

TargetID	RefSeq	EntrezID	Symbol	FC	adj.P.Val	PredictedTF	KEGG	GO_Biological_Process
scl000973.1_27-S	NM_030724	80914	Uck2	-1.98	0.00147	-	Pyrimidine metabolism (00240)	biosynthetic process (GO:0009058)
scl40832.13.1_18-S	NM_010858	17896	Myl4	-2.32	0.00176	-	-	cytoskeleton organization and biogenesis (GO:0007010)
scl0015312.2_169-S	NM_008251	15312	Hmgn1	-1.53	0.00238	-	-	pyrimidine dimer repair via nucleotide-excision repair (GO:0000720) transcription-coupled nucleotide-excision repair (GO:0006283) establishment and/or maintenance of chromatin architecture (GO:0006325) response to UV-B (GO:0010224) response to UV-C (GO:0010225)
scl20444.23.1_130-S	NM_009773	12236	Bub1b	-1.87	0.003	-	Cell cycle (04110)	protein amino acid phosphorylation (GO:0006468) apoptosis (GO:0006915) cell cycle (GO:0007049) mitosis (GO:0007067) negative regulation of progression through cell cycle (GO:0045786) cell division (GO:0051301)
scl35677.8_443-S	NM_173413	235442	Rab8b	-1.61	0.0033	-	-	transport (GO:0006810) intracellular protein transport (GO:0006886) small GTPase mediated signal transduction (GO:0007264) protein transport (GO:0015031)
scl23564.6_587-S	NM_010329	14726	Pdpn	-2.36	0.00332	-	-	cell morphogenesis (GO:0000902) lymphangiogenesis (GO:0001946) water transport (GO:0006833) amino acid transport (GO:0006865) cell adhesion (GO:0007155) multicellular organismal development (GO:0007275) regulation of cell shape (GO:0008360) folic acid transport (GO:0015884) lung development (GO:0030324) positive regulation of cell migration (GO:0030335) tube morphogenesis (GO:0035239) positive regulation of cell motility (GO:0051272)
scl17978.10_263-S	NM_172654	227094	5330401P04Rik	-1.51	0.00438	-	-	-
scl48834.5_262-S	NM_033149	93961	B3galt5	-3.17	0.00442	-	Glycosphingolipid biosynthesis - lactoseries (00601) Glycosphingolipid biosynthesis - globoseries (00603) Glycan structures - biosynthesis 2 (01031)	protein amino acid glycosylation (GO:0006486)
scl0054613.2_126-S	NM_018784	54613	St3gal6	-1.67	0.00504	-	Glycosphingolipid biosynthesis - neo-lactoseries (00602) Glycan structures - biosynthesis 2 (01031)	protein amino acid glycosylation (GO:0006486)
scl00235442.1_185-S	NM_173413	235442	Rab8b	-1.72	0.00537	-	-	transport (GO:0006810) intracellular protein transport (GO:0006886) small GTPase mediated signal transduction (GO:0007264) protein transport (GO:0015031)
scl48937.1.1_21-S	NM_001025192 NM_009988	13052	Cxadr	-2.76	0.00555	-	-	mitochondrion organization and biogenesis (GO:0007005) cell adhesion (GO:0007155) heart development (GO:0007507) cardiac muscle fiber development (GO:0048739)
scl27561.16.206_36-S	NM_013470	11745	Anxa3	-1.92	0.00662	-	-	negative regulation of coagulation (GO:0050819)
scl37307.8.1_29-S	NM_010809	17392	Mmp3	-3.79	0.00669	-	-	peptidoglycan metabolic process (GO:0000270) proteolysis (GO:0006508) collagen catabolic process (GO:0030574)
scl30680.4.1_44-S	NM_019738	56312	Nupr1	-1.88	0.00768	-	-	cell growth (GO:0016049)
scl51527.5.1_25-S	NM_027222	69816	2010001M09Rik	-4.41	0.00845	-	-	-
scl53221.10_351-S	NM_133775	77125	Il33	-2.35	0.00962	-	-	biological_process (GO:0008150)
scl15984.9.1_5-S	NM_030724	80914	Uck2	-2.52	0.0101	-	Pyrimidine metabolism (00240)	biosynthetic process (GO:0009058)
scl24307.19_191-S	NM_018761	54366	Ctnnal1	-1.69	0.0109	-	-	cell adhesion (GO:0007155) Rho protein signal transduction (GO:0007266)
scl27593.5.1_239-S	NM_053087	71920	Epgn	-3.27	0.0114	-	-	MAPKKK cascade (GO:0000165) activation of MAPK activity (GO:0000187) positive regulation of epidermal growth factor receptor activity (GO:0045741) positive regulation of mitosis (GO:0045840) positive regulation of epithelial cell proliferation (GO:0050679)
scl0217847.1_55-S	NM_144834	217847	Serpina10	-1.69	0.0114	-	-	D- repair (GO:0006281)
scl48501.9_645-S	NM_019388	12524	Cd86	-1.68	0.0127	-	Cell adhesion molecules (CAMs) (04514) Toll-like receptor signaling pathway (04620) Type I diabetes mellitus (04940)	defense response (GO:0006952)
scl0098878.2_247-S	NM_133838	98878	Ehd4	-1.63	0.0132	-	-	-
scl018103.3_14-S	NM_001077529 NM_008705	18103	Nme2	-1.58	0.0135	-	Purine metabolism (00230) Pyrimidine metabolism (00240)	GTP biosynthetic process (GO:0006183) UTP biosynthetic process (GO:0006228) CTP biosynthetic process (GO:0006241) nucleotide metabolic process (GO:0009117) pyrimidine ribonucleoside triphosphate biosynthetic process (GO:0009209)
scl38155.8_378-S	NM_009397	21929	Tnfrsf3	-1.99	0.0136	TF	-	ubiquitin cycle (GO:0006512) apoptosis (GO:0006915)
scl49348.7_351-S	NM_054052	108105	B3gnt5	-2.25	0.0136	-	Glycosphingolipid biosynthesis - lactoseries (00601) Glycosphingolipid biosynthesis - neo-lactoseries (00602) Glycan structures - biosynthesis 2 (01031)	protein amino acid glycosylation (GO:0006486) multicellular organismal development (GO:0007275) sphingolipid biosynthetic process (GO:0030148)
scl069745.1_205-S	NM_027196	69745	Pold4	-1.57	0.0136	-	Purine metabolism (00230) Pyrimidine metabolism (00240) D- polymerase (03030)	positive regulation of endothelial cell proliferation (GO:0001938) D- replication (GO:0006260)

scl028071.4_2-S	NM_172253	28071	Twistnb	-2.41	0.0138	-	-	transcription (GO:0006350)
scl22946.3.1_72-S	NM_025393	66166	S100a14	-2.69	0.014	-	-	-
scl47358.1_193-S	NM_027395	70350	Basp1	-2.31	0.0143	-	-	regulation of transcription, D--dependent (GO:0006355)
scl53313.7_541-S	NM_008137	14675	Gna14	-2.42	0.0143	-	Calcium signaling pathway (04020)	protein amino acid ADP-ribosylation (GO:0006471) signal transduction (GO:0007165) G-protein coupled receptor protein signaling pathway (GO:0007186)
scl25940.13_350-S	NM_020044 NM_022964	56743	Lat2	-1.92	0.0144	-	-	immune response (GO:0006955) B cell activation (GO:0042113) mast cell degranulation (GO:0043303) B cell receptor signaling pathway (GO:0050853)
scl0003597.1_94-S	NM_010809	17392	Mmp3	-2.45	0.0152	-	-	peptidoglycan metabolic process (GO:0000270) proteolysis (GO:0006508) collagen catabolic process (GO:0030574)
scl067283.1_285-S	NM_026071	67283	Slc25a19	-1.71	0.0152	-	-	transport (GO:0006810)
scl068219.2_2-S	NM_026623	68219	Nudt21	-1.63	0.0165	-	-	mR- cleavage (GO:0006379) mR- processing (GO:0006397)
scl32962.7.1_133-S	NM_011113	18793	Plaur	-2.48	0.0167	-	Complement and coagulation cascades (04610)	cell surface receptor linked signal transduction (GO:0007166)
scl19399.8_192-S	NM_013515	13830	Stom	-2.5	0.018	-	-	protein homooligomerization (GO:0051260)
scl37305.10.1_6-S	NM_019471	17384	Mmp10	-2.02	0.0187	-	-	peptidoglycan metabolic process (GO:0000270) proteolysis (GO:0006508) collagen catabolic process (GO:0030574)
scl15828.17_286-S	NM_133815	98386	Lbr	-1.57	0.0192	-	-	-
scl40029.6_18-S	NM_013415	11932	Atp1b2	-2.13	0.0192	-	-	transport (GO:0006810) ion transport (GO:0006811) potassium ion transport (GO:0006813) sodium ion transport (GO:0006814) cell adhesion (GO:0007155)
scl31147.9.1_14-S	NM_175640	103968	Plin	-1.51	0.0209	-	PPAR signaling pathway (03320)	lipid metabolic process (GO:0006629) lipid catabolic process (GO:0016042)
scl000253.1_401-S	NM_009982	13032	Ctsc	-1.66	0.021	-	-	proteolysis (GO:0006508)
scl42015.3_219-S	NM_028023	71963	Cdca4	-1.53	0.0218	-	-	biological_process (GO:0008150) cell division (GO:0051301)
scl020400.3_29-S	NM_011364	20400	Sh2d1a	-1.52	0.0222	-	Natural killer cell mediated cytotoxicity (04650)	humoral immune response (GO:0006959) intracellular signaling cascade (GO:0007242)
scl41002.6.1_5-S	NM_001038664 NM_023121	14710	Gngt2	-1.69	0.0222	-	-	signal transduction (GO:0007165) G-protein coupled receptor protein signaling pathway (GO:0007186)
scl0067742.1_215-S	NM_023380	67742	Samsn1	-2.39	0.0222	-	-	-
scl33579.4.1_22-S	NM_008535	17095	Lyl1	-1.53	0.0233	TF	-	transcription (GO:0006350) regulation of transcription, D--dependent (GO:0006355) regulation of transcription (GO:0045449)
scl31371.4.1_45-S	NM_008654	17872	Myd116	-1.62	0.0238	-	-	multicellular organismal development (GO:0007275) cell differentiation (GO:0030154)
scl49057.5_195-S	NM_008099	14525	Gcet2	-1.81	0.0243	-	-	-
scl0002999.1_1356-S	NM_009373	21817	Tgm2	-1.87	0.0246	-	Huntington's disease (05040)	proteolysis (GO:0006508) G-protein coupled receptor protein signaling pathway (GO:0007186) G-protein signaling, coupled to IP3 second messenger (phospholipase C activating) (GO:0007200) peptide cross-linking (GO:0018149) positive regulation of cell adhesion (GO:0045785)
scl36156.3_7-S	NM_010333	14739	Edg5	-1.88	0.0255	-	Neuroactive ligand-receptor interaction (04080)	signal transduction (GO:0007165) G-protein coupled receptor protein signaling pathway (GO:0007186) behavior (GO:0007610)
scl23887.17.1_103-S	NM_016748	51797	Ctps	-1.76	0.0256	-	Pyrimidine metabolism (00240)	pyrimidine nucleotide biosynthetic process (GO:0006221) glutamine metabolic process (GO:0006541)
scl0107321.9_13-S	NM_134152	107321	Lpxn	-2.04	0.0264	-	-	protein complex assembly (GO:0006461) cell adhesion (GO:0007155) signal transduction (GO:0007165)
scl34188.7.1_72-S	NM_009606	11459	Acta1	-3.1	0.0264	-	-	muscle contraction (GO:0006936) cytoskeleton organization and biogenesis (GO:0007010) muscle development (GO:0007517) skeletal muscle fiber development (GO:0048741)
scl0326619.1_58-S	NM_178192	326619	t1h4c Hist1h4f Hi	-2.58	0.0265	-	-	nucleosome assembly (GO:0006334) chromosome organization and biogenesis (sensu Eukaryota) (GO:0007001)
scl0002898.1_1-S	NM_009214	20603	04511 OTTMUSG	-1.56	0.0265	-	Urea cycle and metabolism of amino groups (00220) beta-Alanine metabolism (00410)	spermine metabolic process (GO:0008215)
scl000111.1_99-S	NM_009898	12721	Coro1a	-2.23	0.0293	-	-	-
scl0003450.1_9-S	NM_133978	102545	Cmtm7	-1.67	0.0304	-	-	chemotaxis (GO:0006935)

ri C130028H04 PX00168D15 AK047994 1392-S	NM_025282	17260	Mef2c	-1.73	0.0314	-	MAPK signaling pathway (04010)	blood vessel remodeling (GO:0001974) transcription (GO:0006350) regulation of transcription, D--dependent (GO:0006355) transcription from R- polymerase II promoter (GO:0006366) nervous system development (GO:0007399) heart development (GO:0007507) muscle development (GO:0007517) positive regulation of transcription (GO:0045941)
scl0014017.1_112-S	NM_001033711 NM_010161	14017	Evi2a	-1.61	0.0314	-	-	cell proliferation (GO:0008283) cellular process (GO:0009987)
scl0020135.2_120-S	NM_009104	20135	Rrm2	-1.67	0.032	-	Purine metabolism (00230) Pyrimidine metabolism (00240) p53 signaling pathway (04115)	D- replication (GO:0006260) deoxyribonucleoside diphosphate metabolic process (GO:0009186) deoxyribonucleotide metabolic process (GO:0009262)
scl18808.6.1_35-S	NM_028104	72112	Ppp1r14d	-11.3	0.0322	-	-	-
scl0217151.1_189-S	NM_207231	217151	Arl5c	-1.91	0.0322	-	-	intracellular protein transport (GO:0006886) small GTPase mediated signal transduction (GO:0007264) protein transport (GO:0015031)
scl19931.7.1_28-S	NM_026323	67701	Wfdc2	-2.21	0.0325	-	-	-
scl014528.1_141-S	NM_008102	14528	Gch1	-2.16	0.0331	-	Folate biosynthesis (00790)	tetrahydrobiopterin biosynthetic process (GO:0006729) aromatic compound biosynthetic process (GO:0019438)
scl0319159.1_95-S	NM_178210	319159	1h4c Hist1h4f Hi	-2.21	0.0332	-	-	nucleosome assembly (GO:0006334) chromosome organization and biogenesis (sensu Eukaryota) (GO:0007001)
scl0067475.1_65-S	NM_026184	67475	Ero1lb	-1.51	0.0337	-	-	electron transport (GO:0006118) transport (GO:0006810)
scl48625.8_280-S	NM_009744	12053	Bcl6	-1.93	0.0341	TF	-	negative regulation of transcription from R- polymerase II promoter (GO:0000122) cell morphogenesis (GO:0000902) negative regulation of cell-matrix adhesion (GO:0001953) germinal center formation (GO:0002467) negative regulation of T-helper 2 type immune response (GO:0002829) transcription (GO:0006350) regulation of transcription, D--dependent (GO:0006355) Rho protein signal transduction (GO:0007266) spermatogenesis (GO:0007283) protein localization (GO:0008104) negative regulation of cell proliferation (GO:0008285) actin cytoskeleton organization and biogenesis (GO:0030036) B cell differentiation (GO:0030183) positive regulation of B cell proliferation (GO:0030890) regulation of Rho GTPase activity (GO:0032319) negative regulation of mast cell cytokine production (GO:0032764) negative regulation of Rho protein signal transduction (GO:0035024) T-helper 2 type immune response (GO:0042092) regulation of cell proliferation (GO:0042127) negative regulation of apoptosis (GO:0043066) regulation of memory T cell differentiation (GO:0043380) negative regulation of cell differentiation (GO:0045596) negative regulation of T-helper 2 cell differentiation (GO:0045629)
scl40499.12_425-S	NM_019549	56193	Plek	-1.54	0.0352	-	-	intracellular signaling cascade (GO:0007242)
scl53341.4_558-S	NM_026640	107373	4632417K18Rik	-1.93	0.0369	-	-	-
scl0003917.1_104-S	NM_015781	53605	Nap1l1	-1.63	0.0376	-	-	nucleosome assembly (GO:0006334)
scl42728.4.1_1-S	NM_013929	30954	Siva1	-1.77	0.0376	-	-	apoptosis (GO:0006915) positive regulation of apoptosis (GO:0043065)
scl30689.14.1_1-S	NM_009844	12478	Cd19	-1.98	0.0377	-	Hematopoietic cell lineage (04640) B cell receptor signaling pathway (04662)	-
scl0012514.2_91-S	NM_009853	12514	Cd68	-1.56	0.038	-	-	-
scl42747.5_440-S	NM_001099792 NM_001099793 NM_177374	328162	6720458F09Rik	-1.67	0.0401	-	-	tR- processing (GO:0008033)
scl41469.8_427-S	NM_021349	57916	Tnfrsf13b	-2.18	0.0401	-	Cytokine-cytokine receptor interaction (04060)	B cell homeostasis (GO:0001782) immune response (GO:0006955) negative regulation of B cell proliferation (GO:0030889)
scl21758.4.1_5-S	NM_013486	12481	Cd2	-1.67	0.0404	-	Cell adhesion molecules (CAMs) (04514) Hematopoietic cell lineage (04640)	protein amino acid phosphorylation (GO:0006468) defense response (GO:0006952) cell adhesion (GO:0007155)
scl38756.3.1_44-S	NM_009514	22364	Vpreb3	-2.27	0.0404	-	-	-
scl068011.3_46-S	NM_026506	68011	Snrpg	-1.57	0.0413	-	-	nuclear mR- splicing, via spliceosome (GO:0000398) mR- processing (GO:0006397) R- splicing (GO:0008380) mR- metabolic process (GO:0016071)
ri 9630007E23 PX00115M09 AK035814 1461-S	XR_035190 XR_035416	67647	4930523C07Rik	-1.56	0.0425	-	-	-

scl00319161.1_8-S	NM_175657	319161	t1h4c Hist1h4f Hi	-2.54	0.0434	-	-	nucleosome assembly (GO:0006334) chromosome organization and biogenesis (sensu Eukaryota) (GO:0007001)
scl0014700.2_203-S	NM_025277	14700	Gng10	-1.65	0.0444	-	-	signal transduction (GO:0007165) G-protein coupled receptor protein signaling pathway (GO:0007186)
scl44840.4_185-S	NM_009856	12522	Cd83	-2.26	0.0449	-	-	-
scl44948.10_526-S	NM_013674	16364	Irf4	-1.6	0.0458	TF	-	transcription (GO:0006350) regulation of transcription, D--dependent (GO:0006355) myeloid dendritic cell differentiation (GO:0043011)
scl37649.7_307-S	NM_027878	71712	1200002N14Rik	-1.57	0.0469	-	-	autophagy (GO:0006914) apoptosis (GO:0006915)
scl35001.15_103-S	NM_031257	83436	Plekha2	-1.5	0.0476	-	-	-