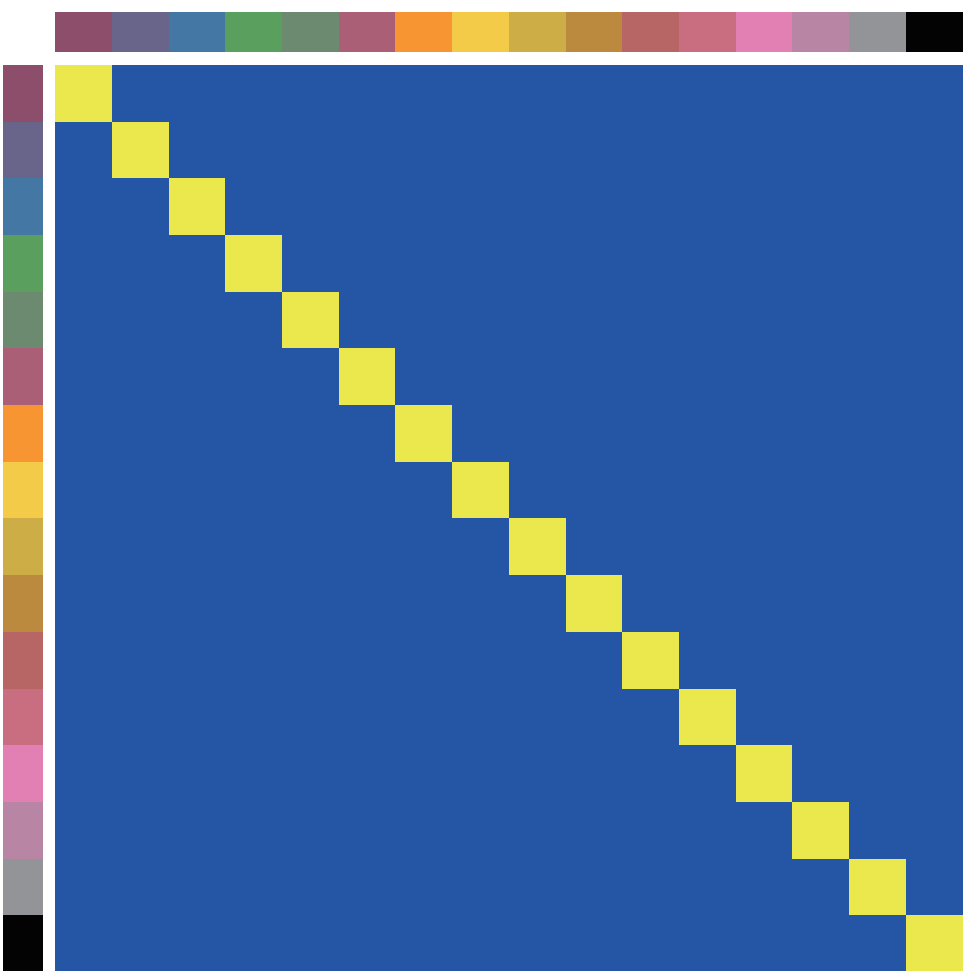
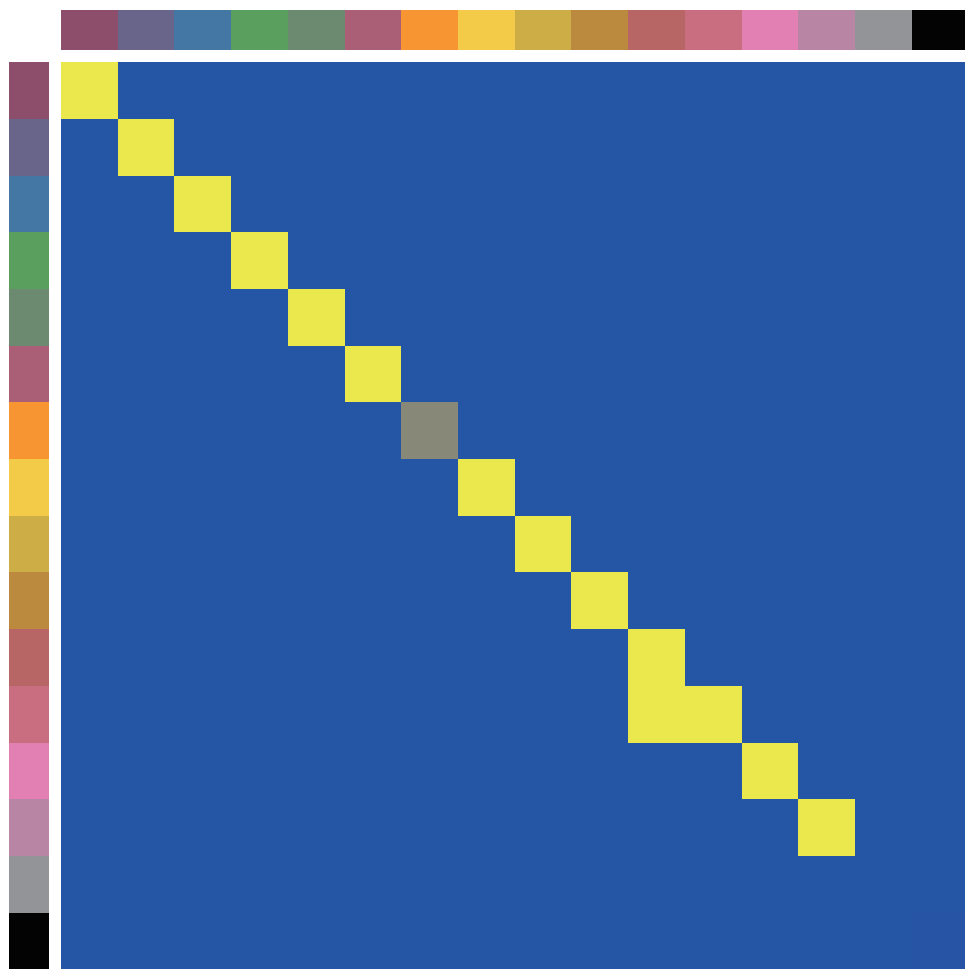


threshold m = 14

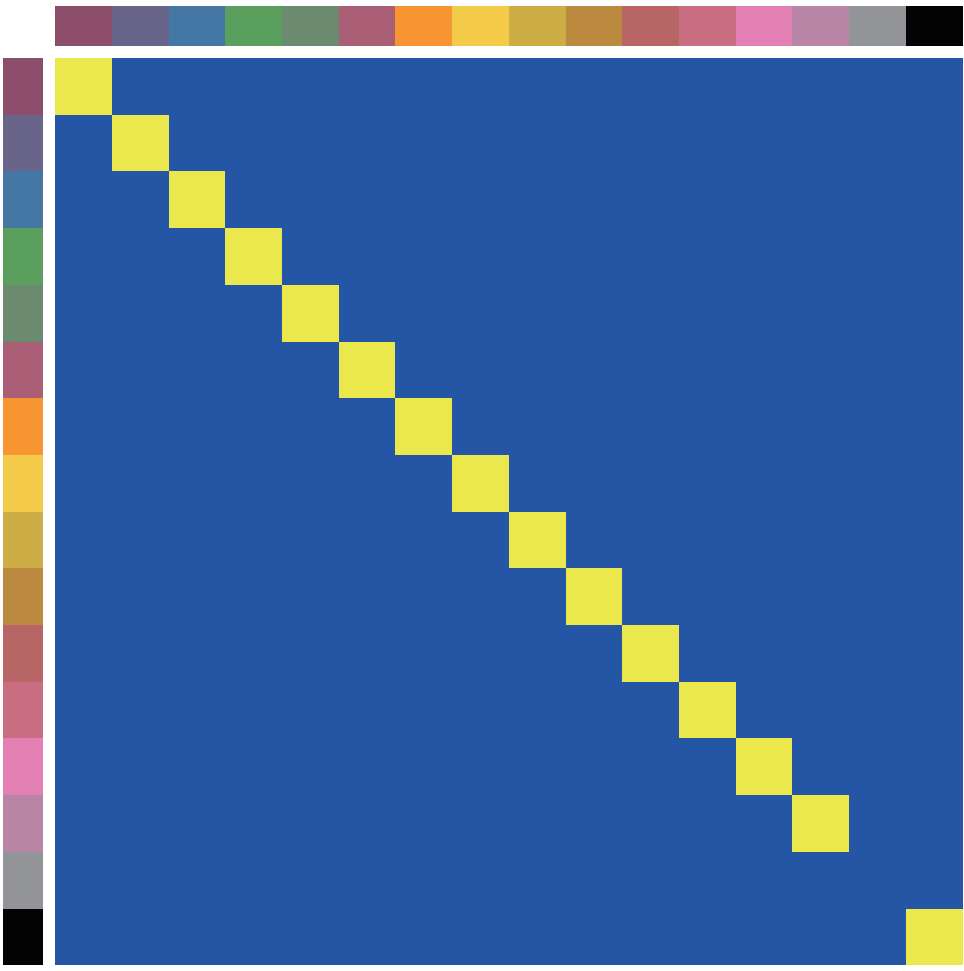
A H3K4me1 on associated enhancers



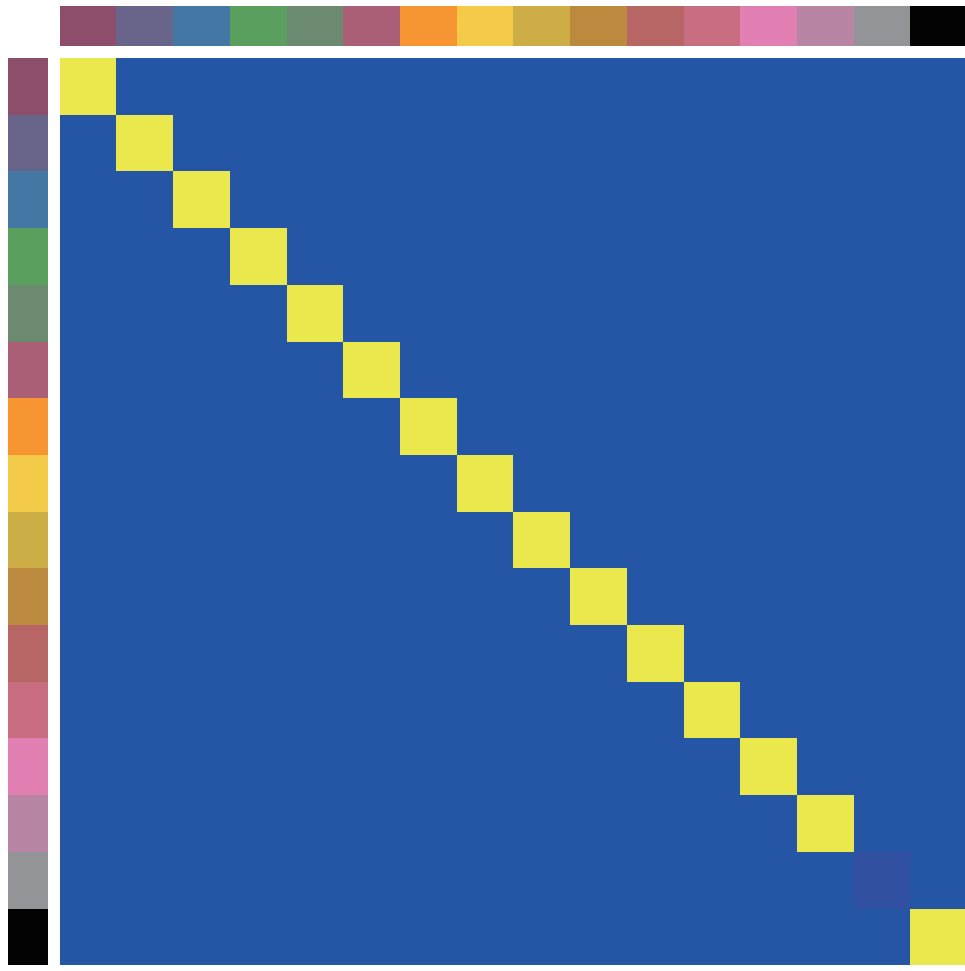
B H3K4me1 on associated promoters



C H3K27ac on associated enhancers

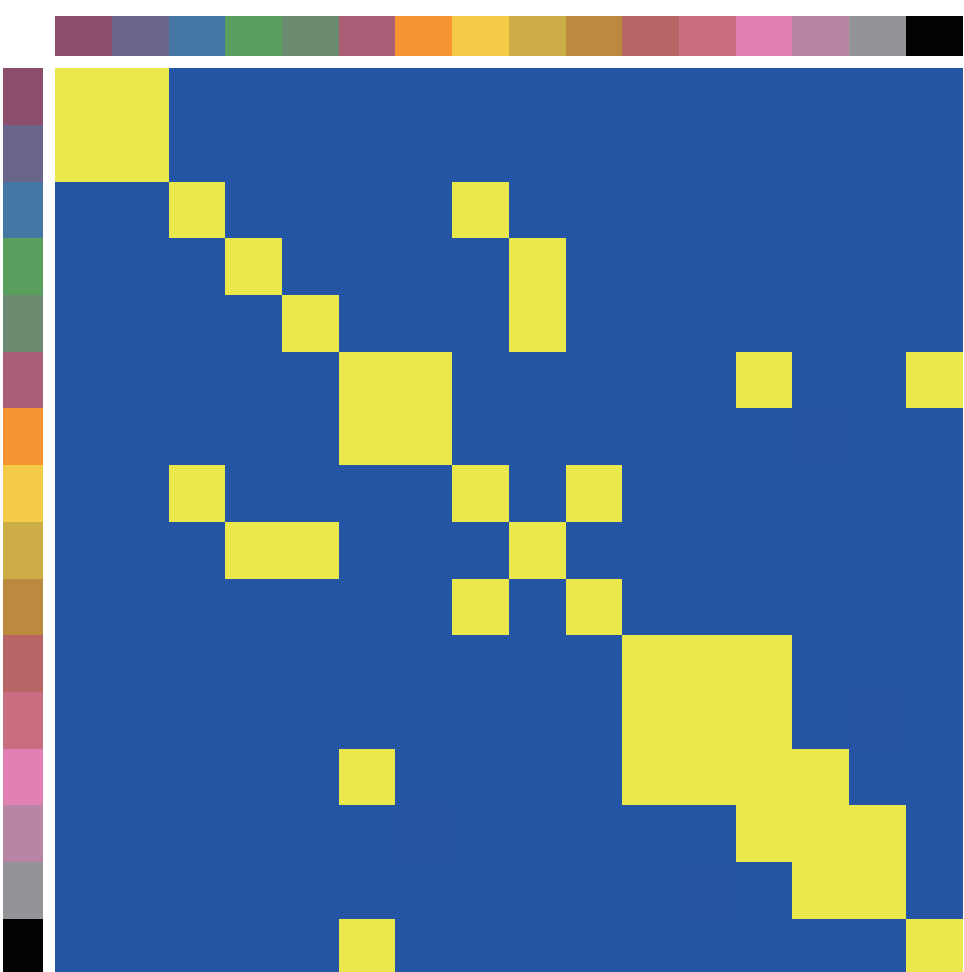


D H3K27ac on associated promoters

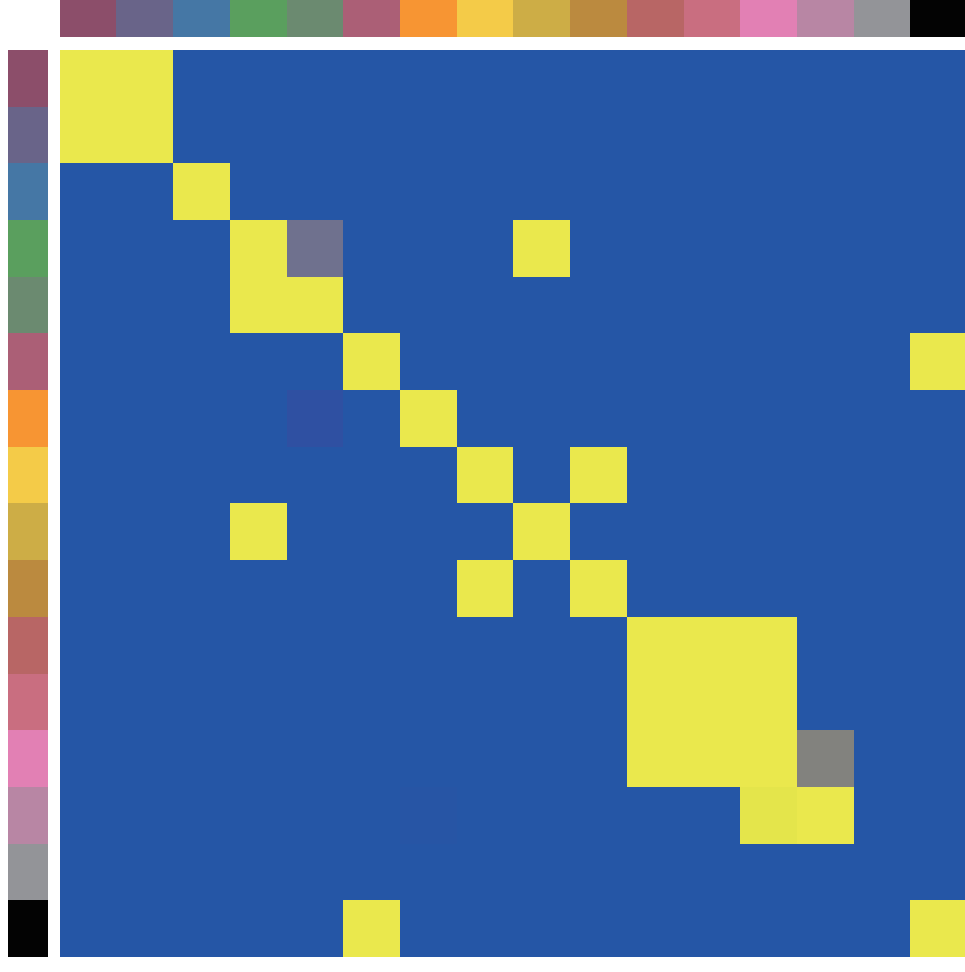


threshold m = 13

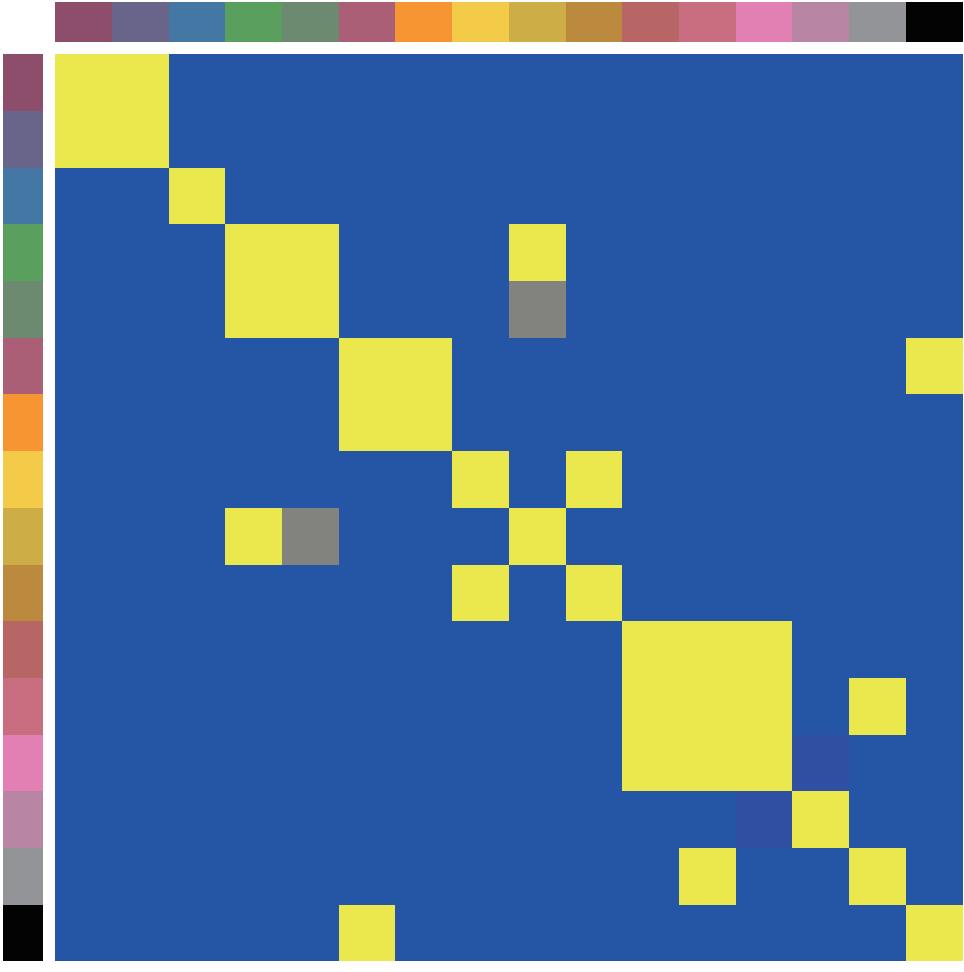
E H3K4me1 on associated enhancers



F H3K4me1 on associated promoters



G H3K27ac on associated enhancers



H H3K27ac on associated promoters

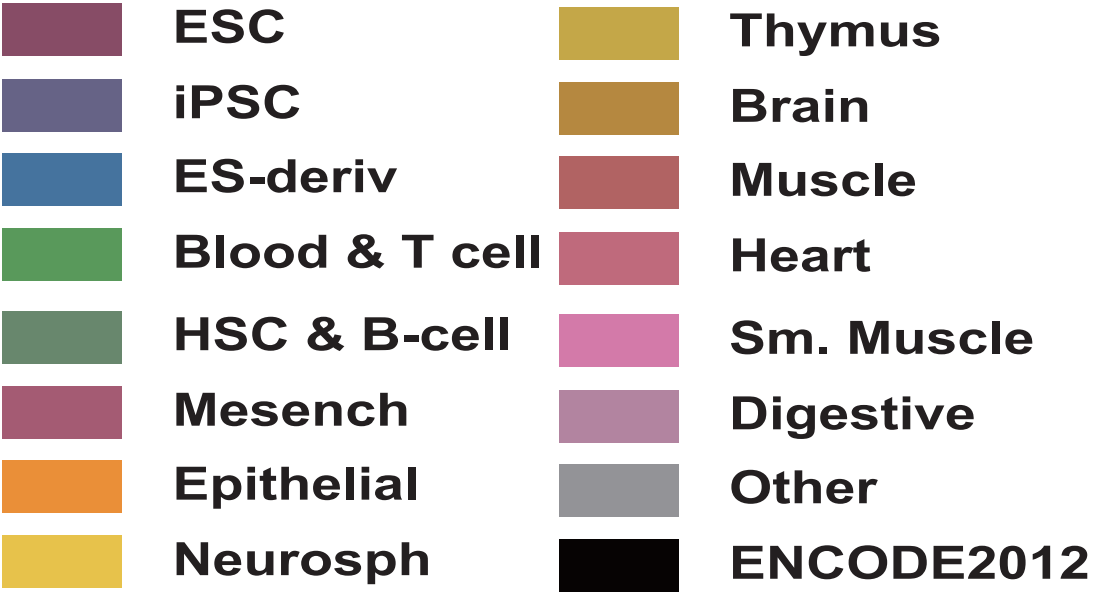
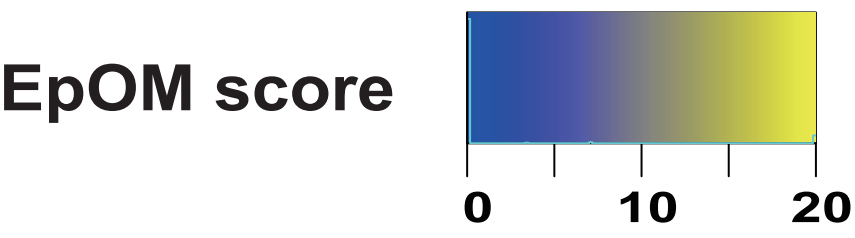
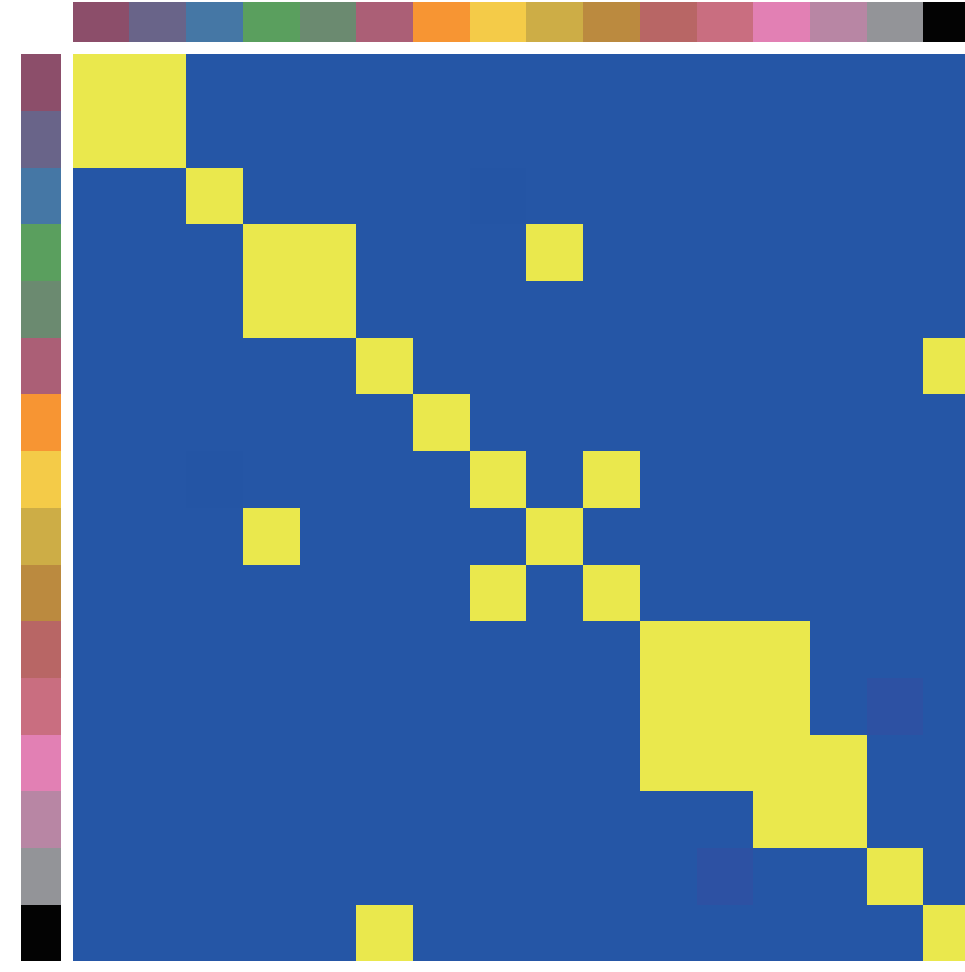


Figure S2. Correspondence maps of EpOM scores saturated at 20. Each heatmap plots the EpOM scores calculated from associated regions (enhancers or promoters) identified through one histone modification mark (H3K4me1 or H3K27ac) in step 2. A-D: threshold m=14 in step 3. E-H: threshold m=13 in step 3.