, TIAL1, YB-1			
HAX1	Intron Retention	2.05	1.63E-04	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, KSRP, Nova-1, RBM5, SC35, TIA-1, TIAL1, YB-1			
SLC50A1	Exon Cassette	1.59	1.28E-03	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HuB, KSRP, Nova-1, Sam68, SC35, TDP43, TIA-1, TIAL1, YB-1, ZRANB2			
USP21	Intron Retention	1.89	7.40E-04	ETR-3, Fox-1, Fox-2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, KSRP, Nova-1, RBM5, Sam68, SC35, YB-1			
NDUFS2	Intron Retention	1.82	3.36E-02	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), HuB, KSRP, Nova-1, Sam68, SC35, TIA-1, TIAL1, YB-1			
UHMK1	Intron Retention	1.60	6.06E-03	ETR-3, hnRNP A1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F5, hnRNP H1, hnRNP H2, hnRNP I (PTB), HuB, KSRP, Nova-1, Sam68, SC35, SRp20, SRp30c, YB-1, ZRANB2			
MPZL1	Exon Cassette	3.71	1.01E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2			
DCAF6	Exon Cassette	1.59	2.23E-02	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP H2, hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2			
SOAT1	Exon Cassette	1.81	4.84E-03	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2			
TSEN15	Exon Cassette	2.10	1.04E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2			
CD46	Exon Cassette	1.73	4.30E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2			
SYT14	Complex (e2-4)	1.84	1.06E-03	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2			
VASH2	Alter. Terminal Exon (e9-11)	1.59	2.08E-03	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, HuR, KSRP,			
PROGRAM	Complex	1.59	9.62E-03	MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2			
RPS6KC1	Intron Retention	2.54	9.59E-05	EIK-3, INKIV A1, INKIV A2/B1, INKIV PDL, INRIVP F, INRIVP H2, INRIVP H2, INRIVP PTLIS, INTR2Alpha, HTra2beta1, HuB, MBNL1, Nova-1, Sam68, SC35, SRp20, SRp30c, YB-1, ZRANB2			
PROX1	Complex	3.00	2.29E-05	UG-BF1, E1R-3, F0X-1, F0X-2, NNRNP A1, NNRNP A2, NNRNP A2, NNRNP D, NNRNP E1, NNRNP E2, NNRNP F, NNRNP H1, NNRNP H2, NNRNP F (PTB), NNRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2			
MARK1	Exon Cassette	1.73	1.69E-02	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP,			

				MBNI 1 Nova-1 Sam68 SC35 SE1 SRn20 SRn30c TIA-1 TIA11 YR-1 7RANR2
COG2	Intron Retention	1.51	5.80E-03	ETR.3, Fox 1, Fox 2, Fo
GNPAT	Exon Cassette	1.65	4.70E-03	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SRo20, SRo30c, TIA-1, TIAL1, YB-1, ZRANB2
LGALS8	Exon Cassette	2.00	3.64E-03	ETR-3, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP K, HuB, KSRP, MBNL1, Nova-1, Sam68, SC35, TIA-1, TIAL1, YB-1
	Alter. Terminal Exon (e6)	1.60	7.64E-04	FTR-3 Fox-1 Fox-2 hnRNP A1 hnRNP C1 hnRNP F1 hnRNP F2 hnRNP F2 hnRNP F2 hnRNP H1 hnRNP H2 hnRNP H2 hnRNP H2 hnRNP F (DTIS) HTra2heta1 HuR HuD KSRP MRN11 Nova-1 Nova-2 PSF
SLC35E2B	Intron Retention	1.63	1.83E-04	RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, VB-1, ZRANB2
WRAP73	Intron Retention	1 79	5 83E-04	FTR-3 bnRNP A1 bnRNP C1 bnRNP F bnRNP H1 bnRNP H2 bnRNP H/PTR) bnRNP P (TLS) HuR KSRP MRNI 1 SC35 SRo30c TIA-1 TIAL1 YR-1
	Alter, First Exon (e1-2.e4)	2.90	1.08E-03	CIG-RPI FIR-3 Gov-1 Fox-2 hoRNP A1 hoRNP A2/B1 hoRNP C1 hoRNP D1 hoRNP D1 hoRNP F1 h
CTNNBIP1	Alter. Terminal Exon (e2,e4-7)	1.83	4.60E-04	HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
EXOSC10	Intron Retention	1.79	1.17E-04	CUG-BP1, ETR-3, hnRNP C1, hnRNP F1, hnRNP H2, hnRNP H2, hnRNP I (PTB), HTra2beta1, Nova-1, Sam68, SC35, TIA-1, TIAL1, YB-1
CASP9	Alter. Acceptor Site	1.62	1.13E-02	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, RBM5, SC35, SRp20, YB-1
MFAP2	Intron Retention	3.86	1.45E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP P (TLS), KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, TIA-1, TIAL1, YB-1, ZRANB2
AKR7A2	Alter. Terminal Exon (e3)	1.60	2.84E-03	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
UD1DD2	Alter. Acceptor Site	1.75	1.66E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP H, hnRNP P (TLS), HTra2beta1, HuB, HuD,
TIFIDES	Complex (e3)	1.72	1.50E-03	KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
RAP1GAP	Complex (e2,e4)	2.29	5.01E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
C1orf63	Alter. Acceptor Site	1.61	5.84E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP CL, hnRNP F, hnRNP H1, hnRNP H2, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Sam68, SC35, TIA-1, TIAL1, YB-1, ZRANB2
STMN1	Intron Retention	2.03	1.21E-04	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, KSRP, Nova-1, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
00054	Exon Cassette	2.35	1.37E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (TEB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP,
SRSF4	Intron Retention	2.36	3.03E-04	MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
BAI2	Alter. First Exon (e2-4)	1.61	1.02E-02	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
BSDC1	Intron Retention	1.97	4.79E-04	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SRp20c, STLA-1, TIAL1, YB-1, ZRANB2
FHL3	Intron Retention	1.58	2.95E-02	ETR-3, hnRNP K, hnRNP P (TLS), MBNL1, SC35, SF1, YB-1
EBNA1BP2	Intron Retention	2.44	4.97E-04	ETR-3, Fox-1, Fox-2, hnRNP I (PTB), hnRNP F (TLS), HuB, KSRP, Nova-1, Sam68, SC35, SRp30c, YB-1
HYI	Intron Retention	2.00	1.43E-04	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, PSF, SC35, SRp30c, TIA-1, TIAL1, YB-1
POMGNT1	Intron Retention	2.31	5.16E-03	hnRNP A1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP P (TLS), KSRP, MBNL1, Nova-1, SC35, TIA-1, TIAL1, YB-1, ZRANB2
FAF1	Exon Cassette	1.75	1.33E-02	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
FPS15	Alter. First Exon (e1-8,e10-13)	1.74	1.81E-02	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP A1, hnRNP K, hnRNP LL, hnRNP P (TLS),
21010	Alter. Terminal Exon (e9)	1.64	8.46E-03	HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
LRP8	Exon Cassette	1.55	9.70E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
HSPB11	Intron Retention	1.57	6.56E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1
CDCP2 //	Alter. Terminal Exon (e6,e7-10)	1.91	1.16E-03	FTR.3 Fox.1 Fox.2 hnRNP 41 hnRNP 42/R1 hnRNP C1 hnRNP C1 hnRNP C1 hnRNP C1 hnRNP F2 hnRNP F2 hnRNP F4 hnRNP H2 hnRNP H2 hnRNP F4
CYB5RL	Complex	1.64	1.32E-02	HUD, HUR, KSPP, MBNLI Nova-I, Nova-Z, PSF, RBM5, Sam68, S235, SFI, SF2/ASF, SRo20, SR030c, TDP43, TIA-1, TIA-1, YB-1, ZRANB2
-	Exon Cassette	1.91	1.98E-02	
MYSM1	Intron Retention	1.86	3.06E-03	ETR3, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Sam68, SC35, SRp20, TIA-1, TIAL1, YB-1, ZKANB2
ITGB3BP	Alter. Terminal Exon (e8)	1.8/	1.06E-03	EIR3, Fox1, Fox2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H2, hnRNP H2, hnRNP H2, hnRNP P (ILS), HIra2alpha, HIra2beta1, HuB, KSRP, MBNL1,
704000	Exon Cassette	1.91	1.85E-04	N074-1, N074-2, P51, R5003, Salitos, SUS3, S11, SRD20, SRD302, LUP43, IIA-1, IIAL1, IST-1, ZRANSZ
ZKAINB2 7772	Intron Retention	1.50	6.04E-03	EIK-3, MIKIWE CL, MIKIWE P (115), MIKIWE P (115), MIKZOERIJ, HUB, NSKE, NOVEL, FSF, SAMOS, SFJ, SKP2U, 114-1, 114CL, 151
LLLJ	Evon Cassette	1.54	1.65E.02	בודאס, החושים הביסבו, החושים בביסבו, החושים בין החושים בין החושים בין החושים בין החושים ביודאס, החושים הביסבו, החושים בביסבו, החושים ביודאס, החושים הביסבו, החושים ביודאס, החושים ביודאס ביודאס, החושים ביודאס, החושים ביודאס, החושים ביודאס, החושים ביודאס, החושים ביודאס, החושים ביודאס
FUBP1	Intron Retention	2.63	7.925.05	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), HuB, HuD, Nova-1, RBM5, Sam68, SC35, SF2/ASF, TIA-1, TIAL1, YB-1, ZRANB2
TTLL7	Exon Cassette	1.65	2.38E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2, B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, KSPB, MDNI 1, March 1, DSC, Samee SC25, SE1, SEx20, SEx20
DDAH1	Alter. First Exon (e4)	2.16	3.84E-04	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F2, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTr-221bb HTr-27bbt H1, BHD, H1, BHB, H1, BK, SPD, BMB, 1, Nora-2, PCE BBMS, S2n68, SC35, SE1, SE2/ASE, SPc30, SPc30, TDPA3, TIA, 1, TIA, 1, YB, 1, ZPAMP2
DBT	Alter. Acceptor Site	1.64	4.54E-03	ETR2 approx 1 Feb 1 Feb 2 Feb
				ouniou, oooo, onpeo, onpeo, onpeo, in i, inci, ib i, ennote

EXTL2	Exon Cassette	2.20	1.69E-02	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
DPH5	Exon Cassette	2.14	1.23E-04	CUG-BP1, ETR-3, hnRNP A1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
01 5140	Alter. First Exon	2.28	2.00E-05	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS),
OLFM3	Exon Cassette	13.23	2.78E-06	HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
	Complex	12.17	2.95E-07	ETR-3. hnRNP C1. hnRNP E1. hnRNP E2. hnRNP F. hnRNP H1. hnRNP H2. hnRNP / (PTB). hnRNP P (TLS). HTra2beta1. HuB. KSRP. MBNL1. Nova-1. RBM5. Sam68. SC35. SRb20. SRb20. SRb20. TIA-1. TIAL1.
DRAM2	Exon Cassette	12.01	2.95E-07	YB-1, ZRANB2
RSBN1	Exon Cassette	2.16	1.12E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
750400	Alter. Terminal Exon (e16)	1.66	6.12E-03	ETR-3. Fox-1. Fox-2. hnRNP A1. hnRNP A2/B1. hnRNP C1. hnRNP D. hnRNP D1. hnRNP E1. hnRNP E2. hnRNP F. hnRNP H1. hnRNP H2. hnRNP I (PTB). hnRNP K. hnRNP P (TLS). HTra2beta1. HuB. HuD. KSRP.
TRIM33	Exon Cassette	1.82	3.48E-03	MBNL1, Nova-1, Nova-2, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
NOTCH2	Exon Cassette	5.23	8.60E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MRNI 1, Nova-2, PSE, RRM5, Sam68, SC35, SE1, SE2/ASE, SRn20, SRn30c, TDP43, TIA-1, TIA-1, YB-1, ZRANR2
APH1A	Intron Retention	1.67	2.50F-03	hnRNP D. hnRNP F1. hnRNP F2. hnRNP L(PTB). hnRNP K. hnRNP P. (TLS). HuB. KSRP. MBNL1. Nova-1. SC35. SF2/ASE. SRo20. SRo30c. TIA-1. TIAL1. YB-1
ARNT	Exon Cassette	1.67	2.38E-02	CUG-BJ, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP H3, hnRNP I, hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, HuR, KSRP, MBN1 1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRo20, SRo30c, TDP43, TIA-1, TIA1 1, YP-1, ZRANB2
CDC42SE1	Intron Retention	1.62	2 56E-04	TRA: hnRNP E hnRNP H hnRNP H2 hnRNP (PTR) hnRNP PTI(S) HTRA: hnRNP PTI(S) HTRA: http://www.isano.com/iter.isa
VPS72	Complex	1.78	2 84F-03	TR3 bRNP 41 bRNP 42/B1 bRNP C1 bRNP (1/FR) bRNP F KIRNP F (1/S) HuB HuD KSPP MRI 1 braz-1 braz-2 Sam68 SC35 SR20 TA1 TA11 YR-1
ITB	Intron Retention	1.67	1.30E-03	Erres handling (Erres Handling) (Erres H
SHC1	Alter. First Exon (e2)	3.28	7.76E-05	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, RM5, Sam68, SC35, SRb20, SRb30c, TIA-1, TIA1, 1, VB-1, ZRANB2
GBA // GBAP1	Alter. First Exon (e1)	3.17	4.61E-04	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E2, hnRNP E2, hnRNP F, hnRNP H2, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
YY1AP1	Exon Cassette	1.50	2.62E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
0073	Exon Cassette	2.20	1.98E-03	ETR-3, hnRNP A1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, PSF, Sam68, SC35, SRp30c, TIA-
0015	Exon Cassette	1.54	1.14E-02	1, TIAL1, YB-1, ZRANB2
ARHGEF11	Intron Retention	1.67	4.06E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, SC35, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
IGSF9	Exon Cassette	2.28	5.23E-04	ETR-3, FMRP, hnRNP DL, hnRNP F, hnRNP H1, hnRNP H2, hnRNP P (TLS), HTra2beta1, KSRP, Nova-1, SC35, YB-1, ZRANB2
USF1	Alter. First Exon (e1)	2.41	6.04E-04	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SRo30c, TIA-1, TIAL1, YB-1, ZRANB2
B4GALT3	Intron Retention	1.58	6.36E-04	ETR-3, hnRNP A1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HuB, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
B4GALT3 ASTN1	Intron Retention Alter. Acceptor Site	1.58 2.90	6.36E-04 6.36E-03	ETR-3, hnRNP A1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HuB, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HuB, KSRP, Nova-1, Nova-2, SC35, SF1, SRp20, TIA-1, TIAL1, YB-1
B4GALT3 ASTN1	Intron Retention Alter. Acceptor Site Alter. Term Exon (e3,e4,e8-13)	1.58 2.90 3.74	6.36E-04 6.36E-03 3.50E-06	ETR-3, hnRNP A1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HuB, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HuB, KSRP, Nova-1, Nova-2, SC35, SF1, SRp20, TIA-1, TIAL1, YB-1 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP A2/B1, hnRNP D, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP H2, hnRNP F (TLS), HTra2alpha, HTra2beta1,
B4GALT3 ASTN1 FAM129A	Intron Retention Alter. Acceptor Site Alter. Term Exon (e3,e4,e8-13) Exon Cassette	1.58 2.90 3.74 1.90	6.36E-04 6.36E-03 3.50E-06 1.76E-02	ETR-3, hnRNP A1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP F (TLS), HuB, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HuB, KSRP, Nova-1, Nova-2, SC35, SF1, SRp20, TIA-1, TIAL1, YB-1 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP A2, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP I (PTB), hnRNP H2, hnRNP I (PTB), hnRNP F, hnRNP H1, hnRNP H2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP F, hnRNP H2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP F, hnRNP H2, hnRNP H2, hnRNP H2, hnRNP F, hnRNP H2, hnRNP F, hnRNP H2, hnRNP H2, hnRNP F, hnRNP H2, hnRNP H2, hnRNP F, hnRNP H2, hnRNP H2, hnRNP H2, hnRNP F, hnRNP H2, hnRNP H2, hnRNP H2, hnRNP F, hnRNP H2, hnRN
B4GALT3 ASTN1 FAM129A TRMT1L	Intron Retention Alter. Acceptor Site Alter. Term Exon (e3,e4,e8-13) Exon Cassette Exon Cassette	1.58 2.90 3.74 1.90 2.02	6.36E-04 6.36E-03 3.50E-06 1.76E-02 1.33E-02	ETR-3, hnRNP A1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP F (tLS), HuB, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HuB, KSRP, Nova-1, Nova-2, SC35, SF1, SRp20, TIA-1, TIAL1, YB-1 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP D1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP F, hnRNP H2, hnRNP F, hnRNP H2, hnRNP H2, hnRNP H2, hnRNP F, hnRNP H2, hnRNP H2, hnRNP F, hnRNP H2, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SR920, SR920, STP30, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
B4GALT3 ASTN1 FAM129A TRMT1L	Intron Retention Alter. Acceptor Site Alter. Term Exon (e3,e4,e8-13) Exon Cassette Exon Cassette Exon Cassette	1.58 2.90 3.74 1.90 2.02 7.80	6.36E-04 6.36E-03 3.50E-06 1.76E-02 1.33E-02 9.62E-05	ETR-3, hnRNP A1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP F, hnRNP P (TLS), HuB, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP E2, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HuB, KSRP, Nova-1, Nova-2, SC35, SF1, SRp20, TIA-1, TIAL1, YB-1 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP H2, hnRNP H1, hnRNP H2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP F, hnRNP F, hnRNP H2, hnRNP F, hnRNP F, hnRNP H2, hnRNP F, hn
B4GALT3 ASTN1 FAM129A TRMT1L PLEKHA6	Intron Retention Alter. Acceptor Site Alter. Term Exon (e3,e4,e8-13) Exon Cassette Exon Cassette Exon Cassette Muthalk Exclusive Exons (e10)	1.58 2.90 3.74 1.90 2.02 7.80 3.42	6.36E-04 6.36E-03 3.50E-06 1.76E-02 1.33E-02 9.62E-05 7.59E-05	ETR-3, hnRNP A1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP F (TLS), HuB, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HuB, KSRP, Nova-1, Nova-2, SC35, SF1, SRp20, TIA-1, TIAL1, YB-1 CUG-B91, ETR-3, Fox-1, Fox-2, hnRNP A2/B1, hnRNP A2/B1, hnRNP D, hnRNP D, hnRNP D1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP P (TLS), HUB, KSRP, Nova-1, Nova-2, SC35, SF1, SRp20, TIA-1, TIAL1, YB-1 CUG-B91, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP D, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuK, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 CUG-B91, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP D, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP F (TLS), HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
B4GALT3 ASTN1 FAM129A TRMT1L PLEKHA6	Intron Retention Alter. Acceptor Site Alter. Term Exon (e3,e4,e8-13) Exon Cassette Exon Cassette Exon Cassette Mutualy Exclusive Exons (e10) Alter. First Exon (e1)	1.58 2.90 3.74 1.90 2.02 7.80 3.42 1.89	6.36E-04 6.36E-03 3.50E-06 1.76E-02 1.33E-02 9.62E-05 7.59E-05 1.66E-03	ETR-3, hnRNP A1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP F (TLS), HuB, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HuB, KSRP, Nova-1, Nova-2, SC35, SF1, SRp20, TIA-1, TIAL1, YB-1 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP E1, hnRNP D, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP H2, hnRNP H2, hnRNP F, hnRNP H1, hnRNP A2/B1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP F, HS, and S, SC35, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-1, Fox-2, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP F, (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1
B4GALT3 ASTN1 FAM129A TRMT1L PLEKHA6 ANGEL2	Intron Retention Alter. Acceptor Site Alter. Term Exon (e3,e4,e8-13) Exon Cassette Exon Cassette Exon Cassette Mutualy Exclusive Exons (e10) Alter. First Exon (e1) Complex (e4)	1.58 2.90 3.74 1.90 2.02 7.80 3.42 1.89 2.75	6.36E-04 6.36E-03 3.50E-06 1.76E-02 1.33E-02 9.62E-05 7.59E-05 1.66E-03 1.86E-03	ETR-3, hnRNP A1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP F, hnRNP P (TLS), HuB, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP E2, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP H2, hnRNP H1, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E2, hnRNP F2, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, SRB5, SC35, SP20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-2, hnRNP A1
B4GALT3 ASTN1 FAM129A TRMT1L PLEKHA6 ANGEL2	Intron Retention Alter. Acceptor Site Alter. Term Exon (e3,e4,e8-13) Exon Cassette Exon Cassette Exon Cassette Mutualy Exclusive Exons (e10) Alter. First Exon (e1) Complex (e4) Complex (e10)	1.58 2.90 3.74 1.90 2.02 7.80 3.42 1.89 2.75 5.07	6.36E-04 6.36E-03 3.50E-06 1.76E-02 1.33E-02 9.62E-05 7.59E-05 1.66E-03 1.86E-03 4.53E-06	ETR-3, hnRNP A1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP E2, hnRNP P (TLS), HuB, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP E2, hnRNP E2, hnRNP P, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HuB, KSRP, Nova-1, Nova-2, SC35, SF1, SRp20, TIA-1, TIAL1, YB-1 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP H1, hnRNP H2, hnRNP F (TLS), HUB, KSRP, MBNL1, Nova-1, Nova-2, SF5, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-1, Fox-2, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP F (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-1, Fox-2, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP F (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF2/ASF, SRp20, SRp30
B4GALT3 ASTN1 FAM129A TRMT1L PLEKHA6 ANGEL2 ESRRG	Intron Retention Alter. Acceptor Site Alter. Term Exon (e3,e4,e8-13) Exon Cassette Exon Cassette Exon Cassette Mutualy Exclusive Exons (e10) Alter. First Exon (e1) Complex (e4) Complex (e10) Exon Cassette	1.58 2.90 3.74 1.90 2.02 7.80 3.42 1.89 2.75 5.07 5.07	6.36E-04 6.36E-03 3.50E-06 1.76E-02 1.33E-02 9.62E-05 7.59E-05 1.66E-03 1.86E-03 4.53E-06	ETR.3, hnRNP A1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP F, hnRNP P (TLS), HuB, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 ETR.3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP F (TLS), HuB, KSRP, Nova-1, Nova-2, SC35, SF1, SRp20, TIA-1, TIAL1, YB-1 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A2/B1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H1, hnRNP H2, hnRNP H1, hnRNP P (TLS), HUB, KSRP, Nova-1, Nova-2, SC35, SF1, SRp20, TIA-1, TIAL1, YB-1 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H1, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuK, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP F (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP F (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP F (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, SBM68, SC35, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP F (TLS), HTra2beta1, HuB, HuD
B4GALT3 ASTN1 FAM129A TRMT1L PLEKHA6 ANGEL2 ESRRG NVL	Intron Retention Alter. Acceptor Site Alter. Term Exon (e3,e4,e8-13) Exon Cassette Exon Cassette Mutualy Exclusive Exons (e10) Alter. First Exon (e1) Complex (e4) Complex (e10) Exon Cassette Exon Cassette	1.58 2.90 3.74 1.90 2.02 7.80 3.42 1.89 2.75 5.07 5.07 1.60	6.36E-04 6.36E-03 3.50E-06 1.76E-02 1.33E-02 9.62E-05 7.59E-05 1.66E-03 1.86E-03 4.53E-06 4.01E-04	ETR-3, hnRNP A1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP E2, hnRNP P (TLS), HuB, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP E2, hnRNP E2, hnRNP F, hnRNP H2, hnRNP E2, hnRNP F, hnRNP H2, hnRNP E1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H2, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP H2, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP F, hnRNP H1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP F, hnRNP H2, hnRNP F, hnRNP H1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP K, hnRNP F (TLS), HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, SBM5, Sam68, SC35, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP F (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, SBM5, Sam68, SC35, SRp20, SRp30c, TD4-3, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C
B4GALT3 ASTN1 FAM129A TRMT1L PLEKHA6 ANGEL2 ESRRG NVL WDR26	Intron Retention Alter. Acceptor Site Alter. Term Exon (e3,e4,e8-13) Exon Cassette Exon Cassette Mutualy Exclusive Exons (e10) Alter. First Exon (e1) Complex (e10) Exon Cassette Exon Cassette Exon Cassette	1.58 2.90 3.74 1.90 2.02 7.80 3.42 1.89 2.75 5.07 5.07 1.60 1.51	6.36E-04 6.36E-03 3.50E-06 1.76E-02 1.33E-02 9.62E-05 7.59E-05 1.66E-03 1.86E-03 4.53E-06 4.53E-06 4.01E-04 7.62E-03	ETR.3, hnRNP A1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP E, hnRNP P (TLS), HuB, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 ETR.3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP F (TLS), HuB, KSRP, Nova-1, Nova-2, SC35, SF1, SRp20, TIA-1, TIAL1, YB-1 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP H2, hnRNP P (TLS), HUB, KSRP, Nova-1, Nova-2, SC35, SF1, SRp20, TIA-1, TIAL1, YB-1 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuK, KSRP, MBNL1, Nova-1, Nova-2, SFR, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 9G8, CUG-BP1, ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP D1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H1, hnRNP H2, hnRNP H2
B4GALT3 ASTN1 FAM129A TRMT1L PLEKHA6 ANGEL2 ESRRG NVL WDR26	Intron Retention Alter. Acceptor Site Alter. Term Exon (e3,e4,e8-13) Exon Cassette Exon Cassette Mutualy Exclusive Exons (e10) Alter. First Exon (e1) Complex (e4) Complex (e10) Exon Cassette Exon Cassette Exon Cassette	1.58 2.90 3.74 1.90 2.02 7.80 3.42 1.89 2.75 5.07 5.07 1.60 1.51 2.04	6.36E-04 6.36E-03 3.50E-06 1.76E-02 1.33E-02 9.62E-05 7.59E-05 1.66E-03 1.86E-03 4.53E-06 4.53E-06 4.01E-04 7.62E-03 5.58E-04	 ETR.3, hnRNP A1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP E, hnRNP P (TLS), HuB, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 ETR.3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP F (TLS), HuB, KSRP, Nova-1, Nova-2, SC35, SF1, SRp20, TIA-1, TIAL1, YB-1 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP H2, hnRNP H2, hnRNP H2, hnRNP F, hnRNP H2, hnRNP H2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP F, fnRNP M1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-2, NF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D1, hnRNP D2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SRp20, SRp30c, TD+3, TIA-1, TIAL1, YB-1, ZRANB2 GSG, CUG-BP1, ETR-3, FMRP, Fox-1, hnRNP A2/B1, hnRNP D1, hnRNP D2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H1, hnRNP H2
B4GALT3 ASTN1 FAM129A TRMT1L PLEKHA6 ANGEL2 ESRRG NVL WDR26 MRPL55	Intron Retention Alter. Acceptor Site Atter. Term Exon (e3,e4,e8-13) Exon Cassette Exon Cassette Mutualy Exclusive Exons (e10) Alter. First Exon (e1) Complex (e4) Complex (e10) Exon Cassette Exon Cassette Exon Cassette Exon Cassette Exon Cassette	1.58 2.90 3.74 1.90 2.02 7.80 3.42 1.89 2.75 5.07 5.07 1.60 1.51 2.04 1.73	6.36E-04 6.36E-03 3.50E-06 1.76E-02 1.33E-02 9.62E-05 7.59E-05 1.66E-03 4.53E-06 4.01E-04 7.62E-03 5.58E-04 3.6EE-04	 ETR-3, hnRNP A1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP E, hnRNP P (TLS), HuB, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP E2, hnRNP E, hnRNP P (TLS), HuB, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP H2, hnRNP F, hnRNP H1, hnRNP F, hnRNP H1, hnRNP F, hnRNP H2, hnRNP F, hnRNP H1, hnRNP F, hnRNP F (TLS), HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, SF, SRB05, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, SBM5, Sam68, SC35, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, SBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP D, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H1, hnRNP H2, hnRNP H1, hnRNP H2, hnRNP H1, hnRNP H2, hnRNP H
B4GALT3 ASTN1 FAM129A TRMT1L PLEKHA6 ANGEL2 ESRRG NVL WDR26 MRPL55 TAF5L	Intron Retention Alter. Acceptor Site Alter. Term Exon (e3,e4,e8-13) Exon Cassette Exon Cassette Mutualy Exclusive Exons (e10) Alter. First Exon (e1) Complex (e4) Complex (e10) Exon Cassette Exon Cassette Exon Cassette Complex Exon Cassette Alter. Terminal Exon (e4)	1.58 2.90 3.74 1.90 2.02 7.80 3.42 1.89 2.75 5.07 5.07 1.60 1.51 2.04 1.73 1.62	6.36E-04 6.36E-03 3.50E-06 1.76E-02 1.33E-02 9.62E-05 7.59E-05 1.66E-03 1.86E-03 4.53E-06 4.53E-06 4.01E-04 7.62E-03 5.58E-04 3.65E-04 5.64E-04	 ETR.3, hnRNP A1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP E, hnRNP P (TLS), HuB, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 ETR.3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP F (TLS), HuB, KSRP, Nova-1, Nova-2, SC35, SF1, SRp20, TIA-1, TIAL1, YB-1 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP H2, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2, ASF, SRp20, SRp30c, TD43, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP F, (K, hnRNP P (TLS), HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TD43, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TD43, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP H2, hnRNP H2, hnRNP H1, hnRNP H2, hnR
B4GALT3 ASTN1 FAM129A TRMT1L PLEKHA6 ANGEL2 ESRRG NVL WDR26 MRPL55 TAF5L TTC13	Intron Retention Alter. Acceptor Site Atter. Term Exon (e3,e4,e8-13) Exon Cassette Exon Cassette Mutualy Exclusive Exons (e10) Alter. First Exon (e1) Complex (e4) Complex (e10) Exon Cassette Exon Cassette Exon Cassette Complex Exon Cassette Alter. Terminal Exon (e4) Exon Cassette	1.58 2.90 3.74 1.90 2.02 7.80 3.42 1.89 2.75 5.07 5.07 1.60 1.51 2.04 1.73 1.62 1.83	6.36E-04 6.36E-03 3.50E-06 1.76E-02 1.33E-02 9.62E-05 7.59E-05 1.66E-03 1.86E-03 4.53E-06 4.01E-04 7.62E-03 5.58E-04 3.65E-04 5.64E-04 8.29E-05	 ETR-3, hnRNP A1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP E, hnRNP E, hnRNP E, thnRNP F (TLS), HuB, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP E1, hnRNP E, hnRNP E1, hnRNP E2, hnRNP F, thRNP F, hnRNP F1, hnRNP E2, hnRNP F, hnRNP F1, hnRNP E2, hnRNP F, hnRNP F1, hnRNP E2, hnRNP F, hnRNP F1, hnRNP F2, hnRNP F1, hnRNP F1, hnRNP F2, hnRNP F3, hnRNP F1, hnRNP F2, hnRNP F1, hnRNP F2, hnRNP F1, hnRNP F2, hnRNP F2, hnRNP F2, hnRNP F2, hnRNP F2, hnRNP F1, hnRNP F2, hnRNP F1, hnRNP F2, hnRNP F1, hnRNP F2, hnRNP F3, hnRNP F1, hnRNP F2, hnRNP F1, hnRNP F2, hnRNP F1, hnRNP F2, hnRNP F3, hnRNP F1, hnRNP F2, hnRNP F3, hnRNP F1, hnRNP F2, hnRNP F1, hnRNP F2, hnRNP F1, hnRNP F2, hnRNP F1, hnRNP F2, hnRNP F3, hnRNP F1, hnRNP F2, hnRNP F3, hnRNP F1, hnRNP F2, hnRNP F1, hnRN
B4GALT3 ASTN1 FAM129A TRMT1L PLEKHA6 ANGEL2 ESRRG NVL WDR26 MRPL55 TAF5L TTC13 NID1	Intron Retention Alter. Acceptor Site Alter. Term Exon (e3,e4,e8-13) Exon Cassette Exon Cassette Mutualy Exclusive Exons (e10) Alter. First Exon (e1) Complex (e10) Exon Cassette Exon Cassette Exon Cassette Complex Exon Cassette Alter. Terminal Exon (e4) Exon Cassette Exon Cassette Exon Cassette Exon Cassette Exon Cassette Exon Cassette Exon Cassette	1.58 2.90 3.74 1.90 2.02 7.80 3.42 1.89 2.75 5.07 5.07 1.60 1.51 2.04 1.73 1.62 1.83	6.36E-04 6.36E-03 3.50E-06 1.76E-02 1.33E-02 9.62E-05 7.59E-05 1.66E-03 1.86E-03 4.53E-06 4.53E-06 4.01E-04 7.62E-03 5.58E-04 3.65E-04 5.64E-04 8.29E-05 7.00E-03	ETR-3, hnRNP A1, hnRNP F1, hnRNP H2, hnRNP L2, hnRNP L2, hnRNP L3, hnRNP F1, L3, HuB, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP E1, hnRNP F2, hnRNP F1, hn

				HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRo20, SRo30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
				FTR-3. Fox-1. Fox-2. bnRNP A1. bnRNP A2/B1. bnRNP C1. bnRNP C1. bnRNP F1. bnRNP F2. bnRNP F4. bnRNP H1. bnRNP H2. bnRNP H2. bnRNP K4. bnRNP K4. bnRNP F4. bn
OPN3	Alter. Donor Site	1.79	2.02E-04	Nova-2, PSF, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
				FTR-3, Fox-1, Fox-2, bnRNP A1, bnRNP A2/B1, bnRNP C1, bnRNP C1, bnRNP D1, bnRNP F2, bnRNP F2, bnRNP H1, bnRNP H2, bnRNP H2, bnRNP K, bnRNP K, bnRNP P, (TLS), HTra2aloba, HTra2beta1, HuB.
OPN3	Alter. First Exon (e1-2)	2.33	3.69E-05	HuD, HuR, KSRP, MBNLI, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRo20, SRo30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
	Complex	1.55	2.94F-03	
ZNF692	Intron Retention	1.86	1.36F-04	ETR-3, hnRNP A1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, KSRP, MBNL1, Nova-1, RBM5, SC35, TIA-1, TIAL1
		1.00	11002.01	CUIC-RP1 FTR-3 Fox-1 Fox-2 bnRNP A1 bnRNP A2/B1 bnRNP C1 bnRNP C1 bnRNP F1 bnRNP F2 bnRNP F bnRNP H1 bnRNP H2 bnRNP H3 bnRNP L(PTR) bnRNP K bnRNP P (TLS) HTra2beta1 HuR HuD
FBX018	Alter. First Exon (e4-5)	2.04	1.16E-02	KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF2/ASF, SRc20, SRc30c, TIA-1, TIAL1, YB-1, ZRANB2
				FTR-3 Fox-1 Fox-2 hoRNP A1 hnRNP A2/B1 hnRNP C1 hnRNP C1 hnRNP F1 hnRNP F2 hnRNP F2 hnRNP F1 hnRNP H2 hnRNP H2 hnRNP L(PTB) hnRNP K hnRNP P (TLS). HTra2beta1. HuB. HuD. HuR. KSRP. MBNI 1.
CACNB2	Mutualy Exclusive Exons (e11)	2.25	9.75E-04	Nova-1, Nova-2, Sam68, SC35, SF1, SRo20, SRo30c, TIA-1, TIAL1, YB-1, ZRANB2
				CUG-BP1. ETR-3. Fox-1. Fox-2. hnRNP A1. hnRNP A2/B1. hnRNP C1. hnRNP C1. hnRNP DL. hnRNP E1. hnRNP E2. hnRNP F1. hnRNP H1. hnRNP H2. hnRNP I (PTB). hnRNP K. hnRNP P (TLS). HTra2alpha. HTra2beta1.
MLLI 10	Exon Cassette	1.59	1.12E-03	HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
BMI1//COMMD3	Intron Retention	1.61	6.08E-05	ETR-3, hnRNP A1, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HuB, Nova-1, Sam68, SC35, TIA-1, TIAL1, YB-1
00104	5 0 "	0.04	5 655 65	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D1, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP H, hnRNP K, hnRNP M, hnRNP C1, hnRNP
SPAG6	Exon Cassette	2.96	5.65E-05	KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
10/001		1.04		9G8. CUG-BP1. ETR-3. Fox-1. Fox-2. hnRNP A1. hnRNP A2/B1. hnRNP C1. hnRNP D. hnRNP DL. hnRNP E1. hnRNP E2. hnRNP F. hnRNP H1. hnRNP H2. hnRNP H3. hnRNP H (PTB). hnRNP K. hnRNP K. hnRNP C1. hnRNP P
MY03A	Alter. First Exon (e1-33)	1.86	1.55E-02	(TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
7504				CUG-BP1, ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS),
ZEBI	Alter. First Exon	2.18	1.78E-02	HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
	Complex	2.71	1.04E-04	
MAPK8	Mutualy Exclusive Exons (e7)	5.44	1.34E-06	ETR-3, Fox-1, Fox-2, hnRNP F4, hnRNP F2, B1, hnRNP C1, hnRNP C1, hnRNP E2, hnRNP F4, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP F (TLS), HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1,
	Exon Cassette	2.90	5.01E-04	Nova-1, Nova-2, Sam68, SC35, SKp20, SKp30c, TDP43, TIA-1, TIAL1, YB-1, ZKANB2
				CUIG-BP1, FTR-3, Fox-1, Fox-2, bnRNP A1, bnRNP A2/B1, bnRNP C1, bnRNP C1, bnRNP F1, bnRNP F2, bnRNP F4, bnRNP H2, bnRNP H3, bnRNP H3, bnRNP K, bnRNP F4, bnRNP P (TI S), HTra2aloba, HTra2beta1,
PHYHIPL	Exon Cassette	2.60	1.36E-04	HuB, HuD, KSRP, MBNLI, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRo20, SRo30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
				CUIC-RPT FTR-3 Fox-1 Fox-2 bnRNP A1 bnRNP A2/B1 bnRNP C1 bnRNP C1 bnRNP F1 bnRNP F2 bnRNP F bnRNP H2 bnRNP H2 bnRNP H2 bnRNP I (PTR) bnRNP K bnRNP P (TLS) HTra2beta1 HuR HuD HuR KSRP
VPS26A	Exon Cassette	1.84	1.67E-02	MBNI 1, Nova-2, PSE, RBM5, Sam68, SC35, SF1, SRn20, SRn30c, TDP43, TIA-1, TIAI, 1, YP-1, ZRANB2
	Exon Cassette	1.67	1.22E-04	FTR-3 Fox-1 Fox-2 hnRNP C1 hnRNP C1 hnRNP F2 hnRNP F2 hnRNP F4 hnRNP H1 hnRNP H2 hnRNP I (PTB) hnRNP P (TI S) HuB KSRP MBNI 1 Nova-1 Nova-2 PSE RBM5 Sam68 SC35 SRo20 SRo30c
SEC24C	Intron Retention	1.75	3.25F-04	TIA-1, TIAL1, YB-1, ZRANB2
				CUG-BP1_FTR-3_Fox-1_Fox-2_bnRNP_A1_bnRNP_A2/B1_bnRNP_C1_bnRNP_D2_bnRNP_F1_bnRNP_F2_bnRNP_F4_bnRNP_H2_bnRNP_H2_bnRNP_H2_bnRNP_F4_b
ZSWIM8	Alter. Terminal Exon (e1-2)	1.59	1.02E-03	KSRP, MBNI 1, Nova-1, Nova-2, PSE, RBM5, Sam68, SC35, SE2/ASE, SRo20, SRo30c, TDP43, TIA-1, TIA1, 1, YB-1, ZRANB2
				CUG-RP1, FTR-3, Fox-1, Fox-2, bnRNP A1, bnRNP A2/B1, bnRNP C1, bnRNP C1, bnRNP F1, bnRNP F2, bnRNP F4, bnRNP H2, bnRNP H2, bnRNP H2, bnRNP H2, bnRNP F4, bnR
VDAC2	Exon Cassette	2.09	1.19E-04	MBNI 1, Nova-1, Nova-2, Sam68, SC35, SE1, SRo20, TIA-1, TIA-1, YR-1, ZRANB2
ZMIZ1	Exon Cassette	3.18	3.45E-04	ETR-3. hnRNP C1. hnRNP F. hnRNP H., hnRNP H.2. hnRNP I (PTB). hnRNP K. hnRNP P (TLS). HuB. KSRP. MBNL1. Nova-1. Nova-2. SC35. SRb20. TIA-1. TIAL1. YB-1. ZRANB2
BTAF1	Alter, Donor Site	2.70	7.80E-04	CUG-BP1, ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP F, hnR
AS3MT/C10orf32	Alter, First Exon (e7)	1.70	3.92F-05	hnRNP F1, hnRNP F2, SC35, SR030c, TIA-1, TIA1, 1
SFR1	Intron Retention	2.52	4.63F-04	TR-3, bRNP (1, bnRNP F1, bnRNP H2, bnRNP I/ (PTB), bnRNP K, bnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNI 1, Nova-1, PSE, RBM5, Sam68, SC35, SF2/ASE, TIA-1, TIAI 1, YB-1, ZRANB2
01112		2.02	11002.01	CIIC/ENF TRAS FAMP Fox 1 Fox 2 hoRNP 41 hoRNP 42 (81 hoRNP 1 hoRNP 1 hoRNP F1 hoRNP F1 hoRNP H1 hoRNP H2 hoRNP [1 PRIN] F1 hoRNP
MXI1	Exon Cassette	2.32	1.96E-03	HuB, HuD, KSRP, MBN11, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRa20, SRo30c, TDP43, TIA-1, TIA11, VB-1, ZRANB2
				FTR-3 FMRP Fox-1 Fox-2 hoRNP A1 hoRNP A2/R1 hoRNP C1 hoRNP C1 hoRNP F1 hoRNP F2 hoRNP F2 hoRNP F1 hoRNP H1 hoRNP H2 hoRNP L(PTR) hoRNP K hoRNP F (TLS) HTra2beta1 HuR KSRP MRNI 1 Nova-
VTI1A	Exon Cassette	1.62	1.10E-02	1 Nova-2 RBM5 Sam68 SC35 SR30c TDP43 TIA-1 TIA1 / VB-1 ZRANB2
				TR3 F0x1 F0x2 bnRNP 41 bnRNP 42/R1 bnRNP C1 bnRNP C1 bnRNP F1 bnRNP F2 bnRNP F2 bnRNP F1 bnRNP H2 bnRNP H2 bnRNP L(PTR) bnRNP P(TLS) HuR HuD KSRP MRN1 1 Nova-1 Nova-2 Sam68 SC35
TRUB1	Complex	1.83	1.83E-04	SR020. SR030c. TIA-11 VI: 1. VB-12, MARK 21, MAR
WDR11	Intron Retention	1.67	6.85F-04	FTR-3, brRNP C1, brRNP E, brRNP H1, brRNP H2, brRNP I (PTB), brRNP P (TLS), HuB, KSRP, MBN 1, Nova-1, PSE, SC35, SE1, SRo20, SRo30c, YB-1, ZRANB2
				FTR-3 Fox-1 Fox-2 bnRNP A1 bnRNP A2/B1 bnRNP C1 bnRNP C1 bnRNP E1 bnRNP E2 bnRNP E bnRNP H1 bnRNP H2 bnRNP L(PTR) bnRNP K bnRNP P (TLS) HTra2beta1 HuB KSRP MRNI 1 Nova-1
TACC2	Exon Cassette	2.68	5.60E-03	Nux-2 PERMS Sanda S(2) SE2/ASE SER00 SR30C 1141 TIAL 1 VAL 124. TRANS 2
	Evon Cassette	1 71	6 37E-04	CIICLEPT FTR3 Fox1 Fox2 broRNP of horPC/02/R1 horRNP C1 horRNP C1 horRNP H2 horRNP H2 horRNP H2 horRNP P/TLS) HTra2aloha HTra2bata1 HuR KSRP MRNI 1 Nova1 Sam68 SC35 SF1
PLEKHA1	Intron Retention	1.76	6.37E-04	SE2/ASE_SR030c_TDP43_TIA1_TIA1_YB-1_ZRANP2
		1.70	0.07201	
BCCIP	Alter. Terminal Exon (e6)	2.16	3.69E-02	SSPP_INTN_Nova-2_PSF_RBM5_Sam68_S23_S52/ASF_SR20_SB000_TLA_TIAL1_YB_1_FRANR2
LRRC27	Exon Cassette	2.26	1.50E-03	MRNI 1 Nova-1 Nova-2 PSF RBMS Sam68 SC3 SE1 SE2 VSG SR 300 SR 30C TDP43 TIA-1 TIA1 19L 7 RANR2
			l	968. CUG-RP1. FTR-3. FMRP. Fox-1. fox-9. hnRNP A1. hnRNP A2/B1. hnRNP C1. hnRNP F1. hnRNP F2. hnRNP F1. hnRNP H1. hnRNP H3. hnRNP H3. hnRNP K. hnRNP K. hnRNP P /TI S1. HTra2alnha
DIP2C	Alter. Terminal Exon	1.68	1.76E-03	HTra2beta1, HuB, HuD, KSRP, MBN1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRa20, SRo30c, TDP43, TLA1, TA11, YF1, 7RANR2
	Alter Dopor Site	2 07	6 99F-04	
SEPHS1	Alter, Terminal Exon (e6)	2.17	6.48F-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68,
02.1.01	Exon Cassette	1 90	3 24F-04	SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
∆ RI1	Exon Cassette	1.50	4 19E-04	FTR.3 Fow.1 Fow.2 hoRNP &1 hoRNP &2/R1 hoRNP C1 hoRNP C1 hoRNP F1 hoRNP F2 hoRNP F hoRNP H1 hoRNP H2 hoRNP H2 hoRNP H hORNP
דומי	LAUN GASSELLE	1.34	7.1JL-04	E E ROUTE ON A LEVEL DE LE CONTRALE DE L

				Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1
ANKRD26	Exon Cassette	1.51	6.49E-05	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Sam68, SC35,
ZNF438	Exon Cassette	3.02	1.20E-03	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, INRIVE A1, INRIVE A2/B1, INRIVE D1, INRIVE D1, INRIVE D1, INRIVE B1, INRIVE
ITGB1	Exon Cassette	1.83	1.77E-02	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MRN11, Nova-1, Nova-2, Sam68, SC35, SRo20, SRo30, TLA1, TLA1, YR-1, ZRANR2
ZNE37BP	Intron Retention	1.68	6.82F-04	TR3. FOX. FOX. PRIVE C1. INRVE F1. INRVE F2. INRVE F. INRVE F. INRVE F. INRVE F. INRVE F. INRVE K. INRVE F1. INRVE F2. INRVE F1. INRVE F1. TR41 TR41 F2. INRVE F1. INRVE F1
FRCC6 //		1.00	OIOLL OI	FIR-3, brRNP A1, brRNP A2/B1, brRNP C1, brRNP C1, brRNP F1, brRNP F2, brRNP F1, brRNP F1, brRNP F1, brRNP F2, brRNP F2, brRNP F1, brRNP F2, brRNP
ERCC6-PGBD3 //	Intron Retention	1.53	2.12E-03	PSF, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
ZWINT	Intron Retention	2.15	5.41E-04	ETR-3, hnRNP P (TLS), HTra2beta1, Nova-1, SC35, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
FAM13C	Alter. Terminal Exon (e13-14)	2.42	1.10E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Sam68, SC35, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
RTKN2	Exon Cassette	1.81	7.60E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
RUFY2	Alter. First Exon (e1)	1.84	4.62E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, RBM5, Sam68, SC35, SRb20, SRb
LRRC20	Alter. First Exon (e2)	1.52	1.03E-02	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP F (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MRN1 1, Nova-2, RMR5, Sam68, SC35, SE1, SRo20, SRo30, TIA-1, TIA-1, 7RANR2
	Exon Cassette	1.67	5 00F-04	
CAMK2G	Exon Cassette	1.60	9.82E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP,
	Exon Cassette	2.08	1.54E-03	MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
ATAD1	Exon Cassette	1.59	9.14E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SRo20, SRo30c, TIA-1, TIAL1, YB-1, ZRANB2
ACTA2	Exon Cassette	2.47	6.23E-05	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, PSE, Sam68, SC35, SRn20, SRn30c, TIA-1, TIA-1, TIA-1, TRANB2
	Alter, Acceptor Site	3.57	2.42E-04	
SORBS1	Complex	3.60	1.61E-04	CUG8P1, ETR-3, Fox-2, Fox-2, FnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP A2,
	Exon Cassette	1.59	4.83E-04	HIR2/Deta1, HUB, HUU, KSKP, MBINL1, Nova-1, Nova-2, PSF, KBMS, Samb8, SC35, SF1, SF2/ASF, SKp2U, SKp3Uc, HA-1, HAL1, YB-1, ZKANB2
ARHGAP19 // SLIT1	Alter. Terminal Exon (e21,e22- 27,e29-54)	1.92	1.06E-03	9G8, CUG-BP1, ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP H1, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
POLL	Alter. Terminal Exon (e7)	1.60	4.78E-04	CUG-BP1, ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
LDB1	Alter. Terminal Exon (e11)	2.31	7.56E-05	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
	Exon Cassette	2.01	1.22E-04	FTR.3 hnRNP 01/R1 hnRNP 02/R1 hnRNP C1 hnRNP C1 hnRNP F2 hnRNP F2 hnRNP F4 hnRNP H2 hnRNP H2 hnRNP P/TI S1 HTra2hata1 HuR KSPP MRN11 Nova1 Nova2 Sam68 SC35
NT5C2	Intron Retention	2.00	1.78E-04	SRp20, TIA-1, TIAL1, YB-1, ZRANB2
COD001	Alter. Terminal Exon (e25)	1.53	1.70E-03	9G8, CUG-BP1, ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP H1, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP LL,
SURCSI	Complex (e2)	1.62	2.83E-04	hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
SMNDC1	Intron Retention	1.58	4.00E-03	ETR-3, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, Nova-1, Sam68, SC35, SF2/ASF, SRp20, YB-1, ZRANB2
	Alter. Terminal Exon (e4)	1.96	9.74E-05	FTR-3 Fox-1 Fox-2 hoRNP A1, hoRNP A2/B1, hoRNP C1, hoRNP C1, hoRNP F1, hoRNP F2, hoRNP F, hoRNP H1, hoRNP H2, hoRNP J (PTB), hoRNP K, hoRNP P (TI S1) HTra2aloba HTra2beta1 HuR Hu1) KSRP
BBIP1	Exon Cassette	2.41	1.42E-04	MBNL1, Nova-2, PSF, RBMS, Sam68, SC35, SF1, SF2/ASF, SRo20, SRo30c, TIA-1, TIAL1, YB-1, ZRANB2
C10orf118	Alter. Acceptor Site	1.71	1.95E-05 1.80E-02	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Sam68, SC35,
	Altern Terminal From (+10)	1.02	4 205 04	
TIAL1	Alter. Terminal Exon (e12)	1.83	4.38E-04	EIK-3, FOX-1, FOX-2, INRKWP A1, INRKWP A2/B1, INRKWP C1, INRKWP E2, INRKWP E4, INRKWP H1, INRKWP H2, INRKWP H2, INRKWP P (ILS), HTR32Deta1, HUB, HUU, KSKP, MIBINLI, NOVA-1, NOVA-2, DDMs C-song Co26 C-2010 CHall Tild I VD 1 ZONDO
NSMCE/A	Intron Retention	1.71	2.17E-04	NOME, SANDO, SUSS, SNEZO, SNESO, INFEL, IDEL, IDEL, IDEL, SINTOZ ETEL: ANDRA IL ANDRA IL ANDRE HADDRE ITA NOMEN IL INVESTI PRIS SANGE SCIESCI SECON SDA 30A TIALI TIALI VEL
NONICLAA	intron netention	1./1	4.012-04	Erres, minure ra, minure ra, minure raz, minure raz, minure rates, monte, nome, samos, source, source, source, source, meter, meter, meter, source, so
OAT	Alter. Acceptor Site	1.71	1.92E-03	Sam68, SC35, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
STK32C	Alter. First Exon	3.01	1.35E-07	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
TMEM80	Intron Retention	2.18	1.60E-04	ETR-3, hnRNP A1, hnRNP C1, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, Nova-2, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
BRSK2	Complex	1.78	1.93E-02	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, RBM5, SC35, SF2/ASF, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
RRM1	Alter. Donor Site	1.77	1.19E-02	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SRp20, TIA-1, TIAL1, YB1
11.17	Intron Retention	1.61	1.57E-02	ETR-3, hnRNP A1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP P (TLS), HTra2beta1, KSRP, SRo30c

	Complex	2.06	1 005 00	
TEAD1	Complex	2.00	1.02E-03	
	Exon Cassette	2.06	1.02E-03	
NAV2	Exon Cassette	2.40	3.40E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1,
				Nova-2, PSF, Sam68, SC35, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
	Alter. Terminal Exon (e4-5)	1.70	1.62E-02	
DNAJC24	Complex	2.14	8.40E-04	CODED 1, ETCS, TAX1, TAX2, TAX1, TAX2, TAXA, ATTACAPTING C, TITATA O, TITATA
	Exon Cassette	2.05	8.40E-04	Nonr, mbnei, nova-i, nov
HIPK3	Exon Cassette	1.53	8.38E-05	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP I (PTB), HuB, Nova-1, PSF, Sam68, SC35, SRp30c, TIA-1, TIAL1, YB-1
				CUC-BP1 FTR-3 EMRP Fox-1 Fox-2 bnRNP A1 bnRNP A2/B1 bnRNP C1 bnRNP D1 bnRNP D1 bnRNP F1 bnRNP F2 bnRNP F4 bnRNP H2 bnRNP
KIAA1549L	Exon Cassette	1.87	3.96E-04	HTra/beta1 HuB KSRP MRNI1 Nova-1 Nova-2 PSF RBMS Sam68 SC35 SE1 SE2/ASE SR0/0 SR0/20 CTIA-1 TIAI 1 YR-1 ZRANR2
	Altor Terminal Even (c19 c20			
ACCS // EXT2	Alter. Terminal Exon (e19,e20-	1.86	6.72E-03	
	21,023-23,027-33)			
PRDM11	Alter, Terminal Exon	1.96	8.33E-05	9G8, E1R-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP P (1ES), H1ra2alpha, H1ra2beta1, HuB, KSRP,
				MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
DGK7	Alter First Evon (e1-29)	1 74	3 32E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha,
DUITE	/itel: 113t Ex61 (e1 25)	1.7 4	5.52E 05	HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
TTOOO	E	1.74	0.705.04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, Sam68,
TIC9C	Exon Cassette	1./4	8.79E-04	SC35, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
VEGEB	Alter, Acceptor Site	1.54	2.42F-04	hrRNP A1, hrRNP F, hrRNP H1, hrRNP H2, hrRNP H2, hrRNP K, MBNI 1, Nova-1, Nova-2, Sam68, SRo30c, TIA-1, TIA11, YB-1
MUS81	Intron Retention	1 70	2.62E-03	FTR-3 hpRNP (1 hpRNP (1PTR) hpRNP P(TTS) KSRP Noval SC35 SR-20 SR-30c TIAL TIALI VR.1
	Intron Potention	1.64	2.0E 04	ETTO 2 handhold prilled Hund Kophine (Cophine Cophine) (Starborn Hardines) (Starborn H
ANNOT JD	Intron Retention	1.04	8.40L-04	
NDUFV1	Intron Retention	2.62	8.41E-04	nikiw Al, nikiw D, nikiw EL, nikiw F, nikiw H, nikiw HL, nikiw H, nikiw F (F1B), nikiw F (L3), N3K, P5-, 3C33, 5F2/ASF, 3Kp30C, TB-1
TPCN2	Exon Cassette	2.16	1.58E-04	CUG-BP1, ETR-3, hnRNP A1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, Nova-2, RBM5, SC35, SF2/ASF, SRp30c, TIA-1, TIAL1, YB-1
MPPL // 8	Evon Cassette	1.60	2 /0E-02	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2beta1, HuB, HuD, HuR, KSRP,
WINF L40	EXOIT Casselle	1.00	2.40L-02	MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
11/040	F 0 "	1.00	6.065.00	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1,
UVRAG	Exon Cassette	1.96	6.36E-03	HuB, KSRP, MBNL1, Nova-2, Sam68, SC35, SF2/ASF, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
				FTR-3, Fox-1, Fox-2, bnRNP A1, bnRNP A2/B1, bnRNP C1, bnRNP C1, bnRNP F2, bnRNP F2, bnRNP H1, bnRNP H2, bnRNP H2, bnRNP P (TLS), bnRNP P (TLS), HTra2aloba, HTra2beta1, HuB, KSRP, MBNI 1, Nova-1, Nova-2, PSE
C11orf30	Exon Cassette	1.56	3.95E-05	RBM5_Sam68_SC35_SE1_SRo20_SRo30c_TIA-1_TIA11_YR-1_ZRANB2
TMEM126B	Exon Cassette	1.84	1.80E-03	Entroy for 1, 0x2, initial A2, initial A2, 01, initial 0, initial 1, initial 12, initial 12, initial 12, initial 12, initial 12, initial 14, initial 1
011-472	Altern Termeinel Freez (+C 7)	0.10	1.025.04	
C110ff73	Alter. Terminal Exon (e6-7)	2.19	1.23E-04	
C11orf54	Exon Cassette	1.78	1.48E-03	EIR-3, INRKIP AL, INRKIP ZJ, BI, INRKIP EJ, INRKIP EJ, INRKIP F, INRKIP HI, INRKIP HZ, INRKIP F (PIB), INRKIP F (ILS), HIRZZIPRA, HIRZZPETAI, HUB, HUU, KSKP, MENLI, NOVA-I, NOVA-Z,
-				RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
DIXDC1	Alter First Evon (e3-7 e10-12)	1 75	1.02E-02	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD,
DIADOI	/itel: 113t Ex61 (657,610 12)	1.75	1.022.02	KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
CDUD	Exon Cassette	1.77	8.06E-03	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1,
SUHU	Mutualy Exclusive Exons	2.26	1.62E-03	Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
	Complex (e17-20)	3.21	1.67E-05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2aloha, HTra2beta1, HuB, HuD,
NCAM1	Evon Cassette	4.05	2 36E-05	KSRP MRNI 1 Nova 1 Nova 2 PSF RRM5 Sam68 SC35 SRo20 SRo30c TDP43 TIAL TIALI 1 KL 1 ZANR2
V/DC11	Compley	2.01	2 77E 04	
LIMDS	Intron Batantian	1.72	2.776-04	
HIVES		1./3	3./0E-U3	
HINFP	Intron Retention	1.50	8.25E-05	EIK-3, INKINP AL, INKINP U, INKINP EL, INKINP EL, INKINP HI, INKINP HI, INKINP HZ, INKINP I (FIB), INKINP Y, INKINP P (ILS), HUB, KSKP, MBINLI, Nova-1, Nova-2, Sam68, SC35, SRp30c, TIA-1, TIAL1, Y
ARHGFF12	Exon Cassette	1,51	1.92E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP H2, hnRNP K, hnRNP F, TLa2beta1, HuB, HuD, KSRP,
	Elen ousselle	1.01	1.522.00	MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SRp20c, TIA-1, TIAL1, YB-1, ZRANB2
	Complex	1.59	4.24E-04	
TBCEL				Ency rock, rock, mixer Az, mixer Az, original of, mixer D, mixer D, mixer T, mixer T
	Exon Cassette	1.70	9.42E-04	MDNE1, NOVA1, NOVA2, F31, NDM3, 341100, 3033, 311, 3NP20, 3NJ300, 11A1, 11A11, 10-1, 2NNN52
TBRG1	Exon Cassette	1.70	2.32E-05	ETR-3, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1
07701	5 0 11	1.05	6 955 94	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2,
STI3A	Exon Cassette	1.95	6.35E-04	PSF. Sam68. SC35. SF1. SRo30c. TIA-1. TIAL1. YB-1. ZRANB2
FOXRED1	Alter Donor Site	1 74	1 74F-03	FTR-3 Fox-1 Fox-2 hoRNP A1 hoRNP A2/R1 hoRNP E hoRNP H1 hoRNP H2 hoRNP P (TLS) HTra2aloba HTra2beta1 HuB KSRP MBNI 1 Nova-1 Nova-2 Sam68 SC35 SR020 SR030c TIA-1 TIAI 1 YB-1
TOMILEDI	Compley	1.0 1	1.59E 02	ETC2 Ev2 beach and the registration of the most of the
ACAD8	Intron Detention	1.31	1.300-02	בוריס, ועיבן שאריבן שוואד אבן שנו שוואד אבן שנו שוואד ט, ושואד ט, ושואד ט, ושוואד ט, ושואד ב, ושואד ב, ושוואד ב, ושואד ב, ושואד ב, שוואד
	Intron Retention	1./1	1.33E-02	Sanido, Sussi, Sakisu, Sakisu, 114-1, 114-1, 118-1, 24anbz
	Alter. Acceptor Site	1.56	3.00E-03	
RNH1	Alter. First Exon (e1)	1.60	3.52E-03	ETR-3, hnRNP A1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SRp20,
100111	Complex	1.71	4.99E-04	SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
	Exon Cassette	1.54	3.82E-03	

MOB2	Alter. First Exon (e1)	1.99	1.86E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SRb30c, TDP43, TIA-1, TIA-1, TRA-1, ZRANB2
NAP1L4	Exon Cassette	1.54	1.88E-02	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SF1, SF2/ASF, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
ZNF195	Exon Cassette	2.48	2.16E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
APBB1	Intron Retention	1.64	1.64E-02	ETR-3, Fox-1, Fox-2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), KSRP, MBNL1, RBM5, SC35, SF2/ASF, TIA-1, TIAL1, YB-1
	Alter. Acceptor Site	2.00	2.83E-04	
ARFIP2	Alter. Terminal Exon (e3)	1.65	1.80E-04	ETR-3, hnRNP A1, hnRNP A1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1
	Intron Retention	2.07	7.98E-05	
	Alter. First Exon (e1-3)	5.91	4.20E-06	9G8. CUG-BP1. ETR-3. Fox-1. Fox-2. hnRNP A1. hnRNP A2/B1. hnRNP C1. hnRNP D. hnRNP D1. hnRNP E1. hnRNP E1. hnRNP F. hnRNP H1. hnRNP H2. hnRNP H3. hnRNP I (PTB). hnRNP K. hnRNP P (TLS).
DKK3	Complex	1.53	3.21F-04	HTra2alpha. HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
FBX03	Alter. Terminal Exon (e11)	1.99	1.06E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
PHF21A	Mutualy Exclusive Exons (e16)	5.71	1.07E-07	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
AMBRA1	Exon Cassette	1.52	1.45E-02	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
LPXN	Exon Cassette	1.53	3.72E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
GANAB	Exon Cassette	1.50	7.84E-03	ETR-3, hnRNP A1, hnRNP C1, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, Nova-1, RBM5, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
	Intron Retention	2.01	7.64E-05	
UBXN1	Intron Retention	2.92	2.81E-04	ETR-3, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, Nova-1, Sam68, SC35, SF2/ASF, SRp30c, TDP43, TIA-1, TIAL1, YB-1
	Intron Retention	2.25	8.44E-04	
SNHG1// SNORD22	Intron Retention	1.70	3.84E-04	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP P (TLS), HuB, KSRP, Sam68, SC35, TIA-1, TIAL1, YB-1, ZRANB2
	Alter. Acceptor Site	2.73	4.56E-04	
RELA	Intron Retention	2.34	7.51E-05	EI N-3, IIIIKINF F1, IIIIKINF F1, IIIIKINF F (11-3), F3F, 3C-33, SR/30C, 18-1
SUV420H1	Exon Cassette	1.77	1.14E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
	Alter. First Exon (1-6)	1.79	8.78E-04	
NUMA1	Complex	1.64	4.43E-05	
	Exon Cassette	2.34	2.25E-05	
CTSC	Alter. Donor Site	2.03	2.16E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Sam68, SC35, SF1, SRp20, TIA-1, TIAL1, YB-1, ZRANB2
MRE11A	Alter. Terminal Exon	1.52	5.95E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
CWC15	Intron Retention	1.94	9.80E-04	ETR-3, hnRNP A1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, HTra2beta1, HuB, Nova-1, Sam68, SC35, TIA-1, TIAL1
	Alter. First Exon (e1-10)	1.86	1.06E-03	
CADM1	Exon Cassette	2.60	3.89E-06	
	Mutualy Exclusive Exons	1.92	1.44E-04	יוואבעקווא, ווואבטעאבן האבן האבן האני, האון הסווי, ואסורבן, וסערבן, וסערבן, וסיויס, ספווסט, סססט, סו בן סו בי אסו, סוועבע, סוקטעט, וסו אס, ווארב, וואבן, וסיב, באאוועבע
	Alter. Acceptor Site	1.56	3.01E-02	
TMEM218	Complex (e1-3)	2.23	2.11E-05	LINGS 1042, UNC 1, UNC 1, UNC 7, COS CEI COS CEI COS
	Exon Cassette	2.17	3.03E-04	100/022, NDIHJ, SAIIUO, 3033, SI 1, SI 2/NSI, SNP2U, SNP3U, IUT43, HA11, HA11, ID-1, ZNHIDZ
ETC1	Complex	1.68	2.66E-03	9G8, CUG-BP1, ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD,
EISI	Exon Cassette	2.53	2.31E-05	KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20c, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
ARHGAP32	Intron Retention	2.15	3.98E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
	Alter. Term Exon (e10,e11-16)	1.57	2.66E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD,
DINNA	Exon Cassette	1.95	3.96E-04	KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
	Alter. First Exon	2.29	2.24E-05	
CD9	Alter. Terminal Exon	2.81	1.76E-03	
	Complex (e3-7)	3.21	1.68E-05	
PTMS	Alter. Acceptor Site	2.64	4.99E-04	FTR-3, hnRNP I (PTR), hnRNP P (TLS), HTra2aloha, HTra2beta1, KSRP, MRNI 1, Nova-2, PSE, SC35, SRn30, TIA-1, TIA1 1, YR-1, 7RANR2
	Alter. First Exon (e1)	1.90	8.19E-04	
ATN1//C12orf57	Intron Retention	1.85	1.21E-04	ETR-3, hnRNP P (TLS), HuB, KSRP, Nova-1, SC35, SRp30c, TIA-1, TIAL1

FAM66C	Exon Cassette	1.73	7.45E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
	Complex	2.05	3.28E-03	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5,
GADARAFLI	Exon Cassette	2.52	1.70E-03	Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
ATF7IP	Alter. First Exon (e1)	2.29	5.59E-05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
ECEP1OP2	Alter. Terminal Exon (e5)	2.38	1.78E-03	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5,
FGFR10F2	Exon Cassette	2.60	5.98E-05	Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
CCDC91	Exon Cassette	2.24	2.36E-04	9G8, CUG-BP1, ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP F, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20c, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
PICD1	Complex	1.92	1.88E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1,
BIODI	Exon Cassette	1.92	1.02E-02	HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
IRAK4	Exon Cassette	1.50	3.62E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
ARID2	Exon Cassette	1.96	5.90E-03	9G8, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
PFKM	Intron Retention	3.04	1.86E-03	ETR-3, hnRNP I (PTB), hnRNP P (TLS), MBNL1, Nova-1, Nova-2, SRp30c, YB-1, ZRANB2
SPATS2	Exon Cassette	2.84	6.64E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
LETMD1	Exon Cassette	1.62	2.49E-05	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
EIF4B	Exon Cassette	2.24	1.02E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP P (TLS), HuB, Nova-1, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
RAB5B	Complex	1.85	4.78E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SF2/ASF, SRo20, SRo30c, TIA-1, TIAL1, YB-1, ZRANB2
ERBB3	Complex	2.46	2.42E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP F (TLS), HTra2alpha, HTra2beta1, HuB, HUD, KSRP, MRNI 1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRb20, SRb30, TIA-1, TIA1, YB-1, ZRANB2
	Alter. Terminal Exon (e7-8)	1.90	8.75E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP E2, hnRNP E1, hnRNP H2, hnRNP H2, hnRNP H2, hnRNP F, hnRNP F, hnRNP F, hnRNP H2, hnRNP F, hnRNP F
MYL6	Complex	1.65	9.60E-04	ZRANB2
NABP2	Alter. First Exon (e1)	1.63	2.72E-02	ETR-3, hnRNP A1, hnRNP C1, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), KSRP, Nova-1, Sam68, SC35, SRp20, YB-1, ZRANB2
	Alter. Acceptor Site	2.56	6.92E-03	ETP 2 hadned 11 hadned E1 Had
DIX3	Intron Retention	2.20	5.97E-04	
ARHGEF25 //	Complex	1.74	1.60E-02	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, KSRP, MBNL1, Nova-1, PSF, Sam68,
SLC26A10	Exon Cassette	1.89	5.20E-03	SC35, SRp30c, YB-1, ZRANB2
SRGAP1	Alter. Terminal Exon (e10)	1.50	1.10E-03	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
TBC1D30	Alter. Terminal Exon (e14-16)	1.90	1.10E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
HELB	Exon Cassette	1.58	1.01E-02	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP LL, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
FRS2	Exon Cassette	1.80	1.04E-02	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
CNOT2	Intron Retention	1.84	1.08E-02	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
LGR5	Complex	2.43	1.20E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, KSRP, Nova-1, RBM5, Sam68, SC35, SE1, SRb20, SRb30c, TLA-1, TLA-1, VB-1, ZRANB2
SYT1	Complex	1.58	9.99E-04	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP D1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (IIS) HTra2beta1 HuB HUD HUB KSPP MRNI 1 Nova1 Nova2 PSE RRM5 Sam68 SC35 SE1 SE2/ASE SRo20 SRo30, TDP43 TIA1 TIA1 YB1 7RANR2
MRPL42	Exon Cassette	3.45	8.84E-04	ETR3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP D1, hnRNP D2, hnRNP E1, hnRNP F2, hnRNP F1, hnRNP F1, hnRNP F1, hnRNP F4, hnRNP F1, hnRNP F4, hnR
PLXNC1	Alter. First Exon	1.89	5.98E-03	CUG BP1, ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP A2, B1, hnRNP D1, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS),
VEZT	Exon Cassette	2.33	8.80E-04	ETR3 pixel, The pixel,
				Samoo, SUSS, STI, STZ/MST, STRZU, SKRSUC, IIA-I, IIALI, IIALI, ISE-I, ZKANKZ ETT2 S. KANDA II. KANDA O'LO MADO CI. KANDA CI. KANDA CI. KANDA CI. KANDA DI MADO DI M
VEZT	Exon Cassette	1.72	5.62E-05	LINCY, HINTY 24,
	Alter, Terminal Exon (e4-5)	2.24	1.56F-04	CIJCSPI FTR-3 Frox-1 FCA; DA 1 MORDE 42/R1 MNRP C1 MNRP F1 MNRP F1 MNRP F MNRP F1 MNRP H1 MNRP H2 MNRP H2 MNRP F MNRP F MNRP F1 MNRP F
TMPO	Exon Cassette	4.45	3.79E-04	MBNL1, Nova-1, Nova-2, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
SLC25A3	Intron Retention	1.55	2.10E-03	CUG-BP1, ETR-3, FMRP, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2

PARPBP	Exon Cassette	1.75	2.08E-03	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNI 1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRo20, SRo30c, TDP43, TIA-1, TIAI 1, YB-1, 7RANB2
RIC8B	Exon Cassette	1.95	1.64E-02	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP D1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MRN1, Nova-2, PSE, RBM5, Sam68, SC35, SE1, SRo20, SRo30, TDP43, TIA-1, TIA-1, TIA-1, TRANR2
	Complex	1.51	1.17E-02	FTR-3. Ex-1. Ex-2. bnRNP A1. bnRNP A2/B1. bnRNP C1. bnRNP D. bnRNP F1. bnRNP F2. bnRNP F2. bnRNP H1. bnRNP H2. bnRNP H2. bnRNP P (TLS). HTra2beta1. HuB. HuD. KSRP. MBN1 1. Nova-1. Nova-2.
UBE3B	Exon Cassette	1.80	3.88E-03	Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
IFT81	Exon Cassette	1.83	2.78E-03	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Sam68, SC35, SF1, SRo20, SRo20, TIA-1, TIA1, YB-1, ZRANB2
ERP29	Exon Cassette	2.04	1.40E-03	ETR-3, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MR1, Lova-2, DSF, RBM5, Sam68, SC35, SF1, SRo20, SRo30, TIA-1, TIA-1, YR-1, ZRANB2
SETD8	Alter. First Exon (e1)	1.52	4.48E-03	ETR-3, FMRP, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRo20, SRo30, TIA-1, TIA1, YB-1
ZNF10 // ZNF268	Complex	1.65	2.50E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP D, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MRN1, Nova-1, Nova-2, Sam68, SC35, SF1, SF2/ASF, SRo20, SRo30, TDP43, TIA-1, TIA 1, YB-1, ZRANR2
DCP1B	Exon Cassette	1.71	1.94E-03	CUG-BP1, ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MRN 1, Nova-1, Nova-2, PSE, BRM5, Sam68, SC35, SF1, SF2/ASE, SRo20, SRo30c, TDP43, TIA-1, TIA11, YB-1, ZRANB2
FOXM1	Exon Cassette	2.06	3.62E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SRo20, SRo20, SRo20, CTDP43, TIA-1, TIA-1, TRA-1, TRANB2
PARP11	Exon Cassette	2.08	1.50E-02	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP D1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, NSR-8, SC35, SF1, SF2/ASF, SRo20, SRo30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
TNFRSF1A	Alter. First Exon (e1,e3,5-6,8-11)	1.74	3.16E-04	CUG-BP1, ETR3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRo20, SRo30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
LMO3	Alter. First Exon (e3)	7.88	7.84E-05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRo20, SRo30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
CAPRIN2	Exon Cassette	2.22	3.35E-06	CUG-BP1, ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, PSF, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
DENND5B	Exon Cassette	1.89	1.98E-03	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
KIF21A	Exon Cassette	2.62	4.43E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
	Exon Cassette	2.06	1.20E-02	
HDAC7	Intron Retention	2.09	7.62E-03	
	Complex	1.68	6.00E-04	11112200121, 1102, 10111, 101121, 10121, 10121, 10110, 301100, 3033, 3022, 30200, 10143, 1141, 1041, 1041, 1042
MCRS1	Intron Retention	1.60	2.22E-03	ETR-3, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP K, hnRNP P (TLS), HuB, Nova-1, Nova-2, SC35, TIA-1, TIAL1, YB-1, ZRANB2
LIMA1	Alter. First Exon (e1-3)	2.05	2.84E-04	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
CSAD	Exon Cassette	1.60	6.86E-03	ETR-3, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, Sam68, SC35, SF2/ASF, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
CALCOC01	Intron Retention	1.73	1.97E-02	ETR-3, hnRNP A1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, PSF, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
CBX5	Alter. First Exon (e1)	1.60	5.52E-03	ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
ITOAF	Exon Cassette	3.03	7.38E-04	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF,
TIGAD	Alter, First Exon (e1)	3.71	2.17E-05	RBM5, Sam68, SC35, SRp20, TIA-1, TIAL1, YB-1, ZRANB, CUG-BP1, ETR-3, Fox-1, Fox-2
GTSF1	Alter. First Exon (e1)	3.71	2.17E-05	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5. Sam68. SC35. SRo20. TIA-1. TIAL1. YB-1. ZRANB2
RNF41	Exon Cassette	1.54	9.98E-04	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP P (TLS), HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
CS	Exon Cassette	2.07	2.20E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
DCTN2	Complex (e4)	2.22	3.34E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
IKPID	Complex (e1-2)	2.10	1.39E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1,
II/DIF	Exon Cassette	2.19	3.45E-04	HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
SART3	Intron Retention	1.82	1.24E-03	ETR-3, hnRNP C1, hnRNP I (PTB), HTra2beta1, HuB, KSRP, Nova-1, SC35, SRp20, TIA-1, TIAL1, YB-1
	Ind on Actendion			
GIT2	Exon Cassette	4.53	9.24E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
GIT2	Exon Cassette Complex	4.53 2.14	9.24E-04 1.14E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP D1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD,

171/10	Complex	1.68	9.50E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P, (TLS), HTra2beta1, HuB, HuD, HuR, KSRP,
ATXN2	Exon Cassette	1.52	6.04E-03	MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRo20, SRo30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
TBX3	Exon Cassette	2.63	3.67F-05	FTR-3, Fox-1, Fox-2, bnRNP A1, bnRNP A2/B1, bnRNP C1, bnRNP ((TB), bnRNP K, bnRNP P (TLS), HuB, Nova-1, RBM5, Sam68, SC35, SRo30c, TIA-1, TIA-1, YB-1
RPI P0	Intron Retention	1.65	9.19F-04	FTR-3, hnRNP A1, hnRNP A2/B1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP P (TLS), KSRP, Sam68, SC35, YB-1
	Alter Dopor Site	2.07	3 12E-03	TR3 F0x1 F0x2 bnRNP 41 bnRNP 42/R1 bnRNP F1 bnRNP F1 bnRNP F2 bnRNP F1 bnRNP H1 bnRNP H2 bnRNP H2 bnRNP H bnRNP F4 bnRNP F4 bnRNP F4 bnRNP H1 bnRNP F4 bnRNP
RSRC2	Evon Cassette	1.55	6.52E-03	Elico, tox1, tox2, minut A1, minut A2, b1, minut A2, minut A1, minut A1, minut A2, minut A1, min
CDK2AP1	Alter. First Exon (e1)	1.55	2.21E-04	CUG BP1, ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, DFC RBMR Samp8 SC35 SE2/AFS S
FIF2B1	Alter Terminal Exon (e5)	1 52	2 16E-03	TR3 F0x1 F0x2 hRNPR 1 hRNPR 2/B hRNPD C hRRNP (17B) hRNP K hRNP P (TIS) HTra2heta1 HuB KSRP MRNI 1 Nova-1 Nova-2 PSF Sam68 SC35 SF1 SRn20 SRn30 C TIA-1 TIAL1 YR-1
20201	Autor: Forfininda Exter (66)	THE	Elifet de	FTR-3 Fox-1 Fox-2 hnRNP A1 hnRNP A2/B1 hnRNP C1 hnRNP D hnRNP F2 hnRNP F hnRNP F4 hnRNP F4 hnRNP F4 hnRNP F1 hnRNP F1 hnRNP F1 hnRNP F1 hnRNP F2 hnRNP F4 hn
SCARB1	Exon Cassette	3.91	4.69E-06	RM5. Scar68. SC35. SRo20. SRo30. SRo30. IA4. TIAI 1. YB-1. ZRAM2.
SLC15A4	Exon Cassette	1.97	5.82E-05	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
RIMBP2	Exon Cassette	2.07	1.81E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
ZMYM2	Exon Cassette	1.89	2.12E-03	9G8, CUG-BP1, ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP DL, hnRNP E1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
IET00	Complex	1.53	2.58E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, KSRP,
IFTOO	Exon Cassette	1.52	1.30E-03	MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
POLR1D	Complex	1.66	5.02E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
GPR180	Exon Cassette	2.71	4.94E-06	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
	Alter. First Exon (e1)	2.86	3.63E-04	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP DL, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP K, thrRNP P (TLS),
ARTIGET /	Exon Cassette	2.11	3.89E-05	HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
CDC16	Intron Retention	1.61	5.02E-03	ETR-3, hnRNP A1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, MBNL1, Nova-1, Sam68, SC35, SRp20, TIA-1, TIAL1, YB-1, ZRANB2
DCLK1	Alter. Terminal Exon (e8)	2.49	1.24E-04	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
MTRF1	Intron Retention	1.83	5.84E-05	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP I (PTB), HTra2beta1, HuB, HuD, KSRP, Nova-1, SC35, SRp20, TIA-1, TIAL1, YB-1
SUCLA2	Alter. First Exon (e1-2,e5)	1.56	8.90E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
DHRS12	Exon Cassette	1.59	6.80E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
MRPS31P5 // THSD1P1	Complex	2.60	1.17E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, KSRP, Nova-1, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
DOCK9	Alter. Acceptor Site	2.40	4.45E-04	ETR-3, Fox-1, Fox-2, hnRNP C1, hnRNP I (PTB), hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, Sam68, SC35, SRp20, TIA-1, TIAL1, YB-1, ZRANB2
TMTC4	Alter. Terminal Exon (e15)	2.27	3.61E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
GAS6	Alter. First Exon (e1-2,e4)	1.67	2.72E-03	9G8, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
RASA3	Exon Cassette	1.99	3.46E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
PARP2	Alter. Donor Site	5.19	1.14E-06	hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), HuB, Nova-1, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1
OXA1L	Intron Retention	2.16	4.31E-06	ETR-3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), Nova-1, SRp20, TIA-1, TIAL1, YB-1, ZRANB2
	Alter. Acceptor Site	3.21	1.88E-05	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2,
ULIK92	Alter. First Exon (e1-5)	3.29	3.29E-06	PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
IRF9 // RNF31	Alter. Terminal Exon (e29-31)	1.68	1.56E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, PSF, Sam68, SC35, SRp20c, STR-1, TIAL1, YB-1, ZRANB2
AKAP6	Alter. First Exon (e1-2)	1.81	4.92E-03	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
PRPF39	Exon Cassette	1.69	2.50E-03	ETR-3, hnRNP A1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HuB, HuD, KSRP, Nova-1, Sam68, YB-1
SAMD4A	Exon Cassette	2.06	2.41E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
1/111	Exon Cassette	1.71	1.84E-03	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, KSRP, MBNL1, Nova-1,
N (N1	Intron Retention	1.81	1.84E-03	RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1
PRKCH	Alter First Evon (e1-11)	5 88	1.83E-04	9G8, CUG-BP1, ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP A2/B1, hnRNP P (TLS),
FINGH	Allel. HISLEXUIT (e1-11)	5.00	1.03L-04	HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
ZBTB1	Exon Cassette	1.93	1.62E-02	9G8, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP A2/B1, hnRNP K, hnRNP P (TLS), HTra2alpha,

				HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
CHURC1 //	Even Orienthe	1.01	4 705 04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1,
FNTB	Exon Cassette	1.91	4.78E-04	Nova-1, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
ELITO.	Complex (e3-4)	1.61	4.40E-04	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP L, hnRNP L,
FUI8	Exon Cassette	1.61	4.40E-04	hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
GPHN	Exon Cassette	2.19	6.13E-05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSPP, MRNI 1, March 1, March 2, DEC 2006, SC26, SC1 SC2 (ASE, SC26), SC26, SC1 SC2 (ASE, SC26), SC26, SC26
GALNT16	Complex	1.60	1.55E-04	Hra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
	Alter. Acceptor Site	1.94	8.24E-04	
SRSF5	Alter. Terminal Exon (e6,e7-9)	1.80	5.59E-05	Encommute As a mixed as a mixed by mixe
	Intron Retention	2.24	7.90E-05	
RBM25	Intron Retention	1.63	2.13E-02	hnRNP A1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Sam68, SC35, SRp30c, TIA-1, TIAL1, YB-1
PTGR2 //	Alter. Donor Site	2.05	5.10E-03	CUG-BP1, ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68,
ZNF410	Complex	2.05	5.10E-03	SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
PAPOLA	Intron Retention	1.63	2.46E-02	CUG-BP1, ETR-3, hnRNP C1, hnRNP I (PTB), HuB, Nova-1, Sam68, SC35, SRp30c, TIA-1, TIAL1, YB-1
EVL	Alter. Terminal Exon (e14)	1.86	8.22E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP DL, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIA-1, YB-1, ZRANB2
				CUG-BPI_ETR-3. Fox-1. Fox-2. hnRNP A1. hnRNP C1. hnRNP D. hnRNP E1. hnRNP E2. hnRNP F. hnRNP H1. hnRNP H2. hnRNP H2. hnRNP H2. hnRNP F. hn
MARK3	Exon Cassette	2.42	4.11E-05	Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
	Alter, Donor Site	1.69	4.75E-04	
	Alter, Terminal Exon (e19-23)	1.82	1.37F-04	9G8. CLIG-BP1. FTR-3. Eox-1. Eox-2. hnRNP A1. hnRNP A2/B1. hnRNP C1. hnRNP D. hnRNP F2. hnRNP F2. hnRNP F4. hnRNP H2. hnRNP H2. hnRNP H2. hnRNP K. hnRNP K. hnRNP F1. hnRNP P (TLS). HTra2aloha.
APOPT1 // KLC1	Complex	3.63	1.61E-05	HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRo20, SRo30c, TDP43, TIA-1, TIA11, YB-1, ZRANB2
	Exon Cassette	1.90	2.83F-04	
SIVA1	Intron Retention	1.60	4.94E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP I (PTB), hnRNP F, hnRNP P (TLS), HuB, HuD, KSRP, MBNL1, Nova-1, PSF, RBM5, Sam68, SC35, SPc30, SPc30, TLA1, TLA1, VB-1, ZEMP2
	Alter First Evon (e2-3)	1 70	1 80E-02	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP,
ADJJLI	Alter: Tirst Exolit (e2-3)	1.70	1.80L-02	MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
CONR1IP1	Evon Cassette	2.07	3 36E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2,
CCNB1IP1	EXOII Casselle	2.07	3.30L-04	Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
HNRNPC	Complex	2.29	1.40E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP K, hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP,
THAT C	Exon Cassette	1.99	7.16E-04	MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
AJUBA // HAUS4	Alter. Terminal Exon (e1-9)	3.76	1.56E-05	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRo20, SRo30c, TIA-1, TIAL1, YB-1, ZRANB2
				CUG-BPJ. ETR-3. Fox-1. Fox-2. hnRNP AJ. hnRNP AJ. hnRNP AL. hnRNP C1. hnRNP C1. hnRNP EJ. hnRNP EJ. hnRNP F. hnRNP F. hnRNP HJ. hnRNP HJ. hnRNP H. hnRNP K. hnRNP Y. (TLS). HTra2alpha. HT
C14orf93	Complex (e2-3)	2.03	5.03E-04	KSRP. MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
TINF2	Intron Retention	1.54	9.14E-03	ETR-3, hnRNP C1, HuB, HuD, MBNL1, SC35, TIA-1, TIAL1, YB-1
SDR39U1	Intron Retention	1.53	5.72E-03	ETR-3, hnRNP F, hnRNP H1, hnRNP H2, HuB, KSRP, Nova-1, Nova-2, SC35, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
D4714	5 0 "	1.07	6 005 04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, Nova-1, Nova-2,
BAZIA	Exon Cassette	1.97	6.99E-04	Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
CAV/1	Even Orienthe	1.70	2 205 04	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SF1,
SAV1	Exon Cassette	1.76	3.39E-04	SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
NIN	Exon Cassette	3.68	5.00E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, PSF, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
PYGL	Exon Cassette	9.18	2.67E-06	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSE Sam68, SC35, SRx20, SRx30, TLA1, TLA1, YB, 172, 2008
	Alter Terminal Exon (e12)	3.16	6 15E-04	
DDHD1		3.10	0.132.04	CUG-BPL, EIK-3, Fox-1, Fox-2, Fox-4,
	EXOII Casselle	5.76	2.37E-04	
GCH1	Alter. Terminal Exon (e5)	1.80	2.0/E-05	EIR3, Fox-1, Fox-2, InKNP A1, InKNP A2/B1, INKNP C1, INKNP E2, INKNP F2, INKNP F1, INKNP F2, INK
	Complex	1.82	1.38E-03	
RTN1	Exon Cassette	2.95	1.24E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP DL, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H
AREL1	Exon Cassette	1.93	2.72E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H2, hnRNP H2, hnRNP H2, hnRNP F, KnRNP
NEK9	Intron Retention	1 54	9 52E-03	TRUE, TRUE, TRUE, TRUE TRUE T, TRUE T, TRUE T, TRUE SATING
GALC	Alter First Evon (e1.2)	4.70	2.83E-06	
FMI 5	Fxon Cassette	2 40	1 18E-03	FTR-3 hnRNP A1 hnRNP A2/R1 hnRNP F hnRNP H1 hnRNP H2 hnRNP H(PTR) hnRNP P (TIS) HTra2heta1 HuR KSRP Noval PSE Sam68 SC35 TIA1 TIA1 VR-1 7RANR2
LINES	ENOTI OUSSELLO	2.40	1.102.03	

SMFK1	Alter. Terminal Exon (e8)	1.53	4.21E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD,
	Exon Cassette	1.51	4.61E-04	KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
MOK	Exon Cassette	1.51	1.27E-02	968, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP 01, hnRNP DL, hnRNP B1, hnRNP E2, hnRNP F, hnRNP H2, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2beta1, HuB, HuB, HuB, HuB, HuB, HuB, HuB, HuB
VPCC2	Even Cascotte	2.00	1.29E.02	
ARCUS	Exoli Casselle	2.99	1.20E-03	בוראי, ווווגיער כן, ווווגיער רן, וווגיער גער רן, וווגיער רן
C14orf2	Evon Cassette	2.43	2.48E-03	ETR-3, hnRNP A1, hnRNP C1, hnRNP F1, hnRNP H1, hnRNP H2, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Sam68, SC35, SRp30c, YB-1, ZRANB2
EMC4	Complex (e5)	2.16	3.76E-04	ETR-3, hnRNP A1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Sam68, SC35, SRp20, SRp30c. TLA-1. TIA11, YR-1, ZRANR2
SRP14-AS1	Alter. Terminal Exon (e3-4)	1.59	6.36E-04	CUG-BP1, ETR-3, Fox1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBN1, Nova-2, PSE, RBM5, Sam68, SC35, SE2/ASE, SRb20, SRb30c, TIA-1, TIA1, YB-1, ZRANB2
RAD51	Exon Cassette	1.81	8.79E-04	ETR-3, hnRNP A1, hnRNP C1, hnRNP DL, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, PSF, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
TUBGCP4	Exon Cassette	1.57	5.08E-03	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, PSF, Sam68, SC35, SRp20, TIA-1, TIAL1, YB-1, ZRANB2
	Alter. Acceptor Site	1.79	2.74E-03	ETR-3, hnRNP A1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, PSF, RBM5, Sam68, SC35, SRp30c, TIA-1,
HIPK // SERF2	Complex	1.91	2.48E-03	TIAL1, YB-1, ZRANB2
CTDSPL2	Complex	1.69	5.05E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HUB. HuD. HuR. KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRo20, SRo30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
SORD	Alter. Acceptor Site	1.87	7.84E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP DL, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
SEMA6D	Exon Cassette	2.55	4.18E-06	9G8, CUG-BP1, ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SRo20, SRo30c, TIA-1, TIAL1, YB-1, ZRANB2
GALK2	Exon Cassette	1.88	6.20E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I, hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
70510	Alter. First Exon (e2-4)	1.70	1.16E-03	968. CUG-BP1. ETR-3. FMRP. Fox-1. Fox-2. hnRNP A1. hnRNP A2/B1. hnRNP C1. hnRNP D. hnRNP DL hnRNP E1. hnRNP E2. hnRNP F. hnRNP H1. hnRNP H3. hnRNP H3. hnRNP H3. hnRNP K. hnRNP LL.
ICF12	Exon Cassette	5.09	8.28E-05	hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
	Alter. First Exon (e1-3)	2.83	1.64E-05	
TPM1	Complex	4.27	2.41E-05	CUGBP1, EIK-3, Fox-1, Fox-2, InKNP A1, INKNP A2/B1, INKNP C1, INKNP C1, INKNP E1, INKN
	Exon Cassette	3.59	2.41E-05	H ITAZDERAL, HUB, HUU, NSKY, MEINLI, NOVA-1, NOVA-2, PSF, KEWIO, SAMOS, SC30, SF1, SF2/, SKp2U, SKp3UC, HA-1, HALL, TB-1, ZKANBZ
USP3	Alter. First Exon (e1-2)	1.69	7.45E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SF2/ASF, SRo20, SRo30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
LRRC49	Exon Cassette	3.26	1.01E-04	CUG-BP1, ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SF1, SRo20, SRo30c, TI4-1, TIA1 1, YR-1
	Alter, Terminal Exon (e5-10)	1.52	2.00E-02	
PML	Complex	1.51	1.04E-02	908, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP D, hnRNP E1, hnRNP E1, hnRNP E1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP I (PTB), hnRNP A2/B1, hnRNP A2/B1, hnRNP D, hnRNP D, hnRNP E1, hnRNP E1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP I (PTB), hnRNP A2/B1, hnRNP A2/B1, hnRNP D, hnRNP D, hnRNP E1, hnRNP E1, hnRNP E1, hnRNP H3, hnRNP H3, hnRNP I (PTB), hnRNP A2/B1, hnRNP A2/B1, hnRNP D, hnRNP D, hnRNP E1, hnRNP E1, hnRNP E1, hnRNP H3, hnRNP H3, hnRNP I (PTB), hnRNP A2/B1, hnRNP A2/B1, hnRNP D, hnRNP D, hnRNP E1, hnRNP E1, hnRNP E1, hnRNP H3, hnRNP H3, hnRNP I (PTB), hnRNP A2/B1, hnRNP A2/B1, hnRNP D, hnRNP D, hnRNP E1, hnRNP E1, hnRNP E1, hnRNP H3, hnRNP H3, hnRNP I (PTB), hnRNP A2/B1, hnRNP A2/B1, hnRNP D, hnRNP D, hnRNP E1, hnRNP E1, hnRNP E1, hnRNP H3, hnRNP
	Exon Cassette	1.52	1.57E-02	HIRAZDETAI, HUB, KSKP, MBINLI, NOVA-I, NOVA-Z, PSF, KBMS, SAMOS, SU3S, SF2/ASF, SKP2US, SKP3UC, HA-I, HALI, YB-I, ZKANBZ
SCAMP5	Mutualy Exclusive Exons (e2)	5.63	3.86E-05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
COMMD4	Intron Retention	1.69	1.42E-03	hnRNP P (TLS), KSRP, SC35, SRp30c, YB-1
C15orf27	Alter First Evon (e1-11)	2 59	3 40E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS),
01301127		2.05	5.402.04	HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-2, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, bnRNP A1, bnRNP A2/R1, bnRNP C1, bnRNP C1, bnRNP F1, bnRNP F2, bnRNP F1, bnRNP H1, bnRNP H2, bnRNP K, bnRNP F4, bnRNP F4
IREB2	Intron Retention	2.00	3.50E-03	SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
PSMA4	Intron Retention	1.94	3.78E-04	ETR-3, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HuB, MBNL1, Nova-1, Sam68, SC35, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
7544104	Alter. First Exon (e1-2,e5-7)	1.69	3.90E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1,
ZFAND6	Exon Cassette	2.17	4.02E-03	HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
AKAP13	Exon Cassette	3.89	9.02E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
EANO	Complex	1.65	1.03E-02	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2alpha, HTra2beta1. HuB. HuD. KSRP.
FANCI	Intron Retention	1.65	1.98E-03	MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
SLCO3A1	Alter. First Exon (e1-4)	3.21	4.01E-05	
1	Alter. Terminal Exon (e16-17)	7.53	5.98E-05	suos, Juu-ber J, Ein-S, Friker, Fork-J, Fork-J, Fork-J, Finker AZ/BJ, FINKIW GJ, FINKIW GJ, FINKIW FL, FINKIW
	Complex	8.28	5.98E-05	INTRATE T (123), THE220/04, THE220/04, THE220/04, THE220/04, THE2, THE TRUE TO THE TOTAL TOTAL TO THE TOTAL TOTAL TO THE TOTAL TO THE
CHD2//MIR3175	Intron Retention	1.85	1.53E-02	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP P (TLS), HTra2beta1, HuB, KSRP, Nova-1, Sam68, SC35, SRp30c, YB-1, ZRANB2
GABRB3	Exon Cassette	3.97	8.40E-05	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP F, (hnRNP F, thrRNP P, thrRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP F, thrRNP F, thrRNP H2, hnRNP F, thrRNP F, thrRNP H2, hnRNP F, thrRNP H2, hnRNP F, thrRNP H2, hnRNP F, thrRNP H2, hnRNP F, thrRNP F, thrRNP F, thrRNP F, thrRNP F, thrRNP H2, hnRNP F, thrRNP F, th

				RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
TJP1	Exon Cassette	2.33	1.18E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, KSRP, Nova-1, PSF, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
C15orf57 //	Alter. Donor Site	2.03	7.96E-05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, Nova-2, Sam68,
WIRFL42F0				
EHD4	Complex	1.50	5.44E-04	
VPS39	Complex	2.21	2.14E-03	Soc, Erros, Tors, Tors, Tors, Index AS, Index CJ, Index CJ, Index CJ, Index CJ, Index CJ, Index LJ, Index
				TH2, TH2, TOTAL, HOMEL, HOMEL, HOMEL, HOMEL, HOMEN, HOMEN, HOMEN, HOMEN, HOMEN, HOMEN, HOMEN, HARL, HOMEN, HO
TTBK2	Exon Cassette	2.06	1.50E-03	KSRP_MRN11, Nova-1 PSE_sam68, SC35, SRo20, SRo30, TDP43, TIA-1, TIA-1, ZRANB2
PPIP5K1	Complex	1.65	1.09E-02	ETR-3. hnRNP A1. hnRNP C1. hnRNP F. hnRNP H1. hnRNP H2. hnRNP I (PTB). hnRNP P (TLS). HTra2beta1. HuB. HuD. KSRP. Nova-1. Nova-2. PSF. Sam68. SC35. SRo20. SRo30c. YB-1. ZRANB2
MYEF2	Intron Retention	2.10	3.02E-03	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP P (TLS), HuB, Nova-1, Nova-2, SC35, TIA1, TIAL1, YB-1, ZRANB2
DMXL2	Exon Cassette	1.76	2.62E-03	ETR-3. Fox-1. Fox-2. hnRNP A1. hnRNP A2/B1. hnRNP C1. hnRNP D. hnRNP E1. hnRNP E2. hnRNP F. hnRNP H1. hnRNP H2. hnRNP I (PTB). hnRNP P (TLS). HTra2alpha. HTra2abeta1. HuB. KSRP. MBNL1. Nova-1.
	Alter. Terminal Exon	4.94	8.32E-05	Nova-2, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
SLTM	Intron Retention	1.56	1.17E-02	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, KSRP, Nova-1, Nova-2, SC35, SRp20, SRp30c, YB-1, ZRANB2
0410	E	1.50	1 425 00	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D1, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F1, hnRNP H1, hnRNP H3, hnRNP H3, hnRNP H7, hnRNP K, hnRNP F(TLS), HTra2alpha,
CAIZ	Exon Cassette	1.59	1.43E-02	HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
CSNK1G1 //	Altor Terminal Even (65)	2.40	1 555 04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha,
KIAA0101	Alter: Terminal Exolt (e3)	2.45	1.552-04	HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
IGDCC4	Alter First Evon (e1-18)	3 50	1 78F-05	CUG-BP1, ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F1, hnRNP H1, hnRNP H3, hnRNP H3, hnRNP I (PTB), hnRNP P (TLS),
Idb004	Alter: Thist Exolit (e1-10)	5.50	1.702-05	HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
DPP8	Exon Cassette	2.20	3.56F-04	CUG-BP1, ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP DL, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1,
				Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
MYO9A	Exon Cassette	2.23	8.48E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF,
				Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
PKM	Complex	1.67	9.02E-03	ETR3, Fox 1, Fox 2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP F2, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K2/B1, hnRNP C1, hnRNP C1, hnRNP E2, hnRNP F2, hnRNP F1, hnRNP H2, hnRNP H2, hnRNP F3, hnRNP F4, hnRNP
ADPGK	Exon Cassette	1.52	5.16E-04	CUG-BPL, ELK-3, Fox-1, Fox-2, InKNP AL, INKNP CL, INKNP CL, INKNP CL, INKNP EL, INKNP EL, INKNP FL, INKNP HL, INKNP HL, INKNP HL, INKNP KL, INKNP FL, INKNP KL, INKNP
WDDC1	latera Datastica	1.00	2 705 02	
WDR61	Intron Retention	1.00	3.70E-03	EIRS, FORT, FORZ, INRIVE CL, MIRIVE CL, MIRIVE EL, MIRIVE EL, MIRIVE FL, MIRIVE FL, MIRIVE FL, MIRIVE TLEIB, MIRIVE FL, M
CHRNB4	Alter. Donor Site	2.40	1.76E-05	
-				
MFGE8	Exon Cassette	2.18	4.71E-06	
PFX11A	Exon Cassette	2.35	1.81F-04	TR3. Fox: Fox: P RNP A1 hoRNP A1 (R) PAT A TRAVE A HORN P 1 hoRNP P 1 hoRNP P 2 hoRNP F hoRNP H 1 hoRNP H 2 hoRNP I (PTR) hoRNP K hoRNP F (TIS) HTra2beta1 HuR Hu/D KSRP
AP3S2/C15orf38	Exon Cassette	1.59	5.70F-03	MBNL1, Nova-1, RBM5, Sam68, SC35, SF1, SF2/ASF, SRo20, SRo30c, TIA-1, TIAL1, YB-1, ZRANB2
	Complex	1.62	2.88E-03	FTR-3. Fox-1. Fox-2. hnRNP A1. hnRNP A2/B1. hnRNP C1. hnRNP E. hnRNP H1. hnRNP H2. hnRNP I (TI S). HTra2beta1. HuB. KSRP. MBNI 1. Nova-1. Nova-2. PSE. RBM5. Sam68. SC35. SRo20.
PRC1	Exon Cassette	1.73	1.18E-03	SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
RHOT2	Intron Retention	1.78	7.36E-03	ETR-3, hnRNP I (PTB), hnRNP P (TLS), MBNL1, Nova-1, SRp30c, YB-1, ZRANB2
110501	5 0 1	1.05		ETR-3, hnRNP A1, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c,
UBE21	Exon Cassette	1.95	1.56E-04	TIA-1, TIAL1, YB-1, ZRANB2
TELOO	0	1.50	7.675.04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, Nova-1, Nova-1
TELUZ	Complex (e13-15)	1.52	7.57E-04	2, RBM5, Sam68, SC35, SF2/ASF, SRp30c, YB-1, ZRANB2
MADIZOIDO	Intron Potentian	0.50	1 695 05	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, RBM5, Sam68, SC35, SF2/ASF,
WAFKOFS	Intron Retention	9.09	1.66E-05	SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
C16orf59	Intron Retention	2.00	1.56E-02	ETR-3, Fox-1, Fox-2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP P (TLS), KSRP, PSF, SC35, SF2/ASF, SRp30c
MCRN1	Evon Cassette	2 51	6.22E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1,
manni	Exon ousselle	2.51	0.222 04	Nova-1, Nova-2, RBM5, Sam68, SC35, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
MKL2	Intron Retention	2 79	2 62E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, HuB, KSRP, MBNL1, Nova-1, PSF, Sam68, SC35, SRp30c, TIA-
		2.05	LIGEE 00	1, TIAL1, YB-1
TNRC6A	Alter. First Exon (e14)	1.55	2.29E-05	FTR-3. hnRNP A1. hnRNP A2/B1. hnRNP C1. hnRNP L(PTB). hnRNP K. hnRNP P (TLS). HuB. KSRP. Nova-1. Sam68. SC35. SRn20. TIA-1. TIAL1. YB-1. ZRANB2
	Exon Cassette	2.07	2.80E-04	
TAOK2	Alter. Terminal Exon (e16-17)	1.67	3.30E-03	EIK-3, INRIVIP A1, INRIVIP C1, INRIVIP C1, INRIVIP C2, INRIVIP E2, INRIVIP F, INRIVIP H1, INRIVIP H2, INRIVIP H2, INRIVIP A2/B1, INRIVIP C1, INRIVIP C2, INRIVIP E2, INRIVIP F, INRIVIP H1, INRIVIP H2, INRIVIP A2/B1, INRIVIP C1, INRIVIP C2, INRIVIP E2, INRIVIP F, INRIVIP H1, INRIVIP H2, INRIVIP C1, INRIVIP C2, INRIVIP
000014		1.00	0.105.00	PSF, KBMS, Samos, SU35, SF2/ASF, SKp2U, SKp3US, HA-I, HALI, YB-I, ZKANB2
CORUIA	Intron Retention	1.88	3.16E-03	
51X4	Intron Retention	18/	9611-04	I ETR-3. NOKINE ET UDKINE ET UDKINE HT
ELLO	Intron Notonidon	0.00	0.005.04	
FUS	Intron Retention	2.82	8.22E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP F1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, SC35, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2

				MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20c, TIA-1, TIAL1, YB-1, ZRANB2
CVLD	Even Cessette	1.05	E 24E 02	CUG-BP1, ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD,
CTLD	EXOII Casselle	1.60	0.54E-05	KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
SI CEA2	Even Cassette	4.02	4 225 05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P, (TLS), HuB, KSRP, MBNL1, Nova-1, Nova-2,
SLUGAZ	Exon Casselle	4.03	4.23E-00	PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
COQ9	Intron Retention	1.55	5.60E-03	ETR-3, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HuB, KSRP, Nova-1, SC35, TIA-1, TIAL1, YB-1
ODDEC	Complex (e7)	3.50	2.42E-05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F1, hnRNP H1, hnRNP H3, hnRNP H3, hnRNP H1, hnRNP K, hnRNP P (TLS), HTra2beta1,
GFR00	Exon Cassette	3.19	1.50E-03	HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
	Alter. Acceptor Site	2.54	3.48E-06	
NDRG4	Complex (e8)	1.82	3.67E-05	UDED 1, EIN-0, 1042, 1042, IMANY A2, BINNY A2, DI, BINNY D3, BINNY D4, BINNY
	Exon Cassette	1.86	2.19E-04	
SETDE	Intron Potention	1.60	5 725 02	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, Nova-1, Sam68, SC35, SRp20,
JEIDO	introl Netention	1.00	5.722-05	SRp30c, TIA-1, TIAL1, YB-1
FAM65A	Complex	1.62	3.48E-03	ETR-3, Fox-1, Fox-2, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, Sam68, SC35, SRp30c, TDP43, TIA-1, TIAL1, YB-1,
EDC4	Intron Retention	1.71	4.38E-03	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP I (PTB), hnRNP K, HuB, KSRP, Nova-1, SC35, TIA-1, TIAL1, YB-1
NEATC3	Alter First Evon (e3)	2.06	1.07E-02	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1,
INTATO5	Alter: Thist Exoti (es)	2.00	1.07 2-02	HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
ΝΕΔΤ5	Evon Cassette	1 96	4 34F-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP F, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD,
		1.50		KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
7NRF1	Exon Cassette	2 11	6 04F-05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A1, hnRNP C1, hnRNP D1, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP H, hnRNP K, hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1,
2		2.11	0.012.00	HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
NUDT7	Exon Cassette	2.56	1.96F-05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2beta1,
				HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
MAP1LC3B	Exon Cassette	2.13	2.82E-03	CUG-BP1, ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, HuD, HuR, KSRP, Nova-1, Nova-2, Sam68, SC35, SRp20, TIA-1, TIAL1, YB-1, ZRANB2
JPH3	Alter, Terminal Exon (e3)	1.72	2.60F-03	9G8, CUG-BP1, ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP K, hnRNP K, hnRNP P (TLS), HTra2alpha,
				HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
7C3H18	Exon Cassette	2.65	1.41F-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A1, hnRNP C1, hnRNP C1, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F1, hnRNP H1, hnRNP H3, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1,
				HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
TRAPPC2L	Complex	1.61	5.56E-04	ETR3, hnRNP A1, hnRNP A2/B1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, SC35, SF2/ASF, SRp30c, TIA-
		11.05		I, HALI, YB-I, ZHANBZ
	Alter. First Exon (e3-8)	14.05	2.20E-07	ETR-3, hnRNP A1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F1, hnRNP H2, hnRNP H (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-2, PSF, RBM5.
10BB3	Complex	11.53	4.3/E-05	Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
014 // 0	Exon Cassette	4.69	1./1E-05	
C16ort13	Intron Retention	1.79	2.43E-05	Fox-1, Fox-2, hnRMP F (PIB), hnRMP F (ILS), HUB, KSRP, Nova-1, Nova-2, SC35, SKP2U, SKp3Uc, YB-1
RNPS1	Exon Cassette	1.78	1.39E-02	ETR3, Fox 1, Fox2, InRRP A1, INRRP C1, INRRP D1, INRRP E1, INRRP E2, INRRP F1, INRRP H1, INRRP H2, INRRP H2, INRRP H2, INRRP F1 (PTB), INRRP F1 (PTB), INRRP F1 (PTB), INRRP F1, INRP F1, INRRP F1, INRR
POODL		0.01	1 205 02	
RUGDI	Intron Retention	2.01	1.32E-03	EIR-3, INRIVE A1, INRIVE A2/B1, INRIVE E2, INRIVE E2, INRIVE P (ILS), INRIVE P (ILS), INRIVE A2, ISI, INRIVE A2, ISI, INRIVE E2, INRIVE P (ILS), INRIVE P (ILS), INRIVE A2, ISI, INRIVE E2, INRIVE E2, INRIVE P (ILS), INRIVE
NAGPA	Exon Cassette	1.56	1.54E-03	
TVP23A	Alter. Acceptor Site	3.14	1.50E-06	CUG-BP1, EIK-5, FMKP, Fox-1, Fox-2, InKMP F41, INKMP F21, INKMP F1, INKMP F1, INKMP F2, INKMP F1, INKMP F42, INKMP F1, INKMP F
TXNDC11	Complex (e1-2)	2.31	2.80E-04	
KINN0420	Intron Potention	2 21	4 755 04	Sallido, 3C33, STZ/RAT, STRZU, STR20U, THAT, THELT, TE-T, ZNATOZ
CDIDT	Intron Retention	3.21	4.7 JL-04	
CDIF1		2.10	2.02E-04	
KCID13	Complex	1.81	2.92E-03	
DOC2A	Alter Deven Cite	1.95	3.04E-04	
	Alter Acceptor Site	2.24	0.43E-04	ויטרא , אטארבו, אטארבו, אטארבו, ויטראט , אוויטס אטאטע , אטאראט , איז
016 art02	Alter, Acceptor Site	2.01	2.125.02	9G8, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35,
C100Ш33	Aiter. Terminal Exon (e4-9)	1.93	2.12E-U3	SF2/ASF, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
		1.83	9.82E-03	
ZNF423	Alter. First Exon (e1-4)	2.46	2.61E-04	905, UU-911, LIF-3, FOX-1, FOX-2, DRIVEY AL, DRIVEY AL, DRIVEY U, DRIVEY U, DRIVEY U, DRIVEY E, DRIVEY F, DRIVEY H, DRIVEY H, DRIVEY H, DRIVEY H, DRIVEY H, DRIVEY AL, DRIVEY AL
DDCO	Intron D-tti	1 57	1.005.00	(LIS), ITTRZAUJIA, ITTRZUBIA, ITUD, TUU, TUU, NOKY, MISHLI, NOR2-I, NOR2-, FSY, TOMO, SATIOS, SOLS, SFI, SFZ/ASF, SKP2U, SKP3UC, IUF4S, IN4-I, INE-I, ZKANBZ (LIC PDI TO 2 & DOID 0.1 E-DDI 0.1 E-DDI 0.1 E-DDI 0.1 E-DDI 0.1 E-DDI 0.1 E-DDI 0.2 E
BBS2	Intron Retention	1.5/	1.92E-02	UUSOFT, EINS, HIRNY RA, HIRNY RAZIST, RINKY F, RINKY FT, RINKY FT, RINKY FT, RINKY FT, RINKY FT, SUBJER, HUB, KSKP, NOVA-1, SC33, SF2/RS7, SKP2U, SKP3UC, RF4, THAL, TS41, ZKANDZ
	Intron Retention	1./8	3./2E-U3	LING, TOX, TOX, TIMENT AL, TIMENT F.
FAM96B	Intron Retention	1.58	5.60E-05	INTRIVEL (FIS), INTRIVE F (ILS), NOVA-I, KBMB, SU33, SKP3UC, KE-I, ZKANBZ
ACD	Intron Retention	1.94	2.42E-04	
MISSIL	Complex	1.55	3.02E-03	CUG-BELLEIK-3, FOX-1, FOX-2, INKINP A1, INKINP A2/B1, INKINP G1, I

				HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20c, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
COG4	Intron Retention	2.04	1.94E-03	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP P (TLS), HTra2beta1, Nova-1, Sam68, SC35, SRp20, YB-1, ZRANB2
AP1G1	Exon Cassette	1.60	4.19E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, HuB, KSPP, MRNI 1, Nore-1, Nore-2, BRM5, Sam6a, SC35, SE2/ASE, SBn30, TIA1, TIA1, YE-1, ZRANB2
				That, Non-minuter, Hower, Homer, and Society of 27Abil, Millor, Stoport, Harris, Trict, Trict, 200002 ETD 3: Env 2: hoRND 41 hoRND 41/31 hoRND 1: Hill Hull Hull Hull KCRD MRNI 1: Nava 1: Nava 2: Sam68
ZNF821	Exon Cassette	2.01	4.20E-05	
				TRA: For Jerve bitNPD 41 hnRNP 47/81 hnRNP C1 hnRNP C1 hnRNP F2 hnRNP F hnRNP H1 hnRNP H2 hnRNP H2 hnRNP P (TIS) HTra2heta1 HuR HuD KSRP MRNI 1 Nova. 1 Nova. 2 PSF
RFWD3	Exon Cassette	1.76	1.50E-03	SameB. Sci SBn20. Sanot Tial 1 Ye-1 / RANB2
THE				CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H (PTB), hnRNP P (TLS), HTra2alpha,
IMEM170A	Alter. First Exon (e1)	1.56	4.24E-05	HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
70,007	E	0.24	C 225 05	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1,
ZDHHC7	Exon Cassette	2.34	6.33E-05	Nova-1, Nova-2, PSF, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
DPH1 // OVCA2	Intron Retention	1.67	2.10E-03	ETR-3, hnRNP A1, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, KSRP, Nova-1, Nova-2, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
SGSM2	Exon Cassette	1.68	4.17E-05	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, Nova-1, Nova-2, PSF, Sam68,
0001112	Intron Retention	1.70	3.46E-03	SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1
RABFP1	Exon Cassette	1.76	2.11E-02	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, PSF, Sam68,
				SC35, SRp20, SRp30c, Ti4-1, Ti41, YB-1, ZRANB2
RPAIN	Intron Retention	2.15	3.77E-05	ETR3, hnRNP A1, hnRNP P (TLS), HuB, MBNL1, Nova-1, SC35, YB-1, ZRANB2
ELP5	Alter. Terminal Exon (e6)	2.58	5.23E-04	ETR3, Fox1, Fox2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, Nova-1, Nova-2, RBM5, Sam68,
	latara Datastian	0.04	1 275 04	SU35, SF2/RSF, SKp2U, SKp3UC, TIA-1, TIALI, TSF1, ZKANBZ
CD68//EIF4A	Intron Retention	2.24	1.37E-04	EIK-3, INRIVE AJ, INRIVE AZ/BJ, INRIVE F, INRIVE FL, INRIVE T, INRIVE T (FIS), INRIVE F (ILS), SU33, SKp20, TA-1, TALI, TB-1
CNIROB	Intron Retention	1.00	4.01E-04	
MAP2K4	Exon Cassette	2.49	2.76E-03	UGBP1, EIK-5, F0X-1, F0X-2, F0X-1, F0
	Complex (e2-3)	1.66	7.91E-05	
C17orf76-4S1	Evon Cassette	1.00	2 29E-05	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha,
0170170431	Intron Retention	2.01	3.84E-05	HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
	ind on recention	2.01	5.04E 05	
MPRIP	Exon Cassette	1.52	7.57E-04	MRN1, Nov-1, Nov-2, DSR 2005, SET, SR202, SR302, DSR302, TPJ 2014, TAJ, TAJ, TAJ, TAJ, TAJ, TAJ, TAJ, TAJ
LLGL1	Intron Retention	2.16	2.15E-02	ETR-3. hnRNP I (IPTB). hnRNP P (TLS). KSRP, MBNLL SC35. SF2/ASF. SRo30c. YB-1. ZRANB2
55110	5 0 1	1.74		ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB,
EPN2	Exon Cassette	1.76	8.42E-04	HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
K0D1	E	1.02	0.055.04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF,
K2K1	Exon Cassette	1.03	9.65E-04	RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
ERAL1	Complex	1.87	4.90E-03	ETR-3, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
ADAP2	Evon Cassette	1.86	1.04E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1,
ADAI 2	EXON Gasselle	1.00	1.04E-04	Nova-1, Nova-2, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
NF1	Exon Cassette	4.86	9.84F-05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP H2, hnRNP K, hnRNP F (TLS), HTra2beta1, HuB, HuD, HuR, KSRP,
	Elen eusselle		5101200	MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
TMUB2	Exon Cassette	2.26	6.79E-04	9G8, ETR-3, hnRNP A1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SRp20, TIA-1, TIAL1, YB-1
C17orf104	Alter. Terminal Exon	2.90	2.21E-04	ETR3, Fox 1, Fox 2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP F, hnRNP F (TLS), H1ra2beta1, HuB, HuD, KSRP,
				MBRLL, Nova-1, Nova-2, PSF, RBMD, SambB, SU35, SF1, SHp2U, SHp2UC, IA-1, IAL1, PB-1, ZKANBZ
NSF // NSFP1	Complex	1.85	1.32E-02	
NEE2L1	Even Cassette	1.54	2 145 02	
PDK2	Alter First Evon (e1 e4)	2 44	4.63E-04	Erres market in market in index in the index is a market in the index is a market index index index is a solution of the index
SPATA20	Intron Retention	1.52	2 15E-04	ETR3 hRNP1 hRNP1 hrsNP1 hrsNP5 hrsNP5 hrsNP1 HrsNP1 hrsNP1 hrsNP1 hrsNP1 hrsNP1 hrsNP1 hrsNP3 hrsNp3 hrs25 5 114 114 11 42.1
GITTITIZO	ind on Neteridon	1.52	2.152.04	Erres handball handball by National Estimated in the manual of the manual of the manual structure for the manual structure of the structure of
LUC7L3	Intron Retention	2.20	4.41E-04	
PSMC5	Intron Retention	1.82	1.16E-04	ETR-3, hnRNP A1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SRp30c, TIA-1, TIAL1, YB-1
DITOLIO	5 0 "	4 77		CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E2, hnRNP E2, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP F7, hnRNP P7 (TLS), HTra2alpha, HTra2alpha, HTra2alpha, HTra2beta1, HuB, HuD,
PITPINCI	Exon Cassette	1.//	1.74E-03	KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20c, STA-1, TIAL1, YB-1, ZRANB2
DDTC	Alter. Terminal Exon (e32)	1.83	1.99E-05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD,
BEIL	Exon Cassette	1.77	1.36E-04	HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
	Alter. Donor Site	1.50	8.43E-04	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP D1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS),
FRNARIA	Alter. First Exon (e3)	1.66	3.66E-03	HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
COG1	Exon Cassette	1.53	4.48E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Sam68, SC35, SRp30c, TIA-1, TIAL1, YB-1
RPL38	Alter. Terminal Exon (e3)	1.88	1.52E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-2, RBM5, Sam68, SC35,

				SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
SNHG16	Complex	2.38	1.94E-05	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
MGAT5B	Exon Cassette	2.05	2.48E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D1, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
CCDC40	Alter. First Exon (e1-7)	2.10	7.42E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2alpha, HTra2alpha, HTra2beta1, HuB, HuD,
	Alter. Terminal Exon (e11,e13)	1.94	1.20E-03	HUR, KSKP, MBNLI, Nova-1, Nova-2, PSF, KBMS, Sam68, SC35, SF1, SF2/ASF, SKp2U, SKp3Uc, 1DF43, 1IA-1, 1IAL1, YB-1, ZKANB2
NARF	Exon Cassette	2.45	1.14E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP C1, hnRNP CL, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2 (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1 V P.1
	Intron Retendon	2.4J	1.771-04	TRA: bRNP 01 bnRNP 01 bnRNP 01 bnRNP 01 bnRNP 01 bnRNP 02 bnRNP 02 bnRNP 04
GLOD4	Complex	1.84	2.50E-03	TIAL1, YB-1
C17orf85	Complex	1.97	1.53E-02	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, Nova-1, Nova-2, Sam68, SC35, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
SLC25A11	Intron Retention	1.51	5.02E-03	hnRNP P (TLS), HTra2beta1, HuB, KSRP, TIA-1, TIAL1, YB-1
CAMTA2	Exon Cassette	1.52	1.16E-03	ETR-3, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), KSRP, Nova-1, RBM5, SC35, SF2/ASF, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
DLG4	Alter. First Exon (e1-3,e5)	3.62	2.98E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
PLSCR3 // TMEM256	Alter. First Exon	1.57	4.37E-06	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
ZNF18	Alter. First Exon (e2-4)	1.57	2.13E-05	ETR-3, hnRNP A1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
CDRT4 //	Alter. Terminal Exon (e6)	2.00	5.36E-03	9G8, CUG-BP1, ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP H4/B1, hnRNP K, hnRNP LL,
TVP23C	Exon Cassette	1.88	2.88E-03	hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
NCOR1	Exon Cassette	2.36	1.70E-05	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
SLC46A1	Exon Cassette	1.86	1.43E-04	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
ALDOC	Alter. Donor Site	1.59	7.19E-04	ETR-3, hnRNP A1, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, Nova-1, SC35, TIA-1, TIAL1, YB-1, ZRANB2
SDF2	Complex	1.77	1.04E-03	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
	Complex (e2)	1.76	1.16E-03	CUG-BP1. ETR-3. Fox-1. Fox-2. hnRNP A1. hnRNP A2/B1. hnRNP C1. hnRNP D. hnRNP DL. hnRNP E1. hnRNP E2. hnRNP F. hnRNP H1. hnRNP H2. hnRNP H (PTB). hnRNP P (TLS). HTra2aloha. HTra2beta1.
FAM222B	Exon Cassette	1.76	1.16E-03	HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
PHF12	Complex	2.16	1.72E-03	ETR-3, Fox-1, Fox-2, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
MYO18A // TIAF1	Exon Cassette	3.55	6.77E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
SANDO	Alter. Donor Site	2.57	4.28E-05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP,
31111.0	Exon Cassette	4.81	3.63E-06	MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SRp20, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
DDX52	Intron Retention	1.92	1.14E-02	ETR-3, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP K, hnRNP P (TLS), HuB, KSRP, Nova-1, SC35, SRp30c, TIA-1, TIAL1, YB-1
MIEN1	Intron Retention	1.70	5.96E-05	hnRNP E1, hnRNP E2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HuB, KSRP, Nova-1, Nova-2, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1
	Alter. First Exon (e1)	1.60	3.05E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A1, hnRNP D2, hnRNP E2, hnRNP F2, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP H, hnRNP F, hnRNP A, hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35,
MED24	Complex	2.39	1.18E-03	SRp20, SRp30c, TIA-1, TIAL1, YB-1
KRT222//SMARC	Exon Cassette	5.92	8.48E-05	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, VPL-1 ZPANP2
I FPRFI 4	Alter First Exon (e1)	2 14	2 98F-04	TR3 Fxx1 Fxx2 bnRNP F bnRNP H1 bnRNP H2 bnRNP I (PTR) bnRNP P (TIS) KSRP PSF RRM5 SC35 SF2/ASF SRb30r TIA.1 TIAI 1 YR-1 7RANR2
	Alter, Donor Site	2.17	7.84E-04	ETR3. Fox2. InRNP A1. InRNP A2/B1 InRNP C1. InRNP C5. INRNP H2 INRNP H2 INRNP H3 INRNP H2 INRNP H3. INRNP H1 INRNP H2 INRNP H2 INRNP H2 INRNP H3.
PSMC3IP	Intron Retention	2.17	7.79E-04	PSF, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
ETV/4	Alter. First Exon (e1-4)	3.67	8.54E-03	
EIV4	Exon Cassette	7.00	2.00E-05	
MPP3	Intron Retention	2.92	1.08E-03	CUG-BP1, ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
GPATCH8	Exon Cassette	2.37	6.74E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
PLEKHM1	Exon Cassette	1.86	4.04E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
KANSL1	Exon Cassette	2.35	3.62E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SRp30c, TIA-1, TIAL1, YB-1

SPAG9	Alter. First Exon (e1-4)	6.50	8.88E-08	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2, B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F2, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS),
	Exon Cassette	1.68	2.50E-03	HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
MOTO 1	Exon Cassette	2.13	6.03E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1,
MBIDI	Intron Retention	1.62	4.80E-03	HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SF1, SF2/ASF, SRo20, SRo30c, TIA-1, TIAL1, YB-1, ZRANB2
SRSF1	Intron Retention	1.73	6.22E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, PSE, RBM5, Sam68, SC35, SE1, SRx20, SR30c, TLA1, VB1, ZRANB2
	Alter Dopor Site	/ 98	2.63E-04	
ICAM2	Alter. Donor Site	4.50	2.031-04	
	Complex (e1)	5.13	4.04E-04	NSRY, WBNLI, NOVA-2, PSF, KBMS, Samos, Sc3, SF1, SKp2U, SKp3UC, HA-1, HAL1, TB-1, ZKANBZ
PLEKHM1P	Alter. Donor Site	1.56	1.12E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1,
TEERINII	Exon Cassette	2.43	1.15E-04	HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
AMZ2P1	Intron Retention	2.20	9.01E-04	ETR-3, hnRNP C1, hnRNP I (PTB), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SRo20, YB-1
HN1	Exon Cassette	1.83	1.22E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MRN11, Nova-1, Nova-2, BRM5, Sam68, SC35, SRa20, SRa30, TLA1, TLA11, VR-1, ZRANR2
	Intron Potention	2.09	261504	
		3.50	2.011-04	
FBF1 // MRPL38	Complex	1.64	7.62E-03	ETR-3, NNKNP AI, NNKNP AZ/BI, NNKNP CI, NNKNP FI, NNKNP HI, NNKNP H2, NNKNP I (PIB), NNKNP K, NNKNP P (TLS), HIRazbetaI, HUB, KSKP, MBNLI, Nova-I, Sam68, SC35, SKp20, SKp30c, HA-I, HALI, YB-I,
ACOX1	Complex	1.64	4.82E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
	Alter. Acceptor Site	2.70	1.68E-02	
	Alter Terminal Exon (e4)	1.62	7 01E-04	
EXOC7	Complex	2.26	9.955.04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD,
EXUC/	Complex	2.30	0.00E-04	HuR, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
	Exon Cassette	2.99	1.90E-05	
	Intron Retention	1.73	1.10E-02	
CYTH1	Exon Cassette	1.96	6.63E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF. RBM5. Sam68. SC35. SRo20. SRo20. STA-1. TIAL1. YB-1. ZRANB2
	Alter First Exon (e1 e3)	1 56	1 02E-03	9G8 FTR-3 Fox-1 Fox-2 bnRNP 41 bnRNP 42/81 bnRNP C1 bnRNP C1 bnRNP D1 bnRNP D1 bnRNP F1 bnRNP F2 bnRNP F1 bnRNP H1 bnRNP H2 bnRNP H3 bnRNP H2 bnRNP H2 bnRNP F4 bnRNP
CSNK1D	Compley	1.50	6.100.04	
	Complex	1.50	0.19E-04	
ANKRD12	Alter. Terminal Exon (e12-16)	1.72	5.78E-03	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS),
TINNE	Exon Cassette	1.52	2.06E-03	HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
005011	5 0 "	0.41	5 055 04	CUG-BP1, ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P, (TLS), HTra2alpha, HTra2beta1, HuB, KSRP, MBNL1,
GREBIL	Exon Cassette	2.41	5.05E-04	Nova-1. Nova-2. RBM5. Sam68. SC35. SF1. SF2/ASF. SRo20. SRo30c. TDP43. TIA-1. TIAI 1. YB-1. ZRANB2
	Complex	2.02	4 19E 04	
ZNF271	Complex	2.03	4.100-04	
	Exon Cassette	1.90	4.18E-04	NSRF, WDIVLI, NUV4-2, FSF, RDWJ, Saliloo, SUSS, SF1, SF2/ASF, SR/20, SR/200, 114-1, 114L1, 15-1, ZRAWD2
C18orf25	Exon Cassette	1.84	5.48E-03	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
D1154.65	5 0 1		1 7 6 5 6 1	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H (PTB), hnRNP K, hnRNP LL, hnRNP P
RNF165	Exon Cassette	1.88	1.76E-04	(TIS) HTra2alpha HTra2bata1 HuR HuR KSPP MRNI1 Nova 2 PSE RRM5 Sam68 SC35 SE1 SE2/ASE SP020 SP030c TDP/3 TIA.1 TIA.1 TVR.1 7PANR2
ELAC1 // SMAD4	Exon Cassette	2.80	5.01E-04	
			-	Samba, SC35, SF1, SF2/ASF, Skp20, Skp30c, TIA-1, TIAL1, YB-1, ZKANB2
POLI	Intron Retention	1.87	3.60E-03	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
7115520	Alter First Free (c1 - C 10 - 10)	1 77	2 625 04	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS),
ZINFUUZ	Alter. First EXOII (e1,e6-10,e12)	1.//	3.03E-04	HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
				CUG-BP1. FTR-3. Fox-1. Fox-2. hnRNP A1. hnRNP A2/B1. hnRNP C1. hnRNP D. hnRNP D1. hnRNP F1. hnRNP F2. hnRNP F1. hnRNP H1. hnRNP H2. hnRNP H2. hnRNP J. (PTB). hnRNP K. hnRNP P. (TLS). HTra2alpha. HTra2beta1.
TNFRSF11A	Exon Cassette	1.88	2.62E-03	HUR HUD HUR KSRP MRNI 1 Nova 2 PSE RRM5 Sam68 \$C35 SE1 SP020 SP030c TIA 1 TIA 1 VR.1 ZPANR2
ATP9B	Exon Cassette	1.51	4.88E-03	
			-	HUB, HUD, KSRP, MBNLI, NOVA-I, NOVA-Z, PSF, RBM5, Samo8, SC35, SFI, SF2/ASF, SRp2U, SKp3Uc, TDP43, TIA-I, TIALI, YB-I, ZKANB2
NEATC1	Evon Cassette	2.62	3 13E-06	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP,
MINIOI	Exon ousselle	2.02	5.15E 00	MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
				9G8, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP H3, hnRNP K, hnRNP K, hnRNP P, (TLS), HTra2alpha,
LAMAI	Complex	2.99	9.39E-04	HTra2beta1 HuB HuD KSRP MBNL1 Nova-1 Nova-2 PSE RBM5 Sam68 SC35 SE1 SE2/ASE SRo20 SRo30c TIA-1 TIAL1 YB-1 7RANR2
ZNF519	Exon Cassette	1.52	4.94E-03	DDMS Considered and the constraints of minute L, minute
-			-	RBWD, Samod, SU33, Sr2/ASr, SRp2U, SRp3UC, 11A-1, 11A-1, ZKAND2
FSC01	Evon Cassette	1 84	1 72E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha,
20001	Exon ousselle	1.04	1.722.03	HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
TMEMOAL	From On control	1.50	0.025.04	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, KSRP, Nova-1, Nova-2, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1,
TMEWI241	Exon Cassette	1.53	8.63E-04	YB-1, ZRANB2
				CLIG-RP1 FTR-3 Fox-1 Fox-2 hnRNP A1 hnRNP A2/R1 hnRNP C1 hnRNP C1 hnRNP F1 hnRNP F2 hnRNP F2 hnRNP F1 hnRNP H1 hnRNP H2 hnRNP F1 (PTR) hnRNP P (TI S) HTra2hata1 HuR HuD KSRP MRNI 1 Noua-
SS18	Exon Cassette	2.77	6.96E-04	1 Nurs 2 DBMS Cambridge SC25 CE1 Sb20 (Sb20) That Tai 1 Tai 1 VR.1 7 DANE2
70041120	Alter Dever Cite	1.50	1 705 00	
ZSCAN30	Alter. Donor Site	1.59	1./6E-03	UGGBELLERGS, FOX-1, FOX-2, ONKNE A1, DNKNE A2/B1, DNKNE G1, DNKNE G1, DNKNE G1, DNKNE G2, DNKNE F, DNKNE H1, DNKNE H2, DNKNE H2, DNKNE H, DNKNE K, DNKNE P (TLS), HTra2alpha, HTra2beta1, HuB, HuD,

			1	
470541	All D 0''	0.50	5.665.00	Noter, MBRLL, Nova-1, Nova-2, PSF, KBMD, Samos, Sc33, SFL, SFZ/ASF, SKRZU, SKRZUG, LIDP43, HALL, HALL, YB-1, ZKANSZ
ATP5AT	Alter. Donor Site	2.50	5.66E-03	CUG-BP1, E1R-3, INKIVP A1, INKIVP F1, INKIVP F1, INKIVP H2, INKIVP H2, INKIVP K, INKIVP P (ILS), H1ra2beta1, HuB, HuD, KSKP, Nova-1, Samb8, SC39, SKp30c, IIA-1, IIAL1, YB-1, ZKAINB2
MBD1	Complex	1.52	2.98E-04	ETR-3. Fox-1. Fox-2. hnRNP A1. hnRNP A2/B1. hnRNP P (TLS), KSRP, Nova-1. SC35. SRo30c, TIA-1. TIAL1. YB-1. ZRANB2
	Exon Cassette	1.53	2.98E-04	
TCF4	Alter. First Exon (e1-2,e4-	3.27	5.47F-07	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D1, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F1, hnRNP H1, hnRNP H3, hnRNP H3, hnRNP H3, hnRNP K, hnRNP P (TLS),
-	20,e23)			HIra2alpha, HIra2beta1, HuB, HuD, HuK, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/, SF5, SKp20, SRp30c, IDP43, IA-1, IIAL1, YE-1, ZKANB2
CBLN2	Alter, First Exon (e1-3)	2.80	5.76E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F1, hnRNP H2, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, PSF, RBM5, Sam68,
-			-	SC35, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
CIRBP	Intron Retention	1.89	2.15E-04	ETR-3, Fox-1, Fox-2, hnRNP C1, hnRNP DL, hnRNP F1, hnRNP H1, hnRNP P2, hnRNP P (TLS), HuB, KSRP, MBNL1, RBM5, SC35, SF2/ASF, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
NEIC	Exon Cassette	1 55	2 11E-05	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, KSRP, MBNL1,
	Exern edubberto	1.00	2.112.00	Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
HMG20B	Intron Retention	2.61	1.92E-03	hnRNP F, hnRNP H1, hnRNP H2, hnRNPI (PTB), hnRNP P (TLS), HTra2beta1, HuB, Nova-1, Nova-2, SC35, TIA-1, TIAL1, YB1
	Alter. First Exon (e3-4,e6-	2 69	9 52F-05	9C8 CUCARD FTR.3 Fox.2 F
ATCAY	15,e17)	2.05	51022.00	IIIS) HTra2alna HTra2alna HTra2alna HUD HUR KSRP MRNI 1 Nova-2 PSF RRM5 Sam68 SC35 SE1 SE2/ASF SR/20 SR/20 TDP43 TIAL TIAL 1 VR-1 ZRANR2
	Complex	3.45	8.08E-05	
MAP2K7	Exon Cassette	1.88	2 39F-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, RBM5,
	Exern edubberto	1.00	2.052.01	Sam68, SC35, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1
SNAPC2	Alter. First Exon (e2)	1.64	6.28E-03	hnRNP A1, hnRNP A2/B1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, KSRP, Nova-1, SC35, SRp30c, TIA-1, TIAL1, YB-1
ZNF317	Intron Retention	1.52	7.72E-03	ETR-3, Fox-1, Fox-2, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HuB, KSRP, Nova-1, PSF, RBM5, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1
PIN1	Evon Cassette	1.67	1.40E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, Nova-2, SC35, SRp20,
1 1141	EXOII Gasselle	1.07	1.402-04	SRp30c, TIA-1, TIAL1, YB-1
DNM2 // OTPT1	Intron Retention	2.07	4.40E-04	ETD 2 Env 1 Env 2 hadned E hadned H1 hadned H2 hadned (Jack Hadned D (TIS) Hurd KCDD MONII 1 Navia 1 DSE DDME Sames SC25 SE2/ASE SDa20 SDa20 TH 1 TH 1 VD 1 7DAND2
DINNZ // QINII	Mutualy Exclusive Exons (e22)	1.52	7.18E-04	
CMADCA4	Complex	1.86	9.08E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRN
SWARCA4	Exon Cassette	1.86	9.08E-03	HuD, HuR, KSRP, MBNL1, Nova-2, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
ANKLE1/BABAM	Intron Retention	1.63	5.06E-03	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), KSRP, SC35, SF2/ASF, YB-1, ZRANB2
MAU2	Intron Retention	1.77	2.50E-02	ETR-3. Fox-1. Fox-2. hnRNP A1. hnRNP I (PTB). hnRNP P (TLS). KSRP. SC35. SRp30c. YB-1. ZRANB2
				FTR-3. Fox-1. Fox-2. hnRNP A1. hnRNP A2/B1. hnRNP C1. hnRNP C1. hnRNP C1. hnRNP F2. hnRNP F2. hnRNP F4. hnRNP H1. hnRNP H2. hnRNP F (TI S). HTra2alpha. HTra2beta1. HuB. HuD. KSRP.
ZNF257	Exon Cassette	2.78	1.60E-04	MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SRo20, SRo30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
71/5054		1.00		9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP K, hnRNP K, hnRNP P (TLS),
ZNF254	Alter. First Exon (e1-2,4,e11-12)	1.89	2.56E-04	HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
71/5507			0.005.00	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P, (TLS), HTra2alpha, HTra2beta1, HuB,
ZNF507	Alter. Terminal Exon (e4)	1.69	3.06E-03	HuD, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
EVVDE	Altern First From (c.1.F)	0.07	2.515.00	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP,
FXTDS	Alter. First Exon (e1-5)	2.97	3.51E-06	MBNL1, Nova-1, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
1.00	F	0.00	2 005 02	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2, B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP K, hnRNP L1, hnRNP P (TLS),
LSR	Exon Cassette	2.69	3.82E-03	HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
LIKP1	F 0 11	1.70	0.045.04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP H, hnRNP K, hnRNP M, hnRNP C1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP H4, hnRNP H4, hnRNP K3,
HKRI	Exon Cassette	1.79	9.24E-04	KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
0.01117.0	5 0 1		1.005.00	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP,
SPIN12	Exon Cassette	4.10	1.68E-06	MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
		1.00	1 705 00	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5,
HNRNPULI	Alter. Donor Site	1.86	1.76E-03	Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
7115574		1.01	0.505.00	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F1, hnRNP H1, hnRNP H3, hnRNP H3, hnRNP H1, hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB,
ZINF574	Alter. First Exon (e3)	1.81	2.58E-03	HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
71/5000		4.50	1 105 00	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP,
ZINF283	Alter. Terminal Exon (e7)	1.59	1.40E-02	MBNL1, Nova-1, Nova-2, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
D) (D		1.07	1 405 00	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SRp20, SRp30c, TIA-1,
PVR	Alter. Donor Site	1.97	1.42E-03	TIAL
01.4000		1.50	6 005 05	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP H7, hnRNP K, hnRNP K, hnRNP P (TLS),
CLASRP	Alter. First Exon (e1-11)	1.50	6.20E-05	HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
PPP5C	Intron Retention	1.84	4.16E-03	ETR-3, Fox-1, Fox-2, hnRNP E1, hnRNP E2, hnRNP I (PTB), hnRNP P (TLS), MBNL1, Nova-1, TIA-1, TIAL1
0100	Complex	2.24	6.21E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, PSF, RBM5, Sam68, SC.35, SRn30e, TIA-1,
SNRNP70	Exon Cassette	2.45	3.45E-04	TIAL1, YB-1, ZRANB2
PRMT1	Alter, Donor Site	3.66	4.45E-04	
	Alter, First Exon (e1-4)	1.96	1.73E-05	CUG-BP1, ETR-3, hnRNPA1, hnRNPC1, hnRNPD, hnRNPE1, hnRNPE2, hnRN F, hnRNPH1, hnRNPH2, hnRNPI (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuD, KSRP, MBNL1, Nova-1, RBM5, SC35, SF2/ASF,
	Evon Cassette	1.55	1.28E-03	SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
7NE480	Evon Cassette	1.55	3.72E-02	
2111 400	LAUH GASSELLE	1.00	J./ 2L-UJ	

MYADM	Alter. First Exon (e2)	1.80	8.99E-04	KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, hnRNP A1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP F (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, PSF, RBM5, Sam68, SC35,
CNOT3	Intron Retention	1.58	6.98E-03	SRp30c, TIA-1, TIAL1, TB-1 ETR-3, hnRNP A1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H (PTB), hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, KSRP, MBNL1, Nova-1, RBM5, Sam68, SC35, SRp30c, TIA-1,
	Altar Dapar Sita	1 0 1	1 225 02	IIALI, YB-1
RPS9	Intron Retention	1.79	2.48F-03	ETR-3, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, PSF, Sam68, SC35, SRp20, TIA-1, TIAL1, YB-1, ZRANB2
RPL28	Alter. Terminal Exon (e3)	1.99	5.64E-04	ETR-3, Fox-1, Fox-2, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Sam68, SC35, SF2/ASF. SRo20, SRo30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
71155.40	Alter. First Exon (e2)	3.35	5.80E-04	
ZINF042	Complex	3.51	4.15E-04	
ZNF551	Exon Cassette	1.71	1.44E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
ZNF135	Exon Cassette	2.50	3.64E-04	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, HuR, KSRP, Nova-1, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1
MFSD12	Complex	1.72	1.36E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
PTPRS	Exon Cassette	2.59	4.00E-05	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
ZNF266	Intron Retention	2.50	5.00E-03	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H (PTB), hnRNP K, hnRNP P (TLS), HuB, Nova-1, Nova-2, SC35, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
TYK2	Complex (e6-7)	1.88	3.63E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
EPOR // RGL3	Complex	1.98	4.99E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
STX10	Intron Retention	2.07	3.59E-04	ETR-3, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP P (TLS), HuB, KSRP, Nova-1, Sam68, SC35, SRp30c, YB-1, ZRANB2
GIPC1	Exon Cassette	1.94	1.41E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
NOTCH3	Exon Cassette	2.29	3.05E-04	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SRp30c, YB-1, ZRANB2
RAB3A	Alter. First Exon (e1)	2.29	1.57E-04	FTR.3 Frv.1 Frv.2 hoRNP A1 hoRNP D hoRNP F1 hoRNP F2 hoRNP F hoRNP H1 hoRNP H2 hoRNP H2 hoRNP P (TI S) HUR KSRP Nova.1 RRM5 SC35 SRo20 SRo30 VR.1 7BANR2
10103/1	Intron Retention	1.56	1.02E-03	
C19orf12	Exon Cassette	1.79	5.40E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
ZNF565	Alter. First Exon (e1,e4) Exon Cassette	1.75	1.58E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB HuD HuB KSPP MRNI 1, Nova-2, PSF, RBM5, Sam68, SC35, SE1, SE2/ASF, SRa20, SRa30, TDP43, TIA-1, TIA-1, TIA-1, TRA1, PANR2
	Complex	2.59	4.78F-03	THUS THAT FOR THAT FOR THAT THAT THAT THAT THAT THAT THAT THA
ZNF260	Exon Cassette	2.41	3.45E-04	KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SRp20, SRp30c, TiA-1, TIAL1, YB-1, ZRANB2
ZNF571	Exon Cassette	2.02	2.22E-03	9G8, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF2/ASF, SRo20, SRo30c, TIA-1, TIAL1, YB-1, ZRANB2
ZNF573	Exon Cassette	1.74	7.53E-05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNI 1, Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SF2/ASF, SRo20, SRo30c, TDP43, TIA-1, TIAI 1, YR-1, ZRANB2
HNRNPL	Exon Cassette	2.32	1.02E-03	ETR-3, hnRNP A1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F2, hnRNP H1, hnRNP H2, hnRNP I(PTB), hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1,
FBX017//SARS2	Intron Retention	1.82	1.55E-04	Fox-1, Fox-2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP P (TLS), HuB, Nova-1, Sam68, SC35, SF2/ASF, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
ZNF780B	Exon Cassette	2.26	9.12E-03	ETR-3, hnRNP A1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1
AKT2	Exon Cassette	1.76	1.14E-03	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
RTN2	Exon Cassette	1.81	6.45E-04	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
PIH1D1	Alter. Acceptor Site	3.02	1.72E-05	ETR-3, hnRNP A1, hnRNP I (PTB), hnRNP P (TLS), HuB, RBM5, Sam68, SC35, SRp30c, TIA-1, TIAL1, YB-1
NOSIP	Complex	2.54	4.40E-03	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
SYT3	Alter. First Exon (e1-2)	1.50	6.02E-03	9G8, ETR-3, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1
ZNF615	Exon Cassette	2.03	7.80E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SF2/ASF, SRp20c, STRp30c, TIA-1, TIAL1, YB-1, ZRANB2
711500	Alter. First Exon (e1.3,e8)	2.09	1.90E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha,
ZINF83	Exon Cassette	3.03	8.12E-05	HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
ZNF611	Exon Cassette	3.38	1.99E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
ZNF415	Exon Cassette	9.39	2.33E-05	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HuB, HuD, KSRP, MBNL1, Nova-1,

				Nova-2, PSF, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
ZNF667	Alter. First Exon (e1-2)	5.77	2.13E-05	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP F, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
ZNF772	Exon Cassette	1.55	5.29E-07	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, SC35, SF2/ASF, SRp30c, TIA-1, TIAL1, YB-1
ZNF550	Exon Cassette	2.35	2.08E-05	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SRp20c, TIA-1, TIAL1, YB-1, ZRANB2
7115606	Alter. Terminal Exon	2.01	1.58E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD,
ZNF606	Exon Cassette	1.54	3.12E-03	HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
ZNF329	Exon Cassette	2.44	1.64E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
RNF144A	Alter. First Exon (e1)	4.83	1.77E-06	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
HPCAL1	Alter. First Exon (e1,e3-5)	2.16	7.69E-05	CUG-BP1, ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H3, hnRNP H3, hnRNP H3, hnRNP A2/B1, hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRo20, SRo30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
EAM228A //	Complex (e4)	2.14	2.40F-03	
FAM228R	5011plax (61)	1.64	0.005.00	EIR-S, FW-L, FW-C, HINNYF AL, HINNYF AL, HINNYF CL, HINNYF CL, HINNYF CL, HINNYF FL, HINNYF FL
174112200	Exon Cassette	1.64	8.26E-03	
CENPO	Complex	1.54	5.64E-05	CUG-BP1, E1R-3, FOX-1, FOX-2, INRIVE A1, INRIVE A2/B1, INRIVE C1, INRIVE C1, INRIVE E1, INRIVE E2, INRIVE F, INRIVE F1, INRIVE H2, INRIVE H2, INRIVE H2, INRIVE F2, INRIVE F4, I
КНК	Exon Cassette	2.17	4.39E-05	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP F, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
SNX17	Exon Cassette	1.57	2.14E-03	ETR-3, hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, PSF, SC35, SRp30c, TIA-1, TIAL1, YB-1
BRE	Exon Cassette	1.99	5.28E-03	CUG-BP1, ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
PPP1CB // SPDYA	Complex	1.66	5.32E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRo20, SRo30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
NDUFAF7	Intron Retention	2.37	1.03E-04	ETR-3, hnRNP A1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, HuB, KSRP, Nova-1, Sam68, SC35, TIA-1, TIAL1, YB-1, ZRANB2
EML4	Exon Cassette	9.66	2.44E-05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
МТАЗ	Alter. Terminal Exon	2.20	1.63E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HUB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
DADOLO	Exon Cassette	1.58	8.70E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1,
PAPULG	Intron Retention	1.66	1.98E-02	Nova-2, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
KIAA1841	Complex (e18-19)	1.81	4.33E-05	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
	Alter. First Exon (e1)	3.00	1.10E-03	
CEP68	Complex	2.51	1.43E-04	
	Exon Cassette	1.71	3.28E-03	
MEIS1	Intron Retention	1.94	4.38E-03	hnRNP C1, hnRNP I (PTB), Nova-1, SRp20, SRp30c, YB-1, ZRANB2
NAGK	Intron Retention	1.66	2.65E-04	ETR3, hnRVP F, hnRVP H1, hnRVP H2, hnRVP F (PIB), hnRVP P (TLS), HUB, KSRP, Nova-1, Nova-2, PSF, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1
MPHOSPH10	Alter. Terminal Exon (e5)	1.56	8.40E-03	ETR-3, Fox-1, Fox-2, INDRIVE A1, INDRIVE P2/B1, INDRIVE C1, INDRIVE C1, INDRIVE E2, INDRIVE F2, INDRIVE F1, INDRIV
ZNF638	Alter. Acceptor Site	2.41	8.03E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A2/B1, hnRNP A2/B1, hnRNP D, hnRNP D, hnRNP E2, hnRNP F, hnRNP F1, hnRNP H1, hnRNP H1, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-
TT001	Complex	2.43	8.90E-03	1, Nova-2, PSF, HRMb, Sambd, SC3b, SF1, SF2/ASF, SKp2U, Skp3Uc, IDP44, TIA-1, HIAL1, YIAL1, ZKANB2
11031	Intron Retention	1.70	2.38E-03	nRRWP AL, NRRWP F, NRRWP HZ, NRRWP P(LDS), HTR22010B, HTR2202B1, HUE, NBWLI, RBWCJ, SU35, SK530C, TS-1
ELMOD3	EXOII Casselle	2.02	9.44E-04	EIK-3, INKWE CL, INKWE F, INKWE H, INKWE H, INKWE H, INKWE K, INKWE K, INKWE K, INKWE K, INKWE K, INKWE F, INKWE H, INK
CIA01	Intron Retention	1.00	1.11E-02	TET 2: A DRINE F ADDRE F ADDRE MADE MADE AT A DRIVE A TRANSPORT A DRIVE A DRIV
00/01	introl heternon	1.75	1.152.04	ETR3 brenze
ITPRIPL1	Exon Cassette	2.12	7.66E-05	
INPP4A	Alter. Donor Site	2.39	2.02E-04	EIR-3, FOX-1, FOX-2, HURINF A1, HURINF 61, BRRINF 61, BRRINF E2, BRRINF F2, BRRINF F1, BRRINF F1, BRRINF F1, BRRINF F1, BRRINF F2, B
MAP4K4	Alter. Terminal Exon (e18-33)	2.31	5.39E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
BCI 2I 11	Complex (e3,e9-13)	1.73	1.50E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP D, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD,
	Exon Cassette	1.91	3.06E-03	HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
POLR1B	Exon Cassette	2.35	5.62E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2

DPI	Complex (e2-3)	2.30	4.58E-04	ETD 2 handle E handle 1 handle 1 handle 1 (DTD) handle K handle D (TE) Hug MONIT Nova 1 Sames SC25 SD20 SD206 SD11 TALL VD 1 7DAND2
DBI	Exon Cassette	2.28	6.60E-04	ETR-5, INITAR 1, INITAR 11, INITAR 112, INITAR 1, ITED, INITAR K,
PKP4	Alter. Terminal Exon (e17)	1.93	4.36E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
DNAJC10	Complex	1.85	1.54E-03	CUG-BP1, ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1
CARF	Exon Cassette	1.56	6.26E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
FASTKD2	Intron Retention	1.66	1.79E-02	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
PIKFYVE	Alter. Terminal Exon (e13)	1.83	3.64E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
MAP2	Exon Cassette	3.56	1.94E-06	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
SPAG16	Complex (e1)	1.82	1.74E-03	9G8, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
PLCD4	Alter. Terminal Exon (e11)	2.54	6.05E-05	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB,
D0011	Complex	2.67	9.88E-03	
BUSIL	Complex	1.57	4.00E-04	
ZFAND2B	Alter. Terminal Exon (e8)	1.92	2.16E-04	ETR3, Fox1, Fox2, InRNP E1, INRNP E2, INRNP F1, INRNP F1, INRNP F1, INRNP F1 (PIB), INRNP F1 (LS), HTrazbeta1, HuB, Nova-1, FS, SambB, SC35, SF1, SKp20, SKp30c, YB-1, ZKANB2
DNAJB2	Intron Retention	1.87	4.60E-04	ETR-3, hnRNP A1, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, SC35, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
ASIC4	Intron Retention	3.53	1.91E-05	ETR-3, hnRNP F, hnRNP H1, hnRNP H2, hnRNP P (TLS), KSRP, Nova-1, SC35, SRp30c, YB-1
STK11IP	Intron Retention	1.73	2.03E-04	ETR-3, hnRNP A1, hnRNP C1, hnRNP I (PTB), hnRNP P (TLS), HuB, HuD, KSRP, Nova-1, SC35, TDP43, TIA-1, TIAL1, YB-1
NYAP2	Exon Cassette	1.74	3.40E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2, B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
RHBDD1	Exon Cassette	1.79	5.56E-05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
MFF	Exon Cassette	1.59	3.99E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SF1, SRo20, SRo30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
GIGYF2	Alter. Terminal Exon (e8)	1.57	1.88E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2, B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F2, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRo20, SRo30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
	Alter, First Exon (e1.e3-20.e23)	2.78	2.16F-04	9G8 CLIG-RP1 FTR-3 Fox-1 Fox-2 bnRNP A1 bnRNP A2/B1 bnRNP C1 bnRNP D1 bnRNP D1 bnRNP E2 bnRNP E2 bnRNP E1 bnRNP H1 bnRNP H2 bnRNP H3 bnRNP H3 bnRNP L(PTR) bnRNP K bnRNP L(bnRNP L)
LRRFIP1	Alter Terminal Exon (e21)	4.06	5.00E-06	(TIS), HTra2abha, HTra2betal, HuB, HuD, HuB, KSRP, MBNI, Nova-1, Nova-2, PSE, RBMS, Sam68, SC35, SF1, SF2/ASE, SRo20, SRo30c, TDP43, TIA-1, TIA1, VB-1, ZRANB2
	Complex (e6)	1.81	1 18E-03	
ATG4B	Even Cassette	1.69	9.495.02	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
CLI2VL1	Alter First From (c2)	2.77	3.460-03	CHE DD1 FTD 2 Few 1 Few 2 ADDD 14 ADDD F ADDD 11 ADDD 10 ADDD 10 FDDD ADDD 10 FDDD D FEDD OF A DDD 7 CO HDD 10 NORE 1 DDAE CO2C CT0/ACT CD-20 CD-20 TA 1 TA11 VD 1
SHOTLI	Alter. First Exoli (e2)	2.11	3.00E-03	
KIDINS220	Exon Cassette	2.30	1.38E-04	ETR-3, Fox-1, Fox-2, DRKNP A1, DRKNP A2/B1, DRKNP D1, DRKNP E1, DRKNP E2, DRKNP F, DRKNP H1, DRKNP H2, DRKNP H2, DRKNP K, DRKNP P (TLS), HTrazalpha, Htrazbeta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
SMC6	Exon Cassette	1.66	2.05E-02	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
SDC1	Alter. First Exon (e1-2,e4-6)	1.53	1.28E-03	CUG-BP1, ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
PUM2	Exon Cassette	1.75	1.26E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
DNAJC27	Exon Cassette	1.97	2.02E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
DNMT3A	Alter. First Exon (e1)	2.85	4.72E-03	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
DTNB	Exon Cassette	1.58	1.14E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRo20, SRo30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
HADHA	Alter. Terminal Exon	2.93	5.96E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
PREB	Intron Retention	1.65	2.84E-03	ETR-3, hnRNP A1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HuB, KSRP, Nova-1, RBM5, SC35, SRo20, TIA-1, TIAL1, YB-1, ZRANB2
				CUG-BP1. ETR-3. Fox-1. Fox-2. hnRNP A1. hnRNP A2/B1. hnRNP C1. hnRNP DL. hnRNP E1. hnRNP E2. hnRNP F. hnRNP H1. hnRNP H2. hnRNP [/[PTB]. hnRNP [/[TTS]. HnRNP P (TTS). HTra2beta1. HuB. HuD. HuR.
GTF3C2	Exon Cassette	1.75	2.44E-03	KSRP_MBNI1_Nova-1_Nova-2_PSF_RBM5_Sam68_SC35_SF1_SF2/ASF_SRp20_SRp30c_TDP43_TIA-1_TIA_1_VF1_ZRANR2
FIF2B4	Intron Retention	1.74	1.60F-03	FTR-3, hnRNP C1, hnRNP F1, hnRNP H1, hnRNP H2, HuB, KSRP, Nova-1, Nova-2, Sam68, SC35, YB-1
SUPT7I	Intron Retention	3.24	3 89E-05	TR3 bRNP A1 brRNP D1 brRNP F1 brRNP F1 brRNP F1 brRNP H1 brRNP H2 brRNP [PTR] brRNP P (TIS) HuR KSRP Nova-1 SC35 YR-1
SOS11/L	Evon Cassette	2.24	4 96E-07	ETRA: Frequencies of particle and the particle and the particle partite particle particle particle particle particle par
3031	LAUIT GUSSELLE	2.30	T.JUL-0/	

MANCH Part Counter					MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
Interface Interface <t< td=""><td>MAD4K2</td><td>Even Consette</td><td>1 57</td><td>4.215.04</td><td>ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1,</td></t<>	MAD4K2	Even Consette	1 57	4.215.04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1,
HMPRI Description End 50 End	MAP4K3	Exon Cassette	1.57	4.21E-04	Nova-1, Nova-2, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
Internet Open Subject Dist Open Subject Status Control Status	TUUMDDO	F	1.50	6 005 00	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1,
MCH Origin 1.710 <th< td=""><td>THUMPD2</td><td>Exon Cassette</td><td>1.52</td><td>6.80E-03</td><td>Nova-2, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2</td></th<>	THUMPD2	Exon Cassette	1.52	6.80E-03	Nova-2, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
Instrument Descurate 2.000 Hand R (200) Mills (Rec) (Rec) (Rec) (Rec) (Sec)	DDEDI	Complex	1.71	1.71E-02	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP F (TLS), HTra2alpha, HTra2beta1, HuB,
NBT Data Count Los Data Count	PREPL	Exon Cassette	2.03	2.60E-04	HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
Hor Data Links Links Resp. 2 sentis Statis S	5105		1.07		ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1,
MASS Mass Desc Company	PIGF	Exon Cassette	1.87	1.00E-04	Nova-2, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
Name Addition Addition <th< td=""><td>1000 // 00075</td><td></td><td>1.50</td><td>4 005 00</td><td>CUG-BP1, ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP A2/B1, hnRNP A2/B1, hnRNP D, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP K, hnRNP M2/B1, hnRNP A2/B1, hnRNP D, hnRNP D, hnRNP E2, hnRNP F2, hnRNP H1, hnRNP H2, hnRNP H, hnRNP K, hnRNP M2/B1, hnRNP A2/B1, hnRNP D, hnRNP D, hnRNP E2, hnRNP F2, hnRNP H1, hnRNP H2, hnRNP H, hnRNP K, hnRNP H2, hnRNP K, hnRNP M2/B1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E2, hnRNP F2, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP M2/B1, hnRNP A2/B1, hnRNP A2/B1, hnRNP D, hnRNP D, hnRNP E2, hnRNP F2, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP H2, hnRNP K, hnRNP K, hnRNP A2/B1, hnRNP A2/B1, hnRNP E3, hnRNP E4, hnRNP H1, hnRNP H4, hnRNP H2, hnRNP H</td></th<>	1000 // 00075		1.50	4 005 00	CUG-BP1, ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP A2/B1, hnRNP A2/B1, hnRNP D, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP K, hnRNP M2/B1, hnRNP A2/B1, hnRNP D, hnRNP D, hnRNP E2, hnRNP F2, hnRNP H1, hnRNP H2, hnRNP H, hnRNP K, hnRNP M2/B1, hnRNP A2/B1, hnRNP D, hnRNP D, hnRNP E2, hnRNP F2, hnRNP H1, hnRNP H2, hnRNP H, hnRNP K, hnRNP H2, hnRNP K, hnRNP M2/B1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E2, hnRNP F2, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP M2/B1, hnRNP A2/B1, hnRNP A2/B1, hnRNP D, hnRNP D, hnRNP E2, hnRNP F2, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP H2, hnRNP K, hnRNP K, hnRNP A2/B1, hnRNP A2/B1, hnRNP E3, hnRNP E4, hnRNP H1, hnRNP H4, hnRNP H2, hnRNP H
BBC Bonc basels 1.76 4.56.3 CPR.3 res.1 res.2 https://dxibid/2.01.https://dxibid/2.01.https://dxi/bid/2.1.bid/2.01.https://dxi/bid/2.1.bid/2.01.https://dxi/bid/2.1.bid/2.01.bid/2.1	ASB3 // GPR/5	Alter. Donor Site	1.58	4.98E-03	HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
PN310 Data Casetti 11:54 6.522 FTRS, Faul, Faul	SMEK2	Exon Cassette	1.76	4.62E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), HuB, KSRP, Nova-1, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
Photo Land Land <thland< th=""> Land Land <th< td=""><td>D11010</td><td></td><td></td><td>0.005.04</td><td>ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1,</td></th<></thland<>	D11010			0.005.04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1,
PMEIL Pinnet 1.1.5 2.4423 Pinnet Pin	PUSIO	Exon Cassette	1.54	8.63E-04	Sam68, SC35, SF1, SRp20, TIA-1, TIAL1, YB-1, ZRANB2
PMR1/A Devi Custom 1.30 2.4940 Nove2. Sam68, SS35. Step300, TH4.1, TH4.1, TH4.1, TH4.1, TH4.2, PMR2 COT4 Conclusate 1.31 4.2164 TH58, Four J, Four J, PMR2 AL, IMMRP CJ, ImMRP CJ, ImMRP LJ, ImMRP HL, Im	54441614	F 0 "	1.50	0.405.00	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, KSRP, MBNL1, Nova-1,
CitCle	FAM161A	Exon Cassette	1.58	2.40E-03	Nova-2, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
UDI Ease 1.71 4.21E44 1094.1, No.1, No.1, No.1, No.1, No.2, MoNR 2 FM316A Compte 2.33 2.555.40 FR3, Table PA, Link PP 2, Link PP 1, Link PP 2, Link PP 1, Lin	0.07.4	Complex	1.63	1.63E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SRp30c,
PMU364 Corpus 2.03 2.28824 First, hindle AL, hindle AZ, hindle EL, hindle EL, hindle EL, hindle EL, hindle PL, hindle PC, hindle PL, hindle	CC14	Exon Cassette	1.71	4.21E-04	TDP43, TIA-1, TIAL1, YB-1, ZRANB2
PMIAB Exerc Causale 1.85 5.955/2 First, Exerc (http://www.set/set/set/set/set/set/set/set/set/set/		Complex	2.03	2.58E-04	
PRION Alter. Find Exer (e13) 2.59 2.0766 Find Exer (e14) 2.59 2.0766 Find Exer (e14) 2.59 2.0766 Find Exer (e14) 1.58 3.2067 CODCL42 // MPR53 Alter. Find Exer (e14) 1.58 3.2060 CODE#D: TERS, Find Find PD (L, InRPP CL, InRPP CL, InRPP CL, InRPP CL, InRPP CL, INRPP EL, InRPP CL, INRPP F, INRPP FL, INRPP FL	FAM136A	Exon Cassette	1.85	3.99E-04	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, Nova-2, SC35, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
RNN Aller, Frat Exo (k1) 2.59 2.00 https://rightstand.sci.sci.sci.sci.sci.sci.sci.sci.sci.sci					FTR-3. Fox-1. Fox-2. hnRNP A1. hnRNP C1. hnRNP C1. hnRNP D1. hnRNP F1. hnRNP F2. hnRNP F5. hnRNP H1. hnRNP H2. hnRNP F1 (PTB). hnRNP F (In S). HTra2beta1. HuB. HuD. KSRP. MBN11. Nova-1.
ODCL42 // MRPL3 Alter. Fird Exer (b 4) 1.58 3.00.00 UCLEPT, ETR3, Food, Food PAL, InteRP PAL, InteRP PAL, InteRP PL, I	RTKN	Alter. First Exon (e1)	2.59	2.07E-05	Nova-2, FSF, RBM5, Sam68, SC35, SRo20, SRo30, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
Minute Market Tests Stop Minute Loss	CCDC142 //				CUG-BP1. FTR-3. Fox-1. Fox-2. hnRNP A1. hnRNP A2/B1. hnRNP C1. hnRNP D1. hnRNP D1. hnRNP F2. hnRNP F2. hnRNP F4. hnRNP H1. hnRNP H2. hnRNP J (PTB). hnRNP F4. hnRNP F7. hnRNP F4. hnRNP F4
AllPI Intro. Retrotom 169 8.65/C4 TFR3. shmRP1 (PTR), homP P (TG), KEPP, Max (SMS, SSGS, SMS, CD, TAJ, TML), YMS, ZMARG SNRP200 Exerc Stateth 173 6.79/C4 ETR3. shmRP1, IntRNP P (TG), KEPP, Max (SMR, SGSS, SMS, CD, TAJ, TML), YMS, ZMARG ANR0368 Exer Casceth 152 2.28/C3 Max (TW, YMS, ZMR, SWR, SWR, SWR, SWR, SWR, SWR, SWR, SW	MRPI 53	Alter. First Exon (e1-8)	1.58	3.20E-03	KSRP, MBNI I, Nova-1, Nova-2, PSE, Sam68, SC35, SE1, SRo20, SRo30c, TDP43, TIA-1, TIA-1, TRANB2
SNRMP 200 Exon Cassette 1.7.3 6.79E-04 Strong 201 Strong 201 InstRP 21, InstRP 12, I	AUP1	Intron Retention	1.69	8.63E-04	ETR-3, hnRNP / (PTB), hnRNP P (TLS), KSRP, Nova-1, RBM5, SC35, SRo20, TIA-1, TIAL1, YB-1, ZRANB2
SNRP200 Exerc Cassette 1.73 6.79E-04 Stypp:0; That, 1.191, 1.201, 22AH22 ANG036B Exerc Cassette 1.52 2.28E-03 Stypp:0; That, 1.191, 22AH22 Concentration Stype:0; Stypp:0; That, 1.101, 1.191, 22AH22 CMG036B Exerc Cassette 3.27 1.58E-05 Stype:0; That, 1.1002, 1.196 Stype:0; That, 1.1002, 1.196 Stype:0; That, 1.1002, 1.196 Stype:0; That, 1.1002, 1.196 Stype:0; Stype					TR3. bnRNP 41 bnRNP 42/R1 bnRNP C1 bnRNP C1 bnRNP F1 bnRNP F2 bnRNP F1 bnRNP H1 bnRNP H2 bnRNP L(PTR) bnRNP P(TLS) HTra2beta1 HuB KSRP MRN11 Nova-1 PSE Sam68 SC35 SRn20
ANK0036B Exon Cassette 1.52 2.28E.03 963. C10.68P1. [TR3.1 col., 1 froz.1, col., 1 froz.1, col., 1 froz.1, 2 col., 1 froz.1, 2 col., 2 mbW 2, 1 mb	SNRNP200	Exon Cassette	1.73	6.79E-04	SR030C TIA-1 TIAI 1 YR-1 / ZRANB2
ANKRO368 Exon Cassette 1.52 2.286.03 MMNL I hosa J. Home?, PFC RBMS 2005, SPJ 527.485, SR02, SPb 2005, DPb 32, The J. Tue					9(3) CILCRP1 FTR3 Fox1 Fox2 hoRNP 41 hoRNP 42/R1 hoRNP C1 hoRNP C1 hoRNP F1 hoRNP F2 hoRNP F2 hoRNP F1 hoRNP H2 hoRNP H2 hoRNP F(PTR) hoRNP F(PTR) hoRNP F(PTR) hoRNP F(PTR) hoRNP F(PTR) hoRNP F(PTR) hoRNP F1 hoRNP F1 hoRNP F2 hoRNP F2 hoRNP F2 hoRNP F1 hoRNP F1 hoRNP F1 hoRNP F1 hoRNP F1 hoRNP F2 hoRNP F1 hO
CLASP1 Exm Castellin 3.37 1 69:E02 036; ETR3, Fea1, Fea2, FindPl AL, InRRP A2[1, InRRP D1, InRRP D1, InRRP D2, InRRP E1, INRRP E2, INRRP E1, INRRP E1, INRRP E2, INRRP E1, INRR	ANKRD36B	Exon Cassette	1.52	2.28E-03	MBN 1, Nova-2, PSE, RBM5, Sam68, SC35, SF1, SF2/ASE, SRo20, SRo30c, TDP43, TIA-1, TIA1, YR-1, ZRANR2
OL(SP1 Mutualy Exclusive Exons 4.88 1.69E-05 HuB, HuO, KSPP, MBNL1, Nova, J, Nova, PEF, Sam68, S235, SF1, SR200, SR309, TDP43, THA1, THA1, TVB1, ZAM82 BIN1 Exon Cassette 1.84 1.04E-03 COUGEPT, ETR3, Fou, I, Fou, 2, mRNP A1, ImRNP P Z1, ImRNP F Z1, ImRNP F, I		Exon Cassette	3.97	1.69F-05	9G8 FTR-3 For-1 For-2 hor-2 ho
BIN1 Exon Cassette 1.42 COUGP1 ETR3, Fast, Fas	CLASP1	Mutualy Exclusive Exons	4 88	1 69F-05	HuB, HuD, KSRP, MBN11, Nova-1, Nova-2, PSE, Sam68, SC35, SF1, SRo20, SRo30c, TDP43, TIA-1, TIA11, VR-1, ZRANB2
BIN1 Exon Cassette 1.84 1.04 55b20 Stp302. TDP31 TML1, YB1, ZPANB2 ERC03 Intron Relation 1.70 1.7663 ETR3, INNPP F, INRPP LI, PTBJ, Hull, YB1, ZPANB2 CACM84 Alter. Termin Exon (12:15,e)77 1.62 1.02623 CusPSP Link, Tink P L, InRNP F, InRNP LI, InRNP F, InRNP LI, InRNP F, InRNP F, InRNP FL, INRNP F		Indiana Elononio Elono		11002.00	CIICREPTETES For 1 For 2 horRNP 41 horRNP 47(81 horRNP F1 horRNP F2 horRNP F1 horRNP H2 horRNP H2 horRNP H2 horRNP H2 horRNP F1 (F1 horRNP F2 horR
ERCC3 Intron Retention 1.70 1.76(-0.3 ETR3, horRNP F, hmRNP H1, hmRNP 42, hmRNP Q1, hmRNP Q2, BandB, SC35, SE35, SC15, SC25, SC15, SC20, SC20, TA1, TAL1, YE1, ZANHB2 CACNB4 Alter, Termin Econ (e12-15,e17) 1.62 1.02620 CUG_BP1, ETR3, Fox1, Fox2, hmRNP A, hmRNP Q2,B1, hmRNP Q1, hmRNP Q2,B1, hmRNP L, hmRNP H2, hmRNP H1, hmRNP H2, hmRNP H1, hmRNP H2, hmRNP I (PTB), hmRNP L1, hmRNP 1, YE1, ZANHB2 PRPF40A Econ Cassette 3.71 9.84E-05 ETR3, Fox1, Fox2, hmRNP A, hmRNP Q2/B1, hmRNP C1, hmRNP E1, hmRNP E2, hmRNP F1, hmRNP H1, hmRNP H1, fmRNP M2, MBL1, Nova-1, Sam6B, SC35, SF1, SF2/ASF, SR620, STA02, TTN1, TAL1, YE1, ZANHB2 BA22B Complex 1.58 2.39E-02 ETR3, Fox1, Fox2, hmRNP A, hmRNP Q2/B1, hmRNP C1, hmRNP E1, hmRNP E2, hmRNP F1, hmRNP H1, hmRNP H1, hmRNP H1, hmRNP H2, hmRNP P (TLS), HTra2beta1, HuB, KSCP, MBL11, Nova-1, Nova-2, Sam6B, SC35, SF1, SF2/ASF, SR620, STA02, TLA1, TAL1, YE1, ZAMHB2 KCNH7 Alter, Terminal Econ (e1-019) 3.18 1.63E-05 968, CUG4P1, ETR3, Fox1, Fox2, hmRNP A, ImRNP A2/B1, hmRNP C1, hmRNP E2, hmRNP F1, hmRNP H1, hmRNP H2, hmRNP H1, ImRNP H2, hmRNP H1, ImRNP H2, ImRNP F1, ImRNP H1, hmRNP H2, ImRNP F1, ImRNP H1, hmRNP H2, ImRNP F1, ImRNP H2, ImRNP F1, ImRNP H2, ImRNP F1, ImRNP H2, ImRNP F1, ImRNP H2, ImRNP H1, ImRNP H2, ImRNP F1, ImRNP H2, ImRNP F1, ImRNP F1, ImRNP F3, SS5, SS5, SS5, SS5, SS5, SS5, SS5, SS	BIN1	Exon Cassette	1.84	1.04E-03	SRo20, SRo30, TDP43, TIA-1, TIA-1, YB-1, ZRAMP2
Alter. Termina Exon (e12-15.e17) 1.62 1.02E02 CUG BPI, ETR3, Fox1, Fox2, hnRNP A1, hnRNP A2, B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP E1, hnRNP E1, hnRNP E2, hnRNP E1, hnRNP	FRCC3	Intron Retention	1.70	1.76F-03	FTR-3, bnRNP FL, bnRNP H2, bnRNP H2, bnRNP I (PTB), HuB, MRNI 1, Nova-2, Sam68, SC35, SRb30c, TIA-1, TIA 1, YB-1, ZRANB2
CACINE4 Exon Cassette 1.70 5.64E03 HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30e, TA-1, TAL1, YB-1, ZRANB2 PRPF40A Exon Cassette 3.71 9.84E05 ETR3, Toral, Torac, Jank Z/alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30e, TA-1, TAL1, YB-1, ZRANB2 BAZ2B Complex 1.58 2.39E02 ETR3, Toral, Torac, Jank Z/alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, SST, MSP Z, ST, SPS Z, ST, SP		Alter Termin Exon (e12-15 e17)	1.62	1 02F-02	CIG-RPI FTR-3 Fox-1 Fox-2 hnRNP A1 hnRNP A2/B1 hnRNP C1 hnRNP C1 hnRNP C1 hnRNP C1 hnRNP F2 hnRNP F2 hnRNP F4 hnRNP F4 hnRNP H3 hnRNP H3 hnRNP H3 hnRNP H3 hnRNP H4
PRP40A Exon Cassette 3.71 9.84E05 ETR3, Fox, 1, Fox2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP P42, hnRNP P (TLS), HTra2abta1, HuB, HuD, MBNL1, Nova-1, Sam68, SC35, SF1 BA22B Complex 1.58 2.39E02 ETR3, Fox1, Fox2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP P42, hnRNP P (TLS), HTra2abta1, HuB, KSP, MBNL1, Nova-1, Sam68, SC35, SF1 KCNH7 Alter. Terminal Exon (e10-19) 3.18 1.65E05 968, CUG4P1, ETR3, Fox1, Fox2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP H1, hnRNP H2, hnRNP H1, hnRNP H2, hnRNP H1, hnRNP H2, hnRNP F1, hnRNP F2, hnRNP F1, h	CACNB4	Exon Cassette	1.70	5.64E-03	Hrazaloha Hirazheta Huß Huß KSRP MENI Nova-2 PSE REMS Sam68 SC35 SF1 SF2/ASE SRo20 SRo30c TIA 1 TIA11 YR-1 ZRANR2
PRPF40A Exon Cassette 3.71 9.84E.05 SRp200, TIAL, TIAL, YBJ, ZRANB2 BA22B Complex 1.58 2.39E.02 ETR3, Fox1, Fox2, honRVP A1, hnRNP A2/B1, hnRNP C1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP F,			1.70	0101200	TR3. FOX, ENDPAID https://www.inter.inte
BAZ2B Complex 1.58 2.39E02 EfR3, Fox1, Fox2, InRNP A1, InRNP A2/B1, InRNP A2/B1, InRNP A2/B1, InRNP E2, InRNP F, InRNP H1, InRNP H2, InRNP P1, InRNP P2, InRNP F1, InRNP A2/B1, INRNP A2/B1	PRPF40A	Exon Cassette	3.71	9.84E-05	SR-20 TIAL TIAL 178-1 7 PANRS
BAZ2B Complex 1.58 2.39E02 Stands, SC35, SF1, SRp30c, TA-J, TIAL, YE1, ZARAB2 Common Commo					TR3. Fxv2 hoRNP &1 hoRNP &2/B1 hoRNP C1 hoRNP C1 hoRNP F2 hoRNP F2 hoRNP F1 hoRNP H1 hoRNP H2 hoRNP H2 hoRNP [/PTR) hoRNP P (TIS) HTra2aloha HTra2hotal HuR KSRP MBNI 1 Nova-1 Nova-2
KCNH7 Alter. Terminal Exon (e10-19) 3.18 1.63E-05 968, CUG-BP1, ETR-3, Fox-1, Fox-2, InRNP A1, InRNP A2/B1, InRNP C1, InRNP D, InRNP D, InRNP E1, InRNP E2, InRNP F, InRNP H1, InRNP H2, INRNP H1,	BAZ2B	Complex	1.58	2.39E-02	Sam68, SC35, SF1, SR030c, TIA-1, TIA1 1, YB-1, ZRANB2
KCNH7 Alter. Terminal Exon (e10-19) 3.18 1.63E05 (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 LRP2 Alter. First Exon (e1-50) 2.19 7.98E04 968, OUG-BP1, ETR-3, Fox-1, Fox-2, InRNP A1, InRNP P A2, IB1, InRNP P C1, InRNP E1, InRNP E2, INRNP F, IN					9G8. CUG-RP1 FTR-3, Fox-1, Fox-2, bnRNP A1, bnRNP A2/B1, bnRNP C1, bnRNP D, bnRNP D1, bnRNP F1, bnRNP F2, bnRNP F1, bnRNP H2, bnRNP H2, bnRNP H3, bnRNP H2, bnRNP K, bnRNP H4, bnRNP F2, bnRNP H4, b
LRP2 Alter. First Exon (e1-50) 2.19 7.98E-04 9G8, CUG-BP1, ETR-3, Fox1, Fox2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP D, hnRNP P,	KCNH7	Alter. Terminal Exon (e10-19)	3.18	1.63E-05	(TLS). HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBN11, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIA11, YB-1, ZRANR2
LRP2 Alter. First Exon (e1-50) 2.19 7.98E-04 HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 GPR155 Exon Cassette 2.49 2.63E-04 ETR3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-2, Sma68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 ATF2 Alter. Terminal Exon (e9) 1.75 4.59E-04 968, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E2, hnRNP F, hnRNP F1, hnRNP F2, hnRNP H1, hnRNP F2, hnRNP F1, hnRN					9G8. CUG-BP1. FTR-3. Fox-1. Fox-2. hoRNP A1. hnRNP A2/B1. hnRNP C1. hnRNP C1. hnRNP D1. hnRNP F1. hnRNP F2. hnRNP F5. hnRNP F1. hnRNP F4. hnRNP F4
GPR155 Exon Cassette 2.49 2.63E-04 ETR3, Fox1, Fox2, InRNP A1, InRNP A2/B1, InRNP C1, InRNP E1, InRNP E2, InRNP F, InRNP H1, InRNP H2, InRNP F, IN	LRP2	Alter. First Exon (e1-50)	2.19	7.98E-04	HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRo20, SRo30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
GPR155Exon Cassette2.492.63E-04Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2ATF2Alter. Terminal Exon (e9)1.754.59E-04968, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H2, hnRNP H3, hnRNP P (TLS), HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2PRKRAExon Cassette2.972.42E-05HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2ORMDL1Intron Retention1.772.86E-03ETR-3, hnRNP A1, hnRNP C1, hnRNP C1, hnRNP P (TLS), HUB, MBNL1, Nova-1, SRp20, TIA-1, TIAL1, YB-1PGAP1Exon Cassette1.778.20E-04CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP F, hnRNP H1, hnRNP A2/B1, hnRNP A2/B1, hnRNP A2/B1, hnRNP A2/B1, hnRNP A2/B1, hnRNP C1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP F, fnRNP H1, hnRNP P, fnRNP H1, hnRNP P, fnRNP H1, hnRNP A2/B1, hnRNP C1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP C1, hnRNP F, hnRNP F, hnRNP H1, hnRNP H2, hnRNP F, fnRNP H1, hnRNP F, fnRNP H1, hnRNP F, fnRNP H1, hnRNP F, fnRNP H1, hnRNP F, fnRNP F, fnRNP H1, hnRNP F, fnRNP H1, hnRNP F, fnRNP F, fnRNP F, fnRNP H1, hnRNP F, fnRNP					FTR-3. Fox-1. Fox-2. hnRNP A1. hnRNP A2/B1. hnRNP C1. hnRNP F1. hnRNP F2. hnRNP F2. hnRNP H1. hnRNP H2. hnRNP H2. hnRNP H2. hnRNP K. hnRNP K. hnRNP P. (TI S). HTra2beta1. HuB. HuD. KSRP. MBN 11. Nova-1. Nova-2.
Atter. Terminal Exon (e9) 1.75 4.59E-04 968, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP H3, hnRNP H2, hnRNP H2, hnRNP H2, hnRNP H3, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 PRKRA Exon Cassette 2.27 2.16E-03 ETR-3, hnRNP A1, hnRNP C1, hnRNP D, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Sam68, SC35, SF1, TIA-1, TIAL1, YB-1 ORMDL1 Intron Retention 1.77 2.86E-03 ETR-3, hnRNP C1, hnRNP I (PTB), hnRNP C1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H1, hnRNP H2, hnRNP H1, hnRNP H2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP F, hnRNP H1, hnRNP A2/B1, hnRNP C1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E1, hnRNP E1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP F, hnRNP H1, hnRNP A2/B1, hnRNP C1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP F, fnRNP H1, hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SF1, SF2, SR20, SR30c, TIA-1, TIAL1, YB-1 ORMDL1 Alter. Acceptor Site 1.93 6.56E-03 G8, ETR-3, fox-1, fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, SSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SR20, SR30c, TIA-1, TIAL1, YB-1, ZRANB2 CLK1 // PPIL3	GPR155	Exon Cassette	2.49	2.63E-04	Sam68, SC35, SF1, SF2/ASF, SRo20, SRo30c, TIA-1, TIA-1, YB-1, ZRANB2
ATF2 Exon Cassette 2.97 2.42E05 HuD, HuR, KSRP, MBNL1, Nova-1, Rova-2, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 PRKRA Exon Cassette 2.27 2.16E03 ETR-3, InRNP C1, InRNP C1, InRNP C1, InRNP E2, InRNP F, InRNP H2, InRNP H2, InRNP F, InRNP H2, InRNP F, InRNP F, InRNP H1, InRNP P, TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Sam68, SC35, SF1, TIA-1, TIAL1, YB-1 ORMDL1 Intron Retention 1.77 2.86E03 ETR-3, InRNP C1, InRNP P (TLS), HuB, MBNL1, Nova-1, SRp20, TIA-1, TIAL1, YB-1 PGAP1 Exon Cassette 1.77 8.20E04 CUGBP1, ETR-3, Fox-2, InRNP A1, InRNP A2/B1, InRNP C1, InRNP D, InRNP E1, InRNP E1, InRNP E2, InRNP F, InRNP H1, InRNP H2, InRNP F, INRNP H1, INRNP K, InRNP F, MNL1, Nova-1, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1 CLK1 // PPIL3 Atter. Acceptor Site 1.93 6.56E03 Atter. First Exon (e1-3,5-8,10-11) 1.82 7.01E04 Sea ETR-3, Fox-1, Fox-2, InRNP A2/B1, InRNP C1, InRNP D, InRNP D, InRNP E1, InRNP E1, INRNP F, INRNP H1, INRNP H2, InRNP F, INRNP H1, INRNP K, INRNP F (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, Sen SRB, SC35, SF1, SP20, SR30c, TIA-1, TIAL1, YB-1, ZRANB2 ALS2 Alter. Terminal Exon (e23) 1.55 3.68E03 PG8, CUG-BP1, ETR-3, Fox-1, Fox-2, INRNP A2, INRNP A2, HINRNP C1, INRNP D1, INRNP E1, INRNP E1, INRNP E1, INRNP F2, INRNP F, INRNP F, INRNP H1, INRNP H2, INRNP F, INRNP F, IN		Alter, Terminal Exon (e9)	1.75	4.59F-04	9G8. CLIG-BP1. FTR-3. Exx-1. Exx-2. hnRNP A1. hnRNP A2/B1. hnRNP C1. hnRNP D. hnRNP F1. hnRNP F2. hnRNP F. hnRNP H1. hnRNP H2. hnRNP H3. hnRNP H (PTB). hnRNP K. hnRNP P (TLS). HTra2beta1. HuB.
PRKRA Exon Cassette 2.17 2.16E-03 ETR-3, hnRNP A1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP I(PTB), hnRNP F, fnRNP I(PTB), hnRNP F, fnRNP I(PTB), hnRNP F, fnRNP F, fnR	ATF2	Exon Cassette	2.97	2.42F-05	HuD, HuR, KSRP. MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
PRKRA Exon Cassette 2.27 2.16E03 TIAL1, YB-1, ZRANB2 ORMDL1 Intron Retention 1.77 2.86E03 ETR-3, hnRNP C1, hnRNP P (TLS), HuB, MBNL1, Nova-1, SRp20, TIA-1, TIAL1, YB-1 PGAP1 Exon Cassette 1.77 2.86E03 ETR-3, hnRNP C1, hnRNP P (TLS), HuB, MBNL1, Nova-1, SRp20, TIA-1, TIAL1, YB-1 PGAP1 Exon Cassette 1.77 8.20E04 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP F, hnRNP F, hnRNP H1, hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 CLK1 // PPIL3 Alter. Acceptor Site 1.93 6.56E03 Alter. First Exon (e1-3,5-8,10-11) 1.82 7.01E04 968, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP E1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 ALS2 Alter. Terminal Exon (e23) 1.55 3.68E03 968, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A2/B1, hnRNP A2/B1, hnRNP C1, hnRNP D1, hnRNP E1, hnRNP E2, hnRNP F1, hnRNP H2, hnRNP H1, hnRNP K, hnRNP P (TLS), HTra2alpha, HUB, HuB, HUB, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sm68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 ALS2 Alter					FTR-3 bnRNP A1 bnRNP C1 bnRNP D bnRNP F1 bnRNP F2 bnRNP F1 bnRNP H1 bnRNP H2 bnRNP L(PTR) bnRNP K bnRNP P (TLS) HTra2beta1 HuR HuD KSRP MRNL1 Nova-1 Sam68 SC35 SE1 TLA-1
ORMDL1 Intron Retention 1.77 2.86E03 ETR-3, hnRNP C1, hnRNP I (PTB), hnRNP P (TLS), HuB, MBNL1, Nova-1, SRp20, TIA-1, TIAL1, YB-1 PGAP1 Exon Cassette 1.77 8.20E04 CUG-BP1, ETR-3, Fox.1, Fox.2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP F2, hnRNP F1, hnRNP F2, hnRNP F2, hnRNP F2, hnRNP F2, hnRNP F2, hnRNP	PRKRA	Exon Cassette	2.27	2.16E-03	TIAL1, YB-1, ZRANB2
PGAP1 Exon Cassette 1.77 8.20E-04 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/91, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 CLK1 // PPIL3 Alter. Acceptor Site 1.93 6.56E-03 968, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/91, hnRNP C1, hnRNP D, hnRNP D, hnRNP E1, hnRNP E2, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-2, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 CLK1 // PPIL3 Alter. First Exon (e1-3,5-8,10-11) 1.82 7.01E-04 968, ETR-3, Fox-1, Fox-2, hnRNP A2/91, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 ALS2 Alter. Terminal Exon (e23) 1.55 3.68E-03 968, CUG-BP1, ETR-3, Fox-1, Fox-2, nRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP F, hnRNP H1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP F, hnRNP H1, hnRNP F, hnRNP H2, hnRNP F, hnRNP F, hnRNP H2, hnRNP F, hnRNP F, hnRNP H2, hnRNP F, hnRNP	ORMDL1	Intron Retention	1.77	2.86E-03	ETR-3, hnRNP C1, hnRNP I (PTB), hnRNP P (TLS), HuB, MBNL1, Nova-1, SRp20, TIA-1, TIAL1, YB-1
PGAP1 Exon Cassette 1.77 8.20E-04 MBNL1, Nova-1, Nova-2, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 CLK1 // PPIL3 Alter. Acceptor Site 1.93 6.56E-03 9G8, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP D, hnRNP D, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F1, hnRNP H2, hnRNP I, PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuB, HuB, HuB, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 Alter. Terminal Exon (e23) 1.55 3.68E-03 9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A2/B1, hnRNP A2/B1, hnRNP D, hnRNP D, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F1, hnRNP H2, hnRNP H1, hnRNP F2, hnRNP F1, hnRNP F2, hnRNP		5			CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1. HuB. HuD. KSRP
Alter. Acceptor Site 1.93 6.56E03 CLK1 // PPIL3 Alter. Acceptor Site 1.93 6.56E03 Alter. First Exon (e1-3,5-8,10-11) 1.82 7.01E-04 Intron Retention 1.98 4.42E03 Alter. Terminal Exon (e23) 1.55 3.68E-03 Alter. Terminal Exon (e23) 1.55 3.68E-03	PGAP1	Exon Cassette	1.77	8.20E-04	MBNL1, Nova-1, Nova-2, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
CLK1 // PPIL3 Alter. First Exon (e1-3,5-8,10-11) 1.82 7.01E04 968. ETR-3, Fox-1, Fox-2, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP D, hnRNP D, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I, hnRNP F, hnRNP H1, hnRNP H2, hnRNP F, hnRNP H1, hnRNP K, hnRNP F, KnRNP F, HTR-2alpha, HTra2alpha,		Alter, Acceptor Site	1.93	6.56E-03	
Intron Retention 1.98 4.42E-03 HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 ALS2 Alter. Terminal Exon (e23) 1.55 3.68E-03 9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP DL, hnRNP E1, hnRNP E1, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP H1, hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2	CLK1 // PPIL3	Alter. First Exon (e1-3.5-8.10-11)	1.82	7.01E-04	908, ETR-3, Fox-1, hox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP B1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (TES), HTra2alpha, HTra2beta1,
ALS2 Alter. Terminal Exon (e23) 1.55 3.68E-03 9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP D1, hnRNP E1, hnRNP E1, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP H2, hnRNP F, hnRNP H2, hnRNP F, hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2	,,	Intron Retention	1.98	4.42E-03	Hub, Hub, HuR, KSRP, MBINLI, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
ALS2 Atter. Terminal Exon (e23) 1.55 3.68E-03 HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, VB-1, ZRANB2					968. CLIG-RP1, FTR-3, Fox-1, Fox-2, bnRNP A1, bnRNP A2/B1, bnRNP C1, bnRNP D, bnRNP D1, bnRNP F1, bnRNP F2, bnRNP F4, bnRNP H1, bnRNP H2, bnRNP H2, bnRNP K, bnRNP P (TLS), HTra2alnba
	ALS2	Alter. Terminal Exon (e23)	1.55	3.68E-03	HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2

ABCA12	Exon Cassette	1.68	6.20E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
OBSL1	Alter. Terminal Exon (e9)	1.57	7.76E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
PAX3	Alter. Term Exon (e6-8,e10-11)	1.75	8.84E-03	9G8, CUG-BP1, ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP DL, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNI 1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAI 1, YB-1, ZRANB2
FARSB	Exon Cassette	1.68	4.39E-04	ETR-3, Fox-1, Fox-2, InRNP A1, InRNP A2/B1, InRNP C1, InRNP C1, INRNP E1, INRNP E2, INRNP F2, INRNP F1, INRNP H1, INRNP H2, INRNP F, INRNP F, INRNP F1, INRNP F4, INRN
DOCK10	Exon Cassette	2.08	2.81E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1
NDUFA10	Intron Retention	1.87	2.45E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
SEC23B	Complex	1.57	1.16E-03	ETR-3, hnRNP A1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
EPB41L1	Alter. First Exon (e3-6)	1.53	2.50E-02	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F2, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha,
	Complex (e3-7,e9)	2.21	1.44E-04	HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
SRSF6	Exon Cassette	2.23	4.93E-06	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP I (PTB), hnRNP P (TLS), HuB, KSRP, Nova-1, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
STK4	Alter. Terminal Exon (e2,e10)	1.52	8.16E-03	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H, hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
PCIF1	Intron Retention	1.54	6.13E-05	hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, SC35, SRp30c, YB-1
ARFGEF2	Exon Cassette	1.53	7.28E-03	ETR-3, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP I (PTB), hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SF1, SRp20, TIA-1, TIAL1, YB-1, ZRANB2
DDX27	Intron Retention	1.56	2.48E-02	ETR-3, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Sam68, SC35, SRp30c, YB-1
ZFAS1	Exon Cassette	2.79	4.80E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
NELECD	Alter. Donor Site	1.74	8.60E-04	FTR-3 Fox-1 Fox-2 hoRNP A1 hoRNP A2/R1 hoRNP C1 hoRNP C1 hoRNP H1 hoRNP H2 hoRNP I (PTR) hoRNP P (TIS) HTra2heta1 HuR KSRP MRNI 1 Nova-1 Nova-2 PSE SC35 YR-1 ZRANR2
	Intron Retention	2.15	3.57E-04	
	Alter. Acceptor Site	1.83	5.02E-03	CUG-RP1, FTR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP D1, hnRNP F2, hnRNP F2, hnRNP F4, hnRNP H2, hnRNP H2, hnRNP F4, hnRNP F4, hnRNP P(TLS), hnRNP P(TLS), HTra2alpha, HTra2
LSM14B	Alter. Terminal Exon (e6)	1.97	5.44E-03	HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
	Exon Cassette	2.01	1.62E-03	
ADEOAD1		1 60	C 005 04	ETD 3 & DND 41 & DND 61 & DND 111 & DND 110 & DND 110 D DND 1100 U DND 0035 VD 1
ARFGAP1	Intron Retention	1.62	6.96E-04	ETR3, hnRNP A1, hnRNP C1, hnRNP F1, hnRNP F1, hnRNP 1(FTB), hnRNP F1 (FTB), KSRP, SC35, YB-1
ARFGAP1 TCEA2	Intron Retention Complex	1.62 1.72	6.96E-04 5.22E-03	ETR-3, hnRNP A1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H(PTB), hnRNP P (TLS), HuB, KSRP, SC35, YB-1 ETR-3, Fox1, Fox2, hnRNP A1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H(PTB), hnRNP F, hnRNP P (TLS), HuB, HuD, KSRP, Nova-1, Nova-2, RBM5, Sam68, SC35, SC2/ASE_SCA2_SCA2_DTLA_TIA1_YB_1_ZBANP2
ARFGAP1 TCEA2	Intron Retention Complex Intron Retention	1.62 1.72 2.22 2.70	6.96E-04 5.22E-03 1.82E-05	ETR-3, hnRNP A1, hnRNP C1, hnRNP F1, hnRNP H2, hnRNP H2, hnRNP H2, hnRNP P (TLS), HuB, KSRP, SC35, YB-1 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H(PTB), hnRNP F (TLS), HuB, HuD, KSRP, Nova-1, Nova-2, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
ARFGAP1 TCEA2 LINC00266- 1/MYT1/PCMTD	Intron Retention Complex Intron Retention Alter. Terminal Exon (e21-25) Exon Cassette	1.62 1.72 2.22 2.70 2.44	6.96E-04 5.22E-03 1.82E-05 3.51E-05 4.01E-06	ETR-3, hnRNP A1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP P (TLS), HuB, KSRP, SC35, YB-1 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H (PTB), hnRNP P (TLS), HuB, HuD, KSRP, Nova-1, Nova-2, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP D1, hnRNP E1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP H2, hnRNP H2, hnRNP F, hnRNP H2, hnRNP F, hnRNP F, hnRNP H2, hnRNP F, hnRNP H2, hnRNP F, hnRNP H2, hnRNP F, hnRNP H2, hnRNP F, hnRNP F, hnRNP F, hnRNP H2, hnRNP F, hnRNP F, hnRNP F, hnRNP H2, hnRNP F, hnRNP F, hnRNP H2, hnRNP F, hnR
ARFGAP1 TCEA2 LINC00266- 1/MYT1/PCMTD TBC1D20	Intron Retention Complex Intron Retention Alter. Terminal Exon (e21-25) Exon Cassette Intron Retention	1.62 1.72 2.22 2.70 2.44 1.99	6.96E-04 5.22E-03 1.82E-05 3.51E-05 4.01E-06 6.86E-03	ETR-3, hnRNP A1, hnRNP C1, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HuB, KSRP, SC35, YB-1 ETR-3, Fow.1, Fox-2, hnRNP A1, hnRNP C1, hnRNP DL, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HuB, HuD, KSRP, Nova-1, Nova-2, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRAMB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP F (TLS), HuB, HuD, KSRP, Nova-1, Nova-2, RBM5, Sam68, SC35, SF2/ASF, SRp30c, TIA-1, TIAL1, YB-1, ZRAMB2 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP P, hnRNP D, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H2, hnRNP H2, hnRNP F, NOVa-2, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRAMB2 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP F, hnRNP H2, hnRNP H2, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRAMB2
ARFGAP1 TCEA2 LINC00266- 1/MYT1/PCMTD TBC1D20 SNRPB	Intron Retention Complex Intron Retention Alter. Terminal Exon (e21-25) Exon Cassette Intron Retention Exon Cassette	1.62 1.72 2.22 2.70 2.44 1.99 2.20	6.96E-04 5.22E-03 1.82E-05 3.51E-05 4.01E-06 6.86E-03 4.22E-04	ETR-3, hnRNP A1, hnRNP C1, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HuB, KSRP, SC35, YB-1 ETR-3, Fox1, Fox2, hnRNP A1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HuB, HuD, KSRP, Nova-1, Nova-2, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP F, hnRNP H2, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP F, hnRNP H2, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
ARFGAP1 TCEA2 LINC00266- 1/MYT1/PCMTD TBC1D20 SNRPB IDH3B	Intron Retention Complex Intron Retention Alter. Terminal Exon (e21-25) Exon Cassette Intron Retention Exon Cassette Intron Retention	1.62 1.72 2.22 2.70 2.44 1.99 2.20 1.80	6.96E-04 5.22E-03 1.82E-05 3.51E-05 4.01E-06 6.86E-03 4.22E-04 1.20E-02	ETR-3, hnRNP A1, hnRNP C1, hnRNP F1, hnRNP H2, hnRNP H2, hnRNP P (TLS), HuB, KSRP, SC35, YB-1 ETR-3, Fox-1, Fox-2, hnRNP C1, hnRNP C1, hnRNP C1, hnRNP E2, hnRNP F, hnRNP F1, hnRNP H2, hnRNP H2, hnRNP H(PTB), hnRNP K, hnRNP P (TLS), HuB, HuD, KSRP, Nova-1, Nova-2, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP F, hnRNP H1, hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP F, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-2, PSF, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-2, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HUB, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, hnRNP E1, hnRNP A2/B1, hnRNP C1, hnRNP F, H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HUB, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, TRAL1, YB-1, INRNP E1, hnRNP E
ARFGAP1 TCEA2 LINC00266- 1/MYT1/PCMTD TBC1D20 SNRPB IDH3B CPYM1	Intron Retention Complex Intron Retention Alter. Terminal Exon (e21-25) Exon Cassette Intron Retention Exon Cassette Intron Retention	1.62 1.72 2.22 2.70 2.44 1.99 2.20 1.80 2.73	6.96E-04 5.22E-03 1.82E-05 3.51E-05 4.01E-06 6.86E-03 4.22E-04 1.20E-02 9.39E.04	ETR-3, hnRNP A1, hnRNP C1, hnRNP F1, hnRNP H2, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HuB, KSRP, SC35, YB-1 ETR-3, Fox-1, Fox-2, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HuB, HuD, KSRP, Nova-1, Nova-2, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP F (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-1, Fox-2, hnRNP A2/B1, hnRNP C1, hnRNP F1, hnRNP H2, hnRNP H2, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP P (TLS), HUB, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, hnRNP E1, hnRNP E2, hnRNP F (ITS), HuB, KSRP, MBNL1, SC35, TIA-1, TIAL1, YB-1 ETR-3, hnRNP E1, hnRNP E40, hnRNP F (TLS), HuB, KSRP, MBNL1, SC35, TIA-1, TIAL1, YB-1 ETR-3, hnRNP E1, hnRNP E40, hnRNP F (TIS), MBNL1, Nova-1, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1
ARFGAP1 TCEA2 LINC00266- 1/MYT1/PCMTD TBC1D20 SNRPB IDH3B CPXM1 PCED1A	Intron Retention Complex Intron Retention Alter. Terminal Exon (e21-25) Exon Cassette Intron Retention Exon Cassette Intron Retention Complex Intron Retention	1.62 1.72 2.22 2.70 2.44 1.99 2.20 1.80 2.73 2.11	6.96E-04 5.22E-03 1.82E-05 3.51E-05 4.01E-06 6.86E-03 4.22E-04 1.20E-02 9.39E-04 3.24E-03	ETR-3, hnRNP C1, hnRNP F1, hnRNP F1, hnRNP F1, hnRNP F1, hnRNP F2, hnRNP F (TLS), HuB, KSRP, SC35, YB-1 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HuB, HuD, KSRP, Nova-1, Nova-2, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP H2, hnRNP H2, hnRNP H2, hnRNP F, hnRNP H1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP D, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP F2, hnRNP F, hnRNP H1, hnRNP F2, hnRNP F, hnRNP H1, hnRNP C1, hnRNP F1, hnRNP F2, hnRNP F1, hnRNP F1, F0x-2, hnRNP A1, hnRNP F1, hnRNP F1, hnRNP H2, hnRNP H3, hnRNP F (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-2, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HUB, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1 ETR-3, hnRNP E1, hnRNP E2, hnRNP F (TLS), HuB, KSRP, MBNL1, SC35, TIA-1, TIAL1, YB-1 ETR-3, hnRNP A1, hnRNP F1, hnRNP P (TLS), HuB, KSRP, MBNL1, SC35, SRp20, SRp30c, YB-1 ETR-3, hnRNP A1, hnRNP F1, hnRNP P (TLS), MBNL1, Nova-1, BRM5, SRp30c,
ARFGAP1 TCEA2 LINC00266- 1/MYT1/PCMTD TBC1D20 SNRPB IDH3B CPXM1 PCED1A SIC4A11	Intron Retention Complex Intron Retention Alter. Terminal Exon (e21-25) Exon Cassette Intron Retention Exon Cassette Intron Retention Complex Intron Retention Alter. Accentor Site	1.62 1.72 2.22 2.70 2.44 1.99 2.20 1.80 2.73 2.11 1.76	6.96E-04 5.22E-03 1.82E-05 3.51E-05 4.01E-06 6.86E-03 4.22E-04 1.20E-02 9.39E-04 3.24E-03 1.83E-04	ETR-3, hnRNP A1, hnRNP C1, hnRNP F1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HuB, KSRP, SC35, YB-1 ETR-3, Fow.1, Fow.2, hnRNP A1, hnRNP C1, hnRNP DL, hnRNP DL, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP F, thRNP P (TLS), HuB, KSRP, Nova-1, Nova-2, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, Fow-1, Fow-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP H2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP F (TLS), HUB, KSRP, MBNL1, Nova-2, Sam68, SC35, SF2/ASF, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fow.1, Fow.2, hnRNP A1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, fow.1, Fow.2, hnRNP A1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HUB, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1 ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HUB, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1 ETR-3, hnRNP E1, hnRNP E2, hnRNP P (TLS), HuB, KSRP, MBNL1, SC35, TIA-1, TIAL1, YB-1 ETR-3, hnRNP F1, hnRNP F1, hnRNP P (TLS), MBNL1, Nova-1, SC35, SRp20, SRp30c, YB-1 ETR-3, hnRNP F1, hnRNP F1, hnRNP P (TLS), MBNL1, NOva-1, SC35, SRp20, SRp30c, YB-1 ETR-3, hnRNP F1, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP P (TLS), KSRP, Nova-1, RBM5, SRp20, SRp30c, TIA-1 ETR-3, hnRNP F1, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP P (TLS), KSRP, Nova-1, RSM5, SRp20, SRp30c, TIA-1 ETR-3, fow.2, fow.2, hnRNP F1, hnRNP F1, hnRNP H2, hnRNP P (TLS), KSRP, Nova-1, SC35, SF2/ASE, SRp20, SRp30c, TIA-1 ETR-3, fow.2, fow.2, hnRNP F1, hnRNP H2, hnRNP H2, H1S, KSRP, N
ARFGAP1 TCEA2 LINC00266- 1/MYT1/PCMTD TBC1D20 SNRPB IDH3B CPXM1 PCED1A SLC4A11	Intron Retention Complex Intron Retention Alter. Terminal Exon (e21-25) Exon Cassette Intron Retention Exon Cassette Intron Retention Complex Intron Retention Alter. Acceptor Site Alter. First Exon (e1-3)	1.62 1.72 2.22 2.70 2.44 1.99 2.20 1.80 2.73 2.11 1.76 1.64	6.96E-04 5.22E-03 1.82E-05 3.51E-05 4.01E-06 6.86E-03 4.22E-04 1.20E-02 9.39E-04 3.24E-03 1.83E-04 1.08E-03	ETR-3, hnRNP A1, hnRNP C1, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HuB, KSRP, SC35, YB-1 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP C1, hnRNP D2, hnRNP P, hnRNP P, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HuB, HuD, KSRP, Nova-1, Nova-2, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP C1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP H2, hnRNP H2, hnRNP F (TLS), HUB, KSRP, MBNL1, Nova-1, Nova-2, SF, RBM5, Sam68, SC35, SF2/ASF, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, TIAL1, Y
ARFGAP1 TCEA2 LINC00266- 1/MYT1/PCMTD TBC1D20 SNRPB IDH3B CPXM1 PCED1A SLC4A11 NAPB	Intron Retention Complex Intron Retention Alter. Terminal Exon (e21-25) Exon Cassette Intron Retention Exon Cassette Intron Retention Complex Intron Retention Alter. Acceptor Site Alter. First Exon (e1-3) Alter. Terminal Exon	1.62 1.72 2.22 2.70 2.44 1.99 2.20 1.80 2.73 2.11 1.76 1.64 2.12	6.96E-04 5.22E-03 1.82E-05 3.51E-05 4.01E-06 6.86E-03 4.22E-04 1.20E-02 9.39E-04 3.24E-03 1.83E-04 1.08E-03 3.83E-04	ETR-3, hnRNP A1, hnRNP C1, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HuB, KSRP, SC35, YB-1 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP C1, hnRNP D1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HuB, HuD, KSRP, Nova-1, Nova-2, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E2, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP F, hnRNP H1, hnRNP A2/B1, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, SF, RBM5, Sam68, SC35, SF2/ASF, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HUB, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1 ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HUB, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1 ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F, H2, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HUB, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1 ETR-3, hnRNP A1, hnRNP F, hnRNP H1, hnRNP P (TLS), KBRP, Nova-1, SC35, SRp20, SRp30c, YB-1 ETR-3, hnRNP A1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP P (TLS), KSRP, Nova-1, RBM5, SRp20, SRp30c, TIA-1, TIAL1, YB-1 ETR-3, fox-1, fox-2, hnRNP A1, hnRNP A2/B1, hnRNP P (TLS), KSRP, Nova-1, RSM5, SRp20, SRp30c, TIA-1, TIAL1, YB-1 CUG-BP1, ETR-3, fox-1, fox-2, hnRNP A1, hnRNP A2/B1, hnRNP P (TLS), KSRP, Nova-1, RSM5, SRp20, SRp30c, TIA-1, TIAL1, YB-1 CUG-BP1, ETR-3, fox-1, fox-2, hnRNP A1, hnRNP A2/B1, hnRNP P (TLS), HNRP E2, hnRNP F1, hnRNP F42, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HUB, HURN, HUB, HUB, HUB, HUB, HU
ARFGAP1 TCEA2 LINC00266- 1/MYT1/PCMTD TBC1D20 SNRPB IDH3B CPXM1 PCED1A SLC4A11 NAPB	Intron Retention Complex Intron Retention Alter. Terminal Exon (e21-25) Exon Cassette Intron Retention Exon Cassette Intron Retention Complex Intron Retention Alter. Acceptor Site Alter. First Exon (e1-3) Alter. Terminal Exon Exon Cassette	1.62 1.72 2.22 2.70 2.44 1.99 2.20 1.80 2.73 2.11 1.76 1.64 2.12 1.56	6.96E-04 5.22E-03 1.82E-05 3.51E-05 4.01E-06 6.86E-03 4.22E-04 1.20E-02 9.39E-04 3.24E-03 1.83E-04 1.08E-03 3.83E-04 1.16E-02	ETR-3, hnRNP A1, hnRNP C1, hnRNP F1, hnRNP H2, hnRNP H2, hnRNP 1(PTB), hnRNP P (TLS), HuB, KSRP, SC35, YB-1 ETR-3, Fox-1, Fox-2, hnRNP C1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HuB, HuD, KSRP, Nova-1, Nova-2, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP F, KnRNP F (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP F1, hnRNP H2, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HUB, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1 ETR-3, hnRNP E1, hnRNP E2, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HUB, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1 ETR-3, hnRNP F1, hnRNP E2, hnRNP F (TLS), HUB, KSRP, MBNL1, SC35, TIA-1, TIAL1, YB-1 ETR-3, hnRNP F1, hnRNP H2, hnRNP P (TLS), KBRP, Nova-1, RBM5, SRp20, SRp30c, YB-1 ETR-3, fox-1, Fox-2, hnRNP F1, hnRNP H2, hnRNP P (TLS), KSRP, Nova-1, RGM5, SRp20, SRp30c, TIA-1, TIAL1, YB-1 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP P (TLS), KSRP, Nova-1, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E2, hnRNP F, hnRNP H1, hnRNP F, MLS, hnRNP C1, hnRNP C1, hnRNP D, hnRNP E2, hnRNP F, hnRNP H1, hnRNP F, MLS, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, SRP3, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1
AREGAP1 TCEA2 LINC00266- 1/MYT1/PCMTD TBC1D20 SNRPB IDH3B CPXM1 PCED1A SLC4A11 NAPB	Intron Retention Complex Intron Retention Alter. Terminal Exon (e21-25) Exon Cassette Intron Retention Exon Cassette Intron Retention Complex Intron Retention Alter. Acceptor Site Alter. First Exon (e1-3) Alter. Terminal Exon Exon Cassette Complex	1.62 1.72 2.22 2.70 2.44 1.99 2.20 1.80 2.73 2.11 1.76 1.64 2.12 1.56 1.95	6.96E.04 5.22E.03 1.82E.05 3.51E.05 4.01E.06 6.86E.03 4.22E.04 1.20E.02 9.39E.04 3.24E.03 1.83E.04 1.08E.03 3.83E.04 1.16E.02 4.84E.04	ETR-3, hnRNP A1, hnRNP C1, hnRNP F1, hnRNP H2, hnRNP L2, hnRNP I(PTB), hnRNP P (TLS), HuB, KSRP, SC35, YB-1 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HuB, HuD, KSRP, Nova-1, Nova-2, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP F1, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, fox-1, Fox-2, hnRNP A1, hnRNP F1, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HUB, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-3, ZRANB2 ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1 ETR-3, hnRNP F1, hnRNP F2, hnRNP P (TLS), HuB, KSRP, MBNL1, SC35, TIA-1, TIAL1, YB-1 ETR-3, hnRNP F1, hnRNP F2, hnRNP P (TLS), MBNL1, Nova-1, SC35, SRp20, SRp30c, YB-1 ETR-3, hnRNP A1, hnRNP F1, hnRNP P (TLS), MBNL1, Nova-1, RBM5, SRp20, SRp30c, YB-1 ETR-3, fox-1, fox-2, hnRNP F1, hnRNP F1, hnRNP F2, hnRNP F (TLS), KSRP, Nova-1, RBM5, SRp20, SRp30c, TIA-1, TIAL1, YB-1 CUG-BP1, ETR-3, fox-1, fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP P (TLS), KSRP, Nova-1, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1 CUG-BP1, ETR-3, fox-1, fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F1, hnRNP F2, hnRNP F1, hnRNP H2, hnRNP F (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TD43, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, fox-1, fox-2, hnRNP A1
ARFGAP1 TCEA2 LINC00266- 1/MYT1/PCMTD TBC1D20 SNRPB IDH3B CPXM1 PCED1A SLC4A11 NAPB BCL2L1	Intron Retention Complex Intron Retention Alter. Terminal Exon (e21-25) Exon Cassette Intron Retention Exon Cassette Intron Retention Complex Intron Retention Alter. Acceptor Site Alter. First Exon (e1-3) Alter. Terminal Exon Exon Cassette Complex Exon Cassette	1.62 1.72 2.22 2.70 2.44 1.99 2.20 1.80 2.73 2.11 1.76 1.64 2.12 1.56 1.95 2.20	6.96E-04 5.22E-03 1.82E-05 3.51E-05 4.01E-06 6.86E-03 4.22E-04 1.20E-02 9.39E-04 3.24E-03 1.83E-04 1.08E-03 3.83E-04 1.16E-02 4.84E-04 4.21E-04	ETR-3, hnRNP A1, hnRNP C1, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HuB, KSRP, SC35, YB-1 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP D1, hnRNP D2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HuB, HuD, KSRP, Nova-1, Nova-2, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, SBF, SBM5, Sam68, SC35, SF2/ASF, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YZ, ZRANB2 ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YZ, ZRANB2 ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1 ETR-3, hnRNP F1, hnRNP F1, hnRNP P (TLS), HuB, KSRP, MBNL1, SC35, TIA-1, TIAL1, YB-1 ETR-3, hnRNP F1, hnRNP F1, hnRNP P (TLS), MBNL1, Nova-1, SC35, SRp20, SRp30c, YB-1 ETR-3, hnRNP F1, hnRNP F1, hnRNP H2, hnRNP P (TLS), KSRP, Nova-1, RBM5, SRp20, SRp30c, YB-1 ETR-3, fox-1, Fox-2, hnRNP F1, hnRNP H2, hnRNP P (TLS), KSRP, Nova-1, RBM5, SRp20, SRp30c, TIA-1, TIAL1, YB-1 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP H2, hnRNP P (TLS), KSRP, Nova-1, RBM5, SRp20, SRp30c, TIA-1, TIAL1, YB-1 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F1, hnRNP H1, hnRNP K, hnRNP F (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, TRA1, YB-1, ZRANB2
ARFGAP1 TCEA2 LINC00266- 1/MYT1/PCMTD TBC1D20 SNRPB IDH3B CPXM1 PCED1A SLC4A11 NAPB BCL2L1	Intron Retention Complex Intron Retention Alter. Terminal Exon (e21-25) Exon Cassette Intron Retention Exon Cassette Intron Retention Complex Intron Retention Alter. Acceptor Site Alter. First Exon (e1-3) Alter. Terminal Exon Exon Cassette Complex Exon Cassette Alter. Terminal Exon (e8)	1.62 1.72 2.22 2.70 2.44 1.99 2.20 1.80 2.73 2.11 1.76 1.64 2.12 1.56 1.95 2.20 1.87	6.96E-04 5.22E-03 1.82E-05 3.51E-05 4.01E-06 6.86E-03 4.22E-04 1.20E-02 9.39E-04 3.24E-03 1.83E-04 1.08E-03 3.83E-04 1.16E-02 4.84E-04 4.21E-04 3.76E-04	 ETR-3, hnRNP A1, hnRNP C1, hnRNP F1, hnRNP H2, hnRNP L2, hnRNP I (PTB), hnRNP P (TLS), HuB, KSPP, SC35, YB-1 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP D1, hnRNP D2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HuB, HuD, KSRP, Nova-1, Nova-2, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP D2, hnRNP D1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, SFF, RBM5, Sam68, SC35, SF2/ASF, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H (PTB), hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1 ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1 ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP F, InRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1 ETR-3, hnRNP F1, hnRNP F2, hnRNP F (TLS), HuB, KSRP, MBNL1, SC35, TIA-1, TIAL1, YB-1 ETR-3, hnRNP F1, hnRNP F1, hnRNP H2, hnRNP P (TLS), KSRP, Nova-1, RS5, SRp20, SRp30c, YB-1 ETR-3, hnRNP F, hnRNP H1, hnRNP H2, hnRNP P (TLS), KSRP, Nova-1, RBM5, SRp20, SRp30c, TIA-1, TIAL1, YB-1 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP F, hnRNP H2, hnRNP P (TLS), KSRP, Nova-1, RS5, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP F (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, SRB5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A2/B1, hnRNP A2/B1, hnRNP D, hnRNP D, hnRNP E2, hnRNP F, h
ARFGAP1 TCEA2 LINC00266- 1/MYT1/PCMTD TBC1D20 SNRPB IDH3B CPXM1 PCED1A SLC4A11 NAPB BCL2L1 UQCC	Intron Retention Complex Intron Retention Alter. Terminal Exon (e21-25) Exon Cassette Intron Retention Exon Cassette Intron Retention Complex Intron Retention Alter. Acceptor Site Alter. First Exon (e1-3) Alter. Terminal Exon Exon Cassette Complex Exon Cassette Alter. Terminal Exon (e8) Complex	1.62 1.72 2.22 2.70 2.44 1.99 2.20 1.80 2.73 2.11 1.76 1.64 2.12 1.56 1.95 2.20 1.87	6.96E-04 5.22E-03 1.82E-05 3.51E-05 4.01E-06 6.86E-03 4.22E-04 1.20E-02 9.39E-04 3.24E-03 1.83E-04 1.08E-03 3.83E-04 1.16E-02 4.84E-04 4.21E-04 3.30E-03	 ETR-3, hnRNP A1, hnRNP C1, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HuB, KSRP, SC35, YB-1 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP D1, hnRNP D2, hnRNP F1, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HuB, HuD, KSRP, Nova-1, Nova-2, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP C1, hnRNP D, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP F (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, SF, RBM5, Sam68, SC35, SF2/ASF, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H (PTB), hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1 ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1 ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F, InRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1 ETR-3, hnRNP A1, hnRNP F, hnRNP H1, hnRNP P (TLS), KSRP, Nova-1, RSM5, SRp20, SRp30c, YB-1 ETR-3, hnRNP A1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP P (TLS), KSRP, Nova-1, RSM5, SRp20, SRp30c, TIA-1 ETR-3, fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP F, hnRNP F, hnRNP F, hnRNP H1, hnRNP H2, hnRNP P (TLS), KSRP, Nova-1, RSM5, SRp20, SRp30c, TIA-1 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP P (TLS), KSRP, Nova-1, RSM5, SRp20, SRp30c, TDH3, TIA-1, TIAL1, YB-1 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP D, hnRNP D, hnRNP E1, hnRNP F2, hnRNP F1, hnRNP H3, hnRNP H3, hnRNP I (PTB), hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP D1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H3, hnRNP H3, hnRNP P (
ARFGAP1 TCEA2 LINC00266- 1/MYT1/PCMTD TBC1D20 SNRPB IDH3B CPXM1 PCED1A SLC4A11 NAPB BCL2L1 UQCC	Intron Retention Complex Intron Retention Alter. Terminal Exon (e21-25) Exon Cassette Intron Retention Exon Cassette Intron Retention Complex Intron Retention Alter. Acceptor Site Alter. First Exon (e1-3) Alter. Terminal Exon Exon Cassette Complex Exon Cassette Alter. Terminal Exon (e8) Complex Alter. Terminal Exon (e21-38)	1.62 1.72 2.22 2.70 2.44 1.99 2.20 1.80 2.73 2.11 1.76 1.64 2.12 1.95 2.20 1.87 1.62	6.96E-04 5.22E-03 1.82E-05 3.51E-05 4.01E-06 6.86E-03 4.22E-04 1.20E-02 9.39E-04 3.24E-03 1.83E-04 1.08E-03 3.83E-04 1.16E-02 4.84E-04 4.21E-04 3.30E-03 5.80E-04	 ETR-3, hnRNP C1, hnRNP F1, hnRNP H1, hnRNP L2, hnRNP E1, hnRNP E1, hnRNP F (TLS), HuB, KSRP, SC35, YE-1 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP DL, hnRNP E1, hnRNP E1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP F (TLS), HuB, HuD, KSRP, Nova-1, Nova-2, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YE-1, ZRANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP F, hnRNP D1, hnRNP D2, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H1, hnRNP H2, hnRNP F (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp30c, TIA-1, TIAL1, YE-1, ZRANB2 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2 (PTB), hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YE-1, ZRANB2 ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2 (PTB), hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1 ETR-3, hnRNP E2, hnRNP E2, hnRNP F (TLS), HuB, KSRP, MBNL1, SC35, TIA-1, TIAL1, YB-1 ETR-3, hnRNP E2, hnRNP H2, hnRNP P (TLS), HuB, KSRP, MBNL1, SC35, SRp20, SRp30c, YB-1 ETR-3, hnRNP F4, hnRNP H1, hnRNP H2, hnRNP P (TLS), MBNL1, Nova-1, SC35, SRp20, SRp30c, YB-1 ETR-3, Fox-1, Fox-2, hnRNP F1, hnRNP H2, hnRNP F (TLS), KSRP, Nova-1, SC35, SRp20, SRp30c, YB-1 ETR-3, Fox-1, Fox-2, hnRNP F1, hnRNP H2, hnRNP F (TLS), KSRP, Nova-1, SC35, SRp20, SRp30c, YB-1 ETR-3, Fox-1, Fox-2, hnRNP F1, hnRNP H2, hnRNP F1, hnRNP F1, hnRNP F2, hnRNP F1, hnRNP F2, hnRNP F1, hnRNP F2, hnRNP F1, hnRNP F2, hnRNP F1, hnRNP F4, hnRNP
ARFGAP1 TCEA2 LINC00266- 1/MYT1/PCMTD TBC1D20 SNRPB IDH3B CPXM1 PCED1A SLC4A11 NAPB BCL2L1 UQCC CPNEL // NFS1	Intron Retention Complex Intron Retention Alter. Terminal Exon (e21-25) Exon Cassette Intron Retention Exon Cassette Intron Retention Complex Intron Retention Alter. Acceptor Site Alter. First Exon (e1-3) Alter. Terminal Exon Exon Cassette Complex Exon Cassette Alter. Terminal Exon (e8) Complex Alter. Terminal Exon (e8) Complex Alter. Terminal Exon (e1-38) Complex	1.62 1.72 2.22 2.70 2.44 1.99 2.20 1.80 2.73 2.11 1.76 1.64 2.12 1.56 1.95 2.20 1.87 1.62 1.53 1.62 1.53 1.62	6.96E-04 5.22E-03 1.82E-05 3.51E-05 4.01E-06 6.86E-03 4.22E-04 1.20E-02 9.39E-04 1.20E-02 9.39E-04 1.20E-02 9.39E-04 1.83E-04 1.16E-02 4.84E-04 3.76E-04 3.76E-04 3.30E-03 5.80E-04 2.02E-03 5.80E-04 2.02E-03	 ETR-3, hnRNP C1, hnRNP F1, hnRNP F1, hnRNP F2, hnRNP F1(PTB), hnRNP F (TLS), HuB, KSRP, SC35, YB-1 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP DL, hnRNP E1, hnRNP F, hnRNP F1, hnRNP H2, hnRNP F, hnRNP F, hnRNP F1, hnRNP F2, hnRNP F1, hnRNP F2, hnRNP F1, hnRNP F2, hnRNP F1, hnRNP F1, hnRNP F1, hnRNP F1, hnRNP F2, hnRNP F1, hnRNP F2, hnRNP F1, hnRNP F2, hnRNP F1, hnRNP F1, hnRNP F2, hnRNP F1, hnRNP F2, hnRNP F1, hnRNP F2, hnRNP F1, hnRNP F2, hnRNP F1, hnRNP F1, hnRNP F2, hnRNP F1, hnRNP F1, hnRNP F1, hnRNP F1, hnRNP F1, hnRNP F2, hnRNP F1, hnRNP F2, hnRNP F1, hnRNP F1, hnRNP F1, hnRNP F1, hnRNP F1, hnRNP F2, hnRNP F1, hnRNP F1, hnRNP F2, hnRNP F2, hnRNP F1, hnRNP F2, hnRNP
ARFGAP1 TCEA2 LINC00266- 1/MYT1/PCMTD TBC1D20 SNRPB IDH3B CPXM1 PCED1A SLC4A11 NAPB BCL2L1 UQCC CPNE1 // NFS1 // RBM12	Intron Retention Complex Intron Retention Alter. Terminal Exon (e21-25) Exon Cassette Intron Retention Exon Cassette Intron Retention Complex Intron Retention Alter. Acceptor Site Alter. First Exon (e1-3) Alter. Terminal Exon Exon Cassette Complex Exon Cassette Alter. Terminal Exon (e8) Complex Alter. Terminal Exon (e8) Complex Alter. Terminal Exon (e21-38) Complex	1.62 1.72 2.22 2.70 2.44 1.99 2.20 1.80 2.73 2.11 1.76 1.64 2.12 1.56 1.95 2.20 1.87 1.62 1.53 1.62 1.75 2.55	6.96E.04 5.22E.03 1.82E.05 3.51E.05 4.01E.06 6.86E.03 4.22E.04 1.20E.02 9.39E.04 3.24E.03 3.83E.04 1.08E.03 3.83E.04 1.08E.03 3.83E.04 1.08E.03 3.83E.04 4.21E.04 3.76E.04 3.30E.03 5.80E.04 2.02E.03 3.44E.03	 ETR-3, hnRVP A1, hnRNP C1, hnRNP F, hnRNP H2, hnRNP H2, hnRNP F (IJE), hnRNP P (TLS), HuB, KSRP, SC35, Y8-1 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP F (TLS), HuB, HuD, KSRP, Nova-1, Nova-2, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TA-1, TIAL1, Y8-1, ZRANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP H2, hnRNP F, hnRNP H1, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SF2/ASF, SRp30c, TIA-1, TIAL1, Y8-1, ZRANB2 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP F, hnRNP H2, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HUB, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1 ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP F1, hnRNP F1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HUB, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1 ETR-3, hnRNP A1, hnRNP E2, hnRNP H1, hnRNP P (TLS), KSRP, MSH1, SC35, TIA-1, TIAL1, YB-1 ETR-3, hnRNP A1, hnRNP F, hnRNP H1, hnRNP P (TLS), KSRP, Nova-1, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1 ETR-3, fox-1, fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D (TLS), KSRP, Nova-1, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1 CUG-BP1, ETR-3, fox-1, fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, fox-1, fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D1, hnRNP E1, hnRNP E2, hnRNP F, hnRN
ARFGAP1 TCEA2 LINC00266- 1/MYT1/PCMTD TBC1D20 SNRPB IDH3B CPXM1 PCED1A SLC4A11 NAPB BCL2L1 UQCC CPNE1 // NFS1 // RBM12	Intron Retention Complex Intron Retention Alter. Terminal Exon (e21-25) Exon Cassette Intron Retention Exon Cassette Intron Retention Complex Intron Retention Alter. Acceptor Site Alter. First Exon (e1-3) Alter. Terminal Exon Exon Cassette Complex Exon Cassette Alter. Terminal Exon (e8) Complex Alter. Terminal Exon (e8) Complex Alter. Terminal Exon (e8) Complex Exon Cassette Intron Retention	1.62 1.72 2.22 2.70 2.44 1.99 2.20 1.80 2.73 2.11 1.76 1.64 2.12 1.56 1.95 2.20 1.87 1.62 1.53 1.62 1.75 2.95	6.96E-04 5.22E-03 1.82E-05 3.51E-05 4.01E-06 6.86E-03 4.22E-04 1.20E-02 9.39E-04 3.24E-03 1.83E-04 1.08E-03 3.83E-04 1.16E-02 4.84E-04 4.21E-04 3.76E-04 3.30E-03 5.80E-04 2.02E-03 3.44E-03 9.27E-07	 ETR-3, hnRNP AL, hnRNP F, hnRNP FL, hnRNP FL, hnRNP P (IPTB), hnRNP F (TLS), HuB, KSRP, SC35, VB-1 ETR A, Fox-2, hor RNP AL, hnRNP C1, hnRNP C1, hnRNP E2, hnRNP F, hnRNP FL, hnRNP FL, hnRNP FL, hnRNP P (TLS), HuB, HuD, KSRP, Nova-1, Nova-2, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, VB-1, ZANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP AL, hnRNP AL, hnRNP E1, hnRNP E2, hnRNP FL, hnRNP F
ARFGAP1 TCEA2 LINC00266- 1/MYT1/PCMTD TBC1D20 SNRPB IDH3B CPXM1 PCED1A SLC4A11 NAPB BCL2L1 UQCC CPNE1 // NFS1 // RBM12 RBM39	Intron Retention Complex Intron Retention Alter. Terminal Exon (e21-25) Exon Cassette Intron Retention Exon Cassette Intron Retention Complex Intron Retention Alter. First Exon (e1-3) Alter. First Exon (e1-3) Alter. Terminal Exon Exon Cassette Alter. Terminal Exon (e8) Complex Alter. Terminal Exon (e8) Complex Alter. Terminal Exon (e8) Complex Exon Cassette Intron Retention Exon Cassette	1.62 1.72 2.22 2.70 2.44 1.99 2.20 1.80 2.73 2.11 1.76 1.64 2.12 1.56 1.95 2.20 1.87 1.62 1.53 1.62 1.75 2.95 1.90	6.96E-04 5.22E-03 1.82E-05 3.51E-05 4.01E-06 6.86E-03 4.22E-04 1.20E-02 9.39E-04 3.24E-03 1.83E-04 1.08E-03 3.83E-04 1.08E-03 3.83E-04 4.21E-04 3.76E-04 3.76E-04 3.30E-03 5.80E-04 2.02E-03 3.44E-03 9.27E-07 1.34E-03	 ETR-3, hnRNP A1, hnRNP C1, hnRNP F, hnRNP H2, hnRNP F1, hnRNP P CTLSJ, HuB, KSRP, SC35, V8-1 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP D1, hnRNP D1, hnRNP E1, hnRNP P CTLSJ, HnRNP F, hnRNP H1, hnRNP P, hnRNP F, hnRNP P (TLS), HuB, HuD, KSRP, Nova-1, Nova-2, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, Y8-1, ZRANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP F, hnRNP C1, hnRNP DL, hnRNP DL, hnRNP E1, hnRNP F, hnRNP F, hnRNP H1, hnRNP H2, hnRNP F, hnRNP H1, hnRNP F, hnRNP H2, hnRNP F, hnRNP H2, hnRNP F (TLS), HUB, KSRP, MBNL1, Nova-1, Nova-2, SBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, nnRNP E1, hnRNP E2, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1 ETR-3, nnRNP E1, hnRNP F2, hnRNP F1, hnRNP F1, hnRNP H2, hnRNP H2, hnRNP F (TLS), HuB, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1 ETR-3, hnRNP E1, hnRNP F1, hnRNP F1, hnRNP F1, hnRNP F1, SRp20, SRp30c, YB-1 ETR-3, nnRNP A1, hnRNP F1, hnRNP F1, hnRNP F1, NNRNP F (TLS), KBR, Nova-1, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1 ETR-3, fox1, fox2, hnRNP A1, hnRNP F2, hnRNP F1, hnRNP F1, hnRNP F1, hnRNP F2, hnRNP F1, hnRNP F1, hnRNP F2, hnRNP F1, HNRNP F2, SRp20, SRp30c, TIA-1, TIAL1, YB-1 ETR-3, fox1, fox2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP F1, hnRNP E2, hnRNP F1, hnRNP H2, hnRNP F (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, SRB5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, fox1, fox2, hnRNP A1, hnRNP A2/B1, hnRNP C1, h
ARFGAP1 TCEA2 LINC00266- 1/MYT1/PCMTD TBC1D20 SNRPB IDH3B CPXM1 PCED1A SLC4A11 NAPB BCL2L1 UQCC CPNE1 // NFS1 // RBM12 RBM39 DSN1	Intron Retention Complex Intron Retention Alter. Terminal Exon (e21-25) Exon Cassette Intron Retention Exon Cassette Intron Retention Complex Intron Retention Alter. Acceptor Site Alter. First Exon (e1-3) Alter. Terminal Exon Exon Cassette Complex Exon Cassette Alter. Terminal Exon (e8) Complex Alter. Terminal Exon (e8) Complex Alter. Terminal Exon (e8) Complex Alter. Terminal Exon (e8) Complex Alter. Terminal Exon (e8) Complex Exon Cassette Intron Retention Exon Cassette	1.62 1.72 2.22 2.70 2.44 1.99 2.20 1.80 2.73 2.11 1.76 1.64 2.12 1.56 1.95 2.20 1.87 1.62 1.53 1.62 1.75 2.95 1.90 1.64	6.96E-04 5.22E-03 1.82E-05 3.51E-05 4.01E-06 6.86E-03 4.22E-04 1.20E-02 9.39E-04 3.24E-03 1.83E-04 1.08E-03 3.83E-04 1.08E-03 3.83E-04 1.08E-03 3.83E-04 3.30E-03 3.44E-03 9.27E-07 1.34E-03 4.06E-03	 ETR-3, InRNP A1, InRNP C1, InRNP F, InRNP H2, InRNP F1, INRNP P (ICS), INRNP P (TLS), HuB, KSP, S25, V8-1 ETR-3, Fox-1, Fox-2, InRNP A1, InRNP D2, INRNP E1, INRNP E2, INRNP F, INRNP H1, INRNP L2, INRNP F, INRNP F, INRNP P (TLS), HUB, KSRP, Nova-1, Nova-2, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, Y9-1, ZRANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, INRNP A1, INRNP A2, B1, INRNP C1, INRNP D1, INRNP D1, INRNP E1, INRNP E2, INRNP F, INRNP F, INRNP H1, INRNP H2, INRNP F, INRNP F, INRNP F, INRNP F, INRNP A1, INRNP A2, B1, INRNP F, INRNP H1, INRNP H2, INRNP F (TLS), HUB, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SF2/ASF, SRp30c, TIA-1, TIAL1, Y9-1, ZRANB2 ETR-3, Fox-1, Fox-2, INRNP A1, INRNP A2, INRNP F, INRNP H1, INRNP H2, INRNP H2, INRNP F (TLS), HUB, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, Y9-1, ZRANB2 ETR-3, INRNP A1, INRNP PA2/B1, INRNP F, INRNP H1, INRNP H2, INRNP H2, INRNP F (TLS), HUB, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, Y8-1 ETR-3, INRNP F, INRNP H1, INRNP H2, INRNP F (TLS), HUB, KSRP, MBNL1, SC35, TIA-1, TIAL1, Y8-1 ETR-3, INRNP F, INRNP H1, INRNP H2, INRNP F (TLS), MBNL1, Nova-1, SC35, SRp20, SRp30c, Y8-1 ETR-3, INRNP F, INRNP H1, INRNP H2, INRNP F (TLS), MBNL1, Nova-1, SC35, SRp20, SRp30c, Y8-1 ETR-3, INRNP F, INRNP H1, INRNP H2, INRNP F (TLS), MBNL1, Nova-1, SC35, SRp20, SRp30c, Y8-1 ETR-3, TAC-1, Fox-2, INRNP A1, INRNP A2/B1, INRNP C1, INRNP D, INRNP E1, INRNP E2, INRNP F, INRNP H1, INRNP F, INRNP
ARFGAP1 TCEA2 LINC00266- 1/MYT1/PCMTD TBC1D20 SNRPB IDH3B CPXM1 PCED1A SLC4A11 NAPB BCL2L1 UQCC CPNE1 // NFS1 // RBM12 RBM39 DSN1 SNHG17	Intron Retention Complex Intron Retention Alter. Terminal Exon (e21-25) Exon Cassette Intron Retention Exon Cassette Intron Retention Complex Intron Retention Alter. Acceptor Site Alter. Acceptor Site Alter. Terminal Exon Exon Cassette Complex Exon Cassette Alter. Terminal Exon (e1-3) Complex Alter. Terminal Exon (e21-38) Complex Exon Cassette Intron Retention Exon Cassette Intron Retention Exon Cassette	1.62 1.72 2.22 2.70 2.44 1.99 2.20 1.80 2.73 2.11 1.76 1.64 2.12 1.56 1.95 2.20 1.87 1.62 1.53 1.62 1.75 2.95 1.90 1.64	6.96E-04 5.22E-03 1.82E-05 3.51E-05 4.01E-06 6.86E-03 4.22E-04 1.20E-02 9.39E-04 3.24E-03 1.83E-04 1.08E-03 3.83E-04 1.16E-02 4.84E-04 3.30E-03 5.80E-04 3.30E-03 3.44E-03 9.27E-07 1.34E-03 4.06E-03 1.14E-03	 ETR-3, InnRNP A1, InnRNP C1, InnRNP F1, InnRNP F2, InnRNP E2, InnRNP F (LTS), HuB, KSP (SS, YE-1 ETR-3, Fox-1, Fox-2, InnRNP A1, InnRNP D, InnRNP E1, InnRNP E2, InnRNP F, InnRNP H1, InnRNP H2, InnRNP F (PTB), InnRNP F (TLS), HuB, HuD, KSRP, Nova-1, Nova-2, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YE-1, ZRANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, InnRNP A1, InnRNP A2, B1, InnRNP C1, InnRNP D, InnRNP D, InnRNP E2, InnRNP F (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SF2/ASF, SRp30c, TIA-1, TIAL1, YE-1, ZRANB2 ETR-3, Fox-1, Fox-2, InnRNP A1, InnRNP C1, InnRNP F1, InnRNP H2, InnRNP H2, InnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YE-1, ZRANB2 ETR-3, InnRNP A1, InnRNP A2/B1, InnRNP C1, InnRNP F1, InnRNP H2, InnRNP H2, InnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YE-1, ZRANB2 ETR-3, InnRNP A1, InnRNP A2/B1, InnRNP C1, InnRNP F1, InnRNP H2, InnRNP H2, InnRNP P (TLS), HUB, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YE-1 ETR-3, InnRNP E1, InnRNP E1, InnRNP P C1, IS, MBNL1, Nova-1, SC35, STA-1, TIAL1, YE-1 ETR-3, InRNP E1, InnRNP E1, InnRNP P (TLS), MBNL1, Nova-1, SC35, STA-1, TIAL1, YE-1 ETR-3, InRNP E1, InnRNP E1, InnRNP P (TLS), MBNL1, Nova-1, SC35, SRp20, SRp30c, YE-1 ETR-3, InRNP E1, InnRNP E1, InNRNP E1, InNRNP P (TLS), INRNP F (TLS), INRNP F, INRNP H1, InNRNP H2, InRNP F (TLS), HIRNP E2, INRNP F, INRNP H1, INRNP H2, INRNP P (TLS), INRNP F, INRNP H1, INRNP H2, INRNP F, INRNP F, INRNP F, INRNP F, INRNP F, INRNP F (TLS), INRNP E1, INRNP F (TLS), INRNP E2, INRNP F, INRNP H1, INRNP H2, INRNP F (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Rova-2, RSR, SRB5, SRF5, SRP20, SRp30c, TDA-1, TIAL1, YE-1, ZRANB2 CUG-BP1, ETR-3, Fox1, Fox2, InRNP A1, INRNP A2/B1, INRNP C1, INRNP D, INRNP

	Complex	2.16	5 455 07	
	Even Cascotto	1.79	1.24E.02	
	Litera Datastica	1.70	1.546-03	
ELMO0	Intron Retention	1.95	2.56E-03	
ELIVIUZ	Introl Retention	1.01	1.40E-03	CUC+OF1, ETR-S, INKWE CL, NIKWE FL,
PREXI	Intron Retention	2.12	1.80E-04	NNKNP F, NNKNP H1, NNKNP H2, NNKNP I (PIB), NNKNP P (ILS), HUB, NOVA-I, SC35, SKp2U, SKp3Uc, YB-I
	Alter. First Exon (e1,3,e5-7,e15)	1.94	1.26E-03	
TMEM189//UBE	Complex	2.18	2.60E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1,
2V1	Exon Cassette	2.18	2.49E-03	HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
	Mutualy Exclusive Exons (e11,e14)	2.18	2.49E-03	
DID01	Alter. Term Exon (e7-8,e17-18)	1.56	4.28E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
ARFRP1	Alter. First Exon (e1)	1.56	4.68E-03	ETR-3, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP F (, hnRNP P (TLS), KSRP, MBNL1, Nova-1, SC35, SRp30c, TIA-1, TIAL1, YB-1
USP25	Exon Cassette	1.61	1.88E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSPB, MDNI 1, Marci 1, Ma
LISP16	Intron Retention	1 55	3 75E-02	TRA: Fry, Bry, hendberg in hower, rsi, now, salido, sees, signo, signo, signo, north, inter,
ITSN1	Exon Cassette	2.39	4.24E-03	CUGBP1, ETR-3, Fox-1, Fox-2, InRNP 41, InRNP 42/B1, InRNP C1, InRNP C1, INRNP C1, INRNP E1, INRNP E2, INRNP F1, INRN
	Alter Terminal Even (s12.16)	2.25	1 525 05	
PCBP3	Alter. Terminal Exon (e12-16)	2.25	1.52E-05	905, UU-BPT, ETK-3, FOX-1, FOX-2, FOX-2, ANRIVE AL, ANRIVE AL, ANRIVE PL, ANRIVE PL, ANRIVE FL, ANR
	Exoli Casselle	2.02	0.02E-04	
MCM3AP-AS1	Alter. Terminal Exon (e5)	1.82	2.14E-03	LINCS, DWA, DWA, MINNER, ALL, MINNER, MI
PRMT2	Evon Cassette	1 71	2 99F-04	THU, HOM, HIDRET, HOWE, TOL, HOME, SAINOU, OCCU, U.E./OU, OLDEV, OLDEV, HOLEV, TOL, TOL, TOL, TOL, TOL, TOL, TOL, TOL
110012	Exon ousselle	1.7 1	2.552.04	CICCRPT FTR3 Ford FC, broker C, maker F, maker F, maker F, DD, maker F, maker F, CG, maker F, CG, maker C, Maker K, Maker F, Barker F, B
APP	Exon Cassette	5.04	1.05E-04	Hrazhet Hurb Hurb Hurb KSRE MRN 1 Nova- DS. RMS 525 SE1 SK20 SR30 CTD43 THAT TAL TALL YARRA
				TR3.5 (x) F
SCAF4	Alter. Terminal Exon (e19)	1.55	2.76E-04	Sam68, SC35, SF1, SRo20, SRo30c, Ti-4, TiAL1, YB-1, ZRANB2
ATP50/CRYZL1/ /DONSON	Alter. Acceptor Site	1.64	8.16E-04	9G8, ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, Nova-1, Nova-2, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
ZBTB21	Exon Cassette	1.52	2.26E-03	CUG-BP1, ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRo20, SRo30c, TIA-1, TIAL1, YB-1, ZRANB2
	Alter, First Exon (e1)	1.59	1.69F-02	FTR-3 Fox-1 Fox-2 hoRNP A1 hoRNP A2/R1 hoRNP C1 hoRNP D hoRNP F1 hoRNP F2 hoRNP F hoRNP H1 hoRNP H2 hoRNP (PTR) hoRNP K hoRNP P (FTR) H172/heta1 HuR KSRP MRNI 1 Nova-1
U2AF1	Intron Retention	1.58	6.34F-03	Sam68, SC35, SF1, SF2/ASF, SRo20, TIA-1, TIAL1, VB-1, ZRANB2
HSF2BP	Exon Cassette	1.61	2.33E-02	9G8, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
DGCR8	Intron Retention	2.11	1.40E-03	ETR-3, Fox-1, Fox-2, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, 784NR2
MED15	Complex	1.58	5.18E-03	CUGBP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2beta1,
				HUS, HUD, HUK, KSKP, MENLI, NOVAZ, PSF, KBMS, SAMOS, SZS, SF1, SF2/ASS, SKD20, SKD30C, HAT, HALL, YB-1, ZKANBZ
SLC2A11	Alter. Terminal Exon	1.56	6.18E-04	EIK-S, FOR-L, FOR-C, RINKIY AL, RINKIY CL, RINKIY CL, RINKIY EL, RINKIY FL,
SGSM1	Exon Cassette	3.67	2.19E-05	ETR.3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP F (TLS), HTra2beta1, HuB, KSRP, MBNL1,
MTED1 //				
SEC14L2	Complex	1.52	1.48E-03	EIR-S, FOX-2, HURRINF AL, HURRINF AZ, 51, HURRINF CL, HURRINF CL, HURRINF EZ, HURRINF F, HURRINF FL, HURRINF FZ, HURRINF F, FEB, HURRINF F, FEB, HURRINF F, FEB, HURRINF FZ, HURRINF F, HURRINF FZ, H
TUG1	Exon Cassette	1.56	6.78E-04	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, PSF, RBM5, Sam68, SC35, SRp200, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
LIMK2	Alter. First Exon (e1-2)	1.54	6.19E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
TIMP3	Complex	1.63	2.19E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRo20, SRo30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
MCM5	Intron Retention	1.52	1.38E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP F1, hnRNP H2, hnRNP H2, hnRNP ((TEB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, SC35, SRn30c, TIA-1, TIA-1, YB-1
MPST	Intron Retention	1.76	8.45E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF,
				RBMS, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YE-1, ZRANB2
SGSM3	Alter. First Exon (1-17)	1.56	5.02E-03	200, 00-00 F, CHNS, LOW, DWS, MINTER, MINTER, MINTER D, MINTER D, MINTER D, MINTER E, MINTER E, MINTER F,

			-	
RBX1 // XPNPEP3	Exon Cassette	1.94	4.79E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRo20, SRo30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
PANX2	Exon Cassette	1.92	5.66E-03	ETR-3, hnRNP A1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, RBM5, Sam68, SC35, SRb30, SRb30, TIA1, TIA1, YRJ, ZRANR2
DID	Alter. First Exon (e2,e4-7)	1.61	1.66E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB,
BID	Complex (e4-6)	1.66	1.20E-03	HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
	Exon Cassette	2.03	5.64F-05	
DGCR2 //	Complex (e2)	1.52	3.24E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, Hug Hug KSPP, MRNI 1, Mara 1, Mara 2, PSE PRM5, Sam68, S238, S21, S22(ASE, SPa20, SPa30, TDP43, TLA, 1, TLA, 1, YB, 1, ZPANP2, ASE, SPa30, SPa30
TRMT2A	Intron Retention	1.52	4.18F-04	The instruction of the second se
YPEL1	Complex	2.57	8.96E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, PSF, RBM5, Sam68, SC35, SPA30, TDP43, TIA1, TIA1, VB1, ZPANB2
	Alter First Evon (e1)	3.60	1 52E-05	OIRCAPT FTR. F. IDT 40, ITF. F. IDT 42, ITF. F. IDT 42, ITF. FTR. TO 42, ITF. FTR. FTR. FTR. FTR. FTR. FTR. FTR. F
PRAME	Complex	1.64	2.25E-05	MBNL1, Nova-1, Nova-2, PSF, Sam68, S.C35, SF1, SF2/ASF, SR502, SR302, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
FAM211B	Alter. Donor Site	1.76	4.75E-06	CUG-BP1, ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SRb30, SRb30
HPS4	Intron Retention	1.77	2.70F-03	TRA: Fox: FoxX: PRMPE F. bnRNP F. bnRNP L bnRNP LPTB). bnRNP K. bnRNP P (TIS). HuB. KSRP. MBNI I. Nova-2. PSE. SC35. TIA-1. TIAI J. YR-1
THOC5	Exon Cassette	1.62	7.38E-03	ETR-3, Fox-1, Fox-2, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP K, Nova-1, SC35, SF2/ASF, TIA-1, TIAL1, YB-1
DAT71	Alter. Terminal Exon (e4)	1.67	2.43E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2beta1, HuB, HuD,
PAIZI	Exon Cassette	1.58	1.08E-03	KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
CSNK1E	Alter. Terminal Exon (e8)	2.24	8.44E-04	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
DDX17	Intron Retention	5.12	1.11E-06	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, Nova-1, Nova-2, PSF, Sam68, SC35, SE1, SRn20, SRn30c, TIA-1, TIA11, YB-1, ZRANB2
RPL3	Alter. Acceptor Site	4.77	5.71E-05	ETR-3, Fox1, Fox2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, KSRP, Nova-1, Sam68, SC35, SRp30c, YB-1, ZRANB2
MKL1	Exon Cassette	1.83	1.80E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1,
	5 0 1			HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H, hnRNP H, hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP,
SLC25A17	Exon Cassette	2.90	6.62E-04	MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
RANGAP1	Alter. First Exon (e1,e6)	1.80	6.30E-03	9G8, CUG-BP1, ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E2, hnRNP F2, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNI1, Nova-1, Nova-2, PSE, RBM5, Sam68, SC35, SE1, SE2/ASE, SRo20, SRo30c, TDP43, TIA1, TIA11, YB-1, ZRANB2
CENPM	Complex (e4)	1.85	9.56E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, Nova-1, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1,
KIAA0930	Alter. First Exon (e4)	2.42	6.57E-04	ETR-3, Fox-1, Fox-2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H (PTB), hnRNP K, hnRNP P (TLS), HuB, KSRP, Nova-1, Nova-2, SC35, SF2/ASF, SRp30c, YB-1
HDAC10 // MAPK12	Alter. Terminal Exon (e13)	1.95	3.99E-05	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
DENND6B	Intron Retention	2.51	1.41E-04	ETR-3, hnRNP P (TLS), SC35, YB-1
DADLOD	Alter. Donor Site	1.66	1.12E-02	
RADLZD	Intron Retention	1.68	2.34E-03	בוהי, ווותיתי אנו ווותיתי אבים, ווותיתי בנ, ווותיתי ד, ווותיתי ד, ווותיתי ד, ווותיתי ד, ווותיתי ה, ווותיתי ד, ווותיתי ה, ווותיתי ה, ווותיתי ה, ווותיתי אבים, אסאבו, אסא
CNTN4	Alter. First Exon (e1-3,e6-8)	2.97	1.43E-04	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
LRRN1	Alter. First Exon (e1)	6.09	7.65E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNI 1, Nova-1, Nova-2, PSE, RBM5, Sam68, SC35, SE1, SE2/ASE, SRb20, SRb30c, TDP43, TIA-1, TIAI 1, YB-1, ZRANB2
SETD5	Complex	1.87	4.35E-04	ETR-3, hnRNP D, hnRNP E1, hnRNP E2, hnRNP I (PTB), hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, SC35, SRp3oc, TIA-1, TIAL1, YB-1
11 1700	Complex	1.62	5.77E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP H (TLS), HTra2beta1, HuB, HuD, HuR,
IL17RC	Exon Cassette	1.97	3.04E-04	KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20c, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
NP2C2	Exon Cassette	1.62	1.18E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP,
NR202	Intron Retention	2.72	4.20E-04	MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
RAB5A	Exon Cassette	1.91	6.98E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
CMTM8	Exon Cassette	1.71	2.91E-02	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP D1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF. SRo20. SRo30c. TDP43. TIA-1. TIAL1. YB-1. ZRANB2
OXSR1	Exon Cassette	1.87	4.14E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MRN1 I, Nuva-2, PSE, Sam68, SC35, SE1, SRo20, SRo30c, TDP43, TIA-1, TIA-1, TRANB2
	1		1	TR3.5 (ox 1, Fox 2, InRVP A1) InRNP A2/B1, InRNP C1, InRNP C1, INRNP C2, INRNP F, INRNP F, INRNP H1, INRNP H2, INRNP K, INRNP K, INRNP H1, INRNP A2/B1, INRNP A1, INRNP A2, INRNP A1, INRNP A2, INRNP A1, INRNP A2, INRNP A1, INRNP A2, INRN
XYLB	Alter. Terminal Exon (e18)	1.60	2.93E-02	HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TiA-1, TIAL1, YB-1, ZRANB2
ARIH2	Exon Cassette	1.80	5.41E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1,

1				
				HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
	Complex	1.68	9.08E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha,
KDINIO // KDINIO	Intron Retention	1.98	1.66E-03	HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
				ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P, (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-
TEX264	Exon Cassette	1.63	4.00E-04	1 Nova-2 PSE Sam68 SC35 SE1 SE2/ASE SRo20 SRo30c TIA.1 TIA11 VR.1 7RANR2
				This deploy is a second of the provide second and the provide second
PDE12	Intron Retention	1.74	4.57E-02	
-				SKp3uc, IIA-1, IIAL1, YA-1
RPP14	Alter First Evon (e1 e3)	1 55	1 12E-03	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2,
	7 (1017 - 1101 EXCIT (01900)	1.00	1.122.00	Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
DVK	Even Cassette	1 5 2	7 065 02	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1,
FAN	EXON Casselle	1.55	7.90E-03	HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
				CUG-BP1. ETR-3. Fox-1. Fox-2. hnRNP A1. hnRNP A2/B1. hnRNP C1. hnRNP C1. hnRNP E1. hnRNP E2. hnRNP F1. hnRNP H1. hnRNP H2. hnRNP I (TLS). HTra2aloha. HTra2beta1. HuB. HuD. KSRP.
KCTD6	Alter. First Exon (e2)	1.58	6.44E-04	MBNI 1 Nova-1 Nova-2 RBM5 Sam68 SC35 SE1 SRn20 SRn30c TDP43 TIA-1 TIAI 1 YB-1 ZRANB2
	1			Ministration of the second sec
EPHA3	Alter. Terminal Exon (e9-19)	2.01	2.05E-04	Subjection 1, Encorrect the second se
				HIAZUPELI, HUD, HUD, HUD, HUR, HSKR, MONELI, NUVAZI, FSF, HOMOS, SAIILOS, SOSO, SFI, SFZ/ASF, SREVEJ, SREJEJ, STAL, IDFAS, HAFL, HAEL, HSFL, ZRANDZ
NIT2	Complex	1.62	1.18F-03	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP Y (FIB), hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1,
	• - · · · P · · · ·			Nova-2, Sam68, SC35, SF1, SRp20, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
C2arfE0	Even Consette	1 5 2	2 665 05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1,
C30H32	EXON Casselle	1.55	3.00E-00	HuB, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
				CUG-BP1. FTR-3. Fox-1. Fox-2. bnRNP A1. hnRNP A2/B1. hnRNP C1. hnRNP D1. hnRNP F1. hnRNP F2. hnRNP F4. hnRNP H1. hnRNP H2. hnRNP H2. hnRNP K. hnRNP K. hnRNP A. HTra2beta1. HuB. KSRP. MBNI 1.
UMPS	Exon Cassette	2.61	1.09E-02	Nova-1 Nova-2 PSE Sam68 SC35 SE2/ASE SRo20 SRo30c TDP43 TIA-1 TIAI 1 VB-1 ZRANB2
IFT122	Intron Retention	1 57	3 39E-04	TED 2 horber 1 di James (1990) (JCTR) horber 2 (SCP MR) 1 Noval Samés COS SE2/ASE SE2/
11 1 1 2 2	Intron Netendon	1.57	3.35E-04	
CEP63	Exon Cassette	1.58	1.01E-04	CUG-Br1, EIR-S, Fox-1, FOX-2, ADRIVE AL, BI, ADRIVE AZ, BI, ADRIVE P, ADRIVE P, ULT, ADRIVE P, ADRIV
				KSRP, MBNLI, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, IDP43, IIA-1, IIAL1, YB-1, ZKANB2
FAIM	Mutualy Exclusive Exons (e3)	2 18	1 99F-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha,
174141	matualy Exclusive Exons (co)	2.10	1.552.04	HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
707000		0.04	1 755 05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP A, hnRNP A, hnRNP K, hnRNP LL, hnRNP P (TLS),
ZB1B38	Alter. First Exon (e1-5,e7,e9)	2.24	1./5E-05	HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNI1, Nova-1, Nova-2, PSE, RBM5, Sam68, SC35, SF1, SF2/ASE, SRo20, SRo30c, TDP43, TIA-1, TIAI 1, YB-1, ZRANB2
	Complex	1.67	2 02E-02	
RNF7	Even Generatte	1.67	2.020.02	
	Exoli Casselle	1.07	2.021-02	
TSC22D2	Exon Cassette	1.83	8.21E-04	CUG-BP1, EIR-3, Fox-1, Fox-2, INRRVP A1, INRRVP A2, B11, INRRVP C1, INRRVP C1, INRRVP E2, INRRVP F1, INRRVP H2, INRRVP H2, INRRVP H2, INRRVP H2, INRRVP F1 (PIB), INRRVP A2, INRRVP A1, INRRVP A2, INRRVP A2
				HUB, HUU, HUR, KSRP, MBNLI, Nova-1, Nova-2, PSF, RBMS, Samo8, SC35, SF1, SRp2U, SRp3UC, HA-1, HAL1, YB-1, ZKANB2
GEM1	Evon Cassette	1 78	8 52E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35,
GI III 1	Exon ousselle	1.70	0.022 00	SRp20, SRp30c, TIA-1, TIAL1, YB-1
	5 0 "	6.05	0 705 07	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP K, hnRNP LL, hnRNP P
IQCJ // SCHIPT	Exon Cassette	6.05	3.73E-07	(TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
SMC4	Intron Retention	1.54	1.33F-02	FTR-3, hnRNP F1, hnRNP F2, hnRNP F1, hnRNP F1, hnRNP F2, hnRNP F2, hnRNP F2, hnRNP F2, hnRNP F3,
MYNN	Evon Cassette	1.65	2 20E-03	FTR-3, hnRNP C1, hnRNP F1, hnRNP F2, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP P (T1S), HTra2beta1, HuR, KSRP, MRN1, Nova-1, Sam68, SC35, SE2/ASE, TIA.1, TIAL1, YRA,1, ZRANR2
LILODE	Intron Batantian	1.03	1 705 04	
EIFZDD	Intron Retention	1.07	1.79E-04	
FIF4A2	Alter, Terminal Exon (e10)	2.61	4.12F-05	EIF-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP Y (ILS), H1ra2beta1, HuB, KSRP, MBNL1, Nova-1, Sam68, SC35,
				SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
I PP	Alter First Evon	1 01	4 37E-04	9G8, CUG-BP1, ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H3, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP LL,
	Aller: Hist Exert	1.51	4.57 2 04	hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
000050	5 0 "	1.01	5 605 00	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD,
CCDC50	Exon Cassette	1.81	0.08E-03	KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
				FTR-3 Fox-1 Fox-2 bnRNP A1 bnRNP A2/R1 bnRNP C1 bnRNP C1 bnRNP F1 bnRNP F1 bnRNP F2 bnRNP F4 bnRNP H2 bnRNP H2 bnRNP H2 bnRNP F4
OPA1	Exon Cassette	2.12	1.32E-03	MDNI 1 Nova 1 Nova 2 DEE DDME Camede CC28 EE1 EE2/AEE EDA 00 CDa200 TH 1 TM1 1 VD 1 7DAND2
CDDN	Intron Potention	1 76	1.605.02	
		1./0	1.00E-02	
VGLL4	Alter. First Exon (e1-6)	2.93	4.50E-05	Story Conserved Teles, Foxel,
	. ,		l	HIRAZAIDNA, HIRAZDETAI, HUB, HUD, HUK, NSKY, MIBNLI, NOVA-I, NOVA-2, YSF, KBMB, SAMOS, SC35, SF1, SF2/ASF, SKp20, SKp30c, IDP43, IIA-1, IIALI, YB-1, ZRANB2
П БН3	Complex	1.84	9.00E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1,
DELLO	Exon Cassette	1.91	5.21E-04	Nova-2, PSF, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
01.0.117	5 0 1	1.74		ETR-3. Fox-1. Fox-2. hnRNP A1. hnRNP A2/B1. hnRNP C1. hnRNP C1. hnRNP E1. hnRNP E2. hnRNP F. hnRNP H1. hnRNP H2. hnRNP H2. hnRNP H2. hnRNP P. (TLS). HTra2beta1. HuB. HuD. KSRP. MRNI 1. Nova-1. Nova-2.
SLC4A/	Exon Cassette	1./6	1.34E-03	Sam68, SC35, SF1, SRo20, SRo30c, TIA-1, TIAL1, YB-1, ZRANB2
	Alter Acceptor Site	1 54	4 50E-02	FTR.3 For LARVE ALL RAVE ALL
EOMES	Complex	1.00	3.040.04	
	Alter First First (1.7, 00.01)	1.90	5.04E-04	
1	Alter First Exon (e1-/ e2()-21)	3.52	6.48E-05	9G8, CUG-BY1, ETK-3, FOX-1, FOX-2, DRKNY A1, DRKNY A2/B1, DRKNY C1, DRKNY D, DRKNY E1, DRKNY E2, DRKNY F, DRKNY H1, DRKNY H2, DRKNY H3, DRKNY F, DRKNY F, DRKNY H3, DRKNY H3, DRKNY F, DRKNY F
CLASP2	-	-		

LRRFIP2	Exon Cassette	2.60	2.40E-04	9G8, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
IP6K2	Alter. Terminal Exon (e9-11)	1.55	7.96E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR,
	Intron Retention	1.61	1.84E-04	
QRICH1	Exon Cassette	1.62	5.48E-03	Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
QARS	Alter. Acceptor Site	2.54	1.36E-03	ETR-3, hnRNP A1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HuB, KSRP, Nova-1, Sam68, SC35, TIA-1, TIAL1, YB-1, ZRANB2
CAMKV	Complex	1.68	2.14E-03	ETR-3, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, Nova-1, Nova-2, RBM5, SC35, SRp20, TIA-1, TIAL1, YB-1, ZRANB2
DCDD4	Exon Cassette	2.15	2.05E-05	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, SC35,
FUDF4	Intron Retention	2.68	3.43E-04	SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
NT5DC2	Alter. Donor Site	1.58	9.56E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
PBRM1	Exon Cassette	1.59	7.18E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
CADPS	Alter. First Exon (e1-6,e8- 14.e16-21.e60-27.e29-31)	2.65	9.98E-04	9G8, CUG-BP1, ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRo20, SRo30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
	Complex (e14,e17)	1.53	1.72E-02	
FOXP1	Exon Cassette	1.53	1.02E-03	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, INRNP A1, INRNP A2/B1, INRNP C1, INRNP D, INRNP C1,
	Intron Retention	1.62	2.94E-02	(ILS), HIra2alpha, HIra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, IDP43, IIA-1, IIAL1, YB-1, ZRANB2
PDZRN3	Alter. First Exon (e1-3,e7)	6.25	7.62E-05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2aloba, HTra2beta1, HuB, HuD, KSRP, MBNI 1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SE1, SE2/ASF, SRb20, SRb30c, TDP43, TIA-1, TIA11, YB-1, ZRANR2
CCDC14	Intron Retention	2.00	5.06F-03	FTR-3, hnRNP C1, hnRNP F1, hnRNP H2, HuB, Nova-1, Sam68, TDP43, YB-1, ZRANB2
GATA2	Intron Retention	3.27	3.84F-04	FTR-3, bnRNP A1, bnRNP C1, bnRNP F1, bnRNP F2, bnRNP F1, bnRNP H1, bnRNP H2, bnRNP P (TLS), HuB, KSRP, MBNI 1, Nova-1, RBM5, Sam68, SC35, SRb30c, TDP43, TIA-1, TIA-1, YB-1, ZRANB2
ASTE1	Exon Cassette	1.64	1.21E-02	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP K, hnRNP P (TLS), HuB, HuD, KSRP, MBNL1, Nova-1, Sam68, SC35, SRo20, TLA-1, TLA-1, ZRANB2
ACAD11/NPHP3	Intron Retention	2 29	1.81E-05	GOOG GREEV AND ALL TO A
NonDil/ NITH 5	Alter Terminal Evon (e10)	1.86	1.30E-03	
STAG1	Evon Cassette	2.15	1.01E-02	(IS) Hiradoha Hiradoha Hiradoha Huh KSPP MRNI hova-2 PSE RRM5 Sam68 Sam58 SatS SEI SEZ ASE SRA20
CONL1	Intron Petention	1.52	1.01E-02	(TO), THE LUDIA IN THE CALL THE
B3GALNT1	Exon Cassette	3.63	4.20E-05	CUGSP1. ctrj, hox-1, fox-2, hnRVP A2, b1, hnRVP A2, b1, hnRVP D, hnRVP D, hnRVP D, hnRVP E, hnRVP F, hnRVP F1, hnRVP H2, hnRVP H3, hnRVP H3, hnRVP A2, hnRVP A2, hnRVP D, hnRVP D, hnRVP D, hnRVP E2, hnRVP F2, hnRVP F1, hnRVP H3, hnRVP H3, hnRVP I (PTB), hnRVP F2, hnRVP F3, hnRVP F4, h
PHC3	Alter. Terminal Exon (e4)	1.60	4.46E-03	HTraZbeta1, HuB, HuU, HUK, KSHP, MBRLL, NOWa-1, NOWa-2, FSF, KBMO, Samo6, SC-33, S-1, SH2-0, SRP30C, TH-1, TH2L, TB-1, ZKANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP D, hnRNP D, hnRNP E1, hnRNP F, hnRNP H1, hnRNP H3, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSP, MBNLL, Nova-1, Nova-2, RBMS, Sam68, SC35, SF1, SF2/ASF, SN20, SRb30c, TIA-1, TIAL1, YB-1, ZRANB2
NCEH1	Exon Cassette	1.52	1.02E-02	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP H3, hnRNP K, hnRNP P (TLS), HTra2aloba, HTra2beta1, HuB, HuD, HuR, KSRP, MBN11, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRo20, SRo30c, TDP43, TIA-1, TIA-1, TIA-1, TIA-1, TRANB2
	Alter First Exon (e1-2)	1 53	5 00E-03	938 CILCERPT FIRST STRUCTURE THE THE THE THE THE THE THE THE THE TH
TBL1XR1	Complex	1.35	2 30E-03	HTs23blb HTs2bbl Hug Hug Hug Hug KS2 Starte 1 Note2 PERMS Sam68 Sc35 SE1 SE2/ASE SE20 SR30C TDP43 TILL 1 TILL 1 VEL 7 RAN2
	Complex	1.75	2.502.05	TTD2 Exp. Thrusteral, not not not index index index in the internet of a none of the prove of the prove of the prove of the internet of the index inde
CLDN1	Complex (e2-4)	5.08	1.24E-06	Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
NCBP2	Intron Retention	2.46	1.85E-04	ETR-3, hnRNP A1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, Nova-1, Sam68, SC35, TIA-1, TIAL1, YB-1
KIAA0226	Exon Cassette	2.46	3.08E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
KIAA0226	Intron Retention	2.22	1.14E-03	ETR-3, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP P (TLS), HuB, Nova-1, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1
FAM114A1	Complex	1.93	1.04E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2, B1, hnRNP C1, hnRNP D, hnRNP D1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRo20, SRo30c, TIA-1, TIAL1, YB-1, ZRANB2
	Alter. First Exon (e2)	2.50	2.21E-04	CUG-BP1. ETR-3. Fox-1. Fox-2. hnRNP A1. hnRNP A2/B1. hnRNP C1. hnRNP C1. hnRNP DL. hnRNP E1. hnRNP E2. hnRNP F. hnRNP H1. hnRNP H2. hnRNP H3. hnRNP H. hnRNP I (PTB). hnRNP K. hnRNP P (TLS). HTra2alaba.
KLHL5	Exon Cassette	2.19	7.95E-05	HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
LIMCH1	Exon Cassette	3.52	1.40E-03	CUG-BP1, ETR-3, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
GUF1	Exon Cassette	2.09	8.35E-04	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, RBM5, Sam68, SC35, SF2/ASF, SRp20, TIA-1, TIAL1, YB-1
DCUN1D4	Exon Cassette	4.06	1.90E-06	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2, B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1. TIAL1. YB-1. ZRANB2
	Alter, First Exon (e1)	2.46	2.44E-03	
	Alter, Terminal Exon (e5-12)	2,09	3.61F-04	
REST	Complex	2 38	8.03E-04	Job, Jober J, Erros, Iwaz, Iwaz, Iwaz, Iwaz, De ReMS, Sanka S (23, SE) Sey Jober J, Illiant L, Illi
	Mutualu Evaluaiva Eva	2.30	7.425.04	
NDEEDO	Widtualy Exclusive Exons	2.41	7.43E-04	
INPEERZ	Alter, First Exon (e1)	14./2	1.U3E-U4	300, OUG-DET, ETK-3, FUX-2, FUX-2, FUX-2, FUX-2, FUX-1, FUX-1, FUX-1, FUX-1, FUX-1, FUX-1, FUX-1, FUX-2, FU

1				
				(ILS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
MTHED21	Alter. Terminal Exon (e16)	1.80	2.70E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1,
WITTI DZE	Exon Cassette	1.86	2.50E-03	HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
TUADO	Alter Terminal Even (ed)	1 5 4	2 425 02	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-2, Sam68,
THAFO	Alter. Terminal Exon (e4)	1.04	2.43E-02	SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
000110			6.045.05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1,
PRDM8	Alter. First Exon (e2-7)	2.60	6.24E-05	HuB, KSRP, MBNI 1, Nova-1, Nova-2, PSE, RBM5, Sam68, SC35, SF1, SF2/ASE, SRo20, SRo30c, TDP43, TIA-1, TIAI 1, YB-1, ZRANB2
				CIIG-REI FTR-3 Fox-1 Fox-2 hoRNP A1 hoRNP A2/R1 hoRNP C1 hoRNP D1 hoRNP D1 hoRNP F1 hoRNP F2 hoRNP F hoRNP H1 hoRNP H2 hoRNP H2 hoRNP I (FTR) hoRNP F (TLS). HTra2aloba HTra2beta1
THAP9	Exon Cassette	1.63	2.76E-04	Hurk KSPP MRNI 1 Noval Noval Sam68 SC35 SRR30 TIALI TIALI VELT TRANSC
AFF1	Alter. First Exon (e1-3)	2.08	1.86E-05	
	-			
TET2	Exon Cassette	1.61	1.30E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, DRRWP A1, DRRWP A2, DRRWP C1, DRRWP C1, DRRWP C2, DRRWP F2, DRRWP F1, DRRWP F1, DRRWP F1, DRRWP F2, DRRWP F1, DRRWP
				MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
AP1AR	Evon Cassette	1 77	1 24F-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB,
70 1700	EXON OUSSELLE	1.77	1.242.00	HuD, KSRP, MBNL1, Nova-1, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
EXOCO0	Intron Datantian	1.04	1 205 04	CUG-BP1, ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, Nova-1, Sam68, SC35, SF1, SRp20,
EXUSUS	Intron Retenuon	1.04	1.59E-04	TIA-1, TIAL1, YB-1, ZRANB2
				ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1,
INTU	Exon Cassette	1.55	1.23E-04	Nova-1. Nova-2. PSF. RBM5. Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
				9G8 CLIG-BP1 FTR-3 EMRP Fox-1 Fox-2 hoRNP A1 hoRNP A2/B1 hoRNP C1 hoRNP C1 hoRNP D1 hoRNP F1 hoRNP F1 hoRNP F4 hoRNP H3 hoRNP H3 hoRNP H3 hoRNP H3 hoRNP K hoRNP H1
ARHGAP10	Alter. First Exon (e1-18)	1.54	4.62E-04	browney of the structure of the structur
ARFIP1	Exon Cassette	2.45	7.76E-04	
		0.04	2.005.04	
TRIM2	Alter. First Exon	2.04	3.99E-04	CUGBP1, EIR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP F1, hnRNP H2, hnRNP F (ILS), HIR22alpha,
	Alter. Terminal Exon (e6-7)	2.15	7.17E-04	HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
GUCY1B3	Exon Cassette	4.09	3.07E-03	ETR-3, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HuB, KSRP, PSF, RBM5, SC35, YB-1
FTEDU	Even Cessette	1.04	2 725 02	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2alpha, HTra2beta1,
EIFUN	EXOIT Casselle	1.94	2.72E-03	HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
ENIDO		1.74	2.565.04	CUG-BP1, ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Sam68, SC35,
ENIP2	Intron Retention	1./4	3.56E-04	SF1. SRp20. SRp30c. TIA-1. TIAL1. YB-1. ZRANB2
				CIG-BP1 FTR-3 EMRP Fox-1 Fox-2 boRNP A1 boRNP A2/B1 boRNP C1 boRNP C1 boRNP F1 boRNP F2 boRNP F2 boRNP F1 boRNP H1 boRNP H2 boRNP L(PTR) boRNP K boRNP P (TLS) HTra2beta1 HuB HuD
CEP44	Alter. Donor Site	2.72	2.54E-06	KSRP MRN11 Nova-2 RBM5 Sam68 SC35 SE1 SRo20 SRo30c TIA-1 TIA11 YR-1 ZRANB2
CVP/IV2	Intron Retention	1.86	2 2/E-03	TER 2 FOR L For 2 hold 1, HOND A 1 hold ND A 2/R1 hold P 1 1 hold P 1 hold
011 412	intron Netention	1.00	2.246-03	
RNF212	Exon Cassette	2.94	2.03E-05	CUCPCT, EIRS, FUX-1, FUX-2, INITATE AL, INITATE AL, INITATE T, INI
THEN100		1.55	1.055.00	
TMEM128	Intron Retention	1.55	1.05E-02	ETR-3, NNRNP CI, NNRNP EJ, NNRNP EZ, NNRNP EZ, NNRNP I (PTB), NNRNP K, NNRNP K (TLS), HIRAZAIPNA, HIRAZDETAI, HUB, MBINLI, NOVA-Z, SAMO8, SC35, SKP2U, SKP3UC, TIA-I, TIALI, YE-I, ZKANBZ
RAB28	Exon Cassette	2.26	1 59E-02	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB,
101020	Elen edesette	2.20	11052.02	KSRP, MBNL1, Nova-1, PSF, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
ADDDO	Alter. First Exon (e1-13)	1.60	4.54E-03	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P
AFDDZ	Intron Retention	1.89	1.09E-02	(TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
170011			0.005.00	ETR-3. Fox-1. Fox-2. hnRNP A1. hnRNP A2/B1. hnRNP C1. hnRNP C1. hnRNP E1. hnRNP E2. hnRNP F. hnRNP H1. hnRNP H2. hnRNP H2. hnRNP K. hnRNP K. hnRNP P. (TLS). HTra2beta1. HuB. HuD. KSRP. MBNL1. Nova-1.
AIP8AI	Mutualy Exclusive Exons (e/)	1.56	2.90E-03	Nova-2, PSE, Sam68, SC35, SE1, SRo20, SRo30c, TIA-1, TIAI 1, YB-1, ZRANB2
	T			
FRYL	Alter. Terminal Exon (e5)	1.62	8.80E-04	HTra2alpha HTra2bata HuR HUD HUR KSPR MRNI Nota. Nota: 9 RRM5 Sam68 Sam68 Sam68 S(35 ST SE) (SC) (SC) SC) CR36 TDP43 TIA1 TIA1 VE. TPANP2
NUP54	Exon Cassette	1.98	2.44E-04	
RASGEF1B	Exon Cassette	2.59	8.35E-05	EIT-3, DRRWP AL, DRRWP PZ, VBL, DRRWP EL, DRRWP EL, DRRWP FL, DRRWP FL
				SRp20, SRp30c, TIA-1, TIALI, YB-1, ZKANB2
HNRNPD	Exon Cassette	3.92	1.18E-04	CUG-BP1, ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F1, hnRNP F1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HuB, KSRP, Nova-1, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
HNRNPDL	Exon Cassette	2.01	3.38E-04	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, KSRP, Nova-1, Nova-2, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
LIDEE	Complex	2.29	6.24E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F1, hnRNP H1, hnRNP H3, hnRNP H3, hnRNP H3, hnRNP K, hnRNP K, hnRNP P (TLS), HTra2alpha,
HPSE	Exon Cassette	2.18	3.87E-05	HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
				FTR-3. Fox-1. Fox-2. bnRNP A1. bnRNP A2/B1. bnRNP C1. bnRNP C1. bnRNP F1. bnRNP F2. bnRNP F5. bnRNP H1. bnRNP H2. bnRNP H2. bnRNP L(PTB). bnRNP K. bnRNP P (TLS). HTra2beta1. HuR. KSRP. MRN11. Nova-1
WDFY3	Exon Cassette	1.60	3.48E-03	Nova-2, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIA11, YB-1, ZRANR2
-		-	1	
PPM1K	Exon Cassette	1.72	9.70E-03	Ency rest, rest, innoverat, innoverat, or innoveration, in
	1		1	
FAM13A	Alter. First Exon (e1-9,e11-23)	2.71	7.62E-05	
	. itol. 1 ibt Ex01 (e1-5,e11-25)		1	(ILS), HTRZZAIPNA, HTRZZIETAT, HUB, HUD, HUK, KSKP, MBNLT, Nova-1, Nova-2, PSF, RBM5, SAm68, SC35, SF1, SF2/ASF, SKp20, SKp30c, TDP43, TIA-1, TIALT, YB-1, ZRANB2

UNC5C	Exon Cassette	4.29	3.77E-05	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
ADH5	Alter. Terminal Exon (e6)	2.34	1.56E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, PSF, RBM5, Sam68, SC35, SF1, SRp20c, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
DNAJB14	Alter. Terminal Exon (e2-5)	1.90	5.95E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
MANBA	Exon Cassette	1.90	1.08E-02	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
SLC9B2	Alter. Terminal Exon (e13)	1.95	6.12E-03	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
ТВСК	Exon Cassette	1.79	1.52E-05	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
ТВСК	Exon Cassette	2.47	2.97E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1
LEF1	Exon Cassette	2.74	6.41E-04	ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
PITX2	Exon Cassette	2.02	5.91E-05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
C4orf21	Alter. Terminal Exon (e22-31)	1.54	7.70E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
SORBS2	Complex (e6-8)	9.13	1.62E-05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha,
0011202	Exon Cassette	7.86	8.41E-05	HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
BRIX1	Intron Retention	1.86	5.80E-03	ETR-3, HuB, Nova-1, Sam68, TIA-1, TIAL1
SLC1A3	Complex	2.97	1.93E-05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
C7	Alter. First Exon	5.42	1.60E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha,
	Alter. Terminal Exon	1.78	7.46E-03	HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, VB-1, ZRANB2
MAP3K1	Intron Retention	1.98	1.11E-02	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, HuB, MBNL1, Nova-1, Sam68, SC35, SF1, SRp20, TIA-1, TIAL1, YB-1
GPBP1	Exon Cassette	1.91	5.40E-04	CUG-BP1, ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
SREK1	Exon Cassette	2.68	7.65E-05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-
	Intron Retention	1.67	2.16E-02	1, Nova-2, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
OCLN	Complex (e4) Exon Cassette	1.67	1.94E-03 2.21E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
FCH02	Alter. First Exon (e1-17,e12-17)	1.53	1.62E-02	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP D1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H, hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
ARHGEF28	Alter. Terminal Exon (e16-38)	1.59	3.84E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
DACA1	Complex	1.65	2.90E-03	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha,
NAJAI	Exon Cassette	2.08	2.96E-03	HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
PPIP5K2	Exon Cassette	2.24	5.81E-05	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1
	Alter. First Exon (e1)	1.58	9.48E-03	
PHF15	Alter. Terminal Exon (e12-13)	1.98	1.98E-03	
	Complex	1.75	2.08E-03	
	Exon Cassette	2.42	6.52E-03	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2alpha, HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Sam68, SC35, SRp30c, TIA-1, TIAL1,
DDA40	Intron Retention	1.67	1.87E-02	YB-1
MATR3 //	Alter. First Exon (e1-4,e6-7)	2.27	3.45E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (TES), hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB,
SNHG4	Alter. Terminal Exon (e4)	2.48	6.34E-05	HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
WDR55	Intron Retention	2.02	1.59E-04	ETR-3, Fox-1, Fox-2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, Nova-2, SRp20, YB-1, hnRNP H2, SC35, SRp30
HARS2	Intron Retention	2.74	3.77E-04	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP I (PTB), hnRNP P (TLS), HuB, KSRP, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
PCDHGA1- 12/3/PCDHGB1- 7/PCDHGC3-5	Alter. Donor Site	2.75	1.78E-03	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
	Alter. Donor Site	1.58	8.86E-03	
ARHGAP26	Complex (e23-24)	1.59	5.85E-04	UU-BYL, LIK-5, DX-1, DX-2, DX-4, DX-14, DX-1
	Exon Cassette	1.59	5.85E-04	111122/08/21, 11/02, 11/02, 11/07, 11/07, 11/07/22, 137, TOM2, 341100, 30/32, 51, 57/7437, 37/22, 37/32/2, 11/42, 11/41, 11/4
CPLX2	Alter. First Exon (e1-2,e4-6)	2.07	1.18E-03	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP D1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I, (hTB), hnRNP K, hnRNP LL, hnRNP P

	Complex	2.69	1.18F-03	(TLS), HTra2alpha, HTra2heta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSE, RBM5, Sam68, SC35, SE1, SE2/ASE, SRo20, SRo30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
	o on piox	2.05	11102.00	TR3. FX2 bRV p1 brBVP 0 brBVP p1 brBVP F2 brBVP F2 brBVP F1 brBVP
TSPAN17	Intron Retention	1.55	1.50E-03	
				SUPPORT, 10-1
UNC5A	Exon Cassette	5.59	3.97E-05	
TDIM41	Intron Datantian	1.02	4 095 03	TTP 2 For 1 For 2
1 K11V141	Introl Retention	1.92	4.90E-03	
BRD9	Complex	1.54	5.76E-04	908, EIK-3, FOX-1, FOX-2, INRINP AJ, INRINP AZ/BL, INRINP U, INRINP U, INRINP EI, INRINP E, INRINP F, INRINP H, INRINP H, INRINP H, INRINP K, INRI
MYO10	Complex (e1-3)	2.97	6.04E-04	
				H razalpna, H razbeta1, HuB, HuD, HuK, KSKP, MBNL1, Nova-1, Nova-2, PSF, KBMB, Samo8, SC33, SF1, SF2/ASF, SKp20, SKp30c, IDP43, IA-1, IIAL1, YB-1, ZKANBZ
ZFR	Intron Retention	1.81	3.24E-03	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HuB, KSRP, Nova-1, Sam68, SC35, SF1, TIA-1, TIAL1, YB-1, ZRANB2
NADK2	Evon Cassette	1 98	9 17E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, PSF, Sam68, SC35,
TUBILE		1.50	5.17201	SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
PDF4D	Evon Cassette	3 01	1.955-04	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P
T DE#D	Exon Gasselle	5.51	1.552-04	(TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
CLICBDO	Even Cessette	1 70	4 005 02	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD,
GUSBF9	EXOII Casselle	1./0	4.90E-03	HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
THENICIP		1.00	4.145.00	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP F (TLS), HTra2alpha, HTra2beta1,
IMEM101B	Exon Cassette	1.62	4.14E-03	HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
ND051 401		1.70	1.505.00	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A3, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP K, hnRNP K, hnRNP P (TLS),
NR2F1-AS1	Exon Cassette	1.78	1.50E-03	HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
				CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H2, hnRNP H2, hnRNP H3, hnRNP I, (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS).
ELL2	Complex	3.34	8.14E-05	HTra2aloha, HTra2beta1, HuB, HuD, HuR, KSRP, MBN 1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRo20, SRo30c, TDP43, TIA-1, TIAI 1, YB-1, 7RANB2
NUDT12	Intron Retention	1.62	3 59E-02	FTR-3 bnRNP A1 bnRNP A2/B1 bnRNP C1 bnRNP L(PTR) bnRNP P (TLS) HTra2beta1 HuR MRN11 Nova-1 Nova-2 PSE Sam68 SC35 SRn20 SRn30c TLA-1 TLA11 YR-1
HODTIE	Alter First Evon (e1-3)	4 52	7.60E-05	
MCC	Alter Terminal Evon (e19)	1.96	6.96E-04	Society (10) HTraslanda HTraslanda Hurk Hurk Hurk (10) Hurk (20) HTV (10) HURK (10) HTV (10) HURK (10) HURK (10) HTV (10) HURK (10) HURK (10) HTV (10) HURK (10) H
	Alter: Terminal Exon (e15)	1.50	0.502-04	
CEP120	Complex	1.67	5.02E-04	
	Albert Territy (* 15 - 17 42)	1.50	0.505.00	
FBN2	Alter. Term Exon (e15,e17-43)	1.58	2.50E-02	908 (UG-BPT), ELR-3, FOX-1, FOX-2, RAKIVE AL, RAKIVE AZ, BLI, RAKIVE CL, RAKIVE PL, RAKIVE PL, RAKIVE PL, RAKIVE PL, RAKIVE HJ, RAKI
	Exon Cassette	2.43	4.56E-04	(ILS), HIRZ2IDRA, HIRZDERI, HUE, HUU, HUK, NOKY, WINLL, NOVAZ, PSY, KWO, SAMOS, SCJ, ST, ST/ ASY, SKD2U, SKDSUC, IDP43, IA41, IA41, TB-1, ZKANDZ
HINT1	Alter. Donor Site	1.88	7.22E-04	EIK-3, FOX-1, FOX-2, DIRKIP A1, DIRKIP C1, DIRKIP C1, DIRKIP C1, DIRKIP C2, DIRKIP C, DIRKIP C1, DIRKIP C1, DIRKIP C1, DIRKIP C1(LS), HTrazbeta1, Hub, Hub, KSRP, Nova-1, Nova-2, Samba, Dirkip C1, Di
	Exon Cassette	2.15	6.24E-05	5135, 5Kp20, 5Kp30C, 10P43, 1A41, 1AL1, 1B-1, ZKANBZ
FNIP1 //	Alter, First Exon (e1-2,e20-24)	3.70	7.42E-04	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP A2/B1, hnRNP L1, hnRNP P
RAPGEF6				(ILS), HIra2alpha, HIra2beta1, Hub, Hub, Hub, KoktP, MbNLL, Nova-2, PSF, KBM5, Sam68, SC35, SF1, SF2/ASF, Skp20, Skp30c, IDP43, IIA-1, IIA-1, Y8-1, ZKANB2
CDKL3 //	Alter. Terminal Exon (e11-	1.68	1.19F-02	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP H (PTB), hnRNP K1, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD,
PPP2CA	14,e17)			HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
FAM13B	Exon Cassette	1 70	1.30E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H (PTB), hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-
				1, Nova-2, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
HARS	Intron Retention	1.88	1.02E-02	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP P (TLS), HuB, KSRP, Nova-1, Nova-2, SC35, SRp20, SRp30c, YB-1, ZRANB2
CNPDA1	Complex	1.74	2.24E-04	ETD 3 hnDND 61 hnDND F1 hnDND F1 hnDND F7 F1S1 KSDD Nova 1 Sam68 SC35 SDn304 T16.1 T16.1 VR.1 7DAND2
UNI DAI	Intron Retention	1.61	1.92E-03	
EAVDC2	Even Cassette	1.67	7 005 04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D1, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP,
TAXD62	EXOIT Casselle	1.07	7.55L-04	MBNL1, Nova-1, Nova-2, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
CONU	Even Cessette	4.12	6.010.05	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D1, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP,
CONJE	EXOII Casselle	4.15	0.21E-05	MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
05 /54		0.00	2.045.02	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1,
C5orf54	Exon Cassette	2.82	3.04E-03	Nova-2, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
RNF44	Intron Retention	1.97	2.76E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP K, hnRNP P, (TLS), HuB, KSRP, MBNL1, Nova-1, RBM5, SC35, TIA-1, TIAL1, YB-1, ZRANB2
DBN1	Intron Retention	1.69	4.02F-04	hnRNP I (PTB), hnRNP P (TI S), PSE, SC35, YB-1
DDX41	Intron Retention	2.96	3.52E-05	ETR-3. hnRNP A1. hnRNP A2./B1. hnRNP C1. hnRNP F1. hnRNP H2. hnRNP H2. hnRNP P (TLS). HTra2alpha. HTra2beta1. HuB. KSRP. Nova-1. Nova-2. SC35. SRo20. YB-1
CI K4	Intron Retention	2.03	3.25F-04	FTR.3. hnRNP AJ, hnRNP AZ/B1, hnRNP CL, hnRNP DL, hnRNP I (I/TB), hnRNP P (TLS), HuB, KSRP, MBNL1, Nvva-1, Sam68, SC35, SF1 TLA-1 TLA-1 YR-1
FI T4	Alter Acceptor Site	2.64	1.60E-03	harRNP F1 harRNP F2 harRNP P (III) KSRP Nova-1 SC35 SR030 SR030 SR030 F1 778AB2
1617	Alter: Acceptor one	2.04	1.002.03	CICCDE ETD.2 Excl Ency hopburgh hopburg
DUSP22	Intron Retention	2.27	1.50E-03	Social States (Second States)
			1	
JARID2	Alter. First Exon (e1-4)	3.00	1.83E-04	
			1	
MYLIP	Exon Cassette	1.70	2.08E-02	
			1	MDNET MOVAT MOVAT FOR MOVAT FOR MOVE STATUCE ST

BTN2A3P	Alter. Acceptor Site	1.96	4.22E-04	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1
BTN2A1	Alter. First Exon (e1-7,e10)	2.89	5.92E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP DL, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
70040110	Alter. Terminal Exon (e3)	1.50	1.40E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, Sam68, SC35,
ZSCANIB	Intron Retention	2.01	3.54E-03	SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1
HLA-F	Alter. Terminal Exon (e5-6,e8-9)	1.81	3.61E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
ZNRD1	Intron Retention	1.56	3.80E-04	ETR-3, Fox-1, Fox-2, hnRNP C1, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, PSF, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
PPP1R11	Exon Cassette	1.70	4.70E-03	ETR-3, hnRNP A1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, MBNL1, Nova-1, PSF, RBM5, SC35, TIA-1, TIAL1, YB-1
DDR1	Alter. Acceptor Site	1.65	2.52E-03	ETR-3, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), KSRP, Nova-1, Nova-2, PSF, RBM5, SC35, SRp20, TIA-1, TIAL1, YB-1
PHF1	Intron Retention	2.14	1.30E-03	hnRNP A1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP P (TLS), HTra2beta1, KSRP, SC35, TIA-1, TIAL1, YB-1, ZRANB2
ANKS1A	Exon Cassette	1.58	1.90E-03	ETR-3. hnRNP F. hnRNP H1. hnRNP H2. hnRNP I (PTB). hnRNP K. hnRNP P (TLS). HuB. KSRP. MBNL1. Nova-1. SC35. SRo30c. TIA-1. TIAL1. YB-1. ZRANB2
ZNF76	Alter. Terminal Exon (e10)	1.74	2.38E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
PPARD	Alter. Terminal Exon (e9-10)	1.69	7.66E-05	ETR-3, hnRNP A1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
MAPK14	Mutualy Exclusive Exons (e9)	1.90	3.74E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
SRSF3	Exon Cassette	1.87	3.77E-05	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP DL, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H (PTB), hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
POLR1C	Intron Retention	1.66	1.36E-03	ETR-3, hnRNP P (TLS), HTra2beta1, HuB, KSRP, Nova-1, Sam68, SC35, SF2/ASF, TIA-1, TIAL1, YB-1
TMEM63B	Exon Cassette	3.97	2.38E-06	ETR-3, hnRNP A1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, RBM5, SC35, SRp20, TIA-1, TIAL1, YB-1, ZRANB2
EFHC1	Intron Retention	2.66	2.50E-03	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SRp20, TIA-1, TIAL1, YB-1, ZRANB2
54441054	Alter. First Exon (e1-10,e12-15)	1.67	4.37E-04	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H (PTB), hnRNP K, hnRNP P (TLS),
FAM135A	Exon Cassette	3.30	2.01E-04	HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
KCNQ5	Exon Cassette	1.67	9.79E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
BCKDHB	Exon Cassette	1.79	2.40E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P(TLS), HTra2beta1, HuB, KSRP, Nova-1, Nova-2, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1
RWDD2A	Intron Retention	2.50	1.09E-02	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HuB, Nova-1, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
ORC3	Exon Cassette	2.30	4.26E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
GRIK2	Exon Cassette	6.77	6.27E-05	9G8, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
F0X03	Alter. First Exon (e2)	14.11	1.57E-05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
TD450100 401	Alter. Terminal Exon (e2-5)	2.18	7.41E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I, hnRNP I, hnRNP A, hnRNP LL, hnRNP P (TLS), HTra2alpha,
TRAF3IP2-AS1	Exon Cassette	1.70	2.42E-04	HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
DNE146	Complex	1.50	1.16E-02	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP H, hnRNP A, hnRNP P (TLS), HTra2alpha,
RINF146	Exon Cassette	2.08	1.84E-05	HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
10/0	Complex (e10-12)	1.72	1.62E-03	ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Sam68,
MAR	Exon Cassette	2.36	7.45E-04	SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
STXBP5	Exon Cassette	2.61	2.22E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
000111	Complex	2.35	4.04E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha,
OPRIVIT	Exon Cassette	1.74	6.79E-04	HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
ARID1B	Exon Cassette	1.79	1.50E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
QKI	Intron Retention	1.59	6.56E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
TEADOA	Alter. First Exon (e3)	3.37	2.77E-06	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F2, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP H (TLS), HTRa2alpha. Httra2alpha. Htra2alpha. Httra2alpha. Httra2alph
IFAP2A	Exon Cassette	3.16	2.17E-05	MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
KIF13A	Exon Cassette	2.22	1.78E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
TDP2	Alter. Donor Site	1.53	5.78E-03	9G8, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2

PH191 Alter for work 9.34 3.44 000000000000000000000000000000000000	TRIM27	Intron Retention	1.70	4.40E-04	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, Nova-1, Nova-2, Sam68, SC35, SRp200, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
$ \frac{9000}{900} = 8 km [\log k (((($	PPP1R18	Alter. First Exon (e1)	2.48	3.41E-04	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, SC35, SRp20c, TIA-1, TIAL1, YB-1, ZRANB2
UDDA1 General 2.56 4.566 Space (n. N. 2000) IAG General 2.58 4.566 Space (n. N. 2000) Space (n. N. 2000) </td <td>0011001</td> <td>Alter. Terminal Exon (e16)</td> <td>1.72</td> <td>2.63E-04</td> <td>ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2alpha, HTra2beta1, HuB, KSRP, Nova-1, Nova-2, PSF, Sam68, SC35, SRp20,</td>	0011001	Alter. Terminal Exon (e16)	1.72	2.63E-04	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2alpha, HTra2beta1, HuB, KSRP, Nova-1, Nova-2, PSF, Sam68, SC35, SRp20,
HBAC Domain 27:0 458:06 Antifer Disa Description Descripion	CCHCRI	Complex	2.06	4.54E-03	SRp30c, YB-1, ZRANB2
BABS Alter, Face Sci Li Li Corp. 103. AddP J. MOP T. MOP L. MoP T. MOP L. MoP T. MoP R. MoP P. TOS, R. MULL MARK 2015, TPR3, TAL TULL 1, Li 20002 BALDON // IVP Multic Face Sci Li 103. Li Corp. 103. AddP J. MOP L. MoP T. MoP P. TUL, MOP L. MOP P. TUL,	HLA-C	Complex	2.25	4.50E-06	hnRNP P (TLS), KSRP, Nova-1, Nova-2, SC35, SF2/ASF, SRp20, SRp30c, YB-1
Humber biologic Alter Arge biologic The Arge biologic	BAG6	Alter. First Exon (e1)	1.82	1.57E-04	CUG-BP1, ETR-3, hnRNP A1, hnRNP F1, hnRNP H2, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), KSRP, MBNL1, RBM5, SC35, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
Discop These Tensor Ison Iso		Alter. First Exon (e1-11)	2.00	1.12E-03	
Info Operate 2.12 3.5460 Norm Host, Line J, Park J, Park J, Sterk	HLA-DUB //	Alter. Terminal Exon (e18-20)	1.59	1.10E-02	
Amb. Tensor Use sp2.eds 2.23 2.243 Operation of the space of	TAP2	Complex	2.10	3.54E-05	KSKP, MENLI, Nova-1, Nova-2, PSF, Samos, SU39, SF1, SKp20, SKp30C, HA-1, HALI, YB-1, ZKANBZ
Her Adva Compare Lin2 307 4486 Use PL 1014 (1 resp) (2), 1102 (2)		Alter. Terminal Exon (e2,e4-6)	2.67	2.94E-03	
Inter Relation 2.10 1.82.4 New F, Haller S, Haller S, Jacking S, Statu,	HLA-DMA	Complex (e2)	3.07	4.48E-05	CUG4P1, EIR-3, Fox-1, Fox-2, InRNP A1, INRNP A2/B1, INRNP C1, INRNP E1, INRNP E1, INRNP F2, INRNP F1, INRNP F2, INRN
MBB Attern Terminal from fan 1.44 L BECO ETRS 7-or 1, Fand P., Harling P. J., Ha		Intron Retention	2.10	1.43E-04	Nova-1, Nova-2, KBM3, Sam68, SC35, SKp20, SKp30c, TIA-1, TIAL1, YB-1, ZKAINB2
Mode Holes Relation 1.75 4.18644 TH4, TR4, T64, 200482 WRS2 Meth. Terrors Exercise Conference	DVDD	Alter. Terminal Exon (e7)	1.64	1.48E-03	ETR-3. Fox-1. Fox-2. hnRNP A1. hnRNP A2/B1. hnRNP A2, hnRNP F. hnRNP H1. hnRNP H2. hnRNP I (PTB). hnRNP K. hnRNP P (TLS). HuB. KSRP. MBNL1. Nova-1. RBM5. Sam68. SC35. SF2/ASF. SRo20. SRo30c.
Mess Output State Clubble hash State Clubble hash State State <td>RXRB</td> <td>Intron Retention</td> <td>1.78</td> <td>4.16E-04</td> <td>TIA-1, TIAL1, YB-1, ZRANB2</td>	RXRB	Intron Retention	1.78	4.16E-04	TIA-1, TIAL1, YB-1, ZRANB2
VPSI2 Intern Retention 2.22 7.987.05 Hex, RSRP, MSRL, Nova, LNova, PSF, BBMS, Sams, Spi3,		Alter, Terminal Exon (e13)	1.77	8.21E-04	CUG-BP1. ETR-3. Fox-1. Fox-2. hnRNP A1. hnRNP A2/B1. hnRNP C1. hnRNP D1. hnRNP D1. hnRNP E2. hnRNP E2. hnRNP F1. hnRNP H1. hnRNP H2. hnRNP I (PTB). hnRNP A. hnRNP P (TLS). HTra2beta1. HuB. HuD.
Op/Inst. 65:30 196 2.24653 TIR3. hm/PA /L holl/P C, hm/PP CL, hm/PP CL, hm/PP CL, hm/PP P (TS, Hm22/pha, Hm22/ph	VPS52	Intron Retention	2.32	7.89F-05	HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRo20, SRo30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
WD84 Intern Networds 2.32 6.56/2 FTRS, InteRP 21, InteRP 41, InteRP 21, InteRP 41, InteRP 21, InteRP 41, InteRP 42, InteRP 41, IntER 42, InteRP 41, IntER 42, InteRP 41, IntER 42, InteRP 41, IntER 44, InteRP 42, InteRP 41, IntER 44, InteRP 42, InteRP 41, IntER 44, InteRP 4		Complex (e2-3)	1.96	2.04F-05	
B012 Dom Cassette 1.58 6.356/04 FTR3. httpPL AL, httpPL AL, httpPL AL, httpPL F, httpPL P, htttpPL P, httpPL P, httttpPL P, httpPL P, httpPL P, h	WDR46	Intron Retention	2.32	8 56F-04	ETR-3, hnRNP A1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP P (TLS), HTra2alpha, HTra2alpha, HTra2beta1, KSRP, Nova-1, PSF, RBM5, Sam68, SC35, SRp30c, TIA-1, TIAL1, YB-1
Intern Retention 2.12 6.452-04 ZMM/E Control Contro Control Contro Contro Contro <		Exon Cassette	1.58	6.36E-04	FTR-3 hnRNP &1 hnRNP F1 hnRNP F1 hnRNP F2 hnRNP F hnRNP H1 hnRNP H2 hnRNP H2 hnRNP H hnRNP K hnRNP P (TIS) HTra2alnha HTra2hata1 HuR KSRP MRNI 1 Nova-1 RRM5 SC35 SRn30c VR-1
Alter fund tions (e) 161 2.26604 CUTA Competition 151 2.26604 Intron Relation 188 3.71605 Intron Relation 188 3.71605 WPE3 Intron Relation 162 2.8563 ETR3, IntRNP F, In	RGL2	Intron Retention	2.12	8.42E-04	
OUTA Description 151 2.02033 ETR3. hmRPP 1, hmRPP 12, hmRPP 12, hmRPP 17, BMP P1, hmRPP P1(15), Hm32 2015 YPE3 Inton Relation 152 2.02633 ETR3. hmRPP 1, ImRPP 17, ImRPP 17, ImRPP 17, ImRPP 17, ImRPP 17, ImRPP 20, ImRPP 17, ImRPP 17		Alter First Evon (e1)	1.61	2 76E-04	
Other Intern Relation 1.86 \$71E46 Other Manual Y, Linkink Y, Dawler Y, Dia Manuel Y, Manuel Y, Dialy, Novel Y, Dialy K,	CLITA	Compley	1.51	2.60E-03	FTR-3 hnDND 61 hnDND F hnDND H1 hnDND H2 hnDND H (DTR) hnDND P (TIS) Nova 1 DRM5 Sam68 SC35 VE.1 7RAND2
WP3 Initial Institution 1.62 2.586.03 ETR. Institution (FL) PTR3 Initial Institution PTR3 PTR3<	COTA	Introp Retention	1.91	3.71E-05	
Instrumentary 1.00 Loss Part 1, sol, the L, ball MP, CL, ball MP,	VIDE2	Intron Retention	1.60	2.26E.02	ETD 2. hsDND L (DTD), hsDND D (TLS), Hup, KCDD, MDNL1, Nave 1, Nave 2, SC25, VD 1
DST Jackbox Long Cost Long Cost Jackbox Long Cost Long Cost <thlong cost<="" th=""> Long Cost <thlong cost<="" t<="" td=""><td>TIFT 3</td><td>Altor First Even (c1.2)</td><td>2.40</td><td>1.49E.02</td><td></td></thlong></thlong>	TIFT 3	Altor First Even (c1.2)	2.40	1.49E.02	
Data Zold Custom Zold Science Total Science Total Science Total Science Total Science Total Science Total Science SNPP1 Explore 6.09 2.15605 Sci CGP1; ETRA, Too, 1, Fao2, JinNP 4, JinNP 402, JinNP 402, JinNP 60, LinNP 2, JinNP 2, JinNP 2, JinNP 1, JinNP 11, TinNP	DST	Firen Cossette	3.40	7.005.05	
SNAP91 Exon Cassette 6.09 2.186.05 9eb. GOADSPT, EPRS, FOG. 1, rock, marker Ag, marke		EXOII Casselle	2.00	7.99E-00	
MAP3K7 Exon Cassette 11/22 3.00E03 Compton	SNAP91	Exon Cassette	6.09	2.15E-05	
MAPSK7 Exon Cassette 1.52 3.00C33 ROUGH 1, ETOS, TOTAL TODA, TODA					
PNISR Intron Retention 1.72 1.96E-03 ETR3, Kev, J,	MAP3K7	Exon Cassette	1.52	3.00E-03	
PNISR Introl Reletion 1.172 1.90cco First, Fox 2, Fox 2, InRNP A, J, InRNP A, J, InRNP E, J, InRNP E, J, InRNP F, EJ, InRNP F, EJ, INRNP F, EJ, INRNP F, IN		Intron Potention	1 72	1.065.02	Nova-1, Nova-2, Saliloo, 50-50, 51 1, Sty2co, Sty2ou, 101-45, 114-1, 16-1, 204402
Introd 1.34 <	PNISR	Intron Retention	1.72	1.30E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, Nova-1, Sam68, SC35, YB-1
HACE1 Exon Cassette 1.86 8.36E03 COOLENT, LINK, Prod., Tuber, Link, Hanne, 2, Jinkhor EJ, Jinkh		Introl Retention	1.55	1.49L-02	
MICAL1// Alter. Terminal Exon (e2) 1.69 1.74E.03 ETRAS, FMRP, Fox1, Fox2, hnRNP P, (nLRNP Z, binRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP F1, hnRNP H2, hnRNP I, thRNP P, (nLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TDP43, TiA-1, TIAL1, YE1, ZRANB2 WASF1 Exon Cassette 1.56 5.50E.03 EURophy, LNRNP P, (nLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YE1, ZRANB2 HDDC2 Exon Cassette 1.68 4.83E.06 ETR3, Fox1, Fox2, hnRNP A1, hnRNP A2/B, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E1, hnRNP H2, hnRNP H, HNRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YE1, ZRANB2 ECHDC1 Exon Cassette 1.91 9.16E.04 ETR3, Fox1, Fox2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YE1, ZRANB2 PTPRK Complex 2.52 1.83E.04 CUG491, ETR3, Fox1, Fox2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP D, hnRNP F1, hnRNP F2, hnRNP F1, hnRNP F1, hnRNP F1, hnRNP F2, hnRNP F1, hnRNP F	HACE1	Exon Cassette	1.86	8.36E-03	WRNI N. N. 2. Samba S. 25 Shoro C. Sano Tala Tala Y. J. Pakinz
Inter-terminal conflexity 100 <td>MICALL //</td> <td>Alter Terminal Evon (e2)</td> <td>1.69</td> <td>1 7/F-03</td> <td></td>	MICALL //	Alter Terminal Evon (e2)	1.69	1 7/F-03	
Lorder Internation 2.01 Houring and the second and t	7BTB24	Intron Retention	2 31	1.0 4E 00	
WASF1 Exon Cassette 1.56 5.50E-03 OUGSE, Initiat PL, Initiat PL, Disc, Initat PL, Disc, PL, Disc, PL, Disc, PL, Disc, PL, Disc, PL, Disc,	LUIDEA	intron Netention	2.31	4.002-04	
HDDC2 Exon Cassette 1.68 4.83E-06 ETR3, Fox.1, Fox.2, InRNP A1, InRNP A2[1, InRNP C1, InRNP D, InRNP E1, InRNP E1, InRNP E1, InRNP E1, InRNP F1,	WASF1	Exon Cassette	1.56	5.50E-03	Hrazhatal Hurk Hur KSP MRNI Nova. 1 Nova. 2 NER REMS Samfa Sci SE SE SE SESSE SR20 SR30- TDALI TILL TILL VI. 17. TRANZ
HDDC2 Exon Cassette 1.68 4.83E-06 Complex (e.g., minder 4, minder 4, minder 4, minder 4, minder 1, minder 12, minder 14, minder 1					TTD 2 Grave Levy a hour hour, monther, more and the relation of the second of the seco
ECHDC1 Exon Cassette 1.91 9.16E-04 ETR3, for.1, for.2, fnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP D, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H1, hnRNP H2, hnRNP F (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SF20, SR30c, TIA-1, TIAL1, YB-1, ZRAMB2 PTPRK Complex 2.52 1.83E-04 CUGBP1, ETR3, for.1, For.2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HUB, HUR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRAMB2 AHI1 Exon Cassette 3.58 3.92E-05 HTra2beta1, HuB, HUD, HUR, KSRP, MBNL1, Nova-1, Nova-2, SR, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRAMB2 BCLAF1 Exon Cassette 3.81 3.62E-05 ETR3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP P (TLS), HTra2beta1, HUB, Nova-1, Nova-2, SBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRAMB2 WYMAI // PLAGL1 Alter. First Exon (e2) 3.09 3.16E-04 CUG-BP1, ETR3, for.1, For.2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP F, (TLS), HTra2alpha, HTra2beta1, HUB, HUD, HUR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRAMB2 BCLAF1 Alter. First Exon (e2) 1.68 7.	HDDC2	Exon Cassette	1.68	4.83E-06	MRNI Nova-1 Nova-2 PS Sam68 C35 SR020 SR030C TA-1 TAI 1 YAI 7PA NB2
ECHDC1 Exon Cassette 1.91 9.16E-04 Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 PTPRK Complex 2.52 1.83E-04 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D1, hnRNP D1, hnRNP E1, hnRNP E2, hnRNP F1, hnRNP H2, hnRNP H1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP H1, hnRNP H2, hnRNP F1 (PTB), hnRNP F1, Nova-2, RBM5, Sam68, SC35, SF1, SF20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 BCLAF1 Exon Cassette 3.81 3.62E-05 ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, Nova-1, Nova-2, RBM5, Sam68, SC35, SF1, SF20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 BCLAF1 Alter. Donor Site 1.77 4.58E-03 SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 PLAGL1 CUG-B91, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D2, hnRNP F, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP H2, hnRNP F, hnRNP H2, hnRNP F, hnRNP H2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP P (TLS), HTra2alpha, HTra2beta					TR3-F 6x21 F0x2 brokP41 brokP41 brokP0 4/R1 brokP0 C1 brokP0 C1 brokP0 F1 brokP0 F2 brokP0 F2 brokP0 F4 brokP0 H1 brokP0 H2 brokP0 F(JS) H7ra2beta1 Hu/B KSRP MRNI 1
PTPRK Complex 2.52 1.83E04 CluBeP1, ETR-3, fox1, fox2, nnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP D, hnRNP D, hnRNP D, hnRNP L, hnRNP H2, hnRNP H2, hnRNP H2, hnRNP H3, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2alpha, AHI1 Exon Cassette 3.58 3.92E05 HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 AHI1 Exon Cassette 1.53 1.08E02 ETR-3, InRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E2, hnRNPF, hnRNH1, hnRNPH2, hnRNP(TLS), HTra2alpha, HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1 BCLAF1 Exon Cassette 3.81 3.62E05 ETR-3, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP D, hnRNP E1, hnRNP H2, hnRNP H1, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, Nova-1, Nova-2, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1 BCLAF1 Exon Cassette 3.81 3.62E05 ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP H2, hnRNP H1, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, Nova-1, Nova-2, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 HYMAI // PLAGL1 Alter. Donor Site 1.77 4.58E03 CUGBP1, ETR-3, fox-1, fox-2, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, SF, RBM5, Sam68, SC35, SF1,	ECHDC1	Exon Cassette	1.91	9.16E-04	Nova-1 Nova-2 PSE Sam68 SC35 SE1 SBn20 SBn30c TIA-1 TIAI 1 VB-1 ZRANR2
DURDER Dist Dist <thdist< th=""> Dist Dist <t< td=""><td></td><td>Complex</td><td>2 52</td><td>1 83E-04</td><td>CICLRPT FTR.3 Fox 1 Fox 2 hoRNP H3 hoRNP 621 KBNRD FC1 hoRNP F0 hoRNP F1 hoRNP F1 hoRNP F2 hoRNP F1 hoRNP H3 hoRNP H3 hoRNP H3 hoRNP H3 hoRNP K hoRNP F (IS) HTra2aloha</td></t<></thdist<>		Complex	2 52	1 83E-04	CICLRPT FTR.3 Fox 1 Fox 2 hoRNP H3 hoRNP 621 KBNRD FC1 hoRNP F0 hoRNP F1 hoRNP F1 hoRNP F2 hoRNP F1 hoRNP H3 hoRNP H3 hoRNP H3 hoRNP H3 hoRNP K hoRNP F (IS) HTra2aloha
Bits Dissection Dissection <td>PTPRK</td> <td>Exon Cassette</td> <td>3 58</td> <td>3 92F-05</td> <td>HTra2beta1. HuB. HuD. HuR. KSRP. MBN11. Nova-2. PSF. RBM5. Sam68. SC35. SF1. SF2/ASF. SRo20. SRo30c. TDP43. TIA-1. TIA1. YB-1. ZRANB2</td>	PTPRK	Exon Cassette	3 58	3 92F-05	HTra2beta1. HuB. HuD. HuR. KSRP. MBN11. Nova-2. PSF. RBM5. Sam68. SC35. SF1. SF2/ASF. SRo20. SRo30c. TDP43. TIA-1. TIA1. YB-1. ZRANB2
AHI1 Exon Cassette 1.53 1.08E-02 SRp30c, TDP43, TIAL, TALL, YB1 BCLAF1 Exon Cassette 3.81 3.62E-05 SRp30c, TDP43, TIAL, TALL, YB1 BCLAF1 Exon Cassette 3.81 3.62E-05 SRp30c, TDP43, TIAL, TALL, YB1 BCLAF1 Exon Cassette 3.81 3.62E-05 SRp30c, TDP43, TIAL, TALL, YB1 BCLAF1 Exon Cassette 1.77 4.58E-03 SRp20c, SRp30c, TIA-1, TIALL, YB-1, ZRANB2 HYMAI // PLAGL1 Complex (e8-19) 3.09 3.16E-04 CUG-BP1, ETR-3, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 EPM2A Alter. First Exon (e2) 1.68 7.76E-04 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A2/B1, hnRNP C1, hnRNP D2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H, hnRNP H2, hnRNP F, MRNP H1, hnRNP H2, hnRNP H2, hnRNP H1, hnRNP H2, hnRNP F, hnRNP H1, hnRNP P, (TLS), HTra2alpha, HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 SYNE1 Alter. First Exon (e1-6,e8- 1.58 3.62E-04 hnRNP F, MSNP, A1, hnRNP A2/B1, hnRNP C1, hnRNP A2		Elen edesette	0.00	0.0EE 00	FTR-3 bnRNP A1 bnRNP A2/R1 bnRNP C1 bnRNPF1 bnRNPF2 bnRNPF bnRNH1 bnRNH2 bnRNPH3 bnRNPI/PTR3 bnRNP/I/TR3 bnRNPP/I/S1 Hrz2beta1 Huß KSRP MRNI1 Nova-1 Nova-2 Sam68 SC35 SE1 SRo20
BCLAF1 Exon Cassette 3.81 3.62E-05 ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, Nova-1, Nova-2, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 HYMAI // PLAGL1 Alter. Donor Site 1.77 4.58E-03 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP D, hnRNP D, hnRNP D, hnRNP E1, hnRNP E1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H1, hnRNP P, TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 EPM2A Alter. First Exon (e2) 1.68 7.76E-04 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A2/B1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MSNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 SYNE1 Alter. First Exon (e1-6,e8- 15, e19-88, e90-133,e135) 1.58 3.62E-04 NGRP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MSNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 SYNE1 Alter. First Exon (e1-6,e8- 15, e19-88, e90-133,e135) 1.58 3.62E-04 NGNP P (TLS), HTra2alpha, HTra2beta1, HuB, HUD, HUR, KSRP, MSNL1, Nova-1, No	AHI1	Exon Cassette	1.53	1.08E-02	SR030C TDP43 TIAI TIAI 1 KB1
BCLAF1 Exon Cassette 3.81 3.62E-05 SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 HYMAI // PLAGL1 Alter. Donor Site 1.77 4.58E-03 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP D, hnRNP D, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP F (TLS), HTra2alpha, Hra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 EPM2A Alter. First Exon (e2) 1.68 7.76E-04 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2alpha, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 SYNE1 Alter. First Exon (e1e-6,e8- 15, e19-88, e90-133,e135) 1.58 3.62E-04 PGR, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A2/B1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP I (PTB), HNRNP F TIR-3, FOX-1, Fox-2, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP D, hnRNP F2, hnRNP F, hnRNP F1, hnRNP F1, hnRNP F2, hnRNP F3, hnRNP F1, hnRNP F4, hnRN					FTR-3, bnRNP A1, bnRNP A2/R1, bnRNP C1, bnRNP C1, bnRNP F1, bnRNP F2, bnRNP F5, bnRNP H1, bnRNP H2, bnRNP L(PTB), bnRNP P (TLS), HTra2aloba, HTra2beta1, HuB, Nova-1, Nova-2, RBM5, Sam68, SC35,
Alter. Donor Site 1.77 4.58E-03 HYMAI // PLAGL1 Complex (e8-19) 3.09 3.16E-04 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP D, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 EPM2A Alter. First Exon (e2) 1.68 7.76E-04 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP K, hnRNP I (PTB), hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 SYNE1 Alter. First Exon (e16,e8- 15,e19-88,e90-133,e135) 1.58 3.62E-04 SRP, FRB.4, SC35, SF1, SRP20, SRP, MSL1, Nova-1, Pox-2, PSF, RBM5, Sam68, SC35, SF1, SRP20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2	BCLAF1	Exon Cassette	3.81	3.62E-05	SRb20, SRb30c, TIA-1, TIALI, YB-1, ZRANB2
HYMAI // PLAGL1 Complex (e8-19) 3.09 3.16E-04 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP DL, hnRNP F2, hnRNP F, hnRNP H3, hnRNP H2, hnRNP H2, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP FX, HnRAP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 EPM2A Alter. First Exon (e2) 1.68 7.76E-04 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP F, INRNP H1, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 SYNE1 Alter. First Exon (e1-6,e8- 15,e19-88, e90-133,e135) 1.58 3.62E-04 SRP. For A1, Fox-2, hnRNP A2/B1, hnRNP A2/B1, hnRNP A2/B1, hnRNP D, hnRNP D, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H2, hnRNP F, H2, hnRNP F, H2,		Alter, Donor Site	1.77	4.58E-03	
PLAGL1 Exon Cassette 1.97 3.58E-05 HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 EPM2A Alter. First Exon (e2) 1.68 7.76E-04 CUG-BP1, ETR-3, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP F2, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 SYNE1 Alter. First Exon (e1-6,e8- 15,e19-88,e90-133,e135) 1.58 3.62E-04 PG8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A2/B1, hnRNP A2/B1, hnRNP D, hnRNP D, hnRNP D, hnRNP E1, hnRNP E1, hnRNP E1, hnRNP F2, hnRNP F1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP I (PTB), hnRNP K, hnRNP I, HUB, HUD, HUR, KSRP, MSNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2	HYMAI //	Complex (e8-19)	3.09	3.16E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F2, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha,
EPM2A Alter. First Exon (e2) 1.68 7.76E-04 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E1, hnRNP H2, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSPP, MBNL1, Now-2, PSF, RBM5, Sam68, SC35, SF1, SRp.20, SRp.30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 SYNE1 Alter. First Exon (e1-6,e8- 15.e19-88.e90-133,e135) 1.58 3.62E-04 FRRM P, Fox-2, hnRNP F, hnRNP A2/B1, hnRNP A2/B1, hnRNP A2/B1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP E1, hnRNP E1, hnRNP F2, hnRNP F1, hnRNP H2, hnRNP H2, hnRNP H2, hnRNP H1, hnRNP H2, hnRNP F1, HNRNP H2,	PLAGL1	Exon Cassette	1.97	3.58E-05	HIra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
EPM2A Alter. First Exon (e2) 1.68 7.76E-04 Hub. Hub. Hub. Hub. Hub. Hub. Hub. Hub.					CUG-RP1, FTR-3, Fox-1, Fox-2, bnRNP A1, bnRNP A2, bnRNP A2, bnRNP A2, bnRNP A2, bnRNP A2, bnRNP A2, bnRNP A1, bnRNP A2, bnRNP A2, bnRNP A2, bnRNP A2, bnRNP A3, bnRNP A3, bnRNP A4, bnRNP
SYNE1 After. First Exon (e1-6,e8- 15,e19-88,e90-133,e135) 1.58 3.62E-04 9G8, CUG-BP1, ETR-3, FMRP, Fox-1, Fox-2, hRNP A1, hnRNP A2/B1, hnRNP A2/B1, hnRNP DL, hnRNP DL, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP H2, hnRNP F, h	EPM2A	Alter. First Exon (e2)	1.68	7.76E-04	HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRo20, SRo30c, TDP43, TIA-1, TIA1, YB-1, 7RANR2
SYNE1 15,e19-88,e90-133,e135) 1.58 3.62E-04 hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRo30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2	0.0.7	Alter. First Exon (e1-6.e8-		0.00	9G8, CUG-BP1, ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D1, hnRNP D2, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP H4, hnRNP H4
	SYNE1	15.e19-88.e90-133.e135)	1.58	3.62E-04	hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRo20, SRo30c, TDP43, TIA-1, TIA-1, YR-1, 7RANR/2

			1	
PDE10A	Complex (e5)	2.17	1.66E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2, B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H2, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MRNI 1, Mova-1, Nova-2, PSE, RBM5, Sam68, SC35, SE1, SE2/4SE, SRn20, SRn30, TDP43, TI41, TI41, YB, TRANR2
DLL1	Alter. Terminal Exon (e5-11)	3.05	1.22E-04	CUG-BP1, ETR-3, hnRNP A1, hnRNP A2, B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, KSRP, MBNL1, Nova-1, PSF, RBM5,
PSMG3-AS1	Exon Cassette	1.53	5.64E-03	9GS, Super, Supe
NUDT1	Alter. First Exon (e2-3)	1.75	7.02E-03	968, CUG-BP1, ETR3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP D, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H3, hnRNP H3, hnRNP H7, hnRNP K, hnRNP LL, hnRNP P (TIS) HTT-Salaba
WIPI2	Exon Cassette	1.62	1.12E-03	ETR3, Fox1, Fox2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP F, hnRNP F, hnRNP F, hnRNP H2, hnRNP F,
RAC1	Exon Cassette	3.26	3.80E-04	VOV#2, FST, Sallido, SCST, ST2/KST, SRD2D, SRD3DL, TDP45, TR41, TR41, TB-1, ZRAIN52 CUG5P1, ETR-3, Fox-1, Fox-2, InRNP A1, hnRNP A2/B1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Num 2, Competer ScST ST2/KST, SRD2D, SRD3DL, TDP43, TA1, TA1, YD1, ZRAIN52
KLHL7	Alter. Terminal Exon (e6-7)	2.15	6.04E-04	968, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha,
FAM221A	Exon Cassette	3.31	9.40E-04	HITAZDEBIAL, HUD, HSKY, MBIVLI, NOVAZ, HSKY, KBMS, SARDAS, SC3S, SF1, SF2/ASF, SKD2O, SKD3OC, TDF43, TIAL1, TIAL1, TIAL1, TAL1, KANBZ CUG5P1, ETR-3, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E2, hnRNP F2, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP F (TLS), HTra2beta1, HuB, HuD, KSRP, MBNI 1, hup 1, hup 2, DEC Space SC32, SC32, SC32, SC4, TADAN22
	Alter Terminal Evon (e6)	2 15	6.04E-04	MBILL, NUWAY, NUWAY, FST, SAINDO, SC33, SME2U, SME2U, INFJ, INFJ, INFJ, ISAINT, ISAINDO, ISAINT, ISAIN
KLHL7	Alter, Terminal Even	2.13	0.04L-04	
FAM221A	Exon Cassette	3.31	9.40E-04	CUGBP1, ETR-3, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP D, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP,
PPIA	Exon Cassette	2.21	1.34E-03	ETR-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, RBM5, Sam68, S225, Speace, TIA 1, TU V 1, VP 1, ZPANP2
	Alter Acceptor Site	2.04	5 14E 02	
UPP1	Aiter: Acceptor Site	2.04	5.142-03	CUG49P1, EIR-3, Fox-1, Fox-2, Fox-1,
	Exon Cassette	1.66	6.83E-04	Nova-1, Nova-2, PST, RBMS, Samos, SU3S, SRp2U, SRp3U, 104-1, 114-1, 114-1, 12-1, ZRAWS2
ZNF138	Exon Cassette	1.78	7.56E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
STAG3L4	Exon Cassette	1.77	1.56E-05	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Sam68, SC35, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1
AUTS2	Exon Cassette	1.68	7.60E-03	CUG-BP1, ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
WBSCR22	Intron Retention	1.62	5.06E-03	ETR-3, hnRNP F, hnRNP H1, hnRNP H2, hnRNP K, hnRNP P (TLS), HuB, KSRP, SC35, TIA-1, TIAL1, YB-1, ZRANB2
FLN	Complex	1.57	4.63E-04	CUG-BP1, ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2,
LLIN	Exon Cassette	3.75	2.56E-04	PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
GTF2IRD1	Intron Retention	1.51	4.04E-03	ETR-3, hnRNP I (PTB), hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SRp30c, YB-1
MAGI2-AS3	Exon Cassette	2.39	5.44E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
DMTF1	Alter. Acceptor Site	1.58	2.87E-02	ETR-3, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, KSRP, Nova-1, Sam68, SC35, TDP43, TIA-1, TIAL1, YB-1
ADAM22	Alter. Terminal Exon (e29)	1.53	6.17E-05	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D1, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
GTPBP10	Exon Cassette	2.41	4.78E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SF2/ASF, SRp20c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
ZNF655	Alter. Terminal Exon (e4-7)	2.67	4.84E-06	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E2, hnRNP F2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MRNI 1, Nova-1, Nova-2, PSE, Sam68, SC35, SF1, SF2/ASE, SRo20, SRo30c, TDP43, TIA-1, TIA-1, YB-1, ZRANB2
ZNHIT1	Exon Cassette	1.66	2.42E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP H2, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SRo20, SRo30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
PMPCB	Intron Retention	2.16	2.21E-04	ETR-3, hRNP A1, hRNP A2/B1, hRNP C1, hRNP E1, hRNP E2, hRNP F, hRNP H1, hRNP H2, hRNP I (PTB), hRNP P (TLS), HuB, KSRP, Nova-1, Nova-2, Sam68, SC35, SRo20, TIA-1, TIAL1, YB-1, ZRANB2
DLD	Alter. Acceptor Site	1.65	2.68E-02	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP I (PTB), hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, Sam68, SC35, SRp30c, TIA-1, TIAL1, YB-1
	Alter. First Exon (e1)	4.12	1.54E-05	
ST7 // ST7-0T3	Alter. Terminal Exon (e25)	2.26	7.15E-04	905, CUG-BYL, ELK-3, FWIRF, FOX-1, FOX-2, INKIVP AZ, INKIVP AZ, INKIVP CL, INKIVP UL, INKIVP EL, INKIVP EZ, INKIVP FL, INKIVP HZ, IN
	Exon Cassette	2.56	8.78E-04	nnrinr r (ils), Hirazaipna, Hirazbetai, Hub, Hub, Hub, KSKY, MBINLI, Nova-1, Nova-2, PSF, KBMS, Sambb, SC39, SFI, SF2/ASF, SKp2U, SKp3UC, IDP43, IIA-1, IIALI, YB-1, ZKANB2
NAA38	Intron Retention	1.69	2.70E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
CALU	Exon Cassette	1.59	7.94E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, PSE, RBM5, Sam68, SC35, SE1, SRo20, SRo30c, TDP43, TIA-1, TIA1, 1, YB-1
NDUFB2	Exon Cassette	1.79	2.62E-03	ETR-3, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, KSRP, MBNL1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRa20, SRa30, TIA-1, TIA-1, PB-1, ZRAMR2
GSTK1	Intron Retention	1.56	6.56E-03	ETR-3, hnRNP 1 (PTB), hnRNP 7 (ILS), Nova-1, Nova-2, SRp30c, TJA-1, TIAL1, YB-1

				FTR-3 Fox-1 Fox-2 hoRNP &1 hoRNP &1 hoRNP C1 hoRNP C1 hoRNP H1 hoRNP H2 hoRNP L(PTR) hoRNP K hoRNP P(TLS) HTra2heta1 HuR HuD KSRP Nova-1 PSE Sam68 SC35 SE1 SRo20
CASP2	Intron Retention	2.33	7.81E-04	SR30c TIAL TIAL YEA 7 RAMP2
				TR3 Fox1 Fox2 Fox2 Fox2 Fox2 Fox2 Fox2 Fox2 Fox2
ATP6V0E2	Exon Cassette	1.59	9.00E-04	SE2/ASE SR030c. TIA-1. TIAL1, YB-1. ZRANB2
	5 9 11			CUG-BP1, ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP P (TLS), HTra2alpha, HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-
INSIG1	Exon Cassette	1./1	3.38E-04	1, Nova-2, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
DNE20	F 0 11	1.50	0.005.00	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD,
RNF32	Exon Cassette	1.56	2.63E-02	KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
ICA1	Exon Cassette	2.80	1.50E-05	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, KSRP, Nova-1, Sam68, SC35, SRp30c, TIA-1, TIAL1, YB-1
ET)/1	Alter. First Exon (e4-8)	1.70	9.97E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1,
EIVI	Exon Cassette	2.97	5.67E-05	HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20c, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
TRA2A	Intron Retention	1.85	2.30E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP F1, hnRNP H2, hnRNP H (PTB), hnRNP P (TLS), HTra2beta1, HuB, KSRP, Nova-1, Sam68, SC35, SRp30c, YB-1
HNRNPA2B1	Intron Retention	1.93	3.20E-04	ETR-3, hnRNP C1, hnRNP I (PTB), hnRNP P (TLS), HuB, KSRP, Nova-1, PSF, Sam68, SC35, TIA-1, TIAL1, ZRANB2
ELMO1	Complex (e19)	6.02	3.51E-05	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
	Alter. First Exon (e1-2,4-6,e8-10)	1.60	2.65E-02	
COA1	Alter. Terminal Exon (e9)	1.70	2.16E-04	
	Exon Cassette	1.61	1.23E-04	
POLM	Intron Retention	1.65	1.62E-02	hnRNP F, hnRNP H1, hnRNP H2, hnRNP P (TLS), Nova-1, Nova-2, RBM5, SC35, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
CAMK2B	Exon Cassette	1.81	2.23E-05	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
FIGNL1	Intron Retention	1.85	5.18E-04	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP P (TLS), HTra2beta1, HuB, MBNL1, Nova-1, PSF, Sam68, SC35, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
000	F 0 11	0.00	0.015.04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, RBM5,
DDC	Exon Cassette	2.23	2.01E-04	Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
DMC2D4	Alter. Acceptor Site	1.82	2.55E-02	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB,
PINS2P4	Alter. Terminal Exon (e5-6)	2.13	1.64E-03	HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
TMEM120A	Intron Retention	1.84	1.81E-04	hnRNP F, hnRNP H1, hnRNP H2, hnRNP P (TLS), KSRP, Nova-2, SC35, SRp20, SRp30c, YB-1
MAGI2	Alter. First Exon (e1,e3,e6-7)	1.69	1.62E-04	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
1/14.4.1.20.41	Altern First From	2.10	4 705 04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha,
KIAA1324L	Alter. First Exon	3.19	4.78E-04	HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
ADOD1	Alter. First Exon	1.72	1.10E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha,
ADCDI	Complex	1.61	1.50E-03	HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
SGCE	Exon Cassette	2 70	8 94F-07	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HuB, MBNL1, Nova-1, Sam68, SC35, SRp20, SRp30c,
OGOE	Exon ousselle	2.70	0.542.07	TIA-1, TIAL1, YB-1, ZRANB2
PON2	Complex (e2)	1.65	1 80F-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD,
10112	Complex (C2)	1.00	1.002.00	KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
C7orf43	Alter. Acceptor Site	2.35	1.06E-03	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
EPHB4	Alter. Donor Site	1.64	1.10E-02	ETR-3, hnRNP C1, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
RABL5	Intron Retention	1.91	7.28E-03	ETR-3, hnRNP A1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HuB, KSRP, Nova-1, Nova-2, Sam68, SC35, SF2/ASF, TIA-1, TIAL1, YB-1
PNPI A8	Complex (e3-5)	1.81	1.54E-03	CUG-BP1, ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1,
	Exon Cassette	2.90	1.05E-04	HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF2/ASF, SRp20c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
DPAGT1	Intron Retention	1.52	6.56E-04	ETR-3, hnRNP A1, hnRNP C1, hnRNP I (PTB), hnRNP P (TLS), HuB, Nova-1, Nova-2, SC35, SRp20, TIA-1, TIAL1, YB-1
AASS	Exon Cassette	1.93	8.37E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
СНСНДЗ	Exon Cassette	1.87	3.16E-02	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2bata1 HuB, KSPP, MRNI 1, Mara1, Mara2, PSF, BRM5, Sam68, SC35, SE1, SPa30, TDP/3, TIA.1, TIA.1, TIA.1, ZRANB2
				TITIZZEGEL, THOL, NOTI, MOTEL, TOVEL, TOTAL, TOTAL, TOTAL, AND COSO, OT 1, OT 22, OT 200, TOT 30, THE T, THEL, TOT, TOTAL, T
HIPK2	Alter. Acceptor Site	2.63	4.66E-06	Nova-1, Nova-2, NSE, RBMS, Sam68, SC35, SF1, SR600, SR630C, TIA-1, TIA1, 1, VE-1, ZRANB2
F7H2	Intron Retention	1 53	6 28E-03	FTR-3 hRRNP A1 hrRNP A2/R1 hrRNP C1 hrRNP E hrRNP H1 hrRNP H2 hrRNP P (TIS) HTra2alpha HTra2heta1 HuR KSRP MRNI 1 Nova-1 RRM5 SC35 SRn30c TIA-1 TIAI 1 YR1
				ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H4, hnRNP H2, hnRNP H2, hnRNP H2, hnRNP F, hnRNP P, (LS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1.
ZNF746	Complex	1.58	9.18E-03	Nova-2, PSF, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
ZNF767	Exon Cassette	1.93	4.85E-04	ETR-3, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
CDK5	Intron Retention	2.72	3.70E-06	hnRNP F, hnRNP H1, hnRNP H2, RBM5, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
SMARCD3	Intron Retention	1.90	7.85E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP E1, hnRNP E2, hnRNP I (PTB), hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
DDKACO	Compley (e7)	1 50	1 565 02	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP H(PTB), hnRNP K, hnRNP P (TLS), HTra2alpha,
FRAG2	Complex (e7)	1.00	1.00E-03	HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2

				FTR-3 Fox-1 Fox-2 hnRNP 41 hnRNP 42/81 hnRNP C1 hnRNP C1 hnRNP F1 hnRNP F2 hnRNP F2 hnRNP F1 hnRNP H1 hnRNP H2 hnRNP H2 hnRNP K hnRNP F (TIS) HTra2hata1 HuR KSRP MRNI 1 Nova-1
KMT2C	Intron Retention	1.57	2.20E-02	Nova-2, PS, Sanda, S.G.S. Shalo, S. Sola, Tikal, J. Kala, Kakika L., Innova L
FDFT1	Alter. First Exon (e1)	2.86	1.55E-05	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP D, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRo20, SRo30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
ATP6V1B2	Intron Retention	1.82	9.99E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, Nova-2, Sam68, score, scor
BNIP3L	Alter. First Exon (e2)	2.30	3.80E-03	CUG, BLZ, Kair, Micolog, Treat, Test, Test
FZD3	Exon Cassette	2.43	2.37E-04	CUG-BP1, ETR3, Fox-1, Fox-2, hnRNP A1, hnRNP A2, bnRNP C1, hnRNP D, hnRNP C1, hnRNP F, hnRNP F, hnRNP H1, hnRNP H2, hnRNP P (TLS), HTra2alpha, HTra2alpha, HTra2beta1, HuB, KSRP, MBNL1, Number 2, Phys. Rev. D (1997) 1000 (1
	Complex	2.08	6.00E-04	
HMBOX1	Intron Retention	3.86	2 30F-05	Upper Line, Low, Low, Low, Low, Low, Low, Low, Low
	Complex (e6-10)	2.53	1.08F-03	CIG-BELTRA_FOX_FOX_DRAVPAL. https://cit.html/file.cit.html/fi
NRG1	Exon Cassette	2.10	2.45E-04	HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
TACC1	Alter. Terminal Exon	2.45	9 365 04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP D1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha,
TACCI	(e8,e10,e12-21)	2.40	8.36E-04	HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
AP3M2	Exon Cassette	1.60	2.98E-02	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HuB, HuD, KSRP, MBNL1, Nova-1, Sam68, SC35, SF2/ASF, SRp20, TIA-1, TIAL1, YB-1
CHCHD7	Exon Cassette	2.06	5.05E-04	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, TIA-1, TIAL1, YB-1
CSPP1	Exon Cassette	1.68	5.94E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
CTMNO	Alter. First Exon (e1)	2.43	5.97E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB,
STMIN2	Exon Cassette	10.17	1.83E-05	HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
LRRCC1	Alter. Donor Site	2.21	2.25E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
OTUD6B	Exon Cassette	1.66	5.36E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
OVD1	Alter. First Exon (e1-11,e13)	2.32	2.22E-05	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS),
UNNI	Exon Cassette	3.49	4.56E-06	HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
ENY2	Intron Retention	2.27	4.04E-04	CUG-BP1, ETR-3, hnRNP A1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SF1, SRp30c, TIA-1, TIAL1, YB-1
RPL23AP53	Exon Cassette	2.08	8.08E-05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2, B1, hnRNP C1, hnRNP D, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
FAM167A	Alter. First Exon (e2,e4)	2.11	5.76E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2, B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
STMN4	Exon Cassette	5.15	2.80E-06	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, KSRP, MBNL1, Nova-1, RBM5, SC35, SRp20c, YB-1
KIF13B	Exon Cassette	2.15	2.54E-02	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2, B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
FUT10	Alter. Terminal Exon (e5)	1.56	1.10E-02	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I, PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
PLAT	Complex	5.33	1.20E-04	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F2, hnRNP H1, hnRNP H2, hnRNP P (TLS), HTra2beta1, HuB, KSRP, Nova-1, Nova-2, PSF, Sam68, SC35, SRp30c, TIA-1, TIAL1, YB-1
RPS20	Alter. First Exon (e1-4)	1.68	1.17E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP P (TLS), HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
COPS5	Intron Retention	1.65	9.76E-04	ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1
	Alter. Acceptor Site	3.42	1.81E-05	
EYA1	Complex	3.39	1.81E-05	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP K, HuB, Nova-1, Sam68, SC35, SRp30c, TIA-1, TIAL1, YB-1
	Intron Retention	4.49	1.81E-05	
STAU2	Alter. Terminal Exon (e18)	1.55	9.21E-04	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2, B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I, PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
11.7	Complex (e6)	1.79	1.62E-03	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-2, Sam68, SC35,
127	Exon Cassette	2.03	1.62E-03	SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
1				
C8orf59	Exon Cassette	1.51	2.02E-04	9G8, EIK-3, INRKIP AL, INRKIP AZ/BL, INRKIP CL, INRKIP D, INRKIP EL, INRKIP EZ, INRKIP F, INRKIP HL, INRKIP HZ, INRKIP F (ILS), HIRZOEtal, HUB, KSKP, Nova-1, Samos, SC35, SKp2U, SKp3UC, TIA-1, TIAL1, YB-1, ZRAINB2
C8orf59 RUNX1T1	Exon Cassette Exon Cassette	1.51 2.21	2.02E-04 1.08E-03	9G8, CIG-SP1, TRAL PA2, B1, BRKNP C1, BRKNP C1
C8orf59 RUNX1T1 TRIOK	Exon Cassette Exon Cassette Complex (e6)	1.51 2.21 1.92	2.02E-04 1.08E-03 3.64E-03	9G8, CIR-3, InnRVP AJ, InnRVP AZ, BI, INNRVP CJ, INNRVP D, INRRVP EJ, INNRVP F, INRRVP F, INRRVP HJ, INRRVP HJ, INRRVP F (ILS), HIT220eta1, HUB, KSRP, Nova-1, Samba, SC35, SKp2U, SKp3U, TIA-1, TIA-1, TIA-1, TIA-1, TIA-1, TZRANB2 9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, INRVP A1, INRVP A2/B1, INRVP C1, INRVP D, INRVP DL, INRVP E1, INRVP E2, INRVP F, INRVP F, INRVP H1, INRVP H2, INRVP H3, INRVP H3, INRVP H4, INRVP F, INRVP H7, INR
C8orf59 RUNX1T1 TRIQK	Exon Cassette Exon Cassette Complex (e6) Exon Cassette	1.51 2.21 1.92 1.97	2.02E-04 1.08E-03 3.64E-03 3.64E-03	9G8, E1K-3, InRKNP AZ, BI, INRKNP CI, INRKNP D, INRKNP D, INRKNP E2, INRKNP F, INRKNP H2, INRKNP H2, INRKNP F (TLS), H1ra2beta1, HUB, KSKP, Nova-1, Samba, SC35, SKp2U, SKp3Uc, TIA-1, TIAL1, TIAL1, YB-1, ZRANB2 9G8, CUG-BP1, ETR-3, Fox-2, INRKNP A1, INRKNP A2/B1, INRKNP C1, INRKNP C1, INRKNP DL, INRKNP E1, INRKNP E2, INRKNP F, INRKNP H1, INRKNP H2, INRKNP H3, INRKNP H1, INRKNP H7, IN

	Exon Cassette	1.92	8.24E-05	SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2	
KLF10	Alter. First Exon (e1)	2.60	3.92E-03	ETR-3, hnRNP A1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, TIA-1, TIAL1, YB-1, ZRANB2	
VPS28	Intron Retention	1.96	2.67E-07	ETR-3, hnRNP A1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP K, hnRNP P (TLS), KSRP, Nova-1, RBM5, SC35, SRp30c, YB-1, ZRANB2	
PRSS3	Alter. First Exon (e1,e3)	25.11	1.24E-06	9G8, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP H, hnRNP H2, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNI 1, Nova-1, Nova-2, PSE, RBM5, Sam68, SC35, SF1, SF2/ASE, SRo20, SRo30c, TDP43, TIA-1, TIAI 1, YB-1, ZRANB2	
NUDT2	Exon Cassette	1.58	2.66E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MRN1 Nova-2 PSE RBM5 Sam68 SC35 SE1 SBo20 SRo30c TIA-1 TIA1 YB-1 ZRANB2	
GALT	Intron Retention	1.87	8.61E-04	Instruct, Hord Protect, Hord Hubble Boots of States States (States) and States	
RUSC2	Alter. Donor Site	1.89	1.00E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRo20, SRo30c, TIA-1, TIAL1, YB-1, ZRANB2	
00500	Intron Retention	1.74	2.02E-04	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Sam68, SC35,	
CREB3	Exon Cassette	1.65	2.61E-04	SF1, SF2/ASF, TIA-1, TIAL1, YB-1	
RMI1	Complex (e1-2)	2.09	1.66E-02	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2	
NTRK2	Alter. Terminal Exon (e20-22)	1.65	6.77E-04	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP D1, hnRNP E1, hnRNP E2, hnRNP F1, hnRNP H2, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS),	
MINAZ	Alter. First Exon (e1-3)	1.57	8.98E-04	HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2	
ANKRD19P	Alter. Terminal Exon (e11-12)	2.65	2.59E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2	
PTPDC1	Alter. Terminal Exon (e8)	1.66	1.00E-02	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2	
ERCC6L2	Exon Cassette	1.75	6.85E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2	
CCDC180	Alter. First Exon (e1-12,e14-15)	2.00	6.39E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2	
MSANTD3 // TMEFF1	Alter. Terminal Exon (e5-6)	2.11	5.66E-05	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2	
SMC2	Exon Cassette	1.74	3.34E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, Nova-1, PSF, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2	
MDDE	Complex	2.34	6.37E-05	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1,	
WIRKE	Exon Cassette	2.22	1.19E-04	Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2	
MVB12B	Alter. Terminal Exon (e8)	2.37	5.96E-05	CUG-BP1, ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP I, hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2	
GARNL3	Exon Cassette	2.42	5.78E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2	
CERCAM	Complex	1.64	1.66E-03	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP LL, hnRNP P (TLS), HuB, KSRP, Nova-1, Nova-2, PSF, RBM5, SC35, SRp20, SRo30c, TIA-1, TIAL1, YB-1, ZRANB2	
ODF2	Exon Cassette	2.34	3.40E-03	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SE2/ASE, SRb30c, TIA-1, TIA11, YR-1, ZRANR2	
FUBP3	Exon Cassette	1.55	1.09E-02	9G8, CUG-B91, Share Carlos and Annu a	
0.51114	Alter. Terminal Exon (e20-21)	2.53	9.64E-04	ETR-3. hnRNP A1. hnRNP D. hnRNP E1. hnRNP E2. hnRNP F1. hnRNP H2. hnRNP H2. hnRNP P (TLS). HTra2beta1. HuB. KSRP. Nova-1. Nova-2. RBM5. Sam68. SC35. SF2/ASF. SRo20. SRo30c. TIA-1.	
GRINI	Exon Cassette	2.20	9.79E-04	TIAL1, YB-1	
CDWD1	Alter. Terminal Exon (e4)	1.56	1.87E-02	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha,	
CBWD1	Exon Cassette	1.55	4.99E-04	HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2	
MPDZ	Exon Cassette	1.55	1.10E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2	
LINCO2	Complex (e3-5)	5.74	1.96E-06	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP D1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P	
EINGOZ	Exon Cassette	4.34	1.96E-06	(TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2	
DCTN3	Intron Retention	2.64	2.59E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Sam68, SC35, SF1, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2	
C9orf41	Exon Cassette	1.61	5.04E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2	
GKAP1	Exon Cassette	1.96	4.64E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2	
ZCCHC6	Intron Retention	1.54	2.94E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Sam68, SC35, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2	
SEMA4D	Alter. First Exon (e1-17,e19)	1.95	2.30E-02	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP D1, hnRNP E1, hnRNP E2, hnRNP F2, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P	
NUL Descharter 140 2.800 140 1.8000 1.800 1.800 <th< th=""><th></th><th></th><th></th><th></th><th></th></th<>					
---	----------	------------------------------	------	----------	--
Dec/1920 Conciliant Concilian	NOL8	Evon Cassette	3.07	3 78E-04	(ILS), HTR22BPR3, HTR22BPR3, HTR22BPR3, HTR2ABPR3, HTR2ABPR3, HTR2ABPR3, SAMBS, SAMBS, SAMBS, SCH35, SKP2/SKP30C, IDP43, ITA-1, IAL1, IFS-1, ZKANBZ ETD 3, hpr1D A1 hpr1DP 1 hpr1DP H2 hpr1DP H2 hpr1DP H1 (SIL) HTr22het3 Htr32het3 Htr32 (SamB3, SCH35, SCH25, SCH
9.00000 Desc Constitu 1000 990000 1000000000000000000000000000000000000	NOLO	Exon Gasselle	5.07	3.702-04	
Implified Operating is a set of	SLC35D2	Exon Cassette	1.63	8.50E-03	CUC-DT, EIR-S, FOR-1, FOR-2, INITIATE AL, INITIATE AL/DL, INITIATE CL, INITIATE CL, INITIATE CL, INITIATE T, INITI
TIME Ame. Terms Dox (9-10) Col. Col. 224 (Col. State)					
DAtt Amr. Fm Exc. (pl.) 2.85 1.44.01 CDC/PT (178, 1.4.9.2, 1.9.9.2, 1.9.9.2, 2.9.9.2, 2.9.9.2, 2.9.9.2, 2.9.9.9.2, 2.9.9.2, 2.9.9.9.2, 2.9.9.2, 2.9.9.9.2, 2.9.9.9.2, 2.9.9.9.2, 2.9.9.9.9.9.9.9.9.9.9.9.9.9.9.9.9.9.9.9	TRIM14	Alter. Terminal Exon (e9-10)	2.61	2.26E-05	CUG-DT1, EIR-3, F0X-1, F0X-2, F0X-1, F0X-2, F0X-1,
IPAP Absr. Ref. box (x):0. 2.80 1.4400 Character, and an equipment, and equipment, and equipment, and					
COCK2// TRYTIS Atter. First Can. Reb. 9.4 1.54 4.64.0 Biology (1, B), and an (2, B), and an (2, B), and an (2, B), and an (2, B), and (2, B), a	LPAR1	Alter. First Exon (e2-3)	2.85	1.44E-03	UU-5PT, EIK-5, FOX-1, FOX-1, FOX-2, IDRIVE AL, DIRKVE CL, DIRKVE CL, DIRKVE CL, DIRKVE EL, DIRKVE FL, DIRKVE F
Charge 1 Atter Trans Cone (20.3.0) 1.99 4.44.0. Description (20.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.	00000 //			1	
P0013 Jobs Nambaria Lot 2250 P0013 Jobs Nambaria Lot P0013 Jobs Nambaria	CDC26 //	Alter. First Exon (e20-34)	1.59	4.64E-03	UU-BPL, ELK-5, FOX-1, FOX-2, IDKIVE AL, DIKKVE CL, DIKKVE CL, DIKKVE CL, DIKKVE EL, DIKKVE EL, DIKKVE FL, DIKK
Process Instrument Process	FNDF10	latera Detention	1.67	7.005.05	
MM Metr. Fred Exervel of 1 182 52.204 Collst. Links. J. Supp. 25.204 Coll Link	FULES	Intron Retention	1.07	7.96E-00	
FBND Amer. Door Sign 111 FBND Amer. Door Sign 111 FBND Amer. Door Sign 111 FBND	AKNA	Alter. First Exon (e1-5)	1.82	5.22E-04	EIRS, FOR J, FOR Z, DIRKIP AJ, DRIVP AZ, BI, DIRKIP CJ, DRIVP CJ, DRIVP CZ, DRIVP F, DRIVP F AJ, DRIVP
Fibred Alter. Devror Sile 1.95 1.1122 Name: Stacks 2 Sta					MDNLL, NOVA-L, NOVA-L, NOVA-C, FSF, NOWO, SAITIOS, SC33, SF1, SF2/RSF, SND2O, SND3OC, HAT, TINLT, TO, LT, LTNNT, LAND LL, NOVA-L, NOVA-
AV07102 Compton 2.00 3.00 Col CTR3, Final Final Science Av070 AV Linder 21, Linder 21	FBXW2	Alter. Donor Site	1.95	1.11E-02	
AMPT12 Comptex 2.59 1.950:00 Comptex 2.59 1.950:00 Comptex					
Seconds 4.79 6.455.07 Attract (1, 20, 1000), 30000, 30	ANGPTL2	Complex	2.59	3.90E-03	EIRS), TOR 1, TOR 2, HINNY AL, HINNY AZ, DI, HINNY EZ, HINNY EZ, HINNY EZ, HINNY FA, HINNY FAZ, HINNY FAZ
Strolog Darbate 1.24 200002 Clock and the structure of the structure		Queren la co	4.70	C AFF OF	
Description 1.64 2.5862 TTUST / Jan Mark Mark Mark Mark Mark Mark Mark Mark	SH2D3C	Complex	4.79	0.45E-05	CUG-BPL, ELK-5, Fox-1, Fox-2, Fox-4, Fox-4, IDRIVE PL,
IMAGE/T1 Down Cosselfe 1.59 1.88/2 Files, Tex, Tex, Tex, Tex, Tex, Tex, Tex, Tex		EXOII Casselle	1.04	2.96E-04	
DOX31 Alter. First Exon (e1-2) 1.54 2.684:03 First Exon (e1-2) First Exon (e1-2	RAPGEF1	Exon Cassette	1.59	1.88E-02	EIR3, FOR1, FOR2, INRIVE AL, INRIVE AZ, INRIVE AZ, INRIVE D, INRIVE D, INRIVE D, INRIVE AZ, INRIVE H, INRIVE AZ, INRIVE H, INRIVE AZ, INRIV
D031 Aller, First Exon (e1-2) 1.14 2.68433 Links, more A, more A, Min Per AJ, Min Per Z, Min Per J, Min Per J, Min Per J, Min Per JJ, Min Per J					
Matr. Doto: 28 219 20065 Constraints 323.57.27.27.97.39000, 20000, 101.1 (1.1.1.1.1.) 200000 GBDT1//F Atter. Exist Loss: 162.2.00 163.8 110562 CONSTRAINED Constraint	DDX31	Alter. First Exon (e1-2)	1.54	2.68E-03	ETER3, DRRWP A1, DRRWP A2/B1, DRRWP C1, DRRWP C1, DRRWP C2, DRRWP F2, DRRWP F4, DRRWPF
GBG11// PALCOS Date: Intel Context Current PL Date: Intel Context Current PL Date: Intel Context Date: Intel		Alter Dener Cite	0.10	0.005.05	NOVA-2, PSF, KBWO, SAMOS, SU30, SF2/ASF, SKP2U, SKP3UC, TIA-1, TIAL1, TB-1, ZKANSZ
PARCIOS Attern First Exercise 1 1.18 1.108-02 Intern Retention 2.21 1.976-65 ETR3 , Fou 1, Fou 2, IntRV E 1, IntRV	GBGT1 //	Alter. Donor Site	2.19	2.09E-05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP H3, hnRNP K, hnRNP K, hnRNP L1, hnRNP P (TLS),
Intro. Network 221 1.97L59 FTR3, Fox J, Fox Z, InsNP C1, InsNP E1, InsNP E2, InsNP P F, InsNP P (TS), InsNP P (TS), HTra2eba1, HuB, HuD, KSPP, MBNL1, News J, Sam6B, SC3S, SR2S, SR2S, O, TDP43, TL41, TL41, Yz J, ZAMB22 ABCA2 Intron. Retention 1.87 6.64EA FTR3, Fox J, Fox Z, InsNP E1, InsNP E2, InsNP P (TS), KSPP, RBM5, SC35 ABCA2 Intron. Retention 1.87 1.166.3 ETR3, Fox J, Fox Z, InsNP E1, InsNP F2, InsNP F1, InsNP F4, In	RALGDS	Alter. First Exon (e2-7,e9)	1.88	1.10E-02	HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
SECIAR Env Cassets 157 6.64624 EIR 3, Feb. 1, Feb. 2, InsRVP C1, InsRVP F2, InsRVP F1, InsRVP F2, InsRVP F1, InsRVP F2, InsRVP F1, InsRVP F2, InsRVP F1, InsRVP F2, InsRVP F2, InsRVP F1, InsRVP F2, InsRVP F2, InsRVP F1, InsRVP F1, InsRVP F2, InsRVP F1, InsRVP F2, InsRVP F1, InsRVP F2, InsRVP F1, InsRVP F1, InsRVP F1		Intron Retention	2.21	1.97E-05	
ABC/2 Intron Retention 1.87 11.603 ETHs, Fex1, Fex2, InRNP AL, IndRNP P (TLS), KSRP, RBM5, S235 MSMF Addre, Finit Exer (e1-5) 1.52 2.806/23 ETHs, Fex1, Fex2, InRNP AL, IndRNP P (TLS), KSRP, RBM5, S235, S25 NSMF Exer (Finit Exer (e1-5) 1.52 2.806/23 ETHs, Fex1, Fex2, InRNP AL, IndRNP AZ/B1, InRNP AL, InRNP FL, INRNP	SEC16A	Exon Cassette	1.57	6.64E-04	ETR3, Fox-1, Fox-2, hnRNP C1, hnRNP E2, hnRNP F2, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Sam68, SC35, SRp20, TDP43, TIA-1, TIAL1,
Abd/2 Intron Relation 1.87 I.16.4.3 ETR3, row, 1, row, 1, row, 2, rohRP A1, InnRNP P (L), INSRP, RBM5, SU35 NSMF Complex 2.94 4.11E-05 ETR3, row, 1, row, 2, rohRP A1, InnRNP P (L), INRNP F, InRNP H1, InRNP P (L, INRNP F, I					YB-1, ZKANBZ
Alter. First Exon (e1-5) 1.52 2.804-03 ETR3, Fox 1, Fox 2, InRRP A1, InRRP A2/B1, InRRP C1, InRRP F, InRRP F1, InRRP F2, InRRP P1 (FTB), InRRP FX, INRRPP1 (FTB), INRRP FX, INRRP P1 (FTB), INRRP FX, INRRP	ABCA2	Intron Retention	1.87	1.16E-03	ETR-3, Fox-1, Fox-2, hnRNP AI, hnRNP P (TLS), KSRP, RBM5, SC35
NMF Complex 2.94 4.112.06 ETR3.5 ro.1, For2, JmRP A1, JmRNP 22/B1, JmRNP C1, JmRNP F1, JmRNP F2, JmRNP F1, JmRNP F, ImRNP F1, JmRNP F1,		Alter. First Exon (e1-5)	1.52	2.80E-03	
Lond Exon Link 1.7.3 3.586-04 1, T/3 3.586-04 Hinton Retention 1.6.3 1.990-30 CUG 4PI, TER3, Fox J, Fox Z, InRNP A1, InRNP A2/B1, InRNP C1, InRNP E2, InRNP F, InRNP H1, InRNP H2, InRNP H3, InRNP I (PTB), InRNP K, InRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, LHK, RSRP, MBNL1, Noa-1, Noa-2, RBMS, Sam68, S235, S17, S72/ASF, SR020, SR030, TPA1, TLA11, Y91, ZAMB2 DDX3X Alter. Terminal Exon (e4) 1.58 4.40E-4 ETR3, Fox J, Fox Z, InRNP A1, InRNP A2/B1, InRNP C1, InRNP C1, InRNP E2, InRNP F, InRNP H1, InRNP H2, InRNP F, IL, ISRNP F, IL, INRNP F,	NSME	Complex	2.94	4.11E-06	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, SC35, SF2/ASF, SRp30c, TIA-
Intron Retention 1.63 1.906.33 PPEFI Alter. First Exon (e1-3) 4.83 3.376-04 CUGBPI, ETR3, Fox1, Fox2, hnRNP A1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2al		Exon Cassette	1.73	3.58E-04	1, TIAL1, YB-1, ZRANB2
PPE1 Alter. First Exon (e1-3) 4.83 3.37E-04 CUGGP1 [TR3, Fox 2], fnRNP A1, nRNP A2/B1, nRNP C1, nRNP E2, nRNP F1, nRNP F1, nRNP F1, nRNP F1, INRNP F1, INRNP F (L, NRNP F A1, NRNP A2/B1, nRNP A2/B1, nRNP A2/B1, nRNP C1, nRNP E2, nRNP F1, nRNP F1, INRNP F2, INRNP F2, INRNP F1, INRNP F2, INRNP F2, INRNP F2, INRNP F1, INRNP F2, IN		Intron Retention	1.63	1.90E-03	
Hub Alter. Terminal Exon (e4) 15.8 Hub	PPFF1	Alter First Exon (e1-3)	4 83	3 37F-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2alpha, HTra2beta1, HuB,
DDX3X Alter. Terminal Exon (e4) 1.58 4.40E4 ETR3, Fox 1, Fox 2, InNP A2, Ibi, InRNP P A2, IBI, InRNP P D, InRNP E1, INRNP E2, INRNP E1, INRNP E2, INRNP E1, INRNP E1, INRNP E2, INRNP E1, INRNP E1,		Alter: Thist Exoti (e1-5)		+	HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
Name Name <th< td=""><td>DDX3X</td><td>Alter Terminal Exon (e4)</td><td>1 58</td><td>4 40F-04</td><td>ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP,</td></th<>	DDX3X	Alter Terminal Exon (e4)	1 58	4 40F-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP,
KRB0X4 Complex (e5-6) 2.49 1.34E03 FTR3, Took, 1, noRNP A2, nnRNP A1, nnRNP A2/81, nnRNP E1, nnRNP E1, nnRNP E1, nnRNP E1, nnRNP E2, nnRNP P, tnRNP F, nnRNP P, tnRNP P, trRNP P, trRN	BBROK	Autor: Forthinda Exort (61)	1.00		MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
Exon Cassette 2.42 1.34E03 PFS, RBMS, Sam68, SC35, SF1, SR20, SR30bc, TLA1, TLA1, YB1, ZRAMB2 CDKLid Intron Retention 1.91 1.67E02 InRNP P, InRNP PE, INRNP PE	KRBOX4	Complex (e5-6)	2.49	1.34E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1,
CDK16 Intron Retention 1.91 1.67c2 hnRNP E1, hnRNP E2, hnRNP E1, hnRNP E2, hnRNP F (ILS), KSRP, Sam68, SC35, VS1 USP11 Alter. Donor Site 1.98 9.78E-05 CUG6P1, ETR3, Fox-1, Fox-2, hnRNP A1, hnRNP A2, hnRNP C2, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP I(PTB), hnRNP F, hnRNP H1, hnRNP F, hn	паволя	Exon Cassette	2.42	1.34E-03	PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
Alter_Donor Site 1.98 9.78E-05 CUGPL; ETR-3; Fox-1; Fox-2; hnRNP A1, hnRNP A2[81, hnRNP C], hnRNP C], hnRNP E1, hnRNP E1, hnRNP H2, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, HDAC6 Intron Retention 1.58 1.08E-0 MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF2, OSE, TLA1, TLA1, YB-1, ZRANB2 PQBP1 Intron Retention 1.54 7.72E-03 hnRNP P (TLS), KSRP, Nova-1, Nova-2, Sam68, SC35, SF2, OSE, SF2/ASF, SRp30c, TLA1, TLA1, YB-1 NUDT10 Alter. First Exon (e1) 2.55 1.72E-07 ETR-3, hnRNP I (PTB), hnRNP K, hnRNP P, L, hnRNP C, hnRNP D, hnRNP C, hnRNP D, I, hnRNP E, I, hnR	CDK16	Intron Retention	1.91	1.67E-02	hnRNP D, hnRNP E1, hnRNP E2, hnRNP P (TLS), KSRP, Sam68, SC35, YB-1
Intron Retention 2.18 1.91E-02 MBNL1, Nova-1, Robar-2, RBM5, Sam68, SC35, SF1, SR20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 HDAC6 Intron Retention 1.58 1.68E-03 hnRNP P (TLS), KSRP, Nova-1, Rova-2, Sam68, SC35, SR20, TIA-1, TIAL1, YB-1 PQBP1 Intron Retention 1.54 7.72E-03 InRNP P (TLS), KSRP, Nova-1, Rova-2, Sam68, SC35, SR20, TIA-1, TIAL1, YB-1 NUDT10 Alter. First Exon (e1) 2.55 1.72E-07 ETR3, hnRNP I (PTB), hnRNP P A2(B1, hnRNP P C1, SRNP P, InNRP P, I, hnRNP P, I, INRNP P, I, INRN	USP11	Alter. Donor Site	1.98	9.78E-05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP,
HDAC6 Intron Retention 1.58 1.682.03 hnRNP P (TLS), KSRP, Nova-1, Nova-2, Sam68, SC35, SR202, TIA-1, TIAL1, YB-1 PQBP1 Intron Retention 1.54 7.72E.03 hnRNP P (TLS), KSRP, Nova-1, Nova-2, Sam68, SC35, SR202, TIA-1, TIAL1, YB-1 NUDT10 Alter. First Exon (e1) 2.55 1.72E.07 ETR.3, hnRNP 1 (PTB), hnRNP P, CLS, KSRP, MSNL1, Nova-1, PSF, SC35, SF2/ASF, SRp30c, TIA-1, TIAL1, YB-1 MAGED1 Alter. First Exon (e1) 5.02 2.32E.06 968, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D2, hnRNP D1, hnRNP E1, hnRNP E1, hnRNP E1, hnRNP E1, hnRNP H2, hnRNP H1, hnRNP H2, hnRNP H1, hnRNP H2, hnRNP H1, hnRNP A2/B1, hnRNP A2/B1, hnRNP C1, SN30c, YB-1, ZRANB2, SN30c, YB-1, ZRANB2 XAGE1D Complex 2.71 1.98E-07 ETR.3, hnRNP 1 (PTB), hnRNP A2/B1, hnRNP C1, hnRNP F2, SS35, SR200c, YB-1, ZRANB2 TRO Alter. Donor Site 2.02 1.88E-03 ETR.3, hnRNP C1, hnRNP C1, hnRNP C1, hnRNP C2, hnRNP F1, hnRNP P1, hnRNP P1	00111	Intron Retention	2.18	1.91E-02	MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
PQBP1 Intron Retention 1.54 7.72E-03 hnRNP A1, hnRNP A2/B1, hnRNP H2, hnRNP H2, hnRNP P (TLS), hnRNP K, hnRNP P (TLS), htTra2beta1, Nova-1, SC35, YB-1 NUDT10 Alter. First Exon (e1) 2.55 1.72E-03 PRNP A1, hnRNP A2/B1, hnRNP P (TLS), KSRP, MBNL1, Nova-1, SC35, SF2/ASF, SRp3oc, TLA1, TLAL, YB-1 MAGED1 Alter. First Exon (e1) 5.02 2.32E-06 9G8, CUG-BP1, ETR-3, fox1, Fox-2, hnRNP A2/B1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E1, hnRNP E1, hnRNP E1, hnRNP H2, hnRNP H2, hnRNP H1, hnRNP H2, hnRNP H1, hnRNP A2/B1, hnRNP A2/B1, hnRNP A2/B1, hnRNP A2/B1, hnRNP C1, hnRNP A2/B1, hnRNP C1, hnRNP A2/B1, hnRNP C1, hnRNP A2/B1, hnRNP H1, hnRNP H2, hnRNP H1, hnRNP H2, hnRNP F (TLS), HTra2beta1, HUB, KSRP, MBNL1, Nova-1, RBM5, Sam68, SC35, SF2/ASF, SRp3oc, YB-1, ZRANB2 XAGE1D Complex 2.71 1.98E-07 ETR-3, hnRNP C1, hnRNP C1, hnRNP C1, hnRNP F2, hnRNP H1, hnRNP H2, hnRNP P (TLS), HTra2beta1, HUB, KSRP, MBNL1, Nova-1, RBM5, Sam68, SC35, SF2/ASF, SRp3oc, YB-1, ZRANB2 TRO Alter. First Exon (e1-3) 2.30 3.75E-05 ETR-3, fox-1, fox-2, hnRNP A1, hnRNP C1, hnRNP C1, hnRNP C1, hnRNP F2, hnRNP F1, hnRNP F1, hnRNP F2, hnRNP F2, hnRNP F1, hnRNP F2, hnRNP F1, hnRNP F2, hnRNP F1	HDAC6	Intron Retention	1.58	1.68E-03	hnRNP P (TLS), KSRP, Nova-1, Nova-2, Sam68, SC35, SRp20, TIA-1, TIAL1, YB-1
NUDT10 Alter. First Exon (e1) 2.55 1.72E-07 ETR-3, hnRNP L (PTB), hnRNP F, hnRNP P (TLS), KSRP, MBNL1, Nova-1, PSF, SC35, SF2/ASF, SRp30c, TIA-1, TIAL1, YB-1 MAGED1 Alter. First Exon (e1) 5.02 2.32E-00 968, CUG GPI, ETR-3, fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP D, hnRNP D, hnRNP E1, hnRNP F2, hnRNP F1, hnRNP H3, hnRNP H3, hnRNP H3, hnRNP H2, hnRNP F (TLS), Hinton Retention 1.54 9.86E-03 HTra2alpha, HTra2abeta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBMS, Sam68, SC35, SF1, SF2/ASF, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 XAGE1D Complex 2.71 1.98E-07 ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F1, hnRNP H2, hnRNP H2, hnRNP H2, hnRNP H2, hnRNP H2, hnRNP H2, hnRNP P (TLS), HTra2abeta1, HuB, KSRP, MSN.1, Nova-1, RBM5, Sam68, SC35, SRp30c, TB-1, TAL1, YB-1 MAGED2 Intron Retention 1.84 4.22E-04 ETR-3, hnRNP A1, hnRNP C1, hnRNP C1, hnRNP F2, hnRNP H1, hnRNP H2, hnRNP P (TLS), HTra2abeta1, HuB, KSRP, Nova-1, RBM5, Sam68, SC35, SRp30c, YB-1, ZRANB2 TRO Alter. Donor Site 2.02 1.88E-03 ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP P2, hnRNP P, fLS, hnRNP P (TLS), HTra2abeta1, HuB, KSRP, Nova-1, RBM5, Sc35, SRp30c, YB-1, ZRANB2 NLGN3 <u>Alter. First Exon (e1-3) 2.30 3.75E-05 ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP P, hnRNP P, fLS, hnRNP F, hnRNP H1, hnRNP H2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP F, hnRNP H1, hnRNP A2/B1, hnRNP C1, hnRN</u>	PQBP1	Intron Retention	1.54	7.72E-03	hnRNP A1, hnRNP A2/B1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, Nova-1, SC35, YB-1
Alter. First Exon (e1) 5.02 2.32E-06 968, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP I (PTB), hnRNP F, (LS), HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2, ASF, SRp20, SRp30c, TDH-43, TIA-1, TAL1, YB-1, ZRANB2 XAGE1D Complex 2.71 1.98E-07 ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP F, hnRNP H1, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, RBM5, Sam68, SC35, SF1, SF2, ASF, SRp20, SRp30c, TDH-43, TIA-1, TAL1, YB-1, ZRANB2 MAGED2 Intron Retention 1.84 4.22E-04 ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP E1, hnRNP E1, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, RBM5, Sam68, SC35, SRp30c, TB-1, ZRANB2 TRO Alter. Donor Site 2.02 1.88E-03 ETR-3, hnRNP A1, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP P (TLS), HTra2beta1, HuB, KSRP, Nova-1, RBM5, Sam68, SC35, SRp30c, TB-1, ZRANB2 NLGN3 Alter. First Exon (e1-3) 2.30 3.75E-05 ETR-3, forx-1, forx-2, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP F, hnRNP F, hnRNP H1, hnRNP H2, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, RSKP, MBNL1, Nova-1, RSKP, MBNL1, Nova-1, RSKP, MBNL1, Nova-1, PSF, Exon Cassette 2.89 1.28E-03 RBM5, Sam68, SC35, SRp20, RB42, TIA-1, TAL1, YB-1, ZRANB2 NONO Exon Cassette 2.51 2.21E-05 ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F, hnRNP H2, hnRNP F (TLS	NUDT10	Alter. First Exon (e1)	2.55	1.72E-07	ETR-3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), KSRP, MBNL1, Nova-1, PSF, SC35, SF2/ASF, SRp30c, TIA-1, TIAL1, YB-1
Introl Number Intron Retention 1.54 9.86E03 HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 XAGE1D Complex 2.71 1.98E03 HTra2beta1, HuB, HuD, HuR, KSRP, MRNP 41, hnRNP F, hnRNP H, hnRNP H(PTB), hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, RBM5, Sam68, SC35, SRp30c, TIA-1, TIAL1, YB-1 MAGED2 Intron Retention 1.84 4.22E04 ETR-3, hnRNP H, INRNP E1, hnRNP E1, hnRNP E1, hnRNP F, INSNP F, SRp30c, YB-1, ZRANB2 TRO Alter. Donor Site 2.02 1.88E03 ETR-3, hnRNP H1, hnRNP 21, hnRNP E1, hnRNP E1, hnRNP E1, hnRNP F, INRNP H1, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, KSRP, Nova-1, RBM5, Sar68, SC35, SF2/ASF, SRp30c, YB-1, ZRANB2 NLGN3 Alter. First Exon (e1-3) 2.30 3.75E-05 ETR-3, hnRNP H1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E	MAGED1	Alter. First Exon (e1)	5.02	2.32E-06	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS),
XAGE1D Complex 2.71 1.98E-07 ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, RBM5, Sam68, SC35, SRp30c, TIA-1, TIAL1, YB-1 MAGED2 Intron Retention 1.84 4.22E-04 ETR-3, hnRNP 1 (PTB), hnRNP P (TLS), HTra2beta1, HuB, KSRP, PSF, SC35, SRp30c, YB-1, ZRANB2 TRO Alter. Donor Site 2.02 1.88E-03 ETR-3, hnRNP C1, hnRNP P (TLS), HnRNP E2, hnRNP F, hnRNP P 1, hnRNP P (TLS), HTra2beta1, HuB, KSRP, Nova-1, RBM5, SC35, SF2/ASF, SRp30c, YB-1, ZRANB2 NLGN3 Alter. First Exon (e1-3) 2.30 3.75E-05 ETR-3, fox-2, hnRNP A2/B1, hnRNP A2/B1, hnRNP C1, hnRNP E2, hnRNP F, hnRNP P1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP H1, hnRNP H2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP F, for Cassette 2.51 2.21E-05 ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP A2/B1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H1, hnRNP H2, hnRNP F, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SRp20, SRp30c, TLA-1, TIAL1, YB-1, ZRANB2 OGT Alter. Acceptor Site 1.63 1.68E-03 ETR-3, fox-1, fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HUB, KSRP,	MAGEDI	Intron Retention	1.54	9.86E-03	HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
MAGED2 Intron Retention 1.84 4.22E-04 ETR-3, hnRNP P (ILS), HTra2beta1, HuB, KSRP, PSF, SC35, SRp30c, YB-1, ZRANB2 TRO Alter. Donor Site 2.02 1.88E-03 ETR-3, hnRNP C1, hnRNP C1, hnRNP C1, hnRNP C2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP P (ILS), HTra2alpha, HTra2beta1, HuB, KSRP, Nova-1, RBM5, SC35, SF2/ASF, SRp30c, YB-1, ZRANB2 NLGN3 Alter. First Exon (e1-3) 2.30 3.75E-05 ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H1, hnRNP H2, hnRNP H1, hnRNP H2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP F, fnRNP H1, hnRNP A2/B1, hnRNP A2/B1, hnRNP A2/B1, hnRNP F, hnRNP H1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP F, fnRNP H1, hnRNP A2/B1, hnRNP A2/B1, hnRNP A2/B1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP F (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, NSA-2, RBM5, Sam68, SC35, SRp20, SRp30c, TI-4.1, TIAL1, YB-1, ZRANB2 OGT Alter. Acceptor Site 1.63 1.68E-03 ETR-3, fox-1, fox-2, hnRNP A2/B1, hnRNP A2/B1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HUB, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SRp20, SRp30c, TI-4.1, TIAL1, YB-1, ZRANB2 OGT Alter. Terminal Exon (e4-6) 1.63 1.68E-03 ETR-3, fox-1, fox-2, hnRNP A2/B1, hnRNP A2/B1, hnRNP E1, hnRNP E1, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HUB, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SRp20, SRp30c, TI-4.1, TIAL1, YB-1, ZRANB2 OCK111 Exon Cassette 1.63 1.64E-03 ETR-3, fox-1,	XAGE1D	Complex	2.71	1.98E-07	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP (PTB), hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, KSRP, MBNL1, Nova-1, RBM5, Sam68, SC35, SRp30c, TIA-1, TIAL1, YB-1
TRO Alter. Donor Site 2.02 1.88E-03 ETR-3, hnRNP A1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP P (TLS), HTra2beta1, HuB, KSRP, Nova-1, RBM5, SC35, SF2/ASF, SRp30c, YB-1, ZRANB2 NLGN3 Alter. First Exon (e1-3) 2.30 3.75E-05 ETR-3, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H1, hnRNP K, hnRNP F (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, PSF, Exon Cassette 2.89 1.28E-03 RBM5, San68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 NONO Exon Cassette 2.51 2.21E-05 ETR-3, forXIP A2/B1, hnRNP C1, hnRNP C1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP MD, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 OGT Alter. Acceptor Site 1.63 1.68E-03 ETR-3, forXIP A2/B1, hnRNP C1, hnRNP E1, hnRNP E1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HUB, HuD, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 OGT Alter. Terminal Exon (e4-6) 1.63 ETR-3, forXIP A2/B1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E1, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HUB, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 DOCK11 Exon Cassette 1.65 SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 DOCK11	MAGED2	Intron Retention	1.84	4.22E-04	ETR-3, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, KSRP, PSF, SC35, SRp30c, YB-1, ZRANB2
Alter. First Exon (e1-3) 2.30 3.75E-05 ETR.3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP F, I, KnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, PSF, Exon Cassette NONO Exon Cassette 2.89 1.28E-03 RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 NONO Exon Cassette 2.51 2.21E-05 ETR.3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP F, INRNP H1, hnRNP P, INRNP F, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 OGT Alter. Acceptor Site 1.63 1.68E-03 ETR.3, Fox-1, Fox-2, hnRNP A2/B1, hnRNP A2/B1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP P (TLS), HTB, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 OGT Alter. Acceptor Site 1.63 1.68E-03 ETR.3, Fox-1, Fox-2, hnRNP A2/B1, hnRNP A2/B1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP P (TLS), HUB, HuD, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SRp20, Alter. Terminal Exon (e4-6) 8.47E-05 SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 DOCK11 Exon Cassette 1.85 2.24E-03 CUGBB1, ETR.3, Fox-1, Fox-2, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRN	TRO	Alter. Donor Site	2.02	1.88E-03	ETR-3, hnRNP A1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP P (TLS), HTra2alpha, HTra2alpha, HTra2beta1, HuB, KSRP, Nova-1, RBM5, SC35, SF2/ASF, SRp30c, YB-1, ZRANB2
INLING Exon Cassette 2.89 1.28E-03 RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 NONO Exon Cassette 2.51 2.21E-05 ETR-3, InRNP A1, InRNP A2/B1, InRNP C1, InRNP F, InRNP H1, InRNP H2, InRNP H1, InRNP H2, InRNP H1, InRNP H2, InRNP H1, InRNP A2/B1, InRNP F, InRNP H1, InRNP H2, InRNP H1, InRNP H2, InRNP H1, InRNP P2, InRNP H1, InRNP A2/B1, InRNP A2/B1, InRNP A2/B1, InRNP A2/B1, InRNP A2/B1, InRNP F, InRNP H1, InRNP H2, InRNP H1, InRNP H2, InRNP H1, InRNP P2, InRNP F, InRNP H1, InRNP P2, InRNP F, InRNP H1, InRNP A2/B1, INR	NI OND	Alter. First Exon (e1-3)	2.30	3.75E-05	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, PSF,
NONO Exon Cassette 2.51 2.21E-05 ETR.3, hnRNP A1, hnRNP A2/B1, hnRNP A2/B1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP F, thrRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 OGT Alter. Acceptor Site 1.63 1.68E-03 ETR.3, 6vx-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SRp20, SRp20, Alter. Terminal Exon (e4-6) OCK11 Exon Cassette 1.85 2.24E-03 SRp30c, TIA-1, TIAL1, YB-1, ZRANB2	INLGIN3	Exon Cassette	2.89	1.28E-03	RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
NUNU Exon Cassette 2.01 2.21E-05 SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 OGT Alter. Acceptor Site 1.63 1.682 8.78,30c, TIA-1, TIAL1, YB-1, ZRANB2 OGT Alter. Terminal Exon (e4-6) 1.63 1.68E-05 STR3,50c, TIA-1, TIAL1, YB-1, ZRANB2 DOCK11 Exon Cassette 1.85 2.24E-05 SRp30c, TIA-1, TIAL1, YB-1, ZRANB2	NONO	Even Orienthe	0.51	0.015.05	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SRp20,
Alter. Acceptor Site 1.63 1.68E-03 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E1, hnRNP H2, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SRp20, Alter. Terminal Exon (e4-6) 1.82 8.47E-05 SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 DOCK11 Exon Cassette 1.85 2.24E-03 CUG-BP1, ETR-3, Fox-2, hnRNP A2/B1, hnRNP A2/B1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP H2, hnRNP H, hnRNP H2, hnRNP H, hnRNP H2, hnRNP	NUNU	Exon Cassette	2.51	2.21E-05	SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
Otsi Alter. Terminal Exon (e4-6) 1.82 8.47E-05 SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 DOCK11 Exon Cassette 1.85 2.24E-03 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E1, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP H1, hnRNP H2, hnRNP H, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1,	0.07	Alter. Acceptor Site	1.63	1.68E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E2, hnRNP F2, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP P (TLS), HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SRp20,
DOCK11 Exon Cassette 1.85 2.24E-03 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E1, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP I (TLS), HTra2beta1, HuB, KSRP, MBNL1,	UGI	Alter. Terminal Exon (e4-6)	1.82	8.47E-05	SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
	DOCK11	Exon Cassette	1.85	2.24E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1,

				Nova-1, Nova-2, PSF, Sam68, SC35, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
ZBTB33	Exon Cassette	1.90	8.76E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, Constant of the second s
				Samoo, SU33, SF1, SND2U, SND3UC, 10F43, 11F41, 14E1, TK4NDZ
STAG2	Complex (4e4-15)	1.66	5.58E-03	
STAG2	Exon Cassette	2.37	2.04E-05	CUGBP1, ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E2, hnRNP E2, hnRNP F1, hnRNP F1, hnRNP F2, hnRNP F, hnRNP F1 (PTB), hnRNP P (TLS), HTra2alpha, HTra2batH Jung Hung Hung KNRP MRN1 Jung-2, PSF BRM5, Sam68, SC35, SE1, SE7/ASF, SR206, SR206, TDP44, TIA1, TIA1, TIA1, TABR2
FMR1	Exon Cassette	1.82	6.17E-04	ETR-3, hnRNPA1, hnRNP A2/B1, hnRNPC1, hnRNPC1, hnRNPE2, hnRNP F, hnRN H1, hnRNPH2, hnRNPI (PTB), hnRNPK, hnRNPP (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SP-20, TLA1, TLA1, 1, VP1
RPI 10	Intron Retention	1.88	1 58E-04	CIRCL WRAPP AL INRINE 4/AL INRIP CL INRIP CL INRIP CL INRIP F2 INRIP F2 INRIP F4 INR
GDI1	Intron Retention	2.02	1.02F-04	FTR-3, bnRNP C1, bnRNP F1, bnRNP H2, bnRNP H2, bnRNP I (PTB), bnRNP P (TLS), HuB, KSRP, Nova-1, PSE, RBM5, SC35, SRo30c, TIA-1, TIA-1, VB-1, ZRANB2
	Alter, First Exon (e1.e3.e14-15)	3.01	1.15E-04	
MID1	Complex	1.88	2.38E-04	9G8, CUG-BP1, ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP I, hnRNP K, hnRNP LL,
	Exon Cassette	2.07	2.01E-04	hnRNP P (ILS), HIraZalpha, HIraZbeta1, HuB, HuD, HuK, KSKP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SKp20, SKp30c, IDP43, IIA-1, IIAL1, YB-1, ZKANB2
	Complex	1.52	1.04E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP D1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H, hnRNP K, hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB,
MAP7D2	Exon Cassette	1.56	2.92E-03	HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
TAB3	Intron Retention	1.82	1.17E-02	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
ZNF182 // ZNF630	Exon Cassette	1.70	5.26E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
SYP	Intron Retention	1.51	4.78E-03	ETR-3, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), KSRP, Nova-1, PSF, SC35, SRp30c, YB-1, ZRANB2
FAM120C	Alter. Terminal Exon (e2)	2.33	1.20E-03	9G8, CUG-8P1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F2, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRo20, SRo30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
FGD1	Intron Retention	1.54	5.41E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP P (TLS), KSRP, Nova-1, Nova-2, RBM5, SC35, SF2/ASF, YB-1, ZRANB2
FAM104B	Alter. Donor Site	1.70	4.48E-03	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, MBNL1, Nova-1, Nova-2, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1
	Alter. First Exon (e1)	2.26	6.01E-05	
ZC4H2	Exon Cassette	2.46	7.62E-04	CUG-BP1, EIK-3, FOX-1, FOX-2, INRIVE P41, INRIVE P2/B1, INRIVE C1, INRIVE P2, INRIVE P2, INRIVE P2, INRIVE P4,
	Intron Retention	1.82	3.98E-03	
BRWD3	Exon Cassette	1.87	2.80E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
RPS6KA6	Exon Cassette	3.29	7.45E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
ARMCX2	Alter. Donor Site	1.74	1.11E-02	ETR-3, hnRNP I (PTB), hnRNP P (TLS), HuB, KSRP, Nova-1, RBM5, SC35, TIA-1, TIAL1, YB-1
ZMAT1	Exon Cassette	1.57	2.73E-02	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
MORF4L2	Exon Cassette	1.56	2.94E-03	ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
NUP62CL	Exon Cassette	1.88	1.76E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
KLHL13	Alter. First Exon (e1-4)	2.86	1.02E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
CUL4B	Alter. First Exon (e1-2)	1.91	1.44E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
CUL4B	Intron Retention	1.84	4.86E-03	ETR-3, hnRNP C1, HuB, MBNL1, Nova-1, Sam68, SC35, TIA-1, TIAL1, YB-1
	Alter. First Exon (e1-2,e4-10)	1.52	1.22E-02	
AIFM1	Complex	2.89	6.31E-05	
	Exon Cassette	4.52	7.35E-04	
HS6ST2	Alter. First Exon (e1-2)	1.73	3.15E-04	CUG-BP1, ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, PSF, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
CSAG4 //	Complex	2.16	1.52E-03	FTR.3 hnRNP A1 hnRNP D hnRNP F1 hnRNP F2 hnRNP F4 hnRNP H2 hnRNP H2 hnRNP P (TI S) HTra2hata1 HuR KSRP Nova.1 SC35 SRn20 S
MAGEA2B	Exon Cassette	1.61	2.64E-03	
HAUS7 // TREX2	Alter. Terminal Exon (e8)	2.18	1.85E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D1, hnRNP DL, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
NAA10	Intron Retention	1.65	3.84E-04	ETR-3, Fox-1, Fox-2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP P (TLS), RBM5, SC35, TIA-1, TIAL1
MECP2	Complex (e1,e3)	1.62	7.02E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
CMC4 // MTCP1	Complex	1.61	2.56E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2

CTGLF9P //	Alter. Terminal Exon (e18-25)	1.74	4.32E-05	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP H4, hnRNP A2, hnRNP A4, hnRNP L4, hnRNP L4, hnRNP L4, hnRNP A4, hnRNP A4
	Altern Terminel From (+10.05)	1.05	2.005.00	
CIGLF9P //	Alter. Terminal Exon (e18-25)	1.85	3.99E-06	906, UUG-BF1, ELF3, FOX-J, FOX-J, FOX-Z, INRIVE PJ, INRIVE PJ
FARG	EXOII Casselle	4.20	1.40E-04	
LINC01001	Exon Cassette	1.69	1.82E-03	EIK-3, FOX-1, FOX-2, FIRKIP A1, FIRKIP A2/B1, FIRKIP C1, FIRKIP C1, FIRKIP E1, FIRKIP E2, FIRKIP F1, FIRKIP F1
	Alter Terminal Exon (e3 e6-8)	1 72	2 60F-03	
GTE2IRD2	Evon Cassette	1.65	1.65E-02	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1,
diff Embe	Intron Retention	1.50	1.46E-03	HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
	intron neterition	1.50	1.402.00	9G8 FTR-3 Fox-1 Fox-2 hnRNP A1 hnRNP A2/R1 hnRNP C1 hnRNP C1 hnRNP F1 hnRNP F2 hnRNP F2 hnRNP H1 hnRNP H2 hnRNP H2 hnRNP K hnRNP K hnRNP F(TI S) HTra2beta1 HuR HuD HuR KSRP
ZNF26	Exon Cassette	1.81	3.32E-03	MBNL1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRo20, SRo30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
				FTR-3, bnRNP A1, bnRNP C1, bnRNP D, bnRNP F1, bnRNP F2, bnRNP F2, bnRNP H1, bnRNP H2, bnRNP H (PTB), bnRNP K, bnRNP P (TLS), HTra2aloba, HTra2beta1, HuB, KSRP, MBNI 1, Nova-1, Nova-2, Sam68,
ZNF302	Complex	1.61	1.84E-03	SC35, SF1, SRo20, TIA-1, TIAL1, YB-1, ZRANB2
RABGGTB	Complex	1.52	3.80E-02	ETR-3, hnRNP A1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, Sam68, SC35, SRo20, TDP43, TIA-1, TIAL1, YB-1
	Complex	2.33	8.27E-05	
C1orf85	Exon Cassette	2.31	8.27F-05	ETR-3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1
				FTR-3, bnRNP A1, bnRNP A2/B1, bnRNP C1, bnRNP C1, bnRNP F1, bnRNP F2, bnRNP F, bnRNP H2, bnRNP H2, bnRNP I (PTB), bnRNP K, bnRNP P (TLS), HTra2beta1, HuB, MBNI 1, Nova-1, Nova-2, Sam68, SC35,
FAS	Exon Cassette	1.91	8.36E-04	SF1. SRo20. SRo30c. TIA1. TIA11. YB-1. ZRANB2
C11orf80 //	Alter, First Exon (e1.e4-15)	1.64	4.60E-03	CUG-RP1_FTR-3_Fox-1_Fox-2_hnRNP_A1_hnRNP_A2/B1_hnRNP_C1_hnRNP_D1_hnRNP_D1_hnRNP_F2_hnRNP_F2_hnRNP_F4_hnRNP_H2_hnRNP_H2_hnRNP_H2_hnRNP_F4_nRNP_F4_hn
RCE1	Exon Cassette	3.04	5.95E-05	HuB. HuD. HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRo20, SRo30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
ALG9 // CRYAB				FTR-3. Fox-1. Fox-2. bnRNP A1. bnRNP A2/B1. bnRNP C1. bnRNP E1. bnRNP H1. bnRNP H2. bnRNP H2. bnRNP K. bnRNP P (TIS). HTra2beta1. HuB. HuD. KSRP. MBN11. Nova-1. Nova-2. RBM5. Sam68. SC35.
// FDXACB1	Alter. First Exon (e6)	1.77	2.66E-03	STI. SF2/ASF. SRb20. SRb30c. TIA.1. TIAL1. YB-1. ZRANB2
	Alter, First Exon (e1.e3-8)	1.56	1.16F-04	9G8 CIIC-RP1 FTR-3 Fox-1 Fox-2 hoRNP A1 hoRNP A2/R1 hoRNP C1 hoRNP D hoRNP F1 hoRNP F2 hoRNP F1 hoRNP H1 hoRNP H2 hoRNP H2 hoRNP K hoRNP F (TIS) HTra2aloba HTra2beta1 HuR
PPHLN1	Exon Cassette	3 10	1 19E-04	
LRRC23	Complex	1.51	8.62E-03	TRA: hnPNUP A1 hnPNUP in hnPNUP in hnPNUP H2 hnPNUP (JPTR) hnPNUP (IS) HTra2beat Hur KCRP MRNI 1 Nuva. PSE SC35 SE2/ASE SR30c TIA.1 TIAL1 VR.1
TRIM13	Intron Retention	1.31	4 21F-05	Erros force for a force for the force of the
1100115		1.77	4.212.05	CICCRPT TR3.5 rv.1 row 2 running to many training to the many to the many to the many state to the running to the many to them
CLK3	Intron Retention	1.77	3.58E-03	
IPW//SNORD116	Intron Retention	4 18	3.01E-06	CICLER TETRA FOR TRANSPORT AT A BARNE C1 ANRALE 1 ANTAL 1
II W// ONONDITO	Alter Terminal Exon (e10-11)	1.56	2 20E-03	GOOD F, ELTY A, TWAE, MARKA TA, MARKA D, MARKA
CCNDBP1	Intron Retention	1.50	3 34E-03	Erros rust, rusz, minut Az, minut Az, minut Az, minut Er, minut Er, minut Er, minut Hz, minut Hz, minut R, minut R, minut F, fild, rub, rub, rub, rub, rub, rub, rub, rub
	ind on riciclation	1.7 1	5.54E 05	CICARD TERLS FOR LEWARD AL MARNE AL MARNE AL MARNE CL MARNE CL MARNE DL MARNE DL MARNE EL MARNE EL MARNE EL MARNE HI
MAPT	Alter. First Exon (e1-3)	2.29	1.39E-04	Hrazhari Huik Hui Huik KSP MRNI Nova, I Nova, P. RMK Sama Sri Star Sz (Sz St I Sz Astronov T, Innov T,
				TR3 Fox1 Fox2 bran PLA bran PL
ABCA5	Exon Cassette	2.16	3.22E-04	Sam68, Sci SF1, SR020, SR020, TDP43, TIA1, TIA1, TP, TRANB2
				CIIG-RPI FTR-3 Fox-2 hoRNP A1 hoRNP A2/B1 hoRNP C1 hoRNP C1 hoRNP C1 hoRNP C1 hoRNP C1 hoRNP C2 hoRNP C4 hoRNP
ZNF583	Alter. First Exon (e1-3)	2.02	7.64E-03	KSRP. MRNI 1. Nova-2. PSE. RBM5. Sam68. SC35. SF1. SRo20. SRo30c. TIA-1. TIA 1. VR-1. ZRANB2
	Intron Retention	1.60	5 18E-03	FTR-3 Fox-1 Fox-2 brRNP A1 bnRNP A2/R1 bnRNP C1 bnRNP C1 bnRNP F1 bnRNP F2 bnRNP F1 bnRNP H1 bnRNP H2 bnRNP I (PTR) bnRNP K bnRNP P (TIS) HuB HuD KSRP MRNI 1 Nova-1 PSF RBM5
CARD8	Exon Cassette	3.27	8.10F-05	Sam68, SC35, SF1, SF2/ASE, SRo20, SRo30c, TDP43, TIA-1, TIA-1, YB-1, ZRANB2
	Alter Acceptor Site	1 95	8 25F-04	
WDR6	Complex (e4)	2.32	1.06F-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP DL, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5,
	Intron Retention	2.41	8.06F-05	Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
	Complex (e2 e4)	5.98	4.16F-04	CUG-RP1, FTR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2, B1, hnRNP C1, hnRNP D, hnRNP D, hnRNP F1, hnRNP F2, hnRNP F hnRNP F1, hnRNP H1, hnRNP H2, hnRNP F4, hnRNP
CNR1	Exon Cassette	5.98	4.16F-04	HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam66, SC35, SF1, SRo20, SRo30c, TDP43, TIA-1, TIAL1, YE-1, ZRANB2
	Alter, First Exon (e2)	1.80	7.01F-04	FTR-3. F0x-1. F0x-2. hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP D1, hnRNP F1, hnRNP F2, hnRNP F hnRNP F1 hnRNP H2 hnRNP H2 hnRNP H2 hnRNP F1 hnRNP F1 hnRNP H2 hnRNP F1 hnRNP F1 hnRNP F1
ERAP1	Alter Terminal Exon (e20)	2 16	2 14E-03	MBNI 1, Nova-1, Nova-2, RBM5, Sam68, SC35, SE2/ASE, SRo20, SRo30, TIA-1, TIA11, VB-1, ZRANB2
RAR24	Intron Retention	1.87	1 12E-02	TR.3 bnRNP A1 bnRNP F bnRNP H1 bnRNP H2 bnRNP (/DTR) bnRNP P (TIS) HTra2baba1 KSPP RRM5 SC35 SRn30r VR.1
APBB3	Intron Retention	1.98	8.55F-04	TR-3, brRNP A1, brRNP F1, brRNP H1, brRNP H2, brRNP I (TB), brRNP P (TB), brRNP P (TB), brRNP F1, DRMS, SQ35, SR530c, YB-1, ZRANB2
POL R2 12 //		1.50	0.002.04	
RASA4 //	Exon Cassette	2.47	1.12F-03	CUG-BP1, ETR-3, hnRNP A1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1,
UPK3BL			-	IIALI, YB-1, ZKANBZ
NSUN5P1//TRIM		0.10	2 265 02	
73/74	Intron Retention	2.12	3.36E-03	ETR-3, RIRKIYE D, RIRKIYE ET, RIRKIAE ET, ULEN, ULEN, HILASDERTT, KRAN, NOVA-1, KRANS, SAMOS, SC35, SKb2U, SKb2U, HA-1, HAL1, YB-1
NSUN5	Intron Retention	2.42	6.76E-04	ETR-3, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP P (TLS), HTra2beta1, KSRP, Nova-1, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1
4055	Intron Retention	1.66	9.61E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS),
ARF5	Alter. First Exon (e22-23,e36)	1.69	7.61E-04	HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
		1.50	1 505 02	

				KODD MDNI 1 Nave 1 Nave 2 DOC DDME Came 0 CO2E CC1 CC2/ACC CD-20 CD-20 TA 1 TAL 1 VD 1 7DAND2
EDVI C		0.00	1.005.00	
FBXL0	Intron Retention	2.00	1.96E-03	EIR-3, NNKINP F, NNKINP HI, NNKINP HZ, KSRP, MBINLI, NOVA-1, SC39, SF2/ASF, TIA-1, TIALI, YB-1
	Alter. First Exon (e1-2)	2.10	4.76E-03	
WASH3P	Intron Retention	1.57	2.71E-02	EITES 1021, 1022, INTRUE AL, INTRUE AZ, DI, INTRUE D, INTRUE D, INTRUE D, INTRUE D, INTRUE L, IN
	Exon Cassette	1.92	2.68E-03	NSRF, MIDINEL, NUVA-2, FSF, RDM3, SAII100, SUS3, SF1, SR/2U, SR/SUC, IDF43, HA-1, HAL1, ID-1, ZRAINDZ
				CUG-RP1 FTR-3 Eox-1 Eox-2 bnRNP A1 bnRNP A2/R1 bnRNP C1 bnRNP D bnRNP D1 bnRNP D1 bnRNP E1 bnRNP E2 bnRNP E1 bnRNP H1 bnRNP H2 bnRNP L(PTR) bnRNP K bnRNP P (TLS) HTra2alnba HTra2beta1
GPR161	Alter. First Exon (e1-2,e6)	1.63	1.05E-04	HuR HUD KSRP MRN1 Nova-2 PSE RM5 Sam68 SC35 SE2/ASE SRa00 SR30c TDP43 TIA1 TIA11 VR1 7RANR2
-				
AHNAK	Alter. Terminal Exon (e5-7)	1.84	4.36E-03	506, ETRO, FORZ, FORZE, TORVET AL, MILARE AZ, DT, MILARE A, MILARE A, MILARE A, MILARE AZ, MILARE T, MILAR
				HIRZZAIPNA, HIRZZBETAI, HUB, HUU, HUK, KSKP, MISNLI, NOVA-2, PSF, KBM5, SAM68, SC35, SF1, SF2/ASF, SKp2U, SKp3Uc, TDP43, TIA-1, TIAL1, YB-1, ZKANB2
EXYD2 // EXYD6	Exon Cassette	1 95	1.63E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP KL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB,
1,1102 // 1,1100	Elon oubbollo	1.50	1.002.01	HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
FAM101A //	Even Cesette	1 5 4	1.045.04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1,
ZNF664	EXOIT Casselle	1.04	1.04E-04	HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
				FTR-3, Fox-1, Fox-2, bnRNP A1, bnRNP A2/B1, bnRNP C1, bnRNP C1, bnRNP F1, bnRNP F2, bnRNP F1, bnRNP H2, bnRNP H2, bnRNP H2, bnRNP K, bnRNP K, bnRNP P, (T1S), HTra2alpha, HTra2beta1, HuB, HuD, KSRP,
GPR19	Alter. First Exon (e1-2)	6.22	1.61E-04	MBNI 1 Nova-1 Nova-2 PSE RBM5 Sam68 SC35 SE1 SE2/ASE SR020 SR030c TIA-1 TIAL1 YR-1 ZRANB2
RRN3P1	Alter. First Exon (e3-8)	1.59	1.32E-03	
SLC7A5P1	Alter, First Exon (e1)	1.74	1.15E-02	9G8, CUG-BP1, E1R-3, FMRP, Fox-1, Fox-2, NRRVP A1, NRRVP A2/B1, NNRVP D1, NNRVP D, NNRVP D1, NNRVP E2, NNRVP F1, NNRVP F1, NNRVP H2, NNRVP H3, NNRVP H3
				HTraZalpha, HTraZbeta1, HuB, HuD, HuK, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
NPIPB3 //	Alton First Evon (o11)	1.52	2 105 02	CUG-BP1, ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha,
SLC7A5P2	Alter. Hist Exoli (e11)	1.JZ	2.10L-03	HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
TPM3P9 //		1.50	1 105 00	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D1, hnRNP D2, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB,
7NF761	Alter. First Exon (e1,e4-6)	1.52	1.10E-03	HuD, KSRP, MBNI 1, Nova-1, Nova-2, PSE, RBM5, Sam68, SC35, SE2/ASE, SRo20, SRo30c, TIA-1, TIAI 1, YB-1, ZRANB2
				FIR-3 Fox-1 Fox-2 bnRNP 41 bnRNP 42/81 bnRNP C1 bnRNP C1 bnRNP C1 bnRNP F1 bnRNP F2 bnRNP F bnRNP H1 bnRNP H2 bnRNP H2 bnRNP H2 bnRNP K bnRNP F (TIS) HTra2alnba HTra2beta1 HuR
ARL17B	Alter. Terminal Exon (e5)	2.70	1.14E-03	HID KORD MRNI I Nova 1 Nova 2 PEC RMK Sam68 SO35 SE1 SCY AGE SPACE SPACE SPACE TO ATAL 1 ALL 1 VE 1 ZAMRY
010(20 /DDI 17	0	1.50	0.005.04	
C180ff32/RPL17	Complex	1.53	2.80E-04	EIK-3, NNKWP H, NNKWP H2, NNKWP H2, NNKWP K, NNKWP K, NNKWP K (113), HUB, NSKP, WOVA-2, Samoo, SU-39, SKp3uc, 10P43, 11A-1, 11AL1, 18-1
OAZ1	Intron Retention	2.37	3.16E-04	hnRNP F, hnRNP H1, hnRNP H2, hnRNP P (TLS), Nova-1, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
CALR3/CHERP/	Evon Cassette	1 73	1 98E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1,
MED26/SLC35E	Exon Gassette	1.75	4.502-05	Nova-1, Nova-2, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
ANUCODOC	5 0 "	1.54	1 105 00	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP,
ANKRD36	Exon Cassette	1.54	1.12E-03	MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
				FTR-3 Fox-1 Fox-2 bnRNP A1 bnRNP A2/B1 bnRNP C1 bnRNP D1 bnRNP D1 bnRNP D1 bnRNP F2 bnRNP F2 bnRNP F4 bnRNP H2 bnRNP H2 bnRNP H2 bnRNP K4 bnRNP F4
SCLY // UBE2F	Exon Cassette	1.62	5.20E-03	KSPP MRV1 Nova-2 PSF Sam68 SC35 SF1 SF2/ASF SRo20 SRo30c TDPA3 TIAL TIAL 12, TANNA TAL TANA TAL TAL TAL TAL TAL
	Albert Assessment City	1 71	1.025.00	
51011.1	Alter. Acceptor Site	1./1	1.03E-02	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1,
FIPILI	Exon Cassette	1.83	4.02E-04	Nova-2, PSF. Sam68. SC35. SF1. SRp20. SRp30c. TIA-1. TIAL1. YB-1. ZRANB2
	Intron Retention	1.83	4.02E-04	
MECDO	Even Cassette	2 22	2 645 02	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP,
WII 300	Exon Gassette	2.52	3.042-03	MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
GTF2H4//VARS2	Intron Retention	1.70	9.26E-03	ETR-3, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP I (PTB), hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, Sam68, SC35, SF2/ASF, TIA-1, TIAL1, YB-1
				CUG-BP1_FTR-3_EMRP_Fox-1_Fox-2_bnRNP A1_bnRNP A2/B1_bnRNP C1_bnRNP D_bnRNP D1_bnRNP F1_bnRNP F2_bnRNP F2_bnRNP F1_bnRNP H2_bnRNP H2_bnRNP H3_bnRNP H3_bnRNP H2_bnRNP
MCM9	Alter. Terminal Exon	1.68	1.18E-03	HTra2alpha HTra2beta1 HuR HuD KSRP MRNI 1 Nova-2 PSE RRM5 Sam68 SC35 SE1 SE2/ASE SR020 SR030c TDP43 TIA1 TIA11 VR.1 ZRANR2
MDDS24 //	Alter First Evon (e1 e4-5)	1.64	5 30E-03	
	Intron Datantian	1.04	2.300-03	Encorrections as innover as innover as innover of innover of innover of innover of innover of the innover of the innover of innover
		1.52	2.30E-02	
ADCYTOPT //	Complex	2.73	2.26E-05	ETR3, FOR-1, FOR-2, RIKTER AL, RIKT
NFYA				KSRP, MBNL1, Nova-1, PSF, Sambe, SU35, SKp2U, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
ARMOVE //	Alter. Acceptor Site	1.68	5.74E-03	ETD.3 hADND A1 HADND A2/R1 HADND C1 HADND C1 HADND L1 HADND L1 HADND L1 HADND L1 HADND L (TES) HADND D (TES) LT-20-44-1 LILD KODD MONIT New 1 DOC DDMC CO2C CT1 CD-20 CD-20- TH 1
	Complex (e3)	2.70	9.97E-05	This to T Toble 2 with a contrast of the contrest of the contrast of the contrest of the contrest of the contr
GENAOFZ	Exon Cassette	2.70	9.97E-05	Inct, 10-1, 200102, 104-1, 104-2
	Complex (e5)	1.55	3.16F-03	
WAC	Evon Cassette	1.55	2.66E-02	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, HuD, HuR, KSRP, Nova-1, RBM5, Sam68, SC35,
into		1.33	1.200.02	SF2/ASF, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
	Intron Retention	1./3	1.39E-02	
RBM26	Intron Retention	1.69	2.82F-03	EIK-3, NNKIV AL, NNKIV AL, NNKIV CL, NNKIV EL, NNKIV EL, NNKIV F, NNKIV HL, NNKIV HZ, NNKIV K, NNKIV P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, RBM5, Sam68, SC35,
		1.05	2.021-03	SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
AKT101 // 0.401	Alter. First Exon (e2-4,e19,e22)	1.74	4.02E-04	
ANTIST // IL411	Complex	1.56	6.40E-04	
// NUP62	Intron Retention	2.55	2.43E-04	(12), HIRAZOERAI, HUB, HUU, NƏKY, WBIYLI, NOVA-2, NƏF, KBMƏ, ƏRMƏS, ƏCƏƏ, ƏFZ/AƏF, ƏKPZU, ƏKPZUÇ, IUP43, IIA-1, IALI, YB-1, ZKANBZ
COX17 //	Exon Cassette	2 04	2 97F-04	CIG_RP1 FTR-3 Fox-1 Fox-2 hoRNP A1 hoRNP A2/B1 hoRNP C1 hoRNP C1 hoRNP D1 hoRNP D1 hoRNP F1 hoRNP F2 hoRNP F hoRNP H1 hoRNP H1 hoRNP H2 hoRNP H2 hoRNP A hoRNP H1 hoRNP H1 hoRNP H2 hoRNP H1 hoR
POPDC2	Mutualy Evolucity Evone (c4 E)	2.01	1.22E.04	
r Ur DGZ	mutually Exclusive EXOIIS (e4-3)	2.30	1.22E-U4	111α2.05α1, 1105, 1107, 1107, 11071, 11074-1, 11074-2, FOL, NONO, 3033, 311, 312/A31, 3Nβ20, 3Nβ20C, LDF43, HA-1, HAL1, TD-1, ZNANDZ

	Complex (e3-4,9-10)	1.58	4.00E-05	
CSNK2B //	Complex (e3-4)	1.52	2.01E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35,
LY6G5B	Exon Cassette	1.65	6.26E-05	SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
	Intron Retention	2.06	1.57E-04	
01100.101	Complex	1.58	9.04E-04	CUG-BP1, ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F1, hnRNP H1, hnRNP H3, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha,
GMDS-AS1	Alter, First Exon (e1-2)	1.72	6.63F-04	HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
AOTDAD	F 0 "	1 70	2 705 02	
AGTRAP	Exon Cassette	1.78	3.70E-03	EIR'S, FOX-1, FOX-2, INRIVE AL, INRIVE F, INRIVE HZ, INRIVE 1 (P18), INRIVE P (LS), HUE, KSKP, MBIVEL, Samos, SG35, SF2/ASF, SOF30C, IA-1, IAL, YB-1, ZKANBZ
VPS13D	Complex (e40)	1.75	5.88E-03	EIR3, F0x-1, F0x-2, INRNP A1, INRNP A2/B1, INRNP C1, INRNP E1, INRNP E2, INRNP F, INRNP H1, INRNP H2, INRNP H3, INRNP H3, INRNP F (ILS), INRNP A2/B1, INRNP C1, INRNP
-	Exon Cassette	1.74	5.88E-03	MBNL1, Nova-1, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZKANB2
PDPN	Exon Cassette	5.20	2.14E-05	9G8, CUG-BP1, ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
RCC1 // SNHG3	Exon Cassette	2.03	9.70E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
SERINC2	Exon Cassette	1.78	1.38E-03	ETR-3, hnRNP A1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), KSRP, MBNL1, Nova-1, RBM5, SC35, SRp20, TIA-1, TIAL1, YB-1
ADC	Alter. First Exon	1.73	1.25E-02	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, RBM5, Sam68, SC35, SRp30c, TIA-1, TIAL1,
DNALI1	Alter. Terminal Exon	2.33	1.28E-03	9G8, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
PTPRF	Exon Cassette	7.31	3.01E-06	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
DMAD1	Alter. Acceptor Site	1.70	2.58E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP P (TLS), HTra2beta1, HuB, KSRP, Nova-1, PSF, Sam68, SC35,
DMAP1	Intron Retention	2.21	2.36E-04	SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
NSUN4	Alter. First Exon (e1)	2.95	2.30E-03	ETR-3, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F1, hnRNP H2, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2alpha, HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, SC35, TIA-1, TIAL1, YB-1
	Complex (e16)	2.07	9.38E-04	FTR-3. Fox-1. Fox-2. bnRNP A1. bnRNP A2/B1. bnRNP C1. bnRNP C1. bnRNP F1. bnRNP F2. bnRNP F5. bnRNP H1. bnRNP H2. bnRNP L (PTB). bnRNP K. bnRNP P (TLS). HTra2aloba. HTra2beta1. HuB. KSRP. MBNI 1.
OSBPL9	Exon Cassette	2.17	9.38F-04	Nova-1, Nova-2, RBM5, Sam68, SC35, SF1, SRo20, SRo30c, TIA-1, TIAL1, YB-1, ZRANB2
TCEANC2	Exon Cassette	1.92	1.72E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRo20, SRo30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
	Alter, First Exon (e1-9)	6.11	9.61F-07	9G8 CLIG-BP1 FTR-3 Fox-1 Fox-2 hnRNP A1 hnRNP A2/B1 hnRNP C1 hnRNP D1 hnRNP D1 hnRNP F1 hnRNP F1 hnRNP F1 hnRNP H1 hnRNP H2 hnRNP H3 hnRNP H3 hnRNP H7 hnRNP K hnRNP H hnRNP F1
PDE4B	Complex (e3-4)	7 15	1.67E-05	(IS) HTra/alpha HTra/betal HuB HuD HuR KSRP MRN1 Nova-2 PSF RBMS Sam68 SC35 SF1 SF2/ASF SRa/0 SRa/0 CTDP43 TIA-1 TIA1 1 R-1 7RANR2
	Alter First Evon (e1-3)	2.69	8 43E-04	(100) The second s
SRSF11	Evon Cassette	3.50	3 70E-05	Judy Judy and Lines (1997) and a structure of the structu
	Alter First Evon (e1-6)	2.41	1.57E-05	
LPHN2	Even Corretto	1.90	6.00E.04	500, 000-01, LTR-3, IMICT, 104-1, 104-1, 104-04, IMICT 22, D1, IMICT 21, IMICT 9, IMICT 21, IMICT 21, IMICT 21, IMICT 12, IMICT 13, IMICT 112, IMICT 112, IMICT 112, IMICT 14, I
PRKACB	Alter. First Exon (e1,e7)	1.67	6.59E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP D, hnRNP E2, hnRNP F2, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP H, hnRNP H3, hnRNP F4, hnRNP
SH3GLB1	Exon Cassette	4.73	4.43E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SF1, SRo20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
HS2ST1	Alter. First Exon (e2-7)	1.94	1.71E-05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
KIAA1324	Complex	1.53	3.26E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
AMPD2	Exon Cassette	1.57	1.90E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, RBM5, SC35, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
	Alter. First Exon (e1)	2.64	1.34E-06	
1101/10	Complex	1.54	4.64E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB,
MOVIO	Intron Retention	1.59	8.60E-03	HuD, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
	Exon Cassette	1.58	6.74E-03	
700044	Complex	1.58	1.72E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP F1, hnRNP F1, hnRNP H2, hnRNP H3, hnRNP H (PTB), hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, RBM5, SC35, SF2/ASF, SRp30c, TDP43, TIA-1,
TRIM46	Exon Cassette	1.93	8.02E-04	TIAL1, YB-1
RGS4	Complex	2.46	2.41E-04	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP K, Nova-1, Nova-2, Sam68, SC35, TIA-1, TIAL1, YB-1
PBX1	Exon Cassette	1.59	1.62E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
RABGAP1L	Alter. Terminal Exon (e32-37)	2.65	9.60E-03	9G8, CUG-8P1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
FAM163A	Alter. Terminal Exon (e8-9)	14.59	1.87E-05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
DHX9 // NPL	Alter. First Exon (e1,4-6,9-12-15)	1.86	1.34E-02	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP DL, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB,

Appendices

	F 0	0.1.0	0.005.00	
	Exon Cassette	2.10	3.88E-03	HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
SMG7	Exon Cassette	2.17	4.33E-05	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1
RGL1	Exon Cassette	1.54	5.19E-04	9G8, CUG-8P1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRo20, SRo30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
PLA2G4A	Exon Cassette	1.84	1.01E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP D1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MRN11, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRo20, SRo30c, TDP43, TIA-1, TIA11, YB-1, ZRAWR2
CAMSAP2	Exon Cassette	2.07	1.58E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F1, hnRN
SHISA4	Complex	2 59	8 55E-04	hardy the phase is the second s
NEASC	Alter. Terminal Exon (e21,e22-25,e27- 29 e34-36)	1.77	1.19E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1,
1117100	Evon Cassette	2.03	1 28E-03	HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
CDK19	Intron Potention	1.52	1.202-03	CO25 CD-20 VD 1
CDK10	Altern Derren Site	1.55	1.00L-02	3033, 30j20, 15-1
	Alter. Donor Site	3.86	6.05E-05	ETR-3. Fox-1. Fox-2. hnRNP A1. hnRNP A2/B1. hnRNP C1. hnRNP C1. hnRNP DL. hnRNP E1. hnRNP E2. hnRNP F. hnRNP H1. hnRNP H2. hnRNP I (PTB). hnRNP K. hnRNP P (TLS). HTra2aloha. HTra2beta1. HuB.
CD55	Exon Cassette	4.69	3.34E-03	HuD, KSRP, MBNI 1, Nova-1, Nova-2, RBM5, Sam68, SC35, SE1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
	Intron Retention	3.86	6.05E-05	
PSEN2	Exon Cassette	1.85	1.16E-02	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
ZNF678	Exon Cassette	1.81	5.38E-04	CUG-BP1, ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H3, hnRNP H3, hnRNP H3, hnRNP I4, hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
CUK1	Exon Cassette	1.61	4.48E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1,
GONI	Intron Retention	1.51	6.35E-04	RBM5, Sam68, SC35, SF2/ASF, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
ACTN2	Exon Cassette	2.85	1.12E-03	CUG-BP1, ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, SC35, SRo30c, TIA-1, TIAL1, YB-1
KIF26B	Complex	3.79	2.59E-06	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
SDF4	Complex	3.77	3.22E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP K, hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF2/ASF, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
CDK11A/B //	Exon Cassette	1.95	3.83E-04	CUG-BP1. ETR-3. Fox-1. Fox-2. hnRNP C1. hnRNP E1. hnRNP E2. hnRNP F. hnRNP H1. hnRNP H2. hnRNP H2. hnRNP P. (PTB). hnRNP P. (TLS). HuB. HuD. KSRP. MBNL1. Nova-1. Sam68. SC35. SF1. SF2/ASF. SRo20. SRo30c.
GNB1	Intron Retention	1.51	2.09F-02	TDP43, TIA1, TIAL1, YB-1, ZRANB2
	Complex	1.59	4.21E-04	
ACOT7	Even Connette	0.15	5.0EF.0E	
	EXON Casselle	2.10	5.95E-05	
RERE	Alter. First Exon (e1-9)	1.56	1.44E-03	9G8, CUG-BP1, ETR-3, FMRP, Fox-1, Fox-2, hnRNP F A2, B1, hnRNP F C1, hnRNP F D1, hnRNP F L1, hnRNP F L1, hnRNP F H2, hnRNP F H3, hnRNP F H3, hnRNP F H3, hnRNP F H3, hnRNP F H2, HNRNP F L1, HNRNP F L
	Exon Cassette	1.64	1.18E-03	hnKNP P (ILS), H1ra2alpha, H1ra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, KBM5, Sam68, SC35, SF1, SF2/ASF, SKp20, SKp30c, IDP43, IIA-1, IIAL1, YB-1, ZKANB2
RCC2	Alter. First Exon (e1)	1.53	2.15E-02	ETR-3, hnRNP A1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SRp30c, TIA-1, TIAL1, YB-1
TMEM234	Exon Cassette	1.71	8.41E-04	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP LL, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
MEAF6	Exon Cassette	7.44	1.82E-05	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP L1, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, Sam68,
	Mutualy Exclusive Exons (e7)	5.41	2.42E-05	SC35, SRd20, SRd30c, TIA-1, TIAL1, YB-1, ZRANB2
LEPRE1	Intron Retention	1.67	2 70F-03	Fox-2 bnRVP P (TLS) HTra2beta1 Nova1 SC35 SRn30c YB-1
ATPAF1 // EFCAB14	Exon Cassette	1.94	6.70E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, PSF, Sam68, SC35, SRp20, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
TTC39A	Alter. Terminal Exon (e17-18)	1.56	2.21E-05	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
YIPF1	Exon Cassette	2.14	1.82E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
DOCK7	Exon Cassette	2.57	1.16E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
WLS	Exon Cassette	5.99	8.34E-05	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
DEPDC1	Exon Cassette	2.04	1.10E-02	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, KSRP, MBNL1, Nova-1, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
MCOLN3	Exon Cassette	4.14	2.85E-06	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
TMED5	Exon Cassette	2.16	8.32E-05	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, PSF, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
SLC16A1	Complex	1.89	1.06E-03	9G8, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2

MTMR11	Exon Cassette	1.60	9.80E-03	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1
ENSA	Alter. Terminal Exon (e5)	1.79	1.83E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, PSF, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
	Alter. Acceptor Site	2.23	4.41E-04	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35,
SELENBPI	Intron Retention	4.98	8.39E-05	SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
0100412	Alter. First Exon (e1-3)	1.81	1.42E-03	CUG-BP1, ETR-3, hnRNP A1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5,
S100A13	Complex	2.57	2.02E-04	Sam68, SC35, SF2/ASF, TIA-1, TIAL1, YB-1, ZRANB2
	Alter. First Exon (e5-9)	1.63	3.41E-04	
TPM3	Exon Cassette	1.51	1.58E-03	CUG&P1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E1, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP H, hnRNP F, hnRNP F, hnRNP A2/B1, hnRNP A2/B1, hnRNP A2/B1, hnRNP E1, hnRNP E1
	Intron Retention	2.38	1 74F-03	MBNL1, NOVA-1, NOVA-2, PSF, SAMO8, SU35, SF1, SF2/ASF, SKp2U, SKp3UC, IUP43, IIA-1, IIAL1, YB-1, ZKANBZ
NES	Complex	1.95	2.18E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRo30c, TIA-1, TIAL1, YB-1, ZRANB2
TMC01	Complex	3.81	2.03E-04	ETR-3, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
TNR	Alter. First Exon (e1-2)	2.36	7.78E-05	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I, hnRNP I, hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
KCNT2	Complex	3.12	4.36E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
KCNT2	Exon Cassette	2.42	4.36E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SRp20c, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
IRF6	Exon Cassette	2.08	3.99E-05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
ENAH	Exon Cassette	1.59	4.44E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
TMEM63A	Alter. Terminal Exon (e22-26)	2.87	3.84E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
AKT3	Complex	2.17	6.37E-05	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
HSPA14	Exon Cassette	1.56	2.68E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
PTER	Exon Cassette	2.19	2.12E-03	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
	Alter. Acceptor Site	2.39	2.84E-04	
CDH23	Alter. First Exon (e1–27,49-66)	3.63	2.40E-04	Socy Conserve Lines, Inter, Totes, To
	Alter. Terminal Exon (e34-38)	1.54	3.25E-02	הוותיו ד (רבט), ההצבושות, ההצבושות, המני, המני, המני, המני, המניב, המניב, המנים, סבוויס, סבוט, מרבי, סבי, מקבר, מקבר, מקבר, מקבר, מרבי, האבי, ה
AGAP11/FAM25A	Intron Retention	2.01	4.00E-03	ETR-3, hnRNP A1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, TIA-1, TIAL1, YB-1
SUFU	Alter. Terminal Exon (e13-14)	1.65	6.22E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
ADD3	Exon Cassette	4.47	8.44E-05	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
SHOC2	Exon Cassette	1.52	1.16E-03	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP H, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
1	Alter. First Exon (e1-3,e5-6,e10)	2.34	2.44E-04	
TCF7L2	Exon Cassette	2.67	2.32E-03	borking for the first state in the first state in the first state of the first state sta
	Mutualy Exclusive Exons (e20)	1.86	1.13E-02	
INPP5F	Alter. Terminal Exon (e11-16,e18-22)	2.04	5.23E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
PITRM1	Intron Retention	2.91	8.60E-03	ETR-3, Fox-1, Fox-2, hnRNP D, hnRNP E1, hnRNP E2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
ARHGAP21	Alter. First Exon (e9)	3.61	9.76E-05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP D1, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1,
	Exon Cassette	3.54	1.53E-05	HUB, HUD, KSHY, MBNLI, NOA-1, NOA-2, HBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
EPC1	Complex	1.75	3.64E-05	9G8, CUG-BP1, E1K-3, Fox-1, Fox-2, INKNP A1, INKNP A2, B1, INRNP C1, INRNP D, INRNP DL, INRNP E1, INRNP E2, INRNP F, INRNP H1, INRNP H2, INRNP H3, INRNP H (PTB), INRNP K, INRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
NRP1	Alter. Terminal Exon (e11,e13-14)	2.58	1.21E-06	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2aloha, HTra2beta1, HuB, HuD, HuB, KSRP, MBNI 1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRo20, SRo30c, TDP43, TIA-1, TIAI 1, YR-1, ZRANR2
	Exon Cassette	1.73	4.04E-03	

ZNF248	Alter. Terminal Exon (e7)	1.56	1.53E-05	CUG-BP1, ETR-3, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2alpha, HTra2beta1, Hun Hun KSPP MBN11, Nata-1, Nata-2, PSE, PBM5, Sam68, SC35, SE1, SE2/ASE, SPa30, TDPA3, TIA-1, TIA-1, TIA-1, ZANB2,
	Intron Retention	1.70	5.28E-03	
MARCH8	Complex	1.80	9.80E-04	9G8, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
ANIKO	Complex (e2)	2.68	1.02E-02	9G8, CUG-BP1, ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP DL, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP H2, hnRNP K, hnRNP LL,
ANNS	Exon Cassette	4.39	2.40E-04	hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
TYSND1	Alter. First Exon (e1-2)	1.54	8.21E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
ASCC1	Alter. Donor Site	3.97	1.19E-04	ETR-3, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
P4HA1	Exon Cassette	1.61	3.30E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
PPP3CB	Exon Cassette	1.70	4.94E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
	Alter. First Exon (e1,e8,e10-15)	1.69	7.92E-03	
KCNMA1	Alter. Terminal Exon (e1,5,10- 23,25,29-30e32-34,36-39,41)	3.46	5.25E-09	9G9, COG-DF1, ETRS, FMRP, F0x-2, F0x-2, HIRAYP A1, HIRAYP A2/B1, HIRAYP C1, HIRAYP D2, HIRAYP E1, HIRAYP F, HIRAYP F, HIRAYP F1, HIRAYP F2, HIRAYP F3, HIRAYP F3, HIRAYP F3, HIRAYP F3, HIRAYP F4, HIRAYP4, HIRAYPA F4, HIRAYP4, H
TCTN3	Intron Retention	1.93	1.80E-04	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, MBNL1, Nova-1, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1
NDUFB8 //	Complex	1.98	1.24E-02	ETR-3, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, KSRP, MBNL1, Nova-1, SC35, SF2/ASF, SRp30c, TIA-
SEC31B	Exon Cassette	2.96	3.36E-06	1, TIAL1, YB-1
SH3PXD2A	Alter. First Exon (e1-3,e5-6,e9,e12)	3.55	4.48E-05	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP D1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
SFXN4	Intron Retention	1.59	1.42E-02	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
RGS10	Alter. First Exon	2.80	6.64E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
EGER2	Complex (e15)	6.62	2.42E-05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB,
TOTAL	Exon Cassette	1.63	5.67E-05	HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
ATE1	Exon Cassette	1.56	1.02E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
MKI67	Exon Cassette	2.46	1.64E-05	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, PSF, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
PTDSS2	Alter. First Exon (e1)	1.67	4.79E-06	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, PSF, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
CD151	Alter. First Exon (e1,e4)	1.53	1.40E-04	ETD 2 HADNID C1 HADNID E HADNID E/ HADNID E/ TADNID E/ DATO O TTO E TTO 2 HADNID E/ HAD
CD151	Complex	1.51	2.59E-04	LINS, IIINAR 01, IIINAR 11, IIINAR 12, IIINAR 17, IIINAR 17, IIINAR 17, IIINAR 17, IIINAR 17, IIINAR 11, IIINAR 12, IIINAR 17, IIINA
TSPAN4	Alter. First Exon (e1)	1.69	7.05E-04	ETR-3, Fox 1, Fox 2, hnRNP A1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H (PTB), hnRNP K, hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, RBM5, SC35, SRp20, SRp30c,
-	Exon Cassette	1.61	7.79E-04	
STIM1	Alter. Donor Site	1.57	6.04E-04	CUC-BP1, E1R-3, Fox-1, Fox-2, INKINP A1, INKINP A2/B1, INKINP C1, INKINP C1, INKINP E2, INKINP F, INKINP F, INKINP H2, INKINP H2, INKINP K, INKINP K, INKINP P (TLS), HTrazbeta1, HUB, KSKP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
SYT9	Exon Cassette	2.26	2.28E-05	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
LDLRAD3	Exon Cassette	1.54	1.18E-03	9G8, CUG-BP1, ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
DDB2	Complex	1.64	9.77E-04	FTR.3 bnRNP C1 bnRNP F bnRNP H2 bnRNP H2 bnRNP I (PTR) bnRNP P (TI S) HuR MRNI 1 Noval PSE SC35 SR530c TIAL TIALI YR.1 ZRANR2
0002	Exon Cassette	1.71	9.77E-04	Enco, mixed 04, mixed 14, mixed 14, mixed 14, mixed 14 (16), mixed 14 (16), mixed 14, mixed 14, 100 (17), 0000, mixed 14, mixe
MADD	Exon Cassette	2.93	3.99E-05	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
SLC39A13	Alter. First Exon (e6-7)	1.58	9.58E-03	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
CTNND1 //	Alter. Acceptor Site	1.71	2.60E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD,
TMX2	Complex	1.84	8.50E-03	HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
SLC3A2	Exon Cassette	2.15	2.54E-03	EIK-3, INKIV A1, INKIV A2/B1, INKIV F, INKIV F1, INKIV F1, INKIV F1 (PTB), INKIV P (TLS), HTra2beta1, HUB, KSRP, MBUL1, Nova-1, PSF, RBM5, Sam66, SC35, SRp20, STp40, TIA-1, YB-1
RTN3	Exon Cassette	2.95	3.61E-04	CUG-BP1, E1R-3, F0X-2, DNKNP H2, DNKNP H2, DNKNP C1, DNKNP D1, DNKNP D1, DNKNP D1, DNKNP E2, DNKNP F2, DNKNP F1, DNKNP F4, DNKNP F3, DNKNP F3, DNKNP F4, DNKNP F2, DNKNP F3, DNKNP F2, DNKNP F4, DNKNP F3, DNKNP F4, DNKNP F2, DNKNP F3, DNKNP F3, DNKNP F4, DNKNP F4, DNKNP F3, DNKNP F4, DNKNP F3, DNKNP F3, DNKNP F4, DNKNP F3, DNK

FAM89B	Complex	3.00	4.26E-05	ETR-3, hnRNP A1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, KSRP, Nova-1, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
SIPA1	Alter. Terminal Exon (e9-11,e13-19)	2.00	1.43E-04	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HuB, HuD, KSRP, MBNL1, Nova-1, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
CCND1	Complex	3.26	8.20E-05	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HuB, KSRP, Nova-1, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
005144	Complex	2.37	7.84E-04	CUG-BP1. ETR-3. Fox-1. Fox-2. hnRNP A1. hnRNP A2/B1. hnRNP C1. hnRNP C1. hnRNP DL. hnRNP E1. hnRNP E2. hnRNP F. hnRNP H1. hnRNP H2. hnRN
PPFIAI	Exon Cassette	5.07	2.19E-04	HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
1701610	Complex	2.18	3.01E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, RBM5, Sam68,
AIG16L2	Exon Cassette	2.01	1.38E-04	SC35, SF1, SF2/ASF, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
TMEM135	Complex	1.57	5.36E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
C11orf63	Alter. Terminal Exon (e5-10)	1.55	1.72E-03	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP D1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
PIDD	Intron Retention	1.59	1.82E-04	ETR-3, Fox-1, Fox-2, hnRNP E1, hnRNP E2, hnRNP P (TLS), HuB, KSRP, Nova-1, Nova-2, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
IFITM10	Alter. Donor Site	1.79	1.34E-03	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
1110	Complex (e5)	1.73	2.62E-02	TTD 2 HERND C1 HERND HERND R (TC1) HER NEW 1 DOC DRIVE CO2E OF 40 TIA 1 TIAL1 VD 1
HI9	Exon Cassette	1.88	3.42E-03	E1K-3, NIRKIY C1, NIRKIY F (F1B), NIRKY F (1L5), HUB, NOVA-1, P5F, KBM9, SC33, SKP2U, 11A-1, 11AL1, TB-1
ICE2 // INS	Alter. First Exon (e1-2,e4-5)	3.98	1.17E-04	CUG-BP1, ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F1, hnRNP H1, hnRNP H3, hnRNP H3, hnRNP I, hnRNP I, hnRNP P (TLS),
101 2 // 1113	Alter. Terminal Exon (e11-13)	4.90	7.76E-05	HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
PIC3	Complex	3.15	1.64E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1,
RIC3	Exon Cassette	3.40	1.64E-04	HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
CYP2R1	Alter. First Exon (e2)	2.03	2.19E-02	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
ABCC8	Exon Cassette	1.73	3.43E-06	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
DAVE	Alter. Donor Site	6.28	5.84E-05	TTD 2 Faul Faul A HEADER 1 HEADER F HEADER 11 HEADER 10 HEADER 10 HEADER AND A THE UTER SHARE 1 HEAD KODE NEWS COLOR CARE COLOR COLOR COLOR THAT THAT YO I TRANSPO
PAX6	Intron Retention	6.30	3.78E-05	
CD59	Alter. First Exon (e1-3,e6)	2.94	8.48E-05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
FAM168A	Exon Cassette	4.08	4.92E-07	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
DADCA	Exon Cassette	1.86	2.23E-05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1,
RADOA	Mutualy Exclusive Exons	2.14	1.70E-03	HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
XRRA1	Exon Cassette	1.93	3.66E-05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
CODCOOR	Complex	2.41	2.36E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB,
CCDC30B	Exon Cassette	1.79	5.97E-04	HuD, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
PICAL M	Evon Cassette	1 59	2 30E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD,
	Exert eduberte	1.05	2.002.00	KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
EXPH5	Exon Cassette	1.52	4.00E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
	Alter. First Exon (e1-2)	2.03	1.02E-03	
SLC37A4	Complex	1.73	1.96E-03	ETR-3, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), KSRP, MBNL1, Nova-1, Sam68, SC35, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
	Exon Cassette	1.71	2.40E-03	
MSANTD2	Exon Cassette	1.72	7.63E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
PUS3	Exon Cassette	1.78	5.22E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP P (TLS), HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
WNK1	Exon Cassette	2.10	3.95E-05	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, Nova-1, Nova-2, Sam68, SC35, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
ERC1	Exon Cassette	4.10	6.08E-05	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
MGST1	Alter. First Exon (e2)	3.66	1.10E-03	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SRb30c, TIA-1, TIAL1, YB-1, ZRANB2
ARNTL2	Alter. Donor Site	1.85	5.54E-03	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP H, hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1 HuB HuD KSRP MRNL1 Nova-1 Nova-2 PSE Sam68 SC35 SE1 SE2/ASE SRo20, SRo30, TIA-1 TIA11 VR-1 ZPANR2
FGD4	Alter. First Exon (e2)	2.63	5.89E-05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP F1, hnRNP E2/161, hnRNP D1, hnRNP D1, hnRNP D2, hnRNP E3, hnRNP F1, hRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP F, hnRNP P (TLS).

	Alter. Terminal Exon (e21)	2.28	1.92E-03	HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
CACNB3	Exon Cassette	2.41	4.95E-04	ETR-3, hnRNP I (PTB), hnRNP P (TLS), HuB, KSRP, Nova-1, SC35, SF2/ASF, SRp30c, TIA-1, TIAL1, YB-1
SLC4A8	Alter. Terminal Exon (e10-23,e25-30)	1.58	1.40E-03	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2aloha, HTra2aloha, HTra2beta1, HuB, HuD, KSRP, MBNI 1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAI 1, YB-1, ZRANB2
	Alter First Evon (e2-3)	3.62	6 60E-07	
MDM2	Complex	1.61	1 16E-02	Erres, twel, twee, mixed A2, mixed A2, mixed B3, mixed B4, mixed B
BTBD11	Alter. First Exon (e1-3)	2.58	2.40E-05	CUG-BP1, ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP A2, B1, hnRNP G1, hnRNP G1, hnRNP G1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP H3, hnRNP K, hnRNP K, hnRNP LL, hnRNP P (US) HTT-3/Johas HTT-3/Johas HTT-3/Johas HTT-3/Johas A2, PSE RPMS Same SC38, SS1 SS1 SS2/Johas HTT-3/JOHAT H11, VB1, 720/NP2
RPH3A	Alter. First Exon (e2-19)	2.03	3.73E-05	9G8, CUG-BPI, ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H2, hnR
DODY7	Exon Cassette	2.23	4.28E-05	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP F, (PTLS), HTRa2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, RBM5,
P2RX7	Mutualy Exclusive Exons (e5)	1 74	4 07F-05	Sam68, SC35, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
RAD52	Alter. Terminal Exon (e2)	2.08	1.85E-05	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2, B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alnba HT
SLC2A14	Alter. First Exon (e3,e8-14)	3.18	1.96E-03	CUGBP1, ETR-3, Fox-1, Fox-2, fnRNP A1, horn PA2/B1, hnRNP D, hnRNP D, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F1, hnRNP H2, hnRNP H2, hnRNP H3, hnRNP H2, hnRNP K, hnRNP F1, hnRNP F1, hnRNP F2, hnRNP H2, hnRNP H2
ITPR2	Alter. Terminal Exon (e27-43,e45-61)	1.80	2.84E-04	CUG-BP1, ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP A2, hord, sail of social starting startin
CPNE8	Alter. First Exon (e2)	1.62	1.19E-02	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP P4, hnRNP P2/B1, hnRNP C1, hnRNP C1, hnRNP C2, hnRNP F, hnRNP H2, hnRNP H2, hnRNP H2, hnRNP F (TLS), HTra2alpha, H
SLC38A1	Alter. First Exon (e1)	1.68	3.18E-03	CUG-BP1, ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRc20, SRc30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
STAT2	Complex	1.75	1.52E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SRn20, SRn30, TIA-1, TIA-1, TIA-1, TRANB2
R3HDM2 // STAC3	Exon Cassette	1.69	1.00E-03	ETR-3, Fox-1, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, PSF, Sam68, SC35, SRb30c, YB-1, ZRANR2
GNS	Exon Cassette	1.75	3.77E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SF2/ASF, SRp200, STp30c, TIA-1, TIAL1, YB-1, ZRANB2
	Alter, First Exon (e1-8)	2.14	4.71E-06	
OSBPI 8	Complex	2.55	1.61F-05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F1, hnRNP H2, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP K, hnRNP P (TLS), HTra2alpha,
	Exon Cassette	2.54	1.61F-05	HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
SLC6A15	Alter. Terminal Exon (e5)	1.70	3.44E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNI 1, Nova-1, Nova-2, PSE, Sam68, SC35, SE1, SRo20, SRo30c, TDP43, TIA-1, TIA-1, YR-1, ZRANB2
LTA4H	Complex	3.21	2.01E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
CDK17	Intron Retention	1.61	4.17E-04	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F, hnRNP HJ, hnRNP H2, hnRNP (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Sam68, SF1, SRb20, SRb30c, TIA-1, TIAL1, YB-1
ALDH112	Alter, Acceptor Site	2.88	7.22F-07	FTR-3, hnRNP A1, hnRNP C1, hnRNP F1, hnRNP F2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TI S), HTra2beta1, HuB, KSRP, MBNI 1, Nova-1, Sam68, SC35, SRn20, SRn30c, TIA-1, TIAI 1, YR-1
TAOK3	Alter. First Exon (e1-8,e10-15)	2.04	1.55E-02	CUG-BP1, ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP H4, hnRNP H4, hnRNP H4, hnRNP H4, hnRNP K, hnRNP LL, hnRNP P (TLS) HTra2alpha HTra2beta1 HuB HuD HuR KSRP MRNL1 Nova-2 PSE RBM5 Sam68 SC35 SE1 SE2/ASE SRo20 SRo30 CTDP43 TIA-1 TIA-1 YB-1 ZRANR2
CAMKK2	Exon Cassette	1.61	1.32E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIA-1, YB-1, ZRANB2
WASF3	Mutualy Exclusive Exons (e7)	1.64	8.22E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, PSE, RBM5, Sam68, SC35, SF1, SRo20, SRo30, TI4-1, TIA1, YR-1, ZRANB2
	Alter, Acceptor Site	1.94	3.69E-05	
EXOSC8	Intron Retention	1.75	6.38F-03	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HuB, HuD, KSRP, MBNL1, Nova-1, Sam68, SC35, SRp20, TIA-1, TIAL1, YB-1, ZRANB2
COG3	Alter. Terminal Exon (e13-23)	1.58	9.40E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
SETDB2	Exon Cassette	1.54	1.60E-02	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP F (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
DIFUI	Complex	2.26	9.74E-03	9G8, CUG-BP1, ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP DL, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP H2, hnRNP K, hnRNP LL,
DLEUI	Exon Cassette	2.04	7.39E-04	hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
CLAIN1	Alter. First Exon (e2-3)	2.67	1.76E-05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP F, thRNP F (TLS), HTra2alpha, HTra2abeta1.
SLAIN1	Exon Cassette	3.76	1.62E-06	HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
ZIC2	Complex	4.68	3.08E-07	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRo20, SRo30c, TIA-1, TIAL1, YB-1, ZRANB2
MCF2L	Complex	2.14	4.60E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2

Appendices

Hat Addres for Sol 111111315 2:36 9:4846 Opport 1118, bits / 1118, bit	MTIF3	Alter. First Exon (e1-3)	1.83	8.04E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
Image: International Link Link (mit provided and provided an	FI T1	Alter. First Exon (e1-11,e13,e15- 16,e18,e21-27,e29-35)	2.16	9.94E-05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS),
SIPPLH Find Guarda 1/3 6.426-0. Find Lamber 2/J. Baller 2/L. Baller 2/L	1211	Alter. Terminal Exon (e4-11,e13,e15- 16,e18,e21-24,e26-27,e29-35,e37-38)	3.08	2.44E-04	HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
ID002// UR00098 Mex. Perc Exer (eq) 2.13 L00044 Construct F, Veritor L, Ve	SUPT20H	Exon Cassette	1.78	6.75E-04	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP I (PTB), hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, Sam68, SC35, SRp20, TIA-1, TIAL1, YB-1
Decoupy Internet ban (n1) 1.6 1.0024 (mail of a 1, and 2 an	F0X01 //	Alter. First Exon (e2)	2.73	1.60E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F1, hnRNP H1, hnRNP H3, hnRNP H3, hnRNP H3, hnRNP K, hnRNP LL, hnRNP P (TLS),
COMUDE Even Causeds 1.62 COURDPLIC TALL TALL TALE 2, LINER 24, LINER 247, LINER 27, LINER 21, TRADE 1000 (LINER 21, LINER 2, LINER 21, LINER 2	TSC22D1	Alter. First Exon (e1)	1.56	1.09E-02	CUG-BP1, ETR-3, Fox-1, Fox-2, hRNP A1, hRNP A2/B1, hnRNP C1, hnRNP D, hnRNP D, hnRNP F2, hnRNP F2, hnRNP F2, hnRNP F1, hnRNP F1, hnRNP F1, hnRNP F2, hnRNP F2, hnRNP F2, hnRNP F1, hnRNP F
Col. 411 Comptain L 66 2004 31 ETR3, RepR, Feo J, Fool 2, And PE A, Linder Z, Citt, Meder LL, Inder D, Linder D, Li	COMMD6	Exon Cassette	1.62	1.82E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, RBM5. Sam68, SC35, SF1, SRo20, SRo30c, TIA-1, TIAL1, YB-1
MR010 Alter Fer Ender (k.1.3) 2.007 Z. BEGG COULD PT: TR3, Ford, Ferder AL, Ferder (MRN LA, No.1, Kerder (K. MARRY F, MRN LA, MARRY F, MRN LA, No.1, Kerder (K. MARRY F, MRN LA, MARRY F, M	COL4A1	Complex	1.66	2.20E-03	ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
Instruction Dex Causelle 1.73 1.37 LOG MRR/L (hoo), Hoo2, LPS RMS, Sandé, SCIS, ST, JAG, SRUD, TORA, TUAL, YAL, ZMARZ SYD1 Exon Causelle 1.66 1.76 Corp. 1.77 Log		Alter. First Exon (e1-3)	2.07	7.18E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP H, hnRNP F, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP,
SST01 End 1762 (2) FTR8.7 fool, <i>Toole</i> , <i>Inited</i> P 2, <i>IniteD</i> P 2, <i>IniteD</i> 2, <i>IniteD</i> 2, <i>IniteD</i> 4, <i>InitD</i> 4, <i>InitD</i> 4, <i>IniteD</i> 4, <i>InitD</i> 4, <i>IniteD</i> 4, <i>InitD</i> 4, <i></i>	ANIMEDIO	Exon Cassette	1.73	1.37E-04	MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
DAMI Den Cassette 1.84 5.84-C3 Tins, Fai, Fai, Fai, Fai, Fai, Fai, Fai, Fai	SCFD1	Exon Cassette	1.56	1.76E-02	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP F, tra2alpha, HTra2alpha, HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
JKMP Complex (b1-2) 1.54 1.73.00 FTR3, hmRP C1, hmRP F1, hmRP H1, hmRP L2, hmRP P1 (D3, Hm2zball, Hab, KSP, MBNL, Ikoa-J, Sanda, SC35, S27,457, Sb200, Sb200, Th4, TM41, YB-1, ZMMB2 SW12 Kanc Assatte 2.15 8.72.04 FTR3, Tea, Ta, TabP L1, ImRP C1, hmRP C1, ImRP	DAAM1	Exon Cassette	1.84	5.84E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
JANNE Long Cossette 1.13 1.4002 International manual manua	IKAMD	Complex (e1-2)	1.54	1.73E-02	
SYR2 Exon Casada 21.15 87.926.4 ETR3, Fou L Fou 2, IndRP AL IndRP C, IndRP F, IndRP H, IndRP C, IndRP P, IndRP K, IndRP P, IndRP A, IndRP	JKAWP	Exon Cassette	1.83	1.40E-02	
PPP285C Mutualy Exclusive Exons (s3) 1.96 L08.602 905, CUG 4P1, LTRA3, FooL, FooZ, JmRPA AJ, LINN RV Z, JML, Neu JL, Neu JL, Zug JML, TML VEL J, JMRVP L, JMRVP P, TS, JMRV AJ, MRVP L, JMRVP L, JMRVP D, LMRVP L, JMRVP L	SYNE2	Exon Cassette	2.15	8.79E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
MTA1 Euro Cassette 160 9.16E4 CTR3, Foul, Frozz, ImNRP AL, IntRIP P. QL, ImNRP D., ImRNP EL, ImRNP EL, ImRNP FL, ImRNP HL, ImRNP P. (TS), KSPP, MBILL, Nova, I, Rosz, P. (RBMS, SS), SSP0, 269, 200, TLA, TLAL, TY, JZ, ZMAR2 CRIP2 Euro Cassette 2.10 1.886.6 SSp0, 269, 200, TLA, TLAL, TY, JZ, ZMAR2 HECTD1 Alter, First Euro (e13, a6620, a22-20) 1.60 1.446.20 TCR3, Foul, Frozz, ImRNP AL, ImRNP P. Z, ImRNP CJ, ImRNP LJ, ImRNP LJ, ImALLY LJ, ZJAAR2 IND2 Euro Cassette 3.84 2.0366 CUG BPJ, CTR3, Fou J, Foo2, ImNNP AL, ImRNP AZ, BJ, ImANP CJ, ImRNP	PPP2R5C	Mutualy Exclusive Exons (e3)	1.96	1.08E-02	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
CRIP2 Exon Cassette 2.10 1.856-05 CUGGPU_TR3, Food_Food_Number 2, IndRNP E1, IndRNP E1, IndRNP E1, IndRNP E1, IndRNP P1(IS), Hulk, KSRP, MBNL1, Non-1, PSF, RBM5, SC35, ST2/ASF, HECTD1 Alter. First Exon (a1-3,66-20,e22-29) 160 1.44-60 9936, CUG P1, TT3, Food_Food_Number 2A, IndRNP A1, IndRNP A2, IndRNP E1, IndR	MTA1	Exon Cassette	1.60	9.15E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
HECTD1 Alter. First Exon (e1-3, 6-20, 22229) 1.60 1.44E02 903, CUCPUP, ETR3, Fao, 1, Fao, 2, InRNP A2, InI, INRNP A2/B1, InRNP A1, INRNP A2, ISS, SB30, CTP34, TAI, TAI, TAI, TAI, TAI, TAI, TAI, TAI	CRIP2	Exon Cassette	2.10	1.85E-05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, PSF, RBM5, SC35, SF2/ASF, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
PRILCHAPAI // BALGAPAI // BALGAPAI // BALGAPAI P Alter. Tarminal Exon (e6.0) 2.22 1.7E.6.3 ETR3, Faol., FaoJ., FaoJ., FaoJ., HanNP AZ/El, JunNPP CJ, JunNPP CJ, LunNPP E, JunNPP E, JunNP E,	HECTD1	Alter. First Exon (e1-3,e6-20,e22-29)	1.60	1.44E-02	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
PALGAPALP Complex (e20) 2.56 8.83E-04 Howa2, PSF, RBMS, Samska, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TVA1, TY8-1, ZRANB2 NID2 Exon Cassette 3.84 2.03E-06 CUGGP1; ETR3, Fox1, Fox2, InSPP, AL, INSPP, Z(B, LINRPR Z), LINRPR Z), InSPP Z, INS	RALGAPA1 //	Alter. Terminal Exon (e46)	2.22	1.76E-03	ETR-3. Fox-1. Fox-2. hnRNP A1. hnRNP A2/B1. hnRNP C1. hnRNP D. hnRNP E1. hnRNP E2. hnRNP F. hnRNP H1. hnRNP H2. hnRNP H2. hnRNP H2. hnRNP K. hnRNP P. (TLS). HTra2beta1. HuB. KSRP. MBNL1. Nova-1.
NID2 Exon Cassette 3.84 2.016-0F CUCGBP1. ETR3, Fox.1, Fox2, InRNP A1, InRNP C1, InRNP C1, InRNP C1, InRNP E2, InRNP F1, InRNP F2, InRNP F1, INRNP F1, INRNP F1, INRNP F2, INRNP F1, INRNP F1, INRNP F2, INRNP F1, INRNP F1, INRNP F2, INRN	RALGAPA1P	Complex (e20)	2.56	8.83E-04	Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
TIMM9 Exon Cassette 2.68 1.10E-03 CUG-GP1_ETR3_Froat_Foc2_hnRNP A1, hnRNP A2[bit hnRNP C1, hnRNP C1, hnRNP E2, hnRNP F1, hnRNP F2, hnRNP F, hnRNP F1, hnRNP F4, hnRNP P (TLS), HTra2beta1, Hug, HuD, Hug, KSRP, MBNL1, Nova-1, Nova-2, Nova-2, PSF, RBM5, Sam68, SC35, SF1_SF2/ASF, SRp20, SRp30c, TD43, TLA1, TLA1, YB1, ZRANB2 ACTN1 Alter. First Exon (e1-13) 1.69 1.95Ec0 96.0 (CuG-P1_ETR3, Froat_Foc2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, InRNP D, InRNP E2, hnRNP F, InRNP H1, hnRNP H2, hnRNP F4, InRNP F4, INRN	NID2	Exon Cassette	3.84	2.03E-06	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
ACTN1 Alter. First Exon (e1-13) 1.69 1.95E02 9G8, CUGBP1, ETR3, FMRP, Fox 1, Fox 2, hnRNP A1, hnRNP 2/B1, hnRNP D, hnRNP D, hnRNP D, hnRNP D, hnRNP D, hnRNP L, hnRNP A3, TAJ, TAL, TAL, TB-1, ZRANB2 ATXN3 Complex (e2.3,e5.6,e8-11) 1.81 4.14E02 CUGBP1, ETR3, Fox 1, Fox 2, hnRNP A1, hnRNP 2/B1, hnRNP D, h	TIMM9	Exon Cassette	2.68	1.10E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRo20, SRo30c, TIA-1, TIAL1, YB-1, ZRANB2
ATXN3 Complex (e23,e56,e8-11) 1.81 4.14E02 CUG BP1, ETR3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E1, hnRNP P1, hnRNP P2, hnRNP P1, hnRNP P1, hnRNP P2, hnRNP P1, hnRNP P1, h	ACTN1	Alter. First Exon (e1-13)	1.69	1.95E-02	9G8, CUG-BP1, ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2aloha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRo20, SRo30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
AIXN3 Exon Cassette 2.17 7.24E.03 HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 WARS Alter. First Exon (e1) 1.50 1.20E.03 968, CUGBP1, ETR-3, nnRNP A1, nnRNP A2/B1, nnRNP D, nnRNP D, nnRNP E1, nnRNP H1, nnRNP H2, nnRNP H1, nnRNP H2, nnRNP H1, nnRNP H2, nnRNP H2, nnRNP H2, nnRNP F, nnRNP H2, nnRNP F, nnRNP H2, nnRNP H3, nnRNP I, (PTB), nnRNP K, nnRNP P (TLS), HTra2beta1, HuB, KDSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, Shp20, Shp30c, TD43, TIA-1, TIAL1, YB-1, ZRANB2 BRF1 Complex 1.64 1.62E-02 CUGBP1, ETR-3, Fox-1, Fox-2, nnRNP A1, nnRNP A2/B1, nnRNP C1, nnRNP D, nnRNP E1, nnRNP F, nnRNP H3, nnRNP H2, nnRNP H3, nnRNP I (PTB), nnRNP K, nnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, Shp20, Shp30c, TD43, TIA-1, TIAL1, YB-1, ZRANB2 ELK2AP // IGHD Alter. First Exon (e15-16,e101) 2.78 4.07E-05 968, CUGBP1, ETR-3, Fox-1, Fox-2, nnRNP A1, nnRNP A2/B1, nnRNP C1, nnRNP C1	17010	Complex (e2-3,e5-6,e8-11)	1.81	4.14E-02	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP F, hnRNP F, hnRNP H2, hnRNP H2, hnRNP F, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E2, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP F, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP F, hnRNP A2/B1, hnRNP A2/B1, hnRNP D, hnRNP D, hnRNP D, hnRNP E2, hnRNP E2, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP F, hnRNP F, hnRNP H2, hnRNP H2, hnRNP F, hnRNP H2, hnRNP F, hnRNP H2, hnRNP A2/B1, hnRNP A2/B1, hnRNP D, hnRNP D, hnRNP D, hnRNP E2, hnRNP E2, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP F, hnRNP F, hnRNP H2, hnRNP H2, hnRNP F, hnRNP H2, hnRNP H2, hnRNP F, hnRNP H2,
WARS Alter. First Exon (e1) 1.50 1.20E-03 9G8, CUG-BP1, ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HSP90A11 HSP90A11 Alter. First Exon (e1-2) 2.95 2.99E-04 CUG-BP1, ETR-3, fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP D, hnRNP E1, hnRNP F, hnRNP F, hnRNP H1, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 ELK2AP // IGHD // IGHG1 Alter. First Exon (e15-16,e101) 2.78 4.07E-05 968, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F1, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2abeta1, HuB, HUD, HKK, SRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TD43, TIA-1, TIAL1, YB-1, ZRANB2 ELK2AP // IGHD Alter. First Exon (e15-16,e101) 2.78 4.07E-05 968, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNPA A2/B1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP F1, hnRNP F2, hnRNP F1, hnRNP F1, hnRNP F1, hnRNP F1, hnRNP F1, hnRNP F1, hn	ATXN3	Exon Cassette	2.17	7.24E-03	HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
WARS Exon Cassette 2.53 1.21E-04 HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 HSP90AA1 Alter. First Exon (e1-2) 2.95 2.99E-04 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP L, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 ELK2AP // IGH0 Alter. First Exon (e15-16,e101) 2.78 4.07E-05 9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP D, I, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P // IGH0 Alter. First Exon (e15-16,e101) 2.78 4.07E-05 9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP D, I, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HDD, Hut, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SR20, SR30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 C15orf41 Intron Retention 1.61 1.70E-03 ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP A2/B1, hnRNP P (TLS), HBM, MBNL1, Nova-1, Nova-2, Sam68, SC35, SF1, SR20, SR30c, TIA-1, TIAL1, YB-1	WARA	Alter. First Exon (e1)	1.50	1.20E-03	9G8, CUG-BP1, ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB,
HSP90Al1 Alter. First Exon (e1-2) 2.95 2.99E04 CUG-BP1, ETR-3, Fox-1, Fox-2, InRNP A1, InRNP A2/B1, InRNP C1, InRNP D, InRNP E1, InRNP E2, InRNP F1, InRNP F1, INRNP H1, InRNP H2, InRNP F1, INRNP H2, INRNP F1, INRNP	WARS	Exon Cassette	2.53	1.21E-04	HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
BRF1 Complex 1.64 1.62E-02 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, PSF, RBM5, Sam66, SC35, SF2/ASF, SR20, SR30c, TLA-1, TLAL1, YB-1, ZRANB2 ELK2AP // IGHD // IGHG1 Alter. First Exon (e15-16,e101) 2.78 4.07E-05 9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP D, hnRNP D, hnRNP D, inNRNP E1, inRNP E1, inRNP E1, inRNP E1, inRNP F1, inRNP F1, inRNP F1, inRNP F2, inRNP F1, inRNP F2, inRNP F1, inRNP F	HSP90AA1	Alter. First Exon (e1-2)	2.95	2.99E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
ELK2AP // IGHD // IGHG1 Alter. First Exon (e15-16,e101) 2.78 4.07E-05 9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H1, hnRNP A2/B1, hnRNP A2/B1, hnRNP A2/B1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H1, THAL1, YB-1, ZRANB2 APBA2 Exon Cassette 2.36 6.84E-04 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E1, hnRNP H1, hnRNP H2, hnRNP F, hnRNP H1, hnRNP K, hnRNP P (TLS), HUB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SR20, SRp30c, TIA-1, TIAL1, YB-1 C15orf41 Intron Retention 1.61 1.70E-03 ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP P (TLS), HUB, MBNL1, Nova-1, Nova-2, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1 MAPKBP1 Complex (e29-30) 1.75 1.04E-03 ETR-3, hnRNP F, hnRNP H1, hnRNP A2/B1, hnRNP C1, hnRNP P (TLS), HNRNP C1, hnRNP E1, hnRN	BRF1	Complex	1.64	1.62E-02	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2, B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
APBA2 Exon Cassette 2.36 6.84E-04 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP P (TLS), hnR	ELK2AP // IGHD // IGHG1	Alter. First Exon (e15-16,e101)	2.78	4.07E-05	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I, hnRNP I, hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
C15orf41 Intron Retention 1.61 1.70E-03 ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP A2/B1, hnRNP F (TEB), hnRNP P (TLS), HuB, MBNL1, Nova-1, Nova-2, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1 MAPKBP1 Complex (e29-30) 1.75 1.04E-03 ETR-3, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP F1, hnRNP P (TLS), KSRP, Nova-1, RBM5, SC35, SRp30c, TIA-1, TIAL1, YB-1 CAPN3 // GANC Alter. First Exon (e30-31,e33-35,e37- 42) 1.82 8.81E-04 CUG-BP1, ETR-3, fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E1, hnRNP F4, hnRNP H2, hnRNP H2, hnRNP F, hnRNP P (TLS), HTra2alpha, HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 NEO1 Alter. Acceptor Site 7.98 1.78E-06 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP F (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TD43, TIA-1, TIAL1, YB-1, ZRANB2 NEO1 Exon Cassette 3.31 1.72E-05 Nova-2, Sam68, SC35, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2	APBA2	Exon Cassette	2.36	6.84E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
MAPKBP1 Complex (e29-30) 1.75 1.04E-03 ETR-3, hnRNP F, hnRNP H1, hnRNP H2, hnRNP F (JTR), hnRNP P (TLS), KSRP, Nova-1, RBM5, SC35, SRp30c, TIA-1, TIAL1, YB-1 CAPN3 // GANC Alter. First Exon (e30-31,e33-35,e37- 42) 1.82 8.81E-04 CUG-BP1, ETR-3, fox-1, fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E1, hnRNP E1, hnRNP F4, hnRNP H2, hnRNP H3, hnRNP F (TLS), KSRP, Nova-1, RBM5, SC35, SRp30c, TIA-1, TIAL1, YB-1 NEO1 Alter. Acceptor Site 7.98 1.78E-06 ETR-3, fox-1, fox-2, hnRNP A1, hnRNP C1, hnRNP C1, hnRNP C1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP F (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, NSRP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP C1, hnRNP C1, hnRNP D4, hnRNP F, hnRNP H1, hnRNP H2, hnRNP F, H1, H2, H2, H2, H2, H2, H2, H2, H2, H2, H2	C15orf41	Intron Retention	1.61	1.70E-03	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HuB, MBNL1, Nova-1, Nova-2, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1
CAPN3 // GANC Alter. First Exon (e30-31,e33-35,e37- 42) 1.82 8.81E-04 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP DL, hnRNP E2, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuC, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 NEO1 Alter. Acceptor Site 7.98 1.78E-06 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP DL, hnRNP E1, hnRNP F4, hnRNP H2, hnRNP H2, hnRNP F (TLS), HTra2beta1, HuB, KSRP, MBNL1, Neve-1, Nova-2, sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2	MAPKBP1	Complex (e29-30)	1.75	1.04E-03	ETR-3, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP P (TLS), KSRP, Nova-1, RBM5, SC35, SRp30c, TIA-1, TIAL1, YB-1
Alter. Acceptor Site 7.98 1.78E-06 ETR-3, Fox-1, Fox-2, hnRNP A2/B1, hnRNP A2/B1, hnRNP DL, hnRNP DL, hnRNP DL, hnRNP E1, hnRNP E1, hnRNP H2, hnRNP H1, hnRNP H2, hnRNP H, hnRNP H2, hnRNP H2, hnRNP H, hnRNP H2, hnRNP H, hnRNP H2, hnRNP H, hnRNP H2, hnRNP H	CAPN3 // GANC	Alter. First Exon (e30-31,e33-35,e37- 42)	1.82	8.81E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2, B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuC, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
NEU1 Exon Cassette 3.31 1.72E-05 Nova-1, Nova-2, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2	NEO1	Alter. Acceptor Site	7.98	1.78E-06	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP H, hnRNP F (TLS), HTra2beta1, HuB, KSRP, MBNL1,
	NEU1	Exon Cassette	3.31	1.72E-05	Nova-1, Nova-2, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2

.

PPCDC	Alter. First Exon (e1-2)	1.76	4.50E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
NGRN // TTLL13	Complex	1.77	1.39E-04	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
WHAMMP3	Exon Cassette	1.51	5.15E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1
OCA2	Exon Cassette	1.50	2.62E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
HERC2	Alter. First Exon (e1-2,e4,e6-49)	1.72	7.54E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP I, hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
SLC12A6	Alter. First Exon (e1-3)	3.45	2.19E-05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS),
GEGIZNO	Exon Cassette	2.07	8.45E-05	HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
ZSCAN29	Alter. First Exon (e1)	2.16	1.58E-04	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, PSF, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1
MY05C	Exon Cassette	2.04	7.58E-03	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
NEDD4	Exon Cassette	1.82	6.34E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP K, hnRNP P (TLS), HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
ΔΝΧΔ2	Alter. First Exon (e1-2)	3.44	1.63E-04	CUG-BP1, ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP I (PTB), hnRNP P (TLS), HTra2alpha, HTra2beta1,
7117012	Exon Cassette	2.93	1.63E-04	HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
RORA	Complex (e2)	1.99	1.24E-03	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
VP\$120	Alter. Terminal Exon (e83)	2.31	2.44E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP,
VF3130	Exon Cassette	12.31	2.84E-06	MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
CELF6 // HEXA	Exon Cassette	13.77	5.68E-07	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP I (PTB), hnRNP F (TLS), HTra2beta1, HuB,
// PARP6	Intron Retention	3.17	6.36E-04	HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
CTSH	Exon Cassette	2.42	8.56E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, Nova-1, Sam68, SC35, SF2/ASF, TIA-1, TIAL1, YB-1
SEC11A	Exon Cassette	2.51	1.58E-05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
CIB1	Complex	1.58	2.54E-03	ETR-3, hnRNP I (PTB), hnRNP P (TLS), RBM5, SC35, SRp30c, ZRANB2
RGMA	Alter. First Exon	3.35	5.04E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SE2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
TTCOO	Exon Cassette	1.63	3.94E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP,
11625	Alter. Terminal Exon (e4)	1.52	4.05E-05	MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
	Alter. First Exon (e1)	3.37	2.18E-04	
ABAT	Alter. Terminal Exon (e5-18)	2.62	3.90E-05	
	Exon Cassette	3.52	3.61E-05	
C16orf45	Complex	2.23	1.37E-04	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
ZNF720	Complex	1.81	1.54E-02	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
PLA2G15	Alter. First Exon (e1)	1.88	5.96E-05	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
ZFP90	Alter. First Exon (e3-6)	1.90	5.78E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F1, hnRNP H2, hnRNP H2, hnRNP H3, hnRNP H (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2aloha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
CDH1	Alter. First Exon (e1-2)	5.20	1.40E-06	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuB, KSRP, MBN 1, Nova-1, Nova-2, PSE, RBM5, Sam68, SC35, SF1, SF2/ASE, SRo20, SRo30c, TDP43, TIA-1, TIA1, 1, YB-1, ZRANB2
HAGH	Exon Cassette	1.65	4.95E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, PSF, Sam68, SC35, SF2/ASE, SRo20, SRo30, TDP43, TIA-1, TIA-1, TRA-1, ZRANR2
ZSCAN32	Exon Cassette	1.70	1.34E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30, CTDP43, TIA-1, TIA11, YB-1, ZRAMB2
RPS15A	Complex	2.06	3.19E-04	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Sam68, SC35, SF2/ASF, TIA-1, TIAL1, YB-1, ZRANB2
DCUN1D3 // ERI2	Alter. Acceptor Site	1.52	2.82E-03	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, HTra2alpha, HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
DNAH3	Alter. Terminal Exon (e46-66)	1.70	2.80E-02	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
SULT1A1	Alter. First Exon (e1-4)	2.39	1.99E-04	CUG-BP1, ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2

			1	
DOK4	Exon Cassette	1.52	1.72E-03	ETR-3, Fox-1, Fox-2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), KSRP, Nova-1, PSF, RBM5, SC35, TIA-1, TIAL1, YB-1, ZRANB2
PDXDC2P	Exon Cassette	1.71	2.46E-03	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
VAC14	Alter. Terminal Exon (e11-15,e17-21)	1.52	1.47E-02	9G8, CUG-BP1, ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
СҮВА	Complex (e1)	1.72	1.97E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
PIEZ01	Complex	3.53	2.57E-06	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
ANKRD11	Exon Cassette	1.60	7.96E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SRo20, SRo30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
40451/	Alter. Terminal Exon (e12-22)	3.26	1.06E-03	ETR-3, hnRNP A1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, RBM5, Sam68, SC35, SF2/ASF, SRp20,
ACADVL	Intron Retention	2.37	1.82E-05	SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
CHRNB1	Intron Retention	1.79	4.58E-04	CUG-BP1, ETR-3, hnRNP C1, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP P (TLS), HTra2beta1, MBNL1, Nova-1, RBM5, SC35,YB1
	Exon Cassette	2.73	5.72E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD,
ARHGAP44	Exon Cassette	1.74	5.72E-03	KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
TBC1D26 // ZNF286A	Alter. First Exon (e1-6)	1.99	8.24E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
	Alter. First Exon (e2-8)	3.50	4.96E-04	
SI C 47A1	Complex	3.31	2.18E-05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP,
3LC4/A1	Exon Cassette	3.06	2.41E-05	MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
	Intron Retention	2.12	3.17E-04	
DHRS7B	Alter. Terminal Exon (e3)	1.82	7.16E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
11/001	Alter. First Exon (e1-5)	1.69	2.08E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP K, hnRNP K, hnRNP P (TLS), HTra2alpha,
WSB1	Complex	1.74	2.00E-04	HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
ANKRD13B	Complex	2.16	1.56E-04	ETR-3, hnRNP A1, hnRNP F1, hnRNP H2, hnRNP H2, hnRNP P (TLS), KSRP, MBNL1, Nova-1, PSF, SC35, SRp30c, YB-1, ZRANB2
LRRC37B	Alter. Terminal Exon (e13,e15-18)	1.90	1.06E-02	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
50000	Alter. First Exon (e1-8)	1.92	4.12E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2alpha, HTra2beta1, HuB, HuD,
EKBBZ	Alter. Terminal Exon	1.88	8.16E-04	KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
NDD2	Alter. Terminal Exon (e7)	2.26	3.44E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HuB, HuD, HuR, KSRP, MBNL1,
NDRZ	Exon Cassette	1.78	4.24E-03	Nova-1, Nova-2, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
CDKEDADO				FTR-3 Fox-1 Fox-2 bnRNP A1 bnRNP A2 /R1 bnRNP C1 bnRNP C1 bnRNP F1 bnRNP F2 bnRNP F4 bnRNP H1 bnRNP H2 bnRNP H2 bnRNP H2 bnRNP P (TI S) HTra2beta1 HuR KSRP MRNI 1 Nov-2 RRM5
CDKSRAFS	Alter. First Exon (e2-6)	1.66	3.64E-03	Encor, 64,1642, minute A2, minute A2, minute A3, minute A3, minute A4, minute
ATP5G1	Alter. First Exon (e2-6) Alter. First Exon (e1)	1.66 2.53	3.64E-03 5.60E-05	ETR-3, hRNP A1, hRNP C1, hRNP F, hRNP H1, hRNP H2, hRNP I (PTB), hRNP P (TLS), KSRP, Nova-1, SC35, SF2/ASF, SRp30c, TIA-1, TIAL1 ETR-3, hRNP A1, hRNP C1, hRNP F, hRNP H1, hRNP H2, hRNP I (PTB), hRNP P (TLS), KSRP, Nova-1, SC35, SF2/ASF, SRp30c, TIA-1, TIAL1
ATP5G1 ACSF2	Alter. First Exon (e2-6) Alter. First Exon (e1) Alter. First Exon (e1-11)	1.66 2.53 1.74	3.64E-03 5.60E-05 4.20E-04	Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, hnRNP A1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), KSRP, Nova-1, SC35, SF2/ASF, SRp30c, TIA-1, TIAL1 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
ATP5G1 ACSF2 NME1 // NME2	Alter. First Exon (e2-6) Alter. First Exon (e1) Alter. First Exon (e1-11) Complex	1.66 2.53 1.74 13.82	3.64E-03 5.60E-05 4.20E-04 3.09E-06	ETR-3, hnRNP A1, hnRNP A1, hnRNP A1, hnRNP A2, BIAS A 25, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, hnRNP A1, hnRNP C1, hnRNP C1, hnRNP A2, hnRNP A2, hnRNP D1 (PTB), hnRNP P (TLS), KSRP, Nova-1, SC35, SF2/ASF, SRp30c, TIA-1, TIAL1 CUG-BP1, ETR-3, Fox-1, Fox-2, Fox-2, hnRNP A1, hnRNP A2, B1, hnRNP D1, hnRNP D1, hnRNP C1, hnRNP E2, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, hnRNP F1, hnRNP H2, hnRNP H2, hnRNP P (TLS), Nova-1, SC35, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
ATP5G1 ACSF2 NME1 // NME2 AKAP1	Alter. First Exon (e2-6) Alter. First Exon (e1) Alter. First Exon (e1-11) Complex Alter. First Exon (e2)	1.66 2.53 1.74 13.82 1.76	3.64E-03 5.60E-05 4.20E-04 3.09E-06 5.84E-04	ETR-3, hnRVP A1, hnRVP C1, hnRVP A2, hnRVP A2, BNRVP A1, hnRVP P (TLS), hnRVP P (TLS), KSRP, Nova-1, SC35, SF2/ASF, SRp30c, TIA-1, TIAL1 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRVP A1, hnRVP A2, B1, hnRVP P (TLS), hnRVP P (TLS), KSRP, Nova-1, SC35, SF2/ASF, SRp30c, TIA-1, TIAL1 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRVP A1, hnRVP A2/B1, hnRVP C1, hnRVP D, hnRVP DL, hnRVP E1, hnRVP E2, hnRVP F, hnRVP H1, hnRVP H2, hnRVP H3, hnRVP I (PTB), hnRVP P (TLS), HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, hnRVP F, hnRVP H1, hnRVP H2, hnRVP I (PTB), hnRVP P (TLS), Nova-1, SC35, SRp30c, YDP43, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, hnRVP F, hnRVP H1, hnRVP H2, hnRVP P (TLS), Nova-1, SC35, SRp30c, YB-1, ZRANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRVP A1, hnRVP A2/B1, hnRVP D, hnRVP D, hnRVP P, hnRVP F, hnRVP H1, hnRVP H2, hnRVP F (TLS), HTra2beta1, HuB, HuD, HuR, KSRP, MBVL1, Nova-1, Nova-2, SRp30c, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, SRP5, SRb5, SRp30c, SRp30c, TIA-1, ZRANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, SRp50, SRp30c, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, Fox-2, SRp50, SRp30c, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, Fox-2, SRp50, SRp30c, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, Fox-2, SRp50, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, Fox-2, SRp50, SRp30c, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, FOX-2, SRp50, SRp30c, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, FOX-2, SRp50, SRp30c, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, FOX-2, SRp50, SRp30c, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, FOX-2, SRp50, SRp50, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, FOX-2, SRp50, SRp30c, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, FOX-2, SRp50, SRp30c, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, FOX-2, SRp50, SRp30c, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, FOX-2, SRP5, ZBM5, SRp30c, SRp30c, TIA-1, TIA
ATP5G1 ACSF2 NME1 // NME2 AKAP1 BCAS3	Alter. First Exon (e2-6) Alter. First Exon (e1) Alter. First Exon (e1-11) Complex Alter. First Exon (e2) Exon Cassette	1.66 2.53 1.74 13.82 1.76 2.72	3.64E-03 5.60E-05 4.20E-04 3.09E-06 5.84E-04 9.79E-04	ETR-3, hnRNP A1, hnRNP C1, hnRNP F1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP P (TLS), KSRP, Nova-1, SC35, SF2/ASF, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, hnRNP A1, hnRNP C1, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp30c, TD-43, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP F, h
ATP5G1 ACSF2 NME1 // NME2 AKAP1 BCAS3 TBX2	Alter. First Exon (e2-6) Alter. First Exon (e1) Alter. First Exon (e1-11) Complex Alter. First Exon (e2) Exon Cassette Complex	1.66 2.53 1.74 13.82 1.76 2.72 2.08	3.64E-03 5.60E-05 4.20E-04 3.09E-06 5.84E-04 9.79E-04 3.76E-04	 ETR-3, hnRNP AL, hnRNP AL, hnRNP F, hnRNP AL, hnRNP AL, hnRNP AL, hnRNP D, hnRNP CL, hnRNP CL, hnRNP F, hnRNP HL, hnRNP HL, hnRNP HL, hnRNP F, hnRNP HL, hnRNP F, hnRNP HL, hnRNP AL, hnRNP
ATP5G1 ACSF2 NME1 // NME2 AKAP1 BCAS3 TBX2 ARSG	Alter. First Exon (e2-6) Alter. First Exon (e1) Alter. First Exon (e1-11) Complex Alter. First Exon (e2) Exon Cassette Complex Alter. First Exon (e1)	1.66 2.53 1.74 13.82 1.76 2.72 2.08 6.15	3.64E-03 5.60E-05 4.20E-04 3.09E-06 5.84E-04 9.79E-04 3.76E-04 4.32E-05	ETR-3, hnRNP A1, hnRNP C1, hnRNP C1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP C1, hnRNP E2, hnRNP F, hnRNP F, hnRNP H1, hnRNP H2, hnRNP K, hnRNP A2/B1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP F (TLS), HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, PS, RBM5, Sam68, SC35, SRp20s, TA-1, TIAL1, YB-1, ZRANB2 ETR-3, hnRNP F, hnRNP H1, hnRNP H2, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP F (TLS), HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, PS, RBM5, Sam68, SC35, SRp20s, SRp30c, TB-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP F (TLS), HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SRp20s, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP F (TLS), HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-2, PSF, RBM5, Sam68, SC35, SRp20s, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP F (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-2, PSF, RBM5, Sam68, SC35, SRp20s, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP F (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP F (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-1, Fox-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-1, Fox-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-1, Fox-2, HNRNP A2, HINRNP A2, HNRNP D, HNRNP D, HNRNP E1,
ATP5G1 ACSF2 NME1 // NME2 AKAP1 BCAS3 TBX2 ARSG SPHK1	Alter. First Exon (e2-6) Alter. First Exon (e1) Alter. First Exon (e1-11) Complex Alter. First Exon (e2) Exon Cassette Complex Alter. First Exon (e1) Alter. First Exon (e1-8)	1.66 2.53 1.74 13.82 1.76 2.72 2.08 6.15 1.69	3.64E-03 5.60E-05 4.20E-04 3.09E-06 5.84E-04 9.79E-04 3.76E-04 4.32E-05 1.28E-02	 Erres, nake Ag, make Ag, make
ATP5G1 ACSF2 NME1 // NME2 AKAP1 BCAS3 TBX2 ARSG SPHK1 CBX2	Alter. First Exon (e2-6) Alter. First Exon (e1) Alter. First Exon (e1-11) Complex Alter. First Exon (e2) Exon Cassette Complex Alter. First Exon (e1) Alter. First Exon (e1-8) Alter. Terminal Exon (e4-5)	1.66 2.53 1.74 13.82 1.76 2.72 2.08 6.15 1.69 1.83	3.64E-03 5.60E-05 4.20E-04 3.09E-06 5.84E-04 9.79E-04 3.76E-04 4.32E-05 1.28E-02 1.20E-03	ETR-3, hnRNP A1, hnRNP A2, hnRNP A1, hnRNP A2, hnRNP A3, hnRNP A2, hnRNP A3, hnRNP A2, hnRNP A4, hnRNP A2, hnRNP A2, hnRNP A4, hnRNP A2, hnRNP A2, hnRNP A3, hnRNP A4, hnRNP A2, hnRNP A2, hnRNP A4, hnRNP A2, hnRNP A2, hnRNP A4, hnRNP A2, hnRNP A2, hnRNP A3, hnRNP A4, hnRNP A2, hnRNP A2, hnRNP A2, hnRNP A2, hnRNP A2, hnRNP A3, hnRNP A2, hnRNP A3, hnRNP A4, hnRNP A2, hnRNP A4,
ATP5G1 ACSF2 NME1 // NME2 AKAP1 BCAS3 TBX2 ARSG SPHK1 CBX2 ABR	Alter. First Exon (e2-6) Alter. First Exon (e1) Alter. First Exon (e1-11) Complex Alter. First Exon (e2) Exon Cassette Complex Alter. First Exon (e1) Alter. First Exon (e1-8) Alter. Terminal Exon (e4-5) Complex	1.66 2.53 1.74 13.82 1.76 2.72 2.08 6.15 1.69 1.83 1.79	3.64E-03 5.60E-05 4.20E-04 3.09E-06 5.84E-04 9.79E-04 3.76E-04 4.32E-05 1.28E-02 1.20E-03 1.70E-05	 Erres, fox-1, fox-2, hindler A2, hindler A2, hindler A2, hindler A2, hindler A2, hindler A4, hindler A4,
ATP5G1 ACSF2 NME1 // NME2 AKAP1 BCAS3 TBX2 ARSG SPHK1 CBX2 ABR CDRT1 // TRIM16	Alter. First Exon (e2-6) Alter. First Exon (e1) Alter. First Exon (e1-11) Complex Alter. First Exon (e2) Exon Cassette Complex Alter. First Exon (e1) Alter. First Exon (e1-8) Alter. Terminal Exon (e4-5) Complex Alter. Terminal Exon (e10)	1.66 2.53 1.74 13.82 1.76 2.72 2.08 6.15 1.69 1.83 1.79 1.76	3.64E-03 5.60E-05 4.20E-04 3.09E-06 5.84E-04 9.79E-04 3.76E-04 4.32E-05 1.28E-02 1.20E-03 1.70E-05 3.62E-03	 ETR-3, Fox-1, Fox-2, IntRVP A1, IntRVP A2/B1, IntRVP C1, IntRVP C2, IntRVP F2, IntRVP F2, IntRVP F4, IntRVP F4,
ATP5G1 ACSF2 NME1 // NME2 AKAP1 BCAS3 TBX2 ARSG SPHK1 CBX2 ABR CDRT1 // TRIM16 FAM83G	Alter. First Exon (e2-6) Alter. First Exon (e1) Alter. First Exon (e1-11) Complex Alter. First Exon (e2) Exon Cassette Complex Alter. First Exon (e1) Alter. First Exon (e1-8) Alter. Terminal Exon (e4-5) Complex Alter. Terminal Exon (e10) Alter. Terminal Exon (e7)	1.66 2.53 1.74 13.82 1.76 2.72 2.08 6.15 1.69 1.83 1.79 1.76 2.40	3.64E-03 5.60E-05 4.20E-04 3.09E-06 5.84E-04 9.79E-04 3.76E-04 4.32E-05 1.20E-03 1.20E-03 1.70E-05 3.62E-03 1.18E-03	 ETR3, Fox1, Fox2, InRNP A1, INRNP A2/B1, INRNP C1, INRNP C1, INRNP D2, INRNP C1, INRNP C2, INRNP A1, INRNP A2, B1, INRNP A2/B1, INRNP C1, INRNP C2, INRNP A1, INRNP C1, INRNP C1, INRNP C1, INRNP C1, INRNP C1, INRNP C2, INRNP C2, INRNP C3, SF2/ASF, SRp30c, TD43, TL11, TL11, YB-1, ZRANB2 ETR3, INRNP A1, INRNP C1, INRNP A2/B1, INRNP C1, INRNP C1, INRNP C1, INRNP C2, INRNP C4, INRNP C4, INRNP C4, INRNP C1, INRNP C1, INRNP C1, INRNP C1, INRNP C2, INRNP C4, INRNP C4, INRNP C4, INRNP C1, INRNP C1, INRNP C1, INRNP C2, INRNP C4, INRNP C4, INRNP C4, INRNP C1, INRNP C1, INRNP C1, INRNP C4, INR
ATP5G1 ACSF2 NME1 // NME2 AKAP1 BCAS3 TBX2 ARSG SPHK1 CBX2 ABR CDRT1 // TRIM16 FAM83G RDM1	Alter. First Exon (e2-6) Alter. First Exon (e1) Alter. First Exon (e1-11) Complex Alter. First Exon (e2) Exon Cassette Complex Alter. First Exon (e1) Alter. First Exon (e1-8) Alter. Terminal Exon (e4-5) Complex Alter. Terminal Exon (e10) Alter. Terminal Exon (e7) Exon Cassette	1.66 2.53 1.74 13.82 1.76 2.72 2.08 6.15 1.69 1.83 1.79 1.76 2.40 1.90	3.64E03 5.60E05 4.20E04 3.09E06 5.84E04 9.79E04 3.76E04 4.32E05 1.28E02 1.20E03 1.70E05 3.62E03 1.18E03 2.20F03	 ETR3, Tosk, F, KSR, Shp2O, Shp3Oc, TIA-I, TIALI, YE-I, ZRANB2 ETR3, hnRNP AL, hnRNP C.I, hnRNP F, hnRNP H.I, hnRNP H.2, hnRNP I (PTB), hnRNP P (TLS), KSRP, Nova-I, SC35, SF2/ASF, SRp3Oc, TIA-I, TIALI CUG-BP1, ETR3, Fox-I, Fox-2, hnRNP AL, hnRNP AL, hnRNP CI, hnRNP D, hnRNP D, hnRNP D, hnRNP EL, hnRNP F, hnRNP H.1, hnRNP H.2, hnRNP F, hnRNP H.2, hnRNP F, hnRNP H.1, hnRNP F, hnRNP H.2, hnRNP F, hnRNP H.2, hnRNP F, hnRNP H.2, hnRNP F, hnRNP H.2, hnRNP F, hnRNP H.1, hnRNP F, hnRNP H.2, hnRNP F, hnRNP H.2, hnRNP F, hnRNP H.2, hnRNP F, hnRNP H.1, hnRNP H.2, hnRNP F, hnRNP H.1, hnRNP H.2, hnRNP F, hnRNP AL, hnRNP AL, hnRNP C, TLS), MSR-2, SSF, SRp3Oc, TD-43, TIA-I, TIALI, YE-I, ZRANB2 ETR3, Fox-I, Fox-2, hnRNP AL, hnRNP AL, hnRNP C, I, hnRNP D, hnRNP E, hnRNP F, hnRNP F, hnRNP H.1, hnRNP H.2, hnRNP F, TLS), HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, SFF, RBM5, Sam68, SC35, SF2/ASF, SRp2O, SRp3Oc, TIA-1, TIALI, YE-I, ZRANB2 ETR3, Fox-I, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E2, hnRNP F, hnRNP F, hnRNP H1, hnRNP H2, hnRNP F (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SSP2O, STD43, TIA-1, TIALI, YE-I, ZRANB2 ETR3, Fox-I, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E2, hnRNP F, hnRNP F, hnRNP H1, hnRNP H2, hnRNP F (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SR2O, SRp3Oc, TIA-1, TIALI, YE-1, ZRANB2 ETR3, Fox-I, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP F, KNRP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, NSF, RBM5, Sam68, SC35, SF2/ASF, SR2O, SRp3Oc, TLA-1, TIALI, YE-1, ZRANB2 CUG-BP1, ETR3, Fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP D, hnRNP D, hnRNP D, hnRNP F H1, hnRNP H2, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP F, HSRNP H1, hnRNP H2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1,

				KSRP, MBNL1, Nova-1, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
C17orf58	Alter. Donor Site	1.98	2.58E-04	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HuB, HuD, KSRP, MBNL1, Nova-1, Sam68, SC35, SRp30c, TIA-1, TIAL1, YB-1
SLC25A19	Alter. First Exon (e1-3)	1.66	2.00E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP P (TLS), HuB, HuD, KSRP, MBNL1, Nova-1, PSF, Sam68, SC35, SF2/ASE_SRn20_SRn30c_TIA-1_TIAI_1_YB-1_ZRANB2
CANT1	Intron Retention	1.53	2.66F-03	TR-3. Fox-1. Fox-2. hnRNP E. hnRNP H.1. hnRNP H.2. hnRNP I (PTB). hnRNP P (TLS). KSRP. Nova-1. RBM5. SF2/ASE. SRn30c. YB-1
TBC1D16	Alter. First Exon (e1-5,7)	1.52	8.64E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP H3, hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, HuB, KSPP, MRN11, Nore 2, DEC REMS Same S235, S51, S52 (ASE SEP 20, CRD23), CRD23, TLA1, TUA1, VB1, 720 NP2
MYL12B	Alter. First Exon (e1)	1.51	2.48E-03	ETRA, Fox2, hnRVP 41, hnRVP 42/B1, hnRVP 61, hnRVP 61, hnRVP 61, hnRVP 62, hnRVP 74, h
TGIF1	Alter. First Exon (e7)	1.50	2.10E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2, B1, hnRNP D, hnRNP D, hnRNP D, hnRNP E1, hnRNP E1, hnRNP F2, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP I (PTB), hnRNP P (TLS), HTra2alpha, HTr
RBBP8	Alter First Evon (e2)	2 36	7.66E-03	TTR2> NRDV A1 NRDVP A1 NRDVP A1 NRDVP A1 NRDVP AND NRDVP (JPR) PARVP (JPR) NRDVP AND N
ZNF397	Alter. Terminal Exon (e3)	1.61	1.28E-02	9G8, CUG-BPI, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP D1, hnRNP E1, hnRNP E1, hnRNP E1, hnRNP F1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP I (PTB), hnRNP K1, hnRNP P (TLS), HTra2abab HTra2abab HTra2abab HTra2baba HuB KNP MRNI 1 Nova-2 PSR RBMS Sam68 SC35 SE1 SF2/ASE SRa20 SRa20 TDP43 Tha TTA1 TV F1 ZARNP2
	Alter, Donor Site	1.77	1.84F-03	
C18orf54	Complex	1.97	2.96E-03	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP CL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), HTra2beta1, HuB, KSRP, Nova-1, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1
	Alter. First Exon (e1-10)	4.27	1.01E-04	
NEDD4L	Complex (e7)	1.72	9.72E-05	CUGBP1, ETR-3, FMRP, Fox-1, Fox-2, InRNP A1, InRNP A2/B1, InRNP C1, InRNP D1, InRNP E1, InRNP E2, INRNP F2, INRNP H3, INRNP H3, INRNP H3, INRNP K, INRNP LL, INRNP P4, INRNP H3,
	Exon Cassette	1.67	5.64E-04	(ILS), HIraZalpha, HIraZbeta1, HuB, HuD, HuK, KSKY, MBINLI, Nova-1, Nova-2, PSF, KBMS, Samos, SC3S, SF1, SF2/ASF, SKp2U, SKp3UC, IDP43, IIA-1, IIAL1, YB-1, ZKANBZ
COLEC12	Alter. First Exon (e1)	2.79	9.79E-05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
EDD 411 2	Complex (e23-25)	4.96	1.18E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB,
EPB41L3	Exon Cassette	3.24	2.20E-04	HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
DSC3	Exon Cassette	2.25	9.01E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SRp20c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
DSC2	Exon Cassette	2.77	2.79E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, Nova-1, Nova-2, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
IN080C	Exon Cassette	1.55	1.60E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
SYT4	Complex	1.99	4.56E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
BSG	Alter. First Exon (e2,e4)	1.64	1.64E-04	CUG-BP1, ETR-3, hnRNP A1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
FSD1	Complex	1.68	3.95E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP P (TLS), HTra2beta1, HuB, KSRP, Nova-1, SC35, SF2/ASF, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
PNPLA6	Alter. First Exon (e2,e4)	1.53	6.17E-04	hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HuB, KSRP, Nova-1, RBM5, SC35, SRp20, SRp30c, YB-1, ZRANB2
7NF177 //	Alter. Acceptor Site	2.10	3.24E-03	
ZNF559	Exon Cassette	1.79	1.82E-03	HIR HID KSPP MRN 1 Nva-1 Nu-2 RBMS Sam68 SC35 SE1 SR00 SR30r TA-1 TIA1 14 1- YA-1 ZAMR2
	Intron Retention	2.23	5.62E-03	
SI C44A2	Complex	2.42	1.79E-04	FTR-3 Fox-1 Fox-2 hnRNP C1, hnRNP F1, hnRNP F2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (T1S), KSRP, MBNI 1, Nova-1, Nova-2, PSE, RBM5, SC35, SRo30, STIA-1, TIAI 1, YB-1
	Exon Cassette	1.93	1.28E-03	
CARM1	Exon Cassette	3.81	3.62E-05	ETR-3, Fox-1, Fox-2, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF2/ASF, SRp30c, TIA- 1, TIAL1, YB-1, ZRANB2
ZNF69	Alter. First Exon (e1-4,e6)	1.88	3.70E-03	9G8, CUG-BP1, ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
ZNF136	Exon Cassette	1.53	1.20E-03	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
	Alter. Acceptor Site	1.52	1.06E-03	ETD 2 hADNO DI HADNO E1 HADNO E HADNO LI HADNO LI HADNO LI (DTD) HADNO LI (DTD) HADNO LI (LU LI LU LI
GTPBP3	Alter. First Exon (e3-4)	1.97	1.20E-02	Elico, mixer E, mixer E, mixer E, mixer E, mixer E, mixer E, mixer E E, mixer E E, mixer E E, mixer E E, mixer
	Complex	2.38	3.96E-04	
IFI30 // PIK3R2	Alter. First Exon (e1-19)	13.13	1.89E-05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
ZNF90	Exon Cassette	2.08	8.02E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
ZNF85	Alter. First Exon (e1-3)	2.17	5.95E-05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
LTDD4	Alter. First Exon (e1-4)	1.94	5.61E-04	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2,
LIBP4	Exon Cassette	1.53	1.38E-03	PSF, RBM5, Sam68, SC35, SF2/ASF, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
EGLN2 // MIA //	Alter, Terminal Exon (e8-14)	1.62	4.18E-03	CUG-BP1. ETR-3. Fox-1. Fox-2. hnRNP A1. hnRNP A2/B1. hnRNP C1. hnRNP C1. hnRNP E1. hnRNP E2. hnRNP F1. hnRNP F1. hnRNP F1. hnRNP F2. hnRNP F1. hnRNP F2. hnRNP F1. hnRNP F3. hnRNP F3. hnRNP F4. hnRNP F4

RAB4B				HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
BCAM	Complex	1.87	5.60E-04	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HuB, KSRP, Nova-1, Nova-2, RBM5, SC35, SRp20, TIA-1, TIAL1, YB-1, ZRANB2
FCGRT	Alter. Terminal Exon (e6)	1.77	2.23E-03	ETR-3, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, RBM5, Sam68, SC35, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
MED25	Complex (e9)	1.55	1.29E-02	hnRNP I (PTB), KSRP, MBNL1, Nova-1, Nova-2, SRp30c, YB-1
ZNF610	Exon Cassette	3.48	6.36E-05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
ZNF525 // ZNF765	Mutualy Exclusive Exons (e2)	1.64	2.71E-02	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
	Alter. First Exon (e1-11)	1.67	9.84E-04	
BRSK1	Alter. Terminal Exon (e14-22)	1.59	2.80E-03	CUG-BP1, ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
ZNF586//ZNF58 7/B // ZNF776	Complex	1.51	3.22E-04	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
TMEM205	Complex	1.67	2.23E-04	ETR-3, hnRNP A1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, PSF, RBM5, Sam68, SC35, SRp30c, TIA-1, TIAL1, YB-1
ZNF20 //ZNF625	Alter. First Exon (e1-5)	8.44	2.62E-06	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
ZNF564 // ZNF709	Alter. Terminal Exon (e6-8)	1.78	8.41E-05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
DMKN	Complex	1.69	1.86E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F2, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP F, hnRNP F, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, KSRP, MBNL1, Nova-1,
DIVIKIN	Exon Cassette	3.06	8.58E-04	Nova-2, Sam68, SC35, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
ATP5SL	Exon Cassette	1.56	4.26E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
SLC8A2	Exon Cassette	2.20	3.59E-05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
ZNF28	Alter. First Exon (e1-3)	3.94	1.04E-04	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRo20, SRo30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
ZNF320	Alter. Terminal Exon (e10)	1.92	2.82E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E2, hnRNP F2, hnRNP F, hnRNP H2, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP F (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuB, KSRP MRN1 I, Nova-1, Nova-2, PSE, Sam68, SC35, SF2/ASE, SRb20, SRb20, TLA-1, TLA 1, YB-1, ZRANB2
ZNF321P // ZNF816	Alter. Terminal Exon (e4-5)	1.86	5.96E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRb20, SRb30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
71/51/60	Alter. Acceptor Site	4.64	6.11E-05	9G8, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD,
ZINF100	Alter. Terminal Exon (e5-8)	2.87	4.36E-03	KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
ZNF677	Alter. Terminal Exon (e5)	1.79	9.61E-04	9G8, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
SYT5	Exon Cassette	5.63	2.13E-05	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SRp20, SRp30c, TDP43, YB-1, ZRANB2
CHMP2A	Complex	1.92	9.97E-04	9G8, ETR-3, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP P (TLS), HTra2beta1, HuB, MBNL1, Nova-1, SC35, SF2/ASF, SRp20, SRp30c, YB-1
COLEC11	Exon Cassette	2.60	4.04E-04	9G8, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB,
COLLCII	Exon Cassette	2.67	4.04E-04	HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
GREB1	Complex	2.48	9.74E-05	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
I PIN1	Alter. Terminal Exon (e14-19,e21-29)	1.84	2.03E-04	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H, hnRNP K, hnRNP P (TLS), HTra2alpha,
	Exon Cassette	1.77	1.00E-02	HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
ABHD1	Exon Cassette	1.65	2.74E-03	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNPD, hnRNPE1, hnRNP E2, hnRN F, hnRN H1, hnRNPH2, hnRNPK, hnRNP P (TLS), HTra2alpha, HTra2beta1, KSRP, MBNL1, SC35, TIA-1, TIAL1, YB1
ATRAID	Complex (e1)	1.57	3.76E-04	ETR-3, Fox-1, Fox-2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HuB, Nova-1, SC35, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
GPN1 // ZNF512	Alter. First Exon (e1-6,e8-15,e19)	1.66	5.18E-03	CUG-BP1, ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
SLC30A6	Exon Cassette	1.64	8.40E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, TIA-1, TIAL1, YB-1, ZRANB2
PLEKHH2	Alter. First Exon (e1-9)	1.82	5.36E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuC, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
EPAS1	Alter. First Exon (e1-11)	1.86	1.22E-03	9G8, CUG-BP1, ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
SPTBN1	Alter. First Exon (e2-3)	1.54	2.41E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2aloha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBMS, Sam68, SC35, SF1, SF2/ASF, SRo20, SRo30c, TDP43, TIA-1, TIAL1, YB-1, 7RANB2
VRK2	Complex	2,86	7,57F-05	CUG-BP1_ETR-3_Fox-1_Fox-2_hnRNP_A1_hnRNP_A2/B1_hnRNP_C1_hnRNP_C1_hnRNP_PD_hnRNP_F1_hnRNP_F2_hnRNP_F1_hnRNP_H1_hnRNP_H2_hnRNP_L[PTR)_hnRNP_K_hnRNP_P(TI_S)_HTra2heta1_HuB_HuD
VI VI VE	Complex	2.00	7.372.03	

	Exon Cassette	2.71	7.57E-05	KSRP, MBNL1, Nova-2, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
DOI 42 401	Complex	1.95	5.84E-03	EDND AT E-DND K LED New 1 2005 VD 1
BULA3-AS1	Intron Retention	1.75	1.24E-02	חרגיער או, חרגיער א, אוש, אופאי, 50, 15-1
SUILT1C4	Alter. Terminal Exon (e4-7)	2.95	2.19E-04	9G8, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1,
30E1104	Exon Cassette	2.73	3.83E-05	HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
MERTK	Alter. Terminal Exon (e19-20)	1.67	2.17E-05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
DPP10	Alter. First Exon (e1-6)	1.96	1.82E-03	9G8, CUG-BP1, ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (ITLS), HTra2abha, HTra2beta1, HuB, HuD, HuB, KSRP, MBNI 1, Nova-1, Nova-2, PSE, RBM5, Sam68, SC35, SE1, SE2/ASE, SRo20, SRo30c, TDP43, TIA-1, TIA11, YB-1, ZRANB2
GLI2	Complex	2.91	1.56E-03	ETR-3, hnRNP A1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I(PTB), hnRNP K, hnRNP P(TLS), HuB, KSRP, Nova-1, Nova-2, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1
ONTHADS	Alter. Terminal Exon (e18-24)	2.35	1.01E-02	CUG-BP1, ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP DL, hnRNP E1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS),
CNTNAP5	Complex	2.44	8.46E-03	HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
LICOT1	Alter. Donor Site	1.84	8.24E-07	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR,
UGGTI	Exon Cassette	1.80	2.05E-04	KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
R3HDM1	Exon Cassette	1.68	1.24E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
EMNIL 2	Complex	1.58	4.24E-03	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP D1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS),
FIMINEZ	Exon Cassette	1.66	4.12E-03	HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
DYNC1I2	Exon Cassette	8.47	6.10E-05	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Sam68, SC35, SF1, SRn20, SRn30c, TIA-1, TIAI 1, YB-1, ZRANB2
0100551	Alter. First Exon (e1)	3.13	9.24E-03	CUG-BPJ, ETR-3. Fox-1. Fox-2. hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F2, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alaba.
RAPGEF4	Complex	1.97	1.82E-02	HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
CDCA7	Exon Cassette	2.02	3.33E-06	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, HCSP, MONULA, New 1, Sense SC35, SC1, Sense SC1, Sense SC1, Sense SC1, SC1, Sense SC1, SC1, SC1, SC1, SC1, SC1, SC1, SC1,
OSBPL6	Exon Cassette	1.98	1.24E-03	Soc, Fire, for a more ray more ray more of more as more as more as more ray more ray more ray more ray more respectively. The applies that be readed and respectively more ray more r
COL3A1	Alter. First Exon (e1-47)	2.25	2.16E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MRN1 I, Nuxa2, RRM5, Sam68, SC33, SE1, SRb30, SRb30, CTP43, TLA1, TLA1, YE4, 7RANR2
NABP1	Exon Cassette	1.98	2.39F-04	TR3. https://www.article.com/procession/score/sc
	Alter, First Exon (e1-2.e5.e8-12.e14-		7.075.04	
CCDC150	17,e20-21,e23-25)	1.88	7.37E-04	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP D1, hnRNP E1, hnRNP E2, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
	Exon Cassette	1.79	1.10E-02	
CACDO	Alter. Termi Exon (e13,16-18)	4.29	5.80E-05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP F (TLS), HTra2beta1, HuB, HuD,
CASEO	Evon Cassette	2.12	2.65E-04	KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
INPP5D	Alter Eirst Exon (e1-5)	5.01	2 27E-05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1,
		0.01	2.272.00	HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
FAM132B	Alter. First Exon (e1-2)	3.65	1.70E-05	ETR-3, hnRNP E1, hnRNP E2, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP P (TLS), KSRP, Nova-1, Nova-2, Sam68, SC35, SKp20, TIA-1, TIAL1, YB-1, ZRANB2
MYT1L	Alter. First Exon (e1-2,e4-5)	4.53	5.98E-04	9G8, CUG-BPI, ETR-3, Fox-1, Fox-2, InRNP A1, InRNP A2/B1, InRNP C1, INRNP D, INRNP E1, INRNP F2, INRNP F4,
XWIIAO	Alter. Terminal Exon (e25,28)	4.82	8.16E-07	(ICS), HTT222[DR3, HTT220Eta1, HUB, HUU, HUK, NSR*, WISHLI, NOV3-1, NOV3-2, F5*7, ROMO, SATIOS, SATIOS, SCJ. SF/ZASF, SKP2U, SKP3UC, IUF43, IIA-1, IAL1, TB-1, ZKAN52 TT2.2, CPU, JANDE C, JANDHE C, JANDHE C, JANDHE C, JANDE JANDE JANDE JANDE JANDE JANDE C, JANDE C, JANDHE C, J
TWHAQ	Complex	4.22	1.10E-03	
WDR35	Exon Cassette	5.90	4.14E-05	LINGS, INDEXT AC, INDEXT AC DUI, INDEXT C, IND
C2orf43	Exon Cassette	1.62	1.38E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNI 1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRo20, SRo30c, TDP43, TIA-1, TIA-1, YB-1, ZRANB2
ATL2			1	
	Complex	4.22	5.61E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, KSRP, Nova-1, Sam68, SC35, SRn20, SRn20, SRn20, TIA-1, TI
NRXN1	Complex Alter First Exon (e1-3 e5 e8-	4.22	5.61E-04	ETR-3, Fox 1, Fox 2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, KSRP, Nova-1, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 GR C1/C4RP1 ETR-3, Fox 1, Fox 2, hoRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP D1, hnRNP F1, hnRNP F2, hnRNP F2, hnRNP F1, hnRNP F4, hnR
INKANI	Complex Alter. First Exon (e1-3,e5,e8- 19,e21,e24-26)	4.22 3.59	5.61E-04 4.91E-06	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, KSRP, Nova-1, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
RTN4	Complex Alter. First Exon (e1-3,e5,e8- 19,e21,e24-26) Exon Cassette	4.22 3.59 2.50	5.61E-04 4.91E-06 6.18E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, KSRP, Nova-1, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP F (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
RTN4	Complex Alter. First Exon (e1-3,e5,e8- 19,e21,e24-26) Exon Cassette Alter. Terminal Exon (e14-18)	4.22 3.59 2.50 1.64	5.61E-04 4.91E-06 6.18E-03 2.21E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, KSRP, Nova-1, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HUD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F1, hnRNP H2, hnRNP H2, hnRNP F (TLS), HTra2alpha, HTra2beta1, HuB, HUD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E2, hnRNP F2, hnRNP F1, hnRNP H2, hnRNP H2, hnRNP F (TLS), HTra2alpha, HTra2beta1, HuB, HUD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D1, hnRNP E1, hnRNP E1, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HUD, HUR, LNRNP A2/B1, hnRNP C1, hnRNP P (TLS), HNRP E1, hnRNP E
RTN4 AAK1	Complex Alter. First Exon (e1-3,e5,e8- 19,e21,e24-26) Exon Cassette Alter. Terminal Exon (e14-18) Complex	4.22 3.59 2.50 <u>1.64</u> 2.61	5.61E-04 4.91E-06 6.18E-03 2.21E-04 5.77E-05	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, KSRP, Nova-1, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HUD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H1, hnRNP H2, hnRNP F (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H, hnRNP F (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H (PTB), hnRNP F (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
RTN4 AAK1 ASPRV1 //	Complex Alter. First Exon (e1-3,e5,e8- 19,e21,e24-26) Exon Cassette Alter. Terminal Exon (e14-18) Complex Alter. First Exon (e1)	4.22 3.59 2.50 1.64 2.61 2.09	5.61E-04 4.91E-06 6.18E-03 2.21E-04 5.77E-05 8.19E-05	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, KSRP, Nova-1, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP F, KNRNP F, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP F (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP D, hnRNP D, hnRNP D, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP D, hnRNP D, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D1, hnRNP E2, hnRNP F2, hnRNP F4, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, NOVA-1, NOVA-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, S
AAK1 AAK1 ASPRV1 // PCBP1-AS1	Complex Alter. First Exon (e1-3,e5,e8- 19,e21,e24-26) Exon Cassette Alter. Terminal Exon (e14-18) Complex Alter. First Exon (e1) Alter. Terminal Exon (e11)	4.22 3.59 2.50 1.64 2.61 2.09 1.74	5.61E-04 4.91E-06 6.18E-03 2.21E-04 5.77E-05 8.19E-05 9.95E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, KSRP, Nova-1, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/OS, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP D, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2abeta1, HuB, HuD, KSRP, MBNL1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SD30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP D1, hnRNP D1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2abeta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SD30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
RTN4 AAK1 ASPRV1 // PCBP1-AS1 PCGF1	Complex Alter. First Exon (e1-3,e5,e8- 19,e21,e24-26) Exon Cassette Alter. Terminal Exon (e14-18) Complex Alter. First Exon (e1) Alter. First Exon (e1) Alter. First Exon (e1)	4.22 3.59 2.50 1.64 2.61 2.09 1.74 1.73	5.61E-04 4.91E-06 6.18E-03 2.21E-04 5.77E-05 8.19E-05 9.95E-04 1.02E-02	 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, KSRP, Nova-1, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H1, hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP F (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP C1, hnRNP DL, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP F (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP D, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A2/B1, hnRNP D1, hnRNP D, hnRNP D, hnRNP E4, hnRNP F4, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP K,

				MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
FHL2	Complex	1.80	2.48E-02	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, HuC, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
CD302 // LY75	Alter. Terminal Exon (e14-35,e37-41)	1.67	3.41E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
SLC25A12	Exon Cassette	4.01	2.12E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
	Complex	2.03	1.90E-03	FTR-3. Fox-1. Fox-2. hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP D1, hnRNP F1, hnRNP F2, hnRNP F4, hnRNP H2, hnRNP H2, hnRNP H2, hnRNP F(TIS), HTra2beta1, HuB, HuD, KSRP
FKBP7	Exon Cassette	1.99	1.90E-03	MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
TTN	Exon Cassette	1.92	1.98E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, KSRP, MBNL1, Nova-1, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
ICA1L	Intron Retention	1.70	3.12E-03	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
EN1	Complex	1.79	2.20E-05	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-2, Sam68, SC35,
1111	Exon Cassette	4.63	1.18E-06	SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
ABCB6 // ATG9A	Alter. Terminal Exon (e16,e17-30,e32- 35)	1.76	3.18E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP I (PTB), hnRNP F, thrRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
SERPINE2	Alter. First Exon (e3-4)	2.34	9.21E-04	9G8, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
KIF1A	Complex (e2,e3-38,e40-47)	2.22	1.18E-03	CUG-BP1, ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP I, hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
PRNP	Complex	2.18	6.38E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D1, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
PLCB1	Alter. First Exon (e2,e4-5,e7)	1.98	6.38E-04	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I, hnRNP I, hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
BTBD3	Alter. First Exon (e2)	1.85	1.57E-02	ETR-3, hnRNP I (PTB), HTra2alpha, HTra2beta1, HuB, Nova-1, Sam68, SC35, YB-1
CBFA2T2	Exon Cassette	1.51	1.24E-03	9G8, CUG-BP1, ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
AAR2	Complex	1.99	2.02E-05	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP DL, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
RPN2	Exon Cassette	1.87	1.60E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
PPP1R16B	Alter. Terminal Exon (e3-12)	3.35	1.64E-05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
CDAP1L1	Alter. First Exon (e2)	5.59	3.22E-07	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP,
ODAI ILI	Exon Cassette	2.62	8.19E-05	MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
TTPAL	Alter. First Exon (e1-2)	1.72	8.74E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP F, TLS), HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
DBNDD2// SYS1	Complex	1.72	6.96E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP P (TLS), HuB, KSRP, Nova-1, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1
UBE2C	Alter. First Exon (e1)	1.77	5.59E-04	9G8, hnRNP A1, hnRNP C1, hnRNP E1, hnRNP E1, hnRNP F, hnRNP H2, hnRNP H2, hnRNP P (TLS), KSRP, Nova-1, SC35, S2/ASF, SRp30c, YB-1, ZRANB2
SLC9A8	Alter. Acceptor Site	2.04	1.24E-03	C0C9P1, EIK3, Fox1, Fox2, InRKIP F1, INRKIP F1, INRKIP F1, INRKIP F4, INRKIP F, INRKIP F1, INRKIP F
STX16	Alter. First Exon (e9,e12)	1.82	1.66E-02	EIK-3, FOX-1, FOX-2, FIRKIWE AL, FIRKIWE GL, FIRKIWE EL, FIRKIWE EL, FIRKIWE FL, FIRKIWE F
01/10	Alter, First Exon (e2.e8)	1.57	4.40E-03	1968 CIIG-BP1 FTR-3, FORM-0, MRNP A1, INRNP A2/F1, INRNP C1, INRNP D1, INRNP F1, INRNP F2, INRNP F1, INRNP H1, INRNP H3, INRNP H3, INRNP H3, INRNP K, INRNP P (TI S).
GNAS	Complex (e10,e13)	1.52	1.76E-03	HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
TPD52L2	Exon Cassette	11.59	6.51E-07	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E2, hnRNP F2, hnRNP F1, hnRNP H2, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
CSNK2A1	Exon Cassette	1.83	6.14E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRo20, SRo30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
TMEM230	Complex	1.97	2.32E-06	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP V, hnRNP P (TLS), HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SF1, SRp30c, TIA-1, TIAL1, YB-1,
SNX5	Alter. First Exon (e1-2)	1.62	2.76E-03	CUG-BP1, ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP DL, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF1, SRp20c, TIA-1, TIAL1, YB-1, ZRANB2
0077	Alter. First Exon (e1-3)	1.94	1.00E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS). HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1.
GGT /	Exon Cassette	2.12	8.38E-04	Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
STAU1	Exon Cassette	1.66	2.40E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2, B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuC, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
ZFP64	Alter. First Exon (e1-5)	3.35	1.36E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS),

		1	1	
BTG3	Evon Cassette	1 70	9 18E-04	HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 9G8, ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SF1, SRp20,
DEMC1	Even Gassette	1.70	1.250.00	SRp30c, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H (PTB), hnRNP K, hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SF1,
PSWG1	Exon Cassette	1.00	1.35E-02	SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
UBE2G2	Alter. First Exon (e1,e3-5)	1.86	3.59E-04	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, INRIVE P1, INRIVE P2, INRIVE P2, INRIVE P2, INRIVE P3, INRIVE P1, INRIVE P3, INRIVE P3, INRIVE P3, INRIVE P4, INRI P4, INRIVE P4, INRIVE P4,
TPTEP1	Exon Cassette	1.59	5.82E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
EWSP1	Alter. First Exon (e1-8)	11.13	2.16E-05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1,
LW3N1	Complex	1.88	3.80E-03	HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
NF2	Exon Cassette	1.51	8.62E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
SMTN	Complex	1.56	2.70E-02	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP L1, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, KSRP, Nova-1, Nova-2,
Giintt	Intron Retention	1.86	3.28E-03	Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
KCTD17	Complex	1.78	5.04E-04	hnRNP L (PTB), Nova-1, RBM5, SC35, SRo20, TIA-1, TIAL1, YB-1
101517	Complex	1.53	1.40E-03	
NOL12 //	Alter. First Exon (e1-9,14,16-17)	2.05	9.75E-05	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP K, hnRNP P (TLS), HTra2alpha,
TRIOBP	Exon Cassette	3.64	5.38E-04	HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
	Intron Retention	1.86	1./3E-05	
SYNGRI // TABI	Intron Retention	2.35	1.00E-04	ETR3, INRIVEPT, INRIVEPT, INRIVEPT, INRIVEPT (F15), INRIVEPT (F15), INRIVEPT, INVA-1, ROWAL, ROWAL, SAMDAS, SC35, SF2/ASF, SK520, SK520C, ITA-1, ITAL1, YE-1
AKHGAP8 //	Alter. First Exon (e4-19,e12)	2.99	1.23E-04	
	Exon Cassette	1.8/	3.36E-04	(ICS), HIRZ2001, HUE, HUE, HUE, KNORAL, NORAL, YOF, KBMO, SATTOS, SCISS, ST. J. STZ/ASF, SKD2U, SHD3UC, IDF43, IIA-I, ITALI, ISL, ZKANGZ OLA DDI TET 2 - L-I - L- L- DDI TE I - DDI L-
URELD2	Introl Retention	1.04	1.30E-03	CUC+DF1, ETK-3, F0K-1, F0K-4, F0K-4, IIIIRNY F1, IIIIRNY F1, IIIRNY F1, F1B, IIIRNY F1(F1B), IIIRNY F1(F1S), IIIRNY F1, F1S, FR, FNK-3, SAIRO, SU-33, S72/AST, F1Z-43, F1K-1, F1L-1, F1-1, F1Z-4, F1Z-
CLTCL1	Alter. Donor Site	1.57	8.38E-03	EIR-5, F0x-2, F0x-2, IIIRINF A1, IIIRINF A2, D1, IIIRINF C1, IIIRINF E1, IIIRINF E2, IIIRINF F1, IIIRINF F1, IIIRINF F1, IIIRINF F1 (F15), IIIRINF F1 (F15), IIIR206141, HD5, NSRF, NOVA-1, SAI1106, SU33, SR[20, 114-1, TIAL1, YB-1]
TXNRD2	Alter. First Exon (e3)	1.56	4.21E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
PI4KA	Alter. First Exon (e1-32)	1.81	1.70E-02	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
GSTT1	Exon Cassette	1.56	1.42E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
CHEK2	Exon Cassette	1.51	4.52E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
C1QTNF6	Intron Retention	1.98	2.54E-03	ETR-3, FMRP, Fox-1, Fox-2, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SRp30c, TIA-1, TIAL1, YB-1
DNAL4 // SUN2	Complex	2.24	1.04E-03	ETR-3, Fox-1, Fox-2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, KSRP, Nova-1, SC35, SF2/ASF, SRp30c, TIA-1, TIAL1, YB-1
ITPR1	Exon Cassette	1.59	1.70E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Sam68, SC35, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
ARPC4 // TTLL3	Alter. Terminal Exon (e5-6)	3.93	1.84E-05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20c, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
BTD	Alter. First Exon (e1)	2.20	3.82E-04	CUG-BP1, ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20c, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
	Alter. Donor Site	1.73	2.22E-04	
RPL15	Complex (e1)	1.75	4.97E-04	hnRNP I (PTB), hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, SC35, TIA-1, TIAL1, YB-1, ZRANB2
	Intron Retention	1.82	4.58E-03	
MI LI 1	Complex	1.96	1.26E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D1, hnRNP DL, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP K (TLS), HTra2alpha, HTra2beta1, HuB,
IVILIII	Exon Cassette	3.00	3.91E-05	HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
GOLGA4	Exon Cassette	2.08	5.63E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP P (TLS), HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
MYD88	Exon Cassette	1.99	6.14E-05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, RBM5, SC35, SF2/ASF, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
EXOG	Complex	2.73	7.36E-04	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNPE2, hnRNP F, hnRNPH1, hnRNP H2, hnRNP(PTB), hnRNP P(TLS), HTra2beta1, HuB, KSRP, Nova-1, Sam68, SC35, SRp20, TIA-1, TIAL1, YB1
CTNND1	Complex	1.90	1.18E-03	TTD 2 HUDDID A1 HUDDID A1 HUDDID A HUDDID AT SU HITUNALMAA 1 HUD HUD VODD NUMB 1 SAMED SO22 SD2204 TA 1 TAI 1 VD 1 7DANDO
CINNBI	Intron Retention	1.78	8.56E-04	E1r-3, IIIIRINA A2, IIIIRINA A2/D1, IIIIRINA C1, IIIRINA C1
NKTR	Alter. First Exon (e1-7)	1.92	5.80E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D1, hnRNP DL, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP H(PTB), hnRNP K, hnRNP P (TLS), HTra2alpha,
DUATIA	Exon Cassette	1.67	4.70E-03	HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2

	Alter. First Exon (e1-4,e6-14)	1.58	1.76E-03	
SACM1L	Complex	1.85	1.34E-03	
	Exon Cassette	1.88	2.40E-03	
DAC1	Alter. First Exon (e1-6)	1.79	1.22E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP H2, hnRNP K, hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB,
DAGI	Complex	1.50	9.75E-05	HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
МАРКАРКЗ	Alter. First Exon (e1-3)	1.97	2.36E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, PSF, RBM5, Sam68, SC35, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
FLNB	Alter. First Exon (e1-26)	1.69	7.46E-03	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H, hnRNP K, hnRNP K, hnRNP LL, hnRNP P (TLS),
	Alter First Evon	1.67	2.19E-03	
PTPRG	Complex	1.07	8 70E-03	500,000-01, Citos, mike, roze, inder, inder az bi, inder az bi, inder Ci, in
	Complex	5.40	9.86E-05	
CADM2	Exon Cassette	4.99	3.78E-05	HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
PVRL3	Alter. Donor Site	1.82	1.77E-04	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
PHLDB2 // PLCXD2	Alter. First Exon (e1-3)	3.88	7.76E-05	9G8, CUG-BP1, ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
CD200	Exon Cassette	2.03	4.18E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, HuR, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
MAATS1	Exon Cassette	3.75	2.08E-03	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF1, SF2/ASF, SRb20, SRb30c, TIA-1, TIAL1, YB-1, ZRANB2
PDIA5	Intron Retention	2.31	3.20E-03	ETR-3, hnRNP A1, hnRNP C1, hnRNP F1, hnRNP H2, hnRNP H2, hnRNP P (TLS), HuB, Sam68, SC35, TIA-1, TIAL1, YB-1
DDDDDD	5 0 "	0.54	7 505 05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha,
PPP2R3A	Exon Cassette	2.54	7.53E-05	HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
CLSTN2	Complex	6.58	4.24E-04	9G8, CUG-BP1, ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
PLS1	Alter. First Exon (e2,e5)	1.70	5.44E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP H3, hnRNP K, hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
TRPC1	Exon Cassette	1.83	1.58E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP DL, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
AGTR1	Exon Cassette	1.51	4.84E-03	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H, hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
GPR160	Exon Cassette	5.14	4.01E-05	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
ATP11B	Exon Cassette	2.12	1.17E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E2, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HUB, HUD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRo20, SRo30c, TIA-1, TIAL1, YB-1, ZRANB2
MAP3K13	Alter. Terminal Exon (e13-19)	1.53	2.63E-02	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
LRCH3	Exon Cassette	3.88	1.22E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
TADA3	Complex (e2-4)	1.52	6.82E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP (PTB), hnRNP K, hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SRp30c, TIA-1, TIAL1, Y
ATP2B2	Complex	1.92	4.70E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MRNI 1, Nova-1, Nova-2, PSF, RRM5, Sam68, SC35, SF2/ASF, SRn30c, TIA-1, TIA-1, YR-1, ZRANB2
FGD5-AS1	Alter. Terminal Exon (e4)	1.65	9.56E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E5, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP K, hnRNP F (TLS), HTra2alpha, HTra2beta1, HuB, H0L, KSRP, MRNI I, Nova-1, Rova-2, ESE, RBMS, Sam68, SC35, SF1, SRo20, SRo30c, TDP43, TIA-1, TIAI 1, YB-1, ZRAMB2
RFTN1	Alter. First Exon (e1-6,e8-9)	1.89	1.15E-02	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP H4, hnRNP H5, hnRNP H4, hnRNP H5, hnRNP H5, hnRNP H4, hnRNP H4, hnRNP H5, h
TOP2B	Alter. First Exon (e1)	2.34	6.63E-04	CUG-BP1, ETR-3, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), KSRP, MBNL1, Nova-1, SC35, SF2/ASF, SRp30c, TIA-1, TIAL1
GLB1 // TMPPE	Exon Cassette	1.55	2.50E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
SLC26A6	Intron Retention	1.54	1.72E-03	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HuB, KSRP, Nova-1, Nova-2, SC35, SRp30c, YB, Fox-1, Fox-2
D41 DD2	Alter. Acceptor Site	2.68	7.83E-04	TTD 1 HOND 61 HOND 6 HOND 11 HOND 10 HOND 10 HOND 14 HOND 7 HOND 7 HOND 14 HOND 14 HOND 10
DALKD3	Complex	3.16	3.17E-04	EIR-S, HIRVAR CI, HIRVAR F, HIRVAR FI, NRKVAR FI, NRKVAR F (FIB), NRKVAR K, NRKVAR K (FIS), HIRZOBERI, HUB, KSKK, MBNLI, NOVA-I, NOVA-Z, KBMS, SG3S, SKP2U, SKP3U, IA-I, HALI, YB-I
AMT	Complex (e5)	1.82	1.25E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, KSRP, MBNL1,
AIVIT	Exon Cassette	1.85	1.44E-04	Nova-1, Nova-2, PSF, Sam68, SC35, SF2/ASF, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
MAGI1	Exon Cassette	2.56	2.21E-05	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2

EOGT	Alter. First Exon (e1-2)	1.81	1.04E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MRNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SE1, SRo20, SRo30, TLA-1, TLA1, 1, YR-1, ZRANR2
	Complex	1.74	6.72E-03	
ABI3BP	Alter. Terminal Exon (e14,e15-31,e36- 43)	1.62	2.37E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD,
	Exon Cassette	3.05	8.61E-04	HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
CD47	Alter. Ter Exon (e9,e10-12)	4.44	9.80E-05	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H(PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1,
0047	Exon Cassette	4.93	2.45E-04	Nova-2, Sam68, SC35, SF1, SRp20, TIA-1, TIAL1, YB-1, ZRANB2
LSAMP	Alter. Terminal Exon	2.04	9.72E-05	9G8, CUG-BP1, ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP H2, hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
HEG1	Exon Cassette	1.61	1.34E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1
PFN2	Complex	3.38	2.50E-07	ETR-3, Fox-1, Fox-2, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Sam68, SC35, SRp20, TIA-1, TIAL1, YB-1, ZRANB2
TNIK	Exon Cassette	3.39	3.53E-05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNPA1, hnRNPA2/B1, hnRNPC1, hnRNPF1, hnRNPH1, hnRNPI(PTB), hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova1, Nova2, PSF, Sam68, SC35, SF1, TIA-1, TIAL1, YB-1
DI C1	Exon Cassette	3.81	4.29E-05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1,
DLGI	Mutualy Exclusive Exons (e23)	4.03	2.29E-05	HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
PIGG	Complex	1.87	1.20E-03	ETR-3, hnRNP A1, hnRNP C1, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
PCGF3	Exon Cassette	1.82	2.77E-04	ETR-3, hnRNP A1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP K, hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1
TMEM175	Alter. Acceptor Site	1.88	2.78E-04	ETR-3, Fox-1, Fox-2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP P (TLS), KSRP, Nova-1, Nova-2, PSF, SC35, TIA-1, TIAL1, YB-1
FGFR3	Complex	2.08	1.12E-03	ETR-3, hnRNP E1, hnRNP E2, hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, SC35, SRp30c, YB-1, ZRANB2
WHSC1	Exon Cassette	1.70	1.02E-02	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
E4M1024	Alter. First Exon (e3-7)	1.90	3.64E-05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD,
FAW195A	Exon Cassette	1.76	1.66E-03	KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
	Alter. Donor Site	2.88	3.94E-03	
ADD1	Exon Cassette	6.87	2.23E-07	
	Alter. First Exon (e2-8)	8.73	2.80E-06	11102/0001, 1100, 1100, 1100, 100, 100, 100,
EXOC1	Exon Cassette	2.38	9.64E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
81.0444	Alter. First Exon (e1-5)	3.86	3.55E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP H (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS),
SLC4A4	Complex	1.81	2.32E-03	HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
SHROOM3	Alter. Terminal Exon (e8-11,e13-15)	1.91	1.20E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-2, NSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
NDNT	Complex	2.83	1.20E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP,
INPINI	Exon Cassette	11.30	2.24E-05	MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SRp20c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
CYP2U1	Alter. Terminal Exon (e3-7)	1.69	1.27E-02	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
	Alter. First Exon	3.04	2.44E-05	
ANK2	Complex	4.37	4.22E-05	908, CUG-PT, ELK-3, FOX-1, FOX-2, FOX-2, FOX-2, FOX-1, FOX-10, FOX-10, FOX-10, FOX-10, FOX-10, FOX-10, FOX-2, FOX-
	Exon Cassette	2.49	1.84E-05	ה הוצבאוטוג, הוצבעיגו, העם, העם, העם, העם, האסיגר, אוסאבי, היא האסיגר אסיגי, אסאר אסיגר, אסגר אסגר, ארש אסיגר, אסגר אסגר אסגר אסגר אסגר אסגר אסגר אסגר
UGT8	Alter. First Exon (e1)	1.52	5.75E-05	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
USP53	Exon Cassette	1.63	2.14E-02	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
TMEM144	Intron Retention	2.80	7.38E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SF1, TIA-1, TIAL1, YB-1
CLCN3	Alter. Terminal Exon (e5,e6-15,e17)	1.51	2.38E-05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
	Alter. Acceptor Site	1.68	8.78E-04	
HAND2-AS1	Complex	7.13	3.83E-05	ETK-S, DRKWF AL, DRKWF AZ/BL, DRKWF U, DRKWF U, DRKWF DL, DRKWF EZ, DRKWF F, DRKWF H, DRKWF HZ, DRKWF I (PTB), DRKWF V, DRKWF V (LS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-0, Nova-0, Nova-0, DRAW, DR
	Exon Cassette	2.89	6.31E-05	2, 341100, 3U-33, 3NP2U, 3NP3UC, 1IA-1, 1IAL1, TB-1, ZIXAINB2
	Alter. Term Exon (e7-8,23-32)	3.21	8.80E-04	
HAUS3 // POLN	Complex (e19,e20-21)	2.32	6.02E-04	
	Exon Cassette	2.32	6.02E-04	
SEPSECS	Exon Cassette	1.67	3.14E-02	ETR-3, hnRNP A1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP P (TLS), HuB, HuD, KSRP, MBNL1, Nova-1, PSF, Sam68, SC35, SF2/ASF, SRp20, TIA-1, TIAL1, YB-1
UGDH	Exon Cassette	1.70	2.43E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1,

1				
				Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
LIN54	Alter. Donor Site	1.53	6.32E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2, b1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
	Alter. Terminal Exon	1.53	7.38E-04	
	Exon Cassette	1.65	7.00E-03	
MAPK10	Alter. First Exon (e3)	2.79	7.01E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
CAMK2D	Exon Cassette	2.54	4.36E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP H, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
	Alter. First Exon (e1-4,e6,e8-10)	1.83	1.72E-03	9G8. CUG-BP1. ETR-3. Fox-1. Fox-2. hnRNP A1. hnRNP A2/B1. hnRNP C1. hnRNP D. hnRNP DL. hnRNP E1. hnRNP E1. hnRNP F. hnRNP H1. hnRNP H2. hnRNP H3. hnRNP I (PTB). hnRNP K. hnRNP P (TLS).
SCLIT	Exon Cassette	3.66	1.45E-04	HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
SLC10A7	Complex (e7)	1.56	1.40E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
PDLIM3	Alter. Donor Site	1.83	1.31E-02	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
FAT1	Exon Cassette	6.37	4.15E-06	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
LINC01001	Complex (e5-7)	13.04	4.11E-05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP H, hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha,
LINCUIUZI	Exon Cassette	12.45	3.95E-05	HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20c, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
KIF2A	Exon Cassette	5.88	4.26E-05	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, HuR, KSRP, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
SLC30A5	Alter. Acceptor Site	2.03	3.20E-04	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, KSRP, Nova-1, Sam68, SC35, TIA-1, TIAL1, YB-1, ZRANB2
TNP01	Alter. First Exon (e1)	2.75	3.22E-06	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
BTF3	Complex	1.61	9.18E-04	ETR-3, hnRNP F, hnRNP H1, hnRNP H2, hnRNP P (TLS), HuB, Nova-1, PSF, RBM5, SC35, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
IQGAP2	Exon Cassette	2.23	2.05E-05	9G8, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MRNL1, Nova-2, PSE, Sam68, SC35, SE1, SRo20, SRn30c, TDP43, TIA-1, TIA-1, TRANB2
SCAMP1	Alter. First Exon (e1-7)	5.18	7.66E-05	CUG-BPJ, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D1, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F2, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
PAPD4	Complex (e3)	9.26	3.45E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
VCAN	Exon Cassette	2.62	5.23E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
GPR98	Alter. First Exon (e1-22,e24-26,e28- 85)	1.54	5.76E-03	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I, hnRNP I, hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
CAST	Alter. First Exon (e2)	4.27	1.41E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF1, SF2/ASF, SRo20, SRo30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
PAM	Exon Cassette	2.12	2.24E-05	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
SMAD5	Exon Cassette	1.52	1.02E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
TCERG1	Exon Cassette	1.80	5.20E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D1, hnRNP D1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
CAROOL	Complex	1.54	3.30E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1,
SAP3UL	Exon Cassette	1.73	3.78E-03	Nova-2, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
CNOT8	Complex	1.77	5.81E-05	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP I, hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
NSD1	Intron Retention	1.63	2.97E-04	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP P (TLS), HTra2beta1, HuB, KSRP, Nova-1, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
	Alter. Donor Site	2.75	1.17E-04	
ZNF454	Alter. First Exon (e1)	8.16	5.70E-05	EIK-3, INRIVIP AL, INRIVIP AZ/BL, INRIVIP U, INRIVIP EI, INRIVIP E, INRIVIP F, INRIVIP H1, INRIVIP H2, INRIVIP H2, INRIVIP AZ/BL, INRIVIP U, INRIVIP EI, INRIVIP EI, INRIVIP EI, INRIVIP EI, INRIVIP EI, INRIVIP H2, INRIVIP H
	Complex	2.60	9.89E-05	572/AST, 5KD3UC, 11A-1, 11AL1, 115-1, ZKAINBZ
DDADGA	Complex (e1-2)	2.08	4.99E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha.
PPAP2A	Exon Cassette	1.87	4.22E-04	HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
P4HA2	Alter. First Exon (e1)	2.91	1.82E-03	ETR-3, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), KSRP, Nova-1, SC35, YB-1, ZRANB2
SPOCK1	Complex (e3)	1.52	3.90E-03	9G8, CUG-BP1, ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2

ARAP3	Exon Cassette	1.67	4.44E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, PSF, Sam68, SC35, SF2/ASF, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
5051	Complex	2.22	6.39E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha,
FGF1	Exon Cassette	2.31	5.88E-05	HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
DPYSL3	Complex	5.80	3.00E-06	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
PHYKPL	Complex	1.57	6.56E-03	ETR-3, Fox-1, Fox-2, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, KSRP, Nova-1, Nova-2, Sam68, SC35, SRp200, SRp30c, YB-1, ZRANB2
TFAP2A-AS1	Intron Retention	1.70	8.70E-03	ETR-3, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP P (TLS), KSRP, Nova-1, Nova-2, Sam68, SC35, SF2/ASF, TIA-1, TIAL1, YB-1
CDKAL1	Alter. Terminal Exon (e8-17)	1.83	1.08E-02	9G8, CUG-BP1, ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
PRSS16	Exon Cassette	4.45	7.56E-05	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, PSF, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
HLA-E	Complex	1.69	7.99E-04	Fox-1, Fox-2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), MBNL1, Nova-1, SC35, SRp20, SRp30c, YB-1, ZRANB2
	Alter. Terminal Exon (e10-11)	1.53	1.80E-03	FTR-3. bnRNP A1. bnRNP A2/B1. bnRNP C1. bnRNP F1. bnRNP F2. bnRNP F. bnRNP H1. bnRNP H2. bnRNP H2. bnRNP H2. bnRNP F. (bnRNP P. (TLS). HTra2beta1. HuB. HuD. KSRP. MBNI 1. Nova-1. RBM5. Sam68. SC35.
ATAT1	Complex	1.52	7.61E-05	SF1, SRb20, SRb30c, TIA-1, TIAL1, YB-1, ZRANB2
	Intron Retention	1.81	3.94E-03	
MSH5-SAPCD1	Alter. Acceptor Site	1.71	2.88E-03	CUG-BP1, ETR-3, hnRNP A1, hnRNP A2, B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP F (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1,
// SAPCDI	Exon Cassette	1.6/	5.61E-04	
SKIV2L	Intron Retention	1.//	1.69E-02	CUG-BP1, EIR-3, F0X-1, F0X-2, F0X-1P41, F0RRWP Z/B1, F0RRWP C1, F0RRWP C1, F0RRWP C2, F0RRWP F1, F0RRWP F1, F0RRWP F2, F0RRWP F1, F0
	Alter. Donor Site	3.00	1.65E-04	MDILL; NUX#1, NUX#2, SAIIDO, SUS3, SF1, SF2/RSF, SND2U, SND3UC, INF1, IAL1, IDF1, ZANDZ TT2 2, Car J, DENDRA L-DENDRA (D LENDR 2) LENDR 2) LENDR 2 LENDR 2 LENDR 2 LENDR 2 LENDR 1/LENDR 1/LENDR 2/LENDR 2/L
HLA-DPB1	Alter. Terminal Exon (e2-4)	3.13	1.44E-06	
LIMCA1	Complex	1.06	1.025.02	Nort, molect, nover, nover, nover, nover, nover, samoo, see, si, shee, sheeper, net, net, net, net, net, net, net, net
TIMOAT	Complex	3 20	3.84E-04	
τιδρ1	Evon Cassette	4 51	4 14E-05	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, PSF, RBM5, Sam68, SC35, SRp30c, TIA-1,
10/11 1	Intron Retention	1.76	7 42F-03	TIAL1, YB-1, ZRANB2
VEGFA	Alter. First Exon (e1-3)	1.68	2.76E-03	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
DIMC 1	Alter. First Exon (e7,e10-22,e25,e30)	2.20	5.36E-04	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP D1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS),
NIWI31	Exon Cassette	2.66	1.81E-07	HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
	Alter. Terminal Exon	2.74	3.87E-05	
CD109	Alter. Terminal Exon	2.70	4.39E-05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD,
CD109				
00105	Complex	2.78	3.87E-05	KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, IDP43, IIA-1, IIAL1, YB-1, ZRANB2
	Complex Complex	2.78 2.74	3.87E-05 4.39E-05	KSRP, MBNLI, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp2U, SRp3Uc, IDP43, IIA-1, IIALI, YB-1, ZKANB2
DOPEY1	Complex Complex Alter. First Exon (e1)	2.78 2.74 1.85	3.87E-05 4.39E-05 4.78E-03	KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SKp2U, SKp3Uc, IDP43, IIA-1, IIAL1, YB-1, ZKANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
DOPEY1 C6orf165 // SLC35A1	Complex Complex Alter. First Exon (e1) Alter. First Exon (e1-11)	2.78 2.74 1.85 1.55	3.87E-05 4.39E-05 4.78E-03 2.83E-04	KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SKp2U, SKp3Uc, IDP43, IIA-1, IIAL1, YB-1, ZKANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H, hnRNP F, KhRNP F, KhRNP F, KhRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp2O, SRp3Oc, TDP43, TIA-1, TIAL1, YB-1, ZKANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp2O, SRp3Oc, TDP43, TIA-1, TIAL1, YB-1, ZKANB2
DOPEY1 C6orf165 // SLC35A1 SOBP	Complex Complex Alter. First Exon (e1) Alter. First Exon (e1-11) Alter. Terminal Exon (e7-11)	2.78 2.74 1.85 1.55 1.65	3.87E-05 4.39E-05 4.78E-03 2.83E-04 2.90E-03	KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SKp20, SKp30c, IDP43, IIA-1, IIAL1, YB-1, ZKANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
DOPEY1 C6orf165 // SLC35A1 SOBP DCBLD1	Complex Complex Alter. First Exon (e1) Alter. First Exon (e1-11) Alter. Terminal Exon (e7-11) Alter. First Exon (e1)	2.78 2.74 1.85 1.55 1.65 8.42	3.87E-05 4.39E-05 4.78E-03 2.83E-04 2.90E-03 4.95E-04	 KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SKp2U, SKp3Uc, IDP43, IIA-1, IIAL1, YB-1, ZKANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP D, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP F, hnRNP F, hnRNP F, hnRNP H2, hnRNP F, hnRNP F,
DOPEY1 C6orf165 // SLC35A1 SOBP DCBLD1	Complex Complex Alter. First Exon (e1) Alter. First Exon (e1-11) Alter. Terminal Exon (e7-11) Alter. First Exon (e1) Alter. First Exon (e1)	2.78 2.74 1.85 1.55 1.65 8.42 4.78	3.87E-05 4.39E-05 4.78E-03 2.83E-04 2.90E-03 4.95E-04 7.65E-05	 KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SKp20, SKp30c, 1DP43, 1IA-1, 1IAL1, YB-1, ZKANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF20, SKp30c, TDP43, TIA-1, TIAL1, YB-1, ZKANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP D, hnRNP D, hnRNP DL, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2, SKp30c, TDP43, TIA-1, TIAL1, YB-1, ZKANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZKANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZKANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP D, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP F (TLS), HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZKANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP D, hnRNP D, hnRNP E1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP F (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, NOva-2, NOVA-2,
DOPEY1 C6orf165 // SLC35A1 SOBP DCBLD1 SMPDL3A	Complex Complex Alter. First Exon (e1) Alter. First Exon (e1-11) Alter. Terminal Exon (e7-11) Alter. First Exon (e1) Alter. First Exon (e1) Exon Cassette	2.78 2.74 1.85 1.55 1.65 8.42 4.78 3.28	3.87E.05 4.39E.05 4.78E.03 2.83E.04 2.90E.03 4.95E.04 7.65E.05 1.35E.06	 KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SKp20, SKp30c, 1DP43, 1IA-1, 1IAL1, YB-1, ZKANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP F (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
DOPEY1 C6orf165 // SLC35A1 SOBP DCBLD1 SMPDL3A	Complex Complex Alter. First Exon (e1) Alter. First Exon (e1-11) Alter. Terminal Exon (e7-11) Alter. First Exon (e1) Alter. First Exon (e1) Exon Cassette Alter. First Exon (e1)	2.78 2.74 1.85 1.55 1.65 8.42 4.78 3.28 6.09	3.87E.05 4.39E.05 4.78E.03 2.83E.04 2.90E.03 4.95E.04 7.65E.05 1.35E.06 3.71E.06	 KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SKp20, SKp30c, 1DP43, 1IA-1, 1IAL1, YB-1, ZKANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E1, hnRNP E1, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-2, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP F (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, F
DOPEY1 C6orf165 // SLC35A1 SOBP DCBLD1 SMPDL3A TPD52L1	Complex Complex Alter. First Exon (e1) Alter. First Exon (e1-11) Alter. Terminal Exon (e7-11) Alter. First Exon (e1) Alter. First Exon (e1) Exon Cassette Alter. First Exon (e1) Alter. Terminal Exon (e8-9)	2.78 2.74 1.85 1.55 1.65 8.42 4.78 3.28 6.09 3.59	3.87E-05 4.39E-05 4.78E-03 2.83E-04 2.90E-03 4.95E-04 7.65E-05 1.35E-06 3.71E-06 8.38E-07	 KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SKp20, SKp30c, 1DF43, 1IA-1, 1IAL1, YB-1, ZKANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP D, hnRNP D, hnRNP DL, hnRNP E2, hnRNP F2, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP F1 (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E1, hnRNP F1, hnRNP H2, hnRNP F1, hnRNP F1 (PTB), hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP F (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-1, Fox-2, hnRNP A
DOPEY1 C6or1165 // SLC35A1 SOBP DCBLD1 SMPDL3A TPD52L1 NC0A7	Complex Complex Alter. First Exon (e1) Alter. First Exon (e1-11) Alter. Terminal Exon (e7-11) Alter. First Exon (e1) Alter. First Exon (e1) Exon Cassette Alter. First Exon (e1) Alter. Terminal Exon (e8-9) Alter. Acceptor Site	2.78 2.74 1.85 1.55 8.42 4.78 3.28 6.09 3.59 5.14	3.87E-05 4.39E-05 4.78E-03 2.83E-04 2.90E-03 4.95E-04 7.65E-05 1.35E-06 3.71E-06 3.38E-07 9.75E-05	 KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SKp20, SKp30c, 1DP43, 1IA-1, 1IAL1, YB-1, ZKANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP D, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP D, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP D, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-1, Fox-2, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP D, hnRNP F, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP F, K, hnRNP P (TLS), HTra2beta1, HuB, HuD, HuZ, Stams, Stams,
DOPEY1 C6orf165 // SLC35A1 SOBP DCBLD1 SMPDL3A TPD52L1 NCOA7	Complex Complex Alter. First Exon (e1) Alter. First Exon (e1-11) Alter. Terminal Exon (e7-11) Alter. First Exon (e1) Alter. First Exon (e1) Exon Cassette Alter. First Exon (e1) Alter. Acceptor Site Alter. First Exon (e3,e5,e7-14)	2.78 2.74 1.85 1.55 8.42 4.78 3.28 6.09 3.59 5.14 1.96	3.87E-05 4.39E-05 4.78E-03 2.83E-04 2.90E-03 4.95E-04 7.65E-05 1.35E-06 3.71E-06 8.38E-07 9.75E-05 6.62E-04	 KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SKp20, SKp30c, 1DF43, 1IA-1, 1IAL1, YB-1, ZKANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF20, SKp30c, TDP43, TIA-1, TIAL1, YB-1, ZKANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SKp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZKANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2abeta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZKANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP D1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP F (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZKANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP D, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP F (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZKANB2 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP F, hnRNP H1, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZKANB2 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E2, hnRNP F, hnRNP H1
DOPEY1 C6ort165 // SLC35A1 SOBP DCBLD1 SMPDL3A TPD52L1 NCOA7 TRMT11	Complex Complex Alter. First Exon (e1) Alter. First Exon (e1-11) Alter. Terminal Exon (e7-11) Alter. First Exon (e1) Alter. First Exon (e1) Exon Cassette Alter. First Exon (e1) Alter. First Exon (e2) Alter. First Exon (e3,e5,e7-14) Alter. Terminal Exon (e12-16)	2.78 2.74 1.85 1.55 8.42 4.78 3.28 6.09 3.59 5.14 1.96 1.58	3.87E-05 4.39E-05 4.78E-03 2.83E-04 2.90E-03 4.95E-04 7.65E-05 1.35E-06 3.71E-06 8.38E-07 9.75E-05 6.62E-04 1.74E-02	 KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SKp2U, SKp3UC, IDF43, IIA-1, IIAL1, YB-1, ZKANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp2O, SRp3Oc, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP D, hnRNP D, hnRNP DL, hnRNP E2, hnRNP F2, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp2O, SRp3Oc, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP D, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp2O, SRp3Oc, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP D, hnRNP D, hnRNP DL, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam66, SC35, SF1, SRp2O, SRp3Oc, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP D, hnRNP D, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp2O, SRp3Oc, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E2, hnRNP F, hnRNP F, hnRNP H1, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp2O, SRp3Oc, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 GG6, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnR
DOPEY1 C6orf165 // SLC35A1 SOBP DCBLD1 SMPDL3A TPD52L1 NCOA7 TRMT11 L3MBTL3	Complex Complex Alter. First Exon (e1) Alter. First Exon (e1-11) Alter. Terminal Exon (e7-11) Alter. First Exon (e1) Alter. First Exon (e2) Alter. Acceptor Site Alter. Terminal Exon (e3,e5,e7-14) Alter. Terminal Exon (e12-16) Exon Cassette	2.78 2.74 1.85 1.55 8.42 4.78 3.28 6.09 3.59 5.14 1.96 1.58 5.99	3.87E-05 4.39E-05 4.78E-03 2.83E-04 2.90E-03 4.95E-04 7.65E-05 1.35E-06 3.71E-06 3.38E-07 9.75E-05 6.62E-04 1.74E-02 2.64E-04	 KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SKp20, SKp30c, 1DP43, 1IA-1, 1IAL1, YB-1, ZKANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP D, hnRNP D, hnRNP DL, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP D, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP D, hnRNP D, hnRNP DL, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP D, hnRNP D, hnRNP DL, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 eTR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP DL, hnRNP E2, hnRNP F, hnRNP H1, hnRNP P (TLS), HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP D
DOPEY1 C6orf165 // SLC35A1 SOBP DCBLD1 SMPDL3A TPD52L1 NCOA7 TRMT11 L3MBTL3 ULBP2	Complex Complex Alter. First Exon (e1) Alter. First Exon (e1-11) Alter. Terminal Exon (e7-11) Alter. First Exon (e1) Alter. Terminal Exon (e8-9) Alter. Terminal Exon (e3-65,e7-14) Alter. Terminal Exon (e12-16) Exon Cassette Alter. Terminal Exon (e4-5)	2.78 2.74 1.85 1.55 8.42 4.78 3.28 6.09 3.59 5.14 1.96 1.58 5.99 2.23	3.87E-05 4.39E-05 4.78E-03 2.83E-04 2.90E-03 4.95E-04 7.65E-05 1.35E-06 8.38E-07 9.75E-05 6.62E-04 1.74E-02 2.64E-04 3.76E-04	 KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SKp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D1, hnRNP D1, hnRNP E1, hnRNP E4, hnRNP F1, hnRNP F4, hnRNP H1, hnRNP H2, hnRNP F (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP D, hnRNP P (TLS), hnRNP F4, hnRNP F1 (PTB), hnRNP F4, hnRNP F1, hnRNP F2, hnRNP F1, hnRNP F2, hnRNP F1, hnRNP F4, hnRNP F4, hnRNP F4, hnRNP F4, hnRNP C1, hnRNP C1, hnRNP D, hnRNP D, hnRNP P1, hnRNP F2, hnRNP F4, hnRNP F1 (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 GG8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP D, hnRNP P (TLS), hnRNP F2, hnRNP F4, hnRNP F1, hnRNP F4, hnRNP F1
DOPEY1 C6orf165 // SLC35A1 SOBP DCBLD1 SMPDL3A TPD52L1 NCOA7 TRMT11 L3MBTL3 ULBP2 ZDHHC14	Complex Complex Alter. First Exon (e1) Alter. First Exon (e1-11) Alter. Terminal Exon (e7-11) Alter. First Exon (e1) Alter. Terminal Exon (e3) Alter. Acceptor Site Alter. Terminal Exon (e1-6) Exon Cassette Alter. Terminal Exon (e1-2-16) Exon Cassette Alter. Terminal Exon (e4-5) Alter. Acceptor Site	2.78 2.74 1.85 1.55 1.65 8.42 4.78 3.28 6.09 3.59 5.14 1.96 1.58 5.99 2.23 2.65	3.87E-05 4.39E-05 4.78E-03 2.83E-04 2.90E-03 4.95E-04 7.65E-05 1.35E-06 3.71E-06 8.38E-07 9.75E-05 6.62E-04 1.74E-02 2.64E-04 3.76E-04 1.01E-04	 KSRP, MBNL1, Nova-1, Nova-2, PSF, RBMS, Sam68, SC35, SF1, SF2/ASF, SKp20, SKp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP F (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP P (TLS), hnRNP F (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HK, SRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP F (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HK, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SP2/OS, SP30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2 9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, h

C6orf70	Exon Cassette	2.10	1.60E-02	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
ΑΤΥΝΙ1	Complex	2.11	9.78E-04	9G8, CUG-BP1, ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP LL,
AIANI	Exon Cassette	2.22	2.19E-04	hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
ZNF204P	Alter. First Exon (e1-3)	1.61	1.74E-02	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
GNL1	Complex (e1-7)	1.61	3.78E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta 1, HuB, KSRP, MBNL1, Nova-1, PSF, RBM5, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
HLA-DQB1	Alter. First Exon (e1)	1.78	1.41E-04	ETR-3, Fox-1, Fox-2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, PSF, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1
	Alter. Terminal Exon (e3)	2.20	2.22E-03	
HLA-DMB	Exon Cassette	2.44	4.19E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E2, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, PSF, DPME 5 CPA2 0 CPA2 1 HUL XP1 2 FUE 2 FUE 2 CPA2 1 HUL XP1 2 FUE
	Mutualy Exclusive Exons (e4)	1.92	1.52E-03	ndino, 30/30, 3n/200, 11/41, 11/41, 11/41, 11/41, 11/41, 11/41, 11/41, 11/41, 11/41, 11/41, 11/41, 11/41, 11/41
DEVIC	Alter. Terminal Exon (e9,e10-18)	1.58	2.38E-02	ETR-3, Fox-1, Fox-2, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F5, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF2/ASF,
PEX6	Complex (e11-12)	1.55	3.06E-03	SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
0111.7	Alter. First Exon (e9-10)	1.51	7.85E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP D1, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-
CUL/	Intron Retention	1.97	5.53E-05	1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
ENPP5	Exon Cassette	4.01	5.82E-05	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1
ME1	Exon Cassette	1.71	2.22E-02	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
DADCO	Alter. Donor Site	1.55	1.53E-02	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1,
RARGZ	Alter. First Exon (e1)	2.38	4.16E-03	HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
USP45	Exon Cassette	2.57	3.39E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
00//10	Complex	1.75	1.72E-03	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP F (TLS),
CDK19	Exon Cassette	1.71	2.78E-03	HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
TRAF3IP2	Exon Cassette	1.93	2.12E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
EVN	Exon Cassette	3.35	1.22E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2,
1 IN	Mutualy Exclusive Exons (e11)	2.30	1.22E-04	Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
CEP85L	Alter. First Exon (e4)	1.69	4.96E-02	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
	Complex	7.69	1.85E-05	
EPB41L2	Exon Cassette	9.63	1.71E-05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP,
	Alter. First Exon (e2-3)	2.92	1.64E-04	MBNL1, Nova-1, Nova-2, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
	Exon Cassette	2.30	2.96E-04	
ADAT2	Alter. First Exon (e1)	1.94	7.22E-04	CUG-BP1, ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP F, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
ULBP3	Complex	6.21	4.08E-06	ETR-3, hnRNP A1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1,
SFT2D1	Intron Retention	1.62	1.35E-02	ETR-3, hnRNP A1, hnRNPA2/B1, hnRNP C1, hnRNP F, hnRNPH1, hnRNPH2, hnRNP (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova1, Nova2, Sam68, SC35, SRp30c, TIA-1, TIAL1, YB-1
PHF10	Alter. Terminal Exon (e12)	1.88	4.36E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
IQCE	Exon Cassette	1.66	1.14E-02	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, HuD,
SDK1	Alter. First Exon (e27-40)	1.53	2.36E-02	KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
RBAK// RBAKDN // RNF216P1	Alter. Terminal Exon (e15)	1.67	1.54E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
PMS2CL	Alter. Terminal Exon (e5-15)	3.23	6.40E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRo20, SRo30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
MPP6	Exon Cassette	1.50	1.22E-02	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP D1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MRNI 1, Nova-2, PSE, RBM5, Sam68, SC35, SF1, SF2/ASE, SRo20, SRo30c, TDP43, TIA-1, TIA-1, YB-1, ZRANR2
AQP1//FAM188 B // INMT	Complex (e27,e31)	2.31	7.57E-05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP D1, hnRNP E1, hnRNP E2, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MRN1, Nova-1, Nova-2, SSR, SSR5, SS25, SS27, ASS, SS25, SS27, S
BBS9	Exon Cassette	2.32	1.02E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP D, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuR, KSRP, MRN1, Nova-1, Nova-2, Sam68, SC35, SF1, SF2/CASE, SRb20, CTA-1, TIAI 1, YB-1, 7RANB2
ZMIZ2	Complex	1.69	1.42E-03	ETR-3, Fox-1, hnRNP A1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF_RBM5_Sam68_SC35_SF1_SF2/ASF_SRb20_SRb30_SRb30_ST1A-1_TIA1_1_YB-1_ZRANR2
CCM2	Exon Cassette	1.61	5.84E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP D1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha,

			1	
				HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
LANCL2	Complex	1.57	9.64E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP DL, hnRNP E2, hnRNP F, hnRNP F1, hnRNP H2, hnRNP F2, hnRNP F4, hnR
CRCP	Exon Cassette	1.55	3.30E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D1, hnRNP DL, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
RHBDD2	Exon Cassette	1.51	5.78E-04	ETR-3, hnRNPA1, hnRNP A2/B1, hnRN C1, hnRNPE1, hnRNPE2, hnRNPF, hnRNPH1, hnRNPH2, hnRNI(PTB), hnRNPK, hnRNPP(TLS), HuB, HuD, KSRP, MBNL1, Nova1, Nova2, PSF, RBM5, Sam68,SC35, SRo20,SRo30c, TDP43, TIA1, TIA11, TIA11, YB1
	Alter, First Exon (e1-6)	1.77	1.39E-02	
CCDC146	Complex	1.69	1.34E-03	HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
STEAP1	Alter. Terminal Exon (e5)	2.64	1.40E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
STEAP2	Alter. First Exon (e2-3)	2.09	4.41E-05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
AKAP9	Exon Cassette	2.13	2.40E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, HuD, MBNL1, Nova-1, Nova-2, Sam68, SC35, SRp20, TIA-1, TIAL1, YB-1, ZRANB2
TRIP6	Exon Cassette	2.98	1.78E-04	hnRNP A1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HuB, KSRP, MBNL1, RBM5, SC35, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
	Alter. Terminal Exon (e18-25)	3.43	7.50E-05	
FOXP2	Complex (e8-9)	1.75	2.10E-03	UU-SPI, EIK-3, F0X-1, F0X-2, F0X-1, F0X-2, F0X-1,
	Exon Cassette	3.68	1.96E-04	n Irazaijila, n Irazuela 1, nub, nub, nub, nub, n
CAV1	Alter. Donor Site	2.99	5.99E-04	ETR-3, hnRNP A1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNPH1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HuB, KSRP, MBNL1, Nova1, RBM5, SC35, SF2/ASF, SRp20c, TIA-1, TIAL1, YB-1
C7orf55 //	Alter. First Exon (e2,e4)	2.02	4.18E-03	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha,
LUC7L2	Exon Cassette	1.73	2.96E-03	HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
CNTNADO	Alter First Even (e1 17)	0.30	1 795 09	9G8, CUG-BP1, ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C, hnRNP C1, hnRNP D1, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP H, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP K, hnRNP
CINTINAP2	Alter. First Exon (e1-17)	9.38	1.78E-08	LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
NUB1	Alter. Terminal Exon (e9)	1.52	1.99E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNI 1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAI 1, YB-1, ZRANB2
PAXIP1-AS2	Alter. Terminal Exon	3.49	4.14E-05	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SRn20, SRn30, TIA-1, TIA-1, TIA-1, TRANB2
PDGFA	Alter. First Exon (e1-2)	1.95	5.55E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, RBMS, Sam68, SG35, SF2/ASE, SRo20, SRo30, TIA-1, TIA1, YR-1, ZRAMB2
PRKAR1B	Alter. First Exon (e1-6,e8-11)	1.70	3.39E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
FTSJ2	Complex	1.72	7.18E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP P (TLS), HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1
RADIL	Exon Cassette	1.79	3.04E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRo20, SRo30c, TIA-1, TIAL1, YB-1, ZRANB2
FAM126A	Exon Cassette	1.58	1.02E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MRN 1, Nova-2, PSE, RBM5, Sam68, SC35, SF1, SF2/ASE, SRo20, SRo30c, TIA-1, TIA-1, YR-1, ZRANR2
POLR2J4	Alter. Terminal Exon (e9-10,e12-15)	2.15	1.79E-04	9G8, CUG-BPI, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1 HuB HuD HuR KSRP MRN1 Nova-1 Nova-2 NSF RBM5 Sam68 SQ35 SE2/ASF SR020 SR030c TDP43 TLA TIAL 1 VA-1 ZRANB2
HUS1	Intron Retention	1.68	7.77E-04	ETR-3. hnRNP C1. hnRNP I (IPTB). hnRNP P (TLS). HuB. KSRP. MBNL1. Nova-1. Nova-2. Sam68. SRo20. SRo30c. TIA-1. TIAL1. YB-1
GUSB	Intron Retention	1.56	7.79E-05	ETR-3, hnRNP C1, hnRNP H, hnRNP H, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Sam68, SC35, SF2/ASF, SRo20, TIA-1, TIAL1, YB-1, ZRANB2
TBL2	Alter. Acceptor Site	1.66	2.88E-03	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSE, RBM5, Sam68, SC35, SRn30c, TDP43, TIA-1, TIA-1, TIA-1, TRANB2
STX1A	Complex	1.85	2.11E-05	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, RBM5 Sam68 S035 SF2/ASF SR0/0 SR300 TLA_1 TLA1 1 YE-1 7RANB2
SEMA3C	Alter. First Exon (e2)	1.64	1.51E-02	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SC2/ASE, SRp20, Spa30, TDP43, TLA1, TLA1, VB-1, ZRAMR2
ASNS	Exon Cassette	1.77	1.16E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sarda S, Sarda
GAI 3ST4/GPC2	Complex	2.03	2.18F-04	CIIG-RPT FR3. InRIP AL INRIA 1.03. LINET DAL INTER ALL INRIP F. IN
PMS2P1	Exon Cassette	1.61	3.10E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2, B1, hnRNP C1, hnRNP C1, hnRNP E2, hnRNP F2, hnRNP F1, hnRNP F4, hnRNP H2, hnRNP H2, hnRNP F4, h
C7orf49	Alter. First Exon (e1-4)	1.64	8.56E-04	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP E1, hnRNP E1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, PSF, RBM5, Sam68, SC35, SRp30, SRp30r, TIA-1 TIA1 1, YR-1, ZRANR2
	Alter, First Exon (e1-5.e7-16)	3,37	1.22F-06	CIIG-RPI - FR-3 fox1- Rox2- bnRNP F1 hnRNP A/B1, hnRNP C1, hnRNP D, hnRNP F1, hnRNP F2, hnRNP F hnRNP H1 hnRNP H2 hnRNP H3 hnRNP H3 hnRNP K hnRNP P (TIS) HT/2/heta1 HuR KSRP
KCNH2	Complex	6.20	1.22E-08	MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
· · · · · · · · · · · · · · · · · · ·				

FASTK	Alter. First Exon (e1)	1.59	2.12E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SRp20, SRp30c,
	Intron Retention	1.52	1.14E-02	
PTPRN2	Complex (e1,e4)	1.77	2.52E-03	9G8, CUG-BP1, ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP DL, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP H3, hnRNP H2, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP H2, hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
ESYT2	Exon Cassette	1.69	9.22E-03	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRo20, SRo30c, TIA-1, TIAL1, YB-1, ZRANB2
DPYSL2	Complex	2.43	1.25E-04	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2,B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP H3, hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alaba, HTra2beta1, HuB, HuD, HuB, KSRP, MBNI 1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRo20, SRo30c, TDP43, TIA-1, TIA-1, YB-1, ZRANB2
IKBKB	Exon Cassette	1.74	3.24E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, KSRP, Nova-1, RBM5, Sam68, SC35, SRp20, TIA-1, TIAL1, YB-1
01/01	Alter First Even (s1 E)	4.00	1.005.05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS),
CLV31	Alter: First Exoli (e1-5)	4.00	1.90E-05	HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
VPS13B	Exon Cassette	1.50	1.84E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, PSF, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
RIMS2	Exon Cassette	1.95	5.19E-04	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
MTUS1	Alter. Terminal Exon (e8-9,e11,e13-20)	1.98	6.94E-03	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
ASAH1	Alter. First Exon (e1)	1.72	3.88E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
LZTS1	Complex (e1-2)	2.76	6.18E-05	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
FOEDI	Complex	2.62	4.41E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1,
FGFRI	Exon Cassette	2.58	9.51E-05	HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
MRPS28 // TPD52	Exon Cassette	3.65	6.44E-05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
FIE2E	Alter. First Exon (e1)	1.95	9.24E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP F, hnRNP F, hnRNP H2, hnRNP H2, hnRNP A1, hnRNP P (TLS), HTra2alpha, HTra2beta1,
EIFSE	Alter. Terminal Exon (e6)	1.94	1.26E-02	HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
	Complex (e2,e5-6)	1.58	9.36E-04	
EEF1D	Complex	8.74	1.30E-06	ETR-3, Fox 1, Fox 2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1,
	Exon Cassette	5.26	7.74E-07	Nova-2, PSF, RBMS, Sam68, SC35, SF1, SF2/XSF, SRp30c, TDP43, TIA-1, TIAL1, PSF1, ZRABE2
PLEC	Alter. First Exon (e4)	3.38	7.91E-05	CUG-BP1, E1R-3, Fox-1, Fox-2, INKINP A1, INKINP A2/B1, INKINP D2, INKINP D2, INKINP E2, INKINP F2, INKINP F1, INKINP F2,
CYHR1	Alter. First Exon (e2)	1.68	1.50E-03	ETR-3, hnRNP FI, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), SC35, SF2/ASF, SRp30c, YB-1
COMMD5 //	Alter. First Exon (e1-5,e7-10)	2.29	2.35E-02	
ZNF250	Complex	1.69	1.64E-03	CUG8P1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E1, hnRNP F1, hnRNP H2, hnRNP H2, hnRNP I, hnRNP P (FLS), HTra2beta1, httra2beta1, hnRNP A2/B1, hnRN
	Exon Cassette	4.72	4.41E-04	HuB, HuD, HuK, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SKp20, SKp30c, HA-1, HAL1, YB-1, ZKANB2
	Mutualy Exclusive Exons	2.59	2.52E-03	
CHMP5	Exon Cassette	1.87	5.79E-04	ETR-3, F0x-1, F0x-2, INRIVE A1, INRIVE A2/ B1, INRIVE C1, INRIVE C1, INRIVE E1, INRIVE E2, INRIVE F1, INRIVE F1, INRIVE F2, INRIVE F
TJP2	Complex	1.81	6.35E-04	ETR-3, hnRNP A1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SF2/ASF, SRp30c, TIA-1, TIAL1, YB-1
C9orf89	Alter. First Exon (e1-2)	1.65	1.12E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
DAR2IP	Alter. Acceptor Site	1.56	2.10E-02	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I, hnRNP I, hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2beta1, HuB, HuD,
DADZII	Alter. First Exon (e5-7)	2.06	1.40E-03	KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
NEK6	Alter. First Exon (e2)	1.54	4.36E-02	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
DNM1	Mutualy Exclusive Exons (e10)	2.02	3.45E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
0004	Alter. First Exon (e2-4)	1.50	2.66E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2beta1,
CUQ4	Intron Retention	1.86	1.23E-04	HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
POMT1	Alter. First Exon (e1,e4)	1.61	1.02E-02	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP CL, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5,
100011	Exon Cassette	1.55	2.24E-03	Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
KIAA1984 //	Alter. First Exon (e1-4)	1.97	4.58E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP D1, hnRNP D2, hnRNP F2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H, hnRNP K, hnRNP F, tra2beta1, HuB, KSRP, MBNL1,
RABL6	Alter. Terminal Exon (e25-33)	1.77	2.72E-03	
KIAA0020	Alter. Terminal Exon (e3-19)	2.00	2.90E-02	UG-BF1, E1K-3, F0X-2, DRKNP A1, DRKNP A2, DRKNP C1, DRKNP D, DRKNP D, DRKNP D1, DRKNP D2, DRKNP E2, DRKNP F2, DRKNP F1, DRKNP F2, DRKNP
RFX3	Exon Cassette	1.57	9.30E-03	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2

NFIB	Alter. First Exon (e1,e3)	3.43	1.81E-05	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRo20, SRo30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
ELAVL2	Alter. First Exon (e1,e4)	2.63	4.02E-04	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2ahaba HTra2beta1 HuB HuD HuB KSPP MRNI 1 Nova-1 Nova-2 PSF RBM5 Sam68 SC35 SE1 SE2/ASF SRo20 SRo30 TDP43 TIA1 TIA1 VB-1 ZBANR2
BAG1	Complex	2.23	5.72E-03	ETR-3, Fox-1, Fox-2, hnRNP 41, hnRNP 42, hnRNP 42, hnRNP 02, hnRNP 02, hnRNP 62, hnRNP 6, hnRNP 6, hnRNP 1, hnRNP 1, hnRNP 1 (PTB), hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova- 1, Nova-2, Sam68, SC25, SPo20, SPo30, TIA, 1, TIA, 1, YB-1, ZBAMB2
AOP3	Intron Retention	3.8/	2 38E-04	1, Novae, samoo, ossa, snpev, neva, incat, nevi, incl. 10-1, zovine ETB 2, hopDer Fundburg hi hopDer 10-10 hopDer 0 mil Novae, 1 90-25 SDn20 SDn20 SDn20 - TIA, 1 TIAL 1 VR.1 ZDAND2
	ind on Retendon	3.04	2.30L-04	ETR2 Cav, INITAT 1, INITAT 12, INITAT 1(C), INITAT 1(C), INITAT 1(C), INITAT 1(C), INITAT 1, INITAT 1, INITAT 12, INITAT 1, INITAT 1(C), INITAT 1, INITAT 1(C), INITAT 1, INITAT 1(C), INIT
FAM95C	Alter. Terminal Exon (e16-18,e20-22)	2.85	5.67E-05	KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
TMEM2	Alter. First Exon (e20-22)	2.28	1.06E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
BICD2	Intron Retention	2.08	2.66E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1
IKBKAP	Alter. First Exon (e1-8)	1.61	1.11E-02	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F1, hnRNP H2, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1,
TOR24	Intron Retention	2.25	3.51E-05	TILD, TAU, TSAT, MONTLI, MOVAZ, TOMO, SAITIO, SUSS, ST., ST2/AST, ST2/AST
TONEN	Alter First Even (o1.7)	1.62	4 79E 04	CIC DDI TD 2 Cov 2 hondbar 1 hondbar
SH3GLB2	Intron Retention	2.17	4.70E-04	
	Alter First First (a1 10 a12 a14	2.17	2.232-04	MOLES, HOVES, HOVES, FOR, HOVES, FOR, HOVES, GUID, GUID, HOVES, HIELS, HELS, H
FNBP1	Alter: First Exol1 (e1-10,e12,e14-	1.68	5.36E-04	
-	10,620)			THE DEVELOPMENT AND THE
TTF1	Exon Cassette	2.57	1.85E-04	MRN1 Nova-1 Nova-1 PSF RBM5 Sam68 Sci25 SEP/ASE SRo20 SRo30 CHA1 TIAI 1 YE1 7RANR2
				monte, nova , row to money cannot go occor, or provide in the propose, not a contract, to relate the provide in the provide interval of the provide in
STS	Alter. First Exon (e2)	1.56	8.81E-04	HIGH HURKSEP MENT Nova-19 REMOVED ANT
MSL3	Alter First Exon (e1)	1 78	2 18F-04	
moleo	Alter First Evon (e1)	1.64	2 11E-02	
	Intron Retention	2.10	1 18E-03	ETR-3, hnRNP A1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HuB, KSRP, Nova-1, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
	Introl Retention	2.10	1.102-03	
PRRG1	Complex	5.72	6.12E-05	Hrazbela, Hub, Hub, KSP, MBNL, Nova-J, Nova-2, PSF, RBNS, Sanda, SZ, SFL, SF2/ASF, SR20, SR30, Th4. TH4L YB-1, ZRANB2
RRAGB	Exon Cassette	2.04	7.18E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
7115744	Exon Cassette	2.10	2.18E-03	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP P (TLS), HTra2beta1, HuB, HuD, Nova-1, PSF, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-
ZNF/11	Intron Retention	1.73	4.45E-02	1, ZRANB2, TDP43
CSTF2	Exon Cassette	3.06	5.56E-04	CUG-BP1, ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
	Alter. First Exon (e1)	1.58	1.76E-02	ETR-3. Fox-1. Fox-2. hnRNP A1. hnRNP A2/B1. hnRNP C1. hnRNP E1. hnRNP E2. hnRNP F. hnRNP H1. hnRNP H2. hnRNP H (PTB). hnRNP K. hnRNP P. (TLS). HTra2beta1. HuB. KSRP. MBNL1. Nova-1. Nova-2. PSF.
ALG13	Exon Cassette	2.09	2.16E-03	RBM5, Sam68, SC35, SF2/ASF, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
FHL1	Exon Cassette	5.02	3.75E-05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
MTMR1	Alter. First Exon (e2-3,e5-11)	1.82	1.20E-02	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
ATDODO	Alter. Terminal Exon (e21,e23)	2.23	3.60E-04	9G8, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP,
AIFZDO	Exon Cassette	2.22	1.56E-04	MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
TAZ	Intron Retention	1.83	1.51E-05	hnRNP P (TLS), RBM5, YB-1
GEMIN8	Alter. First Exon (e1)	1.69	2.50E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
40100	Alter. Terminal Exon (e4,e8)	2.05	1.41E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP H, hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD,
AP152	Complex (e5)	2.62	5.41E-04	KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
MAOR	Even Carcotto	1.61	1 965 02	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1,
IWIAUB	EXOII Casselle	1.61	4.00E-03	Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
SMC1A	Alter. First Exon (e1)	1.77	7.90E-03	ETR-3, hnRNP I (PTB), hnRNP P (TLS), Nova-1, SC35, SF2/ASF, TIA-1, TIAL1, YB-1
ARHGEF9	Complex	1.59	1.71E-05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
XIST	Alter. Acceptor Site	1.55	1.04E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB,
	Complex	4.29	1.10E-03	KSRP, MBNL1, Nova-1, Nova-2, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
0002	Alter. First Exon (e1)	12.44	3.56E-05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP LL, hnRNP P (TLS),
6763	Exon Cassette	5.68	3.53E-05	HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2

ATP11C	Exon Cassette	3.08	4.98E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
BCAP31	Alter. First Exon (e3)	1.57	2.12E-05	ETR-3, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Sam68, SC35, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
FAM3A	Exon Cassette	1.73	4.96E-03	ETR-3, hnRNP A1, hnRNP C1, hnRNP F1, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), KSRP, Nova-1, SC35, SRp20, TIA-1, TIAL1, YB-1
MPP1	Exon Cassette	2.10	7.84E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP F (FTB), hnRNP F (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
TRA/TRAC/TRAV	Alter. Term Exon (e35,144,e152-155)	1.74	1.48E-03	9G8, CUG-BP1, ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP H1, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP K, hnRNP K, hnRNP LL,
12-1/TRAV20	Intron Retention	1.69	2.16E-02	hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
LINC00338 // SEC14L1	Alter. Terminal Exon (e8-9,e11-25)	2.34	9.64E-04	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
SDHAP1	Exon Cassette	2.83	3.80E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
GTF2I	Alter. Terminal Exon (e12-35)	1.79	2.06E-05	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
CD99	Alter. Terminal Exon (e3-11)	6.59	4.83E-07	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
	Complex	4.23	2.88E-07	
	Complex	1.83	9.17E-04	
SH3D21	Alter. First Exon (e1-3)	1.84	2.14E-03	ETR-3, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, KSRP, Nova-1, Nova-2, PSF, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1
	Complex	1.59	4.46E-03	
MDM4	Exon Cassette	1.82	1.98E-04	CUG-BP1, E1R-3, Fox-1, Fox-2, INKINP A1, INKINP A2/B1, INKINP C1, INKINP C1, INKINP E1, INKINP E2, INKINP F1, INKINP H1, INKINP H2, INKINP I (P1B), INKINP K, INKINP LL, INKINP P (ILS), H1ra2alpha, H1ra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
PLEKHA5	Alter. First Exon (e1)	1.61	8.84E-03	CUG-BP1, ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP K, hnRNP P (TLS),
	Complex	2.50	3.76E-03	HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
	Alter. First Exon (e2)	1.59	3.42E-03	
SLC12A4	Complex (e22-29)	1.78	3.63E-04	903, CUG-BYL, EIK-3, FOX-1, FOX-2, INRIVP AL, INRIVP AL, INRIVP CL, INRIVP EL, INRIVP EL, INRIVP EL, INRIVP F, INRIVP HL, INRIP
	Even Correctto	1.70	3.03E-04	MDHLI, NOVA-2, NUM2, SAINO, SOJ, SI 2/NJ, SN2OC, TH-1, TRL1, TD-1, ZNAND2
	Alter First Evon (e1-2)	2.58	5 15E-04	
SLC13A3	Evon Cassette	2.30	4.03E-05	300, 00-00 r, cites, row, row, may an internal of a mixer of mixer
	Alter, First Exon (e8-12)	3.64	3.40F-03	
AHRR // PDCD6	Exon Cassette	2.02	1.04E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP F4, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP K, hnRNP LL, hnRNP P (TL
///////////////////////////////////////	Intron Retention	2.40	1.36E-03	HIraZalpha, HIraZbeta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, KBM5, Sam68, SC35, SF1, SF2/ASF, SKp20, SKp30c, TDP43, TIA-1, TIAL1, YB-1, ZKANB2
ANXA1	Complex (e2-3)	2.19	1.95E-02	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
MKNK1 // MOB3C	Alter. Terminal Exon (e3-5)	1.67	4.22E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
DIP2B	Alter. First Exon (e1-16)	1.77	4.78E-03	9G8, CUG-BP1, ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2al
CHMP4A/PO4/M	Alter. Donor Site	2.14	2.07E-05	
DP1/NEDD8/TM 9SF1	Alter. Terminal Exon (e24,e25-54)	2.05	2.42E-04	ETR-3, F0X-1, F0X-2, INRIVE A1, INRIVE A2/B1, INRIVE C1, INRIVE C1, INRIVE E1, INRIVE E2, INRIVE F1, INRIVE F1, INRIVE F2, INRI
SDHAP3	Alter. Terminal Exon (e4,e6-8)	1.77	3.21E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, KSRP, MBNL1, Nova-1, Nova-2, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
MAST4	Exon Cassette	3.19	2.66E-03	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H2, hnRNP K, hnRNP P (TLS), HTra2beta1, HuB, HuD, KSRP, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
ZNRD1-AS1	Alter. First Exon (e1)	1.51	1.14E-02	ETR-3, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HuB, KSRP, Nova-1, PSF, Sam68, SC35, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
ATF6B	Complex	1.54	2.62E-04	ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP C1, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF2/ASF, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2
	Alter. First Exon (e6-7,e9,e11)	2.94	5.96E-05	9G8, CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS),
BLUGIS5/EEFIE 1/TXNDC5	Alter. Terminal Exon (e7,e9,e11-12)	1.82	1.03E-02	
1/ TANDUS	Exon Cassette	1.60	1.84E-03	1112 Legina, 1112 Lower, 1102, 1101, 1111,
PCSK5	Alter. Terminal Exon (e7-22)	3.29	1.17E-04	9G8, CUG-BP1, ETR-3, FMRP, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP DL, hnRNP DL, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP LL,
	Exon Cassette	3.37	1.06E-03	hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, HuR, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
SLC16A10	Alter. Terminal Exon (e3)	1.59	7.04E-03	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP DL, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP H3, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, HuD, KSRP, MBNL1, Nova-1, Nova-2, PSF, RBM5, Sam68, SC35, SF1, SF2/ASF, SRp20, SRp30c, TDP43, TIA-1, TIAL1, YB-1, ZRANB2
NBPF10 // NOTCH2NL	Complex	2.18	6.17E-04	CUG-BP1, ETR-3, Fox-1, Fox-2, hnRNP A1, hnRNP A2/B1, hnRNP C1, hnRNP D, hnRNP E1, hnRNP E2, hnRNP F, hnRNP H1, hnRNP H2, hnRNP I (PTB), hnRNP K, hnRNP P (TLS), HTra2alpha, HTra2beta1, HuB, KSRP, Nova-1, Sam68, SC35, SF1, SRp20, SRp30c, TIA-1, TIAL1, YB-1, ZRANB2