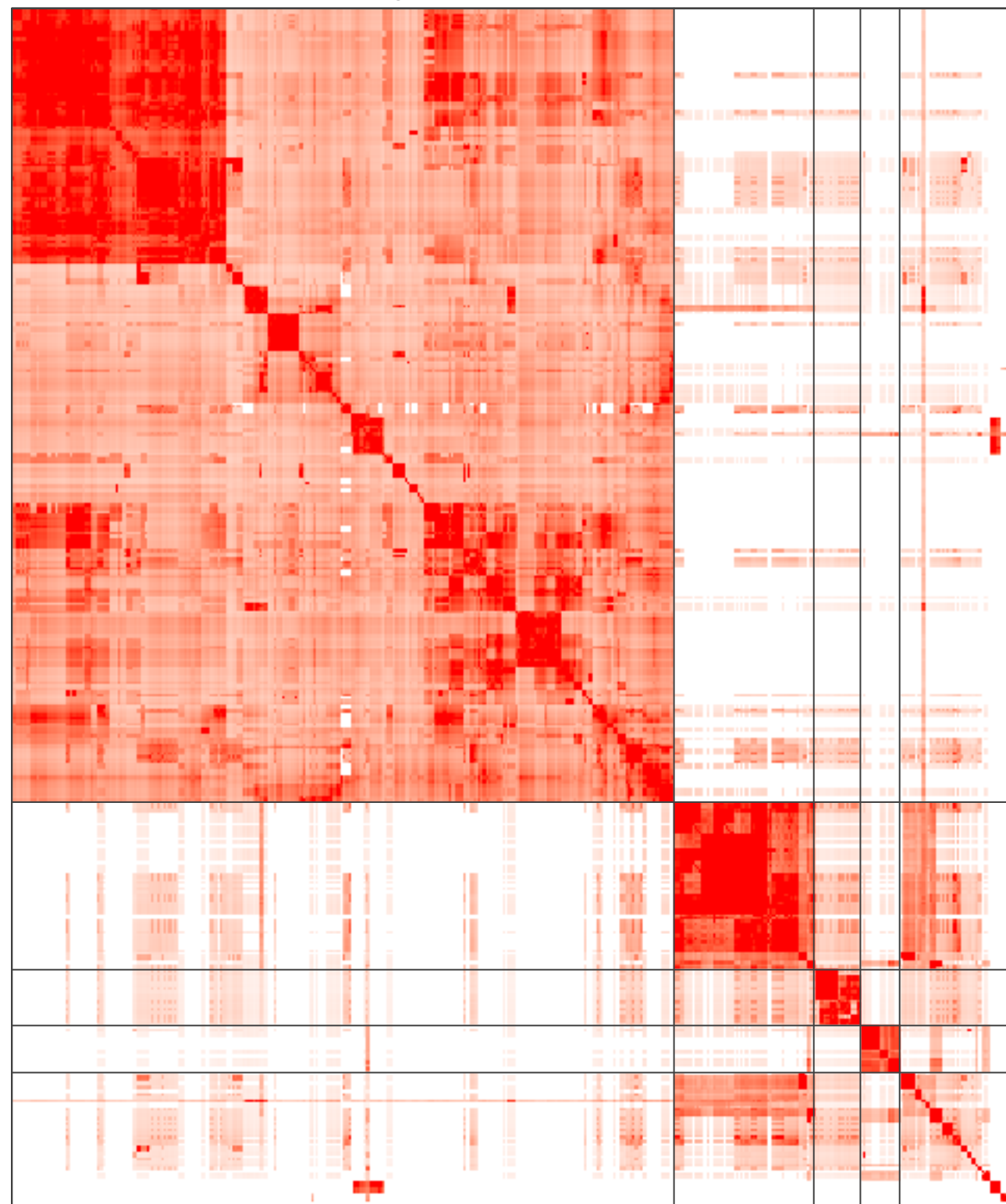


ot_detected-with_ChIP_rna_bg_all_proximal.inactive.accUp.H3K27me3_GO_BP



differentiation cell formation involved tubule process metanephric
development morphogenesis regulation

compound positive cellular macromolecule transcription rna
process regulation biosynthetic metabolic

cohesion division segregation chromosome maintenance
regulation positive sister chromatid mitotic

glucose peroxide hydrogen
response cellular acid stimulus retinoic monosaccharide hexose

Similarity
0.8
0.6
0.4
0.2
0