

Full g:Profiler Results: Proband, Normoxia (4) vs. Control, Normoxia (3)

Source	Term	Adj. P	$-\log_{10}$ Adj. P	Sig. Genes in Term		
GO: Molecular Function	peptide binding	0.0158	1.7986	CLTB CRIP1 HSPG2	ITM2C LRP1 OXTR	RPS6KB2
	structural molecule activity	0.0418	1.3786	AHNAK CAV2 CLTB COL12A1	HSPB6 HSPG2 IGFBP7	MRPL20 RPL26L1 TNC
GO: Biological Process	tissue development	0.0095	2.0214	ACTA2 ADAMTSL4 ANKRD1 CAV2 COL12A1 CRIP1 FLNB	FZD1 GAA HES4 ITGB1BP1 KLF2 LMO4 PHLDA2	PKDCC SEMA7A SOX4 SRGN TNC
GO: Cellular Compartment	extracellular region	0.0383	1.4163	ACTA2 ADAMTSL4 AHNAK C1R CFD COL12A1 FGF5 FH FLNB	GAA HSPB6 HSPG2 IGFBP7 IL17RA IL1R1 ITM2C MARCKSL1 MYL12B	PKDCC PRDX6 RHOBTB3 RPL26L1 SEMA7A SRGN TIMP3 TNC
	collagen-containing extracellular matrix	0.0464	1.3326	ADAMTSL4 COL12A1 HSPG2	IGFBP7 SEMA7A	TIMP3 TNC
	adherens junction	0.0472	1.3253	AHNAK CAV2 FLNB	FZD1 HSPG2 LRP1	OXTR TNC
KEGG Pathway	Proteoglycans in cancer	0.0146	1.8348	CAV2 FLNB	FZD1 HSPG2	RPS6KB2 TIMP3
Transcription Factor	Factor: MAZ; motif: GGGGAGGG	0.0074	2.1302	ADAMTSL4 AHNAK BEX1 C1R CAV2 CFD COL12A1 CRIP1 EBNA1BP2 FAM43A FGF5 FH FLNB FTSJ1 HES4	HSPB6 HSPG2 IGFBP7 IL17RA ITGB1BP1 ITM2C KLC LMO4 LRP1 MARCKSL1 MRPL20 OSMR PHLDA2 PKDCC PLK3	PPP1R14A PRDX6 PRRC2B PRRC2C RHOBTB3 RPS6KB2 RRP36 SELENOH SELENOW SEMA7A SLC25A23 SOX4 TIMP3 WFS1
	Factor: MAZ; motif: GGGGAGGG; match class: 0	0.0074	2.1302	ADAMTSL4 AHNAK BEX1 C1R CAV2 CFD COL12A1 CRIP1 EBNA1BP2 FAM43A FGF5 FH FLNB	HSPB6 HSPG2 IGFBP7 IL17RA ITGB1BP1 ITM2C KLC1 LMO4 LRP1 MARCKSL1 MRPL20 OSMR PHLDA2	PPP1R14A PRDX6 PRRC2B PRRC2C RHOBTB3 RPS6KB2 RRP36 SELENOH SELENOW SEMA7A SLC25A23 SOX4 TIMP3

			FTSJ1	PKDCC	WFS1
			HES4	PLK3	
			AHNAK	HSPG2	PPP1R14A
			BEX1	IL17RA	PRDX6
			C1R	ITM2C	PRRC2B
			CAV2	KLC1	RHOBTB3
			CFD	LMO4	RPS6KB2
			COL12A1	LRP1	RRP36
	Factor: CKROX; motif: SCCCTCCCC	0.0335	1.4748	MARCKSL1	SELENOW
				MRPL20	SEMA7A
				OSMR	SLC25A23
				PHLDA2	SOX4
				PKDCC	TIMP3
				PLK3	WFS1
			HSPB6		
			AHNAK	HSPG2	PRDX6
			BEX1	IL17RA	PRRC2B
			C1R	ITM2C	RHOBTB3
			CAV2	KLC1	RPS6KB2
			CFD	LMO4	RRP36
			COL12A1	LRP1	SELENOW
	Factor: CKROX; motif: SCCCTCCCC; match class: 0	0.0335	1.4748	MARCKSL1	SEMA7A
				MRPL20	SLC25A23
				OSMR	SOX4
				PHLDA2	TIMP3
				PKDCC	WFS1
				PLK3	
			HSPB6	PPP1R14A	
			AHNAK	HSPG2	PKDCC
			BEX1	IL17RA	PRDX6
			CFD	KLF2	PRRC2B
			COL12A1	LMO4	RHOBTB3
			FH	LRP1	SEMA7A
	Factor: Egr-1; motif: GCGGGGCGG; match class: 1	0.0382	1.4170	MARCKSL1	SLC25A23
				MRPL20	TIMP3
				PHLDA2	WFS1
			HES4		

S5 Table . g:Profiler results from the analysis of 58 genes differentially expressed in four proband fibroblast lines cultured at normoxia compared to 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.