

SUPPLEMENTARY TABLES

Supplementary Table 4. List of all KEGG pathways under the pathway enrichment analysis for mice subjected to 7 and 30 days of BCAS.

| Description | ID | q-value | geneID | Count |
|----------------------------------|----------|----------|---|-------|
| MAPK signaling pathway | mmu04010 | 0.002396 | Gna12/Cacna1e/Hspa11/Gadd45b/Fos/Gadd45g/Rasgrf2/Cacna2d3/Nr4a1/Cacna1h/Dusp1/Pdgfrb/Fgfr2/Ikbkb/Pla2g3/Ntf3/Prkca/Prkcb/Fgfr3/Cacnb2/Mapk3 | 21 |
| Gastric acid secretion | mmu04971 | 0.00249 | Car2/Itpr2/Gnai2/Plcb2/Kcnj2/Chrm3/Sstr2/Prkca/Ezr/Prkcb | 10 |
| Long-term depression | mmu04730 | 0.007753 | Gna12/Itpr2/Ryr1/Gnai2/Pla2g3/Plcb2/Prkca/Prkcb/Mapk3 | 9 |
| Regulation of actin cytoskeleton | mmu04810 | 0.011272 | Gna12/Itgb4/Iqgap2/Pdgfrb/Fn1/Gsn/Nckap1/Fgfr2/Itga11/Itga9/Chrm4/Chrm3/Ezr/Fgfr3/Mapk3/Chrm5 | 16 |
| Calcium signaling pathway | mmu04020 | 0.013768 | Cacna1e/Plcg1/Cacna1h/Pdgfrb/Phkg1/Itpr2/Ryr1/Phka1/Drd5/Plcb2/Chrm3/Prkca/PrkB/Chrm5 | 14 |
| Axon guidance | mmu04360 | 0.026275 | Efnb3/Sema6a/Slit1/Epha7/Sema3c/Plxna4/Srgap3/Gnai2/Epha6/Mapk3/Sema3e | 11 |

Supplementary Table 5. List of all significantly ($q<0.05$) enriched upregulated and downregulated GO terms for mice subjected to 7 and 30 days of BCAS.

| Description | ID | Category | q-value |
|---|------------|----------|----------|
| cellular response to growth factor stimulus | GO:0071363 | BP | 0.007679 |
| positive regulation of endothelial cell migration | GO:0010595 | BP | 0.007679 |
| regulation of endothelial cell migration | GO:0010594 | BP | 0.009149 |
| endothelial cell migration | GO:0043542 | BP | 0.009149 |
| positive regulation of neuron death | GO:1901216 | BP | 0.009149 |
| posttranscriptional regulation of gene expression | GO:0010608 | BP | 0.009149 |
| regulation of cell morphogenesis | GO:0022604 | BP | 0.009149 |
| protein serine/threonine kinase activity | GO:0004674 | MF | 0.015801 |
| negative regulation of protein phosphorylation | GO:0001933 | BP | 0.023866 |
| modulation of synaptic transmission | GO:0050804 | BP | 0.023866 |
| postsynapse | GO:0098794 | CC | 0.026809 |
| negative regulation of protein modification process | GO:0031400 | BP | 0.029445 |
| regulation of cellular amide metabolic process | GO:0034248 | BP | 0.029445 |
| regulation of mitochondrial fission | GO:0090140 | BP | 0.033902 |
| negative regulation of phosphorylation | GO:0042326 | BP | 0.048738 |