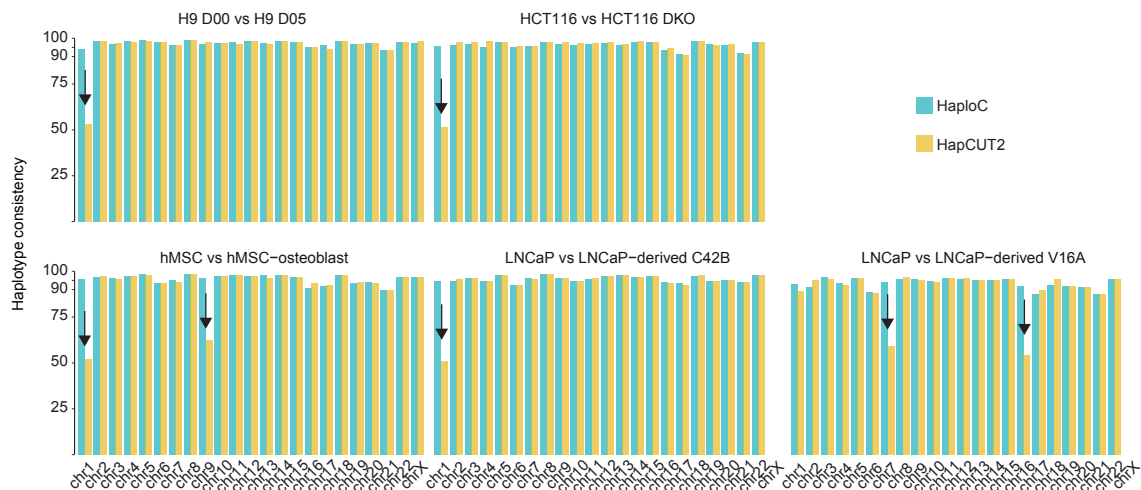
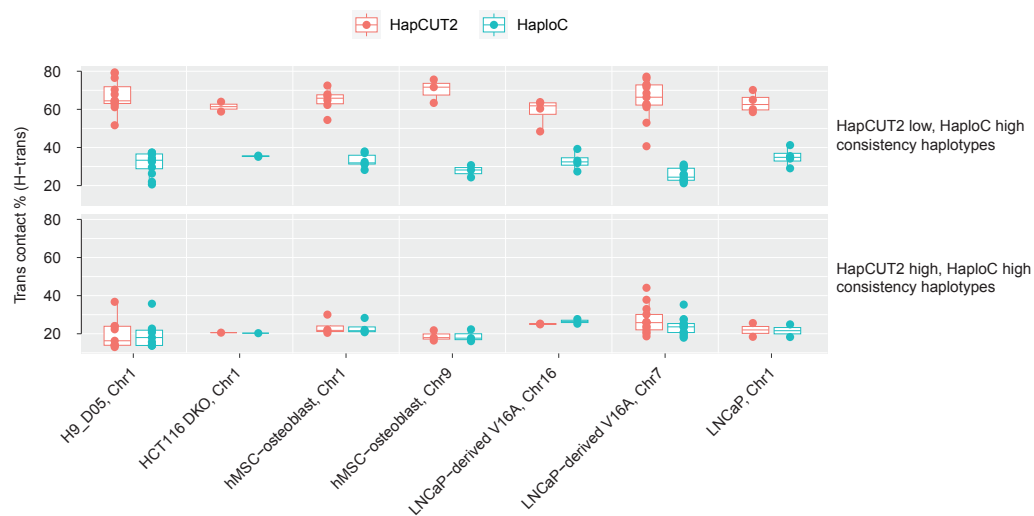


Supplementary Figure 1

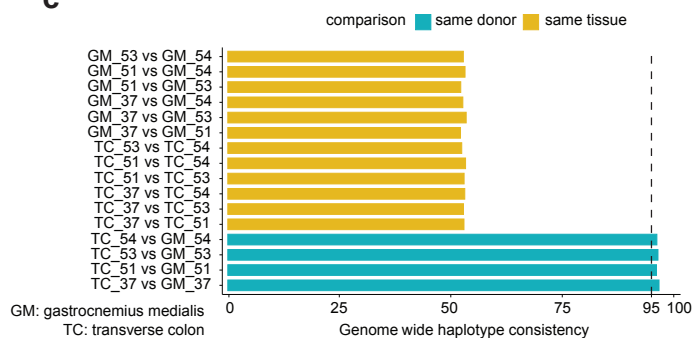
a



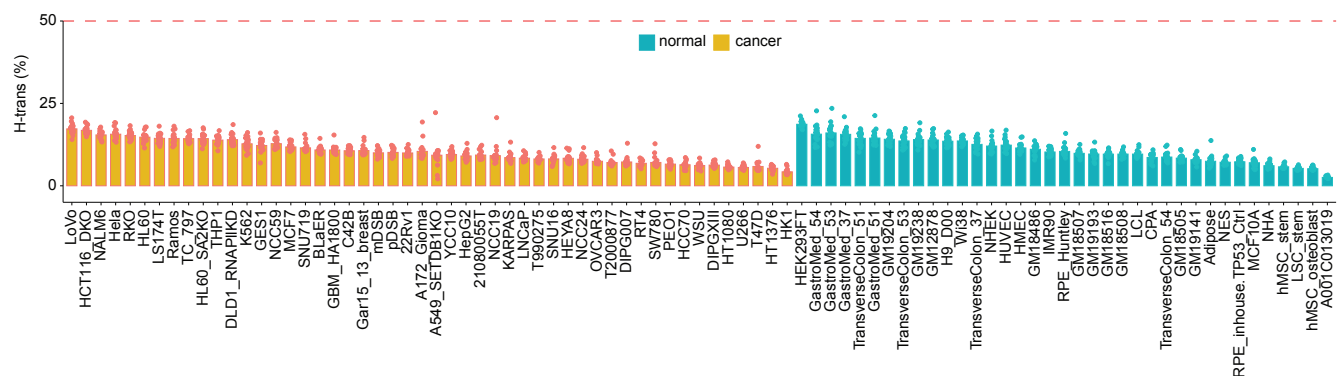
b



c

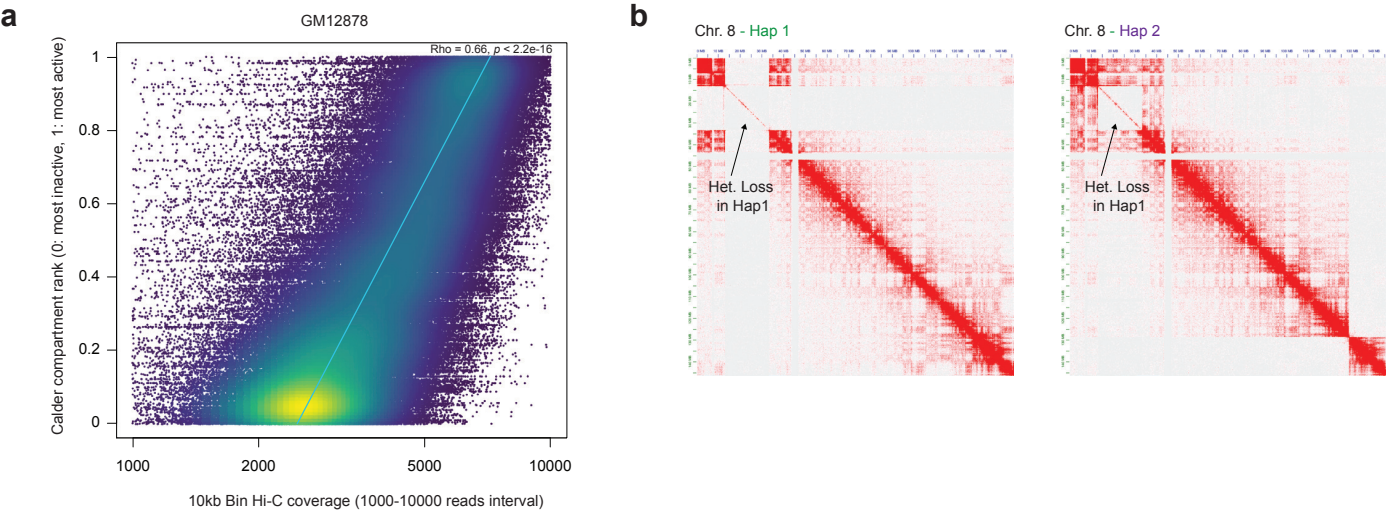


d



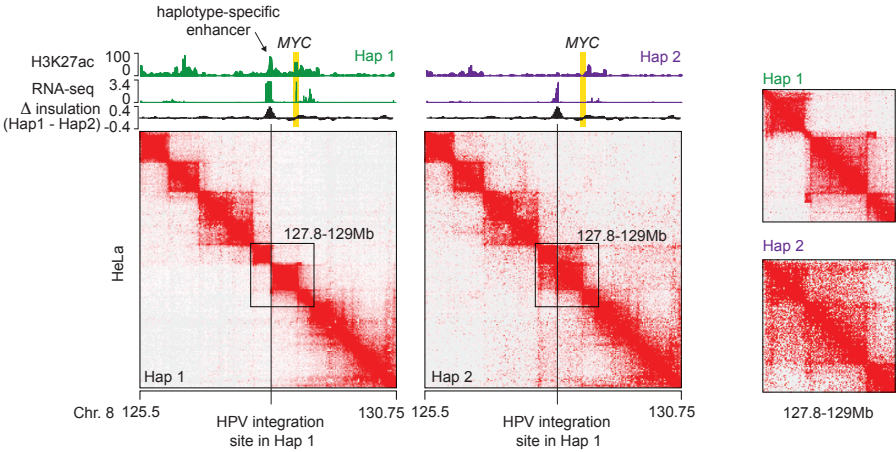
Supplementary Fig. 1. a) Bars indicate the consistency between haplotypes inferred from Hi-C datasets generated under different conditions or by different laboratories for the same cell line (data shown for six comparisons) by HaploC (blue) and HapCUT2 (yellow). Arrows indicate the largest differences between HaploC and HapCUT2. Chromosome X for LNCaP and HCT-116 was left blank, as both originate from male donors. **b)** Upper panel: H-trans contact rates between regions with low phasing consistency by HapCUT2 but high consistency by HaploC. Lower panel: H-trans rates between regions consistently phased by both methods. Each point represents a pair of regions. **c)** Genome-wide consistency between haplotypes derived from Hi-C dataset from different tissues (gastrocnemius medialis - GM - or transverse colon - TC) of the same donor (blue), or same tissue from different donors (yellow – the number in the label indicate the donor). **d)** H-trans rate for phased chromosomes of 87 dataset. Each point represents a single phased chromosome.

Supplementary Figure 2



Supplementary Fig. 2. a) Calder compartment rank plotted against Hi-C coverage for 10kn bins in the GM12878 cell line. Color brightness (from blue to yellow) is proportional to point density. **b)** Example of heterozygous loss on chromosome 8 of U266 cell line. A region exhibiting loss of heterozygosity (LoH) appears as an “empty square” corresponding to lack of phased contacts. However, the region exhibits interactions with other phased regions in Hap1 but not with Hap2, allowing to infer that Hap2 is lost in this region.

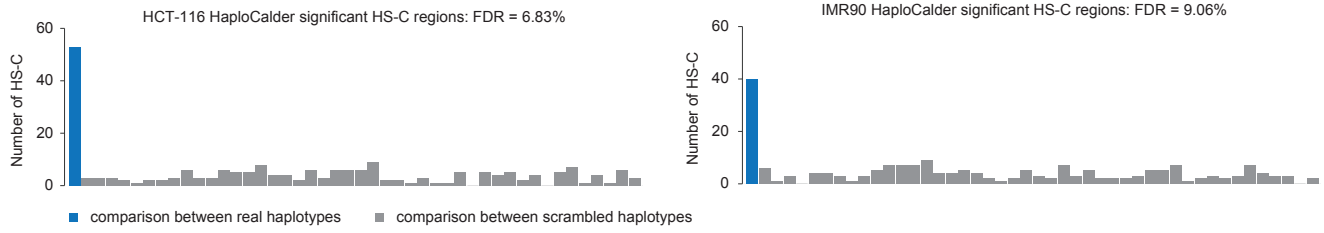
Supplementary Figure 3



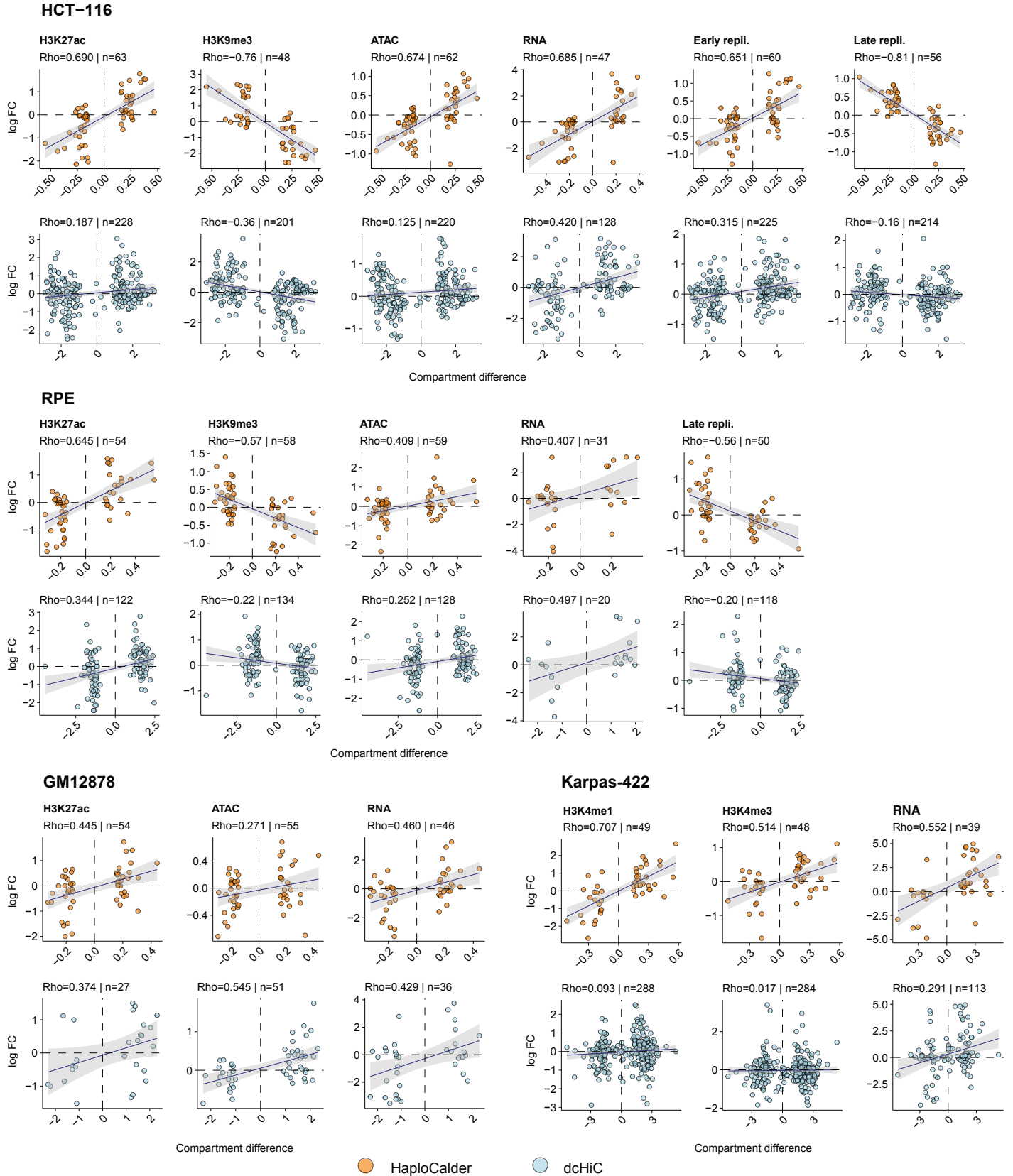
Supplementary Fig. 3. Left: Annotated Hi-C maps of the two haplotypes of the HeLa cell line, chr. 8q, in the indicated regions. Annotations track on top of the Hi-C maps include (from the top): H3K27ac track, RNA-sequencing read coverage, delta contact insulation. The HPV integration site is indicated in the Hi-C maps, while the MYC genomic locus is highlighted in yellow in the annotation tracks. Right: Zoom-in Hi-C maps of the genomic regions surrounding the HPV integration site corresponding to the boxed regions on the Hi-C maps on the left.

Supplementary Figure 4

a



b



Supplementary Fig. 4. a) FDR estimation of HaploCalder calls on HCT116 and IMR90 samples. Each random pair of haplotypes ($n=45$) was segmented using the same threshold ($T=.15$), and the number of positive events is reported. The FDR was estimated as the fraction of the median of positive events across random haplotypes and the total number of positive events in the correctly phased pair. b. Scatterplot comparisons of distinct molecular signals in regions exhibiting significantly different compartments as detected by HaploCalder (orange) or dcHiC (blue). Y-axis (from left to right, when available for the corresponding cell line): log fold change ($\log FC$ – Hap1/Hap2) of histone mark (ChIP-seq), chromatin accessibility (ATAC-seq), mRNA expression (RNA-seq), and replication time. X-axis: compartment difference as quantified by the corresponding tools; positive (negative) values indicate Hap 1 is in a more active (inactive) compartment than Hap 2. Each point represents an individual HS-C region. The number of HS-C regions (n), the Pearson correlation coefficient (Rho) between X and Y values, and the regression line with a 95% confidence interval are indicated in each plot.

Comparisons between results obtained at original resolution (1500M contacts) and:	Intermediate resolution (1000M contacts)	Low resolution (500M contacts)
Correlation of differential contact insulation (HaploCI) 50kb bin-size	0.84	0.8
Correlation of differential contact insulation (HaploCI) 25kb bin-size	0.73	0.56
Percentage of concordant HSC (min size = 100 kb, min Δ rank = 0.15)	71%	57%
Percentage of concordant HSC (min size = 100 kb, min Δ rank = 0.25)	77%	71%
Percentage of concordant total copy number status	99.9%	99.9%
Percentage of concordant haplotype-specific copy number status	99.9%	98.7-99.5%

Supplementary Table 1: Comparison of results obtained by HaploCI, HaploCalder, and HaploCNV using HCT116 Hi-C maps at original resolution (1500M contacts), intermediate resolution (1000M contacts), and low resolution (500M contacts)