

TargetID	RefSeq	EntrezID	Symbol	FC	adj.P.Val	PredictedTF	KEGG	GO_Biological_Process
scl34295.23_345-S	NM_172466	208936	Adamts18	2.19	5.47E-09	-	-	proteolysis (GO:0006508) integrin-mediated signaling pathway (GO:0007229)
scl000613.1_842-S	NM_172466	208936	Adamts18	1.85	8.78E-08	-	-	proteolysis (GO:0006508) integrin-mediated signaling pathway (GO:0007229)
ri 1810010H13 R000022C24 AK007420 1588-S	NR_003518	66776	4933439C20Rik	3.81	1.75E-06	-	-	-
scl00244867.2_39-S	NM_175535	244867	Arhgap20	1.71	2.14E-06	-	-	signal transduction (GO:0007165) neuropeptide signaling pathway (GO:0007218)
scl42604.11_253-S	NM_015764	268527	Greb1	1.74	3.14E-06	-	-	electron transport (GO:0006118)
scl21552.7_36-S	NM_011674	22239	Ugt8a	2.26	3.16E-06	-	Sphingolipid metabolism (00600)	metabolic process (GO:0008152) glycolipid biosynthetic process (GO:0009247) myelination (GO:0042552)
scl39519.5.1_59-S	NM_145435	217212	Pyy	2.14	9.91E-06	-	-	eating behavior (GO:0042755)
ri B930090K24 PX00167E03 AK081122 949-S	NM_172466	208936	Adamts18	4.32	9.91E-06	-	-	proteolysis (GO:0006508) integrin-mediated signaling pathway (GO:0007229)
scl00268527.2_292-S	NM_015764	268527	Greb1	2.1	2.72E-05	-	-	electron transport (GO:0006118)
scl35270.3.1_8-S	NM_027294	70031	Cmtm8	2.18	2.92E-05	-	-	chemotaxis (GO:0006935)
scl000323.1_2-S	NM_021472 NM_201239	58809	Rnase4 Ang	3.27	3.02E-05	-	-	angiogenesis (GO:0001525) response to hypoxia (GO:0001666) positive regulation of endothelial cell proliferation (GO:0001938) diacylglycerol biosynthetic process (GO:0006651) phospholipase C activation (GO:0007202) multicellular organismal development (GO:0007275) central nervous system development (GO:0007417) rR- transcription (GO:0009303) negative regulation of translation (GO:0017148) actin filament polymerization (GO:0030041) cell differentiation (GO:0030154) activation of phospholipase A2 (GO:0032431) negative regulation of smooth muscle cell proliferation (GO:0048662) positive regulation of protein secretion (GO:0050714)
scl52981.3.767_203-S	NM_007417	11551	Adra2a	3.36	4.46E-05	-	Neuroactive ligand-receptor interaction (04080)	signal transduction (GO:0007165) G-protein coupled receptor protein signaling pathway (GO:0007186) fear response (GO:0042596)
scl20335.12.1_10-S	NM_011978	26458	Slc27a2	2.58	4.52E-05	-	PPAR signaling pathway (03320)	long-chain fatty acid metabolic process (GO:0001676) lipid metabolic process (GO:0006629) fatty acid metabolic process (GO:0006631) metabolic process (GO:0008152)
scl37900.17.1_109-S	NM_145419	216019	Hkdc1	1.79	7.07E-05	-	-	glycolysis (GO:0006096)
scl29888.9.1_8-S	NM_001035228 NM_011375	20454	St3gal5	2.3	7.69E-05	-	Glycosphingolipid biosynthesis - ganglioseries (00604) Glycan structures - biosynthesis 2 (01031)	protein amino acid glycosylation (GO:0006486)
scl076279.3_16-S	NM_029562	76279	Cyp2d26	1.87	0.000127	-	-	electron transport (GO:0006118)
scl50076.19.1_35-S	NM_144855 NM_178224	12411	Cbs	1.64	0.000131	-	Glycine, serine and threonine metabolism (00260) Methionine metabolism (00271) Selenoamino acid metabolism (00450) Huntington's disease (05040)	amino acid metabolic process (GO:0006520) cysteine biosynthetic process from serine (GO:0006535) metabolic process (GO:0008152) amino acid biosynthetic process (GO:0008652) cysteine biosynthetic process via cystathionine (GO:0019343) cysteine biosynthetic process (GO:0019344)
ri D830018K05 PX00198P18 AK085856 791-S	NM_011845	23947	Mid2	1.65	0.000164	-	-	-
scl000377.1_101-S	NM_134079	11534	Adk	1.89	0.000176	-	Purine metabolism (00230)	purine ribonucleoside salvage (GO:0006166)
scl0019299.2_231-S	NM_008991	19299	Abcd3	1.69	0.000178	-	ABC transporters - General (02010)	transport (GO:0006810)
scl0003908.1_61-S	NM_011361	20393	Sgk Sgk1	2.67	0.000194	-	-	protein amino acid phosphorylation (GO:0006468) apoptosis (GO:0006915) response to D- damage stimulus (GO:0006974)
scl38793.6_454-S	NM_025807	66859	Slc16a9	3.01	0.000203	-	-	transport (GO:0006810)
scl0023972.1_63-S	NM_011864	23972	Papss2	2.26	0.000206	-	Purine metabolism (00230) Selenoamino acid metabolism (00450) Sulfur metabolism (00920)	sulfate assimilation (GO:0000103)
scl22634.5_179-S	NM_001042502 NM_001042504 NM_011098	18741	Pitx2	1.54	0.000243	TF	TGF-beta signaling pathway (04350)	patterning of blood vessels (GO:0001569) extraocular skeletal muscle development (GO:0002074) regulation of transcription, D- -dependent (GO:0006355) multicellular organismal development (GO:0007275) determination of left/right symmetry (GO:0007368) pattern specification process (GO:0007389) heart development (GO:0007507) Wnt receptor signaling pathway (GO:0016055) regulation of cell migration (GO:0030334) regulation of cell proliferation (GO:0042127) regulation of transcription (GO:0045449)
scl48545.9.1_240-S	NM_145932	106407	Osta	2.24	0.000243	-	-	transport (GO:0006810)

ri 9530095G06 PX00114P05 AK035716 3465-S	NM_021353	13487	Slc26a3	1.95	0.000243	-	-	transport (GO:0006810) sulfate transport (GO:0008272)
scl0056808.2_258-S	NM_020263	56808	Cacna2d2	1.73	0.000256	-	MAPK signaling pathway (04010)	calcium ion transport (GO:0006816) neuromuscular junction development (GO:0007528) regulation of body size (GO:0040014) muscle fiber development (GO:0048747) rhythmic synaptic transmission (GO:0060024)
scl0026458.2_190-S	NM_011978	26458	Slc27a2	2.34	0.000286	-	PPAR signaling pathway (03320)	long-chain fatty acid metabolic process (GO:0001676) lipid metabolic process (GO:0006629) fatty acid metabolic process (GO:0006631) metabolic process (GO:0008152)
scl015493.1_155-S	NM_153193	15493	Hsd3b2	2.3	0.000299	-	C21-Steroid hormone metabolism (00140) Androgen and estrogen metabolism (00150)	steroid biosynthetic process (GO:0006694) C21-steroid hormone biosynthetic process (GO:0006700)
scl29084.12.1_24-S	NM_022413	64177	Trpv6	2.28	0.000309	-	-	regulation of transcription, D--dependent (GO:0006355) transport (GO:0006810) ion transport (GO:0006811) cation transport (GO:0006812) calcium ion transport (GO:0006816)
scl22846.10_380-S	NM_010232	14263	Fmo5	1.76	0.000369	-	-	electron transport (GO:0006118)
scl0012499.2_107-S	NM_001026214 NM_007647	12499	Entpd5	1.93	0.00041	-	Purine metabolism (00230) Pyrimidine metabolism (00240)	-
scl23969.12.1_3-S	NM_007823	13120	Cyp4b1	2.58	0.000463	-	-	electron transport (GO:0006118)
scl020393.12_71-S	NM_011361	20393	Sgk Sgk1	3.48	0.000501	-	-	protein amino acid phosphorylation (GO:0006468) apoptosis (GO:0006915) response to D- damage stimulus (GO:0006974)
scl42754.12.1_99-S	NM_033603	93835	Amn	2.04	0.000561	-	-	multicellular organismal development (GO:0007275) excretion (GO:0007588) protein localization (GO:0008104)
scl0001451.1_53-S	NM_145373	209588	Sectm1a	1.52	0.000626	-	-	-
scl44053.7_337-S	NM_175417	109254	9530008L14Rik	1.65	0.00086	-	-	dicarboxylic acid transport (GO:0006835)
scl19516.4.19_7-S	NM_013677	20930	Surf1	1.6	0.000874	-	-	-
scl00170460.2_242-S	NM_023377	170460	Stard5	2.22	0.000924	-	-	steroid biosynthetic process (GO:0006694) transport (GO:0006810) lipid transport (GO:0006869)
scl00217732.2_273-S	NM_173735	217732	2310044G17Rik	2.34	0.001	-	-	regulation of transcription, D--dependent (GO:0006355)
scl22709.30_314-S	NM_020505 NM_146139	57257	Vav3	1.84	0.00143	-	Focal adhesion (04510) Natural killer cell mediated cytotoxicity (04650) T cell receptor signaling pathway (04660) B cell receptor signaling pathway (04662) Fc epsilon RI signaling pathway (04664) Leukocyte transendothelial migration (04670) Regulation of actin cytoskeleton (04810)	vesicle fusion (GO:0006906) integrin-mediated signaling pathway (GO:0007229) intracellular signaling cascade (GO:0007242) small GTPase mediated signal transduction (GO:0007264) cell migration (GO:0016477) cell projection biogenesis (GO:0030031) lamellipodium biogenesis (GO:0030032) regulation of Rho protein signal transduction (GO:0035023) regulation of GTPase activity (GO:0043087) positive regulation of phosphoinositide 3-kinase activity (GO:0043552) positive regulation of cell adhesion (GO:0045785)
scl30125.1_25-S	NM_175408	109218	Tmem139	1.89	0.0015	-	-	-
GI_38085084-S	-	-	Cyp2c65	2.07	0.00156	-	-	electron transport (GO:0006118)
scl020535.23_4-S	NM_009207	20535	Slc4a2	1.97	0.00174	-	-	transport (GO:0006810) ion transport (GO:0006811) anion transport (GO:0006820)
scl0213989.1_4-S	NM_145987	213989	Tmem82	1.76	0.00184	-	-	-
scl0003546.1_11-S	NM_026381 NM_025858	66940	Scotin	1.53	0.00207	-	p53 signaling pathway (04115)	induction of apoptosis (GO:0006917) apoptotic program (GO:0008632)
scl39681.11.1_111-S	NM_008081	14422	B4galnt2	1.94	0.00208	-	-	UDP-N-acetylglucosamine metabolic process (GO:0006047) protein amino acid glycosylation (GO:0006486) UDP-N-acetylgalactosamine metabolic process (GO:0019276) negative regulation of cell-cell adhesion (GO:0022408) lipid glycosylation (GO:0030259)
scl46912.2.1_27-S	NM_029562	76279	Cyp2d26	1.96	0.00208	-	-	electron transport (GO:0006118)
scl0235674.1_219-S	NM_146230	235674	Acaa1a Acaa1b	2.38	0.00208	-	Fatty acid metabolism (00071) Bile acid biosynthesis (00120) Valine, leucine and isoleucine degradation (00280) Benzoate degradation via hydroxylation (00362)	fatty acid metabolic process (GO:0006631) metabolic process (GO:0008152)
scl16430.4.1_256-S	NM_178779	320311	Rnf152	3.73	0.00208	-	-	-
scl0002745.1_20-S	NM_133348	70025	Acot7	1.77	0.00208	-	-	fatty acid metabolic process (GO:0006631) fatty acid catabolic process (GO:0009062)
scl43045.31_238-S	XM_126961 XM_904513	211945	Plekhh1	2.04	0.00208	-	-	-
scl0019116.1_207-S	NM_011169	19116	Prlr	1.9	0.00208	-	Cytokine-cytokine receptor interaction (04060) Neuroactive ligand-receptor interaction (04080) Jak-STAT signaling pathway (04630)	lactation (GO:0007595) regulation of cell adhesion (GO:0030155) regulation of epithelial cell differentiation (GO:0030856)
ri 9130003P18 PX00026I05 AK033572 2560-S	NM_172791	237625	Pla2g3	2.46	0.00208	-	-	lipid catabolic process (GO:0016042)
scl00242585.2_286-S	NM_177732	242585	Slc35d1	1.61	0.00208	-	-	-

scl3957.1.1_88-S	-	-	Ppp1r3d	1.64	0.00218	-	-	-
scl020541.2_143-S	NM_011406	20541	Slc8a1	1.59	0.00238	-	Calcium signaling pathway (04020)	cardiac inotropy (GO:0002026) transport (GO:0006810) ion transport (GO:0006811) sodium ion transport (GO:0006814) calcium ion transport (GO:0006816) cell communication (GO:0007154)
scl33431.12_111-S	NM_172759	234673	Ces5	1.7	0.00253	-	-	-
scl51764.24.1_222-S	NM_027727	69190	Dym	2.08	0.00258	-	-	biological_process (GO:0008150)
scl51015.5.49_29-S	NM_010023	13177	Dci	1.56	0.00269	-	Fatty acid metabolism (00071)	lipid metabolic process (GO:0006629) fatty acid metabolic process (GO:0006631) fatty acid beta-oxidation (GO:0006635) metabolic process (GO:0008152)
scl44201.10.1_39-S	NM_177016	319848	Slc17a4	1.68	0.00289	-	-	transport (GO:0006810)
scl25200.12.1_24-S	NM_025909	67013	Oma1	1.55	0.00289	-	-	proteolysis (GO:0006508)
scl0020646.1_10-S	NM_001082961 NM_001082962 NM_013670	20646	Snrpn	1.58	0.00291	-	-	mR- metabolic process (GO:0016071)
scl33211.11.6_30-S	NM_007876	13479	Dpep1	2.62	0.00291	-	-	proteolysis (GO:0006508)
scl29247.11.6_29-S	NM_138587	27999	D6Wsu176e	1.5	0.00292	-	-	biological_process (GO:0008150)
scl31918.5.1_81-S	NM_009475	22264	Prap1	2.17	0.00349	-	-	-
scl0056428.2_17-S	NM_019758	56428	Mtch2	1.7	0.00383	-	-	transport (GO:0006810)
scl064385.1_89-S	NM_022434	64385	Cyp4f14	2.53	0.00383	-	Arachidonic acid metabolism (00590)	electron transport (GO:0006118)
scl24656.12.1_25-S	NM_133348	70025	Acot7	1.52	0.00395	-	-	fatty acid metabolic process (GO:0006631) fatty acid catabolic process (GO:0009062)
scl000797.1_375-S	NM_145079	94284	Ugt1a6a	1.59	0.00438	-	Pentose and glucuronate interconversions (00040) Androgen and estrogen metabolism (00150) Starch and sucrose metabolism (00500) Porphyrin and chlorophyll metabolism (00860) Metabolism of xenobiotics by cytochrome P450 (00980)	metabolic process (GO:0008152) glucuronate metabolic process (GO:0019585)
scl000252.1_5-S	NM_033174	84704	Snurf Snrpn	1.87	0.00438	-	-	response to hormone stimulus (GO:0009725) mR- metabolic process (GO:0016071)
scl27110.7.1_2-S	NM_021719	60363	Cldn15	1.67	0.00438	-	Cell adhesion molecules (CAMs) (04514) Tight junction (04530) Leukocyte transendothelial migration (04670)	calcium ion transport (GO:0006816) calcium-independent cell-cell adhesion (GO:0016338)
scl011727.2_300-S	NM_007447	11727	Ang	1.66	0.00438	-	-	angiogenesis (GO:0001525) multicellular organismal development (GO:0007275) negative regulation of protein biosynthetic process (GO:0017148) cell differentiation (GO:0030154)
scl0394435.1_1-S	NM_201410	394435	Ugt1a6b Ugt1a6a	2.08	0.00447	-	Pentose and glucuronate interconversions (00040) Androgen and estrogen metabolism (00150) Starch and sucrose metabolism (00500) Porphyrin and chlorophyll metabolism (00860) Metabolism of xenobiotics by cytochrome P450 (00980)	metabolic process (GO:0008152) glucuronate metabolic process (GO:0019585)
scl48036.13_340-S	NM_020332	11732	Ank	2.07	0.00447	-	-	transport (GO:0006810) phosphate transport (GO:0006817) regulation of bone mineralization (GO:0030500)
scl24051.10_612-S	NM_177732	242585	Slc35d1	2.12	0.0046	-	-	-
scl16606.3_174-S	NM_010544	16147	Ihh	1.74	0.00474	-	Hedgehog signaling pathway (04340)	skeletal development (GO:0001501) patterning of blood vessels (GO:0001569) osteoblast differentiation (GO:0001649) proteolysis (GO:0006508) cell communication (GO:0007154) cell-cell signaling (GO:0007267) multicellular organismal development (GO:0007275) pattern specification process (GO:0007389) positive regulation of cell proliferation (GO:0008284) intein-mediated protein splicing (GO:0016539) cell differentiation (GO:0030154) negative regulation of cell differentiation (GO:0045596) cell maturation (GO:0048469)
scl30281.25_19-S	NM_021414	74340	4631427C17Rik	3.29	0.0049	-	Methionine metabolism (00271) Selenoamino acid metabolism (00450)	one-carbon compound metabolic process (GO:0006730)
scl31608.7.1_161-S	NM_181593	233011	Itpkc	1.59	0.00499	-	-	-
scl074754.9_24-S	NM_053272	74754	Dhcr24	1.8	0.00517	-	Biosynthesis of steroids (00100)	cholesterol biosynthetic process (GO:0006695) protein localization (GO:0008104) cholesterol metabolic process (GO:0008203) tissue development (GO:0009888) membrane organization and biogenesis (GO:0016044) sterol metabolic process (GO:0016125) male genitalia development (GO:0030539) plasminogen activation (GO:0031639) amyloid precursor protein catabolic process (GO:0042987)
scl18615.14.1325_54-S	NM_198029	241639	5830467P10Rik	1.8	0.00518	-	-	cell adhesion (GO:0007155)
scl50117.17_16-S	NM_010220	14229	Fkbp5	1.58	0.00529	-	-	protein folding (GO:0006457)

ri 4732462B05 PX00051O12 AK028848 2782-S	NM_177047	319974	Auts2	1.91	0.00529	-	-	biological_process (GO:0008150)
scl20253.5_8-S	NM_007694	12653	Chgb	1.6	0.00529	-	-	protein targeting (GO:0006605) intracellular protein transport (GO:0006886)
scl000929.1_30-S	NM_145079	94284	Ugt1a6b Ugt1a6a	2.06	0.00537	-	Pentose and glucuronate interconversions (00040) Androgen and estrogen metabolism (00150) Starch and sucrose metabolism (00500) Porphyrin and chlorophyll metabolism (00860) Metabolism of xenobiotics by cytochrome P450 (00980)	metabolic process (GO:0008152) glucuronate metabolic process (GO:0019585)
scl47787.2_58-S	NM_182805	76282	Gpt1	2.75	0.00537	-	Glutamate metabolism (00251) Alanine and aspartate metabolism (00252) Carbon fixation (00710)	biosynthetic process (GO:0009058)
scl53247.20_415-S	NM_013703	22359	Vldlr	1.57	0.00546	-	-	lipid metabolic process (GO:0006629) transport (GO:0006810) lipid transport (GO:0006869) endocytosis (GO:0006897) steroid metabolic process (GO:0008202) cholesterol metabolic process (GO:0008203) positive regulation of protein kinase activity (GO:0045860)
GI_38078281-S	XM_001473077 XM_194139	269529	Fbxo10	1.62	0.00547	-	-	biological_process (GO:0008150)
scl51356.6_394-S	NM_021296	17714	Grpel2	1.51	0.00581	-	-	protein folding (GO:0006457) biological_process (GO:0008150)
ri E130318A13 PX00208H22 AK053879 2944-S	NM_133942	101476	Plekha1	1.52	0.00631	-	-	-
ri B430202L17 PX00071I21 AK080899 3551-S	NM_153417	225997	Trpm6	1.79	0.00643	-	-	protein amino acid phosphorylation (GO:0006468) transport (GO:0006810) ion transport (GO:0006811) calcium ion transport (GO:0006816) metal ion transport (GO:0030001)
scl0067972.1_167-S	-	-	Atp2b1	1.53	0.00659	-	-	transport (GO:0006810) cation transport (GO:0006812) calcium ion transport (GO:0006816) metabolic process (GO:0008152)
scl0001019.1_73-S	NM_026159	67442	Retsat	1.64	0.00662	-	-	electron transport (GO:0006118) carotenoid biosynthetic process (GO:0016117) retinol metabolic process (GO:0042572)
scl47733.1_175-S	NM_010795	17309	Mgat3	1.6	0.00668	-	N-Glycan biosynthesis (00510) Glycan structures - biosynthesis 1 (01030)	protein amino acid N-linked glycosylation (GO:0006487)
scl0066552.1_146-S	NM_023220	66552	2010106G01Rik	1.9	0.00676	-	-	cell surface receptor linked signal transduction (GO:0007166)
ri A830081L15 PX00155H24 AK044025 2877-S	NM_029475	75894	Adal	2.17	0.00743	-	-	nucleotide metabolic process (GO:0009117) purine ribonucleoside monophosphate biosynthetic process (GO:0009168)
ri D230004H07 PX00187J04 AK084159 1630-S	NM_015747	20515	Slc20a1	1.51	0.00743	-	-	transport (GO:0006810) phosphate transport (GO:0006817)
scl0239827.3_270-S	NM_172822	239827	Pigz	1.75	0.00743	-	Glycosylphosphatidylinositol(GPI)-anchor biosynthesis (00563) Glycan structures - biosynthesis 2 (01031)	GPI anchor biosynthetic process (GO:0006506)
scl0264895.2_92-S	NM_153807	264895	BC018371 Acsf2	1.72	0.00743	-	-	metabolic process (GO:0008152)
scl17624.26.1_101-S	NM_145519	227377	Farp2	1.82	0.00768	-	Focal adhesion (04510) Adherens junction (04520)	intracellular signaling cascade (GO:0007242) neuron remodeling (GO:0016322) Rac protein signal transduction (GO:0016601) regulation of Rho protein signal transduction (GO:0035023)
scl0073296.1_60-S	NM_028493	73296	Rhobtb3	1.51	0.00768	-	-	-
scl0020732.2_76-S	NM_016907	20732	Spint1	1.55	0.00794	-	-	morphogenesis of a branching structure (GO:0001763) embryonic placenta development (GO:0001892)
scl00101476.1_284-S	NM_133942	101476	Plekha1	1.88	0.00808	-	-	-
scl074104.1_75-S	NM_023732	74104	Abcb6	1.58	0.00809	-	ABC transporters - General (02010)	transport (GO:0006810)
scl27391.19_438-S	NM_133904	100705	Acacb	1.72	0.00821	-	Fatty acid biosynthesis (00061) Pyruvate metabolism (00620) Propanoate metabolism (00640) Insulin signaling pathway (04910) Adipocytokine signaling pathway (04920)	phosphoenolpyruvate-dependent sugar phosphotransferase system (GO:0009401)
scl36356.8_626-S	NM_133710	69274	Ctdspl	1.58	0.00852	-	-	-
scl076263.8_129-S	NM_029555	76263	Gstk1	2.34	0.00899	-	Glutathione metabolism (00480) Metabolism of xenobiotics by cytochrome P450 (00980)	protein targeting (GO:0006605) glutathione metabolic process (GO:0006749)
scl094178.12_1-S	NM_053177	94178	Mcoln1	1.52	0.00944	-	-	transport (GO:0006810) ion transport (GO:0006811) calcium ion transport (GO:0006816) endosome transport (GO:0016197)
scl40598.13.96_215-S	NM_172439	170835	Pib5pa	2.61	0.00947	-	Inositol phosphate metabolism (00562) Phosphatidylinositol signaling system (04070)	biological_process (GO:0008150)
scl33167.10_5-S	NM_145608	234878	BC021891	1.67	0.0095	-	-	protein amino acid phosphorylation (GO:0006468)
scl34488.15.1_131-S	NM_144930	234564	AU018778	1.61	0.0096	-	-	-
ri B230353G19 PX00161I13 AK046215 2735-S	NM_172791	237625	Pla2g3	1.71	0.0097	-	-	lipid catabolic process (GO:0016042)

scl0001589.1_43-S	NM_134021	103711	Pnpo	1.82	0.01	-	Vitamin B6 metabolism (00750)	pyridoxine biosynthetic process (GO:0008615)
scl22543.4.4_13-S	NM_007410	11532	Adh5	1.73	0.01	-	Glycolysis / Gluconeogenesis (00010) Fatty acid metabolism (00071) Bile acid biosynthesis (00120) Tyrosine metabolism (00350) Glycerolipid metabolism (00561) 1- and 2-Methylnaphthalene degradation (00624) Methane metabolism (00680) Metabolism of xenobiotics by cytochrome P450 (00980)	retinoid metabolic process (GO:0001523)
scl23440.19_602-S	NM_001039079 NM_008860	18762	Prkcz	1.78	0.0107	-	Tight junction (04530) Insulin signaling pathway (04910) Type II diabetes mellitus (04930)	microtubule cytoskeleton organization and biogenesis (GO:0000226) protein amino acid phosphorylation (GO:0006468) intracellular signaling cascade (GO:0007242)
scl35792.9_485-S	NM_020270	56807	Scamp5	1.78	0.0109	-	-	transport (GO:0006810) protein transport (GO:0015031)
scl068338.3_10-S	NM_026680	68338	Golt1a Kiss1	1.63	0.0111	-	-	transport (GO:0006810) protein transport (GO:0015031) vesicle-mediated transport (GO:0016192)
scl052710.5_1-S	NM_029643	52710	Gpr172b	1.56	0.0112	-	-	-
scl32856.10.1_9-S	NM_016772	51798	Ech1	1.76	0.0114	-	Tyrosine metabolism (00350) Benzoate degradation via hydroxylation (00362) Fluorene degradation (00628)	lipid metabolic process (GO:0006629) fatty acid metabolic process (GO:0006631) metabolic process (GO:0008152)
scl50306.11.1_132-S	NM_009202	20517	Slc22a1	1.77	0.0115	-	-	ion transport (GO:0006811) cation transport (GO:0006812)
scl0338521.2_75-S	NM_178086	338521	Fa2h	2.26	0.0116	-	-	metabolic process (GO:0008152)
scl23466.19.1_1-S	NM_019585 NM_207687 NM_207688 NM_207689 NM_207690 NM_207691	56226	Espn	1.61	0.0118	-	-	locomotory behavior (GO:0007626) parallel actin filament bundle formation (GO:0030046) actin filament bundle formation (GO:0051017) negative regulation of cytoskeleton organization and biogenesis (GO:0051494) actin filament network formation (GO:0051639)
ri 4732465J04 PX00051C18 AK076359 1632-S	NM_001001499	414105	4732465J04Rik	2.07	0.0118	-	-	-
scl0017289.2_279-S	NM_008587	17289	Mertk	1.87	0.0118	-	-	regulation of progression through cell cycle (GO:0000074) protein amino acid phosphorylation (GO:0006468) cellular process (GO:0009987)
scl54377.16.1_8-S	NM_172778	109731	Maob	1.87	0.0118	-	Urea cycle and metabolism of amino groups (00220) Glycine, serine and threonine metabolism (00260) Histidine metabolism (00340) Tyrosine metabolism (00350) Phenylalanine metabolism (00360) Tryptophan metabolism (00380)	electron transport (GO:0006118)
scl33196.2.1635_134-S	NM_133955	69581	Rhou	1.66	0.012	-	-	G1/S transition of mitotic cell cycle (GO:0000082) small GTPase mediated signal transduction (GO:0007264) regulation of cell shape (GO:0008360) Rac protein signal transduction (GO:0016601) actin cytoskeleton organization and biogenesis (GO:0030036)
scl39660.7_333-S	NM_134021	103711	Pnpo	2.01	0.012	-	Vitamin B6 metabolism (00750)	pyridoxine biosynthetic process (GO:0008615)
scl37827.3_399-S	NM_134007	52637	Cisd1	1.56	0.012	-	-	-
scl30493.4.19_120-S	NM_011328	20287	Sct	1.95	0.0132	-	-	-
scl20027.27_426-S	-	-	Epb4.1l1	1.57	0.0135	-	-	cortical actin cytoskeleton organization and biogenesis (GO:0030866)
scl45408.20.1_29-S	NM_007940	13850	Ephx2	1.55	0.0136	-	Arachidonic acid metabolism (00590) Tetrachloroethene degradation (00625)	aromatic compound metabolic process (GO:0006725) xenobiotic metabolic process (GO:0006805) metabolic process (GO:0008152) response to toxin (GO:0009636) aromatic compound catabolic process (GO:0019439)
scl31382.5.64_0-S	-	-	Ppfia3	1.74	0.0138	-	-	regulation of transcription, D--dependent (GO:0006355)
scl070337.5_268-S	NM_027391	70337	lyd	2.2	0.0139	-	-	electron transport (GO:0006118) biological_process (GO:0008150)
scl0004017.1_1-S	NM_007819	13113	Cyp3a13	1.73	0.0142	-	gamma-Hexachlorocyclohexane degradation (00361) Linoleic acid metabolism (00591) Metabolism of xenobiotics by cytochrome P450 (00980)	electron transport (GO:0006118) xenobiotic metabolic process (GO:0006805)
ri 4732478E01 PX00052A23 AK028984 2945-S	NM_020258	56857	Slc37a2	3.87	0.0145	-	-	glycerol-3-phosphate metabolic process (GO:0006072) glycerophosphate shuttle (GO:0006127) glycerol-3-phosphate transport (GO:0015794)
scl063955.10_154-S	NM_022021	63955	Cables1	2.04	0.0145	-	-	regulation of progression through cell cycle (GO:0000074) G1/S transition of mitotic cell cycle (GO:0000082) cell cycle (GO:0007049) nervous system development (GO:0007399) cell division (GO:0051301) regulation of cell division (GO:0051302) regulation of cell cycle (GO:0051726)
scl25160.11.1_73-S	NM_145550	230584	Yipf1	1.56	0.015	-	-	-

scl30605.20_54-S	NM_010207 NM_201601	14183	Fgfr2	1.89	0.015	-	MAPK signaling pathway (04010) Regulation of actin cytoskeleton (04810) Prostate cancer (05215)	angiogenesis (GO:0001525) positive regulation of mesenchymal cell proliferation (GO:0002053) protein amino acid phosphorylation (GO:0006468) signal transduction (GO:0007165) cell-cell signaling (GO:0007267) salivary gland morphogenesis (GO:0007435) positive regulation of cell proliferation (GO:0008284) fibroblast growth factor receptor signaling pathway (GO:0008543) morphogenesis of embryonic epithelium (GO:0016331) bone mineralization (GO:0030282) lung development (GO:0030324) regulation of cell proliferation (GO:0042127) inner ear morphogenesis (GO:0042472) cell fate commitment (GO:0045165) embryonic organ morphogenesis (GO:0048562) epithelial cell proliferation (GO:0050673)
scl22833.10_29-S	NM_008256	15360	Hmgcs2	3.73	0.015	-	Synthesis and degradation of ketone bodies (00072) Valine, leucine and isoleucine degradation (00280) Butanoate metabolism (00650) PPAR signaling pathway (03320)	acetyl-CoA metabolic process (GO:0006084) steroid biosynthetic process (GO:0006694) cholesterol biosynthetic process (GO:0006695) lipid biosynthetic process (GO:0008610) sterol biosynthetic process (GO:0016126)
scl25177.9.1_28-S	NM_053272	74754	Dhcr24	2.32	0.0153	-	Biosynthesis of steroids (00100)	cholesterol biosynthetic process (GO:0006695) protein localization (GO:0008104) cholesterol metabolic process (GO:0008203) tissue development (GO:0009888) membrane organization and biogenesis (GO:0016044) sterol metabolic process (GO:0016125) male genitalia development (GO:0030539) plasminogen activation (GO:0031639) amyloid precursor protein catabolic process (GO:0042987)
scl0003580.1_5-S	NM_019793	56434	Tspan3	2.02	0.0158	-	-	visual perception (GO:0007601)
scl39304.10.1_23-S	XM_001481297 XM_181343	67763	Prpsap1	1.62	0.0158	-	-	nucleoside metabolic process (GO:0009116) nucleotide biosynthetic process (GO:0009165)
scl41473.7.1_27-S	NM_145428	216820	Dhrs7b	1.53	0.016	-	-	metabolic process (GO:0008152) enterobactin biosynthetic process (GO:0009239)
scl000268.1_28-S	NM_175105	66333	Aqp11	1.68	0.0163	-	-	proteolysis (GO:0006508) transport (GO:0006810)
scl20654.12_238-S	NM_019758	56428	Mtch2	1.6	0.0163	-	-	transport (GO:0006810)
GI_18079338-S	NM_080633	11429	Aco2	1.5	0.0169	-	Citrate cycle (TCA cycle) (00020) Glyoxylate and dicarboxylate metabolism (00630) Reductive carboxylate cycle (CO2 fixation) (00720)	tricarboxylic acid cycle (GO:0006099) citrate metabolic process (GO:0006101) metabolic process (GO:0008152)
scl0170460.6_30-S	NM_023377	170460	Stard5	1.65	0.017	-	-	steroid biosynthetic process (GO:0006694) transport (GO:0006810) lipid transport (GO:0006869)
GI_33468898-S	NM_010359	14864	Gstm3	2.01	0.0172	-	Glutathione metabolism (00480) Metabolism of xenobiotics by cytochrome P450 (00980)	metabolic process (GO:0008152)
scl0003764.1_13-S	NM_024435	67405	Nts	2.03	0.0174	-	-	regulation of blood vessel size (GO:0050880)
scl018641.1_29-S	NM_008826	18641	Pfkl	1.88	0.0174	-	Glycolysis / Gluconeogenesis (00010) Pentose phosphate pathway (00030) Fructose and mannose metabolism (00051) Galactose metabolism (00052) Insulin signaling pathway (04910)	glycolysis (GO:0006096)
scl42940.8_203-S	NM_173735	217732	2310044G17Rik	2.1	0.0182	-	-	regulation of transcription, D--dependent (GO:0006355)
scl39804.8.1_101-S	NM_177564	192970	BC022224	1.85	0.0186	-	-	metabolic process (GO:0008152)
scl16823.6.1_161-S	NM_172499	211798	Mfsd9	1.82	0.0187	-	-	transport (GO:0006810)
scl36950.1.1_88-S	NM_176846	320051	ExpH5	1.61	0.0187	-	-	biological_process (GO:0008150)
scl056448.1_20-S	NM_019823	56448	Cyp2d22	2.54	0.0187	-	-	electron transport (GO:0006118)
scl21752.24.8_3-S	NM_144900	11928	Atp1a1	1.77	0.0187	-	-	cardiac inotropy (GO:0002026) transport (GO:0006810) ion transport (GO:0006811) cation transport (GO:0006812) potassium ion transport (GO:0006813) sodium ion transport (GO:0006814) metabolic process (GO:0008152) blood pressure regulation (GO:0008217) monovalent inorganic cation transport (GO:0015672) ATP hydrolysis coupled proton transport (GO:0015991) sperm motility (GO:0030317) cellular hydrogen ion homeostasis (GO:0030641) negative regulation of glucocorticoid biosynthetic process (GO:0031947) response to drug (GO:0042493) negative regulation of heart contraction (GO:0045822) positive regulation of heart contraction (GO:0045823) positive regulation of striated muscle contraction (GO:0045989)
scl19223.5.1_16-S	NM_008100	14526	Gcg	1.63	0.019	-	-	regulation of insulin secretion (GO:0050796)

scl30075.6.1_112-S	NM_029638	76507	Abp1	4.48	0.0193	-	Urea cycle and metabolism of amino groups (00220) Glycine, serine and threonine metabolism (00260) Histidine metabolism (00340) Tyrosine metabolism (00350) Phenylalanine metabolism (00360) Tryptophan metabolism (00380) beta-Alanine metabolism (00410) Alkaloid biosynthesis II (00960)	transport (GO:0006810) amiloride transport (GO:0015898)
scl44383.15_255-S	NM_172593	218613	Mier3	1.6	0.0195	-	-	-
scl42524.16_317-S	NM_009132	20259	Scin	2.66	0.0197	-	-	barbed-end actin filament capping (GO:0051016)
scl0268822.14_46-S	NM_172960	268822	Adck5	1.8	0.0201	-	-	protein amino acid phosphorylation (GO:0006468)
scl14261.1.1_139-S	NM_009579	22782	Slc30a1	1.83	0.0203	-	-	in utero embryonic development (GO:0001701) transport (GO:0006810) ion transport (GO:0006811) cation transport (GO:0006812) zinc ion transport (GO:0006829) cellular zinc ion homeostasis (GO:0006882) nutrient import (GO:0009935)
scl0074754.1_5-S	NM_053272	74754	Dhcr24	1.56	0.0205	-	Biosynthesis of steroids (00100)	cholesterol biosynthetic process (GO:0006695) protein localization (GO:0008104) cholesterol metabolic process (GO:0008203) tissue development (GO:0009888) membrane organization and biogenesis (GO:0016044) sterol metabolic process (GO:0016125) male genitalia development (GO:0030539) plasminogen activation (GO:0031639) amyloid precursor protein catabolic process (GO:0042987)
scl0004026.1_20-S	NM_145558	231086	Hadhb	1.66	0.0205	-	Fatty acid elongation in mitochondria (00062) Fatty acid metabolism (00071) Bile acid biosynthesis (00120) Valine, leucine and isoleucine degradation (00280) Benzoate degradation via hydroxylation (00362)	lipid metabolic process (GO:0006629) fatty acid metabolic process (GO:0006631) fatty acid beta-oxidation (GO:0006635)
scl29880.12.1_23-S	NM_026159	67442	Retsat	2.14	0.0205	-	-	electron transport (GO:0006118) carotenoid biosynthetic process (GO:0016117) retinol metabolic process (GO:0042572)
scl36620.9_485-S	NM_178711	235527	Plscr4	1.55	0.021	-	-	-
scl000152.1_1-S	NM_133670	20887	Sult1a1	4.09	0.0214	-	Sulfur metabolism (00920)	lipid metabolic process (GO:0006629) steroid metabolic process (GO:0008202)
scl00394432.2_137-S	NM_201642	394432	Ugt1a10 Ugt1a9 Ugt1a7c Ugt1a6b Ugt1a6a Ugt1a5 Ugt1a2 Ugt1a1	1.9	0.0222	-	Pentose and glucuronate interconversions (00040) Androgen and estrogen metabolism (00150) Starch and sucrose metabolism (00500) Porphyrin and chlorophyll metabolism (00860) Metabolism of xenobiotics by cytochrome P450 (00980)	metabolic process (GO:0008152)
scl0002605.1_2-S	NM_133348	70025	Acot7	1.62	0.0223	-	-	fatty acid metabolic process (GO:0006631) fatty acid catabolic process (GO:0009062)
scl40004.19.1_140-S	NM_017366	11370	Acadvl	1.57	0.023	-	Fatty acid metabolism (00071)	electron transport (GO:0006118) lipid metabolic process (GO:0006629) fatty acid metabolic process (GO:0006631) metabolic process (GO:0008152)
scl098952.11_256-S	NM_153560	98952	C230093N12Rik	1.8	0.0231	-	-	-
scl0076608.2_255-S	NM_175244	76608	Hectd3	1.51	0.0233	-	-	protein modification process (GO:0006464) ubiquitin cycle (GO:0006512) regulation of mitotic metaphase/anaphase transition (GO:0030071)
ri C130089K18 PX00172G15 AK081952 639-S	NM_008991	19299	Abcd3	1.64	0.024	-	ABC transporters - General (02010)	transport (GO:0006810)
scl0330260.1_61-S	NM_183308	330260	Pon2	1.53	0.0243	-	gamma-Hexachlorocyclohexane degradation (00361) Bisphenol A degradation (00363)	-
scl25766.4.1_97-S	NM_007673	12591	Cdx2	1.5	0.0243	TF	-	blood vessel development (GO:0001568) blastocyst development (GO:0001824) placenta development (GO:0001890) transcription (GO:0006350) regulation of transcription, D--dependent (GO:0006355) multicellular organismal development (GO:0007275) pattern specification process (GO:0007389) cell differentiation (GO:0030154) regulation of transcription (GO:0045449)
scl17562.16_159-S	NM_023755	81879	Tcfcp2l1	2.22	0.0243	-	-	negative regulation of transcription from R- polymerase II promoter (GO:0000122) cell morphogenesis (GO:0000902) epithelial cell maturation (GO:0002070) transcription (GO:0006350) regulation of transcription, D--dependent (GO:0006355) cytoplasm organization and biogenesis (GO:0007028) salivary gland development (GO:0007431) determination of adult life span (GO:0008340) positive regulation of growth (GO:0045927)
scl52455.6.1_68-S	NM_030703	93721	Cpn1	1.84	0.0243	-	-	proteolysis (GO:0006508)
scl38855.11.1_294-S	NM_026085	67307	3110049J23Rik	2.29	0.0245	-	-	biosynthetic process (GO:0009058)

scl0020404.1_267-S	NM_019535	20404	Sh3gl2	1.86	0.0246	-	-	-
scl068738.1_270-S	NM_080575	68738	Acss1	1.76	0.0247	-	Glycolysis / Gluconeogenesis (00010) Pyruvate metabolism (00620) Propanoate metabolism (00640) Reductive carboxylate cycle (CO2 fixation) (00720)	acetyl-CoA biosynthetic process (GO:0006085) metabolic process (GO:0008152)
scl0002198.1_20-S	NM_177470	52538	Acaa2	1.85	0.0248	-	Fatty acid elongation in mitochondria (00062) Fatty acid metabolism (00071) Bile acid biosynthesis (00120) Valine, leucine and isoleucine degradation (00280) Benzoate degradation via hydroxylation (00362)	lipid metabolic process (GO:0006629) fatty acid metabolic process (GO:0006631)
Gl_40786427-S	NM_199366	381334	Gal3st2	1.57	0.0256	-	-	biosynthetic process (GO:0009058)
scl0013195.2_156-S	NM_016672	13195	Ddc	2.37	0.0259	-	Histidine metabolism (00340) Tyrosine metabolism (00350) Phenylalanine metabolism (00360) Tryptophan metabolism (00380) Alkaloid biosynthesis I (00950)	amino acid and derivative metabolic process (GO:0006519) carboxylic acid metabolic process (GO:0019752) catecholamine biosynthetic process (GO:0042423)
scl000186.1_92-S	NM_001082961 NM_001082962 NM_013670	20646	Snrpn	1.69	0.0259	-	-	mR- metabolic process (GO:0016071)
scl00209760.1_40-S	NM_172476	209760	Tmc7	1.62	0.0259	-	-	-
scl27904.14.1_131-S	NM_019447	54426	Hgfac	1.59	0.0264	-	-	proteolysis (GO:0006508)
scl35940.9_671-S	NM_027865	71687	Tmem25	1.7	0.0265	-	-	biological_process (GO:0008150)
scl47769.4_85-S	NM_138670	246221	Mpst	1.82	0.0287	-	Cysteine metabolism (00272)	sulfate transport (GO:0008272)
scl00320508.1_241-S	NM_198037	320508	Cachd1	1.57	0.029	-	-	transport (GO:0006810) ion transport (GO:0006811) calcium ion transport (GO:0006816)
scl20425.11_54-S	NM_016907	20732	Spint1	1.72	0.0319	-	-	morphogenesis of a branching structure (GO:0001763) embryonic placenta development (GO:0001892)
scl000333.1_26-S	NM_009366 NM_207652	21807	Tsc22d1	1.97	0.0322	-	-	transcription (GO:0006350) regulation of transcription, D--dependent (GO:0006355)
scl0001961.1_16-S	NM_007382	11364	Acadm	1.9	0.0331	-	Fatty acid metabolism (00071) Valine, leucine and isoleucine degradation (00280) beta-Alanine metabolism (00410) Propanoate metabolism (00640) PPAR signaling pathway (03320)	electron transport (GO:0006118) lipid metabolic process (GO:0006629) fatty acid metabolic process (GO:0006631) metabolic process (GO:0008152)
scl40593.13.11_2-S	NM_015749	21452	Tcn2	1.56	0.0331	-	-	transport (GO:0006810) ion transport (GO:0006811) cobalt ion transport (GO:0006824) cobalamin transport (GO:0015889)
scl21370.9_11-S	NM_007382	11364	Acadm	1.87	0.0336	-	Fatty acid metabolism (00071) Valine, leucine and isoleucine degradation (00280) beta-Alanine metabolism (00410) Propanoate metabolism (00640) PPAR signaling pathway (03320)	electron transport (GO:0006118) lipid metabolic process (GO:0006629) fatty acid metabolic process (GO:0006631) metabolic process (GO:0008152)
scl27972.10.1_31-S	NM_008439	16548	Khk	1.5	0.0337	-	Fructose and mannose metabolism (00051)	carbohydrate metabolic process (GO:0005975)
Gl_31981976-S	NM_153176	234847	Spg7	1.56	0.0341	-	-	mitochondrion organization and biogenesis (GO:0007005) cell adhesion (GO:0007155) anterograde axon cargo transport (GO:0008089) regulation of cell adhesion (GO:0030155)
scl41029.2_494-S	NM_009427	22057	Tob1	1.61	0.0353	-	-	SMAD protein nuclear translocation (GO:0007184) negative regulation of BMP signaling pathway (GO:0030514) negative regulation of osteoblast differentiation (GO:0045668)
scl0232409.1_160-S	NM_153506	232409	Clec2e	2.11	0.0355	-	-	-
scl50172.5.1_49-S	NM_026633	68241	9530058B02Rik	1.5	0.0364	-	-	biological_process (GO:0008150)
scl51647.25_267-S	NM_008720	18145	Npc1	1.77	0.0364	-	-	endocytosis (GO:0006897) lysosomal transport (GO:0007041) bile acid metabolic process (GO:0008206) cholesterol transport (GO:0030301) cholesterol homeostasis (GO:0042632)
scl54768.23.4_19-S	NM_010417 NM_181273	15203	Heph	1.52	0.0365	-	-	transport (GO:0006810) ion transport (GO:0006811) copper ion transport (GO:0006825) iron ion transport (GO:0006826) erythrocyte differentiation (GO:0030218)
scl014651.8_3-S	NM_024284	14651	Hagh	1.54	0.0376	-	Pyruvate metabolism (00620)	-
scl35187.16.1_30-S	NM_133979	102566	Tmem16k	1.59	0.0382	-	-	-
scl011429.19_155-S	NM_080633	11429	Aco2	1.58	0.039	-	Citrate cycle (TCA cycle) (00020) Glyoxylate and dicarboxylate metabolism (00630) Reductive carboxylate cycle (CO2 fixation) (00720)	tricarboxylic acid cycle (GO:0006099) citrate metabolic process (GO:0006101) metabolic process (GO:0008152)
scl39104.23_0-S	NM_008635	17761	Mtap7	1.51	0.0393	-	-	response to osmotic stress (GO:0006970) microtubule-based process (GO:0007017)
scl34490.14.1_30-S	NM_053200	104158	Ces3	2.53	0.0394	-	-	acyl-CoA metabolic process (GO:0006637) response to toxin (GO:0009636)
scl26170.7.4_26-S	NM_007383	11409	Acads	1.51	0.0395	-	Fatty acid metabolism (00071) Valine, leucine and isoleucine degradation (00280) Butanoate metabolism (00650)	electron transport (GO:0006118) lipid metabolic process (GO:0006629) fatty acid metabolic process (GO:0006631) metabolic process (GO:0008152)
scl26568.9_443-S	NM_145923	100532	Rel1	1.51	0.0395	-	-	-

scl0114664.1_62-S	NM_053262	114664	Hsd17b11	1.54	0.04	-	-	steroid biosynthetic process (GO:0006694) metabolic process (GO:0008152) lipid biosynthetic process (GO:0008610)
scl46993.2.1_42-S	NM_009437	22117	Tst	1.96	0.0401	-	-	sulfate transport (GO:0008272)
scl29310.11_209-S	NM_013743	27273	Pdk4	1.53	0.041	-	-	carbohydrate metabolic process (GO:0005975) glucose metabolic process (GO:0006006) acetyl-CoA biosynthetic process from pyruvate (GO:0006086) phosphorylation (GO:0016310) peptidyl-histidine phosphorylation (GO:0018106)
scl0170716.1_183-S	NM_130882	170716	Cyp4f13	1.97	0.0413	-	Arachidonic acid metabolism (00590)	electron transport (GO:0006118)
scl36816.23_421-S	NM_020043	56741	Nope	1.67	0.0415	-	-	-
scl0012808.2_292-S	NM_172496	12808	Cobl	1.74	0.0422	-	-	neural tube closure (GO:0001843)
scl058809.2_14-S	NM_021472 NM_201239	58809	Rnase4	1.73	0.0423	-	-	-
scl43044.8.1_17-S	NM_009705	11847	Arg2	1.59	0.0424	-	Urea cycle and metabolism of amino groups (00220) Arginine and proline metabolism (00330)	urea cycle (GO:0000050) arginine metabolic process (GO:0006525) arginine catabolic process (GO:0006527) striated muscle contraction (GO:0006941)
scl19581.12.1_39-S	NM_172204	241275	Noxa1	1.58	0.0424	-	-	superoxide metabolic process (GO:0006801)
scl35355.5_339-S	NM_010017	13138	Dag1	1.56	0.0423	-	ECM-receptor interaction (04512)	morphogenesis of an epithelial sheet (GO:0002011)
scl54593.13.1_30-S	NM_175326	102871	D330045A20Rik	2.29	0.0438	-	-	-
scl40512.21.1_20-S	NM_016672	13195	Ddc	1.82	0.0438	-	Histidine metabolism (00340) Tyrosine metabolism (00350) Phenylalanine metabolism (00360) Tryptophan metabolism (00380) Alkaloid biosynthesis I (00950)	amino acid and derivative metabolic process (GO:0006519) carboxylic acid metabolic process (GO:0019752) catecholamine biosynthetic process (GO:0042423)
scl32956.7.1_6-S	NM_023154	66071	Ethe1	1.62	0.0451	-	-	-
scl51376.2_283-S	-	-	Synpo	1.74	0.0458	-	-	-
scl0001696.1_24-S	NM_021793	60455	Tmem8	1.5	0.0458	-	-	cell adhesion (GO:0007155) biological_process (GO:0008150)
scl0015016.1_231-S	XM_001475314 NM_010393	15016	H2-Q5	1.52	0.046	-	-	defense response (GO:0006952)
scl0394435.7_126-S	NM_201410	394435	Ugt1a10 Ugt1a9 Ugt1a7c Ugt1a6b Ugt1a6a Ugt1a5 Ugt1a2 Ugt1a1	1.82	0.0467	-	Pentose and glucuronate interconversions (00040) Androgen and estrogen metabolism (00150) Starch and sucrose metabolism (00500) Porphyrin and chlorophyll metabolism (00860) Metabolism of xenobiotics by cytochrome P450 (00980)	metabolic process (GO:0008152) glucuronate metabolic process (GO:0019585) response to nutrient (GO:0007584) biphenyl metabolic process (GO:0018879) response to drug (GO:0042493) response to starvation (GO:0042594) response to ethanol (GO:0045471) response to steroid hormone stimulus (GO:0048545) response to glucocorticoid stimulus (GO:0051384)
scl51768.11.1_9-S	NM_177470	52538	Acaa2	1.8	0.0472	-	Fatty acid elongation in mitochondria (00062) Fatty acid metabolism (00071) Bile acid biosynthesis (00120) Valine, leucine and isoleucine degradation (00280) Benzoate degradation via hydroxylation (00362)	lipid metabolic process (GO:0006629) fatty acid metabolic process (GO:0006631)
scl50698.5_378-S	NM_032003	83965	Enpp5	1.74	0.0475	-	-	metabolic process (GO:0008152) nucleotide metabolic process (GO:0009117) nucleotide catabolic process (GO:0009166)
scl0002163.1_25-S	NM_177470	52538	Acaa2	1.76	0.0476	-	Fatty acid elongation in mitochondria (00062) Fatty acid metabolism (00071) Bile acid biosynthesis (00120) Valine, leucine and isoleucine degradation (00280) Benzoate degradation via hydroxylation (00362)	lipid metabolic process (GO:0006629) fatty acid metabolic process (GO:0006631)
scl38682.6_297-S	NM_139292	70335	Reep6	1.63	0.0492	-	-	translation (GO:0006412) homoiothermy (GO:0042309) response to freezing (GO:0050826) G-protein coupled receptor protein signaling pathway (GO:0007186)