

Table S1. Enriched functions for upregulated differentially expressed genes (DEGs) with an enrichment score >2.5.

Enrichment score/ Term	Description	Count	P	DEGs
5.258				
GO:0006091	Generation of precursor metabolites and energy	37	1.21E-07	<i>UQCRC2, ATP5D, TMX1, NDUFB8, PHKB, TMX4, ATP6AP1, NDUFB1, CYB561D2, NDUFS...</i>
GO:0006119	Oxidative phosphorylation	18	3.51E-07	<i>UQCRC2, ATP5D, NDUFA2, NDUFB8, ATP6AP1, NDUFA7, ATP6VIH, ATP6V1D, NDUFA1, NDUFB1...</i>
GO:0015980	Energy derivation by oxidation of organic compounds	22	1.73E-06	<i>UQCRC2, NDUFA2, NDUFB8, PHKB, NDUFA7, CS, CRAT, PPP1CC, NDUFA1, NDUFB1...</i>
GO:0006120	Mitochondrial electron transport, NADH to ubiquinone	10	1.06E-05	<i>NDUFS7, NDUFA2, NDUFB8, NDUFV1, NDUFV2, NDUFA7, DLD, NDUFS3, NDUFA1, NDUFB1</i>
GO:0045333	Cellular respiration	16	1.33E-05	<i>UQCRC2, NDUFA2, NDUFB8, CS, NDUFA7, NDUFA1, NDUFB1, NDUFS7, NNT, UQCRC1...</i>
GO:0042775	Mitochondrial ATP synthesis coupled electron transport	11	1.77E-05	<i>NDUFS7, NDUFA2, UQCRC1, NDUFB8, NDUFV1, NDUFV2, NDUFA7, DLD, NDUFS3, NDUFA1...</i>
GO:0042773	ATP synthesis coupled electron transport	11	1.77E-05	<i>NDUFS7, NDUFA2, UQCRC1, NDUFB8, NDUFV1, NDUFV2, NDUFA7, DLD, NDUFS3, NDUFA1...</i>
GO:0042773	Respiratory electron transport chain	12	1.77E-05	<i>NDUFS7, NDUFA2, SLC1A3, UQCRC1, NDUFB8, NDUFV1, NDUFV2, NDUFA7, DLD, NDUFS3...</i>
GO:0055114	Oxidation reduction	41	6.81E-04	<i>UQCRC2, TMX1, NDUFB8, TMX4, PRDX3, PRDX1, NDUFB1, CYB561D2, NDUFS7, SLC1A3...</i>
4.449				
GO:0006396	RNA processing	50	3.89E-09	<i>RPP38, RPL14, SYNCRIP, INTS1, ZNF638, SFRS2B, DDX23, RRP1B, CLP1, LSM4...</i>
GO:0008380	RNA splicing	33	3.27E-07	<i>POLR2G, POLR2F, STRAP, SYNCRIP, ZNF638, IVNSIABP, PRPF19, SFRS2B, DDX23, FRG1...</i>
GO:0006397	mRNA processing	33	3.31E-06	<i>POLR2G, POLR2F, STRAP, SYNCRIP, PRPF19, SFRS2B, DDX23, FRG1, CLP1, DHX15...</i>
GO:0016071	mRNA metabolic process	33	5.19E-05	<i>POLR2G, POLR2F, STRAP, SYNCRIP, PRPF19, SFRS2B, DDX23, FRG1, CLP1, DHX15...</i>
GO:0000375	RNA splicing, via transesterification reactions	16	6.92E-03	<i>PABPN1, POLR2G, DHX9, POLR2F, PTBP1, HNRNPA2B1, HNRNPR, PAPOLA, DDX23, CLP1...</i>
GO:0000377	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	16	6.92E-03	<i>PABPN1, POLR2G, DHX9, POLR2F, PTBP1, HNRNPA2B1, HNRNPR, PAPOLA, DDX23, CLP1...</i>
GO:0000398	Nuclear mRNA splicing, via spliceosome	16	6.92E-03	<i>PABPN1, POLR2G, DHX9, POLR2F, PTBP1, HNRNPA2B1, HNRNPR, PAPOLA, DDX23, CLP1...</i>
3.040				
GO:0006511	Ubiquitin-dependent protein catabolic process	24	3.82E-05	<i>PSMB10, USP7, RAD23B, UBE2A, UFD1L, PPP2R5C, UBE2I, UBE2C, CCNB1, PSMC6...</i>
GO:0010498	Proteasomal protein catabolic process	15	1.26E-04	<i>PSMB10, RAD23B, PPP2R5C, UBE2C, CCNB1, PSMC6, PSMD13, PSMC5, PSMB6, PSME1...</i>
GO:0043161	Proteasomal ubiquitin-dependent protein catabolic process	15	1.26E-04	<i>PSMB10, RAD23B, PPP2R5C, UBE2C, CCNB1, PSMC6, PSMD13, PSMC5, PSMB6, PSME1...</i>
GO:0009057	Macromolecule catabolic process	46	1.38E-04	<i>PSMB10, USP7, RAD23B, SPG7, PPP2R5C, RNASEH1, UBE3C, DNASE1L1, RPA2, UBE2D2...</i>
GO:0044265	Cellular macromolecule catabolic process	42	2.84E-04	<i>PSMB10, USP7, RAD23B, PPP2R5C, RNASEH1, UBE3C, DNASE1L1, RPA2, UBE2D2, PSMB6...</i>
GO:0019941	Modification-dependent protein catabolic process	33	2.99E-04	<i>PSMB10, USP7, RAD23B, PPP2R5C, UBE3C, PSMB6, UBE2D2, CUL7, CUL9, FBXO28...</i>
GO:0043632	Modification-dependent macromolecule catabolic process	33	2.99E-04	<i>PSMB10, USP7, RAD23B, PPP2R5C, UBE3C, PSMB6, UBE2D2, CUL7, CUL9, FBXO28...</i>
GO:0031145	Anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process	12	3.72E-04	<i>CCNB1, PSMB10, PSMC6, PSMD13, PSMB6, PSMC5, PSME1, PSMC3, PSMD10, PSMD5...</i>
GO:0051437	Positive regulation of ubiquitin-protein ligase activity during mitotic cell cycle	12	5.10E-04	<i>CCNB1, PSMB10, PSMC6, PSMD13, PSMB6, PSMC5, PSME1, PSMC3, PSMD10, PSMD5...</i>
GO:0030163	Protein catabolic process	35	5.22E-04	<i>PSMB10, USP7, RAD23B, SPG7, PPP2R5C, UBE3C, PSMB6, UBE2D2, CUL7, CUL9...</i>
GO:0051443	Positive regulation of ubiquitin-protein ligase activity	12	6.90E-04	<i>CCNB1, PSMB10, PSMC6, PSMD13, PSMB6, PSMC5, PSME1, PSMC3, PSMD10, PSMD5...</i>
GO:0051439	Regulation of ubiquitin-protein ligase activity during mitotic cell cycle	12	7.98E-04	<i>CCNB1, PSMB10, PSMC6, PSMD13, PSMB6, PSMC5, PSME1, PSMC3, PSMD10, PSMD5...</i>
GO:0051603	Proteolysis involved in cellular protein catabolic process	33	9.88E-04	<i>PSMB10, USP7, RAD23B, PPP2R5C, UBE3C, PSMB6, UBE2D2, CUL7, CUL9, FBXO28...</i>
GO:0044257	Cellular protein catabolic process	33	1.04E-03	<i>PSMB10, USP7, RAD23B, PPP2R5C, UBE3C, PSMB6, UBE2D2, CUL7, CUL9, FBXO28...</i>
GO:0051351	Positive regulation of ligase activity	12	1.06E-03	<i>CCNB1, PSMB10, PSMC6, PSMD13, PSMB6, PSMC5, PSME1, PSMC3, PSMD10, PSMD5...</i>
GO:0051436	Negative regulation of ubiquitin-protein ligase activity during mitotic cell cycle	11	1.28E-03	<i>PSMB10, PSMC6, PSMD13, PSMB6, PSMC5, PSME1, PSMC3, PSMD10, PSMD5, UBE2C...</i>

GO:0051352	Negative regulation of ligase activity	11	1.70E-03	<i>PSMB10, PSMC6, PSMD13, PSMB6, PSMC5, PSME1, PSMC3, PSMD10, PSMD5, UBE2C...</i>
GO:0051444	Negative regulation of ubiquitin-protein ligase activity	11	1.70E-03	<i>PSMB10, PSMC6, PSMD13, PSMB6, PSMC5, PSME1, PSMC3, PSMD10, PSMD5, UBE2C...</i>
GO:0032269	Negative regulation of cellular protein metabolic process	19	1.76E-03	<i>IBTK, HSP90AB1, PSMB10, CLN3, YWHAB, UBE2C, EIF4A3, PSMC6, PSMC5, PSMB6...</i>
GO:0051438	Regulation of ubiquitin-protein ligase activity	12	1.78E-03	<i>CCNB1, PSMB10, PSMC6, PSMD13, PSMB6, PSMC5, PSME1, PSMC3, PSMD10, PSMD5...</i>
GO:0031398	Positive regulation of protein ubiquitination	12	1.78E-03	<i>CCNB1, PSMB10, PSMC6, PSMD13, PSMB6, PSMC5, PSME1, PSMC3, PSMD10, PSMD5...</i>
GO:0051340	Regulation of ligase activity	12	2.55E-03	<i>CCNB1, PSMB10, PSMC6, PSMD13, PSMB6, PSMC5, PSME1, PSMC3, PSMD10, PSMD5...</i>
GO:0051248	Negative regulation of protein metabolic process	19	2.80E-03	<i>IBTK, HSP90AB1, PSMB10, CLN3, YWHAB, UBE2C, EIF4A3, PSMC6, PSMC5, PSMB6...</i>
GO:0000278	Mitotic cell cycle	29	2.92E-03	<i>PSMB10, CETN3, CETN2, CCNG2, PSMB6, PSMD5, NUDC, PSMD9, PDS5A, PAPD7...</i>
GO:0031397	Negative regulation of protein ubiquitination	11	3.25E-03	<i>PSMB10, PSMC6, PSMD13, PSMB6, PSMC5, PSME1, PSMC3, PSMD10, PSMD5, UBE2C...</i>
GO:0031400	Negative regulation of protein modification process	14	5.46E-03	<i>PSMB10, IBTK, YWHAB, UBE2C, PSMC6, PSMC5, PSMB6, PSMD13, PSME1, PSMC3...</i>
GO:0031396	Regulation of protein ubiquitination	12	6.60E-03	<i>CCNB1, PSMB10, PSMC6, PSMD13, PSMB6, PSMC5, PSME1, PSMC3, PSMD10, PSMD5...</i>
GO:0006508	Proteolysis	49	1.23E-02	<i>UQCRC2, SPG7, MMP9, PPP2R5C, MMP7, MIPEP, MMP1, CUL7, FAP, CD46...</i>

GO: gene ontology.

Table S2. Enriched functions for downregulated differentially expressed genes (DEGs) with an enrichment score >2.5.

Enrichment score/ Term	Description	Co unt	P	DEGs
3.467				
GO:0035295	Tube development	24	1.32E-05	<i>DLC1, CAV2, FGFR4, NRP1, EPAS1, TMBIM6, SMAD4, MGP, CXCL12, SLIT2...</i>
GO:0030324	Lung development	13	7.37E-04	<i>CAV2, FGFR4, EPAS1, TMBIM6, MGP, ASAH1, ALDH1A2, TCF21, LAMA5, HOXA5...</i>
GO:0030323	Respiratory tube development	13	9.15E-04	<i>CAV2, FGFR4, EPAS1, TMBIM6, MGP, ASAH1, ALDH1A2, TCF21, LAMA5, HOXA5...</i>
GO:0060541	Respiratory system development	13	1.53E-03	<i>CAV2, FGFR4, EPAS1, TMBIM6, MGP, ASAH1, ALDH1A2, TCF21, LAMA5, HOXA5...</i>
2.802				
GO:0032970	Regulation of actin filament-based process	12	5.94E-04	<i>DLC1, SIPRI, TSC1, TNNC1, CAPZA2, ILK, ELN, SPTBN1, MYO1F, ARPC5...</i>
GO:0032956	Regulation of actin cytoskeleton organization	11	1.76E-03	<i>DLC1, SIPRI, TSC1, CAPZA2, ILK, ELN, SPTBN1, MYO1F, ARPC5, CXCL12...</i>
GO:0051493	Regulation of cytoskeleton organization	13	3.75E-03	<i>DLC1, CAV2, CAV1, CAPZA2, ELN, MYO1F, ARPC5, CXCL12, DSTN, SIPRI...</i>
2.672				
GO:0051270	Regulation of cell motion	22	7.21E-05	<i>RTN4, DLC1, IL6, F10, NRP1, SP100, MYO1F, JAG1, CXCL12, LAMA2...</i>
GO:0040012	Regulation of locomotion	21	1.64E-04	<i>RTN4, DLC1, IL6, F10, MYO1F, JAG1, CXCL12, AGER, SLIT2, LAMA2...</i>
GO:0030334	Regulation of cell migration	19	3.57E-04	<i>RTN4, DLC1, IL6, F10, MYO1F, JAG1, CXCL12, LAMA2, MAPK1, LAMA3...</i>
GO:0040017	Positive regulation of locomotion	11	1.32E-02	<i>MAPK1, IL6, F10, SIPRI, ILK, PDGFRA, HBEGF, MYO1F, CXCL12, AGER...</i>
GO:0051272	Positive regulation of cell motion	10	3.37E-02	<i>MAPK1, IL6, F10, SIPRI, ILK, PDGFRA, HBEGF, MYO1F, BCL6, CXCL12</i>
GO:0030335	Positive regulation of cell migration	9	4.96E-02	<i>MAPK1, IL6, F10, SIPRI, ILK, PDGFRA, HBEGF, MYO1F, CXCL12</i>
2.646				
GO:0035295	Tube development	24	1.32E-05	<i>DLC1, CAV2, FGFR4, NRP1, EPAS1, TMBIM6, SMAD4, MGP, CXCL12, SLIT2...</i>
GO:0001763	Morphogenesis of a branching structure	13	8.02E-05	<i>NRP1, COL13A1, SMAD4, MGP, CXCL12, SEMA5A, TCF21, GPC3, LAMA5, HOXA5...</i>
GO:0048754	Branching morphogenesis of a tube	12	9.03E-05	<i>SEMA5A, TCF21, NRP1, GPC3, HOXA5, LAMA5, FOXF1, ILK, NOTCH4, SMAD4...</i>
GO:0035239	Tube morphogenesis	14	1.03E-03	<i>DLC1, NRP1, SMAD4, MGP, CXCL12, SEMA5A, TCF21, GPC3, TSC1, LAMA5...</i>
GO:0048729	Tissue morphogenesis	17	1.08E-03	<i>DLC1, TNNC1, RXRA, DAG1, SMAD4, JAG1, SLIT2, ALDH1A2, TCF21, GPC3...</i>
GO:0002009	Morphogenesis of an epithelium	12	1.34E-03	<i>DLC1, TCF21, ALDH1A2, GPC3, TSC1, HOXA5, LAMA5, FOXF1, ILK, SMAD4...</i>
GO:0060562	Epithelial tube morphogenesis	9	3.32E-03	<i>DLC1, TCF21, GPC3, TSC1, HOXA5, LAMA5, FOXF1, ILK, SMAD4</i>
GO:0060675	Ureteric bud morphogenesis	5	1.27E-02	<i>TCF21, GPC3, LAMA5, ILK, SMAD4</i>
GO:0001658	Branching involved in ureteric bud morphogenesis	5	1.27E-02	<i>TCF21, GPC3, LAMA5, ILK, SMAD4</i>
GO:0001657	Ureteric bud development	6	1.29E-02	<i>TCF21, GPC3, LAMA5, ILK, SMAD4, SLIT2</i>
GO:0001656	Metanephros development	6	3.10E-02	<i>TCF21, GPC3, LAMA5, ILK, SMAD4, SLIT2</i>
GO:0060429	Epithelium development	15	3.13E-02	<i>DLC1, SMAD4, DAG1, JAG1, ALDH1A2, TCF21, SIPRI, GPC3, LAMA3, TSC1...</i>
GO:0001822	Kidney development	9	4.12E-02	<i>TCF21, ALDH1A2, GPC3, TSC1, LAMA5, ILK, SMAD4, ZBTB16, SLIT2</i>

GO: gene ontology.