Table 1

Probe set	p-value	fc	Gene Symbol	Gene Title	Gene Ontology Biological Process
	Samples 3-4				
LIF-induced genes					
1456212_x_at	2,1214E-06	26,69	Socs3	suppressor of cytokine signaling 3	7242 // intracellular signaling cascade // inferred from electronic annotation /// 1558 // regulation of cell growth // inferred from electroni
1455899_x_at	9,61616E-06	25,71	Socs3	suppressor of cytokine signaling 3	7242 // intracellular signaling cascade // inferred from electronic annotation /// 1558 // regulation of cell growth // inferred from electroni
1416576_at	3,64506E-06	16,83	Socs3	suppressor of cytokine signaling 3	7242 // intracellular signaling cascade // inferred from electronic annotation /// 1558 // regulation of cell growth // inferred from electroni
1423100_at	7,03917E-05	11,06	Fos	FBJ osteosarcoma oncogene	8151 // cell growth and/or maintenance // inferred from electronic annotation /// 7399 // neurogenesis // inferred from mutant phenotype
1415899_at	2,28315E-05	8,66	Junb	Jun-B oncogene	8151 // cell growth and/or maintenance // inferred from direct assay /// 74 // regulation of cell cycle // inferred from direct assay /// 6355
1459961_a_at	5,41643E-06	5,41	Stat3Loc	---	---
1452519_a_at	3,03454E-06	4,59	Zfp36	zinc finger protein 36	6402 // mRNA catabolism // inferred from sequence or structural similarity
1417065_at	0,001515205	4,06	Egr1	early growth response 1	6355 // regulation of transcription, DNA-dependent // inferred from mutant phenotype /// 46652 // thymocyte differentiation // inferred fro
1427683_at	0,001121372	3,45	Egr2	early growth response 2	42552 // myelination // inferred from mutant phenotype /// 6355 // regulation of transcription, DNA-dependent // inferred from mutant ph
1458308_at	0,001864448	2,41	Sbno2	cDNA sequence BC019206	---
1416442_at	0,009872621	2,26	Ier2	immediate early response 2	---
1417483_at	0,000599049	2,25	Nfkbiz	nuclear factor of kappa light polypeptide	6954 // inflammatory response // inferred from direct assay /// 6355 // regulation of transcription, DNA-dependent // inferred from seque
1419647_a_at	0,000199306	2,04	Ier3	immediate early response 3	---
1423619_at	0,000481877	2,03	Rasd1	RAS, dexamethasone-induced 1	7264 // small GTPase mediated signal transduction // inferred from sequence or structural similarity
1443721_x_at	0,00027872	1,99	Sbno2	cDNA sequence BC019206	---
1447337_at	0,000435249	1,92	Dapp1	Dual adaptator for PY and PI3K	PI3K regulator
1439349_at	4,97613E-05	1,78	Sbno2	cDNA sequence BC019206	---
1438331_at	0,001060547	1,77	Ypel2	Yippee-like 2 (Drosophila)	Nucleus
1457824_at	0,004058413	1,66	Plscr1	---	---
1451739_at	0,001302309	1,58	Klf5	Kruppel-like factor 5	6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation
1457404_at	0,004809154	1,52	Nfkbiz	nuclear factor of kappa light polypeptide	6954 // inflammatory response // inferred from direct assay /// 6355 // regulation of transcription, DNA-dependent // inferred from seque
1458075_at	0,011830034	1,51	Dst	Dystonin	7155 // cell adhesion // inferred from electronic annotation /// 7050 // cell cycle arrest // inferred from sequence or structural similarity ///
1444598_at	0,000468387	1,51	Etv6	Ets variant 6 (Tel oncogen)	Transcription factor
1441177_at	0,00069422	1,50	Pabpc1	Poly A binding protein, cytoplasmic 1	---

LIF-repressed genes					
1459137_at	0,000442857	-1,92	---	---	---
1444320_at	0,013829571	-1,90	Ddhd2	DDHD domain containing 2	---
1457304_at	0,044704995	-1,68	---	---	---
1441333_at	0,037545575	-1,67	Trps1	Trichorhinophalangeal syndrome I (hum	6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation
1442445_at	0,010491985	-1,63	2610027H17Rik	RIKEN cDNA 2610027H17 gene	---
1438824_at	0,002016909	-1,62	Slc20a1	Solute carrier family 20, member 1	Receptor activity, phosphate transport, extracellular membrane
1440717_at	0,014256571	-1,58	---	---	---
1443729_at	0,024234385	-1,58	Mtss1	metastasis suppressor 1	7015 // actin filament organization // inferred from direct assay /// 30041 // actin filament polymerization // inferred from direct assay
1457712_at	0,025091997	-1,56	Chd8	chromodomain helicase DNA binding pr	Embryonic development
1443088_at	0,03757275	-1,53	9930031P18Rik	RIKEN cDNA 9930031P18 gene	---
1458031_at	0,001767302	-1,52	B230315F11Rik	RIKEN cDNA B230315F11 gene	6810 // transport // inferred from sequence or structural similarity
1438896_at	0,042316337	-1,51	DNajc6	Adult male pituitary gland cDNA	Phosphatase activity

Table 2

Probe set	pvalue	fc	Gene Symbol	Gene Title	Gene Ontology Biological Process
	Samples 5-6				
LIF-induced genes					
1456212_x_at	6,56769E-06	17,32	Socs3	suppressor of cytokine signaling 3	7242 // intracellular signaling cascade // inferred from electronic annotation /// 1558 // regulation of cell growth // inferred fro
1455899_x_at	1,72347E-05	16,97	Socs3	suppressor of cytokine signaling 3	7242 // intracellular signaling cascade // inferred from electronic annotation /// 1558 // regulation of cell growth // inferred fro
1416576_at	4,24304E-05	9,23	Socs3	suppressor of cytokine signaling 3	7242 // intracellular signaling cascade // inferred from electronic annotation /// 1558 // regulation of cell growth // inferred fro
1423100_at	0,000524225	4,44	Fos	FBJ osteosarcoma oncogene	8151 // cell growth and/or maintenance // inferred from electronic annotation /// 7399 // neurogenesis // inferred from mutant
1415899_at	0,000428514	3,41	Junb	Jun-B oncogene	8151 // cell growth and/or maintenance // inferred from direct assay /// 74 // regulation of cell cycle // inferred from direct ass
1459961_a_at	0,001754324	3,03	Stat3Loc	---	---
1452519_a_at	0,000126269	2,48	Zfp36	zinc finger protein 36	6402 // mRNA catabolism // inferred from sequence or structural similarity
1417065_at	0,004307178	2,37	Egr1	early growth response 1	6355 // regulation of transcription, DNA-dependent // inferred from mutant phenotype /// 46652 // thymocyte differentiation //
1416442_at	0,027960612	1,83	Ier2	immediate early response 2	---
1427683_at	0,010852284	1,80	Egr2	early growth response 2	42552 // myelination // inferred from mutant phenotype /// 6355 // regulation of transcription, DNA-dependent // inferred from
1451739_at	0,000710647	1,63	Klf5	Kruppel-like factor 5	6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation
1423619_at	0,000183761	1,63	Rasd1	RAS, dexamethasone-induced 1	7264 // small GTPase mediated signal transduction // inferred from sequence or structural similarity
1417395_at	0,018605917	1,54	Klf4	Kruppel-like factor 4 (gut)	6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation
1419647_a_at	0,000271929	1,52	Ier3	immediate early response 3	---

Table 3

Probe set	pvalue	fc	Gene Symbol	Gene Title	Gene Ontology Biological Process	
	Samples 3-1					
1455899_x_at	5,68149E-05	11,11	*Socs3*	suppressor of cytokine signaling 3	7242 // intracellular signaling cascade // inferred from electronic annotation /// 1558 // regulation of cell growth // in	
1456212_x_at	3,69929E-05	9,77	*Socs3*	suppressor of cytokine signaling 3	7242 // intracellular signaling cascade // inferred from electronic annotation /// 1558 // regulation of cell growth // in	
1416576_at	0,000256498	7,08	*Socs3*	suppressor of cytokine signaling 3	7242 // intracellular signaling cascade // inferred from electronic annotation /// 1558 // regulation of cell growth // in	
1418133_at	7,88695E-05	4,58	Bcl3	B-cell leukemia/lymphoma 3	6355 // regulation of transcription, DNA-dependent // inferred from sequence or structural similarity	
1429833_at	0,000836675	3,75	Ly6g6e	lymphocyte antigen 6 complex, locus G6E	Transmembrane receptor/TGFb receptor activity	
1416715_at	0,000528589	3,08	Gjb3	gap junction membrane channel protein bet	7154 // cell communication // inferred from electronic annotation /// 7267 // cell-cell signaling // inferred from electro	
1429377_at	0,00344185	2,99	2410004A20Rik	RIKEN cDNA 2410004A20 gene	---	
1416454_s_at	0,009344918	2,92	Acta2 /// 0610041G0	actin, alpha 2, smooth muscle, aorta /// RIK	7010 // cytoskeleton organization and biogenesis // inferred from electronic annotation /// 7517 // muscle developm	
1430208_at	0,011955854	2,82	2410039E07Rik	RIKEN cDNA 2410039E07 gene	---	
1418569_at	0,003580766	2,77	2410043F08Rik	RIKEN cDNA 2410043F08 gene	---	
1449590_a_at	0,001071447	2,70	Mras	muscle and microspikes RAS	7264 // small GTPase mediated signal transduction // inferred from electronic annotation	
1415899_at	0,010046099	2,66	*Junb*	Jun-B oncogene	8151 // cell growth and/or maintenance // inferred from direct assay /// 74 // regulation of cell cycle // inferred from	
1424719_a_at	0,005072824	2,59	Mapt	microtubule-associated protein tau	7026 // microtubule stabilization // inferred from electronic annotation /// 7017 // microtubule-based process // infer	
1418467_at	0,002263181	2,56	Smarcd3	SWI/SNF related, matrix associated, actin d	18342 // protein prenylation // inferred from sequence or structural similarity	
1449141_at	0,000642355	2,56	2410043F08Rik	RIKEN cDNA 2410043F08 gene	---	
1448213_at	0,010601507	2,56	Anxa1	annexin A1	50482 // arachidonic acid secretion // inferred from mutant phenotype /// 7049 // cell cycle // inferred from mutant p	
1449204_at	0,00011577	2,51	Gjb5	gap junction membrane channel protein bet	7154 // cell communication // inferred from electronic annotation /// 7267 // cell-cell signaling // inferred from electro	
1431057_a_at	0,001819217	2,49	2310046G15Rik	RIKEN cDNA 2310046G15 gene	6508 // proteolysis and peptidolysis // inferred from electronic annotation	
1417395_at	0,003998489	2,49	*Klf4*	Kruppel-like factor 4 (gut)	6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation	
1417013_at	0,000397666	2,38	Hspb8 *	heat shock 27kDa protein 8	6457 // protein folding // inferred from electronic annotation /// 6986 // response to unfolded protein // inferred from	
1418091_at	0,00315329	2,38	Tcfcp2l1	transcription factor CP2-like 1	122 // negative regulation of transcription from Pol II promoter // inferred from direct assay	
1421830_at	0,000833105	2,28	Ak3l1	Adenylate kinase 3-like 1	Nucleic acid metabolism/ Mitochondria	
1418470_at	0,000531266	2,26	Yes	Yamaguchi sarcoma viral (v-yes) oncogene	8151 // cell growth and/or maintenance // inferred from electronic annotation /// 15758 // glucose transport // inferre	
1439757_s_at	0,000335774	2,20	Epha4	Eph receptor A4	7628 // adult walking behavior // inferred from mutant phenotype /// 7411 // axon guidance // inferred from mutant p	
1433977_at	0,008966506	2,20	AW536289	expressed sequence AW536289	---	
1417394_at	0,004902775	2,18	*Klf4*	Kruppel-like factor 4 (gut)	6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation	
1434500_at	0,00191481	2,14	Ttyh2	Tweety homolog-like 2 (Drsophila)	Integral to membrane	
1450387_s_at	0,000766493	2,11	Ak3l1	Adenylate kinase 3-like 1	Nucleic acid metabolism/ Mitochondria	
1460700_at	0,001390044	2,10	Stat3	signal transducer and activator of transcript	7259 // JAK-STAT cascade // inferred from direct assay /// 6953 // acute-phase response // inferred from electroni	
1423669_at	0,009401474	2,10	Col1a1	procollagen, type I, alpha 1	7155 // cell adhesion // inferred from electronic annotation /// 6817 // phosphate transport // inferred from electroni	

1450641_at	3,91911E-05	2,09	Vim *	vimentin	45103 // intermediate filament-based process // inferred from mutant phenotype	
1437277_x_at	0,013512365	2,06	Tgm2	transglutaminase 2, C polypeptide	18149 // peptide cross-linking // inferred from electronic annotation /// 6508 // proteolysis and peptidolysis // inferre	
1442434_at	0,009138947	2,05	D8Ertd82e *	NA segment, Chr 8, ERATO Doi 82, express	---	
1436926_at	0,003857986	2,02	**Esrrb**	estrogen related receptor, beta	6605 // protein targeting // inferred from sequence or structural similarity /// 6355 // regulation of transcription, DNA	
1422914_at	0,008086304	1,99	Sp5	trans-acting transcription factor 5	6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation	
1427238_at	0,008815546	1,96	Fbxo15	F-box protein 15	6512 // ubiquitin cycle // inferred from electronic annotation	
1423786_at	0,00826878	1,96	8430410A17Rik	RIKEN cDNA 8430410A17 gene	---	
1453419_at	0,00408252	1,95	2900078C09Rik	RIKEN cDNA 2900078C09 gene	---	
1437247_at	0,001893341	1,93	Fosl2	fos-like antigen 2	6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation	
1422965_at	0,001686477	1,93	Agtrap	angiotensin II, type I receptor-associated pr	8217 // regulation of blood pressure // inferred from mutant phenotype	
1449254_at	0,002689271	1,91	Spp1	secreted phosphoprotein 1	7155 // cell adhesion // inferred from electronic annotation /// 1503 // ossification // inferred from electronic annotati	
1421829_at	0,016071757	1,91	Ak3l1	Adenylate kinase 3-like 1	Nucleic acid metabolism/ Mitochondria	
1435040_at	0,005097718	1,91	Irak3	interleukin-1 receptor-associated kinase 3	6915 // apoptosis // inferred from sequence or structural similarity /// 6468 // protein amino acid phosphorylation // i	
1422937_at	0,008822928	1,90	Fzd5	frizzled homolog 5 (Drosophila)	7186 // G-protein coupled receptor protein signaling pathway // inferred from electronic annotation /// 16055 // Wnt	
1422912_at	0,002271737	1,89	**Bmp4**	bone morphogenetic protein 4	30509 // BMP signaling pathway // inferred from direct assay /// 1525 // angiogenesis // inferred from mutant phen	
1420973_at	0,005555001	1,88	Arid5b	AT rich interactive domain 5B (Mrf1 like)	6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation	
1456434_x_at	0,00652875	1,88	Hspb8 *	heat shock 27kDa protein 8	6457 // protein folding // inferred from electronic annotation /// 6986 // response to unfolded protein // inferred from	
1460454_at	0,004294003	1,86	2010001H14Rik	RIKEN cDNA 2010001H14 gene	---	
1449090_a_at	0,011111787	1,86	**Yes**	Yamaguchi sarcoma viral (v-yes) oncogene	8151 // cell growth and/or maintenance // inferred from electronic annotation /// 15758 // glucose transport // inferre	
1437100_x_at	6,01632E-05	1,84	Pim3	proviral integration site 3	6468 // protein amino acid phosphorylation // inferred from electronic annotation	
1417500_a_at	0,010379111	1,84	Tgm2	transglutaminase 2, C polypeptide	18149 // peptide cross-linking // inferred from electronic annotation /// 6508 // proteolysis and peptidolysis // inferre	
1421929_at	0,00525225	1,81	Epha4	Eph receptor A4	7628 // adult walking behavior // inferred from mutant phenotype /// 7411 // axon guidance // inferred from mutant p	
1456292_a_at*	0,005481956	1,81	Vim*	vimentin	45103 // intermediate filament-based process // inferred from mutant phenotype	
1451123_at	0,001313395	1,79	C330016O10Rik	RIKEN cDNA C330016O10 gene	6605 // protein targeting // inferred from sequence or structural similarity	
1450781_at	0,000705393	1,79	Hmga2	high mobility group AT-hook 2	6323 // DNA packaging // inferred from electronic annotation /// 7001 // chromosome organization and biogenesis (	
1438684_at	0,000101018	1,78	Nuak1	Znuak- SNF1-like kinase 1	Kinase activity	
1438118_x_at	0,001001756	1,78	Vim *	vimentin	45103 // intermediate filament-based process // inferred from mutant phenotype	
1460220_a_at	0,014210962	1,78	Csf1	colony stimulating factor 1 (macrophage)	8151 // cell growth and/or maintenance // inferred from electronic annotation /// 40018 // positive regulation of body	
1417193_at	0,001234577	1,78	Sod2	superoxide dismutase 2, mitochondrial	6801 // superoxide metabolism // inferred from mutant phenotype	
1448819_at	0,003414435	1,76	Eif2s2	eukaryotic translation initiation factor 2, sub	6412 // protein biosynthesis // inferred from electronic annotation /// 6413 // translational initiation // inferred from el	
1438175_x_at	0,001734614	1,75	Myom2	myomesin 2	6936 // muscle contraction // inferred from physical interaction /// 7517 // muscle development // inferred from sequ	
1429388_at	0,004540293	1,75	**Nanog**	Nanog homeobox	17145 // stem cell division // inferred from direct assay	
					902 // cellular morphogenesis // inferred from sequence or structural similarity /// 7010 // cytoskeleton organization	

Table 4

Probe set	pvalue	fc	Gene Symbol	Gene Title	Gene ontology Biological Process
	Samples 5-1				
1456212_x_at	4,90167E-05	-14,21	*Socs3*	suppressor of cytokine signaling 3	7242 // intracellular signaling cascade // inferred from electronic annotation /// 1558 // regulation of cell growth // inf
1455899_x_at	1,9022E-05	-13,35	*Socs3*	suppressor of cytokine signaling 3	7242 // intracellular signaling cascade // inferred from electronic annotation /// 1558 // regulation of cell growth // inf
1426858_at	0,00069156	-7,86	Inhbb	Inhibin beta-B	8151 // cell growth and/or maintenance // inferred from electronic annotation /// 40007 // growth // inferred from elec
1456242_at	0,008279581	-7,20	Esgp	Embryonic stem cell and germ cell specific	---
1416576_at	9,88461E-06	-6,32	*Socs3*	suppressor of cytokine signaling 3	7242 // intracellular signaling cascade // inferred from electronic annotation /// 1558 // regulation of cell growth // inf
1417394_at	0,002060175	-5,74	*Klf4*	Kruppel-like factor 4 (gut)	6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation
1416529_at	0,001312135	-5,70	Emp1	epithelial membrane protein 1	16049 // cell growth // inferred from sequence or structural similarity
1418133_at	1,11764E-05	-5,41	Bcl3	B-cell leukemia/lymphoma 3	6355 // regulation of transcription, DNA-dependent // inferred from sequence or structural similarity
1425538_x_at	0,001222694	-5,34	Ceacam1	CEA-related cell adhesion molecule 1	---
1417395_at	0,002966638	-5,25	*Klf4*	Kruppel-like factor 4 (gut)	6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation
1449590_a_at	0,000317026	-5,19	Mras	muscle and microspikes RAS	7264 // small GTPase mediated signal transduction // inferred from electronic annotation
1418091_at	0,001331556	-4,89	Tcfcp2l1	transcription factor CP2-like 1	122 // negative regulation of transcription from Pol II promoter // inferred from direct assay
1429377_at	0,000785436	-4,84	2410004A20Rik	RIKEN cDNA 2410004A20 gene	---
1436905_x_at	0,001865856	-4,40	Laptm5	lysosomal-associated protein transmembra	---
1429366_at	0,003097511	-4,28	Lrrc34	Leucin rich repeat containing 34	---
1431416_a_at	0,003572981	-4,26	Jam2	junction adhesion molecule 2	---
1435040_at	0,000609101	-4,21	Irak3	interleukin-1 receptor-associated kinase 3	6915 // apoptosis // inferred from sequence or structural similarity /// 6468 // protein amino acid phosphorylation // i
1436568_at	0,003603632	-4,11	Jam2	junction adhesion molecule 2	---
1437165_a_at	0,000700267	-4,10	Pcolce	procollagen C-proteinase enhancer protei	6508 // proteolysis and peptidolysis // inferred from direct assay
1436926_at	0,002052319	-4,09	Esrrb	estrogen related receptor, beta	6605 // protein targeting // inferred from sequence or structural similarity /// 6355 // regulation of transcription, DNA-
1418569_at	0,001666767	-4,08	Fblim1	Filamin binding LIM 1 protein	---
1427630_x_at	0,002191884	-3,78	Ceacam1	CEA-related cell adhesion molecule 1	Positive regulation of MAPK activity/ Receptor activity
1422458_at	0,003825208	-3,76	Tcl1	T-cell lymphoma breakpoint 1	---
1449408_at	0,004782744	-3,68	Jam2	junction adhesion molecule 2	---
1434025_at	0,003231977	-3,64	---	---	---
1436291_a_at	0,001913821	-3,59	Dpys	dihydropyrimidinase	---
1416715_at	0,000235973	-3,53	Gjb3	gap junction membrane channel protein be	7154 // cell communication // inferred from electronic annotation /// 7267 // cell-cell signaling // inferred from electro
1448029_at	0,004623186	-3,49	Tbx3	T-box 3	7569 // cell aging // inferred from direct assay /// 7275 // development // inferred from electronic annotation /// 1648
1460682_s_at	0,000704938	-3,43	Ceacam2	CEA-related cell adhesion molecule 2	---
1448433_a_at	0,000370218	-3,41	Pcolce	procollagen C-proteinase enhancer protei	6508 // proteolysis and peptidolysis // inferred from direct assay

1455604_at	0,000902695	-3,37	---	---	---
1434917_at	0,001386305	-3,34	Cobl	cordon-bleu	1843 // neural tube closure // inferred from genetic interaction
1421840_at	0,000503398	-3,29	Abca1	ATP-binding cassette, sub-family A (ABC1	8203 // cholesterol metabolism // inferred from direct assay /// 30301 // cholesterol transport // inferred from direct a
1429833_at	0,001107136	-3,29	Ly6g6e	lymphocyte antigen 6 complex, locus G6E	---
1424719_a_at	0,004445954	-3,26	Mapt	microtubule-associated protein tau	7026 // microtubule stabilization // inferred from electronic annotation /// 7017 // microtubule-based process // inferr
1435374_at	0,000462542	-3,26	---	---	---
1449530_at	0,001257967	-3,24	Trps1	trichorhinophalangeal syndrome I (human)	6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation
1449141_at	0,0005966	-3,23	Fblim1	Filamin binding LIM 1 protein	---
1431417_at	0,00154475	-3,23	Jam2	junction adhesion molecule 2	---
1449090_a_at	0,001960297	-3,21	Yes	Yamaguchi sarcoma viral (v-yes) oncogen	8151 // cell growth and/or maintenance // inferred from electronic annotation /// 15758 // glucose transport // inferre
1422986_at	0,002795399	-3,14	Esrrb	estrogen related receptor, beta	6605 // protein targeting // inferred from sequence or structural similarity /// 6355 // regulation of transcription, DNA
1427238_at	0,005693231	-3,13	Fbxo15	F-box protein 15	6512 // ubiquitin cycle // inferred from electronic annotation
1418470_at	0,004845082	-3,06	Yes	Yamaguchi sarcoma viral (v-yes) oncogen	8151 // cell growth and/or maintenance // inferred from electronic annotation /// 15758 // glucose transport // inferre
1455300_at	0,005488317	-3,05	E130014J05Rik	RIKEN cDNA E130014J05 gene	---
1422123_s_at	0,000461485	-3,05	Ceacam2 /// Ceacam	CEA-related cell adhesion molecule 2 /// C	---
1449254_at	0,001719978	-3,04	Spp1	secreted phosphoprotein 1	7155 // cell adhesion // inferred from electronic annotation /// 1503 // ossification // inferred from electronic annotati
1444390_at	0,005246027	-3,02	Prdm14	PR domain containing 14	Transcription factor
1430125_s_at	0,006272053	-3,00	Pqlc1	PQ loop repeat containing 1	---
1416808_at	0,003817271	-2,95	Nid1	nidogen 1	7155 // cell adhesion // inferred from electronic annotation /// 7160 // cell-matrix adhesion // inferred from direct ass
1420619_a_at	0,002084343	-2,90	Aes1/2	amino-terminal enhancer of split	16055 // Wnt receptor signaling pathway // inferred from electronic annotation /// 16481 // negative regulation of tra
1456521_at	0,00704939	-2,86	---	---	---
1450624_at	0,001014706	-2,85	Bhmt	betaine-homocysteine methyltransferase	9086 // methionine biosynthesis // traceable author statement
1433735_a_at	0,003455084	-2,81	Tmem64	Transmembrane protein 64	---
1430208_at	0,000507045	-2,80	2410039E07Rik	RIKEN cDNA 2410039E07 gene	---
1450494_x_at	0,000230263	-2,80	Ceacam1	CEA-related cell adhesion molecule 1	---
1440739_at	0,004191212	-2,79	Vegfc	vascular endothelial growth factor C	1525 // angiogenesis // inferred from electronic annotation /// 8151 // cell growth and/or maintenance // inferred fro
1419417_at	0,003048127	-2,78	Vegfc	vascular endothelial growth factor C	1525 // angiogenesis // inferred from electronic annotation /// 8151 // cell growth and/or maintenance // inferred fro
1418362_at	0,008414517	-2,78	Zfp42	zinc finger protein 42	6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation
1422912_at	0,000914813	-2,74	Bmp4	bone morphogenetic protein 4	30509 // BMP signaling pathway // inferred from direct assay /// 1525 // angiogenesis // inferred from mutant pheno
1423508_at	0,001766282	-2,73	Myst4	MYST histone acetyltransferase monocyti	16573 // histone acetylation // inferred from direct assay
1449204_at	0,000151742	-2,72	Gjb5	gap junction membrane channel protein b	7154 // cell communication // inferred from electronic annotation /// 7267 // cell-cell signaling // inferred from electro
1435084_at	0,005389269	-2,72	C730049O14Rik	RIKEN cDNA C730049O14 gene	---
1434286_at	0,007516694	-2,72	Trps1	trichorhinophalangeal syndrome I (human)	6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation
1425675_s_at	0,000944016	-2,71	Ceacam1	CEA-related cell adhesion molecule 1	---

1419288_at	0,005219055	-2,70	Jam2	junction adhesion molecule 2	---
1421375_a_at	0,009926975	-2,70	S100a6	S100 calcium binding protein A6 (calcyclin	7049 // cell cycle // inferred from electronic annotation /// 8283 // cell proliferation // inferred from electronic annotat
1420973_at	0,0010852	-2,69	Arid5b	AT rich interactive domain 5B (Mrf1 like)	6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation
1438214_at	0,006528131	-2,67	Trps1	trichorhinophalangeal syndrome I (human)	6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation
1418467_at	0,005009153	-2,67	Smarcd3	SWI/SNF related, matrix associated, actin	18342 // protein prenylation // inferred from sequence or structural similarity
1423786_at	0,000188725	-2,63	8430410A17Rik	RIKEN cDNA 8430410A17 gene	---
1451021_a_at	0,000767349	-2,62	*Klf5*	Kruppel-like factor 5	6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation
1417760_at	0,002974581	-2,61	Nr0b1	clear receptor subfamily 0, group B, membe	16481 // negative regulation of transcription // inferred from direct assay /// 6355 // regulation of transcription, DNA
1423281_at	0,005197813	-2,57	Stmn2	stathmin-like 2	7242 // intracellular signaling cascade // inferred from electronic annotation
1419418_a_at	0,004558273	-2,57	Morc	microrchidia	7283 // spermatogenesis // inferred from mutant phenotype
1421830_at	0,004155014	-2,56	Ak3l1	Adenylate kinase 3 alpha-like 1	Nucleic acid metabolism
1430781_at	0,00067255	-2,56	Ak7	adenylate kinase 7	---
1454974_at	0,006595416	-2,55	Ntn1	netrin 1	6915 // apoptosis // inferred from electronic annotation /// 7411 // axon guidance // inferred from mutant phenotype
1429525_s_at	0,004447781	-2,54	Myo1f	myosin IF	7010 // cytoskeleton organization and biogenesis // inferred from electronic annotation
1433596_at	0,007070887	-2,53	Dnajc6	DnaJ (Hsp40) homolog, subfamily C, mem	---
1436419_a_at	0,008144789	-2,53	1700097N02Rik	RIKEN cDNA 1700097N02 gene	---
1449187_at	0,004908424	-2,50	Pdgfa	platelet derived growth factor, alpha	30036 // actin cytoskeleton organization and biogenesis // inferred from direct assay /// 8151 // cell growth and/or
1426587_a_at	0,002388451	-2,49	Stat3	signal transducer and activator of transcrip	7259 // JAK-STAT cascade // inferred from direct assay /// 6953 // acute-phase response // inferred from electronic
1429388_at	0,005157615	-2,48	Nanog	Nanog homeobox	17145 // stem cell division // inferred from direct assay
1451835_at	0,000457924	-2,47	Sox21	SRY-box containing gene 21	6355 // regulation of transcription, DNA-dependent // inferred from direct assay
1445669_at	0,007603938	-2,44	Spry4	sprouty homolog 4 (Drosophila)	7275 // development // inferred from electronic annotation /// 9966 // regulation of signal transduction // inferred fro
1424067_at	0,001793668	-2,43	Icam1	intercellular adhesion molecule	7155 // cell adhesion // inferred from direct assay /// 16337 // cell-cell adhesion // inferred from electronic annotatio
1453419_at	0,000938459	-2,42	2900078C09Rik	RIKEN cDNA 2900078C09 gene	---
1437435_at	0,000408331	-2,42	1700061G19Rik	RIKEN cDNA 1700061G19 gene	8152 // metabolism // inferred from sequence or structural similarity
1417073_a_at	0,006763115	-2,40	Qk	quaking	7626 // locomotory behavior // inferred from electronic annotation /// 42692 // muscle cell differentiation // inferred f
1429021_at	0,009751397	-2,40	Epha4	Eph receptor A4	7628 // adult walking behavior // inferred from mutant phenotype /// 7411 // axon guidance // inferred from mutant
1438781_at	0,008461031	-2,40	---	Adult male aorta and vein cDNA, RIKEN f	---
1452242_at	0,005550964	-2,40	Cep55	Centrosomal protein 55	---
1432229_a_at	0,000112905	-2,39	Cdyl2	chromodomain protein, Y chromosome-lik	---
1453683_a_at	0,005072065	-2,38	Cep55	Centrosomal protein 55	---
1422937_at	0,000885572	-2,35	Fzd5	frizzled homolog 5 (Drosophila)	7186 // G-protein coupled receptor protein signaling pathway // inferred from electronic annotation /// 16055 // Wnt
1452532_x_at	0,001729847	-2,35	Ceacam1	CEA-related cell adhesion molecule 1	---
1450387_s_at	0,000552887	-2,34	Ak3l1	Adenylate kinase 3 alpha-like 1	Nucleic acid metabolism
1429399_at	0,002536554	-2,34	Rnf125	ring finger protein 125	---

1460700_at	0,000758697	-2,34	Stat3	signal transducer and activator of transcrip	7259 // JAK-STAT cascade // inferred from direct assay /// 6953 // acute-phase response // inferred from electronic
1420410_at	0,002645406	-2,31	Nr5a2	nuclear receptor subfamily 5, group A, me	8206 // bile acid metabolism // inferred from mutant phenotype /// 42632 // cholesterol homeostasis // inferred from
1429802_at	0,004729104	-2,27	Dhrs10	dehydrogenase/reductase (SDR family) m	---
1427004_at	0,000660207	-2,26	Fbxo2	F-box only protein 2	30163 // protein catabolism // inferred from electronic annotation /// 6512 // ubiquitin cycle // inferred from electroni
1457445_at	0,003639341	-2,26	Trps1	Trichorhinophalangeal syndrome I (human	6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation
1436932_at	0,009428344	-2,24	Grhl3	Grainy head-like 3 (Drosophila)	Transcription factor/ ectoderm/ Epiderm/ wound healing
1423280_at	0,00200439	-2,24	Stmn2	stathmin-like 2	7242 // intracellular signaling cascade // inferred from electronic annotation
1454984_at	0,004898549	-2,23	---	---	---
1451782_a_at	0,001654787	-2,22	Slc29a1	solute carrier family 29 (nucleoside transp	15858 // nucleoside transport // inferred from direct assay /// 6810 // transport // inferred from sequence or structura
1438223_at	0,001358643	-2,21	Vps54	Vacuolar protein sorting 54 (Yeast)	Protein binding
1432227_at	0,008582055	-2,19	Suv39h1	suppressor of variegation 3-9 homolog 1 (	6323 // DNA packaging // traceable author statement /// 6333 // chromatin assembly or disassembly // inferred from
1434283_at	0,00164546	-2,19	Arid5b	AT-rich interacting domain 5B	---
1450929_at	0,00373745	-2,17	Zfp57	zinc finger protein 57	122 // negative regulation of transcription from Pol II promoter // inferred from direct assay /// 6355 // regulation of t
1422965_at	0,000412674	-2,14	Agtrap	angiotensin II, type I receptor-associated p	8217 // regulation of blood pressure // inferred from mutant phenotype
1431786_s_at	0,003706514	-2,14	1190003J15Rik	RIKEN cDNA 1190003J15 gene	6810 // transport // inferred from electronic annotation
1443621_at	0,008138386	-2,11	---	---	---
1438474_at	0,000593221	-2,11	Ankrd 35	Ankyrin repeat domain 5	---
1448610_a_at	0,003206376	-2,10	Sod2	superoxide dismutase 2, mitochondrial	6801 // superoxide metabolism // inferred from mutant phenotype
1417804_at	0,007629084	-2,10	Rasgrp2	RAS, guanyl releasing protein 2	7242 // intracellular signaling cascade // inferred from sequence or structural similarity /// 7264 // small GTPase me
1420361_at	0,002852296	-2,09	Slc11a1	solute carrier family 11 (proton-coupled di	6826 // iron ion transport // inferred from electronic annotation /// 6810 // transport // inferred from electronic annota
1438672_at	0,005246238	-2,08	Parvb	Parvin beta	Actin binding/ Cell adhesion
1423686_a_at	0,000223554	-2,08	1110020C13Rik	Prr13	Prolin rich 13
1441921_x_at	0,001201237	-2,08	Esrrb	estrogen related receptor, beta	6605 // protein targeting // inferred from sequence or structural similarity /// 6355 // regulation of transcription, DNA-
1417193_at	0,000412356	-2,06	Sod2	superoxide dismutase 2, mitochondrial	6801 // superoxide metabolism // inferred from mutant phenotype
1431979_at	0,00159004	-2,06	4930444M15Rik	RIKEN cDNA 4930444M15 gene	---
1448469_at	0,003256379	-2,04	Nid1	nidogen 1	7155 // cell adhesion // inferred from electronic annotation /// 7160 // cell-matrix adhesion // inferred from direct ass
1454946_at	0,002289226	-2,04	Mybl2	myeloblastosis oncogene-like 2	8151 // cell growth and/or maintenance // inferred from electronic annotation /// 74 // regulation of cell cycle // inferr
1453063_at	0,000449131	-2,04	Cltb	clathrin, light polypeptide (Lcb)	---
1454709_at	0,000666778	-2,04	Tmem 64	Transmembrane protein 64	---
1448890_at	0,004449204	-2,02	Klf2	Kruppel-like factor 2 (lung)	45941 // positive regulation of transcription // inferred from direct assay /// 6355 // regulation of transcription, DNA-
1448845_at	0,0039053	-2,02	Rpp25	ribonuclease P 25 subunit (human)	---
1415899_at	0,000175953	-2,01	*Junb*	Jun-B oncogene	8151 // cell growth and/or maintenance // inferred from direct assay /// 74 // regulation of cell cycle // inferred from
1444531_at	0,001478207	-2,01	Sod2	Superoxyde Dismutase 2	---
1451123_at	0,001730809	-2,01	C330016O10Rik	RIKEN cDNA C330016O10 gene	6605 // protein targeting // inferred from sequence or structural similarity

1460235_at	0,001771319	-2,00	Scarb2	scavenger receptor class B, member 2	7155 // cell adhesion // inferred from sequence or structural similarity
1449231_at	0,002307877	-1,99	Zfp296	zinc finger protein 296	---
1450860_at	0,000610729	-1,99	Lap3	leucine aminopeptidase 3	6508 // proteolysis and peptidolysis // inferred from electronic annotation
1428092_at	0,002493174	-1,98	Cdc5l	cell division cycle 5-like (S. pombe)	910 // cytokinesis // inferred from electronic annotation /// 6605 // protein targeting // inferred from sequence or stru
1423187_at	0,00224195	-1,98	Gabarapl2	gamma-aminobutyric acid (GABA-A) recep	6891 // intra-Golgi transport // inferred from sequence or structural similarity /// 6886 // intracellular protein transpor
1444779_s_at	0,00648575	-1,97	Zfp59	zinc finger protein 59	---
1457435_x_at	0,002031946	-1,96	Myom2	myomesin 2	6936 // muscle contraction // inferred from physical interaction /// 7517 // muscle development // inferred from sequ
1434307_at	0,005028081	-1,95	Tmem 64	Transmembrane protein 64	---
1419896_at	0,002145264	-1,94	BB001228	Expressed sequence BB001228	---
1451416_a_at	0,002590676	-1,94	Tgm1	transglutaminase 1, K polypeptide	9887 // organogenesis // inferred from mutant phenotype /// 19538 // protein metabolism // traceable author statem
1454666_at	0,007951118	-1,93	Klf3	Kruppel-like factor 3 (basic)	6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation
1417656_at	0,008468401	-1,93	Mybl2	myeloblastosis oncogene-like 2	8151 // cell growth and/or maintenance // inferred from electronic annotation /// 74 // regulation of cell cycle // inferr
1434836_at	0,000635058	-1,93	Nfatc2ip	nuclear factor of activated T-cells, cytoplas	6355 // regulation of transcription, DNA-dependent // inferred from direct assay
1460429_at	0,000419498	-1,93	Cdc5l	cell division cycle 5-like (S. pombe)	910 // cytokinesis // inferred from electronic annotation /// 6605 // protein targeting // inferred from sequence or stru
1416239_at	0,00168276	-1,93	Ass1	argininosuccinate synthetase 1	6526 // arginine biosynthesis // inferred from electronic annotation /// 50 // urea cycle // inferred from electronic ann
1426511_at	0,002454152	-1,93	Susd2	sushi domain containing 2	---
1428440_at	0,00695347	-1,92	Slc25a12	solute carrier family 25 (mitochondrial carri	6810 // transport // inferred from sequence or structural similarity
1425503_at	0,00370915	-1,92	Gcnt2	glucosaminyl (N-acetyl) transferase 2, I-bra	---
1426733_at	0,000228377	-1,92	Itpk1	inositol 1,3,4-triphosphate 5/6 kinase	---
1449064_at	0,001820895	-1,91	Tdh	L-threonine dehydrogenase	---

Table 5

					Genes	
	p-value				also expressed	
Probe set	Samples 3-1	fc	Gene Symbol	Gene Title	in irrev. com. Cells	Gene Ontology Biological Process
1436398_at	0,000698423	-3,89	**Lef1**	Lymphoid enhancer binding factor 1	YES	16055 // Wnt receptor signaling pathway // inferred from electronic annotation /// 42475 // odontogen
1425995_s_at	0,000139441	-3,85	Wt1	Wilms tumor homolog	YES	30855 // epithelial cell differentiation // inferred from mutant phenotype /// 1654 // eye morphogenesis
1442655_at	4,00665E-05	-3,59	**Dnmt3b**	DNA methyltransferase 3B	YES	Imprinting
1436964_at	7,40368E-05	-3,59	D7Ertd715e	DNA segment, Chr 7, ERATO Doi 715	NO	---
1454734_at	0,000525552	-3,50	**Lef1**	lymphoid enhancer binding factor 1	YES	16055 // Wnt receptor signaling pathway // inferred from electronic annotation /// 42475 // odontogen
1421299_a_at	0,002056782	-3,37	**Lef1**	lymphoid enhancer binding factor 1	YES	16055 // Wnt receptor signaling pathway // inferred from electronic annotation /// 42475 // odontogen
1439260_a_at	0,001747708	-3,29	Enpp3	ectonucleotide pyrophosphtase/phosphod	NO	9117 // nucleotide metabolism // inferred from sequence or structural similarity
1441145_at	0,004056552	-3,20	D030065N23Rik	RIKEN cDNA D030065N23 gene	NO	---
1460038_at	0,005745518	-3,19	Oct6/Tst-1		YES	---
1427133_s_at	2,81388E-05	-3,17	Lrp2	Low density lipoprotein receptor-related p	YES	6898 // receptor mediated endocytosis // inferred from mutant phenotype /// 6766 // vitamin metabolis
1452320_at	4,99127E-05	-3,14	Lrp2	Low density lipoprotein receptor-related p	YES	6898 // receptor mediated endocytosis // inferred from mutant phenotype /// 6766 // vitamin metabolis
1438454_at	0,00378768	-3,10	B430203M17Rik	RIKEN cDNA B430203M17 gene	YES	---
1425926_a_at	0,003414321	-2,98	**Otx2**	orthodenticle homolog 2 (Drosophila)	YES	9952 // anterior/posterior pattern formation // inferred from mutant phenotype /// 45165 // cell fate cor
1443167_at	0,002470274	-2,84	Rnf12	Ring finger protein 12	NO	16567 // protein ubiquitination // inferred from electronic annotation /// 6355 // regulation of transcripti
1454866_s_at	0,00687868	-2,78	Clic6	chloride intracellular channel 6	NO	6821 // chloride transport // inferred from sequence or structural similarity /// 6811 // ion transport // ir
1453361_at	0,008555241	-2,76	Hells	Helicase, lymphoid specific	NO	DNA methylation, chromatin silencing/ apoptosis
1439123_at	0,003963268	-2,74	Bhc80 **	BRAF35/HDAC2 complex	NO	6355 // regulation of transcription, DNA-dependent // inferred from sequence or structural similarity
1455029_at	0,001597536	-2,74	Kif21a	Kinesin family member 21A	YES	---
1419639_at	0,001235348	-2,74	Ephb2	EphrinB2	YES	---
1439231_at	0,001969269	-2,73	---	---	NO	---
1437548_at	0,005915598	-2,73	Bicd1	BicaudalD,homolog1(Drosophila)	NO	---
1423063_at	0,005813525	-2,72	**Dnmt3a**	DNA methyltransferase 3A	YES	6306 // DNA methylation // inferred from direct assay /// 6349 // imprinting // inferred from mutant phe
1460324_at	0,009058634	-2,72	**Dnmt3a**	DNA methyltransferase 3A	YES	6306 // DNA methylation // inferred from direct assay /// 6349 // imprinting // inferred from mutant phe
1446526_at	0,003670747	-2,70	9330199F22Rik	RIKEN cDNA 9330199F22 gene	NO	---
1460006_at	0,001272593	-2,68	Atbf1	AT motif binding factor 1	YES	6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation
1418391_at	0,001112074	-2,67	Phf21a	PHD finger protein 21A	NO	---
1443526_at**	0,004013711	-2,66	Bhc80**	BRAF35/HDAC2 complex	NO	6355 // regulation of transcription, DNA-dependent // inferred from sequence or structural similarity
1436766_at	0,008667766	-2,66	Luc7l2	LUC7-like 2 (S. cerevisiae)	NO	---
1459722_at	0,002234879	-2,65	Zswim6	Zinc finger Zwim domain containing 6	YES	---
1444646_at	0,00192628	-2,61	8430420F16Rik	RIKEN cDNA 8430420F16 gene	NO	---

1419204_at	0,005644524	-2,60	Dll1	delta-like 1 (Drosophila)	YES	7154 // cell communication // inferred from electronic annotation /// 30154 // cell differentiation // infer
1418390_at	0,003680635	-2,59	Bhc80 **	BRAF35/HDAC2 complex	NO	6355 // regulation of transcription, DNA-dependent // inferred from sequence or structural similarity
1455087_at	0,003031932	-2,59	D7Ertd715e	DNA segment, Chr 7, ERATO Doi 715, ex	NO	---
1419959_s_at	0,000823195	-2,56	C330003B14Rik	RIKEN cDNA C330003B14 gene	NO	6355 // regulation of transcription, DNA-dependent // inferred from sequence or structural similarity
1436082_at	0,002787121	-2,54	Slc24a5	Solute carrier family 24, member 5	NO	---
1416638_at	0,002121067	-2,52	Sall2	sal-like 2 (Drosophila)	YES	6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation
1431633_x_at	0,001918816	-2,52	4930526L06Rik	RIKEN cDNA 4930526L06 gene	NO	---
1419638_at	0,001241028	-2,52	Efnb2	ephrin B2	YES	7275 // development // inferred from electronic annotation /// 7399 // neurogenesis // inferred from ele
1439998_at	0,001823303	-2,50	Jmjd1C	Jumonji domain containing 1C, chromatin	NO	---
1445710_x_at	0,001143813	-2,50	1110051B16Rik	RIKEN cDNA 1110051B16 gene	NO	---
1456960_at	0,007543746	-2,48	Adk	Adenosine kinase	NO	6166 // purine ribonucleoside salvage // inferred from direct assay
1459973_x_at	0,001467471	-2,46	Dpp4	Dipeptidylpeptidase 4	NO	---
1439665_at	0,009035862	-2,42	Gpr23	G protein-coupled receptor 23	YES	---
1454617_at	0,001761097	-2,42	Arrdc3	arrestin domain containing 3	NO	---
1456159_at	0,008150022	-2,41	2900045N06Rik	RIKEN cDNA 2900045N06 gene	NO	---
1456862_at	0,004851524	-2,40	Six4	Sine oculis-related homeobox 4 homolog	NO	Transcription factor/ Development/ muscle/ migration myoblast
1440896_at	0,001652504	-2,36	AA517739	Expressed sequence AA517739	NO	---
1423064_at	0,000422429	-2,36	Dnmt3a	DNA methyltransferase 3A	YES	6306 // DNA methylation // inferred from direct assay /// 6349 // imprinting // inferred from mutant phe
1454806_at	0,002106775	-2,33	D12Ertd553e	DNA segment, Chr 12, ERATO Doi 553, e	NO	---
1444320_at	0,002429669	-2,33	Ddhd2	DDHD domain containing 2	NO	---
1455121_at	0,007693128	-2,32	Mlr2**	Mblk1-related protein-2	NO	6366 // transcription from Pol II promoter // inferred from direct assay
1440011_at	0,001286189	-2,32	Ext1	Exostoses (multiple) 1	NO	8151 // cell growth and/or maintenance // inferred from electronic annotation /// 7492 // endoderm de
1438802_at	0,000235708	-2,32	Foxp1	Forkhead box-1	NO	---
1418911_s_at	0,006289806	-2,32	Acsl4	acyl-CoA synthetase long-chain family me	NO	6631 // fatty acid metabolism // inferred from electronic annotation /// 8152 // metabolism // inferred fr
1426043_a_at	0,002100261	-2,32	Capn3	calpain 3	NO	6508 // proteolysis and peptidolysis // inferred from electronic annotation
1439753_x_at	0,003818434	-2,31	Six4	Sine oculis-related homeobox 4 homolog	NO	---
1448733_at	0,004360239	-2,31	Bmi1	B lymphoma Mo-MLV insertion region 1	NO	7420 // brain development // inferred from mutant phenotype /// 8151 // cell growth and/or maintenan
1427242_at	0,008070486	-2,30	Ddx4	DEAD (Asp-Glu-Ala-Asp) box polypeptide	NO	7275 // development // inferred from electronic annotation
1435952_at	0,004658253	-2,29	---	---	NO	---
1457072_at	0,003396674	-2,28	Bcl11A	B cell lymphoma 11A	NO	B and T cell differentiation
1458031_at	0,002796464	-2,28	B230315F11Rik	RIKEN cDNA B230315F11 gene	NO	6810 // transport // inferred from sequence or structural similarity
1427046_at	0,009888514	-2,27	Tcfcp2l3	transcription factor CP2-like 3	NO	45449 // regulation of transcription // inferred from sequence or structural similarity
1441243_at	0,001147825	-2,26	Zfp532	Zinc finger protein 532	NO	---
1418345_at	0,003981161	-2,26	Tnfsf13	tumor necrosis factor (ligand) superfamily	NO	16064 // humoral defense mechanism (sensu Vertebrata) // inferred from mutant phenotype /// 6955

1451687_a_at	0,009269916	-2,25	Tcf2	Transcription factor 2	NO	---
1442744_at	0,006993936	-2,23	C79248	expressed sequence C79248	NO	---
1452142_at	0,009383967	-2,23	Slc6a1	solute carrier family 6 (neurotransmitter tr	NO	6836 // neurotransmitter transport // inferred from electronic annotation /// 6810 // transport // inferred
1447360_at	0,001298136	-2,23	Tsc22d1	Tsc 22 domain family, member 1	NO	---
1427427_at	0,000729202	-2,22	Ryr3	ryanodine receptor 3	NO	6811 // ion transport // inferred from electronic annotation /// 6810 // transport // inferred from electron
1454138_a_at	0,004823638	-2,22	Stk31	serine threonine kinase 31	NO	6468 // protein amino acid phosphorylation // inferred from electronic annotation
1444851_at	0,002998057	-2,21	Zfp532	Zinc finger protein 532	NO	---
1450044_at	0,000755881	-2,20	**Fzd7**	frizzled homolog 7 (Drosophila)	YES	7186 // G-protein coupled receptor protein signaling pathway // inferred from electronic annotation ///
1437217_at	0,001058179	-2,20	Ankrd6	Ankyrin repeat domain 6	NO	---
1455355_at	0,004336498	-2,19	6030408C04Rik	RIKEN cDNA 6030408C04 gene	NO	---
1423065_at	0,001315052	-2,18	**Dnmt3a**	DNA methyltransferase 3A	YES	6306 // DNA methylation // inferred from direct assay /// 6349 // imprinting // inferred from mutant phe
1456632_at	0,004211458	-2,18	Bcl11A	B cell lymphoma 11A	YES	B and T cell differentiation
1438130_at	0,008941028	-2,15	Taf15	TAF15 RNA polymerase II, TATA box bin	NO	---
1452384_at	0,000843063	-2,15	Enpp3	ectonucleotide pyrophosphatase/phospho	NO	9117 // nucleotide metabolism // inferred from sequence or structural similarity
1437372_at	0,004264305	-2,15	Cpsf6	Cleavage and polyA specific factor 6	NO	---
1442959_at	0,005438897	-2,14	Birc6	baculoviral IAP repeat-containing 6	NO	6916 // anti-apoptosis // inferred from sequence or structural similarity /// 6915 // apoptosis // inferred
1446550_at	0,009820767	-2,14	Gspt1	G1 to S phase transition 1	NO	82 // G1/S transition of mitotic cell cycle // inferred from sequence or structural similarity /// 8283 // ce
1444615_x_at	0,000131032	-2,13	Cbfa2t1h	CBFA2T1 identified gene homolog (huma	NO	6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation
1437660_at	0,006631425	-2,12	Nktr	Natural killer tumor recognition sequence	NO	6457 // protein folding // inferred from electronic annotation
1443729_at	0,004190799	-2,12	Mtss1	metastasis suppressor 1	NO	7015 // actin filament organization // inferred from direct assay /// 30041 // actin filament polymerizati
1427193_at	0,003225889	-2,12	Brd8 **	bromodomain containing 8	NO	---
1459384_at	0,002721374	-2,12	**Dnmt3b**	DNA methyltransferase 3B	YES	---
1438701_at	0,000881439	-2,11	B830009D06Rik	RIKEN cDNA B830009D06 gene	NO	---
1438542_at	0,008859682	-2,11	---	---	NO	---
1427202_at	0,002113065	-2,11	AI256744	RIKEN cDNA 4833442J19 gene	NO	---
1456670_at	0,002007733	-2,10	A930007A09Rik	RIKEN cDNA A930007A09 gene	NO	---
1440910_at	0,003312345	-2,10	Bicd1	Bicaudal D homolog 1	NO	---
1443305_at	0,00163503	-2,09	Sall1	Sal-like 1 (Drosophila)	NO	9887 // organogenesis // inferred from mutant phenotype /// 6355 // regulation of transcription, DNA-
1442671_at	0,007115851	-2,08	Hip2	Huntingtin-interacting protein 2	NO	---
1449947_s_at	0,006366194	-2,08	Atbf1	AT motif binding factor 1	NO	6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation
1437127_at	0,008074357	-2,08	C730040L01Rik	RIKEN cDNA C730040L01 gene	NO	---
1453133_at	0,002144548	-2,08	Slc25a31	Solute carrier family 25, member 31	NO	6810 // transport // inferred from sequence or structural similarity
1439138_at	0,005736702	-2,08	---	---	NO	---
1419241_a_at	0,003684106	-2,06	Aire **	autoimmune regulator (autoimmune polye	NO	6959 // humoral immune response // inferred from mutant phenotype /// 6355 // regulation of transcri

1431632_at	0,004187513	-2,06	4930526L06Rik	RIKEN cDNA 4930526L06 gene	NO	---
1450292_a_at	0,000824094	-2,06	Hormad1	Horma domain containing 1	NO	---
1430526_a_at	0,000161766	-2,05	Smarca2 **	SWI/SNF related, matrix associated, actin	NO	6325 // establishment and/or maintenance of chromatin architecture // traceable author statement ///
1458687_at	0,006861406	-2,04	---	Gene model 177, (NCBI)	NO	---
1440806_x_at	0,003813544	-2,04	5730526G10Rik	RIKEN cDNA 5730526G10 gene	NO	---
1438349_at	0,009701756	-2,04	BC043476	CDNA sequence BC043476	NO	---
1434558_at	0,000662873	-2,04	Wdr47	WD repeat domain 47	NO	---
1438675_at	0,000440531	-2,04	Sfrs8	Splicing factor, arginine/serine-rich 8	NO	6376 // mRNA splice site selection // inferred from electronic annotation
1454809_at	0,000571753	-2,04	Ncoa7	Nuclear receptor coactivator 7	NO	---
1436203_a_at	0,009386969	-2,03	1110059G02Rik	RIKEN cDNA 1110059G02 gene	NO	---
1440764_at	0,001711533	-2,03	Araf	V-ras sarcoma 3611 viral oncogen homol	NO	---
1439775_at	0,005594815	-2,03	Brwd3	Bromo domain and WD repeat domain 3	NO	---
1437766_at	0,008660672	-2,03	---	---	NO	---
1456266_at	0,006943412	-2,03	Rpl30	Ribosomal protein like 30	NO	6412 // protein biosynthesis // inferred from electronic annotation
1452309_at	0,001045822	-2,02	Cgnl1	Cingulin like 1	NO	---
1425035_s_at	0,00280301	-2,02	Dnmt3l	DNA (cytosine-5-)-methyltransferase 3-lik	NO	1701 // embryonic development (sensu Mammalia) // inferred from mutant phenotype /// 6349 // impr
1448665_at	0,003233149	-2,02	Dmd	dystrophin, muscular dystrophy	NO	7517 // muscle development // inferred from mutant phenotype
1437495_at	0,005405981	-2,02	Mbtps2	membrane-bound transcription factor prot	NO	6508 // proteolysis and peptidolysis // inferred from sequence or structural similarity
1436386_x_at	0,001413203	-2,01	---	---	NO	---
1431830_at	0,006254673	-2,00	Zfp329	RIKEN cDNA 4632409L22 gene	NO	---
1434272_at	0,001507326	-1,99	Cpeb2	cytoplasmic polyadenylation element bind	NO	---
1435222_at	0,002079249	-1,99	Foxp1	Forkhead box P1	NO	16481 // negative regulation of transcription // inferred from direct assay /// 6355 // regulation of trans
1457883_at	0,009791883	-1,99	---	Adult male aorta and vein cDNA, RIKEN f	YES	---
1440095_at	0,009608755	-1,99	---	---	NO	---
1438215_at	0,001332298	-1,98	Sfrs3	splicing factor, arginine/serine-rich 3 (SRp	NO	6376 // mRNA splice site selection // inferred from electronic annotation /// 398 // nuclear mRNA splic
1455340_at	0,003087599	-1,97	AI852444	Expressed sequence AI852444	NO	---
1438398_at	0,003679596	-1,97	Rnpc2	RNA binding protein containing 2	NO	6397 // mRNA processing // inferred from electronic annotation /// 398 // nuclear mRNA splicing, via
1438234_at	0,004270877	-1,97	Wdr26	WD repeat domain 26	NO	---
1442566_at	0,005116018	-1,97	---	---	NO	---
1438084_at	0,003915902	-1,97	Adam23	---	NO	---
1447624_s_at	0,001426344	-1,97	Stox2	Storkhead box2	NO	---
1440929_at	0,007529099	-1,96	Ggnbp2	RIKEN cDNA D330017P12 gene	NO	---
1450853_at	0,000558409	-1,96	Tle4 **	transducin-like enhancer of split 4, homol	NO	16055 // Wnt receptor signaling pathway // inferred from direct assay /// 7222 // frizzled signaling pat
1443088_at	0,004066847	-1,95	9930031P18Rik	RIKEN cDNA 9930031P18 gene	NO	---

1439852_at	0,004793771	-1,95	---	---	NO	---
1435931_at	0,003178361	-1,95	---	---	NO	---
1457712_at	0,009868308	-1,94	Chd8	chromodomain helicase DNA binding prot	NO	---
1436153_a_at	0,003185974	-1,93	Zmynd11	Zinc finger, MYND domain containing 11	NO	8151 // cell growth and/or maintenance // inferred from sequence or structural similarity /// 8283 // ce
1440847_at	0,002446985	-1,93	Mtss1	metastasis suppressor 1	NO	7015 // actin filament organization // inferred from direct assay /// 30041 // actin filament polymerizati
1443527_at	0,009612528	-1,93	Terf1	telomeric repeat binding factor 1	NO	7049 // cell cycle // inferred from electronic annotation /// 7001 // chromosome organization and bioge
1436240_at	0,00878518	-1,93	Sost	Sclerotin	NO	Ossification/ repressor of BMP pathway
1424458_at	0,005107134	-1,92	Jmjd2c	jumonji domain containing 2C	NO	6355 // regulation of transcription, DNA-dependent // inferred from sequence or structural similarity
1423066_at	0,002710222	-1,92	Dnmt3a	DNA methyltransferase 3A	YES	6306 // DNA methylation // inferred from direct assay /// 6349 // imprinting // inferred from mutant phe
1428467_at	0,008493213	-1,91	1190002A23Rik	RIKEN cDNA 1190002A23 gene	NO	---
1417850_at	0,00137721	-1,91	Rb1	retinoblastoma 1	NO	45786 // negative regulation of cell cycle // inferred from mutant phenotype /// 122 // negative regulat
1435436_at	0,003535318	-1,91	Epas1	Endothelial PAS domain binding 1	NO	---
1425087_at	0,004814494	-1,91	2310003F16Rik	RIKEN cDNA 2310003F16 gene	NO	---
1441429_at	0,00392271	-1,91	Irs4	Insulin receptor substrate 4	YES	---
1455337_at	0,003911565	-1,90	Fgd4	Fyve, RhoGef and PH domain containing	YES	---
1457731_at	0,002911932	-1,90	Snapc3	small nuclear RNA activating complex, po	NO	---
1438980_x_at	0,004523629	-1,90	4732466D17Rik	RIKEN cDNA 4732466D17 gene	NO	6508 // proteolysis and peptidolysis // inferred from sequence or structural similarity
**** :**	Genes with transient expression in reversibly committed cells					
	(Genes in Cluster 7, Figure 3A)					

Table 6

Probe set	pvalue	fc	Gene Symbol	Gene Title	Gene Ontology Biological Process
	Samples 3-5				
1438883_at	0,004777313	4,61	Fgf5	fibroblast growth factor 5	8151 // cell growth and/or maintenance // inferred from electronic annotation /// 8283 // cell prolifera
1419700_a_at	0,000434875	3,33	Prom1	prominin 1	7602 // phototransduction // inferred from electronic annotation
1416846_a_at	0,005570535	3,21	Pdzrn3	PDZ domain containing RING finger 3	7242 // intracellular signaling cascade // inferred from sequence or structural similarity
1418094_s_at	0,000904162	3,14	Car4	carbonic anhydrase 4	6730 // one-carbon compound metabolism // inferred from electronic annotation
1456329_at	0,006459913	3,12	Prtg	Protogenin	---
1456326_at	0,00198988	3,12	---	Gene model 784, (NCBI)	---
1417216_at	0,00314975	3,07	Pim2	proviral integration site 2	6916 // anti-apoptosis // inferred from direct assay /// 8637 // apoptotic mitochondrial changes // inf
1416454_s_at	0,005101781	3,04	Acta2	actin, alpha 2, smooth muscle, aorta /// RIKEN cDNA	7010 // cytoskeleton organization and biogenesis // inferred from electronic annotation /// 7517 // m
1448949_at	0,006911907	2,95	Car4	carbonic anhydrase 4	6730 // one-carbon compound metabolism // inferred from electronic annotation
1450047_at	0,000956516	2,84	Hs6st2	heparan sulfate 6-O-sulfotransferase 2	---
1426186_a_at	0,001978461	2,83	Fgf5	fibroblast growth factor 5	8151 // cell growth and/or maintenance // inferred from electronic annotation /// 8283 // cell prolifera
1452294_at	0,000394643	2,77	Pcdh1	Protocadherin 1	7156 // homophilic cell adhesion // inferred from sequence or structural similarity /// 6355 // regulati
1452249_at	0,005064851	2,76	Prickle1	prickle like 1 (Drosophila)	---
1436512_at	0,001222169	2,63	Arl4c	ADP-ribosylation factor-like 4C	6886 // intracellular protein transport // inferred from sequence or structural similarity /// 7264 // sma
1454838_s_at	0,004982912	2,58	AW548124	expressed sequence AW548124	---
1421053_at	0,002870865	2,53	Kif1a	kinesin family member 1A	7017 // microtubule-based process // inferred from electronic annotation
1442434_at	0,000100762	2,53	D8Ertd82e *	DNA segment, Chr 8, ERATO Doi 82, expressed	---
1448182_a_at	0,005939422	2,51	Cd24a	CD24a antigen	---
1423104_at	0,003558124	2,47	Irs1	insulin receptor substrate 1	---
1447623_s_at	0,000340965	2,39	---	---	---
1460444_at	0,002379187	2,36	Arrb1	arrestin, beta 1	8277 // regulation of G-protein coupled receptor protein signaling pathway // inferred from mutant p
1433770_at	0,007863733	2,17	Dpysl2	dihydropyrimidinase-like 2	---
1431057_a_at	0,002609858	2,13	Prss23	Protease, serine 23	6508 // proteolysis and peptidolysis // inferred from electronic annotation
1452968_at	0,004169029	2,13	Cthrc1	collagen triple helix repeat containing 1	---
1434442_at	0,004052645	2,12	D5Ertd593e	DNA segment, Chr 5, ERATO Doi 593, expressed	---
1417895_a_at	0,002598594	2,11	Tmem54	Transmembrane protein 54	---
1454788_at	0,004726676	2,11	Arl7	ADP-ribosylation factor-like 7	6886 // intracellular protein transport // inferred from sequence or structural similarity /// 7264 // sma
1434822_at	0,000720744	2,07	Pphln1	periphilin 1	---
1420928_at	0,003888065	2,06	St6gal1	beta galactoside alpha 2,6 sialyltransferase 1	6486 // protein amino acid glycosylation // inferred from electronic annotation
1422962_a_at	0,006706184	2,06	Psmb8	proteosome (prosome, macropain) subunit, beta type	6955 // immune response // inferred from electronic annotation /// 6511 // ubiquitin-dependent prote

1434909_at	0,002403773	2,06	Rragd	Ras-related GTP binding D	---
1417962_s_at	0,004429903	2,03	Ghr	growth hormone receptor	6897 // endocytosis // inferred from electronic annotation
1439485_at	0,009695658	1,99	---	---	---
1445503_at	0,000634457	1,97	---	Gene model 715, (NCBI)	---
1460411_s_at	0,005482096	1,97	AW548124	expressed sequence AW548124	---
1429051_s_at	0,000758536	1,96	Sox11	SRY-box containing gene 11	---
1449022_at	0,003243992	1,96	Nes	nestin	7399 // neurogenesis // inferred from direct assay
1452127_a_at	0,002918082	1,94	Ptpn13	protein tyrosine phosphatase, non-receptor type 13	7242 // intracellular signaling cascade // inferred from sequence or structural similarity /// 6470 // pr
1434112_at	0,001929385	1,93	Lphn2	latrophilin 2	7186 // G-protein coupled receptor protein signaling pathway // traceable author statement
1422917_at	0,001713479	1,91	Epha1	Eph receptor A1	6468 // protein amino acid phosphorylation // inferred from electronic annotation /// 7165 // signal tr
1429315_at	0,00231076	1,91	Syt11	synaptotagmin 11	6810 // transport // inferred from electronic annotation
1425884_at	0,002977836	1,91	Bxdc1	brix domain containing 1	---
* :	Genes with transient repression in Rev. Com. Cells				
	(Genes in Cluster 2, Figure 3A)				

Table 7

Probe set	pvalue	fc	Gene Symbol	Gene Title	Gene Ontology Biological Process
	Samples1-5				
1438883_at	0,001926601	11,34	Fgf5	fibroblast growth factor 5	8151 // cell growth and/or maintenance // inferred from electronic annotation /// 8283 // cell proliferation // in
1448949_at	4,37912E-05	6,05	Car4	carbonic anhydrase 4	6730 // one-carbon compound metabolism // inferred from electronic annotation
1460038_at	0,000995487	4,69	Oct6/pou3f1***	POU domain, class 3, transcription factor 1	6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation
1418094_s_at	1,27225E-05	4,51	Car4	carbonic anhydrase 4	6730 // one-carbon compound metabolism // inferred from electronic annotation
1417216_at	0,000171305	4,47	Pim2	proviral integration site 2	6916 // anti-apoptosis // inferred from direct assay /// 8637 // apoptotic mitochondrial changes // inferred fro
1425995_s_at	0,000900575	4,32	Wt1***	Wilms tumor homolog	30855 // epithelial cell differentiation // inferred from mutant phenotype /// 1654 // eye morphogenesis // infe
1422068_at	3,20269E-06	3,93	Oct6/pou3f1***	POU domain, class 3, transcription factor 1	6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation
1442655_at	0,00187938	3,76	Dnmt3b***	DNA methyltransferase 3B	Imprinting
1441429_at	0,001057555	3,75	Irs4***	Insulin receptor substrate 4	Insulin signaling
1455029_at	0,000343138	3,45	Kif21a***	Kinesin family member 21A	Kinesin complex, microtubule associated
1452294_at	0,000252338	3,44	Pcdh1	Protocadherin 1	7156 // homophilic cell adhesion // inferred from sequence or structural similarity /// 6355 // regulation of tra
1416638_at	0,000218472	3,44	Sall2***	sal-like 2 (Drosophila)	6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation
1418351_a_at	4,96538E-05	3,28	Dnmt3b***	DNA methyltransferase 3B	6306 // DNA methylation // inferred from electronic annotation /// 6349 // imprinting // inferred from mutant p
1449052_a_at	0,000127272	3,09	Dnmt3b***	DNA methyltransferase 3B	6306 // DNA methylation // inferred from electronic annotation /// 6349 // imprinting // inferred from mutant p
1454681_at	0,004696315	3,06	Rbm35a	RNA binding motif protein 35A	RNA binding
1418376_at	0,000272991	3,06	Fgf15	fibroblast growth factor 15	7165 // signal transduction // inferred from electronic annotation
1426186_a_at	0,000815148	3,03	Fgf5	fibroblast growth factor 5	8151 // cell growth and/or maintenance // inferred from electronic annotation /// 8283 // cell proliferation // in
1418517_at	0,000177847	3,02	Irx3	Iroquois related homeobox 3 (Drosophila)	6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation
1447825_x_at	0,00049708	3,01	Pcdh8	protocadherin 8	16331 // morphogenesis of embryonic epithelium // inferred from mutant phenotype /// 1756 // somitogenes
1419638_at	0,000115998	3,01	Efnb2***	ephrin B2	7275 // development // inferred from electronic annotation /// 7399 // neurogenesis // inferred from electroni
1425926_a_at	7,82871E-05	2,96	Otx2***	orthodenticle homolog 2 (Drosophila)	9952 // anterior/posterior pattern formation // inferred from mutant phenotype /// 45165 // cell fate commitme
1452127_a_at	0,001601088	2,94	Ptpn13	protein tyrosine phosphatase, non-receptor type 1	7242 // intracellular signaling cascade // inferred from sequence or structural similarity /// 6470 // protein am
1450738_at	0,000215887	2,94	Kif21a	Kinesin family member 21A	Kinesin complex, microtubule associated
1436600_at	0,000748192	2,78	Tnrc9	trinucleotide repeat containing 9	---
1440542_at	0,00090133	2,78	---	RIKEN cDNA 7420416P09	---
1435192_at	0,001352773	2,70	Sox3	SRY-box containing gene 3	establishment and maintenance of chromatin structure
1419639_at	0,000290409	2,68	Efnb2***	Ephrin B2	Develpment/ Lymph vessel/ Integral to membrane
1436398_at	0,003952368	2,60	Lef1***	Lymphoid enhancer binding factor 1	16055 // Wnt receptor signaling pathway // inferred from electronic annotation /// 42475 // odontogenesis (s
1436512_at	0,001526224	2,56	Arl4c	ADP-ribosylation factor-like 4C	GTPase activity/ rRNA processing
1455114_at	0,002037889	2,55	Ung2	Uracil DNA glycosylase 2	Regulation of progression through cell cycle

1418533_s_at	4,6606E-06	2,54	**Fzd2**	frizzled homolog 2 (Drosophila)	7186 // G-protein coupled receptor protein signaling pathway // inferred from electronic annotation /// 16055
1419700_a_at	0,00203052	2,53	**Prom1**	prominin 1	7602 // phototransduction // inferred from electronic annotation
1434909_at	0,001751451	2,48	Rragd	Ras-related GTP binding D	---
1421072_at	0,000277559	2,48	Irx5	Iroquois related homeobox 5 (Drosophila)	6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation
1415856_at	0,000601252	2,47	**Emb**	embigin	---
1448690_at	0,003942414	2,46	Kcnk1	potassium channel, subfamily K, member 1	6811 // ion transport // inferred from electronic annotation /// 6813 // potassium ion transport // inferred from
1454877_at	0,00093237	2,45	Sertad4	SERTA domain containing 4	---
1450047_at	0,000423416	2,45	Hs6st2	heparan sulfate 6-O-sulfotransferase 2	---
1421299_a_at	0,002904802	2,42	**Lef1*** **	lymphoid enhancer binding factor 1	16055 // Wnt receptor signaling pathway // inferred from electronic annotation /// 42475 // odontogenesis (s
1439015_at	0,000510657	2,41	Gfra1	glial cell line derived neurotrophic factor family rec	9653 // morphogenesis // traceable author statement /// 7399 // neurogenesis // inferred from mutant pheno
1418532_at	4,17886E-05	2,40	**Fzd2**	frizzled homolog 2 (Drosophila)	7186 // G-protein coupled receptor protein signaling pathway // inferred from electronic annotation /// 16055
1419204_at	0,00156238	2,40	Dll1***	delta-like 1 (Drosophila)	7154 // cell communication // inferred from electronic annotation /// 30154 // cell differentiation // inferred fro
1452320_at	7,86496E-05	2,40	Lrp2***	Low density lipoprotein receptor-related protein 2	6898 // receptor mediated endocytosis // inferred from mutant phenotype /// 6766 // vitamin metabolism // in
1435437_at	0,000101004	2,39	Set7	SET domain-containing protein 7	16568 // chromatin modification // inferred from electronic annotation
1439665_at	0,005832407	2,38	Gpr23***	G protein-coupled receptor 23	---
1415857_at	0,0004022	2,36	**Emb**	embigin	---
1436959_x_at	0,009948701	2,35	Nelf	nasal embryonic LHRH factor	---
1452270_s_at	0,000200308	2,34	Cubn	Cubilin (intrinsic factor-cobalamin receptor)	6898 // receptor mediated endocytosis // traceable author statement /// 6418 // tRNA aminoacylation for pro
1448182_a_at	0,000559301	2,33	Cd24a	CD24a antigen	---
1457883_at	0,004982177	2,32	***	Adult male aorta and vein cDNA, RIKEN full-lengt	---
1434362_at	0,000562069	2,30	---	---	---
1433983_at	0,001672966	2,30	Magi1	membrane associated guanylate kinase interactin	---
1417574_at	0,000748404	2,27	Cxcl12	chemokine (C-X-C motif) ligand 12	42098 // T-cell proliferation // inferred from mutant phenotype /// 7420 // brain development // inferred from
1456632_at	0,001544229	2,26	Bcl11A***	B cell lymphoma 11A	---
1427133_s_at	0,000283254	2,26	Lrp2***	Low density lipoprotein receptor-related protein 2	6898 // receptor mediated endocytosis // inferred from mutant phenotype /// 6766 // vitamin metabolism // in
1454788_at	0,000640249	2,22	Arl7	ADP-ribosylation factor-like 7	6886 // intracellular protein transport // inferred from sequence or structural similarity /// 7264 // small GTPa
1434822_at	0,001698319	2,22	Pphln1	periphilin 1	---
1416846_a_at	0,003448645	2,20	Pdzrn3	PDZ domain containing RING finger 3	7242 // intracellular signaling cascade // inferred from sequence or structural similarity
1456329_at	0,000132902	2,19	A230098A12Rik	RIKEN cDNA A230098A12 gene	---
1423064_at	0,004126925	2,17	**Dnmt3a*** **	DNA methyltransferase 3A	6306 // DNA methylation // inferred from direct assay /// 6349 // imprinting // inferred from mutant phenotype
1456326_at	0,00580299	2,16	Gm784	Gene model 784, (NCBI)	Membrane
1426990_at	0,000121874	2,14	Cubn	Cubilin (intrinsic factor-cobalamin receptor)	6898 // receptor mediated endocytosis // traceable author statement /// 6418 // tRNA aminoacylation for pro
1436030_at	0,000359697	2,13	Cachd1	Cache domain containing 1	Membrane
1429690_at	0,001592878	2,12	1300003B13Rik	RIKEN cDNA 1300003B13 gene	---

1433939_at	0,004522205	2,12	A730046J16	hypothetical protein A730046J16	---
1429372_at	0,007349799	2,12	Sox11	SRY-box containing gene 11	Transcription factor
1423470_at	0,001571354	2,12	Ptbp2	polypyrimidine tract binding protein 2	6376 // mRNA splice site selection // inferred from direct assay
1433575_at	0,002631655	2,11	Sox4	SRY-box containing gene 4	6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation
1448566_at	0,002717423	2,11	Slc40a1	solute carrier family 40 (iron-regulated transporter	6826 // iron ion transport // inferred from direct assay /// 6810 // transport // inferred from sequence or struct
1440206_at	0,00153026	2,11	A930024E05Rik	RIKEN cDNA A930024E05 gene	---
1455374_at	0,001166749	2,11	---	---	---
1426614_at	0,001177913	2,10	Prkcbp1	protein kinase C binding protein 1	---
1451589_at	0,006781723	2,08	Gats	opposite strand transcription unit to Stag3	---
1422631_at	0,000762828	2,08	Ahr	aryl-hydrocarbon receptor	7049 // cell cycle // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependen
1423065_at	0,000309895	2,08	Dnmt3a***	DNA methyltransferase 3A	6306 // DNA methylation // inferred from direct assay /// 6349 // imprinting // inferred from mutant phenotype
1420928_at	0,004967884	2,08	St6gal1	beta galactoside alpha 2,6 sialyltransferase 1	6486 // protein amino acid glycosylation // inferred from electronic annotation
1438200_at	0,002274333	2,08	Sulf1	sulfatase 1	6915 // apoptosis // inferred from electronic annotation /// 8152 // metabolism // inferred from electronic ann
1436031_at	0,000738994	2,07	Cachd1	Cache domain containing 1	Membrane
1450070_s_at	0,000996867	2,07	Pak1	P21 (CDKN1A)-activated kinase 1	16358 // dendrite morphogenesis // inferred from direct assay /// 6468 // protein amino acid phosphorylation
1449147_at	0,001736324	2,07	Chst1	carbohydrate (keratan sulfate Gal-6) sulfotransfera	---
1438454_at	0,00491412	2,06	B430203M17Rik***	RIKEN cDNA B430203M17 gene	---
1416840_at	0,002542451	2,06	Mid1ip1	Mid1 interacting protein 1 (gastrulation specific G1	7026 // microtubule stabilization // inferred from genetic interaction
1417051_at	0,001439205	2,05	Pcdh8	protocadherin 8	16331 // morphogenesis of embryonic epithelium // inferred from mutant phenotype /// 1756 // somitogenes
1447623_s_at	0,00441528	2,05	---	---	---
1416034_at	0,008998349	2,05	Cd24a	CD24a antigen	---
1439485_at	0,008190403	2,05	Zfp608	Zinc finger protein 608	---
1448393_at	0,004570949	2,04	Cldn7	claudin 7	---
1417965_at	0,000103836	2,03	Plekha1	Pleckstrin homology domain A1	Lipid binding
1454890_at	0,003302907	2,03	Amot	angiomotin	6935 // chemotaxis // inferred from mutant phenotype /// 1570 // vasculogenesis // inferred from mutant phe
1427912_at	0,002270304	2,02	Cbr3	carbonyl reductase 3	8152 // metabolism // inferred from sequence or structural similarity
1420650_at	0,001734803	2,02	Atbf1	AT motif binding factor 1	Transcription factor
1457402_at	0,004084036	2,02	Sulf1	Sulfatase 1	6915 // apoptosis // inferred from electronic annotation /// 8152 // metabolism // inferred from electronic ann
1433745_at	0,000444489	2,00	Trio	triple functional domain (PTPRF interacting)	---
1421973_at	0,001038046	2,00	Gfra1	glial cell line derived neurotrophic factor family rec	9653 // morphogenesis // traceable author statement /// 7399 // neurogenesis // inferred from mutant pheno
1443221_at	0,002606729	2,00	Wt1***	Wilms tumor homolog	30855 // epithelial cell differentiation // inferred from mutant phenotype /// 1654 // eye morphogenesis // infe
1436319_at	0,00366735	1,99	Sulf1	sulfatase 1	6915 // apoptosis // inferred from electronic annotation /// 8152 // metabolism // inferred from electronic ann
1450779_at	0,002761892	1,99	Fabp7	fatty acid binding protein 7, brain	6810 // transport // inferred from electronic annotation
1434699_at	0,001092619	1,98	6030408C04Rik	RIKEN cDNA 6030408C04 gene	---

1454734_at	0,0019642	1,98	Lef1***	lymphoid enhancer binding factor 1	16055 // Wnt receptor signaling pathway // inferred from electronic annotation /// 42475 // odontogenesis (s
1437181_at	4,0939E-05	1,97	Peli2	pellino 2	8063 // Toll signaling pathway // inferred from mutant phenotype
1426926_at	0,003934178	1,97	Plcg2	phospholipase C, gamma 2	---
1434967_at	0,001155773	1,96	Zswim6	zinc finger, SWIM domain containing 6	---
1428647_at	0,00064212	1,95	2310056B04Rik	RIKEN cDNA 2310056B04 gene	---
1421053_at	0,001172874	1,95	Kif1a	kinesin family member 1A	7017 // microtubule-based process // inferred from electronic annotation
1418534_at	0,000611859	1,94	---	---	---
1416407_at	0,004228778	1,94	Pea15	phosphoprotein enriched in astrocytes 15	6915 // apoptosis // inferred from sequence or structural similarity /// 7242 // intracellular signaling cascade
1419550_a_at	0,003471077	1,94	Stk39	serine/threonine kinase 39, STE20/SPS1 homolo	6468 // protein amino acid phosphorylation // inferred from electronic annotation
1456377_x_at	0,003643206	1,94	Limd2	LIM domain containing 2	Metal ion binding
1448747_at	0,001526431	1,94	Fbxo32	F-box only protein 32	6810 // transport // inferred from electronic annotation /// 6512 // ubiquitin cycle // inferred from electronic ar
1419355_at	0,004046662	1,94	Klf7	Kruppel-like factor 7 (ubiquitous)	6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation
1428826_at	0,000813379	1,93	Nr6a1	nuclear receptor subfamily 6, group A, member 1	122 // negative regulation of transcription from Pol II promoter // inferred from mutant phenotype /// 6355 //
1417217_at	0,000196783	1,93	Magel2	melanoma antigen, family L, 2	45449 // regulation of transcription // inferred from direct assay
1434570_at	0,000508411	1,93	AK122525	cDNA sequence AK122525	---
1459722_at	0,002840789	1,93	Zswim6***	zinc finger, SWIM domain containing 6	Zinc ion binding
1436925_at	0,003986037	1,93	Ches1	checkpoint supressor 1	77 // DNA damage checkpoint // inferred from sequence or structural similarity /// 85 // G2 phase of mitotic
1460006_at	0,009918604	1,92	Atbf1***	AT motif binding factor 1	6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation
1428738_a_at	0,00050716	1,92	D14Ertd449e	DNA segment, Chr 14, ERATO Doi 449, expresse	---
1435554_at	0,003573525	1,92	Tmcc3	Transmembrane and coiled domains 3	---
1450044_at	0,009316424	1,91	Fzd7***	frizzled homolog 7 (Drosophila)	7186 // G-protein coupled receptor protein signaling pathway // inferred from electronic annotation /// 16055
1448688_at	0,000170745	1,91	Podxl	podocalyxin-like	8151 // cell growth and/or maintenance // inferred from electronic annotation
1434709_at	0,000880605	1,91	C130076O07Rik	RIKEN cDNA C130076O07 gene	7155 // cell adhesion // inferred from electronic annotation
1438410_at	0,001657393	1,90	Prtg	Protogenin homolog	Striated muscle/ Thick filament membrane
1452670_at	0,000454139	1,90	Myl9	Myosin, light polypeptide 9, regulatory	7517 // muscle development // inferred from sequence or structural similarity /// 6937 // regulation of muscle
1417612_at	0,005223441	1,90	Ier5	immediate early response 5	---

Additional file 1

Tables 1 to 7 and legends

For all tables, the Affymetrix probe set numbers, genes annotation (from NetAffx data base, last release from 21 July 2008) and fold change (fc) in expression are documented. Genes have been classified from the highest to the lowest fc. Cut off parameters have been chosen, for each table, as a way to include known regulated genes. Those ones served as positive controls for each analysis. More exhaustive analysis, with other parameter set up, could be done by using the complete data deposited at the GeneArray database under the accession number (pending). Sample numbers, 1 to 6, are referring to those indicated in Figure 1B, 1C, and 1D of the main text.

For all the Tables, multiple testing corrections have been performed using the Benjamini and Hochberg procedure and all genes in these tables have an FDR< 0,05.

Table 1: Genes whose expression is induced (20 genes) or repressed (12 genes) by LIF at 24h upon LIF withdrawal: Pair wise comparisons of samples 3 versus 4 after a student t-test and the following cut off parameters : pvalue < or equal to 0,05 and fc > or equal to 1,5 (for the induced genes) and < or equal to -1,5 (for the repressed genes).

Table 2: Genes whose expression is induced (12 genes) or repressed (no genes) by LIF at 48h upon LIF withdrawal: Pair wise comparisons of samples 5 versus 6 after a student t-test and the following cut off parameters : pvalue < or equal to 0,05 and fc > or equal to 1,5 (for the induced genes) and < or equal to -1,5 (for the repressed genes).

Table 3: Genes whose expression is induced in pluripotent cells versus cells in which LIF has been withdrawn for 24h (59 genes): Pair wise comparisons of samples 3 versus 1 after a student t-test and the following cut off parameters : pvalue < or equal to 0,017 and fc > or equal to 1,75. Known pluripotent markers are in bold and *Lifind* genes (see table 1) are in bold, italique.

Table 4: Genes whose expression is repressed at 48h upon LIF withdrawal versus pluripotent cells (143 genes): Pair wise comparisons of samples 5 versus 1 after a student t-test and the following cut off parameters : pvalue < or equal to 0,01 and fc < or equal to -1,9. Known pluripotent markers are in bold and *Lifind* genes (from Table 1) are in bold, italique.

Table 5: Genes whose expression is repressed in pluripotent cells versus cells grown 24h without LIF (140 genes): Pair wise comparisons of samples 3 versus 1 after a student t-test and the following cut off parameters : pvalue < or equal to 0,01 and fc < or equal to -1,9. Informations regarding profiling of these genes at 48h upon LIF withdrawal versus pluripotent cells are also documented. The genes quoted « NO » correspond to a new category of genes whose expression is transiently induced 24h after LIF withdrawal (reversible commitment state). Genes present in Cluster 7 (Figure 3A of the main text) are indicated by a double asterisk (**) and known differentiation markers are bolded.

Table 6: Genes whose expression is induced at 48h upon LIF withdrawal versus 24h upon LIF withdrawal (41 genes): Pair wise comparisons of samples 3 versus 5 after a student t-test and the following cut off parameters : pvalue < or equal to 0,01 and fc > or equal to 1,9.

Table 7: Genes whose expression is induced at 48h upon LIF withdrawal versus pluripotent cells (114 genes): Pair wise comparisons of samples 1 versus 5 after a student t-test and the following cut off parameters : pvalue < or equal to 0,01 and fc > or equal to 1,9. Genes induced at 24h of LIF withdrawal and whose expression was sustained at 48h are quoted by a triple asterisk (***). Known differentiation markers are bolded.

Additional file 2

Characterisation of *Stat3Loc*: probe set n°: 1459961_a_at

<u>Sequence of the probe set :</u>

atgcacacatgctagacggatgaatggtgctggcggcacatgcccttaattccagcacttggaaggcagcagcagtggatctctaa
gaattaagggccagctggtctacaaattgagttccaggccagctaagaccctggcttaagatgaacaggaacaaaacactaagcagaa
gctggccatggatgtttcatgtctgcag

This sequence is complementary to the BAC where are located the *Stat3* and *Stat5a* loci as defined by BLAST search.

LOCUS AF246978 : 83848 bp

DEFINITION: Mus musculus transcription factor Stat5a (Stat5a) and transcription factor Stat3 (Stat3) genes, complete cds.

ACCESSION AF246978

VERSION AF246978.2 GI:18087725

78371 ctgcagacat gaaacatcca tggccagctt ctgcttagtg ttttgttcct
78421 gttcatctta agccagggtc ttagctggcc tggaactcaa tttgtagacc agctggccct
78481 taattcttag agatccactg ctgctgcctt ccaagtgctg gaattaaggg catgtgccgc
78541 cagcaccatt catccgtcta **gcatgtgtgc at (78572)**

The sequence corresponding to probe set 1459961_a_at (*Stat3Loc*) is located 5’ to the ATG codon of *Stat3* on mouse chromosome 11 and therefore does not correspond to *Stat3* gene. Numbers in parenthesis correspond to nucleotide positions in the BAC sequence.
We renamed this gene *Stat3Loc*. to indicate the proximity of this unknown gene with the *Stat3* locus.

Additional file 3

Complete list of genes in Figure 3

Lanes 15 to 74:	Cluster 1	"Com. and Dif." genes
Lanes 75 to 86:	Cluster 2	Transient repression
Lanes 87 to 130:	Cluster 3	"Dif." Markers
Lanes 131 to 160:	Cluster 4	"Pluri" genes
Lanes 161 to 222:	Cluster 5	"Pluri" genes
Lanes 223 to 248:	Cluster 6	"Pluri and Com." genes
Lanes 249 to 291:	Cluster 7	Transient induction
Lanes 292 to 306:	Cluster 8	"Lifind" genes

Pluri: Pluripotent	Com.: Commitment	Dif. Differentiation

Lane 15	1426043_a_at: Capn3; calpain 3
	1436266_x_at: Cbx1 /// E430007M08Rik; chromobox homolog 1 Drosophil
	1428647_at: 2310056B04Rik; RIKEN cDNA 2310056B04 gene
	1435221_at: Foxp1; Forkhead box P1
	1435222_at: Foxp1; Forkhead box P1
	1444679_at: Bhc80; BRAF35/HDAC2 complex
	1420965_a_at: Enc1; ectodermal-neural cortex 1
	1427046_at: Tcfcp2l3; transcription factor CP2-like 3
	1440542_at: ---; Similar to Protein C14orf115
	1434853_x_at: Mkrn1; makorin, ring finger protein, 1
	1426401_at: Ppp3ca; protein phosphatase 3, catalytic subunit, alpha isoform
	1435434_at: Braf; Braf transforming gene
	1449947_s_at: Atbf1; AT motif binding factor 1
	1427302_at: Enpp3; ectonucleotide pyrophosphatase/phosphodiesterase 3
	1452384_at: Enpp3; ectonucleotide pyrophosphatase/phosphodiesterase 3
	1425926_a_at: Otx2; orthodenticle homolog 2 Drosophila
	1420980_at: Pak1; P21 CDKN1A-activated kinase 1
	1458218_s_at: Pde7a; phosphodiesterase 7A
	1417051_at: Pcdh8; protocadherin 8
	1447825_x_at: Pcdh8; protocadherin 8
	1450738_at: ---; ---
	1425995_s_at: Wt1; Wilms tumor homolog
	1456632_at: ---; ---
	1455029_at: ---; ---
	1452214_at: 9130011J04Rik; RIKEN cDNA 9130011J04 gene
	1424008_a_at: Rbpms2; RNA binding protein with multiple splicing 2
	1419638_at: Efnb2; ephrin B2
	1419639_at: ---; ---
	1438973_x_at: Gja1; gap junction membrane channel protein alpha 1
	1438650_x_at: Gja1; gap junction membrane channel protein alpha 1
	1460038_at: ---; ---
	1416638_at: Sall2; sal-like 2 Drosophila
	1440206_at: A930024E05Rik; RIKEN cDNA A930024E05 gene
	1420979_at: Pak1; P21 CDKN1A-activated kinase 1

	1445710_x_at: 1110051B16Rik; RIKEN cDNA 1110051B16 gene
	1455114_at: C86987; expressed sequence C86987
	1434967_at: Zswim6; zinc finger, SWIM domain containing 6
	1422553_at: Pten; phosphatase and tensin homolog
	1454990_at: Arid2; AT rich interactive domain 2 Arid-rfx like
	1420649_at: Atbf1; AT motif binding factor 1
	1442655_at: ---; ---
	1455087_at: D7Ertd715e; DNA segment, Chr 7, ERATO Doi 715, expressed
	1436964_at: D7Ertd715e; DNA segment, Chr 7, ERATO Doi 715, expressed
	1437217_at: ---; ---
	1426722_at: Slc38a2; solute carrier family 38, member 2
	1454734_at: Lef1; lymphoid enhancer binding factor 1
	1418390_at: Bhc80; BRAF35/HDAC2 complex
	1418391_at: ---; ---
	1436398_at: Lef1; Lymphoid enhancer binding factor 1
	1450044_at: Fzd7; frizzled homolog 7 Drosophila
	1452309_at: 4933421H10Rik; RIKEN cDNA 4933421H10 gene
	1450655_at: Herc1; hect homologous to the E6-AP UBE3A carboxyl termin
	1454722_at: Herc1; hect homologous to the E6-AP UBE3A carboxyl termin
	1423064_at: Dnmt3a; DNA methyltransferase 3A
	1423065_at: Dnmt3a; DNA methyltransferase 3A
	1428843_at: Rnf153; ring finger protein 153
	1417392_a_at: Slc7a7; solute carrier family 7 cationic amino acid transporte
	1421299_a_at: Lef1; lymphoid enhancer binding factor 1
	1450396_at: Stag2; stromal antigen 2
Lane 74	1435603_at: Sned1; sushi, nidogen and EGF-like domains 1
Lane 75	1454729_at: B130017P16Rik; RIKEN cDNA B130017P16 gene
	1448871_at: Mapk13; mitogen activated protein kinase 13
	1442434_at: D8Ertd82e; DNA segment, Chr 8, ERATO Doi 82, expressed
	1437760_at: Galnt12; UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-
	1449752_at: ---; ---
	1449198_a_at: Siat9; sialyltransferase 9 CMP-NeuAc:lactosylceramide alph
	1436865_at: Slc26a11; solute carrier family 26, member 11
	1456434_x_at: Hspb8; heat shock 27kDa protein 8
	1438118_x_at: Vim; vimentin
	1450350_a_at: Jundm2; Jun dimerization protein 2
	1450641_at: Vim; vimentin
Lane 86	1436141_at: ---; ---
Lane 87	1460556_at: D15Mit260; DNA Segment, Chr 15 Massachusetts Institute of
	1420611_at: Prkacb; protein kinase, cAMP dependent, catalytic, beta
	1448747_at: Fbxo32; F-box only protein 32
	1448949_at: Car4; carbonic anhydrase 4
	1418094_s_at: Car4; carbonic anhydrase 4
	1416407_at: Pea15; phosphoprotein enriched in astrocytes 15
	1417829_a_at: Rab15; RAB15, member RAS oncogene family
	1451589_at: Gats; opposite strand transcription unit to Stag3
	1434822_at: Pphln1; periphilin 1
	1426926_at: Plcg2; phospholipase C, gamma 2

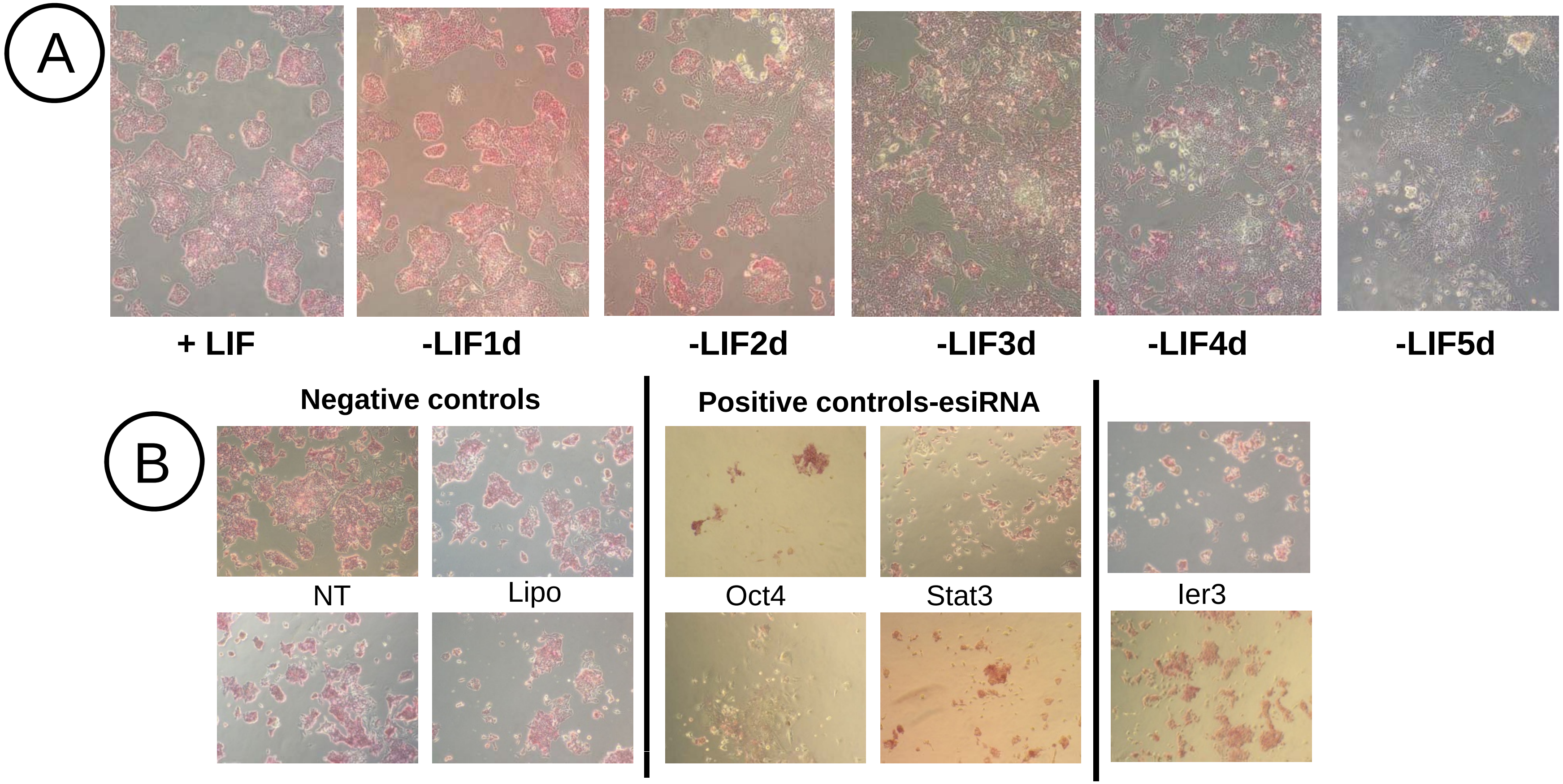
	1438883_at: Fgf5; fibroblast growth factor 5
	1415856_at: Emb; embigin
	1415857_at: Emb; embigin
	1434362_at: ---; ---
	1452127_a_at: Ptpn13; protein tyrosine phosphatase, non-receptor type 13
	1417965_at: AA960558; expressed sequence AA960558
	1423272_at: Polg; polymerase DNA directed, gamma
	1425940_a_at: Ssbp3; single-stranded DNA binding protein 3
	1420842_at: Ptprf; protein tyrosine phosphatase, receptor type, F
	1426794_at: Ptprs; protein tyrosine phosphatase, receptor type, S
	1418517_at: Irx3; Iroquois related homeobox 3 Drosophila
	1427917_s_at: Ssbp3; single-stranded DNA binding protein 3
	1417379_at: Iqgap1; IQ motif containing GTPase activating protein 1
	1426186_a_at: Fgf5; fibroblast growth factor 5
	1452294_at: 2010005A06Rik; RIKEN cDNA 2010005A06 gene
	1437064_at: AW320017; expressed sequence AW320017
	1425266_a_at: Rap1gds1; RAP1, GTP-GDP dissociation stimulator 1
	1449368_at: Dcn; decorin
	1451912_a_at: Fgfrl1; fibroblast growth factor receptor-like 1
	1445503_at: ---; Gene model 715, NCBI
	1456603_at: 1500005K14Rik; RIKEN cDNA 1500005K14 gene
	1427894_at: Slitl2; Slit-like 2 Drosophila
	1417389_at: Gpc1; glypican 1
	1435256_at: AI844915; RIKEN cDNA 1500005P14 gene
	1418445_at: ---; ---
	1425784_a_at: Olfm1; olfactomedin 1
	1434442_at: D5Ertd593e; DNA segment, Chr 5, ERATO Doi 593, expresse
	1417189_at: Psme2; proteasome prosome, macropain 28 subunit, beta
	1417056_at: Psme1; proteasome prosome, macropain 28 subunit, alpha
	1431008_at: 0610037M15Rik; RIKEN cDNA 0610037M15 gene
	1422673_at: Prkcm; protein kinase C, mu
	1417978_at: Eif4e3; eukaryotic translation initiation factor 4E member 3
	1449461_at: Rbp7; retinol binding protein 7, cellular
Lane 130	1448436_a_at: Irf1; interferon regulatory factor 1
Lane 131	1448113_at: Stmn1; stathmin 1
	1431979_at: 4930444M15Rik; RIKEN cDNA 4930444M15 gene
	1455604_at: ---; ---
	1449090_a_at: Yes; Yamaguchi sarcoma viral v-yes oncogene homolog
	1417976_at: Ada; adenosine deaminase
	1454704_at: 9330185J12Rik; RIKEN cDNA 9330185J12 gene
	1439947_at: Cyp11a1; cytochrome P450, family 11, subfamily a, polypeptid
	1452076_at: 4633402N23Rik; RIKEN cDNA 4633402N23 gene
	1423281_at: Stmn2; stathmin-like 2
	1460235_at: Scarb2; scavenger receptor class B, member 2
	1430125_s_at: Pqlc1; PQ loop repeat containing 1
	1460227_at: Timp1; tissue inhibitor of metalloproteinase 1
	1437165_a_at: Pcolce; procollagen C-proteinase enhancer protein
	1416529_at: Emp1; epithelial membrane protein 1

	1448433_a_at: Pcolce; procollagen C-proteinase enhancer protein
	1448491_at: Ech1; enoyl coenzyme A hydratase 1, peroxisomal
	1422458_at: Tcl1; T-cell lymphoma breakpoint 1
	1434025_at: ---; ---
	1429399_at: Rnf125; ring finger protein 125
	1456242_at: ---; LOC433110
	1436905_x_at: Laptm5; lysosomal-associated protein transmembrane 5
	1433596_at: Dnajc6; DnaJ Hsp40 homolog, subfamily C, member 6
	1420410_at: Nr5a2; nuclear receptor subfamily 5, group A, member 2
	1425538_x_at: Ceacam1; CEA-related cell adhesion molecule 1
	1427630_x_at: Ceacam1; CEA-related cell adhesion molecule 1
	1460682_s_at: Ceacam2; CEA-related cell adhesion molecule 2
	1426858_at: Inhbb; Inhibin beta-B
	1449530_at: Trps1; trichorhinophalangeal syndrome I human
	1438214_at: Trps1; trichorhinophalangeal syndrome I human
Lane 160	1449706_s_at: ---; ---
Lane 161	1433657_at: A130092J06Rik; RIKEN cDNA A130092J06 gene
	1437100_x_at: Pim3; proviral integration site 3
	1425991_a_at: Ankrd25; ankyrin repeat domain 25
	1430781_at: Ak7; adenylate kinase 7
	1426025_s_at: Laptm5; lysosomal-associated protein transmembrane 5
	1453063_at: Cltb; clathrin, light polypeptide Lcb
	1454974_at: Ntn1; netrin 1
	1449064_at: Tdh; L-threonine dehydrogenase
	1460681_at: Ceacam2; CEA-related cell adhesion molecule 2
	1422937_at: Fzd5; frizzled homolog 5 Drosophila
	1422566_at: Tcfeb; transcription factor EB
	1435195_at: D930046M13Rik; RIKEN cDNA D930046M13 gene
	1420361_at: Slc11a1; solute carrier family 11 proton-coupled divalent metal
	1448610_a_at: Sod2; superoxide dismutase 2, mitochondrial
	1460429_at: Cdc5l; cell division cycle 5-like S. pombe
	1436926_at: Esrrb; estrogen related receptor, beta
	1418091_at: Tcfcp2l1; transcription factor CP2-like 1
	1434283_at: ---; ---
	1421840_at: Abca1; ATP-binding cassette, sub-family A ABC1, member 1
	1435040_at: Irak3; interleukin-1 receptor-associated kinase 3
	1426511_at: Susd2; sushi domain containing 2
	1449590_a_at: Mras; muscle and microspikes RAS
	1452532_x_at: Ceacam1; CEA-related cell adhesion molecule 1
	1422123_s_at: Ceacam2 /// Ceacam1; CEA-related cell adhesion molecule 2
	1450494_x_at: Ceacam1; CEA-related cell adhesion molecule 1
	1423686_a_at: 1110020C13Rik; RIKEN cDNA 1110020C13 gene
	1423280_at: Stmn2; stathmin-like 2
	1429377_at: 2410004A20Rik; RIKEN cDNA 2410004A20 gene
	1450860_at: Lap3; leucine aminopeptidase 3
	1437435_at: 1700061G19Rik; RIKEN cDNA 1700061G19 gene
	1423786_at: 8430410A17Rik; RIKEN cDNA 8430410A17 gene
	1422965_at: Agtrap; angiotensin II, type I receptor-associated protein

	1416715_at: Gjb3; gap junction membrane channel protein beta 3
	1418569_at: 2410043F08Rik; RIKEN cDNA 2410043F08 gene
	1449141_at: 2410043F08Rik; RIKEN cDNA 2410043F08 gene
	1451123_at: C330016O10Rik; RIKEN cDNA C330016O10 gene
	1449204_at: Gjb5; gap junction membrane channel protein beta 5
	1418133_at: Bcl3; B-cell leukemia/lymphoma 3
	1460700_at: Stat3; signal transducer and activator of transcription 3
	1417193_at: Sod2; superoxide dismutase 2, mitochondrial
	1453419_at: 2900078C09Rik; RIKEN cDNA 2900078C09 gene
	1429833_at: Ly6g6e; lymphocyte antigen 6 complex, locus G6E
	1418467_at: Smarcd3; SWI/SNF related, matrix associated, actin dependent
	1460596_at: Agtrap; angiotensin II, type I receptor-associated protein
	1418417_at: Msc; musculin
	1434500_at: ---; ---
	1417013_at: Hspb8; heat shock 27kDa protein 8
	1430208_at: 2410039E07Rik; RIKEN cDNA 2410039E07 gene
	1436164_at: Slc30a1; solute carrier family 30 zinc transporter, member 1
	1455229_x_at: 4933424M23Rik /// LOC260345; RIKEN cDNA 4933424M2
	1454045_a_at: 4933424M23Rik /// LOC260345; RIKEN cDNA 4933424M2
	1454046_x_at: 4933424M23Rik /// LOC260345; RIKEN cDNA 4933424M2
	1433645_at: 2210409B22Rik; RIKEN cDNA 2210409B22 gene
	1424719_a_at: Mapt; microtubule-associated protein tau
	1418470_at: Yes; Yamaguchi sarcoma viral v-yes oncogene homolog
	1460253_at: Cklfsf7; chemokine-like factor super family 7
	1426733_at: Itpk1; inositol 1,3,4-triphosphate 5/6 kinase
	1416066_at: Cd9; CD9 antigen
	1460454_at: 2010001H14Rik; RIKEN cDNA 2010001H14 gene
	1453442_at: 2310043M15Rik; RIKEN cDNA 2310043M15 gene
	1421839_at: Abca1; ATP-binding cassette, sub-family A ABC1, member 1
Lane 222	1425396_a_at: Lck; lymphocyte protein tyrosine kinase
Lane 223	1433436_s_at: Thtpa; thiamine triphosphatase
	1417460_at: Ifitm2; interferon induced transmembrane protein 2
	1436155_at: Nmnat2; nicotinamide nucleotide adenylyltransferase 2
	1454991_at: Slc7a1; Solute carrier family 7 cationic amino acid transporter,
	1452093_at: 2500001K11Rik; RIKEN cDNA 2500001K11 gene
	1417804_at: Rasgrp2; RAS, guanyl releasing protein 2
	1447678_at: ---; ---
	1426808_at: Lgals3; lectin, galactose binding, soluble 3
	1455333_at: BC023928; cDNA sequence BC023928
	1434917_at: Cobl; cordon-bleu
	1455300_at: E130014J05Rik; RIKEN cDNA E130014J05 gene
	1419417_at: Vegfc; vascular endothelial growth factor C
	1440739_at: Vegfc; vascular endothelial growth factor C
	1438781_at: ---; Adult male aorta and vein cDNA, RIKEN full-length enrich
	1454984_at: ---; ---
	1438872_at: BC050188; cDNA sequence BC050188
	1423465_at: Sdfr2; stromal cell derived factor receptor 2
	1417234_at: Mmp11; matrix metalloproteinase 11

	1439766_x_at: Vegfc; vascular endothelial growth factor C
	1415849_s_at: Stmn1; stathmin 1
	1453230_at: Zfp74; zinc finger protein 74
	1427140_at: Pvt1; plasmacytoma variant translocation 1
	1458295_at: BC038331; cDNA sequence BC038331
	1427087_at: Luc7l2; LUC7-like 2 S. cerevisiae
	1436994_a_at: Hist1h1c; histone 1, H1c
Lane 248	1456546_at: 1700097N02Rik; RIKEN cDNA 1700097N02 gene
Lane 249	1438802_at: ---; ---
	1419537_at: Tcfec; transcription factor EC
	1451687_a_at: ---; ---
	1435436_at: ---; ---
	1439123_at: Bhc80; BRAF35/HDAC2 complex
	1443526_at: Bhc80; BRAF35/HDAC2 complex
	1453976_at: 4432414F05Rik; RIKEN cDNA 4432414F05 gene
	1439582_at: ---; ---
	1423277_at: Ptprk; protein tyrosine phosphatase, receptor type, K
	1452940_x_at: Pitpnc1; phosphatidylinositol transfer protein, cytoplasmic 1
	1459973_x_at: ---; ---
	1456670_at: A930007A09Rik; RIKEN cDNA A930007A09 gene
	1417822_at: D17H6S56E-5; DNA segment, Chr 17, human D6S56E 5
	1454617_at: Arrdc3; arrestin domain containing 3
	1453013_at: 1110034O07Rik; RIKEN cDNA 1110034O07 gene
	1438084_at: ---; ---
	1444851_at: ---; ---
	1457314_at: ---; Similar to hypothetical protein FLJ10884
	1441243_at: ---; ---
	1430798_x_at: Mrpl15; mitochondrial ribosomal protein L15
	1437984_x_at: Bat1a; HLA-B-associated transcript 1A
	1457113_at: ---; ---
	1456705_at: C530030I18Rik; RIKEN cDNA C530030I18 gene
	1435669_at: Zfp532; zinc finger protein 532
	1438107_x_at: ---; ---
	1427193_at: Brd8; bromodomain containing 8
	1460600_at: ---; Hypothetical LOC245350
	1452657_at: Ap1s2; adaptor-related protein complex 1, sigma 2 subunit
	1430526_a_at: Smarca2; SWI/SNF related, matrix associated, actin depende
	1444426_at: F730031O20Rik; RIKEN cDNA F730031O20 gene
	1455544_at: Zranb3; zinc finger, RAN-binding domain containing 3
	1451559_a_at: Dhrs4; Dehydrogenase/reductase SDR family member 4
	1440522_at: B930075F07; hypothetical protein B930075F07
	1418388_s_at: 4930548G07Rik; RIKEN cDNA 4930548G07 gene
	1450853_at: Tle4; transducin-like enhancer of split 4, homolog of Drosophil
	1453208_at: 2700089E24Rik; RIKEN cDNA 2700089E24 gene
	1460588_at: ---; ---
	1455121_at: Mlr2; Mblk1-related protein-2
	1434004_at: Dhps; deoxyhypusine synthase
	1460490_at: Mrpl15; mitochondrial ribosomal protein L15

	1419241_a_at: Aire; autoimmune regulator autoimmune polyendocrinopathy				
	1452340_at: 6820424L24Rik; RIKEN cDNA 6820424L24 gene				
Lane 291	1443167_at: Rnf12; Ring finger protein 12				
Lane 292	1446583_at: ---; ---				
	1438331_at: ---; ---				
	1439349_at: BC019206; cDNA sequence BC019206				
	1458308_at: BC019206; cDNA sequence BC019206				
	1443721_x_at: BC019206; cDNA sequence BC019206				
	1457824_at: ---; ---				
	1447337_at: ---; ---				
	1423619_at: Rasd1; RAS, dexamethasone-induced 1				
	1416576_at: Socs3; suppressor of cytokine signaling 3				
	1456212_x_at: Socs3; suppressor of cytokine signaling 3				
	1455899_x_at: Socs3; suppressor of cytokine signaling 3				
	1415899_at: Junb; Jun-B oncogene				
	1459961_a_at: ---; ---				
	1452519_a_at: Zfp36; zinc finger protein 36				
Lane 306	1423100 at: Fos; FBJ osteosarcoma oncogene				

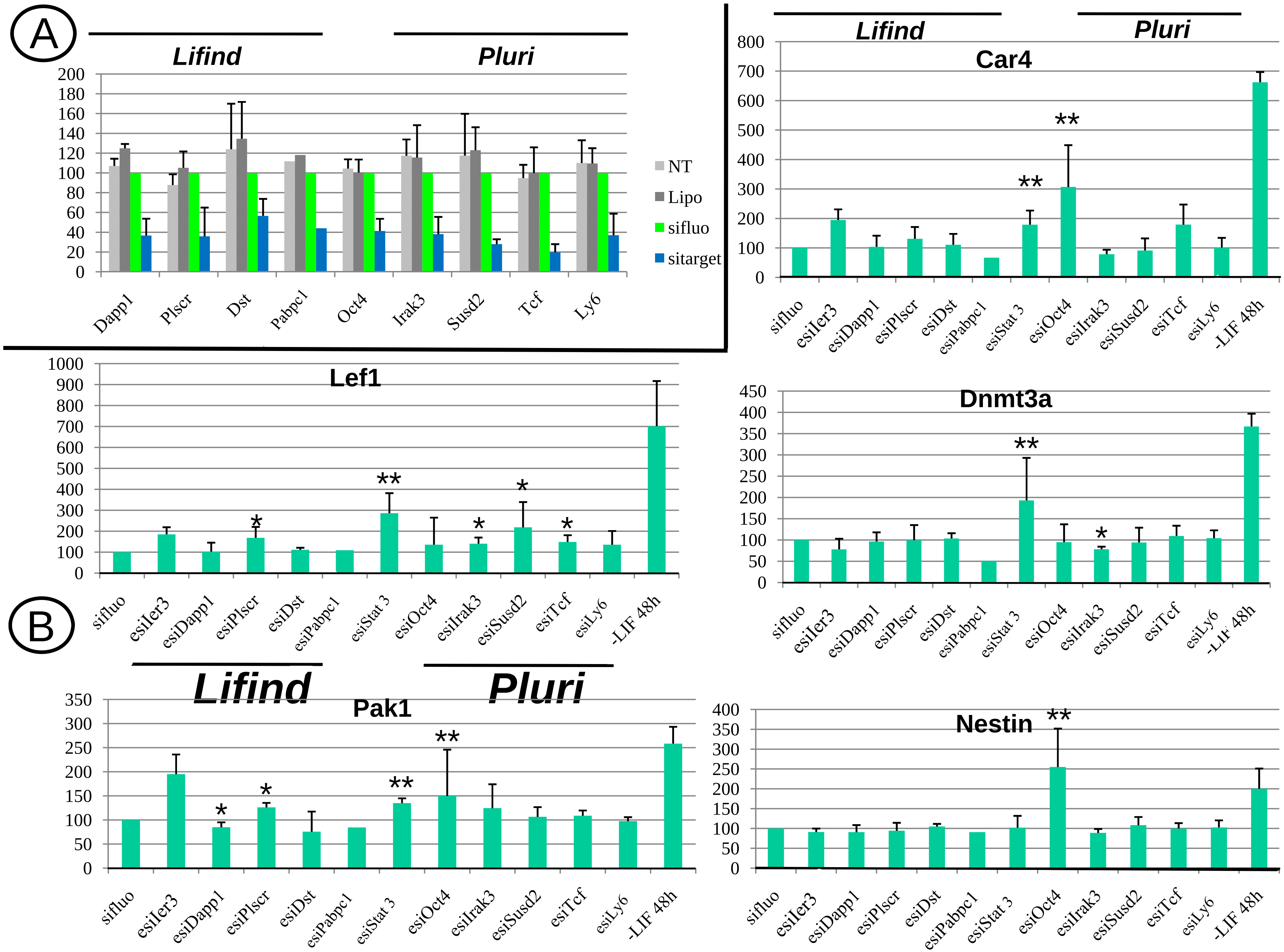


Additional file 4

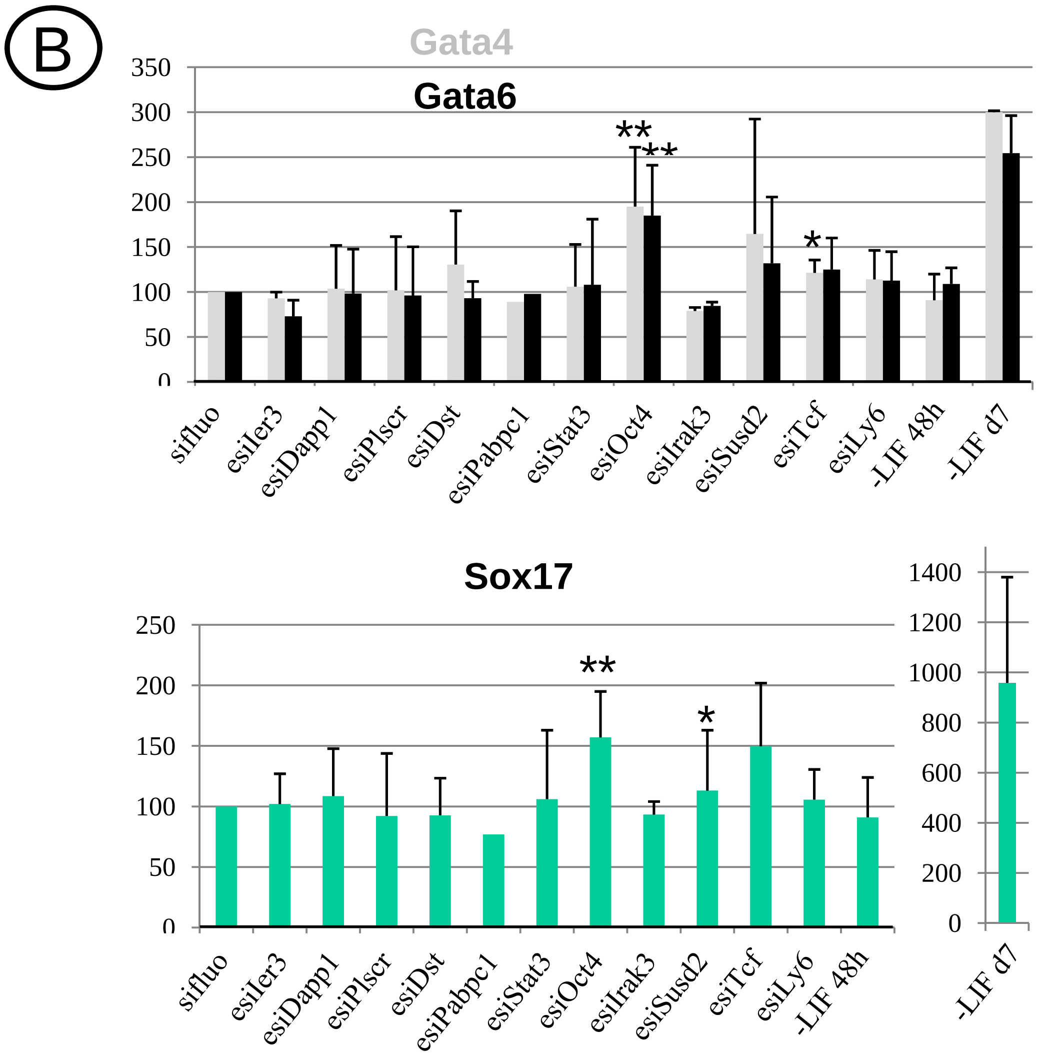
Morphological changes of Alkaline phosphatase stained cells in various cell growth conditions

Pictures of Alkaline Phosphatase (ALP) staining of ES cells **A)** grown with LIF or depleted of LIF for the indicated times (d=day) or **B)** transfected twice with *Oct4*, *Stat3* or *Ier3* esiRNA. Fixation and ALP staining have been performed at day 5 after the first round of transfection. NT: Non Transfected cells, Lipo: Lipofectamine mocked transfected cells.

Significant fields of two independent experiments are shown. Magnication is X400 in **A)** and X100 in **B)**.



Additional file 5



Additional file 5: Knock-down of a selection of *Lifind* and *Pluri* genes by the esiRNA strategy leads to minor changes in expression of early differentiation markers : A) Histogram representation of expression levels of a selection of *Lifind* and *Pluri* genes following RT-qPCR performed from ES cells transfected with the indicated esiRNAs (si target). NT and Lipo are as in Additional file 4. Sifluo: ES cells transfected with a fluorescent siRNA used as the base line control. **B)** Histogram representation of the expression levels of the indicated genes following transfection with the esiRNAs. The expression level of each marker, in cells grown without LIF for 48h (-LIF 48h) or for 7 days (-LIF d7), has also been included. The average of a minimum of three independent experiments has been plotted with standard deviations. Experiments with esi*Pabpc1* have been done twice. The estimated pvalue between samples was assessed by randomisation test according to Pfaffl. et al. (2002), Nucleic Acids Research, **30**, p36.

*: pvalue = 0.1; **: pvalue < or equal to 0,05.

Additional file 6

List of primers used for semi-quantitative RT-PCR analyses.

Genes	Forward	reverse	PCR Products
Pak1	TGCAACTGGACGAGTAATCC	GGGATGGCTGAGATTCTGTT	136bp
Lef1	AAGAAATGAGAGCGAATGTCGT	TTCTGGGACCTGTACCTGAAGT	249bp
Fzd7	TGTGTCTCTCTTTCGCATCC	GGAAGGCCTGCTCATAAAAG	155bp
Dnmt3a	GCAGTCTCAACAGCACCATT	AGGTTTCCTGTGTGGTAGGC	123bp
Mapk13	TGACCCAGATCCTGAAAGTG	GTGGGAAGAGCTGTGTGAAA	132bp
D8Ertd82e	GGGATGTCATTTCACACACG	AACTTGGTTCTGTCGGGATG	132bp
Hspb8	TCATTGGCTCACCTCAGTGT	CTTGGTGGTGATGGTTTGAG	153bp
Car4	GTAATGGCCCACTTCTGGAT	AGGCTGGGATTAAAGGTGTG	145bp
embigin	CTCAGTGACGGAAAAGTCCA	GGGCTCATCATCTTTCTTCC	142bp
Ptpn13	CCTCACGTGCCATCAGTATT	CCATGAACCTCTGGCTGATA	141bp
Irx3	GACGACGAGGATGAGGAGAT	GTCGTCCGAGTCGCTAGTTT	144 bp
1434025_at	ACTGACTCGTCTGCCTTTGA	TTTGCTTGTGGTTTCTGTCC	113bp
Ceacam1	ACTTCAGCCCCTTCTTCTCC	AGACCCTCCAGTGAGGAACA	137bp
Ceacam2	GCACTCTCAGGAAACCTTGG	AGCACTGGTCCACTGGAAGT	136bp
Inhbb	GAGACAGGTGGAATGTGGTG	CAGCTGTCACACTGCACATC	139bp
Mras	ACAGGGCTACAGCTTCCAAA	GCGTTGTATGTGGGTAAGCA	125bp
1429377_at	TGTCCCAGAAGTGTCCTGAG	TATCCTGGCTCACACCAGAG	140bp
1423786_at	GCAGCAGTCAAAGGATGATG	TGGGCTCTTCTGGAGAAACT	125bp
Gjb3	ACTGCTGCTTGAGACACACC	CCGGGGATATGACAGGATAC	140bp
Gjb5	CCCTTCCCTGATTCTGACAT	ACACTCCAGTTCATGGTGGA	137bp
Bcl3	GAGAGCAGCAGTCGTCTCAG	GGCAGGTGTAGATGTTGTGG	138bp
Vegfc	AAGACCGTGTGCGAATCGA	CACAGCGGCATACTTCTTC	70bp
1438781_at	CCGTACGTTATTGCTGGGTA	TGTCAGGAGAACCTTCGTGT	158bp
1454984_at	GGATCGGTTATGATGTGCAA	TTTTGAGTCGGAGTGAATCG	124bp
Zfp74	AGCACCAGAAAATCCAGGAC	GACTGTGCATGGAAGGAATG	129bp
Smarca2	TAAAGACCCCGTGAAGGAAG	CGCCCTGAACTGTCTTTGTA	150bp
Tle4	GGCTGTTTTGTGTCATGCTC	GGCTCTTCTTTGTGGCTTTC	143bp
Aire	ACACCACCCTTCTCTTCCTG	GCCAGCTCTTGGTCCTAATC	137bp
1443167_at	AATGAGTGACCAGAGGCTTT	TCTTCATGGCCTAGCTTTCT	138bp
Sbno2	TATGAGATCAAGGCCACAGG	TGGAAGGCTGAGTCATGTTC	130bp
Plscr1	TGGGCTTTGGTGTGTTACAT	CAGCTCATTTGCATAGCTTC	134bp
Dapp1	AGAGCTTAGCCTTTCCCACA	GCTCTCACTTGGGTTCACCT	130bp

Rasd1	AATCGGATTCCTGGACTAGC	TTCCTTTCACAGCAGGTGAC	122bp
Socs3	CGTTGTGAAGAGGCAGTAGC	ACAAAGCAGAACCCTCCATC	147bp
JunB	CCATCAACATGGAAGACCAG	CGTTCTCAGCCTTGAGTGTC	144bp
1459961_a_at	CATGCTAGACGGATGAATGG	TAGCTGGCCTGGAACTCAAT	124bp
Zfp36	CTTCACGACACACCAGATCC	TGGGAGTGCTGTAGTTGAGC	136bp
Fos	GGCTCTCCTGTCAACACACA	CCGCTTGGAGTGTATCTGTC	382bp
Nfkbiz	TGATAATGCCCGACAAGAAT	AATCCAATCCAATCCAAAGG	160bp
Klf5	ATTATTTGGGCCTGAGGTTG	TCTTCTGGCACCTGTCAACT	123bp
Klf4	TATACATTCCGCCACAGCAG	TCTGGGCTTCCTTTGCTAAC	136bp
Egr1	GAGCAAAAACGAGGAAGAGG	CCACAACACTCCAACTCCTG	151bp
Egr2	GTTCTGAACCTTCGGGAAAA	CACAAGGCACAGAGGACACT	138bp
Egr3	GATCCACCTCAAGCAAAAGG	AGGGAAAAGAAGGGATCTGG	137bp
Ier2	GTGAGCCTGAACTGAACCAA	GTCTACGGCAGCAACTACGA	139bp
Ier3	GGCAACGCTAACTCAGAACA	CATACACCCCTCCTTCACCT	143bp
Hprt	TACAGGCCAGACTTTGTTGG	CAACTTGCGCTCATCTTAGG	153bp
Ypel2	GCTGTGCTGTGTGGTGTCTT	GCAATGCGATAGCCTTATCA	153bp

Additional file 7		
List of primers used for RT-qPCR experiments		
nm_013556	HPRT F	tcagtcaacgggggacataaa
	HPRT R	ggggctgtactgcttaaccag
nm_010703	Lef1 F	aagaaatgagagagcgaatgtcgt
	Lef1 R	ttctgggacctgtacctgaagt
nm_011035	Pak1 F	tgcaactggacgagtaatcc
	Pak1 R	gggatggctgagattctgtt
nm_007607	Car4 F	gacaacggttcagagcacag
	Car4 R	aagcccttgttcaccttgtc
nm_007872	Dnmt3a F	gcagtctcaacagcaccatt
	Dnmt3a R	aggtttcctgtgtggtaggc
nm_016701	Nestin F	agaatgtgcagtcaccaagg
	Nestin R	gggtctcattttcaggtgggt
nm_008092	Gata4 F	ccctacccagcctacatgg
	Gata4 R	acatatcgagattggggtgtct
nm_010258	Gata6 F	ttgctccggtaacagcagtg
	Gata6 R	gtggtcgcttgtgtagaagga
nm_011441	Sox17 F	gatgcgggatacgccagtg
	Sox17 R	ccaccacctcgcctttcac
nm_0133662	Ier3 F	gctctggtcccgagattttca
	Ier3 R	agatgatggcgaacaggagaa
nm_011932	Dapp1 F	gcagaacttctaggagggaaca
	Dapp1 R	ccgtgataccaccccaaatc
nm_011636	Plscr1 F	ttctggaagtcttagcaggct
	Plscr1 R	cagtttcgggtacagcagtca
nnm_133833	Dst F	agaacggaacctatttgcatgaa
	Dst R	ctggtgctgagccatgatctt
nm_008774	Pabpc1 F	caagccagtacgcatcatgtg
	Pabpc1 R	tgcttcctgtgtttcaaagtgt
nm_013633	Oct4 F	gaggagtcccaggacatgaa
	Oct4 R	agatggtggtctggctgaac
nm_213659	Stat3 F	caacatcctggtgtctccac
	Stat3 R	caatggtattgctgcaggtc
nm_028679	Irak3 F	acatggggcatcaacgagc
	Irak3 R	ggaagctgataggggttttctg
nm_027890	Susd2 F	tgatgggtggcaaagacttcg
	Susd2 R	agcaagggtgatatgcagtgc
nm_023755	Tcfcp2l1 F	gaatcggaagctaggggactt
	Tcfcp2l1 R	ccctggggtccaagataccaa
nm_027366	Ly6g6e F	tactggtcacggtcctactct
	Ly6g6e R	ggcagcattgcataggtcct