Probe Set	Gene name	Genbank	LocusLink	cytogenet band	avg Ctrl	avg PSA	diff	t-test	mean fold change
218659_at	KIAA1685 protein (additional sex combs like 2 (Drosophila))	NM_018263	55252	2p24	**9417.71**	16804.31	7386.59	2.08E-08	1.78
209964_s_at	spinocerebellar ataxia 7 (olivopontocerebellar atrophy with retinal degeneration)	AF032105	6314	3p21	**2681.55**	4719.953	2038.40	2.71E-07	1.76
201991_s_at	kinesin family member 5B	BF223224	3799	10pter	**4152.82**	6936.916	2784.10	2.51E-06	1.67
216022_at	WNK lysine deficient protein kinase 1 (WNK1)	AL049278	65125	12p13	**233.25**	703.1368	469.88	1.28E-05	3.01
215452_x_at	SMT3 suppressor of mif two 3 homolog 4 (yeast) (SUMO4)	AL031133	387082	6q25	**2932.81**	4638.637	1705.83	1.53E-05	1.58
205863_at	S100 calcium binding protein A12 (calgranulin C)	NM_005621	6283	1q21	**7604.28**	23690.1	16085.82	1.87E-05	3.12
206765_at	potassium inwardly-rectifying channel, subfamily J, member 2	AF153820	3759	17q23	**7088.88**	11591.51	4502.63	3.11E-05	1.64
217868_s_at	DORA reverse strand protein 1 (DREV1) CGI-81 protein	NM_016025	51108	16p13	**6514.16**	10604.53	4090.36	3.18E-05	1.63
209555_s_at	CD36 antigen (collagen type I receptor, thrombospondin receptor)	M98399	948	7q11	**2498.94**	4625.216	2126.28	3.96E-05	1.85
205191_at	retinitis pigmentosa 2 (X-linked recessive)	NM_006915	6102	Xp11	**496.72**	870.4368	373.72	4.35E-05	1.75
213524_s_at	putative lymphocyte G0/G1 switch gene	NM_015714	50486	1q32	**670.46**	1174.832	504.37	7.27E-05	1.75
204071_s_at	tumor protein p53-binding protein	NM_005802	10210	12p12	**548.71**	976.0895	427.38	9.02E-05	1.78
220122_at	hypothetical protein FLJ22344	NM_024717	79772	5q15	**561.71**	1051.811	490.10	0.000113	1.87
216210_x_at	putative nuclear protein	AA046650	11078	22q13	**5184.37**	7903.2	2718.83	0.000207	1.52
204859_s_at	apoptotic protease activating factor	NM_013229	317	12q23	**1205.06**	1824.542	619.48	0.000257	1.51
214182_at	ADP-ribosylation factor 6	AA243143	382	7q22	**2177.39**	4852.868	2675.48	0.00026	2.23
222320_at	Hyperparathyroidism 2 (with jaw tumor)	AW970584	79577	1q25	**159.71**	309.9053	150.19	0.000273	1.94
202917_s_at	S100 calcium binding protein A8 (calgranulin A)	NM_002964	6279	1q21	**66247.22**	126618	60370.74	0.000308	1.91
217769_s_at	hypothetical protein	NM_015932	51371	13q12	**5595.99**	9220.453	3624.46	0.000313	1.65
213902_at	N-acylsphingosine amidohydrolase (acid ceramidase)	AI379338	427	8p22	**2607.45**	4043.926	1436.47	0.00032	1.55
204059_s_at	malic enzyme 1, NADP(+)-dependent, cytosolic	NM_002395	4199	6q12	**332.89**	534.2158	201.32	0.000371	1.60
202626_s_at	LYN	NM_002350	4067	8q13	**16212.88**	25824.29	9611.41	0.000375	1.59
205070_at	inhibitor of growth family, member 3	NM_019071	54556	7q31	**1921.62**	3077.316	1155.69	0.000414	1.60
221829_s_at	karyopherin (importin) beta 2	AI307759	3842	17p11	**7214.05**	11470.59	4256.54	0.000435	1.59
214807_at	MRNA; cDNA DKFZp564O0862 (from clone DKFZp564O0862)	AI278204	278204	X	**872.23**	1352.763	480.53	0.000442	1.55
205551_at	synaptic vesicle protein 2B homolog	NM_014848	9899	15q26	**126.92**	243.2579	116.34	0.000447	1.92
206420_at	immunoglobulin superfamily, member 6 (DORA, down-regulation by activation)	NM_005849	10261	16p12	**3568.95**	5944.853	2375.90	0.000451	1.67
202437_s_at	cytochrome P450, subfamily I (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile)	NM_000104	1545	2p21	**755.45**	1720.389	964.94	0.000468	2.28
213805_at	abhydrolase domain containing 5 (ABHD5)	AI692428	51099	3p21	**1188.64**	2518.495	1329.86	0.000498	2.12
202600_s_at		AI824012	8204	21q11	**614.34**	1081.463	467.13	0.000533	1.76
214800_x_at	basic transcription factor 3 (BTF3)	R83000	689	5q13	**5064.20**	9554.953	4490.75	0.000534	1.89
202381_at	a disintegrin and metalloproteinase domain 9 (meltrin gamma)	NM_003816	8754	8p11	**413.39**	758.7263	345.33	0.000553	1.84
215779_s_at	H2B histone family, member A	BE271470	8339	6p21	**412.68**	810.9684	398.29	0.000568	1.97
215039_at	Hypothetical protein LOC339524	AK002179	339524	1p22	**183.07**	396.2	213.13	0.000576	2.16
208864_s_at	Thioredoxin (TXN)	AF313911	7295	9q31	**964.60**	2541.179	1576.58	0.000577	2.63
201738_at	translation factor sui1 homolog	NM_005875	10289	3p21	**5670.44**	10115.67	4445.23	0.000606	1.78
207234_at	regulatory factor X, 3 (influences HLA class II expression)	NM_002919	5991	9p22	**365.32**	601.6526	236.34	0.000609	1.65
211201_at	follicle stimulating hormone receptor	M95489	2492	2p21	**85.86**	179.1789	93.32	0.000612	2.09
206343_s_at	neuregulin 1	NM_013959	3084	8p21	**307.83**	751.8632	444.03	0.000616	2.44
213624_at	acid sphingomyelinase-like phosphodiesterase	AA873600	10924	6q22	**539.25**	957.3895	418.14	0.000652	1.78
220330_s_at	SAM domain, SH3 domain and nuclear localisation signals, 1	NM_022136	64092	21q11	**780.83**	1624.895	844.06	0.000667	2.08
206145_at	Rhesus blood group-associated glycoprotein	NM_000324	6005	6p21	**220.28**	399.0526	178.77	0.000698	1.81
208523_x_at	H2B histone family, member K	NM_003525	8346	6p21	**633.21**	1052.063	418.85	0.000698	1.66
202430_s_at	phospholipid scramblase 1	NM_021105	5359	3q23	**1191.89**	1989.284	797.39	0.000709	1.67
203672_x_at	thiopurine S-methyltransferase	U12387	7172	6p22	**1120.08**	1923.311	803.23	0.000783	1.72
215438_x_at	G1 to S phase transition 1	BE906054	2935	16p13	**7369.60**	16038.47	8668.87	0.000791	2.18
215786_at	Hepatitis B virus x associated protein (HBXAP)	AK022170	51773	11q13	**969.56**	1659.184	689.63	0.000806	1.71
203735_x_at	PTPRF interacting protein, binding protein 1 (liprin beta 1)	N35896	8496	12p11	**512.91**	1110.5	597.59	0.000816	2.17
207500_at	caspase 5, apoptosis-related cysteine protease	NM_004347	838	11q22	**470.27**	768.1947	297.92	0.000822	1.63
222303_at	Homo sapiens ETS2 intronic transcript 1 mRNA, complete sequence.	AV700891	AY216265	21q22	**1742.03**	3015.974	1273.94	0.000861	1.73

221205_at	hypothetical protein FLJ10254	NM_018041	55694	0	**610.95**	982.1842	371.24	0.000869	1.61
220411_x_at	hypothetical protein FLJ23447	NM_024825	79883	19p13	**675.44**	1080.495	405.06	0.000874	1.60
220327_at	colon carcinoma related protein	NM_016206	51159	3p11	**67.99**	206.4895	138.49	0.000937	3.04
219754_at	hypothetical protein FLJ11016	NM_018301	55285	Xq22	**421.26**	859.1368	437.87	0.000957	2.04
201963_at	fatty-acid-Coenzyme A ligase, long-chain 2	NM_021122	2180	4q34	**12906.13**	22462.58	9556.45	0.000976	1.74
218303_x_at	hypothetical protein LOC51315	NM_016618	51315	2p11	**1308.72**	2055.305	746.58	0.000984	1.57

Probe Set	Gene name	Genbank	LocusLink	cytogenet band	mean Ctrl	mean PSA	difference	t-test	mean fold change	NP1	NP2	NP3
212890_at	integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29)	BF663461	3688	10p11	**3750.65**	2225.43	-1525.22	7.40889E-06	1.69	3183.4	2079.8	3539.1
209916_at	hypothetical protein DKFZp762M115	BC002477	55526	10p14	**1010.71**	412.72	-597.99	7.27289E-06	2.45	103.6	1310.7	1347.3
57715_at	hypothetical protein	W72694	51063	10pter	**3279.82**	2164.68	-1115.14	4.99349E-06	1.52	3692.9	2804.1	3321.5
212359_s_at	KIAA0913 protein	W89120	23053	10q22	**2515.19**	1575.46	-939.73	0.000274577	1.60	1577.6	1501.3	2709.5
214617_at	perforin 1 (pore forming protein)	AI445650	5551	10q22	**21817.15**	12032.79	-9784.36	1.11306E-05	1.81	20608.6	17911	21347.2
210461_s_at	actin binding LIM protein 1	BC002448	3983	10q25	**1688.97**	881.56	-807.42	0.00010207	1.92	712.6	2323.1	1911.8
201135_at	enoyl Coenzyme A hydratase, short chain, 1, mitochondrial	NM_00409	1892	10q26	**4117.77**	2741.93	-1375.85	0.000151637	1.50	4774.2	3776	6739.2
209489_at	CUG triplet repeat, RNA binding protein 1	N25915	10658	11p11	**7749.12**	4734.17	-3014.95	2.52584E-05	1.64	6278.1	6803.1	8196.8
217759_at	DIPB protein	BF431488	54765	11p13	**3995.38**	2623.15	-1372.24	0.000958805	1.52	2319.7	2647.9	3459.5
200675_at	CD81 antigen (target of antiproliferative antibody 1)	NM_00435	975	11p15	**6766.15**	3812.25	-2953.90	2.91655E-05	1.77	7942.1	3724.1	7177.7
218921_at	single Ig IL-1R-related molecule, SIGIRR, TOLL/IL1R 8 (TIR8)	NM_02180	59307	11p15	**2318.33**	1312.86	-1005.46	5.62297E-05	1.77	1749.5	1822.2	1800.3
219359_at	hypothetical protein FLJ22635	NM_02509	80162	11p15	**2397.29**	1358.50	-1038.79	0.000284479	1.76	1346.7	2165.8	2697.2
202109_at	partner of RAC1 (arfaptin 2)	NM_01240	23647	11p15	**2192.48**	1460.65	-731.83	0.000161908	1.50	2072.2	1027	1983.3
203942_s_at	ELKL motif kinase	NM_01749	2011	11q12	**1072.21**	231.43	-840.78	4.46731E-06	4.63	572.7	132.2	950.9
212969_x_at	metastasis-associated 1-like 1	BE222618	9219	11q12	**4035.78**	2514.90	-1520.88	8.8396E-06	1.60	2815.1	2361.9	4245.7
208922_s_at	nuclear RNA export factor 1	BC004904	10482	11q12	**6152.21**	3955.62	-2196.59	9.51777E-06	1.56	6469.8	3922.6	7234.5
43511_s_at	MRNA; cDNA DKFZp762M127 (from clone DKFZp762M127)	AI201594	Hs.550621	11q13	**5443.93**	3608.85	-1835.08	0.000281279	1.51	4423.4	4749.4	5224.8
204178_s_at	RNA binding motif protein 14	NM_00632	10432	11q13	**1379.41**	690.30	-689.11	8.6055E-05	2.00	710.3	1783.7	2486.5
214450_at	cathepsin W (lymphopain)	NM_00133	1521	11q13	**6304.16**	3874.74	-2429.42	0.000463977	1.63	8268.9	2853.7	6959.8
204164_at	signal-induced proliferation-associated gene 1 (SIPA1)	NM_00674	6494	11q13	**3595.89**	2185.49	-1410.40	0.000819438	1.65	3902.9	1065.9	4347.7
208313_s_at	splicing factor 1	NM_00463	7536	11q13	**7412.59**	4149.27	-3263.32	1.45357E-06	1.79	4318.5	4351.7	7372.7
208206_s_at	RAS guanyl releasing protein 2 (calcium and DAG-regulated)	NM_00582	10235	11q13	**5054.04**	2811.86	-2242.18	1.60517E-05	1.80	4598.2	5664.5	5379.5
203252_at	tumor suppressor deleted in oral cancer-related 1	NM_00585	10263	11q13	**1559.28**	920.44	-638.84	2.02701E-05	1.69	2128.3	772.3	1784.8
202116_at	requiem, apoptosis response zinc finger gene (REQ)	NM_00626	5977	11q13	**4534.62**	2678.69	-1855.92	0.000312244	1.69	3773	341.3	7327.3
205436_s_at	H2A histone family, member X	NM_00210	3014	11q23	**1659.92**	922.74	-737.18	5.24891E-05	1.80	2225.7	863.4	1881.3
206126_at	Burkitt lymphoma receptor 1, GTP binding protein (CXCR5)	NM_00171	643	11q23	**1472.51**	850.28	-622.22	0.000663654	1.73	2190.6	800	956.7
212078_s_at	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila)	AA704766	4297	11q23	**2127.07**	1193.93	-933.14	9.49095E-07	1.78	1669.8	2253.4	1722.6
218774_at	HSPC015 protein	NM_01402	28960	11q24	**1147.89**	477.58	-670.32	5.65139E-05	2.40	797.5	1457.3	1858.2
201600_at	B-cell associated protein, PHB2	NM_00727	11331	12p13	**14897.88**	9669.92	-5227.96	2.21678E-06	1.54	20508.6	8635.4	15360.3
206150_at	tumor necrosis factor receptor superfamily, member 7 (CD27)	NM_00124	939	12p13	**7068.02**	4239.03	-2828.99	1.4667E-05	1.67	6680.2	5296.3	5893.5
218338_at	early development regulator 1 (homolog of polyhomeotic 1)	NM_00442	1911	12p13	**1854.32**	890.05	-964.27	6.39289E-05	2.08	592.8	257.5	1428.1
206687_s_at	protein tyrosine phosphatase, non-receptor type 6 (SHP1)	NM_00283	5777	12p13	**20430.79**	12753.10	-7677.69	9.82807E-05	1.60	16243.3	9724.5	23074.9
201184_s_at	chromodomain helicase DNA binding protein 4	NM_00127	1108	12p13	**4967.67**	3128.62	-1839.05	0.000295648	1.59	1626.1	2983.7	4751.3
201313_at	enolase 2, (gamma, neuronal)	NM_00197	2026	12p13	**1341.41**	837.41	-504.00	0.000366967	1.60	387.8	1695.1	1133.5
204255_s_at	vitamin D (1,25- dihydroxyvitamin D3) receptor	AA772285	7421	12q12	**1436.70**	858.75	-577.95	1.54002E-05	1.67	1169.5	780	939.9
218841_at	ankyrin repeat and SOCS box-containing 8, ASB8	NM_02409	79076	12q13	**1713.59**	983.01	-730.59	0.000328604	1.74	1004.4	854.3	1620.2
208858_s_at	KIAA0747 protein	BC004998	23344	12q13	**4511.08**	2327.21	-2183.87	1.25645E-05	1.94	3060.5	2482.1	4351
207170_s_at	DKFZP586A011 protein	NM_01541	25875	12q13	**3309.81**	2090.96	-1218.84	1.47686E-05	1.58	3145.7	2190.8	4248.1
201440_at	prp28, U5 snRNP 100 kd protein	NM_00481	9416	12q13	**2432.45**	1130.87	-1301.58	0.00017181	2.15	539.5	348.1	3072.1
202519_at	KIAA0867 protein	NM_01493	22877	12q21	**3416.23**	1699.07	-1717.15	3.50758E-06	2.01	1997.7	1343.9	2314.2
212139_at	GCN1 general control of amino-acid synthesis 1-like 1 (yeast)	D86973	10985	12q24	**2027.58**	1278.73	-748.85	3.16396E-06	1.59	1359.7	2161	1839.8
211941_s_at	prostatic binding protein	BE969671	5037	12q24	**5333.61**	3442.97	-1890.64	7.29422E-05	1.55	6620.2	4828.9	4948.3
219267_at	glycolipid transfer protein	NM_01643	51228	12q24	**1361.58**	840.28	-521.29	0.000537235	1.62	1341.4	802.8	1711
202723_s_at	forkhead box O1A (rhabdomyosarcoma)	AW117498	2308	13q14	**4630.12**	1713.26	-2916.86	3.05558E-08	2.70	2192.5	2671.6	3614.3
213398_s_at	HCDI protein	AI347090	56948	14q11	**3577.32**	2245.89	-1331.43	1.48204E-07	1.59	2370.4	2970.5	3825.4
213594_x_at	FUS interacting protein (serine-arginine rich) 1	AU130523	63902	14q22	**2385.14**	1486.56	-898.58	3.34258E-06	1.60	1741.5	2348.2	1820.3
202761_s_at	synaptic nuclei expressed gene 2	NM_01518	23224	14q23	**3142.78**	2066.57	-1076.21	2.62017E-05	1.52	1704.5	2449.1	3408.7
215210_s_at	dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex)	S72422	1743	14q24	**1966.37**	1245.33	-721.04	3.27901E-06	1.58	1620.9	2641.7	2309.4
222285_at	immunoglobulin heavy constant delta, IGHD	AW134608	3495	14q32	**1321.20**	710.12	-611.08	0.000629334	1.86	1415.7	1165.5	1253.3
212827_at	immunoglobulin heavy constant mu	X17115	3507	14q32	**12491.85**	5911.85	-6580.01	3.27329E-07	2.11	11073.6	7683.7	11229.8

220439_at	hypothetical protein FLJ11700	NM_02489	79952	14q32	**1840.77**	1082.14	-758.63	7.99153E-07	1.70	1702	2664.7	1235.1
217838_s_at	RNB6	NM_01633	51466	14q32	**6942.84**	4307.28	-2635.56	1.52111E-06	1.61	5483.7	6713.7	7884.2
211783_s_at	metastasis associated 1	BC006177	9112	14q32	**1596.25**	968.18	-628.07	8.82161E-06	1.65	707.4	1189.8	1443.9
204756_at	mitogen-activated protein kinase kinase 5 (MEK5 or MAP2K5)	NM_00275	5607	15q22	**636.21**	250.88	-385.33	0.000401234	2.54	1590.3	1253.9	542.6
219066_at	hypothetical protein MDS018	NM_02182	60490	15q23	**1340.00**	716.53	-623.47	3.41498E-05	1.87	1283.6	1606.4	1934.1
74694_s_at	hypothetical protein FLJ23282	AA907940	79874	16p11	**1310.18**	803.11	-507.08	3.56862E-06	1.63	892.1	1944.7	1451
209685_s_at	protein kinase C, beta 1	M13975	5579	16p11	**15980.18**	10215.49	-5764.69	6.72917E-07	1.56	18589.6	10912.7	21108.9
207907_at	tumor necrosis factor (ligand) superfamily, member 14	NM_00380	8740	16p11	**3184.18**	1796.98	-1387.20	5.56093E-06	1.77	2366.9	2578.2	2980.8
218714_at	hypothetical protein MGC3121	NM_02403	78994	16p11	**2987.41**	1623.93	-1363.48	6.50458E-06	1.84	2262.6	1550.9	3599
212275_s_at	Snf2-related CBP activator protein	NM_00666	10847	16p11	**1594.47**	954.98	-639.49	0.000300706	1.67	1545.6	928.4	1698.8
217891_at	hypothetical protein FLJ13868	NM_02274	64755	16p11	**812.99**	383.93	-429.06	0.000780614	2.12	286.8	45	844.7
203709_at	phosphorylase kinase, gamma 2 (testis)	NM_00029	5261	16p12	**1500.31**	913.85	-586.46	0.000346663	1.64	1848.2	1331	1578.6
212576_at	KIAA0544 protein	AB011116	23295	16p13	**4054.53**	2672.60	-1381.93	6.42807E-05	1.52	3292.1	3624.7	4636.7
204524_at	3-phosphoinositide dependent protein kinase-1	NM_00261	5170	16p13	**2606.04**	955.02	-1651.03	8.77156E-09	2.73	1595.8	1363.2	2619.8
218848_at	hypothetical protein MGC2655	NM_02433	79228	16p13	**1423.15**	826.41	-596.74	4.21631E-06	1.72	1322.2	1347.8	995.2
213639_s_at	KIAA0557 protein	AI871396	26048	16p13	**1566.04**	794.95	-771.09	8.9682E-06	1.97	878.5	1862.4	1091.2
219040_at	coronin 7 (CORO7)	NM_02453	79585	16p13	**1815.69**	1098.34	-717.35	0.000599124	1.65	1032.5	2182.9	2227.1
210555_s_at	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3 (NFATC3)	U85430	4775	16q13	**2860.70**	1679.10	-1181.60	0.000490762	1.70	2452.5	1019.5	2475.5
1729_at	TNFRSF1A-associated via death domain (TRADD)	L41690	8717	16q22	**2762.66**	1559.04	-1203.63	0.000349393	1.77	1556.4	2846.4	3217.3
219384_s_at	adenosine deaminase, tRNA-specific 1	NM_01209	23536	16q23	**2141.31**	1230.87	-910.44	1.24572E-08	1.74	1799	1691.7	1625.4
203644_s_at	KIAA0872 protein	AI629033	22879	16q23	**1077.56**	534.28	-543.28	0.000250469	2.02	1163.1	142.6	1585.1
202771_at	KIAA0233 gene product	NM_01474	9780	16q24	**2459.15**	1314.02	-1145.13	0.000162999	1.87	1962.9	1364.7	2426.8
202104_s_at	spastic paraplegia 7, paraplegin (pure and complicated autosomal recessive)	NM_00311	6687	16q24	**1792.44**	1023.52	-768.92	0.000122766	1.75	1326.3	1188.1	1516.6
214494_s_at	paraplegin or cell matrix adhesion regulator (SPG7)	NM_00520	1216	16q24	**2914.23**	1902.26	-1011.97	0.000586139	1.53	2144	2569.1	2530.3
203219_s_at	adenine phosphoribosyltransferase	NM_00048	353	16q24	**3560.99**	2330.05	-1230.94	3.44966E-05	1.53	4680.4	2752.1	3208.2
203938_s_at	TATA box binding protein (TBP)-associated factor, RNA polymerase I, C, 110kD	NM_00567	9013	16q24	**1018.95**	434.01	-584.95	0.000494592	2.35	350	929.3	1447
213036_x_at	ATPase, Ca++ transporting, ubiquitous	Y15724	489	17p13	**5056.52**	1983.10	-3073.42	1.15652E-05	2.55	1945.8	3807.5	6815.5
219184_x_at	translocase of inner mitochondrial membrane 22 homolog (yeast)	NM_01333	29928	17p13	**1509.43**	614.83	-894.60	8.38403E-09	2.46	1078.1	1403.9	1495.3
203871_at	sentrin/SUMO-specific protease 3	NM_01567	26168	17p13	**1059.61**	406.91	-652.71	3.80476E-06	2.60	1862.6	464.8	1048.3
218526_s_at	homolog of yeast MOG1	NM_01418	29098	17p13	**1568.39**	911.92	-656.47	0.000127288	1.72	1570.6	1627.7	1844.6
204925_at	cystinosis, nephropathic	NM_00493	1497	17p13	**1023.45**	634.08	-389.36	0.000201927	1.61	658.7	971.7	1097.8
200000_s_at	PRP8 pre-mRNA processing factor 8 homolog (yeast)	NM_00644	10594	17p13	**3224.97**	2092.31	-1132.67	0.000107744	1.54	2615.8	3171.3	4090.6
207522_s_at	ATPase, Ca++ transporting, ubiquitous	NM_00517	489	17p13	**2541.39**	1318.79	-1222.59	0.000125933	1.93	927.5	1471.2	3288.3
219435_at	hypothetical protein FLJ22170	NM_02509	80169	17p13	**1691.87**	1079.08	-612.79	0.000221387	1.57	1129.1	1263.5	1441.4
218828_at	phospholipid scramblase 3	NM_02036	57048	17p13	**3868.98**	1612.28	-2256.69	0.000502174	2.40	7794.1	629.8	5294.2
211300_s_at	tumor protein p53 (Li-Fraumeni syndrome)	K03199	7157	17p13	**876.10**	424.12	-451.98	0.000609195	2.07	616.5	671.9	887.2
201729_s_at	KIAA0100 gene product	NM_01468	9703	17q11	**3142.98**	1946.01	-1196.97	0.000618515	1.62	1810.5	1668.1	3184.4
209163_at	cytochrome b-561	AL514271	1534	17q11	**1439.45**	908.52	-530.93	0.000277325	1.58	1573.3	1317.6	1507.5
208831_x_at	suppressor of Ty 6 homolog (S. cerevisiae)	D79984	6830	17q11	**826.90**	295.93	-530.97	0.000620253	2.79	246.2	143.8	819
208991_at	signal transducer and activator of transcription 3 (acute-phase response factor)	AA634272	6774	17q21	**27432.17**	16069.52	-11362.65	3.11912E-05	1.71	20651	9289.5	22003.7
216836_s_at	v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived	X03363	2064	17q21	**479.40**	229.98	-249.42	0.000140646	2.08	250.6	881.4	445.6
210230_at	RNA, U2 small nuclear	BC003629	6066	17q21	**1037.15**	356.65	-680.50	2.42447E-05	2.91	291.4	977	1105.4
220684_at	T-box 21 (T-bet)	NM_01335	30009	17q21	**4275.31**	2691.73	-1583.58	2.0365E-05	1.59	4296.3	3644.2	4074.8
221554_at	protein kinase LYK5	AF308302	92335	17q23	**2208.07**	1249.74	-958.33	0.000232062	1.77	1185.4	1596.7	2813.5
205297_s_at	CD79B antigen (immunoglobulin-associated beta)	NM_00062	974	17q23	**1991.54**	1287.24	-704.31	0.000430736	1.55	1406.2	1853.9	1577.4
203514_at	mitogen-activated protein kinase kinase kinase 3	BF971923	4215	17q23	**9968.25**	2725.36	-7242.89	2.56836E-08	3.66	3686.6	2514.3	10388.9
217973_at	carbonyl reductase	NM_01628	51181	17q25	**2591.47**	1313.93	-1277.55	1.09007E-05	1.97	2914.9	1817.4	3852.7
204970_s_at	v-maf musculoaponeurotic fibrosarcoma oncogene homolog G (avian)	NM_00235	4097	17q25	**1289.57**	740.05	-549.52	0.000520058	1.74	1097	1645.8	814.7
208657_s_at	MLL septin-like fusion	AF142408	10801	17q25	**1861.36**	1074.76	-786.59	0.000744162	1.73	1226.6	2168.4	2050.5
219173_at	hypothetical protein FLJ22686	NM_02495	80022	17q25	**1429.32**	715.13	-714.19	0.000163063	2.00	1157.2	112.3	1268.7
202812_at	glucosidase, alpha; acid (Pompe disease, glycogen storage disease type II)	NM_00015	2548	17q25	**2803.28**	1571.84	-1231.44	0.000187186	1.78	3653.5	1008.2	2599.8
218058_at	CpG binding protein	NM_01459	30827	18q12	**1807.27**	1082.16	-725.11	0.000166356	1.67	1268.3	1257.8	1597.7

213489_at	microtubule-associated protein, RP/EB family, member 2	BE671156	10982	18q12	**1334.89**	655.81	-679.08	0.000355344	2.04	534.9	272.5	1578.1
218913_s_at	Gem-interacting protein (GMIP)	NM_01657	51291	19p11	**2191.96**	1089.97	-1101.99	2.21101E-05	2.01	1264.5	2392.8	3224.7
213505_s_at	splicing factor, arginine/serine-rich 14, SFRS14	BG252853	10147	19p12	**1311.32**	717.53	-593.79	0.000182815	1.83	1312	1656.6	682.1
206722_s_at	endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 4	NM_00472	9170	19p12	**2471.56**	1558.99	-912.57	0.000250387	1.59	2029.5	1394.1	3249.2
213039_at	Rho-specific guanine nucleotide exchange factor p114	AB011093	23370	19p13	**13395.23**	8566.14	-4829.08	3.11007E-06	1.56	9773.9	10428.9	18580.7
221506_s_at	karyopherin beta 2b, transportin	BG258639	30000	19p13	**2275.92**	1351.09	-924.83	3.67379E-06	1.68	2907.8	2689.4	2065.9
208336_s_at	glycoprotein, synaptic 2	NM_00486	9524	19p13	**1674.74**	712.65	-962.08	4.25581E-06	2.35	2368.1	981	1666.5
203782_s_at	polymerase (RNA) mitochondrial (DNA directed)	NM_00503	5442	19p13	**1703.73**	1013.69	-690.04	1.27576E-05	1.68	1905.6	2405.9	1527.6
213045_at	KIAA0561 protein	AB011133	23031	19p13	**4180.32**	2596.31	-1584.01	2.63654E-05	1.61	3814.7	2554.6	4740.7
202102_s_at	bromodomain-containing 4	BF718610	23476	19p13	**11075.67**	6770.53	-4305.14	5.26303E-05	1.64	13179	4260.6	8845.7
202574_s_at	casein kinase 1, gamma 2	NM_00131	1455	19p13	**2604.34**	1303.17	-1301.17	8.0763E-05	2.00	3045.6	1141.3	3630.7
206929_s_at	nuclear factor I/C (CCAAT-binding transcription factor)	NM_00559	4782	19p13	**1051.56**	459.89	-591.67	0.000150598	2.29	1066.4	160.3	784.5
210463_x_at	hypothetical protein FLJ20244	BC002492	55621	19p13	**1256.53**	618.15	-638.38	0.000169002	2.03	1082.3	997.2	1331.9
43977_at	hypothetical protein FLJ20422	AI660497	54929	19p13	**2199.58**	1369.61	-829.97	0.000951018	1.61	3283.8	3133.6	2261.5
217804_s_at	hypothetical protein FLJ20011	BC003086	54783	19pter	**3241.88**	1577.26	-1664.62	3.49916E-07	2.06	3478.4	3435.1	3009.4
200094_s_at	eukaryotic translation elongation factor 2	AI004246	1938	19pter	**37678.31**	24633.16	-13045.15	0.000221877	1.53	40996.4	28636.1	43324.9
221998_s_at	VRK3 for vaccinia related kinase 3	BF062886	51231	19q13	**4300.79**	2721.53	-1579.26	0.000181748	1.58	3771.4	1619	4375
207740_s_at	nucleoporin 62kD	NM_01234	23636	19q13	**1288.71**	470.93	-817.78	2.29564E-10	2.74	1321.5	942.9	1050.9
205182_s_at	zinc finger protein	NM_01434	25799	19q13	**1787.86**	623.09	-1164.77	2.76382E-06	2.87	1745.5	180.7	672.3
214339_s_at	mitogen-activated protein kinase kinase kinase kinase 1	AA744529	11184	19q13	**4436.88**	2419.86	-2017.02	3.12866E-06	1.83	4954.1	3060.3	3128.1
201770_at	small nuclear ribonucleoprotein polypeptide A	NM_00459	6626	19q13	**3561.45**	2095.21	-1466.25	4.66611E-06	1.70	3698.1	861.8	3320.4
201221_s_at	small nuclear ribonucleoprotein 70kD polypeptide (RNP antigen)	NM_00308	6625	19q13	**4634.22**	3030.81	-1603.42	9.22175E-06	1.53	4594.7	4817.2	5978.3
209282_at	protein kinase D2	AF309082	25865	19q13	**3552.44**	2066.21	-1486.23	5.52158E-05	1.72	2916.5	2206.7	4120.1
208308_s_at	glucose phosphate isomerase	NM_00017	2821	19q13	**5637.11**	3515.21	-2121.90	0.000166266	1.60	6025.9	2024.3	6326.7
214907_at	hypothetical protein R29124_1	BF110434	90273	19q13	**1674.47**	968.47	-706.00	0.000297971	1.73	976.1	1610.9	1907.5
205861_at	Spi-B transcription factor (Spi-1/PU.1 related)	NM_00312	6689	19q13	**2174.87**	1270.76	-904.12	0.000343503	1.71	1645.3	507.9	1860.3
202621_at	interferon regulatory factor 3	NM_00157	3661	19q13	**3264.74**	2015.18	-1249.56	0.000361377	1.62	2927.6	1847.9	4213.5
204139_x_at	zinc finger protein 42 (myeloid-specific retinoic acid- responsive)	NM_00342	7593	19q13	**868.37**	444.32	-424.05	0.000495012	1.95	253.8	335	915.4
213915_at	natural killer cell group 7 sequence	NM_00560	4818	19q13	**16013.97**	9075.55	-6938.42	0.000728691	1.76	27099.1	12257.5	19509.3
202726_at	ligase I, DNA, ATP-dependent	NM_00023	3978	19q13	**1096.96**	630.67	-466.28	0.000924727	1.74	683.4	2164.5	876
200990_at	tripartite motif-containing 28	NM_00576	10155	19q13	**3898.12**	2167.54	-1730.58	0.000101259	1.80	4551.6	1098	3964.2
220948_s_at	ATPase, Na+/K+ transporting, alpha 1 polypeptide	NM_00070	476	1p21	**4260.67**	2486.13	-1774.54	8.95748E-05	1.71	3586.5	2001.8	5156
204263_s_at	carnitine palmitoyltransferase II	M58581	1376	1p32	**1029.10**	289.31	-739.79	1.56061E-06	3.56	666.7	1180.7	1655.5
204731_at	transforming growth factor, beta receptor III (betaglycan, 300kD)	NM_00324	7049	1p33	**1970.90**	999.42	-971.48	4.71675E-05	1.97	2408.8	2003.6	1322.4
213798_s_at	adenylyl cyclase-associated protein	AA806142	10487	1p34	**39407.80**	22992.82	-16414.98	1.33695E-08	1.71	33499.7	21811.8	32945.7
212103_at	karyopherin alpha 6 (importin alpha 7)	BG403834	23633	1p35	**2056.81**	941.06	-1115.75	4.86333E-06	2.19	1208.3	1332.4	2118.2
219235_s_at	hypothetical protein FLJ13171	NM_02392	65979	1p35	**1520.68**	569.46	-951.22	7.61909E-09	2.67	1214	686.7	1466
204891_s_at	lymphocyte-specific protein tyrosine kinase (LCK)	NM_00535	3932	1p35	**12494.76**	7292.54	-5202.23	5.36542E-06	1.71	11810.5	10347.1	11356.7
219423_x_at	TNFRSF25	NM_00379	8718	1p36	**1890.59**	972.63	-917.97	1.84883E-07	1.94	1325.1	2132	1602.8
202178_at	protein kinase C, zeta	NM_00274	5590	1p36	**2120.71**	1288.08	-832.63	1.6054E-05	1.65	1656.8	2349.1	2875.4
221790_s_at	LDL receptor adaptor protein	AL545035	26119	1p36	**3676.73**	2195.16	-1481.57	0.000434582	1.67	3357.4	3260.8	1995.9
202481_at	short-chain dehydrogenase/reductase 1	NM_00475	9249	1p36	**1782.37**	1143.85	-638.52	0.000677678	1.56	2305.9	907.7	1948.2
205025_at	GLI-Kruppel family member HKR3	NM_00534	3104	1p36	**1096.91**	584.37	-512.54	0.000712967	1.88	791.2	44.1	1336.4
219865_at	HSPC157 protein	NM_01417	29092	1p36	**1778.71**	1177.34	-601.36	0.000867841	1.51	2083.7	2278.5	2151.4
204198_s_at	runt-related transcription factor 3, RUNX3	AA541630	864	1p36	**7168.09**	3720.07	-3448.02	1.51716E-06	1.93	7546.8	5843.8	6942.8
218608_at	putative ATPase	NM_02208	23400	1p36	**524.13**	256.48	-267.65	0.00065546	2.04	550.5	122.8	888
215967_s_at	lymphocyte antigen 9	AL582804	4063	1q21	**2155.73**	1377.46	-778.27	6.53258E-05	1.57	2106.2	1712.6	2014.5
203229_s_at	CDC-like kinase 2	NM_00399	1196	1q21	**3274.61**	1962.32	-1312.28	1.26349E-05	1.67	3280.5	1793.4	3642.6
210031_at	CD3Z antigen, zeta polypeptide (TiT3 complex)	J04132	919	1q22	**13903.41**	7077.09	-6826.32	6.47456E-07	1.96	11929.4	10369.8	13173.6
202250_s_at	WD repeat domain 42A (WDR42A)	NM_01572	50717	1q22	**1976.98**	1307.21	-669.77	0.000566177	1.51	1361.1	1163.5	2801.8
205988_at	CD84 antigen (leukocyte antigen)	NM_00387	8832	1q24	**4434.46**	2887.02	-1547.45	1.40203E-05	1.54	3752.7	2833.9	3301.6
221601_s_at	regulator of Fas-induced apoptosis, Fas apoptotic inhibitory molecule 3 FAIM3	AI084226	9214	1q32	**13072.28**	8472.66	-4599.62	5.4766E-07	1.54	11212.3	11266.9	9606.2

207734_at	hypothetical protein FLJ20340	NM_01777	54900	1q32	**2561.47**	1552.86	-1008.61	3.43844E-06	1.65	2492.8	1713.2	2034.6
214833_at	transmembrane protein 63A, TMEM63A	AB007958	57243	1q42	**2197.91**	1224.75	-973.16	5.08598E-05	1.79	904.9	1155.6	1194.1
201853_s_at	cell division cycle 25B	NM_02187	994	20p13	**8988.00**	5770.62	-3217.38	3.45802E-05	1.56	5220.1	6752.3	7222.3
209026_x_at	FK506 binding protein 1A (12kD)	AF141349	2280	20p13	**9290.43**	6029.44	-3260.99	0.000153246	1.54	13283.3	3754.6	8590.5
210706_s_at	ring finger protein 24	BC000213	11237	20p13	**10237.35**	4914.46	-5322.88	1.60725E-06	2.08	3826.5	3579.2	8957.9
209144_s_at	core-binding factor, runt domain, alpha subunit 2; translocated to, 2	AI810484	9139	20q11	**404.07**	170.41	-233.66	0.000753068	2.37	387.7	196.3	106.1
201704_at	ectonucleoside triphosphate diphosphohydrolase 6 (putative function)	NM_00124	955	20q11	**1417.91**	825.78	-592.13	2.98541E-05	1.72	1498.1	596	1610.2
212750_at	protein phosphatase 1, regulatory (inhibitor) subunit 16B	AB020630	26051	20q11	**1618.48**	963.78	-654.70	0.000267292	1.68	1369.3	2103.9	1455.2
217770_at	CGI-06 protein	NM_01593	51604	20q12	**2106.82**	1260.86	-845.96	3.62654E-05	1.67	1263.7	1928.3	2550.1
202789_at	phospholipase C, gamma 1 (formerly subtype 148), PLCG1	AL022394	5335	20q12	**2207.17**	1276.25	-930.93	5.58447E-05	1.73	2012.1	3820.5	568.1
209048_s_at	protein kinase C binding protein 1	AB032951	23613	20q13	**2490.32**	1408.96	-1081.36	1.96708E-09	1.77	2395.2	1774.2	1480.6
218494_s_at	GLUT4 enhancer factor	NM_02006	56731	20q13	**1468.46**	783.82	-684.64	0.000117993	1.87	1370.8	1677.4	1450.2
208880_s_at	putative mitochondrial outer membrane protein import receptor	AB019219	24148	20q13	**3002.42**	1842.13	-1160.29	0.000176694	1.63	4472.2	2953	1682.3
218533_s_at	hypothetical protein FLJ20517	NM_01785	54963	20q13	**760.49**	390.36	-370.13	0.000787465	1.95	586.5	1225.2	621.8
209042_s_at	ubiquitin-conjugating enzyme E2G 2 (UBC7 homolog, yeast)	BC001738	7327	21q22	**2243.79**	740.21	-1503.59	2.34613E-09	3.03	2135.3	2284.4	1643.4
220918_at	hypothetical protein FLJ20856	NM_02514	80215	21q22	**4892.77**	2205.66	-2687.11	6.85673E-07	2.22	2656.3	2483.9	3444.4
202217_at	ES1 (zebrafish) protein, human homolog of	NM_00464	8209	21q22	**4489.32**	2901.46	-1587.86	2.80467E-06	1.55	4024.5	5037.1	6141.8
203660_s_at	pericentrin 2 (kendrin)	NM_00603	5116	21q22	**1994.98**	1328.94	-666.04	0.000281865	1.50	1722.3	1663.9	1566
213408_s_at	phosphatidylinositol 4-kinase, catalytic, alpha polypeptide	AK024034	5297	22q11	**5419.34**	3133.67	-2285.67	6.87213E-07	1.73	3868.3	3403.9	4994.5
202624_s_at	calcineurin binding protein 1, CABIN1	NM_01229	23523	22q11	**3881.08**	2348.05	-1533.04	0.000423192	1.65	4362.9	2992.8	3425.9
208024_s_at	DiGeorge syndrome critical region gene 6	NM_00567	8214	22q11	**2207.15**	1455.07	-752.08	0.000586466	1.52	1971.3	1088.7	2013.5
217497_at	endothelial cell growth factor 1 (platelet-derived)	AW613387	1890	22q13	**3111.95**	1280.62	-1831.34	5.12583E-06	2.43	2116.5	1698.5	2851.9
213579_s_at	E1A binding protein p300	AI459462	2033	22q13	**2527.84**	1284.63	-1243.21	6.15501E-08	1.97	1150.1	1748.1	1719.2
204193_at	choline kinase-like	NM_00519	1120	22q13	**3664.56**	2271.21	-1393.35	1.32581E-05	1.61	2479.8	3637.6	3443.3
212682_s_at	hypothetical protein BC002942	AI081535	91289	22q13	**1599.85**	658.27	-941.58	9.13476E-05	2.43	637.8	426.2	1734.8
204008_at	dynein, axonemal, light polypeptide 4	NM_00574	10126	22q13	**776.62**	471.72	-304.89	0.000170345	1.65	730.8	679.4	867
205291_at	interleukin 2 receptor, beta	NM_00087	3560	22q13	**11609.94**	6515.04	-5094.89	0.000315863	1.78	8036	6777.3	8506
201755_at	MCM5 minichromosome maintenance deficient 5, cell division cycle 46 (S. cerevisiae)	NM_00673	4174	22q13	**1146.18**	645.93	-500.25	0.000464999	1.77	1861.9	97.3	1257.5
39835_at	SET binding factor 1	U93181	6305	22q13	**1230.35**	686.99	-543.36	0.00095242	1.79	1211.9	670.3	1556.1
212040_at	trans-golgi network protein 2	BG249599	10618	2p11	**3616.76**	2052.39	-1564.36	6.18492E-05	1.76	2753.5	2798.5	3298.5
221671_x_at	immunoglobulin kappa constant	M63438	3514	2p12	**45808.52**	23671.46	-22137.06	7.65207E-06	1.94	43425.6	23507.7	41159.5
206036_s_at	v-rel reticuloendotheliosis viral oncogene homolog (avian)	NM_00290	5966	2p13	**1491.20**	892.84	-598.36	3.03971E-05	1.67	1655	1040.1	1447.1
201082_s_at	dynactin 1 (p150, glued homolog, Drosophila)	NM_00408	1639	2p13	**1203.40**	717.34	-486.06	0.00043947	1.68	697.2	456.7	1483.2
212071_s_at	spectrin, beta, non-erythrocytic 1 (barbed-end actin filament capping), SPTBN1	BE968833	6711	2p21	**5333.96**	3390.97	-1942.99	0.000101961	1.57	3861.5	3251.9	5620.1
212645_x_at	brain and reproductive organ-expressed (TNFRSF1A modulator)	AL566299	9577	2p23	**1770.85**	1082.30	-688.55	0.000114657	1.64	1099.3	1797.3	2579.8
210249_s_at	nuclear receptor coactivator 1	U59302	8648	2p23	**13397.93**	8351.06	-5046.87	5.36895E-05	1.60	10349.2	5126.8	11061.2
212274_at	lipin 1	AV705559	23175	2p25	**2360.67**	1175.61	-1185.06	0.000115052	2.01	1064.8	3596.9	1680.3
214032_at	zeta-chain (TCR) associated protein kinase (70 kD)	AI817942	7535	2q12	**2924.46**	1613.97	-1310.49	4.26213E-07	1.81	2541.5	4260.5	2652.4
212752_at	CLIP-associating protein 1	AA176798	23332	2q14	**1644.55**	1075.33	-569.22	0.000276933	1.53	889.2	1377.1	1602.5
201937_s_at	aspartyl aminopeptidase	NM_01210	23549	2q36	**724.26**	262.73	-461.54	0.000387003	2.76	449.7	358.9	1087.7
212280_x_at	ATG4 autophagy related 4 homolog B (S. cerevisiae), ATG4B - KIAA0943 protein	AA532726	23192	2q37	**2157.68**	1399.95	-757.73	0.000722711	1.54	2443	1117.6	2055.3
202208_s_at	ADP-ribosylation factor-like 7	BC001051	10123	2q37	**5813.04**	2799.65	-3013.39	9.36618E-09	2.08	5743.1	4443.7	4281.8
219997_s_at	COP9 (constitutive photomorphogenic, Arabidopsis, homolog) subunit 7B	NM_02273	64708	2q37	**1722.63**	1084.84	-637.79	9.84915E-06	1.59	1390.2	1577.1	1680.5
221548_s_at	integrin-linked kinase-associated serine/threonine phosphatase 2C	AY024365	80895	2q37	**1531.84**	978.41	-553.43	3.4268E-05	1.57	1250.9	1057.6	1498.3
221934_s_at	DALR anticodon binding domain containing 3, DALRD3	BF941492	55152	3p21	**3313.04**	2066.04	-1247.00	2.88096E-05	1.60	2295.7	1955.5	3043.1
201040_at	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2 (GN	NM_00207	2771	3p21	**13325.14**	5815.91	-7509.23	2.53759E-06	2.29	10194	4189	18122.4
203281_s_at	ubiquitin-activating enzyme E1-like	NM_00333	7318	3p21	**4071.51**	2517.64	-1553.86	0.000424629	1.62	2927.5	1978.6	6743.2
204346_s_at	Ras association (RalGDS/AF-6) domain family 1	NM_00718	11186	3p21	**2902.84**	1643.79	-1259.05	7.98554E-07	1.77	1407.2	3004.2	4376.4
204355_at	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 30	NM_01496	22907	3p21	**1974.74**	1000.55	-974.19	6.41031E-06	1.97	1969.1	856.1	2483.1
205875_s_at	three prime repair exonuclease 1	NM_01638	11277	3p21	**2763.69**	1311.53	-1452.17	0.000426427	2.11	2115.7	514.3	3683.1
209950_s_at	villin-like (actin bundling)	BC004300	50853	3p21	**595.09**	312.55	-282.54	0.000533727	1.90	132.7	718.3	675.9
203246_s_at	homologous to yeast nitrogen permease (candidate tumor suppressor)	NM_00654	10641	3p21	**2503.97**	1217.42	-1286.55	0.000697322	2.06	913.7	1267.5	2866.1

217817_at	actin related protein 2/3 complex, subunit 4 (20 kD)	BE891920	10093	3p25	**5677.56**	2259.06	-3418.50	3.42349E-06	2.51	5283.5	3419.7	7940.6
203906_at	KIAA0763 gene product	AI652645	9922	3p25	**5602.08**	3435.18	-2166.90	0.000227741	1.63	3691.1	3159	7796.8
214739_at	hypothetical protein MGC4126	AI357539	84859	3q29	**955.42**	607.85	-347.57	0.00074771	1.57	601.1	1570.5	947
208021_s_at	transcription regulation of transcription)	NM_00291	5981	4p14	**1254.89**	819.37	-435.52	0.00050463	1.53	1211	1106.7	1074.1
210137_s_at	dCMP deaminase	BC001286	1635	4q35	**2347.53**	1365.12	-982.41	7.54476E-06	1.72	1962.6	1375.8	3103.8
222152_at	Programmed cell death 6 (PDCD6)	AK024175	10016	5pter	**2057.41**	1092.06	-965.35	0.000137832	1.88	979.5	1621.4	1006.8
202531_at	interferon regulatory factor 1	NM_00219	3659	5q31	**14403.07**	9407.78	-4995.29	1.33441E-05	1.53	12635	8860.9	19191.9
205254_x_at	transcription factor 7 (T-cell specific, HMG-box)	AW027359	6932	5q31	**1963.48**	976.09	-987.39	2.82568E-05	2.01	867	729.2	1509.3
212193_s_at	KIAA0731 protein	BE881529	23367	5q33	**1700.56**	634.32	-1066.24	1.73971E-07	2.68	768.6	406.1	1266.8
40420_at	serine/threonine kinase 10	AB015718	6793	5q35	**9149.38**	5758.27	-3391.12	2.5456E-05	1.59	7053.3	5880.6	10253.5
212605_s_at	AF034176 Human mRNA (Tripodis and Ragoussis) Homo sapiens cDNA clone ntcon5 c	AK025759	AK025759	6p21	**2014.16**	937.81	-1076.36	3.9005E-07	2.15	1630	1852.1	1901.4
200905_x_at	major histocompatibility complex, class I, E	NM_00551	3133	6p21	**98505.23**	63128.26	-35376.97	3.40127E-08	1.56	88149.3	89402.3	96804.8
200041_s_at	HLA-B associated transcript 1	NM_00464	7919	6p21	**16317.91**	9742.19	-6575.71	3.35984E-05	1.67	11192.6	7660.5	20030
203146_s_at	gamma-aminobutyric acid (GABA) B receptor, 1	NM_00147	2550	6p21	**2303.58**	1361.92	-941.66	9.2316E-05	1.69	1646.7	1105.7	1873.7
207169_x_at	discoidin domain receptor family, member 1	NM_00195	780	6p21	**763.95**	443.14	-320.81	0.000166598	1.72	979.4	766.2	457.2
212671_s_at	major histocompatibility complex, class II, DQ alpha 1	BG397856	3117	6p21	**12018.31**	6005.98	-6012.33	0.000449149	2.00	18088.9	4242.9	16708
201797_s_at	valyl-tRNA synthetase 2	NM_00629	7407	6p21	**427.57**	187.95	-239.62	0.00045514	2.27	483.2	62.7	519.2
204265_s_at	chromosome 6 open reading frame 9	NM_02210	63940	6p21	**18681.22**	10588.76	-8092.45	0.00046363	1.76	26466.5	6348.2	18247.3
217478_s_at	major histocompatibility complex, class II, DM alpha	X76775	3108	6p21	**10318.13**	6835.93	-3482.21	0.000800624	1.51	9596.3	3825.6	15020.9
221866_at	transcription factor EB	AL035588	7942	6p21	**2056.25**	1262.29	-793.96	0.000390188	1.63	2182.9	1553.8	1975.9
201700_at	cyclin D3	NM_00176	896	6p21	**20631.00**	13226.92	-7404.08	2.98559E-05	1.56	16174.9	14920.8	25299.6
201189_s_at	inositol 1,4,5-triphosphate receptor, type 3	NM_00222	3710	6p21	**1934.41**	961.12	-973.29	9.05612E-05	2.01	1683.9	146.9	1615.4
212118_at	ret finger protein	AL523814	5987	6p22	**4764.13**	3130.88	-1633.24	0.000267267	1.52	6331.9	3047.2	4446.4
208622_s_at	villin 2 (ezrin)	AA670344	7430	6q25	**2515.68**	1148.03	-1367.65	7.47928E-05	2.19	1250	392	1984.3
221073_s_at	caspase recruitment domain 4 (CARD4 or NOD1)	NM_00609	10392	7p15	**2841.76**	1795.15	-1046.62	4.40718E-05	1.58	3323	1752.5	2707
216899_s_at	src family associated phosphoprotein 2 (SCAP2)	AC003999	8935	7p21	**4137.27**	2323.79	-1813.48	0.000555963	1.78	3243	1194.2	4242.4
212212_s_at	DKFZP586J0619 protein	BF055496	26173	7p22	**1542.03**	997.02	-545.01	0.000211435	1.55	1237.7	2545.9	1282
218425_at	TRIAD3 protein	BC000787	54476	7p22	**2061.71**	1354.61	-707.10	0.000363666	1.52	2918.6	1867.1	1198.9
203802_x_at	NOL1R protein	NM_01804	55695	7q11	**2734.32**	1363.16	-1371.16	0.000196783	2.01	287.5	901.7	3207.3
211031_s_at	cytoplasmic linker 2	BC006259	7461	7q11	**517.36**	225.93	-291.43	0.000268425	2.29	693.4	644.4	434
221191_at	DKFZp434A0131 protein	NM_01899	54441	7q11	**1105.16**	627.39	-477.77	0.000309327	1.76	313.3	653.6	698.4
217529_at	hypothetical LOC401394/hypothetical LOC402578	BE547674	401394	7q22	**1084.64**	704.65	-379.99	0.000748217	1.54	1099.2	855.2	1002
220954_s_at	paired immunoglobulin-like receptor beta	NM_01344	29990	7q22	**2005.49**	1247.89	-757.60	5.57503E-05	1.61	1174.8	1435.4	2023.4
213444_at	KIAA0543 protein	AB011115	23145	7q36	**1661.37**	582.51	-1078.87	5.63034E-05	2.85	377.1	260.9	1775.7
217437_s_at	transforming, acidic coiled-coil containing protein 1	AB029026	6867	8p11	**1582.20**	890.08	-692.12	7.86993E-06	1.78	1379.3	1217.5	2137.2
209342_s_at	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase beta (IKBKB)	AF080158	3551	8p11	**1404.94**	887.24	-517.70	0.000124645	1.58	969.1	631.1	1075.4
206255_at	B lymphoid tyrosine kinase, BLK	NM_00171	640	8p23	**753.22**	207.33	-545.88	1.23361E-07	3.63	758.2	856.8	684.1
215874_at	ST3 beta-galactoside alpha-2,3-sialyltransferase 1	AK026820	6482	8q24	**807.80**	425.62	-382.18	0.000357192	1.90	885.5	1810.4	411.9
208322_s_at	sialyltransferase 4A (beta-galactosidase alpha-2,3-sialytransferase)	NM_00303	6482	8q24	**1380.48**	489.67	-890.81	1.05133E-06	2.82	934.1	1157.2	1330
201639_s_at	cleavage and polyadenylation specific factor 1, 160kD subunit	NM_01329	29894	8q24	**2153.25**	1146.92	-1006.33	2.64714E-06	1.88	2440.8	940.9	2524.6
204773_at	interleukin 11 receptor, alpha	NM_00451	3590	9p13	**1684.05**	1052.81	-631.24	0.000179772	1.60	1194.5	1215.2	1533.5
215925_s_at	CD72 antigen	AF283777	971	9p13	**1197.51**	679.37	-518.13	0.000378212	1.76	975.6	925.5	906.8
209432_s_at	cAMP responsive element binding protein 3 (luman)	AF029674	10488	9pter	**1545.39**	935.79	-609.60	7.22393E-05	1.65	1797.4	1059.2	1786.8
207540_s_at	spleen tyrosine kinase, SYK	NM_00317	6850	9q22	**7254.79**	3851.60	-3403.19	3.41971E-05	1.88	3312	2724.1	6922.5
203147_s_at	tripartite motif-containing 14	BE962483	9830	9q22	**3163.69**	1696.01	-1467.68	0.000236294	1.87	1505.3	4256.7	2102.1
218555_at	anaphase-promoting complex subunit 2 (ANAPC2)	NM_01336	29882	9q34	**1395.85**	827.77	-568.08	0.000835778	1.69	884.7	567.1	1407.4
203198_at	cyclin-dependent kinase 9 (CDC2-related kinase), (CDK9)	NM_00126	1025	9q34	**1233.65**	660.32	-573.33	0.000103141	1.87	193.1	895.8	1460.8
202123_s_at	v-abl Abelson murine leukemia viral oncogene homolog 1	NM_00515	25	9q34	**1506.52**	996.45	-510.07	0.000262415	1.51	1421.8	964.9	1306.2
208723_at	ubiquitin specific protease 11	BC000350	8237	Xp21	**3558.94**	1886.54	-1672.41	3.3838E-08	1.89	2507.9	2812.8	3407.2
209439_s_at	phosphorylase kinase, alpha 2 (liver)	D38616	5256	Xp22	**3165.22**	2099.45	-1065.77	3.09546E-05	1.51	1733.7	1455.4	2770
208806_at	chromodomain helicase DNA binding protein 3	BE379542	1107	Xq13	**1652.78**	1030.54	-622.24	1.68398E-05	1.60	1461.9	979.5	1700.2

NP4	NP5	NP6	NP7	NP8	NP9	NP10	NP11	NP12	NP13	NP14	NP15	NP16	NP17	NP18	NP19	PSA1	PSA2	PSA3	PSA4	PSA5	PSA6
2849.7	4489.6	4970.6	3331.1	4813.2	4682	5684.5	2849.5	4942.7	3192.4	4038.8	4276.9	3007.2	2672.8	3294.6	3364.4	2672.8	2233.4	2158.2	1482	2196.2	3305.5
555.3	1088.7	1089	1203.6	696.9	1215.5	1539.6	1202	1608.3	947.6	1431.8	748.3	613.5	956.7	1120.6	424.5	370	374.4	305.4	1175.8	475.6	567.7
3014.9	3643.2	2229.7	3315.7	4146.2	2637.5	3381.5	3611.5	2899.3	2262.2	4437.4	3114.8	4314.2	3253.5	2822.7	3413.8	2786.6	2520.3	1941.6	2104	2866.7	2125.9
2908.6	3366.9	3731.8	1719.7	1963.1	1640.4	3493.4	2293.7	3359.2	1899.4	2283.8	2715.8	2151.8	3027.7	2365	3080	1575.5	1525.6	1279.5	702.2	2300.6	2671.1
25358.9	16731	25885.4	24570.3	25522.6	24052.1	28128.6	11404	13027.1	23674.9	30507.8	15946.7	30797.2	15120.9	18063.9	25867.7	11745.7	16299.5	2893.2	13041.7	25836.1	7399.9
1885.4	1992	1939.3	1084.7	1632.1	1242.4	724.7	795.6	1209.7	1875.8	2649.2	2655.6	2840.9	1914.8	1289.9	1410.9	1023.9	202.8	340.8	738.5	852.6	837
2983.5	4942.5	4304.5	3381.3	4762.5	3482.2	3425.3	3992.6	5134.6	3575.9	3105.5	3580.9	4737.6	3470	4158.3	3911.1	2560.6	1983	2192.2	4047.1	3293.5	2643.7
8196.7	8017.6	8405.4	9482.9	8755.8	8590.6	6931.7	5583.6	9553.8	10092.3	7020.6	6733	6284.4	6449.1	6297	9560.8	4282.2	2911	6066.1	3698	3079.7	3702.6
4065.4	5086.9	5161.7	3006.1	4918.3	4530.8	3884.3	3143.8	4395.9	5439.9	3684.3	4629.2	4161.5	4262.5	2642.9	4471.7	2403.8	1868.9	1595.3	1820.4	1828.4	1972.1
7668.6	7609.4	6066.6	8266.7	5803.6	4488.4	7756.9	5374.8	9640	5927.8	9509.7	8038.6	6623.8	7383.1	5031.6	4523.3	5974.6	3896.8	2780.3	4193.3	5078	5310.5
2042.8	3581.8	2355.8	2521.3	2732.8	2372.3	2487.7	1345.5	4145.3	2590.4	2077.3	3240.7	2221	1830.1	1214.7	1916.7	1924.3	1093.4	1123.9	2263.6	918.8	1078.9
3235.6	3637.1	4155.8	1607.5	1088.8	1787.9	2032.1	941.6	3877.1	1280.1	3417.5	2782.4	1847.8	2788.4	2107.1	2752	1419.9	1203.6	802.4	1362.2	2117.7	698.7
2783.1	2161.9	2234.6	2133.3	2204.1	1260.9	2032.3	1770.6	2857.7	1761.5	3236.8	2386.9	2983.7	1996.9	2208	2562.3	1622.9	1427.1	2338.2	1873.7	1651.7	1411.9
2059.4	2028.4	1580.1	159.2	1508.1	1106.5	1123	974.2	1747.3	1138.9	100.9	1050.5	1325.5	912.8	1183.9	717.5	165.7	100.1	448.3	117.5	88.2	314.1
4656.7	5277.9	3820.7	3815.8	4425.1	3509.7	3068.6	4098.4	4863.2	3605.5	2224.8	3970.6	5226.2	4881	5526.8	4286.2	2900.2	2743.2	3082.2	3601.5	3473.2	3236.5
5399.7	6823.4	6983.6	4644.1	6828.8	5270.8	7726	6691.1	7323.5	4450	6565.7	7061.7	4894.1	6230.1	4284.5	8088	4934	3230.6	3599.1	3033.5	4349.6	4903.3
5271.6	6281.9	6979.1	4976.1	7345	5015.4	5077.3	5125.4	7780.2	5433.4	5593.7	4282.2	5577.5	5000.4	4688.7	4609.2	4083.3	3957.6	2871.9	4189.8	3677.7	5907.2
1056.9	1059.5	2005.5	1757.4	1357.7	1835	2004.7	681.7	1992.9	1370.9	1434.8	1362.1	905.5	792.1	456.8	1154.8	367.4	1137.6	590.2	428.5	442.6	1161.6
6627.7	5231	8659.5	4881.1	7634.7	5022.7	4310	5947.3	6971.5	5056.2	8121.3	4841.8	9536.7	4800.7	5361.4	8693	4606.2	4424	2446.9	6443.8	7584.3	4287.5
4182.7	3844	3825.9	3727.9	3949.7	2390.7	3755.3	2329.1	6223	2163.4	4339.3	4932.5	3055.4	5009.3	2632.6	2644.7	3184.3	2670.6	2576.2	2144.2	3467.9	3784.6
7283.2	6837.5	8518.1	9242.5	10777.8	7921.8	8875.2	6970.9	9360.2	7394.5	9473.5	6500.2	6632.4	6211.8	5283.6	7513.2	4702.2	4058.3	2626.8	5596.8	4336.2	4551.7
5917.6	6587.3	6854.1	2788	5257.5	3215.5	4737	4155.5	5835.9	4707.1	5541.3	6586.7	3323.2	6085.9	3526.3	5265.7	2951.2	2604.8	2139.3	3718.8	2721.2	3941.4
1197.6	1673.4	1487.4	1514.1	1493.9	1374	1355.2	1336	1855.7	1146.8	2308.7	1958.2	1041.5	1830.6	1425.6	1942.2	1635.5	939	1143.4	922.4	851	1237.6
3001.2	4021.5	5332.5	4456	4726.7	6101	5575	4135.1	6644.8	4306.8	4624.5	5641.7	4584.6	4028	3690	3846.7	5933.8	2973.9	1320.3	2205.4	2360.4	3012.9
1477.1	2167.1	2076.8	1858.8	1476.1	1067.7	1853.1	1614.7	3304.2	1444.1	1496.3	1707.2	1118.9	1354.2	1138.6	1413.2	1723.6	705.4	185.4	1146.1	838	1117.6
1508.4	1729.5	1165.1	2038.3	699.5	1639.1	1757.9	928.1	2479.9	1377.2	1444.2	2025.7	1395	1970.4	767.3	1104.7	1237.4	471.5	883.5	1179.9	242.4	604.4
2477.9	3049.1	1508.4	2543.6	2266	1446.2	1612.3	1249.7	1823.6	2434.8	2371.2	2507.5	2451.6	2078.2	1893	3055.5	1365.3	915	1649.6	1349.3	1298.7	1250.3
522.2	1721.2	1440.6	662.1	1482.4	542.2	1262.5	1265.5	1290.4	1592.9	1069.9	1177.2	1199.5	1218.9	163.7	1085.8	919.6	378.2	133.4	293.4	155.7	195.7
14482.9	14405.5	13765.9	15339.7	16470.9	14932.7	15693.9	15005.8	17853.7	15822.8	13824.7	12966.6	17061	15288	11391.5	14249.8	11927	10339.9	8483.6	11335.5	9656.7	9176
6910	8522.6	5990.1	6977.4	6275	7742.4	7330.5	5219.4	8779.4	4799.4	8022.3	9044.2	6619.5	8647.1	7243.1	8299.9	5888.6	1700.3	3666.5	6135.4	3944.9	5163
2657.3	1872.7	2445.2	2770.7	2095.9	1763.9	1795.4	1879.2	2501.7	1767	2364.8	1696	1953.7	2304.5	1236.3	1849.3	1172.9	329.8	359.2	2194.6	402.2	1161.5
22954.6	22540.6	22250.4	22682.1	24613.4	22188.5	30034.8	14750.2	30194.5	12969.9	25618.9	21228.3	20405.1	22634.1	13940.1	10136.8	20851.6	14065.2	12379.7	8745.7	12149.7	19193
7029	6106.6	8184.6	5362	4610.6	5697.5	5779.7	3583.6	7012.6	5525.8	4988.2	4984.8	4996	3427	3220.1	4516.6	3641.9	3075.8	4045.1	4894.1	3170.5	3797.5
1647.2	1870	1386.5	1161.8	1521.3	1085.5	1047.1	587.8	2103	1416.5	1222.1	1362.5	1561.5	1334.5	1301	1662.1	909.5	506.2	651.3	1522.3	936.2	832.7
1290.5	1111.4	2105.6	1160.7	1460.9	1748.6	1843.2	1055.8	1798.2	1337.6	1192.2	1551.8	2032.7	1455.9	1950.4	1312.4	925.2	732.9	1225.8	263.1	712.1	594.9
2012.4	1531.1	1539.7	1707.9	1444.3	1631	1783.6	2614.6	2169.5	1299.5	3844	978.7	1625.2	1513.3	2064.2	1320.4	1519.4	712.3	953.3	1099.9	1102.1	853
5057.5	4274.3	5325.8	5394.6	4992.3	6064.8	6902.5	4331.8	6178	4121.1	5923.9	3886.6	3336.2	2938.9	2746	4342.7	3284.3	1848.8	325.9	4299	429.3	2877.5
2942.3	3493.8	3103.8	2328.9	3662.9	3444.8	3780.2	3275.6	2929	4559.5	3510.4	3323.1	3051.9	3577.2	2461	3857.3	2259.5	1959.1	258.1	3365.8	1907.7	2211.4
1782.5	2156.2	3171.2	1931	4066.7	3019.3	4374.7	1881.4	2792.2	2910.6	2855.7	2844.8	2367.3	2795.7	2740.9	566.7	2038.3	1812.6	477.9	1464.4	785.8	2174.7
1911.8	4457.1	4637.4	3134.5	4614.2	3722.5	5600.6	3107.6	4364.9	3547	4966.7	2511.1	3614.4	2845.3	3498.7	2718.7	1374.4	999.3	1252.4	2053.8	1750.6	2576.5
2044.4	2151.3	1776.3	3027.5	2446.3	2111.9	2041.5	1374.4	1711	1548.3	2524.9	2414.3	2313.2	1575	1454.6	2648.7	1643.3	821.2	1082.4	1093.6	1317	1086.1
4135.3	5008.4	3334.3	6243.8	6401	5556.1	6370.4	6518.6	4649.9	4952	6732.6	4560.8	5022.8	4013.6	4979.6	6462	3666.1	2412.2	2090.6	4065.4	3046	3382.3
1502.9	2280.1	1050.6	1496.9	1080.2	1149.6	1361.1	1662.9	1753.6	1873.7	729	1488.1	978.2	1483	949.2	1175.7	872.8	1649	478.5	1020.3	650.2	965.6
4420.6	6285.7	4872.1	5179.5	5460.8	5187	5163.2	4040.5	6503.7	5322.9	4274.4	4062.4	5670.4	4451.5	4351.6	4247.6	1427.7	544.1	416.9	1331.5	1298.7	1178.3
2764.7	3408.7	2731.4	4255.5	3699	3291.9	3212.9	3295.6	4023.8	3453.5	4281.7	3665.7	4398.8	3207.4	4205.5	4906.6	2143.6	1666.8	1609.6	2107.6	2052.7	2342.6
2194.5	2051.4	2047.1	2663	2440.5	2563.6	2442.6	2860.5	2268.9	3681.2	2271.5	2430.6	2183.4	2679.9	2062.8	2566.2	1763.5	1196.2	1008.3	1542.8	1046.6	797.2
2550.6	3485.1	2695.1	2435	4086.2	3748.4	4934.5	3420.5	3333.7	3460.2	3867	2608.2	2709.8	2703.8	2835	3277.4	2275	1543.1	920.8	1534.4	2002.2	2602.4
1898.8	2635.1	1731	2203.4	1414.1	2383.9	2292.7	1647	2207.1	1629.2	1664.5	1880	1598.8	1854.5	1799.3	1949.6	1155.7	1548.7	504.4	993.4	1562.7	1205.3
1970.3	2163.9	523.2	1414.9	750	1098	971.2	599.6	2225.6	1219.1	936.9	1546	1956.8	1717.1	1024.9	1150.8	1347.4	261.7	130.1	743.6	794.7	682.1
12495.6	14887.1	7645.4	8940.6	11176.1	12030.5	13100.7	12909.4	18176.3	13029	13843.2	18291.1	15695.2	16520.7	8511.6	10105.6	11017.1	2149.4	3326	9270.1	5080.6	5589.7

1761.1	1619.4	1532.5	1493.5	1795.5	1162.3	1540.6	2126.6	1809.1	1730.6	2440.4	2087.4	2554	2034.3	1635.4	2050.1	1475.8	915.1	1046.2	1149.7	809.8	892
7279.6	7326.6	5898.7	7589.2	7773.5	6153.9	7780.1	6186.6	10276.5	8100.5	7510.3	5672.2	6575.6	6191.9	3925.8	7591.4	3659.5	2950.1	3019.1	4543.4	3206.5	4140.6
1894	1935.6	1611.3	1917.9	1761.5	1149.3	1858.6	1661.2	2461.9	1697.5	1449.8	1247.1	1546.5	1380	1413.7	2001.8	1205.5	812	508.8	1370.7	1096.4	1358.7
189.2	430.6	729.2	166.2	1144.6	264.9	362.6	660.8	798.2	417.1	288.2	574.5	542.2	579.8	1048.2	504.8	362.1	119.6	225.6	316.8	187.1	187.9
373.2	1359.9	1710.6	1189.7	1032.8	1404.8	1627.9	769.6	1692.5	1417.5	1126.9	1507.3	825.4	1547.7	1323	1727.1	1256.5	982.8	144.7	269.4	294.9	561.3
1152.8	1493.3	838.9	1018	1185	1006.9	1010.9	1272.2	1554.2	951.3	1571.8	1673.5	1616.5	1549.3	1256.4	1454.7	892	575.5	467.2	848.7	1020.5	1068.1
14164.6	15504.9	16622.4	16452.2	15509.3	19539.2	16926.7	14045.9	15597.6	19255.1	19894.1	10931.7	17295.9	11976.2	15106.4	14190.1	9429	7548.9	8450.5	8407.3	10375.8	14805.4
3072.4	3174	5070.5	3330.9	3207	2889.8	2161	4276	3377.2	3764.7	2438.1	4200.2	3046	3836.4	3266.1	1463.2	2584.1	1384.5	726.5	1742.9	1637.7	1405.2
3348.9	3770.2	4369.3	2332.6	3170.3	3092.9	3107.4	1323.8	4706.2	2268	3064.4	3581.4	1900.6	3559.3	2792.5	2960.5	2600.6	1889.8	1098	1303.7	1709	2511.3
1987.4	2209.8	2566.9	2178.8	1512.8	1199.7	1344.4	1321.1	1646.3	1564.7	2055.2	1534.5	1233.8	895.7	1444.2	1426.8	1051.8	461.6	690	2127	1500.6	1339.1
1324.9	929.6	600.6	1411.5	1291.3	722.9	1089.1	467.8	1506.7	954.9	1191.8	875.9	188.3	959.8	430.1	325.2	627.7	223.5	365.3	229.7	424	325.5
1290.6	2435.4	1865.3	1543.6	1662.3	1025.2	1192.5	725.9	1712.2	1480.8	1846.1	1661.5	1009.7	1071	1574.7	1651.2	874.6	362.6	440.5	1140.3	1964.4	1533
4000.3	4012.3	3997.8	2754.8	3795.1	4104.8	5131	3092.3	7359.5	2107.3	5061.4	4840.8	3338.4	3788.7	3727.1	4370.9	2135	2371.8	1739.6	2980.1	2316.2	3868.4
2300.7	3922.8	2954.1	2401.3	2420.2	2500.6	2982.1	2236.6	2852.1	2925.5	1875.2	2927.1	3452.3	3501.7	1889.6	2794.1	458.5	1004.9	467.1	712.1	392.2	761.6
1912.4	1412.6	1551.5	2062.1	1476	1358.4	1309.6	966.3	1030.4	846	1735	1487	1545.6	1540.9	1805.9	1334.9	1366.3	1036.9	943.5	1095.9	274.9	842.4
2034.6	1515.9	1444.8	1538.8	1357.6	1462.5	1187.3	941.2	1548.6	1698.1	1105.7	2029.9	2073.5	2548.2	996.8	2439.2	579.5	378.9	394.8	433.2	701.7	613
2170.5	1918.4	2229.7	1832.2	1570.8	1250.6	2026.2	966.5	2686.5	1825.8	1626	1863	1589	2287.2	2070.9	1142.3	1905.4	1293.1	1187.5	1166.8	1048.2	2223.4
2580.2	2281.2	3219.6	3185.1	3064.8	3189	3444.4	1468.4	3799.7	3408.1	4966.2	2549.8	2186	4278.2	991.9	3793.2	2359.2	1258.3	1410.6	1573.9	906.2	1884.1
1718	2787.4	2723.2	4758.6	3502.8	4087.4	2578.9	1766.7	3928.1	2828.6	2401.5	3412.9	1714.2	3257.6	1846.6	1558	979.8	522.2	536.5	1311.9	616.9	2565.8
2902.6	1732.5	2514.1	1430.1	2259.2	2095.9	2560	1984.3	2183.3	2790.7	2317.3	2183.7	2562.2	2273	1992.2	1787.7	1041.1	1264.8	813.1	960.8	1290.1	1388.7
319.5	1258.5	1927.1	1086.6	1353.5	1345.5	1250.9	844.5	801.6	742.1	785.6	1801.8	1042.2	1042.3	819.2	1162	851.9	270.6	505.4	153.5	388.6	1101.2
2434.7	2999.9	3503	2053.1	2728.9	2633.3	3294.1	1016.3	2105	2748.7	2038	2424	2590.7	2496	2128	3775.8	2002.1	942.7	1403.1	1580	1218	1466.2
1519.1	1813.7	2059.9	1969.9	1920	2087.7	1873.2	939.5	1838.1	2274.5	1658.8	2101.7	1758.7	2193.2	1177.3	2840	1928.5	1155.6	1774.4	695.6	778.8	2192.1
3115.2	3030.3	1860.4	3286.2	2484.5	2226.2	2704.7	3381.5	3229.7	2115.7	4317.2	2284.4	3286.8	3084.7	2715.1	5004.4	1319.4	1284.8	3641.7	2396.5	2677.2	2898.2
4278	4013.8	2868	3910.9	4201.1	2889.7	2964.1	3806.8	3493.5	3253.3	3508.4	4058.6	4170.9	3089.7	3242.8	3268.5	2622.3	2994.8	2577.6	2646.1	2297.3	3021.5
1790.4	2039.4	1466.8	270	1199.1	836.4	847	762.5	1011.5	1555.1	417.6	338.7	773.1	1109	809.5	1407.7	185.4	243.6	259.6	369.5	277.9	770.3
5327	7624.1	7846.9	2949.3	3297.3	2125.1	6888.5	3014.3	9185.6	4315.5	5837.2	6461.5	2856.7	7081.6	4624.8	4069.6	2962.2	2236.7	1376.9	1012	2605.1	5069.2
1587.8	1264.7	1253.8	1561	1638.2	1450.8	1453.3	1041.5	1533.4	1714.3	1893.6	1361.9	2290.5	1477.8	1489.7	1689.6	616.4	588.1	154.7	1616.5	777.9	125.3
1188.4	1365.6	1002	212.7	1059.1	743.8	1088.7	777.5	1640.4	1222.4	356	1456.8	1260.8	962.5	1189.2	1231	270	431.3	180.9	356.7	211.1	132.8
2080.3	1730.3	1525.9	2119.2	1338.5	1439.7	1344.7	1002.9	2421.5	1597.6	1426.7	1751.5	1605.8	1218.4	1109.4	1044.2	1374.3	732.4	220.3	675.6	1425	894.6
1042.1	1094.5	1338.7	657.2	1015.6	1017.2	1225.2	930	1095.3	654.8	604.1	1424.7	1329.6	1164.8	995.8	1127.7	421.3	471.9	225.4	901.7	1076.1	627.9
3069	3418.6	3201.9	2830.5	4207.7	4159.8	4651.6	1878.7	4505	2503.2	4020.2	2246.1	2433.7	2569.9	2646.4	3054.5	3422.1	1716.4	1534	2558.5	1434.6	2962.2
2993.8	4044.5	3264.6	1414.3	2279.3	2218.9	3449	1945.9	4480.7	2689.8	3334.8	2487.3	2036.2	2616.4	1347.5	1996.4	1935.3	1251.5	2367.9	1417.4	1159.6	2390.9
1235.7	1970.2	1809.1	1373.7	2173	3008.9	1949.8	1484.4	1580.2	1766.3	1377.8	2079	1452.8	1901.9	1254.2	1894.5	1006.2	677	344.1	1284.3	865.9	1256.9
4182.7	5046.9	5069.4	4094.5	3152.7	2687.4	3477.2	741.2	8059.1	2294	7422	2549.3	907.8	2190.5	2846.3	5071.5	1588.5	2280.1	1275.4	1320.3	760.7	2097.7
907.7	1287.2	936.8	784.3	897.8	350.3	1118.2	1109.2	1063.6	865.4	762.2	1209.4	834.5	1584.3	674.3	85.1	1575.7	461.4	126.9	286.7	332	527.7
4073	4529.1	3546.8	3130.9	4466.4	3228.2	3489.3	2582.7	4044.7	2023.3	2696.8	3530.2	2686.9	3707.7	1988.3	3329.4	3265.9	2225.3	2193.7	2211.2	1946	2700.5
1143.8	1654.7	1558.2	2292.2	1378.8	898.5	1430.8	1414.8	1501.1	1313.5	2048.5	1214.6	1026.5	1059	1303.6	1712.5	1168.6	785.4	253.7	1056.7	1142.3	946.1
1083.2	793.2	1156.2	1080.7	1048.1	1320.2	1423.7	174.9	2213.1	1067.4	682.4	1252	217.8	544	211.5	233.7	448.4	427.4	524.2	237.3	171.6	362.1
29773.8	30495.2	47095.3	31731.6	32348.7	27609.8	33872.2	22960.7	30265.7	32599.8	37196.6	23233	27902.8	21346.9	25433.2	15401.8	19189.4	18119.3	14951.9	12123.6	20744.6	21751.8
495.8	195.1	619.7	685	575.3	230.3	263.9	811.8	593.3	216.8	325.5	329.9	699.8	674.4	251.4	563	300	135.8	364.2	265.3	322.9	124.5
1332.5	847.4	2059.2	754.4	894.4	981.4	969.4	157.8	1511.7	1457.7	1558.9	885.8	1042.2	1026.4	561.4	1291.5	100.3	179.7	174.1	439.2	133.2	243.3
4091.2	4506.8	3223	3821.4	6768.3	3729.5	6271.5	3563.7	2931.6	5230.1	4429.8	3366.7	4604.1	3508	3003.7	6166.1	2944.2	3190.8	1299.2	3194.6	3788.8	2629.7
2094.8	2188.8	2585.2	1950.7	3218.3	2234.2	2650.3	2073.7	2237.7	2317.1	1531.9	2842.9	2548.7	2032.3	2772.5	1078.7	2981.2	1617.9	590.3	928.5	682.1	2043.1
1964.8	2677.4	1463.8	1376	1942.1	1807.8	1369.4	1953.2	2221.3	1814.6	1972.7	3172.2	2646.3	3077.8	1672.9	1869.5	2001.1	676	1451.1	1911.5	1149.4	774.3
10090.5	15128.9	15441.9	6443.2	11442.4	8139.5	12153	9726.9	13775.8	9843.5	11885.3	12387.6	8715.1	11382	9860.4	6391	2663.5	3088.3	2957.2	3300.4	2557.2	3224.3
1807	2939.7	2499.8	3617.4	3420	3159.4	2020.9	1542	4188.6	2028.6	1905.9	2048.1	2924.3	2032.1	2309.6	2209.6	1714.8	2356	2229.8	1465.7	1287.4	1525
1174.6	2059.1	1080.3	1687.4	1144.9	1461.9	1137.5	2358.1	1885.3	1112.7	488.6	732.5	1454	1109.3	1357.7	700.4	358.2	398.3	276.2	647.7	855.1	765.6
1585.1	1954.5	2339	3291.7	1592.7	2298.8	1988.4	1679	3416.6	2218.9	2103.5	1750.8	1069	986.1	304.9	1341.3	1395.3	624	1119.3	1613.2	873.5	700.1
778.8	1965.7	1552.2	753.9	1810.5	1195	1839.9	1119.5	2528.4	821.7	1926.9	1726.2	1608.1	1875.2	1509.4	1607.5	241.1	212	190.3	1175.5	932.6	1470.2
2807.1	3497	3108.3	3103.9	2559.2	2589.2	3230.2	2998.9	3958.9	1650.4	2995.4	3612.3	2516.4	3360.6	2101.4	1911.6	2776.9	1808.5	933.5	974	2477.9	3198.1
1558.6	2207.4	1877.2	1628.6	1859.8	1441.3	1755.3	1924.4	2562.4	990.2	2174.9	1982.8	1869.1	1926.2	1930.2	2526	1521	1166.5	588.4	695.8	1470.2	1753.4

1645.8	673.9	1788.6	400.3	2164.5	1113.3	1333.2	1487.6	2764.3	1005.3	1537.7	2048.5	1405.9	1660.4	703.1	1245.1	689.1	875	1147.1	151.1	229.8	300.3
1990.7	2323.8	4145.9	1791.5	1951.1	2699.2	2805.8	2282	3078.7	1959.3	1610.5	1863.2	1633.2	1589.6	1749.6	1291.2	1651	1032.6	268.6	1240.5	778.7	2469.3
1341.4	1436.9	1745.7	1163	1271	945.1	1166.5	955.2	1656.4	1084.4	496.6	1785.7	1434.9	1558.7	1013.2	2209.7	776.6	704.9	360.8	287.5	893.1	525.9
2445.2	2365.3	2376	2470.9	2283.6	1868.7	3614.2	2551.9	2464.2	1927.7	2928.3	3667.1	2037.3	2101.3	2791.2	2393.9	1190.7	1451.9	1665.9	2142.7	1972.8	2329.3
13166.6	14905	12108.7	9282.9	18927.8	15810.3	14509.1	9869.8	13730.6	11711.9	18301.7	12170.6	12873.5	10310.7	15828.7	12217.9	10001.1	6605.5	7047.4	6489.5	8149.4	10367.4
2913.3	2463.5	2131	2503.4	1884.1	1997.7	2657.4	2730.8	1862.5	1852.6	1622.3	1968.5	1729.8	1961.4	3141	2160	2067.7	863.7	459.9	2024.7	1741.5	2133.2
1551.6	2803.5	1279.6	1343	1230.7	1177.7	1603	1202.8	2248.7	1124.8	1697	2366.3	1979.3	1872.4	1936.5	1387.5	1791.9	1035.4	492.7	198.4	309.2	1088.5
2046.7	1763.6	1454.7	1886.3	1713.1	1075.6	1510	1613.6	2131.1	1176.3	1766.2	1689.2	2022.1	2126.1	1231.7	1325.4	1312.7	1030.2	325.5	1327.2	968.5	1404.1
4063.2	3184.8	6045.2	4263.6	4003.4	4110.5	4048.5	3463	5909.4	3731.3	4673.7	6456.3	3636	4344.3	2725.3	3657.5	2924.3	2448.6	2804.6	2329	2356.1	3256.2
14193.9	13028.7	10637.9	9441.1	7243.6	10736.7	13649.7	6772.7	17466.3	7581.8	16701.7	10360.8	12347.1	9321.1	13102.7	11566.7	7932.6	6305.5	6921.6	5301.5	7572.6	7713.8
4088.2	5009.7	2920.2	1124.6	1242.5	1382.1	2633.6	2434.1	2720	1988	1765.2	3211.4	2435.1	3411.4	3077.9	2220.9	1793.6	921.2	987.3	1375.2	1740.5	2189.4
1350.1	1271.2	1396.6	146.7	1186.8	1830.6	403.1	510.4	1255.9	620.9	1113	1335.2	1503.2	1513.8	1225.9	1305.1	480	570.7	1407.8	1015.7	169.9	154.5
1793.8	1425.4	946.8	829.5	1287.9	936.8	632	876.9	1287	845.8	1572.4	1184.9	1531	1679.5	1625.4	2007.6	515.7	186.8	227.2	923	1133.4	826.6
1314.8	2015.2	1587.8	1510.9	2212.7	1756.9	1705	2146.9	2511.9	1530.2	1792	2366.7	2828.4	2908.6	2323.8	2601.3	1374.5	363.8	691.9	1595.6	2454.6	2521.2
2777	2518.2	2878.1	2649.1	3639.2	2512.5	2997.4	3566	4423.4	2004.9	4053.2	3999.5	2177.1	3264.6	3162.9	5049.7	2298.1	678.5	951.6	3016.5	2552.4	2835.9
37122.7	40167.6	47140.8	42121.3	35807.5	38898.2	33178.6	26008.5	56845.9	43224.6	32868.9	43648.4	23447	40597.2	27639.6	34213.7	35561.7	21684.7	20734.5	31412.5	21944.1	29553.5
2938.6	4346.3	5938.8	4947.3	4586.2	5846.8	5127.5	2278	6257.1	3667.9	5373.9	4652.4	4201.5	4756	4438.2	2593.2	3420.4	2298.5	1880.9	3560.9	2971.6	3073
1883.1	1794.3	1179.6	998.8	1370.8	865.3	1216.1	1219.3	1714.4	1176.4	1073.5	1463	1772.1	1017	1147.8	1278.6	579.6	468.3	467.8	704.1	279.1	564.2
896.6	1999.5	1642.3	2615.1	1868.7	1941.6	1757.6	1868.4	2989.1	1804.4	2050.9	2495.4	1850	2437.6	2716.2	437.5	1747.6	1022.2	628.8	633.3	423.6	376
4962.9	4351.7	5040	5149.7	4170.8	3093.1	4827.9	2841.3	8012.7	2971.5	4468.1	5969.8	5102.3	5203.6	2462.8	4530.1	3635.5	2204.7	4343.6	2533	1898.8	3003.1
4010	3846.5	3871.7	3543.5	4442.4	3769.6	3265.9	3234	4189.6	2877.4	3739.4	3859.7	3796.7	3200.8	3861.2	4278.9	2715.6	2111.1	2878.3	2475.7	3090.5	2791.9
4968.9	4434	6182.4	4000.1	3595.2	4576.4	4473.7	3915.5	6389.6	3114	4085.8	4871.5	3872.2	4713.5	4435	5032.2	2924.1	2383.8	3107.7	5672	2844.4	4018.8
2346.7	3155	3472.6	2535.7	4316.6	3795.4	5468.8	3131.7	5808.3	2969.5	4206.1	3094.8	3819.7	3705.2	3660.6	2766.4	2992.8	1693.5	1239.7	2469.7	2491.1	3815.5
5826.6	6286.4	6227.6	4721.2	6771.4	6621.4	8960.8	3232.8	8278.1	5180	6685.2	5284	5381.8	4850.7	3387.3	5032.9	4138.5	4116.1	3267.1	4338.8	3114.8	5294.5
1962	2647.5	2112	1005.1	2731.9	1822.2	1840.1	1471.2	1954.2	1467.8	2098.9	1173.6	1560.3	810	977.9	1685.8	1370.2	1183.8	354.3	1161.5	1199.3	1344
2236.5	1973.3	1523	1417.6	1502.9	2180.3	1887.5	3004	3921.7	2044.7	3130.8	3035.4	3475.3	2284.1	2144	1548	1848.9	843.5	1119.6	1447.8	840.1	1341.5
3259	4126	2649.8	1726	3698	2439.5	2560.3	1930.1	5465	2016.2	4080.7	3987.1	3766.9	3522.1	2995.5	4818.9	3619	1982.8	2078	2482.6	2840	2581.8
1155.1	1329	1177.5	165.8	773.9	610.2	1009.1	196.3	1493.5	982.8	1092.3	1157	1104	1134.9	392.4	1221	571.2	193.2	655.7	842.1	298.9	350.8
12718.7	9720	12714.5	10716.1	20256.1	9242.8	16647.3	13912.5	11018.1	13588.3	18209.8	18319.1	29100.4	19956.9	10599.2	18679.7	8970.7	14199.9	3097.9	9953.7	14060.8	6648.1
1398.8	1218.4	1181.3	1020.1	878.9	867.4	729.3	801.8	1879.6	1026.4	1414.3	615	934.4	1329	619.2	1204.4	782.7	473.6	1075.8	696	536.1	327.9
4221.8	5008.2	4340.5	3240	3786.2	3206.4	4450	3103.3	6865.9	3437.5	5730.4	3760	3354.5	3394	3284.1	3267.7	4445.7	2015.1	292.8	2271.4	1863.5	3726.8
4292.8	4131.4	3843.4	2726.6	5799.2	5278	5880.9	3002.1	6827.5	5095.2	4489.1	4766.5	3333.1	3269.4	3693.1	3780.2	2222.2	2158.7	1506.8	2371.2	2299.4	3535.9
506.2	698.3	1302.6	888.1	1564.3	1719	1392.6	187.8	1327.5	910	1692.1	970	1217.5	840.8	470.9	362.3	562.8	404.2	268.4	414.6	559.7	282.1
1774.6	1580.6	1518.8	3386.7	2730.7	2059.2	2718.4	1017.1	806.8	1825.1	2099	1250.9	2342.3	1587	1487.5	3527.6	1033.9	842.6	159.3	695.8	995.5	696.1
42303.2	47783.1	56578.7	43031.3	34809.4	46132.7	44387.7	40502.3	37947.9	36266.5	35523.7	44960.5	39476	43761	30997.3	36029.7	22283.7	32561.4	20235.7	20333.3	25130.3	25590.3
2253	2442.3	2339.5	2623.4	2559.9	1806	2604.2	930.6	3710.5	2794.2	2201.1	1359.3	1969.4	1338.3	1329.3	2159.4	1314.3	982.4	609.9	276.1	623	238.2
1112.3	1742.6	1045.5	1329.7	1435	1968.7	1778	1401.7	1862.8	1378.7	1873.3	1854.7	1717.1	1581.1	1677.9	1767.1	429.7	446.3	1816.7	739.7	239.9	750.2
12627.4	14084.2	11752.1	11132.4	15454.1	9542.6	15130.8	7925.8	18934.7	11790.7	14514.8	13449.8	8541.4	12534.5	12286.7	14184.2	6515.8	3437.1	2795.2	8166.7	5086.8	6870.7
2082.3	2243.3	1811.5	1823.8	1938.9	1043.1	1588.7	1391.4	2252.9	1554.8	1575.2	2503.5	1996.1	1923.5	2213.7	2918.7	799.7	678.6	340.7	1015.8	1015.1	1291.4
1389.2	2157	1728.9	1929.2	2505.4	2011.9	2036.1	2154	2840.6	1869.6	2534.5	2145.6	2323	1976.3	1744.2	2066.6	1983	962.2	1761.8	2248	689	1655.8
3468.5	4295.5	2379.6	3742.5	4183.6	5142	4090.3	2436.5	5835.3	5346.2	3370.1	3535.8	2584.3	3380.8	3858.8	3593.9	1456.9	1103.1	2111.6	4505.8	1731.6	2528.7
1925.4	2206.3	2377.2	1239.8	1746.4	2208.9	1605.1	1426.9	1947.8	1733.6	1441.5	1648.1	1514.4	1775.1	1437.1	2469.6	1842.8	961.9	1949	577.3	1580.8	1382.6
866.6	1231.3	1558.1	300.4	1408.7	1203.7	746.7	973.4	1734.9	1160.4	988	1158.2	1170.8	1843.8	1668.3	656.3	892	302.2	330.3	194.5	1108.6	1121.5
1511.4	1864.5	1400.2	1876.6	2990.5	935.3	940.8	2408.3	2079.9	1955.3	1833.6	1129.1	2157.4	910.7	1340.1	1948.1	897.1	795.7	403.7	400.9	941	660.9
7596.6	7039.3	8577	6753.1	7625	6558.5	11349.2	5443.2	11588.8	7673.9	9147	3272.6	7308.7	3096.3	5928.8	6902.3	3009	3757.2	970	4674.4	5815.1	3655.9
634.1	642.2	730.5	92.9	512.3	718.3	681.4	203.1	1049.2	497.6	632.1	552.9	445.6	694	179.6	131.4	299.4	257.5	200	281.7	118.6	351.3
2262.7	2554.4	2112.9	2796.1	2273.5	1818	1625.3	1341.6	3332	1927.4	2748.9	2582.3	1347.6	2256.4	1379.5	2767	1732.5	795.8	584.6	1620.4	977.4	1034.9
2828.7	3301.1	2952.2	2580.5	4161.2	3406.2	3939.7	2970.3	4268	2326.8	3601.4	4874.4	3128.3	3134.3	2071.2	3956.7	2808.8	1287.5	887.1	1002.6	3310	2548.8
13919.8	13794.6	14610.8	15902.2	15491.7	16429.1	15362.9	6359.6	17190.8	12265.1	12409.5	14543.3	18210.9	13277.9	9455	19468.8	9221.9	7923	1831.7	10374.9	9083	5911.5
2164.4	2021.4	2191.8	1562.2	2046.4	2498.2	2870.4	1927.2	2883.4	1938.5	2436.9	1316.3	1751.9	1522.9	1382.9	1721.4	1409.1	782.6	711.5	2107.5	1338.6	1435.7
6579.3	5327.7	4440.2	4851.3	4323.3	3685.1	6312.1	4688.4	5462.9	5087.7	4914.6	2866.7	3932.8	4580.5	2851.8	4462.2	2996.4	4085.4	2597	2904.1	4350.4	3068.4
12672.2	14350.8	11880	12980.2	11185.1	15077.9	13526.4	13653.2	15319.3	15468.3	15503.7	11897.7	13927.6	14436.2	12267.3	12142	10137.8	4175	4837.7	13345.7	8198.1	9613.2

3258.5	2811.6	2017.8	1207.2	3334.9	2415	2442.8	2431.1	2095.2	2732	3398.6	1920.1	2915.1	3134.8	2944.5	3368.1	1300.2	1348.3	1646.6	1739.1	1780.3	1446
2570.1	2824	2353.9	1703.3	2424.2	1633.2	2426.7	1703.3	3114.7	2435.3	2640.5	2558.5	2210.9	2626.1	2375.4	2905.5	1471.5	1025.4	1106.4	1129.5	1468.4	1218.5
9594.1	9483	10038.7	11567.8	9752.3	9490.9	11126.5	5636.9	14497.1	8874.5	9980.3	8699.6	6858.8	8529.2	5881.3	11566.3	6041.9	4000.3	6254.8	7802	4719.3	6756.2
9301.5	8928.7	11944.5	6294.9	11552	8311.8	9586.8	7452.9	10765.3	7345.8	10539	11976.7	8623.9	8883.6	8198.6	11183.8	8757.3	4861.5	7438	6600	6591.9	6392.2
9095	10923.6	11988.3	8190	8565.4	10384.1	12545.1	12496.4	15226	6463.9	12887.3	13775.1	10190.9	13555.5	14394.1	7465.3	5042.2	4512.6	7936.8	5010.6	6331.2	6635.9
326.3	425.1	312.1	1017.9	264.9	165.4	943.3	197.1	413.6	515.5	403.6	575.7	206.9	556.6	225	438.2	211.2	68.5	225.9	126.6	136.2	112.6
1590.9	1684.6	1694.2	1596	1173.7	1076.8	1366.3	1398.2	1929.4	1046.6	1655.7	1448.7	1752.2	1216	953.8	1652.8	959.2	737.4	520.8	1140	1361.1	854.3
1256.9	1705.5	2138.3	1990.7	2205.8	1595.7	2050.4	1149.6	1557.4	1852.3	1331.5	2548.9	1056.7	1459.1	390.6	1533.3	840.7	320.6	163.2	1214.6	1487.4	1120.4
2293	2500.9	2664.7	1855.8	2217.6	2351.4	2469	1935	2487.5	1790.3	2299.3	1504	1804.9	1635	1787.7	2691.3	1730.2	711	2315.4	652.6	1021.6	1866.1
1741.9	1999.7	2288.7	2111.1	2009.6	2047.9	2758.3	1726	3451.3	1530.3	2010.3	2197.4	2540.6	2585.2	1669.7	2867.6	1251.7	855.2	806.9	2007.8	1936.8	936.7
2416.9	2897.2	2015.9	2247.2	2647.9	3086.1	2378.9	2377.4	2660.8	2164.3	3303.8	2801.1	2608.6	2572	2395.1	3092.9	1181.5	666.1	1077.9	1558.9	1429.3	1627.5
2064.6	1448.7	1505.9	2164.1	1110.1	835.3	1717.3	1207.3	2320	1142.8	1963.3	1461.7	1002.7	1274.9	468.1	1715.5	349.5	565.8	1184.4	2146.6	658.8	1259
3913.4	2038.3	2306.9	3197.9	2477	2942.9	3403.9	2861.8	3948.5	2986.1	1906	2866.6	4018.8	3190.2	3074.7	2805.5	3058.3	2491.6	2635.7	2879.3	2029.3	713.3
836.8	784.7	694.5	1456.1	681.5	614.7	737.6	671.5	1318.5	538.8	228.1	929.6	169.2	930.7	368.9	1054.6	719	96	175.8	216.3	108	739.7
2160.3	2667.8	3875.9	1373.9	2555.1	2520.6	2465.6	1378	2236.9	3017.3	2208.9	2231.4	1834.8	2009.3	1283.8	2749.4	1260.6	802.4	457.7	155.1	424.5	300.9
3958.2	5264.4	5017.3	4767.4	6261.5	5062.8	6139.8	4423.9	5215.6	5198.6	6724.6	5133	4294.6	5229.2	3343.3	8343.8	1857.3	1590.1	1424.2	160.3	1560.9	2244.3
3578.5	4657	4811.1	4817.7	5731	4518.3	3926.7	4404.3	5309.2	3245.7	3861.7	4355.9	4688.2	3314.6	3914.5	4959.3	2919.4	3243.6	3344.9	4940.9	2948.3	2712.9
2231.3	1685.6	2170.5	2033.2	2215.2	2125.7	2140.3	2227.5	2028.5	1623.7	1449.7	1917.4	2608.6	1978.4	1553.5	2963.3	692.4	1304.2	144.6	1105.2	1901.9	1148.2
4106	6992.3	5827.8	5054.5	6258.4	5049.8	5747.8	3053.4	6584.2	6025.9	6759.4	6831.9	5132	6364	4763.9	6149.4	3845.1	2934.1	3065.8	4377.5	2453.6	4567.9
4816.9	3268.9	3537.5	1491.8	3614.5	2644.9	4753	4656.6	7545.5	2056	4580.4	4219.8	3730.6	5089.8	4010.2	2942.6	3860.6	2638.8	3093.1	1521.5	1920.1	2718.1
2184.6	2251.5	1950.7	2786.4	2747.7	1594.5	2188	2282.5	2856.5	1900.6	2863.6	2409.9	2358.3	1836.9	2421.4	2229.3	1619	1410.8	1978.7	2269.4	1585.6	1382.2
3509.4	5418.7	6260.4	2495.9	1539.5	2143.8	2912.2	2437.4	3289.3	3390.4	2979.2	3320.4	2903.8	4096.8	3857.1	1905.9	1232	715.5	1108.5	1044.6	597.3	1187.6
2370.5	3069.2	3200.3	3433.2	2977.2	3002.5	2503.3	2247.8	2014.1	2793.6	3286.8	2325.4	2985.2	2065.7	2851.6	2285.1	1146.2	649.7	1036.5	1105.6	837.2	766.5
3712.6	3142	3824.6	2347.6	3419.6	2768.1	4967.2	2966.1	3977.7	2463	3411.9	5612.4	2795.8	5042.9	4025.5	5588.9	2377.1	2019.4	1007.8	2581.2	2425.3	2490.1
1909.4	1957.1	1321.7	839	935.1	866.5	2376.3	1138.3	2523.8	1350.1	1361.7	2834.4	2684.8	2385.2	873.1	2241.9	736.7	286	1343.2	771.3	518.7	1565
877.9	474.5	339.1	885.5	1002.7	774.7	528.2	683	983.4	631.4	952.3	768.4	1171.7	707.7	831.6	866.4	301.5	348.8	392.8	491.3	887	469.6
8195.4	10371.2	10420.9	11813.7	15506.6	14242.6	11503.9	9891.1	11233	10101.3	17067.4	8122.3	27316.8	6201.8	10630.3	14651.2	8073	6562.2	6098.9	7152.3	10855.7	5247.3
1289.5	1272.8	1033.3	1102.6	904.5	854.9	1662.8	1002.6	1773.7	1096.2	823.3	1108.3	1208.2	1651.4	875	901.6	1607.6	685.9	851.7	663.9	667.2	1058.5
1691.3	1566.5	1845.8	582.5	1327	579.2	1351.1	1209.1	1564.5	1546.7	439	1723.4	735.8	1629	519.1	1628.4	733.8	576.9	280.9	1188.7	1017.6	1481.7
4705.8	5996.7	6078.8	3079.6	2569.5	4891	4263.6	2529.7	3935.8	3267.8	4677.9	2763.6	2613.1	2792.5	2976.6	2725.9	2097.9	2326.6	1669.6	1379.2	1686.9	2518.8
30575.2	58878.9	31911.7	32048.9	36320.7	38264.3	45299.8	45781	52424.4	41683.7	55157.2	72152.3	59346.8	72985.9	41290.6	48147.6	37190.4	5612.9	16757.8	33274.1	19865.5	26350.6
2220.7	1664.6	1298	1078	1726.4	1425.4	1342.9	1757.3	1495.1	1702.5	2120.3	1305.4	861	1017.1	1316.2	1859.7	1878.7	963	549.9	475.9	717.2	1104.5
1111.6	1871.3	1294.5	1239.4	1465.7	909.1	1646.5	1091.1	1877.4	722.7	1453.5	987.6	756.3	1577.9	752.2	1470.7	1070.5	1009.5	238.9	521.2	1214.9	970.2
5480.8	5668.6	4503.8	4400.7	5291.7	5301	8998.6	4280.3	4747.5	6353.4	6109.3	5620.7	3831.3	7844.1	4721.9	5458	3542.9	1973.8	2196.1	3786.4	3001.7	4104.8
1425	1732.9	1526.5	1592.1	1942.9	2412.6	2387.2	1255.5	2545.9	1563.8	1465	2181.5	1476.1	1548.6	908.1	2206.1	1095.8	786.2	314.1	1016.6	917.8	1359
15419	13310.7	11680.2	17222.2	13970.3	15240.9	18135.1	13225.1	14204.6	14051.4	12219.3	14647.6	14322.6	15224.3	13915.8	11234.4	8627.7	7091.5	8055.8	6312.9	7685	6038.2
2560.9	1823.2	2241.4	2901.9	3160.6	2534.6	2303	2201.9	1596.1	2416.4	1936.5	1733.5	3096.4	2293.6	2471.1	3239.6	705.5	746.7	456.1	555.8	557.6	528.5
2660.7	2958.8	3225.3	3869.2	3716.6	2132.6	2828.7	1742.6	2856.5	2654.9	2982.9	3088.7	3059.5	2895.3	1661.9	3776.2	1696.3	1413.5	506.6	963.3	1876.9	1398.9
1628.6	1995.1	1481	1948.8	1310.4	1021.4	2673.8	1368	2311.1	1553.1	1741.4	1855.7	1932	1530.7	1384.2	1642.3	1155.8	1268.6	1052.5	256	1226	1675
221.2	1293.5	1317.4	211	1388.8	478.4	1111	602.1	1133.5	139.8	613.4	1063.4	781.5	229.5	1064.8	215.4	612.3	709.1	136.9	211.8	327.2	150.5
1908.4	2362.3	2540.4	1561.3	2743.4	1037.8	1804.9	1901.1	3275.3	1671.2	2420.1	2583.4	2256.1	2436.4	2641	2236.9	2829.3	1450.9	1898.7	721.9	1563.6	2233.6
6281.2	5024.7	6596.6	8798.4	5632.9	5244.7	7808.2	3986.5	4710.6	7109.8	5122.5	6125.7	6062.8	5911.2	4414	7149.4	2647.1	3241.5	901.2	2276.5	2721.9	2238.6
1863.4	1591.9	1736.2	1823.8	2139.2	1410.1	1908.2	1582.5	2467.6	1812.7	1141.1	1521.6	1528.5	1436.1	1554	2565.3	956.5	1051	719	502.5	1170.3	1340.2
1800.1	1873.3	1347.8	2026.7	1485.7	1007.4	1493	1386.9	1616.3	1622.7	1191.7	1695.5	1890.7	1565	1177.8	2117.5	1020.7	778.4	169	407.7	1082.3	736.5
3633	2899.1	2755.8	2814.2	5393.3	3564.8	3922.5	3885.5	3830.1	2495.7	3370.4	3517.2	3919.7	3137.8	2927.2	3587.2	2029.9	1673.4	1237.9	3114.9	1981.9	2425.7
12220.2	16406.3	14473	9031.5	8966.1	13222.6	20170.4	12365.9	26236.9	8587.4	10459.1	15650.1	13819.3	14833.5	12714.5	11515.4	7103.1	7000	8535.8	7063.6	5129.1	8577.2
4849.9	3984.7	4340.4	4060.1	3666.9	4058.4	4782.6	3137.9	6731.8	3821.7	4171.8	4987.4	4028.2	4177.4	2112.8	2797.3	3822.7	3930.5	4262.4	1920.3	2002.4	2857.4
3119.3	2595.4	3301.8	3454.3	2647.3	2756.2	3650.5	2434	3641.1	2772.9	3967.2	2214.1	2069.1	2783.2	2160.6	2799.2	1770.1	1781.7	1352.5	2813.1	1589.2	1309.3
2294.7	2238.3	2173.4	1351.4	2322.6	2193.9	2868.2	2242.4	2643.1	1764.9	1846.4	1555.8	1318.7	1917.3	1518.2	1962.5	1584.1	679.8	1202	1614.9	1904.5	2034.4
3458.1	2558	3843.9	1810.1	2614.1	3453	2145.7	1016.5	4714.5	1590.3	2666	4793.7	4082.7	3595.8	905.5	2949.2	1772.6	1539.6	2357.6	1469.9	396	1390.7
220	668.4	764.6	377.9	574.8	374.5	481.9	476.5	1259.4	925.1	391.1	584.5	584.8	877.9	665.5	553	178.5	637.7	270.2	397	166.9	228.3
2077.1	3020	5077.8	2196.7	2130.1	4116.8	2356.8	1655.5	2575.6	2581.3	2973.7	3037.8	2247.9	2302.7	1301.8	2876.6	1570.4	1150.7	278.1	345.5	369.7	797

5820.2	9606.1	7341.1	6910	3842.7	3534.4	6202.9	3966.6	7798.7	3120.5	4719.3	9242	4116.7	6750.2	4054.4	4204	6293.5	4612.3	1362	716.3	761.9	2208.7
4257	5775.8	8845	5196.7	8175.8	7173	7255.9	6476.5	8655.1	4797.8	5873.6	5564.9	2754.4	4410	3352.9	3228.2	4041.1	3521.4	1377.8	3377.9	2608.8	4154.3
1076.9	916.3	550	1164.5	990.5	630	715	1013.2	825.9	659.6	1395.5	983.9	807.7	954.7	1085.1	1265.6	624	425.5	122.6	886.8	525.3	617.4
1356.8	1115.6	1133.7	1685	1687.9	1536.5	1183.1	1549.2	1117.5	1185.3	473.1	1221.2	1208.9	1419.7	979	1598.6	986.1	529.2	149.7	1670.3	590.5	742
2924.1	2635.5	2235.3	1788.9	3343.2	2150.1	2252.6	2317.8	2612.5	2122.4	2771.2	2320.5	1813.6	2431.9	1296.7	3144.5	2318	1743.9	344.4	1022.5	1099	1179.3
1605.8	2128.1	1725	2122.1	1738.4	2385.7	1931	1509.4	2183.7	2580	1881.5	2817	3123.8	2160.6	1625	3966	1434.6	700.3	1632.4	1350.9	540.9	804.7
11929.6	13073.8	19347.5	14426.3	16545.6	12558.2	18325.6	17659.2	15218	14389.3	15376.3	13591.8	13436.7	12512.7	14964.8	9615.2	11704.5	12210.2	12423.2	7133.9	10845.3	10534.3
1890.2	2487.4	1866	1707.7	1772.3	1789.2	1953.3	1765.4	4203.2	2007.2	2834.7	1984.9	1586.9	2122.7	1918.9	2310.6	1311.9	494.4	295.1	1746.1	717.8	1187.4
1796	2755.4	1468.3	1590.1	1571.9	1481.7	2468.2	1399.2	2517.9	1184.9	1884.5	1618.7	2010.5	1784.6	2198.7	2138.5	683	435.8	685.7	105.2	768.6	872.7
8864	10148.1	12687.2	6677.3	11208.7	10235.4	9671.6	7615.2	9087.2	10048.8	7967.4	9714.4	8041.4	11261.9	9074.1	8348.2	8298.2	5354.1	5379.2	7109.7	5875.8	9714.2
2371.8	2976.8	1987	1494.3	2258.9	2323.4	2935.1	2119.7	2914.2	2529.7	2535.8	1366.6	1472.6	1252.6	1103	1244.1	858	1004.2	362.6	568.4	620.3	918.3
101851.9	99489.9	125651.3	113381.6	96863.5	92541.7	69521.9	84777.3	105605.1	106492.9	90183.4	102337	113428.4	98577.3	106527.3	90012.5	67869.8	69191.2	66013.6	61496.5	69061.1	63069.7
18195.4	18978.9	20165.1	14949.9	16591.8	13124.5	22433.7	15698.5	27040.2	15674.6	16128.5	14192.3	12642.9	16243	13282.4	15815.4	11861	12611.8	7943.7	7254	9672.5	13863.2
2234.9	2326.7	2453.4	1785.8	3256.4	1344.3	2507.9	2501.2	4023.8	1252.6	2419.6	2837.9	2840.3	2360	1846.2	3151	1787.4	1373.6	564.2	1616	1525.2	1331.3
1093.5	774.7	980.1	558.6	906.4	1016.9	807.9	498.3	1308.2	1024.6	463.7	665.5	351.4	669.9	718.5	474.1	673.2	564.9	412	595.7	571.4	663.1
13185.7	9486.7	11543.4	5556.1	4284.7	14031	10548.5	14760.7	13317	20073.9	5391.1	19410.3	15403.5	17345.2	5883	9087.2	12627.7	9289.9	2829.3	9205.9	5182.8	2635.9
503.8	329.6	726.8	709.7	436.5	395.1	698.4	318.9	585.8	303	104.3	745.9	356.5	438.1	250.2	156.1	595.8	48.1	179.2	205.3	64.8	101.9
23284.6	28910.4	33213.8	14821.3	13632.4	15890.9	22751.2	12540.5	30627.8	10566.4	25955.6	17490.2	11028.2	16876.8	15834.7	10456.3	12170.4	12369.8	13694.5	6451.2	13085	17760
9533.1	10671.4	9257.6	8199.8	10975.3	8994.1	10801	10150.2	15265.6	11288	8838	12368.7	12353	10180.5	8906.6	9818.8	13523.4	8253.5	6229.4	6394.7	5308.8	6722.1
2295.3	1980.4	2943.7	3222.1	2038.3	1435.5	1809.1	1276.8	3606.2	1329.6	1766.1	3054.5	1079.9	2366.2	1839.7	1312.7	1215.6	1089.6	1298.7	1540.8	1482.6	2038.8
19311	19451.5	23065.7	11162.4	23517.8	19881.5	23875.9	20447.9	20095.8	16441.6	17867.9	30035.5	23309.7	27337.2	18546.4	21245.9	12855.4	16044.4	9568	14507.2	17673.5	12810.2
3148.3	1686	1978.7	2133.3	2118.5	1552.2	2283.9	1195.1	2604.2	2549.4	3081.2	2034.5	1967.5	1630.4	1775	1569.4	1219.6	1089.5	838.7	474.8	1549.1	1390.1
3070.7	3918.9	5386.2	3903	4153	5523.4	6119.4	5022	4844.2	3723.8	6050.2	4289.4	6340.2	4172.6	3654.4	6521.5	2774.4	1945.3	2525	2933.6	4307.2	3977.4
2881.9	2869.4	3953.7	2713.3	4606.7	2827.1	2857.4	1920.4	3186.2	1720.4	1907.9	3723.4	1823.8	3143.7	1608.2	2428.1	1487.2	720.3	1132.8	588.5	529.5	1035
3730	2222.5	2768.1	3500.3	3381.7	2095.8	3554.8	3041.4	2802.2	2346.2	3193.6	2096.2	3069	2915.6	3075.4	2418.2	1701.2	992	908.2	2576.8	972.1	3265
6565.5	3560.7	7684.6	3731.2	3491.2	3406.3	3594.7	7586.5	3009	6013.6	4695.7	3795.8	2496	4585.9	4524.5	1187.4	2926.7	2395.7	1258.5	1651.9	2548.1	2204.1
1989.5	1347.3	1377.2	2090	1368	1310.8	1416.4	808.2	1988.7	1702.4	1587.5	1379.4	1471.6	1056.8	1527.6	1811.5	1259.2	1049.5	972.7	1588.8	1488.8	1040.7
2795	2378.1	1460.6	2441.1	1411.1	1384	1803.5	1831.6	2866.4	1804.6	3446.3	1367.4	2595.6	1778.4	1950.9	1873.3	1687.2	1037.6	2086.7	886.9	1369.3	1640.6
3077.8	3635.4	4401	2872.4	3124.6	2349.5	2055.1	1937.1	3890.8	3750.4	1971.3	3926.3	1994.2	3298.7	1804.4	3466.6	1803.6	1431.9	1373.5	145.6	1233.9	1417.9
938.9	616.4	624.8	1036.1	322.8	286.6	432.6	75.8	524.7	441.2	429.8	839	704.1	207.2	312.6	265.4	96.3	96.7	133.8	637.1	114.6	294.5
986	1277	1152.2	1398.7	1030.1	766.7	1105.5	937.7	1110.8	943.5	1784	1196.4	1303.5	1876.7	1000.4	1463.5	456.8	179.6	122.9	1425.7	540.6	656.9
812.4	1458.5	1129.8	845.3	1083.7	856.5	1002	1013.5	1364.1	976.7	1556.7	1347.7	1087.6	1470.4	852.4	794.5	655.5	623.1	265.9	304.7	633.1	932.5
2157.2	2605.9	2593.7	1525.3	2100.3	1558	2580.5	2180.2	2351	2613.8	1931.5	1811.3	1769.5	2108.8	1533.4	2050.3	1579.8	741.2	1187	1174.7	1328.8	2582.9
1644.9	1720.4	2540.3	2117.8	1503.1	2646	2255.9	650.6	3080.4	2313.5	2892.7	2219.9	663.2	1580.2	403.5	920	616.8	489.7	924.2	618.5	462.1	435.9
1812.6	1978.7	2231.5	1256.2	1674.9	1726.8	1994.5	1951.7	1092.7	2085.2	1977.8	1145.7	739.1	1245.7	1271.5	1143.2	1301.3	723.4	285.4	409.1	565.6	1382.3
1412.7	1569.2	1546	1746.9	1502.3	1555	1380	1261	2067.5	1222	1374.1	1706.6	1097.7	1692.1	1143.5	1741.7	1242.3	547.3	1170.7	244.5	535.5	1597.2
576	1123.5	460.2	1071.3	457.3	98.5	598.9	778.7	897.6	510.7	745.8	1374.4	1010.8	1056.4	614.3	637.6	724	24.8	155.4	123.5	104.1	71.4
473.6	524.8	984.5	663.3	488.6	845.9	713.9	567.8	679.7	745.9	576.1	1182	1312.6	529.5	959.1	993.1	699.1	122.9	166.2	290.5	670.2	488.8
1384.6	1796.7	1954.5	1298.4	1249	1364.6	1348.4	980.5	1603.5	1927.7	3032.3	1128.7	365.8	1401.1	1192.4	779.7	641.9	780.1	1021.4	614	350.6	507.1
2324.6	2166.3	3203	3333.7	2520.9	2421.9	2253.5	1886.2	2862.7	2007.2	1841.8	1992.2	2175.8	1148.2	1635	1232.4	1485.3	1146.9	721.8	1040.9	1305.5	1824.9
2158.2	1484.9	1403.1	1548.7	1694.9	1655.6	1242.1	1828	2500.7	1480	1835.7	1678.2	1743.6	1564.1	2212.2	2023.7	848.7	720.7	298.4	1857	1140.3	1869.9
1491	1329.7	456.2	1045.9	1127.1	988.4	1109.6	1399.1	1479.5	1178.9	1102.5	1494.1	1755.3	1067.5	1393.2	1526.7	1198.7	490.3	233.3	1273.7	762.2	423.3
1592.5	1604	1429.3	1668	1450.1	1651.5	1299.6	826.4	1568	1288.8	2397	1704.5	1483.5	1428.8	1638.1	1689	1000.1	468.9	387.5	1479.7	986.8	1446.2
7325.6	8783	11701.4	4311.8	8251.1	8280.4	8534	7588	5936.7	9321.1	6080.4	9329.7	8264	9765	6309.7	5100.6	4921.8	3736	2443.4	3141.9	2663.3	6688.9
2436.6	2873	1737.1	3892.8	2815.1	2714	1891.2	1949.4	3820.6	4801.9	4332.5	2353	6816.6	1994.6	4019.5	3798.1	2513.6	1068.1	721.6	2456.8	1607.3	1280
1808.8	1939.8	1442.7	2706.8	1346.3	701.2	723.3	1143.8	2111	1511.8	894.2	1258.4	1222.8	1454.3	1286.8	2110	1579	796.5	632	818.7	863.5	933.6
926.1	1741.5	1167.5	1085.6	1772.5	1255.5	1262	946.6	1391.5	1242.9	1627.8	1270	848.8	1376.8	1193	1781.5	848.8	500.5	504.4	547.8	676.9	934.4
1465.3	1412	1804.8	604.1	2101.2	1345.4	1792	875.9	1836.5	1602.3	1488.2	1220	2331.4	1840.4	1407.3	1804.1	1011.6	456.3	1223.4	1142.9	1097.2	1181.9
3700.6	3573.5	3302.1	2873.9	3126.7	3624.4	3830.1	2736.1	5752.4	2623.6	4711.3	4262.2	4077.4	3870.3	3784	3043.4	1721.7	1250.4	1200.9	1951	2087.8	2546.4
2609.3	3719.1	3638	2438.8	4117.4	3834.2	4646.9	2729.6	3606.4	3224.4	3688.8	3221.2	2926.3	3244.2	2924.7	3610.8	1934	1832.5	1608.2	1438	2698.3	2678.9
2038.3	2027.3	2217.8	1696.4	1817.3	1762.3	2041.8	1116.8	2003.2	1247.5	1264.5	1591.4	1773.3	1820.8	1040.6	1801.9	1085.8	811.5	1108.7	1136.5	658.8	1858.8

PSA7	PSA8	PSA9	PSA10	PSA11	PSA12	PSA13	PSA14	PSA15	PSA16	PSA17	PSA18	PSA19	Description
1855.1	1576.3	3071.3	2812.1	2666.6	2819	3833.9	2269.9	2157.4	1695.4	2101.1	1001.7	375.3	Consensus includes gb:BF663461 /FEA=EST /DB_XREF=gi:11937356 /DB_XREF=est:602144623
265.9	244	613.5	204.7	211.5	930.5	494.4	251.3	113.7	41.8	667.6	222.3	311.5	gb:BC002477.1 /DEF=Homo sapiens, clone MGC:3090, mRNA, complete cds. /FEA=mRNA /PRO
2002.1	2429	3272.9	2483.6	2518.6	2309.4	2028.2	2248.9	2955.1	1206.2	1625.9	907.7	796.3	Cluster Incl. W72694:zd68f10.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-345835 /clone_end=3
2630.7	1677.6	1576.5	1402.4	1967.4	1944.9	1220.2	2528.6	2265.4	561.4	1409.1	222.2	472.9	Consensus includes gb:W89120 /FEA=EST /DB_XREF=gi:1404482 /DB_XREF=est:zh69b03.s1 /C
8230.3	11780.5	16572.2	14776.2	8636.7	5435	20779.4	12482.8	20392.4	8164.2	12650.4	3309.3	8197.5	Consensus includes gb:AI445650 /FEA=EST /DB_XREF=gi:4289772 /DB_XREF=est:tj08g03.x1 /C
491.1	759.3	806.2	826.7	770.5	554	676.5	1487.8	1014.6	2130	934	649.2	1654.1	gb:BC002448.1 /DEF=Homo sapiens, Similar to actin binding LIM protein 1, clone MGC:1224, mRN
2261.1	1838.3	3763.6	3714.1	2118.4	3600	4139.4	3191.9	4073.6	2183.3	3340.9	678.2	473.7	gb:NM_004092.2 /DEF=Homo sapiens enoyl Coenzyme A hydratase, short chain, 1, mitochondrial
3532.7	4468.9	3469.4	5250.4	3087.4	4851.3	4406.6	6595.4	4253.7	10657.3	9611.3	1172.7	4852.5	Consensus includes gb:N25915 /FEA=EST /DB_XREF=gi:1140263 /DB_XREF=est:yx87a02.s1 /CL
1538.7	1589.8	2398.3	3294.6	1490.6	2056.1	3104.8	4313.4	2976.8	3994	5782.6	627.7	5183.5	Consensus includes gb:BF431488 /FEA=EST /DB_XREF=gi:11443602 /DB_XREF=est:7o14f01.x1
3670	4789.1	4982.5	8070.5	2858.7	5242.8	2681.8	4643.6	5602.2	754.2	786.7	815.1	302	gb:NM_004356.1 /DEF=Homo sapiens CD81 antigen (target of antiproliferative antibody 1) (CD81),
770.4	1063.6	1196.8	1939.7	1454.6	1385.4	1553.5	2719.8	1607	52.7	1021.6	1270	506.4	gb:NM_021805.1 /DEF=Homo sapiens single Ig IL-1R-related molecule (SIGIRR), mRNA. /FEA=m
723	1323.2	1243.4	1100.3	600.3	1389	1516.1	1701.8	1964.3	1962.5	1324.9	2342.8	1015.4	gb:NM_025092.1 /DEF=Homo sapiens hypothetical protein FLJ22635 (FLJ22635), mRNA. /FEA=m
1134.5	2061.9	1661.7	1414.6	762.5	1143.1	1796	1426.4	1947.4	2007.9	1158.3	288.8	623.7	gb:NM_012402.1 /DEF=Homo sapiens partner of RAC1 (arfaptin 2) (POR1), mRNA. /FEA=mRNA /
170	59.5	172.9	420.7	86.9	562.6	811.9	150.1	258	189.9	28	169.8	82.9	gb:NM_017490.1 /DEF=Homo sapiens ELKL motif kinase (EMK1), transcript variant 1, mRNA. /FE
1815.7	1563.2	3014.9	2109.5	2935.7	2935.6	3017.4	2903.3	2761.1	2092.4	2110.3	124.2	1363	Consensus includes gb:BE222618 /FEA=EST /DB_XREF=gi:8909936 /DB_XREF=est:hu49a11.x1
3999.5	3106.6	4143.4	4345.7	4696.4	4620.8	5180.3	7071.2	4745.2	2613.2	4061.1	951.2	1572.1	gb:BC004904.1 /DEF=Homo sapiens, nuclear RNA export factor 1, clone MGC:4612, mRNA, comp
4064.5	4754.9	5653.5	3861.6	3099.4	5980.4	3262.6	5652.5	3417.1	1481.7	1713.7	402.2	536.6	Cluster Incl. AI201594:qc02h12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1708487 /clone_en
401.4	271.8	823.1	1486.7	646.1	1266.6	417.5	699.9	785.6	617.1	487.4	89.9	994.7	gb:NM_006328.1 /DEF=Homo sapiens RNA binding motif protein 14 (RBM14), mRNA. /FEA=mRN
4778	1869.2	5474.1	3889	4764	3005.5	5529.3	6167.9	4603.2	735.8	1558	256.1	1197.2	Consensus includes gb:NM_001335.1 /DEF=Homo sapiens cathepsin W (lymphopain) (CTSW), m
2292.2	1750.2	2829.9	2396.4	3796.8	2531.1	3160.1	1903.2	1922.5	56.6	233.4	158.6	665.6	gb:NM_006747.1 /DEF=Homo sapiens signal-induced proliferation-associated gene 1 (SIPA1), mR
4407.2	4145.8	3956.6	4400.5	5970.9	3405.4	4793.7	8814.1	5749.5	2135	2586.1	1154.4	1445	gb:NM_004630.1 /DEF=Homo sapiens zinc finger protein 162 (ZNF162), mRNA. /FEA=mRNA /GE
3148.9	2236	3703.6	5687.6	4547.3	4406.7	2413.3	4278.3	2849.1	1372.2	90.2	280.9	334.5	gb:NM_005825.1 /DEF=Homo sapiens RAS guanyl releasing protein 2 (calcium and DAG-regulate
1375.8	917.4	1297.9	1244.6	556.3	1140.1	846.5	1154.9	853.3	38.3	827.8	260.1	246.4	gb:NM_005851.1 /DEF=Homo sapiens tumor suppressor deleted in oral cancer-related 1 (DOC-1R)
169.7	2870.7	3879.4	3145.7	3580.3	4669.8	2729.5	2684.9	2917.3	1734.2	2727.2	145.3	1834.5	gb:NM_006268.2 /DEF=Homo sapiens requiem, apoptosis response zinc finger gene (REQ), mRN
851.9	1209.5	1319.1	1281.3	956.8	1129.2	544	644.5	1048.9	256.4	1494	216.4	864	gb:NM_002105.1 /DEF=Homo sapiens H2A histone family, member X (H2AFX), mRNA. /FEA=mR
257.9	818.8	650.1	1912.7	587.4	1184.2	531.3	1128.2	654.5	1885.3	342.7	287.9	1295.3	gb:NM_001716.1 /DEF=Homo sapiens Burkitt lymphoma receptor 1, GTP-binding protein (BLR1), m
297	1165.7	1284.4	935.3	1105.9	600.5	2098.4	1505.1	1405.6	1515.7	1081.6	286	1575.3	Consensus includes gb:AA704766 /FEA=EST /DB_XREF=gi:2714684 /DB_XREF=est:zj34h05.s1 /
71.2	364.1	225.2	1730.5	241.1	1260	218.3	1148.4	143	257	757.4	448.5	133.3	gb:NM_014026.1 /DEF=Homo sapiens HSPC015 protein (HSPC015), mRNA. /FEA=mRNA /GEN=
9470.5	11946.9	9588.6	12387.2	10967.7	10208.1	10257.2	14312	10516.3	4743.2	13054.2	3004.8	2353	gb:NM_007273.1 /DEF=Homo sapiens B-cell associated protein (REA), mRNA. /FEA=mRNA /GEN
3393.6	4606.3	4525.7	6844.2	3771.4	5488.3	3194.2	8407.4	6506	2579	2242	309.9	2174.8	gb:NM_001242.1 /DEF=Homo sapiens tumor necrosis factor receptor superfamily, member 7 (TNF
249.1	1247.1	1785.1	976.8	348.1	1693.7	464.5	1308.6	1928.3	130.8	148.6	800.8	209.2	gb:NM_004426.1 /DEF=Homo sapiens early development regulator 1 (homolog of polyhomeotic 1)
11926.3	12708	18885.7	15423	15768.6	17077.7	9097	10194.7	6062.6	16027.7	10194.1	2191.2	9367.4	gb:NM_002831.1 /DEF=Homo sapiens protein tyrosine phosphatase, non-receptor type 6 (PTPN6),
586.3	2378.8	3117.8	3045.9	1103.6	3143.7	4006	4810.8	3306.7	696.8	3095.2	4185.2	3342.1	gb:NM_001273.1 /DEF=Homo sapiens chromodomain helicase DNA binding protein 4 (CHD4), mR
502.1	921.1	572.5	1203.6	541.7	499.3	955.5	1675.2	1060.5	1091.3	895.1	100.7	534	gb:NM_001975.1 /DEF=Homo sapiens enolase 2, (gamma, neuronal) (ENO2), mRNA. /FEA=mRN
1153.2	779.1	772.7	657.6	959.6	351	1633.8	731.8	719.3	883.3	957.4	928.6	1334.8	Consensus includes gb:AA772285 /FEA=EST /DB_XREF=gi:2824068 /DB_XREF=est:ai42d11.s1 /
748.6	1014.6	1077.3	333.3	753.1	339	1947.7	644.3	1279.7	601.2	1448.3	902.1	1347.9	gb:NM_024095.1 /DEF=Homo sapiens hypothetical protein MGC5540 (MGC5540), mRNA. /FEA=m
510.1	1526.5	2397.1	3612.4	343.4	3540.5	2217.8	3677.6	2731.7	4479.6	3274.3	501.8	2339.4	gb:BC004998.1 /DEF=Homo sapiens, Similar to membrane bound C2 domain containing protein, cl
2408.4	2378.6	2145.3	2556.3	881.5	2330	2484	3222.8	2784.3	1937.8	2475.8	108.1	2053.8	gb:NM_015416.1 /DEF=Homo sapiens DKFZP586A011 protein (DKFZP586A011), mRNA. /FEA=m
1114.9	1522.4	2140.1	2397.3	452.6	1920	437.5	1342.1	505.7	174.7	249.4	133.5	342.7	gb:NM_004818.1 /DEF=Homo sapiens prp28, U5 snRNP 100 kd protein (U5-100K), mRNA. /FEA=
1261.9	1618.9	2040	2064.2	2098.7	1412.3	1915.3	1693.8	2276.5	1269.2	2327.9	340.7	1956	gb:NM_014938.1 /DEF=Homo sapiens KIAA0867 protein (MONDOA), mRNA. /FEA=mRNA /GEN=
916.4	1466.4	1659.4	1157.5	1439.4	1578.7	1186.8	909.1	1199.1	1618.2	1147.4	787	2186.9	Consensus includes gb:D86973.1 /DEF=Human mRNA for KIAA0219 gene, partial cds. /FEA=mRN
2084.2	2915.6	2760.7	4610.7	3088.2	3277.4	4271.6	6558.1	7221.3	2696.4	4035.5	2116	1118.2	Consensus includes gb:BE969671 /FEA=EST /DB_XREF=gi:10582604 /DB_XREF=est:601679610
728.8	831.4	799	1591.3	432.2	1051.6	1050	1115.1	1460.9	39.6	379.2	761.8	88.1	gb:NM_016433.1 /DEF=Homo sapiens glycolipid transfer protein (LOC51228), mRNA. /FEA=mRN
1160.9	1216.7	585.4	730.4	864.1	1080.5	829.1	2046.2	1517.8	4273.6	4197.7	2403.5	5448.8	Consensus includes gb:AW117498 /FEA=EST /DB_XREF=gi:6086082 /DB_XREF=est:xd92e10.x1
1607.3	1940.1	2706.7	2771.3	1527.8	2139.9	2089.4	3415.9	2253.7	1355.3	2934.5	3446.1	2561	Consensus includes gb:AI347090 /FEA=EST /DB_XREF=gi:4084296 /DB_XREF=est:qp60d11.x1 /
1213.5	1403.8	1283.4	1638.3	1334.9	1754.2	1477	2404.1	2906.1	2053.5	1737.6	480.1	1203.5	Consensus includes gb:AU130523 /FEA=EST /DB_XREF=gi:10990877 /DB_XREF=est:AU130523
1474.4	1907.9	2007.7	2643.3	1200.8	2669.5	1842.9	2083.2	2561.5	1586.7	3613.2	2320.6	2475.2	gb:NM_015180.1 /DEF=Homo sapiens synaptic nuclei expressed gene 2; KIAA1011 protein (KIAA1
1592.5	1477.1	1669.5	1675.9	1642.4	1696.1	936.9	1323.7	1492	1364.6	1038.3	256.7	525.3	Consensus includes gb:S72422.1 /DEF=E2k=alpha-ketoglutarate dehydrogenase complex dihydroli
380.2	360.5	450.6	1653.2	412.5	1027.3	351.3	583.5	1081.4	1168.1	116.6	182.4	1765.1	Consensus includes gb:AW134608 /FEA=EST /DB_XREF=gi:6138154 /DB_XREF=est:UI-H-BI1-ab
3314.1	6038.8	4685.2	14459.2	5102	9441.5	6373.7	5898.8	7511.3	5325.5	2094.3	1747.7	3900.1	Consensus includes gb:X17115.1 /DEF=Human mRNA for IgM heavy chain complete sequence. /F

1410.1	486.6	998.8	886.6	608.8	869.1	1461.6	1760	1338.9	1026.2	654.3	1820.6	950.5	gb:NM_024892.1 /DEF=Homo sapiens hypothetical protein FLJ11700 (FLJ11700), mRNA. /FEA=m
2893.4	4949.1	3569	4684.6	4273.7	4508	3128	7365.3	5779	5398.6	6614.6	1255.9	5900	gb:NM_016337.1 /DEF=Homo sapiens RNB6 (RNB6), mRNA. /FEA=mRNA /GEN=RNB6 /PROD=
797.7	947.9	1328.4	1098.4	548.6	973.4	785.3	1413.5	1625.6	318.4	525.5	816.3	864.4	gb:BC006177.1 /DEF=Homo sapiens, Similar to metastasis associated 1, clone MGC:13258, mRN
219.7	190.3	495.5	485.5	144.3	188.2	155	170.4	164.9	307.6	128.4	446.5	271.3	gb:NM_002757.1 /DEF=Homo sapiens mitogen-activated protein kinase kinase 5 (MAP2K5), mRN
1066.3	1071.5	156.4	1309.8	940.4	647.3	1100.2	449.1	499.2	954.9	1382.2	271.2	255.9	gb:NM_021823.1 /DEF=Homo sapiens hypothetical protein MDS018 (MDS018), mRNA. /FEA=mR
593.3	615.9	925.5	1496.5	558.1	984.2	919.9	866.6	757.3	890.1	396.1	721	662.5	Cluster Incl. AA907940:ol24e02.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1524410 /clone_en
9839.1	6450.7	9912.1	8446.2	10191.3	10596.3	12516.9	11405.1	10504.8	12100.3	15285.6	3069.5	14759.6	gb:M13975.1 /DEF=Homo sapiens protein kinase C beta-II type (PRKCB1) mRNA, complete cds. /
1500	1577.6	2078.3	1596.6	3333.1	1760.7	2062.9	2703.1	1767	2656	2647.7	877.7	101	gb:NM_003807.1 /DEF=Homo sapiens tumor necrosis factor (ligand) superfamily, member 14 (TNF
1048.2	2406	1219.6	2068.5	2243.1	1883.4	1523.1	1925.1	1753.6	811.8	2067.6	180.6	611.6	gb:NM_024031.1 /DEF=Homo sapiens hypothetical protein MGC3121 (MGC3121), mRNA. /FEA=m
589.6	1298.2	1176.4	1068	1103.9	1400.2	1077	1100	1377.9	172.8	163.5	219.1	227.9	Consensus includes gb:NM_006662.1 /DEF=Homo sapiens Snf2-related CBP activator protein (SR
396	176.9	587.6	454.3	572.7	908.6	695.2	146.7	604.1	77.4	318.7	85.2	75.6	gb:NM_022744.1 /DEF=Homo sapiens hypothetical protein FLJ13868 (FLJ13868), mRNA. /FEA=m
890.8	754.5	1301.9	1268.2	690.1	1542.1	653.8	1427	563	122	1167.1	292.2	375	gb:NM_000294.1 /DEF=Homo sapiens phosphorylase kinase, gamma 2 (testis) (PHKG2), mRNA. /
3047.7	2002.3	2908.7	2373.3	3524.9	3374.5	2429.6	2357.8	2520.6	3939.6	2992.4	1532.1	2364.8	Consensus includes gb:AB011116.1 /DEF=Homo sapiens mRNA for KIAA0544 protein, partial cds.
412.7	475.6	1164.8	657.1	237.8	724.4	2465.3	2314.2	1625.2	1483.8	2093.9	239.1	455	gb:NM_002613.1 /DEF=Homo sapiens 3-phosphoinositide dependent protein kinase-1 (PDPK1), m
969.2	893.6	1034.7	899.9	1076	632.1	810.2	1569.7	520	601.4	401.8	561.6	171.7	gb:NM_024339.1 /DEF=Homo sapiens hypothetical protein MGC2655 (MGC2655), mRNA. /FEA=m
683.9	762.7	753.8	796	698.4	555.8	1606.8	804.6	807.4	1301	1507	113.5	1612	Consensus includes gb:AI871396 /FEA=EST /DB_XREF=gi:5545445 /DB_XREF=est:wl81f07.x1 /C
1508.3	936.8	1213.2	2036.2	1760.7	1768	980.3	924.6	230.9	205.7	128.7	229.8	120.9	gb:NM_024535.1 /DEF=Homo sapiens hypothetical protein FLJ22021 (FLJ22021), mRNA. /FEA=m
1165.8	1659.9	1758.7	2591	2358.8	2793.3	1858	2300.8	3545	787.5	869.8	82.3	739.7	gb:U85430.1 /DEF=Human transcription factor NFATx4 mRNA, complete cds. /FEA=mRNA /PROD
621.5	1508.9	1826.8	3598.2	571.9	1878.8	660.1	2938.2	1294.8	1839.4	3178.8	1429.9	1741.3	L41690 /FEATURE= /DEFINITION=HUMTRADD Homo sapiens TNF receptor-1 associated protein
1192.4	1037	928.4	1136.4	1659.8	1115.4	1849.3	830.5	2019.3	1669.3	1373.4	874.8	941.9	gb:NM_012091.2 /DEF=Homo sapiens adenosine deaminase, tRNA-specific 1 (ADAT1), mRNA. /F
206.4	309	765.2	1129.7	306.8	703.5	854.4	1148	862.6	72.8	207.6	165.2	149	Consensus includes gb:AI629033 /FEA=EST /DB_XREF=gi:4665833 /DB_XREF=est:ty79g04.x1 /C
1036.9	965.1	1107.4	2437.6	496.2	1515.9	1552.5	4517	836	212.4	837.8	396.4	443.1	gb:NM_014745.1 /DEF=Homo sapiens KIAA0233 gene product (KIAA0233), mRNA. /FEA=mRNA /
488	774	539.1	1497.1	851.2	1633.3	1100.3	1458.1	1420.2	78	802.8	149.6	130.2	gb:NM_003119.1 /DEF=Homo sapiens spastic paraplegia 7, paraplegin (pure and complicated auto
639	2055.8	2307.5	2035.8	2421.5	2340.8	1571.7	2407	2103.2	1910.2	1640.6	258	234	Consensus includes gb:NM_005200.1 /DEF=Homo sapiens cell matrix adhesion regulator (CMAR),
2440.1	3282.1	2355	2486.4	2038.1	2480.8	2614.7	3625.2	3594.6	260.6	1415.7	1207.4	310.7	gb:NM_000485.1 /DEF=Homo sapiens adenine phosphoribosyltransferase (APRT), mRNA. /FEA=n
225.3	134.4	128.7	803.7	201.9	360.9	168.5	929.1	199.3	438.9	374	236	1939.1	gb:NM_005679.1 /DEF=Homo sapiens TATA box binding protein (TBP)-associated factor, RNA pol
2157.3	3102.5	4238.5	3547.2	1200.5	3366.9	855.7	1059.5	1269.7	613.4	660.9	137.6	207.1	Consensus includes gb:Y15724 /DEF=Homo sapiens SERCA3 gene, exons 1-7 (and joined CDS) /
104.2	326.2	456.4	891.3	87.1	649.6	616.5	1027.4	590	131.6	806.4	1264	852.2	gb:NM_013337.1 /DEF=Homo sapiens translocase of inner mitochondrial membrane 22 (yeast) hon
292.9	136.7	575.3	1047.9	466.7	532.5	326.3	1031.1	277	941.8	90.5	296.7	133	gb:NM_015670.1 /DEF=Homo sapiens sentrinSUMO-specific protease 3 (SENP3), mRNA. /FEA=m
365.2	1444.8	1192.6	1857.4	740.7	1100.2	444.3	1971.8	1119.9	181	857.9	174	554.5	gb:NM_014185.1 /DEF=Homo sapiens HSPC165 protein (HSPC165), mRNA. /FEA=mRNA /GEN=
273.5	341.4	1100.3	1067.5	640.1	928.2	1096.7	790.4	424.8	735.5	577.6	139.9	207.4	gb:NM_004937.1 /DEF=Homo sapiens cystinosis, nephropathic (CTNS), mRNA. /FEA=mRNA /GE
1284.2	2185	2480.3	3127.2	2004.7	2884	1463.9	2462.5	2071.6	2918.8	1519.3	1233	491.5	gb:NM_006445.1 /DEF=Homo sapiens U5 snRNP-specific protein (220 kD), ortholog of S. cerevisia
1493.6	1314.5	2885.1	2245.1	1161.9	1507.4	1105.5	1198.2	243.9	420.1	363.4	126.7	469.1	gb:NM_005173.1 /DEF=Homo sapiens ATPase, Ca++ transporting, ubiquitous (ATP2A3), mRNA. /
740.1	1065.4	1364.4	1607.4	1243.1	374.5	1295.5	1554.1	1251	1870.5	1623.2	124.3	954.6	gb:NM_025099.1 /DEF=Homo sapiens hypothetical protein FLJ22170 (FLJ22170), mRNA. /FEA=m
858.7	2035	1561.6	2643.2	764.5	3024.8	776.9	4380	1377.3	895.1	1912.9	538.5	542.2	gb:NM_020360.1 /DEF=Homo sapiens phospholipid scramblase 3 (PLSCR3), mRNA. /FEA=mRNA
203.1	471.9	1248.6	766.5	472.3	304	366	485.2	133.8	153.8	53.3	54.8	34.6	gb:K03199.1 /DEF=Human p53 cellular tumor antigen mRNA, complete cds. /FEA=mRNA /GEN=T
975.5	2202.5	3251.5	3137.5	1312.2	3031.1	2399.5	3036.3	1980.6	748.3	176.2	138.5	41.9	gb:NM_014680.1 /DEF=Homo sapiens KIAA0100 gene product (KIAA0100), mRNA. /FEA=mRNA /
695.1	1012.1	348.9	716.4	1026.8	1466.7	1375.7	645.8	1265.4	138.1	2016.9	489.6	711.6	Consensus includes gb:AL514271 /FEA=EST /DB_XREF=gi:12777765 /DB_XREF=est:AL514271 /
223.7	134	179	465.9	228.6	250.3	243.8	775.2	251.1	351.8	139.9	125.3	83	gb:D79984.1 /DEF=Human mRNA for KIAA0162 gene, complete cds. /FEA=mRNA /GEN=KIAA016
18348.4	12773.8	23807.8	14375.2	25638.4	17790.8	16583.9	15087.6	23649.1	9348.1	10663.5	1735.6	8638.1	Consensus includes gb:AA634272 /FEA=EST /DB_XREF=gi:2557486 /DB_XREF=est:ac75h05.s1 /
126.4	186.3	179.5	548.2	212.5	157.3	367.7	169.5	266.8	180	139.2	170.7	152.9	Consensus includes gb:X03363.1 /DEF=Human c-erb-B-2 mRNA. /FEA=mRNA /DB_XREF=gi:311
103.9	378.1	237.6	1818	161.1	207.2	64	766.8	786.1	115	211	600.1	57.7	gb:BC003629.1 /DEF=Homo sapiens, clone MGC:2854, mRNA, complete cds. /FEA=mRNA /PRO
3058.3	2221.4	2981.7	3349.9	3297.6	2036	3542.1	2941.1	3197.5	2766	1241.5	2789.2	673.2	gb:NM_013351.1 /DEF=Homo sapiens T-box 21 (TBX21), mRNA. /FEA=mRNA /GEN=TBX21 /PR
1563.1	513.2	1582.8	1632.9	628.4	2559.5	572.8	2597.8	392.5	390.7	267.9	1206.4	994	gb:AF308302.1 /DEF=Homo sapiens serologically defined breast cancer antigen NY-BR-96 mRNA,
919	1216.5	592.4	2042.6	680.2	1940.8	470.6	1412.7	955.9	2437.2	1127	1715	984.2	gb:NM_000626.1 /DEF=Homo sapiens CD79B antigen (immunoglobulin-associated beta) (CD79B),
2759.8	2138.8	2520.3	2427.8	3900.4	2942.4	2790	2704.5	1907.2	3228.2	3698	1606.2	1367.4	Consensus includes gb:BF971923 /FEA=EST /DB_XREF=gi:12339138 /DB_XREF=est:602240326
817.3	1571.5	2243.7	2484	248.2	1656.6	229.7	2102.8	844.9	765.1	716.9	609.4	95.8	gb:NM_016286.1 /DEF=Homo sapiens carbonyl reductase (LOC51181), mRNA. /FEA=mRNA /GE
384.5	340.6	1149.1	592	539.1	128	1019	975.2	903.3	1687.8	1402.8	789.5	848.9	gb:NM_002359.1 /DEF=Homo sapiens v-maf musculoaponeurotic fibrosarcoma (avian) oncogene f
1437.6	731.3	1002.8	1431.2	1342.1	1477.8	1099.5	2516.4	1018.5	173.9	1173.1	509.4	181.5	gb:AF142408.1 /DEF=Homo sapiens cell division control protein septin D1 mRNA, complete cds. /
332.5	504.8	1036.7	971.3	1034.5	1561.5	1395.5	784.5	663.2	217.1	493.7	323.6	46.9	gb:NM_024957.1 /DEF=Homo sapiens hypothetical protein FLJ22686 (FLJ22686), mRNA. /FEA=m
1628.2	776.2	3937.8	1521.8	2373.4	2228	1380.9	987.2	1268.3	191.7	496.9	745.1	160.5	gb:NM_000152.2 /DEF=Homo sapiens glucosidase, alpha; acid (Pompe disease, glycogen storage
646.4	1480.7	1472.1	1834.4	61.8	1332.4	1870.4	1360.1	1670.9	167.1	1084.9	219.2	165.4	gb:NM_014593.1 /DEF=Homo sapiens CpG binding protein (CGBP), mRNA. /FEA=mRNA /GEN=C

850.3	738.3	453.5	792.1	481.8	376.9	403.4	1253.8	551.2	1024.3	1195.9	671.5	275	Consensus includes gb:BE671156 /FEA=EST /DB_XREF=gi:10031697 /DB_XREF=est:7e46f09.x1
498.1	963.7	1882.5	1810.6	1068	1590.6	469.5	1894	377	366.5	1421.6	375	551.7	gb:NM_016573.1 /DEF=Homo sapiens Gem-interacting protein (LOC51291), mRNA. /FEA=mRNA /
148.3	547.2	885.2	1232.8	159.6	844.5	180.2	1510.8	441.4	481.4	915.7	1897.9	839.2	Consensus includes gb:BG252853 /FEA=EST /DB_XREF=gi:12762669 /DB_XREF=est:602365438
2610.4	1427.5	2421.9	1963.5	2718	1898.2	1253.7	1746.1	1122.9	1136.9	198.2	258.4	111.8	gb:NM_004720.3 /DEF=Homo sapiens endothelial differentiation, lysophosphatidic acid G-protein-c
6205.5	6044.3	7493	9845.7	10218.7	12619.9	5909.2	10586.8	6182	8906.1	7982.8	8917.6	13184.8	Consensus includes gb:AB011093.1 /DEF=Homo sapiens mRNA for KIAA0521 protein, partial cds.
1170.9	1170.9	1687.3	1743.1	1302.1	1757.8	1441.7	2039	1335.1	481.2	1159.9	362.6	728.4	Consensus includes gb:BG258639 /FEA=EST /DB_XREF=gi:12768455 /DB_XREF=est:602380357
405.8	945.6	1029.3	1807.8	282.9	1602.6	202.8	860.5	1041.2	109.1	71.7	145.4	119.6	gb:NM_004868.1 /DEF=Homo sapiens glycoprotein, synaptic 2 (GPSN2), mRNA. /FEA=mRNA /GE
881.4	921	1308.8	1476.1	1627.9	1035.9	1400.5	1305.9	1546	273.3	616	198.1	301	gb:NM_005035.1 /DEF=Homo sapiens polymerase (RNA) mitochondrial (DNA directed) (POLRMT)
3244.6	2365.9	4331.6	2860.3	4693.8	3285.6	2374.4	2542.3	1797	1218.9	2582.7	528.1	1385.8	Consensus includes gb:AB011133.1 /DEF=Homo sapiens mRNA for KIAA0561 protein, partial cds.
8415.2	5762.1	6970.2	4004.5	8882	6895.2	10796.3	6123.6	8833.5	8012.3	6775.6	1529.2	3892.8	Consensus includes gb:BF718610 /FEA=EST /DB_XREF=gi:12019523 /DB_XREF=est:KEST81 /C
1676.7	1695.3	1642.7	2211.9	2176.7	1810.2	1276.9	1499.6	878.6	62.2	219.2	272.4	330.6	gb:NM_001319.2 /DEF=Homo sapiens casein kinase 1, gamma 2 (CSNK1G2), mRNA. /FEA=mRN
352.5	222.3	191.3	190.9	187.7	204.2	145.9	841.9	244.8	820.7	88.1	838.9	610.2	gb:NM_005597.1 /DEF=Homo sapiens nuclear factor IC (CCAAT-binding transcription factor) (NFIC
211.4	1357.8	1842.2	954	1016.1	909.7	86.9	112.4	1061.2	91.2	95.8	103.2	90.2	gb:BC002492.1 /DEF=Homo sapiens, hypothetical protein FLJ20244, clone MGC:1066, mRNA, con
721.4	1322.6	2317.4	2059	2061.5	1950.5	895.2	2547.9	1353.3	303.7	814.1	219.5	454.8	Cluster Incl. AI660497:we67h06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2346203 /clone_en
2135.4	1507.3	1955.7	2241.5	543	2259.9	401.7	1648.9	1480.4	147.6	688.8	1765.7	859.1	gb:BC003086.1 /DEF=Homo sapiens, hypothetical protein FLJ20011, clone MGC:1080, mRNA, con
25441.3	27201.4	29274.3	26883.2	25799.1	32403.7	20367.1	54331.3	27571.8	10475.1	12438.2	2993.1	11959.4	Consensus includes gb:AI004246 /FEA=EST /DB_XREF=gi:3213756 /DB_XREF=est:ou03g06.x1 /
3138.2	3457	4877.5	3551	3311.1	3875.4	2121.6	3042.5	2165.7	1462.7	1060.3	609.8	1831	Consensus includes gb:BF062886 /FEA=EST /DB_XREF=gi:10821796 /DB_XREF=est:7h71f04.x1
419.9	289.2	583.4	569.5	540.7	443.6	1180.3	769	643	188.9	52.5	96.3	108.2	gb:NM_012346.1 /DEF=Homo sapiens nucleoporin 62kD (NUP62), mRNA. /FEA=mRNA /GEN=NU
465.7	358.3	354.9	893.2	531.7	359.6	898.4	850.9	564.3	242.1	1117.6	207.2	163.4	gb:NM_014347.1 /DEF=Homo sapiens zinc finger protein (ZF5128), mRNA. /FEA=mRNA /GEN=ZF
1564.4	2188.9	2074.8	2450.5	2457.9	2815.6	2370.9	2811.9	2789	1810.9	1847.5	1497.3	1679.1	Consensus includes gb:AA744529 /FEA=EST /DB_XREF=gi:2783293 /DB_XREF=est:ny79a04.s1 /
1837.2	2271.9	2501.9	2247.8	1977.3	2931.5	1787.5	2859.1	2822.3	269.3	1569.1	348.8	322.1	gb:NM_004596.1 /DEF=Homo sapiens small nuclear ribonucleoprotein polypeptide A (SNRPA), mR
2653.3	3989.5	3088.6	4203.6	2772.9	2938.6	3389.8	3287.2	3078.9	872	2063	2969.6	1327.5	gb:NM_003089.1 /DEF=Homo sapiens small nuclear ribonucleoprotein 70kD polypeptide (RNP anti
1784.2	1878.8	2856.8	2815.5	2133.3	2082.4	3700	2970.7	1910.2	66.7	518.5	1502.4	336.2	gb:AF309082.1 /DEF=Homo sapiens protein kinase D2 mRNA, complete cds. /FEA=mRNA /PROD
3599.4	3528.6	5363.9	4820.4	3296.6	4352.1	4582.5	5276.4	3091.3	1664.3	1161.5	671.6	1110.6	gb:NM_000175.1 /DEF=Homo sapiens glucose phosphate isomerase (GPI), mRNA. /FEA=mRNA /
407.6	297.9	979.6	1663.1	845.1	344.2	1961.7	1142.5	1134.3	1532.9	149.4	1266.5	63.1	Consensus includes gb:BF110434 /FEA=EST /DB_XREF=gi:10940124 /DB_XREF=est:7n52h07.x1
999.3	1043	1368.7	2964.7	926.9	1259.3	1176.8	1118.2	1510.2	860.7	602.4	1845.6	1027.2	gb:NM_003121.1 /DEF=Homo sapiens Spi-B transcription factor (Spi-1PU.1 related) (SPIB), mRNA
3044.6	2039.9	1637.4	3085.8	1812.7	1920.5	2487.2	1797.1	2179	383.3	1252.5	382.8	681.5	gb:NM_001571.1 /DEF=Homo sapiens interferon regulatory factor 3 (IRF3), mRNA. /FEA=mRNA /
360.8	385.3	782.8	692.4	396.3	490	347.9	569.2	293.1	99.9	92.2	461.5	558.8	gb:NM_003422.1 /DEF=Homo sapiens zinc finger protein 42 (myeloid-specific retinoic acid- respons
5580.8	11749.5	12670.8	16340.7	7862.8	3624	17356.6	11827.6	20757.6	834.8	4325.4	1667.3	906.4	Consensus includes gb:NM_005601.1 /DEF=Homo sapiens natural killer cell group 7 sequence (NK
564	821.5	356.5	636.5	221.9	814.6	1219.5	1589.1	878.2	331.3	123.5	373.8	160.3	gb:NM_000234.1 /DEF=Homo sapiens ligase I, DNA, ATP-dependent (LIG1), mRNA. /FEA=mRNA
3058.9	2784.3	3826.8	3832.4	2127.4	2161.1	2044.1	2337	1987.6	855.8	854.1	604.9	93.6	gb:NM_005762.1 /DEF=Homo sapiens KRAB-associated protein 1 (TIF1B), mRNA. /FEA=mRNA /
2614.3	2233.2	3338.7	4954.2	1541	3911.9	3152.7	4391.7	3572.7	1172.6	1309.7	106.1	843.5	gb:NM_000701.1 /DEF=Homo sapiens ATPase, Na+K+ transporting, alpha 1 polypeptide (ATP1A1)
146.1	166.3	170.5	244	127.6	188.5	509.6	777.2	257.2	89.3	143.1	77.9	107.7	gb:M58581.1 /DEF=Human carnitine palmitoyltransferase (CPT1) mRNA, complete cds. /FEA=mR
766.9	794.2	928.5	594.3	818.3	464.5	1979.8	1810	2039.1	662.3	1562.2	1169.4	976.3	gb:NM_003243.1 /DEF=Homo sapiens transforming growth factor, beta receptor III (betaglycan, 30
25149.2	13250.1	22233.8	21529.6	25904.5	21386.7	21982.4	25063	19004.4	29059.9	34429.1	7450.9	24285.3	Consensus includes gb:AA806142 /FEA=EST /DB_XREF=gi:2874892 /DB_XREF=est:oe29d06.s1 /
1073.8	806.7	1080.3	945.5	271.7	242.7	1222.9	1911.7	1392.3	2149.4	1684.7	211.6	842.9	Consensus includes gb:BG403834 /FEA=EST /DB_XREF=gi:13297282 /DB_XREF=est:602419675
467.9	371.5	479.8	360.5	567.5	494.3	1358.7	684.1	605.1	120.9	789.7	58.7	38.5	gb:NM_023923.1 /DEF=Homo sapiens hypothetical protein FLJ13171 (FLJ13171), mRNA. /FEA=m
4592.4	7591.4	6734.2	13465.6	4639.6	6563.2	4761.5	11140.5	10622	9233.2	13130.6	2666.8	10544.9	gb:NM_005356.1 /DEF=Homo sapiens lymphocyte-specific protein tyrosine kinase (LCK), mRNA. /
1265.5	780	749.7	1397.1	1067	1345.8	1560.1	775.5	1387.2	1022.5	1629.6	119.3	239.3	gb:NM_003790.1 /DEF=Homo sapiens tumor necrosis factor receptor superfamily, member 12 (tran
247.8	754.9	1353.5	1822.9	1572.6	1877.4	1115.6	1364.2	906.8	122.5	852.6	1888.7	1294.2	gb:NM_002744.2 /DEF=Homo sapiens protein kinase C, zeta (PRKCZ), mRNA. /FEA=mRNA /GEN
1913.5	2771.2	2674.5	3506	1852.7	3040.5	1322.8	3359.9	5111.7	277.3	1333.5	340.1	766.6	Consensus includes gb:AL545035 /FEA=EST /DB_XREF=gi:12877516 /DB_XREF=est:AL545035 /
1007.9	1238.3	1189.6	1773	1676.7	1529.1	1061.3	531.6	1906.5	65.5	160.5	120.8	1177.9	gb:NM_004753.1 /DEF=Homo sapiens short-chain dehydrogenasereductase 1 (SDR1), mRNA. /FE
603.2	457.9	783	1162.8	676.4	936.8	799.8	833.8	536.7	149.7	40.8	105.2	67.8	gb:NM_005341.1 /DEF=Homo sapiens GLI-Kruppel family member HKR3 (HKR3), mRNA. /FEA=m
1477.2	1733.6	1282.3	1013.8	939.2	1307.7	1477.1	2087.6	1307.4	1324.1	1227.2	1818	1275	gb:NM_014179.1 /DEF=Homo sapiens HSPC157 protein (HSPC157), mRNA. /FEA=mRNA /GEN=
2330.9	2613	3176.9	3971.1	2530.4	2152.4	5338.7	3579	4118.8	4201.4	6274.9	3577.9	4934.4	Consensus includes gb:AA541630 /FEA=EST /DB_XREF=gi:2288064 /DB_XREF=est:ni99e01.s1 /
72.5	168.6	430.4	417.3	216.9	587.4	341.7	165.9	97.9	69.7	370.8	208.5	217.1	gb:NM_022089.1 /DEF=Homo sapiens putative ATPase (HSA9947), mRNA. /FEA=mRNA /GEN=H
999.5	1426.8	1489	1473.8	1681.8	1412	397.9	2541.8	1901.2	1560.6	1098.2	1847.3	1596.3	Consensus includes gb:AL582804 /FEA=EST /DB_XREF=gi:12951151 /DB_XREF=est:AL582804 /
1783.7	1377.3	2188.9	2220.4	2131.8	1926.5	1886.4	2886.3	2328.6	1502.9	3358.6	285.1	1562.8	gb:NM_003993.1 /DEF=Homo sapiens CDC-like kinase 2 (CLK2), transcript variant phclk2, mRNA.
2716.7	10850.5	7418.6	14290.1	3621.4	6169.6	6122.6	13970.4	10287.9	5404.9	3935.3	2452.6	2878.1	gb:J04132.1 /DEF=Human T cell receptor zeta-chain mRNA, complete cds. /FEA=mRNA /PROD=T
1730.4	853.8	1706	1470.5	1277	1672.6	1650.7	2022.5	1645.2	98	1686.7	285.6	953	gb:NM_015726.1 /DEF=Homo sapiens H326 (H326), mRNA. /FEA=mRNA /GEN=H326 /PROD=H3
2792.4	2143.5	3161.9	3473	2170	2860.5	3516.2	2399.6	4040.7	2382.4	2152.7	1466.7	2292	gb:NM_003874.1 /DEF=Homo sapiens CD84 antigen (leukocyte antigen) (CD84), mRNA. /FEA=m
6240.5	7887.6	7302.1	10941.4	7712.9	10070.9	7515.8	9441.2	11278.6	9421.9	7794	2999	12067.1	Consensus includes gb:AI084226 /FEA=EST /DB_XREF=gi:3422649 /DB_XREF=est:oy72g09.x1 /

1330.8	1179.5	1803.7	2074.2	1634.8	1435.3	2357.1	1672.3	2760.8	1146.7	1406.1	678.9	763.7	gb:NM_017773.1 /DEF=Homo sapiens hypothetical protein FLJ20340 (FLJ20340), mRNA. /FEA=m
820.2	1034.3	1225.9	1494	982.6	792.4	2167.8	2070.1	3035.9	1258.2	554.7	312.9	101.5	Consensus includes gb:AB007958.1 /DEF=Homo sapiens mRNA, chromosome 1 specific transcript
4322.2	8588.5	6687.3	7116.5	5915.4	5542.5	5019.5	8425	7036.4	4461.1	5972	2203.2	2777.6	gb:NM_021873.1 /DEF=Homo sapiens cell division cycle 25B (CDC25B), transcript variant 3, mRN
6339.6	7578.2	6839.1	7775.9	6022.3	8569.6	6367.8	9237.3	7885.1	2329.7	2443.6	1384.9	1145.4	gb:AF141349.1 /DEF=Homo sapiens beta-tubulin mRNA, complete cds. /FEA=mRNA /PROD=beta-
6573.5	4302.3	5741.7	4702.5	6570.3	4572.2	5526.3	3553.4	5404	2669	6049.9	1621.1	619.3	gb:BC000213.1 /DEF=Homo sapiens, ring finger protein 24, clone MGC:1815, mRNA, complete cds
181.3	217.9	47.6	478.5	266.6	187.5	129.1	254.5	195.5	138.3	42.7	156.4	60.8	Consensus includes gb:AI810484 /FEA=EST /DB_XREF=gi:5397050 /DB_XREF=est:wb89b11.x1 /
425.5	1462.7	866.4	1130.9	360	1053.4	416.3	1708.1	875	855.5	321	170.9	471.3	gb:NM_001247.1 /DEF=Homo sapiens ectonucleoside triphosphate diphosphohydrolase 6 (putative
432.9	1005.8	1010.5	1806.4	926.8	1046.8	391	1587.5	643.2	1492.9	1582.1	209.7	1029.3	Consensus includes gb:AB020630.1 /DEF=Homo sapiens mRNA for KIAA0823 protein, partial cds.
515.3	819.7	2167.7	1666.8	1832.4	1595.5	1989.4	1583.8	1170.2	557.7	938.7	174.4	647.8	gb:NM_015937.1 /DEF=Homo sapiens CGI-06 protein (LOC51604), mRNA. /FEA=mRNA /GEN=L
1394.4	1295.8	707.5	1514.5	2037.8	1217.1	1578.6	1254.8	1858.8	201.5	783.8	1667.3	941.7	Consensus includes gb:AL022394 /DEF=Human DNA sequence from clone RP3-511B24 on chrom
1337.9	1081.2	813.4	1874.7	1512.5	1996.8	1455.1	1254.5	2058.9	1368.6	1790.2	1541.4	1143.8	Consensus includes gb:AB032951.1 /DEF=Homo sapiens mRNA for KIAA1125 protein, partial cds.
952.5	962.5	1143.3	925.7	1179.9	788	183	861.9	903.7	420.9	125.2	176.8	105.1	gb:NM_020062.1 /DEF=Homo sapiens GLUT4 enhancer factor (GEF), mRNA. /FEA=mRNA /GEN=
1275.3	2736.5	744.9	1796.9	2475	3132.4	2125.1	2576.7	1778.2	384.4	728	337.4	1102.2	gb:AB019219.1 /DEF=Homo sapiens mRNA, complete cds, similar to yeast pre-mRNA splicing fact
401.7	53.3	121.5	545.6	310	755.6	725.6	623.4	186.8	771.9	609.4	196.6	60.6	gb:NM_017859.1 /DEF=Homo sapiens hypothetical protein FLJ20517 (FLJ20517), mRNA. /FEA=m
492.4	697.6	138	1521.5	231.7	1065.6	519.5	1756.3	1268.9	1027.5	1646.8	144.4	152.5	gb:BC001738.1 /DEF=Homo sapiens, Similar to ubiquitin-conjugating enzyme E2G 2 (homologous
1295.6	1244.5	1721.8	2531.8	1572.8	1782.1	2754.6	5145.6	4720.4	3478.9	3446.6	98.3	3277.5	gb:NM_025143.1 /DEF=Homo sapiens hypothetical protein FLJ20856 (FLJ20856), mRNA. /FEA=m
2226.8	2231.2	3451	3360	2463.4	2710	3782.9	3308.2	2802.4	2563.6	3980.9	155.7	1981.6	gb:NM_004649.1 /DEF=Homo sapiens ES1 (zebrafish) protein, human homolog of (C21ORF33), m
1031.8	1297.1	1088.8	1179.4	1678.3	1019.5	2085.3	2127.9	1472.6	2080.5	1750.1	155.1	1987	gb:NM_006031.1 /DEF=Homo sapiens pericentrin (PCNT), mRNA. /FEA=mRNA /GEN=PCNT /PR
2334.9	2532.6	4158.2	4081.5	4426.2	4375.5	3340	4588.9	2195.4	2288.1	1538.3	1249.8	1186.3	Consensus includes gb:AK024034.1 /DEF=Homo sapiens cDNA FLJ13972 fis, clone Y79AA10015
3700.5	1583.3	2937	2312	3509	2832.3	3445	2262.6	3441.9	780.8	880	1084	92.3	gb:NM_012295.1 /DEF=Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA. /FEA=mR
1203.6	1185.3	1256.2	2035.6	1644	1761.6	1898.8	2951	2004.3	211.1	857.8	60.1	331.2	gb:NM_005675.1 /DEF=Homo sapiens DiGeorge syndrome critical region gene 6 (DGCR6), mRNA.
1107.7	474.3	1111.7	1865.5	896.1	502.2	1008.8	1206.7	1358.8	2553.1	4093.3	1424	844	Consensus includes gb:AW613387 /FEA=EST /DB_XREF=gi:7318573 /DB_XREF=est:hh71e04.x1
1361.6	1129.3	1180.9	863.4	970	1017.9	1417.5	1691.4	1118.4	2373.8	2256.1	1369.2	2116.8	Consensus includes gb:AI459462 /FEA=EST /DB_XREF=gi:4312343 /DB_XREF=est:ar86e07.x1 /
2116.7	1997.9	1721.5	2952.7	1975.4	2492.4	2692.1	3510.4	2037.2	1587.6	2707.3	2014.1	2446.8	gb:NM_005198.2 /DEF=Homo sapiens choline kinase-like (CHKL), mRNA. /FEA=mRNA /GEN=CH
478.1	394.7	1716	1499.2	488.2	853.1	814.5	174	365.4	106.8	118.1	160.4	117.8	Consensus includes gb:AI081535 /FEA=EST /DB_XREF=gi:3418327 /DB_XREF=est:on04g03.x1 /
448.6	671.6	537.3	726.8	1050.1	608.7	251.9	213.2	628.7	121.8	210	336	267	gb:NM_005740.1 /DEF=Homo sapiens dynein, axonemal, light polypeptide 4 (DNAL4), mRNA. /FE
5651.1	4233.3	4297.8	3989.9	6503.8	4565.7	8235.8	11089.1	9944	7485.4	7022.4	3372	3406.1	gb:NM_000878.1 /DEF=Homo sapiens interleukin 2 receptor, beta (IL2RB), mRNA. /FEA=mRNA /
152.5	320.6	884.9	927.8	711.9	1107.9	390.6	800	565.5	121.3	129.9	494.4	130.6	gb:NM_006739.1 /DEF=Homo sapiens minichromosome maintenance deficient (S. cerevisiae) 5 (c
226.6	778.8	932.9	1656.8	483.1	557.8	250.3	968.6	673.9	90.4	243.3	819.3	91.4	Cluster Incl. U93181:Homo sapiens nuclear dual-specificity phosphatase (SBF1) mRNA, partial cds
2020.9	1126.1	2307.9	1440.5	2755.1	2446.1	4287.3	3363.3	3369.5	1058.5	1790.4	500	850.9	Consensus includes gb:BG249599 /FEA=EST /DB_XREF=gi:12759426 /DB_XREF=est:602319692
10803.4	28187.1	35641.3	41825.8	23483	33323.9	15614.6	23981.6	38363.4	38891.1	15330.3	852.6	4408.3	gb:M63438.1 /DEF=Human Ig rearranged gamma chain mRNA, V-J-C region and complete cds. /F
1165.5	813.9	1076.9	1087.5	744.6	1010.4	947.8	1295.9	1285.2	34.6	780.5	333.4	698.5	gb:NM_002908.1 /DEF=Homo sapiens v-rel avian reticuloendotheliosis viral oncogene homolog (R
852.8	943.9	1026.7	572.2	553.1	983.7	1095.8	716.1	797.4	637.8	196.4	167.7	60.7	gb:NM_004082.2 /DEF=Homo sapiens dynactin 1 (p150, Glued (Drosophila) homolog) (DCTN1), tr
2203	3447.4	4065.6	3964.8	2183	3490.3	3183.6	3003.1	4493.6	2682	2295.3	2695.2	8115.8	Consensus includes gb:BE968833 /FEA=EST /DB_XREF=gi:10579538 /DB_XREF=est:601649861
981	691.4	1320.1	1858.7	1529.4	1099.7	435.6	980.8	1400.9	279.2	1255.8	1036.8	2204.8	Consensus includes gb:AL566299 /FEA=EST /DB_XREF=gi:12918529 /DB_XREF=est:AL566299 /
4343.5	3799.2	9570.1	4884.5	8722.8	10658.6	8806.7	6790.6	6849.7	16855.8	13684.3	3479.7	16413.6	gb:U59302.1 /DEF=Human steroid receptor coactivator-1 F-SRC-1 mRNA, complete cds. /FEA=mR
232.9	941.3	645.6	751.8	447.1	1130.3	1108	2218	1935.9	3166.6	2663.6	253.2	3292	Consensus includes gb:AV705559 /FEA=EST /DB_XREF=gi:10722858 /DB_XREF=est:AV705559
1630.8	1917.1	1081.9	2677.3	1354.4	1748.1	1863.3	2837.7	2273.2	2185	1396.6	1455.5	389	Consensus includes gb:AI817942 /FEA=EST /DB_XREF=gi:5437110 /DB_XREF=est:wk41f07.x1 /
1011.6	1046.2	1270	1198.5	1320.5	1028.5	1490.6	1098.9	1659.2	84.1	1284.1	146.4	1158.7	Consensus includes gb:AA176798 /FEA=EST /DB_XREF=gi:1757939 /DB_XREF=est:zp32e12.s1
117.9	87.5	289.7	749	326.4	77.7	643	60.8	150.8	53.8	116.8	120.9	49.7	gb:NM_012100.1 /DEF=Homo sapiens aspartyl aminopeptidase (DNPEP), mRNA. /FEA=mRNA /G
777.9	1014.9	1761.1	1975.2	1465.4	2284	1829.8	1297	1261.2	693	933.1	184	424.5	Consensus includes gb:AA532726 /FEA=EST /DB_XREF=gi:2278302 /DB_XREF=est:nj21e02.s1 /
1462.1	2903.9	1907.6	3765	1919.6	2729.2	5263.7	4787.2	4648.6	3242.9	3537.7	984.9	2014.1	gb:BC001051.1 /DEF=Homo sapiens, ADP-ribosylation factor-like 7, clone MGC:1575, mRNA, com
1299.7	1025.8	1118.1	1611.6	580.9	759.2	1089.4	1661	1540	1957.5	807.5	586.6	835.2	gb:NM_022730.1 /DEF=Homo sapiens hypothetical protein FLJ12612 similar to COP9 (constitutive
828.3	1326.8	932.4	1361.2	833.3	972.9	1373.2	1696.1	1489.3	366.1	1244.6	898.4	1072.6	gb:AY024365.1 /DEF=Homo sapiens integrin-linked kinase-associated serinethreonine phosphatas
1431.1	2103.5	1629.5	2231.6	1535.1	2566.5	3613.6	3004.7	2940.4	2042	2653.3	147.1	892.7	Consensus includes gb:BF941492 /FEA=EST /DB_XREF=gi:12358812 /DB_XREF=est:nac74d09.x
8379.4	4994.1	4458.5	4975.7	10820.7	9127.6	8076.6	4706.9	4720	3420.9	1695.7	1203.6	513.7	gb:NM_002070.1 /DEF=Homo sapiens guanine nucleotide binding protein (G protein), alpha inhibiti
2682.9	2788.3	2565.3	4129.3	3224.5	3975.9	2640.7	1957.8	1908.2	1077.3	1390	385.2	314.1	gb:NM_003335.1 /DEF=Homo sapiens ubiquitin-activating enzyme E1-like (UBE1L), mRNA. /FEA=
1956.6	1707.8	1878	2286.7	1850.5	1654.4	2061.1	1788.5	1352.7	77.3	1731.7	907.7	1363.2	gb:NM_007182.2 /DEF=Homo sapiens Ras association (RalGDSAF-6) domain family 1 (RASSF1),
864.4	882.2	1564.8	1466.1	902.7	730.2	172	1232.3	1353.2	42.6	89.4	595.1	95.8	gb:NM_014966.1 /DEF=Homo sapiens KIAA0890 protein (KIAA0890), mRNA. /FEA=mRNA /GEN=
293	1883.4	1938.6	4221.3	1331.6	1485.1	450.6	2435.8	1163.1	279.6	131.7	168	210.8	gb:NM_016381.1 /DEF=Homo sapiens hypothetical protein (DKFZp434J0310), mRNA. /FEA=mRN
220.5	805.6	233.7	543.4	280.5	210.1	197	146.8	140	291.8	554	290.9	145.6	gb:BC004300.1 /DEF=Homo sapiens, Similar to villin-like, clone MGC:10896, mRNA, complete cds.
128.7	392.8	373.1	3966.2	183.8	1952.1	577.6	2050.2	1452.6	2221.4	3648.5	92.7	1579.9	gb:NM_006545.1 /DEF=Homo sapiens homologous to yeast nitrogen permease (candidate tumor s

1511.5	2567.9	4208.9	1429.7	4441.3	1896.6	4407.8	3391.5	1637.5	261.1	261	613.5	339.1	Consensus includes gb:BE891920 /FEA=EST /DB_XREF=gi:10351728 /DB_XREF=est:601435490
2223.8	3244.9	4830.1	3087	5670.1	4112.5	3629.7	3858.2	3412.5	3740.1	3370.3	1394.7	3613.2	Consensus includes gb:AI652645 /FEA=EST /DB_XREF=gi:4736624 /DB_XREF=est:wb30b07.x1 /
671.8	467.6	856.1	827.2	271.6	421.8	585.9	809.7	1171.6	89.3	638.7	1209.1	327.1	Consensus includes gb:AI357539 /FEA=EST /DB_XREF=gi:4109160 /DB_XREF=est:qu20a12.x1 /
530.4	732	1102	914.1	790.9	648.5	837	1257.6	1377.3	158.5	1158.2	369	1024.8	gb:NM_002913.1 /DEF=Homo sapiens replication factor C (activator 1) 1 (145kD) (RFC1), mRNA.
956.1	1201.7	2012.7	1650.1	946.8	1852.6	940.9	2215.4	2200.2	1694	1360.2	635.3	564.1	gb:BC001286.1 /DEF=Homo sapiens, Similar to dCMP deaminase, clone MGC:5160, mRNA, comp
59.9	668.4	753.5	593.3	900.9	654	845.4	2028.8	1576.6	2892.8	1744.3	314.1	1253.3	Consensus includes gb:AK024175.1 /DEF=Homo sapiens cDNA FLJ14113 fis, clone MAMMA1001
12702.2	9521	9963.8	11126.6	13571.5	9319.7	9730.7	10863.5	7792.4	6891.6	8237.2	1671.5	2504.7	gb:NM_002198.1 /DEF=Homo sapiens interferon regulatory factor 1 (IRF1), mRNA. /FEA=mRNA /
997.9	1064.2	841.6	1161.5	691.5	788.9	1010.3	1987	1729.1	1104.9	1048.8	158.3	209	Consensus includes gb:AW027359 /FEA=EST /DB_XREF=gi:5886115 /DB_XREF=est:wt73f08.x1 /
905.7	592.1	735.5	682.2	358.4	531.9	1337	968	1322	163.4	575.7	132.9	196.3	Consensus includes gb:BE881529 /FEA=EST /DB_XREF=gi:10330305 /DB_XREF=est:601490242
4428.7	5115	9317.9	7609	6300.3	6930.5	7431.4	7705.1	5065.5	2242.4	2349.3	1490.2	1690.6	Cluster Incl. AB015718:Homo sapiens lok mRNA for protein kinase, complete cds /cds=(50,2956) /
868.5	881.1	925.1	1117.5	803.5	1087.9	1464.2	1185.6	872.3	2127.5	1200.4	54.6	898.3	Consensus includes gb:AK025759.1 /DEF=Homo sapiens cDNA: FLJ22106 fis, clone HEP17675. /
62809.1	62301.2	71183.1	65941.4	69190.4	60998.1	89326.4	91993.7	67373.5	46096.4	67535.5	10242.4	37743.9	gb:NM_005516.1 /DEF=Homo sapiens major histocompatibility complex, class I, E (HLA-E), mRNA.
9352.8	13913.6	11979.2	12852.3	11953.3	12679.3	9743.6	12754	14910	3089.5	6472.5	370.9	1824.5	gb:NM_004640.1 /DEF=Homo sapiens HLA-B associated transcript-1 (D6S81E), mRNA. /FEA=mR
1705.5	1379.6	1547.2	2011.1	894.1	1531.1	2127.2	2023.4	1893.2	96.2	918.9	789	762.3	gb:NM_001470.1 /DEF=Homo sapiens gamma-aminobutyric acid (GABA) B receptor, 1 (GABBR1),
433.4	797.1	373.4	442.4	282.1	394.4	273.1	186.4	130	235.5	795.9	408.3	187.4	gb:NM_001954.2 /DEF=Homo sapiens discoidin domain receptor family, member 1 (DDR1), transcr
1460.1	12899.7	6958	10627	6672.5	7888.4	8117.4	9807.7	6441.3	104.9	816	476.4	72.7	Consensus includes gb:BG397856 /FEA=EST /DB_XREF=gi:13291304 /DB_XREF=est:602438950
68	106.2	348.1	631.5	134.4	320.9	124	122.4	69.6	76.1	76.7	237.3	60.8	gb:NM_006295.1 /DEF=Homo sapiens valyl-tRNA synthetase 2 (VARS2), mRNA. /FEA=mRNA /GE
19061.7	8420.7	13773.4	11027.7	15805.1	12665.2	11176	7838.9	7376.3	5030.8	8691.9	1762.4	3025.5	gb:NM_022107.1 /DEF=Homo sapiens G18.2 protein (G18.2), mRNA. /FEA=mRNA /GEN=G18.2 /
6284.3	7824.2	9893.3	9874.8	6646	8208.7	6934	10789.9	8388.2	1793.2	5521.9	225.4	1066.8	Consensus includes gb:X76775 /DEF=H.sapiens HLA-DMA gene /FEA=mRNA_1 /DB_XREF=gi:51
838.4	1341.4	1823.4	1783.8	2228.1	1444.7	1243	1136.6	1005.5	1093.1	554.4	325.9	499.1	Consensus includes gb:AL035588 /DEF=Human DNA sequence from clone 696P19 on chromosom
10733.4	13736.1	19197.2	20579.7	16039.2	17124.8	13110.6	14781.1	19735.8	5844.3	9518.4	4113.9	3338.3	gb:NM_001760.1 /DEF=Homo sapiens cyclin D3 (CCND3), mRNA. /FEA=mRNA /GEN=CCND3 /P
144.2	1636.3	930.5	1686.7	1602	648	516.9	1300	2573.5	260.2	76.3	221.8	103.1	gb:NM_002224.1 /DEF=Homo sapiens inositol 1,4,5-triphosphate receptor, type 3 (ITPR3), mRNA.
4260.9	4029	2606.9	2929.5	4931.9	4992.3	4015.4	3830.4	4182.3	304.4	2829	801.6	1310.3	Consensus includes gb:AL523814 /FEA=EST /DB_XREF=gi:12787307 /DB_XREF=est:AL523814 /
441.6	1908.6	1362.2	3343.1	469.5	2769.5	1253.5	2153.5	1101.3	433.6	260.3	234.9	587.6	Consensus includes gb:AA670344 /FEA=EST /DB_XREF=gi:2631843 /DB_XREF=est:ad16b08.s1
840.8	1115.3	2646.5	1425.4	2421	2344.2	2254.6	1999.1	2685.4	353.4	1723.6	2262.3	1620.9	gb:NM_006092.1 /DEF=Homo sapiens caspase recruitment domain 4 (NOD1), mRNA. /FEA=mRN
2209.4	2336	2555.5	2849.7	4037.4	4022.7	1241.7	2020.3	3306.1	1601	2570.2	534.7	1882.4	Consensus includes gb:AC003999 /DEF=Human PAC clone RP5-1139P1 from 7p15-p21 /FEA=CD
1149.4	861.5	1100.7	967.1	1769	1210.1	1333.6	813.5	775	350.7	445.7	307.4	460	Consensus includes gb:BF055496 /FEA=EST /DB_XREF=gi:10809392 /DB_XREF=est:7j80h12.x1
1436.2	778.8	1605.3	1587.1	1694.9	1738.8	1716	1549.4	1675.9	773.8	1310.9	704.4	457.8	gb:BC000787.1 /DEF=Homo sapiens, TRIAD3 protein, clone MGC:998, mRNA, complete cds. /FEA
114.1	1978.7	925.2	2656.5	920.8	1997.2	480.5	3976.7	939.1	876.6	1781.1	143.7	1703.4	gb:NM_018044.1 /DEF=Homo sapiens hypothetical protein FLJ10267 (FLJ10267), mRNA. /FEA=m
192.3	36.5	317.2	366.3	38.1	228.4	483.8	525.8	338.2	68.7	130.8	111.5	82.1	gb:BC006259.1 /DEF=Homo sapiens, clone MGC:11333, mRNA, complete cds. /FEA=mRNA /PRO
258	430.8	527.6	747.1	656.7	316	1038.4	678.3	1177.3	483.3	699.3	1203.9	321.2	gb:NM_018991.1 /DEF=Homo sapiens DKFZp434A0131 protein (DKFZP434A0131), mRNA. /FEA=
1053.3	960.9	471.2	978.8	1008.4	554	582	1006.1	829.1	60	767.2	1570	132.5	Consensus includes gb:BE547674 /FEA=EST /DB_XREF=gi:9776319 /DB_XREF=est:601076255F
999.9	797.6	1532.5	2485.5	1249.2	1075.3	821.2	1980.6	1206.9	729	871.8	776.3	589.7	gb:NM_013440.1 /DEF=Homo sapiens paired immunoglobulin-like receptor beta (PILR(BETA)), mR
689.6	310.3	198.1	937.2	454.3	440.4	590.3	1711.4	614.3	331	296.9	342.1	604.5	Consensus includes gb:AB011115.1 /DEF=Homo sapiens mRNA for KIAA0543 protein, partial cds.
966.1	639.5	981.3	789.9	979.3	807.6	1246.6	1139.7	1156.9	1141.4	1353.9	68.6	973.7	Consensus includes gb:AB029026.1 /DEF=Homo sapiens mRNA for KIAA1103 protein, partial cds.
1105.9	1150.2	1220	1307.4	743.2	1121.5	555.7	1176.6	872	215.9	976.2	267.3	808.2	gb:AF080158.1 /DEF=Homo sapiens IkB kinase-b (IKK-beta) mRNA, complete cds. /FEA=mRNA /
146.8	91	350.7	307	197.6	128.1	264	225.7	445	404.2	27.5	112	36.5	gb:NM_001715.1 /DEF=Homo sapiens B lymphoid tyrosine kinase (BLK), mRNA. /FEA=mRNA /GE
305.1	355.6	358.1	646.2	276.6	609.3	317.5	863.7	782.5	261.5	445.6	92.7	334.7	Consensus includes gb:AK026820.1 /DEF=Homo sapiens cDNA: FLJ23167 fis, clone LNG09902. /
305.1	208.3	362	393	158	237.8	548.1	331.2	529.8	930.4	636.9	207.8	540.3	gb:NM_003033.1 /DEF=Homo sapiens sialyltransferase 4A (beta-galactosidase alpha-2,3-sialytran
1270.5	1225.5	1058.2	1705.2	1697.7	1013.3	1357	1471.9	1284.1	590.5	977.4	332.9	281.9	gb:NM_013291.1 /DEF=Homo sapiens cleavage and polyadenylation specific factor 1, 160kD subu
971.8	1084.4	1477.3	1392.5	1326.7	1093	1139.8	1515.6	1844.8	218	602	232.1	370.3	gb:NM_004512.1 /DEF=Homo sapiens interleukin 11 receptor, alpha (IL11RA), mRNA. /FEA=mRN
135.1	1156.1	136.7	1180.2	806.8	1263.1	1284.4	1085.5	895.9	263.9	35.9	222.3	60.7	Consensus includes gb:AF283777.2 /DEF=Homo sapiens clone TCBAP0702 mRNA sequence. /FE
1131.9	1310.1	1485.2	1357.7	1335.5	1207.1	534	1563.5	865.3	547.3	359.3	172.9	141.1	gb:AF029674.1 /DEF=Homo sapiens basic leucine zipper protein LZIP (LZIP) mRNA, complete cds.
4317	3910.2	3914.9	4364.6	2542.6	4634.5	7630.1	8226.6	4870.1	1601.9	2970.2	174.1	428.3	gb:NM_003177.1 /DEF=Homo sapiens spleen tyrosine kinase (SYK), mRNA. /FEA=mRNA /GEN=S
1281.7	956.7	1664.6	2089.1	1262.3	1183.8	1601.7	2102.3	2032.9	3057.5	2878.4	1028.5	1437.3	Consensus includes gb:BE962483 /FEA=EST /DB_XREF=gi:11765431 /DB_XREF=est:601655782
433.3	1169.1	293.8	898.7	438	1159.9	862.3	1026.2	1015.6	78.4	1489.8	742.5	496.7	gb:NM_013366.2 /DEF=Homo sapiens anaphase-promoting complex subunit 2 (APC2), mRNA. /FE
101.6	568.2	1207.1	987.6	389.3	635.5	1161.7	1667.6	1016.3	246.8	294.8	138.4	118.3	gb:NM_001261.1 /DEF=Homo sapiens cyclin-dependent kinase 9 (CDC2-related kinase) (CDK9),
1032.8	1124.4	1135.5	1141.6	357.3	710.1	1089.9	1263.9	1445	921.9	412.1	1631.2	553.5	gb:NM_005157.2 /DEF=Homo sapiens v-abl Abelson murine leukemia viral oncogene homolog 1 (
988.2	1025.7	1511.3	2524.3	2123.6	2050.7	2989.2	2044.3	1892	2275.4	2553.1	490.5	2617.7	gb:BC000350.1 /DEF=Homo sapiens, ubiquitin specific protease 11, clone MGC:8620, mRNA, com
3243.7	1241	2003.6	1755.6	2756.1	1903.2	2779.6	2848.9	1940.8	1642.2	1781.6	1775.1	2028.2	gb:D38616.1 /DEF=Human mRNA for phosphorylase kinase alpha subunit, complete cds. /FEA=m
459.4	839.1	1334.1	1285.9	1250.7	1361.3	999.8	1284.1	1677.8	317.6	679.8	616	814.6	Consensus includes gb:BE379542 /FEA=EST /DB_XREF=gi:9324907 /DB_XREF=est:601238148F

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LONE=IMAGE:417293 /UG=Hs.65135 KIAA0913 protein
LONE=IMAGE:2140948 /UG=Hs.2200 perforin 1 (pore forming protein) /FL=gb:M28393.1 gb:NM_005041.1
A, complete cds.  /FEA=mRNA /PROD=Similar to actin binding LIM protein 1 /DB_XREF=gi:12803266 /UG=Hs.158203 actin binding LIM protein 1 /FL=gb:BC002448.1
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, mRNA.  /FEA=mRNA /GEN=DOC-1R /PROD=tumor suppressor deleted in oral cancer-related1 /DB_XREF=gi:5031668 /UG=Hs.25664 tumor suppressor deleted in oral cancer-related 1 /FL=gb:BC002850.1 gb:AF089814.1 gb:NM_005851.1
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 (TRADD) mRNA, 3  end of cds
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GBP /PROD=CpG binding protein /DB_XREF=gi:7656974 /UG=Hs.180933 CpG binding protein /FL=gb:AL136862.1 gb:AF149758.1 gb:NM_014593.1 gb:AB031069.1
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F1 /CLONE=IMAGE:4473753 /UG=Hs.190452 KIAA0365 gene product
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nplete cds.  /FEA=mRNA /PROD=hypothetical protein FLJ20011 /DB_XREF=gi:13111838 /UG=Hs.256583 interleukin enhancer binding factor 3, 90kD /FL=gb:BC003086.1 gb:NM_004516.1 gb:U10324.1 gb:AF167570.1 gb:NM_012218.1
CLONE=IMAGE:1625242 /UG=Hs.75309 eukaryotic translation elongation factor 2
 /CLONE=IMAGE:3321439 /UG=Hs.98289 VRK3 for vaccinia related kinase 3
P62 /PROD=nucleoporin 62kD /DB_XREF=gi:6912543 /UG=Hs.278511 nucleoporin 62kD /FL=gb:NM_012346.1
5128 /PROD=zinc finger protein /DB_XREF=gi:7657692 /UG=Hs.296365 zinc finger protein /FL=gb:AF060503.1 gb:NM_014347.1
CLONE=IMAGE:1284462 /UG=Hs.86575 mitogen-activated protein kinase kinase kinase kinase 1
NA.  /FEA=mRNA /GEN=SNRPA /PROD=small nuclear ribonucleoprotein polypeptide A /DB_XREF=gi:4759155 /UG=Hs.173255 small nuclear ribonucleoprotein polypeptide A /FL=gb:BC000405.1 gb:NM_004596.1
gen) (SNRP70), mRNA.  /FEA=mRNA /GEN=SNRP70 /PROD=small nuclear ribonucleoprotein 70kD polypeptide(RNP antigen) /DB_XREF=gi:4507118 /UG=Hs.174051 small nuclear ribonucleoprotein 70kD polypeptide (RNP antigen) /FL=gb:B
=protein kinase D2 /DB_XREF=gi:12659006 /UG=Hs.91146 protein kinase D2 /FL=gb:AF309082.1 gb:AF151021.1 gb:NM_016457.1
EN=GPI /PROD=glucose phosphate isomerase /DB_XREF=gi:4504086 /UG=Hs.180532 glucose phosphate isomerase /FL=gb:BC004982.1 gb:K03515.1 gb:NM_000175.1
  /CLONE=IMAGE:3568380 /UG=Hs.230424 Homo sapiens cDNA FLJ13540 fis, clone PLACE1006754, weakly similar to BILIARY GLYCOPROTEIN 1 PRECURSOR
.  /FEA=mRNA /GEN=SPIB /PROD=Spi-B transcription factor (Spi-1PU.1 related) /DB_XREF=gi:4507176 /UG=Hs.192861 Spi-B transcription factor (Spi-1PU.1 related) /FL=gb:NM_003121.1
EN=IRF3 /PROD=interferon regulatory factor 3 /DB_XREF=gi:4504724 /UG=Hs.75254 interferon regulatory factor 3 /FL=gb:NM_001571.1
sive) (ZNF42), mRNA.  /FEA=mRNA /GEN=ZNF42 /PROD=zinc finger protein 42 (myeloid-specificretinoic acid- responsive) /DB_XREF=gi:4508024 /UG=Hs.169832 zinc finger protein 42 (myeloid-specific retinoic acid- responsive) /FL=gb:M582
G7), mRNA. /FEA=CDS /GEN=NKG7 /PROD=natural killer cell group 7 sequence /DB_XREF=gi:5031948 /UG=Hs.10306 natural killer cell group 7 sequence /FL=gb:NM_005601.1
 /GEN=LIG1 /PROD=DNA ligase I /DB_XREF=gi:4557718 /UG=Hs.1770 ligase I, DNA, ATP-dependent /FL=gb:M36067.1 gb:NM_000234.1
EN=TIF1B /PROD=KRAB-associated protein 1 /DB_XREF=gi:5032178 /UG=Hs.228059 KRAB-associated protein 1 /FL=gb:BC004978.1 gb:U78773.1 gb:U95040.1 gb:NM_005762.1
), mRNA.  /FEA=mRNA /GEN=ATP1A1 /PROD=ATPase, Na+K+ transporting, alpha 1polypeptide /DB_XREF=gi:4502268 /UG=Hs.76549 ATPase, Na+K+ transporting, alpha 1 polypeptide /FL=gb:NM_000701.1 gb:U16798.1
A /GEN=CPT1 /PROD=carnitine palmitoyltransferase /DB_XREF=gi:180988 /UG=Hs.274336 carnitine palmitoyltransferase II /FL=gb:U09648.1 gb:BC002445.1 gb:BC005172.1 gb:M58581.1 gb:NM_000098.1
kD) (TGFBR3), mRNA.  /FEA=mRNA /GEN=TGFBR3 /PROD=transforming growth factor, beta receptor III(betaglycan, 300kD) /DB_XREF=gi:4507470 /UG=Hs.79059 transforming growth factor, beta receptor III (betaglycan, 300kD) /FL=gb:NM
CLONE=IMAGE:1409963 /UG=Hs.104125 adenylyl cyclase-associated protein
F1 /CLONE=IMAGE:4526611 /UG=Hs.301553 karyopherin alpha 6 (importin alpha 7) /FL=gb:AF060543.1 gb:NM_012316.1
RNA /GEN=FLJ13171 /PROD=hypothetical protein FLJ13171 /DB_XREF=gi:12965188 /UG=Hs.225641 hypothetical protein FLJ13171 /FL=gb:AF130081.1 gb:NM_023923.1
FEA=mRNA /GEN=LCK /PROD=lymphocyte-specific protein tyrosine kinase /DB_XREF=gi:4885448 /UG=Hs.1765 lymphocyte-specific protein tyrosine kinase /FL=gb:M36881.1 gb:U07236.1 gb:NM_005356.1
slocating chain-association membrane protein) (TNFRSF12), mRNA.  /FEA=mRNA /GEN=TNFRSF12 /PROD=tumor necrosis factor receptor superfamily,member 12 /DB_XREF=gi:4507568 /UG=Hs.180338 tumor necrosis factor receptor super
=PRKCZ /PROD=protein kinase C, zeta /DB_XREF=gi:10864649 /UG=Hs.78793 protein kinase C, zeta /FL=gb:NM_002744.2 gb:L14283.1
CLONE=CS0DI013YH20 (3 prime) /UG=Hs.184482 DKFZP586D0624 protein
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RNA /GEN=HKR3 /PROD=GLI-Kruppel family member HKR3 /DB_XREF=gi:4885418 /UG=Hs.2364 GLI-Kruppel family member HKR3 /FL=gb:L16896.1 gb:NM_005341.1
HSPC157 /PROD=HSPC157 protein /DB_XREF=gi:7661813 /UG=Hs.279842 HSPC157 protein /FL=gb:AF161506.1 gb:NM_014179.1
CLONE=IMAGE:984984 /UG=Hs.170019 runt-related transcription factor 3 /FL=gb:NM_004350.1
SA9947 /PROD=putative ATPase /DB_XREF=gi:13435128 /UG=Hs.128866 putative ATPase /FL=gb:NM_022089.1
CLONE=CS0DL011YC18 (3 prime) /UG=Hs.153042 lymphocyte antigen 9
  /FEA=mRNA /GEN=CLK2 /PROD=CDC-like kinase 2  isoform hclk2 /DB_XREF=gi:4502882 /UG=Hs.73986 CDC-like kinase 2 /FL=gb:NM_003993.1 gb:L29218.1
-cell receptor zeta chain /DB_XREF=gi:623041 /UG=Hs.97087 CD3Z antigen, zeta polypeptide (TiT3 complex) /FL=gb:NM_000734.1 gb:J04132.1
26 /DB_XREF=gi:7657147 /UG=Hs.110707 H326 /FL=gb:U06631.1 gb:NM_015726.1
NA /GEN=CD84 /PROD=CD84 antigen (leukocyte antigen) /DB_XREF=gi:4502686 /UG=Hs.137548 CD84 antigen (leukocyte antigen) /FL=gb:U82988.1 gb:NM_003874.1 gb:AF054815.1
CLONE=IMAGE:1671424 /UG=Hs.58831 regulator of Fas-induced apoptosis /FL=gb:AF057557.1 gb:NM_005449.1
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RNA /GEN=FLJ20340 /PROD=hypothetical protein FLJ20340 /DB_XREF=gi:8923315 /UG=Hs.272794 hypothetical protein FLJ20340 /FL=gb:NM_017773.1
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A.  /FEA=mRNA /GEN=CDC25B /PROD=cell division cycle 25B, isoform 3 /DB_XREF=gi:11641412 /UG=Hs.153752 cell division cycle 25B /FL=gb:NM_021873.1
-tubulin /DB_XREF=gi:4929137 /UG=Hs.179661 tubulin, beta polypeptide /FL=gb:BC000222.1 gb:BC002347.1 gb:BC001938.1 gb:AF070561.1 gb:AF070593.1 gb:AF070600.1 gb:AF141349.1
.  /FEA=mRNA /PROD=ring finger protein 24 /DB_XREF=gi:12802985 /UG=Hs.30524 ring finger protein 24 /FL=gb:BC000213.1
CLONE=IMAGE:2312829 /UG=Hs.153934 core-binding factor, runt domain, alpha subunit 2; translocated to, 2 /FL=gb:AF068266.1 gb:AF069747.1
 function) (ENTPD6), mRNA.  /FEA=mRNA /GEN=ENTPD6 /PROD=ectonucleoside triphosphate diphosphohydrolase 6(putative function) /DB_XREF=gi:4557422 /UG=Hs.12330 ectonucleoside triphosphate diphosphohydrolase 6 (putative funct
 /FEA=mRNA /GEN=KIAA0823 /PROD=KIAA0823 protein /DB_XREF=gi:4240131 /UG=Hs.45719 KIAA0823 protein
C51604 /PROD=CGI-06 protein /DB_XREF=gi:7706257 /UG=Hs.84038 CGI-06 protein /FL=gb:AF132940.1 gb:NM_015937.1
osome 20q11.2-12. Contains the 3 end of the TOP1 gene for topoisomerase (DNA) I, the PLCG1 gene for phospholipase C gamma 1, gene KIAA0395 for a possible homeobox protein, a 60S Ribosomal Protein L... /FEA=mRNA_1 /DB_XREF=gi
 /FEA=mRNA /GEN=KIAA1125 /PROD=KIAA1125 protein /DB_XREF=gi:6329748 /UG=Hs.75871 protein kinase C binding protein 1 /FL=gb:BC001004.1
GEF /PROD=GLUT4 enhancer factor /DB_XREF=gi:13236503 /UG=Hs.170088 GLUT4 enhancer factor /FL=gb:AF249267.3 gb:NM_020062.1
ors, Prp1Zer1 and Prp6.  /FEA=mRNA /DB_XREF=gi:4164165 /UG=Hs.31334 putative mitochondrial outer membrane protein import receptor /FL=gb:BC001666.1 gb:AF026031.1 gb:AB019219.1 gb:NM_012469.1 gb:AF221842.1
RNA /GEN=FLJ20517 /PROD=hypothetical protein FLJ20517 /DB_XREF=gi:8923486 /UG=Hs.39850 hypothetical protein FLJ20517 /FL=gb:NM_017859.1
to yeast UBC7), clone MGC:1589, mRNA, complete cds.  /FEA=mRNA /PROD=Similar to ubiquitin-conjugating enzyme E2G 2(homologous to yeast UBC7) /DB_XREF=gi:12804628 /UG=Hs.192853 ubiquitin-conjugating enzyme E2G 2 (homolog
RNA /GEN=FLJ20856 /PROD=hypothetical protein FLJ20856 /DB_XREF=gi:13376728 /UG=Hs.288916 hypothetical protein FLJ20856 /FL=gb:NM_025143.1
RNA.  /FEA=mRNA /GEN=C21ORF33 /PROD=ES1 (zebrafish) protein, human homolog of /DB_XREF=gi:5031690 /UG=Hs.182423 ES1 (zebrafish) protein, human homolog of /FL=gb:BC002370.1 gb:BC003587.1 gb:D86061.1 gb:U53003.1 gb:
D=pericentrin /DB_XREF=gi:5174478 /UG=Hs.15896 pericentrin /FL=gb:U52962.1 gb:NM_006031.1
48, highly similar to PHOSPHATIDYLINOSITOL 4-KINASE ALPHA (EC 2.7.1.67).  /FEA=mRNA /DB_XREF=gi:10436297 /UG=Hs.171625 phosphatidylinositol 4-kinase, catalytic, alpha polypeptide
NA /GEN=KIAA0330 /PROD=calcineurin binding protein 1 /DB_XREF=gi:6912457 /UG=Hs.7840 calcineurin binding protein 1 /FL=gb:AF072441.1 gb:NM_012295.1
.  /FEA=mRNA /GEN=DGCR6 /PROD=DiGeorge syndrome critical region protein 6 /DB_XREF=gi:5031662 /UG=Hs.153910 DiGeorge syndrome critical region gene 6 /FL=gb:AF228707.1 gb:NM_005675.1
 /CLONE=IMAGE:2968254 /UG=Hs.278541 ESTs, Moderately similar to TYPH_HUMAN THYMIDINE PHOSPHORYLASE PRECURSOR H.sapiens
CLONE=IMAGE:2152164 /UG=Hs.25272 E1A binding protein p300
KL /PROD=choline kinase-like /DB_XREF=gi:6978648 /UG=Hs.154886 choline kinase-like /FL=gb:AB029886.1 gb:NM_005198.2
CLONE=IMAGE:1555732 /UG=Hs.150540 Homo sapiens, clone IMAGE:3954961, mRNA, partial cds
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EN=IL2RB /PROD=interleukin 2 receptor, beta /DB_XREF=gi:4504664 /UG=Hs.75596 interleukin 2 receptor, beta /FL=gb:M26062.1 gb:NM_000878.1
ll division cycle 46) (MCM5), mRNA.  /FEA=mRNA /GEN=MCM5 /PROD=minichromosome maintenance deficient (S.cerevisiae) 5 (cell division cycle 46) /DB_XREF=gi:6981191 /UG=Hs.77171 minichromosome maintenance deficient (S. cerevis
 /cds=(0,5095) /gb=U93181 /gi=3015537 /ug=Hs.112049 /len=5228
F1 /CLONE=IMAGE:4414895 /UG=Hs.110771 Homo sapiens cDNA: FLJ21904 fis, clone HEP03585
EA=mRNA /DB_XREF=gi:184847 /UG=Hs.156110 immunoglobulin kappa constant /FL=gb:M63438.1
L), mRNA.  /FEA=mRNA /GEN=REL /PROD=v-rel avian reticuloendotheliosis viral oncogenehomolog /DB_XREF=gi:4506472 /UG=Hs.44313 v-rel avian reticuloendotheliosis viral oncogene homolog /FL=gb:NM_002908.1
anscript variant 1, mRNA.  /FEA=mRNA /GEN=DCTN1 /PROD=dynactin 1, isoform 1 /DB_XREF=gi:13259509 /UG=Hs.74617 dynactin 1 (p150, Glued (Drosophila) homolog) /FL=gb:NM_023019.1 gb:NM_004082.2
F1 /CLONE=IMAGE:3933782 /UG=Hs.324648 Homo sapiens cDNA FLJ13700 fis, clone PLACE2000216, highly similar to SPECTRIN BETA CHAIN, BRAIN
CLONE=CS0DF015YB11 (3 prime) /UG=Hs.80426 brain and reproductive organ-expressed (TNFRSF1A modulator)
NA /PROD=steroid receptor coactivator-1 F-SRC-1 /DB_XREF=gi:1480645 /UG=Hs.74002 nuclear receptor coactivator 1 /FL=gb:U40396.1 gb:U59302.1 gb:U90661.1 gb:NM_003743.1
CLONE=ADBAPE04 /UG=Hs.81412 lipin 1
CLONE=IMAGE:2417989 /UG=Hs.234569 zeta-chain (TCR) associated protein kinase (70 kD)
CLONE=IMAGE:611182 /UG=Hs.11238 KIAA0622 protein; Drosophila multiple asters (Mast)-like homolog 1
EN=DNPEP /PROD=aspartyl aminopeptidase /DB_XREF=gi:6912247 /UG=Hs.258551 aspartyl aminopeptidase /FL=gb:BC000653.1 gb:AF005050.2 gb:NM_012100.1
CLONE=IMAGE:993146 /UG=Hs.272586 KIAA0943 protein
plete cds.  /FEA=mRNA /PROD=ADP-ribosylation factor-like 7 /DB_XREF=gi:12654450 /UG=Hs.111554 ADP-ribosylation factor-like 7 /FL=gb:BC001051.1 gb:AB016811.1 gb:NM_005737.2
 photomorphogenic), subunit 7b (Arabidopsis) (FLJ12612), mRNA.  /FEA=mRNA /GEN=FLJ12612 /PROD=hypothetical protein FLJ12612 similar to COP9(constitutive photomorphogenic), subunit 7b (Arabidopsis) /DB_XREF=gi:12232384 /UG=H
 2C mRNA, complete cds.  /FEA=mRNA /PROD=integrin-linked kinase-associatedserinethreonine phosphatase 2C /DB_XREF=gi:13432041 /UG=Hs.92033 integrin-linked kinase-associated serinethreonine phosphatase 2C /FL=gb:AL136850.1
1 /CLONE=IMAGE:3439937 /UG=Hs.280978 hypothetical protein FLJ10496
ng activity polypeptide 2 (GNAI2), mRNA.  /FEA=mRNA /GEN=GNAI2 /PROD=guanine nucleotide binding protein (G protein),alpha inhibiting activity polypeptide 2 /DB_XREF=gi:4504040 /UG=Hs.77269 guanine nucleotide binding protein (G pro
mRNA /GEN=UBE1L /PROD=ubiquitin-activating enzyme E1-like /DB_XREF=gi:4507766 /UG=Hs.16695 ubiquitin-activating enzyme E1-like /FL=gb:NM_003335.1 gb:L13852.1
mRNA.  /FEA=mRNA /GEN=RASSF1 /PROD=Ras association (RalGDSAF-6) domain family 1 /DB_XREF=gi:9256633 /UG=Hs.26931 Ras association (RalGDSAF-6) domain family 1 /FL=gb:AF061836.1 gb:AF132676.1 gb:AF040703.2 gb:NM_
KIAA0890 /PROD=KIAA0890 protein /DB_XREF=gi:7662361 /UG=Hs.323462 KIAA0890 protein /FL=gb:AB020697.1 gb:NM_014966.1
A /GEN=DKFZp434J0310 /PROD=hypothetical protein /DB_XREF=gi:7705352 /UG=Hs.278408 hypothetical protein /FL=gb:AF319568.1 gb:AL137745.1 gb:NM_016381.1
.  /FEA=mRNA /PROD=Similar to villin-like /DB_XREF=gi:13279166 /UG=Hs.103665 villin-like /FL=gb:BC004300.1
uppressor) (NPR2L), mRNA.  /FEA=mRNA /GEN=NPR2L /PROD=homologous to yeast nitrogen permease (candidatetumor suppressor) /DB_XREF=gi:5729948 /UG=Hs.169780 homologous to yeast nitrogen permease (candidate tumor suppres
```

F1 /CLONE=IMAGE:3920590 /UG=Hs.323342 actin related protein 23 complex, subunit 4 (20 kD) /FL=gb:AF006087.1 gb:NM_005718.1
CLONE=IMAGE:2307157 /UG=Hs.4764 KIAA0763 gene product /FL=gb:AB018306.1 gb:NM_014869.1
CLONE=IMAGE:1965310 /UG=Hs.289038 Homo sapiens cDNA: FLJ20994 fis, clone CAE02453
/FEA=mRNA /GEN=RFC1 /PROD=replication factor C (activator 1) 1 (145kD) /DB_XREF=gi:4506484 /FL=gb:NM_002913.1
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715. /FEA=mRNA /DB_XREF=gi:10436491 /UG=Hs.323409 Homo sapiens cDNA FLJ14113 fis, clone MAMMA1001715
GEN=IRF1 /PROD=interferon regulatory factor 1 /DB_XREF=gi:4504720 /UG=Hs.80645 interferon regulatory factor 1 /FL=gb:NM_002198.1
/CLONE=IMAGE:2513127 /UG=Hs.169294 transcription factor 7 (T-cell specific, HMG-box) /FL=gb:NM_003202.1
F1 /CLONE=IMAGE:3892546 /UG=Hs.6214 KIAA0731 protein
gb=AB015718 /gi=4001687 /ug=Hs.16134 /len=4221
FEA=mRNA /DB_XREF=gi:10438374 /UG=Hs.323470 Homo sapiens cDNA: FLJ22106 fis, clone HEP17675
. /FEA=mRNA /GEN=HLA-E /PROD=major histocompatibility complex, class I, E /DB_XREF=gi:5031744 /UG=Hs.181392 major histocompatibility complex, class I, E /FL=gb:BC002578.1 gb:NM_005516.1
NA /GEN=D6S81E /PROD=HLA-B associated transcript-1 /DB_XREF=gi:4758111 /UG=Hs.55296 HLA-B associated transcript-1 /FL=gb:BC004350.1 gb:NM_004640.1
transcript variant 1, mRNA. /FEA=mRNA /GEN=GABBR1 /PROD=gamma-aminobutyric acid (GABA) B receptor 1,isoform a precursor /DB_XREF=gi:10835014 /UG=Hs.167017 gamma-aminobutyric acid (GABA) B receptor, 1 /FL=gb:NM_0014
ipt variant 2, mRNA. /FEA=mRNA /GEN=DDR1 /PROD=discoidin receptor tyrosine kinase isoform b /DB_XREF=gi:7669486 /UG=Hs.75562 discoidin domain receptor family, member 1 /FL=gb:NM_001954.2
F1 /CLONE=IMAGE:4564956 /UG=Hs.198253 major histocompatibility complex, class II, DQ alpha 1
EN=VARS2 /PROD=valyl-tRNA synthetase 2 /DB_XREF=gi:5454157 /UG=Hs.159637 valyl-tRNA synthetase 2 /FL=gb:NM_006295.1
PROD=G18.2 protein /DB_XREF=gi:11545816 /UG=Hs.288316 chromosome 6 open reading frame 9 /FL=gb:NM_022107.1 gb:AF155657.1
2468 /UG=Hs.77522 major histocompatibility complex, class II, DM alpha
e 6p12.3-21.2. Contains the gene for TFEB, an NPM1 (Nucleophosmin, Numatrin) pseudogene and the MDFI gene for MyoD family inhibitor (myogenic repressor I-MF). Contains ESTs, STSs, GSSs and two putat... /FEA=mRNA_2 /DB_XREF=g
ROD=cyclin D3 /DB_XREF=gi:4502618 /UG=Hs.83173 cyclin D3 /FL=gb:M90814.1 gb:M92287.1 gb:NM_001760.1
/FEA=mRNA /GEN=ITPR3 /PROD=inositol 1,4,5-triphosphate receptor, type 3 /DB_XREF=gi:4504794 /UG=Hs.77515 inositol 1,4,5-triphosphate receptor, type 3 /FL=gb:D26351.1 gb:NM_002224.1 gb:U01062.1
CLONE=CS0DC003YH03 (3 prime) /UG=Hs.142653 ret finger protein /FL=gb:AF230393.1 gb:J03407.1 gb:NM_006510.1
/CLONE=IMAGE:878391 /UG=Hs.155191 villin 2 (ezrin) /FL=gb:J05021.1 gb:AL162086.1 gb:NM_003379.2
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S /DB_XREF=gi:2772566 /UG=Hs.52644 SKAP55 homologue
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RNA /GEN=FLJ10267 /PROD=hypothetical protein FLJ10267 /DB_XREF=gi:8922321 /UG=Hs.272820 hypothetical protein FLJ10267 /FL=gb:NM_018044.1
D=Unknown (protein for MGC:11333) /DB_XREF=gi:13623312 /FL=gb:BC006259.1
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1 /CLONE=IMAGE:3462325 /UG=Hs.204169 ESTs
NA. /FEA=mRNA /GEN=PILR(BETA) /PROD=paired immunoglobulin-like receptor beta /DB_XREF=gi:7305386 /UG=Hs.9408 paired immunoglobulin-like receptor beta /FL=gb:AF161081.1 gb:NM_013440.1
/FEA=mRNA /GEN=KIAA0543 /PROD=KIAA0543 protein /DB_XREF=gi:3043609 /UG=Hs.98507 KIAA0543 protein
/FEA=mRNA /GEN=KIAA1103 /PROD=KIAA1103 protein /DB_XREF=gi:5689542 /UG=Hs.173159 transforming, acidic coiled-coil containing protein 1
GEN=IKK-beta /PROD=IkB kinase-b /DB_XREF=gi:4185274 /UG=Hs.226573 inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase beta /FL=gb:AF031416.1 gb:AF080158.1
N=BLK /PROD=B lymphoid tyrosine kinase /DB_XREF=gi:4502412 /UG=Hs.2243 B lymphoid tyrosine kinase /FL=gb:NM_001715.1
FEA=mRNA /DB_XREF=gi:10439765 /UG=Hs.287730 Homo sapiens cDNA: FLJ23167 fis, clone LNG09902
sferase) (SIAT4A), mRNA. /FEA=mRNA /GEN=SIAT4A /PROD=sialyltransferase 4A (beta-galactosidasealpha-2,3-sialytransferase) /DB_XREF=gi:4506950 /UG=Hs.301698 sialyltransferase 4A (beta-galactosidase alpha-2,3-sialytransferase) /FL
nit (CPSF1), mRNA. /FEA=mRNA /GEN=CPSF1 /PROD=cleavage and polyadenylation specific factor 1,160kD subunit /DB_XREF=gi:9558724 /UG=Hs.83727 cleavage and polyadenylation specific factor 1, 160kD subunit /FL=gb:U37012.1 gb:
A /GEN=IL11RA /PROD=interleukin 11 receptor, alpha /DB_XREF=gi:4758593 /UG=Hs.64310 interleukin 11 receptor, alpha /FL=gb:BC003110.1 gb:NM_004512.1 gb:U32324.1
A=mRNA /DB_XREF=gi:10281735 /UG=Hs.116481 CD72 antigen
. /FEA=mRNA /GEN=LZIP /PROD=basic leucine zipper protein LZIP /DB_XREF=gi:2599559 /UG=Hs.287921 cAMP responsive element binding protein 3 (luman) /FL=gb:AF211848.1 gb:AF009368.1 gb:AF029674.1 gb:NM_006368.1
YK /PROD=spleen tyrosine kinase /DB_XREF=gi:4507328 /UG=Hs.74101 spleen tyrosine kinase /FL=gb:NM_003177.1
R1 /CLONE=IMAGE:3846116 /UG=Hs.179703 KIAA0129 gene product /FL=gb:D50919.1 gb:NM_014788.1
A=mRNA /GEN=APC2 /PROD=anaphase-promoting complex 2 /DB_XREF=gi:7549800 /UG=Hs.23076 anaphase-promoting complex subunit 2 /FL=gb:AF191337.1 gb:NM_013366.2
nRNA. /FEA=mRNA /GEN=CDK9 /PROD=cyclin-dependent kinase 9 (CDC2-related kinase) /DB_XREF=gi:4502746 /UG=Hs.150423 cyclin-dependent kinase 9 (CDC2-related kinase) /FL=gb:BC001968.1 gb:NM_001261.1 gb:L25676.1
BL1), transcript variant a, mRNA. /FEA=mRNA /GEN=ABL1 /PROD=v-abl Abelson murine leukemia viral oncogenehomolog 1 isoform a /DB_XREF=gi:6382056 /UG=Hs.146355 v-abl Abelson murine leukemia viral oncogene homolog 1 /FL=gb:
plete cds. /FEA=mRNA /PROD=ubiquitin specific protease 11 /DB_XREF=gi:12653164 /UG=Hs.171501 ubiquitin specific protease 11 /FL=gb:BC000350.1 gb:U44839.1 gb:NM_004651.1
RNA /PROD=phosphorylase kinase alpha subunit /DB_XREF=gi:1304117 /UG=Hs.54941 phosphorylase kinase, alpha 2 (liver) /FL=gb:D38616.1 gb:NM_000292.1
1 /CLONE=IMAGE:3610234 /UG=Hs.25601 chromodomain helicase DNA binding protein 3 /FL=gb:U91543.1

rt chain, 1, mitochondrial /FL=gb:NM_004092.2 gb:D13900.

25.1 gb:AF043723.

:NM_003807.1

ctor, RNA polymerase I, C, 110kD /FL=gb:NM_005679.1 gb:L39059.1

2324.1 gb:AF155330.1 gb:NM_013337.1

gb:AB007510.1 gb:AF092565.1 gb:NM_006445.1

e family, protein G /FL=gb:AF059195.1 gb:NM_002359.1

b:M34424.1

protein-coupled receptor, 4 /FL=gb:NM_004720.3 gb:AF197929.1 gb:AF011466.1 gb:AF233092.

000342.1 gb:M22636.1 gb:NM_003089.

7.1 gb:NM_003422.1

_003243.1 gb:L07594.1

family, member 12 (translocating chain-association membrane protein) /FL=gb:U72763.1 gb:U74611.1 gb:U78029.1 gb:U94501.1 gb:U94502.1 gb:NM_003790.1

ion) /FL=gb:AF039916.1 gb:NM_001247.1

:11345540 /UG=Hs.268177 phospholipase C, gamma 1 (formerly subtype 148) /FL=gb:M34667.1 gb:NM_002660.1

ous to yeast UBC7) /FL=gb:BC001738.1 gb:AF032456.1 gb:NM_003343.1

NM_004649.1

siae) 5 (cell division cycle 46) /FL=gb:D83986.1 gb:BC000142.1 gb:BC003656.1 gb:NM_006739.1

s.114432 hypothetical protein FLJ12612 similar to COP9 (constitutive photomorphogenic), subunit 7b (Arabidopsis) /FL=gb:NM_022730.1
gb:AY024365.1

tein), alpha inhibiting activity polypeptide 2 /FL=gb:J03004.1 gb:NM_002070.

_007182.2

ssor) /FL=gb:BC002791.1 gb:AF040707.1 gb:NM_006545.1

70.1 gb:AF301005.1 gb:AF099148.1

ji:5419648 /UG=Hs.23391 Human DNA sequence from clone 696P19 on chromosome 6p12.3-21.2. Contains the gene for TFEB, an NPM1 (Nucleophosmin, Numatrin) pseudogene and the MDFI gene for MyoD family inhibitor (myogenic repress

=gb:L13972.1 gb:NM_003033.1 gb:L29555.1
AB046744.1 gb:NM_013291.

M14752.1 gb:NM_005157.2

sor I-MF). Contains ESTs, STSs, GSSs and two putative CpG