

Supplementary table 1: RNA-seq analysis of gene expression in high-invasive and low-invasive HepG2 cells

TOP 20 up regulation genes

TOP 20 down regulation genes

Gene	FPKM.High	FPKM.Low	FC	LOG2FC	Gene	FPKM.High	FPKM.Low	FC	LOG2FC
TPI1	707.50	2.62	270.13	8.08	DSG2	0.19	36.66	0.01	-7.58
DYRK1A	15.23	0.09	173.77	7.44	HIST1H2E	6.99	1261.04	0.01	-7.50
SELENOI	16.03	0.10	157.66	7.30	LASP1	0.30	52.79	0.01	-7.45
APLP2	51.51	0.33	156.22	7.29	HIST1H2A	15.97	1263.82	0.01	-6.31
CTSD	175.46	1.73	101.60	6.67	MYOF	0.20	16.14	0.01	-6.30
PAICS	108.62	1.13	95.75	6.58	TGOLN2	0.25	19.92	0.01	-6.30
ABCC4	27.69	0.33	83.59	6.39	MGAT1	0.34	25.13	0.01	-6.20
ACTB	286.22	3.62	78.96	6.30	NCAPG2	0.31	20.03	0.02	-6.02
CLUH	19.20	0.26	72.95	6.19	NUP214	0.21	13.74	0.02	-6.00
LASP1	191.45	2.71	70.67	6.14	COPS7A	0.76	48.21	0.02	-5.99
TUBB3	36.55	0.53	68.41	6.10	PDXDC1	0.25	13.97	0.02	-5.79
HDLBP	23.82	0.36	66.50	6.06	NUTF2	0.86	45.95	0.02	-5.74
NCLN	35.10	0.54	65.22	6.03	DBNDD1	0.43	21.99	0.02	-5.68
USP19	13.38	0.22	60.69	5.92	LIF	0.24	12.28	0.02	-5.65
FGFRL1	56.73	0.98	57.81	5.85	PSMG2	0.90	43.63	0.02	-5.60
ECE1	15.90	0.30	53.40	5.74	ARID1A	0.21	10.14	0.02	-5.57
SPECC1L	8.59	0.16	53.12	5.73	GSPT1	0.95	44.19	0.02	-5.54
FDFT1	21.81	0.43	50.22	5.65	SCRN1	0.76	34.12	0.02	-5.49
MDM4	6.13	0.12	49.50	5.63	DDX17	1.57	70.78	0.02	-5.49
EIF3L	33.22	0.67	49.49	5.63	HNRNPH1	0.75	33.06	0.02	-5.46