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Pluralistic and stochastic gene regulation: examples, models and consistent theory

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ABSTRACT

We present a theory of pluralistic and stochastic gene regulation. To bridge the gap between empirical studies and mathematical models, we integrate pre-existing observations with our meta-analyses of the ENCODE ChIP-Seq experiments. Earlier evidence includes fluctuations in levels, location, activity, and binding of transcription factors, variable DNA motifs, and bursts in gene expression. Stochastic regulation is also indicated by frequently subdued effects of knockout mutants of regulators, their evolutionary losses/gains and massive rewiring of regulatory sites. We report wide-spread pluralistic regulation in ≈800 000 tightly co-expressed pairs of diverse human genes. Typically, half of ≈50 observed regulators bind to both genes reproducibly, twice more than in independently expressed gene pairs. We also examine the largest set of co-expressed genes, which code for cytoplasmic ribosomal proteins. Numerous regulatory complexes are highly significant enriched in ribosomal genes compared to highly expressed non-ribosomal genes. We could not find any DNA-associated, strict sense master regulator. Despite major fluctuations in transcription factor binding, our machine learning model accurately predicted transcript levels using binding sites of 20+ regulators. Our pluralistic and stochastic theory is consistent with partially random binding patterns, redundancy, stochastic regulator binding, burst-like expression, degeneracy of binding motifs and massive regulatory rewiring during evolution.

INTRODUCTION

Most disease-associated mutations are located outside of protein coding regions, likely affecting transcriptional regulation or chromosomal organization (1,2). To draw objective and *consistent* biological and clinical conclusions from the over two million human genomes to be sequenced by 2020 (3), we need new models and theories of gene regulation that are highly consistent with observations and minimally biased (4). Almost inherent biases include the number and selection of transcriptional regulators (TRs), knockout mutants, amplification and sequencing bias. However, we can avoid biased interpretation. Struggling with vast complexity, human perception is naturally biased toward simplifications. Many simplifications had been practical before the Encyclopedia of DNA Elements (ENCODE) Project (5) probed the complexity of transcriptional regulation. In the *lac* operon and similar prokaryotic models, only a few agents regulate each target gene (6). These models were extrapolated to higher eukaryotes, which regulate gene expression by over a thousand sequence- or shape-specific transcription factors, histone modifying enzymes and chaperones (for brevity, TRs; 7). To handle this complexity, diverse concepts of master regulators were introduced. This term occurs in over 28 700 publications, two-thirds of which are related to cancer or cellular differentiation according to our full-text Scopus search. We present multiple lines of evidence that typically, rather than singular master regulators or oligarchies, large numbers of TRs regulate genes. We report and test our pluralistic and stochastic, minimally biased computational models. Stochastic is defined as 'partially randomly determined; a process that follows some random probability distribution or pattern, so that its behavior may be analyzed statistically but not predicted precisely' (8) (quoted verbatim in the Oxford English Dictionary as well). At first glance, stochastic processes may appear vague. Inherently, they are more difficult to understand, reproduce and verify than comparable deterministic processes. Hence demanding high reproducibility leads to ignoring mid-to-low probability events. However, stochastic models allow for more accurate predictions than deterministic simplifications. For example, differentiated fibroblasts

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can be reprogrammed into pluripotent stem cells in multiple ways (9). OCT4 and SOX2, two essential but insufficient agents, along with either KLF4 and MYC (10) or NANOG and LIN28 (11) can induce such reprogramming. Stochasticity means that either KLF4 and MYC or NANOG and LIN28 can bind in partially random processes (but with similar effects). These four TRs bind to pluripotency targets with probabilities much below certainty but higher than those TRs that cannot induce pluripotency. In this well-established example, deterministic master regulators were replaced by stochastic regulation (12). Similar probabilistic patterns form the very essence of this publication.

A theory of transcriptional regulation is presented which is consistent with our new results reported here:

- 20–25 TRs bind reproducibly in ≈800 000 co-expressed gene pairs, indicating pluralistic regulation.
- 20 or more TRs are needed to predict transcript levels of cytoplasmic ribosomal protein genes (cRPGs).
- TR binding shows stochastic enrichment patterns in cRPGs compared to high-expression non-ribosomal genes (HE-NRGs).

Pluralistic and stochastic gene regulation is also supported by a novel synthesis of earlier observations:

- Cellular levels, location, activity and binding of TRs and polymerases undergo major fluctuations
- Transcription bursts and pauses even in the genes of TRs themselves (11,13–16)
- A wide variety of ≈1700 human DNA-associated proteins have evolved and been preserved (7)
- Transcription factors bind with different strength and regulatory effect to highly variable DNA motifs/shapes (17)
- Several double knockout mutants of TRs are viable (18)
- Several TRs have been replaced during evolution (Table 1) and their binding sites have been rewired even between human and mouse (19).

Surprisingly, as we will show in the Discussion, *concepts* of master regulators have already evolved from strict hierarchies to more participative regulation. We continue this trend by integrating the above observations with highly sophisticated stochastic models and computational simulations of transcriptional regulation (9,13,20–26), which were partly validated by experiments (16). To help the experimental community to embrace stochastic gene regulation, we propose a theory of widespread pluralistic and stochastic regulation based on the above wide spectrum of evidence.

MATERIALS AND METHODS

We analyzed six human and two murine cell lines for which twenty or more regulators have been mapped by the (mouse) ENCODE Project to the *hg19, hg38* and *mm9* genome assemblies. Two pairs of cell lines are comparable across human and mouse: myelogeneous leukemia (K562 and MEL) and lymphoblastoid (GM12878 and CH12.LX). Additional human cell types include embryonic stem cells (h1-hESC1), hepatocarcinoma (HepG2), adenocarcinoma (A549) and cervical cancer (HeLa-S3) cells. Pseudogenes were eliminated, leaving 98 human and 87 mouse cRPGs and 84 human and 76 mouse mRPGs (Supplementary Table S1). cRPGs and mRPGs were compared to either all non-ribosomal genes (NRGs), or their subset, the HE-NRGs (Supplementary Table S2). We compare cRPGs to 169 human and 107 mouse HE-NRGs, the latter defined as genes expressed at higher levels than the least intensively expressed 25% of cRPGs in the Expression Atlas (27). All data have been stored in our MySQL relational database and queried by a PERL Database Interface library and scripts. The human part of the MySQL Database, its documentation, and all the gene pairs with the number of jointly bound and separately bound TRs, are available at our web site: https://git.unl.edu/sladunga2/genereg/tree/master. Other data can be obtained upon request.

TR binding site observations derived from chromatin immunoprecipitation combined with deep sequencing (ChIP-Seq) were downloaded from the ENCODE web sites (https://www.encodeproject.org). Gene coordinates and annotations were taken from the ENSEMBL annotations (Homo_sapiens.GRCh37.59.gtf and Mus_musculus.NCBIM37.67.gtf). From among overlapping gene annotations, the longest splice variant was chosen. Binding sites were mapped to genes as follows: when a binding site was localized within a gene's coding sequence or its up- or downstream 5000 base pair environment (excluding potentially overlapping genes), the binding site was associated with the gene. Five thousand base pairs represent a compromise between the inclusion of not overly distant enhancer regions and the minimization of the number of TRs that do not affect the transcription of the particular gene. To examine the impact of selecting the longest coding regions with 5000 base pair upstream and downstream segments (Gene5kb), we compared the results to the most frequent transcripts and to predicted 600 base pair promoter regions in K562 cells (Supplementary Information, Figure S4 and Tables S4 and S5). The predicted promoter regions largely reproduced the Gene5kb patterns of enrichments although with higher fold changes.

Statistical analyses

High genewise counts of single TRs allowed evaluating the statistical significance of enrichment using the Wilcoxon–Mann–Whitney test. Due to the lower genewise counts of TR dimers and trimers, enrichment was assessed using Fisher's exact test. Both tests are robust against large differences in sample size. Unless otherwise noted, all results reported here are statistically significant at the 0.01 level after multiple test correction by tailwise False Discovery Rate (28).

Statistical/machine learning models

How many TRs are necessary to relatively accurately predict transcript levels from TR binding sites? To answer this question, we use Least Angle Regression (LARS) (29). LARS applies ordinary least squares to minimize the sum of the absolute values of weights assigned to generalized linear models. This parsimonious feature works as Occam's razor by regressing transcript levels using the fewest possible TRs. LARS performs cross-validation, i.e. training the

Table 1. Few regulators of human cRPGs have orthologs in *Saccharomyces cerevisiae*. A few double knockout mutants of the orthologous mouse genes are still viable

Regulator		Mouse mutant phenotype	
human	*Scer*	-/-	+/-
IRF1		phenotype	phenotype
SIX5		phenotype	phenotype
BRCA1		phenotype	phenotype
MYC		lethal	phenotype
KAT2A	GCN5	lethal	reduced transcription elongation
ETS1		partially lethal	phenotype
ELK1		mostly normal	normal
GTF2B	SUA7	lethal	?
ZZZ3		lethal	lethal
TAF1	TAF1		phenotype
TAF7	TAF7	lethal	phenotype
ATF2	ATF2	phenotype	phenotype
HDAC6	HDA1	normal	normal
RCOR1	SNT1	lethal	phenotype
NFKB1		phenotype	phenotype
CEPB		lethal	normal
CHD1	CHD1	phenotype	phenotype
CJUN		phenotype	phenotype
EJUN		phenotype	phenotype
JUNB		phenotype	phenotype
CTCF	CTCF	lethal	phenotype
MAFF		lethal	phenotype
NELFE		?	phenotype
NFYB	HAP3	?	phenotype
NRF1		lethal	phenotype
RFX5		phenotype	phenotype
SETDB1	SET2	lethal	phenotype/lethal

models on one subset of input data and testing performance on the complementary subset. Transcript levels were taken from the Genevestigator database (30) and from the human and mouse ENCODE experiments (31).

RESULTS

Genome-wide functional pluralistic TR binding in the human genome

We found that TR binding sites were about twice as highly reproducible in 799 695 co-expressed human gene pairs than in 100 000 independently expressed genes in six human cell types. We compared five co-expressed and one independently expressed gene sets: all 4851 gene pairs within cRPGs (Supplementary Table S1), all 3486 pairs of mitochondrial ribosomal protein genes (mRPGs, Supplementary Table S1) and all 14 196 pairs high-expression NRGs (HE-NRG's, Supplementary Table S2). Pseudogenes were eliminated. We considered a gene as a HE-NRG if its median RNA-seq transcript level exceeds the 25$^{\text{th}}$ percentile of the transcript levels in cRPGs in the Expression Atlas Database (32) (Supplementary Table S2, Materials and Methods). We also analyzed 17 846 pairs of very strongly co-expressed genes ($R \geq 0.9$, NRG_A's); 759 316 pairs of strongly co-expressed ($0.9 > R \geq 0.8$) genes (NRG_B's), and a sample of 100 000 independently expressed (abs(R) < 0.1) gene pairs (NRG_C's, Figures 1 and 2). Co-expression was measured by Pearson correlation coefficients of transcript levels for each pair of human protein-coding gene over 120 diverse samples in the Expression Atlas (27) (see Materials and Methods).

We quantified the reproducibility of binding for each TR using a simple adaptation of the Jaccard coefficient: $J = \frac{n_2}{n_1}$ Here n_2 is the number of gene pairs where the TR in question is observed in both genes of the pair and n_1 is the number of gene pairs where the TR is observed in at least one of the two genes.

First, we examined individual TRs and their binding sites. Binding events of PolII, YY1, (C)MYC, KDM5B, TAF1, MAX, PHF8, ELF1 and MAZ are highly reproducible ($J \geq 0.9$) in NRG_A's, cRPGs and HE-NRGs (Figure 1). This high between-gene reproducibility is the lower bound of ChIP-Seq reproducibility in the ENCODE experiments (33), as discussed below. In NRG_C's however, the reproducibility of most TRs remains below 0.25. The only three exceptions are RUNX3, CTCF and RAD21.

Which TRs bind most reproducibly across cell types? To answer this question, we compared the cell-wise distributions of the 50 most reproducibly bound TRs in the six gene pair sets (Figure 2). In the five co-expressed sets of gene pairs, about 25 TRs bind with a median reproducibility exceeding 0.5 compared to 0.23 in independently expressed gene pairs. The interquartile ranges show that reproducibility is very similar in all cell types studied for RUNX3, PolII, PHF8, IRF1, KDM5B, POU2F2, CTCF, RAD21 and CREB1, indicating largely cell-independent functions.

We found that twice as many regulators mapped reproducibly in co-expressed pairs than in independently expressed gene pairs (Figure 3). This difference persists independently of gene length (Supplementary Information and Figure S1). While co-regulated gene pairs tend to be expressed at higher levels than independently transcribed

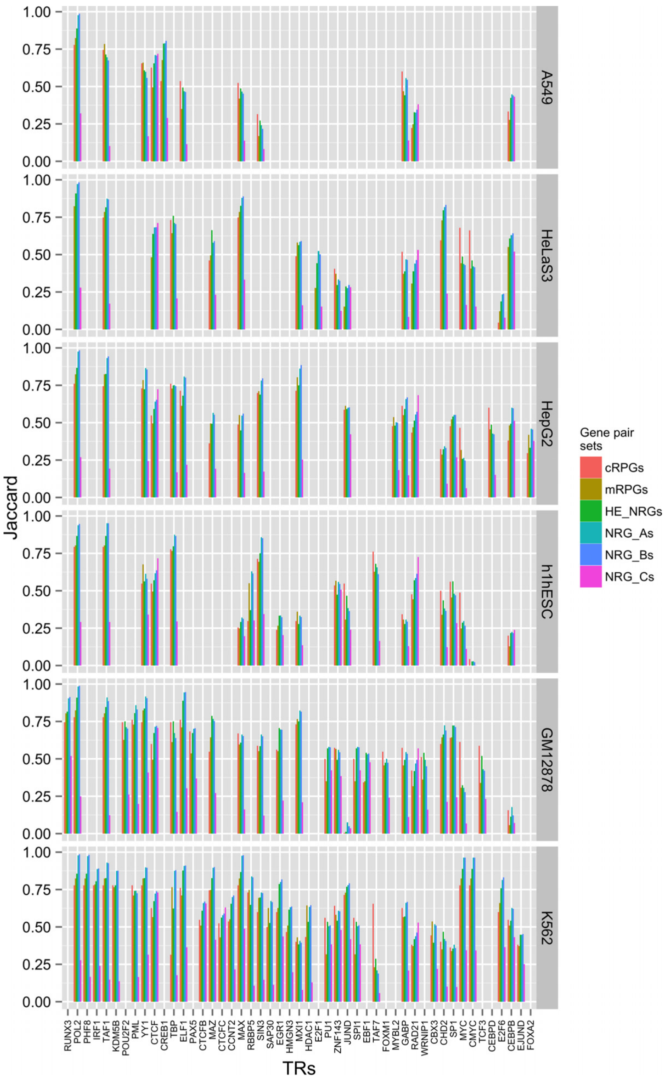


Figure 1. High reproducibility of ChIP-Seq peaks in pairs of co-expressed genes. Jaccard coefficients show reproducibility for the following sets of gene pairs: cRPGs ($n = 4851$ pairs); mRPGs ($n = 3486$); HE_NRGs (high-expression NRGs, $n = 14\,196$, see Materials and Methods); NRG_A's (diverse gene pairs co-expressed with $R \geq 0.9$, $n = 17\,846$); NRG_B's (diverse gene pairs co-expressed with $0.9 > R \geq 0.8$, $n = 759\,316$); and NRG_C's (a sample of independently expressed, diverse gene pairs, $\mathrm{abs}(R) < 0.1$, $n = 100\,000$). TR binding in NRG_C's is about 50% less reproducible than in co-expressed gene sets, indicating that a large portion of the binding events in gene regions is functional.

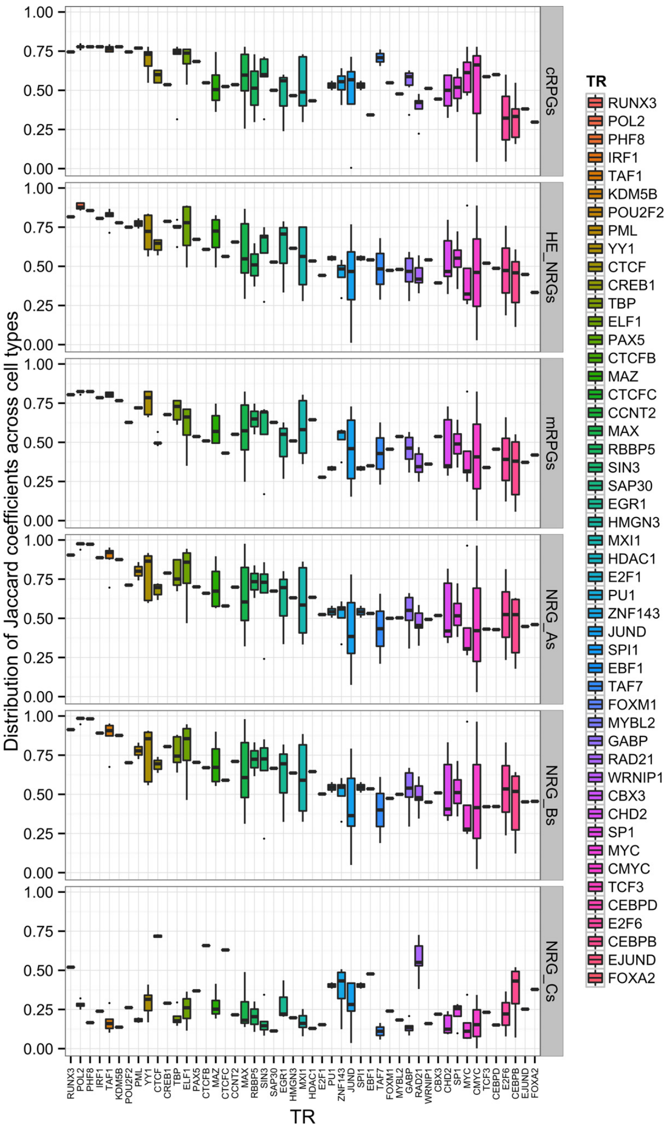


Figure 2. TRs bind with similar reproducibility in diverse human cells. Box plots show the distribution of Jaccard coefficients for individual TR. Sets of gene pairs are defined in Figure 1. In all co-expressed sets of gene pairs, over 25 TRs bind with a median reproducibility exceeding 0.5. In independently expressed gene pairs, reproducibility is only about 0.22, corresponding to the magnitude of nonspecific TR binding. Highly significant differences between co-expressed and independently expressed gene sets ($P < 10^{-256}$, Wilcoxon–Mann–Whitney test) indicate that even those TRs, which bind in highly stochastic processes, may have biological roles.

ones, the effect of co-regulation on reproducibility is much stronger than the level of expression (Supplementary Information and Figure S2). In K562 cells, at least one gene of an independently expressed (NRG_C) pair binds to a median of 62 TRs (Figure 3). Only 10 of these TRs bind to both genes ($J = 0.16$). In highly co-expressed pairs (NRG_A), at least one gene of a pair binds to a median of 75 TRs. Of these, 37 TRs bind to both genes ($J = 0.49$). The significantly more reproducible binding ($P < 10^{-16}$, Fisher's exact test) in co-expressed versus independently expressed gene pairs indicates markedly pluralistic regulation.

Specific model: co-regulation of 98 cRPGS

We present a model based primarily on binding sites of less than three hundred TRs in six human and two murine cell types (Materials and Methods), gain/loss-of-function mutants and evolutionary studies. The ENCODE Consortium mapped these TR binding sites to the human and mouse genomes using Chromatin ImmunoPrecipitation followed by deep sequencing (ChIP-Seq; 5). Despite the strong co-expression of ribosomal protein genes (RPGs, see below), the observed binding patterns of TRs show differences between genes and cell types (Figure 5 and Supplementary Figure S1). As we discuss in Supplementary Information,

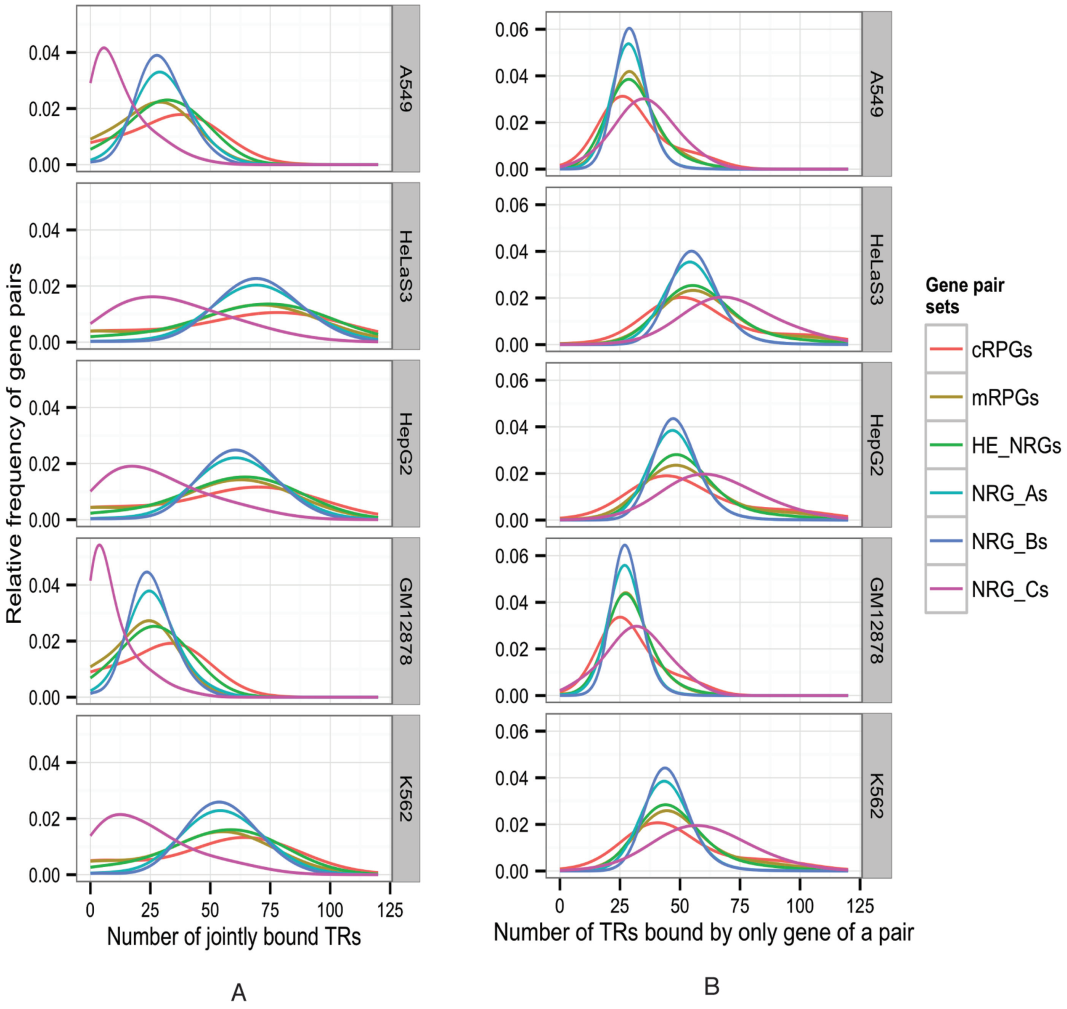


Figure 3. **(A)**. More TRs bind to both genes in co-expressed gene pairs than in independently expressed pairs (NRG_C's, max(P) < 10^{-32}, Wilcoxon test). **(B)** Conversely, fewer TRs bind to only one gene in co-expressed gene pairs than in NRG_C's (max(P) < 10^{-32}). The number of TRs that may be associated with co-regulation depends on the TRs mapped in a cell type. The number of TRs implicated in co-regulation ranges from 25 (in A549 and GM12878 cells) to over 50 (in HeLaS3, HepG2 and K562 cells).

these differences are largely due to stochastic TR binding, not to experimental error.

To increase confidence and to estimate experimental error in TR binding site observations and to narrow the gray zone, it would be ideal to map all regulators in tens of ChIP-Seq replicates for several cell types. However, such a megaproject would cost multiples of the ENCODE Project Consortium's budget. To increase confidence without astronomic costs, we analyze a relatively homogeneous subpopulation of genes, which are tightly co-regulated to minimize waste in synthesizing stoichiometric amounts of ribosomal proteins (34). Each gene serves as an experimental unit, analogously to clinical trials, where individual patients are not replicates but experimental units, which also facilitate drawing robust conclusions (35). Dispersed across 22 chromosomes, the 98 cytoplasmic RPGs (cRPGs) form the largest co-expressed gene network in the human genome (Figure 4 and Supplementary Table S1) (36,37). Their vital importance is another major advantage: viable null mutants of a TR indicate that the TR is not necessary for cRPG expression.

RPG co-regulation has been reported a quarter century ago (36) and in 2006 (37) based on very limited data sets. As the tight co-expression of RPGs is critical to our results, it is necessary to confirm and quantify RPG co-expression by Pearson correlation coefficients on a large data set. For every possible pairs of RPGs across 28 032 microarray samples in the Genevestigator Database (30), the median of the correlation coefficients is as high as 0.788 for cRPGs and 0.514 for mRPGs (Figure 4). The probability of such co-expression across 28K samples is less than 10^{-256}. Its most plausible cause is co-regulation. Imperfect correlations are likely due to possible translational efficiencies and the about one hundred extraribosomal functions that RPs perform (38). However, as extraribosomal RP accumulation evokes nucleolar stress and potentially, cell cycle arrest, most cytoplasmic RP molecules are constrained to the ribosomes and the nucleoli (39). Co-expression is not due to constitutive expression as cells repress or induce RPG transcription

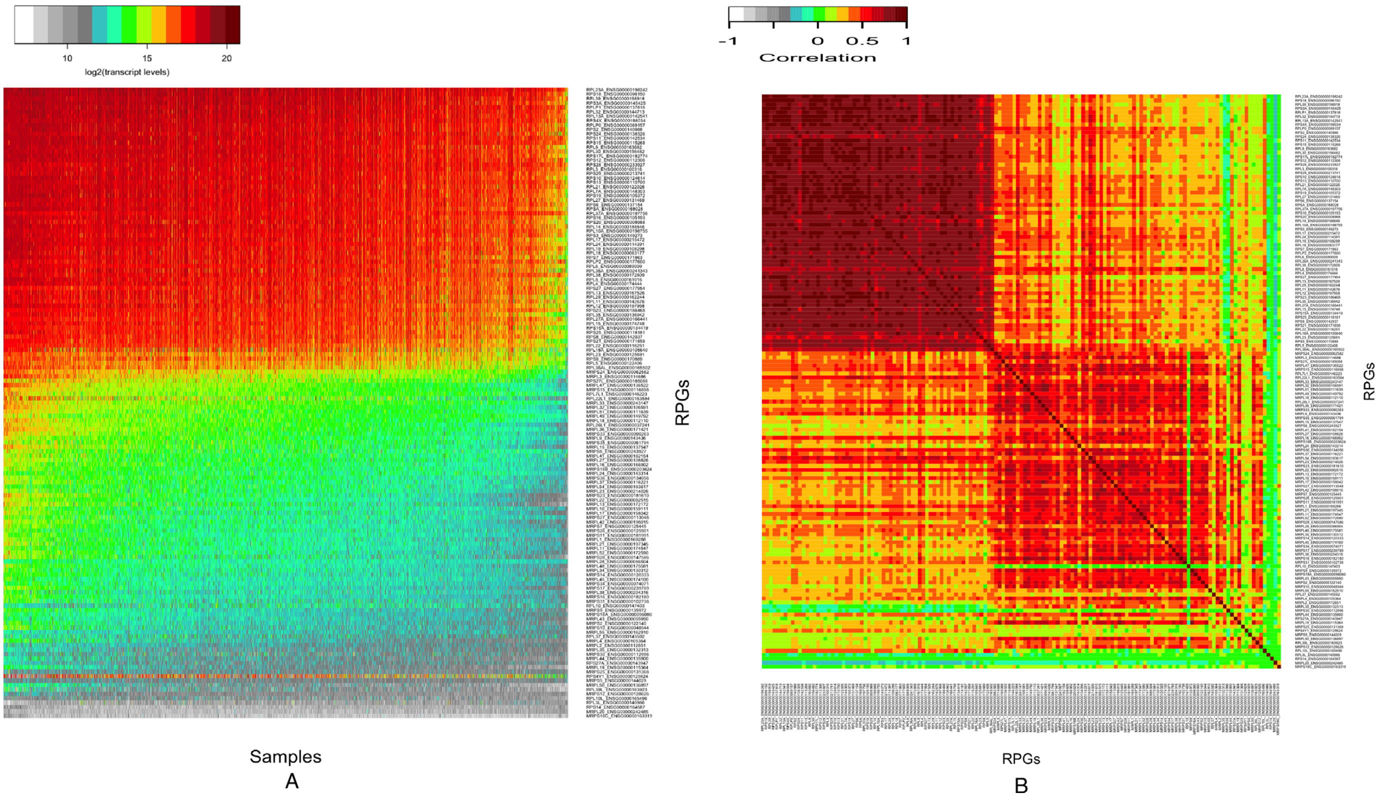


Figure 4. Confirmation of tight RPG co-expression across a wide range of conditions and cell types. **(A)** Base 2 logarithms of transcript levels (horizontal axis) are shown in arbitrary but normalized units from 28,032 Affymetrix microarrays from the Genevestigator Database (30). Transcripts are over hundredfold more abundant in cRPGs than in mRPGs and also vary between families of RPGs. **(B)** Pearson correlation coefficients (*R*) for cRPG transcript levels for each RPG pair indicate that variations in transcript levels are reproducible and tightly correlated. The high median correlation of 0.7875 for all cRPGs is very likely due to co-regulation. High co-expression is in accordance with the earlier observation that only a small proportion of RP molecules are located outside the ribosome and the nucleolus (39).

in response to changes in energy levels and nutrient availability (37,40,41). Were co-regulation a deterministic process, translational efficacy identical, extraribosomal function, experimental error and nonfunctional binding absent, identical TRs would bind in identical amounts to all of the 98 cRPGs. In sharp contrast, the observed distribution of TRs in six cell types shows a mixture of experimental error and *highly stochastic binding of TRs* in diverse human cells (Figure 5 and Supplementary Figure S1).

We systematically compared TR binding sites in cRPG to those of all non-ribosomal genes (NRGs) as well as HE-NRGs. We searched for DNA-bound master regulators for cRPGs but could find none. We looked for strong correlations between TR binding and cRPG transcript levels but none exceeded 0.45. Binding sites of ≈20 regulators were needed to accurately predict cRPG transcript levels by machine learning. Most TR knockout mutants in mice are viable (18) indicating that these cannot be necessary controllers of protein synthesis. On the evolutionary scale, the most important RPG regulators in *S. cerevisiae* does not have mammalian orthologs and the two third of the mammalian cRPG regulators do not have orthologs in fungi (Table 1). Instead of masters, we found that only RNA Polymerase II (POL2), CTCF, MYC, YY1 and IRF1 bind to most cytoplasmic and mitochondrial RPGs in K562 cells (Figure 5) and other human and mouse cells (Supplemen-

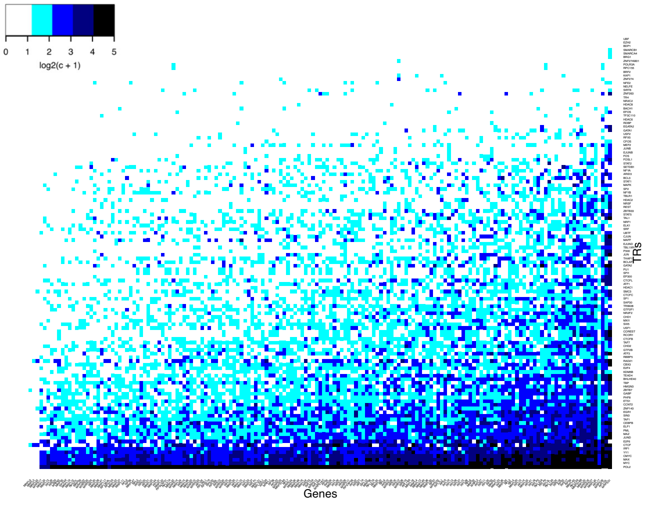


Figure 5. Stochastic TR binding to DNA does not show evident master regulators. The unfiltered numbers of observed binding sites for individual TRs (c) in cytoplasmic and mitochondrial RPGs in human K562 cells. Statistical preferences for several TRs emerge despite considerable randomness, which is partly due to experimental noise. For scalability, $\log_2(c + 1)$ values are shown. Stochastic TR binding is also confirmed for all other analyzed human and mouse cell types (Supplementary Figure S3). The network of cRPG regulation also shows rich and highly variable binding of TRs to diverse cRPGs (Supplementary Figure S5).

tary Figure S3). None of these TRs are specific to cRPGs and the rest of TRs bind to RPGs in stochastic patterns (Figure 5).

We examined peaks of binding sites for each TR separately, regardless of overlapping peaks predicted from ChIP-Seq experiments (5), and for brevity, called them single TRs. We also analyzed pairs and triplets of overlapping peaks of distinct TRs and named them putative dimers and trimers, regardless of overlaps with yet other TRs. We called them putative as individual peaks are 'snapshots' taken at different times and from different samples, hence some of these binding events may occur in different times.

Enriched TR complexes indicate pluralistic and stochastic regulation and signal integration

We observed statistically *highly* significant enrichment of several TRs, hundreds of heterodimers and tens of thousands of trimers in cRPGs as compared to HE-NRGs and/or all NRGs (Figure 6 and Supplementary Tables S6–S11). Unless otherwise mentioned, we compared cRPGs to HE-NRGs and all comparisons were significant at the $P \leq 0.01$ level (Wilcoxon or Fisher's Exact test, see Materials and Methods) followed by multiple test correction using tail-wise False Discovery Rate (28). We present evidence that these enrichment patterns indicate pluralistic and stochastic integration of external and cellular signals and regulatory mechanisms that are far more complex than earlier reported *cis*-regulatory modules (42).

For the biological roles of these complexes, we extrapolated from the roles of individual TRs based on previous experiments to the functions of the multimolecular complexes. These extrapolations provide a reasonably informed *hypothetical framework* to guide future experiments.

Importantly, the enriched di- and trimers include several well-studied TRs that have not yet been implicated in RPG regulation. Of these, SIX5 (a.k.a. DMAHP or BOR2) preferentially binds together with MYC, CHD1, TAF7, GTF2B, and with cohesin constituents including RAD21, CTCF, SMC3 and ZNF143. Consistent with SIX5 roles in a wide array of disorders (43,44), in one or more of the six human cell types studied, SIX5 binds to 6,779 protein-coding genes. One could expect that homozygous knockout mutants of such a wide-spectrum TR to be lethal. However, both the murine (44) and *Drosophila* (45) null mutants are impaired in organ development but still viable. Because ribogenesis is critical to protein synthesis, viable null mutants indicate that the ribosome-specific functions of SIX5 can be substituted by other TRs. This and the highly significant enrichment of SIX5 and its complexes show that SIX5 has a stochastic contribution to cRPG regulation, which is robust against SIX5 mutations.

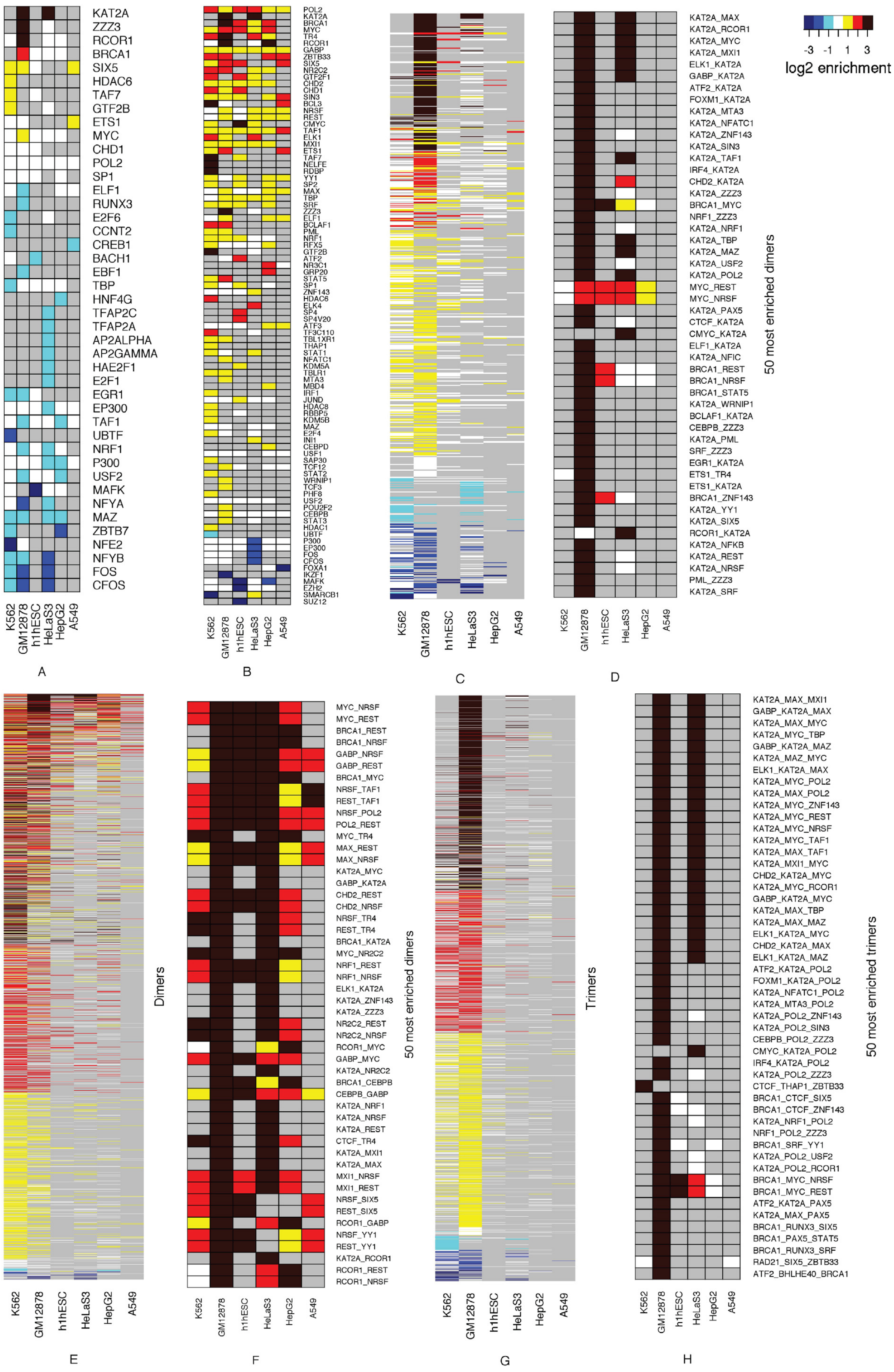
Similarly, the highly enriched BRCA1 (Figure 6) has not been implicated in *direct* RPG regulation. Indirectly, BRCA1 is known to interact with the nucleoli and the ribosomal protein RPSA (46) to suppress the cell cycle upon DNA damage (47). Preferential co-binding of BRCA1 with CTCF and RAD21 indicates a role in modulating chromosome conformation (Figure 6). Preferred association with GABP1, a known integrator of cellular signaling pathways (48) suggests that GABP1 may interact with BRCA1 to downregulate cRPGs under adverse conditions.

Specific pre-initiation complexes (PICs)

We extend RPG-specific PICs reported earlier (49) with several novel stochastic patterns. The strong enrichment of the transcriptional activator KAT2A (GCN5) indicates that it contributes more to the regulation of cRPGs than to most other genes including HE-NRGs. By acetylating histones, KAT2A prepares the chromatin for intensive transcription. Like HDAC6, one of its antagonists, KAT2A has been conserved between yeast and mammals (50). GCN5, its ortholog in yeast, is known to regulate RPGs directly (51). KAT2A is scaffolded to histones by the similarly enriched ZZZ3. This latter protein is specific to ATAC and only either ATAC or S(T)AGA, but not both, can bind to a highly expressed gene (52). Thus, ZZZ3 enrichment (Figure 6, and Supplementary Tables S6–S11) indicates strong preference for the ATAC complex in cRPGs. As intrinsically disordered regions within KAT2A are known to initiate the formation of PICs (53), we speculate that KAT2A's preferential associations may orchestrate the formation of RPG-specific PIC's. Preferential association with MYC (Figure 6 and Supplementary Tables S8–S11) is consistent with the need for KAT2A-mediated histone acetylation to recruit MYC (54). MYC, a widespread nonspecific regulator of RPGs in vertebrates, has similarly extensive disordered transactivation domains (55). In vitro, these domains can recruit hundreds of regulators but *in vivo*, the interactors are constrained by the co-bound partners and adjacent DNA motifs (15,56). MYC, its activator, MAX, and repressor, MXI1 appear to interact with TAF7, HDAC6, REST, NELF (RDBP) and BRCA1 (Figure 6, Supplementary Tables S6–S11). Such complex binding events indicate a network far exceeding the MAX/MYC/MXI1 axis for the regulation and deregulation of oncogenic activity. In a positive feedback loop, KAT2A acetylates histones in the genes of MYC, Yin Yang 1 (YY1) and other direct regulators of RPGs. Subsequently, MYC induces the *KAT2A* gene (57). Enriched complexes of the histone deacetylase HDAC6 or similar agents can break this positive feedback loop.

The robust enrichment of HDAC6 (Figure 6, Supplementary Tables S6–S11) raises the possibility that its influence on the cell cycle (58) may be partly mediated via the regulation of ribogenesis. HDAC6 preferentially co-binds with PolII, P300, estrogen receptor, RUNX2, NFκB and HSP90; an activity likely to be organized by the ubiquitin-binding domain of HDAC6 (59). Despite the fundamental roles of HDAC6, its null mutants display normal phenotype both in *Drosophila* (60) and mouse (61), strongly indicating that other enzymes, possibly paralogous HDAC family members, can effectively perform HDAC6 functions.

The strongly enriched overlapping peaks of KAT2A and chromodomain helicase DNA binding protein 1 (CHD1) may indicate coupled histone acetylation and methylation (62). This dimer and its superset with ZZZ3 are known to evict nucleosomes to facilitate the passing of the transcriptional machinery (63). KAT2A also forms enriched di- and trimers with TBP/TRF2-associated factors TAF1 and TAF7. These factors form enriched complexes with


KAT2A
ZZZ3
RCOR1
BRCA1
SIX5
HDAC6
TAF7
GTF2B
ETS1
MYC
CHD1
POL2
SP1
ELF1
RUNX3
E2F6
CCNT2
CREB1
BACH1
EBF1
TBP
HNF4G
TFAP2C
TFAP2A
AP2ALPHA
AP2GAMMA
HAE2F1
E2F1
EGR1
EP300
TAF1
UBTF
NRF1
P300
USF2
MAFK
NFYA
MAZ
ZBTB7
NFE2
NFYB
FOS
CFOS
K562
GM12878
h1hESC
HeLaS3
HepG2
A549
A
POL2
KAT2A
BRCA1
MYC
TR4
RCOR1
GABP
ZBTB33
SIX5
NR2C2
GTF2F1
CHD2
CHD1
SIN3
BCL3
NRSF
REST
CMYC
TAF1
ELK1
MXI1
ETS1
TAF7
NELFE
RDBP
YY1
SP2
MAX
TBP
SRF
ZZZ3
ELF1
BCLAF1
PML
NRF1
RFX5
GTF2B
ATF2
NR3C1
GRP20
STAT5
SP1
ZNF143
HDAC6
ELK4
SP4
SP4V20
ATF3
TF3C110
TBL1XR1
THAP1
STAT1
NFATC1
KDM5A
TBLR1
MTA3
MBD4
IRF1
JUND
HDAC8
RBBP5
KDM5B
MAZ
E2F4
INI1
CEBPD
USF1
SAP30
TCF12
STAT2
WRNIP1
TCF3
PHF8
USF2
POU2F2
CEBPB
STAT3
HDAC1
UBTF
P300
EP300
FOS
CFOS
FOXA1
IKZF1
MAFK
EZH2
SMARCB1
SUZ12
K562
GM12878
h1hESC
HeLaS3
HepG2
A549
B
K562
GM12878
h1hESC
HeLaS3
HepG2
A549
C
KAT2A_MAX
KAT2A_RCOR1
KAT2A_MYC
KAT2A_MXI1
ELK1_KAT2A
GABP_KAT2A
ATF2_KAT2A
FOXM1_KAT2A
KAT2A_MTA3
KAT2A_NFATC1
KAT2A_ZNF143
KAT2A_SIN3
KAT2A_TAF1
IRF4_KAT2A
CHD2_KAT2A
KAT2A_ZZZ3
BRCA1_MYC
NRF1_ZZZ3
KAT2A_NRF1
KAT2A_TBP
KAT2A_MAZ
KAT2A_USF2
KAT2A_POL2
MYC_REST
MYC_NRSF
KAT2A_PAX5
CTCF_KAT2A
CMYC_KAT2A
ELF1_KAT2A
KAT2A_NFIC
BRCA1_REST
BRCA1_NRSF
BRCA1_STAT5
KAT2A_WRNIP1
BCLAF1_KAT2A
CEBPB_ZZZ3
KAT2A_PML
SRF_ZZZ3
EGR1_KAT2A
ETS1_TR4
ETS1_KAT2A
BRCA1_ZNF143
KAT2A_YY1
KAT2A_SIX5
RCOR1_KAT2A
KAT2A_NFKB
KAT2A_REST
KAT2A_NRSF
PML_ZZZ3
KAT2A_SRF
50 most enriched dimers
K562
GM12878
h1hESC
HeLaS3
HepG2
A549
D
-3 -1 1 3
log2 enrichment
K562
GM12878
h1hESC
HeLaS3
HepG2
A549
Dimers
E
MYC_NRSF
MYC_REST
BRCA1_REST
BRCA1_NRSF
GABP_NRSF
GABP_REST
BRCA1_MYC
NRSF_TAF1
REST_TAF1
NRSF_POL2
POL2_REST
MYC_TR4
MAX_REST
MAX_NRSF
KAT2A_MYC
GABP_KAT2A
CHD2_REST
CHD2_NRSF
NRSF_TR4
REST_TR4
BRCA1_KAT2A
MYC_NR2C2
NRF1_REST
NRF1_NRSF
ELK1_KAT2A
KAT2A_ZNF143
KAT2A_ZZZ3
NR2C2_REST
NR2C2_NRSF
RCOR1_MYC
GABP_MYC
KAT2A_NR2C2
BRCA1_CEBPB
CEBPB_GABP
KAT2A_NRF1
KAT2A_NRSF
KAT2A_REST
CTCF_TR4
KAT2A_MXI1
KAT2A_MAX
MXI1_NRSF
MXI1_REST
NRSF_SIX5
REST_SIX5
RCOR1_GABP
NRSF_YY1
REST_YY1
KAT2A_RCOR1
RCOR1_REST
RCOR1_NRSF
50 most enriched dimers
K562
GM12878
h1hESC
HeLaS3
HepG2
A549
F
Trimers
K562
GM12878
h1hESC
HeLaS3
HepG2
A549
G
KAT2A_MAX_MXI1
GABP_KAT2A_MAX
KAT2A_MAX_MYC
KAT2A_MYC_TBP
GABP_KAT2A_MAZ
KAT2A_MAZ_MYC
ELK1_KAT2A_MAX
KAT2A_MYC_POL2
KAT2A_MAX_POL2
KAT2A_MYC_ZNF143
KAT2A_MYC_REST
KAT2A_MYC_NRSF
KAT2A_MYC_TAF1
KAT2A_MAX_TAF1
KAT2A_MXI1_MYC
CHD2_KAT2A_MYC
KAT2A_MYC_RCOR1
GABP_KAT2A_MYC
KAT2A_MAX_TBP
KAT2A_MAX_MAZ
ELK1_KAT2A_MYC
CHD2_KAT2A_MAX
ELK1_KAT2A_MAZ
ATF2_KAT2A_POL2
FOXM1_KAT2A_POL2
KAT2A_NFATC1_POL2
KAT2A_MTA3_POL2
KAT2A_POL2_ZNF143
KAT2A_POL2_SIN3
CEBPB_POL2_ZZZ3
CMYC_KAT2A_POL2
IRF4_KAT2A_POL2
KAT2A_POL2_ZZZ3
CTCF_THAP1_ZBTB33
BRCA1_CTCF_SIX5
BRCA1_CTCF_ZNF143
KAT2A_NRF1_POL2
NRF1_POL2_ZZZ3
BRCA1_SRF_YY1
KAT2A_POL2_USF2
KAT2A_POL2_RCOR1
BRCA1_MYC_NRSF
BRCA1_MYC_REST
ATF2_KAT2A_PAX5
KAT2A_MAX_PAX5
BRCA1_RUNX3_SIX5
BRCA1_PAX5_STAT5
BRCA1_RUNX3_SRF
RAD21_SIX5_ZBTB33
ATF2_BHLHE40_BRCA1
50 most enriched trimers
K562
GM12878
h1hESC
HeLaS3
HepG2
A549
H

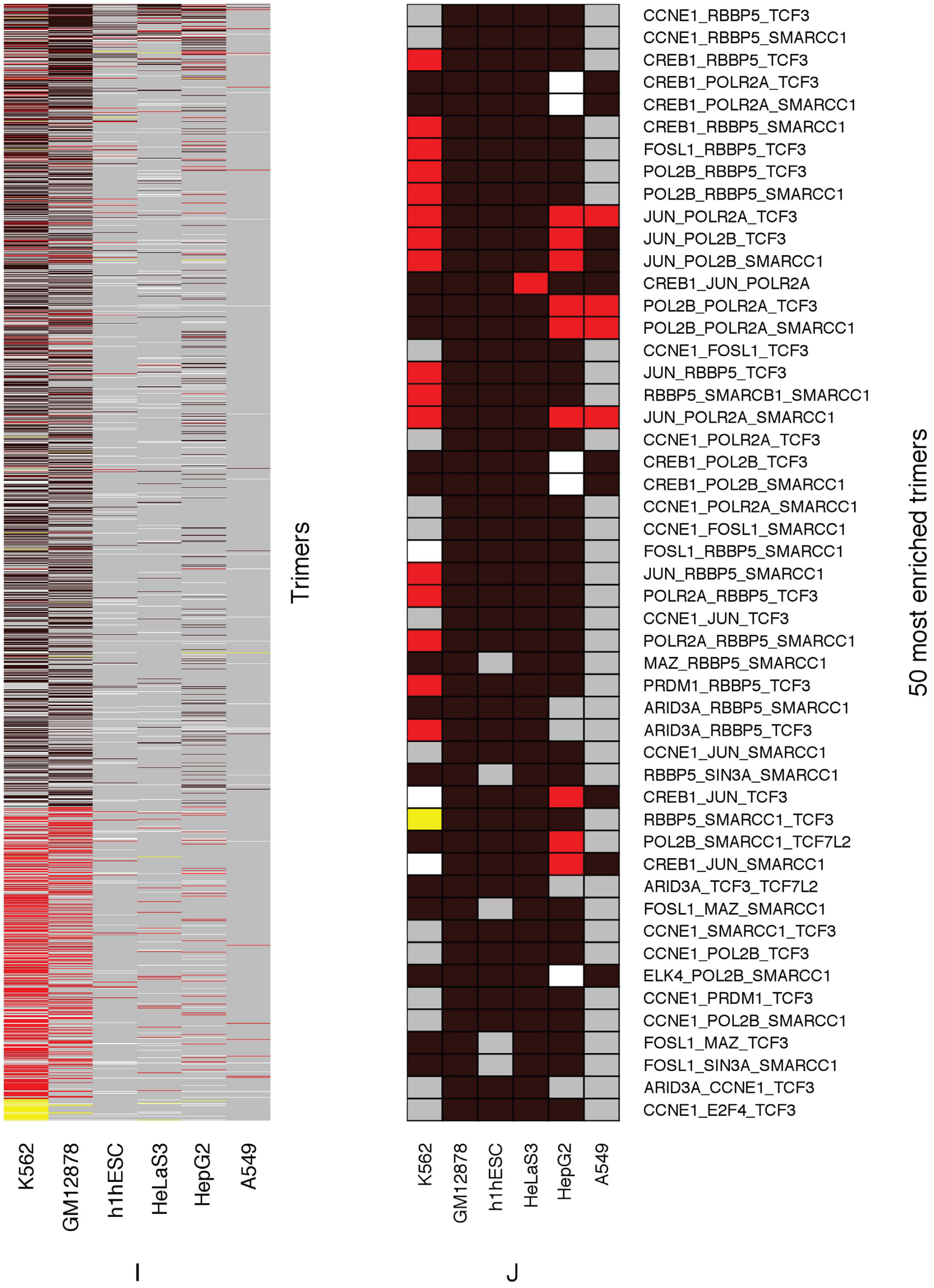


Figure 6. cRPG regulatory binding events show highly specific and statistically significant patterns of enrichment or depletion of single transcriptional regulators, putative TR heterodimers and heterotrimers. Human cRPGs are compared to HE-NRGs and NRGs in separate panels. For single TRs, the significance of enrichment was assessed by the Wilcoxon–Mann–Whitney test, for dimers and trimers, by Fisher's Exact Test. Multiple test corrections were performed using Benjamini and Hochberg's False Discovery Rate (28). Numerical data are available in Supplementary Tables S4–S8. **(A)** Single TRs, cRPGs versus HE-NRGs. **(B)** Single TRs, cRPGs versus all NRGs. **(C)** Heterodimers, cRPGs versus HE-NRGs. **(D)** The 50 most highly enriched heterodimers, cRPGs versus HE-NRGs. **(E)** Heterodimers, cRPGs versus all NRGs. **(F)** The 50 most highly enriched heterodimers, cRPGs versus all NRGs. **(G)** Heterotrimers, cRPGs versus HE-NRGs. **(H)** The 50 most highly enriched heterotrimers, cRPGs versus HE-NRGs. **(I)** Heterotrimers, cRPGs versus all NRGs. **(J)** The 50 most highly enriched heterotrimers, cRPGs versus all NRGs.

KAT2A, MYC, MAX, MXI1, Pol II, SIX5, YY1, G2F2B, ZZZ3, IRF1, CHD1 and ZNF143 (Figure 6).

GTF2 subunits are among the most enriched regulators (Figure 6). GTF2 is known to link the TFIID complex to Pol II (64). We found that several joint members of the *quantitative* regulator complexes TFIID and S(T)AGA complexes are enriched in RPG promoters (Figure 6). Taken together, these observations show that PICs of RPGs display significantly different distributions of regulators than PICs of other genes including HE-NRGs.

Pol II is enriched in cRPGs compared to NRGs, but not compared to HE-NRGs (Figure 6 and Supplementary Tables S6–S11). An inducer of polymerase pausing, RD RNA binding protein (RDBP a.k.a. NELF) is enriched in cRPGs relative to NRGs (Supplementary Tables S6–S11) but not compared to HE-NRGs. Pausing is known to counteract nucleosome reconstitution hence to prepare the chromatin for active transcription (65). On this basis, we speculate that RPG-specific PICs and transcriptional machinery modulate polymerase performance and pausing. Relief from pausing allows rapid RPG induction in timely response to improved growth conditions. In cancer cells, the MAX-MYC dimer relieves Pol II from pausing and amplifies transcription (66). In both malignant transformation and experimental overexpression, MYC and MAX may overinduce thousands of active genes by interacting with members of the basal transcriptional machinery during PIC formation (67). Under such conditions, MYC and MAX indeed act as master regulators. We found that MYC and MAX bind to 148 of the 183 human RPGs in at least one of the six major cell lines (Figure 5 and Supplementary Figure S1). Unlike MAX, MYC by itself is enriched in RPGs relative to both HE-NRGs and NRGs. In differentiated cells, MAX forms the four most enriched pairs with REST, G2F2F1, KAT2A and ZNF143, followed by KAT2A_ MAX (Figure 6). PIC constituents MYC, MAX, KAT2A, TAF1, TAF7 and SIX5 form the most enriched triplets with the sole exception of A549 cells (Figure 6). These observations and the presence of MYC and MAX in mRPGs, which are expressed at hundredfold lower levels than cRPGs (Figure 4) indicate MYC and MAX functions that are not related to intensive transcription.

Stochasticity is the most plausible resolution for the ostensible controversy regarding the ternary complex factor ELK1. Despite its high enrichment, ELK1 is redundant for the regulation of ribogenesis and other processes. Its deletion mutants in mice are not impaired in immune reaction, brain and spleen function (68). Were ELK1 roles deterministic, it would be either enriched and essential or unenriched and unnecessary. Instead, we observed enrichment because it *frequently but not necessarily regulates* cRPGs. TRs like ELK1 can be substituted by other TRs in stochastic processes.

The tumor suppressor REST is enriched in cRPGs as compared to NRGs both as a monomer and when co-bound with MYC, STAT5A, Pol II, TAF7, TCF3 and TAF1 (Figure 6 and Supplementary Tables S6–S11). The enriched complex of IRF1, yet another tumor suppressor, with MYC and Pol II may counteract the hyperactivation of the cell cycle by inhibiting MYC (69). These negative feedback mechanisms are critical to cRPG regulation.

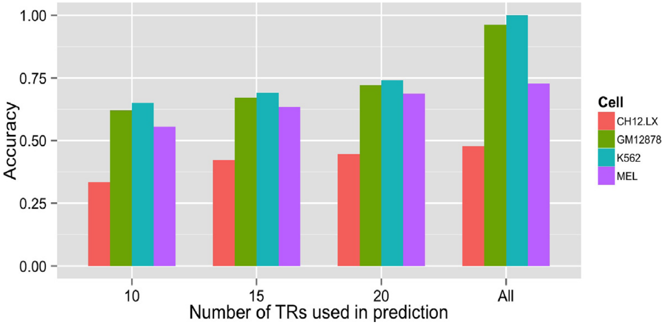


Figure 7. Accurate prediction of transcript levels by Least Angle Regression (29) models (see Materials and Methods) requires binding sites of no less than 20 TRs in human and mouse cell types. Cross-validation prediction accuracy is shown in the function of the number of TRs selected by Least Angle Regression.

Machine learning models of transcriptional regulation

Next we asked: how many TRs bound to cRPGs can predict the observed transcript levels? To avoid inaccurate predictions on untrained observations (known as overtraining), machine learning methods need to be trained on about three-to-five times fewer carefully selected TRs than genes. For example, K562 cells transcribe 98 cRPGs. Therefore we had to select subsets of 98/4–25 or fewer TRs to maximize prediction accuracy for untrained observations. For this purpose, Least Angle Regression (LARS) (29) provided for the highest accuracy (see Materials and Methods). Note that TR selection (in computer science terms, feature selection) methods maximize regression accuracy, not the biological importance of the TRs. For example, if two or more TRs, such as the mandatory components of the PIC or transcriptional machinery, bind to similar genes in similar quantity under similar conditions, only one is necessary for regression despite similar biological necessity of the other proteins. For this reason, regression typically demands fewer TRs than transcriptional regulation, making our estimates for the numbers of necessary TRs conservative.

LARS achieved 74% cross-validation prediction accuracy for K562 cells using binding sites of 20 TRs (Figure 7, Supplementary Table S5). Higher accuracy would demand more TRs but the number of cRPGs limits the number of TRs that can account for robust predictions. These findings implicate a minimum of twenty TRs in the regulation of cRPGs in human and mouse. As several TRs correlate moderately ($0.3 < R < 0.45$) with transcript levels (Figure 8), were these TRs acting independently, four TRs would account for almost all of the regulation and would allow for accurate predictions. This is not the case, indicating strongly interdependent effects of these agents. Therefore none of the above TRs is sufficient for the regulation of cRPGs under the conditions of the ChIP-Seq experiments. Despite moderate correlations between the binding of individual TRs and transcript levels, the complexes that regulate cRPG transcription contain no less than 29 different TRs which are both enriched and predictive for cRPG expression in one or more cell type studied.

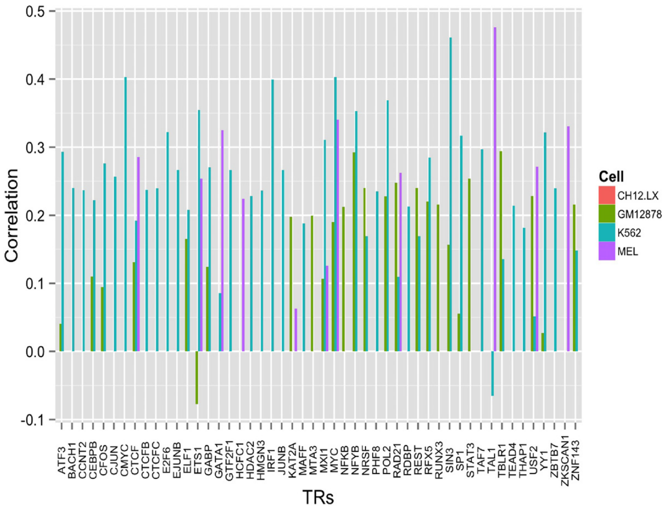


Figure 8. No master regulator emerges from the moderate correlations between TR binding sites and transcript levels in cRPGs. Transcript levels for human K562 and GM12878 cells were taken as the average transcript levels from the Genevestigator Database (30); for mouse MEL and CH12.LX cells RNA sequencing transcript levels were calculated from raw data of the mouse ENCODE Project (31).

DISCUSSION

We report a general theory of pluralistic and stochastic regulation of PolII-mediated transcription in human. This theory is a synthesis of our above results with a broader spectrum of published evidence. In our studies, most of the ≈800 000 tightly co-expressed gene pairs are bound reproducibly by over twenty TRs, indicating widespread pluralistic regulation. In RPGs, the largest co-expressed network of genes in human, observed TR binding sites vary greatly among individual RPGs (Figure 5 and Supplementary Figure S1) despite their tight co-expression (36,37). A particular RPG in a particular cell type can be regulated by very diverse TRs. This variation significantly exceeds the level of ChIP-Seq error. We searched for DNA-associated master regulators of cRPGs but could find none. We looked for strong correlations between TR binding and cRPG transcript levels but none exceeded 0.45. Binding sites of ≈20 regulators were needed to accurately predict cRPG transcript levels by machine learning. Most TR knockout mutants in mice are viable (18) indicating that these cannot be necessary controllers of protein synthesis. On the evolutionary scale, the most important RPG regulators in *S. cerevisiae* does not have mammalian orthologs and the two third of the mammalian cRPG regulators do not have orthologs in fungi (Table 1). Instead of master regulators, we found significant enrichment of 41 individual TRs, 700 putative dimers, and 9827 trimers in cRPGs compared to HE-NRGs (Supplementary Tables S6–S11). The probability of the random occurrence for such strong patterns is close to zero. This enrichment shows that a large number of TRs, dimers, trimers, and likely higher order complexes collectively regulate cRPGs. MYC, NFκB and other widely bound TRs act as regulatory hubs recruiting other TRs. Under most normal, stress and disease conditions, repressors like HDAC6, MXI1, NELF1, REST, IRF1 and BRCA1 prevent regulatory hubs from becoming uncontrolled master regulators. When negative feedback fails, MYC and MAX may become master regulators and amplify the transcription of thousands of genes in cancer (66). The observed stochastic TR binding and interactions are more robust against regulatory malfunctions (such as mutations and evolutionary substitution of regulators and their binding sites) than rigid hierarchies controlled by masters (70).

We also found that accurate predictions of cRPG transcript levels demand a minimum of 20 regulators. This is in concordance with the viability of null mutants for several orthologous murine (18) and *Drosophila* TRs (45). These observations show that TRs regulating cRPGs can substitute each other to a large extent. A high number of TRs, even some of those that bind to thousands of genes, are not critical to survival (71). In a study of the control of growth arrest and differentiation in a leukemia cell line, none of the 52 TRs knocked down by short interfering RNAs proved to be as necessary (master) regulators (72).

Many regulators disappear and others emerge during evolution. Despite the vital role of ribogenesis and the strong conservation of most RPs in eukaryotes (73), their regulators and regulator binding sites have evolved rapidly (74). We have implicated 27 TRs in the regulation of cRPGs. This is the union of highly predictive TRs in machine learning experiments and the enriched single TRs in all six human cell types. We hypothesize that several other TRs contribute to the governance of cRPG expression. The confirmation of this hypothesis requires additional experiments. Of the 27 TRs implicated here, only 11 have apparent orthologs in *Saccharomyces cerevisiae* (CTCF, KAT2A, GTF2, TBP, TAF1, TAF7, ATF2, HDAC6, RCOR1, NFYB and SETDB1; Supplementary Table S6). MYC binds to most RPGs in mammals (56) but neither MYC nor its prime interactors, MAX and MXI1, nor the also widely bound BRCA1 have detectable homologs in yeast (Supplementary Table S6, Wu, Y.-C., Bansal, M.S., Rasmussen, M.D., Herrero, J. and Kellis, M. (2014) Phylogenetic Identification and Functional Characterization of Orthologs and Paralogs across Human, Mouse, Fly and Worm. *bioRxiv*, doi:10.1101/005736). In *S. cerevisiae,* RAP1 is one of the most important regulators of RPGs; whereas in another yeast, *Candida albicans,* TBF1 plays a similar role (75). Neither have detectable homologs in humans. Such extensive gains and losses of TRs have not caused lethal impairments to protein synthesis in the ancestors of contemporary species, indicating that these TRs were not necessary at some times and in some lineages. Compared to prokaryotes and yeasts, over 1200 additional TRs evolved in the lineage of mammals (7). The resulting vast combinatorics also facilitates sophisticated responses to internal and external signals. For example, the mTORC1 kinase complex governs RPGs by directly or indirectly phosphorylating MYC, YY1, STAT's, JUN, histone deacetylases, BRCA1, RAD21, ZZZ3, KDM5A and TAF1 (76,77). To a limited extent, even the mTORC1 kinase complex can be substituted by the phosphatidylinositol 3-kinase and ERK-MAP pathways (78,79).

DNA binding sites of transcription factors evolve very fast. The resulting variability modulates the strength and the regulatory effects of individual sites (17). As old binding sites are transferred to new loci or deteriorate and new sites emerge, a large part of the regulatory network changes during evolution. Only 36% of the mouse regulatory regions (DNase hypersensitivity sites) maps to human regions and only 14% of them are conserved in both content and position (19,31). Such mutations in regulatory regions are responsible for massive evolutionary rewiring of the regulatory networks.

In RPGs and 800 000 co-expressed gene pairs, regulatory specificity is generated by as many as 20–25 TRs. The distribution of TR binding sites and associations follow statistical patterns ranging from strictly preferential to highly random. A wide spectrum of stochastic protein–protein and protein–DNA interactions are promoted by an unusual abundance of intrinsically disordered domains in transcription factors (15). TRs like MYC and KAT2A with exceptionally large intrinsically disordered domains (15) may bind to a large variety of other regulators. Widely bound TRs such as MYC and NFκB recruit other TRs. These interactions are built and broken in a matter of seconds (80), further increasing probabilistic binding, which is the plausible cause for burst-like expression patterns (14). Stochastic TR binding may cause stochastic regulatory effects, including pauses and bursts of transcription. The binding of different TRs is considerably but not fully preferential and is affected by random effects such as the availability and Brownian motion of TRs in the nucleus (81).

Surprisingly, pluralistic and stochastic gene regulation can be reconciled with what most recent authors call master regulators. Masters can be defined as inducers of a cascade of regulatory events that guide the cell cycle, cellular differentiation and other biological processes (82). Note that this definition requires neither necessity nor rigorous sufficiency of the master for inducing a process or a phenotype. As more and more TRs are implicated in the governance of animal development, Chan and Kyba (83) pointed out that 'the genome might have more masters than servants'. Hence the metaphor of masters taken from human societies may lose its relevance.

With the emergence of regulatory information, authors relaxed the concepts of master regulators. Originally, a master regulator was defined as 'a gene which… should not be under the regulatory influence of any other gene' (84). However, the ENCODE Project (85) demonstrated that even TR genes are bound by numerous other TRs. According to a somewhat later definition, master regulators are necessary and sufficient agents for producing a phenotype or differential gene expression (72). Necessity means that no other TR is sufficient and sufficiency means that no other TR is necessary. As the number of genes is strictly controlled in *Metazoa* (86), hundreds of nonfunctional TR genes would have been eliminated. Second, being known targets of signaling pathways, many of the implied 'servants' integrate and convey a wide variety of cellular information to improve regulatory decisions (87).

Such a 'dictatorial' concept may be overly strict and several proposed masters were not verified rigorously. Necessity can be validated using homozygous knockout mutants (18). For example, the transcription factor BCL11A is necessary for the developmental stage-specific downregulation of the γ-globin gene as shown using $BCL11A^{-/-}$ transgenic mice (88). However, its sufficiency remains unproven as DEAD and/or SIX6 may also be necessary for downregulation (88). Proving the sufficiency of individual candidates by overinducing the expression of their genes can be problematic (89). In an ideal overinduction experiment, no other specific regulator would bind to synthetic promoters and enhancers, and no cofactors would be associated with the candidate master. As such *in vivo* experiments are hardly feasible in higher eukaryotes given that co-binding specific regulators confound practical sufficiency tests. At far beyond physiological levels, MYC and MAX flood low-affinity DNA sites and outcompete repressors. This low-specificity upregulation of several thousand genes (90,91) is named as transcriptional amplification (66). Under such conditions, MYC and MAX act as strict sense master regulators.

Hierarchy may exist in the regulation of the transcriptional regulators themselves. This complex network problem requires additional studies. Necessary and sufficient masters including MyoD (92) and SCL (93) do exist even under physiological conditions. However, their number could be far lower than previously thought (83). Considerably random effects were found even in the action of classic masters including Bicoid, Hunchback, Caudal and Nanos, which orchestrate the segmentation of *Drosophila* embryos (94). Therefore, compared to deterministic approaches, thermodynamic models of multiple TRs predict the transcription of segmentation-related genes more accurately (95).

The concept of master regulators can be extended to sets of a few TRs (96), which we call 'oligarchies'. To prevent the uncontrolled growth of oligarchies, we require that none of the individual oligarchs is sufficient to induce a phenotype but each of them is necessary. These criteria disqualify several previous claims for master regulators and oligarchies. In the fibroblast reprogramming example (9) mentioned in the Introduction, OCT4 and SOX2 are essential but insufficient for reprogramming and none of the four TRs, KLF4 and MYC (10) or NANOG and LIN28 (11) is necessary. Hence none of these six TRs is a strict sense master regulator.

According to a Scopus search, over 28 700 publications mention master regulators. Most authors use this metaphor solely to indicate the well-established differential importance of TRs (85). Calling the most important TRs as 'masters' may be somewhat inaccurate, but this does not conflict with stochastic and pluralistic regulation.

We recognize the limitations of our insight into the vast complexity of transcriptional regulation. As of August 2015, the ENCODE Project (5) mapped about three hundred of the ≈1700 DNA-associated proteins and a fraction of histone modifications in human cells (7). False negative observations and unknown distal enhancer regions (97) may lead to overlooking numerous regulator binding sites. To a lesser extent, false positives also present a concern. We have limited information about the differences in the stability, lifespan and regulatory effects of TR binding sites. Our stochastic and pluralistic model of gene regulation is biased toward highly expressed genes with specific transcriptional machinery. Another potential bias is that cRPGs are governed by a higher number of TRs including a larger percentage of general regulators than most medium-to-low-expression genes. ENCODE's selection of TRs, amplification bias in ChIP-Seq, and phantom peaks may further bias analyses including ours. However, using objective statistics, machine learning methods, evolutionary observations and gain-/loss-of-function mutants, we reduced interpretational and simplification bias.

In summary, the stochastic distribution of TR binding sites across the human genome, the viability of null mutants for most TRs and the evolutionary rewiring of the regulatory networks indicate the wide extent of stochastic regulation. TRs bind to DNA and associate with each other in partially random manner but with probabilistic preferences. Deterministic regulation cannot produce stochastic, burst-like transcription. Stochastic mechanisms have a major evolutionary advantage over rigid, deterministic systems. Positive Darwinian selection for increasingly adaptive regulators (98) and binding site patterns improves adaptation to new environments and elevate organismal complexity during evolution. Neither positive selection for mutants with improved fitness nor negative selection against less adaptive mutants was able to eliminate stochastic regulation. Also, degrading most of the ≈1700 human TRs to mere 'servants' would eliminate robustness against mutations, the large majority of regulatory repertoire, and hence the pool for evolutionary adaptation. The ≈800 000 co-regulated gene pairs and the cRPGs indicate that pluralistic and stochastic mechanisms are widespread in the human and likely other genomes. This does not contradict most of the ≈28 700 publications that discuss master regulators in some relaxed sense. We recommend evaluating both stochastic and more or less hierarchical regulation as well. Sophisticated and minimally biased interpretations of transcriptional regulation will guide us to understand the effects of regulatory mutations in the millions of human genomes soon to be sequenced (3) and to design therapeutic interventions.

AVAILABILITY

Key data are available in Supplementary Tables. All data have been stored in our MySQL relational database. The human part of the MySQL Database and its documentation are available at our web site: https://git.unl.edu/sladunga2/genereg/tree/master. Other data can be obtained upon request.

ACCESSION NUMBERS

Are available in Supplementary Tables S1 and S2.

SUPPLEMENTARY DATA

Supplementary Data are available at NAR Online.

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Authors' contributions: Designed the study: I.L. Analyzed the data: I.L., M.F.C. and J.S. Wrote the manuscript: I.L., D.P.W. and E.N.S. All authors read and approved the final manuscript.

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SUPPLEMENTARY INFORMATION

E.N. Salas, J. Shu, M.F. Cserhati, D.P. Weeks, and I. Ladunga:

Pluralistic and stochastic gene regulation: examples, models, and consistent theory

Table of Contents

ChIP-Seq reproducibility and quality are critical to our conclusions. In the absence of "standards of truth", experimental error cannot be quantified directly. Instead, reproducibility has been evaluated rigorously using Irreproducible Discovery Rate (IDR) (1). IDR evaluates the consistency of ranking for all peaks in a pair of ChIP-Seq duplicates. IDR is robust to the choice of the peak calling algorithm and its parameters. High ChIP-Seq standards used in the ENCODE experiments for highly localized "point-source" TR experiments required: an IDR ≤ 0.01 (2), a minimum of two replicates, no less than 10 million mapped reads in each replicate, and secondary confirmation for antibody specificity (3). Note that the IDR criterion makes our assessments of stochasticity conservative. In addition to reproducibility analyses, ChIP-Seq peaks were also compared to negative controls obtained by nonspecific antibodies. Additional quality metrics such as the Fraction of Reads in Peaks (FRiP), strand cross-correlation, library complexity, and the fraction of nonredundant mapped reads in a data set are discussed elsewhere (3). Substandard replicates and experiments were removed from further analyses. Despite strict quality assurance, a gray zone remains between confidently called ChIP-Seq peaks and experimental noise. False peaks may occur even in control datasets due to overrepresentation of reads from unknown copy number variants or amplification bias (4). Other "phantom" peaks may originate from the increased shearing efficiency of open chromatin (5). Numerous potentially false peaks have been removed from the ChIP-Seq datasets but an unknown number of them may have escape detection (2). Weak binding sites may escape detection, which requires more than 10 million mapped reads per replicate (6,7). The reasonably high quality of the ENCODE ChIP-Seq experiments have been confirmed by a recent study (2).

TR binding in the most abundant transcripts and in promoter regions

To examine the impact of selecting the longest coding regions with 5,000 base pair upstream and downstream segments (Gene5kb), we compared the results to the most frequent transcripts and to predicted promoter regions as well in K562 cells. The most frequent transcript for each gene was determined Cap Assessment of Gene Expression (CAGE) studies by the FANTOM Consortium (8). The most frequent transcripts (from the TSS to the end of the 3'UTR) contained as few as 65,951 TR binding sites (3.8 percent of all the 1,736,829 sites observed). Most of the binding sites in coding regions are flatly distributed due to the movement of the transcription machinery. To address this issue, we used broad peaks from the Hudson Alpha Institute predicted by the SPP method (9). Unfortunately, the ENCODE Project has not published other broad peaks. Instead of peaks, one may analyze counts of sequencing reads but normalization remains an open problem. Therefore a potentially large number of binding sites were missed within the transcripts. An average of ~3 binding site per gene is insufficient for any of our statistical analyses.

Next, we analyzed **putative promoter regions**. Promoter predictions are not available from the FANTOM Consortium (8). In K562 cells, the average length of the combined ChromHMM (10) and Segway (11) predictions is as high as 1,165 base pairs. Such wide promoters would largely reproduce the Gene5kb analyses. For more conservative promoter predictions, we enumerated the binding sites for every transcription start site (TSS) for each gene. Following the conventions of the Eukaryotic Promoter Database (12), we included the 499 base pairs upstream and 100 base pair downstream of each TSS. We selected the most densely bound region as the putative promoter. Typically, this was different from the most abundantly transcribed TSS as indicated by CAGE. In the predicted promoter regions, 543,316 binding sites were mapped (31.3 percent), while in the 5,000 base pair regions of the longest transcripts, 653,386 binding sites (37.6 percent) were found. Taking into account the relatively small difference between the two datasets, our major analyses are based on Gene5kb. This approach balances between avoiding sites with limited or no regulatory effects and including important regulators binding outside the promoter region including moderately distant enhancers. Narrowing the search space to putative promoter regions would have weakened our claim of not finding master regulators as they could bind to more upstream or downstream locations.

Promoter regions show stronger enhancement of the same TRs as Gene5kb (Fig. S1 and Tables S3-S5). This may indicate some combination of more specific TR binding, fewer less functional binding, and less ChIP-Seq noise due to nucleosomes in promoters compared to Gene5kb. TRA4, TAF7, and TAF1 show particularly stronger enrichment in promoter regions compared to Gene5kb.

Supplementary Figures

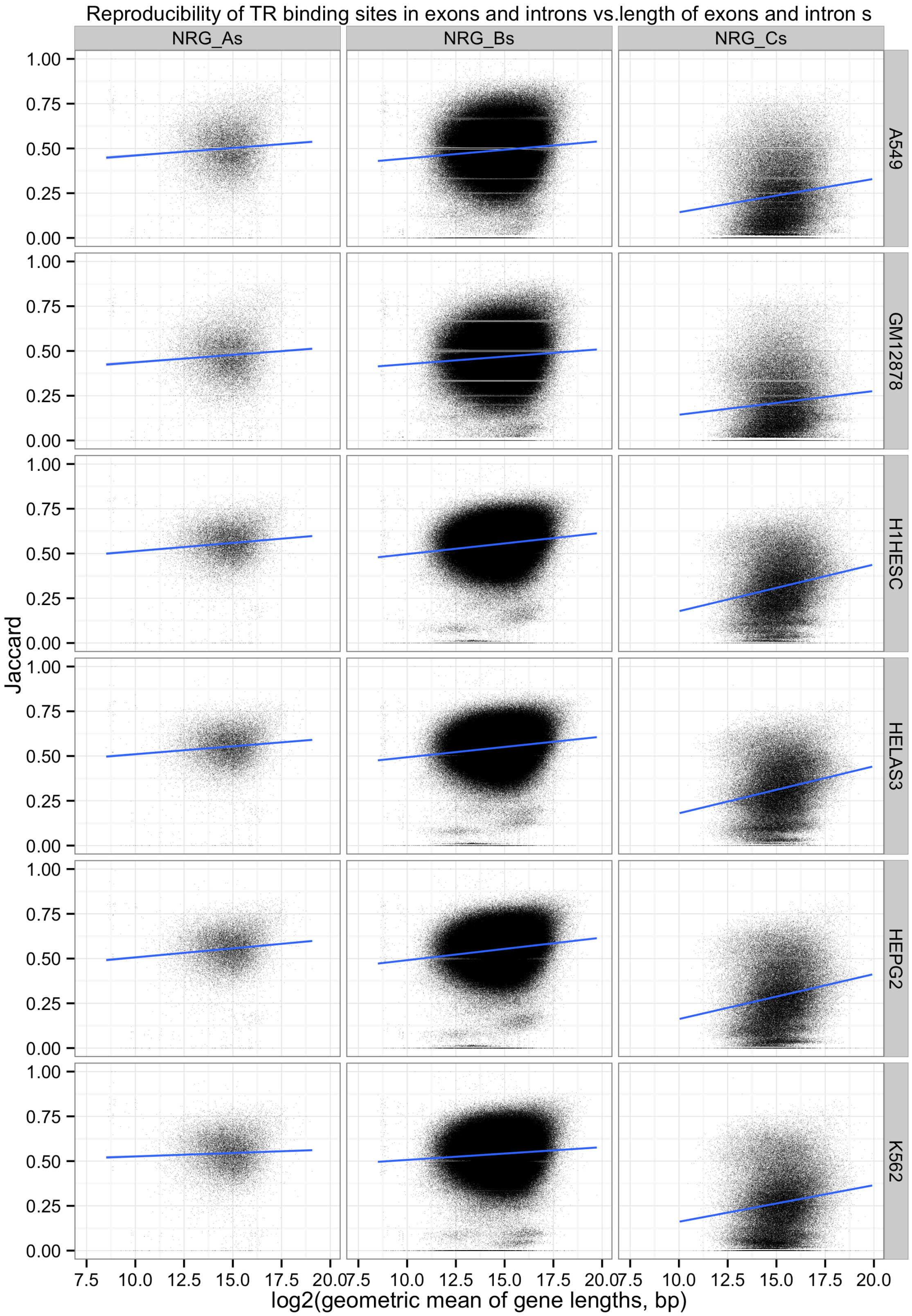


Figure S1. Reproducibility of TR binding between gene pairs improves very slowly with the combined length of exons and introns (for brevity, gene length). Base 2 logarithms of the geometric means of gene lengths are displayed. The Jaccard similarity coefficient increases moderately with gene length for NRG_A's, NRG_B's, and NRG_C's in six human cell types. Gene length is similarly distributed in all co-expression sets.

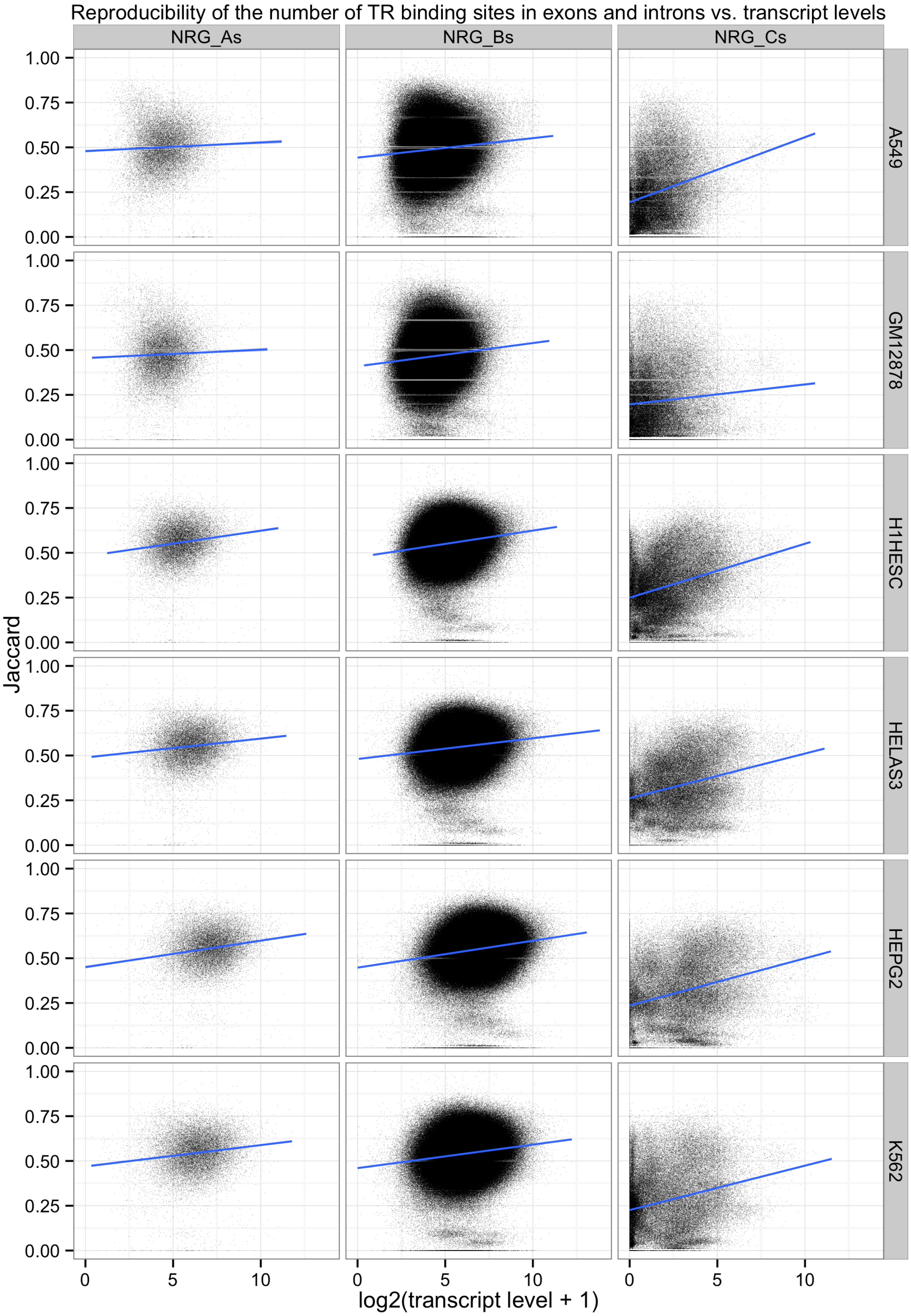
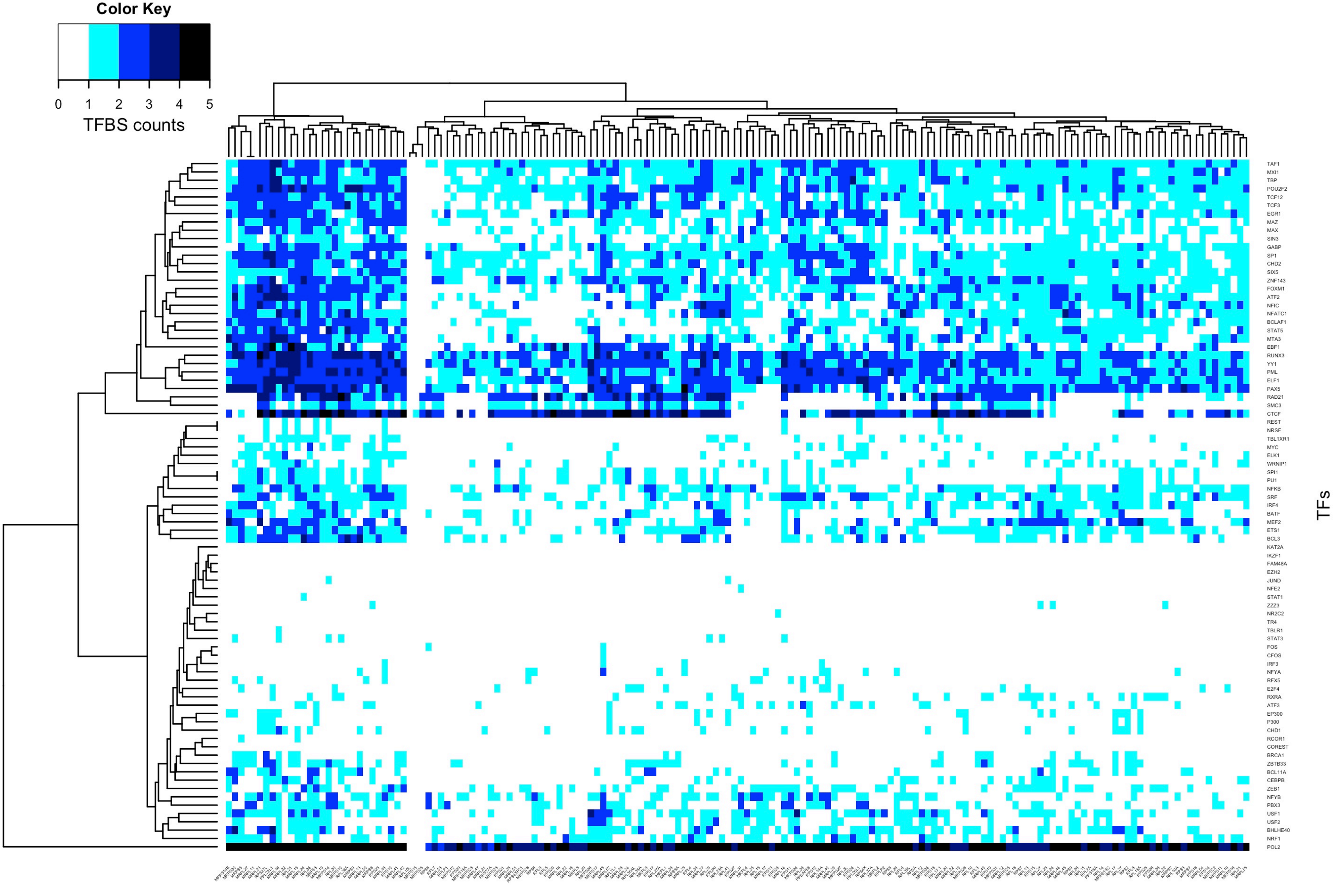
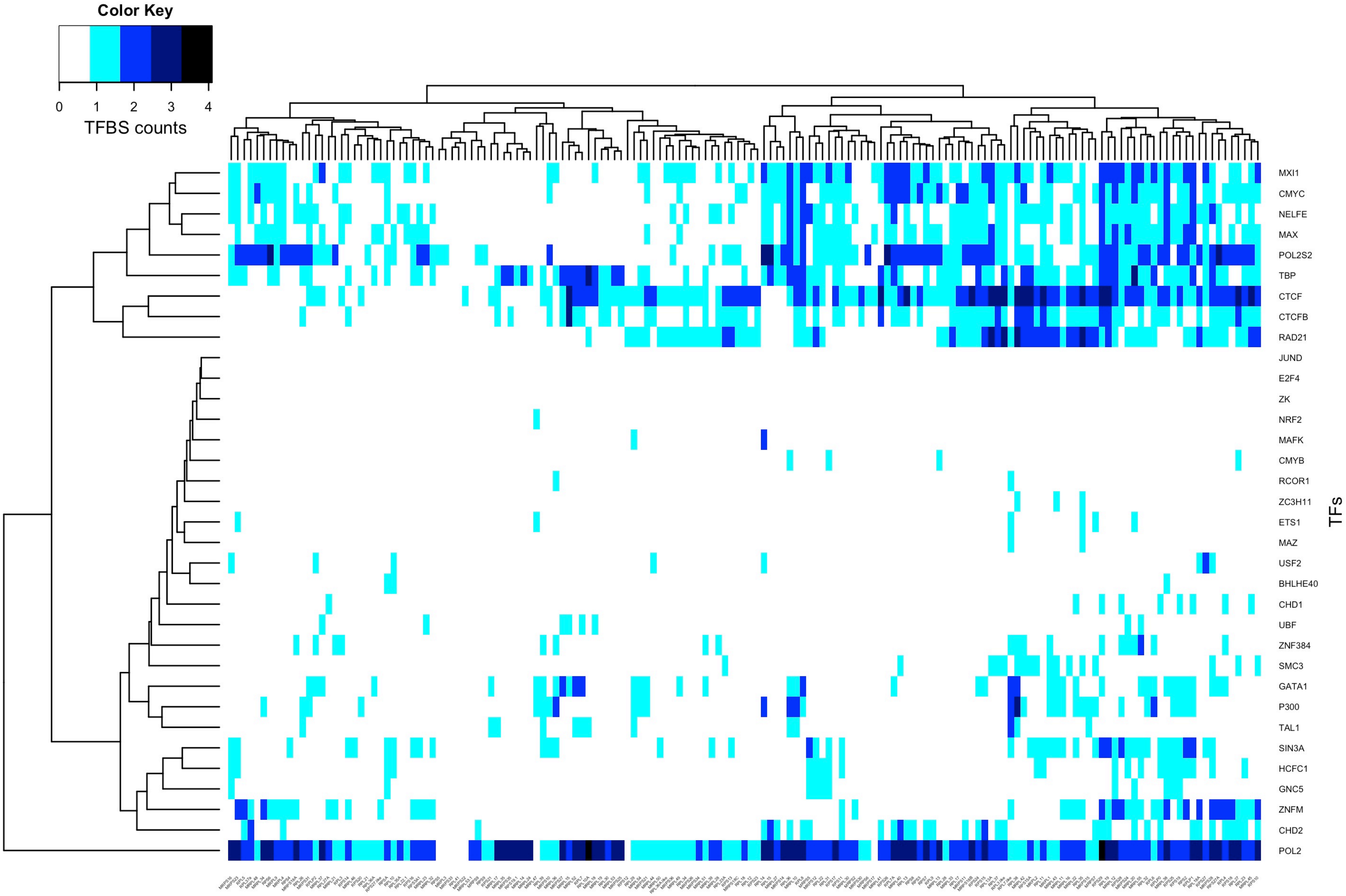

Reproducibility of the number of TR binding sites in exons and introns vs. transcript levels
NRG_As
NRG_Bs
NRG_Cs
A549
GM12878
H1HESC
HELAS3
HEPG2
K562
Jaccard
1.00
0.75
0.50
0.25
0.00
0
5
10
log2(transcript level + 1)

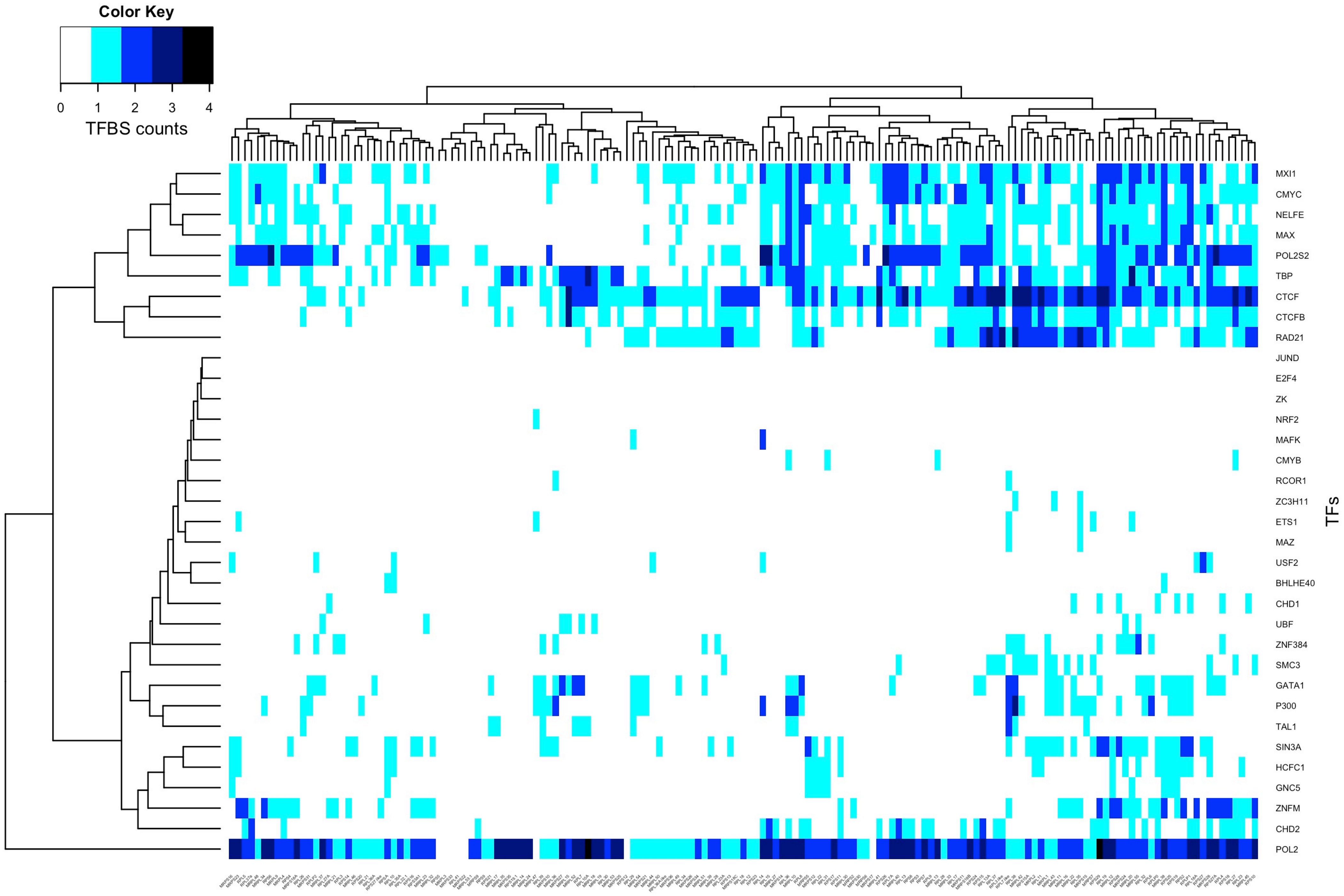
Figure S2. Transcript levels have small effects on the reproducibility of TR binding in co-regulated and independently expressed gene pairs. Base 2 logarithms of the geometric mean of transcript levels are shown. Although transcript levels are mostly lower in NRG_C's (non-logarithmic median: 1.4, interquartile range [IQR]: 0.05 – 6.4) than in NRG_A's (median: 44.9, IQR: 21.2 – 85.7, $p < 10^{-32}$) and in NRG_B's (median: 41.6, IQR: 20.2-73.3, $p < 10^{-32}$), the regression line remains twice as high at most transcript levels in NRG_A's and NRG_B's than in NRG_C's.



A, human GM12878 cells



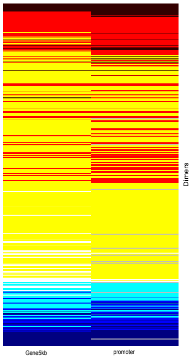
B, mouse MEL cells



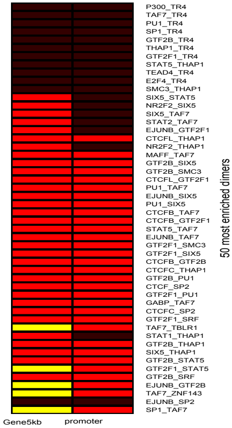
C, mouse CH12.LX cells

Figure S3. Stochastic TR binding to DNA does not show evident master regulators. The unfiltered numbers of observed binding sites for individual TRs (*c*) in cytoplasmic and mitochondrial RPGs in human K562 cells. Statistical preferences for several TRs emerge despite considerable randomness, which is partly due to experimental noise. For scalability, $\log_2(c+1)$ values are shown. For K562 cells, see in-text Fig. 5. For network representation, see Fig. S2. **A**. human GM12878 cells, **B**. mouse MEL cells, and **C**. mouse CH12.LX cells.

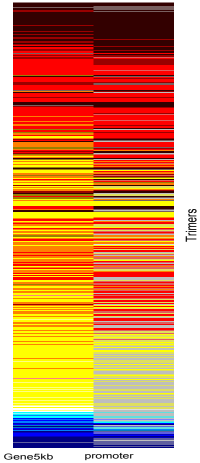
A, Single TRs



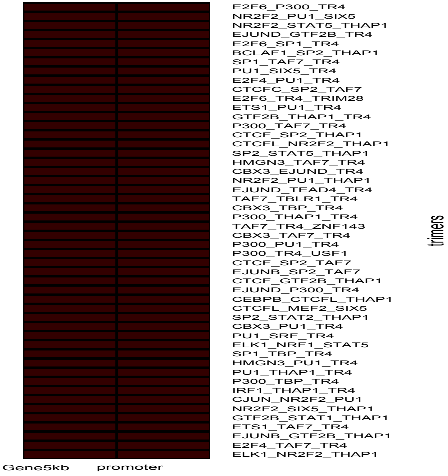
B, Putative TR dimers



D



D, Putative TR trimers



the top 50 most enriched trimers

Fig. S4. Enrichment or depletion of single TRs **(A)**, putative TR dimers **(B)**, and putative TR trimers (**C**). In genes and their 5kb environments (Gene5kb) and in the predicted promoter regions of K562 cells, we compared cRPGs to HE-NRGs. Gray color indicates TRs that are not significantly enriched/depleted, all other TRs are significantly enriched or depleted at the FDR ≤ 0.01 level. Numerical fold change data are shown in Tables S3-S5.

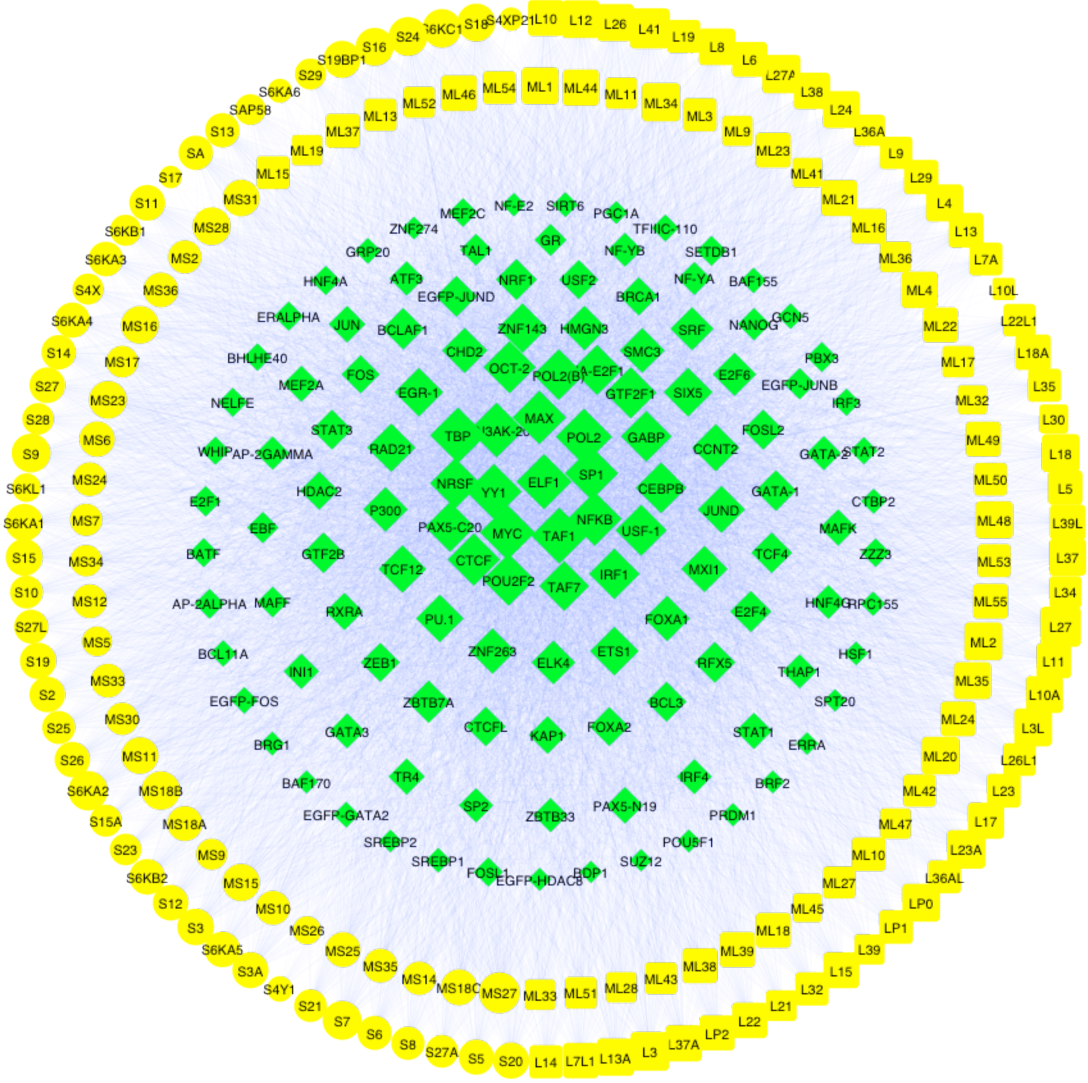


Figure S5. The network of RPG regulation. RPGs are regulated by large and diverse sets of agents that are also implicated in the governance of the cell cycle and cancer. Edges represent binding of a TR to an RPG. Yellow circles represent small subunit RPGs, yellow rectangles stand for large subunit RPGs and green diamonds indicate regulators. Sizes of RPG icons are proportional to the number of bound regulators. Most RPGs are bound by a high number of regulators, and those that are not are likely variants or conditionally translated genes. Sizes of green diamonds are proportional to the number of RPGs to which the TR binds. This Figure was drawn using Cytoscape (13).

Supplementary Table Legends

Table S1. Genes coding for functional cytoplasmic and mitochondrial proteins **(A)** in the human genome, and **(B)** in the mouse genome.

Table S2. Highly expressed non-ribosomal genes (HE-NRGs) in human and mouse, defined as genes expressed at higher levels than the least intensively expressed 25 percent of cRPGs in the Expression Atlas (26).

Table S3. Enrichment of single TRs in genes and their 5kb environments (Gene5kb) and in the predicted promoter regions of K562 cells cRPGs compared to HE-NRGs. NS indicates TRs that are not significantly enriched/depleted, all other TRs are significantly enriched or depleted at the FDR $\leq$ 0.01 level.

Table S4. Enrichment of putative TR dimers in genes and their 5kb environments (Gene5kb) and in the predicted promoter regions of K562 cells cRPGs compared to HE-NRGs. NS indicates TRs that are not significantly enriched/depleted, all other TRs are significantly enriched or depleted at the FDR $\leq$ 0.01 level.

Table S5. Enrichment of putative TR trimers in genes and their 5kb environments (Gene5kb) and in the predicted promoter regions of K562 cells cRPGs compared to HE-NRGs. NS indicates TRs that are not significantly enriched/depleted, all other TRs are significantly enriched or depleted at the FDR $\leq$ 0.01 level.

Table S6. Enrichment of single TRs in cRPGs compared to HE-NRGs in human cell types in Gene5kb regions.

Table S7. Enrichment of single TRs in cRPGs compared to all NRGs in human cell types in Gene5kb regions.

Table S8. Enrichment of putative TR dimers in cRPGs compared to HE-NRGs in human cell types in Gene5kb regions.

Table S9. Enrichment of putative TR dimers in cRPGs compared to all NRGs in human cell types in Gene5kb regions.

Table S10. Enrichment of putative TR trimers in cRPGs compared to HE-NRGs in human cell types in Gene5kb regions.

Table S11. Enrichment of TR trimers in cRPGs compared to all NRGs in human cell types in Gene5kb regions.

Table S12. TRs selected for most accurate prediction of transcript levels. Sets of 20 TRs identified by LARS are shown for human and mouse cell lines.

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Table S1. Genes coding for functional cytoplasmic and mitochondrial proteins (A) in the human genome, and (B) in the mouse genome.

	human cRPGs
Symbol	*Accession*
RPSAP58	ENSG00000205246
RPSA	ENSG00000168028
RPS9	ENSG00000170889
RPS8	ENSG00000142937
RPS7	ENSG00000171863
RPS6	ENSG00000137154
RPS5	ENSG00000083845
RPS4Y2	ENSG00000157828
RPS4Y1	ENSG00000129824
RPS4XP21	ENSG00000186008
RPS4X	ENSG00000198034
RPS3	ENSG00000149273
RPS3A	ENSG00000145425
RPS2	ENSG00000140988
RPS29	ENSG00000213741
RPS28	ENSG00000233927
RPS27L	ENSG00000185088
RPS27	ENSG00000177954
RPS27A	ENSG00000143947
RPS26	ENSG00000197728
RPS25	ENSG00000118181
RPS24	ENSG00000138326
RPS23	ENSG00000186468
RPS21	ENSG00000171858
RPS20	ENSG00000008988
RPS19	ENSG00000105372
RPS18	ENSG00000231500
RPS17L	ENSG00000182774
RPS17	ENSG00000184779
RPS16	ENSG00000105193
RPS15	ENSG00000115268
RPS15A	ENSG00000134419
RPS14	ENSG00000164587

RPS13	ENSG00000110700
RPS12	ENSG00000112306
RPS11	ENSG00000142534
RPS10	ENSG00000124614
RPLP2	ENSG00000177600
RPLP1	ENSG00000137818
RPLP0	ENSG00000089157
RPL9	ENSG00000163682
RPL8	ENSG00000161016
RPL7L1	ENSG00000146223
RPL7	ENSG00000147604
RPL7A	ENSG00000148303
RPL6	ENSG00000089009
RPL5	ENSG00000122406
RPL4	ENSG00000174444
RPL41	ENSG00000229117
RPL3L	ENSG00000140986
RPL3	ENSG00000100316
RPL39L	ENSG00000163923
RPL39	ENSG00000198918
RPL38	ENSG00000172809
RPL37	ENSG00000145592
RPL37A	ENSG00000197756
RPL36	ENSG00000130255
RPL36AL	ENSG00000165502
RPL36A	ENSG00000241343
RPL35	ENSG00000136942
RPL35A	ENSG00000182899
RPL34	ENSG00000109475
RPL32	ENSG00000144713
RPL31	ENSG00000071082
RPL30	ENSG00000156482
RPL29	ENSG00000162244
RPL28	ENSG00000108107
RPL27	ENSG00000131469
RPL27A	ENSG00000166441
RPL26L1	ENSG00000037241
RPL26	ENSG00000161970
RPL24	ENSG00000114391
RPL23	ENSG00000125691
RPL23A	ENSG00000198242
RPL22L1	ENSG00000163584

RPL22	ENSG00000116251
RPL21	ENSG00000122026
RPL19	ENSG00000108298
RPL18	ENSG00000063177
RPL18A	ENSG00000105640
RPL17	ENSG00000265681
RPL17	ENSG00000215472
RPL15	ENSG00000174748
RPL14	ENSG00000188846
RPL13	ENSG00000167526
RPL13A	ENSG00000142541
RPL12	ENSG00000197958
RPL11	ENSG00000142676
RPL10L	ENSG00000165496
RPL10	ENSG00000147403
RPL10A	ENSG00000198755

human A147mRPGS

Symbol	*Accession*
MRPS9	ENSG00000135972
MRPS7	ENSG00000125445
MRPS6	ENSG00000243927
MRPS5	ENSG00000144029
MRPS36	ENSG00000134056
MRPS35	ENSG00000061794
MRPS34	ENSG00000074071
MRPS33	ENSG00000090263
MRPS31	ENSG00000102738
MRPS30	ENSG00000112996
MRPS2	ENSG00000122140
MRPS28	ENSG00000147586
MRPS27	ENSG00000113048
MRPS26	ENSG00000125901
MRPS25	ENSG00000131368
MRPS24	ENSG00000062582
MRPS23	ENSG00000181610
MRPS22	ENSG00000175110
MRPS18C	ENSG00000163319
MRPS18B	ENSG00000204568
MRPS18A	ENSG00000096080
MRPS17	ENSG00000239789

MRPS16	ENSG00000182180
MRPS15	ENSG00000116898
MRPS14	ENSG00000120333
MRPS12	ENSG00000128626
MRPS11	ENSG00000181991
MRPS10	ENSG00000048544
MRPL9	ENSG00000143436
MRPL55	ENSG00000162910
MRPL54	ENSG00000183617
MRPL53	ENSG00000204822
MRPL52	ENSG00000172590
MRPL51	ENSG00000111639
MRPL50	ENSG00000136897
MRPL4	ENSG00000105364
MRPL49	ENSG00000149792
MRPL48	ENSG00000175581
MRPL47	ENSG00000136522
MRPL46	ENSG00000259494
MRPL45	ENSG00000174100
MRPL44	ENSG00000135900
MRPL43	ENSG00000055950
MRPL42	ENSG00000198015
MRPL41	ENSG00000182154
MRPL40	ENSG00000185608
MRPL3	ENSG00000114686
MRPL39	ENSG00000154719
MRPL38	ENSG00000204316
MRPL37	ENSG00000116221
MRPL36	ENSG00000171421
MRPL35	ENSG00000132313
MRPL34	ENSG00000130312
MRPL33	ENSG00000243147
MRPL32	ENSG00000106591
MRPL30	ENSG00000185414
MRPL2	ENSG00000112651
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MRPL27	ENSG00000108826
MRPL24	ENSG00000143314
MRPL23	ENSG00000214026
MRPL22	ENSG00000082515
MRPL21	ENSG00000197345
MRPL20	ENSG00000242485

MRPL1	ENSG00000169288
MRPL19	ENSG00000115364
MRPL18	ENSG00000112110
MRPL17	ENSG00000158042
MRPL16	ENSG00000166902
MRPL15	ENSG00000137547
MRPL14	ENSG00000180992
MRPL13	ENSG00000172172
MRPL12	ENSG00000262814
MRPL11	ENSG00000174547
MRPL10	ENSG00000159111
MRP63	ENSG00000173141

mouse cRPGs+A231

RPL10	ENSMUSG00000008682
RPL10A	ENSMUSG00000037805
RPL10L	ENSMUSG00000060499
RPL11	ENSMUSG00000059291
RPL12	ENSMUSG00000038900
RPL13	ENSMUSG00000000740
RPL13A	ENSMUSG00000074129
RPL14	ENSMUSG00000025794
RPL15	ENSMUSG00000012405
RPL17	ENSMUSG00000062328
RPL18	ENSMUSG00000059070
RPL18A	ENSMUSG00000045128
RPL19	ENSMUSG00000017404
RPL21	ENSMUSG00000041453
RPL22	ENSMUSG00000028936
RPL22L1	ENSMUSG00000039221
RPL23	ENSMUSG00000071415
RPL23A	ENSMUSG00000058546
RPL26	ENSMUSG00000060938
RPL27	ENSMUSG00000063316
RPL27A	ENSMUSG00000046364
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RPL7A	ENSMUSG00000062647
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RPS14	ENSMUSG00000024608
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RPS2	ENSMUSG00000044533
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RPS21	ENSMUSG00000039001
RPS23	ENSMUSG00000049517
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RPS25	ENSMUSG00000009927
RPS26	ENSMUSG00000025362
RPS27	ENSMUSG00000090733

RPS27A	ENSMUSG00000020460
RPS27L	ENSMUSG00000036781
RPS28	ENSMUSG00000067288
RPS29	ENSMUSG00000034892
RPS3	ENSMUSG00000030744
RPS3A	ENSMUSG00000028081
RPS4X	ENSMUSG00000031320
RPS4Y2	ENSMUSG00000063171
RPS5	ENSMUSG00000012848
RPS6	ENSMUSG00000028495
RPS7	ENSMUSG00000061477
RPS8	ENSMUSG00000047675
RPS9	ENSMUSG00000006333
RPSA	ENSMUSG00000032518

mouse mRPGs

MRPL1	ENSMUSG00000029486
MRPL10	ENSMUSG00000001445
MRPL11	ENSMUSG00000024902
MRPL12	ENSMUSG00000039640
MRPL13	ENSMUSG00000022370
MRPL14	ENSMUSG00000023939
MRPL15	ENSMUSG00000033845
MRPL16	ENSMUSG00000024683
MRPL17	ENSMUSG00000030879
MRPL18	ENSMUSG00000057388
MRPL19	ENSMUSG00000030045
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MRPL20	ENSMUSG00000029066
MRPL21	ENSMUSG00000024829
MRPL22	ENSMUSG00000020514
MRPL23	ENSMUSG00000037772
MRPL24	ENSMUSG00000019710
MRPL27	ENSMUSG00000024414
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MRPL3	ENSMUSG00000032563
MRPL30	ENSMUSG00000026087
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MRPL33	ENSMUSG00000029142
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MRPL36	ENSMUSG00000021607

MRPL37	ENSMUSG00000028622
MRPL38	ENSMUSG00000020775
MRPL39	ENSMUSG00000022889
MRPL4	ENSMUSG00000003299
MRPL40	ENSMUSG00000022706
MRPL41	ENSMUSG00000036850
MRPL42	ENSMUSG00000062981
MRPL43	ENSMUSG00000025208
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MRPL47	ENSMUSG00000037531
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MRPL51	ENSMUSG00000030335
MRPL52	ENSMUSG00000010406
MRPL53	ENSMUSG00000030037
MRPL54	ENSMUSG00000034932
MRPL55	ENSMUSG00000036860
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MRPS10	ENSMUSG00000034729
MRPS11	ENSMUSG00000030611
MRPS12	ENSMUSG00000045948
MRPS14	ENSMUSG00000058267
MRPS15	ENSMUSG00000028861
MRPS16	ENSMUSG00000049960
MRPS17	ENSMUSG00000034211
MRPS18A	ENSMUSG00000023967
MRPS18B	ENSMUSG00000024436
MRPS18C	ENSMUSG00000016833
MRPS2	ENSMUSG00000035772
MRPS21	ENSMUSG00000054312
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MRPS23	ENSMUSG00000023723
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MRPS26	ENSMUSG00000037740
MRPS27	ENSMUSG00000041632
MRPS28	ENSMUSG00000040269
MRPS30	ENSMUSG00000021731
MRPS31	ENSMUSG00000031533

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MRPS35	ENSMUSG00000040112
MRPS36	ENSMUSG00000061474
MRPS5	ENSMUSG00000027374
MRPS6	ENSMUSG00000039680
MRPS9	ENSMUSG00000060679

Table S2. **Highly expressed non-ribosomal genes (HE-NRGs) in human and mouse** were selected from the Expression Atlas Database (Kolesnikov et al., 2015).

Human HE-NRGs

Ensembl Gene ID	**Description**	**HGNC symbol**
ENSG00000011052	NME/NM23 nucleoside diphosphate kinase 2 [Source:HGNC Symbol;Acc:HGNC:7850]	NME2
ENSG00000019582	CD74 molecule, major histocompatibility complex, class II invariant chain [Source:HGNC Symbol;Acc:HGNC:1697]	CD74
ENSG00000034510	thymosin beta 10 [Source:HGNC Symbol;Acc:HGNC:11879]	TMSB10
ENSG00000063046	eukaryotic translation initiation factor 4B [Source:HGNC Symbol;Acc:HGNC:3285]	EIF4B
ENSG00000065518	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4, 15kDa [Source:HGNC Symbol;Acc:HGNC:7699]	NDUFB4
ENSG00000065978	Y box binding protein 1 [Source:HGNC Symbol;Acc:HGNC:8014]	YBX1
ENSG00000067225	pyruvate kinase, muscle [Source:HGNC Symbol;Acc:HGNC:9021]	PKM
ENSG00000067560	ras homolog family member A [Source:HGNC Symbol;Acc:HGNC:667]	RHOA
ENSG00000070756	poly(A) binding protein, cytoplasmic 1 [Source:HGNC Symbol;Acc:HGNC:8554]	PABPC1
ENSG00000074800	enolase 1, (alpha) [Source:HGNC Symbol;Acc:HGNC:3350]	ENO1
ENSG00000075415	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 3 [Source:HGNC Symbol;Acc:HGNC:10989]	SLC25A3
ENSG00000075624	actin, beta [Source:HGNC Symbol;Acc:HGNC:132]	ACTB
ENSG00000075785	RAB7A, member RAS oncogene family [Source:HGNC Symbol;Acc:HGNC:9788]	RAB7A
ENSG00000078369	guanine nucleotide binding protein (G protein), beta polypeptide 1 [Source:HGNC Symbol;Acc:HGNC:4396]	GNB1
ENSG00000080824	heat shock protein 90kDa alpha (cytosolic), class A member 1 [Source:HGNC Symbol;Acc:HGNC:5253]	HSP90AA1
ENSG00000084207	glutathione S-transferase pi 1 [Source:HGNC Symbol;Acc:HGNC:4638]	GSTP1
ENSG00000084234	amyloid beta (A4) precursor-like protein 2 [Source:HGNC Symbol;Acc:HGNC:598]	APLP2
ENSG00000087086	ferritin, light polypeptide [Source:HGNC Symbol;Acc:HGNC:3999]	FTL
ENSG00000088986	dynein, light chain, LC8-type 1 [Source:HGNC Symbol;Acc:HGNC:15476]	DYNLL1
ENSG00000092199	heterogeneous nuclear ribonucleoprotein C (C1/C2) [Source:HGNC Symbol;Acc:HGNC:5035]	HNRNPC
ENSG00000092841	myosin, light chain 6, alkali, smooth muscle and non-muscle [Source:HGNC Symbol;Acc:HGNC:7587]	MYL6
ENSG00000096384	heat shock protein 90kDa alpha (cytosolic), class B member 1 [Source:HGNC Symbol;Acc:HGNC:5258]	HSP90AB1
ENSG00000100097	lectin, galactoside-binding, soluble, 1 [Source:HGNC Symbol;Acc:HGNC:6561]	LGALS1
ENSG00000100650	serine/arginine-rich splicing factor 5 [Source:HGNC Symbol;Acc:HGNC:10787]	SRSF5
ENSG00000100823	APEX nuclease (multifunctional DNA repair enzyme) 1 [Source:HGNC Symbol;Acc:HGNC:587]	APEX1
ENSG00000101439	cystatin C [Source:HGNC Symbol;Acc:HGNC:2475]	CST3
ENSG00000102265	TIMP metallopeptidase inhibitor 1 [Source:HGNC Symbol;Acc:HGNC:11820]	TIMP1
ENSG00000103363	transcription elongation factor B (SIII), polypeptide 2 (18kDa, elongin B) [Source:HGNC Symbol;Acc:HGNC:11619]	TCEB2
ENSG00000103495	MYC-associated zinc finger protein (purine-binding transcription factor) [Source:HGNC Symbol;Acc:HGNC:6914]	MAZ
ENSG00000104529	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein) [Source:HGNC Symbol;Acc:HGNC:3211]	EEF1D
ENSG00000104904	ornithine decarboxylase antizyme 1 [Source:HGNC Symbol;Acc:HGNC:8095]	OAZ1
ENSG00000104964	amino-terminal enhancer of split [Source:HGNC Symbol;Acc:HGNC:307]	AES
ENSG00000105373	glioma tumor suppressor candidate region gene 2 [Source:HGNC Symbol;Acc:HGNC:4333]	GLTSCR2
ENSG00000105701	FK506 binding protein 8, 38kDa [Source:HGNC Symbol;Acc:HGNC:3724]	FKBP8
ENSG00000106153	coiled-coil-helix-coiled-coil-helix domain containing 2 [Source:HGNC Symbol;Acc:HGNC:21645]	CHCHD2
ENSG00000106211	heat shock 27kDa protein 1 [Source:HGNC Symbol;Acc:HGNC:5246]	HSPB1
ENSG00000107223	endothelial differentiation-related factor 1 [Source:HGNC Symbol;Acc:HGNC:3164]	EDF1
ENSG00000108518	profilin 1 [Source:HGNC Symbol;Acc:HGNC:8881]	PFN1
ENSG00000108953	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon [Source:HGNC Symbol;Acc:HGNC:12851]	YWHAE
ENSG00000109971	heat shock 70kDa protein 8 [Source:HGNC Symbol;Acc:HGNC:5241]	HSPA8
ENSG00000110651	CD81 molecule [Source:HGNC Symbol;Acc:HGNC:1701]	CD81
ENSG00000110717	NADH dehydrogenase (ubiquinone) Fe-S protein 8, 23kDa (NADH-coenzyme Q reductase) [Source:HGNC Symbol;Acc:HGNC:7715]	NDUFS8
ENSG00000110955	ATP synthase, H+ transporting, mitochondrial F1 complex, beta polypeptide [Source:HGNC Symbol;Acc:HGNC:830]	ATP5B
ENSG00000111640	glyceraldehyde-3-phosphate dehydrogenase [Source:HGNC Symbol;Acc:HGNC:4141]	GAPDH
ENSG00000111669	triosephosphate isomerase 1 [Source:HGNC Symbol;Acc:HGNC:12009]	TPI1
ENSG00000111678	chromosome 12 open reading frame 57 [Source:HGNC Symbol;Acc:HGNC:29521]	C12orf57
ENSG00000111716	lactate dehydrogenase B [Source:HGNC Symbol;Acc:HGNC:6541]	LDHB
ENSG00000111775	cytochrome c oxidase subunit VIa polypeptide 1 [Source:HGNC Symbol;Acc:HGNC:2277]	COX6A1
ENSG00000112695	cytochrome c oxidase subunit VIIa polypeptide 2 (liver) [Source:HGNC Symbol;Acc:HGNC:2288]	COX7A2
ENSG00000113558	S-phase kinase-associated protein 1 [Source:HGNC Symbol;Acc:HGNC:10899]	SKP1
ENSG00000114942	eukaryotic translation elongation factor 1 beta 2 [Source:HGNC Symbol;Acc:HGNC:3208]	EEF1B2
ENSG00000116288	parkinson protein 7 [Source:HGNC Symbol;Acc:HGNC:16369]	PARK7
ENSG00000117450	peroxiredoxin 1 [Source:HGNC Symbol;Acc:HGNC:9352]	PRDX1
ENSG00000117984	cathepsin D [Source:HGNC Symbol;Acc:HGNC:2529]	CTSD
ENSG00000118816	cyclin I [Source:HGNC Symbol;Acc:HGNC:1595]	CCNI
ENSG00000120885	clusterin [Source:HGNC Symbol;Acc:HGNC:2095]	CLU
ENSG00000122566	heterogeneous nuclear ribonucleoprotein A2/B1 [Source:HGNC Symbol;Acc:HGNC:5033]	HNRNPA2B1
ENSG00000123349	prefoldin subunit 5 [Source:HGNC Symbol;Acc:HGNC:8869]	PFDN5

ENSG00000123416	tubulin, alpha 1b [Source:HGNC Symbol;Acc:HGNC:18809]	TUBA1B
ENSG00000125534	pancreatic progenitor cell differentiation and proliferation factor [Source:HGNC Symbol;Acc:HGNC:16142]	PPDPF
ENSG00000125743	small nuclear ribonucleoprotein D2 polypeptide 16.5kDa [Source:HGNC Symbol;Acc:HGNC:11159]	SNRPD2
ENSG00000125971	dynein, light chain, roadblock-type 1 [Source:HGNC Symbol;Acc:HGNC:15468]	DYNLRB1
ENSG00000125995	reactive oxygen species modulator 1 [Source:HGNC Symbol;Acc:HGNC:16185]	ROMO1
ENSG00000126247	calpain, small subunit 1 [Source:HGNC Symbol;Acc:HGNC:1481]	CAPNS1
ENSG00000126267	cytochrome c oxidase subunit VIb polypeptide 1 (ubiquitous) [Source:HGNC Symbol;Acc:HGNC:2280]	COX6B1
ENSG00000126432	peroxiredoxin 5 [Source:HGNC Symbol;Acc:HGNC:9355]	PRDX5
ENSG00000127022	calnexin [Source:HGNC Symbol;Acc:HGNC:1473]	CANX
ENSG00000127184	cytochrome c oxidase subunit VIIc [Source:HGNC Symbol;Acc:HGNC:2292]	COX7C
ENSG00000127922	split hand/foot malformation (ectrodactyly) type 1 [Source:HGNC Symbol;Acc:HGNC:10845]	SHFM1
ENSG00000128272	activating transcription factor 4 [Source:HGNC Symbol;Acc:HGNC:786]	ATF4
ENSG00000130770	ATPase inhibitory factor 1 [Source:HGNC Symbol;Acc:HGNC:871]	ATPIF1
ENSG00000131143	cytochrome c oxidase subunit IV isoform 1 [Source:HGNC Symbol;Acc:HGNC:2265]	COX4I1
ENSG00000132341	RAN, member RAS oncogene family [Source:HGNC Symbol;Acc:HGNC:9846]	RAN
ENSG00000132507	eukaryotic translation initiation factor 5A [Source:HGNC Symbol;Acc:HGNC:3300]	EIF5A
ENSG00000133112	tumor protein, translationally-controlled 1 [Source:HGNC Symbol;Acc:HGNC:12022]	TPT1
ENSG00000134333	lactate dehydrogenase A [Source:HGNC Symbol;Acc:HGNC:6535]	LDHA
ENSG00000135390	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit C2 (subunit 9) [Source:HGNC Symbol;Acc:HGNC:842]	ATP5G2
ENSG00000135404	CD63 molecule [Source:HGNC Symbol;Acc:HGNC:1692]	CD63
ENSG00000135486	heterogeneous nuclear ribonucleoprotein A1 [Source:HGNC Symbol;Acc:HGNC:5031]	HNRNPA1
ENSG00000135940	cytochrome c oxidase subunit Vb [Source:HGNC Symbol;Acc:HGNC:2269]	COX5B
ENSG00000138668	heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kDa) [Source:HGNC Symbol;Acc:HGNC:5036]	HNRNPD
ENSG00000139644	transmembrane BAX inhibitor motif containing 6 [Source:HGNC Symbol;Acc:HGNC:11723]	TMBIM6
ENSG00000140264	small EDRK-rich factor 2 [Source:HGNC Symbol;Acc:HGNC:10757]	SERF2
ENSG00000140319	signal recognition particle 14kDa (homologous Alu RNA binding protein) [Source:HGNC Symbol;Acc:HGNC:11299]	SRP14
ENSG00000141522	Rho GDP dissociation inhibitor (GDI) alpha [Source:HGNC Symbol;Acc:HGNC:678]	ARHGDIA
ENSG00000142089	interferon induced transmembrane protein 3 [Source:HGNC Symbol;Acc:HGNC:5414]	IFITM3
ENSG00000142192	amyloid beta (A4) precursor protein [Source:HGNC Symbol;Acc:HGNC:620]	APP
ENSG00000143761	ADP-ribosylation factor 1 [Source:HGNC Symbol;Acc:HGNC:652]	ARF1
ENSG00000143933	calmodulin 2 (phosphorylase kinase, delta) [Source:HGNC Symbol;Acc:HGNC:1445]	CALM2
ENSG00000145741	basic transcription factor 3 [Source:HGNC Symbol;Acc:HGNC:1125]	BTF3
ENSG00000149806	Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed [Source:HGNC Symbol;Acc:HGNC:3597]	FAU
ENSG00000149925	aldolase A, fructose-bisphosphate [Source:HGNC Symbol;Acc:HGNC:414]	ALDOA
ENSG00000150991	ubiquitin C [Source:HGNC Symbol;Acc:HGNC:12468]	UBC
ENSG00000152082	mitotic spindle organizing protein 2B [Source:HGNC Symbol;Acc:HGNC:25886]	MZT2B
ENSG00000155368	diazepam binding inhibitor (GABA receptor modulator, acyl-CoA binding protein) [Source:HGNC Symbol;Acc:HGNC:2690]	DBI
ENSG00000156467	ubiquinol-cytochrome c reductase binding protein [Source:HGNC Symbol;Acc:HGNC:12582]	UQCRB
ENSG00000156508	eukaryotic translation elongation factor 1 alpha 1 [Source:HGNC Symbol;Acc:HGNC:3189]	EEF1A1
ENSG00000159199	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit C1 (subunit 9) [Source:HGNC Symbol;Acc:HGNC:841]	ATP5G1
ENSG00000159335	parathymosin [Source:HGNC Symbol;Acc:HGNC:9629]	PTMS
ENSG00000160014	calmodulin 3 (phosphorylase kinase, delta) [Source:HGNC Symbol;Acc:HGNC:1449]	CALM3
ENSG00000161960	eukaryotic translation initiation factor 4A1 [Source:HGNC Symbol;Acc:HGNC:3282]	EIF4A1
ENSG00000163041	H3 histone, family 3A [Source:HGNC Symbol;Acc:HGNC:4764]	H3F3A
ENSG00000164405	ubiquinol-cytochrome c reductase, complex III subunit VII, 9.5kDa [Source:HGNC Symbol;Acc:HGNC:29594]	UQCRQ
ENSG00000164919	cytochrome c oxidase subunit VIc [Source:HGNC Symbol;Acc:HGNC:2285]	COX6C
ENSG00000165119	heterogeneous nuclear ribonucleoprotein K [Source:HGNC Symbol;Acc:HGNC:5044]	HNRNPK
ENSG00000166165	creatine kinase, brain [Source:HGNC Symbol;Acc:HGNC:1991]	CKB
ENSG00000166598	heat shock protein 90kDa beta (Grp94), member 1 [Source:HGNC Symbol;Acc:HGNC:12028]	HSP90B1
ENSG00000166710	beta-2-microglobulin [Source:HGNC Symbol;Acc:HGNC:914]	B2M
ENSG00000166794	peptidylprolyl isomerase B (cyclophilin B) [Source:HGNC Symbol;Acc:HGNC:9255]	PPIB
ENSG00000167468	glutathione peroxidase 4 [Source:HGNC Symbol;Acc:HGNC:4556]	GPX4
ENSG00000167552	tubulin, alpha 1a [Source:HGNC Symbol;Acc:HGNC:20766]	TUBA1A
ENSG00000167553	tubulin, alpha 1c [Source:HGNC Symbol;Acc:HGNC:20768]	TUBA1C
ENSG00000167658	eukaryotic translation elongation factor 2 [Source:HGNC Symbol;Acc:HGNC:3214]	EEF2
ENSG00000167815	peroxiredoxin 2 [Source:HGNC Symbol;Acc:HGNC:9353]	PRDX2
ENSG00000167996	ferritin, heavy polypeptide 1 [Source:HGNC Symbol;Acc:HGNC:3976]	FTH1
ENSG00000168653	NADH dehydrogenase (ubiquinone) Fe-S protein 5, 15kDa (NADH-coenzyme Q reductase) [Source:HGNC Symbol;Acc:HGNC:7712]	NDUFS5
ENSG00000169020	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit E [Source:HGNC Symbol;Acc:HGNC:846]	ATP5I
ENSG00000169045	heterogeneous nuclear ribonucleoprotein H1 (H) [Source:HGNC Symbol;Acc:HGNC:5041]	HNRNPH1
ENSG00000169100	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6 [Source:HGNC Symbol;Acc:HGNC:10992]	SLC25A6
ENSG00000169218	R-spondin 1 [Source:HGNC Symbol;Acc:HGNC:21679]	RSPO1
ENSG00000170144	heterogeneous nuclear ribonucleoprotein A3 [Source:HGNC Symbol;Acc:HGNC:24941]	HNRNPA3
ENSG00000170296	GABA(A) receptor-associated protein [Source:HGNC Symbol;Acc:HGNC:4067]	GABARAP
ENSG00000170315	ubiquitin B [Source:HGNC Symbol;Acc:HGNC:12463]	UBB

ENSG00000170906	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 3, 9kDa [Source:HGNC Symbol;Acc:HGNC:7686]	NDUFA3
ENSG00000171530	tubulin folding cofactor A [Source:HGNC Symbol;Acc:HGNC:11579]	TBCA
ENSG00000172270	basigin (Ok blood group) [Source:HGNC Symbol;Acc:HGNC:1116]	BSG
ENSG00000172354	guanine nucleotide binding protein (G protein), beta polypeptide 2 [Source:HGNC Symbol;Acc:HGNC:4398]	GNB2
ENSG00000172757	cofilin 1 (non-muscle) [Source:HGNC Symbol;Acc:HGNC:1874]	CFL1
ENSG00000173113	tRNA methyltransferase 11-2 homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:HGNC:26940]	TRMT112
ENSG00000173660	ubiquinol-cytochrome c reductase hinge protein [Source:HGNC Symbol;Acc:HGNC:12590]	UQCRH
ENSG00000173915	up-regulated during skeletal muscle growth 5 homolog (mouse) [Source:HGNC Symbol;Acc:HGNC:30889]	USMG5
ENSG00000176340	cytochrome c oxidase subunit VIIIA (ubiquitous) [Source:HGNC Symbol;Acc:HGNC:2294]	COX8A
ENSG00000179010	Morf4 family associated protein 1 [Source:HGNC Symbol;Acc:HGNC:24549]	MRFAP1
ENSG00000179218	calreticulin [Source:HGNC Symbol;Acc:HGNC:1455]	CALR
ENSG00000180879	signal sequence receptor, delta [Source:HGNC Symbol;Acc:HGNC:11326]	SSR4
ENSG00000181163	nucleophosmin (nucleolar phosphoprotein B23, numatrin) [Source:HGNC Symbol;Acc:HGNC:7910]	NPM1
ENSG00000184009	actin, gamma 1 [Source:HGNC Symbol;Acc:HGNC:144]	ACTG1
ENSG00000185201	interferon induced transmembrane protein 2 [Source:HGNC Symbol;Acc:HGNC:5413]	IFITM2
ENSG00000185624	prolyl 4-hydroxylase, beta polypeptide [Source:HGNC Symbol;Acc:HGNC:8548]	P4HB
ENSG00000185787	mortality factor 4 like 1 [Source:HGNC Symbol;Acc:HGNC:16989]	MORF4L1
ENSG00000185883	ATPase, H+ transporting, lysosomal 16kDa, V0 subunit c [Source:HGNC Symbol;Acc:HGNC:855]	ATP6V0C
ENSG00000186010	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 13 [Source:HGNC Symbol;Acc:HGNC:17194]	NDUFA13
ENSG00000187514	prothymosin, alpha [Source:HGNC Symbol;Acc:HGNC:9623]	PTMA
ENSG00000189403	high mobility group box 1 [Source:HGNC Symbol;Acc:HGNC:4983]	HMGB1
ENSG00000196230	tubulin, beta class I [Source:HGNC Symbol;Acc:HGNC:20778]	TUBB
ENSG00000196262	peptidylprolyl isomerase A (cyclophilin A) [Source:HGNC Symbol;Acc:HGNC:9253]	PPIA
ENSG00000196531	nascent polypeptide-associated complex alpha subunit [Source:HGNC Symbol;Acc:HGNC:7629]	NACA
ENSG00000196683	translocase of outer mitochondrial membrane 7 homolog (yeast) [Source:HGNC Symbol;Acc:HGNC:21648]	TOMM7
ENSG00000197111	poly(rC) binding protein 2 [Source:HGNC Symbol;Acc:HGNC:8648]	PCBP2
ENSG00000197746	prosaposin [Source:HGNC Symbol;Acc:HGNC:9498]	PSAP
ENSG00000198258	ubiquitin-like 5 [Source:HGNC Symbol;Acc:HGNC:13736]	UBL5
ENSG00000198830	high mobility group nucleosomal binding domain 2 [Source:HGNC Symbol;Acc:HGNC:4986]	HMGN2
ENSG00000204525	major histocompatibility complex, class I, C [Source:HGNC Symbol;Acc:HGNC:4933]	HLA-C
ENSG00000204628	guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1 [Source:HGNC Symbol;Acc:HGNC:4399]	GNB2L1
ENSG00000205352	proline rich 13 [Source:HGNC Symbol;Acc:HGNC:24528]	PRR13
ENSG00000205542	thymosin beta 4, X-linked [Source:HGNC Symbol;Acc:HGNC:11881]	TMSB4X
ENSG00000206503	major histocompatibility complex, class I, A [Source:HGNC Symbol;Acc:HGNC:4931]	HLA-A
ENSG00000219200	ribonuclease, RNase K [Source:HGNC Symbol;Acc:HGNC:33911]	RNASEK
ENSG00000228474	oligosaccharyltransferase 4 homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:HGNC:32483]	OST4
ENSG00000232112	translation machinery associated 7 homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:HGNC:26932]	TMA7
ENSG00000234745	major histocompatibility complex, class I, B [Source:HGNC Symbol;Acc:HGNC:4932]	HLA-B
ENSG00000241468	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit F2 [Source:HGNC Symbol;Acc:HGNC:848]	ATP5J2
ENSG00000254772	eukaryotic translation elongation factor 1 gamma [Source:HGNC Symbol;Acc:HGNC:3213]	EEF1G
ENSG00000255823	MT-RNR2-like 8 [Source:HGNC Symbol;Acc:HGNC:37165]	MTRNR2L8
ENSG00000256045	MT-RNR2-like 10 [Source:HGNC Symbol;Acc:HGNC:37167]	MTRNR2L10
ENSG00000256222	MT-RNR2-like 3 [Source:HGNC Symbol;Acc:HGNC:37157]	MTRNR2L3
ENSG00000256618	MT-RNR2-like 1 [Source:HGNC Symbol;Acc:HGNC:37155]	MTRNR2L1

Mouse HE-NRGs

Ensembl Gene ID	Description	MGI symbol
ENSMUSG00000000682	CD52 antigen [Source:MGI Symbol;Acc:MGI:1346088]	Cd52
ENSMUSG00000001666	D-dopachrome tautomerase [Source:MGI Symbol;Acc:MGI:1298381]	Ddt
ENSMUSG00000011752	phosphoglycerate mutase 1 [Source:MGI Symbol;Acc:MGI:97552]	Pgam1
ENSMUSG00000015656	heat shock protein 8 [Source:MGI Symbol;Acc:MGI:105384]	Hspa8
ENSMUSG00000016319	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5 [Source:MGI Symbol;Acc:MGI:1353496]	Slc25a5
ENSMUSG00000017778	cytochrome c oxidase subunit VIIc [Source:MGI Symbol;Acc:MGI:103226]	Cox7c
ENSMUSG00000018293	profilin 1 [Source:MGI Symbol;Acc:MGI:97549]	Pfn1
ENSMUSG00000019505	ubiquitin B [Source:MGI Symbol;Acc:MGI:98888]	Ubb
ENSMUSG00000020018	small nuclear ribonucleoprotein polypeptide F [Source:MGI Symbol;Acc:MGI:1917128]	Snrpf
ENSMUSG00000020163	ubiquinol-cytochrome c reductase, complex III subunit XI [Source:MGI Symbol;Acc:MGI:1913844]	Uqcr11
ENSMUSG00000020219	translocase of inner mitochondrial membrane 13 [Source:MGI Symbol;Acc:MGI:1353432]	Timm13
ENSMUSG00000020372	guanine nucleotide binding protein (G protein), beta polypeptide 2 like 1 [Source:MGI Symbol;Acc:MGI:101849]	Gnb2l1
ENSMUSG00000020738	SMT3 suppressor of mif two 3 homolog 2 (yeast) [Source:MGI Symbol;Acc:MGI:2158813]	Sumo2
ENSMUSG00000020857	NME/NM23 nucleoside diphosphate kinase 2 [Source:MGI Symbol;Acc:MGI:97356]	Nme2

ENSMUSG00000021131	enhancer of rudimentary homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:108089]	Erh
ENSMUSG00000021520	ubiquinol-cytochrome c reductase binding protein [Source:MGI Symbol;Acc:MGI:1914780]	Uqcrb
ENSMUSG00000021660	basic transcription factor 3 [Source:MGI Symbol;Acc:MGI:1202875]	Btf3
ENSMUSG00000022982	superoxide dismutase 1, soluble [Source:MGI Symbol;Acc:MGI:98351]	Sod1
ENSMUSG00000023004	tubulin, alpha 1B [Source:MGI Symbol;Acc:MGI:107804]	Tuba1b
ENSMUSG00000024653	secretoglobin, family 1A, member 1 (uteroglobin) [Source:MGI Symbol;Acc:MGI:98919]	Scgb1a1
ENSMUSG00000024661	ferritin heavy chain 1 [Source:MGI Symbol;Acc:MGI:95588]	Fth1
ENSMUSG00000026162	nonhomologous end-joining factor 1 [Source:MGI Symbol;Acc:MGI:1922820]	Nhej1
ENSMUSG00000026238	prothymosin alpha [Source:MGI Symbol;Acc:MGI:97803]	Ptma
ENSMUSG00000027907	S100 calcium binding protein A11 (calgizzarin) [Source:MGI Symbol;Acc:MGI:1338798]	S100a11
ENSMUSG00000027944	HCLS1 associated X-1 [Source:MGI Symbol;Acc:MGI:1346319]	Hax1
ENSMUSG00000028333	acidic (leucine-rich) nuclear phosphoprotein 32 family, member B [Source:MGI Symbol;Acc:MGI:1914878]	Anp32b
ENSMUSG00000028367	thioredoxin 1 [Source:MGI Symbol;Acc:MGI:98874]	Txn1
ENSMUSG00000028773	fatty acid binding protein 3, muscle and heart [Source:MGI Symbol;Acc:MGI:95476]	Fabp3
ENSMUSG00000029075	tumor necrosis factor receptor superfamily, member 4 [Source:MGI Symbol;Acc:MGI:104512]	Tnfrsf4
ENSMUSG00000029368	albumin [Source:MGI Symbol;Acc:MGI:87991]	Alb
ENSMUSG00000029580	actin, beta [Source:MGI Symbol;Acc:MGI:87904]	Actb
ENSMUSG00000030695	aldolase A, fructose-bisphosphate [Source:MGI Symbol;Acc:MGI:87994]	Aldoa
ENSMUSG00000031146	proteolipid protein 2 [Source:MGI Symbol;Acc:MGI:1298382]	Plp2
ENSMUSG00000031231	cytochrome c oxidase subunit VIIb [Source:MGI Symbol;Acc:MGI:1913392]	Cox7b
ENSMUSG00000031765	metallothionein 1 [Source:MGI Symbol;Acc:MGI:97171]	Mt1
ENSMUSG00000032294	pyruvate kinase, muscle [Source:MGI Symbol;Acc:MGI:97591]	Pkm
ENSMUSG00000033307	macrophage migration inhibitory factor [Source:MGI Symbol;Acc:MGI:96982]	Mif
ENSMUSG00000034566	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit D [Source:MGI Symbol;Acc:MGI:1918929]	Atp5h
ENSMUSG00000035215	LSM7 homolog, U6 small nuclear RNA associated (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1913344]	Lsm7
ENSMUSG00000035242	ornithine decarboxylase antizyme 1 [Source:MGI Symbol;Acc:MGI:109433]	Oaz1
ENSMUSG00000036752	tubulin, beta 4B class IVB [Source:MGI Symbol;Acc:MGI:1915472]	Tubb4b
ENSMUSG00000036835	presenilin enhancer 2 homolog (C. elegans) [Source:MGI Symbol;Acc:MGI:1913590]	Psenen
ENSMUSG00000038274	Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed (fox derived) [Source:MGI Symbol;Acc:MGI:102547]	Fau
ENSMUSG00000038717	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit G [Source:MGI Symbol;Acc:MGI:1351597]	Atp5l
ENSMUSG00000041697	cytochrome c oxidase subunit VIa polypeptide 1 [Source:MGI Symbol;Acc:MGI:103099]	Cox6a1
ENSMUSG00000049775	thymosin, beta 4, X chromosome [Source:MGI Symbol;Acc:MGI:99510]	Tmsb4x
ENSMUSG00000050708	ferritin light chain 1 [Source:MGI Symbol;Acc:MGI:95589]	Ftl1
ENSMUSG00000052305	hemoglobin, beta adult s chain [Source:MGI Symbol;Acc:MGI:5474852]	Hbb-bs
ENSMUSG00000053317	Sec61 beta subunit [Source:MGI Symbol;Acc:MGI:1913462]	Sec61b
ENSMUSG00000054106	trypsin 4 [Source:MGI Symbol;Acc:MGI:102757]	Try4
ENSMUSG00000055302	Morf4 family associated protein 1 [Source:MGI Symbol;Acc:MGI:1914818]	Mrfap1
ENSMUSG00000057113	nucleophosmin 1 [Source:MGI Symbol;Acc:MGI:106184]	Npm1
ENSMUSG00000057506	biogenesis of lysosomal organelles complex-1, subunit 2 [Source:MGI Symbol;Acc:MGI:1920939]	Bloc1s2
ENSMUSG00000058126	tropomyosin 3, related sequence 7 [Source:MGI Symbol;Acc:MGI:99705]	Tpm3-rs7
ENSMUSG00000059040	enolase 1B, retrotransposed [Source:MGI Symbol;Acc:MGI:3648653]	Eno1b
ENSMUSG00000060591	interferon induced transmembrane protein 2 [Source:MGI Symbol;Acc:MGI:1933382]	Ifitm2
ENSMUSG00000060802	beta-2 microglobulin [Source:MGI Symbol;Acc:MGI:88127]	B2m
ENSMUSG00000060803	glutathione S-transferase, pi 1 [Source:MGI Symbol;Acc:MGI:95865]	Gstp1
ENSMUSG00000061315	nascent polypeptide-associated complex alpha polypeptide [Source:MGI Symbol;Acc:MGI:106095]	Naca
ENSMUSG00000061482	histone cluster 1, H4d [Source:MGI Symbol;Acc:MGI:2448423]	Hist1h4d
ENSMUSG00000061518	cytochrome c oxidase subunit Vb [Source:MGI Symbol;Acc:MGI:88475]	Cox5b
ENSMUSG00000062070	phosphoglycerate kinase 1 [Source:MGI Symbol;Acc:MGI:97555]	Pgk1
ENSMUSG00000062248	CDC28 protein kinase regulatory subunit 2 [Source:MGI Symbol;Acc:MGI:1913447]	Cks2
ENSMUSG00000062683	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit C2 (subunit 9) [Source:MGI Symbol;Acc:MGI:1915192]	Atp5g2
ENSMUSG00000062825	actin, gamma, cytoplasmic 1 [Source:MGI Symbol;Acc:MGI:87906]	Actg1
ENSMUSG00000062867	inosine 5'-phosphate dehydrogenase 2 [Source:MGI Symbol;Acc:MGI:109367]	Impdh2
ENSMUSG00000063229	lactate dehydrogenase A [Source:MGI Symbol;Acc:MGI:96759]	Ldha
ENSMUSG00000063524	enolase 1, alpha non-neuron [Source:MGI Symbol;Acc:MGI:95393]	Eno1

ENSMUSG00000064213	defensin, alpha, 24 [Source:MGI Symbol;Acc:MGI:3630383]	Defa24
ENSMUSG00000064341	mitochondrially encoded NADH dehydrogenase 1 [Source:MGI Symbol;Acc:MGI:101787]	mt-Nd1
ENSMUSG00000064345	mitochondrially encoded NADH dehydrogenase 2 [Source:MGI Symbol;Acc:MGI:102500]	mt-Nd2
ENSMUSG00000064351	mitochondrially encoded cytochrome c oxidase I [Source:MGI Symbol;Acc:MGI:102504]	mt-Co1
ENSMUSG00000064356	mitochondrially encoded ATP synthase 8 [Source:MGI Symbol;Acc:MGI:99926]	mt-Atp8
ENSMUSG00000064357	mitochondrially encoded ATP synthase 6 [Source:MGI Symbol;Acc:MGI:99927]	mt-Atp6
ENSMUSG00000064360	mitochondrially encoded NADH dehydrogenase 3 [Source:MGI Symbol;Acc:MGI:102499]	mt-Nd3
ENSMUSG00000064363	mitochondrially encoded NADH dehydrogenase 4 [Source:MGI Symbol;Acc:MGI:102498]	mt-Nd4
ENSMUSG00000064367	mitochondrially encoded NADH dehydrogenase 5 [Source:MGI Symbol;Acc:MGI:102496]	mt-Nd5
ENSMUSG00000064368	mitochondrially encoded NADH dehydrogenase 6 [Source:MGI Symbol;Acc:MGI:102495]	mt-Nd6
ENSMUSG00000064370	mitochondrially encoded cytochrome b [Source:MGI Symbol;Acc:MGI:102501]	mt-Cytb
ENSMUSG00000069117	predicted gene 10260 [Source:MGI Symbol;Acc:MGI:3642298]	Gm10260
ENSMUSG00000069744	proteasome (prosome, macropain) subunit, beta type 3 [Source:MGI Symbol;Acc:MGI:1347014]	Psmb3
ENSMUSG00000069919	hemoglobin alpha, adult chain 1 [Source:MGI Symbol;Acc:MGI:96015]	Hba-a1
ENSMUSG00000070493	coiled-coil-helix-coiled-coil-helix domain containing 2 [Source:MGI Symbol;Acc:MGI:1261428]	Chchd2
ENSMUSG00000071528	upregulated during skeletal muscle growth 5 [Source:MGI Symbol;Acc:MGI:1891435]	Usmg5
ENSMUSG00000071866	peptidylprolyl isomerase A [Source:MGI Symbol;Acc:MGI:97749]	Ppia
ENSMUSG00000073940	hemoglobin, beta adult t chain [Source:MGI Symbol;Acc:MGI:5474850]	Hbb-bt
ENSMUSG00000074516	predicted gene 10709 [Source:MGI Symbol;Acc:MGI:3642754]	Gm10709
ENSMUSG00000074695	interleukin 22 [Source:MGI Symbol;Acc:MGI:1355307]	Il22
ENSMUSG00000075014	predicted gene 10800 [Source:MGI Symbol;Acc:MGI:3641657]	Gm10800
ENSMUSG00000075602	lymphocyte antigen 6 complex, locus A [Source:MGI Symbol;Acc:MGI:107527]	Ly6a
ENSMUSG00000078193	predicted gene 2000 [Source:MGI Symbol;Acc:MGI:3780170]	Gm2000
ENSMUSG00000078427	SAP domain containing ribonucleoprotein [Source:MGI Symbol;Acc:MGI:1913368]	Sarnp
ENSMUSG00000078672	major urinary protein 20 [Source:MGI Symbol;Acc:MGI:3651981]	Mup20
ENSMUSG00000078974	SEC61, gamma subunit [Source:MGI Symbol;Acc:MGI:1202066]	Sec61g
ENSMUSG00000079010	predicted gene 11032 [Source:MGI Symbol;Acc:MGI:3779255]	Gm11032
ENSMUSG00000079018	lymphocyte antigen 6 complex, locus C1 [Source:MGI Symbol;Acc:MGI:96882]	Ly6c1
ENSMUSG00000079019	insulin-like 3 [Source:MGI Symbol;Acc:MGI:108427]	Insl3
ENSMUSG00000079523	thymosin, beta 10 [Source:MGI Symbol;Acc:MGI:109146]	Tmsb10
ENSMUSG00000079600	predicted gene, 17604 [Source:MGI Symbol;Acc:MGI:4937238]	Gm17604
ENSMUSG00000079740	predicted gene 11172 [Source:MGI Symbol;Acc:MGI:3779427]	Gm11172
ENSMUSG00000090592	predicted gene, 17571 [Source:MGI Symbol;Acc:MGI:4937205]	Gm17571
ENSMUSG00000090625	predicted gene, 20721 [Source:MGI Symbol;Acc:MGI:5313030]	Gm20721
ENSMUSG00000090841	myosin, light polypeptide 6, alkali, smooth muscle and non-muscle [Source:MGI Symbol;Acc:MGI:109318]	Myl6
ENSMUSG00000090889	predicted gene, 17428 [Source:MGI Symbol;Acc:MGI:4937062]	Gm17428
ENSMUSG00000091159	predicted gene, 17545 [Source:MGI Symbol;Acc:MGI:4937179]	Gm17545
ENSMUSG00000091228	predicted gene 20390 [Source:MGI Symbol;Acc:MGI:5141855]	Gm20390

Table S3. Enrichment of single TRs in genes and their 5kb environments (Gene5kb) and in the predicted promoter regions of K562 cells cRPGs compared to HE-NRGs. NS indicates TRs that are not significantly enriched/depleted, all other TRs are significantly enriched or depleted at the FDR <= 0.01 level.

TR	**Gene5kb**	**promoter**
TR4	1.255	2.032
SIX5	0.793	1.012
GTF2B	0.758	0.936
TAF7	0.951	1.244
NELFE	0.989	1.238
SRF	0.07	0.916
ELK1	NS	0.883
PU1	-0.057	0.771
GTF2F1	0.592	0.76
ZNF143	0.156	0.712
ZBTB33	0.561	NS
PML	NS	0.259
ZBTB7	-0.937	-0.693
CFOS	-1.065	-0.811
UBTF	-1.444	NS
TBP	-0.817	-0.778
NFE2	-3.047	-9.509

Table S4. Enrichment of putative TR dimers in genes and their 5kb environments and in the predicted promoter regions of K562 cells cRPGs compared to HE-NRGs. NS indicates TRs that are not significantly enriched/depleted, all other TRs are significantly enriched or depleted at the FDR <= 0.01 level.

TR pairs	**Gene5kb**	**promoter**
P300_TR4	4.247	4.219
TAF7_TR4	3.732	4.598
PU1_TR4	4.095	4.067
SP1_TR4	4.095	4.067
GTF2B_TR4	3.625	3.705
THAP1_TR4	3.095	3.897
GTF2F1_TR4	3.041	3.598
STAT5_THAP1	2.851	3.705
TEAD4_TR4	3.247	3.219
E2F4_TR4	2.732	3.598
SMC3_THAP1	3.063	2.804
SIX5_STAT5	2.384	2.823
NR2F2_SIX5	2.173	2.897
SIX5_TAF7	2.312	2.62
STAT2_TAF7	2.166	2.705
EJUNB_GTF2F1	1.995	2.823
CTCFL_THAP1	2.205	2.357
NR2F2_THAP1	1.925	2.598
MAFF_TAF7	2.013	2.482
GTF2B_SIX5	2.195	2.276
GTF2B_SMC3	2.003	2.338
CTCFL_GTF2F1	2.205	2.09
PU1_TAF7	1.961	2.326
EJUNB_SIX5	2.013	2.219
PU1_SIX5	1.925	2.245
CTCFB_TAF7	1.684	2.482
CTCFB_GTF2F1	2.072	2.055
STAT5_TAF7	1.873	2.219
EJUNB_TAF7	2.077	1.897
GTF2F1_SMC3	1.714	2.219
GTF2F1_SIX5	2.041	1.859
CTCFB_GTF2B	1.645	2.082
CTCFC_THAP1	1.662	2.013
GTF2B_PU1	1.694	1.971
CTCF_SP2	1.714	1.897

GTF2F1_PU1	1.625	1.897
GABP_TAF7	1.662	1.841
CTCFC_SP2	1.662	1.804
GTF2F1_SRF	1.613	1.848
TAF7_TBLR1	1.489	1.968
STAT1_THAP1	2.095	3.4
GTF2B_THAP1	1.677	1.668
SIX5_THAP1	1.732	1.598
GTF2B_STAT5	1.662	1.656
GTF2F1_STAT5	1.478	1.83
GTF2B_SRF	1.631	1.668
EJUNB_GTF2B	1.44	1.823
TAF7_ZNF143	1.463	1.79
EJUNB_SP2	3.247	3.705
SP1_TAF7	1.41	1.827
EJUND_GTF2B	1.562	1.67
CEBPB_SIX5	1.478	1.745
ELK1_SIX5	1.603	1.617
EJUND_GTF2F1	1.567	1.575
PU1_SRF	1.23	1.897
EJUND_TAF7	1.492	1.634
GTF2B_TAF7	1.521	1.604
NELFE_PU1	2.51	3.12
CMYC_TAF7	1.528	1.576
NR2F2_TAF7	1.51	1.56
SRF_TR4	2.095	3.067
TR4_ZNF143	2.51	3.067
CMYC_TR4	2.431	3.067
GTF2F1_TAF7	1.379	1.675
ELK1_PU1	1.542	1.507
BCLAF1_GTF2B	1.294	1.755
ELF1_TAF7	1.348	1.675
GTF2B_TBLR1	1.451	1.569
ELK1_GTF2B	1.44	1.567
TAF7_THAP1	1.233	1.72
GTF2B_ZNF143	1.444	1.497
ELK1_ZNF143	1.481	1.433
E2F6_TR4	2.003	2.897
ELK1_GTF2F1	1.384	1.463
THAP1_ZNF143	1.324	1.482
PU1_STAT5	1.51	2.804
GTF2F1_STAT2	1.321	1.482

SIX5_SRF	1.177	1.613
STAT1_TAF7	2.51	2.79
IRF1_TAF7	1.34	1.446
MEF2_SIX5	2.188	2.772
ELK1_P300	1.262	1.507
P300_SIX5	1.34	1.404
GABP_GTF2B	1.301	1.431
CBX3_SIX5	1.188	1.535
PU1_TBLR1	1.036	1.668
CMYC_GTF2B	1.197	1.482
SIX5_SP1	1.235	1.433
MAX_TAF7	1.33	1.337
GTF2B_MXI1	1.299	1.348
CEBPB_GTF2F1	1.294	1.345
CBX3_TR4	2.662	2.634
TAF7_YY1	1.167	1.464
CTCFB_SIX5	1.44	1.187
CEBPB_GTF2B	1.225	1.392
P300_TAF7	1.155	1.459
ETS1_GTF2B	1.207	1.402
NR2F2_PU1	1.361	2.598
BHLHE40_TAF7	1.066	1.522
GTF2B_JUND	1.158	1.405
GTF2B_USF1	1.124	1.433
JUND_TAF7	1.107	1.443
SIX5_ZNF143	1.103	1.442
GABP_GTF2F1	1.284	1.245
GTF2F1_THAP1	1.247	1.281
ETS1_SIX5	1.045	1.482
CBX3_TAF7	1.111	1.412
GTF2B_NRF1	1.139	1.383
GTF2B_YY1	1.157	1.35
STAT2_THAP1	2.34	2.482
ETS1_TR4	1.818	2.482
CTCFB_NELFE	1.773	2.482
ATF1_GTF2B	1.288	1.16
E2F4_TAF7	1.009	1.435
ETS1_TAF7	1.026	1.383
CHD2_TAF7	0.925	1.482
PML_TAF7	1.029	1.375
SIX5_TBLR1	1.089	1.312
CTCF_GTF2B	1.372	2.383

NELFE_NRF1	2.247	2.383
ATF1_TAF7	1.209	1.17
PML_SIX5	1.102	1.269
E2F4_GTF2B	1.08	1.286
GABP_SIX5	1.087	1.276
SIX5_TR4	1.925	2.357
CJUN_PU1	1.069	1.287
GTF2F1_TBLR1	1.147	1.202
GTF2F1_ZNF143	1.087	1.251
IRF1_TR4	2.557	2.33
CEBPB_TAF7	1.083	1.234
CBX3_GTF2B	1.113	1.2
IRF1_SIX5	1.14	1.157
GTF2B_SP1	1.069	1.228
POL2_TR4	1.968	2.284
SIN3_TAF7	0.925	1.34
SIN3_SIX5	1.113	1.142
TAF1_TAF7	1.093	1.151
GTF2B_TRIM28	1.063	1.151
CTCFB_GABP	0.988	1.219
CMYC_GTF2F1	1.081	1.125
GTF2F1_IRF1	1.247	0.957
ELF1_GTF2B	0.966	1.231
TR4_YY1	2.109	2.193
ELF1_GTF2F1	1.084	1.109
GTF2B_MAX	1.075	1.118
GTF2F1_TRIM28	0.972	1.208
PML_TR4	2.173	2.177
JUND_TR4	1.818	2.16
EJUNB_SRF	1.51	2.16
GTF2B_IRF1	1.016	1.142
E2F4_SIX5	0.995	1.16
GTF2B_GTF2F1	0.991	1.142
GTF2F1_USF1	1.131	0.997
GABP_NELFE	1.818	2.12
ELK1_STAT1	1.603	2.12
ELF1_TR4	1.662	2.12
JUND_SIX5	0.988	1.132
SIX5_ZBTB33	2.118	NS
GTF2F1_YY1	1.054	1.054
CTCFC_GTF2B	1.288	2.09
SRF_STAT1	1.118	2.09

ETS1_THAP1	0.893	1.191
ATF1_GTF2F1	1.141	0.937
GTF2B_P300	1.003	1.072
HMGN3_TAF7	0.785	1.269
EGR1_SIX5	0.964	1.084
GTF2F1_JUND	1.046	0.997
CJUN_TAF7	0.815	1.227
GTF2F1_P300	0.925	1.101
CCNT2_TAF7	0.804	1.212
CTCFB_STAT5	1.395	2.013
BCLAF1_THAP1	1.366	2.013
NELFE_SIX5	1.41	2.013
ELF1_SIX5	0.897	1.114
IRF1_PU1	0.866	1.141
MAX_SIX5	0.994	1.003
CJUN_GTF2F1	0.628	1.369
ELK1_TAF7	1.478	1.985
POL2_SIX5	0.853	1.113
MAX_TR4	1.662	1.961
ELK1_STAT5	1.925	1.4
NELFE_POL2	0.526	1.92
GTF2F1_MAX	1.069	0.85
SIX5_YY1	0.778	1.137
PML_PU1	0.843	1.053
GTF2B_SIN3	0.811	1.083
CMYC_SIX5	1.009	0.879
BHLHE40_GTF2B	0.925	0.935
GTF2B_HMGN3	0.795	1.063
RAD21_THAP1	1.851	1.79
PU1_ZNF143	0.727	1.848
SMC3_SP2	1.843	1.357
PU1_ZBTB33	1.843	NS
PML_SRF	0.84	1
GABP_PU1	0.671	1.16
JUND_PU1	0.609	1.21
BCLAF1_PU1	0.925	1.815
ETS1_GTF2F1	0.853	0.945
CBX3_GTF2F1	0.806	0.985
CTCFL_GTF2B	1.273	1.79
E2F4_NELFE	1.372	1.782
GTF2F1_SIN3	0.811	0.97
CJUN_GTF2B	0.751	1.026

CTCF_THAP1	1.773	1.772
ELK1_SP2	1.773	1.177
CMYC_NELFE	1.103	1.768
IRF1_ZNF143	1.046	0.716
ELK1_THAP1	1.588	1.76
ETS1_NELFE	1.34	1.755
MXI1_NELFE	1.925	1.745
CBX3_NELFE	1.051	1.727
JUND_THAP1	0.828	0.897
GTF2B_STAT1	1.131	1.705
E2F4_GTF2F1	0.826	0.871
E2F6_GTF2B	0.681	1.016
GTF2B_PML	0.771	0.915
BCLAF1_SIX5	1.34	1.686
CEBPB_PU1	0.662	1.686
GTF2F1_SP1	0.823	0.862
ELF1_NELFE	1.466	1.675
NELFE_TAF7	1.032	1.675
POL2_TAF7	0.723	0.941
E2F4_GABP	0.766	0.897
CTCFB_PU1	0.556	1.663
RAD21_SP2	1.662	1.772
ELF1_STAT5	0.878	1.634
BCLAF1_CTCFB	1.032	1.634
BHLHE40_GTF2F1	0.766	0.863
JUND_NELFE	1.41	1.613
CEBPB_ELK1	0.925	1.608
BCLAF1_TAF7	1.259	1.589
BCLAF1_SP2	1.588	1.482
GTF2B_MAFF	1.588	1.482
POL2_ZNF143	0.856	0.727
CTCFB_THAP1	1.569	1.575
PU1_YY1	0.568	0.989
GABP_STAT5	0.974	1.549
GTF2F1_PML	0.788	0.742
NELFE_ZNF143	0.636	1.525
SRF_TAF7	1.147	1.519
CEBPB_CTCFB	0.306	1.519
HMGN3_NELFE	1.51	1.519
GTF2B_STAT2	1.127	1.519
NRF1_SIX5	1.118	1.514
BCLAF1_GTF2F1	1.041	1.51

E2F4_STAT5	1.378	1.482
GABP_STAT1	0.584	1.482
CCNT2_NELFE	1.106	1.482
CBX3_PU1	0.613	1.482
CBX3_THAP1	0.986	1.482
STAT1_ZNF143	0.744	1.482
GTF2B_POL2	0.634	0.847
NELFE_YY1	0.654	1.468
TAF7_ZBTB33	1.456	NS
NELFE_SIN3	0.732	1.454
CCNT2_GTF2F1	0.609	0.845
CTCF_ZNF143	0.323	1.45
CTCFB_ELK1	1.106	1.445
NRF1_TAF7	1.102	1.433
CMYC_ZNF143	0.69	0.738
NRF1_TBLR1	0.925	1.428
TBLR1_THAP1	1.137	1.421
MXI1_TAF7	0.719	1.418
NRSF_SIX5	1.063	1.412
GTF2F1_NR2F2	1.23	1.412
CTCFB_MXI1	1.147	1.412
GTF2B_TAF1	0.68	0.73
MXI1_SIX5	0.982	1.404
TAF7_USF1	1.095	1.395
GTF2F1_STAT1	0.925	1.395
SP1_SRF	0.984	1.395
SRF_YY1	0.666	1.374
SIN3_STAT1	0.847	1.371
GTF2F1_NELFE	0.925	1.371
ELK1_SP1	1.44	1.371
SP2_TAF7	1.188	1.333
IRF1_NELFE	0.967	1.33
CTCFB_ZNF143	0.301	1.33
ETS1_PU1	0.662	1.325
SIX5_STAT1	1.032	1.312
EJUND_ELK1	1.003	1.312
EJUND_SIX5	1.072	1.312
SRF_ZNF143	0.778	1.312
EJUND_SRF	0.858	1.29
ELF1_STAT1	0.732	1.281
GTF2F1_POL2	0.698	0.582
YY1_ZNF143	0.545	0.699

CMYC_PU1	0.765	1.244
STAT1_YY1	0.432	1.238
CBX3_ELK1	1.215	1.234
CBX3_CTCFB	0.719	1.234
NELFE_PML	0.765	1.232
IRF1_SRF	0.948	1.23
STAT1_TBLR1	1.077	1.219
CBX3_SRF	1.056	1.219
GTF2F1_MXI1	0.879	1.21
SIN3_SRF	0.654	1.193
GABP_THAP1	1.188	1
TAF7_TRIM28	0.835	1.181
HMGN3_THAP1	0.747	1.177
GTF2F1_TAF1	0.639	0.524
JUND_SRF	0.803	1.151
SRF_TBLR1	0.762	1.149
GTF2B_NELFE	0.744	1.149
E2F6_TAF7	0.612	1.136
IRF1_YY1	0.622	0.513
E2F4_PU1	0.681	1.134
NRSF_TAF7	0.83	1.132
PU1_SIN3	0.534	1.12
E2F4_ELK1	0.995	1.111
TBLR1_ZNF143	0.662	1.107
CEBPB_GABP	0.687	1.104
E2F6_SIX5	0.858	1.102
MAX_NELFE	0.481	1.085
GTF2B_ZBTB33	1.045	NS
MXI1_TBLR1	0.703	1.035
ELK1_PML	0.845	1.032
ELK1_SIN3	0.81	1.023
SIX5_TAF1	1.006	0.971
ELK1_JUND	0.878	0.973
ELF1_ELK1	0.535	0.968
BCLAF1_GABP	0.963	0.954
ELF1_PU1	0.178	0.963
CCNT2_GTF2B	0.684	0.957
SP1_TBLR1	0.498	0.945
CEBPB_ELF1	0.414	0.942
CBX3_TBLR1	0.259	0.942
CJUN_SIX5	0.888	0.939
ELK1_GABP	0.969	0.935

EGR1_TAF7	0.573	0.935
PML_ZNF143	0.478	0.922
POL2_SRF	0.851	0.921
ELK1_IRF1	1.038	0.916
MAZ_TAF7	0.902	NS
CMYC_SRF	0.751	0.897
GTF2F1_NRF1	0.818	0.897
PML_TBLR1	0.449	0.897
TAF7_TEAD4	0.777	0.897
MAX_PU1	0.386	0.878
MAX_STAT1	0.538	0.866
IRF1_PML	0.435	0.425
ELK1_YY1	0.641	0.86
CBX3_ZNF143	0.495	0.857
MAZ_SIX5	0.847	NS
GTF2B_RCOR1	0.845	0.897
ELF1_ZNF143	0.34	0.843
JUND_ZNF143	0.378	0.841
ELK1_MAX	0.824	0.831
GABP_ZNF143	0.64	0.83
IRF1_TBLR1	0.767	0.83
GTF2F1_NRSF	0.61	0.825
GTF2B_NRSF	0.603	0.821
GTF2B_MAZ	0.811	NS
THAP1_YY1	0.63	0.807
GTF2F1_MAZ	0.806	NS
CHD2_GTF2B	0.466	0.782
CTCFB_IRF1	0.782	0.897
ELF1_TBLR1	0.283	0.779
EGR1_GTF2B	0.562	0.774
E2F6_GTF2F1	0.525	0.756
ELK1_POL2	0.706	0.752
POL2_PU1	-0.089	0.751
CMYC_ELK1	0.971	0.743
GTF2B_TEAD4	0.618	0.741
GTF2F1_HMGN3	0.549	0.731
POL2_STAT1	-0.253	0.715
TBLR1_YY1	0.34	0.715
CMYC_PML	0.564	0.699
CJUN_ZNF143	0.371	0.686
GABP_PML	0.547	0.661
MAX_TBLR1	0.447	0.646

GABP_YY1	0.546	0.623
IRF1_JUND	0.617	0.589
MAX_ZNF143	0.548	0.595
JUND_YY1	0.248	0.575
ELF1_PML	0.312	0.529
MAX_PML	0.26	0.251
JUND_PML	0.302	0.501
ELF1_GABP	0.195	0.477
PML_YY1	0.281	0.185
MAZ_TBP	-0.567	NS
CMYC_ZBTB7	-0.325	-0.62
SIN3_TBP	-0.646	-0.615
PML_TBP	-0.65	-0.688
E2F6_ZBTB7	-0.685	-0.626
MAX_ZBTB7	-0.441	-0.688
IRF1_TBP	-0.243	-0.553
CMYC_TBP	-0.293	-0.574
HMGN3_ZBTB7	-0.959	-0.816
E2F4_TBP	-0.964	-0.789
ATF3_TBP	-1.174	-1.103
MAX_TBP	-0.463	-0.734
CHD2_TBP	-1.263	-1.054
RCOR1_UBTF	-1.66	-1.273
MAZ_UBTF	-1.29	NS
POL2_ZBTB7	-0.699	-0.66
GABP_UBTF	-1.001	-1.425
POL2_TBP	-0.386	-1.055
ETS1_TBP	-0.826	-0.652
CMYC_USF2	-1.092	-1.491
TAF1_TBP	-0.741	-0.791
SIN3_UBTF	-1.102	-1.562
CFOS_EGR1	-1.586	-1.425
TAF1_ZBTB7	-0.699	-0.948
E2F6_TBP	-0.901	-0.795
NFYB_TBP	-1.156	-1.781
CFOS_TBP	-1.162	-1.825
TAL1_UBTF	-1.338	-2.041
ATF3_EFOS	-2.075	-6.069
EGR1_TBP	-1.186	-0.947
BHLHE40_USF2	-0.66	-2.162
ELF1_USF2	-1.075	-2.218
E2F6_UBTF	-1.09	-1.181

USF1_USF2	-0.859	-2.325
CCNT2_TAL1	-1.227	-2.325
CCNT2_USF2	-1.508	-2.425
CCNT2_TBP	-1.203	-1.23
RAD21_UBTF	-2.49	-3.103
IRF1_UBTF	-1.245	-1.266
POL2_UBTF	-1.3	-1.359
CTCFC_UBTF	-2.699	-2.351
TBP_ZBTB7	-1.151	-1.612
CTCF_UBTF	-2.775	-2.01
EFOS_HMGN3	-2.775	-2.688
HMGN3_TBP	-1.608	-1.282
TBP_UBTF	-1.373	-1.614
UBTF_YY1	-1.845	-1.149
ELF1_UBTF	-1.534	-1.481
CMYC_UBTF	-1.424	-1.6
CCNT2_UBTF	-1.277	-1.775
JUND_UBTF	-1.633	-1.657
TAF1_UBTF	-1.577	-1.791
EFOS_ZBTB7	-3.467	-9.528
MAX_UBTF	-1.54	-1.951
EGR1_UBTF	-1.586	-2.041
BHLHE40_UBTF	-1.694	-2.066
CCNT2_EFOS	-3.775	-3.19
GATA2_TBP	-3.775	-2.803
PML_UBTF	-2.075	-1.887
E2F4_UBTF	-2.075	-1.944
HMGN3_UBTF	-1.444	-2.614
ETS1_UBTF	-2.075	-1.996
NFE2_POL2	-4.204	-10.823
UBTF_ZBTB7	-2.271	-1.944
CHD2_UBTF	-2.323	-1.951
CMYC_NFE2	-4.342	-10.975
NRSF_UBTF	-2.36	-3.19
HMGN3_TAL1	-2.699	-2.91
ETS1_NFE2	-9.966	-8.876
NFE2_RCOR1	-10.059	-8.876
NFE2_TEAD4	-10.059	-8.069
EGR1_NFE2	-10.146	-8.654
NFE2_ZBTB7	-10.146	-9.238
NFE2_SIN3	-10.229	-9.39
NFE2_P300	-10.229	-8.876

ELF1_NFE2	-10.307	-9.39
NFE2_PML	-10.381	-8.876
MAZ_NFE2	-10.451	NS
BHLHE40_NFE2	-10.518	-9.528
CCNT2_NFE2	-10.518	-9.39
HMGN3_NFE2	-10.582	-9.39
JUND_NFE2	-10.644	-9.528
ATF3_NFE2	-10.703	-8.654
IRF1_NFE2	-10.759	-10.069
E2F6_NFE2	-10.866	-10.316
NFE2_YY1	-11.146	-10.069
MAX_NFE2	-11.416	-10.39

Table S5. Enrichment of putative TR trimers in genes and their 5kb environments (Gene5kb) and in the predicted promoter regions of K562 cells cRPGs compared to HE-NRGs. NS indicates TRs that are not significantly enriched/depleted, all other TRs are significantly enriched or depleted at the FDR <= 0.01 level.

TR triplets	**Gene5kb**	**promoter**
E2F6_P300_TR4	10.569	10.587
NR2F2_PU1_SIX5	10.443	10.462
NR2F2_STAT5_THAP1	10.569	10.172
EJUND_GTF2B_TR4	10.306	10.324
E2F6_SP1_TR4	10.443	10.172
BCLAF1_SP2_THAP1	10.443	10.002
SP1_TAF7_TR4	10.154	10.172
PU1_SIX5_TR4	10.154	10.172
E2F4_PU1_TR4	10.154	10.172
CTCFC_SP2_TAF7	10.306	10.002
E2F6_TR4_TRIM28	9.984	10.172
ETS1_PU1_TR4	9.984	10.172
GTF2B_THAP1_TR4	10.154	10.002
P300_TAF7_TR4	9.984	10.002
CTCF_SP2_THAP1	10.306	9.587
CTCFL_NR2F2_THAP1	10.306	9.587
SP2_STAT5_THAP1	10.306	9.587
HMGN3_TAF7_TR4	9.984	9.81
CBX3_EJUND_TR4	9.984	9.81
NR2F2_PU1_THAP1	9.984	9.81
EJUND_TEAD4_TR4	9.984	9.81
TAF7_TBLR1_TR4	9.569	10.172
CBX3_TBP_TR4	9.791	9.81
P300_THAP1_TR4	9.791	9.81
TAF7_TR4_ZNF143	9.791	9.81
CBX3_TAF7_TR4	9.791	9.81
P300_PU1_TR4	9.791	9.81
P300_TR4_USF1	9.791	9.81
CTCF_SP2_TAF7	9.984	9.587
EJUNB_SP2_TAF7	9.984	9.587
CTCF_GTF2B_THAP1	9.791	9.587
EJUND_P300_TR4	9.791	9.587
CEBPB_CTCFL_THAP1	9.791	9.587
CTCFL_MEF2_SIX5	9.791	9.587
SP2_STAT2_THAP1	9.791	9.587

CBX3_PU1_TR4	9.569	9.587
PU1_SRF_TR4	9.569	9.587
ELK1_NRF1_STAT5	9.569	9.587
SP1_TBP_TR4	9.569	9.587
HMGN3_PU1_TR4	9.569	9.587
PU1_THAP1_TR4	9.569	9.587
P300_TBP_TR4	9.569	9.587
IRF1_THAP1_TR4	4.925	11.002
CJUN_NR2F2_PU1	5.013	10.81
NR2F2_SIX5_THAP1	4.625	10.324
GTF2B_STAT1_THAP1	9.984	4.934
ETS1_TAF7_TR4	4.384	10.324
EJUNB_GTF2B_THAP1	4.384	10.324
E2F4_TAF7_TR4	4.384	10.324
ELK1_NR2F2_THAP1	10.154	4.393
CTCFC_NR2F2_THAP1	4.51	9.81
EJUNB_ETS1_SP2	4.247	10.002
CTCFC_GTF2B_USF1	4.247	10.002
E2F4_THAP1_TR4	4.095	10.002
EJUNB_GTF2B_SMC3	4.095	10.002
EJUND_GTF2F1_TR4	4.095	10.002
SIX5_TAF7_TR4	4.095	10.002
E2F4_EJUNB_SP2	4.247	9.81
E2F6_EJUNB_GTF2F1	2.449	11.587
EJUND_TAF7_TR4	3.925	10.002
CTCF_NR2F2_THAP1	4.247	9.587
CTCFB_NR2F2_THAP1	4.247	9.587
EGR1_NELFE_PU1	9.569	4.256
NR2F2_SRF_THAP1	3.925	9.81
GTF2F1_MAFF_STAT5	3.925	9.81
CCNT2_EJUNB_SP2	3.925	9.81
EJUNB_HMGN3_SP2	3.925	9.81
CTCF_GTF2B_USF1	3.925	9.81
EJUNB_GTF2F1_SP2	3.925	9.81
CEBPB_SRF_THAP1	3.925	9.81
BHLHE40_EJUNB_SP2	4.095	9.587
GTF2F1_NR2F2_PU1	3.247	10.324
EJUNB_SP2_ZNF143	3.925	9.587
CEBPB_EJUNB_SIX5	3.247	10.172
GABP_MXI1_NELFE	9.569	3.634
POL2_TAF1_ZBTB33	0.823	NS
ARID3_CEBPB_PU1	2.925	10.172

E2F4_NR2F2_PU1	2.51	10.462
CTCFC_PU1_SP2	3.095	9.81
CTCF_PU1_SP2	3.095	9.81
CTCFB_PU1_SP2	3.095	9.81
ELK1_GTF2B_STAT1	9.791	3.104
BCLAF1_NR2F2_PU1	2.662	10.002
ATF3_GTF2B_PU1	2.8	9.587
NR2F2_PU1_TEAD4	2.025	10.324
POL2_PU1_TR4	5.095	5.519
SP2_STAT1_USF1	2.732	10.462
NELFE_PU1_TAF7	3.732	10.462
CTCFB_THAP1_ZBTB33	10.306	NS
MAX_P300_TR4	5.013	5.256
IRF1_P300_TR4	5.384	4.841
CJUN_TAF7_TR4	3.925	10.172
NELFE_PU1_TEAD4	3.732	10.172
IRF1_PU1_TR4	4.832	5.182
NELFE_NRF1_STAT1	6.984	10.002
CBX3_EHDAC8_USF1	NS	10.002
NR2F2_NRF1_SIX5	2.925	10.002
EJUND_NRF1_STAT5	3.51	10.002
CTCFC_NR2F2_PU1	1.925	10.002
NRF1_STAT2_STAT5	3.51	10.002
CTCFB_NR2F2_PU1	1.662	10.002
EJUNB_THAP1_ZBTB33	9.984	NS
TF3C110_YY1_ZNF143	9.984	9.002
STAT1_TAF7_ZBTB33	9.984	NS
EJUNB_SMC3_SP2	9.984	9.324
CTCFC_SMC3_ZBTB33	9.984	NS
EJUNB_SP2_THAP1	9.984	9.324
IRF1_SP1_TR4	5.095	4.841
CTCF_STAT1_USF1	1.662	9.81
NRF1_SIN3_STAT5	3.51	9.81
NELFE_PU1_SIX5	8.569	9.81
CBX3_MAFK_PU1	2.732	9.81
EJUNB_NRF1_STAT5	2.925	9.81
CEBPB_PU1_STAT1	2.662	9.81
CTCFL_NR2F2_PU1	1.773	9.81
EJUND_SRF_TR4	3.732	9.81
MXI1_NRF1_STAT5	2.925	9.81
GTF2F1_THAP1_TR4	3.732	9.81
NRF1_SP1_STAT5	9.306	9.81

NR2F2_NRF1_STAT5	3.247	9.81
CEBPB_CTCFC_PU1	1.51	9.81
NRF1_STAT5_THAP1	9.306	9.81
CEBPB_NELFE_NRF1	8.984	9.81
ELF1_TF3C110_ZNF143	9.791	8.587
EJUNB_SP1_SP2	9.791	9.324
CTCFL_ELK1_SP2	9.791	2.741
NFYA_SIX5_ZBTB33	9.791	NS
BCLAF1_CTCF_TAF7	9.791	9.324
CTCFL_SP2_THAP1	9.791	9.002
CTCFL_SMC3_ZBTB33	9.791	NS
ELK1_PU1_ZBTB33	9.791	NS
MAFK_PU1_ZNF143	1.925	9.587
BCLAF1_NELFE_SP2	8.569	9.587
MAFK_NRF1_TBLR1	2.51	9.587
ATF1_NRF1_STAT5	3.247	9.587
MXI1_NELFE_PU1	1.925	9.587
ARID3_PU1_SP2	3.732	9.587
MEF2_NRF1_TBLR1	2.51	9.587
EJUND_THAP1_TR4	3.732	9.587
CTCF_PU1_SRF	3.732	9.587
CEBPB_NELFE_PU1	2.925	9.587
TAF7_THAP1_TR4	3.732	9.587
CTCF_NR2F2_PU1	1.603	9.587
CEBPB_CTCF_PU1	1.118	9.587
NRF1_THAP1_TR4	8.984	9.587
TBP_THAP1_TR4	3.51	9.587
NELFE_PU1_SP2	7.984	9.587
CCNT2_EJUNB_NELFE	3.732	9.587
ELK1_NR2F2_NRF1	8.984	9.587
CTCFB_NELFE_STAT5	9.306	9.587
TAF7_TR4_TRIM28	3.51	9.587
EJUNB_ELF1_NELFE	3.51	9.587
CTCFC_STAT1_USF1	1.247	9.587
PU1_TBLR1_TR4	9.306	9.587
CTCFB_STAT1_USF1	1.247	9.587
SRF_TBP_TR4	3.51	9.587
MEF2_NELFE_NRF1	6.984	9.587
MAFK_PU1_TBLR1	1.925	9.587
MAFF_STAT5_TAF7	3.732	9.587
NRF1_P300_TR4	8.984	9.587
CTCF_EJUNB_GTF2B	2.147	9.587

MEF2_NRF1_SIX5	3.51	9.587
GTF2B_MAFF_NFYA	9.569	9.324
CTCFL_GTF2B_THAP1	9.569	9.324
GTF2F1_MAFF_NFYA	9.569	9.324
CTCF_THAP1_ZBTB33	9.569	NS
CTCFL_NR2F2_NRF1	9.569	9.002
CTCFC_THAP1_ZBTB33	9.569	NS
SP2_THAP1_ZBTB33	9.569	NS
E2F6_GTF2B_TR4	4.625	4.934
POL2_THAP1_TR4	4.34	5.182
E2F6_TEAD4_TR4	4.732	4.634
CMYC_GTF2B_TR4	3.851	5.426
P300_PML_TR4	4.625	4.634
ETS1_GTF2B_TR4	4.625	4.634
GTF2B_STAT5_THAP1	4.732	4.519
MAX_SP1_TR4	4.832	4.393
GTF2B_SMC3_THAP1	4.625	4.519
E2F4_GTF2B_TR4	4.51	4.634
E2F6_STAT5_THAP1	3.864	5.256
SP1_TR4_YY1	5.247	3.841
E2F6_EJUND_TR4	4.832	4.256
GTF2B_TAF7_TR4	4.51	4.519
POL2_SP1_TR4	3.662	5.326
MAX_PU1_TR4	5.173	3.741
E2F6_TR4_ZNF143	4.51	4.393
RAD21_SIX5_THAP1	4.732	4.104
GTF2B_SIX5_TR4	4.384	4.393
E2F6_PU1_TR4	4.384	4.393
P300_TAF1_TR4	4.51	4.256
PML_SP1_TR4	4.51	4.256
NR2F2_SMC3_THAP1	4.625	4.104
POL2_TAF7_TR4	2.879	5.841
CMYC_P300_TR4	3.832	4.888
CTCFL_SMC3_THAP1	4.732	3.934
ELF1_P300_TR4	4.384	4.256
CTCFL_NR2F2_SIX5	4.51	4.104
CMYC_SP1_TR4	4.247	4.326
GTF2B_POL2_TR4	4.198	4.326
CMYC_EJUNB_SP2	5.21	3.312
P300_POL2_TR4	2.773	5.741
E2F4_P300_TR4	4.247	4.256
JUND_P300_TR4	4.247	4.256

CBX3_TEAD4_TR4	4.247	4.256
CBX3_GTF2B_TR4	4.247	4.256
P300_SIX5_TR4	4.247	4.256
GTF2B_TR4_ZNF143	4.247	4.256
GTF2B_P300_TR4	4.247	4.256
CBX3_E2F4_TR4	4.247	4.256
E2F4_TEAD4_TR4	4.247	4.256
GTF2F1_P300_TR4	4.247	4.256
ETS1_TEAD4_TR4	4.247	4.256
E2F6_EJUNB_SP2	4.095	4.393
GTF2B_PU1_STAT5	3.832	4.634
E2F6_GTF2F1_TR4	3.832	4.634
TAF1_TAF7_TR4	3.925	4.519
PML_TAF7_TR4	3.51	4.934
IRF1_TAF7_TR4	4.041	4.393
EJUNB_GTF2B_SIX5	3.732	4.634
NRF1_SIX5_TAF7	3.625	4.741
ETS1_P300_TR4	4.095	4.256
ELK1_SMC3_THAP1	4.247	4.104
CTCFL_GTF2B_TAF7	4.247	4.104
STAT1_TAF7_USF1	4.095	4.256
GTF2B_TBP_TR4	4.095	4.256
SP1_TAF1_TR4	4.247	4.104
E2F6_TAF7_TR4	3.832	4.519
E2F4_E2F6_TR4	3.588	4.741
SMC3_STAT5_THAP1	4.384	3.934
EJUNB_STAT2_TAF7	4.384	3.934
MAX_TAF7_TR4	4.198	4.104
GTF2F1_TAF7_TR4	3.625	4.634
ELF1_TAF7_TR4	3.625	4.634
SMC3_SP2_THAP1	4.51	3.741
JUND_PU1_TR4	4.095	4.104
CBX3_TR4_ZNF143	4.095	4.104
CBX3_GTF2F1_TR4	4.095	4.104
TEAD4_TR4_ZNF143	4.095	4.104
GTF2B_PU1_TR4	4.095	4.104
E2F4_SP1_TR4	4.095	4.104
GTF2B_TR4_USF1	4.095	4.104
EJUNB_NR2F2_SIX5	4.095	4.104
EJUNB_NR2F2_THAP1	4.095	4.104
TAF7_TEAD4_TR4	4.095	4.104
GTF2B_SP1_TR4	4.095	4.104

GTF2F1_SP1_TR4	4.095	4.104
ELF1_PU1_TR4	4.095	4.104
ELF1_SP1_TR4	4.095	4.104
CTCFL_TAF7_TRIM28	4.247	3.934
PU1_TAF1_TR4	4.247	3.934
CTCFB_GTF2B_THAP1	4.247	3.934
CEBPB_SMC3_THAP1	4.247	3.934
GTF2B_IRF1_TR4	3.51	4.634
CMYC_E2F4_TR4	4.121	4.021
PU1_TR4_YY1	4.732	3.349
GTF2F1_POL2_TR4	4.054	4.021
E2F4_STAT5_THAP1	3.428	4.634
TAF7_TR4_YY1	4.384	3.671
EJUNB_SMC3_STAT2	4.095	3.934
GTF2B_SRF_TR4	4.095	3.934
P300_SIN3_TR4	3.925	4.104
CEBPB_STAT5_THAP1	4.095	3.934
E2F4_GTF2F1_TR4	3.51	4.519
GABP_P300_TR4	4.095	3.934
CTCFC_GTF2B_TAF7	4.095	3.934
EJUNB_GTF2F1_SIX5	3.247	4.741
EJUNB_SMC3_THAP1	4.247	3.741
GTF2F1_IRF1_TR4	4.198	3.741
PML_PU1_TR4	3.384	4.519
SIX5_STAT5_TAF7	3.51	4.393
CBX3_STAT5_THAP1	3.625	4.256
BHLHE40_TAF7_TR4	3.925	3.934
SP1_TR4_ZNF143	3.925	3.934
CBX3_SP1_TR4	3.925	3.934
CBX3_EGR1_TR4	3.925	3.934
NRF1_SMC3_THAP1	3.925	3.934
GTF2F1_TR4_USF1	3.925	3.934
CCNT2_P300_TR4	3.925	3.934
SIX5_TEAD4_TR4	3.925	3.934
GTF2F1_HMGN3_TR4	3.925	3.934
JUND_SP1_TR4	3.925	3.934
SP1_TEAD4_TR4	3.925	3.934
EGR1_SP1_TR4	3.925	3.934
SRF_TEAD4_TR4	3.925	3.934
BHLHE40_P300_TR4	3.925	3.934
GTF2B_MAX_TR4	4.041	3.808
GTF2B_RAD21_THAP1	4.095	3.741

E2F6_ETS1_TR4	3.095	4.741
P300_TR4_YY1	4.095	3.741
CTCFB_SP2_TAF7	4.095	3.741
CTCFL_NRF1_THAP1	4.095	3.741
CMYC_PU1_TR4	4.013	3.808
STAT1_TAF7_TBLR1	3.925	3.872
E2F4_IRF1_TR4	3.984	3.808
ETS1_GTF2F1_TR4	3.384	4.393
CMYC_TAF7_TR4	3.638	4.135
SIX5_STAT5_THAP1	3.247	4.519
NR2F2_PU1_TAF7	3.51	4.256
GABP_TAF7_TR4	3.51	4.256
CBX3_SMC3_THAP1	3.625	4.104
GTF2F1_MAX_TR4	4.041	3.671
CMYC_THAP1_TR4	3.603	4.104
CTCF_GTF2B_TAF7	3.925	3.741
EJUNB_POL2_SP2	4.925	2.741
GABP_PU1_TR4	3.925	3.741
EGR1_HMGN3_TR4	3.925	3.741
CTCFC_GTF2B_THAP1	3.925	3.741
CCNT2_TAF7_TR4	3.384	4.256
JUND_TAF7_TR4	3.384	4.256
E2F6_THAP1_TR4	3.384	4.256
CTCFC_PU1_SIX5	3.384	4.256
EJUNB_PML_SP2	3.51	4.104
E2F6_SMC3_THAP1	3.569	4.021
PU1_SIX5_STAT5	3.041	4.519
IRF1_TEAD4_TR4	3.449	4.104
HMGN3_NR2F2_THAP1	3.147	4.393
CCNT2_STAT5_THAP1	3.013	4.519
TEAD4_TR4_YY1	4.095	3.436
GTF2F1_SIX5_TR4	3.247	4.256
NRF1_STAT2_TAF7	3.247	4.256
GABP_NR2F2_SIX5	3.662	3.841
MXI1_SMC3_THAP1	3.095	4.393
EJUNB_STAT5_THAP1	3.384	4.104
E2F6_SRF_TR4	3.095	4.393
GTF2B_SIX5_STAT5	3.51	3.934
GTF2B_PU1_SIX5	3.569	3.872
NR2F2_PU1_YY1	2.173	5.256
JUND_SMC3_THAP1	3.662	3.741
CBX3_IRF1_TR4	4.247	3.156

NR2F2_THAP1_ZNF143	3.147	4.256
E2F4_MAX_TR4	3.188	4.182
ATF1_EJUNB_GTF2F1	2.732	4.634
STAT1_STAT2_TAF7	3.925	3.436
CTCF_PU1_SIX5	3.247	4.104
ETS1_THAP1_TR4	3.247	4.104
ELF1_THAP1_TR4	3.247	4.104
BCLAF1_SMC3_THAP1	3.384	3.934
SRF_STAT5_THAP1	2.925	4.393
GABP_MEF2_SIX5	3.041	4.256
CTCFL_IRF1_THAP1	3.449	3.841
POL2_TEAD4_TR4	3.34	3.934
GTF2B_GTF2F1_TR4	3.625	3.634
PU1_SIX5_TAF7	3.662	3.597
PU1_TAF7_THAP1	3.732	3.519
ELF1_GTF2B_TR4	3.732	3.519
GTF2B_STAT2_THAP1	3.832	3.393
GTF2F1_TBP_TR4	3.095	4.104
E2F4_SRF_TR4	3.095	4.104
GTF2F1_TR4_ZNF143	3.095	4.104
TAF7_TBP_TR4	3.095	4.104
CMYC_TEAD4_TR4	2.984	4.207
PU1_STAT5_THAP1	3.247	3.934
EJUNB_ELF1_SP2	3.247	3.934
CEBPB_NR2F2_THAP1	3.247	3.934
ATF1_GTF2B_MAFF	3.247	3.934
ATF1_STAT5_THAP1	3.247	3.934
CTCFC_SIN3_SP2	3.041	4.104
BHLHE40_STAT5_THAP1	3.041	4.104
PML_STAT5_THAP1	2.51	4.634
CEBPB_PU1_SIX5	2.625	4.519
GTF2B_JUND_TR4	3.51	3.634
EJUND_SP2_STAT5	3.384	3.741
EJUNB_MAX_SP2	3.732	3.393
GTF2B_TAF1_TR4	3.732	3.393
CEBPB_SIX5_THAP1	3.732	3.393
ETS1_NELFE_PU1	3.095	4.021
ELK1_SIX5_STAT5	3.832	3.256
CMYC_GTF2F1_TR4	3.68	3.393
MAX_THAP1_TR4	3.428	3.634
CTCFB_PU1_SRF	3.095	3.934
JUND_THAP1_TR4	3.095	3.934

MEF2_SIX5_THAP1	3.095	3.934
EGR1_TAF7_TR4	3.095	3.934
EJUNB_NR2F2_TAF7	3.095	3.934
BCLAF1_PU1_THAP1	3.095	3.934
SIX5_THAP1_TR4	3.095	3.934
EJUNB_SP1_TAF7	3.625	3.393
IRF1_STAT5_THAP1	3.557	3.457
MAX_TEAD4_TR4	3.662	3.349
GTF2F1_TR4_YY1	3.8	3.197
GABP_HMGN3_NELFE	3.732	3.256
ELK1_THAP1_ZNF143	3.832	3.156
EJUNB_JUND_SP2	3.247	3.741
GABP_STAT1_TAF7	3.247	3.741
E2F4_PML_TR4	3.34	3.634
STAT5_THAP1_ZNF143	3.428	3.519
EJUNB_GTF2F1_SRF	2.662	4.256
NR2F2_SIX5_USF1	2.662	4.256
CBX3_EJUNB_THAP1	2.8	4.104
ELK1_GTF2B_STAT5	4.384	2.519
NR2F2_SIX5_STAT5	3.51	3.393
EJUNB_SIX5_TAF7	3.51	3.393
ELF1_GTF2F1_TR4	3.147	3.741
CTCF_NR2F2_SIX5	3.625	3.256
E2F4_PU1_STAT5	3.247	3.634
E2F6_SIX5_STAT5	3.198	3.671
EJUND_STAT5_THAP1	2.925	3.934
ELF1_MEF2_PU1	2.925	3.934
CBX3_POL2_TR4	3.247	3.597
EJUNB_P300_SP2	3.095	3.741
EGR1_EJUNB_SP2	3.095	3.741
EJUNB_SP2_TEAD4	3.095	3.741
CTCF_SIX5_THAP1	3.732	3.104
GABP_THAP1_TR4	3.095	3.741
EJUND_SIX5_STAT5	2.41	4.393
EJUNB_GTF2F1_TRIM28	2.147	4.634
TR4_YY1_ZNF143	3.625	3.156
EJUND_GTF2B_SMC3	3.147	3.634
GABP_GTF2B_TR4	3.384	3.393
ELF1_TEAD4_TR4	3.384	3.393
GTF2B_TEAD4_TR4	3.384	3.393
GTF2B_NR2F2_PU1	2.384	4.393
GTF2B_SIX5_THAP1	3.449	3.326

CEBPB_CTCFB_TAF7	2.662	4.104
EJUNB_GABP_TAF7	3.247	3.519
STAT1_STAT5_TAF7	3.51	3.256
EJUNB_GTF2F1_SMC3	2.662	4.104
GTF2F1_TAF1_TR4	3.247	3.519
SIN3_STAT2_THAP1	3.247	3.519
CTCF_SIN3_SP2	2.8	3.934
ELK1_NRF1_SIX5	3.925	2.808
CTCFL_SIX5_THAP1	3.625	3.104
GTF2B_TR4_YY1	3.588	3.135
POL2_STAT5_THAP1	3.428	3.256
GTF2B_PML_TR4	3.428	3.256
GTF2F1_SMC3_THAP1	3.625	3.049
PU1_STAT5_TAF7	3.147	3.519
BCLAF1_SIX5_TAF7	3.147	3.519
ELF1_NR2F2_THAP1	3.013	3.634
STAT5_TBLR1_THAP1	3.384	3.256
CTCFL_PU1_SIX5	3.384	3.256
TAF1_TEAD4_TR4	3.384	3.256
CTCF_GTF2F1_SP2	3.384	3.256
GTF2B_SIN3_TR4	3.247	3.393
E2F6_EJUNB_TAF7	3.449	3.182
GTF2B_STAT1_TAF7	3.625	2.993
ELK1_SP2_THAP1	3.51	3.104
SMC3_SP1_THAP1	3.51	3.104
GTF2F1_PU1_SIX5	3.188	3.393
HMGN3_STAT5_THAP1	2.925	3.634
CEBPB_CTCFB_PU1	2.025	4.519
E2F4_NR2F2_THAP1	3.147	3.393
ELF1_STAT5_THAP1	2.691	3.841
GABP_STAT5_THAP1	3.013	3.519
E2F6_JUND_TR4	3.173	3.349
EGR1_PU1_SIX5	2.925	3.597
GTF2F1_STAT1_TAF7	3.51	3.004
GTF2F1_TEAD4_TR4	3.247	3.256
EJUND_SMC3_THAP1	3.247	3.256
CBX3_ETS1_TR4	3.247	3.256
GTF2F1_MAFF_TAF7	3.34	3.156
STAT5_TAF7_THAP1	2.384	4.104
E2F4_ELF1_TR4	2.832	3.634
GTF2F1_PML_TR4	3.013	3.436
EJUNB_SP2_YY1	3.013	3.436

SIX5_SP1_TAF7	3.247	3.197
GABP_SMC3_THAP1	3.51	2.934
E2F6_SIX5_TR4	2.925	3.519
SMC3_THAP1_ZNF143	3.51	2.934
GTF2F1_SIX5_STAT5	2.603	3.841
EJUNB_SIX5_SP1	3.041	3.393
ELK1_NR2F2_SIX5	3.384	3.049
JUND_STAT5_THAP1	2.691	3.741
GTF2B_SIX5_USF1	3.247	3.182
NR2F2_STAT5_TAF7	3.147	3.256
EJUNB_GTF2F1_STAT5	2.732	3.634
MAX_SMC3_THAP1	3.557	2.808
EGR1_SMC3_THAP1	3.428	2.934
GTF2B_SMC3_USF1	3.247	3.104
EJUNB_GABP_GTF2B	2.832	3.519
STAT5_THAP1_TRIM28	2.832	3.519
SIN3_STAT5_THAP1	2.691	3.634
CTCFB_GABP_TAF7	2.691	3.634
CEBPB_ELK1_SIX5	2.8	3.519
EJUNB_GTF2F1_THAP1	2.925	3.393
GTF2B_MEF2_SIX5	2.925	3.393
CTCFL_GTF2B_GTF2F1	2.925	3.393
HMGN3_STAT2_THAP1	3.147	3.156
GABP_MEF2_TAF7	3.041	3.256
CHD2_SMC3_THAP1	3.041	3.256
NR2F2_PU1_STAT5	2.188	4.104
GTF2B_SIX5_TAF7	3.072	3.207
GTF2F1_SIX5_TAF7	2.969	3.303
GABP_STAT5_TAF7	2.662	3.597
MAX_NELFE_PU1	2.8	3.457
STAT5_TEAD4_THAP1	2.732	3.519
CHD2_MAFF_TAF7	2.732	3.519
CTCFL_ETS1_THAP1	3.147	3.104
GTF2B_STAT1_USF1	2.51	3.741
PU1_TAF7_TBLR1	3.247	3.004
E2F6_EJUNB_THAP1	3.127	3.104
ELF1_STAT1_TAF7	2.832	3.393
SMC3_TBLR1_THAP1	3.095	3.104
BHLHE40_GTF2F1_TR4	3.095	3.104
CBX3_JUND_TR4	3.095	3.104
JUND_TEAD4_TR4	3.095	3.104
CBX3_SRF_TR4	3.095	3.104

ELK1_STAT5_THAP1	2.8	3.393
GTF2F1_JUND_TR4	2.8	3.393
NR2F2_SIX5_TAF7	2.8	3.393
GTF2F1_NR2F2_THAP1	3.384	2.808
MXI1_STAT5_THAP1	3.384	2.808
CMYC_NR2F2_SIX5	2.51	3.681
CCNT2_GABP_NELFE	3.247	2.934
EGR1_MAFF_TAF7	2.925	3.256
EJUNB_GTF2F1_TAF7	2.925	3.256
BCLAF1_CTCFB_TAF7	2.925	3.256
EJUNB_STAT5_TAF7	3.247	2.934
EJUNB_SIX5_THAP1	2.925	3.256
CCNT2_MAFF_TAF7	2.925	3.256
SP1_STAT5_THAP1	2.925	3.256
SIX5_TAF7_ZNF143	2.995	3.182
PU1_SIX5_TBLR1	2.851	3.326
EJUNB_GABP_GTF2F1	2.428	3.741
EJUND_GTF2F1_SIX5	2.703	3.457
GTF2F1_STAT5_THAP1	2.625	3.519
ELF1_MEF2_SIX5	2.625	3.519
E2F4_ETS1_TR4	2.625	3.519
E2F4_JUND_TR4	2.625	3.519
E2F4_TAF1_TR4	2.732	3.393
CTCFC_NR2F2_SIX5	2.732	3.393
EGR1_STAT5_THAP1	2.603	3.519
EJUNB_GTF2B_GTF2F1	2.588	3.519
ETS1_SMC3_THAP1	3.173	2.934
BCLAF1_GTF2B_SIX5	2.925	3.182
E2F4_GABP_NELFE	2.925	3.182
E2F4_POL2_TR4	3.417	2.684
CTCFB_SMC3_THAP1	3.428	2.671
IRF1_SMC3_THAP1	3.162	2.934
GTF2F1_NR2F2_SIX5	3.041	3.049
ETS1_NR2F2_PU1	2.247	3.841
CEBPB_NR2F2_SIX5	2.8	3.256
GABP_GTF2F1_TR4	2.8	3.256
ETS1_GTF2B_SIX5	2.961	3.086
BCLAF1_PU1_SIX5	2.41	3.634
GTF2F1_PU1_TAF7	2.879	3.156
E2F4_TR4_YY1	2.773	3.256
CTCFB_NR2F2_SIX5	2.925	3.104
HMGN3_SMC3_THAP1	3.095	2.934

P300_STAT5_THAP1	2.925	3.104
EJUND_GTF2B_USF1	2.925	3.104
GTF2B_PU1_ZNF143	2.662	3.367
CTCF_SMC3_THAP1	3.34	2.671
CTCFC_SMC3_THAP1	3.34	2.671
ELF1_STAT2_TAF7	2.662	3.349
BCLAF1_SIX5_THAP1	2.603	3.393
HMGN3_STAT2_TAF7	2.732	3.256
GTF2B_TBLR1_USF1	2.662	3.326
EJUNB_IRF1_SP2	3.173	2.808
SIX5_SP2_TAF7	3.041	2.934
CEBPB_SIX5_TAF7	3.041	2.934
CBX3_ELK1_THAP1	3.041	2.934
EJUNB_GTF2B_SP1	3.041	2.934
CMYC_SMC3_THAP1	2.951	3.004
NRF1_TAF7_TBLR1	2.625	3.326
MAX_STAT5_THAP1	2.925	3.021
ELK1_GTF2B_USF1	3.247	2.699
JUND_NR2F2_SIX5	2.588	3.349
ELK1_SIX5_SP1	3.34	2.597
BHLHE40_NR2F2_PU1	2.188	3.741
E2F4_ELK1_SP2	3.732	2.197
CJUN_GTF2B_PU1	2.625	3.303
GTF2B_PU1_TAF7	2.843	3.081
CTCFC_SIX5_THAP1	3.247	2.671
CTCFB_GTF2B_STAT5	2.662	3.256
MAFF_MXI1_TAF7	2.662	3.256
ATF1_EJUNB_SIX5	2.8	3.104
ATF1_EJUNB_TAF7	2.8	3.104
EJUNB_SIX5_STAT5	2.51	3.393
NR2F2_THAP1_TRIM28	2.51	3.393
CEBPB_SIX5_STAT5	2.51	3.393
E2F4_SIX5_TR4	2.51	3.393
EJUND_NR2F2_SIX5	2.51	3.393
CHD2_STAT5_THAP1	2.51	3.393
CTCFB_GTF2F1_PU1	2.832	3.049
IRF1_TR4_YY1	2.843	3.038
EJUNB_GTF2F1_SP1	2.247	3.634
CTCFB_TAF7_ZNF143	2.247	3.634
E2F4_STAT2_TAF7	2.51	3.349
GTF2B_RFX5_TAF7	3.925	1.934
ELF1_STAT2_THAP1	2.925	2.934

CEBPB_GTF2F1_SIX5	2.603	3.256
ETS1_STAT2_THAP1	2.588	3.256
ETS1_STAT5_THAP1	2.588	3.256
STAT5_THAP1_YY1	2.641	3.182
GABP_SIX5_STAT5	2.641	3.182
EJUND_GTF2B_SIX5	2.873	2.934
ETS1_NR2F2_SIX5	2.366	3.436
CTCFB_GTF2B_TAF7	2.773	3.021
CTCFB_GTF2F1_TAF7	2.773	3.021
CMYC_TR4_YY1	2.662	3.126
ETS1_PU1_STAT5	2.041	3.741
CTCF_ETS1_GTF2B	2.732	3.049
SP1_STAT5_TAF7	2.732	3.049
NR2F2_P300_SIX5	2.732	3.049
CJUN_PU1_TAF7	2.732	3.049
E2F4_GABP_TR4	2.51	3.256
MAFK_SIX5_ZNF143	2.662	3.104
CTCFB_SP1_TAF7	2.662	3.104
E2F4_EGR1_TR4	2.662	3.104
EJUNB_GTF2F1_IRF1	2.553	3.207
HMGN3_NR2F2_TAF7	2.603	3.156
IRF1_SIX5_TR4	3.063	2.671
ELK1_PU1_STAT5	2.8	2.934
PML_TEAD4_TR4	2.8	2.934
EJUNB_GTF2F1_MAX	2.384	3.349
GTF2F1_MAFF_MXI1	2.925	2.808
CCNT2_SIX5_TAF7	2.68	3.049
RCOR1_STAT5_THAP1	2.625	3.104
SIX5_STAT5_YY1	2.783	2.934
IRF1_STAT2_TAF7	2.691	3.021
PU1_SIX5_SRF	2.691	3.021
STAT5_TAF1_THAP1	2.603	3.104
P300_SIX5_TAF7	2.925	2.782
CTCFL_GTF2F1_YY1	3.294	2.408
CBX3_CTCFB_TAF7	2.304	3.393
ELF1_SIX5_STAT5	2.51	3.182
CTCFB_GTF2F1_MXI1	2.34	3.349
STAT2_TAF7_TBLR1	2.428	3.256
CTCF_THAP1_ZNF143	3.013	2.671
CBX3_CMYC_TR4	2.613	3.071
ETS1_SIX5_TAF7	2.557	3.126
E2F6_STAT5_TAF7	2.569	3.104

E2F4_MAFF_TAF7	2.732	2.934
BCLAF1_GTF2B_THAP1	2.732	2.934
MAX_NR2F2_SIX5	2.294	3.367
CTCFB_IRF1_TAF7	2.473	3.182
SIX5_STAT5_TEAD4	2.603	3.049
GABP_GTF2B_STAT1	2.51	3.135
E2F6_NR2F2_SIX5	2.641	3.004
BCLAF1_NR2F2_SIX5	2.384	3.256
CTCFB_P300_TAF7	2.384	3.256
TBLR1_THAP1_USF1	2.384	3.256
GTF2B_PU1_STAT1	2.384	3.256
EJUNB_P300_SIX5	2.384	3.256
JUND_MEF2_SIX5	2.384	3.256
CTCFB_GTF2B_USF1	2.384	3.256
CEBPB_GTF2F1_PU1	2.288	3.349
CEBPB_GTF2B_PU1	2.288	3.349
PML_STAT1_TAF7	2.925	2.711
CMYC_STAT2_THAP1	2.158	3.478
GTF2B_SMC3_YY1	3.304	2.332
ETS1_GABP_NELFE	2.625	3.004
ETS1_SIX5_STAT5	2.51	3.104
ATF1_SIX5_STAT5	2.51	3.104
GTF2B_SMC3_STAT5	2.8	2.808
E2F4_EJUNB_SRF	2.8	2.808
CTCFL_GTF2F1_TRIM28	2.8	2.808
CTCFL_ETS1_GTF2B	2.8	2.808
CBX3_ELF1_TR4	2.8	2.808
GTF2B_NR2F2_THAP1	2.8	2.808
CTCFC_ELK1_NR2F2	2.8	2.808
EJUNB_ELF1_GTF2F1	2.003	3.597
CEBPB_EJUNB_TAF7	2.925	2.671
CTCFC_CTCFL_THAP1	2.925	2.671
ELF1_SMC3_THAP1	2.851	2.741
HMGN3_STAT5_TAF7	2.428	3.156
SIN3_SIX5_STAT5	2.428	3.156
CTCFC_ELK1_SIX5	3.384	2.197
BHLHE40_EJUNB_GTF2F1	2.041	3.519
CTCFC_PML_TAF7	2.304	3.256
STAT2_TBLR1_THAP1	2.625	2.934
CJUN_GTF2F1_PU1	2.818	2.741
CTCFB_PU1_SIX5	2.625	2.934
NR2F2_SIX5_TRIM28	2.625	2.934

ELK1_RCOR1_THAP1	3.247	2.312
CBX3_MAX_TR4	2.925	2.634
E2F4_STAT2_THAP1	2.732	2.808
SIX5_TAF7_THAP1	2.691	2.841
GABP_JUND_NELFE	2.925	2.597
E2F4_STAT1_TAF7	2.662	2.86
ELK1_SIX5_ZNF143	3.063	2.457
ELK1_SIX5_TAF7	2.41	3.104
GTF2B_NRF1_SIX5	2.51	3.004
PU1_SIX5_ZNF143	2.51	3.004
GTF2B_PU1_TBLR1	2.641	2.872
PU1_SP1_TAF7	2.577	2.934
CTCFL_GTF2F1_IRF1	3.461	2.049
SIX5_SMC3_THAP1	2.832	2.671
CBX3_TR4_YY1	3.247	2.256
MAX_PU1_TAF7	2.51	2.988
JUND_PU1_SIX5	2.613	2.881
NRSF_SIX5_THAP1	2.384	3.104
MAFF_TAF7_TEAD4	2.384	3.104
BHLHE40_GABP_NELFE	3.095	2.393
GTF2B_NR2F2_SIX5	2.732	2.741
EJUND_GTF2F1_PU1	2.732	2.741
CTCFL_GTF2F1_TAF7	2.8	2.671
ETS1_STAT2_TAF7	2.215	3.256
CTCFC_GTF2F1_SP2	2.8	2.671
JUND_SIX5_STAT5	2.44	3.021
CTCF_GTF2B_HMGN3	2.304	3.156
ATF1_EJUNB_GTF2B	2.41	3.049
ELK1_SP1_THAP1	3.147	2.312
NR2F2_RCOR1_SIX5	2.41	3.049
ELK1_SIX5_SP2	3.147	2.312
JUND_SIX5_TAF7	2.51	2.934
CTCFB_GTF2B_PU1	2.51	2.934
ELF1_SIX5_TAF7	2.51	2.934
E2F4_SIX5_TAF7	2.562	2.881
EJUNB_GTF2F1_POL2	2.405	3.038
IRF1_MAFF_TAF7	2.751	2.689
SIX5_STAT2_TAF7	2.625	2.808
ELF1_MAFF_TAF7	2.625	2.808
CMYC_STAT5_TAF7	2.281	3.149
POL2_SIX5_TAF7	2.484	2.934
ETS1_GTF2B_PU1	2.354	3.063

CBX3_GABP_NELFE	2.247	3.156
STAT1_TAF7_YY1	1.925	3.478
GTF2B_MAX_SIX5	2.709	2.689
EJUNB_IRF1_SIX5	2.51	2.881
P300_PU1_TAF7	2.773	2.612
PU1_TAF7_ZNF143	2.449	2.934
E2F6_EJUNB_SIX5	2.51	2.872
CMYC_GTF2B_PU1	2.395	2.98
CMYC_GABP_NELFE	2.873	2.498
PU1_SIX5_SP1	2.428	2.934
EJUNB_ETS1_GTF2B	2.428	2.934
ELK1_GTF2F1_SIX5	2.773	2.586
ATF1_GTF2F1_STAT5	2.304	3.049
NRF1_SIN3_SIX5	2.095	3.256
EJUND_GTF2B_STAT5	2.603	2.741
CTCFB_PML_TAF7	2.34	3.004
CMYC_STAT5_THAP1	2.818	2.519
CMYC_CTCFB_TAF7	2.247	3.089
SIX5_TAF7_ZBTB7	2.662	2.671
E2F4_SMC3_THAP1	2.691	2.634
GTF2F1_STAT2_TAF7	2.384	2.934
CMYC_MAFF_TAF7	2.577	2.741
BCLAF1_THAP1_ZNF143	2.51	2.808
CTCFL_EGR1_GTF2B	2.51	2.808
EJUNB_TAF7_TBLR1	2.925	2.393
CMYC_PU1_TAF7	2.523	2.784
GTF2F1_SIX5_USF1	2.925	2.374
ELF1_GABP_NELFE	2.625	2.671
SMC3_THAP1_TRIM28	2.625	2.671
NR2F2_SIX5_SMC3	2.625	2.671
EJUNB_MAX_TAF7	3.013	2.282
BCLAF1_NR2F2_TAF7	2.188	3.104
ELK1_PU1_SIX5	2.691	2.597
ELF1_GTF2F1_STAT5	2.215	3.071
IRF1_PML_TR4	2.864	2.419
E2F6_GTF2B_STAT5	2.51	2.77
PML_SIX5_TAF7	2.428	2.851
STAT1_TAF1_TAF7	2.691	2.586
ETS1_NR2F2_THAP1	2.118	3.156
GTF2F1_PU1_ZNF143	2.399	2.872
CBX3_PU1_TAF7	2.428	2.841
ELF1_NR2F2_SIX5	2.247	3.021

CJUN_PU1_SIX5	2.215	3.049
MAFF_MAX_TAF7	2.324	2.934
CCNT2_STAT2_TAF7	2.51	2.741
STAT5_TAF7_ZNF143	2.51	2.741
BHLHE40_NR2F2_SIX5	2.304	2.934
EJUNB_SIX5_ZNF143	2.304	2.934
CTCFC_GTF2B_SMC3	2.304	2.934
GABP_SIX5_TAF7	2.456	2.77
CEBPB_CTCFB_GTF2F1	2.205	3.021
SIX5_THAP1_ZNF143	2.703	2.519
EJUND_ELK1_GTF2B	2.41	2.808
CJUN_GTF2B_THAP1	2.428	2.782
PU1_SIN3_SRF	2.095	3.104
BCLAF1_CTCFB_GTF2F1	2.147	3.049
NR2F2_SIX5_SP1	2.147	3.049
GTF2B_IRF1_SMC3	2.714	2.481
E2F4_EJUNB_GTF2F1	2.173	3.021
E2F6_MAFF_TAF7	2.384	2.808
CMYC_STAT2_TAF7	1.999	3.188
E2F6_GTF2B_SIX5	2.173	3.012
IRF1_SRF_TR4	2.925	5.182
CBX3_EJUNB_TAF7	2.51	2.671
ETS1_MAFF_TAF7	2.34	2.841
CTCFC_GABP_NR2F2	2.662	2.519
E2F4_MAFF_MXI1	2.51	2.671
EJUNB_TAF7_ZNF143	2.51	2.671
CBX3_GTF2B_PU1	2.317	2.86
ELK1_PU1_TAF7	2.428	2.741
E2F4_NR2F2_SIX5	2.118	3.049
CHD2_STAT5_TAF7	2.118	3.049
BHLHE40_PU1_TAF7	2.384	2.782
EJUNB_GTF2F1_YY1	2.327	2.827
STAT5_TAF7_TBLR1	2.41	2.741
JUND_TR4_YY1	2.703	2.448
CTCFB_GTF2F1_YY1	2.603	2.548
SIX5_SP1_STAT5	2.51	2.634
GABP_STAT2_TAF7	2.51	2.634
E2F4_STAT5_TAF7	2.44	2.699
SMC3_THAP1_YY1	3.198	1.934
EGR1_NR2F2_SIX5	2.288	2.841
ATF1_SIX5_TAF7	2.428	2.699
ELK1_P300_SIX5	2.732	2.393

GTF2B_TBLR1_THAP1	2.34	2.782
GTF2B_PU1_SRF	2.603	2.519
RCOR1_SMC3_THAP1	2.603	2.519
EJUND_GTF2F1_TAF7	2.648	2.474
NRSF_STAT2_TAF7	2.603	2.519
GABP_NR2F2_TAF7	2.51	2.612
ELK1_GTF2B_THAP1	2.51	2.612
POL2_SIX5_STAT5	1.897	3.223
CMYC_MEF2_SIX5	2.181	2.934
P300_STAT5_TAF7	2.304	2.808
ELF1_NELFE_TAF7	2.304	2.808
CBX3_SRF_THAP1	2.304	2.808
E2F4_PU1_SIX5	2.399	2.711
CBX3_GTF2B_SIX5	2.449	2.65
E2F6_STAT2_TAF7	1.773	3.326
CJUN_SMC3_THAP1	5.095	2.393
EJUNB_GTF2B_MAX	2.428	2.656
CTCFL_JUND_THAP1	2.691	2.393
CTCFB_CTCFL_THAP1	2.691	2.393
EGR1_NR2F2_PU1	2.41	2.671
CHD2_SIX5_TAF7	2.34	2.741
CEBPB_ETS1_SIX5	2.215	2.86
EJUNB_GTF2F1_PML	2.063	3.004
IRF1_NR2F2_SIX5	2.273	2.792
GTF2B_MXI1_THAP1	2.691	2.374
EJUND_SIX5_TAF7	2.366	2.699
E2F6_GTF2F1_STAT5	2.41	2.65
POL2_SMC3_THAP1	2.288	2.77
CTCF_GTF2F1_SIX5	2.8	2.256
E2F4_MEF2_SIX5	2.384	2.671
CTCFB_SIX5_TAF7	2.384	2.671
CTCFB_GABP_GTF2B	2.384	2.671
CTCF_GABP_GTF2B	2.384	2.671
CTCFB_MXI1_TRIM28	2.384	2.671
GABP_PU1_TAF7	2.288	2.764
CBX3_SIX5_THAP1	2.205	2.841
CCNT2_IRF1_NELFE	1.925	3.121
EJUNB_GTF2B_STAT5	2.41	2.634
CTCFL_ETS1_GTF2F1	2.625	2.419
GTF2B_SRF_THAP1	2.41	2.634
CMYC_PML_TR4	2.553	2.49
IRF1_NR2F2_THAP1	2.109	2.934

TAF7_USF1_ZNF143	2.428	2.612
BCLAF1_GTF2B_PU1	2.013	3.021
CEBPB_CTCFB_MXI1	2.51	2.519
E2F4_SP2_TAF7	2.247	2.782
NR2F2_SIX5_TAF1	2.288	2.741
EJUND_GTF2B_THAP1	2.773	2.256
GTF2B_NR2F2_SMC3	2.51	2.519
STAT5_TAF7_TRIM28	2.095	2.934
GTF2B_NR2F2_STAT5	2.51	2.519
CBX3_ELF1_NELFE	2.188	2.841
GTF2B_STAT2_TAF7	2.247	2.782
PML_SIX5_STAT5	2.247	2.782
IRF1_SIX5_STAT5	2.636	2.393
GTF2B_P300_SIX5	2.569	2.457
CMYC_SIX5_TAF7	2.374	2.65
NR2F2_POL2_THAP1	2.23	2.792
CMYC_EJUNB_NELFE	2.851	5.021
GTF2F1_MAX_SIX5	2.843	2.165
ELF1_STAT5_TAF7	2.147	2.86
GTF2B_PU1_YY1	2.53	2.474
CJUN_PU1_SRF	2.063	2.934
MAX_SIX5_TAF7	2.535	2.461
CTCF_GTF2B_SP2	2.188	2.808
CBX3_EJUNB_SIX5	2.188	2.808
SIN3_SMC3_THAP1	2.603	2.393
GTF2B_HMGN3_SIX5	2.42	2.571
CTCFB_TAF7_YY1	2.147	2.841
EJUNB_POL2_SIX5	2.51	2.47
EJUNB_TAF7_TRIM28	2.304	2.671
CTCFB_SIX5_THAP1	2.773	2.197
GTF2B_TAF7_THAP1	2.449	2.519
CJUN_GTF2B_USF1	2.366	2.597
GABP_GTF2B_STAT5	2.51	2.448
NR2F2_SIN3_SIX5	2.147	2.808
POL2_STAT1_TAF7	2.051	2.903
SIX5_TAF1_TAF7	2.434	2.519
NRSF_SIX5_TAF7	2.34	2.612
CBX3_SIX5_TAF7	2.34	2.612
ELK1_PU1_ZNF143	2.428	2.519
E2F6_ELK1_STAT5	2.691	2.256
IRF1_SIX5_TAF7	2.372	2.574
NR2F2_SIX5_ZNF143	2.205	2.741

ELK1_SIX5_THAP1	2.247	2.699
EJUNB_GTF2F1_JUND	1.925	3.021
CMYC_GTF2B_SIX5	2.281	2.661
SIX5_TAF7_YY1	2.449	2.492
ELK1_HMGN3_SP2	2.625	2.312
ETS1_GTF2B_USF1	2.166	2.77
STAT2_TAF7_TRIM28	2.095	2.841
SIX5_TAF7_TRIM28	2.41	2.519
CEBPB_SIX5_SP1	2.41	2.519
GTF2B_SIX5_STAT2	2.41	2.519
GABP_GTF2B_SMC3	2.51	2.419
CEBPB_GTF2F1_TAF7	2.34	2.586
ELK1_SP1_TAF7	2.34	2.586
ELK1_P300_TAF7	2.118	2.808
E2F4_PU1_TAF7	2.051	2.872
ETS1_PU1_TAF7	2.032	2.888
GTF2B_SIX5_SP1	2.569	2.349
HMGN3_SIX5_TAF7	2.399	2.519
STAT2_TAF7_YY1	2.198	2.718
P300_PU1_SIX5	2.317	2.597
ELF1_GTF2B_SIX5	2.473	2.436
CBX3_GTF2F1_SRF	2.205	2.699
CBX3_PU1_SIX5	2.205	2.699
EJUNB_PML_TAF7	2.384	2.519
ELK1_PU1_SRF	2.384	2.519
GTF2B_SRF_USF1	2.51	2.393
GTF2F1_SMC3_SP2	2.51	2.393
JUND_NR2F2_PU1	1.851	3.049
EJUND_GTF2B_PU1	2.247	2.65
CTCFB_GTF2B_GTF2F1	2.247	2.65
E2F6_SIX5_TAF7	2.198	2.689
GABP_IRF1_NELFE	2.51	2.374
E2F4_ELK1_STAT5	2.625	2.256
EJUND_GTF2F1_SP2	2.832	2.049
IRF1_PU1_TAF7	2.333	2.543
EGR1_GTF2B_SIX5	2.41	2.464
CBX3_ELK1_SIX5	2.691	2.182
IRF1_JUND_TR4	2.577	2.296
CTCF_ETS1_GTF2F1	2.832	2.033
EGR1_PU1_STAT5	1.925	2.934
PU1_SIX5_THAP1	2.34	2.519
SIX5_TAF7_USF1	2.34	2.519

ELK1_GTF2B_SIX5	2.34	2.519
GTF2B_SIX5_ZNF143	2.34	2.519
SIX5_STAT5_USF1	2.188	2.671
EJUNB_GABP_SIX5	2.34	2.519
E2F4_GTF2B_SIX5	2.384	2.474
CTCFB_ELF1_TAF7	2.013	2.841
BHLHE40_STAT2_TAF7	2.428	2.419
CTCFC_IRF1_THAP1	2.41	2.436
ELF1_PU1_TAF7	2.188	2.656
GTF2B_HMGN3_SMC3	2.588	2.256
CBX3_CTCFB_GTF2F1	2.247	2.597
EHDAC8_TAF7_YY1	NS	4.841
GABP_GTF2B_SIX5	2.354	2.474
CEBPB_ELF1_GTF2F1	2.083	2.741
CTCFC_GABP_GTF2B	2.304	2.519
CTCFL_GABP_GTF2F1	2.625	2.197
CBX3_E2F6_TR4	2.188	2.634
GTF2B_THAP1_USF1	2.51	2.312
CTCFC_EGR1_THAP1	2.428	2.393
PU1_TAF7_YY1	2.032	2.788
CCNT2_NR2F2_THAP1	2.147	2.671
BCLAF1_GTF2F1_SIX5	2.205	2.612
EJUND_PU1_SIX5	2.205	2.612
GTF2B_POL2_SIX5	2.168	2.647
GTF2F1_SIX5_THAP1	2.44	2.374
CCNT2_STAT2_THAP1	2.41	2.393
ELF1_GTF2B_SMC3	2.366	2.436
HMGN3_SP2_TAF7	2.366	2.436
ETS1_PU1_SIX5	2.166	2.634
EGR1_ELK1_SIX5	2.449	2.349
GTF2B_P300_USF1	2.279	2.519
NR2F2_THAP1_YY1	2.279	2.519
GTF2B_GTF2F1_SIX5	2.434	2.363
EJUNB_ETS1_SIX5	2.095	2.699
CTCFB_GABP_GTF2F1	2.569	2.223
GTF2B_SIN3_SIX5	2.273	2.519
MAFF_TAF7_YY1	2.34	2.448
JUND_PU1_TAF7	2.269	2.519
CTCFB_ETS1_THAP1	2.366	2.419
BHLHE40_PU1_SRF	2.147	2.634
EJUNB_GTF2B_YY1	2.843	1.934
CTCF_HMGN3_SP2	1.843	2.934

GTF2B_SP1_STAT5	2.428	2.349
GTF2B_SMC3_TAF7	2.384	2.393
GTF2F1_SMC3_TAF7	2.384	2.393
PU1_SIN3_SIX5	2.188	2.586
E2F6_GTF2B_SMC3	2.003	2.77
GTF2B_JUND_SMC3	2.173	2.597
CCNT2_GTF2B_SIX5	2.198	2.571
JUND_STAT2_THAP1	2.247	2.519
CTCFL_ELF1_GTF2F1	2.51	2.256
ELK1_GTF2F1_PU1	2.51	2.256
PML_STAT2_THAP1	2.247	2.519
GTF2F1_MAFF_SIN3	2.51	2.256
ELK1_HMGN3_THAP1	2.247	2.519
PU1_RCOR1_SIX5	2.247	2.519
EGR1_STAT2_THAP1	2.247	2.519
EJUND_GABP_GTF2B	2.294	2.47
MAX_SIX5_STAT5	2.395	2.367
GTF2B_MAFF_TAF7	2.34	2.419
EJUND_NRF1_TAF7	2.41	2.349
SIX5_TAF7_TBLR1	2.366	2.393
CTCFB_GTF2F1_IRF1	2.573	2.185
CHD2_EJUNB_GTF2F1	1.818	2.934
ELK1_GTF2F1_SP2	2.625	2.126
E2F6_HMGN3_NELFE	2.366	2.381
ELK1_IRF1_STAT5	3.198	1.547
GTF2F1_IRF1_SMC3	2.588	2.156
CTCF_GTF2F1_IRF1	2.925	1.818
IRF1_TR4_TRIM28	3.732	4.741
EJUNB_ELK1_GTF2F1	2.732	4.741
THAP1_TR4_YY1	3.247	4.741
E2F4_GTF2B_PU1	2.118	2.622
EJUNB_SIX5_TEAD4	2.063	2.671
GTF2F1_SRF_TBLR1	2.384	2.349
ETS1_GTF2B_THAP1	2.384	2.349
EGR1_GABP_NELFE	2.384	2.349
CEBPB_SIX5_TRIM28	1.925	2.808
MAZ_TAF7_TR4	4.732	NS
E2F4_E2F6_STAT5	2.473	2.256
CTCFC_SIN3_TRIM28	2.205	2.519
MAFF_PML_TAF7	2.205	2.519
BHLHE40_STAT5_TAF7	2.205	2.519
CTCFL_GTF2F1_HMGN3	2.304	2.419

CMYC_IRF1_TR4	2.705	2.018
CBX3_STAT5_TAF7	2.41	2.312
CJUN_PU1_STAT5	1.366	3.349
GTF2B_MXI1_PU1	2.34	2.374
HMGN3_NELFE_TAF7	2.34	2.374
GTF2B_PU1_SP2	2.013	2.699
CTCFL_GTF2B_YY1	2.625	2.086
CEBPB_GTF2F1_SRF	2.188	2.519
BHLHE40_ELK1_TAF7	2.188	2.519
ATF1_GTF2B_STAT5	2.188	2.519
GTF2B_PU1_THAP1	2.51	2.197
CEBPB_PML_SIX5	2.003	2.699
ETS1_GTF2F1_SIX5	2.366	2.336
MAX_STAT2_TAF7	2.225	2.474
PU1_THAP1_ZNF143	2.304	2.393
GTF2B_NRF1_USF1	2.384	2.312
PML_STAT2_TAF7	2.109	2.586
GTF2B_THAP1_ZNF143	2.317	2.374
GTF2F1_PU1_SRF	2.34	2.349
ELF1_HMGN3_NELFE	2.428	2.256
CEBPB_GABP_GTF2B	2.22	2.464
CTCFC_E2F6_TRIM28	2.025	2.65
CTCFC_GTF2F1_SMC3	2.041	2.634
GTF2B_PML_SIX5	2.195	2.478
CTCFB_POL2_TAF7	1.461	3.207
E2F6_PU1_SIX5	2.198	2.47
E2F4_ELK1_THAP1	2.147	2.519
CTCFC_E2F6_SP2	2.147	2.519
MAFF_SIN3_TAF7	2.147	2.519
E2F4_EJUNB_SIX5	2.247	2.419
ELF1_SP1_TAF7	2.188	2.478
CTCF_GTF2F1_RCOR1	2.147	2.519
JUND_MAFF_TAF7	2.147	2.519
ELF1_GTF2B_STAT5	2.34	2.326
CBX3_ELK1_GTF2B	2.41	2.256
CTCF_NR2F2_ZNF143	1.858	2.808
GTF2B_PU1_SP1	2.215	2.448
CEBPB_SIN3_SIX5	2.025	2.634
GABP_HMGN3_TAF7	1.889	2.764
GTF2F1_P300_SIX5	2.304	2.349
CCNT2_EJUNB_TAF7	2.603	2.049
GTF2B_SIX5_YY1	1.898	2.753

EJUNB_PML_THAP1	2.013	2.634
MAX_PML_TR4	1.976	2.671
HMGN3_NR2F2_SIX5	2.013	2.634
GTF2B_SIX5_TBLR1	2.279	2.367
GABP_GTF2B_TAF7	2.218	2.426
NR2F2_SP1_TAF7	2.205	2.436
GTF2B_GTF2F1_SMC3	2.205	2.436
POL2_STAT2_THAP1	2.858	1.782
CTCFC_RAD21_SP2	2.247	2.393
GTF2B_JUND_SIX5	2.247	2.393
CBX3_SIX5_STAT5	2.118	2.519
E2F4_SIX5_STAT5	2.288	2.349
EJUND_GTF2B_NRF1	2.118	2.519
CCNT2_EGR1_NELFE	2.34	2.296
POL2_PU1_SIX5	2.417	2.219
CTCFL_GTF2F1_PML	2.603	2.033
E2F6_GTF2F1_SMC3	1.864	2.77
CJUN_NELFE_PU1	3.247	4.634
CMYC_TR4_TRIM28	3.603	4.634
GABP_GTF2F1_NELFE	2.304	2.326
SIX5_STAT5_TAF1	2.279	2.349
ELK1_GTF2B_PU1	2.34	2.287
EJUNB_ELF1_SIX5	2.013	2.612
MAFF_TAF1_TAF7	2.205	2.419
P300_SIX5_STAT5	2.205	2.419
CTCFB_GTF2B_YY1	2.137	2.486
CTCF_SP2_TAF1	2.366	2.256
EJUND_GTF2F1_USF1	2.247	2.374
CMYC_EJUNB_GTF2F1	1.72	2.897
GTF2F1_NR2F2_STAT5	2.304	2.312
SIX5_STAT5_ZNF143	2.095	2.519
NR2F2_PML_SIX5	2.095	2.519
EGR1_SIX5_TAF7	2.279	2.326
GTF2B_STAT1_TBLR1	2.147	2.457
EJUNB_GTF2B_TAF7	2.34	2.256
GTF2F1_TBLR1_USF1	1.925	2.671
BCLAF1_THAP1_YY1	1.925	2.671
CCNT2_EJUNB_GTF2B	2.34	2.256
ELK1_GTF2F1_P300	2.366	2.229
ETS1_GTF2B_SMC3	2.288	2.296
CEBPB_GABP_SIX5	2.147	2.436
CTCF_GTF2B_GTF2F1	2.188	2.393

GTF2F1_HMGN3_SIX5	2.198	2.381
CHD2_SIX5_THAP1	2.317	2.256
ELK1_TAF7_TBLR1	2.247	2.326
EGR1_EJUNB_GTF2F1	1.832	2.741
PML_POL2_TR4	2.553	2.016
CMYC_GTF2B_MAFF	1.991	2.578
PML_PU1_TAF7	2.247	2.321
ELK1_GTF2B_SP1	2.41	2.156
E2F4_HMGN3_NELFE	2.118	2.448
EJUND_SP1_TAF7	2.279	2.287
E2F4_GTF2B_STAT5	2.384	2.182
CTCFC_JUND_THAP1	2.366	2.197
NR2F2_PU1_TRIM28	1.755	2.808
GTF2F1_MXI1_PU1	2.041	2.519
PU1_SIX5_SP2	2.041	2.519
ELF1_GTF2F1_TAF7	2.22	2.34
CTCFC_GTF2B_SP2	2.041	2.519
CTCF_PML_SP2	1.925	2.634
GTF2B_THAP1_TRIM28	2.247	2.312
CBX3_GTF2B_THAP1	2.247	2.312
ELK1_SP1_STAT5	2.51	2.049
BCLAF1_CTCFB_YY1	2.113	2.443
ATF1_GTF2B_USF1	2.34	2.214
HMGN3_NELFE_NRSF	2.118	2.436
IRF1_PU1_STAT5	2.032	2.519
ELK1_P300_PU1	2.288	2.256
JUND_NR2F2_THAP1	2.025	2.519
E2F4_GABP_TAF7	1.887	2.656
GTF2F1_NRF1_SIX5	2.095	2.448
GTF2B_SP1_SRF	2.384	2.156
EJUND_ELK1_GTF2F1	2.147	2.393
EJUNB_JUND_THAP1	2.147	2.393
EJUNB_SIN3_THAP1	2.147	2.393
CHD2_SIX5_STAT5	2.147	2.393
EJUND_STAT5_TAF7	2.147	2.393
EJUNB_JUND_SIX5	2.118	2.419
CTCFC_ETS1_GTF2F1	2.603	1.934
EGR1_SIX5_STAT5	2.013	2.519
E2F4_GTF2F1_STAT5	2.095	2.436
CBX3_EJUND_SIX5	1.858	2.671
HMGN3_NELFE_YY1	2.179	2.349
GTF2F1_SMC3_YY1	2.225	2.303

EJUND_GTF2B_GTF2F1	2.247	2.275
CTCFC_NR2F2_ZNF143	1.851	2.671
GTF2B_TAF7_USF1	2.127	2.393
SIX5_STAT1_THAP1	3.925	4.519
EJUNB_IRF1_NELFE	2.304	4.519
MAX_TR4_TRIM28	2.8	4.519
GABP_GTF2F1_STAT5	1.995	2.519
EJUNB_GTF2F1_TAF1	1.995	2.519
MAX_PU1_SIX5	2.331	2.182
IRF1_STAT5_TAF7	1.992	2.519
BHLHE40_GTF2B_PU1	2.063	2.448
ATF1_GTF2B_SIX5	2.247	2.256
CTCFL_E2F6_TRIM28	1.984	2.519
GTF2F1_IRF1_PU1	2.18	2.321
MXI1_PU1_SP1	2.188	2.312
CTCFL_GTF2F1_RCOR1	2.188	2.312
CTCFB_ELF1_STAT5	1.755	2.741
GTF2B_SMC3_TAF1	2.147	2.349
CEBPB_E2F6_GTF2F1	2.018	2.478
CMYC_GTF2B_STAT5	2.312	2.177
EJUNB_TAF1_TAF7	2.44	2.049
GTF2B_MXI1_SIX5	2.095	2.393
BCLAF1_GABP_THAP1	2.095	2.393
ELK1_GTF2B_ZNF143	2.428	2.059
BCLAF1_ELF1_THAP1	1.851	2.634
CTCF_GTF2B_IRF1	2.198	2.287
CMYC_STAT1_TAF7	1.662	2.821
CMYC_CTCFL_THAP1	1.963	2.519
GTF2B_NRF1_TBLR1	2.025	2.457
GTF2B_JUND_PU1	2.077	2.403
JUND_PU1_STAT5	1.636	2.841
GTF2F1_MXI1_SIX5	2.025	2.448
CTCFB_TAF1_TAF7	1.858	2.612
GTF2B_MAFF_YY1	2.466	2.004
CTCFL_E2F6_GTF2F1	2.077	2.393
BHLHE40_GTF2B_THAP1	2.384	2.086
E2F6_SIX5_STAT2	2.077	2.393
ATF1_GTF2B_SRF	2.095	2.374
EJUND_GTF2F1_SRF	2.095	2.374
BHLHE40_GTF2F1_SIX5	2.372	2.091
MAX_STAT2_THAP1	2.358	2.104
HMGN3_SIX5_STAT5	2.205	2.256

BCLAF1_GTF2F1_SP2	2.41	2.049
MXI1_PU1_ZNF143	2.41	2.049
ELK1_PU1_THAP1	2.41	2.049
CMYC_NELFE_PU1	2.188	4.457
BCLAF1_EJUND_GTF2F1	1.755	2.699
GTF2B_SRF_YY1	1.992	2.461
E2F6_ELK1_SIX5	1.748	2.699
ETS1_GTF2F1_PU1	1.972	2.474
EGR1_ELK1_THAP1	2.095	2.349
CEBPB_CHD2_CTCFB	1.925	2.519
GTF2B_SIX5_STAT1	1.925	2.519
GTF2F1_TAF7_THAP1	2.051	2.393
ETS1_PU1_SRF	1.925	2.519
CTCFC_ETS1_GTF2B	1.925	2.519
CTCFB_GTF2F1_TRIM28	2.025	2.419
E2F4_ELK1_SIX5	2.288	2.156
SIX5_STAT5_TRIM28	1.925	2.519
CEBPB_NRF1_SIX5	1.925	2.519
SIN3_STAT5_TAF7	1.925	2.519
P300_TAF7_USF1	2.147	2.296
JUND_PU1_SRF	1.995	2.448
GTF2F1_SRF_YY1	2.37	2.071
PU1_SIN3_TAF7	2.032	2.408
HMGN3_SP1_TAF7	1.969	2.47
CTCFB_GTF2F1_POL2	1.866	2.571
CEBPB_STAT5_TAF7	2.041	2.393
SIX5_SRF_STAT5	2.041	2.393
GTF2F1_IRF1_STAT5	2.376	2.056
SP1_STAT2_TAF7	2.118	2.312
EJUND_GTF2B_SRF	2.247	2.182
RCOR1_SIX5_THAP1	2.077	2.349
E2F6_GTF2F1_SIX5	2.304	2.121
CTCFB_PML_PU1	1.984	2.436
GABP_GTF2F1_TAF7	2.08	2.338
RCOR1_SP2_THAP1	2.025	2.393
CTCF_E2F6_SP2	1.995	2.419
GTF2B_TAF7_TBLR1	2.131	2.275
E2F4_ELK1_GTF2B	2.147	2.256
SP2_TAF7_TBLR1	2.147	2.256
CEBPB_GTF2B_SIX5	2.247	2.156
CEBPB_IRF1_PU1	2.169	2.233
BCLAF1_HMGN3_SP2	2.205	2.197

CTCFB_E2F4_TAF7	1.788	2.612
E2F6_GTF2F1_SRF	2.095	2.303
GABP_NELFE_POL2	2.762	1.634
CBX3_ELF1_TAF7	2.083	2.312
CCNT2_NELFE_PU1	2.925	4.393
GTF2B_RFX5_USF1	9.306	4.393
CTCF_E2F6_GTF2B	2.288	2.104
PML_TR4_YY1	2.562	1.827
HMGN3_SIX5_THAP1	2.166	2.223
CMYC_EJUNB_SIX5	2.484	1.902
CTCFL_EGR1_GTF2F1	2.188	2.197
EJUND_GABP_GTF2F1	2.294	2.091
MAZ_P300_TR4	4.384	NS
BCLAF1_ELK1_SP2	4.384	1.934
E2F4_ELF1_NELFE	1.925	2.457
GTF2F1_SIN3_SIX5	2.147	2.229
GTF2B_GTF2F1_SRF	2.147	2.229
ELK1_GTF2B_P300	2.118	2.256
PU1_SP2_TAF7	2.118	2.256
ELK1_PU1_SP1	2.247	2.126
CTCFB_GTF2F1_SIX5	2.34	2.033
ELK1_GTF2F1_USF1	2.188	2.182
ELF1_GTF2F1_SIX5	2.266	2.104
ETS1_HMGN3_NELFE	2.173	2.197
GTF2F1_HMGN3_STAT2	2.147	2.223
GTF2B_SRF_TBLR1	2.147	2.223
GABP_GTF2B_NELFE	2.041	2.326
CTCF_GTF2B_RCOR1	1.732	2.634
GABP_TAF7_TBLR1	1.984	2.381
EJUNB_PML_SIX5	2.013	2.349
E2F4_EJUNB_GTF2B	2.013	2.349
CBX3_CTCFB_GTF2B	1.925	2.436
HMGN3_JUND_NELFE	2.147	2.214
GTF2B_GTF2F1_PU1	1.965	2.393
ETS1_GTF2F1_SMC3	2.173	2.182
ATF1_TAF7_USF1	2.041	2.312
CHD2_GTF2F1_SMC3	2.041	2.312
EJUND_GABP_TAF7	2.095	2.256
GTF2B_STAT5_ZNF143	2.247	2.104
CTCFB_EGR1_TAF7	1.832	2.519
BHLHE40_SIX5_TAF7	2.127	2.223
CMYC_GTF2F1_PU1	1.83	2.519

EJUNB_IRF1_TAF7	1.879	2.47
MAX_STAT5_TAF7	2.304	2.041
BCLAF1_ELK1_SIX5	2.188	2.156
EJUND_SIX5_THAP1	1.925	2.419
CTCFB_GTF2F1_SMC3	1.925	2.419
EJUNB_ELF1_STAT5	1.925	2.419
BCLAF1_PU1_TAF7	2.147	2.197
PML_PU1_SIX5	2.032	2.312
PU1_TAF7_USF1	2.147	2.197
BHLHE40_SIX5_STAT5	2.025	2.312
CEBPB_GABP_GTF2F1	1.873	2.464
E2F4_GTF2B_THAP1	2.109	2.223
GTF2F1_JUND_SIX5	2.205	2.126
GTF2B_SIX5_TAF1	2.113	2.214
CTCFB_JUND_TAF7	1.714	2.612
POL2_TR4_ZNF143	2.51	4.326
ELK1_GTF2B_SP2	2.304	2.021
CEBPB_PU1_TAF7	2.013	2.312
GTF2F1_JUND_SRF	2.22	2.104
GTF2B_GTF2F1_STAT5	2.063	2.256
CEBPB_GTF2F1_YY1	2.247	2.071
E2F4_GTF2B_STAT2	1.989	2.326
CBX3_SP1_THAP1	2.118	2.197
E2F4_GABP_GTF2B	1.892	2.419
GTF2B_SIX5_SRF	2.095	2.214
CTCFL_E2F4_GTF2F1	2.147	2.156
GTF2B_IRF1_SIX5	2.304	1.998
ELK1_STAT5_YY1	2.317	1.984
GTF2F1_MAX_SMC3	2.072	2.229
CMYC_NR2F2_THAP1	1.871	2.429
CTCFB_ETS1_GTF2F1	2.077	2.223
GABP_GTF2F1_PU1	2.086	2.214
CTCFB_ETS1_GTF2B	1.925	2.374
MAX_NR2F2_THAP1	1.925	2.374
GTF2B_MAFF_MAX	2.179	2.118
CEBPB_JUND_SIX5	1.858	2.436
CTCFL_TRIM28_YY1	1.925	2.367
E2F6_THAP1_ZNF143	1.925	2.367
GTF2F1_STAT5_TAF7	1.773	2.519
GTF2F1_SIX5_TBLR1	2.188	2.104
CHD2_PU1_TAF7	1.995	2.296
GTF2B_PU1_TRIM28	2.077	2.214

GABP_PU1_SIX5	1.976	2.312
GABP_GTF2F1_SIX5	2.205	2.081
ATF1_EJUND_GTF2F1	2.109	2.175
PU1_TAF1_TAF7	2.113	2.171
GTF2B_USF1_ZNF143	2.127	2.156
ELF1_JUND_NELFE	2.147	2.135
SIX5_TBLR1_USF1	2.025	2.256
BCLAF1_GTF2B_SP2	2.025	2.256
CCNT2_ELF1_NELFE	2.025	2.256
CTCF_RAD21_SP2	2.025	2.256
E2F4_GTF2B_SMC3	2.247	2.033
BHLHE40_TBLR1_THAP1	1.843	2.436
E2F4_ELK1_PU1	2.34	1.934
GTF2F1_PU1_TBLR1	2.215	2.059
BHLHE40_GTF2B_SIX5	2.095	2.175
CTCFB_GTF2B_POL2	1.393	2.877
CMYC_SP1_TAF7	1.835	2.433
ELF1_GTF2B_THAP1	2.225	2.041
GTF2B_STAT1_ZNF143	2.041	2.223
ETS1_SIX5_THAP1	2.106	2.156
GTF2B_STAT5_TAF7	2.077	2.182
NR2F2_PU1_SP1	1.703	4.256
CEBPB_CTCFC_GTF2F1	2.095	4.256
NELFE_PU1_SIN3	2.732	4.256
NELFE_NRF1_SIN3	8.569	4.256
PML_TR4_TRIM28	3.095	4.256
NRF1_RFX5_TAF7	1.925	4.256
MXI1_NELFE_NRF1	8.569	4.256
SP2_STAT1_THAP1	3.51	4.256
ELF1_NELFE_STAT1	8.569	4.256
CBX3_NELFE_PU1	2.732	4.256
HMGN3_NELFE_PU1	2.51	4.256
STAT2_TAF7_THAP1	2.384	4.256
STAT1_STAT5_THAP1	3.51	4.256
GABP_NELFE_STAT1	7.984	4.256
SMC3_STAT1_THAP1	2.925	4.256
PML_THAP1_TR4	3.384	4.256
EJUNB_GTF2B_NRF1	2.732	4.256
GABP_GTF2B_PU1	2.041	2.214
STAT2_TAF7_TEAD4	2.205	2.049
ELK1_SP2_STAT5	4.247	1.612
CTCFC_SP2_THAP1	4.247	3.519

SIX5_SP1_ZBTB33	4.247	NS
MAZ_THAP1_TR4	4.247	NS
CTCF_ELK1_SP2	4.247	2.349
SP1_THAP1_ZBTB33	4.247	NS
CTCFC_ELK1_SP2	4.247	2.349
MAZ_PU1_TR4	4.247	NS
CTCFL_E2F6_GTF2B	2.025	2.214
CHD2_ELK1_SIX5	2.304	1.934
EGR1_EJUNB_SIX5	1.925	2.312
CTCFC_GTF2B_GTF2F1	1.925	2.312
SP1_TAF7_TBLR1	1.925	2.312
CCNT2_SIX5_STAT5	1.925	2.312
E2F6_EJUND_STAT5	2.147	2.086
ETS1_STAT5_TAF7	1.858	2.374
CTCF_GTF2B_TAF1	1.553	2.671
POL2_PU1_SRF	1.562	2.66
ELK1_STAT5_TRIM28	2.188	2.033
CTCFB_GTF2B_HMGN3	1.925	2.296
IRF1_PU1_SIX5	2.215	2.004
CCNT2_GABP_TAF7	1.805	2.412
GABP_GTF2F1_NR2F2	2.003	2.214
CTCFB_GTF2F1_PML	2.34	1.877
BHLHE40_GTF2F1_PU1	1.989	2.223
BCLAF1_E2F4_THAP1	1.691	2.519
ELF1_TAF7_TBLR1	1.873	2.336
HMGN3_PU1_SIX5	1.773	2.436
CCNT2_NELFE_TAF7	2.118	2.086
GTF2F1_TAF7_TBLR1	1.925	2.275
CHD2_GTF2B_SIX5	2.095	2.104
GTF2F1_SIX5_YY1	2.194	2.004
CTCFB_CTCFL_GTF2F1	2.147	2.049
CTCFL_ELF1_TRIM28	1.773	2.419
GTF2F1_MAFF_MAX	2.072	2.118
ELK1_JUND_THAP1	2.003	2.182
E2F6_ELF1_STAT5	2.029	2.156
MAFF_POL2_TAF7	1.858	2.326
E2F6_STAT1_THAP1	2.384	4.182
MXI1_PU1_TBLR1	1.925	2.256
CTCFB_GTF2F1_SIN3	1.925	2.256
CTCFC_PML_SP2	1.925	2.256
ELK1_P300_STAT5	2.51	1.671
CTCFB_GTF2F1_ZNF143	1.925	2.256

EJUNB_ETS1_STAT5	1.925	2.256
GABP_GTF2F1_SRF	1.925	2.256
EJUND_GTF2B_SP2	2.025	2.156
TAF7_TBLR1_ZNF143	2.063	2.118
CEBPB_CTCFB_GTF2B	1.925	2.256
CEBPB_SP1_TAF7	2.025	2.156
EJUND_ELK1_SIX5	2.147	2.033
ELK1_SIX5_SRF	2.147	2.033
EJUNB_POL2_TAF7	2.449	1.73
CTCFL_GTF2F1_MAX	1.995	2.182
CTCFC_GTF2B_RCOR1	1.755	2.419
E2F4_PU1_SP2	1.755	2.419
SP1_TAF7_USF1	1.755	2.419
EJUNB_ELF1_TAF7	2.013	2.156
ELK1_PU1_TBLR1	2.147	2.021
E2F4_EJUNB_STAT5	2.118	2.049
E2F4_EJUNB_TAF7	2.118	2.049
NR2F2_SIX5_YY1	1.773	2.393
EGR1_PU1_ZNF143	1.384	2.782
BCLAF1_IRF1_PU1	1.783	2.381
CTCF_JUND_SP2	2.003	2.156
CCNT2_SP1_TAF7	1.925	2.233
ELK1_ETS1_GTF2B	2.173	1.984
CMYC_TR4_ZNF143	3.732	4.156
CCNT2_PU1_TAF7	1.762	2.393
JUND_STAT5_TAF7	1.858	2.296
ELF1_GTF2B_TAF7	1.979	2.175
CJUN_PU1_THAP1	2.41	1.741
GTF2B_HMGN3_THAP1	1.976	2.175
EJUND_GTF2F1_THAP1	2.118	2.033
GTF2B_NRF1_TAF7	2.109	2.041
GTF2F1_RCOR1_SIX5	2.063	2.086
PU1_SIX5_YY1	1.855	2.291
BHLHE40_GTF2F1_TAF7	1.887	2.256
EJUNB_JUND_TAF7	2.205	1.934
ELF1_GTF2F1_SMC3	1.925	2.214
CTCFC_IRF1_SP2	2.312	1.827
CBX3_GTF2B_SRF	2.013	2.126
GTF2F1_IRF1_SIX5	2.348	1.786
CMYC_GABP_TAF7	1.751	2.381
GABP_SIX5_THAP1	2.072	2.059
ELK1_SIX5_TEAD4	2.304	1.827

GTF2F1_POL2_SRF	1.78	2.349
BCLAF1_E2F4_PU1	1.691	2.436
GTF2B_MAX_PU1	1.845	2.282
GTF2F1_PML_SIX5	2.113	2.012
EJUND_GTF2F1_TRIM28	1.732	2.393
CMYC_PU1_SIX5	2.136	1.987
GTF2B_USF1_YY1	2.129	1.993
HMGN3_PU1_TAF7	1.748	2.374
PU1_SIX5_TRIM28	1.925	2.197
GTF2B_IRF1_PU1	1.849	2.266
GTF2B_HMGN3_STAT2	1.858	2.256
GTF2B_JUND_THAP1	2.179	1.934
CTCFB_GTF2B_SMC3	2.041	2.071
EJUND_GTF2F1_NRF1	2.025	2.086
CMYC_SIX5_STAT5	2.147	1.964
PML_SIX5_THAP1	1.976	2.135
ATF1_GTF2B_PU1	1.925	2.182
CJUN_SIX5_STAT5	1.925	2.182
BCLAF1_SIX5_YY1	1.636	2.47
CMYC_GTF2F1_SRF	1.962	2.144
ELF1_TAF7_THAP1	1.818	2.287
ELF1_PU1_SIX5	1.876	2.229
GTF2F1_NRF1_STAT5	2.51	4.104
E2F4_TBP_TR4	2.51	4.104
CTCF_ETS1_NELFE	3.247	4.104
EJUNB_NELFE_YY1	3.247	4.104
EJUNB_SRF_THAP1	2.51	4.104
POL2_TR4_TRIM28	2.732	4.104
NR2F2_TBLR1_THAP1	2.34	4.104
CEBPB_CTCF_GTF2F1	1.925	4.104
NRF1_STAT1_THAP1	7.984	4.104
CEBPB_NR2F2_PU1	2.063	4.104
NRF1_STAT5_TBLR1	2.51	4.104
NR2F2_PU1_TBLR1	0.925	4.104
PU1_STAT1_STAT5	2.384	4.104
CMYC_GTF2F1_SIX5	2.047	2.055
GTF2B_JUND_USF1	1.925	2.175
GTF2B_NRF1_SIN3	1.773	2.326
E2F4_GTF2F1_SIX5	2.018	2.081
GTF2B_HMGN3_STAT5	2.077	2.021
SIN3_SIX5_TAF7	1.81	2.287
CTCF_SP2_YY1	1.81	2.287

ELK1_GTF2F1_TAF7	1.925	2.171
CTCFL_ZBTB33_ZNF143	4.095	NS
CTCFB_EJUNB_THAP1	4.095	3.519
CTCFC_STAT5_THAP1	4.095	3.519
GABP_SP1_TAF7	1.969	2.126
CTCFB_STAT5_THAP1	4.095	3.519
EJUNB_EJUND_SP2	4.095	9.324
BCLAF1_CTCF_THAP1	4.095	3.519
MAZ_SP1_TR4	4.095	NS
RAD21_SP2_THAP1	4.095	3.519
CTCFC_GTF2F1_USF1	4.095	2.934
THAP1_ZBTB33_ZNF143	4.095	NS
SMC3_THAP1_ZBTB33	4.095	NS
CTCFB_PU1_THAP1	4.095	3.519
MAFF_THAP1_ZBTB33	4.095	NS
GTF2B_IRF1_THAP1	2.028	2.066
JUND_SIX5_THAP1	1.972	2.118
ATF1_EJUND_GTF2B	2.041	2.049
GTF2F1_SIX5_TAF1	2.069	2.021
E2F6_PU1_TAF7	1.569	2.519
EJUND_GTF2B_TAF7	2.106	1.978
GABP_TAF7_THAP1	1.788	2.296
GABP_NELFE_YY1	2.041	2.041
PU1_SIN3_ZNF143	1.432	2.65
BCLAF1_HMGN3_TAF7	1.925	2.156
GTF2B_SIN3_SMC3	1.925	2.156
PU1_SP2_ZNF143	1.925	2.156
NRF1_SIX5_THAP1	1.925	2.156
CTCF_GTF2F1_ZNF143	1.925	2.156
CTCFB_GTF2B_TRIM28	1.925	2.156
EJUNB_TAF7_YY1	2.147	1.934
ETS1_P300_SIX5	1.972	2.104
CTCFB_GTF2B_MAX	2.137	1.934
ELF1_GTF2B_STAT1	1.662	2.408
GTF2F1_SIX5_SRF	1.773	2.296
EJUNB_MAX_SIX5	2.072	1.993
ELF1_GTF2B_PU1	1.828	2.236
GTF2F1_POL2_SIX5	2.239	1.824
GTF2F1_SRF_ZNF143	1.732	2.326
ETS1_PU1_THAP1	1.843	2.214
BCLAF1_EJUND_GTF2B	1.843	2.214
BCLAF1_GTF2B_TAF7	1.8	2.256

ATF1_PU1_TAF7	2.118	1.934
ELK1_GABP_STAT5	2.288	1.764
CBX3_E2F4_SP2	2.003	2.049
TBLR1_THAP1_ZNF143	1.925	2.126
GABP_P300_SIX5	2.063	1.988
GTF2B_PML_SMC3	1.925	2.126
CMYC_GTF2B_SMC3	2.645	1.398
PU1_SIX5_TAF1	1.925	2.118
CBX3_EJUND_GTF2B	1.925	2.118
CTCFB_ELF1_GTF2F1	2.109	1.934
ELK1_JUND_SIX5	2.051	1.988
GTF2B_POL2_THAP1	2.188	1.851
CTCFL_ETS1_TRIM28	1.832	2.197
CMYC_EJUNB_TAF7	1.953	2.076
E2F6_PU1_SRF	1.843	2.182
GABP_GTF2B_THAP1	2.147	1.877
IRF1_PU1_SRF	1.744	2.278
ETS1_STAT1_THAP1	2.384	4.021
CMYC_GTF2B_TAF7	1.96	2.061
ELK1_GTF2B_TAF7	1.925	2.091
ETS1_GTF2B_NR2F2	1.858	2.156
CJUN_SP2_THAP1	4.013	4.519
CCNT2_GTF2B_SRF	2.077	1.934
CBX3_GTF2F1_SIX5	2.077	1.934
EJUNB_GTF2B_JUND	1.714	2.296
CBX3_GTF2F1_PU1	1.714	2.296
ETS1_GABP_GTF2B	1.925	2.083
E2F4_GTF2B_MXI1	1.976	2.027
GTF2B_PU1_TEAD4	1.788	2.214
CEBPB_SIX5_ZNF143	1.843	2.156
CCNT2_CTCFB_GTF2F1	2.063	1.934
BHLHE40_GTF2B_TAF7	1.925	2.071
E2F4_SIX5_THAP1	1.984	2.012
GTF2F1_MAX_PU1	2.247	1.748
GABP_MAX_NELFE	2.003	1.988
GTF2F1_PU1_TRIM28	1.832	2.156
ATF1_PU1_SIX5	1.832	2.156
GTF2B_MXI1_TBLR1	2.003	1.984
GTF2F1_JUND_SMC3	1.691	2.296
GTF2F1_JUND_PU1	2.008	1.978
SIX5_TBLR1_ZNF143	1.868	2.118
GTF2B_P300_PU1	1.8	2.182

CTCFB_MAX_TAF7	1.557	2.419
GTF2B_SIX5_SMC3	2.041	1.934
E2F6_GTF2F1_STAT2	1.719	2.256
CTCFB_GTF2B_SP1	2.041	1.934
EJUND_GTF2B_TBLR1	1.984	1.988
ELF1_GABP_TAF7	1.699	2.271
CCNT2_GTF2F1_SIX5	2.083	1.885
BCLAF1_GABP_TAF7	1.864	2.104
ATF1_GTF2B_MXI1	2.095	1.867
GTF2B_RCOR1_SMC3	2.025	1.934
CJUN_GTF2B_SIX5	1.868	2.091
EGR1_HMGN3_NELFE	2.025	1.934
E2F4_GTF2B_MAFF	2.025	1.934
RCOR1_SP2_TAF7	1.925	2.033
CTCFC_GTF2F1_RCOR1	1.925	2.033
P300_SIX5_THAP1	1.925	2.033
GTF2F1_P300_USF1	1.8	2.156
CMYC_NRF1_TAF7	1.855	2.1
GTF2B_STAT1_YY1	1.773	2.182
ATF1_ELK1_P300	2.188	1.764
E2F4_PU1_THAP1	2.013	1.934
CEBPB_POL2_SIX5	2.013	1.934
CEBPB_ELF1_SIX5	1.732	2.214
ELF1_NR2F2_TAF7	1.925	2.021
EJUND_P300_SIX5	1.732	2.214
CEBPB_IRF1_SIX5	2.008	1.934
GTF2B_PU1_SIN3	1.8	2.14
ATF1_GTF2F1_SRF	1.925	2.012
JUND_PU1_THAP1	2.003	1.934
ELK1_GTF2F1_SP1	2.118	1.818
ETS1_THAP1_ZNF143	1.876	2.059
EJUNB_MAX_NELFE	3.095	3.934
GTF2B_TR4_TRIM28	3.925	3.934
SRF_STAT1_THAP1	2.925	3.934
EHDAC8_GTF2F1_USF1	NS	3.934
NRF1_SIX5_STAT5	2.925	3.934
EJUNB_GTF2F1_STAT2	3.247	3.934
EHDAC8_GTF2B_USF1	NS	3.934
SP1_STAT1_THAP1	3.925	3.934
ETS1_SP1_TR4	3.925	3.934
E2F4_EJUND_TR4	3.095	3.934
NELFE_PU1_ZNF143	1.34	3.934

CEBPB_CTCFL_GTF2F1	2.732	3.934
ELK1_P300_TR4	9.306	3.934
CTCFC_NRF1_THAP1	2.51	3.934
ELF1_STAT1_THAP1	2.51	3.934
GTF2F1_TBLR1_TR4	3.51	3.934
ELF1_TR4_TRIM28	2.732	3.934
EJUNB_GTF2B_STAT2	3.095	3.934
CTCFB_PU1_STAT5	2.095	3.934
CTCFL_NELFE_ZNF143	3.247	3.934
CTCF_NRF1_SP2	2.51	3.934
ELK1_TAF7_TR4	3.247	3.934
NR2F2_NRF1_TBLR1	0.603	3.934
CTCFL_GABP_NELFE	3.51	3.934
BHLHE40_NELFE_PU1	2.51	3.934
GTF2B_TBLR1_TR4	3.51	3.934
CBX3_NELFE_USF1	3.247	3.934
EJUNB_NELFE_PML	1.925	3.934
MXI1_RFX5_SMC3	6.984	3.934
SRF_TR4_ZNF143	2.925	3.934
GTF2B_NRF1_TR4	3.247	3.934
POL2_TAF7_THAP1	1.829	2.104
CTCFB_E2F4_GTF2B	1.925	2.004
CHD2_GTF2F1_SIX5	1.995	1.934
CTCFC_EGR1_GTF2B	1.732	2.197
MXI1_SIX5_THAP1	1.714	2.214
CTCFC_GTF2B_MAX	2.131	1.796
CTCFB_SP2_THAP1	3.925	2.934
MEF2_PU1_TAF7	3.925	3.256
CTCF_STAT5_THAP1	3.925	3.256
GTF2B_P300_RFX5	3.925	1.282
E2F4_MAFF_THAP1	3.925	3.519
GTF2F1_MAFF_THAP1	3.925	2.519
NR2F2_RAD21_THAP1	3.925	3.256
CEBPB_CTCF_THAP1	3.925	3.519
MAZ_NELFE_PU1	3.925	NS
CTCFL_P300_THAP1	3.925	3.256
CTCFL_MEF2_PU1	3.925	3.256
GTF2B_RFX5_SIN3	3.925	1.474
EJUNB_TAF7_ZBTB33	3.925	NS
MEF2_MXI1_PU1	3.925	3.256
BCLAF1_CTCFC_TAF7	3.925	3.519
CEBPB_GTF2B_TAF7	1.925	1.998

CEBPB_ETS1_GTF2F1	1.818	2.104
CTCF_GTF2B_MAX	2.247	1.671
EJUND_GTF2B_MXI1	1.925	1.993
EJUND_GTF2F1_MXI1	1.925	1.993
GABP_GTF2B_NR2F2	1.788	2.126
GTF2F1_MAX_TAF7	2.023	1.89
EJUNB_SIX5_YY1	1.979	1.934
GTF2F1_P300_TAF7	1.925	1.984
IRF1_TAF7_TBLR1	1.67	2.236
SP1_TBLR1_THAP1	1.691	2.214
SP1_TAF7_THAP1	1.773	2.126
CTCFL_GTF2F1_POL2	1.965	1.934
CTCFB_EGR1_GTF2B	1.773	2.126
CEBPB_GABP_TAF7	1.641	2.256
CTCFB_GTF2B_IRF1	1.762	2.135
GABP_JUND_TAF7	1.773	2.121
CBX3_E2F4_PU1	1.788	2.104
CTCFL_EGR1_TRIM28	1.843	2.049
POL2_STAT2_TAF7	1.777	2.114
GTF2B_MAX_SMC3	2.372	1.519
CMYC_CTCFC_SP2	1.956	1.934
P300_SIN3_SIX5	1.818	2.071
JUND_TAF7_ZNF143	1.675	2.214
CTCFB_ELK1_SIX5	2.147	1.741
BCLAF1_GTF2B_HMGN3	1.8	2.086
GTF2F1_MAX_STAT5	2.086	1.8
JUND_TAF7_THAP1	1.662	2.223
SIN3_SIX5_THAP1	1.873	2.012
P300_PML_SIX5	1.792	2.091
GTF2B_NRSF_SIX5	1.755	2.126
E2F4_PU1_SRF	1.755	2.126
CCNT2_E2F4_NELFE	1.553	2.326
CJUN_IRF1_PU1	1.851	2.027
P300_SIX5_SRF	1.843	2.033
CMYC_CTCFC_THAP1	2.308	1.566
BHLHE40_PU1_SIX5	1.858	2.012
CTCFC_GTF2B_IRF1	1.765	2.104
CBX3_ETS1_SIX5	1.662	2.207
HMGN3_TAF7_TBLR1	1.662	2.207
GTF2F1_TAF7_ZNF143	1.847	2.021
CTCFL_GTF2B_IRF1	2.41	1.457
GTF2B_JUND_STAT1	1.818	2.049

CBX3_GTF2B_SMC3	1.818	2.049
EGR1_PU1_TAF7	1.684	2.182
CMYC_ELF1_TAF7	1.647	2.219
GTF2B_MAX_STAT5	2.147	1.718
BCLAF1_GTF2B_SP1	1.843	2.021
GTF2F1_NRSF_SIX5	1.843	2.021
GTF2B_TAF7_ZNF143	1.889	1.973
CTCFB_GTF2B_PML	1.744	2.118
GTF2F1_PU1_SP1	1.925	1.934
CTCFL_GTF2F1_JUND	1.925	1.934
GTF2F1_RCOR1_SP2	1.925	1.934
E2F4_ELF1_STAT5	1.703	2.156
E2F6_STAT5_ZNF143	1.925	1.934
GABP_NELFE_PML	1.662	2.197
EJUND_ELF1_GTF2F1	2.003	1.856
ELK1_IRF1_TAF7	1.925	1.934
CBX3_GABP_TAF7	1.925	1.934
GTF2F1_SP1_STAT5	1.925	1.934
ELK1_GTF2B_TRIM28	1.925	1.934
ARID3_CEBPB_GTF2B	1.925	1.934
GTF2B_PML_PU1	1.81	2.049
EJUND_SIX5_TEAD4	1.925	1.934
GABP_NELFE_TAF1	1.925	1.934
GTF2F1_SIX5_ZNF143	1.976	1.881
CEBPB_ETS1_GTF2B	1.984	1.872
CHD2_CTCFB_GTF2F1	2.013	1.841
CMYC_TAF7_ZNF143	1.785	2.068
ELK1_SIN3_THAP1	1.832	2.021
ELF1_POL2_TAF7	1.721	2.13
EJUND_TAF7_ZNF143	2.051	1.796
EGR1_PU1_SP2	1.691	2.156
ELF1_IRF1_TAF7	1.786	2.061
GTF2B_MAFF_POL2	1.648	2.197
IRF1_TAF7_ZNF143	1.773	2.071
ATF1_CEBPB_GTF2F1	1.662	2.182
GTF2F1_TBLR1_THAP1	1.832	2.012
GTF2B_JUND_ZNF143	1.81	2.033
TR4_TRIM28_YY1	2.662	3.841
MXI1_STAT1_TAF7	2.147	3.841
ELK1_GABP_TAF7	1.684	2.156
GTF2F1_MAFF_YY1	1.972	1.867
GTF2F1_TAF7_USF1	1.703	2.135

CMYC_CTCFL_GTF2F1	2.201	1.634
POL2_TAF7_TBLR1	1.862	1.971
CTCFL_GABP_THAP1	3.832	2.934
CTCFC_GTF2B_TAF1	1.312	2.519
ELK1_GTF2F1_ZNF143	2.013	1.818
CMYC_EJUND_GTF2B	2.092	1.732
ELK1_GABP_SIX5	2.041	1.782
CTCF_SP2_ZNF143	1.773	2.049
BCLAF1_ELF1_GTF2F1	1.762	2.059
E2F4_GABP_STAT5	1.8	2.021
TAF7_YY1_ZNF143	1.691	2.126
GTF2B_JUND_TAF7	1.795	2.021
E2F4_GTF2F1_PU1	1.925	1.885
CMYC_EJUNB_GTF2B	2.009	1.799
SP1_TAF7_ZNF143	1.81	1.998
BCLAF1_GABP_GTF2B	1.873	1.934
CTCFB_IRF1_PU1	1.873	1.934
CBX3_THAP1_ZNF143	1.755	2.049
JUND_SP1_TAF7	1.732	2.071
E2F4_GTF2B_SRF	1.868	1.934
EGR1_ELK1_PU1	2.003	1.796
E2F4_SIN3_STAT5	1.864	1.934
ELK1_RCOR1_SIX5	2.013	1.782
E2F6_GTF2B_SRF	1.703	2.091
CEBPB_EJUND_GTF2B	1.858	1.934
CTCF_ELF1_SP2	1.636	2.156
CEBPB_EJUND_GTF2F1	1.925	1.867
CTCFB_GTF2F1_HMGN3	1.925	1.867
BCLAF1_POL2_TAF7	1.535	2.256
E2F6_SIX5_TEAD4	1.703	2.086
GTF2F1_SIX5_SP2	2.118	1.671
GTF2B_SMC3_ZNF143	1.755	2.033
RCOR1_SIX5_TAF7	1.755	2.033
EJUND_MAX_TAF7	2.067	1.72
GTF2B_SIN3_STAT5	1.851	1.934
CJUN_SIX5_THAP1	2.003	1.782
BHLHE40_THAP1_ZNF143	1.851	1.934
CTCFC_JUND_SP2	1.851	1.934
GTF2B_SIX5_TEAD4	1.851	1.934
GTF2B_TEAD4_THAP1	1.851	1.934
EJUNB_GTF2B_ZNF143	1.732	2.049
BCLAF1_GTF2B_GTF2F1	1.662	2.118

GABP_P300_TAF7	1.719	2.059
GTF2F1_SP2_TBLR1	1.925	1.851
E2F4_GTF2B_USF1	1.703	2.071
ELF1_NELFE_YY1	2.032	1.741
EJUND_GTF2B_YY1	1.792	1.981
CEBPB_E2F6_GTF2B	1.792	1.981
ELK1_GABP_GTF2B	1.925	1.846
BHLHE40_TAF7_ZNF143	1.684	2.086
CEBPB_GTF2B_YY1	2.107	1.662
GTF2B_SIX5_TRIM28	2.003	1.764
SIN3_SIX5_ZNF143	1.696	2.071
EJUND_PU1_TAF7	1.925	1.841
EJUND_TAF7_USF1	1.832	1.934
GTF2F1_PU1_SP2	1.832	1.934
ELF1_GTF2F1_NELFE	1.832	1.934
SRF_TAF7_TBLR1	1.832	1.934
CHD2_GTF2B_MAFF	1.832	1.934
IRF1_TAF7_THAP1	1.586	2.178
GTF2B_POL2_PU1	1.625	2.137
CMYC_EJUND_TAF7	1.752	2.007
PML_PU1_ZNF143	1.571	2.188
CJUN_PML_PU1	1.703	2.056
GTF2F1_JUND_TAF7	1.79	1.964
GTF2B_GTF2F1_MAFF	2.013	1.741
CJUN_GTF2F1_SIX5	1.873	1.881
CTCFB_GTF2F1_MAX	1.893	1.86
CTCF_E2F4_GTF2B	1.818	1.934
CCNT2_JUND_NELFE	1.818	1.934
NR2F2_POL2_SIX5	1.925	1.827
EGR1_GTF2B_SMC3	1.925	1.827
POL2_PU1_TAF7	1.728	2.021
GTF2F1_MXI1_THAP1	1.662	2.086
CTCFC_ELF1_SP2	1.714	2.033
GTF2B_SP1_TBLR1	1.762	1.984
E2F6_GABP_STAT5	1.879	1.867
SIN3_THAP1_ZNF143	1.641	2.104
CEBPB_P300_PU1	1.588	2.156
CTCFB_E2F4_GTF2F1	1.925	1.818
JUND_P300_SIX5	1.755	1.988
E2F6_SIX5_TRIM28	1.744	1.998
CTCFC_GTF2B_PU1	2.51	3.741
GTF2F1_STAT1_USF1	2.34	3.741

SP1_SRF_TR4	3.732	3.741
GTF2F1_PU1_TR4	3.732	3.741
NRF1_NRSF_SIX5	2.925	3.741
GTF2F1_TR4_TRIM28	2.732	3.741
SP1_TBLR1_TR4	3.51	3.741
CBX3_TR4_TRIM28	3.732	3.741
E2F4_NRF1_TR4	3.247	3.741
EJUNB_GTF2B_SP2	2.925	3.741
ELK1_PU1_TR4	9.306	3.741
SIN3_THAP1_TR4	2.925	3.741
E2F4_MXI1_TR4	2.51	3.741
GTF2B_PU1_RFX5	3.51	3.741
GTF2B_HMGN3_TR4	3.925	3.741
CTCFB_STAT5_TAF7	3.732	3.741
BHLHE40_PU1_TR4	3.732	3.741
MEF2_PU1_SIX5	2.34	3.741
EJUNB_NELFE_SIN3	1.925	3.741
CBX3_P300_TR4	3.732	3.741
GABP_NRF1_STAT5	2.732	3.741
TEAD4_TR4_TRIM28	3.732	3.741
CTCFC_NELFE_SIN3	2.925	3.741
EJUNB_GTF2F1_PU1	1.603	3.741
CTCF_EJUNB_GTF2F1	1.925	3.741
E2F4_TR4_USF1	2.732	3.741
P300_TEAD4_TR4	3.732	3.741
CTCF_GTF2B_PU1	2.34	3.741
ETS1_TR4_USF1	2.925	3.741
CTCF_NRF1_THAP1	2.51	3.741
EGR1_SRF_TR4	2.732	3.741
TBP_TEAD4_TR4	3.732	3.741
GTF2F1_NRF1_TR4	3.247	3.741
PU1_STAT1_THAP1	3.247	3.741
EJUNB_NELFE_TAF7	2.51	3.741
BCLAF1_CTCFB_NELFE	1.925	3.741
TR4_TRIM28_ZNF143	2.732	3.741
TBLR1_TEAD4_TR4	3.247	3.741
CCNT2_NELFE_STAT5	3.925	3.741
E2F4_HMGN3_TR4	2.925	3.741
EJUNB_PU1_ZNF143	1.34	3.741
CTCFC_PU1_STAT5	2.51	3.741
GABP_NELFE_STAT5	3.247	3.741
HMGN3_NR2F2_NRF1	1.41	3.741

CCNT2_SP1_TR4	3.732	3.741
CHD2_SP1_TR4	3.732	3.741
MXI1_TAF7_TR4	2.51	3.741
NELFE_SP2_USF1	2.51	3.741
MEF2_SP2_ZNF143	2.34	3.741
CTCFC_NR2F2_USF1	1.8	3.741
MAX_TR4_ZNF143	3.588	3.741
SIX5_SP1_TR4	3.732	3.741
P300_TR4_ZNF143	3.732	3.741
E2F4_TR4_TRIM28	2.732	3.741
PU1_SIN3_TR4	3.732	3.741
CEBPB_GTF2F1_RAD21	1.51	3.741
SIN3_TAF7_TR4	2.925	3.741
P300_RCOR1_TR4	3.732	3.741
CTCFC_EJUNB_SIX5	2.925	3.741
GTF2F1_SRF_TR4	2.732	3.741
EJUNB_PU1_STAT5	2.247	3.741
HMGN3_STAT1_THAP1	2.34	3.741
CEBPB_CTCFC_ELK1	2.925	3.741
CFOS_NRF1_TBLR1	1.34	3.741
NELFE_NRSF_PU1	1.925	3.741
IRF1_NELFE_NRF1	3.625	3.741
NRF1_P300_STAT5	2.732	3.741
ATF1_EHDAC8_GABP	NS	3.741
EGR1_P300_TR4	3.732	3.741
EJUNB_GTF2F1_NELFE	2.51	3.741
CTCF_NELFE_SIN3	2.925	3.741
GTF2B_PU1_SMC3	2.925	3.741
CBX3_RCOR1_TR4	3.732	3.741
NELFE_NRSF_SP2	0.925	3.741
GABP_SP1_TR4	3.732	3.741
CTCFC_EJUNB_GTF2F1	2.34	3.741
ELK1_NFYA_TBLR1	2.51	3.741
PU1_TAF7_TR4	3.732	3.741
EJUNB_NRF1_SIX5	2.51	3.741
BCLAF1_CTCFC_NRF1	1.925	3.741
NRF1_STAT5_ZNF143	2.732	3.741
JUND_MEF2_SP2	2.34	3.741
HMGN3_TEAD4_TR4	3.732	3.741
BCL3_NRF1_TBLR1	1.662	3.741
P300_SP1_TR4	3.732	3.741
CEBPB_NFYA_TAF7	2.925	3.741

NRF1_SIX5_TR4	3.247	3.741
ELK1_NFYB_TBLR1	1.925	3.741
BCLAF1_NR2F2_THAP1	3.095	3.741
CTCFC_TAF7_ZNF143	1.773	3.741
ETS1_NRF1_TR4	3.247	3.741
CTCF_NELFE_ZNF143	2.925	3.741
PU1_SRF_STAT1	1.925	3.741
CBX3_EJUNB_NELFE	2.51	3.741
CTCF_TAF7_ZNF143	1.773	3.741
CHD2_TAF7_TR4	2.925	3.741
ATF1_ELK1_SIN3	2.041	1.699
GTF2F1_PU1_SIN3	1.755	1.984
CCNT2_TAF7_ZNF143	1.631	2.104
GTF2B_IRF1_MAFF	2.134	1.601
CMYC_PU1_SRF	1.523	2.211
EJUND_GTF2B_TRIM28	1.864	1.867
SP1_TAF7_YY1	1.498	2.233
GTF2F1_SRF_TAF7	1.714	2.012
GTF2B_SRF_TAF7	1.714	2.012
ATF1_GTF2B_TBLR1	1.732	1.993
CTCFB_GTF2B_ZNF143	1.51	2.214
ELF1_ELK1_STAT5	2.025	1.699
GTF2F1_IRF1_SRF	2.074	1.65
GTF2F1_STAT2_TBLR1	1.788	1.934
ELK1_MAX_TAF7	1.851	1.87
ATF1_GTF2F1_PU1	1.925	1.796
GTF2B_RCOR1_SIX5	1.925	1.796
BCLAF1_E2F6_GTF2F1	1.832	1.888
ETS1_GTF2B_STAT5	1.858	1.86
JUND_THAP1_ZNF143	1.783	1.934
CEBPB_ELF1_GTF2B	1.783	1.934
CCNT2_GTF2B_THAP1	1.719	1.998
MAX_TAF7_TBLR1	1.752	1.961
E2F6_GTF2B_MXI1	1.675	2.038
CTCFB_CTCFC_THAP1	1.662	2.049
GTF2B_RCOR1_SP2	1.851	1.86
GTF2B_SP1_TAF7	1.732	1.978
GTF2B_JUND_SRF	1.773	1.934
CJUN_GABP_GTF2B	1.925	1.782
CJUN_PU1_ZNF143	1.188	2.519
GTF2F1_POL2_SMC3	1.703	2.004
GTF2F1_SIX5_SP1	1.979	1.727

GTF2B_TAF7_YY1	1.802	1.903
EJUND_ELF1_STAT5	1.547	2.156
CHD2_TAF7_TBLR1	1.547	2.156
EJUND_ETS1_GTF2B	1.887	1.815
ETS1_PU1_SP1	1.478	2.223
PML_TAF7_TBLR1	1.662	2.038
CMYC_GTF2B_THAP1	1.998	1.701
CTCFB_GTF2F1_JUND	1.818	1.877
CJUN_SIX5_TAF7	1.925	1.77
GTF2B_JUND_MXI1	1.838	1.856
E2F4_TAF7_TBLR1	1.603	2.091
E2F4_SP1_TAF7	1.535	2.156
CTCFC_IRF1_PU1	1.755	1.934
BHLHE40_ELF1_TAF7	1.662	2.027
CTCFC_E2F4_GTF2B	1.755	1.934
SP1_SRF_TAF7	1.755	1.934
GTF2B_MAX_SRF	1.955	1.732
CTCFB_GTF2B_SIN3	1.473	2.214
BCLAF1_JUND_PU1	1.473	2.214
GTF2F1_STAT5_YY1	2.013	1.671
ETS1_GTF2B_NRF1	1.703	1.981
EJUNB_GTF2B_POL2	1.63	2.054
CCNT2_ETS1_NELFE	1.691	1.993
STAT5_TAF1_TAF7	1.748	1.934
EJUND_GTF2B_SP1	1.925	1.757
E2F4_GTF2F1_TAF7	1.61	2.071
BCLAF1_GTF2B_MAX	1.603	2.078
GABP_PML_TAF7	1.662	2.015
E2F6_EJUND_TAF7	1.882	1.792
ETS1_GTF2B_TAF7	1.739	1.934
ELF1_GTF2B_ZNF143	1.703	1.968
ATF1_ETS1_GTF2B	1.876	1.792
GTF2B_JUND_STAT5	1.8	1.867
PML_TAF7_THAP1	1.732	1.934
GTF2F1_P300_PU1	1.732	1.934
CEBPB_E2F6_SIX5	1.925	1.741
GABP_IRF1_TAF7	1.925	1.741
GTF2B_NRF1_NRSF	1.925	1.741
IRF1_PU1_TBLR1	1.528	2.138
EGR1_GTF2B_PU1	1.662	2.004
BCLAF1_SIX5_TAF1	1.592	2.071
E2F6_GTF2F1_PU1	1.887	1.773

CTCFB_GTF2B_JUND	1.662	1.998
BHLHE40_SP1_TAF7	1.662	1.998
GABP_GTF2F1_P300	1.847	1.808
GTF2B_POL2_STAT5	1.955	1.699
GTF2B_MAX_TAF7	1.925	1.729
GTF2B_IRF1_STAT5	1.893	1.76
CCNT2_THAP1_ZNF143	1.641	2.012
E2F6_SIX5_THAP1	1.662	1.988
CTCF_CTCFC_SP2	1.714	1.934
GABP_TBLR1_THAP1	1.714	1.934
CBX3_ELF1_GTF2B	1.714	1.934
EJUNB_GTF2B_PML	1.577	2.071
GABP_GTF2B_SRF	1.788	1.86
JUND_SP2_TAF7	1.788	1.86
ETS1_RCOR1_SP2	1.788	1.86
CMYC_ELK1_P300	1.811	1.835
E2F4_THAP1_ZNF143	1.864	1.782
CEBPB_CTCFB_PML	1.542	2.104
GTF2B_SMC3_TRIM28	1.818	1.827
ELK1_PU1_SIN3	1.773	1.872
EJUND_ELF1_GTF2B	1.788	1.856
GTF2B_MXI1_TAF7	1.662	1.981
ELF1_TAF7_ZNF143	1.571	2.071
SIX5_THAP1_YY1	2.016	1.626
ETS1_PU1_ZNF143	1.233	2.408
CBX3_GTF2B_TAF7	1.755	1.885
GTF2F1_PU1_YY1	1.925	1.715
ELF1_GTF2F1_SRF	1.762	1.877
GABP_PU1_SRF	1.788	1.851
ETS1_PU1_TBLR1	1.588	2.049
BCLAF1_GABP_GTF2F1	1.703	1.934
ELF1_SP1_STAT5	1.51	2.126
CTCFC_GTF2B_JUND	1.51	2.126
ELK1_STAT1_THAP1	3.732	3.634
EJUNB_GTF2F1_TBLR1	1.703	3.634
STAT1_STAT2_THAP1	3.247	3.634
MXI1_STAT1_THAP1	1.925	3.634
GABP_NELFE_SIX5	3.51	3.634
E2F4_NELFE_PU1	2.34	3.634
EJUND_TR4_YY1	3.925	3.634
CTCFB_P300_PU1	1.51	3.634
CMYC_EJUND_GTF2F1	1.742	1.889

CMYC_CTCFB_THAP1	1.732	1.899
EGR1_TAF7_TBLR1	1.641	1.988
ETS1_NR2F2_TAF7	1.617	2.012
CTCFC_GTF2B_YY1	1.51	2.118
BCLAF1_ELF1_GTF2B	1.51	2.118
ETS1_GTF2F1_TAF7	1.691	1.934
GTF2F1_STAT5_ZNF143	1.691	1.934
GTF2F1_SIX5_TEAD4	1.691	1.934
GTF2B_MAZ_TR4	3.625	NS
EJUND_ELK1_ZNF143	1.773	1.851
ELK1_GTF2B_SIN3	1.832	1.792
ELF1_PML_TAF7	1.712	1.912
CBX3_ETS1_GTF2B	1.732	1.891
ELK1_SIN3_SP1	1.755	1.867
ELK1_IRF1_SIX5	1.847	1.775
GABP_GTF2B_GTF2F1	1.822	1.799
CCNT2_CTCFB_GTF2B	1.588	2.033
ELF1_GTF2F1_STAT2	1.684	1.934
GTF2F1_PML_PU1	1.684	1.934
GTF2F1_SP1_SRF	1.684	1.934
GABP_GTF2B_TBLR1	1.818	1.8
EJUND_GTF2F1_IRF1	2.147	1.47
ELF1_ETS1_STAT5	1.481	2.135
PML_STAT5_TAF7	1.68	1.934
ELK1_GABP_P300	1.925	1.689
CEBPB_P300_SIX5	1.773	1.841
GTF2B_PU1_TAF1	1.596	2.016
CBX3_GABP_GTF2B	1.677	1.934
CEBPB_GTF2F1_MAX	1.61	2.001
BHLHE40_GTF2F1_SRF	1.8	1.808
GTF2F1_IRF1_TAF7	1.674	1.934
CMYC_GTF2F1_TAF7	1.643	1.964
EGR1_GTF2B_THAP1	1.81	1.796
CEBPB_GABP_PU1	1.423	2.182
BCLAF1_CMYC_TAF7	1.519	2.079
ETS1_SP1_TAF7	1.577	2.021
EJUND_ELF1_TAF7	1.709	1.888
CCNT2_IRF1_TR4	3.095	3.597
NRF1_POL2_STAT5	2.51	3.597
GTF2F1_JUND_STAT5	1.662	1.934
CTCFC_SP2_YY1	1.662	1.934
P300_SP2_TAF7	1.755	1.841

CTCF_CTCFC_GTF2F1	1.925	1.671
GTF2B_P300_STAT5	1.755	1.841
GTF2B_NR2F2_SP1	1.755	1.841
E2F6_TAF7_TBLR1	1.259	2.336
BCLAF1_CMYC_GTF2F1	1.776	1.817
GTF2B_YY1_ZNF143	1.818	1.774
SIX5_SRF_ZNF143	1.41	2.182
ETS1_GTF2F1_THAP1	1.744	1.846
BCLAF1_ELF1_TAF7	1.577	2.012
GTF2F1_NRSF_PU1	1.553	2.033
POL2_SP1_TAF7	1.243	2.343
ETS1_GTF2B_TBLR1	1.613	1.973
GTF2F1_MAX_STAT2	1.855	1.73
SIX5_SP1_THAP1	1.843	1.741
BHLHE40_CEBPB_SIX5	1.843	1.741
PU1_TAF7_TRIM28	1.843	1.741
GTF2F1_MAX_SRF	1.864	1.716
CTCFB_NELFE_POL2	0.925	3.578
GTF2B_IRF1_ZNF143	1.879	1.698
GTF2B_STAT2_TBLR1	1.714	1.86
CTCFB_GTF2B_TAF1	1.562	2.012
ELK1_GABP_THAP1	1.714	1.86
MAX_SP1_TAF7	1.925	1.646
GTF2F1_NRF1_TAF7	1.8	1.77
GTF2B_IRF1_TAF7	1.685	1.883
EJUND_GTF2F1_YY1	1.699	1.869
CBX3_PU1_SIN3	1.384	2.182
P300_SIX5_USF1	1.714	1.851
ETS1_GTF2B_IRF1	1.729	1.836
NRF1_SIX5_TAF1	1.569	1.993
STAT5_TAF7_YY1	1.925	1.634
EGR1_GTF2F1_SIX5	1.732	1.827
E2F6_SIX5_ZNF143	1.662	1.897
EGR1_SIX5_THAP1	1.762	1.796
ELF1_SIN3_STAT5	1.399	2.156
NRSF_PU1_TAF7	1.714	1.841
E2F4_EJUND_GTF2B	1.755	1.8
GTF2B_SRF_ZNF143	1.617	1.934
BHLHE40_GABP_TAF7	1.613	1.934
GABP_GTF2B_P300	1.755	1.792
GTF2F1_SP1_TAF7	1.611	1.934
ELF1_GTF2F1_PU1	1.611	1.934

IRF1_PU1_ZNF143	1.643	1.902
CJUN_GABP_PU1	1.308	2.236
ELF1_GTF2B_TBLR1	1.722	1.821
ETS1_GTF2B_SP2	1.662	1.881
GABP_POL2_TAF7	1.427	2.115
BHLHE40_GTF2F1_THAP1	1.8	1.741
GTF2B_IRF1_NRF1	1.645	1.895
CHD2_GTF2B_STAT5	1.603	1.934
E2F4_GTF2F1_SMC3	1.603	1.934
CMYC_E2F4_STAT5	1.811	1.726
CCNT2_GTF2B_NELFE	1.603	1.934
ELF1_GTF2F1_THAP1	1.832	1.704
CBX3_ETS1_THAP1	1.449	2.086
CMYC_ETS1_GTF2B	1.813	1.722
E2F4_GABP_THAP1	1.662	1.872
GTF2F1_SIX5_TRIM28	1.691	1.841
ELF1_MAX_TAF7	1.643	1.887
GTF2F1_STAT5_TAF1	1.748	1.782
GTF2B_P300_TAF7	1.696	1.834
BCLAF1_GTF2F1_TAF7	1.44	2.086
ELK1_IRF1_P300	2.035	1.49
GTF2B_POL2_TAF7	1.847	1.675
BHLHE40_CEBPB_GTF2F1	1.51	2.012
EGR1_ELK1_GTF2B	2.003	1.519
ELK1_GTF2B_JUND	1.588	1.934
GTF2B_HMGN3_SRF	1.662	1.86
CJUN_NRF1_TAF7	2.51	3.519
NELFE_NRF1_TAF7	8.984	3.519
EJUNB_ELK1_GTF2B	3.51	3.519
PU1_STAT1_TAF7	3.384	3.519
NELFE_PU1_TAF1	1.925	3.519
STAT1_TAF7_THAP1	2.147	3.519
GTF2B_SIX5_SP2	1.755	1.764
MXI1_NELFE_STAT1	7.984	3.519
CCNT2_STAT1_THAP1	2.732	3.519
CEBPB_EJUNB_GTF2F1	1.703	3.519
ETS1_GABP_TAF7	1.444	2.071
CMYC_GTF2B_SRF	1.311	2.204
E2F6_TAF7_ZNF143	1.34	2.175
ELK1_JUND_PU1	1.732	1.782
ATF1_GTF2B_TAF7	1.773	1.741
ELF1_THAP1_ZNF143	1.696	1.818

BCLAF1_E2F4_GTF2B	1.577	1.934
ELK1_SIX5_TAF1	1.925	1.586
SIX5_TAF7_ZBTB33	3.51	NS
CJUN_ELK1_SP2	3.51	2.419
CJUN_GABP_GTF2F1	1.662	1.846
CMYC_GABP_GTF2F1	1.897	1.61
GABP_PU1_ZNF143	1.401	2.104
CBX3_E2F4_GTF2B	1.703	1.8
MAX_NR2F2_TAF7	1.269	2.233
EJUND_GTF2F1_POL2	1.6	1.902
EJUND_GTF2B_MAX	1.617	1.885
CBX3_TAF7_YY1	1.597	1.905
GTF2B_MXI1_SP1	1.851	1.65
CMYC_SIX5_THAP1	1.773	1.727
EJUND_PML_TAF7	1.855	1.644
E2F4_GTF2B_TAF7	1.662	1.836
JUND_PU1_ZNF143	1.215	2.282
HMGN3_TAF7_THAP1	1.625	1.872
EGR1_GABP_SIX5	1.611	1.885
ELK1_SIX5_YY1	1.755	1.741
ELK1_GTF2F1_MAX	2.047	1.448
ELK1_TAF1_TAF7	1.703	1.792
ELF1_ELK1_SIX5	1.703	1.792
ELK1_SIX5_TBLR1	2.013	1.481
CCNT2_GTF2B_PU1	1.625	1.867
GTF2B_HMGN3_TAF7	1.596	1.895
GABP_GTF2B_ZNF143	1.675	1.815
E2F4_ETS1_SP2	1.748	1.741
CTCFB_GTF2F1_RCOR1	1.636	1.851
EJUND_GTF2B_ZNF143	1.832	1.654
ETS1_IRF1_PU1	1.476	2.01
GTF2F1_PU1_TAF1	1.639	1.846
EGR1_GABP_TAF7	1.55	1.934
GTF2B_TBLR1_YY1	1.662	1.821
BHLHE40_TAF7_TBLR1	1.423	2.059
CMYC_GTF2B_USF1	1.699	1.782
GTF2F1_POL2_PU1	1.28	2.201
CEBPB_MAX_SIX5	1.662	1.818
ELF1_GTF2B_NELFE	1.662	1.818
GTF2F1_PU1_RCOR1	1.714	1.764
GTF2B_IRF1_USF1	1.588	1.889
SIX5_TRIM28_ZNF143	1.617	1.86

ELK1_TAF7_YY1	1.378	2.096
GABP_MXI1_THAP1	1.732	1.741
GTF2B_MAX_THAP1	1.732	1.741
ATF1_NRSF_TAF7	1.691	1.782
CBX3_GABP_THAP1	1.732	1.741
ATF1_ELF1_TAF7	1.703	1.77
GTF2B_SIX5_TBP	1.773	1.699
GTF2F1_PML_SMC3	1.773	1.699
GTF2B_GTF2F1_THAP1	1.783	1.689
GTF2B_POL2_SMC3	1.493	1.978
EGR1_P300_SIX5	1.662	1.808
CCNT2_GTF2F1_PU1	1.662	1.808
E2F6_IRF1_TR4	3.449	3.47
IRF1_THAP1_ZNF143	1.773	1.696
IRF1_SIX5_THAP1	1.836	1.626
CCNT2_GTF2B_MAFF	1.428	2.033
BCLAF1_ETS1_SIX5	1.44	2.021
ELK1_GTF2B_GTF2F1	1.773	1.686
ATF1_GTF2F1_SIX5	1.788	1.671
GABP_GTF2B_JUND	1.581	1.877
EJUND_SIX5_ZNF143	1.399	2.059
GTF2B_THAP1_YY1	1.418	2.038
BCLAF1_GTF2B_IRF1	1.496	1.959
ELK1_SIN3_SIX5	1.714	1.741
E2F6_SP1_TAF7	1.469	1.984
GTF2B_STAT5_YY1	1.675	1.773
CTCFC_E2F6_GTF2B	1.851	1.597
ATF1_CEBPB_GTF2B	1.588	1.86
GTF2B_MAX_TBLR1	1.68	1.767
GTF2B_GTF2F1_TBLR1	1.648	1.796
EGR1_STAT5_TAF7	1.51	1.934
BHLHE40_ELK1_GTF2F1	1.832	1.612
CTCFB_GTF2F1_TAF1	1.925	1.519
JUND_NR2F2_TAF7	1.51	1.934
CBX3_HMGN3_TAF7	1.51	1.934
BCLAF1_EJUND_GABP	1.51	1.934
E2F6_P300_SIX5	1.51	1.934
ELK1_POL2_SIX5	1.51	1.934
GABP_TAF7_YY1	1.432	2.012
CBX3_ELK1_ZNF143	1.925	1.519
EJUNB_EJUND_GTF2B	1.603	1.841
ELF1_ELK1_THAP1	1.51	1.934

CMYC_ELK1_GTF2F1	1.61	1.832
PU1_SRF_YY1	1.399	2.041
GTF2F1_JUND_MXI1	1.584	1.856
IRF1_NRF1_TAF7	1.556	1.883
EJUNB_NELFE_POL2	2.288	3.436
GABP_STAT1_THAP1	2.34	3.436
IRF1_TR4_ZNF143	3.864	3.436
JUND_STAT1_THAP1	1.925	3.436
BHLHE40_IRF1_TAF7	1.588	1.846
GABP_THAP1_ZNF143	1.762	1.671
IRF1_SP1_TAF7	1.539	1.893
CJUN_GTF2F1_SRF	1.788	1.644
ATF1_TAF7_TBLR1	1.691	1.741
RCOR1_SIX5_SP2	1.691	1.741
E2F4_STAT5_ZNF143	1.732	1.699
E2F4_STAT5_TRIM28	1.732	1.699
ELF1_P300_SIX5	1.648	1.782
GTF2B_SIN3_THAP1	1.818	1.612
CHD2_CTCFB_GTF2B	1.603	1.827
RAD21_SMC3_THAP1	3.428	2.934
CJUN_SMC3_SP2	3.428	1.934
JUND_SIX5_ZNF143	1.675	1.753
CMYC_ELF1_GTF2B	1.459	1.968
CTCFB_GABP_MXI1	1.662	1.764
EGR1_ELK1_P300	1.617	1.808
CEBPB_GTF2F1_IRF1	1.874	1.55
CTCFB_SIX5_YY1	1.596	1.827
CJUN_POL2_PU1	1.233	2.189
E2F6_EJUND_GTF2B	1.451	1.969
CMYC_PU1_TBLR1	1.334	2.086
BHLHE40_CTCFB_GTF2F1	1.636	1.782
CMYC_GTF2F1_SMC3	1.16	2.256
CJUN_ELK1_STAT5	1.562	1.851
GTF2F1_HMGN3_TAF7	1.444	1.969
CTCFL_POL2_TRIM28	1.1	2.312
BHLHE40_GTF2B_USF1	1.603	1.808
ETS1_SIX5_TRIM28	1.542	1.867
EJUND_GTF2B_PML	1.641	1.768
EJUND_GTF2B_IRF1	1.868	1.54
GTF2B_MAFF_TAF1	1.473	1.934
SIN3_TBLR1_THAP1	1.547	1.86
EJUND_GTF2F1_PML	1.639	1.768

POL2_SIX5_THAP1	1.871	1.533
ELF1_SIX5_THAP1	1.677	1.727
EGR1_PU1_TRIM28	1.662	1.741
BCLAF1_SP2_YY1	1.884	1.519
ETS1_SIX5_TEAD4	1.603	1.796
CMYC_GTF2B_MXI1	1.532	1.866
CBX3_SIN3_SIX5	1.399	1.998
GTF2B_GTF2F1_USF1	1.562	1.834
E2F4_GTF2B_TBLR1	1.709	1.686
CTCFC_GTF2B_SIN3	1.925	3.393
EJUNB_GTF2F1_NR2F2	2.063	3.393
CJUN_GTF2B_TR4	4.095	3.393
PU1_STAT5_TEAD4	1.273	3.393
EJUNB_ETS1_SRF	2.063	3.393
E2F4_ELF1_TAF7	1.494	1.899
GTF2F1_PU1_STAT5	2.188	3.393
CEBPB_CTCFB_ELK1	1.603	3.393
CCNT2_NELFE_NRF1	1.51	3.393
EJUNB_ELK1_TAF7	2.247	3.393
BHLHE40_STAT1_THAP1	1.925	3.393
BCLAF1_GABP_SIX5	1.542	1.851
GTF2B_HMGN3_TBLR1	1.592	1.8
CTCFB_E2F6_GTF2F1	1.51	1.881
GABP_SIN3_TAF7	1.493	1.897
CJUN_GABP_TAF7	1.625	1.764
E2F4_TAF7_ZNF143	1.34	2.049
GTF2B_IRF1_TBLR1	1.599	1.789
CMYC_GTF2F1_MAFF	1.143	2.243
BCLAF1_JUND_SP2	1.714	1.671
CTCF_E2F6_GTF2F1	1.714	1.671
ATF1_EJUND_TAF7	1.714	1.671
EGR1_ELK1_SP1	1.714	1.671
ELK1_IRF1_SP1	1.965	1.419
CTCFB_GTF2F1_THAP1	3.384	2.256
BCLAF1_CTCFB_THAP1	3.384	2.934
ATF3_CTCFL_NR2F2	3.384	NS
BCLAF1_CTCFC_THAP1	3.384	2.741
MAZ_TEAD4_TR4	3.384	NS
ELF1_ETS1_GTF2B	1.548	1.834
P300_SIX5_TBLR1	1.641	1.741
EJUND_GTF2F1_MAX	1.8	1.582
GABP_GTF2B_MXI1	1.662	1.718

ATF1_ELF1_GTF2B	1.648	1.73
GTF2B_SP2_ZNF143	1.684	1.693
E2F6_EJUND_GTF2F1	1.51	1.867
CMYC_E2F4_GTF2B	1.68	1.696
GTF2B_SP1_THAP1	1.732	1.644
P300_POL2_SIX5	1.781	1.593
CTCF_GTF2F1_YY1	1.748	1.626
CCNT2_GTF2F1_TAF7	1.586	1.788
P300_SIX5_ZNF143	1.68	1.693
ELK1_GTF2B_TBLR1	1.818	1.555
BHLHE40_HMGN3_TAF7	1.384	1.988
GABP_TAF1_TAF7	1.613	1.757
GTF2F1_P300_SP2	1.851	1.519
CBX3_GTF2F1_TAF7	1.535	1.834
JUND_TAF7_TBLR1	1.391	1.976
EGR1_ELF1_STAT5	1.432	1.934
CTCF_GTF2B_YY1	1.569	1.796
RCOR1_THAP1_ZNF143	1.641	1.722
IRF1_SIX5_SRF	1.567	1.796
CMYC_GABP_GTF2B	1.633	1.729
GTF2F1_STAT2_YY1	1.588	1.773
JUND_SRF_THAP1	1.51	1.851
CEBPB_GTF2B_MXI1	1.662	1.699
E2F4_SIN3_SP2	1.662	1.699
GTF2F1_SIN3_SRF	1.542	1.818
BCLAF1_IRF1_SIX5	1.813	1.547
CBX3_ETS1_PU1	1.423	1.934
CTCFB_ELF1_GTF2B	1.423	1.934
GABP_SIX5_SP1	1.538	1.818
ELK1_ETS1_SIX5	1.662	1.693
CEBPB_CMYC_GTF2B	1.678	1.677
ATF1_CMYC_GTF2B	1.614	1.741
GTF2F1_TAF7_YY1	1.566	1.788
CBX3_E2F4_TAF7	1.481	1.872
CMYC_PU1_ZNF143	1.456	1.895
GABP_GTF2B_USF1	1.542	1.808
IRF1_NR2F2_TAF7	1.469	1.881
BCLAF1_ETS1_GTF2B	1.478	1.872
ELK1_P300_SIN3	1.473	1.877
STAT1_TBLR1_THAP1	2.51	3.349
ELF1_PU1_STAT5	1.553	3.349
CMYC_ELK1_SP1	1.743	1.604

CEBPB_IRF1_TAF7	1.662	1.684
CCNT2_TAF7_TBLR1	1.51	1.834
CBX3_SP1_TAF7	1.603	1.741
ATF1_GTF2F1_MXI1	1.925	1.419
EJUND_TAF7_YY1	1.732	1.612
CEBPB_GTF2B_MAX	1.839	1.501
CMYC_JUND_TAF7	1.449	1.891
RAD21_SIN3_THAP1	3.34	2.519
ATF3_SMC3_THAP1	3.34	7.002
CTCF_GABP_THAP1	3.34	2.349
BCLAF1_GTF2B_PML	1.356	1.984
E2F6_SIN3_TR4	3.34	2.808
EJUND_GTF2B_JUND	1.588	1.751
TAF7_THAP1_YY1	1.327	2.012
ELF1_JUND_TAF7	1.495	1.844
CHD2_GTF2B_PU1	1.478	1.86
CEBPB_GTF2F1_JUND	1.51	1.827
EJUND_GTF2F1_TBLR1	1.703	1.634
ELF1_TAF1_TAF7	1.691	1.644
ELK1_P300_PML	1.569	1.764
GTF2F1_MXI1_TAF7	1.399	1.934
E2F4_ETS1_SIX5	1.475	1.856
GTF2F1_IRF1_THAP1	1.899	1.431
PML_SP1_TAF7	1.494	1.836
STAT5_TAF7_TEAD4	1.588	1.741
P300_PML_TAF7	1.588	1.741
ELF1_GTF2B_SP1	1.588	1.741
CBX3_EJUND_TAF7	1.732	1.597
BCLAF1_JUND_SIX5	1.478	1.851
NELFE_PU1_YY1	3.147	3.326
ETS1_GTF2B_SP1	1.553	1.773
CMYC_SRF_TR4	1.925	3.326
MXI1_THAP1_ZNF143	1.755	1.571
CMYC_GTF2B_IRF1	1.486	1.839
EJUND_SIX5_SP1	1.473	1.851
PU1_SP1_TBLR1	1.473	1.851
CMYC_TAF7_THAP1	1.334	1.988
EJUND_GTF2F1_ZNF143	1.538	1.782
IRF1_SIX5_SP1	1.8	1.519
E2F4_ETS1_GTF2B	1.525	1.794
CBX3_PML_PU1	1.384	1.934
ETS1_GTF2B_SRF	1.577	1.741

BCLAF1_E2F6_SIX5	1.732	1.586
ELF1_TAF7_YY1	1.397	1.919
GTF2F1_SRF_TAF1	1.645	1.671
CMYC_ELK1_PU1	1.569	1.746
E2F4_GTF2F1_SRF	1.603	1.711
BCLAF1_GABP_PU1	1.473	1.841
GTF2F1_JUND_USF1	1.68	1.634
ELF1_PU1_ZNF143	1.106	2.207
CTCFB_SIX5_ZNF143	1.748	1.562
EJUND_SIX5_TBLR1	1.588	1.722
E2F6_GTF2B_THAP1	1.592	1.718
CMYC_NR2F2_TAF7	1.858	1.452
CEBPB_E2F4_GTF2F1	1.481	1.827
E2F4_IRF1_STAT5	1.788	1.519
EJUNB_GTF2B_IRF1	1.492	1.815
CEBPB_CTCFB_IRF1	1.813	1.493
ELF1_NELFE_TAF1	1.662	1.644
CJUN_MAX_PU1	1.399	1.906
EGR1_GABP_GTF2B	1.582	1.722
GTF2B_SIN3_SRF	1.542	1.757
SIN3_SIX5_SP1	1.577	1.722
E2F4_GTF2F1_STAT2	1.577	1.722
CBX3_SIX5_ZNF143	1.481	1.818
CMYC_TAF7_TBLR1	1.471	1.828
ATF1_EJUNB_MAX	1.538	1.757
MAX_TAF7_ZNF143	1.489	1.804
IRF1_SP2_TAF7	1.633	1.66
CJUN_GTF2B_GTF2F1	1.466	1.827
CCNT2_GTF2F1_MAFF	1.773	1.519
GTF2B_JUND_SP1	1.55	1.741
HMGN3_THAP1_ZNF143	1.423	1.867
E2F4_PU1_ZNF143	1.423	1.867
ELK1_GABP_GTF2F1	1.748	1.541
IRF1_P300_SIX5	1.95	1.338
SIX5_SP1_TBLR1	1.478	1.808
ETS1_GTF2B_MXI1	1.535	1.751
GTF2B_JUND_TBLR1	1.489	1.796
BHLHE40_SIX5_SP1	1.542	1.741
MAX_THAP1_ZNF143	1.639	1.644
GTF2F1_TAF7_TRIM28	1.456	1.827
CMYC_HMGN3_TAF7	1.63	1.652
PML_SIX5_ZNF143	1.489	1.792

PML_TAF7_ZNF143	1.596	1.684
ELF1_GTF2B_SRF	1.569	1.711
CCNT2_CMYC_TAF7	1.543	1.735
BHLHE40_PU1_TBLR1	1.41	1.867
CEBPB_CMYC_GTF2F1	1.476	1.8
E2F4_GTF2B_STAT1	1.625	1.65
ETS1_TAF7_THAP1	1.44	1.834
GTF2B_PML_THAP1	1.533	1.741
CTCFC_P300_PML	1.51	1.764
BCLAF1_GTF2B_YY1	1.652	1.618
CMYC_ELK1_GTF2B	1.419	1.85
CEBPB_PU1_YY1	1.55	1.718
BCLAF1_GTF2F1_YY1	1.596	1.671
TAF7_TBLR1_YY1	1.169	2.097
ELF1_ELK1_GTF2B	1.547	1.718
E2F4_GABP_GTF2F1	1.617	1.647
GTF2B_JUND_NRF1	1.423	1.841
BCLAF1_GTF2F1_MAX	1.725	1.538
ELK1_PML_SIX5	1.662	1.601
EJUND_TAF1_TAF7	1.788	1.474
ELK1_MAX_P300	1.528	1.732
ELK1_MAX_SP1	1.8	1.46
E2F6_GTF2B_TBLR1	1.451	1.808
ELF1_GTF2F1_TRIM28	1.378	1.881
SIX5_TEAD4_ZNF143	1.588	1.671
SP1_TAF7_TRIM28	1.662	1.597
CMYC_SP2_TAF7	1.468	1.789
GTF2B_GTF2F1_TAF7	1.56	1.697
CTCFL_E2F4_TAF7	1.818	3.256
JUND_NRF1_STAT5	2.51	3.256
CEBPB_ELF1_NELFE	2.732	3.256
BCLAF1_PU1_STAT5	1.577	3.256
CTCFB_EJUNB_GTF2F1	2.063	3.256
CTCFL_EGR1_PU1	1.41	3.256
ELF1_TR4_ZNF143	2.662	3.256
EGR1_STAT1_THAP1	2.247	3.256
IRF1_NRF1_STAT5	1.925	3.256
CJUN_TEAD4_TR4	3.732	3.256
CTCF_GTF2B_SIN3	1.8	3.256
CBX3_CTCFB_NELFE	2.34	3.256
NR2F2_P300_PU1	1.51	3.256
BCLAF1_ELF1_NELFE	1.925	3.256

CEBPB_NRF1_STAT5	2.34	3.256
CTCFL_EGR1_NELFE	2.51	3.256
E2F4_STAT1_THAP1	2.147	3.256
CTCFB_GABP_NELFE	3.925	3.256
MXI1_SIX5_STAT5	2.247	3.256
E2F6_NELFE_PU1	2.662	3.256
EJUNB_ETS1_PU1	1.925	3.256
MXI1_PU1_STAT1	2.51	3.256
CTCFB_PU1_TRIM28	1.703	3.256
CEBPB_NRF1_STAT2	1.603	3.256
CTCF_E2F6_NELFE	1.662	3.256
NRF1_STAT1_TAF7	1.51	3.256
ELK1_NR2F2_PU1	2.51	3.256
NR2F2_PU1_SIN3	1.703	3.256
ELF1_NRF1_STAT5	2.51	3.256
E2F6_ELK1_STAT1	2.147	3.256
GABP_NELFE_USF1	2.247	3.256
EJUNB_ELK1_THAP1	2.51	3.256
NRF1_SIN3_STAT1	0.188	3.256
BCLAF1_NRF1_SIX5	2.095	3.256
GABP_GTF2B_SIN3	1.573	1.681
CEBPB_GTF2B_GTF2F1	1.562	1.689
E2F4_ETS1_STAT5	1.51	1.741
GTF2F1_MAFF_TAF1	1.51	1.741
EGR1_ETS1_SIX5	1.451	1.8
CCNT2_GTF2B_USF1	1.625	1.626
CMYC_GTF2B_JUND	1.555	1.695
MAX_NRF1_SIX5	1.684	1.566
EJUND_GTF2B_P300	1.538	1.711
CHD2_MAFF_THAP1	3.247	2.741
CHD2_CTCF_THAP1	3.247	3.256
CTCFL_EJUNB_TRIM28	3.247	2.741
CTCFB_TAF7_ZBTB33	3.247	NS
EJUNB_GABP_SP2	3.247	3.256
GTF2B_MAZ_RFX5	3.247	NS
CTCFL_THAP1_ZNF143	3.247	2.519
CTCFL_EJUND_THAP1	3.247	2.519
ATF3_PU1_ZBTB33	3.247	NS
CTCFC_ELK1_THAP1	3.247	2.934
EJUNB_MAZ_SP2	3.247	NS
CTCFB_ELK1_THAP1	3.247	2.934
CTCF_ELK1_SIX5	3.247	2.071

SP2_STAT5_TAF7	3.247	2.934
CTCF_CTCFL_THAP1	3.247	2.519
EJUNB_SP2_TAF1	3.247	3.519
SIX5_THAP1_ZBTB33	3.247	NS
IRF1_TAF7_YY1	1.475	1.771
EJUND_GTF2F1_TAF1	1.788	1.455
CMYC_PML_TAF7	1.489	1.754
ATF1_GTF2F1_TAF7	1.719	1.519
CMYC_IRF1_TAF7	1.514	1.722
CBX3_EJUND_GTF2F1	1.478	1.757
CHD2_GTF2B_MXI1	1.684	1.55
ELK1_PML_ZNF143	1.662	1.571
GTF2F1_THAP1_ZNF143	1.51	1.722
ELK1_GTF2F1_TBLR1	1.925	1.306
CMYC_GTF2F1_STAT5	1.401	1.83
GABP_GTF2B_TRIM28	1.68	1.55
ELF1_GABP_GTF2B	1.51	1.72
E2F6_SIN3_SIX5	1.44	1.789
EJUNB_GTF2B_TAF1	1.617	1.612
ETS1_PML_SIX5	1.392	1.836
CTCFB_PML_YY1	1.615	1.612
BCLAF1_MAX_TAF7	1.586	1.64
GTF2F1_IRF1_STAT2	1.567	1.658
E2F4_GABP_SIX5	1.571	1.654
ETS1_GTF2B_JUND	1.553	1.671
GTF2B_PML_USF1	1.451	1.773
GABP_TAF7_ZNF143	1.288	1.934
JUND_TAF7_USF1	1.478	1.741
ELF1_HMGN3_TAF7	1.43	1.789
ELK1_PML_SP1	1.641	1.578
P300_SIX5_TEAD4	1.547	1.671
ETS1_GTF2B_ZNF143	1.547	1.671
ATF1_E2F4_GTF2B	1.562	1.654
ETS1_SIX5_ZNF143	1.366	1.846
ELF1_P300_TAF7	1.484	1.727
CMYC_GTF2B_GTF2F1	1.338	1.872
E2F4_ELK1_SP1	1.691	1.519
GABP_GTF2F1_TBLR1	1.645	1.562
ATF1_GTF2B_MAX	1.629	1.578
EJUND_GTF2B_SIN3	1.487	1.718
ETS1_SIX5_SP1	1.378	1.827
ETS1_GABP_STAT5	1.481	1.722

ATF1_ELF1_GTF2F1	1.765	1.436
EGR1_SIX5_TEAD4	1.588	1.612
GTF2F1_JUND_THAP1	1.68	1.519
SP1_TAF1_TAF7	1.41	1.789
ELF1_GABP_GTF2F1	1.638	1.559
EGR1_EJUND_TAF7	1.641	1.555
GTF2F1_PML_SRF	1.562	1.634
CJUN_SP1_TAF7	1.542	1.654
GTF2F1_JUND_NR2F2	1.473	1.722
CBX3_TAF7_ZNF143	1.473	1.722
GTF2F1_SP2_ZNF143	1.714	1.481
GTF2B_IRF1_MXI1	1.522	1.671
BHLHE40_GTF2B_TBLR1	1.538	1.654
E2F6_GTF2B_PU1	1.384	1.808
GABP_TAF7_USF1	1.547	1.644
GTF2B_JUND_YY1	1.49	1.699
TAF1_TAF7_TBLR1	1.489	1.699
CBX3_GTF2B_SP1	1.538	1.65
E2F4_EJUND_SIX5	1.538	1.65
ELK1_MAX_SIX5	1.528	1.658
GABP_SIX5_TBLR1	1.481	1.704
BCLAF1_MAX_SIX5	1.384	1.8
POL2_STAT5_TAF7	1.433	1.751
GABP_GTF2B_HMGN3	1.528	1.656
HMGN3_STAT1_TAF7	2.51	3.182
BHLHE40_SIX5_THAP1	1.51	1.671
ETS1_TAF7_TBLR1	1.247	1.934
JUND_SIX5_SP2	1.51	1.671
ELK1_P300_ZNF143	1.732	1.448
NRF1_PML_SIX5	1.384	1.796
E2F4_GTF2B_ZNF143	1.55	1.629
EJUND_JUND_TAF7	1.557	1.622
SIN3_SIX5_SRF	1.317	1.86
CMYC_GTF2F1_STAT2	1.067	2.109
MAX_SIX5_ZNF143	1.769	1.406
ELF1_GTF2F1_ZNF143	1.493	1.682
CMYC_CTCF_SP2	1.392	1.782
ATF1_GTF2B_P300	1.547	1.626
E2F4_GTF2B_SP1	1.529	1.644
EJUND_ETS1_GTF2F1	1.553	1.62
BCLAF1_GTF2B_TAF1	1.294	1.877
MAX_SIX5_THAP1	1.449	1.722

ATF1_GABP_TAF7	1.478	1.693
GTF2F1_IRF1_USF1	1.795	1.376
JUND_MXI1_THAP1	1.361	1.808
GTF2B_MXI1_ZNF143	1.703	1.464
GTF2B_IRF1_SRF	1.423	1.741
EJUND_GTF2F1_SIN3	1.41	1.753
CCNT2_ELF1_TAF7	1.399	1.764
EJUND_IRF1_TAF7	1.67	1.493
IRF1_POL2_TAF7	1.649	1.513
ELF1_GTF2B_GTF2F1	1.463	1.697
ELF1_ETS1_TAF7	1.359	1.799
E2F4_TAF7_THAP1	1.297	1.86
CEBPB_ELF1_TAF7	1.361	1.796
SP2_STAT1_TAF7	2.925	3.156
GTF2F1_STAT1_THAP1	2.925	3.156
EJUND_SIX5_STAT1	2.8	3.156
CBX3_ELK1_USF1	2.188	3.156
ETS1_NELFE_NRF1	2.925	3.156
MAX_PU1_SRF	1.484	1.671
ETS1_IRF1_SIX5	1.575	1.58
GTF2F1_NR2F2_YY1	1.466	1.689
ATF1_BHLHE40_TAF7	1.51	1.644
ELK1_GTF2B_MAX	1.62	1.534
P300_TAF7_TBLR1	1.481	1.671
CJUN_GTF2B_MXI1	1.44	1.711
GTF2B_RCOR1_USF1	1.588	1.562
E2F4_GTF2B_SIN3	1.444	1.706
E2F4_GABP_NR2F2	1.478	1.671
MXI1_SIX5_ZNF143	1.366	1.782
CTCFL_RAD21_THAP1	3.147	2.519
GTF2F1_MAZ_TR4	3.147	NS
CHD2_CTCFB_THAP1	3.147	2.934
HMGN3_PML_TAF7	1.358	1.788
CBX3_CTCFB_ETS1	1.279	1.867
GTF2B_GTF2F1_MXI1	1.487	1.658
BCLAF1_ELF1_SIX5	1.423	1.722
GABP_MAX_TAF7	1.564	1.58
EJUND_ETS1_SIX5	1.209	1.934
CCNT2_SIX5_THAP1	1.662	1.481
BCLAF1_GTF2B_JUND	1.358	1.782
E2F4_SIX5_TEAD4	1.44	1.699
POL2_SIX5_SP1	1.556	1.581

GTF2B_HMGN3_SP1	1.384	1.753
GTF2F1_NRF1_SIN3	1.51	1.626
IRF1_NELFE_PU1	2.732	3.135
E2F6_STAT1_TAF7	2.851	3.135
IRF1_STAT1_THAP1	2.925	3.135
ETS1_SIX5_TBLR1	1.288	1.846
GTF2B_JUND_SP2	1.423	1.711
CJUN_GTF2F1_IRF1	1.678	1.455
GTF2B_SIN3_TAF7	1.452	1.681
E2F6_ETS1_GTF2B	1.453	1.679
CMYC_MAX_TAF7	1.677	1.455
E2F6_GTF2F1_TAF7	1.331	1.799
CCNT2_GTF2B_TAF7	1.51	1.618
RCOR1_SIX5_TBLR1	1.542	1.586
ATF1_GTF2B_GTF2F1	1.691	1.436
GTF2F1_THAP1_YY1	1.573	1.553
GTF2F1_HMGN3_PU1	1.384	1.741
BCLAF1_GTF2B_ZNF143	1.384	1.741
IRF1_MAX_TAF7	1.482	1.641
CBX3_CTCFB_SIX5	1.51	1.612
ELK1_GABP_PU1	1.603	1.519
BHLHE40_EJUND_GTF2F1	1.432	1.689
CHD2_ELF1_TAF7	1.466	1.654
ETS1_GABP_GTF2F1	1.525	1.594
JUND_SRF_TAF7	1.473	1.644
CMYC_ETS1_TAF7	1.3	1.817
GTF2B_P300_TBLR1	1.538	1.578
CMYC_P300_SIX5	1.503	1.612
JUND_NRF1_SIX5	1.317	1.796
ELK1_IRF1_ZNF143	1.806	1.306
CHD2_THAP1_ZNF143	1.44	1.671
GTF2B_MAFF_PML	1.44	1.671
GTF2B_PML_TBLR1	1.418	1.693
GTF2B_IRF1_JUND	1.44	1.671
GTF2B_GTF2F1_JUND	1.498	1.612
GTF2B_PML_ZNF143	1.458	1.652
GTF2F1_HMGN3_THAP1	1.538	1.571
E2F4_SP2_ZNF143	1.547	1.562
CBX3_EGR1_TAF7	1.51	1.597
CJUN_PU1_TBLR1	0.989	2.118
GABP_GTF2B_SP1	1.466	1.64
JUND_MXI1_TAF7	1.279	1.827

ELK1_MAX_STAT1	1.703	3.104
GTF2F1_NRF1_SMC3	2.732	3.104
GABP_GTF2F1_MXI1	1.34	1.764
CTCFL_P300_PU1	1.51	3.104
E2F4_NELFE_SP2	2.51	3.104
CTCFL_ELK1_NR2F2	2.925	3.104
PU1_SP1_STAT5	1.8	3.104
CTCFC_P300_PU1	1.34	3.104
RFX5_TAF7_USF1	1.51	3.104
CCNT2_GTF2F1_TR4	2.51	3.104
EGR1_GTF2F1_TR4	2.51	3.104
PU1_SP2_STAT1	2.925	3.104
CTCFL_EGR1_TAF7	1.577	3.104
GTF2F1_MEF2_SIX5	2.247	3.104
ELK1_NRF1_THAP1	1.925	3.104
EJUNB_GTF2B_SRF	2.095	3.104
ELF1_SP2_TAF7	1.478	1.626
E2F4_TR4_ZNF143	2.51	3.104
CBX3_CJUN_TR4	3.732	3.104
BHLHE40_E2F4_TR4	2.51	3.104
BCLAF1_EJUNB_GTF2F1	1.662	3.104
PU1_STAT5_YY1	1.873	3.104
EJUNB_GTF2F1_NRF1	1.925	3.104
CTCFB_EJUNB_GTF2B	1.925	3.104
CTCF_ELK1_GTF2B	3.51	3.104
JUND_NELFE_SP2	2.51	3.104
ETS1_IRF1_TAF7	1.386	1.718
CTCFB_GTF2F1_STAT5	2.662	3.104
CJUN_GTF2F1_TR4	2.34	3.104
NRF1_SIN3_SRF	1.51	3.104
EGR1_ELK1_STAT1	1.603	3.104
CEBPB_PU1_SRF	2.247	3.104
ELF1_SRF_TR4	2.247	3.104
GTF2F1_SIN3_TAF7	1.37	1.733
ELK1_JUND_P300	1.449	1.654
E2F4_ELK1_GTF2F1	1.662	1.441
ETS1_JUND_SIX5	1.417	1.684
IRF1_NRSF_SIX5	1.326	1.773
POL2_PU1_TBLR1	1.551	1.547
EGR1_ELF1_TAF7	1.376	1.722
TAF7_TRIM28_ZNF143	1.577	1.519
GTF2F1_SP2_TAF7	1.577	1.519

CTCFC_THAP1_USF1	3.095	3.519
CTCFC_GTF2F1_NR2F2	3.095	2.519
CEBPB_PU1_ZBTB33	3.095	NS
CTCFB_PU1_ZBTB33	3.095	NS
CEBPB_NFYA_SIX5	3.095	3.519
CTCF_SMC3_ZBTB33	3.095	NS
NR2F2_SIX5_SP2	3.095	2.934
MAZ_STAT5_THAP1	3.095	NS
CHD2_CTCFL_THAP1	3.095	3.256
CTCFB_SMC3_ZBTB33	3.095	NS
CTCFB_TAF7_THAP1	3.095	2.519
CEBPB_NFYA_THAP1	3.095	2.519
CTCFC_GABP_THAP1	3.095	2.256
ATF1_PU1_ZBTB33	3.095	NS
CTCF_ELK1_THAP1	3.095	2.741
CTCFL_GTF2F1_SP2	3.095	2.349
EJUNB_RCOR1_SP2	3.095	3.519
CTCFC_ZBTB33_ZNF143	3.095	NS
RAD21_THAP1_ZNF143	3.095	2.393
CTCFL_SP2_TAF7	3.095	2.934
CTCFB_SIX5_ZBTB33	3.095	NS
PU1_SIX5_SMC3	3.095	2.934
CTCF_GTF2F1_USF1	3.095	3.104
ARID3_PU1_TAF7	3.095	2.741
CTCFL_ELK1_THAP1	3.095	2.519
GTF2B_SRF_TAF1	1.461	1.634
CJUN_GTF2B_POL2	1.033	2.062
EJUND_GTF2B_TAF1	1.617	1.478
GTF2B_GTF2F1_ZNF143	1.559	1.535
ATF1_ETS1_TAF7	1.542	1.55
GTF2B_TAF1_THAP1	1.722	1.37
E2F4_EJUND_GTF2F1	1.662	1.429
GABP_JUND_SIX5	1.51	1.58
BCLAF1_E2F6_GTF2B	1.324	1.764
GABP_GTF2F1_THAP1	1.569	1.519
GTF2B_JUND_NR2F2	1.366	1.722
CBX3_E2F6_GTF2B	1.219	1.867
GTF2F1_USF1_YY1	1.553	1.533
GTF2B_STAT5_TAF1	1.603	1.481
GABP_SIX5_SRF	1.361	1.722
CBX3_GABP_SIX5	1.432	1.65
ELF1_ELK1_GTF2F1	1.478	1.604

EJUND_POL2_SIX5	1.233	1.848
CMYC_GTF2B_SP1	1.237	1.844
CHD2_ETS1_SIX5	1.41	1.671
GABP_GTF2B_POL2	1.503	1.577
CEBPB_CMYC_SIX5	1.755	1.324
CMYC_SRF_TAF7	1.071	2.007
BHLHE40_PML_TAF7	1.372	1.706
MAX_PML_TAF7	1.631	1.446
JUND_PML_TAF7	1.463	1.612
ELF1_STAT5_ZNF143	1.279	1.796
ETS1_GTF2B_YY1	1.371	1.703
JUND_PU1_TBLR1	1.247	1.827
SIX5_SP1_TAF1	1.44	1.634
ETS1_RCOR1_SIX5	1.42	1.654
CTCFC_MAX_SP2	1.876	1.197
GABP_GTF2F1_POL2	1.826	1.247
GTF2F1_RCOR1_USF1	1.51	1.562
ELF1_NRSF_TAF7	1.299	1.773
MAX_P300_SIX5	1.535	1.536
CJUN_GTF2F1_STAT5	1.372	1.699
ELF1_SIX5_TEAD4	1.399	1.671
GTF2B_SIN3_TBLR1	1.399	1.671
E2F4_IRF1_PU1	1.463	1.607
ELK1_YY1_ZNF143	1.783	1.287
CMYC_ELK1_SIX5	1.533	1.537
MAX_SIX5_SP1	1.496	1.571
ELK1_GTF2F1_JUND	1.547	1.519
ELK1_JUND_SP1	1.547	1.519
E2F4_ETS1_THAP1	1.395	1.671
P300_RCOR1_SIX5	1.51	1.555
GTF2F1_USF1_ZNF143	1.51	1.555
E2F4_SIN3_THAP1	1.247	1.818
GTF2F1_RCOR1_TAF7	1.542	1.519
E2F4_STAT5_YY1	1.649	1.41
CBX3_ELF1_GTF2F1	1.446	1.612
ATF1_JUND_TAF7	1.538	1.519
GTF2B_GTF2F1_P300	1.451	1.604
GABP_NRSF_TAF7	1.273	1.782
ELF1_GTF2B_JUND	1.396	1.654
GTF2B_TBLR1_ZNF143	1.484	1.566
CBX3_ELF1_SIX5	1.308	1.741
CBX3_CTCFB_PU1	1.51	3.049

MAX_SRF_TR4	2.025	3.049
ELF1_NELFE_PU1	2.34	3.049
ELK1_STAT2_TAF7	2.384	3.049
GTF2F1_NELFE_PU1	2.925	3.049
SIN3_STAT1_THAP1	2.34	3.049
GABP_NR2F2_PU1	1.773	3.049
STAT1_TAF1_THAP1	2.662	3.049
ELK1_STAT5_TAF7	2.095	3.049
GTF2B_NELFE_PU1	2.925	3.049
EJUNB_GTF2F1_SIN3	1.456	3.049
IRF1_TBLR1_TR4	4.625	3.049
NR2F2_PU1_TAF1	1.662	3.049
STAT1_THAP1_ZNF143	2.34	3.049
EJUND_SIX5_SRF	1.625	3.049
CTCF_GTF2B_ZNF143	1.732	3.049
CMYC_E2F6_TR4	2.51	3.049
BCLAF1_EJUND_SIX5	1.51	3.049
CBX3_POL2_SIX5	1.736	1.312
ELK1_GABP_SP1	1.617	1.431
BHLHE40_ETS1_GTF2B	1.473	1.575
GTF2F1_MXI1_POL2	1.595	1.453
GTF2B_MAX_ZNF143	1.607	1.44
ETS1_GTF2B_MAX	1.543	1.503
ATF1_CMYC_TAF7	1.326	1.72
GTF2B_TRIM28_YY1	1.359	1.687
ELK1_GTF2F1_IRF1	1.636	1.409
GABP_GTF2F1_JUND	1.54	1.504
ELF1_GTF2F1_IRF1	1.639	1.404
P300_SIX5_YY1	1.542	1.501
GTF2F1_MAX_TBLR1	1.75	1.293
CMYC_E2F4_TAF7	1.229	1.813
IRF1_SIX5_ZNF143	1.547	1.494
IRF1_MAFF_ZBTB33	3.041	NS
E2F4_MAFF_ZBTB33	3.041	NS
CBX3_PML_SIX5	1.44	1.601
CBX3_SP2_THAP1	3.041	2.741
GTF2F1_SIX5_ZBTB33	3.041	NS
PU1_TAF7_ZBTB33	3.041	NS
CHD2_GTF2F1_SRF	1.395	1.644
GTF2B_HMGN3_SP2	1.297	1.741
ETS1_PU1_TRIM28	1.297	1.741
CBX3_CTCFB_TRIM28	1.297	1.741

E2F4_ELF1_GTF2B	1.388	1.65
ELF1_IRF1_STAT5	1.569	1.468
ETS1_JUND_THAP1	1.475	1.562
JUND_MXI1_SIX5	1.279	1.757
PML_SIX5_SP1	1.487	1.547
ELK1_GABP_ZNF143	1.569	1.464
GABP_GTF2B_PML	1.41	1.622
ELF1_SIN3_TAF7	1.264	1.768
ELK1_GTF2B_PML	1.361	1.671
GTF2B_GTF2F1_STAT2	1.361	1.671
GTF2B_P300_YY1	1.551	1.479
HMGN3_IRF1_TAF7	1.294	1.736
GTF2B_HMGN3_ZNF143	1.489	1.541
GTF2B_P300_SP2	1.51	1.519
ATF1_SIN3_TAF7	1.51	1.519
CBX3_E2F6_TAF7	1.247	1.782
BHLHE40_GTF2B_SRF	1.547	1.481
ATF1_GTF2F1_P300	1.478	1.55
CJUN_STAT5_TAF7	1.466	1.562
GTF2B_SP1_YY1	1.372	1.656
MAX_PU1_TBLR1	1.525	1.501
NRSF_SIX5_YY1	1.233	1.792
ELK1_HMGN3_SIX5	1.428	1.597
CCNT2_GTF2B_ZNF143	1.41	1.612
E2F4_HMGN3_TAF7	1.044	1.976
CMYC_GTF2B_TBLR1	1.456	1.564
CHD2_HMGN3_SIX5	1.262	1.757
GTF2F1_IRF1_MXI1	1.536	1.483
CTCFB_GABP_YY1	1.358	1.66
PML_PU1_TBLR1	1.177	1.841
E2F4_GTF2F1_MXI1	1.432	1.586
BHLHE40_EJUND_TAF7	1.569	1.448
IRF1_JUND_TAF7	1.325	1.692
ELF1_GTF2B_NRF1	1.361	1.654
CMYC_P300_TAF7	1.267	1.748
CTCF_E2F4_GTF2F1	1.732	1.282
GTF2F1_POL2_STAT2	0.882	2.132
PML_SMC3_THAP1	3.013	2.671
ETS1_RAD21_THAP1	3.013	2.519
CEBPB_JUND_TAF7	1.34	1.671
E2F6_ELK1_ZNF143	1.34	1.671
JUND_SIX5_SP1	1.432	1.578

EGR1_SIX5_SP1	1.423	1.586
GABP_SIX5_ZNF143	1.354	1.654
GTF2F1_IRF1_YY1	1.495	1.512
EJUND_ETS1_TAF7	1.487	1.519
CTCFB_ETS1_SIX5	1.449	1.555
E2F6_EJUNB_GTF2B	1.925	3.004
CBX3_GABP_PU1	1.378	1.626
TAF1_TAF7_THAP1	1.484	1.519
E2F6_GTF2F1_NR2F2	1.569	1.431
POL2_SRF_TAF7	1.468	1.532
ETS1_GTF2B_TRIM28	1.535	1.464
BCLAF1_GTF2F1_IRF1	1.672	1.326
GTF2B_SP2_TAF7	1.478	1.519
TAF1_TAF7_ZNF143	1.478	1.519
CHD2_GTF2B_TAF7	1.326	1.671
CEBPB_GTF2F1_P300	1.44	1.555
CBX3_GTF2B_ZNF143	1.372	1.622
ETS1_GTF2B_GTF2F1	1.436	1.557
BCLAF1_CTCFB_IRF1	1.584	1.408
SIN3_SP2_TAF7	1.473	1.519
PU1_TBLR1_YY1	1.352	1.638
CEBPB_MAX_TAF7	1.247	1.741
EJUND_GTF2F1_JUND	1.489	1.498
CMYC_GTF2F1_TBLR1	1.257	1.73
CEBPB_CMYC_TAF7	1.387	1.599
ATF1_CMYC_ZBTB33	2.984	NS
SIX5_TBLR1_YY1	1.222	1.761
CMYC_GTF2B_PML	1.422	1.561
E2F6_ETS1_SIX5	1.28	1.702
GTF2F1_POL2_THAP1	1.625	1.357
ELK1_SIN3_ZNF143	1.588	1.393
CJUN_EGR1_TAF7	1.147	1.834
GABP_TAF7_TRIM28	1.423	1.555
BCLAF1_CTCFB_GABP	1.279	1.699
EJUND_SIN3_TAF7	1.399	1.578
ETS1_JUND_PU1	1.162	1.815
EJUND_GTF2B_POL2	1.135	1.841
GABP_IRF1_STAT5	1.719	1.256
ELK1_JUND_ZNF143	1.51	1.464
ELF1_SIX5_SP1	1.34	1.634
PU1_TAF1_ZNF143	1.247	1.727
CMYC_ELK1_ZNF143	1.737	1.236

GTF2F1_TAF1_TAF7	1.468	1.505
IRF1_P300_TAF7	1.453	1.519
CMYC_IRF1_PU1	1.467	1.505
CBX3_GTF2B_YY1	1.151	1.82
CMYC_GTF2B_NRF1	1.234	1.737
SIX5_TAF1_ZNF143	1.528	1.441
JUND_SIX5_TEAD4	1.449	1.519
E2F6_GTF2B_ZNF143	1.363	1.605
ATF1_GTF2B_JUND	1.489	1.478
GABP_SIN3_SIX5	1.395	1.571
GTF2B_PML_TAF7	1.402	1.564
CCNT2_GABP_GTF2B	1.307	1.658
EGR1_MXI1_THAP1	1.41	1.555
GTF2B_GTF2F1_NR2F2	1.366	1.597
ETS1_IRF1_THAP1	1.32	1.642
BHLHE40_E2F4_TAF7	1.235	1.727
ATF1_GTF2F1_TBLR1	1.384	1.578
CCNT2_GTF2B_SP1	1.34	1.622
E2F4_SIN3_SIX5	1.235	1.727
ELF1_GTF2F1_P300	1.38	1.58
EGR1_SP1_TAF7	1.324	1.634
IRF1_TAF1_TAF7	1.453	1.505
GTF2F1_YY1_ZNF143	1.479	1.478
CCNT2_GTF2F1_THAP1	1.321	1.634
ELF1_TAF7_TRIM28	1.304	1.65
ATF1_SP1_TAF7	1.473	1.481
CMYC_GTF2F1_THAP1	1.561	1.393
ELF1_SIX5_ZNF143	1.34	1.612
ELK1_GTF2F1_PML	1.432	1.519
CJUN_JUND_PU1	1.277	1.671
CJUN_ELF1_GTF2F1	1.225	1.722
ETS1_GTF2B_HMGN3	1.276	1.671
CHD2_EJUND_GTF2F1	1.577	1.37
EJUND_PML_SIX5	1.273	1.671
CBX3_SIN3_TAF7	1.233	1.711
GTF2F1_IRF1_TBLR1	1.594	1.349
GABP_GTF2B_YY1	1.372	1.571
JUND_SP1_THAP1	1.423	1.519
CBX3_MAX_TAF7	1.456	1.486
CBX3_PML_TAF7	1.327	1.612
ELF1_ELK1_PU1	1.317	1.622
POL2_TAF7_ZNF143	1.35	1.588

ELF1_GTF2B_MXI1	1.44	1.498
E2F4_E2F6_GTF2B	1.356	1.582
CMYC_GTF2F1_MXI1	1.286	1.651
CCNT2_IRF1_TAF7	1.377	1.56
BHLHE40_GTF2F1_TBLR1	1.324	1.612
EJUND_GTF2F1_SP1	1.542	1.393
JUND_SRF_YY1	1.283	1.652
JUND_NELFE_PU1	3.732	2.934
PU1_STAT5_TRIM28	1.603	2.934
SIX5_TR4_YY1	2.288	2.934
P300_STAT1_TAF7	3.041	2.934
NR2F2_POL2_PU1	1.261	2.934
PML_PU1_STAT5	1.577	2.934
ETS1_MEF2_SIX5	2.304	2.934
GABP_PU1_STAT5	1.851	2.934
GABP_NELFE_TEAD4	2.095	2.934
CEBPB_GTF2F1_THAP1	2.063	2.934
IRF1_STAT2_THAP1	2.832	2.934
EJUNB_GTF2F1_P300	1.456	2.934
ELF1_NELFE_NRF1	3.247	2.934
GTF2F1_NRF1_STAT1	1.662	2.934
PU1_SIN3_STAT5	1.832	2.934
HMGN3_NR2F2_PU1	1.288	2.934
CBX3_EJUNB_GTF2F1	1.34	2.934
CTCFL_HMGN3_NELFE	2.147	2.934
GABP_NELFE_PU1	2.925	2.934
SIX5_STAT1_TAF7	3.095	2.934
PU1_STAT5_ZNF143	1.732	2.934
ELK1_STAT1_TAF7	2.925	2.934
BCLAF1_GTF2F1_NR2F2	1.925	2.934
NRF1_PU1_SIX5	1.925	2.934
NELFE_POL2_PU1	1.095	2.934
GTF2B_SP1_ZNF143	1.584	1.349
ETS1_HMGN3_TAF7	1.158	1.775
E2F4_PML_SIX5	1.352	1.58
CHD2_GABP_TAF7	1.22	1.711
EGR1_GTF2F1_PU1	1.51	1.419
GTF2F1_TRIM28_YY1	1.091	1.838
E2F4_P300_SIX5	1.378	1.55
CJUN_CTCF_THAP1	2.925	1.612
CTCFB_GABP_THAP1	2.925	2.197
SIX5_STAT2_THAP1	2.925	3.104

ATF3_CTCFC_NR2F2	2.925	-6.069
CBX3_MAZ_TR4	2.925	NS
EJUNB_P300_TAF7	2.925	2.519
GABP_NR2F2_THAP1	2.925	2.393
CJUN_SP2_USF1	2.925	3.741
CBX3_GTF2B_JUND	1.312	1.612
NRF1_POL2_SIX5	1.222	1.702
CMYC_GTF2B_ZNF143	1.55	1.373
CBX3_EGR1_SIX5	1.297	1.626
CHD2_EJUND_GTF2B	1.297	1.626
E2F6_GTF2B_TAF7	1.31	1.612
GTF2B_POL2_ZNF143	1.361	1.559
CJUN_ETS1_PU1	1.23	1.689
GTF2B_PML_STAT5	1.432	1.486
GTF2F1_TBLR1_YY1	1.458	1.46
GTF2B_GTF2F1_IRF1	1.494	1.424
STAT5_YY1_ZNF143	1.469	1.448
E2F4_JUND_STAT5	1.361	1.555
ELF1_GTF2B_YY1	1.51	1.404
GTF2F1_MAX_TRIM28	1.525	1.389
GABP_GTF2F1_IRF1	1.543	1.369
CEBPB_TAF7_YY1	1.475	1.436
CEBPB_GTF2B_IRF1	1.474	1.436
GTF2B_GTF2F1_TRIM28	1.391	1.519
JUND_MAX_TAF7	1.29	1.619
GTF2F1_IRF1_JUND	1.717	1.191
SIX5_SP1_YY1	1.247	1.661
IRF1_JUND_PU1	1.41	1.498
ELF1_JUND_STAT5	1.089	1.818
CMYC_PML_SIX5	1.268	1.639
ELF1_GTF2F1_TBLR1	1.294	1.612
CMYC_GTF2B_P300	1.272	1.634
MAX_PU1_ZNF143	1.234	1.671
GABP_GTF2B_IRF1	1.483	1.422
GTF2B_GTF2F1_YY1	1.51	1.395
JUND_SIX5_SRF	1.279	1.626
GTF2B_RCOR1_TAF7	1.51	1.393
CCNT2_GTF2B_TBLR1	1.384	1.519
GTF2B_TAF1_TAF7	1.499	1.403
E2F4_PU1_SIN3	1.288	1.612
E2F4_GTF2B_JUND	1.35	1.55
EJUND_GTF2F1_P300	1.321	1.578

CJUN_ELF1_PU1	1.312	1.586
CHD2_GTF2F1_TAF7	1.225	1.671
ELK1_GTF2F1_POL2	1.536	1.36
SIN3_TAF7_THAP1	1.297	1.597
CHD2_MAX_TAF7	1.242	1.652
ELK1_PU1_YY1	1.535	1.359
GTF2F1_IRF1_ZNF143	1.645	1.247
GABP_JUND_THAP1	1.473	1.419
CMYC_GABP_SIX5	1.467	1.424
PU1_YY1_ZNF143	1.059	1.832
PML_SRF_YY1	1.171	1.72
EGR1_SIX5_ZNF143	1.34	1.55
GABP_GTF2B_NRSF	1.288	1.601
ELF1_GTF2B_MAX	1.413	1.474
CHD2_GTF2B_TBLR1	1.215	1.671
IRF1_TAF7_TRIM28	1.447	1.439
E2F4_GTF2B_GTF2F1	1.322	1.562
GTF2F1_IRF1_TRIM28	1.51	1.374
E2F6_GTF2B_JUND	1.173	1.711
CMYC_GTF2B_TRIM28	1.546	1.337
NELFE_NRF1_YY1	2.304	2.881
CEBPB_PML_TAF7	1.391	1.49
E2F4_GTF2F1_THAP1	1.423	1.457
MAX_PU1_SP1	1.34	1.539
ETS1_GABP_SIX5	1.317	1.562
ETS1_JUND_TAF7	1.207	1.671
ELF1_NRF1_SIX5	1.137	1.741
CMYC_ELF1_GTF2F1	1.56	1.317
ETS1_PML_PU1	1.108	1.768
CJUN_GTF2F1_MAX	1.156	1.72
ETS1_GABP_THAP1	1.38	1.496
E2F6_MAX_STAT5	1.851	1.024
BCLAF1_IRF1_THAP1	1.538	2.872
ETS1_STAT1_TAF7	2.041	2.872
ELK1_MAX_ZNF143	1.625	1.246
GTF2F1_POL2_STAT5	1.352	1.519
CCNT2_GABP_GTF2F1	1.417	1.453
ETS1_TAF7_ZNF143	1.247	1.622
CBX3_CCNT2_TAF7	1.449	1.419
E2F4_GTF2B_NRF1	1.297	1.571
ELK1_GTF2B_IRF1	1.469	1.399
E2F4_IRF1_TAF7	1.367	1.499

ETS1_PML_THAP1	1.219	1.644
E2F4_GTF2B_YY1	1.389	1.471
GABP_NELFE_TAF7	2.063	2.86
E2F6_SIX5_SP1	1.34	1.519
CTCFB_E2F4_TRIM28	1.51	1.349
E2F4_ELK1_GABP	1.51	1.349
GTF2B_TAF7_TRIM28	1.34	1.519
RCOR1_SIX5_ZNF143	1.34	1.519
POL2_PU1_ZNF143	1.357	1.502
E2F4_ETS1_TAF7	1.142	1.716
CBX3_CTCFB_GABP	1.41	1.448
JUND_TAF7_YY1	1.203	1.654
GTF2F1_POL2_TBLR1	1.277	1.579
ETS1_SIN3_SIX5	1.315	1.541
ELF1_GTF2B_TRIM28	1.391	1.464
GABP_GTF2F1_YY1	1.407	1.448
EJUND_GTF2B_HMGN3	1.484	1.37
GTF2B_PML_SRF	1.304	1.55
CBX3_SIX5_YY1	1.137	1.716
GABP_TAF7_TEAD4	1.297	1.555
SMC3_TAF1_THAP1	2.851	2.256
ATF1_GABP_GTF2B	1.432	1.419
MAZ_SMC3_THAP1	2.851	NS
GTF2B_JUND_MAX	1.397	1.453
GTF2F1_PML_TAF7	1.297	1.553
ELK1_GTF2F1_TAF1	1.449	1.399
GTF2B_TAF1_TBLR1	1.366	1.478
E2F4_GTF2B_HMGN3	1.247	1.597
ELK1_P300_YY1	1.41	1.433
GTF2B_MAX_POL2	1.183	1.659
ELF1_ELK1_P300	1.188	1.654
CCNT2_NELFE_ZNF143	1.44	2.841
CCNT2_STAT1_TAF7	3.041	2.841
STAT1_TAF7_ZNF143	2.732	2.841
TBP_TR4_YY1	2.732	2.841
E2F6_ELF1_TR4	1.925	2.841
EJUND_GTF2F1_SMC3	1.925	2.841
CJUN_E2F6_TR4	2.662	2.841
CTCFB_ETS1_TAF7	1.662	2.841
ATF1_ELF1_NELFE	2.095	2.841
BHLHE40_EJUND_GTF2B	1.432	1.408
E2F6_GABP_TAF7	1.118	1.722

GABP_GTF2B_RCOR1	1.432	1.408
BCLAF1_GTF2F1_TAF1	1.288	1.55
BHLHE40_MAX_TAF7	1.256	1.582
CJUN_GTF2F1_TAF7	1.166	1.671
CJUN_GTF2B_YY1	1.316	1.519
E2F4_MAX_TAF7	1.283	1.552
BHLHE40_CMYC_GTF2B	1.421	1.413
E2F4_PU1_TBLR1	1.44	1.393
IRF1_NRF1_SIX5	1.369	1.464
IRF1_SIN3_TAF7	1.198	1.634
ETS1_GTF2F1_TRIM28	1.288	1.544
GTF2F1_STAT2_THAP1	2.832	2.393
IRF1_TAF1_TR4	2.832	2.326
ATF1_GTF2B_SIN3	1.423	1.408
ELF1_ELK1_SP1	1.34	1.49
ETS1_MAX_SIX5	1.298	1.531
SIN3_SRF_TBLR1	1.279	1.55
CHD2_IRF1_TAF7	1.347	1.481
SRF_STAT1_YY1	1.118	2.827
CMYC_POL2_TAF7	1.135	1.69
CMYC_TAF7_YY1	1.328	1.496
JUND_SIN3_SIX5	1.277	1.544
E2F4_PML_TAF7	1.24	1.581
CMYC_NR2F2_PU1	2	2.821
ATF1_GTF2B_ZNF143	1.361	1.457
ATF1_CCNT2_GTF2B	1.361	1.457
GTF2B_GTF2F1_MAX	1.322	1.496
ELF1_TAF7_USF1	1.297	1.519
CJUN_PU1_SP1	1.297	1.519
E2F6_PML_SIX5	1.33	1.486
IRF1_SIX5_TBLR1	1.389	1.425
GTF2F1_JUND_ZNF143	1.328	1.484
CBX3_CTCFB_IRF1	1.463	1.349
ELF1_GTF2B_IRF1	1.244	1.567
E2F4_JUND_TAF7	1.153	1.658
CJUN_GTF2B_SP1	1.684	1.126
ELF1_GTF2F1_SP1	1.473	1.336
CBX3_GTF2F1_YY1	1.147	1.662
GABP_IRF1_PU1	1.418	1.391
CMYC_GTF2F1_JUND	1.506	1.303
NRF1_TBLR1_USF1	0.925	2.808
MAX_TAF7_THAP1	1.444	1.364

GTF2B_NRF1_SMC3	2.34	2.808
STAT1_THAP1_YY1	2.095	2.808
ATF1_MXI1_NELFE	3.51	2.808
ETS1_JUND_TR4	2.188	2.808
JUND_STAT1_TAF7	2.304	2.808
CTCFB_PU1_ZNF143	0.744	2.808
IRF1_STAT1_TAF7	2.818	2.808
CTCF_GTF2F1_P300	1.577	2.808
EJUNB_ELK1_ZNF143	2.147	2.808
CCNT2_NR2F2_SIX5	2.025	2.808
ETS1_NELFE_USF1	2.247	2.808
EJUNB_ELK1_SP1	1.247	2.808
CBX3_NR2F2_SIX5	1.925	2.808
ELK1_SRF_STAT1	1.34	2.808
GTF2B_NRF1_STAT2	1.925	2.808
CBX3_PU1_SRF	1.577	2.808
P300_PU1_STAT5	1.41	2.808
NRSF_PU1_SIX5	2.063	2.808
NR2F2_PU1_ZNF143	1.818	2.808
ELK1_STAT1_USF1	2.51	2.808
ELF1_GTF2F1_MXI1	1.288	1.519
CTCFB_IRF1_YY1	1.416	1.391
GABP_GTF2F1_PML	1.348	1.459
CCNT2_TAF7_THAP1	1.321	1.486
ELF1_GTF2F1_JUND	1.375	1.43
GABP_IRF1_SIX5	1.36	1.445
CJUN_GTF2F1_YY1	0.957	1.846
ELK1_ETS1_ZNF143	1.41	1.393
E2F4_ETS1_PU1	1.131	1.671
EJUND_GABP_SIX5	1.321	1.481
BHLHE40_GABP_GTF2B	1.42	1.381
GTF2B_SIN3_ZNF143	1.215	1.586
CHD2_CTCFC_THAP1	2.8	2.519
ELK1_SP2_TEAD4	2.8	1.808
CTCFL_SIN3_THAP1	2.8	3.519
CMYC_MXI1_NELFE	2.188	2.8
CTCFC_THAP1_TRIM28	2.8	2.156
SP1_SP2_STAT5	2.8	2.349
CHD2_SMC3_ZBTB33	2.8	NS
ELK1_SP2_TBLR1	2.8	1.934
CTCFB_THAP1_TRIM28	2.8	2.156
ELK1_STAT5_USF1	2.8	1.448

GTF2F1_P300_TBLR1	1.358	1.441
CBX3_JUND_SIX5	1.22	1.578
ELF1_GTF2B_USF1	1.22	1.578
ELF1_GABP_SIX5	1.33	1.464
GABP_PML_PU1	1.291	1.502
BHLHE40_GTF2F1_USF1	1.423	1.37
GTF2B_TRIM28_ZNF143	1.399	1.393
ELF1_ETS1_SIX5	1.201	1.591
ETS1_GTF2B_PML	1.306	1.485
E2F6_GTF2B_HMGN3	1.092	1.697
ELF1_SIN3_SIX5	1.293	1.496
E2F4_E2F6_TAF7	0.986	1.803
GABP_PML_SIX5	1.351	1.436
E2F6_GTF2B_RCOR1	1.228	1.558
E2F4_GTF2B_SP2	1.23	1.555
CTCFB_IRF1_ZNF143	1.113	1.671
GTF2B_TAF7_TBP	1.384	1.399
ETS1_POL2_SIX5	1.228	1.554
EJUNB_ETS1_GTF2F1	1.773	2.782
GABP_GTF2F1_MAX	1.623	1.159
GTF2B_MXI1_STAT1	1.773	2.782
GTF2B_MAX_MXI1	1.547	1.235
MAX_STAT1_THAP1	1.818	2.782
EGR1_SIN3_SIX5	1.324	1.457
PML_SIN3_SIX5	1.283	1.498
CMYC_CTCFB_GTF2B	0.972	1.808
CCNT2_MAX_TAF7	1.211	1.567
ATF1_GABP_GTF2F1	1.51	1.268
JUND_SIX5_USF1	1.297	1.481
CMYC_ELK1_THAP1	1.379	1.397
GABP_GTF2B_MAX	1.414	1.361
MAX_SIX5_SRF	1.327	1.448
CBX3_CHD2_GTF2B	1.188	1.586
JUND_POL2_TAF7	1.071	1.703
EJUNB_HMGN3_TAF7	2.773	2.312
CTCFB_SIN3_THAP1	2.773	2.256
ATF1_BHLHE40_GTF2B	1.423	1.349
ETS1_GABP_PU1	1.1	1.671
NRF1_TAF1_TAF7	1.34	1.431
PML_TAF7_YY1	1.317	1.452
ELF1_ETS1_THAP1	1.23	1.538
CJUN_ETS1_GTF2B	1.247	1.519

CJUN_GTF2B_IRF1	1.115	1.65
BCLAF1_CMYC_GTF2B	1.43	1.335
GTF2B_MAX_TRIM28	1.416	1.349
JUND_SP1_SRF	1.279	1.486
E2F4_JUND_SP2	1.361	1.403
GTF2B_MAX_YY1	1.293	1.471
CCNT2_JUND_TAF7	1.188	1.575
BHLHE40_TAF1_TAF7	1.288	1.474
BHLHE40_GABP_GTF2F1	1.428	1.334
GABP_GTF2F1_SIN3	1.392	1.37
CMYC_GTF2B_SP2	1.534	1.227
ELK1_P300_POL2	0.804	1.955
GABP_HMGN3_THAP1	1.41	1.349
E2F6_GTF2F1_P300	1.315	1.443
ELF1_GTF2F1_MAX	1.488	1.27
E2F4_POL2_SIX5	1.209	1.548
MAX_TAF1_TAF7	1.456	1.301
ELF1_ELK1_ZNF143	1.262	1.493
CMYC_NRSF_SIX5	1.67	1.083
E2F6_GTF2F1_ZNF143	1.34	1.413
ETS1_GTF2F1_USF1	1.321	1.431
CJUN_GTF2B_MAX	1.484	1.268
CEBPB_GTF2B_JUND	1.288	1.464
CJUN_PU1_SIN3	1.095	1.654
ETS1_SIX5_TAF1	1.359	1.388
CMYC_JUND_PU1	1.146	1.601
POL2_SIN3_TAF7	1.149	1.597
EJUND_JUND_SIX5	1.288	1.457
GTF2B_IRF1_YY1	1.322	1.422
CTCFB_E2F6_GTF2B	1.051	1.693
EJUND_ELF1_SIX5	1.131	1.612
CMYC_SIX5_SP1	1.696	1.047
GTF2F1_SP1_TBLR1	1.177	1.566
EJUNB_GTF2B_NELFE	1.925	2.741
CEBPB_PU1_TBLR1	1.41	2.741
ELF1_NR2F2_PU1	1.247	2.741
CHD2_STAT2_TAF7	1.662	2.741
BCLAF1_NELFE_PML	0.34	2.741
CJUN_NR2F2_SIX5	2.041	2.741
MAX_NR2F2_PU1	1.755	2.741
CEBPB_CTCFB_TRIM28	1.755	2.741
NELFE_PML_PU1	2.51	2.741

CTCFL_E2F6_NELFE	3.095	2.741
MXI1_NRF1_SIX5	1.8	2.741
POL2_STAT1_THAP1	1.925	2.741
E2F6_NR2F2_PU1	1.843	2.741
CMYC_ELF1_TR4	1.957	2.741
GABP_STAT1_USF1	1.288	2.741
CEBPB_ETS1_NELFE	1.925	2.741
ETS1_PML_TAF7	1.183	1.557
CMYC_GTF2F1_IRF1	1.575	1.165
CJUN_E2F4_PU1	1.247	1.493
CCNT2_CMYC_GTF2B	1.215	1.524
PML_SIX5_TBLR1	1.22	1.519
IRF1_PML_TAF7	1.347	1.39
ETS1_GTF2B_P300	1.356	1.381
GTF2B_SIN3_SP2	1.317	1.419
ELK1_GTF2B_TAF1	1.317	1.419
GTF2F1_P300_YY1	1.458	1.277
GTF2B_IRF1_MAX	1.433	1.302
E2F4_SIX5_SP1	1.304	1.431
EGR1_GTF2B_TAF7	1.315	1.419
GTF2F1_PML_USF1	1.34	1.393
CTCF_PML_THAP1	2.732	1.519
E2F4_SIX5_ZBTB33	2.732	NS
EJUND_SMC3_SP2	2.732	1.741
GTF2F1_MAFF_ZBTB33	2.732	NS
CTCFL_EGR1_THAP1	2.732	2.349
CTCFL_E2F4_THAP1	2.732	2.156
GTF2F1_IRF1_MAX	1.701	1.031
E2F4_MAZ_TR4	2.732	NS
ETS1_SIX5_ZBTB33	2.732	NS
CTCFC_SIN3_THAP1	2.732	2.156
CTCFB_MXI1_THAP1	2.732	2.519
E2F4_E2F6_SIX5	1.247	1.484
GABP_SIX5_YY1	1.312	1.419
ETS1_PU1_SIN3	0.976	1.753
CHD2_GABP_SIX5	1.279	1.448
GABP_GTF2B_TEAD4	1.34	1.386
E2F6_ELF1_TAF7	1.022	1.702
PML_SIX5_YY1	1.45	1.273
CHD2_JUND_SIX5	1.304	1.419
PU1_SIN3_YY1	1.228	1.494
E2F4_JUND_PU1	1.155	1.566

BCLAF1_E2F4_SIX5	1.247	1.474
CCNT2_PML_TAF7	1.173	1.545
BHLHE40_E2F4_GTF2B	1.369	1.349
ATF1_JUND_SRF	1.297	1.419
CMYC_GTF2F1_P300	0.951	1.764
CTCFL_POL2_THAP1	2.714	3.326
IRF1_SIN3_SIX5	1.294	1.419
CMYC_EGR1_SIX5	1.441	1.271
ELF1_POL2_TR4	0.925	2.711
CBX3_JUND_TAF7	1.22	1.49
GABP_GTF2F1_USF1	1.423	1.287
GTF2F1_POL2_TAF7	1.213	1.494
MAX_PML_SIX5	1.456	1.25
CJUN_GTF2B_TAF7	1.072	1.634
CJUN_MAX_TAF7	1.301	1.405
ELF1_ETS1_GTF2F1	1.199	1.506
EGR1_JUND_SIX5	1.34	1.364
PML_SP2_TAF7	1.102	1.601
CJUN_SIX5_SP1	1.617	1.086
E2F6_SP2_STAT5	2.703	2.156
EGR1_ELF1_SIX5	1.228	1.474
GTF2F1_MAX_ZNF143	1.519	1.183
IRF1_PU1_SIN3	1.228	1.474
CMYC_CTCFB_GTF2F1	1.395	1.307
EGR1_THAP1_ZNF143	1.297	1.403
CBX3_PU1_TEAD4	1.16	2.699
MXI1_NRF1_TBLR1	1.118	2.699
CHD2_STAT1_TAF7	2.247	2.699
ATF1_ELK1_TAF7	1.925	2.699
GTF2B_NR2F2_YY1	1.491	1.207
CBX3_E2F4_GTF2F1	1.179	1.519
GABP_P300_PU1	1.147	1.55
E2F4_POL2_TAF7	1.178	1.519
E2F6_GTF2F1_TBLR1	1.327	1.37
BHLHE40_SIX5_ZNF143	1.304	1.393
ELF1_GTF2B_SP2	1.288	1.408
E2F4_GTF2B_IRF1	1.311	1.384
ELF1_PML_SIX5	1.225	1.468
CBX3_E2F6_SIX5	1.312	1.381
E2F6_JUND_TAF7	1.08	1.612
CCNT2_SMC3_THAP1	2.691	2.393
CTCF_ELF1_THAP1	2.691	2.256

CEBPB_E2F4_GTF2B	1.304	1.386
CBX3_GTF2B_HMGN3	1.247	1.441
CMYC_SIN3_TAF7	1.062	1.626
PU1_TAF1_TBLR1	1.109	1.578
ATF1_GTF2F1_SIN3	1.456	1.229
ELF1_IRF1_PU1	1.311	1.374
IRF1_MAX_TR4	2.228	2.684
CMYC_EJUND_SIX5	1.456	1.226
GTF2B_IRF1_SP1	1.288	1.393
EGR1_PML_SIX5	1.299	1.381
CMYC_GTF2B_TAF1	1.278	1.4
GTF2F1_JUND_YY1	1.308	1.37
EGR1_ELK1_GTF2F1	1.547	1.126
EJUND_POL2_TAF7	1.351	1.322
GTF2F1_NRSF_TAF7	1.173	1.499
BCLAF1_STAT5_TAF7	1.925	2.671
CEBPB_CTCFL_EGR1	1.41	2.671
CTCFC_GTF2B_NRF1	1.925	2.671
JUND_NFYA_NRF1	1.247	2.671
ELF1_NELFE_SP2	1.925	2.671
NRF1_SP2_TBLR1	1.732	2.671
ELK1_NRF1_P300	2.51	2.671
GABP_NELFE_NRF1	2.925	2.671
GTF2B_NRF1_SRF	2.34	2.671
NELFE_SMC3_YY1	3.925	2.671
BHLHE40_PU1_STAT5	1.732	2.671
CTCFL_EGR1_MXI1	1.44	2.671
JUND_NR2F2_NRF1	1.51	2.671
BCLAF1_CEBPB_PU1	1.34	2.671
NELFE_NRF1_TBLR1	2.51	2.671
CTCFB_PU1_TBLR1	1.247	2.671
CTCF_ELK1_NR2F2	1.603	2.671
MXI1_NELFE_SIX5	1.925	2.671
MXI1_STAT2_THAP1	2.8	2.671
CEBPB_PU1_STAT5	1.818	2.671
EJUNB_GTF2B_NR2F2	2.247	2.671
BCLAF1_SP2_STAT1	1.247	2.671
ELF1_ELK1_STAT1	1.603	2.671
CBX3_NR2F2_PU1	1.625	2.671
CTCFB_EGR1_PU1	1.273	2.671
MEF2_SIN3_SIX5	2.063	2.671
EJUNB_ELK1_NR2F2	2.247	2.671

CTCF_GTF2B_SMC3	2.063	2.671
E2F4_NELFE_USF1	2.247	2.671
GABP_GTF2F1_RCOR1	1.358	1.312
BHLHE40_JUND_TAF7	1.058	1.612
ELK1_GTF2B_YY1	1.109	1.559
GTF2B_IRF1_P300	1.326	1.341
CCNT2_GTF2F1_IRF1	1.611	1.055
ETS1_GTF2B_SIN3	1.247	1.419
EGR1_EJUND_GTF2B	1.378	1.287
CJUN_EGR1_PU1	0.992	1.671
MAFF_MXI1_ZBTB33	2.662	NS
CTCFB_EJUNB_SIX5	2.662	2.934
CTCFC_NR2F2_SP2	2.662	2.349
CTCFL_ELK1_SIX5	2.662	1.671
CTCF_THAP1_TRIM28	2.662	1.934
CTCFB_ELK1_STAT5	2.662	1.934
ATF1_IRF1_TAF7	1.378	1.284
PU1_ZBTB33_ZNF143	2.662	NS
BCLAF1_RAD21_THAP1	2.662	2.156
CTCFL_GTF2F1_SIX5	2.662	1.782
PU1_SP2_STAT5	2.662	2.934
CTCFB_ELK1_SP2	2.662	1.612
CEBPB_CTCFC_THAP1	2.662	2.934
CMYC_PU1_ZBTB33	2.662	NS
CTCF_NR2F2_SP2	2.662	2.349
GABP_MAFF_TAF7	2.662	2.934
EJUNB_TAF7_THAP1	2.662	2.349
CTCFL_SIX5_TRIM28	2.662	2.349
CEBPB_CTCFB_THAP1	2.662	2.934
P300_SMC3_THAP1	2.662	2.741
RCOR1_THAP1_ZBTB33	2.662	NS
EGR1_MEF2_PU1	2.662	3.519
CTCFB_MAFF_ZBTB33	2.662	NS
ELK1_SMC3_SP2	2.662	1.741
GABP_GTF2F1_SP1	1.384	1.278
CJUN_GTF2F1_POL2	1.264	1.396
CBX3_GTF2B_GTF2F1	1.205	1.455
HMGN3_MAX_TAF7	1.199	1.459
CHD2_IRF1_SIX5	1.376	1.282
GABP_RCOR1_SIX5	1.308	1.349
GABP_GTF2B_TAF1	1.266	1.389
ATF1_PML_TAF7	1.273	1.381

E2F4_GTF2B_TEAD4	1.235	1.419
CCNT2_EJUND_GTF2B	1.304	1.349
TAF7_TRIM28_YY1	1.118	1.535
GTF2F1_P300_POL2	1.318	1.335
ELF1_GTF2B_P300	1.288	1.364
BCLAF1_E2F6_GABP	1.361	1.29
CTCFB_E2F6_TRIM28	1.625	2.65
CEBPB_ELF1_IRF1	1.326	1.323
ETS1_TAF7_YY1	1.113	1.536
E2F4_SIN3_TAF7	1.044	1.604
ATF1_GTF2B_IRF1	1.562	1.086
ELF1_GTF2B_POL2	1.255	1.393
EJUND_GTF2B_RCOR1	1.297	1.349
CMYC_ELK1_STAT5	2.645	1.628
JUND_PML_PU1	1.143	1.502
CMYC_SIX5_TR4	2.366	2.644
JUND_SIX5_YY1	1.257	1.387
GTF2B_POL2_USF1	0.953	1.689
IRF1_SIX5_ZBTB33	2.641	NS
E2F4_SIX5_ZNF143	1.269	1.367
CJUN_CMYC_PU1	1.086	1.548
ELF1_NR2F2_STAT1	1.147	2.634
NR2F2_PML_PU1	1.588	2.634
CEBPB_ELK1_PU1	1.925	2.634
CCNT2_NELFE_SP1	1.51	2.634
PU1_STAT5_TAF1	1.691	2.634
GTF2B_NRF1_STAT1	1.247	2.634
CEBPB_NRF1_TBLR1	0.925	2.634
HMGN3_NFYA_TAF7	1.925	2.634
GABP_SRF_STAT1	1.51	2.634
CTCFB_GTF2F1_TEAD4	1.732	2.634
ELF1_ETS1_TR4	1.818	2.634
ELK1_GTF2B_SMC3	2.34	2.634
ELK1_STAT1_STAT5	3.51	2.634
RFX5_TAF7_YY1	0.925	2.634
ELF1_IRF1_TR4	2.832	2.634
BCLAF1_GTF2F1_PU1	1.818	2.634
ETS1_STAT1_USF1	1.288	2.634
CEBPB_ELK1_TAF7	1.603	2.634
EJUNB_GTF2F1_ZNF143	1.832	2.634
GTF2B_NELFE_NRF1	3.247	2.634
E2F4_NELFE_SIX5	1.732	2.634

GABP_GTF2F1_ZNF143	1.299	1.334
GTF2F1_SIN3_THAP1	1.262	1.37
GTF2F1_TBLR1_ZNF143	1.233	1.399
CHD2_MAX_SIX5	1.283	1.349
CCNT2_GTF2F1_YY1	1.481	1.15
CHD2_JUND_TAF7	1.083	1.547
CMYC_THAP1_ZNF143	1.552	1.077
CHD2_CMYC_TAF7	0.993	1.636
CJUN_GABP_STAT5	1.279	1.349
ATF1_ETS1_GTF2F1	1.41	1.218
GTF2F1_MAX_THAP1	1.417	1.211
CCNT2_EJUND_TAF7	1.321	1.306
E2F4_EJUND_TAF7	1.34	1.287
ETS1_GTF2B_RCOR1	1.294	1.332
GTF2F1_PU1_ZBTB33	2.625	NS
EGR1_EJUNB_TAF7	2.625	2.256
ATF1_GTF2F1_JUND	1.369	1.256
EJUND_SP2_TEAD4	2.625	2.519
SIN3_SIX5_ZBTB33	2.625	NS
MAFF_TAF7_ZBTB33	2.625	NS
ATF1_SIN3_ZBTB33	2.625	NS
SP1_STAT2_THAP1	2.625	2.104
CTCFL_RCOR1_THAP1	2.625	2.519
STAT2_THAP1_ZNF143	2.625	2.256
GABP_STAT2_THAP1	2.625	2.671
EJUNB_GABP_THAP1	2.625	2.519
BHLHE40_SMC3_THAP1	2.625	2.519
EJUNB_PML_SMC3	2.625	2.104
ATF3_CTCF_THAP1	2.625	NS
CTCFB_PU1_YY1	1.372	2.622
ELK1_GTF2F1_YY1	1.102	1.519
ELF1_GTF2F1_YY1	1.285	1.335
ETS1_GTF2F1_TBLR1	1.259	1.361
GTF2B_TAF1_ZNF143	1.304	1.316
GTF2B_SIN3_YY1	1.147	1.473
CBX3_ETS1_TAF7	1.233	1.386
BHLHE40_GTF2B_GTF2F1	1.293	1.324
BHLHE40_GTF2F1_P300	1.198	1.419
P300_POL2_TAF7	0.841	1.776
GTF2B_MXI1_SIN3	1.198	1.419
CJUN_TAF7_ZNF143	1.23	1.386
NR2F2_POL2_TAF7	1.68	0.934

CMYC_E2F4_GTF2F1	1.329	1.285
E2F6_GTF2F1_MXI1	1.111	1.502
TAF7_TBLR1_USF1	1.925	2.612
MXI1_NELFE_TAF7	2.147	2.612
GTF2F1_MAX_RAD21	1.118	2.612
BHLHE40_STAT1_TAF7	2.384	2.612
BCLAF1_E2F6_THAP1	1.473	2.612
GABP_NELFE_NRSF	1.925	2.612
E2F4_MXI1_NELFE	2.925	2.612
BCLAF1_ETS1_PU1	1.553	2.612
CCNT2_PU1_SIX5	1.755	2.612
E2F4_GABP_PU1	1.118	1.493
CHD2_GTF2F1_MXI1	1.147	1.464
ATF1_GTF2B_YY1	1.551	1.059
GTF2F1_MXI1_YY1	1.225	1.385
ETS1_GTF2F1_IRF1	1.483	1.126
ELF1_GTF2F1_SP2	1.423	1.185
NRSF_SP1_TAF7	1.188	1.419
CMYC_GTF2F1_MAX	1.312	1.294
CBX3_CMYC_TAF7	1.009	1.595
CJUN_SIX5_ZNF143	1.233	1.37
ATF3_CTCF_NR2F2	2.603	-6.069
ATF3_NR2F2_RAD21	2.603	NS
GTF2B_MAX_NRF1	1.297	1.306
CMYC_GTF2B_SIN3	1.231	1.372
STAT2_TAF1_THAP1	2.603	1.934
MAZ_STAT2_THAP1	2.603	NS
BHLHE40_GTF2F1_YY1	1.379	1.223
E2F4_GTF2B_MAX	1.211	1.388
EJUND_ELK1_TAF7	1.925	2.597
EGR1_STAT1_TAF7	2.147	2.597
EGR1_ELF1_GTF2B	1.247	1.349
E2F4_GABP_TRIM28	1.247	1.349
CEBPB_TAF1_TAF7	1.34	1.256
CCNT2_GTF2F1_ZNF143	1.258	1.334
E2F4_GTF2B_TRIM28	1.321	1.271
ELF1_SIX5_TBLR1	1.095	1.496
E2F6_GTF2F1_RCOR1	1.277	1.312
E2F4_GTF2F1_ZNF143	1.196	1.393
CJUN_CTCFB_THAP1	2.588	0.571
ATF1_E2F6_STAT5	2.588	2.049
POL2_SP2_TAF7	1.239	1.349

JUND_PU1_SP1	1.102	1.486
GTF2B_GTF2F1_NRF1	1.188	1.399
CEBPB_GTF2F1_PML	1.139	1.448
PML_SP1_SRF	1.137	1.448
GTF2B_JUND_PML	1.166	1.419
GTF2B_RCOR1_TBLR1	1.215	1.37
GTF2B_JUND_SIN3	1.127	1.457
MAX_SP2_TAF7	1.327	1.256
CMYC_TAF7_TRIM28	1.129	1.454
RCOR1_SIX5_YY1	1.175	1.406
CJUN_GTF2B_SRF	1.188	1.393
POL2_PU1_STAT5	0.925	2.578
E2F6_RCOR1_SIX5	1.118	1.46
STAT2_THAP1_YY1	2.577	2.597
CBX3_CEBPB_ELF1	1.095	1.481
BHLHE40_GTF2B_P300	1.304	1.271
CMYC_SIX5_TBLR1	1.426	1.149
BHLHE40_GTF2B_SP1	1.304	1.271
JUND_MAX_SIX5	1.192	1.381
CBX3_MAX_SIX5	1.239	1.334
IRF1_PU1_TAF1	1.276	1.296
ETS1_GTF2F1_P300	1.281	1.29
CCNT2_ETS1_TAF7	1.109	1.461
ELF1_JUND_SIX5	1.158	1.412
BHLHE40_GTF2F1_ZNF143	1.188	1.381
CBX3_EJUND_GABP	1.22	1.349
GTF2B_JUND_TRIM28	1.273	1.296
E2F6_ELF1_GTF2F1	1.265	1.303
GTF2B_P300_ZNF143	1.324	1.242
ATF1_GTF2F1_POL2	1.575	0.99
E2F6_HMGN3_TAF7	0.805	1.76
EGR1_GTF2F1_TAF7	1.256	1.308
IRF1_JUND_THAP1	1.198	1.365
BCLAF1_CMYC_SIX5	1.147	1.414
MAX_SRF_TAF7	1.179	1.381
CBX3_GTF2B_SIN3	1.095	1.464
GTF2F1_P300_PML	1.153	1.406
JUND_P300_TAF7	1.095	1.464
CMYC_MEF2_PU1	2.557	2.374
GTF2B_GTF2F1_SP1	1.219	1.336
MAX_SIX5_TBLR1	1.239	1.316
CBX3_GABP_GTF2F1	1.259	1.296

ATF1_POL2_TAF7	1.282	1.272
PML_PU1_YY1	1.15	1.403
ETS1_SIX5_YY1	1.064	1.488
ETS1_SIN3_TAF7	1.018	1.534
CMYC_GTF2F1_TRIM28	1.222	1.328
ETS1_GTF2B_TAF1	1.253	1.296
MAX_TAF7_TRIM28	1.225	1.324
CBX3_GTF2B_P300	1.118	1.431
ETS1_HMGN3_THAP1	1.129	1.419
BCLAF1_GTF2B_POL2	1.163	1.384
JUND_SIN3_THAP1	1.147	1.399
ELK1_POL2_ZNF143	1.18	1.358
CBX3_CTCFB_POL2	0.741	1.796
CMYC_ETS1_GTF2F1	1.374	1.162
GABP_GTF2F1_TAF1	1.332	1.203
GTF2F1_SIN3_ZNF143	1.124	1.41
CMYC_EGR1_TAF7	1.229	1.304
CMYC_GTF2F1_YY1	1.309	1.224
CEBPB_GABP_IRF1	1.42	1.112
JUND_TAF1_TAF7	1.193	1.338
CMYC_E2F6_TAF7	1.107	1.423
ELF1_SIX5_TAF1	1.283	1.246
BHLHE40_GTF2F1_MAX	1.366	1.163
GTF2B_MAX_SP1	1.319	1.208
E2F6_GTF2B_GTF2F1	1.124	1.402
ELF1_GTF2F1_TEAD4	1.077	1.448
CCNT2_ETS1_GTF2B	1.143	1.379
GABP_PU1_SP1	1.036	1.486
BHLHE40_CMYC_GTF2F1	1.226	1.296
ATF1_GTF2F1_MAX	1.473	1.049
ELF1_HMGN3_THAP1	1.188	1.332
ELK1_TEAD4_THAP1	2.095	2.519
BHLHE40_SP2_STAT1	1.41	2.519
PU1_SRF_TBLR1	1.732	2.519
CTCF_GTF2B_RAD21	1.51	2.519
E2F4_NELFE_NRF1	1.925	2.519
CCNT2_CTCFB_TAF7	1.225	2.519
CTCFC_ELF1_STAT5	1.732	2.519
EJUNB_GTF2F1_MXI1	2.51	2.519
GTF2B_MXI1_NRF1	1.8	2.519
NELFE_SIX5_TAF7	1.925	2.519
BCLAF1_EJUND_MXI1	1.384	2.519

NRF1_TAF7_THAP1	1.662	2.519
GABP_NELFE_P300	2.147	2.519
CTCFC_CTCFL_GTF2F1	2.188	2.519
CEBPB_GTF2F1_USF1	1.703	2.519
STAT2_STAT5_TAF7	2.247	2.519
NR2F2_SIX5_TBLR1	1.773	2.519
MXI1_PU1_TAF7	1.8	2.519
CEBPB_CMYC_PU1	1.362	2.519
ELF1_SIX5_TR4	2.041	2.519
GTF2F1_NELFE_NRF1	3.247	2.519
ELK1_HMGN3_STAT1	1.732	2.519
CTCFC_GTF2B_HMGN3	1.832	2.519
ELK1_HMGN3_TAF7	1.466	2.519
GTF2B_STAT1_STAT5	1.773	2.519
CTCF_GTF2B_PML	1.372	2.519
PU1_STAT1_ZNF143	1.063	2.519
EJUNB_GTF2F1_TEAD4	1.304	2.519
MEF2_PML_SIX5	2.147	2.519
GTF2F1_NR2F2_USF1	2.063	2.519
CBX3_CEBPB_PU1	1.732	2.519
GTF2F1_STAT1_STAT5	1.732	2.519
GTF2B_SIN3_STAT1	2.063	2.519
CEBPB_PU1_ZNF143	1.372	2.519
CTCFC_GTF2F1_RAD21	1.8	2.519
GABP_NELFE_ZNF143	1.603	2.519
ETS1_SP2_STAT1	1.925	2.519
STAT2_TAF7_ZNF143	2.304	2.519
NELFE_STAT1_TBLR1	2.51	2.519
EJUNB_GTF2F1_HMGN3	1.755	2.519
POL2_SIX5_TR4	2.072	2.519
EJUNB_JUND_SRF	1.703	2.519
STAT1_USF1_ZNF143	1.773	2.519
CTCFL_JUND_PU1	0.925	2.519
CEBPB_PU1_SIN3	1.288	2.519
EJUND_MXI1_NRF1	1.247	2.519
CBX3_CTCF_GTF2B	1.703	2.519
CTCF_GTF2F1_SMC3	1.925	2.519
EJUND_NRF1_SIX5	1.34	2.519
ATF1_GABP_NELFE	1.925	2.519
NRF1_STAT2_TBLR1	1.34	2.519
BCLAF1_GTF2F1_NELFE	0.925	2.519
HMGN3_STAT1_STAT2	1.018	2.519

CTCFB_SIN3_TAF7	1.41	2.519
E2F6_PU1_STAT5	2.366	2.519
ETS1_NELFE_SIX5	1.925	2.519
CCNT2_EJUNB_GTF2F1	1.843	2.519
CTCF_E2F6_TRIM28	1.449	2.519
BCLAF1_GTF2B_NR2F2	2.147	2.519
ELK1_TAF7_THAP1	1.925	2.519
MAX_NRSF_TAF7	1.208	1.31
CBX3_CMYC_SIX5	1.006	1.511
GTF2B_NRF1_YY1	0.96	1.557
CBX3_EJUND_PML	1.086	1.429
JUND_PML_SIX5	1.103	1.412
CJUN_ELF1_TAF7	1.036	1.478
CJUN_GABP_SIX5	1.269	1.244
GTF2F1_PML_ZNF143	1.163	1.349
GTF2F1_JUND_MAX	1.315	1.197
BHLHE40_ELF1_GTF2F1	1.247	1.265
CBX3_POL2_TAF7	1.323	1.188
JUND_PU1_ZBTB33	2.51	NS
EJUNB_MAZ_TAF7	2.51	NS
CTCF_RCOR1_THAP1	2.51	2.256
CTCFB_EJUND_THAP1	2.51	2.104
ATF3_GTF2F1_PU1	2.51	2.741
CBX3_ELK1_STAT5	2.51	1.934
NR2F2_SMC3_YY1	2.51	1.562
CJUN_STAT5_THAP1	2.51	1.671
CTCFB_TAF7_TRIM28	2.51	2.256
E2F6_GTF2B_MAFF	2.51	1.711
JUND_RAD21_THAP1	2.51	2.256
E2F4_SP2_ZBTB33	2.51	NS
GTF2B_PU1_ZBTB33	2.51	NS
GABP_GTF2B_MEF2	2.51	2.808
IRF1_PU1_ZBTB33	2.51	NS
MAX_PU1_ZBTB33	2.51	NS
CHD2_MAFF_ZBTB33	2.51	NS
CTCFB_GTF2F1_MAFF	2.51	2.519
ELK1_SIX5_STAT2	2.51	1.808
GABP_PU1_ZBTB33	2.51	NS
E2F4_RAD21_THAP1	2.51	2.071
GTF2B_SIX5_ZBTB33	2.51	NS
ELK1_RCOR1_SP2	2.51	1.464
CTCFL_GABP_NR2F2	2.51	2.671

CTCFL_P300_SIX5	2.51	2.256
E2F6_EJUNB_SMC3	2.51	3.021
CTCFB_GABP_ZBTB33	2.51	NS
EJUND_ELK1_SP2	2.51	2.256
E2F4_SP2_STAT5	2.51	2.256
ATF1_GTF2B_ZBTB33	2.51	NS
EJUNB_RCOR1_TAF7	2.51	2.104
CJUN_PU1_ZBTB33	2.51	NS
CTCFB_GTF2F1_ZBTB33	2.51	NS
ATF3_GTF2B_SIX5	2.51	2.934
CTCF_JUND_THAP1	2.51	2.071
EGR1_MAFF_MXI1	2.51	1.808
PML_PU1_SIN3	1.147	1.363
CBX3_GTF2B_PML	1.288	1.219
CEBPB_POL2_TAF7	1.288	1.219
BHLHE40_GTF2B_ZNF143	1.209	1.296
IRF1_PML_SIX5	1.308	1.197
GTF2B_SIN3_TRIM28	1.233	1.271
GTF2F1_MAX_YY1	1.332	1.17
ELF1_GTF2F1_USF1	1.22	1.282
IRF1_MAX_PU1	1.379	1.123
NRF1_PML_TAF7	1.102	1.399
JUND_THAP1_YY1	1.197	1.304
SIX5_TAF1_YY1	1.172	1.329
CBX3_GTF2B_MAX	1.379	1.122
IRF1_PU1_YY1	1.097	1.402
ATF1_GTF2F1_IRF1	1.381	1.117
MAX_SIN3_TAF7	1.262	1.236
MAX_SIN3_SIX5	1.147	1.349
ETS1_HMGN3_SIX5	1.086	1.41
ELF1_GTF2B_PML	1.126	1.37
E2F4_ELF1_GTF2F1	1.276	1.22
CCNT2_TAF7_YY1	1.102	1.393
GTF2F1_PML_THAP1	1.131	1.364
CMYC_JUND_SRF	0.925	1.569
ELF1_IRF1_SIX5	1.247	1.246
IRF1_SIX5_TAF1	1.404	1.088
HMGN3_JUND_TAF7	1.081	1.41
JUND_PU1_YY1	0.925	1.564
EGR1_ETS1_GTF2B	1.188	1.301
E2F6_PML_TAF7	1.08	1.409
GTF2B_P300_PML	1.086	1.403

GTF2F1_PML_TBLR1	1.304	1.184
CMYC_NRSF_TAF7	1.013	1.474
CBX3_GTF2B_IRF1	1.184	1.303
ETS1_MAX_TAF7	1.206	1.28
BHLHE40_P300_SIX5	1.177	1.306
ELF1_GTF2B_SIN3	1.113	1.37
GTF2B_NRF1_TAF1	1.072	1.41
BCLAF1_CMYC_THAP1	1.34	2.481
GTF2F1_P300_ZNF143	1.131	1.349
EJUND_MAX_SIX5	1.091	1.388
E2F4_IRF1_SIX5	1.362	1.116
GTF2B_IRF1_TRIM28	1.173	1.304
EGR1_GTF2B_TBLR1	1.247	1.229
CMYC_MAX_TR4	1.461	2.476
ATF1_GTF2B_PML	1.312	1.163
GTF2F1_JUND_TBLR1	1.162	1.312
P300_TAF1_TAF7	1.354	1.118
GABP_GTF2F1_HMGN3	1.266	1.205
CMYC_TAF1_TAF7	1.347	1.123
CJUN_ETS1_TAF7	1.432	1.037
GTF2F1_IRF1_P300	1.46	1.009
IRF1_JUND_SRF	1.084	1.384
E2F4_SIX5_TAF1	1.288	1.179
E2F6_GABP_SIX5	1.131	1.336
SP2_STAT1_YY1	1.188	2.464
ELF1_MAX_TR4	2.072	2.464
CEBPB_GTF2F1_POL2	1.181	1.282
ATF1_MAX_TAF7	1.273	1.189
ATF1_CMYC_GTF2F1	1.46	1.002
E2F4_TAF7_YY1	1.121	1.341
JUND_POL2_SIX5	1.147	1.314
GTF2B_IRF1_SIN3	1.064	1.395
GTF2F1_PML_STAT2	1.22	1.239
CEBPB_GTF2B_PML	1.077	1.381
ELF1_GTF2F1_SIN3	1.225	1.233
EGR1_SIX5_YY1	1.038	1.419
GTF2B_MAX_USF1	1.358	1.099
E2F4_ELF1_SIX5	1.166	1.29
GTF2F1_MAX_P300	1.179	1.275
IRF1_PML_PU1	1.259	1.193
SIN3_SIX5_YY1	1.055	1.397
CBX3_IRF1_TAF7	1.306	1.145

GABP_PU1_SIN3	1.041	1.41
ETS1_TAF1_TAF7	1.06	1.389
CTCF_IRF1_THAP1	2.449	1.711
SMC3_SP2_YY1	2.449	2.021
CMYC_PU1_STAT5	2.215	2.448
GABP_NELFE_SIN3	1.8	2.448
CBX3_GTF2F1_POL2	1.198	1.25
MAX_PU1_STAT5	1.677	2.448
CBX3_E2F6_GTF2F1	1.041	1.406
E2F4_GTF2F1_TBLR1	1.083	1.363
E2F4_PML_PU1	1.188	1.256
E2F6_JUND_SIX5	1.038	1.406
JUND_SIN3_TAF7	1.001	1.443
GTF2F1_TAF7_TEAD4	1.147	1.296
IRF1_MAX_SIX5	1.289	1.154
CCNT2_GTF2B_JUND	1.142	1.301
JUND_SIN3_SRF	0.978	1.464
GTF2B_HMGN3_JUND	1.103	1.336
GTF2B_POL2_SRF	1.079	1.36
E2F4_GTF2F1_IRF1	1.292	1.146
POL2_SIX5_ZNF143	1.304	1.134
SIN3_STAT1_TAF7	2.51	2.436
JUND_STAT2_TAF7	1.636	2.436
MXI1_SIX5_TAF7	1.625	2.436
HMGN3_TAF7_YY1	0.86	1.576
CTCFB_JUND_PU1	1.063	2.436
SIN3_STAT1_STAT2	0.547	2.436
ETS1_IRF1_TR4	2.8	2.436
CCNT2_ELF1_GTF2F1	1.152	1.284
SP1_STAT1_TAF7	3.041	2.436
CJUN_CMYC_TAF7	1.145	1.29
CMYC_PML_PU1	0.888	1.547
PML_SIX5_TAF1	1.177	1.256
GTF2B_MAX_SP2	1.329	1.104
CMYC_ELF1_STAT5	1.658	2.429
CTCFC_THAP1_ZNF143	2.428	2.256
CTCFC_E2F4_THAP1	2.428	2.104
CTCFL_E2F6_THAP1	2.428	2.808
CTCF_RAD21_THAP1	2.428	2.393
HMGN3_SIX5_ZNF143	1.139	1.287
ETS1_GTF2F1_YY1	1.239	1.185
CJUN_ELF1_GTF2B	1.063	1.361

CMYC_PU1_TAF1	0.81	1.612
CTCFB_E2F4_GABP	1.147	1.275
ELF1_GTF2F1_NRSF	1.1	1.321
GTF2B_SP2_YY1	1.142	1.279
CMYC_NELFE_SIX5	1.045	2.419
GTF2B_PU1_ZBTB7	1.372	2.419
ELK1_STAT1_STAT2	2.925	2.419
E2F4_EJUNB_ELK1	1.41	2.419
CTCF_CTCFC_GTF2B	1.372	2.419
E2F4_SP2_STAT1	1.925	2.419
GTF2F1_RAD21_YY1	2.025	2.419
GTF2B_PU1_USF1	1.755	2.419
ELK1_SIX5_STAT1	3.925	2.419
BCLAF1_PU1_YY1	1.324	2.419
CBX3_HMGN3_NELFE	1.925	2.419
NRF1_TAF7_ZNF143	1.703	2.419
CTCFB_ETS1_PU1	0.925	2.419
ELK1_SIN3_STAT1	1.51	2.419
CTCFB_ELK1_GTF2F1	2.247	2.419
GABP_NELFE_TBLR1	1.925	2.419
SIX5_STAT5_TBLR1	1.925	2.419
SP2_STAT1_ZNF143	1.51	2.419
CTCF_GTF2B_JUND	1.51	2.419
CTCFB_ETS1_NR2F2	1.205	2.419
EJUNB_EJUND_GTF2F1	1.51	2.419
PU1_SRF_ZNF143	1.662	2.419
EJUND_MXI1_THAP1	1.372	2.419
CTCF_ELF1_GTF2B	1.51	2.419
GTF2F1_SP2_STAT1	1.603	2.419
SP2_STAT1_TBLR1	1.34	2.419
GTF2F1_SIN3_YY1	1.122	1.294
JUND_PU1_SIN3	0.968	1.448
BHLHE40_TAF7_YY1	0.951	1.464
GABP_GTF2F1_NRSF	1.131	1.282
PML_RCOR1_SP2	1.156	1.256
E2F6_GTF2B_SIN3	1.043	1.368
CTCF_SMC3_SP2	2.41	2.104
CTCFL_ELF1_THAP1	2.41	2.671
CTCFB_JUND_ZBTB33	2.41	NS
CTCFL_TAF1_THAP1	2.41	1.256
CHD2_SIX5_ZBTB33	2.41	NS
CTCFC_SMC3_SP2	2.41	2.104

CTCFL_EGR1_NR2F2	2.41	2.934
EJUNB_IRF1_THAP1	2.41	2.182
ATF3_STAT5_THAP1	2.41	8.002
PU1_SIN3_ZBTB33	2.41	NS
CTCFL_MAZ_THAP1	2.41	NS
CTCF_EGR1_THAP1	2.41	1.934
ELF1_JUND_THAP1	1.118	1.29
PML_SIN3_THAP1	1.008	1.399
E2F4_GTF2B_RCOR1	1.22	1.185
ELF1_GTF2B_TEAD4	1.1	1.303
GABP_JUND_PU1	1.029	1.374
CCNT2_GTF2B_GTF2F1	1.014	1.389
CMYC_JUND_TR4	2.51	2.403
CJUN_GTF2F1_JUND	0.882	1.519
MAX_RAD21_THAP1	2.399	1.934
CJUN_ETS1_GTF2F1	1.17	1.227
E2F4_JUND_THAP1	1.067	1.33
GTF2B_JUND_P300	1.106	1.29
CTCFL_GTF2F1_SIN3	1.925	2.393
BCLAF1_GTF2B_NELFE	0.925	2.393
CEBPB_GTF2B_THAP1	2.063	2.393
CTCFB_JUND_NELFE	1.925	2.393
CJUN_JUND_TAF7	0.925	1.468
CHD2_EJUNB_GTF2B	1.34	2.393
CTCF_GTF2F1_RAD21	1.662	2.393
GTF2F1_PU1_STAT1	1.925	2.393
BCLAF1_HMGN3_PU1	1.273	2.393
PU1_USF1_ZNF143	1.131	2.393
JUND_NELFE_NRF1	2.925	2.393
HMGN3_PU1_SRF	1.384	2.393
CBX3_MXI1_NRF1	1.577	2.393
BHLHE40_CFOS_TAF7	1.384	2.393
CTCFC_GTF2F1_TRIM28	1.577	2.393
EJUNB_ELK1_P300	1.732	2.393
BCLAF1_GTF2B_SMC3	2.063	2.393
CEBPB_E2F4_NELFE	1.603	2.393
CTCFB_ELF1_NELFE	1.925	2.393
HMGN3_NELFE_NRF1	3.247	2.393
JUND_SIX5_TR4	1.925	2.393
GTF2F1_NR2F2_SMC3	2.063	2.393
CEBPB_MXI1_SIX5	1.925	2.393
CTCFB_NR2F2_ZNF143	1.51	2.393

CBX3_CEBPB_NELFE	1.34	2.393
GTF2F1_SRF_USF1	1.8	2.393
CBX3_GTF2B_RCOR1	1.137	1.256
EJUNB_GTF2F1_RCOR1	1.51	2.393
EGR1_STAT1_USF1	2.063	2.393
CTCF_ETS1_NR2F2	1.372	2.393
ETS1_NRF1_THAP1	1.288	2.393
JUND_NELFE_SIX5	1.925	2.393
CTCF_EGR1_GTF2B	1.703	2.393
GTF2F1_RFX5_USF1	1.662	2.393
CTCFC_P300_SIN3	1.205	2.393
CTCFC_JUND_PU1	0.744	2.393
CTCF_CTCFL_GTF2F1	2.063	2.393
BCLAF1_CBX3_PU1	1.188	2.393
MXI1_PU1_SRF	2.34	2.393
NRF1_SIX5_USF1	1.773	2.393
SIX5_STAT1_USF1	1.603	2.393
CTCFB_ELK1_NR2F2	1.662	2.393
CTCF_CTCFL_GTF2B	1.51	2.393
BCLAF1_CTCFC_GTF2B	1.925	2.393
BHLHE40_CTCFB_TAF7	1.732	2.393
CTCFC_GTF2B_RAD21	1.732	2.393
ELK1_GTF2B_POL2	0.692	1.699
MAX_P300_TAF7	1.084	1.306
ELF1_TAF7_TEAD4	1.041	1.349
GTF2F1_P300_SIN3	1.025	1.364
GTF2B_NRSF_TAF7	1.09	1.296
ETS1_GTF2F1_JUND	1.194	1.191
GTF2B_HMGN3_YY1	1.002	1.383
JUND_SIX5_TBLR1	1.102	1.282
BCLAF1_SMC3_SP2	2.384	1.741
CTCF_EJUND_THAP1	2.384	1.519
CTCF_SIN3_THAP1	2.384	1.934
CTCF_SP2_STAT5	2.384	2.349
PML_TAF1_TR4	2.384	2.214
E2F4_PU1_ZBTB33	2.384	NS
CEBPB_NR2F2_TAF7	2.384	2.519
EJUNB_RCOR1_THAP1	2.384	1.934
EJUNB_SMC3_TRIM28	2.384	2.519
JUND_MEF2_PU1	2.384	2.741
CTCFB_SIX5_STAT5	2.384	2.349
CTCFB_TAF7_TEAD4	2.384	2.519

CHD2_MAFF_MXI1	2.384	1.934
E2F4_NR2F2_SP2	2.384	2.349
CTCFC_EJUNB_TRIM28	2.384	2.934
CEBPB_SIX5_USF1	2.384	2.519
CTCFC_GTF2F1_SIX5	2.384	1.934
CHD2_CTCFB_MAFF	2.384	2.934
SIX5_SP2_STAT5	2.384	2.519
BHLHE40_RAD21_SP2	2.384	1.519
ATF1_ELF1_ZBTB33	2.384	NS
CTCFC_SP2_STAT5	2.384	2.349
POL2_THAP1_ZNF143	1.172	1.209
CJUN_GTF2B_ZNF143	1.34	1.041
GTF2F1_JUND_SP1	1.277	1.104
MAX_SIX5_TAF1	1.368	1.012
SIN3_TAF7_YY1	0.76	1.619
CMYC_GTF2F1_SIN3	1.191	1.185
BHLHE40_GTF2F1_IRF1	1.226	1.15
MEF2_POL2_SIX5	0.636	2.374
NRF1_SIN3_TAF7	1.288	2.374
JUND_PU1_TAF1	1.025	1.349
BHLHE40_GTF2F1_JUND	1.118	1.256
CBX3_ETS1_GTF2F1	1.118	1.256
CMYC_GTF2B_YY1	1.085	1.289
CBX3_CJUN_PU1	0.925	1.448
GTF2F1_SP1_YY1	1.297	1.076
ELF1_GTF2F1_PML	1.217	1.156
CJUN_CMYC_GTF2B	1.265	1.108
ELK1_POL2_STAT5	2.372	1.027
CMYC_SIX5_ZNF143	1.199	1.17
GTF2F1_MXI1_SIN3	1.083	1.285
GTF2F1_MAX_MXI1	1.384	0.984
BCLAF1_POL2_THAP1	1.677	2.367
MAZ_RAD21_THAP1	2.366	NS
CTCFL_THAP1_YY1	2.366	2.519
CHD2_PML_TAF7	0.888	1.478
CMYC_JUND_SIX5	1.106	1.259
CMYC_IRF1_NELFE	0.84	2.365
CJUN_CMYC_GTF2F1	0.865	1.499
GTF2B_GTF2F1_SIN3	1.121	1.242
GTF2B_MXI1_POL2	1.259	1.104
CMYC_ETS1_TR4	2.23	2.363
MAX_STAT1_TAF7	1.925	2.363

GTF2B_JUND_POL2	0.648	1.711
THAP1_YY1_ZNF143	1.219	1.14
ATF1_E2F6_GTF2B	1.215	1.143
CMYC_ELK1_STAT1	2.879	2.358
HMGN3_SIX5_YY1	0.875	1.479
ETS1_GTF2F1_MAX	1.173	1.181
E2F4_EGR1_TAF7	0.925	1.429
CMYC_GTF2B_HMGN3	1.018	1.335
CCNT2_E2F4_GTF2B	0.992	1.361
SIX5_YY1_ZNF143	0.79	1.562
E2F4_JUND_SIX5	1.095	1.256
CEBPB_ELF1_PML	1.032	1.317
CTCFB_GABP_PU1	1.51	2.349
GABP_STAT1_STAT5	1.703	2.349
TAF7_TBLR1_THAP1	1.456	2.349
ELK1_GTF2F1_STAT1	3.732	2.349
ELK1_GABP_STAT1	2.34	2.349
CTCFC_GTF2B_PML	1.428	2.349
CCNT2_SIX5_YY1	0.802	1.547
GTF2F1_STAT5_TRIM28	1.603	2.349
JUND_SP2_STAT1	1.34	2.349
CMYC_NELFE_NRF1	2.205	2.349
MXI1_PU1_SIX5	1.818	2.349
CTCF_E2F6_P300	1.166	2.349
E2F6_GTF2B_YY1	0.876	1.473
CCNT2_GTF2B_IRF1	1.171	1.175
EJUND_GTF2B_TEAD4	1.201	1.145
CMYC_E2F4_SIX5	1.098	1.248
E2F6_ETS1_GTF2F1	1.063	1.282
E2F4_TAF1_TAF7	1.125	1.219
GTF2B_MAX_PML	1.162	1.182
ATF1_GTF2B_POL2	1.164	1.18
CMYC_SIN3_SIX5	1.172	1.172
TAF1_TR4_YY1	2.34	2.408
E2F4_SP2_TRIM28	2.34	1.808
GABP_PU1_TAF1	1.016	1.324
ATF3_NR2F2_SMC3	2.34	NS
EJUNB_THAP1_YY1	2.34	1.782
PML_SIN3_TAF7	1	1.34
CTCFC_PML_THAP1	2.34	2.071
EJUND_P300_SP2	2.34	2.071
CTCF_E2F4_THAP1	2.34	1.612

CTCF_ETS1_THAP1	2.34	2.256
EGR1_GTF2B_ZNF143	1.294	1.041
E2F4_GTF2F1_YY1	1.033	1.301
EGR1_JUND_TAF7	0.968	1.364
CEBPB_CTCFB_YY1	1.196	2.332
GTF2B_PML_TRIM28	1.166	1.163
CHD2_TAF1_TAF7	1.181	1.148
GTF2B_MXI1_PML	0.968	1.361
CMYC_ELF1_SIX5	1.194	1.135
STAT1_USF1_YY1	1.925	2.326
ETS1_PU1_TEAD4	1.34	2.326
NELFE_SIX5_YY1	1.34	2.326
GTF2B_MAX_SIN3	1.218	1.108
E2F4_GABP_YY1	1.207	1.117
IRF1_SMC3_SP2	2.324	1.998
MAFF_POL2_ZBTB33	2.324	NS
MAZ_PU1_SIX5	2.324	NS
E2F4_GTF2B_PML	1.143	1.18
E2F6_ELF1_GTF2B	1.053	1.268
E2F4_MAX_SIX5	1.201	1.118
EGR1_MAX_SIX5	1.063	1.256
E2F4_ETS1_GABP	1.071	1.248
CMYC_ETS1_SIX5	1.286	1.033
E2F4_GTF2B_TAF1	1.183	1.135
CMYC_CTCFB_PU1	0.791	2.318
CCNT2_SIN3_TAF7	0.956	1.361
MAZ_SIX5_STAT5	2.317	NS
ELF1_MAX_SIX5	1.172	1.144
GTF2B_JUND_TAF1	1.14	1.175
GTF2F1_SIN3_TBLR1	1.036	1.278
ETS1_POL2_THAP1	0.866	1.448
CBX3_CMYC_GTF2B	1.154	1.159
CTCF_CTCFB_GTF2B	1.51	2.312
JUND_STAT1_USF1	2.304	2.312
CCNT2_MXI1_NELFE	1.603	2.312
CEBPB_CTCFB_SIN3	0.843	2.312
GTF2F1_NELFE_SIX5	1.732	2.312
JUND_SRF_STAT1	1.732	2.312
EJUND_GTF2F1_STAT5	1.732	2.312
GTF2F1_NRF1_STAT2	1.925	2.312
RCOR1_SP2_STAT1	1.41	2.312
MXI1_STAT2_TAF7	2.147	2.312

NELFE_SIN3_SIX5	1.732	2.312
BCLAF1_GTF2B_USF1	1.925	2.312
NRF1_SIN3_THAP1	1.41	2.312
ELF1_NELFE_TEAD4	1.925	2.312
GTF2F1_SRF_STAT1	2.147	2.312
ELF1_NELFE_SIX5	1.732	2.312
GTF2B_SMC3_STAT1	2.247	2.312
ATF1_NRSF_SRF	1.925	2.312
ELF1_JUND_TR4	1.925	2.312
ATF1_RFX5_TAF7	2.147	2.312
CTCFB_MAX_NELFE	1.44	2.312
BCLAF1_HMGN3_THAP1	1.603	2.312
CTCFC_GTF2B_ZNF143	1.51	2.312
SIX5_SRF_TAF7	1.818	2.312
E2F6_STAT1_USF1	2.188	2.312
BCLAF1_CTCFB_GTF2B	1.732	2.312
CTCFB_PU1_TAF1	1.266	2.312
P300_STAT1_USF1	1.44	2.312
ETS1_HMGN3_STAT2	1.361	2.312
CTCFC_SIN3_ZNF143	0.542	2.312
CTCFB_PU1_SIN3	1.118	2.312
BHLHE40_GTF2B_IRF1	1.009	1.302
CTCFB_GABP_IRF1	1.268	1.041
GABP_HMGN3_SIX5	1.067	1.242
GABP_MAX_SIX5	1.277	1.031
JUND_PML_SRF	1.131	1.175
E2F4_GTF2F1_MAX	1.113	1.193
GTF2B_GTF2F1_HMGN3	0.989	1.316
EJUND_IRF1_SRF	1.179	1.126
CJUN_PU1_YY1	1.073	1.231
BHLHE40_EJUNB_TAF7	2.304	2.256
RAD21_THAP1_YY1	2.304	1.571
CTCF_TAF1_THAP1	2.304	0.934
PML_SIX5_ZBTB33	2.304	NS
EJUND_RAD21_THAP1	2.304	2.671
CTCF_ETS1_SP2	2.304	2.393
ATF3_NR2F2_SIX5	2.304	NS
MAZ_SIX5_TR4	2.304	NS
JUND_SIX5_ZBTB33	2.304	NS
BCLAF1_STAT5_THAP1	2.304	2.934
CMYC_ELK1_TAF7	1.847	2.304
CTCFC_EJUND_THAP1	2.304	1.934

BHLHE40_GTF2B_YY1	1.209	1.094
E2F6_ETS1_STAT2	1.399	2.303
ETS1_GTF2B_TEAD4	1.162	1.14
CMYC_JUND_NELFE	1.147	2.301
E2F6_GTF2B_P300	0.882	1.419
CMYC_GTF2B_TEAD4	1.184	1.116
ETS1_POL2_TAF7	1.135	1.164
CMYC_SIX5_ZBTB33	2.298	NS
CTCFB_IRF1_JUND	1.118	1.18
GTF2F1_TAF7_TBP	1.041	1.256
GTF2F1_HMGN3_SP1	1.118	1.179
CMYC_E2F6_GTF2F1	1.039	1.257
ELF1_RCOR1_SIX5	1.067	1.229
CTCFB_ELF1_PU1	0.861	2.296
ELK1_STAT1_TBLR1	2.925	2.296
CBX3_ELF1_THAP1	1.384	2.296
EJUND_MXI1_SIX5	1.428	2.296
IRF1_NR2F2_PU1	1.603	2.296
ETS1_MAX_TR4	1.984	2.296
CBX3_TAF1_TAF7	1.17	1.126
ATF1_BHLHE40_GTF2F1	1.177	1.118
GABP_IRF1_THAP1	1.215	1.078
ELF1_PML_PU1	0.874	1.419
JUND_POL2_PU1	0.805	1.488
CHD2_GTF2F1_TBLR1	1.118	1.175
CJUN_PML_TAF7	1.141	1.151
CEBPB_GTF2F1_TAF1	1.147	1.145
CBX3_EGR1_GTF2B	1.166	1.126
E2F4_GTF2F1_SIN3	1.027	1.264
CMYC_GTF2B_MAX	1.023	1.268
ATF1_GTF2F1_YY1	1.161	1.13
BHLHE40_GTF2B_JUND	1.134	1.156
GTF2B_MAX_P300	1.139	1.151
CMYC_GTF2B_POL2	0.927	1.363
EGR1_GTF2B_SP1	1.072	1.218
CCNT2_CMYC_GTF2F1	1.07	1.218
CTCFC_EGR1_NR2F2	2.288	2.104
CJUN_SP1_SP2	2.288	1.223
CTCFC_ETS1_THAP1	2.288	2.197
CTCF_GABP_NR2F2	2.288	2.256
CTCFL_GTF2F1_TAF1	2.288	1.519
ELK1_STAT1_YY1	2.662	2.287

MXI1_NELFE_POL2	2.215	2.287
MXI1_SIX5_TBLR1	1.41	2.287
HMGN3_TAF7_ZNF143	1.279	2.287
ATF1_CMYC_NELFE	0.925	2.287
GTF2F1_HMGN3_ZNF143	1.089	1.197
BHLHE40_CMYC_TAF7	1.029	1.256
GTF2F1_SP1_ZNF143	1.188	1.097
GTF2F1_TAF1_ZNF143	1.225	1.059
E2F6_IRF1_TAF7	0.789	1.494
BCLAF1_MAX_PU1	0.878	2.282
CJUN_GTF2B_PML	0.964	1.318
GTF2B_RCOR1_ZNF143	1.156	1.126
CHD2_TAF7_YY1	0.953	1.328
JUND_RCOR1_SIX5	1.025	1.256
POL2_SMC3_SP2	2.279	1.049
JUND_MXI1_ZNF143	1.22	1.059
IRF1_THAP1_ZBTB33	2.279	NS
HMGN3_TAF1_TAF7	1.129	1.149
CMYC_GABP_PU1	1.015	1.262
BCLAF1_POL2_SIX5	0.535	1.741
GTF2B_POL2_TBLR1	0.925	1.349
CMYC_GTF2B_RFX5	2.273	1.741
CJUN_GTF2B_JUND	1.041	1.231
ELF1_GABP_THAP1	1.173	1.097
IRF1_NRSF_TAF7	0.862	1.408
GTF2F1_JUND_P300	1.054	1.214
SIN3_TAF1_TAF7	1.004	1.263
CMYC_CTCFB_SIX5	1.065	1.201
CCNT2_HMGN3_TAF7	0.982	1.282
GTF2F1_IRF1_SIN3	1.314	0.949
CMYC_E2F6_SIX5	1.096	1.164
CMYC_JUND_THAP1	1.186	1.074
CTCFB_STAT5_YY1	2.127	2.256
ELF1_TR4_YY1	1.773	2.256
GABP_NELFE_SP1	2.095	2.256
GABP_GTF2F1_STAT1	1.925	2.256
E2F6_ELF1_NELFE	2.247	2.256
PU1_TBLR1_ZNF143	1.247	2.256
ELK1_TBLR1_THAP1	1.925	2.256
CEBPB_MAX_NELFE	1.44	2.256
MXI1_SIX5_SP1	1.384	2.256
ATF1_E2F4_NELFE	1.288	2.256

E2F6_GTF2F1_STAT1	2.147	2.256
CEBPB_TAF7_TBLR1	1.51	2.256
MAX_TR4_YY1	1.925	2.256
GTF2B_NRF1_RAD21	2.147	2.256
GABP_SP2_STAT1	1.662	2.256
CBX3_ELK1_TAF7	1.925	2.256
ELF1_NELFE_SP1	1.925	2.256
ELK1_GTF2F1_NR2F2	1.925	2.256
EJUNB_SIX5_TRIM28	1.8	2.256
CJUN_ELK1_TAF7	1.456	2.256
ELF1_ELK1_TAF7	1.266	2.256
ATF1_JUND_NELFE	1.773	2.256
ELF1_STAT1_STAT5	1.577	2.256
CJUN_ETS1_SIX5	1.259	0.995
ETS1_IRF1_ZNF143	1.081	1.173
CMYC_E2F4_GABP	1.061	1.19
GTF2F1_NRSF_YY1	0.878	1.371
CTCFB_E2F4_PML	1.063	1.185
CBX3_CTCFB_THAP1	2.247	2.256
RAD21_RCOR1_THAP1	2.247	2.256
ELK1_JUND_STAT5	2.247	1.349
CTCFL_GTF2F1_MAZ	2.247	NS
E2F4_SMC3_SP2	2.247	1.671
STAT2_TAF1_TAF7	2.247	1.934
EGR1_ELK1_STAT5	2.247	1.312
MAZ_SIX5_TAF7	2.247	NS
NR2F2_TAF1_THAP1	2.247	2.393
GABP_RAD21_THAP1	2.247	1.156
CTCFC_TAF1_THAP1	2.247	1.197
PU1_RCOR1_TAF7	2.247	1.934
CTCFL_GTF2B_SP2	2.247	2.104
ELK1_STAT5_ZNF143	2.247	1.571
CMYC_ELF1_NELFE	1.785	2.246
IRF1_JUND_SIX5	1.288	0.958
ETS1_GTF2B_POL2	0.915	1.33
CMYC_GTF2F1_NR2F2	1.34	2.244
ELF1_JUND_PU1	0.894	1.349
CEBPB_GTF2B_TAF1	1.188	1.054
GTF2B_PML_SP1	1.066	1.175
TAF1_TAF7_YY1	1.035	1.206
CBX3_GTF2F1_MAX	1.151	1.089
CMYC_IRF1_SIX5	1.306	0.934

BHLHE40_E2F6_GTF2B	1.099	1.14
GTF2F1_PML_TRIM28	1.015	1.223
IRF1_MXI1_NELFE	2.366	2.236
CBX3_E2F4_GABP	1.118	1.118
JUND_MAX_PU1	0.925	1.31
MAX_TAF7_YY1	1.057	1.177
GTF2F1_IRF1_PML	1.106	1.128
CMYC_SIX5_SRF	1.1	1.134
POL2_SIX5_SRF	0.995	1.236
ELF1_GTF2B_NRSF	0.882	1.349
IRF1_NELFE_SIX5	1.625	2.229
ELF1_ETS1_NELFE	2.013	2.229
ETS1_GTF2B_STAT1	1.925	2.229
CJUN_JUND_SIX5	1.058	1.171
GTF2B_TAF7_TEAD4	1.131	1.097
EGR1_GTF2B_JUND	1.038	1.189
JUND_POL2_SRF	1.215	1.012
ELF1_GTF2B_HMGN3	0.925	1.301
E2F4_SIX5_YY1	1.002	1.223
CBX3_GTF2F1_ZNF143	0.982	1.242
CJUN_MAX_SIX5	0.898	1.326
CBX3_GTF2F1_PML	1.16	1.063
E2F4_MXI1_SIX5	1.288	2.223
GTF2B_NRSF_YY1	0.948	1.275
E2F4_NELFE_TAF7	1.625	2.223
GTF2B_MAX_TAF1	1.089	1.133
BHLHE40_ELF1_GTF2B	1.051	1.171
ELF1_GTF2F1_RCOR1	1.131	1.091
P300_TAF7_YY1	1.053	1.168
E2F6_GTF2F1_JUND	1.077	1.144
GTF2B_IRF1_PML	1.11	1.109
GTF2F1_STAT1_YY1	0.826	2.219
E2F6_GABP_GTF2B	0.955	1.263
EGR1_IRF1_TAF7	1.029	1.188
MAX_PML_PU1	1.166	1.051
CMYC_GTF2F1_ZNF143	1.115	1.101
GTF2B_RCOR1_YY1	1.161	1.054
ETS1_GTF2F1_SP1	1.106	1.109
JUND_PML_THAP1	0.925	1.29
CEBPB_CTCFB_GABP	1.137	2.214
BCLAF1_PU1_TAF1	0.999	2.214
MXI1_NELFE_SIN3	2.34	2.214

CTCFB_ELK1_P300	1.662	2.214
ELK1_GTF2F1_SRF	2.247	2.214
JUND_RFX5_TAF7	2.147	2.214
GTF2B_SP2_STAT1	1.51	2.214
ELK1_ETS1_STAT1	2.095	2.214
CHD2_MXI1_SIX5	1.553	2.214
SIN3_STAT1_ZNF143	1.625	2.214
EJUNB_ELK1_PML	1.732	2.214
E2F6_ETS1_NELFE	1.788	2.214
CTCFC_POL2_SP2	1.716	0.498
ELK1_IRF1_THAP1	1.976	2.214
CMYC_GTF2B_NRSF	1.143	1.07
HMGN3_IRF1_SIX5	1.083	1.13
CHD2_GTF2B_YY1	1.083	1.13
MAX_PU1_TAF1	1.008	1.201
GTF2B_MXI1_YY1	1.109	1.1
ELF1_GTF2B_RCOR1	1.111	1.097
CBX3_IRF1_THAP1	1.118	2.207
GABP_PU1_YY1	1.07	1.137
CJUN_GTF2F1_SP1	0.925	1.282
GTF2B_IRF1_RCOR1	1.219	0.987
POL2_SIX5_YY1	0.95	1.256
CJUN_MXI1_PU1	2.205	2.004
GABP_POL2_PU1	0.716	1.489
E2F4_ETS1_GTF2F1	0.985	1.22
JUND_SMC3_SP2	2.205	1.808
EJUNB_MAZ_SIX5	2.205	NS
BCLAF1_ELF1_GABP	1.086	1.118
ETS1_GTF2F1_ZNF143	1.054	1.149
GTF2B_HMGN3_IRF1	1.033	1.17
E2F6_MAX_SIX5	1.165	1.037
MAX_POL2_SIX5	1.287	0.915
IRF1_POL2_TR4	2.881	2.201
GTF2B_TAF1_YY1	1.04	1.161
CHD2_GTF2B_JUND	1.013	1.188
ETS1_NELFE_POL2	1.726	2.2
BHLHE40_GABP_SIX5	1.025	1.175
EGR1_STAT2_TAF7	1.755	2.197
EJUNB_ELK1_ETS1	1.118	2.197
CTCFB_GTF2F1_RAD21	1.577	2.197
GTF2F1_TAF1_TBLR1	1.134	1.063
CTCFB_ELK1_PU1	2.063	2.197

PU1_STAT1_TBLR1	1.8	2.197
P300_PU1_SP2	1.818	2.197
BCLAF1_ELF1_NR2F2	1.553	2.197
MXI1_SRF_THAP1	1.288	2.197
CBX3_EJUND_NRF1	1.063	2.197
SP2_TAF7_USF1	1.818	2.197
ATF1_E2F4_STAT5	1.818	2.197
BCLAF1_PU1_ZNF143	1.131	2.197
EJUNB_ELK1_SIX5	1.732	2.197
ELK1_THAP1_TRIM28	1.925	2.197
EJUND_ELK1_STAT5	2.188	2.197
GTF2F1_PU1_ZBTB7	1.51	2.197
EJUNB_GTF2B_TRIM28	1.818	2.197
ELK1_SRF_THAP1	1.773	2.197
PU1_SIX5_TEAD4	1.925	2.197
NRF1_NRSF_TBLR1	1.247	2.197
CEBPB_CTCFC_EGR1	1.106	2.197
CBX3_GTF2F1_SIN3	0.778	1.419
EJUNB_GTF2B_TBLR1	1.8	2.197
RCOR1_SIX5_STAT5	1.732	2.197
ELK1_GTF2F1_SMC3	1.34	2.197
SRF_STAT1_TBLR1	1.732	2.197
CBX3_CTCF_GTF2F1	1.8	2.197
CBX3_CTCFC_GTF2B	1.625	2.197
BCLAF1_GTF2B_STAT1	1.732	2.197
CBX3_NELFE_YY1	1.106	2.197
SP2_TBLR1_USF1	1.384	2.197
CCNT2_GTF2B_YY1	0.907	1.289
CMYC_GTF2F1_POL2	1.214	0.98
GTF2B_GTF2F1_TEAD4	1.015	1.179
BHLHE40_GTF2B_MAX	1.285	0.908
ETS1_GTF2B_NRSF	0.969	1.223
ELF1_PU1_YY1	0.907	1.285
PML_POL2_TAF7	0.839	1.352
GTF2B_PML_YY1	0.983	1.206
CTCFB_GTF2F1_USF1	2.188	2.197
ARID3_GTF2B_PU1	2.188	2.256
CBX3_RAD21_SP2	2.188	1.612
BCLAF1_SP2_TAF7	2.188	1.934
GTF2B_MAFF_MXI1	2.188	1.808
CEBPB_CTCFC_NR2F2	2.188	2.156
E2F6_GTF2B_STAT2	1.137	2.188

BHLHE40_ELK1_STAT5	2.188	1.197
GTF2B_P300_SIN3	1.028	1.156
GTF2B_GTF2F1_RCOR1	1.139	1.045
ELF1_ETS1_STAT2	1.542	2.182
MAX_SIX5_TR4	1.989	2.182
CBX3_PU1_TBLR1	1.205	2.182
MAX_NELFE_NRF1	2.51	2.182
MAX_STAT1_USF1	1.032	2.182
CCNT2_HMGN3_NELFE	1.714	2.182
ELK1_HMGN3_ZNF143	1.553	2.182
ATF1_E2F4_GTF2F1	1.032	1.148
E2F6_IRF1_SIX5	0.843	1.337
MAX_SIX5_YY1	1.073	1.106
CCNT2_GTF2F1_JUND	1.108	1.071
IRF1_TBLR1_THAP1	1.312	2.178
ELF1_GTF2F1_HMGN3	1.059	1.117
ETS1_NELFE_TAF7	1.562	2.175
CTCFC_SP2_TAF1	2.173	1.934
SMC3_SP2_TAF1	2.173	1.256
ELF1_TAF7_ZBTB33	2.173	NS
RAD21_SP2_YY1	2.173	2.519
E2F6_ETS1_TAF7	0.841	1.33
GTF2F1_JUND_SIN3	1.063	1.108
POL2_RCOR1_SIX5	1.271	0.9
EGR1_GABP_GTF2F1	1.118	1.052
ETS1_GTF2F1_PML	1.044	1.126
CCNT2_ELF1_GTF2B	0.895	1.273
CEBPB_POL2_PU1	1.077	2.168
CCNT2_TAF1_TAF7	0.977	1.19
ELK1_MAX_SP2	2.166	1.126
CMYC_RAD21_THAP1	2.166	1.934
CTCFL_IRF1_TRIM28	2.166	1.782
CTCFC_THAP1_YY1	2.166	2.004
EJUNB_MAX_THAP1	2.166	1.741
CTCF_IRF1_SP2	2.166	2.086
CJUN_E2F4_GTF2B	0.778	1.388
CCNT2_PML_SIX5	0.967	1.197
E2F6_SIX5_YY1	1.041	1.123
E2F4_GABP_IRF1	1.324	0.838
GTF2F1_IRF1_TAF1	1.239	0.922
BHLHE40_POL2_TAF7	0.775	1.384
BHLHE40_GTF2B_POL2	1.159	1

NELFE_TAF7_YY1	0.925	2.156
MAX_NRF1_STAT1	1.063	2.156
E2F6_NELFE_SIN3	1.553	2.156
CTCFB_EJUND_GTF2F1	1.625	2.156
ELK1_SP2_TAF7	1.925	2.156
ELK1_GTF2F1_THAP1	1.577	2.156
CBX3_GTF2F1_STAT5	1.732	2.156
CEBPB_CTCFB_EGR1	0.925	2.156
CEBPB_TAF7_ZNF143	1.603	2.156
ELK1_SIX5_USF1	2.063	2.156
MAX_NRF1_STAT5	2.147	2.156
BCLAF1_ETS1_THAP1	1.588	2.156
ELF1_NR2F2_STAT5	1.118	2.156
ELF1_RFX5_TAF7	1.925	2.156
JUND_MXI1_NELFE	2.732	2.156
EJUND_GTF2B_STAT2	2.013	2.156
MXI1_NELFE_PML	1.603	2.156
ELK1_STAT1_ZNF143	2.925	2.156
E2F4_ELK1_STAT1	1.51	2.156
BCLAF1_ELK1_TAF7	1.41	2.156
ETS1_MXI1_STAT1	1.063	2.156
MXI1_NELFE_NRSF	1.925	2.156
GTF2F1_JUND_PML	1.101	1.055
ETS1_GTF2F1_HMGN3	1.02	1.135
CMYC_GTF2F1_PML	0.976	1.175
BHLHE40_E2F4_SIX5	1.032	1.118
BHLHE40_GTF2B_PML	1.063	1.086
GTF2F1_IRF1_SP1	1.288	0.86
NR2F2_PML_THAP1	2.147	2.808
GTF2B_MAFF_ZBTB33	2.147	NS
CCNT2_MAFF_ZBTB33	2.147	NS
GTF2F1_PU1_THAP1	2.147	1.934
CTCFB_E2F4_ZBTB33	2.147	NS
E2F4_EJUNB_THAP1	2.147	1.808
RAD21_SP2_TAF1	2.147	0.711
ELK1_SP2_ZNF143	2.147	1.634
SP2_STAT5_TRIM28	2.147	1.934
BCLAF1_CTCFC_SP2	2.147	2.256
ELK1_P300_SP2	2.147	1.571
TAF7_ZBTB33_ZNF143	2.147	NS
ELK1_MAZ_PU1	2.147	NS
PU1_TAF1_YY1	0.925	1.221

GTF2F1_MAX_USF1	1.35	0.793
ELF1_GABP_PU1	0.816	1.326
CTCFB_ELK1_IRF1	1.449	2.14
NELFE_POL2_SIX5	0.925	2.14
GTF2B_POL2_SP1	0.896	1.243
BHLHE40_ETS1_GTF2F1	1.044	1.094
E2F6_ELF1_SIX5	0.953	1.184
ATF1_GTF2F1_PML	1.162	0.974
EGR1_ELF1_GTF2F1	1.169	0.967
E2F4_NELFE_SIN3	1.147	2.135
CMYC_MAX_SIX5	1.152	0.982
CCNT2_HMGN3_THAP1	0.925	1.207
E2F4_GTF2F1_POL2	1.029	1.102
ATF1_ATF3_GTF2B	2.131	1.741
E2F4_NELFE_POL2	1.805	2.13
GTF2F1_MAX_PML	1.146	0.984
NRSF_TAF7_YY1	0.81	1.319
E2F4_GTF2F1_TEAD4	1.083	1.045
CTCF_POL2_SP2	2.127	1.934
MAX_SIX5_ZBTB33	2.127	NS
CHD2_GTF2B_MAX	0.925	1.202
ELF1_STAT1_STAT2	0.703	2.126
ELF1_NELFE_ZNF143	1.095	2.126
CBX3_SIN3_THAP1	1.317	2.126
CEBPB_ELK1_SIN3	1.662	2.126
CBX3_ETS1_NELFE	1.51	2.126
GTF2B_NRF1_PU1	1.818	2.126
CEBPB_ELK1_GTF2F1	1.288	2.126
BCLAF1_IRF1_NRF1	1.147	2.126
CEBPB_E2F4_PU1	1.013	2.126
CTCFB_GTF2F1_P300	1.428	2.126
NELFE_NRF1_PML	2.247	2.126
BCLAF1_ELF1_PU1	1.086	2.126
IRF1_MEF2_SIX5	2.384	2.126
CEBPB_ETS1_PU1	1.34	2.126
NELFE_PML_SIX5	1.34	2.126
ELK1_SP1_STAT1	2.147	2.126
CMYC_POL2_TR4	2.007	2.124
GTF2B_MAZ_SIX5	2.123	NS
GTF2B_IRF1_TAF1	1.138	0.983
CMYC_SP2_STAT5	2.121	2.19
CMYC_CTCFB_GABP	1.147	0.974

CJUN_CMYC_SIX5	1.201	0.919
CBX3_CMYC_GTF2F1	0.925	1.194
EGR1_ELK1_SP2	2.118	1.282
HMGN3_SP2_THAP1	2.118	2.156
GTF2F1_SIX5_STAT2	2.118	1.827
EJUNB_ETS1_THAP1	2.118	2.156
E2F6_MAZ_TR4	2.118	NS
EJUNB_SIX5_TAF1	2.118	2.519
GABP_TAF7_ZBTB33	2.118	NS
E2F4_EGR1_GTF2B	1.047	1.071
CTCFC_RCOR1_THAP1	2.118	2.071
CTCFC_NR2F2_TRIM28	2.118	1.782
IRF1_JUND_ZNF143	1.166	0.951
EGR1_IRF1_SIX5	0.925	1.191
POL2_SIX5_TAF1	0.597	1.519
CMYC_SIX5_TAF1	1.138	0.975
GTF2F1_MAX_SP1	1.226	0.887
BHLHE40_GTF2B_TAF1	1.137	0.976
CBX3_E2F4_ELF1	0.925	1.188
GTF2F1_POL2_TRIM28	0.684	1.428
IRF1_NRF1_TBLR1	0.978	2.111
EGR1_ETS1_TAF7	0.845	1.266
GTF2F1_MXI1_PML	0.879	1.231
GABP_MAX_PU1	1.069	1.039
POL2_RAD21_THAP1	2.106	1.14
ELK1_PML_TAF7	1.641	2.104
CTCFB_ETS1_TRIM28	1.51	2.104
GTF2F1_MXI1_NELFE	1.925	2.104
ELF1_IRF1_ZNF143	0.994	1.11
POL2_STAT1_ZNF143	0.726	2.104
GTF2B_NRF1_PML	0.925	1.179
CBX3_POL2_PU1	0.905	2.104
CBX3_PU1_ZNF143	1.077	2.104
CEBPB_JUND_PU1	1.051	2.104
CEBPB_PML_PU1	1.137	2.104
ELF1_NR2F2_SP1	0.925	2.104
EJUND_PU1_ZNF143	1.266	2.104
E2F4_MAX_NELFE	1.23	2.104
E2F4_E2F6_GTF2F1	0.995	1.107
E2F4_EGR1_SIX5	1.032	1.065
POL2_TAF7_YY1	0.861	1.236
MAZ_NR2F2_SIX5	2.095	NS

CTCFB_PML_THAP1	2.095	1.296
ELK1_MAZ_THAP1	2.095	NS
CMYC_NELFE_POL2	1.934	2.095
GABP_NR2F2_SMC3	2.095	1.934
CEBPB_GTF2B_POL2	1.041	1.049
E2F4_GTF2F1_JUND	1.022	1.068
ETS1_IRF1_NELFE	1.55	2.089
ATF1_MAX_NELFE	1.041	2.086
E2F4_ELK1_TAF7	1.732	2.086
CTCFB_IRF1_NELFE	1.925	2.086
GTF2F1_PML_YY1	1.101	0.985
HMGN3_NELFE_SIN3	1.273	2.086
NELFE_NRF1_POL2	2.188	2.086
EGR1_MXI1_SIX5	1.395	2.086
CCNT2_ETS1_THAP1	0.962	1.12
CCNT2_ETS1_GTF2F1	0.955	1.126
CTCFB_TRIM28_YY1	1.235	2.081
E2F6_GTF2B_IRF1	0.863	1.218
CMYC_STAT1_THAP1	2.755	2.081
ETS1_GABP_IRF1	1.083	0.997
CMYC_NRF1_TBLR1	0.534	2.079
CMYC_E2F6_GTF2B	0.865	1.214
IRF1_RAD21_SP2	2.077	1.841
E2F6_SIX5_ZBTB33	2.077	NS
CJUN_IRF1_TAF7	1.143	0.934
CCNT2_GTF2F1_MAX	0.925	1.151
CJUN_TAF7_YY1	0.794	1.282
E2F4_GTF2F1_SP1	0.966	1.109
GABP_PML_ZNF143	0.984	1.09
ELF1_GTF2F1_TAF1	1.111	0.962
CMYC_SIX5_YY1	0.739	1.333
E2F6_GABP_NELFE	1.732	2.071
GTF2B_RFX5_SIX5	3.732	2.071
EJUNB_GTF2B_RCOR1	1.703	2.071
CBX3_EJUND_THAP1	1.372	2.071
EJUNB_GTF2B_P300	1.703	2.071
CTCFC_E2F6_P300	1.51	2.071
SP1_SRF_YY1	1.086	2.071
CBX3_SRF_TAF7	1.8	2.071
CBX3_TAF7_TBLR1	1.547	2.071
GTF2F1_TAF1_YY1	0.951	1.119
GTF2F1_MAX_SIN3	1.007	1.062

HMGN3_JUND_THAP1	0.969	1.097
GTF2B_SP1_TAF1	0.999	1.067
CMYC_GTF2B_STAT2	1.623	2.066
BCLAF1_POL2_PU1	1.147	2.065
CTCFB_GTF2B_ZBTB33	2.063	NS
ELK1_SP2_YY1	2.063	1.498
CTCFB_GTF2B_MAFF	2.063	1.934
CMYC_ELF1_IRF1	1.053	1.01
PML_POL2_PU1	0.802	1.259
CMYC_GABP_IRF1	1.262	0.799
ETS1_NRF1_TBLR1	1.131	2.059
GTF2B_GTF2F1_STAT1	1.456	2.059
CHD2_HMGN3_TAF7	1.294	2.059
CBX3_GTF2F1_JUND	0.925	1.133
EJUND_IRF1_SIX5	1.051	1.006
E2F6_POL2_TR4	1.818	2.056
CTCFB_JUND_THAP1	2.051	1.571
CJUN_GTF2F1_PML	0.76	1.291
CTCF_THAP1_YY1	2.051	1.571
CTCFB_ELK1_GTF2B	1.773	2.049
BCLAF1_GTF2F1_USF1	1.562	2.049
E2F6_SRF_STAT1	2.384	2.049
CCNT2_EJUNB_SIX5	1.832	2.049
ELF1_SRF_STAT1	0.925	2.049
SP1_SRF_THAP1	1.562	2.049
BCL3_ELF1_TAF7	1.456	2.049
CTCF_SIN3_ZNF143	0.591	2.049
GTF2F1_PU1_USF1	1.732	2.049
CEBPB_EGR1_PU1	1.188	2.049
GTF2B_NELFE_SIX5	1.41	2.049
SRF_THAP1_YY1	1.613	2.049
CBX3_TBLR1_THAP1	1.625	2.049
CBX3_GTF2F1_SMC3	1.625	2.049
ELK1_NR2F2_SP1	1.662	2.049
BCLAF1_JUND_THAP1	1.395	2.049
ATF1_ELF1_STAT5	1.603	2.049
CEBPB_CTCFB_ZNF143	0.366	2.049
GTF2F1_SMC3_TBLR1	1.456	2.049
CTCFB_GTF2B_MXI1	1.562	2.049
CTCFL_EGR1_P300	1.312	2.049
CTCFB_GABP_TRIM28	1.588	2.049
CTCFB_E2F4_PU1	1.553	2.049

E2F4_ETS1_NELFE	1.691	2.049
CEBPB_ELF1_NR2F2	1.095	2.049
GTF2F1_SRF_TRIM28	1.732	2.049
CBX3_CEBPB_CTCFB	1.095	2.049
CJUN_IRF1_SIX5	1.168	0.88
CMYC_MXI1_SIX5	1.263	2.047
E2F4_GTF2B_NRSF	0.829	1.218
GTF2B_JUND_TEAD4	1.015	1.03
ELK1_SP2_TRIM28	2.041	1.223
ELF1_MAFF_ZBTB33	2.041	NS
GABP_GTF2F1_MAFF	2.041	1.671
EJUNB_NR2F2_TRIM28	2.041	2.256
HMGN3_SP2_STAT5	2.041	1.934
CTCF_ELF1_GTF2F1	2.041	1.634
PU1_RCOR1_SP2	2.041	2.071
BCLAF1_CTCF_SP2	2.041	2.256
E2F4_MXI1_NFYA	2.041	1.197
PML_TAF1_TAF7	1.059	0.982
CBX3_ELK1_SP2	2.041	1.349
BCLAF1_CTCFB_SP2	2.041	2.256
GABP_MAZ_NELFE	2.041	NS
CMYC_GTF2F1_TAF1	1.14	0.898
HMGN3_THAP1_YY1	0.951	1.086
E2F4_GTF2B_POL2	0.881	1.154
E2F6_GABP_GTF2F1	1.045	0.99
GTF2B_GTF2F1_PML	0.986	1.049
GTF2B_MAZ_PU1	2.035	NS
CBX3_EGR1_THAP1	1.366	2.033
TBLR1_TEAD4_THAP1	1.304	2.033
EJUNB_POL2_SRF	0.843	2.033
MXI1_NRF1_TAF7	1.215	2.033
GTF2B_MAX_TEAD4	1.183	0.85
CBX3_E2F4_NELFE	1.34	2.033
PU1_SP1_ZNF143	1.395	2.033
NRF1_STAT1_TBLR1	0.925	2.033
ELK1_PU1_TEAD4	1.925	2.033
CTCF_CTCFB_GTF2F1	1.732	2.033
E2F4_NELFE_ZNF143	0.925	2.033
CBX3_NELFE_SIN3	0.8	2.033
ELK1_HMGN3_PU1	1.703	2.033
ATF1_GTF2B_RFX5	2.34	2.033
ATF1_EJUND_SIX5	1.553	2.033

CMYC_NELFE_SIN3	1.707	2.033
GTF2B_SP1_USF1	1.691	2.033
CBX3_NELFE_TAF7	1.577	2.033
ATF1_HMGN3_SRF	1.34	2.033
GTF2F1_HMGN3_STAT5	1.755	2.033
GTF2B_MXI1_RFX5	3.51	2.033
SIX5_TAF7_TBP	1.662	2.033
CTCFL_EGR1_YY1	0.806	2.033
BHLHE40_ELF1_NELFE	1.925	2.033
CBX3_ELK1_PU1	1.625	2.033
BHLHE40_GTF2F1_STAT5	1.603	2.033
BCLAF1_SP1_TAF7	1.603	2.033
ELK1_JUND_TAF7	1.473	2.033
ETS1_THAP1_YY1	1.127	0.905
GTF2B_GTF2F1_NRSF	0.925	1.104
ELF1_GTF2B_TAF1	0.925	1.104
CJUN_PML_SIX5	1.047	0.98
GTF2F1_HMGN3_YY1	0.965	1.061
BHLHE40_IRF1_SIX5	0.979	1.047
ATF3_CTCFB_NR2F2	2.025	-6.069
EGR1_NR2F2_TAF7	2.025	1.827
SP2_STAT5_ZNF143	2.025	1.808
CTCFC_ELF1_THAP1	2.025	2.197
CCNT2_GTF2B_SMC3	2.025	1.934
ELF1_SP2_STAT5	2.025	1.934
MAFF_TAF1_ZBTB33	2.025	NS
ELK1_PU1_RCOR1	2.025	1.519
CBX3_GTF2B_TAF1	1.038	0.986
IRF1_NELFE_YY1	1.306	2.023
BHLHE40_JUND_SIX5	0.925	1.097
CMYC_GTF2F1_NRSF	0.973	1.049
GTF2B_NRF1_THAP1	1.625	2.021
EJUNB_IRF1_SRF	1.925	2.021
NRF1_SIX5_TBLR1	1.188	2.021
SIN3_SRF_THAP1	1.428	2.021
SIX5_TBLR1_THAP1	1.662	2.021
GTF2F1_HMGN3_NR2F2	1.428	2.021
HMGN3_NRF1_THAP1	1.247	2.021
E2F6_MAX_TR4	2.691	2.021
ELK1_TAF7_TRIM28	1.247	2.021
GTF2B_STAT1_STAT2	0.925	2.021
BCLAF1_ELK1_GTF2B	1.773	2.021

EJUND_NRF1_TBLR1	1.247	2.021
CMYC_SMC3_SP2	2.02	2.063
E2F4_GTF2F1_P300	0.979	1.041
CTCFB_IRF1_THAP1	2.018	1.808
GTF2F1_IRF1_NRSF	0.925	1.093
BHLHE40_GTF2F1_POL2	1.126	0.891
PU1_TAF1_ZBTB33	2.013	NS
CTCFC_RAD21_THAP1	2.013	2.071
CTCFB_THAP1_ZNF143	2.013	1.671
MAZ_NR2F2_THAP1	2.013	NS
JUND_SP2_THAP1	2.013	1.934
CEBPB_GABP_THAP1	2.013	2.049
ELK1_STAT5_TAF1	2.013	1.349
ELK1_HMGN3_SP1	1.755	2.012
GTF2B_P300_STAT1	1.703	2.012
CTCFB_PML_TRIM28	1.449	2.012
ELK1_JUND_STAT1	1.732	2.012
CEBPB_ELF1_PU1	0.984	2.012
E2F4_JUND_MXI1	0.974	1.037
ETS1_GTF2F1_SIN3	0.985	1.025
BCLAF1_CTCFB_POL2	0.759	2.008
CMYC_GTF2F1_SP1	0.973	1.034
GTF2B_TEAD4_YY1	0.948	1.059
CBX3_GTF2F1_IRF1	1.241	0.764
GTF2B_SP1_STAT1	2.384	2.004
CTCF_HMGN3_ZNF143	0.671	2.004
CCNT2_NELFE_SIN3	1.51	2.004
ETS1_MXI1_NELFE	2.095	2.004
E2F6_STAT1_STAT2	1.773	2.004
GTF2F1_NELFE_YY1	1.209	2.004
ETS1_GTF2B_STAT2	1.81	2.004
ELF1_STAT1_ZNF143	1.025	2.004
ELF1_SIN3_STAT1	1.312	2.004
ETS1_POL2_TR4	1.925	2.004
ELK1_GABP_SP2	2.003	1.233
CTCFL_NR2F2_YY1	2.003	1.841
CCNT2_THAP1_YY1	0.999	1.004
MAFF_MAX_ZBTB33	2.003	NS
ELF1_SIX5_YY1	0.684	1.319
GTF2B_IRF1_TEAD4	0.82	1.18
CMYC_MAX_ZNF143	1.302	0.697
NRF1_POL2_TAF7	0.925	1.074

CJUN_POL2_TAF7	0.998	1
CBX3_POL2_THAP1	0.984	1.998
E2F6_NELFE_TAF7	1.662	1.998
E2F4_MXI1_TAF7	1.366	1.998
BCLAF1_E2F6_PU1	1.215	1.998
ETS1_NRF1_SIX5	1.361	1.998
E2F6_GTF2F1_SIN3	0.874	1.123
E2F6_ELK1_NR2F2	1.755	1.993
GTF2B_STAT1_TAF1	1.662	1.993
CCNT2_POL2_TAF7	0.938	1.055
E2F4_GABP_SIN3	0.893	1.099
CMYC_IRF1_SRF	0.708	1.284
BCLAF1_E2F6_SP2	1.989	1.741
MAZ_STAT2_TAF7	1.989	NS
IRF1_STAT1_USF1	1.51	1.988
NRSF_PU1_YY1	1.021	1.988
ELF1_PU1_TBLR1	1.045	1.988
IRF1_SMC3_YY1	1.987	1.208
GTF2B_GTF2F1_TAF1	0.946	1.041
JUND_YY1_ZNF143	0.841	1.144
EGR1_PML_TAF7	0.834	1.151
IRF1_RAD21_THAP1	1.984	2.296
GABP_POL2_STAT5	0.925	1.984
ETS1_GTF2F1_NELFE	1.603	1.984
IRF1_SIX5_YY1	0.813	1.17
CMYC_CTCFL_TRIM28	1.014	1.976
E2F4_NELFE_YY1	1.538	1.976
CMYC_ELK1_SP2	1.976	1.617
GTF2F1_MAX_NR2F2	1.571	1.976
MAZ_PU1_TAF7	1.976	NS
SIX5_SRF_YY1	1.077	1.976
JUND_NELFE_YY1	1.577	1.973
CJUN_GTF2B_TAF1	0.708	1.264
PML_YY1_ZNF143	0.839	1.129
GTF2B_PML_SIN3	0.902	1.066
CMYC_GTF2B_STAT1	1.752	1.967
GTF2F1_IRF1_MAFF	1.967	1.586
CCNT2_GTF2B_SIN3	0.755	1.211
CBX3_CMYC_NELFE	0.755	1.964
GTF2F1_IRF1_POL2	0.637	1.326
GTF2F1_POL2_ZNF143	0.899	1.062
CMYC_GABP_PML	0.96	1

CMYC_CTCF_THAP1	1.959	1.49
BHLHE40_GTF2F1_PML	1.025	0.934
E2F4_GABP_PML	0.954	1.002
ETS1_JUND_ZNF143	0.862	1.094
GABP_IRF1_ZNF143	1.177	0.779
GTF2F1_MAFF_POL2	1.955	1.054
JUND_MAX_SRF	0.953	1.001
CJUN_ELF1_STAT5	0.925	1.021
BHLHE40_E2F4_GTF2F1	0.967	0.977
E2F4_IRF1_ZNF143	0.965	0.976
ELF1_PML_ZNF143	0.726	1.214
PU1_SIN3_STAT1	1.247	1.934
EJUND_ELK1_P300	1.553	1.934
GTF2B_STAT5_TRIM28	1.773	1.934
E2F4_EJUND_STAT5	1.843	1.934
ELK1_PML_THAP1	1.395	1.934
CBX3_P300_PU1	0.925	1.934
ELF1_MAX_NELFE	1.989	1.934
CTCFB_EJUND_GTF2B	1.51	1.934
GTF2F1_HMGN3_NELFE	1.843	1.934
PML_SRF_THAP1	1.018	1.934
NRF1_SIX5_SP1	1.188	1.934
GTF2F1_PU1_TEAD4	1.466	1.934
JUND_NELFE_TAF7	1.51	1.934
ELF1_MXI1_NELFE	1.925	1.934
CEBPB_EGR1_SIX5	1.466	1.934
E2F4_NELFE_PML	1.118	1.934
CTCF_GTF2B_POL2	0.755	1.934
EGR1_ETS1_NELFE	1.818	1.934
CTCFB_ELF1_TRIM28	1.23	1.934
GABP_SIX5_STAT1	1.51	1.934
ELF1_PU1_SRF	1.34	1.934
CTCFB_E2F4_MXI1	1.225	1.934
CBX3_CTCFC_GTF2F1	1.925	1.934
CTCFB_GTF2B_TBLR1	1.304	1.934
EJUND_SIX5_TRIM28	1.662	1.934
E2F6_ELK1_P300	0.989	1.934
ELF1_GTF2F1_NR2F2	1.44	1.934
BCLAF1_CMYC_PU1	1.038	1.934
GTF2F1_SIN3_STAT2	1.925	1.934
CBX3_MXI1_SIX5	1.247	1.934
BCLAF1_SIX5_ZNF143	1.34	1.934

CBX3_NELFE_PML	1.032	1.934
CBX3_JUND_NELFE	1.384	1.934
SIX5_SP1_SRF	1.428	1.934
CEBPB_EJUNB_GTF2B	1.51	1.934
NRF1_TBLR1_ZNF143	1.188	1.934
PU1_RCOR1_ZNF143	0.995	1.934
TAF7_TBLR1_TRIM28	1.225	1.934
HMGN3_TBLR1_THAP1	1.473	1.934
BHLHE40_PU1_ZNF143	0.995	1.934
ELK1_MXI1_TAF7	0.51	1.934
POL2_SRF_TR4	0.832	1.934
EGR1_GTF2F1_SMC3	1.51	1.934
CBX3_SIX5_TEAD4	1.428	1.934
BCLAF1_PML_PU1	0.765	1.934
CTCFB_GTF2F1_TBLR1	1.372	1.934
GTF2F1_NRF1_TBLR1	1.41	1.934
ELF1_NELFE_NRSF	1.384	1.934
CTCFC_ELF1_GTF2B	1.225	1.934
CEBPB_ELK1_GABP	1.41	1.934
ELK1_ETS1_STAT5	1.662	1.934
GTF2F1_SIX5_STAT1	1.577	1.934
CTCFB_GTF2B_TEAD4	1.304	1.934
BCLAF1_CTCFB_PML	1.173	1.934
ELF1_GTF2F1_STAT1	1.34	1.934
GTF2B_SMC3_TBLR1	1.577	1.934
EGR1_ELK1_TAF7	1.553	1.934
NR2F2_TAF7_TBLR1	1.247	1.934
GABP_STAT1_ZNF143	1.032	1.934
E2F6_TAF7_THAP1	1.288	1.934
ELK1_ETS1_THAP1	1.636	1.934
ELK1_P300_USF1	1.384	1.934
GTF2F1_SIN3_STAT1	1.247	1.934
CTCFB_CTCFC_GTF2B	1.34	1.934
GTF2F1_RCOR1_SMC3	1.603	1.934
ELF1_STAT1_TBLR1	1.225	1.934
CEBPB_SIX5_YY1	2.072	1.934
EJUNB_GTF2B_SIN3	1.304	1.934
BCLAF1_E2F4_TAF7	1.266	1.934
ETS1_PU1_STAT1	0.925	1.934
ELK1_ETS1_TAF7	1.225	1.934
CEBPB_ELF1_ELK1	1.041	1.934
CTCFB_MAX_STAT5	1.34	1.934

CCNT2_ELK1_TAF7	1.247	1.934
GABP_SP1_STAT5	1.44	1.934
CTCFL_PML_TAF7	2.041	1.934
CTCFB_P300_SIN3	0.781	1.934
BCLAF1_GTF2B_TBLR1	1.147	1.934
CBX3_CTCFB_SIN3	1.215	1.934
ETS1_NELFE_PML	1.205	1.934
CTCFC_GTF2F1_ZNF143	1.732	1.934
GTF2B_PML_STAT1	1.603	1.934
ELK1_GTF2F1_STAT5	1.925	1.934
CTCFB_GTF2B_P300	1.41	1.934
NRSF_TAF7_THAP1	1.247	1.934
CTCF_ELF1_P300	0.925	1.934
CBX3_NELFE_ZNF143	0.925	1.934
IRF1_SRF_TAF7	1.34	1.934
ETS1_GTF2F1_STAT1	1.562	1.934
CBX3_MAX_NELFE	0.847	1.934
SIX5_SP1_USF1	1.662	1.934
E2F4_SP2_TBLR1	1.603	1.934
E2F4_STAT1_USF1	1.925	1.934
EJUND_GTF2B_STAT1	1.8	1.934
GTF2F1_MAX_NRSF	0.948	0.986
CMYC_PML_ZNF143	0.878	1.055
CHD2_ELF1_GTF2B	0.845	1.086
CHD2_GTF2B_GTF2F1	0.803	1.126
CMYC_JUND_ZNF143	0.778	1.149
ELF1_PU1_ZBTB33	1.925	NS
JUND_RAD21_SP2	1.925	2.519
EJUNB_ETS1_TAF7	1.925	1.934
GABP_RAD21_SP2	1.925	1.419
CTCF_E2F4_SP2	1.925	1.808
GTF2F1_MAZ_SIX5	1.925	NS
RAD21_SP2_ZNF143	1.925	1.782
ARID3_PU1_TAF1	1.925	2.671
ATF3_GTF2F1_SIX5	1.925	1.934
PML_SMC3_SP2	1.925	2.071
MAX_SMC3_SP2	1.925	1.256
CHD2_EJUNB_TAF7	1.925	2.256
EJUNB_SIN3_TAF7	1.925	2.071
JUND_THAP1_ZBTB33	1.925	NS
CTCFC_E2F4_SP2	1.925	1.808
CHD2_ZBTB33_ZNF143	1.925	NS

GTF2B_MAZ_THAP1	1.925	NS
BCLAF1_MAX_SP2	1.925	1.419
CTCFB_EGR1_THAP1	1.925	1.634
CCNT2_TAF7_ZBTB33	1.925	NS
CTCFB_RAD21_THAP1	1.925	1.671
CTCF_ETS1_SIX5	1.925	1.671
CTCFC_NR2F2_SMC3	1.925	2.519
IRF1_ZBTB33_ZNF143	1.925	NS
POL2_RAD21_SP2	1.925	1.519
CTCFL_ETS1_SIX5	1.925	1.634
E2F4_TAF7_ZBTB33	1.925	NS
BCLAF1_E2F4_SP2	1.925	1.808
ELK1_JUND_SP2	1.925	1.349
SP2_THAP1_ZNF143	1.925	1.586
EGR1_RAD21_THAP1	1.925	1.741
GTF2B_SMC3_SP2	1.925	1.808
PML_SMC3_YY1	1.925	1.054
CTCF_P300_SP2	1.925	1.934
CTCFB_EGR1_STAT5	1.925	2.071
CHD2_PU1_ZBTB33	1.925	NS
ELF1_SMC3_SP2	1.925	1.711
ELK1_MAZ_SIX5	1.925	NS
GTF2B_MAZ_SRF	1.925	NS
CTCFB_GTF2F1_SP1	1.925	1.827
EJUND_GTF2B_MAZ	1.925	NS
ELK1_SIN3_SP2	1.925	1.282
EJUNB_TAF7_TEAD4	1.925	2.071
CTCFB_E2F4_THAP1	1.925	1.448
MAFF_PML_ZBTB33	1.925	NS
GABP_GTF2B_ZBTB33	1.925	NS
CMYC_PML_SRF	0.599	1.324
BHLHE40_GTF2F1_TAF1	0.988	0.934
GTF2F1_MAX_TAF1	1.155	0.754
GTF2B_JUND_RCOR1	0.925	0.984
IRF1_POL2_PU1	0.891	1.017
IRF1_PML_ZNF143	0.835	1.065
CMYC_IRF1_ZNF143	1.005	0.893
CMYC_IRF1_YY1	0.875	1.021
CMYC_EJUNB_SRF	1.751	1.895
E2F6_ELK1_HMGN3	0.868	1.893
ATF1_CMYC_NRSF	0.802	1.893
GTF2F1_PML_SP1	0.989	0.9

CTCFL_GTF2B_POL2	1.129	1.888
GTF2F1_POL2_USF1	0.826	1.061
GTF2F1_MAZ_PU1	1.887	NS
CJUN_GTF2F1_TAF1	0.8	1.086
CBX3_THAP1_YY1	1.51	1.885
ETS1_GTF2F1_TAF1	0.975	0.907
CCNT2_E2F6_NELFE	1.636	1.881
E2F6_SRF_ZNF143	1.304	1.881
GABP_PU1_TBLR1	1.297	1.877
ETS1_TBLR1_THAP1	1.247	1.877
GTF2B_PML_SP2	0.832	1.045
NRSF_PML_TAF7	0.83	1.046
E2F6_GTF2F1_IRF1	1.005	0.87
PML_POL2_SIX5	0.823	1.051
GABP_THAP1_YY1	1.009	0.865
GTF2B_HMGN3_NRF1	1.188	1.872
CBX3_SIX5_TBLR1	1.366	1.872
ATF1_IRF1_NELFE	1.077	1.872
CMYC_MAFF_ZBTB33	1.868	NS
SIX5_YY1_ZBTB33	1.868	NS
ETS1_GTF2F1_NR2F2	1.44	1.867
ELF1_NELFE_SIN3	1.577	1.867
CJUN_PU1_TEAD4	1.127	1.867
PML_TBLR1_THAP1	1.077	1.867
EJUNB_ELK1_MAX	1.34	1.867
ETS1_NELFE_YY1	1.41	1.867
E2F6_STAT1_ZNF143	0.662	1.867
HMGN3_NRF1_TBLR1	0.925	1.867
GTF2B_IRF1_NRSF	0.782	1.084
ELK1_POL2_TAF7	1.662	1.865
E2F4_GTF2F1_HMGN3	0.823	1.041
ELF1_PU1_TAF1	0.686	1.175
GABP_PU1_TEAD4	1.077	1.86
ATF1_ELK1_GTF2B	2.095	1.86
ELK1_GTF2F1_TRIM28	1.625	1.86
BCLAF1_PML_SIX5	1.577	1.86
PML_RFX5_TAF7	2.147	1.86
HMGN3_TAF7_TRIM28	1.51	1.86
GTF2B_POL2_SIN3	0.911	0.949
GTF2F1_STAT1_ZNF143	1.44	1.86
NRF1_SIX5_YY1	1.063	1.86
CJUN_GTF2B_STAT5	1.131	1.86

GTF2F1_SMC3_TAF1	1.858	1.934
E2F6_SMC3_SP2	1.858	1.741
CMYC_GTF2F1_USF1	0.889	0.969
CTCFB_GABP_NR2F2	1.858	2.197
CEBPB_CMYC_ELK1	1.397	1.854
GTF2B_IRF1_STAT1	1.279	1.854
JUND_PML_ZNF143	0.758	1.096
GTF2B_PML_POL2	0.903	0.949
GTF2B_POL2_YY1	0.613	1.239
CCNT2_GTF2B_PML	0.71	1.142
CTCFL_EGR1_ETS1	1.147	1.851
PU1_YY1_ZBTB33	1.851	NS
JUND_MXI1_NRF1	1.025	1.851
ELK1_PML_SP2	1.851	1.448
EJUND_PU1_TEAD4	1.44	1.851
GTF2B_MXI1_NELFE	1.925	1.851
EJUNB_GTF2B_MAZ	1.851	NS
CEBPB_PU1_TAF1	1.201	1.851
JUND_MAX_TR4	2.109	1.851
GTF2B_HMGN3_RFX5	3.247	1.851
EJUNB_GTF2F1_MAZ	1.851	NS
EJUND_PU1_TBLR1	1.312	1.851
EGR1_EJUND_ELK1	1.553	1.851
JUND_SIX5_STAT1	0.925	1.851
CBX3_PU1_YY1	1.181	1.851
ELK1_TAF7_ZNF143	1.51	1.851
GTF2F1_NR2F2_TAF7	1.553	1.851
CEBPB_CTCFB_ELF1	0.8	1.851
SIX5_STAT1_TBLR1	1.188	1.851
ETS1_PU1_SP2	1.466	1.851
NRF1_SIN3_TBLR1	1.34	1.851
GTF2F1_MXI1_NRF1	1.384	1.851
CTCFC_GABP_SP2	1.851	1.711
MXI1_STAT1_TBLR1	1.8	1.851
IRF1_JUND_NELFE	1.44	1.851
BCLAF1_CTCFB_ELF1	1.215	1.851
GABP_NRF1_SIX5	1.366	1.851
GTF2B_SP2_TBLR1	1.51	1.851
GTF2F1_NR2F2_SP1	1.428	1.851
CBX3_E2F4_ELK1	1.755	1.851
GTF2B_HMGN3_MAX	0.686	1.164
GABP_IRF1_YY1	0.9	0.95

CCNT2_GTF2B_MAX	0.728	1.121
PML_PU1_TAF1	0.95	0.898
CMYC_NELFE_TAF7	1.099	1.847
CMYC_EJUND_SRF	1.247	1.846
EGR1_MAX_TAF7	0.858	0.988
ATF3_ELK1_SIX5	1.843	1.519
CTCF_NR2F2_SMC3	1.843	2.519
BCLAF1_RCOR1_SP2	1.843	1.827
CTCFB_RCOR1_THAP1	1.843	1.586
RCOR1_SMC3_SP2	1.843	1.393
CTCF_GABP_SP2	1.843	1.671
CTCFB_P300_SIX5	1.843	1.827
CTCF_CTCFC_THAP1	1.843	1.934
ELK1_SP2_TAF1	1.843	0.827
CBX3_ELF1_PML	0.767	1.075
EGR1_GTF2B_IRF1	0.908	0.934
GTF2F1_SMC3_ZNF143	1.372	1.841
GTF2F1_P300_STAT5	1.662	1.841
PU1_SIN3_TEAD4	1.013	1.841
GABP_SRF_THAP1	1.691	1.841
EJUND_ELK1_PU1	1.625	1.841
E2F4_NELFE_SP1	1.077	1.841
CEBPB_ELK1_GTF2B	1.925	1.841
CTCF_EGR1_ZNF143	0.525	1.841
CJUN_EJUNB_GTF2F1	1.41	1.841
CMYC_CTCFB_NELFE	1.51	1.841
ELF1_MXI1_STAT1	1.625	1.841
CTCFB_SIN3_ZNF143	0.625	1.841
BCLAF1_TAF7_ZNF143	1.636	1.841
BHLHE40_ELK1_STAT1	2.732	1.841
CTCFC_ELF1_TRIM28	1.247	1.841
BCLAF1_GTF2B_NRF1	1.577	1.841
EJUND_SRF_YY1	0.925	1.841
GTF2F1_SRF_TEAD4	1.662	1.841
E2F6_JUND_NELFE	1.603	1.841
ELK1_SP1_SRF	1.925	1.841
CBX3_ETS1_SRF	1.312	1.841
ELK1_P300_STAT1	2.147	1.841
MXI1_P300_SIX5	1.562	1.841
GABP_NRSF_SIX5	1.372	1.841
CMYC_CTCFB_TRIM28	0.715	1.841
CBX3_SIX5_SRF	1.466	1.841

CTCFC_E2F6_ELK1	2.34	1.841
GTF2B_HMGN3_NR2F2	1.428	1.841
E2F4_ELK1_NR2F2	1.577	1.841
CBX3_HMGN3_THAP1	1.008	1.841
GTF2B_STAT5_TBLR1	1.925	1.841
ATF1_GTF2B_NELFE	1.095	1.841
GTF2F1_MXI1_SRF	1.51	1.841
ATF1_GTF2F1_NELFE	1.095	1.841
CTCFB_TRIM28_ZNF143	1.23	1.841
GTF2F1_POL2_SIN3	0.513	1.327
ETS1_GABP_PML	0.723	1.113
MAX_PML_SRF	1.008	0.827
E2F6_MXI1_SIX5	1.028	1.834
CTCFL_YY1_ZNF143	0.765	1.834
ELK1_THAP1_YY1	1.976	1.834
ELF1_NELFE_PML	1.428	1.834
CMYC_TAF7_USF1	1.058	1.833
CHD2_GTF2F1_MAFF	1.832	1.934
ELF1_MAZ_NELFE	1.832	NS
BCLAF1_P300_SP2	1.832	1.586
E2F6_GTF2F1_MAFF	1.832	1.741
IRF1_NELFE_TAF7	1.139	1.832
GABP_SMC3_SP2	1.832	1.126
CTCFC_P300_SP2	1.832	1.808
CTCFL_JUND_NR2F2	1.832	2.256
CTCF_MAZ_THAP1	1.832	NS
EGR1_GTF2B_MAX	0.946	0.886
CTCF_SIX5_SMC3	1.832	1.393
CTCFL_NR2F2_ZNF143	1.832	2.934
JUND_SP2_STAT5	1.832	1.586
GTF2B_SRF_STAT1	2.147	1.827
CTCFL_ELF1_GTF2B	1.41	1.827
CTCFL_GTF2B_JUND	1.562	1.827
GTF2B_P300_SMC3	1.625	1.827
ATF1_BCLAF1_GTF2B	1.51	1.827
EGR1_EJUNB_GTF2B	1.562	1.827
GTF2B_NRF1_POL2	1.035	0.789
EJUNB_ELK1_POL2	0.925	1.821
CTCFB_RAD21_SP2	1.818	1.612
ETS1_GABP_STAT1	0.925	1.818
ELK1_SIN3_TAF7	1.147	1.818
CTCFC_ELF1_ELK1	1.818	1.934

CTCFB_SIX5_TEAD4	1.818	1.671
E2F4_GTF2B_NELFE	1.247	1.818
E2F6_ELK1_TAF7	0.818	1.818
E2F6_SP1_SRF	1.23	1.818
GABP_SIN3_STAT1	1.041	1.818
EJUND_TAF7_TBLR1	1.34	1.818
CTCFL_E2F6_EGR1	0.584	1.818
RAD21_SMC3_SP2	1.818	1.519
E2F4_GTF2F1_NELFE	1.247	1.818
BHLHE40_GTF2B_SMC3	1.818	1.711
ELF1_PML_STAT5	0.972	1.818
GABP_MXI1_TAF7	1.173	1.818
ELK1_SRF_YY1	1.773	1.815
GTF2F1_JUND_TAF1	1	0.813
CMYC_PU1_TEAD4	0.755	1.812
GTF2B_MAZ_STAT5	1.81	NS
ATF3_GTF2F1_SRF	1.81	2.156
CTCFL_IRF1_YY1	1.81	1.601
E2F6_IRF1_NELFE	1.8	1.808
CTCFB_MAX_PU1	0.44	1.808
JUND_SIN3_STAT1	1.247	1.808
CJUN_GTF2B_NRF1	1.832	1.808
E2F6_SIN3_STAT1	1.51	1.808
NRF1_POL2_TBLR1	0.784	1.808
MXI1_POL2_SIX5	1.197	1.808
E2F4_ELK1_HMGN3	1.312	1.808
ELF1_GABP_STAT5	1.198	1.808
JUND_SMC3_YY1	1.153	1.808
EGR1_GABP_STAT1	1.273	1.808
MAX_RFX5_TAF7	2.41	1.808
PU1_SIX5_STAT1	1.773	1.808
GTF2B_MAX_NRSF	0.744	1.062
IRF1_JUND_YY1	0.788	1.016
CMYC_IRF1_JUND	0.99	0.814
CBX3_GTF2B_TEAD4	0.868	0.934
IRF1_SRF_THAP1	1.461	1.8
CJUN_PU1_TRIM28	1.8	1.764
CBX3_SRF_YY1	1.235	1.8
CTCF_MAX_THAP1	1.8	1.519
GABP_STAT1_TBLR1	1.41	1.796
GTF2B_NRF1_ZNF143	1.466	1.796
CCNT2_GTF2F1_NELFE	1.428	1.796

ETS1_MXI1_NRF1	1.025	1.796
GTF2B_HMGN3_NELFE	1.553	1.796
CJUN_GTF2F1_MXI1	1.008	1.796
TAF7_TBLR1_TBP	0.925	1.796
ELK1_SP1_TBLR1	1.662	1.796
ETS1_GTF2F1_STAT5	1.44	1.796
PU1_SIN3_TBLR1	1.366	1.796
CHD2_GTF2B_STAT1	1.703	1.796
EJUNB_MAX_SRF	2.077	1.796
GTF2F1_STAT1_TBLR1	1.51	1.796
E2F6_PU1_TEAD4	0.858	1.796
SIN3_STAT1_TBLR1	1.41	1.796
CTCFB_ELF1_ELK1	1.428	1.796
GABP_IRF1_JUND	1.038	0.757
JUND_POL2_THAP1	0.762	1.032
POL2_SIX5_TBLR1	0.827	0.966
MAZ_SIX5_THAP1	1.792	NS
CTCFC_MAX_THAP1	1.792	1.764
CMYC_GABP_THAP1	1.052	0.739
NELFE_SIN3_YY1	0.858	1.789
GTF2B_MAX_STAT1	1.641	1.789
MAZ_STAT5_TAF7	1.788	NS
EJUND_GTF2F1_MAZ	1.788	NS
E2F6_GTF2B_TAF1	0.828	0.959
GABP_POL2_THAP1	0.732	1.052
E2F4_GTF2F1_PML	0.85	0.934
GTF2F1_POL2_SP1	0.573	1.21
CTCF_MAX_SP2	1.783	1.519
GTF2F1_MAZ_SRF	1.783	NS
GTF2B_NRF1_SP1	1.456	1.782
PU1_RCOR1_TBLR1	1.173	1.782
CBX3_JUND_THAP1	1.201	1.782
E2F6_SP2_TBLR1	1.23	1.782
E2F4_ELK1_TRIM28	1.304	1.782
BCLAF1_CTCFB_JUND	1.063	1.782
ELF1_IRF1_NELFE	1.884	1.782
E2F6_JUND_STAT5	1.662	1.782
E2F4_NELFE_NRSF	0.8	1.782
GTF2F1_SIN3_STAT5	1.395	1.782
CCNT2_GTF2F1_SRF	1.51	1.782
NELFE_PML_TAF7	1.118	1.782
SIX5_STAT1_ZNF143	1.166	1.782

CBX3_GTF2B_USF1	1.473	1.782
ELK1_SIN3_SRF	1.456	1.782
CEBPB_GTF2F1_TBLR1	0.925	1.782
CEBPB_CTCFB_MAX	0.41	1.782
ELF1_STAT5_TRIM28	0.858	1.782
NRF1_PML_TBLR1	1.013	1.782
BCLAF1_E2F6_TAF7	1.288	1.782
CBX3_CEBPB_GTF2F1	1.095	1.782
CMYC_MAX_NELFE	1.046	1.779
CHD2_POL2_TAF7	0.45	1.327
GTF2B_POL2_RCOR1	0.49	1.284
MAX_POL2_TAF7	0.826	0.948
BCLAF1_IRF1_SP2	1.773	1.571
CTCFB_THAP1_YY1	1.773	1.711
CTCFB_ELF1_THAP1	1.773	1.741
PML_PU1_ZBTB33	1.773	NS
CTCFB_SP2_TAF1	1.773	1.519
GTF2B_MAZ_SMC3	1.773	NS
CTCFC_MAX_NR2F2	1.773	1.841
CMYC_NELFE_YY1	1.231	1.772
CJUN_ELF1_SIX5	0.788	0.984
CJUN_TAF1_TAF7	0.755	1.016
ETS1_NELFE_SIN3	1.51	1.77
MAX_STAT1_STAT2	0.147	1.77
E2F6_STAT2_ZNF143	1.137	1.77
CTCFB_IRF1_TRIM28	1.696	1.77
E2F6_EJUND_SRF	1.44	1.77
CBX3_GTF2B_TBLR1	1.23	1.77
MXI1_NELFE_YY1	1.925	1.77
MAX_PML_ZNF143	1.043	0.726
E2F4_ELF1_GABP	0.8	0.968
GTF2B_IRF1_POL2	0.553	1.214
CMYC_ETS1_NELFE	0.959	1.766
CTCFL_ETS1_IRF1	1.765	1.689
CEBPB_CTCFB_JUND	0.147	1.764
E2F4_ELK1_MXI1	1.44	1.764
ELF1_NELFE_TBLR1	0.925	1.764
CEBPB_ELK1_P300	1.51	1.764
BCLAF1_ELK1_GTF2F1	1.773	1.764
GTF2F1_RFX5_TAF7	2.34	1.764
ETS1_SRF_THAP1	1.205	1.764
SIX5_TBLR1_TRIM28	1.273	1.764

EJUND_SIX5_USF1	1.288	1.764
SIX5_TBLR1_TEAD4	1.41	1.764
BCLAF1_GTF2F1_P300	1.225	1.764
PML_PU1_SRF	1.395	1.764
CTCFC_ELF1_P300	0.858	1.764
ELF1_GTF2B_RFX5	2.925	1.764
CTCF_E2F6_ELK1	1.925	1.764
CBX3_PU1_RCOR1	0.999	1.764
JUND_THAP1_TRIM28	1.003	1.764
CEBPB_GTF2F1_NRF1	1.304	1.764
ELF1_GTF2B_STAT2	1.44	1.764
CBX3_GTF2F1_NELFE	1.051	1.764
CTCFL_EGR1_GABP	1.109	1.764
GABP_NRF1_TAF7	1.273	1.764
ELK1_IRF1_PU1	1.742	1.764
CEBPB_GTF2B_NRF1	1.456	1.764
CHD2_ELK1_TAF7	1.215	1.764
EJUND_NRF1_SIN3	1.032	1.764
IRF1_RFX5_TAF7	2.691	1.764
CEBPB_GTF2F1_TRIM28	1.205	1.764
EJUNB_ELF1_GTF2B	1.312	1.764
CTCFL_PML_ZNF143	1.188	1.764
JUND_NRSF_THAP1	1.205	1.764
ETS1_HMGN3_SP2	1.762	1.757
CJUN_GABP_THAP1	1.762	1.256
E2F4_IRF1_ZBTB33	1.762	NS
E2F4_GABP_MAX	0.977	0.784
CTCFB_MXI1_POL2	0.824	1.76
JUND_NRF1_TAF7	1.34	1.757
ETS1_JUND_NELFE	1.456	1.757
CMYC_SRF_STAT1	1.925	1.757
EGR1_GTF2B_STAT1	1.732	1.757
E2F4_NRF1_TAF7	1.34	1.757
MXI1_TAF7_TBLR1	1.147	1.757
GTF2F1_JUND_NELFE	1.41	1.757
CEBPB_GTF2F1_SIN3	1.137	1.757
PML_PU1_TEAD4	1.247	1.757
CBX3_E2F6_THAP1	1.025	1.757
EGR1_ELF1_STAT1	1.395	1.757
E2F6_GTF2B_PML	0.798	0.958
EJUNB_MAX_PML	1.755	1.464
ATF1_GTF2B_THAP1	1.755	1.519

CTCFC_MAZ_THAP1	1.755	NS
TAF7_YY1_ZBTB33	1.755	NS
ATF1_GTF2F1_USF1	1.755	1.436
EJUNB_EJUND_TAF7	1.755	1.519
CMYC_POL2_SIX5	0.882	0.872
NRSF_TAF1_TAF7	0.861	0.892
ELF1_PML_SP1	0.818	0.934
E2F6_GTF2B_NRF1	1.22	1.751
CMYC_ELF1_PML	0.711	1.038
GTF2B_POL2_TRIM28	0.943	0.804
JUND_MAX_THAP1	0.808	0.934
HMGN3_PU1_ZNF143	0.369	1.741
CHD2_MXI1_PU1	1.063	1.741
ATF1_CEBPB_TAF7	1.662	1.741
CMYC_P300_PU1	1.503	1.741
ELK1_GTF2B_HMGN3	1.372	1.741
CTCF_GTF2F1_JUND	1.732	1.741
ATF1_ELK1_GTF2F1	1.662	1.741
ETS1_GTF2F1_SRF	1.23	1.741
GTF2F1_STAT5_TBLR1	1.51	1.741
ATF1_ELK1_SIX5	1.8	1.741
BHLHE40_RFX5_TAF7	1.925	1.741
NELFE_TAF7_TBLR1	0.703	1.741
ELF1_STAT5_YY1	1.264	1.741
CTCFB_EGR1_ELK1	1.304	1.741
CTCFB_POL2_TRIM28	1.475	1.741
ELK1_GTF2B_NR2F2	1.732	1.741
BCLAF1_CBX3_SIX5	1.131	1.741
BCLAF1_ELF1_NRF1	1.063	1.741
GABP_TAF7_ZBTB7	1.428	1.741
CJUN_EJUND_GTF2F1	0.989	1.741
SRF_TAF7_ZNF143	1.247	1.741
MXI1_SP1_TAF7	1.225	1.741
EJUND_ELK1_SP1	0.925	1.741
BCLAF1_CTCFB_ZNF143	1.069	1.741
HMGN3_NELFE_PML	1.288	1.741
EJUND_JUND_SRF	1.23	1.741
BHLHE40_GTF2F1_SMC3	1.562	1.741
GTF2F1_THAP1_TRIM28	1.273	1.741
BHLHE40_GTF2B_STAT5	1.755	1.741
ELK1_MXI1_PU1	1.288	1.741
CBX3_GTF2F1_TBLR1	0.858	1.741

GTF2F1_SIN3_SMC3	1.41	1.741
BHLHE40_ELK1_GTF2B	1.8	1.741
CCNT2_GTF2F1_STAT5	1.466	1.741
CBX3_EGR1_PU1	0.843	1.741
GTF2F1_NR2F2_TBLR1	0.925	1.741
CCNT2_GTF2B_STAT5	1.843	1.741
CTCFL_ELF1_P300	0.925	1.741
PU1_SIN3_SP2	1.466	1.741
E2F4_GTF2F1_TAF1	0.925	0.813
CMYC_IRF1_ZBTB33	1.736	NS
GTF2F1_POL2_YY1	0.869	0.866
CMYC_EJUNB_ELK1	1.456	1.733
ELF1_RAD21_SP2	1.732	1.934
CTCFB_MAZ_THAP1	1.732	NS
CHD2_TAF7_ZBTB33	1.732	NS
MAFF_YY1_ZBTB33	1.732	NS
CJUN_E2F6_GTF2F1	0.783	1.732
CMYC_MXI1_THAP1	1.603	1.732
BHLHE40_E2F6_GTF2F1	0.797	0.934
MAX_POL2_TR4	1.162	1.73
BHLHE40_CJUN_TAF7	0.925	0.803
GTF2B_MAX_STAT2	1.847	1.727
ETS1_NRF1_TAF7	1.077	1.727
HMGN3_MAX_NELFE	1.719	1.727
NELFE_YY1_ZNF143	1.032	1.727
JUND_NELFE_PML	1.131	1.727
ETS1_MXI1_SIX5	1.262	1.727
E2F6_ELK1_TRIM28	1.366	1.727
CMYC_CTCFB_STAT5	1.569	1.725
GABP_STAT1_YY1	0.847	1.722
GTF2B_HMGN3_USF1	1.449	1.722
EGR1_TAF7_ZNF143	1.215	1.722
CTCFC_PML_ZNF143	0.925	1.722
TBLR1_THAP1_YY1	1.077	1.722
HMGN3_NRF1_TAF7	0.925	1.722
CEBPB_CMYC_CTCFB	0.972	1.722
ETS1_SP1_SRF	1.16	1.722
CEBPB_CJUN_PU1	1.51	1.722
E2F4_NELFE_TAF1	1.372	1.722
BCLAF1_ELK1_PML	1.147	1.722
ELK1_GTF2F1_MXI1	0.732	1.722
BCLAF1_MAX_THAP1	1.696	1.722

ATF1_ELF1_NRSF	1.003	1.722
CBX3_GTF2B_MXI1	1.428	1.722
GTF2F1_HMGN3_SRF	1.366	1.722
CTCFB_P300_PML	1.262	1.722
GTF2B_JUND_RFX5	2.51	1.722
CMYC_GTF2F1_NELFE	0.958	1.72
GTF2F1_PML_SIN3	0.88	0.839
CTCFB_GABP_SIX5	1.719	1.403
CTCFB_P300_YY1	1.086	1.718
ELK1_POL2_STAT1	0.818	1.718
CCNT2_GTF2B_TAF1	0.68	1.036
GTF2B_POL2_STAT1	1.592	1.716
CTCFB_MAZ_TAF7	1.714	NS
E2F4_GABP_ZBTB33	1.714	NS
GTF2F1_NELFE_TAF7	1.032	1.711
GABP_JUND_STAT1	0.925	1.711
CBX3_CTCFB_YY1	1.262	1.711
IRF1_NELFE_SIN3	0.788	1.711
CTCFL_GTF2B_PML	1.304	1.711
ETS1_HMGN3_STAT1	0.719	1.711
PML_TBLR1_USF1	0.989	1.711
E2F6_SMC3_TRIM28	1.358	1.711
CMYC_ELF1_ZNF143	0.735	0.974
TBLR1_USF1_YY1	1.077	1.706
CCNT2_GTF2F1_PML	0.874	0.832
BCLAF1_CMYC_SP2	1.706	1.72
CMYC_PU1_SIN3	0.765	1.704
SIN3_TAF7_TBLR1	0.992	1.704
E2F6_GTF2F1_NELFE	1.205	1.704
E2F6_GTF2B_NELFE	1.395	1.704
ELK1_POL2_PU1	1.588	1.704
EJUNB_GABP_PML	1.703	1.381
BCLAF1_CBX3_GTF2F1	0.925	1.699
E2F4_STAT5_TEAD4	1.44	1.699
GTF2F1_P300_SRF	1.553	1.699
ELF1_NR2F2_TRIM28	0.925	1.699
EJUND_MXI1_TAF7	1.273	1.699
EJUND_SRF_TBLR1	1.131	1.699
ETS1_SIX5_SRF	1.086	1.699
CBX3_SIN3_SRF	1.44	1.699
BCLAF1_GTF2F1_RCOR1	1.106	1.699
CBX3_GTF2B_STAT5	1.714	1.699

TBLR1_USF1_ZNF143	1.188	1.699
GTF2B_NR2F2_TAF7	1.428	1.699
ELF1_P300_STAT5	1.137	1.699
CEBPB_GTF2F1_MXI1	1.147	1.699
EGR1_GTF2F1_STAT5	1.288	1.699
CEBPB_SIN3_TAF7	1.086	1.699
ELF1_SRF_TAF7	1.395	1.699
JUND_PU1_TEAD4	0.925	1.699
P300_PU1_ZNF143	1.069	1.699
CJUN_GTF2B_TBLR1	0.995	1.699
MXI1_TBLR1_THAP1	1.34	1.699
EGR1_GTF2B_GTF2F1	0.797	0.899
MAX_SIN3_STAT1	0.748	1.696
EJUND_ELK1_YY1	0.588	1.696
GABP_POL2_SIX5	0.714	0.981
HMGN3_IRF1_THAP1	1.28	1.695
GTF2B_GTF2F1_POL2	0.8	0.894
MXI1_PML_THAP1	1.16	1.693
CEBPB_E2F6_TAF7	0.732	1.693
ETS1_MXI1_PU1	1.018	1.693
ATF1_PML_SIX5	1.137	1.693
CEBPB_CJUN_GTF2F1	0.51	1.693
EJUND_ELK1_SIN3	1.131	1.693
CBX3_E2F4_SIX5	1.247	1.693
CHD2_ELF1_STAT1	0.732	1.693
ELF1_ELK1_SP2	1.691	1.296
CTCFC_RCOR1_SP2	1.691	1.711
ELK1_TBLR1_ZNF143	1.691	0.934
CTCF_CTCFB_SP2	1.691	1.711
CTCF_CTCFB_THAP1	1.691	1.671
CTCFL_E2F4_TRIM28	1.691	1.349
ATF1_P300_SIX5	1.691	1.419
CTCF_RCOR1_SP2	1.691	1.934
CCNT2_CHD2_TAF7	1.077	1.689
MAX_NRSF_SIX5	1.063	1.689
ETS1_GTF2B_NELFE	1.34	1.689
CCNT2_NELFE_POL2	1.147	1.689
MAZ_SP1_TAF7	1.687	NS
CTCFB_ELK1_YY1	1.636	1.686
JUND_POL2_TR4	1.118	1.686
E2F4_GABP_JUND	0.744	0.934
GTF2F1_HMGN3_JUND	0.853	0.824

IRF1_PML_SRF	0.925	0.749
CCNT2_E2F4_GTF2F1	0.805	0.867
SP1_SRF_TBLR1	1.16	1.671
CCNT2_NELFE_YY1	1.557	1.671
ATF1_ELK1_PU1	1.247	1.671
BHLHE40_SIX5_SRF	1.466	1.671
CCNT2_ELK1_THAP1	1.41	1.671
ELK1_SP1_YY1	1.748	1.671
CBX3_GTF2B_STAT1	1.818	1.671
PU1_SIN3_TRIM28	1.366	1.671
CBX3_ELF1_STAT5	1.279	1.671
ETS1_MAX_NELFE	1.538	1.671
JUND_NELFE_ZNF143	0.925	1.671
ATF1_E2F4_NRSF	1.025	1.671
BHLHE40_TAF7_THAP1	1.188	1.671
CTCFL_PML_TRIM28	1.205	1.671
CJUN_GTF2F1_USF1	1.312	1.671
CTCFB_TBLR1_ZNF143	0.603	1.671
ATF1_CBX3_TAF7	1.372	1.671
ELF1_GTF2F1_RFX5	1.925	1.671
ETS1_NELFE_NRSF	1.41	1.671
ATF1_NRSF_SP1	1.247	1.671
CEBPB_ETS1_TAF7	1.069	1.671
GTF2B_MXI1_SRF	1.818	1.671
CHD2_ELF1_STAT5	1.23	1.671
CTCFB_ELF1_P300	0.719	1.671
ELK1_PML_PU1	1.719	1.671
GTF2F1_STAT1_STAT2	0.925	1.671
CEBPB_E2F6_SIN3	0.925	1.671
CMYC_CTCF_GTF2B	1.434	1.671
CEBPB_ELF1_STAT5	1.086	1.671
GTF2B_NRSF_SRF	1.372	1.671
CTCFB_CTCFC_GTF2F1	1.755	1.671
SP1_STAT1_STAT5	1.773	1.671
MXI1_PML_SIX5	1.069	1.671
CBX3_P300_SIX5	1.247	1.671
BCLAF1_IRF1_TAF7	1.716	1.671
SIN3_SP1_SRF	1.16	1.671
ELK1_NR2F2_P300	1.703	1.671
CJUN_PML_THAP1	0.861	1.671
GABP_GTF2F1_STAT2	1.773	1.671
MXI1_TAF7_TRIM28	0.925	1.671

ETS1_NRSF_PU1	0.843	1.671
SRF_TAF7_YY1	1.17	1.671
CHD2_SIX5_TBLR1	1.366	1.671
NRSF_SIX5_TAF1	1.317	1.671
ELK1_PU1_TRIM28	1.818	1.671
GTF2B_SIX5_ZBTB7	1.832	1.671
GTF2F1_NRSF_SRF	1.247	1.671
BCLAF1_ELK1_P300	1.625	1.671
CTCFL_EGR1_ZNF143	0.494	1.671
BHLHE40_CBX3_PU1	1.008	1.671
NRSF_PML_THAP1	1.003	1.671
ELF1_PU1_TEAD4	0.542	1.671
E2F6_GTF2F1_YY1	0.748	0.92
E2F4_ELF1_ZNF143	0.732	0.934
CMYC_E2F4_NELFE	1.041	1.664
E2F6_TAF1_TAF7	0.696	0.967
ELF1_GTF2F1_ZBTB33	1.662	NS
CTCFB_SIN3_SIX5	1.662	1.312
GTF2B_MAZ_STAT1	1.662	NS
GTF2B_JUND_MAFF	1.662	1.519
CTCFL_MAX_THAP1	1.662	2.049
CTCFB_GTF2F1_MAZ	1.662	NS
IRF1_TAF7_ZBTB33	1.662	NS
ATF1_ATF3_GTF2F1	1.662	1.612
GTF2B_PU1_RCOR1	1.662	1.612
EJUND_SIX5_TAF1	1.662	1.419
ATF3_THAP1_ZNF143	1.662	2.934
RCOR1_SIN3_SP2	1.662	1.519
CTCFC_JUND_NR2F2	1.662	1.934
GTF2B_HMGN3_POL2	0.861	0.8
NRF1_TBLR1_YY1	0.832	1.66
E2F4_IRF1_NELFE	1.42	1.66
IRF1_YY1_ZNF143	1.079	0.58
E2F6_GTF2F1_TRIM28	1.058	1.658
ELK1_IRF1_NRF1	0.925	1.656
ELK1_GTF2F1_SIN3	1.312	1.656
ELF1_JUND_ZNF143	0.551	1.104
E2F6_STAT2_TBLR1	1.372	1.654
CTCFB_IRF1_MXI1	1.529	1.654
E2F4_E2F6_NELFE	1.788	1.654
ELF1_POL2_STAT5	1.178	1.654
EGR1_GTF2B_YY1	0.575	1.077

POL2_YY1_ZNF143	1.051	0.601
ELF1_NRF1_TAF7	1.16	1.65
ELK1_ETS1_PU1	1.553	1.65
GTF2B_MAX_RFX5	2.51	1.65
CBX3_CTCFB_ELF1	0.971	1.65
GTF2B_JUND_NELFE	1.273	1.65
NR2F2_TAF7_YY1	1.378	1.65
BCLAF1_NRF1_YY1	1.266	1.65
CEBPB_IRF1_SRF	1.925	1.65
GTF2B_PML_TAF1	0.909	0.739
EJUND_MAZ_TAF7	1.648	NS
CBX3_ELK1_YY1	1.095	1.647
ELF1_GTF2F1_POL2	0.703	0.944
IRF1_POL2_ZNF143	0.941	0.706
MAX_PU1_YY1	0.633	1.013
E2F6_SIN3_STAT2	1.645	1.993
CJUN_GTF2F1_THAP1	1.395	1.644
SIN3_SRF_ZNF143	0.995	1.644
E2F4_EJUND_SRF	1.288	1.644
MXI1_PML_TAF7	0.767	1.644
EGR1_ELF1_NELFE	1.925	1.644
STAT1_TBLR1_ZNF143	1.147	1.644
CBX3_GTF2F1_USF1	1.428	1.644
JUND_NELFE_SIN3	1.077	1.644
HMGN3_PU1_TBLR1	0.838	1.644
ATF1_CBX3_GTF2B	1.312	1.644
HMGN3_STAT1_ZNF143	0.925	1.644
CEBPB_E2F6_PU1	0.8	1.644
HMGN3_SP1_SRF	1.008	1.644
CHD2_PU1_TBLR1	1.173	1.644
BCLAF1_GTF2F1_ZNF143	1.266	1.644
CMYC_SIN3_STAT1	1.125	1.644
E2F4_MXI1_THAP1	1.106	1.644
CTCFL_ETS1_PML	1.641	1.644
BCLAF1_GTF2B_SIN3	1.008	1.644
EGR1_GTF2B_STAT5	1.395	1.644
GTF2B_MXI1_TRIM28	1.562	1.644
JUND_MAX_NELFE	1.748	1.64
NRF1_TAF7_YY1	0.968	1.638
CTCFB_JUND_SP2	1.636	1.634
JUND_SIX5_SMC3	1.636	1.634
CTCFC_SP2_ZNF143	1.636	1.827

CTCF_SIX5_ZNF143	1.636	1.464
JUND_NR2F2_SMC3	1.636	1.634
CBX3_IRF1_NELFE	0.732	1.634
ELK1_MAX_THAP1	1.446	1.634
CMYC_EGR1_GTF2B	0.763	0.871
IRF1_MAX_ZNF143	1.073	0.557
GTF2B_STAT2_YY1	1.032	1.629
PU1_TRIM28_YY1	1.277	1.629
E2F6_SIX5_TBLR1	1.188	1.629
MXI1_POL2_TBLR1	1.073	1.628
GTF2F1_PML_STAT5	1.201	1.626
E2F6_GTF2F1_MAX	0.802	0.824
P300_PU1_SIN3	1.118	1.626
PML_STAT1_ZNF143	0.818	1.626
CCNT2_ELK1_GTF2B	1.188	1.626
JUND_TBLR1_THAP1	1.266	1.626
ETS1_STAT1_YY1	0.51	1.626
ETS1_SP2_TAF7	1.41	1.626
E2F4_JUND_NELFE	1.188	1.626
E2F4_TAF7_TRIM28	1.297	1.626
CTCFC_IRF1_SMC3	1.625	1.126
ELK1_P300_TAF1	1.625	1.287
MAX_ZBTB33_ZNF143	1.625	NS
ELF1_YY1_ZNF143	0.634	0.991
CCNT2_MAX_NELFE	1.118	1.622
GTF2F1_MXI1_TBLR1	1.288	1.622
ELF1_NELFE_POL2	1.41	1.621
CMYC_NELFE_PML	1.08	1.621
IRF1_STAT1_YY1	0.878	1.62
E2F6_GTF2F1_NRF1	1.166	1.62
GTF2B_MAZ_TAF7	1.619	NS
CMYC_ETS1_THAP1	1.003	0.616
IRF1_MXI1_SIX5	1.363	1.618
EJUND_GABP_THAP1	1.617	1.059
MAZ_PU1_SRF	1.617	NS
CJUN_SIX5_TEAD4	1.617	1.626
MAX_RAD21_SP2	1.617	2.197
EJUNB_PML_TRIM28	1.617	1.851
CMYC_STAT1_TBLR1	0.725	1.616
IRF1_YY1_ZBTB33	1.614	NS
JUND_NRSF_SRF	1.312	1.612
BCLAF1_GTF2B_RCOR1	1.312	1.612

GTF2F1_STAT5_TEAD4	1.312	1.612
IRF1_NELFE_ZNF143	1.003	1.612
CTCFC_EGR1_ZNF143	0.44	1.612
ELK1_TAF7_TEAD4	1.077	1.612
E2F4_TBLR1_THAP1	1.312	1.612
CBX3_ELF1_PU1	0.874	1.612
BHLHE40_ELF1_STAT5	1.147	1.612
GTF2B_NRSF_PU1	1.288	1.612
E2F4_RCOR1_SP2	1.44	1.612
GTF2B_NELFE_TAF7	1.032	1.612
CTCFB_MXI1_SIN3	1.23	1.612
JUND_SIX5_TRIM28	1.266	1.612
ELF1_GABP_STAT1	1.106	1.612
MAX_NELFE_ZNF143	0.732	1.612
E2F4_ELK1_SRF	0.925	1.612
ELK1_GTF2B_SRF	1.34	1.612
CBX3_SRF_TBLR1	1.34	1.612
RCOR1_TAF7_ZNF143	1.366	1.612
CEBPB_CTCFB_E2F4	0.773	1.612
CEBPB_MAX_PU1	0.886	1.612
GTF2F1_NELFE_ZNF143	0.773	1.612
JUND_NRSF_SIX5	1.106	1.612
CTCFB_POL2_PU1	0.978	1.612
CBX3_CTCFB_TBLR1	0.372	1.612
CTCFB_PML_ZNF143	1.013	1.612
GTF2F1_NR2F2_TRIM28	1.131	1.612
ATF1_CJUN_PU1	1.762	1.612
ELK1_NR2F2_TRIM28	2.188	1.612
ATF1_SP1_SRF	1.118	1.612
SP1_TAF7_TBP	1.118	1.612
CTCFL_EGR1_JUND	0.748	1.612
SIN3_SRF_TAF7	1.118	1.612
E2F4_SRF_TAF7	1.118	1.612
CTCFC_JUND_SMC3	0.375	1.612
E2F6_GTF2F1_PML	0.925	0.686
CTCFB_MAX_THAP1	1.611	1.65
CMYC_YY1_ZNF143	0.818	0.793
ELF1_GABP_IRF1	0.877	0.733
HMGN3_POL2_TAF7	0.708	0.9
GABP_IRF1_PML	0.88	0.726
IRF1_NELFE_POL2	1.321	1.606
IRF1_NELFE_PML	0.84	1.606

STAT1_TAF1_YY1	0.741	1.605
BCLAF1_POL2_SP2	1.603	1.168
P300_PML_PU1	1.155	1.601
CTCFB_POL2_STAT5	1.188	1.601
E2F4_E2F6_STAT2	1.273	1.601
HMGN3_NRSF_TAF7	0.829	1.601
CEBPB_GABP_POL2	1.08	1.6
CTCFL_EGR1_ELF1	0.755	1.597
CTCFB_YY1_ZNF143	0.843	1.597
NELFE_PML_ZNF143	0.44	1.597
GTF2F1_HMGN3_STAT1	1.188	1.597
SRF_TBLR1_ZNF143	1.247	1.597
EJUND_SIN3_SIX5	1.137	1.597
CHD2_TAF7_ZNF143	1.147	1.597
ETS1_TBLR1_USF1	0.714	1.597
ELF1_JUND_SMC3	0.68	1.597
E2F4_EGR1_NELFE	1.51	1.597
BCLAF1_JUND_TAF7	1.147	1.597
MAX_TAF7_ZBTB33	1.595	NS
GTF2B_MAZ_TBLR1	1.595	NS
HMGN3_STAT1_YY1	0.451	1.593
ATF1_MAX_NRSF	0.881	1.593
E2F6_GTF2B_USF1	0.652	1.593
IRF1_MXI1_TAF7	1.091	1.593
E2F6_EJUND_SIX5	1.162	1.593
ELK1_POL2_SP2	1.592	2.168
CMYC_IRF1_PML	0.571	1.018
CTCFC_CTCFL_NR2F2	1.588	2.256
GTF2F1_MAZ_SMC3	1.588	NS
CTCF_JUND_NR2F2	1.588	1.808
ELF1_MXI1_THAP1	1.23	1.586
CBX3_CTCFB_PML	1.384	1.586
GABP_GTF2B_NRF1	1.205	1.586
GTF2F1_JUND_STAT1	1.215	1.586
ELF1_TBLR1_THAP1	1.095	1.586
MAX_MXI1_NELFE	2.118	1.586
GABP_GTF2F1_TRIM28	1.34	1.586
CCNT2_SIX5_SP1	1.127	1.586
MAX_NELFE_TAF7	0.925	1.586
CJUN_ELK1_GTF2F1	1.273	1.586
CMYC_ETS1_PU1	1.038	1.583
POL2_TAF1_TAF7	0.717	0.863

GTF2F1_NELFE_SIN3	0.645	1.578
ELF1_JUND_STAT1	0.925	1.578
CMYC_NELFE_ZNF143	1.215	1.578
GTF2F1_MAZ_STAT5	1.577	NS
E2F4_GTF2B_ZBTB33	1.577	NS
ETS1_GTF2F1_STAT2	1.577	1.808
GABP_MAZ_TAF7	1.573	NS
ELF1_MAX_ZNF143	0.679	0.894
ELF1_MXI1_TAF7	1.137	1.571
CTCFB_GTF2B_RCOR1	1.312	1.571
CTCFC_ELF1_GTF2F1	1.732	1.571
ELK1_SIX5_TRIM28	1.625	1.571
MAX_PU1_TEAD4	0.727	1.571
E2F4_NELFE_TBLR1	0.34	1.571
E2F4_GTF2B_NR2F2	1.131	1.571
CBX3_EJUND_YY1	0.639	1.568
RAD21_RCOR1_SP2	1.562	1.671
ELF1_STAT1_YY1	0.864	1.562
CBX3_EJUND_ELK1	1.34	1.562
GTF2F1_NRF1_ZNF143	1.166	1.562
MAZ_THAP1_ZNF143	1.562	NS
CJUN_NR2F2_TAF7	1.562	2.033
HMGN3_SIX5_TRIM28	1.095	1.562
CTCF_CTCFL_ZNF143	-0.075	1.562
ELF1_GTF2B_NR2F2	1.173	1.562
CHD2_GTF2B_SRF	1.428	1.562
CHD2_TAF7_TRIM28	1.003	1.562
EGR1_EJUND_SIX5	1.147	1.562
GABP_NRSF_PU1	0.925	1.562
ELF1_HMGN3_STAT5	0.999	1.562
NRSF_SIN3_THAP1	0.925	1.562
ATF1_GABP_NRSF	1.008	1.562
SP1_SRF_ZNF143	1.095	1.562
BCLAF1_EJUND_ELF1	1.045	1.562
E2F4_MXI1_PU1	1.372	1.562
GTF2B_RFX5_TBLR1	2.34	1.562
EGR1_STAT1_ZNF143	1.273	1.562
P300_STAT1_ZNF143	0.81	1.562
E2F6_GTF2B_POL2	0.34	1.218
ELK1_TRIM28_YY1	1.317	1.558
CJUN_E2F6_GTF2B	0.481	1.558
GABP_SIN3_SRF	1.215	1.555

ETS1_SIN3_STAT1	0.684	1.555
CEBPB_ELF1_TBLR1	0.395	1.555
CJUN_SIX5_SRF	1.317	1.555
MAX_NRF1_TAF7	1.397	1.555
BHLHE40_P300_TAF7	1.279	1.555
E2F4_STAT1_ZNF143	0.925	1.555
GTF2B_HMGN3_STAT1	1.625	1.555
CEBPB_E2F6_ETS1	0.964	1.555
ATF1_GTF2B_NRSF	1.366	1.555
ETS1_SIX5_STAT1	1.51	1.555
EJUND_RCOR1_SIX5	1.051	1.555
GTF2B_IRF1_ZBTB33	1.553	NS
IRF1_SRF_ZNF143	1.047	1.553
HMGN3_P300_SP2	1.553	1.741
HMGN3_MAZ_NELFE	1.553	NS
ELF1_IRF1_MAX	0.813	0.738
MXI1_PML_PU1	0.851	1.55
E2F6_GABP_STAT1	1.51	1.55
ETS1_SP1_THAP1	1.304	1.55
GTF2F1_MAZ_TAF7	1.548	NS
CBX3_RCOR1_SP2	1.547	1.474
NRF1_TAF1_TBLR1	0.999	1.547
IRF1_SRF_STAT1	1.562	1.547
CEBPB_SIX5_TAF1	1.547	1.741
ELF1_GTF2B_ZBTB33	1.547	NS
BCLAF1_MAZ_PU1	1.547	NS
EJUND_ELK1_PML	1.173	1.547
CJUN_THAP1_ZNF143	1.547	1.14
CEBPB_MAZ_SIX5	1.547	NS
BCLAF1_SP2_TAF1	1.547	1.175
CEBPB_ELK1_IRF1	1.858	1.544
ELK1_POL2_THAP1	1.162	1.544
IRF1_JUND_POL2	0.827	0.717
NRSF_POL2_SIX5	1.308	1.544
GABP_RCOR1_THAP1	1.542	1.321
E2F4_GTF2F1_ZBTB33	1.542	NS
IRF1_JUND_SMC3	1.54	1.393
GTF2F1_IRF1_NR2F2	1.603	1.539
NELFE_POL2_ZNF143	0.732	1.539
HMGN3_IRF1_NELFE	2.077	1.539
GABP_SIN3_STAT5	1.538	1.644
BCLAF1_CMYC_NRF1	0.881	1.536

ELK1_HMGN3_IRF1	0.972	1.536
GTF2B_SIN3_TAF1	0.688	0.848
POL2_SIN3_SIX5	0.747	0.788
IRF1_SP1_SRF	1.222	1.535
CMYC_ELF1_SRF	0.681	1.534
ATF3_GTF2F1_IRF1	1.534	1.059
GTF2B_MAZ_MXI1	1.533	NS
ELF1_GABP_PML	0.659	0.871
CMYC_PU1_SP1	1.136	1.53
NELFE_POL2_TAF7	1.086	1.529
GTF2B_YY1_ZBTB33	1.529	NS
GTF2F1_MAX_POL2	0.769	0.76
GTF2F1_YY1_ZBTB33	1.528	NS
GTF2F1_NRSF_PML	0.703	0.824
EGR1_GTF2B_POL2	0.6	1.519
ELK1_MXI1_P300	1.288	1.519
ELF1_ETS1_STAT1	0.925	1.519
NELFE_SIN3_TAF7	0.81	1.519
PML_SRF_TAF7	1.173	1.519
CBX3_ELK1_GTF2F1	1.304	1.519
E2F4_ELK1_P300	1.225	1.519
EJUND_ELK1_IRF1	1.51	1.519
ELK1_IRF1_STAT1	2.51	1.519
CBX3_RCOR1_SIX5	1.127	1.519
BHLHE40_MXI1_TAF7	0.851	1.519
BCLAF1_CBX3_GTF2B	1.188	1.519
CTCFL_E2F4_ETS1	1.23	1.519
CJUN_PU1_TAF1	1.067	1.519
EJUND_ETS1_PU1	0.992	1.519
CBX3_CMYC_ELF1	0.54	0.979
E2F6_GTF2B_STAT1	0.8	1.519
CBX3_E2F6_SRF	1.641	1.519
CJUN_TAF7_THAP1	1.225	1.519
CBX3_JUND_PU1	0.925	1.519
BCLAF1_CBX3_E2F6	0.826	1.519
IRF1_SIN3_THAP1	1.104	1.519
CEBPB_E2F4_SIX5	1.312	1.519
CTCFC_E2F4_GTF2F1	1.51	1.519
ATF1_P300_TAF7	1.428	1.519
CTCFC_GTF2F1_JUND	1.51	1.519
GTF2F1_PML_STAT1	1.247	1.519
MXI1_NRF1_PML	0.691	1.519

CEBPB_CMYC_SRF	1.328	1.519
GTF2F1_P300_STAT1	0.925	1.519
E2F4_PML_STAT5	1.592	1.519
ELF1_MAX_STAT1	0.711	1.519
CBX3_SP1_SRF	1.428	1.519
CBX3_CTCFB_EGR1	1.247	1.519
ELF1_NRF1_THAP1	0.843	1.519
E2F6_STAT1_TBLR1	1.617	1.519
GTF2F1_NR2F2_ZNF143	1.372	1.519
CTCFC_CTCFL_ZNF143	-0.05	1.519
BCLAF1_GTF2F1_JUND	1.127	1.519
GTF2F1_SIX5_ZBTB7	1.662	1.519
ETS1_STAT1_ZNF143	0.826	1.519
ELK1_P300_TBLR1	1.466	1.519
CHD2_SIX5_SP1	1.247	1.519
CMYC_CTCF_GTF2F1	0.835	1.519
ELK1_JUND_SRF	1.247	1.519
P300_SIN3_SRF	1.247	1.519
BCLAF1_GTF2F1_HMGN3	1.366	1.519
PML_TAF7_USF1	1.247	1.519
GTF2B_PML_TEAD4	0.698	0.821
CTCFB_GTF2B_MAZ	1.51	NS
CCNT2_GTF2B_ZBTB33	1.51	NS
SP2_STAT5_YY1	1.51	2.156
CTCFL_JUND_SIX5	1.51	1.282
CTCFB_ELF1_SP2	1.51	1.741
P300_SIX5_TAF1	1.51	1.306
GABP_GTF2F1_ZBTB33	1.51	NS
CTCFB_MAX_SP2	1.51	1.175
SIN3_SP2_ZNF143	1.51	1.474
GTF2F1_PML_POL2	0.838	0.672
BCLAF1_ELF1_SP2	1.51	1.571
MXI1_POL2_TAF7	0.41	1.505
GABP_IRF1_STAT1	1.41	1.504
E2F4_ELK1_IRF1	1.533	1.503
IRF1_TAF7_USF1	1.452	1.502
IRF1_STAT1_ZNF143	1.423	1.502
GTF2F1_NR2F2_POL2	0.925	1.501
JUND_STAT1_YY1	0.662	1.501
CMYC_TAF7_ZBTB33	1.5	NS
GABP_STAT5_YY1	1.307	1.498
MAX_NRF1_TBLR1	1.308	1.498

IRF1_PU1_TEAD4	1.327	1.496
NELFE_PML_SIN3	0.755	1.493
CJUN_JUND_SRF	0.925	1.493
E2F6_ETS1_STAT1	1.714	1.493
CEBPB_CMYC_GABP	0.863	1.492
CMYC_CTCFB_MXI1	1.072	1.492
GTF2F1_JUND_POL2	0.62	0.871
JUND_MAX_ZNF143	0.597	0.894
GTF2F1_NELFE_POL2	0.401	1.491
E2F4_ELK1_SIN3	1.312	1.49
CTCFB_MAX_TRIM28	1.018	1.49
CMYC_HMGN3_NELFE	1.974	1.49
EGR1_GABP_PU1	0.882	1.49
EGR1_ETS1_PU1	0.711	1.49
E2F6_ELF1_STAT1	1.077	1.49
BCLAF1_GTF2F1_PML	0.868	1.49
SIN3_STAT1_YY1	0.847	1.49
ATF1_GTF2B_MAZ	1.489	NS
BCLAF1_GTF2F1_POL2	0.752	1.488
SIX5_TAF1_THAP1	1.487	1.104
EGR1_SIN3_THAP1	1.036	1.486
EJUND_ELF1_ELK1	0.925	1.486
EJUNB_ELK1_IRF1	2.304	1.486
SIX5_SP1_ZNF143	1.201	1.486
IRF1_STAT1_TBLR1	1.102	1.486
CCNT2_NELFE_PML	1.51	1.486
CMYC_MXI1_ZNF143	1.485	1.08
CMYC_JUND_PML	0.869	0.615
GABP_GTF2B_MAZ	1.484	NS
CTCFB_IRF1_PML	1.235	1.483
E2F4_ELF1_ETS1	0.577	0.906
CTCFB_E2F4_SIN3	0.767	1.481
CBX3_ELF1_SRF	1.201	1.481
CTCFB_E2F6_THAP1	1.481	2.033
ATF3_GABP_GTF2B	1.481	1.671
CBX3_ELK1_P300	1.273	1.481
POL2_TAF7_USF1	0.491	1.481
EGR1_PU1_TBLR1	1.188	1.481
GABP_P300_STAT1	1.025	1.481
GTF2F1_STAT2_TAF1	1.481	1.197
CTCF_CTCFB_ZNF143	0.27	1.481
CTCFB_CTCFL_ZNF143	-0.003	1.481

BHLHE40_CHD2_TAF7	1.056	1.481
RCOR1_TAF7_TBLR1	1.013	1.481
E2F4_EJUND_ELK1	1.041	1.481
BHLHE40_TAF7_USF1	1.077	1.481
BHLHE40_GTF2F1_TRIM28	1.086	1.481
GABP_SP1_THAP1	1.481	1.349
E2F4_NRF1_SIX5	1.086	1.481
SRF_TAF1_TAF7	1.247	1.481
ELK1_NRSF_TAF7	0.603	1.481
ELK1_P300_SP1	1.51	1.481
ELK1_IRF1_SRF	1.23	1.478
GABP_SIX5_TEAD4	1.478	1.436
MXI1_NRF1_YY1	0.478	1.478
GTF2B_MAX_NELFE	0.662	1.478
CTCFB_MXI1_TAF1	1.478	0.934
CMYC_SIN3_SRF	0.527	1.477
MXI1_TAF7_ZNF143	1.273	1.474
BCLAF1_GTF2F1_TBLR1	1.032	1.474
CEBPB_GTF2B_TBP	1.205	1.474
SIN3_SIX5_TEAD4	1.34	1.474
GTF2F1_TEAD4_THAP1	1.312	1.474
EGR1_GTF2B_SRF	1.428	1.474
CBX3_GTF2B_NRF1	0.925	1.474
BCLAF1_GTF2F1_SP1	1.466	1.474
BHLHE40_GTF2B_RFX5	2.925	1.474
MAX_TBLR1_THAP1	1.258	1.474
CBX3_GTF2B_NELFE	0.925	1.474
CBX3_PML_THAP1	0.992	1.474
MAX_NELFE_SIN3	0.855	1.474
ELK1_GTF2B_MAZ	1.473	NS
ELF1_POL2_ZNF143	0.398	1.075
GTF2B_MAX_ZBTB33	1.473	NS
CTCF_JUND_SIX5	1.473	1.282
PML_POL2_SRF	0.77	0.701
CMYC_POL2_STAT1	0.938	1.47
ATF3_GTF2B_GTF2F1	1.469	1.934
GTF2F1_IRF1_NELFE	0.925	1.468
CEBPB_ELK1_YY1	1.636	1.464
CBX3_E2F6_ELK1	1.147	1.464
ETS1_MAX_PU1	0.947	1.464
CTCFC_GTF2B_POL2	1.099	1.464
EGR1_GTF2B_MXI1	1.247	1.464

POL2_TBLR1_THAP1	0.899	1.464
CTCFC_IRF1_SIN3	1.21	1.464
CTCFL_EGR1_IRF1	1.327	1.464
MAZ_TAF7_TBLR1	1.461	NS
GTF2B_POL2_TEAD4	0.665	0.795
CJUN_CMYC_SRF	0.777	1.46
CMYC_ELF1_ELK1	0.969	1.459
E2F6_P300_TAF7	0.818	1.457
CBX3_CMYC_PU1	0.833	1.457
GABP_MXI1_PU1	1.188	1.457
SIN3_TAF7_ZNF143	1.036	1.457
E2F6_PU1_ZNF143	0.986	1.457
CBX3_EJUND_ZNF143	0.925	1.457
CEBPB_E2F4_GABP	0.925	1.457
GABP_MXI1_SIX5	1.23	1.457
E2F4_ELK1_YY1	1.259	1.457
CEBPB_ELK1_MAX	1.542	1.457
EJUND_MAX_SRF	1.147	1.455
BHLHE40_ETS1_TAF7	0.882	1.455
GTF2B_MAX_NR2F2	1.188	1.455
POL2_SRF_YY1	0.979	1.451
POL2_PU1_SIN3	0.925	1.45
ELK1_TAF1_ZNF143	1.449	1.145
ELK1_SIN3_YY1	0.874	1.448
CTCFC_ELF1_GABP	0.744	1.448
ELF1_ELK1_TRIM28	1.118	1.448
E2F4_GTF2F1_STAT1	1.215	1.448
BCLAF1_PML_TAF7	1.198	1.448
JUND_STAT1_ZNF143	1.018	1.448
ATF1_GTF2F1_NRSF	1.366	1.448
CBX3_GTF2F1_RCOR1	0.995	1.448
ELF1_ELK1_SRF	1.025	1.448
CTCFB_EGR1_GABP	1.025	1.448
GABP_JUND_STAT5	0.925	1.448
MAX_STAT1_ZNF143	1.209	1.448
NRSF_TAF7_ZNF143	0.992	1.448
JUND_MXI1_PU1	1.366	1.448
CCNT2_ELK1_SIX5	1.131	1.448
CMYC_GABP_STAT1	1.203	1.448
RCOR1_SIN3_SIX5	1.051	1.448
ETS1_P300_PU1	0.999	1.448
CEBPB_E2F4_TBLR1	0.51	1.448

BCLAF1_E2F4_GTF2F1	1.16	1.448
E2F4_ELK1_ZNF143	1.51	1.448
ELF1_SIX5_SRF	1.056	1.448
GTF2B_IRF1_STAT2	1.203	1.448
CMYC_ZBTB33_ZNF143	1.447	NS
E2F6_GTF2B_MAX	0.592	0.854
CBX3_MAZ_TAF7	1.446	NS
IRF1_STAT5_ZNF143	1.444	1.751
CCNT2_E2F4_TAF7	0.961	1.443
SRF_YY1_ZNF143	1.01	1.443
EJUND_ELK1_MAX	1.215	1.443
CTCFB_ELF1_GABP	1.041	1.441
MXI1_SIN3_TAF7	0.8	1.441
E2F4_NRSF_TAF7	1.067	1.441
CEBPB_ELF1_ETS1	0.792	1.441
NELFE_POL2_YY1	-0.209	1.44
EGR1_ELK1_ZNF143	1.44	1.275
CTCFB_EGR1_SIX5	1.44	1.349
CHD2_GTF2F1_PU1	1.44	1.321
MAZ_SRF_TAF7	1.44	NS
ETS1_GTF2F1_POL2	0.799	0.638
GTF2F1_NRSF_POL2	0.12	1.317
BCLAF1_BHLHE40_GTF2F1	1.288	1.436
CTCFL_EGR1_PML	0.989	1.436
NRSF_PML_SIX5	1.173	1.436
BCLAF1_CTCFB_E2F6	1.056	1.436
SP1_TAF7_TEAD4	1.247	1.436
CEBPB_CHD2_GTF2F1	0.925	1.436
CEBPB_GTF2B_HMGN3	1.366	1.436
GTF2B_STAT1_TEAD4	1.247	1.436
CBX3_CTCFB_P300	0.858	1.436
EGR1_PU1_SP1	1.201	1.436
CBX3_IRF1_SIX5	1.404	1.433
SRF_TBLR1_YY1	1.001	1.433
CMYC_TBLR1_THAP1	1.418	1.433
EJUND_SIX5_YY1	0.843	1.433
ELF1_MAZ_TAF7	1.432	NS
BCLAF1_TAF1_TAF7	1.432	1.321
GTF2F1_MAZ_THAP1	1.432	NS
CTCFB_JUND_SIX5	1.432	1.182
CTCF_E2F6_ZNF143	0.847	1.431
CEBPB_ETS1_GABP	0.925	1.431

ELK1_NR2F2_YY1	1.41	1.431
IRF1_SIN3_STAT1	1.321	1.431
GTF2B_IRF1_NELFE	0.925	1.431
GTF2F1_SIN3_TAF1	0.666	0.764
E2F6_POL2_TAF7	0.48	0.95
CTCFB_MAX_SIX5	1.43	1.156
POL2_TR4_YY1	1.61	1.43
CBX3_MAX_PU1	0.861	1.429
GTF2F1_MAX_STAT1	1.297	1.429
ELF1_ETS1_PU1	0.662	1.427
CCNT2_GTF2F1_POL2	0.646	0.78
CMYC_GTF2F1_STAT1	1.61	1.426
CCNT2_E2F6_GTF2B	0.955	1.425
ELK1_MAZ_P300	1.423	NS
BCLAF1_MAZ_SIX5	1.423	NS
IRF1_JUND_MAX	0.883	0.539
ELF1_NRF1_TBLR1	0.562	1.419
ETS1_GTF2F1_NRF1	1.297	1.419
MXI1_STAT1_YY1	0.818	1.419
GTF2F1_STAT1_TAF1	1.372	1.419
ELK1_ETS1_P300	1.008	1.419
ELK1_ETS1_SP1	1.428	1.419
ELF1_PML_STAT1	1.361	1.419
ELK1_MAX_NRF1	1.603	1.419
ELF1_IRF1_PML	0.686	0.733
MXI1_SIX5_YY1	0.709	1.419
CEBPB_GABP_PML	0.84	1.419
E2F4_ELF1_STAT1	0.818	1.419
CTCFB_JUND_YY1	0.818	1.419
MXI1_SIN3_SIX5	1.063	1.419
CBX3_GTF2F1_STAT1	1.577	1.419
HMGN3_SIX5_SP1	1.127	1.419
E2F4_P300_TAF7	1.262	1.419
HMGN3_MXI1_TAF7	0.533	1.419
CMYC_MAX_STAT1	0.989	1.417
CMYC_POL2_ZNF143	0.592	0.824
ELK1_IRF1_JUND	1.222	1.415
ELK1_MAX_PU1	1.492	1.412
CHD2_SIN3_SIX5	1.41	1.519
GABP_MAX_STAT1	0.978	1.41
GTF2F1_JUND_SP2	1.41	1.156
BCLAF1_GTF2B_MAZ	1.41	NS

CMYC_SIX5_STAT1	1.264	1.409
ELF1_MXI1_SIX5	1.118	1.408
E2F4_GTF2F1_TRIM28	1.109	1.408
HMGN3_SIX5_TBLR1	0.855	1.408
ATF1_CJUN_GTF2F1	0.8	1.408
ETS1_TAF7_TRIM28	1.095	1.408
HMGN3_NR2F2_YY1	0.691	1.408
CCNT2_MXI1_TAF7	0.603	1.408
NELFE_PML_YY1	0.613	1.406
ELF1_IRF1_THAP1	1.026	1.405
E2F6_IRF1_SMC3	1.404	1.09
P300_SIX5_SP1	1.34	1.403
CBX3_EGR1_ELK1	1.312	1.403
EGR1_P300_TAF7	1.069	1.403
CEBPB_GTF2B_TBLR1	0.826	1.403
TAF7_USF1_YY1	1.258	1.403
CJUN_POL2_SIX5	0.844	1.403
BHLHE40_GTF2F1_STAT1	1.077	1.403
E2F6_GTF2F1_POL2	0.642	0.761
CEBPB_E2F4_TAF7	1.008	1.403
JUND_NRF1_THAP1	0.925	1.403
GTF2B_HMGN3_PU1	1.279	1.403
P300_TAF7_ZNF143	1.247	1.403
ELK1_PML_SRF	1.562	1.403
CHD2_ELK1_P300	1.247	1.403
CMYC_NRF1_SIX5	1.453	1.403
GTF2F1_NELFE_NRSF	0.81	1.403
EGR1_TBLR1_THAP1	1.095	1.403
E2F4_SIX5_SRF	1.003	1.403
CBX3_CTCFB_E2F4	1.045	1.403
CCNT2_TBLR1_THAP1	1.473	1.403
ATF1_NELFE_POL2	0.818	1.399
ELK1_MAZ_ZNF143	1.399	NS
CJUN_E2F6_TAF7	0.871	1.399
BHLHE40_CCNT2_TAF7	1.015	1.399
TAF1_TAF7_ZBTB33	1.399	NS
GTF2B_MAZ_ZNF143	1.399	NS
GTF2F1_IRF1_ZBTB33	1.399	NS
E2F4_GABP_POL2	0.556	0.841
EGR1_ELK1_YY1	0.974	1.397
ATF1_CCNT2_TAF7	1.395	1.374
CTCFB_IRF1_SMC3	1.395	1.33

ELF1_PU1_SP1	0.979	1.393
SIN3_SRF_YY1	0.636	1.393
JUND_TAF7_TRIM28	1.166	1.393
CHD2_E2F4_TAF7	0.925	1.393
IRF1_MXI1_THAP1	0.967	1.393
CCNT2_GTF2F1_TRIM28	1.063	1.393
ELK1_PU1_TAF1	1.384	1.393
BCLAF1_ELF1_ZNF143	0.778	1.393
NRSF_TAF7_TBLR1	0.925	1.393
JUND_P300_PU1	0.925	1.393
CEBPB_ELF1_SIN3	0.551	1.393
CJUN_ELK1_PU1	1.147	1.393
E2F4_ELF1_PML	0.534	0.858
ETS1_GTF2B_MAZ	1.391	NS
CMYC_SRF_YY1	0.993	1.39
ETS1_GTF2F1_MXI1	0.982	1.388
GTF2F1_PML_TAF1	0.908	0.48
GABP_STAT5_ZNF143	1.384	1.644
BCLAF1_CMYC_CTCFB	1.065	1.384
GTF2B_TAF7_ZBTB33	1.384	NS
ETS1_MXI1_TAF7	0.805	1.381
GTF2B_NR2F2_ZNF143	1.372	1.381
E2F6_NRF1_TBLR1	1.003	1.381
GABP_MAZ_THAP1	1.38	NS
E2F4_MAX_PU1	0.95	1.379
E2F6_NRF1_SIX5	1.378	1.881
CTCFB_PML_SIX5	1.378	1.374
ELF1_MAX_STAT5	1.147	1.377
CCNT2_ETS1_SIX5	0.965	1.377
ELF1_TBLR1_ZNF143	0.703	1.377
GABP_SRF_YY1	1.175	1.377
CBX3_JUND_SRF	1.215	1.374
CJUN_ELK1_GTF2B	1.818	1.374
ELF1_SIX5_STAT1	1.166	1.374
GTF2F1_TBLR1_TRIM28	1.013	1.374
E2F4_GABP_STAT1	0.925	1.374
P300_SP1_TAF7	1.16	1.374
E2F4_SRF_ZNF143	0.788	1.374
BHLHE40_GTF2B_STAT1	1.384	1.374
EJUND_POL2_SRF	0.925	1.374
ATF1_CEBPB_ELF1	0.805	1.374
EGR1_GTF2F1_THAP1	1.34	1.374

GTF2B_TBLR1_TBP	1.018	1.374
CBX3_NRSF_TAF7	1.147	1.374
E2F4_ELF1_IRF1	0.789	0.584
ETS1_PU1_YY1	1.028	1.373
CMYC_GTF2B_ZBTB33	1.372	NS
CBX3_ELF1_ELK1	0.999	1.37
ETS1_JUND_SRF	1.166	1.37
ETS1_PML_TBLR1	0.773	1.37
ELF1_POL2_TBLR1	0.776	1.37
CEBPB_ETS1_YY1	0.986	1.368
CBX3_CMYC_THAP1	0.982	1.368
EGR1_ETS1_THAP1	0.971	1.367
CEBPB_E2F4_ELF1	0.835	1.367
E2F4_TBLR1_ZNF143	1.198	1.367
E2F6_NELFE_PML	1.317	1.367
ELF1_PML_TBLR1	0.651	1.367
E2F4_SP2_YY1	1.366	1.256
GTF2B_MXI1_TEAD4	1.366	1.086
GTF2B_JUND_ZBTB33	1.366	NS
CHD2_GABP_STAT5	1.366	1.349
ELK1_MAX_POL2	1.16	1.366
BCLAF1_TAF7_YY1	1.283	1.364
GTF2B_MAZ_SP1	1.363	NS
ETS1_PU1_TAF1	0.847	1.363
CBX3_GTF2B_MAZ	1.363	NS
CEBPB_E2F4_E2F6	0.687	1.361
CMYC_MXI1_PU1	0.976	1.361
CTCFB_IRF1_SIN3	0.956	1.361
ETS1_GTF2F1_SP2	1.361	1.33
E2F6_TBLR1_ZNF143	1.021	1.361
EGR1_PU1_YY1	0.304	1.36
MAZ_TAF7_USF1	1.358	NS
CTCFB_ELF1_IRF1	1.057	1.358
CMYC_SRF_TBLR1	0.616	1.356
CMYC_CTCFB_YY1	1.181	1.355
E2F4_ELK1_POL2	1.904	1.355
ELK1_ETS1_TRIM28	1.118	1.349
SIN3_SP1_TAF7	1.041	1.349
CBX3_E2F4_EJUND	1.147	1.349
E2F4_ELF1_ELK1	0.925	1.349
CEBPB_E2F4_SIN3	0.805	1.349
ETS1_P300_TAF7	0.925	1.349

BHLHE40_ELK1_P300	1.553	1.349
E2F6_ELK1_SP1	0.744	1.349
GTF2F1_MXI1_SP1	1.095	1.349
CJUN_GTF2F1_SIN3	1.083	1.349
CTCFB_CTCFC_ZNF143	0.232	1.349
E2F4_PU1_SP1	1.056	1.349
CEBPB_E2F6_GABP	0.773	1.349
EJUND_ELK1_POL2	1.113	1.349
ELK1_HMGN3_P300	0.925	1.349
IRF1_TBLR1_USF1	0.964	1.349
POL2_PU1_YY1	0.364	1.349
CBX3_EJUND_SIN3	0.814	1.349
CTCF_CTCFC_ZNF143	0.281	1.349
GTF2F1_TRIM28_ZNF143	1.201	1.349
MAX_NELFE_NRSF	1.095	1.349
CEBPB_GTF2B_SP1	1.466	1.349
JUND_NRF1_SIN3	0.662	1.349
JUND_SRF_TBLR1	0.986	1.349
CBX3_GTF2F1_NRF1	1.051	1.349
ATF1_TBLR1_ZNF143	0.851	1.349
MXI1_TAF1_TAF7	0.868	1.349
E2F6_PU1_TBLR1	1.177	1.349
E2F6_GTF2B_SP1	0.887	1.349
BCLAF1_ELF1_PML	0.697	1.349
ELF1_P300_PU1	0.925	1.349
CEBPB_GTF2B_SIN3	1.247	1.349
CJUN_POL2_ZNF143	0.47	1.349
BHLHE40_TAF7_TBP	0.925	1.349
CJUN_GTF2F1_ZNF143	1.041	1.349
NELFE_NRSF_PML	0.645	1.349
GTF2F1_NR2F2_PML	1.384	1.349
JUND_NRF1_ZNF143	0.925	1.349
CMYC_EJUNB_PML	1.346	0.91
CBX3_CMYC_ELK1	1.473	1.342
CJUN_MAZ_PU1	1.34	NS
CTCFB_E2F4_IRF1	1.34	0.899
BHLHE40_CJUN_PU1	1.34	0.934
ATF1_MAZ_TAF7	1.34	NS
MAZ_TAF7_ZNF143	1.34	NS
BCLAF1_MAZ_TAF7	1.34	NS
MAZ_P300_SIX5	1.34	NS
GTF2B_JUND_MAZ	1.34	NS

IRF1_JUND_PML	0.777	0.562
ELF1_IRF1_STAT1	1.018	1.338
E2F4_PU1_YY1	0.954	1.338
PU1_SP1_YY1	1.203	1.336
ATF1_IRF1_SRF	0.978	1.336
GTF2B_NELFE_YY1	0.925	1.336
HMGN3_SIN3_TAF7	0.815	1.334
CEBPB_ELF1_GABP	0.781	1.332
CBX3_ELF1_SIN3	0.851	1.332
ETS1_MXI1_THAP1	0.989	1.33
HMGN3_PML_THAP1	0.925	1.33
GTF2F1_JUND_TRIM28	1.109	1.33
MAX_MAZ_SIX5	1.33	NS
POL2_SRF_STAT1	1.366	1.33
ELF1_SIN3_SRF	0.778	1.33
CJUN_GTF2F1_TBLR1	0.723	1.33
MAX_SIN3_SRF	0.895	1.326
E2F4_SP1_SRF	0.992	1.326
ELF1_RCOR1_TAF7	1.201	1.326
GTF2F1_TAF1_USF1	1.326	0.934
ELF1_SP1_SRF	0.925	1.326
CHD2_MXI1_TBLR1	0.925	1.326
GTF2B_TAF1_USF1	1.326	1.223
E2F4_EGR1_PU1	0.652	1.326
JUND_SRF_ZNF143	0.984	1.326
E2F4_EGR1_ELK1	1.288	1.326
ATF1_JUND_SIX5	1.051	1.326
GABP_GTF2F1_NRF1	1.106	1.326
SIN3_SIX5_TBLR1	1.147	1.326
CBX3_ETS1_YY1	0.709	1.325
ETS1_IRF1_TBLR1	1.188	1.324
ATF1_CMYC_SRF	0.647	1.323
GABP_GTF2F1_MAZ	1.322	NS
CMYC_CTCFC_ZNF143	0.557	1.321
E2F4_E2F6_ELK1	0.855	1.321
E2F6_NRSF_TAF7	0.966	1.321
BCLAF1_CTCFB_MAZ	1.321	NS
CBX3_PML_SRF	1.51	1.321
MAZ_TAF7_THAP1	1.321	NS
CBX3_POL2_SRF	1.194	1.321
PML_SIX5_SRF	1.23	1.321
CBX3_CEBPB_GTF2B	1.013	1.321

MXI1_TAF7_YY1	0.703	1.318
MAX_STAT1_TBLR1	1.577	1.317
E2F4_ELK1_PML	1.297	1.317
CHD2_GTF2F1_ZBTB33	1.317	NS
JUND_MXI1_TBLR1	0.925	1.317
ATF3_GTF2B_IRF1	1.316	1.474
ATF1_CJUN_TAF7	0.781	1.312
E2F6_ETS1_SMC3	1.312	1.601
CBX3_EJUND_ETS1	0.976	1.312
CMYC_E2F4_PU1	0.868	1.312
CJUN_ELK1_SIX5	1.312	1.012
CHD2_ETS1_TAF7	0.874	1.312
ATF1_IRF1_SIX5	1.238	1.312
E2F4_MXI1_TBLR1	0.925	1.312
CMYC_MAX_SRF	0.523	1.311
CHD2_CMYC_SIX5	1.179	1.31
CMYC_CTCFB_IRF1	0.406	0.904
E2F4_STAT1_YY1	0.366	1.308
GTF2F1_MAX_NELFE	0.866	1.308
CCNT2_GABP_THAP1	1.308	0.934
MAX_MXI1_SIX5	1.328	1.308
E2F6_ELK1_GTF2F1	0.677	1.308
MXI1_PML_TBLR1	0.603	1.308
GTF2B_MAZ_USF1	1.308	NS
ELF1_POL2_SIX5	0.63	0.677
CEBPB_GABP_SIN3	0.662	1.306
E2F4_SIN3_SRF	0.861	1.306
E2F4_TAF7_TEAD4	1.045	1.306
CBX3_EJUND_TEAD4	0.879	1.306
ELF1_MXI1_PU1	0.925	1.306
PML_SRF_TBLR1	1.056	1.306
E2F4_ETS1_SRF	0.694	1.306
JUND_STAT1_TBLR1	0.925	1.306
EGR1_MXI1_TAF7	0.847	1.306
JUND_NRF1_TBLR1	0.744	1.306
MAX_SRF_YY1	0.909	1.304
MAZ_PU1_TBLR1	1.304	NS
GABP_PU1_TRIM28	1.304	1.374
CBX3_IRF1_PU1	1.266	1.303
IRF1_PML_THAP1	0.969	1.303
JUND_PML_YY1	0.629	0.673
IRF1_PML_YY1	0.782	0.52

CCNT2_E2F6_TAF7	1.171	1.301
CEBPB_CMYC_ELF1	0.789	1.301
NELFE_POL2_SIN3	-0.001	1.301
CCNT2_CMYC_NELFE	1.258	1.3
GTF2F1_MAZ_TBLR1	1.299	NS
CTCFB_JUND_MXI1	1.297	1.474
ATF1_CJUN_GTF2B	0.992	1.296
PML_TBLR1_ZNF143	0.67	1.296
GTF2F1_JUND_NRF1	1.127	1.296
CBX3_TAF7_TEAD4	1.069	1.296
ELF1_GTF2F1_NRF1	1.215	1.296
CHD2_MXI1_TAF7	0.584	1.296
CTCF_POL2_ZNF143	0.658	1.296
CBX3_P300_TAF7	1.173	1.296
GTF2F1_IRF1_STAT1	1.279	1.296
BHLHE40_ELK1_SIX5	1.51	1.296
POL2_STAT1_USF1	1.696	1.296
EJUND_ELF1_SRF	0.999	1.296
GTF2F1_NRF1_YY1	1.351	1.296
CTCF_JUND_ZNF143	0.269	1.296
CEBPB_E2F4_ETS1	1.025	1.296
TAF7_TBLR1_TEAD4	0.832	1.296
PML_SRF_ZNF143	0.858	1.296
MAZ_SIN3_SIX5	1.293	NS
GABP_MAX_PML	0.828	0.464
IRF1_MAX_NELFE	1.331	1.29
ELF1_GTF2F1_MAZ	1.288	NS
SP2_TAF1_TAF7	1.288	1.012
CTCFB_GABP_PML	1.288	1.271
EJUND_TBLR1_ZNF143	0.741	1.287
CBX3_MAX_THAP1	1.175	1.287
ATF1_GTF2F1_ZNF143	1.201	1.287
P300_SIN3_TAF7	0.864	1.287
GTF2F1_RCOR1_TBLR1	1.201	1.287
IRF1_MAX_YY1	0.66	0.627
E2F4_GABP_TEAD4	1.041	1.287
CMYC_SRF_THAP1	1.199	1.285
IRF1_MXI1_ZNF143	1.283	0.811
CCNT2_GTF2F1_MXI1	0.805	1.282
ELK1_IRF1_TBLR1	1.792	1.282
MAZ_P300_TAF7	1.281	NS
CMYC_TBLR1_USF1	0.365	1.28

E2F4_IRF1_MXI1	1.234	1.28
EJUND_POL2_ZNF143	0.812	1.28
POL2_STAT1_TBLR1	1.726	1.28
GABP_SIX5_TAF1	1.279	1.133
MAX_MXI1_TAF7	1.035	1.279
CJUN_P300_SIX5	1.279	1.419
ELK1_POL2_YY1	0.651	1.278
CBX3_IRF1_SRF	1.356	1.278
POL2_PU1_ZBTB33	1.277	NS
CMYC_ELK1_YY1	1.144	1.276
CBX3_CTCFB_ZNF143	0.925	1.275
ELK1_JUND_TRIM28	1.247	1.275
JUND_MAX_STAT1	0.726	1.275
CJUN_SP1_SRF	0.838	1.275
E2F6_ETS1_PU1	0.691	1.275
CBX3_GTF2B_NRSF	0.858	1.275
GABP_STAT5_TAF1	1.273	1.275
RCOR1_SP2_TAF1	1.273	0.764
GTF2F1_IRF1_MAZ	1.273	NS
CMYC_E2F4_ELK1	1.265	1.272
HMGN3_POL2_SIX5	1.467	1.272
PML_RCOR1_SIX5	1.188	1.271
GTF2B_GTF2F1_SP2	1.056	1.271
GABP_POL2_STAT1	1.177	1.271
CMYC_SRF_ZNF143	1.009	1.269
ELF1_SP1_TBLR1	0.636	1.268
IRF1_MXI1_TBLR1	1.277	1.268
CMYC_ELF1_PU1	1.12	1.267
MXI1_POL2_PU1	0.139	1.267
BHLHE40_E2F6_TAF7	0.781	1.266
GTF2F1_HMGN3_TBLR1	1.051	1.266
ETS1_NRSF_TAF7	0.845	1.266
ELF1_PU1_SIN3	0.596	1.266
IRF1_P300_PU1	1.466	1.265
CBX3_ELF1_ETS1	0.675	1.265
IRF1_PU1_SP1	1.331	1.265
CBX3_SIN3_YY1	0.68	1.262
EGR1_TAF7_YY1	0.666	1.261
ELK1_JUND_POL2	1.301	1.26
GTF2F1_MAZ_USF1	1.259	NS
IRF1_MAZ_TAF7	1.259	NS
GTF2F1_TAF1_THAP1	1.259	0.87

GABP_JUND_SRF	1.259	1.197
GABP_SIN3_THAP1	1.258	1.185
ATF3_GTF2F1_MAX	1.258	1.419
ATF3_GTF2B_JUND	1.258	1.349
GTF2F1_MAX_MAZ	1.257	NS
IRF1_SIX5_STAT1	1.617	1.256
BHLHE40_SIX5_TBLR1	1.127	1.256
CMYC_CTCFB_P300	0.619	1.256
GTF2B_P300_POL2	0.808	0.448
CTCF_MAX_ZNF143	0.726	1.256
CTCF_YY1_ZNF143	0.707	1.256
CBX3_TBLR1_ZNF143	0.43	1.256
GTF2B_GTF2F1_NELFE	0.744	1.256
EGR1_SIX5_TBLR1	0.992	1.256
E2F6_SIN3_TAF7	0.832	1.256
ELF1_ELK1_HMGN3	0.562	1.256
JUND_NRSF_TAF7	0.925	1.256
PU1_STAT1_YY1	1.34	1.256
E2F4_PML_THAP1	0.971	1.256
CCNT2_IRF1_THAP1	1.304	1.256
ELK1_MAX_TRIM28	1.273	1.256
E2F4_SIX5_TBLR1	0.861	1.256
CMYC_ELK1_SIN3	0.925	1.256
E2F4_ELF1_PU1	0.684	1.256
ETS1_MAX_THAP1	0.881	1.256
GABP_SP1_TBLR1	0.641	1.256
GTF2F1_MAZ_ZNF143	1.254	NS
IRF1_POL2_SIX5	0.659	0.595
GABP_PML_YY1	0.656	0.597
CBX3_EJUND_POL2	1.202	1.251
ELK1_IRF1_SIN3	1.106	1.25
ELK1_JUND_YY1	1.008	1.25
POL2_STAT1_YY1	-0.84	1.25
MAX_NELFE_YY1	0.586	1.249
GABP_GTF2B_SP2	1.247	1.287
ELF1_IRF1_POL2	0.559	0.688
ATF1_TAF7_YY1	1.317	1.247
ETS1_MAZ_SIX5	1.247	NS
GABP_PML_ZBTB33	1.247	NS
MAZ_SIX5_ZNF143	1.247	NS
JUND_SIN3_ZNF143	0.61	1.246
CMYC_GTF2B_NELFE	1.188	1.244

CCNT2_NRSF_TAF7	0.838	1.244
CEBPB_CTCFB_POL2	0.744	1.244
PML_POL2_ZNF143	0.495	0.749
ELK1_ETS1_GTF2F1	1.288	1.242
E2F4_GABP_MXI1	1.045	1.242
CBX3_EJUND_ELF1	0.882	1.242
E2F4_HMGN3_SIX5	1.072	1.242
ELF1_ETS1_ZNF143	0.667	1.239
CMYC_MAX_PU1	0.478	1.239
CJUN_IRF1_SRF	0.845	1.239
ATF1_ELF1_SIX5	0.984	1.239
CHD2_ELF1_SIX5	1.045	1.239
E2F4_HMGN3_STAT1	0.703	1.239
EGR1_RCOR1_SIX5	1.051	1.239
ETS1_TAF1_THAP1	1.239	0.983
BHLHE40_E2F4_PU1	0.925	1.239
ELK1_SIN3_TBLR1	1.34	1.239
ELF1_IRF1_SMC3	1.237	1.29
POL2_TAF7_TEAD4	1.528	1.237
ELF1_GTF2B_MAZ	1.236	NS
ELK1_PML_SIN3	0.925	1.236
EJUND_MAZ_SIX5	1.235	NS
GTF2B_MAZ_TRIM28	1.235	NS
E2F4_GABP_TBLR1	0.925	1.233
POL2_SIN3_SRF	0.666	1.233
ELK1_JUND_SIN3	1.056	1.233
PU1_SIN3_TAF1	0.815	1.233
BHLHE40_GABP_STAT1	0.8	1.233
MAZ_SP2_TAF7	1.23	NS
CHD2_GTF2B_ZBTB33	1.23	NS
GTF2B_MAZ_YY1	1.23	NS
CTCFC_E2F6_EGR1	0.803	1.229
GTF2B_SIN3_SP1	1.036	1.229
GTF2F1_NELFE_PML	0.843	1.229
GTF2B_MAX_MAZ	1.228	NS
JUND_NELFE_POL2	2.247	1.227
CMYC_ELK1_GABP	1.428	1.225
GTF2F1_RCOR1_YY1	1.225	0.934
PML_PU1_SP1	1.235	1.223
GTF2B_NRSF_TBLR1	0.843	1.223
CBX3_E2F4_ETS1	0.887	1.223
SIN3_TAF7_TRIM28	0.925	1.223

ELK1_GTF2F1_HMGN3	1.032	1.223
ELF1_PML_THAP1	1.035	1.223
ETS1_STAT1_TBLR1	0.826	1.223
GTF2F1_IRF1_NRF1	1.059	1.221
CMYC_MXI1_TBLR1	1.063	1.22
IRF1_SIN3_SRF	0.925	1.22
CBX3_E2F6_ZNF143	0.865	1.219
CBX3_CMYC_SRF	0.925	1.218
CJUN_SIN3_TAF7	0.864	1.218
GTF2B_NELFE_PML	0.62	1.218
IRF1_MAX_PML	0.571	0.646
ELK1_HMGN3_YY1	0.876	1.216
CBX3_GTF2B_POL2	0.599	0.617
CBX3_ELK1_POL2	1.043	1.216
GTF2B_HMGN3_PML	0.925	1.216
IRF1_TAF1_ZNF143	1.215	0.623
GTF2F1_TAF7_ZBTB33	1.215	NS
GABP_HMGN3_STAT1	0.719	1.214
ELF1_ELK1_SIN3	0.81	1.214
JUND_TBLR1_ZNF143	0.64	1.214
MAX_SP1_SRF	1.247	1.214
BCLAF1_E2F4_ELF1	0.783	1.209
BHLHE40_SIN3_TAF7	0.719	1.209
GTF2B_NELFE_SIN3	0.625	1.209
ELK1_ETS1_HMGN3	0.588	1.209
BHLHE40_GTF2B_MXI1	1.063	1.209
BHLHE40_JUND_PU1	0.788	1.209
GTF2B_TBP_ZNF143	0.925	1.209
EGR1_ELK1_IRF1	1.51	1.208
ATF1_MAX_SIX5	1.005	1.207
E2F4_PU1_TAF1	0.925	1.207
GTF2B_IRF1_NR2F2	1.247	1.205
GTF2B_POL2_SP2	0.658	1.205
ATF1_GTF2F1_MAZ	1.205	NS
ELF1_PML_YY1	0.472	0.733
EJUND_GABP_PML	1.025	1.205
GABP_MXI1_PML	0.76	1.204
CMYC_CTCFL_ZNF143	0.427	1.203
CMYC_CTCF_ZNF143	0.698	1.203
JUND_PU1_TRIM28	1.201	1.436
EJUND_IRF1_PU1	1.201	1.247
IRF1_POL2_SRF	0.996	1.2

ELF1_IRF1_YY1	0.571	0.629
ATF1_TAF1_TAF7	1.198	0.875
GTF2B_MAZ_NRF1	1.198	NS
EGR1_ELF1_ELK1	0.979	1.197
CBX3_E2F4_TBLR1	0.684	1.197
CMYC_SIN3_THAP1	0.912	1.197
CHD2_SIN3_TAF7	0.636	1.197
E2F6_TAF7_YY1	0.728	1.197
ELF1_MXI1_TBLR1	0.732	1.197
CBX3_E2F6_PU1	0.481	1.197
CMYC_CTCFB_ELF1	0.767	1.197
CEBPB_GTF2B_RCOR1	1.266	1.197
CBX3_GTF2F1_P300	0.866	1.197
CMYC_MXI1_TAF7	0.833	1.197
EJUND_TAF7_TEAD4	1.247	1.197
BHLHE40_CJUN_GTF2F1	0.684	1.197
ELF1_NRSF_YY1	0.379	1.197
ATF1_EJUND_ELF1	0.726	1.197
CBX3_GTF2F1_HMGN3	1.041	1.197
ELF1_ELK1_YY1	0.54	1.197
BCLAF1_GABP_YY1	1.16	1.197
E2F6_JUND_PU1	0.389	1.197
CHD2_GTF2B_HMGN3	0.703	1.197
CCNT2_ELF1_THAP1	0.884	1.197
ATF3_GTF2F1_JUND	1.196	1.349
GTF2F1_JUND_MAZ	1.193	NS
CMYC_GTF2F1_ZBTB33	1.192	NS
MAZ_POL2_SIX5	1.192	NS
GTF2F1_MAZ_MXI1	1.188	NS
ATF1_GTF2B_TAF1	1.188	0.886
POL2_SIX5_STAT1	1.361	1.188
E2F6_POL2_SIX5	1.433	1.187
POL2_SRF_TBLR1	0.925	1.187
GTF2F1_MXI1_ZNF143	1.077	1.185
CEBPB_GABP_JUND	0.677	1.185
GABP_GTF2F1_TEAD4	1.156	1.185
IRF1_MAX_STAT1	0.305	1.185
EGR1_ELK1_ETS1	0.992	1.185
POL2_SIN3_STAT1	1.005	1.185
BHLHE40_EJUND_SIX5	1.063	1.182
ATF1_CBX3_GTF2F1	1.008	1.182
ETS1_MAX_STAT1	0.925	1.182

ELK1_GABP_IRF1	1.122	1.18
GTF2B_MXI1_TAF1	1.179	0.934
POL2_TBLR1_YY1	0.556	1.179
CBX3_ELF1_ZNF143	0.755	1.179
CJUN_EGR1_GTF2F1	0.449	1.179
NRSF_SIN3_TAF7	0.684	1.179
E2F6_MAX_TAF7	1.01	1.178
E2F4_GTF2B_MAZ	1.178	NS
E2F4_ELK1_MAX	1.063	1.178
IRF1_MAZ_PU1	1.177	NS
E2F4_ELF1_SP2	1.177	1.012
CTCFC_MAX_ZNF143	0.51	1.175
CCNT2_IRF1_SIX5	1.092	1.175
CBX3_MAX_SRF	1.352	1.175
CBX3_E2F6_TBLR1	0.37	1.175
BHLHE40_GTF2F1_MXI1	0.861	1.175
CBX3_CTCFB_E2F6	0.856	1.175
BCLAF1_E2F6_ZNF143	0.925	1.175
BHLHE40_TBLR1_ZNF143	0.979	1.175
MAX_YY1_ZNF143	0.586	0.588
CTCF_ELF1_IRF1	1.173	1.033
GTF2F1_MAZ_YY1	1.172	NS
GABP_SIN3_ZNF143	0.821	1.171
CMYC_GTF2B_MAZ	1.169	NS
EGR1_IRF1_PU1	1.018	1.168
GABP_PML_TBLR1	0.742	1.168
ELF1_SP1_STAT1	1.051	1.168
CBX3_ELF1_YY1	0.562	1.167
GTF2B_TAF1_ZBTB33	1.166	NS
GABP_TAF1_THAP1	1.166	0.702
GABP_IRF1_SP1	1.166	0.685
BCLAF1_GTF2F1_MAZ	1.166	NS
PU1_TEAD4_YY1	0.925	1.165
EGR1_HMGN3_TAF7	0.722	1.165
ELF1_SIN3_THAP1	0.883	1.165
IRF1_MAZ_ZNF143	1.165	NS
E2F4_ELK1_ETS1	0.925	1.165
JUND_MAX_PML	0.657	0.508
CMYC_MAZ_TAF7	1.163	NS
HMGN3_NELFE_POL2	0.925	1.163
CBX3_PML_TBLR1	0.648	1.163
ELF1_SIN3_ZNF143	0.403	1.163

ELF1_ETS1_TBLR1	0.655	1.162
CMYC_STAT1_YY1	1.293	1.161
GTF2B_SIN3_ZBTB33	1.16	NS
CMYC_IRF1_STAT1	1.504	1.16
ELF1_MXI1_ZNF143	1.156	1.059
CTCFB_ELF1_JUND	0.501	1.156
ETS1_PML_SRF	0.868	1.156
BCLAF1_ELK1_YY1	1.225	1.156
CEBPB_ELF1_JUND	0.596	1.156
GTF2B_NRSF_ZNF143	0.858	1.156
ELK1_POL2_SP1	0.855	1.156
EGR1_ELK1_JUND	1.051	1.156
CBX3_ELK1_GABP	1.317	1.156
CBX3_CTCFB_JUND	0.75	1.156
EGR1_MAX_STAT1	0.703	1.156
ETS1_SP1_TBLR1	0.662	1.156
CEBPB_POL2_YY1	0.811	1.156
IRF1_SRF_TBLR1	1.166	1.156
EGR1_ELK1_TBLR1	1.225	1.156
CBX3_ETS1_TBLR1	0.569	1.156
EGR1_ELF1_ZNF143	0.538	1.156
GTF2F1_MXI1_P300	1.018	1.156
BHLHE40_JUND_THAP1	0.984	1.156
ELF1_SP1_THAP1	0.986	1.156
GTF2F1_MAX_ZBTB33	1.155	NS
EJUND_GABP_IRF1	1.155	0.934
IRF1_MAX_SRF	1.159	1.153
E2F4_POL2_SRF	0.608	1.152
CBX3_TBLR1_YY1	0.363	1.151
E2F4_POL2_STAT5	1.437	1.151
ELK1_TBLR1_YY1	0.984	1.151
CMYC_CTCFC_GTF2B	1.232	1.149
P300_PU1_YY1	0.925	1.149
CJUN_E2F4_SIX5	0.767	1.148
BHLHE40_GTF2B_HMGN3	0.971	1.148
CTCFB_E2F6_SIX5	1.147	1.078
GTF2B_MAX_RCOR1	1.147	0.665
SP1_TBLR1_YY1	0.802	1.147
POL2_PU1_SP1	0.993	1.147
CTCFB_GABP_POL2	1.147	1.277
ELF1_STAT5_TAF1	1.147	1.419
E2F4_NRF1_TBLR1	0.838	1.145

CBX3_ELK1_JUND	1.086	1.145
ETS1_PML_ZNF143	0.779	1.145
POL2_SP1_SRF	0.782	1.145
BHLHE40_CBX3_GTF2B	0.989	1.145
CTCFB_POL2_ZNF143	0.73	1.144
IRF1_SRF_YY1	1.297	1.144
GABP_PML_THAP1	1.141	1.175
STAT1_TBLR1_YY1	0.588	1.14
CMYC_ELK1_SRF	0.925	1.14
GABP_MAX_THAP1	1.139	0.699
MAZ_TAF7_TRIM28	1.139	NS
ELF1_GABP_JUND	0.424	0.715
JUND_POL2_ZNF143	0.296	0.842
ETS1_IRF1_STAT1	1.036	1.138
ELF1_ELK1_JUND	0.732	1.137
IRF1_POL2_TBLR1	0.728	1.137
E2F4_MAX_STAT1	0.748	1.137
EGR1_POL2_SIX5	0.33	0.806
BHLHE40_CBX3_GTF2F1	0.864	1.135
CTCFB_ELF1_YY1	0.71	1.135
E2F6_IRF1_STAT1	1.188	1.135
GTF2F1_SIN3_TRIM28	0.741	1.135
CCNT2_ELK1_GTF2F1	0.818	1.135
ELF1_ELK1_IRF1	0.957	1.135
CBX3_GTF2F1_MAZ	1.134	NS
ELK1_GABP_SIN3	1.051	1.133
POL2_PU1_TAF1	0.73	1.132
CTCFC_GABP_IRF1	1.131	0.792
MAZ_PML_SIX5	1.131	NS
MAX_NELFE_POL2	0.761	1.129
E2F4_POL2_PU1	1.034	1.129
CBX3_ETS1_SIN3	0.612	1.126
CBX3_NELFE_POL2	0.765	1.126
GTF2F1_RCOR1_ZNF143	0.986	1.126
MAX_P300_PU1	0.893	1.126
EGR1_GABP_ZNF143	0.714	1.126
CJUN_GTF2F1_TEAD4	0.529	1.126
GTF2B_POL2_STAT2	0.84	1.126
PML_SP1_TBLR1	0.677	1.126
ELK1_JUND_PML	0.972	1.126
IRF1_MAX_TBLR1	1.123	1.126
E2F4_JUND_SRF	0.925	1.126

GTF2B_NELFE_ZNF143	0.395	1.126
SIN3_YY1_ZNF143	0.436	1.126
GTF2F1_MAZ_TRIM28	1.124	NS
E2F4_MXI1_POL2	0.629	1.124
GTF2F1_P300_TAF1	1.123	0.934
CTCF_IRF1_ZNF143	1.123	1.045
EGR1_GTF2B_HMGN3	0.925	1.12
E2F4_ETS1_MXI1	0.739	1.12
POL2_TBLR1_ZNF143	0.826	1.119
CMYC_ELK1_IRF1	1.571	1.119
BHLHE40_GABP_THAP1	1.118	0.934
ETS1_POL2_PU1	0.725	1.118
CBX3_E2F4_SIN3	0.796	1.118
GTF2B_GTF2F1_MAZ	1.118	NS
MAZ_SIX5_SRF	1.118	NS
ELF1_SRF_YY1	0.627	1.117
GTF2B_HMGN3_SIN3	0.925	1.114
TBLR1_YY1_ZNF143	0.684	1.114
CMYC_IRF1_TBLR1	0.862	1.113
E2F4_GTF2B_P300	1.089	1.111
E2F4_ELF1_THAP1	1.1	1.111
EGR1_JUND_THAP1	0.788	1.111
ELF1_RCOR1_SP2	1.109	1.239
E2F4_MXI1_PML	0.835	1.109
ELK1_PML_POL2	0.263	1.109
CEBPB_ELF1_YY1	0.925	1.108
CMYC_E2F4_STAT1	1.143	1.108
ELF1_P300_PML	0.758	1.108
IRF1_SP1_TBLR1	0.79	1.107
CJUN_IRF1_ZNF143	1.06	1.107
ELK1_GABP_POL2	0.741	1.107
EGR1_SIX5_TAF1	1.106	0.993
IRF1_JUND_MXI1	1.042	1.106
ATF1_GTF2F1_TAF1	1.106	0.697
E2F6_GTF2F1_HMGN3	0.765	1.104
ETS1_SIN3_THAP1	0.796	1.104
CCNT2_JUND_THAP1	1.054	1.104
MAX_STAT1_YY1	0.269	1.104
E2F4_E2F6_PU1	0.815	1.104
CCNT2_SIX5_TAF1	1.103	1.223
CTCFB_MAZ_SIX5	1.102	NS
POL2_TBLR1_USF1	0.063	1.1

EJUND_ELF1_PML	0.739	1.1
GABP_MAZ_SIX5	1.099	NS
CMYC_GTF2B_NR2F2	1.133	1.097
CJUN_TAF7_TBLR1	1.008	1.097
ELF1_JUND_SRF	0.716	1.097
EGR1_ELK1_GABP	1.324	1.097
POL2_SRF_ZNF143	0.308	1.096
E2F4_MAZ_TAF7	1.095	NS
SIX5_TAF1_TBLR1	1.095	1.218
MAZ_PML_TAF7	1.095	NS
BHLHE40_MAZ_TAF7	1.095	NS
ELF1_ELK1_POL2	0.127	1.095
CEBPB_E2F6_ELF1	0.684	1.094
ELF1_GABP_TBLR1	0.543	1.094
CEBPB_ETS1_MAX	0.953	1.094
E2F4_E2F6_ZNF143	0.695	1.092
IRF1_PML_TBLR1	0.773	1.092
POL2_TAF7_TRIM28	0.836	1.092
E2F4_GABP_ZNF143	0.847	1.091
E2F4_SIN3_ZNF143	0.62	1.091
CJUN_GTF2B_SIN3	0.873	1.091
CTCFB_IRF1_SIX5	1.09	1.114
SIN3_SIX5_TAF1	1.09	1.059
CEBPB_GTF2B_MAZ	1.089	NS
CJUN_MAZ_TAF7	1.089	NS
POL2_TAF7_ZBTB33	1.087	NS
CMYC_ELK1_PML	0.925	1.087
CBX3_ELF1_TBLR1	0.574	1.086
ELF1_ETS1_PML	0.548	1.086
IRF1_THAP1_YY1	0.698	1.086
CBX3_ETS1_PML	0.679	1.086
E2F4_GTF2F1_NRSF	0.75	1.086
JUND_MAZ_TAF7	1.084	NS
IRF1_TBLR1_ZNF143	1.173	1.083
CEBPB_GABP_YY1	0.925	1.082
ELF1_ELK1_PML	0.709	1.082
EGR1_IRF1_STAT5	1.081	0.622
IRF1_MAZ_SIX5	1.081	NS
E2F4_ELF1_MXI1	0.744	1.081
ELK1_POL2_SIN3	0.429	1.081
CBX3_CHD2_GTF2F1	0.861	1.078
PML_STAT1_TBLR1	1.013	1.078

CBX3_E2F4_E2F6	0.416	1.078
CTCFC_IRF1_ZNF143	1.077	1.104
CBX3_MAZ_SIX5	1.077	NS
GABP_IRF1_TBLR1	0.812	1.076
CBX3_ELK1_MAX	1.258	1.076
E2F4_MAX_STAT5	1.456	1.076
GTF2F1_MAX_NRF1	1.444	1.075
CMYC_HMGN3_THAP1	1.025	1.075
GTF2F1_MAZ_SP1	1.073	NS
HMGN3_SIX5_TAF1	1.073	1.377
CMYC_TAF7_TEAD4	0.974	1.073
CMYC_ELK1_ETS1	0.79	1.073
ETS1_MAZ_THAP1	1.073	NS
ETS1_SIN3_ZNF143	0.44	1.071
CBX3_PML_ZNF143	0.851	1.071
ELF1_STAT1_TAF1	0.636	1.071
GTF2B_TBLR1_TEAD4	0.773	1.071
CMYC_EJUND_ELK1	1.147	1.071
ELK1_IRF1_PML	0.828	1.069
CMYC_RCOR1_SIX5	0.999	1.069
CJUN_ETS1_PML	0.395	1.068
MAZ_PML_SRF	1.067	NS
CMYC_SP1_SRF	1.212	1.066
CJUN_GTF2F1_P300	0.925	1.065
JUND_TAF7_TEAD4	0.925	1.065
PML_SIN3_SRF	0.871	1.065
ATF1_E2F6_GTF2F1	1.063	1.094
ELK1_GABP_JUND	1.072	1.063
MAX_MAZ_TAF7	1.06	NS
BCLAF1_NRF1_POL2	0.737	1.059
ATF3_ELF1_GTF2F1	1.058	0.934
CMYC_SIN3_ZNF143	0.958	1.058
GTF2F1_POL2_TAF1	0.235	0.822
CMYC_MAZ_SIX5	1.056	NS
JUND_MAZ_SIX5	1.056	NS
GTF2B_GTF2F1_ZBTB33	1.056	NS
E2F4_ETS1_TBLR1	0.716	1.056
CHD2_GTF2B_ZNF143	0.814	1.054
CCNT2_GTF2B_HMGN3	0.748	1.052
BCLAF1_CMYC_GABP	0.994	1.051
CCNT2_GTF2B_POL2	0.444	0.607
E2F4_ELK1_JUND	0.925	1.049

JUND_TAF7_TBP	0.773	1.049
CCNT2_PML_THAP1	0.883	1.049
EGR1_TAF1_TAF7	0.684	1.049
ELF1_ELK1_TBLR1	1.173	1.049
GTF2B_P300_TAF1	1.047	0.881
ELF1_MAX_PU1	0.777	1.047
PML_SIN3_ZNF143	0.562	1.046
EJUND_ELF1_ZNF143	0.557	1.045
E2F6_SIX5_TAF1	1.045	1.059
EJUND_ELF1_TBLR1	0.581	1.045
GTF2F1_NRF1_POL2	0.322	1.044
ELF1_IRF1_SRF	0.984	1.043
CMYC_CTCFB_ZNF143	0.527	1.042
CEBPB_EJUND_IRF1	1.041	1.063
GTF2B_SIN3_TEAD4	0.925	1.041
GTF2F1_TAF1_ZBTB33	1.041	NS
BHLHE40_CJUN_GTF2B	0.684	1.041
ELF1_HMGN3_SP2	1.041	1.156
CMYC_JUND_SMC3	0.793	1.041
CMYC_E2F4_MXI1	0.847	1.039
CEBPB_ELF1_MAX	0.498	1.038
ELF1_MAX_PML	0.45	0.588
GTF2B_IRF1_MAZ	1.038	NS
EGR1_POL2_TAF7	0.184	1.038
ELF1_GABP_POL2	0.449	1.038
ELF1_HMGN3_SIX5	0.845	1.037
GTF2B_JUND_NRSF	0.75	1.037
EGR1_HMGN3_SIX5	1.036	1.197
CEBPB_GTF2F1_MAZ	1.036	NS
EGR1_GTF2B_SIN3	0.75	1.033
PML_TAF7_TRIM28	0.8	1.033
MAZ_SIX5_TBLR1	1.032	NS
CMYC_PML_TBLR1	0.605	1.032
JUND_MAZ_THAP1	1.032	NS
MAX_TAF7_USF1	1.23	1.03
ETS1_GTF2F1_TEAD4	0.829	1.03
EGR1_GTF2F1_TBLR1	0.866	1.03
EGR1_GTF2F1_YY1	0.468	1.028
MAZ_SIX5_SP1	1.028	NS
ELF1_ELK1_ETS1	0.641	1.027
E2F6_POL2_STAT1	1.06	1.025
CEBPB_PML_YY1	0.855	1.023

ETS1_GABP_ZNF143	0.662	1.021
JUND_PML_TBLR1	0.51	1.021
CMYC_GTF2B_RCOR1	1.02	1.344
E2F4_GABP_HMGN3	0.893	1.019
BCLAF1_E2F6_ELF1	1.025	1.019
CBX3_IRF1_TBLR1	0.748	1.019
MAX_NELFE_PML	0.874	1.016
GTF2B_TAF1_TRIM28	1.015	0.934
CEBPB_GABP_MAX	0.68	1.014
GABP_JUND_ZNF143	0.716	1.012
ELF1_ELK1_GABP	0.835	1.012
E2F4_PML_TBLR1	0.722	1.01
ETS1_GTF2F1_MAZ	1.009	NS
CJUN_SP1_STAT5	1.008	0.846
CMYC_ETS1_TBLR1	0.735	1.007
EGR1_YY1_ZNF143	0.458	1.005
EGR1_ETS1_GABP	0.525	1.004
CMYC_MAZ_SRF	1.003	NS
ELK1_IRF1_YY1	1.083	1.002
ELK1_PML_YY1	0.679	1.002
GTF2F1_MAZ_P300	1.001	NS
CBX3_GTF2F1_SP1	0.989	1.001
E2F4_IRF1_SRF	0.89	1.001
E2F4_PML_SRF	0.864	1.001
POL2_SP1_TBLR1	0.728	0.999
ELF1_MXI1_PML	0.469	0.999
CMYC_ELF1_STAT1	1.265	0.998
CBX3_GTF2F1_TEAD4	0.652	0.998
ELF1_POL2_PU1	0.149	0.998
ELF1_MAZ_THAP1	0.997	NS
E2F6_GTF2F1_SP1	0.997	0.827
ELF1_POL2_STAT1	0.972	0.994
JUND_SIX5_TAF1	0.994	0.934
MXI1_TBLR1_YY1	0.747	0.994
ETS1_TAF7_TEAD4	0.978	0.993
E2F4_MXI1_YY1	0.652	0.993
CJUN_SIN3_SIX5	0.925	0.993
IRF1_POL2_YY1	0.27	0.721
CTCFC_EGR1_IRF1	0.963	0.99
ELF1_IRF1_TBLR1	0.633	0.989
E2F4_POL2_STAT1	-0.107	0.988
ELK1_ETS1_SIN3	0.588	0.988

PML_POL2_YY1	0.154	0.832
CMYC_ELK1_JUND	1.381	0.986
ELF1_MAZ_SIX5	0.986	NS
CHD2_GTF2F1_HMGN3	0.835	0.986
GABP_MAX_STAT5	1.239	0.986
EGR1_STAT1_YY1	0.553	0.986
BHLHE40_ELF1_SIX5	0.925	0.986
MAZ_SIX5_TAF1	0.984	NS
CJUN_EGR1_GTF2B	0.562	0.984
CJUN_E2F4_TAF7	0.478	0.984
ELK1_ETS1_JUND	0.805	0.983
ELK1_GABP_YY1	0.891	0.983
ETS1_GABP_YY1	0.641	0.983
PML_TAF7_TEAD4	0.813	0.983
BHLHE40_CMYC_SIX5	0.848	0.983
CBX3_CTCFB_MAX	0.553	0.983
CCNT2_E2F6_GTF2F1	0.677	0.982
GABP_TBLR1_YY1	0.662	0.981
CMYC_ELK1_MAX	0.972	0.981
CTCFB_E2F4_YY1	1.156	0.978
CBX3_E2F4_PML	0.668	0.978
CMYC_SP1_TBLR1	0.542	0.978
E2F4_EGR1_GABP	0.61	0.978
E2F4_ETS1_ZNF143	0.714	0.978
EJUND_PML_YY1	0.624	0.977
ETS1_POL2_TBLR1	0.113	0.977
CJUN_EJUND_GTF2B	0.866	0.977
CHD2_GTF2B_PML	0.639	0.974
TAF1_TAF7_TRIM28	0.974	0.934
ELF1_TBLR1_YY1	0.332	0.974
ETS1_PML_SP1	0.687	0.973
MAZ_TAF1_TAF7	0.972	NS
CJUN_SIX5_TAF1	0.972	0.623
JUND_MXI1_PML	0.887	0.971
PML_TBLR1_YY1	0.579	0.97
ELF1_GABP_ZNF143	0.711	0.969
GTF2B_MAZ_RCOR1	0.969	NS
GABP_IRF1_P300	0.969	0.934
CJUN_GTF2B_MAZ	0.969	NS
MAX_TAF7_TEAD4	1.087	0.969
CMYC_IRF1_SMC3	0.968	0.982
MAX_PU1_SIN3	0.782	0.968

GTF2B_MAZ_P300	0.965	NS
GTF2B_MAZ_TEAD4	0.965	NS
BHLHE40_GTF2B_MAZ	0.964	NS
JUND_TAF1_THAP1	0.963	0.565
EJUND_GABP_YY1	0.743	0.963
E2F4_E2F6_GABP	0.773	0.962
E2F4_MAZ_SIX5	0.96	NS
BHLHE40_GTF2F1_MAZ	0.96	NS
CMYC_STAT1_ZNF143	0.952	0.958
ETS1_MAZ_TAF7	0.956	NS
IRF1_PML_ZBTB33	0.953	NS
CMYC_ELK1_POL2	1.019	0.95
ELK1_MAX_YY1	0.878	0.95
CTCFB_IRF1_TAF1	0.949	0.651
CMYC_PU1_YY1	0.798	0.949
E2F6_GTF2F1_MAZ	0.948	NS
CMYC_MAX_PML	0.591	0.348
MAX_POL2_ZNF143	0.191	0.745
MAX_SP1_TBLR1	0.758	0.934
CBX3_EGR1_YY1	0.68	0.934
CBX3_CJUN_GTF2F1	0.547	0.934
ETS1_SIN3_TBLR1	0.432	0.934
EGR1_GABP_YY1	0.271	0.934
ELF1_PML_SRF	0.925	0.934
BCLAF1_ELK1_IRF1	1.641	0.934
ETS1_POL2_ZNF143	0.1	0.934
CJUN_GTF2B_TEAD4	0.478	0.934
STAT1_YY1_ZNF143	0.794	0.934
E2F6_IRF1_TBLR1	0.571	0.934
CBX3_ETS1_GABP	0.81	0.934
CMYC_GTF2F1_NRF1	1.104	0.934
ETS1_GABP_JUND	0.749	0.934
ELK1_GABP_PML	0.925	0.934
CEBPB_E2F4_YY1	1.08	0.934
MAX_TBLR1_ZNF143	0.847	0.934
ELK1_MAX_SIN3	0.855	0.934
MAX_SIN3_THAP1	0.902	0.934
CJUN_E2F4_GTF2F1	0.562	0.934
CJUN_TBLR1_ZNF143	0.378	0.934
ELF1_SIN3_TBLR1	0.375	0.934
E2F4_GTF2F1_NRF1	0.732	0.934
EGR1_ELK1_MAX	1.047	0.934

CJUN_EJUND_SIX5	1.22	0.934
IRF1_STAT5_YY1	1.656	0.934
CTCFB_MAX_ZNF143	0.557	0.934
ELF1_GABP_P300	0.616	0.934
ELK1_ETS1_IRF1	1.16	0.934
CBX3_EJUND_IRF1	0.686	0.934
CMYC_E2F4_SRF	0.623	0.934
ELF1_JUND_TBLR1	0.403	0.934
GTF2F1_TAF1_TRIM28	0.925	0.934
E2F6_MAZ_SIX5	0.925	NS
GABP_MAZ_PU1	0.925	NS
GTF2B_PML_ZBTB33	0.925	NS
E2F4_GABP_SP1	0.925	0.934
MAZ_PML_PU1	0.925	NS
JUND_MAZ_SRF	0.925	NS
CJUN_GTF2F1_MAZ	0.925	NS
IRF1_TBLR1_YY1	0.729	0.922
ELK1_IRF1_MAX	1.458	0.918
CMYC_CTCFB_JUND	0.448	0.918
CBX3_POL2_TBLR1	0.855	0.916
IRF1_JUND_TBLR1	0.579	0.916
ETS1_TBLR1_YY1	0.742	0.913
ETS1_MAX_TBLR1	0.771	0.91
CMYC_PML_YY1	0.366	0.544
EGR1_GTF2F1_IRF1	0.908	0.542
EJUND_IRF1_TBLR1	0.892	0.906
CMYC_POL2_SRF	0.646	0.906
E2F6_ELF1_TBLR1	0.573	0.906
E2F6_ELF1_ZNF143	0.562	0.905
CMYC_TBLR1_ZNF143	0.59	0.901
CCNT2_GTF2F1_SIN3	0.732	0.9
E2F4_GTF2F1_MAZ	0.899	NS
EJUND_IRF1_PML	0.668	0.899
PML_SIN3_TBLR1	0.553	0.896
ATF1_ELF1_PML	0.529	0.895
CMYC_GTF2F1_MAZ	0.894	NS
CBX3_EJUND_MAX	0.949	0.894
ELF1_GABP_MXI1	0.727	0.893
EGR1_JUND_ZNF143	0.414	0.892
E2F4_ELF1_TBLR1	0.567	0.892
CHD2_CMYC_GTF2B	1.198	0.891
CBX3_CMYC_EJUND	0.997	0.891

GTF2F1_SP1_TAF1	0.891	0.815
IRF1_SIN3_ZNF143	0.947	0.891
CJUN_JUND_ZNF143	0.51	0.891
CMYC_ELF1_GABP	0.527	0.89
CMYC_TBLR1_YY1	0.828	0.89
ELK1_IRF1_POL2	0.483	0.889
GTF2F1_NRSF_SIN3	0.612	0.889
BHLHE40_GTF2F1_SIN3	0.722	0.889
GTF2B_NRSF_SIN3	0.716	0.888
GTF2B_JUND_TBP	0.662	0.886
ETS1_JUND_PML	0.593	0.886
GTF2F1_JUND_TEAD4	0.778	0.883
MAX_TBLR1_YY1	0.66	0.882
CHD2_E2F4_GTF2B	0.832	0.881
EGR1_GTF2F1_ZNF143	0.826	0.881
CBX3_ELK1_IRF1	1.535	0.879
CTCFB_IRF1_MAZ	0.878	NS
IRF1_POL2_STAT1	0.063	0.877
CBX3_YY1_ZNF143	0.851	0.874
GTF2B_TEAD4_ZNF143	0.814	0.872
ETS1_GABP_SIN3	0.517	0.871
HMGN3_MAX_THAP1	0.852	0.868
GTF2B_MAZ_SIN3	0.868	NS
SIN3_THAP1_YY1	0.633	0.868
CMYC_GTF2F1_TEAD4	0.657	0.868
GTF2B_MAZ_PML	0.867	NS
CMYC_ETS1_PML	0.84	0.865
GTF2B_HMGN3_MAZ	0.864	NS
CMYC_IRF1_TAF1	0.864	0.335
GABP_IRF1_MAX	0.861	0.342
GTF2B_NRSF_PML	0.582	0.86
CMYC_ELF1_TBLR1	0.737	0.86
CMYC_JUND_YY1	0.797	0.858
EJUND_MAX_TBLR1	0.597	0.858
ELF1_NRSF_PML	0.559	0.858
ELF1_ELK1_MAX	0.622	0.857
GTF2F1_IRF1_TEAD4	1.17	0.854
MAX_PML_POL2	0.591	0.262
IRF1_TAF7_TBP	0.95	0.853
ETS1_GTF2F1_NRSF	0.727	0.851
ELK1_GABP_MAX	0.985	0.851
E2F6_PML_TBLR1	0.51	0.851

CTCFB_E2F6_GABP	0.851	1.104
GABP_IRF1_TAF1	0.85	0.392
CMYC_CTCFB_ELK1	1.292	0.85
GTF2B_MAZ_TAF1	0.85	NS
CBX3_GTF2F1_TAF1	0.849	0.671
GTF2F1_MAZ_TAF1	0.848	NS
E2F6_ETS1_TBLR1	0.639	0.848
GTF2B_HMGN3_TAF1	0.847	0.818
EJUND_ELF1_GABP	0.662	0.846
CMYC_THAP1_YY1	0.776	0.845
CJUN_ELF1_ZNF143	0.055	0.844
CHD2_GTF2B_IRF1	0.717	0.844
EGR1_MAZ_SIX5	0.843	NS
CBX3_ELF1_POL2	0.516	0.843
ELF1_GABP_YY1	0.331	0.841
IRF1_MAX_TAF1	0.841	0.109
ETS1_IRF1_PML	0.639	0.841
IRF1_TAF7_TEAD4	0.977	0.839
EGR1_GTF2F1_SP1	0.838	0.711
E2F4_TBLR1_YY1	0.749	0.838
E2F6_POL2_TBLR1	0.392	0.836
TAF7_TEAD4_YY1	0.807	0.834
ELK1_MAX_PML	1.178	0.832
ELK1_JUND_MAX	1.014	0.831
GTF2F1_HMGN3_IRF1	1.191	0.829
GTF2F1_TEAD4_YY1	0.773	0.829
CCNT2_MAZ_TAF7	0.828	NS
CMYC_GTF2F1_HMGN3	0.58	0.827
CBX3_ETS1_MAX	0.73	0.827
ELF1_SP1_YY1	0.504	0.824
GTF2F1_MAZ_PML	0.824	NS
CJUN_MAX_STAT5	0.595	0.823
CBX3_ELF1_JUND	0.591	0.821
CMYC_ETS1_STAT1	1.293	0.821
GTF2F1_MAZ_POL2	0.821	NS
PML_THAP1_YY1	0.925	0.818
ETS1_PML_SIN3	0.687	0.818
E2F6_GTF2B_MAZ	0.817	NS
GTF2B_MAZ_POL2	0.816	NS
BCLAF1_GABP_POL2	0.907	0.816
JUND_TBLR1_YY1	0.56	0.815
GABP_POL2_YY1	0.389	0.815

MAX_PML_YY1	0.444	0.37
ETS1_MAZ_ZNF143	0.814	NS
CBX3_E2F4_YY1	0.534	0.813
ETS1_MAX_PML	0.564	0.812
GABP_JUND_MAX	0.812	0.342
CMYC_HMGN3_SIX5	1.104	0.811
GABP_PML_POL2	0.268	0.543
GTF2B_POL2_ZBTB33	0.811	NS
E2F4_POL2_ZNF143	0.754	0.81
E2F4_JUND_ZNF143	0.538	0.808
E2F4_YY1_ZNF143	0.798	0.808
ELF1_JUND_YY1	0.467	0.801
CBX3_ETS1_IRF1	0.947	0.799
ELF1_GABP_SIN3	0.45	0.799
CBX3_ELF1_GABP	0.797	0.846
CBX3_CMYC_TBLR1	0.261	0.796
PML_TAF1_ZNF143	0.796	0.484
E2F4_MAX_MXI1	0.729	0.791
EGR1_IRF1_ZNF143	0.796	0.789
GTF2F1_MAZ_SIN3	0.788	NS
GTF2F1_HMGN3_PML	0.695	0.785
CCNT2_GTF2F1_MAZ	0.782	NS
MAZ_POL2_TAF7	0.78	NS
CMYC_GABP_YY1	0.734	0.78
ELF1_ETS1_GABP	0.474	0.779
CBX3_CMYC_CTCFB	0.691	0.779
PML_POL2_TBLR1	0.306	0.779
CMYC_MAX_TBLR1	0.913	0.779
GTF2F1_PML_TEAD4	0.562	0.778
IRF1_TAF1_YY1	0.774	0.555
CCNT2_GTF2F1_HMGN3	0.782	0.771
MAZ_SIX5_YY1	0.769	NS
CMYC_PML_POL2	0.509	0.258
GTF2B_MAZ_NRSF	0.765	NS
GABP_JUND_YY1	0.615	0.762
GTF2F1_HMGN3_POL2	0.25	0.76
CCNT2_GTF2F1_TAF1	0.758	0.875
ELF1_ETS1_JUND	0.28	0.758
E2F6_TBLR1_YY1	0.363	0.758
ELF1_PML_POL2	0.219	0.537
E2F4_ETS1_PML	0.574	0.755
ELF1_JUND_PML	0.437	0.754

CMYC_E2F4_ELF1	0.582	0.754
MAX_POL2_STAT1	0.996	0.754
NELFE_PML_POL2	0.294	0.753
CMYC_GABP_TBLR1	0.802	0.752
CJUN_MAX_PML	0.405	0.749
GABP_JUND_PML	0.582	0.747
EGR1_GTF2F1_JUND	0.747	0.612
E2F4_GABP_TAF1	0.746	0.755
CEBPB_E2F4_PML	0.613	0.734
CMYC_ETS1_GABP	0.709	0.734
GTF2F1_NRSF_TAF1	0.732	0.769
CHD2_GTF2F1_TAF1	0.728	0.349
GTF2B_POL2_TAF1	0.428	0.299
CMYC_POL2_PU1	0.962	0.723
PML_SP1_YY1	0.805	0.723
CJUN_HMGN3_TAF7	0.999	0.722
BHLHE40_SIX5_YY1	0.686	0.721
MAX_SIN3_ZNF143	0.615	0.72
GTF2B_POL2_RFX5	2.304	0.718
ETS1_YY1_ZNF143	0.708	0.718
GABP_MAX_SP1	0.717	0.452
CCNT2_GTF2B_MAZ	0.716	NS
CMYC_ELF1_JUND	0.442	0.714
JUND_MAZ_PU1	0.712	NS
ELF1_IRF1_TAF1	0.712	0.5
HMGN3_POL2_THAP1	0.519	0.711
CMYC_GABP_ZNF143	0.953	0.711
ETS1_MAX_ZNF143	0.649	0.711
MAZ_TAF7_YY1	0.71	NS
GABP_IRF1_MAZ	0.707	NS
EJUND_IRF1_YY1	0.817	0.706
MAX_PML_TBLR1	0.697	0.705
CMYC_IRF1_MAX	0.703	0.952
MAZ_SIN3_TAF7	0.703	NS
CMYC_E2F4_ZNF143	0.443	0.699
E2F4_GABP_MAZ	0.699	NS
EJUND_MAX_PML	0.424	0.691
E2F4_IRF1_PML	0.517	0.689
EGR1_GTF2B_PML	0.478	0.688
CMYC_GABP_JUND	0.932	0.683
CBX3_CMYC_ZNF143	0.613	0.679
CJUN_MAX_ZNF143	0.711	0.677

ETS1_GABP_MAX	0.699	0.674
GTF2F1_POL2_STAT1	0.974	0.671
GABP_POL2_ZNF143	0.555	0.671
GTF2B_NELFE_POL2	0.125	0.661
CJUN_EJUND_TAF7	0.603	0.661
GTF2F1_HMGN3_MAX	0.868	0.66
CBX3_ELF1_MAZ	0.658	NS
GTF2F1_MAX_TEAD4	0.952	0.655
CJUN_ELF1_PML	0.243	0.65
ELF1_IRF1_JUND	0.697	0.649
ATF1_POL2_SRF	0.528	0.648
ELF1_MAX_TBLR1	0.567	0.644
ELF1_PML_SIN3	0.43	0.642
GABP_PML_TAF1	0.639	0.507
JUND_MAX_YY1	0.41	0.638
E2F4_MAX_ZNF143	0.458	0.637
JUND_TAF1_ZNF143	0.636	0.768
P300_PML_YY1	0.582	0.631
ELF1_GABP_SP1	0.63	0.717
MAZ_PML_ZNF143	0.624	NS
E2F4_MAX_TBLR1	0.62	0.623
IRF1_PML_TAF1	0.621	0.141
GTF2B_NR2F2_POL2	0.925	0.619
E2F4_E2F6_TBLR1	0.528	0.618
EGR1_POL2_STAT1	1.125	0.617
GABP_YY1_ZNF143	0.562	0.607
CMYC_ELF1_YY1	0.553	0.607
NRSF_POL2_TAF7	0.579	0.604
CBX3_E2F4_MAX	0.472	0.6
GABP_MAZ_PML	0.599	NS
CBX3_CJUN_GTF2B	0.571	0.599
E2F4_ELF1_JUND	0.349	0.599
PML_SIN3_YY1	0.587	0.598
GTF2B_NRSF_TAF1	0.596	0.73
IRF1_PML_POL2	0.28	0.313
MAX_TAF7_TBP	0.902	0.586
CBX3_POL2_ZNF143	0.947	0.582
CJUN_SIX5_YY1	0.567	0.721
EGR1_GTF2B_TAF1	0.566	0.684
E2F4_ETS1_YY1	0.421	0.565
E2F6_MAX_STAT1	0.496	0.562
GTF2F1_POL2_TEAD4	0.712	0.56

MAZ_YY1_ZNF143	0.559	NS
E2F6_GTF2F1_TAF1	0.555	0.545
ETS1_GABP_POL2	0.327	0.54
E2F4_ELF1_MAX	0.313	0.532
MAZ_POL2_ZNF143	0.528	NS
JUND_MAX_TBLR1	0.406	0.525
CBX3_E2F4_POL2	0.421	0.519
E2F4_ELF1_YY1	0.558	0.519
CMYC_E2F6_TBLR1	0.193	0.519
MAX_TAF1_YY1	0.516	0.258
E2F4_MAX_PML	0.49	0.511
JUND_PML_POL2	0.356	0.502
CTCFB_POL2_SIX5	0.501	0.273
TAF1_YY1_ZNF143	0.497	0.562
ELF1_GABP_MAX	0.558	0.496
E2F4_ELF1_TAF1	0.494	0.457
CJUN_CMYC_ZNF143	0.449	0.488
CMYC_POL2_TBLR1	1.301	0.484
CBX3_CJUN_TAF7	0.372	0.481
CEBPB_ELF1_POL2	0.318	0.479
ELF1_PML_TAF1	0.478	0.405
GABP_MAX_ZNF143	0.89	0.477
CMYC_PML_TAF1	0.468	0.472
MAX_PML_TAF1	0.466	0.295
PML_TAF1_YY1	0.464	0.22
MAX_POL2_PU1	0.593	0.457
ELF1_JUND_MAX	0.409	0.453
ELF1_MAZ_PML	0.45	NS
CMYC_JUND_MAX	0.66	0.441
E2F4_ELF1_POL2	0.508	0.383
ETS1_POL2_STAT1	0.494	0.379
ELF1_JUND_POL2	0.292	0.377
GTF2B_NRSF_POL2	0.311	0.373
MAX_POL2_SRF	0.595	0.359
CMYC_JUND_POL2	0.793	0.351
GABP_TAF1_YY1	0.331	0.556
ELF1_TAF1_YY1	0.304	0.437
MAX_POL2_TBLR1	0.427	0.286
JUND_MAZ_PML	0.277	NS
JUND_MAX_POL2	0.201	0.252
ELF1_POL2_YY1	-0.184	0.251
E2F4_PML_YY1	0.59	0.242

CJUN_MAX_SP1	0.423	0.236
CMYC_TAF1_YY1	0.211	0.597
JUND_POL2_YY1	0.826	0.197
CHD2_GTF2B_POL2	0.364	0.142
GABP_JUND_POL2	0.413	0.117
POL2_TAF1_YY1	0.059	0.145
IRF1_MAZ_TBP	-0.055	NS
CMYC_ELF1_TBP	-0.101	-0.41
MAX_MAZ_TBP	-0.152	NS
CMYC_MAX_TBP	-0.042	-0.167
CMYC_MAZ_TBP	-0.232	NS
CMYC_ETS1_TBP	-0.27	-0.431
CMYC_E2F6_ZBTB7	-0.3	-0.438
ETS1_MAX_TBP	-0.326	-0.279
MAX_SIN3_TBP	-0.34	-0.678
E2F6_IRF1_TBP	-0.343	-0.54
CMYC_SIN3_TBP	-0.416	-0.024
CMYC_MAX_ZBTB7	-0.306	-0.418
MAZ_POL2_TBP	-0.449	NS
IRF1_POL2_TBP	0.032	-0.452
E2F6_MAX_ZBTB7	-0.467	-0.874
E2F4_IRF1_TBP	-0.477	-0.651
E2F4_POL2_TBP	-0.497	-0.097
CMYC_E2F4_TBP	-0.502	-0.132
MAZ_TAF1_TBP	-0.507	NS
ATF3_MAX_TBP	-0.534	-1.204
MAX_POL2_ZBTB7	-0.14	-0.548
CHD2_POL2_TBP	-0.551	-1.231
E2F6_HMGN3_ZBTB7	-0.552	-0.651
CMYC_TAF1_TBP	-0.047	-0.537
CMYC_POL2_TBP	-0.205	-0.391
PML_POL2_TBP	-0.596	-0.098
IRF1_TAF1_TBP	0.009	-0.601
E2F6_YY1_ZBTB7	-0.606	-0.497
E2F6_POL2_ZBTB7	-0.623	-0.956
HMGN3_POL2_ZBTB7	-0.625	-0.349
E2F6_MAZ_TBP	-0.625	NS
IRF1_TAF1_ZBTB7	-0.133	-0.628
CMYC_RCOR1_TBP	-0.632	-0.236
CHD2_MAX_TBP	-0.645	-0.864
MAZ_POL2_UBTF	-0.646	NS
ETS1_TBP_YY1	-0.703	-0.585

E2F6_SIN3_TBP	-0.709	-0.903
CHD2_IRF1_TBP	-0.723	-1.066
CMYC_TAF1_ZBTB7	-0.474	-0.767
E2F6_ELF1_TBP	-0.778	-0.487
E2F4_E2F6_TBP	-0.807	-0.379
ATF3_CMYC_TBP	-0.81	-1.289
E2F4_TAF1_TBP	-0.828	-0.715
POL2_SIN3_TBP	-0.851	-0.68
CMYC_NFYB_TBP	-1.062	-0.851
HMGN3_MAZ_ZBTB7	-0.851	NS
CHD2_MAZ_TBP	-0.871	NS
CMYC_NFYB_ZBTB7	-0.812	-0.886
E2F6_POL2_TBP	-0.257	-0.641
ELF1_HMGN3_ZBTB7	-0.905	-0.725
MAX_TAF1_ZBTB7	-0.477	-0.914
EGR1_MAZ_TBP	-0.923	NS
ATF3_CCNT2_ZBTB7	-0.931	-0.066
CMYC_HMGN3_ZBTB7	-0.941	-0.815
CMYC_POL2_ZBTB7	-0.573	-0.374
MAX_POL2_TBP	-0.423	-0.527
CHD2_TAF1_TBP	-0.956	-0.899
ATF3_POL2_ZBTB7	-0.968	0.033
ATF3_POL2_TBP	-0.971	-0.429
MAZ_TBP_ZBTB7	-0.977	NS
CCNT2_PML_TBP	-0.991	-1.008
EGR1_ETS1_TBP	-0.992	-0.651
EGR1_PML_TBP	-0.994	-0.824
HMGN3_YY1_ZBTB7	-1.009	-0.552
HMGN3_JUND_ZBTB7	-1.011	-1.042
CCNT2_JUND_TBP	-1.014	-0.874
POL2_SIN3_UBTF	-1.283	-1.016
E2F4_TBP_YY1	-1.029	-0.973
ATF3_MAZ_TBP	-1.034	NS
ATF3_MAZ_ZBTB7	-1.036	NS
MAX_TAF1_TBP	-0.297	-0.75
ATF3_TAF1_TBP	-1.055	-0.973
E2F4_EGR1_TBP	-1.055	-0.832
PML_TAF1_ZBTB7	-0.534	-1.066
NFYB_POL2_TBP	-1.352	-1.066
CCNT2_MAZ_UBTF	-1.075	NS
SIN3_UBTF_YY1	-1.605	-1.094
ELF1_TBP_ZBTB7	-0.812	-1.096

EGR1_SIN3_TBP	-1.099	-0.941
E2F6_POL2_UBTF	-0.465	-0.64
CFOS_EGR1_POL2	-1.114	-1.836
CCNT2_MAZ_TBP	-1.121	NS
BHLHE40_UBTF_YY1	-1.803	-1.13
E2F6_MAZ_UBTF	-1.162	NS
MAZ_UBTF_YY1	-1.177	NS
ATF3_ETS1_TBP	-1.182	-0.526
POL2_RCOR1_UBTF	-1.949	-1.188
JUND_UBTF_YY1	-1.546	-1.19
CCNT2_EGR1_UBTF	-0.767	-1.196
ELF1_MAZ_UBTF	-1.2	NS
ATF3_E2F6_TBP	-1.204	-1.066
BHLHE40_CCNT2_TBP	-1.207	-1.099
CMYC_RCOR1_UBTF	-1.413	-1.218
CMYC_MAZ_UBTF	-1.228	NS
ATF3_TBP_YY1	-1.238	-0.718
CCNT2_TBP_USF1	-1.263	-0.973
ETS1_TAF1_TBP	-0.594	-0.671
ELF1_TAF1_UBTF	-1.308	-1.289
HMGN3_RCOR1_ZBTB7	-1.198	-1.289
E2F6_MAX_TBP	-0.484	-0.809
IRF1_NFYB_TBP	-1.312	-1.414
CMYC_E2F6_TBP	-0.576	-0.746
EGR1_IRF1_TBP	-0.568	-0.754
ATF3_SIN3_TBP	-1.323	-0.651
MAX_SIN3_UBTF	-0.987	-1.339
CCNT2_SIN3_UBTF	-0.812	-1.346
MAX_MAZ_UBTF	-1.348	NS
POL2_TAF1_TBP	-0.51	-0.845
CHD2_CMYC_TBP	-0.823	-0.533
HMGN3_JUND_TBP	-1.358	-1.092
CMYC_EGR1_TBP	-0.842	-0.517
E2F6_PML_UBTF	-1.534	-1.364
E2F4_SIN3_UBTF	-1.297	-1.388
EJUND_MAX_UBTF	-1.179	-1.388
IRF1_JUND_UBTF	-0.898	-1.41
ETS1_POL2_TBP	-1.42	-0.777
E2F6_HMGN3_TBP	-1.423	-1.033
JUND_TBP_UBTF	-1.516	-1.424
ELF1_IRF1_UBTF	-1.316	-1.424
CCNT2_IRF1_TBP	-0.429	-0.997

E2F4_ELF1_UBTF	-1.577	-1.435
EGR1_MAZ_UBTF	-1.467	NS
POL2_TAF1_ZBTB7	-0.419	-1.053
EGR1_IRF1_UBTF	-0.727	-1.472
E2F6_TAF1_TBP	-0.73	-0.757
HMGN3_MAZ_UBTF	-1.49	NS
SIN3_TBP_UBTF	-0.962	-1.507
MAX_P300_UBTF	-1.46	-1.544
EGR1_TAF1_UBTF	-1.433	-1.544
CCNT2_RCOR1_TBP	-1.549	-1.276
HMGN3_MAZ_TBP	-1.551	NS
GABP_POL2_UBTF	-1.225	-1.556
GABP_TBP_UBTF	-0.982	-1.569
EGR1_MAX_TBP	-0.925	-0.666
JUND_SIN3_UBTF	-1.126	-1.602
ATF3_EFOS_EJUND	-1.611	-6.069
PML_SIN3_UBTF	-1.66	-1.616
BHLHE40_MAZ_UBTF	-1.619	NS
E2F6_EGR1_UBTF	-1.105	-1.621
CCNT2_IRF1_TAL1	-1.625	-2.236
CMYC_E2F6_UBTF	-1.061	-0.564
E2F4_MAZ_UBTF	-1.625	NS
GTF2F1_TAF1_UBTF	-1.83	-1.651
EGR1_UBTF_YY1	-1.908	-1.651
JUND_TAF1_UBTF	-1.433	-1.651
BHLHE40_TBP_UBTF	-1.397	-1.651
USF1_USF2_YY1	-2.619	-1.651
EGR1_TBP_UBTF	-1.516	-1.651
ATF3_HMGN3_TBP	-1.66	-0.066
ATF3_FOSL1_JUND	-1.66	-7.069
GABP_IRF1_UBTF	-1.034	-1.678
CFOS_IRF1_TBP	-0.882	-1.681
E2F6_NFYB_TBP	-1.684	-1.424
CFOS_CMYC_TBP	-1.215	-1.691
IRF1_SIN3_UBTF	-0.767	-1.694
ATF3_FOSL1_MAX	-1.727	-7.654
MAX_USF1_USF2	-0.753	-1.729
E2F6_JUND_UBTF	-1.288	-1.751
CHD2_HMGN3_TBP	-1.775	-1.544
CCNT2_TBP_YY1	-0.894	-0.881
CMYC_HMGN3_TBP	-1.295	-0.484
ELF1_MAX_USF2	-0.49	-1.789

ATF3_CJUN_EFOS	-1.791	-6.069
HMGN3_MAX_ZBTB7	-0.726	-1.066
SIN3_TAF1_UBTF	-1.263	-1.803
ATF3_CCNT2_TBP	-1.812	-1.651
MAZ_PML_UBTF	-1.812	NS
GABP_TAF1_UBTF	-1.397	-1.832
MAX_NFYB_TBP	-1.183	-1.839
MAZ_UBTF_ZBTB7	-1.848	NS
CMYC_JUND_UBTF	-1.075	-0.789
CHD2_MAZ_UBTF	-1.882	NS
CMYC_RAD21_UBTF	-1.908	-3.111
EGR1_HMGN3_UBTF	-1.727	-1.914
ATF3_IRF1_UBTF	-1.933	-2.236
CCNT2_CFOS_TBP	-1.933	-3.236
ATF3_FOSL1_MAZ	-1.933	NS
CCNT2_MAX_TBP	-0.806	-1.144
NFYB_TAF1_TBP	-1.045	-1.973
GABP_MAX_UBTF	-1.198	-1.973
EGR1_TAF1_TBP	-1.06	-0.914
CCNT2_SIN3_TBP	-1.034	-0.941
CCNT2_FOSL1_MAX	-1.982	-1.767
E2F6_IRF1_UBTF	-1.131	-0.865
CMYC_E2F4_UBTF	-1.181	-0.829
CCNT2_TAF1_TBP	-1.004	-1.008
E2F4_JUND_UBTF	-2.075	-2.02
CCNT2_ELF1_TBP	-1.058	-0.979
IRF1_TBP_ZBTB7	-0.727	-1.329
CMYC_GABP_UBTF	-0.695	-2.066
CMYC_SIN3_UBTF	-0.853	-2.099
CFOS_YY1_ZBTB7	-2.119	-1.204
E2F6_TBP_YY1	-1.054	-1.082
FOSL1_MAX_ZBTB7	-2.145	-3.651
ETS1_MAZ_UBTF	-2.145	NS
GABP_PML_UBTF	-1.882	-2.154
CCNT2_E2F6_UBTF	-0.911	-1.248
CCNT2_NFYB_TBP	-2.162	-2.314
EFOS_P300_POL2	-2.162	-2.651
CCNT2_IRF1_UBTF	-1.323	-0.853
ELF1_USF1_USF2	-1.014	-2.182
CTCFB_CTCFC_UBTF	-2.19	-1.973
HMGN3_IRF1_TBP	-0.949	-1.248
CTCFC_MAX_UBTF	-2.212	-2.182

CCNT2_TAF1_UBTF	-0.968	-1.254
NRSF_TBLR1_UBTF	-1.982	-2.236
EJUND_NRSF_UBTF	-3.323	-2.236
TBP_USF2_YY1	-1.949	-2.236
CMYC_TBP_ZBTB7	-1.099	-1.138
E2F6_EGR1_TBP	-1.259	-0.982
CCNT2_ELF1_UBTF	-1.047	-1.196
ATF3_CFOS_EGR1	-2.245	-1.388
ATF3_EFOS_EJUNB	-2.245	-6.069
NFYB_TBP_ZBTB7	-2.245	-3.066
CTCFC_HMGN3_UBTF	-2.245	-3.236
CCNT2_E2F6_TBP	-1.127	-1.133
IRF1_POL2_UBTF	-0.796	-1.464
CCNT2_MAX_TAL1	-2.271	-2.276
CCNT2_EGR1_TBP	-1.134	-1.142
EGR1_MAX_UBTF	-1.183	-1.094
CTCF_MAX_UBTF	-2.284	-1.874
IRF1_UBTF_YY1	-1.66	-0.624
CTCFC_RAD21_UBTF	-2.297	-2.651
E2F4_RCOR1_UBTF	-2.297	-1.236
HMGN3_MAX_TBP	-1.269	-1.039
NFYB_YY1_ZBTB7	-2.308	-2.821
CCNT2_POL2_UBTF	-1.162	-1.15
CCNT2_CMYC_TBP	-1.069	-1.244
GTF2F1_NRSF_UBTF	-3.075	-2.314
IRF1_TAL1_UBTF	-2.775	-2.314
BHLHE40_CCNT2_USF2	-1.66	-2.314
MXI1_NRSF_UBTF	-1.075	-2.314
ATF3_TBP_ZBTB7	-2.323	-2.388
HMGN3_POL2_TBP	-1.534	-0.799
CMYC_ETS1_UBTF	-1.087	-1.254
ATF3_EFOS_JUND	-2.348	-6.069
FOSL1_HMGN3_JUND	-2.348	-1.729
CTCFB_RAD21_UBTF	-2.348	-2.767
IRF1_MAX_UBTF	-0.772	-1.581
MAX_RAD21_UBTF	-2.36	-3.651
ELF1_HMGN3_TBP	-1.134	-1.236
P300_UBTF_ZBTB7	-3.323	-2.388
CMYC_EGR1_UBTF	-0.944	-1.466
PML_POL2_UBTF	-1.381	-1.036
CCNT2_POL2_TBP	-0.778	-1.641
CMYC_UBTF_YY1	-1.404	-1.021

POL2_TBP_ZBTB7	-1.104	-1.327
NRSF_RCOR1_UBTF	-2.534	-2.459
EFOS_EJUND_HMGN3	-2.467	-2.651
CCNT2_CMYC_TAL1	-2.467	-1.247
MAX_TBP_ZBTB7	-0.862	-1.605
CCNT2_TBP_ZBTB7	-0.927	-1.552
BHLHE40_PML_UBTF	-1.982	-2.481
GATA2_MAX_TBP	-2.49	-3.066
CFOS_MAX_TBP	-0.66	-2.492
HMGN3_TAF1_ZBTB7	-1.166	-1.346
HMGN3_TBP_YY1	-1.497	-1.02
TAF1_TBP_ZBTB7	-1.111	-1.41
SIN3_USF1_USF2	-1.66	-2.526
TAF1_TAL1_UBTF	-2.014	-2.526
HMGN3_TAF1_TBP	-1.427	-1.106
EFOS_HMGN3_JUND	-2.534	-2.651
TBP_YY1_ZBTB7	-1.089	-1.445
EFOS_HMGN3_MAZ	-2.534	NS
HMGN3_PML_TBP	-1.291	-1.247
CMYC_CTCFC_UBTF	-2.556	-2.204
E2F6_UBF_YY1	-6.059	-2.569
E2F6_HMGN3_TAL1	-2.577	-3.02
POL2_TAF1_UBTF	-1.514	-1.066
NFYB_SP2_TBP	-1.444	-2.59
CTCF_MAZ_UBTF	-2.599	NS
E2F6_MAX_UBTF	-1.154	-1.448
CMYC_TAF1_UBTF	-1.49	-1.112
CCNT2_MAX_UBTF	-1.602	-1.001
CHD2_E2F6_TBP	-1.45	-1.154
CTCFC_E2F6_UBTF	-2.619	-2.459
CHD2_ETS1_TBP	-1.368	-1.289
CTCF_CTCFB_UBTF	-2.66	-1.767
BHLHE40_CHD2_UBTF	-2.66	-2.459
CHD2_TAF1_UBTF	-2.66	-1.602
TBP_UBTF_YY1	-1.075	-1.616
CFOS_TBP_YY1	-1.297	-2.691
ELF1_UBTF_YY1	-1.765	-0.933
CTCF_CTCFC_UBTF	-2.719	-1.874
CCNT2_NFYA_TBP	-2.719	-2.874
MAX_RCOR1_UBTF	-1.474	-1.251
NFYA_TBP_YY1	-1.277	-2.729
CCNT2_UBTF_YY1	-1.805	-0.924

BHLHE40_IRF1_UBTF	-0.863	-1.874
HMGN3_SIN3_UBTF	-1.075	-2.767
CMYC_TAL1_UBTF	-1.66	-2.767
EGR1_POL2_TBP	-1.313	-1.456
MAZ_NRSF_UBTF	-2.775	NS
MAZ_RAD21_UBTF	-2.775	NS
CTCF_RAD21_UBTF	-2.775	-2.526
ATF3_EFOS_FOSL1	-2.775	NS
PML_TBP_ZBTB7	-1.234	-1.547
CCNT2_TBP_UBTF	-1.397	-1.388
IRF1_UBTF_ZBTB7	-1.553	-1.236
E2F6_UBTF_YY1	-1.707	-1.084
CCNT2_E2F6_TAL1	-2.812	-2.973
CCNT2_CMYC_UBTF	-1.671	-1.143
CMYC_ELF1_UBTF	-1.338	-1.499
IRF1_TBP_UBTF	-1.233	-1.605
POL2_TAL1_UBTF	-1.49	-2.839
EGR1_TBP_ZBTB7	-1.281	-1.558
ELF1_TBP_UBTF	-1.534	-1.323
E2F6_TBP_ZBTB7	-1.364	-1.516
CHD2_PML_UBTF	-2.882	-1.821
CTCFC_TAF1_UBTF	-2.882	-2.973
BHLHE40_CMYC_USF2	-1.546	-2.899
CCNT2_HMGN3_TBP	-1.625	-1.303
TAF1_UBTF_YY1	-1.472	-1.459
HMGN3_TAF1_TAL1	-2.933	-2.066
FOSL1_JUND_ZBTB7	-2.933	-2.066
E2F4_TBP_ZBTB7	-1.423	-1.511
E2F4_HMGN3_TBP	-1.68	-1.263
E2F6_HMGN3_UBTF	-1.014	-1.941
EGR1_ELF1_UBTF	-1.397	-1.569
CMYC_TBP_UBTF	-0.751	-2.216
CHD2_CMYC_UBTF	-1.927	-1.044
CMYC_MAX_UBTF	-1.518	-1.459
HMGN3_MAZ_TAL1	-2.982	NS
EFOS_EGR1_POL2	-2.982	-3.821
CCNT2_E2F4_TBP	-1.625	-1.388
E2F6_TAL1_UBTF	-2.19	-3.02
JUND_TBP_ZBTB7	-1.37	-1.651
EGR1_HMGN3_TBP	-1.66	-1.362
CCNT2_EFOS_MAX	-3.029	-3.459
CHD2_TBP_UBTF	-3.029	-1.552

CCNT2_CMYC_EFOS	-3.045	-4.314
CCNT2_HMGN3_UBTF	-1.245	-1.813
IRF1_TAF1_UBTF	-1.534	-1.526
ELF1_MAX_UBTF	-1.364	-1.715
EGR1_ETS1_UBTF	-1.738	-1.346
CTCFC_POL2_UBTF	-3.097	-3.424
TAF1_TBP_UBTF	-1.448	-1.651
JUND_MAX_UBTF	-1.564	-1.547
HMGN3_SIN3_TBP	-1.738	-1.414
E2F6_TAF1_UBTF	-1.183	-1.973
MAX_UBTF_YY1	-2.021	-1.168
UBTF_YY1_ZBTB7	-2.045	-1.171
POL2_UBTF_YY1	-2.093	-1.129
E2F6_TBP_UBTF	-1.819	-1.412
CFOS_EGR1_TBP	-1.982	-3.236
CMYC_SIN3_USF2	-1.593	-3.236
JUND_POL2_UBTF	-2.297	-0.978
CMYC_USF1_USF2	-1.183	-3.276
ETS1_IRF1_UBTF	-1.37	-1.914
HMGN3_RCOR1_TBP	-1.763	-1.526
CMYC_ELF1_USF2	-1.348	-3.295
ETS1_TBP_UBTF	-1.625	-1.685
GABP_UBTF_ZBTB7	-1.534	-3.314
E2F4_IRF1_UBTF	-1.911	-1.41
CTCFB_UBTF_ZBTB7	-3.323	-2.874
CMYC_IRF1_UBTF	-1.221	-2.114
E2F6_ETS1_UBTF	-1.933	-1.44
CCNT2_USF1_USF2	-1.397	-3.388
CBX3_CTCFC_UBTF	-3.397	-2.767
EFOS_JUND_ZBTB7	-3.397	-9.528
CTCFC_ETS1_UBTF	-3.397	-2.651
E2F4_E2F6_UBTF	-1.429	-2.005
POL2_UBTF_ZBTB7	-1.565	-1.892
MAX_TAF1_UBTF	-1.66	-1.797
CCNT2_POL2_USF2	-1.36	-3.459
CTCF_UBTF_ZBTB7	-3.467	-2.874
CTCFC_JUND_UBTF	-3.467	-2.874
POL2_USF1_USF2	-1.765	-3.481
HMGN3_IRF1_UBTF	-1.611	-1.892
MAX_POL2_UBTF	-1.475	-2.036
ELF1_UBTF_ZBTB7	-1.59	-1.924
E2F6_UBTF_ZBTB7	-2.022	-1.492

CCNT2_E2F4_UBTF	-1.738	-1.789
EJUND_FOSL1_ZBTB7	-3.534	-2.651
CCNT2_EFOS_MAZ	-3.534	NS
BHLHE40_MAX_UBTF	-1.636	-1.903
PML_TBP_UBTF	-1.791	-1.767
CHD2_EGR1_TBP	-1.83	-1.729
ELF1_PML_UBTF	-2.075	-1.492
JUND_RCOR1_UBTF	-1.962	-1.611
EGR1_NRSF_UBTF	-1.949	-3.59
IRF1_PML_UBTF	-1.927	-1.667
CCNT2_EFOS_JUND	-3.599	-2.973
MAX_TBP_UBTF	-1.743	-1.874
ELF1_POL2_UBTF	-1.672	-1.949
EFOS_HMGN3_POL2	-3.63	-1.803
ELF1_HMGN3_UBTF	-1.397	-2.236
HMGN3_MAX_UBTF	-1.759	-1.874
E2F4_TAF1_UBTF	-1.949	-1.691
POL2_TBP_UBTF	-1.503	-2.145
CCNT2_UBTF_ZBTB7	-1.63	-2.02
JUND_NRSF_UBTF	-2.66	-3.651
CCNT2_EFOS_EJUND	-3.66	-2.973
CCNT2_CMYC_USF2	-1.775	-3.681
HMGN3_UBTF_YY1	-1.765	-1.919
EGR1_POL2_UBTF	-1.486	-2.2
E2F4_TBP_UBTF	-2.038	-1.651
HMGN3_JUND_UBTF	-1.553	-2.137
CHD2_IRF1_UBTF	-1.66	-2.036
BHLHE40_TAF1_UBTF	-1.699	-2.02
CTCFB_MAZ_UBTF	-3.719	NS
ELF1_ETS1_UBTF	-1.848	-1.874
CHD2_E2F6_UBTF	-1.812	-1.914
E2F4_EGR1_UBTF	-1.707	-2.02
E2F4_MAX_UBTF	-1.882	-1.874
BHLHE40_POL2_UBTF	-1.66	-2.117
BHLHE40_CMYC_UBTF	-1.837	-1.941
ETS1_SIN3_UBTF	-2.001	-1.789
CCNT2_CHD2_TBP	-1.958	-1.839
CMYC_PML_UBTF	-2.195	-1.618
ATF3_FOSL1_HMGN3	-3.83	-7.069
BHLHE40_E2F6_UBTF	-1.933	-1.903
CHD2_MAX_UBTF	-2.1	-1.751
CMYC_GATA2_TBP	-3.882	-3.821

ETS1_MAX_UBTF	-2.397	-1.504
CTCFC_UBTF_ZBTB7	-3.933	-3.154
CTCFC_MAZ_UBTF	-3.982	NS
ETS1_TAF1_UBTF	-2.368	-1.616
ETS1_JUND_UBTF	-2.297	-1.699
JUND_PML_UBTF	-1.84	-2.204
CMYC_HMGN3_TAL1	-1.543	-2.504
ETS1_PML_UBTF	-2.179	-1.874
CCNT2_ETS1_UBTF	-2.162	-1.908
GATA2_POL2_TBP	-4.075	-3.526
CMYC_POL2_UBTF	-1.905	-2.175
TAF1_UBTF_ZBTB7	-2.179	-1.914
HMGN3_TBP_UBTF	-1.49	-2.621
PML_UBTF_YY1	-2.245	-1.874
ETS1_HMGN3_UBTF	-2.111	-2.03
E2F4_POL2_UBTF	-1.992	-2.166
CTCFC_UBTF_YY1	-4.162	-2.459
CMYC_HMGN3_UBTF	-1.19	-2.973
E2F4_UBTF_ZBTB7	-1.933	-2.236
EGR1_PML_UBTF	-2.204	-1.992
CCNT2_PML_UBTF	-2.308	-1.908
HMGN3_TAF1_UBTF	-1.605	-2.621
ETS1_POL2_UBTF	-2.534	-1.693
TBP_UBTF_ZBTB7	-2.162	-2.111
MAX_PML_UBTF	-2.227	-2.05
CJUN_EFOS_EGR1	-4.284	-10.069
PML_TAF1_UBTF	-2.19	-2.117
HMGN3_RCOR1_UBTF	-2.204	-2.111
MAX_UBTF_ZBTB7	-2.225	-2.092
E2F4_UBTF_YY1	-1.836	-2.526
CHD2_UBTF_YY1	-2.338	-2.137
E2F4_ETS1_UBTF	-2.323	-2.154
SIN3_UBTF_ZBTB7	-1.797	-2.874
CCNT2_CHD2_UBTF	-2.397	-2.289
RCOR1_UBTF_ZBTB7	-2.66	-2.066
E2F4_PML_UBTF	-2.812	-1.914
HMGN3_PML_UBTF	-2.145	-2.59
CHD2_EGR1_UBTF	-2.719	-2.066
ETS1_UBTF_YY1	-2.304	-2.481
HMGN3_TBP_ZBTB7	-2.438	-2.359
CCNT2_EFOS_POL2	-4.83	-4.066
EGR1_UBTF_ZBTB7	-1.882	-2.973

HMGN3_POL2_UBTF	-1.716	-3.236
BHLHE40_UBTF_ZBTB7	-2.66	-2.314
E2F6_NRSF_UBTF	-2.619	-2.388
CHD2_TBP_ZBTB7	-2.162	-2.874
BHLHE40_CCNT2_UBTF	-2.119	-2.924
NRSF_SIN3_UBTF	-2.245	-2.821
HMGN3_UBTF_ZBTB7	-1.962	-3.111
JUND_UBTF_ZBTB7	-2.297	-2.821
E2F4_NRSF_UBTF	-2.599	-2.59
ELF1_NRSF_UBTF	-2.599	-2.651
CHD2_HMGN3_UBTF	-2.348	-2.924
BHLHE40_HMGN3_UBTF	-2.162	-3.111
NRSF_UBTF_ZBTB7	-2.599	-2.767
E2F4_HMGN3_UBTF	-2.245	-3.236
HMGN3_MAX_TAL1	-2.049	-3.459
CHD2_ETS1_UBTF	-2.882	-2.651
HMGN3_POL2_TAL1	-3.761	-1.851
CCNT2_NRSF_UBTF	-2.882	-2.821
ETS1_TAL1_UBTF	-3.397	-2.314
HMGN3_TAL1_TBP	-2.982	-2.874
NRSF_TBP_UBTF	-2.933	-2.924
HMGN3_IRF1_TAL1	-2.245	-3.621
NRSF_TAF1_UBTF	-2.982	-2.924
BHLHE40_ETS1_UBTF	-2.982	-2.973
CMYC_NFE2_POL2	-6.119	-11.927
CHD2_POL2_UBTF	-3.245	-2.973
ETS1_UBTF_ZBTB7	-3.245	-3.066
CMYC_UBTF_ZBTB7	-2.791	-3.574
PML_UBTF_ZBTB7	-3.882	-2.611
ETS1_NRSF_UBTF	-3.719	-2.874
CHD2_UBTF_ZBTB7	-3.397	-3.388
CHD2_ETS1_TAL1	-3.599	-3.236
CCNT2_HMGN3_TAL1	-3.075	-3.767
NRSF_PML_UBTF	-3.982	-3.02
NRSF_UBTF_YY1	-4.433	-2.59
NRSF_POL2_UBTF	-3.097	-3.949
EGR1_HMGN3_TAL1	-3.775	-3.314
MAX_NRSF_UBTF	-3.747	-3.459
CMYC_NRSF_UBTF	-1.862	-5.37
CHD2_E2F6_TAL1	-4.029	-3.767
IRF1_NRSF_UBTF	-4.284	-3.621
JUND_NFE2_ZBTB7	-9.866	-9.238

NRSF_STAT5_TAL1	-9.866	-8.39
SMC3_UBTF_ZBTB7	-9.866	-9.528
ETS1_MAZ_NFE2	-9.866	NS
CCNT2_NFE2_RCOR1	-9.866	-8.876
EGR1_ELF1_NFE2	-9.866	-8.654
BHLHE40_ETS1_NFE2	-9.866	-8.876
BHLHE40_EGR1_NFE2	-9.866	-8.654
ELF1_JUND_NFE2	-9.866	-9.238
BHLHE40_NFE2_RCOR1	-9.866	-8.876
BHLHE40_NFE2_USF1	-9.866	-8.876
GABP_TAL1_UBTF	-3.162	-9.876
CCNT2_EGR1_NFE2	-9.966	-8.39
EFOS_P300_TEAD4	-9.966	-8.876
ELF1_NFE2_SIN3	-9.966	-9.238
JUND_NFE2_RCOR1	-9.966	-8.876
EGR1_MAZ_NFE2	-9.966	NS
MAZ_NFE2_ZBTB7	-9.966	NS
CCNT2_ETS1_NFE2	-9.966	-8.876
CCNT2_E2F4_NFE2	-9.966	-9.069
EJUND_JUND_NFE2	-9.966	-8.654
EGR1_GATA2_TBP	-9.966	-9.238
JUND_NFE2_P300	-9.966	-8.876
MAFF_MAFK_NRSF	-9.966	-8.876
JUND_MAFF_NFE2	-9.966	-8.654
BHLHE40_NFE2_P300	-9.966	-8.876
TRIM28_UBTF_ZBTB7	-9.866	-9.975
CCNT2_NFE2_SIN3	-10.059	-9.238
BHLHE40_NFE2_SIN3	-10.059	-9.39
CCNT2_EFOS_P300	-10.059	-9.39
CCNT2_EFOS_ZBTB7	-10.059	-9.876
HMGN3_MAZ_NFE2	-10.059	NS
CCNT2_NFE2_ZBTB7	-10.059	-9.238
BHLHE40_ELF1_NFE2	-10.059	-9.39
MAZ_NFE2_SIN3	-10.059	NS
P300_STAT2_TAL1	-10.059	-8.39
ELF1_MAZ_NFE2	-10.059	NS
EFOS_HMGN3_P300	-10.059	-9.238
GABP_NRSF_UBTF	-2.982	-10.069
ELF1_HMGN3_NFE2	-10.146	-9.238
ATF3_NFE2_P300	-10.146	-8.069
EFOS_HMGN3_ZBTB7	-10.146	-9.39
CCNT2_ELF1_NFE2	-10.146	-9.069

CCNT2_HMGN3_NFE2	-10.146	-9.39
CCNT2_EFOS_FOSL1	-10.146	-9.528
EFOS_FOSL1_ZBTB7	-10.146	-9.238
EFOS_EGR1_ZBTB7	-10.146	-9.238
JUND_MAZ_NFE2	-10.146	NS
E2F6_JUND_NFE2	-10.146	-9.975
RAD21_TBP_UBTF	-10.146	-9.654
ATF3_NFE2_SIN3	-10.146	-8.654
CCNT2_EFOS_RCOR1	-10.146	-9.39
CHD2_TAL1_ZBTB7	-10.146	-9.654
HMGN3_JUND_NFE2	-10.229	-9.39
EFOS_EGR1_FOSL1	-10.229	-9.069
BHLHE40_CCNT2_NFE2	-10.229	-9.238
BHLHE40_HMGN3_NFE2	-10.229	-9.39
E2F4_MAX_NFE2	-10.229	-9.39
EJUNB_FOSL1_ZBTB7	-10.229	-9.39
BHLHE40_MAZ_NFE2	-10.229	NS
E2F6_EFOS_P300	-10.229	-9.528
NR2F2_NRSF_TAL1	-10.307	-9.238
ATF3_ELF1_NFE2	-10.307	-8.39
ATF3_MAZ_NFE2	-10.307	NS
ATF3_CCNT2_NFE2	-10.307	-8.39
CCNT2_JUND_NFE2	-10.307	-9.39
BHLHE40_JUND_NFE2	-10.307	-9.528
E2F6_NFE2_SIN3	-10.307	-9.654
BHLHE40_NRSF_UBTF	-3.397	-10.316
NFE2_YY1_ZBTB7	-10.381	-9.528
ATF3_EFOS_EGR1	-10.381	-6.069
CCNT2_MAZ_NFE2	-10.381	NS
ATF3_EFOS_HMGN3	-10.381	NS
ETS1_MAX_NFE2	-10.381	-9.238
EFOS_FOSL1_HMGN3	-10.381	-9.39
E2F4_UBF_YY1	NS	-10.39
GATA2_TBP_YY1	-10.451	-9.769
EJUND_MAX_NFE2	-10.451	-9.39
ATF3_CCNT2_EFOS	-10.451	-6.069
EGR1_MAX_NFE2	-10.451	-8.876
MAX_NFE2_P300	-10.451	-9.654
ATF3_BHLHE40_NFE2	-10.451	-8.654
ELF1_NFE2_YY1	-10.518	-9.876
MAX_NFE2_RCOR1	-10.518	-9.528
MAX_NFE2_USF1	-10.518	-9.654

MAX_NFE2_ZBTB7	-10.518	-9.876
ATF3_JUND_NFE2	-10.582	-8.654
ATF3_E2F6_NFE2	-10.582	-9.238
IRF1_JUND_NFE2	-10.582	-9.769
E2F6_ELF1_NFE2	-10.582	-9.876
BHLHE40_IRF1_NFE2	-10.582	-9.975
NFE2_POL2_TEAD4	-10.582	-8.654
RAD21_UBTF_ZBTB7	-10.582	-9.769
ELF1_IRF1_NFE2	-10.644	-9.654
NFE2_SIN3_YY1	-10.644	-9.654
ETS1_NFE2_POL2	-10.644	-9.769
JUND_NFE2_YY1	-10.644	-9.975
ATF3_IRF1_NFE2	-10.703	-8.39
CCNT2_E2F6_NFE2	-10.703	-9.769
E2F6_HMGN3_NFE2	-10.759	-9.876
E2F6_MAZ_NFE2	-10.759	NS
MAX_NFE2_SIN3	-10.759	-10.069
MAZ_NFE2_POL2	-10.759	NS
BHLHE40_E2F6_NFE2	-10.759	-10.316
MAX_MAZ_NFE2	-10.814	NS
MAZ_NFE2_YY1	-10.814	NS
CCNT2_NFE2_YY1	-10.814	-9.654
ATF3_NFE2_YY1	-10.814	-8.876
BHLHE40_MAX_NFE2	-10.814	-10.316
ATF3_FOSL1_ZBTB7	-10.814	-7.069
JUND_MAX_NFE2	-10.814	-10.069
HMGN3_NFE2_YY1	-10.866	-9.975
E2F6_IRF1_NFE2	-10.866	-10.238
CCNT2_MAX_NFE2	-10.866	-9.975
MAX_NFE2_PML	-10.866	-9.528
ELF1_MAX_NFE2	-10.866	-10.069
ATF3_MAX_NFE2	-10.866	-9.069
BHLHE40_NFE2_YY1	-10.866	-10.069
CMYC_NFE2_RCOR1	-10.866	-10.461
HMGN3_MAX_NFE2	-10.917	-9.528
EGR1_NFE2_POL2	-10.917	-9.39
IRF1_NFE2_YY1	-10.917	-10.069
NFE2_P300_POL2	-10.917	-9.39
NFE2_PML_POL2	-10.966	-9.39
NFE2_POL2_RCOR1	-10.966	-8.654
CMYC_EJUND_NFE2	-11.013	-10.461
NFE2_NRSF_POL2	-11.059	-9.528

NFE2_POL2_ZBTB7	-11.103	-9.654
IRF1_MAX_NFE2	-11.103	-10.769
CJUN_EFOS_HMGN3	-11.188	-10.528
CCNT2_CJUN_EFOS	-11.229	-10.769
HMGN3_NFE2_POL2	-11.268	-9.528
CMYC_NFE2_ZBTB7	-11.268	-10.712
E2F6_NFE2_YY1	-11.307	-10.39
CMYC_NFE2_USF1	-11.344	-10.238
E2F6_MAX_NFE2	-11.381	-10.592
CMYC_NFE2_PML	-11.381	-10.39
CMYC_E2F4_NFE2	-11.381	-9.528
CMYC_ETS1_NFE2	-11.416	-10.069
JUND_NFE2_POL2	-11.416	-10.592
MAX_NFE2_YY1	-11.416	-10.316
CMYC_NFE2_P300	-11.485	-9.876
CMYC_NFE2_SIN3	-11.551	-10.876
CCNT2_NFE2_POL2	-11.582	-9.769
CMYC_EGR1_NFE2	-11.582	-9.876
BHLHE40_NFE2_POL2	-11.582	-10.316
ELF1_NFE2_POL2	-11.613	-10.592
E2F6_NFE2_POL2	-11.644	-10.39
CMYC_ELF1_NFE2	-11.703	-10.975
ATF3_NFE2_POL2	-11.731	-10.069
IRF1_NFE2_POL2	-11.731	-10.654
CMYC_JUND_NFE2	-11.731	-11.023
CMYC_HMGN3_NFE2	-11.731	-10.528
CMYC_MAZ_NFE2	-11.787	NS
CCNT2_CMYC_NFE2	-11.787	-10.238
NFE2_POL2_SIN3	-11.787	-9.975
ATF3_CMYC_NFE2	-11.892	-9.769
BHLHE40_CMYC_NFE2	-11.99	-10.712
CMYC_IRF1_NFE2	-12.036	-10.823
CMYC_E2F6_NFE2	-12.125	-11.495
CMYC_NFE2_YY1	-12.268	-11.426
NFE2_POL2_YY1	-12.307	-10.528
CMYC_MAX_NFE2	-12.582	-11.712
MAX_NFE2_POL2	-12.703	-11.156
HMGN3_TAL1_ZBTB7	-3.66	-10.069
CHD2_TAL1_UBTF	-10.146	-10.069
CTCFC_TBP_UBTF	-10.381	-9.876
JUND_RAD21_UBTF	-10.518	-9.975
HMGN3_TAL1_UBTF	-10.229	-10.316

NRSF_TRIM28_UBTF	-10.307	-10.316
CCNT2_CHD2_TAL1	-10.582	-10.156
CHD2_NRSF_UBTF	-10.518	-10.316
HMGN3_NRSF_UBTF	-10.644	-10.823

Table S6. Enrichment or depletion of single TRs in cRPGs compared to HE-NRGs in human cell types.
For each cell type, the log2 of the fold change (enrichment) and the FDR-corrected *p*-value are shown.
NaN's indicate that the particular TR was not immunoprecipitated in the particular cell type or the enrichment was not at the FDR ≦ 0.01 level.

TR	**Cell type**					
	K562	GM12878	h1hESC	HeLaS3	HepG2	A549
KAT2A	NaN	4.131 2e-06	NaN	3.333 3.7e-06	NaN	NaN
ZZZ3	NaN	4.394 2e-06	NaN	NaN	NaN	NaN
RCOR1	NaN	2.684 0.0064	NaN	NaN	NaN	NaN
BRCA1	NaN	2.095 0.00091	NaN	NaN	NaN	NaN
SIX5	0.696 0.0085	0.579 0.0013	NaN	NaN	NaN	0.809 0.0033
HDAC6	1.472 0.0077	NaN	NaN	NaN	NaN	NaN
RCOR1	NaN	1.394 0.0067	NaN	NaN	NaN	NaN
TAF7	0.824 4.9e-06	NaN	NaN	NaN	NaN	NaN
MYC	NaN	0.536 0.0012	NaN	NaN	0.259 0.0093	NaN
GTF2B	0.667 0.00029	NaN	NaN	NaN	NaN	NaN
CHD1	NaN	NaN	0.394 0.0096	NaN	NaN	NaN
GTF2F1	0.348 0.004	NaN	NaN	NaN	NaN	NaN
POL2	NaN	NaN	0.293 0.0022	NaN	NaN	NaN
SP1	NaN	-0.442 0.0094	NaN	NaN	NaN	NaN
ELF1	NaN	-0.538 0.00091	NaN	NaN	NaN	NaN
RUNX3	NaN	-0.590 0.0031	NaN	NaN	NaN	NaN
EGR1	NaN	-0.715 0.00091	NaN	NaN	NaN	NaN
CREB1	NaN	NaN	NaN	NaN	NaN	-0.789 0.0033
BACH1	NaN	NaN	-0.907 0.0096	NaN	NaN	NaN
EBF1	NaN	-0.932 0.0007	NaN	NaN	NaN	NaN
TBP	-0.943 3.9e-05	NaN	NaN	NaN	NaN	NaN
USF2	NaN	-0.958 0.0055	NaN	NaN	NaN	NaN
TFAP2C	NaN	NaN	NaN	-1.097 6.2e-05	NaN	NaN
TFAP2A	NaN	NaN	NaN	-1.102 6.1e-05	NaN	NaN
AP2ALPHA	NaN	NaN	NaN	-1.102 6.1e-05	NaN	NaN
TAF1	NaN	-0.613 0.00018	-0.493 0.0022	NaN	NaN	NaN
AP2GAMMA	NaN	NaN	NaN	-1.145 3.5e-05	NaN	NaN
HAE2F1	NaN	NaN	NaN	-1.198 2.2e-05	NaN	NaN
E2F1	NaN	NaN	NaN	-1.215 0.00018	NaN	NaN
MAZ	NaN	-0.795 5e-05	NaN	-0.615 0.0026	NaN	NaN
P300	NaN	NaN	NaN	-1.444 0.0069	NaN	NaN
EP300	NaN	NaN	NaN	-1.444 0.0069	NaN	NaN
UBTF	-1.789 4.9e-06	NaN	NaN	NaN	NaN	NaN
NRF1	NaN	-0.609 0.008	NaN	-1.254 0.0032	NaN	NaN
MAFK	NaN	NaN	-2.701 0.0022	NaN	NaN	NaN
NFYA	NaN	-1.913 0.00064	NaN	-0.871 0.004	NaN	NaN
ZBTB7	-1.054 0.0002	NaN	NaN	NaN	-1.869 2.1e-05	NaN
NFE2	-3.145 0.0013	NaN	NaN	NaN	NaN	NaN
NFYB	-0.828 0.0047	-0.756 0.0086	NaN	-1.620 2.1e-05	NaN	NaN
FOS	-1.071 0.0023	-1.913 5e-05	NaN	-2.360 0.00024	NaN	NaN
CFOS	-1.163 0.0033	-2.097 9.5e-05	NaN	-2.360 0.00024	NaN	NaN

Table S12. TRs selected for most accurate prediction of transcript levels. Sets of 20 TRs identified by LARS are shown for human and mouse cell lines.

Cell type	Species	TRs																			
K562	human	SIN3	IRF1	HDAC8	NFYB	MYC	GTF2F1	TAF1	ETS1	EJUNB	JUNB	CTCFC	RFX5	CEBPB	SETDB1	RDBP	MAFF	CJUN	NRF1	CHD1	NELFE
MEL	mouse	TAL1	ZKSCA	MYC	CTCF	USF2	RCOR1	NELFE	RAD21	CHD2	EP300	ZC3H11A	RpII215	KAT2A	GATA1	GABPA	E2F4	ETS1	HCFC1	MYB	SIN3A
GM12898	human	TBLR1	NFYB	RAD21	NRSF	REST	MEF2	USF2	KAT2A	JUND	NFIC	BRCA1	STAT3	ETS1	RCOR1	NFYA	CHD1	MTA3	POL2	PML	TAF1
CH12.LX	mouse	HCFC1	GABPA	EP300	E2F4	CTCF	KAT2A	TBP	ZKSCAN	CHD2	RpII215	RCOR1	USF2	JUN	POLR2Aph	MAZ	ETS1	PAX5	NELFE	ZNF384	UBTF