**Table S3. Summary of pairwise comparisons of RNAseq datasets performed in this study.**

|  |  |  |  |
| --- | --- | --- | --- |
| **Variable** **analyzed** | **Samples** | **Genes****affected** | **Figure** |
| Excitotoxicity | RC-*Abcc8* KO males and females (n=8) vs. RC-WT males and females (n=8) | 7393 | 2 |
| HFD | HFD-WT males and females (n=7) vs. RC-WTmales and females (n=8) | 2372 | 3 |
| Excitotoxicityand HFD | HFD-*Abcc8*KO males and females (n=8) vs. RC-WT males and females (n=8) | 8836 | 4 |
| Sex – WT | RC-WT males (n=4) vs. RC-WT females (n=4)  | 140 | S11 |
| Sex – HFD | HFD-WT males (n=4) vs. HFD-WT females (n=3) | 2618 | S11 |
| Sex – excitotoxicity | RC-*Abcc8*KO males (n=4) vs. RC-*Abcc8*KO females (n=4) | 36 | S11 |
| Sex -excitotoxicity andHFD | HFD-*Abcc8*KO males (n=5) vs. HFD-*Abcc8*KO females (n=3) | 125 | S11 |

Using the 31 RNA-seq datasets collected in this study, we performed a three different pairwise differential expression analyses. All mice contained a single *Ins2Apple* allele. The number of affected (dysregulated) genes based on a padj.< 0.05. HFD, high fat diet. RC, regular chow. WT, wild type. KO, knockout.