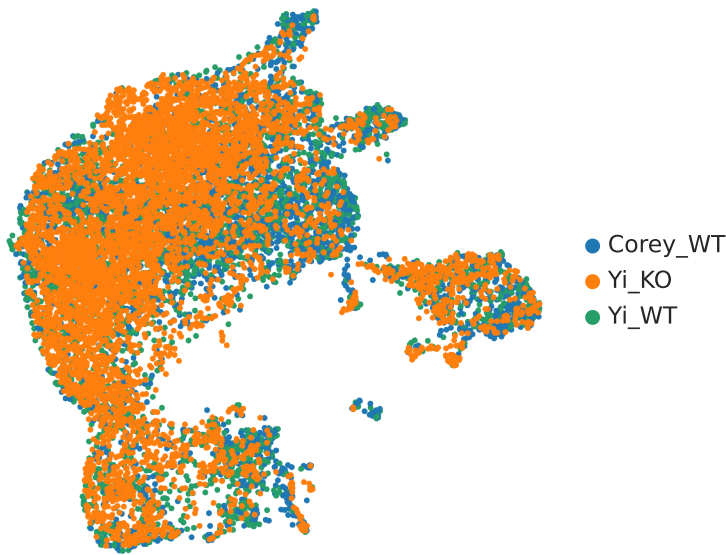
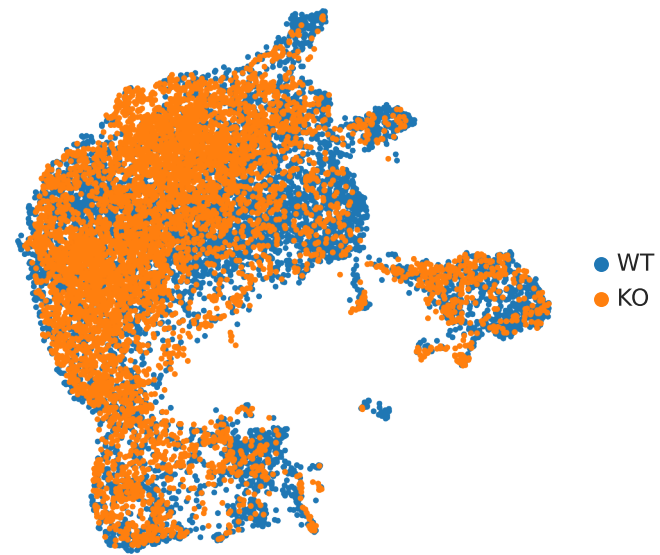


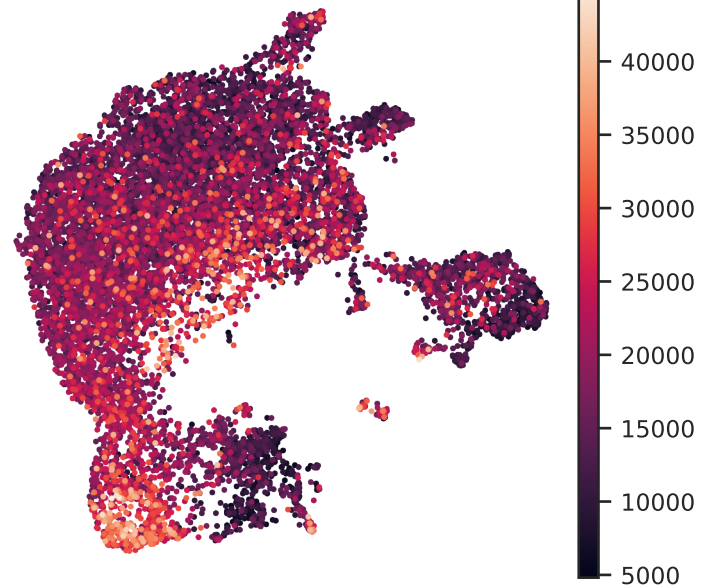
batch



genotype



total_counts



n_genes_by_counts

