Supplementary Material 3. The sub-module of protein-protein interaction network and the enrichment analysis of Module 3

(a) The sub-module from protein-protein interaction network



(b) The detail information of Module 3 enrichment analysis of APA

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| ID | Analysis type | Process | Count | P-value | Genes |
| hsa04020 | KEGG Pathway | Calcium signaling pathway | 4 | 7.60X10-8 | PTGFR, CCKBR, HTR2B, TACR1 |
| hsa04080 | KEGG Pathway | Neuroactive ligand-receptor interaction | 4 | 6.89X10-7 | PTGFR, CCKBR, HTR2B, TACR1 |
| hsa05166 | KEGG Pathway | Human T-cell leukemia virus 1 infection | 3 | 1.46X10-5 | FOS, ETS2, JUN |
| GO: 0045893 | Gene Ontology | positive regulation of transcription, DNA-templated | 5 | 7.04X10-8 | NFYA, FOS, MYB, ETS2, JUN |
| GO: 0007200 | Gene Ontology | phospholipase C-activating G protein-coupled receptor signaling pathway | 3 | 3.29X10-7 | HTR2B, CCKBR, TACR1 |
| GO: 0001228 | Gene Ontology | DNA-binding transcription activator activity, RNA polymerase II-specific | 4 | 2.44X10-6 | NFYA, FOS, MYB, JUN |
| GO: 0007204 | Gene Ontology | positive regulation of cytosolic calcium ion concentration | 3 | 1.45X10-6 | PTGFR, CCKBR, TACR1 |
| GO: 0035994 | Gene Ontology | response to muscle stretch | 2 | 6.34X10-6 | FOS, JUN |

APA: aldosterone-producing adenoma