X3P ID	UniGene ID	Gene Title	Gene Symbol	A	M	*p-fdr*
Hs.273321.1.A1_3p_a_at	Hs.273321	olfactomedin 4	OLFM4	7.6	62.4	0.0047
Hs.184572.0.S2_3p_at	Hs.334562	cell division cycle 2. G1 to S and G2 to M	CDC2	7.7	23.6	0.0023
Hs.75319.0.S3_3p_at	Hs.226390	ribonucleotide reductase M2 polypeptide	RRM2	7.7	19.6	0.0047
Hs.156346.0.S3_3p_at	Hs.156346	topoisomerase (DNA) II alpha 170kDa	TOP2A	6.4	14.9	0.0011
g6466452_3p_s_at	Hs.79078	MAD2 mitotic arrest deficient-like 1 (yeast)	MAD2L1	7.6	14.7	0.0052
Hs.23960.2.S1_3p_a_at	Hs.15740	cyclin B1	CCNB1	5.8	14.2	0.0125
g7705950_3p_at	Hs.279905	nucleolar and spindle associated protein 1	NUSAP1	7.8	14.1	0.0092
g11038651_3p_x_at	Hs.350966	pituitary tumor-transforming 1	PTTG1	9.1	13.9	0.0116
g7661905_3p_s_at	Hs.81892	KIAA0101	KIAA0101	8.1	13.8	0.0037
g12654170_3p_a_at	Hs.434953	high-mobility group box 2	HMGB2	9.3	13.4	0.0062
g13641303_3p_s_at	Hs.435733	cell division cycle associated 7	CDCA7	7.5	12.0	0.0044
g13699823_3p_at	Hs.8878	kinesin family member 11	KIF11	5.4	11.3	0.0109
g5031876_3p_at	Hs.89497	lamin B1	LMNB1	7.1	11.1	0.0112
g5031876_3p_x_at	Hs.89497	lamin B1	LMNB1	7.7	11.0	0.0087
Hs.156346.0.S1_3p_a_at	Hs.156346	topoisomerase (DNA) II alpha 170kDa	TOP2A	7.2	10.3	0.0047
g13529292_3p_at	Hs.164018	leucine zipper protein FKSG14	FKSG14	6.1	10.0	0.0053
g10938017_3p_at	Hs.194698	cyclin B2	CCNB2	8.2	9.4	0.0037
g12804874_3p_a_at	Hs.226390	ribonucleotide reductase M2 polypeptide	RRM2	7.7	9.2	0.0109
g8922501_3p_at	Hs.14559	chromosome 10 open reading frame 3	C10orf3	5.7	9.1	0.0090
Hs.111334.2.S2_3p_at	Hs.356835	epithelial membrane protein 2	EMP2	7.7	9.0	0.0014
g13375855_3p_a_at	Hs.38178	MLF1 interacting protein	MLF1IP	6.6	8.5	0.0108
Hs.77448.2.S1_3p_at	Hs.347524	hypothetical protein MGC24665	MGC24665	7.6	8.3	0.0190
g5453538_3p_a_at	Hs.444439	phosphoribosylaminoimidazole carboxylase. phosphoribosylaminoimidazole succinocarboxamide synthetase	PAICS	7.7	7.9	0.0068
g7661851_3p_at	Hs.77695	discs. large homolog 7 (Drosophila)	DLG7	5.9	7.8	0.0191
g11641252_3p_at	Hs.528669	chromosome condensation protein G	HCAP-G	6.0	7.8	0.0078

Hs.154443.1.S1_3p_a_at	Hs.460184	MCM4 minichromosome maintenance deficient 4 (S. cerevisiae)	MCM4	7.4	7.8	0.0209
g8922180_3p_at	Hs.104859	hypothetical protein DKFZp762E1312	DKFZp762E1312	6.8	7.7	0.0083
g4507750_3p_at	Hs.87491	thymidylate synthetase	TYMS	8.1	7.2	0.0044
g5729749_3p_at	Hs.36708	BUB1 budding uninhibited by benzimidazoles 1 homolog beta (yeast)	BUB1B	5.7	6.8	0.0157
g4885496_3p_at	Hs.407830	v-myb myeloblastosis viral oncogene homolog (avian)	MYB	8.0	6.7	0.0118
g4585861_3p_a_at	Hs.1594	centromere protein A. 17kDa	CENPA	6.0	6.5	0.0398
Hs.23960.0.S1_3p_at	Hs.15740	cyclin B1	CCNB1	5.2	6.4	0.0257
Hs.127797.0.A2_3p_at	Hs.127797	Helicase. lymphoid-specific	HELLS	5.1	6.2	0.0349
Hs.111334.2.S1_3p_at	Hs.356835	epithelial membrane protein 2	EMP2	7.0	6.2	0.0056
Hs.16520.0.S1_3p_a_at	Hs.351623	transcription factor RAM2	RAM2	7.4	6.1	0.0145
g13506815_3p_at	Hs.433278	emopamil binding protein-like	EBPL	8.3	6.0	0.0392
g13375949_3p_at	Hs.94292	FLJ23311 protein	FLJ23311	6.1	5.9	0.0181
g12804750_3p_at	Hs.71827	RRS1 ribosome biogenesis regulator homolog (S. cerevisiae)	RRS1	6.7	5.9	0.0206
g6857828_3p_s_at	Hs.42650	ZW10 interactor	ZWINT	7.7	5.9	0.0138
g5174456_3p_at	Hs.414407	kinetochore associated 2	KNTC2	6.1	5.8	0.0190
g8096220_3p_at	Hs.50813	intelectin 1 (galactofuranose binding)	ITLN1	10.0	5.8	0.0119
Hs.23900.1.S1_3p_a_at	Hs.23900	Rac GTPase activating protein 1	RACGAP1	6.6	5.8	0.0364
g12667400_3p_at	Hs.234545	cell division cycle associated 1	CDCA1	5.4	5.7	0.0142
g13447750_3p_at	Hs.249159	adrenergic. alpha-2A-. receptor	ADRA2A	7.0	5.7	0.0181
Hs.256150.0.S1_3p_at	Hs.335951	Hypothetical protein AF301222	NY-REN-41	6.3	5.7	0.0300
g8923876_3p_at	Hs.104741	T-LAK cell-originated protein kinase	TOPK	5.3	5.7	0.0392
g4502858_3p_s_at	Hs.83758	CDC28 protein kinase regulatory subunit 2	CKS2	7.9	5.5	0.0428
g4506038_3p_a_at	Hs.344037	protein regulator of cytokinesis 1	PRC1	7.9	5.5	0.0257
g4506974_3p_at	Hs.110736	solute carrier family 12 (sodium/potassium/chloride transporters). member 2	SLC12A2	7.0	5.4	0.0054
Hs.127268.0.S1_3p_x_at	Hs.450020	Similar to hypothetical protein FLJ38359	---	10.2	5.3	0.0178
g5902145_3p_at	Hs.93002	ubiquitin-conjugating enzyme E2C	UBE2C	7.5	5.3	0.0101
g2735291_3p_a_at	Hs.367676	dUTP pyrophosphatase	DUT	7.9	5.3	0.0150

g12734643_3p_a_at	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK2-associated dual specificity phosphatase)	CDKN3	6.8	5.2	0.0182
Hs.117950.0.S2_3p_a_at	Hs.444439	phosphoribosylaminoimidazole carboxylase. phosphoribosylaminoimidazole succinocarboxamide synthetase	PAICS	7.6	5.2	0.0347
Hs.78614.3.A1_3p_a_at	Hs.413852	complement component 1. q subcomponent binding protein	C1QBP	9.3	5.1	0.0411
Hs2.145582.1.S1_3p_s_at	Hs.145582	prominin 2	PROM2	6.7	5.0	0.0212
g7661973_3p_at	Hs.184339	maternal embryonic leucine zipper kinase	MELK	7.2	4.9	0.0360
Hs2.105097.2.S1_3p_s_at	Hs.164457	thymidine kinase 1. soluble	TK1	7.2	4.8	0.0134
g9910265_3p_at	Hs.307529	kinesin-like 7	KNSL7	5.3	4.8	0.0182
g4506128_3p_at	Hs.104123	phosphoribosyl pyrophosphate synthetase 2	PRPS2	8.2	4.8	0.0375
g4758169_3p_a_at	Hs.279611	deleted in malignant brain tumors 1	DMBT1	12.6	4.7	0.0450
Hs.18349.1.S1_3p_at	Hs.534827	Similar to RIKEN cDNA 2700049P18 gene	MGC57827	6.1	4.7	0.0153
g4507718_3p_at	---	---	---	5.8	4.7	0.0449
Hs.104696.0.S2_3p_at	Hs.104696	maba1	KIAA1324	7.9	4.6	0.0212
Hs.287440.0.S1_3p_at	Hs.287440	CDNA FLJ11692 fis. clone HEMBA1004983	---	5.3	4.6	0.0376
Hs.80976.1.S1_3p_a_at	Hs.80976	antigen identified by monoclonal antibody Ki-67	MKI67	6.8	4.5	0.0216
g12803002_3p_at	Hs.115474	replication factor C (activator 1) 3. 38kDa	RFC3	7.3	4.5	0.0182
Hs.62180.0.S2_3p_a_at	Hs.62180	anillin. actin binding protein (scraps homolog. Drosophila)	ANLN	6.0	4.5	0.0142
Hs.144687.0.S1_3p_at	Hs.416375	E2F transcription factor 7	E2F7	5.1	4.5	0.0117
g7657047_3p_at	Hs.313544	nucleostemin	NS	8.7	4.4	0.0197
g12653112_3p_a_at	Hs.409065	flap structure-specific endonuclease 1	FEN1	8.9	4.3	0.0214
g4504102_3p_at	Hs.2704	glutathione peroxidase 2 (gastrointestinal)	GPX2	9.0	4.3	0.0233
g4507902_3p_at	Hs.422662	vaccinia related kinase 1	VRK1	6.1	4.2	0.0197
Hs.289721.3.S1_3p_a_at	Hs.19340	growth arrest-specific 5	GAS5	7.0	4.2	0.0114
Hs.76084.1.S1_3p_s_at	Hs.76084	lamin B2	LMNB2	6.5	4.2	0.0451
g13570016_3p_at	Hs.415749	protein kinase. DNA-activated. catalytic polypeptide	PRKDC	7.1	4.2	0.0232

g4504688_3p_s_at	Hs.75432	IMP (inosine monophosphate) dehydrogenase 2	IMPDH2	8.7	4.2	0.0106
Hs.250746.2.S1_3p_a_at	Hs.297792	putative NFkB activating protein 373	FLJ23091	6.6	4.2	0.0138
g7705575_3p_a_at	Hs.436806	RA-regulated nuclear matrix-associated protein	RAMP	6.0	4.1	0.0205
g4506558_3p_a_at	Hs.12013	ATP-binding cassette. sub-family E (OABP). member 1	ABCE1	6.4	4.1	0.0388
g8922941_3p_at	Hs.281895	acid acyltransferase-epsilon	LPAAT-e	8.4	4.1	0.0225
Hs.118064.2.S1_3p_a_at	Hs.510265	nuclear ubiquitous casein kinase and cyclin-dependent kinase substrate	NUCKS	10.3	4.1	0.0019
Hs.133260.0.S2_3p_a_at	Hs.445098	DEP domain containing 1	DEPDC1	5.1	4.1	0.0284
g8922431_3p_a_at	Hs.293257	epithelial cell transforming sequence 2 oncogene	ECT2	6.8	4.0	0.0360
g4758705_3p_s_at	Hs.57101	MCM2 minichromosome maintenance deficient 2. mitotin (S. cerevisiae)	MCM2	7.9	3.9	0.0234
g10800147_3p_at	Hs.360033	KIAA0186 gene product	KIAA0186	6.6	3.9	0.0086
g181154_3p_s_at	Hs.99853	fibrillarin	FBL	9.1	3.9	0.0152
g13537354_3p_s_at	Hs.528353	leucine-rich repeats and immunoglobulin-like domains 1	LRIG1	8.5	3.9	0.0305
Hs.88523.0.S1_3p_at	Hs.507467	chromosome 13 open reading frame 3	C13orf3	4.8	3.9	0.0277
Hs.13421.0.S1_3p_at	Hs.504378	KIAA0056 protein	KIAA0056	6.0	3.9	0.0403
g1277202_3p_a_at	Hs.5337	isocitrate dehydrogenase 2 (NADP+). mitochondrial	IDH2	9.9	3.9	0.0109
g13570016_3p_x_at	Hs.415749	protein kinase. DNA-activated. catalytic polypeptide	PRKDC	7.3	3.8	0.0228
g13543656_3p_s_at	Hs.159557	karyopherin alpha 2 (RAG cohort 1. importin alpha 1)	KPNA2	7.8	3.8	0.0304
g8922484_3p_s_at	Hs.121028	asp (abnormal spindle)-like. microcephaly associated (Drosophila)	ASPM	5.6	3.8	0.0118
g5453793_3p_a_at	Hs.376064	nucleolar protein 5A (56kDa with KKE/D repeat)	NOL5A	8.9	3.8	0.0313
g6224978_3p_a_at	Hs.78853	uracil-DNA glycosylase	UNG	8.9	3.7	0.0151
g3560556_3p_at	Hs.90073	CSE1 chromosome segregation 1-like (yeast)	CSE1L	6.5	3.7	0.0138
Hs.301478.0.S1_3p_at	Hs.525566	KIAA0500 protein	KIAA0500	8.3	3.7	0.0403
g8980659_3p_at	Hs.127797	helicase. lymphoid-specific	HELLS	5.4	3.7	0.0416
g13376819_3p_at	Hs.23723	pseudouridylate synthase 1	PUS1	7.5	3.6	0.0192

Hs.82502.0.S1_3p_at	Hs.82502	polymerase (DNA-directed). delta 3. accessory subunit	POLD3	8.7	3.6	0.0093
Hs.193063.0.S2_3p_at	Hs.132246	Solute carrier family 38. member 1	SLC38A1	9.1	3.6	0.0095
g13376819_3p_x_at	Hs.23723	pseudouridylate synthase 1	PUS1	7.9	3.6	0.0235
g8922408_3p_a_at	Hs.435982	hypothetical protein FLJ10407	FLJ10407	6.2	3.6	0.0382
g8922641_3p_at	Hs.24641	cytoskeleton associated protein 2	CKAP2	7.6	3.6	0.0446
g4504368_3p_at	Hs.47504	exonuclease 1	EXO1	5.7	3.6	0.0476
g5803112_3p_a_at	Hs.74368	cytoskeleton-associated protein 4	CKAP4	8.9	3.6	0.0206
Hs.80976.1.S4_3p_a_at	Hs.80976	antigen identified by monoclonal antibody Ki-67	MKI67	6.7	3.5	0.0232
Hs.165909.0.A1_3p_at	---	---	---	4.8	3.5	0.0446
Hs.274448.1.S1_3p_at	Hs.406639	hypothetical protein LOC146909	LOC146909	4.8	3.5	0.0382
g8922864_3p_at	Hs.38114	BRIX	BRIX	6.3	3.5	0.0228
Hs.105478.0.S1_3p_at	Hs.88139	phosphoribosylformylglycinamidine synthase (FGAR amidotransferase)	PFAS	6.1	3.5	0.0206
g5032012_3p_at	Hs.153546	kinesin family member 20A	KIF20A	7.0	3.5	0.0057
g7661877_3p_at	Hs.3104	Kinesin family member 14	KIF14	5.2	3.5	0.0374
Hs.103135.0.A1_3p_at	---	---	---	7.9	3.4	0.0182
g6631094_3p_x_at	Hs.179565	MCM3 minichromosome maintenance deficient 3 (S. cerevisiae)	MCM3	8.2	3.4	0.0449
g1917006_3p_at	Hs.128453	frizzled-related protein	FRZB	6.1	3.4	0.0332
g8400737_3p_at	Hs.408312	tumor protein p53 (Li-Fraumeni syndrome)	TP53	8.3	3.4	0.0238
Hs.286192.0.S1_3p_at	Hs.286192	protein phosphatase 1. regulatory (inhibitor) subunit 1B (dopamine and cAMP regulated phosphoprotein. DARPP-32)	PPP1R1B	8.2	3.3	0.0035
Hs.318584.0.S1_3p_at	Hs.18919	zinc and ring finger 3	ZNRF3	5.0	3.3	0.0332
g5729983_3p_at	Hs.241517	polymerase (DNA directed). theta	POLQ	5.4	3.3	0.0351
Hs.104696.0.S1_3p_a_at	Hs.104696	maba1	KIAA1324	9.2	3.3	0.0170
Hs.21331.0.S2_3p_at	---	---	---	8.3	3.3	0.0446
g4503986_3p_at	Hs.78619	gamma-glutamyl hydrolase (conjugase. folylpolygammaglutamyl hydrolase)	GGH	5.3	3.3	0.0418
Hs.293514.0.A1_3p_at	Hs.479612	hypothetical protein FLJ14001	FLJ14001	5.9	3.3	0.0138
g13436073_3p_a_at	Hs.286049	phosphoserine aminotransferase 1	PSAT1	6.9	3.2	0.0267
g4758323_3p_a_at	Hs.444082	enhancer of zeste homolog 2 (Drosophila)	EZH2	8.1	3.2	0.0182

g7657205_3p_a_at	Hs.405465	integrin beta 3 binding protein (beta3-endonexin)	ITGB3BP	7.9	3.2	0.0385
Hs.288928.0.S1_3p_s_at	Hs.134885	zinc finger protein 300	ZNF300	5.1	3.2	0.0257
Hs.93121.1.S1_3p_at	Hs.93121	G-protein signalling modulator 2 (AGS3-like. C. elegans)	GPSM2	9.0	3.2	0.0349
g9506436_3p_at	Hs.49932	chromosome 21 open reading frame 45	C21orf45	6.5	3.2	0.0327
g12804598_3p_a_at	Hs.500995	small nuclear ribonucleoprotein D1 polypeptide 16kDa	SNRPD1	9.8	3.2	0.0491
Hs.133294.1.S1_3p_a_at	Hs.133294	IQ motif containing GTPase activating protein 3	IQGAP3	6.9	3.2	0.0058
Hs.296585.0.S1_3p_s_at	Hs.376064	nucleolar protein 5A (56kDa with KKE/D repeat)	NOL5A	7.7	3.1	0.0162
g7706484_3p_at	Hs.183803	TNF receptor-associated protein 1	TRAP1	8.3	3.1	0.0319
g6841461_3p_at	Hs.119908	nucleolar protein NOP5/NOP58	NOP5/NOP58	10.1	3.1	0.0146
Hs2.433010.1.S1_3p_at	Hs.433010	Transcribed locus. weakly similar to XP_343448.1 similar to ORF4 [Rattus norvegicus]	---	8.3	3.1	0.0106
Hs.111749.1.S1_3p_a_at	Hs.111749	PMS1 postmeiotic segregation increased 1 (S. cerevisiae)	PMS1	7.0	3.1	0.0389
Hs.62711.0.S1_3p_at	---	---	---	7.4	3.1	0.0023
g4557796_3p_at	Hs.118638	non-metastatic cells 1. protein (NM23A) expressed in	NME1	7.4	3.0	0.0223
Hs.110080.0.S1_3p_s_at	Hs.512260	ovostatin	OVOS	7.8	3.0	0.0385
g4557436_3p_s_at	Hs.82906	CDC20 cell division cycle 20 homolog (S. cerevisiae)	CDC20	7.2	3.0	0.0232
g4505408_3p_s_at	Hs.433416	non-metastatic cells 2. protein (NM23B) expressed in	NME2	11.2	3.0	0.0343
Hs.121536.0.S1_3p_at	Hs.121536	DUF729 domain containing 1	DUFD1	5.7	3.0	0.0411
Hs.12969.1.S1_3p_a_at	Hs.186649	hypothetical protein LOC54103	LOC54103	6.6	3.0	0.0343
Hs.17731.0.S1_3p_at	Hs.17731	hypothetical protein FLJ12892	FLJ12892	9.9	3.0	0.0275
Hs.9842.0.S1_3p_at	---	---	---	6.7	3.0	0.0312
g1000093_3p_a_at	Hs.77204	centromere protein F. 350/400ka (mitosin)	CENPF	5.0	3.0	0.0349
g8400737_3p_x_at	Hs.408312	tumor protein p53 (Li-Fraumeni syndrome)	TP53	8.4	3.0	0.0203
g13376746_3p_x_at	Hs.288981	chromosome 14 open reading frame 127	C14orf127	5.0	3.0	0.0487
g10864014_3p_a_at	Hs.432799	signal recognition particle receptor. B subunit	SRPRB	9.0	3.0	0.0182

g4885132_3p_a_at	Hs.77204	centromere protein F. 350/400ka (mitosin)	CENPF	6.8	3.0	0.0109
g7770071_3p_a_at	Hs.172801	isoleucine-tRNA synthetase	IARS	8.6	3.0	0.0212
Hs.133294.1.A1_3p_a_at	---	---	---	5.8	3.0	0.0225
g13623694_3p_s_at	Hs.128861	hypothetical protein MGC4308	MGC4308	5.5	2.9	0.0490
Hs.289721.1.S1_3p_s_at	Hs.19340	growth arrest-specific 5	GAS5	10.3	2.9	0.0254
g7657426_3p_at	Hs.49760	origin recognition complex. subunit 6 homolog-like (yeast)	ORC6L	7.8	2.9	0.0114
g12052970_3p_s_at	Hs.299208	coenzyme Q3 homolog. methyltransferase (yeast)	COQ3	7.6	2.9	0.0363
Hs.27931.0.S1_3p_at	Hs.478025	glucosamine-phosphate N-acetyltransferase 1	GNPNAT1	8.5	2.9	0.0166
Hs.108106.0.A2_3p_at	Hs.108106	ubiquitin-like. containing PHD and RING finger domains. 1	UHRF1	6.0	2.9	0.0294
g1695881_3p_at	Hs.69360	kinesin family member 2C	KIF2C	7.2	2.9	0.0225
Hs.127264.0.A1_3p_at	---	---	---	7.6	2.9	0.0416
Hs.180582.0.S1_3p_at	Hs.502848	hypothetical protein FLJ40869	FLJ40869	5.9	2.9	0.0365
g12232386_3p_a_at	Hs.510265	nuclear ubiquitous casein kinase and cyclin-dependent kinase substrate	NUCKS	9.1	2.8	0.0338
g12655170_3p_s_at	Hs.23348	S-phase kinase-associated protein 2 (p45)	SKP2	8.6	2.8	0.0274
g4505332_3p_a_at	Hs.446206	nuclear autoantigenic sperm protein (histone-binding)	NASP	8.1	2.8	0.0207
Hs.182490.0.S1_3p_s_at	Hs.182490	leucine-rich PPR-motif containing	LRPPRC	9.8	2.8	0.0430
g7656903_3p_s_at	Hs.102336	Rho GTPase activating protein 8	ARHGAP8	6.8	2.8	0.0207
Hs.30212.2.S1_3p_x_at	Hs.356247	Aminoacylase 1-like 2	ACY1L2	7.4	2.8	0.0476
Hs.112193.1.S2_3p_at	Hs.132399	mutS homolog 5 (E. coli)	MSH5	7.8	2.8	0.0037
Hs.15243.0.S1_3p_at	Hs.15243	nucleolar protein 1. 120kDa	NOL1	8.2	2.8	0.0037
Hs.93589.0.S1_3p_s_at	Hs.444229	Rho GTPase activating protein 24	ARHGAP24	6.6	2.8	0.0408
g13111771_3p_a_at	Hs.436849	hypothetical protein FLJ10521	FLJ10521	8.6	2.8	0.0236
214662_3p_at	Hs.169863	WD repeat domain 43	WDR43	7.3	2.8	0.0206
g6325471_3p_a_at	Hs.448396	ribosomal protein L10a	RPL10A	9.8	2.8	0.0423
Hs.111496.0.S1_3p_at	Hs.111496	hypothetical protein LOC139886	LOC139886	6.1	2.8	0.0480
g12652570_3p_s_at	Hs.424551	chromosome 15 open reading frame 22	C15orf22	9.2	2.8	0.0235
g2739055_3p_a_at	Hs.125124	EPH receptor B2	EPHB2	7.6	2.8	0.0054
g6652811_3p_at	Hs.226391	anterior gradient 2 homolog (Xenopus laevis)	AGR2	11.4	2.8	0.0314
g10445222_3p_at	Hs.454495	ribosomal protein L36a	RPL36A	10.3	2.8	0.0360

g4502712_3p_s_at	Hs.114311	CDC45 cell division cycle 45-like (S. cerevisiae)	CDC45L	6.5	2.8	0.0343
g4502612_3p_at	Hs.85137	cyclin A2	CCNA2	4.3	2.8	0.0332
g177109_3p_s_at	Hs.182490	leucine-rich PPR-motif containing	LRPPRC	9.5	2.8	0.0239
Hs.173802.0.S2_3p_at	Hs.173802	TBC1 domain family. member 4	TBC1D4	8.5	2.8	0.0157
g6631086_3p_s_at	Hs.528686	high mobility group AT-hook 2	HMGA2	6.9	2.8	0.0104
g4506960_3p_x_at	Hs.102456	survival of motor neuron protein interacting protein 1	SIP1	5.0	2.7	0.0436
g12056970_3p_at	Hs.436527	anaphase promoting complex subunit 1	ANAPC1	7.6	2.7	0.0398
g4504896_3p_at	Hs.159557	karyopherin alpha 2 (RAG cohort 1. importin alpha 1)	KPNA2	10.3	2.7	0.0138
g12232404_3p_at	Hs.195345	hypothetical protein FLJ22390	FLJ22390	5.9	2.7	0.0385
g5031794_3p_at	---	---	---	7.2	2.7	0.0188
g4504960_3p_at	Hs.435166	lamin B receptor	LBR	11.1	2.7	0.0138
g11967984_3p_at	Hs.74899	chromosome 10 open reading frame 117	C10orf117	7.2	2.7	0.0257
Hs.288809.0.S2_3p_at	Hs.288809	basic. immunoglobulin-like variable motif containing	BIVM	9.3	2.7	0.0189
g7661865_3p_at	Hs.443866	KIAA0020	KIAA0020	6.2	2.7	0.0449
g400340_3p_s_at	Hs.326249	ribosomal protein L22	RPL22	10.1	2.7	0.0333
Hs.1192.0.S1_3p_at	Hs.308045	barren homolog (Drosophila)	BRRN1	6.9	2.6	0.0359
g9558738_3p_at	Hs.23642	likely ortholog of mouse Sac3 homology domain 1 (S. cerevisiae)	SHD1	8.7	2.6	0.0430
g6841565_3p_a_at	Hs.9081	phenylalanine-tRNA synthetase-like. beta subunit	FARSLB	9.1	2.6	0.0191
g9963834_3p_at	Hs.421956	kinetochore protein Spc25	Spc25	5.6	2.6	0.0154
Hs.22123.0.A1_3p_at	Hs.238889	Unc-5 homolog D (C. elegans)	UNC5D	7.5	2.6	0.0128
Hs.98402.0.A1_3p_at	---	---	---	6.3	2.6	0.0333
Hs.180789.0.S2_3p_at	Hs.197184	RNA binding motif protein 25	RBM25	10.2	2.6	0.0350
g12804374_3p_at	Hs.27693	peptidylprolyl isomerase (cyclophilin)-like 1	PPIL1	7.1	2.6	0.0422
Hs.4747.1.S1_3p_a_at	Hs.4747	dyskeratosis congenita 1. dyskerin	DKC1	7.6	2.6	0.0275
g4758849_3p_at	Hs.17908	origin recognition complex. subunit 1-like (yeast)	ORC1L	4.7	2.6	0.0430
g5729733_3p_a_at	Hs.152759	activator of S phase kinase	ASK	6.9	2.6	0.0362
g11386144_3p_s_at	Hs.239	forkhead box M1	FOXM1	7.1	2.6	0.0188
g7657117_3p_at	Hs.54609	glycine C-acetyltransferase (2-amino-3-ketobutyrate coenzyme A ligase)	GCAT	7.4	2.6	0.0090

Hs.113503.0.S2_3p_a_at	Hs.113503	RAN binding protein 5	RANBP5	6.5	2.6	0.0179
Hs.2316.0.S1_3p_a_at	Hs.2316	SRY (sex determining region Y)-box 9 (campomelic dysplasia. autosomal sex-reversal)	SOX9	6.1	2.5	0.0476
g9558738_3p_x_at	Hs.23642	likely ortholog of mouse Sac3 homology domain 1 (S. cerevisiae)	SHD1	8.8	2.5	0.0435
g6912339_3p_s_at	Hs.367821	deoxythymidylate kinase (thymidylate kinase)	DTYMK	8.4	2.5	0.0183
229700_3p_at	Hs.444206	hypothetical protein LOC148203	LOC148203	6.0	2.5	0.0257
g13514830_3p_at	Hs.41706	DEAD (Asp-Glu-Ala-Asp) box polypeptide 10	DDX10	7.4	2.5	0.0292
Hs.117487.0.S1_3p_a_at	Hs.398178	chromosome 4 open reading frame 9	C4orf9	8.1	2.5	0.0274
g13376157_3p_at	Hs.370147	hypothetical protein FLJ22490	FLJ22490	8.6	2.5	0.0385
g12053106_3p_at	Hs.273294	Abelson helper integration site	AHI1	7.6	2.5	0.0312
g179364_3p_x_at	Hs.371468	cyclin D1 (PRAD1: parathyroid adenomatosis 1)	CCND1	8.5	2.5	0.0428
g4506694_3p_at	Hs.381184	ribosomal protein S19	RPS19	11.4	2.5	0.0381
g7705402_3p_a_at	Hs.369284	chromosome 20 open reading frame 6	C20orf6	9.2	2.5	0.0277
g7661729_3p_a_at	Hs.55097	mitochondrial ribosomal protein S28	MRPS28	7.5	2.5	0.0408
g13376651_3p_at	Hs.353181	hypothetical protein FLJ22635	FLJ22635	8.5	2.5	0.0450
Hs.292457.0.S1_3p_at	Hs.356331	peptidylprolyl isomerase A (cyclophilin A)	PPIA	10.4	2.5	0.0225
Hs.288809.1.S1_3p_x_at	Hs.288809	basic. immunoglobulin-like variable motif containing	BIVM	4.9	2.5	0.0138
g409069_3p_s_at	Hs.326249	ribosomal protein L22	RPL22	10.2	2.5	0.0430
g4506648_3p_s_at	Hs.119598	ribosomal protein L3	RPL3	12.1	2.4	0.0211
222761_3p_at	Hs.288809	basic. immunoglobulin-like variable motif containing	BIVM	7.9	2.4	0.0239
214042_3p_s_at	Hs.326249	ribosomal protein L22	RPL22	10.0	2.4	0.0402
Hs.117102.0.S2_3p_at	Hs.311097	exportin 4	XPO4	7.8	2.4	0.0446
g8922791_3p_at	Hs.144407	nudix (nucleoside diphosphate linked moiety X)-type motif 15	NUDT15	8.8	2.4	0.0387
Hs.115660.0.S2_3p_at	Hs.115660	DNA cross-link repair 1B (PSO2 homolog. S. cerevisiae)	DCLRE1B	4.0	2.4	0.0294
Hs.38178.2.S1_3p_at	Hs.38178	MLF1 interacting protein	MLF1IP	5.4	2.4	0.0138
g13376190_3p_at	Hs.326725	FLJ22624 protein	FLJ22624	7.1	2.4	0.0087
g13129021_3p_at	Hs.208912	chromosome 22 open reading frame 18	C22orf18	7.5	2.4	0.0223
g12653842_3p_a_at	Hs.20830	Kinesin family member C1	KIFC1	7.0	2.4	0.0103

Hs.122908.1.S1_3p_at	Hs.122908	DNA replication factor	CDT1	7.0	2.4	0.0387
g8922949_3p_at	Hs.303573	meiosis-specific nuclear structural protein 1	MNS1	4.5	2.4	0.0172
Hs.62918.0.S1_3p_at	Hs.62918	CDC91 cell division cycle 91-like 1 (S. cerevisiae)	CDC91L1	8.7	2.4	0.0130
g2317691_3p_at	Hs.90280	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase	ATIC	9.6	2.4	0.0385
g10445222_3p_x_at	Hs.454495	ribosomal protein L36a	RPL36A	11.6	2.4	0.0350
g5453631_3p_at	Hs.16244	sperm associated antigen 5	SPAG5	7.6	2.4	0.0166
Hs.28540.0.S1_3p_at	Hs.28540	Transcribed locus. weakly similar to XP_375099.1 hypothetical protein LOC283585 [Homo sapiens]	---	7.2	2.4	0.0463
g7661965_3p_a_at	Hs.433653	Mediator of DNA damage checkpoint 1	MDC1	6.6	2.4	0.0182
Hs.62918.0.S1_3p_x_at	Hs.62918	CDC91 cell division cycle 91-like 1 (S. cerevisiae)	CDC91L1	8.6	2.4	0.0108
Hs.168950.0.S2_3p_at	Hs.168950	Ganglioside-induced differentiation-associated protein 1	GDAP1	5.5	2.3	0.0239
g4504520_3p_a_at	Hs.79037	heat shock 60kDa protein 1 (chaperonin)	HSPD1	11.7	2.3	0.0392
g8923012_3p_at	Hs.311559	Notch homolog 1. translocation-associated (Drosophila)	NOTCH1	7.1	2.3	0.0249
g4507506_3p_a_at	Hs.118631	timeless homolog (Drosophila)	TIMELESS	7.5	2.3	0.0364
g4505460_3p_at	Hs.104925	ectodermal-neural cortex (with BTB-like domain)	ENC1	10.5	2.3	0.0458
Hs.24724.1.A2_3p_at	Hs.379414	malignant fibrous histiocytoma amplified sequence 1	MFHAS1	8.7	2.3	0.0228
g4502780_3p_at	Hs.75573	centromere protein E. 312kDa	CENPE	6.7	2.3	0.0126
208712_3p_at	Hs.371468	cyclin D1 (PRAD1: parathyroid adenomatosis 1)	CCND1	7.8	2.3	0.0413
Hs.292570.0.S1_3p_at	Hs.292570	chromosome 9 open reading frame 112	C9orf112	8.7	2.3	0.0238
g4505154_3p_at	Hs.298289	mesoderm specific transcript homolog (mouse)	MEST	9.2	2.3	0.0327
Hs.112160.0.S1_3p_at	Hs.458571	chromosome 15 open reading frame 20	C15orf20	6.8	2.3	0.0364
Hs.7517.0.S1_3p_at	Hs.7517	Chromosome 9 open reading frame 123	C9orf123	9.6	2.3	0.0405
g12654424_3p_s_at	Hs.534522	epsin 3	EPN3	6.2	2.3	0.0092
g7705424_3p_at	Hs.44298	mitochondrial ribosomal protein S17	MRPS17	6.8	2.3	0.0310

200089_s_at	Hs.186350	ribosomal protein L4 /// ribosomal protein L4	RPL4	11.4	2.3	0.0430
Hs.31442.0.S1_3p_at	---	---	---	8.2	2.3	0.0364
g13375698_3p_at	Hs.418233	mitochondrial ribosomal protein L24	MRPL24	8.7	2.3	0.0294
g6031190_3p_a_at	Hs.75323	prohibitin	PHB	8.0	2.3	0.0395
g13129079_3p_a_at	Hs.530463	hypothetical protein MGC3196	MGC3196	9.4	2.3	0.0415
g12056472_3p_at	Hs.274424	N-acetylneuraminic acid synthase (sialic acid synthase)	NANS	9.1	2.3	0.0189
g10280619_3p_a_at	Hs.243960	NDRG family member 2	NDRG2	9.9	2.3	0.0239
Hs.116206.0.S1_3p_at	Hs.191583	Opa-interacting protein 5	OIP5	6.9	2.3	0.0170
g6382077_3p_a_at	Hs.24763	RAN binding protein 1	RANBP1	7.1	2.3	0.0206
g13775227_3p_s_at	Hs.91103	hypothetical protein MGC4293	MGC4293	7.6	2.2	0.0382
g12652540_3p_s_at	Hs.386392	nucleolar protein family A. member 2 (H/ACA small nucleolar RNPs)	NOLA2	9.0	2.2	0.0230
g8923292_3p_a_at	Hs.18616	more than blood homolog	MTB	5.8	2.2	0.0478
g4759155_3p_at	Hs.173255	small nuclear ribonucleoprotein polypeptide A	SNRPA	9.1	2.2	0.0182
Hs.69559.0.S1_3p_a_at	Hs.446197	HBxAg transactivated protein 2	XTP2	11.1	2.2	0.0261
Hs.44860.0.S1_3p_at	Hs.293533	glutathione S-transferase omega 2	GSTO2	8.3	2.2	0.0163
Hs.16727.0.A1_3p_at	---	---	---	7.2	2.2	0.0025
216449_3p_x_at	Hs.192374	tumor rejection antigen (gp96) 1	TRA1	7.9	2.2	0.0430
Hs.250655.0.S1_3p_x_at	Hs.264317	prothymosin. alpha (gene sequence 28)	PTMA	13.2	2.2	0.0156
215946_3p_x_at	Hs.407693	similar to bK246H3.1 (immunoglobulin lambda-like polypeptide 1. pre-B-cell specific) /// immunoglobulin lambda-like polypeptide 1	LOC91316 /// IGLL1	8.4	2.2	0.0277
g2367403_3p_at	Hs.30035	splicing factor. arginine/serine-rich 10 (transformer 2 homolog. Drosophila)	SFRS10	6.7	2.2	0.0350
214723_3p_x_at	Hs.469358	KIAA1641	KIAA1641	6.1	2.2	0.0239
g7657235_3p_at	Hs.367992	inositol(myo)-1(or 4)-monophosphatase 2	IMPA2	8.1	2.2	0.0365
Hs.324470.1.S1_3p_a_at	Hs.324470	adducin 3 (gamma)	ADD3	8.3	2.2	0.0184
g13623708_3p_s_at	Hs.119598	ribosomal protein L3	RPL3	12.3	2.2	0.0458
g10864016_3p_a_at	Hs.18442	E-1 enzyme	MASA	8.3	2.2	0.0442
g7705422_3p_at	Hs.279913	processing of precursor 5. ribonuclease P/MRP subunit (S. cerevisiae)	POP5	9.0	2.2	0.0238

g13436139_3p_s_at	Hs.433427	ribosomal protein S17	RPS17	12.2	2.2	0.0372
g4506692_3p_s_at	Hs.433427	ribosomal protein S17	RPS17	12.2	2.1	0.0380
g4504168_3p_at	Hs.82327	glutathione synthetase	GSS	9.9	2.1	0.0225
g5454101_3p_at	Hs.104019	transforming. acidic coiled-coil containing protein 3	TACC3	7.4	2.1	0.0436
Hs.76989.0.S1_3p_a_at	Hs.201253	KIAA0097 gene product	ch-TOG	9.0	2.1	0.0309
g3282822_3p_at	Hs.107474	NGFI-A binding protein 1 (EGR1 binding protein 1)	NAB1	8.6	2.1	0.0182
Hs.306794.0.S1_3p_at	Hs.269777	Protein phosphatase 1. regulatory (inhibitor) subunit 12B	PPP1R12B	6.7	2.1	0.0450
Hs.180842.1.A1_3p_x_at	Hs.410817	ribosomal protein L13	RPL13	11.8	2.1	0.0374
Hs.5174.2.S1_3p_s_at	Hs.433427	ribosomal protein S17	RPS17	12.3	2.1	0.0411
Hs2.146973.1.S1_3p_s_at	Hs.94308	RAB35. member RAS oncogene family	RAB35	6.2	2.1	0.0437
g5174448_3p_at	Hs.75307	H1 histone family. member X	H1FX	9.1	2.1	0.0190
Hs.12520.0.S2_3p_at	Hs.12520	hypothetical protein LOC257407	LOC257407	8.2	2.1	0.0232
g4506672_3p_at	Hs.109059	mitochondrial ribosomal protein L12	MRPL12	8.5	2.1	0.0497
Hs.108124.5.A1_3p_a_at	Hs.446628	ribosomal protein S4. X-linked	RPS4X	12.5	2.1	0.0101
g7305204_3p_at	Hs.279766	kinesin family member 4A	KIF4A	7.5	2.1	0.0151
g388890_3p_x_at	Hs.89643	transketolase (Wernicke-Korsakoff syndrome)	TKT	9.5	2.1	0.0460
g2959555_3p_a_at	Hs.72550	hyaluronan-mediated motility receptor (RHAMM)	HMMR	7.4	2.1	0.0387
200061_s_at	Hs.356794	ribosomal protein S24 /// ribosomal protein S24	RPS24	12.1	2.1	0.0332
Hs.105187.1.S1_3p_a_at	Hs.373627	kinesin family member 9	KIF9	6.9	2.1	0.0411
Hs.298262.1.S1_3p_x_at	Hs.381184	ribosomal protein S19	RPS19	11.9	2.1	0.0458
Hs.173310.2.A1_3p_s_at	Hs.315167	defective in sister chromatid cohesion homolog 1 (S. cerevisiae)	DCC1	5.2	2.1	0.0129
Hs.323439.0.A1_3p_at	Hs.6168	KIAA0703 gene product	KIAA0703	8.3	2.1	0.0106
g12805036_3p_s_at	Hs.355750	hypothetical protein MGC5306	MGC5306	9.0	2.1	0.0293
g13112024_3p_a_at	Hs.433180	DNA replication complex GINS protein PSF2	Pfs2	8.1	2.1	0.0312
g4506724_3p_a_at	Hs.446628	ribosomal protein S4. X-linked	RPS4X	12.5	2.1	0.0100
g6325471_3p_s_at	Hs.448396	ribosomal protein L10a	RPL10A	12.6	2.1	0.0232
g6005859_3p_x_at	Hs.182825	ribosomal protein L35	RPL35	12.0	2.0	0.0238
Hs2.429227.1.S1_3p_s_at	Hs.433180	DNA replication complex GINS protein PSF2	Pfs2	4.9	2.0	0.0380
g13399321_3p_at	Hs.438995	N-acetyltransferase-like protein	FLJ10774	9.0	2.0	0.0239

Hs.100555.1.S1_3p_a_at	Hs.363492	DEAD (Asp-Glu-Ala-Asp) box polypeptide 18	DDX18	8.6	2.0	0.0416
Hs.296559.0.S1_3p_at	---	---	---	8.5	2.0	0.0257
Hs.129055.2.S1_3p_at	Hs.129055	outer dense fiber of sperm tails 2	ODF2	7.4	2.0	0.0266
g12653774_3p_s_at	Hs.443796	ribosomal protein. large. P0	RPLP0	12.5	2.0	0.0408
g13027613_3p_at	---	hypothetical protein MGC3032	MGC3032	6.9	2.0	0.0182
g13443017_3p_at	Hs.15277	chromosome 16 open reading frame 33	C16orf33	8.0	2.0	0.0179
g5901939_3p_a_at	Hs.251673	DNA (cytosine-5-)-methyltransferase 3 beta	DNMT3B	5.3	2.0	0.0416
200034_s_at	Hs.416566	ribosomal protein L6 /// ribosomal protein L6	RPL6	10.9	2.0	0.0435
g4503784_3p_at	Hs.360041	frataxin	FXN	7.4	2.0	0.0138
g4507472_3p_a_at	Hs.161999	TGFB-induced factor (TALE family homeobox)	TGIF	8.6	2.0	0.0491
g3126638_3p_a_at	Hs.334562	cell division cycle 2. G1 to S and G2 to M	CDC2	6.1	2.0	0.0305
g4589609_3p_x_at	Hs.75361	chromosome 22 open reading frame 19	C22orf19	7.2	2.0	0.0170
Hs.162246.0.A1_3p_at	Hs.162246	hypothetical protein LOC134285	LOC134285	8.9	2.0	0.0293
g1906010_3p_a_at	Hs.355533	adenosine kinase	ADK	7.8	2.0	0.0441
Hs.18760.0.S1_3p_at	Hs.498063	signal-induced proliferation-associated 1 like 2	SIPA1L2	7.4	2.0	0.0436
g4885104_3p_x_at	Hs.75238	chromatin assembly factor 1. subunit B (p60)	CHAF1B	6.3	2.0	0.0453
g4506742_3p_s_at	Hs.512675	ribosomal protein S8	RPS8	13.2	2.0	0.0197
208837_3p_at	Hs.424551	chromosome 15 open reading frame 22	C15orf22	7.5	2.0	0.0224
Hs.91728.1.A1_3p_at	Hs.85137	cyclin A2	CCNA2	7.0	2.0	0.0264
Hs.80961.1.A2_3p_at	Hs.334828	hypothetical protein FLJ10719	FLJ10719	4.7	2.0	0.0350
g4826859_3p_at	Hs.182255	NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae)	NHP2L1	9.2	2.0	0.0453
g12804504_3p_a_at	Hs.375921	ribosomal protein L31	RPL31	8.1	1.9	0.0364
g4502144_3p_a_at	Hs.1578	baculoviral IAP repeat-containing 5 (survivin)	BIRC5	7.4	1.9	0.0035
g12653502_3p_s_at	Hs.356794	ribosomal protein S24	RPS24	12.7	1.9	0.0170
Hs.113503.0.S4_3p_at	Hs.113503	RAN binding protein 5	RANBP5	8.1	1.9	0.0222
g12006349_3p_a_at	Hs.381219	ribosomal protein L15	RPL15	11.7	1.9	0.0441
g5174722_3p_s_at	Hs.310542	translocase of outer mitochondrial membrane 40 homolog (yeast)	TOMM40	7.9	1.9	0.0138

g7019470_3p_at	Hs.283375	NTF2-like export factor 1	NXT1	6.8	1.9	0.0490
g4508030_3p_at	Hs.127476	zinc finger protein 74 (Cos52)	ZNF74	6.4	1.9	0.0101
Hs2.355309.3.S1_3p_a_at	Hs.412323	KIAA1937 protein	KIAA1937	9.4	1.9	0.0467
200772_3p_x_at	Hs.264317	prothymosin. alpha (gene sequence 28)	PTMA	8.7	1.9	0.0402
g12653688_3p_a_at	Hs.32393	aspartyl-tRNA synthetase	DARS	9.4	1.9	0.0458
g13699831_3p_a_at	Hs.270845	kinesin family member 23	KIF23	3.8	1.9	0.0286
1563796_3p_s_at	Hs.444353	KIAA1970 protein	KIAA1970	6.0	1.9	0.0365
Hs.48480.0.A1_3p_at	Hs.48480	zinc finger protein 367	ZNF367	5.7	1.9	0.0430
Hs.301927.1.A1_3p_a_at	Hs.301927	c6.1A	C6.1A	9.4	1.9	0.0449
208549_3p_x_at	Hs.264317	prothymosin. alpha (gene sequence 28)	PTMA	9.2	1.9	0.0453
Hs.44566.1.A1_3p_x_at	Hs.469358	KIAA1641	KIAA1641	4.4	1.9	0.0460
Hs.226562.0.S1_3p_at	Hs.200228	ets homologous factor	EHF	6.5	1.8	0.0385
Hs.314347.0.S1_3p_at	Hs.272210	activating transcription factor 7 interacting protein	ATF7IP	8.1	1.8	0.0393
g10835100_3p_at	Hs.101067	GCN5 general control of amino-acid synthesis 5-like 2 (yeast)	GCN5L2	9.0	1.8	0.0411
4873394C_3p_s_at	Hs.54702	xylosylprotein beta 1.4-galactosyltransferase. polypeptide 7 (galactosyltransferase I)	B4GALT7	8.7	1.8	0.0449
229220_3p_x_at	Hs.15825	Homo sapiens. clone IMAGE:4151011. mRNA	---	6.6	1.8	0.0125
Hs.17154.0.S1_3p_at	Hs.439530	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 4	DYRK4	7.7	1.8	0.0332
g1255616_3p_a_at	Hs.438720	MCM7 minichromosome maintenance deficient 7 (S. cerevisiae)	MCM7	9.3	1.8	0.0398
g6005859_3p_at	Hs.182825	ribosomal protein L35	RPL35	11.7	1.8	0.0263
Hs.125608.0.A1_3p_at	Hs.125608	chromosome 9 open reading frame 152	C9orf152	6.6	1.8	0.0440
g11038647_3p_at	Hs.28853	CDC7 cell division cycle 7 (S. cerevisiae)	CDC7	5.0	1.8	0.0347
g12053028_3p_at	Hs.183428	sarcospan (Kras oncogene-associated gene)	SSPN	5.8	1.8	0.0206
Hs.31476.0.S1_3p_at	Hs.370420	tubulin. gamma complex associated protein 5	TUBGCP5	6.6	1.8	0.0110
g4506656_3p_a_at	Hs.416566	ribosomal protein L6	RPL6	12.8	1.8	0.0106
g5174446_3p_at	Hs.351839	ovarian zinc finger protein /// guanine nucleotide binding protein (G protein). beta polypeptide 2-like 1	HOZFP /// GNB2L1	12.3	1.8	0.0450

g13376508_3p_at	Hs.194754	hypothetical protein MGC29875	MGC29875	7.5	1.8	0.0403
220176_3p_at	Hs.288981	chromosome 14 open reading frame 127	C14orf127	5.9	1.8	0.0280
Hs.247877.0.S1_3p_at	Hs.421257	ribosomal protein L7	RPL7	7.5	1.8	0.0391
g12653526_3p_a_at	Hs.14468	peter pan homolog (Drosophila)	PPAN	7.9	1.8	0.0389
Hs.296559.0.S1_3p_x_at	---	---	---	8.7	1.8	0.0392
Hs.248080.0.S1_3p_at	---	---	---	8.9	1.8	0.0476
219000_3p_s_at	Hs.315167	defective in sister chromatid cohesion homolog 1 (S. cerevisiae)	DCC1	7.2	1.7	0.0293
g13111838_3p_s_at	Hs.256583	interleukin enhancer binding factor 3. 90kDa	ILF3	8.1	1.7	0.0446
g4506636_3p_s_at	Hs.250895	ribosomal protein L34	RPL34	13.0	1.7	0.0249
g7705838_3p_at	Hs.279209	NY-REN-58 antigen	NY-REN-58	6.5	1.7	0.0244
g11386190_3p_a_at	Hs.274151	ligatin	LGTN	9.0	1.7	0.0087
Hs.323053.0.S1_3p_at	Hs.323053	Hypothetical protein DKFZp547K1113	DKFZp547K1113	6.8	1.7	0.0125
g12654388_3p_a_at	Hs.300141	ribosomal protein L39	RPL39	13.1	1.7	0.0364
g5174636_3p_at	Hs.22516	peptidylprolyl isomerase E (cyclophilin E)	PPIE	8.1	1.7	0.0086
g13654275_3p_s_at	Hs.323084	queuine tRNA-ribosyltransferase 1 (tRNA-guanine transglycosylase)	QTRT1	8.7	1.7	0.0450
Hs2.427928.1.S1_3p_at	Hs.516253	Hypothetical gene supported by BC040598	---	6.4	1.7	0.0341
g8922398_3p_at	Hs.102842	polymerase (RNA) III (DNA directed) polypeptide B	POLR3B	7.9	1.7	0.0182
g4508030_3p_x_at	Hs.127476	zinc finger protein 74 (Cos52)	ZNF74	8.3	1.7	0.0474
g4506654_3p_x_at	Hs.469653	ribosomal protein L5	RPL5	13.1	1.7	0.0398
g9845503_3p_at	Hs.99171	neurotrophin 3	NTF3	6.5	1.7	0.0365
Hs.192789.0.S1_3p_a_at	Hs.334788	nuclear factor of activated T-cells. cytoplasmic. calcineurin-dependent 2 interacting protein	FLJ14639	8.5	1.7	0.0343
g4507274_3p_s_at	Hs.250822	serine/threonine kinase 6	STK6	7.3	1.7	0.0408
g11968036_3p_a_at	Hs.242327	hypothetical protein FLJ13576	FLJ13576	10.8	1.7	0.0383
Hs.133481.0.A1_3p_at	Hs.99472	MRNA; cDNA DKFZp564O0862 (from clone DKFZp564O0862)	---	5.8	1.6	0.0442
Hs.288809.0.S2_3p_a_at	Hs.288809	basic. immunoglobulin-like variable motif containing	BIVM	3.8	1.6	0.0372
Hs.211506.0.S1_3p_at	Hs.521097	pituitary tumor-transforming 3 /// pituitary tumor-transforming 2	PTTG3 /// PTTG2	4.1	1.6	0.0261
g13623450_3p_s_at	Hs.122552	G-2 and S-phase expressed 1	GTSE1	7.2	1.6	0.0332

g7019544_3p_a_at	Hs.109494	secreted protein of unknown function	SPUF	7.9	1.6	0.0218
Hs.142634.0.S1_3p_a_at	Hs.438994	zinc finger protein 544	ZNF544	7.4	1.6	0.0095
Hs.170226.0.S1_3p_at	Hs.170226	chromosome 9 open reading frame 91	C9orf91	5.2	1.6	0.0205
g12653526_3p_x_at	Hs.14468	peter pan homolog (Drosophila)	PPAN	7.7	1.6	0.0203
g5453933_3p_at	Hs.2407	POU domain. class 2. associating factor 1	POU2AF1	5.4	1.6	0.0332
g4503670_3p_at	Hs.61255	fructose-1.6-bisphosphatase 2	FBP2	5.8	1.6	0.0381
g12584207_3p_s_at	Hs.307047	resistin like beta	RETNLB	6.8	1.6	0.0385
Hs.22222.0.S2_3p_at	Hs.410924	hypothetical protein MGC10854	MGC10854	8.4	1.6	0.0087
g5174630_3p_at	Hs.433813	tumor protein p53 inducible protein 11	TP53I11	6.2	1.6	0.0178
Hs.55921.0.S1_3p_a_at	Hs.171292	glutamyl-prolyl-tRNA synthetase	EPRS	5.7	1.6	0.0305
Hs.56966.1.S1_3p_a_at	Hs.292119	nucleoporin 210	NUP210	6.3	1.6	0.0426
g6631094_3p_at	Hs.179565	MCM3 minichromosome maintenance deficient 3 (S. cerevisiae)	MCM3	9.1	1.6	0.0343
g12655140_3p_a_at	Hs.405925	differential display and activated by p53	DDA3	7.5	1.6	0.0476
g7019408_3p_at	Hs.521171	hypoxia-inducible protein 2	HIG2	8.0	1.5	0.0364
g4503308_3p_at	Hs.155597	D component of complement (adipsin)	DF	7.8	1.5	0.0374
Hs.238956.1.A1_3p_x_at	Hs.68714	Splicing factor. arginine/serine-rich 1 (splicing factor 2. alternate splicing factor)	SFRS1	8.2	1.5	0.0053
g7657117_3p_s_at	Hs.54609	glycine C-acetyltransferase (2-amino-3-ketobutyrate coenzyme A ligase)	GCAT	6.5	1.5	0.0206
Hs.24790.0.S1_3p_a_at	Hs.24790	KIAA1573 protein	KIAA1573	5.1	1.5	0.0239
Hs.238956.1.A1_3p_at	Hs.68714	Splicing factor. arginine/serine-rich 1 (splicing factor 2. alternate splicing factor)	SFRS1	8.3	1.5	0.0411
g13097236_3p_a_at	Hs.505572	hypothetical protein from clone 643	LOC57228	8.1	1.5	0.0397
Hs.211506.0.S1_3p_x_at	Hs.511755	pituitary tumor-transforming 2	PTTG2	4.2	1.5	0.0442
g13376283_3p_at	Hs.336866	hypothetical protein FLJ12735	FLJ12735	5.3	1.5	0.0418
g11056055_3p_a_at	Hs.411125	mitochondrial ribosomal protein S12	MRPS12	9.1	1.5	0.0491
g8922608_3p_a_at	Hs.467479	ATPase family. AAA domain containing 3A	ATAD3A	8.1	1.5	0.0212
Hs.105509.1.S2_3p_at	Hs.105509	CTL2 gene	CTL2	7.1	1.5	0.0385
g12597646_3p_x_at	Hs.139709	hypothetical protein FLJ12572	FLJ12572	7.3	1.5	0.0483

Hs.271894.0.A1_3p_at	Hs.446414	CD47 antigen (Rh-related antigen. integrin-associated signal transducer)	CD47	4.6	1.5	0.0430
Hs.6385.0.S1_3p_at	Hs.6385	KIAA1277	KIAA1277	8.1	1.5	0.0440
g179364_3p_at	Hs.371468	cyclin D1 (PRAD1: parathyroid adenomatosis 1)	CCND1	9.0	1.5	0.0429
Hs.123122.1.S1_3p_at	Hs.318398	FSH primary response (LRPR1 homolog. rat) 1	FSHPRH1	4.6	1.4	0.0431
Hs2.376823.1.A1_3p_at	Hs.458418	KIAA1731 protein	KIAA1731	5.7	1.4	0.0380
Hs.114012.0.S1_3p_at	Hs.437205	ataxin 7-like 1	ATXN7L1	7.8	1.4	0.0407
Hs.178617.0.S2_3p_a_at	Hs.327631	retinol dehydrogenase 13 (all-trans and 9-cis)	RDH13	8.4	1.4	0.0376
g4506636_3p_x_at	Hs.250895	ribosomal protein L34	RPL34	13.8	1.4	0.0478
g3462508_3p_a_at	---	---	---	6.3	1.4	0.0476
Hs2.367802.1.A1_3p_at	Hs.406722	chromosome 6 open reading frame 157	C6orf157	3.9	1.4	0.0449
g4757895_3p_at	Hs.377010	carbamoyl-phosphate synthetase 2. aspartate transcarbamylase. and dihydroorotase	CAD	7.1	1.4	0.0402
Hs.62669.0.A1_3p_x_at	Hs.355515	hypothetical protein FLJ25059	FLJ25059	5.0	1.4	0.0385
g5911930_3p_a_at	Hs.278027	LIM domain kinase 2	LIMK2	7.7	1.3	0.0474
g7706546_3p_a_at	Hs.440953	chromosome 9 open reading frame 127	C9orf127	8.0	1.3	0.0319
Hs.30864.0.A1_3p_at	---	---	---	7.3	1.3	0.0408
g8922715_3p_a_at	Hs.17860	oxoglutarate dehydrogenase-like	OGDHL	7.2	1.3	0.0347
Hs.279789.5.A1_3p_x_at	Hs.410396	isovaleryl Coenzyme A dehydrogenase	IVD	8.4	1.3	0.0395
Hs.34779.0.A1_3p_at	---	---	---	5.5	1.3	0.0294