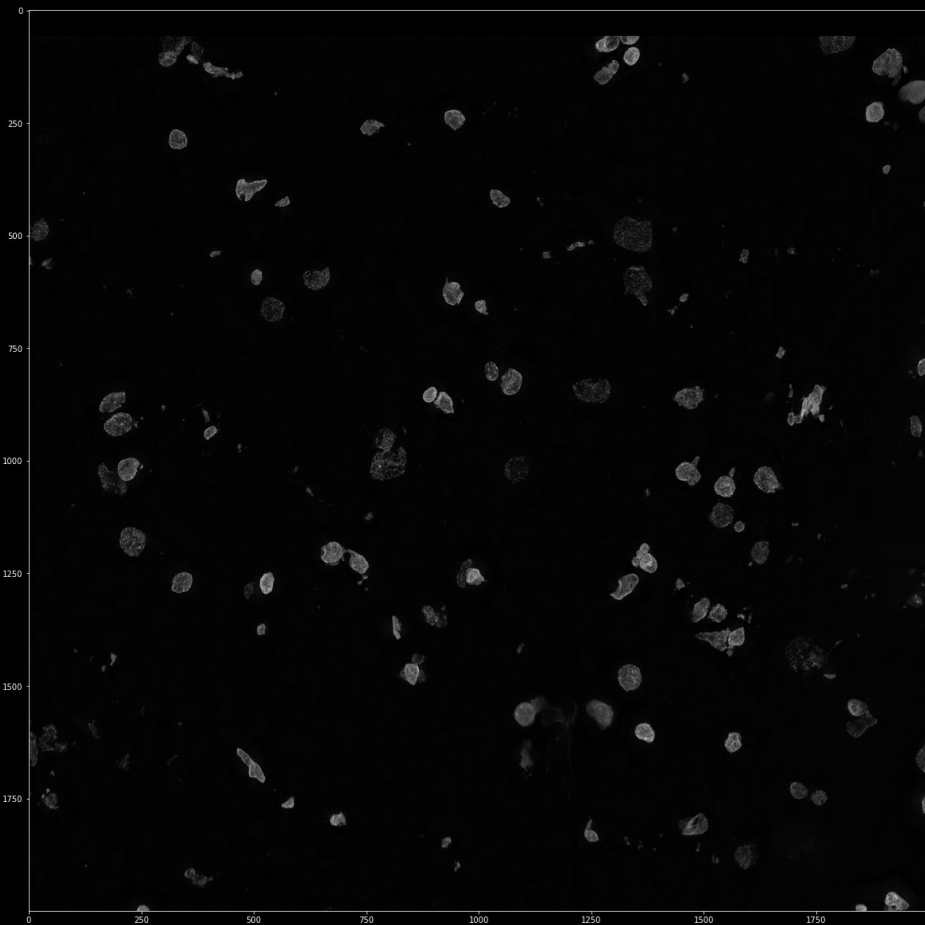
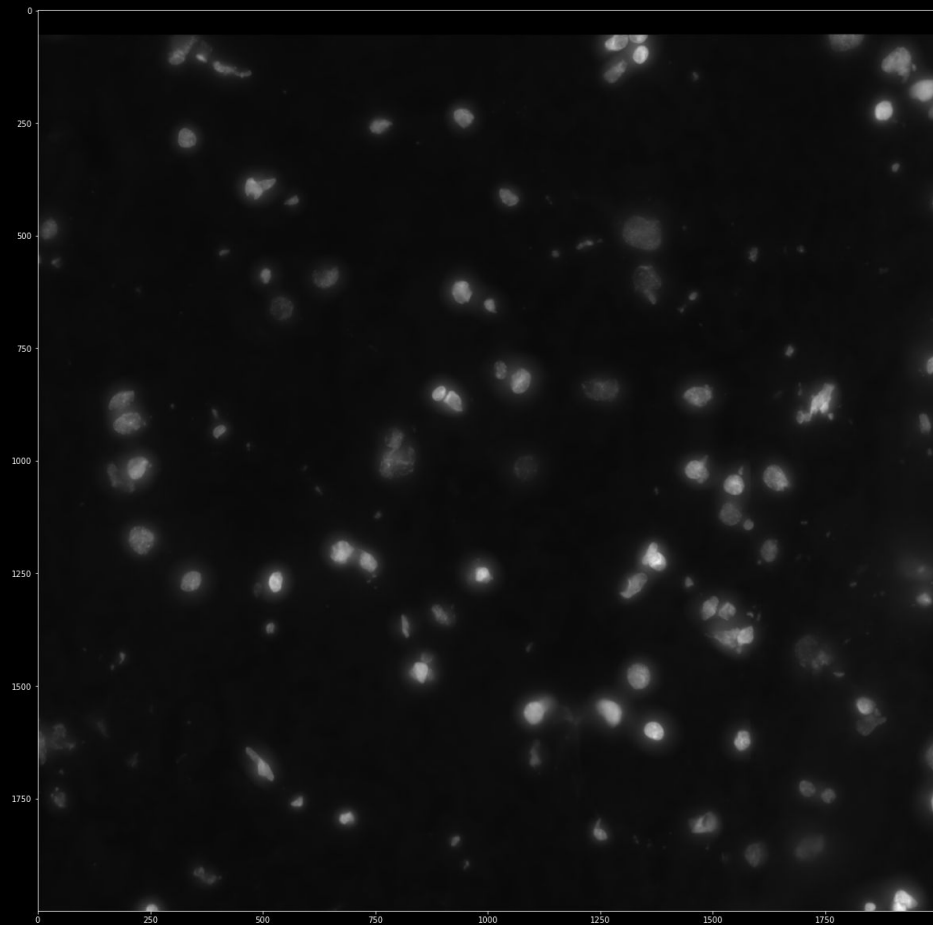


input dapi image

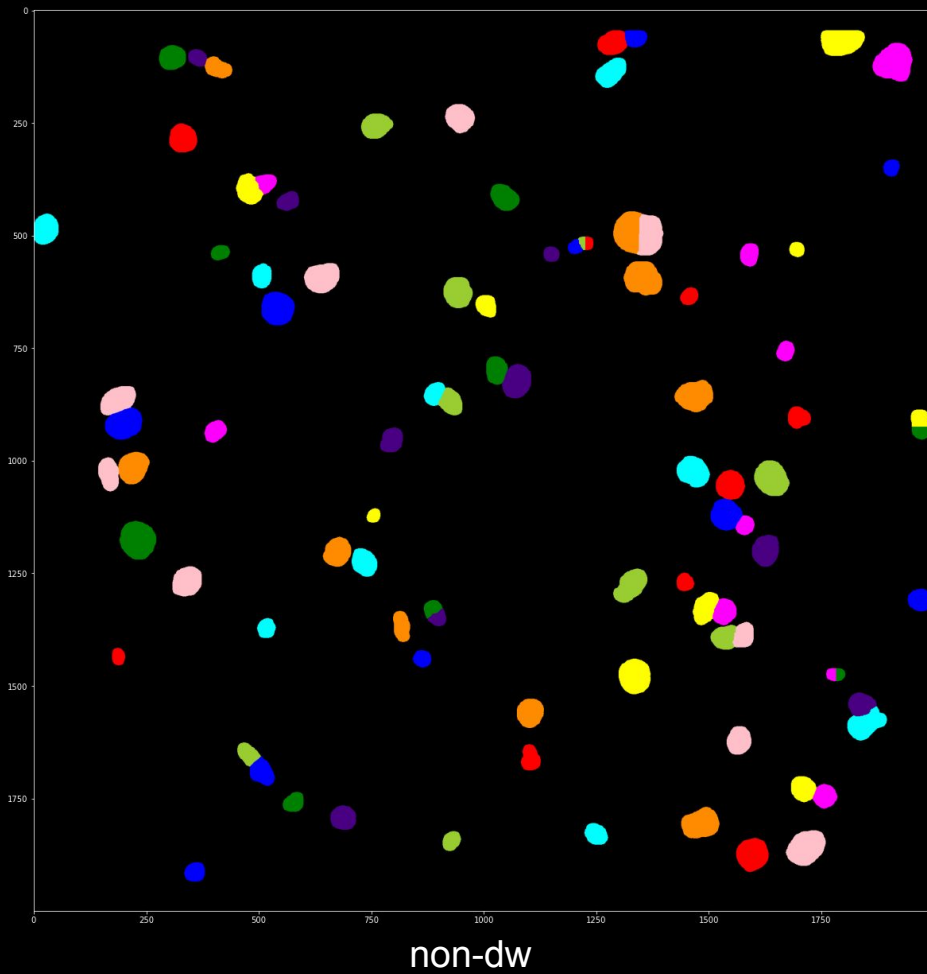
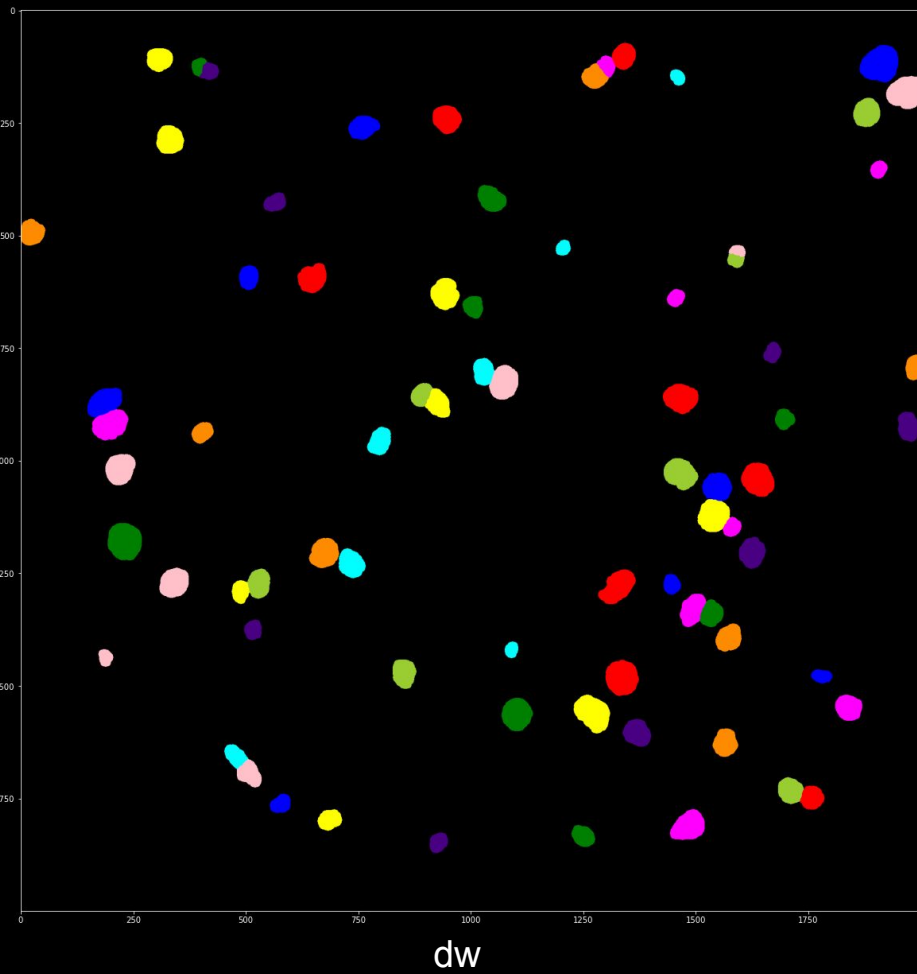


dw

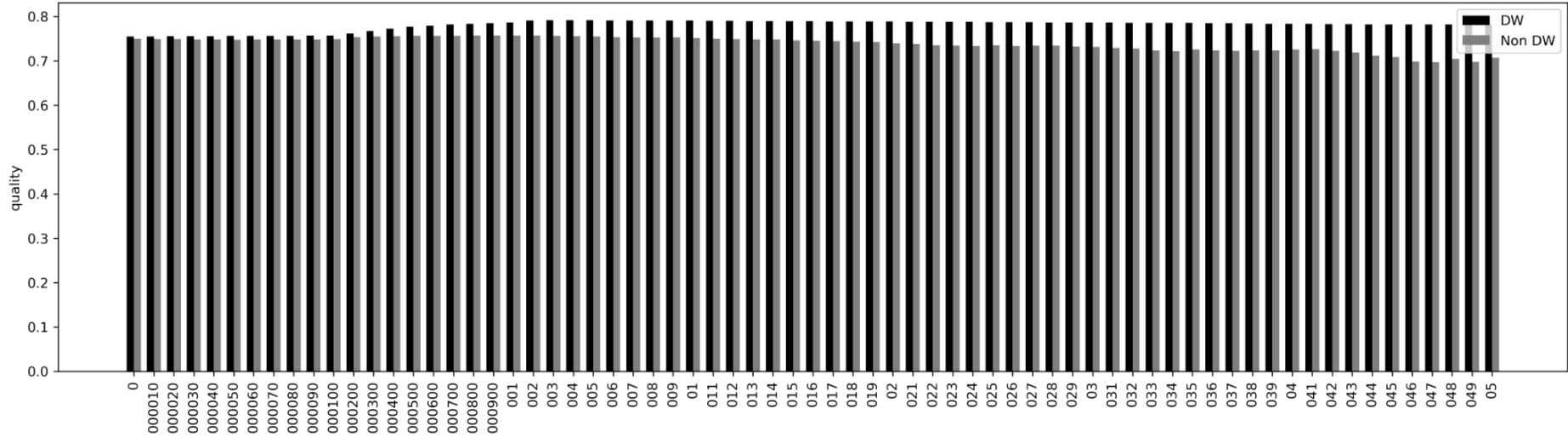


non-dw

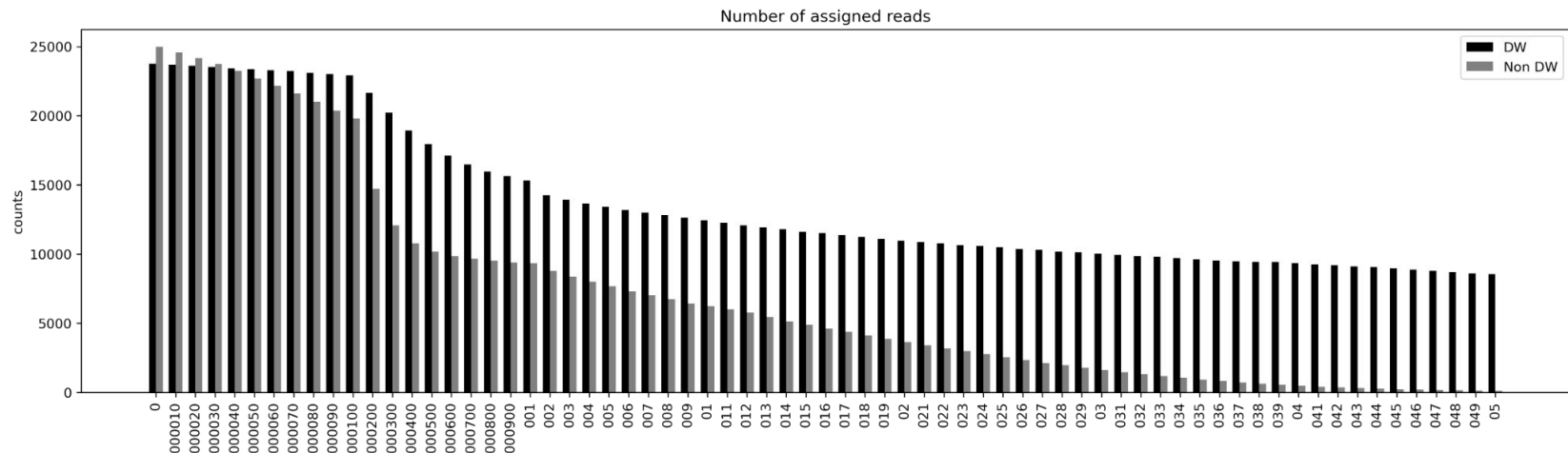
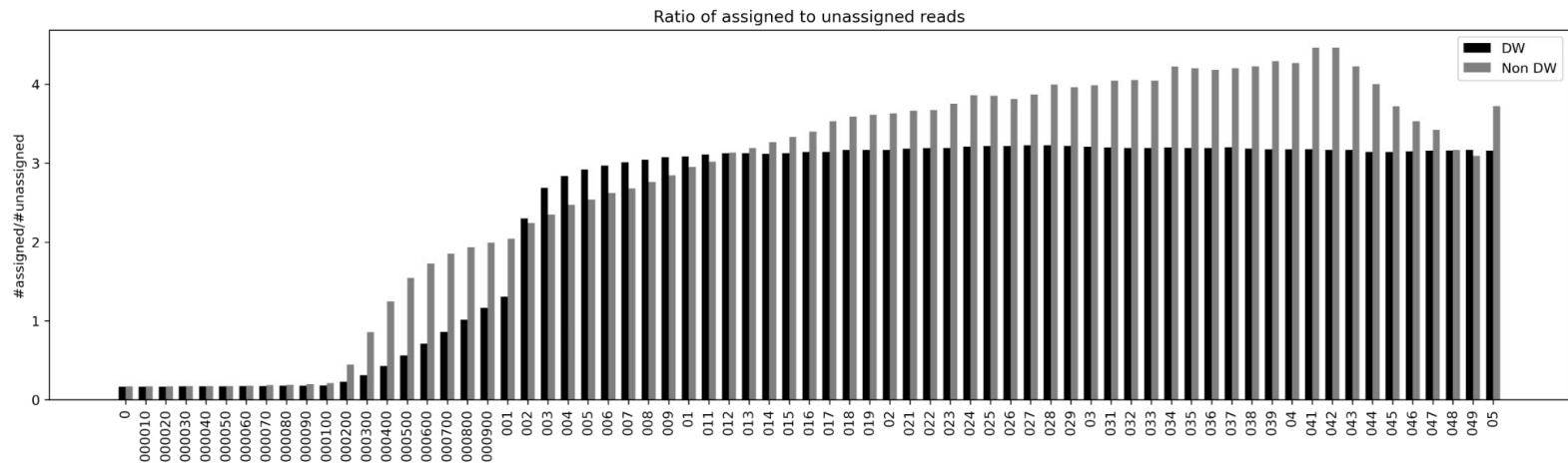
segmentation result



## Quality of spot calling

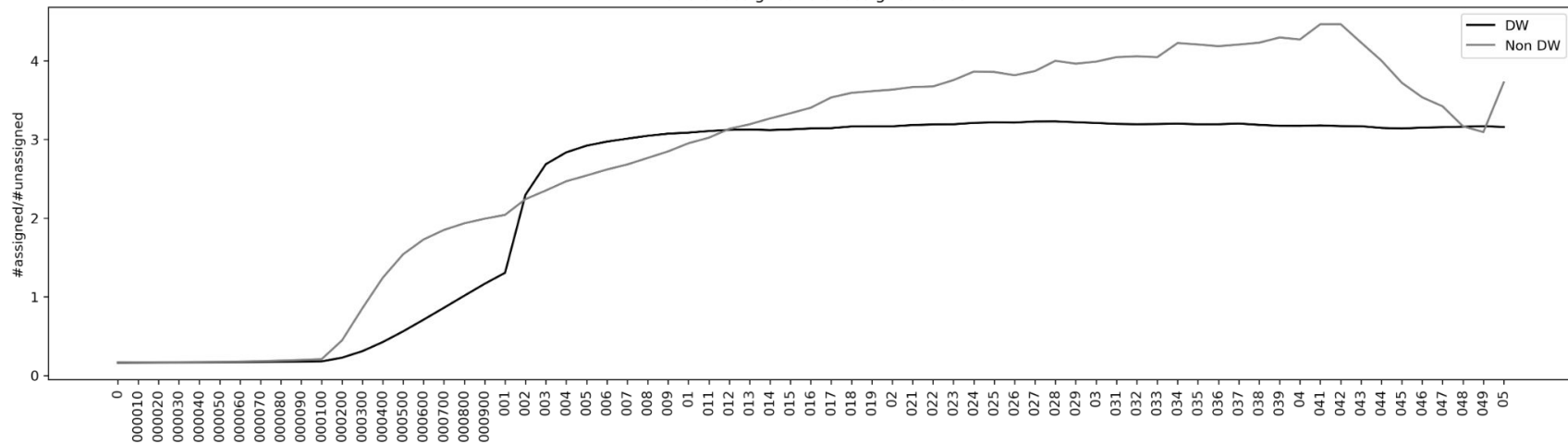


<https://stockholmuniversity.box.com/s/avp326711fzsxhq0sfu90u742j9d746j>

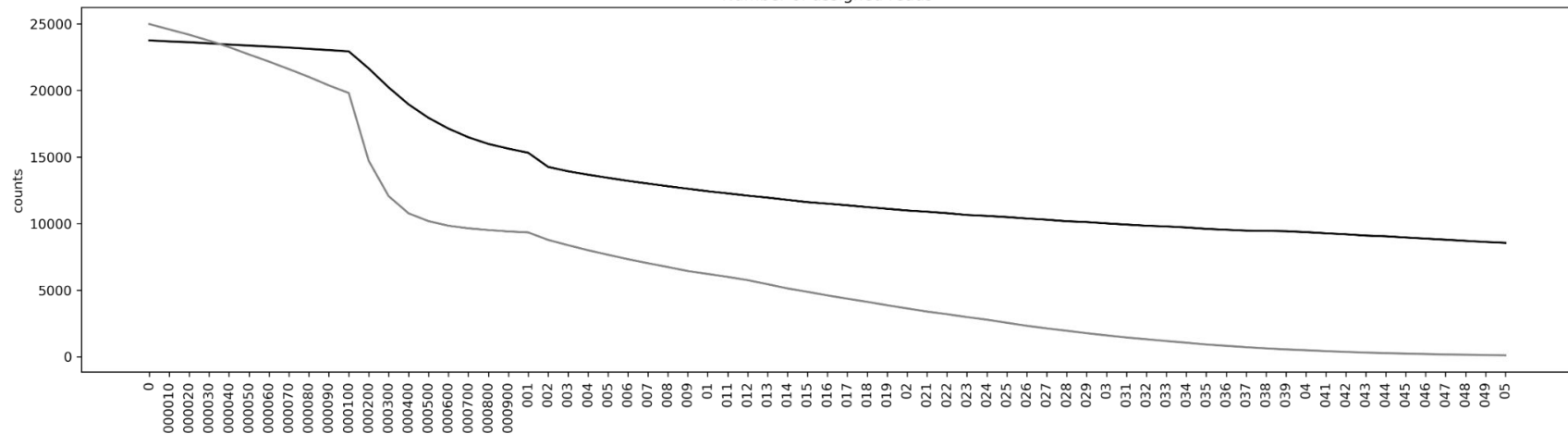


<https://stockholmuniversitv.box.com/s/qy5em2n9e5njqkx7knyk7axv36sla5i>

Ratio of assigned to unassigned reads

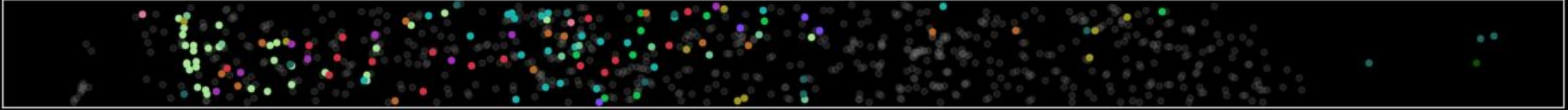


Number of assigned reads

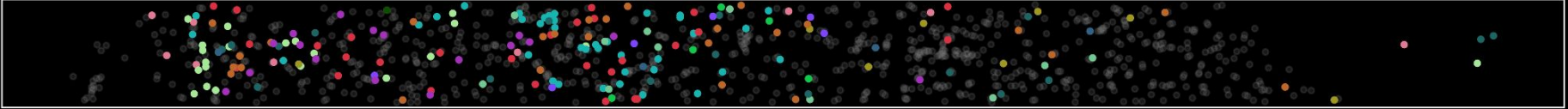


## cell calling results

non-dw

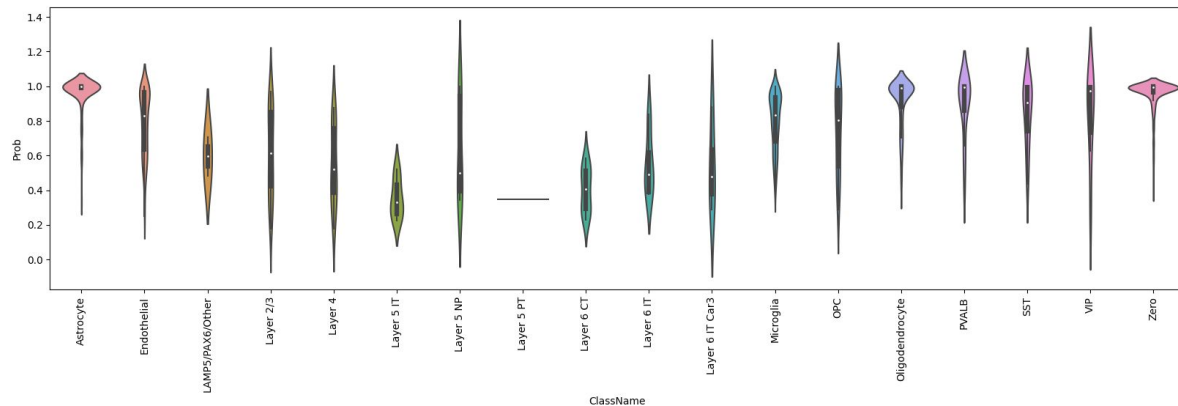


dw



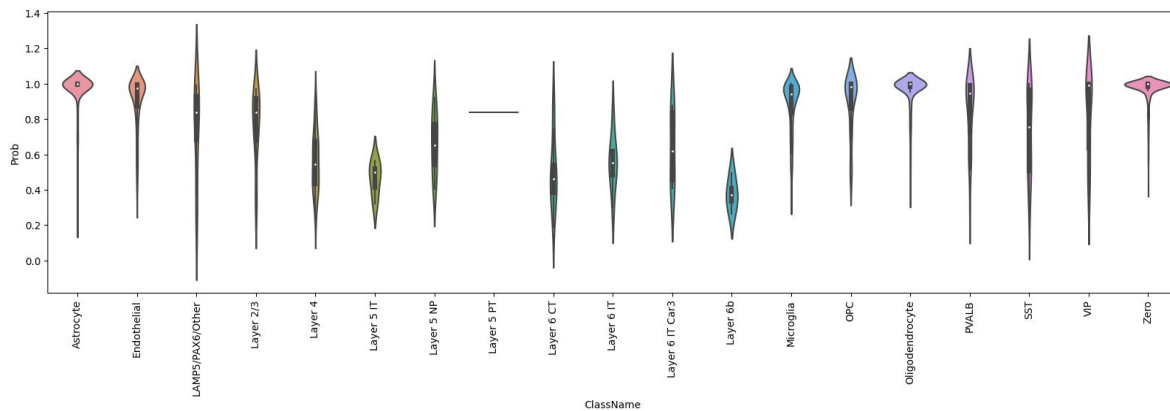
1. nuclei segmentation from non-deconvolved images used
2. plotting the most probable cell type from the calling
3. showing only the neuronal population (that show the most layer specificity)

non-dw

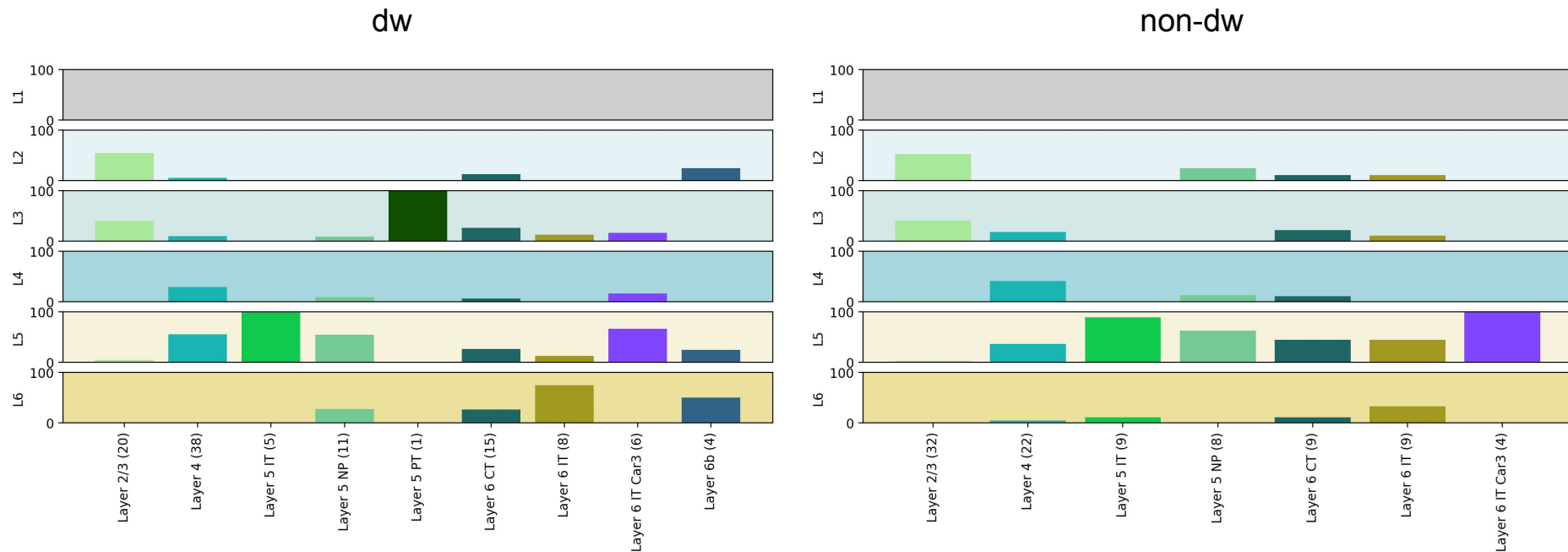


cell calling results: top level probability

dw



# Layer distribution of transcriptomically defined cell types in the human cortex: effect of deconvolution



1. cortical layers were annotated as a part of the original cell typing paper
2. showing the relative across layer distribution of celltypes, e.g. around 50% of cells of the type Layer 2/3 end up in layer 2