**Table 5 The GO and KEGG enrichment of differentially expressed RNAs and DEPs**

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| **Category** | **Enriched Terms** | **Number** | ***P*-value** |
| GO-Biological Process (mRNA) | Defense response | 42 | 9.5E-09 |
| Response to external stimulus | 51 | 7.9E-08 |
| Anatomical structure development | 92 | 5.5E-07 |
| Response to stress | 69 | 5.9E-07 |
| Developmental process | 95 | 1.7E-06 |
| System development | 77 | 5.7E-06 |
| GO-Cellular Components(mRNA) | Extracellular region | 74 | 1.8E-07 |
| Extracellular region part | 58 | 0.000019 |
| Extracellular space | 54 | 0.000079 |
| Extracellular matrix | 12 | 0.00012 |
| Intrinsic component of plasma membrane | 34 | 0.00016 |
| GO-Molecular Function(mRNA) | RAGE receptor binding | 4 | 3.2E-06 |
| Organic acid binding | 10 | 0.000065 |
| Receptor ligand activity | 15 | 0.00013 |
| Carboxylic acid binding | 9 | 0.00022 |
| Growth factor activity | 8 | 0.00029 |
| KEGG pathway(mRNA) | Neuroactive ligand-receptor interaction | 10 | 0.00119 |
| Complement and coagulation cascades | 4 | 0.00891 |
| Cytokine-cytokine receptor interaction | 8 | 0.01029 |
| Cocaine addiction | 3 | 0.01394 |
| MicroRNAs in cancer | 5 | 0.01527 |
| GO-Biological Process(lncRNA) | Transcription from RNA polymerase II promoter | 83 | 0.000013 |
| Nucleic acid-templated transcription | 103 | 0.000015 |
| DNA-templated transcription | 102 | 0.000015 |
| RNA biosynthetic process | 103 | 0.000018 |
| Aromatic compound biosynthetic process | 112 | 0.000032 |
| GO-Cellular Components(lncRNA) | Intracellular membrane-bounded organelle | 242 | 0.00013 |
| Membrane-bounded organelle | 267 | 0.00019 |
| Organelle | 285 | 0.0003 |
| Nucleus | 171 | 0.00055 |
| Nuclear lumen | 104 | 0.00112 |
| GO-Molecular Function(lncRNA) | Transcription regulator activity | 62 | 0.00015 |
| transcriptional activator activity | 20 | 0.00018 |
| Regulatory region DNA binding | 34 | 0.00029 |
| Transcription regulatory region DNA binding | 34 | 0.00029 |
| Regulatory region nucleic acid binding | 34 | 0.0003 |
| KEGG pathway(lncRNA) | Vasopressin-regulated water reabsorption | 5 | 0.00126 |
| Prostate cancer | 7 | 0.00190 |
| Cholinergic synapse | 7 | 0.00479 |
| Insulin secretion | 6 | 0.00491 |
| Colorectal cancer | 6 | 0.00520 |
| GO-Biological Process(circRNA) | Negative regulation of stress fiber assembly | 3 | 0.00014 |
| Negative regulation of wound healing | 2 | 0.00014 |
| Negative regulation of actin filament bundle assembly | 3 | 0.00021 |
| Macromolecule localization | 29 | 0.00023 |
| Regulation of basement membrane organization | 2 | 0.00023 |
| GO-Cellular Components(circRNA) | Basal cortex | 2 | 0.00022 |
| Intracellular organelle part | 57 | 0.00246 |
| Non-membrane-bounded organelle | 32 | 0.0026 |
| Protein complex | 24 | 0.00275 |
| Postsynapse | 9 | 0.00278 |
| GO-Molecular Function(circRNA) | Malonyl-CoA decarboxylase activity | 2 | 0.000024 |
| Histone acetyltransferase binding | 3 | 0.00038 |
| 3',5'-cyclic-GMP phosphodiesterase activity | 2 | 0.00346 |
| 6,7-dihydropteridine reductase activity | 1 | 0.0049 |
| Beta-mannosidase activity | 1 | 0.0049 |
| KEGG pathway(circRNA) | B cell receptor signaling pathway | 4 | 0.000354996 |
| cGMP-PKG signaling pathway | 5 | 0.001159661 |
| Neurotrophin signaling pathway | 4 | 0.002716875 |
| Cortisol synthesis and secretion | 3 | 0.003596882 |
| HTLV-I infection | 5 | 0.004057118 |
| GO-Biological Process(DEPs) | Response to stress | 162 | 1.37E-79 |
| Positive regulation of biological process | 159 | 6.05E-66 |
| Response to stimulus | 135 | 1.39E-63 |
| Localization | 192 | 1.33E-61 |
| Response to chemical | 132 | 1.71E-57 |
| GO-Cellular Components(DEPs) | Extracellular region part | 172 | 6.69E-125 |
| Extracellular region | 189 | 2.23E-123 |
| Membrane-bounded vesicle | 152 | 8E-114 |
| Vesicle | 158 | 6.06E-108 |
| Extracellular organelle | 130 | 6.06E-108 |
| GO-Molecular Function(DEPs) | Protein binding | 223 | 1.63E-80 |
| Antigen binding | 37 | 8.17E-37 |
| Binding | 273 | 7.3E-36 |
| Identical protein binding | 43 | 1.24E-17 |
| Poly(A) RNA binding | 34 | 1.95E-17 |
| KEGG pathway(DEPs) | ECM-receptor interaction | 10 | 0.0000296 |
| Hematopoietic cell lineage | 10 | 0.0000549 |
| Phagosome | 13 | 0.000108 |
| Spliceosome | 11 | 0.000443 |
| Antigen processing and presentation | 8 | 0.000627 |