Duplication percentage (R1 no trim) H3K27ac H3K27me3 60 **-**40 histone_mark H3K27ac H3K27me3 H3K36me3 20 **-**H3K9me3 H3K36me3 H3K9me3 ind 1 2 3 60 -40 -20 interaction(other_time, trt) 24t.5FU ⁻ 144r.VEH ⁻ 144r.VEH ⁻ 144r.5FU ⁻ 24t.DOX -24r.DOX -24r.5FU 24t.VEH 144r.5FU 24t.DOX 24r.VEH 24r.5FU

percent duplication

24t.5FU