***Table S4*: Significant GO Analysis results of all mRNAs in WGCNA Networks**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Category | Term | Count | P\_value | Fold | FDR |
|  |  |  |  | enrichment |  |
| GOTERM | GO:0016525~negative regulation | 10 | 9.93E-08 | 9.518619934 | 8.42E-05 |
| BP DIRECT | of angiogenesis  |  |  |  |  |
| GOTERM | GO:2000181~negative regulation  | 10 | 1.18E-07 | 9.348644578 | 8.42E-05 |
| BP DIRECT | of blood vessel morphogenesis |  |  |  |  |
| GOTERM | GO:1901343~negative regulation | 10 | 2.45E-07 | 8.653290849 | 0.000113078 |
| BP DIRECT | of vasculature development  |  |  |  |  |
| GOTERM | GO:0045765~regulation of | 13 | 2.26E-06 | 4.985943775 | 0.000870704 |
| BP DIRECT | angiogenesis  |  |  |  |  |
| GOTERM | GO:1901653~cellular response | 14 | 5.88E-06 | 4.248891217 | 0.001508964 |
| BP DIRECT | to peptide  |  |  |  |  |
| GOTERM | GO:1901342~regulation of  | 13 | 8.13E-06 | 4.433754562 | 0.001876917 |
| BP DIRECT | vasculature development |  |  |  |  |
| GOTERM | GO:0001525~angiogenesis  | 16 | 1.13E-05 | 3.572019421 | 0.002363251 |
| BP DIRECT |  |  |  |  |  |
| GOTERM | GO:0045444~fat cell | 10 | 3.46E-05 | 4.985943775 | 0.004805018 |
| BP DIRECT | differentiation  |  |  |  |  |
| GOTERM | GO:0019216~regulation of lipid | 12 | 0.000181462 | 3.490160643 | 0.013969425 |
| BP DIRECT | metabolic process  |  |  |  |  |
| GOTERM | GO:0010876~lipid localization  | 12 | 0.000297629 | 3.306467977 | 0.01909348 |
| BP DIRECT |  |  |  |  |  |
| GOTERM | GO:0048545~response to steroid | 12 | 0.000412255 | 3.188979267 | 0.023802321 |
| BP DIRECT | hormone  |  |  |  |  |
| GOTERM | GO:0006869~lipid transport  | 10 | 0.001879136 | 3.01742995 | 0.049882925 |
| BP DIRECT |  |  |  |  |  |
| GOTERM | GO:0052548~regulation of | 10 | 0.005072161 | 2.624180934 | 0.079099122 |
| BP DIRECT | endopeptidase activity  |  |  |  |  |
| GOTERM | GO:0030335~positive regulation | 10 | 0.010091409 | 2.368887314 | 0.094355644 |
| BP DIRECT | of cell migration  |  |  |  |  |
| GOTERM | GO:2000147~positive regulation | 10 | 0.01306692 | 2.276191723 | 0.113450029 |
| BP DIRECT | of cell motility  |  |  |  |  |
| GOTERM | GO:0051272~positive regulation | 10 | 0.015596439 | 2.213632543 | 0.117391947 |
| BP DIRECT | of cellular component movement  |  |  |  |  |
| GOTERM | GO:0040017~positive regulation | 10 | 0.019434668 | 2.136833046 | 0.119055319 |
| BP DIRECT | of locomotion  |  |  |  |  |
| GOTERM | GO:0008201~heparin binding | 9 | 1.77E-05 | 6.101015625 | 0.005404528 |
| MF DIRECT |  |  |  |  |  |
| GOTERM | GO:0005539~glycosaminoglycan | 10 | 2.88E-05 | 5.09213615 | 0.005404528 |
| MF DIRECT | binding |  |  |  |  |
| GOTERM | GO:1901681~sulfur compound | 9 | 0.000306603 | 4.207596983 | 0.028723825 |
| MF DIRECT | binding  |  |  |  |  |
| GOTERM | GO:0017171~serine hydrolase | 7 | 0.01446431 | 2.740929603 | 0.090504248 |
| MF DIRECT | activity  |  |  |  |  |