

Process network analysis report significantly altered proteins in ERO1 KO vs WT hypoxic condition (Wilcoxon Mann Whitney test, p<0.05).								
Enrichment by Process Networks				All_KO vs WT I				
#	Networks	Total	pValue	Min FDR	p-value	FDR	In Data	Network Objects from Active Data
1	Protein folding_Response to unfolded proteins	71	1,962E-09	2,080E-07	1,962E-09	2,080E-07	11	Endoplasmin, HSP90 alpha, HSP90 beta, HSC70, GRP78, DNAJC3, HSP60, HYOU1, HSPA2, VCP, Hdj-2
2	Protein folding_Folding in normal condition	119	4,751E-07	2,518E-05	4,751E-07	2,518E-05	11	Endoplasmin, HSP90 alpha, HSP90 beta, Sti1, HSC70, DNAJC3, HSP60, HYOU1, HSPA2, TCP1-beta, Hdj-2
3	Protein folding_ER and cytoplasm	44	2,395E-05	8,463E-04	2,395E-05	8,463E-04	6	UGCG1, HSC70, GRP78, DNAJC3, HYOU1, VCP
4	Translation_Elongation-Termination	233	6,212E-05	1,646E-03	6,212E-05	1,646E-03	12	DDX1, RPL7A, eEF1D, SRP72, IleRS, GlyRS, DARS, TyrRS, ValRS2, RP40, RPL14, MARS
5	Cytoskeleton_Intermediate filaments	81	1,001E-04	2,122E-03	1,001E-04	2,122E-03	7	TMPOA, Plectin 1, Vimentin, Keratin 18, Lamin B1, TMPOB, Lamin A/C
6	Immune response_Phagosome in antigen presentation	243	3,957E-04	6,990E-03	3,957E-04	6,990E-03	11	Endoplasmin, PSMD14, HSP90 alpha, HSP90 beta, Profilin I, Gelsolin, CDC42, GRP78, NF-kB p65/p65, PSMD11, VCP
7	Transcription_mRNA processing	160	1,353E-03	2,049E-02	1,353E-03	2,049E-02	8	hnRNP A2, Prp8, DDX1, SNRP116, SF3A1, DDX39, Mago nashi, SF3B1
8	Immune response_Antigen presentation	197	4,925E-03	6,526E-02	4,925E-03	6,526E-02	8	Endoplasmin, PSMD14, HSP90 alpha, HSP90 beta, ECM29, GRP78, NF-kB p65/p65, PSMD11
9	Protein folding_Protein folding nucleus	58	7,549E-03	7,790E-02	7,549E-03	7,790E-02	4	HSC70, GRP78, HYOU1, DJ-1
10	Cell adhesion_Integrin-mediated cell-matrix adhesion	214	8,021E-03	7,790E-02	8,021E-03	7,790E-02	8	TGM2, Filamin C, Profilin I, ITGA6, ITGB4, ITGA2, CDC42, Cyr61