

Genes p<0.05 by DESeq2 and Partek - Control, Hypoxia (3) vs. Control, Normoxia (3)

<i>Gene Name</i>	<i>Partek Fold Change</i>	<i>DESeq2 Fold Change</i>	<i>Gene Name</i>	<i>Partek Fold Change</i>	<i>DESeq2 Fold Change</i>
ADAMTSL4	2.12	2.04	MUC1	2.49	2.54
ADH5	-1.95	-1.59	MYADM	1.39	1.57
AIMP2	-2.57	-2.07	NAB2	1.39	1.57
ALDOA	1.68	1.80	NDRG1	3.53	2.86
ALDOC	4.26	2.81	NEU1	-1.99	-1.61
ALKBH5	1.55	1.69	NOL3	2	1.96
ANGPTL4	7.29	4.80	NOP2	-2.16	-1.74
ANKZF1	2.06	2.03	NOP56	-2.01	-1.65
APBB1	1.37	1.55	NPM3	-3.32	-2.42
APEX1	-1.74	-1.45	NQO1	-4.7	-2.76
APLN	19.9	4.34	OBSL1	1.4	1.59
APOL6	-2.45	-1.87	ODC1	-2.53	-1.89
ARRDC3	1.62	1.74	OSMR	1.37	1.55
BCKDK	1.76	1.97	P4HA2	1.81	1.86
BCL2L2	1.28	1.47	P4HB	1.28	1.47
BNIP3	3.81	2.96	PAQR7	1.68	1.89
BNIP3L	2.24	2.16	PCAT6	4.25	3.24
C11orf98	-2.38	-1.88	PCYT2	-2.31	-1.87
C4orf3	2.02	2.08	PFKL	1.82	1.92
CA12	4.57	3.67	PFKP	1.8	1.92
CACNB3	1.46	1.65	PGAM1	1.56	1.71
CCT6A	-1.9	-1.56	PGAM4	2	2.02
CDK4	-1.93	-1.58	PGK1	2.91	2.65
CHST2	-2.95	-2.15	PGM1	1.79	1.97
CLCN7	-1.91	-1.57	PIGY	-1.81	-1.50
CLTA	-1.8	-1.50	PLOD2	2.65	2.23
CNBP	-1.66	-1.39	PLXNA3	1.66	1.82
CNDP2	-1.69	-1.41	PPP1R13L	1.9	1.97
COX14	-1.89	-1.56	PPP1R16A	1.77	1.89
DDX21	-2.09	-1.65	PPP1R3G	3.45	3.53
DDX41	2.49	2.42	PRMT5	-1.76	-1.46
DUSP1	1.99	2.12	PRMT6	-1.91	-1.57
EGLN1	1.83	1.98	PSMC2	-1.75	-1.45
ENO1	1.57	1.75	PSMG1	-2.52	-1.94
ENO2	5.11	3.31	PTPRF	2.94	2.96
EPAS1	-2.99	-2.28	PYURF	-1.81	-1.50
ERO1A	2.46	2.51	RAB29	-2.05	-1.63

ERRFI1	3	2.25	RASSF7	2.04	2.04
FAM57A	1.57	1.74	RHBDD3	-1.96	-1.60
FTH1	-1.91	-1.60	RNASE4	2.4	2.51
FTH1P3	-1.97	-1.60	RNF208	4.12	3.39
FUT11	1.67	1.83	RRP9	-2.77	-2.15
FZD1	1.52	1.69	RRS1	-2.73	-2.10
GAPDH	2.16	2.24	RSAD1	-1.94	-1.59
GLTP	1.43	1.63	SEPHS2	-1.78	-1.48
GNPDA1	-2.64	-2.06	SERPINE1	2.34	2.44
GPATCH4	-2.72	-2.07	SLC16A3	2.69	2.62
GPI	1.76	1.82	SLC2A1	2.95	2.34
GPR176	1.33	1.53	SLC35E1	1.59	1.73
GYS1	3.03	3.03	SLC3A2	-2.09	-1.71
HAS2	2.01	2.02	SMIM3	1.67	1.87
HCFC1R1	2.02	2.00	SNHG15	-2.46	-1.88
HILPDA	3.44	2.75	SNX33	1.61	1.74
HSD17B10	-1.97	-1.62	SPSB2	-3.46	-2.24
HSPD1	-1.81	-1.50	SQSTM1	-3.18	-2.46
HSPH1	-2.14	-1.70	SRPRB	-1.92	-1.56
IGIP	1.66	1.79	SRXN1	-2.07	-1.69
ILF3-DT	-2.13	-1.70	SSSCA1	-1.83	-1.52
INHBB	10.9	6.92	STAT1	-2.25	-1.74
INSIG2	2.39	2.29	STBD1	1.86	1.92
KCTD11	2.57	2.21	STC1	9.86	4.56
KIAA1191	1.55	1.74	SYNPO	5.55	3.39
LARS	-2	-1.63	TALDO1	-2.04	-1.68
LDHA	1.72	1.82	TAP2	-2.64	-1.94
LMAN1	1.53	1.68	TBC1D9B	1.6	1.77
LOX	2.08	2.34	TOB2	1.32	1.50
LSM10	-1.85	-1.53	TPI1	2.45	2.39
MAFF	1.76	1.97	TRMT12	-2.13	-1.68
MAPK7	1.64	1.83	TXNRD1	-2.53	-1.88
MARCKSL1	1.96	2.01	VEGFA	3.95	2.95
MEIS3	1.58	1.76	VKORC1	1.59	1.73
METTL26	1.46	1.64	VWA1	3.85	2.55
MIR210HG	4.75	2.27	WDR54	1.78	1.95
MOSPD3	1.73	1.92	WSB1	2.02	2.04
MPI	1.7	1.78	XYLT2	1.3	1.49
MRPL24	-1.87	-1.54	ZNF395	4.34	3.73
MRPL52	-1.9	-1.56	ZNF593	-1.8	-1.49

S4 Table. 154 differentially expressed genes as determined by both Partek GSA and DESeq2 with $p < 0.05$. Fold change by each algorithm is given.