Liver-specific ablation of KRAB Associated Protein 1 in mice leads to male-predominant hepatosteatosis and development of liver adenoma

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Keywords: steatosis, hepatic adenoma, KRAB-ZFP, sexual dimorphism, transcriptional repressor

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List of Abbreviations: KRAB, Krüppel associated box; KAP1, KRAB-associated protein 1; ERK1/2, extracellular-signal-regulated kinases 1/2; Cyp, cytochrome p450; GST, gluthatione S-transferase; Slp, sex limited protein; Rsl, regulator of sex limitation; ZFP, zinc finger protein; SETDB1, SET domain bifurcated 1; H3K9me3, histone 3 lysine 9 tri-methylation; ESC, embryonic stem cell; Alb, albumin; Cre, Cre recombinase; ORO, Oil Red O; HFD, high fat diet; CD, chow diet; FFA, free fatty acids, AST, aspartate transaminase; ALT, alanine transaminase; IL1β, interleukin 1 β; IL6, interleukin 6; TNFα, tumor necrosis factor α; MAPK, mitogen-activated protein kinase; PTEN, phosphatase and tensin homolog; AKT, protein kinase B; BrdU, bromodeoxyuridine; TUNEL, terminal deoxynucleotidyl transferase dUTP nick end labeling; PPAR; peroxisome proliferator receptor; Mup, major urinary protein; FSP27, fat specific protein 27; c-Cbl, Casitas B-lineage lymphoma; SUMO, small ubiquitin-like modifier

Supported by grants from the Swiss National Science Foundation and the European Research Council (to D.T.).

Abstract

The liver is characterized by sexually dimorphic gene expression translating into sex-specific differences in lipid, drug, steroid hormone and xenobiotic metabolism, with distinct responses of males and females to environmental challenges. Here, we investigated the role of the KRAB-associated protein 1 (KAP1) epigenetic regulator in this process. Liver-specific KAP1 knockout led to strikingly sexually dimorphic phenotypic disturbances, including male-predominant steatosis and hepatic tumors with upregulation of AKT and ERK1/2 mitogen-activated protein kinase signaling. This correlated with sex-specific transcriptional dysregulation of a wide range of metabolic genes, notably those involved in retinol and sex hormone processing as well as in detoxification. Furthermore, chromatin immunoprecipitation followed by deep sequencing indicated that a number of dysregulated genes are direct targets of the KRAB/KAP1 repression system. Those genes include sexually dimorphic *Cyp2d9*, *Gst*π, *Slp Cyp2a*, *Cyp2b* and *Cyp3a* gene clusters. Additionally, we identified a male-restricted KAP1 binding site in the *fsp27* (fat specific protein 27) gene, correlating with its male-predominant upregulation upon *Kap1* deletion, suggesting that the latter might be an important trigger in the development of male-specific hepatosteatosis and secondary tumorigenesis.

Conclusion: This work reveals KRAB/KAP1-mediated transcriptional regulation as a central event in the metabolic control hormones, drugs and xenobiotics in the liver, and further links disturbances in these processes with hepatic carcinogenesis.

Metabolism is orchestrated by complex gene regulatory networks, and the liver is central to this process. This organ is characterized by sexually dimorphic gene expression, with numerous genes transcribed in a sex-dependent manner[1]. In mice, examples of such genes include the male-predominant *Cyp2d9*, which encodes for a testosterone-16-α-hydroxylase inactivating the main male sex hormone and various drugs, and the female-predominant *Cyp2a* and *Cyp2b* genes involved in xenobiotic and drug metabolism[2]. The sex-specific expression of these and other classes of enzymes results in the differential response of males and females to environmental challenges, with males displaying a higher predisposition than females for liver inflammation, cirrhosis and tumors following infections or non-alcoholic steato-hepatitis[3, 4].

Sexually dimorphic gene expression in the liver is established by sex-specific action of liver transcription factors[1]. One of those, regulator of sex limitation (Rsl), belongs to the Krüppel-associated box zinc finger proteins (KRAB-ZFP) family of tetrapod-specific transcription repressors, which counts between 300 and 400 members in mouse and human[5]. KRAB-ZFPs are characterized by the presence of an N-terminal KRAB domain required for repression and a C-terminal array of DNA-binding ZFs. Few have been assigned a physiological role *in vivo*, yet enough data is available to indicate that these proteins display a wide range of biological activities, from the control of imprinting to regulation of metabolic processes in neurons[6, 7].

Whereas the role and gene targets of the vast majority of KRAB-ZFPs remain ill defined, how they repress transcription is comparatively well understood. Many KRAB-ZFPs likely bind DNA in a sequence-specific manner via their ZFs and recruit KRAB-associated protein 1 (KAP1, also known as TIF1β, TRIM28 and KRIP-1), which serves as their universal cofactor.

KAP1 in turn acts as a scaffold for a chromatin-remodeling complex comprising the histone methyltransferase SETDB1, which catalyses histone 3 lysine 9 tri-methylation (H3K9me3), histone deacetylases, nuclear remodeling factors as well as heterochromatin protein 1. The formation of heterochromatin ensues, leading to epigenetic silencing[8].

In the mouse, constitutive *Kap1* knockout is early embryonic lethal, correlating with an absence of gastrulation[9]. Deleting *Kap1* in ESC leads to loss of pluripotentiality, imprinting defects, and failure to silence endogenous and some exogenous retroviruses[6, 8, 10]. In adult tissues, KAP1 regulates spermatogenesis and impacts on the management of behavioral stress[8, 11]. Furthermore, inbred mice heterozygous for a null mutation in *Kap1* were found to exhibit greater variance in body weight than wild type littermates, and for some animals liver steatosis, adipocyte hypertrophy and impaired glucose tolerance[12].

Here, we explored the role of KRAB/KAP1 in liver function. The analysis of hepato-specific conditional *Kap1* KO mouse revealed a sexually dimorphic metabolic syndrome, with male-preominant liver steatosis and tumorigenesis. This correlated with sex-specific transcriptional dysregulation of genes involved in retinol, xenobiotic and drug metabolism. The identification of KAP1-binding sites in the mouse liver further revealed that a number of the affected genes are direct KAP1 targets. This study thus unveils the important contribution of KRAB/KAP1-mediated regulation to liver function and metabolism.

Experimental Procedures

Mice generation and phenotyping. Generation and genotyping of mice with a floxable Kap1 allele (*Kap1*$^{fl/fl}$) and the *Alb.Cre* mouse strain have been previously described[9, 13]. Animals were housed in standard conditions with water and chow or high fat diet provided *ad libitum* - for details see Supporting Experimental Procedures. All animal experiments were approved by the local veterinary office and carried out in accordance with the European Community Council Directive (86/609/EEC) for care and use of laboratory animals. Phenotyping was performed on at least 8 males and females. For details see Supplementary Methods.

Histological tissue processing and analysis. Hematoxylin and erythroeosine and Oil Red O (ORO) stainings were performed according to standard procedures. Histopathology evaluation, ORO scoring and tumor occurrence analysis were done by a board certified pathologist (F.A.). Hepatocellular lesions were classified as foci of cellular alteration, hepatocellular adenomas and hepatocellular carcinoma according to established criteria[14]. For BrdU pulse-labeling, mice received 3 mg/ml of BrdU in drinking water for 6 days and the liver tissue was stained for BrdU (Oxford Biomedical Research). TUNEL assay was performed with the Apoptag kit (Millipore) according to manufacturer's instructions.

Small scale DNA, RNA and protein analysis. Genotyping, RNA extraction and reverse-transcription as well as protein analysis were performed according to standard procedures as previously described, see Supplemental Methods[11].

MicroArray analysis. 8-10-week-old mice were food-deprived at 0700 hrs and liver was isolated at 1100-1400 hrs. Total RNA was extracted with the MirVana kit (Ambion) and treated with DNAse (Ambion), following manufacturer instructions. Three RNA pools from 9 mutant and wild type male livers were prepared, while three individual female KO and wild type livers were used separately. Microarray analysis was performed as previously described[11]. Significantly deregulated genes ($p<0.05$ by unpaired t-test and fold-change ≥ 2) were used to interrogate DAVID bioinformatic database[15].

ChIP-sequencing and ChIP-PCR. Liver chromatin was performed as previously described with minor modifications[16]. For ChIP-seq, chromatin from two male and female *Kap1*$^{fl/fl}$ and one male and female *Alb.Cre Kap1*$^{fl/fl}$ control were prepared. Chromatin immunoprecipitation with an affinity-purified rabbit polyclonal antibody kindly provided by Dr. Rauscher[17] was performed as previously described[18]. Details describing sequencing, read alignment and subsequent analyses are provided in Supporting Methods.

Statistical analysis. Body and organ weight measurements as well as plasma biochemistry were analyzed with the two-tailed Student's *t* test or two-way ANOVA followed by the Bonferroni post-test. Contingency testing was done with Fisher's exact test. For statistical analysis of high throughput data see related paragraphs.

Results

Generation of hepatocyte-specific Kap1 knockout mice. We crossed *Kap1*$^{fl/fl}$ mice[9] in a mixed C57/Bl6-Sv129 background with animals expressing the Cre recombinase under the control of an albumin promoter[13]. We confirmed the liver-specificity of *Kap1*-deletion by locus-specific PCR, and determined that, in whole liver from mutant mice, KAP1 mRNA was reduced by more than 75% and protein was undetectable by Western blot, while immunohistochemistry confirmed that its loss was restricted to hepatocytes (Supporting Fig. 1). Histology combined with Oil Red O (ORO) staining further revealed that 8-10-week-old male *Alb.Cre Kap1*$^{fl/fl}$ mice, but not their female counterparts, suffered from mild liver steatosis (Supporting Fig. 1). These results suggested that loss of KAP1 perturbed metabolic homeostasis in the liver, and pointed to possible sex-specific differences in this process.

Sex-dependent phenotypic consequences of hepatocyte-specific Kap1 KO. Because of this early finding and of known sex-related differences in metabolism and liver function in rodents and other mammals including humans[1, 19], we followed a phenotyping protocol that separately examined male and female mice (see Experimental procedures). At 8-10 weeks of age, no differences in body weight, food intake and plasma markers of liver function and lipid metabolism between mutant and wild type mice were observed (not illustrated). However, histopathology revealed significant fat accumulation with small vacuoles in all of 12 KO male livers compared with only one third (4 out of 12) of controls (Fisher's exact test, p= 0.0013; not shown), while females were exempt of this pathology. The steatosis noted in male KO mice was not due to Cre, because no difference was observed between *Alb.Cre* *Kap1*$^{wt/wt}$ and *Kap1*$^{wt/wt}$ animals (not illustrated).

We then asked whether a metabolic challenge would accentuate the phenotype of male *Kap1* KO mice. For this, we fed 10-week-old male and female *Alb.Cre Kap1*$^{fl/fl}$ and *Kap1*$^{fl/fl}$ littermates with high fat diet (HFD; 60% calories from fat) or chow diet (CD) for 19 weeks. CD-fed *Kap1* KO males displayed progressive hepatosteatosis characterized by increased liver weight and fatty change of mild to moderate degree at 6 months of age (Fig. 1B and 1C, Table 1). In contrast, control littermates exhibited minimal lipid accumulation in the liver as revealed by ORO staining (Fig. 1B and 1C). These changes were not accompanied by weight gain, increased food intake and only by a trend to upregulation of plasma markers of liver function (Fig. 1A and 1D; Table 1 and data not shown). Interestingly, *Kap1*-KO males displayed significantly lower plasma free fatty acid (FFA) concentration than littermate controls, suggesting an increased rate of hepatocytic FFA uptake following *Kap1* deletion (Table 1).

Upon HFD challenge both *Alb.Cre Kap1*$^{fl/fl}$ and *Kap1*$^{fl/fl}$ males developed severe hepatic steatosis (Fig. 1C), but the liver was heavier in *Kap1*-KO animals, which also presented with a bigger epididymal fat pad and a decreased testis weight (Table 1). Although this latter trait suggested an impaired sex hormone balance, a condition also observed in humans in cases of severe liver steatosis[4], total plasma testosterone levels were not different between KO and WT littermates (Table 1).

In contrast to males, CD-fed females did not present significant liver lipid accumulation, although *Kap1*-KO animals showed plasma dyslipidemia and upregulation of liver enzymes (Fig. 1A-D and Table 1). When subjected to HFD, *Kap1* mutant females displayed a higher body weight than littermate controls probably due to increased body fat content as assessed by echoMRI (Fig. 1A and Table 1). Furthermore, these mice were characterized by i) a moderate degree of liver steatosis (Fig. 1C); ii) mildly elevated plasma cholesterol and triglycerides; and iii) significant upregulation of ALT, AST as well as a clear trend in the upregulation of other plasma markers of hepatocytic dysfunction (Fig. 1D and Table 1). Nevertheless, *Kap1*-KO females were comparable to their littermates for food intake, physical activity and energy expenditure (not illustrated).

Development of hepatic adenomas in Kap1 KO males. Anatomo-pathological examination indicated that male *Alb.Cre Kap1*$^{fl/fl}$ mice on HFD had a tendency to develop liver tumors that occasionally reached large size and formed nodular masses distorting the lobar contour (Fig. 2A and 2B). Hepatic adenomas were seen in 4/11 HFD-fed and 1/12 CD-fed males at 29 weeks, while no tumors were found in *Kap1*$^{fl/fl}$ littermates (n=9 and n=10 on CD and HFD, respectively). In one of the HFD-fed *Kap1*-KO males a 2 mm in diameter hepatocellular proliferative focus with features of solid carcinoma was observed. Consistent with the previously reported protective effect of female hormones[3], Kap1-KO female mice appeared largely to escape HFD-induced tumorigenesis as only 1/10 HFD-fed KO females had an adenoma and no tumor was observed in wild type (n=10 on CD and n=10 on HFD) nor in CD-fed female KO mice (n=10). To confirm these results, we analyzed the livers of CD-fed mice at age of 53-72 weeks (Table 2). Macroscopic examination revealed that *Kap1*-KO mice presented with hepatomegaly (Table 2) and 9/15 (64%) male *Alb.Cre Kap1*$^{fl/fl}$ mice developed tumors compared to 2/13 (15%; $p<0.024$) wild type controls, while females appeared partially protected against this process with only 4/15 (27%) KO and 1/15 (7%) wild type controls showing hepatocellular tumors (Table 2 and Fig. 2C). Histopathological examination performed on a subset of animals (13-15 in each subgroup) confirmed that all tumors observed in *Kap1*-deleted mice were adenomas, while focal cellular alterations were detected in both control and knockout mice. In addition, minimal infiltration by mixed inflammatory cells was noted in about a quarter of the animals, but no significant association with Kap1 status was found (not illustrated). We verified that similar results were obtained in a C57/Bl6 background (Supporting Fig. 2).

Although inflammation was not a prominent histological feature of *Kap1* KO livers, we observed higher intrahepatic levels of pro-inflammatory cytokines IL1β, IL6 and TNFα in this setting (Fig. 1E, Tables 1 and 2). IL6 and TNFα contribute to hepato-protection and induce hepatocyte proliferation during liver injury[20] and have been implicated in the development of fatty liver and tumors in other mouse models of liver tumorigenesis[3]. Since cytokine signaling involves several transduction pathways previously implicated in liver oncogenic transformation[21], we analyzed the activity of the mitogen-activated protein kinase (MAPK) pathway, the phosphorylation levels of AKT as well as the expression levels of PTEN, key regulators of the PI3 kinase pathway (Fig. 2D and 2E). Total levels of p38 MAPK were similar in wild type and KO animals, irrespective of their genetic background. However, levels of phosphorylated p38 were increased in knockout livers. As an expected corollary, there also was a significant hyperphosphorylation ERK1/2 MAPK and MEK1 in KAP1-depleted tissue (Fig. 2D and 2E). Furthermore, tumor tissue harvested from *Kap1* KO liver displayed a marked upregulation of both total and phosphorylated ERK1/2, despite normal levels of activity of other components of the MAPK pathway. Additionally, we observed AKT hyperphosphorylation in the tumor tissue despite normal total protein levels. These results suggest that amplification of ERK1/2 and increase of AKT signaling plays a prominent role in the development of adenomas in *Kap1* KO livers. In contrast, there was no significant change in the phosphorylation status of JNK/SAPK nor abnormalities in PTEN levels (Fig. 2D).

To assess the contribution to the observed phenotype of hepatocyte proliferation and hepatic cell death, we performed BrdU pulse in 35- and 68-week-old mice and found that hepatocyte proliferation was comparable between KO and controls (Fig. 2F). Similarly, histological examination and TUNEL staining in KAP1-depleted livers did not reveal any significant signs of cell death in *Kap1*-KO livers (data not shown).

In summary these results indicate that loss of KAP1 in the liver leads to sexually dimorphic phenotypes, with males exhibiting progressive steatosis and age-related tumorigenesis, and females suffering from a less dramatic syndrome with mild metabolic defects, including obesity and steatosis revealed only upon exposure to an environmental stress.

Sex-specific gene dysregulation in Kap1 knockout liver. We performed gene expression profiling in liver from CD-fed 8- to 10-week-old wild type and mutant male and female mice, choosing this young age in order to minimize the potential impact of compensatory changes. Loss of KAP1 led to at least two-fold dysregulation of 170 and 149 genes in male and female mice, respectively. Interestingly, less than 50% of the deregulated genes were common to the two sexes (Fig. 3A), suggesting that the KRAB/KAP1 system targets different genes in males and females. Gene ontology analysis of 2-fold dysregulated transcripts (Supporting Table 1) indicated that loss of KAP1 impacted on genes encoding protein endowed with oxidoreductase activity involved in xenobiotic metabolism by cytochrome P450 (Cyp450) as well as the pathways of retinol, drug and arachidonic acid metabolism (Fig. 3B). Additionally, GO terms and Kegg pathway analyses singled out genes relevant for steroid hormone biosynthesis and metabolism, peptidase inhibitor activity and PPAR signaling in male KO mice, contrasting with genes linked to pheromone binding in their female counterparts. About 50% of genes with the highest fold-change differed between male and female mice. For example, the most highly upregulated genes in males belong to phenobarbital-inducible Cyp2b family, while in females those include Spink3, Krt23 and Cyp2d9 (Fig. 3C). We verified that the transcriptional changes noted upon *Kap1* deletion were not due to the mixed genetic background of the mice nor to Cre expression (Supporting Fig. 2).

KAP1 controls expression of Rsl-target genes. Female-restricted changes in Cyp2d9, sex-limited protein (Slp) and major urinary proteins (Mup), are hallmarks of the *Rsl* loss-of-function phenotype[5]. While we could document both *Cyp2d9* and *Slp* derepression in female *Kap1* KO livers (Fig. 3D), *Slp* appeared affected to a far lower extent than reported in *rsl*-deleted female mice, although a direct comparison is difficult owing to differences in the mouse strains used in the two studies. Furthermore, we observed a downregulation, rather than an upregulation of *Mups* in *Kap1* mutant mice at both RNA and protein level (Fig. 3D and Supporting Fig. 3), suggesting that either Rsl2-mediated female-specific repression[5] is not mediated by KAP1 or that *Mups* are indirect KAP1 or Rsl targets.

KAP1 binding sites and KAP1-related chromatin modifications in the mouse liver. To understand better the molecular mechanisms of KAP1-mediated gene expression control in the liver, we performed chromatin immunoprecipitation (ChIP) followed by deep sequencing on male and female wild type and KAP1-depleted nuclei, using an antibody directed against the RBCC domain of KAP1[8]. False-positive peaks originating from non-hepatocytic cells present in the samples were minimized by following a protocol optimized for hepatocyte-centered ChIP experiments[16], and data obtained in *Kap1*-deleted hepatocytes served as a control sample for peak calling. We identified 7158 and 5223 KAP1 peaks in male and female livers, respectively (Fig. 4A), a number comparable to that extrapolated from genome-wide KAP1 binding studies previously performed in other tissues[22]. Surprisingly few of the identified peaks (~10%) were common to males and females (Fig. 4A), consistent with the observed sex-specific gene dysregulations induced by the *Kap1* knockout (Fig. 2). KAP1 peaks were significantly enriched in vicinity of transcriptional start sites (TSS; Fig. 4B).

We then searched the nearest peak for each of the genes dysregulated at least 1.5-fold upon KAP1 removal (Supporting Table 1). We observed that relatively few of them had a KAP1-binding site in the gene body (less than 20%; not shown), however the average distance between both upregulated and downregulated genes and the nearest KAP1 peak was significantly shorter than for all protein-coding genes present on our Illumina chip (Fig. 4C). Furthermore, these peaks were usually found just upstream of the TSS of deregulated genes (Fig. 4D). This suggests that KAP1 might directly control many of the genes perturbed in its absence, but that it may not always be through repression.

Surprisingly, for several genes expressed and deregulated in a sex-discriminating fashion, KAP1-binding was found in both males and females (Fig. 3 and 5). These included peaks in the promoter of the male-predominant *Cyp2d9* and *Slp* genes, both strongly upregulated in *Kap1* KO females; and in the *glutathione S-transferase* π (*Gst*π) cluster, a late-phase drug-responsive gene preferentially expressed in males, with strong downregulation upon KAP1 removal. Of note, the *Gst*π cluster bears a male-specific KAP1 binding site downstream of the locus that could explain sex-biased dysregulation. Moreover we identified putative KAP1-binding sites in an intron of the gene encoding fat specific protein 27 (FSP27), which plays a role in lipid droplet formation[23] and was strongly upregulated in male KO livers and in the gene encoding for the cellular homologue of the viral Casitas B-lineage lymphoma proto-oncogene (c-Cbl), a regulator of various tyrosine kinase signaling pathways[24] upregulated in KO livers of both sexes (Fig. 3E, 5 and 6A). We also identified KAP1 binding sites in a cluster of phenobarbital-responsive, female predominant *Cyp2b* genes that were upregulated in males and downregulated in females upon loss of KAP1 and in clusters of other xenobiotics-processing *Cyp450* genes, such as *Cyp2a* and *Cyp3a* (Fig. 3E, 5, 6A and Supporting Fig. 4).

KAP1 recruits the SETDB1 histone methyltransferase, which induces deposition of the H3K9me3 repressive mark, and HDAC-containing complexes, which result in histone deacetylation[17]. We thus compared the presence of the relevant chromatin marks in wild type and *Kap1* knockout liver at both nearest KAP-binding site and promoter of a few genes suspected to represent direct KAP1 targets. Loss of KAP1 correlated with a loss of H3K9me3 at the binding site for genes upregulated in *Kap1*-mutant livers, such as *Cyp2d9* in females and *fsp27*, *c-Cbl* or the *Cyp2b* cluster in males. However, for male-downregulated *Gstπ*, *Cyp2d9* or *Slp* no change in H3K9me3 at the KAP1-binding site was detected. Notably, gain of H3K9me3 at the male KAP1-binding site in the *fsp27* locus in female liver suggests local chromatin changes that could be the cause of mild female-upregulation of the corresponding transcript. Finally, increase in H3Ac at the promoters of *Cyp2d9* in females and *Fsp27* in males coincided with gene dysregulation, however this was not the case for all tested KAP1-target loci (Fig. 6B-C).

Discussion

The present work reveals the prominent role of KRAB/KAP1-mediated regulation in the control of liver metabolism and endo/xenobiotics-detoxifying genes. The liver-targeted knockout of KAP1, the universal cofactor of KRAB-ZFPs, resulted in a markedly sexually dimorphic phenotype in mice, which included male-predominant steatosis and hepatic tumors. This correlated with sex-specific transcriptional dysregulation of a wide range of metabolic genes, notably those involved in retinol and sex hormone processing as well as in detoxification. An examination of KAP1 genomic binding sites in the liver and of chromatin marks at the promoters of some of these genes further revealed that a number of detoxifying genes such as *Cyp2d9*, *Gst*π, and the *Cyp2a*, *Cyp2b* and *Cyp3a* gene clusters are direct KAP1 targets. Moreover, loss of KAP1 binding at the *fsp27* locus was associated with the male-predominant upregulation of its product.

Male liver-specific *Kap1* knockout mice displayed early onset hepatosteatosis and age-related development of liver adenomas, while their female counterparts exhibited milder metabolic disturbances revealed only by a high fat diet challenge and had lower incidences of liver adenomas than their male counterparts. This correlates with the reported resistance of the female liver to environmental insults, which has been attributed to its greater ability to inactivate toxins and neutralize reactive oxygen species, and to the protective action of estrogens against inflammation and steatofibrosis, including during the course of chronic viral hepatitis[19, 25]. Our results suggest that these mechanisms are influenced by KRAB/KAP1-mediated transcriptional control.

What specific mechanisms account for the accumulation of fat and tumor development in the *Kap1*-deleted male liver remains to be determined. We observed a male-predominant, *Kap1* deletion-induced upregulation of the fat-specific protein 27 (FSP27), correlating with a male-restricted strong KAP1 binding site in the body of this gene. FSP27 promotes fat droplet formation in adipocytes and its hepatocytic overexpression results in hepatosteatosis[23, 26]. This phenotypic abnormality, which represents an early sign of hepatocyte suffering common to many pathological circumstances, has been linked to increased liver damage, inflammation and development of hepatocellular carcinoma in other mouse models[3]. Interestingly, KAP1 KO mice displayed an upregulation of liver levels of pro-inflammatory cytokines IL6 and TNFα, which is a sign of response to hepatocyte damage. Aberrant activity of signaling pathways downstream of these cytokines have been linked to increased fat accumulation in hepatocytes and development of liver tumors and our results suggest a role of the MAPK and AKT pathways in the increased incidence of tumors in *Kap1* KO animals[3]. The early development of hepatosteatosis due to de-repression of *fsp27* in KAP1 KO males may be one important trigger in a cascade of events leading to development of liver steatosis and tumors in these mice.

Indirectly, our analyses suggest that xenobiotic stress, which if prolonged can lead to tumorigenesis[27], might contribute to the observed phenotype. In *Kap1*-deleted livers, we measured a dysregulation of drug and xenobiotic metabolizing phase I genes such as members of the *Cyp2a*, *Cyp2b* and *Cyp3a* families, of phase II and III genes such as *Gst*π and θ, and of genes coding for various UDP-glucuronosyltransferases required for conjugation of molecules that need this modification for efficient excretion[2]. We identified KAP1-binding sites in the vicinity of several of these genes, suggesting that they are direct targets of the transcriptional regulator.

The combined results of our transcriptome and chromatin analyses exclude a simple model for KAP1 action, whereby a given KRAB-ZFP would tether the cofactor to specific sequences, with secondary heterochromatin formation and gene silencing. Some sexually dimorphic genes, such as the male-predominant *Cyp2d9*, *Gst*π and *Slp*, carry KAP1 signatures inconsistent with such a model. For instance, the *Cyp2d9* and *Slp* genes are Rsl1-targeted, male-predominant genes upregulated upon *Kap1* KO only in female mice. However, KAP1 was detected at similar sites, such as the promoter of *Cyp2d9*, in liver chromatin from both sexes. As well, KAP1 binds upstream of the *Gst*π locus in both male and female, whereas this gene is highly expressed in the former and strongly repressed in the latter. These observations might reflect the effect of sex-specific dominant factors counteracting the repressing influence of KAP1, or sex-differential post-translational modifications of the transcription regulator. KAP1 SUMOylation appears to be required for its co-repressor activity, while phosphorylation stimulates its chromatin-opening properties[8]. In the case of *Cyp2d9*, it could be that phospho-KAP1 keeps the promoter accessible for transcription factors in males, whereas SUMO-KAP1 recruits SETDB1 and heterochromatin protein 1 to close it down in females.

It is generally acknowledged that KAP1 exerts its gene repressor activity via an interaction with DNA-binding KRAB-ZFP family members. It will be important to identify the mediators of its activity in the liver; however it remains that our data strongly suggest that KAP1 sometimes acts as a transcriptional activator rather than as a repressor. Future studies should explore this possibility, which challenges the current view of KAP1 function.

Acknowledgments

We thank the Histology Core Facility at EPFL, the NCCR Genomics Platform at University of Geneva and the EPFL Transgenic Core Facility for technical assistance, Jacques Rougemont for bioinformatics support, and Juergen Ripperger, Walter Wahli, Gianpaolo Rando and Kristina Schoonjans for discussions. The computations were performed on the Vital-IT facility of the Swiss Institute of Bioinformatics.

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Figure Legends

Figure 1. Phenotypic analyses of *Kap1* KO mice.

A. Body weight of male (n=9-12; top) and female (n=10; bottom) mice fed indicated diets. *: $p<0.05$ as assessed by two-way ANOVA followed by Bonferroni post-test. CD - chow diet, HFD - high fat diet. **B**. HE staining of liver sample from chow diet-fed 29-week-old indicated mice. Inlet: ORO staining. Scale bar: 50 μm. **C**. Semi-quantitate ORO staining score of male (top) and female (bottom) mice fed indicated diets ***: $p<0.001$ as assessed by two-way ANOVA followed by Bonferroni post-test. **D**. **& E.** Plasma levels of alanine transaminase (ALT) and lactate dehydrogenase (LDH) (n=7-9; D.) and liver protein levels of pro-inflammatory cytokines IL6 and TNFα (n=5; E.) in 29-week-old female (left) and male (right) mice. Black bars: CD, grey bars: HFD. *: $p<0.05$ as assessed by two-way ANOVA followed by Bonferroni post-test. Error bars represent S.E.M.

Figure 2. Liver tumorigenesis in KAP1 KO mice.

A. Left, liver adenoma with a well demarcated nodular proliferation and a clear expansile growth; right, hepatocellular carcinoma with poorly demarcated irregular borders suggestive of infiltrative growth (black solid line), increased anisocytosis and anisokaryosis within the tumor, when compared to the adjacent normal hepatocytes (right) in male mouse fed HFD for 19 weeks. Scale bar in A: 2 mm. Scale bar in B: 100 μm. **B.** Macroscopic view of rostral (left) and caudal (right) face of livers from indicated CD-fed, 58-week-old male mice. **C.** Gross necropsy analysis of tumor occurrence in livers of mice at age 53-70 weeks. *: $p<0.024$ by Fisher's exact test. **D.** Western blot of indicated proteins in *Kap1* KO tumor tissue and normal liver from WT and *Kap1* KO mice (left) with quantification of band intensity normalized to actin and represented as fold-change over average WT liver (right). *** - $p<0.001$ by one-way ANOVA **E.** Phosphorylation status and total protein content of AKT and various MAPK in indicated samples determined by ELISA and represented as fold-change over average WT liver. *** - p<0.001 by one-way ANOVA **F.** Hepatocyte proliferation in livers of 35- and 68-week-old female (n=3-5; left) and male (n=4-5; right) mice. Data represent mean number of BrdU-positive nuclei per field of view. Error bars in **D.**, **E.** and **F.** represent S.E.M.

Figure 3. Hepato-specific KAP1 deletion leads to sex-specific gene dysregulation.

A. Venn diagram of genes ≥ 2-fold deregulated in 10-week-old female and male KO vs WT mice. Less than 50% of deregulated genes are shared between sexes. **B.** Functional annotation chart of significantly deregulated (fold change ≥ 2) in *Kap1*-mutant livers. **C.** Top 10 up- and down-regulated genes in male (left) and female (right) livers. **D.** Expression of Rsl-regulated sexually dimorphic genes in Kap1 KO and WT male and female livers (n≥5). Error bars represent SEM. **E.** Dysregulation of mRNA levels of selected direct KAP1-target genes; n=3-4. Error bars represent SEM.

Figure 4. KAP1 binding sites in mouse liver.

A. Number of KAP1 peaks on genome from male and female hepatocytes. **B.** Distribution of KAP1 putative binding sites relative to all annotated transcriptional start sites (TSS). For distance of -200, 0 and 200 bp relative to TSS KAP1 is significantly enriched (P<0.05) as assessed by the Wilcoxon sum rank test. **C.** KAP1-responsive genes are closer to the nearest KAP1 peak than random genes. Distance to the nearest peak was calculated for all KAP1 up- or down-regulated genes and compared to the average distance for all genes probed by the Illumina chip. **D.** Frequency of KAP1 peaks in different intervals from the TSS for genes downregulated (left) or upregulated (right) in *Kap1* mutant livers. Frequency is defined at the % of peaks normalized for the interval size.

Figure 5. Selected KAP1 putative binding sites in mouse liver.

Screen-shots from the UCSC Genome Browser illustrating the KAP1 ChIP-seq data from female and male *Kap1* KO (n=1) and WT (n=2) hepatocytes for indicated loci. Direction of transcription is indicated by arrow. Regions targeted by primers used for the validation by qPCR are shown.

Figure 6. Chromatin studies on KAP1-regulated genes.

A. qPCR validation of KAP1 binding in female and male livers (n=4). Data are represented as an enrichment of wild type over KO sample relative to an average of KAP1 unbound control loci (*Foxp3*, *RPS9* and *β-actin*) at sites depicted in A. Error bar is S.E.M. **B. & C.** H3K9me3 (B.) and H3 acetylation (C.) ChIP-qPCR in female and male nuclei (n=3) of wild type and KAP1-depleted liver. Data are represented as an enrichment of wild type over KO sample relative to an average of three control loci (*GAPDH*, *RPS9* and *β-actin*). Error bar is S.E.M.

Table 1. Plasma markers of lipid metabolism and liver function in 29-week-old mice.

Parameter	Female KO CD (n=7)	Female WT CD (n=8)	Female KO HFD (n=8)	Female WT HFD (n=8)	Male KO CD (n =10)	Male WT CD (n=7)	Male KO HFD (n=10)	Male WT HFD (n=9)
Body weight (g)	31.4 ± 1.4	30.0 ± 1.4	46.2 ± 2.2	41.0 ± 2.6	38.0 ± 1.4	35.9 ± 1.5	51.5 ± 2.2	52.4 ± 1.2
Body fat (%)	27.6 ± 3.0	26.1 ± 1.8	48.2 ± 1.4	41.6 ± 2.2	23.0 ± 1.6	23.3 ± 3.0	39.4 ± 0.6	38.6 ± 1.1
Liver (% BW)	4.1 ± 0.2	3.8 ± 0.2	4.0 ± 0.3**	3.0 ± 0.2	4.8 ± 0.2	4.0 ± 0.2	6.3 ± 0.4*	5.3 ± 0.3
PG-WAT (% BW)	6.3 ± 0.9	6.4 ± 0.6	10.9 ± 0.3	10.3 ± 0.6	4.7 ± 0.2	4.4 ± 0.4	4.5 ± 0.3	3.8 ± 0.2
Ovaries/Testes (% BW)	0.33 ± 0.03	0.34 ± 0.03	0.23 ± 0.02	0.25 ± 0.04	0.91 ± 0.03	0.93 ± 0.03	0.62 ± 0.02*	0.72 ± 0.04
Testosterone (ng/ml)	ND	ND	ND	ND	3.8 ± 1.4	2.2 ± 0.5	1.3 ± 0.6	4.5 ± 2.4
Cholesterol (mM)	4.8 ± 0.4	4.5 ± 0.3	6.0 ± 0.6*	4.1 ± 0.5	5.7 ± 0.2	4.5 ± 0.3	8.2 ± 0.4	7.9 ± 0.4
HDL Cholesterol (mM)	1.34 ± 0.25*	1.67 ± 0.17	2.11 ± 0.10	1.98 ± 0. 17	2.19 ± 0.09	2.33 ± 0.11	2.11 ± 0.10	2.95 ± 0.08
LDL Cholesterol (mM)	1.25 ± 0.55*	0.86 ± 0.33	0.73 ± 0.18	0.38 ± 0.06	0.44 ± 0.04	0.24 ± 0.03	1.10 ± 0.09**	0.83 ± 0.06
Triglycerides (mM)	1.46 ± 0.13**	1.20 ± 0.09	1.15 ± 0.05*	0.86 ± 0.03	1.56 ± 0.15	1.38 ± 0.16	1.10 ± 0.08	0.92 ± 0.09
Tot. Protein (g/l)	63.4 ± 1.2	63.1 ± 0.7	68.2 ± 1.4*	63.5 ± 1.8	63.9 ± 0.7	63.1 ± 1.3	68.6 ± 1.4	67.5 ± 0.7
Free Fatty Acids (mM)	1.60 ± 0.40	1.70 ± 0.21	1.66 ± 0.14	1.28 ± 0.09	1.06 ± 0.11*	1.75 ± 0.40	1.50 ± 0.14	1.77 ± 0.13
AST (U/l)	252 ± 79	173 ± 50	342 ± 82**	123 ± 18	118 ± 19	173 ± 67	373 ± 58	239 ± 72
γGT (U/l)	10.3 ± 2.1***	6.4 ± 1.4	3.7 ± 0.4	4.6 ± 0.5	7.3 ± 0.6	6.3 ± 0.6	6.4 ± 0.5	4.9 ± 0.6
IL-1β (ng/ml/mg protein)	4355 ± 106*	3881 ± 91	4380 ± 140	4257 ± 180	4234 ± 195	3614 ± 164	4021 ± 241	4485 ± 184
ALP (U/l)	79.8 ± 5.8	86.8 ± 4.3	104.3 ± 20.0*	66.8 ± 5.8	72.5 ± 3.8	67.1 ± 4.8	114.5 ± 14.7*	82.1 ± 5.1
Tot. Bilirubin (μM/l)	2.7 ± 0.6	2.2 ± 0.4	2.7 ± 0.5	1.5 ± 0.3	1.6 ± 0.2	2.1 ± 0.5	2.4 ± 0.4	1.3 ± 0.1
Glucose (mM)	15.8 ± 0.8	16.1 ± 0.9	17.0 ± 1.4	16.4 ± 1.3	17.5 ± 1.1	18.7 ± 1.2	17.9 ± 0.7	19.1 ± 1.0

Wild-type mice (WT) and animals bearing liver-specific KAP1 KO were fed chow diet (CD) or high fat diet (HFD) for 19 weeks and fasted for 4 hours prior to experiment.
 - p<0.05; ** - p<0.01; *** - p<0.001 as compared to control KAP1 WT of the same sex and diet by two-way ANOVA followed by Bonferroni post-test
ND – not determined; WAT – white adipose tissue; HDL – high density lipoprotein; LDL – low density lipoprotein; AST – aspartate transaminase; ALT – alanine transaminase; LDH – lactate dehydrogenase; γGT – gamma glutamyl transpeptidase; ALP – alkaline phosphatase

Table 2. Parameters describing 53-72-week-old KAP1 KO mice.

Parameter	*Female KO CD (n=15)*	*Female WT CD (n=15)*	*Male KO CD (n=15)*	*Male WT CD (n=13)*
Body weight	40.1 ± 2.5	46.2 ± 2.7	43.9 ± 2.7	45.9 ±2.8
Liver weight (% BW)	5.1 ± 0.3*	3.8 ± 0.1	6.5 ± 0.7*	4.5 ± 0.3
Age (weeks)	60.3 ± 3.9	59.3 ± 1.6	63.5 ± 1.6	62.1 ± 2.0
Liver IL1β (ng/ml/mg protein)	1611 ± 95	1606 ± 63	1962 ± 32*	1674 ± 78
Liver IL6 (ng/ml/mg protein)	1178 ± 79	1258 ± 51	1504 ± 87*	1255 ± 47
Liver TNFα (ng/ml/mg protein)	2085 ±161	2123 ± 156	2682 ±128*	2360 ±145

Wild-type mice (WT) and animals bearing liver-specific KAP1 KO were fed chow diet (CD) and fasted for 4 hours prior to experiment.
- significantly different ($p<0.05$) as compared to control KAP1 WT of the same sex by *Student's t* test.

Figure 1 - HEP-11-2341 - Bojkowska et al

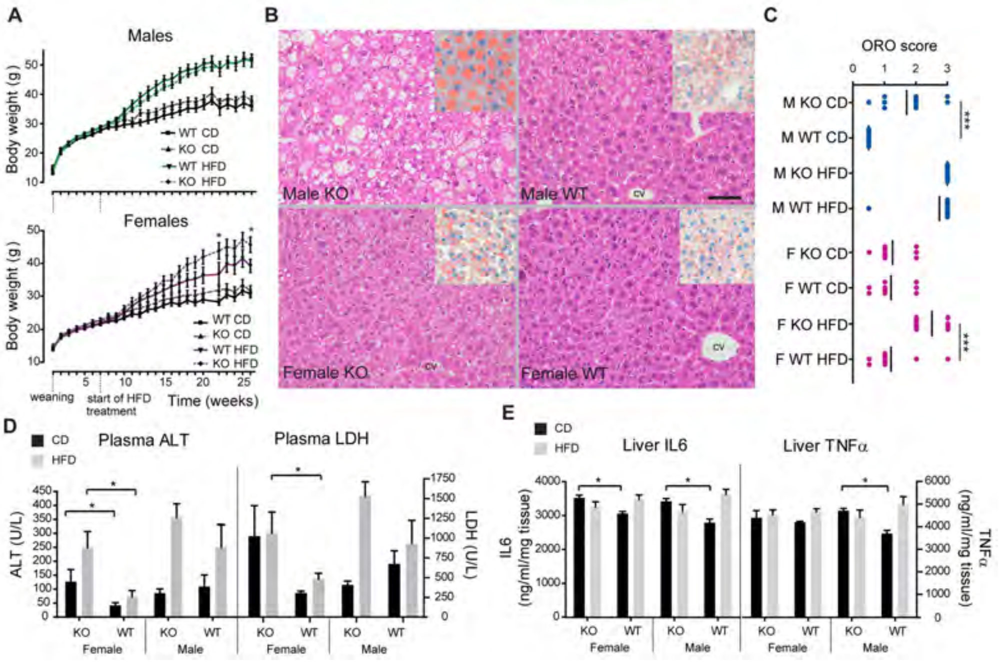

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Figure 2 - HEP-11-2341 - Bojkowska et al

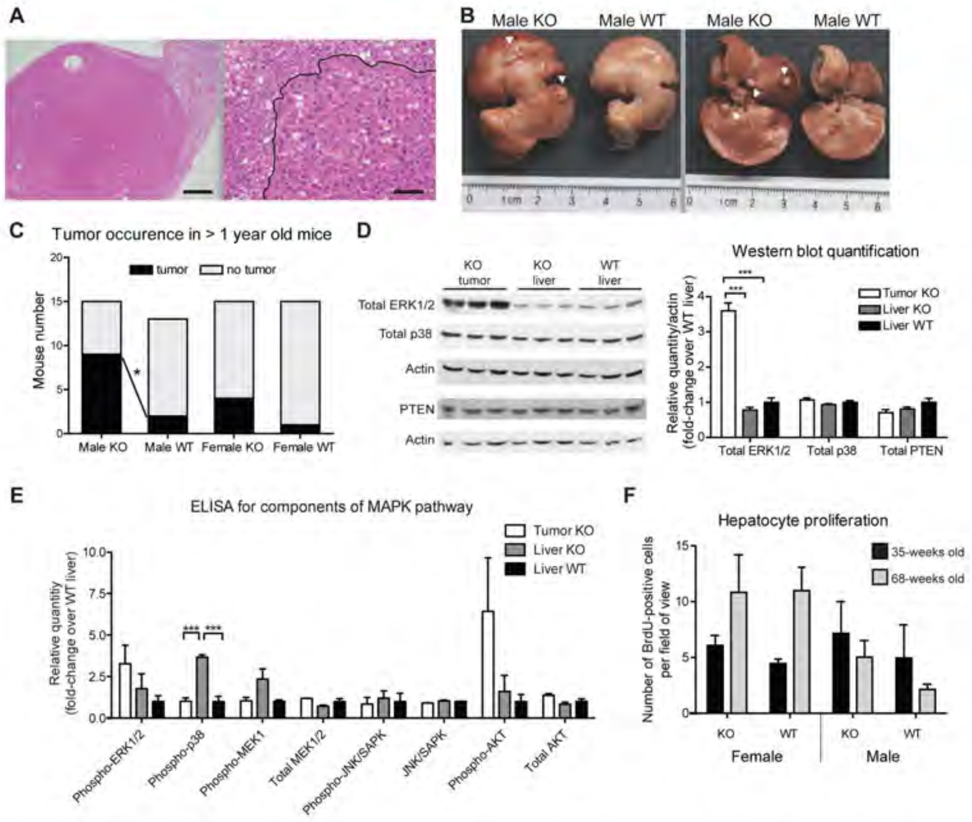

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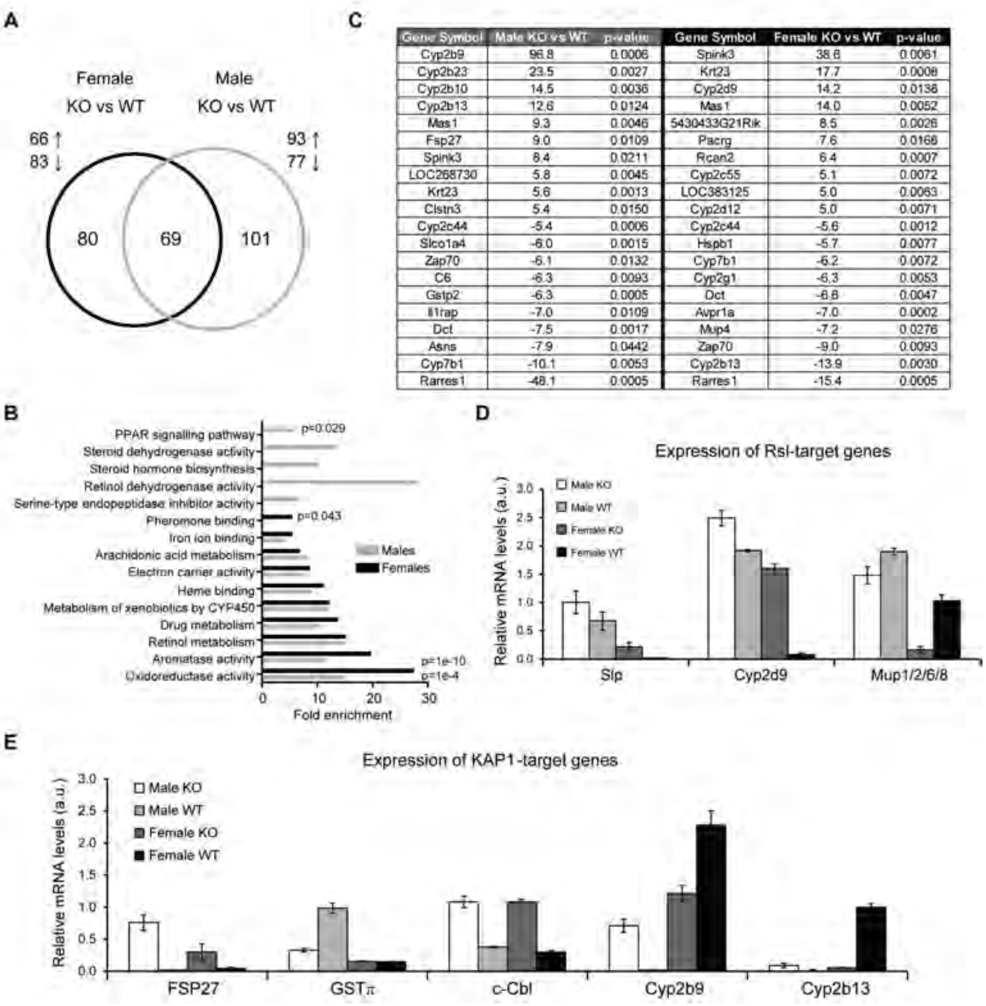
Figure 3 - HEP-11-2341 - Bojkowska et al



Gene Symbol	Male KO vs WT	p-value	Gene Symbol	Female KO vs WT	p-value
Cyp2b9	96.8	0.0006	Spink3	38.6	0.0061
Cyp2b23	23.5	0.0027	Krt23	17.7	0.0008
Cyp2b10	14.5	0.0036	Cyp2d9	14.2	0.0136
Cyp2b13	12.6	0.0124	Mas1	14.0	0.0052
Mas1	9.3	0.0046	5430433G21Rik	8.5	0.0026
Fsp27	9.0	0.0109	Pacrg	7.6	0.0168
Spink3	8.4	0.0211	Rcan2	6.4	0.0007
LOC268730	5.8	0.0045	Cyp2c55	5.1	0.0072
Krt23	5.6	0.0013	LOC383125	5.0	0.0063
Clstn3	5.4	0.0150	Cyp2d12	5.0	0.0071
Cyp2c44	-5.4	0.0006	Cyp2c44	-5.6	0.0012
Slco1a4	-6.0	0.0015	Hspb1	-5.7	0.0077
Zap70	-6.1	0.0132	Cyp7b1	-6.2	0.0072
C6	-6.3	0.0093	Cyp2g1	-6.3	0.0053
Gstp2	-6.3	0.0005	Dct	-6.6	0.0047
Il1rap	-7.0	0.0109	Avpr1a	-7.0	0.0002
Dct	-7.5	0.0017	Mup4	-7.2	0.0276
Asns	-7.9	0.0442	Zap70	-9.0	0.0093
Cyp7b1	-10.1	0.0053	Cyp2b13	-13.9	0.0030
Rarres1	-48.1	0.0005	Rarres1	-15.4	0.0005

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Figure 4 - HEP-11-2341 - Bojkowska et al

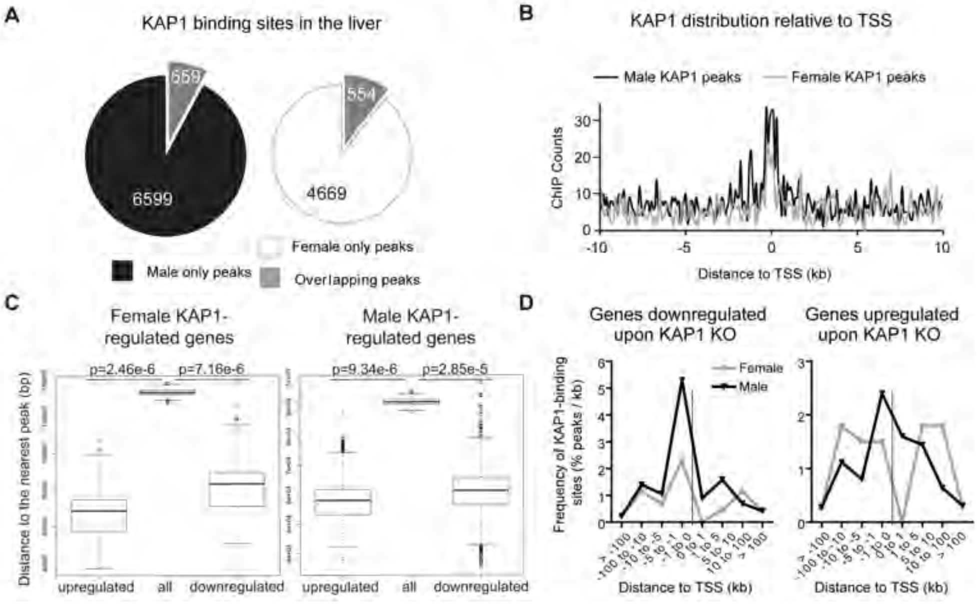

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Figure 5 - HEP-11-2341 - Bojkowska et al

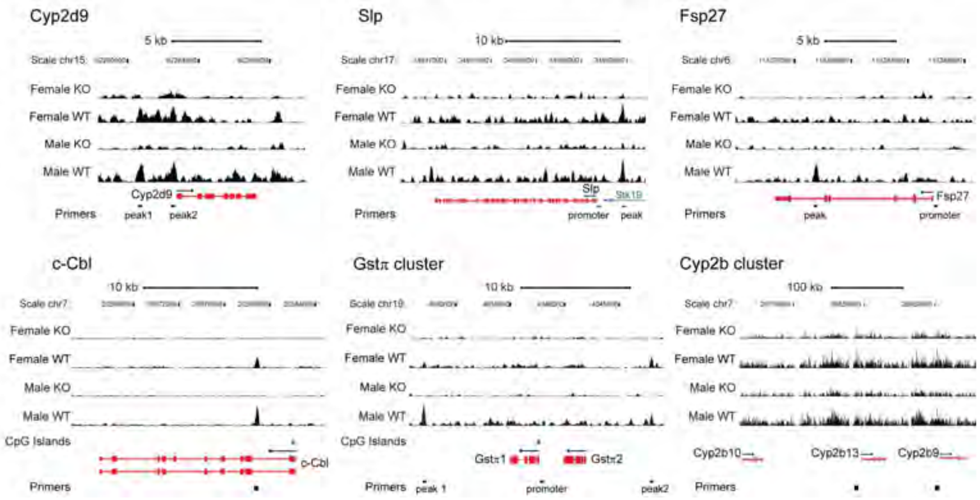

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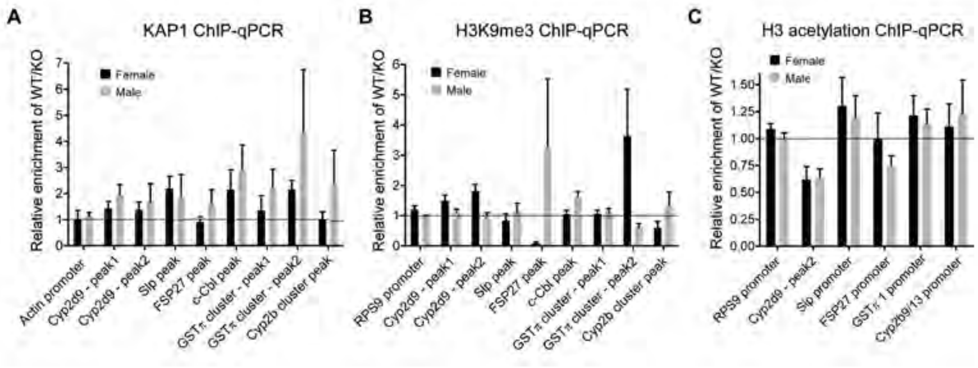
Figure 6 - HEP-11-2341 - Bojkowska et al



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Supporting text

We verified that the transcriptional deregulation observed in *Kap1* KO mice was due neither to the presence of Cre itself nor to the genetic background of the mice, we bred the original C57/Bl6 strain of the *Kap1*$^{fl/fl}$ mice[3] with *Alb.Cre* mice in a pure C57/Bl6 background[4]and validated the deregulation of several genes by RT-qPCR on 8-10-week-old livers. The KAP1 deletion-associated transcriptional changes were confirmed irrespective of genetic background and Cre expression (Supporting Fig. 2).

Detailed description of pathology analysis

Hepatic adenomas were characterized by well demarcated, unencapsulated, nodular proliferations causing distinct compression of the surrounding hepatic parenchyma. Neoplastic plates had regular cords, one to two cells thick, frequently impinging at a right or oblique angle at the adjacent normal hepatic parenchyma. Portal areas were not seen. Neoplastic hepatocytes were well differentiated with minimal anisocytosis, regular nuclei having mild anisokaryosis that resembled normal hepatocytes. Tinctorial affinity of the cytoplasm was variable among the different nodules with cases having vacuolar changes throughout the neoplasm.

Features of solid carcinoma observed in one of *Kap1* KO males fed HFD included: disruption of lobular architecture by solid plates of hepatocyte-like cells with peripheral infiltrative to slightly compressive growth (Fig 2A), increased cellular polymorphism characterized by marked anisocytosis and anisokaryosis with larger cells having large hyperchromatic nuclei, occasionally oval shaped, alternated to smaller or larger cells than surrounding normal hepatocytes with hyperchromatic nuclei, evident mitotic activity, cytoplasmic and nuclear vacuolation.

Supporting Experimental Procedures

Mice

Alb.Cre KAP1$^{fl/fl}$ mice were generated in a mix C57/Bl6-129sv background or C57/Bl6 as specified by crossing of previously described mouse strains[1, 2]. Mice were housed at 22°C–24°C with a 12 hr light/12 hr dark cycle (lights on at 0700 hrs) with standard mouse chow (Harlan Teklad diet 2919, 3.6 kcal/g digestible energy and 3.4 kcal/g metabolizable energy, 23% kcal from fat) or high fat diet (Taconic Research Diets, D12492; 5.24 kcal/g, 60% kcal from fat) as indicated and water provided *ad libitum*. All animal experiments were approved by the local veterinary office and carried out in accordance with the European Community Council Directive (86/609/EEC) for care and use of laboratory animals.

Phenotyping protocol

Cohorts of at least 8 male and female mice with indicated genotypes were generated and body-weight was measured starting at weaning, twice a week for groups sacrificed at 10 weeks and once a week for those sacrificed at 6 months. For food intake measurements, mice were placed in individual cages for a period of 5 says and food intake was measured twice for 10-week-old mice.

For sacrifice, after 4h period of fasting (staring at 0700 hrs), mice were anaesthetized by CO_2 inhalation and blood was collected into a heparinized tube by cardiac puncture, spun for 10 min at 4°C at 5000 rmp to isolate plasma, which was stored at -80°C until processing. Various organs were harvested, weighed and stored at -80°C, including: liver (a piece embedded in OCT, fixed in 4% paraformaldehyde, submerged in RNAlater (Ambion) or snap-frozen and stored at -80°C), gallbladder, kidney, adipose tissue (subcutaneous, perirenal, epididymal), intestines (duodendum, ileum, jejunum, colon), heart, skeletal muscles (gastrocnemius and soleus), brain, spleen, adrenal gland, reproductive organs and spleen.

Determination of energy expenditure, physical activity, food and water intake in the high fat diet challenged groups was performed in the Comprehensive Lab Animal Monitoring System (CLAMS) with the set-up of 16 cages (Columbus Instruments, Columbus, OH, USA). Mice at age of 24-25 weeks were placed in individual cages for a 22h period of habituation staring at 1300 hrs (room temperature 22 ± 1°C), followed by a measurement period of 22 hrs: 1 entire dark cycle (12 hrs) at room temperature (15°C±1°C). Parameters measured during CLAMS include: i) oxygen consumption (VO_2 in mL/Kg/h): VO_2 is directly correlated to energy expenditure. Oxygen consumption is measured every 40 min thanks to a zirconia oxide based oxygen sensor; ii) carbon dioxide production (VCO_2 in mL/Kg/h). CO_2 production is measured every 40 min thanks to a single beam non dispersed infra-red beam based sensor; iii) Respiratory Exchange Ratio (RER): VCO_2 / VO_2: RER is an indicator of the use of energy substrate. In a steady state, RER is equivalent to the Respiratory Quotient (RQ). Pure carbohydrate use gives RER=1, whereas pure fat burning yields an RER=0.7. A mixed diet gives a RER=0.85; iv) ambulatory activity is measured thanks to infra-red beams surrounding the cages on the X and Z axis. Every 40 min, the system compiles the data corresponding to the number of breaks of the infra-red beams by the animal inside the cage; v) water intake and food intake are measured thanks to high precision scales. Body composition was measured via EchoMRI 3-in-1 (Echo Medical Systems, Houston, TX, USA) according to manufacturers' instructions. Body weight was simultaneously recorded to allow normalization for total body weight.

Levels of metabolic parameters in the plasma, such as Alanine transaminase (ALAT), Aspartate transaminase (ASAT), lactate dehydrogenase (LDH), D-glucose, creatinine, free-fatty-acids, total cholesterol, high density lipoprotein (HDL) and low density lipoprotein cholesterol (LDL) cholesterol, triglycerides, total protein, albumin, gamma-glutamyltransferase (γGT) and bilirubin were determined with the Dimension Xpand automat, (Siemens Healthcare Diagnostics, Deerfield, IL, USA) according to manufacturer's instructions. Liver levels of cytokines were determined as previously described[3]. Total testosterone was measured with the Testosterone ELISA kit (Fitzgerald Industries International, cat. Number 55R-RE52151) according to manufacturer's instructions.

Histological tissue processing and analysis

For hematoxylin and erythroeosine (HE) staining and KAP1 immunohistochemistry (IHC), liver was fixed overnight in 4% PFA in PBS and, upon dehydratation, embedded in paraffin before being cut into 4 μm sections on a microtome. For HE staining, liver sections were de-waxed and hydrated to water before being placed in Harris hematoxylin for 5 min, washed and differentiated in 1% acid-alcohol followed by cytoplasm staining with 0.25% erythrosine, dehydration, clearing and mounting. KAP1 immunohistochemistry on paraffin-embedded liver sections was performed with the polyclonal anti-TRIM28 antibody (Proteintech, UK).

For Oil Red O staining fresh liver tissue was directly embedded in OCT (Medite), frozen on dry ice and 10 μm sections were cut on a cryostat. Sections were fixed in 4% PFA incubated in 50% Ethanol for 3 min then in Oil Red O (Sigma) for 15 min for fat staining, washed in 50% Ethanol for 1 min and Distilled water for 2 min and nuclear staining was performed in Mayer's Hematoxyline (Medite) for 2 min. Slides were then washed in tap water for 5 min before mounting with aqueous mounting media (Aquamount).

Histopathology evaluation of histology sections was performed in a blind fashion by a board certified pathologist (F.A.). Degree of vacuolar change was considered as mild, moderate or marked according to extent of the affected hepatocytes and degree of cytoplasmic vacuolation in the single hepatocytes. Semiquantitative measurement of fat accumulation within hepatocytes was performed on ORO stained liver sections and arbitrative values of 1 (mild), 2 (moderate) and 3 (marked) were assigned according to the intensity of stained tissue observed. For tumor occurence analysis, criteria were used as previously described [4].

Small scale DNA, RNA and protein analysis

For genotyping, DNA from an ear punch was extracted with the TissueDirectTM Multiplex kit (Genscript) and subjected to a PCR reaction with HotMasterMix mix (Vwr) and primers for KAP1 previously described in[1] or cre and x-globin primers (Supporting Table 2). RNA was extracted with the RNeasy kit (Qiagen), treated with Dnase (Turbo Dna-free kit, Ambion), reverse transcribed with the Superscript II RT (Qiagen) and the qPCR was performed on 7900HT Fast Real-Time PCR (Applied Biosystem) using SybrGreen Master Mix (Roche). Primer specificity was confirmed by dissociation curve analysis. β-actin and RPS9 were used for normalization. Primers used in this work are listed in the Supporting Table 2[5-7]. For protein analysis total liver, or hepatocyte nuclei isolated with the buffer containing 10mM Tris, 10mM NaCl, 0.2% NP-40, protease inhibitors (PIC; Roche) and 1 mM PMSF (Sigma), were lysed in RIPA buffer containing PIC and PMSF by sonication or glass-glass potter homogenization and, upon BCA quantification (Pierce), equal amounts of protein were loaded on 4-12% B-T NuPage gels (Invitrogen). After the transfer on a nitrocellulose membrane, proteins were stained with primary monoclonal rabbit anti-KAP1 (anti-TRIM28; Proteintech labs, UK), mouse anti-ERK1/2 MAPK (Zymed Laboratories), rabbit anti-p38 MAPK

(Cell Signaling), goat anti-PTEN (Santa Cruz), mouse anti-pan-actin (Sigma) antibodies as loading controls, followed by HRP-conjugated anti-mouse or anti-rabbit Ig secondary antibodies. HA-tag Western blot was performed with the anti-HA-HRP conjugated antibody and revealed with the SuperSignal West Pico Chemiluminescent Substrate (Thermo Scientific). Phospho-protein ELISA was performed with PathScan Signaling Nodes Multi-Target Sandwich ELISA Kit or PathScan MAP Kinase Multi-Target Sandwich ELISA Kit according to manufacturer’s instructions using 50 µg of liver protein extract (Cell Signaling).

MicroArray analysis

8-10-week-old mice were food-deprived at 0700 hrs and liver was isolated at 1100-1400 hrs. Total RNA was extracted with the MirVana kit (Ambion) and treated with DNAse (Turbo DNA free kit, Ambion), following manufacturer instructions. After quality control for RNA integrity by capillary electrophoresis on Agilent 2100 Bioanalyzer, three RNA pools from 9 mutant and wild type male livers were prepared, while three individual female KO and wild type livers were used separately. 100 ng of RNA was amplified and labeled using the Illumina TotalPrep RNA Amplification kit (Ambion). cRNA quality was assessed by capillary electrophoresis on Agilent 2100 Bioanalyzer. Hybridization on Mouse WG 6 v2 expression arrays (Illumina) was carried out according to the manufacturer’s instructions. Data were normalized and analyzed using Illumina Beadstudio 3.1.3 (background correction and quantile normalization). Expression profiles of each sample were imported into GeneSpringGX 7.3.1 (Agilent Technologies, USA). In addition to expression values, Illumina BeadStudio software computes a detection p-value. Based on this, each probe was assigned a detection flag (P (present): $p < 0.045$; M (Marginal): p between 0.050 and 0.045, A (Absent): $p>0.05$). Expression values below a defined threshold (i.e. 20) are set to the threshold in order to remove negative values after background correction. To identify deregulated genes in KO mice (i.e. differentially expressed transcripts between KO and control samples), t-test and/or ANOVA and additional steps of filtering were carried out. Significantly deregulated genes (p value <0.05 by unpaired t-test and fold-change ≥ 2) were used to interrogate DAVID bioinformatic database [8], where analysis was performed by using medium default stringency.

ChIP-sequencing and ChIP-PCR

Liver ChIP was performed as previously described with minor modifications [9]. Livers from 8-10-week-old mice were dounce homogenized in 6 ml per liver of 1x PBS including 1% formaldehyde for 10 min at room temperature. Cross-linking was stopped by the addition of 24 ml of ice-cold 2.2 M sucrose in 150 mM glycine, 10 mM HEPES pH 7.6, 15 mM KCl, 2 mM EDTA, 0.15 mM spermine, 0.5 mM spermidine, 0.5 mM DTT and 0.5 mM PMSF. The homogenate was layered on top of a 7 ml cushion of 2.05 M sucrose (containing the same ingredients and including 10% glycerol and 125 mM glycine) and centrifuged for 60 min at 24,000 rpm at 4 °C in a Beckmann SW28 rotor. The nuclei were resuspended in 1 ml of 20 mM Tris, pH 7.5, 150 mM NaCl, 2 mM EDTA, and spun at 5000 rpm for 30 sek prior to storage at -80C. For sonication, they were counted and 2 x10^7 nuclei were resuspended in 300 μl per liver of the same buffer supplemented with 1% SDS. Nuclei were sonicated for 20 s on ice ten times. The fragmented cross-linked chromatin was then diluted tenfold in the ChIP buffer [10]. Chromatin was immunoprecipitated with an affinity-purified rabbit polyclonal antibody raised against KAP1 amino acids 20–418 (RBCC) kindly provided by Dr. Rauscher [11]. Detailed protocol for Chromatin immunoprecipitation is described elsewhere [10]. After de-crosslinking of both IP and total input, DNA was quantified with the Qubit fluorometer (Invitrogen) and 10 ng were used to prepare libraries for sequencing, following the ChIP Seq library preparation protocol (including End Repair for blunted end fragments, addition of "A" base to the 3' end and ligation of adapters to DNA fragments (kit IP-102-1001). Ligation products were then purified on 2% E Gels Size Select (Invitrogen, fragments of 200 bp recovered), followed by enrichment of DNA fragments by PCR (18 cycles). No more than two libraries were loaded per gel to avoid cross contamination. Libraries were purified on AMP XP beads (Agencourt), quantified with Qubit fluorometer and size distribution determined on the Agilent Bioanalyzer (High Sensitivity DNA chip). Sequencing was performed on an Illumina Genome Analyzer IIx with each library sequenced in a 38 bases single read run.

Reads with less than five matches were aligned to the *Mus musculus* genome (assembly NCBI37/mm9) using bowtie[12]. Peak calling was performed with the model-based analysis of ChIP-seq algorithm[13] for wild type samples, using as a background the KO control. The male and female peak lists were intersected and any two peaks distant by <1kb were called overlapping. Distribution of KAP1 peaks around TSS was done with Chip-Cor tool (http://ccg.vital-it.ch/chipseq/chip_cor.html) using *M. musculus* ENSEMBL59 TSS collection as the input feature. For intersection with transcriptome analysis, Illumina probes were mapped to their corresponding ENSEMBL genes and overlapping peaks annotated with the bioconductor package ChIPpeakAnno (PMID: 20459804) were identified. Comparison between the distance of deregulated genes and all the UCSC annotated genes (used as control) was done using a Wilcoxon rank sum test. Frequency of KAP1 peaks was calculated as a percentage of peaks found in a given region divided by the region length in kb. Correction for multiple testing issues was done using the Benjamini-Hochberg procedure[14] .

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SUPPLEMENTAL FIGURE LEGENDS

Supporting Fig. 1. KAP1 deletion in *Alb.Cre Kap1*$^{fl/fl}$ mice is specific to hepatocytes and causes male-specific hepatosteatosis at age of 10 weeks.

A. Top: KAP1 recombination PCR in various organs of *Alb.Cre Kap1*$^{fl/fl}$ mice. Upper band corresponds to the PCR product from the deleted locus upon Cre-mediated recombination, while the lower band to the unrecombined *Kap1*^{fl} locus. Bottom: Cre-specific PCR (upper band). X-globin was used as an internal control in Cre-specific PCR reactions (lower band). **B.** KAP1 mRNA levels relative to β-actin in *Alb.Cre Kap1*$^{fl/fl}$ and *Kap1*$^{fl/fl}$ livers of female (left) and male (right) mice. **C.** KAP1 protein levels as assessed with KAP1-specific antibody in *Alb.Cre Kap1*$^{fl/fl}$ and *Kap1*$^{fl/fl}$ livers of male (left) and female (right) mice. Blotting against β-actin was done for loading control. **D.** Liver KAP1 immunohistochemistry in an *Alb.Cre Kap1*$^{fl/fl}$ male (left) and a *KapP1*$^{fl/fl}$ littermate (right). Positive staining in the interstitial cells in the *Alb.Cre Kap1*$^{fl/fl}$ liver indicates that KAP1 KO is specific to hepatocytes. Scale bar is 100 μm. **E.** HE staining of liver sample from chow diet-fed 10-week-old indicated mice. Inlet: ORO staining. Arrows indicate intrahepatic lipid droplets.

Supporting Table 1. List of genes dysregulated in KAP1-mutant mice.

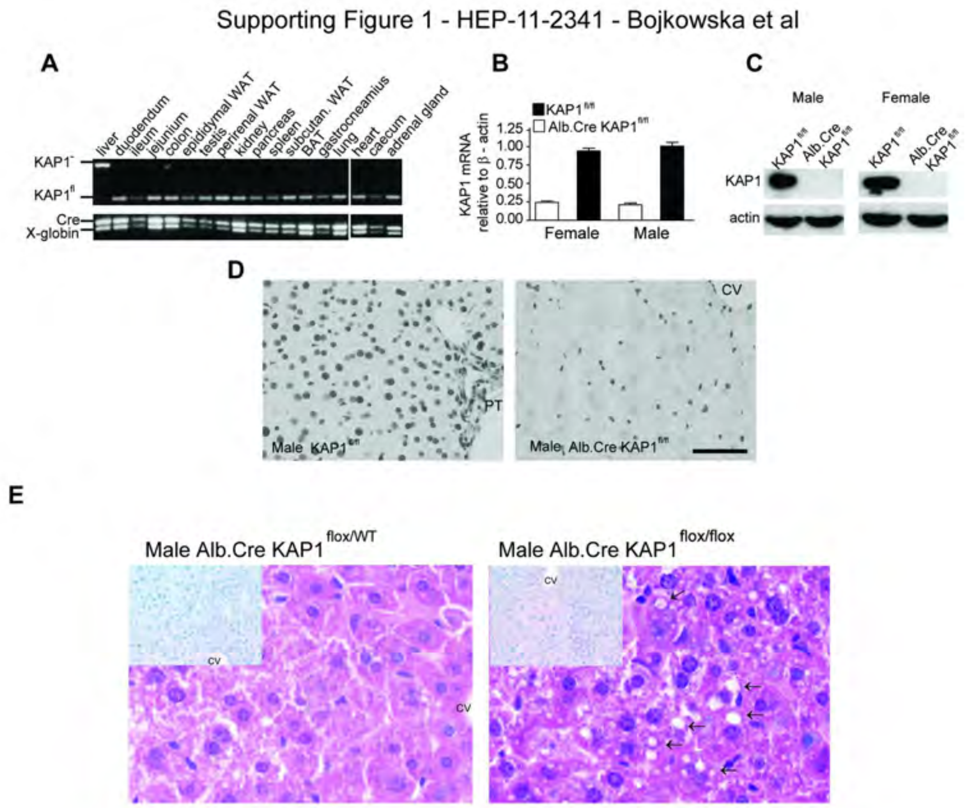
Supporting Table 2. List of primers used in the current study.

Supporting Fig. 2. Phenotype of mice with liver-specific KAP1 deletion is background independent. **A.** Gross necropsy analysis of C57/Bl6 Kap1-KO mice at age of 53-70 weeks. Top: characteristics of mice used in the study, **: $p<0.01$ as assessed by Students t-test. Data are represented as mean ± S.E.M. Bottom: Quantification of tumor occurrence in C57/Bl6 Kap1-KO mice. **B.** Histopathological analysis of tumor occurrence in C57/Bl6 Kap1-KO mice at age of 53-70 weeks. Indicated p-value was obtained by Fisher's exact test. **C.** and **D.** Correlation between gene deregulation in *Kap1* KO vs wild-type mice generated in mixed background and C57/Bl6 mice. Log2 ratio of mix *Alb.Cre Kap1*$^{fl/fl}$ vs *Kap1*$^{fl/fl}$ is plotted against the Log2 ratio of C57/Bl6 *Alb.Cre Kap1*$^{fl/fl}$ vs *Alb.Cre Kap1*$^{wt/wt}$ for males (C) and females (D).

A. Comparisons between male KAP1-responsive genes and STAT5b, STAT5a and Rsl-regulated. **B.** Similar comparisons as in A but with female gene expression data.

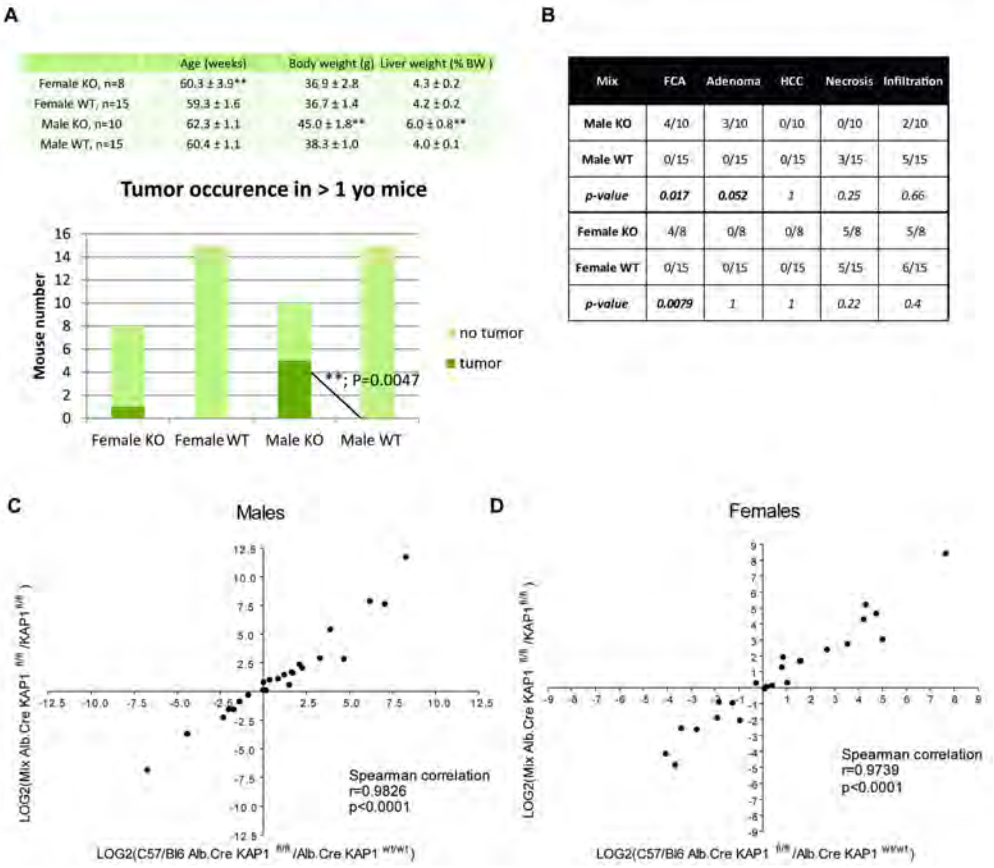
Supporting Fig. 3. KAP1 binding at chosen loci in male and female hepatocytes.

Screen-shots from the UCSC illustrating KAP1 binding sites in xenobiotic and drug metabolizing cytochrome P450 (Cyp) clusters, *Cyp2a* and *Cyp3a*. Green rectangles indicate peaks identified by a peak calling program using KO sample as a background reference.



170x142mm (300 x 300 DPI)

Supporting Figure 2 - HEP-11-2341 - Bojkowska et al

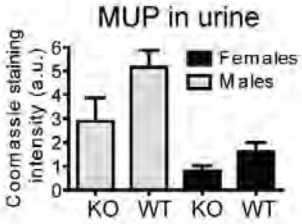


	Age (weeks)	Body weight (g)	Liver weight (% BW)
Female KO, n=8	60.3 ± 3.9**	36.9 ± 2.8	4.3 ± 0.2
Female WT, n=15	59.3 ± 1.6	36.7 ± 1.4	4.2 ± 0.2
Male KO, n=10	62.3 ± 1.1	45.0 ± 1.8**	6.0 ± 0.8**
Male WT, n=15	60.4 ± 1.1	38.3 ± 1.0	4.0 ± 0.1

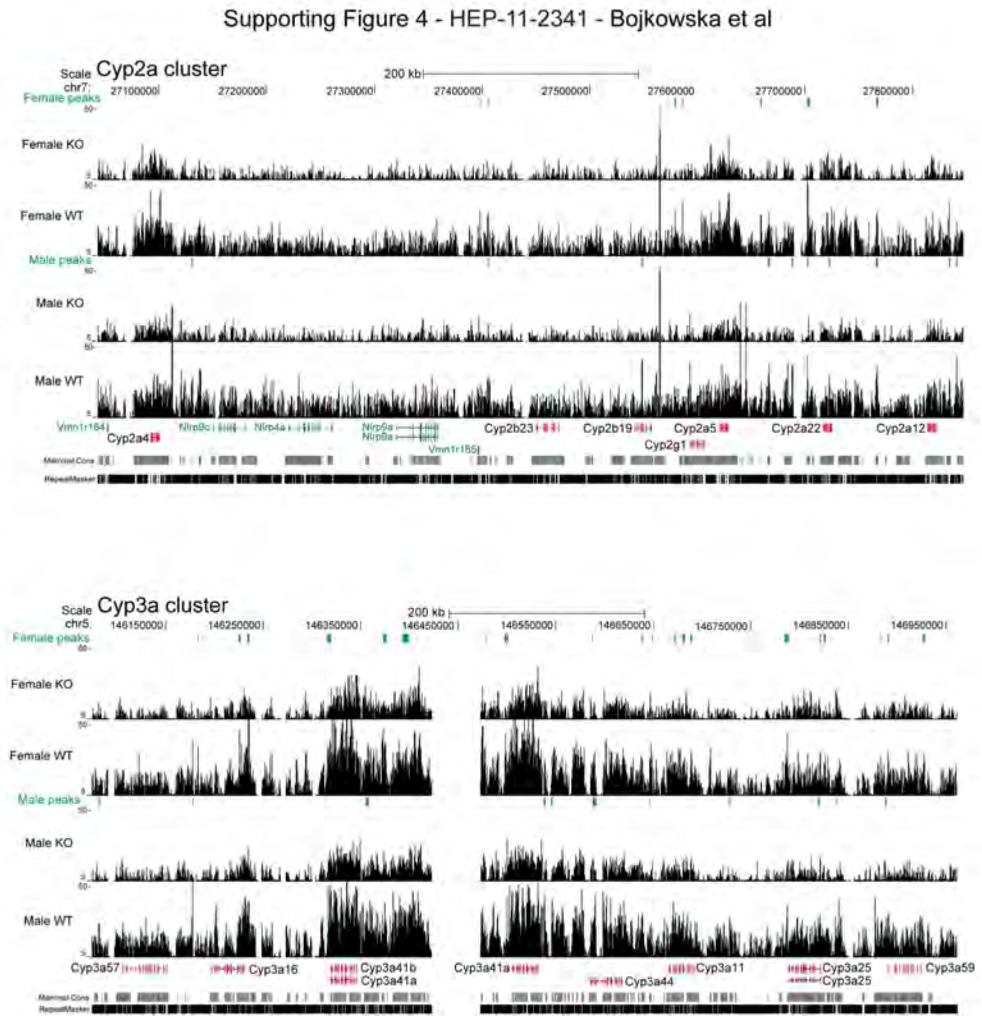
Mix	FCA	Adenoma	HCC	Necrosis	Infiltration
Male KO	4/10	3/10	0/10	0/10	2/10
Male WT	0/15	0/15	0/15	3/15	5/15
p-value	***0.017***	***0.052***	*1*	*0.25*	*0.66*
Female KO	4/8	0/8	0/8	5/8	5/8
Female WT	0/15	0/15	0/15	5/15	6/15
p-value	***0.0079***	*1*	*1*	*0.22*	*0.4*

209x194mm (300 x 300 DPI)

Supporting Figure 3 - HEP-11-2341 - Bojkowska et al



113x56mm (300 x 300 DPI)


Supporting Figure 4 - HEP-11-2341 - Bojkowska et al

Cyp2a cluster

Cyp3a cluster

181x184mm (300 x 300 DPI)

Description

BeadChip	Mouse WG-6 v2
Annotation file	Mouse WG-6_v2_0_R2_11278593_A

Gene identification			
Illumina ID	beadtype identifier Illumina's probe design pipeline makes use of alternative splicing information documented in the RefSeq database		
	"A"	*all isoforms*	meaning the probe will hit all splice isoforms of the gene
Probe Type	"I"	*isoform specific*	meaning the probe is designed to a gene with multiple isoforms, but will hit only one specific isoform
	"S"	*single isoform*	meaning that the gene has only one splice isoform recorded
Gene Symbol	approved gene symbol		
Description	sequence definition, extracted from the RefSeq record		
Chr	chromosomal location		
Representative ID	identifier for the sequence record in the NCBI RefSeq database used in probe design		

Compilation of the comparisons	
Fold Change - Female KO vs WT	mean of KAP1 -KO replicates / mean of KAP1-WT replicates
Welch t-test p-value - Female KO vs WT	p-value of the Welch t-test between the KAP1-KO mean and the KAP1-WT mean in log2 scale

Analysis	
normalization	background subtraction & quantile normalization (BeadStudio software) Expression values below a defined threshold (i.e. 20) are set to the threshold in order to remove negative values after background correction.
filtering	fold change >= 2 & Welch t-test p-value <= 0.05 (log2 scale)

Genes dysregulated in KAP1-mutant females

Illumina ID	Probe Type	Gene Symbol	Description	Chr	Representative ID	Fold Change - Female KO vs WT	Fold Change - Male KO vs WT	Welch t-test p-value - Female KO vs WT	Welch t-test p-value - Male KO vs WT
ILMN_2708477	S	**Spink3**			NM_009258.2	**38,60**	8,38	**0,0061**	0,0211
ILMN_2671165	S	**Krt23**	Mus musculus keratin 23 (Krt23), mRNA.	11	NM_033373.1	**17,72**	5,60	**0,0008**	0,0013
ILMN_2687507	S	**Cyp2d9**	Mus musculus cytochrome P450, family 2, subfamily d, polypeptide 9 (Cyp2d9), mRNA.	15	NM_010006.1	**14,15**	1,25	**0,0138**	0,0211
ILMN_1253860	S	**Mas1**	Mus musculus MAS1 oncogene (Mas1), mRNA.	17	NM_008552.3	**14,02**	9,27	**0,0052**	0,0046
ILMN_2728134	S	**5430433G21Rik**	PREDICTED: Mus musculus RIKEN cDNA 5430433G21 gene (5430433G21Rik), mRNA.		XM_001480745.1	**8,51**	3,74	**0,0026**	0,0021
ILMN_2625279	S	**Pacrg**	Mus musculus Park2 co-regulated (Pacrg), mRNA.	17	NM_027032.2	**7,63**	2,50	**0,0168**	0,0165
ILMN_3106592	A	**Rcan2**	Mus musculus regulator of calcineurin 2 (Rcan2), transcript variant 1, mRNA.	17	NM_207649.1	**6,40**	3,36	**0,0007**	0,0010
ILMN_2736539	S	**Cyp2c55**	Mus musculus cytochrome		NM_028089.3	**5,07**	1,74	**0,0072**	0,0864

			P450, family 2, subfamily c, polypeptide 55 (Cyp2c55), mRNA.						
ILMN_1230375	S	**LOC383125**			XM_356890.1	**5,02**	4,14	**0,0063**	0,0042
ILMN_2875737	S	**Cyp2d12**	Mus musculus cytochrome P450, family 2, subfamily d, polypeptide 12 (Cyp2d12), mRNA.	15	NM_201360.1	**5,01**	1,98	**0,0071**	0,0683
ILMN_1236308	S	**LOC268730**			XM_193754.2	**4,61**	5,80	**0,0323**	0,0045
ILMN_2611027	S	**Pmm1**	Mus musculus phosphomannomutase 1 (Pmm1), mRNA.	15	NM_013872.2	**4,58**	4,46	**0,0041**	0,0017
ILMN_1225985	S	**Serpina7**	Mus musculus serine (or cysteine) peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 7 (Serpina7), mRNA.	X	NM_177920.4	**4,49**	4,32	**0,0234**	0,0196
ILMN_3122845	A	**H1fx**	Mus musculus H1 histone family, member X (H1fx), mRNA.	6	NM_198622.1	**4,36**	2,56	**0,0222**	0,0262
ILMN_1244484	S	**Robo1**	Mus musculus roundabout homolog 1 (Drosophila) (Robo1), mRNA.	16	NM_019413.2	**4,36**	4,16	**0,0002**	0,0135
ILMN_2974041	S	**Pmm1**	Mus musculus phosphomannomutase 1 (Pmm1), mRNA.	15	NM_013872.1	**4,33**	3,75	**0,0037**	0,0099
ILMN_3023451	I	**LOC433801**	Mus musculus similar to RIKEN cDNA 6330416L07 gene (LOC433801), mRNA.		NM_001013808.1	**4,20**	2,35	**0,0301**	0,0028
ILMN_1212612	S	**Rcan2**	Mus musculus regulator of calcineurin 2 (Rcan2), transcript variant 1, mRNA.	17	NM_207649.1	**4,17**	2,07	**0,0305**	0,0082

ILMN_1238820	S	**LOC332788**			XM_285750.2	**4,06**	4,19	**0,0447**	0,0060
ILMN_1258330	S	**LOC384348**			XM_357593.1	**4,01**	3,65	**0,0040**	0,0033
ILMN_2738699	S	**Cblc**	Mus musculus Casitas B-lineage lymphoma c (Cblc), mRNA.	7	NM_023224.4	**3,99**	3,47	**0,0003**	0,0039
ILMN_1246061	S	**LOC239727**			XM_156408.2	**3,84**	1,74	**0,0268**	0,2146
ILMN_2718638	S	**Hao3**	Mus musculus hydroxyacid oxidase (glycolate oxidase) 3 (Hao3), mRNA.	3	NM_019545.3	**3,81**	1,00	**0,0152**	NA
ILMN_1253233	S	**Dsg1c**			NM_181680	**3,80**	1,67	**0,0197**	0,0365
ILMN_1245582	S	**Chrna4**	Mus musculus cholinergic receptor, nicotinic, alpha polypeptide 4 (Chrna4), mRNA.	2	NM_015730.4	**3,71**	3,25	**0,0203**	0,0601
ILMN_1228211	S	**Tff2**	Mus musculus trefoil factor 2 (spasmolytic protein 1) (Tff2), mRNA.	17	NM_009363.3	**3,68**	2,61	**0,0253**	0,0093
ILMN_2618148	S	**C330008K14Rik**			XM_128979	**3,55**	1,45	**0,0045**	0,4983
ILMN_2425229	S	**Serpina7**			NM_177920	**3,47**	2,25	**0,0321**	0,0705
ILMN_1244169	S	**Sftpd**	Mus musculus surfactant associated protein D (Sftpd), mRNA.	14	NM_009160.1	**3,42**	2,99	**0,0325**	0,0038
ILMN_2535566	S	**LOC382691**			XM_356627.1	**3,40**	2,63	**0,0144**	0,0292
ILMN_2621708	S	**Abcc4**	Mus musculus ATP-binding cassette, sub-family C (CFTR/MRP), member 4 (Abcc4), mRNA.	14	NM_001033336.2	**3,13**	1,79	**0,0185**	0,0098
ILMN_2491526	S	**Zkscan3**	Mus musculus zinc finger with KRAB and SCAN domains 3 (Zkscan3), mRNA.	13	NM_023685.3	**3,12**	1,20	**0,0496**	0,4954
ILMN_1247074	S	**Gm379**	PREDICTED: Mus musculus gene model 379, (NCBI)		XM_908711.1	**3,08**	-1,08	**0,0153**	0,6071

			(Gm379), mRNA.						
ILMN_2627328	S	**Dnase2a**			NM_010062	**2,93**	2,60	**0,0058**	0,0069
ILMN_2591342	S	**BC021614**	Mus musculus cDNA sequence BC021614 (BC021614), mRNA.	19	NM_144869.2	**2,93**	1,98	**0,0230**	0,0031
ILMN_2440679	S	**D1Ertd471e**				**2,87**	2,14	**0,0070**	0,0029
ILMN_1254927	S	**Ly6c1**	Mus musculus lymphocyte antigen 6 complex, locus C1 (Ly6c1), mRNA.	15	NM_010741.2	**2,86**	2,63	**0,0292**	0,0295
ILMN_1215877	S	**Extl1**			NM_019578	**2,79**	4,07	**0,0065**	0,0016
ILMN_2748680	S	**Fhit**	Mus musculus fragile histidine triad gene (Fhit), mRNA.	14	NM_010210.2	**2,74**	2,28	**0,0103**	0,0303
ILMN_2661971	S	**Gm2a**	Mus musculus GM2 ganglioside activator protein (Gm2a), mRNA.	11	NM_010299.2	**2,73**	2,48	**0,0030**	0,0001
ILMN_2874352	S	**Cyp17a1**	Mus musculus cytochrome P450, family 17, subfamily a, polypeptide 1 (Cyp17a1), mRNA.	19	NM_007809.2	**2,58**	4,26	**0,0133**	0,0380
ILMN_2893081	S	**Mbd1**	Mus musculus methyl-CpG binding domain protein 1 (Mbd1), mRNA.	18	NM_013594.1	**2,57**	2,59	**0,0001**	0,0003
ILMN_1223880	S	**Tmprss2**	Mus musculus transmembrane protease, serine 2 (Tmprss2), mRNA.	16	NM_015775.2	**2,51**	2,07	**0,0047**	0,0288
ILMN_2864290	S	**BC049806**	Mus musculus cDNA sequence BC049806 (BC049806), mRNA.	1	NM_172513.2	**2,50**	1,99	**0,0256**	0,0096
ILMN_1230557	S	**D2Wsu81e**	Mus musculus DNA segment, Chr 2, Wayne State University 81, expressed (D2Wsu81e), mRNA.	2	NM_172660.2	**2,50**	2,85	**0,0283**	0,0081

ILMN_3079804	I	**Cyp2a5**	Mus musculus cytochrome P450, family 2, subfamily a, polypeptide 5 (Cyp2a5), mRNA.	7	NM_007812.2	**2,47**	1,77	**0,0190**	0,0553
ILMN_2939652	S	**Selenbp2**	Mus musculus selenium binding protein 2 (Selenbp2), mRNA.	3	NM_019414.2	**2,47**	1,60	**0,0061**	0,0492
ILMN_2674620	S	**Ela2a**	Mus musculus elastase 2A (Ela2a), mRNA.	4	NM_007919.2	**2,39**	-1,52	**0,0086**	0,0460
ILMN_1247646	S	**H1fx**	Mus musculus H1 histone family, member X (H1fx), mRNA.	6	NM_198622.1	**2,38**	1,64	**0,0383**	0,0615
ILMN_2628629	S	**Cdh1**	Mus musculus cadherin 1 (Cdh1), mRNA.	8	NM_009864.2	**2,37**	1,21	**0,0293**	0,2318
ILMN_2596421	S	**A430079E08**			NM_175018.2	**2,37**	-1,27	**0,0148**	0,2937
ILMN_2632073	S	**Sfxn5**	Mus musculus sideroflexin 5 (Sfxn5), mRNA.	6	NM_178639.2	**2,35**	1,51	**0,0097**	0,2683
ILMN_2476948	S	**Gabrb3**	Mus musculus gamma-aminobutyric acid (GABA-A) receptor, subunit beta 3 (Gabrb3), transcript variant 2, mRNA.	7	NM_001038701.1	**2,33**	3,53	**0,0117**	0,0023
ILMN_2894396	S	**Tmem184a**	Mus musculus transmembrane protein 184a (Tmem184a), mRNA.	5	NM_144914.2	**2,29**	2,59	**0,0015**	0,0032
ILMN_2623536	S	**Golm1**	Mus musculus golgi membrane protein 1 (Golm1), transcript variant 1, mRNA.	13	NM_027307.4	**2,28**	2,09	**0,0059**	0,0148
ILMN_2829250	S	**Serpinb8**	Mus musculus serine (or cysteine)	1	NM_011459.2	**2,23**	1,40	**0,0450**	0,2666

			peptdiase inhibitor, clade B, member 8 (Serpinb8), mRNA.						
ILMN_2646369	S	**Slc13a2**	Mus musculus solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2 (Slc13a2), mRNA.		NM_022411.3	**2,20**	-1,13	**0,0194**	0,6482
ILMN_2535582	S	**LOC382707**			XM_356635.1	**2,18**	3,46	**0,0242**	0,0120
ILMN_1244281	S	**D2Wsu81e**	Mus musculus DNA segment, Chr 2, Wayne State University 81, expressed (D2Wsu81e), mRNA.	2	NM_172660.2	**2,17**	1,79	**0,0119**	0,0463
ILMN_2971479	S	**Trp53inp1**	Mus musculus transformation related protein 53 inducible nuclear protein 1 (Trp53inp1), mRNA.	4	NM_021897.1	**2,13**	1,48	**0,0122**	0,3608
ILMN_2954474	S	**Enpp2**	Mus musculus ectonucleotide pyrophosphatase/phosphodiesterase 2 (Enpp2), mRNA.	15	NM_015744.1	**2,11**	1,16	**0,0044**	0,1039
ILMN_1219440	S	**Rdh16**	Mus musculus retinol dehydrogenase 16 (Rdh16), mRNA.	10	NM_009040.2	**2,09**	2,44	**0,0072**	0,0041
ILMN_2907214	S	**Tcea3**	Mus musculus transcription elongation factor A (SII), 3 (Tcea3), mRNA.	4	NM_011542.1	**2,09**	1,43	**0,0063**	0,0008
ILMN_1218651	S	**Dnmbp**	Mus musculus dynamin binding protein (Dnmbp), mRNA.	19	NM_028029.2	**2,09**	2,05	**0,0247**	0,0700
ILMN_2650428	S	**4833442J19Rik**			NM_177101.2	**2,08**	1,18	**0,0079**	0,0808
ILMN_1241789	S	**Sucnr1**	Mus musculus succinate receptor 1 (Sucnr1), mRNA.	3	NM_032400.1	**2,08**	1,00	**0,0298**	0,9652

ILMN_2747886	S	**Ndufb11**	Mus musculus NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 11 (Ndufb11), mRNA.	X	NM_019435.2	**2,04**	1,11	**0,0078**	0,7556
ILMN_2683138	S	**Smek2**	Mus musculus SMEK homolog 2, suppressor of mek1 (Dictyostelium) (Smek2), mRNA.	11	NM_134034.1	**2,03**	-1,17	**0,0217**	0,1536
ILMN_2802952	S	**Narg2**	Mus musculus NMDA receptor-regulated gene 2 (Narg2), mRNA.	9	NM_145618.3	**2,03**	1,19	**0,0110**	0,3349
ILMN_2656884	S	**Tmem53**	Mus musculus transmembrane protein 53 (Tmem53), mRNA.	4	NM_026837.2	**2,02**	1,42	**0,0021**	0,0228
ILMN_2598715	S	**Tubb2b**	Mus musculus tubulin, beta 2b (Tubb2b), mRNA.	13	NM_023716.1	**2,01**	-1,13	**0,0122**	0,6071
ILMN_1214448	S	**9030619P08Rik**	Mus musculus RIKEN cDNA 9030619P08 gene (9030619P08Rik), mRNA.	15	NM_001039720.1	**2,00**	2,41	**0,0298**	0,0209
ILMN_3143358	A	**Adora1**	Mus musculus adenosine A1 receptor (Adora1), transcript variant 1, mRNA.	1	NM_001008533.2	**1,98**	-1,19	**0,0014**	0,3970
ILMN_2421064	S	**Gtf3c4**			NM_172977	**1,98**	1,10	**0,0235**	0,7185
ILMN_1228849	S	**Hist2h2aa1**			NM_013549	**1,97**	-1,02	**0,0187**	0,9390
ILMN_1248603	S	**Treh**	Mus musculus trehalase (brush-border membrane glycoprotein) (Treh), mRNA.	9	NM_021481.2	**1,97**	2,48	**0,0120**	0,0292
ILMN_1222760	S	**Zfp579**	Mus musculus zinc finger protein 579	7	NM_026741.2	**1,97**	2,40	**0,0008**	0,0128

			(Zfp579), mRNA.						
ILMN_1240515	S	**Wipi2**	Mus musculus WD repeat domain, phosphoinositide interacting 2 (Wipi2), mRNA.		NM_178398.4	**1,96**	1,34	**0,0148**	0,0938
ILMN_2965613	S	**Abca6**	Mus musculus ATP-binding cassette, sub-family A (ABC1), member 6 (Abca6), mRNA.	11	NM_147218.1	**1,96**	1,13	**0,0165**	0,3273
ILMN_2702519	S	**D630004N19Rik**			NM_207274.1	**1,95**	-1,05	**0,0339**	0,7625
ILMN_2746812	S	**2410012H22Rik**	PREDICTED: Mus musculus RIKEN cDNA 2410012H22 gene (2410012H22Rik), mRNA.	11	XM_126343.5	**1,94**	1,78	**0,0007**	0,0012
ILMN_2492961	S	**6530401N04Rik**			NM_029545	**1,93**	1,81	**0,0184**	0,1392
ILMN_2747820	S	**Dhrs7**	Mus musculus dehydrogenase/reductase (SDR family) member 7 (Dhrs7), mRNA.		NM_025522.3	**1,93**	2,38	**0,0246**	0,0078
ILMN_2742152	S	**Gadd45a**	Mus musculus growth arrest and DNA-damage-inducible 45 alpha (Gadd45a), mRNA.	6	NM_007836.1	**1,93**	1,93	**0,0223**	0,0116
ILMN_1239129	S	**A530076E23Rik**			AK041063	**1,93**	-1,25	**0,0104**	0,3269
ILMN_2589350	S	**Ces5**	Mus musculus carboxylesterase 5 (Ces5), mRNA.	8	NM_172759.2	**1,92**	2,57	**0,0336**	0,0011
ILMN_2666747	S	**G3bp2**	Mus musculus GTPase activating protein (SH3 domain) binding protein 2 (G3bp2), transcript variant 1, mRNA.	5	NM_011816.3	**1,92**	1,80	**0,0221**	0,0169
ILMN_2505095	S	**Usp48**			XM_485461	**1,92**	1,16	**0,0051**	0,1535
ILMN_2710139	S	**Ppargc1a**	Mus musculus peroxisome	5	NM_008904.1	**1,91**	1,44	**0,0127**	0,1521

			proliferative activated receptor, gamma, coactivator 1 alpha (Ppargc1a), mRNA.						
ILMN_2489360	S	**Pdia6**	Mus musculus protein disulfide isomerase associated 6 (Pdia6), mRNA.		NM_027959.3	**1,91**	1,09	**0,0271**	0,6704
ILMN_1229267	S	**Cyp2a5**	Mus musculus cytochrome P450, family 2, subfamily a, polypeptide 5 (Cyp2a5), mRNA.		NM_007812.4	**1,91**	1,69	**0,0062**	0,0055
ILMN_1213456	S	**Dhrs7**	Mus musculus dehydrogenase/reductase (SDR family) member 7 (Dhrs7), mRNA.		NM_025522.3	**1,91**	2,46	**0,0126**	0,0026
ILMN_2939702	S	**Dhrs7**	Mus musculus dehydrogenase/reductase (SDR family) member 7 (Dhrs7), mRNA.	12	NM_025522.1	**1,90**	2,73	**0,0124**	0,0145
ILMN_2534783	S	**LOC245069**			XM_159529.3	**1,89**	1,83	**0,0052**	0,0500
ILMN_2776283	S	**Tcea3**			NM_011542	**1,89**	1,54	**0,0021**	0,0002
ILMN_2856157	S	**Pgam1**	Mus musculus phosphoglycerate mutase 1 (Pgam1), mRNA.	19	NM_023418.2	**1,89**	1,75	**0,0057**	0,0051
ILMN_2808751	S	**Bcl9**	Mus musculus B-cell CLL/lymphoma 9 (Bcl9), mRNA.	3	NM_029933.3	**1,88**	-1,05	**0,0322**	0,6500
ILMN_1235255	S	**Klf15**	Mus musculus Kruppel-like factor 15 (Klf15), mRNA.	6	NM_023184.3	**1,88**	-1,05	**0,0291**	0,8054
ILMN_3148550	A	**Golm1**	Mus musculus golgi membrane protein 1 (Golm1), transcript variant 2, mRNA.	13	NM_001035122.2	**1,88**	1,63	**0,0057**	0,0073
ILMN_2691815	S	**G3bp2**	Mus musculus GTPase activating protein (SH3 domain) binding	5	NM_011816.3	**1,88**	1,52	**0,0265**	0,0397

			protein 2 (G3bp2), transcript variant 1, mRNA.						
ILMN_2671689	S	**Cox7b**	Mus musculus cytochrome c oxidase subunit VIIb (Cox7b), nuclear gene encoding mitochondrial protein, mRNA.	X	NM_025379.2	**1,87**	-1,14	**0,0117**	0,4732
ILMN_2859917	S	**Tmem53**	Mus musculus transmembrane protein 53 (Tmem53), mRNA.	4	NM_026837.1	**1,85**	1,49	**0,0195**	0,0007
ILMN_1239180	S	**Rprd1a**	Mus musculus regulation of nuclear pre-mRNA domain containing 1A (Rprd1a), mRNA.	18	NM_144861.2	**1,85**	1,81	**0,0078**	0,0921
ILMN_2984793	S	**1500001M20 Rik**	Mus musculus RIKEN cDNA 1500001M20 gene (1500001M20Rik), mRNA.	6	NM_026894.1	**1,83**	1,51	**0,0182**	0,1524
ILMN_3092653	A	**Palld**	Mus musculus palladin, cytoskeletal associated protein (Palld), mRNA.	8	NM_001081390.1	**1,82**	1,46	**0,0391**	0,0492
ILMN_2853739	S	**Nadsyn1**	Mus musculus NAD synthetase 1 (Nadsyn1), mRNA.	7	NM_030221.1	**1,82**	1,10	**0,0195**	0,6135
ILMN_2608043	S	**Hes6**	Mus musculus hairy and enhancer of split 6 (Drosophila) (Hes6), mRNA.	1	NM_019479.3	**1,82**	1,66	**0,0234**	0,0328
ILMN_1213185	S	**LOC385792**			XM_358947.1	**1,81**	1,99	**0,0183**	0,0374
ILMN_2587863	I	**2410091N08Rik**			XM_146886.1	**1,80**	-1,68	**0,0332**	0,0266
ILMN_2506012	S	**Trp53inp1**	Mus musculus transformation related protein 53 inducible nuclear	4	NM_021897.1	**1,80**	1,28	**0,0105**	0,1055

			protein 1 (Trp53inp1), mRNA.						
ILMN_2771665	S	**Pafah2**	Mus musculus platelet-activating factor acetylhydrolase 2 (Pafah2), mRNA.	4	NM_133880.1	**1,79**	1,53	**0,0068**	0,0063
ILMN_1230710	S	**C730039N23Rik**			AK050344	**1,79**	-1,96	**0,0477**	0,0009
ILMN_3074952	I	**Copg**	Mus musculus coatomer protein complex, subunit gamma (Copg), transcript variant 2, mRNA.	6	NM_201244.1	**1,78**	-1,15	**0,0489**	0,5887
ILMN_2977903	S	**BC057627**	Mus musculus cDNA sequence BC057627 (BC057627), mRNA.	7	NM_198631.1	**1,78**	1,18	**0,0092**	0,5610
ILMN_1222258	S	**Mid2**	Mus musculus midline 2 (Mid2), mRNA.	X	NM_011845.2	**1,78**	1,47	**0,0036**	0,1093
ILMN_2722455	S	**Prmt5**	Mus musculus protein arginine N-methyltransferase 5 (Prmt5), mRNA.	14	NM_013768.2	**1,78**	1,03	**0,0494**	0,8824
ILMN_2755915	S	**Pet112l**	Mus musculus PET112-like (yeast) (Pet112l), mRNA.		NM_144896.4	**1,76**	1,20	**0,0014**	0,2074
ILMN_2857143	S	**Rft1**	Mus musculus RFT1 homolog (S. cerevisiae) (Rft1), mRNA.	14	NM_177815.3	**1,76**	1,09	**0,0035**	0,3714
ILMN_2589770	S	**Fam179a**	Mus musculus family with sequence similarity 179, member A (Fam179a), mRNA.		NM_177087.4	**1,76**	-1,11	**0,0227**	0,7249
ILMN_2711045	S	**Sirt5**	Mus musculus sirtuin 5 (silent mating type information regulation 2 homolog) 5 (S. cerevisiae) (Sirt5), mRNA.	13	NM_178848.3	**1,76**	1,78	**0,0188**	0,0023

ILMN_1257020	S	**Aldh1b1**	Mus musculus aldehyde dehydrogenase 1 family, member B1 (Aldh1b1), nuclear gene encoding mitochondrial protein, mRNA.	4	NM_028270.4	**1,76**	1,03	**0,0258**	0,4497
ILMN_2526042	S	**LOC217372**			XM_126827.4	**1,75**	-1,20	**0,0493**	0,5909
ILMN_1242689	S	**LOC236371**			XM_135639.2	**1,75**	2,15	**0,0319**	0,0463
ILMN_2763983	S	**Sds**	Mus musculus serine dehydratase (Sds), mRNA.	5	NM_145565.1	**1,75**	-1,04	**0,0463**	0,8396
ILMN_1232093	S	**LOC386330**			XM_359173.1	**1,75**	-1,20	**0,0130**	0,0050
ILMN_1236637	S	**Trim33**	Mus musculus tripartite motif-containing 33 (Trim33), transcript variant 1, mRNA.	3	NM_053170.2	**1,75**	-1,08	**0,0313**	0,5618
ILMN_1250364	S	**Cyp2a4**	Mus musculus cytochrome P450, family 2, subfamily a, polypeptide 4 (Cyp2a4), mRNA.	7	NM_009997.2	**1,75**	10,95	**0,0337**	0,1208
ILMN_2708263	S	**Madd**	Mus musculus MAP-kinase activating death domain (Madd), mRNA.	2	NM_145527.3	**1,74**	1,42	**0,0263**	0,1936
ILMN_2602687	S	**Rpa2**	Mus musculus replication protein A2 (Rpa2), mRNA.	4	NM_011284.3	**1,74**	1,36	**0,0349**	0,1533
ILMN_2606415	S	**Adra1b**			NM_007416	**1,74**	1,13	**0,0357**	0,6613
ILMN_2747311	S	**Atp6v0a2**	Mus musculus ATPase, H+ transporting, lysosomal V0 subunit A2 (Atp6v0a2), mRNA.		NM_011596.4	**1,74**	1,27	**0,0396**	0,1987
ILMN_2656871	S	**Tmem97**	Mus musculus transmembrane protein 97 (Tmem97), mRNA.	11	NM_133706.2	**1,74**	1,46	**0,0026**	0,0352

ILMN_2692942	S	**Sntb2**	Mus musculus syntrophin, basic 2 (Sntb2), mRNA.	8	NM_009229.2	**1,74**	-1,51	**0,0335**	0,2066
ILMN_1236941	S	**Csnk2a1-rs3**			AK031617	**1,73**	1,04	**0,0479**	0,7347
ILMN_2487358	S	**Eif3s6**			NM_008388	**1,73**	-1,20	**0,0079**	0,4302
ILMN_2586024	S	**Nup98**			AK089973	**1,73**	-1,28	**0,0498**	0,2040
ILMN_1255363	S	**Fkbp14**	Mus musculus FK506 binding protein 14 (Fkbp14), mRNA.	6	NM_153573.1	**1,73**	1,05	**0,0220**	0,5261
ILMN_2734598	S	**Cyp2a5**	Mus musculus cytochrome P450, family 2, subfamily a, polypeptide 5 (Cyp2a5), mRNA.		NM_007812.4	**1,73**	1,85	**0,0036**	0,0101
ILMN_1256271	S	**Atp13a3**	PREDICTED: Mus musculus ATPase type 13A3, transcript variant 1 (Atp13a3), mRNA.	16	XM_001480958.1	**1,72**	-1,03	**0,0149**	0,8462
ILMN_2945374	S	**Gm806**	Mus musculus gene model 806, (NCBI) (Gm806), mRNA.	13	NM_001033400.1	**1,72**	1,22	**0,0476**	0,2197
ILMN_2789425	S	**Polb**	Mus musculus polymerase (DNA directed), beta (Polb), mRNA.	8	NM_011130.1	**1,72**	-1,22	**0,0440**	0,5765
ILMN_2490536	S	**Aldh5a1**			NM_172532	**1,72**	1,65	**0,0001**	0,0000
ILMN_2727309	S	**LOC100044204**	PREDICTED: Mus musculus hypothetical protein LOC100044204 (LOC100044204), mRNA.		XM_001471696.1	**1,71**	1,45	**0,0368**	0,0481
ILMN_2734564	S	**Tmem53**	Mus musculus transmembrane protein 53 (Tmem53), mRNA.	4	NM_026837.2	**1,71**	-1,02	**0,0050**	0,9299
ILMN_1216900	S	**Rabl3**	Mus musculus RAB, member of RAS oncogene family-like 3 (Rabl3), mRNA.	16	NM_001042499.1	**1,71**	1,16	**0,0481**	0,5394
ILMN_2844963	S	**Nos1ap**	Mus musculus nitric oxide synthase 1 (neuronal) adaptor		NM_027528.1	**1,71**	-1,27	**0,0262**	0,2712

			protein (Nos1ap), mRNA. XM_994037						
ILMN_2728255	S	**6430526O11Rik**			XM_110937.4	**1,71**	1,21	**0,0456**	0,5553
ILMN_2707079	S	**Sirt5**	Mus musculus sirtuin 5 (silent mating type information regulation 2 homolog) 5 (S. cerevisiae) (Sirt5), mRNA.	13	NM_178848.3	**1,70**	1,90	**0,0001**	0,0171
ILMN_1224487	S	**Ddx26b**	Mus musculus DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 26B (Ddx26b), mRNA.	X	NM_172779.1	**1,70**	-1,02	**0,0009**	0,8531
ILMN_2603377	S	**Dnase2b**	Mus musculus deoxyribonuclease II beta (Dnase2b), mRNA.	3	NM_019957.3	**1,68**	1,63	**0,0378**	0,0019
ILMN_2536687	S	**LOC383077**			XM_356845.1	**1,68**	1,22	**0,0223**	0,3258
ILMN_1244477	S	**Garnl4**	Mus musculus GTPase activating RANGAP domain-like 4 (Garnl4), mRNA.	11	NM_001015046.2	**1,68**	1,26	**0,0435**	0,2537
ILMN_2674001	S	**Smyd2**	Mus musculus SET and MYND domain containing 2 (Smyd2), mRNA.	1	NM_026796.1	**1,68**	1,39	**0,0198**	0,0337
ILMN_1215965	S	**Ubr1**			AK086900	**1,67**	-1,10	**0,0080**	0,4226
ILMN_2791952	S	**Hes6**	Mus musculus hairy and enhancer of split 6 (Drosophila) (Hes6), mRNA.	1	NM_019479.2	**1,67**	1,25	**0,0342**	0,2520
ILMN_2757641	S	**Efna5**	Mus musculus ephrin A5 (Efna5), transcript variant 2, mRNA.	17	NM_010109.2	**1,67**	1,80	**0,0141**	0,0162
ILMN_2527923	S	**LOC228966**			XM_141580.1	**1,66**	-1,13	**0,0193**	0,6422
ILMN_2820703	S	**Scarf1**	Mus musculus scavenger receptor	11	NM_001004157.2	**1,66**	1,04	**0,0093**	0,8431

			class F, member 1 (Scarf1), mRNA.						
ILMN_1216174	S	**Parp16**	Mus musculus poly (ADP-ribose) polymerase family, member 16 (Parp16), mRNA.	9	NM_177460.3	**1,66**	1,89	**0,0469**	0,0052
ILMN_2431619	S	**Ube2l6**			NM_019949	**1,66**	1,57	**0,0461**	0,0062
ILMN_2774690	S	**LOC677317**	PREDICTED: Mus musculus similar to Mod1 protein, transcript variant 4 (LOC677317), mRNA.		XM_001004685.1	**1,66**	2,11	**0,0341**	0,0123
ILMN_1245447	S	**Abcd1**	Mus musculus ATP-binding cassette, sub-family D (ALD), member 1 (Abcd1), mRNA. XM_973409	X	NM_007435.1	**1,66**	1,12	**0,0236**	0,3710
ILMN_1244847	S	**Cyp2a5**	Mus musculus cytochrome P450, family 2, subfamily a, polypeptide 5 (Cyp2a5), mRNA.		NM_007812.4	**1,66**	1,63	**0,0017**	0,0014
ILMN_2605013	S	**Sec14l4**	Mus musculus SEC14-like 4 (S. cerevisiae) (Sec14l4), mRNA.	11	NM_146013.1	**1,64**	1,14	**0,0127**	0,3773
ILMN_2562109	S	**A630091F01Rik**			AK042432	**1,64**	1,41	**0,0249**	0,0343
ILMN_2655126	S	**Gchfr**	Mus musculus GTP cyclohydrolase I feedback regulator (Gchfr), mRNA.	2	NM_177157.4	**1,63**	1,80	**0,0136**	0,0114
ILMN_1258242	S	**2310031L18Rik**			NM_026507.2	**1,63**	1,22	**0,0250**	0,2179
ILMN_2938973	S	**C330005M16Rik**	Mus musculus RIKEN cDNA C330005M16 gene (C330005M16Rik), mRNA.	7	NM_175319.2	**1,63**	1,21	**0,0212**	0,4226
ILMN_1247075	S	**Npc1**	Mus musculus Niemann Pick type C1 (Npc1), mRNA.	18	NM_008720.2	**1,62**	1,09	**0,0009**	0,2599
ILMN_1226783	S	**Irak4**	Mus musculus interleukin-1	15	NM_029926.4	**1,62**	-1,23	**0,0104**	0,2957

			receptor-associated kinase 4 (Irak4), mRNA.						
ILMN_1227874	S	**LOC100048589**	PREDICTED: Mus musculus similar to CDNA sequence BC052040, transcript variant 1 (LOC100048589), mRNA.		XM_001480260.1	**1,62**	1,25	**0,0320**	0,1979
ILMN_1222773	S	**Exoc4**	Mus musculus exocyst complex component 4 (Exoc4), mRNA.	6	NM_009148.3	**1,62**	1,70	**0,0232**	0,1558
ILMN_2581065	S	**6030460N08Rik**			AK077954	**1,62**	-1,21	**0,0356**	0,2651
ILMN_2752624	S	**Ccrl2**	Mus musculus chemokine (C-C motif) receptor-like 2 (Ccrl2), mRNA.	9	NM_017466.4	**1,62**	1,45	**0,0074**	0,0085
ILMN_1214126	S	**Hes6**	Mus musculus hairy and enhancer of split 6 (Drosophila) (Hes6), mRNA.	1	NM_019479.2	**1,62**	1,57	**0,0408**	0,0540
ILMN_2812935	S	**Atp6v1h**	Mus musculus ATPase, H+ transporting, lysosomal V1 subunit H (Atp6v1h), mRNA.	1	NM_133826.2	**1,62**	1,21	**0,0399**	0,1691
ILMN_2744603	S	**Gchfr**	Mus musculus GTP cyclohydrolase I feedback regulator (Gchfr), mRNA.	2	NM_177157.4	**1,61**	1,43	**0,0033**	0,0040
ILMN_1224408	S	**Eif2ak3**			AK046355	**1,61**	-1,15	**0,0269**	0,6766
ILMN_2993473	S	**Sp6**	Mus musculus trans-acting transcription factor 6 (Sp6), mRNA.	11	NM_031183.1	**1,61**	1,18	**0,0473**	0,6508
ILMN_1234693	S	**Nipbl**	Mus musculus Nipped-B homolog (Drosophila) (Nipbl), transcript variant A, mRNA.	15	NM_027707.2	**1,61**	1,14	**0,0453**	0,1072
ILMN_1256775	S	**Thrsp**	Mus musculus	7	NM_009381.2	**1,60**	2,05	**0,0368**	0,1520

			thyroid hormone responsive SPOT14 homolog (Rattus) (Thrsp), mRNA.						
ILMN_2637203	S	**Rfc5**	Mus musculus replication factor C (activator 1) 5 (Rfc5), mRNA.	5	NM_028128.1	**1,60**	1,45	**0,0154**	0,0483
ILMN_1221288	S	**Lgals8**	Mus musculus lectin, galactose binding, soluble 8 (Lgals8), mRNA.	13	NM_018886.3	**1,60**	1,46	**0,0258**	0,0025
ILMN_2622761	S	**Pccb**	Mus musculus propionyl Coenzyme A carboxylase, beta polypeptide (Pccb), nuclear gene encoding mitochondrial protein, mRNA.	9	NM_025835.2	**1,60**	-1,46	**0,0403**	0,0557
ILMN_2534278	S	**LOC327992**			XM_282974.2	**1,60**	-1,26	**0,0069**	0,4226
ILMN_2908485	S	**Ap1s3**	Mus musculus adaptor-related protein complex AP-1, sigma 3 (Ap1s3), mRNA.	1	NM_183027.1	**1,60**	-1,19	**0,0071**	0,5077
ILMN_1244292	S	**Sox13**	Mus musculus SRY-box containing gene 13 (Sox13), mRNA.	1	NM_011439.2	**1,60**	-1,05	**0,0345**	0,8752
ILMN_2453120	S	**C130065N10Rik**				**1,59**	1,79	**0,0011**	0,0025
ILMN_2933022	S	**Plekhb1**	Mus musculus pleckstrin homology domain containing, family B (evectins) member 1 (Plekhb1), mRNA.	7	NM_013746.1	**1,59**	1,57	**0,0259**	0,0141
ILMN_2589556	S	**Ikbkb**			NM_010546	**1,59**	1,00	**0,0062**	0,9820
ILMN_1248444	S	**BC002230**	PREDICTED: Mus musculus cDNA sequence BC002230, transcript	12	XM_484171.3	**1,59**	-1,55	**0,0226**	0,0553

			variant 1 (BC002230), mRNA.						
ILMN_1218042	S	**LOC383483**			XM_357088.1	**1,59**	-1,13	**0,0120**	0,6428
ILMN_2425032	S	**Zfp445**			NM_173364.3	**1,59**	1,08	**0,0100**	0,6740
ILMN_1241366	S	**Rshl3**	PREDICTED: Mus musculus radial spokehead-like 3 (Rshl3), mRNA.	10	XM_137041.6	**1,58**	1,02	**0,0274**	0,4226
ILMN_1217489	S	**LOC671878**	PREDICTED: Mus musculus similar to spermine synthase (LOC671878), mRNA.	X	XM_001473434.1	**1,58**	1,27	**0,0360**	0,0494
ILMN_2524100	S	**Zswim6**			XM_358311	**1,58**	1,16	**0,0285**	0,6639
ILMN_1214224	S	**Zfp1**	Mus musculus zinc finger protein 1 (Zfp1), transcript variant 1, mRNA.	8	NM_001037665.2	**1,58**	1,10	**0,0486**	0,6673
ILMN_1239770	S	**Peli1**	Mus musculus pellino 1 (Peli1), mRNA.	11	NM_023324.2	**1,58**	1,58	**0,0432**	0,0664
ILMN_2852737	S	**Cdkl1**	Mus musculus cyclin-dependent kinase-like 1 (CDC2-related kinase) (Cdkl1), mRNA.	12	NM_183294.1	**1,57**	-1,27	**0,0378**	0,1986
ILMN_2674924	S	**Pcca**	Mus musculus propionyl-Coenzyme A carboxylase, alpha polypeptide (Pcca), mRNA.	14	NM_144844.1	**1,57**	1,27	**0,0016**	0,0270
ILMN_1257291	S	**D030029J20Rik**				**1,57**	1,16	**0,0469**	0,2400
ILMN_1242852	S	**Wdr45l**	Mus musculus Wdr45 like (Wdr45l), mRNA.	11	NM_025793.2	**1,57**	1,51	**0,0118**	0,0912
ILMN_2865016	S	**Cd83**	Mus musculus CD83 antigen (Cd83), mRNA.	13	NM_009856.1	**1,57**	1,31	**0,0258**	0,2265
ILMN_1258600	S	**LOC100043671**	PREDICTED: Mus musculus hypothetical protein	11	XM_001481024.1	**1,56**	1,59	**0,0164**	0,0635

			LOC100043671 (LOC100043671), mRNA.						
ILMN_1221362	S	**Esr1**			AK039911	**1,55**	-1,08	**0,0379**	0,4226
ILMN_2551945	S	**E130209G04Rik**			AK021406	**1,55**	1,10	**0,0281**	0,4410
ILMN_1240738	S	**Rdh19**	Mus musculus retinol dehydrogenase 19 (Rdh19), mRNA.	10	NM_147222.2	**1,55**	1,00	**0,0068**	0,9919
ILMN_2873862	S	**Lrrc30**	Mus musculus leucine rich repeat containing 30 (Lrrc30), mRNA.	17	NM_001033340.1	**1,55**	-1,32	**0,0185**	0,2806
ILMN_1213636	S	**C330023D02Rik**			AK049320	**1,55**	1,02	**0,0176**	0,8129
ILMN_1235366	S	**LOC100045628**	PREDICTED: Mus musculus similar to X-linked PEST-containing transporter (LOC100045628), misc RNA.		XR_031850.1	**1,55**	1,02	**0,0365**	0,9474
ILMN_2937261	S	**Mod1**	Mus musculus malic enzyme, supernatant (Mod1), mRNA.	9	NM_008615.1	**1,54**	1,88	**0,0022**	0,0364
ILMN_2860242	S	**Klhl24**	Mus musculus kelch-like 24 (Drosophila) (Klhl24), mRNA.	16	NM_029436.3	**1,54**	1,20	**0,0446**	0,3019
ILMN_2458184	S	**Upp2**	Mus musculus uridine phosphorylase 2 (Upp2), mRNA.	2	NM_029692.1	**1,54**	1,06	**0,0494**	0,4644
ILMN_2681057	S	**Phca**	Mus musculus phytoceramidase, alkaline (Phca), mRNA.	7	NM_025408.2	**1,54**	1,52	**0,0026**	0,0061
ILMN_1237758	S	**LOC382153**			XM_356249.1	**1,53**	1,68	**0,0385**	0,0268
ILMN_2486267	S	**Ube2l6**	Mus musculus ubiquitin-conjugating enzyme E2L 6 (Ube2l6), mRNA.	2	NM_019949.1	**1,53**	1,99	**0,0035**	0,0251
ILMN_1256868	S	**C130005N09Rik**			AK081324	**1,53**	-1,18	**0,0434**	0,5649
ILMN_1238995	S	**BC062650**			NM_177650.2	**1,52**	-1,06	**0,0370**	0,8355
ILMN_2946410	S	**Slc36a2**	Mus musculus solute carrier family 36	11	NM_153170.1	**1,52**	-1,21	**0,0365**	0,2460

			(proton/amino acid symporter), member 2 (Slc36a2), mRNA.						
ILMN_3038404	I	**Tcf25**	Mus musculus transcription factor 25 (basic helix-loop-helix) (Tcf25), transcript variant 3, mRNA.	8	NM_001037878.1	**1,52**	1,31	**0,0337**	0,2685
ILMN_2473692	S	**1110059G02Rik**				**1,52**	1,43	**0,0118**	0,0149
ILMN_2879614	S	**Zbp1**	Mus musculus Z-DNA binding protein 1 (Zbp1), mRNA.	2	NM_021394.1	**1,51**	-1,02	**0,0454**	0,8625
ILMN_1234020	S	**scl0002007.1_97**				**1,51**	1,26	**0,0447**	0,1245
ILMN_2747381	S	**Ddx24**	Mus musculus DEAD (Asp-Glu-Ala-Asp) box polypeptide 24 (Ddx24), mRNA.	12	NM_020494.2	**1,51**	1,04	**0,0095**	0,7959
ILMN_2560602	S	**Centd1**	PREDICTED: Mus musculus centaurin, delta 1, transcript variant 5 (Centd1), mRNA.		XM_001001363.1	**1,51**	-1,16	**0,0072**	0,4909
ILMN_2640752	S	**Ces1**	Mus musculus carboxylesterase 1 (Ces1), mRNA.	8	NM_021456.2	**1,51**	-1,06	**0,0143**	0,7371
ILMN_2425691	S	**A930009E05Rik**			XM_489135	**-1,50**	-1,16	**0,0377**	0,2111
ILMN_2970691	S	**Ppie**	Mus musculus peptidylprolyl isomerase E (cyclophilin E) (Ppie), mRNA.	4	NM_019489.2	**-1,51**	1,16	**0,0374**	0,1012
ILMN_1220036	S	**C130032M10Rik**			AK048065	**-1,51**	1,02	**0,0189**	0,9126
ILMN_2700550	S	**Ddx11**			XM_128714.3	**-1,51**	-1,07	**0,0430**	0,5757
ILMN_2637094	S	**Pcsk6**	PREDICTED: Mus musculus proprotein convertase subtilisin/kexin type 6, transcript variant 4 (Pcsk6), mRNA.		XM_919493.2	**-1,51**	-1,17	**0,0128**	0,1208
ILMN_3003631	S	**Ppap2c**	Mus musculus phosphatidic acid phosphatase type 2c	10	NM_015817.2	**-1,51**	-1,40	**0,0045**	0,0102

			(Ppap2c), mRNA.						
ILMN_2958207	S	**Nsdhl**	Mus musculus NAD(P) dependent steroid dehydrogenase-like (Nsdhl), mRNA.	X	NM_010941.3	**-1,51**	-1,23	**0,0443**	0,0917
ILMN_2773936	S	**Edg5**			NM_010333	**-1,51**	1,03	**0,0334**	0,3811
ILMN_2588737	S	**Rab3d**	Mus musculus RAB3D, member RAS oncogene family (Rab3d), mRNA.	9	NM_031874.4	**-1,52**	-1,01	**0,0429**	0,9407
ILMN_2532923	S	**LOC245066**			XM_142398.1	**-1,52**	1,04	**0,0087**	0,4226
ILMN_1214166	S	**Odf2**			BC057001	**-1,52**	-1,25	**0,0370**	0,4790
ILMN_2630710	S	**Zfp623**	Mus musculus zinc finger protein 623 (Zfp623), mRNA.	15	NM_030199.3	**-1,52**	-1,44	**0,0021**	0,0242
ILMN_1254827	S	**D830041I17Rik**			AK052921	**-1,53**	-1,59	**0,0436**	0,0847
ILMN_1242772	S	**Adal**	Mus musculus adenosine deaminase-like (Adal), mRNA. XM_900859 XM_900862 XM_917792 XM_925262 XM_925265 XM_925269 XM_925272 XM_925275 XM_986097 XM_986134 XM_986169 XM_986201 XM_986236 XM_986298	2	NM_029475.1	**-1,53**	1,18	**0,0394**	0,1555
ILMN_1242246	S	**Scamp5**	Mus musculus secretory carrier membrane protein 5 (Scamp5), mRNA.	9	NM_020270.2	**-1,53**	-1,49	**0,0145**	0,0702

ILMN_2714787	S	**1110038B12Rik**	PREDICTED: Mus musculus RIKEN cDNA 1110038B12 gene, transcript variant 6 (1110038B12Rik), mRNA.		XM_922038.2	**-1,53**	-1,13	**0,0086**	0,3205
ILMN_2774563	S	**Mug4**	PREDICTED: Mus musculus murinoglobulin 4 (Mug4), misc RNA.		XR_035729.1	**-1,53**	-1,52	**0,0107**	0,0017
ILMN_2707782	S	**Afg3l1**	Mus musculus AFG3(ATPase family gene 3)-like 1 (yeast) (Afg3l1), mRNA.	8	NM_054070.2	**-1,55**	1,24	**0,0392**	0,4234
ILMN_1224110	S	**Bst2**	Mus musculus bone marrow stromal cell antigen 2 (Bst2), mRNA.	8	NM_198095.2	**-1,55**	-1,20	**0,0322**	0,1516
ILMN_2709392	S	**Zfp707**	Mus musculus zinc finger protein 707 (Zfp707), mRNA.	15	NM_001081065.1	**-1,56**	-1,39	**0,0153**	0,0504
ILMN_2534207	S	**LOC380706**			XM_354621.1	**-1,56**	-1,29	**0,0459**	0,1030
ILMN_1247450	S	**B430005K18Rik**			AK046551	**-1,56**	-1,43	**0,0084**	0,0486
ILMN_2635348	S	**Iqcb1**	Mus musculus IQ calmodulin-binding motif containing 1 (Iqcb1), mRNA.	16	NM_177128.3	**-1,56**	-1,11	**0,0256**	0,3012
ILMN_2539511	S	**Mpeg1**			XM_129176.3	**-1,57**	-1,23	**0,0083**	0,4226
ILMN_1236610	S	**Socs6**	Mus musculus suppressor of cytokine signaling 6 (Socs6), mRNA.	18	NM_018821.3	**-1,57**	-1,01	**0,0300**	0,9651
ILMN_2901626	S	**Tnfrsf21**	Mus musculus tumor necrosis factor receptor superfamily, member 21 (Tnfrsf21), mRNA.	17	NM_178589.2	**-1,57**	-1,26	**0,0069**	0,5203
ILMN_1241328	S	**Kcnd1**			NM_008423	**-1,57**	-1,37	**0,0303**	0,0985
ILMN_2699052	S	**Nrn1**	Mus musculus neuritin 1 (Nrn1), mRNA.	13	NM_153529.1	**-1,57**	-2,42	**0,0155**	0,0038
ILMN_2714222	S	**Elovl2**	Mus musculus elongation of very long chain fatty acids	13	NM_019423.1	**-1,57**	-1,54	**0,0423**	0,0427

			(FEN1/Elo2, SUR4/Elo3, yeast)-like 2 (Elovl2), mRNA.						
ILMN_1232151	S	**C130023I09Rik**			AK047956	**-1,57**	-1,21	**0,0249**	0,2496
ILMN_2460653	S	**Unc93b1**	Mus musculus unc-93 homolog B1 (C. elegans) (Unc93b1), mRNA.	19	NM_019449.1	**-1,57**	1,10	**0,0325**	0,6867
ILMN_2597332	S	**1700123O20Rik**	Mus musculus RIKEN cDNA 1700123O20 gene (1700123O20Rik), mRNA.	14	NM_021437.1	**-1,57**	-1,12	**0,0419**	0,3240
ILMN_2790144	S	**Tomm34**	Mus musculus translocase of outer mitochondrial membrane 34 (Tomm34), mRNA.	2	NM_025996.1	**-1,57**	-1,09	**0,0430**	0,0780
ILMN_2741277	S	**Snurf**	Mus musculus SNRPN upstream reading frame (Snurf), mRNA.	7	NM_033174.2	**-1,58**	1,18	**0,0086**	0,0530
ILMN_3041906	I	**Timm9**	Mus musculus translocase of inner mitochondrial membrane 9 homolog (yeast) (Timm9), nuclear gene encoding mitochondrial protein, transcript variant 2, mRNA.	12	NM_001024853.1	**-1,58**	-1,50	**0,0480**	0,0597
ILMN_2915689	S	**Dhx58**	Mus musculus DEXH (Asp-Glu-X-His) box polypeptide 58 (Dhx58), mRNA.	11	NM_030150.2	**-1,58**	-1,47	**0,0232**	0,0499
ILMN_2516338	S	**D430019H16Rik**	PREDICTED: Mus musculus RIKEN cDNA D430019H16 gene	12	XM_001476158.1	**-1,59**	1,06	**0,0216**	0,7151

			(D430019H16Rik), mRNA.						
ILMN_1236246	S	**D4Wsu132e**	Mus musculus DNA segment, Chr 4, Wayne State University 132, expressed (D4Wsu132e), mRNA.	4	NM_138590.2	**-1,59**	1,00	**0,0066**	0,9981
ILMN_2693403	S	**Ela1**	Mus musculus elastase 1, pancreatic (Ela1), mRNA.	15	NM_033612.1	**-1,59**	-1,50	**0,0223**	0,0875
ILMN_2423372	S	**2310014D11Rik**				**-1,59**	1,09	**0,0250**	0,7254
ILMN_1220307	S	**LOC100046025**	PREDICTED: Mus musculus similar to mKIAA1230 protein, transcript variant 1 (LOC100046025), mRNA.		XM_001475823.1	**-1,60**	-1,82	**0,0104**	0,0106
ILMN_1243900	S	**LOC626152**	PREDICTED: Mus musculus similar to epiplakin (LOC626152), misc RNA.		XR_032670.1	**-1,60**	-1,21	**0,0388**	0,1544
ILMN_2760619	S	**Tinagl1**	Mus musculus tubulointerstitial nephritis antigen-like 1 (Tinagl1), mRNA.	4	NM_023476.2	**-1,60**	-1,01	**0,0284**	0,9264
ILMN_1250837	S	**Rangap1**			NM_011241	**-1,60**	-1,15	**0,0147**	0,2237
ILMN_2824683	S	**Usp4**	Mus musculus ubiquitin specific peptidase 4 (proto-oncogene) (Usp4), mRNA.	9	NM_011678.1	**-1,60**	-1,14	**0,0015**	0,4089
ILMN_1242437	S	**C130090G16Rik**			AK081969	**-1,60**	-1,15	**0,0255**	0,4226
ILMN_1244991	S	**Fbxo21**	Mus musculus F-box protein 21 (Fbxo21), mRNA.	5	NM_145564.3	**-1,60**	-1,24	**0,0146**	0,3290
ILMN_1244804	S	**D430042O09Rik**	Mus musculus RIKEN cDNA D430042O09 gene (D430042O09Rik), mRNA.	7	NM_001081022.1	**-1,61**	-1,32	**0,0145**	0,0544
ILMN_1222734	S	**Aldh1a1**	Mus musculus	19	NM_013467.3	**-1,61**	-1,06	**0,0438**	0,7363

			aldehyde dehydrogenase family 1, subfamily A1 (Aldh1a1), mRNA.						
ILMN_3007540	S	**Krtap5-5**	Mus musculus keratin associated protein 5-5 (Krtap5-5), mRNA. XM_925516	7	NM_001037822.1	**-1,61**	-1,31	**0,0398**	0,2277
ILMN_2682928	S	**Rai14**	Mus musculus retinoic acid induced 14 (Rai14), mRNA.	15	NM_030690.2	**-1,61**	-1,47	**0,0272**	0,0488
ILMN_2920800	S	**Sip1**	Mus musculus survivor of motor neuron protein interacting protein 1 (Sip1), mRNA.	12	NM_025656.1	**-1,62**	-1,46	**0,0025**	0,2301
ILMN_2658815	S	**Tmem98**	Mus musculus transmembrane protein 98 (Tmem98), mRNA.	11	NM_029537.1	**-1,62**	-1,20	**0,0244**	0,3805
ILMN_2476174	S	**Zfp264**			XM_486050	**-1,62**	-1,06	**0,0268**	0,7924
ILMN_1252776	S	**LOC100044812**	PREDICTED: Mus musculus similar to cornichon homolog 2 (Drosophila) (LOC100044812), mRNA.		XM_001473093.1	**-1,62**	-1,29	**0,0342**	0,4299
ILMN_2548010	S	**Hopx**	Mus musculus HOP homeobox (Hopx), mRNA.	5	NM_175606.2	**-1,63**	-1,17	**0,0068**	0,0360
ILMN_2588882	S	**Slc41a2**	Mus musculus solute carrier family 41, member 2 (Slc41a2), mRNA.	10	NM_177388.3	**-1,63**	-2,39	**0,0328**	0,1036
ILMN_2600720	S	**2310007H09Rik**	Mus musculus RIKEN cDNA 2310007H09 gene (2310007H09Rik), mRNA.	7	NM_029609.1	**-1,63**	-1,28	**0,0427**	0,1144
ILMN_2494707	S	**LOC381232**			XM_358531	**-1,63**	1,09	**0,0332**	0,4226
ILMN_1226216	S	**Rnf123**	Mus musculus ring	9	NM_032543.1	**-1,64**	1,06	**0,0174**	0,7823

			finger protein 123 (Rnf123), mRNA.						
ILMN_3162960	I	**EG214403**	Mus musculus predicted gene, EG214403 (EG214403), mRNA.	1	NM_001029977.2	**-1,64**	1,14	**0,0424**	0,4770
ILMN_2779703	S	**Ercc1**	Mus musculus excision repair cross-complementing rodent repair deficiency, complementation group 1 (Ercc1), mRNA.	7	NM_007948.1	**-1,64**	1,21	**0,0263**	0,5058
ILMN_2929572	S	**Ccdc68**	Mus musculus coiled-coil domain containing 68 (Ccdc68), mRNA.	18	NM_201362.1	**-1,65**	-1,28	**0,0438**	0,1922
ILMN_1235585	S	**D930040M24Rik**			NM_177278	**-1,65**	-1,31	**0,0279**	0,4257
ILMN_2907964	S	**Crim2**	Mus musculus cysteine rich BMP regulator 2 (chordin like) (Crim2), mRNA.	6	NM_001029985.1	**-1,65**	-1,67	**0,0061**	0,0125
ILMN_2597778	S	**Gna14**	Mus musculus guanine nucleotide binding protein, alpha 14 (Gna14), mRNA.	19	NM_008137.3	**-1,65**	-2,05	**0,0068**	0,0728
ILMN_2677792	S	**Cyp2c39**	Mus musculus cytochrome P450, family 2, subfamily c, polypeptide 39 (Cyp2c39), mRNA.	19	NM_010003.1	**-1,65**	1,02	**0,0164**	0,4226
ILMN_1249666	S	**Ppap2c**	Mus musculus phosphatidic acid phosphatase type 2c (Ppap2c), mRNA.	10	NM_015817.2	**-1,66**	-1,55	**0,0108**	0,0163
ILMN_1231939	S	**Ccbl2**	Mus musculus cysteine conjugate-beta lyase 2 (Ccbl2),	3	NM_173763.3	**-1,66**	-2,36	**0,0072**	0,0010

			mRNA.						
ILMN_3115677	A	**Ilf3**	Mus musculus interleukin enhancer binding factor 3 (Ilf3), transcript variant 3, mRNA.	9	NM_001042708.1	**-1,66**	-1,04	**0,0205**	0,8180
ILMN_2453076	S	**Ypel3**	Mus musculus yippee-like 3 (Drosophila) (Ypel3), mRNA.	7	NM_025347.2	**-1,67**	-1,24	**0,0136**	0,3231
ILMN_2785454	S	**Hist2h2ab**	Mus musculus histone cluster 2, H2ab (Hist2h2ab), mRNA.	3	NM_178213.3	**-1,67**	-1,46	**0,0395**	0,0155
ILMN_1218058	S	**Atp1a1**	Mus musculus ATPase, Na+/K+ transporting, alpha 1 polypeptide (Atp1a1), mRNA.	3	NM_144900.1	**-1,68**	-1,78	**0,0029**	0,0017
ILMN_1218551	S	**Mapk3**	Mus musculus mitogen-activated protein kinase 3 (Mapk3), mRNA.	7	NM_011952.2	**-1,68**	1,21	**0,0404**	0,5653
ILMN_2776056	S	**Rassf3**	Mus musculus Ras association (RalGDS/AF-6) domain family member 3 (Rassf3), mRNA.	10	NM_138956.3	**-1,68**	-3,03	**0,0026**	0,0027
ILMN_2635105	S	**Nme7**	Mus musculus non-metastatic cells 7, protein expressed in (nucleoside-diphosphate kinase) (Nme7), transcript variant 1, mRNA.	1	NM_138314.2	**-1,68**	-1,24	**0,0484**	0,1349
ILMN_2825020	S	**Rassf5**	Mus musculus Ras association (RalGDS/AF-6) domain family 5 (Rassf5), mRNA.	1	NM_018750.2	**-1,69**	-1,29	**0,0389**	0,1097

ILMN_2962584	S	**Tspan4**	Mus musculus tetraspanin 4 (Tspan4), mRNA.	7	NM_053082.2	**-1,69**	1,09	**0,0022**	0,7562
ILMN_3027751	I	**Sorbs1**	Mus musculus sorbin and SH3 domain containing 1 (Sorbs1), transcript variant 5, mRNA.	19	NM_001034964.1	**-1,69**	1,34	**0,0009**	0,0665
ILMN_1240839	S	**Golt1a**	Mus musculus golgi transport 1 homolog A (S. cerevisiae) (Golt1a), mRNA.	1	NM_026680.4	**-1,69**	-1,62	**0,0204**	0,0390
ILMN_1219717	S	**Sort1**	Mus musculus sortilin 1 (Sort1), mRNA.	3	NM_019972.2	**-1,69**	-1,60	**0,0386**	0,0184
ILMN_1259939	S	**Trim3**	Mus musculus tripartite motif-containing 3 (Trim3), mRNA.	7	NM_018880.2	**-1,69**	1,08	**0,0220**	0,8074
ILMN_2776922	S	**Glrx1**			NM_053108	**-1,70**	-1,60	**0,0051**	0,0030
ILMN_1249775	S	**Lrp8**	Mus musculus low density lipoprotein receptor-related protein 8, apolipoprotein e receptor (Lrp8), transcript variant 2, mRNA.		NM_001080926.1	**-1,70**	1,11	**0,0430**	0,4226
ILMN_1228189	S	**Med14**	Mus musculus mediator complex subunit 14 (Med14), transcript variant 2, mRNA.	X	NM_012005.3	**-1,70**	-1,09	**0,0026**	0,8079
ILMN_1220360	S	**Unc13b**	Mus musculus unc-13 homolog B (C. elegans) (Unc13b), mRNA.	4	NM_001081413.1	**-1,72**	-1,72	**0,0307**	0,0610
ILMN_1216145	S	**Np220**			AK043029	**-1,73**	-1,06	**0,0248**	0,4226
ILMN_2707694	S	**D10Wsu102e**	Mus musculus DNA segment, Chr 10, Wayne State University 102, expressed (D10Wsu102e),	10	NM_026579.2	**-1,73**	-1,19	**0,0106**	0,1342

			mRNA.						
ILMN_1247430	S	**LOC383681**			XM_357183.1	**-1,74**	1,19	**0,0216**	0,4605
ILMN_1239742	S	**Atp2a2**	Mus musculus ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 (Atp2a2), mRNA.	5	NM_009722.2	**-1,74**	-1,28	**0,0439**	0,0420
ILMN_2794608	S	**Bcat2**	Mus musculus branched chain aminotransferase 2, mitochondrial (Bcat2), mRNA.	7	NM_009737.1	**-1,75**	-1,13	**0,0108**	0,6196
ILMN_1257953	S	**5730598B06**			XM_135809.3	**-1,76**	-1,02	**0,0036**	0,9337
ILMN_2463006	S	**LOC100047208**	PREDICTED: Mus musculus similar to trypsinogen 15 (LOC100047208), mRNA.		XM_001477976.1	**-1,76**	-1,12	**0,0323**	0,5565
ILMN_3071907	I	**Nme2**	Mus musculus non-metastatic cells 2, protein (NM23B) expressed in (Nme2), transcript variant 1, mRNA.	11	NM_008705.4	**-1,77**	-1,01	**0,0380**	0,9592
ILMN_2710449	S	**Crip2**	Mus musculus cysteine rich protein 2 (Crip2), mRNA.	12	NM_024223.1	**-1,77**	-1,58	**0,0216**	0,0101
ILMN_2526468	S	**LOC217591**			XM_138082.2	**-1,77**	-1,30	**0,0314**	0,2597
ILMN_1231483	S	**D230017B08Rik**			AK051900	**-1,77**	1,00	**0,0341**	NA
ILMN_2637241	S	**Dhps**	Mus musculus deoxyhypusine synthase (Dhps), mRNA.	8	NM_001039514.1	**-1,77**	-1,20	**0,0026**	0,2282
ILMN_2660364	S	**Nudt14**	Mus musculus nudix (nucleoside diphosphate linked moiety X)-type motif 14 (Nudt14), mRNA.		NM_025399.3	**-1,78**	-1,01	**0,0313**	0,9535
ILMN_2773835	S	**LOC670044**	PREDICTED: Mus musculus similar to Mothers against decapentaplegic homolog 6 (SMAD 6) (Mothers against DPP homolog 6) (Smad6)		XM_978692.1	**-1,78**	-1,78	**0,0472**	0,0379

			(Mad homolog 7) (LOC670044), mRNA.						
ILMN_1256699	S	**Sfi1**	Mus musculus Sfi1 homolog, spindle assembly associated (yeast) (Sfi1), mRNA.	11	NM_030207.2	**-1,78**	-1,12	**0,0385**	0,3218
ILMN_2907878	S	**H2afx**	Mus musculus H2A histone family, member X (H2afx), mRNA.	9	NM_010436.2	**-1,78**	-1,08	**0,0287**	0,6958
ILMN_2449986	S	**EG640530**	PREDICTED: Mus musculus predicted gene, EG640530 (EG640530), mRNA.		XM_917532.3	**-1,78**	-1,53	**0,0236**	0,0025
ILMN_2751948	S	**Hist2h2aa1**			NM_013549	**-1,79**	-1,51	**0,0087**	0,0440
ILMN_1238542	S	**2810405K02Rik**	Mus musculus RIKEN cDNA 2810405K02 gene (2810405K02Rik), mRNA.	4	NM_025582.3	**-1,80**	-1,79	**0,0057**	0,0077
ILMN_2769877	S	**Reck**			NM_016678	**-1,80**	-1,44	**0,0180**	0,1834
ILMN_2894057	S	**Srrd**	Mus musculus SRR1 domain containing (Srrd), mRNA. XM_913540 XM_922786 XM_922800 XM_922805 XM_922818	5	NM_027323.1	**-1,81**	1,15	**0,0080**	0,6954
ILMN_2903734	S	**Siah1b**	Mus musculus seven in absentia 1B (Siah1b), mRNA.	X	NM_009173.1	**-1,82**	-1,18	**0,0441**	0,5724
ILMN_2496163	S	**LOC100044165**	PREDICTED: Mus musculus hypothetical protein LOC100044165 (LOC100044165), mRNA.		XM_001471936.1	**-1,83**	1,00	**0,0412**	NA
ILMN_2597469	S	**LOC544904**	PREDICTED: Mus musculus similar to idiotypic anti-NP IgG(1) heavy chain V-D-J (LOC544904), mRNA.		XM_914633.2	**-1,83**	-1,03	**0,0087**	0,8567
ILMN_2642339	S	**Slc1a2**	Mus musculus solute	2	NM_011393.2	**-1,83**	-1,48	**0,0295**	0,0836

			carrier family 1 (glial high affinity glutamate transporter), member 2 (Slc1a2), transcript variant 3, mRNA.						
ILMN_3160416	S	**2900024O10Rik**	Mus musculus RIKEN cDNA 2900024O10 gene (2900024O10Rik), mRNA.	13	NM_028372.1	**-1,83**	1,07	**0,0060**	0,8300
ILMN_2636508	S	**8030411F24Rik**	Mus musculus RIKEN cDNA 8030411F24 gene (8030411F24Rik), mRNA.	2	NM_030135.2	**-1,84**	-1,33	**0,0231**	0,3423
ILMN_2667091	S	**Ppp1r3c**	Mus musculus protein phosphatase 1, regulatory (inhibitor) subunit 3C (Ppp1r3c), mRNA.		NM_016854.2	**-1,84**	-2,03	**0,0250**	0,0025
ILMN_2686700	S	**Abca8a**	Mus musculus ATP-binding cassette, sub-family A (ABC1), member 8a (Abca8a), mRNA.		NM_153145.3	**-1,86**	-1,49	**0,0273**	0,0263
ILMN_1227403	S	**Rtn4rl1**	Mus musculus reticulon 4 receptor-like 1 (Rtn4rl1), mRNA.	11	NM_177708.5	**-1,86**	-1,14	**0,0408**	0,5632
ILMN_2739843	S	**Metrn**			NM_133719	**-1,86**	-1,55	**0,0242**	0,0103
ILMN_2945940	S	**Rapgef4**	Mus musculus Rap guanine nucleotide exchange factor (GEF) 4 (Rapgef4), mRNA.	2	NM_019688.1	**-1,87**	1,00	**0,0059**	0,9792
ILMN_2945348	S	**Glrx**	Mus musculus glutaredoxin (Glrx), mRNA.	13	NM_053108.2	**-1,87**	-1,65	**0,0007**	0,0159
ILMN_1231720	S	**Zfp385a**	Mus musculus zinc finger protein 385A (Zfp385a), mRNA.	15	NM_013866.2	**-1,87**	-1,25	**0,0445**	0,0699
ILMN_3064283	I	**Pde4dip**	Mus musculus	3	NM_001039376.1	**-1,87**	-1,40	**0,0494**	0,0498

			phosphodiesterase 4D interacting protein (myomegalin) (Pde4dip), transcript variant 1, mRNA.						
ILMN_2961216	S	**Slco2a1**	Mus musculus solute carrier organic anion transporter family, member 2a1 (Slco2a1), mRNA.		NM_033314.2	**-1,89**	-2,49	**0,0181**	0,0053
ILMN_2692927	S	**Srd5a1**			NM_175283.2	**-1,89**	-1,85	**0,0148**	0,0008
ILMN_3050362	I	**Nt5dc3**	Mus musculus 5'-nucleotidase domain containing 3 (Nt5dc3), transcript variant 3, mRNA.	10	NM_001003910.1	**-1,89**	-1,22	**0,0016**	0,5165
ILMN_2534556	S	**LOC195150**			XM_111306.1	**-1,89**	-1,08	**0,0072**	0,6913
ILMN_2962575	S	**A830080D01 Rik**	Mus musculus RIKEN cDNA A830080D01 gene (A830080D01Rik), mRNA.	X	NM_001033472.2	**-1,89**	-1,11	**0,0380**	0,5816
ILMN_2918732	S	**Ugt3a1**	Mus musculus UDP glycosyltransferases 3 family, polypeptide A1 (Ugt3a1), mRNA.	15	NM_207216.1	**-1,90**	-1,35	**0,0136**	0,1093
ILMN_2678355	S	**Amigo2**	Mus musculus adhesion molecule with Ig like domain 2 (Amigo2), mRNA.	15	NM_178114.3	**-1,90**	-1,83	**0,0478**	0,0094
ILMN_1236522	S	**Cbr1**	Mus musculus carbonyl reductase 1 (Cbr1), mRNA.	16	NM_007620.2	**-1,90**	-1,57	**0,0204**	0,0010
ILMN_1256103	S	**Ccbl2**	Mus musculus cysteine conjugate-beta lyase 2 (Ccbl2), mRNA.	3	NM_173763.3	**-1,90**	-2,18	**0,0090**	0,0140
ILMN_1241208	S	**C030017I19Rik**			AK047722	**-1,90**	-1,32	**0,0017**	0,3939
ILMN_2685203	S	**Mrgprg**	Mus musculus MAS-related GPR, member G (Mrgprg), mRNA.	7	NM_203492.2	**-1,91**	-1,11	**0,0001**	0,7860

ILMN_2918317	S	**Adck5**	Mus musculus aarF domain containing kinase 5 (Adck5), mRNA.	15	NM_172960.1	**-1,91**	-1,03	**0,0257**	0,8920
ILMN_3145814	A	**Ogfrl1**	Mus musculus opioid growth factor receptor-like 1 (Ogfrl1), mRNA.	1	NM_001081079.1	**-1,91**	-1,64	**0,0248**	0,0026
ILMN_2436561	S	**Tmem19**	Mus musculus transmembrane protein 19 (Tmem19), mRNA.		NM_133683.3	**-1,92**	-2,68	**0,0220**	0,0011
ILMN_1229529	S	**Hsd17b7**	Mus musculus hydroxysteroid (17-beta) dehydrogenase 7 (Hsd17b7), mRNA.	1	NM_010476.3	**-1,92**	-1,38	**0,0254**	0,0392
ILMN_2631948	S	**Gulo**	Mus musculus gulonolactone (L-) oxidase (Gulo), mRNA.	14	NM_178747.2	**-1,93**	-1,99	**0,0071**	0,0001
ILMN_3138743	A	**Acsl3**	Mus musculus acyl-CoA synthetase long-chain family member 3 (Acsl3), transcript variant 1, mRNA.	1	NM_028817.2	**-1,93**	-2,27	**0,0491**	0,0037
ILMN_1227386	S	**Aig1**	Mus musculus androgen-induced 1 (Aig1), mRNA.	10	NM_025446.1	**-1,93**	-1,40	**0,0491**	0,1299
ILMN_1222039	S	**Dhx58**	Mus musculus DEXH (Asp-Glu-X-His) box polypeptide 58 (Dhx58), mRNA.	11	NM_030150.2	**-1,93**	-1,42	**0,0144**	0,1396
ILMN_1218662	S	**Tpp2**			AK040859	**-1,94**	1,10	**0,0321**	0,4063
ILMN_1213148	S	**Slc2a8**	Mus musculus solute carrier family 2, (facilitated glucose transporter), member 8 (Slc2a8), mRNA.	2	NM_019488.4	**-1,95**	-1,35	**0,0196**	0,0194
ILMN_2535846	S	**LOC383738**			XM_357217.1	**-1,95**	-1,74	**0,0182**	0,0671
ILMN_1240671	S	**LOC382058**			XM_356133.1	**-1,96**	1,09	**0,0381**	0,7865

ILMN_1236134	S	**EG434674**	Mus musculus predicted gene, EG434674 (EG434674), mRNA. XM_922736 XM_922739 XM_922744 XM_922747	19	NM_001013820.2	**-1,96**	-1,54	**0,0452**	0,0018
ILMN_1250776	S	**Arhgap6**			AK048162	**-1,97**	-1,88	**0,0365**	0,0219
ILMN_2605819	S	**Egln3**	Mus musculus EGL nine homolog 3 (C. elegans) (Egln3), mRNA.	12	NM_028133.1	**-2,00**	-1,44	**0,0365**	0,0202
ILMN_2691067	S	**Dhdds**	Mus musculus dehydrodolichyl diphosphate synthase (Dhdds), mRNA.		NM_026144.4	**-2,01**	-1,15	**0,0158**	0,5467
ILMN_2531212	S	**LOC232619**			XM_145207.2	**-2,01**	-1,17	**0,0206**	0,3675
ILMN_2961221	S	**Slco2a1**	Mus musculus solute carrier organic anion transporter family, member 2a1 (Slco2a1), mRNA.		NM_033314.2	**-2,01**	-1,90	**0,0310**	0,0010
ILMN_1214193	S	**D430006M22Rik**			AK084896	**-2,01**	-1,24	**0,0454**	0,5527
ILMN_1254358	S	**Igfbp5**	Mus musculus insulin-like growth factor binding protein 5 (Igfbp5), mRNA.	1	NM_010518.2	**-2,02**	1,01	**0,0348**	0,9504
ILMN_1227913	S	**Pmpca**	Mus musculus peptidase (mitochondrial processing) alpha (Pmpca), nuclear gene encoding mitochondrial protein, mRNA.	2	NM_173180.3	**-2,03**	-1,04	**0,0422**	0,9115
ILMN_2521965	S	**Slc30a3**			NM_011773	**-2,04**	-1,70	**0,0173**	0,0748
ILMN_2900617	S	**Tle6**	Mus musculus transducin-like enhancer of split 6, homolog of Drosophila E(spl) (Tle6), mRNA.	10	NM_053254.2	**-2,04**	-1,22	**0,0082**	0,1901

ILMN_2761046	S	**Slc25a33**	Mus musculus solute carrier family 25, member 33 (Slc25a33), mRNA.	4	NM_027460.2	**-2,05**	-1,13	**0,0238**	0,4411
ILMN_2671435	S	**LOC223672**			XM_128064.4	**-2,06**	-3,17	**0,0153**	0,0025
ILMN_2627733	S	**Slc46a3**	Mus musculus solute carrier family 46, member 3 (Slc46a3), mRNA.	5	NM_027872.3	**-2,06**	-2,41	**0,0068**	0,0144
ILMN_1257220	S	**Mfn2**	PREDICTED: Mus musculus mitofusin 2, transcript variant 9 (Mfn2), mRNA.		XM_001002419.1	**-2,07**	1,24	**0,0184**	0,3101
ILMN_2685022	S	**C730048C13Rik**	Mus musculus RIKEN cDNA C730048C13 gene (C730048C13Rik), mRNA.	19	NM_177002.2	**-2,07**	-1,52	**0,0442**	0,0025
ILMN_1258442	S	**Adh4**	Mus musculus alcohol dehydrogenase 4 (class II), pi polypeptide (Adh4), mRNA.	3	NM_011996.2	**-2,08**	-1,40	**0,0302**	0,0186
ILMN_2704318	S	**D16Bwg1494e**	PREDICTED: Mus musculus DNA segment, Chr 16, Brigham & Women's Genetics 1494 expressed (D16Bwg1494e), mRNA.	16	XM_358773.6	**-2,11**	1,09	**0,0137**	0,7056
ILMN_2699367	S	**1190005I06Rik**	Mus musculus RIKEN cDNA 1190005I06 gene (1190005I06Rik), mRNA.	8	NM_197988.1	**-2,12**	-1,45	**0,0079**	0,0267
ILMN_3123195	A	**Slc1a2**	Mus musculus solute carrier family 1 (glial high affinity glutamate transporter), member 2 (Slc1a2), transcript variant 1, mRNA.		NM_001077514.1	**-2,12**	-1,57	**0,0160**	0,0508

ILMN_2617625	S	**Cyp2b9**	Mus musculus cytochrome P450, family 2, subfamily b, polypeptide 9 (Cyp2b9), mRNA.	7	NM_010000.2	**-2,14**	96,77	**0,0007**	0,0006
ILMN_2723190	S	**Guca1a**	Mus musculus guanylate cyclase activator 1a (retina) (Guca1a), mRNA.	17	NM_008189.2	**-2,15**	-1,69	**0,0466**	0,1557
ILMN_2569894	S	**D630011D02Rik**			AK052644	**-2,16**	-1,26	**0,0297**	0,2902
ILMN_1218127	S	**Pcp4l1**	PREDICTED: Mus musculus Purkinje cell protein 4-like 1 (Pcp4l1), mRNA.	1	XM_484933.5	**-2,17**	-1,23	**0,0244**	0,4392
ILMN_2484679	S	**Prei4**	Mus musculus preimplantation protein 4 (Prei4), transcript variant 4, mRNA.	2	NM_001042672.1	**-2,17**	-1,21	**0,0368**	0,2502
ILMN_2793806	S	**Mug2**	Mus musculus murinoglobulin 2 (Mug2), mRNA.	6	NM_008646.1	**-2,20**	-1,91	**0,0244**	0,0001
ILMN_3076439	I	**Slc1a2**	Mus musculus solute carrier family 1 (glial high affinity glutamate transporter), member 2 (Slc1a2), transcript variant 2, mRNA.	2	NM_001077515.1	**-2,21**	-1,56	**0,0030**	0,0811
ILMN_2686513	S	**Cbara1**			NM_144822.1	**-2,21**	-1,21	**0,0292**	0,2849
ILMN_2634667	S	**Mep1b**			NM_008586	**-2,23**	-1,14	**0,0384**	0,4226
ILMN_1229187	S	**Prhoxnb**	Mus musculus parahox cluster neighbor (Prhoxnb), mRNA.	5	NM_001039678.1	**-2,25**	-1,59	**0,0305**	0,0171
ILMN_2692527	S	**5730593N15Rik**			NM_175263	**-2,28**	-1,76	**0,0482**	0,0232
ILMN_1250358	S	**Acot8**	Mus musculus acyl-CoA thioesterase 8 (Acot8), mRNA.	2	NM_133240.1	**-2,28**	2,11	**0,0249**	0,0376
ILMN_2793062	S	**Rasl11b**	Mus musculus RAS-like, family 11,	5	NM_026878.1	**-2,29**	-1,63	**0,0298**	0,0925

			member B (Rasl11b), mRNA.						
ILMN_2658355	S	**Ugt3a2**	Mus musculus UDP glycosyltransferases 3 family, polypeptide A2 (Ugt3a2), mRNA.	15	NM_144845.3	**-2,30**	-1,69	**0,0071**	0,0026
ILMN_2986051	S	**Ccbl1**	Mus musculus cysteine conjugate-beta lyase 1 (Ccbl1), mRNA.	2	NM_172404.2	**-2,32**	-1,75	**0,0132**	0,0125
ILMN_1243129	S	**Slc11a2**			AK049856	**-2,33**	-1,40	**0,0117**	0,0190
ILMN_2749717	S	**Bcl3**	Mus musculus B-cell leukemia/lymphoma 3 (Bcl3), mRNA.	7	NM_033601.1	**-2,34**	-2,62	**0,0336**	0,0169
ILMN_2614432	S	**Egfr**			NM_207655.1	**-2,34**	-1,71	**0,0170**	0,0153
ILMN_2685043	S	**Mug2**	Mus musculus murinoglobulin 2 (Mug2), mRNA.		NM_008646.3	**-2,34**	-2,30	**0,0331**	0,0011
ILMN_2598103	S	**Emp2**	Mus musculus epithelial membrane protein 2 (Emp2), mRNA.	16	NM_007929.2	**-2,35**	-1,77	**0,0158**	0,2209
ILMN_2683613	S	**Nlk**	Mus musculus nemo like kinase (Nlk), mRNA.	11	NM_008702.2	**-2,39**	-1,30	**0,0468**	0,5149
ILMN_3143404	A	**Mup2**	Mus musculus major urinary protein 2 (Mup2), transcript variant 1, mRNA.	4	NM_008647.3	**-2,39**	1,07	**0,0340**	0,1440
ILMN_1242024	S	**Setd4**	Mus musculus SET domain containing 4 (Setd4), mRNA.	16	NM_145482.2	**-2,40**	-1,38	**0,0009**	0,2990
ILMN_1217352	S	**EG381806**	Mus musculus predicted gene, EG381806 (EG381806) on chromosome 6.		NR_003624.1	**-2,43**	-1,38	**0,0191**	0,0507
ILMN_2818498	S	**OTTMUSG00000000231**	Mus musculus predicted gene, OTTMUSG00000000231 (OTTMUSG00000000231), mRNA.	4	NM_001009550.1	**-2,44**	-4,37	**0,0212**	0,0001
ILMN_2819424	S	**Prhoxnb**	Mus musculus	5	NM_001039678.1	**-2,45**	-1,56	**0,0056**	0,0366

			parahox cluster neighbor (Prhoxnb), mRNA.						
ILMN_2433848	S	**Slco2a1**			NM_033314	**-2,46**	-2,41	**0,0112**	0,0039
ILMN_1221533	S	**5830445I20Rik**			AK030893	**-2,47**	-1,02	**0,0260**	0,8993
ILMN_3125606	A	**D12Ertd647e**	Mus musculus DNA segment, Chr 12, ERATO Doi 647, expressed (D12Ertd647e), transcript variant 5, mRNA.	12	NM_194069.1	**-2,52**	-2,77	**0,0015**	0,0037
ILMN_2693922	S	**Egfr**	Mus musculus epidermal growth factor receptor (Egfr), transcript variant 1, mRNA.	11	NM_207655.2	**-2,53**	-1,95	**0,0211**	0,0078
ILMN_2814865	S	**Qpct**	Mus musculus glutaminyl-peptide cyclotransferase (glutaminyl cyclase) (Qpct), mRNA.		NM_027455.1	**-2,60**	-1,52	**0,0014**	0,0392
ILMN_2881620	S	**Nfe2**	Mus musculus nuclear factor, erythroid derived 2 (Nfe2), mRNA.	15	NM_008685.2	**-2,63**	-1,43	**0,0329**	0,2186
ILMN_1254902	S	**Rdh9**	Mus musculus retinol dehydrogenase 9 (Rdh9), mRNA.	10	NM_153133.2	**-2,68**	-2,44	**0,0043**	0,0040
ILMN_2711948	S	**LOC100047619**	PREDICTED: Mus musculus similar to solute carrier family 7 (cationic amino acid transporter, y+ system), member 5 (LOC100047619), misc RNA.		XR_033736.1	**-2,71**	-1,63	**0,0055**	0,0710
ILMN_1213838	S	**Arhgap26**	Mus musculus Rho GTPase activating protein 26 (Arhgap26), mRNA.	18	NM_175164.4	**-2,71**	-3,74	**0,0055**	0,0283
ILMN_2622856	S	**Apol9b**	Mus musculus apolipoprotein L 9b (Apol9b), mRNA.	15	NM_173743.3	**-2,77**	-4,34	**0,0077**	0,0001

ILMN_2976211	S	**Cyp2b23**	Mus musculus cytochrome P450, family 2, subfamily b, polypeptide 23 (Cyp2b23), mRNA.	7	NM_001081148.1	**-2,77**	23,54	**0,0033**	0,0027
ILMN_2681232	S	**D12Ertd647e**	Mus musculus DNA segment, Chr 12, ERATO Doi 647, expressed (D12Ertd647e), transcript variant 4, mRNA.	12	NM_194068.1	**-2,81**	-3,14	**0,0011**	0,0095
ILMN_2618176	S	**Socs3**	Mus musculus suppressor of cytokine signaling 3 (Socs3), mRNA.	11	NM_007707.2	**-2,84**	-1,33	**0,0248**	0,5701
ILMN_1221060	S	**Pparg**	Mus musculus peroxisome proliferator activated receptor gamma (Pparg), mRNA.	6	NM_011146.2	**-2,86**	-1,25	**0,0353**	0,2762
ILMN_2685157	S	**Abcc3**	Mus musculus ATP-binding cassette, sub-family C (CFTR/MRP), member 3 (Abcc3), mRNA.	11	NM_029600.3	**-2,87**	-2,22	**0,0116**	0,0109
ILMN_2684316	S	**P2ry1**	Mus musculus purinergic receptor P2Y, G-protein coupled 1 (P2ry1), mRNA.		NM_008772.4	**-2,89**	1,11	**0,0137**	0,5978
ILMN_2623735	S	**Ccbl1**	Mus musculus cysteine conjugate-beta lyase 1 (Ccbl1), mRNA.	2	NM_172404.2	**-2,91**	-1,87	**0,0295**	0,0051
ILMN_1246137	S	**1810005K13Rik**				**-2,97**	-3,14	**0,0176**	0,0019
ILMN_3029849	I	**Cebpe**	Mus musculus CCAAT/enhancer binding protein (C/EBP), epsilon (Cebpe), mRNA.	14	NM_207131.1	**-3,05**	-4,66	**0,0050**	0,0032
ILMN_2696026	S	**Npr2**	Mus musculus	4	NM_173788.3	**-3,10**	-2,45	**0,0141**	0,0233

			natriuretic peptide receptor 2 (Npr2), mRNA.						
ILMN_3000236	S	**F11**	Mus musculus coagulation factor XI (F11), mRNA.	8	NM_028066.1	**-3,23**	-2,99	**0,0002**	0,0044
ILMN_3128725	A	**Egfr**	Mus musculus epidermal growth factor receptor (Egfr), transcript variant 2, mRNA.	11	NM_007912.4	**-3,25**	-1,76	**0,0020**	0,0005
ILMN_1239293	S	**Sulf2**	Mus musculus sulfatase 2 (Sulf2), mRNA.	2	NM_028072.4	**-3,29**	-4,12	**0,0085**	0,0016
ILMN_3138904	A	**Ntrk2**	Mus musculus neurotrophic tyrosine kinase, receptor, type 2 (Ntrk2), transcript variant 1, mRNA.	13	NM_001025074.1	**-3,29**	1,12	**0,0148**	0,4226
ILMN_2609762	S	**F11**	Mus musculus coagulation factor XI (F11), mRNA.	8	NM_028066.1	**-3,32**	-3,41	**0,0000**	0,0003
ILMN_1225528	S	**Trib3**	Mus musculus tribbles homolog 3 (Drosophila) (Trib3), mRNA.	2	NM_175093.2	**-3,34**	-4,74	**0,0366**	0,0366
ILMN_3052260	I	**Egfr**	Mus musculus epidermal growth factor receptor (Egfr), transcript variant 2, mRNA.	11	NM_007912.4	**-3,37**	-1,77	**0,0025**	0,0140
ILMN_1257851	S	**LOC384273**			XM_357532.1	**-3,43**	-2,41	**0,0041**	0,0189
ILMN_1241818	S	**Cyp2c54**	Mus musculus cytochrome P450, family 2, subfamily c, polypeptide 54 (Cyp2c54), mRNA.	19	NM_206537.1	**-3,44**	-1,71	**0,0065**	0,0162
ILMN_1241496	S	**9030024J15Rik**				**-3,45**	-1,82	**0,0049**	0,0238
ILMN_1220301	S	**Cebpe**	Mus musculus CCAAT/enhancer	14	NM_207131.1	**-3,52**	-2,91	**0,0062**	0,0065

			binding protein (C/EBP), epsilon (Cebpe), mRNA.						
ILMN_1226469	S	**Cyp2g1**	Mus musculus cytochrome P450, family 2, subfamily g, polypeptide 1 (Cyp2g1), mRNA.	7	NM_013809.1	**-3,62**	-1,74	**0,0179**	0,1810
ILMN_1243228	S	**Il1rap**	Mus musculus interleukin 1 receptor accessory protein (Il1rap), transcript variant 2, mRNA.	16	NM_134103.1	**-3,75**	-4,43	**0,0065**	0,0013
ILMN_2744879	S	**Dnaic1**	Mus musculus dynein, axonemal, intermediate chain 1 (Dnaic1), mRNA.	4	NM_175138.3	**-3,77**	-2,05	**0,0366**	0,2189
ILMN_1227404	S	**C8b**	Mus musculus complement component 8, beta polypeptide (C8b), mRNA.	4	NM_133882.2	**-3,78**	-1,62	**0,0201**	0,0063
ILMN_2740465	S	**Il1rap**	Mus musculus interleukin 1 receptor accessory protein (Il1rap), transcript variant 1, mRNA.	16	NM_008364.1	**-3,84**	-4,28	**0,0011**	0,0004
ILMN_2621752	S	**Irf5**	Mus musculus interferon regulatory factor 5 (Irf5), mRNA.		NM_012057.3	**-3,94**	-4,74	**0,0017**	0,0096
ILMN_2641201	S	**Sp5**	Mus musculus trans-acting transcription factor 5 (Sp5), mRNA.	2	NM_022435.2	**-4,00**	-1,78	**0,0108**	0,0967
ILMN_2504842	S	**Ugt1a12**			NM_201644	**-4,08**	-3,03	**0,0144**	0,0017
ILMN_2740464	S	**Il1rap**	Mus musculus interleukin 1 receptor accessory protein (Il1rap), transcript variant 1, mRNA.	16	NM_008364.1	**-4,09**	-4,08	**0,0014**	0,0013
ILMN_2931918	S	**4432416J03R**	Mus musculus	9	NM_030069.1	**-4,14**	-2,26	**0,0014**	0,0067

		ik	RIKEN cDNA 4432416J03 gene (4432416J03Rik), mRNA.						
ILMN_3005740	S	**Zap70**	Mus musculus zeta-chain (TCR) associated protein kinase (Zap70), mRNA.	1	NM_009539.2	**-4,28**	-4,36	**0,0146**	0,0001
ILMN_1236044	S	**F11**	Mus musculus coagulation factor XI (F11), mRNA.	8	NM_028066.1	**-4,28**	-3,90	**0,0002**	0,0006
ILMN_2890935	S	**Avpr1a**	Mus musculus arginine vasopressin receptor 1A (Avpr1a), mRNA.	10	NM_016847.2	**-4,41**	-4,74	**0,0058**	0,0047
ILMN_2903945	S	**Gadd45g**	Mus musculus growth arrest and DNA-damage-inducible 45 gamma (Gadd45g), mRNA.	13	NM_011817.1	**-4,50**	-3,37	**0,0418**	0,1872
ILMN_2424150	S	**1500017E21Rik**				**-4,60**	-3,72	**0,0316**	0,0057
ILMN_1226650	S	**Il1rap**	Mus musculus interleukin 1 receptor accessory protein (Il1rap), transcript variant 2, mRNA.	16	NM_134103.1	**-4,68**	-7,03	**0,0012**	0,0109
ILMN_2881950	S	**OTTMUSG00000007485**	Mus musculus predicted gene, OTTMUSG00000007485 (OTTMUSG00000007485), mRNA.	4	NM_001012323.1	**-4,71**	-1,45	**0,0164**	0,0374
ILMN_1227225	S	**Trim28**	Mus musculus tripartite motif protein 28 (Trim28), mRNA.	7	NM_011588.2	**-5,36**	-5,15	**0,0078**	0,0013
ILMN_1254622	S	**Pcp4l1**	PREDICTED: Mus musculus Purkinje cell protein 4-like 1 (Pcp4l1), mRNA.	1	XM_484933.5	**-5,48**	-5,02	**0,0176**	0,0123
ILMN_2654582	S	**Cyp2c44**	Mus musculus	19	NM_001001446.2	**-5,56**	-5,41	**0,0012**	0,0006

			cytochrome P450, family 2, subfamily c, polypeptide 44 (Cyp2c44), mRNA.						
ILMN_2706269	S	**Hspb1**	Mus musculus heat shock protein 1 (Hspb1), mRNA.	5	NM_013560.1	**-5,72**	-4,47	**0,0077**	0,0002
ILMN_2601215	S	**Cyp7b1**	Mus musculus cytochrome P450, family 7, subfamily b, polypeptide 1 (Cyp7b1), mRNA.	3	NM_007825.3	**-6,20**	-10,15	**0,0072**	0,0053
ILMN_2959757	S	**Cyp2g1**	Mus musculus cytochrome P450, family 2, subfamily g, polypeptide 1 (Cyp2g1), mRNA.	7	NM_013809.1	**-6,32**	-1,92	**0,0053**	0,0556
ILMN_2770040	S	**Dct**	Mus musculus dopachrome tautomerase (Dct), mRNA.	14	NM_010024.1	**-6,61**	-7,50	**0,0047**	0,0017
ILMN_1242999	S	**Avpr1a**	Mus musculus arginine vasopressin receptor 1A (Avpr1a), mRNA.	10	NM_016847.2	**-7,01**	-3,27	**0,0002**	0,0108
ILMN_2592166	S	**Mup4**	Mus musculus major urinary protein 4 (Mup4), mRNA.	4	NM_008648.1	**-7,24**	-1,12	**0,0276**	0,4385
ILMN_2513870	S	**Zap70**	Mus musculus zeta-chain (TCR) associated protein kinase (Zap70), mRNA.	1	NM_009539.2	**-9,00**	-6,08	**0,0093**	0,0132
ILMN_1251894	S	**Dct**	Mus musculus dopachrome tautomerase (Dct), mRNA.	14	NM_010024.2	**-9,25**	-8,57	**0,0107**	0,0165
ILMN_1214531	S	**Cyp2b13**	Mus musculus cytochrome P450, family 2, subfamily b, polypeptide 13	7	NM_007813.1	**-13,91**	12,62	**0,0030**	0,0124

			(Cyp2b13), mRNA.						
ILMN_2664202	S	**Rarres1**	PREDICTED: Mus musculus retinoic acid receptor responder (tazarotene induced) 1 (Rarres1), mRNA.	3	XM_001475793.1	**-15,35**	-48,08	**0,0005**	0,0005

Genes dysregulated in KAP1-mutant males

Illumina ID	Probe Type	Gene Symbol	Description	Chr	Representative ID	Fold Change - Female KO vs WT	Fold Change - Male KO vs WT	Welch t-test p-value - Female KO vs WT	Welch t-test p-value - Male KO vs WT
ILMN_2617625	S	**Cyp2b9**	Mus musculus cytochrome P450, family 2, subfamily b, polypeptide 9 (Cyp2b9), mRNA.	7	NM_010000.2	-2,14	**96,77**	0,0007	**0,0006**
ILMN_2976211	S	**Cyp2b23**	Mus musculus cytochrome P450, family 2, subfamily b, polypeptide 23 (Cyp2b23), mRNA.	7	NM_001081148.1	-2,77	**23,54**	0,0033	**0,0027**
ILMN_2594926	S	**Cyp2b10**	Mus musculus cytochrome P450, family 2, subfamily b, polypeptide 10 (Cyp2b10), transcript variant 2, mRNA.	7	NM_009999.3	3,44	**14,47**	0,0843	**0,0036**
ILMN_1214531	S	**Cyp2b13**	Mus musculus cytochrome P450, family 2, subfamily b, polypeptide 13 (Cyp2b13), mRNA.	7	NM_007813.1	-13,91	**12,62**	0,0030	**0,0124**
ILMN_1253860	S	**Mas1**	Mus musculus MAS1 oncogene (Mas1), mRNA.	17	NM_008552.3	14,02	**9,27**	0,0052	**0,0046**

ILMN_1222679	S	**Cidec**	Mus musculus cell death-inducing DFFA-like effector c (Cidec), mRNA.	6	NM_178373.3	1,05	**9,03**	0,1990	**0,0109**
ILMN_2708477	S	**Spink3**			NM_009258.2	38,60	**8,38**	0,0061	**0,0211**
ILMN_1236308	S	**LOC268730**			XM_193754.2	4,61	**5,80**	0,0323	**0,0045**
ILMN_2671165	S	**Krt23**	Mus musculus keratin 23 (Krt23), mRNA.	11	NM_033373.1	17,72	**5,60**	0,0008	**0,0013**
ILMN_2827217	S	**Clstn3**	Mus musculus calsyntenin 3 (Clstn3), mRNA.	6	NM_153508.2	2,02	**5,39**	0,0876	**0,0150**
ILMN_2695360	S	**Lcn13**	Mus musculus lipocalin 13 (Lcn13), mRNA.	2	NM_153558.1	1,00	**5,33**	NA	**0,0044**
ILMN_2611027	S	**Pmm1**	Mus musculus phosphomannomutase 1 (Pmm1), mRNA.	15	NM_013872.2	4,58	**4,46**	0,0041	**0,0017**
ILMN_1225985	S	**Serpina7**	Mus musculus serine (or cysteine) peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 7 (Serpina7), mRNA.	X	NM_177920.4	4,49	**4,32**	0,0234	**0,0196**
ILMN_2874352	S	**Cyp17a1**	Mus musculus cytochrome P450, family 17, subfamily a, polypeptide	19	NM_007809.2	2,58	**4,26**	0,0133	**0,0380**

			1 (Cyp17a1), mRNA.						
ILMN_1238820	S	**LOC332788**			XM_285750.2	4,06	**4,19**	0,0447	**0,0060**
ILMN_1244484	S	**Robo1**	Mus musculus roundabout homolog 1 (Drosophila) (Robo1), mRNA.	16	NM_019413.2	4,36	**4,16**	0,0002	**0,0135**
ILMN_1230375	S	**LOC383125**			XM_356890.1	5,02	**4,14**	0,0063	**0,0042**
ILMN_1215877	S	**Extl1**			NM_019578	2,79	**4,07**	0,0065	**0,0016**
ILMN_2709810	S	**Acnat2**	Mus musculus acyl-coenzyme A amino acid N-acyltransferase 2 (Acnat2), mRNA.	4	NM_145368.2	1,22	**4,04**	0,2550	**0,0310**
ILMN_2974041	S	**Pmm1**	Mus musculus phosphomannomutase 1 (Pmm1), mRNA.	15	NM_013872.1	4,33	**3,75**	0,0037	**0,0099**
ILMN_2728134	S	**5430433G21Rik**	PREDICTED: Mus musculus RIKEN cDNA 5430433G21 gene (5430433G21Rik), mRNA.		XM_001480745.1	8,51	**3,74**	0,0026	**0,0021**
ILMN_1258330	S	**LOC384348**			XM_357593.1	4,01	**3,65**	0,0040	**0,0033**
ILMN_2476948	S	**Gabrb3**	Mus musculus gamma-aminobutyric acid (GABA-A) receptor, subunit beta 3 (Gabrb3), transcript variant 2, mRNA.	7	NM_001038701.1	2,33	**3,53**	0,0117	**0,0023**
ILMN_2738699	S	**Cblc**	Mus musculus Casitas B-lineage	7	NM_023224.4	3,99	**3,47**	0,0003	**0,0039**

			lymphoma c (Cblc), mRNA.						
ILMN_2535582	S	**LOC382707**			XM_356635.1	2,18	**3,46**	0,0242	**0,0120**
ILMN_3106592	A	**Rcan2**	Mus musculus regulator of calcineurin 2 (Rcan2), transcript variant 1, mRNA.	17	NM_207649.1	6,40	**3,36**	0,0007	**0,0010**
ILMN_1245604	S	**LOC100044218**	PREDICTED: Mus musculus hypothetical protein LOC100044218 (LOC100044218), mRNA.		XM_001471913.1	1,15	**3,36**	0,2877	**0,0115**
ILMN_2960044	S	**Cyp4a31**	Mus musculus cytochrome P450, family 4, subfamily a, polypeptide 31 (Cyp4a31), mRNA.	4	NM_201640.1	1,20	**3,34**	0,3381	**0,0018**
ILMN_1251714	S	**LOC673589**	PREDICTED: Mus musculus similar to Cytochrome P450 2B9 (CYPIIB9) (Testosterone 16-alpha hydroxylase) (P450-16-alpha) (Clone PF26) (LOC673589), mRNA.		XM_001005911.1	-1,41	**3,28**	0,2528	**0,0333**
ILMN_2693019	S	**Acpp**	Mus musculus acid phosphatase, prostate (Acpp), transcript variant 1, mRNA.	9	NM_207668.2	3,48	**3,20**	0,0763	**0,0216**
ILMN_3133095	A	**Slc35f2**	Mus musculus solute carrier family 35, member F2 (Slc35f2), mRNA.	9	NM_028060.2	1,28	**3,07**	0,4226	**0,0030**

ILMN_1259180	S	**Rcan1**	Mus musculus regulator of calcineurin 1 (Rcan1), transcript variant 2, mRNA.	16	NM_019466.3	1,18	**3,04**	0,2006	**0,0250**
ILMN_2832675	S	**Chrna4**	Mus musculus cholinergic receptor, nicotinic, alpha polypeptide 4 (Chrna4), mRNA.	2	NM_015730.4	4,82	**3,03**	0,0557	**0,0086**
ILMN_1244169	S	**Sftpd**	Mus musculus surfactant associated protein D (Sftpd), mRNA.	14	NM_009160.1	3,42	**2,99**	0,0325	**0,0038**
ILMN_3156010	A	**Pdzrn3**	Mus musculus PDZ domain containing RING finger 3 (Pdzrn3), mRNA.	6	NM_018884.1	1,39	**2,97**	0,2234	**0,0006**
ILMN_2879534	S	**Extl1**	Mus musculus exostoses (multiple)-like 1 (Extl1), mRNA.	4	NM_019578.1	1,74	**2,96**	0,1884	**0,0017**
ILMN_2669714	S	**Ctsa**	Mus musculus cathepsin A (Ctsa), transcript variant 2, mRNA.	2	NM_001038492.1	1,26	**2,95**	0,5932	**0,0066**
ILMN_1229577	S	**Sstr2**			NM_009217.1	1,00	**2,89**	0,4226	**0,0019**
ILMN_2839877	S	**Hectd2**	Mus musculus HECT domain containing 2 (Hectd2), mRNA.	19	NM_172637.1	1,33	**2,87**	0,3034	**0,0116**

ILMN_1230557	S	**D2Wsu81e**	Mus musculus DNA segment, Chr 2, Wayne State University 81, expressed (D2Wsu81e), mRNA.	2	NM_172660.2	2,50	**2,85**	0,0283	**0,0081**
ILMN_1257547	S	**Tox**	Mus musculus thymocyte selection-associated high mobility group box (Tox), mRNA. XM_919293 XM_919306	4	NM_145711.3	-1,02	**2,84**	0,9047	**0,0008**
ILMN_2529509	S	**LOC666168**	PREDICTED: Mus musculus similar to cytochrome P450, family 4, subfamily a, polypeptide 10 (LOC666168), mRNA.	4	XM_001475399.1	1,17	**2,83**	0,4507	**0,0064**
ILMN_2939702	S	**Dhrs7**	Mus musculus dehydrogenase /reductase (SDR family) member 7 (Dhrs7), mRNA.	12	NM_025522.1	1,90	**2,73**	0,0124	**0,0145**
ILMN_2526851	S	**LOC227393**			XM_129965.3	1,55	**2,66**	0,0905	**0,0016**
ILMN_2535566	S	**LOC382691**			XM_356627.1	3,40	**2,63**	0,0144	**0,0292**
ILMN_1254927	S	**Ly6c1**	Mus musculus lymphocyte antigen 6 complex, locus C1 (Ly6c1), mRNA.	15	NM_010741.2	2,86	**2,63**	0,0292	**0,0295**

ILMN_1228211	S	**Tff2**	Mus musculus trefoil factor 2 (spasmolytic protein 1) (Tff2), mRNA.	17	NM_009363.3	3,68	**2,61**	0,0253	**0,0093**
ILMN_2627328	S	**Dnase2a**			NM_010062	2,93	**2,60**	0,0058	**0,0069**
ILMN_2893081	S	**Mbd1**	Mus musculus methyl-CpG binding domain protein 1 (Mbd1), mRNA.	18	NM_013594.1	2,57	**2,59**	0,0001	**0,0003**
ILMN_2619639	S	**AI428936**	Mus musculus expressed sequence AI428936 (AI428936), mRNA.	7	NM_153577.2	2,18	**2,59**	0,1689	**0,0007**
ILMN_1224291	S	**Mbd1**	Mus musculus methyl-CpG binding domain protein 1 (Mbd1), mRNA.	18	NM_013594.1	1,17	**2,59**	0,4226	**0,0023**
ILMN_2591264	S	**Orm2**			NM_011016.1	2,03	**2,59**	0,0635	**0,0010**
ILMN_2894396	S	**Tmem184a**	Mus musculus transmembrane protein 184a (Tmem184a), mRNA.	5	NM_144914.2	2,29	**2,59**	0,0015	**0,0032**
ILMN_2589350	S	**Ces5**	Mus musculus carboxylesterase 5 (Ces5), mRNA.	8	NM_172759.2	1,92	**2,57**	0,0336	**0,0011**
ILMN_1219079	S	**Serpina9**			NM_027997	1,13	**2,56**	0,2006	**0,0169**
ILMN_3122845	A	**H1fx**	Mus musculus H1 histone family, member X (H1fx), mRNA.	6	NM_198622.1	4,36	**2,56**	0,0222	**0,0262**
ILMN_2673332	S	**9530051K01Rik**			XM_485965	1,03	**2,54**	0,4226	**0,0431**

ILMN_1233860	S	**Tmem162**	Mus musculus transmembrane protein 162 (Tmem162), mRNA.	7	NM_175240.3	1,93	**2,50**	0,1674	**0,0045**
ILMN_2625279	S	**Pacrg**	Mus musculus Park2 co-regulated (Pacrg), mRNA.	17	NM_027032.2	7,63	**2,50**	0,0168	**0,0165**
ILMN_2661971	S	**Gm2a**	Mus musculus GM2 ganglioside activator protein (Gm2a), mRNA.	11	NM_010299.2	2,73	**2,48**	0,0030	**0,0001**
ILMN_1248603	S	**Treh**	Mus musculus trehalase (brush-border membrane glycoprotein) (Treh), mRNA.	9	NM_021481.2	1,97	**2,48**	0,0120	**0,0292**
ILMN_1213456	S	**Dhrs7**	Mus musculus dehydrogenase/reductase (SDR family) member 7 (Dhrs7), mRNA.		NM_025522.3	1,91	**2,46**	0,0126	**0,0026**
ILMN_1219440	S	**Rdh16**	Mus musculus retinol dehydrogenase 16 (Rdh16), mRNA.	10	NM_009040.2	2,09	**2,44**	0,0072	**0,0041**
ILMN_1233122	S	**Bglap-rs1**	Mus musculus bone gamma-carboxyglutamate protein, related sequence 1 (Bglap-rs1), mRNA.	3	NM_031368.3	1,63	**2,44**	0,2478	**0,0199**
ILMN_1214448	S	**9030619P08Ri**	Mus musculus	15	NM_00103972	2,00	**2,41**	0,0298	**0,0209**

		k	RIKEN cDNA 9030619P08 gene (9030619P08Rik), mRNA.		0.1				
ILMN_2838564	S	**Tsku**	Mus musculus tsukushin (Tsku), mRNA.	7	NM_001024619.1	1,00	**2,41**	NA	**0,0433**
ILMN_1222760	S	**Zfp579**	Mus musculus zinc finger protein 579 (Zfp579), mRNA.	7	NM_026741.2	1,97	**2,40**	0,0008	**0,0128**
ILMN_2747820	S	**Dhrs7**	Mus musculus dehydrogenase/reductase (SDR family) member 7 (Dhrs7), mRNA.		NM_025522.3	1,93	**2,38**	0,0246	**0,0078**
ILMN_2665715	S	**Gstt3**	Mus musculus glutathione S-transferase, theta 3 (Gstt3), mRNA.	10	NM_133994.3	1,63	**2,36**	0,0614	**0,0064**
ILMN_3023451	I	**LOC433801**	Mus musculus similar to RIKEN cDNA 6330416L07 gene (LOC433801), mRNA.		NM_001013808.1	4,20	**2,35**	0,0301	**0,0028**
ILMN_2573694	S	**B430219N15Rik**			AK046650	1,19	**2,32**	0,2725	**0,0454**
ILMN_2421890	S	**Acacb**			NM_133904	1,08	**2,30**	0,7034	**0,0028**
ILMN_2852756	S	**Rbm26**	Mus musculus RNA binding motif protein 26 (Rbm26), mRNA.	14	NM_134077.4	1,43	**2,30**	0,2228	**0,0074**
ILMN_2748680	S	**Fhit**	Mus musculus fragile histidine triad gene (Fhit), mRNA.	14	NM_010210.2	2,74	**2,28**	0,0103	**0,0303**
ILMN_2756311	S	**1110006G14Rik**	PREDICTED: Mus musculus RIKEN cDNA 1110006G14 gene (1110006G14Rik), mRNA.		XM_989766.1	1,88	**2,27**	0,0913	**0,0432**
ILMN_2772070	S	**Dio1**	Mus musculus	4	NM_007860.3	1,24	**2,26**	0,2097	**0,0012**

			deiodinase, iodothyronine, type I (Dio1), mRNA.						
ILMN_2782841	S	**BC050811**	Mus musculus cDNA sequence BC050811 (BC050811), mRNA.	3	NM_178418.2	1,32	**2,25**	0,3300	**0,0383**
ILMN_2970429	S	**Uck1**	Mus musculus uridine-cytidine kinase 1 (Uck1), mRNA.	2	NM_011675.1	2,38	**2,22**	0,0729	**0,0030**
ILMN_2620166	S	**Prpsap1**	PREDICTED: Mus musculus phosphoribosyl pyrophosphate synthetase-associated protein 1 (Prpsap1), mRNA.	11	XM_181343.5	2,10	**2,18**	0,0532	**0,0009**
ILMN_1242689	S	**LOC236371**			XM_135639.2	1,75	**2,15**	0,0319	**0,0463**
ILMN_2440679	S	**D1Ertd471e**				2,87	**2,14**	0,0070	**0,0029**
ILMN_2435392	S	**Dnase2a**			NM_010062	1,52	**2,13**	0,0647	**0,0056**
ILMN_1250358	S	**Acot8**	Mus musculus acyl-CoA thioesterase 8 (Acot8), mRNA.	2	NM_133240.1	-2,28	**2,11**	0,0249	**0,0376**
ILMN_2589401	S	**Pltp**	Mus musculus phospholipid transfer protein (Pltp), mRNA.	2	NM_011125.2	-1,05	**2,11**	0,9182	**0,0481**
ILMN_1256676	S	**Ddah1**			NM_026993	1,44	**2,11**	0,0673	**0,0013**
ILMN_2774690	S	**LOC677317**	PREDICTED: Mus musculus similar to Mod1 protein, transcript variant 4 (LOC677317), mRNA.		XM_001004685.1	1,66	**2,11**	0,0341	**0,0123**

ILMN_1223997	S	**Crtap**	Mus musculus cartilage associated protein (Crtap), mRNA.	9	NM_019922.1	2,07	**2,09**	0,1233	**0,0071**
ILMN_2623536	S	**Golm1**	Mus musculus golgi membrane protein 1 (Golm1), transcript variant 1, mRNA.	13	NM_027307.4	2,28	**2,09**	0,0059	**0,0148**
ILMN_2771219	S	**LOC669660**	PREDICTED: Mus musculus similar to PDZ and LIM domain protein 5 (Enigma homolog) (Enigma-like PDZ and LIM domains protein) (LOC669660), mRNA.		XM_976375.1	-1,14	**2,09**	0,6798	**0,0243**
ILMN_2693827	S	**Atg16l2**	PREDICTED: Mus musculus autophagy related 16 like 2 (S. cerevisiae), transcript variant 1 (Atg16l2), mRNA.	7	XM_001476186.1	1,70	**2,09**	0,0846	**0,0077**
ILMN_3077758	I	**Unc93a**	Mus musculus unc-93 homolog A (C. elegans) (Unc93a), mRNA.	17	NM_199252.1	1,48	**2,08**	0,2698	**0,0125**
ILMN_3007971	S	**Gm826**	Mus musculus gene model 826, (NCBI) (Gm826), mRNA.	2	NM_001033411.1	1,01	**2,08**	0,4226	**0,0037**
ILMN_1212612	S	**Rcan2**	Mus musculus	17	NM_207649.1	4,17	**2,07**	0,0305	**0,0082**

			regulator of calcineurin 2 (Rcan2), transcript variant 1, mRNA.						
ILMN_2647234	S	**Dio1**	Mus musculus deiodinase, iodothyronine, type I (Dio1), mRNA.	4	NM_007860.3	1,49	**2,07**	0,0488	**0,0131**
ILMN_1223880	S	**Tmprss2**	Mus musculus transmembrane protease, serine 2 (Tmprss2), mRNA.	16	NM_015775.2	2,51	**2,07**	0,0047	**0,0288**
ILMN_2853619	S	**Abhd6**	Mus musculus abhydrolase domain containing 6 (Abhd6), mRNA.	14	NM_025341.3	1,39	**2,05**	0,3100	**0,0045**
ILMN_1249246	S	**LOC384022**			XM_357375.1	1,74	**2,04**	0,0619	**0,0298**
ILMN_2453351	S	**Ugt1a5**			NM_201643	-1,35	**2,03**	0,0381	**0,0042**
ILMN_2543657	S	**Mbd1**			AK007371	1,08	**2,03**	0,4226	**0,0077**
ILMN_1213185	S	**LOC385792**			XM_358947.1	1,81	**1,99**	0,0183	**0,0374**
ILMN_2864290	S	**BC049806**	Mus musculus cDNA sequence BC049806 (BC049806), mRNA.	1	NM_172513.2	2,50	**1,99**	0,0256	**0,0096**
ILMN_2486267	S	**Ube2l6**	Mus musculus ubiquitin-conjugating enzyme E2L 6 (Ube2l6), mRNA.	2	NM_019949.1	1,53	**1,99**	0,0035	**0,0251**
ILMN_2836246	S	**3110023B02Rik**	Mus musculus RIKEN cDNA	11	NM_152807.1	1,34	**1,98**	0,1415	**0,0169**

			3110023B02 gene (3110023B02Rik), mRNA.						
ILMN_2591342	S	**BC021614**	Mus musculus cDNA sequence BC021614 (BC021614), mRNA.	19	NM_144869.2	2,93	**1,98**	0,0230	**0,0031**
ILMN_2599751	S	**Rabep2**	Mus musculus rabaptin, RAB GTPase binding effector protein 2 (Rabep2), mRNA.	7	NM_030566.2	1,07	**1,98**	0,7842	**0,0031**
ILMN_2432458	S	**Top3b**	Mus musculus topoisomerase (DNA) III beta (Top3b), mRNA.	16	NM_011624.2	1,19	**1,97**	0,6004	**0,0014**
ILMN_2800813	S	**Cabc1**	Mus musculus chaperone, ABC1 activity of bc1 complex like (S. pombe) (Cabc1), nuclear gene encoding mitochondrial protein, mRNA.	1	NM_023341.2	-1,05	**1,97**	0,9076	**0,0437**
ILMN_1242101	S	**Tmem184a**	Mus musculus transmembrane protein 184a (Tmem184a), mRNA.	5	NM_144914.2	1,35	**1,97**	0,4601	**0,0275**
ILMN_2724294	S	**Gpx7**	Mus musculus glutathione peroxidase 7 (Gpx7), mRNA.	4	NM_024198.3	2,17	**1,97**	0,0835	**0,0257**

ILMN_1227348	S	**LOC100044218**	PREDICTED: Mus musculus hypothetical protein LOC100044218 (LOC100044218), mRNA.		XM_001471913.1	1,11	**1,96**	0,3974	**0,0147**
ILMN_2619107	S	**Lgals1**			NM_008495.1	1,82	**1,95**	0,0762	**0,0275**
ILMN_2631813	S	**Gemin6**	Mus musculus gem (nuclear organelle) associated protein 6 (Gemin6), mRNA.	17	NM_026053.1	1,38	**1,95**	0,3240	**0,0276**
ILMN_2947568	S	**Gadd45a**	Mus musculus growth arrest and DNA-damage-inducible 45 alpha (Gadd45a), mRNA.	6	NM_007836.1	1,31	**1,94**	0,1390	**0,0400**
ILMN_2619307	S	**LOC100047052**	PREDICTED: Mus musculus similar to Aptx protein (LOC100047052), mRNA.		XM_001477288.1	-1,02	**1,93**	0,9522	**0,0269**
ILMN_2639360	S	**Slc7a4**	Mus musculus solute carrier family 7 (cationic amino acid transporter, y+ system), member 4 (Slc7a4), mRNA.	16	NM_144852.3	1,61	**1,93**	0,3069	**0,0454**
ILMN_2742152	S	**Gadd45a**	Mus musculus growth arrest and DNA-damage-inducible 45 alpha (Gadd45a), mRNA.	6	NM_007836.1	1,93	**1,93**	0,0223	**0,0116**

ILMN_2721337	S	**G6pdx**	Mus musculus glucose-6-phosphate dehydrogenase X-linked (G6pdx), mRNA.	X	NM_008062.2	1,19	**1,93**	0,5889	**0,0066**
ILMN_2904686	S	**Cyb5r3**	Mus musculus cytochrome b5 reductase 3 (Cyb5r3), mRNA.	15	NM_029787.2	1,38	**1,93**	0,1552	**0,0037**
ILMN_2852624	S	**Hamp2**	Mus musculus hepcidin antimicrobial peptide 2 (Hamp2), mRNA.	7	NM_183257.1	-1,30	**1,92**	0,0658	**0,0338**
ILMN_2479690	S	**1700048O20Rik**				1,14	**1,92**	0,4292	**0,0284**
ILMN_2740965	S	**Prss8**	Mus musculus protease, serine, 8 (prostasin) (Prss8), mRNA.	7	NM_133351.1	2,21	**1,91**	0,0884	**0,0164**
ILMN_2974720	S	**Igf2bp2**	Mus musculus insulin-like growth factor 2 mRNA binding protein 2 (Igf2bp2), mRNA.	16	NM_183029.1	-1,02	**1,91**	0,9223	**0,0013**
ILMN_2707079	S	**Sirt5**	Mus musculus sirtuin 5 (silent mating type information regulation 2 homolog) 5 (S. cerevisiae) (Sirt5), mRNA.	13	NM_178848.3	1,70	**1,90**	0,0001	**0,0171**
ILMN_1226366	S	**Uck1**	Mus musculus	2	NM_011675.1	1,24	**1,90**	0,4036	**0,0105**

			uridine-cytidine kinase 1 (Uck1), mRNA.						
ILMN_1216174	S	**Parp16**	Mus musculus poly (ADP-ribose) polymerase family, member 16 (Parp16), mRNA.	9	NM_177460.3	1,66	**1,89**	0,0469	**0,0052**
ILMN_2742311	S	**Cyp39a1**	Mus musculus cytochrome P450, family 39, subfamily a, polypeptide 1 (Cyp39a1), mRNA.	17	NM_018887.3	1,40	**1,89**	0,3073	**0,0356**
ILMN_2937261	S	**Mod1**	Mus musculus malic enzyme, supernatant (Mod1), mRNA.	9	NM_008615.1	1,54	**1,88**	0,0022	**0,0364**
ILMN_1256967	S	**AI875142**				1,38	**1,88**	0,0044	**0,0084**
ILMN_2544603	S	**2610015J01Rik**			AK011403	1,32	**1,87**	0,2269	**0,0095**
ILMN_1252183	S	**BC004004**	Mus musculus cDNA sequence BC004004 (BC004004), mRNA.	17	NM_030561.2	-1,04	**1,87**	0,8735	**0,0213**
ILMN_2697256	S	**Klk1b4**	Mus musculus kallikrein 1-related pepidase b4 (Klk1b4), mRNA.	7	NM_010915.2	1,20	**1,87**	0,5047	**0,0206**
ILMN_2631894	S	**Pafah2**	Mus musculus platelet-activating factor acetylhydrolas	4	NM_133880.1	1,80	**1,86**	0,0849	**0,0031**

			e 2 (Pafah2), mRNA.						
ILMN_2709051	S	**BC049806**	Mus musculus cDNA sequence BC049806 (BC049806), mRNA.	1	NM_172513.2	1,49	**1,86**	0,0131	**0,0142**
ILMN_2734598	S	**Cyp2a5**	Mus musculus cytochrome P450, family 2, subfamily a, polypeptide 5 (Cyp2a5), mRNA.		NM_007812.4	1,73	**1,85**	0,0036	**0,0101**
ILMN_3155626	A	**EG245297**	Mus musculus predicted gene, EG245297 (EG245297), mRNA.	12	NM_001018086.2	-1,08	**1,84**	0,5914	**0,0051**
ILMN_2984153	S	**Zfp667**	Mus musculus zinc finger protein 667 (Zfp667), mRNA.	7	NM_001024928.2	1,57	**1,84**	0,0782	**0,0404**
ILMN_1214888	S	**Ugt1a2**	Mus musculus UDP glucuronosyltransferase 1 family, polypeptide A2 (Ugt1a2), mRNA.	1	NM_013701.1	-1,28	**1,84**	0,1180	**0,0009**
ILMN_1220829	S	**Bglap-rs1**	Mus musculus bone gamma-carboxyglutamate protein, related sequence 1 (Bglap-rs1), mRNA.	3	NM_031368.3	1,21	**1,84**	0,4226	**0,0176**
ILMN_2467800	S	**Uap1l1**	Mus musculus UDP-N-acteylglucosamine	2	NM_001033293.2	1,13	**1,83**	0,7828	**0,0159**

			pyrophosphorylase 1-like 1 (Uap1l1), mRNA.						
ILMN_2786567	S	**Nln**	XM_918982 Mus musculus neurolysin (metallopeptidase M3 family) (Nln), mRNA.	13	NM_029447.1	1,38	**1,83**	0,0292	**0,0203**
ILMN_1258830	S	**Ppap2a**	Mus musculus phosphatidic acid phosphatase 2a (Ppap2a), transcript variant 1, mRNA.	13	NM_008247.2	1,70	**1,83**	0,0860	**0,0072**
ILMN_2685569	S	**Pus10**	Mus musculus pseudouridylate synthase 10 (Pus10), transcript variant 3, mRNA.	11	NM_028304.2	-1,01	**1,82**	0,9547	**0,0231**
ILMN_2832608	S	**Fvt1**	Mus musculus follicular lymphoma variant translocation 1 (Fvt1), mRNA.	1	NM_027534.1	1,05	**1,81**	0,7034	**0,0370**
ILMN_3141781	A	**Ttc19**	XM_921793 XM_985103 Mus musculus tetratricopeptide repeat domain 19 (Ttc19), transcript variant 2, mRNA.	11	NM_029704.1	-1,11	**1,81**	0,4226	**0,0207**

ILMN_1213070	S	**1700037H04Rik**	Mus musculus RIKEN cDNA 1700037H04 gene (1700037H04Rik), mRNA.	2	NM_026091.2	1,49	**1,80**	0,0288	**0,0482**
ILMN_1253155	S	**Dcbld1**	Mus musculus discoidin, CUB and LCCL domain containing 1 (Dcbld1), mRNA.	10	NM_025705.2	-1,04	**1,80**	0,8895	**0,0070**
ILMN_2666747	S	**G3bp2**	Mus musculus GTPase activating protein (SH3 domain) binding protein 2 (G3bp2), transcript variant 1, mRNA.	5	NM_011816.3	1,92	**1,80**	0,0221	**0,0169**
ILMN_2604263	S	**8430410A17Rik**	Mus musculus RIKEN cDNA 8430410A17 gene (8430410A17Rik), mRNA.	6	NM_173737.2	2,14	**1,80**	0,1254	**0,0002**
ILMN_2655126	S	**Gchfr**	Mus musculus GTP cyclohydrolase I feedback regulator (Gchfr), mRNA.	2	NM_177157.4	1,63	**1,80**	0,0136	**0,0114**
ILMN_2757641	S	**Efna5**	Mus musculus ephrin A5 (Efna5), transcript variant 2, mRNA.	17	NM_010109.2	1,67	**1,80**	0,0141	**0,0162**

ILMN_2674602	S	**Rapgef5**	Mus musculus Rap guanine nucleotide exchange factor (GEF) 5 (Rapgef5), mRNA.	12	NM_175930.4	-1,02	**1,80**	0,9267	**0,0391**
ILMN_1216842	S	**Aifm2**	Mus musculus apoptosis-inducing factor, mitochondrion-associated 2 (Aifm2), nuclear gene encoding mitochondrial protein, transcript variant 3, mRNA.	10	NM_001039194.2	1,52	**1,80**	0,3077	**0,0271**
ILMN_1244281	S	**D2Wsu81e**	Mus musculus DNA segment, Chr 2, Wayne State University 81, expressed (D2Wsu81e), mRNA.	2	NM_172660.2	2,17	**1,79**	0,0119	**0,0463**
ILMN_1225154	S	**Ugt1a5**	Mus musculus UDP glucuronosyltransferase 1 family, polypeptide A5 (Ugt1a5), mRNA.		NM_201643.2	-1,13	**1,79**	0,1843	**0,0022**
ILMN_2621708	S	**Abcc4**	Mus musculus ATP-binding cassette, sub-family C (CFTR/MRP), member 4 (Abcc4), mRNA.	14	NM_001033336.2	3,13	**1,79**	0,0185	**0,0098**
ILMN_2636832	S	**Cyb5r3**	Mus musculus	15	NM_029787.2	1,29	**1,79**	0,0781	**0,0096**

			cytochrome b5 reductase 3 (Cyb5r3), mRNA.						
ILMN_2453120	S	**C130065N10Rik**				1,59	**1,79**	0,0011	**0,0025**
ILMN_2746812	S	**2410012H22Rik**	PREDICTED: Mus musculus RIKEN cDNA 2410012H22 gene (2410012H22Rik), mRNA.	11	XM_126343.5	1,94	**1,78**	0,0007	**0,0012**
ILMN_2524167	S	**4631434O19Rik**			XM_130859.4	1,27	**1,78**	0,3249	**0,0302**
ILMN_1249959	S	**Tom1l1**	Mus musculus target of myb1-like 1 (chicken) (Tom1l1), mRNA.	11	NM_028011.2	1,27	**1,78**	0,4917	**0,0334**
ILMN_1246471	S	**Ctr9**	Mus musculus Ctr9, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae) (Ctr9), mRNA.		NM_009431.2	1,11	**1,78**	0,4226	**0,0236**
ILMN_2711045	S	**Sirt5**	Mus musculus sirtuin 5 (silent mating type information regulation 2 homolog) 5 (S. cerevisiae) (Sirt5), mRNA.	13	NM_178848.3	1,76	**1,78**	0,0188	**0,0023**
ILMN_2600744	S	**Rgs16**	Mus musculus regulator of G-protein signaling 16 (Rgs16), mRNA.	1	NM_011267.2	1,64	**1,77**	0,2333	**0,0052**
ILMN_2631892	S	**Pafah2**	Mus musculus platelet-activating factor acetylhydrolas	4	NM_133880.1	1,46	**1,77**	0,2301	**0,0482**

			e 2 (Pafah2), mRNA.						
ILMN_2701991	S	**Dscr1**			NM_019466.2	1,38	**1,77**	0,1032	**0,0263**
ILMN_3102467	A	**Rab34**	Mus musculus RAB34, member of RAS oncogene family (Rab34), mRNA.	11	NM_033475.2	1,02	**1,75**	0,9673	**0,0171**
ILMN_1218317	S	**LOC100048616**	PREDICTED: Mus musculus similar to regulatory factor X domain containing 2 homolog (LOC100048616), mRNA.		XM_001480824.1	-1,00	**1,75**	0,9973	**0,0319**
ILMN_2856157	S	**Pgam1**	Mus musculus phosphoglycerate mutase 1 (Pgam1), mRNA.	19	NM_023418.2	1,89	**1,75**	0,0057	**0,0051**
ILMN_2506757	S	**LOC100048280**	PREDICTED: Mus musculus similar to crooked legs CG14938-PB, transcript variant 1 (LOC100048280), mRNA.		XM_001480149.1	1,25	**1,75**	0,1552	**0,0047**
ILMN_1223710	S	**Pmm1**			AK013805	1,05	**1,75**	0,4226	**0,0329**
ILMN_2720429	S	**Pla2g6**	Mus musculus phospholipase A2, group VI (Pla2g6), mRNA.	15	NM_016915.3	2,25	**1,74**	0,0550	**0,0057**
ILMN_2604814	S	**Fgf22**	Mus musculus fibroblast growth factor 22 (Fgf22), mRNA.	10	NM_023304.1	1,22	**1,74**	0,4373	**0,0155**
ILMN_2729235	S	**Ccdc126**	Mus musculus coiled-coil domain containing 126 (Ccdc126), mRNA.	6	NM_175098.2	1,26	**1,74**	0,4847	**0,0497**
ILMN_1246446	S	**Lrrc59**	Mus musculus leucine rich	11	NM_133807.1	1,01	**1,74**	0,4226	**0,0122**

			repeat containing 59 (Lrrc59), mRNA.						
ILMN_1252131	S	**Klk1b27**	Mus musculus kallikrein 1-related peptidase b27 (Klk1b27), mRNA.		NM_020268.3	1,00	**1,74**	NA	**0,0368**
ILMN_1219670	S	**Gpatch4**	Mus musculus G patch domain containing 4 (Gpatch4), mRNA.	3	NM_025663.2	1,42	**1,73**	0,1664	**0,0252**
ILMN_2664040	S	**Alas1**	Mus musculus aminolevulinic acid synthase 1 (Alas1), mRNA.	9	NM_020559.1	1,16	**1,73**	0,6807	**0,0402**
ILMN_3029727	I	**Shf**	Mus musculus Src homology 2 domain containing F (Shf), mRNA.		NM_001013829.2	1,53	**1,73**	0,0990	**0,0187**
ILMN_2704285	S	**Pklr**	Mus musculus pyruvate kinase liver and red blood cell (Pklr), mRNA.	3	NM_013631.1	1,15	**1,72**	0,5076	**0,0366**
ILMN_2662885	S	**B230120H23Rik**	Mus musculus RIKEN cDNA B230120H23 gene (B230120H23Rik), transcript variant 1, mRNA.	2	NM_023057.1	-1,04	**1,72**	0,8200	**0,0076**
ILMN_2711410	S	**Pmf1**	Mus musculus polyamine-modulated factor 1 (Pmf1), mRNA.		NM_025928.3	1,26	**1,72**	0,2476	**0,0133**
ILMN_2592496	S	**Dis3l2**	Mus musculus DIS3 mitotic control	1	NM_153530.1	1,70	**1,71**	0,0550	**0,0307**

			homolog (S. cerevisiae)-like 2 (Dis3l2), mRNA.						
ILMN_2700265	S	**Pex11a**	Mus musculus peroxisomal biogenesis factor 11a (Pex11a), mRNA.	7	NM_011068.1	1,06	**1,71**	0,6988	**0,0230**
ILMN_2587638	S	**C230080E09Rik**			AK082664	1,03	**1,71**	0,4226	**0,0224**
ILMN_1224736	S	**Zmiz1**	Mus musculus zinc finger, MIZ-type containing 1 (Zmiz1), mRNA.	14	NM_183208.2	1,00	**1,70**	NA	**0,0354**
ILMN_2515349	S	**Zfp64**	Mus musculus zinc finger protein 64 (Zfp64), mRNA.	2	NM_009564.1	-1,10	**1,70**	0,7100	**0,0167**
ILMN_1219786	S	**Morn2**	Mus musculus MORN repeat containing 2 (Morn2), mRNA.	17	NM_194269.1	1,21	**1,70**	0,4155	**0,0324**
ILMN_1222599	S	**Zubr1**	PREDICTED: Mus musculus zinc finger, UBR1 type 1, transcript variant 1 (Zubr1), mRNA.	4	XM_001479450.1	1,19	**1,70**	0,1202	**0,0350**
ILMN_1247257	S	**Gpd2**	Mus musculus glycerol phosphate dehydrogenase 2, mitochondrial	2	NM_010274.2	1,30	**1,69**	0,1206	**0,0084**

			(Gpd2), nuclear gene encoding mitochondrial protein, mRNA.						
ILMN_1229267	S	**Cyp2a5**	Mus musculus cytochrome P450, family 2, subfamily a, polypeptide 5 (Cyp2a5), mRNA.		NM_007812.4	1,91	**1,69**	0,0062	**0,0055**
ILMN_2479666	S	**Uck1**	Mus musculus uridine-cytidine kinase 1 (Uck1), mRNA.	2	NM_011675.1	1,19	**1,69**	0,1231	**0,0075**
ILMN_1229318	S	**Pdk1**	Mus musculus pyruvate dehydrogenase kinase, isoenzyme 1 (Pdk1), nuclear gene encoding mitochondrial protein, mRNA.	2	NM_172665.3	1,11	**1,68**	0,2267	**0,0013**
ILMN_1237758	S	**LOC382153**			XM_356249.1	1,53	**1,68**	0,0385	**0,0268**
ILMN_2470799	S	**LOC100047579**	PREDICTED: Mus musculus similar to transmembrane protein 20 (LOC100047579), mRNA.		XM_001478437.1	-1,13	**1,68**	0,6603	**0,0482**
ILMN_2766596	S	**Gmds**	Mus musculus GDP-mannose 4, 6-dehydratase (Gmds), mRNA.	13	NM_146041.2	1,59	**1,68**	0,0529	**0,0068**
ILMN_2738845	S	**Olfr1269**	Mus musculus olfactory receptor 1269 (Olfr1269), mRNA.	2	NM_146342.1	1,02	**1,68**	0,9567	**0,0240**
ILMN_2512986	S	**Zfyve27**	Mus musculus zinc finger, FYVE domain containing 27	19	NM_177319.2	-1,18	**1,68**	0,5925	**0,0074**

			(Zfyve27), mRNA.						
ILMN_2970742	S	**Rnf170**	Mus musculus ring finger protein 170 (Rnf170), mRNA.	8	NM_029965.2	-1,16	**1,68**	0,3834	**0,0228**
ILMN_2684388	S	**1700034H14Rik**	Mus musculus RIKEN cDNA 1700034H14 gene (1700034H14Rik), mRNA.		NM_025969.3	-1,08	**1,68**	0,7722	**0,0039**
ILMN_1253233	S	**Dsg1c**			NM_181680	3,80	**1,67**	0,0197	**0,0365**
ILMN_1247760	S	**2210016L21Rik**	Mus musculus RIKEN cDNA 2210016L21 gene (2210016L21Rik), mRNA.	5	NM_028211.1	1,29	**1,67**	0,4455	**0,0074**
ILMN_2877541	S	**Crtap**	Mus musculus cartilage associated protein (Crtap), mRNA.	9	NM_019922.1	2,04	**1,67**	0,2502	**0,0087**
ILMN_2673889	S	**Mcm7**			NM_008568.1	-1,10	**1,67**	0,6605	**0,0317**
ILMN_2608043	S	**Hes6**	Mus musculus hairy and enhancer of split 6 (Drosophila) (Hes6), mRNA.	1	NM_019479.3	1,82	**1,66**	0,0234	**0,0328**
ILMN_2858399	S	**D930001I22Rik**	Mus musculus RIKEN cDNA D930001I22 gene (D930001I22Rik), mRNA.	2	NM_173397.2	1,24	**1,66**	0,1275	**0,0240**
ILMN_2561986	S	**A130046C05Rik**			AK037745	-1,11	**1,66**	0,6982	**0,0222**
ILMN_1214866	S	**Eml1**	Mus musculus echinoderm microtubule associated protein like 1	12	NM_001043335.1	1,25	**1,65**	0,5136	**0,0031**

			(Eml1), transcript variant 1, mRNA. XM_901775 XM_901779 XM_978946 XM_978978 XM_979015 XM_979053 XM_979124 XM_979166 XM_979204						
ILMN_1241980	S	**Cdc2l1**	Mus musculus cell division cycle 2-like 1 (Cdc2l1), mRNA.	4	NM_007661.3	1,25	**1,65**	0,2525	**0,0289**
ILMN_1245424	S	**Ppat**	PREDICTED: Mus musculus phosphoribosyl pyrophosphate amidotransferase, transcript variant 8 (Ppat), mRNA.		XM_001002886.2	1,61	**1,65**	0,0801	**0,0031**
ILMN_1256633	S	**LOC100045567**	PREDICTED: Mus musculus similar to purine nucleoside phosphorylase (LOC100045567), mRNA.		XM_001474536.1	1,48	**1,65**	0,0027	**0,0101**
ILMN_2760979	S	**Tgfbr2**	Mus musculus transforming growth factor, beta receptor II (Tgfbr2), transcript variant 1, mRNA.	9	NM_009371.2	1,09	**1,65**	0,4032	**0,0349**
ILMN_2490536	S	**Aldh5a1**			NM_172532	1,72	**1,65**	0,0001	**0,0000**
ILMN_2611532	S	**Slc25a19**	Mus musculus solute carrier family 25 (mitochondrial thiamine pyrophosphate	11	NM_026071.2	1,04	**1,65**	0,4226	**0,0187**

			carrier), member 19 (Slc25a19), nuclear gene encoding mitochondrial protein, mRNA.					
ILMN_2639714	S	**2700078E11Rik**	Mus musculus RIKEN cDNA 2700078E11 gene (2700078E11Rik), mRNA.	19	NM_030197.1	-1,17	**1,64**	0,4564	**0,0467**
ILMN_3126933	A	**Tacc1**	Mus musculus transforming, acidic coiled-coil containing protein 1 (Tacc1), transcript variant 2, mRNA.	8	NM_199323.2	1,32	**1,64**	0,1962	**0,0067**
ILMN_2726448	S	**Bbs4**	Mus musculus Bardet-Biedl syndrome 4 (human) (Bbs4), mRNA.	9	NM_175325.2	1,49	**1,64**	0,1288	**0,0193**
ILMN_2746556	S	**Dkk3**	Mus musculus dickkopf homolog 3 (Xenopus laevis) (Dkk3), mRNA.	7	NM_015814.2	1,25	**1,64**	0,5458	**0,0322**
ILMN_3148550	A	**Golm1**	Mus musculus golgi membrane protein 1 (Golm1), transcript variant 2, mRNA.	13	NM_001035122.2	1,88	**1,63**	0,0057	**0,0073**

ILMN_1258578	S	**Ahnak**	Mus musculus AHNAK nucleoprotein (desmoyokin) (Ahnak), transcript variant 3, mRNA.	19	NM_001039959.1	1,55	**1,63**	0,2831	**0,0094**
ILMN_3139693	A	**Rab11fip5**	Mus musculus RAB11 family interacting protein 5 (class I) (Rab11fip5), transcript variant 1, mRNA.	6	NM_001003955.2	1,26	**1,63**	0,0911	**0,0322**
ILMN_2517060	S	**9630015D15Rik**			NM_181401	1,17	**1,63**	0,0914	**0,0259**
ILMN_2467578	S	**scl000416.1_19**			AK049709.1	1,22	**1,63**	0,2613	**0,0072**
ILMN_2747070	S	**Fpgs**	Mus musculus folylpolyglutamyl synthetase (Fpgs), mRNA.	2	NM_010236.1	-1,01	**1,63**	0,9498	**0,0203**
ILMN_2598990	S	**Lnx2**	Mus musculus ligand of numb-protein X 2 (Lnx2), mRNA.	5	NM_080795.3	1,21	**1,63**	0,3681	**0,0334**
ILMN_2603377	S	**Dnase2b**	Mus musculus deoxyribonuclease II beta (Dnase2b), mRNA.	3	NM_019957.3	1,68	**1,63**	0,0378	**0,0019**
ILMN_1244847	S	**Cyp2a5**	Mus musculus cytochrome P450, family 2, subfamily a, polypeptide 5 (Cyp2a5), mRNA.		NM_007812.4	1,66	**1,63**	0,0017	**0,0014**
ILMN_2707198	S	**As3mt**			NM_020577.1	1,32	**1,62**	0,0178	**0,0035**
ILMN_2788073	S	**Hmox1**	Mus musculus heme oxygenase (decycling) 1 (Hmox1), mRNA.	8	NM_010442.1	1,11	**1,62**	0,6448	**0,0015**

ILMN_2470039	S	**D930001I22Rik**			NM_173397	1,22	**1,62**	0,1877	**0,0040**
ILMN_2756113	S	**Nln**	Mus musculus neurolysin (metallopeptidase M3 family) (Nln), mRNA.	13	NM_029447.1	1,30	**1,62**	0,0720	**0,0074**
ILMN_1231651	S	**LOC100045439**	PREDICTED: Mus musculus similar to testis-specific adriamycin sensitivity protein (LOC100045439), mRNA.		XM_001474279.1	1,04	**1,61**	0,3894	**0,0385**
ILMN_2614966	S	**Rab27a**	Mus musculus RAB27A, member RAS oncogene family (Rab27a), mRNA.		NM_023635.4	1,82	**1,61**	0,0989	**0,0131**
ILMN_2659415	S	**Atp8b2**	Mus musculus ATPase, class I, type 8B, member 2 (Atp8b2), mRNA.	3	NM_001081182.1	-1,50	**1,61**	0,2657	**0,0270**
ILMN_1229935	S	**LOC434200**	PREDICTED: Mus musculus similar to Thymine DNA glycosylase (LOC434200), misc RNA.	7	XR_034036.1	-1,03	**1,61**	0,7930	**0,0257**
ILMN_2756379	S	**Aqp8**	Mus musculus aquaporin 8 (Aqp8), mRNA.	7	NM_007474.1	1,08	**1,61**	0,7983	**0,0488**
ILMN_2939652	S	**Selenbp2**	Mus musculus selenium binding protein 2 (Selenbp2), mRNA.	3	NM_019414.2	2,47	**1,60**	0,0061	**0,0492**
ILMN_1254631	S	**AI481316**			XM_148986.1	1,45	**1,60**	0,0067	**0,0046**
ILMN_2637757	S	**Hlx**	Mus musculus H2.0-like homeobox (Hlx), mRNA.	1	NM_008250.1	1,00	**1,59**	NA	**0,0187**
ILMN_1232972	S	**Stk19**	Mus musculus serine/threonin	17	NM_019442.3	-1,11	**1,59**	0,2050	**0,0259**

			e kinase 19 (Stk19), mRNA.						
ILMN_2636525	S	**Kcna3**	Mus musculus potassium voltage-gated channel, shaker-related subfamily, member 3 (Kcna3), mRNA.	3	NM_008418.1	1,09	**1,59**	0,5023	**0,0484**
ILMN_2698564	S	**Khk**	Mus musculus ketohexokinase (Khk), mRNA.	5	NM_008439.3	1,23	**1,58**	0,0362	**0,0010**
ILMN_2953277	S	**EG433182**	Mus musculus predicted gene, EG433182 (EG433182), mRNA.	18	NM_001025388.1	1,26	**1,58**	0,4250	**0,0320**
ILMN_2648100	S	**LOC676974**	PREDICTED: Mus musculus similar to Glucose phosphate isomerase 1, transcript variant 2 (LOC676974), mRNA.		XM_001003154.1	1,12	**1,58**	0,2030	**0,0112**
ILMN_2704119	S	**Cul4a**	Mus musculus cullin 4A (Cul4a), mRNA.	8	NM_146207.1	1,36	**1,58**	0,1745	**0,0384**
ILMN_2929723	S	**Zfp64**	Mus musculus zinc finger protein 64 (Zfp64), mRNA.	2	NM_009564.1	-1,16	**1,58**	0,7127	**0,0192**
ILMN_3084087	A	**Ivns1abp**	Mus musculus influenza virus NS1A binding protein (Ivns1abp), transcript variant 1,	1	NM_001039511.1	1,44	**1,58**	0,0725	**0,0260**

			mRNA.						
ILMN_3144820	A	**LOC329575**	Mus musculus hypothetical LOC329575 (LOC329575), mRNA.	2	NM_001024849.1	1,01	**1,58**	0,4226	**0,0327**
ILMN_2472708	S	**5730402C02Rik**			NM_027442	1,27	**1,58**	0,0999	**0,0409**
ILMN_1220641	S	**Pgrmc2**	PREDICTED: Mus musculus progesterone receptor membrane component 2, transcript variant 3 (Pgrmc2), mRNA.		XM_911696.2	1,16	**1,57**	0,2381	**0,0065**
ILMN_1244134	S	**Lrp4**	Mus musculus low density lipoprotein receptor-related protein 4 (Lrp4), mRNA.	2	NM_172668.2	1,10	**1,57**	0,2621	**0,0186**
ILMN_2845839	S	**1700065O13Rik**	Mus musculus RIKEN cDNA 1700065O13 gene (1700065O13Rik), mRNA.	17	NM_028543.1	1,75	**1,57**	0,1491	**0,0271**
ILMN_2824012	S	**Timm17b**	Mus musculus translocase of inner mitochondrial membrane 17b (Timm17b), mRNA.	X	NM_011591.2	1,00	**1,57**	NA	**0,0147**
ILMN_2431619	S	**Ube2l6**			NM_019949	1,66	**1,57**	0,0461	**0,0062**
ILMN_3057482	I	**4833426J09Rik**	Mus musculus RIKEN cDNA 4833426J09 gene (4833426J09Rik), mRNA.	8	NM_001024606.1	1,14	**1,57**	0,6847	**0,0164**
ILMN_2933022	S	**Plekhb1**	Mus musculus pleckstrin	7	NM_013746.1	1,59	**1,57**	0,0259	**0,0141**

			homology domain containing, family B (evectins) member 1 (Plekhb1), mRNA.						
ILMN_1240471	S	**Retsat**	Mus musculus retinol saturase (all trans retinol 13,14 reductase) (Retsat), mRNA.	6	NM_026159.4	1,33	**1,57**	0,1602	**0,0156**
ILMN_1257579	S	**Nup210**	Mus musculus nucleoporin 210 (Nup210), mRNA.	6	NM_018815.1	1,42	**1,57**	0,0088	**0,0022**
ILMN_2588055	S	**Actb**	Mus musculus actin, beta (Actb), mRNA.		NM_007393.3	-1,39	**1,57**	0,4101	**0,0281**
ILMN_2681186	S	**Rab7l1**	Mus musculus RAB7, member RAS oncogene family-like 1 (Rab7l1), mRNA.	1	NM_144875.1	1,24	**1,57**	0,0029	**0,0446**
ILMN_2777293	S	**Pafah2**	Mus musculus platelet-activating factor acetylhydrolase 2 (Pafah2), mRNA.	4	NM_133880.1	1,38	**1,57**	0,1649	**0,0197**
ILMN_2622613	S	**Acot4**	Mus musculus acyl-CoA thioesterase 4 (Acot4), mRNA.	12	NM_134247.2	1,05	**1,57**	0,8637	**0,0477**
ILMN_2721083	S	**Catsper2**	Mus musculus cation channel,	2	NM_153075.2	1,39	**1,56**	0,2371	**0,0219**

			sperm associated 2 (Catsper2), mRNA.						
ILMN_2783519	S	**Acadl**	Mus musculus acyl-Coenzyme A dehydrogenase, long-chain (Acadl), mRNA.	1	NM_007381.2	-1,15	**1,56**	0,4662	**0,0260**
ILMN_1260112	S	**2400003C14Rik**	Mus musculus RIKEN cDNA 2400003C14 gene (2400003C14Rik), mRNA.	8	NM_028018.1	-1,17	**1,56**	0,6951	**0,0146**
ILMN_2638721	S	**Csrnp2**	Mus musculus cysteine-serine-rich nuclear protein 2 (Csrnp2), mRNA.	15	NM_153407.2	1,00	**1,56**	NA	**0,0377**
ILMN_2641032	S	**Epb7.2**			NM_013515.1	1,39	**1,56**	0,3715	**0,0121**
ILMN_2667550	S	**Ppil1**	Mus musculus peptidylprolyl isomerase (cyclophilin)-like 1 (Ppil1), mRNA.		NM_026845.3	1,21	**1,56**	0,1534	**0,0233**
ILMN_1254228	S	**EG241041**	Mus musculus predicted gene, EG241041 (EG241041), non-coding RNA.	1	NR_002858.1	1,00	**1,56**	NA	**0,0301**
ILMN_1235374	S	**Decr1**	Mus musculus 2,4-dienoyl CoA reductase 1, mitochondrial (Decr1), nuclear gene encoding	4	NM_026172.3	-1,27	**1,56**	0,1870	**0,0002**

			mitochondrial protein, mRNA.						
ILMN_3004221	S	**Cyp2u1**	Mus musculus cytochrome P450, family 2, subfamily u, polypeptide 1 (Cyp2u1), mRNA.		NM_027816.1	1,42	**1,56**	0,2161	**0,0341**
ILMN_2653696	S	**Abcd3**			NM_008991	-1,01	**1,56**	0,8749	**0,0001**
ILMN_3159131	A	**Cyp2a5**	Mus musculus cytochrome P450, family 2, subfamily a, polypeptide 5 (Cyp2a5), mRNA.	7	NM_007812.2	1,30	**1,55**	0,0051	**0,0198**
ILMN_2418855	S	**Ugt1a6a**	Mus musculus UDP glucuronosyltransferase 1 family, polypeptide A6A (Ugt1a6a), mRNA.	1	NM_145079.2	1,27	**1,55**	0,2118	**0,0002**
ILMN_1251885	S	**Hist1h4d**	Mus musculus histone cluster 1, H4d (Hist1h4d), mRNA.	13	NM_175654.1	1,29	**1,55**	0,4080	**0,0021**
ILMN_2606825	S	**Cmah**			NM_007717.1	1,34	**1,55**	0,2183	**0,0381**
ILMN_2497067	S	**Zmynd11**			NM_144516.1	1,59	**1,55**	0,1019	**0,0378**
ILMN_2549039	S	**4930487N19Rik**			AK015640	1,28	**1,54**	0,2014	**0,0105**
ILMN_3003864	S	**Cgnl1**	Mus musculus cingulin-like 1 (Cgnl1), mRNA.	9	NM_026599.4	1,00	**1,54**	NA	**0,0492**
ILMN_3031099	I	**Coq10b**	Mus musculus coenzyme Q10 homolog B (S. cerevisiae) (Coq10b), transcript variant 1, mRNA.	1	NM_001039710.1	1,46	**1,54**	0,2963	**0,0372**

ILMN_2626114	S	**Rab3ip**	Mus musculus RAB3A interacting protein (Rab3ip), mRNA.	10	NM_001003950.2	-1,16	**1,54**	0,5043	**0,0336**
ILMN_2620583	S	**Pacs2**	Mus musculus phosphofurin acidic cluster sorting protein 2 (Pacs2), mRNA.	12	NM_001081170.1	1,42	**1,54**	0,1325	**0,0096**
ILMN_2776283	S	**Tcea3**			NM_011542	1,89	**1,54**	0,0021	**0,0002**
ILMN_2628271	S	**LOC100045967**	PREDICTED: Mus musculus hypothetical protein LOC100045967 (LOC100045967), misc RNA.		XR_032154.1	1,25	**1,54**	0,0140	**0,0014**
ILMN_2901029	S	**Zfp532**	Mus musculus zinc finger protein 532 (Zfp532), mRNA.	18	NM_207255.1	1,21	**1,54**	0,0477	**0,0292**
ILMN_2808811	S	**Gpd1**	Mus musculus glycerol-3-phosphate dehydrogenase 1 (soluble) (Gpd1), mRNA.	15	NM_010271.2	-1,68	**1,54**	0,1134	**0,0076**
ILMN_1234388	S	**Twf2**	Mus musculus twinfilin, actin-binding protein, homolog 2 (Drosophila) (Twf2), mRNA.	9	NM_011876.3	-1,04	**1,54**	0,8387	**0,0314**
ILMN_1233813	S	**Ss18**	Mus musculus synovial sarcoma translocation, Chromosome 18 (Ss18), mRNA.	18	NM_009280.1	1,14	**1,53**	0,5846	**0,0081**

ILMN_1229225	S	**D030016E14Rik**			NM_177240.2	1,11	**1,53**	0,7878	**0,0151**
ILMN_2672113	S	**Ddhd2**	PREDICTED: Mus musculus DDHD domain containing 2 (Ddhd2), mRNA.	8	XM_356065.5	-1,03	**1,53**	0,8430	**0,0084**
ILMN_2904819	S	**9530058B02Rik**	Mus musculus RIKEN cDNA 9530058B02 gene (9530058B02Rik), mRNA.	17	NM_026633.1	1,25	**1,53**	0,1879	**0,0048**
ILMN_1226755	S	**E030007N04Rik**			AK086880	-1,16	**1,53**	0,4226	**0,0364**
ILMN_2771665	S	**Pafah2**	Mus musculus platelet-activating factor acetylhydrolase 2 (Pafah2), mRNA.	4	NM_133880.1	1,79	**1,53**	0,0068	**0,0063**
ILMN_2949021	S	**Aadacl1**	Mus musculus arylacetamide deacetylase-like 1 (Aadacl1), mRNA.	3	NM_178772.2	-1,05	**1,53**	0,7097	**0,0156**
ILMN_2623886	S	**A030007L17Rik**	Mus musculus RIKEN cDNA A030007L17 gene (A030007L17Rik), mRNA.	6	NM_026637.3	1,25	**1,53**	0,2699	**0,0146**
ILMN_1231810	S	**Ube2e1**	Mus musculus ubiquitin-conjugating enzyme E2E 1, UBC4/5 homolog (yeast) (Ube2e1),	14	NM_009455.3	1,16	**1,53**	0,4633	**0,0027**

			mRNA.						
ILMN_1233402	S	**LOC100045981**	PREDICTED: Mus musculus similar to synaptotagmin XI (LOC100045981), mRNA.		XM_001475298.1	1,49	**1,52**	0,0510	**0,0498**
ILMN_2691815	S	**G3bp2**	Mus musculus GTPase activating protein (SH3 domain) binding protein 2 (G3bp2), transcript variant 1, mRNA.	5	NM_011816.3	1,88	**1,52**	0,0265	**0,0397**
ILMN_2688888	S	**Gca**	Mus musculus grancalcin (Gca), mRNA.	2	NM_145523.3	1,00	**1,52**	NA	**0,0088**
ILMN_2980323	S	**Cldn2**	Mus musculus claudin 2 (Cldn2), mRNA.	X	NM_016675.3	1,19	**1,52**	0,1092	**0,0045**
ILMN_1232601	S	**Cyb561**	Mus musculus cytochrome b-561 (Cyb561), mRNA.		NM_007805.4	1,46	**1,52**	0,2309	**0,0452**
ILMN_1226760	S	**LOC619973**	PREDICTED: Mus musculus similar to LRRGT00183 (LOC619973), mRNA.	4	XM_884359.3	-1,01	**1,52**	0,8992	**0,0027**
ILMN_2647170	S	**Serhl**	Mus musculus serine hydrolase-like (Serhl), mRNA.	15	NM_023475.2	1,17	**1,52**	0,0913	**0,0400**
ILMN_2681057	S	**Phca**	Mus musculus phytoceramidase, alkaline (Phca), mRNA.	7	NM_025408.2	1,54	**1,52**	0,0026	**0,0061**
ILMN_1258834	S	**Chd1**			AK042202	1,00	**1,52**	NA	**0,0100**
ILMN_3068197	I	**Slc12a2**	Mus musculus solute carrier family 12,	18	NM_009194.2	-1,12	**1,52**	0,6279	**0,0375**

			member 2 (Slc12a2), mRNA.						
ILMN_1222471	S	**Gmfg**	Mus musculus glia maturation factor, gamma (Gmfg), transcript variant 1, mRNA.	7	NM_022024.2	1,40	**1,51**	0,0974	**0,0135**
ILMN_1244836	S	**Tmem41a**	Mus musculus transmembrane protein 41a (Tmem41a), mRNA.		NM_025693.3	1,43	**1,51**	0,0490	**0,0228**
ILMN_1228641	S	**E330022B15Rik**			AK054393	1,40	**1,51**	0,2252	**0,0028**
ILMN_2742068	S	**Csrp3**	Mus musculus cysteine and glycine-rich protein 3 (Csrp3), mRNA.	7	NM_013808.3	-1,03	**1,51**	0,9086	**0,0027**
ILMN_2630884	S	**Aplf**	Mus musculus aprataxin and PNKP like factor (Aplf), mRNA.	6	NM_024251.3	1,10	**1,51**	0,6631	**0,0212**
ILMN_1237670	S	**Entpd2**	Mus musculus ectonucleoside triphosphate diphosphohydrolase 2 (Entpd2), mRNA.	2	NM_009849.1	-1,01	**1,51**	0,9870	**0,0041**
ILMN_2702894	S	**Afmid**	Mus musculus arylformamidase (Afmid), mRNA.	11	NM_027827.2	1,26	**1,51**	0,5146	**0,0458**
ILMN_2960982	S	**Pex11a**	Mus musculus peroxisomal biogenesis factor 11a (Pex11a),	7	NM_011068.1	-1,01	**1,50**	0,9640	**0,0015**

			mRNA.						
ILMN_1234241	S	**Mrap**	Mus musculus melanocortin 2 receptor accessory protein (Mrap), mRNA.		NM_029844.3	1,30	**1,50**	0,0257	**0,0411**
ILMN_1233334	S	**Fpgs**	Mus musculus folylpolyglutamyl synthetase (Fpgs), mRNA.	2	NM_010236.1	1,16	**1,50**	0,4169	**0,0214**
ILMN_2539489	S	**Myo5b**	Mus musculus myosin Vb (Myo5b), mRNA.	18	NM_201600.2	-1,22	**1,50**	0,2962	**0,0391**
ILMN_2738629	S	**Acot8**	Mus musculus acyl-CoA thioesterase 8 (Acot8), mRNA.	2	NM_133240.1	1,08	**1,50**	0,5759	**0,0016**
ILMN_2862465	S	**Ghdc**	Mus musculus GH3 domain containing (Ghdc), mRNA.	11	NM_031871.1	1,29	**1,50**	0,2652	**0,0274**
ILMN_2633096	S	**Gstm6**	Mus musculus glutathione S-transferase, mu 6 (Gstm6), mRNA.	3	NM_008184.3	-1,29	**-1,50**	0,1662	**0,0006**
ILMN_2800151	S	**Lsm2**	Mus musculus LSM2 homolog, U6 small nuclear RNA associated (S. cerevisiae) (Lsm2), mRNA.	17	NM_030597.2	-1,10	**-1,50**	0,6440	**0,0342**
ILMN_2558520	S	**A430104D08Rik**			AK040509	1,20	**-1,50**	0,4467	**0,0433**
ILMN_2461871	S	**scl0003651.1_17**			XM_356680.1	1,01	**-1,50**	0,9389	**0,0422**
ILMN_2982200	S	**Mrpl13**	Mus musculus mitochondrial ribosomal protein L13 (Mrpl13),	15	NM_026759.2	-1,52	**-1,51**	0,1997	**0,0091**

			mRNA.						
ILMN_1230318	S	**Cbs**			NM_144855.1	-1,26	**-1,51**	0,1218	**0,0447**
ILMN_1243997	S	**A530052I19Rik**			AK040969	-1,16	**-1,51**	0,4218	**0,0005**
ILMN_1245352	S	**Dclk3**	Mus musculus doublecortin-like kinase 3 (Dclk3), mRNA.		NM_172928.3	-1,85	**-1,51**	0,1972	**0,0380**
ILMN_2655184	S	**2810007J24Rik**	Mus musculus RIKEN cDNA 2810007J24 gene (2810007J24Rik), mRNA.	7	NM_175250.4	-1,44	**-1,51**	0,0350	**0,0089**
ILMN_1245382	S	**Tmem102**	Mus musculus transmembrane protein 102 (Tmem102), mRNA.		NM_001033433.3	-1,44	**-1,51**	0,3992	**0,0032**
ILMN_2751948	S	**Hist2h2aa1**			NM_013549	-1,79	**-1,51**	0,0087	**0,0440**
ILMN_2860479	S	**Arpc1b**	Mus musculus actin related protein 2/3 complex, subunit 1B (Arpc1b), mRNA.	5	NM_023142.1	-1,05	**-1,52**	0,7285	**0,0256**
ILMN_2622209	S	**Rnaseh2b**	Mus musculus ribonuclease H2, subunit B (Rnaseh2b), mRNA.	14	NM_026001.2	-1,25	**-1,52**	0,4106	**0,0055**
ILMN_2775910	S	**Olfr1023**	Mus musculus olfactory receptor 1023 (Olfr1023), mRNA.	2	NM_146587.2	1,11	**-1,52**	0,7410	**0,0305**
ILMN_2932164	S	**Notum**	Mus musculus notum pectinacetylesterase homolog (Drosophila) (Notum), mRNA.	11	NM_175263.3	-2,49	**-1,52**	0,0532	**0,0098**
ILMN_1245112	S	**Aldh16a1**	Mus musculus aldehyde	7	NM_145954.1	-1,18	**-1,52**	0,3467	**0,0009**

			dehydrogenase 16 family, member A1 (Aldh16a1), mRNA.						
ILMN_1227951	S	**Gcnt2**	Mus musculus glucosaminyl (N-acetyl) transferase 2, I-branching enzyme (Gcnt2), transcript variant 3, mRNA.	13	NM_133219.1	-1,25	**-1,52**	0,0962	**0,0110**
ILMN_2599997	S	**Ncor1**	Mus musculus nuclear receptor co-repressor 1 (Ncor1), mRNA.	11	NM_011308.2	1,00	**-1,52**	NA	**0,0075**
ILMN_2674620	S	**Ela2a**	Mus musculus elastase 2A (Ela2a), mRNA.	4	NM_007919.2	2,39	**-1,52**	0,0086	**0,0460**
ILMN_1214703	S	**Nme7**	Mus musculus non-metastatic cells 7, protein expressed in (nucleoside-diphosphate kinase) (Nme7), transcript variant 1, mRNA.	1	NM_138314.2	-1,18	**-1,52**	0,1499	**0,0193**
ILMN_2642815	S	**Slc44a3**	Mus musculus solute carrier family 44, member 3 (Slc44a3),	3	NM_145394.2	-1,36	**-1,52**	0,3129	**0,0269**

			mRNA.						
ILMN_2685022	S	**C730048C13Rik**	Mus musculus RIKEN cDNA C730048C13 gene (C730048C13 Rik), mRNA.	19	NM_177002.2	-2,07	**-1,52**	0,0442	**0,0025**
ILMN_1219904	S	**Tspan33**	Mus musculus tetraspanin 33 (Tspan33), mRNA.	6	NM_146173.2	-1,90	**-1,52**	0,1206	**0,0383**
ILMN_2814865	S	**Qpct**	Mus musculus glutaminyl-peptide cyclotransferase (glutaminyl cyclase) (Qpct), mRNA.		NM_027455.1	-2,60	**-1,52**	0,0014	**0,0392**
ILMN_2774563	S	**Mug4**	PREDICTED: Mus musculus murinoglobulin 4 (Mug4), misc RNA.		XR_035729.1	-1,53	**-1,52**	0,0107	**0,0017**
ILMN_1213443	S	**LOC433261**	PREDICTED: Mus musculus similar to Sid393p (LOC433261), misc RNA.	19	XR_034247.1	-1,05	**-1,52**	0,7901	**0,0184**
ILMN_2631423	S	**H2-Ab1**	Mus musculus histocompatibility 2, class II antigen A, beta 1 (H2-Ab1), mRNA.	17	NM_207105.2	1,24	**-1,53**	0,3786	**0,0357**
ILMN_2941728	S	**Nenf**	Mus musculus neuron derived neurotrophic factor (Nenf), mRNA.	1	NM_025424.1	-1,45	**-1,53**	0,1003	**0,0339**
ILMN_1241278	S	**Rdh11**			NM_021557	-1,60	**-1,53**	0,0983	**0,0312**
ILMN_2607675	S	**LOC641240**	PREDICTED: Mus musculus similar to MHC class II antigen beta chain (LOC641240), mRNA.		XM_918601.3	1,20	**-1,53**	0,5256	**0,0481**
ILMN_2982764	S	**Ugt2a3**	Mus musculus	5	NM_028094.1	-1,23	**-1,53**	0,1292	**0,0110**

			UDP glucuronosyltransferase 2 family, polypeptide A3 (Ugt2a3), mRNA.						
ILMN_2852217	S	**Gnpda1**	Mus musculus glucosamine-6-phosphate deaminase 1 (Gnpda1), mRNA.	18	NM_011937.1	1,06	**-1,53**	0,8088	**0,0121**
ILMN_1231053	S	**Hist2h2aa1**	Mus musculus histone cluster 2, H2aa1 (Hist2h2aa1), mRNA.	3	NM_013549.1	-1,35	**-1,53**	0,0046	**0,0016**
ILMN_2449986	S	**EG640530**	PREDICTED: Mus musculus predicted gene, EG640530 (EG640530), mRNA.		XM_917532.3	-1,78	**-1,53**	0,0236	**0,0025**
ILMN_1256905	S	**Creb3**	Mus musculus cAMP responsive element binding protein 3 (Creb3), mRNA.	4	NM_013497.3	-1,08	**-1,54**	0,5089	**0,0494**
ILMN_2714222	S	**Elovl2**	Mus musculus elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 2 (Elovl2), mRNA.	13	NM_019423.1	-1,57	**-1,54**	0,0423	**0,0427**
ILMN_2540844	S	**LOC385583**			XM_358296.1	-1,08	**-1,54**	0,8243	**0,0109**
ILMN_1236134	S	**EG434674**	Mus musculus predicted gene, EG434674	19	NM_001013820.2	-1,96	**-1,54**	0,0452	**0,0018**

			(EG434674), mRNA. XM_922736 XM_922739 XM_922744 XM_922747						
ILMN_2651831	S	**2310039L15Rik**			XM_290098.1	1,02	**-1,54**	0,9582	**0,0085**
ILMN_2840091	S	**Ugcg**	Mus musculus UDP-glucose ceramide glucosyltransferase (Ugcg), mRNA.	4	NM_011673.2	-1,23	**-1,54**	0,3586	**0,0102**
ILMN_1236517	S	**Il18**	Mus musculus interleukin 18 (Il18), mRNA.	9	NM_008360.1	-1,35	**-1,54**	0,0841	**0,0040**
ILMN_2607408	S	**Pcbp4**	Mus musculus poly(rC) binding protein 4 (Pcbp4), mRNA.	9	NM_021567.2	-1,22	**-1,55**	0,0979	**0,0066**
ILMN_1244515	S	**Tmem50b**	Mus musculus transmembrane protein 50B (Tmem50b), mRNA.	16	NM_030018.3	-1,48	**-1,55**	0,0040	**0,0222**
ILMN_1236553	S	**Gimap9**	Mus musculus GTPase, IMAP family member 9 (Gimap9), mRNA.	6	NM_174960.2	-1,68	**-1,55**	0,0912	**0,0351**
ILMN_1250576	S	**2810439F02Rik**	Mus musculus RIKEN cDNA 2810439F02 gene (2810439F02Rik), mRNA.	18	NM_028341.2	1,33	**-1,55**	0,0932	**0,0390**
ILMN_1249666	S	**Ppap2c**	Mus musculus phosphatidic acid phosphatase	10	NM_015817.2	-1,66	**-1,55**	0,0108	**0,0163**

			type 2c (Ppap2c), mRNA.						
ILMN_2739843	S	**Metrn**			NM_133719	-1,86	**-1,55**	0,0242	**0,0103**
ILMN_1250498	S	**Gm317**	PREDICTED: Mus musculus gene model 317, (NCBI) (Gm317), mRNA.	17	XM_139904.6	-1,12	**-1,55**	0,6830	**0,0085**
ILMN_2749556	S	**Mupcdh**	Mus musculus mucin-like protocadherin (Mupcdh), mRNA.	7	NM_028069.2	-1,21	**-1,56**	0,0274	**0,0102**
ILMN_1216182	S	**2810439F02Rik**	Mus musculus RIKEN cDNA 2810439F02 gene (2810439F02Rik), mRNA.	18	NM_028341.2	1,24	**-1,56**	0,1172	**0,0313**
ILMN_1236107	S	**Ogfrl1**	PREDICTED: Mus musculus opioid growth factor receptor-like 1 (Ogfrl1), mRNA.		XM_973033.1	-1,18	**-1,56**	0,2199	**0,0025**
ILMN_2819424	S	**Prhoxnb**	Mus musculus parahox cluster neighbor (Prhoxnb), mRNA.	5	NM_001039678.1	-2,45	**-1,56**	0,0056	**0,0366**
ILMN_1252204	S	**Sepw1**	Mus musculus selenoprotein W, muscle 1 (Sepw1), mRNA.	7	NM_009156.2	-1,25	**-1,56**	0,3405	**0,0062**
ILMN_2775885	S	**Calm2**			NM_007589	-1,28	**-1,56**	0,2201	**0,0469**
ILMN_2776278	S	**Ly6e**			NM_008529	-1,37	**-1,56**	0,0372	**0,0114**
ILMN_2454339	S	**2310010J17Rik**				1,13	**-1,57**	0,7299	**0,0444**
ILMN_1229329	S	**2700049H19Rik**				-1,30	**-1,57**	0,0141	**0,0158**
ILMN_1236522	S	**Cbr1**	Mus musculus carbonyl	16	NM_007620.2	-1,90	**-1,57**	0,0204	**0,0010**

			reductase 1 (Cbr1), mRNA.						
ILMN_2668778	S	**Use1**	Mus musculus unconventional SNARE in the ER 1 homolog (S. cerevisiae) (Use1), transcript variant 2, mRNA.	8	NM_029768.3	-1,21	**-1,57**	0,4874	**0,0443**
ILMN_1236588	S	**Car1**	Mus musculus carbonic anhydrase 1 (Car1), transcript variant 1, mRNA.		NM_009799.4	-1,54	**-1,57**	0,3076	**0,0269**
ILMN_2977762	S	**Tnpo3**	Mus musculus transportin 3 (Tnpo3), mRNA.	6	NM_177296.4	-1,13	**-1,58**	0,6544	**0,0153**
ILMN_2710449	S	**Crip2**	Mus musculus cysteine rich protein 2 (Crip2), mRNA.	12	NM_024223.1	-1,77	**-1,58**	0,0216	**0,0101**
ILMN_2656511	S	**Bbs7**	Mus musculus Bardet-Biedl syndrome 7 (Bbs7), mRNA.	3	NM_027810.2	-1,51	**-1,58**	0,1335	**0,0464**
ILMN_2645662	S	**Tmem86a**	Mus musculus transmembrane protein 86A (Tmem86a), mRNA.		NM_026436.3	-1,35	**-1,58**	0,2195	**0,0216**
ILMN_1255634	S	**Pigyl**	Mus musculus phosphatidylinositol glycan anchor biosynthesis, class Y-like (Pigyl), mRNA.	9	NM_001082532.1	-1,14	**-1,59**	0,2258	**0,0108**
ILMN_1229187	S	**Prhoxnb**	Mus musculus parahox cluster neighbor (Prhoxnb), mRNA.	5	NM_001039678.1	-2,25	**-1,59**	0,0305	**0,0171**

ILMN_1249941	S	**Gdf10**	Mus musculus growth differentiation factor 10 (Gdf10), mRNA.	14	NM_145741.2	-1,62	**-1,59**	0,0947	**0,0100**
ILMN_2546596	S	**2310076E21Rik**			AK010195	1,60	**-1,59**	0,1854	**0,0385**
ILMN_2476804	S	**Ube2a**	Mus musculus ubiquitin-conjugating enzyme E2A, RAD6 homolog (S. cerevisiae) (Ube2a), mRNA.	X	NM_019668.3	-1,02	**-1,60**	0,8608	**0,0095**
ILMN_2520174	S	**6530402F18Rik**				-1,01	**-1,60**	0,9751	**0,0313**
ILMN_2776922	S	**Glrx1**			NM_053108	-1,70	**-1,60**	0,0051	**0,0030**
ILMN_2944666	S	**Ifit3**	Mus musculus interferon-induced protein with tetratricopeptide repeats 3 (Ifit3), mRNA.	19	NM_010501.1	-1,65	**-1,60**	0,1051	**0,0010**
ILMN_2678755	S	**Rpl22l1**	Mus musculus ribosomal protein L22 like 1 (Rpl22l1), mRNA.	3	NM_026517.2	1,00	**-1,60**	NA	**0,0450**
ILMN_3123759	A	**Gas2l1**	Mus musculus growth arrest-specific 2 like 1 (Gas2l1), transcript variant beta, mRNA.	11	NM_144560.2	-1,57	**-1,60**	0,1403	**0,0114**
ILMN_1219717	S	**Sort1**	Mus musculus sortilin 1 (Sort1), mRNA.	3	NM_019972.2	-1,69	**-1,60**	0,0386	**0,0184**
ILMN_2921383	S	**Serpina6**	Mus musculus serine (or	12	NM_007618.2	-1,13	**-1,60**	0,6448	**0,0411**

			cysteine) peptidase inhibitor, clade A, member 6 (Serpina6), mRNA.						
ILMN_1236696	S	**1700007B13Rik**	PREDICTED: Mus musculus RIKEN cDNA 1700007B13 gene (1700007B13Rik), mRNA.		XM_913577.2	-1,46	**-1,61**	0,0754	**0,0231**
ILMN_2728802	S	**Arnt**	Mus musculus aryl hydrocarbon receptor nuclear translocator (Arnt), transcript variant 2, mRNA.	3	NM_009709.3	-1,03	**-1,61**	0,4226	**0,0142**
ILMN_2604179	S	**Lrrc3**	Mus musculus leucine rich repeat containing 3 (Lrrc3), mRNA.	10	NM_145152.3	-1,59	**-1,61**	0,0646	**0,0152**
ILMN_1255490	S	**D930042J21Rik**			AK086627	1,23	**-1,61**	0,3553	**0,0489**
ILMN_2511089	S	**Ugcg**			NM_011673	-1,37	**-1,61**	0,2051	**0,0074**
ILMN_1242167	S	**Hist2h2aa2**	Mus musculus histone cluster 2, H2aa2 (Hist2h2aa2), mRNA.		NM_178212.1	-1,32	**-1,62**	0,0305	**0,0061**
ILMN_1253316	S	**Polr3f**			NM_027417	-1,22	**-1,62**	0,1544	**0,0061**
ILMN_1250103	S	**Tle2**	Mus musculus transducin-like enhancer of split 2, homolog of Drosophila E(spl) (Tle2), mRNA.	10	NM_019725.1	-1,19	**-1,62**	0,3079	**0,0260**
ILMN_1249158	S	**Nfs1**	Mus musculus nitrogen fixation gene 1 (S. cerevisiae)	2	NM_010911.1	1,03	**-1,62**	0,9436	**0,0203**

			(Nfs1), mRNA.						
ILMN_2718266	S	**Fkbp5**	Mus musculus FK506 binding protein 5 (Fkbp5), mRNA.	17	NM_010220.2	-1,61	**-1,62**	0,1200	**0,0049**
ILMN_1240839	S	**Golt1a**	Mus musculus golgi transport 1 homolog A (S. cerevisiae) (Golt1a), mRNA.	1	NM_026680.4	-1,69	**-1,62**	0,0204	**0,0390**
ILMN_1227404	S	**C8b**	Mus musculus complement component 8, beta polypeptide (C8b), mRNA.	4	NM_133882.2	-3,78	**-1,62**	0,0201	**0,0063**
ILMN_2985497	S	**Naip2**	Mus musculus NLR family, apoptosis inhibitory protein 2 (Naip2), mRNA.	13	NM_010872.1	-1,25	**-1,63**	0,2952	**0,0325**
ILMN_2771331	S	**Hao1**	Mus musculus hydroxyacid oxidase 1, liver (Hao1), mRNA.	2	NM_010403.2	-1,33	**-1,63**	0,0501	**0,0070**
ILMN_3158509	A	**Mup5**	Mus musculus major urinary protein 5 (Mup5), mRNA.	4	NM_008649.2	-1,73	**-1,63**	0,0962	**0,0021**
ILMN_1246194	S	**LOC667370**	PREDICTED: Mus musculus similar to interferon-induced protein with tetratricopeptide repeats 3 (LOC667370), mRNA.		XM_001480084.1	-1,98	**-1,63**	0,2163	**0,0253**
ILMN_1247377	S	**Mpeg1**	Mus musculus macrophage	19	NM_010821.1	1,03	**-1,63**	0,7867	**0,0036**

			expressed gene 1 (Mpeg1), mRNA.						
ILMN_1242466	S	**Psmb9**	Mus musculus proteasome (prosome, macropain) subunit, beta type 9 (large multifunctional peptidase 2) (Psmb9), mRNA.	17	NM_013585.2	-1,39	**-1,64**	0,0895	**0,0247**
ILMN_2825803	S	**Parp14**	Mus musculus poly (ADP-ribose) polymerase family, member 14 (Parp14), mRNA. XM_901644 XM_916789 XM_924484 XM_924488	16	NM_001039530.1	1,01	**-1,64**	0,9517	**0,0068**
ILMN_1213448	S	**LOC669658**	PREDICTED: Mus musculus similar to melanoma antigen (LOC669658), mRNA.		XM_976371.1	-1,15	**-1,64**	0,7626	**0,0393**
ILMN_3068722	I	**Mapk6**	Mus musculus mitogen-activated protein kinase 6 (Mapk6), transcript variant 2, mRNA.	9	NM_027418.1	-1,04	**-1,64**	0,8435	**0,0393**
ILMN_3145814	A	**Ogfrl1**	Mus musculus opioid growth factor receptor-like 1 (Ogfrl1), mRNA.	1	NM_001081079.1	-1,91	**-1,64**	0,0248	**0,0026**

ILMN_2445548	S	**C330006A16Rik**				-1,60	**-1,64**	0,0655	**0,0152**
ILMN_2879921	S	**Phf8**	Mus musculus PHD finger protein 8 (Phf8), mRNA.	X	NM_177201.2	-1,62	**-1,64**	0,2233	**0,0404**
ILMN_2591782	S	**LOC100048313**	PREDICTED: Mus musculus similar to ABC transporter, transcript variant 1 (LOC100048313), mRNA.		XM_001480281.1	-1,14	**-1,65**	0,4946	**0,0131**
ILMN_2945348	S	**Glrx**	Mus musculus glutaredoxin (Glrx), mRNA.	13	NM_053108.2	-1,87	**-1,65**	0,0007	**0,0159**
ILMN_1221501	S	**5730469M10Rik**	Mus musculus RIKEN cDNA 5730469M10 gene (5730469M10Rik), mRNA.		NM_027464.3	-1,40	**-1,65**	0,0377	**0,0001**
ILMN_1230893	S	**LOC100045542**	PREDICTED: Mus musculus similar to FERMRhoGEF (Arhgef) and pleckstrin domain protein 1 (LOC100045542), mRNA.		XM_001473941.1	-1,47	**-1,65**	0,0412	**0,0203**
ILMN_2686069	S	**Gyg**	Mus musculus glycogenin (Gyg), mRNA.	3	NM_013755.2	1,10	**-1,66**	0,3850	**0,0035**
ILMN_1229183	S	**Nubp1**			AK020876	1,04	**-1,66**	0,7813	**0,0373**
ILMN_2457054	S	**Ung**	Mus musculus uracil DNA glycosylase (Ung), transcript variant 2, mRNA.	5	NM_011677.2	-1,01	**-1,66**	0,9697	**0,0350**
ILMN_2939681	S	**Lyzs**	Mus musculus lysozyme (Lyzs), mRNA.	10	NM_017372.2	2,13	**-1,66**	0,1608	**0,0408**
ILMN_3127932	A	**Tmem77**	Mus musculus transmembrane protein 77 (Tmem77), transcript variant 2, mRNA.	3	NM_026013.2	1,01	**-1,67**	0,9233	**0,0141**

ILMN_2763498	S	**Pycard**	Mus musculus PYD and CARD domain containing (Pycard), mRNA.	7	NM_023258.3	1,03	**-1,67**	0,8423	**0,0293**
ILMN_1242134	S	**D330003G07Rik**			AK052176	-1,08	**-1,67**	0,8474	**0,0397**
ILMN_2716838	S	**Hspa4**	Mus musculus heat shock protein 4 (Hspa4), mRNA.	11	NM_008300.3	1,00	**-1,67**	NA	**0,0239**
ILMN_2907964	S	**Crim2**	Mus musculus cysteine rich BMP regulator 2 (chordin like) (Crim2), mRNA.	6	NM_001029985.1	-1,65	**-1,67**	0,0061	**0,0125**
ILMN_1256128	S	**LOC100046469**	PREDICTED: Mus musculus similar to Plec1 protein, transcript variant 1 (LOC100046469), mRNA.		XM_001476518.1	-1,18	**-1,68**	0,3992	**0,0156**
ILMN_2587863	I	**2410091N08Rik**			XM_146886.1	1,80	**-1,68**	0,0332	**0,0266**
ILMN_2538010	S	**LOC385989**			XM_359026.1	1,06	**-1,68**	0,8313	**0,0233**
ILMN_2602597	S	**Sh3rf1**	Mus musculus SH3 domain containing ring finger 1 (Sh3rf1), mRNA.	8	NM_021506.2	1,05	**-1,68**	0,8022	**0,0317**
ILMN_2899318	S	**Rdh11**	Mus musculus retinol dehydrogenase 11 (Rdh11), mRNA.	12	NM_021557.2	-1,61	**-1,68**	0,1680	**0,0121**
ILMN_2658355	S	**Ugt3a2**	Mus musculus UDP glycosyltransferases 3 family, polypeptide A2 (Ugt3a2),	15	NM_144845.3	-2,30	**-1,69**	0,0071	**0,0026**

			mRNA.						
ILMN_2612117	S	**Agxt**	Mus musculus alanine-glyoxylate aminotransferase (Agxt), mRNA.	1	NM_016702.2	1,14	**-1,69**	0,4531	**0,0165**
ILMN_2677046	S	**Gstp1**	Mus musculus glutathione S-transferase, pi 1 (Gstp1), mRNA.	19	NM_013541.1	1,08	**-1,69**	0,3134	**0,0170**
ILMN_2665063	S	**Slc11a2**	Mus musculus solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2 (Slc11a2), mRNA.	15	NM_008732.1	-1,03	**-1,69**	0,4727	**0,0478**
ILMN_1245637	S	**A930015C19Rik**			AK044477	-1,15	**-1,69**	0,5418	**0,0114**
ILMN_2964324	S	**Igfbp5**	Mus musculus insulin-like growth factor binding protein 5 (Igfbp5), mRNA.	1	NM_010518.2	-1,32	**-1,70**	0,3234	**0,0453**
ILMN_1259808	S	**LOC386235**			XM_359130.1	1,25	**-1,70**	0,6603	**0,0487**
ILMN_2620871	S	**Hrh1**	Mus musculus histamine receptor H1 (Hrh1), mRNA.	6	NM_008285.3	-1,14	**-1,70**	0,7318	**0,0067**
ILMN_2596183	S	**Syde1**	PREDICTED: Mus musculus synapse defective 1, Rho GTPase, homolog 1 (C.	10	XM_359260.3	1,15	**-1,70**	0,5908	**0,0361**

			elegans) (Syde1), mRNA.						
ILMN_1253156	S	**LOC381502**			XM_355459.1	1,17	**-1,70**	0,5419	**0,0406**
ILMN_1254276	S	**Hist2h2ac**	Mus musculus histone cluster 2, H2ac (Hist2h2ac), mRNA.	3	NM_175662.1	-1,35	**-1,71**	0,0657	**0,0030**
ILMN_2576431	S	**Lpin2**			AK048657	-1,13	**-1,71**	0,5947	**0,0192**
ILMN_2614432	S	**Egfr**			NM_207655.1	-2,34	**-1,71**	0,0170	**0,0153**
ILMN_2683113	S	**Ang1**			NM_007447	-1,29	**-1,71**	0,4913	**0,0346**
ILMN_1249220	S	**Col6a3**	Mus musculus procollagen, type VI, alpha 3 (Col6a3), mRNA.		NM_009935.1	-1,02	**-1,71**	0,9631	**0,0084**
ILMN_1241818	S	**Cyp2c54**	Mus musculus cytochrome P450, family 2, subfamily c, polypeptide 54 (Cyp2c54), mRNA.	19	NM_206537.1	-3,44	**-1,71**	0,0065	**0,0162**
ILMN_1251504	S	**Cyp4v3**	Mus musculus cytochrome P450, family 4, subfamily v, polypeptide 3 (Cyp4v3), mRNA.	8	NM_133969.2	-1,45	**-1,71**	0,0755	**0,0050**
ILMN_2732707	S	**Kcnq1**	Mus musculus potassium voltage-gated channel, subfamily Q, member 1 (Kcnq1), mRNA.	7	NM_008434.2	1,09	**-1,71**	0,7113	**0,0122**
ILMN_2814107	S	**Olfr725**	Mus musculus olfactory receptor 725 (Olfr725),	14	NM_146317.1	-1,02	**-1,72**	0,9262	**0,0012**

			mRNA.						
ILMN_2615837	S	**Cstf3**	Mus musculus cleavage stimulation factor, 3' pre-RNA, subunit 3 (Cstf3), transcript variant 1, mRNA.	2	NM_145529.2	-1,06	**-1,72**	0,7464	**0,0381**
ILMN_2625280	S	**Grb14**	Mus musculus growth factor receptor bound protein 14 (Grb14), mRNA.	2	NM_016719.1	-1,66	**-1,72**	0,0906	**0,0018**
ILMN_2701582	S	**Cbs**	Mus musculus cystathionine beta-synthase (Cbs), transcript variant 1, mRNA.	17	NM_144855.2	-1,26	**-1,72**	0,1464	**0,0127**
ILMN_1233339	S	**Nme4**	Mus musculus non-metastatic cells 4, protein expressed in (Nme4), nuclear gene encoding mitochondrial protein, mRNA.	17	NM_019731.1	-1,05	**-1,73**	0,4226	**0,0033**
ILMN_1228366	S	**Cdkn2c**	Mus musculus cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4) (Cdkn2c), mRNA.	4	NM_007671.2	-1,99	**-1,73**	0,0543	**0,0290**
ILMN_2447658	S	**Rgp1**	Mus musculus	4	NM_172866.3	-1,35	**-1,73**	0,0863	**0,0274**

			RGP1 retrograde golgi transport homolog (S. cerevisiae) (Rgp1), mRNA.						
ILMN_2570875	S	**E130309L16Rik**			AK053808	1,35	**-1,74**	0,1121	**0,0109**
ILMN_2748164	S	**Hist1h3f**	Mus musculus histone cluster 1, H3f (Hist1h3f), mRNA.	13	NM_013548.2	1,07	**-1,74**	0,8186	**0,0133**
ILMN_2965737	S	**Klhl34**	Mus musculus kelch-like 34 (Drosophila) (Klhl34), mRNA.	X	NM_001081667.1	-1,47	**-1,75**	0,3304	**0,0205**
ILMN_2663281	S	**2310045A20Rik**	Mus musculus RIKEN cDNA 2310045A20 gene (2310045A20Rik), mRNA.		NM_172710.3	-1,09	**-1,75**	0,8041	**0,0324**
ILMN_2986051	S	**Ccbl1**	Mus musculus cysteine conjugate-beta lyase 1 (Ccbl1), mRNA.	2	NM_172404.2	-2,32	**-1,75**	0,0132	**0,0125**
ILMN_3128725	A	**Egfr**	Mus musculus epidermal growth factor receptor (Egfr), transcript variant 2, mRNA.	11	NM_007912.4	-3,25	**-1,76**	0,0020	**0,0005**
ILMN_2881864	S	**Cfhr1**	Mus musculus complement factor H-related 1 (Cfhr1), mRNA.	1	NM_015780.1	-1,14	**-1,76**	0,4485	**0,0081**
ILMN_2692527	S	**5730593N15Rik**			NM_175263	-2,28	**-1,76**	0,0482	**0,0232**
ILMN_2500533	S	**Amigo2**	Mus musculus adhesion	15	NM_178114.3	-2,29	**-1,76**	0,0688	**0,0311**

			molecule with Ig like domain 2 (Amigo2), mRNA.						
ILMN_3041654	I	**BC026782**	Mus musculus cDNA sequence BC026782 (BC026782), mRNA.	1	NM_001025575.1	1,07	**-1,77**	0,6234	**0,0091**
ILMN_3160137	S	**Aldoc**	Mus musculus aldolase C, fructose-bisphosphate (Aldoc), mRNA.		NM_009657.3	-2,01	**-1,77**	0,0930	**0,0038**
ILMN_3052260	I	**Egfr**	Mus musculus epidermal growth factor receptor (Egfr), transcript variant 2, mRNA.	11	NM_007912.4	-3,37	**-1,77**	0,0025	**0,0140**
ILMN_2739797	S	**Olfr427**	Mus musculus olfactory receptor 427 (Olfr427), mRNA.		NM_207158.1	1,18	**-1,77**	0,7244	**0,0213**
ILMN_2773835	S	**LOC670044**	PREDICTED: Mus musculus similar to Mothers against decapentaplegic homolog 6 (SMAD 6) (Mothers against DPP homolog 6) (Smad6) (Mad homolog 7) (LOC670044), mRNA.		XM_978692.1	-1,78	**-1,78**	0,0472	**0,0379**
ILMN_1218058	S	**Atp1a1**	Mus musculus ATPase, Na+/K+ transporting, alpha 1 polypeptide (Atp1a1), mRNA.	3	NM_144900.1	-1,68	**-1,78**	0,0029	**0,0017**
ILMN_1252185	S	**Rbp4**	Mus musculus retinol binding protein 4, plasma (Rbp4),	19	NM_011255.2	-1,33	**-1,79**	0,0764	**0,0077**

			mRNA.						
ILMN_1238542	S	**2810405K02Rik**	Mus musculus RIKEN cDNA 2810405K02 gene (2810405K02Rik), mRNA.	4	NM_025582.3	-1,80	**-1,79**	0,0057	**0,0077**
ILMN_1221684	S	**Scp2**	Mus musculus sterol carrier protein 2, liver (Scp2), mRNA.	4	NM_011327.2	-1,41	**-1,80**	0,1605	**0,0104**
ILMN_1245298	S	**D130050K19Rik**			AK051465	-1,21	**-1,80**	0,5128	**0,0107**
ILMN_2823778	S	**Sc4mol**	Mus musculus sterol-C4-methyl oxidase-like (Sc4mol), mRNA.	8	NM_025436.1	-1,32	**-1,80**	0,5180	**0,0161**
ILMN_1221822	S	**Rbm12**	Mus musculus RNA binding motif protein 12 (Rbm12), transcript variant 2, mRNA.	2	NM_170598.2	-1,48	**-1,81**	0,2246	**0,0053**
ILMN_1224485	S	**Eme2**			XM_128555.4	1,29	**-1,82**	0,5598	**0,0376**
ILMN_1220307	S	**LOC100046025**	PREDICTED: Mus musculus similar to mKIAA1230 protein, transcript variant 1 (LOC100046025), mRNA.		XM_001475823.1	-1,60	**-1,82**	0,0104	**0,0106**
ILMN_1241496	S	**9030024J15Rik**				-3,45	**-1,82**	0,0049	**0,0238**
ILMN_2678355	S	**Amigo2**	Mus musculus adhesion molecule with Ig like domain 2 (Amigo2), mRNA.	15	NM_178114.3	-1,90	**-1,83**	0,0478	**0,0094**
ILMN_1221272	S	**LOC381294**	PREDICTED: Mus musculus complement factor H-like (LOC381294), mRNA.		XM_981749.1	-1,51	**-1,83**	0,1699	**0,0160**

ILMN_2796798	S	**5730469M10Rik**	Mus musculus RIKEN cDNA 5730469M10 gene (5730469M10Rik), mRNA.	14	NM_027464.1	-1,35	**-1,83**	0,1043	**0,0060**
ILMN_2727273	S	**Swap70**	Mus musculus SWA-70 protein (Swap70), mRNA.	7	NM_009302.2	-1,24	**-1,84**	0,2126	**0,0147**
ILMN_1237259	S	**Mug-ps1**				-1,88	**-1,85**	0,0661	**0,0049**
ILMN_2692927	S	**Srd5a1**			NM_175283.2	-1,89	**-1,85**	0,0148	**0,0008**
ILMN_2468635	S	**MJ-1000-77_495**				-1,02	**-1,86**	0,9231	**0,0368**
ILMN_2674643	S	**Tdo2**	Mus musculus tryptophan 2,3-dioxygenase (Tdo2), mRNA.	3	NM_019911.2	1,55	**-1,87**	0,1027	**0,0455**
ILMN_2724433	S	**B3gat1**	Mus musculus beta-1,3-glucuronyltransferase 1 (glucuronosyltransferase P) (B3gat1), mRNA.	9	NM_029792.1	1,15	**-1,87**	0,5683	**0,0150**
ILMN_2623735	S	**Ccbl1**	Mus musculus cysteine conjugate-beta lyase 1 (Ccbl1), mRNA.	2	NM_172404.2	-2,91	**-1,87**	0,0295	**0,0051**
ILMN_1250776	S	**Arhgap6**			AK048162	-1,97	**-1,88**	0,0365	**0,0219**
ILMN_2645275	S	**Mvd**	Mus musculus mevalonate (diphospho) decarboxylase (Mvd), mRNA.	8	NM_138656.1	-2,03	**-1,88**	0,4237	**0,0465**
ILMN_3150724	A	**Ppfibp1**	Mus musculus PTPRF interacting	6	NM_026221.1	-1,08	**-1,88**	0,7505	**0,0167**

			protein, binding protein 1 (liprin beta 1) (Ppfibp1), mRNA.						
ILMN_1215824	S	**Sec22l2**			NM_133704.3	-1,13	**-1,89**	0,6216	**0,0107**
ILMN_2619574	S	**Slc35e3**	Mus musculus solute carrier family 35, member E3 (Slc35e3), mRNA.	10	NM_029875.2	-1,29	**-1,89**	0,0711	**0,0083**
ILMN_1243763	S	**B230349N02Rik**			AK046195	1,11	**-1,89**	0,5293	**0,0408**
ILMN_2900042	S	**Gba2**	Mus musculus glucosidase beta 2 (Gba2), mRNA.	4	NM_172692.1	-2,01	**-1,89**	0,1192	**0,0225**
ILMN_2772077	S	**Bok**			NM_016778	-1,08	**-1,90**	0,5668	**0,0020**
ILMN_2961221	S	**Slco2a1**	Mus musculus solute carrier organic anion transporter family, member 2a1 (Slco2a1), mRNA.		NM_033314.2	-2,01	**-1,90**	0,0310	**0,0010**
ILMN_1258645	S	**4833442A19Rik**			AK029468	1,09	**-1,90**	0,7797	**0,0456**
ILMN_2913855	S	**Olfr1166**	Mus musculus olfactory receptor 1166 (Olfr1166), mRNA.	2	NM_146650.2	1,03	**-1,91**	0,9395	**0,0360**
ILMN_2793806	S	**Mug2**	Mus musculus murinoglobulin 2 (Mug2), mRNA.	6	NM_008646.1	-2,20	**-1,91**	0,0244	**0,0001**
ILMN_2731024	S	**Pah**	Mus musculus phenylalanine hydroxylase (Pah), mRNA.	10	NM_008777.2	1,03	**-1,92**	0,8392	**0,0025**
ILMN_1231439	S	**Aatk**	Mus musculus apoptosis-associated tyrosine kinase (Aatk), mRNA.	11	NM_007377.3	-1,64	**-1,92**	0,0531	**0,0248**

ILMN_1214562	S	**4933405P16Rik**			AK016678	-1,21	**-1,93**	0,2980	**0,0141**
ILMN_2826264	S	**Serinc2**	Mus musculus serine incorporator 2 (Serinc2), mRNA.	4	NM_172702.1	-2,29	**-1,94**	0,0681	**0,0159**
ILMN_2693922	S	**Egfr**	Mus musculus epidermal growth factor receptor (Egfr), transcript variant 1, mRNA.	11	NM_207655.2	-2,53	**-1,95**	0,0211	**0,0078**
ILMN_1230710	S	**C730039N23Rik**			AK050344	1,79	**-1,96**	0,0477	**0,0009**
ILMN_2683432	S	**Mug1**	Mus musculus murinoglobulin 1 (Mug1), mRNA. XM_981606	6	NM_008645.2	-1,51	**-1,96**	0,0608	**0,0002**
ILMN_2600348	S	**Sqle**	Mus musculus squalene epoxidase (Sqle), mRNA.	15	NM_009270.3	-1,73	**-1,96**	0,2189	**0,0068**
ILMN_1221503	S	**Ccnd1**			NM_007631.1	-1,97	**-1,97**	0,0926	**0,0148**
ILMN_2740187	S	**LOC100044443**	PREDICTED: Mus musculus similar to cytochrome P450IIIA25 (LOC100044443), misc RNA.		XR_030683.1	1,09	**-1,97**	0,7756	**0,0091**
ILMN_1242082	S	**4632408I12Rik**			AK076276	-1,13	**-1,98**	0,4757	**0,0055**
ILMN_1221786	S	**LOC383698**			XM_357193.1	1,37	**-1,98**	0,4360	**0,0352**
ILMN_2747302	S	**Slc25a32**	Mus musculus solute carrier family 25, member 32 (Slc25a32), mRNA.	15	NM_172402.2	-1,08	**-1,99**	0,6933	**0,0057**
ILMN_2631948	S	**Gulo**	Mus musculus gulonolactone (L-) oxidase (Gulo), mRNA.	14	NM_178747.2	-1,93	**-1,99**	0,0071	**0,0001**

ILMN_1252762	S	**Trib3**	Mus musculus tribbles homolog 3 (Drosophila) (Trib3), mRNA.	2	NM_175093.2	-1,64	**-1,99**	0,0633	**0,0054**
ILMN_1242911	S	**Hmgb1**	Mus musculus high mobility group box 1 (Hmgb1), mRNA.	5	NM_010439.3	1,52	**-2,00**	0,2082	**0,0054**
ILMN_2531773	S	**BC048546**	Mus musculus cDNA sequence BC048546 (BC048546), mRNA.	6	NM_001001179.2	-1,67	**-2,01**	0,1258	**0,0044**
ILMN_2984219	S	**BC048546**	Mus musculus cDNA sequence BC048546 (BC048546), mRNA.	6	NM_001001179.1	-1,48	**-2,02**	0,1496	**0,0042**
ILMN_2667091	S	**Ppp1r3c**	Mus musculus protein phosphatase 1, regulatory (inhibitor) subunit 3C (Ppp1r3c), mRNA.		NM_016854.2	-1,84	**-2,03**	0,0250	**0,0025**
ILMN_1243188	S	**Chchd3**	Mus musculus coiled-coil-helix-coiled-coil-helix domain containing 3 (Chchd3), mRNA.	6	NM_025336.1	-1,41	**-2,06**	0,4808	**0,0184**
ILMN_2737163	S	**Sqle**	Mus musculus squalene epoxidase (Sqle), mRNA.	15	NM_009270.3	-1,43	**-2,08**	0,3056	**0,0063**
ILMN_2705424	S	**Slc39a5**	Mus musculus solute carrier family 39	10	NM_028051.2	1,03	**-2,08**	0,8323	**0,0039**

			(metal ion transporter), member 5 (Slc39a5), mRNA.						
ILMN_2596917	S	**LOC100044475**	PREDICTED: Mus musculus similar to SH2/SH3 adaptor protein (LOC100044475), mRNA.		XM_001472256.1	-1,27	**-2,10**	0,1958	**0,0090**
ILMN_2636004	S	**9530064J02**			XM_489200	-1,44	**-2,13**	0,0191	**0,0000**
ILMN_2601471	S	**Ccnd1**			NM_007631.1	-1,97	**-2,14**	0,0728	**0,0045**
ILMN_1234449	S	**Hsd3b5**	Mus musculus hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 5 (Hsd3b5), mRNA.	3	NM_008295.2	-3,28	**-2,15**	0,3152	**0,0041**
ILMN_1254987	S	**Mbnl2**	Mus musculus muscleblind-like 2 (Mbnl2), transcript variant 1, mRNA.	14	NM_175341.4	-1,10	**-2,16**	0,5446	**0,0033**
ILMN_1256103	S	**Ccbl2**	Mus musculus cysteine conjugate-beta lyase 2 (Ccbl2), mRNA.	3	NM_173763.3	-1,90	**-2,18**	0,0090	**0,0140**
ILMN_2957054	S	**Cyp26a1**	Mus musculus cytochrome P450, family 26, subfamily a, polypeptide 1 (Cyp26a1), mRNA.	19	NM_007811.1	-1,40	**-2,19**	0,4908	**0,0058**
ILMN_2685157	S	**Abcc3**	Mus musculus ATP-binding	11	NM_029600.3	-2,87	**-2,22**	0,0116	**0,0109**

			cassette, sub-family C (CFTR/MRP), member 3 (Abcc3), mRNA.						
ILMN_3054914	I	**Usp18**	Mus musculus ubiquitin specific peptidase 18 (Usp18), mRNA.	6	NM_011909.1	-1,42	**-2,26**	0,4327	**0,0089**
ILMN_2931918	S	**4432416J03Rik**	Mus musculus RIKEN cDNA 4432416J03 gene (4432416J03Rik), mRNA.	9	NM_030069.1	-4,14	**-2,26**	0,0014	**0,0067**
ILMN_3138743	A	**Acsl3**	Mus musculus acyl-CoA synthetase long-chain family member 3 (Acsl3), transcript variant 1, mRNA.	1	NM_028817.2	-1,93	**-2,27**	0,0491	**0,0037**
ILMN_1216539	S	**Cml4**	Mus musculus camello-like 4 (Cml4), mRNA.	6	NM_023455.2	1,21	**-2,27**	0,2300	**0,0479**
ILMN_2806439	S	**Slc17a8**	Mus musculus solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 8 (Slc17a8), mRNA.	10	NM_182959.2	-2,67	**-2,28**	0,1045	**0,0122**

ILMN_1223230	S	**Gstp1**	Mus musculus glutathione S-transferase, pi 1 (Gstp1), mRNA.	19	NM_013541.1	1,11	**-2,28**	0,4067	**0,0000**
ILMN_2685043	S	**Mug2**	Mus musculus murinoglobulin 2 (Mug2), mRNA.		NM_008646.3	-2,34	**-2,30**	0,0331	**0,0011**
ILMN_2629191	S	**Cpm**	PREDICTED: Mus musculus carboxypeptidase M (Cpm), mRNA.	10	XM_994613.1	-1,41	**-2,32**	0,1738	**0,0260**
ILMN_1231939	S	**Ccbl2**	Mus musculus cysteine conjugate-beta lyase 2 (Ccbl2), mRNA.	3	NM_173763.3	-1,66	**-2,36**	0,0072	**0,0010**
ILMN_2769991	S	**Cyp2c29**	Mus musculus cytochrome P450, family 2, subfamily c, polypeptide 29 (Cyp2c29), mRNA.	19	NM_007815.3	-1,20	**-2,36**	0,3581	**0,0098**
ILMN_1240332	S	**Zdhhc14**	Mus musculus zinc finger, DHHC domain containing 14 (Zdhhc14), mRNA.	17	NM_146073.3	-1,68	**-2,37**	0,1053	**0,0085**
ILMN_1229990	S	**Agxt2l1**	Mus musculus alanine-glyoxylate aminotransferase 2-like 1 (Agxt2l1), mRNA.	3	NM_027907.2	-1,34	**-2,40**	0,5417	**0,0203**
ILMN_2627733	S	**Slc46a3**	Mus musculus solute carrier family 46,	5	NM_027872.3	-2,06	**-2,41**	0,0068	**0,0144**

			member 3 (Slc46a3), mRNA.						
ILMN_1257851	S	**LOC384273**			XM_357532.1	-3,43	**-2,41**	0,0041	**0,0189**
ILMN_2669793	S	**Ccnd1**	Mus musculus cyclin D1 (Ccnd1), mRNA.	7	NM_007631.2	-2,24	**-2,41**	0,1204	**0,0050**
ILMN_2433848	S	**Slco2a1**			NM_033314	-2,46	**-2,41**	0,0112	**0,0039**
ILMN_1213458	S	**Fbxo18**	Mus musculus F-box protein 18 (Fbxo18), mRNA.	2	NM_015792.1	-1,01	**-2,41**	0,9506	**0,0217**
ILMN_2699052	S	**Nrn1**	Mus musculus neuritin 1 (Nrn1), mRNA.	13	NM_153529.1	-1,57	**-2,42**	0,0155	**0,0038**
ILMN_1254902	S	**Rdh9**	Mus musculus retinol dehydrogenase 9 (Rdh9), mRNA.	10	NM_153133.2	-2,68	**-2,44**	0,0043	**0,0040**
ILMN_2696026	S	**Npr2**	Mus musculus natriuretic peptide receptor 2 (Npr2), mRNA.	4	NM_173788.3	-3,10	**-2,45**	0,0141	**0,0233**
ILMN_2961216	S	**Slco2a1**	Mus musculus solute carrier organic anion transporter family, member 2a1 (Slco2a1), mRNA.		NM_033314.2	-1,89	**-2,49**	0,0181	**0,0053**
ILMN_2661820	S	**Agxt2l1**	Mus musculus alanine-glyoxylate aminotransferase 2-like 1 (Agxt2l1), mRNA.	3	NM_027907.1	-1,32	**-2,51**	0,5594	**0,0069**
ILMN_2698499	S	**Nox4**	Mus musculus NADPH oxidase 4 (Nox4), mRNA.		NM_015760.4	-1,33	**-2,51**	0,0379	**0,0044**
ILMN_1223285	S	**Hspa2**	Mus musculus heat shock	12	NM_001002012.1	-1,62	**-2,53**	0,1419	**0,0105**

			protein 2 (Hspa2), transcript variant 2, mRNA.						
ILMN_2749717	S	**Bcl3**	Mus musculus B-cell leukemia/lymphoma 3 (Bcl3), mRNA.	7	NM_033601.1	-2,34	**-2,62**	0,0336	**0,0169**
ILMN_1238433	S	**Rbp1**			NM_011254.2	-1,03	**-2,62**	0,8852	**0,0047**
ILMN_2436561	S	**Tmem19**	Mus musculus transmembrane protein 19 (Tmem19), mRNA.		NM_133683.3	-1,92	**-2,68**	0,0220	**0,0011**
ILMN_2543285	S	**Elovl3**			AK004901	-1,16	**-2,69**	0,6936	**0,0399**
ILMN_2590923	S	**Idi1**	Mus musculus isopentenyl-diphosphate delta isomerase (Idi1), transcript variant 2, mRNA.	13	NM_177960.3	-1,98	**-2,77**	0,1955	**0,0045**
ILMN_3125606	A	**D12Ertd647e**	Mus musculus DNA segment, Chr 12, ERATO Doi 647, expressed (D12Ertd647e), transcript variant 5, mRNA.	12	NM_194069.1	-2,52	**-2,77**	0,0015	**0,0037**
ILMN_2433990	S	**LOC100048346**	PREDICTED: Mus musculus similar to ubiquitin specific protease UBP43 (LOC100048346), mRNA.		XM_001480051.1	-1,92	**-2,88**	0,1206	**0,0041**
ILMN_1220301	S	**Cebpe**	Mus musculus CCAAT/enhancer binding protein (C/EBP),	14	NM_207131.1	-3,52	**-2,91**	0,0062	**0,0065**

			epsilon (Cebpe), mRNA.						
ILMN_1215252	S	**Bmp4**	Mus musculus bone morphogenetic protein 4 (Bmp4), mRNA.	14	NM_007554.2	-1,18	**-2,92**	0,4679	**0,0035**
ILMN_2772632	S	**Saa3**	Mus musculus serum amyloid A 3 (Saa3), mRNA.	7	NM_011315.3	-1,55	**-2,96**	0,2225	**0,0020**
ILMN_2752545	S	**Lama3**			XM_128926.3	1,00	**-2,98**	NA	**0,0035**
ILMN_3000236	S	**F11**	Mus musculus coagulation factor XI (F11), mRNA.	8	NM_028066.1	-3,23	**-2,99**	0,0002	**0,0044**
ILMN_2776056	S	**Rassf3**	Mus musculus Ras association (RalGDS/AF-6) domain family member 3 (Rassf3), mRNA.	10	NM_138956.3	-1,68	**-3,03**	0,0026	**0,0027**
ILMN_2504842	S	**Ugt1a12**			NM_201644	-4,08	**-3,03**	0,0144	**0,0017**
ILMN_2596522	S	**Mt1**	Mus musculus metallothionein 1 (Mt1), mRNA.	8	NM_013602.2	-1,36	**-3,04**	0,4390	**0,0090**
ILMN_3120510	A	**Gvin1**	Mus musculus GTPase, very large interferon inducible 1 (Gvin1), transcript variant B, mRNA.	7	NM_001039160.2	-1,33	**-3,12**	0,5215	**0,0129**
ILMN_2682207	S	**Elovl3**	Mus musculus elongation of	19	NM_007703.1	1,00	**-3,12**	NA	**0,0383**

			very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 3 (Elovl3), mRNA.						
ILMN_1246137	S	**1810005K13Rik**				-2,97	**-3,14**	0,0176	**0,0019**
ILMN_2681232	S	**D12Ertd647e**	Mus musculus DNA segment, Chr 12, ERATO Doi 647, expressed (D12Ertd647e), transcript variant 4, mRNA.	12	NM_194068.1	-2,81	**-3,14**	0,0011	**0,0095**
ILMN_2671435	S	**LOC223672**			XM_128064.4	-2,06	**-3,17**	0,0153	**0,0025**
ILMN_1242999	S	**Avpr1a**	Mus musculus arginine vasopressin receptor 1A (Avpr1a), mRNA.	10	NM_016847.2	-7,01	**-3,27**	0,0002	**0,0108**
ILMN_2609762	S	**F11**	Mus musculus coagulation factor XI (F11), mRNA.	8	NM_028066.1	-3,32	**-3,41**	0,0000	**0,0003**
ILMN_3131679	A	**Usp18**	Mus musculus ubiquitin specific peptidase 18 (Usp18), mRNA.	6	NM_011909.1	-1,70	**-3,43**	0,0774	**0,0054**
ILMN_2424150	S	**1500017E21Rik**				-4,60	**-3,72**	0,0316	**0,0057**
ILMN_1213838	S	**Arhgap26**	Mus musculus Rho GTPase activating protein 26 (Arhgap26), mRNA.	18	NM_175164.4	-2,71	**-3,74**	0,0055	**0,0283**

ILMN_1236044	S	**F11**	Mus musculus coagulation factor XI (F11), mRNA.	8	NM_028066.1	-4,28	**-3,90**	0,0002	**0,0006**
ILMN_1234552	S	**Hsd17b6**	Mus musculus hydroxysteroid (17-beta) dehydrogenase 6 (Hsd17b6), mRNA.	10	NM_013786.2	1,06	**-4,08**	0,8426	**0,0003**
ILMN_2740464	S	**Il1rap**	Mus musculus interleukin 1 receptor accessory protein (Il1rap), transcript variant 1, mRNA.	16	NM_008364.1	-4,09	**-4,08**	0,0014	**0,0013**
ILMN_1239293	S	**Sulf2**	Mus musculus sulfatase 2 (Sulf2), mRNA.	2	NM_028072.4	-3,29	**-4,12**	0,0085	**0,0016**
ILMN_2740465	S	**Il1rap**	Mus musculus interleukin 1 receptor accessory protein (Il1rap), transcript variant 1, mRNA.	16	NM_008364.1	-3,84	**-4,28**	0,0011	**0,0004**
ILMN_2622856	S	**Apol9b**	Mus musculus apolipoprotein L 9b (Apol9b), mRNA.	15	NM_173743.3	-2,77	**-4,34**	0,0077	**0,0001**
ILMN_2677824	S	**Susd4**	Mus musculus sushi domain containing 4 (Susd4), mRNA.		NM_144796.4	-1,01	**-4,35**	0,4226	**0,0119**
ILMN_3005740	S	**Zap70**	Mus musculus zeta-chain (TCR) associated protein kinase (Zap70),	1	NM_009539.2	-4,28	**-4,36**	0,0146	**0,0001**

			mRNA.						
ILMN_2818498	S	**OTTMUSG00000000231**	Mus musculus predicted gene, OTTMUSG00000000231 (OTTMUSG00000000231), mRNA.	4	NM_001009550.1	-2,44	**-4,37**	0,0212	**0,0001**
ILMN_1243228	S	**Il1rap**	Mus musculus interleukin 1 receptor accessory protein (Il1rap), transcript variant 2, mRNA.	16	NM_134103.1	-3,75	**-4,43**	0,0065	**0,0013**
ILMN_2793329	S	**Gstp1**	Mus musculus glutathione S-transferase, pi 1 (Gstp1), mRNA.	19	NM_013541.1	-1,28	**-4,46**	0,1887	**0,0006**
ILMN_2706269	S	**Hspb1**	Mus musculus heat shock protein 1 (Hspb1), mRNA.	5	NM_013560.1	-5,72	**-4,47**	0,0077	**0,0002**
ILMN_1237485	S	**2310040A07Rik**	PREDICTED: Mus musculus RIKEN cDNA 2310040A07 gene (2310040A07Rik), mRNA.		XM_912979.2	-3,47	**-4,55**	0,1072	**0,0068**
ILMN_3029849	I	**Cebpe**	Mus musculus CCAAT/enhancer binding protein (C/EBP), epsilon (Cebpe), mRNA.	14	NM_207131.1	-3,05	**-4,66**	0,0050	**0,0032**
ILMN_2890935	S	**Avpr1a**	Mus musculus arginine vasopressin receptor 1A	10	NM_016847.2	-4,41	**-4,74**	0,0058	**0,0047**

			(Avpr1a), mRNA.						
ILMN_1225528	S	**Trib3**	Mus musculus tribbles homolog 3 (Drosophila) (Trib3), mRNA.	2	NM_175093.2	-3,34	**-4,74**	0,0366	**0,0366**
ILMN_2621752	S	**Irf5**	Mus musculus interferon regulatory factor 5 (Irf5), mRNA.		NM_012057.3	-3,94	**-4,74**	0,0017	**0,0096**
ILMN_1254622	S	**Pcp4l1**	PREDICTED: Mus musculus Purkinje cell protein 4-like 1 (Pcp4l1), mRNA.	1	XM_484933.5	-5,48	**-5,02**	0,0176	**0,0123**
ILMN_1227225	S	**Trim28**	Mus musculus tripartite motif protein 28 (Trim28), mRNA.	7	NM_011588.2	-5,36	**-5,15**	0,0078	**0,0013**
ILMN_2798129	S	**C6**	Mus musculus complement component 6 (C6), mRNA.	15	NM_016704.1	-1,34	**-5,25**	0,1849	**0,0092**
ILMN_1246808	S	**Serpine2**			AK045954	-1,44	**-5,26**	0,2285	**0,0016**
ILMN_2654582	S	**Cyp2c44**	Mus musculus cytochrome P450, family 2, subfamily c, polypeptide 44 (Cyp2c44), mRNA.	19	NM_001001446.2	-5,56	**-5,41**	0,0012	**0,0006**
ILMN_2479977	S	**2310040A07Rik**	PREDICTED: Mus musculus RIKEN cDNA 2310040A07 gene (2310040A07Rik), mRNA.		XM_912979.2	-3,72	**-5,48**	0,0599	**0,0313**
ILMN_1258323	S	**Slco1a4**	Mus musculus solute carrier organic anion transporter family, member	6	NM_030687.1	-1,91	**-6,05**	0,0534	**0,0015**

			1a4 (Slco1a4), mRNA.						
ILMN_2513870	S	**Zap70**	Mus musculus zeta-chain (TCR) associated protein kinase (Zap70), mRNA.	1	NM_009539.2	-9,00	**-6,08**	0,0093	**0,0132**
ILMN_1216720	S	**C6**	Mus musculus complement component 6 (C6), mRNA.	15	NM_016704.1	-1,87	**-6,27**	0,1022	**0,0093**
ILMN_2917386	S	**Gstp2**	Mus musculus glutathione S-transferase, pi 2 (Gstp2), mRNA.	19	NM_181796.2	-1,16	**-6,27**	0,6768	**0,0005**
ILMN_1226650	S	**Il1rap**	Mus musculus interleukin 1 receptor accessory protein (Il1rap), transcript variant 2, mRNA.	16	NM_134103.1	-4,68	**-7,03**	0,0012	**0,0109**
ILMN_2770040	S	**Dct**	Mus musculus dopachrome tautomerase (Dct), mRNA.	14	NM_010024.1	-6,61	**-7,50**	0,0047	**0,0017**
ILMN_2643513	S	**Asns**	Mus musculus asparagine synthetase (Asns), mRNA.		NM_012055.3	1,00	**-7,92**	NA	**0,0442**
ILMN_1251894	S	**Dct**	Mus musculus dopachrome tautomerase (Dct), mRNA.	14	NM_010024.2	-9,25	**-8,57**	0,0107	**0,0165**
ILMN_2601215	S	**Cyp7b1**	Mus musculus cytochrome P450, family 7, subfamily b, polypeptide 1	3	NM_007825.3	-6,20	**-10,15**	0,0072	**0,0053**

			(Cyp7b1), mRNA.						
ILMN_2664202	S	**Rarres1**	PREDICTED: Mus musculus retinoic acid receptor responder (tazarotene induced) 1 (Rarres1), mRNA.	3	XM_001475793.1	-15,35	**-48,08**	0,0005	**0,0005**

Supporting Table 2. Sequences of primers used in the current study.

Name	***Forward (5'-)***	***Reverse (5'-)***
	RT-qPCR	
β-actin	CTAAGGCCAACCGTGAAAAGAT	CACAGCCTGGATGGCTACGT
18S rRNA	CGC CGC TAG AGG TGA AAT TC	CCA GTC GGC ATC GTT TAT GG
FSP27	GAC CTC CTG AAC AAG GTC CA	TAG CTG GGC TCT CTT CTT GC
c-Cbl	AAA GGA CGG CAT CTT CCT C	GAT CCT CAC GTC CTT GTC C
Cyp17a1	TGC CCC TGG TGG GTA GTC TA	CAT GCA TAT GAC CAC GTC TGG
Cyp2a4	AGC AGG CTA CCT TCG ACT GG	GCT GCT GAA GGC TAT GCC AT
Cyp2b13	GAA CTG AGA CTA CCA GCA CCA CTC T	TGA GCA TGA GCA GGA AAC CAC T
Cyp2b9	CTG AGA CCA CAA GCG CCA C	CTT GAG CAT GAG CAG GAC TCC
Cyp2d9	AGT CTC TGG CTT AAT TCC TGA GGT T	CGC AAG AGT ATC GGG AAT GC
Cyp7b1	TGA GGT TCT GAG GCT GTG CTC	TCC TGC ACT TCT CGG ATG ATG
Elovl3	GGA CAG AGG CAC ACA CAA ACA	GCG CCT ACC AGG CCT AGA AT
GSTπ	TGA GGA TGG AGA CCT CAC CC	AGG TGT CTC AAG ATG GCA TTA GAT T
Hsd3b5	AGT CCT AAG CAC TTG CCC AGT AAT	CAC AGC AGC TGA GTC ACA ACA G
KAP1	TCA GCT GGC TAC CGA CTC TAC A	GGC GAG CAC GAA TCA AGG T
Krt23	TCA AGG CTG AAA GGA TCT G	CTT GAG AAA GAA CGA TTC TTC C
Lcn13	CCA GTC ACA AGA TAC CCA G	CCA TTG TTC CAG AAT ACA ACT G
Mas1	AAG CCT CTA GCC CTC TGT CC	TGG TCC ATG AGG AGT TCT TGC
mTBP	TTG ACC TAA AGA CCA TTG CAC TTC	TTC TCA TGA TGA CTG CAG CAA A
Mup1/2/6/8	GAC TTT TTC TGG AGC AAA TCC ATG	GAG CAC TCT TCA TCT CTT ACA G
Mup3	GAA GAG TGC ACC GAA ATG ACT G	TGC CAG CCT TTT CTG TTT GTT
Rarres1	CAG GAA GGT GGA CGT TTG	GCG CAC GTT ACA TTA ACG GC
RPS9	GAC CAG GAG CTA AAG TTG ATT GGA	TCT TGG CCA GGG TAA ACT TGA
Rsl1	CCT TGG GAC ATG AAG AGA C	GAT CAT TGG GTA TTA TTC CTG G
Rsl2	GTA CCC AGG AAT AAC ACC C	GCC TTA CCA AAT TCT CCA C
Slp	AGG TCC GGG ACA TGG TGA ATT TG	CGC ACT GTC AAC AGT TTG GAG C
Spink3	ATG CAG TGG CGG GAT GTC	CAG AAC ACA TTC ATT GGC ATA AGT AA
STAT5a	TGC GCC AGA TGC AAG TGT T	CAA GTC AAT AGC ATC CCA CGG
STAT5b	GAG AAT TTG CCA GGA CGG AA	CAC GCC ATC AAA CCA CTG C
TRIM24	GAG GCC TCC GTC AAA CAG AAC	GAG CCA GAG CTT CCT CGA CTT
Zfp169	CTA TAG CCA CCT TGT CTC C	AAT TCT GTC CTG GGT TCT G
Zfp445	TCTAGAGGACCACTTGGAG	GAGACAGCAGGAGAATCAG
Zfp780b	TAC TAG AGC AGG AGA AAG AG	CAT AAT CTG TCT CCA AGT CTG
	Genotyping	
Cre	GAA CCT GAT GGA CAT GTT CAG G	AGT GCG TTC GAA CGC TAG AGC CTG T
GAPDH	TCC ACC ACC ATG GAG AAG GC	GGC ATG GAC TGT GGT CAT GA
KAP1 - 1	TTG GTG AGT GGG AAG ATA ACC AGG	Comment: use of those three primers in the PCR reaction allows distinguishing between different KAP1 loci (Cammas et al., 2000).
KAP1 - 2	AAA GAT CTA GGT CTG GAA GC	
KAP1 - 3	GCG AGC ACG AAT CAA GGT CAG	
X-globin	CAA GAT CAT GAC CGC CGT AGG	CAT GAA CTT GTC CCA GGC TTC
	ChIP	
Actin	TAG GCA CCA GGG TGT GAT GG	CAT GGC TGG GGT GTT GAA GG
FSP27 – promoter	GGG TTC CTC AGT CAG CTA CTA TGC	GCA GGG ATC TAA GTG GCT TGA
FSP27 – peak	GGC GCA TTG GGT CAA AGA	GAC CTA GAA CAC AGG CAG AAG CTT
Cyp2b – peak	TTT CAG CAG TTC AGG ACC TTC TT	CAC ATG AAA CAG GAC TTC CAA CA
c-Cbl - peak	CTG AGT TTG AGA TCA GGA TG	TCT CTG TGC TCA TAA GGT TC
Cyp2b9/13 promoter	AAA GTC TAG GGT GGT TGT AAT GGA A	CCA GGA ATG TGA GCA CCA TAG TT
Cyp2d9 – peak1	GAA AAT GGC AAA CCT GGG AAT	CAA CAG GAT GCT GGG ACT GA
Cyp2d9 – peak2	GCC TCT TTC CCT CCA CTG TAG A	GCT TGA CTG CCT TCC TGT GAA
Foxp3	GCT CTG GAA GCC CTG TGA	GCCCTGGCTGTCTTCTGA
GAPDH	GGC CGC CGC CAT GT	AGC TAG GAA GAA GGA AGG CCT AAG
GSTπ - peak2	CAA TGT GCG TCC TCT GTG TGT	GGC GCA AGT GTC TCA CAA GTT
GSTπ - promoter	TGA AGC TCT TTG GGA GGA GAA A	TCC CCA TCT ACC AAC CTC TGT AG
GSTπ - peak1	ATC CAC TCG AGG CTT CTC	GGC TTC TAC CCA GAC ATG
RPS promoter	CGA AGG TGG CTG GAA GTT ACA	CCA ACT CGG CTC TCA GAG AAA T
Slp – peak	CCC CTG CGT GGG ATA	ACC GTC CTT GCT GCA
Slp – promoter	GGA GGA TCC AGG AGA GGT CAA	TCA AAC TCT GCC CCA AAC CTA