

Supplementary Fig. S1: Overall performance evaluation of *iNeuroAkita* model on internal NPC test data. The figure shows prediction accuracy related to MSE and Pearson correlation across genomic regions in internal NPC test data.

Supplementary Fig. S2: Examples of contact map predicted by *iNeuronAkita* model, and baseline model versus experimental contact maps related to *PSEN2*, *CLU*, and *TOMM40* from the independent NPC test data.

Supplementary Fig. S3: Predicted chromatin disruption scores for 42 functional variants.

Composite disruption Z-scores quantify 3D contact perturbation induced by each variant, with significant loci ($|Z| > 2$, $\text{adj-}p < 0.001$) highlighted.

Supplementary Fig. S4: Predicted chromatin disruption scores for top 37 variants from microglia eQTL. Composite disruption Z-scores quantify 3D contact perturbation induced by each variant, with significant loci ($|Z| > 2$, $\text{adj-}p < 0.001$) highlighted.

Supplementary Fig. S5: Predicted 3D chromatin contact maps for the *PLCG2* structural variant (chr16:81,885,235-81,893,072 (hg38), DEL-7837) for the wild type (WT), mutated (MUT) and differential map (Diff). The bottom are genes impacted by mutation.