***Table S3*: Significant GO analysis results of co-expressed genes with each core lncRNA**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Category** | **Term** | **Count** | **P\_value** | **Fold Enrichment** | **FDR** |
| **AC005550.4** |
| GOTERM  | GO:0016042~lipid catabolic process  | 5 | 0.000568424 | 7.306010929 | 0.039744544 |
| BP DIRECT |  |  |  |  |  |
| GOTERM  | GO:0010876~lipid localization  | 5 | 0.001519835 | 5.864035088 | 0.039744544 |
| BP DIRECT |  |  |  |  |  |
| **AC093850.2** |
| GOTERM  | GO:0005788~endoplasmic reticulum lumen  | 7 | 1.98E-10 | 36.11399108 | 1.11E-09 |
| CC DIRECT |  |  |  |  |  |
| GOTERM  | GO:0005581~collagen trimer  | 5 | 1.67E-09 | 87.6467803 | 7.03E-09 |
| CC DIRECT |  |  |  |  |  |
| GOTERM  | GO:0030574~collagen catabolic process  | 5 | 6.12E-10 | 106.5012255 | 3.76E-08 |
| BP DIRECT |  |  |  |  |  |
| GOTERM  | GO:0032963~collagen metabolic process  | 5 | 1.35E-08 | 57.93666667 | 4.15E-07 |
| BP DIRECT |  |  |  |  |  |
| GOTERM  | GO:0005539~glycosaminoglycan binding  | 5 | 1.96E-07 | 33.94757433 | 1.55E-06 |
| MF DIRECT |  |  |  |  |  |
| **AL035610.1** |
| GOTERM  | GO:0009746~response to hexose  | 5 | 0.000190713 | 9.344623656 | 0.029394495 |
| BP DIRECT |  |  |  |  |  |
| GOTERM  | GO:0034284~response to monosaccharide  | 5 | 0.000215737 | 9.1 | 0.029394495 |
| BP DIRECT |  |  |  |  |  |
| GOTERM  | GO:0016042~lipid catabolic process  | 6 | 0.000230734 | 6.83842623 | 0.029394495 |
| BP DIRECT |  |  |  |  |  |
| GOTERM  | GO:0006066~alcohol metabolic process  | 6 | 0.000298584 | 6.517875 | 0.029394495 |
| BP DIRECT |  |  |  |  |  |
| GOTERM  | GO:0009743~response to carbohydrate  | 5 | 0.000349208 | 8.198584906 | 0.029394495 |
| BP DIRECT |  |  |  |  |  |
| GOTERM  | GO:1901615~organic hydroxy compound  | 7 | 0.000485828 | 4.945813008 | 0.029394495 |
| BP DIRECT | metabolic process |  |  |  |  |
| GOTERM  | GO:0019216~regulation of lipid  | 6 | 0.000557845 | 5.793666667 | 0.029394495 |
| BP DIRECT | metabolic process  |  |  |  |  |
| GOTERM  | GO:0032868~response to insulin  | 5 | 0.000712896 | 7.008467742 | 0.030310276 |
| BP DIRECT |  |  |  |  |  |
| GOTERM  | GO:0010876~lipid localization  | 6 | 0.000740437 | 5.488736842 | 0.030310276 |
| BP DIRECT |  |  |  |  |  |
| GOTERM  | GO:0006732~coenzyme metabolic process  | 5 | 0.003446646 | 4.896056338 | 0.044584318 |
| BP DIRECT |  |  |  |  |  |
| GOTERM  | GO:0006631~fatty acid metabolic process  | 5 | 0.003488251 | 4.882303371 | 0.044584318 |
| BP DIRECT |  |  |  |  |  |
| **RP11-175K6.1** |
| GOTERM | GO:0048545~response to steroid hormone  | 8 | 0.000349048 | 4.583294878 | 0.061563108 |
| BP DIRECT |  |  |  |  |  |
| GOTERM  | GO:0007623~circadian rhythm  | 5 | 0.001696775 | 5.817713215 | 0.109878754 |
| BP DIRECT |  |  |  |  |  |
| GOTERM  | GO:0051896~regulation of protein kinase | 5 | 0.002446909 | 5.348987505 | 0.109878754 |
| BP DIRECT |  B signaling  |  |  |  |  |
| GOTERM  | GO:0048511~rhythmic process  | 6 | 0.002767099 | 4.285960875 | 0.109878754 |
| BP DIRECT |  |  |  |  |  |
| GOTERM  | GO:0009755~hormone-mediated  | 5 | 0.003609241 | 4.885871704 | 0.109878754 |
| BP DIRECT | signaling pathway  |  |  |  |  |
| GOTERM  | GO:0043491~protein kinase B signaling  | 5 | 0.004629571 | 4.606679035 | 0.109935635 |
| BP DIRECT |  |  |  |  |  |
| GOTERM  | GO:0071383~cellular response to steroid  | 5 | 0.005840724 | 4.357669358 | 0.120171405 |
| BP DIRECT | hormone stimulus |  |  |  |  |
| GOTERM  | GO:0050900~leukocyte migration  | 6 | 0.018031837 | 2.875506659 | 0.124991999 |
| BP DIRECT |  |  |  |  |  |
| GOTERM  | GO:0001667~ameboidal-type cell migration  | 5 | 0.020178014 | 3.197270152 | 0.127543689 |
| BP DIRECT | ameboidal-type |  |  |  |  |
| GOTERM  | GO:0001228~transcriptional  | 7 | 0.001556398 | 4.105095972 | 0.047120464 |
| MF DIRECT | activator activity, RNA polymerase  |  |  |  |  |
|  | II transcription regulatory  |  |  |  |  |
|  | region sequence-specific binding |  |  |  |  |
| GOTERM  | GO:0017171~serine hydrolase activity  | 5 | 0.005855657 | 4.350681909 | 0.057642405 |
| MF DIRECT |  |  |  |  |  |