**Table S2. Top10 GO enrichment results.**

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| Ontology | ID | Description | pvalue | p.adjust |
| BP | GO:0031331 | positive regulation of cellular catabolic process | 1.20E-09 | 4.32E-06 |
| BP | GO:0034248 | regulation of cellular amide metabolic process | 1.79E-09 | 4.32E-06 |
| BP | GO:0009896 | positive regulation of catabolic process | 2.41E-09 | 4.32E-06 |
| BP | GO:0001701 | in utero embryonic development | 7.01E-09 | 8.91E-06 |
| BP | GO:0060537 | muscle tissue development | 8.28E-09 | 8.91E-06 |
| BP | GO:1903829 | positive regulation of cellular protein localization | 1.09E-08 | 9.80E-06 |
| BP | GO:0051098 | regulation of binding | 1.85E-08 | 1.42E-05 |
| BP | GO:0007050 | cell cycle arrest | 5.84E-08 | 3.54E-05 |
| BP | GO:0010720 | positive regulation of cell development | 5.93E-08 | 3.54E-05 |
| BP | GO:0016049 | cell growth | 7.25E-08 | 3.90E-05 |
| CC | GO:0031519 | PcG protein complex | 9.69E-08 | 5.97E-05 |
| CC | GO:0000151 | ubiquitin ligase complex | 8.40E-07 | 0.000259 |
| CC | GO:0005667 | transcription regulator complex | 1.72E-06 | 0.000297 |
| CC | GO:0061695 | transferase complex, transferring phosphorus-containing groups | 2.15E-06 | 0.000297 |
| CC | GO:1902911 | protein kinase complex | 2.41E-06 | 0.000297 |
| CC | GO:0035097 | histone methyltransferase complex | 1.22E-05 | 0.00125 |
| CC | GO:0001650 | fibrillar center | 1.63E-05 | 0.001409 |
| CC | GO:1902554 | serine/threonine protein kinase complex | 1.83E-05 | 0.001409 |
| CC | GO:0017053 | transcription repressor complex | 3.34E-05 | 0.002118 |
| CC | GO:0072686 | mitotic spindle | 3.44E-05 | 0.002118 |
| MF | GO:0031625 | ubiquitin protein ligase binding | 3.41E-09 | 3.14E-06 |
| MF | GO:0044389 | ubiquitin-like protein ligase binding | 8.16E-09 | 3.76E-06 |
| MF | GO:0046332 | SMAD binding | 4.09E-08 | 1.26E-05 |
| MF | GO:0004674 | protein serine/threonine kinase activity | 5.32E-07 | 0.000105 |
| MF | GO:0001228 | DNA-binding transcription activator activity, RNA polymerase II-specific | 5.68E-07 | 0.000105 |
| MF | GO:0001216 | DNA-binding transcription activator activity | 7.48E-07 | 0.000115 |
| MF | GO:0008013 | beta-catenin binding | 4.87E-06 | 0.000567 |
| MF | GO:0061629 | RNA polymerase II-specific DNA-binding transcription factor binding | 4.93E-06 | 0.000567 |
| MF | GO:0043021 | ribonucleoprotein complex binding | 6.56E-06 | 0.000672 |
| MF | GO:0048185 | activin binding | 8.11E-06 | 0.000747 |