**Suppl. Table 2. GO pathway for positively correlated genes.**

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| **GO biological process complete** | **Fold Enrichment** | **upload\_1 (raw P-value)** | **FDR** |
| cellular macromolecule catabolic process (GO:0044265) | 2.5 | 2.77E-04 | 4.92E-02 |
| positive regulation of nucleobase-containing compound metabolic process (GO:0045935) | 1.91 | 2.48E-04 | 4.47E-02 |
| cell division (GO:0051301) | 3.08 | 2.46E-04 | 4.48E-02 |
| negative regulation of metabolic process (GO:0009892) | 1.71 | 2.28E-04 | 4.20E-02 |
| macromolecule modification (GO:0043412) | 1.72 | 2.09E-04 | 3.90E-02 |
| regulation of ubiquitin-dependent protein catabolic process (GO:2000058) | 5.22 | 2.06E-04 | 3.90E-02 |
| positive regulation of cellular metabolic process (GO:0031325) | 1.68 | 1.79E-04 | 3.43E-02 |
| regulation of RNA biosynthetic process (GO:2001141) | 1.66 | 1.73E-04 | 3.35E-02 |
| positive regulation of macromolecule metabolic process (GO:0010604) | 1.66 | 1.72E-04 | 3.37E-02 |
| regulation of nucleic acid-templated transcription (GO:1903506) | 1.66 | 1.68E-04 | 3.33E-02 |
| regulation of transcription, DNA-templated (GO:0006355) | 1.66 | 1.67E-04 | 3.37E-02 |
| regulation of cellular process (GO:0050794) | 1.25 | 1.62E-04 | 3.29E-02 |
| CRD-mediated mRNA stabilization (GO:0070934) | 36.51 | 1.51E-04 | 3.12E-02 |
| biological\_process (GO:0008150) | 1.1 | 1.47E-04 | 3.08E-02 |
| Unclassified (UNCLASSIFIED) | 0.35 | 1.47E-04 | 3.12E-02 |
| heterochromatin organization (GO:0070828) | 11.18 | 1.27E-04 | 2.73E-02 |
| negative regulation of cellular metabolic process (GO:0031324) | 1.82 | 1.24E-04 | 2.70E-02 |
| positive regulation of macromolecule biosynthetic process (GO:0010557) | 1.98 | 1.21E-04 | 2.67E-02 |
| regulation of DNA metabolic process (GO:0051052) | 3.52 | 1.15E-04 | 2.57E-02 |
| protein metabolic process (GO:0019538) | 1.63 | 1.11E-04 | 2.53E-02 |
| cellular protein catabolic process (GO:0044257) | 2.9 | 1.10E-04 | 2.53E-02 |
| posttranscriptional regulation of gene expression (GO:0010608) | 3.17 | 1.08E-04 | 2.52E-02 |
| negative regulation of chromosome organization (GO:2001251) | 8.65 | 1.00E-04 | 2.38E-02 |
| positive regulation of ATP-dependent activity (GO:0032781) | 12.17 | 8.76E-05 | 2.11E-02 |
| alternative mRNA splicing, via spliceosome (GO:0000380) | 19.91 | 8.31E-05 | 2.03E-02 |
| regulation of ATP-dependent activity (GO:0043462) | 9 | 8.14E-05 | 2.03E-02 |
| positive regulation of nitrogen compound metabolic process (GO:0051173) | 1.76 | 7.55E-05 | 1.91E-02 |
| proteolysis involved in cellular protein catabolic process (GO:0051603) | 3.03 | 6.35E-05 | 1.63E-02 |
| regulation of DNA duplex unwinding (GO:1905462) | 54.76 | 5.88E-05 | 1.54E-02 |
| protein localization to nucleus (GO:0034504) | 5.57 | 5.12E-05 | 1.36E-02 |
| negative regulation of nitrogen compound metabolic process (GO:0051172) | 1.9 | 4.91E-05 | 1.33E-02 |
| biological regulation (GO:0065007) | 1.24 | 4.73E-05 | 1.30E-02 |
| DNA repair (GO:0006281) | 3.44 | 4.40E-05 | 1.23E-02 |
| regulation of biological process (GO:0050789) | 1.26 | 4.27E-05 | 1.22E-02 |
| cellular process (GO:0009987) | 1.17 | 4.07E-05 | 1.18E-02 |
| organelle organization (GO:0006996) | 1.75 | 3.74E-05 | 1.11E-02 |
| negative regulation of macromolecule metabolic process (GO:0010605) | 1.84 | 3.53E-05 | 1.06E-02 |
| protein modification by small protein conjugation or removal (GO:0070647) | 2.67 | 3.41E-05 | 1.05E-02 |
| cellular component organization (GO:0016043) | 1.55 | 2.58E-05 | 8.08E-03 |
| RNA splicing, via transesterification reactions (GO:0000375) | 5.06 | 1.76E-05 | 5.62E-03 |
| mRNA splicing, via spliceosome (GO:0000398) | 5.15 | 1.51E-05 | 5.04E-03 |
| RNA splicing, via transesterification reactions with bulged adenosine as nucleophile (GO:0000377) | 5.15 | 1.51E-05 | 4.93E-03 |
| cellular component organization or biogenesis (GO:0071840) | 1.55 | 1.49E-05 | 5.07E-03 |
| cellular protein metabolic process (GO:0044267) | 1.79 | 1.39E-05 | 4.83E-03 |
| cellular response to DNA damage stimulus (GO:0006974) | 3.04 | 1.36E-05 | 4.85E-03 |
| regulation of RNA metabolic process (GO:0051252) | 1.76 | 6.03E-06 | 2.20E-03 |
| chromatin organization (GO:0006325) | 3.56 | 4.69E-06 | 1.75E-03 |
| DNA conformation change (GO:0071103) | 4.94 | 3.83E-06 | 1.46E-03 |
| mRNA processing (GO:0006397) | 4.02 | 3.81E-06 | 1.49E-03 |
| regulation of cellular biosynthetic process (GO:0031326) | 1.76 | 1.47E-06 | 5.92E-04 |
| regulation of biosynthetic process (GO:0009889) | 1.76 | 1.08E-06 | 4.44E-04 |
| regulation of macromolecule biosynthetic process (GO:0010556) | 1.8 | 9.48E-07 | 4.01E-04 |
| regulation of gene expression (GO:0010468) | 1.69 | 9.22E-07 | 4.02E-04 |
| regulation of cellular macromolecule biosynthetic process (GO:2000112) | 1.81 | 5.75E-07 | 2.57E-04 |
| nucleocytoplasmic transport (GO:0006913) | 6.38 | 2.51E-07 | 1.19E-04 |
| nuclear transport (GO:0051169) | 6.38 | 2.51E-07 | 1.16E-04 |
| nucleobase-containing compound transport (GO:0015931) | 6.44 | 2.27E-07 | 1.11E-04 |
| mRNA transport (GO:0051028) | 8.92 | 9.41E-08 | 4.76E-05 |
| establishment of RNA localization (GO:0051236) | 7.87 | 8.82E-08 | 4.61E-05 |
| RNA transport (GO:0050658) | 7.96 | 7.79E-08 | 4.36E-05 |
| nucleic acid transport (GO:0050657) | 7.96 | 7.79E-08 | 4.21E-05 |
| regulation of nucleobase-containing compound metabolic process (GO:0019219) | 1.87 | 7.70E-08 | 4.47E-05 |
| DNA metabolic process (GO:0006259) | 3.66 | 6.75E-08 | 4.07E-05 |
| RNA splicing (GO:0008380) | 5.24 | 5.25E-08 | 3.29E-05 |
| RNA localization (GO:0006403) | 7.57 | 3.86E-08 | 2.52E-05 |
| mRNA metabolic process (GO:0016071) | 4.1 | 3.77E-08 | 2.57E-05 |
| metabolic process (GO:0008152) | 1.53 | 2.68E-08 | 1.91E-05 |
| regulation of metabolic process (GO:0019222) | 1.63 | 1.11E-08 | 8.30E-06 |
| regulation of primary metabolic process (GO:0080090) | 1.71 | 1.05E-08 | 8.25E-06 |
| RNA processing (GO:0006396) | 3.6 | 6.71E-09 | 5.53E-06 |
| regulation of cellular metabolic process (GO:0031323) | 1.7 | 5.98E-09 | 5.20E-06 |
| regulation of nitrogen compound metabolic process (GO:0051171) | 1.74 | 4.70E-09 | 4.34E-06 |
| organic substance metabolic process (GO:0071704) | 1.6 | 1.10E-09 | 1.08E-06 |
| cellular macromolecule metabolic process (GO:0044260) | 1.92 | 7.69E-10 | 8.04E-07 |
| regulation of macromolecule metabolic process (GO:0060255) | 1.73 | 5.97E-10 | 6.68E-07 |
| chromosome organization (GO:0051276) | 3.75 | 3.62E-10 | 4.37E-07 |
| RNA metabolic process (GO:0016070) | 3.1 | 1.82E-10 | 2.37E-07 |
| primary metabolic process (GO:0044238) | 1.7 | 5.86E-11 | 8.35E-08 |
| gene expression (GO:0010467) | 2.72 | 5.38E-11 | 8.44E-08 |
| cellular metabolic process (GO:0044237) | 1.7 | 2.46E-11 | 4.29E-08 |
| nitrogen compound metabolic process (GO:0006807) | 1.76 | 2.21E-11 | 4.32E-08 |
| cellular nitrogen compound metabolic process (GO:0034641) | 2.36 | 2.08E-12 | 4.65E-09 |
| organic cyclic compound metabolic process (GO:1901360) | 2.46 | 1.30E-12 | 3.41E-09 |
| cellular aromatic compound metabolic process (GO:0006725) | 2.55 | 9.00E-13 | 2.82E-09 |
| nucleobase-containing compound metabolic process (GO:0006139) | 2.73 | 7.29E-14 | 2.86E-10 |
| macromolecule metabolic process (GO:0043170) | 1.93 | 5.20E-14 | 2.71E-10 |
| heterocycle metabolic process (GO:0046483) | 2.69 | 3.05E-14 | 2.39E-10 |
| nucleic acid metabolic process (GO:0090304) | 3.31 | 2.36E-17 | 3.70E-13 |