

**Table S1.** Functional enrichments of Biological Processes in the network created by STRING with the proteins more abundant in PTX3 silenced cells.

#Term ID	Term description	Observed gene count	Background gene count	Strength	False discovery rate	Matching proteins in your network (labels)
GO:0000398	mRNA splicing, via spliceosome	6	294	1.24	0.0128	SRSF9, SNRPC, U2AF2, PSPC1, SNRPB, ALYREF
GO:0045765	Regulation of angiogenesis	6	303	1.23	0.01280	GRN, ITGA5, ATP2B4, EPHA2, ENG, ANXA1
GO:0001649	Osteoblast differentiation	4	127	1.43	0.0254	CCDC47, EPHA2, RRBP1, ALYREF