**Supplementary Table S10. Top 20 REACTOME gene sets from GSEA of down-regulated and up-regulated genes in PG1**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Gene set | Overlap | Size | pval | FDR |
| **Top 20 REACTOME gene sets from GSEA of down-regulated genes in PG1** |   |   |   |   |
| REACTOME\_BIOLOGICAL\_OXIDATIONS | 53 | 219 | 6.58E-40 | 1.06E-36 |
| REACTOME\_PHASE\_I\_FUNCTIONALIZATION\_OF\_COMPOUNDS | 32 | 104 | 3.20E-28 | 2.56E-25 |
| REACTOME\_METABOLISM\_OF\_AMINO\_ACIDS\_AND\_DERIVATIVES | 42 | 375 | 2.91E-18 | 1.56E-15 |
| REACTOME\_METABOLISM\_OF\_LIPIDS | 59 | 742 | 8.02E-18 | 3.21E-15 |
| REACTOME\_CYTOCHROME\_P450\_ARRANGED\_BY\_SUBSTRATE\_TYPE | 19 | 66 | 1.06E-16 | 3.39E-14 |
| REACTOME\_FATTY\_ACID\_METABOLISM | 26 | 178 | 1.48E-14 | 3.97E-12 |
| REACTOME\_PHASE\_II\_CONJUGATION\_OF\_COMPOUNDS | 19 | 108 | 1.74E-12 | 3.48E-10 |
| REACTOME\_SYNTHESIS\_OF\_BILE\_ACIDS\_AND\_BILE\_SALTS\_VIA\_24\_HYDROXYCHOLESTEROL | 9 | 14 | 1.65E-12 | 3.48E-10 |
| REACTOME\_BILE\_ACID\_AND\_BILE\_SALT\_METABOLISM | 13 | 43 | 3.67E-12 | 6.54E-10 |
| REACTOME\_SYNTHESIS\_OF\_BILE\_ACIDS\_AND\_BILE\_SALTS\_VIA\_7ALPHA\_HYDROXYCHOLESTEROL | 10 | 24 | 2.87E-11 | 4.19E-09 |
| REACTOME\_ARACHIDONIC\_ACID\_METABOLISM | 14 | 60 | 2.67E-11 | 4.19E-09 |
| REACTOME\_COMPLEMENT\_CASCADE | 18 | 114 | 4.39E-11 | 5.79E-09 |
| REACTOME\_XENOBIOTICS | 10 | 25 | 4.69E-11 | 5.79E-09 |
| REACTOME\_SYNTHESIS\_OF\_BILE\_ACIDS\_AND\_BILE\_SALTS | 11 | 34 | 7.42E-11 | 8.50E-09 |
| REACTOME\_FATTY\_ACIDS | 8 | 15 | 2.41E-10 | 2.57E-08 |
| REACTOME\_METABOLISM\_OF\_STEROIDS | 19 | 151 | 7.06E-10 | 7.07E-08 |
| REACTOME\_AMINO\_ACID\_CONJUGATION | 6 | 9 | 7.52E-09 | 6.70E-07 |
| REACTOME\_SYNTHESIS\_OF\_16\_20\_HYDROXYEICOSATETRAENOIC\_ACIDS\_HETE | 6 | 9 | 7.52E-09 | 6.70E-07 |
| REACTOME\_TRANSPORT\_OF\_SMALL\_MOLECULES | 42 | 729 | 9.88E-09 | 8.34E-07 |
| REACTOME\_CYP2E1\_REACTIONS | 6 | 11 | 3.99E-08 | 3.20E-06 |
| **Top 20 REACTOME gene sets from GSEA of up-regulated genes in PG1** |   |   |   |   |
| REACTOME\_NEURONAL\_SYSTEM | 15 | 410 | 9.08E-06 | 0.004998 |
| REACTOME\_SIGNALING\_BY\_GPCR | 21 | 699 | 3.49E-06 | 0.004998 |
| REACTOME\_GPCR\_LIGAND\_BINDING | 16 | 463 | 9.35E-06 | 0.004998 |
| REACTOME\_POTASSIUM\_CHANNELS | 7 | 103 | 5.43E-05 | 0.017418 |
| REACTOME\_G\_ALPHA\_I\_SIGNALLING\_EVENTS | 12 | 314 | 4.67E-05 | 0.017418 |
| REACTOME\_EXTRACELLULAR\_MATRIX\_ORGANIZATION | 11 | 301 | 0.000142 | 0.038037 |
| REACTOME\_ACTIVATION\_OF\_KAINATE\_RECEPTORS\_UPON\_GLUTAMATE\_BINDING | 4 | 30 | 0.00017 | 0.039003 |
| REACTOME\_CHEMOKINE\_RECEPTORS\_BIND\_CHEMOKINES | 5 | 57 | 0.000196 | 0.039234 |
| REACTOME\_CLASS\_B\_2\_SECRETIN\_FAMILY\_RECEPTORS | 6 | 94 | 0.000262 | 0.04669 |
| REACTOME\_INTEGRATION\_OF\_ENERGY\_METABOLISM | 6 | 108 | 0.000552 | 0.088537 |
| REACTOME\_RND1\_GTPASE\_CYCLE | 4 | 42 | 0.000636 | 0.092804 |
| REACTOME\_VOLTAGE\_GATED\_POTASSIUM\_CHANNELS | 4 | 43 | 0.000697 | 0.093109 |
| REACTOME\_REGULATION\_OF\_INSULIN\_SECRETION | 5 | 78 | 0.000841 | 0.103735 |
| REACTOME\_TRANSMISSION\_ACROSS\_CHEMICAL\_SYNAPSES | 9 | 269 | 0.001054 | 0.106136 |
| REACTOME\_PRESYNAPTIC\_FUNCTION\_OF\_KAINATE\_RECEPTORS | 3 | 21 | 0.000952 | 0.106136 |
| REACTOME\_METABOLISM\_OF\_FAT\_SOLUBLE\_VITAMINS | 4 | 48 | 0.001059 | 0.106136 |
| REACTOME\_CLASS\_A\_1\_RHODOPSIN\_LIKE\_RECEPTORS | 10 | 331 | 0.001225 | 0.115541 |
| REACTOME\_ANTI\_INFLAMMATORY\_RESPONSE\_FAVOURING\_LEISHMANIA\_PARASITE\_INFECTION | 8 | 224 | 0.001311 | 0.116844 |
| REACTOME\_SYNTHESIS\_OF\_VERY\_LONG\_CHAIN\_FATTY\_ACYL\_COAS | 3 | 24 | 0.001419 | 0.119827 |
| REACTOME\_ADORA2B\_MEDIATED\_ANTI\_INFLAMMATORY\_CYTOKINES\_PRODUCTION | 6 | 133 | 0.001628 | 0.130597 |