

Table S4. Enriched GO biological process terms in up-regulated genes

GO ID	Enrichment (p-value)	Number up-regulated	Total	Term	Ontology
GO:0006418	4.9E-07	12	51	tRNA aminoacylation for protein translation	BP
GO:0001666	8.2E-07	17	110	response to hypoxia	BP
GO:0070059	2.2E-06	7	17	intrinsic apoptotic signaling pathway in response to endoplasmic reticulum stress	BP
GO:1990622	3.9E-06	4	4	CHOP-ATF3 complex	CC
GO:0042493	4.5E-06	23	209	response to drug	BP
GO:0007565	6.8E-06	11	54	female pregnancy	BP
GO:1900745	1.0E-05	5	8	positive regulation of p38MAPK cascade	BP
GO:0019953	1.2E-05	4	5	sexual reproduction	BP
GO:1990440	1.4E-05	6	13	positive regulation of transcription from RNA polymerase II promoter in response to endoplasmic reticulum stress	BP
GO:0004826	2.1E-05	4	5	phenylalanine-tRNA ligase activity	MF
GO:0006432	2.1E-05	4	5	phenylalanyl-tRNA aminoacylation	BP
GO:0009328	2.1E-05	4	5	phenylalanine-tRNA ligase complex	CC
GO:0048146	2.4E-05	8	33	positive regulation of fibroblast proliferation	BP
GO:0004812	2.5E-05	9	43	aminoacyl-tRNA ligase activity	MF
GO:0033210	2.7E-05	4	6	leptin-mediated signaling pathway	BP
GO:0045669	3.1E-05	9	42	positive regulation of osteoblast differentiation	BP
GO:0004832	3.2E-05	4	7	valine-tRNA ligase activity	MF
GO:1990441	4.4E-05	4	6	negative regulation of transcription from RNA polymerase II promoter in response to endoplasmic reticulum stress	BP
GO:0006954	5.3E-05	14	108	inflammatory response	BP
GO:0005021	5.3E-05	3	3	vascular endothelial growth factor-activated receptor activity	MF
GO:0042730	5.4E-05	4	6	fibrinolysis	BP
GO:0003779	5.5E-05	18	189	actin binding	MF
GO:0046850	6.2E-05	4	7	regulation of bone remodeling	BP
GO:2000144	6.2E-05	4	6	positive regulation of DNA-templated transcription, initiation	BP
GO:0014032	6.9E-05	4	7	neural crest cell development	BP

GO:0000976	8.6E-05	7	29	transcription regulatory region sequence-specific DNA binding	MF
GO:0031118	8.8E-05	3	3	rRNA pseudouridine synthesis	BP
GO:0044548	1.1E-04	4	7	S100 protein binding	MF
GO:0032040	1.1E-04	8	37	small-subunit processome	CC
GO:0060561	1.2E-04	3	3	apoptotic process involved in morphogenesis	BP
GO:0031668	1.2E-04	5	15	cellular response to extracellular stimulus	BP
GO:0008285	1.2E-04	23	261	negative regulation of cell proliferation	BP
GO:0036488	1.3E-04	3	3	CHOP-C/EBP complex	CC
GO:0010941	1.3E-04	5	12	regulation of cell death	BP
GO:0030515	1.8E-04	6	22	snoRNA binding	MF
GO:0036499	2.0E-04	5	13	PERK-mediated unfolded protein response	BP
GO:0005737	2.1E-04	157	3272	cytoplasm	CC
GO:0060022	2.7E-04	3	4	hard palate development	BP
GO:0030546	2.8E-04	4	9	receptor activator activity	MF
GO:0030308	3.1E-04	11	81	negative regulation of cell growth	BP
GO:0008284	3.2E-04	22	246	positive regulation of cell proliferation	BP
GO:0060674	3.2E-04	4	9	placenta blood vessel development	BP
GO:0009314	3.2E-04	6	25	response to radiation	BP
GO:0001077	3.2E-04	15	139	transcriptional activator activity, RNA polymerase II core promoter proximal region sequence-specific binding	MF
GO:0006968	3.2E-04	4	10	cellular defense response	BP
GO:0042542	3.4E-04	8	41	response to hydrogen peroxide	BP
GO:0006936	3.4E-04	9	54	muscle contraction	BP
GO:0000978	3.4E-04	17	172	RNA polymerase II core promoter proximal region sequence-specific DNA binding	MF
GO:0045471	4.0E-04	10	72	response to ethanol	BP
GO:0008237	4.1E-04	10	76	metallopeptidase activity	MF
GO:0038021	4.5E-04	2	2	leptin receptor activity	MF
GO:0009612	4.7E-04	7	37	response to mechanical stimulus	BP
GO:0006865	4.8E-04	6	34	amino acid transport	BP
GO:0009615	5.3E-04	9	58	response to virus	BP
GO:0038028	5.5E-04	2	2	insulin receptor signaling pathway via phosphatidylinositol 3-kinase	BP
GO:0051591	5.8E-04	7	39	response to cAMP	BP

GO:0004888	6.0E-04	8	56	transmembrane signaling receptor activity	MF
GO:0070410	6.7E-04	4	11	co-SMAD binding	MF
GO:0051973	6.8E-04	5	19	positive regulation of telomerase activity	BP
GO:0071394	6.8E-04	3	6	cellular response to testosterone stimulus	BP
GO:0008203	7.5E-04	6	31	cholesterol metabolic process	BP
GO:2000379	7.8E-04	5	18	positive regulation of reactive oxygen species metabolic process	BP
GO:0046628	7.9E-04	4	14	positive regulation of insulin receptor signaling pathway	BP
GO:0010593	8.1E-04	2	2	negative regulation of lamellipodium assembly	BP
GO:0030199	8.4E-04	4	16	collagen fibril organization	BP
GO:0070561	8.5E-04	2	2	vitamin D receptor signaling pathway	BP
GO:0006438	8.6E-04	2	2	valyl-tRNA aminoacylation	BP
GO:0008140	9.0E-04	4	13	cAMP response element binding protein binding	MF
GO:0032355	9.0E-04	10	78	response to estradiol	BP
GO:0000982	9.0E-04	4	12	transcription factor activity, RNA polymerase II core promoter proximal region sequence-specific binding	MF
GO:0071260	9.2E-04	8	55	cellular response to mechanical stimulus	BP
GO:0061029	9.4E-04	4	13	eyelid development in camera-type eye	BP
GO:0043066	9.4E-04	27	350	negative regulation of apoptotic process	BP
GO:0030506	9.7E-04	3	9	ankyrin binding	MF