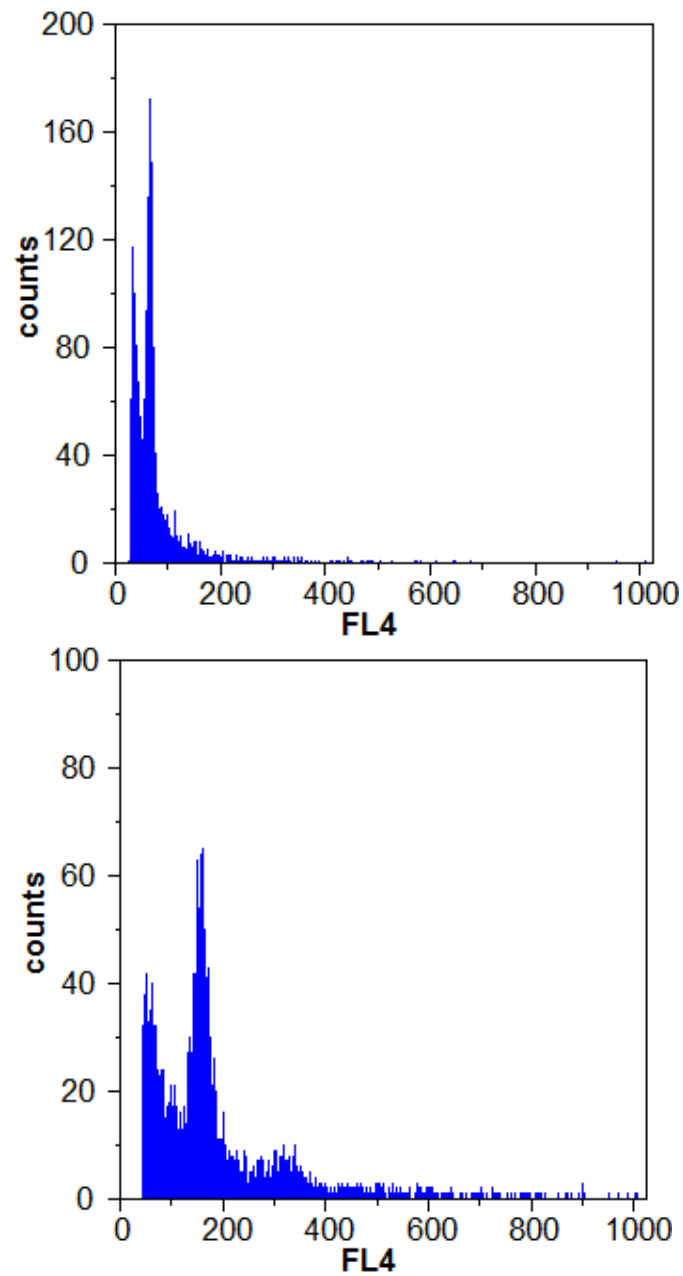
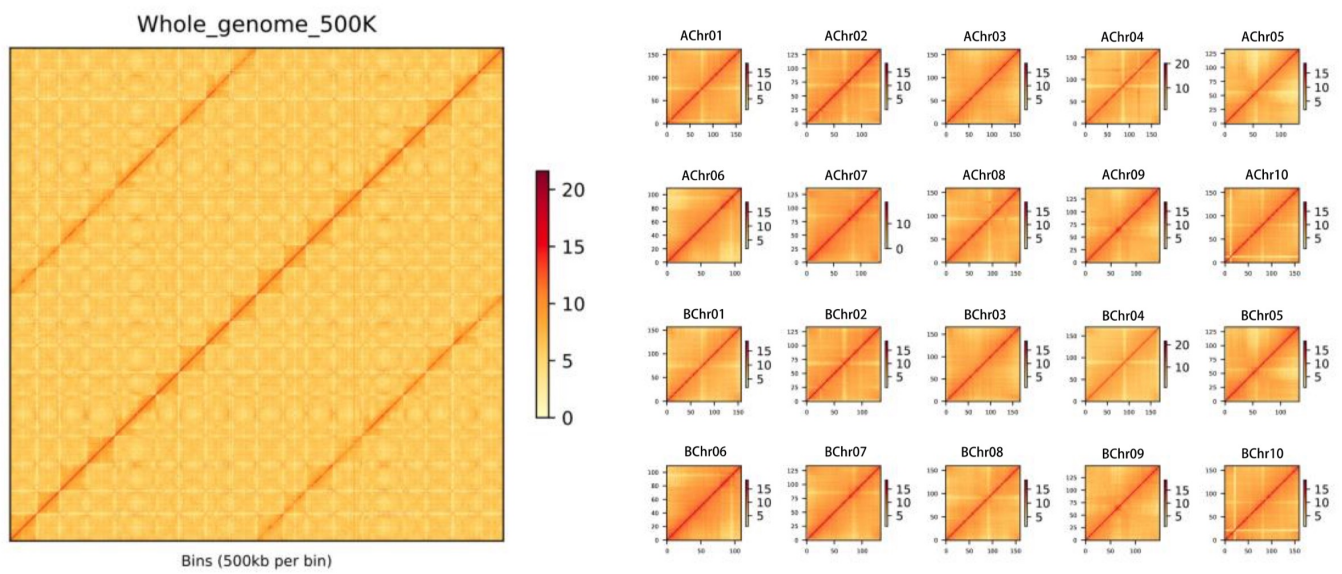
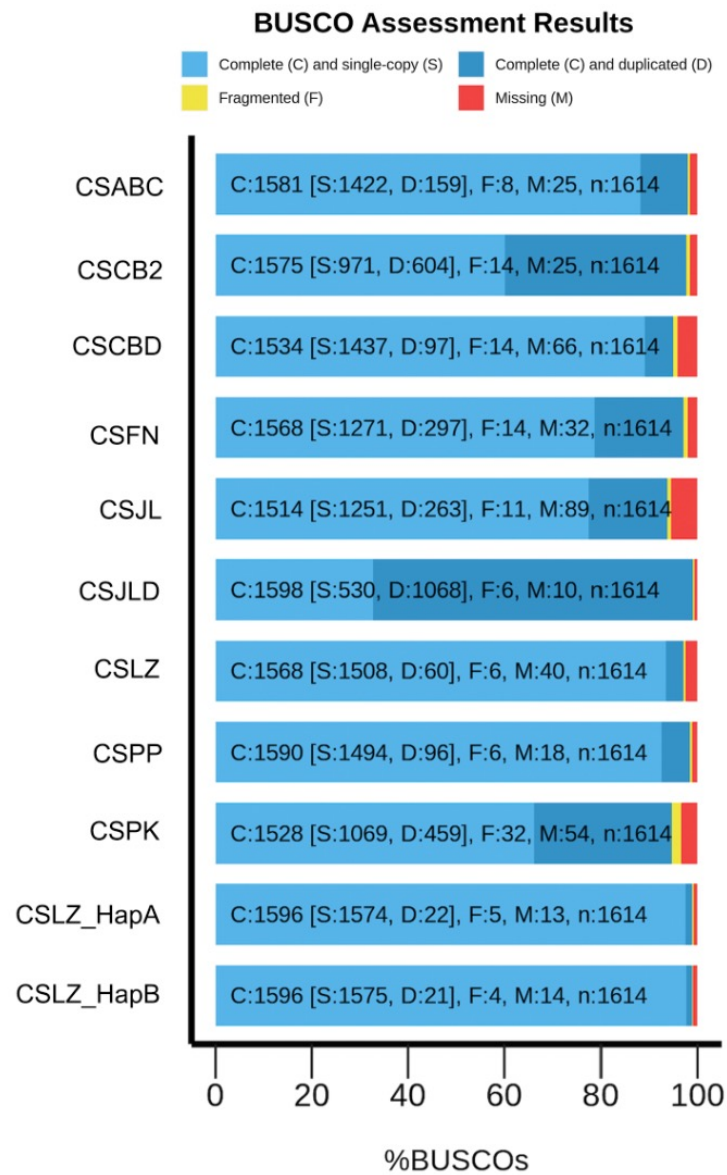




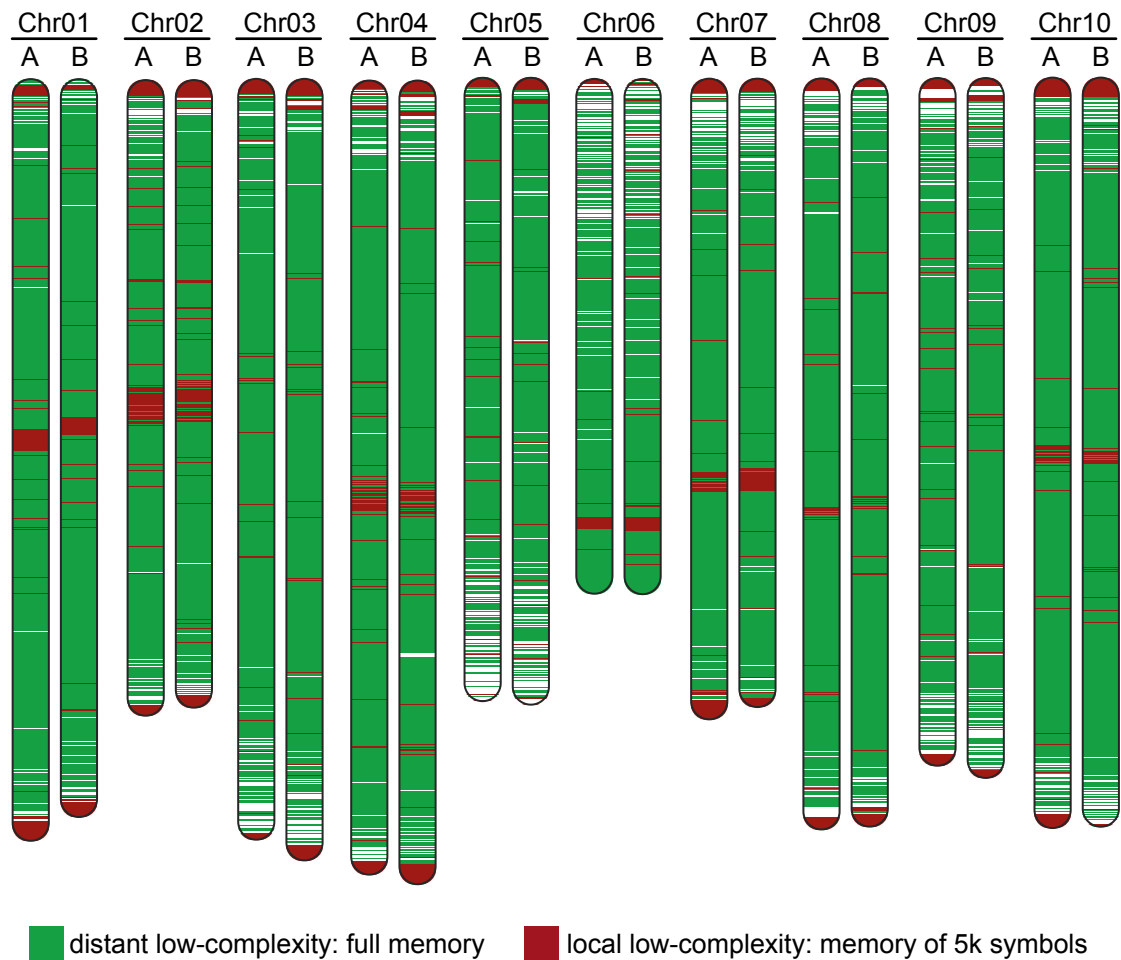
FigS1. Genome size estimation using flow cytometry. Histogram of fluorescence intensity for nuclei isolated from the internal reference *Oryza sativa* ssp. japonica (up) and CSLZ (down).



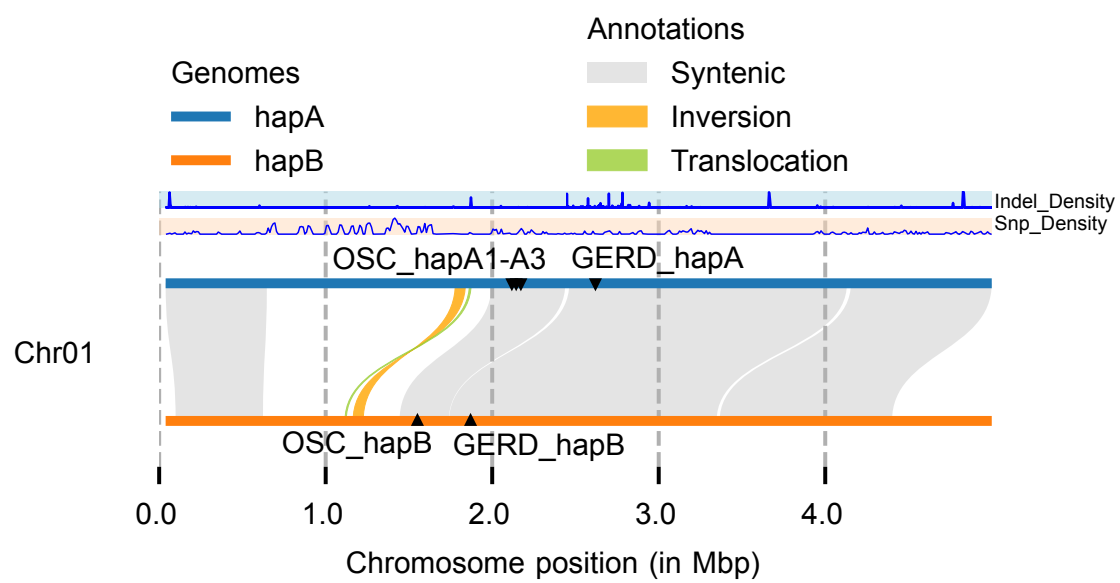
FigS2. Heatmap of the intensity signal of Hi-C chromosome interactions (bin=200 kb)



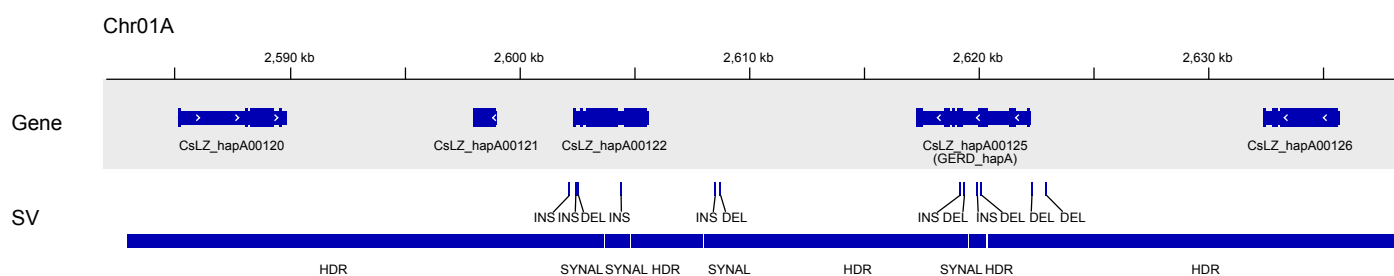
FigS3. BUSCO assessment results for CSLZ and other cannabis genomes



FigS4. Chromosome low-complexity (redundancy) map using different memories. The green color stands for the identification of LCRs using a setup of a model that uses the full memory, while the red color uses a memory of $p = 5,000$ symbols. In the map, the regions with the red color overlap the green; therefore, regions marked with red are also green, and the green regions that are visible stand for low complexity related to distant patterns.



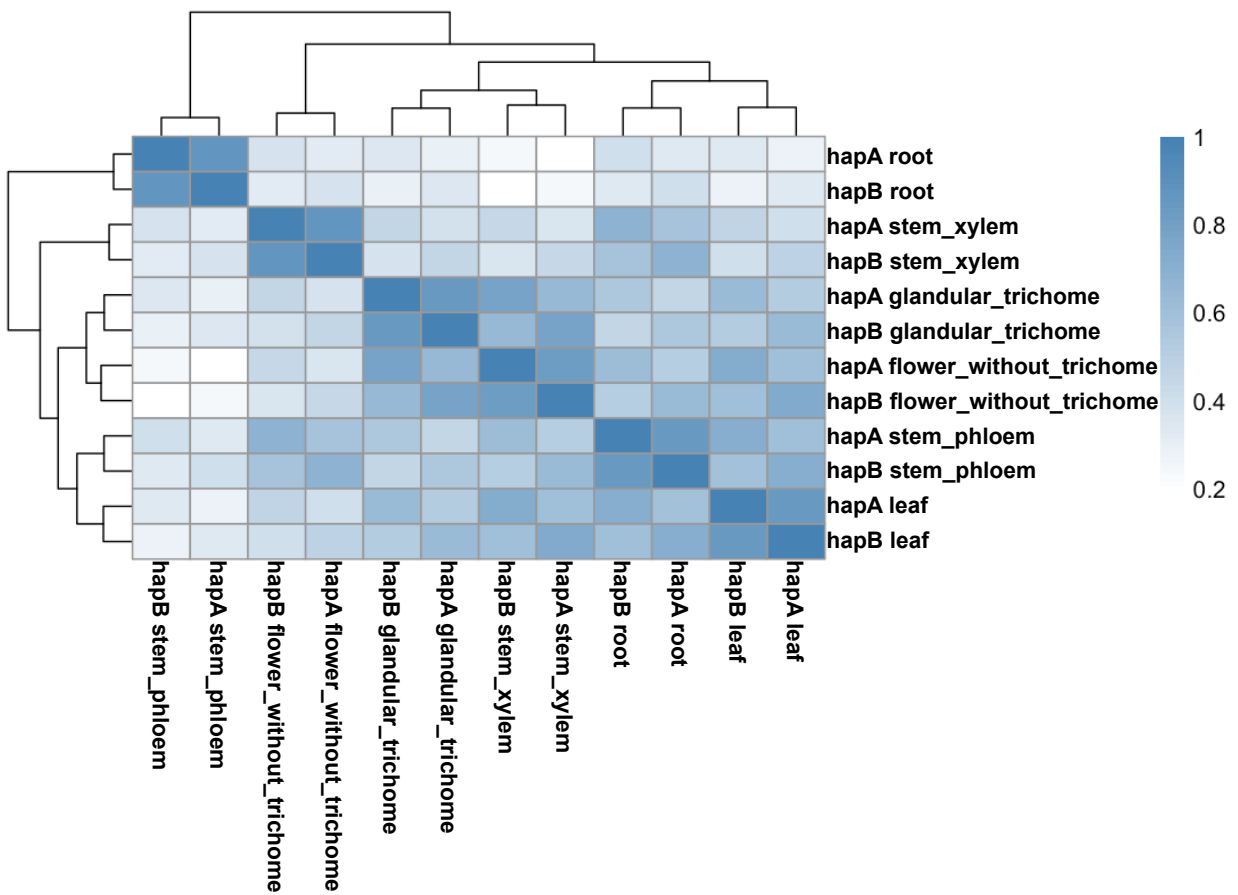
FigS5. Linear visualization of structural variants and gene synteny at the *GERD* and *OSC* loci.



FigS6. Linear visualization of structural variants and gene synteny at the *GERD_hapA* loci. INS: insertion in query, DEL: deletion in query, HDR: highly diverged regions, SYNAL: alignment in syntenic region.

CsLZ_hapA0012	1	MSPCEDTIDEKRPNMPKFTPTIWGDYFMSSASNNHHSSLMETMENNNKES	50
CsLZ_hapB0013	1	-----MPKFTPTIWGDYFMSSHSS-HHSSLMETMENNNKES	35
CsLZ_hapA0012	51	YEKIIEMKEQVKNKLLHGLHLENPLETLEYIDDIQRLGLSYYFENEIEQ	100
CsLZ_hapB0013	36	YEKIIEMKEQVKNKLLHGLHLENPLETLEYIDDIQRLGLSYYFENEIEQ	85
CsLZ_hapA0012	101	IL-EQFHNNYQNLIDFGDNNLYADALCFRLLRQQGYNIACDIFDKYKNEK	149
		: :	
CsLZ_hapB0013	86	VLMKQFHNN-QNLIDFGDNNLYADALCFRLLRQQGYNIACDIFDKYKNEK	134
CsLZ_hapA0012	150	GKFKEISSDIRGMLNLYEAAQMRVHGEKILDEALIFTTTHLESSVKTCQ	199
		.	
CsLZ_hapB0013	135	GKFKEISLSDIRGMLNLYEAAQMRVHGEKILDEALIFTTTHLESSVKTCQ	184
CsLZ_hapA0012	200	LSSPYLDLVKHALMHPIRKSQRREARLYISLYHQLPSHEEILLTLAKLD	249
CsLZ_hapB0013	185	LSSPYLDLVKHALMHPIRKSQRREARLYISLYHQLPSHEEILLTLAKLD	234
CsLZ_hapA0012	250	FNLLQKLHQKELSYITRWKEDYKSKHSFIKDRIVECYFWVYGVFFAE	299
CsLZ_hapB0013	235	FNLLQKLHQKELSYITRWKEDYKSKHSFIKDRIVECYFWVYGVFFAE	284
CsLZ_hapA0012	300	TSQIRLIITKLIAILTIIDDAYDSFGTLEELPFTQAIERWDICAIDTLP	349
CsLZ_hapB0013	285	TSQIRLIITKLIAILTIIDDAYDSFGTLEELPFTQAIERWDICAIDTLP	334
CsLZ_hapA0012	350	EYMKIFYMKLLEIYNEIEQFSKEKSYCPSYAKKGVQSLIRAYFKEAKWLH	399
CsLZ_hapB0013	335	EYMKIFYMKLLEIYNEIEQFSKERSYCPSYAKKGVQSLIRAYFKEAKWLH	384
CsLZ_hapA0012	400	TKYIPTLDEYMPVGVDSSAGSFMLISMVFIGMGDIVTKHSMDWIFSNPQPK	449
CsLZ_hapB0013	385	TKYIPTLDEYMPVGVDSSAGSFMLISMVFIGMGDIVTKHSMDWIFSNPQPK	434
CsLZ_hapA0012	450	IIQTMAIVGRVMNDIGYHKSERKKSSGEIVASTVECYMKQYGVPGEEAIE	499
CsLZ_hapB0013	435	IIQTMAIVGRVMNDIGYHKSERKKSSGEIVASTVECYMKQYGVPGEEAIE	484
CsLZ_hapA0012	500	KLSEQVKDSWKDLNEDLLNPITIPRLLMQVLKLRVNHEIYREGDGFTQ	549
		:	
CsLZ_hapB0013	485	KLSQQVKDSWKDLNEDLLNPITIPRLLMQVLKLRVNHEIYREGDGFTQ	534
CsLZ_hapA0012	550	PTLLKNLIHSLIINPIDF*	568
CsLZ_hapB0013	535	PTLLKNLIHSLIINPIDF*	553

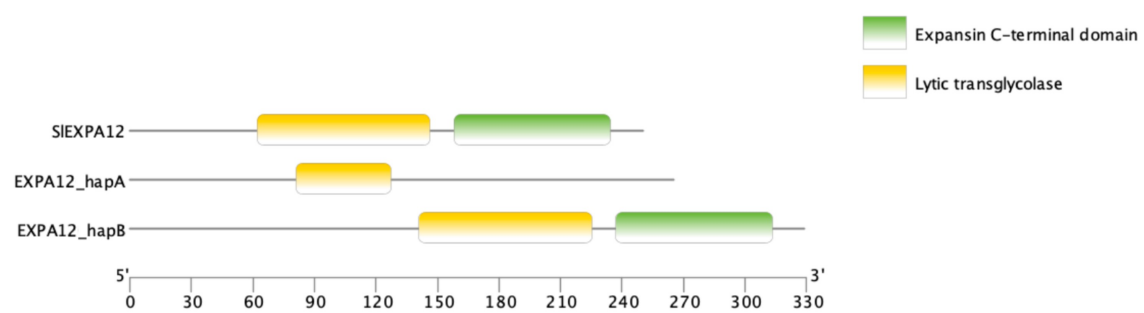
FigS7. Pairwise sequence alignment between GERD_HapA and GERD_HapB.



FigS8. Correlation analysis between roots, stem xylem, stem phloem, leaves, female flowers (without trichomes), and glandular trichomes.



FigS9. Differences in HCT expression and promoter region in different haplotypes.



FigS10. Domains of SIEXPA12, EXPA12_hapA and EXPA12_hapB.