

Full g:Profiler Results: Control, Hypoxia (3) vs. Control, Normoxia (3)

Source	Term	Adj. P	$-\log_{10}$ Adj. P	Sig. Genes in Term		
GO: Molecular Function	monosaccharide binding	2.74 E-07	6.5624	ALDOA EGLN1 GPI GYS1	LMAN1 P4HA2 PFKL	PFKP PLOD2 TALDO1
	intramolecular oxidoreductase activity, interconverting aldoses and ketoses	0.0003	3.5110	GNPDA1 GPI	MPI	TPI1
	carbohydrate binding	0.0012	2.8872	ALDOA EGLN1 GPI GYS1	LMAN1 P4HA2 PFKL PFKP	PLOD2 PPP1R3G STBD1 TALDO1
	oxidoreductase activity	0.0013	2.8668	ADH5 ALKBH5 APEX1 EGLN1 ERO1A FTH1 GAPDH	HSD17B10 KIAA1191 LDHA LOX NQO1 P4HA2 P4HB	PGK1 PLOD2 RSAD1 SRXN1 TXNRD1 VKORC1
	intramolecular oxidoreductase activity	0.0015	2.8113	ERO1A GNPDA1	GPI MPI	P4HB TPI1
GO: Biological Process	glucose catabolic process to pyruvate	4.17 E-14	13.3793	ALDOA ALDOC ENO1 ENO2	GAPDH GPI PFKL PFKP	PGAM1 PGK1 TPI1
	canonical glycolysis	4.17 E-14	13.3793	ALDOA ALDOC ENO1 ENO2	GAPDH GPI PFKL PFKP	PGAM1 PGK1 TPI1
	NADH regeneration	4.17 E-14	13.3793	ALDOA ALDOC ENO1 ENO2	GAPDH GPI PFKL PFKP	PGAM1 PGK1 TPI1
	glycolytic process through fructose-6-phosphate	7.19 E-14	13.1434	ALDOA ALDOC ENO1 ENO2	GAPDH GPI PFKL PFKP	PGAM1 PGK1 TPI1
	glycolytic process through glucose-6-phosphate	7.19 E-14	13.1434	ALDOA ALDOC ENO1 ENO2	GAPDH GPI PFKL PFKP	PGAM1 PGK1 TPI1
GO: Cellular Compartment	cytoplasmic part	4.64 E-06	5.3334	N=107		
	cytoplasm	6.67 E-06	5.17577	N=119		
	cytosol	1.85 E-05	4.7333	N=69		
	extracellular exosome	0.0001	3.8590	ADH5	LDHA	PGM1
				ALDOA ALDOC CCT6A CNDP2 ENO1 ENO2 FTH1 GAPDH	LMAN1 MARCKSL1 MPI MUC1 NDRG1 NEU1 P4HB PFKL	PLOD2 PTPRF RAB29 SERPINE1 SLC2A1 SLC3A2 SQSTM1 TALDO1

				GNPDA1	PFKP	TPI1
				GPI	PGAM1	TXNRD1
				HSPD1	PGAM4	VWA1
				HSPH1	PGK1	
				ADH5	LDHA	
				ALDOA	LMAN1	PGM1
				ALDOC	MARCKSL1	PLOD2
				CCT6A	MPI	PTPRF
				CNDP2	MUC1	RAB29
				ENO1	NDRG1	SERPINE1
extracellular vesicle	0.0001	3.7423		ENO2	NEU1	SLC2A1
				FTH1	P4HB	SLC3A2
				GAPDH	PFKL	SQSTM1
				GNPDA1	PFKP	TALDO1
				GPI	PGAM1	TPI1
				HSPD1	PGAM4	TXNRD1
				HSPH1	PGK1	VWA1
				ADH5	GAPDH	PGAM1
				ALDOA	GPI	PGAM4
Glycolysis / Gluconeogenesis	6.99 E-15	14.1556		ALDOC	LDHA	PGK1
				ENO1	PFKL	PGM1
				ENO2	PFKP	TPI1
				ADH5	GAPDH	PGAM4
				ALDOA	GPI	PGK1
Carbon metabolism	5.20 E-10	9.2842		ALDOC	PFKL	TALDO1
				ENO1	PFKP	TPI1
				ENO2	PGAM1	
				ALDOA	GAPDH	PGAM4
				ALDOC	PFKL	PGK1
Biosynthesis of amino acids	6.23 E-10	9.2058		ENO1	PFKP	TALDO1
				ENO2	PGAM1	TPI1
				ALDOA	GAPDH	
				EGLN1	LDHA	SERPINE1
HIF-1 signaling pathway	3.13 E-07	6.5042		ENO1	PFKL	SLC2A1
				ENO2	PGK1	VEGFA
				ALDOA		
				ALDOC	PFKL	PGM1
Pentose phosphate pathway	1.15 E-06	5.9405		GPI	PFKP	TALDO1
				ALDOA	GAPDH	PFKP
				ALDOC	GNPDA1	PGAM1
Glycolysis	4.51 E-10	9.3455		ENO1	GPI	PGK1
				ENO2	PFKL	TPI1
				ALDOA	GPI	PGK1
				ALDOC	GYS1	PGM1
				CHST2	HAS2	SLC2A1
Metabolism of carbohydrates	2.39 E-09	8.6215		ENO1	PFKL	TALDO1
				ENO2	PFKP	TPI1
				GAPDH	PGAM1	XYLT2
				GNPDA1		
				ALDOA	ENO2	PGAM1
				ALDOC	GAPDH	PGK1
Gluconeogenesis	4.18 E-09	8.3785		ENO1	GPI	TPI1
				ALDOA	GAPDH	PFKP
				ALDOC	GNPDA1	PGAM1
Glucose metabolism	8.59 E-09	8.0658		ENO1	GPI	PGK1
				ENO2	PFKL	TPI1
				ADH5	GNPDA1	PFKP
				AIMP2	GPI	PGAM1
				ALDOA	GYS1	PGK1
				ALDOC	HAS2	PGM1
Metabolism	3.28 E-05	4.48433		ANGPTL4	HILPDA	PSMC2
				BCKDK	HSD17B10	SEPHS2
				CA12	INSIG2	SLC16A3
				CACNB3	LARS	SLC2A1
				CHST2	LDHA	SLC3A2

				CNDP2	NEU1	TALDO1
				COX14	NQO1	TPI1
				ENO1	ODC1	TXNRD1
				ENO2	PCYT2	VKORC1
				GAPDH	PFKL	XYLT2
				GLTP		
Wiki Pathways	Pathways in clear cell renal cell carcinoma	1.01 E-13	12.9958	ALDOA ALDOC ENO1 ENO2 GAPDH GPI	LDHA PFKL PFKP PGK1 PGM1	PLOD2 SLC2A1 SQSTM1 TPI1 VEGFA
	Glycolysis and Gluconeogenesis	1.48 E-13	12.8290	ALDOA ALDOC ENO1 ENO2 GAPDH	GPI LDHA PFKL PFKP	PGAM1 PGK1 SLC2A1 TPI1
	Cori Cycle	2.81 E-12	11.5512	GAPDH GPI LDHA	PFKP PGAM1 PGK1	SLC2A1 TALDO1 TPI1
	Metabolic reprogramming in colon cancer	2.96 E-09	8.5287	ENO1 GAPDH GPI LDHA	PFKL PGAM1 PGK1	SLC16A3 SLC2A1 TALDO1
	Photodynamic therapy-induced HIF-1 survival signaling	2.51 E-08	7.6000	BNIP3 BNIP3L EGLN1	LDHA PFKL PGK1	SERPINE1 SLC2A1 VEGFA
	Factor: Churchill; motif: CGGGNN	3.51 E-05	4.4548	N=135		
Factor: Churchill; motif: CGGGNN; match class: 0	3.51 E-05	4.4548	N=135			
Transcription Factor	Factor: HIF1A; motif: NNACGTGCNN; match class: 0	3.81 E-05	4.4195	ALDOA BCKDK BNIP3 BNIP3L C11ORF98 C4ORF3 CA12 CACNB3 CCT6A DDX21 DDX41 ENO1 ENO2 ERO1A FUT11	GAPDH HAS2 HILPDA KCTD11 LDHA MAPK7 METTL26 MOSPD3 NAB2 NOP56 NPM3 OSMR P4HA2 PFKL PFKP	PLXNA3 PPP1R3G PRMT6 PTPRF RSAD1 SEPHS2 SLC16A3 SMIM3 STAT1 STC1 TPI1 VEGFA VKORC1 WDR54
	Factor: HIF1A; motif: NNACGTGCNN	3.81 E-05	4.4195	ALDOA BCKDK BNIP3 BNIP3L C11ORF98 C4ORF3 CA12 CACNB3 CCT6A DDX21 DDX41 ENO1 ENO2 ERO1A FUT11	GAPDH HAS2 HILPDA KCTD11 LDHA MAPK7 METTL26 MOSPD3 NAB2 NOP56 NPM3 OSMR P4HA2 PFKL PFKP	PLXNA3 PPP1R3G PRMT6 PTPRF RSAD1 SEPHS2 SLC16A3 SMIM3 STAT1 STC1 TPI1 VEGFA VKORC1 WDR54

	Factor: HIF1; motif: GNNKACGTGCGGNN; match class: 0	4.17 E-05	4.3796	n = 56		
miRNA Sites	hsa-miR-331-3p	0.0182	1.7394	APBB1 APOL6 DDX21 FUT11 GAPDH	GPI HSPD1 LARS LDHA MARCKSL1	NOP2 PFKL PGAM1 TPI1
Human Protein Atlas	urinary bladder; urothelial cells [Approved, Low]	0.0313	1.5042	n = 62		

S8 Table. Top five g:Profiler results for each category from the analysis of 154 genes differentially expressed in three control fibroblast lines cultured at hypoxia compared to the same three control fibroblast lines cultured at normoxia. Analysis was performed using the default settings and selecting the Ensembl ID with the most annotations for each gene name. The p-value cut-off was 0.05 after g:SCS significance adjustment. If number of significant genes in g:Profiler term is greater than 50, *n* is shown; full lists are available upon request.