Antibodies

The following monoclonal antibodies were used for fluorescence activated cell sorting For immunoprecipitation and western blotting experiments, anti– β 3 integrin (N-20 and C-20, Santa Cruz Biotechnology, Santa Cruz, CA), anti–c-Src^{PY418} (100F9, Cell Signaling Technology, Danvers, MA), Syk (N-19, Santa Cruz Biotechnology), anti-pTyr (PY99, Santa Cruz Biotechnology) and anti- β 3^{PY747} (Biosource International, Camarillo, CA) antibodies were used. Peroxidase-conjugated secondary antibody (GE healthcare science, Arlington Heights, IL) was used for western blotting.

Induction of outside-in signaling via integrin β 3 by anti-mouse β 3 integrin antibody, 2C9.G2, in platelets

Washed platelets were prepared from C57/BL6 mice as described previously.¹ Platelets were incubated with 2C9.G2 or hamster IgG in Tyrode-Hepes buffer (137 mM NaCl, 12.1 mM NaHCO₃, 2.7 mM KCl, 5 mM HEPES, BSA 0.1%, D-glucose 0.1%, 0.5 mM CaCl₂, 1 mM MgCl₂, pH7.4) for 15 min at room temperature. After incubation, the platelets lysed in lysis buffer (50 mM Tris-HCl (pH7.4), 150 mM NaCl, 1% Nonidet P-40, 0.5 mM EDTA, 0.1 mM PMSF, 10 μ g/ml Leupeptin and 10 μ g/ml aprotinin), and the lysates were subjected to immunoprecipitation with specific antibody and protein A or G Sepharose (Amersham Biosciences, Arlington Heights, IL) for 3 h at 4°C. Immunoprecipitated proteins were used for western blotting as described previously.¹

Whole transcriptome analysis using a SOLiD system

After sorting 1,000–1,500 CD34⁻KSL cells, total RNA was extracted as previously described,² and first strand cDNA were synthesized using a SMARTer Pico cDNA amplification kit (Clonetech, Mountain View, CA). Double-stranded cDNA was then amplified by 20 cycles of PCR. The amplified cDNA was sheared into small fragments (80–130 bp) using a Covaris S2 system (Covaris, Inc., Woburn MA), which was followed by the repair and subsequent ligation of SOLiD P1 and P2 adaptors to the ends of target DNAs. To amplify a pool of cDNA fragments, the ligated fractions were subjected to limited rounds of PCR using primers complementary to the P1 and P2 adaptor sequences. After purification of the cDNA fragments, emulsion PCR was run using 1-µm–diameter beads with P1 primers covalently attached to their surfaces. We then sequenced ~120,000,000 beads on a SOLiD sequencer (Applied Biosystems). All of these procedures were carried out according to the manufacturer's instructions. After SOLiD sequencing, we analyzed the raw data using Applied Biosystems' whole transcriptome software (http://www.solidsoftwaretools.com/). In addition, the expression signals were normalized by dividing the tag number of each gene by the total tag number. The whole transcriptomes obtained through SOLiD sequencing were analyzed using GeneSpring (Agilent Technologies). Following filtration based on p<0.05 and >2-fold change, the selected genes were subjected to hierarchical cluster analysis. In addition, whole transcriptomes were subjected to gene set enrichment analysis using GSEA v2.06 software available from the Broad Institute (http://www.broad.mit.edu/gsea). Changed gene sets were selected based on a threshold set at a p-value <0.05 and FDR (q-value) <0.25.

DNA microarray analysis

After CD34⁻KSL cells were cultured with 2C9.G2 or control IgG for 5 days in S-Clone SF-03 medium supplemented with 50 ng/ml SCF and/or 50 ng/ml TPO, total RNA was extracted as described previously² from 5,000 sorted CD48⁻KSL cells, a population containing putative HSCs after culture.³ Using the extracted total RNA, fluorescently-labeled cRNA was prepared with a ULS aRNA Fluorescent Labeling Kit (Kreatech, Amsterdam, The Netherlands), after which the cRNA was amplified using an OvationTM Aminoallyl System (NuGEN Technologies, San Carlos, CA). The prepared cRNA was then hybridized into Whole Mouse Genome $(4 \times 44K)$ arrays (Agilent Technologies, Santa Clara, CA). After washing with a Gene Expression Wash Pack (Agilent Technologies), the microarrays were scanned using an Agilent MicroArray Scanner (Agilent Technologies). All of these procedures were carried out according to the manufacturer's instructions. The distribution of remaining average intensities for each chip was normalized to the quantile value for all chips, and the signal values for genes were normalized to the median value for all genes. The expression value (signal) and detection call (Present or Absent) for each probe set were calculated using Feature Extraction Ver.9.5.3 (Agilent Technologies). All experiments were performed in duplicate or triplicate using sorted cells that were independently prepared in separate experiments. To analyze the data, we first removed the probe sets that were used for quality control and consistently yielded high negative values, resulting in extraction of 35,791 genes. Additionally, all values less than 1 were set to 1 when addressing fold changes. To identify differentially expressed genes, we selected probe sets that showed more than a 1.4-fold upregulation or downregulation upon addition of 2C9.G2 to HSCs in the presence of TPO (Fig. S2). Genes from 2C9.G2-treated HSCs that showed more than a 1.0-fold upregulation or downregulation only in the presence of SCF were filtered out of the selected probe sets so as to clearly identify the effects of the combination of TPO and outside-in signaling from β 3 integrin (Fig. S2). Gene ontology analysis was performed using Onto-Express on the Onto-tools website (http://vortex.cs.wayne.edu/projects.htm).

Single cell culture

Single CD34⁻KSL cells were clonally sorted into the wells of 96-well U bottom plates (BD falcon, Franklin Lakes, NJ) and cultured with 2C9.G2 or hamster IgG for 5 days in the indicated medium. After 5 days, the total cell number was counted in the individual wells using a phase-contrast microscope.

BrdU uptake assay

To determine cell cycle rates *in vivo*, BrdU (100 mg/kg; BD Biosciences) was intraperitoneally injected into Wt and Y747A mice. Two hours after administration, the % BrdU⁺ cells were determined in individual mice using a BrdU Flow Kit (BD Biosciences). Following the manufacturer's instructions, whole BMCs were stained with antibodies to detect CD34⁻KSL or CD34⁺KSL cells, and were examined individually. The cells were treated with DNase I for 1 h at 37°C, stained with anti-BrdU antibody (BD Biosciences) and assayed using flow cytometry.

REFERENCES

1. Takizawa H, Nishimura S, Takayama N, et al. Lnk regulates integrin alphaIIbbeta3 outside-in signaling in mouse platelets, leading to stabilization of thrombus development *in vivo. J Clin Invest.* 2010;120(1):179–190. Prepublished on 2009/12/30 as DOI 39503 [pii] 10.1172/JCI39503.

 Umemoto T, Yamato M, Nishida K, Yang J, Tano Y, Okano T. Limbal epithelial side-population cells have stem cell-like properties, including quiescent state. *Stem Cells*. 2006;24(1):86–94. Prepublished on 2005/09/10 as DOI 2005-0064 [pii] 10.1634/stemcells.2005-0064.

3. Noda S, Horiguchi K, Ichikawa H, Miyoshi H. Repopulating activity of *ex vivo*-expanded murine hematopoietic stem cells resides in the CD48–c-Kit+Sca-1+lineage marker– cell population. *Stem Cells*. 2008;26(3):646–655. Prepublished on 2007/12/15 as DOI 2007-0623 [pii] 10.1634/stemcells.2007-0623.

Table S1. Gene sets upregulated in Wt CD34⁻KSL cells, as compared to Y747A cells

The whole transcriptomes of wild-type and Y747A HSCs were subjected to gene set enrichment analysis (GSEA), and the threshold was set at p-value <0.05 and FDR (q value) <0.25. The normalized enrichment score (NES) reflects the degree to which a gene set is overrepresented at the top or bottom of a ranked list of genes. Bold indicates the gene sets in which p<0.01 and q<0.1.

	Signal pathway	
	Cytokine response	
	Transcription factor-reguated gene set	
	CMV infection	
	UV treatment	
	Cell proliferation & Cell cycle	
NAME	DESTRIBUTION	NES NOM p-val FDR q-val
DORSAM_HOXA9_UP	Genes upregulated by HOXA9	3.780879 <0.001 0.089415
CMV HCMV TIMECOURSE 4HRS DN	Down-regulated in fibroblasts following infection with human cytomegalovirus with maximum change at 4 hours	3.622293 <0.001 0.081843
DER IFNG UP	Genes up-regulated by interferon-gamma in HT1080 (fibrosarcoma)	3.5233 <0.001 0.071108
UVC XPCS 4HR DN	Down-regulated at 4 hours following treatment of XPB/CS fibroblasts with 3 J/m^2 UVC	3.428252 <0.001 0.090449
CALCINEURIN NF AT SIGNALING	Mouse genes associated with signal transduction through calcium, calcineurin, and NF-AT.	3.340477 <0.001 0.088111
IFN ANY UP	Upregulated 2-fold in HT1080 cells 6 hours following treatment with any of interferons alpha, beta and gamma	3.280988 <0.001 0.08798
DER IFNB UP	Genes up-regulated by interferon-beta in HT1080 (fibrosarcoma)	3.220002 <0.001 0.097217
IFN GAMMA UP	Upregulated 2-fold in HT1080 cells 6 hours following treatment with interferon gamma	3.146951 <0.001 0.113284
LEI MYB REGULATED GENES	Myb-regulated genes	3.063134 <0.001 0.106041
UV-CMV UNIQUE HCMV 6HRS UP	Up-regulated in fibroblasts at 6 hours following infection with UV-inactivated CMV, but not untreated CMV	2.937503 <0.001 0.113874
CMV-UV HCMV 6HRS UP	Up-regulated in fibroblasts at 6 hours following infection with UV-inactivated human cytomegalovirus	2.936515 <0.001 0.105794
IEN ALPHA UP	Upregulated 2-fold in HT1080 cells 6 hours following treatment with interferon alpha	2.93507 <0.001 0.099061
UVB NHEK1 C1	Upregulated by UV-B light in normal human epidermal keratinocytes, cluster 1	2.918387 <0.001 0.097381
CMV HCMV TIMECOURSE ALL UP	Up-regulated in fibroblasts following infection with human cytomegalovirus.	2.849963 <0.001 0.105456
IL6PATHWAY	IL-6 binding to its receptor activates JAK kinases and a variety of transcription factors, with effects in neuronal differentiation, bone loss, and inflammation.	2.764113 <0.001 0.129641
FCER1PATHWAY	In mast cells, Fc epsilon receptor 1 activates BTK, PKC, and the MAP kinase pathway to promote degranulation and arachnidonic acid release	2.759928 <0.001 0.123101
PENG LEUCINE UP	Genes upregulated in response to leucine starvation	2.756302 <0.001 0.119043
CMV 8HRS UP	Upregulated at 8hrs following infection of primary human foreskin fibroblasts with CMV	2.710537 0.037209 0.125483
IFN_BETA_UP	Upregulated 2-fold in HT1080 cells 6 hours following treatment with interferon beta	2.67786 <0.001 0.130361
SMOOTH_MUSCLE_CONTRACTION		2.657845 <0.001 0.132751
PRMT5_KD_DN	Down-regulated by stable RNAi knock-down of PRMT5 in NIH 3T3 cells	2.642075 <0.001 0.135555
P53GENES_ALL	p53 transcriptional targets	2.640601 <0.001 0.132046
IFN_ALL_UP	Upregulated 2-fold in HT1080 cells 6 hours following treatment with interferons alpha, beta and gamma	2.61445 <0.001 0.141137
ST_FAS_SIGNALING_PATHWAY	The Fas receptor induces apoptosis and NF-kB activation when bound to Fas ligand.	2.602091 <0.001 0.13878
CMV_HCMV_TIMECOURSE_12HRS_UP	Up-regulated in fibroblasts following infection with human cytomegalovirus (at least 3-fold, with Affymetrix change call, in at least two consectutive timepoints), with maximum change at 12 hours	2.589036 <0.001 0.142917
	IA Genes involved in Toll-like receptor signaling pathway	2.588033 <0.001 0.138382
CMV_ALL_UP	Upregulated at any timepoint following infection of primary human foreskin fibroblasts with CMV	2.582003 <0.001 0.135179
SHEPARD_CELL_PROLIFERATION	Cell proliferation genes determined in zebra fish	2.566925 <0.001 0.135996
CELL_PROLIFERATION	The multiplication or reproduction of cells, resulting in the rapid expansion of a cell population.	2.566925 <0.001 0.140853
	L Genes involved in amyotrophic lateral sclerosis (ALS)	2.559734 <0.001 0.135745
BRG1_SW13_UP	Up-regulated by transient expression of BRG1 at 24 hours in human, BRG1-lacking SW-13 cells	2.552981 <0.001 0.135817
DER_IFNA_UP	Genes up-regulated by interferon-alpha in HT1080 (fibrosarcoma)	2.552463 <0.001 0.132354
EPOPATHWAY	Erythropoietin, which activates the MAPK pathway, stimulates erythrocyte production and is an effective treatment for anemia. N Genes preferentially excressed in breast cancers, especially those involved in estrogen-receptor-dependent signal transduction.	2.528966 <0.001 0.136674
	N Genes preferentially expressed in breast cancers, especially those involved in estrogen-receptor-dependent signal transduction. Positive regulators of cell provingeration in zeptar fish	2.517045 <0.001 0.137332
IDX TSA UP CLUSTER1	Postive regulators of cell proliferation in zebra hish Strongly up-cepulated at 2 hours during differentiation of 3T3-L1 fibroblasts into adipocytes with IDX (insulin, dexamethasone and isobutylxanthine), vs. fibroblasts treated with IDX + TSA to prevent differentiation (cluster 1)	2.484177 0.037209 0.143191
ET743 HELA UP		2.482752 <0.001 0.139908 2.428896 <0.001 0.156943
UVC XPCS ALL DN	Upregulated by Et-743 in HeLa cells Down-regulated at any timepoint following treatment of XPB/CS fibroblasts with 3 J/m ⁴ 2 UVC	2.428896 <0.001 0.156943
UVC_XPCS_ALL_DN UVB_NHEK4_24HRS_DN	Down-regulated at 24 hours by UV-B light in normal human exidemal readermal kerses and a construction of the construction of t	2.379913 <0.001 0.174079
TAKEDA NUP8 HOXA9_8D_UP	Lowmeguates at 24 hours by Uv-B light in formal keratinocytes Effect of NUPSH-IOXA9 one retranscription at 8 d after transduction UP	2.379913 <0.001 0.174079
LEE MYC E2F1 DN	Effect of NOPSCHOARS on gene transcription at s of after transportation UP Genes down-regulated in heaptoma tissue of Mix+E2F1 transperic mice	2.372752 <0.001 0.169055
		2.512152 ~0.001 0.109055

KERATINOCYTEPATHWAY	Keratinocyte differentiation, which models the differentiation of epidermal cells, requires the four main MAP kinase pathways.	2.368144	
ENEDINI_MEGAKARYOCYTIC_GENES	Genes essential to the development of megakaryocytes, as expressed in normal cells and essential thrombocythemic cells (ET).	2.360362	<0.001 0.1
YPOXIA REVIEW	Genes known to be induced by hypoxia	2.33619	0.025532 0.1
ETT UP	Upregulated by expression of mutant MeCP2 (Rett syndrome) vs. wt MeCP2 in fibroblasts	2.331012	< 0.001 0.1
ADIATION SENSITIVITY	Genes related to radiation sensitivity	2.325312	<0.001 0.
/B SCC UP	Upregulated by UV-B light in squamous cell carcinoma cells	2.322484	0.029021 0.1
ROONQUIST RAS STROMA DN	Genes downregulated in multiple myeloma cells with N-ras-activating mutations versus those co-cultured with bone marrow stromal cells.	2.282837	< 0.001 0.1
DACI COLON BUT48HRS UP	Upregulated by butyrate at 48 hrs in SW260 colon carcinoma cells	2.259198	
NG RAPAMYCIN UP	Genes uprequiated in estonse to rapamycin starvation	2.255989	< 0.001 0.1
UCCHI EPITHELIAL DN	Dense of physical and a physical and physical and physical and a physical and a physical and a p	2.254453	<0.001 0
D12 ANY DN	The set mast definition of the set of the se	2.229415	<0.001 0.
ASSERINI PROLIFERATION	Down-regulated 2-rold in reta cens by Additional type 12 (Ad12) at any unequality to bosc-intection of Genes associated with cellular adhesion that are differentially expressed in endothelials for acrtas from regions of disturbed flow (inner aortic arch) versus regions of undisturbed laminar flow (descending thoracic aorta).	2.229413	
	Comers associated with central admession that are interentially expressed in encoursenance of plantas non-regions of disturbed now (inter admit admitsurbed naminal now (descending indiacid admits)). 350 neurologically relevant transcripts with highest abundance fold range among strains	2.220455	<0.001 0
NDSTEDT_DEND_8H_VS_48H_UP	Genes up-regulated in DC stimulated for 8 h as compared to DC stimulated for 48 h	2.21318	<0.001 0.1
PCRDB_OTHER		2.210764	
AKEDA_NUPB_HOXA9_10D_DN	Effect of NUP98-HOXA9 on gene transcription at 10 d after transduction Down	2.210015	
S3_FIBRO_C4	Downregulated early by sodium arsenite in fibroblasts (Cluster 4)	2.185448	
ALRES_MOUSE_NEOCORTEX_DN	Downregulated in the neocortex of aged (30-month) mice subjected to caloric restriction since young adulthood vs. age-matched controls		0.045614 0.1
D12_24HRS_DN	Down-regulated 2-fold in HeLa cells by Adenovirus type 12 (Ad12) at 24 hours post-infection	2.181267	
	Genes involved in Jak-STAT signaling pathway		0.039735 0.1
DIP_HUMAN_UP	Up-regulated in primary human adipocytes, versus preadipocytes	2.171569	
TRESS GENOTOXIC SPECIFIC UP	Genes up-regulated 4 hours following genotoxic stress that discriminate genotoxic from non-genotoxic stress	2.142541	< 0.001 0.1
	Genes that are upregulated in AML NPM1 mutant versus AML NPM1 wild type	2.135005	
	Genes involved in B cell receptor signaling pathway	2.132378	
OGERKORP ANTI CD44 UP	Genes differentially expressed in human B cells cultured in vitro in the presence or absence of CD44 ligation, together with anti-immunoglobulin and anti-CD40 antibodies	2.091393	
DACI COLON BUT UP	Dense amonghaine to physical an initiation of the presence of absence of other spaces, ogener was another and an other analysis and an other analysis and an other analysis and an other analysis and an		0.029666 0.2
	Genes implicated in drug resistance and metabolism Genes implicated in drug resistance and metabolism	2.028933	<0.001 0.2
TSPATHWAY		2.020933	<0.001 0.2
	The Ets transcription factors are activated by Ras and promote macrophage differentiation.		
IVB_NHEK4_6HRS_DN	Downregulated at 6 hours by UV-B light in normal human epidermal keratinocytes	2.012101	
ALRES_RHESUS_DN	Downregulated in the vastus lateralis muscle of middle-aged rhesus monkeys subjected to caloric restriction since young adulthood vs. age-matched controls	2.009319	0.034 0.1
SA05212_PANCREATIC_CANCER	Genes involved in pancreatic cancer	1.976935	<0.001 0
	Genes with reduced expression in mouse embryonic stem cells with a targeted deletion of BRCA1, whose expression was rescued by ectopic expression of a BRCA1 transgene	1.976375	<0.001 0.2
IDPATHWAY	On ligand binding, interferon gamma receptors stimulate JAK2 kinase to phosphorylate STAT transcription factors, which promote expression of interferon responsive genes.	1.966672	<0.001 0.2
ST_ADRENERGIC	Adrenergic receptors respond to epinephrine and norepinephrine signaling.	1.938831	<0.001 0.2
TIRPATHWAY	Binding of angiotensin II to AT1-R activates Ca2+ signaling and the JNK pathway.	1.934715	< 0.001 0.2
GFPATHWAY	The epidermal growth factor (EGF) peptide stimulates the EGF receptor to promote cell proliferation via the MAP kinase and Ras pathways.	1.930149	< 0.001 0.2
AF57 BT549 DN	Down-regulated following stable re-expression of BAF57 in Bt549 breast cancer cells that lack functional BAF57	1.926494	0.032694 0.1
GED RHESUS DN	Downregulated in the vastus lateralis muscle of aged vs. young adult rhesus monkeys	1.924703	< 0.001 0.2
	Negative regulators of cell proliferation in zebra fish	1.902596	<0.001 0.3
MV HCMV TIMECOURSE 48HRS DN	n-genero regulated in fibroblasts following infection with human cytomegalovirus (at least 3-fold, with Affymetrix change call, in at least two consectutive timepoints), with maximum change at 48 hours	1.89314	
CRPATHWAY	Commodulate in motoriast comming metabolism with names and transiently increase transient and name in the metabolism commodulate in motoriast comming in the set of t	1.889467	<0.001 0.2
HANG SERUM RESPONSE UP	D cen angen teophysika (Dorsy durinae from kinados and unitatenty increade troame prodphotytation on binding to angen. CSR (Serum Response) signature for activated genes (Stanford)		0.024641 0.2
H EXOGENOUS ANY DN	Con Certain response) signature for activated genes (statitud) Down-regulated at any time point (1-24 hours) following treatment of mammary carcinoma cells (MCF-7) with exogenous human growth hormone	1.876963	<0.024641 0.2
SH_EXOGENOUS_LATE_DN	Down-regulated at late time points (12-24 hours) following treatment of mammary carcinoma cells (MCF-7) with exogenous human growth hormone	1.872325	
ASSERINI_SIGNAL	Genes associated with cellular adhesion that are differentially expressed in endothelial cells of pig aortas from regions of disturbed flow (inner aortic arch) versus regions of undisturbed laminar flow (descending thoracic aorta).	1.866323	<0.001 0.2
PCRPATHWAY	G-protein coupled receptors activate adenylyl cyclase, which converts ATP to cAMP, to activate second messenger pathways.	1.864519	<0.001 0.2
ISA04640_HEMATOPOIETIC_CELL_LINEA		1.862582	<0.001 0.3
NEREAR_UP	Genes prefentially expressed in human inner ear tissue (cochlea and vestibule), at least 10-fold higher from a mixture of 29 other tissues	1.859108	<0.001 0.1
HAN_MMPC_PC	Microarray-derived expression levels of genes differentially expressed during PC development	1.854972	<0.001 0.2
ICALPAINPATHWAY	In integrin-mediated cell migration, calpains digest links between the actin cytoskeleton and focal adhesion proteins.		0.048485 0.3
UIZ_TENASCIN_TARGETS	Tenascin-C target genes		0.045455 0.1
2PATHWAY	IL-2 promotes proliferation via JAK and MAP kinase and has surface receptors on activated B cells, LPS-treated monocytes, and many T cells.	1.837445	0.033 0.1
ROONQUIST_IL6_STROMA_UP	Genes upregulated in multiple myeloma cells exposed to the pro-proliferative cytokine IL-6 versus those co-cultured with bone marrow stromal cells.	1.837135	< 0.001 0.1
1RPATHWAY	The cytokine IL-1 stimulates its primary receptor, IL-1R1, which induces transcription of inflammation-related genes such as interferons.	1.835865	<0.001 0.1
IG BCR_SIGNALING_PATHWAY	The optimine is naminated in pathway Membershow and the BCR signaling pathway	1.832386	<0.001 0.
REB BRAIN 2WKS LIP	Memory of the Der signaling patients Up-regulated in the nucleus accumbers of mice after 2 weeks of induction of transgenic CREB	1.813879	<0.001 0.
ARK MSCS_DIFF	Opregulated in the nocleus accuments of mice area z weeks on induction of namingenic OFCE	1.807054	
ELL_CYCLE_KEGG			0.024 0
	Party regulated in Electricate following infection with human schementarious (at least 2 fold with Affordation shares and in at least hus especiality threesalds) with mendation (at least 2 fold with Affordation shares and in at least hus especiality threesalds) with mendation (at least 2 fold with Affordation scheme and the statement of the sta	1.795203	
MV_HCMV_TIMECOURSE_18HRS_DN	Down-regulated in fibroblasts following infection with human cytomegalovirus (at least 3-fold, with Affymetrix change call, in at least two consectutive timepoints), with maximum change at 18 hours		< 0.001 0.3
EMETH_TNF_DN ARIES_PULP_UP	Genes down-regulated after 3 h in LPS-stimulated RAW 2647 macrophages	1.786664	
	Up-regulated in pulpal tissue from extracted carious teeth (cavities), compared to tissue from extracted healthy teeth		0.029835 0.2

			for 5 days CF + TPO
	Fresh	lgG	2C9.G2
Total cell number	40	4498 ± 1254	4360 ± 1169
HSC frequency	1 in 3.5	1 in 43.2	1 in 90.2
No. of HSCs	11.4	104.2	48.2
RU	1.115 ± 0.489	3.652 ± 1.433	5.732 ± 2.330

Table S2. Integrin β3-mediated signaling contributes to successful *ex vivo* expansion of HSCs without loss of LTR activity per single HSC

The results obtained with single-cell transplantation were used to determine HSC frequency among fresh CD34⁻KSL cells (Fig. 5D). HSC numbers were calculated from the total cell number and HSC frequency. Repopulation unit (RU) values reflect that ability in HSCs (see Materials and Methods).

Table S3. Genes upregulated in 2C9.G2-treated HSCs cultured in the presence of TPO

The values are the fold changes in 2C9.G2-treated vs. IgG-treated cells under the indicated conditions. A and P represent the detection calls "Absence" and "Presence," respectively.

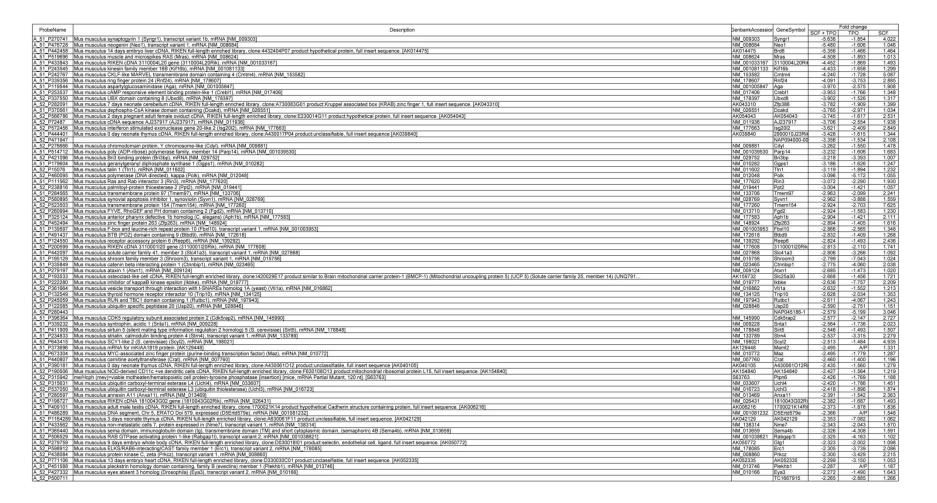
ProbeName	Description	GenbankAccession	CanaSumbal		Fold change	
				SCF + TPO	TPO	SCF
		AK046685 NM 032543	Pan3 Rnf123	8.753	5.542 2.837	-1.190 -6.250
A 52 P300305	inius insocius ing inger protein 125 (mil 125), initiva (two US264) Mus musculus vacular protein statis (Strating Stratis), initia (Stratis)	NM 022997	Vps35	4.443	1.587	-2.263
A 51 P169401	Mus musculus low density lipoprotein receptor-related protein 6 (Lrp6), mRNA [NM_008514]	NM_008514	Lrp6	4.005	2.997	-2.224
A 52 P1083868	Mus musculus 16 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A130020M21 product:unclassifiable, full insert sequence. [AK037475]	AK037475	AK037475	3.733	2.467	-1.093
A_51_P498388		NM_145587	Sbk1	3.679	3.412 4.170	-1.014
A_52_P138267	wus musculus milochondria moosoma protein Sz5 (wipsz5), mkrak [vwu25578]	NM_025578	Mrps25 TC1711987	3.649	1.866	-3.230
A 52 P183345		AK080831	Nucb1	3.385	4.726	-1.109
A 52 P52311	AF052147 cul-3 {Homo sapiens} (exp=-1; wop=0; cq=0), partial (27%) [TC1620610]		TC1620610	3.374	2.441	-1.168
		NM_009406 XM_901554	Tnni3 Rc3h2	3.350	3.177	-1.083
A 52 P131972		AK038326	Nt5c2	3.339	4.011	-1.693
A 51 P248304	Mus musculus vacuolar protein sorting 26 homolog B (veast) (Vos26b), mRNA (NM 178027)	NM 178027	Vps26b	3.295	1.429	-1.700
A_52_P213561	Mus musculus inositol polyphosphate-5-phosphatase F (Inpp5f), mRNA [NM_178641]	NM_178641	Inpp5f	3.245	3.444	-1.087
A 52 P907652		AK087575	AK087575	3.232	2.406	-2.448
A 52 P472583		NM_133626 AK137301	Rrbp1	3.115 3.033	2.046	-1.223
A 52 P318683	Mus misculus to days neorate cerebenant CDMA, Nitch numerigin enticitie introduction to polacitation and international	NM 001081132	Apc Upf2	3.035	3.062	-1.249
A 52 P6328	Mus musulus PF2 regulator of nonsense transcripts homolog (yeast) (Up2), mFNA [NM.001081132] Mus musulus pre-Secilitodov-menorging for of (PoPI), mRNA [NM.001081132]	NM_021524	Pbef1	2.957	3.641	-1.783
A 52 P246716	Mus musculus adult male corpora guadrigemina cDNA, RIKEN full-length enriched library, clone:B230325K18 product:hypothetical protein, full insert sequence (AK080825)	AK080825	B230325K18F	2.862	4.100	-1.522
A_52_P81101		NM_027184	Ipmk	2.841	1.590	A/P
	Mus musculus SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily, a, member 4 (Smarcad), mRNA [NM_011417] Dna) (Hop40) homolog, subfamily B, member 14 (Smarcad), mRNA [NM_011417] Dna) (Hop40) homolog, subfamily B, member 14 (Smarcad), mRNA [NM_011417]	NM_011417	Smarca4 Dnajb14	2.759	2.542	-2.154
A_51_P233267 A_52_P157101			NAP053724-1	2.632	2.853	-1.161
A 52 P262275	Mus musculus ataxin 2 (Atxn2), mRNA (NM 009125)	NM_009125	Atxn2	2.513	1.634	-1.019
A_52_P18317	Mus musculus translocase of outer mitochondrial membrane 40 homolog (yeast), mRNA (cDNA clone MGC:48245 IMAGE:3326417), complete cds. [BC038887]	BC038887	Tomm40	2.502	1.425	-1.660
A_52_P568651	Mus musculus Alstrom syndrome 1 homolog (human) (Alms1), mRNA [NIM_145223]	NM_145223	Alms1	2.494	2.559	-1.126
A 52 P676744		NM_016973 NM_029166	St6galnac6 E030041M21F	2.477 2.411	1.475	-2.494
A 51 P2/4633	mus maculas ruicex curve coulou mazi gene (cosuou nazi rene, mena curve) (mena curv	NM_026430	Uxs1	2.411	3.875	-1.342
A 52 P239850	Mus musculus CREB binding protein (Crebbp), mRNA [NM_001025432]	NM 001025432	Crebbp	2.408	3.875 2.273	-2.193
A_52_P211759	Mus musculus pleckstrin homology domain containing, family A member 7 (Plekha7), mRNA [NM_172743]	NM_172743	Plekha7	2.386	2.537	-2.742
		AK020759	A430103D13F	2.353	2.074	-1.384
A 52 P118958		NM_023041 NM_007970	Pex19 Ezh1	2.353	1.866	-1.965
A 52 P1140541	mus indicause enhanced or zeste formiolity of constraints (carr), interver (www.dor/ard) Mus musculus enhanced or zeste formiolity (carr), interver (www.dor/ard) Mus musculus enhanced care (carr), interver (www.dor/ard)	AK078575	Uxs1	2.351	1.846	-1.236
A_52_P95471			NAP055900-1	2 3 3 9	1.796	-1.585
A 52 P444785	Mus musculus cDNA sequence BC037393 (BC037393), mRNA [NM_201369]	NM_201369	BC037393	2.328	1.726	-1.181
A_51_P155714		AK014457	Traf3ip1	2.301	2.476	-1.759
A_51_P160293	Mus musculus 0 day neonate lung CDNA, RIKEN full-length enriched Ibrary, clone: E030004.15 product unclassifiable, full insert sequence. [AK053116] Mus musculus mitogen-activated protein kinase kinase 4 (Map44), mRNA (MiN 006966)	AK053116 NM 008696	AK053116 Map4k4	2.301 2.300	2.285 2.064	-1.757
A 52 P237522		14141_000030	NAP049780-1	2.299	1.444	-1.092
A 51 P492456	Mus musculus hyaluronan synthase1 (Has1), mRNA [NM_008215]	NM_008215	Has1	2.277	2.135	-1.435
A_52_P222096	Mus musculus RIKEN cDNA 4931428F04 gene (4931428F04Rik), mRNA [NM_028888]	NM_028888	4931428F04R		4.433	-1.527
		AK032094 NM 172620	Zfp182	2.238	1.488	-2.749
A 51 P205170		NM 146175	Vps52 Zfp282	2.220	1.730	-1.174
A 52 P491273	Mars maculate and ingenerative (approximative (approximative)	AK046543	B430006D22F	2.197	1.986	-1.463
A 52 P199019	Mus musculus tripartite motif protein 6 (Trim6), mRNA [NM 001013616]	NM_001013616	Trim6	2.177	1.411	-1.315
A_52_P128612			NAP123204-1	2.166	1.643	-3.274
A 52 P185639	Mus musculus valy4:RNA synthetiase 2, mitochondrial (putathet) (Van2), mRNA [NM, 175137] Mus musculus soluto carrier family 2 fourcelobase transporters), membra [NM, 176137]	NM_175137 NM_011397	Vars2 Slc23a1	2.149	2.107 4.382	-1.121
A 51 P299393	www.smusculus.solute.camer.tamily.cs.intoiceoase transporters), memoer. 1(c)ccca1), mrxva (vm/ 0.132/1 PREDICTED. Www.smusculus.Ritken CONA 6720475.1098(k), mrXva (vm/ 0.132/1) PREDICTED. Www.smusculus.Ritken CONA 6720475.1098(k), mrXva (vm/ 0.132/1)	XM_983620	6720475J19R	2.124	4.302	-2.520
A_52_P674418	Mus musculus RIKEN cDNA 4930430F08 gene (4930430F08Rik), mRNA [NM_175128]	NM_175128	4930430F08R	il 2.117	2.761	-3.013
A 52 P502828	Mus musculus phosphodiesterase 2A, cGMP-stimulated (Pde2a), mRNA [NM_001008548]	NM_001008548		2.112	1.646	-1.122
A_52_P240020		NM_146165	Jtv1	2.071	2.222	-1.270
A 52 P429749		NM_019704 NM_001081251	Tmem115 Pbrm1	2.062	1.757 4.526	-1.570
A 51 P350752	Inter insedue payation (form), interventing (intervention) Nos musculus (2033 mitiger (2033), intervention (2007 665)	NM_007645	Cd37	2.057	2.505	-1.034
A_51_P326015	Mus musculus AXIN1 up-regulated 1 (Axud1), mRNA [NM_153287]	NM_153287	Axud1	2.055 2.052	1.979	-2.260
A_52_P368262		AK049064	Bcl7c	2.052	2.857	-1.085
A 52 P4937	Mus musculus Igase III, DNA, ATP-dependent (Lg3), mRNA (NM, 010716) Mus musculus ginde assembly 6 homolog (C. eligants (NM, 023246) Mus musculus ginde assembly 6 homolog (C. eligants (Sassb), mRNA (NM, 023246)	NM_010716 NM_028349	Lig3	2.052 2.046	10.447	-1.128
A 52 P538515	Muis misculus spinole assembly 6 nomicog (L. elegans) [cassas), mirkva [kw. [cos4] Muis musculus RH domain 1 (binki single-strander Juckie ass), mirkva [kw. [cos4] Muis musculus RH domain 1 (binki single-strander Juckie ass), mirkva [kw. [cos4]	BC049181	Sass6 R3hdm1	2.046	2.378	-1.021
A 52 P408237	mus maculas kar comain r (one anglessanded nucles acas), minure (other dominence) compare cas, compare cas, compare cas, compare cas,	AK044401	Sestd1	2.034	1.473	-3.081
A_51_P339344	Mus musculus transmembrane protein 81 (Tmem81), mRNA [NM_029025]	NM_029025	Tmem81	2.033	4.973	-3.694
A_52_P561377		NM_145505	AI450540	2.022	2.796	-1.138
A_51_P176797	Mus musculus LIM domain containing 2 (Limd2), mRNA [MN, 172397]	NM_172397	Limd2	2.022	1.574	-3.150 A/P
A 51 P319141	Mus musculus ecotropic viral Integration site 5 (EviS), mRNA [MN 007964] Mus musculus Are-related light stransfer (START) domain containing (5 Stard), mRNA [NM 023377]	NM_007964 NM_023377	Evi5 Stard5	2.013	2.216	-1.153
A 52 P534355	mus insolutes of exceeding ligit an and/or (or her/) during of logar up, move (ewe 223377) Mus musculus 3 days encorate thymus cDNA, RIKEN full-length enriched library, clone A83042FCB0 productanexin A7, full insert sequence. [AK041855]	AK041855	AK041855	2.003	1.522	-1.132
A 51 P464769	Mus musculus asp (abnormal spindle)-like, microcephaly associated (Drosophila) (Aspm), mRNA [NM 009791]	NM 009791	Aspm	1.989	1.531	-1.925
A_51_P477779	Mus musculus RAR-related orphan receptor alpha (Rora), mRNA (NM 013646)	NM_013646	Rora	1.978	1.957	-1.102
A_52_P660142	PREDICTED: Mus musculus SFT2 domain containing 3 (Stt2d3), mRNA [XM_464715]	XM_484715	Sft2d3	1.976	1.424	-1.145

A 51 D214906 Hillium murculus personal equamous malformation 2 bomolon (bumon) (Com2), mD10 D114 1460141	NM 146014	Ccm2	1 060	4 050	-1.742
A 51 P314895 Mus musculus cerebrai cuerebrai malformation 2 homolog (humana) (Com2), mRNA [NM 146014] A 52 P424000 Mus musculus molegne activated protein in Age beford protein 1 (Age beford), mRNA [NM 146014] A 52 P424000 Mus musculus CASP8 and FADD-like apoptosis regulator (Cfan, transcript variant 2, mRNA [NM 146014] A 51 P31409 Mus musculus CASP8 and FADD-like apoptosis regulator (Cfan, transcript variant 1, mRNA [NM 17089] A 51 P31409 Mus musculus transforming, acidi coled-coil containing protein 1 (Tacob); transcript variant 1, mRNA [NM 17089]	NM_146014 NM_011941	Mapkbp1	1.969 1.965	4.050 1.571	-1.879
A 51 P135491 Mus musculus CASP8 and FADD-like apoptosis regulator (Cflar), transcript variant 2, mRNA [NM_009805]	NM_009805	Cflar	1.950	2 351	-1.011
A 51 P331409 Mus musculus transforming, acidic coiled-coil containing protein 1 (Tact1), transcript variant 1, mRNA [NM 177089]	NM_177089 NM_173048	Tacc1	1.948	3.280	-1.148
A 52, Posse424 [Mus musculus Bpla pendentanderanderand are containing, Ark binaing protein a (sgaa), mkNA [NM_173048]	NM_173048 NM_153597	Gga3	1.945	1.906	-4.542
	NM 023243	Trpt1 Ccnh	1.936	1.454	-1.046
A, 51, 2531409 [Mus musculus trainstorming, acidic collection containing protein 1 (1 acid); trainscript variant 1, mitrVA [Mu, 17/089] A, 52, P53954, Mus musculus group associated, gamma adaptin era contraining, AFF bring protein 3 (Gga3), mRNA [Mu, 173048] A, 52, P19554, Mus musculus group associated, gamma adaptin era contraining, AFF bring protein 3 (Gga3), mRNA [Mu, 173048] A, 52, P19554, Mus musculus group associated, gamma adaptin era contraining, AFF bring protein 3 (Gga3), mRNA [Mu, 173048] A, 51, P48002, Mus musculus group associated, gamma adaptin era contraining, BFC bring Mu, 173048] A, 51, P48002, Mus musculus group associated, gamma (Gda6), mRNA [Mu, 008001] A, 51, P48002, Mus musculus acide-coil doratin containing (B (Ccod6)), mRNA [Mu, 17747] A, 52, P420344, Mus musculus acide-coil doratin containing (B (Ccod6)), mRNA [Mu, 17747]	NM_008801 NM_177471	Pde6d	1.928	1.991	-1.184 -1.046 -1.052
A 52 P423364 Mus musculus colled-coil domain containing 69 (Ccdc69), mRNA (NM 177471)	NM_177471	Ccdc69	1.925	2.495	-4.692
	AF180471 AK020736	Lpin1 A330105O20R	1.913	2.971	-1.623
A 52 P67510 Mus musculus auti male spinal cord CON, RIKER Mul-length enriched library, clone A330105O20 product unclassifiable, full insert sequence. [AK020736] A 52 P675101 Mus musculus auti male spinal cord CON, RIKER Mul-length enriched library, clone A330105O20 product unclassifiable, full insert sequence. [AK020736] A 51 P5195073 Mus musculus RIKEN CDNA A230050P20 gene (A230050P2018), mRNA [MU 01051331] A 52 P875174 Mus musculus RIKEN CDNA 4305056A11 gene (4930569A11 Rene (4930	NM 175687	A230050P20Ri	1.899	1 4 1 5	-1.083
A_51_P311905 Mus musculus transmembrane protein 103 (Tmem103), mRNA [NM_001081381]	NM 001081381	Tmem103	1.896	2.245 6.961	-1.607
A 52_P367774 Mus musculus RIKEN cDNA 4930566A11 gene (4930566A11 Rik), mRNA [NM_022468]	NM_029468	4930566A11Ri	1.884		-1.484
A 52, P288733 Mus musculus zinc finger, CCHC domain containing 7 (Zchc7), mRNA (NM, 177027) A 51, P128336 Mus musculus serine incorporator 5 (Serinc5), mRNA (NM, 172588)	NM_177027 NM_172588	Zcchc7 Serinc5	1.873	2.471 1.604	-1.225
A 52 P67388 Mus musculus 0 day neonate lung CDA, RICKE Null-length enriched library, clone E030038D23 product hypothetical protein, full insert sequence [AK087243]	AK087243	Tmcc1	1.852	1.515	-2.493
5 2 D563765 Mus musculus 12 days embryonic body between displayam ration and pack cDNA RIKEN full-length enriched library clone 0430038800 producticine element full insert eaguance (AK020450)	AK020459	Wtap	1.850	3.206	-4.002
A 51 P445765 Mus musculas dut mai by temp to employ temp to te	NM_053073	Lrp8	1.850	1.449	-1.456
A 52 P415385 Mus musculus adult male liver tumor cDNA, RIKEN full-length enriched library, clone CT30013012 product unclassinable, full insert sequence, [AK050084]	AK050084 AK048089	AK050084 9130206l24Rik	1.847	3.451	-1.236 -1.298
n 22 records must muscule to day employ near containing 5 (blue), mark the mark contect records and brock in insert sequence. (who evolg)		Otud5	1.844	1.460	-1.502
A 52_P537663 Mus musculus transformation related protein 53 binding protein 2 (Trp53bp2), mRNA [NM_173378]	NM_138604 NM_173378	Trp53bp2	1.843	2.847	-1.502 -1.109
A 52 P11192 Mus musculus 0 day neonate lung CDNA, RIKEN full-length enriched library, cione E030027N17 product hypothetical protein, full insert sequence. [AK063186] A 52 P12322 Mus musculus KH-Hype splicing regulatory protein (Khuny), mRNA [MN, 01613]	AK053185	Ccdc66	1.839	1.516	-1.048
A 52 P12325 Mus musculus KH-type splicing regulatory protein (Khsp), mRNA [NM_010613] A 52 P20329 Mus musculus KH-type splicing regulatory protein (Khsp), mRNA [NM_010613] A 52 P20329 Mus musculus KH-type splicing regulatory protein (Khsp), mRNA [NM_010613]	NM_010613 AK053567	Khsrp Cflar	1.837	2.214 2.506 2.035 2.696	-2.222
A 52 P23016 Mus musculus 0 day neovale cerebelium channel hearth ender the cerebelium channel hearth e	AK049083	Rbm26	1.822	2.035	-1.464
A 52 P83888 Mus musculus 0 day neonate eyebail CDNA, RIKEN full-length enriched library, clone E130111C10 product unclassifiable, full insert sequence. [AK053567] A 52 P329105 Mus musculus 0 day neonate cerebeltum CDNA, RIKEN full-length enriched library, clone E130111C10 product CTCL TUMOR ANTIGEN SE70-2 (CUTANEOUS T-CELL LYMPHOMA TUMOR ANTIGEN SE70-2) homolog [Homo sapiens], full insert sequence. [AK049083] A 52 P42796		NAP043943-1	1.822 1.819		-1.592
A 52 P476902 [Mus musculus Abelson helper integration site (Ahi1), mPNA [MN, 028203]	NM_026203	Ahi1	1.817	1.886	-1.174
A 52 P476602 Mus musculus Abelson helper integration site (Ah1), mRNA (NM_026203) A 51 P168355 Mus musculus adult male urinary bladder cDNA, RIKEN full-length enriched library, clone 9530081E14 product unclassifiable, full insert sequence [AK035649] A 52 P276251	AK035649	1700047A11Ri NAP106897-1	1.813	1.582	-1.974 -1.079
	AK081258	AK081258	1.805	1.608	-1.386
A 52 P395324 Mus maculus adut male corpus striatum cDNA. RIKEN Nul-length enriched library, clone C030033C23 product unclassifiable, full insert sequence. [AK081258] A 51 P395077 Mus maculus aequivilin (SW), ranscript variant 1, man (PMA), PMA 19515]	NM_153153	Svil	1.805	1.683	-1.032
	BC090643	2210418O10Ri	1,797	2.486	-1.086
A SE P11357 (Mus musculus Anket Cutrix a 21 via 10/10 gene, minink (Lufrix dute musc. 110/27, minuec. 30/62/260), complete cuts. [eCusuo45] A ST P12564 (Mus musculus myelioid)ymphoid or mixed-inaege leukemia 1 (Mi1), mRVA (NM 018521) A ST P455409 (Mus musculus ST A3332 (AS333), mRVA (MN 018521) A ST P25108 (Mus musculus ST A3332 (AS333), mRVA (MN 018521) A ST P25108 (Mus musculus ST A3332 (AS333), mRVA (MN 018521)	NM_019521 NM_001081049	Gas6 MII1	1.796	1.649	-1.846
In strength induction intercontain reproducting the strength induction inductination i	NM_001081049 NM 025275	X83328	1.792	1.419	-1.541 -1.021
A 52_P39326 Mus musculus poly A binding protection, https://www.anscript.variant.2, mRNA [NM_148917] A 52_P3932131 Mus musculus activin A receptor, type 1 (Acvr1), mRNA [NM_007394]	NM_148917	Pabpc4	1.782	1.637	-1.322
A 52 P352131 Mus musculus activin A receptor, type 1 (Acv1), mRNA [NM 007394]	NM_007394	Acvr1	1.774	1.439	-1.700
A 51 P372828 Mus musculus spermine oxidase (Smox), mRNA (NM 145533)	NM_145533 NM_145414	Smox Nsun5	1.767	1.521	-1.330
A 51_P221495 Mus musculus NOL1NOP2/Sun domain family, member 5 (Nsun5), mRNA [NM_145414] A 52_P92514 Mus musculus DNA segment, Chr 3, ERATO Doi 300, expressed, mRNA (cDNA clone MGC.64649 IMAGE 6400922), complete cds. [BC052702]	BC052702	D3Ertd300e	1.763	2.072	-1.369 -1.237
A 51 P344770 Mus musculus 12 days embry eveball CDNA, RIKEN Nill-length enriched library, clone D230019K20 product hypothetical Proline-rich region containing protein, full insert sequence, [AK051922]	AK051922	Tnrc6b	1.753	3.565	
A 51_P347770 Mus musculus 12 days embryo eyeball CDNA, RIKEN full-length enriched library, clone D230019K20 product hypothetical Proline-rich region containing protein, full insert sequence. [AK051922] A 51_P321958 Mus musculus Zwilch, kinetochore associated, homolog (Drosophila) (Zwilch), mRNA [NM_026507]	NM_026507	Zwilch	1.749	3.221	-1.114
A. 51_P366290 [Mus musculus RIKEN cDNA 6430526N21 gene (6430526N21Rik), mRNA [NM_001033383]	NM_001033383	6430526N21Ri	1.744	2.013	
A 51 P45130 Mus misculus tryptophan hydroxylase 1 (Dh1), mRNA (NM. 009414) A 52 P13971 Mus misculus tryptophan hydroxylase 1 (Dh1), mRNA (NM. 009414)	NM_009414 NM_008231	Tph1 Hdgf	1.744	1.610	-1.006
A 31 - Press to this insculus a pupulant hypotoxytes (1) (1) (1) (1) (1) (1) (1) (1) (1) (1)	AK004569	Cdc40	1.737	3.877	-2.013 -1.026 -2.366 -1.045 -1.627
A_51_P165984 Mus musculus ancient ubiquitous protein (Aup1), mRNA [NM_007517]	NM_007517	Aup1	1 732	2.125	-2.366
A 51 P453502 Mus musculus survival motor neuron 1 (Smn1), mRNA [NM_011420]	NM_011420	Smn1 BC050092	1.730 1.730	1.760	-1.045
A: 52 2495099 [Mus musculus cUNA sequence BC030092 (E0050092); mrNA [NM_151419] A: 51 P264929 [Mus musculus Mouse marmary turnor virus clore 68 An en ynecusior (env) and VSAG protein (vSAG) mRNA, complete cds [AF043688]	NM_181419 AF043688	Igkv14-111	1.730	1.553	-1.627
A 51 P394585 Mus musculus sorting nexin 22 (Snx22): mRNA INM 0010256121	NM_001025612	Snx22	1.707	1.917	-1.044
A 51 P224468 Mus musculus RIKEN CDNA 9430016H08 gene (9430016H08R), mRNA [NM 001081181] A 52 P224468 [Mus musculus RIKEN CDNA 9430016H08R), mRNA [NM 001081181] A 52 P204242 [Mus musculus RIKEN CDNA 9430016H08R), mRNA [NM 005082]	NM_001081181	9430016H08Ri	1,705	1.668	-1 443
A 52 P302422 Mus musculus mitogen activated protein kinase kinase kinase 12 (Map3k12), mRNA [NM_009582]	NM_009582	Map3k12	1.701	3.681 2.264	-1.211 -1.275 -1.059
A 51 P15030 Mus musculus phosphathylefananamine N-metrymarkersae (Permit, Nank (NML 00005)) A 52 P655167 Mus musculus 16 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:9630005N12 product unclassifiable, full insert sequence [AK035805]	NM_008819 AK035805	Pemt A630026N12Ri	1.698	2.264	-1.275
A DZ POSOTO Mus misculas to days resonate determinant durves, rocen numeringar emicines numering and emicines	AJ001373	ltgb1bp1	1.687	2.194 2.407	-1.039
A_52_P346438 [Mus musculus adult male medulla oblongata cDNA, RIKEN full-length enriched library, clone:6330547J17 product:unclassifiable, full insert sequence [AK032020]	AK032020	Atpaf1	1.682	1.513	-1.465
A 52 P206492 Mus musculus processing of precursor 4, ribonuclease P/MRP family, (S. cerevisiae) (Pop4), mRNA [NM 025390]	NM_025390	Pop4	1.675	1.612	-1.289
A 52 P996429 [Mus musculus 15 days embryo head cDNA, PilkEM full-length enriched library, clone D5300/31N17 product unclassifiable, full insert sequence [AK086649] A 52 P446205 [Mus musculus adsyntemin 1, mRNA (CDNA clone MCG): 45505], Morapite et al. (Eds. 2540) [MuS CB 2005	AK086649 BC053843	D930043N17R Clstn1	1.672	1.924	-1.791
A 51 P328926 Mus musculus thymopoletin (Tmpo) transprint variant 1 mRNA INM 0116051	NM 011605		1.659	1 4 3 5	-1.037
A 52 P13/F12/ Mus muscules and information of the second s	NM_029704 AK080694	Tmpo Ttc19	1.655	9.663	-1.810
A 52 P1004616[Mus musculus adult retina cDNA, RiKEN full-length enriched library, clone: A930001J16 product unclassifiable, full insert sequence. [AK080694]	AK080694	AK080694	1.653	1.805	-1.192
A 51 P483373 IMus musculus thioredoxin domain containing 5 (Txndc5), mRNA INM 1453671	NM_145367	Txndc5 TC1677196	1.648	2.647	-3.851 -1.572
A 52 P459750 Mus musculus ubiguitin protein ligase E3 component n-recognin 2 (Ubr2), mRNA (NM 146078)	NM_146078	Ubr2	1.648	1.771	-1.960
A 51 P509518 Mus musculus ral quanine nucleotide dissociation stimulator (Ralods). mRNA (NM 009058)	NM 009058	Ralgds	1.645	1.611	-2.308 -1.889
A_52_P433137 [Mus musculus DNA segment, Chr 12, ERATO Doi 551, expressed (D12Ertd551e), mRNA [NM_028731]	NM_028731	D12Ertd551e	1.642	2.776	-1.889
A 52 P88266 PREDICTED: Mus musculus similar to putative retrovirus-related gag protein (LOC686759), mRNA (ZM, X97691] A 52 P198767 (Mus musculus 1 days embys foreing hol-RAP, RIKER Hol-RAP, and RAP (ARA)	XM_976961 AK020029	LOC669759 Ints7	1.640	1.480	-1.803 -2.135
A 52 P14321 PREDICTED Mus musculus Wolf-Hirschtom syndrome candidate (fuman), trainer grupting strategy by the syndrome candidate (fuman), trainer grupting	XM_898331	Whsc1	1.627	1.513	-1.061
A 52, P14321 PREDICTED: Mus musculus Wolf-Hirschhorn syndrome candidate 1 (human), transcript variant 9 (Whsc1), mRNA [XM_898331] A 52, P322141 Mus musculus coiled-coil domain containing 88 (Ccdc88), mRNA [NM_001081291]	NM_001081291	Ccdc88	1.626	3.228	-1.046
	NM_144558	Bivm	1.626	P/A	-1.429
A 52 Pr20223 (mis madculs state, minimapolarineme variance front obtaining (semi), mixed (vec, "44-00) A 52 Pr20223 (Mis musculs statutin-conjugation errorme E23 f 102 F honolog, C 450 pr2023), mRNA (NM. 025895) A 52 Pr43351 (Mis musculs statutin-state) (Usp40), mRNA (NM. 0210323) (Mis Mis Mis Mis Mis Mis Mis Mis Mis Mis	NM_025985 NM_001033291	Ube2g1 Usp40	1.615	2.223	-1.170 A/P
A 51 P212107 Mus musculus catenin, beta like 1 (Cirmbit), mRNA (MM 025860)	NM_025680 NM_138598	Ctnnbl1	1.611	1.443	-1.149
		Ctnnbl1 D11Wsu99e	1.608	4.470	-1.470
A 52 P318667 Mus musculus prenatal alcohol-1 mRNA, complete cds. [AY223547] A 51 P377856 Mus musculus glutathione S-transferase, theta 3 (Gstt3), mRNA [NM_133994]	AY223547	AY223547	1.608	2.599	-1.257
A 51 - 2777350 Mus musculus glutatinone 5-transferase, theta 3 (15813), mirrAn [r/m 135994] A 52 - P251658 Mus musculus di days neonate stim toDNA, RIKEN full-lengti enriched library, done 4732465/J09 product MYOSIN-IXA homolog [Homo sapiens], full insert sequence. [AK028873]	NM_133994 AK028873	Gstt3 Myo9a	1.607	3.143 4.149	-3.022
A 51 P437737 Mus musculus dihydroorotate dehydrooenase (Dhodh). mRNA INM 0200461	NM 020046	Dhodh	1.601	1.693	A/P
A 52 P439932 Mus musculus colled-coll domain containing 130 (Codc130) mRNA INM 026350	NM 026350	Ccdc130	1.601	3.475	A/P
A 52 P302463 Mus musculus ADP-ribosylation factor-like \$A (Arl5a), mRNA [NM, 182994] A 51 P363564 Mus musculus transformation related protein 53 binding protein 2 (Trp53bp2), mRNA [NM, 173378]	NM_182994 NM_173378	Arl5a	1.600 1.600	1.741	-1.152
(A_D) _ 2003009 [MUIS musculus transformation related protein 3.2 linking frolem 2 (1(p):0502), mtVA [MM_112376] 6.5 D 1913260 [Muis musculus transformation related protein X3376] 6.5 D 1913260 [Muis musculus calcium/calmonders incluse]. Imama (Camk/D) Langer(p) L	NM_173378 NM_178597	Trp53bp2 Camk2g	1.600	2.553 2.101	-1.192
A 51 P132480 Mus musculas traismoniantor related protein y contracting protein y (mov (mov (mov (mov (mov (mov (mov (mov	NM 023040	Gfer	1.596	1.803	-1.009
IA 52 P532841 IMus musculus expressed sequence C87436 (C87436), mRNA INM 146170	NM 146170	C87436	1.592	1.401	-1.655
A 52 P326399 Mus musculus EK506 binding protein 11 (Ekbn11) mRNA INM 0241691	NM_024169	Fkbp11	1.587	3.505	-3.994
A 52 P674847 Mus musculus 5-azacytidine induced gene 2 (Azi2), transcript variant 1, mRNA (NM 013227) A 52 P16516 Mus musculus CDNA clone IMAGE 5368151	NM_013727 BC028949	Azi2 EG668383	1.585	1.649	-1.404
A 52_P641758 Mus musculus RIKEN CDNA A030007L17 gene (A030007L17Rik), mRNA (NM, 026637)	NM 026637	A030007L17Ri	1.579	1.723	-1.956
A_51_P234283 Mus musculus RAB5B, member RAS oncogene family (Rab5b), mRNA [NM, 011229]	NM_011229	Rab5b	1.578	1.571	-2.008

A_52_P555913 Mus musculus neurofibromatosis 2 (N/2), mRNA [NM_010898]	NM_010898	Nf2	1.576	2.133	-1.180
A_52_P24722 Mus musculus 16 days neonate thymus cDNA, RIKEN full-length enriched library, clone: A130073N12 product: unclassifiable, full insert sequence [AK038044]	AK038044	AK038044	1.572	1.540	-1.161
A 52 P331382 Mus musculus premature mRNA for mKIAA1167 protein [AK173119]	AK173119	Gripap1	1.566	1.419	-1.266
A 52 P419973 Mus musculus retinoblastoma 1 (Rb1), mRNA [NM 009029] A 51 P405290 Mus musculus tretinoblastoma 1 (Rb1), mRNA [NM 03553]	NM_009029 NM_033563	Rb1 Klf7	1.566	1.547	-1.909
A ST Prevose) Mus musculus krupperinke indiciti / (duiquitous) (km/), minva (twin Usasos) A S2 Prečeská Mus musculus pervisional membrane protein 4 (Pampel, minka (twin Usasos)	NM 021534	Pxmp4	1.562	2.372	-1.061
A 22 processor was indexide performance inclusion in the index of the	NM_028711	Sic25a27	1.551	1.642	-2.561
A 51 P125771 Mus musculus solute carrier family 25. member 27 (Sic25a27, mRNA PM, 108 025711) A 51 P125771 Mus musculus solute carrier family 25. member 27 (Sic25a27, mRNA PM, 108 105) A 51 P125827 Mus musculus solute carrier family 25. member 27 (Sic25a27, mRNA PM, 108 105)	NM 198108	BC023055	1.544	2.145	-1.393
A 51 P251245 Mus musculus plakophilin 4 (Pkp4), mRNA INM 0263611	NM 026361	Pkp4	1.541	1.744	-1.285
A_51_P477018 Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4930532K22 product:hypothetical Ribonuclease Rh-like structure containing protein, full insert sequence. [AK015947]	AK015947	Rnaset2a	1.539	1.605	-1.526
A 51 P272046 Mus musculus catenin (cadherin associated protein), beta 1 (Ctrinb1), mRNA INM 0076141	NM_007614	Ctnnb1	1.537	1.555	-1.113
A 52 P188593 Mus musculus gene model 447, (NCB) (Gm447), mRNA [NM, 001007590]	NM_001007590	Gm447	1.534	1.617	-2.945
A 52 P80021 Mus musculus CKLF-like MARVEL transmembrane domain containing 7, mRNA (cDNA clone IMAGE 3982549), complete cds. [BC026773]	BC026773	Cmtm7	1.530	1.544	-1.271
A 51 P457113 Mus maculus retinoblastoma-like 2 (RbI2), mRNA [NM 011250] A 52 P427394 Mus maculus activitational-like 2 (RbI2), mRNA [NM 011250] A 52 P427394 Mus maculus activitational activitational bitrary, clone A530076C18 product unclassifiable, full insert sequence. [AK080173]	NM_011250 AK080173	Rbl2 E130112N10Ri	1.527	1.653 3.222	-1.716
A: 32, P#2739 With inductive adult miler adult and vent curver, intern univerging remote adults, full insert sequence, protocol 15 A 51 P253527 With simulations info finger and PVPV like domains containing proteine (RR), transcriptive advantation, run insert sequence, protocol 15 A 51 P253527 With simulations info finger and PVPV like domains containing proteine (RR), transcriptive advantation, run insert sequence, protocol 15 A 51 P253527 With simulation advantation advantation (RR), transcriptive advantation, run insert sequence, protocol 15 A 51 P253527	NM 026097	Rff	1.525	2.568	-1.440
A 51 P199410 [Mus musculus mRNA for Gh3-3, isoform of Gb2, complete cash, D85748]	D85748	Grb2	1.522	1.912	-1.225
A 52_P152468 [Mus musculus 3 days neonate thymus CDNA, RIKEN full-length enriched library, clone A630010G17 product unclassifiable, full insert sequence. [AK153595]	AK153595	AK153595	1.520	1.558	-1.274
A 52 P569759 Mus musculus 12 days embryo female mullerian duct includes surrounding region cDNA, RIKEN full-length enriched library, clone 6820426C07 product BETA-CENTRACTIN (ACTIN-RELATED PROTEIN 1B) (ARP1B) homolog (Homo sapiens), full insert sequence (AK078508)	AK078508	Actr1b	1.519	1.774	-1.185
A_51_P401527 Mus musculus RNA methyltransferase like 1 (Rnmt/1), mRNA [NM_183263]	NM_183263	Rnmtl1	1.515	1.621	-1.088
A_52_P373480 Mus musculus adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone:B230345H22 product unclassifiable, full insert sequence. [AK046154]	AK046154	AK046154	1.514	3.111	-1.151
A_51_P316129 Mus musculus autophagy-related 4A (yeast) (Atg4a), mRNA [NM_174875]	NM_174875	Atg4a	1.508	1.642	-1.167
A 52_P91359 Mus musculus zinc finger protein 655 (Zfp655), transcript variant 2, mRNA [NM_001083958]	NM_001083958		1.505	1.725	-1.913
A 51 P310254 Mus musculus RIKEN cDNA 3110048E14 gene (3110048E14Rik), transcript variant 1, mRNA [NM_133750]	NM_133750	3110048E14Ri	1.504	1.897	-1.090
A 51 P462546 [Mus musculus GDP-mannose prophosphorylase A (Gmppa), mPNA [MM, 133708]	NM_133708	Gmppa	1.500	2.429	-1.885
A 52 P590038 [Mus musculus bifunctional apoptosis regulator (Bar), mPNA [NM, 025976]	NM_025976 NM_026295	Bfar Ctdp1	1.496	2.145	-1.565
A 51 P313467 [Mus musculus CTD (carboxy-terminal domain, RNA polymerase), polypeptide A) phosphatase, suburul 1 (clopt), mRNA [Mu 302328] A 52 P5954 [Mus musculus adult male offactor with Unil-ength enriched library, doi:ef30402612 product.hypothetical protein, full insert sequence, [AK032149]	AK032149		1.495	1.518	-2.600
A: 52 Post93 Mus musculus adui male omacory orain c.Urv., Nicken Yui-lengin eminine linaray, come e4.94/U/2:12 product rypometical protein, fui insert sequence. [ANU32149] A: 51 Post9954 [Mus musculus aduitinate omacory postpolicity aduitination of the sequence and the sequence aduitination of the sequenc	NM 172276	Ppargc1a Sfrs8	1.492	5.538	-1.300
A 52 P86771 Mus muscula spincing ladvin, agiminativing muncup muscular agiminative muscular spincing ladvin agiminativing muncup muscular spincing ladving agiminativing ladving agiminativing muncup muncup muscular spincing ladving agiminativing muncup muscular spincing ladving agiminativing ladving agiminativin	AK050998	AK050998	1.488	1.553	-2.110
A 52 P67464 Mus musculas BREN CDNA 281005622 (2RX), mRN 10005611	NM_080561	2810055G22Ri	1.487	3.228	-1.463
A 51 P314264 Mus musculus signal sequence receptor, beta (Ssr2), mRNA [NM 025448]	NM_025448	Ssr2	1.487	1.950	-2.163
A 52 P595006 Mus musculus vacuolar protein sorting 72 (veast) (Vps72), mRNA [NM 009336]	NM_009336	Vps72	1.485	2.535	-1.361
A 52 P636394 Mus musculus membrane-associated ring finger (C3HC4) 6 (March6), mRNA [NM 172606]	NM_172606	March6	1.485	1.446	-1.224
A 52 P51936 Mus musculus 13 days embryo lung cDNA, RIKEN full-length enriched library, clone: D430022A14 product unclassifiable, full insert sequence [AK084992]	AK084992	D430022A14R	1.482	2.167	-1.598
A 52_P597800 Mus musculus ets variant gene 6 (TEL oncogene) (Etv6), mRNA [NM_007961]	NM_007961	Etv6	1.480	1.731	-1.977
A 52 P755438 Mus musculus 7 days neonate cerebelium cDNA, RIKEN full-length enriched library, clone A730094G16 productunspliced dna for. PROLIFERATION RELATED ACIDIC LEUCINE RICH PROTEIN PAL31 (SIMILAR TO ACIDIC PROTEIN RICH IN LEUCINES) homolog [Mus musculus]	AK043419	Anp32b	1.479	2.375	-1.236
A 52 P256279 Mus musculus zinc finger and BTB domain containing 11, mRNA (cDNA clone IMAGE 6485438) [BC055403]	BC055403 AK049524	Zbtb11 AK049524	1.479	1.858	-1.390
A 52 P695324 [Mus musculus 7 days embryo whole body CDNA, RIKEN Nul-Hength enriched library, cohore C430019H13 product RIKEN CDNA 4930421J07 gene, Lill insert sequence [AK049524] A 52 P495977 [Mus musculus 9 days embryo whole body CDNA, RIKEN Nul-Hength enriched library, cohore C430019H13 product RIKEN CDNA 4930421J07 gene, Lill insert sequence [AK049524]	AK049524 AK083507	D030036P13R	1.477	1.629	-1.004
A 32 - Passor I mus musculus 5 days eminyo wine daug 5 curve, nice ni umengar eminicagi curve a product uncassimate, numiniseri sequence (nkrodsor) A 52 - Passor I mus musculus 5 dai poli pagi curve, nice ni umengar eminicagi curve a product uncassimate, numiniseri sequence (nkrodsor)	NM_001002897	Atagh	1.469	1.514	-1.553
A 51 P37152 [PREDICTED: Mus musculus on of sevenies and onling (Concernance) (market (Musculus) (market (XM 127051	Sos2	1.467	1.848	-1.276
A 51 P314929 Mus musculus 0 day meonate head cDNA, RIKEN full-length enriched library, clone 483242SN18 product DIACYLGLYCEROL KINASE, DELTA (EC 2.7.1.107) (DIGLYCERIDE KINASE) (DGK-DELTA) (DAG KINASE DELTA) (130 KDA DIACYLGLYCEROL KINASE) (FRAGMENT) homolog (Homo	AK076439	Dgkd	1.467	2.081	-1.400
A_51_P185701 Mus musculus dynamin 1-like (Dnm1i), transcript variant 1, mRNA [NM_152816]	NM 152816	Dnm1I	1.465	1.435	-1.370
A 52 P394561 Mus musculus adult male small intestine cDNA. RIKEN full-length enriched library. clone:2010001F03 product:ADULT MALE SMALL INTESTINE CDNA. RIKEN FULL-LENGTH ENRICHED LIBRARY. CLONE:2010001F03. FULL INSERT SEQUENCE. full insert sequence. [AK008004]	AK008004	Txnrd2	1.461	2.034	-1.074
A_51_P101858 Mus musculus discs, large homolog 1 (Drosophila) (DIg1), mRNA [NM_007862]	NM_007862	Dlg1	1.460	1.481	-1.339
A 51 P463270 Mus musculus aduit male hippocampus cDNA. RIKEN full-length enriched library, clone C630012M08 product: SNRNA ACTIVATING PROTEIN COMPLEX 50 KDA SUBUNIT (SNAPC 50 KDA SUBUNIT) (PROXIMAL SEQUENCE ELEMENT-BINDING TRANSCRIPTION FACTOR BETA SUBUNIT) (PSE-B	AK049933	Snapc3	1.460	1.983	-1.042
A 51 P491835 Mus musculus adult male hippocampus cDNA, RIKEN full-length enriched library, clone 2900009J20 product inferred: RIKEN cDNA 2900009J20 gene, full insert sequence. [AK013507]	AK013507	2900009J20Ril	1.453	1.528	-1.623
A 51 P411874 Mus musculus 3 days neonate thymus CDNA. RIKEN Villength enriched library. clone A630074J11 product:unclassifiable, full insert sequence. [AK042243]	AK042243	Ankhd1	1.452	4.256	-1.146
A 52 P24593 Mus musculus zinc finger, DHHC domain containing 20 (Zdhike20), mRNA [NM 022492] A 51 P244593 Mus musculus zinc informerich Gia (Gestratorogylatamic acid) polypegiba 2 (Prog2), mRNA [NM 022499]	NM_029492 NM_022999	Zdhhc20	1.452	2.193	-1.472
A.51 F 254725 Into a misculus plantima do local and control to a control do local and control and c	AK039370	Prrg2 AK039370	1.450	1.806	-1.191
A 51 p1/25/8 Mix mission control mission (crick) mRA INM CONTRCT:	NM_007652	Cd59a	1.446	4.622	-1.321
A. 51; P142896 [Mus musculus CD59a antigen (Cd59a), mRNA [PM. 007652] A. 52; P242386 [Mus musculus mRNA for PEP2Pa protein, complete co.ds. [D1302]	D13802	Runx1	1.444	2.224	-1.886
A_52_P137145 Mus musculus 13 days embryo male testis cDNA, RIKEN full-length enriched library, clone:6030423J02 product:weakly similar to CDNA FLJ14936 FIS, CLONE PLACE1010194, WEAKLY SIMILAR TO SPLICING FACTOR, ARGININE/SERINE-RICH 2 [Homo sapiens], full insert	AK031401	Prpf38a	1.443	2.878	-5.650
A_51_P203710 Mus musculus taube nuss (Tbn), mRNA [NM_022015]	NM_022015	Tbn	1.441	1.704	-1.291
A_51_P465988 Mus musculus glucosidase, alpha; neutral C (Ganc), mRNA [NM_172672]	NM_172672	Ganc	1.439	1.880	-2.121
A_51_P257684 Mus musculus staufen (RNA binding protein) homolog 1 (Drosophila) (Stau1), mRNA [NM_011490]	NM_011490	Stau1	1.433	2.528	-2.159
A 52 P497193 Mus musculus nucleolar complex associated 2 homolog (S. errevisiae) (Noc2), mRNA [NM_021303]	NM_021303	Noc2l	1.433	1.482	-1.206
A 51 P359983 Mus musculus Rho GTP3es activating protein 17 (Arhgap17), mRNA [NM, 144529]	NM_144529	Arhgap17	1.431	1.478	-1.170
A. 52, P303595, Mus musculus RIKEN CDNA 170022003 gene (170022003Rik), mRNA [Mu 027405] A. 54, P303195, Mus musculus RIKEN CDNA 170022003. gene (170022003Rik), mRNA [Mu 027405]	NM_027405 NM_025822	1700020003Ri	1.430	1.527	-1.553
A. 51. P139165 Mus musulus arginne/seiner-ich colled-coil 1 (farc1), mRNA [MM 025822] A. 52. P52049 [Mus musulus Stel2:04] keinase (yeast (5k), mRNA [MN.009289]	NM_025822 NM_009289	Rsrc1 Sik	1.428	1.519	-1.409
A 32 F020V9 INUS INSCUIS O TEZVINE ATIABE (VESS) (JOK, INTON [VM, OUZ20] A 51 F22032 (JUK unsculute arriter family 19 (haimine transporter), member 2 (SIc19a2), mRNA [NM_ 054087]	NM 054087	Sic19a2	1.425	1.894	-1.004
A 51 - 733138 Mus musculus Buck/like Z (Bick) Res Z (Bick	NM 007537	Bcl2l2	1.425	2.604	-1.161
A 51 P130824 Mus musculus component of oligomenic golgi complex 8 (Cog8), mRNA [NM, 139229]	NM_139229	Cog8	1.420	2.536	-1.561
A_51_P250433 Mus musculus additional sex combs like 2 (Drosophila) (Asxl2), mRNA [NM_172421]	NM 172421	Asxi2	1.418	1.581	-1.076
A_52_P135155 Mus musculus two pore segment channel 2 (Tpcn2), mRNA [NM_146206]	NM_146206	Tpcn2	1.411	2.298	-2.821
A_51_P300717 Mus musculus syntaxin binding protein 1 (Stxbp1), mRNA [NM_009295]	NM_009295	Stxbp1	1.410	2.816	-1.272
A_51_P422369 Mus musculus RIKEN cDNA 2010001/J22 gene (2010001J22Rik), mRNA [NM_001013022]	NM_001013022		1.409	3.152	-1.396
A 52 P137361 Mus musculus transmembrane channel-like gene family 4 (Tmc4), mRNA [NM_181820]	NM_181820	Tmc4	1.408	1.874	-1.904
A 51 P207940 Mus musculus transmembrane protein 117 (Timem117), mRNA [NM] 178789	NM_178789	Tmem117	1.406	1.435	-1.450
A 52 PB64057 (Mus musculus snurpotini 1 (Snupn), mRNA (NM, 178374) 6 51 P079070 (Mus musculus 5 funz methods and falls (Musch and administrational and administrational administr	NM_178374 AK048190	Snupn AK048190	1.404	2.414	-1.209
A_51_P220040 [Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched library, clone:C130039105 product.unclassifiable, full insert sequence. [AK048190]	IMR.048190	AN048190	1.403	2.51/	-1.052

Table S4. Genes downregulated in 2C9.G2-treated HSCs cultured in the presence of TPO

The values are fold changes in 2C9.G2-treated vs. IgG-treated cells under the indicated conditions. A and P represent detection the calls "Absence" and "Presence," respectively.



A 52 P258291 Mus musculus E26 avian leukemia onogene 1. 5' domain (Ets1), transcript variant 1, mRNA [NM_011808] A 51 P275496 Mus musculus cDNA clone IMAGE 5065404 [BC029971] A 52 P38393 T	NM_011808 BC029971	Ets1 BC026762	-2.261	-1.405 -1.552	1.980
		TC1685454	-2.234 -2.246 -2.229 -2.224 -2.211 -2.211 -2.209 -2.209	-2.225	1.082 1.265 1.182
A. 52, P898397	NM_011828	Hs2st1	-2.229	-1.429	1.265
A 52 P410449 Mus musculus interleukin 4 induced 1 (I4i1), mRNA (INM 010215)	NM_010215 NM_028834	II4i1 2210009G21Ri	-2.224	A/P -1.954	1.182
[A_5] P2/1762 Mus musculus Ritken CDNA 2210009521 gene (221000952) Riski, transford varianti, I, mKNA [MM] (22854) [A_51] P262107. Mus musculus Ritken CDNA 2210009521 Riski, transford varianti, I, mKNA [MM] (22854) [A_51] P262107. Mus musculus Ritken CDNA 221009521 Riski, transford varianti, I, mKNA [MM] (22854)	AK028913	1700041B20Ri	-2.212	-1.954	1.196
A 51 F 2004D Mus musculus to days module sin Lotive, Intel numerity entroped interview and structure protein, but miser sequence (Process of Last Structure) and the sequence (Process of Last Structu	NM_028666	5430432M24Ri	-2.209	-2.124 -2.427 -5.144	1.704 4.972
A 52_P505584 Mus musculus expressed sequence Al314976 (Al314976), mRNA (NM, 207219)	NM_207219	AI314976	-2.205	-5.144	1.439
A_52_P373846 Mus musculus polycomb group ring finger 3 (Pcgf3), mRNA [NM_172716]	NM_172716	Pcgf3			4.040
A 52 P390227 Mus musculus Rho guanine nucleotide exchange factor (GEF) 12 (Angerl2), mRNA (Mu, 027144)	NM_027144 NM_001039530	Arhgef12 Parp14	-2.198	-1.629 -1.491	2.029
A 52 PY9/580 Mus musculus poy (ADP-nose) poymerase taminy, member 14 (Parp14), mKrNa [NM, u1/1039530] A 52 PY9/581 Mus musculus GB22-aleladador proteina (Zarp2), mBAI [NM, u1/1039530]	NM 010815	Parp14 Grap2	-2.181	-1.491 A/P	1.517
A 52 P125238 Mus musculus additional sectorshila (Assimily, mink) (min (Min 2003))	NM 001039939	AsxI1	-2.169 -2.169 -2.145	10 717	2011
A_51_P125629 Mus musculus regulator of G-protein signaling 12 (Rgs12), mRNA [NM_173402]	NM 173402	Rgs12	-2.169	-2.309	2.448 2.205 4.746
A 52 P402394 Mus musculus transmembrane protein 121 (Tmem121), mRNA [NM] 153776]	NM_153776 NM_172717	Tmem121	-2.145	-2.160	2.205
A 52 P327971 Mus musculus checkpoint with forkhead and ring Inger domains (chr), mRNA [NM 172717] A 52 P327972 Mus musculus checkpoint with forkhead and ring Inger domains (chr), mRNA [NM 172717]	NM_172717 NM_010840	Chfr Mthfr	-2.145		4.746
A 52 P413947 Mus musculus 5:10-methylenetetrahydrofolate reductase (Mhrf), mRNA [NM_010840] A 52 P284588 Mus musculus DNA segment, Chr 11, ERATO DO 497 expressed (D11E/n5497e), mRNA [NM_029976] A 52 P39459 Mus musculus michaes (DNA) B (D104, mRNA [NM_0108440] C 52 P3945 Mus musculus michaes (DNA) B (D104, mRNA [NM_0108446] C 52 P3945 Mus musculus michaes (DNA) B (D104, mRNA [NM_0108446] C 52 P3945 Mus musculus michaes (DNA) B (D10446) C 52 P3945 Mus musculus musculus michaes (DNA) B (D10446) C 52 P3945 Mus musculus michaes (DNA) B (D10446) C 52 P3945 Mus musculus musculus michaes (DNA) B (D10446) C 52 P3945 Mus musculus musculus michaes (DNA) B (D10446) C 52 P3945 Musculus michaes (DNA) B (D10446) C 52 P3945 Musculus musculus michaes (DNA) B (D10446) C 52 P3945 Musculus michaes (NM_029976	D11Ertd497e	-2.143 -2.130 -2.125 -2.124 -2.122 -2.108 -2.108 -2.107	-1.975	1.387 2.307 1.619
A 52 P6994 Mus musculus helicase (DNA) B (Helb), mRNA [NM. 080466]	NM 080446	Helb	-2.130	-1.439	1.619
A_52_P81928 Mus musculus Smg-5 homolog, nonsense mediated mRNA decay factor (C. elegans) (Smg5), mRNA [NM_178246]	NM_178246 NM_033521	Smg5	-2.125	-7.673	1.160
A 52_P470316 Mus musculus lysosomal-associated protein transmembrane 4B (Laptm4b), mRNA (NM_033521)	NM_033521	Laptm4b	-2.124	-1.452	1.180
A 51_P140590 Mus musculus staffmm-like 3 (Stm3), mKNe [NR (00133] A 52_P0110 - Mus musculus staffmented afficience packet (Mode)) mPNA (ML 04090)	NM_009133 NM_016969	Stmn3	-2.122	A/P	1.254
A 52 PPR341 Mixe miseuite calcula is (canch) mRNA MIM 072602	NM_007602	Myadm Cann5	-2.100	-2.201	1 129
A. 52 P254458 Mus musculus bAA segrenes Chri 11, ERATO Doi 497, expressed (D11End497e), mRNA [NM_029976] A. 52 P5954 Mus musculus financiase (DNA) E [Hubb, mRNA [NM_008446] A. 52 P59152 Mus musculus financiase (DNA) E [Hubb, mRNA [NM_008446] A. 52 P59162 Mus musculus sociase (DNA) E [Hubb, mRNA [NM_008446] A. 52 P10569 Mus musculus sociase (DNA) E [Hubb, mRNA [NM_009133] A. 54 P104590 Mus musculus sociase (Jacobia (Hubb, mRNA [NM_009133] A. 54 P104590 Mus musculus and differentiation marker (Mgadm), mRNA [NM_01696] A. 52 P61516 Mus musculus and protein transmere (Mgadm), mRNA [NM_01696] A. 52 P6159 Mus musculus and protein transmere (Mgadm), mRNA [NM_01762] A. 52 P6150 Mus musculus and protein transmere (Mgadm), mRNA [NM_1762] A. 52 P6150 Mus musculus and protein transmere (Mgadm), mRNA [NM_1762] A. 52 P65050 Mus musculus and protein transmere (Mgadm), mRNA [NM_1762] A. 52 P650507 Mus musculus transfing finger protein 157, mRNA (CNA come IMAGE EA011088) [ECOS0707] A. 51 P257530 Mus musculus transfing finger protein 157, mRNA (CNA come IMAGE EA011088) [ECOS0707] </td <td>NM_133214</td> <td>Capn5 BC017612</td> <td>-2.102</td> <td>A/P -2.281 -2.163 -1.511</td> <td>1.254 1.356 1.129 1.207 2.252 2.465 1.050 1.535 2.130 1.439 1.834 1.663</td>	NM_133214	Capn5 BC017612	-2.102	A/P -2.281 -2.163 -1.511	1.254 1.356 1.129 1.207 2.252 2.465 1.050 1.535 2.130 1.439 1.834 1.663
A_52_P508506 Mus musculus RIKEN cDNA 4930025D01 gene (A930025D01 Rik), mRNA [NM, 178762]	NM 178762	A930025D01R	-2.102 -2.082 -2.080 -2.074	-2.062 -1.714 -1.495	2.252
A 51 P170641 Mus musculus WD repeat domain 21 (Wdr21), mRNA [NM_030246]	NM_030246	Wdr21	-2.080	-1.714	2.465
A 22_P900b93 [Mus musculus dematan suitate epimerase-like (Use), mRNA [MM 001081316] 6.51_2754007 [Mus musculus dematan suitate epimerase-like (Use), mRNA [MM 001081316] 1.51_2754007 [Mus musculus dematan suitate epimerase-like (Use), mRNA [MM 001081316]	NM_001081316 BC053070	Dsel Rnf157	-2.074	-1.495	1.050
In the second se	AK163829		-2.065	-2.011	2 130
A 51 P21530 Mus musculus bone marcow marcophage cDNA, RIKEN full-ender index of the control product hypothetical Z-finger, RING/Zim finare RIN	AK151379	Mapk8 Rnf180	-2.065 -2.050 -2.050 -2.045	-2.011 -3.507 -5.529 -1.571	1.439
A_51_P278103 Mus musculus Stam binding protein (Stambp), mRNA [NM_024239]	NM_024239	Stambp	-2.045	-1.571	1.834
A_51_P111259 Mus musculus CDK2-associated protein 2 (Cdit2ap2), mRNA [NM 026373]	NM_026373	Cdk2ap2		-2.057	1.663
A 52 P244098 [Mus musculus adult male thymus cDNA, RIKEN full-length enriched library, clone; 5330488H16 product unclassifiable, full insert sequence [AK031010] 520 P24698 [Mus musculus adult male thymus cDNA, RIKEN full-length enriched library, clone; 5330488H16 product unclassifiable, full insert sequence [AK031010]	AK031010 NM 015824	AK031010 Orc3l	-2.035	-3.283 -1.843	2.405
A 25 2944039 Mus musculus adult male thymus CDNA. RIKEN full-length enriched library, done 3530489116 product unclassifiable, full insert sequence [AK031010] A 52 P10609 Mus musculus adomucediate triphosphate diphosphotycrolase 5 (Enrpds), transcript variant 1, mRNA [NM 007647] A 52 P450046 Mus musculus adomucediate triphosphate diphosphotycrolase 5 (Enrpds), transcript variant 1, mRNA [NM 007647] A 51 P450046 Mus musculus adomucediate triphosphate diphosphotycrolase 5 (Enrpds), transcript variant 1, mRNA [NM 007647] A 52 P450146 Mus musculus adamucediate triphosphate diphosphotycrolase 5 (Enrpds), transcript variant 1, mRNA [NM 007647] A 51 P37772 Mus musculus aparagnen linked group dipersate strates (JAg0), mRNA [NM 007647] A 52 P451371 Mus musculus adamucediate domain containing 1 (Papd1), mRNA [NM 026157] A 51 P30772 Mus musculus protein tito (IRDB), mRNA [NM 0076179] A 51 P30723 Mus musculus aphermannositic (IRDB), mRNA [NM 00708179] A 51 P30732 Mus musculus aphermannositic (IRDB), mRNA [NM 00708179] A 51 P30732 Mus musculus aphermannositic (IRDB), mRNA [NM 00708179] A 51 P30732 Mus musculus aphermannositic (IRDB), mRNA [NM 00708179] A 51 P30732 Mus musculus aphermannositic (IRDB), mRNA [NM 00708179] A 51 P30732 Mus musculus aphermannositic (IRDB), mRNA [NM 00708179] A 51 P308235 Mus musculus aphermannositic (IRDB), mRNA [NM 00708179] A 52 P258464 Mus musculus aphermannositic (IRDB), mRNA [NM 00708174] A 52 P258464 Mus musculus aphermannositic (IRDB), mRNA [NM 00708174] A 52 P59587 Mus musculus aphermannositic (IRDB), mRNA [NM 00708774] A 52 P59587 Mus musculus aphermannositic (IRDB), mRNA [NM 00708774] A 52 P59587 Mus musculus aphermannositic (IRDB), mRNA [NM 00708714] A 52 P59587 Mus musculus aphermannositic (IRDB), mRNA [NM 02714] A 52 P59587 Mus musculus aphermannositic (IRDB), mRNA [NM 02714] A 52 P59587 Mus musculus aphermannositic (IRDB), mRNA [NM 02714] A 52 P59587 Mus musculus aphermannositic (IRDB), mRNA [NM 02714] A 52 P59587 Mus musculus aphermannositic (IRDB), mRNA [NM 02714] A 52 P59587 Mus m	NM_015824 NM_007647		-2.035 -2.030 -2.026 -2.025 -2.023 -2.023 -2.023	-1.843	2.405 2.382 2.937 3.218 1.221 3.122 3.408
A 52 PE51371 Mus musculus asparanie-inter dycosylation 8 homolog versa table 1.3-but h	NM 199035	Entpd5 Alg8	-2.025	-1.476	3.218
A 51 P367772 Mus musculus PAP associated domain containing 1 (Papd1), mRNA [NM, 026157]	NM 026157	Papd1	-2.023	-3.038 -1.456	1.221
A_52_P358138 MMANB01 Mus musculus lysosomal alpha-mannosidase (Man2b) gene, exon 1 [AF044174]	AF044174	Papd1 AF044174	-2.022	-1.456	3.122
A 51_P111018 [Mus musculus HEAT repeat containing 58 (Heatr5b), mRNA [NM, 001081179]	NM_001081179	Heatr5b		-2.524 -3.893 -1.837	3.408
A 51 P2053C Mus musculus gene trap locus F36 (Gli3b), mRNA [NN 025294]	NM_025294 NM_001033142	Gtlf3b Rnf166	-2.000	-3.893	1.217
A 51 P2668/T Mus musculus ring imger protein 126 (Rritchin 126 Rritchin 144528)	NM 144528	Rnf126	-2.000	-6.187	2 548
A 52 P602771 Mus musculus serine/arginine-rich protein secific kinase 2 (Smk2), mRNA (NM .009274)	NM 009274	Srpk2	-2.000	-3.925	2.548
A 52 P265945 Mus musculus 12 days embryo eyeball cDNA, RIKEN full-length enriched library, clone D230026F01 product unclassifiable, full insert sequence. [AK142083]	AK142083	Srpk2 C330050A14R	-1.985	-1.780	1.085
A_51_P380527 Mus musculus RIKEN cDNA 4631427C17 gene (4631427C17Rik), mRNA [NM_021414]	NM_021414	4631427C17Ri		-1.780 -1.420 -1.626	1.660
A 52 P505827 Mus nusculus cytochrome b5 reductase 4 (cyto5r4), mRAA [NM, 024195]	NM_024195	Cyb5r4	-1.969	-1.626	1.505
[A: 52 PS0623 [Mus musculus 1b days neonate trymus curva, knckn full-indign entitiched lidrary, coline at Jource 1b product L2-inducibile 1-cell kinase, full insert sequence. [AkU3/554] [A: 52 PS1621] [Mus musculus home homeing in [Amore 1] (Amore 1) area (III Amore 1) (Amore 1) area (IIII Amore 1) (Amore 1) area (IIII Amore 1) (Amore 1)	AK037554 NM_152134	Homer1	-1.969	-1.947 -2.374	1.524 1.085 1.660 1.505 2.014 2.563 1.036 1.458
A 51 P4658 Mus musculus RilkEN cDNA 430473A06 gene (4330473A06Rk), mRNA [NM. 001081012]	NM 001081012	4930473A06Ri	-1.961	-1.826	1.036
A 52 P239381 Mus musculus 12 days embryo embryonic body between diaphragm region and neck cDNA, RIKEN full-length enriched library, clone 9430032H24 product unclassifiable, full insert sequence. [AK034763] A 51 P362973 Mus musculus ADP-ribosylation factor GTPase activating protein 3 (Artgap3), mRNA [NM 025445]	AK034763	E330009E22Ri	-1.954	-1.667	1.458
A 51 P362973 Mus musculus ADP-ribosylation factor GTPase activating protein 3 (Artgap3), mRNA [NM. 025445]	NM_025445 NM_023168	Arfgap3	-1.937	-1.725 -1.869	1.272
A 51 P200053 Mus musculus glutamate receptor, ionoropic, N-methyl D-asparate-associated protein 1 (glutamate binding) (Grna), mRNA [NM_023168]	NM_023168 NM_173181	Grina 3110050N22Ri	-1.935	-1.869	1.141
A. ST P 50267/3 Mus muscula ALP-recognition factor ST Para excitating protein s (Artiglio), mixika (NM 202446) A. ST P 200058 A. ST P 200058 A. ST P 20058 A. ST P 20057 Mus musculas RIKEN cDNA S11050N22 gene (311050N22RA), miXik (NM 173181) A. SZ P 20177 A. SZ P 20177 A. SZ P 20177 Mus musculas RIKEN cDNA 150061N15 gene (150061N15 gene (150061N1640), miXik (NM 202339) A. SZ P 20177 A. SZ P 20177 A. SZ P 20177 Mus musculas RIKEN cDNA 150061N15 gene (150061N15 gene (150061N1640), miXik (NM 202339) A. SZ P 20177 A. SZ P 20177 A. SZ P 20177 Mus musculas RIKEN cDNA 150061N15 gene (150061N15 gene (150061N1640), miXik (NM 202339) A. SZ P 20177 A. SZ P 20177 A	14141_173101	NAP123168-1	-1.931 -1.930	-2.051 -3.059	1.013
A 52 P405177 Mus musculus C1q and tumor necrosis factor related protein 6 (C1qthf6), mRNA [NM_028331]	NM_028331	C1qtnf6	-1.918	_2 220	1 164
A_52_P110257 Mus musculus RIKEN cDNA 1500041N16 gene (1500041N16Rik), mRNA [NM_026399]	NM_026399	1500041N16Ri	-1.917	-1.518 -2.116	1.397
	NM_028166	1600014C10Ri	-1.905	-2.116	1.332
(A, 51 P153882 [Mus musculus sperm antigen with calponin homology and colled-coil domains 1 (Specc1), mRNA [NM_001029936] A, 52 P15166	NM_001029936	Specc1 NAP108265-1	-1.898	-1.484 A/P	1.397 1.332 2.360 4.004
A 24 P10100 A 25 P10100 A 25 P10100 A 26 P10100 A 27 P	NM 008326		-1.889	-1.400	4.004 1.277 1.622 2.285 1.088 1.292 1.223 1.027
A_51_P183940 Mus musculus serinethreonine kinase 39, STE20/SPS1 homolog (yeast) (SIK39), mRNA [NM_016866]	NM 016866	Irgm Stk39	-1.886	-1.400 -2.537 -1.586	1.622
A_51_P230799 Mus musculus ATPase, Ca++ transporting, plasma membrane 1 (Atp2b1), mRNA [NM_026482]	NM_026482	Atp2b1	-1.885	-1.586	2.285
A 52 P522754 Mus musculus EBNA1 binding protein 2 (Ebna1692).mENA [MM_026932]	NM_026932	Ebna1bp2	-1.885	-2.341	1.088
(r. 2) [72:1100] mus musuus guga automingen, gugai suuraminge, 2) (suugada), mirkva (rob. 10/1/4/) (h. 5) 129/2473) Mus musuuk autu maa coho CDNA. RIKEN bilanoh anoiteen dihaan coho CDNA (RIKK1) moduci unclassifable. full insert senuence (AK1)18518)	NM_013747 AK018518	Golga5 9030418K01Ril	-1.881	-1.437 -1.401	1.292
A 51 P211903 Mus musculus adul male colon cDNA. RIKEH full-length enriched library, clones 900418K01 product unclassifiable, full insert sequence [AK018518] A 51 P284700 Mus musculus adult male colon cDNA. RIKEH full-length enriched library, clones 900418K01 product unclassifiable, full insert sequence [AK018518] A 52 P64048 Mus musculus inpartite modi protein 21 (rim21), transcript variant (mRNA [NM 009277]	NM 009277	Trim21	-1.869	-2.210	1.027
A 52 P632191 Mus musculus nuclear transcription factor, X-box binding 1 (Nkrt), mRNA [NM 023739]	NM_023739 NM_008577	Nfx1	-1.866	-1.571 -1.597	2.105
A 22 Poistor into intoacous guarder transcription factor, X-box briefing 1 (MrJ), mRNs (Mm 02273) A 51 Pa72801 Mus musculus solute carrier family 3 (adivators of dibasic and neutral amino add transport), member 2 (Sic3a2), mRNA [NM_008577] A 51 Pa72801 Mus musculus solute carrier family 3 (adivators of dibasic and neutral amino add transport), member 2 (Sic3a2), mRNA [NM_008577] A 52 Pa72839 Mus musculus solute carrier family 7 (cationic amino add transport, y+ system), member 5 (Sic7a5), mRNA [NM_011404]	NM_008577	Slc3a2	-1.859	-1.597	1.173
A 52_P249228 Mus musculus KIKEN CDNA 25103040308 gene (25103046008K), mRNA tak MM 027434]	NM_027434 NM_011404	2610304G08Ri	-1.857	-2.990 -2.747	3.305
In service more investment assumed warment entity / (calcinit, attitude antipotente), yr systemin, inemaet 3 (sit/ad), intriver pre- (a 51) P200356 Miles misecular biotecholicaete C. beta 2 (PE02), mRNA INN 177568	NM_011404 NM_177568	SIc7a5 Picb2	-1.854	-2 424	1.004
A. 51 P260356 Mus musculus phospholipase C, beta 2 (Picb2), mRNA [NM_177568] A. 51 P270146 Mus musculus cyclin H (Conh), mRNA [NM_023243]	NM_023243	Ccnh	-1.833	-2.424 -3.706 -2.706	2.471
A 52 P341373 Mus musculus SLAIN motif family, member 1 (Slain1), mRNA (NM, 198014) A 51 P421876 Mus musculus interferon regulatory factor 7 (H7), mRNA (NM, 018850)	NM 198014	Slain1	-1.833	-2.706	2.471 2.929 1.041
A 51 P421876 Mus musculus interferon regulatory factor 7 (H7), mRNA (INM 016850)	NM_016850	lrf7	-1.828		1.041
	NM_011960	Parg	-1.827	-1.746	1.354 1.050 2.334 1.533 1.160
mos moscinia presentigradovanime reprincipationali mental and	NM_013796 NM_177305	Nagpa Arl4c	-1.827	-1.571 -3.119	2 334
A 51 P496804 Mus musculus deaminase domain containing 1 (Deadc1), mRNA (NM 025748)	NM_025748	Deadc1	-1.813	-1.613	1.533
A 51 Pr3050 Mus musculus N-acetylquicosamines (Parg. Introductional Programmes (Parg. Introductiona	AK041653	Stil	-1.810	-3.047	1.160
[A_52_P1083688 [Mus musculus adult male diencephalon cUNA, KIKEN full-length enriched library, clone:9330184N06 product unclassifiable, full insert sequence. [AK034379]	AK034379	AK034379	-1.809	-1.775	6.558
[A: 52: P3224/9] Mus musuulus 12 days embryo spinal cord cDNA. RIKEN full-length emriched library, clone C530045D03 product; pryuvate kinase 3, full insert sequence. [AK083076] [A: 51: P130038]	AK083076 NM 013509	Pkm2 Eno2	-1.802	-1.839 -1.664	6.558 1.052 1.278
(x, 5) r 1 souzo mus eriuses z, gamia rezuriais (zniz), mitve (MM U1509) 16.51 P33897: Miss missulus colorbone 5 for MSA III M 255581	NM_013509 NM_025558	Eno2 Cyb5b	-1.798	-1.004	1.2/8
A 51 P30825 [Miss musculos shorts/me b5 yes (Cybb), mRNA MR 02558] A 51 P218612 [Miss musculos 16 days neonate thymus cDNA, RIKEN full-length enriched library, clone A130029B16 product.5-methyltetrahydrofolate-homocysteine methyltransferase, full insert sequence. [AK037599]	AK037599	Mtr	-1.795	-2.006	1.022 1.038 2.935 1.276
A 52_P9392		NAP037484-1	-1.792	-1.439	2.935
A_52_P590474 Mus musculus cyclin L1 (Ccni1), mRNA (NM_019937)	NM_019937	Ccnl1	-1.789	A/P	1.276
A 52 P50972 miles intescues to dars incremente infinites Curriers, nuclei numerary endites induces to produce entities infinites integration access to produce entities induces to produce entities integration access in integration access in integration access in integration access in access integration access in access in access integration access in access integration access in access integration access in access in access integration access in access integration access in access integration access a	NM_009371	Tgfbr2	-1.786	-2.206	1.671
A. 22, 297229 CleUX57, HUMAN (GeUX57) ALtH2996, partial (47%) [TC1619366] A. 52, 293537 J. Misa musculus alamyirkNa synthesis (rans): (AML 146217]	NM 146217	TC1619366 Aars	-1.781	-5.249 -2.416	5.279 1.963
A 22 P30337 Wus initiacuus adamy-invok synthetiae (valis), initive (valis) more (valis) mo	NM 028922	Ppapdc2	-1.779	-1.871	1.555
A 51 P118024 Mus musculus trigatite motif-containing 65 (Trim65) mRNA INM 1788021	NM_178802	Ppapdc2 Trim65	-1.779	-2.040	1.389
A 52 P407022 Mus musculas tradicis more or financia or (minor)	NM_177411	Rab5b	-1.771	-1.801	1.222

A 52 P9260	Mus musculus expressed sequence AA536717 (AA536717), transcript variant 1, mRNA (NM_001024512] Mus musculus expressed sequence AA536717 (AA536717), transcript variant 1, mRNA (NM_001024512] Mus musculus pressor of used fromodig Orosophila (Sub), transcript variant 1, mRNA (NM_001752] Mus musculus gene masociated appressor of used fromodig Orosophila (Sub), transcript variant 1, mRNA (NM_001752] Mus musculus gene masociated appressor of used fromodig Orosophila (Sub), transcript variant 1, mRNA (NM_001752] Mus musculus gene masociated appressor of used from transcript variant 1, mRNA (NM_001752] Mus musculus gene masociated appressor of used from transcript variant 1, mRNA (NM_001752] Mus musculus gene masociated gene (Sappa), transcript variant 1, mRNA (NM_001752] Mus musculus gene masociated gene (Sappa), transcript variant 1, mRNA (NM_001752] Mus musculus gene (Sappa), transcript variant 1, mRNA (NM_001752) Mus musculus gene masociated gene (Sappa), transcript variant 1, mRNA (NM_001752) Mus musculus gene (Sappa), transcript variant 1, mRNA (NM_001752) Mus musculus gene masociated gene (Sappa), transcript variant 1, mRNA (NM_001752) Mus musculus gene (Sappa), transcript variant 1, mRNA (NM_001753) Mus musculus gene (Sappa), transcript variant 1, mRNA (NM_001753) Mus musculus gene (Sappa), transcript variant 1, mRNA (NM_001773) Mus musculus gene methylionanferase 3 (Sapta), mRNA (NM_0020241] Mus musculus gene methylionanferase 3 (Sappa), mRNA (NM_0020241] Mus musculus gene methylionanferase 3 (Sappa), mRNA (NM_0020241] Mus musculus gene (MACE 6413001, containing frame ethilt register (Sappa), fragociated methylionanferase 3 (Sappa), fragociated methylionanferase 5 (Sappa), fragociated methylionanferase 5 (Sappa), fragociated methylionanferase 3 (Sapp	NM_001024512	44536717	-17	55 -5.63	3 2452
A 52 P331212	Mus missious senses sequence recourt / rectourt / instant in mitror (mitror fun borezo)	NM_026493	Cspp1	-1.7	55 -5.63 55 -1.71	3 2.452 1 1.131
A_52_P603184	Mus musculus suppressor of fused homolog (Drosophila) (Sufu), transcript variant 1, mRNA [NM_015752]	NM_015752	Sufu	-1.7	51 -2.36	8 3.342
A_52_P628067	Mus musculus cell division cycle associated 3 (Cdca3), mRNA [NM_013538]	NM_013538	Cdca3	-1.7	50 -2.53	1.408
A_51_P359259	Mus musculus sperm associated antigen 9 (Spage), transcript variant 1, mRNA (NM, 027569)	NM_027569	Spag9	-1.7	50 -2.55	0 1.814
A_51_P382500	Mus musculus adult male drain UNDEFINED_CELL_LINE CUNA, NICEN Tui-length enriched library, clone.MSC.10/9K13 product.Hypothetical AMP-dependent synthetase and ligase containing protein nomolog [Mus musculus], tuil insert sequence. [AK14/562]	AK147562 NM 009662	Dip2b Alox5	-1.7	40 -2.68 36 -3.50	0 1.960 3 1.153
A 51 P127279	Mills millscalad analytication and employing the second state of t	NM 133858	4930504E06R	-17	36 -1.93	6 1.320
A 51 P391825	Mus musculus exosome component 10 (Exosc1) .mRNA (NM 016699)	NM_133858 NM_016699	Exosc10	-1.7	25 -1.46	
A_52_P605122	Ras and Rab interactor 2 [Source:MarkerSymbol/Acc:MGI:1921280] [ENSMUST00000071473]		Rin2	-1.73	23 -3.40	4 1.117
A_52_P181468	Mus musculus SET domain containing (lysine methyltransferase) 8 (Setd8), mRNA [NM_030241]	NM_030241	Setd8	-1.7	19 -1.44	5 1.419
A_52_P366980	Mus musculus tetraspanin 17 (1span17), mRNa [NM 028841]	NM_028841 BC059816	Tspan17	-1.7	18 -2.16	1.495
A 52 P568/81	Mus musculus CUNA clone IMAGE 5413001, containing trame-sinit errors (5CUS9816)	NM_198176	Sec63 Fastkd5	-1.7	12 -1.77	0 1 202
A 51 P485800	Nus musculus rAST Milase dufitatis 5 (raskuds), mirtve [twin_1stor1o] Mus musculus rAST Milase dufitatis 5 (raskuds), mirtve [twin_1stor1o]	NM_196176		-1.7	11 -2.29 10 -2.77 09 -1.67	1.303 7 4.362 76 1.334 18 1.521 15 1.256 16 1.350 12 1.684
A 51 P450123	Mus musculus mitchondria ribosomal protein L36 (Mrc/30, mRNA (NM 503/63)	NM_010048 NM_053163	Dgcr2 MrpI36	-1.70	-1.67	6 1.334
A 52 P287492	Mus musculus zinc finger, DHHC domain containing 13 (Zdhhc13), mRNA [NM_028031]	NM_028031 NM_178051	Zdhhc13	-1.70	-2.13	8 1.521
A_52_P69756	Mus musculus MTERF domain containing 2 (Mterfd2), mRNA [NM_178051]	NM_178051	Mterfd2	-1.70	-1.92	5 1.256
A_51_P170050	Mus musculus zinc finger protein 248 (Zfp248), mRNA [NM_028335]	NM_028335 BC055403	Zfp248	-1.70	-1.64	3 1.350
A 52 P 154005	Mus musculus zinc imiger and bill biomain containing 11, mittee (cDirec cline whole 5-965945) [BCU059403] Mus musculus duit majo cholo cDMA. Differ thill particular theory of contract. Different containing 11, mittee (cDirec cline 2003/2003)	AK033450	Zbtb11 Gapud1	-1.70	01 -3.92 00 -1.56	2 1.004
A 51 P387123	Mus misculas aduri male coon curves, kincur tionengui eminuted undary, curve sodozor dou productimeneo. Kincur curve enzore sequence [kincurded]	NM 011854	Gapvd1 Oasl2	-1.6	-1.84	6 1.724
A 52 P31125	Mus musculus 6-phosphofructo-2-kinase/fructose-2.6-biphosphatase 2, mRNA (cDNA clone MGC:25723 IMAGE:3979400), complete cds. [BC018418]	BC018418	Pfkfb2	-1.6	-1.62	4 1.017
A_51_P332602	Mus musculus surfeit gene 1 (Surf1), mRNA [NM 013677]	NM_013677	Surf1	-1.6	90 -1.90	9 2.370
A_51_P517157	Mus maculus cDNA done INAČE 5413001, containing tame-shift errors [BC05816] Mus maculus FX1 kinase donianis 5 (Fask50, InRNA [NM, 18917] Mus maculus DiGeorge syndrome ortical region gene 2 (Dg20), mRNA [NM, 05183] Mus maculus DiGeorge syndrome ortical region gene 2 (Dg20), mRNA [NM, 05183] Mus maculus DiGeorge syndrome ortical region gene 2 (Dg20), mRNA [NM, 05183] Mus maculus DiGeorge syndrome ortical region gene 2 (Dg20), mRNA [NM, 05183] Mus maculus DiGeorge syndrome ortical region gene 2 (Dg20), mRNA [NM, 05183] Mus maculus AITERF domain containing 2 (MinefQ), mRNA [NM, 17051] Mus maculus arc finger and BTB domain containing 11, mRNA (DNA clone IMAGE 645438) [BC055403] Mus maculus 2:nt finger and BTB domain containing 11, mRNA (DNA clone IMAGE 645438) [BC055403] Mus maculus 2:nt finger and BTB domain containing 11, mRNA [NM 01854] Mus maculus 2:nt finger and BTB domain containing 11, mRNA [NM 17854] Mus maculus 2:nt finger and BTB domain containing 11, mRNA [NM 018543] Mus maculus 2:-5 oligoaderiyates z (macultis z) Mus maculus z (macultis z)	NM_011854 BC018418 NM_013677 NM_028766 NM_001081230	Tmem43	-1.6	-2.51	8 1.344
A_52_P681659	Mus musculus microbubile-associated protein 9 (Mtag9), mRNA [ML_001081230]	NM_001081230	Mtap9	-1.6	37 -1.47	9 1.153
A 52 P209942	Nus musculus camtine paimito/irtansrerase 1c (cptro), mNNA [NM 1530/9]	NM_153679 NM_001001932	Cpt1c Eea1	-1.6	33 -4.63 79 -1.43	1 1.013
A 52 P299832		NM 018797	Pixnc1	-1.6	79 -1 96	3 1 209
A_51_P521216	Mus musculus CCAAT/enhancer binding protein (C/EBP), gamma (Cebpg), mRNA [NM_009884]	NM 009884	Cebpg	-1.6	76 -2.12	0 1 184
A_52_P473644	Mus musculus septin 6, mRNA (cDNA clone MGC: 19033 IMAGE: 4168214), complete cds. [BC010489]	BC010489 NM_021542	Sept6	-1.6	73 -1.53	5 1.357
A_51_P267861	Mus musculus potassium channel, subfamily K, member 5 (Kcnk5), mRNA [NM, 021542]	NM_021542	Kcnk5	-1.6	-2.35	15 1.357 11 1.907 15 1.777
A_52_P681488	Mus maculus sufeti giene 1 (Surf1), mRNA [NM, 013577] Mus musculus microtubule associated protein 9 (Mag5), mRNA [NM, 027876] Mus musculus microtubule associated protein 9 (Mag5), mRNA [NM, 027876] Mus musculus microtubule associated protein 9 (Mag5), mRNA [NM, 027876] Mus musculus microtubule associated protein (Surf1), mRNA [NM, 027876] Mus musculus and y molosome antigen 1 (East1), mRNA [NM, 027876] Mus musculus and y molosome antigen 1 (East1), mRNA [NM, 027876] Mus musculus active molosome antigen 1 (East1), mRNA [NM, 027876] Mus musculus Active molosome antigen 1 (East1), mRNA [NM, 029884] Mus musculus Active molosome antigen 1 (East1), mRNA [NM, 029884] Mus musculus Active molosome antigen 1 (East1), mRNA [NM, 029884] Mus musculus Active molosome antigen 1 (East1), mRNA [NM, 02984] Mus musculus Active molosome antigen 1 (East1), mRNA [NM, 02984] Mus musculus Active molosome antigen 1 (East1), mRNA [NM, 02984] Mus musculus Active molosome antigen 1 (East1), mRNA [NM, 02984] Mus musculus Active molosome antigen 1 (East1), mRNA [NM, 02984] Mus musculus Active molosome antigen 1 (East1), mRNA [NM, 02984] Mus musculus Active molosome antigen 1 (East1), mRNA [NM, 02984] Mus musculus Active molosome antigen 1 (East1), mRNA [NM, 02984] Mus musculus Active molosome antigen 1 (East1), mRNA [NM, 02084] Mus musculus Active molosome antigen 1 (East1), mRNA [NM, 02084] Mus musculus Active molosome antigen 1 (East1), mRNA [NM, 02084] Mus musculus Active molosome antigen 1 (East1), mRNA [NM, 02084] Mus musculus Active molosome antigen 2 (East1), mRNA [NM, 02084] Mus musculus Active molosome antigen 2 (East2), mRNA [NM, 02084] Mus musculus Active molosome antigen 2 (East2), mRNA [NM, 02084] Mus musculus Active molosome antigen 2 (East2), mRNA [NM, 02083] Mus musculus Active molosome antigen 2 (East2), mRNA [NM, 02083] Mus musculus Active molosome antigen 2 (East2), mRNA [NM, 02083] Mus musculus Active molosome antigen 2 (East2), mRNA [NM, 02083] Mus musculus Active molosome antigen 2 (East2), mRNA [NM, 02083] Mus musculu	NM_026343	Stx17	-1.6	70 -1.94	5 1.777
A 51 P2/1208	Intus musculus angiovernismi ir, type i receptior-associated protein (-kgrup), mKNA [NM_U09642]	NM_009642 NM_011014	Agtrap Opre1	-1.6	30 -2.04	1 3.452
A 51 P424959	Instantiation of the technologies, instantiation of the technologies in technologies in the technologies in techno	NM 007528	Oprs1 Bcl6b	-1.6	57 -2.04	0 1.403
A_52_P251425	Mus musculus RIKEN cDNA D030074E01 gene (D030074E01Rik), mRNA [NM 029491]	NM 020401	D030074E01F	-1.6	57 -3.07 54 -1.58	1.405 1.568 2 2.289 12 3.617 19 1.581 18 1.091
A_51_P397003	Mus musculus abhydrolase domain containing 13 (Abhd13), mRNA [NM_001081119]	NM_001081119	Abhd13	-1.6	51 -1.93	2 3.617
A_52_P507305	Mus musculus isoamyl acetate-hydrolyzing esterase 1 homolog (S. cerevisiae) (lah1), mRNA [NM_026347]	NM_026347	lah1	-1.64	45 -1.78	9 1.581
A_51_P292073	Mus musculus hydroxyacy[glutathione hydrolase-like (Hagh), mRNA [NM 026897]	NM_026897	Haghl AK051825	-1.64	43 -1.67	8 1.091
A 51 P152892	Mus musculus 12 days emoryo eyedani cuNA, Kitken tui-lengtin enniched library, clone U230Uber 19 product CU3 antigen, zeta polypeptide, tuil insert sequence. [AKUS1825]	AK051825 NM 030263	AK051825 Psd3	-1.6	39 -1.91 37 -2.02	1 097
A 52 P590701	Mus musculus previsioni and Secri Volnain Containing 3 (* 500), transvink vanani 1, interver (vm. 500203)	AK122344	2310047C04R	-1.63	31 -1.44	7 1.007
A 52 P27864	Mus musculus sarcoglycan, epsilon (Sqce), mRNA [NM 011360]	NM 011260	Sgce	-1.6	29 -1.45	9 1.222
A 51 P430014	Mus musculus platelet-activating factor receptor (Ptafr), mRNA [NM_001081211]	NM_001081211 NM_009748	Sgce Ptafr	-1.6	27 -2.23 26 -1.52	6 1.953
A_51_P432449	Mus musculus blocked early in transport 1 homolog (S. cerevisiae) (Bet1), mRNA [NM_009748]	NM_009748	Bet1	-1.63	26 -1.52	3 2.721
A_52_P510877	Mus musculus Bcl2-like 1 (Bcl211), mRNA [NM_009743]	NM_009743	Bcl2l1	-1.6	24 -1.58	5 1.777
A 52 P/4/190	Mus musculus u day neonate thymus CUNA, KIKEN tull-length enrinced library, clone A43009 KUV product unclassinable, tull insert sequence. [AK040400]	AK040400 NM_001081077	AK040400 Cwf19I1	-1.6	22 -1.77 16 -1.52	8 12.101 2 1.464
A 51 P461219	Mas miscular converting the control of the control	NM_178693	Coq4	-1.6	14 -1.56	3 6.395
A 52 P254174	Mus musculus nuclear receptor subfamily 3, group C, member 1 (Nr3c1), mRNA [NM_008173]	NM 008173	Nr3c1	-1.6		1.107 13 6.395 1.292 1.008 12 1.507
A_52_P569240	Mus musculus NACHT and WD repeat domain containing 1 (Nwd1), mRNA [NM_176940]	NM_176940	Nwd1	-1.6	11 -1.73	2 1.008
A 52 P291428	Mus musculus RIKEN cDNA 1700001E04 gene (1700001E04Rik), mRNA (NM 029288)	NM_029288	1700001E04R	-1.6	11 -1.52	2 1.507
A 52 P514352	Mus musculus potassium channel, subfamily K, member 5 (Kcrk5), mRNA [NM_021542]	NM_021542 Z78155	Kcnk5 Z78155	-1.6	11 -1.58 10 -2.58	15 1.035 13 1.354
A 51 P217369	M. musculus partai cochear inntva (coche 4975)[27:0150] Mus musculus ET2 (a talometer mainteanance) bomolon (\$ peravidia) /Talo?) mRNA (NM 027880)	NM_027880	Telo2	-1.6	-2.50	4 1.134
A 52 P423021	Mus muscular Lizer, from and the manufactor of managed to careful and the mass (managed to careful and the managed to careful and	NM 028059	Zfp654	-1.6	-2.31	2 1611
A_51_P301052	Mus musculus RIKEN cDNA 1810008A18 gene (1810008A18Rik), mRNA [NM, 133998]	NIM 133008	Zfp654 1810008A18R	-1.6	2.78	8 2.000
A_52_P314571	Mus musculus chitinase domain containing 1 (Chid1), mRNA [NM_026522]	NM_026522 NM_173750	Chid1 2700007P21R	-1.6	-1.79	1 1.470
A 51 P126835	M musculus partial cochiese mRNA (clone 48°F) [Z78155] Mks musculus TE2, telomere ministerance 2, henologi (S cerviaige) (Telo2), mRNA [NM, 02780] Mks musculus TE2, telomere ministerance 2, henologi (S cerviaige) (Telo2), mRNA [NM, 02780] Mks musculus TE2, telomere ministerance 2, henologi (S cerviaige) (Telo2), mRNA [NM, 02780] Mks musculus TERCI coOA (15 Obox 13 gene (17000x81 Rein, minister) (Telo2), mRNA [NM, 02780] Mks musculus TERCI coOA (15 Obox 13 gene (17000x7124) segme (270007724) se	NM_173750	2700007P21R		-1.63	6 2.000 11 1.470 18 1.248 /P 1.735
A 52 P467439	INUS INUSCUUS AUULITINEE UTIVIS CUTVA, TRICEN UNI-INTERIO ENTRY, CONCESS/APOUSTU DIPOLICIT/OPOTECIA (DOTE), ALIA 154/15/ INUS INUSCUUS 2 Class programma dulli fangle purch child landh anno entroped (INTA) (Concer Research Eurol 2), Ika 1. full insert sequence. [AK054364]	AK134157 AK054364	5033406O09R Cd99l2	i -1.6	06 A	1./35
A 52 P507368	Mus musculus alutathione 5-transferase, C-terminal domain containing (Soticity, MRAN NM) (2023)	NM 026231	Gstcd	-1.5	-1.63	1.388
A 52 P512877	Mus musculus adult male bone cDNA, RiKEN full-length enriched library, clone:9830005E11 product.unclassifiable, full insert sequence. [AK036397]	NM_026231 AK036397	AK036397	-1.5	98 -4.79	8 2.272
A_51_P372874	Mus musculus D4, zinc and double PHD fingers family 2 (Dpf2), mRNA [NM_011262]	NM 011262	Dpf2	-1.5	-2.53	9 1.115
A 52 P771228	INUS musculus 2 days pregnant adult temate ovary CLIVA, KIKLEN tul-length enriched library, clone:E330010G20 product unclassifiable, full insert sequence. [AK054284]	AK054284 NM_021887	AK054284	-1.5		3 1.771
A 52 P263870	Integritude Integritude Internet Lincopput (IJCI), Internet (Immung Linco) (Code2), ImRNA [NM 178347]	NM_021887 NM_178347	ll21r Cdc23	-1.5	53 -1.52 77 -1.94	6 1.611
A 51 P468531	Mus musculus ATP-binding cassette, sub-family F (GCN20), member 3 (AbC1), mRA (NM 013852)	NM_013852	Abcf3	-1.5	73 -1.58	4 2.120
A_52_P588262	PREDICTED. Mus musculus RIKEN cDNA C730024G19 gene, transcript variant 1 (C730024G19Rik), mRNA [XM_132975]		C730024G19F	-1.5	72 -1.46	
A_51_P442838	Mus musculus RIKEN cDNA 2810422020 gene (2810422020Rik), mRNA [NM_027279]	NM_027279	2810422O20R	i -1.5	72 -1.60	9 1.207
A 51 P325889	Nus musculus 16 days neonate thymus cDNA, RIKEN Nul-length enriched library, clone:A130019C19 product unclassifiable, full insert sequence [AK037440]	AK037440	4933407L21R	-1.5	71 -1.72	4 1.028
A 52 P682456	Mus maculus interfeukin 21 receptor (II21), mRNA [NM. 021867] Mus maculus AIRCPACC33 cell division projet 23, yeash. https://www.networks.interfeukin 21 receptor (II21), mRNA [NM. 02187] Mus maculus AIR2-binding cassetts, sub-family F (GCN20), member 3 (AbcB), mRNA [NM. 178347] Mus maculus AIR2-binding cassetts, sub-family F (GCN20), member 3 (AbcB), mRNA [NM. 178347] Mus maculus RIKEN CONA 2310422020 gene (2810422020H3), mRNA [NM. 178347] Mus maculus RIKEN CONA 2310422020 gene (2810422020H3), mRNA [NM. 178347] Mus maculus RIKEN CONA 2310422020 gene (2810422020H3), mRNA [NM. 101807] Mus maculus RIKEN CONA 2310422020 gene (2810422020H3), mRNA [NM. 1019019 product unclassifiable, full insert sequence [AK037440] Mus maculus RIKEN CONA 231042104 [NM. 20164] binary, clone C230030421 product unclassifiable, full insert sequence [AK037440] Mus maculus RIKEN CONA 231042104 [NM. 20164] binary, clone C230030421 product unclassifiable, full insert sequence [AK037440] Mus maculus RIKEN CONA RIKEN full-heigh enricheel binary, clone C23003421 product hypothetical protein, full insert sequence [AK03740] Mus maculus RIKEN CONA RIKEN full-heigh enricheel binary, clone C30034311 product hypothetical protein, full insert sequence [AK03740] Mus maculus RIKEN CONA RIKEN full-heigh enricheel binary, clone C30034311 product hypothetical eliademai/ymphona 2, full insert sequence [AK077913] Mus maculus RIKEN CONA RIKEN full-heigh enricheel binary, clone C30034311 product B-cell eliademai/ymphona 2, full insert sequence [AK077913] Mus maculus RIKEN CONA RIKEN full-heigh enricheel binary, clone C30034311 product B-cell eliademai/ymphona 2, full insert sequence [AK077913] Mus maculus RIKEN CONA A 2010207105 gene (2610207105Rik), mRNA [NM, 02011] Mus maculus RIKEN CONA 2610207105Rik, mRNA [NM, 2011] Mus maculus RIKEN CONA 2610207105Rik, mRNA [NM, 201018141 Mus maculus RIKEN CONA 2610207105Rik, mRNA [NM, 20101814]	NM_027421 AK082305 AK077913	Ints2 Dev1	-1.5	71 -1.42 71 -1.49	1.465 19 1.207 14 1.028 13 1.104 10 1.210 10 1.038 14 1.230 5 1.033
A 52 P438280	Internetworks of very increase devocation doney, maker thermagnet simulation linety, control could unit by proteins, cut in test sequence. [AV07213]	AK077913	Pex1 Bcl2	-1.5	70 -2.10	0 1.038
A_51_P347728	Mus musculus NFU1 iron-sulfur cluster scaffold homolog (S. cerevisiae) (Mu1), mRNA (NM, 020045)	NM_020045	Nfu1	-1.5	70 -1.89	4 1.230
A_52_P178904	Mus musculus SEH1-like (S. cerevisiae (Seh1i), transcript variant 2, mRNA [NM_028112]	NM_028112	Seh1I	-1.56	59 -1.47	5 1.033
A_51_P457171	Mus musculus RIKEN EDNA 2810207/05 gene (2810207/05 Rik), mRNA [NM_001031814]	NM_001031814	2610207105Ril	-1.5	58 -1.53 58 -1.52	1.989 3 1.537
A 51 P242027	Intus musculus syrosine 3-monoxygenase artivation protein, beta polypeptide (YMAB), mKNA (INM U19/53) Illum musculus yrosine 3-monoxygenase artivation protein, beta polypeptide (YMAB), mKNA (INM U19/53) Illum musculus yrosine 3-monoxygenase artivation protein, beta polypeptide (YMAB), mKNA (INM U19/53) Illum musculus yrosine 3-monoxygenase artivation protein, beta polypeptide (YMAB), mKNA (INM U19/53) Illum musculus yrosine 3-monoxygenase artivation protein, beta polypeptide (YMAB), mKNA (INM U19/53) Illum musculus yrosine 3-monoxygenase artivation protein, beta polypeptide (YMAB), mKNA (INM U19/53) Illum musculus yrosine 3-monoxygenase artivation protein, beta polypeptide (YMAB), mKNA (INM U19/53) Illum musculus yrosine 3-monoxygenase artivation protein, beta polypeptide (YMAB), mKNA (INM U19/53) Illum musculus yrosine 3-monoxygenase artivation protein, beta polypeptide (YMAB), mKNA (INM U19/53) Illum musculus yrosine 3-monoxygenase artivation protein, beta polypeptide (YMAB), mKNA (INM U19/53) Illum musculus yrosine 3-monoxygenase artivation protein, beta polypeptide (YMAB), mKNA (INM U19/53) Illum musculus yrosine 3-monoxygenase artivation protein, beta polypeptide (YMAB), mKNA (INM U19/53) Illum musculus yrosine 3-monoxygenase artivation protein polypetide (YMAB), mKNA (INM U19/53) Illum yrosine 3-monoxygenase artivation protein polypetide (YMAB), mKNA (INM U19/53) Illum yrosine 3-monoxygenase artivation protein polypetide (YMAB), mKNA (INM U19/53) Illum yrosine 3-monoxygenase artivation protein polypetide (YMAB), mKNA (INM U19/53) Illum yrosine 3-monoxygenase artivation protein polypetide (YMAB), mKNA (INM U19/53) Illum yrosine 3-monoxygenase artivation protein polypetide (YMAB), mKNA (INM U19/53) Illum yrosine 3-monoxygenase artivation protein polypetide (YMAB), mKNA (INM U19/53) Illum yrosine 3-monoxygenase artivation protein polypetide (YMAB), mKNA (INM U19/53) Illum yrosine 3-monoxygenase artivation polypetide (YMAB), mKNA (INM U19/53) Illum yrosine 3-monoxygenase artivation protei	NM_018753 AK160833	Ywhab	-1.5	38 -2.40	3 1.537
A 51 P160344	Inter Instantia Krich Cubrick and Dockhold (2017) Borger (AK014046	Etaa1 Prr6	-1.5	58 -3.18 57 -2.50	0 1.832 10 1.765
A_51_P432504	Mus musculus phosphate cylidylyltransferase 2, ethanolamine (Pcyt2), mRNA (NM, 024229)	NM 024229	Pcvt2	-1.56	55 -1.44	1 1.200
A_52_P300730	Mus musculus high mobility group AT-hook 2 (Hmga2), mRNA [NM_010441]	NM_010441	Hmga2 ENSMUST000	-1.56	54 -2.41	0 1.635
A_52_P1026507			ENSMUST000	-1.5	54 -1.49	1 1.986
A_51_P202954	Nus musculus death effector domain-containing DNA binding protein 2 (Dedd2), mRNA [NM_207677]	NM_207677	Dedd2	-1.5	53 -1.41	7 1.048
A 52 P306217	Intus musulus interrityialatiserates/inter-actional (Interrity) (I	NM_019721 NM_173028	Metti3 Vps13a	-1.5	52 -2.63 52 -1.48	1.665
A 52 P967353	Mus musculus amvotrophic lateral sclerosis 2 (une lice) tronscent revision, candidate 13 (human) (Als2cr13), transcript variant 2, mRNA INM_0010039461	NM_001003946	Als2cr13	-1.5	52 -1.40	9 1.954
A_51_P228974	Mus musculus 2-oxoglutarate and iron-dependent oxygenase domain containing 2 (Ogfod2), mRNA [NM_025671]	NM_025671	Ogfod2	-1.5	57 -1.97	6 2.594
A_52_P533779	Mus musculus ankyrin repeat domain 40 (Ankrd40), transcript variant 1, mRNA [NM_027799]	NM 027799	Ankrd40	-1.5	57 -2.45	i4 1.502
A 51 P115334	Nus musculus surfeit gene 4 (Surfe), mPINA [NM 011512]	NM 011512	Surf4	-1.5	56 -1.49	2 1.122
A 52 P635898	Nus musculus myosin va (Nyosa), miXNa [NM, U10864] Nus musculus myosin va (Nyosa), miXNa [NM, U10864]	NM_010864 AK037470	Myo5a AK037470	-1.5	56 -1.59 53 -1.52	3 1.359 8 1.067
A 51 P409595	Mus musculus protein tyrosine phosphatase-like A domain containing 2 (Plplad2), mRNA [NM_025760]	AK037470 NM_025760	AK037470 Ptplad2	-1.5		
1.01_1400120		020100	I. MIGUE	-1.0	-2.10	1.202

A 52 P508812 Mus musculus RIKEN cDNA 4932438A13 gene, mRNA (cDNA clone IMAGE:30536256), complete cds. IBC0796231			-		
A 51 D170246 Mux musculus PDNA DIVEN full leads and back and back along MEC1001D17 and using to VV1 according Management (MV147575)	BC079623 AK147575	4932438A13Ri 5830417110Rik	-1.548	-1.481 -1.507	1.276 2.527 2.019 1.597 1.376
A 52 P508912 [Mus musculus RIKEN LODNA 4932438A13 gene, mRNA (cDNA done MAGE 30359256), complete oct 3 A 51 P170346 [Mus musculus CDNA, RIKEN full-length enriched library, clone M5C1061D17 product weakly similar to YY1 associated protein [Homo sapiens], full insert sequence [AK147575] A 52 P201984 [Mus musculus adult mate unitary biadder CDNA, RIKEN full-length enriched library, clone 9530001023 product weakly similar to MHC CLASS I 17 ANTIGEN (FRAGMENT) [Mus musculus], full insert sequence [AK035206]	AK147575 AK035206	E330021A06Ri	-1.546	-1.507 A/P	2.027
A 22_P2019e Initia Initiaziona adui mitaziona adui vita, kinici tui mengare minateo unary, bune sossoo 122 poudoc, veeday similari o amito UC-03 117 AVI 136/r (Privileev 1) priva musiculus (Initiaziona adui nella sequence privaszoo) A 51_P31492 PREDICTED Nus masculus (Initiaziona adui nella seguence privaszoo) A 52_P36947 (Nus musiculus private dehydrogenae complex, component, Nongo (yeast), transcript variant 1 (Up20), mRNA (XM_12967] A 52_P36242 (Nus musiculus private dehydrogenae complex, component, Nongo (yeast), transcript variant 1 (Up20), mRNA (XM_12967] A 52_P36242 (Nus musiculus 20121112 gene (192211127km), mRNA (NM_175094] A 52_P36242 (Nus musiculus 2012112 gene (192211127km), mRNA (NM_17500)	XM 125867	Utp20	-1.542	-1.487	1.597
A 52_P168047 Mus musculus pyruvate dehydrogenase complex, component X (Pdhx), mRNA [NM_175094]	NM_175094	Pdhx	-1.542	-1.680	1.376
A_52_P582424 Mus musculus RIKEN cDNA 9130221H12 gene (9130221H12Rik), mRNA [NM_178400]	NM_178400	9130221H12Ri	-1.541	-1.581	6.604
A 52, P28228 Muss musculus milogen-activated protein kinase 12 (Mapk 12), mRNA [NM, 01371] A 52, P191468 Muss musculus ubiquitin family domain containing (1) (LIM51), mRNA [NM, 17356] A 52, P191468 Muss musculus centromere protein T (Centpl), mRNA [NM, 01081098] A 52, P325366 Muss musculus DEADHI (Asp-Giu-Alla-Asp1ris) box polypeptide 285, mRNA (DNA clone MGC:56742 [IAAGE:6466142], complete cds. [BC051161] A 51, P201043 Muss musculus DEADHI (Asp-Giu-Alla-Asp1ris) box polypeptide 285, mRNA (DNA clone MGC:56742 [IAAGE:6466142], complete cds. [BC051161] A 51, P201043 Muss musculus DEADHI (Asp-Giu-Alla-Asp1ris) box polypeptide 288, mRNA (DNA clone MGC:56742 [IAAGE:6466142], complete cds. [BC051161] A 51, P201043 Muss musculus DEADHI (Asp-Giu-Alla-Asp1ris) box polypeptide 288, mRNA (DNA clone MGC:56742 [IAAGE:6466142], complete cds. [BC051161] A 52, P17058 Muss musculus DnaJ (Hsp4) formolog, audiamity 8, member 1 (Dnag) 1, mRNA (NM 01808) A 52, P17058 Muss musculus DnaJ (Hsp4) formolog, audiamity 8, member 1 (Dnag) 1, mRNA (NM 02017) A 51, P48252 Muss musculus DnaJ (Hsp4) formolog, audiamity 8, member 1 (Dnag) 1, mRNA (NM 02017) A 51, P48252 Muss musculus Dday mante cembelum control mitoritadi manty and contex cancel matchills momber and containing protein-full insert sequence. [AK048766] A 52, P38267 Muss musculus Dday RA118, member 1482 (Raddatin ORG2), representadi (Ratiditin, mRNA NM 020187), ompteler	NM_013871 NM_138589	Mapk12	-1.541	-2.214 -1.760	1.828
A 52 P191468 [Mus musculus bubqutin family domain containing] 1 (bbt1), mk1vA [MM] 138589]	NM_138589 NM_177150	Ubfd1 Cennt	-1.540 -1.538	-1.760	1.425
A 52 P37300 With most musculus companies proteint (Certip), minve (wm.17.130)	NM_001081098	Cenpt BC039093	-1.538	-3.181	6.912
A 51_P280043 Mus musculus DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 26B, mRNA (cDNA clone MGC:56742 IMAGE:6466142), complete cds. [BC051161]	BC051161	Ddx26b	-1.538 -1.537	-2.383	2.464
A_51_P210143 Mus musculus synaptic nuclear envelope 2 (Syne2), mRNA [NM_001005510]	NM 001005510	Syne2	-1.537	-1.648	1.249
A 52_P171663 Mus musculus DnaJ (Hsp40) homolog, subfamily B, member 1 (Dnajb1), mRNA [NM_018808]	NM_018808 NM_022018	Dnajb1	-1.533 -1.530	-2.363	1.475
A 51 P46798 Mus musculus niban protein (Nban), mRNA [MM 022018]	NM_022018	Niban	-1.530	-3.110	1.178
A 51 P489285 Mus musculus cancer susceptibility candidate 5 (Casc5), mRVA (NM 029617)	NM_029617 AK048766	Casc5	-1.527 -1.526	-1.837 -3.740 -1.725	1.209
A 51 P30052 Two musculus Q agrieonae cereverium Conv, ricken numeringer emitore unairy, obiene cosocioenza product ryportencial cysineence region containing protein, our insert sequence. (Acoested)	NM_008997	Vps13c Rab11b	-1.526	-1.725	1.107
5 22 P30970 Times mascadas How THO, Timemeen How Oncogene learning (Haav TUD), Timetee Team Oracity	BC027244	Seh1l	-1.525 -1.521	-2.866	1.271
A 51 P108931 Mas musculas nuclear fragle X mental relatation protein interacting protein 1 (Nufp1), mRNA (NM, 013746) A 52, P346458 Mas musculas toli interacting protein (Tolip), mRVA (NM, 023764) A 52, P171933 Mas musculas toli interacting protein (Tolip), mRVA (NM, 023764) A 52, P171933 Mas musculas toli interacting protein (Tolip), mRVA (NM, 023764) A 52, P171933 Mas musculas toli interacting protein (Tolip), mRVA (NM, 023764) A 52, P171933 Mas musculas toli interacting protein (Tolip), mRVA (NM, 023764)	NM_013745	Nufip1	-1.521	-2.866 -1.500	1.494
A_52_P346458 Mus musculus toll interacting protein (Tollip), mRNA [NM_023764]	NM_023764	Tollip	-1.517	-1.450	1.030
A 52_P171993 Mus musculus 11 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2700060P05 product:proteasome (prosome, macropain) 26S subunit, non-ATPase, 7, full insert sequence. [AK012463]	AK012463	Psmd7	-1.516	-1.564	2.897
A_51_F378967 Mus musculus citary neurotrophic factor (cht), transcript variant 2, mkNA [NM_053007]	NM_053007 NM_011589	Cntf Timeless	-1.514 -1.513	-2.402 -1.427	1.654
A 52 P376331 Mus musculus timeless homolog [Drosophila] (Timeless) mRNA [MM 01589] A 51 P37605 Muser musculus timeless homolog (Drosophila) (Timeless) mRNA [MM 01589]	NM_011589 NM_177319	Zfyve27	-1.513	-1.427	1.127
A 51 P17307 Mus musculus polarizassembly stacking protein 2 (c)yezz1, mittely (wij 17616)	NM_027352	Gorasp2	-1.511	-1.821	1.734
A_51_P383822 Mus musculus ecotropic viral integration site 2b (Evi2b), transcript variant 2, mRNA [NM_146023]	NM_146023	Evi2b	-1.508 -1.508	-1.427	1.187
A_51_P361359 Mus musculus asparagine-linked glycosylation 11 homolog (yeast, alpha-1,2-mannosyltransferase) (Alg11), mRNA [NM_183142]	NM_183142	Evi2b Alg11	-1.508	-1.635	1.128
A 52_P676510 [Mus musculus T-cell specific GTPase (Tgtp), mRNA [NM_011579]	NM 011579	Tgtp Tnfsf5ip1	-1.508	-1.413	1.299
A 51 P33515 Mus musculus tumor necrosis tactor supertamily, member 5-induced protein 1 (Trifstig)), mRNA [NM_134138]	NM_134138	Intsf5ip1	-1.506	-1.583	1.210
rx 3.c_m×nez/ mois inuscuos giucusenime>prospinate deaminate 2 (sippaz), mixixa [ixik 2013]	NM_001038015 NM_026686	Gnpda2 0610011F06Ri	-1.504	-1.665	1.4/3
A 22 P37633 [Mus musculus timeless homolog [Drosophila] (Timeless), mRNA [NM, 011589] A 51 P33590 [Mus musculus timeless homolog [Drosophila] (Timeless), mRNA [NM, 177319] A 51 P735197 [Mus musculus golg reasembly stacking protein 2 (Gorasp2), mRNA [NM, 177319] A 51 P381392 [Mus musculus septragine hinked glycosphilation 11 homolog (veest, gibh=12-mannecy/transferase) (Ag11), mRNA [NM_183142] A 51 P38135 [Mus musculus septragine-hinked glycosphilation 11 homolog (veest, gibh=12-mannecy/transferase) (Ag11), mRNA [NM_183142] A 52 P376513 [Mus musculus tumor necrosis factor superfamily, member 5-induced protein 1 (Tinfs/5p1), mRNA [NM_1134138] A 52 P475513 [Mus musculus tumor necrosis factor superfamily, member 5-induced protein 1 (Tinfs/5p1), mRNA [NM_1134138] A 52 P474513 [Mus musculus tumor necrosis factor superfamily, member 5-induced protein 1 (Tinfs/5p1), mRNA [NM_1134138] A 52 P474513 [Mus musculus SIREM CONA 0610011F05Rik), mRNA [NM_01025015] A 51 P443613 [Mus musculus SIREM CONA 0610011F05Rik), mRNA [NM_010787]	NM_020000 NM_019787	Sec23b	-1.501	-1.665 -2.000 -2.797 -1.668	1.299 1.210 1.473 1.231 1.217 1.545 1.020 2.044 1.028 1.122
A 51 P348456 Mus musculus RE1-silencing transcription factor (Rest). mRNA INM 011263	NM_011263	Rest	-1.495	-1.668	1.545
A 51 P485542 Mus musculus cytidine 51-triphosphate synthase 2 (C(ps2), mRNA [NM_018737] A 52 P283835 Mus musculus cyclin K (Conk), mRNA [NM_009832]	NM_018737	Ctps2	-1.495	-1.464	1.020
A 52_P283835 Mus musculus cyclin K (Conk), mRNA [NM_009832]	NM_009832	Ccnk	-1.495	-1.940	2.044
A 52 P551496 Mus musculus nuclear factor I/C (Nfic), transcript variant 1, mRNA [NM. 008688]	NM_008688	Nfic	-1.491	-3.435	1.028
A 51 P101006 RIKEN cDNA 1190002A17 gene [Source MarkerSymbol/.ac.MGI-1916120] [ENSMUST00000074156]	1111 000 100	1190002A17Ri	-1.486	-1.911	1.122
A 51 P24941 Mus musculus expressed sequence 2 embryonic lethal (Es2el), transcript variant 1, mRNA [NM_022408] A 51 P24191 Mus musculus 1, 2 hudrowingtende debudgemeent (2 hudro), Broth NBA 154421	NM_022408 NM_145443	Es2el L2hgdh	-1.484 -1.484	-5.096	1.362 1.022 1.592
A 51 P221132 Mus musculus L-2-hydroxyglutarate dehydrogenase (L2hgdh), mRNA (NM, 145443) A 51 P305027 Mus musculus formin binding protein 1 (FhpP1), transcript variant 2, mRNA (NM, 019406)	NM_019406	Ezilgun Fnbp1	-1.484	-1.955	1.592
	NM_057173	Lmo1	-1.482	-1.522	1 176
A 22 P2857 Mus musculus allehyde delytogrames 9 sublami A1 (Albha1) mRNA [NM 01998] A 22 P2857 Mus musculus allehyde delytogrames 9 sublami A1 (Albha1) mRNA [NM 01998] A 51 P102582 Mus musculus RIKEH CON 151034A23 pare (151034A23RA) RAVA [NM 025307] A 51 P102582 Mus musculus RIKEH CON 151034A23 pare (151034A23RA) RAVA [NM 025307]	NM_019993	Aldh9a1	-1.482	-2.011	1.236 2.217 2.474
A_51_P102652 Mus musculus RIKEN cDNA 1810034K20 gene (1810034K20 Rik), mRNA [NM_023397]	NM_023397	1810034K20Ri	-1.477	-1.701	2.217
A. 51_P160202 Mus musculus N-ethylmaleimide sensitive fusion protein (Nsf), mRNA [NM_008740]	NM_008740	Nsf	-1.476	-1.557	2.474
A 51 P185465 Mus musculus solute carrier family 29 (nucleoside transporters), member 3 (Sic29a3), mRNA (NM 023596)	NM_023596 NM_144931	Slc29a3	-1.476	-2.145 -1.457	2.681
A. 51 P/20035 Mus musculus any/old beta precursor protein o inding protein 1 (Appop), mitrix4 (MM) 144931	AB029397	Appbp1 Patz1	-1.4/4	-1.457	2.830
A 52 PAID38 Mus muscula industri more no tanaccipion raccin moz.r. complete das processori in a fait more no tanaccipion raccin moz.r. complete das processori in a fait more no tanaccipion raccin moz.r. complete das processori in a fait more no tanaccipion raccin moz.r. complete das processori in a fait more no tanaccipion raccin moz.r. complete das processori in a fait more no tanaccipion raccin more no tanaccipion raccin moz.r. complete das processori in a fait more no tanaccipion raccin moz.r. complete das processori in a fait more no tanaccipion raccin moz.r. complete das processori in a fait more no tanaccipion raccin moz.r. complete das processori in a fait more no tanaccipion raccin more no tanaccin more no tanaccipion raccin more no tanaccin more no tanaccin	AK031650	Stxbp4	-1.462	-3.082	2.987
A 3 1 P169460 Mus musculus solute carrer raminy 24 (nucleosite transporters), memore (soluc2as), mirove [mu 225996] A 5 1 P20038 Mus musculus solute carrer raminy 24 (nucleosite transporters), memore (soluc2as), mirove [mu 225997] A 5 1 P276522 Mus musculus mazr mRNA for transcription factor MAZP, complete dds [AB02397] A 5 2 P47153 Mus musculus inde tests CDNA, FIKIS Null-Hagft memore Haded Biology, clone 5030470/M02 product unclassifiable, full insert sequence. [AK031650] A 5 2 P471597 Mus musculus frombide tests CDNA, FIKIS Null-Hagft memore rotational (JR041), mRNA [NM 029777] A 5 1 P203576 Mus musculus frombide domain containing 1 (Rh041), mRNA [NM 029777] A 5 1 P203576 Mus musculus frombide domain containing 1 (Rh041), mRNA [NM 019776]	NM_029777	Rhbdd1	-1.462	-1.685	2.681 1.999 2.830 2.987 2.007 1.233 1.129 2.008 2.251 1.005 1.155
A 51 P233578 [Mis musculus RanBP-type and C3HC4-type zinc finger containing 1 (BbcH); transcript variant 2, mRNA [NM_019705] A 52, P574527 [Mus musculus zinc finger protein 286 (Zfp295); transcript variant 1, mRNA [NM_175428] A 51 P174773 [Mus musculus RinCH cDNA 2900010M23 gene (2900010M23Risk, mRVA [NM_0050])	NM_019705	Rbck1	-1.459	-2.121 -1.884	1.233
A 52_P574527 Mus musculus zinc finger protein 295 (Zfp296), transcript variant 1, mRNA [NM_175428]	NM_175428	Zfp295	-1.459	-1.884	1.129
A 51 P174773 [Mus musculus RIKEN cDNA 290010M23 gene (2900010M23 fik), mRNA [MI, 025063]	NM_026063 NM_153525	2900010M23R	-1.457	-1.470	2.008
A, 52, P4389 Mus musulus transmembrane protein 418 (Timen41b), mRNA [NM, 153525] A, 52, P46434 Mus musulus protein phsphateat = 1, tablytis suburint, gamma isoform (Ppp tot), mRNA [NM, 013636]	NM_013636	Tmem41b Ppp1cc	-1.456	-1.462 -1.569	2.251
A 22 F24554 (https://mdoi.org/pii/add/). (add/nc.gad/n	NM_001001491	Tpm4	-1.455	-1.420	1 155
A 52 P464268 Mus musculus fractured callus expressed transcript (Fxc1), mRNA [NM, 019502] A 51 P281334 Mus musculus RIKEN CDNA 2410187C168 gene (2410187C16Rik), mRNA [NM, 029734]	NM 019502	Fxc1	-1.454	-1.793	1.441
A 51 P201284 Mile milesule PIKEN a DNA 2410187016 apps (2410187018016) mPNA (NM 020724)	NM_029734	2410187C16Ri	-1.453	-1.692	1.414
			-1.453	-2.240	1.185
A_51_P125260 Mus musculus acetyl-Coenzyme A acytransterase 2 (mitochondrial 3-3x8acyl-Coenzyme A thiolase) (Acaa2), mRNA [NM_1774/0]	NM_177470	Acaa2		-2.182	1.945
A_51_P125260 Mus musculus acetyl-Coenzyme A acytransterase 2 (mitochondrial 3-0x0acyl-Coenzyme A thiolase) (Acaa2), mRNA [NM_1774/0]	BC021831	BC021831	-1.451		1.557
A_51_P125260 Mus musculus acetyl-Coenzyme A acytransterase 2 (mitochondrial 3-0x0acyl-Coenzyme A thiolase) (Acaa2), mRNA [NM_1774/0]	BC021831	BC021831 2600009E05Ri	-1.451	-1.743	
A_51_P125260 Mus musculus acetyl-Coenzyme A acytransterase 2 (mitochondrial 3-0x0acyl-Coenzyme A thiolase) (Acaa2), mRNA [NM_1774/0]	BC021831 NM_029832 NM_007735	BC021831 2600009E05Ri Col4a4	-1.451 -1.451 -1.447 -1.446	-1.743	1.249
A_51_P125260 Mus musculus acetyl-Coenzyme A acytransterase 2 (mitochondrial 3-0x0acyl-Coenzyme A thiolase) (Acaa2), mRNA [NM_1774/0]	BC021831 NM_029832 NM_007735 NM_172705 NM_028292	BC021831 2600009E05Ri Col4a4 Phf13	-1.451 -1.447	-1.743 A/P -1.502 -1.949	1.249 1.101 1.934
A_51_P125260 Mus musculus acetyl-Coenzyme A acytransterase 2 (mitochondrial 3-0x0acyl-Coenzyme A thiolase) (Acaa2), mRNA [NM_1774/0]	BC021831 NM_029832 NM_007735 NM_172705 NM_028292 AK080240	BC021831 2600009E05Ril Col4a4 Phf13 Ppme1 Gpd2	-1.451 -1.447 -1.446 -1.445 -1.437	-1.743 A/P -1.502 -1.949	1.249 1.101 1.934 1.104
A 51 P125260 Muss musculus adetp1-CentYme A adytransterate 2 (mtochonhal -50xadey1-CentYme A minaste) (Acad2), mtox [Nuk _ 17/470] A 52 P68200 Muss musculus (one MAGE 39823321, mtNA, panti dots) [E0021831] A 52 P68200 Muss musculus (one MAGE 39823321, mtNA, panti dots) [E0021831] A 51 P32705 Muss musculus profolgen, type (V, panti 4 (CotAd4), mtNA [Nuk (29832] A 51 P32705 Muss musculus profolgen, type (V, panti 4 (CotAd4), mtNA [Nuk (29832] A 51 P32705 Muss musculus profolgen, type (V, panti 4 (CotAd4), mtNA [Nuk (29735] A 52 P68670 Muss musculus profein protein 13 (Phf13), mtNA [Nuk (29232] A 52 P69870 Muss musculus adult male aonte and vien (DonA, RIKEN full-length enriched library, clone A530087K12 product.unclassifiable, full insert sequence [AK080240] A 51 P403105 Muss musculus adult male aonte and vien (DonA, RIKEN full-length enriched library, clone A530087K12 product.unclassifiable, full insert sequence [AK080240] A 51 P40105 Muss musculus adult male aonte and vien (DonA, RIKEN full-length enriched library, clone A530087K12 product.unclassifiable, full insert sequence [AK080240]	BC021831 NM_029832 NM_007735 NM_172705 NM_028292 AK080240 NM_011637	BC021831 2600009E05Ri Col4a4 Phf13 Ppme1 Gpd2 Trex1	-1.451 -1.447 -1.446 -1.445 -1.437 -1.437	-1.743 A/P -1.502 -1.949 -1.647 -1.715	1.249 1.101 1.934 1.104 1.109
A 51 P125260 Muss musculus adetp1-CentYme A adytransterate 2 (mtochonhal -50xadey1-CentYme A minaste) (Acad2), mtox [Nuk _ 17/470] A 52 P68200 Muss musculus (one MAGE 39823321, mtNA, panti dots) [E0021831] A 52 P68200 Muss musculus (one MAGE 39823321, mtNA, panti dots) [E0021831] A 51 P32705 Muss musculus profolgen, type (V, panti 4 (CotAd4), mtNA [Nuk (29832] A 51 P32705 Muss musculus profolgen, type (V, panti 4 (CotAd4), mtNA [Nuk (29832] A 51 P32705 Muss musculus profolgen, type (V, panti 4 (CotAd4), mtNA [Nuk (29735] A 52 P68670 Muss musculus profein protein 13 (Phf13), mtNA [Nuk (29232] A 52 P69870 Muss musculus adult male aonte and vien (DonA, RIKEN full-length enriched library, clone A530087K12 product.unclassifiable, full insert sequence [AK080240] A 51 P403105 Muss musculus adult male aonte and vien (DonA, RIKEN full-length enriched library, clone A530087K12 product.unclassifiable, full insert sequence [AK080240] A 51 P40105 Muss musculus adult male aonte and vien (DonA, RIKEN full-length enriched library, clone A530087K12 product.unclassifiable, full insert sequence [AK080240]	BC021831 NM_029832 NM_007735 NM_172705 NM_028292 AK080240 NM_011637 NM_053082	BC021831 2600009E05Ril Col4a4 Phf13 Ppme1 Gpd2 Trex1 Tspan4	-1.451 -1.447 -1.446 -1.445 -1.437 -1.437 -1.437	-1.743 A/P -1.502 -1.949 -1.647 -1.715 -1.796	1.249 1.101 1.934 1.104 1.109 1.808
A 51 P125200 Mus musculus adetp:-Centyme A apriramistrate 2 (mtochnoma) 50x00etp://cetryme A mioase) (AcBaz), mtox [NM 17/4/U] A 52 P68200 Mus musculus (one MAGE 39823321, mtNA, paint dots, [BCC21832], mtNA [NM 22932] A 51 P327156 Mus musculus proceedings, mtRA [NM 22932] A 51 P32705 Mus musculus proteing nosphate methylesterase (Pome 1), mtNA [NM 22932] A 52 P68207 Musculus adult male aonta and vein CDNA. RIKEN full-length enriched library, clone A50087K12 product unclassifiable, full insert sequence [AK08240] A 51 P32703 Mus musculus adult male aonta and vein CDNA. RIKEN full-length enriched library, clone A50087K12 product unclassifiable, full insert sequence [AK080240] A 51 P30708 Musculus adult male aonta and vein CDNA. RIKEN full-length enriched library, clone A50087K12 product unclassifiable, full insert sequence [AK080240] A 51 P405078 Mus musculus adult male aonta and vein CDNA. RIKEN full-length enriched library, clone A50087K12 product unclassifiable, full insert sequence [AK080240] A 51 P405078 Musculus adult male aonta and vein CDNA. RIKEN full-length enriched library, clone A50087K12 product unclassifiable, full insert sequence [AK080240] A 51 P40508 Musculus adult male aonta and vein CDNA. RIKEN full-length enriched library, clone A50087K12 product unclassifiable, full insert sequence [AK080240] A 51 P40508 Musculus adult male aborta and vein CDNA. RIKEN full-length enriched library, clone A50087K12 product product patelet-activating factor acetylhydrolase, isoform 1b, beta1 subunit, full insert sequence [AK147309]	BC021831 NM_029832 NM_007735 NM_172705 NM_028292 AK080240 NM_011637 NM_053082 AK147309	BC021831 2600009E05Ri Col4a4 Phf13 Ppme1 Gpd2 Trex1 Tspan4 Pafah1b1	-1.451 -1.447 -1.446 -1.445 -1.437 -1.437 -1.437 -1.437 -1.436	-1.743 A/P -1.502 -1.949 -1.647 -1.715 -1.796 -1.426	1.249 1.101 1.934 1.104 1.109 1.808 2.338 1.107
A 51 P42080 Muss musculus adure marketinase (mitocionnas 3-social/pri a Agringinasteriase (mitocionnas 3-social/pri a Agringinasteriase) A 61 A 52 P8680 Muss musculus, done MAGE 3880321, mRNA, paint doit, BICC/1830303 A 61 A 52 P86807 Muss musculus, done MAGE 3880321, mRNA paint doit, BICC/1830303 A 61 A 51 P480176 Muss musculus, done MAGE 3880321, mRNA, paint doit, BICC/18303 A 61 A 51 P480176 Muss musculus, protein prophotate methylesteriase 1 Prost 11, mRNA paint A 51 P480176 Muss musculus, protein prophotate methylesteriase 1 Prost 11, mRNA paint A 51 P480176 Muss musculus, protein prophotate methylesteriase 1 Prost 11, mRNA paint Prost 2000 A 52 P58407 Muss musculus, protein prophotate methylesteriase 1 Prost 11, mRNA pill, protein 2000 Paint A 52 P58407 Muss musculus, adult male odit and vien CVAN, RINKEN full-Regiment role for acetylinylogiose, isoform 1b, beta1 subunit, full insert sequence. [AK147309] A 51 A 51 P480176 Muss musculus adult male orana metric olival, RINKEN full-Regiment role for acetylinyloilase, isoform 1b, beta1 subunit, full insert sequence. [AK147309] A 52 A 52	BC021831 NM_029832 NM_07735 NM_172706 NM_028292 AK080240 NM_011637 NM_053082 AK147309 NM_029752	BC021831 2600009E05Ri Col4a4 Phf13 Ppme1 Gpd2 Trex1 Tspan4 Pafah1b1 Bri3bp	-1.451 -1.447 -1.446 -1.445 -1.437 -1.437 -1.437 -1.437 -1.436 -1.434	-1.743 A/P -1.502 -1.949 -1.647 -1.715 -1.796 -1.426 -2.453	1.557 1.249 1.101 1.934 1.104 1.109 1.808 2.338 1.107 1.788
A 3 P12380 Mus musculus steep:Centryme A acjurateristicate 2 (mtochonical 3-social/-centryme A ministeristicate 2 (mtochonical 3-social/-centryme A ministeristicate) (mtochonical 3-social/-centryme A ministeristicate) (mtochonical 3-social/-centryme A ministeristicate) (mtochonical 3-social/-centryme A ministeristicate) (mtochonicate 3-social/-centryme A ministeristicate) (mtochonicate) (m	BC021831 NM_029832 NM_17735 NM_172705 NM_028292 AK080240 NM_011637 NM_053082 AK147309 NM_029752 NM_029752 NM_013871	BC021831 2600009E05Ri Col4a4 Phf13 Ppme1 Gpd2 Trex1 Tspan4 Pafah1b1 Bri3bp Mapk12	-1.451 -1.447 -1.446 -1.445 -1.437 -1.437 -1.437 -1.437 -1.436 -1.434 -1.434	-1.743 A/P -1.502 -1.949 -1.647 -1.715 -1.796 -1.426 -2.453 -2.564	1.249 1.101 1.934 1.104 1.109 1.808 2.338 1.107 1.788 2.214
A 3 P12380 Mus musculus steep:Centryme A acjurateristicate 2 (mtochonical 3-social/-centryme A ministeristicate 2 (mtochonical 3-social/-centryme A ministeristicate) (mtochonical 3-social/-centryme A ministeristicate) (mtochonical 3-social/-centryme A ministeristicate) (mtochonical 3-social/-centryme A ministeristicate) (mtochonicate 3-social/-centryme A ministeristicate) (mtochonicate) (m	BC021831 NM_029832 NM_07735 NM_172705 NM_028292 AK080240 NM_011637 NM_053082 AK147309 NM_029752 NM_013871 XM_908122	BC021831 260009E05Ri Col4a4 Phf13 Ppme1 Gpd2 Trex1 Tspan4 Pafah1b1 Bri3bp Mapk12 Iars2 ENSMUST000	-1.451 -1.447 -1.446 -1.445 -1.437 -1.437 -1.437 -1.437 -1.436 -1.434 -1.434 -1.433 (-1.433	-1.743 A/P -1.502 -1.949 -1.647 -1.715 -1.796 -1.426 -2.453 -2.564 -1.793 -1.833	1.249 1.101 1.934 1.104 1.109 1.808 2.338 1.107 1.788 2.214 2.730
A 3 P12380 Mus musculus steep:-Centryme A aprimatistate 2 (mitochonnal 3-social-process;me A misales) (AcBaz), mitox (Mitor 1/4/0] A 52, P6802 Mus musculus (Centryme A aprimatistate 2 (mitochonnal 3-social-process;me A misales) (AcBaz), mitox (Mitor 1/4/0] A 52, P6802 Mus musculus (Centryme A aprimatistate 2 (mitochonnal 3-social-process;me A misales) (AcBaz), mitox (Mitor 1/4/0] A 51, P82718 Mus musculus (Centryme A aprimatistate 2 (mitochonnal 3-social-process;me A misales) (AcBaz), mitox (Mitor 1/4/0] A 51, P82718 Mus musculus (Centryme A aprimatistate 2 (mitochonnal 3-social-process;me A misales) (AcBaz), mitox (Mitor 1/4/0] A 51, P82718 Mus musculus (Centryme A aprimatistate 2 (mitochonnal 3-social-process;me A misales) (AcBaz), mitox (Mitor 1/4/0] A 51, P8270 Mus musculus (Centryme A aprimatistate 2 (mitochonnal 3-social-process;me A misales) (AcBaz) A 51, P8260 Mus musculus (Centryme A aprimatistate 2 (mitochonnal 3-social-process;me A misales) (AcBaz) A 51, P8260 Mus musculus (Centryme A misales) (Centryme A misale	BC021831 NM 029832 NM 007735 NM 172705 NM 028292 AK080240 NM NM 01637 NM 02952 AK147309 NM NM 029752 NM 03871 XM 908122 BC025200	BC021831 260009E05Ri Col4a4 Phf13 Ppme1 Gpd2 Trex1 Tspan4 Pafah1b1 Bri3bp Mapk12 Iars2 ENSMUST000 S110073H01Ri	-1.451 -1.447 -1.446 -1.445 -1.437 -1.437 -1.437 -1.437 -1.436 -1.434 -1.434 -1.434 -1.433 -1.433 -1.433	-1.743 A/P -1.502 -1.949 -1.647 -1.715 -1.796 -1.426 -2.453 -2.564 -1.793 -1.833 -1.413	1.788 2.214 2.730 1.266
A 3 P 128200 Multis multicults adely: Londong Multis adely: London	BC021831 NM_029832 NM_007735 NM_172705 NM_028292 AK080240 NM_01637 NM_053082 AK147309 NM_029752 NM_013871 XM_908122 BC025200 AK078937	BC021831 2600009E05Ril Col4a4 Phf13 Ppme1 Gpd2 Trex1 Tspan4 Pafan1b1 Bri3bp Mapk12 Iars2 ENSMUST000 3110073H01Ril 9130206124Rik	-1.451 -1.447 -1.446 -1.445 -1.437 -1.437 -1.437 -1.437 -1.437 -1.436 -1.434 -1.434 -1.433 (-1.433 (-1.433 (-1.432 (-1.432) (-1.432) (-1.432) (-1.432) (-1.432) (-1.432) (-1.432) (-1.432) (-1.432) (-1.432) (-1.432) (-1.435) (-1.445) (-1.437) (-1.432) (-1.433) (-1.433) (-1.432) (-1.432) (-1.432) (-1.432) (-1.432) (-1.432) (-1.433) (-1.432) (-1.4	-1.743 A/P -1.502 -1.949 -1.647 -1.715 -1.795 -1.426 -2.453 -2.564 -1.793 -1.833 -1.413 -1.713	1.788 2.214 2.730 1.266
A 3 P 128200 Multis multicults adely: Londong Multis adely: London	BC021831 NM 029832 NM 07735 NM 172705 NM 028292 AK080240 NM 011637 NM 053082 AK147309 NM 029752 NM 013871 XM 906122 BC025200 AK078937 NM 07700	BC021831 2600009E05Ril 260484 Phf13 Ppme1 Gpd2 Trex1 Tspan4 Pafah1b1 Bri3bp Mapk12 Iars2 ENSMUST000 3110073H01Ril 9130206124Rik Chuk	-1.451 -1.447 -1.446 -1.445 -1.437 -1.437 -1.437 -1.437 -1.436 -1.434 -1.434 -1.433 -1.433 -1.433 -1.432 -1.432 -1.432	-1.743 A/P -1.502 -1.949 -1.647 -1.715 -1.796 -1.426 -2.453 -2.453 -2.453 -2.564 -1.793 -1.833 -1.413 -1.713 -1.713	1.788 2.214 2.730 1.266 2.460 1.997
A 3 P 128200 Multis multicults adely: Londong Multis adely: London	BC021831 NM 029832 NM 07735 NM 172705 NM 07735 NM 08292 AK080240 NM 01637 NM 053082 AK1309 AK147309 AK147309 AK198752 BC025200 AK078937 NM 07700 BC034876	BC021831 2600009E05Ril Col4a4 Phf13 Ppme1 Gpd2 Trex1 Tspan4 Pafah1b1 Bri3bp Mapk12 Iars2 ENSMUST000 3110073H01Ri 9130206I24Rik Chuk	-1.451 -1.447 -1.446 -1.445 -1.437 -1.437 -1.437 -1.437 -1.437 -1.434 -1.434 -1.434 -1.433 -1.433 -1.432 -1.432 -1.432 -1.432 -1.432	-1.743 A/P -1.502 -1.949 -1.647 -1.715 -1.795 -1.426 -2.453 -2.2564 -1.793 -1.833 -1.833 -1.413 -1.713 -1.418 -1.536	1.788 2.214 2.730 1.266 2.460 1.997 3.616 1.038
A 3 P 128200 Multis multicults adely: Londong Multis adely: London	BC021831 NM 028832 NM 07735 NM 172705 NM 028292 NM 028292 NM 011637 NM 029752 NM 029752 BC025200 AK147306 NM 018871 XM 908122 BC025200 AK078937 NM 009190 NM 019650	BC021831 2600009E05Ril Col4a4 Phf13 Ppme1 Gpd2 Trex1 Trex1 Fasan4 Pafah1b1 Bri3bp Mapk12 Iars2 ENSMUST000 3110073H01Ril 9130206124Rik Ung4b1 110008L16Rii Vps4b	1 -1.451 -1.447 -1.446 -1.445 -1.437 -1.437 -1.437 -1.437 -1.437 -1.438 -1.433 (-1.433 (-1.433) (-1.432 -1.435 -1.437 -1.438 -1.437 -1.437 -1.438 -1.437 -1.438 -1.437 -1.438 -1.437 -1.438 -1.437 -1.438 -1.437 -1.438 -1.437 -1.438 -1.437 -1.438 -1.437 -1.438 -1.432 -1.	-1.743 A/P -1.502 -1.949 -1.647 -1.715 -1.768 -1.426 -2.453 -2.564 -1.793 -1.413 -1.713 -1.713 -1.713 -1.418 -1.538 -2.006	1.788 2.214 2.730 1.266 2.460 1.997 3.616 1.038
A 3 P 128200 Multis multicults adely: Londong Multis adely: London	BC021831 NM 029832 NM 07735 NM 028292 NM 028292 AK080240 NM 011637 NM 028292 AK147309 NM 013871 XM 908122 BC025200 AK078937 NM 013871 SC025200 BC034876 NM 019650 XM 919663	BC021831 2600009E05Ril Col4a4 Phf13 Ppme1 Gpd2 Trex1 Tspan4 Pafah1b1 Bri3bp Mapk12 Iars2 ENSMUST000 3110073H01Ri 9130206I24Rik Chuk	 -1.451 -1.447 -1.446 -1.448 -1.437 -1.437 -1.437 -1.437 -1.438 -1.434 -1.433 -1.433 -1.433 -1.432 	-1.743 A/P -1.502 -1.949 -1.647 -1.715 -1.796 -1.426 -2.453 -2.564 -1.793 -1.433 -1.413 -1.713 -1.418 -1.536 -2.006 -1.939 -1.939 -1.405	1.788 2.214 2.730 1.266 2.460 1.997 3.616 1.038 3.228 4.460
A 32 P128200 Mu6 mukadus adept. Longtomer. A 84' ambrates & (Index-nonous 3' stoept-Locker, mex A Mode2, mexA (Mu 17/4/g) A 51 P2716 Mus mukadus Adept. Longtomer. A 84' ambrates & (Index-nonous 3' stoept-Locker, mex A Mode2, mexA (Mu 17/4/g) A 51 P27278 Mus mukadus REVEX LOCA 2000956058, mex (Index-nonous 3' stoept-Locker, mex A Mode2, mexA (Mu 17/4/g) A 51 P27278 Mus mukadus PIC high storp and a 40' colored and a mexature and a mexat	BC021831 NM_028932 NM_07735 NM_07735 NM_07735 NM_07735 NM_017735 NM_01637 NM_01637 NM_01637 NM_028292 AK147309 NM_01871 SC052500 AK078037 NM_009190 NM_009190 NM_009196 NM_019669 NM_019669 NM_019669 NM_019669 NM_019669 NM_019669 NM_019669 NM_019669	BC021831 2600009E05Ril Col4a4 Phrf13 Ppme1 Gpd2 Trex1 Tspan4 Parlan1b1 Bri3bp Mapk12 lars2 ENSMUST000 3110073H01Ri 9130206124Rik Chuk 1110008L16Ril Vps4b Gosr2 EG631624 Usp47	$\begin{array}{c} -1.451\\ -1.447\\ -1.446\\ -1.437\\ -1.436\\ -1.437\\ -1.437\\ -1.437\\ -1.436\\ -1.434\\ -1.434\\ -1.433\\ -1.433\\ -1.432\\$	-1.743 A/P -1.502 -1.949 -1.647 -1.715 -1.769 -1.426 -2.453 -2.453 -2.564 -1.793 -1.413 -1.713 -1.413 -1.413 -1.418 -1	1.788 2.214 2.730 1.266 2.460 1.997 3.616 1.038 3.228 3.228
A 32 P128200 Mu6 mukadus adept. Longtomer. A 84' ambrates & (Index-nonous 3' stoept-Locker, mex A Mode2, mexA (Mu 17/4/g) A 51 P2716 Mus mukadus Adept. Longtomer. A 84' ambrates & (Index-nonous 3' stoept-Locker, mex A Mode2, mexA (Mu 17/4/g) A 51 P27278 Mus mukadus REVEX LOCA 2000956058, mex (Index-nonous 3' stoept-Locker, mex A Mode2, mexA (Mu 17/4/g) A 51 P27278 Mus mukadus PIC high storp and a 40' colored and a mexature and a mexat	BC021831 NM 029832 NM 07735 NM 027735 NM 028292 AK080240 NM NM 01637 NM 01637 NM 013871 SKM 909122 BC025200 AK07700 BC034876 NM NM 019650 NM 019663 NM 193754	BC021831 2600009E05Ri Col4a4 Phf13 Ppf13 Ppf13 Prex1 Tex1 Tspan4 Trex1 Tspan4 Br3bp Mapk12 Iars2 ENSMUSTOD0 3110073H01Ri 9130206124Rik Chuk Chuk Chuk Chuk Chuk Chuk Cos2 Cos2 Top2 Top2 Top2 Top2 Top2 Top2 Top2 Top	$\begin{array}{c} -1.451\\ -1.447\\ -1.446\\ -1.437\\ -1.437\\ -1.437\\ -1.437\\ -1.437\\ -1.438\\ -1.433\\ -1.433\\ -1.433\\ -1.433\\ -1.433\\ -1.433\\ -1.432\\ -1.422\\$	-1.743 A/P -1.502 -1.949 -1.647 -1.715 -1.706 -2.463 -2.464 -2.564 -2.564 -2.564 -1.793 -1.413 -1.713 -1.418 -1.538 -2.006 -1.939 -1.939 -1.405 -3.515 -1.832	1.788 2.214 2.730 1.266 2.460 1.997 3.616 1.038 3.228 3.228
A 32 P128200 Mu6 mukadus adept. Longtomer. A 84' ambrates & (Index-nonous 3' stoept-Locker, mex A Mode2, mexA (Mu 17/4/g) A 51 P2716 Mus mukadus Adept. Longtomer. A 84' ambrates & (Index-nonous 3' stoept-Locker, mex A Mode2, mexA (Mu 17/4/g) A 51 P27278 Mus mukadus REVEX LOCA 2000956058, mex (Index-nonous 3' stoept-Locker, mex A Mode2, mexA (Mu 17/4/g) A 51 P27278 Mus mukadus PIC high storp and a 40' colored and a mexature and a mexat	BC021831 NM 029832 NM 07735 NM 027735 NM 028292 AK080240 NM NM 01637 NM 01637 NM 013871 SKM 909122 BC025200 AK07700 BC034876 NM NM 019650 NM 019663 NM 193754	BC021831 2600009E05RI Col4a4 Phf13 Ppme1 Gpd2 Trex1 Tepart Bribbp Parah1b1 Bribbp Bribbb Bribbp Bribbb Bribbb Bri	-1.451 -1.447 -1.446 -1.447 -1.446 -1.445 -1.437 -1.437 -1.436 -1.434 -1.433 -1.433 -1.433 -1.433 -1.432 -1.442 -1.432 -1.447 -1.447 -1	-1.743 A/P -1.502 -1.949 -1.647 -1.715 -1.706 -2.463 -2.464 -2.564 -2.564 -2.564 -1.793 -1.413 -1.713 -1.418 -1.538 -2.006 -1.939 -1.939 -1.405 -3.515 -1.832	1.788 2.214 2.730 1.266 2.460 1.997 3.616 1.038 3.228 4.460
A 32 P128200 Mu6 mukadus adept. Longtomer. A 84' ambrates & (Index-nonous 3' stoept-Locker, mex A Mode2, mexA (Mu 17/4/g) A 51 P2716 Mus mukadus Adept. Longtomer. A 84' ambrates & (Index-nonous 3' stoept-Locker, mex A Mode2, mexA (Mu 17/4/g) A 51 P27278 Mus mukadus REVEX LOCA 2000956058, mex (Index-nonous 3' stoept-Locker, mex A Mode2, mexA (Mu 17/4/g) A 51 P27278 Mus mukadus PIC high storp and a 40' colored and a mexature and a mexat	BC021831 NM0 029832 NM0 07735 NM0 07735 NM0 02832 NM0 07735 NM0 028752 NM0 055082 NM0 028752 BC02870 NM0 013871 XM 098122 BC028200 NM0 013871 XM 069180 BC024875 NM0 013871 XM 919633 NM0 010338 NM1 010833	BC021831 260009E05Ril 260009E05Ril 260009E05Ril Pprif3 Ppr	-1.451 -1.447 -1.446 -1.446 -1.445 -1.437 -1.437 -1.437 -1.436 -1.434 -1.434 -1.434 -1.434 -1.434 -1.433 -1.432 -1.435 -1.445 -1	-1.743 A/P -1.502 -1.949 -1.647 -1.715 -1.775 -1.775 -1.726 -2.453 -2.453 -2.453 -1.833 -1.413 -1.713 -1.713 -1.713 -1.713 -1.713 -1.713 -1.418 -1.536 -2.006 -1.939 -1.405 -3.515 -1.882 -1.447 -2.128	1.788 2.214 2.730 1.266 2.460 1.997 3.616 1.038 3.228 4.460
A 3 F 128200 Mus mukabus adept-concernme A aprimativase 2 (mice-concernme A miceacy metva (Mu 17/4/g) A 5 F 22716 Mus mukabus adept-concernme A aprimativase 2 (mice-concernme A miceacy metva (Mu 17/4/g) A 5 F 22716 Mus mukabus REVEK ICOAX 20009E0058, mice (20009E0058), mice (20009E058), mice (20009E058), mice (20009E058), mice (20009E058), mice (20009E08), mice (20009E0	BC021831 NM 029832 NM 07735 NM 027735 NM 028292 AK080240 NM NM 01637 NM 01637 NM 013871 SKM 909122 BC025200 AK07700 BC034876 NM NM 019650 NM 019663 NM 193754	BC021831 260009E05R 260009E05R 260009E05R Phf13 Pome1 God2 Trex1 Trex1 Trex1 Trex1 Trex1 Trex1 Trex1 Trex1 Trex1 Trex1 Palantb1 Bri3bp Maph12 Iars2 Bri3bp Maph12 Iars2 S102012AF Bri3bp S102012AF Bri3bp S102012AF S1020075555555555555555555555555555555555	-1.451 -1.447 -1.446 -1.447 -1.446 -1.445 -1.437 -1.437 -1.436 -1.434 -1.433 -1.433 -1.433 -1.433 -1.432 -1.442 -1.432 -1.447 -1.447 -1	-1.743 A/P -1.502 -1.949 -1.647 -1.715 -1.775 -1.428 -2.564 -1.773 -1.413 -1.413 -1.413 -1.418 -2.506 -1.939 -1.405 -1.939 -1.405 -1.939 -1.405 -1.939 -1.405 -1.939 -1.405 -1.407 -1.405 -1.407 -1.405 -1.407 -	1.788 2.214 2.730 1.266 2.460 1.997 3.616 1.038 3.228 3.228
A 19 P12050 Multian Inductions addity in the apyrimatives as a (index control as 4 proceeding of a pyrimatives as a (index control as 4 proceeding). The A 19 P2150 A 3 19 P2150 Multian Inductions addity in the A pyrimatives as a (index control as 4 pyrimatives as a pyrimatives as a (index control as 4 pyrimatives as a (in	BC021831 NM 026832 NM 07735 NM 07735 NA 052042 NA 052042 NA 052042 NA 052042 NA 052042 NM 015371 NM 025752 GC025200 6C025200 AK07700 BC026200 NM 019550 NM 019550 NM 019653 NM 019653 NM 019654 NM 027915 NM 0275915	8C021831 260009E05R4 260009E05R4 Phf13 Ppme1 Gpd2 Trex1 Pagan4 Pagan1b1 Bra5p2	(-1.451 -1.447 -1.446 -1.446 -1.446 -1.437 -1.437 -1.437 -1.437 -1.437 -1.437 -1.437 -1.433 -1.432 -1.442 -1.441 -	$\begin{array}{c} -1,743\\ APP\\ -1,602\\ -1,949\\ -1,647\\ -1,746\\ -1,746\\ -1,746\\ -1,746\\ -1,746\\ -2,463\\ -2,462\\ -2,463\\ -2,462\\ -2,462\\ -2,462\\ -2,462\\ -2$	1.788 2.214 2.730 1.266 2.460 1.997 3.616 1.038 3.228 1.196 2.507 1.223 1.078 1.931 2.519 1.834 1.410
A 31 P12580 Multip multiplication Multip multiplication Multip multiplication A 32 P58500 Multip multiplication Multip multiplication Multip multiplication A 32 P58500 Multip multiplication Multip multiplication Multip multiplication A 32 P58500 Multip multiplication Multiplication Multiplication A 51 P48010 Multip multiplication Multiplication Multiplication A 52 P58030 Multip multiplication Multiplication Multiplication A 51 P48010 Multip multiplication Multiplication Multiplication A 52 P58030 Multiplication Multiplication Multiplication Multiplication A 52 P48033 Multiplication Multiplication Multiplication Multiplication A 52 P48033 Multiplication Multiplication Multiplication Multiplication A 52 P48043 Multiplication Multiplication Multiplication Multiplication A 52 P48043 Multiplication Multiplication Multiplication Multiplication Multiplication A 52 P48043 Multiplication Multiplication Multiplication	BC021831 BC021831 MM 029832 MM 07735 MM 07735 MM 07735 MM 07735 MM 0785 MM 0785 MM 0785024 AK080240 MM 01837 MM 01837 MM 01837 MM 01837 XM 09812 S0827 AK0812 S0812 MM 01700 BC024476 MM 01700 BC024476 MM 01700 BC024476 MM 0100186 MM 010018	BC021831 260009E05R/ 260009E05R/ Phf13 Ppme1 Gpd2 Trex1 Papen4 Pa	(-1.451 -1.447 -1.446 -1.446 -1.445 -1.437 -1.437 -1.437 -1.436 -1.432 -1.434 -1.434 -1.434 -1.434 -1.433 -1.432 -1.435 -1.441 -1.440 -1.440 -	-1,743 APP -1,502 -1,949 -1,647 -1,745 -1,745 -1,745 -1,745 -1,426 -2,453 -1,447 -1,745 -1,426 -2,453 -1,447 -1,745 -1,426 -1,426 -1,425 -1,425 -1,425 -1,425 -1,447 -1,425 -1,455 -	1,788 2,214 2,730 1,266 1,997 3,616 1,038 3,228 1,196 2,507 1,223 1,078 1,931 1,931 1,834 1,410 1,008
A 3 P 12350 Mus musculus stepp: Concernme A aprimativase 2 (Micconomics - Society-Concernme A mission) (Calaz), mixed (Mic 17/4/0] A 5 P 22750 Mus musculus (Eller) (CAL 2000/0016/05 Musculus (Calaz), mixed (Micconomics - Society-Concernme A mission) A 5 P 22750 Mus musculus processing (Calaz), mixed (Calaz), mixed (Micconomics - Society-Concernme A mission) A 5 P 22750 Mus musculus processing (Calaz), mixed (Calaz), mixed (Micconomics - Society-Concernme A mission) A 5 P 22750 Mus musculus processing (Calaz), mixed (Calaz), mixed (Micconomics - Society-Concernme A mission) A 5 P 24870 Mus musculus and (Micconomics - Society-Concernme A mission) A 5 P 24870 Mus musculus and (mission), mixed (Micconomics - Society-Concernme A mission), mixed (Micconomics - Society), mixed (Micconomics - Micconomics - Mic	BC021831 NM 029832 NM 07735 NM 027735 NM 027735 NM 02795 NM 029752 NM 029752 NM 029752 BC027500 BC027500 BC0276037 RM NM 019571 NM 019612 NM 0196700 RC026200 RC026200 RC026200 RC026200 RC0265200 RC019196 NM 019650 NM 019651 NM 027504 NM 027504 NM 027504 NM 027593 NM 0275935	80221831 260009E05R4 260009E05R4 Phf13 Ppme1 Gpd2 Trex1 Pagan4 Pagah1b1 Bra52 ENSMUST000 Bra52 ENSMUST000 Bra52 ENSMUST000 Bra52 ENSMUST000 Bra52 ENSMUST000 Bra52 ENSMUST000 Bra52 ENSMUST000 Bra52 ENSMUST000 Bra52 ENSMUST000 Bra52 ENSMUST000 Bra52 ENSMUST00 ENSMUST00 Bra52 ENSMUST00 ENSMUST0	(-1.451 -1.447 -1.446 -1.445 -1.446 -1.445 -1.437 -1.437 -1.437 -1.436 -1.434 -1.434 -1.434 -1.434 -1.434 -1.433 -1.432 -1.442 -1.442 -1.442 -1.442 -1.442 -1.442 -1.442 -1.442 -1.442 -1.442 -1.442 -1.442 -1.442 -1.442 -1.442 -1.442 -1.442 -1.442 -1.442 -1.4417 -1.441 -1.441 -1.441 -1.441 -1.4410 -1.4410 -1.4410 -1.4410 -1.4410 -1.4410 -1.4410 -1.4410 -1.4410 -1.4410 -1.4410 -1.4410 -1.4410 -1.4410 -1.4410 -1.4410 -1.4410 -1.4410 -1.4410 -1.4400 -	-1,743 APP -1,602 -1,949 -1,647 -1,745 -1,745 -1,748 -1,743 -1,428 -	1.788 2.214 2.730 1.266 1.997 3.616 1.038 3.228 1.196 2.507 1.223 1.078 1.931 2.519 1.834 1.410 1.008
A 3 P 12350 Mus musculus stepp: Concernme A aprimativase 2 (Micconomics - Society-Concernme A mission) (Calaz), mixed (Mic 17/4/0] A 5 P 22750 Mus musculus (Eller) (CAL 2000/0016/05 Musculus (Calaz), mixed (Micconomics - Society-Concernme A mission) A 5 P 22750 Mus musculus processing (Calaz), mixed (Calaz), mixed (Micconomics - Society-Concernme A mission) A 5 P 22750 Mus musculus processing (Calaz), mixed (Calaz), mixed (Micconomics - Society-Concernme A mission) A 5 P 22750 Mus musculus processing (Calaz), mixed (Calaz), mixed (Micconomics - Society-Concernme A mission) A 5 P 24870 Mus musculus and (Micconomics - Society-Concernme A mission) A 5 P 24870 Mus musculus and (mission), mixed (Micconomics - Society-Concernme A mission), mixed (Micconomics - Society), mixed (Micconomics - Micconomics - Mic	BC021831 BC021831 MM 029832 MM 07735 MM 07735 MM 07735 MM 07735 MM 07735 MM 075302 AK060240 MM 011637 MM 053082 AK06122 MM 029752 MM 029752 MM 029752 MM 029752 MM 013871 XM 060120 MM 013871 MM 013871 MM 013871 MM 0109180 MM 0109180 MM 0109180 MM 01001883 MM 01001883 MM 027504 MM 027515 MM 02753 MM 02753	BC021831 260009E05R/ 260009E05R/ Phf13 Ppme1 Gpd2 Trex1 Parent Pa	(-1.451 -1.447 -1.446 -1.445 -1.445 -1.437 -1.437 -1.437 -1.437 -1.436 -1.434 -1.434 -1.434 -1.434 -1.432 -1.435 -1.435 -1.435 -1.435 -1.435 -1.435 -1.435 -1.435 -1.435 -1.435 -1.435 -1.435 -1.435 -1.435 -1.435 -1.435 -1.435 -1.435 -1.435 -1.432 -1.435 -1.455 -	-1,743 APP -1,602 -1,949 -1,647 -1,745 -1,745 -1,748 -1,743 -1,428 -	1,788 2,214 2,730 1,266 1,266 1,038 3,228 1,196 2,507 1,223 1,078 1,931 1,078 1,931 1,834 1,401 1,008 1,442
A 3 P 20250 MUC Induction Setty-Conference and provide source water provide a source prove A model (New 17747) A 5 P 2015 Mus musculus processing on the Vision and the set of the source and the source	BC021831 NM0 029832 NM0 07735 NM0 07735 NM0 07735 NM0 07735 NM0 07735 NM0 07037 NM0 07037 NM0 07037 NM0 053082 RC102730 NM0 053082 BC025200 AK147309 NM0 013871 XM0 001700 NM0 013871 XM0 001900 NM0 019500 NM1 019530 NM1 019540 NM1 0103376 NM1 01033760 NM1 027815 NM1 027815 NM1 027804 NM1 026055 AK027953	BC021831 260009E05R/ 260009E05R/ Phf13 Ppme1 Gpd2 Gpd2 Gpd2 Gpd2 Gpd2 Gpd2 Gpd2 Gpd2	(-1.451 -1.447 -1.447 -1.446 -1.445 -1.445 -1.437 -1.437 -1.437 -1.436 -1.434 -1.434 -1.434 -1.434 -1.434 -1.433 -1.432 -1.442 -1.442 -1.442 -1.442 -1.442 -1.442 -1.442 -1.442 -1.442 -1.442 -1.442 -1.442 -1.442 -1.442 -1.442 -1.442 -1.442 -1.442 -1.441 -1.441 -1.441 -1.441 -1.441 -1.441 -1.441 -1.400	$\begin{array}{c} -1,743\\ -1,743\\ -MP\\ -1,602\\ -1,942\\ -1,942\\ -1,942\\ -1,745\\ -1,745\\ -1,765\\ -2,564\\ -2,564\\ -1,763\\ -2,564\\ -2,564\\ -1,763\\ -2,654\\ -2,564\\ -1,763\\ -2,664\\ -1,763\\ -2,664\\ -1,763\\ -2,664\\ -2,728\\ -2,728\\ -2,728\\ -2,785\\ -2$	1,788 2,214 2,730 1,266 2,460 1,997 3,616 1,038 3,228 1,196 2,507 1,223 1,078 1,931 2,519 1,834 1,410 1,008 1,442 1,481
A 3 P 20250 MUC Induction Setty-Conference and provide source water provide a source prove A model (New 17747) A 5 P 2015 Mus musculus processing on the Vision and the set of the source and the source		BC021831 260009E0584 260009E0584 Phrif3 Ppris3 Ppris3 Ppris3 Ppris4 Ppris3 Ppris4 Ppris4 Parlan1b1 Bri3bp Bri3bp Bri3bp Bri3bp Bri3bp Bri3bp Bri2b S100/216/0184 S100/216/	(-1.451 -1.447 -1.446 -1.445 -1.445 -1.437 -1.437 -1.437 -1.437 -1.436 -1.434 -1.434 -1.434 -1.434 -1.434 -1.432 -1.435 -1.435 -1.435 -1.435 -1.435 -1.435 -1.435 -1.435 -1.435 -1.435 -1.435 -1.435 -1.435 -1.435 -1.435 -1.435 -1.435 -1.432 -1.432 -1.432 -1.432 -1.432 -1.432 -1.432 -1.432 -1.432 -1.432 -1.432 -1.432 -1.435 -1.432 -1.422 -1.422 -1.422 -1.422 -1.422 -1.422 -1.422 -1.422 -1.422 -1.422 -1.422 -1.422 -1.422 -1.422 -1.422 -1.422 -1.421 -1.441 -1.440 -1.408 -1.408 -1.408 -1.408 -1.406	-1,743 -7,743 -7,743 -7,744 -7,745	1.788 2.214 2.730 1.266 1.997 3.616 1.038 3.228 3.228 3.228 1.196 2.507 1.223 1.078 1.931 1.223 1.078 1.931 1.233 1.078 1.931 1.235 1.96 1.235 1.078 1.931 1.2519 1.2551 1.410 1.008 1.4451 1.4451 1.4451 1.4451 1.4451
A 3 P 20250 MUC Induction Setty-Conference and provide source water provide a source prove A model (New 17747) A 5 P 2015 Mus musculus processing on the Vision and the set of the source and the source	BC021831 NM 026832 NM 07735 NM 07735 NA 052042 NA 052042 NM 01735 NM 016374 NM 016371 NM 02752 GC025200 640470 AK079037 609122 NM 019501 AK079037 6001950 NM 020196 NM 020196 NM 020196 NM 0201950 NM 0201950 NM 0201950 NM 0201950 NM 027591 NM 0275953 AK030238 AK030236 NM 0175933 AK020357132 05037132	BC021831 260009E05R/ 260009E05R/ Phrif3 Ppme1 Gpd2 Gpd2 Gpd2 Gpd2 Gpd2 Gpd2 Gpd2 Gpd2		$\begin{array}{c} -1,743\\ -1,743\\ -MP\\ -1,566\\ -1,867\\ -1,867\\ -1,867\\ -1,867\\ -1,766\\ -1,766\\ -1,766\\ -1,766\\ -2,563\\ -1,763\\ -2,563\\ -1,426\\ -2,563\\ -1,426\\ -2,563\\ -1,426\\ -2,563\\ -1,413\\ -1,413\\ -1,413\\ -1,413\\ -1,413\\ -1,413\\ -1,413\\ -1,413\\ -1,413\\ -1,413\\ -1,413\\ -1,413\\ -1,413\\ -1,413\\ -1,413\\ -1,413\\ -1,413\\ -2,563\\ -2$	1.788 2.214 2.730 1.226 2.480 2.490 1.997 1.038 3.616 3.626 2.507 1.223 1.078 1.931 2.519 1.634 1.491 1.634 1.400 1.008 1.442 1.442 1.442 1.442 1.447 1.064 1.777
A 31 P 12550 Not miscula scipt-Centry at a syntaments 2 (microninitia south-Centry in a histoge) (Acade), micka (wa (1747o) A 51 P 25719 Not micro-centry (1974) (1972) (1974) (1974) (1974) (1974) (1972) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1972) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1972) (1974) (BC021831 BC021831 MM 029832 MM 07735 MM 07735 MM 07735 MM 07735 MM 07735 MM 07850240 MM 0785082 AK080240 MM 0785082 AK08739 MM 07887 MM 07887 MM 07887 MM 07887 MM 07887 MM 0790 BC024476 MM 07700 BC024476 MM 07700 BC024476 MM 07700 BC024477 MM 0790 BC024477 MM 0790 BC024477 MM 0790 BC024477 MM 0790 BC02477 MM 0790 BC0247 MM 0790 BC024 MM 0790 BC0247 MM 0790 BC024 MM 0 0790 BC024 MM 0 0790 BC024 MM 0 0790 BC024 MM 0 0790 MM 0	BC021831 260009E05R4 260009E05R4 Phr13 Phr13 Col444 Phr13 Phr13 Col444 Phr13 Phr13 Phr13 Phr13 Phr13 Phr13 Phr13 Phr13 Phr13 Phr13 Phr13 Phr24 P		$\begin{array}{c} -1,743\\ -1,743\\ -MP\\ -1,602\\ -1,947\\ -1,947\\ -1,947\\ -1,947\\ -1,947\\ -1,946\\ -1,976\\ -1,476\\ -1,776\\ -1,476\\ -1,776\\ -1,476\\ -1,776\\ -1,476\\ -1,778\\ -2,564\\ -1,778\\ -2,564\\ -1,778\\ -2,564\\ -1,778\\ -2,564\\ -2,564\\ -1,778\\ -2,564\\ -2$	1.788 2.214 2.730 1.266 2.460 1.997 3.616 1.038 3.228 1.196 3.228 1.196 3.228 1.196 3.228 1.196 3.228 1.078 1.251 1.251 1.251 1.251 1.251 1.251 1.251 1.251 1.251 1.251 1.251 1.251 1.2555 1.255 1.2555 1.2555 1.2555 1.2555 1.2555 1.2555 1.2555 1.25
A 31 P 12550 Not miscula scipt-Centry at a syntaments 2 (microninitia south-Centry in a histoge) (Acade), micka (wa (1747o) A 51 P 25719 Not micro-centry (1974) (1972) (1974) (1974) (1974) (1974) (1972) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1972) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1972) (1974) (BC021831 BC021831 MM 029832 MM 07735 MM 07735 MM 07735 MM 07735 MM 07735 MM 07850240 MM 0785082 AK080240 MM 0785082 AK08739 MM 07887 MM 07887 MM 07887 MM 07887 MM 07887 MM 0790 BC024476 MM 07700 BC024476 MM 07700 BC024476 MM 07700 BC024477 MM 0790 BC024477 MM 0790 BC024477 MM 0790 BC024477 MM 0790 BC02477 MM 0790 BC0247 MM 0790 BC024 MM 0790 BC0247 MM 0790 BC024 MM 0 0790 BC024 MM 0 0790 BC024 MM 0 0790 BC024 MM 0 0790 MM 0	BC021831 260009E05R4 260009E05R4 Phr13 Phr13 Col444 Phr13 Phr13 Col444 Phr13 Phr13 Phr13 Phr13 Phr13 Phr13 Phr13 Phr13 Phr13 Phr13 Phr13 Phr24 P		$\begin{array}{c} -1,743\\ -1,743\\ -MP\\ -1,602\\ -1,947\\ -1,947\\ -1,947\\ -1,947\\ -1,947\\ -1,946\\ -1,976\\ -1,476\\ -1,776\\ -1,476\\ -1,776\\ -1,476\\ -1,776\\ -1,476\\ -1,778\\ -2,564\\ -1,778\\ -2,564\\ -1,778\\ -2,564\\ -1,778\\ -2,564\\ -2,564\\ -2,564\\ -1,778\\ -2,564\\ -2$	1.788 2.214 2.730 1.286 2.460 1.997 3.616 1.997 1.038 3.1286 3.1286 1.937 1.038 3.228 1.937 2.507 1.223 1.078 1.077 1.078 1.077 1.078 1.077 1.078 1.077 1.078 1.077 1.078 1.0777 1.07777 1.0777 1.07777 1.07777 1.07777 1.0777777 1.07777 1.07777777 1.07777777777
A 3 P 20250 MUC Induction Setty-Conference and provide source water provide a source prove A model (New 17747) A 5 P 2015 Mus musculus processing on the Vision and the set of the source and the source	BC021831 BC021831 MM 029832 MM 07735 MM 07735 MM 07735 MM 07735 MM 07735 MM 07850240 MM 0785082 AK080240 MM 0785082 AK08739 MM 07887 MM 07887 MM 07887 MM 07887 MM 07887 MM 0790 BC024476 MM 07700 BC024476 MM 07700 BC024476 MM 07700 BC024477 MM 0790 BC024477 MM 0790 BC024477 MM 0790 BC024477 MM 0790 BC02477 MM 0790 BC0247 MM 0790 BC024 MM 0790 BC0247 MM 0790 BC024 MM 0 0790 BC024 MM 0 0790 BC024 MM 0 0790 BC024 MM 0 0790 MM 0	BC021831 260009E05R/ 260009E05R/ Phrif3 Ppme1 Gpd2 Gpd2 Gpd2 Gpd2 Gpd2 Gpd2 Gpd2 Gpd2		$\begin{array}{c} -1,743\\ -1,743\\ -MP\\ -1,602\\ -1,947\\ -1,947\\ -1,947\\ -1,947\\ -1,947\\ -1,946\\ -1,946\\ -1,766\\ -1,4766\\ -1,4766\\ -1,4766\\ -1,4766\\ -1,476\\ -1,476\\ -1,476\\ -1,476\\ -1,476\\ -1,476\\ -1,476\\ -1,476\\ -1,476\\ -1,476\\ -1,476\\ -1,476\\ -1,476\\ -2,276\\ -2,276\\ -1,276\\ -2,276\\ -1,276\\ -2,276\\ -1,276\\ -2,276\\ -1,276\\ -2,276\\ -1,276\\ -2,276\\ -1,276\\ -2,276\\ -1,276\\ -2,276\\ -1,276\\ -2,276\\ -1,276\\ -2,276\\ -1,276\\ -2,276\\ -1,276\\ -2,276\\ -1,276\\ -2,276\\ -1,276\\ -2,276$	1.788 2.214 2.730 1.226 2.460 1.997 1.926 2.460 1.997 1.927 1.928 3.616 3.228 3.228 1.196 2.507 1.223 1.078 1.931 2.519 1.834 1.401 1.008 1.442 1.442 1.447 1.064 1.777

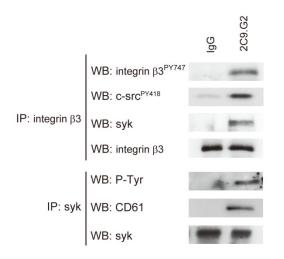


Figure S1. 2C9.G2 induces phosphorylation of Tyr747 (pY747) of $\beta 3$ integrin in mouse platelets

Washed platelets were incubated for 15 min in the presence of 2C9.G2 or IgG, after which cell lysates were prepared. After immunoprecipitation using anti- β 3 integrin or anti-Syk antibodies, western blotting was carried out with the indicated antibodies.

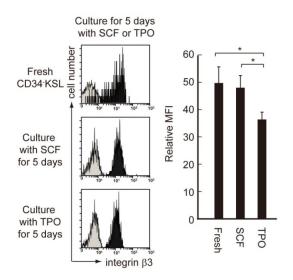


Figure S2. TPO did not enhanced expression of β3 integrin on HSCs

One thousand sorted Wt CD34⁻KSL cells were cultured for 5 days in the presence SCF or TPO. Following the culture, the level of integrin β 3 expression was determined by flow cytometry. "Fresh" indicates uncultured CD34⁻KSL cells. The histograms depict expression of integrin β 3; the graphs depict the relative mean fluorescence intensity (MFI). Data are means ± S.D (*p<0.01).

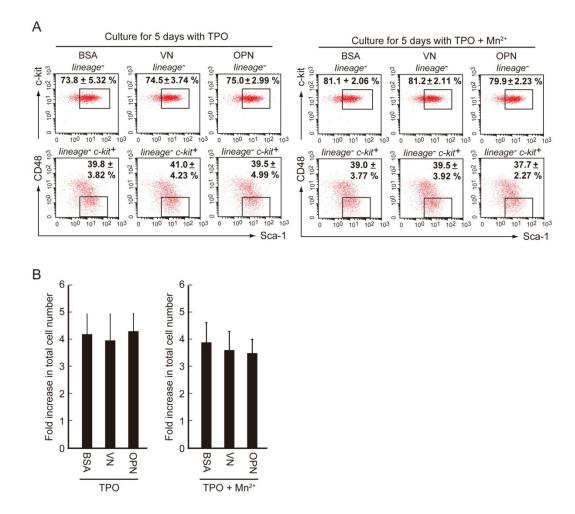


Figure S3. Natural ligands have little effect on HSC expansion

One thousand sorted Wt CD34⁻KSL cells were cultured for 5 days on plates coated with the indicated ligand, with or without Mn^{2+} in the presence of TPO. (A) The percentages of KSL and CD48⁻KSL cells were determined by flow cytometry after culture. The values in the dot plots are means \pm S.D. (B) After the culture, total cell numbers were also counted. The graphs show the fold-increase of total cell number after 5 days of culture. Data are means \pm S.D.

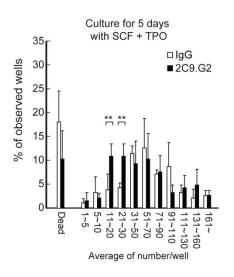


Figure S4. 2C9.G2 suppresses cell division during ex vivo expansion of HSC

Single CD34⁻KSL cells were cultured with 2C9.G2 or IgG in 96-well plates. The Y-axis shows the % observed wells among the 96 wells in each plate, and the X-axis shows the number of cells derived from the single cells in the individual wells after 5 days of culture. Data are means \pm S.D (**p<0.05, *p<0.01, n=6 of independent experiments).

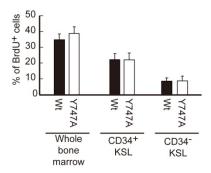


Figure S5. Y747A mutation has little effect on the cell cycle state of HSCs *in vivo* The frequency of BrdU⁺ cells among BMCs was examined using flow cytometry 2 h after administration of BrdU. The graphs depict the % BrdU⁺ cells among the indicated populations. Data are presented as means \pm S.D. (*p<0.01, n>3).