**Table S4. Functional annotation of Clusters from TMT-MS data.**
List of significant (false discovery rate [FDR]<0.05) gene ontology terms associated with proteins differentially expressed in WT vs. PCKO mice.

### Cluster 1 - Gene ontology: Biological Processes (GO:BP)

| GO term | Description | p-value | FDR |
|---|---|---|---|
| GO:1901566 | organonitrogen compound biosynthetic process | 0 | 0 |
| GO:0043603 | cellular amide metabolic process | 0 | 0 |
| GO:0006518 | peptide metabolic process | 0 | 0 |
| GO:0043604 | amide biosynthetic process | 0 | 0 |
| GO:0043043 | peptide biosynthetic process | 0 | 0 |
| GO:0006412 | translation | 0 | 0 |
| GO:0022613 | ribonucleoprotein complex biogenesis | 0 | 0 |
| GO:0042254 | ribosome biogenesis | 0 | 0 |
| GO:0002181 | cytoplasmic translation | 0 | 0 |
| GO:0042255 | ribosome assembly | 0 | 0 |
| GO:0022618 | ribonucleoprotein complex assembly | 4.22E-15 | 3.46E-12 |
| GO:0042274 | ribosomal small subunit biogenesis | 5.33E-15 | 4.00E-12 |
| GO:0071826 | ribonucleoprotein complex subunit organization | 1.11E-14 | 7.70E-12 |
| GO:0042273 | ribosomal large subunit biogenesis | 1.93E-14 | 1.24E-11 |
| GO:0000027 | ribosomal large subunit assembly | 8.84E-13 | 5.31E-10 |
| GO:0000028 | ribosomal small subunit assembly | 8.48E-11 | 4.78E-08 |
| GO:0006364 | rRNA processing | 1.14E-09 | 6.04E-07 |
| GO:0016072 | rRNA metabolic process | 5.22E-09 | 2.61E-06 |
| GO:0006417 | regulation of translation | 2.86E-08 | 1.36E-05 |
| GO:0005977 | glycogen metabolic process | 7.59E-08 | 3.11E-05 |
| GO:0006073 | cellular glucan metabolic process | 7.59E-08 | 3.11E-05 |
| GO:0044042 | glucan metabolic process | 7.59E-08 | 3.11E-05 |
| GO:0034248 | regulation of cellular amide metabolic process | 1.20E-07 | 4.72E-05 |
| GO:0065003 | protein-containing complex assembly | 1.69E-07 | 6.34E-05 |
| GO:0034660 | ncRNA metabolic process | 2.26E-07 | 8.16E-05 |
| GO:0006112 | energy reserve metabolic process | 2.91E-07 | 1.01E-04 |
| GO:0000462 | maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) | 3.11E-07 | 1.04E-04 |
| GO:0043933 | protein-containing complex subunit organization | 4.49E-07 | 1.45E-04 |
| GO:0044264 | cellular polysaccharide metabolic process | 5.18E-07 | 1.61E-04 |
| GO:0034470 | ncRNA processing | 5.55E-07 | 1.67E-04 |
| GO:0070925 | organelle assembly | 6.08E-07 | 1.77E-04 |
| GO:0010608 | posttranscriptional regulation of gene expression | 8.05E-07 | 2.27E-04 |
| GO:0005976 | polysaccharide metabolic process | 9.97E-07 | 2.72E-04 |

| | | | |
|---|---|---|---|
| GO:0030490 | maturation of SSU-rRNA | 1.38E-06 | 3.66E-04 |
| GO:0034622 | cellular protein-containing complex assembly | 2.87E-06 | 7.39E-04 |
| GO:0015980 | energy derivation by oxidation of organic compounds | 3.26E-05 | 0.008168703 |
| GO:0005978 | glycogen biosynthetic process | 5.03E-05 | 0.011938724 |
| GO:0009250 | glucan biosynthetic process | 5.03E-05 | 0.011938724 |

## Cluster 2 - Gene ontology: Biological Processes (GO:BP)

| GO term | Description | p-value | FDR |
|---|---|---|---|
| GO:0007010 | cytoskeleton organization | 2.52E-08 | 2.27E-04 |
| GO:0007519 | skeletal muscle tissue development | 1.71E-07 | 5.22E-04 |
| GO:0061061 | muscle structure development | 1.74E-07 | 5.22E-04 |
| GO:0060538 | skeletal muscle organ development | 2.39E-07 | 5.40E-04 |
| GO:0030029 | actin filament-based process | 5.50E-07 | 9.31E-04 |
| GO:0007517 | muscle organ development | 6.20E-07 | 9.31E-04 |
| GO:0014706 | striated muscle tissue development | 9.87E-07 | 0.001271472 |
| GO:0060537 | muscle tissue development | 1.47E-06 | 0.001654921 |
| GO:0042692 | muscle cell differentiation | 2.82E-05 | 0.02705853 |
| GO:0048641 | regulation of skeletal muscle tissue development | 3.00E-05 | 0.02705853 |
| GO:0055001 | muscle cell development | 3.38E-05 | 0.027669422 |
| GO:0030036 | actin cytoskeleton organization | 4.51E-05 | 0.033883856 |

## Cluster 3 - Gene ontology: Biological Processes (GO:BP)

| GO term | Description | p-value | FDR |
|---|---|---|---|
| GO:0046907 | intracellular transport | 2.22E-15 | 1.00E-11 |
| GO:0034613 | cellular protein localization | 2.66E-15 | 1.00E-11 |
| GO:0070727 | cellular macromolecule localization | 3.33E-15 | 1.00E-11 |
| GO:0045184 | establishment of protein localization | 1.67E-14 | 3.75E-11 |
| GO:0015031 | protein transport | 4.37E-14 | 7.89E-11 |
| GO:0015833 | peptide transport | 1.15E-13 | 1.71E-10 |
| GO:0006886 | intracellular protein transport | 1.33E-13 | 1.71E-10 |
| GO:0042886 | amide transport | 1.94E-13 | 2.19E-10 |
| GO:0051649 | establishment of localization in cell | 1.66E-12 | 1.67E-09 |
| GO:0033365 | protein localization to organelle | 6.07E-10 | 5.47E-07 |
| GO:0044248 | cellular catabolic process | 4.55E-08 | 3.73E-05 |
| GO:0016192 | vesicle-mediated transport | 3.58E-07 | 2.69E-04 |
| GO:0007034 | vacuolar transport | 4.07E-07 | 2.81E-04 |
| GO:0036503 | ERAD pathway | 4.36E-07 | 2.81E-04 |
| GO:0009894 | regulation of catabolic process | 6.58E-07 | 3.74E-04 |
| GO:0072657 | protein localization to membrane | 6.64E-07 | 3.74E-04 |
| GO:1901575 | organic substance catabolic process | 9.10E-07 | 4.83E-04 |
| GO:0072594 | establishment of protein localization to organelle | 1.10E-06 | 5.49E-04 |

| | | | |
|---|---|---|---|
| GO:0072665 | protein localization to vacuole | 2.33E-06 | 0.001107194 |
| GO:0050821 | protein stabilization | 5.45E-06 | 0.002457095 |
| GO:0007031 | peroxisome organization | 5.73E-06 | 0.002462005 |
| GO:0009057 | macromolecule catabolic process | 9.20E-06 | 0.003772423 |
| GO:0072666 | establishment of protein localization to vacuole | 1.03E-05 | 0.004024816 |
| GO:0030433 | ubiquitin-dependent ERAD pathway | 1.24E-05 | 0.004666264 |
| GO:0016236 | macroautophagy | 1.53E-05 | 0.005411462 |
| GO:0031329 | regulation of cellular catabolic process | 1.56E-05 | 0.005411462 |
| GO:0006457 | protein folding | 2.46E-05 | 0.008214725 |
| GO:0006914 | autophagy | 2.99E-05 | 0.009303523 |
| GO:0061919 | process utilizing autophagic mechanism | 2.99E-05 | 0.009303523 |
| GO:1904292 | regulation of ERAD pathway | 4.17E-05 | 0.012536745 |
| GO:0007029 | endoplasmic reticulum organization | 4.59E-05 | 0.013363737 |
| GO:0008333 | endosome to lysosome transport | 5.06E-05 | 0.014161841 |
| GO:0009895 | negative regulation of catabolic process | 5.18E-05 | 0.014161841 |
| GO:0044265 | cellular macromolecule catabolic process | 5.62E-05 | 0.014726019 |
| GO:0006623 | protein targeting to vacuole | 5.72E-05 | 0.014726019 |
| GO:0140029 | exocytic process | 7.02E-05 | 0.017396138 |
| GO:0009896 | positive regulation of catabolic process | 7.32E-05 | 0.017396138 |
| GO:0007041 | lysosomal transport | 7.48E-05 | 0.017396138 |
| GO:0002026 | regulation of the force of heart contraction | 7.64E-05 | 0.017396138 |
| GO:0031330 | negative regulation of cellular catabolic process | 7.72E-05 | 0.017396138 |
| GO:0061024 | membrane organization | 8.74E-05 | 0.019220065 |
| GO:1904294 | positive regulation of ERAD pathway | 1.01E-04 | 0.021707869 |
| GO:0043933 | protein-containing complex subunit organization | 1.14E-04 | 0.023975191 |
| GO:0009225 | nucleotide-sugar metabolic process | 1.28E-04 | 0.026186294 |
| GO:1903441 | protein localization to ciliary membrane | 1.31E-04 | 0.026186294 |
| GO:0006605 | protein targeting | 1.34E-04 | 0.026316189 |
| GO:1901565 | organonitrogen compound catabolic process | 1.65E-04 | 0.031708906 |
| GO:1901698 | response to nitrogen compound | 1.74E-04 | 0.03249617 |
| GO:0048193 | Golgi vesicle transport | 1.77E-04 | 0.03249617 |
| GO:0007033 | vacuole organization | 2.00E-04 | 0.036102939 |
| GO:0031647 | regulation of protein stability | 2.11E-04 | 0.037232303 |
| GO:1905897 | regulation of response to endoplasmic reticulum stress | 2.31E-04 | 0.040089763 |
| GO:1990778 | protein localization to cell periphery | 2.61E-04 | 0.044330295 |
| GO:0090150 | establishment of protein localization to membrane | 2.88E-04 | 0.048138393 |
| GO:0003009 | skeletal muscle contraction | 3.03E-04 | 0.049432208 |
| GO:0060341 | regulation of cellular localization | 3.07E-04 | 0.049432208 |