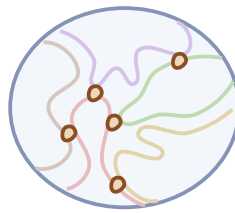


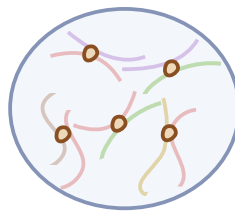
1: Maize nuclei



2: Crosslink chromatin



3: DpnII digestion



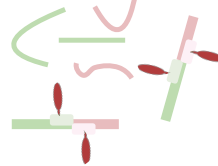
4: Repair and Biotinylate ends



5: Ligation



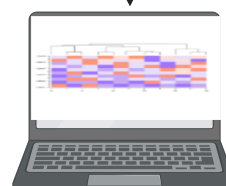
6: Shear DNA and pull down biotinylated DNA



7: Paired end sequencing

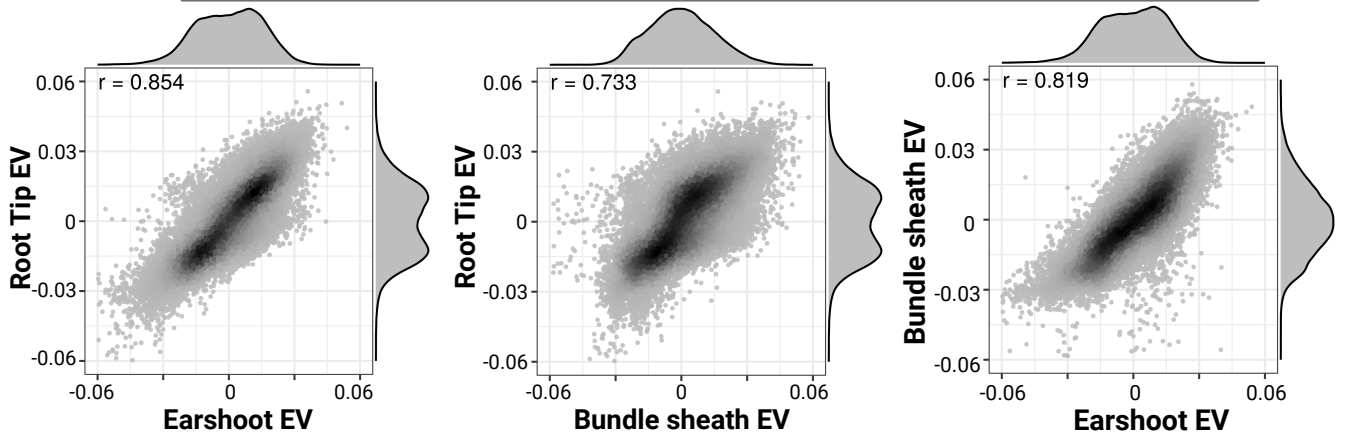


8: Bioinformatics
(HiC-pro,
JuicerTool, FanC,
R libraries)

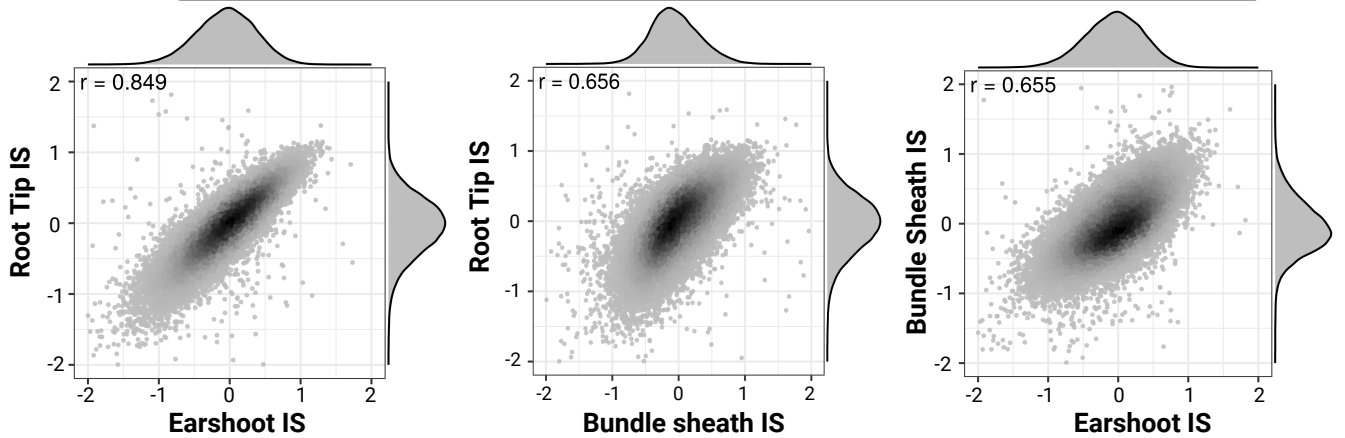


a

Different tissues EV correlation genomewide

**b**

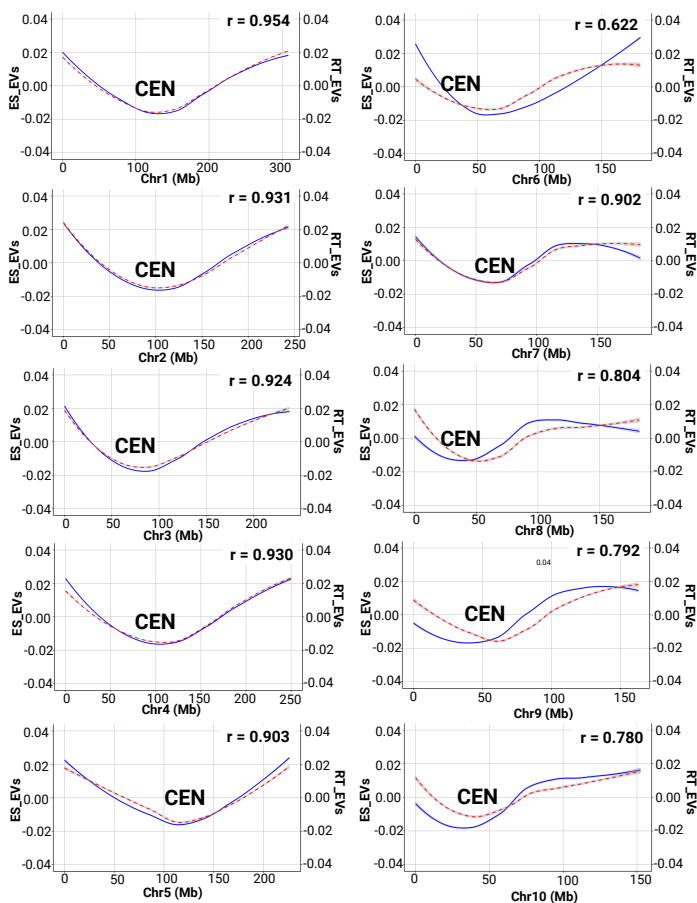
Different tissues IS correlation genomewide



Correlation between HiC eigenvalues for pairs of samples across each chromosome

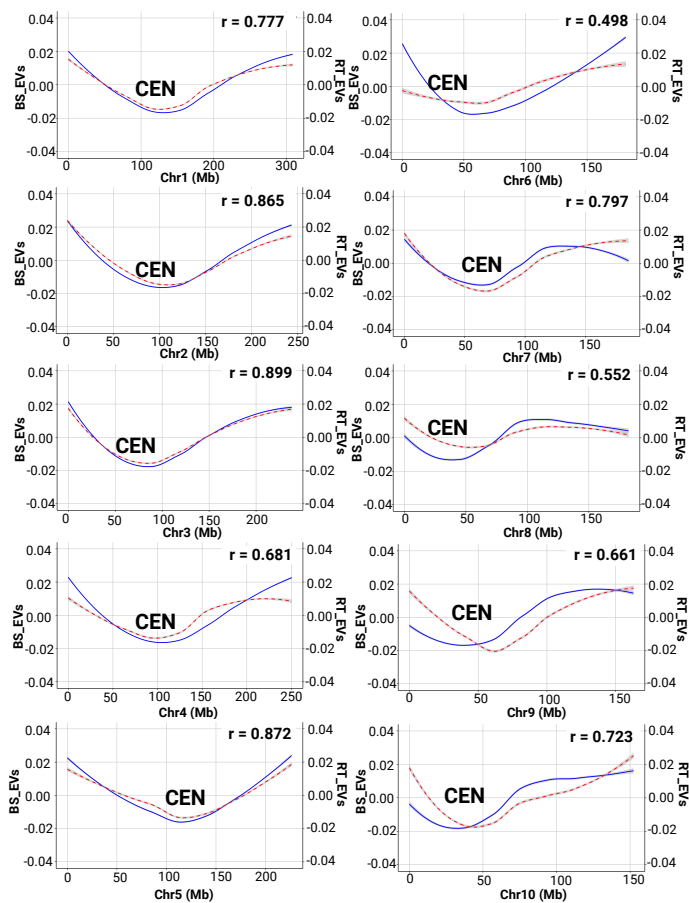
a

Root tip (blue) and Ear shoot (red)

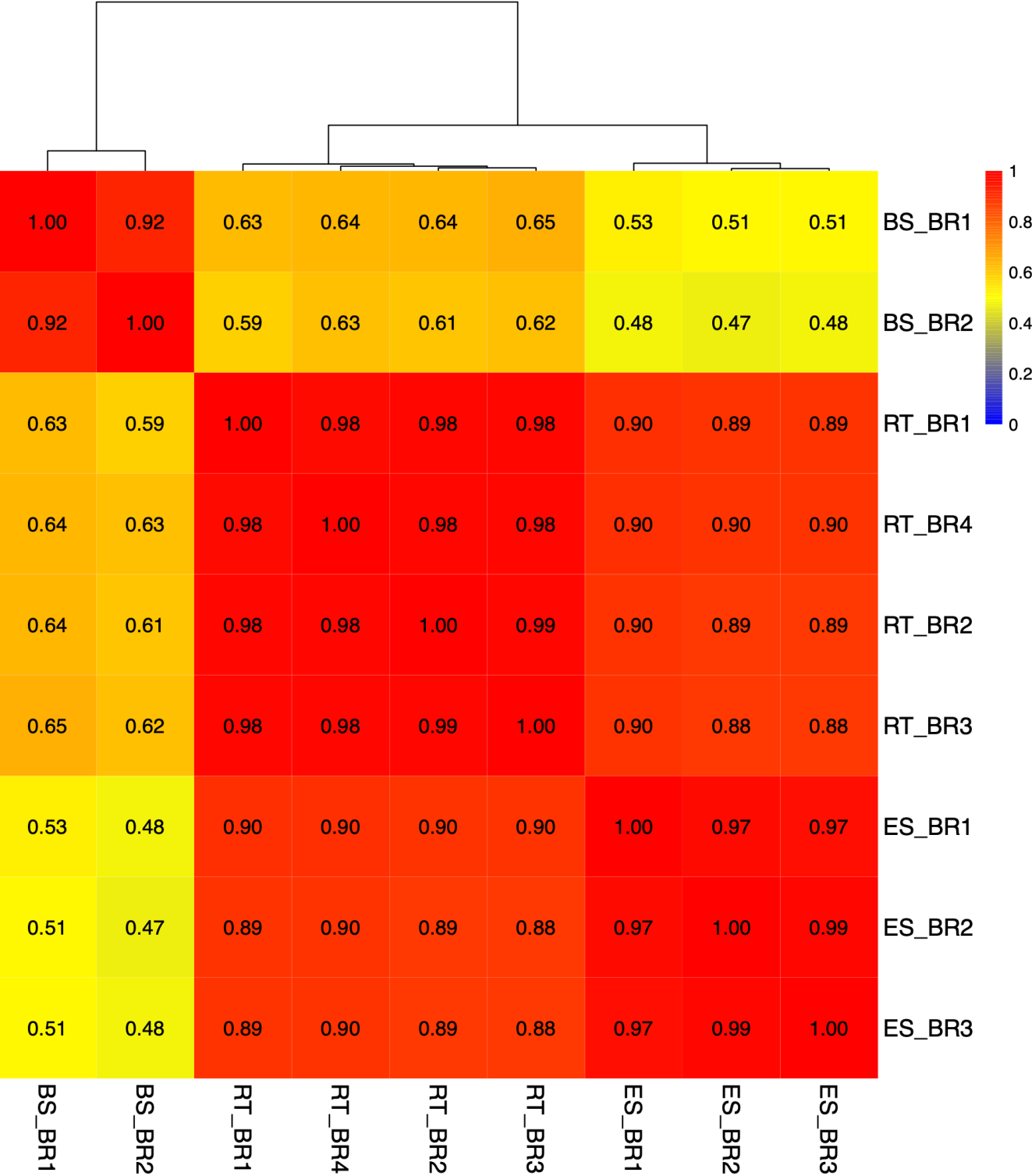


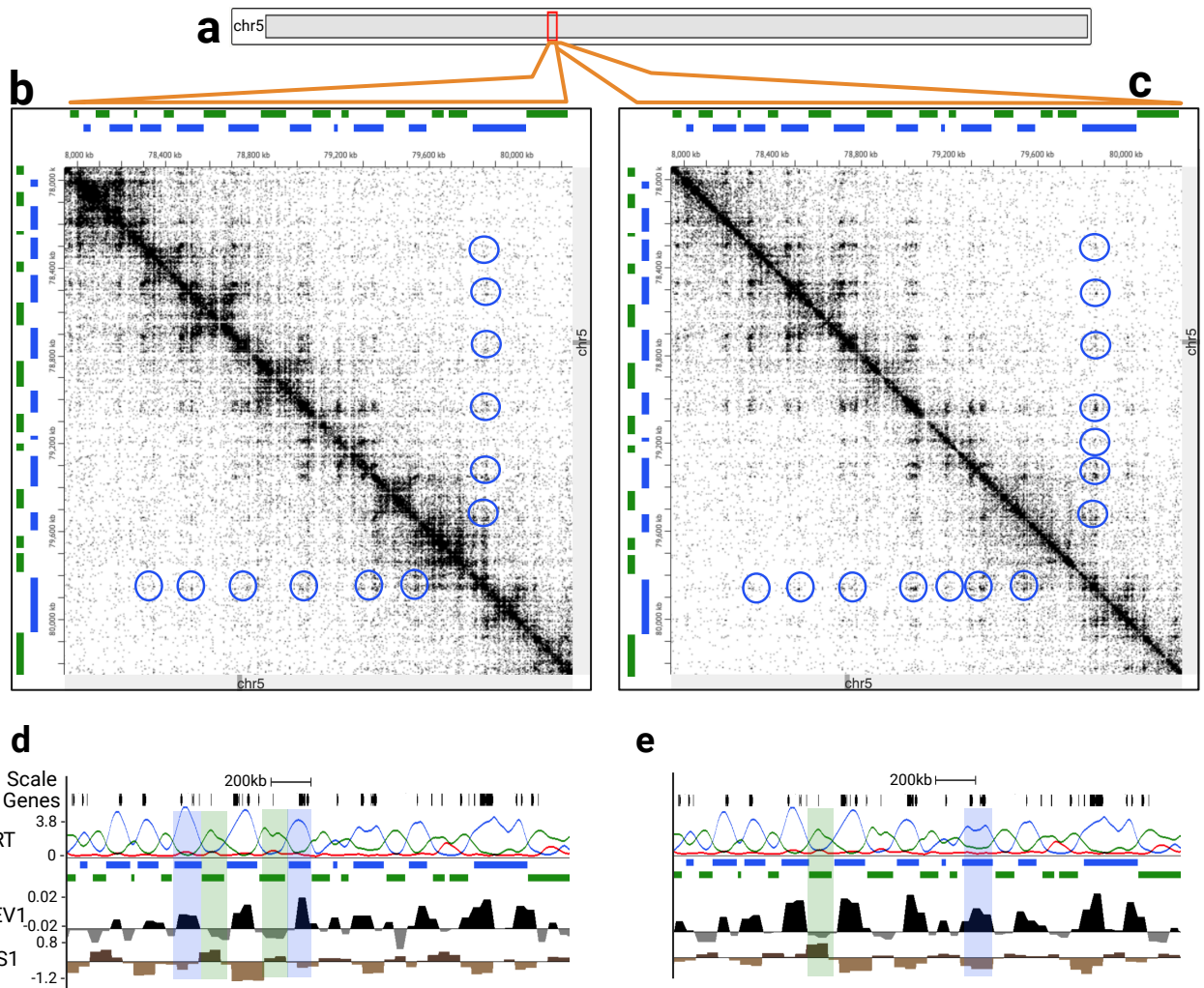
b

Root tip (blue) and Bundle sheath (red)

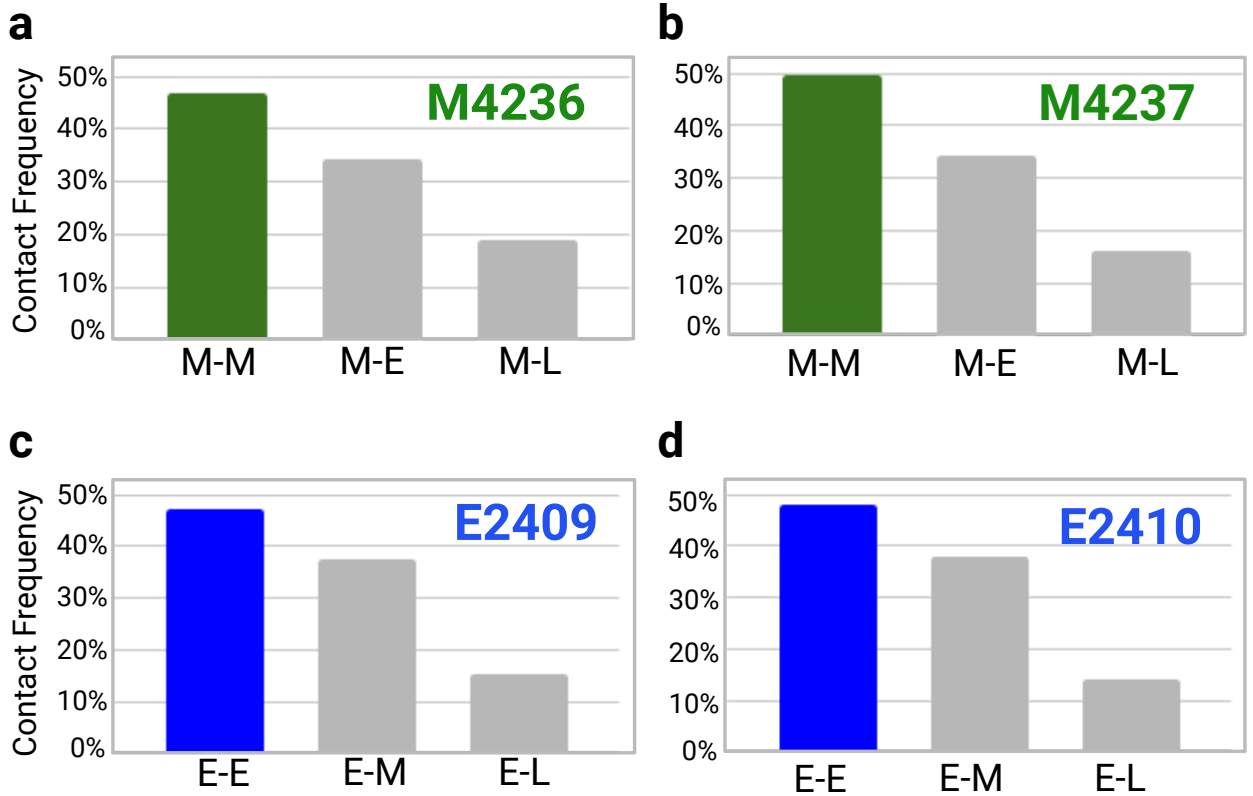


SCC score heat map across tissues and replicates

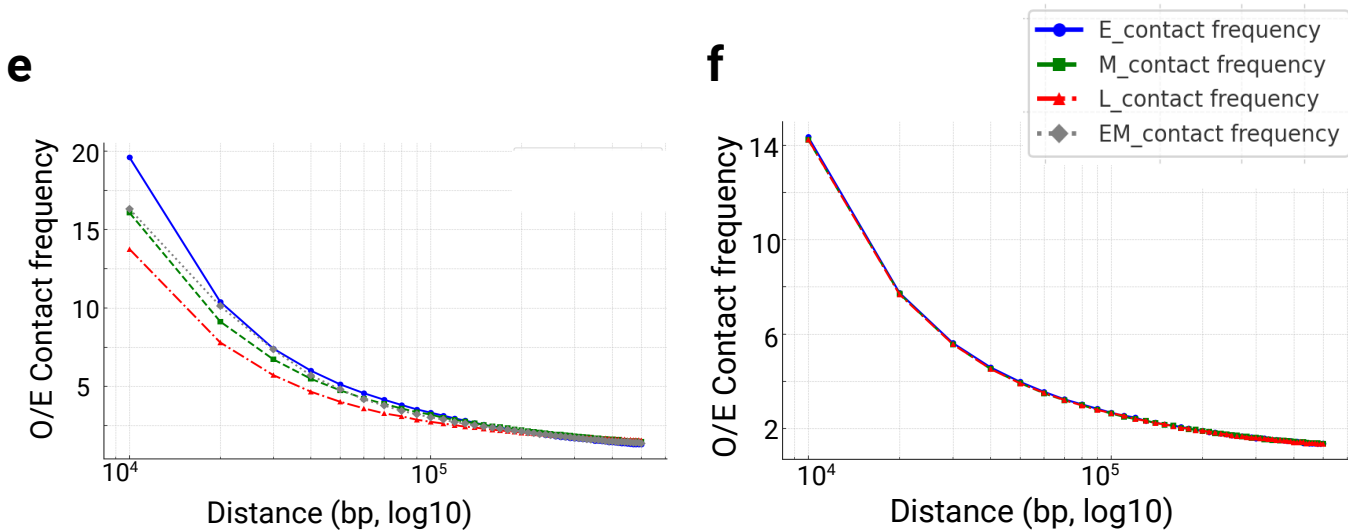


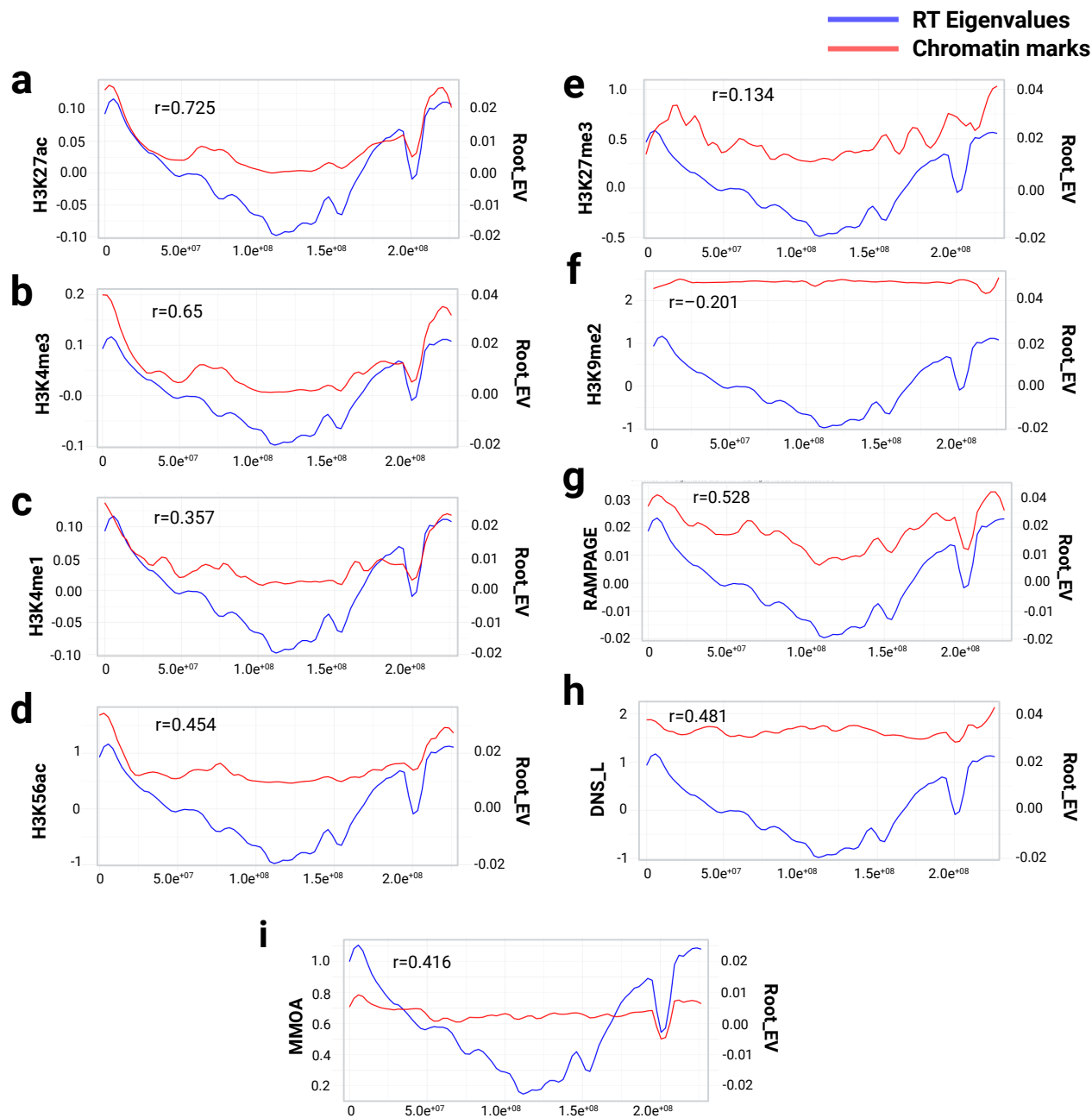


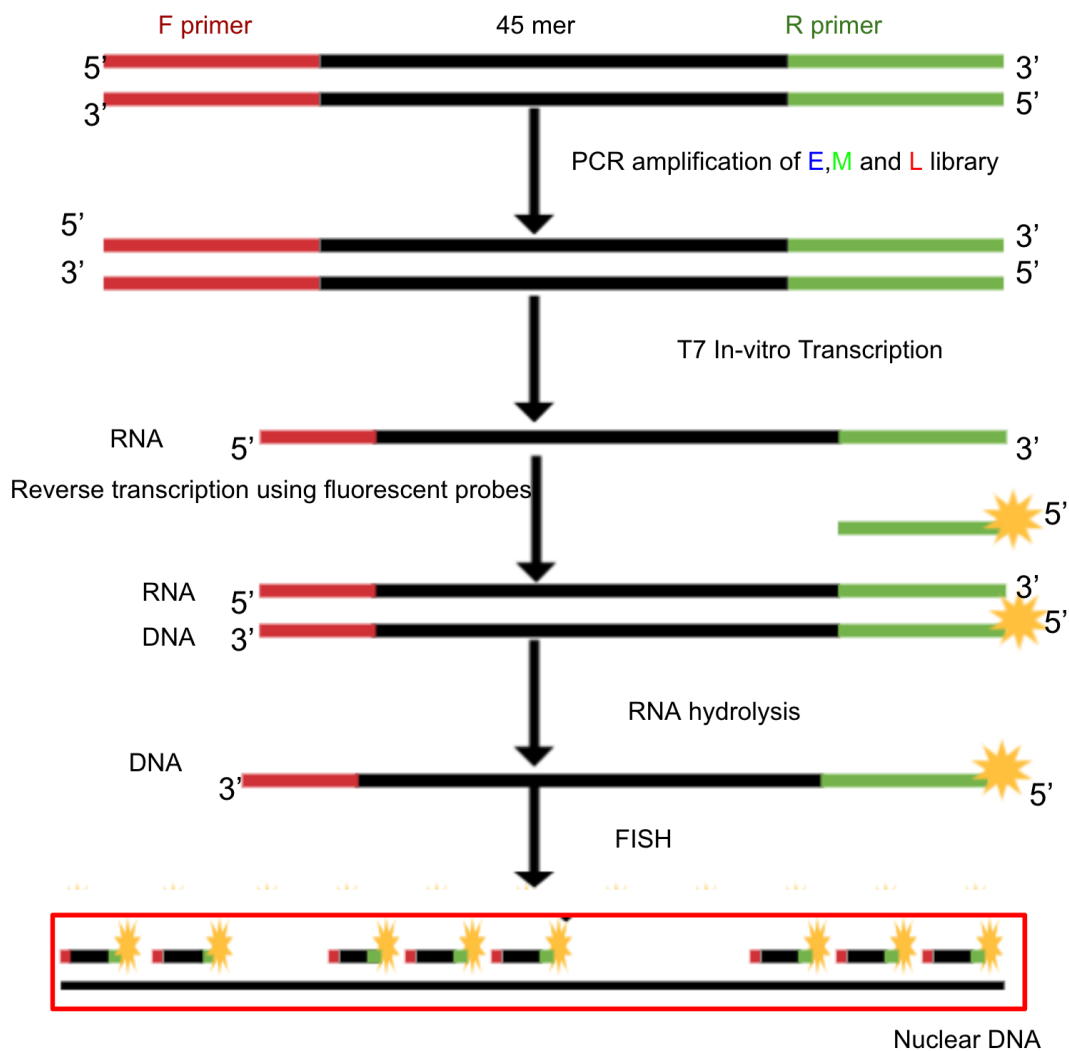
Per-bait contact pair frequencies



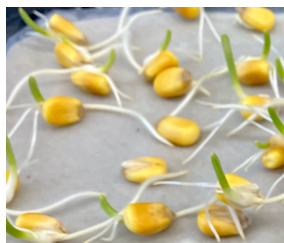
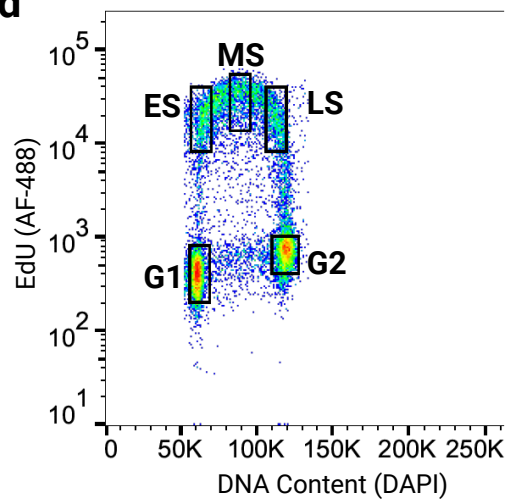
EvsE and MvsM contact pair frequencies normalised by distance





a**b**

EdU in vivo pulse-labeling

**c****d**

Supplementary Table 1. HiC Summary Statistics.

HiC libraries ^A	Total Reads ^B	Valid Contacts ^C	PCR Duplicates	Trans Interactions	Cis Interactions	Cis Short Range	Cis Long Range
Root tip rep1	148,529,729	46,277,361	8,646,492	5,815,255	31,815,614	6,593,800	25,221,814
Root tip rep2	146,330,218	42,912,077	8,065,453	7,005,296	27,841,328	5,889,328	21,952,000
Root tip rep3	187,537,189	58,057,354	9,410,986	9,507,348	39,139,020	7,684,329	31,454,691
Root tip rep4	143,438,961	41,549,774	6,834,567	7,190,483	27,524,724	5,603,289	21,921,435
Ear shoot rep1	127,467,879	27,730,693	4,505,474	4,769,700	18,455,519	4,162,271	14,293,248
Ear shoot rep2	308,506,330	95,879,933	18,220,265	20,675,903	56,983,765	8,711,364	48,272,401
Ear shoot rep3	253,912,920	74,369,477	14,472,034	17,325,131	42,572,312	42,572,312	35,915,439
Bundle sheath rep1	448,399,207	110,363,506	39,723,571	36,158,855	74,204,651	18,148,355	56,056,296
Bundle sheath rep2	867,566,517	294,700,726	86,109,501	88,319,269	206,381,451	51,183,865	155,197,592

Footnotes:

- A. Root tip and Ear shoot samples from this study. Bundle sheath libraries are from Dong *et al.*, (2017)³².
- B. Total read pairs are from initial sequencing.
- C. The remaining columns are output values from HiC-pro pipeline Servant *et al.*, (2015)³³.