

Nandhu et al.

Tumor-derived fibulin-3 activates pro-invasive NF-kappa B signaling in glioblastoma cells and their microenvironment

Supplementary Table S-III:

List of NF-kB-regulated genes and their correlation with fibulin-3

Target gene:	EFEMP1	NM_001039348	EGF containing fibulin like extracellular r	HGNC: 3218	2p16.1
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TCGA GLIOBLASTOMA MICROARRAY DATA

Genes regulated by or correlated with NFKB

Total genes: 348

(blank cells mean that the gene ID was not found in TCGA)

Symbol	RefSeq	Approved Name	HGNC ID	Location	CORRELATION WITH EFEMP1			Correlation
					Pearson's Rho	p value	p.adjusted	
ABCA1	NM_005502	ATP binding cassette subfamily A membe	HGNC:29	9q31.1	0.7766	2.27E-100	7.82E-98	High positive correl
ABCB1	NM_000927	ATP binding cassette subfamily B membe	HGNC:40	7q21.12	0.4908	3.50E-31	1.20E-28	
ABCB4	NM_018849	ATP binding cassette subfamily B membe	HGNC:45	7q21.12	-0.0909	0.043856771	1	Poor correl
ABCC6	NM_001171	ATP binding cassette subfamily C membe	HGNC:57	16p13.11	-0.1914	1.91E-05	0.00657115	Poor correl
ABCG8	NM_022437	ATP binding cassette subfamily G membe	HGNC:13887	2p21	-0.3561	3.75E-16	1.29E-13	
ADH1A	NM_000667	alcohol dehydrogenase 1A (class I), alpha	HGNC:249	4q23	0.3901	2.48E-19	8.52E-17	
ADORA1	NM_000674	adenosine A1 receptor	HGNC:262	1q32.1	0.7170	8.36E-79	2.87E-76	High positive correl
ADORA2A	NM_000675	adenosine A2a receptor	HGNC:263	22q11.23	-0.8507	6.24E-139	2.15E-136	High negative correl
AFP	NM_001134	alpha fetoprotein	HGNC:317	4q13.3	-0.8360	8.16E-130	2.81E-127	High negative correl
AGER	NM_001136	advanced glycosylation end-product spec	HGNC:320	6p21.32	-0.1601	0.000363332	0.12498608	Poor correl
AGT	NM_000029	angiotensinogen	HGNC:333	1q42.2	0.6580	2.38E-62	8.18E-60	
AICDA	NM_020661	activation induced cytidine deaminase	HGNC:13203	12p13.31	-0.3007	9.72E-12	3.34E-09	Poor correl
ALOX12	NM_000697	arachidonate 12-lipoxygenase, 12S type	HGNC:429	17p13.1	-0.1845	3.84E-05	0.01320317	Poor correl
AMACR	NM_014324	alpha-methylacyl-CoA racemase	HGNC:451	5p13.2	-0.2116	2.20E-06	0.00075635	Poor correl
AMH	NM_000479	anti-Mullerian hormone	HGNC:464	19p13.3	-0.3674	3.59E-17	1.23E-14	
ANGPT1	NM_001146	angiopoietin 1	HGNC:484	8q23.1	0.3300	5.77E-14	1.99E-11	
APOBEC2	NM_006789	apolipoprotein B mRNA editing enzyme c	HGNC:605	6p21.1	0.2478	2.55E-08	8.76E-06	Poor correl
APOC3	NM_000040	apolipoprotein C3	HGNC:610	11q23.3	-0.8599	3.61E-145	1.24E-142	High negative correl
APOD	NM_001647	apolipoprotein D	HGNC:612	3q29	0.6612	3.77E-63	1.30E-60	
APOE	NM_000041	apolipoprotein E	HGNC:613	19q13.32	0.8639	5.05E-148	1.74E-145	High positive correl
AQP4	NM_001650	aquaporin 4	HGNC:637	18q11.2	0.8248	1.92E-123	6.62E-121	High positive correl
AR	NM_000044	androgen receptor	HGNC:644	Xq12	0.7243	3.65E-81	1.26E-78	High positive correl
ARFRP1	NM_003224	ADP ribosylation factor related protein 1	HGNC:662	20q13.33	-0.6521	6.59E-61	2.27E-58	High negative correl

ART1	NM_004314	ADP-ribosyltransferase 1	HGNC:723	11p15.4	-0.1408	0.001736935	0.59750547	Poor correl
ASPH	NM_004318	aspartate beta-hydroxylase	HGNC:757	8q12.3	-0.6749	1.11E-66	3.80E-64	High negative correl
ASS1	NM_000050	argininosuccinate synthase 1	HGNC:758	9q34.11	-0.5568	2.11E-41	7.25E-39	
ATP1A2	NM_000702	ATPase Na+/K+ transporting subunit alph	HGNC:800	1q23.2	0.7421	3.50E-87	1.20E-84	High positive correl
B2M	NM_004048	beta-2-microglobulin	HGNC:914	15q21.1	0.8711	1.87E-153	6.44E-151	High positive correl
BACE1	NM_012104	beta-secretase 1	HGNC:933	11q23.3	0.7149	3.73E-78	1.28E-75	High positive correl
BAX	NM_004324	BCL2 associated X, apoptosis regulator	HGNC:959	19q13.33	-0.2365	1.11E-07	3.81E-05	Poor correl
BCL2	NM_000633	BCL2, apoptosis regulator	HGNC:990	18q21.33	0.5324	2.32E-37	7.97E-35	
BCL2A1	NM_004049	BCL2 related protein A1	HGNC:991	15q25.1	0.6673	1.08E-64	3.71E-62	
BCL2L1	NM_138578	BCL2 like 1	HGNC:992	20q11.21	0.4476	1.30E-25	4.47E-23	
BCL2L11	NM_138621	BCL2 like 11	HGNC:994	2q13	0.0513	0.255901567	1	Poor correl
BCL3	NM_005178	B-cell CLL/lymphoma 3	HGNC:998	19q13.32	-0.5468	1.05E-39	3.61E-37	
BDKRB1	NM_000710	bradykinin receptor B1	HGNC:1029	14q32.2	-0.2544	1.04E-08	3.58E-06	Poor correl
BDNF	NM_001709	brain derived neurotrophic factor	HGNC:1033	11p14.1	-0.6051	1.79E-50	6.14E-48	
BIRC4	NM_001167	X-linked inhibitor of apoptosis	HGNC:592	Xq25	0.4265	3.60E-23	1.24E-20	
BLNK	NM_013314	B-cell linker	HGNC:14211	10q24.1	0.2179	1.06E-06	0.00036385	Poor correl
BLR1	NM_001716	C-X-C motif chemokine receptor 5	HGNC:1060	11q23.3	-0.3862	6.02E-19	2.07E-16	
BMI1	NM_005180	BMI1 proto-oncogene, polycomb ring fin	HGNC:1066	10p12.2	0.7203	7.27E-80	2.50E-77	High positive correl
BMP2	NM_001200	bone morphogenetic protein 2	HGNC:1069	20p12.3	0.6795	6.64E-68	2.28E-65	
BMP4	NM_001202	bone morphogenetic protein 4	HGNC:1071	14q22.2	-0.8474	8.35E-137	2.87E-134	High negative correl
BNIP3	NM_004052	BCL2 interacting protein 3	HGNC:1084	10q26.3	-0.5051	3.23E-33	1.11E-30	
BRCA2	NM_000059	BRCA2, DNA repair associated	HGNC:1101	13q13.1	0.0190	0.673948881	1	Poor correl
BTK	NM_000061	Bruton tyrosine kinase	HGNC:1133	Xq22.1	0.5997	2.21E-49	7.60E-47	
C3	NM_000064	complement C3	HGNC:1318	19p13.3	0.6562	6.47E-62	2.23E-59	
C4A	NM_007293	complement C4A (Rodgers blood group)	HGNC:1323	6p21.33	N/A			
C4BPA	NM_000715	complement component 4 binding protei	HGNC:1325	1q32.2	-0.7205	6.49E-80	2.23E-77	High negative correl
CALCB	NM_000728	calcitonin related polypeptide beta	HGNC:1438	11p15.2	0.1464	0.00112919	0.38844142	Poor correl
CASP4	NM_001225	caspase 4	HGNC:1505	11q22.3	-0.0150	0.739845237	1	Poor correl
CCL1	NM_002981	C-C motif chemokine ligand 1	HGNC:10609	17q12	-0.4183	2.91E-22	1.00E-19	
CCL11	NM_002986	C-C motif chemokine ligand 11	HGNC:10610	17q12	-0.1340	0.00289026	0.99424951	Poor correl
CCL15	NM_032965	C-C motif chemokine ligand 15	HGNC:10613	17q12	0.7268	5.74E-82	1.98E-79	High positive correl
CCL17	NM_002987	C-C motif chemokine ligand 17	HGNC:10615	16q21	0.2497	1.98E-08	6.82E-06	Poor correl
CCL19	NM_006274	C-C motif chemokine ligand 19	HGNC:10617	9p13.3	0.6564	5.83E-62	2.01E-59	
CCL2	NM_002982	C-C motif chemokine ligand 2	HGNC:10618	17q12	0.8231	1.72E-122	5.92E-120	High positive correl
CCL20	NM_004591	C-C motif chemokine ligand 20	HGNC:10619	2q36.3	0.0378	0.40297742	1	Poor correl
CCL22	NM_002990	C-C motif chemokine ligand 22	HGNC:10621	16q21	-0.2469	2.88E-08	9.92E-06	Poor correl

CCL23	NM_005064	C-C motif chemokine ligand 23	HGNC:10622	17q12	0.5760	8.11E-45	2.79E-42	
CCL28	NM_148672	C-C motif chemokine ligand 28	HGNC:17700	5p12	-0.8465	3.03E-136	1.04E-133	High negative correl
CCL3	NM_002983	C-C motif chemokine ligand 3	HGNC:10627	17q12	0.6574	3.39E-62	1.17E-59	
CCL4	NM_002984	C-C motif chemokine ligand 4	HGNC:10630	17q12	0.8187	3.73E-120	1.28E-117	High positive correl
CCL5	NM_002985	C-C motif chemokine ligand 5	HGNC:10632	17q12	0.7534	3.01E-91	1.04E-88	High positive correl
CCND1	NM_053056	cyclin D1	HGNC:1582	11q13.3	-0.7898	4.48E-106	1.54E-103	High negative correl
CCND2	NM_001759	cyclin D2	HGNC:1583	12p13.32	0.4367	2.48E-24	8.53E-22	
CCR5	NM_000579	C-C motif chemokine receptor 5 (gene/ps	HGNC:1606	3p21.31	0.8403	2.33E-132	8.02E-130	High positive correl
CCR7	NM_001838	C-C motif chemokine receptor 7	HGNC:1608	17q21.2	-0.7140	6.85E-78	2.36E-75	High negative correl
CD209	NM_021155	CD209 molecule	HGNC:1641	19p13.2	-0.4773	2.35E-29	8.08E-27	
CD274	NM_014143	CD274 molecule	HGNC:17635	9p24.1	0.6604	6.03E-63	2.08E-60	
CD38	NM_001775	CD38 molecule	HGNC:1667	4p15.32	-0.2119	2.12E-06	0.0007283	Poor correl
CD3G	NM_000073	CD3g molecule	HGNC:1675	11q23.3	-0.5271	1.57E-36	5.39E-34	
CD40	NM_001250	CD40 molecule	HGNC:11919	20q13.12	-0.3566	3.36E-16	1.15E-13	
CD40LG	NM_000074	CD40 ligand	HGNC:11935	Xq26.3	0.5614	3.27E-42	1.13E-39	
CD44	NM_000610.3	CD44 molecule (Indian blood group)	HGNC:1681	11p13	0.3152	8.20E-13	2.82E-10	
CD48	NM_001778	CD48 molecule	HGNC:1683	1q23.3	-0.1625	0.00029655	0.10201336	Poor correl
CD69	NM_001781	CD69 molecule	HGNC:1694	12p13.31	0.4003	2.36E-20	8.11E-18	
CD74	NM_004355	CD74 molecule	HGNC:1697	5q33.1	0.8473	9.46E-137	3.25E-134	High positive correl
CD80	NM_005191	CD80 molecule	HGNC:1700	3q13.33	0.6402	4.25E-58	1.46E-55	
CD83	NM_004233	CD83 molecule	HGNC:1703	6p23	0.3652	5.70E-17	1.96E-14	
CD86	NM_175862	CD86 molecule	HGNC:1705	3q13.33	0.7996	1.31E-110	4.52E-108	High positive correl
CDX1	NM_001804	caudal type homeobox 1	HGNC:1805	5q32	N/A			
CEBPD	NM_005195	CCAAT/enhancer binding protein delta	HGNC:1835	8q11.21	0.8413	5.43E-133	1.87E-130	High positive correl
CFB	NM_001710	complement factor B	HGNC:1037	6p21.33	0.2187	9.63E-07	0.00033137	Poor correl
CFLAR	NM_003879	CASP8 and FADD like apoptosis regulator	HGNC:1876	2q33.1	-0.0001	0.99870732	1	Poor correl
CHI3L1	NM_001276	chitinase 3 like 1	HGNC:1932	1q32.1	0.8758	4.35E-157	1.49E-154	High positive correl
CIDEA	NM_001279.3	cell death-inducing DFFA-like effector a	HGNC:1976	18p11.21	0.3503	1.18E-15	4.07E-13	
COL1A2	NM_000089	collagen type I alpha 2 chain	HGNC:2198	7q21.3	-0.4395	1.17E-24	4.03E-22	
CR2	NM_001006658	complement C3d receptor 2	HGNC:2336	1q32.2	-0.5328	2.03E-37	6.98E-35	
CREB3	NM_006368	cAMP responsive element binding protein	HGNC:2347	9p13.3	0.2866	9.35E-11	3.21E-08	Poor correl
CRP	NM_000567	C-reactive protein	HGNC:2367	1q23.2	0.1088	0.015720942	1	Poor correl
CSF1	NM_000757	colony stimulating factor 1	HGNC:2432	1p13.3	0.5659	5.26E-43	1.81E-40	
CSF2	NM_000758	colony stimulating factor 2	HGNC:2434	5q31.1	-0.3978	4.23E-20	1.45E-17	
CSF3	NM_000759	colony stimulating factor 3	HGNC:2438	17q21.1	-0.3298	6.00E-14	2.06E-11	
CTSB	NM_001908	cathepsin B	HGNC:2527	8p23.1	0.7390	4.28E-86	1.47E-83	High positive correl

CXCL1	NM_001511	C-X-C motif chemokine ligand 1	HGNC:4602	4q13.3	-0.3761	5.56E-18	1.91E-15	
CXCL3	NM_002090	C-X-C motif chemokine ligand 3	HGNC:4604	4q13.3	-0.1894	2.36E-05	0.00811433	Poor correl
CXCL5	NM_002994	C-X-C motif chemokine ligand 5	HGNC:10642	4q13.3	-0.1129	0.012223017	1	Poor correl
CXCL9	NM_002416	C-X-C motif chemokine ligand 9	HGNC:7098	4q21.1	0.7481	2.49E-89	8.56E-87	High positive correl
CYP19A1	NM_000103	cytochrome P450 family 19 subfamily A n	HGNC:2594	15q21.2	-0.0587	0.193906754	1	Poor correl
CYP27B1	NM_000785	cytochrome P450 family 27 subfamily B n	HGNC:2606	12q14.1	0.0722	0.109513702	1	Poor correl
CYP7B1	NM_004820	cytochrome P450 family 7 subfamily B m	HGNC:2652	8q12.3	0.6024	6.44E-50	2.22E-47	
DEFB4	NM_004942	defensin beta 4A	HGNC:2767	8p23.1	-0.2457	3.35E-08	1.15E-05	Poor correl
DIO2	NM_000793	iodothyronine deiodinase 2	HGNC:2884	14q31.1	0.5261	2.22E-36	7.65E-34	
DMP1	NM_001079911	dentin matrix acidic phosphoprotein 1	HGNC:2932	4q22.1	0.4467	1.65E-25	5.67E-23	
DNASE1L2	NM_001374	deoxyribonuclease 1 like 2	HGNC:2958	16p13.3	0.4456	2.27E-25	7.81E-23	
E2F3	NM_001949	E2F transcription factor 3	HGNC:3115	6p22.3	-0.6186	2.81E-53	9.66E-51	High negative correl
EBI3	NM_005755	Epstein-Barr virus induced 3	HGNC:3129	19p13.3	-0.1218	0.006835804	1	Poor correl
EDN1	NM_001955	endothelin 1	HGNC:3176	6p24.1	-0.0280	0.534825663	1	Poor correl
EGFR	NM_005228	epidermal growth factor receptor	HGNC:3236	7p11.2	0.4196	2.09E-22	7.20E-20	
ELF3	NM_004433	E74 like ETS transcription factor 3	HGNC:3318	1q32.1	-0.7532	3.39E-91	1.17E-88	High negative correl
ENG	NM_000118	endoglin	HGNC:3349	9q34.11	-0.2157	1.37E-06	0.00047218	Poor correl
EPHA1	NM_005232	EPH receptor A1	HGNC:3385	7q34-q35	-0.8169	3.51E-119	1.21E-116	High negative correl
EPO	NM_000799	erythropoietin	HGNC:3415	7q22.1	-0.7047	4.81E-75	1.65E-72	High negative correl
ERBB2	NM_001005862	erb-b2 receptor tyrosine kinase 2	HGNC:3430	17q12	-0.6141	2.45E-52	8.42E-50	
ERVWE1	NM_014590	endogenous retrovirus group W member	HGNC:13525	7q21.2	-0.4151	6.41E-22	2.21E-19	
F3	NM_001993	coagulation factor III, tissue factor	HGNC:3541	1p21.3	0.7683	5.57E-97	1.92E-94	High positive correl
F8	NM_000132	coagulation factor VIII	HGNC:3546	Xq28	0.4584	6.24E-27	2.15E-24	
FABP6	NM_001445	fatty acid binding protein 6	HGNC:3561	5q33.3	-0.3945	8.98E-20	3.09E-17	
FAS	NM_000043	Fas cell surface death receptor	HGNC:11920	10q23.31	0.6700	2.13E-65	7.32E-63	
FASLG	NM_000639	Fas ligand	HGNC:11936	1q24.3	0.7267	6.33E-82	2.18E-79	High positive correl
FCER2	NM_002002	Fc fragment of IgE receptor II	HGNC:3612	19p13.2	0.8038	1.37E-112	4.70E-110	High positive correl
FCGRT	NM_004107	Fc fragment of IgG receptor and transpor	HGNC:3621	19q13.33	0.8451	2.19E-135	7.53E-133	High positive correl
FGF8	NM_006119	fibroblast growth factor 8	HGNC:3686	10q24.32	0.7105	8.20E-77	2.82E-74	High positive correl
FN1	NM_002026	fibronectin 1	HGNC:3778	2q35	-0.4305	1.28E-23	4.39E-21	
FSTL3	NM_005860	follistatin like 3	HGNC:3973	19p13.3	-0.1158	0.010155616	1	Poor correl
FTH1	NM_002032	ferritin heavy chain 1	HGNC:3976	11q12.3	-0.4290	1.91E-23	6.57E-21	
G6PC	NM_000151	glucose-6-phosphatase catalytic subunit	HGNC:4056	17q21.31	-0.7220	2.07E-80	7.12E-78	High negative correl
GADD45B	NM_015675	growth arrest and DNA damage inducible	HGNC:4096	19p13.3	0.5676	2.61E-43	8.98E-41	
GATA3	NM_001002295	GATA binding protein 3	HGNC:4172	10p14	-0.8237	7.82E-123	2.69E-120	High negative correl
GBP1	NM_002053	guanylate binding protein 1	HGNC:4182	1p22.2	0.8415	3.78E-133	1.30E-130	High positive correl

GNAI2	NM_002070	G protein subunit alpha i2	HGNC:4385	3p21.31	0.3350	2.43E-14	8.35E-12	
GNB2L1	NM_006098	receptor for activated C kinase 1	HGNC:4399	5q35.3	-0.4926	1.92E-31	6.62E-29	
GNRH2	NM_001501	gonadotropin releasing hormone 2	HGNC:4420	20p13	-0.4333	6.15E-24	2.11E-21	
GRM2	NM_000839	glutamate metabotropic receptor 2	HGNC:4594	3p21.2	-0.5173	5.06E-35	1.74E-32	
GSTP1	NM_000852	glutathione S-transferase pi 1	HGNC:4638	11q13.2	0.2359	1.20E-07	4.13E-05	Poor correl
GZMB	NM_004131	granzyme B	HGNC:4709	14q12	0.7606	5.67E-94	1.95E-91	High positive correl
HAMP	NM_021175	hepcidin antimicrobial peptide	HGNC:15598	19q13.12	0.1225	0.006536631	1	Poor correl
HAS1	NM_001523	hyaluronan synthase 1	HGNC:4818	19q13.41	0.3562	3.67E-16	1.26E-13	
HBE1	NM_005330	hemoglobin subunit epsilon 1	HGNC:4830	11p15.4	-0.7916	6.87E-107	2.36E-104	High negative correl
HBZ	NM_005332	hemoglobin subunit zeta	HGNC:4835	16p13.3	-0.8228	2.58E-122	8.86E-120	High negative correl
HIF1A	NM_001530	hypoxia inducible factor 1 alpha subunit	HGNC:4910	14q23.2	-0.6885	2.26E-70	7.76E-68	High negative correl
HLA-B	NM_005514	major histocompatibility complex, class I,	HGNC:4932	6p21.33	0.3889	3.29E-19	1.13E-16	
HLA-G	NM_002127	major histocompatibility complex, class I,	HGNC:4964	6p22.1	0.8187	3.77E-120	1.30E-117	High positive correl
HMGNI	NM_004965	high mobility group nucleosome binding	HGNC:4984	21q22.2	-0.7346	1.37E-84	4.73E-82	High negative correl
HMOX1	NM_002133	heme oxygenase 1	HGNC:5013	22q12.3	0.6502	1.90E-60	6.53E-58	
HOXA9	NM_152739	homeobox A9	HGNC:5109	7p15.2	0.1247	0.005621592	1	Poor correl
HSD11B2	NM_000196	hydroxysteroid 11-beta dehydrogenase 2	HGNC:5209	16q22.1	-0.5429	4.56E-39	1.57E-36	
HSP90AA1	NM_001017963	heat shock protein 90 alpha family class A	HGNC:5253	14q32.31	-0.4394	1.21E-24	4.17E-22	
ICAM1	NM_000201	intercellular adhesion molecule 1	HGNC:5344	19p13.2	-0.4372	2.22E-24	7.64E-22	
ICAM1	NM_000201	intercellular adhesion molecule 1	HGNC:5344	19p13.2	-0.4372	2.22E-24	7.64E-22	
IER3	NM_003897	immediate early response 3	HGNC:5392	6p21.33	-0.4440	3.46E-25	1.19E-22	
IFNB1	NM_002176	interferon beta 1	HGNC:5434	9p21.3	0.3556	4.12E-16	1.42E-13	
IFNG	NM_000619	interferon gamma	HGNC:5438	12q15	0.8483	2.08E-137	7.16E-135	High positive correl
IGFBP2	NM_000597	insulin like growth factor binding protein	HGNC:5471	2q35	0.4004	2.29E-20	7.88E-18	
IGHG3	M12958	immunoglobulin heavy constant gamma 3	HGNC:5527	14q32.33	N/A			
IGHG4	K01316	immunoglobulin heavy constant gamma 4	HGNC:5528	14q32.33	N/A			
IL10	NM_000572	interleukin 10	HGNC:5962	1q32.1	0.7303	3.99E-83	1.37E-80	High positive correl
IL11	NM_000641	interleukin 11	HGNC:5966	19q13.42	-0.7362	3.90E-85	1.34E-82	High negative correl
IL12A	NM_000882	interleukin 12A	HGNC:5969	3q25.33	-0.7400	1.92E-86	6.60E-84	High negative correl
IL12B	NM_002187	interleukin 12B	HGNC:5970	5q33.3	0.0621	0.169181662	1	Poor correl
IL13	NM_002188	interleukin 13	HGNC:5973	5q31.1	0.5219	1.00E-35	3.44E-33	
IL15	NM_172174	interleukin 15	HGNC:5977	4q31.21	-0.2376	9.69E-08	3.33E-05	Poor correl
IL15RA	NM_172200	interleukin 15 receptor subunit alpha	HGNC:5978	10p15.1	-0.0622	0.168052133	1	Poor correl
IL17A	NM_002190	interleukin 17A	HGNC:5981	6p12.2	0.2610	4.21E-09	1.45E-06	Poor correl
IL1A	NM_000575	interleukin 1 alpha	HGNC:5991	2q14.1	-0.7417	5.11E-87	1.76E-84	High negative correl
IL1B	NM_000576	interleukin 1 beta	HGNC:5992	2q14.1	0.5693	1.34E-43	4.60E-41	

IL1RN	NM_173842	interleukin 1 receptor antagonist	HGNC:6000	2q14.1	-0.5233	6.13E-36	2.11E-33	
IL2	NM_000586	interleukin 2	HGNC:6001	4q27	0.0171	0.704917697	1	Poor correl
IL23A	NM_016584	interleukin 23 subunit alpha	HGNC:15488	12q13.3	0.1876	2.80E-05	0.00964529	Poor correl
IL27	NM_145659	interleukin 27	HGNC:19157	16p12.1-p1	0.4755	4.03E-29	1.39E-26	
IL2RA	NM_000417	interleukin 2 receptor subunit alpha	HGNC:6008	10p15.1	0.8219	8.06E-122	2.77E-119	High positive correl
IL32	NM_001012635	interleukin 32	HGNC:16830	16p13.3	0.2682	1.48E-09	5.11E-07	Poor correl
IL6	NM_000600	interleukin 6	HGNC:6018	7p15.3	0.3412	7.10E-15	2.44E-12	
IL8	NM_000584	C-X-C motif chemokine ligand 8	HGNC:6025	4q13.3	-0.3100	2.04E-12	7.02E-10	
IL8RA	NM_000634	C-X-C motif chemokine receptor 1	HGNC:6026	2q35	0.3083	2.73E-12	9.39E-10	
IL8RB	NM_001557	C-X-C motif chemokine receptor 2	HGNC:6027	2q35	0.8344	7.53E-129	2.59E-126	High positive correl
IL9	NM_000590	interleukin 9	HGNC:6029	5q31.1	-0.4773	2.30E-29	7.90E-27	
INHBA	NM_002192	inhibin beta A subunit	HGNC:6066	7p14.1	-0.5943	2.70E-48	9.27E-46	
IRF1	NM_002198	interferon regulatory factor 1	HGNC:6116	5q31.1	0.2657	2.14E-09	7.36E-07	Poor correl
IRF2	NM_002199	interferon regulatory factor 2	HGNC:6117	4q35.1	0.6906	5.70E-71	1.96E-68	
IRF4	NM_002460	interferon regulatory factor 4	HGNC:6119	6p25.3	-0.8527	2.91E-140	1.00E-137	High negative correl
IRF7	NM_001572	interferon regulatory factor 7	HGNC:6122	11p15.5	-0.3495	1.39E-15	4.78E-13	
JUNB	NM_002229	JunB proto-oncogene, AP-1 transcription	HGNC:6205	19p13.13	0.7563	2.50E-92	8.60E-90	High positive correl
KCNK5	NM_003740	potassium two pore domain channel sub	HGNC:6280	6p21.2	-0.7311	2.13E-83	7.31E-81	High negative correl
KCNN2	NM_021614	potassium calcium-activated channel sub	HGNC:6291	5q22.3	0.6645	5.44E-64	1.87E-61	
KISS1	NM_002256	KiSS-1 metastasis-suppressor	HGNC:6341	1q32.1	-0.1013	0.024605362	1	Poor correl
KITLG	NM_000899	KIT ligand	HGNC:6343	12q21.32	0.5748	1.59E-44	5.48E-42	
KLK3	NM_001030047	kallikrein related peptidase 3	HGNC:6364	19q13.33	-0.4455	2.31E-25	7.93E-23	
KLRA1	NM_006611	killer cell lectin like receptor A1, pseudog	HGNC:6372	12p13.2	-0.5841	2.42E-46	8.34E-44	
KRT15	NM_002275	keratin 15	HGNC:6421	17q21.2	-0.8310	6.40E-127	2.20E-124	High negative correl
KRT3	NM_057088	keratin 3	HGNC:6440	12q13.13	-0.7768	1.82E-100	6.28E-98	High negative correl
KRT5	NM_000424	keratin 5	HGNC:6442	12q13.13	0.1686	0.00017205	0.05918534	Poor correl
KRT6B	NM_005555	keratin 6B	HGNC:6444	12q13.13	-0.1574	0.000457433	0.15735699	Poor correl
LAMB2	NM_002292	laminin subunit beta 2	HGNC:6487	3p21.31	0.3435	4.55E-15	1.57E-12	
LBP	NM_004139	lipopolysaccharide binding protein	HGNC:6517	20q11.23	0.2374	9.84E-08	3.38E-05	Poor correl
LCN2	NM_005564	lipocalin 2	HGNC:6526	9q34.11	0.0088	0.845410962	1	Poor correl
LEF1	NM_016269	lymphoid enhancer binding factor 1	HGNC:6551	4q25	-0.2489	2.19E-08	7.54E-06	Poor correl
LIPG	NM_006033	lipase G, endothelial type	HGNC:6623	18q21.1	0.0888	0.049057932	1	Poor correl
LTA	NM_000595	lymphotoxin alpha	HGNC:6709	6p21.33	-0.3671	3.84E-17	1.32E-14	
LTB	NM_002341	lymphotoxin beta	HGNC:6711	6p21.33	0.7232	8.29E-81	2.85E-78	High positive correl
LYZ	NM_000239	lysozyme	HGNC:6740	12q15	-0.4753	4.31E-29	1.48E-26	
MADCAM1	NM_130760	mucosal vascular addressin cell adhesion	HGNC:6765	19p13.3	-0.5692	1.37E-43	4.72E-41	

MBP	NM_001025081	myelin basic protein	HGNC:6925	18q23		0.0430	0.340736724	1	Poor correl
MDK	NM_001012334	midkine (neurite growth-promoting facto	HGNC:6972	11p11.2		-0.8215	1.26E-121	4.35E-119	High negative correl
MMP1	NM_002421	matrix metalloproteinase 1	HGNC:7155	11q22.2		-0.7758	4.75E-100	1.63E-97	High negative correl
MMP13	NM_002427	matrix metalloproteinase 13	HGNC:7159	11q22.2		-0.3128	1.25E-12	4.29E-10	
MMP3	NM_002422	matrix metalloproteinase 3	HGNC:7173	11q22.2		-0.7594	1.56E-93	5.38E-91	High negative correl
MMP9	NM_004994	matrix metalloproteinase 9	HGNC:7176	20q13.12		0.1135	0.0117634	1	Poor correl
MTHFR	NM_005957	methylenetetrahydrofolate reductase	HGNC:7436	1p36.22		0.0150	0.739618611	1	Poor correl
MUC2	NM_002457	mucin 2, oligomeric mucus/gel-forming	HGNC:7512	11p15.5	N/A				
MYB	NM_005375	MYB proto-oncogene, transcription facto	HGNC:7545	6q23.3		-0.8563	1.10E-142	3.77E-140	High negative correl
MYC	NM_002467	v-myc avian myelocytomatosis viral onco	HGNC:7553	8q24.21		-0.7788	2.67E-101	9.20E-99	High negative correl
MYLK	NM_053025	myosin light chain kinase	HGNC:7590	3q21.1		0.8882	1.26E-167	4.33E-165	High positive correl
MYOZ1	NM_021245	myozenin 1	HGNC:13752	10q22.2		0.2913	4.47E-11	1.54E-08	Poor correl
NCAM1	NM_000615	neural cell adhesion molecule 1	HGNC:7656	11q23.2		0.4209	1.52E-22	5.23E-20	
NFKB1	NM_003998	nuclear factor kappa B subunit 1	HGNC:7794	4q24		-0.5275	1.36E-36	4.68E-34	
NFKB2	NM_001077493	nuclear factor kappa B subunit 2	HGNC:7795	10q24.32		-0.5131	2.16E-34	7.44E-32	
NFKBIA	NM_020529	NFKB inhibitor alpha	HGNC:7797	14q13.2		0.6513	1.03E-60	3.54E-58	
NFKBIE	NM_004556	NFKB inhibitor epsilon	HGNC:7799	6p21.1		0.1401	0.001842458	0.63380548	Poor correl
NFKBIZ	NM_001005474	NFKB inhibitor zeta	HGNC:29805	3q12.3		0.3776	4.01E-18	1.38E-15	
NGFB	NM_002506	nerve growth factor	HGNC:7808	1p13.2		0.1880	2.69E-05	0.00926919	Poor correl
NLF1	NM_207322	C2 calcium dependent domain containing	HGNC:33627	15q22.2		0.6705	1.54E-65	5.31E-63	
NLRP2	NM_017852	NLR family pyrin domain containing 2	HGNC:22948	19q13.42		-0.7787	2.89E-101	9.92E-99	High negative correl
NOD2	NM_022162	nucleotide binding oligomerization doma	HGNC:5331	16q12.1		0.7052	3.42E-75	1.17E-72	High positive correl
NOS1	NM_000620	nitric oxide synthase 1	HGNC:7872	12q24.22		0.4648	9.67E-28	3.33E-25	
NOS2A	NM_000625	nitric oxide synthase 2	HGNC:7873	17q11.2		0.6619	2.53E-63	8.69E-61	
NOX1	NM_007052	NADPH oxidase 1	HGNC:7889	Xq22.1		-0.0018	0.968532915	1	Poor correl
NPY1R	NM_000909	neuropeptide Y receptor Y1	HGNC:7956	4q32.2		-0.7841	1.49E-103	5.12E-101	High negative correl
NQO1	NM_000903	NAD(P)H quinone dehydrogenase 1	HGNC:2874	16q22.1		-0.7990	2.63E-110	9.03E-108	High negative correl
NR4A2	NM_006186	nuclear receptor subfamily 4 group A me	HGNC:7981	2q22-q23		-0.1502	0.000833208	0.2866237	Poor correl
NRG1	NM_004495	neuregulin 1	HGNC:7997	8p12		0.2567	7.63E-09	2.63E-06	Poor correl
NUAK2	NM_030952	NUAK family kinase 2	HGNC:29558	1q32.1		-0.2439	4.26E-08	1.47E-05	Poor correl
OLR1	NM_002543	oxidized low density lipoprotein receptor	HGNC:8133	12p13.2		0.8031	2.88E-112	9.92E-110	High positive correl
OPN1SW	NM_001708	opsin 1 (cone pigments), short-wave-sen	HGNC:1012	7q32.1		0.2054	4.38E-06	0.00150562	Poor correl
OPRD1	NM_000911	opioid receptor delta 1	HGNC:8153	1p35.3		-0.0389	0.389389852	1	Poor correl
OPRM1	NM_000914	opioid receptor mu 1	HGNC:8156	6q25.2		-0.7340	2.19E-84	7.53E-82	High negative correl
ORM1	NM_000607	orosomuroid 1	HGNC:8498	9q32		-0.7930	1.58E-107	5.43E-105	High negative correl
OXTR	NM_000916	oxytocin receptor	HGNC:8529	3p25.3		0.4853	1.98E-30	6.82E-28	

PFAH2	NM_000437	platelet activating factor acetylhydrolase	HGNC:8579	1p36.11	0.5995	2.42E-49	8.31E-47	
PDGFB	NM_002608	platelet derived growth factor subunit B	HGNC:8800	22q13.1	0.3916	1.78E-19	6.13E-17	
PDYN	NM_024411	prodynorphin	HGNC:8820	20p13	0.3065	3.68E-12	1.27E-09	
PENK	NM_006211	proenkephalin	HGNC:8831	8q12.1	0.5364	5.39E-38	1.85E-35	
PGLYRP1	NM_005091	peptidoglycan recognition protein 1	HGNC:8904	19q13.32	0.6921	2.13E-71	7.32E-69	
PGR	NM_000926	progesterone receptor	HGNC:8910	11q22.1	-0.8366	3.56E-130	1.22E-127	High negative correl
PI3	NM_002638	peptidase inhibitor 3	HGNC:8947	20q13.12	0.5088	9.32E-34	3.21E-31	
PIGF	NM_002643	phosphatidylinositol glycan anchor biosyr	HGNC:8962	2p21	-0.3324	3.71E-14	1.28E-11	
PIK3AP1	NM_152309	phosphoinositide-3-kinase adaptor prote	HGNC:30034	10q24.1	0.5830	3.94E-46	1.36E-43	
PIK3CA	NM_006218	phosphatidylinositol-4,5-bisphosphate 3-	HGNC:8975	3q26.32	0.2732	7.15E-10	2.46E-07	Poor correl
PIM1	NM_002648	Pim-1 proto-oncogene, serine/threonine	HGNC:8986	6p21.2	-0.6783	1.40E-67	4.81E-65	High negative correl
PLA2G1B	AF058921.1	phospholipase A2 group IB	HGNC:9030	12q24.31	0.4433	4.23E-25	1.45E-22	
PLAU	NM_002658	plasminogen activator, urokinase	HGNC:9052	10q22.2	-0.0092	0.838294295	1	Poor correl
PLCD1	NM_006225	phospholipase C delta 1	HGNC:9060	3p22.2	0.4412	7.48E-25	2.57E-22	
PLK3	NM_004073	polo like kinase 3	HGNC:2154	1p34.1	0.0386	0.393123054	1	Poor correl
POMC	NM_000939	proopiomelanocortin	HGNC:9201	2p23.3	0.5773	4.59E-45	1.58E-42	
PPARGC1B	NM_001172698.1	PPARG coactivator 1 beta	HGNC:30022	5q32	0.1490	0.000917893	0.31575527	Poor correl
PRDM1	NM_00198	PR/SET domain 1	HGNC:9346	6q21	-0.1490	0.000915498	0.31493118	Poor correl
PRF1	NM_005041	perforin 1	HGNC:9360	10q22.1	0.5258	2.52E-36	8.66E-34	
PRKACA	NM_002730	protein kinase cAMP-activated catalytic s	HGNC:9380	19p13.1	0.3463	2.60E-15	8.95E-13	
PRKCD	NM_006254	protein kinase C delta	HGNC:9399	3p21.1	0.0061	0.891804543	1	Poor correl
PRL	NM_000948	prolactin	HGNC:9445	6p22.3	0.5621	2.50E-42	8.60E-40	
PSMA2	NM_002787	proteasome subunit alpha 2	HGNC:9531	7p14.1	0.4196	2.11E-22	7.27E-20	
PSMB9	NM_002800	proteasome subunit beta 9	HGNC:9546	6p21.32	0.5917	8.46E-48	2.91E-45	
PSME1	NM_006263	proteasome activator subunit 1	HGNC:9568	14q12	0.2680	1.54E-09	5.28E-07	Poor correl
PSME2	NM_002818	proteasome activator subunit 2	HGNC:9569	14q12	-0.5047	3.73E-33	1.28E-30	
PTAFR	NM_000952	platelet activating factor receptor	HGNC:9582	1p35.3	-0.2117	2.16E-06	0.00074418	Poor correl
PTEN	NM_000314	phosphatase and tensin homolog	HGNC:9588	10q23.31	-0.2403	6.82E-08	2.35E-05	Poor correl
PTGDS	NM_000954	prostaglandin D2 synthase	HGNC:9592	9q34.3	0.8775	1.72E-158	5.92E-156	High positive correl
PTGS2	NM_000963	prostaglandin-endoperoxide synthase 2	HGNC:9605	1q31.1	-0.4099	2.32E-21	7.98E-19	
PTH1H	NM_002820	parathyroid hormone like hormone	HGNC:9607	12p11.22	-0.5371	4.05E-38	1.39E-35	
PTPN1	NM_002827	protein tyrosine phosphatase, non-recep	HGNC:9642	20q13.13	0.3022	7.50E-12	2.58E-09	
PTX3	NM_002852	pentraxin 3	HGNC:9692	3q25.32	-0.0402	0.373020307	1	Poor correl
PYCARD	NM_013258	PYD and CARD domain containing	HGNC:16608	16p11.2	0.4292	1.80E-23	6.18E-21	
RAG1	NM_000448	recombination activating 1	HGNC:9831	11p12	-0.3792	2.84E-18	9.78E-16	
RAG2	NM_000536	recombination activating 2	HGNC:9832	11p13	-0.2265	3.83E-07	0.00013188	Poor correl

RBBP4	NM_005610	RB binding protein 4, chromatin remodeli	HGNC:9887	1p35.1	0.1187	0.008393826	1	Poor correl
REL	NM_002908	REL proto-oncogene, NF-kB subunit	HGNC:9954	2p16.1	-0.4225	1.02E-22	3.50E-20	
RELB	NM_006509	RELB proto-oncogene, NF-kB subunit	HGNC:9956	19q13.32	-0.1543	0.000593485	0.20415886	Poor correl
S100A4	NM_002961	S100 calcium binding protein A4	HGNC:10494	1q21.3	-0.2190	9.29E-07	0.00031967	Poor correl
S100A6	NM_014624	S100 calcium binding protein A6	HGNC:10496	1q21.3	0.2594	5.27E-09	1.81E-06	Poor correl
SAA1	NM_000331	serum amyloid A1	HGNC:10513	11p15.1	0.5888	3.16E-47	1.09E-44	
SAA2	NM_030754	serum amyloid A2	HGNC:10514	11p15.1	0.6890	1.65E-70	5.66E-68	
SAA3P	S73444.1	serum amyloid A3 pseudogene	HGNC:10515	11p15.1	-0.3841	9.72E-19	3.34E-16	
SAT1	NM_002970	spermidine/spermine N1-acetyltransfera	HGNC:10540	Xp22.11	0.5038	5.04E-33	1.73E-30	
SCNN1A	NM_001038	sodium channel epithelial 1 alpha subuni	HGNC:10599	12p13	-0.4049	7.72E-21	2.65E-18	
SDC4	NM_002999	syndecan 4	HGNC:10661	20q13.12	0.2579	6.48E-09	2.23E-06	Poor correl
SELE	NM_000450	selectin E	HGNC:10718	1q24.2	0.5833	4.31E-46	1.48E-43	
SELP	NM_003005	selectin P	HGNC:10721	1q24.2	0.7419	4.34E-87	1.49E-84	High positive correl
SELS	NM_018445	selenoprotein S	HGNC:30396	15q26.3	0.5897	2.07E-47	7.14E-45	
SEN2	NM_021627	SUMO1/sentrin/SMT3 specific peptidase	HGNC:23116	3q27.2	0.1347	0.002756768	0.94832818	Poor correl
SERPINA1	NM_000295	serpin family A member 1	HGNC:8941	14q32.13	-0.4414	7.14E-25	2.46E-22	
SERPINA3	NM_001085	serpin family A member 3	HGNC:16	14q32.13	0.7732	5.53E-99	1.90E-96	High positive correl
SERPINB1	NM_030666	serpin family B member 1	HGNC:3311	6p25.2	0.2934	3.19E-11	1.10E-08	Poor correl
SERPINE1	NM_000602	serpin family E member 1	HGNC:8583	7q22.1	-0.1242	0.005788889	1	Poor correl
SERPINE2	NM_006216	serpin family E member 2	HGNC:8951	2q36.1	-0.7652	8.81E-96	3.03E-93	High negative correl
SH3BGRL	NM_003022	SH3 domain binding glutamate rich prote	HGNC:10823	Xq21.1	-0.1061	0.018540919	1	Poor correl
SKP2	NM_005983	S-phase kinase associated protein 2	HGNC:10901	5p13.2	-0.6768	3.47E-67	1.19E-64	High negative correl
SLC11A2	NM_000617	solute carrier family 11 member 2	HGNC:10908	12q13.12	0.1720	0.000125737	0.04325342	Poor correl
SLC16A1	NM_003051	solute carrier family 16 member 1	HGNC:10922	1p13.2	0.0032	0.944093737	1	Poor correl
SLC2A5	NM_003039	solute carrier family 2 member 5	HGNC:11010	1p36.23	0.8171	2.57E-119	8.83E-117	High positive correl
SLC3A2	NM_001012661	solute carrier family 3 member 2	HGNC:11026	11q12.3	-0.6220	5.03E-54	1.73E-51	High negative correl
SLC6A6	NM_003043	solute carrier family 6 member 6	HGNC:11052	3p25.1	-0.6275	3.16E-55	1.09E-52	High negative correl
SNAI1	NM_005985	snail family transcriptional repressor 1	HGNC:11128	20q13.13	-0.2357	1.22E-07	4.21E-05	Poor correl
SOD1	NM_000454	superoxide dismutase 1, soluble	HGNC:11179	21q22.11	-0.0686	0.12855924	1	Poor correl
SOD2	NM_000636	superoxide dismutase 2, mitochondrial	HGNC:11180	6q25.3	0.4566	1.05E-26	3.61E-24	
SOX9	NM_000346	SRY-box 9	HGNC:11204	17q24.3	0.7704	7.90E-98	2.72E-95	High positive correl
SP7	AF477981.1	Sp7 transcription factor	HGNC:17321	12q13.13	-0.2800	2.68E-10	9.23E-08	Poor correl
SPI1	NM_001080547.1	Spi-1 proto-oncogene	HGNC:11241	11p11.2	0.4501	6.51E-26	2.24E-23	
SPP1	NM_001040058	secreted phosphoprotein 1	HGNC:11255	4q22.1	0.7789	2.38E-101	8.18E-99	High positive correl
ST6GAL1	NM_173216	ST6 beta-galactoside alpha-2,6-sialyltrans	HGNC:10860	3q27.3	-0.1095	0.015127921	1	Poor correl
ST8SIA1	NM_003034	ST8 alpha-N-acetyl-neuraminide alpha-2,	HGNC:10869	12p12.1	0.0288	0.523244155	1	Poor correl

STAT5A	NM_003152	signal transducer and activator of transcr	HGNC:11366	17q21.2	-0.7340	2.19E-84	7.54E-82	High negative correl
TACR1	NM_015727	tachykinin receptor 1	HGNC:11526	2p12	0.0523	0.246995209	1	Poor correl
TAP1	NM_000593	transporter 1, ATP binding cassette subfa	HGNC:43	6p21.32	-0.1932	1.66E-05	0.00571583	Poor correl
TAPBP	NM_003190	TAP binding protein	HGNC:11566	6p21.32	-0.5331	1.76E-37	6.04E-35	
TERT	NM_198253	telomerase reverse transcriptase	HGNC:11730	5p15.33	-0.8454	1.52E-135	5.24E-133	High negative correl
TFEC	NM_001018058	transcription factor EC	HGNC:11754	7q31.2	0.8005	4.86E-111	1.67E-108	High positive correl
TFF3	NM_003226	trefoil factor 3	HGNC:11757	21q22.3	-0.6935	8.76E-72	3.01E-69	High negative correl
TFPI2	NM_006528	tissue factor pathway inhibitor 2	HGNC:11761	7q21.3	-0.6699	2.34E-65	8.06E-63	High negative correl
TGM1	NM_000359	transglutaminase 1	HGNC:11777	14q12	0.4976	3.89E-32	1.34E-29	
TGM2	NM_004613	transglutaminase 2	HGNC:11778	20q11.23	-0.5790	2.20E-45	7.56E-43	
TICAM1	NM_014261	toll like receptor adaptor molecule 1	HGNC:18348	19p13.3	-0.4808	7.89E-30	2.71E-27	
TLR2	NM_003264	toll like receptor 2	HGNC:11848	4q31.3	0.9061	3.30E-185	1.13E-182	High positive correl
TLR9	NM_017442	toll like receptor 9	HGNC:15633	3p21.2	-0.4845	2.53E-30	8.72E-28	
TNC	NM_002160	tenascin C	HGNC:5318	9q33.1	0.7952	1.50E-108	5.16E-106	High positive correl
TNF	NM_000594	tumor necrosis factor	HGNC:11892	6p21.33	-0.6425	1.29E-58	4.43E-56	High negative correl
TNFAIP3	NM_006290	TNF alpha induced protein 3	HGNC:11896	6q23.3	-0.3342	2.65E-14	9.10E-12	
TNFRSF4	NM_003327	TNF receptor superfamily member 4	HGNC:11918	1p36.33	0.6970	8.91E-73	3.07E-70	
TNFRSF9	NM_001561	TNF receptor superfamily member 9	HGNC:11924	1p36.23	-0.3996	2.74E-20	9.41E-18	
TNFSF10	NM_003810	tumor necrosis factor superfamily memb	HGNC:11925	3q26	0.7665	2.83E-96	9.74E-94	High positive correl
TNFSF13B	NM_006573	tumor necrosis factor superfamily memb	HGNC:11929	13q33.3	0.8317	2.84E-127	9.77E-125	High positive correl
TNFSF15	NM_005118	tumor necrosis factor superfamily memb	HGNC:11931	9q32	0.6932	1.04E-71	3.58E-69	
TNIP1	NM_006058	TNFAIP3 interacting protein 1	HGNC:16903	5q33.1	-0.5861	1.00E-46	3.46E-44	
TNIP3	NM_024873	TNFAIP3 interacting protein 3	HGNC:19315	4q27	0.4624	1.97E-27	6.77E-25	
TP53	NM_000546	tumor protein p53	HGNC:11998	17p13.1	-0.8041	9.83E-113	3.38E-110	High negative correl
TPMT	NM_000367	thiopurine S-methyltransferase	HGNC:12014	6p22.3	-0.4280	2.48E-23	8.54E-21	
TRAF1	NM_005658	TNF receptor associated factor 1	HGNC:12031	9q33.2	0.1280	0.004456815	1	Poor correl
TRAF2	NM_021138	TNF receptor associated factor 2	HGNC:12032	9q34.3	-0.2325	1.83E-07	6.28E-05	Poor correl
TREM1	NM_018643	triggering receptor expressed on myeloid	HGNC:17760	6p21.1	0.8699	1.67E-152	5.74E-150	High positive correl
TRPC1	NM_003304	transient receptor potential cation chann	HGNC:12333	3q23	0.6310	5.47E-56	1.88E-53	
TWIST1	NM_000474	twist family bHLH transcription factor 1	HGNC:12428	7p21.1	0.0480	0.287544937	1	Poor correl
UPK1B	NM_006952	uroplakin 1B	HGNC:12578	3q13.32	-0.2160	1.32E-06	0.00045357	Poor correl
UPP1	NM_003364	uridine phosphorylase 1	HGNC:12576	7p12.3	0.1332	0.003076028	1	Poor correl
VCAM1	NM_001078	vascular cell adhesion molecule 1	HGNC:12663	1p21.2	0.8616	2.27E-146	7.80E-144	High positive correl
VEGFC	NM_005429	vascular endothelial growth factor C	HGNC:12682	4q34.3	-0.1191	0.008188162	1	Poor correl
VIM	NM_003380	vimentin	HGNC:12692	10p13	0.1521	0.000710518	0.24441813	Poor correl
WT1	NM_000378	Wilms tumor 1	HGNC:12796	11p13	-0.7916	6.45E-107	2.22E-104	High negative correl

YY1	NM_003403	YY1 transcription factor	HGNC:12856 14q32.2	0.5446	2.46E-39	8.48E-37
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