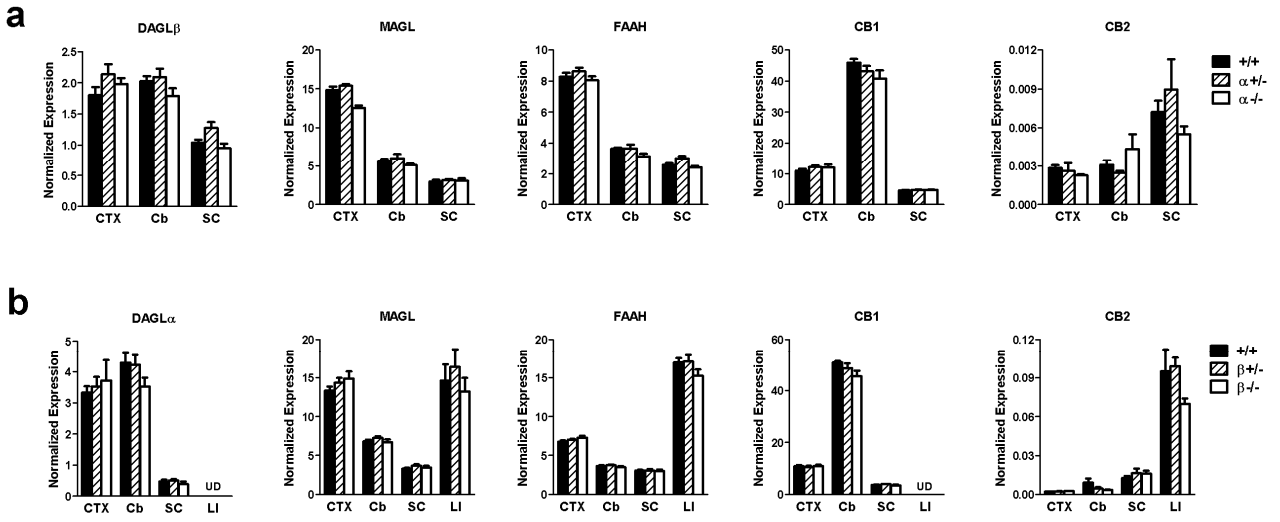
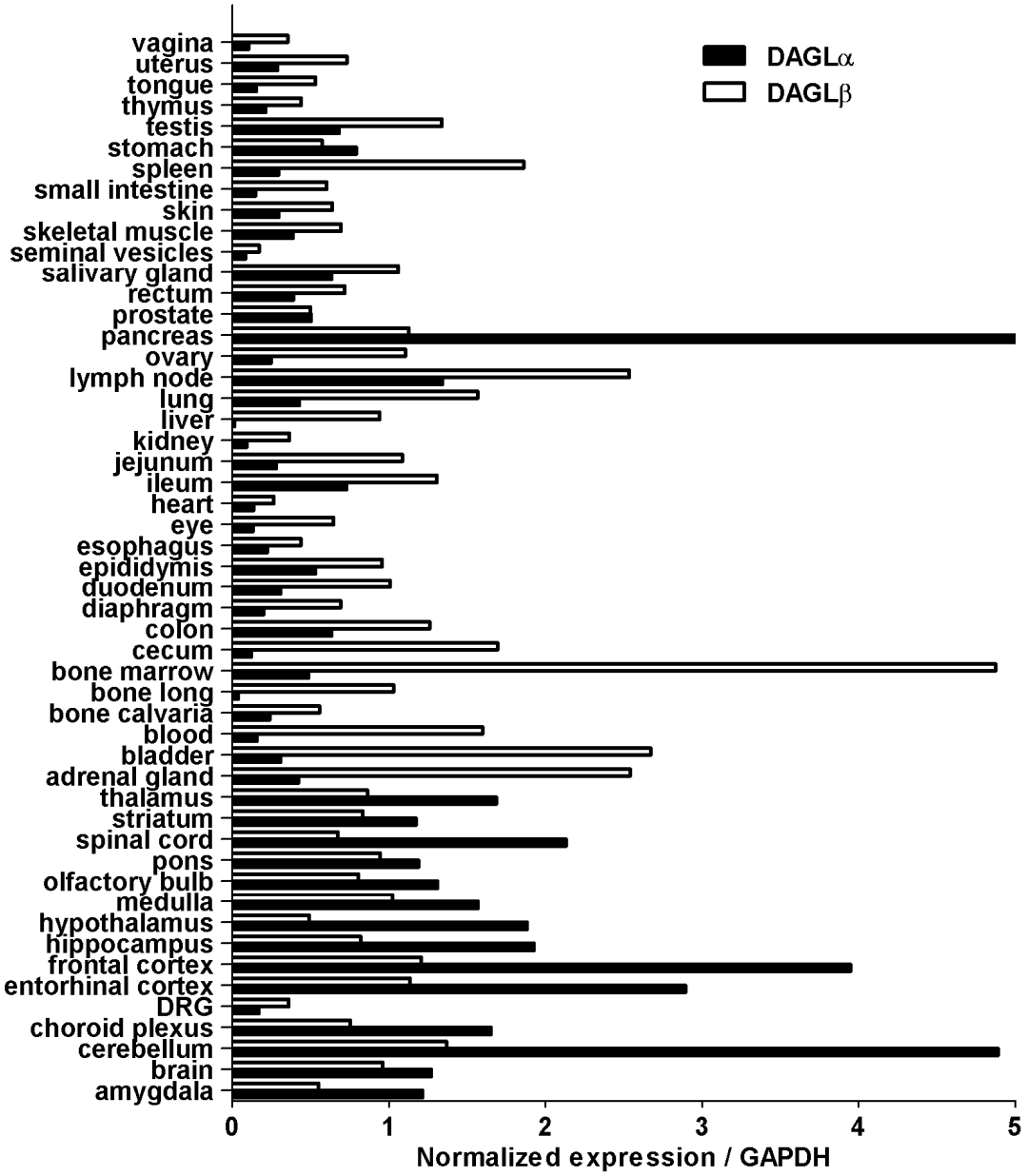



**Supplementary Fig 1. Loss of either DAGLα or DAGLβ has no impact on expression of other eCB pathway transcripts.** Taqman analysis for mRNA levels of DAGLα, DAGLβ, MAGL, FAAH, CB1, and CB2 in the cortex (CTX), cerebellum (Cb), spinal cord (SC), and liver (LI) from 3-5 wt (+/+),DAGL$\alpha^{+/-}$ (α+/-), DAGL$\alpha^{-/-}$ (α-/-), DAGL$\beta^{+/-}$ (β+/-), and DAGL$\beta^{-/-}$ (β-/-) mice. mRNA expression is normalised as the percentage of GAPDH levels.




**Supplementary Fig 2. Tissue distribution of DAGLα/β transcripts.** TaqMan qRT-PCR was performed on RNA samples extracted from multiple mouse tissue samples to detect DAGLα/β mRNA. Data were fitted to a standard curve generated with varying amounts of cDNA. Expression levels of DAGLα/β were normalized to GAPDH.