**Table 3: Summarized gene set enrichment analysis of pathways.** Selected pathway enriched in subcutaneous adipose tissue from Cushing’s disease patients via GSEA analysis. NES is the net enrichment score, asterisk indicates q<0.25. For a complete list see Supplementary Tables 2-3.

|  |  |  |
| --- | --- | --- |
| Pathway | Dataset | NES |
| M\_PHASE\_OF\_MITOTIC\_CELL\_CYCLE | Gene Ontology | 2.60\* |
| KEGG\_CITRATE\_CYCLE\_TCA\_CYCLE | KEGG | 2.41\* |
| KEGG\_BIOSYNTHESIS\_OF\_UNSATURATED\_FATTY\_ACIDS | KEGG | 2.41\* |
| REACTOME\_TRIGLYCERIDE\_BIOSYNTHESIS | Reactome | 2.24\* |
| PYRUVATE\_METABOLISM | Gene Ontology | 2.24\* |
| KEGG\_VALINE\_LEUCONE\_AND\_ISOLEUCINE\_DEGRADATION | KEGG | 2.16\* |
| STEROID\_BIOSYNTHETIC\_PROCESS | Gene Ontology | 2.11\* |
| KEGG\_STARCH\_AND\_SUCROSE\_METABOLISM | KEGG | 2.08\* |
| PROTEASOME\_COMPLEX | Gene Ontology | 1.78\* |
| KEGG\_ALLOGRAFT\_REJECTION | KEGG | -1.87\* |
| KEGG\_BASAL\_CELL\_CARCINOMA | KEGG | -1.86\* |
| KEGG\_RIBOSOME | KEGG | -2.33\* |