



Additional file 2: Figure S2. Loss of *TSC2* triggers expression changes related to inflammatory response, metabolism, and neuronal function. **A** *Bar graphs* representing the total number of transcripts significantly upregulated or downregulated in *TSC2* heterozygous and homozygous mutant cells as compared to wild-type lines. Threshold: Benjamini–Hochberg adjusted p value < 0.05. **B** *Bar charts* showing biological processes significantly enriched for genes upregulated and downregulated in *TSC2* depleted cells as determined by gene set enrichment analysis. **C** *Heat map* of expression levels of genes associated with “inflammatory response” in the indicated cell lines and biological replicates. Gene expression levels are normalized to have zero average and unit (one) standard variance. **D** Expression levels of genes associated with “metabolism,” as shown in (C). **E** Expression levels of genes associated with “neural function,” as shown in (C). **F** *Dot plots* for examples of genes involved in the glycolytic pathway (displayed in Fig. 3g). Data are shown for biological replicates of two independent cell clones (*circle, triangle*) of the indicated genotypes. *Solid lines* indicate average values of all replicates. **G** Expression of proteins indicative of inflammation in control and *TSC2*-deficient 6-week-old cell cultures ($n = 3$) determined by a human protein array. Expression levels in control cells are set to 1 and significance of differential expression is determined by Student’s two tailed t-test, $*p < 0.05$, $**p < 0.01$, $***p < 0.001$.