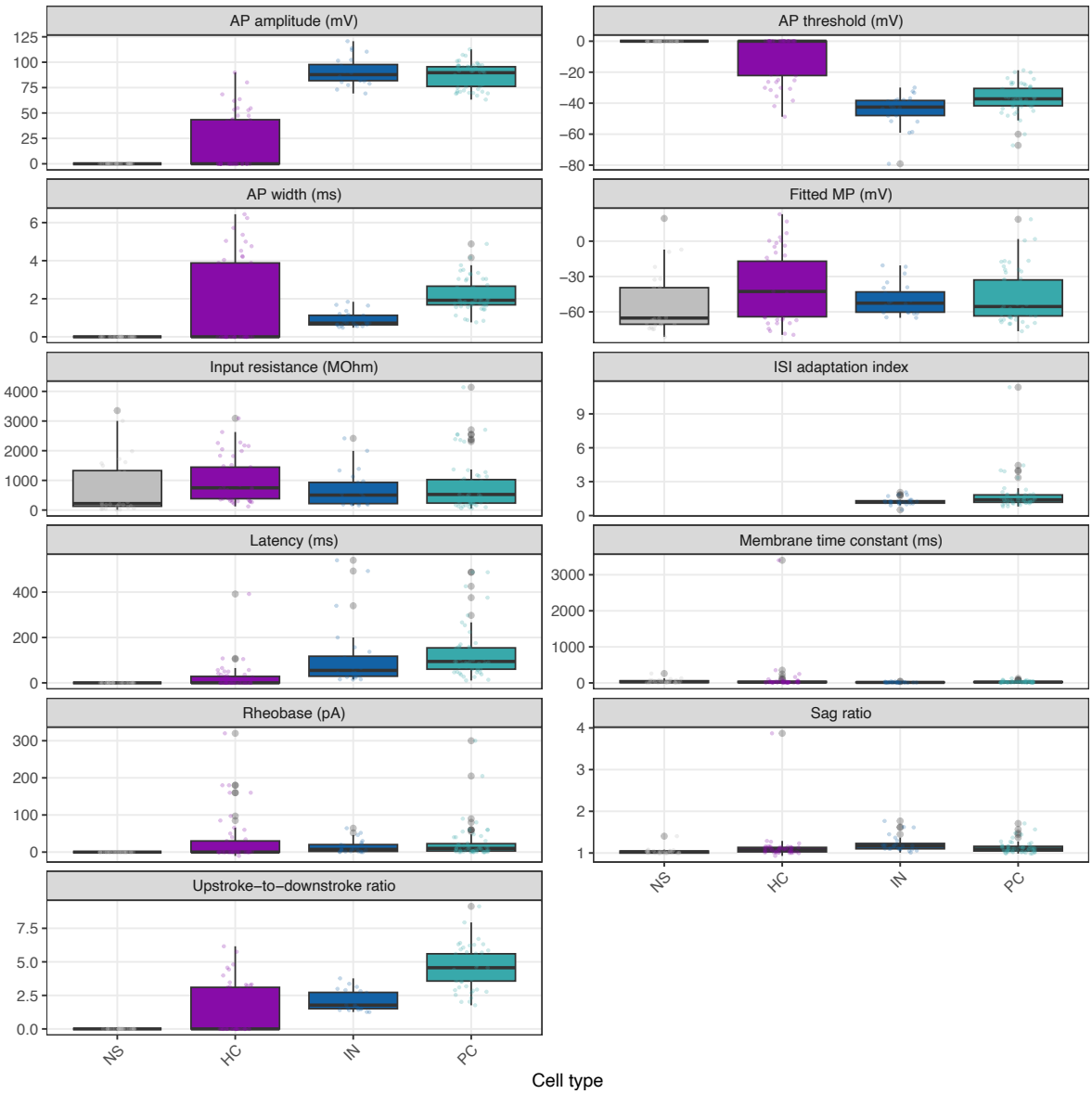
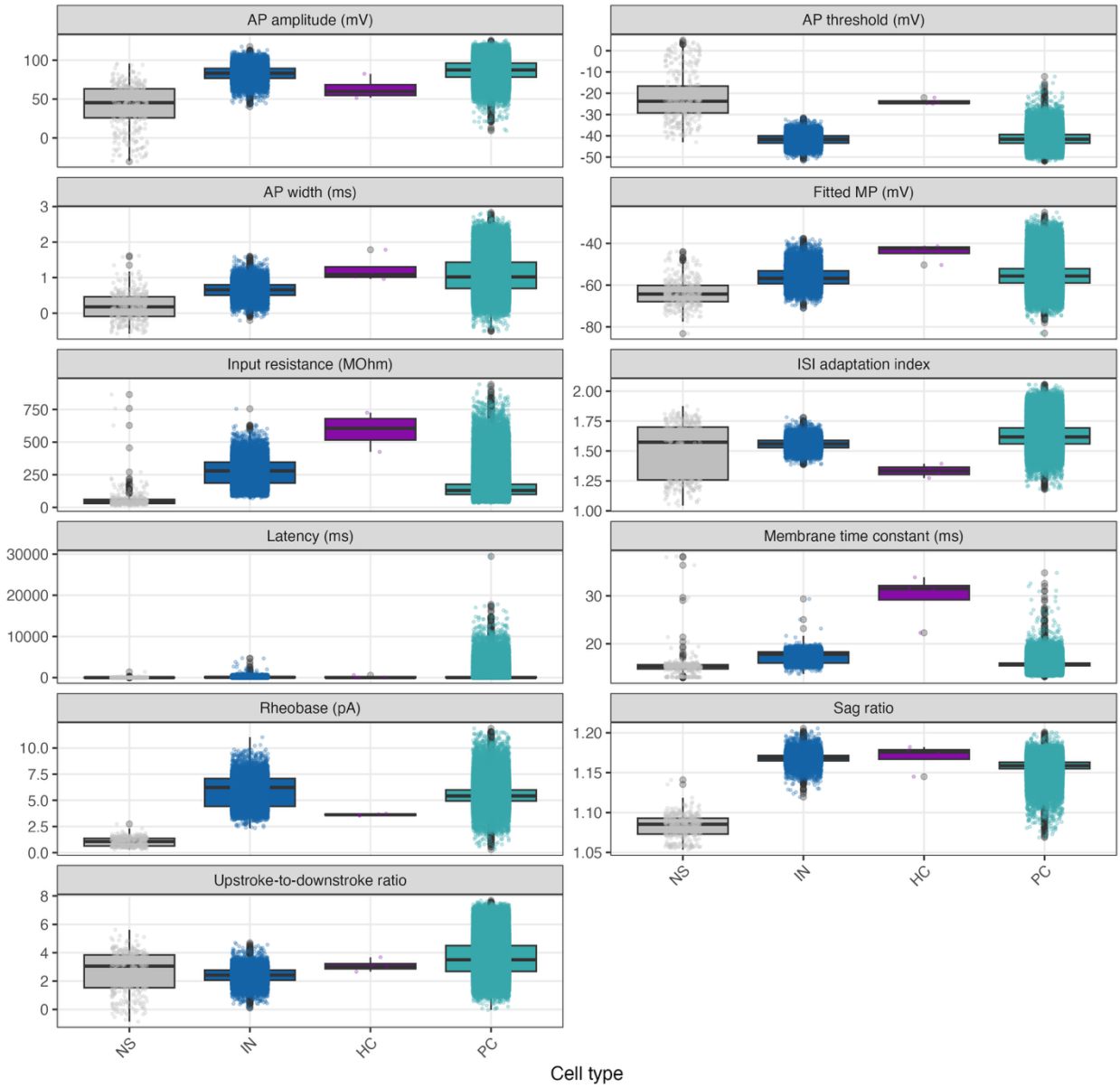


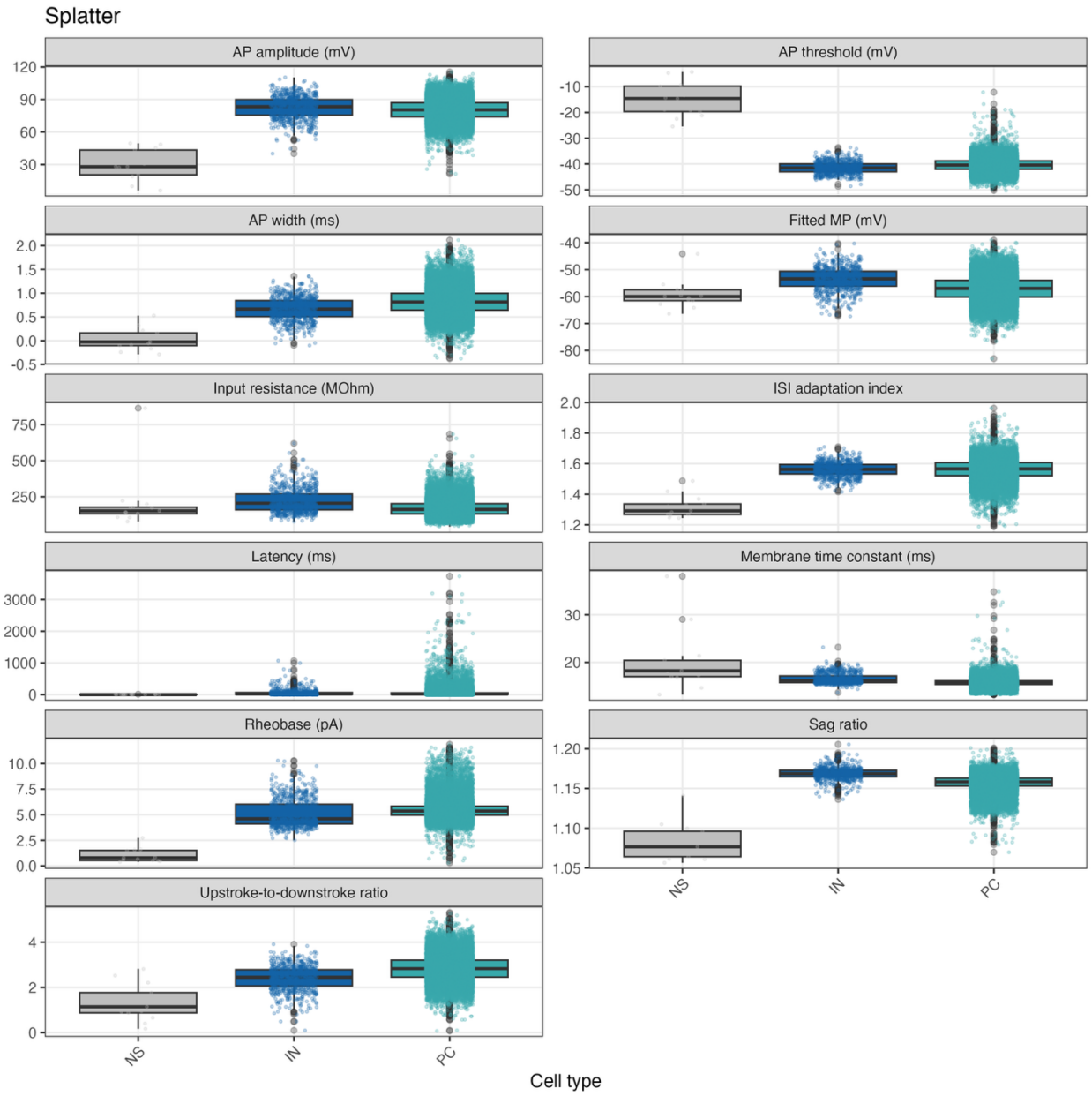
Supp Fig1. Boxplots of electrophysiological (EPHYS) features across cell types in the Patch-seq training data. NS = Non-spiking cell; HC = Hybrid cell; IN = Inhibitory neuron; PC = Pyramidal cell.

Feature Name	model	alpha	l1_ratio	corr	MAE
AP threshold (mV)	pcs	0.95	0.7	0.829	8.599
Input resistance (MOhm)	embs	0.95	0	0.817	470.228
AP amplitude (mV)	embs	0.95	0.7	0.801	17.56
Upstroke-to-downstroke ratio	embs	0.85	0.05	0.54	1.596
Membrane time constant (ms)	embs	0.1	0.05	0.537	16.943
Rheobase (pA)	embs	0.05	0	0.376	34.342
Latency (ms)	embs	0.05	0.85	0.372	58.346
Sag ratio	embs	0.2	0	0.367	0.086
Fitted MP (mV)	embs	0.95	0	0.337	17.014
AP width (ms)	embs	0.3	0.05	0.298	0.915
ISI adaptation index	embs	0.15	0.75	0.113	0.457

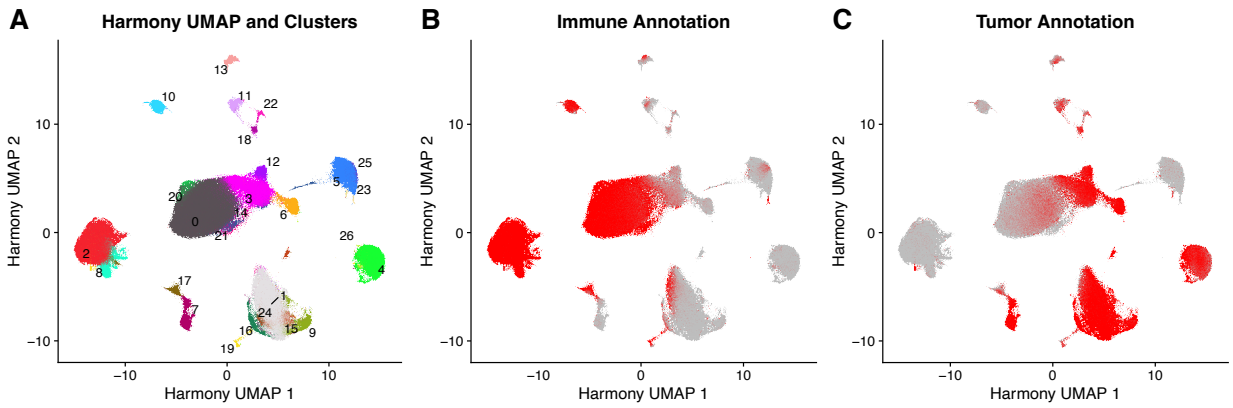
Supp Table 2. Elastic Net performance on held-out Patch-seq test set. Rows are electrophysiological features; models use transformer embeddings (embs) or principal components (pcs). Columns: α (regularization strength), l1_ratio (L1–L2 mix; 0=ridge, 1=lasso), corr (Pearson r; higher is better), MAE (mean absolute error in feature units; lower is better).



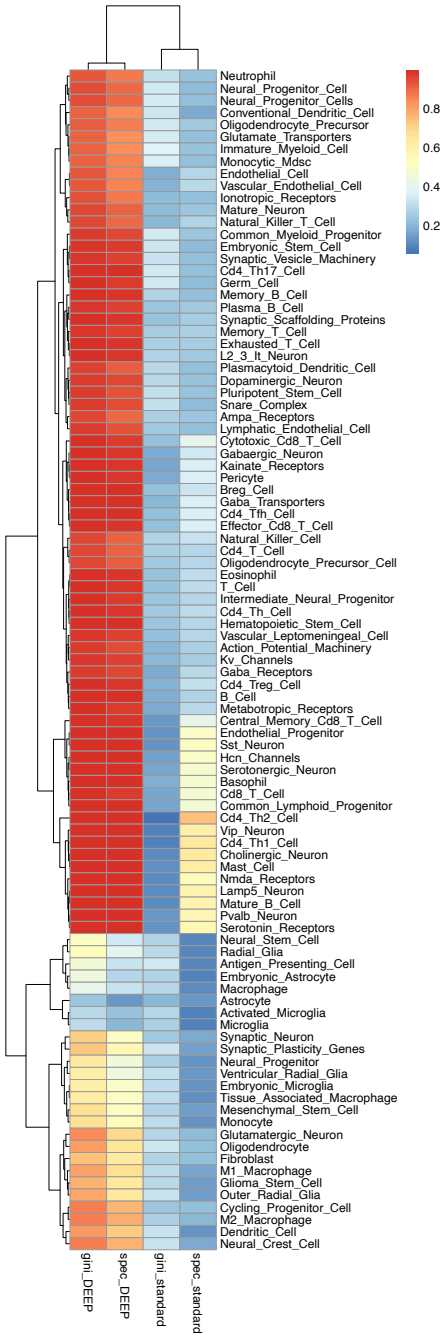
Supp Fig. 3. Boxplots of PREPS-predicted electrophysiological features across PREPS-assigned cell types in the Allen Brain Atlas neuronal dataset. NS = Non-spiking cell; HC = Hybrid cell; IN = Inhibitory neuron; PC = Pyramidal cell.



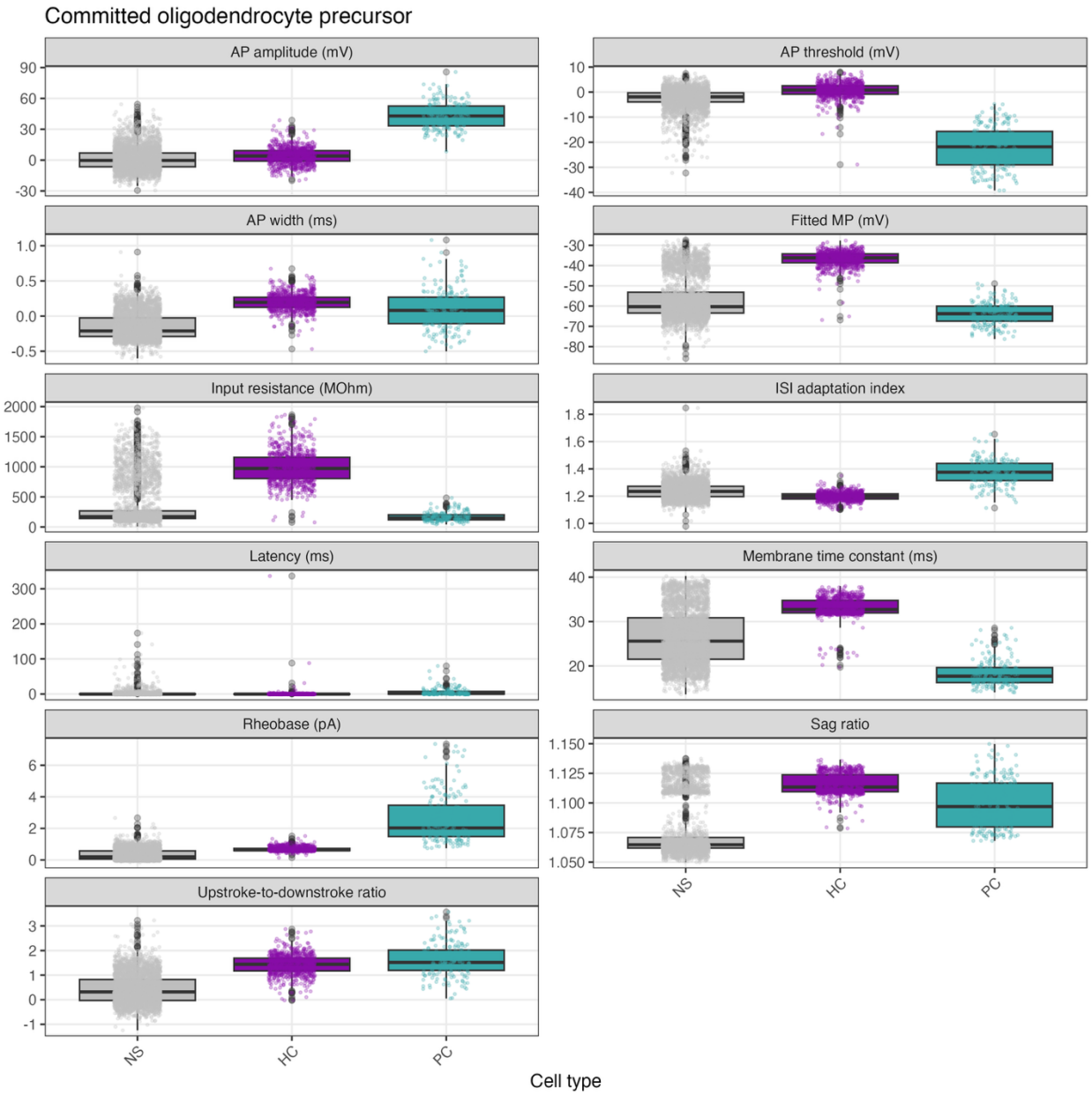
Supp Fig4. Boxplots of PREPS-predicted electrophysiological features across PREPS-assigned cell types in the Allen Brain Atlas Splatter cluster cells.



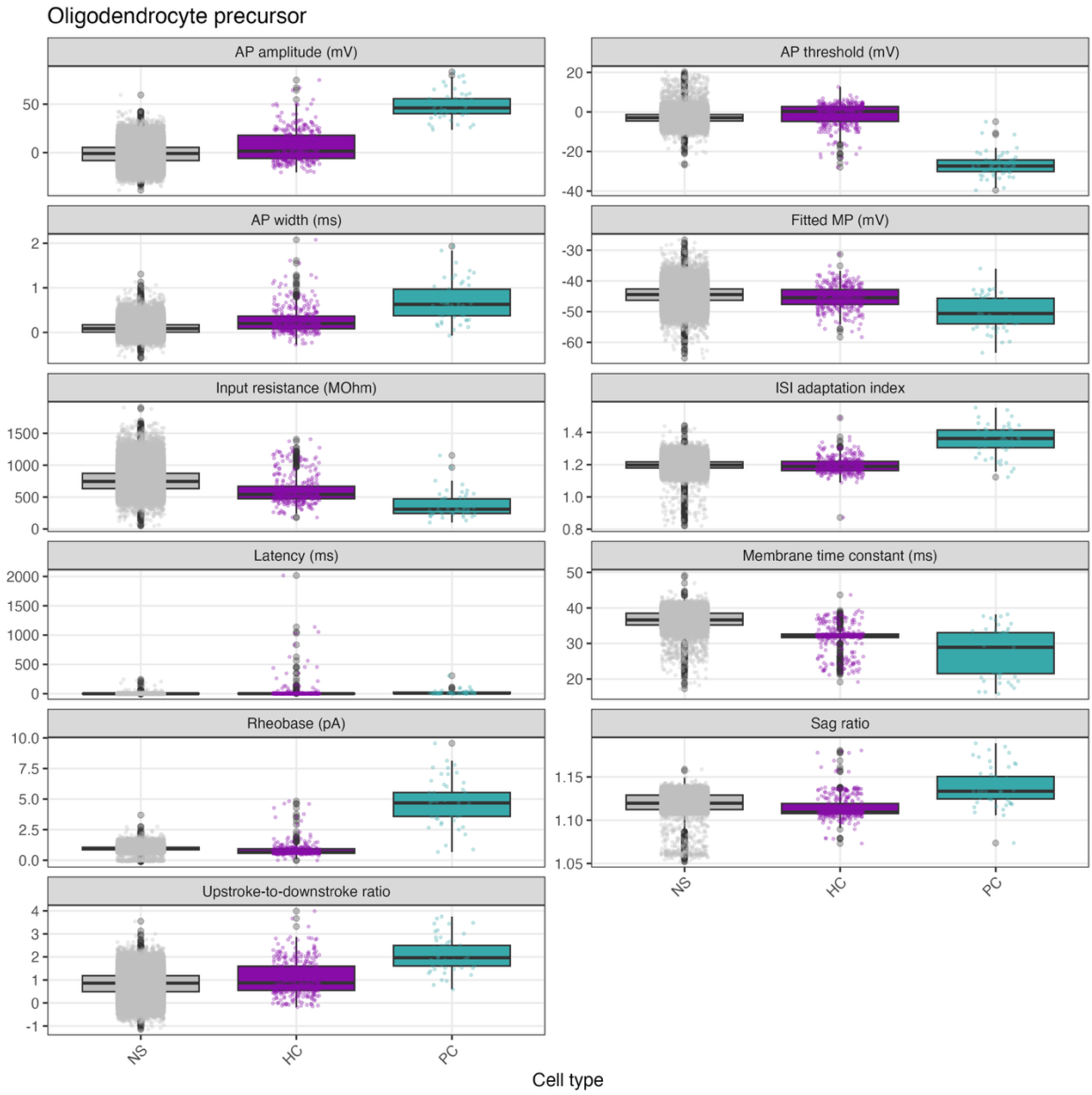
Supp Fig5. Harmony-integrated UMAP of glioma scRNA-Seq data. (A) UMAP of Harmony-corrected data showing seurat clusters (numeric labels). **(B)** Immune annotation: immune cells highlighted in red; non-immune in grey. **(C)** Tumor annotation: malignant cells highlighted in red; non-tumor in grey.



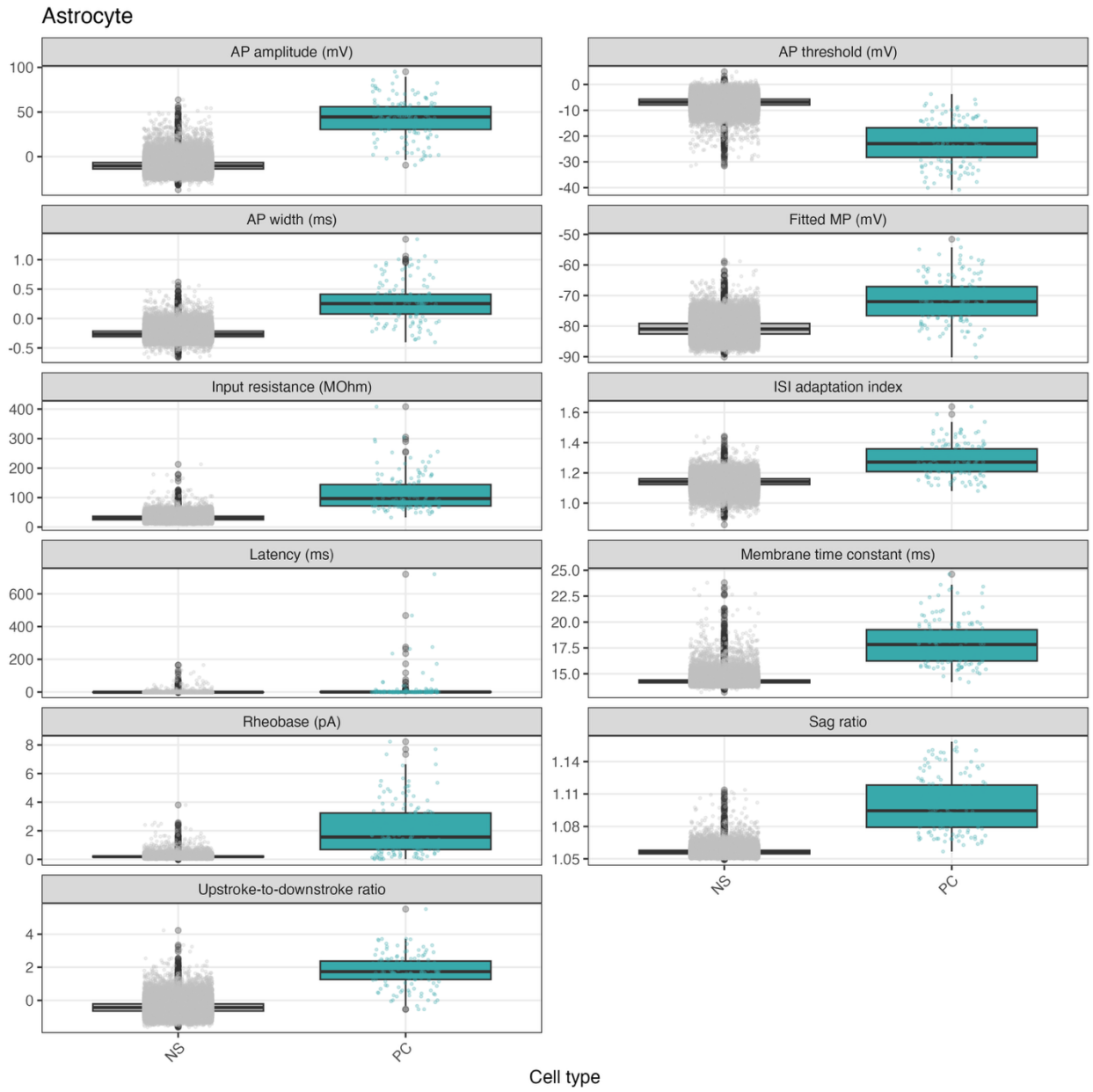
Supp Fig6. Heatmap of distribution of sharpness metrics for DEEPS vs standart gene-set scores. Rows are gene sets; columns report gini_DEEP, spec_DEEP, gini_standard, and spec_standard, computed from per-cell score distributions. Gini quantifies inequality of scores; specificity score values indicate sharper distributions. Across gene sets, DEEPS showed higher Gini score and specificity than standard module scores, indicating sharper, more cell-type-restricted distributions.



Supp Fig7. Boxplots of PREPS-predicted electrophysiological features across PREPS-assigned cell types in the Allen Brain Atlas Committed Oligodendrocyte Precursor cluster cells.



Supp Fig8. Boxplots of PREPS-predicted electrophysiological features across PREPS-assigned cell types in the Allen Brain Atlas Oligodendrocyte Precursor cluster cells.



Supp Fig9. Boxplots of PREPS-predicted electrophysiological features across PREPS-assigned cell types in the Allen Brain Atlas Astrocyte cluster cells.