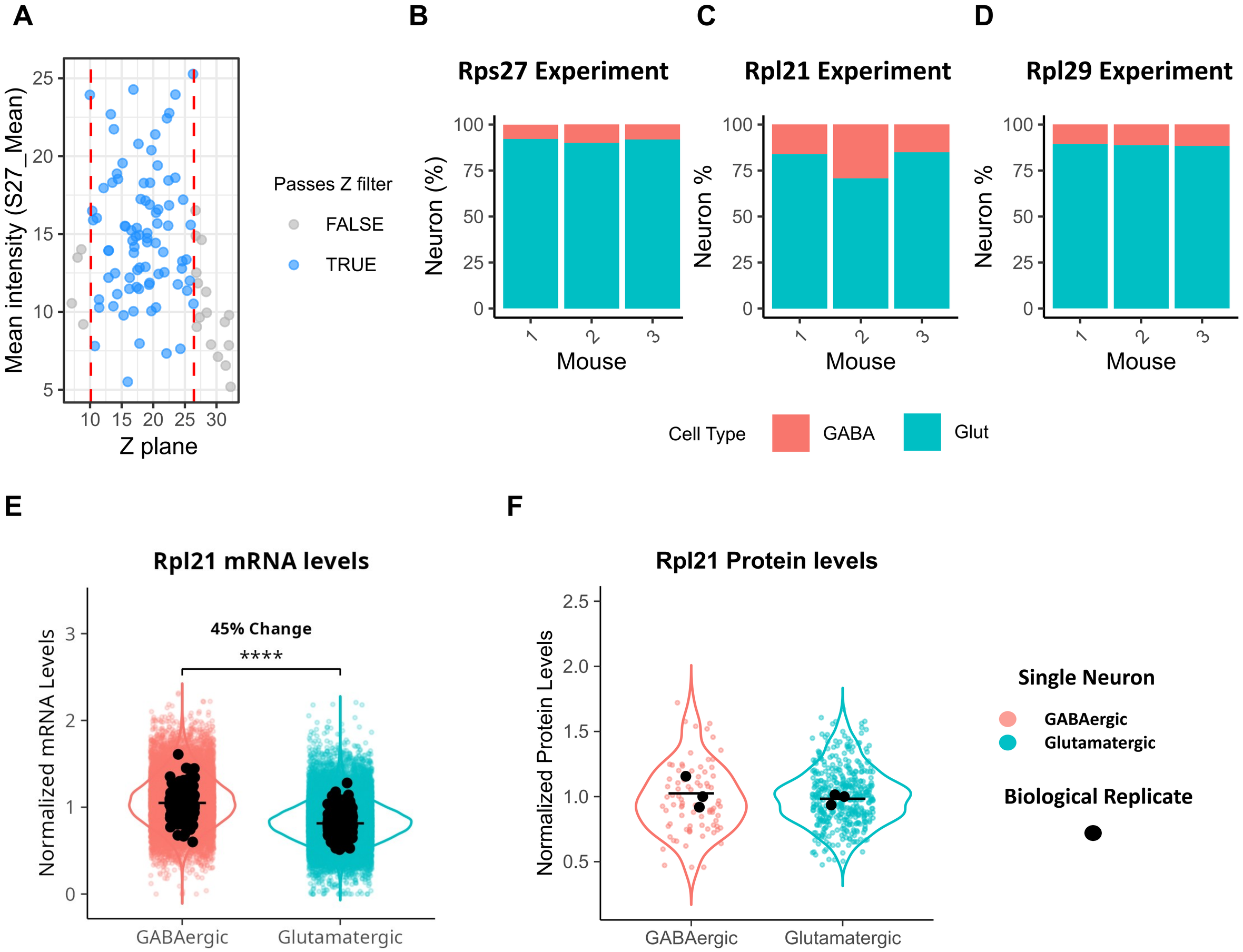

Figure S9. Supporting data and quality control for immunofluorescence-based protein quantification. (A) Example of the Z-plane filtering strategy, where cells with centroids at the edges of the Z-stack (outside the red dashed lines) were excluded to avoid intensity artifacts. (B-D) Bar plots showing the percentage of neuronal cell types identified in each mouse for the Rps27 (B), Rpl21 (C), and Rpl29 (D) experiments. (E) Rpl21 mRNA levels from the Smart-seq2 dataset showing significant expression differences with p-adj < 0.0001. (F) In contrast, quantification of Rpl21 protein levels by mean fluorescence intensity shows no significant differences. (G) Rpl29 mRNA levels from Smart-seq2 dataset showing significant expression differences between neuronal classes. (H) In contrast, protein quantification shows no significant difference. In all violin plots, black dots represent the mean for each biological replicate, and coloured dots individual neuron measurements.