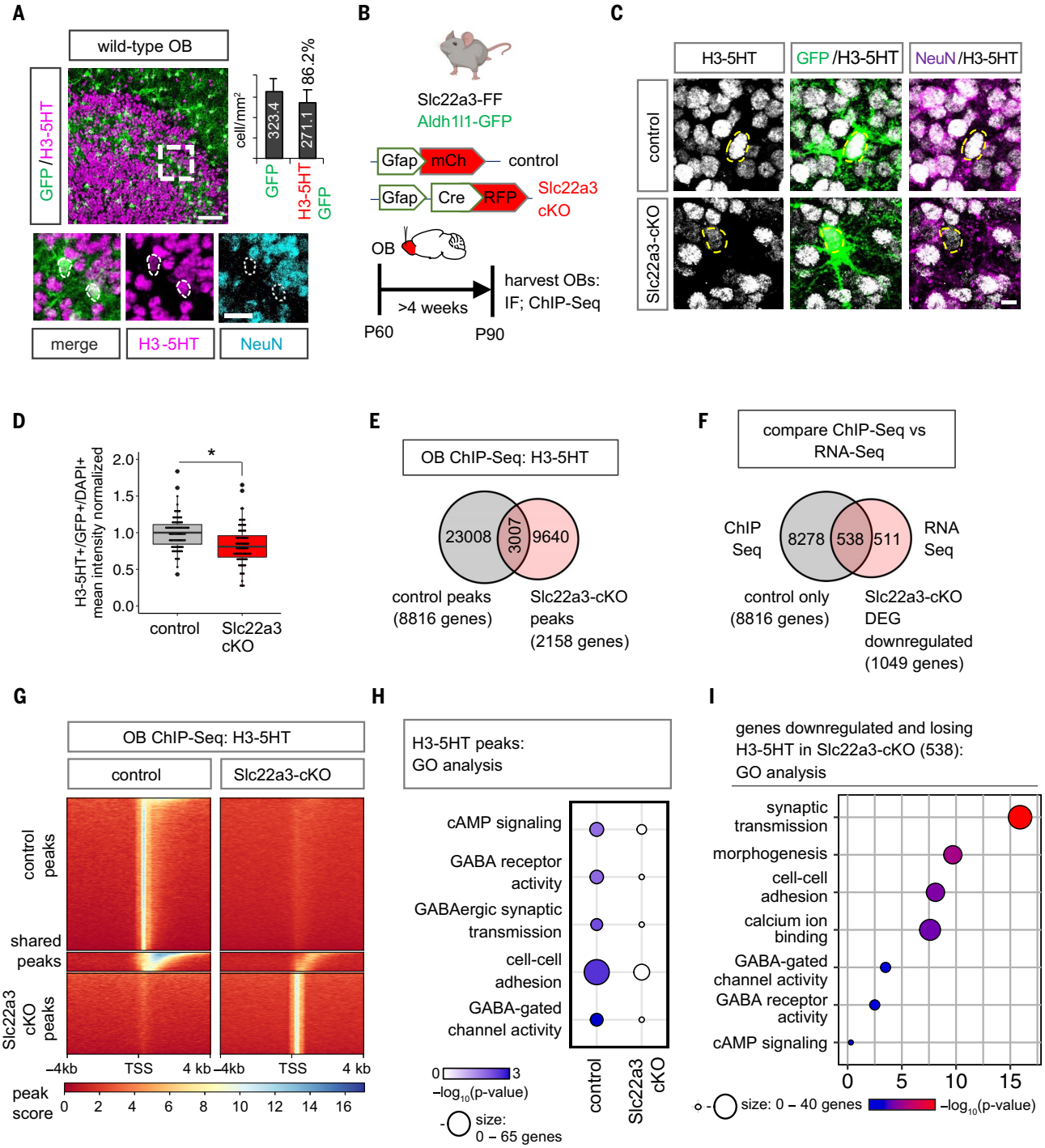

Fig. 5. Slc22a3 regulates histone serotonylation in OB astrocytes. (**A**) Immunostaining of H3-serotonin in OBs of Aldh1l1-GFP mice and quantification of GFP$^+$H3-5HT$^+$ colabeling (n = 3, 25 to 45 cells). White dashed lines in the zoom-in views represent the boundary of the astrocyte nucleus. Error bars represent mean ± SEM. Scale bar, 50 μm; zoom-in scale bar, 20 μm. (**B**) Schematic illustrating viral vectors and timelines for H3-5HT quantification and ChIP-seq. IF, immunofluorescence. (**C** and **D**) H3-5HT immunostaining (C) and quantification (D) in control and Slc22a3-cKO OB astrocytes (74 to 79 cells per cohort; *p = 0.0377, unpaired Student's two-tailed t test on n = 4 mice per cohort). Yellow dashed lines represent the boundary of the astrocyte nucleus. Scale bar, 5 μm. In the box plot, the center line represents the median, box limits are upper and lower quartiles, and whiskers are minimum and maximum values. DAPI, 4′,6-diamidino-2-phenylindole. (**E**) Venn diagram depicting the number of H3-5HT ChIP-seq peaks that are specific to or shared between control and Slc22a3-cKO OBs (n = 4 OBs per cohort). (**F**) Venn diagram depicting number of genes that both lose H3-5HT peaks and are down-regulated in Slc22a3-cKO astrocytes. (**G**) Heatmaps comparing ChIP H3-5HT at 4 kb from the peak center in control versus Slc22a3-cKO OBs. TSS, transcription start site. (**H**) GO analysis of genes at H3-5HT peaks revealing a loss of H3-5HT regulation at GABA-associated pathways in Slc22a3-cKO OBs. (**I**) GO analysis of the 538 overlapping genes shown in (F). See table S3 for data summary. Illustrations were created with Biorender.com.