|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Condition** | **Genotype** | **Strain** | **Sex** | **Diet** | **N** |
| Excitotoxicity | *Abcc8-/- ; Ins2Apple/+* | C57Bl6/J | Male | Chow | 4 |
| Excitotoxicity | *Abcc8-/- ; Ins2Apple/+* | C57Bl6/J | Female | Chow | 4 |
| HFD | *Ins2Apple/+* | C57Bl6/J | Male | HFD | 4 |
| HFD | *Ins2Apple/+* | C57Bl6/J | Female | HFD | 3 |
| Normal | *Ins2Apple/+*  | C57Bl6/J | Male | Chow | 4 |
| Normal | *Ins2Apple/+* | C57Bl6/J | Female | Chow | 4 |
| Excitotoxicity and HFD | *Abcc8-/- ; Ins2Apple/+* | C57Bl6/J | Male | HFD | 5 |
| Excitotoxicity andHFD | *Abcc8-/- ; Ins2Apple/+* | C57Bl6/J | Female | HFD | 3 |

**Table S2. Summary of RNAseq datasets obtained in this study.**

The table summarizes -cell RNA-seq datasets obtained in this study. Characteristics and treatment conditions of mice used for -cell isolations were as follows. All mice were 60 +/- 2 days of age at the time of β-cell isolation. A high fat diet (HFD) was fed to wild type or *Abcc8-/-* mice for 5 weeks beginning at the time of weaning. β-cells were purified by FACS based on the red fluorescence of the *Ins2Apple* allele present in all animals. A total of 31 different datasets were generated. N=3-5 for each group.