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Supplemental Data

XBP1 Links ER Stress to Intestinal Inflammation and Confers Genetic Risk for Human Inflammatory Bowel Disease

Arthur Kaser, Ann-Hwee Lee, Andre Franke, Jonathan N. Glickman, Sebastian Zeissig, Herbert Tilg, Edward E.S. Nieuwenhuis, Darren E. Higgins, Stefan Schreiber, Laurie H. Glimcher, and Richard S. Blumberg

Supplemental Figure legends

Figure S1. Generation of *Xbp1*$^{\text{flox}}$ mice. A. Schematic representation of the gene targeting strategy. A floxed *Xbp1* allele was generated by homologous recombination in W4/129 embryonic stem (ES) cells. The targeting vector contains a *lox*P site in intron 2 and a floxed neomycin resistance gene cassette (neo) in intron 1 of the *Xbp1* gene. A targeted ES cell clone identified by Southern blot was injected into C57BL/6 blastocysts to obtain chimeras, which were subsequently bred to establish the *Xbp1*$^{\text{floxneo}}$ strain. *Xbp1*$^{\text{floxneo}}$ mice were mated with *EIIacre* transgenic mice to induce a partial *Cre*-mediated recombination. Male mice with the greatest deletion of the neo cassette were mated with wild type female mice to obtain an *Xbp1*$^{\text{flox}}$ strain. **B.** Breeding of *Xbp1*$^{\text{flox}}$ mice with Villin-(V)*Cre* transgenic mice resulted in the deletion of exon 2 of the *Xbp1* gene as confirmed by Southern blot. Total RNAs were isolated from small intestinal mucosal scrapings of untreated (NT) or mice injected with 1 mg/kg tunicamycin and harvested 6h later, and analyzed for the expression of XBP1 mRNA by Northern blot and RT-PCR followed by DNA sequencing. The mutant XBP1 mRNA produced by *Xbp1*$^{\Delta/\Delta}$ mice is slightly smaller than the wild type XBP1 mRNA, due to the deletion of exon 2 as confirmed by DNA sequencing of the cDNA. The IRE1 splicing site of XBP1 mRNA is located downstream of the floxed exon 2 in exon 4, which hence allowed us to monitor splicing status in mRNA transcribed from floxed and *Cre*-deleted *Xbp1* alleles alike. Absence of XBP1 protein was confirmed by Western blotting of small intestinal mucosal scraping protein lysates from untreated and tunicamycin-injected mice (*, nonspecific band). **C.** Deletion of exon 2 in the mutant XBP1 mRNA resulted in the change of the translational reading frame, introducing a premature translational termination codon. **D.** Truncated XBP1 protein is not functional as evidenced by its failure to upregulate expression of a prototypical XBP1s target gene, ERdj4 (*Dnajb9*) upon ER stress induction through tunicamycin injection (Lee et al., 2003), as determined by qPCR on small intestinal mucosal scraping specimens (mean ± SEM). In contrast, tunicamycin injection led to upregulation of Chop (*Ddit3*) mRNA expression, transcriptionally regulated by PERK-Atf4 during ER stress, in XBP1$^{\text{flox/flox}}$V*Cre* mice, indicating that other branches of the UPR are intact in the presence of a non-functional, truncated XBP1. **E.** Livers and spleens of *Xbp1*$^{\text{flox/flox}}$V*Cre* (*Xbp1*$^{-/-}$) and *Xbp1*$^{\text{flox/flox}}$ (*Xbp1*$^{+/+}$) mice were analyzed for XBP1 mRNA levels (primers binding in the floxed region) quantified by qPCR (*n* = 2 per group, mean ± SEM)

Figure S2. Villin*Cre*-mediated *Xbp1* deletion leads to Chop induction, intestinal inflammation, and does not affect colonic goblet cells or small intestinal enteroendocrine cells. A. Chop (*Ddit3*) mRNA expression was analyzed in small intestinal mucosal scrapings from *Xbp1*$^{+/+}$ and *Xbp1*$^{-/-}$ mice ($n = 7$ per group, mean ± SEM). **B.** H&E stains of *Xbp1*$^{+/-}$ small intestine, showing polymorphonuclear infiltration in the lamina propria (arrows point toward neutrophils between crypts). **C.** Goblet cells in the large intestine were identified by PAS staining ($n = 3$ per genotype). **D.** Chromogranin^{+} cells per immunostained section were quantified by light microscopy ($n = 4$ per group, mean ± SEM).

Figure S3. *Xbp1* deletion does not regulate genes involved in intestinal cell fate decisions. A. Expression of indicated genes was analyzed in small intestinal mucosal scrapings of *Xbp1*$^{+/+}$ and *Xbp1*$^{-/-}$ mice. $n = 11\text{-}19$ per group, mean ± SEM. Two-tailed Student's *t*-test. No significant differences were observed. **B.** Small intestinal paraffin-embedded sections were stained by anti-β-catenin. Representative of 5 specimens per genotype.

Figure S4. *Xbp1* deletion leads to the presence of apoptotic cells in the epithelium. A. Apoptotic nuclei were identified in *Xbp1*$^{+/+}$ (*Xbp1*$^{\text{flox/flox}}$) and *Xbp1*$^{-/-}$ (*Xbp1*$^{\text{flox/flox}}$V*Cre*) sections by TUNEL staining. Arrows point to apoptotic cells. **B.** Deletion of *Xbp1* gene in *Xbp1*$^{\text{floxneo/floxneo}}$V*CreER*^{T2} mice was induced by a 5 day administration of 1 mg tamoxifen intraperitoneally daily, and apoptotic cells stained by an anti-active (cleaved) caspase-3 antibody. Time-points in the figure indicate the length after start of tamoxifen administration. Arrows point to apoptotic cells.

Figure S5. Inhibitors of p38 and ERK1/2 phosphorylation do not affect CXCL1 secretion in XBP1-silenced MODE-K cells. A. MODE-K.iXBP (filled symbols) and MODE-K.Ctrl (open symbols) cells were stimulated for 4h with 50ng/ml TNFα in the presence of the indicated optimal concentrations of inhibitors (PD98059, inhibitor of MAP kinase kinase [MEK]; SB203580, p38 kinase inhibitor; U0126, MEK1/MEK2 inhibitor). Supernatants were assayed for CXCL1. **B.** Experiment as in (A), except for stimulation with 10μg/ml flagellin instead of TNFα. Triplicates, mean ± SEM in (A) and (B).

Figure S6. XBP1-silenced MODE-K cells are more sensitive to TNFα induced apoptosis. A. MODE-K.Control and MODE-K.iXBP cells were cultured for 4 h in medium alone, 50 ng/ml TNFα, or 10 μg/ml flagellin, trypsinized and analyzed for intracellular presence of cleaved caspase-3 by flow cytometry. Duplicates, mean ± SEM. **B.** Same experiment as in (A) with cells stimulated with 50 ng/ml TNFα, except for that adherent cells were fixed and stained for cleaved caspase-3 (red) and nuclei (DAPI; blue) by immunofluorescence.

Figure S7. Antibiotic treatment during 7% DSS colitis abrogates genotype-related differences in susceptibility to colitis. A. *Xbp1*$^{+/+}$ ($n = 6$) and *Xbp1*$^{-/-}$ ($n = 4$) littermates were treated with antibiotics (neomycin sulfate, 1.5g/l; metronidazole, 1.5g/l) in drinking water during the 5 days of high-dose DSS (7%; commensal flora-depleted mice are less susceptible to DSS colitis, which requires an increase in DSS dose to achieve colonic inflammation) administration as well as during the subsequent time on regular drinking water. Wasting was monitored by daily weight measurements. **B.** Colonic specimens harvested on day 8 of 7% DSS colitis in the presence of antibiotics were histologically assessed for inflammation. Two-tailed Mann-Whitney test. Mean ± SEM in (A) and (B).

Figure S8. Regional association plot and structure of linkage disequilibrium (LD) across the *XBP1* gene. A. Plot of the negative logarithm_{10} of the *P*-values obtained in fine mapping of the 120 kb region around the *XBP1* candidate gene. Twenty tagging SNPs were genotyped in overall 5322 controls, 2762 Crohn's disease (**CD**), and 1627 ulcerative colitis (**UC**) patients (combined Panel 1+2+3). Negative log *P*-values are also shown for the combined inflammatory bowel disease (**IBD**) panel (CD+UC). The red dotted line corresponds to a significance threshold of 0.05 and the blue dotted line to the significance threshold according to the Bonferroni correction for multiple testing applied to the fine mapping results (n = 20). Positions are in NCBI‘s build 35 coordinates. For genotype counts see Supplementary Table 2. Panel **B.** shows the plotted recombination rate (in centimorgans [cM] per Mb), while **C.** shows the sequence conservation score based on 16 different species (taken from UCSC Genome Browser, Vertebrate Multiz Alignment & Conservation). **D.** The position and intron/exon structure of underlying genes. Panel **E.** shows the pairwise LD in the combined sample for the 20 genotyped variants using the metric r^2 and the GOLD color scheme.

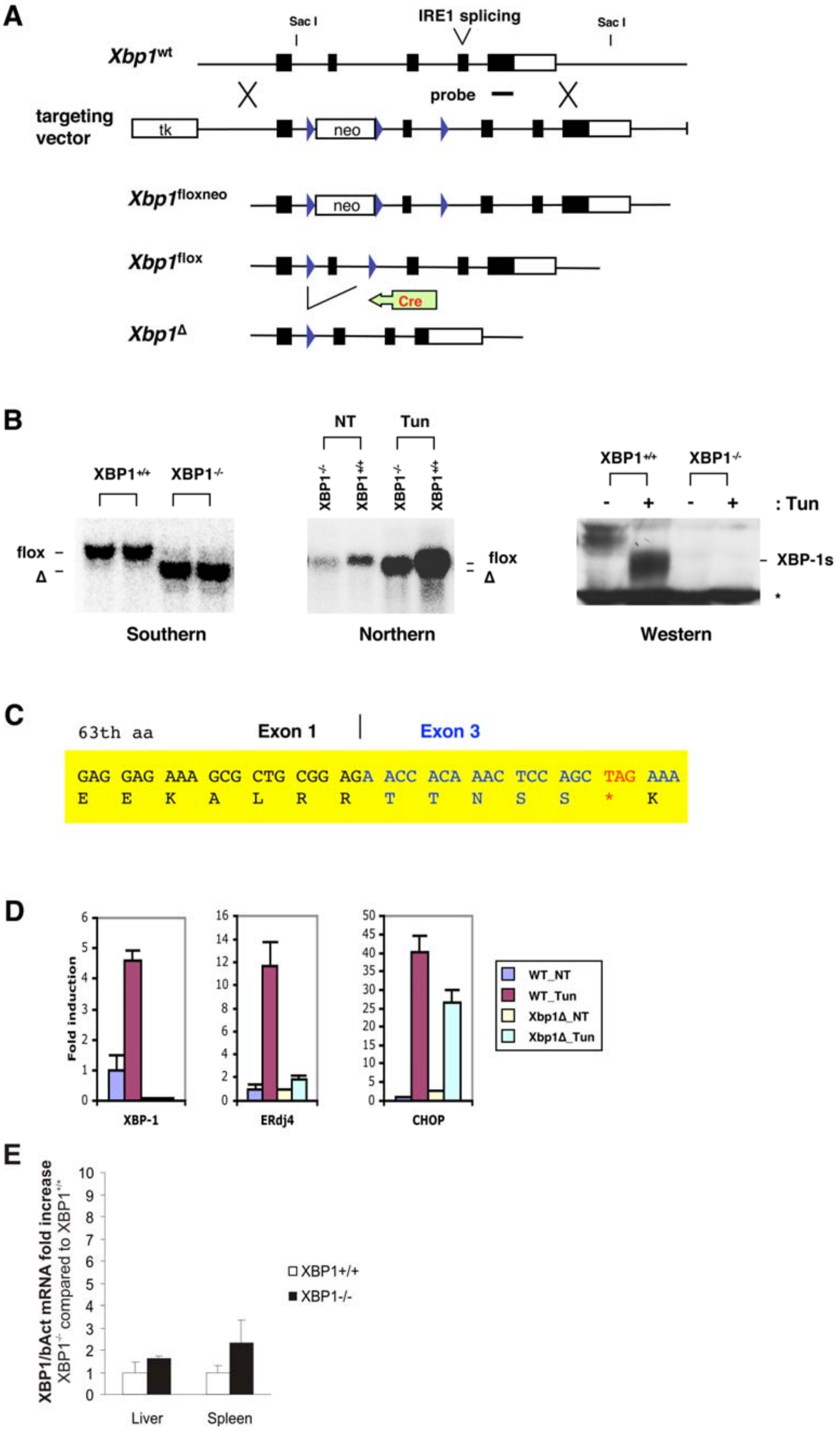
Figure S9. Deep sequencing of *XBP1*. All five exons and 4.3 kb of 5' upstream sequence were resequenced in 282 unaffected controls, 282 Crohn's disease, and 282 ulcerative colitis patients (total of 846 samples); the five *XBP1* exons were sequenced in 282 additional ulcerative colitis patients resulting in a total of 1128 patient and control DNAs analyzed. Chromosomal location of *XBP1* and amplicons used for sequencing are shown in the context of XBP1s and XBP1u transcripts. The panel underneath the transcript panel shows the sequence conservation score based on 16 different species (taken from UCSC Genome Browser, Vertebrate Multiz Alignment & Conservation). SNPs are presented in the context of their genomic localization. SNPs of particular interest are highlighted by color-coding as indicated. The labeling "full panel, genotyping" indicates that in addition to sequencing, actual frequencies were determined in panels 1+2+3 (common SNPs) and panels 1+2 (all 5 novel rare nsSNPs, including *XBP1snp22*), respectively, while "sequencing cohort" refers to the 1128 patients and controls described above. For further details on deep sequencing see Supplementary Table 4.

Figure S10. The rare non-synonymous *XBP1snp22* (P15L) variant does not affect UPRE transactivation. A. MODE-K cells were transfected with UPRE-luciferase and unspliced h*XBP1u* expression plasmids harbouring the rare, minor allele of *XBP1snp22* (P15L), which occurs at equal frequencies in IBD patients and controls (Supplementary Table 4). Luciferase activity (values presented normalized to cotransfected *Renilla* activities) was assessed in transfected cells treated with and without 1 µg/ml tunicamycin. **B.** Experiments as in (A), except that spliced h*XBP1s* cDNA P15L variant was transfected into MODE-K cells (in the absence of tunicamycin treatment). Duplicates, mean ± SD in (A) and (B).

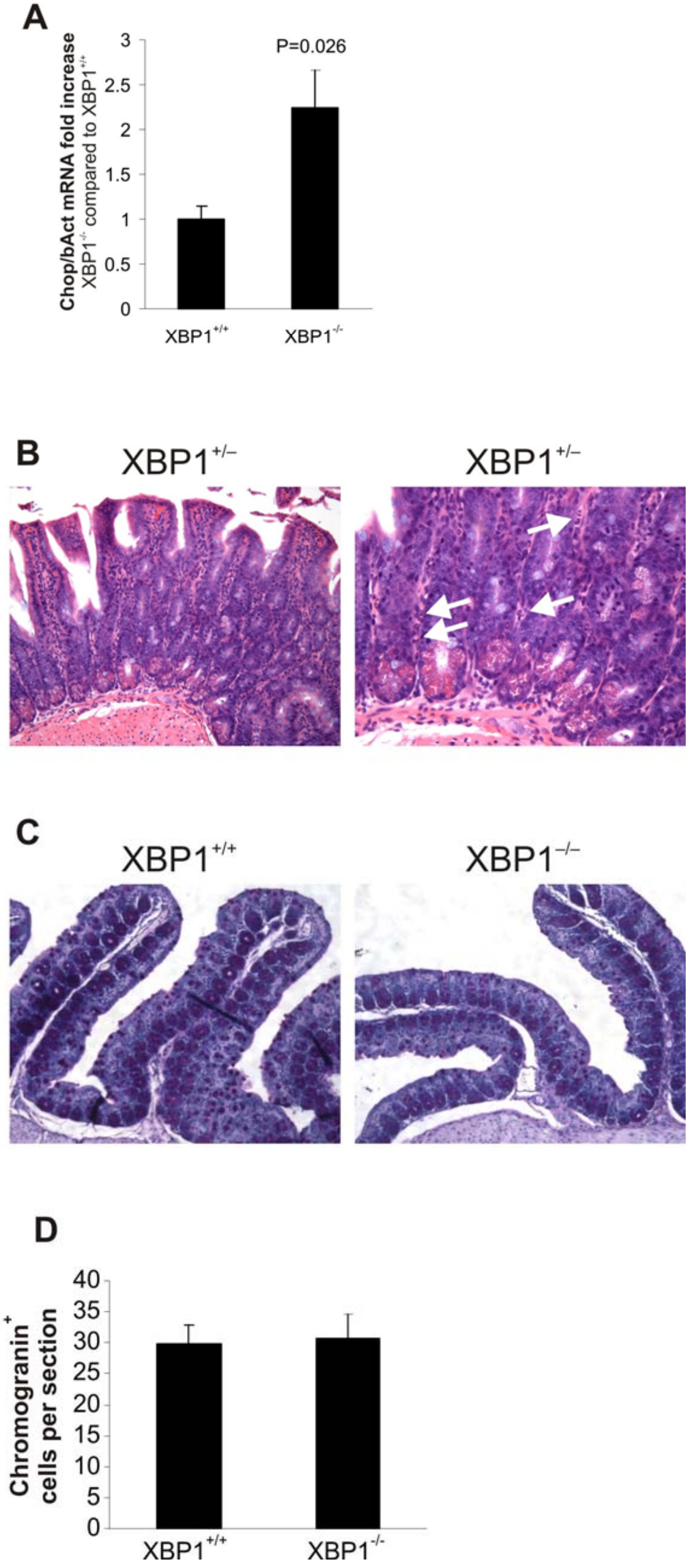
Figure S11. IEC-specific XBP1 deficiency leads to Paneth cell dysfunction and a pro-inflammatory tone of the mucosa. A. Regular function of the IRE1/XBP1 axis. Continuous ER stress due to the high protein burden in IEC (in particular Paneth cells) leads to activation of the UPR and low-level baseline XBP1 splicing. XBP1s protein regulates transcription of XBP1s target genes, required for normal IEC and Paneth cell function. **B.** Decrease or absence of functional XBP1 proteins leads to a decrease in the expression of XBP1s target genes, and hence an inefficient UPR and accumulation of misfolded or unfolded proteins in highly secretory IECs and Paneth cells. This leads to increased ER stress, which leads dominantly to overactivation of IRE1α through a yet to be defined mechanism, which manifests in our model as increased XBP1 splicing and – presumably through TRAF2 – as increased JNK phosphorylation upon ligation of

TNFR1 with TNFα or TLR5 with flagellin. The aforementioned increased ER stress in the absence of XBP1s protein leads further to increased expression of Chop, a major link between the UPR and apoptosis, which results in Paneth cell dysfunction and apoptosis. Alterations in the composition of the intestinal microbiota, or increased bacterial burden due to defensin deficiency in epithelium with impaired or absent Paneth cell function, might lead to increased flagellin expression, further fueling the pro-inflammatory JNK pathway that in turn increases pro-inflammatory gene expression including TNFα. TNFα consequently binds to TNFR1, with the TRAF2-IRE1 interaction further increasing phosphorylation of JNK. As a consequence, intestinal inflammation with features characteristic of IBD develops spontaneously.

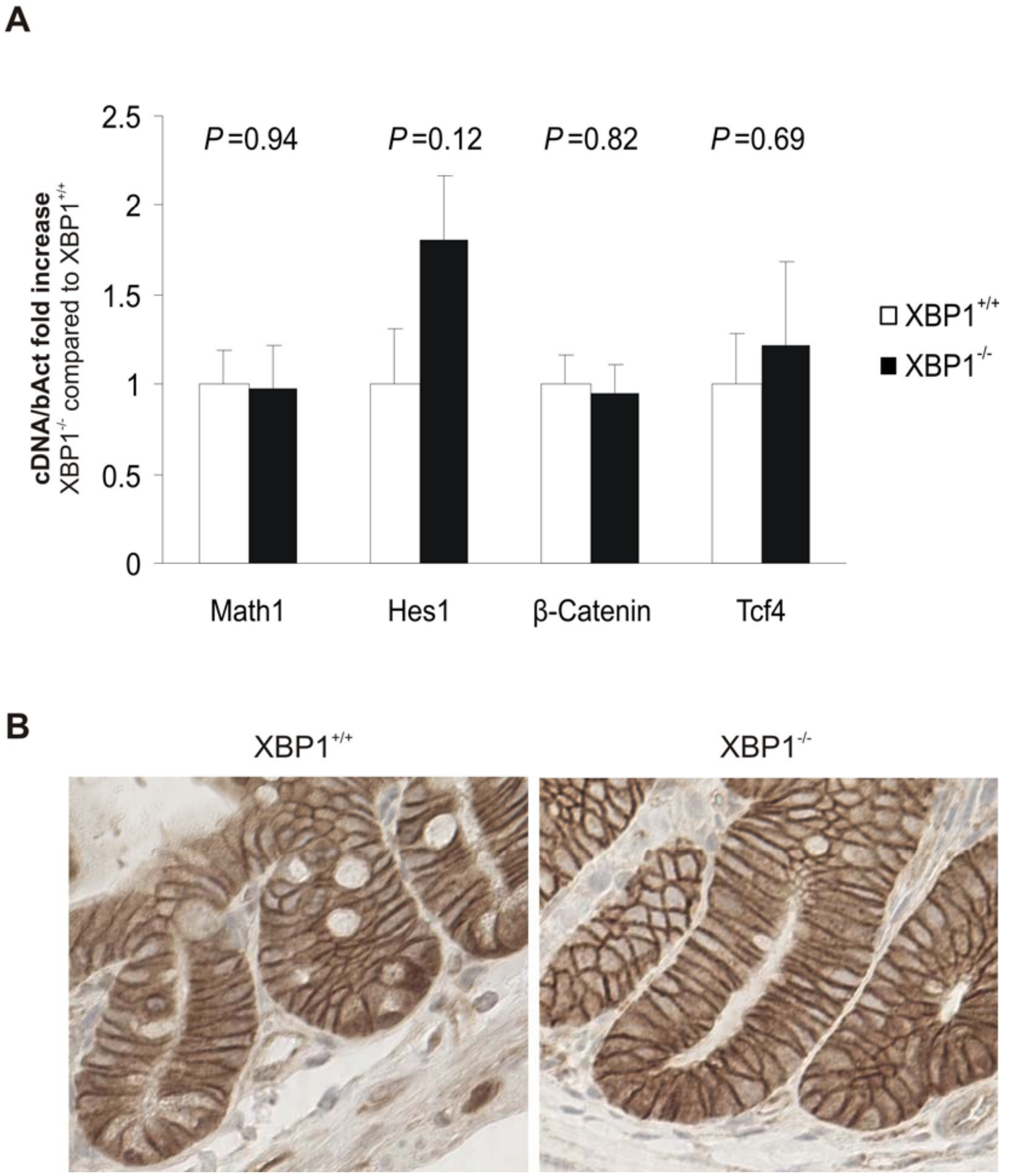
Supplementary Figure 1



Supplementary Figure 2



Supplementary Figure 3



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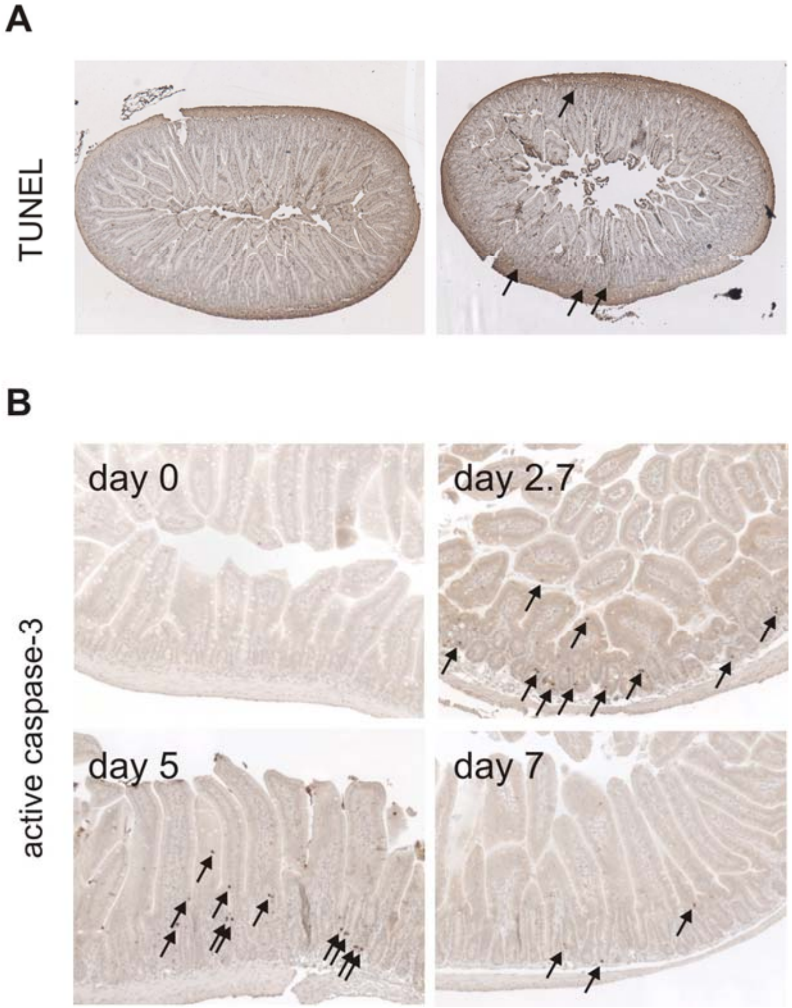
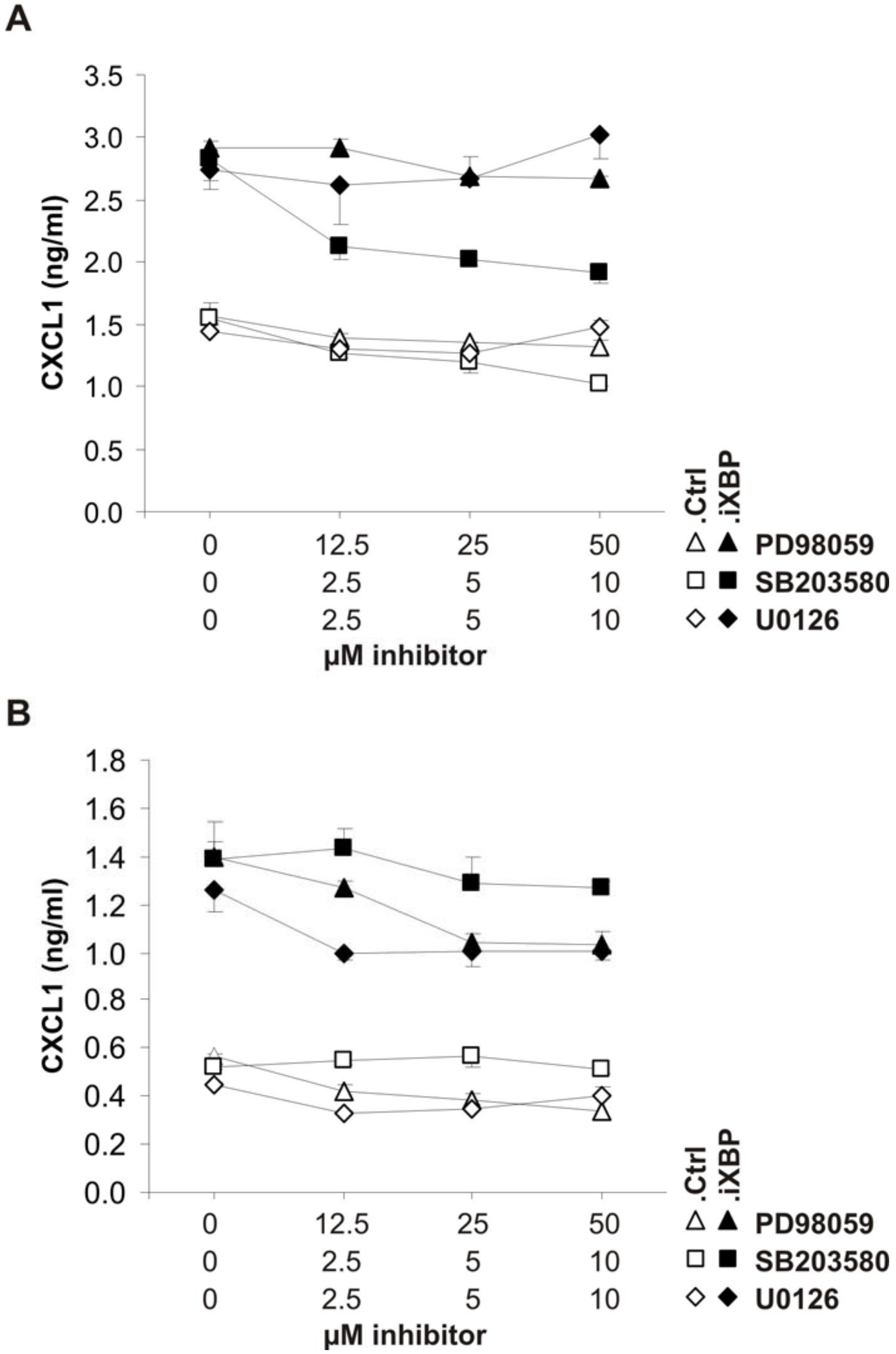


Supplementary Figure 5



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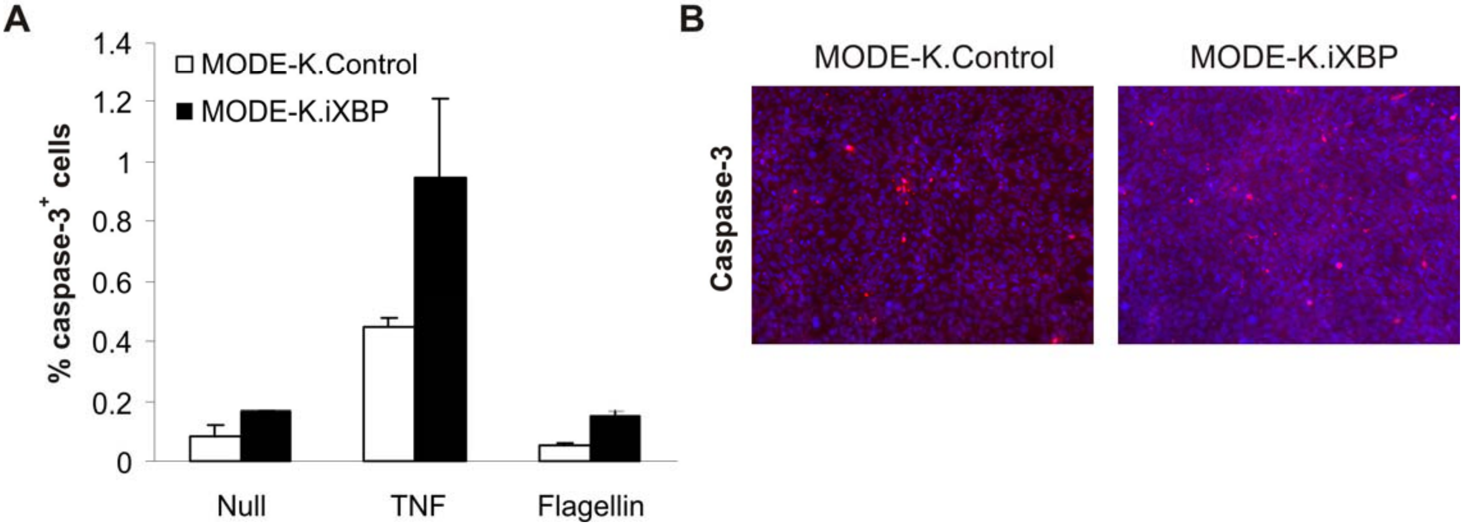

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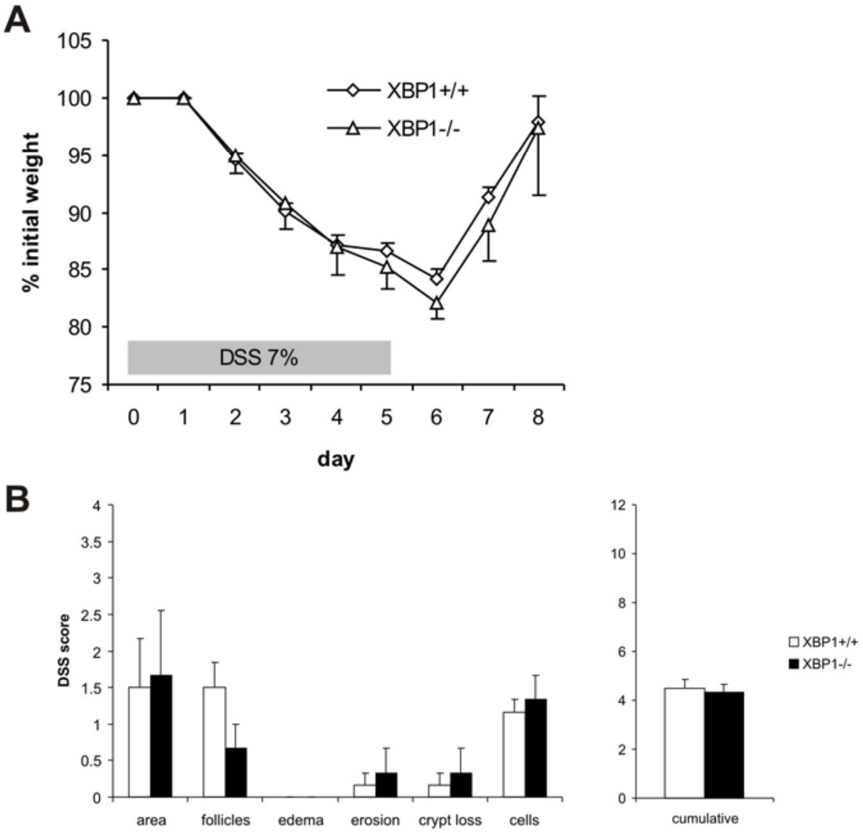
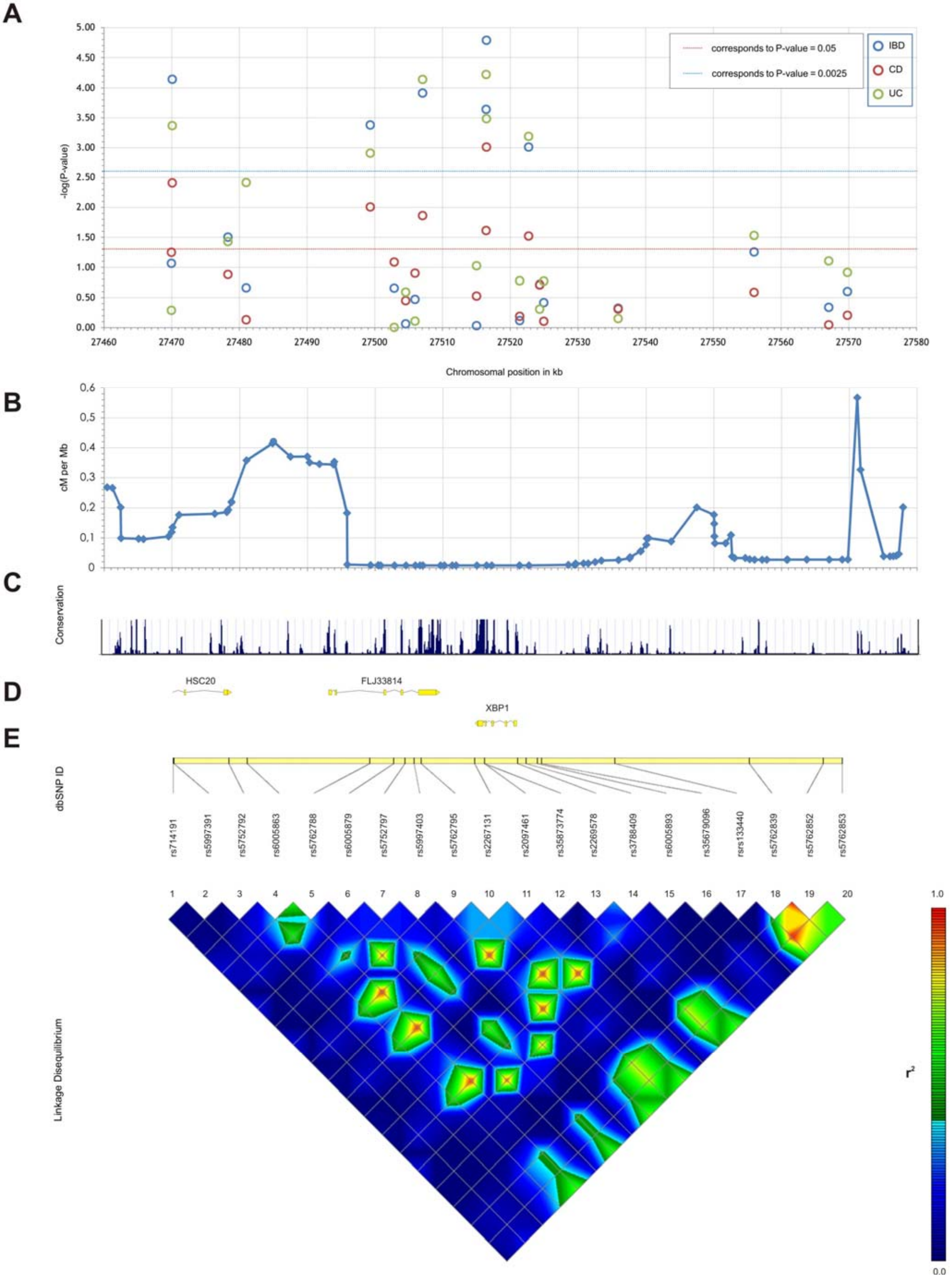


Supplementary Figure 8



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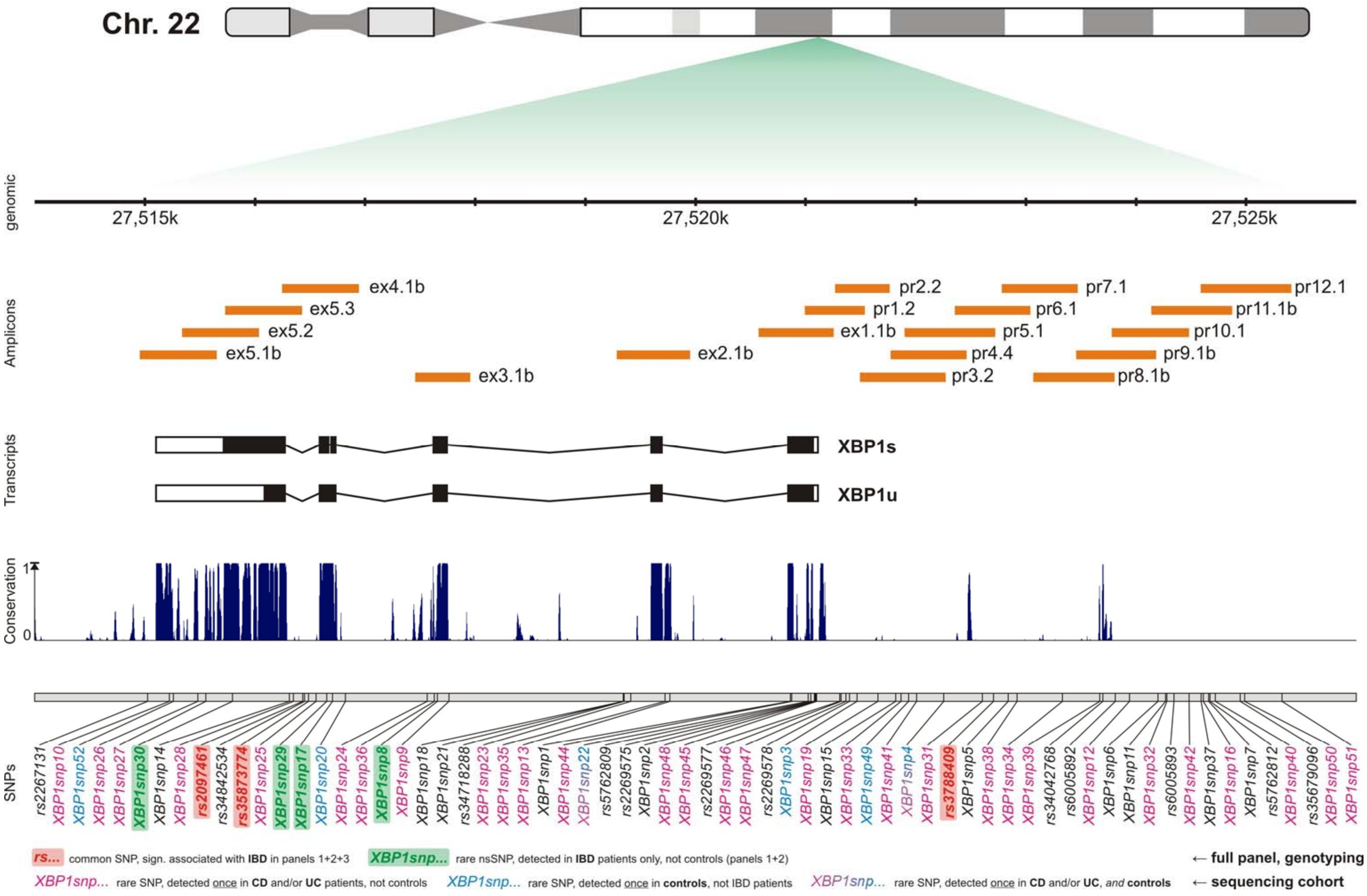

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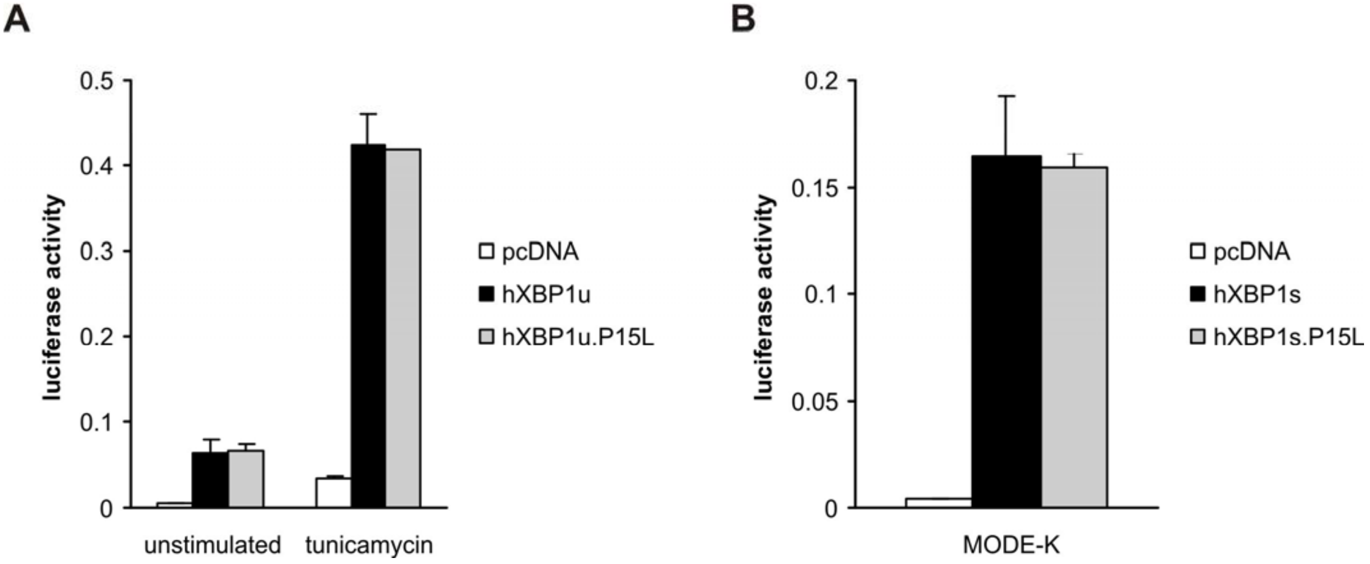

Supplementary Figure 11

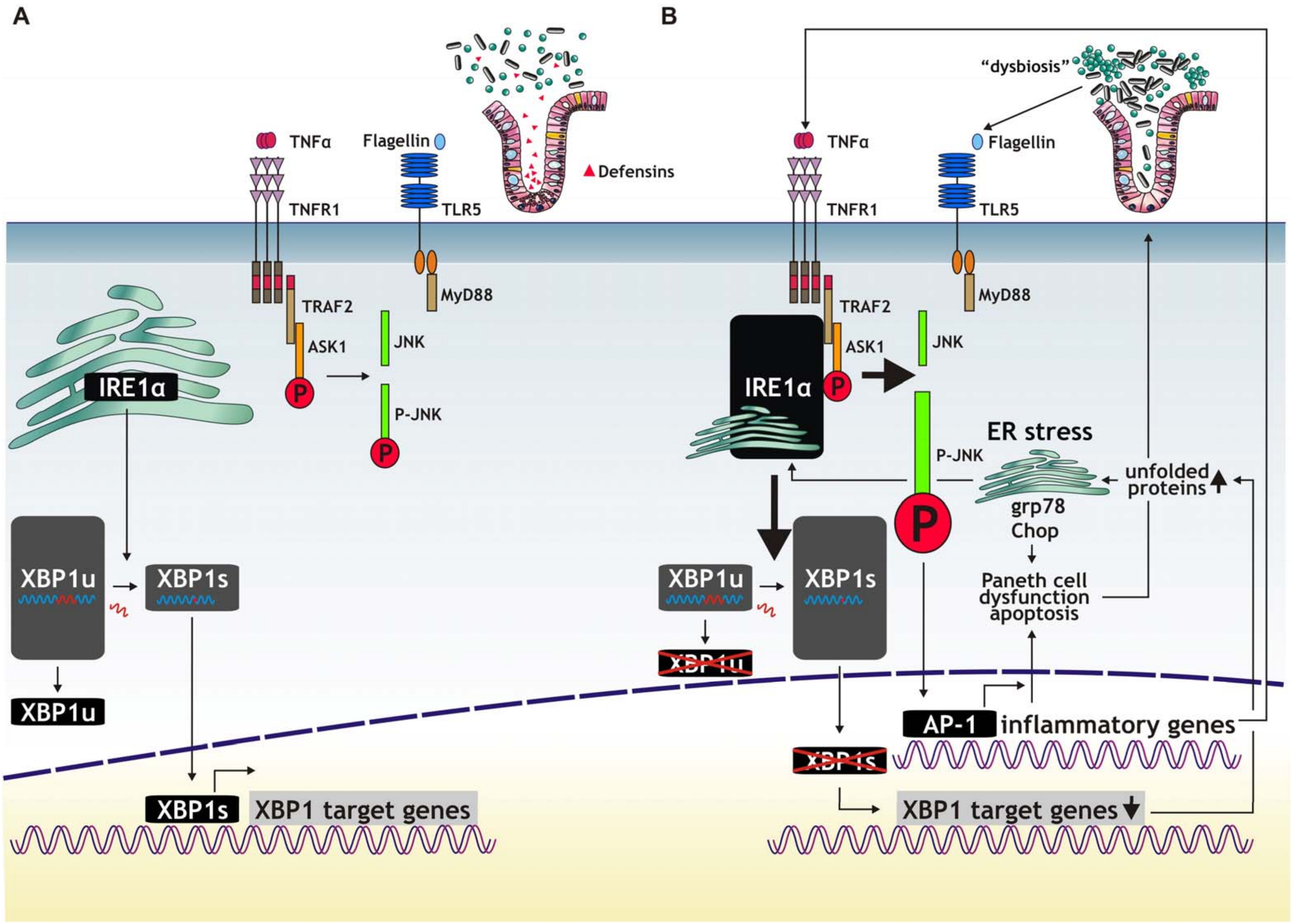

Table S1. Identification of genes that are differentially expressed in the jejunum of the WT and *Xbp1* knock-out mice. Genes with more than two fold changes in the expression level are listed. Total RNAs pooled from three animals per group were subjected to DNA chip experiments using Affymetrix mouse 430 Chips. Data was analyzed by GCOS 1.4 software. P, present; A, absent; D, decrease; I, increase; MI, modest increase. NCBI GEO accession number GSE12038.

Supplementary Table 1. Identification of genes that are differentially expressed in the jejunum of the WT and Xbp1 knock-out mice. Genes with more than two fold changes in the expression level are listed. Total RNAs pool from three animals per each group were subjected to DNA chip experiments using Affymetrix mouse 430 Chips. Data was analyzed by GCOS 1.4 software. P, present; A, absent; D, decrease; I, increase; MI, modest increase

Transcript	WT		KO		Change KO/WT		Gene	
	Signal	Detectio	Signal	Detectio	Fold	Call	Symbol	Title
Defense response								
NM_183253 //	3073	P	4	A	0.00	D	2010016B13R	RIKEN cDNA 2010016B13 gene /// defensin-related cryptdin
NM_007848	546	P	2	A	0.00	D	Defcr-rs7	defensin related cryptdin, related sequence 7
NM_007847	695	P	21	A	0.03	D	Defcr-rs2	defensin related cryptdin, related sequence 2
NM_010039	885	P	45	P	0.07	D	Defcr4	defensin related cryptdin 4
NM_007851	9620	P	385	P	0.07	D	Defcr5	defensin related cryptdin 5
NM_00100758	4263	P	448	P	0.13	D	AY761184	cDNA sequence AY761184
NM_007844	6056	P	814	P	0.14	D	Defcr-rs1	defensin related sequence cryptdin peptide (paneth cells)
NM_007845	63	P	10	A	0.15	D	Defcr-rs10	defensin related cryptdin, related sequence 10
NM_013590	7914	P	1235	P	0.16	D	Lzp-s	P lysozyme structural
NM_013590	8462	P	1516	P	0.22	D	Lzp-s	P lysozyme structural
NM_00101230	8656	P	2043	P	0.23	D	Defcr12 /// De	defensin related cryptdin 12 /// defensin related cryptdin 15 ///
NM_011046	323	P	135	P	0.47	D	Furin	furin (paired basic amino acid cleaving enzyme)
NM_177544	2343	P	5496	P	2.30	I	Ang4	angiogenin, ribonuclease A family, member 4
NM_008330	368	P	1013	P	2.46	I	Ifi47	interferon gamma inducible protein 47
NM_028071	545	P	1356	P	2.46	I	Cotl1	coactosin-like 1 (Dictyostelium)
NM_177544	787	P	1744	P	2.46	I	Ang4	angiogenin, ribonuclease A family, member 4
NM_009684	160	P	404	P	2.46	I	Apaf1	apoptotic peptidase activating factor 1
NM_011541	438	P	1119	P	2.83	I	Tcea1	transcription elongation factor A (SII) 1
NM_011128	202	P	606	P	3.03	I	Pnliprp2	pancreatic lipase-related protein 2
NM_011541	157	P	477	P	3.25	I	Tcea1	transcription elongation factor A (SII) 1
NM_008528	188	P	634	P	3.25	I	Blnk	B-cell linker
NM_008326	125	P	367	P	3.73	I	Irgm	immunity-related GTPase family, M
NM_011128	248	P	832	P	3.73	I	Pnliprp2	pancreatic lipase-related protein 2
NM_010742	24	A	124	P	4.29	I	Ly6d	lymphocyte antigen 6 complex, locus D
Apoptosis								
XM_00100190	7584	P	1286	P	0.16	D	Muc2	mucin 2
NM_020581	494	P	148	P	0.20	D	Angptl4	angiopoietin-like 4
NM_011262	278	P	605	P	2.14	I	Dpf2	D4, zinc and double PHD fingers family 2
NM_011801	212	P	432	P	2.14	I	Cfdp1	craniofacial development protein 1
NM_011585	71	P	119	P	2.14	I	Tia1	cytotoxic granule-associated RNA binding protein 1
NM_023258	1965	P	4347	P	2.14	I	Pycard	PYD and CARD domain containing
NM_018807	101	P	190	P	2.14	I	Plagl2	pleiomorphic adenoma gene-like 2
NM_007661	967	P	2092	P	2.14	I	Cdc2l1	cell division cycle 2-like 1
NM_053157	137	P	325	P	2.14	MI	Tm2d1	TM2 domain containing 1
NM_145452	239	P	446	P	2.14	I	Rasa1	RAS p21 protein activator 1
XM_129968 //	66	P	108	P	2.14	I	Phlpp	PH domain and leucine rich repeat protein phosphatase
NM_172429	151	P	373	P	2.14	I	Smndc1	survival motor neuron domain containing 1
NM_007983	140	P	283	P	2.14	I	Faf1	Fas-associated factor 1
NM_026201	334	P	767	P	2.14	I	Ccar1	cell division cycle and apoptosis regulator 1
NM_181582	452	P	1030	P	2.14	I	Eif5a	eukaryotic translation initiation factor 5A
NM_009810	1127	P	2239	P	2.14	I	Casp3	caspase 3
NM_008960	240	P	619	P	2.14	I	Pten	phosphatase and tensin homolog
NM_009009	120	P	297	P	2.14	I	Rad21	RAD21 homolog (S. pombe)
NM_023229	128	P	329	P	2.14	I	Fastk	Fas-activated serine/threonine kinase
NM_134141	152	A	403	M	2.30	I	Ciapin1	cytokine induced apoptosis inhibitor 1
NM_144541 //	175	P	425	P	2.30	I	Bre	brain and reproductive organ-expressed protein
NM_198176	81	P	183	P	2.30	I	C78212	expressed sequence C78212
NM_134138	47	P	160	P	2.30	MI	Tnfsf5ip1	tumor necrosis factor superfamily, member 5-induced protein 1
NM_019745	245	P	632	P	2.30	I	Pdcd10	programmed cell death 10
NM_134011	155	P	311	P	2.30	I	Tbrg4	transforming growth factor beta regulated gene 4
NM_011997	85	P	181	P	2.30	I	Casp8ap2	caspase 8 associated protein 2
NM_010019	118	P	265	P	2.30	I	Dapk2	death-associated kinase 2
NM_027404	83	P	164	P	2.30	I	Bag5	BCL2-associated athanogene 5
NM_029770	92	P	237	P	2.30	I	Unc5b	unc-5 homolog B (C. elegans)
NM_024239	78	P	191	P	2.46	I	Stambp	Stam binding protein
NM_009172 //	33	P	95	P	2.46	I	Siah1a /// Sial	seven in absentia 1A /// seven in absentia 1B
NM_008960	272	P	716	P	2.46	I	Pten	phosphatase and tensin homolog
XM_905787 //	242	P	681	P	2.46	MI	Rnf7	ring finger protein 7
NM_011615	115	P	294	P	2.46	I	Dedd	death effector domain-containing
NM_009684	160	P	404	P	2.46	I	Apaf1	apoptotic peptidase activating factor 1
NM_009688	167	P	422	P	2.46	I	Birc4	baculoviral IAP repeat-containing 4
XM_905787 //	181	P	453	P	2.46	I	Rnf7	ring finger protein 7
NM_021897	222	P	574	P	2.64	I	Trp53inp1	transformation related protein 53 inducible nuclear protein 1
NM_007530	39	P	88	P	2.64	MI	Bcap29	B-cell receptor-associated protein 29
NM_134138	37	P	103	P	2.64	I	Tnfsf5ip1	tumor necrosis factor superfamily, member 5-induced protein 1
NM_134011	161	P	397	P	2.64	I	Tbrg4	transforming growth factor beta regulated gene 4
NM_023565	97	P	237	P	2.64	I	Cse1l	chromosome segregation 1-like (S. cerevisiae)
NM_172422	80	P	223	P	2.83	I	2810421I24R	RIKEN cDNA 2810421I24 gene
NM_009289	82	P	254	P	2.83	I	Slk	STE20-like kinase (yeast)
NM_178589	158	P	418	P	2.83	I	Tnfrsf21	tumor necrosis factor receptor superfamily, member 21
NM_028133	118	P	278	P	3.03	I	Egln3	EGL nine homolog 3 (C. elegans)
NM_028133	353	P	1101	P	3.03	I	Egln3	EGL nine homolog 3 (C. elegans)
NM_019955	228	P	675	P	3.03	I	Ripk3	receptor-interacting serine-threonine kinase 3
NM_172422	39	P	143	P	3.03	I	2810421I24R	RIKEN cDNA 2810421I24 gene
NM_007859	47	P	84	P	3.25	I	Dffb	DNA fragmentation factor, beta subunit
NM_00101227	96	P	294	P	3.25	I	Birc5	baculoviral IAP repeat-containing 5
NM_009810	164	P	573	P	3.25	I	Casp3	caspase 3
NM_025380	72	P	286	P	3.25	I	Eef1e1	eukaryotic translation elongation factor 1 epsilon 1
NM_023646	156	P	516	P	3.25	I	Dnaja3	DnaJ (Hsp40) homolog, subfamily A, member 3
NM_023646	61	P	291	P	4.00	I	Dnaja3	DnaJ (Hsp40) homolog, subfamily A, member 3
NM_008234	16	A	88	P	4.92	I	Hells	helicase, lymphoid specific
Cell cycle								
NM_007595	93	P	4	A	0.06	D	Camk2b	Calcium/calmodulin-dependent protein kinase II, beta
NM_134101	693	P	1467	P	2.14	I	Psmd2	proteasome (prosome, macropain) 26S subunit, non-ATPase, 2
NM_007661	967	P	2092	P	2.14	I	Cdc2l1	cell division cycle 2-like 1
NM_019750	128	P	269	P	2.14	I	Nat6	N-acetyltransferase 6
NM_010237	384	P	911	P	2.14	I	Frk	fyn-related kinase
NM_013917	188	P	381	P	2.14	I	Pttg1	pituitary tumor-transforming 1
NM_134077	54	P	123	P	2.14	I	1700009P03R	RIKEN cDNA 1700009P03 gene
NM_013812	249	A	572	P	2.14	I	Cdk2ap1	CDK2 (cyclin-dependent kinase 2)-associated protein 1
NM_026904	96	P	236	P	2.14	MI	Anapc10	anaphase promoting complex subunit 10
NM_021535	356	P	808	P	2.14	I	Smu1	smu-1 suppressor of mec-8 and unc-52 homolog (C. elegans)
NM_026201	334	P	767	P	2.14	I	Ccar1	cell division cycle and apoptosis regulator 1
NM_021465	260	P	607	P	2.14	I	Stag2	stromal antigen 2
NM_008960	240	P	619	P	2.14	I	Pten	phosphatase and tensin homolog
NM_030732	80	P	193	P	2.14	MI	Tbl1xr1	transducin (beta)-like 1X-linked receptor 1
NM_029402	136	P	266	P	2.14	I	Cul2	cullin 2
XM_00100040	71	P	153	P	2.14	I	Sbno1	sno, strawberry notch homolog 1 (Drosophila)
NM_133656	486	P	1083	P	2.30	I	Crk	v-crk sarcoma virus CT10 oncogene homolog (avian)
NM_130889	266	P	627	P	2.30	I	Anp32b	acidic nuclear phosphoprotein 32 family, member B
NM_007658	379	P	833	P	2.30	I	Cdc25a	cell division cycle 25 homolog A (S. cerevisiae)
NM_011666	307	P	660	P	2.30	I	Ube1c	ubiquitin-activating enzyme E1C
NM_011317	90	P	130	P	2.30	MI	Khdrbs1	KH domain containing, RNA binding, signal transduction associated 1
NM_009870 //	90	P	231	P	2.30	I	Cdk4 /// LOC	cyclin-dependent kinase 4 /// similar to Cell division protein kinase 4 (Cycli
NM_009870	99	P	276	P	2.30	I	Cdk4	cyclin-dependent kinase 4
NM_011806	113	P	248	P	2.30	I	Dmtf1	cyclin D binding myb-like transcription factor 1
NM_009361 //	180	P	435	P	2.30	I	Tfdp1 /// LOC	transcription factor Dp 1 /// similar to Transcription factor Dp-1 (E2F dimer
NM_027357	395	P	956	P	2.30	I	Psmd1	proteasome (prosome, macropain) 26S subunit, non-ATPase, 1
NM_011666	426	P	735	P	2.30	I	Ube1c	ubiquitin-activating enzyme E1C
NM_008224	138	P	302	P	2.30	I	Hcfc1	host cell factor C1
NM_139269	643	P	1591	P	2.30	I	Hrasls3	HRAS like suppressor 3
NM_134138	47	P	160	P	2.30	MI	Tnfsf5ip1	tumor necrosis factor superfamily, member 5-induced protein 1
NM_009974	170	P	369	P	2.30	I	Csnk2a2	casein kinase II, alpha 2, polypeptide
NM_013715	393	P	950	P	2.30	I	Cops5	COP9 (constitutive photomorphogenic) homolog, subunit 5 (Arabidopsis th
NM_153599 //	262	P	586	P	2.30	I	Cdk8	cyclin-dependent kinase 8
NM_134155	105	P	254	P	2.46	I	Brms1	breast cancer metastasis-suppressor 1
NM_009172 //	33	P	95	P	2.46	I	Siah1a /// Sial	seven in absentia 1A /// seven in absentia 1B
NM_010948 //	213	P	542	P	2.46	I	Nudc /// Nudc	nuclear distribution gene C homolog (Aspergillus) /// nuclear distribution ge
NM_009870 //	43	P	141	P	2.46	I	Cdk4 /// LOC	cyclin-dependent kinase 4 /// similar to Cell division protein kinase 4 (Cycli
NM_008960	272	P	716	P	2.46	I	Pten	phosphatase and tensin homolog
NM_009791	19	A	53	P	2.46	I	Aspm	asp (abnormal spindle)-like, microcephaly associated (Drosophila)
NM_146171	36	P	102	P	2.46	I	2810406C15R	RIKEN cDNA 2810406C15 gene
NM_009668	87	P	175	P	2.46	I	Bin1	bridging integrator 1
NM_145991	202	P	509	P	2.46	I	Cdc73	Vcell division cycle 73, Paf1/RNA polymerase II complex component, hom
NM_011903	69	P	164	P	2.46	I	Tlk2	tousled-like kinase 2 (Arabidopsis)
NM_011666	289	P	728	P	2.46	I	Ube1c	ubiquitin-activating enzyme E1C
NM_013812	196	P	550	P	2.46	I	Cdk2ap1	CDK2 (cyclin-dependent kinase 2)-associated protein 1
NM_009391 //	734	P	1658	P	2.46	I	Ran /// LOC6	RAN, member RAS oncogene family /// similar to RAN, member RAS onc
NM_172301	35	P	149	P	2.46	I	Ccnb1-rs1 ///	cyclin B1, related sequence 1 /// cyclin B1
NM_009831	91	P	255	P	2.46	I	Ccng1	cyclin G1
NM_010898	127	P	339	P	2.46	I	Nf2	neurofibromatosis 2
NM_139269	466	P	1129	P	2.46	I	Hrasls3	HRAS like suppressor 3
NM_133786	168	P	368	P	2.46	I	Smc4l1	SMC4 structural maintenance of chromosomes 4-like 1 (yeast)
NM_013812	244	P	678	P	2.46	I	Cdk2ap1	CDK2 (cyclin-dependent kinase 2)-associated protein 1
NM_007684	130	P	346	P	2.64	I	Cetn3	centrin 3
NM_134138	37	P	103	P	2.64	I	Tnfsf5ip1	tumor necrosis factor superfamily, member 5-induced protein 1
NM_146066	330	P	811	P	2.64	I	Gspt1	G1 to S phase transition 1
NM_00100981	136	P	328	P	2.64	I	38971	septin 11
NM_009391 //	870	P	2336	P	2.64	I	Ran /// LOC6	RAN, member RAS oncogene family /// similar to RAN, member RAS onc
NM_009391 //	432	P	1332	P	2.64	I	Ran /// LOC6	RAN, member RAS oncogene family /// similar to RAN, member RAS onc
NM_011121	25	P	107	P	2.64	I	Plk1	polo-like kinase 1 (Drosophila)
NM_009584	64	P	151	P	2.64	I	Dnajc2	DnaJ (Hsp40) homolog, subfamily C, member 2
NM_146066	337	P	929	P	2.64	I	Gspt1	G1 to S phase transition 1
NM_025415	141	P	481	P	2.83	I	Cks2	CDC28 protein kinase regulatory subunit 2
NM_025415	185	P	506	P	2.83	I	Cks2	CDC28 protein kinase regulatory subunit 2
NM_009584	97	P	319	P	2.83	I	Dnajc2	DnaJ (Hsp40) homolog, subfamily C, member 2
NM_009391 //	556	P	1611	P	2.83	I	Ran /// LOC6	RAN, member RAS oncogene family /// similar to RAN, member RAS onc
NM_007568	26	P	98	P	2.83	I	Btc	betacellulin, epidermal growth factor family member
NM_009773	18	A	63	P	2.83	I	Bub1b	budding uninhibited by benzimidazoles 1 homolog, beta (S. cerevisiae)
NM_007631	129	P	267	P	2.83	I	Ccnd1	cyclin D1
NM_012025	43	A	94	P	2.83	I	Racgap1	Rac GTPase-activating protein 1
NM_023223	117	P	256	P	3.03	I	Cdc20	cell division cycle 20 homolog (S. cerevisiae)
NM_0010404	17	P	63	P	3.03	I	Tacc3	transforming, acidic coiled-coil containing protein 3
NM_019499	72	P	232	P	3.03	I	Mad2l1	MAD2 (mitotic arrest deficient, homolog)-like 1 (yeast)
NM_026758	44	P	198	P	3.03	I	Mphosph6	M phase phosphoprotein 6
NM_010093	121	P	282	P	3.03	I	E2f3	E2F transcription factor 3
NM_0010133	21	P	71	P	3.03	I	E2f8	E2F transcription factor 8
NM_008017	41	P	169	P	3.03	I	Smc2l1	SMC2 structural maintenance of chromosomes 2-like 1 (yeast)
NM_010353	22	P	65	P	3.03	I	Gsg2	germ cell-specific gene 2
NM_173867	33	A	102	P	3.03	I	Rcc2	regulator of chromosome condensation 2
NM_007631	109	P	369	P	3.25	I	Ccnd1	cyclin D1
NM_013726	68	P	212	P	3.25	I	Dbf4	DBF4 homolog (S. cerevisiae)
NM_009772	17	P	65	P	3.25	I	Bub1	budding uninhibited by benzimidazoles 1 homolog (S. cerevisiae)
NM_007951	329	P	897	P	3.25	I	Erh	enhancer of rudimentary homolog (Drosophila)
NM_153547 //	52	P	198	P	3.25	I	Gnl3	guanine nucleotide binding protein-like 3 (nucleolar)
XM_907548 //	52	P	152	P	3.25	I	Ccnjl	cyclin J-like
NM_016904	81	P	276	P	3.48	I	Cks1b	CDC28 protein kinase 1b
NM_016692	77	P	269	P	3.48	I	Incenp	inner centromere protein
NM_007630	58	P	214	P	3.48	I	Ccnb2	cyclin B2

Transcript	WT		KO		Change KO/WT		Gene	
	Signal	Detectio	Signal	Detectio	Fold	Call	Symbol	Title
NM_007900	19	P	84	P	3.73	I	Ect2	ect2 oncogene
NM_145150	46	P	182	P	3.73	I	Prc1	protein regulator of cytokinesis 1
NM_011496	19	A	70	P	3.73	I	Aurkb	aurora kinase B
NM_173867	32	P	127	P	3.73	I	Rcc2	regulator of chromosome condensation 2
NM_026785	112	P	575	P	3.73	I	Ube2c	ubiquitin-conjugating enzyme E2C
NM_009828	50	P	213	P	4.00	I	Ccna2	cyclin A2
NM_007659	65	P	223	P	4.00	I	Cdc2a	cell division cycle 2 homolog A (S. pombe)
NM_010848 //	35	P	98	P	4.59	I	Myb	myeloblastosis oncogene
NM_172301 //	22	P	113	P	4.92	I	Ccnb1-rs1 ///	cyclin B1, related sequence 1 /// cyclin B1 /// similar to G2/mitotic-specifi
NM_007950	76	P	385	P	4.92	I	Ereg	epiregulin
NM_010892	27	A	146	P	4.92	I	Nek2	NIMA (never in mitosis gene a)-related expressed kinase 2
NM_009828	46	P	224	P	5.28	I	Ccna2	cyclin A2
NM_012025	6	P	51	P	5.28	I	Racgap1	Rac GTPase-activating protein 1
NM_172839	20	A	98	P	5.28	I	Ccnj	cyclin J
NM_010848 //	11	A	69	P	7.46	I	Myb	myeloblastosis oncogene
NM_007837	143	P	1258	P	9.19	I	Ddit3	DNA-damage inducible transcript 3
NM_030693	35	P	1136	P	24.25	I	Atf5	activating transcription factor 5
NM_010633 //	1	A	51	P	48.50	I	Uhmk1 /// LO	U2AF homology motif (UHM) kinase 1 /// similar to U2AF homology moti
Unfolded protein response								
NM_007837	143	P	1258	P	9.19	I	Ddit3	DNA-damage inducible transcript 3
NM_011631	539	P	2755	P	5.66	I	Hsp90b1	heat shock protein 90kDa beta (Grp94), member 1
NM_022310	1227	P	5977	P	4.29	I	Hspa5	heat shock 70kD protein 5 (glucose-regulated protein)
NM_015774	349	P	1509	P	4.29	I	Ero1l	ERO1-like (S. cerevisiae)
NM_015774	152	P	624	P	4.29	I	Ero1l	ERO1-like (S. cerevisiae)
NM_015774	314	P	1193	P	3.73	I	Ero1l	ERO1-like (S. cerevisiae)
NM_022310	2292	P	8868	P	3.48	I	Hspa5	heat shock 70kD protein 5 (glucose-regulated protein)
NM_011631	1488	P	4738	P	3.03	I	Hsp90b1	heat shock protein 90kDa beta (Grp94), member 1
NM_009716	245	P	618	P	2.64	I	Atf4	activating transcription factor 4
NM_021305	30	P	86	P	2.46	I	Sec61a2	Sec61, alpha subunit 2 (S. cerevisiae)
NM_023913	175	P	397	P	2.30	I	Ern1	Endoplasmic reticulum (ER) to nucleus signalling 1
NM_138585	70	P	190	P	2.30	I	Cherp	calcium homeostasis endoplasmic reticulum protein
NM_029103	1123	P	2907	P	2.30	I	Armet	arginine-rich, mutated in early stage tumors
NM_009716	1475	P	2986	P	2.14	I	Atf4	activating transcription factor 4
Others								
XM_130038 //	1547	P	146	P	0.08	D	Cubn	cubilin (intrinsic factor-cobalamin receptor)
XM_130038 //	2738	P	218	P	0.08	D	Cubn	cubilin (intrinsic factor-cobalamin receptor)
NM_010584	1962	P	211	P	0.11	D	Itlna	intelectin a
XM_485660 //	64	P	7	A	0.13	D	Pigg	phosphatidylinositol glycan, class G
NM_145424	70	P	11	A	0.13	D	BC089597	cDNA sequence BC089597
NM_013743	249	P	40	P	0.15	D	Pdk4	pyruvate dehydrogenase kinase, isoenzyme 4
NM_0010095	8015	P	1394	P	0.15	D	Naaladl1	N-acetylated alpha-linked acidic dipeptidase-like 1
NM_010776	87	P	10	A	0.19	D	Mbl2	mannose binding lectin (C)
---	71	P	29	P	0.19	D	---	---
NM_007472	1105	P	245	P	0.20	D	Aqp1	aquaporin 1
NM_026384	1768	P	327	P	0.20	D	Dgat2	diacylglycerol O-acyltransferase 2
XM_973716 //	1017	P	167	P	0.20	D	LOC664968 /	hypothetical protein LOC664968 /// hypothetical protein LOC669621 /// h
NM_026384	2267	P	576	P	0.22	D	Dgat2	diacylglycerol O-acyltransferase 2
NM_133213 //	1124	P	236	P	0.23	D	Xpnpep2	X-prolyl aminopeptidase (aminopeptidase P) 2, membrane-bound
NM_134072	118	P	25	P	0.25	D	Akr1c14	aldo-keto reductase family 1, member C14
NM_026701	62	P	5	A	0.25	D	0610038K03	RIKEN cDNA 0610038K03 gene
NM_133970	302	P	80	A	0.25	D	D8Ertd354e	DNA segment, Chr 8, ERATO Doi 354, expressed
NM_011576	51	P	10	A	0.25	D	Tfpi	tissue factor pathway inhibitor
NM_0010395	732	P	177	P	0.27	D	9030012A22	RIKEN cDNA 9030012A22 gene
NM_026501 //	333	P	83	P	0.27	D	1300010M03	RIKEN cDNA 1300010M03 gene
NM_144930	149	P	28	P	0.27	D	AU018778	expressed sequence AU018778
XM_620178 //	2087	P	562	P	0.27	D	Plb1 /// BC03	phospholipase B1 /// cDNA sequence BC033606 /// similar to phospholi
NM_146117	268	P	65	P	0.27	D	BC004853	cDNA sequence BC004853
NM_026159	641	P	220	P	0.31	D	Retsat	retinol saturase (all trans retinol 13,14 reductase)
NM_017473	1119	P	395	P	0.31	D	Rdh7	retinol dehydrogenase 7
---	90	P	32	A	0.31	D	---	---
NM_019521	375	P	110	P	0.33	D	Gas6	growth arrest specific 6
NM_011213	1026	P	403	P	0.33	D	Ptprf	protein tyrosine phosphatase, receptor type, F
NM_023219	818	P	339	P	0.33	D	Slc5a4b	solute carrier family 5 (neutral amino acid transporters, system A), memb
---	55	P	14	P	0.33	D	---	---
NM_028094	779	P	288	P	0.33	D	Ugt2a3	UDP glucuronosyltransferase 2 family, polypeptide A3
NM_010684	4503	P	1469	P	0.35	D	Lamp1	lysosomal membrane glycoprotein 1
NM_009856	68	P	28	A	0.35	D	Cd83	CD83 antigen
NM_146149	901	P	310	P	0.35	D	BC026682	cDNA sequence BC026682
NM_007815	83	P	26	P	0.35	D	Cyp2c29	cytochrome P450, family 2, subfamily c, polypeptide 29
NM_016960	633	P	236	P	0.35	D	Ccl20	chemokine (C-C motif) ligand 20
NM_0010014	55	P	16	P	0.35	D	Cyp2c44	cytochrome P450, family 2, subfamily c, polypeptide 44
NM_027890	1105	P	342	P	0.35	D	Susd2	sushi domain containing 2
---	89	P	44	M	0.35	D	---	Transcribed locus
---	67	P	24	P	0.35	D	9130221J18R	RIKEN cDNA 9130221J18 gene
NM_011213	2391	P	871	P	0.38	D	Ptprf	protein tyrosine phosphatase, receptor type, F
NM_015740	399	P	182	P	0.38	D	Bloc1s1	biogenesis of lysosome-related organelles complex-1, subunit 1
NM_145435	285	P	128	A	0.38	D	Pyy	peptide YY
---	149	P	63	A	0.38	D	---	---
NM_177380	76	P	27	A	0.38	D	Cyp3a44	cytochrome P450, family 3, subfamily a, polypeptide 44
XM_0010011	302	P	110	P	0.38	D	Stim2	stromal interaction molecule 2
NM_031843	50	P	16	A	0.38	D	Dpp7	dipeptidylpeptidase 7
NM_031843	114	P	49	P	0.38	D	Dpp7	dipeptidylpeptidase 7
NM_019577	85	P	46	A	0.38	D	Ccl24	chemokine (C-C motif) ligand 24
NM_008585	2431	P	964	P	0.38	D	Mep1a	meprin 1 alpha
NM_028841	92	P	37	A	0.38	D	Tspan17	tetraspanin 17
NM_007860	1349	P	675	P	0.41	D	Dio1	deiodinase, iodothyronine, type I

Transcript	WT		KO		Change KO/WT		Gene	
	Signal	Detectio	Signal	Detectio	Fold	Call	Symbol	Title
NM_019447	225	P	90	P	0.41	D	Hgfac	hepatocyte growth factor activator
NM_011213	2224	P	861	P	0.41	D	Ptprf	protein tyrosine phosphatase, receptor type, F
NM_0010348	960	P	470	P	0.41	D	1810015C04	RIKEN cDNA 1810015C04 gene
NM_0010335	238	P	84	P	0.41	D	Kcnk6	potassium inwardly-rectifying channel, subfamily K, member 6
NM_0010348	278	P	98	P	0.41	D	1810015C04	RIKEN cDNA 1810015C04 gene
XM_131138 //	181	P	55	P	0.41	D	Gm131 /// LO	gene model 131, (NCBI) /// similar to prochymosin
NM_024264	1133	P	487	P	0.44	D	Cyp27a1	cytochrome P450, family 27, subfamily a, polypeptide 1
NM_033603	2596	P	1158	P	0.44	D	Amn	amnionless
NM_026183	317	P	145	P	0.44	D	1300013J15R	RIKEN cDNA 1300013J15 gene
NM_028749	781	P	401	P	0.44	D	Npl	N-acetylneuraminate pyruvate lyase
NM_009755	107	P	46	A	0.44	D	Bmp1	bone morphogenetic protein 1
NM_008124	278	P	119	P	0.44	D	Gjb1	gap junction membrane channel protein beta 1
NM_021486	101	P	41	P	0.44	D	Bcmo1	beta-carotene 15,15'-monooxygenase
---	177	P	74	P	0.44	D	---	---
NM_010220	739	P	356	P	0.47	D	Fkbp5	FK506 binding protein 5
NM_009899	196	P	83	P	0.47	D	Clca1	chloride channel calcium activated 1
NM_021274	79	P	28	A	0.47	D	Cxcl10	chemokine (C-X-C motif) ligand 10
NM_009467	101	P	29	P	0.47	D	Ugt2b5	UDP glucuronosyltransferase 2 family, polypeptide B5
NM_008013	228	P	116	P	0.47	D	Fgl2	fibrinogen-like protein 2
NM_147776	383	P	172	P	0.47	D	Vwa1	von Willebrand factor A domain containing 1
---	114	P	70	P	0.47	D	---	0 day neonate lung cDNA, RIKEN full-length enriched library, clone:E0300
NM_008585	1683	P	802	P	0.47	D	Mep1a	meprin 1 alpha
NM_010220	285	P	125	P	0.47	D	Fkbp5	FK506 binding protein 5
NM_146131	177	P	109	P	0.47	D	Pbxip1	pre-B-cell leukemia transcription factor interacting protein 1
NM_010284	63	P	33	P	0.47	D	Ghr	growth hormone receptor
NM_008707	696	P	1447	P	2.14	I	Nmt1	N-myristoyltransferase 1
NM_007862	311	P	607	P	2.14	I	Dlgh1	discs, large homolog 1 (Drosophila)
NM_021523	223	P	465	P	2.14	I	Huwe1	HECT, UBA and WWE domain containing 1
XM_898905 //	410	P	856	P	2.14	I	1110019J04R	RIKEN cDNA 1110019J04 gene
NM_026268	1207	P	2487	P	2.14	I	Dusp6	dual specificity phosphatase 6
NM_013507	1813	P	3872	P	2.14	I	Eif4g2	eukaryotic translation initiation factor 4, gamma 2
NM_007563	373	P	833	P	2.14	I	Bpgm	2,3-bisphosphoglycerate mutase
NM_013494	132	P	391	P	2.14	I	Cpe	carboxypeptidase E
NM_008568	87	P	217	P	2.14	I	Mcm7	minichromosome maintenance deficient 7 (S. cerevisiae)
---	115	P	270	P	2.14	I	---	---
NM_011418	159	P	350	P	2.14	I	Smarcb1	SWI/SNF related, matrix associated, actin dependent regulator of chromat
NM_053092 //	300	P	689	P	2.14	I	Kars /// LOC6	lysyl-tRNA synthetase /// similar to lysyl-tRNA synthetase
NM_019703	2146	P	4637	P	2.14	I	Pfkp	phosphofructokinase, platelet
NM_025860	43	P	115	P	2.14	I	Ddx18	DEAD (Asp-Glu-Ala-Asp) box polypeptide 18
NM_009551	641	P	1531	P	2.14	I	Za20d2	zinc finger, A20 domain containing 2
NM_018749	446	P	930	P	2.14	I	Eif3s7	eukaryotic translation initiation factor 3, subunit 7 (zeta)
NM_011899 //	539	P	1142	P	2.14	I	Srp54 /// LOC	signal recognition particle 54 /// similar to signal recognition particle 54
NM_018758	361	P	720	P	2.14	I	Apba3	amyloid beta (A4) precursor protein-binding, family A, member 3
NM_010256	32	A	83	P	2.14	I	Gart	phosphoribosylglycinamide formyltransferase
NM_015729	1333	P	2848	P	2.14	I	Acox1	acyl-Coenzyme A oxidase 1, palmitoyl
NM_016739	1204	P	2579	P	2.14	I	Gpiap1	GPI-anchored membrane protein 1
NM_016897	821	P	1702	P	2.14	I	Timm23	translocase of inner mitochondrial membrane 23 homolog (yeast)
NM_007926	480	P	1065	P	2.14	I	Scye1	small inducible cytokine subfamily E, member 1
NM_009722	161	P	351	P	2.14	I	Atp2a2	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2
NM_019685	28	P	70	P	2.14	I	Ruvbl1	RuvB-like protein 1
NM_026635	845	P	1842	P	2.14	I	5730536A07	RIKEN cDNA 5730536A07 gene
NM_011504	722	P	1421	P	2.14	I	Stxbp3a	syntaxin binding protein 3A
NM_009940	469	P	798	P	2.14	I	Coq7	demethyl-Q 7
NM_026124	1345	P	3054	P	2.14	I	1110008F13	RIKEN cDNA 1110008F13 gene
NM_026499	178	P	371	P	2.14	I	Sfrs6	splicing factor, arginine/serine-rich 6
NM_021537	556	P	1275	P	2.14	I	Stk25	serine/threonine kinase 25 (yeast)
NM_009311	83	P	213	P	2.14	MI	Tac1	tachykinin 1
NM_026438	2957	P	6475	P	2.14	I	Ppa1	pyrophosphatase (inorganic) 1
NM_023721	445	P	881	P	2.14	I	Atp6v1d	ATPase, H+ transporting, lysosomal V1 subunit D
NM_026658	29	P	89	P	2.14	I	Mto1	mitochondrial translation optimization 1 homolog (S. cerevisiae)
NM_0010123	247	P	521	P	2.14	I	Zfp238	zinc finger protein 238
NM_011971	762	P	1563	P	2.14	I	Psmb3	proteasome (prosome, macropain) subunit, beta type 3
NM_022023	100	P	206	P	2.14	I	Gmfb	glia maturation factor, beta
NM_133348	272	P	640	P	2.14	I	Acot7	acyl-CoA thioesterase 7
NM_016661	603	P	1171	P	2.14	I	Ahcy	S-adenosylhomocysteine hydrolase
NM_010773	368	P	901	P	2.14	I	Mbd2	methyl-CpG binding domain protein 2
NM_138599	221	P	599	P	2.14	I	Tomm70a	translocase of outer mitochondrial membrane 70 homolog A (yeast)
NM_007497	152	P	336	P	2.14	I	Atf1	activating transcription factor 1
NM_133888	1225	P	2646	P	2.14	I	Smpdl3b	sphingomyelin phosphodiesterase, acid-like 3B
NM_007927	60	A	122	P	2.14	I	Emd	emerin
NM_009447	768	P	1670	P	2.14	I	Tuba4	tubulin, alpha 4
NM_016721	447	P	934	P	2.14	I	Iqgap1	IQ motif containing GTPase activating protein 1
NM_008907	3109	P	6605	P	2.14	MI	Ppia	peptidylprolyl isomerase A
NM_133825	554	P	1196	P	2.14	I	D1Ertd622e	DNA segment, Chr 1, ERATO Doi 622, expressed
NM_021529	138	P	298	P	2.14	I	4930511A21	RIKEN cDNA 4930511A21 gene
NM_015736	174	P	392	P	2.14	I	Galnt3	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminylt
NM_019440	180	P	449	P	2.14	I	Iigp2	interferon inducible GTPase 2
NM_0010298	385	P	792	P	2.14	I	Slc16a6	solute carrier family 16 (monocarboxylic acid transporters), member 6
NM_023585	84	P	210	P	2.14	I	Ube2v2	ubiquitin-conjugating enzyme E2 variant 2
NM_011192	154	P	330	P	2.14	I	Psme3	proteaseome (prosome, macropain) 28 subunit, 3
NM_025319	254	P	543	P	2.14	I	0610009B22	RIKEN cDNA 0610009B22 gene
NM_007794 //	206	P	487	P	2.14	I	Ctcf	CCCTC-binding factor
NM_013754	311	P	612	P	2.14	I	Insl6	insulin-like 6
NM_008448	720	P	1543	P	2.14	I	Kif5b	kinesin family member 5B
NM_013747	420	P	837	P	2.14	MI	Golga5	golgi autoantigen, golgin subfamily a, 5
NM_025530	55	P	138	P	2.14	I	Cutc	cutC copper transporter homolog (E.coli)

Transcript	WT		KO		Change KO/WT		Gene	
	Signal	Detectio	Signal	Detectio	Fold	Call	Symbol	Title
NM_031179	296	P	628	P	2.14	I	Sf3b1	splicing factor 3b, subunit 1
NM_026023	229	P	407	P	2.14	I	Nudcd2	NudC domain containing 2
---	416	P	812	P	2.14	I	---	---
NM_016884 //	186	P	387	P	2.14	I	Hnrpc /// LOC	heterogeneous nuclear ribonucleoprotein C /// similar to heterogeneous n
NM_011794	1053	P	2298	P	2.14	I	Bpnt1	bisphosphate 3'-nucleotidase 1
NM_025555	357	P	741	P	2.14	I	2410004B18R	RIKEN cDNA 2410004B18 gene
NM_133188	240	P	473	P	2.14	I	Dazap1	DAZ associated protein 1
NM_133669	124	P	264	P	2.14	I	Rp2h	retinitis pigmentosa 2 homolog (human)
NM_145510	181	P	383	P	2.14	I	Rabif	RAB interacting factor
NM_016806 //	1092	P	2492	P	2.14	I	Hnrpa2b1	heterogeneous nuclear ribonucleoprotein A2/B1
NM_026603	117	P	273	P	2.14	I	Denr	density-regulated protein
NM_007548	158	P	332	P	2.14	I	Prdm1	PR domain containing 1, with ZNF domain
NM_008102	700	P	1449	P	2.14	I	Gch1	GTP cyclohydrolase 1
NM_020575	720	P	1336	P	2.14	I	38783	membrane-associated ring finger (C3HC4) 7
NM_008989	322	P	724	P	2.14	I	Pura	purine rich element binding protein A
NM_030250	166	P	356	P	2.14	MI	D10Ertd438e	DNA segment, Chr 10, ERATO Doi 438, expressed
NM_011146	66	A	120	P	2.14	I	Pparg	peroxisome proliferator activated receptor gamma
NM_011225 //	279	P	601	P	2.14	I	Rab18	RAB18, member RAS oncogene family
NM_029556	64	P	143	P	2.14	I	Clybl	citrate lyase beta like
NM_00103823	506	P	1125	P	2.14	I	Banf1	barrier to autointegration factor 1
NM_013631	519	P	1125	P	2.14	I	Pklr	pyruvate kinase liver and red blood cell
NM_009418	71	P	110	P	2.14	I	Tpp2	tripeptidyl peptidase II
NM_008917	280	P	583	P	2.14	I	Ppt1	palmitoyl-protein thioesterase 1
NM_007757	58	P	115	P	2.14	MI	Cpox	coproporphyrinogen oxidase
NM_008775	84	P	181	P	2.14	I	Pafah1b2	platelet-activating factor acetylhydrolase, isoform 1b, alpha2 subunit
NM_019402	2346	P	4169	P	2.14	I	Pabpn1	poly(A) binding protein, nuclear 1
NM_019797	84	P	155	P	2.14	I	Trip4	thyroid hormone receptor interactor 4
NM_009010	50	P	149	P	2.14	I	Rad23a	RAD23a homolog (S. cerevisiae)
NM_023764	227	P	438	P	2.14	I	Tollip	toll interacting protein
NM_007479	1246	P	2758	P	2.14	I	Arf4	ADP-ribosylation factor 4
NM_016858	217	P	424	P	2.14	I	Rab33b	RAB33B, member of RAS oncogene family
NM_020520	356	P	802	P	2.14	I	Slc25a20	solute carrier family 25 (mitochondrial carnitine/acylcarnitine translocase
NM_019425	141	P	288	P	2.14	I	Gnpnat1	glucosamine-phosphate N-acetyltransferase 1
NM_026455	299	P	584	P	2.14	I	2510049I19R	RIKEN cDNA 2510049I19 gene
NM_019737 //	338	P	804	P	2.14	I	B4galt6 /// LO	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 6 /// si
NM_010799	411	P	855	P	2.14	I	Minpp1	multiple inositol polyphosphate histidine phosphatase 1
NM_019772	200	P	478	P	2.14	I	1110004F10R	RIKEN cDNA 1110004F10 gene
NM_133800	57	A	189	P	2.14	I	C78541	expressed sequence C78541
NM_009146 //	159	P	338	P	2.14	I	Frrs1 /// LOC	ferric-chelate reductase 1 /// similar to stromal cell derived factor recepto
NM_009408	740	P	1468	P	2.14	I	Top1	topoisomerase (DNA) I
NM_025927	226	P	493	P	2.14	I	Mrpl45	mitochondrial ribosomal protein L45
NM_021536	132	P	303	P	2.14	I	Rhot1	ras homolog gene family, member T1
NM_052973	154	P	333	P	2.14	I	Strn3	striatin, calmodulin binding protein 3
NM_011969	497	P	1094	P	2.14	I	Psma7	proteasome (prosome, macropain) subunit, alpha type 7
NM_019648	267	P	583	P	2.14	I	Metap2	methionine aminopeptidase 2
NM_027959	180	P	419	P	2.14	MI	Pdia6	protein disulfide isomerase associated 6
NM_146012	158	P	345	P	2.14	MI	Ctdsp2	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) smal
NM_146144	52	P	145	P	2.14	I	Usp1	ubiquitin specific peptdiase 1
NM_025550	483	P	997	P	2.14	I	Psmd6	proteasome (prosome, macropain) 26S subunit, non-ATPase, 6
NM_030018	518	P	1140	P	2.14	I	Tmem50b	transmembrane protein 50B
NM_012010	623	P	1259	P	2.14	I	Eif2s3x	eukaryotic translation initiation factor 2, subunit 3, structural gene X-linke
NM_011816	505	P	1086	P	2.14	I	E430034L04R	RIKEN cDNA E430034L04 gene
NM_145354	173	P	454	P	2.14	I	Nsun2	NOL1/NOP2/Sun domain family 2
NM_133975	842	P	1542	P	2.14	I	Trip12	thyroid hormone receptor interactor 12
XM_00100017	110	P	255	P	2.14	I	4930453N24R	RIKEN cDNA 4930453N24 gene
NM_022989 //	54	P	131	P	2.14	I	Arl6ip6 /// LOC	ADP-ribosylation factor-like 6 interacting protein 6 /// similar to ADP-ribo
NM_027950	363	P	737	P	2.14	MI	1700012B18R	RIKEN cDNA 1700012B18 gene
NM_008704	236	P	573	P	2.14	I	Nme1	expressed in non-metastatic cells 1, protein
NM_146165	225	P	365	P	2.14	I	Jtv1	JTV1 gene
XM_203592 //	261	P	487	P	2.14	MI	Hbld1	HESB like domain containing 1
NM_026759	339	P	628	P	2.14	I	Mrpl13	mitochondrial ribosomal protein L13
NM_053124 //	268	P	694	P	2.14	I	Smarca5 /// 9	SWI/SNF related, matrix associated, actin dependent regulator of chrom
NM_053124 //	142	P	268	P	2.14	I	Smarca5 /// 9	SWI/SNF related, matrix associated, actin dependent regulator of chrom
NM_009011	487	P	898	P	2.14	MI	Rad23b	RAD23b homolog (S. cerevisiae)
NM_028633 //	63	P	149	P	2.14	I	1110020L19R	RIKEN cDNA 1110020L19 gene
NM_025909	152	P	383	P	2.14	I	Oma1	OMA1 homolog, zinc metallopeptidase (S. cerevisiae)
NM_010120	221	P	497	P	2.14	I	Eif1a	eukaryotic translation initiation factor 1A
NM_029271	305	P	798	P	2.14	I	Mrpl32	mitochondrial ribosomal protein L32
NM_029554	467	P	893	P	2.14	I	0610040J01R	RIKEN cDNA 0610040J01 gene
NM_145571	114	P	250	P	2.14	I	Mobk1b	MOB1, Mps One Binder kinase activator-like 1B (yeast)
NM_026368	50	P	119	P	2.14	MI	5830433M19R	RIKEN cDNA 5830433M19 gene
XM_00100107	249	P	572	P	2.14	I	Ighg	Immunoglobulin heavy chain (gamma polypeptide)
NM_011264	89	P	193	P	2.14	I	Rev3l	REV3-like, catalytic subunit of DNA polymerase zeta RAD54 like (S. cer
NM_144535	89	P	193	P	2.14	I	4932432K03R	RIKEN cDNA 4932432K03 gene
NM_028398	148	P	267	P	2.14	I	2900006B13R	RIKEN cDNA 2900006B13 gene
NM_025549	82	P	176	P	2.14	I	Arrdc4	arrestin domain containing 4
NM_020508 //	106	P	230	P	2.14	I	Brd4	bromodomain containing 4
NM_010439	436	P	1084	P	2.14	I	Hmgb1	high mobility group box 1
NM_026998	154	P	341	P	2.14	MI	Snx6	sorting nexin 6
NM_023220	363	P	791	P	2.14	I	2010106G01R	RIKEN cDNA 2010106G01 gene
NM_144544	3669	P	7554	P	2.14	I	2210407C18R	RIKEN cDNA 2210407C18 gene
NM_011151	255	P	640	P	2.14	MI	Ppm1b	protein phosphatase 1B, magnesium dependent, beta isoform
NM_00103858	124	P	298	P	2.14	I	Adar	adenosine deaminase, RNA-specific
NM_010258	289	P	593	P	2.14	I	Gata6	GATA binding protein 6
NM_013830	125	P	260	P	2.14	MI	Prpf4b	PRP4 pre-mRNA processing factor 4 homolog B (yeast)
NM_139144	74	P	175	P	2.14	I	Ogt	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylgluc

Transcript	WT		KO		Change KO/WT		Gene	
	Signal	Detectio	Signal	Detectio	Fold	Call	Symbol	Title
NM_139144	129	P	240	P	2.14	MI	Ogt	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucos
NM_011899 //	396	P	958	P	2.14	I	Srp54 /// LOC	signal recognition particle 54 /// similar to signal recognition particle 54
NM_009652	161	P	316	P	2.14	I	Akt1	thymoma viral proto-oncogene 1
NM_008951	328	P	675	P	2.14	I	Psmd4	proteasome (prosome, macropain) 26S subunit, non-ATPase, 4
NM_011083	82	P	183	P	2.14	I	Pik3c2a	phosphatidylinositol 3-kinase, C2 domain containing, alpha polypeptide
XM_00100145	113	P	245	P	2.14	I	2610301G19R	RIKEN cDNA 2610301G19 gene
NM_007883	39	P	113	P	2.14	I	Dsg2	desmoglein 2
NM_029362	428	P	1077	P	2.14	I	Chmp4b	chromatin modifying protein 4B
NM_198006	589	P	1448	P	2.14	I	6330578E17R	RIKEN cDNA 6330578E17 gene
NM_012008	181	P	430	P	2.14	I	Ddx3y	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, Y-linked
NM_028410	101	P	257	P	2.14	I	Prkrir	protein-kinase, interferon-inducible double stranded RNA dependent inhibi
NM_028410	56	P	131	P	2.14	I	Prkrir	protein-kinase, interferon-inducible double stranded RNA dependent inhibi
NM_026390	242	P	590	P	2.14	I	Ubxd2	UBX domain containing 2
NM_028013	45	P	90	P	2.14	MI	Endod1	endonuclease domain containing 1
NM_025576	667	P	1379	P	2.14	I	Ptpmt1	protein tyrosine phosphatase, mitochondrial 1
NM_177266	124	P	250	P	2.14	I	Gfm2	G elongation factor, mitochondrial 2
NM_026816	116	P	268	P	2.14	I	Gtf2f2	general transcription factor IIF, polypeptide 2
NM_133242	283	P	604	P	2.14	I	Rnpc2	RNA-binding region (RNP1, RRM) containing 2
NM_133916	216	P	499	P	2.14	I	Eif3s9	eukaryotic translation initiation factor 3, subunit 9 (eta)
NM_212484	335	P	681	P	2.14	I	Cnot6	CCR4-NOT transcription complex, subunit 6
NM_178892	206	P	446	P	2.14	I	Tiparp	TCDD-inducible poly(ADP-ribose) polymerase
NM_021720	65	P	154	P	2.14	I	Donson	downstream neighbor of SON
NM_025974	683	P	1852	P	2.14	I	Rpl14	ribosomal protein L14
NM_175224	509	P	1234	P	2.14	I	Metap1	methionyl aminopeptidase 1
NM_172677	236	P	468	P	2.14	I	Ythdf3	YTH domain family 3
NM_024255	159	P	384	P	2.14	I	Hsdl2	hydroxysteroid dehydrogenase like 2
NM_00103315	190	P	376	P	2.14	I	Fbxo33	F-box only protein 33
NM_00103315	197	P	457	P	2.14	I	Fbxo33	F-box only protein 33
NM_172582	68	P	186	P	2.14	I	Coq6	coenzyme Q6 homolog (yeast)
---	418	P	803	P	2.14	MI	---	---
NM_010472	594	P	1255	P	2.14	I	Hrb	HIV-1 Rev binding protein
NM_00100850	143	P	343	P	2.14	I	2700069A02R	RIKEN cDNA 2700069A02 gene
NM_153521	247	P	519	P	2.14	I	Lrrc41	leucine rich repeat containing 41
NM_144802	210	P	453	P	2.14	I	Hnrpll	heterogeneous nuclear ribonucleoprotein L-like
NM_021556	98	P	289	P	2.14	MI	Mrps30	mitochondrial ribosomal protein S30
NM_030147	82	P	251	P	2.14	I	Brd8	bromodomain containing 8
NM_199196	209	P	468	P	2.14	I	Suz12	suppressor of zeste 12 homolog (Drosophila)
NM_009186	397	P	889	P	2.14	I	Sfrs10	splicing factor, arginine/serine-rich 10 (transformer 2 homolog, Drosophila)
NM_181579	720	P	1470	P	2.14	I	Pof1b	premature ovarian failure 1B
XM_621314 //	229	P	509	P	2.14	I	Dsp	desmoplakin
NM_153806	122	P	235	P	2.14	MI	Dnttip2	deoxynucleotidyltransferase, terminal, interacting protein 2
NM_009930	154	P	400	P	2.14	I	Col3a1	procollagen, type III, alpha 1
NM_019660	37	P	86	P	2.14	I	Mycbp	c-myc binding protein
---	884	P	2109	P	2.14	I	---	---
NM_183086	140	P	293	P	2.14	MI	Mrps10	mitochondrial ribosomal protein S10
NM_175187	92	P	167	P	2.14	I	2810446P07R	RIKEN cDNA 2810446P07 gene
NM_00103313	1236	P	2875	P	2.14	I	1200015F23R	RIKEN cDNA 1200015F23 gene
XM_126172 //	147	P	364	P	2.14	I	Larp1 /// LOC	La ribonucleoprotein domain family, member 1 /// similar to la related protei
NM_011221	427	P	934	P	2.14	I	Purb	purine rich element binding protein B
NM_00100198	319	P	713	P	2.14	I	8430427H17R	RIKEN cDNA 8430427H17 gene
NM_028031	201	P	482	P	2.14	MI	Zdhhc13	zinc finger, DHHC domain containing 13
NM_010274	1688	P	3746	P	2.14	I	Gpd2	glycerol phosphate dehydrogenase 2, mitochondrial
NM_029825	493	P	1035	P	2.14	I	Scfd1	sec1 family domain containing 1
NM_025525	27	P	107	P	2.14	I	Rnf113a2	ring finger protein 113A2
NM_025431	157	P	281	P	2.14	I	1190005P17R	RIKEN cDNA 1190005P17 gene
NM_00103920	127	P	270	P	2.14	I	Hdhd2	haloacid dehalogenase-like hydrolase domain containing 2
NM_146087	2026	P	4143	P	2.14	I	Csnk1a1	casein kinase 1, alpha 1
NM_133236 //	251	P	587	P	2.14	I	Glcci1	glucocorticoid induced transcript 1
XM_125901 //	326	P	607	P	2.14	I	Cand1	cullin associated and neddylation disassociated 1
NM_00101339	162	P	344	P	2.14	I	Rreb1	ras responsive element binding protein 1
NM_133225	276	P	509	P	2.14	I	Acbd3	acyl-Coenzyme A binding domain containing 3
---	162	P	337	P	2.14	MI	5630401D06R	RIKEN cDNA 5630401D06 gene
XM_00100425	274	P	522	P	2.14	I	Alkbh3	alkB, alkylation repair homolog 3 (E. coli)
NM_178376	160	P	354	P	2.14	I	Rraga	Ras-related GTP binding A
XM_619008 //	162	P	354	P	2.14	I	2600011C06R	RIKEN cDNA 2600011C06 gene
XM_912953 //	231	P	390	P	2.14	I	1500034J01R	RIKEN cDNA 1500034J01 gene
NM_175172	80	P	167	P	2.14	I	4930506M07R	RIKEN cDNA 4930506M07 gene
NM_00101796	241	P	519	P	2.14	I	Ddi2	DNA-damage inducible protein 2
NM_026757	38	P	88	P	2.14	I	0610010K14R	RIKEN cDNA 0610010K14 gene
XM_985039	310	P	551	P	2.14	I	1810014B01R	RIKEN cDNA 1810014B01 gene
NM_178379	48	P	132	P	2.14	I	Cox10	COX10 homolog, cytochrome c oxidase assembly protein, heme A: farnesy
NM_029508	279	P	490	P	2.14	I	Pcgf5	polycomb group ring finger 5
NM_025690 //	119	P	243	P	2.14	I	Sltm	SAFB-like, transcription modulator
NM_008102	104	P	230	P	2.14	I	Gch1	GTP cyclohydrolase 1
NM_019748	98	P	226	P	2.14	I	Uble1a	ubiquitin-like 1 (sentrin) activating enzyme E1A
NM_028904	113	P	251	P	2.14	I	4932432N11R	RIKEN cDNA 4932432N11 gene
NM_172400 //	173	P	426	P	2.14	I	Dnajc8 /// LOC	DnaJ (Hsp40) homolog, subfamily C, member 8 /// similar to DnaJ (Hsp40
NM_026437	155	P	336	P	2.14	I	1810055E12R	RIKEN cDNA 1810055E12 gene
NM_027652	1069	P	2248	P	2.14	I	D5Wsu178e	DNA segment, Chr 5, Wayne State University 178, expressed
NM_013727	648	P	1362	P	2.14	I	Azi2	5-azacytidine induced gene 2
NM_011672	153	P	352	P	2.14	I	Ufd1l	ubiquitin fusion degradation 1 like
NM_027652	426	P	946	P	2.14	I	D5Wsu178e	DNA segment, Chr 5, Wayne State University 178, expressed
XM_00100252	88	P	155	P	2.14	I	Irf2bp2 /// LOC	interferon regulatory factor 2 binding protein 2 /// similar to interferon regula
NM_00103338	96	P	198	P	2.14	I	Fubp3	far upstream element (FUSE) binding protein 3
NM_025974	901	P	1887	P	2.14	I	Rpl14	ribosomal protein L14
NM_175329	2589	P	5568	P	2.14	I	Ndg2	Nur77 downstream gene 2

Transcript	WT		KO		Change KO/WT		Gene	
	Signal	Detectio	Signal	Detectio	Fold	Call	Symbol	Title
NM_175341 //	605	P	1286	P	2.14	I	Mbnl2	muscleblind-like 2
NM_198033	236	P	533	P	2.14	I	Als4	amyotrophic lateral sclerosis 4 homolog (human)
NM_016806 //	161	P	331	P	2.14	I	Hnrpa2b1	heterogeneous nuclear ribonucleoprotein A2/B1
NM_172704	104	P	209	P	2.14	MI	Dnajc11	DnaJ (Hsp40) homolog, subfamily C, member 11
NM_00100149	285	P	733	P	2.14	I	Tpm4	tropomyosin 4
NM_182994	1136	P	2413	P	2.14	I	Arl5a	ADP-ribosylation factor-like 5A
XM_486797 //	103	P	231	P	2.14	I	Apxl /// LOC6	apical protein, Xenopus laevis-like /// similar to Apical-like protein (APXL
NM_183170	180	P	355	P	2.14	I	BC051227	cDNA sequence BC051227
NM_176843	383	P	829	P	2.14	I	Ints5	integrator complex subunit 5
NM_00100417	3063	P	6682	P	2.14	I	AA467197	expressed sequence AA467197
NM_00103330	1490	P	3163	P	2.14	I	Ndufb6	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6
XM_00100411	142	P	247	P	2.14	I	Fbxo11	F-box protein 11
NM_019648	468	P	1152	P	2.14	I	Metap2	methionine aminopeptidase 2
NM_178627	186	P	427	P	2.14	I	Poldip3	polymerase (DNA-directed), delta interacting protein 3
NM_012023	190	P	395	P	2.14	I	Ppp2r5c	protein phosphatase 2, regulatory subunit B (B56), gamma isoform
NM_033080	324	P	713	P	2.14	I	Nudt19	nudix (nucleoside diphosphate linked moiety X)-type motif 19
NM_019926	267	P	559	P	2.14	I	Mtm1	X-linked myotubular myopathy gene 1
NM_008981 //	142	P	274	P	2.14	I	Ptprg /// LOC	protein tyrosine phosphatase, receptor type, G /// similar to protein tyrosi
XM_194424 //	242	P	486	P	2.14	I	Otud4	OTU domain containing 4
---	384	P	863	P	2.14	I	---	---
NM_178935	144	P	274	P	2.14	MI	4932441K18	RIKEN cDNA 4932441K18 gene
NM_144958	1188	P	2706	P	2.14	I	Eif4a1	eukaryotic translation initiation factor 4A1
NM_178693	171	P	408	P	2.14	I	Coq4	coenzyme Q4 homolog (yeast)
XM_00100102	292	P	616	P	2.14	I	Btaf1	BTAF1 RNA polymerase II, B-TFIID transcription factor-associated, (Mo
XM_00100102	161	P	320	P	2.14	I	Btaf1	BTAF1 RNA polymerase II, B-TFIID transcription factor-associated, (Mo
---	198	P	402	P	2.14	I	2010109N14	RIKEN cDNA 2010109N14 gene
XM_00100087	1534	P	3481	P	2.14	I	LOC667373 /	similar to interferon-induced protein with tetratricopeptide repeats 1 /// si
NM_00103338	182	P	386	P	2.14	I	C430014K11	RIKEN cDNA C430014K11 gene
NM_009536	141	P	302	P	2.14	I	Ywhae	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation prote
NM_011561 //	331	P	742	P	2.14	MI	Tdg /// LOC54	thymine DNA glycosylase /// similar to thymine DNA glycosylase isoform
NM_146154	48	P	115	P	2.14	I	Ppp1r8	protein phosphatase 1, regulatory (inhibitor) subunit 8
NM_011188	643	P	1282	P	2.14	I	Psmc2	proteasome (prosome, macropain) 26S subunit, ATPase 2
NM_026330	207	P	429	P	2.14	I	Nsmce1	non-SMC element 1 homolog (S. cerevisiae)
NM_007622	136	P	270	P	2.14	I	Cbx1	chromobox homolog 1 (Drosophila HP1 beta)
NM_198021	92	P	378	P	2.14	I	Scyl2	SCY1-like 2 (S. cerevisiae)
---	121	P	296	P	2.14	MI	2810001A02	RIKEN cDNA 2810001A02 gene
NM_00100586	208	P	466	P	2.14	I	Mtus1	mitochondrial tumor suppressor 1
NM_00100586	258	P	525	P	2.14	I	Mtus1	mitochondrial tumor suppressor 1
XM_906582 //	364	P	775	P	2.14	I	1810022K09	RIKEN cDNA 1810022K09 gene
NM_025974	877	P	1989	P	2.14	I	Rpl14	ribosomal protein L14
NM_138680	50	P	109	P	2.14	I	Luc7l2	LUC7-like 2 (S. cerevisiae)
NM_00103908	712	P	1620	P	2.14	I	Sel1h	Sel1 (suppressor of lin-12) 1 homolog (C. elegans)
NM_00103344	117	P	263	P	2.14	I	Gm944	gene model 944, (NCBI)
---	227	P	503	P	2.14	I	---	---
NM_172054	488	P	1093	P	2.14	I	Txndc9	thioredoxin domain containing 9
NM_175329	3846	P	7876	P	2.14	I	Ndg2	Nur77 downstream gene 2
NM_009070	444	P	952	P	2.14	I	Rnps1	ribonucleic acid binding protein S1
NM_011968	1548	P	3174	P	2.14	I	Psma6	proteasome (prosome, macropain) subunit, alpha type 6
XM_00100379	59	P	155	P	2.14	I	D330037H05	RIKEN cDNA D330037H05 gene /// similar to La-related protein 4 (La rib
NM_175472	66	P	139	P	2.14	I	Zcchc11	zinc finger, CCHC domain containing 11
NM_00100180	720	P	1173	P	2.14	I	Zfp36l2	zinc finger protein 36, C3H type-like 2
---	359	P	708	P	2.14	I	---	---
NM_009070	219	P	471	P	2.14	I	Rnps1	ribonucleic acid binding protein S1
NM_009738	121	P	274	P	2.14	I	Bche	butyrylcholinesterase
NM_010787	169	P	355	P	2.14	I	Mea1	male enhanced antigen 1
NM_175102	434	P	1167	P	2.14	I	Sf3b5	splicing factor 3b, subunit 5
NM_011826 //	1053	P	2118	P	2.14	I	Silg111 /// Ha	silica-induced gene 111 /// HCLS1 associated X-1
NM_009070	296	P	627	P	2.14	I	Rnps1	ribonucleic acid binding protein S1
NM_010771	535	P	1155	P	2.14	I	Matr3	matrin 3
NM_008214	344	P	729	P	2.14	I	Hars	histidyl-tRNA synthetase
NM_025974	1109	P	2450	P	2.14	I	Rpl14	ribosomal protein L14
NM_016843	105	P	224	P	2.14	I	Atxn10	ataxin 10
NM_00103328	91	P	210	P	2.14	I	Slc30a10	solute carrier family 30, member 10
NM_028779	351	P	735	P	2.14	I	Ampd2	adenosine monophosphate deaminase 2 (isoform L)
XM_00100379	215	P	444	P	2.14	I	D330037H05	RIKEN cDNA D330037H05 gene /// similar to La-related protein 4 (La rib
NM_023240 //	321	P	611	P	2.14	I	Eef1d	eukaryotic translation elongation factor 1 delta (guanine nucleotide excha
NM_009797	1148	P	2291	P	2.14	I	Capza1	capping protein (actin filament) muscle Z-line, alpha 1
NM_178665	313	P	692	P	2.14	MI	Lpp	LIM domain containing preferred translocation partner in lipoma
XM_894489 //	71	P	153	P	2.14	I	Ap4e1	adaptor-related protein complex AP-4, epsilon 1
NM_009427	58	P	128	P	2.14	I	Tob1	transducer of ErbB-2.1
NM_197945	173	P	378	P	2.14	MI	Prosapip1	ProSAPiP1 protein
NM_008229	118	P	243	P	2.14	I	Hdac2	histone deacetylase 2
NM_024287	335	P	662	P	2.14	I	Rab6	RAB6, member RAS oncogene family
NM_009054	89	P	167	P	2.14	I	Trim27	tripartite motif protein 27
NM_013598	137	P	298	P	2.14	I	Kitl	kit ligand
NM_133787	116	P	198	P	2.14	I	Nmd3	NMD3 homolog (S. cerevisiae)
NM_009716	1475	P	2986	P	2.14	I	Atf4	activating transcription factor 4
NM_009005	287	P	586	P	2.14	I	Rab7	RAB7, member RAS oncogene family
NM_011289 //	889	P	2098	P	2.14	I	Rpl27 /// LOC	ribosomal protein L27 /// similar to ribosomal protein L27 /// similar to ribo
NM_019693	444	P	937	P	2.14	I	Bat1a	HLA-B-associated transcript 1A
NM_009462	202	P	380	P	2.14	I	Usp10	ubiquitin specific peptidase 10
NM_00103323	77	P	171	P	2.14	I	Hmgb1 /// 493	high mobility group box 1 /// RIKEN cDNA 4932431P20 gene /// similar t
NM_018829	161	P	336	P	2.14	I	Ap3m1	adaptor-related protein complex 3, mu 1 subunit
NM_019987	191	P	353	P	2.14	I	Ick	intestinal cell kinase
NM_007408	811	P	1751	P	2.14	I	Adfp	adipose differentiation related protein
NM_009242	63	P	146	P	2.14	I	Sparc	secreted acidic cysteine rich glycoprotein

Transcript	WT		KO		Change KO/WT		Gene	
	Signal	Detectio	Signal	Detectio	Fold	Call	Symbol	Title
XM_619533 //	164	P	374	P	2.14	I	Lars	leucyl-tRNA synthetase
NM_010123	551	P	1402	P	2.14	I	Eif3s10	eukaryotic translation initiation factor 3, subunit 10 (theta)
NM_011184	1238	P	2734	P	2.14	I	Psma3	proteasome (prosome, macropain) subunit, alpha type 3
NM_00103396	1798	P	3941	P	2.14	I	Ak2	adenylate kinase 2
NM_026499	720	P	1718	P	2.14	I	Sfrs6	splicing factor, arginine/serine-rich 6
NM_011561 //	152	P	394	P	2.14	I	Tdg /// LOC54	thymine DNA glycosylase /// similar to thymine DNA glycosylase isoform 2
NM_025762 //	379	P	806	P	2.14	I	4933434E20	RIKEN cDNA 4933434E20 gene
NM_015747	148	P	360	P	2.14	I	Slc20a1	solute carrier family 20, member 1
NM_025317	216	P	546	P	2.14	I	Mrpl54	mitochondrial ribosomal protein L54
NM_024194	74	P	181	P	2.14	I	Lrrc40	leucine rich repeat containing 40
NM_011233	132	P	242	P	2.14	I	Rad17	RAD17 homolog (S. pombe)
NM_009194	38	P	84	P	2.14	I	Slc12a2	solute carrier family 12, member 2
NM_019586	183	P	444	P	2.14	I	Ube2j1	ubiquitin-conjugating enzyme E2, J1
NM_026584	115	P	315	P	2.14	I	Gtf2e2	general transcription factor II E, polypeptide 2 (beta subunit)
NM_022329	280	P	691	P	2.14	I	Ifrg15	interferon alpha responsive gene
NM_025999	89	P	151	P	2.14	I	Rnf141	ring finger protein 141
NM_028753	107	P	181	P	2.14	I	Pop7	processing of precursor 7, ribonuclease P family, (S. cerevisiae)
NM_133752	207	P	443	P	2.14	I	Opa1	optic atrophy 1 homolog (human)
NR_002840	285	P	539	P	2.14	MI	Gas5	growth arrest specific 5
NM_022883	278	P	628	P	2.14	I	Lpin3	lipin 3
NM_139308	356	P	777	P	2.14	I	Stard7	START domain containing 7
NM_00102519	334	P	633	P	2.14	I	Cxadr	coxsackievirus and adenovirus receptor
NM_019657	656	P	1487	P	2.14	I	Hsd17b12	hydroxysteroid (17-beta) dehydrogenase 12
---	371	P	835	P	2.14	I	---	---
NM_016745	45	P	105	P	2.14	MI	Atp2a3	ATPase, Ca++ transporting, ubiquitous
NM_008093	207	P	423	P	2.14	I	Gata5	GATA binding protein 5
NM_023063	642	P	1353	P	2.14	I	Lima1	LIM domain and actin binding 1
NM_010771	348	P	755	P	2.14	I	Matr3	matrin 3
NM_025606	246	P	520	P	2.14	I	Mrpl16	mitochondrial ribosomal protein L16
NM_019737 //	297	P	647	P	2.14	I	B4galt6 /// LO	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 6 /// sim
NM_025859	858	P	1647	P	2.14	I	Arl1	ADP-ribosylation factor-like 1
NM_011879	390	P	842	P	2.14	I	Ik	IK cytokine
NM_030147	81	P	178	P	2.14	I	Brd8	bromodomain containing 8
NM_144833	365	P	719	P	2.14	I	Zfp410	zinc finger protein 410
---	51	A	105	P	2.14	I	Myohd1	myosin head domain containing 1
NM_175102	321	P	730	P	2.14	I	Sf3b5	splicing factor 3b, subunit 5
NM_139149	579	P	1224	P	2.14	I	Fus	fusion, derived from t(12;16) malignant liposarcoma (human)
NM_009227	1089	P	2501	P	2.14	I	Snrpe	small nuclear ribonucleoprotein E
NM_130881 //	183	P	404	P	2.14	I	Pabpc4 /// LO	poly A binding protein, cytoplasmic 4 /// similar to Poly(A) binding protein, c
NM_00103969	182	P	436	P	2.14	I	Arhgap12	Rho GTPase activating protein 12
NM_025833	398	P	861	P	2.14	I	Baiap2l1	BAI1-associated protein 2-like 1
NM_175606	199	P	415	P	2.14	I	Hod	homeobox only domain
NM_145398	56	P	120	P	2.14	I	Casd1	CAS1 domain containing 1
NM_146191	41	A	99	P	2.14	I	Lrrk1	leucine-rich repeat kinase 1
NM_027088	218	P	425	P	2.14	I	Bap1	Brca1 associated protein 1
NM_145573	220	P	441	P	2.14	I	Mrps35	mitochondrial ribosomal protein S35
NM_199196	210	P	405	P	2.14	I	Suz12	suppressor of zeste 12 homolog (Drosophila)
NM_175394	532	P	1096	P	2.14	I	Wtap	Wilms' tumour 1-associating protein
NM_172528	164	P	483	P	2.14	I	Lrrc1	leucine rich repeat containing 1
NM_172438	104	P	198	P	2.14	I	Thoc5	THO complex 5
NM_024183	146	P	231	P	2.14	I	Fip1l1	FIP1 like 1 (S. cerevisiae)
NM_010274	684	P	1487	P	2.14	I	Gpd2	glycerol phosphate dehydrogenase 2, mitochondrial
XM_126489 //	90	P	122	P	2.14	MI	Foxk2	forkhead box K2
NM_028632	268	P	553	P	2.14	I	1110008B24	RIKEN cDNA 1110008B24 gene
NM_026673 //	532	P	1092	P	2.14	I	0610008C08	RIKEN cDNA 0610008C08 gene /// hypothetical LOC621156 /// hypothetic
NM_029648	231	P	475	P	2.14	I	D19Ertd737e	DNA segment, Chr 19, ERATO Doi 737, expressed
XM_00100234	110	P	160	P	2.14	MI	1810058I14R	RIKEN cDNA 1810058I14 gene
NM_173441	120	P	248	P	2.14	I	Iws1	IWS1 homolog (S. cerevisiae)
NM_011289 //	953	P	1937	P	2.14	I	Rpl27 /// LOC	ribosomal protein L27 /// similar to ribosomal protein L27 /// similar to ribos
XM_00100355	152	P	317	P	2.14	I	Ppp2r2a	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alpha is
NM_00103862	52	P	130	P	2.14	I	Rabgap1l	RAB GTPase activating protein 1-like
NM_009278	136	P	381	P	2.14	I	Ssb	Sjogren syndrome antigen B
XM_908334 //	97	P	247	P	2.14	I	Etnk1	ethanolamine kinase 1
NM_008453	1611	P	2682	P	2.14	I	Klf3	Kruppel-like factor 3 (basic)
XM_485595 //	714	P	1515	P	2.14	I	D5Ertd579e	DNA segment, Chr 5, ERATO Doi 579, expressed
NM_173364	410	P	840	P	2.14	I	Zfp445	zinc finger protein 445
NM_028099	231	P	504	P	2.14	I	Dusp11	dual specificity phosphatase 11 (RNA/RNP complex 1-interacting)
NM_199469	173	P	412	P	2.14	I	Nploc4	nuclear protein localization 4 homolog (S. cerevisiae)
NM_172469	57	P	155	P	2.14	I	Clic6	chloride intracellular channel 6
NM_019926	104	P	213	P	2.14	MI	Mtm1	X-linked myotubular myopathy gene 1
NM_00103344	81	P	175	P	2.14	I	AU045404	expressed sequence AU045404
NM_00101497	327	P	661	P	2.14	I	Snx13	sorting nexin 13
NM_013671	95	P	230	P	2.14	I	Sod2	superoxide dismutase 2, mitochondrial
XM_283903 //	156	P	360	P	2.14	I	B430201A12	RIKEN cDNA B430201A12 gene
---	281	P	630	P	2.14	I	C130006E23	Hypothetical protein C130006E23
XM_895026 //	169	P	319	P	2.14	I	Pgs1	phosphatidylglycerophosphate synthase 1
XM_00100118	127	P	266	P	2.14	I	Taok1	TAO kinase 1
NM_176840	239	P	515	P	2.14	I	Osbpl11	oxysterol binding protein-like 11
NM_011655	146	P	334	P	2.14	I	Tubb5	tubulin, beta 5
NM_024188	135	P	283	P	2.14	I	Oxct1	3-oxoacid CoA transferase 1
NM_172650	123	P	318	P	2.14	I	Kctd3	potassium channel tetramerisation domain containing 3
NM_175341 //	402	P	843	P	2.14	I	Mbnl2	muscleblind-like 2
NM_178797	100	P	218	P	2.14	I	Mlstd1	male sterility domain containing 1
XM_485063 //	76	P	168	P	2.14	I	3110001I20R	RIKEN cDNA 3110001I20 gene
---	210	P	410	P	2.14	I	Bambi-ps1	BMP and activin membrane-bound inhibitor, pseudogene (Xenopus laevis)
NM_019930	337	P	709	P	2.14	I	Ranbp9	RAN binding protein 9

Transcript	WT		KO		Change KO/WT		Gene	
	Signal	Detectio	Signal	Detectio	Fold	Call	Symbol	Title
NM_00101239	205	P	512	P	2.14	I	Ptpla	protein tyrosine phosphatase-like (proline instead of catalytic arginine), m
---	144	P	269	P	2.14	I	---	PREDICTED: Mus musculus similar to Inward rectifier potassium chann
NM_172153 //	89	P	215	P	2.14	I	A830039H10	RIKEN cDNA A830039H10 gene
NM_008989	227	P	448	P	2.14	I	Pura	purine rich element binding protein A
NM_175151	56	A	152	P	2.14	I	Tatdn1	TatD DNase domain containing 1
NM_133724	143	P	362	P	2.14	I	Cno	cappuccino
NM_008388	702	P	1498	P	2.14	I	Eif3s6	eukaryotic translation initiation factor 3, subunit 6
NM_026465	72	P	154	P	2.14	I	2010316F05	RIKEN cDNA 2010316F05 gene
NM_176835	402	P	843	P	2.14	I	2810451A06	RIKEN cDNA 2810451A06 gene
NM_025279	1244	P	2715	P	2.14	I	Hnrpk	heterogeneous nuclear ribonucleoprotein K
NM_175317	199	P	370	P	2.14	I	Eftud1	elongation factor Tu GTP binding domain containing 1
NM_134129	66	P	149	P	2.14	I	Prpf19	PRP19/PSO4 pre-mRNA processing factor 19 homolog (S. cerevisiae)
NM_011965	860	P	2027	P	2.30	I	Psma1	proteasome (prosome, macropain) subunit, alpha type 1
NM_175565 //	484	P	1122	P	2.30	I	Cdv3	carnitine deficiency-associated gene expressed in ventricle 3
NM_022997	94	P	276	P	2.30	I	Vps35	vacuolar protein sorting 35
NM_009840	375	P	918	P	2.30	I	Cct8	chaperonin subunit 8 (theta)
NM_008722	546	P	1252	P	2.30	I	Npm1	nucleophosmin 1
NM_021510	434	P	1016	P	2.30	I	Hnrph1	heterogeneous nuclear ribonucleoprotein H1
NM_009836	391	P	900	P	2.30	I	Cct3	chaperonin subunit 3 (gamma)
NM_009076	1057	P	2508	P	2.30	I	Rpl12	ribosomal protein L12
NM_024221	850	P	2071	P	2.30	I	Pdhb	pyruvate dehydrogenase (lipoamide) beta
NM_015824	88	P	213	P	2.30	I	Orc3l	origin recognition complex, subunit 3-like (S. cerevisiae)
NM_007839	371	P	912	P	2.30	I	Dhx15	DEAH (Asp-Glu-Ala-His) box polypeptide 15
NM_007839	545	P	1241	P	2.30	I	Dhx15	DEAH (Asp-Glu-Ala-His) box polypeptide 15
NM_013663	54	P	118	P	2.30	I	Sfrs3	splicing factor, arginine/serine-rich 3 (SRp20)
NM_026508	279	P	565	P	2.30	I	Trap1	TNF receptor-associated protein 1
NM_010439	327	P	763	P	2.30	I	Hmgb1	high mobility group box 1
NM_026383	466	P	1178	P	2.30	I	Pnrc2	proline-rich nuclear receptor coactivator 2
NM_010271	648	P	1610	P	2.30	I	Gpd1	glycerol-3-phosphate dehydrogenase 1 (soluble)
NM_010760	474	P	999	P	2.30	I	Magoh	mago-nashi homolog, proliferation-associated (Drosophila)
NM_016682	226	P	607	P	2.30	I	Uble1b	ubiquitin-like 1 (sentrin) activating enzyme E1B
NM_007452	429	P	944	P	2.30	I	Prdx3	peroxiredoxin 3
NM_018829 //	128	P	352	P	2.30	I	Ap3m1 /// LO	adaptor-related protein complex 3, mu 1 subunit /// similar to AP-3 comp
NM_009278	50	P	151	P	2.30	I	Ssb	Sjogren syndrome antigen B
NM_133718	265	P	603	P	2.30	I	Tmem30a	transmembrane protein 30A
NM_016739	925	P	2069	P	2.30	I	Gpiap1	GPI-anchored membrane protein 1
NM_138591	167	P	343	P	2.30	I	Gfm1	G elongation factor, mitochondrial 1
NM_00103396	27	P	52	P	2.30	I	Ube3a	ubiquitin protein ligase E3A
NM_019581	292	P	723	P	2.30	I	Gtpbp2	GTP binding protein 2
NM_025683	219	P	455	P	2.30	I	Rpe	ribulose-5-phosphate-3-epimerase
NM_008320	545	P	1215	P	2.30	I	Irf8	interferon regulatory factor 8
NM_010436	281	P	466	P	2.30	I	H2afx	H2A histone family, member X
NM_011484	140	P	348	P	2.30	I	Stam	signal transducing adaptor molecule (SH3 domain and ITAM motif) 1
NM_025384	298	P	679	P	2.30	I	Dnajc15	DnaJ (Hsp40) homolog, subfamily C, member 15
NM_029397 //	48	P	118	P	2.30	MI	Rbm12	RNA binding motif protein 12
NM_008898	862	P	1876	P	2.30	I	Por	P450 (cytochrome) oxidoreductase
NM_009455 //	362	P	883	P	2.30	I	Ube2e1 /// LO	ubiquitin-conjugating enzyme E2E 1, UBC4/5 homolog (yeast) /// similar
NM_011482	225	P	512	P	2.30	I	Nhp2l1	NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae)
NM_026768	202	P	486	P	2.30	I	Mrps18a	mitochondrial ribosomal protein S18A
NM_026352 //	88	P	192	P	2.30	I	Ppid /// Lamp	peptidylprolyl isomerase D (cyclophilin D) /// lysosomal-associated memb
NM_021524	265	P	575	P	2.30	I	Pbef1	pre-B-cell colony-enhancing factor 1
NM_021336	155	P	336	P	2.30	I	Snrpa1	small nuclear ribonucleoprotein polypeptide A'
NM_00102621	191	P	540	P	2.30	I	Entpd5	ectonucleoside triphosphate diphosphohydrolase 5
NM_00102621	310	P	702	P	2.30	I	Entpd5	ectonucleoside triphosphate diphosphohydrolase 5
NM_013899	263	P	629	P	2.30	I	Timm10	translocase of inner mitochondrial membrane 10 homolog (yeast)
NM_009373	934	P	2164	P	2.30	I	Tgm2	transglutaminase 2, C polypeptide
NM_010325	353	P	786	P	2.30	I	Got2	glutamate oxaloacetate transaminase 2, mitochondrial
NM_016876	363	P	883	P	2.30	I	Eif3s4	eukaryotic translation initiation factor 3, subunit 4 (delta)
NM_023200	181	P	389	P	2.30	I	Ppp1r7	protein phosphatase 1, regulatory (inhibitor) subunit 7
NM_007754	108	P	256	P	2.30	MI	Cpd	carboxypeptidase D
NM_053089	86	P	199	P	2.30	I	Narg1	NMDA receptor-regulated gene 1
NM_007688	187	P	458	P	2.30	I	Cfl2	cofilin 2, muscle
NM_016715	176	P	575	P	2.30	I	Tpte2	transmembrane phosphoinositide 3-phosphatase and tensin homolog 2
NM_026519	300	P	686	P	2.30	I	Tmem85	transmembrane protein 85
---	126	P	459	P	2.30	I	Malat1	metastasis associated lung adenocarcinoma transcript 1 (non-coding RN
NM_022324	220	P	540	P	2.30	I	Sdf2l1	stromal cell-derived factor 2-like 1
NM_010260	36	P	115	P	2.30	I	Gbp2	guanylate nucleotide binding protein 2
NM_027136 //	88	P	193	P	2.30	I	Dph1 /// RP2	DPH1 homolog (S. cerevisiae) /// candidate tumor suppressor OVCA2
NM_009075	217	P	476	P	2.30	I	Rpia	ribose 5-phosphate isomerase A
NM_008448	312	P	693	P	2.30	I	Kif5b	kinesin family member 5B
NM_008448	270	P	615	P	2.30	I	Kif5b	kinesin family member 5B
XM_00100521	107	P	213	P	2.30	I	LOC630509 /	similar to H-2 class I histocompatibility antigen, Q7 alpha chain precurso
NM_025918	58	P	111	P	2.30	I	Ccdc43	coiled-coil domain containing 43
NM_025814	524	P	1174	P	2.30	I	Serbp1	Serpine1 mRNA binding protein 1
NM_025879	120	P	238	P	2.30	I	2410002O22	RIKEN cDNA 2410002O22 gene
NM_007473	117	P	251	P	2.30	I	Aqp7	aquaporin 7
NM_013515	205	P	410	P	2.30	I	Stom	stomatin
NM_009186	314	P	840	P	2.30	I	Sfrs10	splicing factor, arginine/serine-rich 10 (transformer 2 homolog, Drosophi
NM_010281 //	74	P	143	P	2.30	I	Ggh /// LOC6	gamma-glutamyl hydrolase /// similar to Gamma-glutamyl hydrolase prec
NM_138756	197	P	488	P	2.30	I	Slc25a36	solute carrier family 25, member 36
NM_025437	266	P	604	P	2.30	I	Eif1ay	eukaryotic translation initiation factor 1A, Y-linked
NM_033618	182	P	396	P	2.30	I	Supt16h	suppressor of Ty 16 homolog (S. cerevisiae)
NM_025474	345	P	803	P	2.30	I	Mrps14	mitochondrial ribosomal protein S14
NM_00102480	48	P	124	P	2.30	I	Cebpz	CCAAT/enhancer binding protein zeta
NM_026434	83	P	148	P	2.30	I	Rbm18	RNA binding motif protein 18
NM_021507	620	P	1377	P	2.30	I	Sqrdl	sulfide quinone reductase-like (yeast)

Transcript	WT		KO		Change KO/WT		Gene	
	Signal	Detectio	Signal	Detectio	Fold	Call	Symbol	Title
NM_008222	170	P	381	P	2.30	I	Hccs	holocytochrome c synthetase
NM_009847	105	P	232	P	2.30	I	Cd2ap	CD2-associated protein
NM_009847	115	P	308	P	2.30	I	Cd2ap	CD2-associated protein
NM_018785	94	P	206	P	2.30	I	Prpf40a	PRP40 pre-mRNA processing factor 40 homolog A (yeast)
NM_016700	427	P	748	P	2.30	I	Mapk8	mitogen activated protein kinase 8
NM_016856	78	P	189	P	2.30	I	Cpsf2	cleavage and polyadenylation specific factor 2
NM_007690	133	P	266	P	2.30	I	Chd1	chromodomain helicase DNA binding protein 1
NM_00103954	102	P	227	P	2.30	I	Myo6	myosin VI
NM_013631	327	P	747	P	2.30	I	Pklr	pyruvate kinase liver and red blood cell
NM_021526	763	P	1730	P	2.30	I	Psmd14	proteasome (prosome, macropain) 26S subunit, non-ATPase, 14
NM_024174	161	P	360	P	2.30	I	Mrps23	mitochondrial ribosomal protein S23
NM_008740	321	P	819	P	2.30	I	Nsf	N-ethylmaleimide sensitive fusion protein
NM_009667	95	P	218	P	2.30	I	Ampd3	AMP deaminase 3
NM_015756	458	P	1187	P	2.30	I	Shrm	shroom
XM_974161 //	615	P	1348	P	2.30	I	LOC671237	similar to Putative RNA-binding protein 3 (RNA-binding motif protein 3)
NM_00101588	218	P	500	P	2.30	I	Taf9	TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated fac
NM_019402	450	P	990	P	2.30	I	Pabpn1	poly(A) binding protein, nuclear 1
NM_019797	155	P	411	P	2.30	I	Trip4	thyroid hormone receptor interactor 4
NM_019729	183	P	355	P	2.30	I	Usp8	ubiquitin specific peptidase 8
NM_025824	632	P	1232	P	2.30	I	Bzw1	basic leucine zipper and W2 domains 1
NM_016805	562	P	1269	P	2.30	I	Hnrpu	heterogeneous nuclear ribonucleoprotein U
NM_011119	232	P	552	P	2.30	I	Pa2g4	proliferation-associated 2G4
NM_007861	655	P	1478	P	2.30	I	Dld	dihydrolipoamide dehydrogenase
NM_025682	57	P	140	P	2.30	MI	Pspc1	paraspeckle protein 1
NM_007453	1212	P	2636	P	2.30	I	Prdx6	peroxiredoxin 6
NM_010918	63	P	192	P	2.30	I	Nktr	natural killer tumor recognition sequence
NM_008891	167	P	394	P	2.30	I	Pnn	pinin
NM_009677	122	P	271	P	2.30	I	Ap1g1	adaptor protein complex AP-1, gamma 1 subunit
NM_023215	230	P	562	P	2.30	I	2500003M10	RIKEN cDNA 2500003M10 gene
NM_025541	106	P	256	P	2.30	I	Asf1a	ASF1 anti-silencing function 1 homolog A (S. cerevisiae)
NM_145569	222	P	522	P	2.30	I	Mat2a	methionine adenosyltransferase II, alpha
NM_146144	78	P	191	P	2.30	I	Usp1	ubiquitin specific peptdiase 1
NM_011811	102	P	390	P	2.30	I	Farslb	phenylalanine-tRNA synthetase-like, beta subunit
NM_172665	112	P	314	P	2.30	I	Pdk1	pyruvate dehydrogenase kinase, isoenzyme 1
NM_145360 //	74	P	182	P	2.30	I	Idi1	isopentenyl-diphosphate delta isomerase
NM_145540 //	75	P	186	P	2.30	I	Ints3	integrator complex subunit 3
NM_145514	236	P	586	P	2.30	I	Wdr26	WD repeat domain 26
XM_283579 //	149	P	370	P	2.30	I	9430016H08	RIKEN cDNA 9430016H08 gene
NM_053124 //	105	P	259	P	2.30	I	Smarca5 /// 9	SWI/SNF related, matrix associated, actin dependent regulator of chromat
NM_172410	56	P	178	P	2.30	I	Nup93	nucleoporin 93
NM_170591	86	P	166	P	2.30	I	Nupl1	nucleoporin like 1
NM_025690 //	189	P	501	P	2.30	I	Sltm	SAFB-like, transcription modulator
NM_027415	227	P	538	P	2.30	I	Tmem70	transmembrane protein 70
NM_145156	285	P	647	P	2.30	I	Slc25a28	solute carrier family 25, member 28
NM_025786	674	P	1585	P	2.30	I	Rnf186	ring finger protein 186
NM_026313	330	P	793	P	2.30	I	3300001P08	RIKEN cDNA 3300001P08 gene
NM_146087	1683	P	4128	P	2.30	I	Csnk1a1	casein kinase 1, alpha 1
NM_025833	1093	P	2312	P	2.30	I	Baiap2l1	BAI1-associated protein 2-like 1
NM_145512	181	P	537	P	2.30	I	Sft2d2	SFT2 domain containing 2
NM_145512	356	P	793	P	2.30	I	Sft2d2	SFT2 domain containing 2
NM_024282	327	P	713	P	2.30	I	5830417C01	RIKEN cDNA 5830417C01 gene
NM_00103908	247	P	589	P	2.30	I	Sel1h	Sel1 (suppressor of lin-12) 1 homolog (C. elegans)
NM_011743	155	P	348	P	2.30	I	Zfp106	zinc finger protein 106
NM_145542	244	P	512	P	2.30	I	Ahcyl1	S-adenosylhomocysteine hydrolase-like 1
NM_019492 //	93	P	188	P	2.30	MI	Rgs3	regulator of G-protein signaling 3
NM_00100854	286	P	841	P	2.30	I	Mxi1	Max interacting protein 1
XM_00100158	182	P	401	P	2.30	I	1110060D06	RIKEN cDNA 1110060D06 gene /// dedicator of cytokinesis 5
NM_011669	66	P	130	P	2.30	I	Usp12	ubiquitin specific peptidase 12
NM_011826	329	P	662	P	2.30	I	Hax1	HCLS1 associated X-1
NM_145614	361	P	847	P	2.30	I	Dlat	dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrog
NM_011151	314	P	713	P	2.30	I	Ppm1b	protein phosphatase 1B, magnesium dependent, beta isoform
NM_144545	252	P	569	P	2.30	I	Eif3s1	eukaryotic translation initiation factor 3, subunit 1 alpha
NM_144545	61	P	167	P	2.30	I	Eif3s1	eukaryotic translation initiation factor 3, subunit 1 alpha
NM_026474	405	P	989	P	2.30	I	Sugt1	SGT1, suppressor of G2 allele of SKP1 (S. cerevisiae)
NM_028754	84	P	158	P	2.30	I	0610037L13	RIKEN cDNA 0610037L13 gene
NM_011188	560	P	1394	P	2.30	I	Psmc2	proteasome (prosome, macropain) 26S subunit, ATPase 2
NM_145830 //	56	P	158	P	2.30	I	Ehmt2	euchromatic histone lysine N-methyltransferase 2
NM_144808	463	P	1068	P	2.30	I	Slc39a14	solute carrier family 39 (zinc transporter), member 14
NM_178920	501	P	1129	P	2.30	I	Mal2	mal, T-cell differentiation protein 2
NM_011133	29	P	62	P	2.30	I	Pole2	polymerase (DNA directed), epsilon 2 (p59 subunit)
NM_133990	605	P	1336	P	2.30	I	Il13ra1	interleukin 13 receptor, alpha 1
NM_019927	127	P	308	P	2.30	I	Arih1	ariadne ubiquitin-conjugating enzyme E2 binding protein homolog 1 (Drosc
NM_026989	133	P	248	P	2.30	I	Sfrs11	splicing factor, arginine/serine-rich 11
NM_030116	166	P	396	P	2.30	I	Mrpl9	mitochondrial ribosomal protein L9
NM_148945	58	P	136	P	2.30	I	Rps6ka3	ribosomal protein S6 kinase polypeptide 3
---	215	P	556	P	2.30	I	---	---
NM_021353	350	P	744	P	2.30	I	Slc26a3	solute carrier family 26, member 3
NM_023671	88	P	212	P	2.30	MI	Clns1a	chloride channel, nucleotide-sensitive, 1A
NM_148932	200	P	365	P	2.30	I	Pom121	nuclear pore membrane protein 121
NM_00102594	257	P	595	P	2.30	I	Dnm1l	dynamin 1-like
NM_029103	1123	P	2907	P	2.30	I	Armet	arginine-rich, mutated in early stage tumors
---	692	P	1553	P	2.30	I	---	---
NM_00101339	133	P	299	P	2.30	I	Cpsf6	cleavage and polyadenylation specific factor 6
NM_00101339	121	P	275	P	2.30	I	Cpsf6	cleavage and polyadenylation specific factor 6
NM_026932	128	P	304	P	2.30	I	Ebna1bp2	EBNA1 binding protein 2
NM_027420	359	P	782	P	2.30	I	2610034B18	RIKEN cDNA 2610034B18 gene

Transcript	WT		KO		Change KO/WT		Gene	
	Signal	Detectio	Signal	Detectio	Fold	Call	Symbol	Title
XM_140758 //	73	P	178	P	2.30	I	Zfp518	zinc finger protein 518
NM_025333	177	P	425	P	2.30	I	0610038F07	RIKEN cDNA 0610038F07 gene
NM_172712	68	P	173	P	2.30	I	Ube1l2	ubiquitin-activating enzyme E1-like 2
---	109	P	240	P	2.30	I	Malat1	metastasis associated lung adenocarcinoma transcript 1 (non-coding RN
NM_027375	611	P	1340	P	2.30	I	Gcc2	GRIP and coiled-coil domain containing 2
NM_199008	269	P	654	P	2.30	I	Cox11	COX11 homolog, cytochrome c oxidase assembly protein (yeast)
XM_131300 //	39	P	129	P	2.30	I	2310030N02	RIKEN cDNA 2310030N02 gene
NM_172407	63	P	217	P	2.30	I	4921511I16R	RIKEN cDNA 4921511I16 gene
NM_178616	319	P	758	P	2.30	I	Psmd11	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11
NM_026035	169	P	391	P	2.30	I	Mrpl55	mitochondrial ribosomal protein L55
NM_011636 //	173	P	311	P	2.30	I	Plscr1 /// LOC	phospholipid scramblase 1 /// hypothetical LOC433328 /// hypothetical p
NM_026054	305	P	684	P	2.30	I	2810474O19	RIKEN cDNA 2810474O19 gene
NM_173369	229	P	214	P	2.30	I	Cyld	cylindromatosis (turban tumor syndrome)
NM_021394	562	P	1335	P	2.30	I	Zbp1	Z-DNA binding protein 1
NM_024437 //	232	P	471	P	2.30	I	Nudt7	nudix (nucleoside diphosphate linked moiety X)-type motif 7
NM_030116	118	P	271	P	2.30	I	Mrpl9	mitochondrial ribosomal protein L9
XM_00100311	156	P	345	P	2.30	I	1700020I14R	RIKEN cDNA 1700020I14 gene
NM_010485	234	P	659	P	2.30	I	Elavl1	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen
NM_028906	93	P	175	P	2.30	I	Dpp8	dipeptidylpeptidase 8
NM_028677 //	106	P	299	P	2.30	I	Ppih /// LOC4	peptidyl prolyl isomerase H /// similar to peptidyl prolyl isomerase H /// sir
NM_013897	622	P	1515	P	2.30	I	Timm8b	translocase of inner mitochondrial membrane 8 homolog b (yeast)
NM_00101804	330	P	736	P	2.30	I	Sp3	trans-acting transcription factor 3
NM_025714	67	M	91	P	2.30	I	Odf2l	outer dense fiber of sperm tails 2-like
NM_019501	197	P	395	P	2.30	I	Pdss1	prenyl (solanesyl) diphosphate synthase, subunit 1
NM_00102438	175	P	482	P	2.30	I	Crls1	cardiolipin synthase 1
NM_021299	228	P	476	P	2.30	I	Ak3	adenylate kinase 3
NM_026896	63	P	146	P	2.30	I	Crsp8	cofactor required for Sp1 transcriptional activation, subunit 8
NM_016682	185	P	475	P	2.30	I	Uble1b	ubiquitin-like 1 (sentrin) activating enzyme E1B
NM_007636	328	P	693	P	2.30	I	Cct2	chaperonin subunit 2 (beta)
NM_007636	1038	P	2304	P	2.30	I	Cct2	chaperonin subunit 2 (beta)
NM_028932	211	P	565	P	2.30	I	Eaf1	ELL associated factor 1
NM_00103330	142	P	337	P	2.30	I	Gmps	guanine monphosphate synthetase
XR_003788	83	P	167	P	2.30	I	LOC672274	similar to Transcription factor SOX-4
NM_172543	46	P	95	P	2.30	I	5730593F17	RIKEN cDNA 5730593F17 gene
NM_007622	153	P	343	P	2.30	I	Cbx1	chromobox homolog 1 (Drosophila HP1 beta)
NM_173760	320	P	696	P	2.30	I	Hisppd1	histidine acid phosphatase domain containing 1
NM_172254	164	P	368	P	2.30	I	Zcsl2	zinc finger, CSL domain containing 2
NM_00101338	140	P	279	P	2.30	I	Dync1li2	dynein, cytoplasmic 1 light intermediate chain 2
NM_172745	188	P	688	P	2.30	I	Tufm	Tu translation elongation factor, mitochondrial
NM_00103330	1088	P	2393	P	2.30	I	Ndufb6	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6
NM_011967	905	P	2436	P	2.30	I	Psma5	proteasome (prosome, macropain) subunit, alpha type 5
---	277	P	683	P	2.30	I	AI838057	expressed sequence AI838057
XM_194424 //	75	P	188	P	2.30	I	Otud4	OTU domain containing 4
NM_198303	148	P	364	P	2.30	MI	Eif5b	eukaryotic translation initiation factor 5B
NM_198303	61	P	133	P	2.30	I	Eif5b	eukaryotic translation initiation factor 5B
NM_030096	59	P	119	P	2.30	MI	Ddx52	DEAD (Asp-Glu-Ala-Asp) box polypeptide 52
XM_907664 //	121	P	303	P	2.30	I	1810013L24R	RIKEN cDNA 1810013L24 gene
XM_283903 //	278	P	668	P	2.30	I	B430201A12	RIKEN cDNA B430201A12 gene
NM_028768	181	P	421	P	2.30	I	Armc8	armadillo repeat containing 8
NM_028768	58	P	150	P	2.30	I	Armc8	armadillo repeat containing 8
NM_153794	40	P	95	P	2.30	I	4933403F05	RIKEN cDNA 4933403F05 gene
NM_00102989	64	P	178	P	2.30	I	Ate1	arginine-tRNA-protein transferase 1
NM_172714	119	P	250	P	2.30	I	AI461788	expressed sequence AI461788
---	94	P	232	P	2.30	I	---	---
XM_00100339	234	P	499	P	2.30	I	Ppig	peptidyl-prolyl isomerase G (cyclophilin G)
NM_011733 //	381	P	986	P	2.30	I	Csda	cold shock domain protein A
NM_172665	79	P	204	P	2.30	I	Pdk1	pyruvate dehydrogenase kinase, isoenzyme 1
---	337	P	792	P	2.30	I	---	Visual cortex cDNA, RIKEN full-length enriched library, clone:K230008J
NM_00103316	96	P	194	P	2.30	I	2700094K13	RIKEN cDNA 2700094K13 gene
---	42	P	113	P	2.30	I	2310007O11	RIKEN cDNA 2310007O11 gene
NM_177088	35	P	100	P	2.30	I	Ccdc45	coiled-coil domain containing 45
NM_172913	56	P	162	P	2.30	I	Tnrc9	trinucleotide repeat containing 9
NM_153762 //	159	P	398	P	2.30	I	Rnf26 /// LOC	ring finger protein 26 /// similar to ring finger protein 26 /// similar to ring
NM_138585	70	P	190	P	2.30	I	Cherp	calcium homeostasis endoplasmic reticulum protein
NM_178691	70	P	178	P	2.30	I	9930028C20	RIKEN cDNA 9930028C20 gene
NM_019869	197	P	483	P	2.30	I	Rbm14	RNA binding motif protein 14
NM_026054	264	P	579	P	2.30	I	2810474O19	RIKEN cDNA 2810474O19 gene
NM_023913	175	P	397	P	2.30	I	Ern1	Endoplasmic reticulum (ER) to nucleus signalling 1
NM_00104039	146	P	419	P	2.30	I	1110020G09	RIKEN cDNA 1110020G09 gene
NM_026653	184	P	408	P	2.30	I	Rpa1	replication protein A1
NM_026421	55	P	155	P	2.30	I	2310057D15	RIKEN cDNA 2310057D15 gene
NM_026508	101	P	183	P	2.30	I	Trap1	TNF receptor-associated protein 1
---	270	P	447	P	2.30	I	---	---
NM_080708	92	P	301	P	2.30	I	Bmp2k	BMP2 inducible kinase
XM_00100060	489	P	992	P	2.30	I	2310061I04R	RIKEN cDNA 2310061I04 gene
NM_179203	241	P	635	P	2.30	I	Atad3a	ATPase family, AAA domain containing 3A
XM_00100485	42	A	99	P	2.30	I	1110014N23	RIKEN cDNA 1110014N23 gene
NM_010074	94	P	193	P	2.30	I	Dpp4	Dipeptidylpeptidase 4
NM_009054	110	P	193	P	2.30	I	Trim27	tripartite motif protein 27
NM_025408	94	P	240	P	2.30	I	Phca	phytoceramidase, alkaline
XM_00100263	120	P	223	P	2.30	I	Bat2d	BAT2 domain containing 1
NM_011431	242	P	610	P	2.30	I	Eftud2	elongation factor Tu GTP binding domain containing 2
NM_177910	427	P	1018	P	2.30	I	Gmppb	GDP-mannose pyrophosphorylase B
NM_029763	32	P	80	P	2.30	MI	Polr3f	polymerase (RNA) III (DNA directed) polypeptide F
NM_008826	241	P	524	P	2.30	I	Pfkl	phosphofructokinase, liver, B-type
NM_153775	80	P	182	P	2.30	I	2310061F22	RIKEN cDNA 2310061F22 gene

Transcript	WT		KO		Change KO/WT		Gene	
	Signal	Detectio	Signal	Detectio	Fold	Call	Symbol	Title
NM_011276	66	P	166	P	2.30	I	Rnf12	ring finger protein 12
NM_019768 //	1988	P	3812	P	2.30	I	Morf4l2 /// LO	mortality factor 4 like 2 /// similar to Mortality factor 4-like protein 2 (MORF-
XM_976790	84	P	215	P	2.30	I	Tex10	testis expressed gene 10
XM_00100052	39	P	95	P	2.30	I	AI506816	expressed sequence AI506816
---	240	P	637	P	2.30	I	---	---
XM_00100023	432	P	965	P	2.30	I	9130208D14	RIKEN cDNA 9130208D14 gene
NM_009260 //	50	P	117	P	2.30	I	Spnb2	spectrin beta 2
NM_011405	849	P	1638	P	2.30	I	Slc7a7	solute carrier family 7 (cationic amino acid transporter, y+ system), membe
---	149	P	463	P	2.30	I	2410006H16	RIKEN cDNA 2410006H16 gene
NM_010485	330	P	787	P	2.30	I	Elavl1	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R
NM_010664	948	P	2406	P	2.30	I	Krt1-18	keratin complex 1, acidic, gene 18
NM_026506 //	504	P	955	P	2.30	I	Snrpg /// LOC	small nuclear ribonucleoprotein polypeptide G /// similar to small nuclear rib
NM_026310	321	P	811	P	2.30	I	Mrpl18	mitochondrial ribosomal protein L18
NM_00103396	1145	P	2643	P	2.30	I	Ak2	adenylate kinase 2
NM_008320	305	P	637	P	2.30	I	Irf8	interferon regulatory factor 8
NM_029963	91	P	288	P	2.30	I	Mrps5	mitochondrial ribosomal protein S5
NM_025894	296	P	666	P	2.30	I	Psmd12	proteasome (prosome, macropain) 26S subunit, non-ATPase, 12
NM_025531	468	P	1123	P	2.30	I	2310042G06	RIKEN cDNA 2310042G06 gene
NM_010364	57	P	126	P	2.30	I	Gtf2h4	general transcription factor II H, polypeptide 4
NM_00103754	110	P	226	P	2.30	I	Hspa14	heat shock protein 14
NM_027328	62	P	134	P	2.30	I	Prpf31	PRP31 pre-mRNA processing factor 31 homolog (yeast)
NM_013634 //	167	P	380	P	2.30	I	Pparbp	peroxisome proliferator activated receptor binding protein
NM_133825	235	P	541	P	2.30	I	D1Ertd622e	DNA segment, Chr 1, ERATO Doi 622, expressed
NM_013844	35	P	83	P	2.30	I	Zfp68	zinc finger protein 68
NM_022653	33	A	76	M	2.30	MI	Thop1	thimet oligopeptidase 1
NM_010756	97	P	217	P	2.30	I	Mafg	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein G (avian
NM_023514	128	P	273	P	2.30	I	Mrps9	mitochondrial ribosomal protein S9
NM_025368	101	P	233	P	2.30	I	Josd2	Josephin domain containing 2
NM_010407	179	P	512	P	2.30	I	Hck	hemopoietic cell kinase
NM_018869	170	P	363	P	2.30	I	Gprk5	G protein-coupled receptor kinase 5
NM_133358	130	P	324	P	2.30	I	Zfp617	zinc finger protein 617
NM_182999	133	P	300	P	2.30	I	Rnf20	ring finger protein 20
NM_011596	350	P	771	P	2.30	I	Atp6v0a2	ATPase, H+ transporting, lysosomal V0 subunit A2
NM_010122	142	P	348	P	2.30	I	Eif2b4	eukaryotic translation initiation factor 2B, subunit 4 delta
NM_009283	753	P	1882	P	2.30	I	Stat1	signal transducer and activator of transcription 1
NM_009283	313	P	718	P	2.30	I	Stat1	signal transducer and activator of transcription 1
NM_058212	22	A	60	P	2.30	I	Dpf3	D4, zinc and double PHD fingers, family 3
NM_019963	104	P	250	P	2.30	MI	Stat2	signal transducer and activator of transcription 2
NM_026490	59	P	130	P	2.30	I	Mrpl19	mitochondrial ribosomal protein L19
NM_008261	251	P	581	P	2.30	I	Hnf4a	hepatic nuclear factor 4, alpha
XM_485063 //	576	P	1398	P	2.30	I	3110001I20R	RIKEN cDNA 3110001I20 gene
NM_007380	422	P	898	P	2.30	I	Abi1	abl-interactor 1
NM_025527	205	P	468	P	2.30	I	Srp19	signal recognition particle 19
NM_010324	1543	P	3703	P	2.30	I	Got1	glutamate oxaloacetate transaminase 1, soluble
NM_025460	480	P	1071	P	2.30	I	Tmem126a	transmembrane protein 126A
NM_026403	75	P	192	P	2.30	I	2610027L16	RIKEN cDNA 2610027L16 gene
NM_145380	168	P	401	P	2.30	I	Ga17	dendritic cell protein GA17
NM_016980 //	36	P	123	P	2.30	I	Rpl5 /// LOC3	ribosomal protein L5 /// similar to 60S ribosomal protein L5 /// similar to 60
NM_146144	172	P	391	P	2.30	I	Usp1	ubiquitin specific peptdiase 1
NM_012010	399	P	906	P	2.30	I	Eif2s3x	eukaryotic translation initiation factor 2, subunit 3, structural gene X-linked
NM_178603	69	P	137	P	2.30	I	Mrpl50	mitochondrial ribosomal protein L50
NM_007700	278	P	643	P	2.30	I	Chuk	conserved helix-loop-helix ubiquitous kinase
NM_028840 //	178	P	388	P	2.30	I	Armc1 /// LOC	armadillo repeat containing 1 /// similar to armadillo repeat-containing prote
NM_029688	770	P	1968	P	2.30	I	Srxn1	sulfiredoxin 1 homolog (S. cerevisiae)
NM_145457	146	P	352	P	2.30	I	Paip1	polyadenylate binding protein-interacting protein 1
NM_009874	103	P	256	P	2.30	I	Cdk7	cyclin-dependent kinase 7 (homolog of Xenopus MO15 cdk-activating kina
NM_029880	113	P	282	P	2.30	I	Zadh1	zinc binding alcohol dehydrogenase, domain containing 1
NM_133990	542	P	1236	P	2.30	I	Il13ra1	interleukin 13 receptor, alpha 1
NM_030597	59	P	118	P	2.30	I	Lsm2	LSM2 homolog, U6 small nuclear RNA associated (S. cerevisiae)
NM_009786	170	P	430	P	2.30	I	Cacybp	calcyclin binding protein
NM_012008	138	P	306	P	2.30	I	Ddx3y	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, Y-linked
NM_024196	239	P	569	P	2.30	I	Tbc1d20	TBC1 domain family, member 20
NM_183275	33	P	97	P	2.30	MI	1110002N22	RIKEN cDNA 1110002N22 gene
NM_023040	129	P	225	P	2.30	I	Gfer	growth factor, erv1 (S. cerevisiae)-like (augmenter of liver regeneration)
NM_021335	158	P	363	P	2.30	I	Snrpb2	U2 small nuclear ribonucleoprotein B
NM_025434	123	P	311	P	2.30	I	Mrps28	mitochondrial ribosomal protein S28
NM_019660	197	P	317	P	2.30	I	Mycbp	c-myc binding protein
NM_027869	51	P	161	P	2.30	I	Pnpt1	polyribonucleotide nucleotidyltransferase 1
NM_026943	514	P	1153	P	2.30	I	Snrpd2	small nuclear ribonucleoprotein D2
NM_00103313	615	P	1394	P	2.30	I	1200015F23	RIKEN cDNA 1200015F23 gene
NM_012024	54	P	124	P	2.30	I	Ppp2r5e	protein phosphatase 2, regulatory subunit B (B56), epsilon isoform
XM_127221 //	157	P	359	P	2.30	I	Cdc2l5	cell division cycle 2-like 5 (cholinesterase-related cell division controller)
NM_027892	207	P	431	P	2.30	I	Ppp1r12a	protein phosphatase 1, regulatory (inhibitor) subunit 12A
XR_002351 //	81	P	194	P	2.30	I	2700089E24	RIKEN cDNA 2700089E24 gene
XM_618860 //	753	P	1665	P	2.30	I	9030605H24	RIKEN cDNA 9030605H24 gene
NM_009010	98	P	222	P	2.30	MI	Rad23a	RAD23a homolog (S. cerevisiae)
NM_010448	957	P	2116	P	2.30	I	Hnrpab	heterogeneous nuclear ribonucleoprotein A/B
NM_019706 //	125	P	265	P	2.30	I	Rnf138	ring finger protein 138
NM_175411 //	180	P	394	P	2.30	I	C030004A17	RIKEN cDNA C030004A17 gene
---	104	P	230	P	2.30	I	6330549H03	RIKEN cDNA 6330549H03 gene
NM_017381	152	P	325	P	2.30	I	Zfp265	zinc finger protein 265
---	188	P	421	P	2.30	I	Dgkd	diacylglycerol kinase, delta
NM_198102	214	P	493	P	2.30	I	G430041M01	RIKEN cDNA G430041M01 gene
NM_00100586	251	P	592	P	2.30	I	Mtus1	mitochondrial tumor suppressor 1
XM_130985 //	499	P	1181	P	2.30	I	Arfip1	ADP-ribosylation factor interacting protein 1
NM_181517	414	P	967	P	2.30	I	Ipo7	importin 7

Transcript	WT		KO		Change KO/WT		Gene	
	Signal	Detectio	Signal	Detectio	Fold	Call	Symbol	Title
NM_178668	126	P	354	P	2.30	I	E430028B21	RIKEN cDNA E430028B21 gene
NM_0010332	112	P	243	P	2.30	I	Psrc2	proline/serine-rich coiled-coil 2
NM_013761	225	P	533	P	2.30	I	Srr	serine racemase
XM_140308 //	106	P	273	P	2.30	I	Dcp2	DCP2 decapping enzyme homolog (S. cerevisiae)
NM_207633	203	P	432	P	2.30	I	Yipf6	Yip1 domain family, member 6
NM_172153 //	139	P	337	P	2.30	I	A830039H10	RIKEN cDNA A830039H10 gene
NM_025356	1149	P	2516	P	2.30	I	Ube2d3	ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast)
NM_0010249	167	P	349	P	2.30	I	Ddx49	DEAD (Asp-Glu-Ala-Asp) box polypeptide 49
NM_019987	255	P	654	P	2.30	I	Ick	intestinal cell kinase
XM_889805 //	300	P	695	P	2.30	I	Taok3	TAO kinase 3
---	328	P	720	P	2.30	I	---	---
NM_009838	831	P	1961	P	2.30	I	Cct6a	chaperonin subunit 6a (zeta)
NM_0010334	199	P	473	P	2.30	I	A630082K20	RIKEN cDNA A630082K20 gene
NR_002321 //	254	P	478	P	2.30	MI	Tug1	taurine upregulated gene 1
XM_0010007	111	P	207	P	2.30	I	Qrsl1	glutaminyl-tRNA synthase (glutamine-hydrolyzing)-like 1
NM_019768 //	2239	P	4930	P	2.30	I	Morf4l2 /// LO	mortality factor 4 like 2 /// similar to Mortality factor 4-like protein 2 (MOR
NM_203507	51	P	175	P	2.30	I	Rwdd4a	RWD domain containing 4A
NM_009178	109	P	226	P	2.30	I	St3gal4	ST3 beta-galactoside alpha-2,3-sialyltransferase 4
NM_011750	1211	P	2922	P	2.30	I	Sf1	splicing factor 1
NM_008298	238	P	542	P	2.30	I	Dnaja1	DnaJ (Hsp40) homolog, subfamily A, member 1
NM_019661	262	P	597	P	2.30	I	Ykt6	YKT6 homolog (S. Cerevisiae)
NM_026759	90	P	216	P	2.30	I	Mrpl13	mitochondrial ribosomal protein L13
NM_133948	23	P	59	P	2.30	I	Psip1	PC4 and SFRS1 interacting protein 1
NM_172593	197	P	412	P	2.30	I	Mier3	mesoderm induction early response 1, family member 3
---	128	P	287	P	2.30	I	6330564D18	RIKEN cDNA 6330564D18 gene
NM_139144	250	P	554	P	2.30	I	Ogt	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylgluc
NM_134095	177	P	333	P	2.30	I	D15Wsu75e	DNA segment, Chr 15, Wayne State University 75, expressed
XM_127961 //	84	P	178	P	2.30	I	4930461P20	RIKEN cDNA 4930461P20 gene
NM_173363	812	P	2024	P	2.46	I	Eif5	eukaryotic translation initiation factor 5
NM_009031	445	P	1458	P	2.46	I	Rbbp7	retinoblastoma binding protein 7
NM_009196	1013	P	2667	P	2.46	I	Slc16a1	solute carrier family 16 (monocarboxylic acid transporters), member 1
NM_133815	147	P	389	P	2.46	I	Lbr	lamin B receptor
NM_078478	2735	P	6943	P	2.46	I	Ghitm	growth hormone inducible transmembrane protein
NM_133808	62	P	211	P	2.46	I	Hdlbp	high density lipoprotein (HDL) binding protein
NM_008568	131	P	307	P	2.46	I	Mcm7	minichromosome maintenance deficient 7 (S. cerevisiae)
NM_009551	838	P	2064	P	2.46	I	Za20d2	zinc finger, A20 domain containing 2
NM_025364	182	P	444	P	2.46	I	1110005A23	RIKEN cDNA 1110005A23 gene
NM_008300	569	P	1486	P	2.46	I	Hspa4	heat shock protein 4
NM_013663	535	P	1212	P	2.46	I	Sfrs3	splicing factor, arginine/serine-rich 3 (SRp20)
NM_016764	85	P	194	P	2.46	I	Prdx4	peroxiredoxin 4
NM_011655	213	P	669	P	2.46	I	Tubb5	tubulin, beta 5
NM_009794	83	P	217	P	2.46	I	Capn2	calpain 2
NM_008686	263	P	735	P	2.46	I	Nfe2l1	nuclear factor, erythroid derived 2,-like 1
NM_134075 //	100	P	290	P	2.46	I	Gmpr2	guanosine monophosphate reductase 2
NM_019673	101	P	221	P	2.46	I	Actl6a	actin-like 6A
NM_017393	181	P	445	P	2.46	I	Clpp	caseinolytic peptidase, ATP-dependent, proteolytic subunit homolog (E.
NM_010123	269	P	625	P	2.46	I	Eif3s10	eukaryotic translation initiation factor 3, subunit 10 (theta)
NM_025683	253	P	593	P	2.46	I	Rpe	ribulose-5-phosphate-3-epimerase
NM_013902	82	P	260	P	2.46	I	Fkbp3	FK506 binding protein 3
NM_008831 //	282	P	815	P	2.46	I	Phb /// LOC6	prohibitin /// similar to prohibitin /// similar to prohibitin /// similar to prohib
NM_027353	46	P	136	P	2.46	I	Cd2bp2	CD2 antigen (cytoplasmic tail) binding protein 2
NM_024478	238	P	698	P	2.46	I	Grpel1	GrpE-like 1, mitochondrial
NM_026068	56	P	148	P	2.46	I	Med31	mediator of RNA polymerase II transcription, subunit 31 homolog (yeast)
NM_130450	389	P	984	P	2.46	I	Elovl6	ELOVL family member 6, elongation of long chain fatty acids (yeast)
NM_009194	54	P	121	P	2.46	I	Slc12a2	solute carrier family 12, member 2
NM_133801	175	P	469	P	2.46	I	Gtf2f1	general transcription factor IIF, polypeptide 1
NM_011568	272	P	755	P	2.46	I	Thoc4	THO complex 4
NM_011779	238	P	614	P	2.46	I	Coro1c	coronin, actin binding protein 1C
NM_025959	538	P	1309	P	2.46	I	Psmc6	proteasome (prosome, macropain) 26S subunit, ATPase, 6
NM_033075	126	P	341	P	2.46	I	D17H6S56E-	DNA segment, Chr 17, human D6S56E 5
NM_025318	197	P	446	P	2.46	I	Tmem93	transmembrane protein 93
NM_026312	82	P	192	P	2.46	I	2610029G23	RIKEN cDNA 2610029G23 gene
NM_053089	157	P	389	P	2.46	I	Narg1	NMDA receptor-regulated gene 1
NM_026425	461	P	1124	P	2.46	I	Nat5	N-acetyltransferase 5 (ARD1 homolog, S. cerevisiae)
NM_008921	39	P	96	P	2.46	I	Prim1	DNA primase, p49 subunit
NM_009634	56	P	125	P	2.46	MI	Adsl	adenylosuccinate lyase
NM_138755	28	A	76	M	2.46	I	Phf21a	PHD finger protein 21A
NM_0010352	86	P	213	P	2.46	I	Xpo1	exportin 1, CRM1 homolog (yeast)
NM_010178	51	P	130	P	2.46	I	Fusip1	FUS interacting protein (serine-arginine rich) 1
NM_025476	163	P	437	P	2.46	I	2410005O16	RIKEN cDNA 2410005O16 gene
NM_007863	22	A	73	P	2.46	I	Mpp3	membrane protein, palmitoylated 3 (MAGUK p55 subfamily member 3)
NM_013515	225	P	498	P	2.46	I	Stom	stomatin
NM_133905	251	P	580	P	2.46	I	Papd4	PAP associated domain containing 4
NM_025430	371	P	852	P	2.46	I	Mrpl35	mitochondrial ribosomal protein L35
NM_026220	112	P	287	P	2.46	I	Mfap1	microfibrillar-associated protein 1
NM_133196	198	P	394	P	2.46	I	Cstf2	cleavage stimulation factor, 3' pre-RNA subunit 2
XM_0010046	88	P	247	P	2.46	I	Morc3	microrchidia 3
NM_178610	63	P	166	P	2.46	I	Krr1	KRR1, small subunit (SSU) processome component, homolog (yeast)
NM_023554	426	P	1002	P	2.46	I	Nol7	nucleolar protein 7
NM_018785	28	P	76	P	2.46	I	Prpf40a	PRP40 pre-mRNA processing factor 40 homolog A (yeast)
NM_0010020	183	P	522	P	2.46	I	Lmna	lamin A
NM_011396	157	P	402	P	2.46	I	Slc22a5	solute carrier family 22 (organic cation transporter), member 5
NM_013634 //	117	P	314	P	2.46	I	Pparbp	peroxisome proliferator activated receptor binding protein
NM_023647	715	P	1670	P	2.46	I	Nipa2	non imprinted in Prader-Willi/Angelman syndrome 2 homolog (human)
NM_009372	39	P	100	P	2.46	I	Tgif	TG interacting factor
NM_008917	220	P	637	P	2.46	I	Ppt1	palmitoyl-protein thioesterase 1

Transcript	WT		KO		Change KO/WT		Gene	
	Signal	Detectio	Signal	Detectio	Fold	Call	Symbol	Title
NM_011304	93	P	228	P	2.46	I	Ruvbl2	RuvB-like protein 2
NM_031373	102	P	223	P	2.46	I	Ogfr	opioid growth factor receptor
NM_018886	181	P	469	P	2.46	I	Lgals8	lectin, galactose binding, soluble 8
NM_052993	98	P	274	P	2.46	I	C1galt1	core 1 UDP-galactose:N-acetylgalactosamine-alpha-R beta 1,3-galactosylt
NM_013716	183	P	487	P	2.46	I	RP23-336J1.	Ras-GTPase-activating protein SH3-domain binding protein
NM_010266	638	P	1598	P	2.46	I	Gda	guanine deaminase
NM_026095	300	P	804	P	2.46	I	Snrpd3	small nuclear ribonucleoprotein D3
NM_011568 //	152	P	411	P	2.46	I	Thoc4 /// Ref	THO complex 4 /// RNA and export factor binding protein 2
NM_016805	525	P	1335	P	2.46	I	Hnrpu	heterogeneous nuclear ribonucleoprotein U
NM_030259	223	P	566	P	2.46	I	BC003324	cDNA sequence BC003324
NM_025283	309	P	737	P	2.46	I	Prei3	preimplantation protein 3
NM_007917 //	76	P	179	P	2.46	I	Eif4e /// LOC	eukaryotic translation initiation factor 4E /// hypothetical LOC630527
NM_026653	79	P	208	P	2.46	I	Rpa1	replication protein A1
NM_025934	39	P	111	P	2.46	I	Riok2	RIO kinase 2 (yeast)
NM_011552	18	P	59	P	2.46	I	Tcof1	Treacher Collins Franceschetti syndrome 1, homolog
NM_146094	41	P	129	P	2.46	I	Fads1	fatty acid desaturase 1
NM_0010038	253	P	596	P	2.46	I	Tardbp	TAR DNA binding protein
NM_023603	197	P	477	P	2.46	I	Sfpq	splicing factor proline/glutamine rich (polypyrimidine tract binding protein a
NM_145507 //	151	P	269	P	2.46	I	Dars	aspartyl-tRNA synthetase
NM_146083	46	P	132	P	2.46	I	Sfrs7	splicing factor, arginine/serine-rich 7
NM_203507	40	P	96	P	2.46	I	Rwdd4a	RWD domain containing 4A
NM_027002 //	66	P	116	P	2.46	I	Polr2d	polymerase (RNA) II (DNA directed) polypeptide D
NM_145533	139	P	359	P	2.46	I	Smox	spermine oxidase
NM_026053	37	P	94	P	2.46	I	Gemin6	gem (nuclear organelle) associated protein 6
NM_145480	30	P	91	P	2.46	I	Rfc4	replication factor C (activator 1) 4
NM_172054	237	P	584	P	2.46	I	Txndc9	thioredoxin domain containing 9
XM_128528 //	175	P	327	P	2.46	I	BC003965	cDNA sequence BC003965
NM_011967	478	P	1269	P	2.46	I	Psma5	proteasome (prosome, macropain) subunit, alpha type 5
NM_027220	1122	P	2523	P	2.46	I	Prss32	protease, serine, 32
NM_144895	65	P	193	P	2.46	I	Spg20	spastic paraplegia 20, spartin (Troyer syndrome) homolog (human)
NM_144895	147	P	313	P	2.46	I	Spg20	spastic paraplegia 20, spartin (Troyer syndrome) homolog (human)
NM_145381	155	P	434	P	2.46	I	Lactb2	lactamase, beta 2
NM_028521	108	P	255	P	2.46	MI	Phospho2	phosphatase, orphan 2
NM_009333	68	P	183	P	2.46	I	Tcf7l2	transcription factor 7-like 2, T-cell specific, HMG-box
NM_009884	379	P	1005	P	2.46	I	Cebpg	CCAAT/enhancer binding protein (C/EBP), gamma
NM_027296	60	P	190	P	2.46	MI	Trnt1	tRNA nucleotidyl transferase, CCA-adding, 1
NM_011590	492	P	1274	P	2.46	I	Timm17a	translocase of inner mitochondrial membrane 17a
NM_010380	103	P	490	P	2.46	I	H2-D1	histocompatibility 2, D region locus 1
NM_198006	84	P	204	P	2.46	I	6330578E17	RIKEN cDNA 6330578E17 gene
NM_013876	321	P	889	P	2.46	I	Rnf11	ring finger protein 11
NM_009546	91	P	265	P	2.46	I	Trim25	tripartite motif protein 25
NM_0010250	136	P	389	P	2.46	I	Atf2	activating transcription factor 2
NM_144529	232	P	543	P	2.46	I	Arhgap17	Rho GTPase activating protein 17
NM_212484	184	P	418	P	2.46	I	Cnot6	CCR4-NOT transcription complex, subunit 6
NM_144874	122	P	287	P	2.46	I	Cox15	COX15 homolog, cytochrome c oxidase assembly protein (yeast)
NM_175121	373	P	929	P	2.46	I	Slc38a2	solute carrier family 38, member 2
NM_008468	73	P	192	P	2.46	I	Kpna6	karyopherin (importin) alpha 6
NM_172703	178	P	394	P	2.46	I	Eif4g3	eukaryotic translation initiation factor 4 gamma, 3
NM_028399	69	P	168	P	2.46	I	Ccnt2	cyclin T2
NM_011410	78	A	164	P	2.46	I	Slfn4	schlafen 4
NM_019927	124	P	285	P	2.46	I	Arih1	ariadne ubiquitin-conjugating enzyme E2 binding protein homolog 1 (Drosc
NM_009722	1098	P	2596	P	2.46	I	Atp2a2	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2
NM_010431	802	P	1796	P	2.46	I	Hif1a	hypoxia inducible factor 1, alpha subunit
NM_011981 //	36	P	73	P	2.46	I	Zfp260 /// LO	zinc finger protein 260 /// similar to Zinc finger protein OZF (Zinc finger prc
NM_028358 //	246	P	758	P	2.46	I	Ssbp1	single-stranded DNA binding protein 1
NM_030093	94	A	214	P	2.46	I	3300001G02	RIKEN cDNA 3300001G02 gene
NM_026115	63	P	140	P	2.46	I	Hat1	histone aminotransferase 1
NM_028273	93	P	205	P	2.46	I	Pgam5	phosphoglycerate mutase family member 5
NM_027275	92	P	247	P	2.46	I	2810422B04	RIKEN cDNA 2810422B04 gene
XM_0010006	195	P	446	P	2.46	I	1300001I01R	RIKEN cDNA 1300001I01 gene
NM_0010387	138	P	364	P	2.46	I	Cdc42se1	CDC42 small effector 1
NM_033320	140	P	302	P	2.46	I	Glce	glucuronyl C5-epimerase
XM_0010013	387	P	824	P	2.46	I	Hnrpa0	heterogeneous nuclear ribonucleoprotein A0
NM_145215	316	P	657	P	2.46	I	Abhd11	abhydrolase domain containing 11
NM_134156	109	P	272	P	2.46	I	Actn1	actinin, alpha 1
---	119	P	247	P	2.46	I	---	---
NM_027096 //	487	P	1227	P	2.46	I	Prei4	preimplantation protein 4
NM_009333	279	P	571	P	2.46	I	Tcf7l2	transcription factor 7-like 2, T-cell specific, HMG-box
NM_0010391	155	P	372	P	2.46	I	Hnrpa1 /// LO	heterogeneous nuclear ribonucleoprotein A1 /// heterogeneous nuclear ribc
NM_027834	65	P	169	P	2.46	I	9130008F23	RIKEN cDNA 9130008F23 gene
NM_0010400	109	P	266	P	2.46	I	Sco1	SCO cytochrome oxidase deficient homolog 1 (yeast)
NM_016804	414	P	1134	P	2.46	I	Mtx2	metaxin 2
NM_021346 //	31	P	92	P	2.46	I	Zfp318	zinc finger protein 318
NM_026102 //	77	P	183	P	2.46	I	Daam1	dishevelled associated activator of morphogenesis 1
NM_016881	246	P	595	P	2.46	I	Pmm2	phosphomannomutase 2
NM_024258	317	P	732	P	2.46	I	Usp16	ubiquitin specific peptidase 16
NM_0010395	347	P	752	P	2.46	I	Dnm2	dynamin 2
NM_029775	119	P	280	P	2.46	I	Dcun1d5	DCN1, defective in cullin neddylation 1, domain containing 5 (S. cerevisiae
NM_033080	232	P	613	P	2.46	I	Nudt19	nudix (nucleoside diphosphate linked moiety X)-type motif 19
NM_008722	335	P	761	P	2.46	I	Npm1	nucleophosmin 1
NM_009373	896	P	1916	P	2.46	I	Tgm2	transglutaminase 2, C polypeptide
XM_0010024	328	P	712	P	2.46	I	D19Wsu12e	DNA segment, Chr 19, Wayne State University 12, expressed
NM_008515	1095	P	2338	P	2.46	I	Lrrfip1	leucine rich repeat (in FLII) interacting protein 1
XM_0010006	30	P	70	P	2.46	MI	Cdc27	cell division cycle 27 homolog (S. cerevisiae)
NM_175124	25	A	71	P	2.46	MI	Lrrc28	leucine rich repeat containing 28
NM_018747	219	P	547	P	2.46	I	Akap7	A kinase (PRKA) anchor protein 7

Transcript	WT		KO		Change KO/WT		Gene	
	Signal	Detectio	Signal	Detectio	Fold	Call	Symbol	Title
NM_146041	1181	P	2953	P	2.46	I	Gmds	GDP-mannose 4, 6-dehydratase
---	147	P	348	P	2.46	I	B230308N11	RIKEN cDNA B230308N11 gene
NM_198023	143	P	378	P	2.46	I	Rcor1	REST corepressor 1
NM_175312	28	P	79	P	2.46	I	B630005N14	RIKEN cDNA B630005N14 gene
NM_00103915	36	P	103	P	2.46	I	Cd44	CD44 antigen
NM_00102460	78	P	176	P	2.46	I	Ankrd28	ankyrin repeat domain 28
NM_175294	45	P	123	P	2.46	I	Nucks1	nuclear casein kinase and cyclin-dependent kinase substrate 1
NM_00100443	446	P	1097	P	2.46	I	Wapal	wings apart-like homolog (Drosophila)
XM_130548 //	49	P	126	P	2.46	I	2610101J03R	RIKEN cDNA 2610101J03 gene
NM_00103525	62	P	141	P	2.46	MI	Sfrs8	splicing factor, arginine/serine-rich 8
NM_011119	193	P	425	P	2.46	I	Pa2g4	proliferation-associated 2G4
NM_00103363	179	P	462	P	2.46	I	2810482G21	RIKEN cDNA 2810482G21 gene
NM_008433	68	P	159	P	2.46	I	Kcnn4	potassium intermediate/small conductance calcium-activated channel, s
XM_889805 //	508	P	1079	P	2.46	I	Taok3	TAO kinase 3
NM_009579	212	P	627	P	2.46	I	Slc30a1	solute carrier family 30 (zinc transporter), member 1
NM_172687	71	P	194	P	2.46	MI	Coq3	coenzyme Q3 homolog, methyltransferase (yeast)
---	96	P	240	P	2.46	I	1110008H02	RIKEN cDNA 1110008H02 gene
NM_178665	439	P	1057	P	2.46	I	Lpp	LIM domain containing preferred translocation partner in lipoma
NM_178925	73	P	179	P	2.46	I	Nsun3	NOL1/NOP2/Sun domain family 3
NM_175341 //	174	P	363	P	2.46	I	Mbnl2	muscleblind-like 2
NM_138592	107	P	236	P	2.46	I	Usp39	ubiquitin specific peptidase 39
NM_010306	57	P	151	P	2.46	I	Gnai3	guanine nucleotide binding protein, alpha inhibiting 3
NM_179203	142	P	303	P	2.46	I	Atad3a	ATPase family, AAA domain containing 3A
NM_198023	96	P	253	P	2.46	I	Rcor1	REST corepressor 1
NM_007874	86	P	242	P	2.46	I	Reep5	receptor accessory protein 5
NM_025942 //	162	P	365	P	2.46	I	2810409H07	RIKEN cDNA 2810409H07 gene
NM_178665	80	P	192	P	2.46	I	Lpp	LIM domain containing preferred translocation partner in lipoma
NM_133242	76	P	222	P	2.46	I	Rnpc2	RNA-binding region (RNP1, RRM) containing 2
NM_145569	222	P	457	P	2.46	I	Mat2a	methionine adenosyltransferase II, alpha
XM_00100258	119	P	305	P	2.46	I	Thrap1	thyroid hormone receptor associated protein 1
NM_012024	57	P	148	P	2.46	I	Ppp2r5e	Protein phosphatase 2, regulatory subunit B (B56), epsilon isoform
NM_026532 //	146	P	355	P	2.46	I	Nutf2 /// LOC	nuclear transport factor 2 /// similar to Nuclear transport factor 2 (NTF-2)
NM_00103939	124	P	351	P	2.46	I	Pkig	Protein kinase inhibitor, gamma
NM_172745 //	162	P	471	P	2.46	I	Tufm /// LOC	Tu translation elongation factor, mitochondrial /// similar to Tu translation
NM_009836	261	P	687	P	2.46	I	Cct3	chaperonin subunit 3 (gamma)
NM_010688	155	P	386	P	2.46	I	Lasp1	LIM and SH3 protein 1
NM_016682	296	P	650	P	2.46	I	Uble1b	ubiquitin-like 1 (sentrin) activating enzyme E1B
NM_024287	519	P	1358	P	2.46	I	Rab6	RAB6, member RAS oncogene family
NM_008062	499	P	1259	P	2.46	I	G6pdx	glucose-6-phosphate dehydrogenase X-linked
NM_008831	117	P	254	P	2.46	I	Phb	prohibitin
NM_026030	125	P	263	P	2.46	I	Eif2s2	eukaryotic translation initiation factor 2, subunit 2 (beta)
NM_026632	101	P	236	P	2.46	I	Rpa3	replication protein A3
NM_007381	1730	P	4171	P	2.46	I	Acadl	acyl-Coenzyme A dehydrogenase, long-chain
NM_023331	269	P	645	P	2.46	I	Mrpl46	mitochondrial ribosomal protein L46
NM_011699	91	P	218	P	2.46	I	Lin7c	lin-7 homolog C (C. elegans)
NM_026220	195	P	437	P	2.46	I	Mfap1	microfibrillar-associated protein 1
NM_026220	222	P	609	P	2.46	I	Mfap1	microfibrillar-associated protein 1
NM_010810	177	P	428	P	2.46	I	Mmp7	matrix metallopeptidase 7
NM_133808	97	P	310	P	2.46	I	Hdlbp	high density lipoprotein (HDL) binding protein
NM_021305	30	P	86	P	2.46	I	Sec61a2	Sec61, alpha subunit 2 (S. cerevisiae)
NM_019657	351	P	920	P	2.46	I	Hsd17b12	hydroxysteroid (17-beta) dehydrogenase 12
NM_018785	109	P	242	P	2.46	I	Prpf40a	PRP40 pre-mRNA processing factor 40 homolog A (yeast)
NM_018821	56	P	143	P	2.46	I	Socs6	suppressor of cytokine signaling 6
NM_011408	284	P	756	P	2.46	I	Slfn2	schlafen 2
NM_013454	39	P	117	P	2.46	MI	Abca1	ATP-binding cassette, sub-family A (ABC1), member 1
NM_008197	524	P	1467	P	2.46	I	H1f0	H1 histone family, member 0
NM_013585	790	P	2274	P	2.46	I	Psmb9	proteosome (prosome, macropain) subunit, beta type 9 (large multifuncti
NM_025824	573	P	1477	P	2.46	I	Bzw1	basic leucine zipper and W2 domains 1
NM_027000	65	P	168	P	2.46	MI	Gtpbp4	GTP binding protein 4
NM_007917 //	353	P	962	P	2.46	I	Eif4e /// LOC	eukaryotic translation initiation factor 4E /// hypothetical LOC630527
---	102	P	231	P	2.46	I	---	---
NM_025564	68	P	162	P	2.46	MI	2010012C16	RIKEN cDNA 2010012C16 gene
NM_00103908	57	P	164	P	2.46	I	Mrpl1	mitochondrial ribosomal protein L1
NM_018868	37	P	130	P	2.46	I	Nol5	nucleolar protein 5
NM_009569	312	P	752	P	2.46	I	Zfpm1	zinc finger protein, multitype 1
NM_010890	78	P	191	P	2.46	I	Nedd4	neural precursor cell expressed, developmentally down-regulted gene 4
NM_026396	150	P	369	P	2.46	I	Bxdc2	brix domain containing 2
NM_139149	215	P	491	P	2.46	I	Fus	fusion, derived from t(12;16) malignant liposarcoma (human)
NM_00101588	169	P	347	P	2.46	I	Taf9	TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated f
NM_145987	236	P	490	P	2.46	I	BC025833	cDNA sequence BC025833
NM_024282	154	P	316	P	2.46	I	5830417C01	RIKEN cDNA 5830417C01 gene
NM_009884	282	P	610	P	2.46	I	Cebpg	CCAAT/enhancer binding protein (C/EBP), gamma
NM_031403	82	P	227	P	2.46	I	Dbr1	debranching enzyme homolog 1 (S. cerevisiae)
XM_140497 //	29	A	77	P	2.46	I	BC024969	cDNA sequence BC024969
NM_013876	412	P	858	P	2.46	I	Rnf11	ring finger protein 11
NM_178645	97	P	222	P	2.46	I	Blmh	bleomycin hydrolase
NM_028696	75	P	197	P	2.46	I	5830411E10	RIKEN cDNA 5830411E10 gene
NM_172252	166	P	396	P	2.46	I	Mrpl21	mitochondrial ribosomal protein L21
NM_146130 //	128	P	270	P	2.46	I	Hnrpa3	heterogeneous nuclear ribonucleoprotein A3
NM_025645	47	P	147	P	2.46	I	Wdr57	WD repeat domain 57 (U5 snRNP specific)
NM_026157	156	P	384	P	2.46	I	Papd1	PAP associated domain containing 1
NM_019830	81	P	236	P	2.46	I	Prmt1	protein arginine N-methyltransferase 1
---	451	P	1122	P	2.46	I	---	---
XM_910498 //	92	P	232	P	2.46	I	2700029M09	RIKEN cDNA 2700029M09 gene
NM_027314	497	P	1330	P	2.46	I	38781	membrane-associated ring finger (C3HC4) 5
NM_026542	812	P	1980	P	2.46	I	D11Ertd333e	DNA segment, Chr 11, ERATO Doi 333, expressed

Transcript	WT		KO		Change KO/WT		Gene	
	Signal	Detectio	Signal	Detectio	Fold	Call	Symbol	Title
NM_009551	50	P	124	P	2.46	I	Za20d2	zinc finger, A20 domain containing 2
NM_026792	75	P	191	P	2.46	I	Agpat5	1-acylglycerol-3-phosphate O-acyltransferase 5 (lysophosphatidic acid acy
NM_019702	86	P	210	P	2.46	I	Hbs1l	Hbs1-like (S. cerevisiae)
NM_019472	98	P	226	P	2.46	I	Myo10	myosin X
XM_00100060	86	P	212	P	2.46	I	Cdc27	cell division cycle 27 homolog (S. cerevisiae)
NM_026476	207	P	510	P	2.46	I	2610101N10	RIKEN cDNA 2610101N10 gene
NM_013663	178	P	416	P	2.46	I	Sfrs3	splicing factor, arginine/serine-rich 3 (SRp20)
NM_173382	59	P	146	P	2.46	I	2810046L04	RIKEN cDNA 2810046L04 gene
NM_177325	64	P	173	P	2.46	I	Tsr1	TSR1, 20S rRNA accumulation, homolog (yeast)
NM_012000	61	P	122	P	2.46	I	Cln8	ceroid-lipofuscinosis, neuronal 8
NM_133780	79	P	158	P	2.46	I	Tpr	translocated promoter region
NM_009031	814	P	1855	P	2.46	I	Rbbp7	retinoblastoma binding protein 7
NM_025546	52	P	144	P	2.46	I	Rsl1d1	ribosomal L1 domain containing 1
NM_179203	84	P	228	P	2.46	I	Atad3a	ATPase family, AAA domain containing 3A
XM_00100096	340	P	763	P	2.46	I	1500005K14	RIKEN cDNA 1500005K14 gene
NM_025364 //	41	P	134	P	2.46	I	1110005A23	RIKEN cDNA 1110005A23 gene /// similar to cytokine induced protein 29
NM_00103323	399	P	792	P	2.46	I	Trim40	tripartite motif-containing 40
NM_00101239	327	P	749	P	2.46	I	Ptpla	protein tyrosine phosphatase-like (proline instead of catalytic arginine), me
NM_026620	129	P	337	P	2.46	I	2610510H03	RIKEN cDNA 2610510H03 gene
NM_133726	98	P	262	P	2.46	I	St13	suppression of tumorigenicity 13
NM_133978	26	P	67	P	2.46	I	Cmtm7	CKLF-like MARVEL transmembrane domain containing 7
XR_002351 //	89	P	212	P	2.46	I	2700089E24	RIKEN cDNA 2700089E24 gene
NM_025665	624	P	1604	P	2.46	I	2610209M04	RIKEN cDNA 2610209M04 gene
NM_009677	91	P	234	P	2.46	I	Ap1g1	adaptor protein complex AP-1, gamma 1 subunit
NM_010880	484	P	1354	P	2.64	I	Ncl	nucleolin
NM_010655 //	577	P	1509	P	2.64	I	Kpna2 /// LOC	karyopherin (importin) alpha 2 /// similar to Importin alpha-2 subunit (Karyo
NM_078478	1744	P	4412	P	2.64	I	Ghitm	growth hormone inducible transmembrane protein
NM_016737	116	P	326	P	2.64	I	Stip1	stress-induced phosphoprotein 1
NM_026106	58	P	129	P	2.64	I	Dr1	down-regulator of transcription 1
NM_013663	103	P	231	P	2.64	I	Sfrs3	splicing factor, arginine/serine-rich 3 (SRp20)
NM_026383	387	P	834	P	2.64	I	Pnrc2	proline-rich nuclear receptor coactivator 2
NM_133807	759	P	2044	P	2.64	I	Lrrc59	leucine rich repeat containing 59
NM_008567	107	P	259	P	2.64	I	Mcm6	minichromosome maintenance deficient 6 (MIS5 homolog, S. pombe) (S. c
NM_008302	577	P	1594	P	2.64	I	Hsp90ab1	heat shock protein 90kDa alpha (cytosolic), class B member 1
NM_019748	323	P	848	P	2.64	I	Uble1a	ubiquitin-like 1 (sentrin) activating enzyme E1A
NM_010123	49	P	172	P	2.64	I	Eif3s10	eukaryotic translation initiation factor 3, subunit 10 (theta)
NM_007991	186	P	561	P	2.64	I	Fbl	fibrillarin
NM_007444 //	74	P	178	P	2.64	I	Amd1 /// Amd	S-adenosylmethionine decarboxylase 1 /// S-adenosylmethionine decarbox
NM_026524	244	P	587	P	2.64	I	Mid1ip1	Mid1 interacting protein 1 (gastrulation specific G12-like (zebrafish))
NM_013902	70	P	160	P	2.64	I	Fkbp3	FK506 binding protein 3
NM_024172	49	P	77	P	2.64	I	1500019G21	RIKEN cDNA 1500019G21 gene
NM_016917	63	P	211	P	2.64	I	Slc40a1	solute carrier family 40 (iron-regulated transporter), member 1
NM_025591	273	P	732	P	2.64	I	2010309E21	RIKEN cDNA 2010309E21 gene
NM_016675	26	A	84	P	2.64	I	Cldn2	claudin 2
NM_133756	44	P	108	P	2.64	I	Xab1	XPA binding protein 1
NM_030694	178	P	436	P	2.64	I	Ifitm2	interferon induced transmembrane protein 2
NM_026030	487	P	1690	P	2.64	I	Eif2s2	eukaryotic translation initiation factor 2, subunit 2 (beta)
---	111	P	277	P	2.64	I	---	---
NM_009099	40	P	107	P	2.64	I	Trim30	tripartite motif protein 30
NM_019766	599	P	1521	P	2.64	I	Ptges3	prostaglandin E synthase 3 (cytosolic)
NM_020045	113	P	378	P	2.64	I	Hirip5	histone cell cycle regulation defective interacting protein 5
NM_026532 //	174	P	415	P	2.64	I	Nutf2 /// LOC	nuclear transport factor 2 /// similar to Nuclear transport factor 2 (NTF-2) //
NM_007970	24	A	58	P	2.64	I	Ezh1	enhancer of zeste homolog 1 (Drosophila)
NM_026556	581	P	1549	P	2.64	I	Dynll2	dynein light chain LC8-type 2
NM_008448	98	P	249	P	2.64	I	Kif5b	kinesin family member 5B
NM_021512	59	P	143	P	2.64	I	Nup160	nucleoporin 160
NM_017373	72	P	245	P	2.64	I	Nfil3	nuclear factor, interleukin 3, regulated
NM_011206	151	P	321	P	2.64	I	Ptpn18	protein tyrosine phosphatase, non-receptor type 18
NM_018759	45	P	135	P	2.64	I	Zfp326	zinc finger protein 326
NM_009554	51	P	155	P	2.64	I	Zfp37	zinc finger protein 37
NM_138757	37	P	94	P	2.64	I	4933424B01	RIKEN cDNA 4933424B01 gene
NM_028790	216	P	572	P	2.64	I	Acot12	acyl-CoA thioesterase 12
NM_199196	217	P	582	P	2.64	I	Suz12	suppressor of zeste 12 homolog (Drosophila)
NM_053115	104	P	319	P	2.64	I	Acox2	acyl-Coenzyme A oxidase 2, branched chain
NM_019640	84	P	198	P	2.64	I	Pitpnb	phosphatidylinositol transfer protein, beta
NM_009214 //	61	P	143	P	2.64	I	Sms /// LOC6	spermine synthase /// similar to Spermine synthase (Spermidine aminopro
NM_007999	59	P	116	P	2.64	I	Fen1	flap structure specific endonuclease 1
NM_019963	47	P	120	P	2.64	I	Stat2	signal transducer and activator of transcription 2
NM_010437	47	P	147	P	2.64	I	Hivep2	human immunodeficiency virus type I enhancer binding protein 2
NM_008740	115	P	317	P	2.64	I	Nsf	N-ethylmaleimide sensitive fusion protein
NM_00101796	104	P	256	P	2.64	I	Ddi2 /// Rsc1	DNA-damage inducible protein 2 /// regulatory solute carrier protein, family
NM_019666 //	32	P	87	P	2.64	I	Syncrip	synaptotagmin binding, cytoplasmic RNA interacting protein
NM_027432	122	P	299	P	2.64	I	Wdr77	WD repeat domain 77
NM_025695	71	P	174	P	2.64	I	Smc6l1	SMC6 structural maintenance of chromosomes 6-like 1 (yeast)
NM_025824	430	P	1187	P	2.64	I	Bzw1	basic leucine zipper and W2 domains 1
NM_013481	97	P	263	P	2.64	I	Bop1	block of proliferation 1
NM_016776	32	P	109	P	2.64	I	Mybbp1a	MYB binding protein (P160) 1a
NM_008249	70	P	171	P	2.64	I	Tfb2m	transcription factor B2, mitochondrial
NM_010474	38	P	135	P	2.64	I	Hs3st1	heparan sulfate (glucosamine) 3-O-sulfotransferase 1
NM_008972	1201	P	3206	P	2.64	I	Ptma	prothymosin alpha
NM_197982	330	P	889	P	2.64	I	Ddx39	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39
XM_906911 //	18	A	80	P	2.64	I	Rfc3	replication factor C (activator 1) 3
NM_011811	160	P	460	P	2.64	I	Farslb	phenylalanine-tRNA synthetase-like, beta subunit
NM_033073	231	P	568	P	2.64	I	Krt2-7	keratin complex 2, basic, gene 7
NM_203507	88	P	216	P	2.64	I	Rwdd4a	RWD domain containing 4A
NM_010120	231	P	620	P	2.64	I	Eif1a	eukaryotic translation initiation factor 1A

Transcript	WT		KO		Change KO/WT		Gene	
	Signal	Detectio	Signal	Detectio	Fold	Call	Symbol	Title
NM_028233	93	P	242	P	2.64	I	Lrpprc	leucine-rich PPR-motif containing
NM_145632	75	P	242	P	2.64	I	Polr2h	polymerase (RNA) II (DNA directed) polypeptide H
NM_144826	63	P	158	P	2.64	I	Utp6	UTP6, small subunit (SSU) processome component, homolog (yeast)
NM_028876	34	P	77	P	2.64	I	Tmed5	transmembrane emp24 protein transport domain containing 5
XM_358357 //	74	P	191	P	2.64	I	9030416H16	RIKEN cDNA 9030416H16 gene
NM_011743	27	A	73	P	2.64	I	Zfp106	zinc finger protein 106
NM_009338 //	82	P	174	P	2.64	I	Acat2 /// Acat	acetyl-Coenzyme A acetyltransferase 2 /// acetyl-Coenzyme A acetyltrans
NM_145506	45	P	94	P	2.64	I	Epb4.1l5	erythrocyte protein band 4.1-like 5
NM_144808	109	P	293	P	2.64	I	Slc39a14	solute carrier family 39 (zinc transporter), member 14
NM_010773	144	P	372	P	2.64	I	Mbd2	methyl-CpG binding domain protein 2
NM_011400	32	P	93	P	2.64	I	Slc2a1	solute carrier family 2 (facilitated glucose transporter), member 1
NM_025372	39	P	79	P	2.64	I	Tipin	timeless interacting protein
NM_029804	170	P	403	P	2.64	I	Hnrpm	heterogeneous nuclear ribonucleoprotein M
NM_181470	212	P	498	P	2.64	I	Ltv1	LTV1 homolog (S. cerevisiae)
NM_175224	69	P	226	P	2.64	I	Metap1	methionyl aminopeptidase 1
NM_172677	218	P	493	P	2.64	I	Ythdf3	YTH domain family 3
NM_023871	337	P	852	P	2.64	I	Set	SET translocation
NM_00102515	73	P	174	P	2.64	I	Ccdc93	coiled-coil domain containing 93
NM_0010053	73	P	178	P	2.64	I	Eif4g1	eukaryotic translation initiation factor 4, gamma 1
NM_144958	1400	P	3878	P	2.64	I	Eif4a1	eukaryotic translation initiation factor 4A1
NM_028871	134	P	340	P	2.64	I	Hnrpr	heterogeneous nuclear ribonucleoprotein R
XM_907304 //	33	P	124	P	2.64	I	Abcb7	ATP-binding cassette, sub-family B (MDR/TAP), member 7
NM_011358	423	P	1348	P	2.64	I	Sfrs2	splicing factor, arginine/serine-rich 2 (SC-35)
NM_022314	379	P	992	P	2.64	I	Tpm3	tropomyosin 3, gamma
NM_011768	31	P	92	P	2.64	I	Zfx	zinc finger protein X-linked
XM_979471	743	P	1877	P	2.64	I	2310043N10	RIKEN cDNA 2310043N10 gene
NM_173374	64	P	161	P	2.64	I	Sfrs1	splicing factor, arginine/serine-rich 1 (ASF/SF2)
NM_152812	100	P	213	P	2.64	I	Otud6b	OTU domain containing 6B
NM_026276	40	P	111	P	2.64	I	Aasdhppt	aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transfe
NM_027314	1243	P	2958	P	2.64	I	38781	membrane-associated ring finger (C3HC4) 5
NM_00102539	110	P	181	P	2.64	I	Bclaf1	BCL2-associated transcription factor 1
XM_619008 //	64	P	157	P	2.64	I	2600011C06	RIKEN cDNA 2600011C06 gene
NM_172712	79	P	270	P	2.64	I	Ube1l2	ubiquitin-activating enzyme E1-like 2
NM_028108	40	P	129	P	2.64	I	Mak3	Mak3 homolog (S. cerevisiae)
NM_026993	63	P	154	P	2.64	I	Ddah1	dimethylarginine dimethylaminohydrolase 1
NM_009333	75	P	229	P	2.64	I	Tcf7l2	transcription factor 7-like 2, T-cell specific, HMG-box
NM_025408	58	P	120	P	2.64	I	Phca	phytoceramidase, alkaline
NM_176835	112	P	257	P	2.64	I	2810451A06	RIKEN cDNA 2810451A06 gene
NM_028967	201	P	524	P	2.64	I	Batf2	basic leucine zipper transcription factor, ATF-like 2
NM_026276	51	P	157	P	2.64	I	Aasdhppt	aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transfe
NM_028487	123	P	407	P	2.64	I	Gpbp1	GC-rich promoter binding protein 1
NM_020012	54	P	141	P	2.64	I	Rnf14	ring finger protein 14
NM_153587	20	A	63	P	2.64	I	Rps6ka5	ribosomal protein S6 kinase, polypeptide 5
NM_00103969	35	P	76	P	2.64	I	Arhgap12	Rho GTPase activating protein 12
XR_005074	405	P	1059	P	2.64	I	LOC677168	hypothetical protein LOC677168
NM_009691	92	P	245	P	2.64	I	Aplp2	amyloid beta (A4) precursor-like protein 2
NM_175411 //	166	P	406	P	2.64	I	C030004A17	RIKEN cDNA C030004A17 gene
XM_00100252	69	P	168	P	2.64	I	Irf2bp2 /// LO	interferon regulatory factor 2 binding protein 2 /// similar to interferon regu
NM_180600	45	P	148	P	2.64	I	Ube2q2	ubiquitin-conjugating enzyme E2Q (putative) 2
NM_176838	74	P	201	P	2.64	I	Rbm35b	RNA binding motif protein 35b
NM_016806 //	611	P	1553	P	2.64	I	Hnrpa2b1	heterogeneous nuclear ribonucleoprotein A2/B1
NM_016739	65	P	170	P	2.64	I	Gpiap1	GPI-anchored membrane protein 1
NM_009438	280	P	762	P	2.64	I	Rpl13a	ribosomal protein L13a
NM_177474	141	P	500	P	2.64	I	D19Bwg1357	DNA segment, Chr 19, Brigham & Women's Genetics 1357 expressed
NM_013763	62	P	125	P	2.64	I	Tbl2	transducin (beta)-like 2
XM_981031 //	62	P	171	P	2.64	I	BC049349	cDNA sequence BC049349
XM_355205 //	840	P	2209	P	2.64	I	Raph1	Ras association (RalGDS/AF-6) and pleckstrin homology domains 1
XM_355205 //	666	P	2039	P	2.64	I	Raph1	Ras association (RalGDS/AF-6) and pleckstrin homology domains 1
NM_133358	112	P	295	P	2.64	I	Zfp617	zinc finger protein 617
NM_026532	671	P	1732	P	2.64	I	Nutf2	nuclear transport factor 2
NM_198620	176	P	442	P	2.64	I	Gm440	gene model 440, (NCBI)
NM_178936	91	P	169	P	2.64	I	Tmem56	transmembrane protein 56
NM_134163	66	P	189	P	2.64	I	Mbnl3	muscleblind-like 3 (Drosophila)
NM_009980 //	151	P	425	P	2.64	I	Ctbp2 /// Zran	C-terminal binding protein 2 /// zinc finger, RAN-binding domain containi
NM_175092	333	P	990	P	2.64	I	Rhof	ras homolog gene family, member f
XM_484151 //	96	P	259	P	2.64	I	A430041B07	RIKEN cDNA A430041B07 gene
NM_173374	533	P	1481	P	2.64	I	Sfrs1	splicing factor, arginine/serine-rich 1 (ASF/SF2)
NM_175389	19	P	67	P	2.64	MI	Rg9mtd2	RNA (guanine-9-) methyltransferase domain containing 2
NM_008974	757	P	1828	P	2.64	I	Ptp4a2	Protein tyrosine phosphatase 4a2
NM_008831	39	P	107	P	2.64	I	Phb	Prohibitin
NM_027421	29	P	76	P	2.64	I	Ints2	integrator complex subunit 2
NM_146234	44	P	110	P	2.64	MI	Tmem32	transmembrane protein 32
NM_024188	324	P	887	P	2.64	I	Oxct1	3-oxoacid CoA transferase 1
XM_359326 //	60	P	171	P	2.64	I	Jarid1a	jumonji, AT rich interactive domain 1A (Rbp2 like)
XM_899706 //	104	P	274	P	2.64	I	Lsm6	LSM6 homolog, U6 small nuclear RNA associated (S. cerevisiae)
NM_009373	404	P	1034	P	2.64	I	Tgm2	transglutaminase 2, C polypeptide
NM_197982	253	P	731	P	2.64	I	Ddx39	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39
NM_009418	88	P	222	P	2.64	I	Tpp2	tripeptidyl peptidase II
NM_008568	189	P	493	P	2.64	I	Mcm7	minichromosome maintenance deficient 7 (S. cerevisiae)
NM_145569	148	P	358	P	2.64	I	Mat2a	methionine adenosyltransferase II, alpha
NM_009716	245	P	618	P	2.64	I	Atf4	activating transcription factor 4
NM_172381	71	P	215	P	2.64	I	AI314180	expressed sequence AI314180
NM_025364 //	164	P	462	P	2.64	I	1110005A23	RIKEN cDNA 1110005A23 gene /// similar to cytokine induced protein 2
NM_175294	61	P	217	P	2.64	I	Nucks1	nuclear casein kinase and cyclin-dependent kinase substrate 1
---	57	M	139	P	2.64	I	---	Transcribed locus
NM_026542	187	P	567	P	2.64	I	D11Ertd333e	DNA segment, Chr 11, ERATO Doi 333, expressed

Transcript	WT		KO		Change KO/WT		Gene	
	Signal	Detectio	Signal	Detectio	Fold	Call	Symbol	Title
NM_182994	104	P	278	P	2.64	I	Arl5a	ADP-ribosylation factor-like 5A
NM_00103964	52	P	176	P	2.64	I	Mpa2l /// LOC	macrophage activation 2 like /// similar to macrophage activation 2 like /// si
NM_024177	107	P	254	P	2.64	I	Mrpl38	mitochondrial ribosomal protein L38
NM_008894	48	P	115	P	2.64	I	Pold2	polymerase (DNA directed), delta 2, regulatory subunit
NM_019537	88	P	226	P	2.64	I	Dscr2	Down syndrome critical region homolog 2 (human)
NM_018829	106	P	349	P	2.64	I	Ap3m1	adaptor-related protein complex 3, mu 1 subunit
NM_025626	79	P	185	P	2.64	I	3110001A13	RIKEN cDNA 3110001A13 gene
NM_016917	29	P	94	P	2.64	I	Slc40a1	solute carrier family 40 (iron-regulated transporter), member 1
NM_007552	42	P	147	P	2.64	I	Bmi1	B lymphoma Mo-MLV insertion region 1
NM_011338	28	A	54	P	2.64	MI	Ccl9	chemokine (C-C motif) ligand 9
NM_024188	1099	P	2766	P	2.64	I	Oxct1	3-oxoacid CoA transferase 1
NM_033563	41	P	95	P	2.64	MI	Klf7	Kruppel-like factor 7 (ubiquitous)
NM_028790	502	P	1378	P	2.64	I	Acot12	acyl-CoA thioesterase 12
NM_133771 //	131	P	330	P	2.64	I	0610016J10	RIKEN cDNA 0610016J10 gene /// hypothetical LOC619602
NM_016723 //	140	P	332	P	2.64	I	Uchl3 /// Uchl	ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase) /// ubiquitin
NM_019978	32	P	83	P	2.64	I	Dcamkl1	double cortin and calcium/calmodulin-dependent protein kinase-like 1
NM_011723	1803	P	5295	P	2.64	I	Xdh	xanthine dehydrogenase
NM_026744	336	P	900	P	2.64	I	Mrpl53	mitochondrial ribosomal protein L53
---	103	P	233	P	2.64	I	---	---
NM_146251	33	P	94	P	2.64	I	BC027342	cDNA sequence BC027342
NM_0010380	70	P	150	P	2.64	I	Gprk6	G protein-coupled receptor kinase 6
NM_009663	54	P	163	P	2.64	I	Alox5ap	arachidonate 5-lipoxygenase activating protein
NM_009931	72	P	233	P	2.64	I	Col4a1	procollagen, type IV, alpha 1
NM_144545	295	P	765	P	2.64	I	Eif3s1	eukaryotic translation initiation factor 3, subunit 1 alpha
XM_128374 //	86	P	256	P	2.64	I	Zfp294	zinc finger protein 294
NM_028358 //	130	P	372	P	2.64	I	Ssbp1	single-stranded DNA binding protein 1
NM_023136	26	M	83	P	2.64	I	Dtymk	deoxythymidylate kinase
NM_025969	76	P	193	P	2.64	I	1700034H14	RIKEN cDNA 1700034H14 gene
NM_028866	56	P	146	P	2.64	I	Wdr33	WD repeat domain 33
NM_00103908	41	A	111	P	2.64	I	Sel1h	Sel1 (suppressor of lin-12) 1 homolog (C. elegans)
NM_173363	1011	P	2480	P	2.64	I	Eif5	eukaryotic translation initiation factor 5
XM_133073 //	118	P	328	P	2.64	I	Nup205	nucleoporin 205
NM_134086	94	P	219	P	2.64	I	Slc38a1	solute carrier family 38, member 1
NM_0010133	64	P	138	P	2.64	MI	Utp18	UTP18, small subunit (SSU) processome component, homolog (yeast)
NM_0010133	119	P	257	P	2.64	I	Pfdn4	prefoldin 4
NM_024193	59	P	162	P	2.64	I	Nol5a	nucleolar protein 5A
XM_00100379	95	P	260	P	2.64	I	D330037H05	RIKEN cDNA D330037H05 gene /// similar to La-related protein 4 (La ribo
NM_009373	525	P	1356	P	2.64	I	Tgm2	transglutaminase 2, C polypeptide
NM_0010039	167	P	499	P	2.64	I	Mars	methionine-tRNA synthetase
NM_024245	65	P	139	P	2.64	I	Kif23	kinesin family member 23
NM_019682 //	589	P	1569	P	2.64	I	Dynll1 /// LOC	dynein light chain LC8-type 1 /// similar to dynein, cytoplasmic, light peptide
NM_026542	838	P	2389	P	2.64	I	D11Ertd333e	DNA segment, Chr 11, ERATO Doi 333, expressed
NM_0010174	42	P	115	P	2.64	I	Rasef	RAS and EF hand domain containing
NM_011956	50	P	94	P	2.64	I	Nubp2	nucleotide binding protein 2
NM_009836	328	P	749	P	2.64	I	Cct3	chaperonin subunit 3 (gamma)
NM_134095	174	P	432	P	2.64	I	D15Wsu75e	DNA segment, Chr 15, Wayne State University 75, expressed
NM_033074	406	P	973	P	2.64	I	Tars	threonyl-tRNA synthetase
XM_0010024	66	P	152	P	2.64	I	D19Wsu12e	DNA segment, Chr 19, Wayne State University 12, expressed
NM_198030	67	P	259	P	2.64	I	Hsd17b13	hydroxysteroid (17-beta) dehydrogenase 13
NM_139140	46	A	118	P	2.64	I	Spats2	spermatogenesis associated, serine-rich 2
NM_011358	156	P	411	P	2.83	I	Sfrs2	splicing factor, arginine/serine-rich 2 (SC-35)
NM_019641	187	P	545	P	2.83	I	Stmn1	stathmin 1
NM_011830	136	P	367	P	2.83	I	Impdh2	inosine 5'-phosphate dehydrogenase 2
NM_146200	1036	P	2907	P	2.83	I	Eif3s8	eukaryotic translation initiation factor 3, subunit 8
NM_138745	54	P	117	P	2.83	I	Mthfd1	methylenetetrahydrofolate dehydrogenase (NADP+ dependent), methenylte
NM_016777	55	P	171	P	2.83	I	Nasp	nuclear autoantigenic sperm protein (histone-binding)
NM_025706	58	P	160	P	2.83	I	Tbc1d15	TBC1 domain family, member 15
NM_133775	424	P	1094	P	2.83	I	9230117N10	RIKEN cDNA 9230117N10 gene
NM_009226	77	P	222	P	2.83	I	Snrpd1	small nuclear ribonucleoprotein D1
NM_010749	214	P	563	P	2.83	I	M6pr	mannose-6-phosphate receptor, cation dependent
NM_009278	68	P	192	P	2.83	I	Ssb	Sjogren syndrome antigen B
NM_025485	143	P	405	P	2.83	I	Mrps22	mitochondrial ribosomal protein S22
NM_008615 //	330	P	908	P	2.83	I	Mod1 /// LOC	malic enzyme, supernatant /// similar to NADP-dependent malic enzyme (
NM_026499	59	P	158	P	2.83	I	Sfrs6	splicing factor, arginine/serine-rich 6
NM_133777	159	P	494	P	2.83	I	Ube2s	ubiquitin-conjugating enzyme E2S
NM_011014	55	P	134	P	2.83	I	Oprs1	opioid receptor, sigma 1
NM_054099	89	P	243	P	2.83	I	1110038F14	RIKEN cDNA 1110038F14 gene
NM_025626	177	P	550	P	2.83	I	3110001A13	RIKEN cDNA 3110001A13 gene
NM_025297	58	P	178	P	2.83	I	Mecr	mitochondrial trans-2-enoyl-CoA reductase
NM_010738	141	P	453	P	2.83	I	Ly6a	lymphocyte antigen 6 complex, locus A
NM_026504	122	P	285	P	2.83	I	Coq5	coenzyme Q5 homolog, methyltransferase (yeast)
NM_026374	21	P	75	P	2.83	I	Ilf2	interleukin enhancer binding factor 2
NM_053089	94	P	224	P	2.83	I	Narg1	NMDA receptor-regulated gene 1
---	88	P	242	P	2.83	I	Malat1	metastasis associated lung adenocarcinoma transcript 1 (non-coding RNA
NM_008448	263	P	602	P	2.83	I	Kif5b	kinesin family member 5B
NM_0010352	170	P	472	P	2.83	I	Xpo1	exportin 1, CRM1 homolog (yeast)
NM_009883	371	P	1132	P	2.83	I	Cebpb	CCAAT/enhancer binding protein (C/EBP), beta
NM_021792	59	P	150	P	2.83	I	Iigp1	interferon inducible GTPase 1
NM_026527	116	P	337	P	2.83	I	2510006C20	RIKEN cDNA 2510006C20 gene
NM_008009	47	P	124	P	2.83	I	Fgfbp1	fibroblast growth factor binding protein 1
NM_016866	42	P	175	P	2.83	I	Stk39	serine/threonine kinase 39, STE20/SPS1 homolog (yeast)
NM_021394	277	P	796	P	2.83	I	Zbp1	Z-DNA binding protein 1
NM_012010 //	82	P	252	P	2.83	I	Eif2s3x /// LO	eukaryotic translation initiation factor 2, subunit 3, structural gene X-linked
NM_010890	29	P	102	P	2.83	I	Nedd4	neural precursor cell expressed, developmentally down-regulted gene 4
NM_019425	82	P	190	P	2.83	I	Gnpnat1	glucosamine-phosphate N-acetyltransferase 1
NM_134133	55	P	113	P	2.83	I	2010002N04	RIKEN cDNA 2010002N04 gene

Transcript	WT		KO		Change KO/WT		Gene	
	Signal	Detectio	Signal	Detectio	Fold	Call	Symbol	Title
NM_011958	32	P	98	P	2.83	I	Orc4l	origin recognition complex, subunit 4-like (S. cerevisiae)
NM_013885	98	P	210	P	2.83	I	Clic4	chloride intracellular channel 4 (mitochondrial)
NM_133702	45	P	107	P	2.83	I	Nol11	nucleolar protein 11
NM_025500	93	P	204	P	2.83	I	Mrpl37	mitochondrial ribosomal protein L37
NM_026472	61	P	143	P	2.83	I	Mki67ip	Mki67 (FHA domain) interacting nucleolar phosphoprotein
NM_144866	333	P	980	P	2.83	I	Etf1	eukaryotic translation termination factor 1
NM_144904 //	73	P	176	P	2.83	I	Rod1	ROD1 regulator of differentiation 1 (S. pombe)
NM_013872	101	P	278	P	2.83	I	Pmm1	phosphomannomutase 1
NM_027532	74	P	197	P	2.83	I	3200002M19	RIKEN cDNA 3200002M19 gene
NM_198645	120	P	303	P	2.83	I	Ccdc58	coiled-coil domain containing 58
NM_015762	169	A	531	P	2.83	I	Txnrd1	thioredoxin reductase 1
NM_027250	102	P	241	P	2.83	MI	2010305A19	RIKEN cDNA 2010305A19 gene
NM_146083	238	P	695	P	2.83	I	Sfrs7	splicing factor, arginine/serine-rich 7
NM_007516	247	P	782	P	2.83	I	Hnrpd	heterogeneous nuclear ribonucleoprotein D
NM_00103908	310	P	924	P	2.83	I	Sel1h	Sel1 (suppressor of lin-12) 1 homolog (C. elegans)
NM_029735 //	110	P	280	P	2.83	I	Eprs /// LOC6	glutamyl-prolyl-tRNA synthetase /// similar to Bifunctional aminoacyl-tRN
NM_028044	73	P	164	P	2.83	I	Cnn3	calponin 3, acidic
NM_00103343	100	P	286	P	2.83	MI	A630082K20	RIKEN cDNA A630082K20 gene
XM_917085 //	130	P	374	P	2.83	I	AI848100	expressed sequence AI848100
NM_029344	39	P	109	P	2.83	I	Acyp2	acylphosphatase 2, muscle type
NM_026742	96	P	309	P	2.83	I	1110007M04	RIKEN cDNA 1110007M04 gene
NM_173374	621	P	1625	P	2.83	I	Sfrs1	splicing factor, arginine/serine-rich 1 (ASF/SF2)
NM_146130 //	611	P	1904	P	2.83	I	Hnrpa3 /// LO	heterogeneous nuclear ribonucleoprotein A3 /// similar to heterogeneous
NM_028108	94	P	234	P	2.83	I	Mak3	Mak3 homolog (S. cerevisiae)
NM_026560	24	P	75	P	2.83	I	Cdca8	cell division cycle associated 8
NM_026560	67	P	207	P	2.83	I	Cdca8	cell division cycle associated 8
NM_028604	34	A	115	P	2.83	I	2410075D05	RIKEN cDNA 2410075D05 gene
---	1770	P	4853	P	2.83	I	2810423A18	RIKEN cDNA 2810423A18 gene
XM_125902 //	287	P	712	P	2.83	I	Xpot	exportin, tRNA (nuclear export receptor for tRNAs)
NM_011605	63	P	174	P	2.83	I	Tmpo	thymopoietin
NM_027421	45	P	118	P	2.83	I	Ints2	integrator complex subunit 2
NM_172695	159	P	382	P	2.83	I	Plaa	phospholipase A2, activating protein
NM_026250	44	P	149	P	2.83	I	4930429M06	RIKEN cDNA 4930429M06Rik
NM_00102438	167	P	423	P	2.83	I	Crls1	cardiolipin synthase 1
NM_027861	40	P	163	P	2.83	MI	0610010K06	RIKEN cDNA 0610010K06 gene
NM_178112	17	A	54	P	2.83	I	Ints8	integrator complex subunit 8
NM_024437 //	201	P	525	P	2.83	I	Nudt7	nudix (nucleoside diphosphate linked moiety X)-type motif 7
NM_175294	159	P	532	P	2.83	I	Nucks1	nuclear casein kinase and cyclin-dependent kinase substrate 1
NM_173363	473	P	1315	P	2.83	I	Eif5	eukaryotic translation initiation factor 5
NR_002896	99	P	263	P	2.83	I	Snord22	small nucleolar RNA, C/D box 22
NM_175552	52	P	151	P	2.83	I	Wdr3	WD repeat domain 3
NM_172722	84	P	194	P	2.83	I	C330023M02	RIKEN cDNA C330023M02 gene
NM_016805	26	A	83	P	2.83	I	Hnrpu	Heterogeneous nuclear ribonucleoprotein U
NM_00103947	92	P	264	P	2.83	I	Tcerg1	transcription elongation regulator 1 (CA150)
NM_011864	1649	P	5059	P	2.83	I	Papss2	3'-phosphoadenosine 5'-phosphosulfate synthase 2
NM_172594	20	P	57	P	2.83	I	Dhx29	DEAH (Asp-Glu-Ala-His) box polypeptide 29
NM_011811	204	P	504	P	2.83	I	Farslb	phenylalanine-tRNA synthetase-like, beta subunit
NM_010260	37	P	95	P	2.83	I	Gbp2	guanylate nucleotide binding protein 2
NM_030556	47	P	110	P	2.83	I	Slc19a3	solute carrier family 19 (sodium/hydrogen exchanger), member 3
XM_00100133	51	P	171	P	2.83	I	Centd1	centaurin, delta 1
XM_140740 //	82	P	235	P	2.83	I	Dusp5	dual specificity phosphatase 5
NM_016682	215	P	582	P	2.83	I	Uble1b	ubiquitin-like 1 (sentrin) activating enzyme E1B
NM_010480	499	P	1463	P	2.83	I	Hsp90aa1	heat shock protein 90kDa alpha (cytosolic), class A member 1
NM_00101588	103	P	316	P	2.83	I	Taf9 /// LOC5	TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated f
NM_053217	123	P	359	P	2.83	I	2010002M12	RIKEN cDNA 2010002M12 gene
NM_173866	31	P	88	P	2.83	I	Gpt2	glutamic pyruvate transaminase (alanine aminotransferase) 2
NM_181416	57	P	228	P	2.83	I	Arhgap11a	Rho GTPase activating protein 11A
NM_013761	40	P	92	P	2.83	MI	Srr	serine racemase
NM_199146	60	P	180	P	2.83	I	AI451617	expressed sequence AI451617
NM_008567	25	P	90	P	2.83	I	Mcm6	minichromosome maintenance deficient 6 (MIS5 homolog, S. pombe) (S
NM_008568 //	44	P	104	P	2.83	I	Mcm7 /// LOC	minichromosome maintenance deficient 7 (S. cerevisiae) /// similar to mi
NM_146041	116	P	437	P	2.83	I	Gmds	GDP-mannose 4, 6-dehydratase
XM_897902 //	41	P	137	P	2.83	MI	Brwd3	bromodomain and WD repeat domain containing 3
NM_009048	33	P	87	P	2.83	I	Reps1	RalBP1 associated Eps domain containing protein
XM_125902 //	188	P	524	P	2.83	I	Xpot	exportin, tRNA (nuclear export receptor for tRNAs)
NM_028924	51	P	135	P	2.83	I	Mtac2d1	membrane targeting (tandem) C2 domain containing 1
NM_053074	274	P	663	P	2.83	I	Nup62	nucleoporin 62
NM_009846	1073	P	2825	P	2.83	I	Cd24a	CD24a antigen
NM_019553	47	P	77	P	2.83	I	Ddx21	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21
NM_016739	111	P	307	P	2.83	I	Gpiap1	GPI-anchored membrane protein 1
NM_018757	30	A	86	M	2.83	I	Nme6	expressed in non-metastatic cells 6, protein
NM_019682	317	P	830	P	2.83	I	Dynll1	dynein light chain LC8-type 1
NM_026030	282	P	1152	P	2.83	I	Eif2s2	eukaryotic translation initiation factor 2, subunit 2 (beta)
NM_00103865	180	P	534	P	2.83	I	Slc16a3	solute carrier family 16 (monocarboxylic acid transporters), member 3
NM_026613	28	P	98	P	2.83	I	2810027O19	RIKEN cDNA 2810027O19 gene
NM_009836	145	P	465	P	2.83	I	Cct3	chaperonin subunit 3 (gamma)
NM_133249	200	P	556	P	2.83	I	Ppargc1b	peroxisome proliferative activated receptor, gamma, coactivator 1 beta
NM_018871	194	P	578	P	2.83	I	Ywhag	3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamr
---	259	P	616	P	2.83	I	---	---
NM_008303	434	P	1360	P	2.83	I	Hspe1	heat shock protein 1 (chaperonin 10)
NM_025443	129	P	333	P	2.83	I	1810003N24	RIKEN cDNA 1810003N24 gene
NM_007681	38	P	101	P	2.83	I	Cenpa	centromere autoantigen A
NM_025824	342	P	1043	P	2.83	I	Bzw1	basic leucine zipper and W2 domains 1
NM_008889	230	P	598	P	2.83	I	Ppp1r14b	protein phosphatase 1, regulatory (inhibitor) subunit 14B
NM_010817	179	P	471	P	2.83	I	Psmd7	proteasome (prosome, macropain) 26S subunit, non-ATPase, 7
NM_197982	159	P	562	P	2.83	I	Ddx39	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39

Transcript	WT		KO		Change KO/WT		Gene	
	Signal	Detectio	Signal	Detectio	Fold	Call	Symbol	Title
NM_133975	41	P	91	P	2.83	I	Trip12	thyroid hormone receptor interactor 12
NM_025878	87	P	265	P	2.83	I	Mrps18b	mitochondrial ribosomal protein S18B
NM_146130 //	454	P	1352	P	2.83	I	Hnrpa3 /// LO	heterogeneous nuclear ribonucleoprotein A3 /// similar to heterogeneous nu
NM_144866	255	P	769	P	2.83	I	Etf1	eukaryotic translation termination factor 1
XM_358313 //	23	P	73	P	2.83	I	BC018507	cDNA sequence BC018507
NM_009984	343	P	1039	P	2.83	I	Ctsl	cathepsin L
NM_145612	22	P	67	P	2.83	I	BC005471	cDNA sequence BC005471
NM_025782	45	P	133	P	2.83	I	9130422G05	RIKEN cDNA 9130422G05 gene
NM_029735 //	146	P	433	P	2.83	I	Eprs /// LOC6	glutamyl-prolyl-tRNA synthetase /// similar to Bifunctional aminoacyl-tRNA
NM_176979	71	P	196	P	2.83	I	Topbp1	topoisomerase (DNA) II beta binding protein
NM_0010259	29	A	86	P	2.83	I	Dnm1l	dynamin 1-like
NM_026114	293	P	848	P	2.83	I	Eif2s1	eukaryotic translation initiation factor 2, subunit 1 alpha
NM_027350	1583	P	4644	P	2.83	I	Nars	asparaginyl-tRNA synthetase
NM_0010403	42	P	108	P	2.83	I	1110020G09	RIKEN cDNA 1110020G09 gene
NM_019755	216	P	529	P	2.83	I	Plp2	proteolipid protein 2
NM_173374	504	P	1405	P	2.83	I	Sfrs1	splicing factor, arginine/serine-rich 1 (ASF/SF2)
NM_025305	168	P	391	P	2.83	I	Mrps7	mitchondrial ribosomal protein S7
NM_023731	16	A	64	P	2.83	I	Ccdc86	coiled-coil domain containing 86
XM_0010046	63	P	176	P	2.83	I	Ibtk	inhibitor of Bruton agammaglobulinemia tyrosine kinase
NM_020279	92	P	265	P	2.83	I	Ccl28	Chemokine (C-C motif) ligand 28
NM_197982	265	P	783	P	2.83	I	Ddx39	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39
XM_0010057	199	P	575	P	2.83	I	LOC673503	hypothetical protein LOC673503
NM_146200	783	P	2243	P	2.83	I	Eif3s8	eukaryotic translation initiation factor 3, subunit 8
NM_146200	1177	P	3140	P	2.83	I	Eif3s8	eukaryotic translation initiation factor 3, subunit 8
NM_019673	124	P	255	P	2.83	I	Actl6a	actin-like 6A
NM_011830	109	P	346	P	3.03	I	Impdh2	inosine 5'-phosphate dehydrogenase 2
NM_146200	444	P	1345	P	3.03	I	Eif3s8	eukaryotic translation initiation factor 3, subunit 8
NM_011631	1488	P	4738	P	3.03	I	Hsp90b1	heat shock protein 90kDa beta (Grp94), member 1
NM_015751	71	P	149	P	3.03	I	Abce1	ATP-binding cassette, sub-family E (OABP), member 1
NM_009551	189	P	394	P	3.03	I	Za20d2	zinc finger, A20 domain containing 2
NM_029571	31	P	121	P	3.03	I	Kti12	KTI12 homolog, chromatin associated (S. cerevisiae)
NM_013898	152	P	558	P	3.03	I	Timm8a1	translocase of inner mitochondrial membrane 8 homolog a1 (yeast)
NM_013898	51	P	148	P	3.03	I	Timm8a1	translocase of inner mitochondrial membrane 8 homolog a1 (yeast)
NM_130796	54	P	140	P	3.03	I	Snag1	sorting nexin associated golgi protein 1
NM_010790	27	A	87	P	3.03	I	Melk	maternal embryonic leucine zipper kinase
NM_025897	21	A	60	P	3.03	I	1500003O22	RIKEN cDNA 1500003O22 gene
NM_018738	545	P	1820	P	3.03	I	Igtp	interferon gamma induced GTPase
NM_019682 //	619	P	1781	P	3.03	I	Dynll1 /// LOC	dynein light chain LC8-type 1 /// similar to dynein, cytoplasmic, light peptide
NM_007552	89	P	365	P	3.03	I	Bmi1	B lymphoma Mo-MLV insertion region 1
NM_026030	1456	P	4413	P	3.03	I	Eif2s2	eukaryotic translation initiation factor 2, subunit 2 (beta)
NM_133681	145	P	421	P	3.03	I	Tspan1	tetraspanin 1
NM_025829	92	P	265	P	3.03	I	Eif4e3	eukaryotic translation initiation factor 4E member 3
NM_010193	22	A	65	P	3.03	I	Fem1b	feminization 1 homolog b (C. elegans)
NM_007481	102	P	319	P	3.03	I	Arf6	ADP-ribosylation factor 6
NM_008092	72	P	178	P	3.03	I	Gata4	GATA binding protein 4
NM_025505	75	P	171	P	3.03	I	Blzf1	basic leucine zipper nuclear factor 1
NM_025505	54	P	164	P	3.03	I	Blzf1	basic leucine zipper nuclear factor 1
NM_021792	24	P	76	P	3.03	I	Iigp1	interferon inducible GTPase 1
NM_008935	204	P	674	P	3.03	I	Prom1	prominin 1
NM_007792	161	P	547	P	3.03	I	Csrp2	cysteine and glycine-rich protein 2
NM_080452	97	P	295	P	3.03	I	Mrps2	mitochondrial ribosomal protein S2
NM_0010394	51	P	136	P	3.03	I	Tcerg1	transcription elongation regulator 1 (CA150)
NM_008181 //	600	P	1997	P	3.03	I	Gsta1 /// Gsta	glutathione S-transferase, alpha 1 (Ya) /// glutathione S-transferase, alpha
NM_026490	82	P	210	P	3.03	I	Mrpl19	mitochondrial ribosomal protein L19
NM_025777	94	P	192	P	3.03	I	9030623N16	RIKEN cDNA 9030623N16 gene
NM_008062 //	119	P	401	P	3.03	I	G6pd2 /// G6p	glucose-6-phosphate dehydrogenase 2 /// glucose-6-phosphate dehydroge
NM_013820	209	P	602	P	3.03	I	Hk2	hexokinase 2
NM_008775	46	P	116	P	3.03	I	Pafah1b2	platelet-activating factor acetylhydrolase, isoform 1b, alpha2 subunit
NM_027000	21	P	83	P	3.03	I	Gtpbp4	GTP binding protein 4
NM_013885	181	P	519	P	3.03	I	Clic4	chloride intracellular channel 4 (mitochondrial)
NM_0010391	113	P	317	P	3.03	I	Hnrpa1	heterogeneous nuclear ribonucleoprotein A1
NM_025939	54	P	146	P	3.03	I	Paics	phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoribosylan
NM_025378	236	P	863	P	3.03	I	Ifitm3	interferon induced transmembrane protein 3
NM_180678	482	P	1467	P	3.03	I	Gars	glycyl-tRNA synthetase
NM_011654	856	P	2661	P	3.03	I	Tuba2	tubulin, alpha 2
NM_145562	41	A	124	M	3.03	I	9130213B05	RIKEN cDNA 9130213B05 gene
NM_028876	63	P	209	P	3.03	I	Tmed5	transmembrane emp24 protein transport domain containing 5
NM_134015	48	P	144	P	3.03	I	Fbxw11	F-box and WD-40 domain protein 11
NM_009373	114	P	429	P	3.03	I	Tgm2	transglutaminase 2, C polypeptide
XM_0010010	81	P	291	P	3.03	I	Ighg	Immunoglobulin heavy chain (gamma polypeptide)
NM_011319	425	P	1305	P	3.03	I	Sars	seryl-aminoacyl-tRNA synthetase
NM_009371 //	61	P	222	P	3.03	I	Tgfbr2	transforming growth factor, beta receptor II
NM_011400	61	P	170	P	3.03	I	Slc2a1	solute carrier family 2 (facilitated glucose transporter), member 1
NM_010233	55	P	192	P	3.03	I	Fn1	fibronectin 1
NM_028696	73	P	180	P	3.03	I	5830411E10	RIKEN cDNA 5830411E10 gene
NM_023871	396	P	1084	P	3.03	I	Set	SET translocation
NM_013854	132	A	346	P	3.03	I	Abcf1	ATP-binding cassette, sub-family F (GCN20), member 1
NM_023579	40	P	138	P	3.03	I	Ranbp5	RAN binding protein 5
---	24	P	68	P	3.03	I	Atr	ataxia telangiectasia and Rad3 related
NM_009883	198	P	541	P	3.03	I	Cebpb	CCAAT/enhancer binding protein (C/EBP), beta
NM_021414	306	P	830	P	3.03	I	4631427C17	RIKEN cDNA 4631427C17 gene
XM_925560 //	44	A	107	P	3.03	MI	2810026P18	RIKEN cDNA 2810026P18 gene
XM_892627 //	109	P	264	P	3.03	I	Snrpf	small nuclear ribonucleoprotein polypeptide F
XM_125902 //	246	P	830	P	3.03	I	Xpot	exportin, tRNA (nuclear export receptor for tRNAs)
NM_029017	149	P	403	P	3.03	I	Mrpl47	mitochondrial ribosomal protein L47
NM_0010013	99	P	320	P	3.03	I	Vkorc1l1	vitamin K epoxide reductase complex, subunit 1-like 1

Transcript	WT		KO		Change KO/WT		Gene	
	Signal	Detectio	Signal	Detectio	Fold	Call	Symbol	Title
NM_015781	33	P	89	P	3.03	I	Nap1l1	nucleosome assembly protein 1-like 1
XM_127444 //	22	P	93	P	3.03	MI	Trip13	thyroid hormone receptor interactor 13
NM_029673	181	P	546	P	3.03	I	Immt	inner membrane protein, mitochondrial
NM_008615 //	327	P	1153	P	3.03	I	Mod1 /// LOC	malic enzyme, supernatant /// similar to NADP-dependent malic enzyme
NM_028696	53	P	174	P	3.03	I	5830411E10	RIKEN cDNA 5830411E10 gene
NM_173374	144	P	509	P	3.03	I	Sfrs1	splicing factor, arginine/serine-rich 1 (ASF/SF2)
NM_018745	48	P	182	P	3.03	I	Azin1	antizyme inhibitor 1
NM_025881 //	18	A	65	P	3.03	MI	Luc7l	Luc7 homolog (S. cerevisiae)-like
NM_175450	45	A	130	M	3.03	I	Wdr18	WD repeat domain 18
NR_002896	77	P	215	P	3.03	I	Snord22	small nucleolar RNA, C/D box 22
NM_00103774	32	P	102	P	3.03	I	AU021838	expressed sequence AU021838
NM_178907	56	P	305	P	3.03	I	Mapkapk3	mitogen-activated protein kinase-activated protein kinase 3
NM_172746	30	P	105	P	3.03	I	Hirip3	HIRA interacting protein 3
XM_618789 //	21	A	69	P	3.03	I	Brunol5	bruno-like 5, RNA binding protein (Drosophila)
NM_021384	255	P	792	P	3.03	I	Rsad2	radical S-adenosyl methionine domain containing 2
XM_922730 //	64	P	162	P	3.03	I	C330008K14	RIKEN cDNA C330008K14 gene
NM_00103953	129	P	406	P	3.03	I	2210010A19	RIKEN cDNA 2210010A19 gene
NM_00100173	20	A	58	P	3.03	I	5830428H23	RIKEN cDNA 5830428H23 gene
NM_008566	53	P	155	P	3.03	I	Mcm5	minichromosome maintenance deficient 5, cell division cycle 46 (S. cere
NM_028044	115	P	336	P	3.03	I	Cnn3	calponin 3, acidic
NM_026560	54	P	176	P	3.03	I	Cdca8	cell division cycle associated 8
NM_00102450	32	A	89	P	3.03	I	AW495713	expressed sequence AW495713
NM_011468	837	P	2578	P	3.03	I	Sprr2a	small proline-rich protein 2A
NM_00103801	118	P	345	P	3.03	I	Gprk6	G protein-coupled receptor kinase 6
NM_00103030	53	P	169	P	3.03	I	BC068171	cDNA sequence BC068171
XM_907983 //	261	P	816	P	3.03	I	Herc5	hect domain and RLD 5
NM_197982	39	P	75	P	3.03	I	Ddx39	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39
NM_013885	144	P	378	P	3.03	I	Clic4	chloride intracellular channel 4 (mitochondrial)
---	356	P	1128	P	3.03	I	---	Transcribed locus
NM_010480	647	P	2037	P	3.03	I	Hsp90aa1	heat shock protein 90kDa alpha (cytosolic), class A member 1
NM_053074	59	P	224	P	3.03	I	Nup62	nucleoporin 62
XM_980284 //	68	A	147	P	3.03	I	BC010304	cDNA sequence BC010304
XM_980284 //	37	P	91	P	3.03	I	BC010304	cDNA sequence BC010304
NM_175440	40	P	114	P	3.03	I	Prss27	protease, serine 27
XM_131566 //	44	A	99	P	3.03	I	Usp24	ubiquitin specific peptidase 24
NM_010368	123	P	349	P	3.03	I	Gusb	glucuronidase, beta
NM_010431	49	P	185	P	3.03	I	Hif1a	hypoxia inducible factor 1, alpha subunit
NM_016810	60	P	187	P	3.03	I	Gosr1	golgi SNAP receptor complex member 1
NM_023209	53	P	184	P	3.03	I	Pbk	PDZ binding kinase
NM_008012	59	P	186	P	3.03	I	Akr1b8	aldo-keto reductase family 1, member B8
NM_024250	256	P	788	P	3.03	I	Phf10	PHD finger protein 10
NM_023323	39	P	83	P	3.03	I	Bxdc1	brix domain containing 1
NM_008199	184	P	781	P	3.03	I	H2-Bl	histocompatibility 2, blastocyst
NM_016805	157	P	492	P	3.03	I	Hnrpu	heterogeneous nuclear ribonucleoprotein U
NM_024433	21	M	64	P	3.03	I	Mtap	methylthioadenosine phosphorylase
NM_007914	70	P	214	P	3.03	I	Ehf	ets homologous factor
NM_020331	212	P	778	P	3.03	I	Gtf2ird1	general transcription factor II I repeat domain-containing 1
NM_028871	21	P	77	P	3.03	I	Hnrpr	heterogeneous nuclear ribonucleoprotein R
NM_029735 //	68	P	228	P	3.03	I	Eprs /// LOC6	glutamyl-prolyl-tRNA synthetase /// similar to Bifunctional aminoacyl-tRN
XM_907983 //	96	P	275	P	3.03	I	Herc5	hect domain and RLD 5
NM_173363	455	P	1242	P	3.03	I	Eif5	eukaryotic translation initiation factor 5
NM_153089	59	A	104	P	3.03	MI	Ppp1r16b	protein phosphatase 1, regulatory (inhibitor) subunit 16B
NM_00100389	161	P	400	P	3.03	I	Tardbp	TAR DNA binding protein
NM_00103937	25	P	102	P	3.03	MI	Pde4dip	phosphodiesterase 4D interacting protein (myomegalin)
NM_008702	16	P	58	P	3.03	I	Nlk	nemo like kinase
NM_009099 //	35	P	122	P	3.03	I	Trim30 /// AI4	tripartite motif protein 30 /// expressed sequence AI451617
NM_011394	22	P	114	P	3.03	I	Slc20a2	Solute carrier family 20, member 2
---	60	P	143	P	3.03	MI	---	Transcribed locus
NM_007749	31	P	84	P	3.03	MI	Cox7c	cytochrome c oxidase, subunit VIIc
NM_012000	120	P	431	P	3.03	I	Cln8	ceroid-lipofuscinosis, neuronal 8
NM_019766	562	P	1648	P	3.03	I	Ptges3	prostaglandin E synthase 3 (cytosolic)
NM_013470	52	P	154	P	3.03	I	Anxa3	annexin A3
NM_009103	54	P	144	P	3.25	I	Rrm1	ribonucleotide reductase M1
NM_015751	114	P	332	P	3.25	I	Abce1	ATP-binding cassette, sub-family E (OABP), member 1
NM_007657	162	P	463	P	3.25	I	Cd9	CD9 antigen
NM_009687	59	P	177	P	3.25	I	Apex1	apurinic/apyrimidinic endonuclease 1
NM_00103858	70	P	331	P	3.25	I	Usp14	ubiquitin specific peptidase 14
NM_025936	638	P	2110	P	3.25	I	Rars	arginyl-tRNA synthetase
NM_026631	148	P	458	P	3.25	I	Nola2	nucleolar protein family A, member 2
NM_019926	297	P	1052	P	3.25	I	Mtm1	X-linked myotubular myopathy gene 1
NM_026504	54	P	146	P	3.25	I	Coq5	coenzyme Q5 homolog, methyltransferase (yeast)
NM_010325	85	P	271	P	3.25	I	Got2	glutamate oxaloacetate transaminase 2, mitochondrial
NM_025695	28	P	91	P	3.25	I	Smc6l1	SMC6 structural maintenance of chromosomes 6-like 1 (yeast)
NM_011909	449	P	1331	P	3.25	I	Usp18	ubiquitin specific peptidase 18
NM_134090	340	P	1148	P	3.25	I	Kdelr3	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention recept
NM_011819	57	M	228	P	3.25	I	Gdf15	growth differentiation factor 15
NM_009635	63	P	200	P	3.25	I	Avil	advillin
NM_011495 //	25	P	95	P	3.25	I	Plk4	polo-like kinase 4 (Drosophila)
NM_023210	77	P	203	P	3.25	I	Anp32e	acidic (leucine-rich) nuclear phosphoprotein 32 family, member E
NM_021384	77	P	210	P	3.25	I	Rsad2	radical S-adenosyl methionine domain containing 2
NM_023871 //	167	P	540	P	3.25	I	Set /// LOC67	SET translocation /// similar to SET protein (Phosphatase 2A inhibitor I2
NM_011239	271	P	934	P	3.25	I	Ranbp1	RAN binding protein 1
NM_013602	3821	P	14483	P	3.25	I	Mt1	metallothionein 1
NM_144904 //	72	P	269	P	3.25	I	Rod1	ROD1 regulator of differentiation 1 (S. pombe)
NM_146050	799	P	3913	P	3.25	I	Oit1	oncoprotein induced transcript 1
NM_029810	53	P	143	P	3.25	I	Nt5c2	5'-nucleotidase, cytosolic II
NM_010480	405	P	1507	P	3.25	I	Hsp90aa1	heat shock protein 90kDa alpha (cytosolic), class A member 1
NM_172015	110	P	397	P	3.25	I	Iars	isoleucine-tRNA synthetase
XM_00100069	107	P	361	P	3.25	I	Mki67 /// LOC	antigen identified by monoclonal antibody Ki 67 /// similar to Antigen KI-67
NM_00104069	115	P	401	P	3.25	I	Mtmr7	myotubularin related protein 7
NM_199195	23	P	56	P	3.25	I	Bckdhb	branched chain ketoacid dehydrogenase E1, beta polypeptide
NM_00102471	55	P	104	P	3.25	I	LOC544988 /	hypothetical protein LOC544988 /// RIKEN cDNA B930046C15 gene /// hy
NM_153783	85	P	266	P	3.25	I	Paox	polyamine oxidase (exo-N4-amino)
NM_027096 //	39	P	125	P	3.25	I	Prei4	preimplantation protein 4
NM_027297	28	P	94	P	3.25	I	Prpf4	PRP4 pre-mRNA processing factor 4 homolog (yeast)
NM_025942 //	148	P	403	P	3.25	I	2810409H07	RIKEN cDNA 2810409H07 gene
NM_013872	54	A	174	P	3.25	I	Pmm1	phosphomannomutase 1
NM_144958	890	P	2756	P	3.25	I	Eif4a1	eukaryotic translation initiation factor 4A1
XM_907983 //	73	P	247	P	3.25	I	Herc5	hect domain and RLD 5
NM_010768	21	A	52	P	3.25	I	Matk	megakaryocyte-associated tyrosine kinase
NM_145545	56	P	184	P	3.25	I	9830147J24	RIKEN cDNA 9830147J24 gene
NM_011400	93	P	281	P	3.25	I	Slc2a1	solute carrier family 2 (facilitated glucose transporter), member 1
XM_135805 //	67	P	198	P	3.25	I	Wdr44	WD repeat domain 44
NM_026742	74	P	218	P	3.25	I	1110007M04	RIKEN cDNA 1110007M04 gene
NM_030013	13	A	63	P	3.25	I	Cyp20a1	cytochrome P450, family 20, subfamily A, polypeptide 1
NM_175294	34	P	175	P	3.25	I	Nucks1	nuclear casein kinase and cyclin-dependent kinase substrate 1
---	40	A	116	P	3.25	I	4933404O12	RIKEN cDNA 4933404O12 gene
NM_153402	13	A	53	P	3.25	I	Eif2c3	eukaryotic translation initiation factor 2C, 3
---	84	P	272	P	3.25	I	9230110J10	hypothetical protein 9230110J10
NM_013761	125	P	369	P	3.25	I	Srr	serine racemase
NM_007477	22	P	60	P	3.25	I	Arf2	ADP-ribosylation factor 2
NM_008251	331	P	791	P	3.25	I	Hmgn1	high mobility group nucleosomal binding domain 1
NR_002896	137	P	465	P	3.25	I	Snord22	small nucleolar RNA, C/D box 22
NM_00103030	20	P	73	P	3.25	I	BC068171	cDNA sequence BC068171
NM_00103325	60	P	178	P	3.25	I	D130073L02	RIKEN cDNA D130073L02 gene
---	79	P	232	P	3.25	I	---	Transcribed locus
NM_010481	50	P	156	P	3.25	I	Hspa9a	heat shock protein 9A
NM_00104069	101	P	330	P	3.25	I	Mtmr7	myotubularin related protein 7
NM_026506 //	163	P	521	P	3.25	I	Snrpg /// LOC	small nuclear ribonucleoprotein polypeptide G /// similar to small nuclear rib
NM_011690	50	A	199	P	3.25	I	Vars2	valyl-tRNA synthetase 2
NM_021329	34	M	110	P	3.25	I	2400006H24	RIKEN cDNA 2400006H24 gene
NM_009004	16	A	59	P	3.25	MI	Kif20a	kinesin family member 20A
NM_00102485	50	P	87	P	3.25	I	Timm9	translocase of inner mitochondrial membrane 9 homolog (yeast)
NM_025835	288	P	1260	P	3.25	I	Pccb	propionyl Coenzyme A carboxylase, beta polypeptide
NM_028762	17	A	64	P	3.25	I	Rbm19	RNA binding motif protein 19
NM_011319	398	P	1207	P	3.25	I	Sars	seryl-aminoacyl-tRNA synthetase
NM_025782	63	P	148	P	3.25	I	9130422G05	RIKEN cDNA 9130422G05 gene
NM_00100522	27	P	87	P	3.25	I	Znhit3	zinc finger, HIT type 3
NM_028230	80	P	282	P	3.25	I	Shmt2	serine hydroxymethyl transferase 2 (mitochondrial)
NM_146066	48	P	116	P	3.25	I	Gspt1	G1 to S phase transition 1
XM_148595 //	102	P	305	P	3.25	I	4921513D23	RIKEN cDNA 4921513D23 gene
XM_129769 //	643	P	2920	P	3.25	I	Cps1	carbamoyl-phosphate synthetase 1
NM_028044	42	P	148	P	3.25	I	Cnn3	calponin 3, acidic
NM_007573	795	P	2473	P	3.25	I	C1qbp	complement component 1, q subcomponent binding protein
NM_028044	13	A	60	P	3.25	I	Cnn3	calponin 3, acidic
NM_026030	753	P	2415	P	3.25	I	Eif2s2	eukaryotic translation initiation factor 2, subunit 2 (beta)
NM_00103937	29	A	81	M	3.25	I	Pde4dip	phosphodiesterase 4D interacting protein (myomegalin)
NM_134151	101	A	300	P	3.25	I	Yars	tyrosyl-tRNA synthetase
NM_053074	59	A	252	P	3.48	I	Nup62	nucleoporin 62
NM_009846	359	P	1196	P	3.48	I	Cd24a	CD24a antigen
NM_022310	2292	P	8868	P	3.48	I	Hspa5	heat shock 70kD protein 5 (glucose-regulated protein)
NM_007991	135	P	416	P	3.48	I	Fbl	fibrillarin
NM_016669	43	P	165	P	3.48	I	Crym	crystallin, mu
NM_009230	63	P	153	P	3.48	I	Soat1	sterol O-acyltransferase 1
NM_007607	1146	P	4056	P	3.48	I	Car4	carbonic anhydrase 4
NM_023595	31	P	102	P	3.48	I	Dut	deoxyuridine triphosphatase
XM_904332	973	P	3328	P	3.48	I	LOC630729	similar to Glutathione reductase, mitochondrial precursor (GR) (GRase)
NM_010344	745	P	2684	P	3.48	I	Gsr	glutathione reductase 1
NM_053159	45	P	177	P	3.48	I	Mrpl3	mitochondrial ribosomal protein L3
NM_019666 //	32	P	99	P	3.48	I	Syncrip	synaptotagmin binding, cytoplasmic RNA interacting protein
NM_028057	32	P	175	P	3.48	I	Cyb5r1	cytochrome b5 reductase 1
NM_015762	38	A	153	P	3.48	I	Txnrd1	thioredoxin reductase 1
NM_026073	171	P	573	P	3.48	I	Rabl5	RAB, member of RAS oncogene family-like 5
NM_145469	136	P	345	P	3.48	I	Npal2	NIPA-like domain containing 2
NM_145581	33	P	97	P	3.48	I	Siglecf	sialic acid binding Ig-like lectin F
NM_009171	39	P	135	P	3.48	I	Shmt1	serine hydroxymethyl transferase 1 (soluble)
NM_007791	13	P	71	P	3.48	I	Csrp1	cysteine and glycine-rich protein 1
NM_016871	145	P	481	P	3.48	I	Tomm40	translocase of outer mitochondrial membrane 40 homolog (yeast)
NM_010477	608	P	2190	P	3.48	I	Hspd1	heat shock protein 1 (chaperonin)
NM_028315	25	P	80	P	3.48	I	2810028N01	RIKEN cDNA 2810028N01 gene
NM_026195	54	P	212	P	3.48	I	Atic	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyc
XM_00100399	90	P	238	P	3.48	I	Mlkl	mixed lineage kinase domain-like
XM_132538 //	14	A	50	P	3.48	I	5830411G16	RIKEN cDNA 5830411G16 gene
NM_019703	391	P	1540	P	3.48	I	Pfkp	phosphofructokinase, platelet
NM_00103908	165	P	535	P	3.48	I	Sel1h	Sel1 (suppressor of lin-12) 1 homolog (C. elegans)
NM_028035	51	P	179	P	3.48	I	Snx10	sorting nexin 10
XM_907983 //	66	P	225	P	3.48	I	Herc5	hect domain and RLD 5
NM_057172	49	P	127	P	3.48	I	Fubp1	far upstream element (FUSE) binding protein 1
NM_016957	390	P	1523	P	3.48	I	Hmgn2	high mobility group nucleosomal binding domain 2
NM_009104	57	P	185	P	3.48	I	Rrm2	ribonucleotide reductase M2
NM_177715	116	P	383	P	3.48	I	Kctd12	potassium channel tetramerisation domain containing 12
NM_008252 //	117	P	553	P	3.48	I	Hmgb2 /// LO	high mobility group box 2 /// high mobility group box 2 /// high mobility grou

Transcript	WT		KO		Change KO/WT		Gene	
	Signal	Detectio	Signal	Detectio	Fold	Call	Symbol	Title
NM_009846	188	P	669	P	3.48	I	Cd24a	CD24a antigen
XM_978296 //	802	P	2733	P	3.48	I	MGC73635	similar to histone 2a
NM_023136	47	P	141	P	3.48	I	Dtymk	deoxythymidylate kinase
NM_00103964	18	M	88	P	3.48	I	Mpa2l /// LOC	macrophage activation 2 like /// similar to macrophage activation 2 like ///
NM_175356	36	P	117	P	3.48	I	Pik4cb	phosphatidylinositol 4-kinase, catalytic, beta polypeptide
NM_027238	21	P	87	P	3.48	I	1810054D07	RIKEN cDNA 1810054D07 gene
NM_010074	41	P	125	P	3.48	I	Dpp4	Dipeptidylpeptidase 4
XM_921367 //	42	P	131	P	3.48	I	Nbeal1	neurobeachin like 1
NM_178668	19	P	75	P	3.48	I	E430028B21	RIKEN cDNA E430028B21 gene
NM_009103	49	P	130	P	3.48	I	Rrm1	ribonucleotide reductase M1
NM_007573	231	P	756	P	3.48	I	C1qbp	complement component 1, q subcomponent binding protein
NM_023136	34	P	83	P	3.48	I	Dtymk	deoxythymidylate kinase
NM_027159	27	A	96	P	3.48	I	2310061I09R	RIKEN cDNA 2310061I09 gene
NM_013742	130	P	429	P	3.48	I	Cars	cysteinyl-tRNA synthetase
NM_008252 //	119	P	520	P	3.48	I	Hmgb2 /// LO	high mobility group box 2 /// similar to High mobility group protein 2 (HM
NM_025881 //	25	M	72	P	3.48	I	Luc7l	Luc7 homolog (S. cerevisiae)-like
NM_011623	112	P	347	P	3.48	I	Top2a	topoisomerase (DNA) II alpha
NM_021511	21	P	63	P	3.48	I	Rrs1	RRS1 ribosome biogenesis regulator homolog (S. cerevisiae)
NM_010931	22	A	69	P	3.73	I	Uhrf1	ubiquitin-like, containing PHD and RING finger domains, 1
NM_009128	36	P	175	P	3.73	MI	Scd2	stearoyl-Coenzyme A desaturase 2
NM_008566	33	P	125	P	3.73	I	Mcm5	minichromosome maintenance deficient 5, cell division cycle 46 (S. cere
NM_026631	82	P	326	P	3.73	I	Nola2	nucleolar protein family A, member 2
NM_019741	793	P	2956	P	3.73	I	Slc2a5	solute carrier family 2 (facilitated glucose transporter), member 5
NM_007598	568	P	2059	P	3.73	I	Cap1	CAP, adenylate cyclase-associated protein 1 (yeast)
NM_009230	16	M	74	P	3.73	I	Soat1	sterol O-acyltransferase 1
NM_010178	74	P	287	P	3.73	I	Fusip1	FUS interacting protein (serine-arginine rich) 1
NM_025520	67	P	259	P	3.73	I	Lsm5	LSM5 homolog, U6 small nuclear RNA associated (S. cerevisiae)
NM_130452	132	P	496	P	3.73	I	Bbox1	butyrobetaine (gamma), 2-oxoglutarate dioxygenase 1 (gamma-butyrobe
NM_013761	58	P	236	P	3.73	I	Srr	serine racemase
NM_021384	67	P	257	P	3.73	I	Rsad2	radical S-adenosyl methionine domain containing 2
NM_011864	98	P	308	P	3.73	I	Papss2	3'-phosphoadenosine 5'-phosphosulfate synthase 2
NM_011864	325	P	1292	P	3.73	I	Papss2	3'-phosphoadenosine 5'-phosphosulfate synthase 2
NM_009992	67	P	267	P	3.73	I	Cyp1a1	cytochrome P450, family 1, subfamily a, polypeptide 1
NM_008303 //	170	P	495	P	3.73	I	Hspe1 /// LO	heat shock protein 1 (chaperonin 10) /// similar to 10 kDa heat shock pro
NM_008723 //	27	P	113	P	3.73	I	Npm3 /// Np	nucleoplasmin 3 /// nucleoplasmin 3, pseudogene 1 /// similar to Nucleo
NM_030684 //	40	P	130	P	3.73	I	Trim34 /// LO	tripartite motif protein 34 /// similar to Tripartite motif protein 34
NM_145953	318	P	1309	P	3.73	I	Cth	cystathionase (cystathionine gamma-lyase)
XM_00100321	27	A	102	P	3.73	I	Pprc1	peroxisome proliferative activated receptor, gamma, coactivator-related 1
NM_028230	34	A	170	P	3.73	I	Shmt2	serine hydroxymethyl transferase 2 (mitochondrial)
NM_024193	36	M	122	P	3.73	I	Nol5a	nucleolar protein 5A
NM_016966 //	10	A	76	P	3.73	I	Phgdh /// LO	3-phosphoglycerate dehydrogenase /// similar to 3-phosphoglycerate de
NM_133692	22	A	78	P	3.73	I	Pold3	polymerase (DNA-directed), delta 3, accessory subunit
NM_028109	16	A	64	P	3.73	MI	Tpx2	TPX2, microtubule-associated protein homolog (Xenopus laevis)
NM_027350	968	P	3435	P	3.73	I	Nars	asparaginyl-tRNA synthetase
NM_008630	992	P	3103	P	3.73	I	Mt2	metallothionein 2
NM_029600	204	P	780	P	3.73	I	Abcc3	ATP-binding cassette, sub-family C (CFTR/MRP), member 3
NM_207212	56	P	214	P	3.73	I	Wtip	WT1-interacting protein
NM_026476	34	P	125	P	3.73	I	2610101N10	RIKEN cDNA 2610101N10 gene
NM_018876	214	P	902	P	3.73	I	Fut2	fucosyltransferase 2
NM_199146	206	P	797	P	3.73	I	AI451617	expressed sequence AI451617
NM_011710	161	P	689	P	3.73	I	Wars	tryptophanyl-tRNA synthetase
NM_007963	81	P	262	P	3.73	I	Evi1	ecotropic viral integration site 1
XM_894696 //	95	P	441	P	3.73	MI	Dnahc2 /// Dn	dynein, axonemal, heavy chain 2 /// dynein heavy chain domain 3
NM_134188	32	A	188	P	3.73	I	Acot2	acyl-CoA thioesterase 2
NM_012000	67	P	277	P	3.73	I	Cln8	ceroid-lipofuscinosis, neuronal 8
NM_019656	53	P	127	P	3.73	I	Tspan6	tetraspanin 6
NM_013528	87	P	284	P	3.73	I	Gfpt1	glutamine fructose-6-phosphate transaminase 1
NM_015774	314	P	1193	P	3.73	I	Ero1l	ERO1-like (S. cerevisiae)
NM_172616	12	A	51	P	3.73	I	C330027C09	RIKEN cDNA C330027C09 gene
NM_025910	40	P	161	P	3.73	I	Mina	myc induced nuclear antigen
NM_027220	196	P	691	P	3.73	I	Prss32	protease, serine, 32
NM_198414	20	A	84	P	3.73	I	Paqr9	progestin and adipoQ receptor family member IX
NM_008251	200	P	644	P	3.73	I	Hmgn1	high mobility group nucleosomal binding domain 1
---	24	P	137	P	3.73	I	---	---
NM_010880	83	P	337	P	4.00	I	Ncl	nucleolin
NM_053074	57	P	274	P	4.00	I	Nup62	nucleoporin 62
NM_010798	271	P	1122	P	4.00	I	Mif	macrophage migration inhibitory factor
NM_008563 //	28	P	115	P	4.00	I	Mcm3 /// LO	minichromosome maintenance deficient 3 (S. cerevisiae) /// similar to D
NM_010259	47	P	192	P	4.00	I	Gbp1	guanylate nucleotide binding protein 1
NM_008251	162	P	746	P	4.00	I	Hmgn1	high mobility group nucleosomal binding domain 1
NM_023493	267	P	808	P	4.00	I	Cml5	camello-like 5
NM_172952	33	P	122	P	4.00	I	Gphn	gephyrin
---	14	M	68	P	4.00	I	6430710C18	RIKEN cDNA 6430710C18 gene
NM_007646	320	P	1226	P	4.00	I	Cd38	CD38 antigen
NM_029432	37	P	166	P	4.00	I	4930402H24	RIKEN cDNA 4930402H24 gene
NM_007918	265	P	1226	P	4.00	I	Eif4ebp1	eukaryotic translation initiation factor 4E binding protein 1
NM_009104	23	P	111	P	4.00	I	Rrm2	ribonucleotide reductase M2
NM_019395	836	P	3551	P	4.00	I	Fbp1	fructose bisphosphatase 1
NM_007607	1168	P	4775	P	4.00	I	Car4	carbonic anhydrase 4
NM_025872	15	A	54	P	4.00	I	Golt1b	golgi transport 1 homolog B (S. cerevisiae)
NM_007399	57	P	220	P	4.00	I	Adam10	a disintegrin and metallopeptidase domain 10
NM_007646	80	P	278	P	4.00	I	Cd38	CD38 antigen
NM_007599	29	P	132	P	4.00	I	Capg	capping protein (actin filament), gelsolin-like
NM_146217	417	P	1618	P	4.00	I	Aars	alanyl-tRNA synthetase
NM_145588	17	A	73	P	4.00	I	Kif22	kinesin family member 22
NM_011605	94	P	415	P	4.00	I	Tmpo	thymopoietin

Transcript	WT		KO		Change KO/WT		Gene	
	Signal	Detectio	Signal	Detectio	Fold	Call	Symbol	Title
NM_172015	39	P	162	P	4.00	I	Iars	isoleucine-tRNA synthetase
NM_007513	136	P	578	P	4.00	I	Slc7a1	solute carrier family 7 (cationic amino acid transporter, y+ system), membe
NM_007513	119	P	427	P	4.00	I	Slc7a1	solute carrier family 7 (cationic amino acid transporter, y+ system), membe
NM_008538	88	P	510	P	4.00	I	Marcks	Myristoylated alanine rich protein kinase C substrate
NM_172381	20	P	111	P	4.00	I	AI314180	expressed sequence AI314180
NM_0010332	15	P	138	P	4.00	I	Slc4a7	solute carrier family 4, sodium bicarbonate cotransporter, member 7
NM_178883	18	P	83	P	4.00	I	Scyl1bp1	SCY1-like 1 binding protein 1
---	32	P	116	P	4.00	I	---	0 day neonate cerebellum cDNA, RIKEN full-length enriched library, clone
NM_011710	118	P	598	P	4.29	I	Wars	tryptophanyl-tRNA synthetase
NM_008538	117	P	570	P	4.29	I	Marcks	myristoylated alanine rich protein kinase C substrate
NM_025281	37	P	177	P	4.29	I	Lyar	Ly1 antibody reactive clone
NM_007918	284	P	992	P	4.29	I	Eif4ebp1	eukaryotic translation initiation factor 4E binding protein 1
NM_010481	233	P	1159	P	4.29	I	Hspa9a	heat shock protein 9A
NM_010481	503	P	2271	P	4.29	I	Hspa9a	heat shock protein 9A
NM_015774	349	P	1509	P	4.29	I	Ero1l	ERO1-like (S. cerevisiae)
NM_015774	152	P	624	P	4.29	I	Ero1l	ERO1-like (S. cerevisiae)
NM_026515	118	P	430	P	4.29	I	2810417H13	RIKEN cDNA 2810417H13 gene
NM_024184	22	A	77	P	4.29	MI	Asf1b	ASF1 anti-silencing function 1 homolog B (S. cerevisiae)
NM_022310	1227	P	5977	P	4.29	I	Hspa5	heat shock 70kD protein 5 (glucose-regulated protein)
NM_026149	27	P	113	P	4.29	I	Nudcd1	NudC domain containing 1
NM_0010331	52	P	299	P	4.29	I	4930403C10	RIKEN cDNA 4930403C10 gene
NM_145222	107	P	481	P	4.29	I	B3gnt7	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 7
NM_198020	13	A	66	P	4.29	I	Trmt1	TRM1 tRNA methyltransferase 1 homolog (S. cerevisiae)
NM_023835	43	P	254	P	4.29	I	Trim12	tripartite motif protein 12
NM_145495	20	P	94	P	4.29	I	Rin1	Ras and Rab interactor 1
NM_023042	18	A	75	P	4.29	I	Recql	RecQ protein-like
NM_008571	27	A	143	P	4.29	I	Mcpt2	mast cell protease 2
NM_013538	53	P	186	P	4.29	I	Cdca3	cell division cycle associated 3
NM_023731	14	A	57	P	4.29	I	Ccdc86	coiled-coil domain containing 86
NM_173374	121	P	516	P	4.29	I	Sfrs1	splicing factor, arginine/serine-rich 1 (ASF/SF2)
NM_029432	26	A	117	P	4.29	I	4930402H24	RIKEN cDNA 4930402H24 gene
NM_009042	443	P	2057	P	4.59	I	Reg1	regenerating islet-derived 1
NM_008538	267	P	1171	P	4.59	I	Marcks	myristoylated alanine rich protein kinase C substrate
---	88	P	464	P	4.59	I	---	0 day neonate cerebellum cDNA, RIKEN full-length enriched library, clone
NM_023627	31	P	184	P	4.59	I	Isyna1	myo-inositol 1-phosphate synthase A1
NM_008638	43	P	273	P	4.59	I	Mthfd2	methylenetetrahydrofolate dehydrogenase (NAD+ dependent), methenyltet
NM_019578	24	P	156	P	4.59	I	Extl1	exostoses (multiple)-like 1
NM_013559	52	P	302	P	4.59	I	Hsp110	heat shock protein 110
NM_146217	434	P	1971	P	4.59	I	Aars	alanyl-tRNA synthetase
NM_013559	104	P	409	P	4.59	I	Hsp110	heat shock protein 110
NM_0010393	20	P	103	P	4.59	I	Nolc1	nucleolar and coiled-body phosphoprotein 1
---	41	P	176	P	4.59	I	2610024B07	RIKEN cDNA 2610024B07 gene
NM_0010377	13	P	51	P	4.59	I	D330017J20	RIKEN cDNA D330017J20 gene
NM_011710	216	P	1002	P	4.59	I	Wars	tryptophanyl-tRNA synthetase
NM_0010302	274	P	1505	P	4.59	I	Olfm4	olfactomedin 4
NM_178726	15	A	62	P	4.59	I	Ppm1l	protein phosphatase 1 (formerly 2C)-like
NM_145457 //	13	A	57	P	4.59	I	Paip1 /// LOC	polyadenylate binding protein-interacting protein 1 /// similar to poly(A) bind
NM_153171	19	P	177	P	4.59	I	Rgs13	regulator of G-protein signaling 13
NM_028760	18	P	76	P	4.59	I	Cep55	centrosomal protein 55
NM_0010385	11	A	51	P	4.59	MI	Usp14	ubiquitin specific peptidase 14
NM_017397	15	P	82	P	4.92	I	Ddx20	DEAD (Asp-Glu-Ala-Asp) box polypeptide 20
NM_016675	99	P	455	P	4.92	I	Cldn2	claudin 2
NM_007598	256	P	1211	P	4.92	I	Cap1	CAP, adenylate cyclase-associated protein 1 (yeast)
NM_020574	70	P	270	P	4.92	I	Kcne3	potassium voltage-gated channel, Isk-related subfamily, gene 3
NM_053159	82	P	342	P	4.92	I	Mrpl3	mitochondrial ribosomal protein L3
NM_028994	58	P	266	P	4.92	I	Pck2	phosphoenolpyruvate carboxykinase 2 (mitochondrial)
NM_008491	14	A	66	P	4.92	I	Lcn2	lipocalin 2
---	40	A	96	P	4.92	I	---	---
NM_173762	14	A	59	P	4.92	MI	Cenpe	centromere protein E
XM_900254 //	16	A	70	P	4.92	I	Cdc42bpa	Cdc42 binding protein kinase alpha
NM_0010395	30	P	166	P	4.92	I	Ankrd37	ankyrin repeat domain 37
NM_016966 //	25	P	152	P	4.92	I	Phgdh /// LO	3-phosphoglycerate dehydrogenase /// similar to 3-phosphoglycerate dehy
NM_080457 //	29	A	89	P	4.92	I	4933405I11R	RIKEN cDNA 4933405I11 gene /// mucin 4
NM_012000	37	P	256	P	4.92	I	Cln8	ceroid-lipofuscinosis, neuronal 8
NM_030887	61	P	198	P	4.92	I	Jundm2	Jun dimerization protein 2
NM_139148	52	P	286	P	4.92	I	Clca4	chloride channel calcium activated 4
NM_011638	486	P	2416	P	4.92	I	Tfrc	transferrin receptor
NM_0010137	48	M	189	P	4.92	I	Akr1c19	aldo-keto reductase family 1, member C19
NM_033075	55	P	245	P	5.28	I	D17H6S56E-	DNA segment, Chr 17, human D6S56E 5
XM_890672 //	25	A	184	P	5.28	I	LOC624219	similar to hepatocellular carcinoma-associated gene TD26
NM_033149	149	P	816	P	5.28	I	B3galt5	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 5
NM_173757	17	P	75	P	5.28	I	Mrps27	mitochondrial ribosomal protein S27
XM_892623 //	58	P	232	P	5.28	I	D230012E17	RIKEN cDNA D230012E17 gene
NM_029432	64	P	278	P	5.28	I	4930402H24	RIKEN cDNA 4930402H24 gene
---	81	P	495	P	5.28	I	---	0 day neonate cerebellum cDNA, RIKEN full-length enriched library, clone
NM_009128	92	P	513	P	5.66	I	Scd2	stearoyl-Coenzyme A desaturase 2
NM_011710	50	P	279	P	5.66	I	Wars	tryptophanyl-tRNA synthetase
NM_033149	60	P	331	P	5.66	I	B3galt5	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 5
NM_025995	16	A	86	P	5.66	I	Fbxo5	F-box only protein 5
NM_011631	539	P	2755	P	5.66	I	Hsp90b1	heat shock protein 90kDa beta (Grp94), member 1
NM_009801	157	P	910	P	5.66	I	Car2	carbonic anhydrase 2
NM_027342	323	P	2399	P	5.66	I	2310056P07	RIKEN cDNA 2310056P07 gene
NM_0010395	67	P	427	P	5.66	I	2210010A19	RIKEN cDNA 2210010A19 gene
NM_031378	36	P	228	P	6.06	I	Mlze	melanoma-derived leucine zipper, extra-nuclear factor
NM_145447	31	A	117	P	6.06	I	BC011209	cDNA sequence BC011209
NM_027460	37	P	238	P	6.06	I	5730438N18	RIKEN cDNA 5730438N18 gene

Transcript	WT		KO		Change KO/WT		Gene	
	Signal	Detectio	Signal	Detectio	Fold	Call	Symbol	Title
NM_144554 //	127	P	812	P	6.06	I	Trib3	tribbles homolog 3 (Drosophila)
NM_007488	27	P	128	P	6.06	I	Arnt2	aryl hydrocarbon receptor nuclear translocator 2
NM_028274	12	A	100	P	6.06	I	Exosc6	exosome component 6
NM_028355	11	A	69	P	6.06	I	Tmem48	transmembrane protein 48
NM_011234	13	A	103	P	6.50	I	Rad51	RAD51 homolog (S. cerevisiae)
NM_023137	434	P	2825	P	6.50	I	Ubd	ubiquitin D
NM_008570	16	A	116	P	6.50	I	Mcpt1	mast cell protease 1
NM_010416	84	P	429	P	6.50	I	Hemt1	hematopoietic cell transcript 1
NM_198246	12	P	85	P	6.50	I	Yars2	tyrosyl-tRNA synthetase 2 (mitochondrial)
NM_177420	26	A	108	P	6.50	I	Psat1	phosphoserine aminotransferase 1
NM_0010256	15	A	132	P	6.50	I	Gm905	gene model 905, (NCBI)
NM_008638	59	P	352	P	6.96	I	Mthfd2	methylenetetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase
NM_177420	14	P	90	P	6.96	I	Psat1	phosphoserine aminotransferase 1
NM_144554 //	92	P	525	P	6.96	I	Trib3	tribbles homolog 3 (Drosophila)
NM_026041	4	A	58	P	7.46	I	2810430M08	RIKEN cDNA 2810430M08 gene
NM_198119	12	A	103	P	7.46	I	Lrrc24	leucine rich repeat containing 24
NM_197987	6	A	56	P	7.46	MI	Trim37	tripartite motif protein 37
NM_00103344	60	P	484	P	7.46	I	Capn13	calpain 13
NM_018876	12	A	93	P	7.46	I	Fut2	fucosyltransferase 2
NM_019748	6	A	56	P	8.00	I	Uble1a	ubiquitin-like 1 (sentrin) activating enzyme E1A
NM_177912 //	593	P	4409	P	8.00	I	9030605I04R	RIKEN cDNA 9030605I04 gene /// expressed sequence AI987692
NM_012055	216	P	1467	P	8.00	I	Asns	asparagine synthetase
NM_009704	280	P	2568	P	8.57	I	Areg	amphiregulin
NM_012055	118	P	1231	P	8.57	I	Asns	asparagine synthetase
NM_013602	19	A	226	P	8.57	I	Mt1	metallothionein 1
NM_197987	7	A	63	P	9.19	I	Trim37	tripartite motif protein 37
NM_011638	54	P	430	P	9.85	I	Tfrc	transferrin receptor
NM_00100476	381	P	3416	P	9.85	I	Pla2g4c	phospholipase A2, group IVC (cytosolic, calcium-independent)
NM_00103229	74	P	664	P	9.85	I	Bglap-rs1 /// B	bone gamma-carboxyglutamate protein, related sequence 1 /// bone gamma carboxyglutamate protein 1 /// bone gamma-carboxyglutamate protein 2
NM_177912	157	P	1585	P	9.85	I	AI987692	expressed sequence AI987692
NM_030728	9	P	78	P	10.56	I	9930013L23R	RIKEN cDNA 9930013L23 gene
NM_033149	8	A	133	P	10.56	I	B3galt5	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 5
NM_025663	3	A	50	P	11.31	I	Gpatc4	G patch domain containing 4
NM_145457	7	A	86	P	11.31	I	Paip1	polyadenylate binding protein-interacting protein 1
NM_026929	55	P	530	P	11.31	I	Chac1	ChaC, cation transport regulator-like 1 (E. coli)
NM_022018	26	P	356	P	11.31	I	Niban	niban protein
NM_00100476	150	P	2120	P	12.13	I	Pla2g4c	phospholipase A2, group IVC (cytosolic, calcium-independent)
NM_134033	6	A	86	P	12.13	I	BC018601	cDNA sequence BC018601
NM_011638	4	A	69	P	16.00	I	Tfrc	transferrin receptor
NM_016866	5	A	75	P	18.38	I	Stk39	serine/threonine kinase 39, STE20/SPS1 homolog (yeast)
NM_009171	4	A	77	P	18.38	I	Shmt1	serine hydroxymethyl transferase 1 (soluble)
NM_145495	32	P	493	P	21.11	I	Rin1	Ras and Rab interactor 1
NM_021312	4	A	73	P	21.11	I	Wdr12	WD repeat domain 12
NM_00101337	4	A	58	P	22.63	I	E130306D19	RIKEN cDNA E130306D19 gene
NM_023220	2	A	64	P	22.63	I	2010106G01	RIKEN cDNA 2010106G01 gene
NM_029796	1	A	75	P	24.25	I	Lrg1	leucine-rich alpha-2-glycoprotein 1
NM_022018	11	A	343	P	24.25	I	Niban	niban protein
NM_054051	2	A	123	P	39.40	I	Pip5k2b	Phosphatidylinositol-4-phosphate 5-kinase, type II, beta
NM_023881	3	A	182	P	45.25	I	Retnlb	resistin like beta
XM_888097 //	2	A	95	P	51.98	I	U90926	cDNA sequence U90926
NM_0010252	1	A	999	P	194.01	I	H2-Bl /// 2410	histocompatibility 2, blastocyst /// RIKEN cDNA 2410017I17 gene /// similar to MHC class I antigen precursor /// similar to RT1 class Ia, locus A2 /// similar to histocompatibility 2, blastocyst /// similar to RT1 class Ia, locus A1 /// s

Table S2: Genotype counts of the twenty single nucleotide polymorphisms that were genotyped in the three independent case-control IBD sample panels. Marker Positions refer to NCBI's build 35 and nucleotides are listed for each SNP for the minor allele 1 (**A1**) and the major allele 2 (**A2**). Raw genotype counts are listed as A1A1/A1A2/A2A2. **U**: unaffected controls, **CD**: Crohn disease patients, **UC**: ulcerative colitis.

Logistic regression (forward selection) was used to analyse the full German case-control panel for potential epistatic effects with *NOD2*. No statistically significant interaction was observed between any of the 20 SNPs in *XBP1* and the known disease-associated variants in *NOD2* (rs2066844/Arg702Trp, rs2066845/Gly908Arg, rs2066847/Leu1007fs).

					Panel 1			Panel 2			Panel 3		
#	**dbSNP ID**	**Position**	**A1**	**A2**	**U (n=1103)**	**CD (n=550)**	**UC (n=539)**	**U (n=2042)**	**CD (n=1303)**	**UC (n=551)**	**U (n=2177)**	**CD (n=909)**	**UC (n=537)**
1	rs714191	27,469,965	C	T	35/310/732	21/164/365	17/152/347	53/584/1316	34/410/848	20/155/369	72/624/1461	40/278/590	19/162/353
2	rs5997391	27,470,093	T	C	10/134/959	3/56/487	0/51/488	8/242/1792	7/120/1164	0/51/500	17/263/1897	2/102/805	1/57/478
3	rs5752792	27,478,313	C	T	28/287/754	13/157/369	23/143/345	61/535/1313	40/373/849	19/165/339	59/629/1436	32/277/591	19/154/351
4	rs6005863	27,481,002	G	A	172/507/356	77/264/172	69/241/177	283/874/598	187/583/426	63/255/193	375/996/724	166/464/270	81/254/199
5	rs5762788	27,499,324	A	C	104/478/472	47/218/261	29/162/164	185/929/906	114/479/640	29/156/197	233/892/984	88/405/395	49/199/279
6	rs6005879	27,502,868	A	G	2/105/941	0/39/441	1/50/455	5/171/1617	1/82/1051	1/46/479	5/192/1925	1/92/807	0/55/474
7	rs5752797	27,504,552	T	C	31/317/741	19/149/361	14/90/242	74/570/1357	39/331/876	8/105/267	74/605/1467	44/292/561	18/145/368
8	rs5997403	27,505,938	T	C	2/98/979	0/42/504	1/47/469	3/167/1771	0/94/1209	1/44/497	5/177/1974	1/79/822	0/51/483
9	rs5762795	27,507,054	A	C	103/505/479	48/223/263	40/228/251	186/908/922	116/496/658	37/221/271	238/919/995	92/407/400	49/199/284
10	rs2267131	27,515,025	C	T	12/248/834	15/118/415	8/120/408	34/483/1517	25/265/997	6/114/422	33/493/1647	26/231/646	9/103/418
11	rs2097461	27,516,433	C	T	94/492/458	47/230/263	38/227/239	167/829/820	116/510/652	36/214/272	229/906/977	89/410/396	49/197/283
12	rs35873774	27,516,485	C	T	2/170/920	2/52/491	3/56/472	6/263/1758	6/159/1122	2/60/480	7/314/1844	2/95/805	3/45/484
13	rs2269578	27,521,397	C	G	12/245/830	15/104/403	8/80/273	33/473/1511	24/255/985	5/77/309	33/481/1629	26/216/648	9/104/417
14	rs3788409	27,522,705	G	T	105/511/470	47/212/244	29/144/149	186/910/896	115/481/609	30/129/179	237/923/976	89/401/386	49/201/280
15	rs6005893	27,524,344	T	G	2/103/994	0/43/503	1/38/486	5/174/1862	2/86/1200	1/37/506	5/183/1988	1/90/813	0/58/479
16	rs35679096	27,524,947	A	G	2/70/1027	1/29/509	0/19/343	7/137/1882	4/78/1198	1/20/376	2/131/1994	1/60/798	0/33/491
17	rs133440	27,535,932	C	T	5/88/997	1/39/484	0/24/332	7/179/1832	3/113/1122	0/26/354	8/177/1957	1/70/824	1/60/466
18	rs5762839	27,556,001	T	C	22/319/753	21/123/369	11/99/247	51/602/1366	33/299/909	9/90/280	65/596/1495	32/272/598	14/128/387
19	rs5762852	27,567,027	C	T	22/310/726	20/134/343	11/103/244	49/550/1264	33/312/840	9/94/271	65/597/1472	32/272/597	14/129/385
20	rs5762853	27,569,785	G	T	57/393/598	33/193/312	23/193/290	90/701/1015	64/433/778	22/190/319	136/766/1223	67/346/482	34/180/316

Table S3. Results of a seven-marker haplotype analysis at the *XBP1* locus. "f_{controls}" and "f_{IBD}" represent haplotype frequencies among controls and affected individuals, respectively. *P*-values refer to the null hypothesis of equal haplotype frequencies. Nominal *P*-values (P_{nom}) are shown besides *P*-values after 10,000 permutations (P_{Perm}). The two SNPs that achieved the best model fit in a logistic regression analysis among all 20 SNPs in this study are highlighted in red. Numbers given above SNP designations refer to consecutive SNP numbers as assigned in the first column of Table 1.

	2	**3**	**4**	**9**	**10**	**12**	**18**				
Haplotype	**rs5997391**	**rs5752792**	**rs6005863**	**rs5762795**	**rs2267131**	**rs35873774**	**rs5762839**	f_{controls}	f_{IBD}	P_{nom}	P_{perm}
1	T	T	A	C	T	C	C	0.402	0.404	0.81	1
2	T	C	A	C	T	C	C	0.173	0.184	***0.035***	0.212
3	T	T	G	A	C	C	T	0.128	0.127	0.71	1
4	T	T	G	C	T	C	C	0.101	0.115	***0.002***	***0.014***
5	T	2	G	A	T	T	C	0.074	0.058	***0.000020***	***<0.00001***
6	T	T	G	A	T	C	C	0.048	0.051	0.33	0.949
7	C	T	G	A	T	C	T	0.038	0.031	***0.0032***	***0.02***
8	C	T	G	A	T	C	C	0.029	0.024	0.060	0.348

Table S4. Summary of deep sequencing of *XBP1*. All five exons and the promoter were resequenced in 282 unaffected controls (**U**), 282 Crohn's disease (**CD**), and 282 ulcerative colitis (**UC**) patients (total of 846 samples); the five *XBP1* exons were sequenced in 282 additional **UC** patients. Fifty-one not yet annotated polymorphisms were identified (highlighted by bold type), including five rare non-synonymous (ns) SNPs (*XBP1snp30, XBP1snp29, XBP1snp17, XBP1snp8,* and *XBP1snp22*; underlined). Fifteen annotated SNPs were verified. Marker positions are in NCBI's build 35, and Δ indicates the distance in bp from the previous SNP.

Dark gray shading highlights rare SNPs that were only identified once within either **U**, **CD**, and/or **UC** patients; the 3 right columns indicate the panel(s) individual rare SNPs were detected in. Within the 846 controls and patients – with both coding region and promoter sequenced – rare SNPs were detected in 5, 16, and 18, controls, **CD**, and **UC** patients, respectively (in the additional 282 **UC** patients – with only exons sequenced – 3 additional rare SNPs were detected).

† SNPs genotyped as reported in Table 1 and Supplementary Table 2. § Significantly associated with IBD in panels 1+2+3 (see Table 1).

‡ Heterozygote counts of TaqMan-genotyped nsSNPs in Panels 1+2: *XBP1snp17*: 0×**U**, 4×**CD**, 2×**UC**; *XBP1snp8*: 0×**U**, 1×**CD**, 3×**UC**; *XBP1snp30*: 0×**U**, 1×**CD**, 1×**UC**; *XBP1snp29*: 0×**U**, 1×**CD**, 1×**UC**; *XBP1snp22*: 5×**U**, 5×**CD**, 3×**UC**; *rs5762809*: minor allele frequencies of 13% in **U**, 12% in **CD**, and 12% **UC**.

SNP	Position	Δ	Location relative to *XBP1*	Sequence	U	CD	UC
rs2267131†	27,515,025		78bp downstream of exon 5				
XBP1snp10	**27,515,221**	**196**	**exon 5, 496bp 3' UTR; highly conserved region**	**AGGAAAAAATTCCATCAAGCATTTACATAGTAAATTTCTATAATTTC[A/C] CAAAAGATTCTTGATCTTACTTGAAGTATACATGAGGGAAAGAGCCC**			●
XBP1snp52	**27,515,259**	**38**	**exon 5, 458bp 3' UTR**	**TATAATTTCACAAAAGATTCTTGATCTTACTTGAAGTATACATGAGG[G/A] AAAGAGCCCCCTCAGCAGGTGTTCCCGTTGCTTACAGAAGCAAACTA**	●		
XBP1snp26	**27,515,480**	**221**	**exon 5, 237bp 3' UTR**	**AGGGAAAACTACCACCCTTTTAAGATAAAAGTACAATCTTAAAAGCT[G/A] TAGTTCTCAATTATAGTAATATTTCTTACTTCCAGTAATATGTCTCA**			●
XBP1snp27	**27,515,555**	**75**	**exon 5, 162bp 3' UTR; highly conserved region**	**ACTTCCAGTAATATGTCTCAATACCTTGGACTGCTGGATGTCAAAAG[A/G] CAATACCTGGGGGTCATCTATGAGATCTGAACAAATAGAGGAATTCT**			●
***XBP1snp30*‡**	**27,515,798**	**243**	**exon 5; non-synonymous (XBP1s: D350E; XBP1u: 290bp 3' UTR)**	**GCAAAAGTGTCCTCCCAAGAATGGTTTACACCAAGCAGAGAGGACAT[G/C] TCACTGAATGGGGAAAGGGAACCCCCGTATCCACAGTCACTGTAAGC**			●
XBP1snp14	**27,516,314**	**516**	**intron 4/5**	**ATATCAGACTGTAAGAGGCAAAAATTAAATGAAGTACAACTGTCAGA[A/C] TACAATGGAAAATCTAACTGGAACACTTTGTACTGGGTTCCATAATG**			
XBP1snp28	**27,516,350**	**36**	**intron 4/5**	**CAACTGTCAGAATACAATGGAAAATCTAACTGGAACACTTTGTACTG[G/A] GTTCCATAATGTAAATTAGTCATTATGTGATAAGATGACCTCGGGAC**			●
rs2097461†§	27,516,433	83	intron 4/5				
rs34842534	27,516,452	19	intron 4/5				
rs35873774†§	27,516,486	34	intron 4/5				
XBP1snp25	**27,516,557**	**71**	**intron 4/5**	**TCTAGTTAGGGATGTCAAGCATCAAACAGATGGAATTAACTGGTTAT[A/G] TAGCTCTTTAATAAGTCAGAATGATCCCTACCTCTGAATCTGAAGAG**			●
***XBP1snp29*‡**	**27,516,651**	**94**	**exon 4; non-synonymous (XBP1s: V171I; XBP1u: Q179Q); 16bp downstream of splicing site**	**GTCAATACCGCCAGAATCCATGGGGAGATGTTCTGGAGGGGTGACAA[C/T] TGGGCCTGCACCTGCTGCAGAGGTGCACGTAGTCTGAGTGCTGCGGA**			●
***XBP1snp17*‡**	**27,516,704**	**53**	**exon 4; non-synonymous (A162P); 10bp upstream of splicing site**	**CTGCACCTGCTGCAGAGGTGCACGTAGTCTGAGTGCTGCGGACTCAG[C/G] AGACCCGGCCACTGGCCTCACTTCATTCCCCTGGGAGGAAAGACCAA**			
XBP1snp20	**27,516,822**	**118**	**intron 3/4**	**CCAAGGAAATGCTTGCTAGACAGCTGTGATTCTCAACTTTAAAGAAT[T/C] ACTTTTCAAAAAGATTCTAGGGTTAAATTGCTATAGAACTTTATTAT**	●		
XBP1snp24	**27,517,566**	**744**	**intron 3/4**	**AACGCTCTTGATCAGAAGTCCAGACTGTAAACATAATCGCTGGGTCA[T/C] GTCACTTGGAACCAGTACTCACATGAGGCACCAAATAAAGGAGATGA**			●
XBP1snp36	**27,517,628**	**62**	**exon 3, synonymous**	**GTACTCACATGAGGCACCAAATAAAGGAGATGATTTACCTTGGCTTC[C/T] GCCTCCTCTTCAGCAACCAGGGCATCCATCCCCAAGCGCTGTCTTAA**		●	
***XBP1snp8*‡**	**27,517,655**	**27**	**exon 3, non-synonymous (M139I)**	**AGATGATTTACCTTGGCTTCCGCCTCCTCTTCAGCAACCAGGGCATC[C/T] ATCCCCAAGCGCTGTCTTAACTCCTGGTTCTCAACTACAAGGCCATG**		●	●
XBP1snp9	**27,517,762**	**107**	**intron 2/3**	**TAAAAGCTGATTTTCTAGCAAAAGTTTTTGGTTCTGGAAGAAAGTTC[A/G] TAAGAGGCTATTAAAACATCTAATTATTTCAGTTAAGAATCTACCTG**			●
XBP1snp18	**27,519,346**	**1,584**	**intron 2/3**	**TCACGCTTGGCCTTTTTTTTTTTTTTTTTTTGGTATATTTTTGGGT[A/G] GAGACGGGATTTTACCATGTTGGCTAGGCTGGTCTCAAACTGCTGGC**			
XBP1snp21	**27,519,347**	**1**	**intron 2/3**	**CACGCTTGGCCTTTTTTTTTTTTTTTTTTTGGTATATTTTTGGGTA[G/T] AGACGGGATTTTACCATGTTGGCTAGGCTGGTCTCAAACTGCTGGCT**			
rs34718288	27,519,351	4	intron 2/3				
XBP1snp23	**27,519,411**	**60**	**intron 2/3**	**TGTTGGCTAGGCTGGTCTCAAACTGCTGGCTTCAAGTGATCTGCCCA[A/C] CTCAGGCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACCATGCCC**			●
XBP1snp35	**27,519,723**	**312**	**intron 1/2**	**CTACTCTGTTTTTCAGTTTCCTAGGAAGAGAAGGAACATACCACACT[G/A] AGTCATATCAAACCTTATTTATGTCTTTATTTGAAAACTTTACCAGC**		●	
XBP1snp13	**27,519,766**	**43**	**intron 1/2; highly conserved region**	**CACTGAGTCATATCAAACCTTATTTATGTCTTTATTTGAAAACTTTA[C/A] CAGCTGGTGCTTTCATTTTTATTTACAGTATAAGACAGACTAATGAT**		●	

SNP	Position	Δ	Location relative to *XBP1*	Sequence	U	CD	UC
XBP1snp1	**27,520,860**	**1,094**	**exon 1, synonymous**	**GGCCCCAGACCCCGGCCCCTCGCCCACCTCCTCAGCGCCTTCTCCTC[G/A]GGGCTCAGGTGCGTGAGGCGCTGTCGCTTGCGCGCCTGGGGCAGCCC**			
XBP1snp44	**27,520,875**	**15**	**exon 1, synonymous**	**CCCCTCGCCCACCTCCTCAGCGCCTTCTCCTCGGGGCTCAGGTGCGT[G/A]AGGCGCTGTCGCTTGCGCGCCTGGGGCAGCCCCCCGCTCGCTGCCTC**		●	
XBP1snp22[‡]	**27,521,023**	**148**	**exon 1; non-synonymous (P15L)**	**GGGCTCCGGCGGCGGAGGCGGGCTGCCCCGACAGAAGCAGAACTTTA[G/A]GGGTCCCGTCGGCCGGGTTCGGCGCGGCTGCCACCACCACCATAGCT**			●
rs5762809[‡]	27,521,048	25	exon 1, non-synonymous (A7S)				
rs2269575	27,521,080	32	exon 1, 14bp 5'UTR				
XBP1snp2	**27,521,088**	**8**	**exon 1, 22bp 5'UTR**	**TTCGGCGCGGCTGCCACCACCACCATAGCTCCAGACTACGCACCGCG[C/A]ACCGCGCGCCGCAGCCGCCCAGCGCCCAGCCTCGCCGCGCCCGGCCT**			
XBP1snp48	**27,521,091**	**3**	**exon 1, 25bp 5'UTR**	**GGCGCGGCTGCCACCACCACCATAGCTCCAGACTACGCACCGCGCAC[C/T]GCGCGCCGCAGCCGCCCAGCGCCCAGCCTCGCCGCGCCCGGCCTTTC**		●	
XBP1snp45	**27,521,100**	**9**	**exon 1, 34bp 5'UTR**	**GCCACCACCACCATAGCTCCAGACTACGCACCGCGCACCGCGCGCCG[C/T]AGCCGCCCAGCGCCCAGCCTCGCCGCGCCCGGCCTTTCTACGGTCGT**		●	
rs2269577	27,521,311	211	promoter, 197bp upstream of exon 1				
XBP1snp46	**27,521,323**	**12**	**promoter, 209bp upstream of exon 1**	**AAAGGTACTTGGGGTCATTTTCCGCGGGGGGTTACGTGCGGGAGCGT[G/T]TCCTCCACAAACGGATTTTCCCCCCTTAAGCGGACTTATTTCCATCC**		●	
XBP1snp47	**27,521,365**	**42**	**promoter, 251bp upstream of exon 1**	**AGCGTGTCCTCCACAAACGGATTTTCCCCCCTTAAGCGGACTTATTT[C/T]CATCCGGAGTGACAGAATTTAATTCCAAACCGAGAGCTTTCCAGACT**		●	
rs2269578[†]	27,521,397	32	promoter, 283bp upstream of exon 1				
XBP1snp3	**27,521,469**	**72**	**promoter, 355bp upstream of exon 1**	**TTACCGGGACTAACAGAGAATTACCTCAGCCTGACAACATTTTATCT[C/T]GTGCGCCACTTCGGGATCCGAGTGGAGCCGAAAGTCGAGATAGAGCG**	●		
XBP1snp19	**27,521,656**	**187**	**promoter, 542bp upstream of exon 1**	**CCGTCTCAAAAAAAGAAAAAGAAAAAAGCCTGGAAAGAAATTCTGCG[G/T]AATAGAAGTCTTTAAGAAATGAGATCGTGCCCTTTAAAACTAAGTTT**			●
XBP1snp15	**27,521,820**	**164**	**promoter, 706bp upstream of exon 1**	**TTTTTCGTTCCATTTCTAAAGTTTGTACTATGAGCGTGCATTTTTTT[A/T]AATTTAGTTTTATTTTATTTTTTAAATAGAAACGAGGTCTCACTGTG**			
XBP1snp33	**27,521,865**	**45**	**promoter, 751bp upstream of exon 1**	**TTAAATTTAGTTTTATTTTATTTTTTAAATAGAAACGAGGTCTCACT[G/A]TGTTGCCCAGGCTGATCTCGAACTTCTGAGCTCAAGTGAACCTCCCG**			●
XBP1snp49	**27,521,936**	**71**	**promoter, 822bp upstream of exon 1**	**TTCTGAGCTCAAGTGAACCTCCCGCTTCGGCCTCTATTATTTTTATT[T/G]TATTTTTTTTTCTTATTTTTTGAGACGGAGTCAGGCTCTGTCACCAG**	●		
XBP1snp41	**27,522,008**	**72**	**promoter, 894bp upstream of exon 1**	**ACGGAGTCAGGCTCTGTCACCAGGCTGGAGTGCAGTGGCGAGATCTC[A/G]GCTCACTGCAACCTTCGCCTCCGGGTTCAAGCAATTCTCCTGCCTCA**		●	
XBP1snp4	**27,522,253**	**245**	**promoter, 1140bp upstream of exon 1**	**ATTACAGGCGTAAGCCACTGCGCCCAGCCTCTTGTTATTTTAAATGA[G/T]GGGACAGGAAAACGTCACATGTAGAGACTGAGACCCCGGGGTTGACC**	●	●	
XBP1snp31	**27,522,607**	**354**	**promoter, 1493bp upstream of exon 1**	**GGGCAGCACTATTCCAGGTTCTAGGGGTGCAAACAGTAGTAAGACTG[C/T]TACCTGGTATTTGGAGGATATGCAAAAAGTGAAATGTTAAGATAGCA**			●
rs3788409[†§]	27,522,705	98	promoter, 1591bp upstream of exon 1				
XBP1snp5	**27,522,840**	**135**	**promoter, 1726bp upstream of exon 1**	**TTGGTTTTTGCCAGGACTGGGCCACGAGTCTCCTAACGTGTTTTCTC[C/T]CTCTTCGTTGGGAGGGAAATCAATGATTTTTTTTTTTTTAACTGGGC**			
XBP1snp38	**27,522,920**	**80**	**promoter, 1806bp upstream of exon 1**	**TTTTTTTAACTGGGCTGTCCCAACTCCAGAGCCTCCTGAGCACGTGC[T/G]GTCCTGTGGGTTGGAAAAGAGGTGGGGGTGATTGGAGTCTCTGCCGG**			●
XBP1snp34	**27,523,332**	**412**	**promoter, 2218bp upstream of exon 1**	**CCTTGGCCTCCCAAACTGCTGGGATTGCAGGCAGGAACCACAGAGCC[C/A]GGCCCTTTTTATTTATTAAGTGAACATTTATTAATGCCAAGAGAATG**			●
XBP1snp39	**27,523,672**	**340**	**promoter, 2558bp upstream of exon 1**	**ATGCAGTCTTGAACATGTGAGTCCAAACCCTTGGACAGTTTCATATC[C/G]TCTCTATAAAATGAACCTGGTAATTCTTGCATCAGGTGCCATAAGTG**		●	
rs34042768	27,523,699	27	promoter, 2585bp upstream of exon 1				
rs6005892	27,523,812	113	promoter, 2698bp upstream of exon 1				
XBP1snp12	**27,523,940**	**128**	**promoter, 2826bp upstream of exon 1**	**GTGAAACCCAGTCTCTACTAAAAATACAAAAATTAGCCGGACATGGT[G/T]GGGGGCGCCTGTAATCTCAGCTACTGGGGAGGCTGAGGCAGGATAAT**		●	●
XBP1snp6	**27,524,198**	**258**	**promoter, 3085bp upstream of exon 1**	**TAAATAGGCATTCCAGAAAAGGGAAAACAGAAAAATACTGTACACTG[G/A]TAAGCAGAAAACAGAAAATAACATGGCAGGAATAAGTCCAAATATAT**			
XBP1snp11	**27,524,267**	**69**	**promoter, 3153bp upstream of exon 1**	**CATGGCAGGAATAAGTCCAAATATATAAATAATAAAACATAAATGTG[A/G]ATGGGTTATATTATCTTCTTAATCATGCTGTTTTGTTTTATGTATGT**			
XBP1snp32	**27,524,281**	**14**	**promoter, 3167bp upstream of exon 1**	**GTCCAAATATATAAATAATAAAACATAAATGTGAATGGGTTATATTA[T/G]CTTCTTAATCATGCTGTTTTGTTTTATGTATGTCTCTTTATAAACAA**			●
rs6005893[†]	27,524,344	63	promoter, 3230bp upstream of exon 1				
XBP1snp42	**27,524,484**	**140**	**promoter, 3370bp upstream of exon 1**	**ATTTCACATTTTTTGTTTACTATATTTCTCAAGGCAGGAGGATTGCT [T/G]GAGGCCAGGAGTTCAAGACCAGGCTGGGAAACATATTGTGACCTTGT**			●
XBP1snp37	**27,524,592**	**108**	**promoter, 3478bp upstream of exon 1**	**TTAAAAAAATTAACCAGGCGTGGTGACTTGCACCTGTAGTCCCAGCT[G/A]CTCGGAAGACGGAGGTGGTAAGATCCCTTGAACCCAGGAGTTCGAGG**			
XBP1snp16	**27,524,610**	**18**	**promoter, 3496bp upstream of exon 1**	**CGTGGTGACTTGCACCTGTAGTCCCAGCTGCTCGGAAGACGGAGGTG[G/A]TAAGATCCCTTGAACCCAGGAGTTCGAGGCTGCAGTAAACTATGAGC**		●	
XBP1snp7	**27,524,659**	**49**	**promoter, 3546bp upstream of exon 1**	**AAGATCCCTTGAACCCAGGAGTTCGAGGCTGCAGTAAACTATGAGCT[A/G]TGATTGAACCATTGTACTCCAACCTGGGAGACAGAATGAGCTCCTGC**			
rs5762812	27,524,671	12	promoter, 3557bp upstream of exon 1				
XBP1snp40	**27,524,722**	**51**	**promoter, 3608bp upstream of exon 1**	**ACTCCAACCTGGGAGACAGAATGAGCTCCTGCCTCTAAAAAACAAAA[A/C]TTTTTTTAAAAAAAAGGAAAATGACTTACCAGCCATTTTTATGTTTA**			●
rs35679096[†]	27,524,947	225	promoter, 3833bp upstream of exon 1				
XBP1snp50	**27,524,985**	**38**	**promoter, 3871bp upstream of exon 1**	**TAGCATGTCGGCTCACACCTGTAATCTCAGCACTTTGGGAGGCTGAG[G/A]TCAGGGGTTCAAGACCAGCCTGGTCAACATGGCGAAACCCCGTCTCT**		●	
XBP1snp51	**27,525,324**	**339**	**promoter, 4210bp upstream of exon 1**	**AGGTGGGAGGATCATTTGAGCCCAGAAGATTGAGGCTGCAGTGAGCC[G/A]AGATGGTACCACTGCATTCAAGCCTGGGTGACAGAGTGAGATCCTGT**		●	

Table S5. Primer sequences

Gene name (common name)	forward	reverse	Suppl. Ref
Human primers			
HASPA5 (grp78, BiP)	CATCACGCCGTCCTATGTCG	CGTCAAAGACCGTGTTCTCG	(Wang and Seed, 2003)
GAPDH	ATGGGGAAGGTGAAGGTCG	GGGGTCATTGATGGCAACAATA	(Wang and Seed, 2003)
XBP1 splicing	GGAGTTAAGACAGCGCTTGGGGA	TGTTCTGGAGGGGTGACAACTGGG	*
Mouse primers			
Haspa5 (grp78; BiP)	ACTTGGGGACCACCTATTCCT	ATCGCCAATCAGACGCTCC	(Wang and Seed, 2003)
Defcr1 (cryptdin-1)	AAGAGACTAAAACTGAGGAGCAGC	CGACAGCAGAGCGTGTA	(Fre et al., 2005)
Defcr4 (cryptdin-4)	GCTGTGTCTATCTCCTTTGGAGGC	CGTATTCCACAAGTCCCACGAAC	(Kobayashi et al., 2005)
Defcr5 (cryptdin-5)	AGGCTGATCCTATCCACAAAACAG	TGAAGAGCAGACCCTTCTTGGC	(Kobayashi et al., 2005)
Lysz (lysozyme)	ATGGAATGGCTGGCTACTATGG	ACCAGTATCGGCTATTGATCTGA	(Wang and Seed, 2003)
Muc2 (mucin-2)	GCCTGTTTGATAGCTGCTATGTGCC	GTTCCGCCAGTCAATGCAGACAC	*
Camp (cathelicidin)	GCTGTGGCGGTCACTATCAC	TGTCTAGGGACTGCTGGTTGA	(Wang and Seed, 2003)
Xbp1	AGCAGCAAGTGGTGGATTTG	GAGTTTTCTCCCGTAAAAGCTGA	(Wang and Seed, 2003)
Ddit3 (Chop)	CTGGAAGCCTGGTATGAGGAT	CAGGGTCAAGAGTAGTGAAGGT	(Wang and Seed, 2003)
Atoh1 (Math1)	GAGTGGGCTGAGGTAAAAGAGT	GGTCGGTGCTATCCAGGAG	(Wang and Seed, 2003)
Hes1	CCAGCCAGTGTCAACACGA	AATGCCGGGAGCTATCTTTCT	(Wang and Seed, 2003)
Ctnnb1 (β-Catenin)	ATGGAGCCGGACAGAAAAGC	CTTGCCACTCAGGGAAGGA	(Wang and Seed, 2003)
Tcf4	CGAGATATCAACGAGGCTTTCAAG	CATGTGATTCGCTGCGTCTCC	(Fre et al., 2005)
Tnf (TNFα)	CATCTTCTCAAAATTCGAGTGACAA	TGGGAGTAGACAAGGTACAACCC	(Giulietti et al., 2001)
Ifng (IFNγ)	TCAAGTGGCATAGATGTGGAAGAA	TGGCTCTGCAGGATTTTCATG	(Giulietti et al., 2001)
Il4 (IL-4)	ACAGGAGAAGGGACGCCAT	GAAGCCCTACAGACGAGCTCA	(Giulietti et al., 2001)
Il10 (IL-10)	GGTTGCCAAGCCTTATCGGA	ACCTGCTCCACTGCCTTGCT	(Giulietti et al., 2001)
Il1b (IL-1β)	GCAACTGTTCCTGAACTCAACT	GCAACTGTTCCTGAACTCAACT	(Wang and Seed, 2003)
Il1rn (IL-1Ra)	GCTCATTGCTGGGTACTTACAA	CCAGACTTGGCACAAGACAGG	(Wang and Seed, 2003)
Ptgs2 (Cox2)	TGAGCAACTATTCCAAACCAGC	GCACGTAGTCTTCGATCACTATC	(Wang and Seed, 2003)
Nos2 (iNOS)	CAGCTGGGCTGTACAAACCTT	CATTGGAAGTGAAGCGTTTCG	(Giulietti et al., 2001)
Actb (β-actin)	GATGCTCCCCGGGCTGTATT	GGGGTACTTCAGGGTCAG GA	*
Xbp1 splicing	ACACGCTTGGGAATGGACAC	CCATGGGAAGATGTTCTGGG	(Iwakoshi et al., 2003)

* primers designed using Invitrogen VectorNTI software

Table S6. Primers used for resequencing of the *XBP1* locus

Region	Name	Sequence	Touchdown PCR: Tm [°C]	Amplicon length [bp]
Promoter	XBP1_pr1.2_F	5'-GGGCTGCCCCGACAGAAG-3'	64.0/56.0	543
	XBP1_pr1.2_R	5'-TTTCGAACCCAAGGCCCAAC-3'		
	XBP1_pr2.2_F	5'-TCCCTGGCCAAAGGTACTTG-3'	66.5/58.5	498
	XBP1_pr2.2_R	5'-TGAAGGTATTCCCCTCCAACC-3'		
	XBP1_pr3.2_F	5'-GGAGCCGAAAGTCGAGATAG-3'	65.5/57.5	781
	XBP1_pr3.2_R	5'-CATGTGACGTTTTCCTGTCC-3'		
	XBP1_pr4.4_F	5'-TTTTTCGTTCCATTTCTAAAGTTTG-3'	65.5/57.5	690
	XBP1_pr4.4_R	5'-GGCATATTTACGGGGGTTTC-3'		
	XBP1_pr5.1_F	5'-CAAGTGAACCTCCCGCTTCG-3'	66.5/58.5	825
	XBP1_pr5.1_R	5'-TCCCTCCCTACCAAAATAAAATTGACC-3'		
	XBP1_pr6.1_F	5'-AGGGTGGCCAGGTGTTTGTG-3'	66.5/58.5	687
	XBP1_pr6.1_R	5'-CCCCACATCTGAAGGCACATC-3'		
	XBP1_pr7.1_F	5'-GGACATAGTTTTGGTTTTTGCCAGGAC-3'	66.5/58.5	690
	XBP1_pr7.1_R	5'-ATCCCGCACCCTGTGCTTTC-3'		
	XBP1_pr8.1b_F	5'-TGTTTTGGGAGAAGTCTGGAGGTG-3'	66.5/58.5	738
	XBP1_pr8.1b_R	5'-ACCGCGTTTGGCCTCAAAG-3'		
	XBP1_pr9.1b_F	5'-AGCACAGGGTGCGGGATG-3'	66.5/58.5	725
	XBP1_pr9.1b_R	5'-TTCTGTTTTCCCTTTTCTGGAATGC-3'		
	XBP1_pr10.1_F	5'-TCGGTCTTTGAGGCCAAACG-3'	66.5/58.5	701
	XBP1_pr10.1_R	5'-GCAATCCTCCTGCCTTGAGAAATATAG-3'		
	XBP1_pr11.1b_F	5'-AGGAACAGAAATAAATAGGCATTCCAG-3'	66.5/58.5	736
	XBP1_pr11.1b_R	5'-CCTTCAATCAACATGAAATACCCTTC-3'		
	XBP1_pr12.1_F	5'-CCAGCTGCTCGGAAGACG-3'	66.5/58.5	822
	XBP1_pr12.1_R	5'-CGTGCCCAGCCAATTTTC-3'		
Exon 1	XBP1_ex1.1b_F	5'-CGCATCCCCAGCTCTGGTC-3'	60.0/52.0	682
	XBP1_ex1.1b_R	5'-CACGCCGGACTCCATAGCC-3'		
Exon 2	XBP1_ex2.1b_F	5'-GGACTACAGGCACTCACGCTTGG-3'	71.0/63.0	667
	XBP1_ex2.1b_R	5'-CCAGTGCTGTGACGGGGATG-3'		
Exon 3	XBP1_ex3.1b_F	5'-GCCTTTAGGGGAAGAACACTCTG-3'	71.0/63.0	499
	XBP1_ex3.1b_R	5'-TGTTATTCTTGACCCCATGAAGTG-3'		
Exon 4	XBP1_ex4.1b_F	5'-TTGTCCAGAATGCCCAACAGG-3'	71.0/63.0	697
	XBP1_ex4.1b_R	5'-TCCTCCAGGCAAAGATTCAAGC-3'		
Exon 5	XBP1_ex5.1b_F	5'-GCAGGCAGTAATTAAGGTGGAAAAG-3'	71.0/63.0	699
	XBP1_ex5.1b_R	5'-GCCTGTCTGTACTTCATTCAAAAAGC-3'		
	XBP1_ex5.2_F	5'-TGCCAAAAAGGGGGAAGAG-3'	68.0/60.0	699
	XBP1_ex5.2_R	5'-GACAGAGAGCCAAGCTAATGTGG-3'		
	XBP1_ex5.3_F	5'-GCTGGGGAAAGAGTTCATTGG-3'	68.0/60.0	697
	XBP1_ex5.3_R	5'-GGAGTGAAGTGTAGATAAATGGGTCTG-3'		

Table S7. TaqMan primers and probes

XBP1snp17 **(A162P)**

Forward	5'-GAGGCACCAAATAAAGGAGATGAT-3'
Reverse	5'-TGTAGTTGAGAACCAGGAGTTAAGACA-3'
Probe-VIC	5'-CAGGGCATCTATC-3'
Probe-FAM	5'-CAGGGCATCCATC-3'

XBP1snp8 **(M139I)**

Forward	5'-TGCAGAGGTGCACGTAGTCT-3'
Reverse	5'-TCCCAGGGGAATGAAGTG-3'
Probe-VIC	5'-ACTCAGGAGACCCGG-3'
Probe-FAM	5'-CTCAGCAGACCCGG-3'

XBP1snp22 **(P15L)**

Forward	5'-GCCCCGACAGAAGCAGAA-3'
Reverse	5'-GCTATGGTGGTGGTGGCA-3'
Probe-FAM	5'-CGGGACCCTTAAAG-3'
Probe-VIC	5'-ACGGGACCCCTAAAG-3'

XBP1snp29 **(V179I / Q171Q)**

Forward	5'-GAGTCAATACCGCCAGAATCCAT-3'
Reverse	5'-CGCAGCACTCAGACTACGT-3'
Probe-FAM	5'-CCCAATTGTCACCCC-3'
Probe-VIC	5'-CCCAGTTGTCACCCC-3'

XBP1snp30 **(D350E)**

Forward	5'-TGTCCTCCCAAGAATGGTTTACAC-3'
Reverse	5'-CCTGCCTACTGGATGCTTACAG-3'
Probe-FAM	5'-TTCAGTGAGATGTCC-3'
Probe-VIC	5'-CATTCAGTGACATGTCC-3'

rs5762809 **(A7S)**

Forward	5'-GCCCCGACAGAAGCAGAACT-3'
Reverse	5'-AGGGCCACGACCGTAGAAA-3'
Probe-VIC	5'-TTCGGCGTGGCTG-3'
Probe-FAM	5'-TTCGGCGCGGCTG-3'

Supplemental Experimental Procedures

Mice

Xbp1$^{\mathrm{flox/+}}$ (129;B6) and *Xbp1*$^{\mathrm{flox/–}}$ (129;B6;Balb/c) mice were initially mated with Villin (V)-*Cre* transgenic mice (Madison et al., 2002) (Jackson Laboratories) to obtain *Xbp1*$^{\mathrm{flox/flox}}$V*Cre* mice. Colony maintenance involved mating *Xbp1*$^{\mathrm{flox/flox}}$V*Cre* × *Xbp1*$^{\mathrm{flox/flox}}$ as well as *Xbp1*$^{\mathrm{flox/wt}}$V*Cre* × *Xbp1*$^{\mathrm{flox/flox}}$. To exclude XBP1-unrelated phenotypes, we bred *Xbp1*$^{\mathrm{flox/wt}}$V*Cre* × *Xbp1*$^{\mathrm{flox/wt}}$ to obtain *Xbp1*$^{\mathrm{wt/wt}}$V*Cre* mice, which were confirmed to be histologically and clinically indistinguishable from *Xbp1*$^{\mathrm{wt/wt}}$ or *Xbp1*$^{\mathrm{flox/wt}}$ mice. All experiments reported were performed with sex- and age-matched littermate "*Xbp1*$^{–/–}$" (i.e. *Xbp1*$^{\mathrm{flox/flox}}$V*Cre*), "*Xbp1*$^{+/–}$" (i.e. *Xbp1*$^{\mathrm{flox/wt}}$V*Cre*), and "*Xbp1*$^{+/+}$" (i.e. *Xbp1*$^{\mathrm{flox/flox}}$ or *Xbp1*$^{\mathrm{flox/wt}}$) mice obtained as above. For experiments involving time-dependent Cre-mediated deletion of the floxed *Xbp1* gene, we mated *Xbp1*$^{\mathrm{floxneo/+}}$ (129;B6) mice (see Supplementary Fig. 1A) with V*CreER*^{T2} (129;B6) mice kindly provided by Dr. Nicholas Davidson (Washington University, St. Louis) and Dr. Sylvie Robine (Institut Curie-CNRS, Paris) (el Marjou et al., 2004). Cre recombinase was activated by administration of 1mg tamoxifen (MP Biomedicals) intraperitoneally daily over 5 consecutive days. *EIIa*Cre (Lakso et al., 1996; Holzenberger et al., 2000) transgenic mice were obtained from Jackson Laboratories. All mice were genotyped by PCR of genomic DNA isolated by phenol extraction and isopropanol precipitation of proteinase K-digested tails. Primer sequences are available upon request. All mouse protocols were approved by the Harvard Standing Committee on Animals.

Immunohistochemistry

Tissues were collected in 10% neutral buffered formalin and embedded in paraffin. Sections were deparaffinized in isopropanol and graded alcohols, followed by antigen retrieval with Retrievagen A solution according to manufacturer's protocol (Becton Dickinson), and endogenous peroxidase quenched by H_2O_2. Sections were then blocked for 30min with normal goat serum, and incubated overnight at 4°C with primary antibodies at dilutions recommended by the manufacturer. Secondary biotinylated anti-rabbit antibody (1:200) was added for 30 minutes followed by detection with streptavidin-HRP and development with DAB$^+$ chromogen according to manufacturer's (DakoCytomation) recommendations. Slides were counterstained with Mayer's hematoxylin, dehydrated, and mounted with Eukitt.

Electron microscopy

Small intestinal tissue from sex-matched *Xbp1*$^{+/+}$ and *Xbp1*$^{–/–}$ littermates was fixed with 1.25% formaldehyde, 2.5% glutaraldehyde, 0.03% picric acid in 100mM sodium cacodylate buffer. After washing with 100mM sodium cacodylate buffer, tissues were treated for 1h with 1% osmium tetroxide and 1.5% potassium ferrocyanide, and then 30 min with 0.5% uranyl acetate in 50mM maleate buffer, pH 5.15. After dehydration in ethanol, tissues were treated for 1 h in propylenoxide and then embedded in Epon/Araldite resin. Ultrathin sections were collected on EM grids and observed by using a JEOL 1200EX transmission electron microscope at an operating voltage of 60 kV (with the kind assistance of Dr. Susumu Ito, Harvard Medical School).

Oral *L. monocytogenes* infection

For colony forming units (c.f.u.) assay, fecal pellets were aseptically collected 10h after oral infection, and mice euthanized 72 hours after infection, and liver and spleen aseptically harvested. Fecal pellets, liver and spleen were homogenized in PBS, and serial dilutions of the homogenates plated on LB plates containing 200μg/ml streptomycin, incubated at 37 °C for 18 hours and c.f.u.

counted. *L. monocytogenes* burden in feces was expressed as c.f.u. per mg dry weight, whereas liver and spleen data were expressed as c.f.u. per organ. For the determination of dry weight, feces were aseptically collected, divided into two parts, weighed, and one part homogenized and serial dilutions plated. The other part was dried in a speed-vac to allow for accurate weighing to correct the colony counts for differences in water content.

Crypt isolation, stimulation, and bactericidal activity assays

Small intestinal crypts were isolated following published protocols (Ayabe et al., 2000). In brief, the small intestinal lumen of adult mice was rinsed with ice-cold PBS and segments were everted and shaken in Ca^{++} and Mg^{++}-free PBS buffer containing 30mM EDTA to elute crypts. Villi and crypts eluted during 5min intervals were recovered by centrifugation at 700*g* and crypt fractions identified by light microscopy. Crypt numbers were estimated by hemocytometry and 2,000 crypts resuspended in iPIPES buffer containing 10µM carbamyl choline (CCh; Sigma) or 1µg/ml LPS and incubated for 30min at 37°C. For lysozyme detection, supernatants were harvested and proteins precipitated by trichloroacetic acid (TCA), precipitates resuspended in Laemmli's buffer and resolved on 12% SDS-PAGE. Rabbit anti-lysozyme (DakoCytomation) was used for detection by Western blotting. Bactericidal activity of crypt supernatants was assayed against 1×10^3 c.f.u. *Salmonella typhimurium* cs015 as described (Ayabe et al., 2000).

In vivo intestinal permeability experiments

Age-matched *Xbp1*$^{+/+}$ and *Xbp1*$^{-/-}$ littermates were perorally administered 0.6mg/g body weight of a 80mg/ml solution of FITC-dextran (Sigma), and peripheral blood collected 4h later (Karhausen et al., 2004). Dilutions of FITC-dextran in PBS were used as a standard curve, and absorption of 50µl serum or standard measured in a fluorometer at 488nm.

CD1d-restricted antigen presenting function of MODE-K cells (van de Wal et al., 2003) $1x10^5$ MODE-K.iXBP and MODE-K.Ctrl cells were seeded in 96 well plates and allowed to adhere for 2-4h. The CD1d-binding model glycolipid α-galactosyl-ceramide (αGC) was then added at a concentration of 100ng/ml along with the indicated concentrations of SP600125. After 2h of incubation, MODE-K cells (Vidal et al., 1993) were washed and fixed with glutaraldehyde, followed by quenching with glycine, exactly as described (Kang and Cresswell, 2004). After 4 washes with media, the CD1d-restricted NKT cell hybridoma DN32.D3 (Bendelac et al., 1995) (kindly provided by Dr. Albert Bendelac, University of Chicago, Chicago, IL), which is activated upon recognition of αGC presented by CD1d, was added to fixed MODE-K cells, and supernatants harvested after 18h assessed for IL-2 secretion by ELISA (BD Pharmingen).

Genotyping and sequencing

Genomic DNA was prepared using a variety of methods and DNA samples evaluated by gel electrophoresis for the presence of high-molecular weight DNA. One µl of genomic DNA (30-300 ng) was amplified by the GenomiPhi (Amersham) whole genome amplification system and fragmented at 99°C for five minutes. One hundred ngs of DNA was dried overnight in TwinTec hardshell 384well plates (Eppendorf, Hamburg, Germany) at room temperature and genotyping performed using the SNPlex™ Genotyping System (Applied Biosystems, Foster City, CA). All process data were logged into, and administered by, a database-driven LIMS (Teuber et al., 2005). Graphical summaries of LD were created using GOLD 1.0 (Abecasis and Cookson, 2000).

Genomic DNA sequencing traces were visually inspected for the presence of SNPs and InDels using the software tool novoSNP (Weckx et al., 2005). The automated platform used for Taqman genotyping has been previously described (Hampe et al., 2001).

UPRE reporter assays

Expression plasmids h*XBP1u* and h*XBP1s* were engineered to incorporate the *XBP1snp17* (A162P*)*, *XBP1snp8* (M139I) and *XBP1snp22* (P15L) minor variants using the GeneTailor site directed mutagenesis system (Invitrogen). Primers used were *XBP1snp17*_R AGACCCGGCCACTGGCCTCACTTCATTCCC, *XBP1snp17*_F TGAGGCCAGTGGCCGGG-TCTcCTGAGTCCGC; *XBP1snp8*_R ATCCCCAAGCGCTGTCTTAACTCCTGGTTC, *XBP1snp8*_F TTAAGACAGCGCTTGGGGATaGATGCCCTGG; *XBP1snp22*_F CCGACAG-AAGCAGAACTTTAaGGGTCCCGTC, *XBP1snp22*_R TAAAGTTCTGCTTCTGTCGGGG-CAGCCCGC. Transient transfection of MODE-K cells followed by luciferase assays was performed as described previously (Lee et al., 2003). Briefly, cells plated in 24 well plates at 75,000 cells/well were transfected with 50 ng of UPRE-luciferase and various quantities of h*XBP1* plasmids by using lipofectamine 2000 reagent. pcDNA3.1 (Invitrogen) plasmid was added to adjust the total transfected DNA to 0.5 µg. Cells were treated for 16h with 1 µg/ml tunicamycin prior to harvest in certain experiments. Dual luciferase assays were performed following the protocol provided by the manufacturer (Promega). For reconstitution of *Xbp1*$^{-/-}$ MEF cells (Lee et al., 2003), bicistronic retroviral vectors expressing GFP and human XBP1 were constructed by inserting PCR amplified cDNAs for wildtype and *XBP1snp17* and *XBP1snp8* variants of human *XBP1* into RV$_{\mathrm{GFP}}$ vector between *BglII* and *SalI* sites, as described previously (Iwakoshi et al., 2003). Retroviruses produced from 293T cells were used to transduce *Xbp1*$^{-/-}$ MEF cells in the presence of polybrene. Two days later, cells were replated, attached overnight and treated with 1µg/ml tunicamycin for 6 hrs. Retroviral transduction efficiency was determined by FACS analysis of cells for GFP expression, as well as western blot of XBP1s after treating cells with tunicamycin. The levels of ERdj4 and EDEM mRNA were determined by real time PCR and are expressed normalized to β-actin mRNA content.

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