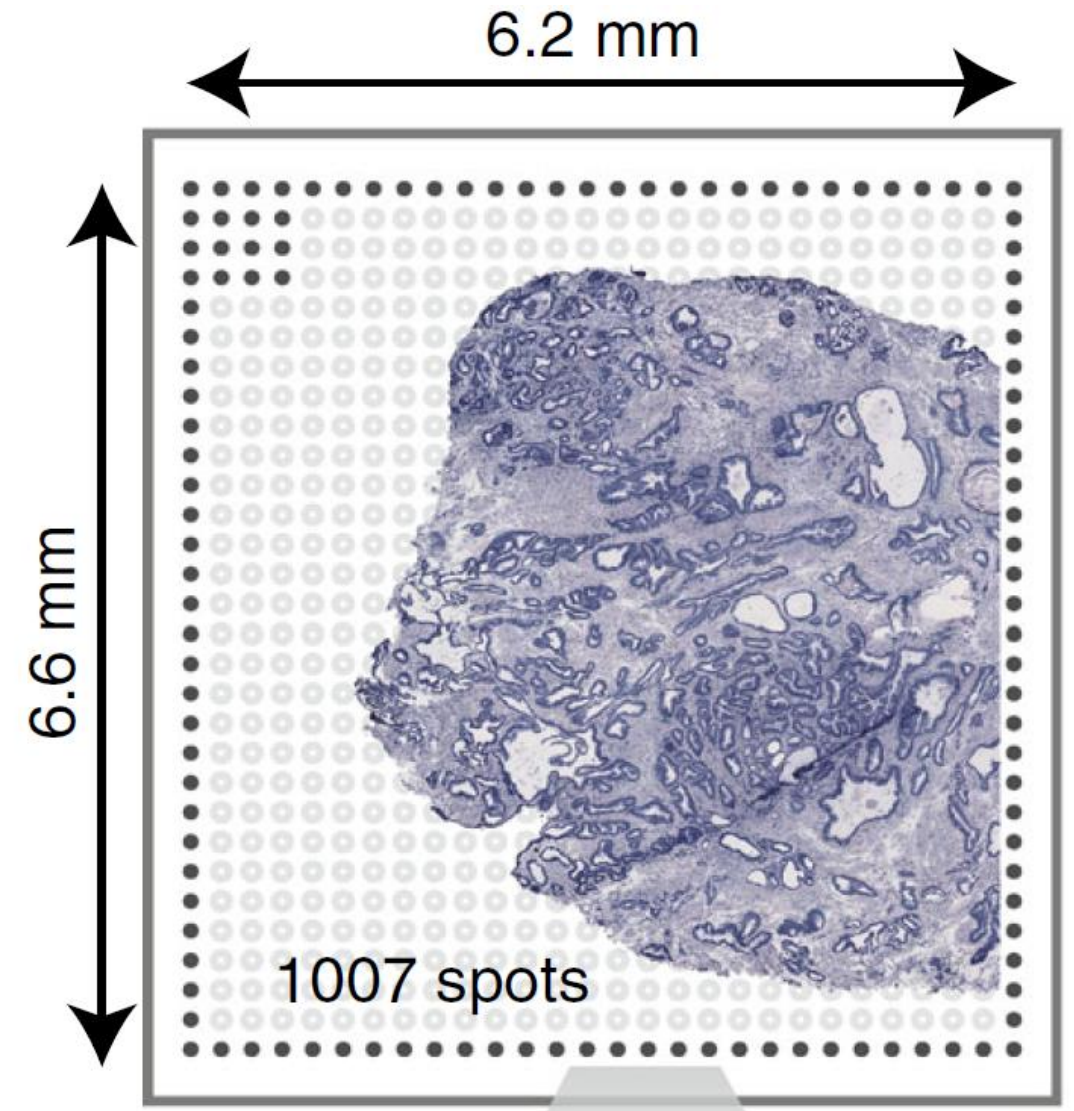
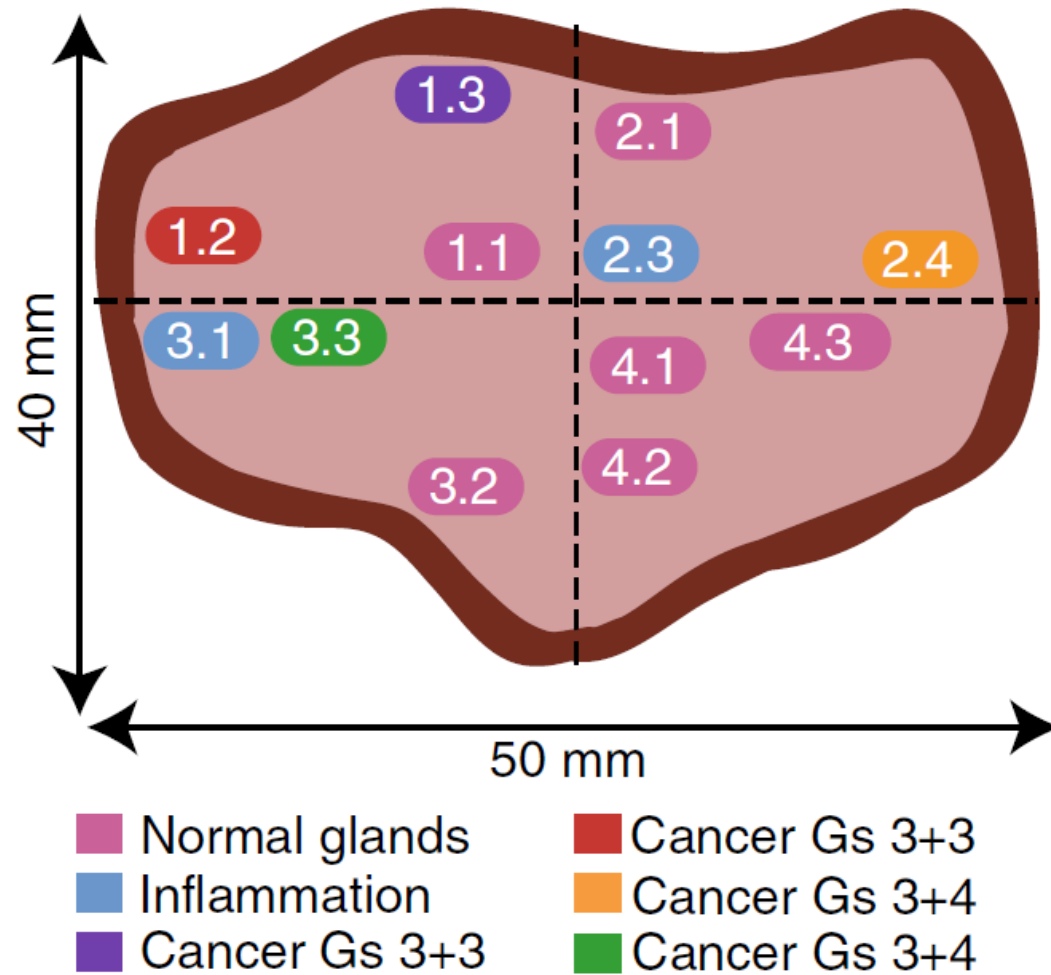


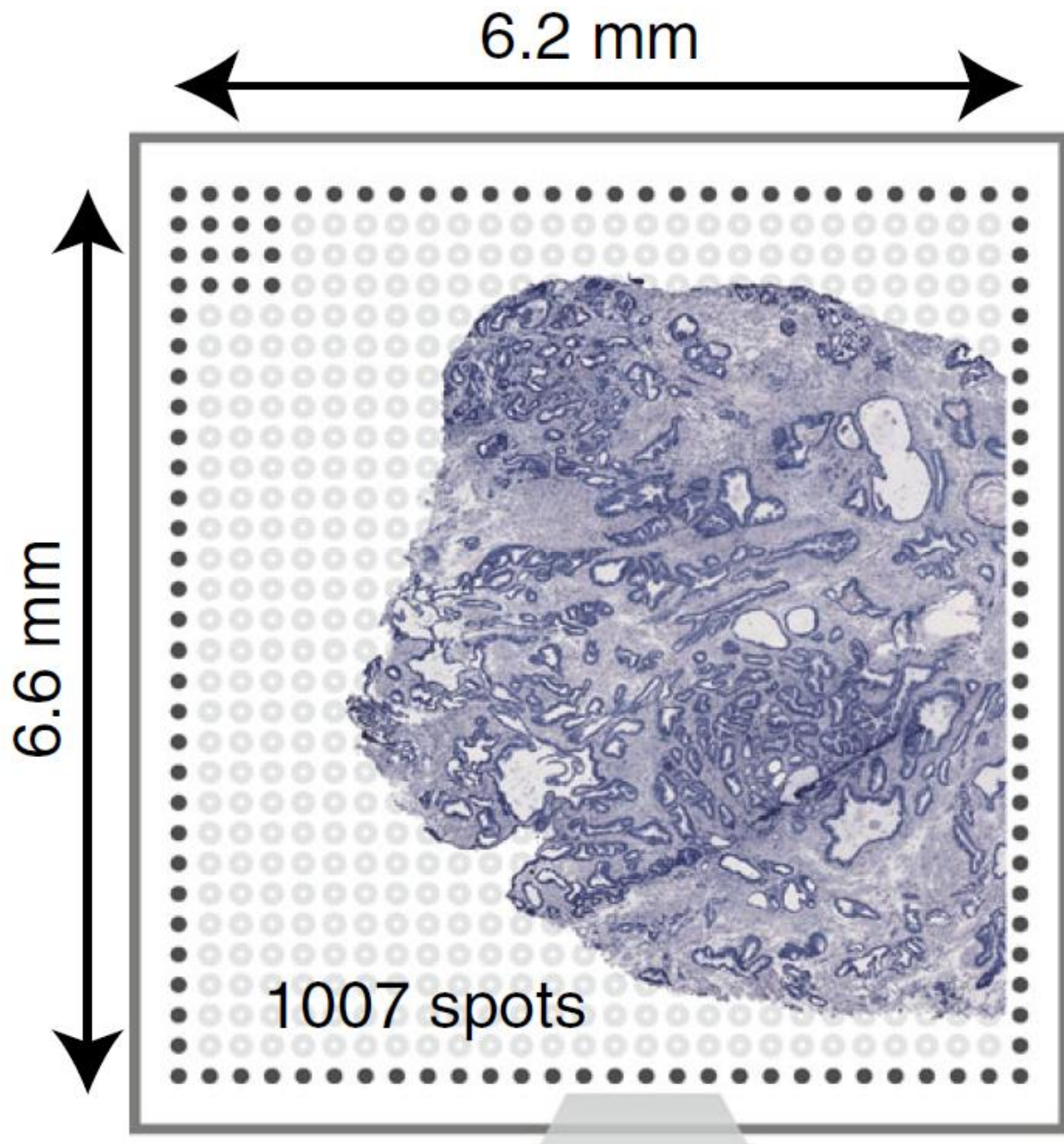
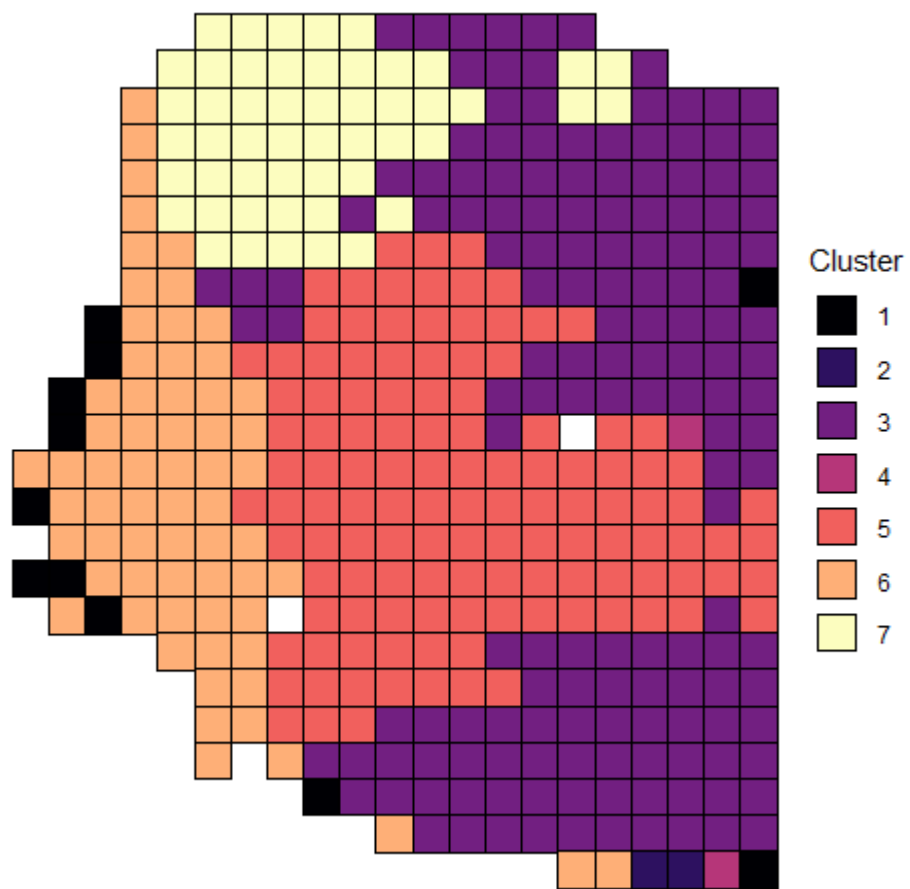
Analysis of Prostate Cancer data from Berglund et al., 2018

4/29

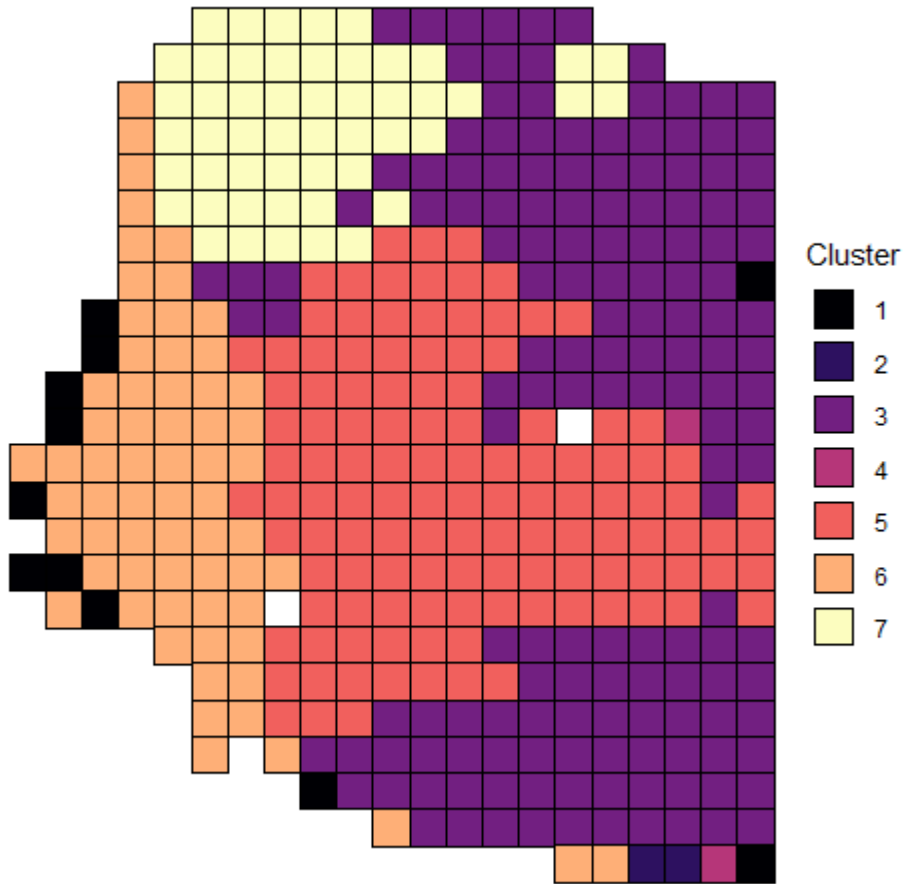
Prostate cancer sample 1.2



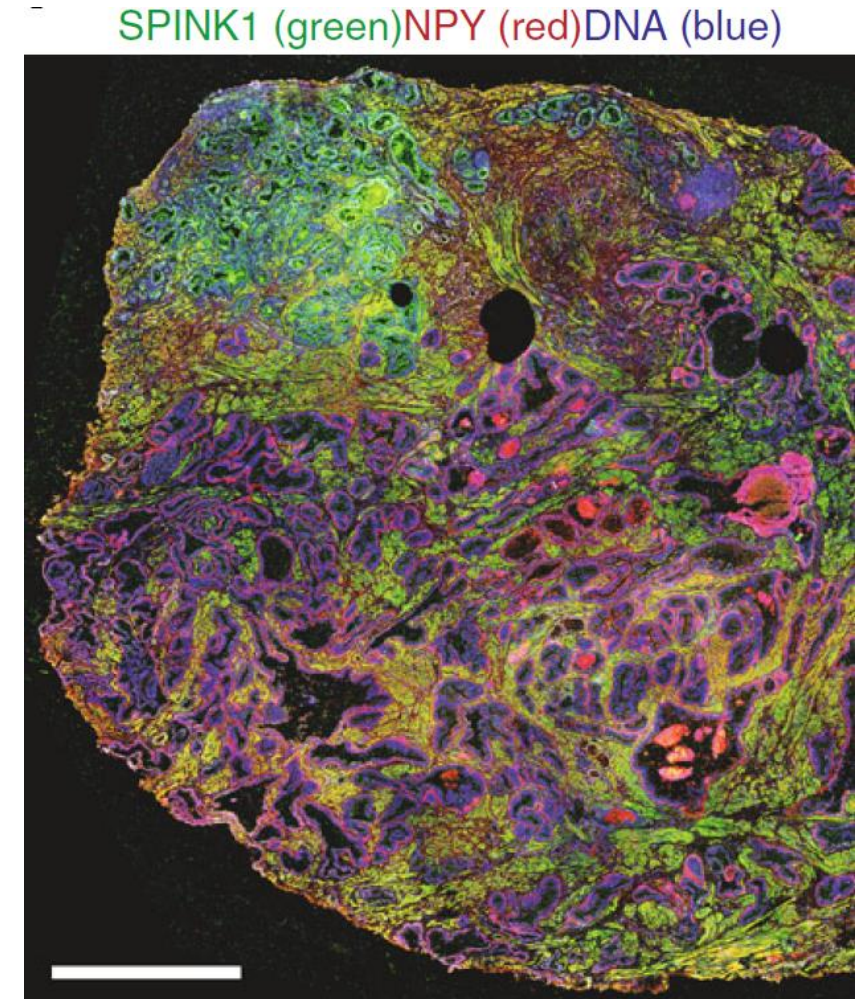
Spatial Clustering



Spatial Clustering

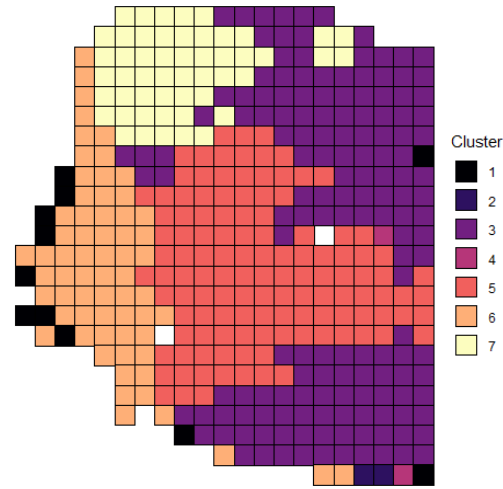


SPINK1 = cancer marker
NPY = PIN marker

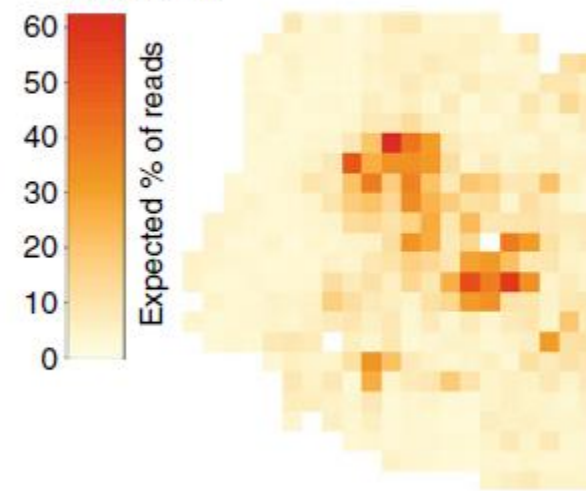


Spatial Clustering

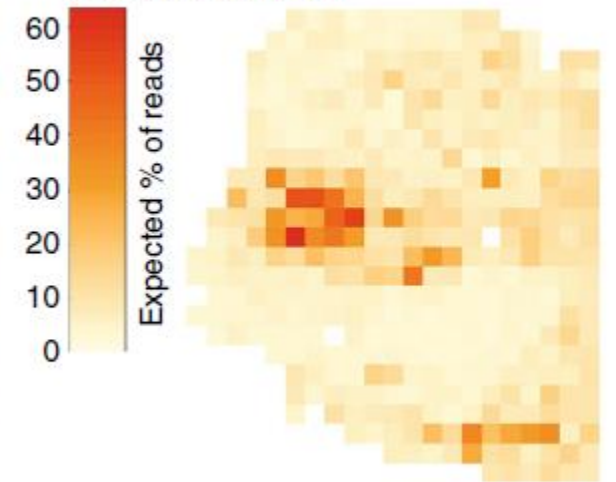
Cluster



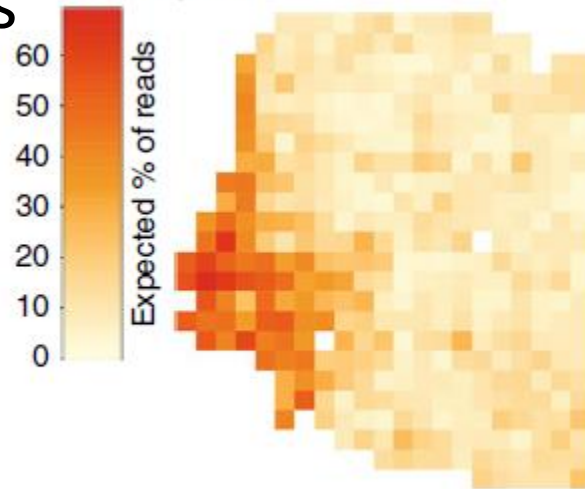
PIN glands



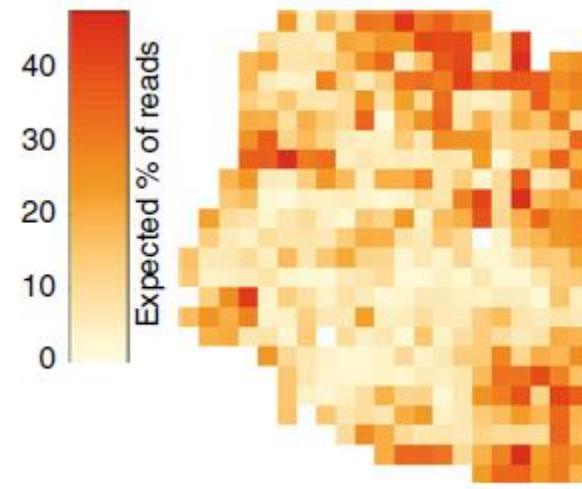
Immune profile - UBC, NR4A1, IER2, JUN, FOS enriched



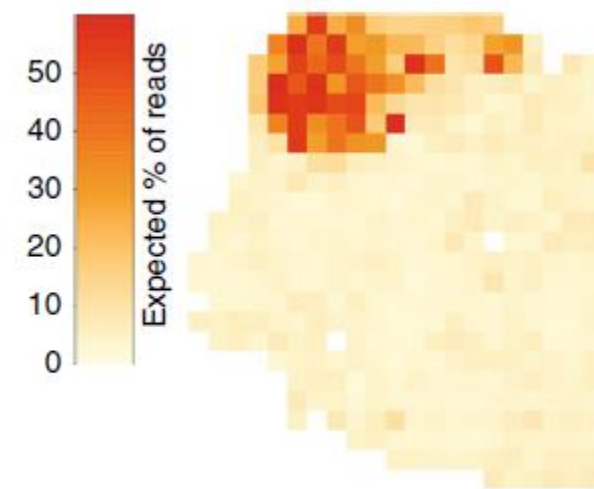
Normal glands



Stroma











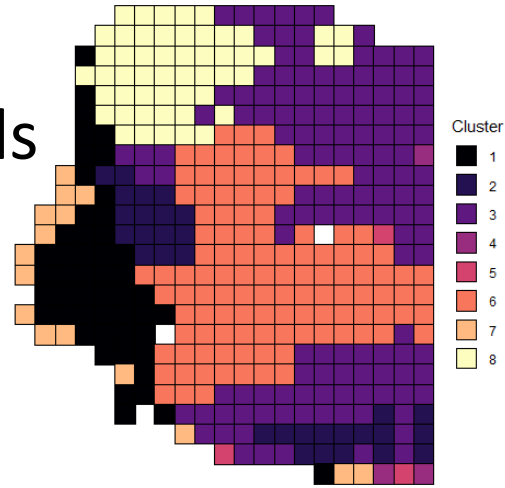
Cancer



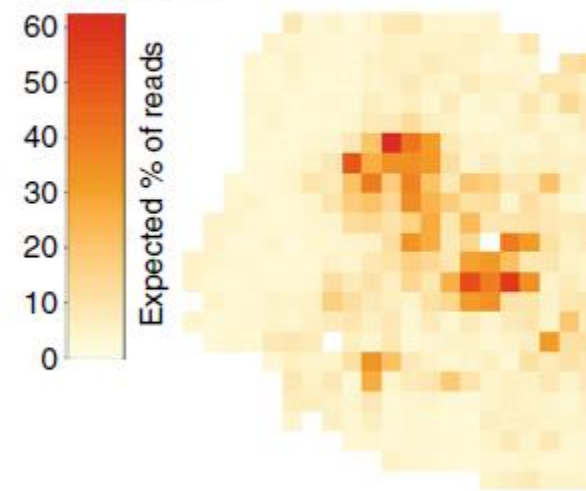
Spatial Clustering

Cluster

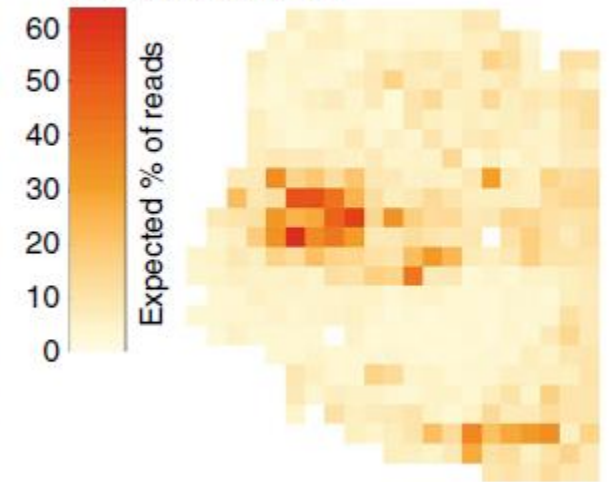
-  1 Normal glands
-  2 Immune
-  3 Stroma
-  4 N/A
-  5 N/A
-  6 PIN glands
-  7 N/A
-  8 Cancer



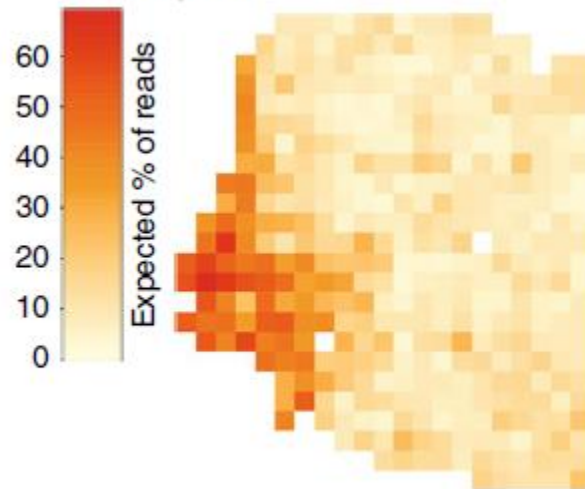
PIN glands



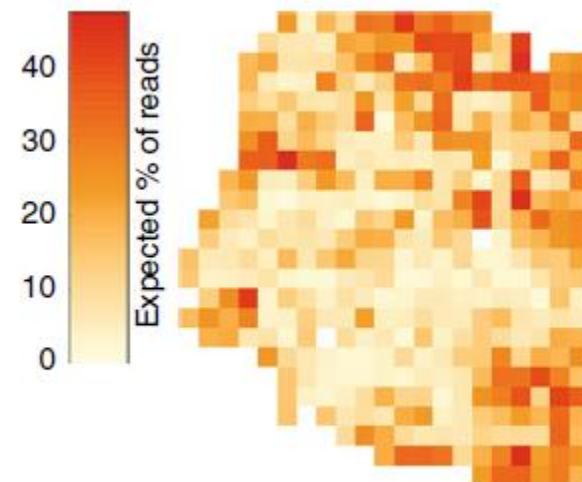
Immune profile - UBC, NR4A1, IER2, JUN, FOS enriched



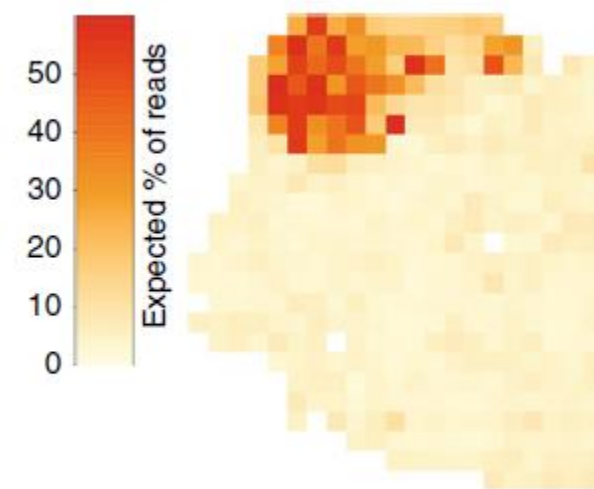
Normal glands



Stroma

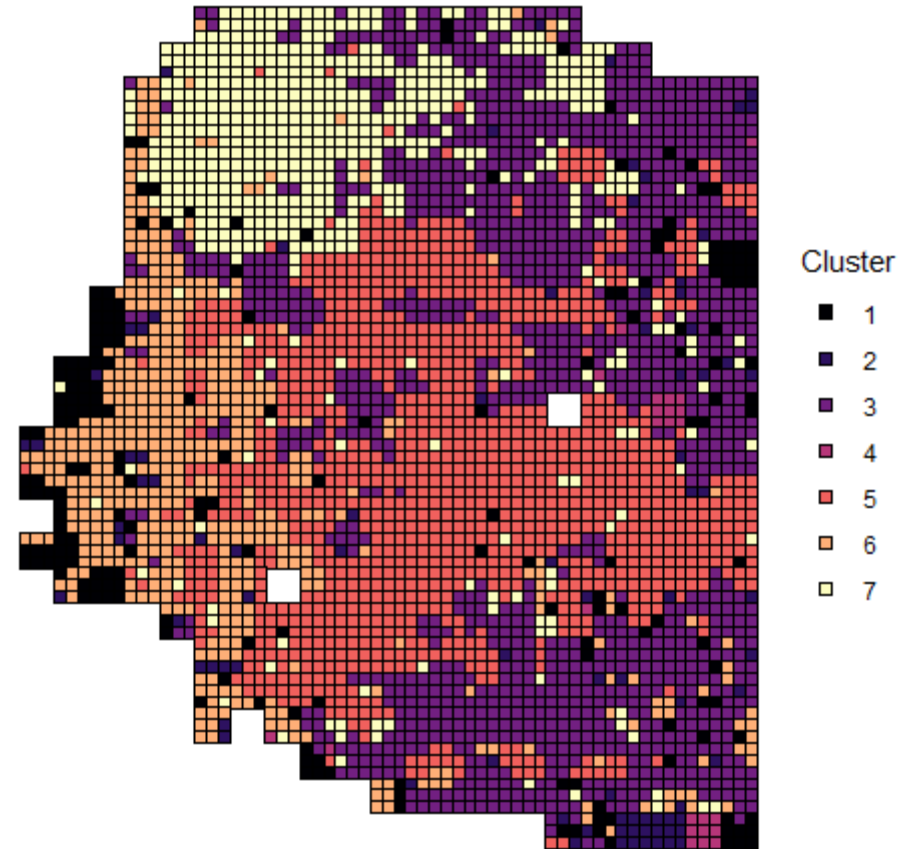


Cancer



Deconvolution

- Can deconvolution increase resolution?
 - Berglund et al. suggest the center and periphery of the cancer have different gene expression (metabolic alteration in center, stress/inflammation in periphery)



Deconvolution

