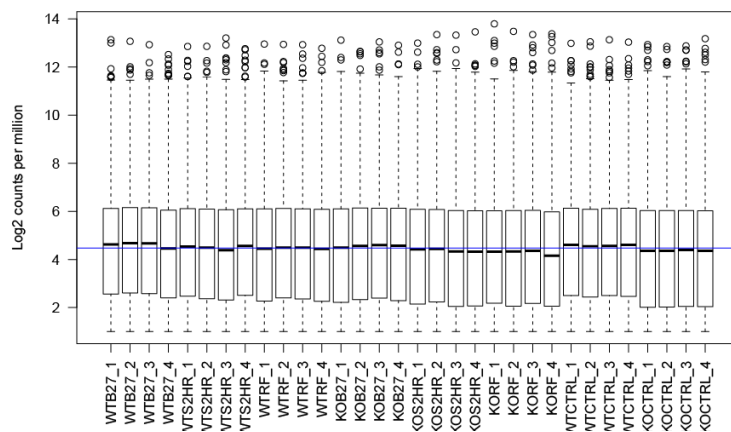# Supplementary Data S1

Transcriptomic

SLC38A10 Regulate Glutamate Homeostasis and modulate the AKT/TSC2/mTOR Pathway in mouse cortex cells

AmpliSeq analysis was performed using a National Genomics Infrastructure (NGI), SciLifeLab platform, Uppsala.

Pre-processing data was performed as follows-

Figures 1. **Boxplot showing data after normalisation for uneven sequencing depth and removal of slow expressed genes. Abbreviations; WTB27: Wild type starved of B27; WTS2HR: Wild type starved for 2HR; WTRF: Wild type refeed after 2h starvation; WTCTRL: Wild type cultured under normal (Basal) conditions; KOB27:KO starved of B27; KOS2HR:KO starved for 2HR; KORF:KO refeed after 2h starvation; KO CTRL:KO cultured under basal conditions**
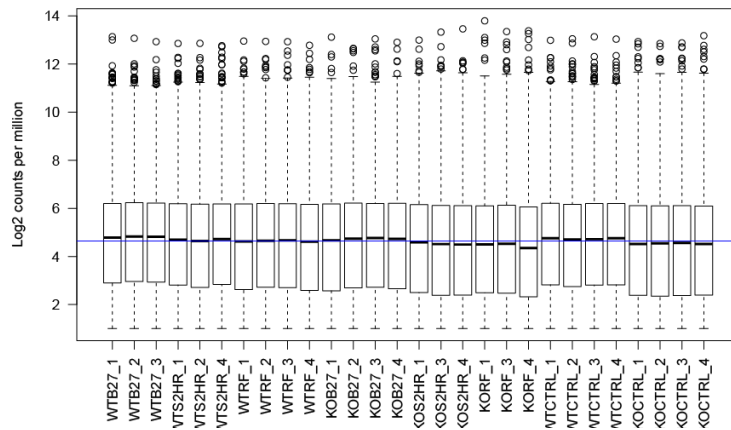

Figure 2. **Box plot showing data after normalisation for uneven sequencing depth and removal of low expressed genes. Based on the clustering in Supplementary Figure 3, four samples: WTB27_4, WTS2HR_3, KOS2HR_2, KORF_2, were**

removed. Abbreviations; WTB27: Wild type starved of B27; WTS2HR: Wild type starved for 2HR; WTRF: Wild type refed after 2h starvation; WTCTRL: Wild type cultured under normal conditions; KOB27:KO starved of B27; KOS2HR:KO starved for 2HR; KORF:KO refeed after 2h starvation; KO CTRL:KO PCCs basal conditions
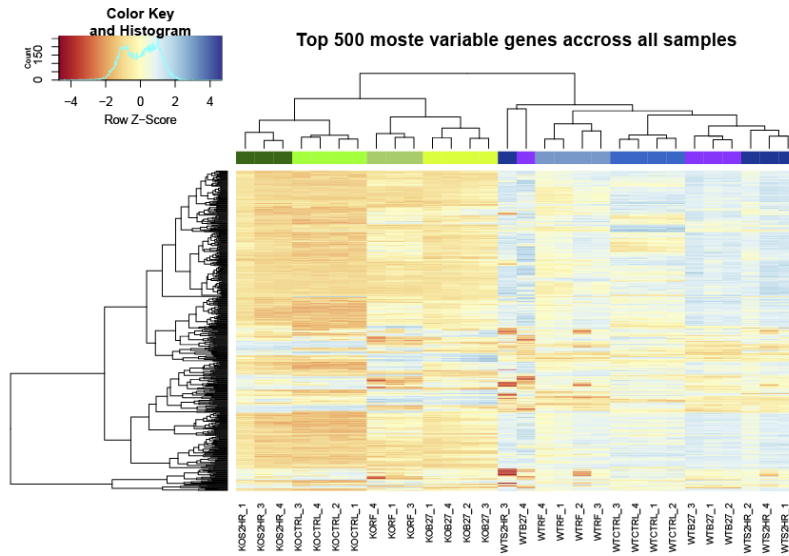

Figure 3. **Heat map over the top 500 most differential expressed genes. Dendograms show clustering by sample, column wise and by gene row wise.**
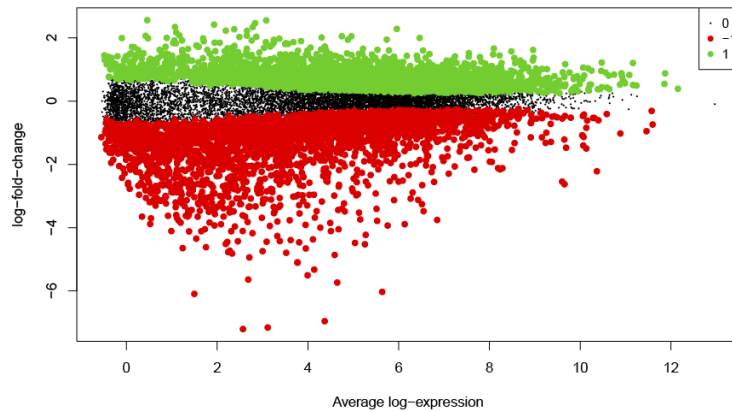

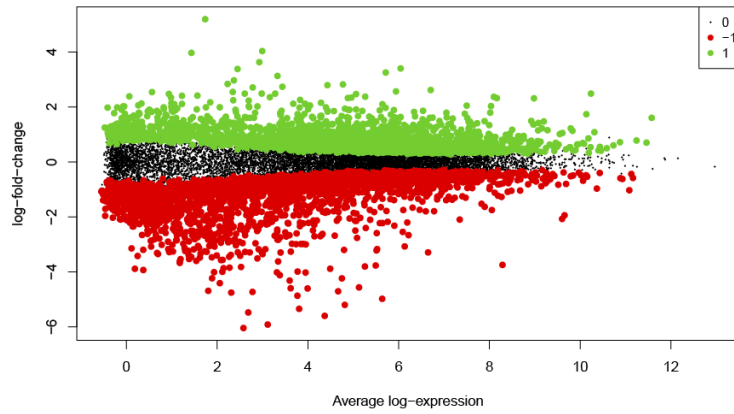*Figure 4.* **MDB plot showing differential expression of all genes between KO and WT basal groups.**

Figure 5. *MDB plot showing differential expression of all genes between KO and WT B27 starvation groups.*
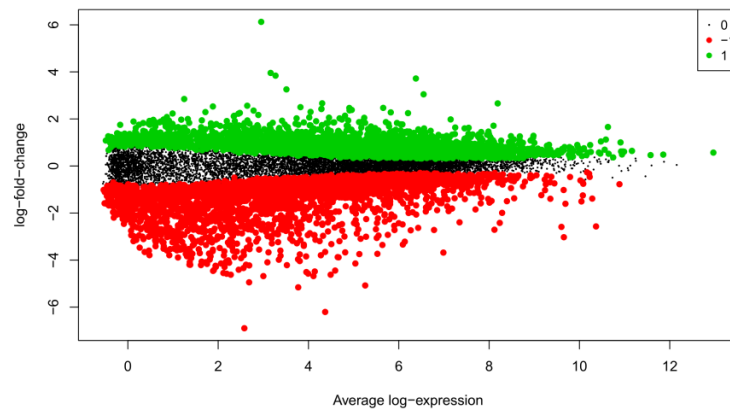

*Figure 6***. MDB plot showing differential expression of all genes between KO and WT starvation groups.**

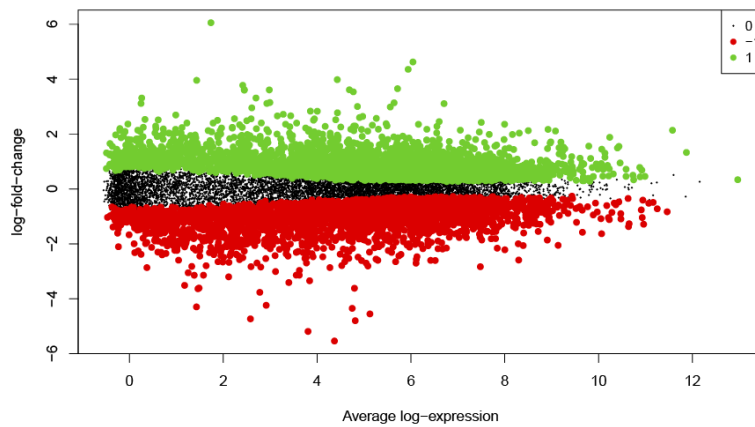*Figure 7.* **MDB plot showing differential expression of all genes between KO and WT refeed groups.**