

**Supplementary Table 1.** Genes correlated to EGFL7 expression in TCGA glioblastoma dataset

Gene	Position	Spearman's correlation	p-value	q-value
ACVRL1	12q13.13	0.796	3.12e-33	6.22e-29
RASIP1	19q13.33	0.785	8.75e-32	8.71e-28
CCM2L	20q11.21	0.780	3.86e-31	2.56e-27
ARHGGEF15	17p13.1	0.767	1.36e-29	6.07e-26
SCARF1	17p13.3	0.767	1.52e-29	6.07e-26
ESAM	11q24.2	0.763	4.01e-29	1.33e-25
GRAP	17p11.2	0.760	1.04e-28	2.94e-25
ADCY4	14q12	0.758	1.62e-28	4.04e-25
USHBP1	19p13.11	0.749	1.60e-27	3.55e-24
DIPK2B	Xp11.3	0.748	2.06e-27	4.10e-24
PEAR1	1q23.1	0.747	2.79e-27	5.06e-24
TMEM204	16p13.3	0.742	7.88e-27	1.31e-23
FUT1	19q13.33	0.737	2.88e-26	4.41e-23
SOX18	20q13.33	0.733	7.96e-26	1.13e-22
ROBO4	11q24.2	0.727	2.92e-25	3.88e-22
SH2D3C	9q34.11	0.725	4.84e-25	6.03e-22
CLEC14A	14q21.1	0.723	6.88e-25	8.06e-22
FLT4	5q35.3	0.720	1.35e-24	1.49e-21
NOTCH4	6p21.32	0.716	2.85e-24	2.98e-21
HSPA12B	20p13	0.716	3.06e-24	3.05e-21
EXOC3L1	16q22.1	0.714	4.27e-24	4.05e-21
BCL6B	17p13.1	0.714	5.13e-24	4.65e-21
TMEM74B	20p13	0.707	2.13e-23	1.84e-20
ECSCR	5q31.2	0.706	2.37e-23	1.96e-20
N4BP3	5q35.3	0.705	3.08e-23	2.45e-20
GIPC3	19p13.3	0.701	7.05e-23	5.40e-20
KANK3	19p13.2	0.700	7.68e-23	5.66e-20
SLC9A3R2	16p13.3	0.691	4.95e-22	3.52e-19
FOXF2	6p25.3	0.689	7.09e-22	4.81e-19
GPR4	19q13.32	0.689	7.25e-22	4.81e-19
ERG	21q22.2	0.688	8.26e-22	5.30e-19
SOX17	8q11.23	0.686	1.22e-21	7.58e-19
PROSER2	10p14	0.683	2.10e-21	1.27e-18
TNFRSF4	1p36.33	0.681	3.15e-21	1.84e-18
ICAM2	17q23.3	0.680	3.55e-21	2.02e-18
MYCT1	6q25.2	0.679	4.18e-21	2.31e-18
HIGD1B	17q21.31	0.679	4.60e-21	2.48e-18
JAG2	14q32.33	0.672	1.56e-20	8.19e-18
CDH5	16q21	0.671	1.92e-20	9.82e-18
EMCN	4q24	0.669	2.76e-20	1.37e-17
ADORA2A	22q11.23	0.669	2.81e-20	1.37e-17
COX4I2	20q11.21	0.668	3.11e-20	1.47e-17
PDGFB	22q13.1	0.667	4.18e-20	1.94e-17
IL3RA	Xp22.33 and Yp11.2	0.666	4.65e-20	2.11e-17
MMRN2	10q23.2	0.661	1.14e-19	5.03e-17
NOSTRIN	2q24.3	0.657	2.26e-19	9.79e-17
PLXDC1	17q12	0.656	2.41e-19	1.02e-16
DLL4	15q15.1	0.656	2.71e-19	1.12e-16
ADGRL4	1p31.1	0.653	4.07e-19	1.65e-16
GJA4	1p34.3	0.652	4.66e-19	1.85e-16
TMEM88	17p13.1	0.649	8.55e-19	3.34e-16
TM4SF18	3q25.1	0.638	4.85e-18	1.86e-15
CLEC1A	12p13.2	0.635	7.12e-18	2.67e-15
MMP25	16p13.3	0.634	8.93e-18	3.29e-15
CYR1	21q21.3	0.629	1.84e-17	6.66e-15
HRC	19q13.33	0.626	2.79e-17	9.91e-15
SLC38A11	2q24.3	0.626	2.96e-17	1.03e-14
CLDN5	22q11.21	0.624	3.78e-17	1.30e-14
FOXO1	20q11.21	0.621	5.89e-17	1.99e-14
LAMC3	9q34.12	0.618	9.27e-17	3.08e-14
LMOD3	3p14.1	0.618	9.68e-17	3.16e-14
TIE1	1p34.2	0.618	1.00e-16	3.22e-14
FAM110D	1p36.11	0.618	1.02e-16	3.22e-14
VWF	12p13.31	0.614	1.67e-16	5.19e-14
FAM162B	6q22.1	0.613	2.01e-16	6.16e-14
SRARP	1p36.13	0.612	2.28e-16	6.88e-14
VSIG2	11q24.2	0.611	2.60e-16	7.72e-14
NOS3	7q36.1	0.611	2.76e-16	8.09e-14
SPAAR	9p13.3	0.609	3.39e-16	9.79e-14
SOX7	8p23.1	0.608	4.06e-16	1.15e-13
ADGRF5	6p12.3	0.608	4.16e-16	1.17e-13
PTGIR	19q13.32	0.606	5.03e-16	1.39e-13
FOXQ1	6p25.3	0.604	7.30e-16	1.99e-13
LRRC70	5q12.1	0.603	7.49e-16	1.99e-13
CARMN	5q32	0.603	7.51e-16	1.99e-13
RGS5	1q23.3	0.603	8.31e-16	2.18e-13
MAGEA12	Xq28	0.603	8.43e-16	2.18e-13
TNFAIP8L1	19p13.3	0.601	1.08e-15	2.75e-13

EGFL7, epidermal growth factor-like domain multiple 7; TCGA, The Cancer Genome Atlas.