

No	Gene symbol	Gene name	Gene function	Location	Probe number	Mean T/R*		Difference (A vs B)	
						Cluster A	Cluster B	p value	p value after BC¶
1	VRK2	vaccinia related kinase 2	apoptosis and growth	2p16.1	4	0.2216578	-0.091428	1.78882E-06	0.026791191
2	XIRP2	xin actin binding repeat containing 2	actin binding	2q24.3	8	0.2525296	0.0062581	1.27706E-06	0.019126541
3	CNTN6	contactin 6	cell adhesion	3p26.3	6	0.00099	-0.322622	8.6214E-07	0.012912274
4	CNTN4	contactin 4	axon connections	3p26.3-p26.2	19	0.1137656	-0.189603	2.02011E-09	3.02551E-05
5	RBMS3	RNA binding motif single stranded interacting protein 3	c-myc gene binding	3p24.1	16	0.0883685	-0.259709	1.30358E-12	1.95238E-08
6	ARPP-21	cAMP regulated phosphoprotein 21	nerve function	3p22.3	5	0.1407465	-0.211016	3.69533E-07	0.005534503
7	STAC	SH3 and cysteine rich domain	SH3 and cysteine rich	3p22.3-p22.2	4	0.0944739	-0.24017	5.63687E-07	0.008442343
8	MYRIP	myosin VIIA and Rab interacting protein	myosin interacting	3p22.1	10	0.1020163	-0.178061	1.24906E-06	0.018707211
9	CACNA2D3	calcium voltage-gated channel auxiliary subunit alpha2delta 3	tumor suppressor gene	3p21.1-p14.3	20	0.1946772	-0.121071	3.18111E-08	0.000476436
10	PTPRG	protein tyrosine phosphatase, receptor type G	tumor suppressor gene	3p14.2	14	0.0442553	-0.238805	3.32493E-06	0.049797535
11	LRIG1	leucine rich repeats and immunoglobulin like domains 1	tumor suppressor gene	3p14.1	3	0.2577084	-0.234233	1.39033E-06	0.020822901
12	SLIT2	slit guidance ligand 2	tumor suppressor gene	4p15.31	11	0.0410187	-0.214485	1.32879E-06	0.019901247
13	SEL1L3	SEL1L family member 3	lymph node/stomach expression	4p15.2	3	0.1200379	-0.272848	5.63456E-07	0.00843888
14	FSTL5	follistatin like 5	tumor suppressor gene	4q32.2	16	0.0087773	-0.252876	1.05674E-06	0.015826866
15	GPM6A	glycoprotein M6A	oncogenic potential gene	4q34.2	9	0.1142247	-0.225603	2.75025E-07	0.004119045
16	MCCC2	methylcrotonoyl-CoA carboxylase 2	carboxylase	5q13.2	3	0.1370447	-0.323169	2.31579E-07	0.003468354
17	NXPH1	neurexophilin 1	nerve function	7p21.3	6	0.4400862	0.0622393	6.47209E-07	0.009693249
18	H2AFV	H2A histone family member V	histones nucleosome	7p13	2	0.6194794	0.1092316	8.29559E-07	0.012424304
19	SUN3	Sad1 and UNC84 domain containing 3	testis expression	7p12.3	2	0.3635659	-0.120918	8.55676E-07	0.012815461
20	COBL	cordon-bleu WH2 repeat protein	actin regulator	7p12.1	8	0.4966139	0.111728	4.98461E-08	0.000746545
21	SEMA3E	semaphorin 3E	proto-oncogene?	7q21.11	7	0.2570146	-0.078017	1.71778E-06	0.025727224
22	MUC12	mucin 12, cell surface associated	tumor suppressor gene	7q22.1	2	0.7944379	0.2106728	8.58551E-08	0.001285852
23	ORAI2	ORAI calcium release-activated calcium modulator 2	calcium modulator	7q22.1	2	0.370068	-0.099438	3.29493E-07	0.004934813
24	PRKD1	protein kinase D1	target for oncogenic KRas signaling	14q12	9	0.0830602	-0.212465	1.15426E-06	0.017287292
25	SLC39A9	solute carrier family 39 member 9	proto-oncogene	14q24.1	3	0.2246334	-0.265776	2.34539E-08	0.000351268
26	NRXN3	neurexin 3	nerve function	14q24.3-q31.1	29	-0.009645	-0.199779	1.05375E-06	0.015782062
27	CHST14	carbohydrate sulfotransferase 14	sulfotransferases	15q15.1	1	0.5904759	-0.107594	2.16714E-06	0.032457219
28	HS3ST3A1	heparan sulfate-glucosamine 3-sulfotransferase 3A1	tumor growth factor related gene	17p12	5	0.1581726	-0.186387	2.87768E-06	0.043099021
29	MAP2K7	mitogen-activated protein kinase kinase 7	tumor growth factor related gene	19p13.2	2	0.3651435	-0.067787	3.70778E-07	0.005553136
30	SCUBE1	signal peptide, CUB domain and EGF like domain containing 1	EGF (epidermal growth factor)-like	22q13.2	4	0.0642863	-0.256986	5.19618E-07	0.007782325
31	MPPED1	metallophosphoesterase domain containing 1	brain/liver expression	22q13.2	3	0.482682	-0.047041	1.24649E-07	0.001866868
32	CELSR1	cadherin EGF LAG seven-pass G-type receptor 1	non-classic-type cadherin	22q13.31	4	0.0170639	-0.325309	2.06694E-06	0.030956486

*T/R: Tumor/Reference fluorescence intensity ratio. ¶BC: Bonferroni correction.