

Supplementary Figure 1: *In-silico* analysis of cell type specificity for DEGs found after comparing Glu-CB1-KO with their respective CB1-WT in the basal state. We used the transcriptomic information derived from single-cell RNA-seq analyses published by the Allen Institute for Brain Sciences (<https://portal.brain-map.org/atlas-and-data/rnaseq>). The heatmap represents the expression levels of the DEGs found in our RNA-seq analysis across different glutamatergic and GABAergic populations, as well as non-neuronal cell-types. The expression levels are color coded, with blue indicating low expression and red being indicative for high expression.

Supplementary Figure 2: *In-silico* analysis of cell type specificity for DEGs found after comparing GABA-CB1-KO with their respective CB1-WT in the basal state. We used the transcriptomic information derived from single-cell RNA-seq analyses published by the Allen Institute for Brain Sciences (<https://portal.brain-map.org/atlas-and-data/rnaseq>). The heatmap represents the expression levels of the DEGs found in our RNA-seq analysis across different glutamatergic and GABAergic populations, as well as non-neuronal cell-types. The expression levels are color coded, with blue indicating low expression and red being indicative for high expression.

Supplementary Figure 3: *In-silico* analysis of cell type specificity for DEGs found after comparing Glu-CB1-KO with their respective CB1-WT after open field exposure. We used the transcriptomic information derived from single-cell RNA-seq analyses published by the Allen Institute for Brain Sciences (<https://portal.brain-map.org/atlas-and-data/rnaseq>). The heatmap represents the expression levels of the DEGs found in our RNA-seq analysis across different glutamatergic and GABAergic populations, as well as non-neuronal cell-types. The expression levels are color coded, with blue indicating low expression and red being indicative for high expression.

Supplementary Figure 4: *In-silico* analysis of cell type specificity for DEGs found after comparing GABA-CB1-KO with their respective CB1-WT after open field exposure. We used the transcriptomic information derived from single-cell RNA-seq analyses published by the Allen Institute for Brain Sciences (<https://portal.brain-map.org/atlas-and-data/rnaseq>). The heatmap represents the expression levels of the DEGs found in our RNA-seq analysis across different glutamatergic and GABAergic populations, as well as non-neuronal cell-types. The expression levels are color coded, with blue indicating low expression and red being indicative for high expression.