



The MNT transcription factor autoregulates its expression and supports proliferation in MYC-associated factor X (MAX)-deficient cells

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M. Carmen Lafita-Navarro^{‡1,2}, Judit Liaño-Pons^{‡1,3}, Andrea Quintanilla^{‡4}, Ignacio Varela[‡], Rosa Blanco[‡], Fabiana Ourique^{‡5}, Gabriel Bretones^{‡6}, Julia Aresti^{‡7}, Ester Molina[‡], Patrick Carroll[§], Peter Hurlin[¶], Octavio A. Romero^{||}, Montse Sanchez-Céspedes^{||8}, Robert N. Eisenman[§], M. Dolores Delgado[‡], and Javier León^{‡9}

From the [‡]Instituto de Biomedicina y Biotecnología de Cantabria (IBBTec), Universidad de Cantabria-CSIC, and Department of Molecular Biology, Universidad de Cantabria, 39005 Santander, Spain, the [§]Division of Basic Sciences, Fred Hutchinson Cancer Research Center, Seattle, Washington 98109, the [¶]Shriners Hospitals for Children Research Center, and Department of Cell, Developmental and Cancer Biology, Knight Cancer Institute, Oregon Health and Science University, Portland, Oregon 97239, and the ^{||}Genes and Cancer Group, Cancer Epigenetics and Biology Program (PEBC), Bellvitge Biomedical Research Institute-IDIBELL, 08908 Barcelona, Spain

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The MAX network transcriptional repressor (MNT) is an MXD family transcription factor of the basic helix-loop-helix (bHLH) family. MNT dimerizes with another transcriptional regulator, MYC-associated factor X (MAX), and down-regulates genes by binding to E-boxes. MAX also dimerizes with MYC, an oncogenic bHLH transcription factor. Upon E-box binding, the MYC-MAX dimer activates gene expression. MNT also binds to the MAX dimerization protein MLX (MLX), and MNT-MLX and MNT-MAX dimers co-exist. However, all MNT functions have been attributed to MNT-MAX dimers, and no functions of the MNT-MLX dimer have been described. MNT's biological role has been linked to its function as a MYC oncogene modulator, but little is known about its regulation. We show here that MNT localizes to the nucleus of MAX-expressing cells and that

MNT-MAX dimers bind and repress the MNT promoter, an effect that depends on one of the two E-boxes on this promoter. In MAX-deficient cells, MNT was overexpressed and redistributed to the cytoplasm. Interestingly, MNT was required for cell proliferation even in the absence of MAX. We show that in MAX-deficient cells, MNT binds to MLX, but also forms homodimers. RNA-sequencing experiments revealed that MNT regulates the expression of several genes even in the absence of MAX, with many of these genes being involved in cell cycle regulation and DNA repair. Of note, MNT-MNT homodimers regulated the transcription of some genes involved in cell proliferation. The tight regulation of MNT and its functionality even without MAX suggest a major role for MNT in cell proliferation.

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This article contains Figs. S1-S9 and Tables S1-S8.

¹ Both authors contributed equally to this work.

² Recipient of an F.P.U. fellowship from the Spanish Government. Present address: Sorrell Lab, Dept. of Cell Biology, UT Southwestern Medical Center, Dallas, TX 75390.

³ Recipient of an F.P.U. fellowship from the Spanish Government.

⁴ Present address: Edinburgh Cancer Research UK Centre, Institute of Genetics and Molecular Medicine, University of Edinburgh, EH4 2XU Scotland, United Kingdom.

⁵ Present address: Dept. of Biochemistry, Universidade Federal de Santa Catarina (UFSC), 88040-900 Florianópolis, Brazil.

⁶ Present address: Dept. de Bioquímica y Biología Molecular, Facultad de Medicina, Instituto Universitario de Oncología (IUOPA), Universidad de Oviedo, 33003 Oviedo, Asturias, Spain.

⁷ Present address: Groningen Biomolecular Sciences and Biotechnology Institute, University of Groningen, 9712 CP Groningen, Netherlands.

⁸ Present address: Josep Carreras Leukemia Research Institute, Campus ICO-Germans Trias i Pujol, 08916 Badalona, Barcelona, Spain.

⁹ To whom correspondence should be addressed. E-mail: leonj@unican.es.

MNT¹⁰ is a basic helix-loop-helix leucine zipper (bHLH-LZ) protein, and it is the most divergent member of the MXD family, which also includes MXD1, MXI1, MXD3, and MXD4. MNT forms heterodimers with MAX through the bHLH-LZ domain and binds to E-box DNA sequences. MYC is one of the most prevalent human oncoproteins (1). MYC can also interact with MAX and bind E-boxes (2, 3). Whereas MYC-MAX, upon binding to E-boxes, acts primarily as a transcriptional activator, the typical effect of MNT-MAX is the transcriptional repression (4, 5). MNT can bind not only to MAX but also to the MAX-like HLH protein MLX (6, 7), which alternatively can interact with MLXIP (MONDOA) and MLXIPL (MONDOB) proteins. Therefore, MNT participates both in the MAX- and MLX-centered networks (8, 9) serving as the link between MAX-MYC and MLX-MONDO.

MNT is expressed constitutively in proliferating and quiescent cells, and the protein levels do not show major fluctuations

¹⁰ The abbreviations used are: MNT, MAX network transcriptional repressor; bHLH-LZ, basic helix-loop-helix leucine zipper; MAX, MYC-associated factor X; qPCR, quantitative PCR; RNA-seq, RNA sequencing; FL, full-length; GSEA, Gene Set Enrichment Analysis; ChIP-seq, ChIP-sequencing; RPKM, reads per kilobase pair per million.

MNT functions in the absence of MAX

when quiescent cells are mitotically stimulated (5, 10, 11). *Mnt*^{-/-} mice are not viable (10, 12), whereas *Mxd1*^{-/-}, *Mxi1*^{-/-}, and *Mxd3*^{-/-} mice survive, suggesting that MNT function is not redundant with that of the other MXD proteins (13–15). Moreover, MNT is the only MXD-related protein in invertebrates (9).

Consistent with MNT functioning as a MYC transcriptional antagonist, enforced MNT expression inhibits cell proliferation and impairs MYC-dependent transformation (5, 11). The deficiency or down-regulation of MNT in fibroblasts leads to increased proliferation (*i.e.* similarly to MYC overexpression) and partially rescues the proliferative arrest caused by MYC deficiency (10, 11, 16, 17). MNT ablation *in vivo* leads to breast and T-cell tumors (10, 12, 17), and according to the Cancer Genome Atlas, about 10% of human tumors show deletion of a MNT allele (1).

Partial or total MNT deficiency in mouse models impairs MYC-dependent tumorigenesis (18, 19), and *MNT* knockout in some cell models inhibits proliferation and promotes apoptosis (10, 16, 17). Thus, MYC and MNT proteins co-exist in proliferating cells, and depending on the model, MNT acts as a MYC antagonist or a cooperators of MYC.

However, there is scarce information about MNT transcriptional regulation, and it is unknown whether MNT exerts functions without MAX. In this work, we studied possible MAX-independent functions of MNT using UR61 cells as the main model. These rat pheochromocytoma cells do not express a functional MAX protein but a truncated form (termed MAX^{PC12}) that lacks the second helix and leucine zipper region of the bHLH-LZ domain, which are the regions responsible for dimerization with MYC and MNT (20). Here, we describe a change of MNT subcellular localization depending on MAX expression and the repression of its own promoter in the presence of MAX. In addition, we show the first examples of MNT functions that are independent of MAX. In the absence of MAX, 1) MNT regulates gene transcription by binding to DNA through the formation of MNT–MNT or MNT–MLX complexes, and 2) MNT is required for optimal cell proliferation.

Results

MNT levels depend on MAX

To explore the effect of MAX on MNT expression, we first compared MNT and MAX levels in proliferating cells from 13 cell lines derived from different tissues and species, including two cell lines lacking MAX: UR61 and the human small-cell lung carcinoma H1417 cells (21). The results showed that although MNT expression varies among the cell lines, the two MAX-deficient cell lines and others with low MAX levels (HeLa and CEM) expressed high MNT levels, whereas other cells with high MAX levels expressed low MNT levels (293T, K562, and Ramos) (Fig. 1A). MNT was expressed in all cell lines as a protein doublet, due to a slower-migrating phosphorylated MNT form (22). MAX was also expressed as a doublet of 21 and 22 kDa (23). Although the correlation was not universal, the high MNT expression in some cell lines with null or low MAX levels led us to explore whether MAX influenced MNT levels.

For this purpose, we transfected UR61 cells with a construct carrying human MAX cDNA driven by the metallothionein promoter, which is activated by Zn²⁺ cations (24). Several clones were isolated, and two of them with robust MAX induction were mixed, and the resulting cells were termed URMax34. We also generated a cell line transfected with the empty vector, termed URMT, which is a pool of five transfected clones. The induction of MAX in response to Zn²⁺ in URMax34 cells was confirmed by immunoblot (Fig. 1B). We examined the effect of MAX induction on MNT levels in URMax34 cells, and we found that MNT was down-regulated upon MAX induction by Zn²⁺ (Fig. 1B). As expected, the treatment of URMT cells with Zn²⁺ did not change the MNT levels (Fig. S1A). To confirm this result and rule out effects potentially related to the generation of stably transfected clones (as the URMax34 system), UR61 cells were transiently transfected with a MAX expression vector, and the results showed a decrease in MNT protein levels in MAX-transfected cells (Fig. 1C). It is noteworthy that the down-regulation of MNT provoked by the re-expression of MAX in these cells also occurred at the mRNA levels, as determined by RT-qPCR (Fig. 1D). We then analyzed the effect of MAX-enforced expression in three human small-cell lung cancer cell lines deficient in MAX (21). MAX-enforced expression was achieved by lentiviral transduction, and the levels of MNT were examined by immunoblot in Lu134, Lu165, and H1417 cell lines (Fig. 1E). In all cell lines, MAX expression resulted in lower MNT protein levels. The MNT mRNA levels were also down-regulated in Lu165 and in H1417 cells upon MAX expression (Fig. 1F).

We next sought to confirm this in a different cell type with endogenous MAX. A MAX expression vector was transfected into human myeloid leukemia K562 cells. The immunoblot results showed lower MNT levels in the cells with MAX overexpression (Fig. 1G). Next, we used the Kmax12 cell line (24), a K562 derivative carrying a MAX transgene in which expression is induced by Zn²⁺. Induction of MAX expression in Kmax12 cells resulted in a concomitant MNT down-regulation (Fig. 1H). We also used the opposite approach, *i.e.* depleting cells of MAX and analyzing the expression of MNT. As shown in Fig. 1I, MNT protein expression was up-regulated when MAX was silenced with siRNA in K562. Interestingly, MNT was also up-regulated in MAX-silenced cells at the mRNA level (Fig. 1J). Altogether, the results showed that low MAX levels result in MNT up-regulation at the mRNA and protein levels.

MNT binds and represses its own promoter in the presence of MAX

The above results showing that MNT down-regulation took place at the mRNA level prompted us to investigate whether MNT impairs the activity of its own promoter. Bioinformatic analysis of human, mouse, and rat *MNT* promoter regions revealed that there are two E-box sequences within 1 kb upstream from the transcriptional start site of *MNT* (one canonical E-box, CACGTG (E-box 1) and one noncanonical CATGTG (E-box 2)) that are conserved among these three different species (Fig. 2A). We then constructed a luciferase reporter carrying the 850-bp upstream region of the transcription start site from the human *MNT* gene. The construct was

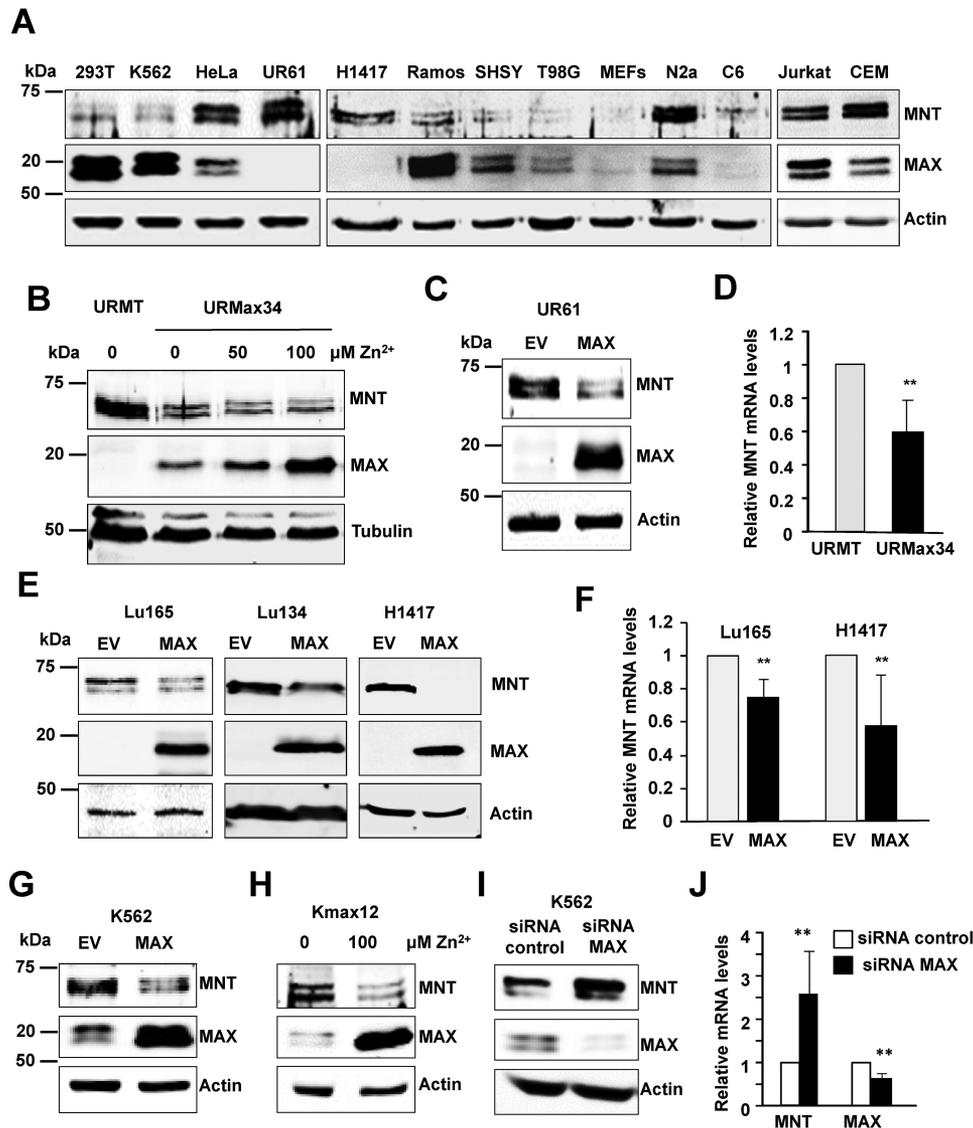


Figure 1. High MNT expression in MAX-deficient cells. *A*, cell lysates of the indicated cell lines were analyzed by immunoblot to determine the levels of MNT and MAX. β -Actin levels were determined as a protein-loading control. The MAX-deficient cell lines analyzed were UR61 (rat pheochromocytoma) and H1417 (human small cell lung carcinoma). The rest are MAX-expressing cells: HEK293T (human embryonic kidney, 293T); K562 (human chronic myeloid leukemia); HeLa (human cervical cancer); Ramos (human B-cell lymphoma); SH-SY5Y (SHSY, human neuroblastoma); T98G (human glioblastoma); mouse embryonic fibroblasts; Neuro-2a (N2a, mouse neuroblastoma); C6 (rat glioma); Jurkat (human T lymphoma); and CEM (human T leukemia). *B*, control URMT and URMx34 cells were treated for 24 h with 50 and 100 μM Zn^{2+} , and the MNT and MAX protein expression was determined by immunoblot. α -Tubulin levels were determined as a protein-loading control. *C*, levels of MNT and MAX determined by immunoblot in UR61 cells 24 h after transfection with a MAX expression vector or the empty vector pCEFL (EV). *D*, mRNA expression determined by RT-qPCR in URMT and URMx34 cells treated for 24 h with 100 μM Zn^{2+} . Data represent the mean \pm S.D. from three independent experiments; **, $p < 0.05$. *E*, protein levels of MNT by immunoblot in Lu165, Lu134, and H1417 cells. The lysates were prepared 72 h after infection with MAX-expressing lentivirus or empty lentivirus (EV). *F*, MNT mRNA expression in Lu165 and H1417 determined 72 h after infection with MAX-expressing lentivirus or empty lentivirus (EV) determined by RT-qPCR. Data are shown as mean \pm S.D. ($n = 3$); **, $p < 0.05$. *G*, MNT and MAX levels determined by immunoblot in K562 cells 24 h after transfection with a MAX expression vector. *H*, MNT and MAX levels determined by immunoblot in Kmax12 cells treated for 48 h with 100 μM Zn^{2+} to induce MAX expression. *I*, MNT and MAX protein expression analyzed by immunoblot in K562 48 h after transfection with siRNA against MAX gene. The results were reproduced in two experiments. *J*, MNT and MAX mRNA expression analyzed by RT-qPCR 48 h after transfection with siRNA against MAX gene. Data are shown as mean \pm S.D. ($n = 4$); **, $p < 0.05$.

termed MNT-Luc (Fig. 2B). HEK293T cells (which express MAX) were transfected with the MNT-Luc and MNT expression vectors (or the corresponding empty vectors). The results showed that MNT overexpression led to a reduction in the luciferase activity (Fig. 2C, left panel), suggesting that MNT-MAX negatively regulates the MNT promoter. To determine the contribution of the two E-boxes in the MNT-mediated negative autoregulation, we constructed two reporters containing each of the E-boxes, termed E-box 2 MNT-Luc (containing the last 220 bp of the MNT-Luc reporter, which includes E-box 2)

and E-box 1 MNT-Luc (containing the first 570 bp of the MNT-Luc reporter which includes E-box 1) (Fig. 2B). The luciferase assays in HEK293T cells suggested that the MNT promoter down-regulation depended on the E-box 2 (Fig. 2C, left panel).

We also investigated the activity of the MNT promoter in UR61 cells, which do not express MAX. UR61 cells were transfected with the MNT-Luc vector together with MNT and MAX expression vectors. The results also showed a decrease in the luciferase activity although less than in HEK293T cells (Fig.

MNT functions in the absence of MAX

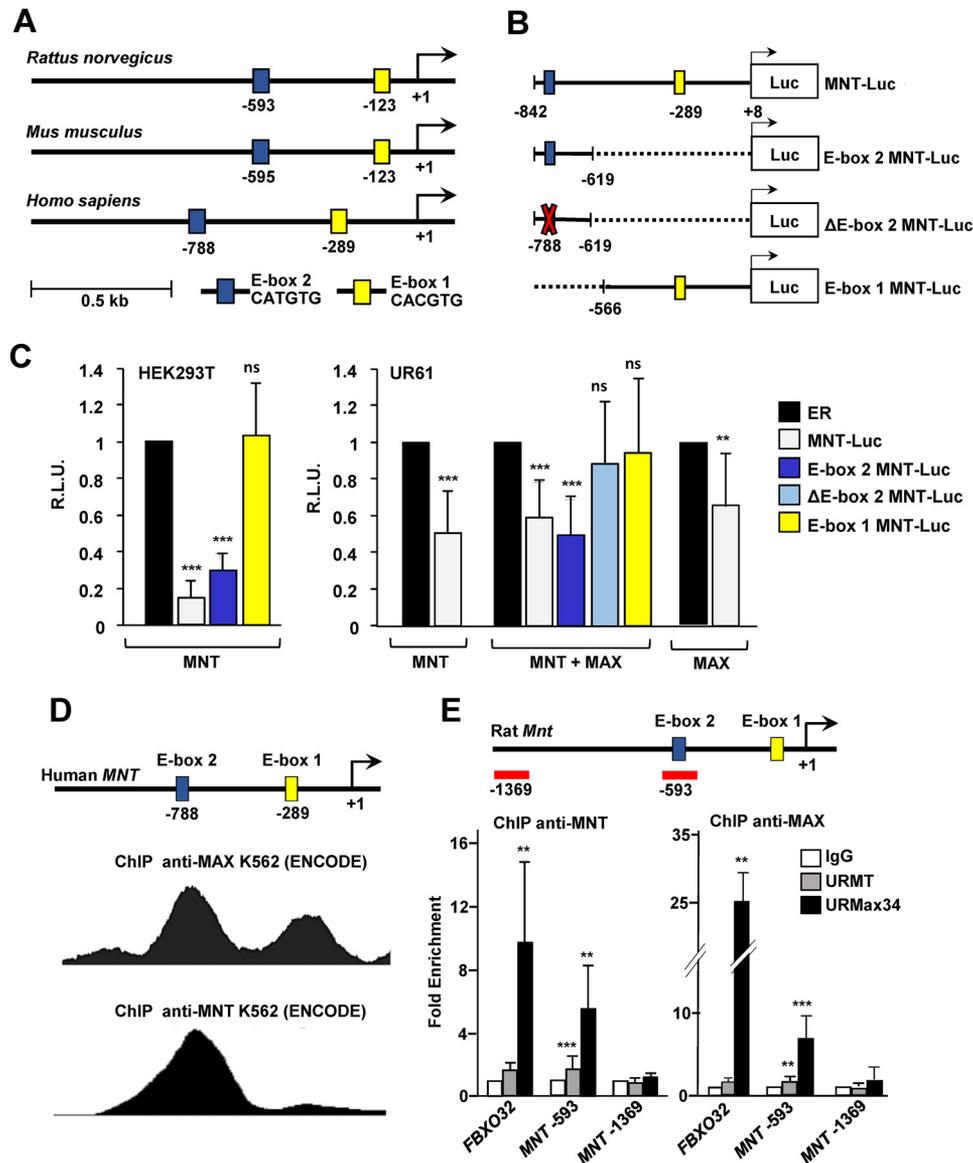


Figure 2. MNT represses its own promoter. *A*, schematic representation of human, rat, and mouse MNT promoters showing two conserved E-boxes. The coordinates correspond to the 5'-nucleotide of each E-box, using the UCSC genome browser. *B*, luciferase reporters driven by human MNT promoter generated in this work. *C*, luciferase assays in HEK293T and UR61, 24 or 36 h after transfection, respectively, with expression vectors for MNT and MAX. Results are expressed in relative luciferase units (R.L.U.) after normalizing each condition first to the luciferase empty reporter (ER; no promoter) and then to the empty expression vector of MNT and/or MAX. The data are shown as the mean \pm S.D. of nine (for MNT-luc) or four independent transfections (for the rest of experimental points). ***, $p < 0.01$; **, $p < 0.05$; ns, nonsignificant. *D*, schematic representation of human MNT promoter showing the peaks for MAX and MNT on human K562 cell line as published by the ENCODE project. *E*, ChIP with anti-MNT (*left*) and anti-MAX (*right*) antibodies of URMT and URMax34 cells, both treated with $100 \mu\text{M Zn}^{2+}$ for 24 h. MNT and MAX binding to MNT gene promoter (below) was studied by qPCR at the amplicons shown with red bars. MNT - 593 corresponds to the region containing the E-box 2, and MNT - 1369 corresponds to an upstream region without E-boxes (negative control). An amplicon from Atrogin-1 (FBXO32) was used as positive control for MNT binding. The data are means \pm S.D. ($n = 3$); ***, $p < 0.01$; **, $p < 0.05$.

2C, right panel). The expression of MNT alone also led to a decrease in the luciferase activity, suggesting that MNT can down-regulate the MNT promoter in UR61 cells in the absence of MAX. The repressive effect of MNT was stronger in HEK293T cells than in UR61 cells, which may be explained by the limited overexpression of MNT protein achieved in transfected UR61 cells (shown below). Co-transfection of MNT and MAX resulted in a decrease in the activity of both promoter constructs (MNT-Luc and E-box 2 MNT-Luc). We next constructed a reporter with a deletion of the -788 E-box (Δ E-box 2 MNT-Luc), and the results showed that in UR61 cells MNT had no effect on the activity of the mutant reporter (Fig. 2C,

right panel), confirming that E-box 2, mapping at -788, was critical for MNT-mediated down-regulation of its own promoter.

Because MNT-MAX bind E-boxes in the promoters to repress transcription, we analyzed the ChIP-seq data published by the ENCODE project. The data revealed two regions bound by MAX in the human MNT promoter that encompass the two E-boxes (Fig. 2D). Interestingly, according to ENCODE, ChIP-seq for MNT also showed that MNT binds to the region encompassing E-box 2 in human K562 cells (Fig. 2D). We also analyzed the ChIP-seq peaks for MAX, MYC, and MXI1 proteins on the MNT promoter as published by the ENCODE project.

We looked at other human cell lines like H1ES, HeLa, NB4, A549, GM78, HEPG, SKSM, and IMR90. The analysis revealed that the three proteins presented peaks at the same positions near the transcription start site of the human MNT gene (Fig. S1B), suggesting that members of the MYC and MXD family bind and possibly regulate the promoter of MNT.

As MNT was significantly down-regulated when MAX was re-expressed, we hypothesized that MNT–MAX heterodimers might bind to the MNT promoter and down-regulate its own expression. To explore this hypothesis, a ChIP assay was performed with anti-MNT and anti-MAX antibodies in URMT and URMax34 cells treated with Zn²⁺, which induces MAX in the URMax34 cells. We studied the –593 E-box of the rat MNT promoter, as well as a region of the *FBXO32* (*Atrogin-1*) promoter as a positive control for MNT binding (25). A region mapping at 1369 bp upstream on MNT transcription start site with no E-boxes was used as negative control. As shown in Fig. 2E, MNT and MAX bound to the MNT promoter in URMax34 cells. However, in the MAX-deficient control URMT cells, the binding of MNT to its promoter was very weak, but above that of the IgG controls. This weak binding could be responsible for the decreased promoter activity detected in the results shown of Fig. 2C in MNT-transfected UR61 cells. MNT and MAX were bound to the positive control *FBXO32/Atrogin-1* promoter in URMax34 but not in URMT control cells (Fig. 2E). These data show that MNT most likely binds to its own promoter as a heterodimer with MAX and suggest a possible negative regulation of MNT's own expression.

Then, to explore the binding of MNT to other regions of the genome in the absence of MAX, we performed ChIP-seq experiments with an anti-MNT antibody in MAX-deficient URMT cells. We sequenced the immunoprecipitated chromatin and the inputs of three independent experiments. The results showed first that MNT bound very weakly to the promoter of MNT in the absence of MAX, while stronger binding was detected in other genes like *CCNG2* (Table S1). This indicates that MNT binds to DNA even in the absence of MAX. The peaks of MNT bound to the regulatory regions of some of these genes (*MNT*, *FBXO32/Atrogin-1*, *CCNG2*, *CDK12*, and *ERCC6*) are shown on Fig. S2A. To evaluate the possible transcriptional effect of MNT binding to these genes, we knocked down MNT in URMT and URMax34 cells through short-hairpin constructs and checked their expression by RT-qPCR. The results showed that upon MNT knockdown, the mRNA expression of these genes increased (Fig. S2B), indicating that MNT binds to their promoters to repress their expression even in the absence of MAX.

Ontology analysis of the genes obtained in our ChIP-seq experiments reveals that MNT-bound genes are involved in cell cycle, DNA replication, and regulation of gene expression (Fig. S3A). We then analyzed whether there were any DNA motifs that were over-represented in the regions bound by MNT. The results revealed that MNT binds to regions with E-boxes in the absence of MAX but also to regions containing DNA-binding motifs for other transcription factors such as forkhead factors, SMAD, VDR, and TBXT (Fig. S3B).

MNT knockdown impairs cell proliferation in MAX-deficient cells

We next asked for a possible biological effect of MNT on cell proliferation in the UR61 MAX-deficient cells. We decided to knock down MNT through siRNAs. For this, we used expression vectors for two short-hairpin constructs against the rat MNT gene. These shMNT constructs efficiently reduced MNT levels and were termed shMNT-1 and shMNT-2 (Fig. 3A). The vectors also carried a puromycin-resistance gene. UR61 cells were transiently co-transfected with the shMNT constructs (or the empty vector) and a GFP expression vector in a proportion of 5:1 (shMNT/GFP vector) to ensure that the GFP-positive cells also incorporated the shMNT plasmid. Six days after transfection, the fraction of GFP-positive cells was analyzed by flow cytometry. The results showed that the fraction of GFP-positive cells was clearly reduced in cells with depleted MNT (Fig. 3B), suggesting that MNT loss resulted in impaired cell proliferation. In a second approach, we transfected the UR61 cells with the shMNT constructs and counted viable cells after 3, 7, and 12 days of transfection. As shown in Fig. 3C, MNT-silenced UR61 cells grew slower than controls. We also performed clonogenic assays in UR61 transfected with the shMNT and/or a MAX expression vector (in 1:3 proportions to ensure that the shMNT-containing cells had also incorporated the MAX vector) as well as the empty vectors. Then, 24 h after transfection puromycin was added and after selection, the colonies were stained with crystal violet, and the dye was solubilized and quantified. The data showed that MNT depletion provoked a dramatic growth inhibition (Fig. 3D). We conclude that MNT depletion impairs cellular proliferation in MAX-deficient cells. This was a striking result as it demonstrates a MAX-independent biological function of MNT. We also observed that UR61 cells overexpressing the MAX protein grew slower than the control (Fig. 3D), confirming the effect previously reported for the MAX-deficient PC12 pheochromocytoma cells (UR61 parental cells) (20). In addition, when MNT silencing was accompanied by MAX-enforced expression, the inhibition of UR61 cell proliferation was stronger (Fig. 3D). Consistent with the anti-proliferative effects of MNT depletion, we failed to generate stable MNT-silenced UR61 cell lines. To generate UR61 cells with MNT overexpression, we transfected UR61 with MNT expression vectors, but we were not able to detect a significant increase in MNT protein levels upon transfection. However, MNT protein was readily detected by immunoblot when the transfected cells were treated with the proteasome inhibitor bortezomib (Fig. S4A).

This could be explained if in the MAX-deficient cells the MNT levels are already high and enforced expressed MNT is degraded by the proteasome. In fact, some increase in the levels of MNT was detected when MNT was transfected in MAX-expressing URMax34 cells (Fig. S4B) or when MNT was co-transfected with MAX in UR61 cells (Fig. S4C).

Because the depletion of MNT impairs cell proliferation of UR61 cells, we wondered whether apoptosis is involved in this process. We found that the fraction of cells with a sub-G₀ amount of DNA was higher in cells transfected with the shMNT vector (Fig. 3E) and an increase in annexin V-positive

MNT functions in the absence of MAX

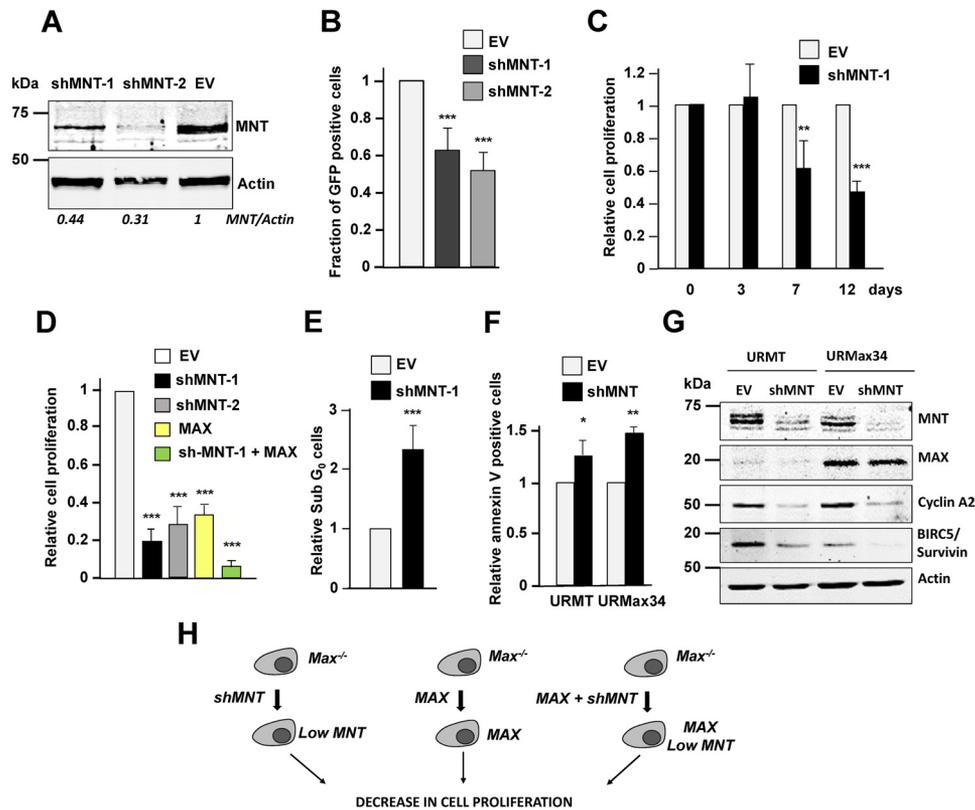


Figure 3. MNT knockdown impairs cell proliferation in MAX-deficient cells. *A*, silencing of MNT by short-hairpin constructs. UR61 cells were transfected with vectors encoding shMNT-1 and shMNT-2. 24 h after transfection, the cells were treated with puromycin (0.3 $\mu\text{g}/\text{ml}$), and 72 h after transfection the cells were lysed, and the levels of MNT were analyzed by immunoblot. β -Actin levels were determined as protein-loading control. *B*, fraction of GFP-expressing UR61 cells assessed by flow cytometry 7 days after co-transfection with GFP and shMNT vectors (in proportion 1:5) and analyzed by flow cytometry. The data are shown as mean \pm S.D. ($n = 3$); ***, $p < 0.01$. *C*, cell proliferation determined by cell counting at 3, 7, and 12 days after transfection of shMNT-1 or the empty vector pLKO. The data are shown as relative mean values \pm S.D. ($n = 3$); ***, $p < 0.01$; **, $p < 0.05$. *D*, cell growth determined by crystal violet staining in UR61 cells transfected with the indicated vectors. After 15 days of puromycin selection, the colonies were stained with crystal violet, and the dye was solubilized and quantified by absorbance at 595 nm. EV, empty vector (pLKO for shMNTs and pCEFL for MAX). ***, $p < 0.01$. Data show mean values \pm S.D. from three (EV and MAX) or six independent experiments (shMNTs). *E*, fraction of sub-G₀ UR61 cells transfected with the shMNT-1 vector relative to the empty vector. Cells were fixed and stained with propidium iodide at day 6 post-transfection and puromycin selection. The percentage of cells containing less than 2C DNA content was determined by flow cytometry. The data are mean values \pm S.D. ($n = 3$); ***, $p < 0.01$. *F*, quantification of annexin V-bound URMT and URMAX cells 4 days after transfection with a mixture of shMNT-1 and shMNT-2 (or the empty vector), and 24 h of treatment with 100 μM Zn²⁺. The data are mean values \pm S.D. ($n = 3$); **, $p < 0.05$; *, $p < 0.1$. *G*, levels of MNT determined by immunoblot in URMT and URMax34 cells 72 h after transfection with a mixture of shMNT-1 and shMNT-2 or the empty vector and treated for 12 h with 100 μM Zn²⁺. MAX, cyclin A2, and survivin (BIRC5) were also determined. *H*, summary of the effects of MNT knockdown and MAX overexpression in the UR61 model.

cells (Fig. 3F). The levels of cyclin A (a marker of cell proliferation) and survivin/BIRC5 (a marker of both proliferation and apoptosis) in URMT and URMax34 were analyzed by immunoblot. The results showed a decrease in survivin and in cyclin A in cells with depleted MNT, both in MAX-deficient cells (URMT) and in MAX-expressing cells (URMax34) (Fig. 3G). However, we did not detect cleavage of PARP1, a marker of apoptosis (data not shown). These results suggest that the depletion of MNT leads to cell proliferation arrest even in the absence of MAX, which can be partially due to the induction of apoptosis. In addition, restoration of MAX expression also impairs proliferation. The results are summarized in Fig. 3H.

MNT regulates gene expression in MAX-deficient cells

Because the data shown above indicated that MNT knockdown in UR61 cells leads to growth arrest, we set out to study whether MNT regulates the transcriptional program in the absence of MAX. For this purpose, we determined the transcriptomes upon MNT depletion in cells with and without MAX. URMT and URMax34 cells were transfected with the

short-hairpin RNA construct against the rat MNT gene (shMNT-1) or the empty vector as control in two different biological replicates. We first checked the depletion of MNT mRNA in the two replicates used for RNA-seq upon transfection of the shMNT-1 construct in URMT and URMax34 cells. URMT and URMax34 cells were transfected with the shMNT-1 construct, and 2 days after transfection, cells were treated with Zn²⁺ for 24 h. The results indicated the induction of MAX mRNA expression in URMax34 as well as significant MNT mRNA depletion in the two independent transfections (Fig. 4A). These RNA preparations were submitted for next generation sequencing, RNA-seq. The data were then processed bioinformatically as described under "Experimental procedures" to obtain the expression values of each experimental replicate. For all of the different comparisons, we grouped the genes that were up-regulated and down-regulated in both biological replicates considering a log₂ RPKM fold change higher than 0.7 or smaller than -0.7 (1.6 \times or 0.6 \times fold change, respectively) of the corresponding control and a p value < 0.1 . The heat maps of the gene expression signatures clearly showed

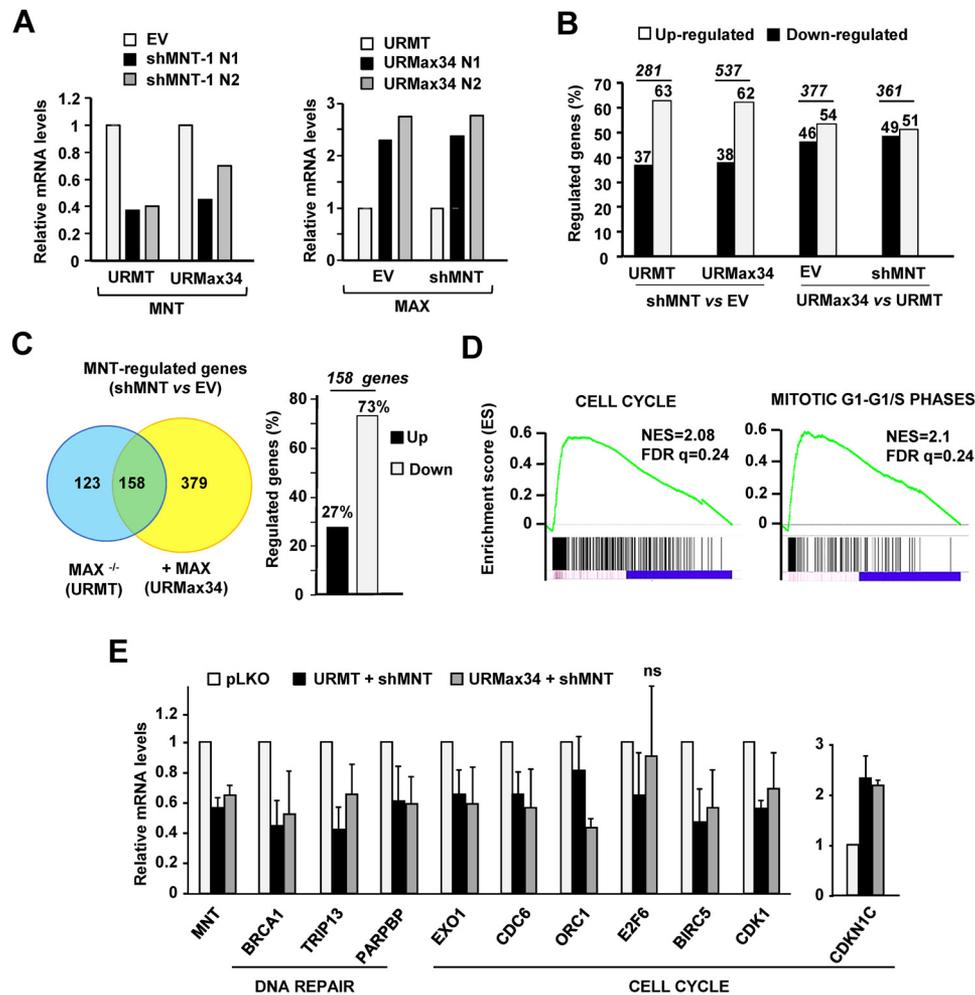


Figure 4. Gene expression changes in MNT knockdown cells. *A*, mRNA expression of MNT and MAX in URMT and URMax34 cells lysed 72 h after transfection with shMNT-1 and 24 h of treatment with $100 \mu\text{M}$ Zn^{2+} . The experiments were performed in duplicated (*N1* and *N2*) biological replicates. These RNAs were subjected to RNA-seq. *B*, percentage of up-regulated and down-regulated genes in cells transfected with the shMNT or pLKO (empty) vectors in URMT and URMax34 cells, as indicated at the *bottom*. The number of genes regulated comparing the different samples are indicated at the *top* of the figure. The gene inclusion criteria used was a change in mRNA level ≥ 0.7 or ≤ -0.7 log₂ fragments per kilobase million fold change. The RNA-seq data are from two independent experiments. The genes regulated in the different comparisons are listed in [Tables S2 and S3](#). *C*, Venn diagram showing the genes that are regulated by MNT in MAX-deficient (URMT) or MAX-expressing cells (URMax34). The *graph at the right* shows the number of up- or down-regulated genes in the group of overlapping genes. *D*, Gene Set Enrichment Analysis (GSEA) plots showing “cell cycle” and “mitotic G₁-G₁/S phases” KEGG pathways enriched in the genes regulated upon MNT depletion in URMT cells. Normalized Enrichment Score and False Discovery Rates are shown for each gene set. *E*, mRNA expression regulation due to MNT silencing in genes selected after the RNA-seq data analysis. URMT and URMax34 were transfected with shMNT-2 or empty vector (pLKO). After 48 h cells were treated for 24 h with $100 \mu\text{M}$ Zn^{2+} , and total RNA was prepared, and mRNA levels of the indicated genes were determined by RT-qPCR. The selected genes are involved in DNA repair or cell cycle as indicated. The data are represented as means \pm S.D. ($n = 3$ independent transfection experiments). In all cases except E2F6 in URMax34 with shMNT: $p < 0.05$. ns, non-significant.

that the depletion of MNT in both URMT and URMax34 induced gene expression changes (Fig. S5) indicating that MNT can be involved in transcriptional regulation without the concurrence of MAX. Specifically, 281 genes were regulated upon MNT depletion in MAX-deficient URMT cells (Table S2) and 537 genes in MAX-expressing cells (*i.e.* URMax34 treated with Zn^{2+}) (Table S3). Of those, $\sim 62\%$ of the genes were down-regulated upon MNT depletion in both cell lines (Fig. 4B). In the presence of MAX (URMax34 cells), MNT regulates more genes than in the absence of MAX (URMT cells): 537 *versus* 281 genes (Fig. 4B). In addition, the URMax34 *versus* URMT gene expression signature heat maps also showed that the expression of MAX induced gene transcriptional changes independently of MNT depletion (Fig. S5). Specifically, 377 genes were found to be differentially expressed when comparing URMax34 and URMT cells (Table S4) and 361 genes when comparing

URMax34 and URMT cells depleted of MNT (Table S5). Among MAX-regulated genes, roughly half of the genes were down-regulated (Fig. 4B). Importantly, the comparison between the lists of differentially expressed genes upon MNT depletion in cells without MAX (URMT) and with MAX (URMax34) revealed 158 shared genes (27% up-regulated and 73% down-regulated) in the two biological replicates (Fig. 4C). These common genes are listed in Table S6. Thus, 56% (158/281) of the genes regulated by MNT in URMT (without MAX) cells are also regulated in URMax34 cells (when MAX is expressed). However, the 30% (158/537) of the genes regulated in URMax34 cells (with MAX) are also regulated in the MAX-less URMT cells (Fig. 4C). Furthermore, we generated a dot plot graph with the RPKM values of the differentially expressed transcripts obtained in our RNA-seq data in URMT and URMax34 cells upon MNT knockdown (Fig. S6). The graph

MNT functions in the absence of MAX

showed that the transcriptional changes induced by *MNT* depletion followed the same pattern in the URMT and URMax34 cells suggesting that the presence of MAX did not affect dramatically the direction of MNT-transcriptional regulation in the UR61 cells. The lists of differentially-regulated genes upon MNT knockdown were compared with the gene sets derived from the biological process gene ontology (based on MsigDB platform, <http://software.broadinstitute.org/gsea/msigdb>),¹¹ and the comparison showed the enrichment in cell cycle-related pathways in both cell lines (Fig. S7A). In addition, the analysis with the Gene Set Enrichment Analysis (GSEA) platform showed that the gene expression signature in URMT cells upon MNT depletion was associated with the cell cycle as the two most enriched pathways (Fig. 4D). A list of these genes is shown in Fig. S7B. Altogether, the functional analysis of the gene transcriptional signatures is consistent with the inhibition of cell proliferation elicited by MNT silencing (Fig. 3).

Thus, to explain and confirm the effects of MNT knockdown on UR61 cell proliferation, we selected several genes involved in cell cycle and DNA replication and repair processes in which expression was changed according to the RNA-seq data to analyze their expression by RT-qPCR. URMT and URMax34 cells were transfected with the shMNT-2 construct and the empty vector following the same conditions as used for the RNA-seq experiment. Fig. 4E shows that genes involved in the cell cycle, DNA replication, and DNA repair were down-regulated upon silencing of *MNT* except *CDKN1C* (p57, a cell cycle inhibitor), which was up-regulated. Altogether, the results are consistent with the negative effect of MNT depletion on cell proliferation in UR61 cells.

MNT localizes in the cytoplasm of MAX-deficient cells

In an attempt to explain the higher MNT levels observed in UR61 cells as compared with the MAX-expressing counterpart, we next examined the subcellular localization of the excess MNT present in MAX-deficient cells. URMT and URMax34 cells were treated with Zn²⁺ to induce MAX, and we performed a cytoplasmic and nuclear fractionation to analyze MNT levels. In control URMT cells, MNT protein was found in the nuclear fraction, as expected, but also at similar levels in the cytoplasm. In contrast, in URMax34-expressing MAX, MNT protein was found only in the nucleus (Fig. 5A), which is the localization typically described for MNT (26). We were not able to use untreated URMax34 cells as a control as they express some MAX even in the absence of Zn²⁺ (Fig. 1B). Cytoplasmic MNT was also observed in H1417 cells, human cells deficient in MAX (Fig. 5A). As a control, the localization of MNT was also analyzed in HEK293T cells, which express the MAX protein. Cytoplasmic/nuclear fractionation revealed that MNT and MAX were localized in the nucleus but not in the cytoplasm of HEK293T cells (Fig. 5A). As controls for nuclear and cytoplasmic proteins, we used SIN3B and RhoGDI, respectively (Fig. 5A). To test whether the localization of MNT depended on MAX, we silenced the MAX protein in K562 cells with siRNA, and we carried out cytoplasmic/nuclear fractionation. In con-

rol K562 cells, MNT and MAX were mainly localized in the nucleus. In contrast, in MAX-depleted cells, a significant amount of MNT was found in the cytoplasm of K562 cells. As controls for nuclear proteins, we used MYC and CTCF (Fig. 5B). It is noteworthy that nuclear MNT levels were similar in URMT and URMax34, as well as in control K562 and MAX-depleted K562 cells. Taken together, the data indicate that the absence of MAX leads to an up-regulation of MNT protein and that the excess of MNT appears to be accumulated in the cytoplasm.

MNT interacts with MLX in the absence of MAX

Besides MAX, MNT can also bind the HLH protein MLX (6, 27). Therefore, MNT would have two partners in UR61-expressing MAX but only one in the absence of MAX, and alternatively, MNT could form homodimers, as schematized in Fig. 5C and previously described *in vitro* (5). To investigate whether the MNT–MLX interaction also takes place in UR61, we transfected MLX–Flag into URMT cells, and 48 h later lysates were immunoprecipitated with anti-MLX and anti-MNT antibodies. The immunoprecipitates were analyzed by immunoblot, and the data demonstrated that MNT interacted with MLX in UR61 cells (Fig. 5D). We next studied this interaction in URMax34 cells treated with Zn²⁺, *i.e.* cells expressing MAX. The immunoblot results showed that MNT and MLX also interacted between them, but the interaction was weaker when MAX expression was induced by Zn²⁺. Thus, the data suggest that, at least in our experimental conditions, MNT–MAX dimers were formed preferentially than MNT–MLX dimers (Fig. 5E). To confirm the MNT–MLX interaction in URMT cells, we prepared a HA-tagged MNT mutant with a deletion of the HLH domain of mouse MNT, termed ΔbHLH MNT-HA (Fig. 5F). This mutant and the WT counterpart were transfected into URMT and the corresponding lysates were immunoprecipitated with anti-HA. The results showed that HLH domain is required for the MNT–MLX interaction (Fig. 5G). As a proof of concept, we performed the same co-immunoprecipitation in HEK293T, obtaining the same result (Fig. 5H).

In contrast to MAX, MLX is found both in the nucleus and cytoplasm (28). By immunoblot analysis, it was found that MLX was present in the cytoplasm and, at a lesser extent, in the nucleus of URMT cells (Fig. 5I). Next, we prepared nuclear and cytoplasmic fractions of URMT cells and studied by immunoprecipitation with anti-MNT and anti-MLX antibodies whether MNT and MLX interacted in these cell compartments. The results showed that MNT and MLX co-immunoprecipitated in both nuclear and cytoplasmic fractions (Fig. 5J).

As mentioned above, it is described that MNT can form homodimers *in vitro* and in two-hybrid experiments in yeasts (4, 5). Thus, another possibility is that MNT acts as a transcription factor by forming homodimers. This homodimerization has not been demonstrated in animal cells, so we tested this in HEK293T and UR61 cells. We first co-transfected HEK293T cells with GFP–MNT and Flag–MNT constructs and immunoprecipitated with anti-GFP antibody. The immunoblot analysis demonstrated the presence of the smaller Flag–MNT protein in the material immunoprecipitated with anti-GFP indicating that MNT forms homodimers in the cell (Fig. 6A). As expected, both

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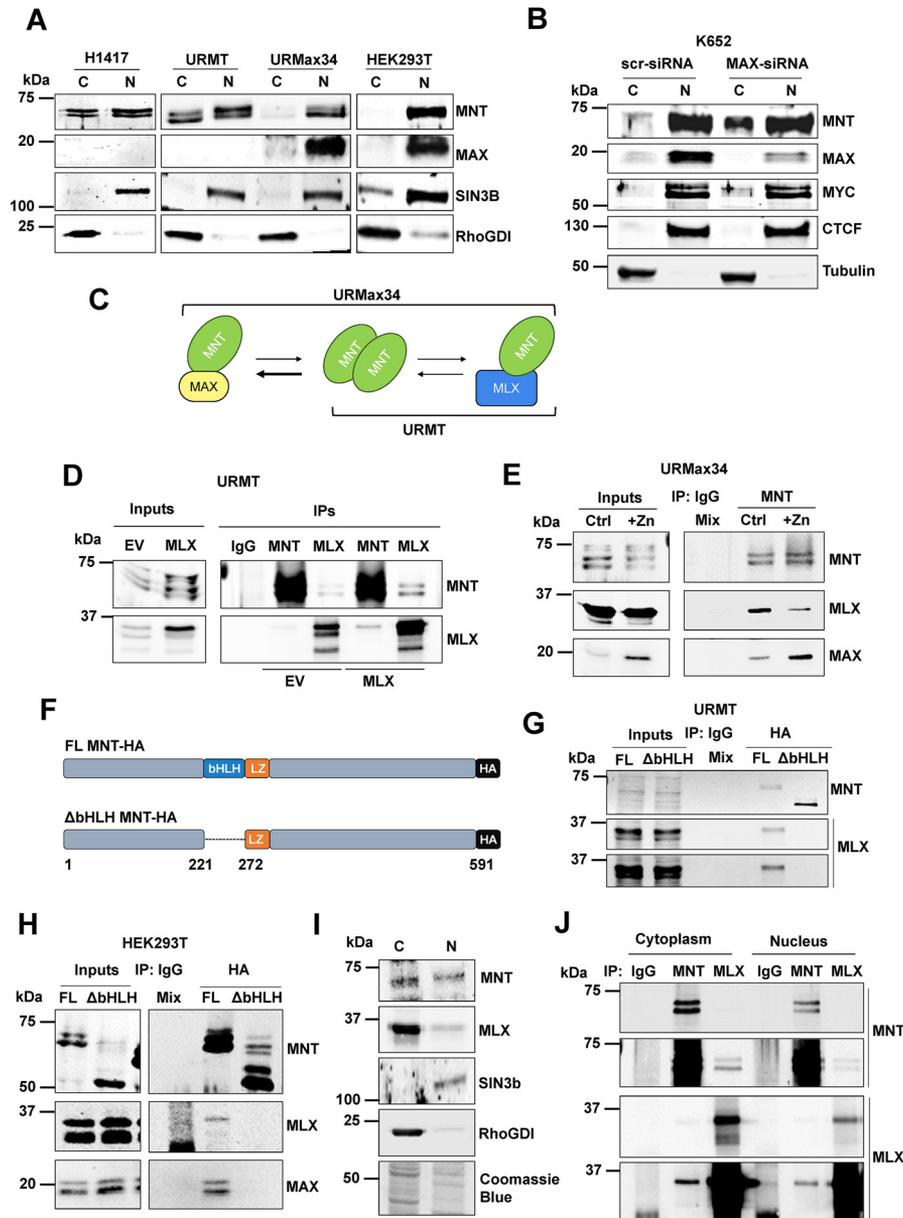


Figure 5. MNT subcellular localization and interaction with MLX depends on MAX. *A*, cell extracts were subjected to cytoplasmic/nuclear fractionation in H1417 (human lung cells deficient in MAX), HEK293T, URMT, and URMax34 treated for 24 h with $100 \mu\text{M Zn}^{2+}$ to induce MAX. The levels of MNT and MAX were determined in each fraction by immunoblot. SIN3B and RhoGDI (ARHGDI) were used as nuclear and cytoplasmic markers, respectively. *C* refers to cytoplasmic fraction, and *N* refers to nuclear fraction. *B*, K562 cells were transfected with siRNA against the *MAX* gene, and 48 h later cell extracts were prepared and subjected to cytoplasmic/nuclear fractionation. The expressions of MAX, MNT, and MYC were analyzed by immunoblot. The expressions of CTCF and α -tubulin were analyzed as a control for nuclear and cytoplasmic proteins, respectively. *scr-siRNA*, control scrambled siRNA. *C*, working hypothesis of the interactions of MNT to test in URMT (MAX-less) and URMax34 (expressing MAX when treated with Zn^{2+}). *D*, URMT cells were transfected with an MLX expression vector or the empty vector (EV). 48 h after transfection, total cell lysates were prepared and immunoprecipitated with anti-MNT or anti-MLX antibodies, as well as unspecific IgG. The presence of MNT and MLX in the immunoprecipitates was detected by immunoblot. *E*, effect of MAX on the MNT-MLX interaction. URMax34 cells were transfected with an MLX expression vector, and 48 h after transfection, cells were treated with $100 \mu\text{M Zn}^{2+}$ for 24 h to induce MAX or left untreated (*Ctrl*). Total cell lysates were immunoprecipitated (IP) with anti-MNT. As a control, a mixture of lysates from cells treated and untreated with Zn^{2+} (*Mix*) was immunoprecipitated with unspecific IgG. The presence of MNT, MLX, and MAX in the immunoprecipitates was analyzed by immunoblot. *F*, schematic representation of the FL and the deletion mutant ΔbHLH MNT-HA used in subsequent experiments. The Sin3-interacting domain, bHLH, LZ domains, HA tag, and amino acids of the murine protein are indicated. *G*, URMT cells were co-transfected with a vector expressing MLX and the constructs shown in *F*, as indicated at the top. 48 h after transfection, cell lysates were prepared, and the cells were immunoprecipitated with mouse anti-HA antibody to pull down the exogenous MNT proteins constructs. The presence of MNT and MLX in the immunoprecipitates was analyzed by immunoblot. As a control, a mixture of lysates from cell transfected with FL MNT and ΔbHLH MNT (*Mix*) were immunoprecipitated with unspecific IgGs. *H*, HEK293T cells were co-transfected with a vector expressing MLX and the constructs shown in *F*, as indicated at the top. 24 h after transfection, cell lysates were prepared, and the cells were immunoprecipitated with mouse anti-HA antibody to pull down the exogenous MNT. As a control, a mixture of lysates from cells transfected with FL MNT and ΔbHLH MNT (*Mix*) were also immunoprecipitated with unspecific IgGs. The presence of MNT and MLX in the immunoprecipitates was detected by immunoblot. MAX co-IP was determined as a positive control. *I*, MLX localization in UR61 cells. Nuclear (N) and cytoplasmic (C) extracts were prepared from URMT cells as described under "Experimental procedures," and the levels of MNT and MLX were determined in each fraction by immunoblot. SIN3B and RhoGDI (ARHGDI) were used as nuclear and cytoplasmic markers, respectively. A picture of the gel stained with Coomassie Blue after transference is also shown as an indicator of the total amount of proteins in the cytoplasmic and nuclear fractions. *J*, interaction between MNT and MLX in the nucleus and cytoplasm. URMT cells were transfected with a MLX expression vector, and 48 h later nuclear and cytoplasmic extracts were prepared and immunoprecipitated with anti-MNT or anti-MLX antibodies. The levels of MNT and MLX in the immunoprecipitates were assayed by immunoblot.

MNT functions in the absence of MAX

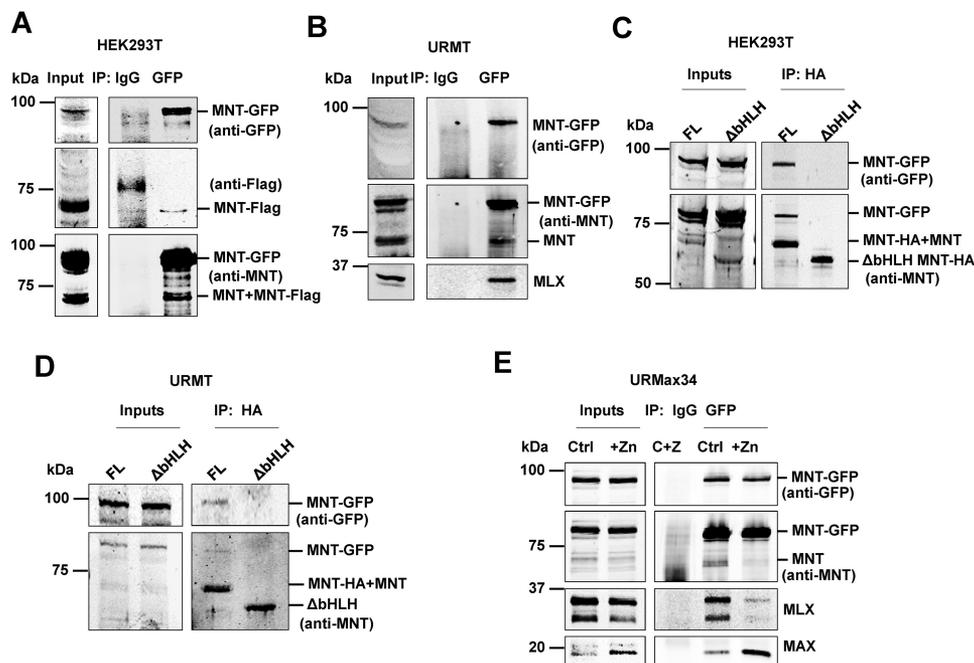


Figure 6. MNT homodimerization in UR61 cells. *A*, HEK293T cells were co-transfected with a GFP–MNT and MNT–Flag expression vectors, and 24 h later lysates were prepared and immunoprecipitated (IP) with an anti-GFP antibody. MNT–GFP and MNT–Flag were detected with the antibodies indicated at the right. As a control, lysates were precipitated with unspecific IgG. The antibodies used in each immunoblot are indicated at the right. The results were reproduced in two immunoprecipitations. *B*, URMT cells were infected with lentivirus encoding a MNT–GFP, and 72 h later were transfected with MNT–Flag and treated with 15 nM bortezomib for 12 h before harvesting. 48 h after transfection, lysates were prepared and immunoprecipitated with anti-GFP antibody. The presence of MNT–GFP, MNT, and MLX in the immunoprecipitates was assessed by immunoblot. The antibodies used in each immunoblot are indicated at the right. The results were reproduced in two experiments. *C*, HEK293T cells were co-transfected with expression vectors for MNT–GFP and expression vectors for FL MNT or Δ bHLH MNT (shown in Fig. 5F) as indicated at the top of each lane. 24 h later, lysates were prepared and immunoprecipitated with anti-HA antibody. The levels of MNT–GFP and MNT were determined by immunoblot using anti-GFP and polyclonal anti-MNT antibody. *D*, URMT cells were infected with lentivirus encoding a GFP–MNT and 72 h later transfected with expression vectors for full-length (FL) MNT or Δ bHLH MNT as indicated at the top of each lane. 48 h after transfection, cell lysates were prepared and immunoprecipitated with anti-HA to pull down the transfected MNT proteins. The levels of MNT–GFP and MNT were determined by immunoblot using anti-GFP and polyclonal anti-MNT antibody. *E*, URMax34 cells were transfected with a MNT–GFP expression vector, and 48 h after transfection cells were left untreated or treated with 100 μ M Zn^{2+} for 24 h to induce MAX. Then total cell lysates were prepared and immunoprecipitated with anti-GFP. As a control, a mixture of lysates from cells treated and untreated with Zn^{2+} was immunoprecipitated with unspecific IgG. The presence of MNT, MLX, and MAX in the immunoprecipitates was analyzed by immunoblot.

big and small MNT forms were detected when the immunoblots were analyzed with anti-MNT antibody. The results suggested the presence of homodimers between GFP–MNT and Flag–MNT in HEK293T cells. As a control, the lysates were immunoprecipitated with anti-MAX antibody, and both MNT and GFP–MNT were found to be bound to MAX (data not shown).

Next, we investigated the MNT homodimerization in the UR61 system. URMT cells were infected with lentiviral particles containing the GFP–MNT construct, immunoprecipitated with the anti-GFP antibody, and the immunoprecipitates analyzed by immunoblot with anti-MNT antibody and anti-GFP antibodies. The results showed that endogenous MNT was present in the immunoprecipitates with anti-GFP (Fig. 6B), suggesting that MNT forms homodimers in human HEK293T cells and in MAX-deficient rat URMT cells. As MNT dimerization in yeast two-hybrid assays depends on the bHLH-LZ (4, 5), we wondered whether HLH was involved in the homodimerization of MNT in our system. We transfected HEK293T cells with HA-tagged MNT constructs that lack the bHLH region (Δ bHLH MNT) (Fig. 5F) or the WT version together with GFP–MNT constructs, and we carried out immunoprecipitations with anti-HA antibodies that should only recognize the HA-tagged proteins. The immunoblot analysis of the immunopre-

cipitates revealed that Δ bHLH MNT was unable to interact with GFP–MNT (Fig. 6C). The same experiment was performed in URMT cells, and the same result was observed, *i.e.* GFP–MNT bound to WT MNT–HA but not to the Δ bHLH form (Fig. 6D). We conclude that MNT homodimerizes through the bHLH domain, as expected. We also wondered whether MNT preferentially binds to MAX or to MLX than to MNT itself. For this, we immunoprecipitated with the antibodies anti-GFP and lysates of URMax34 cells transfected with GFP–MNT that were untreated or treated with Zn^{2+} (to induce MAX). The levels of MAX and MLX after the immunoprecipitation assay were determined by immunoblot, and the results showed that when MAX and MLX are expressed, MNT preferentially binds to MAX than to MLX or MNT (Fig. 6E). Altogether, the results indicate that in URMT cells, MNT can form homodimers or heterodimers with MLX, whereas in URMax34 (in the presence of Zn^{2+}), MNT mainly forms heterodimers with MAX.

The former results showing that MNT can form homodimers open the possibility that in MAX-less cells, MNT can regulate gene expression either as a homodimer or as a heterodimer with MLX. To investigate this, we knocked down both MNT and MLX each with two short-hairpin constructs, in URMT cells (MAX-less) and URMax34 cells (with MAX) and

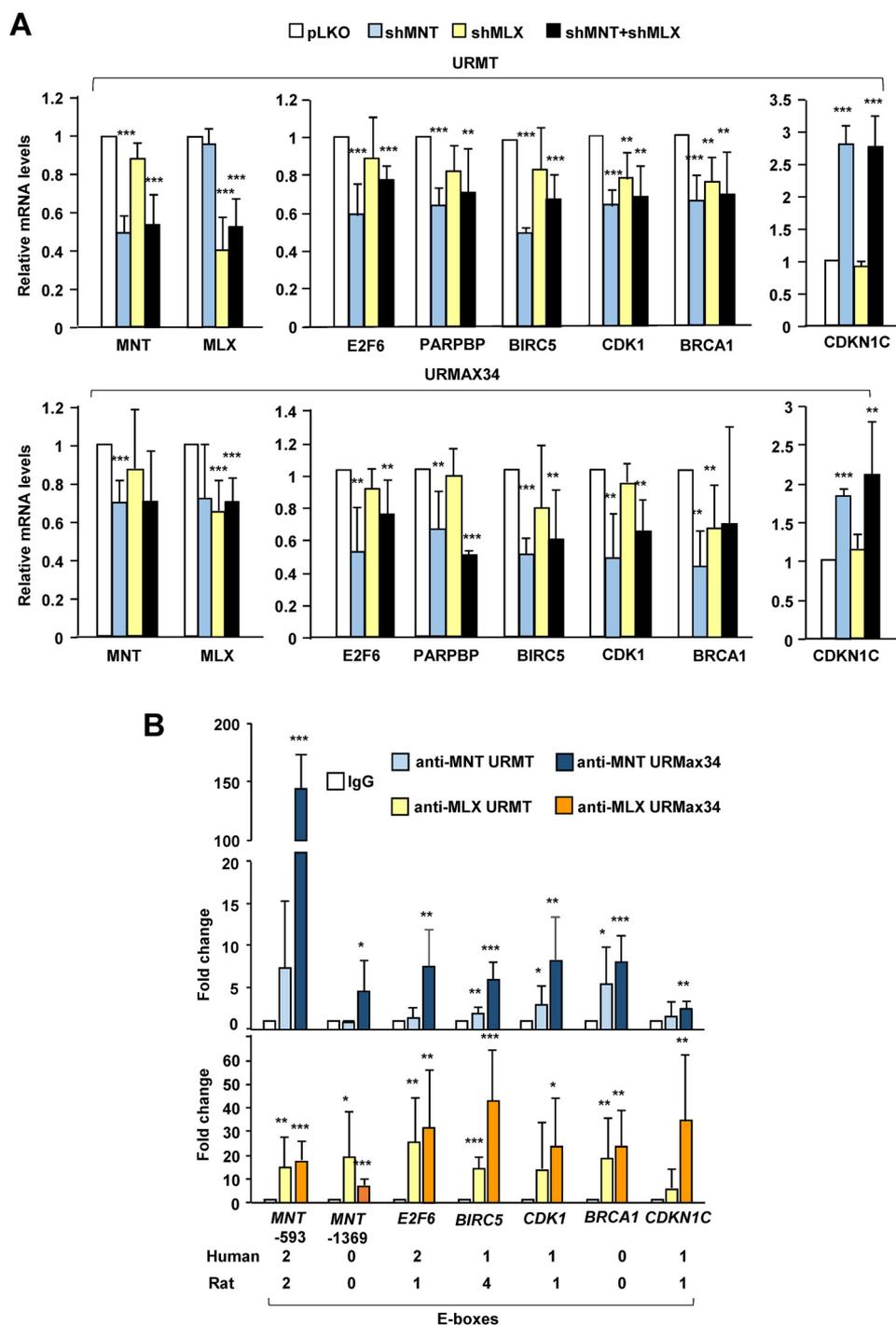


Figure 7. Gene expression changes in MNT and MLX knockdown cells. *A*, mRNA expression regulation due to MNT and MLX silencing in genes selected after the RNA-seq data analysis. URMT (*upper panel*) and URMax34 cells (*lower panel*) were transfected with a mixture of shMNT-1 and shMNT-2 and/or shMLX constructs as indicated. 48 h after transfection, cells were treated for a further 24 h with 100 μM Zn^{2+} , and total RNA was prepared, and mRNA levels of the indicated genes were determined by RT-qPCR. The data are shown as mean \pm S.D. ($n = 3$). ***, $p < 0.01$; **, $p < 0.05$. *B*, ChIP with anti-MNT (*upper panel*) and anti-MLX (*lower panel*) antibodies of URMT and URMax34 cells, both treated with 100 μM Zn^{2+} for 24 h. The genes were those validated from the RNA-seq in *A* and showing a peak of MNT binding in the ENCODE dataset for the K562 cell line. The binding of MNT and MLX was analyzed by qPCR in the amplicons shown in Fig. S9B. The data are means \pm S.D. ($n = 3$), ***, $p < 0.01$; **, $p < 0.05$; *, $p < 0.1$. PARPBP was not included as it does not show any MNT peaks in ENCODE. The presence of E-boxes in the regions bound by MNT in human K562 (according to ENCODE dataset) and in the corresponding regions in rat genome is indicated at the bottom.

determined the expression of some genes that, according to Fig. 4E, showed differential expression upon silencing of MNT. The depletion of MNT and MLX was confirmed at the mRNA (Fig. 7A) and protein levels (Fig. S8A). MLX knockdown led to retarded proliferation (Fig. S8B) to a similar extent as in MNT

depletion. The RT-qPCR analysis showed that in MAX-deficient cells, upon MNT knockdown, CDKN1C/p57 was up-regulated, whereas E2F6, PARPBP, and BIRC5 were down-regulated, as already shown in Fig. 4. However, the expression changes of these four genes were not significantly modified

MNT functions in the absence of MAX

when MLX was depleted or when both MNT and MLX were concomitantly depleted, suggesting that MNT could regulate these genes as homodimers (Fig. 7A). In contrast, *CDK1* and *BRCA1* were down-regulated when *MNT* was silenced but also when *MLX* was silenced (Fig. 7A). However, the expression of *CDK1* and *BRCA1* was not down-regulated further when both *MNT* and *MLX* were silenced. This suggests that both MNT–MNT and MNT–MLX dimers could be regulating the transcription of these genes.

To check whether the transcriptional changes observed upon *MNT* and *MLX* silencing were caused by a direct regulation driven by MNT and/or MLX, we performed ChIP–PCR assays in URMT and URMax34 cells after 24 h of stimulation with Zn^{2+} (i.e. cells in the absence or presence of MAX). From the genes analyzed by RT–qPCR (Fig. 7A), we chose to analyze the genes that showed a peak for MNT binding in the K562 ChIP–seq published in the ENCODE project: *E2F6*, *BIRC5*, *CDK1*, *BRCA1*, and *CDKN1C*. Then, primers for amplifying these regions in the rat genome were designed, and the presence of E-boxes in the amplicons was confirmed in all but *BRCA1* (Fig. 7B, bottom). The coordinates of the E-boxes in human and rat genomes are shown in Fig. S9A. The ChIP–PCR results showed that in the absence of MAX (in URMT cells), MLX and MNT were bound to the promoter of *BRCA1* and *BIRC5* (Fig. 7B).

Together with the results of Fig. 7A, the data suggest that these genes are regulated by MNT homodimers and possibly MNT–MLX dimers in the case of *BRCA1*, as the expression of this gene is affected by MLX knockdown. In the presence of MAX (URMax34 treated with Zn^{2+}), both MNT and MLX were bound to the promoters of the selected genes. MNT showed a much stronger signal in URMax34 cells than in the absence of MAX (Fig. 7B), suggesting a higher affinity of MNT–MAX to DNA and/or higher stability of the heterodimers versus MNT homodimers, as already shown in Fig. 4. We also performed a ChIP–PCR with anti-MAX in the same genes and amplicons in URMax34 cells and (as a negative control) in URMT. The results showed that MAX was bound to all promoters, but the signal in *BIRC5* and *BRCA1* was not statistically significant (Fig. S9B). Altogether, the data identified genes involved in cell cycle regulation and survival that are directly regulated by MNT–MNT or MNT–MLX dimers.

Discussion

In this study, we report several novel findings. (i) MNT is required for optimum proliferation even in the absence of MAX. (ii) In the absence of MAX, MNT expression is elevated, and a significant fraction localizes in the cytoplasm. (iii) MNT represses its own transcription in a MAX-dependent manner. (iv) MNT is able to regulate the expression of genes in the absence of MAX. (v) MNT forms homodimers in the cell. Previous reports suggest that MNT functions as a “MYC buffer,” curbing excessive MYC activity that would lead to cell transformation. For instance, *in vivo* MNT knockdown antagonizes MYC-driven lymphomagenesis (18, 19), whereas *MNT* silencing leads to MYC-like phenotypes (10, 11, 16). Our data show tight control of MNT expression by which MNT limits its own mRNA expression. These controls suggest that MNT plays a critical function in cell biology. Given the relevance of MNT

to modulate MYC activity and its central position between the MYC–MAX and MLX–MONDO networks, the activities and regulation of MNT are key issues for MYC-dependent oncogenesis.

MNT expression was high in some MAX-deficient cells like the rat UR61 cells and human lung carcinoma cell lines deficient in MAX. The absence of MAX was in part responsible for this effect because (i) MAX re-expression in UR61, Lu165, Lu134, and H1417 cells results in decreased MNT protein and mRNA (UR61, H1417, and Lu165), and (ii) MAX overexpression in K562 cells results in MNT down-regulation, whereas MAX knockdown results in MNT up-regulation. The mechanism for this MAX effect on MNT levels depended, at least partially, on the auto-repression of MNT expression by MNT–MAX dimers. Luciferase reporter experiments showed that MNT represses its own promoter (which depends on a conserved E-box), and ChIP assays showed that MNT strongly binds to its own promoter when MAX is ectopically expressed in UR61 cells. MNT binds weaker to its promoter in the absence of MAX, in agreement with the lack of binding to DNA of MNT *in vitro* (5), and a recent report shows reduced MNT binding to chromatin in MAX-deficient lymphocytes (29). In agreement with these results, the excess levels of MNT localize to the cytoplasm of MAX-deficient cells, whereas MNT is predominantly nuclear in MAX-expressing cells. This would explain why MAX re-expression leads to a decrease in MNT levels; MNT–MAX dimers would be formed to repress MNT expression in the nucleus. On the contrary, in the absence of MAX, MNT is expressed at higher levels because there would be no negative MNT autoregulation. We explored possible MAX-independent effects of MNT using the UR61 model. Although originally MAX was defined as an obligate dimerization partner of MYC, work carried out in the PC12 model and in *Drosophila* indicated that MYC can function in a MAX-independent manner, for example in inhibition of differentiation (30–32). MYC overexpression blocks RAS-induced differentiation of UR61 cells (31), although we did not detect a significant effect of MNT depletion on differentiation (data not shown). In contrast, depletion of MNT in MAX-deficient UR61 cells impairs cell proliferation. To our knowledge, this is the first report on a MAX-independent function of an MXD protein. The fact that MNT depletion impairs UR61 proliferation in a MAX-independent manner adds complexity to the MNT–MYC functional interactions. Conversely to our results in UR61 cells, ablation of *Mnt* in rodent fibroblasts leads to increased proliferation and transformation capacities (10, 16). Actually, in human gastric cancer, high MNT expression correlates with shorter survival, whereas MYC overexpression has the opposite effect (<http://kmplot.com/analysis/>).¹¹ Because MNT is a transcription factor, we compared the transcriptomes of parental UR61 cells versus cells with depleted MNT. Upon MNT depletion, a number of genes involved in cell cycle progression and DNA damage response were down-regulated in cells with and without MAX. Also, genes involved in cell cycle arrest such as *CDKN1C/p57* were up-regulated. These gene regulations are concordant with the decrease in proliferation exerted by *MNT* silencing in UR61. It is open to discussion how MNT regulates genes in the absence of MAX. MNT can form heterodimers

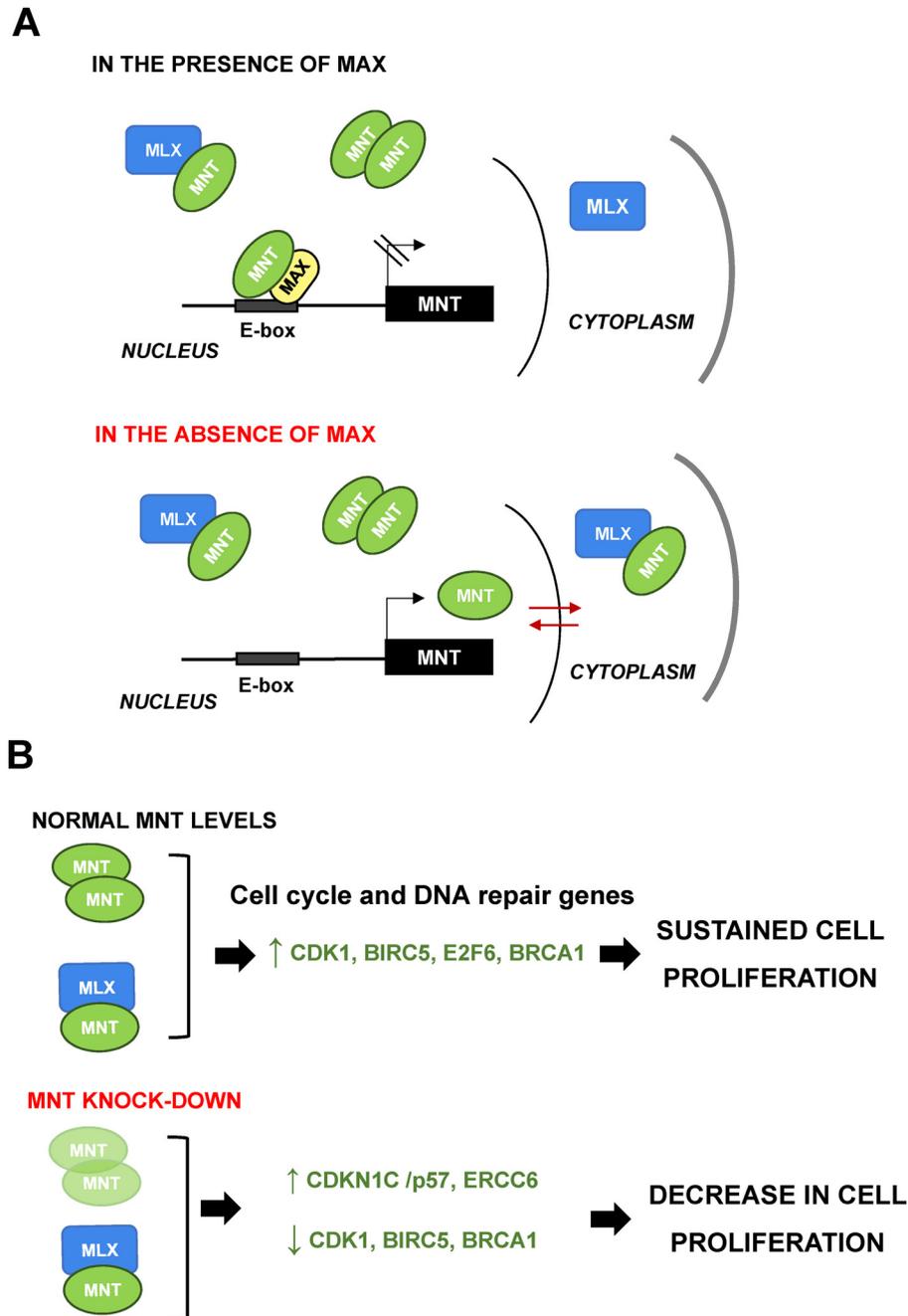


Figure 8. Models of MNT fates and biological roles depending on MAX. *A*, in MAX-expressing cells, most of the MNT is retained in the cell nucleus where it limits its own expression. In MAX-deficient cells as UR61, MNT is distributed in nucleus and cytoplasm and is unable to bind the promoter and regulate its transcriptional activity. The model includes the presence of MNT–MNT homodimers and the interaction MNT–MLX in the cytoplasm, which might be responsible for the MNT partial localization in the cytoplasm in MAX-deficient cells. *B*, model of the biological roles of MNT independent of MAX in UR61 cells. With physiological MNT levels, MNT homodimers and MNT–MLX heterodimers are enhancing cell cycle progression through direct regulation of CDK1 and BIRC5, and DNA repair through BRCA1-dependent mechanisms. However, upon MNT knockdown, this regulation is impaired, with a decrease in CDK1, BIRC5, and BRCA1 and increased levels of CDKN1C, E2F6, and ERCC6. This would cause a cell cycle arrest and the activation of ERCC6-dependent DNA repair mechanisms.

with the HLH protein MLX (6, 27). We have confirmed the ability of MNT to bind MLX in UR61 cells, but when MAX is expressed, the dimers MNT–MAX are favored *versus* MNT–MLX. As a relevant fraction of MLX is cytoplasmic and we have shown that MNT and MLX also interact in the cytoplasm, this interaction could help to explain the increase in cytoplasmic MNT observed in MAX-depleted cells. The model is depicted in Fig. 8A.

Moreover, we have shown that MNT homodimerizes in UR61 cells, and therefore it is likely that MNT regulates genes

as a homodimer as well. In fact, co-depletion of MLX and MNT does not modify the effect of MNT depletion on genes as *CDKN1C/p57*, *BIRC5/Survivin*, *CDK1*, *E2F6*, *BRCA1*, and *PARPB*. Furthermore, ChIP-seq and ChIP–PCR analyses show that MNT binds to some genes in MAX-deficient cells that are regulated by MNT (*BIRC5/Survivin*, *CDK1*, *BRCA1*, *ERCC6*, and *FBXO32*), supporting the possibility of a direct regulation by MNT homodimers or an indirect regulation in other cases where we did not detect MNT binding to the regions assayed (*CDKN1C* and *E2F6*). CDK1 is the only essential CDK protein

MNT functions in the absence of MAX

for cell cycle progression in animal cells (33). BIRC5/Survivin is also a critical protein for cell survival (34), and we have confirmed its regulation by MNT in URMT cells at the protein level. Thus, the MNT-dependent regulation of both genes helps to explain the antiproliferative effect of MNT knockdown in MAX-deficient cells. Altogether, the data suggest that MNT can regulate transcription as a homodimer or heterodimer with MLX or another not yet identified protein. MNT homodimerization has already been shown in yeast two hybrids (4) and *in vitro* (5), although recombinant MNT homodimers did not bind DNA (5). The analysis of MNT-bound regions in our ChIP-seq experiments also revealed the presence of sites for forkhead factors (FOX P1, FOX A2, and FOX O3) in agreement with the reported coordinated regulation between MNT and FOX O of some cell cycle control genes (25). Further work is required to clarify this point. According to our results, MNT homodimers or MNT–MLX heterodimers would be regulating cell cycle and DNA repair checkpoint genes in a MAX-independent manner for correct survival and proliferation of the cells. The model based on these observations is presented in Fig. 8B.

In summary, the results reported here show a strict autoregulation of MNT, supporting a pivotal role of MNT in the control of cell proliferation even in the absence of its canonical dimerization partner MAX.

Experimental procedures

Cell lines and transfections

Cell lines were obtained from ATCC and grown in either RPMI 1640 or Dulbecco's modified Eagle's medium (Lonza) supplemented with 10% fetal bovine serum (Lonza), 150 $\mu\text{g}/\text{ml}$ gentamicin, and 2 $\mu\text{g}/\text{ml}$ ciprofloxacin. UR61 is derived from PC12 cells (35). All cells tested negative for *Mycoplasma* infection by PCR. To generate the URMT and URMax34 cells, UR61 cells were electroporated (260 V, 1 millifarad, Bio-Rad apparatus) with a pHeBo-MT (to generate URMT cells) or pHeBo-MT–Max vector (to generate URMax34 cells), which carries a human MAX cDNA under the control of metallothionein promoter (24). Cells were selected with 0.2 mg/ml hygromycin (Life Technologies, Inc.), and cell clones were isolated by limiting dilution. Two clones transfected with pHeBo-MT–Max showing MAX induction upon Zn^{2+} addition were pooled, and the resulting cell line was termed URMax34. Five clones transfected with pHeBo-MT were pooled and termed URMT cells. Transient transfections were carried out using the Ingenio electroporation solution (Mirus) in an Amaxa nucleofector. The cells were transfected or transduced with expression vectors for the following: MAX (pCEFL-MAX (36)); MLX β isoform (pMS18-MLX (7)); human MNT (pCMVSPORT6-MNT, Origene Technologies); MNT–Flag (human MNT with FLAG at the C-terminal lentiviral Lvl58 vector, Genecopoeia); MNT–GFP (human MNT with GFP at the N-terminal lentiviral Lvl103 vector, Genecopoeia); FL MNT-HA (full-length murine MNT tagged at the C terminus with hemagglutinin epitope (HA)); ΔHLH MNT-HA (murine MNT carrying a deletion of amino acids 221–272 and tagged with HA) (both in pcDNA3 with the Zeocin resistance gene inserted); short-hairpin human

MNT-1 (shMNT-1, pLKO-shMNT from Sigma Mission, TRCN0000085733) or MNT-2 (shMNT-2, pLKO-shMNT from Sigma Mission, TRCN0000235815); siRNA for human MAX (Sigma, SASI_Hs01_00011941).

Immunoblot and immunoprecipitation

Cell lysis, immunoblots, and immunoprecipitations were performed as described (37). Each immunoblot shows a representative experiment out of at least two biological replicates with similar results. The antibodies used are described in Table S7.

Luciferase reporters and assays

To generate the MNT-luc, E-box 1 MNT-luc, and E-box 2 MNT-luc reporter vectors, two pairs of primers were designed for each construct (Table S8), targeting sequences of the human genome corresponding to 850 bp upstream from the transcription start site of the *MNT* gene. The amplified DNA was inserted into the pBV-luc reporter vector at the EcoRV and HindIII sites (38). The sequence of the MNT promoter was from the UCSC genome browser. Cells were transfected with jetPEI[®] reagent (Polyplus), and luciferase assays were performed, as described previously (37).

Cell proliferation, cell cycle, and annexin V–binding analysis

Cell proliferation was monitored with a cell counter (NucleoCounter NC-100, Chemometec) or a cytometer (Guava PCA, Merck Millipore). For the clonogenic assays, $1\text{--}2 \times 10^6$ cells/ml were seeded in a 6-well or 60-mm plate after transfection by electroporation. 48 h post-transfection, cells were selected with puromycin at 0.2–0.5 $\mu\text{g}/\text{ml}$ final concentration. After 8–17 days, the cells were stained with crystal violet, and the dye was measured by absorbance at 595 nm as described (39). To determine the sub- $G_0\text{--}G_1$ population, cells were transfected, and 7 days post-transfection, the DNA concentration was analyzed by propidium iodide staining and flow cytometry as described (40). Apoptosis was assayed by annexin V–positive binding in MACSQuant VYB (Miltenyi Biotec). Roughly, 10^6 cells were harvested and washed twice with previously filtered PBS and 3 mM EDTA. Cells were resuspended in 10 mM HEPES/NaOH, pH 7.4, and stained with 5 μl of annexin V–FITC (BD Biosciences) for 1 h. Cells were washed twice and resuspended in 500 μl of binding buffer with 5 μl of 7-aminoactinomycin D (Immunostep apoptosis detection kit). The results were analyzed with Flow Logic software (Miltenyi Biotec).

RNA analysis and RNA-seq

For qPCR, total RNA was isolated using the TRI Reagent Solution (Invitrogen). cDNA was generated by reverse transcription (RT) using the iScript (Bio-Rad). Quantitative PCR (qPCR) was performed with specific primers (Table S8) using the iTaq Universal SYBR Green Supermix (Bio-Rad) and CFX Connect Real-Time PCR Detection System (Bio-Rad). RNA was converted into cDNA and analyzed as described (41). Levels of mRNA were normalized against actin and RPS14 mRNA levels. For RNA-seq, total RNA was isolated with the RNeasy kit (Qiagen) from two independent experiments of MNT silencing in URMT and URMax34 cells, both treated with 100

μM ZnSO_4 for 24 h. mRNA libraries were prepared using the Illumina TruSeq RNA Sample Prep kit version 2 (kit RS-122-2002, Illumina). A minimum of 40 million 50-base single-end reads per sample were obtained. TopHat algorithm (42) was used to align the data using a set of gene model annotations and/or known transcripts of rat genome obtained from RefSeq database. Cufflinks software (43) was run to estimate transcript abundances represented in RPKM units (reads per kilobase per million reads) as described (44). The gene expression of the genes are represented as RPKM values. The log₂ RPKM values of the transcripts that were differentially expressed in URMT and URMax34 cells were represented in a dot graph with the log₂ RPKM values of the control condition (pLKO) on the *x* axis and the log₂ RPKM values of the experimental condition (shMNT) on the *y* axis.

ChIP and ChIP-seq

Total-cell extracts were first lysed with a hypotonic buffer (described under “Nuclear/cytoplasmic fractionation”) for purifying the nuclear compartment. Then, nuclear lysis and ChIP were performed essentially as described previously (37). Immunoprecipitated DNA was purified with the QIAquick PCR purification kit (Qiagen) and analyzed by qPCR. The antibodies and primers used are described in Tables S7 and S8, respectively. For ChIP-PCR, chromatin was prepared from URMT and URMax34 cells (both treated with 100 μM ZnSO_4 for 24 h) and immunoprecipitated with anti-MNT antibody and unspecific IgG. For ChIP-seq, we used MNT-bound chromatin and the corresponding inputs from URMT cells. Single-end 51-bp ChIP-seq data from three replicate experiments and three input samples of URMT cells were generated by HiSeq. Alignment and peak detection were performed using the ENCODE (phase-3) transcription factor ChIP-seq pipeline specifications (45). Reads were aligned to the rat reference genome (assembly Rnor_6.0) using BWA (46), removing duplicates with PICARD (Picard Toolkit 2018, <http://broadinstitute.github.io/picard>)¹¹ and filtering all reads with a quality score <30. Peaks were called using SPP (47) and input samples as background samples. Enrichment and quality measures were computed with Phantompeakqualtools (48). Reproducibility of peaks identified from the three replicate experiments was measured using IDR with a threshold of 0.1. Peak annotation was performed with Homer (<http://homer.ucsd.edu/homer/motif/motifDatabase.html>)¹¹ (49).

The SYDH ENCODE project was chosen for representation of the binding peaks in the promoter of the human MNT gene. The sequences corresponding to those peaks were analyzed confirming the presence of the E-boxes identified in the human MNT promoter. Enriched motifs on immunoprecipitated regions were identified by HOMER (49) FindMotifsGenome algorithm using the rat genome Rnor_6.0 version as reference, masking common repeats and with a region size of 200 bp (<http://homer.ucsd.edu/homer/motif/motifDatabase.html>).¹¹ The RNA-seq and ChIP-seq data have been deposited to the European Nucleotide Archive with the accession number PRJEB23604.

Nuclear/cytoplasmic fractionation

Cytoplasmic and nuclear extracts were prepared essentially as described (50). The hypotonic buffer to lyse cells was 10 mM HEPES, pH 7, 10 mM KCl, 0.25 mM EDTA, pH 8, 0.125 mM EGTA, pH 8, 0.5 mM spermidine, 0.1% Nonidet P-40, 1 mM DTT, and proteases inhibitors. The hypertonic buffer for nuclear extracts was 20 mM HEPES, 400 mM NaCl, 0.25 mM EDTA, 1.5 mM MgCl_2 , 0.5 mM DTT, and proteases inhibitors.

Statistical analysis

Student's *t* test was used to evaluate the significance of differences between control and experimental groups. A *p* value of less than 0.05 was considered as significant. The threshold for expression changes in the RNA-seq analysis was set as log₂(RPKM fold change) ≥ 0.7 or ≤ -0.7 and a *p* value <0.1.

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The MNT transcription factor autoregulates its expression and supports proliferation in MYC-associated factor X (MAX)-deficient cells

M. Carmen Lafita-Navarro, Judit Liaño-Pons, Andrea Quintanilla, Ignacio Varela, Rosa Blanco, Fabiana Ourique, Gabriel Bretones, Julia Aresti, Ester Molina, Patrick Carroll, Peter Hurlin, Octavio A. Romero, Montse Sanchez-Céspedes, Robert N. Eisenman, M. Dolores Delgado and Javier León

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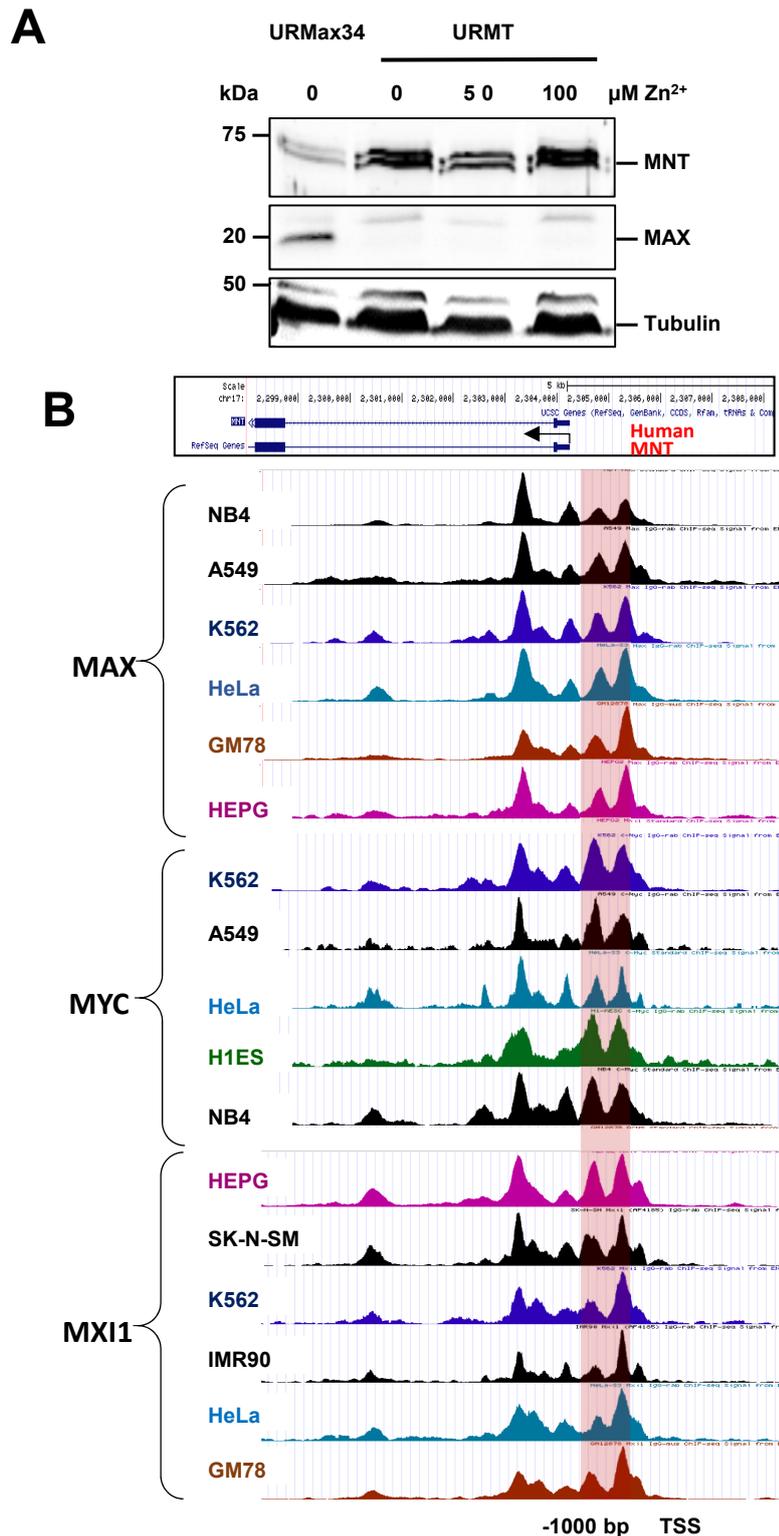
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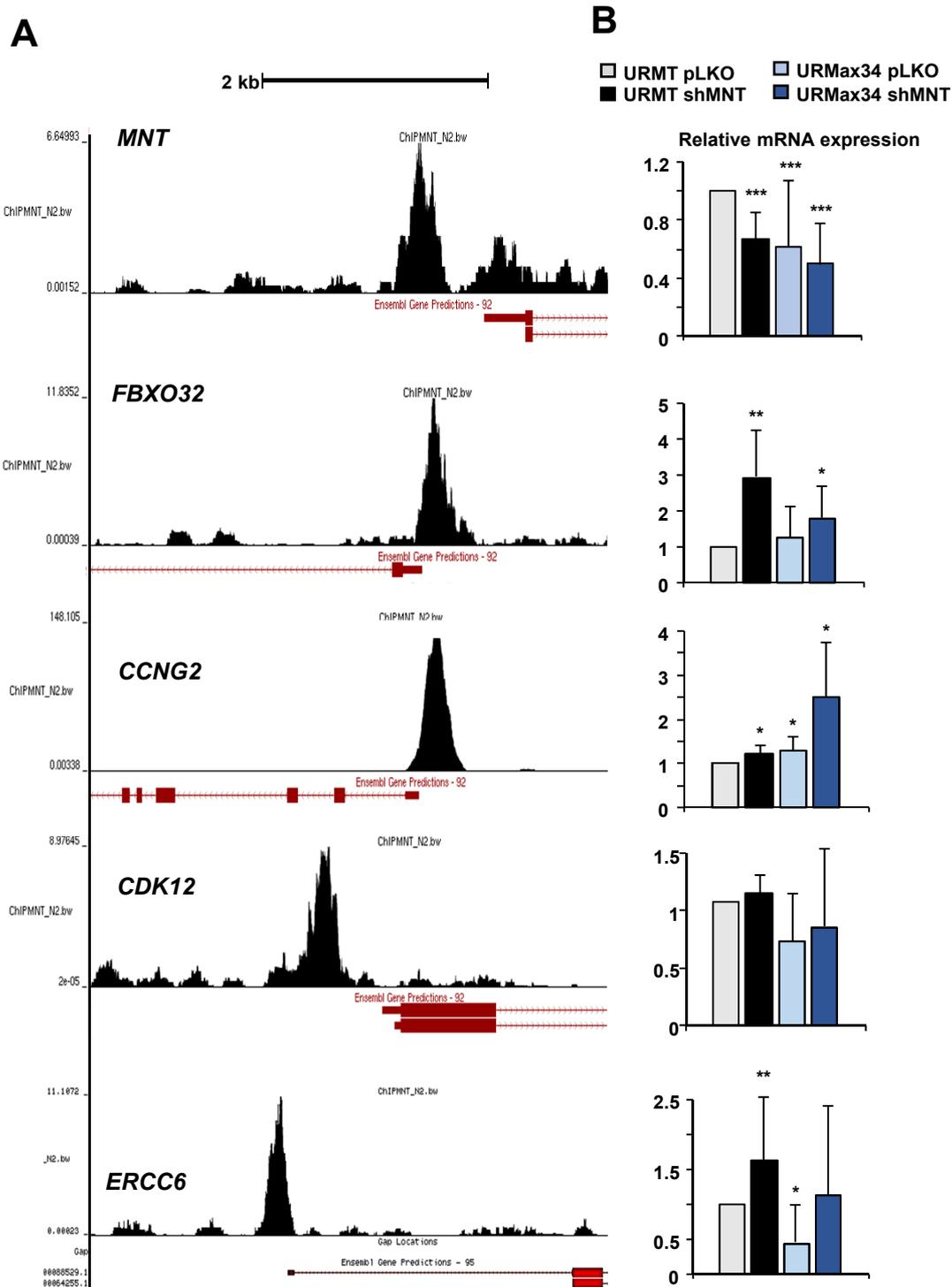
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Supporting Figure S1. MNT levels in URMT cells upon Zn^{2+} treatment and MAX binding to the MNT promoter. A, URMT cells were treated for 24 h with 0, 50 and 100 $\mu\text{M Zn}^{2+}$ and the MNT (a doublet) and MAX protein expression were determined by immunoblot. URMax34 cells without treatment as a comparative control. α -tubulin levels determined as a protein loading control. B, MYC, MAX and MXI1 bound to the MNT promoter. ChIPseq peaks found on the human MNT gene corresponding to signals with anti-MAX, anti-MYC and anti-MXI1 antibodies in the indicated cell lines. The MNT gene and its 5' \rightarrow 3' orientation (from right to left) is indicated at the top. The region 1000 bp upstream from the transcription start site (TSS) is indicated as a pink shadow. The data are from the Stanford/Yale/USC/Harvard (SYDH) ENCODE project (<http://genome.ucsc.edu/ENCODE/>, release GRCh37/hg19).

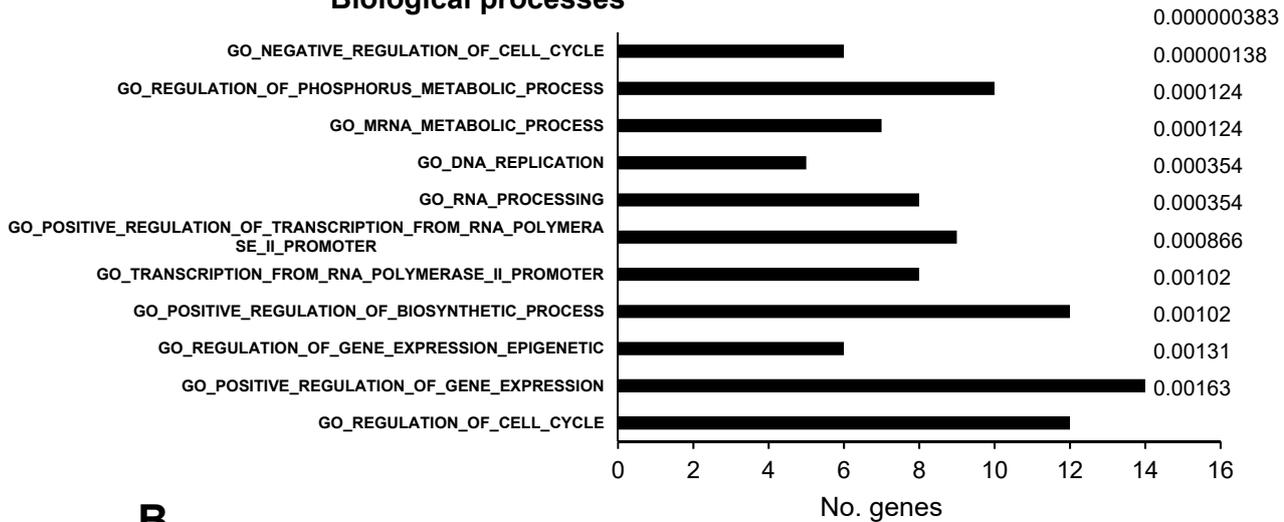


Supporting Figure S2. MNT ChIP-seq peaks on selected genes and MNT effect on their regulation. A, MNT ChIP-seq peaks found on the *MNT*, *FBXO32*, *CCNG2*, *CDK12* and *ERCC6* promoters in URMT cells, using the UCSC rat genome browser (RGSC 6.0/rn6) assembly. The image shows the peaks of one of the three replicates of the assay. B, Expression of *MNT*, *FBXO32*, *CCNG2*, *CDK12* and *ERCC6* in URMT and URMax34 cells 48 h after transfection with shMNT-2 or empty vector pLKO constructs and 24 h of treatment of Zn²⁺. Data obtained by RTqPCR was normalized with RPS14 and related to the expression in URMT with pLKO. The data are mean \pm S.D. (n = 3). *P < 0.1; **P < 0.05.

FDR q-value

A

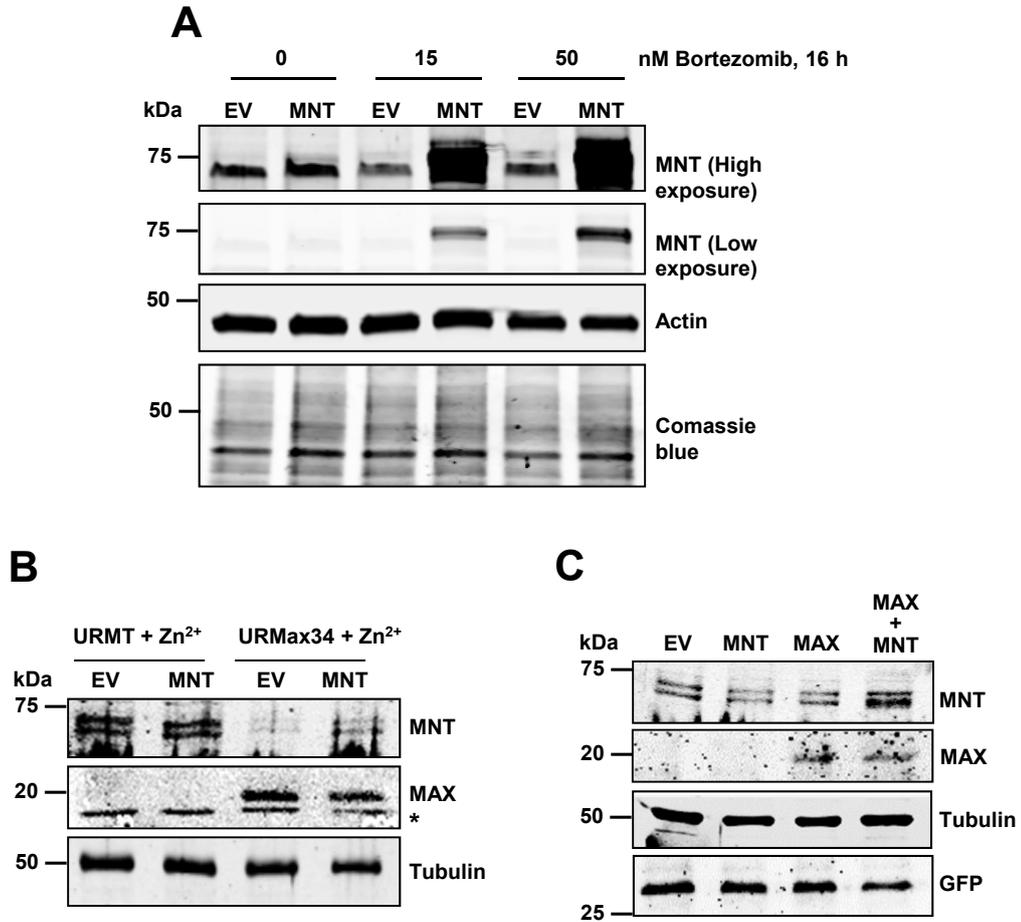
Biological processes



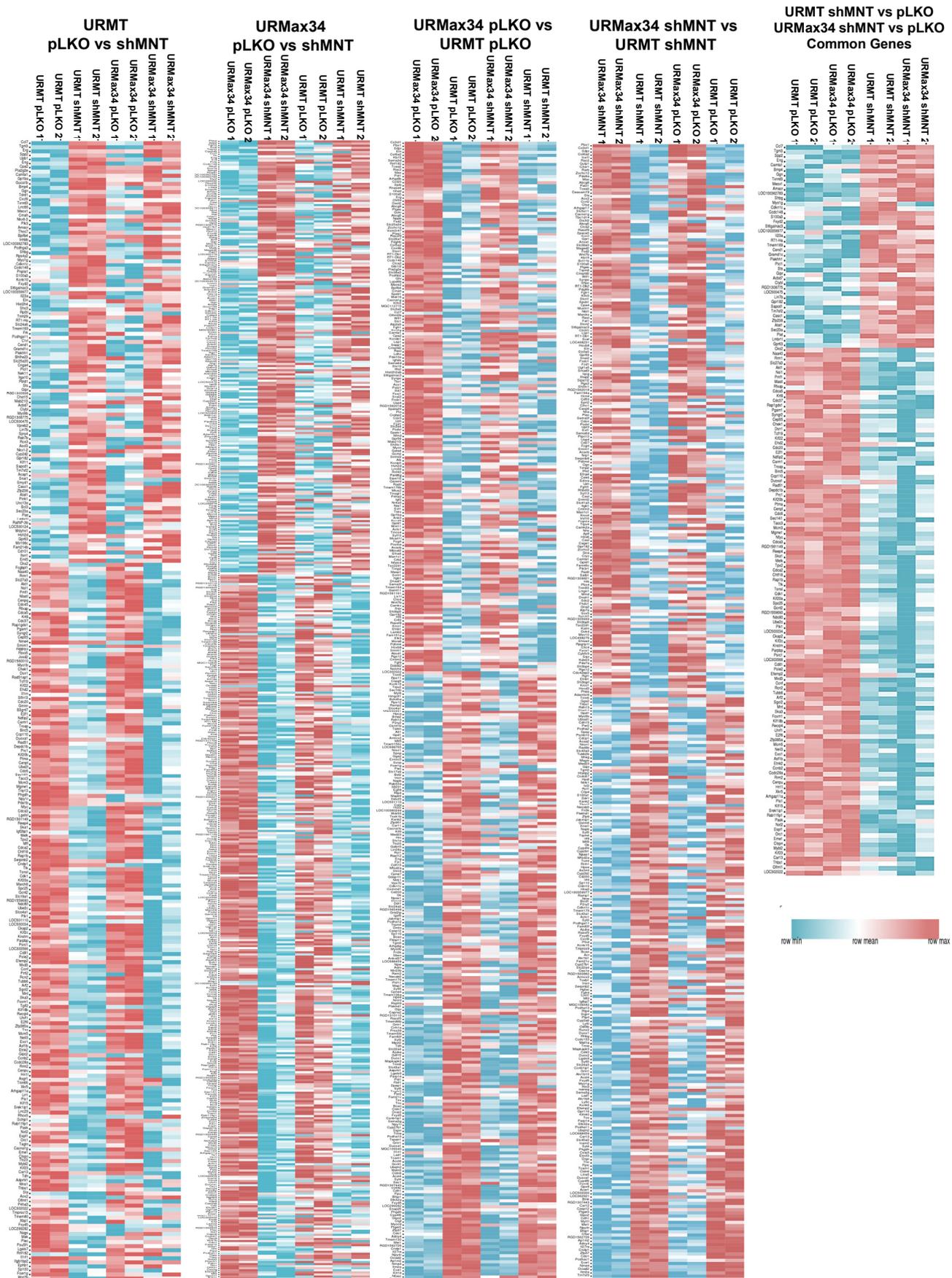
B

Sequence	Factor	log P-value	q-value	No. of targets
	FOXP1	-6.512e+00	0.6148	77
	FOXA2	-5.496e+00	0.8490	164
	SMAD2	-5.441e+00	0.8490	30
	FOXO3	-5.428e+00	0.8490	121
	VDR	-5.235e+00	0.8490	31
	RXR	-5.011e+00	0.8490	135
	E-box 1	-5.006e+00	0.8490	12
	E-box 2	-4.881e+00	0.8490	150
	TBXT	-4.834e+00	0.8490	43
	EWS-FLI	-4.672e+00	0.8490	86

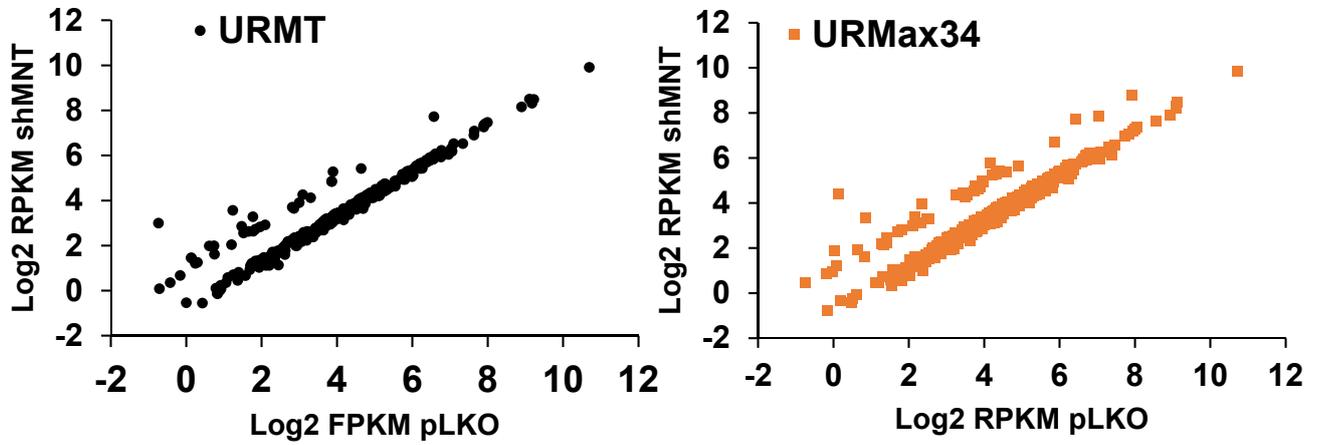
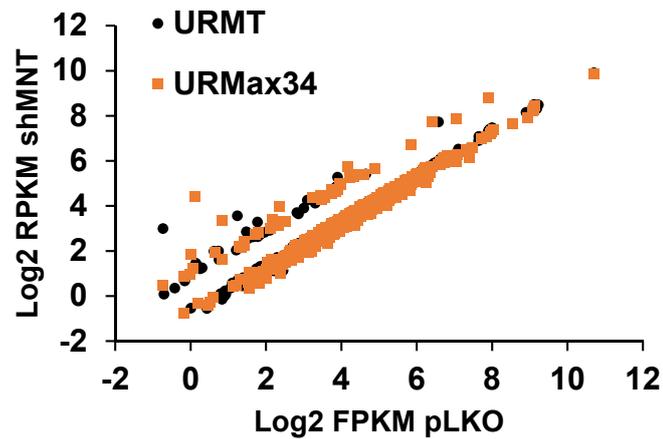
Supporting Figure S3. Analysis of MNT-bound genes. A, Gene ontology of MNT-bound genes. The relevant processes in which the genes are involved are cell cycle, DNA replication and regulation of expression. The genes where MNT was found to be significantly bound (FDR < 0.1) within +/- 3 Kb of their TSS in our ChIPseq experiment were analyzed with the MsigDB platform (<http://software.broadinstitute.org/gsea/msigdb>) using the biological processes gene sets. The 11 top enriched pathways according to FDR value are represented in the graph. B, DNA motifs bound by MNT. HOMER enriched results for known sequence motifs on MNT-immunoprecipated DNA regions on rat genome. The 10 motifs with higher scores are shown. The ChIP-seq data from Supporting Table S1 was analysed by the HOMER algorithm (<http://homer.ucsd.edu/homer/motif/motifDatabase.html>) using the rat genome Rnor_6.0 version as reference



Supporting Figure S4. Reduced MNT stability in the absence of MAX. *A*, MNT expression in UR61 transfected with a MNT expression vector and treated with bortezomib. Cells were transfected with the empty vector (E.V.) and MNT expression vector, and 36 h after transfection the cells were treated for 16 h with 15 nM and 50 nM bortezomib as indicated. The levels of MNT and β -actin were determined by immunoblot. A picture of the gel stained with Coomassie blue is shown at the bottom. *B*, UR61 or URMax34 cells were treated with Zn²⁺ to induce MAX (in URMax34 cells) and transfected with a MNT expression vector or the empty vector (EV, pCMV-Sport6-MNT) and 48 h after transfection the levels of MNT and MAX were analyzed by immunoblot. The asterisk marks an unspecific band. The levels of α -tubulin were also determined as a protein loading control. As expected, URMax34 treated with Zn²⁺ expressed lower MNT levels that MAX-less cells (URMT) but showed MNT overexpression upon transfection. *C*, UR61 cells were transfected with MNT and MAX expression vectors (pCMV-Sport6-MNT and pCEFL-MAX respectively) as indicated at the top, as well as the corresponding empty vectors. In each case a GFP expression vector was also cotransfected. 48 h after transfection the levels of MNT and MAX were analyzed by immunoblot. α -tubulin was determined as a protein loading control and GFP levels as transfection control.



Supporting Figure S5. Heatmaps of gene expression. The heatmaps of the gene expression changes of the comparison indicated at the top of each panel were generated with the Genepattern software and HeatMapView tool, with log2FC data of the genes included in the Supporting Tables 2-5

A**B**

Supporting Figure S6. Distribution of differentially expressed transcripts in URMT and URMax34 upon MNT knockdown. *A*, Dot plot of the Log₂ RPKM values in URMT (black circles) and URMax34 (orange squares) cells where MNT was silenced by shRNA. x-axis values show Log₂ RPKM values in the control condition (pLKO) and y-axis values show Log₂ RPKM values in the shMNT condition. *B*, Overlapped dot plot of the differentially expressed transcripts in the URMT and URMax34 showing similar grades of transcriptional changes in the absence or presence of MAX when MNT is silenced.

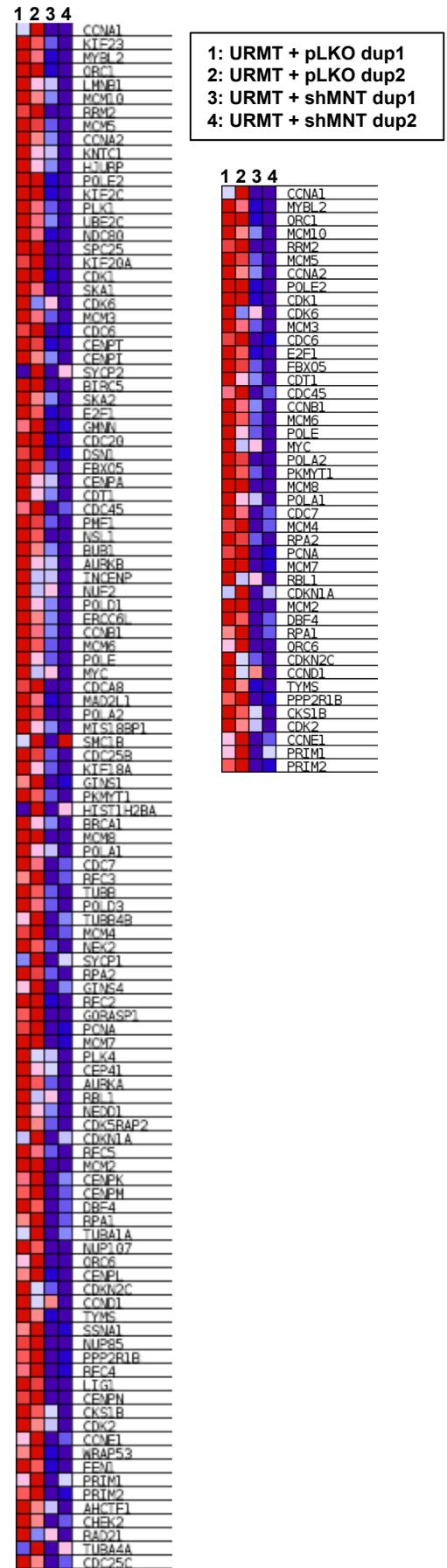
A

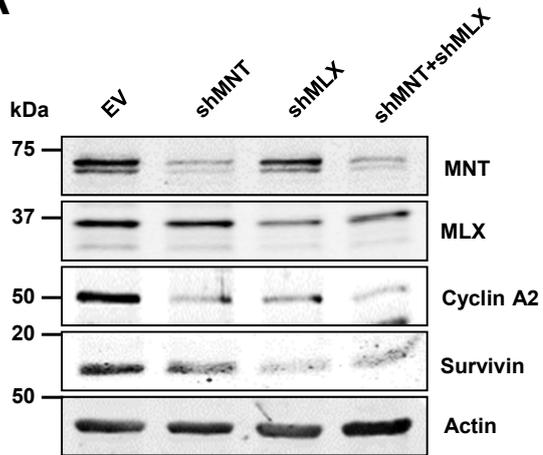
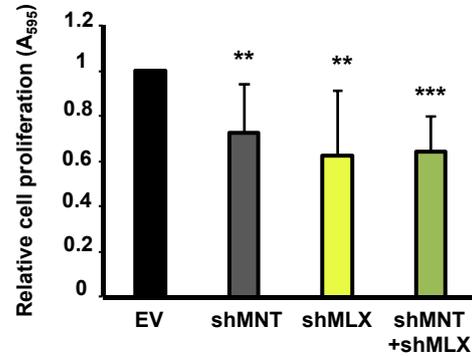
URMT, pLKO vs shMNT-1					
Genes in comparison: 249; Total genes: 45,956					
	Genes in set (K)	# Genes in Overlap (k)	k/K	p-value	FDR qvalue
Cell cycle	1316	69	0.0524	1.63E-47	7.21E-44
Cellular response to DNA damage	720	29	0.0403	6.55E-17	1.94E-14
Regulation of phosphorus metabolic process	1618	36	0.0222	7.96E-13	1.26E-10
Regulation of cellular localization	1277	30	0.0185	9.04E-10	8.02E-08

URMax34, pLKO vs shMNT-1					
Genes in comparison: 474; Total genes: 45,956					
	Genes in set (K)	# Genes in Overlap (k)	k/K	p-value	FDR qvalue
Cell cycle	1081	118	0.1092	7.97E-85	3.54E-81
Regulation of organelle organization	1178	75	0.0637	1.17E-36	4.32E-34
Cellular response to stress	1565	73	0.0466	3.79E-27	7.30E-25
Regulation of phosphorus metabolic process	1618	68	0.0423	8.95E-23	1.24E-20

Supporting Figure S7. Gene Ontology of MNT-regulated genes. A, Gene ontology showing the genes with expression changes in the MNT-depleted URMT and URMax34 cells (shown in Figure 4 –source data 1-4) were analysed with the MsigDB platform (<http://software.broadinstitute.org/gsea/msigdb>). The four top enriched pathways found in the analysis are represented in the table. B, Expression heatmaps of the enriched genes from the REACTOME_CELL_CYCLE (A) and the REACTOME_MITOTIC_G1_G1_S_PHASES (B) gene sets found in the RNA-seq (Fig 4D). Data generated with the Gene Set Enrichment Analysis (GSEA).

B



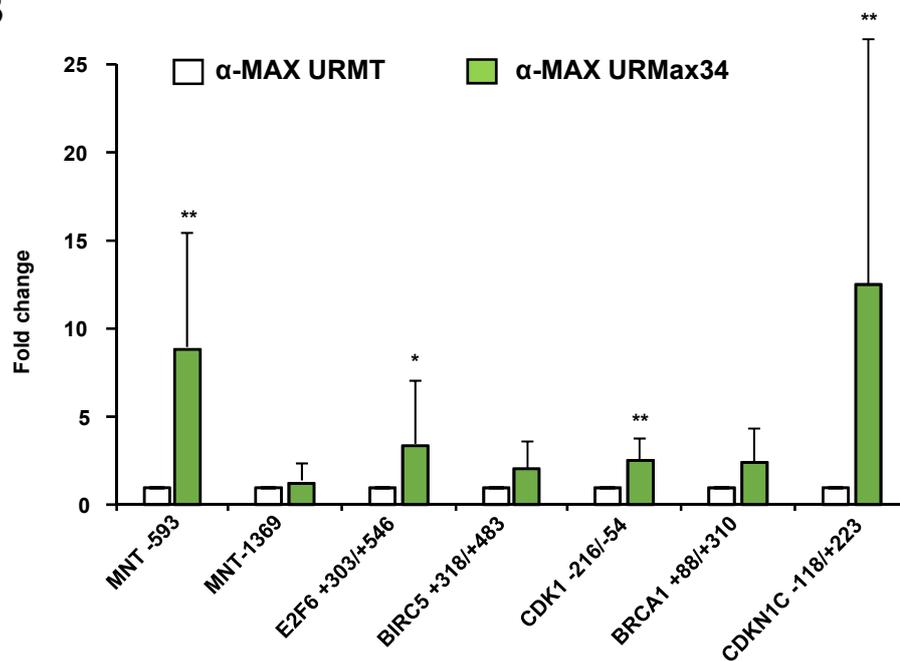
A**B**

Supporting Figure S8. MLX depletion in URMT cells. A, URMT cells were transfected with shMNT2 and shMLX, or the empty vector (EV) as indicated at the top. 5 days after selection with puromycin the cell lysates were subjected to immunoblot to detect MNT and MLX. Cyclin A2 and survivin were determined as control for proliferation and β -actin as protein loading control. B, Cell growth determined by crystal violet staining in URMT cells transfected with the indicated short hairpin vectors. After 15 days of puromycin selection the colonies were stained with crystal violet and the dye was solubilised and quantified by absorbance at 595 nm. EV, empty vector (pLKO) Data show mean values \pm S.D. (n= 4) ** $P < 0.05$; *** $P < 0.005$.

A

Gene	Peak MNT ChIP-seq ENCODE Project (human K562)		Analyzed sequence in rat genome	
	Position	E-boxes	Amplicon	E-boxes
E2F6	-202/+574	CACGTG +109 and +534	+303/+546	CACGTG +309
BIRC5	-335/+365	CACGCG -149	+318/+483	CACGCG -216 bp CACGAG +303 and +477 CATGTG +727
CDK1	-298/+270 +783/+1413	CACGTG +1157	-216/-54	CCACGTG +207
BRCA1	-295/+231	None	+88/+310	None
CDKN1C	-118/+512	CACGAG +890	-118/+223	CACGAG +401

B



Supporting Figure S9. E-boxes in MNT-bound regions and ChIP for MAX. A. Table of the genes found to have a peak for MNT binding in the K562 ChIP-seq published in ENCODE. The position of the peaks and their E-boxes are shown, together with the corresponding regions analyzed in rat and the E-boxes identified around the amplicons. Coordinates correspond to the rat reference genome (assembly Rnor_6.0). B. ChIP with anti-MAX antibody of URMax34 cells relative to URMT, both treated with 100 μ M Zn⁺² for 24 h. Data determined by qPCR on the amplicons listed in A. Represented as means \pm S.D. (n = 3). *P < 0.1; **P < 0.05;

Supporting Table S1. ChIP-seq results of MNT-bound regions in URMT cells genome. The table shows the genes and regions detected in the ChIP-seq experiments (in triplicate) with a q-value <0.7. Chr., chromosome; TSS, transcription start site

Gene	Chr.	Start	End	Distance to TSS	Signal	q-value	Annotation
AABR07003040.1	chr1	94473713	94474035	-19692	141.86198	0.00001	Intergenic
Mcm7	chr12	19312805	19313475	876	105.2951	0.00001	intron (ENSRNOT00000001825, intron 1 of 13)
Ythdc2	chr1	180971723	180972393	1168512	49.84661	0.00001	Intergenic
Ccng2	chr14	16275925	16276657	-223	499.62541	0.00001	promoter-TSS (ENSRNOT00000002876)
Foxk1	chr14	16275925	16276657	-35451	192.85369	0.00001	Intergenic
Riok2	chr1	82452065	82452735	-143	115.75299	0.00001	promoter-TSS (ENSRNOT00000017165)
Cdc40	chr9	41337486	41338156	16	128.25274	0.00001	promoter-TSS (ENSRNOT000000087740)
Phf21b	chr1	180738768	180739438	28364	110.59105	0.00001	intron (ENSRNOT00000017906, intron 2 of 12)
AABR07035428.2	chr12	19328514	19329184	17579	115.50543	0.00001	intron (ENSRNOT00000001466, intron 2 of 8)
Cdk12	chr12	14200676	14200946	-649	131.03918	0.00001	promoter-TSS (ENSRNOT000000082668)
Rps6ka5	chr6	124735773	124736443	-330	113.89653	0.00001	promoter-TSS (ENSRNOT000000091693)
AABR07064998.2	chr10	11205633	11206303	8528	98.78731	1.14956E-05	Intergenic
Klhl24	chr13	89445422	89446092	-10343	101.2998	1.71845E-05	Intergenic
Tnrc6b	chr7	121930127	121930797	-153	85.87448	2.70396E-05	promoter-TSS (ENSRNOT000000033975)
Hbp1	chr6	51257652	51258322	-362	86.06352	3.93079E-05	promoter-TSS (ENSRNOT00000012004)
Kdm5b	chr10	86156624	86157294	-2633	88.85319	5.37023E-05	Intergenic
LOC103690980	chr1	54058156	54058826	-3695	21.96606	6.73184E-05	Intergenic
Gabarapl1	chr20	40913271	40913941	-353	82.66174	8.09128E-05	promoter-TSS (ENSRNOT000000077356)
LOC100911356	chr13	90513902	90514572	-99	80.84637	9.42048E-05	promoter-TSS (ENSRNOT000000088996)
Cdc40	chr1	46329360	46330030	-69	88.46051	0.000108611	promoter-TSS (ENSRNOT000000087740)
Ythdc2	chr6	103938301	103938971	1401239	83.42893	0.000123613	Intergenic
RF00002	chr7	2201465	2202135	20153	80.45633	0.000140917	Intergenic
Mcm7	chr12	19313004	19313674	677	73.05478	0.000158173	promoter-TSS (ENSRNOT00000001827)
Tnrc6b	chr7	121930333	121931003	30	66.555	0.000174939	promoter-TSS (ENSRNOT000000033975)
Tcp11l2	chr7	24893820	24894490	-8380	79.92627	0.00019055	Intergenic
Ccng2	chr6	103798975	103799645	-223	75.17918	0.00020692	promoter-TSS (ENSRNOT00000002876)
Fbxo32	chr7	98098039	98098709	-106	80.31343	0.000224979	promoter-TSS (ENSRNOT00000010361)
Cyp2b1	chr7	98098238	98098908	116213	22.85698	0.00024348	Intergenic
Fcgr2b	chr20	48503654	48504324	-11942	69.35571	0.000264378	Intergenic
LOC683469	chr16	15111110	15111780	140	111.42867	0.000284299	exon (ENSRNOT000000060703, exon 1 of 4)
Zdbf2	chr9	70041233	70041903	-18115	39.51652	0.000304983	Intergenic
Tmem242	chr1	180692356	180693026	-13	76.29343	0.000324734	promoter-TSS (ENSRNOT000000046311)

Vom2r37	chr1	99094686	99095356	40956	71.98416	0.000343835	intron (ENSRNOT00000056515, intron 4 of 4)
Kmt5b	chr1	219001037	219001707	528	75.31798	0.000362686	intron (ENSRNOT00000022486, intron 1 of 11)
Ythdc2	chr1	180692621	180693291	1447614	39.92178	0.000380706	Intergenic
AABR070 20651.1	chr13	33592719	33593389	-555749	71.01038	0.000400596	Intergenic
Vom2r37	chr1	261090347	261091017	40607	74.08927	0.000421532	intron (ENSRNOT00000056515, intron 4 of 4)
Ercc6	chr17	11757325	11757995	-94	75.48635	0.000447244	promoter-TSS (ENSRNOT00000088529)
Klhl24	chr11	84643306	84643976	-10137	68.63935	0.000478866	Intergenic
Frat2	chr11	84643512	84644182	-245	23.3752	0.000509283	promoter-TSS (ENSRNOT00000072055)
Jade1	chr2	128463555	128464225	2666	71.17905	0.000540268	intron (ENSRNOT00000018872, intron 1 of 10)
Cnpy4	chr1	1154969	1155639	-108	71.86791	0.000571608	promoter-TSS (ENSRNOT00000033288)
RF00100	chr7	125677717	125678387	89652	64.84703	0.000605207	Intergenic
Trib1	chr2	49293013	49293683	0	85.17743	0.00063833	promoter-TSS (ENSRNOT00000005885)
LOC50068 4	chr1	59129473	59130143	-3514	71.46528	0.000672414	Intergenic
AABR070 01599.1	chr1	54194237	54194907	-67003	67.95892	0.000707325	Intergenic
Psmg3	chr12	16898649	16899319	-41	70.48702	0.000759004	promoter-TSS (ENSRNOT00000001716)
AABR070 72837.1	chr16	8733606	8734276	115155	65.08933	0.000810198	Intergenic
Fam168b	chr20	48503860	48504530	-323	55.92799	0.000862675	promoter-TSS (ENSRNOT00000039480)
B4galt7	chr17	9558369	9559039	-70	66.42193	0.000922618	promoter-TSS (ENSRNOT00000036223)
Ticrr	chr1	141391129	141391799	202	55.81323	0.000998125	exon (ENSRNOT00000031783, exon 1 of 22)
Gpr19	chr13	51381421	51382091	-10151	64.86881	0.001086841	Intergenic
AABR070 44408.2	chr20	4908400	4909070	-1330	58.00027	0.001172757	intron (ENSRNOT00000082497, intron 3 of 7)
Fbxo32	chr4	163293036	163293706	-305	66.1557	0.001258143	promoter-TSS (ENSRNOT00000010361)
Ythdc2	chr1	180738996	180739666	1447879	80.77813	0.00134206	Intergenic
Nlrp5	chr1	71522380	71523050	-35925	41.05807	0.001424138	Intergenic
Ythdc2	chr7	99273997	99274667	1401467	71.32363	0.001508499	Intergenic
Pim3	chr7	129861410	129862080	1418	59.23681	0.001603877	intron (ENSRNOT00000085835, intron 2 of 3)
LOC10254 7056	chr7	99954157	99954827	-25628	65.3391	0.001698674	Intergenic
Tfap4	chr4	168666489	168667159	-258	59.35772	0.001799633	promoter-TSS (ENSRNOT00000006979)
RF00100	chr2	49293212	49293882	89851	24.84731	0.001908816	Intergenic
AABR070 20651.1	chr13	33475503	33476173	-672965	42.61725	0.002017744	Intergenic
AABR070 20651.1	chr13	33475950	33476620	-672518	39.04096	0.002127086	Intergenic
Exosc5	chr12	14279432	14280102	-69	59.9738	0.002233161	promoter-TSS (ENSRNOT00000027995)
Nlrp5	chr1	71522174	71522844	-35719	57.67713	0.002337707	Intergenic
Gtf2a1	chr6	115351084	115351754	1262	61.47071	0.002443222	intron (ENSRNOT00000005873, intron 1 of 8)

Ppm1d	chr10	72950754	72951424	41539	62.73382	0.002561675	Intergenic
AABR070 55191.1	chr7	507126	507796	91836	57.4641	0.002679705	Intergenic
Cdk5rap1	chr3	149870122	149870792	-44	56.23081	0.002823397	promoter-TSS (ENSRNOT00000021418)
AABR070 55191.1	chr7	507341	508011	92051	21.58931	0.002965384	Intergenic
AABR070 08309.1	chr2	52814728	52815398	31681	55.90037	0.003170881	Intergenic
AABR070 52589.1	chr1	99095035	99095705	-326	59.13497	0.003371631	promoter-TSS (ENSRNOT00000081267)
Gabarap1	chr4	163293250	163293920	-139	53.76585	0.00359703	promoter-TSS (ENSRNOT00000077356)
Msx2	chr3	64852433	64853103	73798	66.28574	0.003818968	Intergenic
AABR070 56118.1	chr7	20244905	20245575	-17440	33.27867	0.004125304	Intergenic
RGD1561 114	chr18	41909267	41909937	-10152	50.33628	0.004483777	Intergenic
RGD1560 718	chr1	54042364	54043034	-6631	69.79567	0.004875936	Intergenic
Harbi1	chr3	80614247	80614917	-355	49.58747	0.005264935	promoter-TSS (ENSRNOT00000065462)
H2afv	chr14	86706689	86707359	-398	93.27539	0.005673173	promoter-TSS (ENSRNOT00000082893)
Nptn	chr8	63367659	63368329	-11093	51.70575	0.006073639	Intergenic
Fcgr2b	chr13	89445627	89446297	-12147	81.88358	0.006483044	Intergenic
Yipf4	chr6	22138194	22138864	-243	51.16993	0.006883051	promoter-TSS (ENSRNOT00000007607)
Lrrc55	chr3	72574884	72575554	27329	51.48408	0.007345223	Intergenic
AABR070 35428.2	chr12	14200707	14201377	17348	59.71487	0.007797978	intron (ENSRNOT00000001466, intron 2 of 8)
Ubf	chr10	90265983	90266653	-1301	58.43918	0.008284189	Intergenic
Stard13	chr12	1107296	1107966	87960	52.35659	0.00876482	intron (ENSRNOT00000001446, intron 1 of 13)
Npas4	chr1	220264833	220265503	604	51.97184	0.009234662	intron (ENSRNOT000000027119, intron 1 of 7)
Smg7	chr13	70321869	70322539	-452	52.52221	0.009715675	promoter-TSS (ENSRNOT00000092336)
AC117971 .2	chr7	19667621	19668291	172813	39.32676	0.01033913	Intergenic
AABR070 01599.1	chr1	54184192	54184862	-56958	59.38015	0.010968267	Intergenic
AABR070 18078.1	chr15	38709374	38710044	275	33.12022	0.011584892	intron (ENSRNOT00000074738, intron 1 of 8)
AABR070 18078.1	chr15	38709701	38710371	-52	28.54126	0.01219596	promoter-TSS (ENSRNOT00000074738)
AABR070 72837.1	chr20	40913486	40914156	114940	23.2056	0.012801091	Intergenic
Ppm1d	chr10	72950964	72951634	41749	40.05863	0.013414578	Intergenic
Selenow	chr1	77301728	77302398	233618	46.3042	0.014049601	Intergenic
Zmiz1	chr16	1750582	1751252	1726	53.35757	0.014718651	intron (ENSRNOT00000014004, intron 1 of 23)
Setdb2	chr15	39680176	39680846	24697	52.78306	0.015386435	Intergenic
Stard13	chr12	1107512	1108182	87744	41.88815	0.016051957	intron (ENSRNOT00000001446, intron 1 of 13)
LOC68346 9	chr16	15111317	15111987	-67	45.20156	0.016733855	promoter-TSS (ENSRNOT00000060703)
LOC10369 0980	chr1	54059171	54059841	-2680	50.97429	0.017407203	Intergenic
RF00002	chr7	2113554	2114224	108064	62.04688	0.018070327	Intergenic

AABR070 38886.1	chrX	63460760	63461430	-23031	59.49312	0.018748261	intron (ENSRNOT00000048127, intron 7 of 9)
RGD1566 337	chr2	194753267	194753937	122360	45.98072	0.019425714	Intergenic
Brca1	chr10	89455019	89455689	-673	47.67085	0.0201037	promoter-TSS (ENSRNOT00000028109)
Vom2r9	chr1	56002976	56003646	-107675	47.04095	0.020971573	Intergenic
RGD1566 337	chr2	194768846	194769516	106781	31.99474	0.02183861	Intergenic
RF00619	chr8	49186038	49186708	-15483	56.46441	0.022690549	Intergenic
RGD1566 337	chr2	194753479	194754149	122148	30.14443	0.023533688	Intergenic
LOC10369 0980	chr1	54058954	54059624	-2897	71.406	0.024373113	Intergenic
Hmga1	chr20	7138481	7139151	2809	56.94055	0.025206991	intron (ENSRNOT00000000580, intron 3 of 3)
RGD1566 337	chr2	194769205	194769875	106422	51.80844	0.02602963	Intergenic
Taco1	chr10	94259818	94260488	-44	48.49478	0.026850291	promoter-TSS (ENSRNOT00000063973)
Msx2	chr17	11759645	11760315	76118	61.04175	0.027684456	Intergenic
AABR070 60519.1	chr4	77447806	77448476	-1517	71.21372	0.028504734	Intergenic
AABR070 01207.1	chr1	38786656	38787326	48516	54.12794	0.02932115	Intergenic
Pcid2	chr16	81757234	81757904	598	46.49768	0.030216141	promoter-TSS (ENSRNOT00000092551)
Trem1	chr9	14795920	14796590	13192	35.94014	0.031099399	intron (ENSRNOT00000049193, intron 1 of 3)
Trem1	chr9	14796225	14796895	12887	30.47532	0.031975769	intron (ENSRNOT00000049193, intron 1 of 3)
Ndufc2	chr1	162364427	162365097	-5039	45.74886	0.032848156	Intergenic
Ndufc2	chr1	162364628	162365298	-4838	22.17121	0.033709398	Intergenic
Mrpl3	chr8	113603484	113604154	286	53.20523	0.034558668	intron (ENSRNOT00000017280, intron 1 of 9)
Rpl18	chr1	101700460	101701130	-1180	45.21348	0.035434067	Intergenic
Trem1	chr9	14795693	14796363	13419	34.77309	0.036343019	intron (ENSRNOT00000049193, intron 1 of 3)
Cdc25c	chr18	27550205	27550875	-316	51.928	0.037277176	promoter-TSS (ENSRNOT00000037368)
Cdc25c	chr18	27550406	27551076	-517	34.61044	0.038203926	promoter-TSS (ENSRNOT00000037368)
Flt1	chr12	9140371	9141041	106398	50.05784	0.039147046	intron (ENSRNOT00000001248, intron 14 of 29)
Brd3	chr3	6025139	6025809	-7877	53.71638	0.040081134	intron (ENSRNOT00000084491, intron 1 of 12)
Gpat4	chr16	73609296	73609966	-6318	49.05042	0.041001713	Intergenic
Potem	chr16	22100886	22101556	15613	45.18363	0.042100475	intron (ENSRNOT00000078734, intron 3 of 3)
Htt	chr14	81279360	81280030	-25058	46.23735	0.043185306	intron (ENSRNOT00000015894, intron 10 of 15)
Tmem101	chr10	90095254	90095924	507	15.76812	0.044262914	exon (ENSRNOT00000081539, exon 2 of 4)
Tmem101	chr10	90095737	90096407	24	37.12887	0.045328568	promoter-TSS (ENSRNOT00000081539)
Fcgr2b	chr13	89445826	89446496	-12346	18.69553	0.046383979	Intergenic
Selenow	chr1	77301266	77301936	234080	27.50438	0.047434246	Intergenic

AABR070 59198.1	chr4	8317599	8318269	61323	50.53929	0.048496679	Intergenic
RF00001	chr10	76492260	76492930	-954	48.17227	0.049617514	promoter-TSS (ENSRNOT00000070730)
Stat3	chr10	88842224	88842894	-326	49.69294	0.050740764	promoter-TSS (ENSRNOT00000026760)
AABR070 25272.1	chr16	31323558	31324228	-22013	40.53565	0.051855879	Intergenic
Galr1	chr18	79272865	79273535	-14630	46.91985	0.053015883	Intergenic
Cyp2b1	chr7	99274196	99274866	116412	36.38855	0.054177131	Intergenic
RF00002	chr2	436776	437446	-27187	44.56362	0.055333992	Intergenic
AABR070 10672.1	chr2	147015512	147016182	9017	37.69849	0.056534298	Intergenic
RGD1561 114	chr18	41908263	41908933	-9148	34.85485	0.057754523	Intergenic
RGD1561 114	chr18	41908463	41909133	-9348	16.48493	0.058965638	Intergenic
AABR070 44408.2	chr20	4906498	4907168	-3232	32.31656	0.060242086	intron (ENSRNOT00000082497, intron 3 of 7)
AC117971 .2	chr7	19741089	19741759	99345	42.06498	0.061507348	Intergenic
AC117971 .2	chr7	19741486	19742156	98948	23.00879	0.062760587	Intergenic
LOC10255 6187	chr6	32923692	32924362	42140	49.21752	0.064032138	Intergenic
AABR070 00639.1	chr1	20659859	20660529	77111	43.88361	0.065312153	Intergenic
Slbp	chr14	82356516	82357186	-65	50.38805	0.066578959	promoter-TSS (ENSRNOT00000040229)
Vps52	chr20	5441259	5441929	112	45.1531	0.0678419	promoter-TSS (ENSRNOT00000037499)
Rps18	chr20	5441508	5442178	-33	18.30675	0.069094583	promoter-TSS (ENSRNOT00000037499)
AABR070 44408.3	chr20	4903285	4903955	-2442	47.96866	0.070335892	intron (ENSRNOT00000082497, intron 3 of 7)
AABR070 20651.1	chr13	33570678	33571348	-57790	30.78465	0.071608075	Intergenic
AABR070 26565.2	chr16	83848477	83849147	-4149	43.55749	0.072887659	TTS (ENSRNOT00000032918)
Potem	chr16	22100636	22101306	15863	51.44588	0.074155608	intron (ENSRNOT00000078734, intron 3 of 3)
Cnpy4	chr12	19328714	19329384	92	30.07372	0.075422166	promoter-TSS (ENSRNOT00000033288)
LOC36579 1	chr2	137390918	137391588	13743	49.14647	0.076678039	intron (ENSRNOT00000090907, intron 6 of 20)
AABR070 01100.1	chr1	38024112	38024782	-34440	22.1122	0.07803025	Intergenic
AABR070 01100.1	chr1	38024463	38025133	-34791	36.73648	0.079371393	Intergenic
Cep250	chr3	151517564	151518234	9538	18.19461	0.080757711	intron (ENSRNOT00000055251, intron 10 of 29)
Cep250	chr3	151517882	151518552	9856	21.92452	0.082130223	intron (ENSRNOT00000055251, intron 10 of 29)
AABR070 44397.1	chr20	4665532	4666202	11167	54.24702	0.083496448	intron (ENSRNOT00000061027, intron 6 of 7)
Stpg2	chr2	244497315	244497985	-24049	42.63433	0.08485765	Intergenic
AABR070 37307.1	chrX	18211837	18212507	48814	25.53123	0.086209872	Intergenic
Txndc11	chr10	4601679	4602349	23545	35.0067	0.087626003	intron (ENSRNOT00000003332, intron 4 of 11)
LOC10255 1100	chr3	92145223	92145893	50444	24.26132	0.089035254	Intergenic

LOC102551100	chr3	92145463	92146133	50684	18.30459	0.090433221	Intergenic
Usp49	chr9	15370131	15370801	4899	34.67345	0.091880214	intron (ENSRNOT00000018550, intron 1 of 6)
Mrpl3	chr8	113603707	113604377	509	30.29603	0.09335466	intron (ENSRNOT00000017280, intron 1 of 9)
AABR07002845.1	chr1	86811240	86811910	-7961	42.62292	0.094841846	Intergenic
Uspl1	chr12	6956613	6957283	-34	40.28789	0.096314129	promoter-TSS (ENSRNOT00000001210)
Borcs8	chr16	21028848	21029518	-49	66.43373	0.097824131	promoter-TSS (ENSRNOT00000041221)
Ccpg1	chr8	79660286	79660956	-36	39.42697	0.099342938	promoter-TSS (ENSRNOT00000089949)
RGD1560718	chr1	54043674	54044344	-7941	45.39796	0.100846307	Intergenic
Acvr1	chr3	44515345	44516015	7250	32.08571	0.102337075	intron (ENSRNOT00000006963, intron 1 of 10)
AABR07063599.1	chr6	36582330	36583000	148669	38.80732	0.103825732	Intergenic
AABR07063599.1	chr6	36582531	36583201	148468	32.14693	0.10530088	Intergenic
AABR07006038.1	chr1	214988416	214989086	16390	24.25222	0.106789856	intron (ENSRNOT00000088263, intron 1 of 1)
AABR07006038.1	chr1	214988209	214988879	16597	43.50945	0.108265229	intron (ENSRNOT00000088263, intron 1 of 1)
AABR07001734.1	chr1	55756034	55756704	48971	54.31549	0.109726367	Intergenic
Stx18	chr14	77482839	77483509	9736	42.14681	0.111175733	intron (ENSRNOT00000008410, intron 1 of 10)
Smpdl3a	chr20	40829099	40829769	50507	39.28369	0.11263309	Intergenic
Pctp	chr10	77523962	77524632	-12265	42.91245	0.114074349	Intergenic
Olr1197	chr8	40266918	40267588	4422	44.19033	0.115501068	Intergenic
Fgf8	chr1	265469367	265469697	29299	47.08488	0.11693136	Intergenic
AABR07027039.1	chr17	11787153	11787823	64047	41.54954	0.118358649	Intergenic
Arhgap26	chr18	32087970	32088640	119444	36.1573	0.119771641	intron (ENSRNOT00000018843, intron 4 of 23)
Rbms2	chr7	2592579	2593249	-4071	21.29832	0.121171086	Intergenic
Rbms2	chr7	2592375	2593045	-3867	41.98764	0.122555837	Intergenic
Tmem220	chr10	53533391	53534061	-37263	49.53787	0.123938147	Intergenic
Zdbf2	chr9	70039232	70039902	-20116	36.6284	0.125323351	Intergenic
Rps6ka5	chr6	124735982	124736652	-539	56.10978	0.126702446	promoter-TSS (ENSRNOT00000091693)
AABR07026339.1	chr16	72588872	72589542	-107740	24.40548	0.128077252	Intergenic
Cdk12	chr10	86156827	86157497	-446	16.5422	0.129442532	promoter-TSS (ENSRNOT00000082668)
RF00026	chr15	108812527	108813197	10811	44.32389	0.130827788	intron (ENSRNOT00000018918, intron 4 of 7)
Ubtf	chr10	90266191	90266861	-1509	21.12087	0.132212647	Intergenic
Kdm5b	chr13	51383994	51384664	-60	42.90754	0.133597706	promoter-TSS (ENSRNOT00000087025)
LOC500876	chr7	100303561	100304231	79001	26.64946	0.134968991	Intergenic
Rab11fip4	chr10	66908793	66909463	-33270	40.52296	0.136336456	intron (ENSRNOT00000089538, intron 50 of 57)

RF00026	chr15	108812728	108813398	10610	32.45569	0.13771841	intron (ENSRNOT00000018918, intron 4 of 7)
Arl15	chr2	45700999	45701669	32365	45.45529	0.139091631	intron (ENSRNOT00000071353, intron 1 of 3)
Vom2r9	chr1	56001576	56002246	-106275	37.09363	0.140456228	Intergenic
Ythdc2	chr1	181286471	181287141	853764	39.78443	0.141817231	Intergenic
Zdhhc7	chr19	52759399	52760069	-9427	44.29964	0.143194059	Intergenic
Agfg2	chr12	22082506	22083176	776	43.96141	0.144583589	intron (ENSRNOT00000077711, intron 1 of 12)
RF00026	chr4	177995315	177995985	72085	45.61466	0.146001057	Intergenic
Ythdc2	chr1	181293703	181294373	846532	15.17243	0.147407303	Intergenic
Mtrr	chr1	37774728	37775398	30966	42.35722	0.148829835	Intergenic
RF00066	chr14	87941136	87941806	200427	34.15902	0.150240839	Intergenic
Stard13	chr12	1209561	1210231	-14305	42.61632	0.151639031	Intergenic
Rad51b	chr6	102684285	102684955	207584	44.53301	0.153026273	Intergenic
Rpl18	chr1	101700670	101701340	-970	35.04478	0.154402383	promoter-TSS (ENSRNOT00000028555)
AABR070 11278.1	chr2	160887674	160888344	596559	34.06527	0.155766837	Intergenic
AABR070 01734.1	chr1	55753361	55754031	46298	41.06458	0.157147328	exon (ENSRNOT00000089548, exon 4 of 4)
Gtpbp2	chr9	17207410	17208080	-751	43.71647	0.158536768	promoter-TSS (ENSRNOT00000026195)
Tdrd3	chr15	70803340	70804010	13550	42.63925	0.15993702	intron (ENSRNOT00000012440, intron 7 of 10)
AABR070 70486.1	chr8	72310334	72311004	25597	42.34552	0.161332179	Intergenic
Potem	chr16	22105288	22105958	11211	47.61771	0.162719649	intron (ENSRNOT00000078734, intron 3 of 3)
Potem	chr16	22105487	22106157	11012	19.52487	0.16409978	intron (ENSRNOT00000078734, intron 3 of 3)
LOC49954 2	chr2	61747525	61748195	10057	31.42507	0.165487045	Intergenic
Ttc17	chr3	83271158	83271828	35288	44.07554	0.166864519	intron (ENSRNOT00000014088, intron 10 of 24)
RF00001	chr9	26775312	26775982	1280	44.61279	0.168231377	Intergenic
Ezh1	chr10	89117056	89117726	12948	44.21249	0.169588735	intron (ENSRNOT00000027640, intron 9 of 19)
LOC50068 4	chr6	103938504	103939174	-3717	40.03171	0.170952714	Intergenic
RGD1563 680	chr3	107177921	107178591	35494	41.80701	0.172310602	intron (ENSRNOT00000006177, intron 1 of 10)
RF00003	chr4	62734611	62735281	-30770	22.47252	0.173692873	intron (ENSRNOT00000014832, intron 17 of 42)
Arhgap11 a	chr3	105297940	105298610	-167	41.00069	0.175064868	promoter-TSS (ENSRNOT00000010994)
RF00026	chr10	63296613	63297283	-7889	39.79422	0.176448918	Intergenic
Slc37a2	chr8	39781308	39781978	-47049	25.19005	0.177827941	intron (ENSRNOT00000040901, intron 10 of 12)
RF00325	chr6	23445640	23446310	2786	43.45538	0.179223106	intron (ENSRNOT00000035320, intron 12 of 18)
Olig3	chr1	14680521	14681191	-116910	44.89101	0.180631713	Intergenic

Gtf2a1	chr6	115352642	115353312	-296	40.76059	0.182030432	promoter-TSS (ENSRNOT00000005873)
AABR070 72979.1	chr4	31943386	31944056	-44546	45.32177	0.183420554	Intergenic
RF00015	chr12	46863012	46863682	-3	43.68909	0.184802142	promoter-TSS (ENSRNOT000000084988)
PsmA8	chr18	6155656	6156326	41290	44.39554	0.186173987	intron (ENSRNOT00000044541, intron 4 of 6)
PsmA8	chr18	6155858	6156528	41492	23.53425	0.187537879	intron (ENSRNOT00000044541, intron 4 of 6)
Brca1	chr10	89455257	89455927	-911	40.43882	0.188893929	promoter-TSS (ENSRNOT00000028109)
Ddx55	chr12	37468689	37469359	-89	41.17471	0.190258908	promoter-TSS (ENSRNOT00000001387)
RF00560	chr2	5836235	5836905	18866	40.83053	0.191618308	Intergenic
Osbpl2	chr3	175493047	175493717	-316	40.11184	0.192991864	promoter-TSS (ENSRNOT000000087356)
AABR070 26137.1	chr16	65168822	65169492	-9006	43.83871	0.194362287	Intergenic
Sgo1	chr9	4408131	4408801	-12603	43.77972	0.195731174	Intergenic
AABR070 68949.1	chr8	2960458	2961128	-113978	44.06365	0.197114694	Intergenic
Brd3	chr3	6025374	6026044	-8112	27.18302	0.198495196	intron (ENSRNOT000000084491, intron 1 of 12)
AABR070 37307.1	chrX	18212299	18212969	49276	43.58759	0.199867877	Intergenic
Mcm8	chr3	125478005	125478675	7789	43.92424	0.20123059	intron (ENSRNOT00000028898, intron 7 of 18)
Cdr4	chr10	49385604	49386274	17625	46.89529	0.202617989	intron (ENSRNOT00000004392, intron 1 of 1)
AC108295 .1	chr3	72424247	72424917	-21046	20.40558	0.204005088	intron (ENSRNOT00000033427, intron 8 of 11)
AC108295 .1	chr3	72423804	72424474	-20603	27.98905	0.205382294	intron (ENSRNOT00000033427, intron 8 of 11)
AC108295 .1	chr3	72424010	72424680	-20809	21.19563	0.206750229	intron (ENSRNOT00000033427, intron 8 of 11)
Prpf31	chr1	64162209	64162879	-83	56.69445	0.208138299	promoter-TSS (ENSRNOT000000089713)
Rfx7	chr8	79239885	79240555	80850	32.94742	0.209520248	intron (ENSRNOT000000086841, intron 2 of 8)
Tmem100	chr10	77602989	77603659	65984	41.42083	0.210904089	Intergenic
Mical1	chr20	46192151	46192821	-7495	42.88688	0.212279961	Intergenic
Abraxas2	chr1	204874747	204875417	13516	43.1005	0.213646115	intron (ENSRNOT00000023214, intron 4 of 8)
RF00003	chr6	75622373	75623043	251	38.99899	0.21501512	TTS (ENSRNOT000000080461)
Kdm5a	chr4	152892138	152892808	85	41.64601	0.216376953	promoter-TSS (ENSRNOT000000075895)
Arl13b	chr7	957773	958443	230057	40.01584	0.217735378	Intergenic
Mrgprx3	chr1	103315304	103315974	7837	41.09048	0.219088206	intron (ENSRNOT00000019051, intron 1 of 1)
RF00100	chr10	21527541	21528211	-140846	42.95519	0.220430659	Intergenic
Evx2	chr3	61583959	61584629	-2696	44.6211	0.221766529	Intergenic
Evx2	chr3	61584165	61584835	-2902	25.6424	0.223092515	Intergenic
Rdh14	chr6	36200085	36200755	90150	37.22685	0.224412477	Intergenic
AABR070 01734.1	chr1	55756233	55756903	49170	40.36103	0.225728294	Intergenic

Insm2	chr6	76367815	76368485	-15296	42.45229	0.227036666	Intergenic
Otos	chr9	99881811	99882481	-60192	38.86717	0.22833527	Intergenic
AABR070 30501.1	chr10	90778122	90778792	-5819	44.03974	0.229627025	Intergenic
RGD1565 784	chr10	14542795	14543465	-70	48.84929	0.230911201	promoter-TSS (ENSRNOT00000047111)
AABR070 27235.1	chr17	20562136	20562806	-56853	44.96364	0.232195608	Intergenic
AABR070 61902.2	chr4	151937421	151938091	48437	42.08587	0.233471568	Intergenic
Pde4a	chr8	22188638	22189308	-627	42.38075	0.234747513	promoter-TSS (ENSRNOT00000061100)
Efcab1	chr11	90050276	90050946	183675	43.36616	0.236027714	Intergenic
Ptprg	chr15	13301405	13302075	-73133	30.8811	0.237301782	Intergenic
AABR070 20651.1	chr13	33593029	33593699	-555439	47.26255	0.238577784	Intergenic
Hagh	chr10	14216423	14217093	603	25.13201	0.23985678	promoter-TSS (ENSRNOT00000019767)
Hagh	chr10	14216104	14216774	284	26.97703	0.241127642	promoter-TSS (ENSRNOT00000019767)
AABR070 35813.1	chr12	23103532	23104202	-26572	23.92431	0.24239854	Intergenic
AABR070 30040.1	chr10	63702268	63702938	5995	44.73366	0.243660426	intron (ENSRNOT00000005100, intron 5 of 13)
AABR070 35813.1	chr12	23103232	23103902	-26872	30.84457	0.244914219	Intergenic
LOC10091 2282	chr7	144391163	144391833	-69258	30.50143	0.246164827	Intergenic
B4galt7	chr17	9557934	9558604	355	31.04011	0.247471961	intron (ENSRNOT00000083492, intron 1 of 6)
AABR070 26915.1	chr17	4763849	4764519	53653	42.00228	0.248772861	Intergenic
Ythdc2	chr1	180926059	180926729	1214176	27.8022	0.250066779	Intergenic
Olig3	chr1	14807972	14808642	10541	42.52161	0.2513709	Intergenic
Tmtc1	chr4	182867899	182868569	-23943	42.14295	0.252669022	Intergenic
Rfxank	chr16	21029074	21029744	-187	42.6359	0.253962153	promoter-TSS (ENSRNOT00000041221)
Cdk5rap1	chr3	149870326	149870996	-248	52.64201	0.255256612	promoter-TSS (ENSRNOT00000021418)
Cdk5rap1	chr3	149870525	149871195	-447	16.70976	0.256543491	promoter-TSS (ENSRNOT00000021418)
Ptprg	chr15	13301606	13302276	-73334	23.67834	0.257832702	Intergenic
MyI10	chr12	22998297	22998967	22885	37.9087	0.259115266	Intergenic
Sik3	chr8	50306629	50307299	-3441	27.83552	0.26038922	Intergenic
Klf9	chr1	240908037	240908707	-111	33.81445	0.261663412	promoter-TSS (ENSRNOT00000019367)
AABR070 24439.1	chr16	42155	42825	3439	46.23418	0.262932941	Intergenic
Cecr2	chr4	153216833	153217503	-614	35.21268	0.264195855	promoter-TSS (ENSRNOT00000015499)
AABR070 01207.1	chr1	38786176	38786846	48996	36.95927	0.265450776	Intergenic
AABR070 56200.1	chr7	21234888	21235558	-30490	44.29807	0.266703675	Intergenic
Ythdc2	chr1	180972145	180972815	1168090	86.86198	0.267948296	Intergenic
Ythdc2	chr1	181014454	181015124	1125781	53.29261	0.269194387	Intergenic
Lysmd4	chr1	128046092	128046762	-152895	40.17272	0.2704388	intron (ENSRNOT00000055877, intron 19 of 22)
Ehf	chr3	93238303	93238973	-22143	16.97553	0.271682084	Intergenic
AABR070 68053.1	chr9	80048682	80049352	-19247	42.58345	0.272921029	Intergenic

AABR070 68053.1	chr9	80048886	80049556	-19043	15.0579	0.274154261	Intergenic
AC110102 .2	chr4	44688638	44689308	-25089	41.72711	0.275381017	Intergenic
Ergic2	chr4	182573732	182574402	20164	34.39535	0.276610715	intron (ENSRNOT00000079291, intron 10 of 12)
Ergic2	chr4	182573527	182574197	20369	41.78626	0.27783375	intron (ENSRNOT00000079291, intron 10 of 12)
Adra1a	chr15	43348639	43349309	50180	40.82661	0.279053195	intron (ENSRNOT00000012736, intron 1 of 1)
Btg1	chr7	37787196	37787866	-25300	29.66325	0.280265732	Intergenic
Btg1	chr7	37787405	37788075	-25091	21.46141	0.281471871	Intergenic
Ttll9	chr3	148457475	148458145	9078	37.81	0.282671485	intron (ENSRNOT00000083812, intron 3 of 14)
AABR070 39256.1	chrX	73074581	73075251	12484	41.71115	0.283870982	Intergenic
LOC36579 1	chr2	137349873	137350543	-19068	33.16023	0.285068349	intron (ENSRNOT00000090907, intron 8 of 20)
Mtmt14	chr4	145194656	145195326	-79	38.90496	0.28626747	promoter-TSS (ENSRNOT00000010723)
Exosc5	chr1	82455347	82456017	3213	41.06529	0.287459721	intron (ENSRNOT00000028026, intron 1 of 5)
AABR070 11057.1	chr2	156939456	156940126	95692	29.56122	0.288648962	Intergenic
Ubl3	chr12	7864536	7865206	-1067	29.66256	0.289832445	Intergenic
Stard13	chr12	1107718	1108388	87538	22.44147	0.291008048	intron (ENSRNOT00000001446, intron 1 of 13)
AABR070 11057.1	chr2	156938927	156939597	96221	28.58462	0.292177656	Intergenic
Rrm2b	chr7	76811846	76812516	-31364	17.87964	0.293348587	intron (ENSRNOT00000009115, intron 36 of 54)
Rrm2b	chr7	76811622	76812292	-31140	39.12752	0.294512003	intron (ENSRNOT00000009115, intron 36 of 54)
Tnni3k	chr2	261229589	261230259	107239	38.98591	0.295677311	intron (ENSRNOT00000030341, intron 16 of 24)
AABR070 13425.1	chr2	236939711	236940381	-116901	46.30904	0.29683766	Intergenic
Ythdc2	chr1	180702682	180703352	1437553	32.92821	0.297995016	Intergenic
Aff4	chr10	38708348	38709018	16472	39.11802	0.299150684	intron (ENSRNOT00000009440, intron 1 of 20)
Samd4a	chr15	23844838	23845508	52242	25.85892	0.30029977	intron (ENSRNOT00000089226, intron 6 of 11)
Ythdc2	chr1	180702381	180703051	1437854	34.55832	0.301444941	Intergenic
Ttc28	chr12	51716189	51716859	-13794	38.29206	0.302593782	Intergenic
Tsc22d1	chr15	58530668	58531338	-23371	40.38992	0.303735112	Intergenic
Cbl	chr8	48557330	48558000	7057	41.45115	0.304869515	intron (ENSRNOT00000067902, intron 1 of 15)
AABR070 01599.1	chr1	54146988	54147658	-19754	30.25511	0.306014496	Intergenic
AABR070 01599.1	chr1	54146746	54147416	-19512	38.30946	0.307155998	Intergenic
RF00001	chr15	46029117	46029787	-10091	36.42182	0.308292529	intron (ENSRNOT00000066864, intron 1 of 10)
AABR070 30034.1	chr10	63527049	63527719	23850	36.00821	0.309421865	Intergenic

Olr392	chr2	209617430	209618100	-35138	34.98077	0.310547473	Intergenic
Esr1	chr1	41311413	41312083	-11446	38.39566	0.311673588	intron (ENSRNOT00000082133, intron 1 of 2)
AABR070 15966.1	chr14	88348663	88349333	165005	35.75353	0.312792982	Intergenic
Nectin2	chr1	80670797	80671467	-4547	41.0805	0.313908445	Intergenic
Nectin2	chr1	80670997	80671667	-4747	16.14251	0.315017732	Intergenic
RF00100	chr13	9937666	9938336	-299809	31.67806	0.316120747	Intergenic
Anapc11	chr10	109774816	109775486	273	37.61317	0.317220321	promoter-TSS (ENSRNOT00000054955)
RF00026	chr4	128802610	128803280	62984	21.15406	0.318320054	Intergenic
RF00026	chr4	128802393	128803063	63201	37.29373	0.319414039	Intergenic
AABR070 01734.1	chr1	55753564	55754234	46501	27.81184	0.320502189	exon (ENSRNOT00000089548, exon 4 of 4)
Mir802	chr11	33618066	33618736	48145	32.82631	0.32158516	Intergenic
AABR070 16141.1	chr14	94548479	94549149	-41951	37.7953	0.322665847	Intergenic
Snx24	chr18	48282288	48282958	80895	43.42386	0.323744203	intron (ENSRNOT00000023507, intron 1 of 6)
Brinp3	chr13	63078136	63078806	-448015	28.07601	0.324820178	Intergenic
Brinp3	chr13	63078374	63079044	-447777	27.91074	0.325889974	Intergenic
Mtmer9	chr15	46740947	46741617	-22030	38.36343	0.326956518	Intergenic
Tmem220	chr10	53533619	53534289	-37035	19.10638	0.328017489	Intergenic
Alg5	chr2	143932369	143933039	-35	36.13159	0.329075083	promoter-TSS (ENSRNOT00000086214)
Fgd6	chr7	35010525	35011195	58849	23.64981	0.330133807	exon (ENSRNOT00000077666, exon 4 of 21)
Mum1	chr7	12337262	12337932	8878	36.42007	0.331192124	intron (ENSRNOT00000060708, intron 6 of 12)
AABR070 00137.1	chr1	1415690	1416360	-23696	15.62408	0.332250773	Intergenic
Ptprm	chr9	115257319	115257989	124791	38.93705	0.333304364	intron (ENSRNOT00000056366, intron 4 of 32)
Polq	chr11	66658538	66659208	36480	41.38872	0.334359756	intron (ENSRNOT00000063995, intron 9 of 29)
AABR070 18457.1	chr15	58777093	58777763	51163	41.74989	0.335412312	Intergenic
Ndor1	chr3	2474567	2475237	11	47.31102	0.336461208	promoter-TSS (ENSRNOT00000014445)
Fosl2	chr6	25780564	25781234	-163904	40.13961	0.33750639	intron (ENSRNOT00000005855, intron 7 of 11)
Fosl2	chr6	25780769	25781439	-164109	25.11107	0.338546244	intron (ENSRNOT00000005855, intron 7 of 11)
AABR070 05838.2	chr1	202882990	202883660	53758	43.76074	0.339583046	Intergenic
AABR070 12426.1	chr2	195065905	195066575	27048	35.54269	0.340618318	Intergenic
RF00066	chr13	53999749	54000419	-100144	23.56796	0.341651239	Intergenic
RGD1306 941	chr9	63970795	63971465	-95449	41.64273	0.342685714	Intergenic
AABR070 44173.1	chr19	61546843	61547513	36296	40.188	0.343717781	Intergenic
Sult2a2	chr1	76584107	76584777	29837	54.13816	0.344745019	intron (ENSRNOT00000041367, intron 3 of 5)
AABR070 01599.1	chr1	54176181	54176851	-48947	40.15342	0.345772938	Intergenic

Lrrc55	chr3	72575083	72575753	27130	34.01583	0.346803922	Intergenic
RF00026	chr1	147838350	147839020	-9856	42.89636	0.347834776	intron (ENSRNOT00000074103, intron 7 of 9)
AC117971 .2	chr7	19667972	19668642	172462	37.85553	0.348862268	Intergenic
RF00181	chr15	88364697	88365367	-75050	40.86949	0.349884739	Intergenic
Kif11	chr1	256034529	256035199	-1002	22.71073	0.350909398	Intergenic
AABR070 31221.1	chr18	4648048	4648718	48358	23.94613	0.351928955	Intergenic
AABR070 22053.1	chr13	104552384	104553054	83782	25.46132	0.352950661	Intergenic
AABR070 27799.1	chr17	44320864	44321534	99397	47.08527	0.353972074	Intergenic
Adam34l	chr16	51530459	51531129	-199658	30.91757	0.354989085	Intergenic
AABR070 20835.1	chr13	43172846	43173516	-212273	20.41749	0.356001641	Intergenic
AABR070 35175.1	chr12	5882411	5883081	-59470	41.55707	0.357008043	Intergenic
AABR070 20835.1	chr13	43172504	43173174	-212615	39.71057	0.358010694	Intergenic
Nr1h5	chr2	205454546	205455216	-3490	41.86567	0.359009549	Intergenic
Slc12a8	chr11	70525850	70526520	-26985	43.11551	0.360005387	intron (ENSRNOT00000002435, intron 7 of 8)
RF00002	chr7	2121437	2122107	100181	24.58253	0.360996507	Intergenic
Cep68	chr14	104535827	104536497	-12865	37.44795	0.361985355	Intergenic
Nlrp1a	chr10	57766748	57767418	-27974	34.58841	0.362971896	intron (ENSRNOT00000037546, intron 1 of 14)
Trim16	chr10	49238833	49239503	7438	44.56281	0.36395526	intron (ENSRNOT00000065335, intron 1 of 5)
Ero1a	chr15	19650485	19651155	4561	18.7531	0.364937086	intron (ENSRNOT00000009404, intron 1 of 15)
Ero1a	chr15	19650217	19650887	4829	39.59818	0.365913135	intron (ENSRNOT00000009404, intron 1 of 15)
Hus1	chr14	89214126	89214796	-5636	29.29639	0.366886727	Intergenic
Gzmf	chr15	35191862	35192532	3528	43.60587	0.367856132	intron (ENSRNOT00000044840, intron 1 of 4)
Ephb4	chr12	22411274	22411944	6371	40.84774	0.368823003	intron (ENSRNOT00000072208, intron 3 of 16)
AABR070 16141.1	chr14	94369468	94370138	-220962	22.14093	0.369786456	Intergenic
Smad7	chr18	71315182	71315852	-80313	22.59928	0.370745595	Intergenic
Smad7	chr18	71315683	71316353	-79812	27.46217	0.371700376	Intergenic
Rgs18	chr13	62051200	62051870	-460396	15.67857	0.37265075	Intergenic
Zfp365	chr20	22086594	22087264	26705	41.24385	0.373601834	TTS (ENSRNOT00000057992)
Lifr	chr2	56418949	56419619	-7083	34.88109	0.374550171	Intergenic
Lifr	chr2	56419154	56419824	-6878	21.28434	0.375493134	Intergenic
Htt	chr14	81279580	81280250	-25278	40.77724	0.37643587	intron (ENSRNOT00000015894, intron 10 of 15)
AC117971 .2	chr7	19628286	19628956	212148	40.747	0.377374022	Intergenic
Stpg2	chr2	244497517	244498187	-23847	29.87006	0.378308413	Intergenic
AC117971 .2	chr7	19628568	19629238	211866	33.43939	0.379239006	Intergenic

Vom2r37	chr1	99095993	99096663	39649	32.2807	0.380171888	intron (ENSRNOT00000056515, intron 4 of 4)
Akap12	chr1	40862821	40863491	-16591	35.55599	0.381100045	intron (ENSRNOT00000060767, intron 2 of 3)
AABR070 35437.1	chr12	14873244	14873914	-166921	30.5759	0.38202431	intron (ENSRNOT00000089775, intron 4 of 46)
Brpf3	chr20	6043809	6044479	-5142	40.16977	0.382944644	Intergenic
Vom2r37	chr1	99095487	99096157	40155	17.88427	0.383860125	intron (ENSRNOT00000056515, intron 4 of 4)
Meis1	chr14	103150528	103151198	170407	22.50471	0.384772478	Intergenic
RF00003	chr9	71678018	71678688	19454	40.75897	0.385685223	Intergenic
Ccdc92b	chr10	61413524	61414194	-7775	18.62671	0.386597463	intron (ENSRNOT00000077649, intron 1 of 5)
Ccdc92b	chr10	61413752	61414422	-7547	16.39032	0.387505615	exon (ENSRNOT00000092490, exon 2 of 4)
Cct6a	chr12	30501445	30502115	54	29.0656	0.388412323	promoter-TSS (ENSRNOT00000090466)
Arhgef37	chr18	56849491	56850161	20975	39.01156	0.389318463	intron (ENSRNOT00000087188, intron 3 of 12)
Usp40	chr9	95066032	95066702	42372	38.98602	0.390219529	intron (ENSRNOT00000035338, intron 27 of 29)
AABR070 68306.1	chr9	97405377	97406047	-20709	32.7787	0.391117276	Intergenic
Epb41l4a	chr18	26628639	26629309	27905	40.95108	0.392012576	intron (ENSRNOT00000038247, intron 7 of 17)
AABR070 53870.1	chr3	131731113	131731783	121857	15.05405	0.392904497	Intergenic
AABR070 53870.1	chr3	131730911	131731581	121655	39.74528	0.393792101	Intergenic
RGD1561 699	chr14	15422069	15422739	4298	45.91843	0.394676256	Intergenic
Tiam2	chr1	44292209	44292879	-18969	41.25456	0.395558754	Intergenic
Ddx31	chr3	7422758	7423428	273	39.09361	0.39643866	promoter-TSS (ENSRNOT00000088339)
Leo1	chr8	82369138	82369808	-11284	19.11065	0.39731412	Intergenic
AABR070 08594.1	chr2	65945037	65945707	-74487	22.50381	0.398186929	Intergenic
AABR070 66188.1	chr9	4627166	4627836	6076	47.99776	0.399061656	Intergenic
Nr1h5	chr2	205454785	205455455	-3729	23.8181	0.39993462	Intergenic
RGD1311 251	chr8	58006464	58007134	23243	35.60556	0.400804879	intron (ENSRNOT00000009562, intron 8 of 9)
Zfp955a	chr7	15787368	15788038	2256	37.43047	0.401670558	exon (ENSRNOT00000073235, exon 2 of 2)
AABR070 58210.1	chr7	105074820	105075490	-26852	37.97686	0.402536253	Intergenic
AABR070 35083.1	chr12	4132844	4133514	-37681	16.23578	0.403396383	Intergenic
Gabrr3	chr11	43081948	43082618	17129	35.31464	0.404258351	intron (ENSRNOT00000002281, intron 2 of 8)
AC126899 .1	chr19	44434377	44435047	-38102	37.16466	0.405117496	Intergenic
Spata19	chr8	28590897	28591567	136270	35.0788	0.405975663	Intergenic
RF00026	chr7	100090838	100091508	27435	24.51339	0.406830964	Intergenic
AABR070 01207.1	chr1	38788697	38789367	46475	16.14867	0.407682435	Intergenic

AABR070 09373.2	chr2	94821735	94822405	46879	36.38803	0.408530984	intron (ENSRNOT00000091734, intron 2 of 2)
Jazf1	chr4	83053446	83054116	83746	39.26844	0.409374701	intron (ENSRNOT00000039580, intron 1 of 4)
Nhlrc3	chr2	142532647	142533317	153595	37.62612	0.410215438	Intergenic
AABR070 59198.1	chr4	8317798	8318468	61522	21.28259	0.411053168	Intergenic
Tars2	chr2	197878773	197879443	-966	23.84583	0.411888816	promoter-TSS (ENSRNOT00000087052)
RF00560	chr2	145957674	145958344	-73129	43.71686	0.412723312	Intergenic
Cd300e	chr10	103637523	103638193	-18775	44.34164	0.413556642	Intergenic
Arl16	chr10	109645256	109645926	-6537	40.28279	0.414387837	intron (ENSRNOT00000054966, intron 6 of 21)
AABR070 44408.2	chr20	4906881	4907551	-2849	58.20608	0.415214967	intron (ENSRNOT00000082497, intron 3 of 7)
AABR070 33357.1	chr11	18083784	18084454	-370025	16.55357	0.416040874	Intergenic
AABR070 33357.1	chr11	18083575	18084245	-370234	40.94862	0.416862664	Intergenic
Sox6	chr1	185738479	185739149	65637	35.24207	0.417681269	intron (ENSRNOT00000048020, intron 2 of 15)
Olr505	chr3	73771281	73771951	8366	40.43475	0.418497627	Intergenic
Asap1	chr7	104717876	104718546	31341	29.50874	0.41931365	intron (ENSRNOT00000079981, intron 7 of 22)
AABR070 25973.1	chr16	56977832	56978502	-53840	37.55585	0.420127394	Intergenic
Crk	chr10	63837780	63838450	8308	37.48417	0.420936902	intron (ENSRNOT00000006407, intron 1 of 2)
AABR070 35864.1	chr12	25898847	25899517	-52775	39.0767	0.421743114	Intergenic
AABR070 00137.1	chr1	1382582	1383252	9412	41.24877	0.422546005	Intergenic
Mybpc3	chr3	79962485	79963155	22259	30.98017	0.423347501	exon (ENSRNOT00000079394, exon 33 of 35)
Mybpc3	chr3	79962690	79963360	22464	29.84595	0.424144656	intron (ENSRNOT00000017360, intron 31 of 33)
AABR070 13718.1	chr2	252972787	252973457	-100720	24.74921	0.4249394	Intergenic
AABR070 13718.1	chr2	252973190	252973860	-101123	15.36227	0.425731711	Intergenic
AABR070 52608.1	chr3	65909623	65910293	-11657	25.88964	0.426523535	Intergenic
AABR070 71287.1	chr8	107750711	107751381	51566	21.40747	0.427311912	intron (ENSRNOT00000019536, intron 13 of 21)
Gas1	chr17	4845957	4846627	-497	42.88763	0.42809879	promoter-TSS (ENSRNOT00000073271)
Rnf217	chr1	28210540	28211210	-91047	38.71662	0.428885141	Intergenic
Emid1	chr14	85405469	85406139	-7272	39.37936	0.429668979	Intergenic
Tom1l2	chr10	46721110	46721780	-535	41.79131	0.430452268	promoter-TSS (ENSRNOT00000067866)
RF00100	chr6	30338041	30338711	105633	39.74827	0.431231026	Intergenic
AABR070 63511.1	chr6	32692721	32693391	-92978	39.5055	0.432010199	Intergenic
Rai14	chr2	60734173	60734843	-51057	39.49238	0.432786794	Intergenic
Apob	chr6	33249503	33250173	73012	40.99665	0.433559793	Intergenic
AC098190 .1	chr2	6080192	6080862	-198990	19.67821	0.434332172	Intergenic

AABR070 27872.1	chr17	47889227	47889897	18951	41.75111	0.435102922	Intergenic
AABR070 39256.1	chrX	73074795	73075465	12270	40.86517	0.435872029	Intergenic
RF01296	chr3	142589532	142590202	132363	32.155	0.436639479	Intergenic
RGD1561 667	chr1	55235076	55235746	15638	51.69435	0.437405259	Intergenic
Dnajb12	chr20	29444573	29445243	-602	35.63217	0.438168346	promoter-TSS (ENSRNOT00000044805)
Fam167a	chr15	46636838	46637508	23363	38.84029	0.438929732	intron (ENSRNOT00000015055, intron 3 of 3)
Ints4	chr1	162444759	162445429	-2586	38.38439	0.439687379	Intergenic
AABR070 65486.1	chr6	130750652	130751322	-40267	36.22255	0.440443292	Intergenic
AABR070 65486.1	chr6	130750880	130751550	-40039	26.58384	0.441195425	Intergenic
Lmod3	chr4	129618339	129619009	468	37.53382	0.441945789	intron (ENSRNOT00000047453, intron 1 of 3)
Adcy2	chr1	37420919	37421589	-86022	36.13434	0.442692333	Intergenic
Sub1	chr2	62039005	62039675	-4712	23.54845	0.443437074	Intergenic
Kng1	chr11	81444988	81445658	-702	39.06264	0.444178977	promoter-TSS (ENSRNOT00000078131)
RF00334	chr4	183486346	183487016	36535	36.34903	0.444919049	intron (ENSRNOT00000071407, intron 17 of 21)
Smpdl3a	chr20	40884490	40885160	105898	33.64674	0.445655222	Intergenic
Sdc4	chr3	160879973	160880643	10882	33.2143	0.446390558	intron (ENSRNOT00000019386, intron 1 of 4)
AABR070 32862.1	chr18	86239198	86239868	40147	38.66309	0.44712196	intron (ENSRNOT00000076159, intron 33 of 35)
RF00026	chr9	58134825	58135495	139053	38.62591	0.447851466	Intergenic
AC117971 .2	chr7	19670707	19671377	169727	40.23774	0.448578031	Intergenic
Olig3	chr1	14808181	14808851	10750	26.24092	0.449302671	Intergenic
Usp8	chr3	119203484	119204154	30001	40.02167	0.450024336	exon (ENSRNOT00000015124, exon 10 of 19)
Usp8	chr3	119203683	119204353	30200	17.7357	0.450744047	intron (ENSRNOT00000015124, intron 10 of 18)
AC109942 .1	chr7	15271732	15272402	-7544	39.31891	0.451461791	Intergenic
RF00100	chr12	6361140	6361810	-12699	38.60211	0.452179636	Intergenic
Zc3hc1	chr4	57702025	57702695	4253	20.08635	0.452895494	intron (ENSRNOT00000013604, intron 2 of 9)
RF00001	chr15	87177985	87178655	-43414	39.58284	0.453608308	Intergenic
AC128582 .1	chr8	80156129	80156799	-293490	40.42716	0.454320151	Intergenic
AABR070 66677.1	chr9	12329471	12330141	-16311	22.64994	0.455027873	Intergenic
Myh8	chr10	53833391	53834061	14908	37.67922	0.455733548	intron (ENSRNOT00000057260, intron 22 of 33)
Zfp827	chr19	32461576	32462246	67054	34.66332	0.456437166	intron (ENSRNOT00000015929, intron 6 of 12)
Zfp827	chr19	32461775	32462445	66855	21.04674	0.457137659	intron (ENSRNOT00000015929, intron 6 of 12)
AABR070 12426.1	chr2	195066154	195066824	27297	26.15949	0.457835011	Intergenic
AABR070 66677.1	chr9	12330219	12330889	-15563	15.59378	0.458530258	Intergenic

AABR070 66677.1	chr9	12360463	12361133	14681	32.52158	0.45922339	Intergenic
AABR070 27128.1	chr17	14932690	14933360	16039	34.72215	0.45991651	Intergenic
Pde5a	chr2	226969787	226970457	69503	37.61649	0.460606434	intron (ENSRNOT00000019638, intron 7 of 20)
Ptprb	chr7	59323507	59324177	-2676	29.50695	0.461294206	intron (ENSRNOT00000085073, intron 12 of 12)
Ptprb	chr7	59323708	59324378	-2475	26.52662	0.461979814	intron (ENSRNOT00000085073, intron 12 of 12)
Vom2r24	chr8	3957100	3957770	46158	37.46989	0.462664311	Intergenic
AABR070 70173.1	chr8	55966929	55967599	57392	25.13457	0.463345554	Intergenic
Pde5a	chr2	226969999	226970669	69715	25.74376	0.464024595	intron (ENSRNOT00000019638, intron 7 of 20)
Eea1	chr7	37140932	37141602	39876	24.59404	0.46470142	intron (ENSRNOT00000087297, intron 12 of 29)
Eea1	chr7	37141154	37141824	40098	24.29395	0.465374947	exon (ENSRNOT00000029764, exon 11 of 28)
Ascc3	chr20	55378855	55379525	125504	37.95091	0.466047304	intron (ENSRNOT00000057016, intron 13 of 41)
Xpo1	chr14	108004580	108005250	-2809	21.68977	0.466720632	Intergenic
Cdca7	chr3	59152702	59153372	-243	40.61047	0.467392781	promoter-TSS (ENSRNOT00000002066)
Selenow	chr1	77202457	77203127	332889	38.418	0.468064819	Intergenic
LOC10255 5038	chr12	3747378	3748048	-59743	19.48606	0.468735666	Intergenic
Wee1	chr1	174751344	174752014	-16281	36.54032	0.46940315	Intergenic
AABR070 66060.1	chr9	1095003	1095673	5061	27.88129	0.470068338	intron (ENSRNOT00000086927, intron 1 of 1)
LOC29927 7	chr6	127882143	127882813	4062	25.21976	0.470731217	intron (ENSRNOT00000057298, intron 3 of 3)
RF00026	chr2	210908259	210908929	-5257	22.46567	0.471391774	intron (ENSRNOT00000026710, intron 3 of 8)
Slc12a1	chr3	117457942	117458612	35573	40.46481	0.472052172	intron (ENSRNOT00000008857, intron 15 of 26)
Pc	chr1	219758810	219759480	-38	30.86416	0.472710229	promoter-TSS (ENSRNOT00000086155)
Cmss1	chr11	45214316	45214986	-89417	36.43496	0.473365933	Intergenic
RF00001	chr3	137388531	137389201	-224259	40.45664	0.474019273	Intergenic
Rock2	chr6	42164924	42165594	-15635	38.30803	0.474671329	Intergenic
Chd1l	chr2	199761464	199762134	10097	26.4966	0.475322092	intron (ENSRNOT00000043937, intron 5 of 24)
Meikin	chr10	39733894	39734564	7722	32.48081	0.475972652	intron (ENSRNOT00000036822, intron 4 of 8)
Meikin	chr10	39734093	39734763	7921	22.29917	0.47662081	intron (ENSRNOT00000036822, intron 4 of 8)
Ninj2	chr4	152622801	152623471	-7333	38.97742	0.477267652	Intergenic
AABR070 72065.1	chr1	269596584	269597254	-251991	32.59809	0.477912071	Intergenic
Galnt5	chr3	43968677	43969347	-56288	30.53329	0.478555156	Intergenic
Agfg2	chr12	22082792	22083462	1062	30.88395	0.479195797	intron (ENSRNOT00000077711, intron 1 of 12)

AABR070 72065.1	chr1	269596959	269597629	-252366	17.21859	0.47983398	Intergenic
Galnt5	chr3	43968876	43969546	-56089	23.71859	0.480470801	Intergenic
Fcgr1a	chr2	198442558	198443228	-3439	41.18348	0.481104036	intron (ENSRNOT00000082450, intron 1 of 5)
Tmem229 a	chr4	52393674	52394344	-43385	41.26326	0.481735887	Intergenic
Spns3	chr10	59086982	59087652	25471	19.90228	0.482366346	intron (ENSRNOT00000041886, intron 7 of 10)
Bmpr1b	chr2	247674141	247674811	-227594	39.06255	0.482994294	Intergenic
RF00066	chr14	87941398	87942068	200165	22.38982	0.483624173	Intergenic
AABR070 70077.1	chr8	47765939	47766609	13783	33.42918	0.484252643	Intergenic
AABR070 70077.1	chr8	47765692	47766362	13536	26.85185	0.484878581	Intergenic
Slco2a1	chr8	111415223	111415893	-79773	35.06414	0.485503092	Intergenic
Tsn	chr13	34251266	34251936	49	34.40878	0.486125049	promoter-TSS (ENSRNOT00000068524)
Cd2ap	chr9	20809299	20809969	44338	39.62093	0.486745562	intron (ENSRNOT00000016291, intron 3 of 17)
Rab11fip4	chr10	66909128	66909798	-32935	42.74078	0.487363499	intron (ENSRNOT00000089538, intron 50 of 57)
AABR070 25272.1	chr16	31323768	31324438	-22223	17.96096	0.487978851	Intergenic
Tcf23	chr6	26743092	26743762	27737	38.9841	0.488593854	Intergenic
AABR070 01734.1	chr1	55755643	55756313	48580	32.22159	0.48920738	Intergenic
Lrp2bp	chr16	49438065	49438735	14994	39.19072	0.489820548	intron (ENSRNOT00000041617, intron 8 of 8)
Mt1m	chr20	3665632	3666302	-11507	15.37424	0.490431097	Intergenic
Mt1m	chr20	3665344	3666014	-11795	21.29246	0.491040146	Intergenic
Tpbpa	chr17	4160426	4161096	-4280	33.21157	0.491647687	Intergenic
AABR070 43598.1	chr19	30533111	30533781	55541	32.72739	0.492252579	Intergenic
AABR070 18038.1	chr15	36861954	36862624	-3259	20.05669	0.492854811	intron (ENSRNOT00000076667, intron 18 of 19)
AABR070 18038.1	chr15	36862234	36862904	-2979	22.58914	0.493456643	intron (ENSRNOT00000076667, intron 19 of 19)
AABR070 33271.1	chr11	14606315	14606985	61045	37.29203	0.494055798	Intergenic
AABR070 32724.3	chr18	78009707	78010377	-267426	29.79499	0.494654541	Intergenic
AABR070 32724.3	chr18	78009936	78010606	-267197	26.8791	0.495252869	Intergenic
AABR070 05886.1	chr1	204175564	204176234	83748	34.68963	0.495847354	Intergenic
Sel1l2	chr3	134474383	134475053	-12065	33.02847	0.49644141	Intergenic
Sel1l2	chr3	134474707	134475377	-12389	28.65316	0.497032743	Intergenic
Lrrc63	chr15	57135190	57135860	34869	38.06213	0.497624782	intron (ENSRNOT00000079097, intron 8 of 10)
RF00026	chr20	45555930	45556600	61828	39.89646	0.498215231	intron (ENSRNOT00000000713, intron 4 of 12)
RF00001	chr18	11608979	11609649	-30887	36.80965	0.498802935	Intergenic
Tagap	chr1	47491701	47492371	10916	26.8029	0.499391332	Intergenic
Tagap	chr1	47491265	47491935	11352	25.89694	0.49997697	Intergenic
Cpne8	chr7	131889613	131890283	-91712	22.37342	0.500562142	Intergenic

Pgap1	chr9	61225518	61226188	-90890	37.44526	0.50114569	Intergenic
Alkal2	chr6	49833289	49833959	8155	39.45371	0.501726454	intron (ENSRNOT00000006921, intron 4 of 4)
Ckap4	chr7	24971470	24972140	32307	36.63971	0.502306734	Intergenic
Fut10	chr16	64649788	64650458	66101	43.08362	0.502885369	exon (ENSRNOT00000071166, exon 4 of 5)
AABR070 34456.1	chr11	72533853	72534523	41098	39.72909	0.503462352	Intergenic
RF00100	chr14	50676522	50677192	128501	24.3497	0.504036515	Intergenic
RF00100	chr14	50676323	50676993	128700	31.2895	0.504610171	Intergenic
AABR070 01018.1	chr1	33767707	33768377	-26761	39.66883	0.505182154	Intergenic
RF00001	chr9	26775567	26776237	1025	41.85998	0.505752455	TTS (ENSRNOT00000070299)
AABR070 01662.1	chr1	54956023	54956693	-72796	49.85121	0.506319904	Intergenic
AABR070 58815.1	chr7	138416811	138417481	7191	40.64553	0.506886821	intron (ENSRNOT00000077822, intron 1 of 2)
AABR070 12426.1	chr2	195066463	195067133	27606	16.87258	0.507450868	Intergenic
Tnik	chr2	113960985	113961655	-23326	38.457	0.508014373	Intergenic
RF00560	chr8	99942202	99942872	11571	31.23834	0.508576162	Intergenic
Pak7	chr3	129381348	129382018	-24192	35.25276	0.509136227	Intergenic
LOC10091 2097	chr1	148918859	148919529	56701	32.98242	0.509696909	Intergenic
AABR070 72065.1	chr1	269597458	269598128	-252865	17.03627	0.510254684	Intergenic
Alkal2	chr6	49833502	49834172	8368	36.44001	0.510811893	intron (ENSRNOT00000006921, intron 4 of 4)
AABR070 66188.1	chr9	4627453	4628123	6363	38.75655	0.511366178	Intergenic
RF00002	chr7	22260383	22261053	193299	15.02309	0.511919885	Intergenic
RF00002	chr7	22260768	22261438	192914	17.12574	0.512471833	Intergenic
Ythdc2	chr1	181294857	181295527	845378	24.2865	0.513022012	Intergenic
AABR070 52263.1	chr3	43790712	43791382	96949	38.11153	0.5135716	Intergenic
Epg5	chr18	74325946	74326616	26350	37.60684	0.514119409	intron (ENSRNOT00000078403, intron 10 of 43)
Arhgap42	chr8	7465666	7466336	-39390	26.06917	0.514665433	Intergenic
Arhgap42	chr8	7465204	7465874	-38928	24.01278	0.51521085	Intergenic
Trem1	chr9	14801070	14801740	8042	38.12187	0.515755657	intron (ENSRNOT00000049193, intron 1 of 3)
Ttc17	chr3	83270871	83271541	35575	18.57264	0.51630104	intron (ENSRNOT00000014088, intron 10 of 24)
Mrs2	chr17	42084909	42085579	20868	39.16784	0.51684581	exon (ENSRNOT00000024196, exon 25 of 25)
Hmbs	chr8	48674832	48675502	-419	40.67761	0.517388772	promoter-TSS (ENSRNOT00000014127)
Klf9	chr1	240929877	240930547	21729	26.49955	0.517931112	intron (ENSRNOT00000019367, intron 1 of 1)
Olr1345	chr9	99693647	99694317	-13003	38.82124	0.518470439	Intergenic
Olig3	chr1	14680731	14681401	-116700	16.00182	0.519010328	Intergenic
Baiap211	chr12	12239610	12240280	12850	41.07283	0.519548386	intron (ENSRNOT00000092610, intron 1 of 12)

Ythdc2	chr1	180925765	180926435	1214470	42.28482	0.520084607	Intergenic
Msx2	chr17	11757529	11758199	74002	24.75199	0.520620182	Intergenic
AABR070 71368.2	chr8	111992244	111992914	-4869	15.94533	0.521153909	Intergenic
AABR070 04992.1	chr1	173327471	173328141	52470	43.56338	0.521686982	Intergenic
AABR070 63599.1	chr6	36582734	36583404	148265	20.10577	0.522218196	Intergenic
AABR070 52750.1	chr3	71653574	71654244	-10686	15.23193	0.522748746	Intergenic
AABR070 01662.1	chr1	54955761	54956431	-72534	44.36614	0.523277426	Intergenic
Rpl32	chr4	147718821	147719491	-84	39.2497	0.523805435	promoter-TSS (ENSRNOT00000090620)
AABR070 04061.1	chr1	123796005	123796675	-173241	37.54712	0.524331561	Intergenic
RF00026	chr8	73322446	73323116	39694	32.87487	0.524857008	Intergenic
Rab11fip4	chr10	66912487	66913157	-29576	26.74302	0.525379351	intron (ENSRNOT00000089538, intron 51 of 57)
Rab11fip4	chr10	66912192	66912862	-29871	18.89435	0.525902215	intron (ENSRNOT00000089538, intron 51 of 57)
Slco1a6	chr4	176362801	176363471	18341	29.35357	0.526423175	exon (ENSRNOT00000048367, exon 8 of 14)
Slco1a6	chr4	176362599	176363269	18543	32.66785	0.526942224	intron (ENSRNOT00000048367, intron 8 of 13)
AABR070 12039.1	chr2	183291200	183291870	-40607	37.05822	0.527459356	Intergenic
AABR070 12039.1	chr2	183291399	183292069	-40806	23.12017	0.527975779	Intergenic
Mir125b1	chr8	45881065	45881735	83140	26.58601	0.528491492	Intergenic
Mir125b1	chr8	45880629	45881299	82704	22.79744	0.52900649	Intergenic
Leo1	chr8	82374015	82374685	-6407	36.71194	0.529518332	Intergenic
Leo1	chr8	82374304	82374974	-6118	27.80668	0.530029449	Intergenic
Atg7	chr4	146700049	146700719	101971	40.12363	0.530538616	intron (ENSRNOT00000067532, intron 17 of 17)
Nfkb2	chr1	265997217	265997887	-55450	19.97737	0.531048272	intron (ENSRNOT00000086041, intron 5 of 40)
Sgcd	chr10	32528939	32529609	-57820	17.94003	0.53155597	Intergenic
RF00619	chr1	245880592	245881262	-10118	41.28352	0.532062928	intron (ENSRNOT00000023762, intron 12 of 14)
RGD1566 337	chr2	194945602	194946272	-69975	39.14376	0.532570369	Intergenic
RGD1565 355	chr4	13991210	13991880	-10216	38.87209	0.53307584	Intergenic
RF00100	chr9	14241934	14242604	-20256	36.73965	0.533580562	Intergenic
B3gnt7	chr9	93335381	93336051	9433	21.95487	0.534084532	Intergenic
B3gnt7	chr9	93335181	93335851	9233	35.8457	0.534587747	Intergenic
AABR070 04130.1	chr1	126315859	126316529	87212	38.18253	0.535088971	Intergenic
Zfp266	chr8	21516284	21516954	2394	38.39512	0.535590666	exon (ENSRNOT00000085060, exon 6 of 6)
Rbm24	chr17	18717799	18718469	-35258	35.43691	0.536090363	Intergenic
LOC68028 8	chr13	37696248	37696918	986	27.92506	0.536588054	TTS (ENSRNOT00000045263)
Plpp1	chr2	44712854	44713524	49065	37.19416	0.537084971	intron (ENSRNOT00000066098, intron 2 of 5)

Hinfp	chr8	48640572	48641242	-6110	40.40759	0.537579873	TTS (ENSRNOT00000030745)
App	chr11	24737337	24738007	-95814	20.62765	0.538073991	Intergenic
Papola	chr6	129581207	129581877	-27532	16.46426	0.538567324	intron (ENSRNOT00000083626, intron 12 of 18)
RF00001	chr13	73005951	73006621	-7370	40.39456	0.539058626	intron (ENSRNOT00000093410, intron 2 of 8)
App	chr11	24737657	24738327	-96134	24.44561	0.539549134	Intergenic
Papola	chr6	129581008	129581678	-27731	39.42789	0.540037602	intron (ENSRNOT00000083626, intron 12 of 18)
Pelo	chr2	47216117	47216787	52173	30.11949	0.540525267	intron (ENSRNOT00000086114, intron 2 of 28)
Ehbp1	chr14	107168465	107169135	-8466	38.75016	0.541012127	Intergenic
Mrpl21	chr1	218531730	218532400	20	47.95239	0.541496932	promoter-TSS (ENSRNOT00000018487)
Rxfp2	chr12	6034913	6035583	43163	17.20734	0.541982171	intron (ENSRNOT00000001197, intron 13 of 17)
Rxfp2	chr12	6035371	6036041	42705	23.79739	0.542465346	intron (ENSRNOT00000001197, intron 13 of 17)
Cnih1	chr15	23583079	23583749	-3019	38.26035	0.542946453	Intergenic
AABR070 42780.1	chr19	7385010	7385680	-862648	26.2169	0.543427986	Intergenic
AABR070 42780.1	chr19	7385588	7386258	-862070	19.1784	0.543907441	Intergenic
Mettl17	chr15	28278638	28279308	-8051	34.74171	0.544386065	Intergenic
Mettl17	chr15	28278848	28279518	-7841	28.86882	0.544862602	Intergenic
AABR070 57590.1	chr7	79320309	79320979	136316	20.08319	0.5453383	Intergenic
AABR070 57590.1	chr7	79320102	79320772	136523	35.58534	0.545813157	Intergenic
Pld5	chr13	94290332	94291002	-1334	36.73405	0.546285911	intron (ENSRNOT00000005332, intron 1 of 9)
Tcf4	chr18	65238868	65239538	-46115	36.90355	0.546757816	intron (ENSRNOT00000081797, intron 3 of 18)
Ipcef1	chr1	43609560	43610230	28266	38.80843	0.547228868	intron (ENSRNOT00000024460, intron 4 of 8)
Mnx1	chr4	2436002	2436672	-55066	39.14824	0.547699066	Intergenic
Gm10642	chr8	77068617	77069287	-19517	17.82482	0.548168405	intron (ENSRNOT00000078685, intron 2 of 8)
AABR070 27501.1	chr17	34558525	34559195	-12592	41.13389	0.548636882	Intergenic
Gm10642	chr8	77068410	77069080	-19724	35.55083	0.549103232	intron (ENSRNOT00000078685, intron 2 of 8)
Ccdc189	chr1	199036754	199037424	178	50.12688	0.549568713	promoter-TSS (ENSRNOT00000025499)
Pin1	chr8	21666454	21667124	-2447	25.05649	0.550032055	Intergenic
Ccdc90b	chr1	157058741	157059411	-344519	26.33451	0.55049452	intron (ENSRNOT00000055401, intron 12 of 21)
Ccdc90b	chr1	157058502	157059172	-344758	32.98443	0.550957374	intron (ENSRNOT00000055401, intron 12 of 21)
Far2	chr4	182489022	182489692	6163	31.24343	0.551418078	intron (ENSRNOT00000002528, intron 1 of 11)
Rfx7	chr8	79240124	79240794	81089	35.44183	0.551877896	intron (ENSRNOT00000086841, intron 2 of 8)

Rfx7	chr8	79240349	79241019	81314	31.32387	0.552336826	intron (ENSRNOT00000086841, intron 2 of 8)
RF00026	chr15	17141454	17142124	-90607	32.87386	0.552796138	Intergenic
RF00100	chr1	184686769	184687439	191617	38.81839	0.553253283	Intergenic
RF00100	chr2	151402254	151402924	-43589	38.33501	0.553709532	Intergenic
Fam3c	chr4	49492050	49492720	-52518	38.91193	0.554164881	Intergenic
Adam10	chr8	77193450	77194120	86249	30.31233	0.554618051	intron (ENSRNOT00000083255, intron 6 of 15)
Adam10	chr8	77193725	77194395	86524	22.37535	0.555071591	intron (ENSRNOT00000083255, intron 6 of 15)
AABR070 19443.1	chr15	106025180	106025850	-36392	35.58976	0.555522943	Intergenic
LOC10255 4127	chr13	41494134	41494804	125183	31.16755	0.555974663	Intergenic
RF00017	chr14	50519797	50520467	152339	42.27633	0.556424187	Intergenic
LOC10255 4127	chr13	41494341	41495011	125390	21.22211	0.556872793	Intergenic
Dusp16	chr4	168495581	168496251	21261	38.2384	0.557320477	intron (ENSRNOT00000009151, intron 3 of 5)
Tmtc1	chr4	182858641	182859311	-14685	15.52916	0.557767236	Intergenic
RGD1561 667	chr1	55235542	55236212	16104	30.65552	0.558213069	Intergenic
Psmg3	chr12	16895849	16896519	-2841	39.78421	0.558659258	Intergenic
Rmi2	chr10	4860433	4861103	49537	41.69852	0.559104516	Intergenic
Rps4x	chr4	35772821	35773491	-42557	35.37	0.559550129	Intergenic
AABR070 42999.1	chr19	15887892	15888562	44358	36.86605	0.559993518	Intergenic
Tmem126 b	chr1	156180669	156181339	-81027	40.6114	0.560437259	Intergenic
Mcam	chr8	48503168	48503838	30679	22.40363	0.560878768	exon (ENSRNOT00000067902, exon 7 of 16)
Mcam	chr8	48503472	48504142	30983	28.1848	0.561320625	intron (ENSRNOT00000067902, intron 6 of 15)
Olfml2a	chr3	23226132	23226802	2988	37.25058	0.561760243	intron (ENSRNOT00000018853, intron 1 of 7)
Sec11a	chr1	142781578	142782248	-22031	33.5727	0.562198911	Intergenic
LOC10835 3037	chr15	53677043	53677713	-181384	27.35354	0.562636626	Intergenic
Dad1	chr15	32887803	32888473	-43	37.48612	0.563073385	promoter-TSS (ENSRNOT00000012233)
AABR070 05838.2	chr1	202953947	202954617	124715	19.64566	0.563507888	Intergenic
AABR070 35437.1	chr12	14731580	14732250	-25257	28.80297	0.563942727	intron (ENSRNOT00000089775, intron 4 of 46)
AABR070 35437.1	chr12	14731366	14732036	-25043	36.46686	0.564376601	intron (ENSRNOT00000089775, intron 4 of 46)
Mkl1	chr7	122385110	122385780	18222	31.41788	0.564808209	intron (ENSRNOT00000088814, intron 1 of 13)
Mkl1	chr7	122384844	122385514	18488	29.40307	0.565240146	intron (ENSRNOT00000088814, intron 1 of 13)
RF00003	chr15	38133053	38133723	-28818	37.71746	0.565669809	intron (ENSRNOT00000063962, intron 4 of 12)
RF00003	chr15	38133256	38133926	-29021	15.51944	0.566098495	intron (ENSRNOT00000063962, intron 4 of 12)

Mc4r	chr18	62664974	62665644	-50584	43.84787	0.566527505	Intergenic
Numb	chr6	107296560	107297230	28450	38.28937	0.566955536	intron (ENSRNOT00000042594, intron 2 of 10)
Phf12	chr10	64859980	64860650	1817	33.36804	0.567381276	intron (ENSRNOT00000056234, intron 2 of 14)
AABR070 56118.1	chr7	20248869	20249539	-13476	42.7376	0.567807337	Intergenic
Depdc5	chr14	83218386	83219056	350	49.69239	0.568232409	intron (ENSRNOT00000067694, intron 1 of 41)
Bet1	chr4	29112519	29113189	-20101	20.28652	0.568655181	Intergenic
RF00108	chr1	194916538	194917208	496	40.98125	0.569078267	TTS (ENSRNOT00000080729)
Sinhcaf	chr4	183417921	183418591	-589	27.28807	0.569499045	promoter-TSS (ENSRNOT00000089160)
Sinhcaf	chr4	183418363	183419033	-1031	28.17777	0.569920134	intron (ENSRNOT00000083310, intron 1 of 6)
LOC10036 2344	chr4	184193693	184194363	-97222	24.28502	0.570338908	Intergenic
Sult2a2	chr1	76584333	76585003	29611	19.31128	0.570756676	intron (ENSRNOT00000041367, intron 3 of 5)
LOC10036 2344	chr4	184194022	184194692	-97551	16.22614	0.571173434	Intergenic
Arrdc4	chr1	129739581	129740251	36360	26.28687	0.571589181	Intergenic
lkbke	chr13	48133332	48134002	-77273	37.78979	0.57200523	intron (ENSRNOT00000086928, intron 4 of 21)
Brat1	chr12	16020626	16021296	6920	38.40834	0.572418946	intron (ENSRNOT00000064726, intron 6 of 12)
AABR070 44836.1	chr20	23017987	23018657	9289	21.51333	0.572832962	Intergenic
AABR070 44836.1	chr20	23018188	23018858	9088	15.13416	0.573244637	Intergenic
AABR070 44836.1	chr20	23017774	23018444	9502	36.89621	0.573656607	Intergenic
Opcml	chr8	29461623	29462293	8315	16.44602	0.57406623	intron (ENSRNOT00000090643, intron 1 of 7)
Opcml	chr8	29461360	29462030	8052	15.98231	0.574476146	intron (ENSRNOT00000090643, intron 1 of 7)
RF00026	chr20	45556132	45556802	62030	29.26027	0.57488503	intron (ENSRNOT00000000713, intron 4 of 12)
RF00100	chr12	2303302	2303972	-3576	41.01002	0.575292881	Intergenic
Col26a1	chr12	22864866	22865536	30182	35.70456	0.575699696	intron (ENSRNOT00000059530, intron 1 of 14)
Tango6	chr19	38884672	38885342	38719	42.66904	0.576105472	intron (ENSRNOT00000030768, intron 7 of 17)
RF00340	chr1	200128405	200129075	28120	28.38494	0.576510206	intron (ENSRNOT00000027644, intron 10 of 15)
Bnip2	chr8	76400393	76401063	355	37.38452	0.576915225	intron (ENSRNOT00000081072, intron 1 of 8)
Med17	chr8	13834938	13835608	-105	38.25651	0.577317869	promoter-TSS (ENSRNOT00000014435)
AABR070 53402.1	chr3	104696227	104696897	-21105	17.81345	0.577720795	Intergenic
AABR070 53402.1	chr3	104696028	104696698	-20906	39.31071	0.57812267	Intergenic
AABR070 53402.1	chr3	104695599	104696269	-20477	18.72493	0.578522161	Intergenic
Flrt3	chr3	135259429	135260099	-563110	35.89679	0.578923261	Intergenic

Eif4g2	chr1	175950469	175951139	-55294	34.6754	0.579321972	Intergenic
Eif4g2	chr1	175950669	175951339	-55494	20.06567	0.579719622	Intergenic
Galk2	chr3	118142463	118143133	-1798	41.29181	0.580116209	intron (ENSRNOT00000083356, intron 1 of 9)
Cep55	chr1	256747664	256748334	2711	37.49069	0.580513067	intron (ENSRNOT00000022133, intron 2 of 8)
Eef2k	chr1	190777437	190778107	-2464	40.77319	0.58090886	Intergenic
AABR070 27799.1	chr17	44388825	44389495	31436	39.782	0.581304922	Intergenic
Vom2r64	chr12	21095124	21095794	-17920	27.5033	0.581701254	Intergenic
Vom2r64	chr12	21095372	21096042	-18168	25.95915	0.582096516	Intergenic
Slc38a2	chr7	138100487	138101157	19	38.77297	0.582490706	promoter-TSS (ENSRNOT00000039002)
Cacna1e	chr13	72023643	72024313	39369	46.75894	0.582885162	intron (ENSRNOT00000090544, intron 2 of 43)
Smg8	chr10	74387504	74388174	948	25.45482	0.583277199	exon (ENSRNOT00000008107, exon 1 of 4)
RF00049	chr2	52255858	52256528	2918	42.0832	0.583670845	intron (ENSRNOT00000033627, intron 6 of 21)
AABR070 27567.1	chr17	36956414	36957084	364	41.32764	0.584062066	intron (ENSRNOT00000024854, intron 1 of 5)
Bcl2l11	chr3	120619608	120620278	-106963	22.92133	0.584453549	intron (ENSRNOT00000021740, intron 14 of 19)
Bcl2l11	chr3	120619092	120619762	-107479	20.03982	0.584843948	intron (ENSRNOT00000021740, intron 14 of 19)
Zc3h8	chr3	121479907	121480577	8298	27.44429	0.58523326	exon (ENSRNOT00000023845, exon 3 of 9)
AABR070 54753.1	chr3	168681371	168682041	38208	26.6816	0.585622831	Intergenic
AABR070 54753.1	chr3	168681726	168682396	38563	26.54094	0.586011313	Intergenic
Cdc42ep3	chr6	2002695	2003365	-60058	39.6763	0.586400052	Intergenic
Cdc42ep3	chr6	2002904	2003574	-60267	17.93321	0.586786346	Intergenic
RF00026	chr4	71157607	71158277	-6801	37.99256	0.587172896	Intergenic
RF00066	chr13	53999366	54000036	-99761	37.39563	0.587558347	Intergenic
AABR070 30501.1	chr10	90778379	90779049	-6076	25.31565	0.58794405	Intergenic
Kctd3	chr13	107393996	107394666	77512	28.97823	0.588328653	intron (ENSRNOT00000004992, intron 65 of 72)
Majin	chr1	221554263	221554933	-3495	23.47628	0.588712151	Intergenic
Majin	chr1	221554057	221554727	-3701	36.00016	0.589094543	Intergenic
Ndufs4	chr2	46477879	46478549	-2011	35.80935	0.589477184	Intergenic
Elmod2	chr19	24477081	24477751	9980	39.7342	0.589858714	intron (ENSRNOT00000031614, intron 5 of 8)
Prpf8	chr10	63634767	63635437	-117	39.37557	0.590237774	promoter-TSS (ENSRNOT00000005016)
AABR070 06436.1	chr1	233538742	233539412	131087	27.60559	0.590618437	intron (ENSRNOT00000019174, intron 2 of 6)
RF00405	chr20	11941278	11941948	-7379	24.41315	0.590996624	Intergenic
Lrguk	chr4	61245079	61245749	-174595	21.32557	0.591373691	intron (ENSRNOT00000075621, intron 18 of 21)

Lrguk	chr4	61245351	61246021	-174323	23.62764	0.591750999	intron (ENSRNOT00000075621, intron 18 of 21)
RF00026	chr4	66283113	66283783	3192	36.32187	0.592127185	intron (ENSRNOT0000007544, intron 1 of 1)
Cdc42ep3	chr6	1991384	1992054	-48747	22.9749	0.592502245	Intergenic
Snx11	chr10	84639048	84639718	-272	41.91292	0.592877542	promoter-TSS (ENSRNOT00000011474)
Ctrb1	chr19	43913868	43914538	-3146	32.70823	0.593253078	Intergenic
AABR070 60145.1	chr4	59075019	59075689	-60938	37.03232	0.593627484	Intergenic
Ctrb1	chr19	43914090	43914760	-3368	30.21621	0.594000759	Intergenic
AABR070 06978.1	chr1	275127793	275128463	-122306	20.04016	0.5943729	Intergenic
AABR070 06978.1	chr1	275127575	275128245	-122088	29.83948	0.594745274	Intergenic
Utp18	chr10	81289009	81289679	298514	41.02921	0.595115141	intron (ENSRNOT00000075163, intron 6 of 8)
lfng2	chr11	31702834	31703504	8830	36.5366	0.595486609	intron (ENSRNOT0000002779, intron 2 of 6)
AABR070 07409.1	chr2	13104347	13105017	-49467	24.08855	0.595855565	Intergenic
AABR070 07409.1	chr2	13104106	13104776	-49226	35.51695	0.59622475	Intergenic
AABR070 20651.1	chr13	33593593	33594263	-554875	15.60296	0.596592789	Intergenic
Tnp1	chr2	29132028	29132698	-11259	19.15742	0.596961056	Intergenic
Dtd1	chr3	138815641	138816311	45361	35.54624	0.597328175	intron (ENSRNOT00000066986, intron 4 of 4)
AABR070 20651.1	chr13	33593985	33594655	-554483	22.18608	0.597694143	Intergenic
Tnp1	chr2	29132404	29133074	-11635	23.04877	0.598058958	Intergenic
Zfp68	chr12	18170817	18171487	18493	30.50515	0.598422618	Intergenic
Zfp68	chr12	18170577	18171247	18253	29.79682	0.598785121	Intergenic
Zfp68	chr12	18171059	18171729	18735	20.44521	0.599147843	Intergenic
Sult2b1	chr1	101731740	101732410	9366	17.93014	0.599509404	intron (ENSRNOT00000067430, intron 1 of 6)
RF00026	chr9	58258512	58259182	262740	35.78552	0.599869802	Intergenic
Ocln	chr2	30567249	30567919	9007	16.77428	0.600230417	intron (ENSRNOT00000024674, intron 1 of 8)
AABR070 58608.1	chr7	127500414	127501084	-65823	38.00714	0.600589866	Intergenic
Clnk	chr14	76627291	76627961	-29685	37.4119	0.600948146	Intergenic
Dcdc5	chr3	97531005	97531675	181886	38.86128	0.601306641	Intergenic
Ctbs	chr2	252310501	252311171	4962	37.07467	0.601663963	intron (ENSRNOT00000020972, intron 3 of 6)
Ctbs	chr2	252310705	252311375	5166	20.73989	0.602020112	intron (ENSRNOT00000020972, intron 3 of 6)
Zfp68	chr12	18187419	18188089	35095	35.8	0.602375084	Intergenic
Plekha5	chr4	174669550	174670220	-22446	38.16478	0.602730266	intron (ENSRNOT00000042291, intron 3 of 31)
Ank3	chr20	20075196	20075866	-29516	20.31577	0.603084268	Intergenic
Med30	chr7	92175148	92175818	-59114	35.25107	0.603438479	Intergenic
Gcnt3	chr8	76475440	76476110	-23221	34.7753	0.603791507	Intergenic

Map4k3	chr6	3310651	3311321	44353	28.04049	0.604143351	intron (ENSRNOT00000078044, intron 16 of 33)
Map4k3	chr6	3310388	3311058	44616	35.23381	0.604494008	intron (ENSRNOT00000078044, intron 16 of 33)
AABR070 17527.1	chr15	25206715	25207385	73234	23.80784	0.604844868	Intergenic
Poln	chr14	81872599	81873269	14191	39.95662	0.605194538	intron (ENSRNOT00000058067, intron 1 of 22)
Ddx20	chr2	208111433	208112103	40411	38.46142	0.605544411	intron (ENSRNOT00000051835, intron 2 of 6)
Rxfp2	chr12	6035624	6036294	42452	15.99938	0.605893091	intron (ENSRNOT00000001197, intron 13 of 17)
AABR070 12384.1	chr2	194716155	194716825	158504	33.93808	0.606240575	intron (ENSRNOT00000070843, intron 1 of 1)
Ypel1	chr11	88197311	88197981	-17104	39.7199	0.606588259	Intergenic
Stmn4	chr15	43033698	43034368	26125	23.57253	0.606934745	Intergenic
Stmn4	chr15	43033474	43034144	25901	32.17106	0.607281428	Intergenic
AABR070 12384.1	chr2	194716435	194717105	158784	29.47654	0.607625512	intron (ENSRNOT00000070843, intron 1 of 1)
Tp53bp1	chr3	113198442	113199112	33013	35.20906	0.60796979	intron (ENSRNOT00000019025, intron 11 of 27)
Vom1r64	chr9	101225367	101226037	2856	20.46717	0.608312863	Intergenic
Kctd6	chr15	18477007	18477677	16024	36.43079	0.60865613	intron (ENSRNOT00000010260, intron 14 of 14)
Vom1r64	chr9	101225168	101225838	2657	29.89276	0.608998187	Intergenic
Olr1382	chr10	12822826	12823496	-5024	15.07465	0.609339034	Intergenic
Olr1382	chr10	12822624	12823294	-4822	37.06901	0.609680072	Intergenic
AABR070 10476.1	chr2	137147953	137148623	5263	36.93045	0.610019896	TTS (ENSRNOT00000083443)
Gpx8	chr2	44916879	44917549	-10184	39.47448	0.610358504	Intergenic
Rcbtb2	chr15	55029670	55030340	-4028	38.06121	0.610695894	Intergenic
Mecom	chr2	117301007	117301677	153427	37.86078	0.61103347	Intergenic
AC129049 .2	chr1	273618460	273619130	-1646	36.90267	0.611371233	Intergenic
Opa1	chr11	74715381	74716051	77957	38.335	0.611706366	Intergenic
Spag17	chr2	201939662	201940332	-260800	48.43836	0.612043091	Intergenic
RF00026	chr1	143504382	143505052	8126	36.32907	0.612377182	intron (ENSRNOT00000087785, intron 1 of 8)
Dync1h1	chr6	134948823	134949493	-9696	36.6921	0.612711455	Intergenic
Lrrc75b	chr20	14062414	14063084	8210	34.6918	0.613045911	Intergenic
AABR070 05596.1	chr1	189803220	189803890	5495	35.71531	0.613379137	intron (ENSRNOT00000091780, intron 1 of 1)
Dlat	chr8	55075988	55076658	11509	23.08651	0.613711131	intron (ENSRNOT00000032152, intron 7 of 13)
St6gal1	chr11	81002213	81002883	-21126	27.26057	0.614043304	Intergenic
St6gal1	chr11	81001901	81002571	-20814	34.48489	0.614375658	Intergenic
Mafg	chr10	109811101	109811771	-113	38.50348	0.614706775	promoter-TSS (ENSRNOT00000054970)
Acsn2	chr1	189385884	189386554	21931	33.1895	0.615036655	intron (ENSRNOT00000084260, intron 7 of 14)

AABR070 30040.1	chr10	63691549	63692219	-4724	31.77518	0.615366713	intron (ENSRNOT00000005100, intron 5 of 13)
Acsm2	chr1	189385672	189386342	21719	33.27613	0.615695529	intron (ENSRNOT000000084260, intron 7 of 14)
Cyp3a62	chr12	18704455	18705125	25001	16.49911	0.616024521	intron (ENSRNOT000000087229, intron 11 of 12)
AABR070 52750.1	chr3	71653299	71653969	-10961	18.21695	0.616353689	Intergenic
AABR070 36010.1	chr12	30501798	30502468	127	37.63197	0.616680193	promoter-TSS (ENSRNOT000000093591)
Spag5	chr10	65556372	65557042	3810	25.01419	0.617008291	TTS (ENSRNOT000000056217)
Wls	chr2	266270556	266271226	-44145	39.44864	0.617333721	Intergenic
Btbd11	chr7	24136469	24137139	-34043	15.22321	0.617659321	intron (ENSRNOT000000044331, intron 17 of 30)
Btbd11	chr7	24135960	24136630	-33534	15.93731	0.617985094	intron (ENSRNOT000000044331, intron 17 of 30)
Dpy19l2	chr8	25805887	25806557	23347	35.09472	0.618309615	intron (ENSRNOT000000071884, intron 6 of 21)
LOC10255 3774	chr8	103011475	103012145	-123070	17.4309	0.618632882	intron (ENSRNOT00000011358, intron 14 of 15)
LOC10255 3774	chr8	103011275	103011945	-123270	37.18964	0.618956317	intron (ENSRNOT00000011358, intron 14 of 15)
AABR070 01662.1	chr1	54980641	54981311	-97414	38.68306	0.619278496	Intergenic
AABR070 01662.1	chr1	54980879	54981549	-97652	33.81832	0.619600843	Intergenic
RF00026	chr3	22079478	22080148	31688	37.07086	0.61992193	intron (ENSRNOT000000025443, intron 18 of 20)
AC112866 .1	chr1	193755986	193756656	-55648	33.35409	0.620243183	Intergenic
RF00026	chr1	147838554	147839224	-9652	30.90831	0.620563174	intron (ENSRNOT000000074103, intron 7 of 9)
AC112866 .1	chr1	193756188	193756858	-55850	20.38142	0.62088333	Intergenic
Stxbp6	chr6	65273470	65274140	45722	37.16753	0.621202221	intron (ENSRNOT00000005618, intron 1 of 5)
LOC68568 0	chr11	60158537	60159207	18742	24.35743	0.621519845	intron (ENSRNOT000000033595, intron 3 of 5)
RF00026	chr2	47385654	47386324	88904	19.09302	0.621837631	Intergenic
RF00026	chr2	47385446	47386116	88696	25.73306	0.622154147	Intergenic
Leo1	chr8	82373576	82374246	-6846	16.63346	0.62246939	Intergenic
Skor2	chr18	73115449	73116119	-42189	30.00738	0.622786228	Intergenic
Skor2	chr18	73115653	73116323	-41985	21.40783	0.623100357	Intergenic
Gtf3a	chr12	9876772	9877442	-12316	20.4148	0.623414645	Intergenic
Gtf3a	chr12	9876573	9877243	-12117	31.17126	0.623727655	Intergenic
Tmtc1	chr4	182985963	182986633	-142007	33.95253	0.624040822	Intergenic
Sft2d1	chr1	53003306	53003976	10825	17.79174	0.624354146	intron (ENSRNOT000000049831, intron 5 of 7)
Foxk1	chr12	14295257	14295927	-51276	40.46599	0.624666189	Intergenic
Apba2	chr1	125514526	125515196	147581	18.67033	0.62497695	intron (ENSRNOT000000022049, intron 5 of 13)
RF00560	chr2	107870087	107870757	-241391	39.19446	0.625287864	Intergenic

RF00015	chr18	64395486	64396156	68093	40.48744	0.625597493	Intergenic
AABR070 27263.1	chr17	21810090	21810760	-24377	17.20843	0.625907276	Intergenic
Als2	chr9	66027044	66027714	6492	27.34722	0.62621577	intron (ENSRNOT00000035209, intron 1 of 33)
Acvr1c	chr3	44380553	44381223	-38533	32.41112	0.626524415	Intergenic
Als2	chr9	66027356	66028026	6180	15.98557	0.62683177	intron (ENSRNOT00000035209, intron 1 of 33)
Gss	chr3	151082300	151082970	23922	29.90443	0.627137832	intron (ENSRNOT00000025657, intron 9 of 12)
Acvr1c	chr3	44380755	44381425	-38735	27.6572	0.627444042	Intergenic
Gss	chr3	151082053	151082723	24169	23.19023	0.627750403	intron (ENSRNOT00000025657, intron 9 of 12)
Serpinb6b	chr17	32809579	32810249	-26487	35.89016	0.62805402	Intergenic
Zbtb10	chr2	94619061	94619731	110912	34.65275	0.628359232	Intergenic
Erap1	chr2	1107770	1108440	-302829	33.07222	0.628663144	Intergenic
Sh3tc2	chr18	57340245	57340915	54258	31.99877	0.628965755	intron (ENSRNOT00000026174, intron 14 of 16)
RF00001	chr9	81052603	81053273	1001	22.37225	0.629268511	TTS (ENSRNOT00000070156)
Psrc1	chr2	211183212	211183882	6991	18.02629	0.629569964	exon (ENSRNOT00000027263, exon 34 of 34)
Psrc1	chr2	211182860	211183530	6639	23.5995	0.629871561	TTS (ENSRNOT00000027263)
RF00001	chr9	81052974	81053644	1372	23.98371	0.630173302	Intergenic
Aldoa	chr1	198231231	198231901	778	28.66814	0.630473737	intron (ENSRNOT00000088473, intron 1 of 8)
AABR070 13288.4	chr2	231927015	231927685	-14444	19.32992	0.630772862	exon (ENSRNOT00000014695, exon 16 of 20)
AABR070 67210.1	chr9	35154863	35155533	6996	37.85453	0.631072129	Intergenic
AABR070 13288.4	chr2	231926812	231927482	-14647	37.68923	0.631370084	intron (ENSRNOT00000014695, intron 15 of 19)
Tmtc3	chr7	39949513	39950183	267208	26.82413	0.63166818	Intergenic
Epb41l5	chr13	35642222	35642892	26411	37.93287	0.631966417	intron (ENSRNOT00000042862, intron 6 of 22)
Proser3	chr1	89005970	89006640	736	32.30102	0.632263338	intron (ENSRNOT00000032363, intron 1 of 10)
Proser3	chr1	89006173	89006843	533	26.92563	0.632558943	intron (ENSRNOT00000032363, intron 1 of 10)
AABR070 05977.1	chr1	210567875	210568545	-50483	37.45443	0.632854686	intron (ENSRNOT00000031734, intron 9 of 11)
Tab2	chr1	2185036	2185706	-111475	19.7902	0.633149109	Intergenic
Gpc6	chr15	102160407	102161077	-4009	37.93478	0.633443669	Intergenic
Alg8	chr1	162340864	162341534	-852	36.85952	0.633736907	promoter-TSS (ENSRNOT00000016478)
Rbm28	chr4	56396904	56397574	40903	42.03954	0.634030281	Intergenic
Pex1	chr4	27697807	27698477	-105	36.88665	0.63432379	promoter-TSS (ENSRNOT00000038136)
Slc25a19	chr10	104204409	104205079	-25221	24.70914	0.634617436	intron (ENSRNOT00000005347, intron 3 of 5)
Jazf1	chr4	83160164	83160834	-22972	17.22157	0.634908293	Intergenic

AABR070 68163.1	chr9	86793140	86793810	18082	37.48657	0.635200747	Intergenic
Slc25a19	chr10	104204167	104204837	-24979	28.13816	0.635491872	intron (ENSRNOT00000005347, intron 3 of 5)
Ptk2	chr7	114551711	114552381	21854	35.16188	0.635781666	intron (ENSRNOT00000011219, intron 3 of 30)
RF00015	chr15	20208729	20209399	-22675	19.87068	0.636071592	Intergenic
Rgs22	chr7	74894274	74894944	7388	36.82466	0.636360186	intron (ENSRNOT00000039378, intron 2 of 27)
Cast	chr2	1512784	1513454	-1528	42.08427	0.63664891	intron (ENSRNOT00000062055, intron 2 of 28)
Zxdc	chr4	122300856	122301526	18912	37.54691	0.636937766	intron (ENSRNOT00000038244, intron 8 of 10)
AABR070 13676.2	chr2	249576536	249577206	-46772	36.21244	0.637226752	Intergenic
Tk2	chr19	930941	931611	14073	39.70674	0.637512934	intron (ENSRNOT00000017269, intron 6 of 9)
AABR070 59140.1	chr4	4549315	4549985	47627	34.60917	0.637800712	Intergenic
RF00100	chr13	16129066	16129736	-190817	48.60631	0.638087152	Intergenic
Rttn	chr18	86075550	86076220	4223	15.60904	0.63837225	intron (ENSRNOT00000064901, intron 5 of 11)
AABR070 42652.1	chr19	1350245	1350915	95138	38.84945	0.638657476	Intergenic
Spats2l	chr9	64777571	64778241	32855	32.45485	0.638941357	intron (ENSRNOT00000021527, intron 3 of 11)
RF00015	chr14	87004010	87004680	-39339	37.68243	0.639226837	Intergenic
Cox5a	chr8	62304003	62304673	5980	35.87633	0.639510972	intron (ENSRNOT00000025525, intron 1 of 4)
Casp3	chr16	48830261	48830931	32608	36.01052	0.639795233	Intergenic
Foxc1	chr17	33706468	33707138	244681	33.56347	0.640078147	intron (ENSRNOT00000023691, intron 7 of 10)
AABR070 35475.1	chr12	16536368	16537038	-122925	26.73417	0.640361186	intron (ENSRNOT00000001709, intron 10 of 17)
Epb41l3	chr9	117598384	117599054	15099	35.73455	0.640642874	intron (ENSRNOT00000088647, intron 2 of 20)
Srpk1	chr20	5875913	5876583	-10394	38.63423	0.640924687	Intergenic
AABR070 35475.1	chr12	16535840	16536510	-123453	19.92187	0.641206624	intron (ENSRNOT00000001709, intron 10 of 17)
AABR070 52263.1	chr3	43535648	43536318	-158115	36.13924	0.641487207	Intergenic
Memo1	chr6	22371871	22372541	9722	15.8475	0.641767914	intron (ENSRNOT00000008687, intron 2 of 7)
Memo1	chr6	22371640	22372310	9491	30.6256	0.642047265	intron (ENSRNOT00000008687, intron 2 of 7)
Ephb3	chr11	83579245	83579915	-32906	39.91358	0.642325258	Intergenic
AABR070 68066.2	chr9	80584769	80585439	84214	32.11818	0.642604851	Intergenic
AABR070 26938.1	chr17	5961978	5962648	85711	36.86683	0.642883086	intron (ENSRNOT00000042145, intron 16 of 17)
Tmem126 b	chr1	156180887	156181557	-80809	24.13254	0.643159961	Intergenic
ltn2c	chr9	92901715	92902385	-14419	39.22961	0.643438436	Intergenic

LOC100911649	chr16	12746196	12746866	-4521	35.93679	0.643715549	Intergenic
Samd13	chr2	252507361	252508031	-1725	31.01525	0.643992782	Intergenic
Snx3	chr20	47262248	47262918	8919	38.04736	0.644268651	intron (ENSRNOT00000074532, intron 5 of 5)
Fam168b	chr9	41337688	41338358	-525	31.36352	0.644544638	promoter-TSS (ENSRNOT00000039480)
AABR07057877.1	chr7	91698882	91699552	57648	36.68224	0.644820743	Intergenic
AABR07051626.2	chr3	18303623	18304293	-11362	17.19037	0.645095482	Intergenic
AABR07051626.2	chr3	18303418	18304088	-11567	36.72644	0.645368851	Intergenic
Gpr150	chr2	2802038	2802708	12317	31.59693	0.645643822	Intergenic
RF00026	chr8	62485831	62486501	-1092	34.07371	0.645917424	intron (ENSRNOT00000026492, intron 1 of 6)
Mnt	chr10	61684289	61684959	-617	41.09961	0.646189653	promoter-TSS (ENSRNOT00000092606)
Mnt	chr10	61684490	61685160	-416	16.57051	0.646463486	promoter-TSS (ENSRNOT00000003933)
Apold1	chr4	168732761	168733431	-19037	37.6397	0.646734457	Intergenic
Barx2	chr8	32923904	32924574	93615	32.27188	0.647007031	Intergenic
AABR07026339.1	chr16	72775690	72776360	79078	33.63011	0.647278229	intron (ENSRNOT00000048602, intron 9 of 9)
RF00026	chr8	87062603	87063273	83278	36.889	0.647549541	intron (ENSRNOT00000077071, intron 51 of 65)
Srrm3	chr12	23908666	23909336	16740	19.70179	0.647819475	intron (ENSRNOT00000001957, intron 1 of 14)
RF00091	chr10	110990549	110991219	28205	35.52946	0.648089522	Intergenic
Gmcl1	chr4	118511159	118511829	22772	42.94741	0.648359681	intron (ENSRNOT00000024414, intron 9 of 13)
Uspl1	chr12	6951297	6951967	5282	41.08753	0.648628459	intron (ENSRNOT00000072129, intron 3 of 8)
Rln1	chr1	247487015	247487685	-1148	35.7548	0.648897349	Intergenic
AABR07057877.1	chr7	91699083	91699753	57447	27.84157	0.649164856	Intergenic
Pcnt	chr20	12985181	12985851	40730	38.23325	0.649432472	intron (ENSRNOT00000048218, intron 13 of 41)
Kcnp2	chr1	265650254	265650924	-77180	19.32571	0.649700199	intron (ENSRNOT00000054703, intron 22 of 25)
LOC306079	chr15	62676467	62677137	155849	37.33569	0.649968037	Intergenic
AABR07032171.1	chr18	50697554	50698224	-75198	36.46217	0.650234487	Intergenic
Tmtc1	chr4	182966090	182966760	-122134	34.09343	0.650499549	Intergenic
Sema6d	chr3	116725276	116725946	-174267	25.24579	0.650764719	Intergenic
Sema6d	chr3	116725719	116726389	-173824	19.31041	0.651029997	Intergenic
RF00026	chr10	63301800	63302470	-2702	36.20998	0.651293884	Intergenic
AABR07031590.1	chr18	21247559	21248229	83948	38.47154	0.651557878	Intergenic
Tfec	chr4	44037588	44038258	98892	34.72576	0.651821978	Intergenic
Tfec	chr4	44037796	44038466	98684	20.32478	0.652084684	Intergenic
Ppp1r1c	chr3	66753300	66753970	80389	33.26751	0.652347496	intron (ENSRNOT00000081338, intron 4 of 4)
Grin2a	chr10	6164669	6165339	234706	24.69599	0.652610414	Intergenic

Grin2a	chr10	6164469	6165139	234506	35.86715	0.652871935	Intergenic
Rdh14	chr6	36289781	36290451	179846	37.71154	0.65313356	Intergenic
RF00003	chr2	73648209	73648879	-182284	36.40747	0.653393786	Intergenic
AABR070 15729.1	chr14	72800864	72801534	-87839	21.72723	0.653654116	Intergenic
Myom2	chr16	79670367	79671037	1017	40.42835	0.653913043	intron (ENSRNOT00000015908, intron 1 of 36)
AABR070 15729.1	chr14	72800623	72801293	-88080	21.48185	0.654172073	Intergenic
AABR070 35471.1	chr12	15943183	15943853	17347	26.64445	0.654431206	intron (ENSRNOT00000001654, intron 2 of 3)
Gucy2g	chr1	276134452	276135122	93787	31.74546	0.654688934	Intergenic
Chn1	chr3	60567370	60568040	44219	39.46294	0.654948271	intron (ENSRNOT00000068745, intron 2 of 8)
Pls1	chr8	103608358	103609028	220	32.35402	0.655204694	intron (ENSRNOT00000013209, intron 1 of 14)
Mtmr3	chr14	84815255	84815925	4825	37.20399	0.655462726	intron (ENSRNOT00000057501, intron 1 of 18)
Myrf1	chr7	59869649	59870319	12093	36.04806	0.65571935	intron (ENSRNOT00000068774, intron 4 of 30)
Setdb2	chr15	39680555	39681225	24318	35.75017	0.655976075	Intergenic
RGD1561 667	chr1	55226666	55227336	7228	45.49114	0.6562329	Intergenic
LOC10254 7963	chr16	5357971	5358641	276067	37.71378	0.656488314	intron (ENSRNOT00000048043, intron 10 of 36)
AABR070 39245.1	chrX	73027329	73027999	4497	36.85978	0.65674534	Intergenic
AABR070 52263.1	chr3	43535363	43536033	-158400	28.61362	0.656999441	Intergenic
Slc28a1	chr1	142973236	142973906	22477	31.09174	0.657255153	intron (ENSRNOT00000077441, intron 8 of 16)
Cbl	chr8	48557538	48558208	6849	25.23311	0.657510965	intron (ENSRNOT00000067902, intron 1 of 15)
AABR070 70151.1	chr8	54351938	54352608	289352	32.60815	0.657765362	Intergenic
RGD1305 938	chr2	53826975	53827645	-135	38.58112	0.658019858	promoter-TSS (ENSRNOT00000078158)
Foxn3	chr6	123716612	123717282	-139252	38.57173	0.658272936	Intergenic
Cd3eap	chr1	80270974	80271644	-308	38.99628	0.658526111	promoter-TSS (ENSRNOT00000034266)
Neto1	chr18	83515839	83516509	44832	34.15187	0.658779384	intron (ENSRNOT00000019384, intron 4 of 10)
Atp5s	chr6	92034540	92035210	-22932	39.74169	0.659031237	intron (ENSRNOT00000006473, intron 6 of 9)
Tsc22d1	chr15	58552402	58553072	-1637	37.02431	0.659283186	Intergenic
Olr1326	chr8	43739241	43739911	6031	27.17487	0.659535232	Intergenic
Scp2d1	chr3	139223978	139224648	249442	34.17257	0.659785854	Intergenic
Myo16	chr16	84957616	84958286	-18628	34.28131	0.660036572	Intergenic
LOC10090 9977	chr11	54099843	54100513	-37461	39.09127	0.660287385	Intergenic
RF00026	chr9	58135026	58135696	139254	19.82878	0.660536772	Intergenic
Mir6326	chr10	62296955	62297625	-2049	34.45459	0.660786254	Intergenic
AC117065 .2	chr12	16299461	16300131	1655	15.26157	0.66103583	intron (ENSRNOT00000060444, intron 6 of 18)

AC117065.2	chr12	16299223	16299893	1893	19.21437	0.6612855	intron (ENSRNOT00000060444, intron 6 of 18)
Pcdha6	chr18	30014622	30015292	-2961	25.05722	0.661533741	intron (ENSRNOT00000084132, intron 1 of 3)
Pcdha6	chr18	30014423	30015093	-3160	35.81061	0.661782075	intron (ENSRNOT00000084132, intron 1 of 3)
AABR07045086.1	chr20	33671215	33671885	-73140	36.08709	0.662028979	Intergenic
RF00015	chr14	86437851	86438521	12994	37.28807	0.662275974	exon (ENSRNOT00000083394, exon 4 of 23)
Irak4	chr7	135805681	135806351	2318	38.29176	0.662523061	intron (ENSRNOT00000007932, intron 1 of 11)
AABR07063755.1	chr6	46320229	46320899	301789	36.09511	0.662770241	Intergenic
Fars2	chr17	29354625	29355295	5862	33.41298	0.663015986	intron (ENSRNOT00000080031, intron 1 of 5)
Fars2	chr17	29354859	29355529	5628	23.87694	0.663261823	intron (ENSRNOT00000080031, intron 1 of 5)
AABR07030919.1	chr10	109418543	109419213	-1308	37.29374	0.663506222	Intergenic
Zfp84	chr1	87709702	87710372	13032	33.14106	0.663750712	exon (ENSRNOT00000028158, exon 4 of 4)
Ccdc14	chr11	69277435	69278105	39078	42.93843	0.663995292	Intergenic
Zfp84	chr1	87709906	87710576	13236	22.95971	0.664238432	exon (ENSRNOT00000028158, exon 4 of 4)
Nup205	chr4	62691263	62691933	-12181	38.74479	0.664481662	Intergenic
Rprd1b	chr3	154501212	154501882	-5488	19.30549	0.664724981	Intergenic
Rprd1b	chr3	154501697	154502367	-5003	18.62042	0.664966857	Intergenic
AABR07061158.1	chr4	107552899	107553569	-109381	34.80436	0.665208822	Intergenic
Adra1a	chr15	43348847	43349517	50388	27.9537	0.665450874	intron (ENSRNOT00000012736, intron 1 of 1)
Drd2	chr8	53666517	53667187	-11925	21.3087	0.665693015	Intergenic
Gpr45	chr9	49856714	49857384	19181	17.59816	0.66593371	exon (ENSRNOT00000079239, exon 11 of 12)
Pole	chr12	52447546	52448216	4159	35.88705	0.666174493	intron (ENSRNOT00000067453, intron 3 of 48)
RGD1566337	chr2	194751540	194752210	124087	44.38886	0.666413828	Intergenic
RGD1566337	chr2	194751739	194752409	123888	20.66922	0.666654784	Intergenic
Tfec	chr4	44163360	44164030	-26880	35.44757	0.666894292	Intergenic
Ryk	chr8	111358978	111359648	32880	18.91204	0.667132349	intron (ENSRNOT00000067203, intron 2 of 14)
Egflam	chr2	56655983	56656653	23637	28.90483	0.667372028	intron (ENSRNOT00000016722, intron 1 of 21)
Ryk	chr8	111359509	111360179	33411	20.10641	0.667610256	intron (ENSRNOT00000067203, intron 3 of 14)
RF00554	chr18	49546284	49546954	-22057	39.80924	0.667848569	Intergenic
Olr1090	chr7	15702435	15703105	4123	24.80639	0.668085429	intron (ENSRNOT00000042742, intron 1 of 1)
Otor	chr3	137239011	137239681	85260	33.93693	0.668323912	Intergenic

Ythdc2	chr1	181198334	181199004	941901	22.35831	0.66856094	Intergenic
AABR070 01662.1	chr1	54956246	54956916	-73019	37.77388	0.668798053	Intergenic
Smpdl3a	chr20	40829977	40830647	51385	38.88539	0.669033709	Intergenic
Stard13	chr12	1229030	1229700	-33774	34.0752	0.669269448	Intergenic
RF00026	chr18	37458562	37459232	-25524	22.05437	0.66950527	Intergenic
AABR070 20983.1	chr13	50702997	50703667	11318	38.91952	0.669741175	intron (ENSRNOT00000076984, intron 2 of 2)
Cpeb2	chr14	72623233	72623903	-243238	34.20649	0.669975621	Intergenic
AABR070 13676.2	chr2	249576743	249577413	-46979	30.09927	0.670210149	Intergenic
Inpp5f	chr1	200088598	200089268	51184	31.07712	0.670444759	exon (ENSRNOT00000027630, exon 8 of 20)
Inpp5f	chr1	200088342	200089012	50928	29.71848	0.670677906	intron (ENSRNOT00000027630, intron 7 of 19)
Pinx1	chr15	47181598	47182268	-29650	35.50565	0.670911135	Intergenic
RF00413	chr19	12646125	12646795	-28042	17.71707	0.671144445	intron (ENSRNOT00000090886, intron 6 of 14)
RF00413	chr19	12645912	12646582	-28255	31.9863	0.67137629	intron (ENSRNOT00000090886, intron 6 of 14)
RF00100	chr14	50676760	50677430	128263	25.55572	0.671609762	Intergenic
Sik3	chr8	50355863	50356533	45793	20.03938	0.671840221	intron (ENSRNOT00000073507, intron 1 of 24)
AABR070 27368.1	chr17	26689677	26690347	-82084	16.01294	0.672072306	Intergenic
Uchl3	chr3	171141186	171141856	-6866	28.7938	0.672302924	Intergenic
Cfap20	chr19	10008991	10009661	-15621	39.04932	0.672533621	intron (ENSRNOT00000016386, intron 11 of 11)
AABR070 27368.1	chr17	26689955	26690625	-81806	16.44992	0.672764396	Intergenic
RF00560	chr4	125381490	125382160	-46273	36.16901	0.672993702	Intergenic
Sel1l2	chr3	134373612	134374282	32629	22.03234	0.673223086	intron (ENSRNOT00000033562, intron 2 of 18)
AABR070 07765.1	chr2	27569327	27569997	-1488	36.08739	0.673452547	Intergenic
RF00026	chr19	44345662	44346332	46158	29.58576	0.673682087	Intergenic
RF00026	chr19	44345351	44346021	45847	18.06606	0.673910154	Intergenic
AABR070 21527.1	chr13	76577155	76577825	-18091	18.69129	0.674138298	intron (ENSRNOT00000039210, intron 2 of 21)
Wnt16	chr4	49293128	49293798	-75833	34.49993	0.674366519	intron (ENSRNOT00000038566, intron 16 of 22)
AABR070 06436.1	chr1	233539059	233539729	130770	19.6566	0.674594817	intron (ENSRNOT00000019174, intron 2 of 6)
Phf19	chr3	13992998	13993668	-15109	16.77091	0.674821638	Intergenic
Phf19	chr3	13992792	13993462	-14903	36.61506	0.675048536	Intergenic
Ldb2	chr14	70789032	70789702	8647	24.71905	0.675275511	intron (ENSRNOT00000083871, intron 1 of 8)
Ldb2	chr14	70788832	70789502	8447	31.56323	0.675501006	intron (ENSRNOT00000083871, intron 1 of 8)
Ccl20	chr9	88878740	88879410	-39358	36.18603	0.675728132	Intergenic

RF00001	chr9	18668481	18669151	-67235	18.33792	0.675953778	intron (ENSRNOT00000061014, intron 5 of 8)
Cyb5r3	chr7	124045776	124046446	-4517	35.32303	0.676177943	Intergenic
Rgs10	chr1	199831892	199832562	-8841	34.13374	0.67640374	Intergenic
AABR070 44167.1	chr19	60559169	60559839	-383038	23.87545	0.676628054	intron (ENSRNOT00000078559, intron 22 of 24)
RF00003	chr18	43118033	43118703	473005	18.07179	0.676852442	Intergenic
RF00003	chr18	43117772	43118442	473266	35.74673	0.677075345	Intergenic
Proser1	chr2	142686464	142687134	75	38.60962	0.677299882	promoter-TSS (ENSRNOT00000014614)
Wwc2	chr16	47404934	47405604	36501	30.96388	0.677522933	intron (ENSRNOT00000017966, intron 1 of 22)
Barhl1	chr3	7464456	7465126	33764	36.00431	0.677744497	intron (ENSRNOT00000064323, intron 17 of 19)
Cobl	chr14	92547914	92548584	29687	17.45604	0.677967694	intron (ENSRNOT00000086154, intron 1 of 15)
Prkaca	chr19	25092763	25093433	-1991	37.66208	0.678189404	TTS (ENSRNOT00000006964)
AABR070 09224.1	chr2	89863561	89864231	-365501	19.87871	0.678411186	Intergenic
Slc22a25	chr1	224666230	224666900	31949	28.12516	0.67863304	intron (ENSRNOT00000024234, intron 6 of 9)
Slc22a25	chr1	224665849	224666519	32330	24.08109	0.678853404	intron (ENSRNOT00000024234, intron 6 of 9)
Dock8	chr1	243060077	243060747	1540	21.97163	0.679073839	intron (ENSRNOT00000092734, intron 1 of 2)
Dock8	chr1	243059877	243060547	1340	33.05171	0.679294346	intron (ENSRNOT00000092734, intron 1 of 2)
Gpr139	chr1	188814535	188815205	80353	35.60888	0.679514925	Intergenic
AABR070 05779.1	chr1	198910686	198911356	-890	26.75229	0.67973401	promoter-TSS (ENSRNOT00000055002)
Srrm3	chr12	23887345	23888015	38061	25.83201	0.679953166	intron (ENSRNOT00000001957, intron 3 of 14)
Srrm3	chr12	23887628	23888298	37778	25.99707	0.680172392	intron (ENSRNOT00000001957, intron 3 of 14)
Helb	chr7	64850175	64850845	36938	33.97085	0.680390122	intron (ENSRNOT00000064448, intron 22 of 23)
Dbr1	chr8	107831595	107832265	5506	21.88242	0.680609489	intron (ENSRNOT00000019769, intron 4 of 7)
RGD1563 680	chr3	107178144	107178814	35717	20.42524	0.68082736	intron (ENSRNOT00000006177, intron 1 of 10)
Dbr1	chr8	107831925	107832595	5836	27.95321	0.681043732	intron (ENSRNOT00000019769, intron 4 of 7)
RF00560	chr4	56503061	56503731	-8605	22.80873	0.681261741	Intergenic
RF00560	chr4	56502859	56503529	-8807	36.48127	0.681478251	Intergenic
AABR070 20835.1	chr13	43363471	43364141	-21648	34.97522	0.68169483	Intergenic
Phlda3	chr13	52596506	52597176	7924	23.48489	0.681911477	Intergenic
AABR070 26441.1	chr16	76654642	76655312	95359	35.57884	0.682126623	Intergenic
AABR070 26441.1	chr16	76654844	76655514	95157	19.90333	0.682343408	Intergenic

Slit2	chr14	66965961	66966631	12203	36.88152	0.68255869	intron (ENSRNOT00000005477, intron 5 of 36)
Cenpv	chr10	48833289	48833959	27278	18.87062	0.682772467	Intergenic
Oxr1	chr7	80577780	80578450	-46895	20.95096	0.682987885	intron (ENSRNOT00000081948, intron 3 of 16)
Myo1d	chr10	68117594	68118264	24935	35.83055	0.683201797	intron (ENSRNOT00000004609, intron 1 of 21)
Myo1d	chr10	68117800	68118470	24729	23.64276	0.683415776	intron (ENSRNOT00000004609, intron 1 of 21)
Usp10	chr19	52589509	52590179	23237	34.4612	0.683629822	intron (ENSRNOT00000022432, intron 3 of 14)
Usp10	chr19	52589715	52590385	23443	27.56103	0.683842361	intron (ENSRNOT00000022432, intron 3 of 14)
Zscan4f	chr7	17852395	17853065	6923	33.32241	0.684056541	exon (ENSRNOT00000030164, exon 3 of 3)
Zscan4f	chr7	17852594	17853264	6724	20.54739	0.684269212	exon (ENSRNOT00000030164, exon 3 of 3)
Fat1	chr16	50538625	50539295	-37039	38.1652	0.684480374	Intergenic
RF00560	chr9	85312851	85313521	-7644	38.36021	0.684693177	Intergenic
Rapgef5	chr6	145433809	145434479	-112451	38.44231	0.684904469	Intergenic
Pop4	chr1	94680062	94680732	-10936	36.51179	0.685115826	Intergenic
RF00425	chr14	105840577	105841247	-65769	39.00918	0.685327249	Intergenic
AABR070 08259.1	chr2	49858483	49859153	1263	36.57383	0.685537158	intron (ENSRNOT00000082762, intron 1 of 1)
Evi5l	chr12	2597869	2598539	-5366	15.66489	0.685748711	intron (ENSRNOT00000001367, intron 4 of 11)
Evi5l	chr12	2597590	2598260	-5087	38.73344	0.68595717	intron (ENSRNOT00000001367, intron 4 of 11)
Wasf3	chr12	10338248	10338918	-3084	15.34726	0.686167272	intron (ENSRNOT00000092340, intron 2 of 4)
S100a10	chr2	193970739	193971409	78485	18.5284	0.686377439	Intergenic
Wasf3	chr12	10337923	10338593	-2759	16.51901	0.686586089	intron (ENSRNOT00000092340, intron 2 of 4)
Best1	chr1	226058288	226058958	-8694	34.98631	0.686793221	Intergenic
AABR070 21612.2	chr13	81462530	81463200	-19728	25.23679	0.687001998	Intergenic
AABR070 21612.2	chr13	81462902	81463572	-19356	29.10849	0.687209255	Intergenic
Rttn	chr18	86123591	86124261	7871	21.64826	0.687416576	intron (ENSRNOT00000076159, intron 5 of 35)
Rttn	chr18	86123388	86124058	7668	33.59155	0.687623958	intron (ENSRNOT00000076159, intron 5 of 35)
Phf2	chr4	10890920	10891590	67974	40.0546	0.687831403	intron (ENSRNOT00000066739, intron 7 of 17)
Helz	chr10	95744704	95745374	-25115	45.21138	0.688037327	Intergenic
Znhit6	chr2	251415909	251416579	-37400	25.59343	0.688243312	intron (ENSRNOT00000019210, intron 59 of 63)
Kitlg	chr7	42263538	42264208	-5911	19.67387	0.688449359	Intergenic
Znhit6	chr2	251416345	251417015	-36964	21.50679	0.688653882	intron (ENSRNOT00000019210, intron 59 of 63)

AABR070 69791.3	chr8	40056795	40057465	-19317	39.51738	0.688860052	Intergenic
RF00156	chr15	101511741	101512411	6882	21.77168	0.689064697	Intergenic
RF00560	chr16	46971887	46972557	-85136	18.73023	0.689269402	Intergenic
RF00004	chr1	232671913	232672583	21245	18.67052	0.689472581	Intergenic
RF00560	chr16	46972250	46972920	-84773	18.98767	0.689677408	Intergenic
RF00004	chr1	232672247	232672917	21579	15.72532	0.689880707	Intergenic
Fat4	chr2	125745860	125746530	-5935	32.22506	0.690084066	Intergenic
Sh3bgrl2	chr8	91040735	91041405	-29003	35.6685	0.690287486	Intergenic
AABR070 30040.1	chr10	63702467	63703137	6194	37.86049	0.690489375	intron (ENSRNOT00000005100, intron 5 of 13)
Polg	chr1	141196709	141197379	-9013	30.97223	0.690692913	Intergenic
Adra1b	chr10	29409255	29409925	41054	34.68766	0.690894921	intron (ENSRNOT00000087937, intron 17 of 17)
AABR070 38886.1	chrX	63462250	63462920	-21541	52.52775	0.691096988	intron (ENSRNOT00000048127, intron 7 of 9)
Dner	chr9	92129400	92130070	-64333	33.79041	0.691299114	intron (ENSRNOT00000093357, intron 4 of 12)
St8sia4	chr9	103146541	103147211	60314	23.88658	0.691499706	intron (ENSRNOT00000026010, intron 4 of 4)
RF00334	chr3	46853457	46854127	-29148	34.90966	0.691700357	intron (ENSRNOT00000087439, intron 3 of 15)
AABR070 07839.1	chr2	30110180	30110850	16094	22.93747	0.691901066	Intergenic
AABR070 32593.1	chr18	72986821	72987491	-65555	34.86975	0.692101834	Intergenic
Scg5	chr3	105250172	105250842	28955	34.06778	0.69230266	exon (ENSRNOT00000010679, exon 3 of 6)
Elovl3	chr1	265876016	265876686	-7004	44.21867	0.692503543	Intergenic
Myh11	chr10	796131	796801	32036	36.51708	0.692702891	intron (ENSRNOT00000084608, intron 4 of 40)
AC115181 .1	chr10	14153890	14154560	17342	22.34758	0.692902295	Intergenic
AC115181 .1	chr10	14153442	14154112	16894	28.68874	0.693101757	Intergenic
Gtf2a1	chr6	115351284	115351954	1062	21.61481	0.69329968	intron (ENSRNOT00000005873, intron 1 of 8)
Samd4b	chr1	85339130	85339800	1660	35.49816	0.69349766	intron (ENSRNOT00000093716, intron 2 of 12)
AABR070 10944.1	chr2	155530203	155530873	-25302	36.70935	0.693697293	Intergenic
Mab2111	chr2	145148823	145149493	-25718	25.8347	0.693895386	Intergenic
Nceh1	chr2	112901116	112901786	-12924	38.52533	0.694091938	intron (ENSRNOT00000017805, intron 1 of 4)
Polq	chr11	66695165	66695835	-147	36.78938	0.694290144	promoter-TSS (ENSRNOT00000063995)
Rps15a	chr1	187573042	187573712	192367	24.31219	0.694486807	Intergenic
Akap13	chr1	136962201	136962871	-51736	33.24553	0.694685126	Intergenic
Cnm2	chr1	266608022	266608692	77880	31.58082	0.694881901	intron (ENSRNOT00000054699, intron 1 of 7)
Thbs1	chr3	109863033	109863703	1248	37.43998	0.695078732	intron (ENSRNOT00000070912, intron 25 of 48)
Siah2	chr2	148918341	148919011	-26776	16.7511	0.695274017	Intergenic

AC119473.1	chr7	117811323	117811993	13721	25.65135	0.695470959	intron (ENSRNOT00000052227, intron 3 of 11)
Selenow	chr1	77202958	77203628	332388	19.85671	0.695666355	Intergenic
AABR07056438.1	chr7	25617780	25618450	32029	33.61341	0.695861806	intron (ENSRNOT00000082493, intron 1 of 1)
Selenow	chr1	77202758	77203428	332588	39.81805	0.696057312	Intergenic
Pdlim3	chr16	49558194	49558864	15785	34.55022	0.696251269	intron (ENSRNOT00000017568, intron 3 of 6)
Bcl2l11	chr3	120893192	120893862	164839	24.21885	0.696446885	Intergenic
Car12	chr8	72437525	72438195	32112	35.03265	0.696640951	intron (ENSRNOT00000023952, intron 2 of 10)
RF00045	chr4	54635078	54635748	300149	34.3948	0.696835071	intron (ENSRNOT00000056996, intron 6 of 8)
Piwil2	chr15	52124540	52125210	-8874	37.84658	0.69702764	Intergenic
Bcl2l11	chr3	120892965	120893635	164612	25.43648	0.697221868	Intergenic
Gfpt1	chr4	118938957	118939627	87173	24.87511	0.697414544	Intergenic
Tnfsf4	chr13	79282198	79282868	12560	36.4094	0.697607273	intron (ENSRNOT00000003969, intron 1 of 2)
Gfpt1	chr4	118938718	118939388	86934	32.40447	0.697800056	Intergenic
Ulk2	chr10	48100026	48100696	29016	25.83746	0.697991285	intron (ENSRNOT00000003792, intron 11 of 27)
Fancl	chr14	110682343	110683013	6588	21.54325	0.698182566	intron (ENSRNOT00000029513, intron 1 of 13)
Ulk2	chr10	48099795	48100465	29247	24.65851	0.698373899	intron (ENSRNOT00000003792, intron 11 of 27)
Vps13c	chr8	73888063	73888733	205511	26.55237	0.698565285	Intergenic
Vps13c	chr8	73888310	73888980	205758	20.49613	0.698756724	Intergenic
Gabrg2	chr10	26934956	26935626	243963	32.90754	0.698946605	Intergenic
Foxn3	chr6	123513387	123514057	63973	33.63558	0.699138148	intron (ENSRNOT00000006604, intron 1 of 6)
Xpo4	chr15	37927693	37928363	-1313	41.39892	0.699328134	Intergenic
Mrpl48	chr1	165606013	165606683	27	37.55053	0.69951817	promoter-TSS (ENSRNOT00000024290)
AABR07013750.1	chr2	254542843	254543513	-6504	22.83937	0.699706648	Intergenic
AABR07013750.1	chr2	254542355	254543025	-6992	20.15118	0.699896787	Intergenic

Supporting Table 2. List of genes which expression changed significantly upon *MNT* silencing in URMT cells. Two independent RNAseq experiments were carried out to compare the transcriptomes of URMT cells (in the presence of Zn²⁺) transfected with the empty pLKO or the shMNT-1. Relative RNA amounts were calculated as FPKM fold change (FC). Data are mean values of the two independent transfections where log₂FC was >0.7 or < -0.7 (i.e., ≥1.6 fold and ≤0.5 fold), and a p-value <0.1.

locus	gene_id	Gene	URMT sh-MNT vs pLKO		
			FC	Log ₂ FC	p-value
chr10:69058108-69059959	NM_001007612	Ccl7	13,36	3,74	0,01
chr3:127438621-127474675	NM_001108959	Tgm3	6,85	2,78	0,01
chr11:39232473-39336438	NM_133397	Erg	5,18	2,37	0,01
chr9:95188005-95207531	NM_053577	Spp2	5,05	2,34	0,04
chr20:16352598-16378743	NM_053845	Upb1	5,02	2,33	0,02
chr3:17021672-17058548	NM_001010968	Eng	4,64	2,21	0,06
chr4:57616942-57640152	NM_001013083	Cpa2	3,92	1,97	0,02
chr5:161068640-161074026	NM_001106696	Pla2g2e	3,74	1,90	0,04
chr5:172507288-172577540	NM_001195560	Camta1	3,72	1,89	0,02
chr10:57006273-57009138	NM_001109654	Gp1ba	3,62	1,86	0,01
chr9:14542072-14550007	NM_001108198	Guca1b	3,60	1,85	0,00
chr15:24735138-24738725	NM_012827	Bmp4	3,55	1,83	0,01
chr1:89288945-89292050	NM_001013065	Ggn	3,03	1,60	0,00
chr1:285021522-285065105	NM_001106202	Tdrd1	2,96	1,56	0,01
chr14:17144965-17150220	NM_145672	Cxcl9	2,90	1,53	0,09
chr4:184234158-184271987	NM_001106609	Txnrd3	2,87	1,52	0,09
chr14:36954230-36976506	NM_001008763	Lrrc66	2,70	1,43	0,01
chr10:89590581-89609632	NM_001108837	Meox1	2,70	1,43	0,01
chr17:44449933-44506535	NM_001024273	Cmah	2,67	1,42	0,09
chr16:73297718-73302932	NM_001109455	Nkx6-3	2,63	1,40	0,05
chr5:139790974-139796149	NM_022187	Plk3	2,62	1,39	0,09
chr2:83723118-83735166	NM_012816	Amacr	2,62	1,39	0,00
chr15:16597090-16611887	NM_001271294	Thoc7	2,60	1,38	0,03
chr3:155802168-155827127	NM_001109209	Bpifb4	2,58	1,37	0,01
chr13:40555698-40561388	NM_080771	Inhbb	2,57	1,36	0,04
chr12:23760924-23767104	NM_001271236	LOC100362783	2,51	1,33	0,05
chr18:30514377-30662065	NM_001037154	Pcdhga3	2,47	1,30	0,06
chr10:55965503-55968684	NM_012650	Shbg	2,45	1,30	0,03
chr4:246879801-246880735	NM_001109612	Rps4y2	2,45	1,29	0,07
chr14:80414798-80429940	NM_001134843	Myo1g	2,41	1,27	0,03
chr1:223521097-223523972	NM_182735	Cdkn1c	2,40	1,26	0,02
chr3:50007272-50327062	NM_001107732	Ccdc148	2,31	1,21	0,07
chr20:8355768-8393371	NM_001191841	Pnpla1	2,27	1,18	0,02
chr2:209427356-209430124	NM_053681	S100a3	2,25	1,17	0,08
chr6:131633745-131760720	NM_023096	Kcnk10	2,25	1,17	0,02
chr8:48338878-48342640	NM_145717	Fxyd2	2,24	1,16	0,04

chr2:278043762-278563294	NM_019123	St6galnac3	2,22	1,15	0,08
chr5:155079202-155083511	NM_001271259	LOC100359977	2,21	1,14	0,07
chr7:2689127-2691242	NM_130410	Il23a	2,20	1,14	0,02
chr12:26978747-27022485	NM_012722	Eln	2,19	1,13	0,06
chr2:217897713-217898109	NM_001123469	Hist2h4	2,19	1,13	0,06
chr17:15743124-15862911	NM_001105743	Shc3	2,13	1,09	0,00
chr10:13910496-13921040	NM_001191589	Rpl3l	2,10	1,07	0,09
chr8:46295149-46319894	NM_001106815	Trim29	2,07	1,05	0,03
chr20:5955098-5960408	NM_001008848	RT1-Ha	2,06	1,04	0,06
chr12:43421505-43444143	NM_001017488	Slc24a6	2,06	1,04	0,03
chr9:79403625-79427523	NM_001109574	Tmem169	2,03	1,02	0,03
chr20:42996502-43115526	NM_024368	Frk	2,02	1,02	0,05
chr18:30598590-30662065	NM_001037153	Pcdhga11	2,01	1,01	0,00
chr4:224126654-224141154	NM_001002804	C1rl	1,99	0,99	0,07
chr1:220887395-220890392	NM_001014163	Cend1	1,98	0,99	0,04
chr11:60714585-60776082	NM_001191826	Gramd1c	1,97	0,98	0,03
chr6:111585027-111633992	NM_001108036	Plekhh1	1,97	0,98	0,07
chr3:179978576-179980791	NM_001109211	Bhlhe23	1,97	0,97	0,01
chr10:55297128-55301123	NM_001109033	Slc25a35	1,95	0,96	0,05
chr1:177249671-177253684	NM_053496	Cnga4	1,94	0,95	0,04
chr9:61824560-62158071	NM_053456	Plcl1	1,93	0,95	0,01
chr8:113173029-113322634	NM_001108182	Nek11	1,91	0,93	0,06
chr2:218259870-218279187	NM_001107699	Itga10	1,89	0,92	0,07
chr20:28943837-28958143	NM_138530	Pbld1	1,89	0,92	0,09
chrX:45646095-45654127	NM_012661	Sts	1,88	0,91	0,00
chr1:81329940-81340229	NM_012714	Gipr	1,86	0,90	0,10
chr2:72846057-72859924	NM_001134548	RGD1305938	1,86	0,90	0,07
chr1:211242706-211272037	NM_173310	Chst15	1,85	0,89	0,03
chr2:223666826-223689474	NM_001106456	Mab21l3	1,84	0,88	0,01
chr17:80546950-80552017	NM_001126079	Acbd7	1,84	0,88	0,05
chr15:111996345-112224036	NM_001100685	Clybl	1,83	0,87	0,08
chr16:19529515-19614171	NM_012984	Myo9b	1,82	0,86	0,01
chr14:84825688-84834332	NM_001107233	RGD1308775	1,81	0,85	0,06
chr5:82503505-82531128	NM_001024346	LOC500475	1,81	0,85	0,06
chr11:90249248-90249959	NM_001134788	Vpreb2	1,80	0,85	0,03
chr1:102422047-102424623	NM_021758	Lin7b	1,80	0,85	0,06
chr18:32272759-32287666	NM_001106150	Spry4	1,79	0,84	0,09
chr13:53528327-53554460	NM_001109328	Rab7b	1,78	0,83	0,00
chr1:102141918-102151178	NM_001008694	Rcn3	1,77	0,83	0,10
chr1:181336763-181337409	NM_001271234	Ascl3	1,76	0,82	0,03
chr1:211596784-211599221	NM_001170476	Nkx1-2	1,75	0,81	0,06
chr7:123636788-123640858	NM_012730	Cyp2d2	1,74	0,80	0,05
chr7:71218205-71221052	NM_053302	Gpr182	1,74	0,80	0,09
chr6:60701427-60713132	NM_001037354	Klf11	1,74	0,80	0,09
chr20:7091295-7093067	NM_001004069	Sapcd1	1,73	0,79	0,07
chr1:228361452-228365776	NM_001013071	Tm7sf2	1,72	0,79	0,10
chr10:56237418-56251565	NM_001105796	Acap1	1,72	0,78	0,05
chr3:170425897-170430384	NM_053805	Snai1	1,72	0,78	0,02

chr4:163851682-163904153	NM_001106595	Smyd1	1,71	0,77	0,03
chr4:243622213-243658236	NM_001106627	Casc1	1,70	0,76	0,04
chr13:100036033-100037602	NM_022678	Zfp238	1,69	0,76	0,05
chr20:5448825-5462082	NM_212498	Atat1	1,69	0,75	0,01
chr5:160425714-160437827	NM_001106694	Pink1	1,67	0,74	0,07
chr16:19917584-19964213	NM_022861	Unc13a	1,66	0,73	0,01
chr1:81996115-82010351	NM_001109422	Bcl3	1,66	0,73	0,02
chr6:89586785-89633108	NM_001105732	Sec23a	1,66	0,73	0,04
chr16:73730260-73754851	NM_013151	Plat	1,66	0,73	0,04
chrX:115098750-115107826	NM_001013950	Lmbr1l	1,66	0,73	0,08
chr16:75129189-75131353	NM_001079898	RatNP-3b	1,66	0,73	0,08
chr4:145013634-145038535	NM_001024329	LOC500124	1,66	0,73	0,01
chr7:98562310-98582049	NM_001025024	Wdyhv1	1,65	0,73	0,07
chr16:19194745-19207342	NM_001271328	Hsh2d	1,65	0,72	0,07
chr5:43958429-43999913	NM_001106640	Gpr63	1,64	0,72	0,07
chr10:83916622-83916702	NR_032269	Mir196c	1,64	0,71	0,09
chr5:63003429-63010436	NM_001013931	Fam214b	1,64	0,71	0,06
chr2:222826871-222863501	NM_001271217	Cd101	1,64	0,71	0,05
chr11:35498916-35672959	NM_001136096	Itsn1	1,63	0,70	0,02
chr6:131991385-132118723	NM_001003402	Eml5	1,63	0,70	0,03
chr17:15662364-15667466	NM_001126083	Cks2	0,61	-0,70	0,04
chr1:86274836-86312788	NM_001164656	Fcgbpl1	0,61	-0,71	0,08
chr1:229468107-229485469	NM_001108518	Naa40	0,61	-0,71	0,01
chr1:173726993-173751295	NM_001013236	Rrm1	0,61	-0,71	0,02
chr2:209191619-209196288	NM_001106439	Slc27a3	0,61	-0,71	0,03
chr6:146226686-146243773	NM_033230	Akt1	0,61	-0,72	0,01
chr13:114264895-114292134	NM_001109083	Nsl1	0,61	-0,72	0,01
chr2:207154780-207174337	NM_001191568	Pmf1	0,61	-0,72	0,02
chr17:91504400-91539143	NM_001107369	Mastl	0,61	-0,72	0,07
chr9:22211292-22226466	NM_001014215	Cenpq	0,61	-0,72	0,02
chr11:89431160-89456065	NM_001105866	Cdc45	0,61	-0,72	0,05
chr2:163630966-163635150	NM_001044263	Rfxap	0,60	-0,73	0,06
chr1:228384096-228394986	NM_001115042	Cdca5	0,60	-0,73	0,07
chr7:141393003-141400457	NM_199370	Krt8	0,60	-0,73	0,07
chr8:22217095-22229971	NM_053743	Cdc37	0,60	-0,73	0,07
chr2:262787595-262899803	NM_001107728	Rap1gds1	0,60	-0,73	0,01
chr1:268610732-268618280	NM_053290	Pgam1	0,60	-0,73	0,05
chr10:106451967-106455900	NM_053553	Syngn2	0,60	-0,74	0,07
chr1:264226026-264241499	NM_001025646	Cep55	0,60	-0,74	0,00
chr10:15275266-15279122	NM_001109478	Nme4	0,60	-0,74	0,01
chr5:174800869-174803561	NM_001163723	Smim1	0,60	-0,74	0,10
chr11:38145427-38153525	NM_001105892	Ripply3	0,60	-0,74	0,06
chr1:43791186-43797556	NM_001106206	Fbxo5	0,60	-0,75	0,02
chr1:101539029-101542739	NM_001106256	Josd2	0,60	-0,75	0,04
chr2:197725439-197728572	NM_001107685	RGD1560010	0,60	-0,75	0,06
chr9:54267752-54472391	NM_053986	Myo1b	0,60	-0,75	0,04
chr8:39184019-39204446	NM_080400	Chek1	0,60	-0,75	0,04
chr3:158598783-158611011	NM_001025768	Dsn1	0,60	-0,75	0,01

chr4:232130923-232143990	NM_001079711	Rad51ap1	0,59	-0,75	0,00
chr20:5831136-5833706	NM_213561	Tcf19	0,59	-0,75	0,05
chr1:205441132-205467610	NM_001009645	Kif22	0,59	-0,75	0,03
chr1:79112278-79130529	NM_001024897	Ehd2	0,59	-0,75	0,05
chr3:1456035-1461452	NM_022194	Il1rn	0,59	-0,75	0,05
chr10:69956874-69970281	NM_001013970	Sifn13	0,59	-0,75	0,00
chr5:141050191-141054395	NM_171993	Cdc20	0,59	-0,75	0,00
chr17:44170133-44178377	NM_001106112	Gmnn	0,59	-0,76	0,03
chr9:93055877-93059829	NM_001012134	B3gnt7	0,59	-0,76	0,03
chr3:156435529-156446390	NM_001100778	E2f1	0,59	-0,76	0,03
chr15:92899713-92951232	NM_001108390	Ndfip2	0,59	-0,76	0,04
chr8:22631827-22676509	NM_001034088	Carm1	0,59	-0,76	0,01
chrX:115263555-115271364	NM_001271243	Troap	0,59	-0,76	0,06
chr10:106494774-106503096	NM_022274	Birc5	0,59	-0,76	0,00
chr1:195361585-195387930	NM_001108501	Ccp110	0,59	-0,76	0,02
chr3:120780502-120790938	NM_001107767	Duoxa1	0,59	-0,77	0,01
chr3:117468880-117493555	NM_001109204	Rad51	0,59	-0,77	0,03
chr2:59075285-59147310	NM_001107651	Depdc1b	0,59	-0,77	0,00
chr1:143039959-143061006	NM_001107529	Prc1	0,59	-0,77	0,05
chr1:260438626-260494019	NM_001107609	Kif20b	0,59	-0,77	0,08
chr9:93273332-93277372	NM_021740	Ptma	0,58	-0,78	0,02
chr19:48680054-48686495	NM_001024257	Cenpt	0,58	-0,78	0,01
chr13:56842244-56852747	NM_001108344	Ube2t	0,58	-0,78	0,00
chr10:86614892-86628265	NM_001108298	Cdc6	0,58	-0,78	0,01
chr10:105718074-105765280	NM_001108309	Sec14l1	0,58	-0,78	0,06
chr14:83025668-83039430	NM_001004424	Tacc3	0,58	-0,79	0,01
chr9:25770287-25788432	NM_001191805	Mcm3	0,58	-0,79	0,04
chr3:144832021-144840679	NM_001009655	Mgme1	0,58	-0,79	0,00
chr1:33392426-33437368	NM_001011930	Trip13	0,58	-0,79	0,00
chr2:219959693-219989012	NM_031620	Phgdh	0,58	-0,79	0,10
chr16:24663044-24671859	NM_001113357	Npy1r	0,58	-0,79	0,07
chr7:142899028-142924626	NM_022710	Pde1b	0,58	-0,79	0,04
chr5:143482582-143542254	NM_012866	Nfyc	0,58	-0,79	0,00
chr4:224365695-224369284	NM_001007648	Cdca3	0,58	-0,79	0,05
chr14:104777089-104784596	NM_001134730	Lgalsl	0,57	-0,80	0,04
chr5:151138848-151147606	NM_001134629	RGD1561149	0,57	-0,80	0,08
chr15:55958799-55962007	NM_001025279	Reep4	0,57	-0,80	0,06
chr18:69317014-69327048	NM_001106134	Ska1	0,57	-0,80	0,04
chr10:83585052-83628434	NM_175594	Igf2bp1	0,57	-0,80	0,04
chr5:64307463-64367854	NM_001108662	Melk	0,57	-0,81	0,02
chr3:154730956-154773179	NM_001107790	Tpx2	0,57	-0,81	0,06
chr9:88237935-88266173	NM_001039015	Mff	0,57	-0,81	0,00
chr15:47186190-47231339	NM_001107273	Cdca2	0,57	-0,81	0,00
chr10:14903482-14911519	NM_001105773	Chtf18	0,57	-0,81	0,02
chr7:60853892-60860953	NM_134346	Rap1b	0,57	-0,81	0,00
chr13:32603845-32612855	NM_021696	Serpib2	0,57	-0,81	0,01
chr18:80511682-80534735	NM_001007687	Cndp1	0,57	-0,82	0,04
chr8:90886761-90924325	NM_001108172	Ttk	0,57	-0,82	0,05

chr7:117676479-117691180	NM_001130572	Tonsl	0,57	-0,82	0,03
chr20:22694920-22709859	NM_019296	Cdk1	0,57	-0,82	0,01
chr18:27137684-27146171	NM_001108426	Kif20a	0,57	-0,82	0,01
chr4:214232833-214345405	NM_001107882	March8	0,56	-0,82	0,01
chr3:62049999-62063264	NM_001009654	Spc25	0,56	-0,82	0,00
chr17:23615670-23657985	NM_001001511	Gcnt2	0,56	-0,83	0,02
chr20:14497057-14514187	NM_017299	Slc19a1	0,56	-0,83	0,05
chr1:163919400-163943710	NM_001126294	RGD1559690	0,56	-0,83	0,04
chr9:119293739-119309561	NM_001126270	Ndc80	0,56	-0,83	0,04
chr3:167422568-167424969	NM_001106542	Ube2c	0,56	-0,83	0,09
chr3:181259386-181278378	NM_133608	Slco4a1	0,56	-0,83	0,08
chr1:199178261-199188238	NM_017100	Plk1	0,56	-0,83	0,07
chr9:26322565-26358469	NM_001024361	LOC501110	0,56	-0,83	0,02
chr4:39891452-39963623	NM_001109221	LOC500034	0,56	-0,84	0,09
chr16:74383676-74410206	NM_001169139	Ckap2	0,56	-0,84	0,01
chr5:139821000-139846566	NM_001085369	Kif2c	0,56	-0,84	0,00
chr3:117157779-117177433	NM_001004264	Knstrn	0,56	-0,84	0,04
chr7:28764493-28825206	NM_001166676	Parpbp	0,56	-0,84	0,05
chr2:230646556-230651000	NM_001044302	Psrc1	0,56	-0,85	0,01
chr10:89978418-90001064	NM_001017988	LOC303566	0,56	-0,85	0,00
chr1:223099327-223114942	NM_013087	Cd81	0,55	-0,85	0,04
chr6:100953299-100977903	NM_001169108	Pole2	0,55	-0,85	0,01
chr1:227783723-227790741	NM_001005907	Efemp2	0,55	-0,86	0,04
chr17:11940005-11943732	NM_145773	Mxd3	0,55	-0,86	0,01
chr10:13410717-13435965	NM_001100474	Ccnf	0,55	-0,86	0,01
chr1:205431759-205435166	NR_077057	Prrt2	0,55	-0,86	0,02
chr8:59280448-59297536	NM_017132	Rcn2	0,55	-0,86	0,02
chr18:62314820-62324460	NM_001025675	Tubb6	0,55	-0,86	0,09
chr10:91783780-91805556	NM_024150	Arf2	0,55	-0,86	0,00
chr9:64698065-64720561	NM_001271191	Sgol2	0,55	-0,86	0,08
chr10:61406976-61422227	NM_001105807	Mnt	0,55	-0,87	0,01
chr15:41919557-41937891	NM_001108379	Ska3	0,55	-0,87	0,00
chr4:226891343-226902365	NM_031633	Foxm1	0,55	-0,87	0,01
chr3:158772764-158787955	NM_001134983	Tgif2	0,54	-0,88	0,04
chr10:90780840-90800011	NM_001039019	Kif18b	0,54	-0,88	0,04
chr7:117753870-117761035	NM_001130494	Recql4	0,54	-0,88	0,05
chr9:9731077-9750175	NM_001008882	Uhrf1	0,54	-0,89	0,03
chr6:51811951-51828131	NM_001100717	E2f6	0,54	-0,89	0,02
chr7:142719644-142746041	NM_001109470	Zfp385a	0,54	-0,89	0,02
chr5:83890951-83950462	NM_053861	Tnc	0,54	-0,90	0,05
chr19:25637491-25681915	NM_001106170	Mcm5	0,54	-0,90	0,02
chr16:40849290-40908352	NM_001170346	Neil3	0,54	-0,90	0,03
chr13:98401024-98427400	NM_001107198	Exo1	0,54	-0,90	0,03
chr19:36055966-36070506	NM_001107160	Asf1b	0,53	-0,90	0,01
chr13:55534038-55551850	NM_001108343	Etnk2	0,53	-0,91	0,06
chr2:275974236-276052941	NM_001037210	Gipc2	0,53	-0,91	0,04
chr1:22625115-22626610	NM_001009470	Ccnb2	0,53	-0,91	0,06
chr1:15072108-15083325	NM_001037789	Ccdc28a	0,53	-0,91	0,02

chr6:60756159-60762351	NM_001025740	Rrm2	0,53	-0,91	0,00
chr16:48613428-48636501	NM_001025673	Cenpu	0,53	-0,91	0,01
chr10:14120127-14139812	NM_001013182	Hn1l	0,53	-0,93	0,02
chr10:56407360-56411205	NM_012503	Asgr1	0,52	-0,93	0,00
chr1:181055796-181108418	NM_001191839	Trim66	0,52	-0,93	0,03
chr16:75349397-75367306	NM_001012228	Xkr5	0,52	-0,94	0,04
chr3:111858564-111874846	NM_001168524	Arhgap11a	0,52	-0,94	0,08
chr6:100922214-100931215	NM_001109483	Lrr1	0,52	-0,94	0,02
chr8:103009499-103046804	NM_001108178	Pls1	0,52	-0,94	0,01
chr8:131187616-131258348	NM_181635	Kif15	0,52	-0,94	0,03
chr7:122151953-122156374	NM_001008373	Srek1ip1	0,52	-0,94	0,03
chr19:48132503-48147429	NM_001195616	Lrrc29	0,52	-0,94	0,04
chrX:124002494-124006340	NM_022175	Rhox5	0,52	-0,95	0,07
chr2:191602248-192429464	NM_001100666	Schip1	0,52	-0,95	0,03
chr16:68718376-68753634	NM_001191555	Rab11fip1	0,52	-0,95	0,05
chr9:100106949-100136087	NM_001009362	Pask	0,51	-0,96	0,00
chrX:111960844-111967052	NM_001108120	Nxt2	0,51	-0,97	0,01
chr7:141693055-141719909	NM_001170602	Espl1	0,51	-0,98	0,06
chr5:132031218-132050961	NM_177931	Orc1	0,50	-0,99	0,01
chr8:48847363-48852838	NM_031549	Tagln	0,50	-0,99	0,02
chr10:81951028-82017885	NM_031601	Cacna1g	0,50	-1,00	0,08
chr10:82185899-82191905	NM_001105830	Eme1	0,50	-1,01	0,02
chr5:148352776-148387685	NM_001106687	Clspn	0,50	-1,01	0,06
chr1:129679808-129753636	NM_001025681	Ttc23	0,49	-1,02	0,02
chr3:165617193-165645609	NM_001106536	Mybl2	0,49	-1,04	0,04
chr8:66598466-66625560	NM_001108155	Kif23	0,49	-1,04	0,04
chr2:108055052-108086130	NM_001134993	Car13	0,48	-1,05	0,00
chr15:50429954-50443496	NM_001106044	Tdh	0,48	-1,05	0,07
chr16:81104695-81120110	NM_001013054	Adprhl1	0,47	-1,08	0,07
chr8:74012276-74033156	NM_001007752	Mns1	0,47	-1,08	0,01
chr3:116411044-116422101	NM_001013062	Thbs1	0,47	-1,09	0,00
chr7:107517378-107566621	NM_178097	Sla	0,45	-1,15	0,06
chr9:64973841-65072436	NM_001008522	Aox2	0,45	-1,15	0,06
chr1:178792339-178816636	NM_001013192	Olfml1	0,44	-1,17	0,03
chr1:171496701-171531029	NM_198775	P4ha3	0,44	-1,18	0,07
chr2:176099246-176179301	NM_001127530	LOC302022	0,44	-1,19	0,03
chr8:48247920-48277215	NM_001127528	Tmprss13	0,41	-1,28	0,10
chr1:221234412-221243406	NR_045203	Tmem80	0,40	-1,31	0,08
chr14:86423838-86428923	NM_001271731	Xbp1	0,40	-1,31	0,02
chr1:90620341-90629734	NM_021909	Fxyd5	0,40	-1,34	0,01
chr6:137256802-137272264	NM_182474	LOC299282	0,39	-1,35	0,01
chr10:89872922-89877057	NM_001107053	Nags	0,36	-1,47	0,04
chr17:23514575-23550277	NM_013136	Mak	0,35	-1,52	0,05
chr7:117215918-117244741	NM_001164304	Plec	0,34	-1,55	0,02
chr20:5833972-5838736	NM_001009178	Pou5f1	0,33	-1,59	0,05
chr1:88226084-88227840	NM_022582	Lgals7	0,32	-1,63	0,05
chr17:26191714-26240098	NM_001109117	Rnf182	0,31	-1,67	0,08
chr9:46849568-46858893	NM_013037	Ii1r1	0,29	-1,77	0,06

chrX:72193461-72198315	NM_001108245	Itgb1bp2	0,28	-1,85	0,06
chr8:109782847-110218328	NM_001104528	Ephb1	0,27	-1,90	0,05
chr9:92411672-92449073	NM_001014220	Sp100	0,24	-2,07	0,08
chr13:94228758-94233191	NM_001131001	Fcer1g	0,23	-2,11	0,02
chr7:126136631-126178957	NM_001009695	Wnt7b	0,18	-2,48	0,06

Supporting Table S3. List of genes which expression changed significantly upon MNT silencing in URMax34 cells. Two independent RNAseq experiments were carried out to compare the transcriptomes of URMax34 cells (in the presence of Zn²⁺) transfected with the empty pLKO or the shMNT-1 vector. Relative RNA amounts were calculated as FPKM fold change (FC). Data are mean values of the two independent transfections where log₂FC was > 0.7 or < -0.7 (i.e., ≥1.6 fold and ≤0.5 fold), and a p-value <0.1.

locus	gene_id	Gene	URMax34 sh-MNT vs pLKO		
			FC	Log ₂ FC	p-value
chr1:82587241-82602923	NM_017350	Plaur	214,51	7,74	0,00
chr9:95188005-95207531	NM_053577	Spp2	19,70	4,30	0,03
chr3:127438621-127474675	NM_001108959	Tgm3	8,22	3,04	0,00
chr15:91201296-91315612	NM_001108388	Scel	7,93	2,99	0,02
chr9:13635293-13645452	NM_001191581	Trem3	6,19	2,63	0,06
chr7:123619361-123623719	NM_173093	Cyp2d3	5,83	2,54	0,04
chr10:69058108-69059959	NM_001007612	Ccl7	5,75	2,52	0,06
chr1:222935461-222942715	NM_012740	Th	5,52	2,47	0,01
chr3:17021672-17058548	NM_001010968	Eng	5,41	2,44	0,04
chr8:53606987-53613608	NM_019165	Il18	5,28	2,40	0,00
chr4:16428813-17031648	NM_020098	Pclo	5,28	2,40	0,04
chr3:50007272-50327062	NM_001107732	Ccdc148	5,24	2,39	0,02
chr11:90312180-90314169	NM_001108846	Gsc2	4,56	2,19	0,06
chr3:59395440-59469573	NM_031686	Scn7a	4,07	2,02	0,02
chr19:9751516-9762543	NM_031967	Ndrp4	3,74	1,90	0,03
chr2:215183198-215191155	NM_001144957	Riad1	3,71	1,89	0,03
chr12:23760924-23767104	NM_001271236	LOC100362783	3,64	1,86	0,01
chr4:180300910-180487010	NM_001107869	Dysf	3,52	1,82	0,03
chr6:137256802-137272264	NM_182474	LOC299282	3,36	1,75	0,01
chr9:92168446-92231811	NM_001108804	Fbxo36	3,17	1,66	0,02
chr2:209427356-209430124	NM_053681	S100a3	3,13	1,65	0,05
chr1:75149297-75154600	NM_001013894	Lilrb4	3,13	1,65	0,03
chr3:136182050-136269422	NM_001270575	Snap25	3,07	1,62	0,06
chr2:83723118-83735166	NM_012816	Amacr	3,07	1,62	0,03
chr8:61379750-61402266	NM_139097	Scn3b	3,03	1,60	0,03
chr19:26487819-26527769	NM_031343	Slc6a2	2,99	1,58	0,03
chr19:26581752-26582695	NM_001109380	Capns2	2,87	1,52	0,05
chr14:84201086-84203507	NR_102354	Patz1	2,86	1,52	0,09
chr2:1422024-1530718	NM_001033715	Cast	2,86	1,51	0,01
chr17:29834673-29877118	NM_053346	Nrn1	2,86	1,51	0,00
chr8:77153118-77169002	NM_019131	Tpm1	2,85	1,51	0,08
chr5:155079202-155083511	NM_001271259	LOC100359977	2,84	1,51	0,01
chr7:34599082-34705727	NM_001106780	Ntn4	2,77	1,47	0,05
chr4:216132958-216172348	NM_001110099	Ret	2,70	1,43	0,02
chr4:216130141-216172348	NM_012643	Ret	2,69	1,43	0,01
chr1:268979487-269121995	NM_134401	Crtac1	2,63	1,40	0,07

chr1:205649565-205652321	NM_012605	Mylpf	2,63	1,39	0,01
chr5:133586292-133592040	NM_001107951	Dmrt2	2,60	1,38	0,07
chr5:155061362-155062328	NM_153727	Gpr3	2,57	1,36	0,06
chr14:84825688-84834332	NM_001107233	RGD1308775	2,55	1,35	0,03
chr13:92917712-92934249	NM_017235	Hsd17b7	2,55	1,35	0,03
chr10:89590581-89609632	NM_001108837	Meox1	2,53	1,34	0,06
chr4:10021507-10170201	NM_001103355	Fbxl13	2,53	1,34	0,03
chr8:48338878-48342640	NM_145717	Fxyd2	2,51	1,33	0,07
chr9:95085453-95170100	NM_134371	Trpm8	2,51	1,33	0,01
chr10:55965503-55968684	NM_012650	Shbg	2,48	1,31	0,00
chr3:116851721-116869739	NM_139258	Bmf	2,48	1,31	0,09
chr1:81329940-81340229	NM_012714	Gipr	2,48	1,31	0,01
chr17:816273-816370	NR_031832	Mir27b	2,45	1,30	0,05
chr3:126571720-126601829	NM_171989	Bcl2l1	2,45	1,29	0,08
chr3:162572667-162574588	NM_019316	Mafb	2,45	1,29	0,09
chr5:37832722-37840896	NM_001271109	Maged2	2,44	1,29	0,01
chr4:224761676-224766884	NM_001024335	Cd27	2,42	1,27	0,04
chr2:147379485-147381731	NM_001014251	LOC365778	2,41	1,27	0,06
chr3:2489157-2516076	NM_001270608	Grin1	2,41	1,27	0,09
chr10:86310807-86319305	NM_001007011	Zbp2	2,41	1,27	0,04
chr2:209437962-209439970	NM_001106438	S100a5	2,41	1,27	0,10
chr5:172507288-172577540	NM_001195560	Camta1	2,39	1,26	0,01
chr2:278043762-278563294	NM_019123	St6galnac3	2,39	1,25	0,00
chr4:184234158-184271987	NM_001106609	Txnrd3	2,38	1,25	0,01
chr2:241308144-241367644	NM_001005555	Ptbp2	2,38	1,25	0,01
chr8:111018331-111059791	NM_001108775	Rab6b	2,37	1,25	0,01
chr5:151552468-151557472	NM_001134689	Ccdc28b	2,36	1,24	0,00
chr20:7091295-7093067	NM_001004069	Sapcd1	2,34	1,23	0,06
chr10:87187795-87203807	NM_001008753	Krt23	2,31	1,21	0,06
chr3:180696182-180698080	NM_001014052	Abhd16b	2,29	1,20	0,02
chr4:7569374-7570566	NM_001177905	LOC100364673	2,28	1,19	0,09
chr12:54119565-54131440	NM_001270418	Lrcol1	2,27	1,18	0,01
chr9:66602088-66639739	NM_199400	Ica1l	2,26	1,18	0,07
chr11:60714585-60776082	NM_001191826	Gramd1c	2,26	1,18	0,01
chr16:49189581-49192471	NM_001108400	Ankrd37	2,22	1,15	0,01
chr17:68050945-68143522	NM_001170325	Actn2	2,20	1,14	0,04
chr19:26436074-26462382	NM_001190375	Ces1a	2,20	1,14	0,02
chr5:62683431-62687950	NM_001108660	Ccl27	2,20	1,14	0,01
chr6:116452995-116459981	NM_001199168	Acyp1	2,18	1,13	0,03
chr20:5448825-5462082	NM_212498	Atat1	2,18	1,12	0,01
chr1:89288945-89292050	NM_001013065	Ggn	2,18	1,12	0,08
chr15:24735138-24738725	NM_012827	Bmp4	2,15	1,11	0,08
chr14:37033184-37103735	NM_001108359	Dcun1d4	2,12	1,09	0,01
chr5:30284069-30290625	NM_019372	Pdp1	2,11	1,08	0,03
chr1:223521097-223523972	NM_182735	Cdkn1c	2,11	1,08	0,06
chr3:17095295-17130517	NM_001108579	Sh2d3c	2,09	1,07	0,07
chr1:226254102-226258660	NM_001108926	Cabp4	2,08	1,06	0,03
chr20:5955098-5960408	NM_001008848	RT1-Ha	2,07	1,05	0,06

chr7:70693374-70727047	NM_212523	Kif5a	2,07	1,05	0,08
chr7:11523424-11547188	NM_001040190	Atcay	2,06	1,05	0,04
chr6:111585027-111633992	NM_001108036	Plekhh1	2,06	1,04	0,06
chrX:115098750-115107826	NM_001013950	Lmbr1l	2,06	1,04	0,05
chr1:268750618-268751978	NM_001044281	MGC93861	2,05	1,04	0,00
chr1:90369375-90386137	NM_001173357	Dmkn	2,05	1,04	0,09
chr9:61824560-62158071	NM_053456	Plcl1	2,05	1,04	0,04
chr19:44812397-44874904	NM_012550	Ednra	2,05	1,03	0,09
chr1:228361452-228365776	NM_001013071	Tm7sf2	2,04	1,03	0,08
chr1:220887395-220890392	NM_001014163	Cend1	2,04	1,03	0,01
chr17:80546950-80552017	NM_001126079	Acbd7	2,03	1,02	0,08
chr16:60750784-60760965	NM_022199	Dusp4	2,03	1,02	0,05
chr7:98669143-98701551	NM_133521	Fbxo32	2,02	1,01	0,04
chr9:79403625-79427523	NM_001109574	Tmem169	2,00	1,00	0,07
chr13:97560709-98000102	NM_019343	Rgs7	1,99	0,99	0,02
chr6:89586785-89633108	NM_001105732	Sec23a	1,99	0,99	0,01
chr10:90521651-90536723	NM_001108300	Adam11	1,99	0,99	0,03
chr3:66535458-66588943	NM_001107811	Gpr155	1,95	0,97	0,02
chrX:907617-910801	NM_001108058	Spaca5	1,94	0,96	0,10
chr16:63619948-63718738	NM_001271118	Nrg1	1,94	0,95	0,07
chrX:56243028-56310184	NM_052803	Atp7a	1,93	0,95	0,04
chr11:46236524-46289103	NM_138897	Gabrr3	1,92	0,94	0,07
chr7:41506396-41510627	NM_053883	Dusp6	1,90	0,93	0,09
chr16:61448505-61456800	NM_001107317	Mboat4	1,90	0,93	0,05
chr1:163663265-163705736	NM_001135013	Ankrd42	1,90	0,93	0,01
chr7:2689127-2691242	NM_130410	Il23a	1,90	0,93	0,03
chr17:29366866-29405082	NM_001012052	Cage1	1,90	0,93	0,00
chr1:143127276-143136513	NM_001108488	Fes	1,89	0,92	0,08
chr5:82503505-82531128	NM_001024346	LOC500475	1,89	0,92	0,07
chr13:95389057-95405643	NM_001107197	Igsf9	1,89	0,92	0,03
chrX:152368704-152397176	NM_001014107	Mospd1	1,89	0,92	0,02
chr1:242484561-242665781	NM_001013151	Gna14	1,88	0,91	0,08
chr8:116993105-117003173	NM_001143817	Slc26a6	1,88	0,91	0,07
chr12:54373896-54377766	NM_001135840	Gtpbp6	1,88	0,91	0,00
chr7:117711348-117718785	NM_198752	Kifc2	1,88	0,91	0,09
chr1:161406478-163514243	NM_022282	Dlg2	1,87	0,90	0,08
chr6:141412600-141443679	NM_001108723	Cyp46a1	1,87	0,90	0,02
chr2:200743298-200775030	NM_001135716	Map9	1,87	0,90	0,04
chr5:172852349-172885677	NM_019622	Espn	1,87	0,90	0,02
chr9:16800669-16835507	NM_181376	Spats1	1,87	0,90	0,03
chr7:71218205-71221052	NM_053302	Gpr182	1,86	0,90	0,00
chr12:24159895-24170247	NM_001107130	Fbxo24	1,86	0,90	0,03
chr7:69263477-69297957	NM_001047962	LOC500846	1,86	0,89	0,06
chr1:245521321-245562970	NM_022407	Aldh1a1	1,85	0,89	0,06
chr14:36042334-36371467	NM_001017499	Scfd2	1,85	0,89	0,07
chr10:3465262-3473936	NM_001034083	Snn	1,85	0,89	0,02
chr17:87260012-87463987	NM_053926	Pip4k2a	1,85	0,89	0,05
chr9:8981381-8984483	NM_001025661	Crb3	1,85	0,89	0,07

chr8:73438095-73451286	NM_001007010	Dyx1c1	1,85	0,89	0,05
chr9:98231203-98273371	NM_031678	Per2	1,84	0,88	0,08
chr15:47927966-47951099	NM_080888	Bnip3l	1,83	0,88	0,04
chr1:75683290-75691003	NM_019350	Syt5	1,80	0,85	0,04
chr11:28966005-28974872	NM_024400	Adamts1	1,80	0,85	0,01
chr3:168659092-168756457	NM_001100838	Zmynd8	1,80	0,85	0,07
chr15:111996345-112224036	NM_001100685	Clybl	1,79	0,84	0,04
chr1:89279380-89288184	NM_001173344	Spred3	1,79	0,84	0,00
chr3:2243500-2252244	NM_001270627	Nsmf	1,79	0,84	0,01
chr9:15761884-15798787	NM_001271230	Ttbk1	1,79	0,84	0,01
chr2:9458242-9501525	NM_001108934	Mblac2	1,78	0,83	0,09
chr10:101978489-102096741	NM_001108303	Sdk2	1,78	0,83	0,04
chr1:82716409-82731463	NM_001106234	Ethe1	1,78	0,83	0,01
chr13:100036033-100037602	NM_022678	Zfp238	1,77	0,83	0,01
chr12:20517049-20519715	NM_001105915	Asmtl	1,77	0,82	0,00
chr1:102388310-102391914	NM_181369	Hrc	1,77	0,82	0,10
chr10:66303608-66327750	NM_031830	Flot2	1,76	0,81	0,08
chr20:13659349-13660300	NM_145679	Lrrc3	1,76	0,81	0,04
chr5:62404325-62409772	NM_001108971	RGD1309821	1,75	0,81	0,01
chr2:215197398-215211497	NM_001109190	Celf3	1,75	0,81	0,02
chr10:75804186-75858297	NM_001108286	Ypel2	1,75	0,81	0,03
chr10:58734594-58737072	NM_001002820	Ggt6	1,75	0,81	0,03
chr14:17448775-17471447	NM_001012035	Cdkl2	1,75	0,80	0,02
chr10:97578113-97614772	NM_001127297	Wipi1	1,74	0,80	0,05
chr3:132822228-132830719	NM_017178	Bmp2	1,74	0,80	0,00
chr5:82342354-82369090	NM_133600	Slc31a1	1,74	0,80	0,06
chr10:110217248-110227797	NM_001109051	Fn3k	1,74	0,80	0,07
chr16:73809852-73863636	NM_053355	Ikbb	1,74	0,80	0,03
chr13:92913182-92937225	NM_001177830	LOC100366054	1,73	0,79	0,01
chr8:76975898-77047482	NM_153317	Rab8b	1,73	0,79	0,05
chr14:3205284-3249200	NM_001105993	Glmn	1,73	0,79	0,01
chr7:29136814-29151275	NM_013041	Sycp3	1,72	0,79	0,04
chr1:102553245-102590188	NM_001012168	Tulp2	1,72	0,78	0,07
chr19:54355769-54407097	NM_001135583	Fa2h	1,72	0,78	0,04
chr3:171105898-171125442	NM_001106544	Dpm1	1,70	0,77	0,03
chr1:90334991-90349297	NM_023964	Gapdhs	1,70	0,76	0,03
chr2:249539690-249552032	NM_001271984	Casp6	1,70	0,76	0,06
chr13:41264899-41329154	NM_001134500	LOC288978	1,70	0,76	0,03
chr20:31629575-31668605	NM_001190237	Psap	1,70	0,76	0,10
chr11:34998541-35001918	NM_001100557	Olig2	1,69	0,76	0,02
chr5:124221009-124370660	NM_001107949	Dnajc6	1,69	0,76	0,06
chr1:102422047-102424623	NM_021758	Lin7b	1,69	0,76	0,02
chr1:268775550-268785855	NM_001024975	Morn4	1,69	0,76	0,06
chr9:65725150-65764334	NM_021265	Mpp4	1,69	0,75	0,00
chr10:77616853-77645126	NM_001007673	Mmd	1,68	0,75	0,07
chr8:76942438-76963484	NM_001047090	Aph1b	1,68	0,75	0,00
chr7:23553830-23958150	NM_017109	Syn3	1,68	0,75	0,03
chr13:31758212-31919850	NM_016993	Bcl2	1,68	0,75	0,03

chr10:55418596-55422465	NM_012663	Vamp2	1,68	0,75	0,10
chr3:111811724-111856137	NM_013175	Scg5	1,67	0,74	0,09
chr15:51053092-51059854	NM_001106045	Sox7	1,67	0,74	0,03
chr10:97225540-97298645	NM_019224	Rgs9	1,67	0,74	0,07
chr19:11137502-11238898	NM_001011925	Nup93	1,67	0,74	0,01
chrX:45646095-45654127	NM_012661	Sts	1,67	0,74	0,07
chr5:43958429-43999913	NM_001106640	Gpr63	1,66	0,73	0,02
chr1:63367660-63393913	NM_080695	Cacng7	1,66	0,73	0,08
chr4:243622213-243658236	NM_001106627	Casc1	1,66	0,73	0,02
chr17:25775675-25873301	NM_001170334	Gfod1	1,66	0,73	0,10
chr20:34297578-34353838	NM_001025113	Kpna5	1,66	0,73	0,06
chr3:110348099-110446527	NM_001109630	Slc12a6	1,66	0,73	0,09
chr5:54950197-54962319	NM_053918	Cga	1,65	0,73	0,01
chr6:33919767-33935175	NM_001035221	Ypel5	1,65	0,73	0,00
chr16:73730260-73754851	NM_013151	Plat	1,65	0,72	0,06
chrX:69500966-69509231	NM_001025747	Yipf6	1,65	0,72	0,00
chr1:235219781-235262757	NM_031124	Stx3	1,64	0,72	0,01
chr7:24683889-24784329	NM_198750	Cry1	1,64	0,71	0,08
chr15:55195151-55213442	NM_001013133	Rhobtb2	1,63	0,71	0,01
chr7:120512620-120552641	NM_001270796	Pla2g6	1,63	0,71	0,06
chr18:79987671-79997023	NM_001106129	Zadh2	1,63	0,70	0,00
chr10:66197473-66208841	NM_001105804	Nek8	1,63	0,70	0,03
chr1:90317628-90330433	NM_012509	Atp4a	1,63	0,70	0,02
chr15:47157958-47185330	NM_001108871	Kctd9	0,61	-0,70	0,07
chr10:89193679-89252502	NM_012514	Brca1	0,61	-0,70	0,03
chr13:107941116-107965561	NM_171990	Bpnt1	0,61	-0,70	0,03
chr10:59488894-59503993	NM_001191647	Ctns	0,61	-0,71	0,01
chr15:30512208-30613262	NM_001108374	RGD1310110	0,61	-0,71	0,09
chr16:5996455-6009258	NM_001107290	Ii17rb	0,61	-0,71	0,10
chr20:13414046-13422144	NM_001004225	RGD1303003	0,61	-0,71	0,01
chr8:70452357-70467298	NM_001108161	Cilp	0,61	-0,71	0,04
chr16:20154957-20164945	NM_052983	Slc5a5	0,61	-0,71	0,00
chr5:141964116-141992634	NM_138827	Slc2a1	0,61	-0,71	0,08
chr18:29211201-29214370	NM_147140	Slc35a4	0,61	-0,71	0,01
chr12:27130768-27143874	NM_053786	Rfc2	0,61	-0,72	0,01
chr3:124038630-124049162	NM_001040271	Dut	0,61	-0,72	0,06
chr7:114371979-114525553	NM_013081	Ptk2	0,61	-0,72	0,03
chr9:112902311-113037023	NM_145094	Rab31	0,61	-0,72	0,03
chr5:43473597-43590298	NM_001135780	Mms22l	0,61	-0,72	0,04
chr4:186066379-186080792	NM_001107873	Mcm2	0,61	-0,72	0,05
chr3:2471128-2471851	NM_001107820	Ssna1	0,61	-0,72	0,01
chr4:224752543-224759995	NM_001106622	Tapbpl	0,60	-0,73	0,00
chr2:49941585-49948770	NM_171991	Ccnb1	0,60	-0,73	0,07
chr5:161781671-161822396	NM_001134703	Iffo2	0,60	-0,73	0,06
chr2:276130292-276151480	NM_139231	Nexn	0,60	-0,73	0,06
chr12:491024-531772	NM_031542	Brca2	0,60	-0,73	0,05
chr8:28095381-28164189	NM_001034000	Ncapd3	0,60	-0,73	0,01
chr20:9338363-9341335	NM_139327	Hmga1	0,60	-0,73	0,01

chr8:84627767-84666187	NM_012815	Gclc	0,60	-0,74	0,01
chr14:59785052-59859229	NM_001106631	Rbpj	0,60	-0,74	0,06
chrX:115782547-115811946	NM_001108112	Racgap1	0,60	-0,74	0,02
chrX:19487953-19491373	NM_001108251	Ubqln2	0,60	-0,74	0,02
chr15:60932333-60988849	NM_001012044	Lcp1	0,60	-0,74	0,09
chr3:158832629-158836243	NM_001100885	Myl9	0,60	-0,74	0,04
chr2:209191619-209196288	NM_001106439	Slc27a3	0,60	-0,74	0,08
chr3:170527446-170539038	NM_001113752	Tmem189	0,60	-0,74	0,00
chr3:130229227-130239028	NM_133572	Cdc25b	0,60	-0,74	0,01
chr7:2622165-2646199	NM_031340	Timeless	0,60	-0,75	0,05
chr1:206178925-206182756	NM_001106298	Bcl7c	0,60	-0,75	0,03
chr3:130344342-130345306	NM_001108591	Rnf24	0,59	-0,75	0,04
chr7:98589667-98631755	NM_001134879	Atad2	0,59	-0,75	0,03
chr2:220640806-220721461	NM_001168641	Wars2	0,59	-0,75	0,03
chr1:232874536-232900880	NM_001106335	Incenp	0,59	-0,75	0,03
chr2:147289991-147308583	NM_001107669	Plk4	0,59	-0,75	0,04
chr15:31571413-31571670	NR_002703	Rmrp	0,59	-0,76	0,09
chr16:80578523-80615804	NM_001025718	MGC112830	0,59	-0,76	0,02
chr6:111632983-111642424	NM_001108714	Pigh	0,59	-0,76	0,01
chr2:249637718-249707661	NM_001106474	Sec24b	0,59	-0,76	0,04
chr3:131376234-131380108	NM_022381	Pcna	0,59	-0,76	0,08
chr9:70668352-70689596	NM_031510	Idh1	0,59	-0,76	0,01
chr10:12880556-12891739	NM_001105766	Pkmyt1	0,59	-0,76	0,02
chr10:66053384-66071009	NM_001044224	Spag5	0,59	-0,76	0,06
chrX:62976408-63291732	NM_053479	Pola1	0,59	-0,76	0,02
chr3:106967784-107028416	NM_001137642	Kif18a	0,59	-0,77	0,05
chr4:187804479-187901455	NM_053322	Nup210	0,59	-0,77	0,03
chr17:71714422-71724533	NM_001039023	Net1	0,59	-0,77	0,03
chr14:37251450-37267486	NM_001271181	Ociad2	0,59	-0,77	0,08
chr1:265106338-265148860	NM_001106371	Hells	0,59	-0,77	0,07
chr6:37442034-37453747	NM_001191874	Gareml	0,59	-0,77	0,05
chrX:2678419-2835212	NM_001271265	Jade3	0,59	-0,77	0,05
chr16:14274049-14285133	NM_001005908	Ghitm	0,59	-0,77	0,02
chr10:65823081-65832165	NM_001008334	Tmem97	0,58	-0,78	0,02
chr1:173726993-173751295	NM_001013236	Rrm1	0,58	-0,78	0,07
chr13:33035660-33058982	NM_001105948	Serpib8	0,58	-0,78	0,09
chr5:63522803-63526373	NM_001106676	Arhgef39	0,58	-0,79	0,04
chr10:45589178-45608591	NM_001271396	Zfp496	0,58	-0,79	0,03
chr3:144832021-144840679	NM_001009655	Mgme1	0,58	-0,79	0,02
chr1:172081903-172089124	NM_001108495	Relt	0,58	-0,79	0,03
chrX:84610338-84767421	NM_017067	Chm	0,58	-0,80	0,03
chr1:208462230-208513824	NM_001079894	Plekha1	0,58	-0,80	0,07
chr20:13892795-13903349	NM_001024295	Sumo3	0,58	-0,80	0,03
chr1:104238666-104243017	NM_001135016	Tmem86a	0,58	-0,80	0,00
chr20:1328648-1330895	NM_001001717	RT1-M2	0,57	-0,80	0,01
chr11:92565513-92579215	NM_033651	Mcm4	0,57	-0,80	0,08
chr2:227591604-227606918	NM_001107713	Fam212b	0,57	-0,80	0,01
chr10:61406976-61422227	NM_001105807	Mnt	0,57	-0,80	0,02

chr7:78317822-78349530	NM_001130536	Fzd6	0,57	-0,80	0,01
chr7:126447843-126464332	NM_001130500	Gtse1	0,57	-0,80	0,03
chr7:141393003-141400457	NM_199370	Krt8	0,57	-0,80	0,09
chr16:73218778-73230596	NM_001030027	Gins4	0,57	-0,81	0,10
chr2:215899667-215907492	NM_001039044	Cdc42se1	0,57	-0,81	0,00
chr6:134008150-134091103	NM_001173557	RGD1311756	0,57	-0,81	0,09
chr16:36936550-36981614	NM_001012050	Fbxo8	0,57	-0,81	0,05
chr7:140043811-140048951	NM_001013107	Dazap2	0,57	-0,81	0,00
chr17:15662364-15667466	NM_001126083	Cks2	0,57	-0,82	0,09
chr6:146226686-146243773	NM_033230	Akt1	0,57	-0,82	0,00
chr15:92899713-92951232	NM_001108390	Ndfip2	0,57	-0,82	0,03
chr12:54138906-54187417	NM_001107152	Pole	0,57	-0,82	0,02
chr4:162316425-162322429	NM_001106594	Mad2l1	0,57	-0,82	0,03
chrX:135621254-135628591	NM_001113786	Rbmx2	0,57	-0,82	0,04
chr8:68780083-68796624	NM_001108158	Lctl	0,56	-0,82	0,02
chr10:106451967-106455900	NM_053553	Syngn2	0,56	-0,82	0,03
chr10:13410717-13435965	NM_001100474	Ccnf	0,56	-0,82	0,07
chr7:44175397-44207232	NM_022959	Rassf9	0,56	-0,83	0,01
chr10:28861942-28867675	NM_022391	Pttg1	0,56	-0,83	0,06
chr3:160322830-160342099	NM_001107796	Fam83d	0,56	-0,83	0,05
chr15:55872253-55883800	NM_001017376	Phyhip	0,56	-0,83	0,02
chr1:229468107-229485469	NM_001108518	Naa40	0,56	-0,83	0,02
chr8:39184019-39204446	NM_080400	Chek1	0,56	-0,83	0,06
chr8:22631827-22676509	NM_001034088	Carm1	0,56	-0,83	0,03
chr20:5519550-5523476	NM_173102	Tubb5	0,56	-0,83	0,01
chr10:55369545-55375203	NM_053749	Aurkb	0,56	-0,83	0,01
chr3:2572743-2577997	NM_001109418	Sapcd2	0,56	-0,84	0,01
chr1:185106505-185164263	NM_001014022	Btbd10	0,56	-0,84	0,05
chr14:91679885-91688408	NM_001011913	Fign1	0,56	-0,84	0,04
chr1:102771803-102776109	NM_001012066	Sphk2	0,56	-0,84	0,01
chr14:17126864-17129062	NM_139089	Cxcl10	0,56	-0,84	0,08
chr2:70696811-70718964	NM_001014037	RGD1306227	0,56	-0,84	0,02
chr4:225098520-225229257	NM_053889	Vwf	0,56	-0,84	0,00
chr5:141050191-141054395	NM_171993	Cdc20	0,55	-0,85	0,06
chr1:228632628-228655003	NM_001011939	Ehd1	0,55	-0,85	0,01
chr9:93273332-93277372	NM_021740	Ptma	0,55	-0,85	0,07
chr3:117392642-117453522	NM_001170594	Casc5	0,55	-0,85	0,08
chr2:172178849-172217986	NM_001107678	Dhx36	0,55	-0,85	0,01
chr2:163630966-163635150	NM_001044263	Rfxap	0,55	-0,85	0,01
chr15:55958799-55962007	NM_001025279	Reep4	0,55	-0,86	0,01
chr5:152101198-152110578	NM_053582	Tinagl1	0,55	-0,86	0,03
chr5:73152086-73198317	NM_001108666	Smc2	0,55	-0,86	0,07
chr16:19652970-19659002	NM_001006964	Babam1	0,55	-0,86	0,00
chr19:11283092-11283867	NM_001137564	Mt2A	0,55	-0,86	0,06
chr15:47186190-47231339	NM_001107273	Cdca2	0,55	-0,86	0,10
chrX:111960844-111967052	NM_001108120	Nxt2	0,55	-0,86	0,07
chr8:74980446-75067087	NM_001014211	Gcom1	0,55	-0,86	0,10
chr8:22217095-22229971	NM_053743	Cdc37	0,55	-0,87	0,00

chr7:119588351-119603850	NM_001044289	Tex33	0,55	-0,87	0,06
chr5:151138848-151147606	NM_001134629	RGD1561149	0,55	-0,87	0,02
chr12:24140328-24142467	NM_032074	Irs3	0,55	-0,87	0,06
chr19:67327712-67343472	NM_001107441	Ccsap	0,55	-0,87	0,08
chr1:195361585-195387930	NM_001108501	Ccp110	0,55	-0,87	0,02
chr5:139821000-139846566	NM_001085369	Kif2c	0,55	-0,88	0,05
chrX:74567729-74583626	NM_001024892	Rlim	0,54	-0,88	0,03
chr13:115071741-115084946	NM_053691	Nek2	0,54	-0,88	0,03
chrX:72862787-72878439	NM_001098674	Ercc6l	0,54	-0,88	0,02
chr17:56598696-57133815	NM_001108415	Elmo1	0,54	-0,88	0,03
chr8:116474846-116519375	NM_001106093	Usp4	0,54	-0,88	0,01
chr3:131075322-131109910	NM_001037096	Rassf2	0,54	-0,88	0,08
chr3:2422871-2425631	NM_199094	Tubb4b	0,54	-0,88	0,03
chr13:114264895-114292134	NM_001109083	Nsl1	0,54	-0,88	0,03
chr1:31347826-31352722	NM_001246319	Cenpw	0,54	-0,88	0,10
chr7:122151953-122156374	NM_001008373	Srek1ip1	0,54	-0,88	0,01
chr17:91504400-91539143	NM_001107369	Mastl	0,54	-0,88	0,02
chr3:129673987-129677772	NM_172022	Lzts3	0,54	-0,89	0,01
chr18:69317014-69327048	NM_001106134	Ska1	0,54	-0,89	0,07
chr10:89282481-89291487	NM_001024967	Tmem106a	0,54	-0,89	0,04
chr14:83025668-83039430	NM_001004424	Tacc3	0,54	-0,89	0,08
chr1:214925921-214952481	NM_001271366	Mki67	0,54	-0,89	0,09
chr13:50127491-50152683	NM_017287	Mcm6	0,54	-0,89	0,03
chr4:187412089-187427229	NM_001007745	Tmem43	0,54	-0,89	0,01
chr7:142719644-142746041	NM_001109470	Zfp385a	0,54	-0,90	0,01
chr8:59280448-59297536	NM_017132	Rcn2	0,54	-0,90	0,00
chr2:42559853-42717753	NM_033443	Arsb	0,54	-0,90	0,04
chr2:230646556-230651000	NM_001044302	Psrc1	0,54	-0,90	0,04
chr10:14903482-14911519	NM_001105773	Chtf18	0,53	-0,90	0,01
chr9:100106949-100136087	NM_001009362	Pask	0,53	-0,90	0,06
chr10:89978418-90001064	NM_001017988	LOC303566	0,53	-0,91	0,05
chr1:268610732-268618280	NM_053290	Pgam1	0,53	-0,91	0,01
chr1:101603484-101614451	NM_021662	Pold1	0,53	-0,91	0,01
chr10:25712356-25740811	NM_012964	Hmmr	0,53	-0,91	0,05
chr20:22694920-22709859	NM_019296	Cdk1	0,53	-0,91	0,07
chr3:167422568-167424969	NM_001106542	Ube2c	0,53	-0,91	0,04
chr4:214232833-214345405	NM_001107882	March8	0,53	-0,91	0,01
chr4:58581529-58628225	NM_138848	Podxl	0,53	-0,91	0,03
chrX:30198506-30217341	NM_001007756	Gemin8	0,53	-0,91	0,00
chr12:48136330-48294184	NM_001029911	Cit	0,53	-0,91	0,01
chr3:9127873-9155507	NM_144745	Gpsm1	0,53	-0,92	0,08
chr4:222461211-222464596	NM_001047864	Dppa3	0,53	-0,92	0,10
chr5:143482582-143542254	NM_012866	Nfyc	0,53	-0,92	0,02
chr6:46660787-46690981	NM_001106717	Gen1	0,53	-0,92	0,00
chr9:94972806-94990037	NM_201423	Ugt1a2	0,53	-0,93	0,01
chr2:207154780-207174337	NM_001191568	Pmf1	0,53	-0,93	0,04
chr19:11277132-11278149	NM_138826	Mt1a	0,53	-0,93	0,04
chr4:39891452-39963623	NM_001109221	LOC500034	0,52	-0,93	0,02

chr10:106494774-106503096	NM_022274	Birc5	0,52	-0,94	0,09
chr3:14598260-14622945	NM_001108578	Aif1l	0,52	-0,94	0,03
chr18:4076914-4088623	NM_001143893	Cabyr	0,52	-0,94	0,04
chr1:205441132-205467610	NM_001009645	Kif22	0,52	-0,94	0,04
chr10:63636585-63637598	NM_021596	Dbil5	0,52	-0,94	0,00
chr4:224365695-224369284	NM_001007648	Cdca3	0,52	-0,94	0,04
chr16:7220776-7223730	NM_001034105	Tnnc1	0,52	-0,94	0,04
chr3:86627763-86646459	NM_001005892	Spi1	0,52	-0,95	0,09
chr7:60853892-60860953	NM_134346	Rap1b	0,52	-0,95	0,00
chr17:34542624-34554071	NM_001007732	Serpib9	0,52	-0,95	0,05
chr10:86699276-86728312	NM_022183	Top2a	0,52	-0,95	0,03
chr10:90780840-90800011	NM_001039019	Kif18b	0,52	-0,95	0,03
chr5:138732241-138762035	NM_001134960	Rad54l	0,52	-0,95	0,01
chr3:126929122-126960429	NM_001106507	Bub1	0,52	-0,95	0,04
chr8:116085075-116104852	NM_001109004	Traip	0,52	-0,96	0,03
chr3:117970748-118001101	NM_001107762	Nusap1	0,52	-0,96	0,01
chr14:80414798-80429940	NM_001134843	Myo1g	0,52	-0,96	0,08
chr3:131132123-131224768	NM_017316	Slc23a2	0,51	-0,96	0,10
chr1:263519575-263570293	NM_001169112	Kif11	0,51	-0,96	0,05
chr10:86614892-86628265	NM_001108298	Cdc6	0,51	-0,96	0,08
chr18:27137684-27146171	NM_001108426	Kif20a	0,51	-0,97	0,05
chr1:199178261-199188238	NM_017100	Plk1	0,51	-0,97	0,02
chr3:144374720-144408658	NM_031555	Bfsp1	0,51	-0,97	0,05
chrX:54466172-54495252	NM_001177824	LOC100363193	0,51	-0,97	0,05
chr3:156435529-156446390	NM_001100778	E2f1	0,51	-0,97	0,03
chr3:127245517-127307875	NM_032462	Kcnip3	0,51	-0,97	0,10
chr5:64307463-64367854	NM_001108662	Melk	0,51	-0,97	0,03
chr7:117676479-117691180	NM_001130572	Tonsl	0,51	-0,97	0,01
chr2:142890983-142897317	NM_053702	Ccna2	0,51	-0,97	0,04
chr9:25770287-25788432	NM_001191805	Mcm3	0,51	-0,97	0,03
chr8:90886761-90924325	NM_001108172	Ttk	0,51	-0,97	0,05
chr9:119293739-119309561	NM_001126270	Ndc80	0,51	-0,97	0,09
chr5:156971023-157004413	NM_022505	Rhd	0,51	-0,98	0,05
chr10:75668740-75686674	NM_001009624	Ska2	0,51	-0,98	0,02
chr15:28108227-28138753	NM_001135802	Dlgap5	0,51	-0,98	0,01
chr13:61564058-61609831	NM_001105955	Aspm	0,51	-0,98	0,02
chr3:154730956-154773179	NM_001107790	Tpx2	0,50	-0,99	0,03
chr19:66090080-66095027	NM_001106192	Cdt1	0,50	-0,99	0,01
chr1:221068625-221076442	NM_001270762	Rnh1	0,50	-0,99	0,05
chr8:70811352-70818568	NM_001044253	Pif1	0,50	-0,99	0,08
chr8:131187616-131258348	NM_181635	Kif15	0,50	-1,00	0,08
chr3:117157779-117177433	NM_001004264	Knstrn	0,50	-1,00	0,01
chr18:50979874-51017524	NM_053905	Lmnb1	0,50	-1,00	0,02
chr16:75349397-75367306	NM_001012228	Xkr5	0,50	-1,00	0,03
chr9:64698065-64720561	NM_001271191	Sgol2	0,50	-1,00	0,04
chr19:36055966-36070506	NM_001107160	Asf1b	0,50	-1,00	0,05
chr1:260438626-260494019	NM_001107609	Kif20b	0,50	-1,00	0,03
chr1:143039959-143061006	NM_001107529	Prc1	0,50	-1,00	0,03

chr15:49092279-49103281	NM_001079937	Pbk	0,50	-1,01	0,03
chr19:49107657-49191221	NM_053605	Smpd3	0,50	-1,01	0,07
chr9:78074907-78145962	NM_022622	Bard1	0,50	-1,01	0,03
chr12:40072617-40146547	NM_001107140	Kntc1	0,50	-1,01	0,05
chr16:68718376-68753634	NM_001191555	Rab11fip1	0,50	-1,01	0,02
chr6:51811951-51828131	NM_001100717	E2f6	0,49	-1,02	0,01
chr17:1642448-1661577	NM_001012051	Zfp367	0,49	-1,02	0,03
chr8:66598466-66625560	NM_001108155	Kif23	0,49	-1,02	0,02
chr1:223099327-223114942	NM_013087	Cd81	0,49	-1,02	0,03
chr3:158598783-158611011	NM_001025768	Dsn1	0,49	-1,02	0,09
chr13:55534038-55551850	NM_001108343	Etnk2	0,49	-1,02	0,00
chr13:112758854-112804965	NM_001100827	Cenpf	0,49	-1,03	0,05
chr2:132490046-132552138	NM_001108547	Ect2	0,49	-1,03	0,04
chr3:62049999-62063264	NM_001009654	Spc25	0,49	-1,03	0,06
chr2:262787595-262899803	NM_001107728	Rap1gds1	0,49	-1,03	0,01
chr20:5831136-5833706	NM_213561	Tcf19	0,49	-1,03	0,00
chr1:236163690-236179257	NM_001109163	Fam111a	0,49	-1,03	0,03
chr6:114998809-115025300	NM_019168	Arg2	0,49	-1,04	0,02
chr10:91783780-91805556	NM_024150	Arf2	0,49	-1,04	0,01
chr3:117468880-117493555	NM_001109204	Rad51	0,49	-1,04	0,03
chr1:163919400-163943710	NM_001126294	RGD1559690	0,49	-1,04	0,07
chr1:15072108-15083325	NM_001037789	Ccdc28a	0,48	-1,05	0,03
chr1:228384096-228394986	NM_001115042	Cdca5	0,48	-1,05	0,03
chr16:74383676-74410206	NM_001169139	Ckap2	0,48	-1,06	0,02
chrX:115263555-115271364	NM_001271243	Troap	0,48	-1,06	0,08
chr4:226891343-226902365	NM_031633	Foxm1	0,48	-1,06	0,05
chr16:49739813-49753271	NM_198791	Tlr3	0,48	-1,06	0,01
chr10:105718074-105765280	NM_001108309	Sec14l1	0,48	-1,07	0,03
chr4:208787163-208847877	NM_001001719	Fancd2	0,48	-1,07	0,02
chr7:53286861-53326929	NM_001108092	E2f7	0,48	-1,07	0,04
chr1:264226026-264241499	NM_001025646	Cep55	0,48	-1,07	0,07
chr13:92450021-92478789	NM_001012028	Nuf2	0,48	-1,07	0,01
chr11:69681012-69786646	NM_001105878	Polq	0,47	-1,07	0,04
chr15:55525396-55544851	NM_001013186	Bin3	0,47	-1,08	0,02
chr16:48613428-48636501	NM_001025673	Cenpu	0,47	-1,08	0,07
chr12:49014185-49024662	NM_001013983	Mlec	0,47	-1,08	0,07
chr1:22625115-22626610	NM_001009470	Ccnb2	0,47	-1,08	0,01
chr11:33551576-33681966	NM_001100558	Tiam1	0,47	-1,08	0,06
chr16:68718376-68753634	NM_001197241	Rab11fip1	0,47	-1,08	0,01
chr5:143777120-143808982	NM_001107974	Zmpste24	0,47	-1,08	0,04
chr18:62314820-62324460	NM_001025675	Tubb6	0,47	-1,09	0,03
chr13:98401024-98427400	NM_001107198	Exo1	0,47	-1,09	0,02
chr20:7567670-7585191	NM_001005878	Kifc1	0,47	-1,09	0,01
chr7:141693055-141719909	NM_001170602	Espl1	0,47	-1,09	0,02
chr2:59075285-59147310	NM_001107651	Depdc1b	0,47	-1,09	0,07
chr15:41919557-41937891	NM_001108379	Ska3	0,47	-1,09	0,04
chrX:105040384-105090804	NM_012955	Cenpi	0,47	-1,10	0,03
chr5:130042065-130066959	NM_001109262	RGD1559493	0,47	-1,10	0,06

chr19:48680054-48686495	NM_001024257	Cenpt	0,47	-1,10	0,04
chr8:103009499-103046804	NM_001108178	Pls1	0,47	-1,10	0,01
chr8:71186711-71198728	NM_201418	Ns5atp9	0,47	-1,10	0,05
chr17:11940005-11943732	NM_145773	Mxd3	0,47	-1,10	0,04
chr5:148352776-148387685	NM_001106687	Clspn	0,46	-1,11	0,03
chr17:78890309-78911578	NM_001107366	Mcm10	0,46	-1,11	0,03
chr17:23615670-23657985	NM_001001511	Gcnt2	0,46	-1,12	0,01
chr14:84955986-84971855	NM_001109090	Sec14I4	0,46	-1,12	0,00
chr3:111858564-111874846	NM_001168524	Arhgap11a	0,46	-1,13	0,03
chr10:106456781-106468109	NM_052800	Tk1	0,46	-1,13	0,01
chr10:14120127-14139812	NM_001013182	Hn1l	0,46	-1,14	0,01
chr3:116411044-116422101	NM_001013062	Thbs1	0,45	-1,14	0,08
chr6:100953299-100977903	NM_001169108	Pole2	0,45	-1,16	0,03
chr3:112080852-112086389	NM_019183	Actc1	0,45	-1,17	0,07
chr19:25637491-25681915	NM_001106170	Mcm5	0,44	-1,17	0,01
chr16:40849290-40908352	NM_001170346	Neil3	0,44	-1,18	0,07
chr2:71808490-71810259	NM_001007634	Pelo	0,44	-1,18	0,04
chr3:165617193-165645609	NM_001106536	Mybl2	0,44	-1,18	0,02
chr9:95036300-95049229	NM_001191813	Hjurp	0,44	-1,18	0,02
chr9:22278198-22282377	NM_001109502	LOC688459	0,44	-1,19	0,05
chr10:94317973-94324597	NM_001007725	Icam2	0,44	-1,19	0,05
chrX:25427593-25491604	NM_022198	Clcn4	0,44	-1,19	0,01
chr9:9731077-9750175	NM_001008882	Uhrf1	0,44	-1,19	0,05
chr3:120780502-120790938	NM_001107767	Duoxa1	0,44	-1,20	0,01
chr5:132031218-132050961	NM_177931	Orc1	0,43	-1,21	0,07
chr7:117753870-117761035	NM_001130494	Recql4	0,43	-1,22	0,10
chr7:28764493-28825206	NM_001166676	Parpbp	0,43	-1,22	0,01
chr6:22325768-22342414	NM_182954	Ston1	0,43	-1,23	0,01
chr2:206725432-206729779	NM_017244	Crabp2	0,43	-1,23	0,05
chr2:206850517-206892647	NM_001191709	Iqgap3	0,42	-1,24	0,01
chr6:60756159-60762351	NM_001025740	Rrm2	0,42	-1,26	0,03
chr16:18621440-18633581	NM_012878	Sftpd	0,41	-1,28	0,04
chr12:21132925-21173248	NM_147206	Cyp3a9	0,40	-1,31	0,00
chr2:223111197-223478957	NM_012830	Cd2	0,40	-1,31	0,05
chr11:93274701-93287932	NM_001106930	Efcab1	0,40	-1,33	0,05
chr9:94910376-94990037	NM_175846	Ugt1a8	0,40	-1,33	0,02
chr13:113312813-113456734	NM_001107200	Ptpn14	0,40	-1,34	0,07
chr10:82185899-82191905	NM_001105830	Eme1	0,39	-1,34	0,05
chr20:31709058-31731465	NM_001044300	MGC112715	0,39	-1,34	0,09
chr2:176099246-176179301	NM_001127530	LOC302022	0,39	-1,36	0,05
chr1:79112278-79130529	NM_001024897	Ehd2	0,38	-1,40	0,08
chr3:119941852-119945947	NM_001011957	Eli3	0,38	-1,40	0,06
chr3:14625723-14686842	NM_001107830	Lamc3	0,37	-1,43	0,08
chr7:141009310-141017951	NM_001008825	Kb15	0,37	-1,44	0,01
chr20:19931568-19932366	NM_001109337	RGD1559903	0,36	-1,46	0,01
chr7:117215918-117273721	NM_001164297	Plec	0,36	-1,47	0,08
chr10:34059638-34067269	NM_172019	Ifi47	0,36	-1,48	0,06
chrX:113502311-113527023	NM_031808	Capn6	0,35	-1,52	0,08

chr8:14190845-14252439	NM_001014087	Ccdc67	0,34	-1,55	0,03
chr2:63940890-63944583	NM_001106411	Gpx8	0,34	-1,56	0,06
chr7:126136631-126178957	NM_001009695	Wnt7b	0,33	-1,61	0,01
chr18:40348060-40362704	NM_052809	Cdo1	0,32	-1,66	0,07
chr8:2681124-2708341	NM_130422	Casp12	0,32	-1,66	0,07
chr9:26283549-26300195	NM_031509	Gsta1	0,31	-1,70	0,05
chr2:72182691-72346118	NM_017094	Ghr	0,31	-1,71	0,06
chr3:163763404-164548723	NM_001108603	Ptprt	0,29	-1,81	0,00
chr18:29810768-29924443	NM_199509	Pcdhac1	0,28	-1,83	0,07
chr11:85926516-85931772	NM_031133	Thpo	0,28	-1,83	0,04
chr9:26210312-26264316	NM_001159739	Gsta3	0,28	-1,84	0,05
chr17:25209367-25713271	NM_214457	Phactr1	0,23	-2,11	0,10
chr14:84201086-84217034	NR_102353	Patz1	0,23	-2,15	0,08
chr3:54349275-54356654	NM_001191070	Tbr1	0,22	-2,21	0,02
chr1:178792339-178816636	NM_001013192	Olfml1	0,20	-2,35	0,09
chr19:47890577-47898167	NM_001106175	Ces2g	0,19	-2,42	0,03
chr1:227783723-227790741	NM_001005907	Efemp2	0,18	-2,44	0,01
chr19:11300013-11301422	NM_053968	Mt3	0,18	-2,48	0,08
chr3:9149729-9155507	NM_001145469	Gpsm1	0,16	-2,62	0,00
chr14:84198775-84203507	NM_001277215	Patz1	0,16	-2,68	0,00
chr2:108055052-108086130	NM_001134993	Car13	0,15	-2,77	0,02

Supporting Table S4. List of genes which expression changed significantly upon MAX expression. Two independent RNAseq experiments were carried out to compare the transcriptomes of URMax34 cells expressing MAX (upon 24h of Zn²⁺ treatment) and URMT without MAX (but also treated with Zn²⁺). Relative RNA amounts were calculated as FPKM fold change (FC). Data are mean values of the two independent transfections where log2FC was >0.7 or < -0.7 (i.e., ≥1.6 fold and ≤0.5 fold), and a p-value <0.1.

locus	gene_id	Gene	URMax34 pLKO vs URMT pLKO		
			FC	Log2FC	p-value
chr19:10638465-10647951	NM_134455	Cx3cl1	37,07	5,21	0,06
chr13:91028025-91307272	NM_001134862	Pbx1	12,64	3,66	0,01
chr9:54940737-54952755	NM_001007712	Sdpr	11,77	3,56	0,01
chr12:26978747-27022485	NM_012722	Eln	11,54	3,53	0,05
chr20:14931525-14959214	NM_001100741	Col6a2	10,55	3,40	0,01
chr7:141009310-141017951	NM_001008825	Kb15	8,46	3,08	0,01
chr4:19169058-19359164	NM_001104633	Sema3d	8,45	3,08	0,05
chr17:26191714-26240098	NM_001109117	Rnf182	7,99	3,00	0,04
chr5:158368888-158402121	NM_001015008	Tcea3	7,59	2,92	0,07
chr7:119772956-119786147	NM_001008384	Rac2	6,55	2,71	0,01
chr6:109380102-109403573	NM_022210	Max	6,54	2,71	0,01
chr9:91403608-91419329	NM_001110493	Pid1	6,29	2,65	0,01
chr4:235170744-235189397	NM_001009600	Arhgdib	5,59	2,48	0,05
chr9:88662801-88665379	NM_019233	Ccl20	5,30	2,41	0,05
chr1:101596930-101602764	NM_001024286	Spib	5,30	2,40	0,03
chr15:31850395-31866405	NM_020082	Rnase4	5,28	2,40	0,02
chr8:129601906-129608906	NM_001106868	Hhat1	4,88	2,29	0,01
chr2:209437962-209439970	NM_001106438	S100a5	4,86	2,28	0,10
chr11:39232473-39336438	NM_133397	Erg	4,74	2,25	0,02
chr1:174082178-174088103	NM_173293	Olr59	4,72	2,24	0,05
chr1:57354079-57362996	NM_001107464	Dact2	4,69	2,23	0,02
chr6:7897004-7916593	NM_130414	Abcg8	4,67	2,22	0,07
chr3:15086725-15098070	NM_021583	Ptges	4,64	2,21	0,05
chr6:36175966-36205241	NM_013120	Gckr	4,54	2,18	0,08
chr6:7871268-7896799	NM_053754	Abcg5	4,49	2,17	0,05
chr5:168454330-168455633	NM_031545	Nppb	4,44	2,15	0,03
chr1:144308591-144336257	NM_001191627	Fsd2	4,44	2,15	0,03
chr5:163890562-163894419	NM_001013936	Slc25a34	4,43	2,15	0,10
chrX:122958361-122961547	NM_001014065	Zcchc12	4,39	2,14	0,04
chr2:174744151-174773776	NM_001099506	Vom2r47	4,31	2,11	0,03
chr5:21569209-21577465	NM_001008316	Plag1	4,22	2,08	0,03
chr7:44175397-44207232	NM_022959	Rassf9	4,16	2,06	0,01
chr5:32678999-32816595	NM_001106638	Slc26a7	4,14	2,05	0,09
chr18:55596757-55637692	NM_031525	Pdgfrb	4,08	2,03	0,01
chr9:51757495-51906270	NM_053488	Col5a2	4,07	2,02	0,03
chr1:220574320-220575781	NM_012786	Cox8b	4,07	2,02	0,04
chr6:22325768-22342414	NM_182954	Ston1	3,78	1,92	0,01
chr20:6167758-6177328	NM_001008884	RT1-Db1	3,72	1,89	0,02
chr20:6186326-6205191	NM_001164826	RT1-Db2	3,65	1,87	0,04
chr4:10265818-10414946	NM_001025044	Ccdc146	3,64	1,86	0,05
chr2:269282796-269305090	NM_001013202	Clca2	3,63	1,86	0,04

chr8:27827459-27872964	NM_001192018	Glb1l2	3,51	1,81	0,10
chr5:161068640-161074026	NM_001106696	Pla2g2e	3,48	1,80	0,03
chr8:115761398-115777438	NM_1457776	Slc38a3	3,48	1,80	0,08
chr18:30083425-30085822	NM_001109123	Pcdhb2	3,32	1,73	0,05
chr2:72182691-72346118	NM_017094	Ghr	3,31	1,72	0,10
chr3:40398134-40555551	NM_001134580	Lypd6b	3,26	1,71	0,08
chr2:71520173-71532083	NM_001007633	Mocs2	3,24	1,69	0,08
chr3:155802168-155827127	NM_001109209	Bpifb4	3,21	1,68	0,01
chr17:44449933-44506535	NM_001024273	Cmah	3,20	1,68	0,09
chr5:170557218-170568525	NM_001107994	Spsb1	3,18	1,67	0,01
chr10:54216433-54257404	NM_001100968	Wdr16	3,17	1,66	0,01
chr10:81951028-82017885	NM_031601	Cacna1g	3,14	1,65	0,05
chr19:10300708-10319286	NM_001103352	Kifc3	3,04	1,60	0,05
chr20:31709058-31731465	NM_001044300	MGC112715	3,04	1,60	0,06
chr16:20154957-20164945	NM_052983	Slc5a5	3,01	1,59	0,00
chr10:69058108-69059959	NM_001007612	Ccl7	2,98	1,58	0,06
chr13:93609912-93647084	NM_001107195	Olfml2b	2,94	1,56	0,02
chr7:63077687-63147646	NM_053738	Wif1	2,90	1,54	0,02
chr15:54622229-54632875	NM_031123	Stc1	2,86	1,52	0,08
chr10:59269278-59299899	NM_012914	Atp2a3	2,80	1,49	0,07
chr16:70925603-70965251	NM_024146	Fgfr1	2,79	1,48	0,00
chr19:47890577-47898167	NM_001106175	Ces2g	2,79	1,48	0,09
chr5:172507288-172577540	NM_001195560	Camta1	2,78	1,47	0,03
chr4:57616942-57640152	NM_001013083	Cpa2	2,77	1,47	0,01
chr2:175102651-175398300	NM_017303	Kcnab1	2,70	1,43	0,07
chr1:222524151-222557295	NM_001025420	Lsp1	2,70	1,43	0,02
chr2:72138279-72148389	NM_019192	Sepp1	2,69	1,43	0,07
chr19:63411525-63452571	NM_138518	Crispld2	2,65	1,40	0,00
chr14:32929168-32944266	NM_031788	Rest	2,61	1,39	0,05
chr1:103989929-104006581	NM_017266	Ldhc	2,56	1,36	0,10
chr1:53617429-53800478	NM_022236	Pde10a	2,50	1,32	0,01
chr10:14056323-14059570	NM_053329	Igfals	2,50	1,32	0,07
chr3:123424950-123482782	NM_001107768	Sema6d	2,49	1,31	0,01
chr7:1133988-1138965	NM_001109460	Stx19	2,45	1,30	0,03
chr5:161781671-161822396	NM_001134703	Iffo2	2,40	1,26	0,03
chr2:217845512-217845905	NM_001111341	Hist2h2ab	2,38	1,25	0,07
chr2:278043762-278563294	NM_019123	St6galnac3	2,38	1,25	0,02
chr18:55104199-55125190	NM_021695	Synpo	2,35	1,24	0,01
chr3:54349275-54356654	NM_001191070	Tbr1	2,34	1,23	0,04
chr9:64726636-64804786	NM_019363	Aox1	2,34	1,23	0,04
chr14:84198775-84203507	NM_001277215	Patz1	2,30	1,20	0,01
chr10:34059638-34067269	NM_172019	Ifi47	2,29	1,19	0,05
chr10:104946568-104948325	NM_053832	Foxj1	2,26	1,18	0,05
chr11:93462644-93464954	NM_013035	Snai2	2,26	1,17	0,05
chr1:48926485-48987223	NM_001038615	Fndc1	2,25	1,17	0,10
chr8:116474846-116519375	NM_001106093	Usp4	2,24	1,16	0,00
chr15:29220348-29287363	NM_001170475	RGD1562018	2,23	1,16	0,00
chr10:82022658-82029499	NM_199402	Spata20	2,21	1,14	0,09
chr4:64063951-64156123	NM_017066	Ptn	2,20	1,14	0,06
chr2:206725432-206729779	NM_017244	Crabp2	2,18	1,13	0,00
chr4:207683201-207699176	NM_019155	Cav3	2,18	1,13	0,08
chr6:34010477-34031267	NM_001129880	Lbh	2,16	1,11	0,01
chr4:26377856-26382255	NM_021266	Fzd1	2,16	1,11	0,01

chr10:56298101-56303606	NM_012751	Slc2a4	2,15	1,10	0,00
chr4:58581529-58628225	NM_138848	Podxl	2,14	1,10	0,05
chr7:117312036-117335715	NM_001115026	Spatc1	2,13	1,09	0,09
chr10:77616853-77645126	NM_001007673	Mmd	2,12	1,08	0,07
chr19:10403000-10442286	NM_152242	Gpr56	2,11	1,08	0,01
chr2:223666826-223689474	NM_001106456	Mab2113	2,11	1,08	0,02
chr14:79829770-79857492	NM_001107226	Sh3tc1	2,11	1,08	0,02
chr6:51348169-51353994	NM_001013096	Mycn	2,09	1,07	0,10
chr15:50151498-50197708	NM_144730	Gata4	2,09	1,06	0,06
chr17:23472658-23481773	NM_001106105	Gcm2	2,05	1,04	0,01
chr10:58690457-58711606	NM_001190998	Smtnl2	2,05	1,03	0,02
chr6:32580743-33082963	NM_001169101	Alk	2,04	1,03	0,06
chr3:127245517-127307875	NM_032462	Kcnip3	2,03	1,02	0,09
chr16:19194745-19207342	NM_001271328	Hsh2d	2,02	1,01	0,03
chr14:36954230-36976506	NM_001008763	Lrrc66	2,01	1,01	0,06
chr10:75073436-75143103	NM_001135921	Rnf43	2,00	1,00	0,10
chr18:72178892-72246274	NM_001100973	Pard6g	1,99	0,99	0,07
chr19:68936976-69098880	NM_001009704	Sipa1l2	1,98	0,99	0,04
chr6:37442034-37453747	NM_001191874	Gareml	1,98	0,99	0,02
chr12:16120531-16185309	NM_001037218	Radil	1,98	0,98	0,01
chr4:143138366-143145822	NM_001270593	Tmem176b	1,97	0,98	0,02
chr12:10197624-10240087	NM_001100989	Mtus2	1,96	0,97	0,09
chr5:152101198-152110578	NM_053582	Tinagl1	1,96	0,97	0,06
chr1:171496701-171531029	NM_198775	P4ha3	1,95	0,97	0,10
chr1:222722920-222729523	NM_001190162	Igf2	1,94	0,96	0,09
chr5:68298771-68338610	NM_031628	Nr4a3	1,94	0,96	0,03
chr19:71984686-72136036	NM_145098	Nrp1	1,93	0,95	0,09
chr7:93245560-93521935	NM_001130540	Ext1	1,91	0,94	0,01
chr1:102004256-102018333	NM_199088	Tsks	1,91	0,93	0,05
chr10:57006273-57009138	NM_001109654	Gp1ba	1,91	0,93	0,05
chr20:22087200-22609936	NM_031805	Ank3	1,91	0,93	0,02
chr9:37980048-38033453	NM_001108792	Bend6	1,90	0,93	0,07
chr17:43952823-43995477	NM_001100512	Gpld1	1,90	0,93	0,03
chr1:170000732-170016829	NM_080401	Wnt11	1,89	0,92	0,07
chr3:112080852-112086389	NM_019183	Actc1	1,88	0,91	0,07
chr5:161163106-161240395	NM_001034949	Tmco4	1,87	0,90	0,03
chr3:88516995-88555163	NM_030839	Syt13	1,87	0,90	0,04
chrX:107500504-107512866	NM_001127602	Mcart1l	1,87	0,90	0,08
chr1:102151856-102161139	NM_033351	Fcgrt	1,87	0,90	0,04
chr12:24171370-24177687	NM_019237	Pcolce	1,85	0,89	0,06
chr12:49914426-50000957	NM_053922	Acacb	1,83	0,88	0,03
chr6:60881776-61003918	NM_001108016	Mboat2	1,81	0,85	0,09
chr2:208065968-208070220	NM_001107692	Efna4	1,80	0,85	0,04
chr5:156559977-156703434	NM_001108687	Man1c1	1,79	0,84	0,02
chr3:27274065-27294580	NM_001135761	Crb2	1,78	0,83	0,02
chr15:38381668-38390744	NM_001107264	Nfatc4	1,78	0,83	0,06
chr15:62249642-62348601	NM_001109912	Tsc22d1	1,77	0,83	0,04
chr10:106973462-107021070	NM_021989	Timp2	1,77	0,82	0,04
chr11:79928628-79998571	NM_022257	Masp1	1,77	0,82	0,09
chr4:149342034-149400634	NM_001025063	Scrn1	1,76	0,82	0,07
chr19:72324611-72372325	NM_017022	Itgb1	1,76	0,82	0,02
chr19:62973795-62994144	NM_001014154	Dnaaf1	1,76	0,81	0,02
chr8:115795105-115824684	NM_001108185	Sema3f	1,76	0,81	0,04

chrX:112397268-112556696	NM_001109014	Tmem164	1,75	0,81	0,05
chr4:6318180-6351691	NM_199393	Galnt11	1,75	0,80	0,04
chr2:64214524-64273495	NM_001134510	RGD1561161	1,74	0,80	0,04
chr2:218213051-218238921	NM_001024303	Lix1l	1,74	0,80	0,04
chr5:157338298-157394464	NM_031818	Clic4	1,73	0,79	0,03
chr7:126136631-126178957	NM_001009695	Wnt7b	1,73	0,79	0,08
chr8:116070038-116084385	NM_024000	Camkv	1,72	0,78	0,09
chr8:36428865-36434949	NM_001034150	Srpr	1,72	0,78	0,00
chr16:7408995-7472907	NM_054011	Sh3bp5	1,69	0,76	0,02
chr7:71218205-71221052	NM_053302	Gpr182	1,69	0,76	0,07
chr12:45839707-45861437	NM_057130	Hrk	1,68	0,75	0,03
chr14:1459623-1464324	NM_134465	Crif2	1,68	0,75	0,01
chr4:244235299-244304646	NM_001191753	Rassf8	1,68	0,75	0,06
chr4:163912883-163925865	NM_001009413	Krcc1	1,67	0,74	0,05
chrX:69764313-69777121	NM_017089	Efnb1	1,67	0,74	0,00
chr8:116613076-116625217	NM_012974	Lamb2	1,66	0,73	0,02
chr5:130179451-130192201	NM_001005558	Fam151a	1,66	0,73	0,05
chr7:34151375-34186857	NM_001108743	Elk3	1,66	0,73	0,03
chr5:176764183-176768534	NM_001007002	Mxra8	1,66	0,73	0,08
chr10:39171367-39185480	NM_017062	Pdlim4	1,66	0,73	0,09
chr10:83934226-83935978	NM_001191649	Hoxb8	1,65	0,72	0,02
chr5:174800869-174803561	NM_001163723	Smim1	1,65	0,72	0,05
chr1:152823435-152844829	NM_001108821	Abcd1	1,64	0,72	0,00
chr14:81671044-81742380	NM_019339	Rgs12	1,63	0,71	0,01
chr19:829210-836078	NM_001106164	Cmtm3	1,63	0,71	0,03
chr15:42177370-42217419	NM_012952	Fgf9	1,63	0,70	0,06
chr11:47430603-47483837	NM_130419	Dcbld2	1,63	0,70	0,01
chr20:6409149-6433141	NM_001002827	Notch4	1,63	0,70	0,00
chr2:176099246-176179301	NM_001127530	LOC302022	0,62	-0,70	0,07
chr1:175586829-175603800	NM_001014023	Trim5	0,61	-0,70	0,08
chr1:102182149-102184258	NM_031110	Rps11	0,61	-0,71	0,10
chr8:117686010-117699636	NM_019284	Cspg5	0,61	-0,71	0,05
chr3:166421476-166427695	NM_130813	Kcnk15	0,61	-0,71	0,08
chr10:48686499-48707996	NM_001270797	Trpv2	0,61	-0,71	0,01
chr13:80091716-80133075	NM_053571	Sec16b	0,61	-0,71	0,01
chr7:2880877-2882604	NM_001109484	Myl6	0,61	-0,71	0,07
chr8:82645961-82780150	NM_001276472	Hmgcl1	0,61	-0,72	0,01
chr1:83684795-83713565	NM_012782	Bckdha	0,61	-0,72	0,07
chr1:24229987-24232144	NM_031709	Rps12	0,61	-0,72	0,09
chr10:88965678-88967458	NM_031646	Ramp2	0,60	-0,73	0,01
chr3:181259386-181278378	NM_133608	Slco4a1	0,60	-0,73	0,10
chr1:268750618-268751978	NM_001044281	MGC93861	0,60	-0,74	0,02
chr5:151029936-151038262	NM_017122	Hpca	0,60	-0,74	0,00
chr3:132822228-132830719	NM_017178	Bmp2	0,60	-0,74	0,00
chr1:75563121-75590916	NM_001108468	Rdh13	0,60	-0,74	0,01
chr1:172227725-172241918	NM_017255	P2ry2	0,60	-0,75	0,01
chr3:119859002-119864004	NM_001012738	Ckmt1b	0,59	-0,75	0,04
chr2:215130623-215152162	NM_001014038	Tdrkh	0,59	-0,75	0,10
chr6:101678898-101819540	NM_001009831	Atf1	0,59	-0,75	0,01
chrX:115875187-115882578	NM_022215	Gpd1	0,59	-0,75	0,01
chrX:105506648-105511422	NM_001014274	Armcx2	0,59	-0,75	0,07
chr1:225500670-225518961	NM_001012069	Mtl5	0,59	-0,76	0,04
chr14:11039579-11110144	NM_001108354	Tmem150c	0,59	-0,76	0,02

chr16:58417283-58419182	NM_001109512	LOC688765	0,59	-0,77	0,02
chr17:43671712-43689290	NM_001106109	Nrsn1	0,59	-0,77	0,06
chr10:83040795-83121507	NM_001100496	Spop	0,59	-0,77	0,01
chr1:198729099-198856174	NM_001100519	Gga2	0,59	-0,77	0,08
chr1:83713976-83723115	NM_001107493	Exosc5	0,58	-0,78	0,04
chr12:50074382-50132727	NM_134404	Svop	0,58	-0,78	0,06
chr13:94228758-94233191	NM_0011131001	Fcer1g	0,58	-0,78	0,08
chr7:117215918-117244741	NM_0011164304	Plec	0,58	-0,78	0,05
chr3:179929442-179946156	NM_001108613	Slc17a9	0,58	-0,78	0,04
chr16:19800347-19803919	NM_198134	Bst2	0,58	-0,79	0,06
chr2:206567014-206586422	NM_022212	Insrr	0,58	-0,79	0,07
chr3:149431211-149473190	NM_0011191966	Napb	0,58	-0,79	0,06
chrX:135420268-135431674	NM_001108257	Rab33a	0,58	-0,80	0,10
chr10:75217842-75227838	NM_001011893	38231	0,58	-0,80	0,03
chr20:6457561-6459956	NM_001165880	Egfl8	0,58	-0,80	0,04
chr11:80084426-80096284	NM_001108321	Rtp4	0,58	-0,80	0,01
chr10:35105632-35146138	NM_001270544	Mapk9	0,57	-0,80	0,07
chr8:36761171-36777206	NM_031630	Ddx25	0,57	-0,81	0,05
chr9:26322565-26358469	NM_001024361	LOC501110	0,57	-0,82	0,01
chr14:92142187-92292689	NM_001107236	Cobl	0,57	-0,82	0,09
chr5:130071414-130088219	NM_001106671	Ttc22	0,56	-0,82	0,07
chr15:65536299-65537142	NM_0011177863	LOC100360244	0,56	-0,83	0,05
chr18:29309023-29312537	NM_001017932	Wdr55	0,56	-0,83	0,06
chr11:90330972-90332396	NM_001011900	Tssk1b	0,56	-0,83	0,04
chr8:22846153-22875377	NM_001270413	Kank2	0,56	-0,84	0,03
chr14:6336172-6350497	NM_001134998	Zfp951	0,56	-0,85	0,08
chr1:102761011-102766123	NM_175708	Car11	0,55	-0,85	0,04
chr3:1727972-1910422	NM_147141	Cacna1b	0,55	-0,85	0,08
chr8:118086486-118136590	NM_001192000	Kif9	0,55	-0,85	0,05
chr1:23019606-23067373	NM_001277054	Med23	0,55	-0,85	0,01
chr1:102388310-102391914	NM_181369	Hrc	0,55	-0,86	0,05
chr12:26682319-26710272	NM_053788	Stx1a	0,55	-0,86	0,01
chr1:129679808-129753636	NM_001025681	Ttc23	0,55	-0,86	0,04
chr11:46236524-46289103	NM_138897	Gabbr3	0,55	-0,87	0,08
chr5:155917437-155935517	NM_001109269	Lin28a	0,55	-0,87	0,08
chr1:254491232-254511641	NM_001013152	Rcl1	0,54	-0,88	0,03
chr8:70607874-70622107	NM_001108162	Rasl12	0,54	-0,88	0,06
chr3:17021672-17058548	NM_001010968	Eng	0,54	-0,88	0,06
chr3:98939478-98941580	NM_001108955	Fjx1	0,54	-0,88	0,06
chr19:66375690-66396016	NM_207613	Cdh15	0,54	-0,89	0,02
chr5:144433449-144448324	NM_001106683	Mfsd2a	0,54	-0,89	0,06
chr1:79987124-80012891	NM_001107480	Strn4	0,54	-0,89	0,08
chr19:66634978-66651622	NM_001108454	Cpne7	0,53	-0,90	0,02
chr3:166016436-166034838	NM_001107798	Gdap11	0,53	-0,90	0,01
chr2:206548565-206565371	NM_021589	Ntrk1	0,53	-0,90	0,01
chr2:215772301-215783863	NM_001107695	Vps72	0,53	-0,93	0,01
chr1:223521097-223523972	NM_182735	Cdkn1c	0,52	-0,93	0,03
chr14:107724469-107835993	NM_001115022	Commd1	0,52	-0,94	0,03
chr11:64474113-64501029	NM_031518	Cd200	0,52	-0,94	0,00
chrX:54426882-54503311	NM_024381	Gk	0,52	-0,95	0,05
chr1:79667892-79687979	NM_001107479	Npas1	0,51	-0,96	0,03
chr3:180518141-180526234	NM_024346	Stmn3	0,51	-0,96	0,00
chr20:5652153-5671944	NM_001166022	Ddr1	0,51	-0,97	0,10

chr3:145760073-146259490	NM_053505	Slc24a3	0,50	-0,99	0,08
chr7:64146260-64159527	NM_001271273	RGD1565498	0,50	-1,00	0,06
chr12:15261533-15291234	NM_001105910	Grid2ip	0,50	-1,01	0,08
chr11:40265271-40305321	NM_001006990	Igsf5	0,49	-1,02	0,02
chr14:78398567-78443092	NM_001033894	Jakmip1	0,49	-1,02	0,03
chr18:29721077-29924443	NM_053940	Pcdha12	0,49	-1,02	0,03
chr1:102357042-102386710	NM_001136229	Trpm4	0,49	-1,02	0,02
chr15:56016281-56043902	NM_001108385	Dmtn	0,49	-1,03	0,03
chr8:2681124-2708341	NM_130422	Casp12	0,49	-1,03	0,08
chr9:92324920-92346959	NM_001034137	Sp110	0,49	-1,03	0,03
chr2:206762690-206775669	NM_001033665	Bcan	0,49	-1,04	0,07
chrX:114908415-114911848	NM_001013105	Fkbp11	0,48	-1,05	0,07
chr3:127438621-127474675	NM_001108959	Tgm3	0,48	-1,06	0,00
chr10:15379684-15381848	NM_001108269	Arhgdig	0,48	-1,06	0,10
chr3:62983083-63336893	NM_001191901	Myo3b	0,48	-1,07	0,01
chr10:110217248-110227797	NM_001109051	Fn3k	0,47	-1,08	0,04
chr1:90357221-90361689	NM_001198591	Sbsn	0,47	-1,08	0,08
chr16:49189581-49192471	NM_001108400	Ankrd37	0,47	-1,08	0,08
chr9:22278198-22282377	NM_001109502	LOC688459	0,47	-1,10	0,05
chr10:13838166-13839432	NM_153294	Npw	0,47	-1,10	0,01
chr1:182433108-182435280	NM_012715	Adm	0,46	-1,11	0,05
chr17:816034-816131	NR_031826	Mir23b	0,46	-1,11	0,07
chr15:37006428-37010908	NM_022685	Rem2	0,46	-1,13	0,09
chr3:156420460-156434946	NM_001098724	Necab3	0,46	-1,13	0,00
chr6:146081899-146092800	NM_001126280	Tmem179	0,45	-1,14	0,04
chr15:42481019-42544097	NM_001024272	Phf11	0,45	-1,14	0,04
chr1:17189223-17293867	NM_001106270	Map7	0,45	-1,15	0,06
chrX:14802670-14891273	NM_178333	Syt5	0,45	-1,15	0,10
chr8:112491425-112972591	NM_001109003	Cpne4	0,45	-1,16	0,04
chr10:89282481-89291487	NM_001024967	Tmem106a	0,45	-1,16	0,10
chr14:10483115-10523890	NM_022605	Hpse	0,45	-1,16	0,05
chr8:51518447-51531215	NM_001106819	Nnmt	0,45	-1,17	0,03
chr9:16120948-16140296	NM_001108205	Rsph9	0,44	-1,18	0,09
chr6:112512062-112543111	NM_001127566	Plekhd1	0,44	-1,20	0,00
chr1:81329940-81340229	NM_012714	Gipr	0,44	-1,20	0,09
chr19:26581752-26582695	NM_001109380	Capns2	0,43	-1,20	0,06
chr15:30512208-30613262	NM_001108374	RGD1310110	0,43	-1,22	0,07
chr13:53032716-53098045	NM_019365	Rassf5	0,43	-1,22	0,01
chr1:75747872-75750239	NM_001109604	Tmem86b	0,42	-1,24	0,02
chr3:2489157-2516076	NM_001270610	Grin1	0,42	-1,26	0,03
chr19:49952332-49980522	NM_001009640	Cirh1a	0,41	-1,27	0,07
chr9:40677389-40683065	NM_001013226	Prss39	0,41	-1,28	0,02
chr16:20547456-20551180	NM_001271055	Tmem59l	0,41	-1,28	0,06
chr7:121880993-121910618	NM_001130502	Fam83f	0,41	-1,28	0,07
chr1:101459651-101473304	NM_019122	Syt3	0,41	-1,29	0,01
chr8:47959126-47980096	NM_001106818	Mpzi2	0,41	-1,29	0,05
chr15:50429954-50443496	NM_001106044	Tdh	0,41	-1,30	0,05
chr10:39059950-39154295	NM_022270	Slc22a4	0,41	-1,30	0,09
chr15:37092298-37102545	NM_053503	Ajuba	0,40	-1,31	0,00
chr16:20411166-20413750	NM_019216	Gdf15	0,40	-1,33	0,01
chr3:120792937-120826088	NM_153739	Duox1	0,39	-1,35	0,10
chr8:115368434-115402229	NM_001012127	Mapkapk3	0,39	-1,36	0,08
chr1:175550132-175563346	NM_001170461	Trim6	0,39	-1,37	0,09

chr3:78760038-78784936	NM_001107742	Slc43a1	0,39	-1,37	0,04
chr16:81104695-81120110	NM_001013054	Adprhl1	0,39	-1,37	0,07
chr10:66863437-66886611	NM_012977	Lgals9	0,38	-1,38	0,08
chr11:71194912-71226980	NM_001191659	Parp14	0,38	-1,39	0,03
chr2:133400608-133554180	NM_030992	Plid1	0,38	-1,39	0,02
chr10:20494592-20496236	NM_001108824	Fbll1	0,38	-1,41	0,07
chr19:66688876-66703636	NM_053591	Dpep1	0,37	-1,43	0,05
chr1:75683290-75691003	NM_019350	Syt5	0,37	-1,43	0,01
chr11:60668451-60681692	NM_031676	Tagln3	0,37	-1,45	0,07
chr9:98231203-98273371	NM_031678	Per2	0,36	-1,46	0,01
chr4:214084982-214143362	NM_199207	Fam21c	0,36	-1,46	0,03
chr5:24669151-24965951	NM_001108654	Tox	0,36	-1,47	0,03
chr5:83890951-83950462	NM_053861	Tnc	0,36	-1,48	0,07
chr2:206767694-206775669	NM_012916	Bcan	0,35	-1,50	0,01
chr10:56321560-56323747	NM_031702	Cldn7	0,35	-1,52	0,04
chr10:102925917-102959579	NM_001007726	Dnai2	0,35	-1,53	0,00
chr1:90620341-90629734	NM_001270688	Fxyd5	0,34	-1,55	0,00
chr15:31552645-31566205	NM_001025141	Ccnb1ip1	0,34	-1,56	0,01
chr16:7231863-7243496	NM_001100882	Sema3g	0,33	-1,58	0,00
chr16:24663044-24671859	NM_001113357	Npy1r	0,33	-1,58	0,07
chr7:70512762-70517707	NM_053763	Cyp27b1	0,32	-1,64	0,01
chr1:220817753-220826497	NM_001024887	Sigirr	0,32	-1,66	0,00
chr8:118480841-118495446	NM_001109299	Tmie	0,31	-1,69	0,07
chr18:29734136-29924444	NM_053934	Pcdha13	0,30	-1,76	0,01
chr5:138803949-138808976	NM_001004236	Tspan1	0,28	-1,81	0,06
chr3:2489157-2516076	NM_001270608	Grin1	0,28	-1,85	0,00
chr3:120780502-120790938	NM_001107767	Duoxa1	0,27	-1,90	0,00
chrX:106632885-106634404	NM_001024267	MGC109340	0,27	-1,91	0,03
chr9:46849568-46858893	NM_013037	Il1rl1	0,26	-1,96	0,02
chr13:57693624-57707987	NM_001107942	Lad1	0,26	-1,96	0,08
chr10:94222777-94228959	NM_021673	Tcam1	0,25	-1,98	0,04
chr6:118021323-118026536	NM_001109440	Acot4	0,25	-1,98	0,01
chr1:243883282-243888286	NM_022276	Gcnt1	0,25	-1,99	0,01
chrX:19487953-19491373	NM_001108251	Ubqln2	0,25	-2,00	0,00
chr6:43852754-43872213	NM_001108013	Matn3	0,25	-2,02	0,00
chr10:12823134-12825903	NM_001102364	Cldn6	0,23	-2,11	0,03
chrX:112046206-112109823	NM_053623	Acsl4	0,23	-2,12	0,03
chr18:23893018-23902428	NM_031693	Syt4	0,23	-2,12	0,04
chr1:102742036-102743268	NM_001135584	Sec1	0,22	-2,16	0,03
chr17:44033615-44094176	NM_001197023	RGD1307443	0,22	-2,21	0,00
chr20:16153342-16160769	NM_001106381	Susd2	0,21	-2,26	0,01
chr19:49635964-49705893	NM_031334	Cdh1	0,20	-2,29	0,07
chr18:47585433-47598040	NM_001004215	Ppic	0,20	-2,29	0,00
chr3:144374720-144408658	NM_031555	Bfsp1	0,19	-2,39	0,00
chr18:37253264-37362844	NM_001191894	Stk32a	0,18	-2,50	0,03
chr1:90620341-90629734	NM_021909	Fxyd5	0,17	-2,52	0,01
chr6:137256802-137272264	NM_182474	LOC299282	0,16	-2,66	0,01
chr3:136182050-136269422	NM_001270575	Snap25	0,14	-2,82	0,02
chr2:219959693-219989012	NM_031620	Phgdh	0,13	-2,92	0,01
chr7:15357399-15384091	NM_153318	Cyp4f6	0,13	-2,95	0,08
chr2:275974236-276052941	NM_001037210	Gipc2	0,13	-2,98	0,01
chr1:23331544-23334660	NM_022266	Ctgf	0,12	-3,11	0,09
chr10:51439730-51534448	NM_182667	Myocd	0,11	-3,15	0,00

chr2:282680843-282760556	NM_012704	Ptger3	0,11	-3,16	0,02
chr5:81394855-82071201	NM_058209	Zfp37	0,11	-3,17	0,04
chr18:40348060-40362704	NM_052809	Cdo1	0,11	-3,21	0,00
chr15:38342433-38358253	NM_019285	Adcy4	0,11	-3,23	0,00
chr12:13876609-13900957	NM_001170399	Tmem130	0,10	-3,31	0,09
chr7:123291486-123344883	NM_001130555	Mei1	0,09	-3,52	0,07
chr11:34833564-34848516	NM_001109052	RGD1562726	0,07	-3,81	0,00
chr18:80511682-80534735	NM_001007687	Cndp1	0,06	-4,05	0,01
chr19:36128872-36140835	NM_001105943	Il27ra	0,06	-4,07	0,00
chr16:8808682-8809939	NM_031581	Npy4r	0,05	-4,23	0,05
chr14:37251450-37267486	NM_001271181	Ociad2	0,05	-4,29	0,03
chr8:22373290-22391178	NM_001108996	Ap1m2	0,05	-4,33	0,00
chr10:15275266-15279122	NM_001109478	Nme4	0,04	-4,77	0,00
chrX:78689824-78695767	NM_001025712	Itm2a	0,03	-4,92	0,09
chr5:159968603-160068655	NM_053596	Ece1	0,02	-5,43	0,01
chr10:87848517-87853235	NM_199498	Krt19	0,02	-5,48	0,04
chr13:54410795-54489201	NM_001160313	Nfasc	0,02	-5,65	0,00
chr4:245073410-245110560	NM_001011970	Tm7sf3	0,02	-5,88	0,00

Supporting Table S5. List of genes which expression was significantly changed upon MAX expression in URMax34 cells with silenced MNT. Two independent RNAseq experiments were carried out to compare the transcriptomes of MNT-silenced URMax34 cells expressing MAX (upon 24h of Zn²⁺treatment) and MNT-silenced URMT without MAX (but also treated with Zn²⁺). Max34 without MAX. Relative RNA amounts were calculated as FPKM fold change (FC). Data are mean values of the two independent transfections where log₂FC was > 0.7 or < -0.7 (i.e., ≥1.6 fold and ≤0.5 fold), and a p-value <0.1.

			URMax34 sh-MNT vs URMT sh-MNT		
locus	gene_id	Gene	FC	Log2FC	p-value
chr13:91028025-91307272	NM_001134862	Pbx1	11,90	3,57	0,01
chr19:10638465-10647951	NM_134455	Cx3cl1	10,26	3,36	0,01
chr9:54940737-54952755	NM_001007712	Sdpr	9,45	3,24	0,00
chr20:14931525-14959214	NM_001100741	Col6a2	8,47	3,08	0,04
chr9:66602088-66639739	NM_199400	Ica1l	7,70	2,95	0,01
chr7:119772956-119786147	NM_001008384	Rac2	6,81	2,77	0,00
chr9:50936853-51211198	NM_001013171	Gulp1	6,30	2,66	0,03
chr4:222704905-222711635	NM_032060	C3ar1	6,00	2,58	0,03
chr15:14166282-14307995	NM_031529	Rarb	5,72	2,52	0,08
chrX:122958361-122961547	NM_001014065	Zcchc12	5,43	2,44	0,05
chr20:12340709-12405855	NM_138543	Pde9a	5,37	2,42	0,05
chr6:109380102-109403573	NM_022210	Max	5,27	2,40	0,00
chr6:7897004-7916593	NM_130414	Abcg8	4,89	2,29	0,03
chr14:84201086-84203507	NR_102354	Patz1	4,80	2,26	0,06
chr5:158368888-158402121	NM_001015008	Tcea3	4,64	2,21	0,01
chr1:82066234-82075018	NM_001198970	Ceacam19	4,57	2,19	0,07
chr7:107517378-107566621	NM_178097	Sla	4,56	2,19	0,00
chr9:64973841-65072436	NM_001008522	Aox2	4,51	2,17	0,06
chr8:118666368-118668671	NM_001108191	Ccl2	4,50	2,17	0,04
chr13:53499149-53521602	NM_012938	Ctse	4,50	2,17	0,03
chr1:200297800-200387135	NM_001270694	Arhgap17	4,39	2,13	0,10
chr1:200246642-200285416	NM_001100482	Slc5a11	4,29	2,10	0,02
chr10:81951028-82017885	NM_031601	Cacna1g	4,24	2,08	0,01
chr14:78978023-79077775	NM_001113365	Tbc1d14	4,05	2,02	0,03
chr9:93495137-93886547	NM_001109007	Dis3l2	3,79	1,92	0,02
chr6:7871268-7896799	NM_053754	Abcg5	3,74	1,90	0,08
chr2:269282796-269305090	NM_001013202	Clca2	3,69	1,88	0,09
chr7:44175397-44207232	NM_022959	Rassf9	3,61	1,85	0,05
chrX:907617-910801	NM_001108058	Spaca5	3,50	1,81	0,03
chr11:37902942-37942470	NM_001107108	Sim2	3,43	1,78	0,06
chr1:10501324-10503331	NM_001197092	Gje1	3,42	1,78	0,00
chr1:245192874-245208894	NM_012904	Anxa1	3,41	1,77	0,09
chr8:115761398-115777438	NM_145776	Slc38a3	3,31	1,73	0,01
chr5:37832722-37840896	NM_001271109	Maged2	3,17	1,67	0,07
chr1:144308591-144336257	NM_001191627	Fsd2	3,15	1,66	0,04
chr7:126136631-126178957	NM_001009695	Wnt7b	3,15	1,66	0,04
chr7:141009310-141017951	NM_001008825	Kb15	3,14	1,65	0,09
chr6:141004476-141096652	NM_001277288	Bcl11b	3,11	1,64	0,00
chr2:209437962-209439970	NM_001106438	S100a5	3,09	1,63	0,08
chr3:15086725-15098070	NM_021583	Ptges	3,04	1,60	0,07

chr9:95085453-95170100	NM_134371	Trpm8	3,02	1,60	0,03
chr19:63411525-63452571	NM_138518	Crispld2	3,01	1,59	0,02
chr7:63077687-63147646	NM_053738	Wif1	2,95	1,56	0,01
chr18:55104199-55125190	NM_021695	Synpo	2,89	1,53	0,02
chr15:55935054-55937997	NM_017342	Sftpc	2,83	1,50	0,05
chr20:6186326-6205191	NM_001164826	RT1-Db2	2,81	1,49	0,08
chr18:55596757-55637692	NM_031525	Pdgfrb	2,77	1,47	0,04
chr16:70925603-70965251	NM_024146	Fgfr1	2,75	1,46	0,01
chr19:10300708-10319286	NM_001103352	Kifc3	2,75	1,46	0,06
chr6:22325768-22342414	NM_182954	Ston1	2,73	1,45	0,04
chr5:170557218-170568525	NM_001107994	Spsb1	2,72	1,44	0,05
chr4:57644769-57668743	NM_001109346	Cpa4	2,70	1,43	0,06
chr16:6889472-6891723	NM_181368	Mustn1	2,68	1,42	0,08
chr5:161263764-161274897	NM_031609	Nbl1	2,67	1,42	0,08
chr20:44693251-44698950	NM_001271090	Marcks	2,65	1,41	0,06
chr14:32929168-32944266	NM_031788	Rest	2,63	1,40	0,02
chr16:50093093-50220784	NM_031819	Fat1	2,61	1,39	0,00
chr6:124654249-124765198	NM_001135874	Ston2	2,60	1,38	0,05
chr2:278043762-278563294	NM_019123	St6galnac3	2,56	1,36	0,01
chr13:56075045-56086477	NM_053560	Chi3l1	2,55	1,35	0,03
chr1:222524151-222557295	NM_001025420	Lsp1	2,51	1,33	0,07
chr20:6167758-6177328	NM_001008884	RT1-Db1	2,51	1,33	0,02
chr15:91201296-91315612	NM_001108388	Scel	2,48	1,31	0,06
chr13:55296140-55315101	NM_001047925	LOC498231	2,47	1,31	0,04
chr10:83934226-83935978	NM_001191649	Hoxb8	2,46	1,30	0,07
chr12:26978747-27022485	NM_012722	Eln	2,44	1,29	0,07
chr16:20154957-20164945	NM_052983	Slc5a5	2,39	1,26	0,01
chr19:10403000-10442286	NM_152242	Gpr56	2,36	1,24	0,00
chr11:93462644-93464954	NM_013035	Snai2	2,29	1,20	0,07
chr1:48926485-48987223	NM_001038615	Fndc1	2,28	1,19	0,09
chr4:26377856-26382255	NM_021266	Fzd1	2,23	1,16	0,00
chr9:94943843-94990037	NM_001039549	Ugt1a5	2,20	1,14	0,09
chr8:68290926-68397727	NM_013095	Smad3	2,17	1,12	0,05
chr11:74052399-74092525	NM_001014230	lqcg	2,16	1,11	0,10
chr9:10049872-10055404	NM_001025026	Stap2	2,15	1,11	0,02
chr19:68936976-69098880	NM_001009704	Sipa1l2	2,12	1,09	0,05
chr13:65831385-65833989	NM_053453	Rgs2	2,10	1,07	0,01
chr14:79829770-79857492	NM_001107226	Sh3tc1	2,10	1,07	0,02
chr15:29220348-29287363	NM_001170475	RGD1562018	2,07	1,05	0,03
chr2:168229961-168256064	NM_001024300	Fam194a	2,07	1,05	0,10
chr8:63367892-63405310	NM_021658	Hcn4	2,07	1,05	0,10
chr2:228956378-229004197	NM_012523	Cd53	2,06	1,05	0,08
chr10:47568778-47630470	NM_001033914	Epn2	2,06	1,04	0,04
chr14:113634941-113673627	NM_001013877	Clhc1	2,04	1,03	0,00
chr2:249539690-249552032	NM_001271984	Casp6	2,02	1,01	0,02
chr5:120364856-120694011	NM_012988	Nfia	2,02	1,01	0,05
chr7:117215918-117244741	NM_001164304	Plec	2,01	1,01	0,05
chr8:115795105-115824684	NM_001108185	Sema3f	2,01	1,01	0,04
chr8:36673131-36725976	NM_017358	Cdon	2,01	1,01	0,03
chr4:58581529-58628225	NM_138848	Podxl	1,98	0,99	0,07
chr5:155061362-155062328	NM_153727	Gpr3	1,96	0,97	0,01
chr7:93245560-93521935	NM_001130540	Ext1	1,95	0,96	0,01
chr3:123424950-123482782	NM_001107768	Sema6d	1,95	0,96	0,01

chr14:7662573-7837443	NM_001100789	Ptpn13	1,94	0,95	0,06
chr8:116474846-116519375	NM_001106093	Usp4	1,93	0,95	0,06
chr4:224761676-224766884	NM_001024335	Cd27	1,93	0,95	0,03
chr1:102151856-102161139	NM_033351	Fcgrt	1,93	0,95	0,06
chr5:174800869-174803561	NM_001163723	Smim1	1,92	0,94	0,05
chr12:49914426-50000957	NM_053922	Acacb	1,92	0,94	0,01
chr19:71984686-72136036	NM_145098	Nrp1	1,91	0,93	0,04
chr13:33035660-33058982	NM_001105948	Serpinb8	1,91	0,93	0,05
chr10:39171367-39185480	NM_017062	Pdlim4	1,91	0,93	0,03
chr17:17506165-17526899	NM_001106103	Ogn	1,90	0,93	0,04
chr10:106973462-107021070	NM_021989	Timp2	1,90	0,93	0,03
chr5:161781671-161822396	NM_001134703	Iffo2	1,89	0,92	0,02
chr2:208065968-208070220	NM_001107692	Efna4	1,89	0,92	0,04
chr13:118334938-118366003	NM_019190	Cd46	1,88	0,91	0,05
chr19:44812397-44874904	NM_012550	Ednra	1,88	0,91	0,01
chr6:34010477-34031267	NM_001129880	Lbh	1,88	0,91	0,03
chr14:2015650-2027710	NM_199114	Fgfr11	1,88	0,91	0,03
chr10:67333795-67387701	NM_001105819	Rhbdl3	1,87	0,91	0,03
chr3:88516995-88555163	NM_030839	Syt13	1,87	0,91	0,06
chr2:1422024-1530718	NM_001033716	Cast	1,87	0,90	0,05
chr10:58690457-58711606	NM_001190998	Smtnl2	1,86	0,89	0,01
chr4:187052886-187078591	NM_001037492	Slc41a3	1,85	0,89	0,06
chr19:72324611-72372325	NM_017022	Itgb1	1,85	0,89	0,01
chr19:829210-836078	NM_001106164	Cmtm3	1,85	0,89	0,01
chr5:156559977-156703434	NM_001108687	Man1c1	1,85	0,88	0,07
chr2:18553025-18803145	NM_001006999	Xrcc4	1,84	0,88	0,01
chr8:44272941-44275041	NR_037614	Vof16	1,84	0,88	0,00
chr13:95665161-95678254	NM_053843	Fcgr2a	1,83	0,87	0,04
chr12:49492069-49529956	NM_023970	Trpv4	1,83	0,87	0,05
chr18:55428486-55529045	NM_012920	Camk2a	1,83	0,87	0,05
chrX:34657416-35015678	NM_001191733	Nhs	1,82	0,86	0,05
chr4:184767520-184819739	NM_001173382	Aplf	1,82	0,86	0,02
chr4:234409180-234409665	NM_001109610	H2afj	1,81	0,86	0,04
chr2:1422024-1530718	NM_001033715	Cast	1,81	0,86	0,02
chr17:29366866-29405082	NM_001012052	Cage1	1,81	0,86	0,00
chr7:71218205-71221052	NM_053302	Gpr182	1,81	0,86	0,01
chr13:31126926-31161268	NM_001271042	Zcchc2	1,81	0,86	0,00
chr3:55291464-55326008	NM_001106483	Gca	1,79	0,84	0,08
chr2:279546018-279573473	NM_001012183	Cryz	1,79	0,84	0,01
chr5:172507288-172577540	NM_001195560	Camta1	1,79	0,84	0,02
chr17:43952823-43995477	NM_001100512	Gpld1	1,79	0,84	0,03
chr2:222244278-222262430	NM_001014041	Fam46c	1,76	0,82	0,03
chr2:50895263-50965217	NM_013005	Pik3r1	1,75	0,81	0,01
chr12:16120531-16185309	NM_001037218	Radil	1,75	0,81	0,02
chr9:2150779-2221991	NM_001012129	Satb1	1,74	0,80	0,04
chr5:62404325-62409772	NM_001108971	RGD1309821	1,74	0,80	0,01
chr12:45839707-45861437	NM_057130	Hrk	1,74	0,80	0,02
chr16:21219920-21253490	NM_001108399	Pbx4	1,74	0,80	0,06
chr2:124140060-124182032	NM_001012218	Trim55	1,74	0,79	0,09
chr8:59844139-59860388	NM_001100722	Lingo1	1,73	0,79	0,09
chr10:77616853-77645126	NM_001007673	Mmd	1,73	0,79	0,08
chr16:7274367-7336001	NM_001033655	Dnah1	1,72	0,78	0,05
chr7:71743894-71856340	NM_013082	Sdc2	1,72	0,78	0,04

chr2:202860603-202896104	NM_001106437	Fhdc1	1,72	0,78	0,04
chrX:30995484-31214065	NM_012568	Glra2	1,72	0,78	0,08
chrX:56243028-56310184	NM_052803	Atp7a	1,72	0,78	0,08
chr4:242270808-242641501	NM_001271267	Sox5	1,71	0,77	0,00
chr1:236425416-236500554	NM_001170606	Spink5	1,70	0,77	0,02
chr7:120839736-120881869	NM_001130581	RGD1305939	1,70	0,77	0,02
chr16:7408995-7472907	NM_054011	Sh3bp5	1,70	0,77	0,04
chr15:62249642-62348601	NM_001109912	Tsc22d1	1,69	0,76	0,07
chr11:72575015-73115328	NM_032062	Kalrn	1,69	0,76	0,01
chr19:10558224-10568896	NM_001108438	Dok4	1,69	0,75	0,04
chr2:226696251-226717439	NM_001107711	Mov10	1,69	0,75	0,09
chr13:95687141-95697538	NM_001135992	LOC498276	1,69	0,75	0,03
chr13:57244748-57248270	NM_001077826	Shisa4	1,69	0,75	0,08
chr19:28182501-28274100	NM_001107414	Rpgrip1l	1,68	0,75	0,04
chr5:157338298-157394464	NM_031818	Clic4	1,68	0,75	0,01
chr8:131995142-132061908	NM_001106870	Fyco1	1,68	0,75	0,10
chr7:124006941-124024503	NM_138877	Cyb5r3	1,68	0,74	0,04
chr8:36428865-36434949	NM_001034150	Srpr	1,67	0,74	0,00
chr7:120742980-120753160	NM_001127546	Kdelr3	1,66	0,73	0,06
chr2:123767823-123856129	NM_031080	Pde7a	1,66	0,73	0,07
chr9:95916237-95994390	NM_022693	Sh3bp4	1,66	0,73	0,02
chr14:81671044-81742380	NM_019339	Rgs12	1,66	0,73	0,02
chr6:1912345-1932818	NM_001048044	Cdc42ep3	1,65	0,72	0,06
chr13:74881864-75145652	NM_001105957	Rgl1	1,64	0,72	0,06
chrX:69764313-69777121	NM_017089	Efnb1	1,64	0,71	0,01
chrX:80392504-80491085	NM_001173339	Sh3bgrl	1,64	0,71	0,04
chr4:163912883-163925865	NM_001009413	Krcc1	1,64	0,71	0,01
chr3:68123928-68135819	NM_001271038	Hoxd3	1,63	0,71	0,10
chr19:33045246-33289198	NM_001014152	Phkb	1,63	0,71	0,05
chr2:217293449-217305079	NM_001034012	Adamts4	1,63	0,70	0,02
chr1:175586829-175603800	NM_001014023	Trim5	0,61	-0,71	0,00
chr1:198729099-198856174	NM_001100519	Gga2	0,61	-0,71	0,07
chr3:116411044-116422101	NM_001013062	Thbs1	0,61	-0,72	0,09
chr1:75563121-75590916	NM_001108468	Rdh13	0,61	-0,72	0,03
chr3:117272041-117274099	NM_001109639	Chst14	0,61	-0,72	0,08
chrX:115875187-115882578	NM_022215	Gpd1	0,61	-0,72	0,08
chr3:62983083-63336893	NM_001191901	Myo3b	0,61	-0,72	0,05
chr5:168904230-168915829	NM_001107993	Ubiad1	0,60	-0,73	0,06
chr19:66375690-66396016	NM_207613	Cdh15	0,60	-0,73	0,03
chr9:98231203-98273371	NM_031678	Per2	0,60	-0,73	0,04
chr18:29657321-29924443	NM_199504	Pcdha2	0,60	-0,74	0,06
chr10:83040795-83121507	NM_001100496	Spop	0,60	-0,74	0,04
chr19:48776574-48779058	NM_001025637	Psmb10	0,60	-0,74	0,07
chr8:131412947-131449580	NM_001106869	Cdcp1	0,60	-0,74	0,06
chr18:69873083-69901836	NM_130433	Acaa2	0,60	-0,74	0,08
chr17:43671712-43689290	NM_001106109	Nrsn1	0,60	-0,75	0,08
chr12:41579809-41610545	NM_001030042	Rad9b	0,59	-0,75	0,01
chr3:78845159-78865590	NM_001107743	Slc43a3	0,59	-0,77	0,07
chr17:33336064-33339112	NM_001013886	Tubb2b	0,59	-0,77	0,06
chr9:79264979-79318250	NM_001192002	Mreg	0,59	-0,77	0,02
chrX:16460416-16467277	NM_001014109	Magix	0,58	-0,78	0,05
chr1:23019606-23067373	NM_001277054	Med23	0,58	-0,79	0,00
chr1:81329940-81340229	NM_012714	Gipr	0,58	-0,79	0,08

chr3:127438621-127474675	NM_001108959	Tgm3	0,58	-0,79	0,04
chr1:106145090-106159702	NM_001106263	Htati2	0,57	-0,80	0,05
chr8:14190845-14252439	NM_001014087	Ccdc67	0,57	-0,81	0,01
chr5:139471944-139473551	NM_001014068	Hpdl	0,57	-0,82	0,10
chr2:206548565-206565371	NM_021589	Ntrk1	0,57	-0,82	0,04
chr8:58696063-58700544	NM_020471	Isl2	0,56	-0,83	0,08
chr1:254491232-254511641	NM_001013152	Rcl1	0,56	-0,84	0,01
chr6:33101205-33183386	NM_001013942	Clip4	0,56	-0,84	0,02
chr2:209331130-209333683	NM_001007636	S100a1	0,55	-0,85	0,08
chr20:5652153-5671944	NM_001166022	Ddr1	0,55	-0,86	0,01
chr8:22846153-22875377	NM_001270413	Kank2	0,55	-0,86	0,06
chr15:16597090-16611887	NM_001271294	Thoc7	0,55	-0,87	0,04
chr3:156420460-156434946	NM_001098724	Necab3	0,54	-0,88	0,00
chr10:110217248-110227797	NM_001109051	Fn3k	0,54	-0,88	0,03
chr6:112512062-112543111	NM_001127566	Plekhd1	0,54	-0,88	0,01
chr4:216439331-216457348	NM_001127635	Zfp9	0,54	-0,89	0,04
chr14:78398567-78443092	NM_001033894	Jakmip1	0,54	-0,89	0,04
chr2:230202465-230207240	NM_001109192	Gstm6	0,54	-0,89	0,07
chr3:170425897-170430384	NM_053805	Snai1	0,54	-0,90	0,02
chr3:149431211-149473190	NM_001191966	Napb	0,54	-0,90	0,07
chr1:75683290-75691003	NM_019350	Syt5	0,53	-0,91	0,02
chr1:102357042-102386710	NM_001136229	Trpm4	0,53	-0,91	0,06
chr19:65037337-65053996	NM_001008722	Irf8	0,53	-0,91	0,02
chr1:225500670-225518961	NM_001012069	Mtl5	0,53	-0,92	0,00
chrX:54426882-54503311	NM_024381	Gk	0,53	-0,92	0,03
chr7:15045083-15061272	NM_173123	Cyp4f4	0,53	-0,92	0,10
chr7:99752107-99775780	NM_001134844	Cyp2b1	0,51	-0,97	0,01
chr1:79667892-79687979	NM_001107479	Npas1	0,50	-0,99	0,04
chr5:144433449-144448324	NM_001106683	Mfsd2a	0,50	-1,00	0,03
chr1:173176766-173178816	NM_001139494	Tomt	0,50	-1,00	0,04
chr1:221068625-221076442	NM_001270762	Rnh1	0,50	-1,01	0,05
chr14:10483115-10523890	NM_022605	Hpse	0,50	-1,01	0,02
chr1:273913119-273945394	NM_080890	As3mt	0,49	-1,02	0,06
chr1:84361235-84376889	NM_001198676	Cyp2b2	0,49	-1,02	0,07
chr11:64474113-64501029	NM_031518	Cd200	0,49	-1,03	0,09
chr17:38499152-38517524	NM_001106108	Irf4	0,49	-1,03	0,06
chr9:92324920-92346959	NM_001034137	Sp110	0,49	-1,03	0,02
chr15:107450002-107539150	NM_001106058	Cldn10	0,49	-1,04	0,09
chr14:79875404-79903558	NM_001271027	Htra3	0,49	-1,04	0,04
chr5:155079202-155083511	NM_001271259	LOC100359977	0,48	-1,05	0,01
chr9:97995668-98041718	NM_031645	Ramp1	0,48	-1,06	0,05
chr10:13838166-13839432	NM_153294	Npw	0,48	-1,06	0,00
chr4:248136720-248283930	NM_001108653	Bicd1	0,47	-1,08	0,03
chr1:172227725-172241918	NM_017255	P2ry2	0,46	-1,11	0,02
chr1:223521097-223523972	NM_182735	Cdkn1c	0,46	-1,12	0,04
chr6:146081899-146092800	NM_001126280	Tmem179	0,46	-1,12	0,05
chr3:78760038-78784936	NM_001107742	Slc43a1	0,46	-1,13	0,00
chr3:112080852-112086389	NM_019183	Actc1	0,45	-1,14	0,10
chr1:101459651-101473304	NM_019122	Syt3	0,45	-1,14	0,06
chr18:30598590-30662065	NM_001037153	Pcdhga11	0,45	-1,16	0,03
chr7:121880993-121910618	NM_001130502	Fam83f	0,43	-1,20	0,07
chr15:37092298-37102545	NM_053503	Ajuba	0,43	-1,21	0,01
chr13:53032716-53098045	NM_019365	Rassf5	0,43	-1,21	0,01

chr1:90620341-90629734	NM_021909	Fxyd5	0,43	-1,22	0,06
chr14:17144965-17150220	NM_145672	Cxcl9	0,43	-1,22	0,03
chr6:39849236-39859320	NM_001009503	Pfn4	0,43	-1,22	0,04
chr3:166421476-166427695	NM_130813	Kcnk15	0,43	-1,23	0,06
chr7:11846110-11866956	NM_001047100	Tmprss9	0,42	-1,24	0,07
chr2:206767694-206775669	NM_012916	Bcan	0,42	-1,25	0,04
chr7:130227694-130233848	NM_012490	Acr	0,42	-1,26	0,04
chr4:61426189-61440279	NM_012498	Akr1b1	0,42	-1,26	0,04
chr4:214084982-214143362	NM_199207	Fam21c	0,41	-1,27	0,04
chr7:70512762-70517707	NM_053763	Cyp27b1	0,41	-1,28	0,04
chr10:39059950-39154295	NM_022270	Slc22a4	0,41	-1,29	0,09
chr12:43140729-43149670	NM_001009492	Oas1e	0,41	-1,29	0,08
chr17:61491660-61536165	NM_001170421	RGD1560860	0,41	-1,30	0,10
chrX:105506648-105511422	NM_001014274	Armox2	0,41	-1,30	0,07
chr5:2044600-2060375	NM_001270561	Tceb1	0,40	-1,31	0,01
chr2:206567014-206586422	NM_022212	Insrr	0,40	-1,33	0,09
chr13:32603845-32612855	NM_021696	Serpnb2	0,40	-1,33	0,08
chr14:81655784-81662339	NM_053320	Hgfac	0,40	-1,33	0,05
chr17:12099382-12113632	NM_001109904	Fgfr4	0,39	-1,34	0,02
chr4:182157292-182163978	NM_021668	Cml1	0,39	-1,36	0,08
chr19:11300013-11301422	NM_053968	Mt3	0,39	-1,36	0,10
chr14:32803850-32863715	NM_001013048	Igfbp7	0,39	-1,38	0,09
chrX:106632885-106634404	NM_001024267	MGC109340	0,38	-1,38	0,03
chr18:29734136-29924444	NM_053934	Pcdha13	0,38	-1,39	0,03
chr11:80084426-80096284	NM_001108321	Rtp4	0,38	-1,40	0,02
chr1:220817753-220826497	NM_001024887	Sigirr	0,38	-1,41	0,01
chr3:163763404-164548723	NM_001108603	Ptprt	0,38	-1,41	0,01
chr12:21132925-21173248	NM_147206	Cyp3a9	0,38	-1,41	0,09
chr7:116315541-116320534	NM_139257	Ly6i	0,38	-1,41	0,09
chr7:130033125-130035751	NM_001191992	Odf3b	0,38	-1,41	0,03
chr9:17529435-17658373	NM_001278484	Runx2	0,37	-1,44	0,04
chr3:120792937-120826088	NM_153739	Duox1	0,37	-1,44	0,00
chr2:207013097-207025362	NM_183054	Rhbg	0,37	-1,45	0,08
chr8:47189964-47196426	NM_001013953	Ccdc153	0,36	-1,46	0,03
chr16:18560491-18578747	NM_012860	Mat1a	0,36	-1,46	0,02
chr8:118480841-118495446	NM_001109299	Tmie	0,36	-1,48	0,09
chr8:115368434-115402229	NM_001012127	Mapkapk3	0,35	-1,51	0,02
chr3:167704323-167719149	NM_134360	Cd40	0,34	-1,54	0,05
chr3:120757632-120775379	NM_024141	Duox2	0,34	-1,57	0,08
chr10:66863437-66886611	NM_012977	Lgals9	0,34	-1,58	0,00
chrX:14802670-14891273	NM_178333	Sytl5	0,33	-1,61	0,03
chr3:145760073-146259490	NM_053505	Slc24a3	0,33	-1,61	0,03
chr15:31552645-31566205	NM_001025141	Ccnb1ip1	0,33	-1,62	0,01
chr3:2489157-2516076	NM_001287423	Grin1	0,32	-1,64	0,02
chr4:61550784-61566177	NM_001013084	Akr1b10	0,32	-1,65	0,08
chrX:112046206-112109823	NM_053623	Acsf4	0,32	-1,65	0,01
chr1:90620341-90629734	NM_001270688	Fxyd5	0,32	-1,65	0,02
chr14:80414798-80429940	NM_001134843	Myo1g	0,31	-1,70	0,03
chr19:36141374-36143406	NM_170667	Rln3	0,30	-1,73	0,01
chr4:222552994-222560653	NM_001100781	Nanog	0,30	-1,73	0,05
chr16:7231863-7243496	NM_001100882	Sema3g	0,29	-1,77	0,05
chr13:57693624-57707987	NM_001107942	Lad1	0,29	-1,78	0,05
chr4:61491239-61503814	NM_173136	Akr1b8	0,29	-1,78	0,09

chr14:22767861-22770928	NM_020103	Ly6c	0,29	-1,79	0,05
chr1:88347072-88355439	NM_053806	Kcnk6	0,29	-1,79	0,07
chr1:227783723-227790741	NM_001005907	Efemp2	0,28	-1,82	0,02
chr9:18970747-19071542	NM_139110	Gpr116	0,27	-1,87	0,03
chr8:129596189-129601706	NM_001108195	Klhl40	0,27	-1,88	0,06
chr5:24669151-24965951	NM_001108654	Tox	0,27	-1,90	0,08
chr11:71194912-71226980	NM_001191659	Parp14	0,26	-1,94	0,09
chr18:37253264-37362844	NM_001191894	Stk32a	0,26	-1,94	0,02
chr18:29715167-29924443	NM_199486	Pcdha11	0,24	-2,06	0,04
chrX:19487953-19491373	NM_001108251	Ubqln2	0,24	-2,07	0,01
chr9:22278198-22282377	NM_001109502	LOC688459	0,24	-2,07	0,01
chr2:108055052-108086130	NM_001134993	Car13	0,23	-2,13	0,00
chr13:53816773-53837091	NM_001135868	Slc45a3	0,23	-2,15	0,06
chr10:94317973-94324597	NM_001007725	Icam2	0,22	-2,15	0,01
chr18:23893018-23902428	NM_031693	Syt4	0,22	-2,16	0,05
chr2:219959693-219989012	NM_031620	Phgdh	0,22	-2,17	0,08
chr1:105206458-105217109	NM_057144	Csrp3	0,22	-2,20	0,01
chr1:273313711-273317540	NM_001107602	Elovl3	0,21	-2,24	0,01
chr16:10789826-10819506	NM_145767	Drgx	0,21	-2,25	0,03
chr5:83890951-83950462	NM_053861	Tnc	0,21	-2,25	0,05
chr18:47585433-47598040	NM_001004215	Ppic	0,21	-2,27	0,01
chr10:94222777-94228959	NM_021673	Tcam1	0,21	-2,28	0,05
chr10:12823134-12825903	NM_001102364	Cldn6	0,20	-2,29	0,05
chr1:74887895-74892461	NM_001076793	Lilra5	0,20	-2,30	0,02
chr3:120780502-120790938	NM_001107767	Duoxa1	0,20	-2,33	0,00
chr7:15357399-15384091	NM_153318	Cyp4f6	0,20	-2,35	0,05
chr20:16153342-16160769	NM_001106381	Susd2	0,20	-2,36	0,01
chr2:63940890-63944583	NM_001106411	Gpx8	0,19	-2,36	0,07
chr9:9062244-9093541	NM_001106875	Acer1	0,18	-2,45	0,01
chr4:214721213-214723298	NM_001024334	LOC500300	0,18	-2,45	0,00
chr7:101766568-101787337	NM_001008878	LOC362921	0,17	-2,54	0,07
chr1:267630219-267697917	NM_001025767	Blnk	0,17	-2,55	0,09
chr17:44033615-44094176	NM_001197023	RGD1307443	0,17	-2,57	0,00
chr8:72072134-72125119	NM_001080756	Car12	0,15	-2,72	0,07
chr8:2681124-2708341	NM_130422	Casp12	0,14	-2,80	0,08
chr2:282680843-282760556	NM_012704	Ptger3	0,13	-2,97	0,01
chr2:275974236-276052941	NM_001037210	Gipc2	0,12	-3,01	0,02
chr19:49635964-49705893	NM_031334	Cdh1	0,12	-3,06	0,02
chr6:57146299-57530068	NM_053888	Myt1l	0,11	-3,19	0,07
chr7:123291486-123344883	NM_001130555	Mei1	0,10	-3,30	0,09
chr16:8808682-8809939	NM_031581	Npy4r	0,10	-3,38	0,04
chr3:144374720-144408658	NM_031555	Bfsp1	0,09	-3,43	0,01
chr9:65342447-65389220	NM_001033864	Cflar	0,09	-3,51	0,03
chr11:34833564-34848516	NM_001109052	RGD1562726	0,08	-3,59	0,02
chr8:22373290-22391178	NM_001108996	Ap1m2	0,08	-3,66	0,04
chr15:38342433-38358253	NM_019285	Adcy4	0,08	-3,74	0,01
chr19:36128872-36140835	NM_001105943	Il27ra	0,06	-4,00	0,01
chr18:80511682-80534735	NM_001007687	Cndp1	0,06	-4,06	0,00
chr5:81394855-82071201	NM_058209	Zfp37	0,05	-4,21	0,06
chr18:40348060-40362704	NM_052809	Cdo1	0,05	-4,27	0,03
chr18:29810768-29924443	NM_199509	Pcdhac1	0,05	-4,35	0,09
chr5:159968603-160068655	NM_053596	Ece1	0,04	-4,57	0,01
chr10:15275266-15279122	NM_001109478	Nme4	0,04	-4,70	0,00

chr14:37251450-37267486	NM_001271181	Ociad2	0,03	-4,92	0,04
chrX:78689824-78695767	NM_001025712	ltn2a	0,03	-4,98	0,01
chr4:245073410-245110560	NM_001011970	Tm7sf3	0,02	-5,83	0,00

Supporting Table S6. Common genes regulated upon MNT depletion in URMT and URMax34 cells. The genes correspond to those shown in the venn diagram of Figure 4C. Relative RNA amounts were calculated as FPKM fold change (FC). Data are mean values of the two independent transfections where log2FC was >0.7 or <-0.7 (i.e., ≥1.6 fold and ≤0.5 fold), and a p-value <0.1.

locus	gene_id	Gene	sh-MNT vs pLKO		
			FC	Log2FC	p-value
chr10:69058108-69059959	NM_001007612	Ccl7	13,36	3,74	0,01
chr3:127438621-127474675	NM_001108959	Tgm3	6,85	2,78	0,01
chr9:95188005-95207531	NM_053577	Spp2	5,05	2,34	0,04
chr3:17021672-17058548	NM_001010968	Eng	4,64	2,21	0,06
chr5:172507288-172577540	NM_001195560	Camta1	3,72	1,89	0,02
chr15:24735138-24738725	NM_012827	Bmp4	3,55	1,83	0,01
chr1:89288945-89292050	NM_001013065	Ggn	3,03	1,60	0,00
chr4:184234158-184271987	NM_001106609	Txnrd3	2,87	1,52	0,09
chr10:89590581-89609632	NM_001108837	Meox1	2,70	1,43	0,01
chr2:83723118-83735166	NM_012816	Amacr	2,62	1,39	0,00
chr12:23760924-23767104	NM_001271236	LOC100362783	2,51	1,33	0,05
chr10:55965503-55968684	NM_012650	Shbg	2,45	1,30	0,03
chr14:80414798-80429940	NM_001134843	Myo1g	2,41	1,27	0,03
chr1:223521097-223523972	NM_182735	Cdkn1c	2,40	1,26	0,02
chr3:50007272-50327062	NM_001107732	Ccdc148	2,31	1,21	0,07
chr2:209427356-209430124	NM_053681	S100a3	2,25	1,17	0,08
chr8:48338878-48342640	NM_145717	Fxyd2	2,24	1,16	0,04
chr2:278043762-278563294	NM_019123	St6galnac3	2,22	1,15	0,08
chr5:155079202-155083511	NM_001271259	LOC100359977	2,21	1,14	0,07
chr7:2689127-2691242	NM_130410	Il23a	2,20	1,14	0,02
chr20:5955098-5960408	NM_001008848	RT1-Ha	2,06	1,04	0,06
chr9:79403625-79427523	NM_001109574	Tmem169	2,03	1,02	0,03
chr1:220887395-220890392	NM_001014163	Cend1	1,98	0,99	0,04
chr11:60714585-60776082	NM_001191826	Gramd1c	1,97	0,98	0,03
chr6:111585027-111633992	NM_001108036	Plekhh1	1,97	0,98	0,07
chr9:61824560-62158071	NM_053456	Plcl1	1,93	0,95	0,01
chrX:45646095-45654127	NM_012661	Sts	1,88	0,91	0,00
chr1:81329940-81340229	NM_012714	Gipr	1,86	0,90	0,10
chr17:80546950-80552017	NM_001126079	Acbd7	1,84	0,88	0,05
chr15:111996345-112224036	NM_001100685	Clybl	1,83	0,87	0,08
chr14:84825688-84834332	NM_001107233	RGD1308775	1,81	0,85	0,06
chr5:82503505-82531128	NM_001024346	LOC500475	1,81	0,85	0,06
chr1:102422047-102424623	NM_021758	Lin7b	1,80	0,85	0,06
chr7:71218205-71221052	NM_053302	Gpr182	1,74	0,80	0,09
chr20:7091295-7093067	NM_001004069	Sapcd1	1,73	0,79	0,07
chr1:228361452-228365776	NM_001013071	Tm7sf2	1,72	0,79	0,10
chr4:243622213-243658236	NM_001106627	Casc1	1,70	0,76	0,04
chr13:100036033-100037602	NM_022678	Zfp238	1,69	0,76	0,05
chr20:5448825-5462082	NM_212498	Atat1	1,69	0,75	0,01

chr6:89586785-89633108	NM_001105732	Sec23a	1,66	0,73	0,04
chr16:73730260-73754851	NM_013151	Plat	1,66	0,73	0,04
chrX:115098750-115107826	NM_001013950	Lmbr1l	1,66	0,73	0,08
chr5:43958429-43999913	NM_001106640	Gpr63	1,64	0,72	0,07
chr17:15662364-15667466	NM_001126083	Cks2	0,61	-0,70	0,04
chr1:229468107-229485469	NM_001108518	Naa40	0,61	-0,71	0,01
chr1:173726993-173751295	NM_001013236	Rrm1	0,61	-0,71	0,02
chr2:209191619-209196288	NM_001106439	Slc27a3	0,61	-0,71	0,03
chr6:146226686-146243773	NM_033230	Akt1	0,61	-0,72	0,01
chr13:114264895-114292134	NM_001109083	Nsl1	0,61	-0,72	0,01
chr2:207154780-207174337	NM_001191568	Pmf1	0,61	-0,72	0,02
chr17:91504400-91539143	NM_001107369	Mastl	0,61	-0,72	0,07
chr2:163630966-163635150	NM_001044263	Rfxap	0,60	-0,73	0,06
chr1:228384096-228394986	NM_001115042	Cdca5	0,60	-0,73	0,07
chr7:141393003-141400457	NM_199370	Krt8	0,60	-0,73	0,07
chr8:22217095-22229971	NM_053743	Cdc37	0,60	-0,73	0,07
chr2:262787595-262899803	NM_001107728	Rap1gds1	0,60	-0,73	0,01
chr1:268610732-268618280	NM_053290	Pgam1	0,60	-0,73	0,05
chr10:106451967-106455900	NM_053553	Syngn2	0,60	-0,74	0,07
chr1:264226026-264241499	NM_001025646	Cep55	0,60	-0,74	0,00
chr8:39184019-39204446	NM_080400	Chek1	0,60	-0,75	0,04
chr3:158598783-158611011	NM_001025768	Dsn1	0,60	-0,75	0,01
chr20:5831136-5833706	NM_213561	Tcf19	0,59	-0,75	0,05
chr1:205441132-205467610	NM_001009645	Kif22	0,59	-0,75	0,03
chr1:79112278-79130529	NM_001024897	Ehd2	0,59	-0,75	0,05
chr5:141050191-141054395	NM_171993	Cdc20	0,59	-0,75	0,00
chr3:156435529-156446390	NM_001100778	E2f1	0,59	-0,76	0,03
chr15:92899713-92951232	NM_001108390	Ndfip2	0,59	-0,76	0,04
chr8:22631827-22676509	NM_001034088	Carm1	0,59	-0,76	0,01
chrX:115263555-115271364	NM_001271243	Troap	0,59	-0,76	0,06
chr10:106494774-106503096	NM_022274	Birc5	0,59	-0,76	0,00
chr1:195361585-195387930	NM_001108501	Ccp110	0,59	-0,76	0,02
chr3:120780502-120790938	NM_001107767	Duoxa1	0,59	-0,77	0,01
chr3:117468880-117493555	NM_001109204	Rad51	0,59	-0,77	0,03
chr2:59075285-59147310	NM_001107651	Depdc1b	0,59	-0,77	0,00
chr1:143039959-143061006	NM_001107529	Prc1	0,59	-0,77	0,05
chr1:260438626-260494019	NM_001107609	Kif20b	0,59	-0,77	0,08
chr9:93273332-93277372	NM_021740	Ptma	0,58	-0,78	0,02
chr19:48680054-48686495	NM_001024257	Cenpt	0,58	-0,78	0,01
chr10:86614892-86628265	NM_001108298	Cdc6	0,58	-0,78	0,01
chr10:105718074-105765280	NM_001108309	Sec14l1	0,58	-0,78	0,06
chr14:83025668-83039430	NM_001004424	Tacc3	0,58	-0,79	0,01
chr9:25770287-25788432	NM_001191805	Mcm3	0,58	-0,79	0,04
chr3:144832021-144840679	NM_001009655	Mgme1	0,58	-0,79	0,00
chr5:143482582-143542254	NM_012866	Nfyc	0,58	-0,79	0,00
chr4:224365695-224369284	NM_001007648	Cdca3	0,58	-0,79	0,05
chr5:151138848-151147606	NM_001134629	RGD1561149	0,57	-0,80	0,08
chr15:55958799-55962007	NM_001025279	Reep4	0,57	-0,80	0,06

chr18:69317014-69327048	NM_001106134	Ska1	0,57	-0,80	0,04
chr5:64307463-64367854	NM_001108662	Melk	0,57	-0,81	0,02
chr3:154730956-154773179	NM_001107790	Tpx2	0,57	-0,81	0,06
chr15:47186190-47231339	NM_001107273	Cdca2	0,57	-0,81	0,00
chr10:14903482-14911519	NM_001105773	Chtf18	0,57	-0,81	0,02
chr7:60853892-60860953	NM_134346	Rap1b	0,57	-0,81	0,00
chr8:90886761-90924325	NM_001108172	Ttk	0,57	-0,82	0,05
chr7:117676479-117691180	NM_001130572	Tonsl	0,57	-0,82	0,03
chr20:22694920-22709859	NM_019296	Cdk1	0,57	-0,82	0,01
chr18:27137684-27146171	NM_001108426	Kif20a	0,57	-0,82	0,01
chr3:62049999-62063264	NM_001009654	Spc25	0,56	-0,82	0,00
chr17:23615670-23657985	NM_001001511	Gcnt2	0,56	-0,83	0,02
chr1:163919400-163943710	NM_001126294	RGD1559690	0,56	-0,83	0,04
chr9:119293739-119309561	NM_001126270	Ndc80	0,56	-0,83	0,04
chr3:167422568-167424969	NM_001106542	Ube2c	0,56	-0,83	0,09
chr1:199178261-199188238	NM_017100	Plk1	0,56	-0,83	0,07
chr4:39891452-39963623	NM_001109221	LOC500034	0,56	-0,84	0,09
chr16:74383676-74410206	NM_001169139	Ckap2	0,56	-0,84	0,01
chr5:139821000-139846566	NM_001085369	Kif2c	0,56	-0,84	0,00
chr3:117157779-117177433	NM_001004264	Knstrn	0,56	-0,84	0,04
chr7:28764493-28825206	NM_001166676	Parbbp	0,56	-0,84	0,05
chr2:230646556-230651000	NM_001044302	Psrc1	0,56	-0,85	0,01
chr10:89978418-90001064	NM_001017988	LOC303566	0,56	-0,85	0,00
chr1:223099327-223114942	NM_013087	Cd81	0,55	-0,85	0,04
chr6:100953299-100977903	NM_001169108	Pole2	0,55	-0,85	0,01
chr1:227783723-227790741	NM_001005907	Efemp2	0,55	-0,86	0,04
chr17:11940005-11943732	NM_145773	Mxd3	0,55	-0,86	0,01
chr10:13410717-13435965	NM_001100474	Ccnf	0,55	-0,86	0,01
chr8:59280448-59297536	NM_017132	Rcn2	0,55	-0,86	0,02
chr18:62314820-62324460	NM_001025675	Tubb6	0,55	-0,86	0,09
chr10:91783780-91805556	NM_024150	Arf2	0,55	-0,86	0,00
chr9:64698065-64720561	NM_001271191	Sgol2	0,55	-0,86	0,08
chr10:61406976-61422227	NM_001105807	Mnt	0,55	-0,87	0,01
chr15:41919557-41937891	NM_001108379	Ska3	0,55	-0,87	0,00
chr4:226891343-226902365	NM_031633	Foxm1	0,55	-0,87	0,01
chr10:90780840-90800011	NM_001039019	Kif18b	0,54	-0,88	0,04
chr7:117753870-117761035	NM_001130494	Recql4	0,54	-0,88	0,05
chr9:9731077-9750175	NM_001008882	Uhrf1	0,54	-0,89	0,03
chr6:51811951-51828131	NM_001100717	E2f6	0,54	-0,89	0,02
chr7:142719644-142746041	NM_001109470	Zfp385a	0,54	-0,89	0,02
chr19:25637491-25681915	NM_001106170	Mcm5	0,54	-0,90	0,02
chr16:40849290-40908352	NM_001170346	Neil3	0,54	-0,90	0,03
chr13:98401024-98427400	NM_001107198	Exo1	0,54	-0,90	0,03
chr19:36055966-36070506	NM_001107160	Asf1b	0,53	-0,90	0,01
chr13:55534038-55551850	NM_001108343	Etnk2	0,53	-0,91	0,06
chr1:22625115-22626610	NM_001009470	Ccnb2	0,53	-0,91	0,06
chr1:15072108-15083325	NM_001037789	Ccdc28a	0,53	-0,91	0,02
chr6:60756159-60762351	NM_001025740	Rrm2	0,53	-0,91	0,00

chr16:48613428-48636501	NM_001025673	Cenpu	0,53	-0,91	0,01
chr10:14120127-14139812	NM_001013182	Hn1l	0,53	-0,93	0,02
chr16:75349397-75367306	NM_001012228	Xkr5	0,52	-0,94	0,04
chr3:111858564-111874846	NM_001168524	Arhgap11a	0,52	-0,94	0,08
chr8:103009499-103046804	NM_001108178	Pls1	0,52	-0,94	0,01
chr8:131187616-131258348	NM_181635	Kif15	0,52	-0,94	0,03
chr7:122151953-122156374	NM_001008373	Srek1ip1	0,52	-0,94	0,03
chr16:68718376-68753634	NM_001191555	Rab11fip1	0,52	-0,95	0,05
chr9:100106949-100136087	NM_001009362	Pask	0,51	-0,96	0,00
chrX:111960844-111967052	NM_001108120	Nxt2	0,51	-0,97	0,01
chr7:141693055-141719909	NM_001170602	Espl1	0,51	-0,98	0,06
chr5:132031218-132050961	NM_177931	Orc1	0,50	-0,99	0,01
chr10:82185899-82191905	NM_001105830	Eme1	0,50	-1,01	0,02
chr5:148352776-148387685	NM_001106687	Clspn	0,50	-1,01	0,06
chr3:165617193-165645609	NM_001106536	Mybl2	0,49	-1,04	0,04
chr8:66598466-66625560	NM_001108155	Kif23	0,49	-1,04	0,04
chr2:108055052-108086130	NM_001134993	Car13	0,48	-1,05	0,00
chr3:116411044-116422101	NM_001013062	Thbs1	0,47	-1,09	0,00
chr1:178792339-178816636	NM_001013192	Olfml1	0,44	-1,17	0,03
chr2:176099246-176179301	NM_001127530	LOC302022	0,44	-1,19	0,03
chr6:137256802-137272264	NM_182474	LOC299282	0,39	-1,35	0,01
chr7:117215918-117244741	NM_001164304	Plec	0,34	-1,55	0,02
chr7:126136631-126178957	NM_001009695	Wnt7b	0,18	-2,48	0,06

Supporting Table S7. Antibodies used in this work. aa, amino acids; FL, full-length; IB, immunoblot; IF, immunofluorescence; IP, immunoprecipitation

Primary antibodies					
Antibody	Immunogen	Type	Origin (reference)	RRID	Technique and dilution
Anti- β -actin	C-terminus (human)	Goat polyclonal	Santa Cruz Biotech. (I-19, sc-1616)	AB_630836	IB (1:1000)
Anti-Bcl-XL	Residues surrounding Asp61 of human Bcl-xL	Rabbit monoclonal	Cell Signalling (54H6, -2764)	AB_2228008	IB (1:1000)
Anti-CCNA2	FL (human)	Rabbit polyclonal	Santa Cruz Biotech. (H-432, sc-751)	AB_631329	IB (1:1000)
Anti-CTCF	659-675 aa (human)	Rabbit polyclonal	Upstate (07-729)	AB_441965	IB (1:1000)
Anti-GFP	GFP from <i>Aequorea victoria</i>	Rabbit polyclonal	Invitrogen (A-11122)	AB_221569	IB (1:1000); IP
Anti-HA	Influenza virus hemagglutinin (HA) epitope	Mouse Monoclonal	Genecopiea (CGAB-HA-0050)	AB_2801472	IP
Anti-HA	Influenza virus hemagglutinin (HA) epitope	Rat monoclonal	Roche (3F10)	AB_2314622	IB (1:2000)
Anti-MAX	C-terminal (human)	Rabbit polyclonal	Santa Cruz Biotech (C-17, sc-197)	AB_2281783	IB (1:1000); ChIP
Anti-MNT	226-361 aa (human)	Rabbit polyclonal	Santa Cruz Biotech (M-132, sc-769)	AB_2145079	IB (1:1000); IF (1:200); IP; ChIP
Anti-MNT	532-582 aa (human)	Rabbit polyclonal	Novus (NBP2-04053)	AB_2801473	IB (1:1000)
Anti-MLX	17-42 aa (human)	Mouse monoclonal	Santa Cruz Biotech (F12, sc-393086)	AB_2801474	IB (1:1000) IP; ChIP
Anti-MYC	1-262 aa (human)	Rabbit polyclonal	Santa Cruz Biotech (N-262, sc-764)	AB_631276	IB (1:1000)
Anti-PARP1	764-1014 aa (human)	Rabbit polyclonal	Santa Cruz Biotech (H-250, sc-7150)	AB_2160738	IB (1:1000)
Anti-RhoGDI	N-terminal (human)	Rabbit polyclonal	Santa Cruz Biotech (A-20, sc-360)	AB_2227516	IB (1:1000)
Anti-Sin3B	172-228 aa (mouse)	Mouse monoclonal	Santa Cruz Biotech (H-4, sc-13145)	AB_628254	IB (1:1000)
Anti-Survivin	1-142 aa (human)	Rabbit polyclonal	Santa Cruz Biotech (FL-142, sc-10811)	AB_2227956	IB (1:1000)
Anti- α -tubulin	149-448 aa (human)	Rabbit polyclonal	Santa Cruz Biotech. (H300, sc-5546)	AB_635001	IB (1:1000)

Secondary antibodies					
Antibody	Immunogen	Type	Origin (reference)	RRID	Technique and dilution
Anti-Rabbit IRDye®800	rabbit heavy and light immunoglobulins chains	Donkey polyclonal	Li-Cor Biosciences (926-32213)	AB_621848	IB (1:10000)
Anti-Rabbit IRDye®680	rabbit heavy and light immunoglobulins chains	Donkey polyclonal	Li-Cor Biosciences (926-68073)	AB_10954442	IB (1:10000)
Anti-Mouse IRDye®800	mouse heavy and light immunoglobulins chains	Donkey polyclonal	Li-Cor Biosciences (926-32212)	AB_621847	IB (1:10000)
Anti-Mouse IRDye®680	mouse heavy and light immunoglobulins chains	Donkey polyclonal	Li-Cor Biosciences (926-68072)	AB_10953628	IB (1:10000)
Anti-Goat IRDye®800	goat heavy and light immunoglobulins chains	Donkey polyclonal	Li-Cor Biosciences (926-32214)	AB_621846	IB (1:10000)
Anti-Goat IRDye®680	goat heavy and light immunoglobulins chains	Donkey polyclonal	Li-Cor Biosciences (926-68074)	AB_10956736	IB (1:10000)

Supporting Table S8. Primers used in this study. The gene and amplicon names, species, sequences and annealing temperature (T_m) are indicated. Primers are arranged by species in this table. Restriction sites are underlined. TSS, transcription start site; ChIP: chromatin immunoprecipitation; RT-qPCR: reverse transcription-quantitative polymerase chain reaction; cloning: cloning strategy.

Gene (amplicon)	Species	Primers sequence (5'→3')	T _m (°C)	Use
ACTB/β-actin	Human.	AAAATCTGGCACCACACCTTC TAGCACAGCCTGGATAGCAA	60	RT-qPCR
RPS14	Human.	TCACCGCCCTACACATCAAACCT CTGCGAGTGCTGTCAGAGG	60	RT-qPCR
MAX	Human..	TGTTGTTGTCGGTACTTCC CATTATGATGAGCCCGTTTG	60	RT-qPCR
MNT	Human	AGCCAGTGGATGGACGTA GACGATGGCTCAGCTTAGGT	60	RT-qPCR
ACTB/β-actin	Rat	CTAAGGCCAACCGTGAAAAG ACCCTCATAGATGGGCACAG	60	RT-qPCR
BIRC5	Rat	GCCTACAAGGAAGTGCAAGG GCGTCCTCATTGAGAAGCTC	60	RT-qPCR
BRCA1	Rat	GCCTACAAGGAAGTGCAAGG GCGTCCTCATTGAGAAGCTC	60	RT-qPCR
BRCA2	Rat	GGCCATGAACCACAGCTATT GGTCCTTTCTGGCCTTCTTT	60	RT-qPCR
CCNG2	Rat	TGACCTTGATGGAGGCTACC CAGGGCCAAGAATCTATCCA	60	RT-qPCR
CDK12	Rat	CCTCCCTCCCCTATTACCTG GTAATTGCCTTTGGCTCTGG	60	RT-qPCR
CDK1	Rat	GCCAGTTCATGGATTCTTCG CCGAAATCTGCCAGTTTGAT	60	RT-qPCR
CDKN1C	Rat	CTCTCCTAACGTGGCTCCTG GATGCCAGCAAGTTCTCTC	60	RT-qPCR
CDC6	Rat	CCCTGAGCAAGACAACTCC GGCGGAGAACATGGAGATAA	60	RT-qPCR
CHEK1	Rat	GCCATAGACTGCCAGAAAA AGCATCTTGTTGAGGCATCC	60	RT-qPCR
E2F6	Rat	CAGTGAAGGCTCCAGAGGAA AGAGGCCCTACTCCATCAG	60	RT-qPCR
E2F7	Rat	ATAAGGGACCGGAGAAGAA GGACAAGGGGTAGCTTGGAT	60	RT-qPCR
ENDOGLIN	Rat	AACCCAGACACCAGTCCAAG GGTATCGATGAGCCAGGAGA	60	RT-qPCR
ERCC6	Rat	GCGCTCTCTCAGACAGACAA GCACTGGGACTTTCTTCTCG	60	RT-qPCR
FANCD2	Rat	AAGCAACCCCTTTCCAAGTT GGACTCCAGGCCATTAACAA	60	RT-qPCR
FBXO32	Rat	CTACGATGTTGAGCCAAAGA GGCAGTCGAGAAGTCCAGTC	60	RT-qPCR
MAX	Rat	CACCATAATGCACTGGAACG CTGGTGCGTATGGTTTTTCC	60	RT-qPCR
MNT	Rat	GAGAAGATTGCCACACAGCA GGACGATGGTTCAGCTTAGG	60	RT-qPCR

MLX	Rat	CTCATGAGGGAGAGGACCAG GGACACCGATCACAATCTCC	60	RT-qPCR
Mycoplasma spp.		GGCGAATGGGTGAGTAACACG CGGATAACGCTTGCACCTATG	64	PCR
ORC1	Rat	GGCATTGTAGGACGGAGA CCAGGACAGCTTCACAAACA	60	RT-qPCR
POLE2	Rat	CGCTTTCCTAGCAGCAGTTT CGGATCGTACTTGTCTGCAA	60	RT-qPCR
NDRG4	Rat	GGATACCAGTCCCCTCCAT CTCCACCAAATCAGGGAAGA	60	RT-qPCR
TXNRD3	Rat	TCATAGCAACAGGGGAAAGG AAGCCACGAAGAAGGACAGA	60	RT-qPCR
RET	Rat	TTGGTCCAGTCCAACAACAA GCACAGACACGTTGAAATGG	60	RT-qPCR
RPS14	Rat	CAAGGGGAAGGAAAAGAAGG GAGGACTCATCTCGGTCAGC	60	RT-qPCR
TRIP13	Rat	AGGGTGGATCTTCGTACAGC GCCTGTAAACGCTCTGCTTT	60	RT-qPCR
NEIL3	Rat	CTTGCAACTAGCAGGGGTTT TTAGCGTTCATTGGAGCAG	60	RT-qPCR
PARPBP	Rat	TGGCGTGCTCATTGTAAGTC CTCAGAGCGCAGAACAAGTG	60	RT-qPCR
FBXO32/Atrogin 1 (-370 bp from TSS)	Rat	ACAAGGCGAGCCATAAAC GGAAGTATGTGGAGGGTTG	60	ChIP
MNT -1369/-1198 bp from TSS	Rat	ATGGCTTCCACCAAAGTAGC CCTCTCTCAACCAACCGTCT	60	ChIP
MNT -654/-478 bp from TSS	Rat	CCGTAATACGACCTGAAG CCGGATTTTGTCTCTGTTCC	60	ChIP
E2F6 +303/+546 bp from TSS	Rat	ACGAGGCACGTGTAGAGCTT ACAAAAGACGGATCCACCAG	60	ChIP
BIRC5 +318/+483 bp from TSS	Rat	CTCTCCCCTCCCTTTACCTG CTCGTGAGCAAGGATCAACA	60	ChIP
BRCA1 +88/+310 bp from TSS	Rat	CGGAAGAAAGGTGAGACAGC GGACTCCCTCACACATCCAT	60	ChIP
CDK1 -216/-54 bp from TSS	Rat	GACGACATTGGAAGGAAAGC TGCACGTAGACGTTCAAAGG	60	ChIP
CDKN1C -118/+223 bp from TSS	Rat	GCGGTGTTGTTGAAACTGAA CTCGATCGTTTGTCTGTCC	60	ChIP
850 MNT (850 bp of MNT promoter flanked with EcoRV/HindIII restriction sites)	Human	TCGATATCATGTGACCTGCAGACACTGG TGAAGCTTGGCACTGCCTCCCTTCTT	70	Reporter construction
220 MNT (220 bp of MNT promoter flanked with EcoRV/HindIII restriction sites)	Human	TCGATATCATGTGACCTGCAGACACTGG TGAAGCTTGGCACTGCCTCCCTTCTT	70	Reporter construction
570MNT (570 bp of MNT promoter TSS MNT EcoRV/HindIII restriction sites)	Human	TCGATATCCAGTCTCTGCCATTCCCAAG TGAAGCTTGGCACTGCCTCCCTTCTT	70	Reporter construction

