probe.set	Gene Title	Gene Symbol	DD rank	LD rank	Phase (CT)	Biological Process I	Biological Process II
1415779_s_at	actin, gamma, cytoplasmic 1	Actg1	1	3	4.5	development	cell organization and biogenesis
1415984_at	acyl-Coenzyme A dehydrogenase, medium chain	Acadm**#**	2	6	4.5	metabolism	
1416178_a_at	pleckstrin homology domain containing, family B (evectins) member 1	Plekhb1**#**	3	9	16.5		
1416203_at	aquaporin 1	Aqp1**#**	4	10	16.5	transport	
1416953_at	connective tissue growth factor	Ctgf**#**	5	16	12.5	cell adhesion	DNA metabolism
1417602_at	period homolog 2 (Drosophila)	Per2**#**	6	23	12.5	RNA metabolism-transcription	signal transduction
1418174_at	D site albumin promoter binding protein	Dbp	7	26	8.5	RNA metabolism-transcription	metabolism
1418829_a_at	enolase 2, gamma neuronal	Eno2	8	31	16.5	metabolism	
1418839_at	glomulin, FKBP associated protein	Glmn**#**	9	32	8.5	cell proliferation-cell cycle	development
1419025_at	retinal S-antigen	Sag**#**	10	33	8.5	signal transduction	
1419740_at	phosphodiesterase 6B, cGMP, rod receptor, beta polypeptide	Pde6b	11	37	4.5	signal transduction	
1420147_at	expressed sequence AA407331	AA407331	12	38	4.5		
1420505_a_at	syntaxin binding protein 1	Stxbp1**#**	13	39	8.5	transport	development
1420772_a_at	TSC22 domain family 3	Tsc22d3**#**	14	41	12.5	death	RNA metabolism-transcription
1421061_at	guanylate cyclase activator 1a (retina)	Guca1a	15	43	8.5		
1421096_at	transient receptor potential cation channel, subfamily C, member 1	Trpc1	16	45	8.5	transport	
1424175_at	thyrotroph embryonic factor	Tef	17	58	8.5	RNA metabolism-transcription	metabolism
1425281_a_at	TSC22 domain family 3	Tsc22d3	18	63	12.5	death	RNA metabolism-transcription
1425557_x_at	TSC22 domain family 3	Tsc22d3	19	67	12.5	death	RNA metabolism-transcription
1427075_s_at	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 2	Pcmtd2	20	76	8.5	protein metabolism	metabolism
1438009_at	similar to histone 2a	MGC73635	21	91	20.5	DNA metabolism	cell organization and biogenesis
1438211_s_at	D site albumin promoter binding protein	Dbp**#**	22	92	8.5	RNA metabolism-transcription	metabolism
1450215_at	recoverin	Rcvrn	23	111	16.5	transport	signal transduction
1434603_at	thyroid hormone receptor associated protein 2	Thrap2**#**	24	137	4.5	RNA metabolism-transcription	metabolism
1444472_at	SNF1-like kinase 2	Snf1lk2**#**	25	154	12.5	signal transduction	protein metabolism
1456487_at	adenylate cyclase 1	Adcy1**#**	26	162	8.5	signal transduction	metabolism
1455140_at	PITPNM family member 3	Pitpnm3	27	170	20.5	transport	metabolism
1439862_at	Visual cortex cDNA, RIKEN full-length enriched library, clone:K530032J01 product:unclassifiab	---	28	175	16.5		
1448383_at	matrix metallopeptidase 14 (membrane-inserted)	Mmp14**#**	29	194	0.5	protein metabolism	metabolism
1427074_at	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 2	Pcmtd2	30	201	8.5	protein metabolism	metabolism
1425138_at	guanylate cyclase activator 1B	Guca1b	31	206	4.5	cell-cell signaling	signal transduction
AFFX-b-ActinM	actin, beta, cytoplasmic	Actb	32	224	4.5		
1435453_at	RIKEN cDNA A930011O12 gene	A930011O12Rik	33	263	16.5		
1422660_at	similar to Putative RNA-binding protein 3 (RNA-binding motif protein 3)	LOC671237	34	281	8.5	RNA metabolism-transcription	stress response
1434150_a_at	methyltransferase like 7A	Mettl7a**#**	35	308	12.5		
1426310_at	zinc finger, DHHC domain containing 5	Zdhhc5**#**	36	488	16.5		
1454714_x_at	3-phosphoglycerate dehydrogenase	Phgdh	37	2125	4.5	metabolism	
1438954_x_at	---	---	38	4950	12.5		
1444347_at	mannoside acetylglucosaminyltransferase 4, isoenzyme A	Mgat4a	39	5362	20.5	metabolism	
1444317_at	protocadherin 15	Pcdh15**#**	40	153	12.5	cell adhesion	development
1450706_a_at	ADP-ribosylation factor-like 3	Arl3	41	187	8.5	signal transduction	
1438040_a_at	heat shock protein 90kDa beta (Grp94), member 1	Hsp90b1	42	2014	16.5	DNA metabolism	stress response
1426645_at	heat shock protein 90kDa alpha (cytosolic), class A member 1	Hsp90aa1	43	74	16.5	stress response	development
1425306_at	cDNA sequence BC027072	BC027072	44	64	8.5		
1423126_at	ATPase, Na+/K+ transporting, beta 3 polypeptide	Atp1b3	45	2365	0.5	transport	
1421007_at	procollagen, type IV, alpha 6	Col4a6	46	17528	8.5	transport	
1420817_at	3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide	Ywhag	47	29176	12.5	cell-cell signaling	transport
1420623_x_at	heat shock protein 8	Hspa8	48	40	16.5	cell proliferation-cell cycle	stress response
1416958_at	nuclear receptor subfamily 1, group D, member 2	Nr1d2**#**	49	18	8.5	RNA metabolism-transcription	metabolism
1453509_at	Ly6/Plaur domain containing 2	Lypd2	50	1831	8.5		
1444172_at	Transcribed locus	---	51	152	20.5		
1443952_at	thyroid hormone receptor alpha	Thra	52	8554	4.5	RNA metabolism-transcription	development
1434572_at	histone deacetylase 9	Hdac9	53	136	4.5	cell proliferation-cell cycle	DNA metabolism
1452499_a_at	kinesin family member 2A	Kif2a	54	123	20.5	transport	cell organization and biogenesis
1450953_at	cytosolic iron-sulfur protein assembly 1 homolog (S. cerevisiae)	Ciao1	55	10989	16.5	cell proliferation-cell cycle	RNA metabolism-transcription
1450391_a_at	monoglyceride lipase	Mgll	56	360	20.5	stress response	protein metabolism
1450377_at	similar to thrombospondin 1	LOC640441	57	407	20.5	cell adhesion	stress response
1438902_a_at	heat shock protein 90kDa alpha (cytosolic), class A member 1	Hsp90aa1	58	563	16.5	stress response	development
1437711_x_at	ornithine decarboxylase, structural 1	Odc1	59	90	8.5	cell proliferation-cell cycle	development
1423933_a_at	RIKEN cDNA 1600029D21 gene	1600029D21Rik	60	277	20.5		
1423862_at	pleckstrin homology domain containing, family F (with FYVE domain) member 2	Plekhf2	61	1460	0.5		
1422230_s_at	cytochrome P450, family 2, subfamily a, polypeptide 4	Cyp2a4	62	446	8.5	metabolism	
1420376_a_at	H3 histone, family 3B	H3f3b	63	215	8.5	DNA metabolism	cell organization and biogenesis
1418022_at	NMDA receptor-regulated gene 1	Narg1	64	22686	8.5	RNA metabolism-transcription	development
1415993_at	squalene epoxidase	Sqle	65	7	4.5	metabolism	
1434867_at	solute carrier family 4, sodium bicarbonate transporter-like, member 11	Slc4a11	66	876	0.5	transport	
1434800_at	synaptic vesicle glycoprotein 2 b	Sv2b	67	788	4.5	cell-cell signaling	transport
1451285_at	fusion, derived from t(12;16) malignant liposarcoma (human)	Fus	68	301	4.5	RNA metabolism-transcription	metabolism
1438761_a_at	ornithine decarboxylase, structural 1	Odc1	69	241	4.5	cell proliferation-cell cycle	development
1433444_at	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1	Hmgcs1	70	274	4.5	metabolism	
1419070_at	cystin 1	Cys1	71	219	12.5		
1417457_at	CDC28 protein kinase regulatory subunit 2	Cks2	72	286	0.5	cell proliferation-cell cycle	signal transduction
1417429_at	flavin containing monooxygenase 1	Fmo1	73	22	12.5	transport	metabolism
1416332_at	cold inducible RNA binding protein	Cirbp	74	12	8.5	stress response	
1454991_at	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1	Slc7a1	75	1405	8.5	transport	metabolism
1436470_at	regulating synaptic membrane exocytosis 2	Rims2	76	146	12.5	cell-cell signaling	transport
1455725_a_at	H3 histone, family 3B	H3f3b	77	183	8.5	DNA metabolism	cell organization and biogenesis
1449434_at	carbonic anhydrase 3	Car3	78	107	8.5	metabolism	
1428082_at	acyl-CoA synthetase long-chain family member 5	Acsl5	79	7259	4.5	metabolism	
1426517_at	guanine nucleotide binding protein, alpha z subunit	Gnaz	80	71	16.5	signal transduction	
1426268_at	RIKEN cDNA C130090K23 gene	C130090K23Rik	81	14527	4.5		
1425441_at	---	---	82	204	0.5		
1425408_a_at	RIKEN cDNA 2610034M16 gene	2610034M16Rik	83	66	4.5	transport	cell organization and biogenesis
1425100_a_at	phosphodiesterase 6G, cGMP-specific, rod, gamma	Pde6g	84	276	16.5	signal transduction	
1423861_at	pleckstrin homology domain containing, family F (with FYVE domain) member 2	Plekhf2	85	458	0.5		
1420622_a_at	heat shock protein 8	Hspa8	86	728	16.5	cell proliferation-cell cycle	stress response
1418705_at	cone-rod homeobox containing gene	Crx	87	29	20.5	RNA metabolism-transcription	development
1443694_at	Regulator of G-protein signaling 20	Rgs20**#**	88	151	8.5	signal transduction	
1418649_at	EGL nine homolog 3 (C. elegans)	Egln3	89	675	0.5	death	protein metabolism
1437989_at	phosphodiesterase 8B	Pde8b	90	292	20.5	RNA metabolism-transcription	signal transduction
1416256_a_at	tubulin, beta 5	Tubb5	91	11	16.5	cell proliferation-cell cycle	death
1435440_at	PDZ domain containing 8	Pdzd8	92	178	0.5	signal transduction	
1456471_x_at	3-phosphoglycerate dehydrogenase	Phgdh	93	1697	4.5	metabolism	
1449821_a_at	RIKEN cDNA 0610016J10 gene	0610016J10Rik	94	562	4.5		
1437277_x_at	transglutaminase 2, C polypeptide	Tgm2	95	936	0.5	cell adhesion	signal transduction
1434799_x_at	aldolase 1, A isoform	Aldoa	96	84	20.5	metabolism	
1422082_a_at	nuclear transcription factor-Y alpha	Nfya	97	20722	8.5	RNA metabolism-transcription	metabolism
1448657_a_at	DnaJ (Hsp40) homolog, subfamily B, member 10	Dnajb10	98	475	20.5	protein metabolism	metabolism
1419638_at	ephrin B2	Efnb2	99	23236	4.5	development	
1417663_a_at	N-myc downstream regulated gene 3	Ndrg3	100	1477	16.5	development	cell organization and biogenesis
1416572_at	matrix metallopeptidase 14 (membrane-inserted)	Mmp14	101	3839	0.5	protein metabolism	metabolism
1435741_at	phosphodiesterase 8B	Pde8b	102	418	20.5	RNA metabolism-transcription	signal transduction
1435319_at	inositol hexaphosphate kinase 2	Ihpk2	103	264	8.5	death	development
1434769_at	BTB (POZ) domain containing 9	Btbd9	104	10063	20.5	cell adhesion	
1456510_x_at	UbiE protein	Ubie	105	2896	12.5		

1452927_x_at	triosephosphate isomerase 1	Tpi1	106	125	16.5	metabolism	
1426311_s_at	zinc finger, DHHC domain containing 5	Zdhhc5	107	202	16.5		
1423784_at	glycyl-tRNA synthetase	Gars	108	672	8.5	RNA metabolism-transcription	transport
1420093_s_at	heterogeneous nuclear ribonucleoprotein D-like	Hnrpdl	109	336	8.5	RNA metabolism-transcription	metabolism
1417664_a_at	N-myc downstream regulated gene 3	Ndrg3	110	721	20.5	development	cell organization and biogenesis
1453782_at	RIKEN cDNA 3021401C12 gene	3021401C12Rik	111	157	8.5		
1435189_at	FERM and PDZ domain containing 1	Frmpd1	112	139	16.5	signal transduction	
1455464_x_at	---	---	113	11130	4.5		
1436338_at	---	---	114	145	16.5		
1433728_at	cDNA sequence BC038479	BC038479	115	510	0.5	metabolism	
1451895_a_at	24-dehydrocholesterol reductase	Dhcr24	116	405	4.5	cell proliferation-cell cycle	death
1450329_a_at	arrestin 3, retinal	Arr3**#**	117	112	12.5	transport	signal transduction
1449039_a_at	heterogeneous nuclear ribonucleoprotein D-like	Hnrpdl	118	1363	8.5	RNA metabolism-transcription	metabolism
1448797_at	ELK3, member of ETS oncogene family	Elk3	119	5944	0.5	cell proliferation-cell cycle	RNA metabolism-transcription
1426464_at	nuclear receptor subfamily 1, group D, member 1	Nr1d1**#**	120	250	4.5	RNA metabolism-transcription	metabolism
1424251_a_at	heterogeneous nuclear ribonucleoprotein D-like	Hnrpdl	121	1577	8.5	RNA metabolism-transcription	metabolism
1423631_at	nuclear receptor subfamily 2, group E, member 3	Nr2e3	122	55	0.5	cell proliferation-cell cycle	RNA metabolism-transcription
1420846_at	mitochondrial ribosomal protein S2	Mrps2	123	1893	8.5	protein metabolism	metabolism
1418892_at	ras homolog gene family, member J	Rhoj	124	568	0.5	development	signal transduction
1433742_at	ankyrin repeat domain 15	Ankrd15	125	3392	20.5	RNA metabolism-transcription	metabolism
1452534_a_at	high mobility group box 2	Hmgb2	126	298	4.5	DNA metabolism	RNA metabolism-transcription
1450193_at	hyperpolarization-activated, cyclic nucleotide-gated K+ 1	Hcn1	127	189	8.5	transport	
1427743_at	Gene model 672, (NCBI)	Gm672	128	19355	20.5		
1455537_at	RIKEN cDNA 6430547I21 gene	6430547I21Rik	129	227	20.5		
1422842_at	5'-3' exoribonuclease 2	Xrn2	130	2669	12.5	DNA metabolism	RNA metabolism-transcription
1455033_at	RIKEN cDNA B430201A12 gene	B430201A12Rik	131	159	8.5		
1442180_at	deleted in lymphocytic leukemia, 7	Dleu7	132	1749	4.5		
1429791_at	RIKEN cDNA A930004D18 gene	A930004D18Rik	133	453	0.5		
1451478_at	angiopoietin-like 7	Angptl7	134	184	12.5	stress response	signal transduction
1426785_s_at	monoglyceride lipase	Mgll**#**	135	249	0.5	stress response	protein metabolism
1422830_s_at	dopamine receptor 4	Drd4**#**	136	50	20.5	signal transduction	
1417458_s_at	CDC28 protein kinase regulatory subunit 2	Cks2	137	448	0.5	cell proliferation-cell cycle	signal transduction
1440683_at	RIKEN cDNA A930004D18 gene	A930004D18Rik	138	607	4.5		
1435436_at	Endothelial PAS domain protein 1	Epas1	139	1694	12.5	RNA metabolism-transcription	stress response
1450892_a_at	ubiquitin specific peptidase 4 (proto-oncogene)	Usp4	140	9817	0.5	protein metabolism	metabolism
1425974_a_at	tripartite motif protein 25	Trim25	141	682	20.5		
1449364_at	aurora kinase C	Aurkc	142	24072	16.5	cell proliferation-cell cycle	protein metabolism
1421095_a_at	transient receptor potential cation channel, subfamily C, member 1	Trpc1	143	213	4.5	transport	
1433819_s_at	1-acylglycerol-3-phosphate O-acyltransferase 3	Agpat3	144	133	20.5	metabolism	
1450725_s_at	carbonic anhydrase 14	Car14	145	7955	12.5	metabolism	
1448276_at	tetraspanin 4	Tspan4	146	325	8.5	protein metabolism	metabolism
1426621_a_at	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), beta isoform	Ppp2r2b	147	73	4.5	signal transduction	
1424638_at	cyclin-dependent kinase inhibitor 1A (P21)	Cdkn1a	148	1675	0.5	cell proliferation-cell cycle	death
1416828_at	synaptosomal-associated protein 25	Snap25	149	4376	16.5	cell-cell signaling	transport
1452964_at	tubulin tyrosine ligase-like family, member 11	Ttll11	150	7718	8.5	protein metabolism	metabolism
1450923_at	transforming growth factor, beta 2	Tgfb2	151	1482	4.5	cell-cell signaling	cell proliferation-cell cycle
1417932_at	interleukin 18	Il18	152	757	20.5	cell adhesion	cell-cell signaling
1415918_a_at	triosephosphate isomerase 1	Tpi1	153	5	16.5	metabolism	
1429251_at	PR domain containing 2, with ZNF domain	Prdm2	154	8448	4.5		
1434487_at	myocyte enhancer factor 2D	Mef2d	155	328	16.5	RNA metabolism-transcription	development
1423078_a_at	sterol-C4-methyl oxidase-like	Sc4mol	156	280	4.5	metabolism	
1422809_at	regulating synaptic membrane exocytosis 2	Rims2	157	48	8.5	cell-cell signaling	transport
1454752_at	similar to RNA binding motif protein 24	LOC380843	158	6993	16.5		
1437445_at	transient receptor potential cation channel, subfamily M, member 1	Trpm1	159	2021	8.5	transport	metabolism
1427612_at	defensin beta 9	Defb9	160	248	4.5		
1422506_a_at	cystatin B	Cstb	161	6542	4.5		
1444487_at	lecithin-retinol acyltransferase (phosphatidylcholine-retinol-O-acyltransferase)	Lrat**#**	162	597	12.5	metabolism	
1448393_at	claudin 7	Cldn7	163	2301	4.5	cell adhesion	
1439150_x_at	GH regulated TBC protein 1	Grtp1	164	94	4.5		
1421087_at	period homolog 3 (Drosophila)	Per3	165	44	8.5	RNA metabolism-transcription	signal transduction
1436818_a_at	Musashi homolog 2 (Drosophila)	Msi2	166	1458	4.5		
1428763_at	single-strand selective monofunctional uracil DNA glycosylase	Smug1	167	343	20.5	DNA metabolism	stress response
1443335_at	PDZ domain containing RING finger 3	Pdzrn3	168	31876	16.5	signal transduction	
1450851_at	WD repeat domain 1	Wdr1	169	1072	4.5		
1448904_at	DNA segment, Chr 6, Wayne State University 176, expressed	D6Wsu176e	170	346	8.5		
1423145_a_at	titin-cap	Tcap**#**	171	212	12.5	development	cell organization and biogenesis
1417168_a_at	ubiquitin specific peptidase 2	Usp2	172	506	12.5	protein metabolism	metabolism
1453287_at	RIKEN cDNA 5730557B15 gene	5730557B15Rik	173	297	4.5		
1434034_at	ceramide kinase	Cerk	174	245	20.5	signal transduction	metabolism
1455643_s_at	TSR1, 20S rRNA accumulation, homolog (yeast)	Tsr1	175	1828	8.5		
1435459_at	flavin containing monooxygenase 2	Fmo2	176	4359	12.5	metabolism	
1426813_at	LTV1 homolog (S. cerevisiae)	Ltv1	177	10906	4.5		
1434096_at	solute carrier family 4 (anion exchanger), member 4	Slc4a4	178	1833	12.5	transport	
1451310_a_at	cathepsin L	Ctsl	179	1999	0.5	protein metabolism	metabolism
1449335_at	tissue inhibitor of metalloproteinase 3	Timp3	180	1819	12.5	signal transduction	
1449214_a_at	optic atrophy 1 homolog (human)	Opa1	181	32135	12.5	death	transport
1434376_at	CD44 antigen	Cd44	182	3048	0.5	cell adhesion	development
1434151_at	methyltransferase like 7A	Mettl7a	183	10197	12.5		
1417802_at	RIKEN cDNA 1110032A04 gene	1110032A04Rik	184	23568	16.5		
1417420_at	cyclin D1	Ccnd1	185	442	12.5	cell proliferation-cell cycle	stress response
1417324_at	microtubule associated serine/threonine kinase 2	Mast2	186	221	4.5	development	signal transduction
1433761_at	phosphodiesterase 4D interacting protein (myomegalin)	Pde4dip	187	580	16.5		
1452732_at	aspartic peptidase, retroviral-like 1	Asprv1	188	19540	0.5	development	protein metabolism
1419273_at	expressed sequence C80913	C80913	189	216	8.5	protein metabolism	metabolism
1457306_at	Transcribed locus	---	190	10072	20.5		
1425933_a_at	5'-nucleotidase, cytosolic II	Nt5c2	191	4956	8.5		
1417841_at	peroxisomal membrane protein 2	Pxmp2	192	24	8.5	cell organization and biogenesis	
1434132_at	RIKEN cDNA E430025E21 gene	E430025E21Rik	193	8028	20.5		
1450376_at	Max interacting protein 1	Mxi1	194	188	12.5	RNA metabolism-transcription	metabolism
1427482_a_at	carbonic anhydrase 8	Car8	195	540	12.5	signal transduction	metabolism
1433913_at	expressed sequence C80913	C80913	196	12836	4.5	protein metabolism	metabolism
1435896_at	sideroflexin 2	Sfxn2	197	895	12.5	transport	
1450387_s_at	adenylate kinase 3 alpha-like 1	Ak3l1	198	113	12.5	metabolism	
1417244_a_at	interferon regulatory factor 7	Irf7	199	20	16.5	RNA metabolism-transcription	protein metabolism
1440605_at	fascin homolog 2, actin-bundling protein, retinal (Strongylocentrotus purpuratus)	Fscn2	200	174	8.5	development	cell organization and biogenesis
1417169_at	ubiquitin specific peptidase 2	Usp2	201	287	8.5	protein metabolism	metabolism
1418300_a_at	MAP kinase-interacting serine/threonine kinase 2	Mknk2	202	430	8.5	stress response	signal transduction
1416468_at	aldehyde dehydrogenase family 1, subfamily A1	Aldh1a1	203	354	12.5	death	development
1428375_at	RIKEN cDNA 4932415G12 gene	4932415G12Rik	204	9591	8.5		
1456542_s_at	glutaminyl-tRNA synthase (glutamine-hydrolyzing)-like 1	Qrsl1	205	421	4.5	protein metabolism	metabolism
1450672_a_at	three prime repair exonuclease 1	Trex1	206	1859	20.5	DNA metabolism	stress response
1449181_at	ferrochelatase	Fech	207	13574	8.5	metabolism	
1423804_a_at	isopentenyl-diphosphate delta isomerase	Idi1	208	369	4.5	metabolism	
1420655_at	patatin-like phospholipase domain containing 3	Pnpla3	209	491	20.5	metabolism	
1450771_at	fucosyltransferase 9	Fut9	210	18262	4.5	protein metabolism	metabolism
1430170_at	Bardet-Biedl syndrome 10 (human)	Bbs10	211	40978	4.5	protein metabolism	metabolism

1420106_at	DNA Segment, Chr 9, Mouse Genome Informatics 7	D9Mgi7	212	13356	16.5		
1452796_at	differentially expressed in FDCP 6	Def6	213	21434	0.5		
1418934_at	mab-21-like 2 (C. elegans)	Mab21l2	214	6633	0.5	cell proliferation-cell cycle	development
1434019_at	PDGFA associated protein 1	Pdap1	215	25639	8.5	cell proliferation-cell cycle	signal transduction
1455180_at	expressed sequence AA407270	AA407270	216	3890	20.5		
1453317_a_at	KH domain containing, RNA binding, signal transduction associated 3	Khdrbs3	217	994	16.5	RNA metabolism-transcription	metabolism
1417860_a_at	spondin 2, extracellular matrix protein	Spon2	218	220	0.5	cell adhesion	development
1425891_a_at	GH regulated TBC protein 1	Grtp1	219	664	4.5		
1449324_at	ERO1-like (S. cerevisiae)	Ero1l	220	104	12.5	stress response	transport
1420820_at	RIKEN cDNA 2900073G15 gene	2900073G15Rik	221	1556	12.5		
1450522_a_at	H1 histone family, member 0	H1f0	222	708	8.5	DNA metabolism	cell organization and biogenesis
1457254_x_at	RIKEN cDNA 6330442E10 gene	6330442E10Rik	223	226	16.5		
1449628_s_at	START domain containing 7	Stard7	224	324	0.5		
1418025_at	basic helix-loop-helix domain containing, class B2	Bhlhb2	225	1234	8.5	RNA metabolism-transcription	metabolism
1449733_s_at	seven in absentia 1A	Siah1a	226	5998	8.5	cell proliferation-cell cycle	death
1449046_a_at	Josephin domain containing 2	Josd2	227	5223	16.5		
1435392_at	WD repeat domain 17	Wdr17	228	142	8.5		
1420562_at	secreted Ly6/Plaur domain containing 1	Slurp1	229	492	12.5	cell adhesion	
1415889_a_at	heat shock protein 90kDa beta (Grp94), member 1	Hsp90b1	230	655	16.5	DNA metabolism	stress response
1416407_at	phosphoprotein enriched in astrocytes 15	Pea15	231	633	0.5	death	transport
1433445_x_at	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1	Hmgcs1	232	81	4.5	metabolism	
1448705_at	zinc finger and BTB domain containing 22	Zbtb22	233	2236	0.5	RNA metabolism-transcription	metabolism
1417864_at	phosphoglycerate kinase 1	Pgk1	234	25	16.5	metabolism	
1448698_at	cyclin D1	Ccnd1	235	2118	12.5	cell proliferation-cell cycle	stress response
1438033_at	thyrotroph embryonic factor	Tef	236	1692	8.5	RNA metabolism-transcription	metabolism
1423684_at	heterogeneous nuclear ribonucleoprotein K	Hnrpk	237	9446	8.5	RNA metabolism-transcription	metabolism
1458506_at	gene model 1582, (NCBI)	Gm1582	238	167	16.5		
1428889_at	alkB, alkylation repair homolog 3 (E. coli)	Alkbh3	239	357	0.5		
1425729_at	bestrophin 2	Best2	240	40677	12.5	transport	
1423108_at	solute carrier family 25 (mitochondrial carnitine/acylcarnitine translocase), member 20	Slc25a20	241	13165	0.5	transport	
1460458_at	cysteine-rich secretory protein LCCL domain containing 2	Crispld2	242	7209	0.5		
1436432_at	RIKEN cDNA B230343J05 gene	B230343J05Rik	243	13330	4.5		
1423707_at	transmembrane protein 50B	Tmem50b	244	8020	16.5		
1419029_at	ERO1-like (S. cerevisiae)	Ero1l	245	1930	16.5	stress response	transport
1428095_a_at	transmembrane protein 24	Tmem24	246	791	12.5		
1418932_at	nuclear factor, interleukin 3, regulated	Nfil3	247	866	20.5	RNA metabolism-transcription	metabolism
1437302_at	adrenergic receptor, beta 2	Adrb2	248	273	12.5	RNA metabolism-transcription	stress response
1455821_x_at	complement component 1, q subcomponent binding protein	C1qbp	249	2563	8.5	stress response	protein metabolism
1431327_at	vacuolar protein sorting 13A (yeast)	Vps13a	250	41011	8.5	development	
1425728_at	---	---	251	26046	16.5		
1416933_at	P450 (cytochrome) oxidoreductase	Por	252	15720	8.5	metabolism	
1430147_a_at	Josephin domain containing 3	Josd3	253	26960	12.5		
1448816_at	prostaglandin I2 (prostacyclin) synthase	Ptgis	254	5738	8.5	metabolism	
1450110_at	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide	Adh7	255	10101	16.5	metabolism	
1418894_s_at	pre B-cell leukemia transcription factor 2	Pbx2	256	4599	20.5	RNA metabolism-transcription	development
1426684_at	CCR4-NOT transcription complex, subunit 6	Cnot6	257	3076	16.5	RNA metabolism-transcription	protein metabolism
1455789_x_at	heat shock protein 8	Hspa8	258	3315	16.5	cell proliferation-cell cycle	stress response
1431788_at	RIKEN cDNA 1700008G05 gene	1700008G05Rik	259	131	20.5	transport	
1431692_a_at	Casitas B-lineage lymphoma c	Cblc	260	5172	0.5	signal transduction	protein metabolism
1425142_a_at	heterogeneous nuclear ribonucleoprotein D	Hnrpd	261	16399	4.5	RNA metabolism-transcription	metabolism
1451862_a_at	perforin 1 (pore forming protein)	Prf1	262	8540	16.5	death	
1425041_at	LIM homeobox protein 3	Lhx3	263	32229	4.5	RNA metabolism-transcription	metabolism
1448830_at	dual specificity phosphatase 1	Dusp1	264	767	12.5	cell proliferation-cell cycle	stress response
1421811_at	thrombospondin 1	Thbs1	265	501	12.5	cell adhesion	stress response
1429139_at	OTU domain containing 7B	Otud7b	266	2886	20.5	protein metabolism	metabolism
1435866_s_at	histone cluster 3, H2a	Hist3h2a	267	2595	12.5	DNA metabolism	cell organization and biogenesis
1437313_x_at	high mobility group box 2	Hmgb2	268	197	4.5	DNA metabolism	RNA metabolism-transcription
1454841_at	RIKEN cDNA 4921511H13 gene	4921511H13Rik	269	21758	8.5		
1421084_at	retinoschisis (X-linked, juvenile) 1 (human)	Rs1	270	214	12.5	cell adhesion	development
1419340_at	Moloney leukemia virus 10-like 1	Mov10l1	271	9862	20.5	cell proliferation-cell cycle	development
1439098_at	RIKEN cDNA E230013L22 gene	E230013L22Rik	272	41166	12.5		
1444403_at	Core-binding factor, runt domain, alpha subunit 2, translocated to, 2 (human)	Cbfa2t2	273	20484	20.5	RNA metabolism-transcription	development
1417010_at	zinc finger protein 238	Zfp238	274	1352	4.5	RNA metabolism-transcription	transport
1428891_at	---	---	275	2184	4.5		
1446068_at	adenosine kinase	Adk	276	31469	8.5	metabolism	
1424118_a_at	spindle pole body component 25 homolog (S. cerevisiae)	Spbc25	277	57	20.5	cell proliferation-cell cycle	