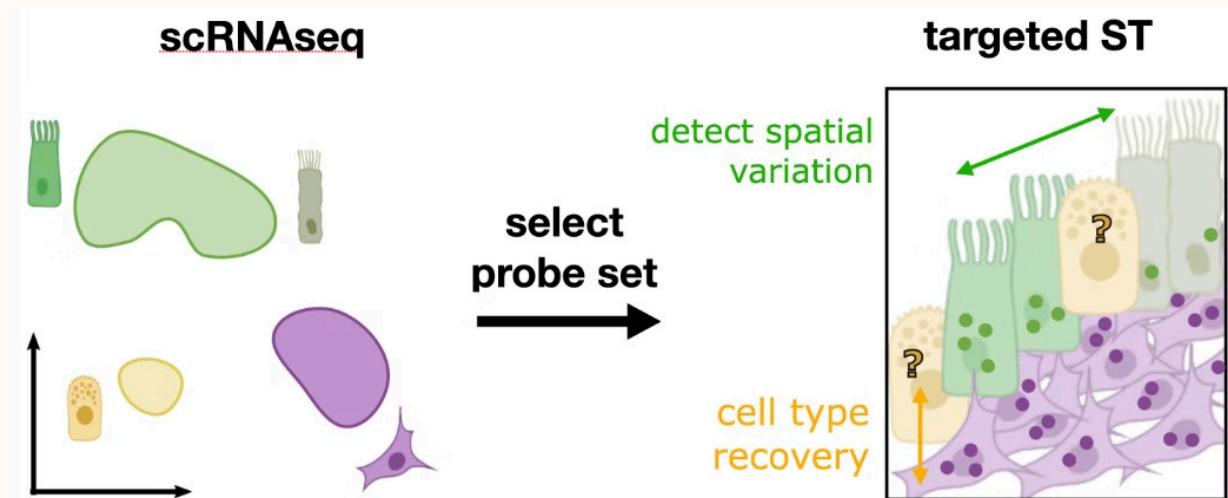


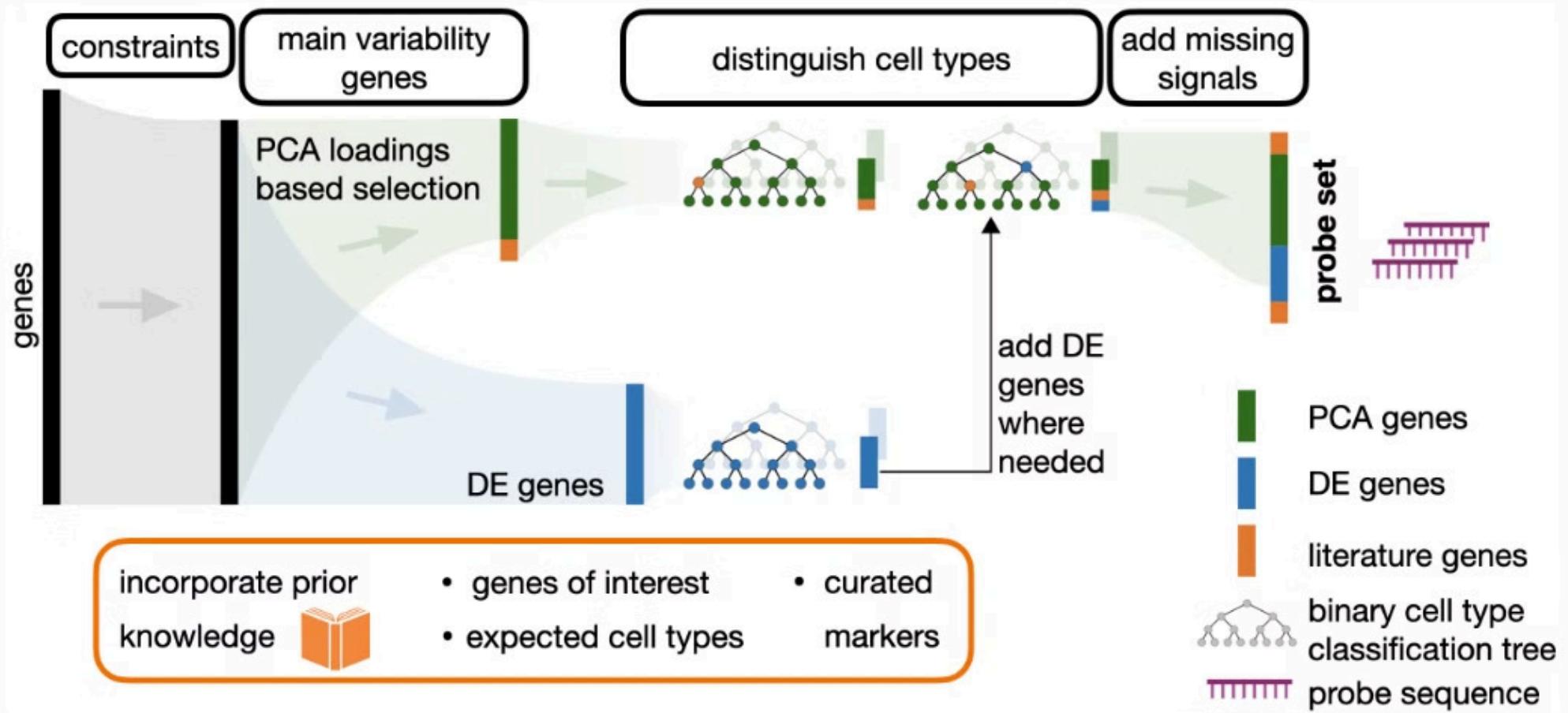


Spapros: A Pipeline for Targeted Spatial Transcriptomics



Spapros is a probe set selection pipeline designed for targeted spatial transcriptomics

Spapros Methodology



Constraints

Spapros begins by defining constraints on the gene set, possibly based on prior knowledge or technical limitations. This ensures that the selected genes are suitable for the specific experiment and available resources.

Main Variability Genes

The pipeline employs principal component analysis (PCA) to identify genes that contribute the most to data variance. This step ensures that the probe set captures the most important signals in the spatial transcriptomics data.

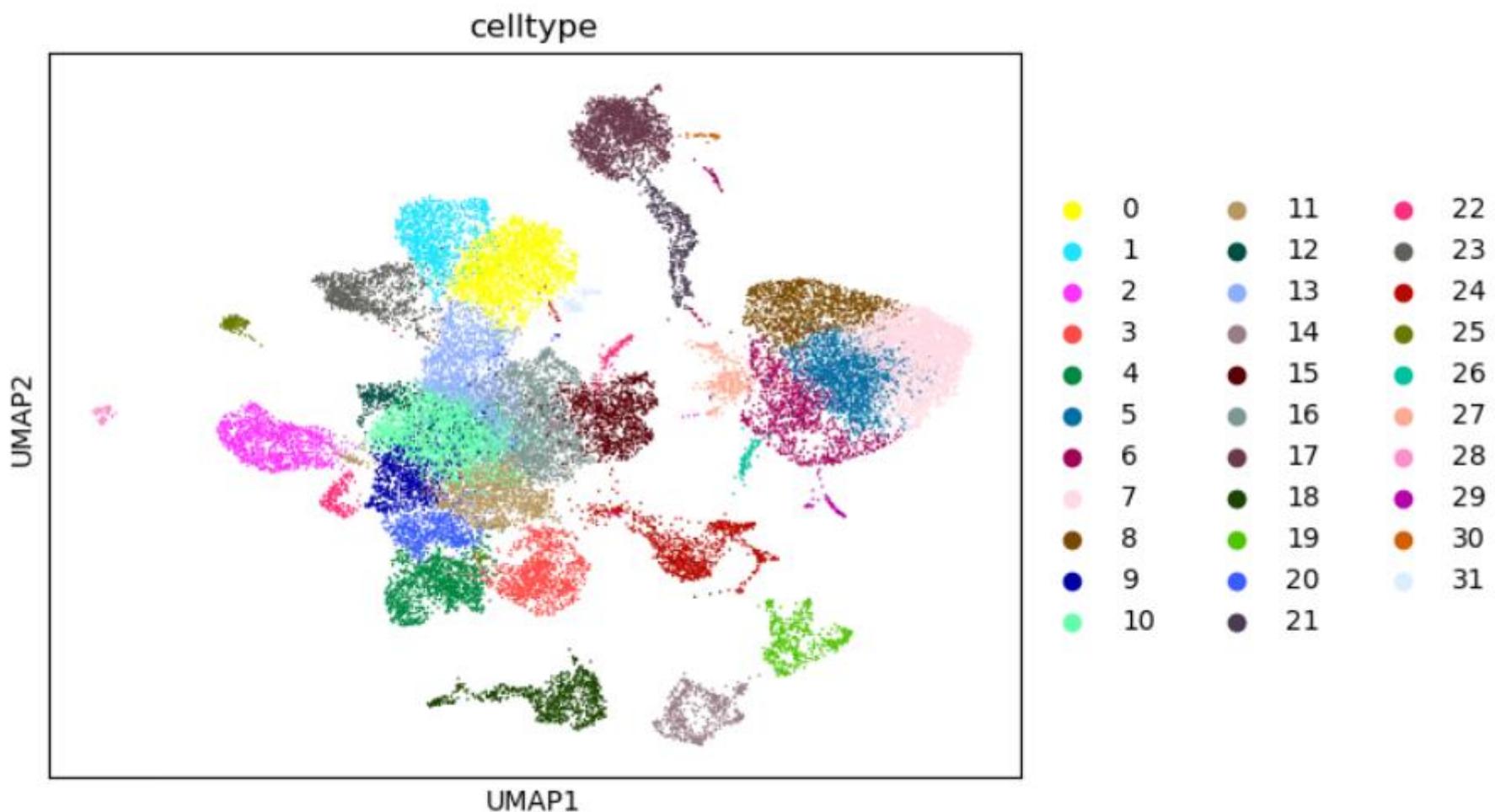
Applications of Spapros

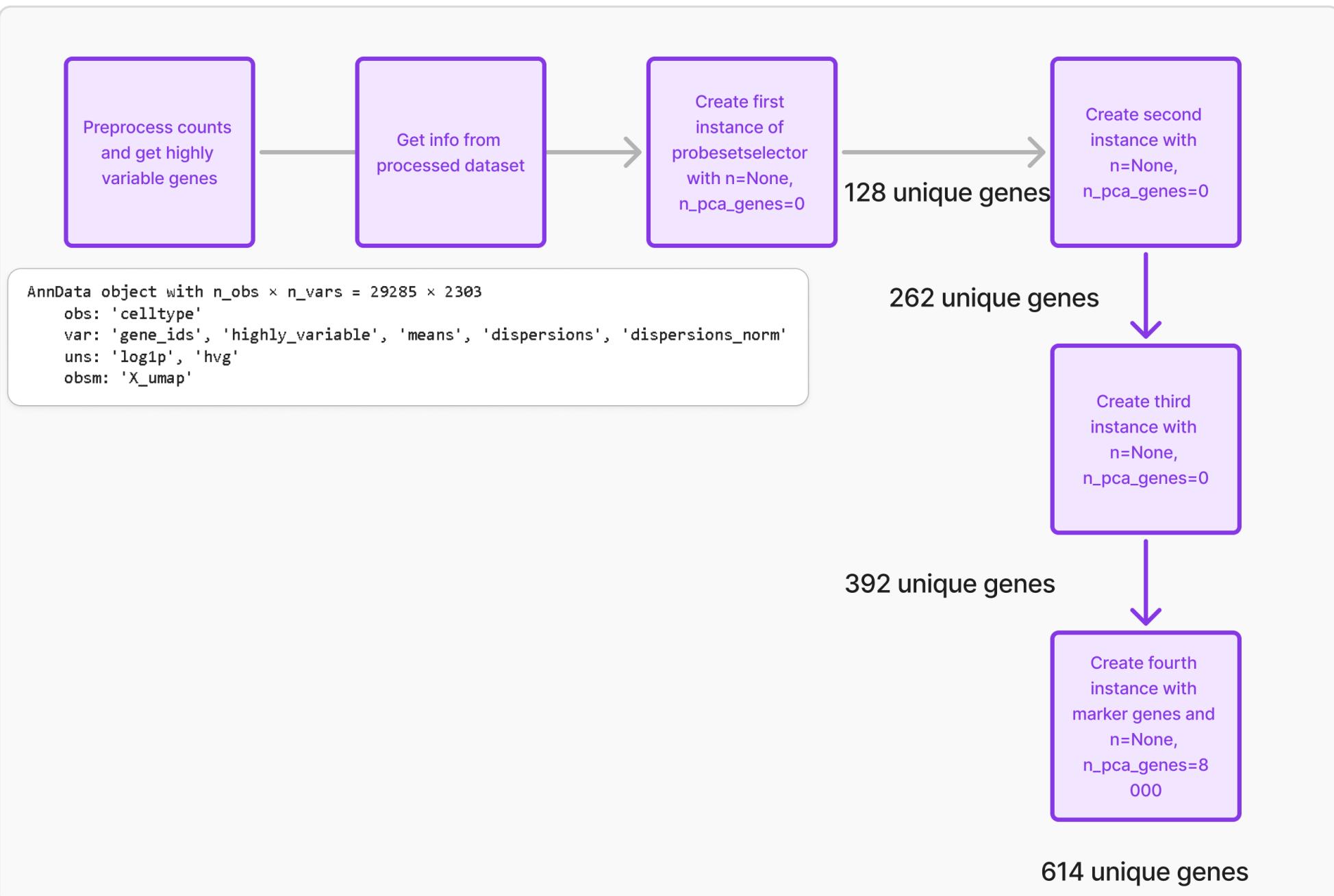
Optimal Probe Set Selection

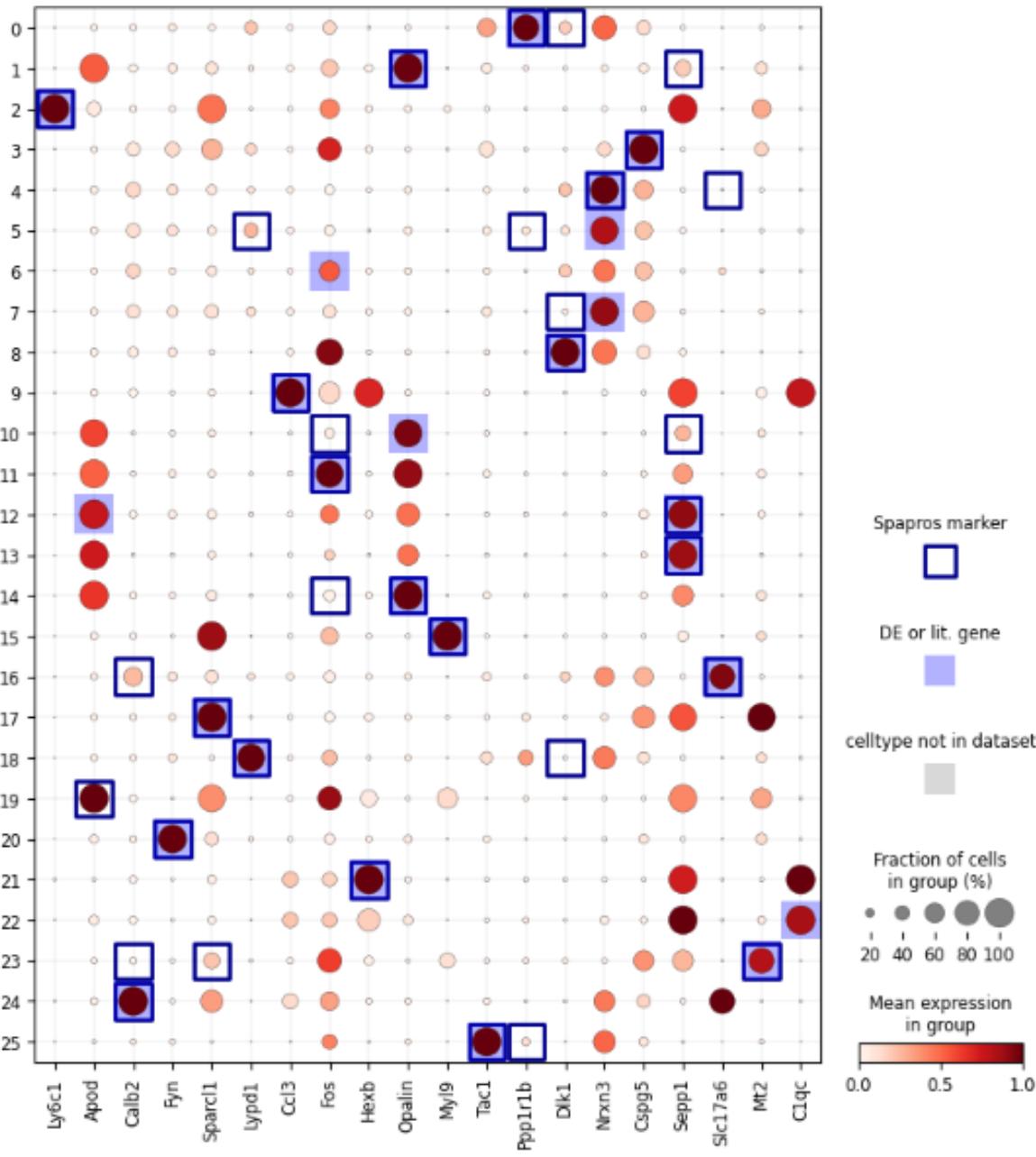
Spapros enables the selection of gene sets optimized for identifying specific cell types and capturing transcriptional variation beyond cell type annotations.

Probe Design

The pipeline includes a probe design component that generates ready-to-order probes based on the selected gene sets, ensuring that the probes meet technical constraints and are suitable for the experimental setup.







	gene_nr	selection	rank	marker_rank	tree_rank	importance_score	pca_score	pre_selected	prior_selected	pca_selected	celltypes_DE_1vsall	celltypes_DE_spec
Ly6c1	1	True	1.0	1.0	1.0	0.975035	0.742810	True	False	False	2	
Sparc1	2	True	1.0	1.0	1.0	0.842713	1.204107	True	False	True	17	
CcB	3	True	1.0	1.0	1.0	0.802680	1.200838	True	False	True	9	
Calb2	4	True	1.0	1.0	1.0	0.780230	0.801069	True	False	False	24	

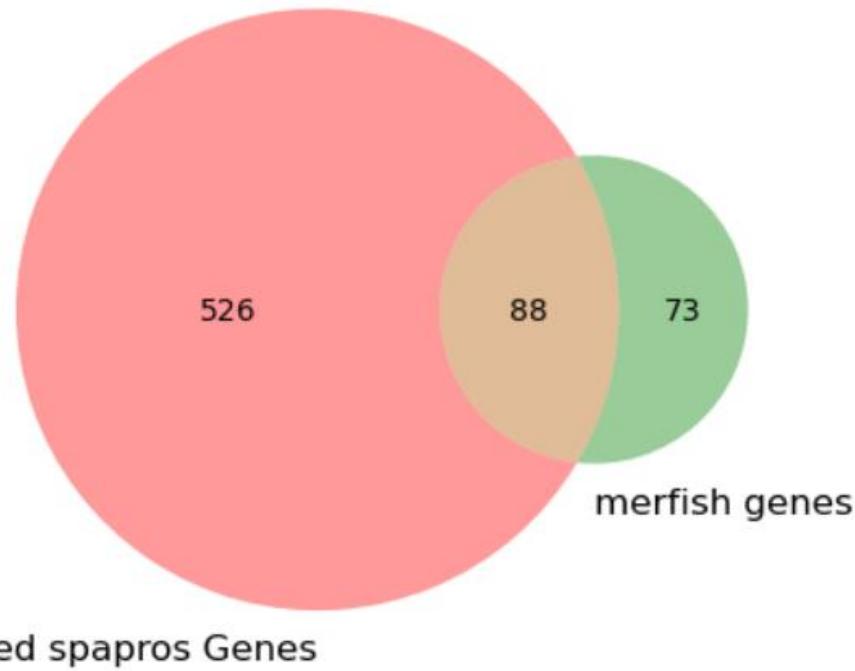
	gene_nr	selection	rank	marker_rank	tree_rank	importance_score	pca_score	pre_selected	prior_selected	pca_selected	celltypes_DE_1vsall	celltypes_DE_spec
Nrxn3	19	True	1.0	1.0	1.0	0.381296	1.670207	True	False	True	4,7,5	
Mal	20	True	1.0	1.0	1.0	0.223368	0.989218	True	False	False	1,10,11	
Mt2	21	True	1.0	1.0	1.0	0.161281	0.737992	True	False	False	23	
Hm2a	22	True	1.0	2.0	1.0	0.492063	0.938224	True	False	False	2	

	gene_nr	selection	rank	marker_rank	tree_rank	importance_score	pca_score	pre_selected	prior_selected	pca_selected	celltypes_DE_1vsall	celltypes_DE_spec
Cc4	49	True	2.0	NaN	1.0	0.052427	1.456800	False	False	True		
Anln	50	True	2.0	NaN	1.0	0.044486	0.400287	False	False	False		
Junb	51	True	2.0	NaN	1.0	0.032562	1.757122	False	False	True		
Xist	52	True	2.0	NaN	1.0	0.024133	2.194393	False	False	True		

[34]: display(selector.probeset.iloc[266:275])

Selpg	267	True	NaN	NaN	NaN	NaN	0.366234	False	False	False	
Calm1	268	True	NaN	NaN	NaN	NaN	0.366160	False	False	False	
Sox4	269	False	NaN	NaN	NaN	NaN	0.364669	False	False	False	
Cxcl12	270	False	NaN	NaN	NaN	NaN	0.362954	False	False	False	
Gdf15	271	False	NaN	NaN	NaN	NaN	0.361086	False	False	False	
Tmem108	272	False	NaN	NaN	NaN	NaN	0.361015	False	False	False	
Fxyd1	273	False	NaN	NaN	NaN	NaN	0.360289	False	False	False	
Mmd2	274	False	NaN	NaN	NaN	NaN	0.360022	False	False	False	
Pde10a	275	False	NaN	NaN	NaN	NaN	0.359962	False	False	False	

Venn Diagram of Gene Overlap
(Overlap: 88 genes)



Venn Diagram of Gene Overlap
(Overlap: 39 genes)

