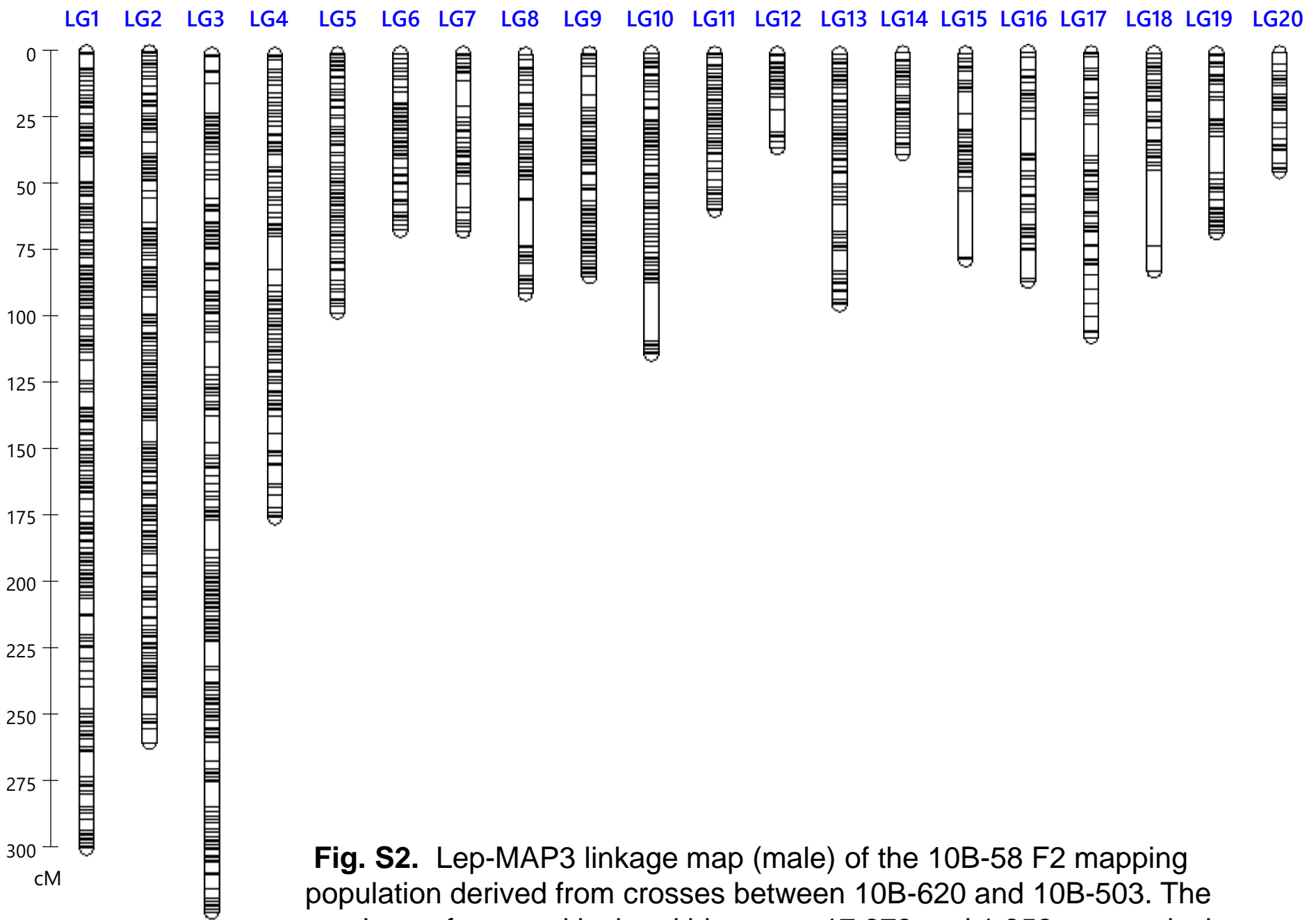
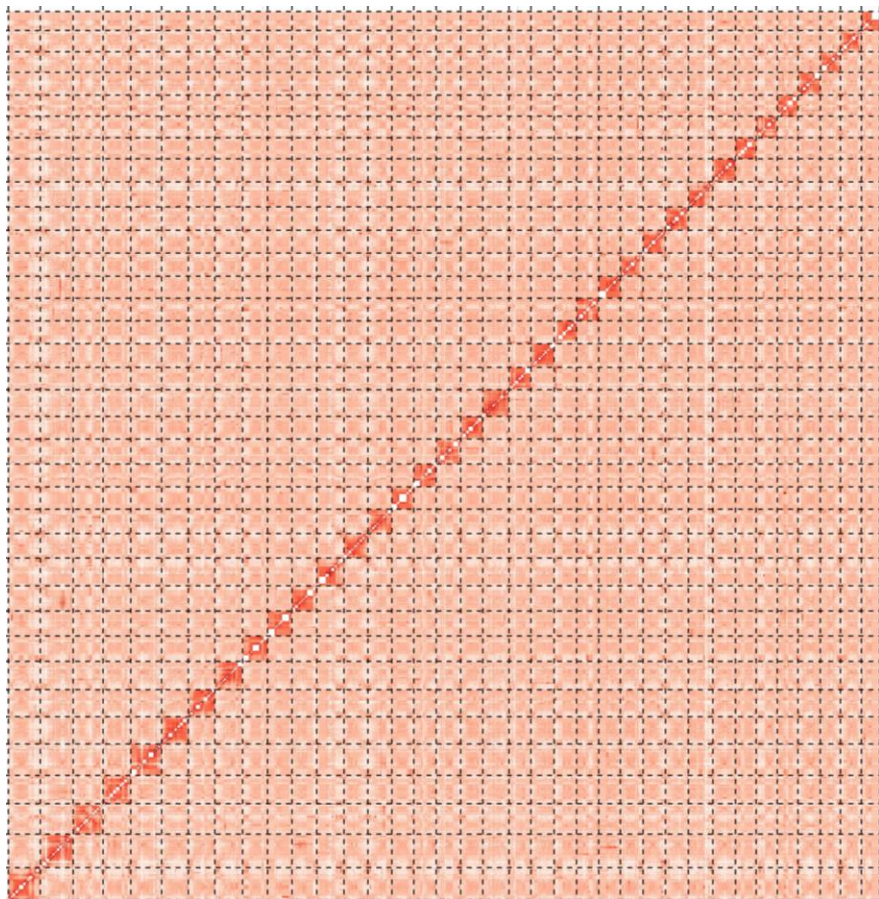


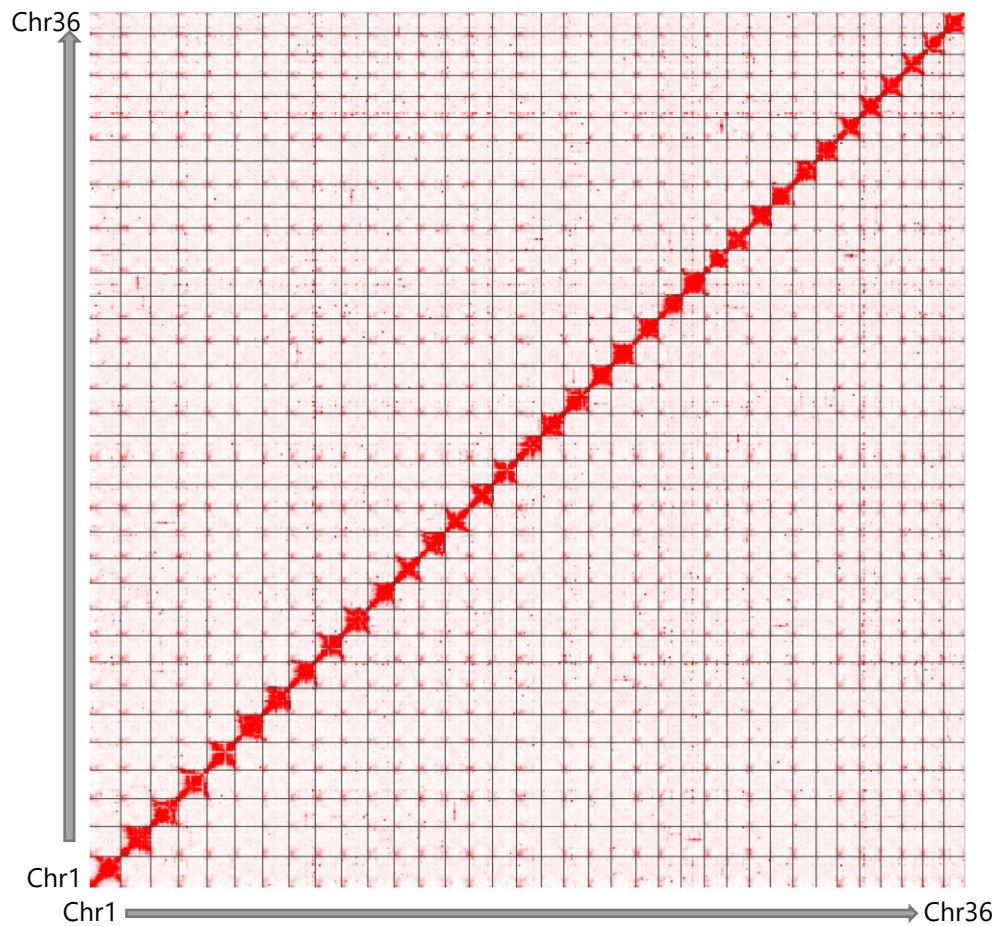
**Fig. S1.** Genome size estimation using Jellyfish with the distribution of the number of distinct kmers (kmer = 17) with the given multiplicity values.



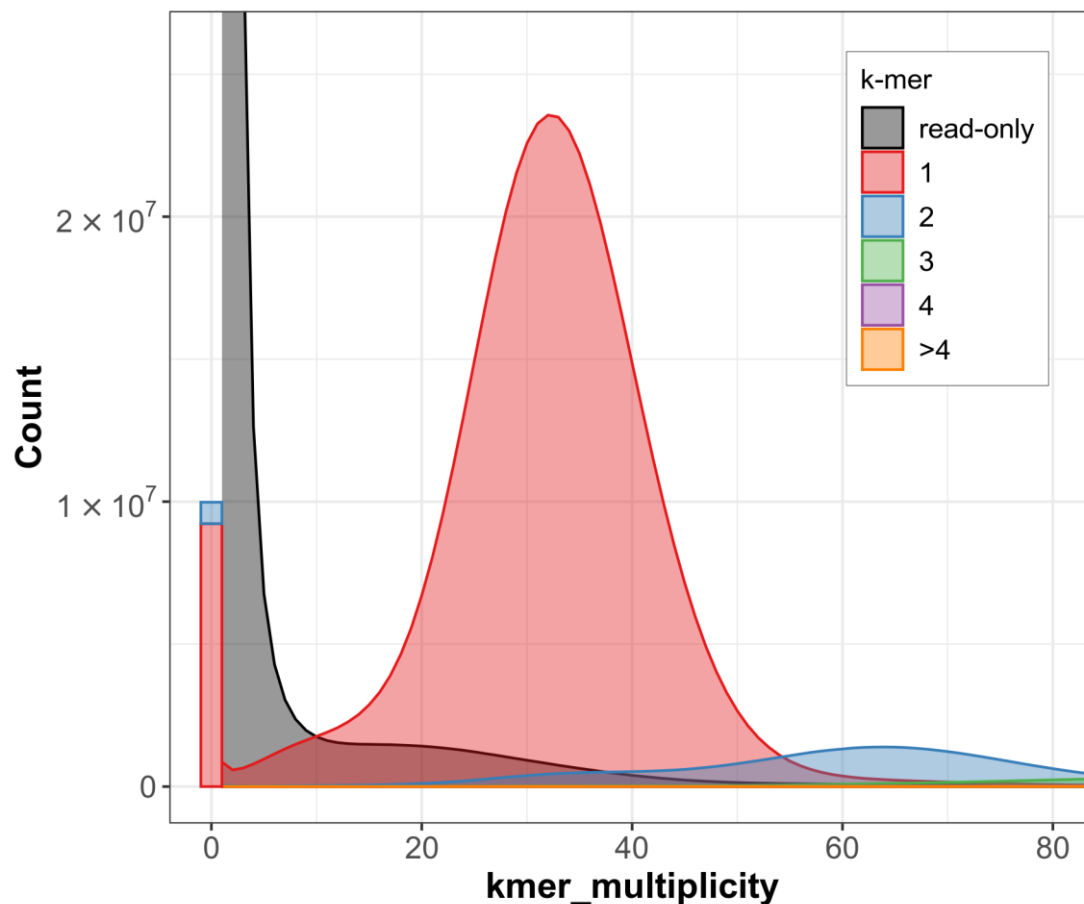
A)



B)



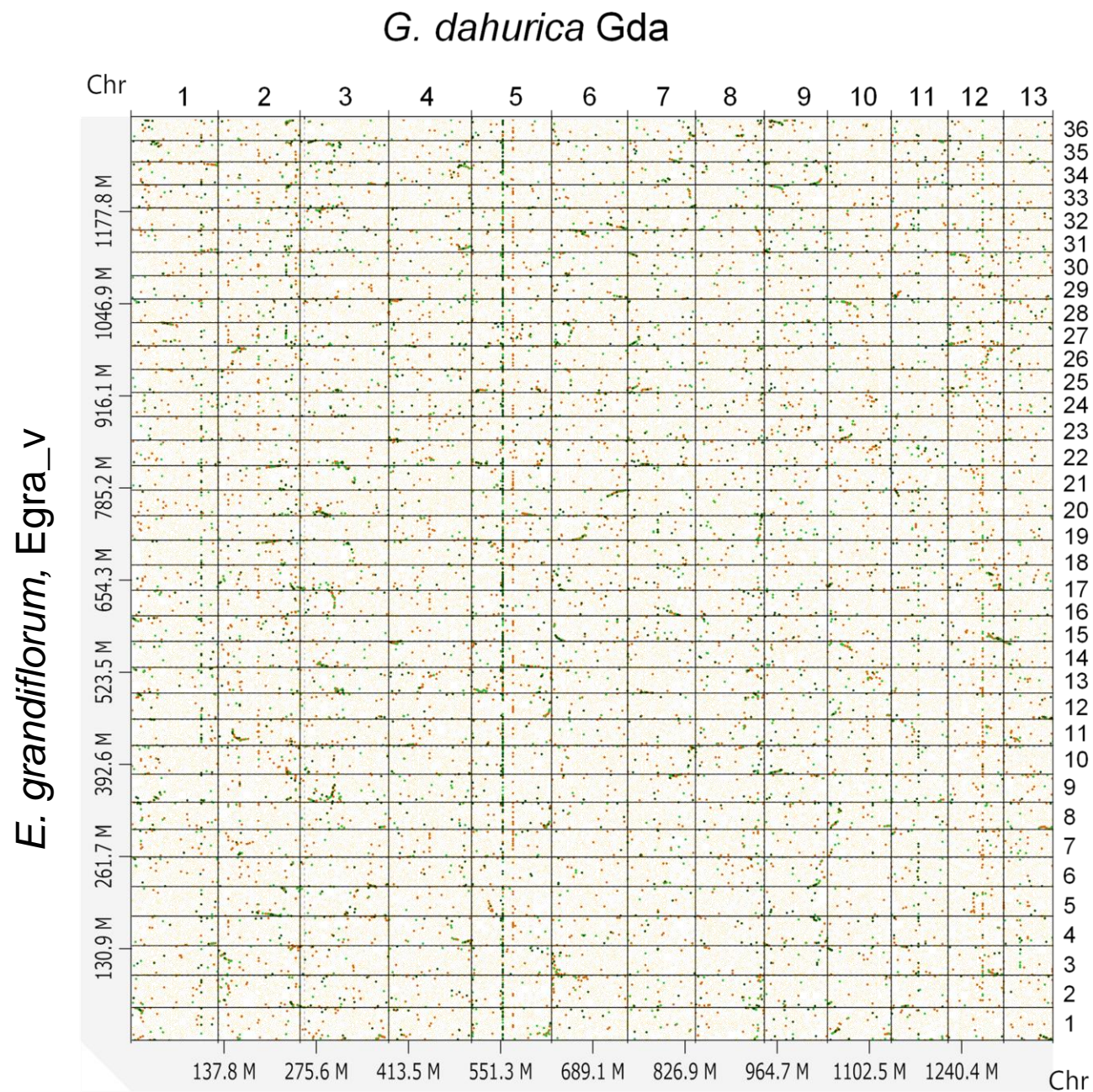
**Fig. S3.** Hi-C contact maps for the 36 pseudomolecules created by Juicebox. A) 36 pseudomolecules (chromosome-level scaffolds) created by Proximo Hi-C. Juicebox was used for creating the map. B) 36 pseudomolecules of Egra\_v1.0. Hi-C was mapped onto the pseudomolecules by juicer.



Sequence	<i>k</i> -mers uniquely found only in the assembly	<i>k</i> -mers found in both assembly and the read set	QV	Error rate	<i>k</i> -mer set used for measuring completeness	solid <i>k</i> -mers in the assembly	Total solid <i>k</i> -mers in the read set	Completeness (%)
Egra_v1	9,978,606	1,323,992,553	34.22	0.00037819	all	587,888,846	626641758.00	93.82

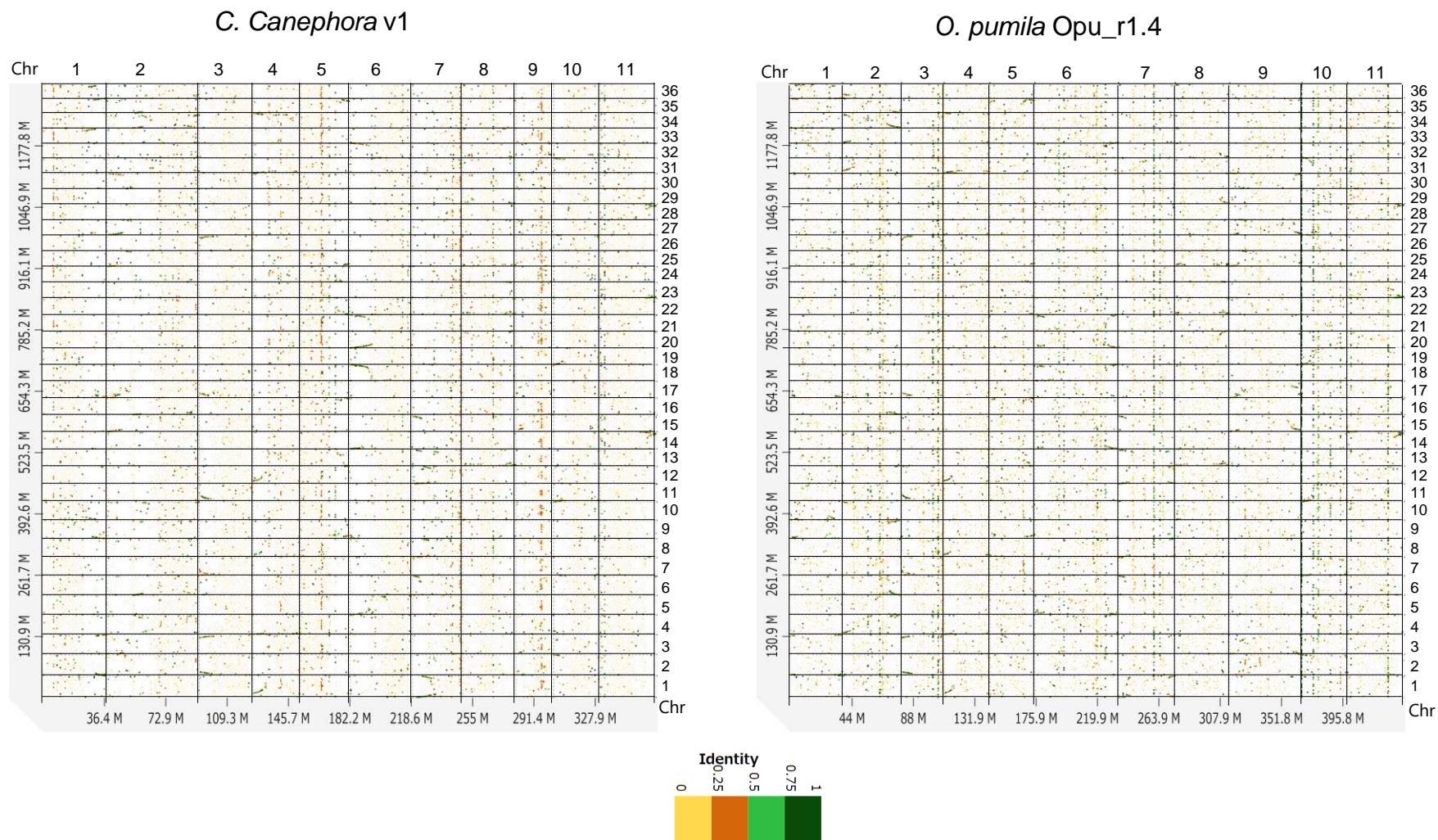
**Fig. S4.** Mercury copy number spectrum plots for the assembled genome, Egra\_v1 (including 36 chr and unplaced scaffolds). The red, blue, green, purple and orange plots represent *k*mer multiplicities peaks with x1, x2, x3, x4 and x >4 copy sequences in Egra\_v1, respectively. The gray plot represents *k*mers identified only on paired end reads of the sequenced line, 10B-620.



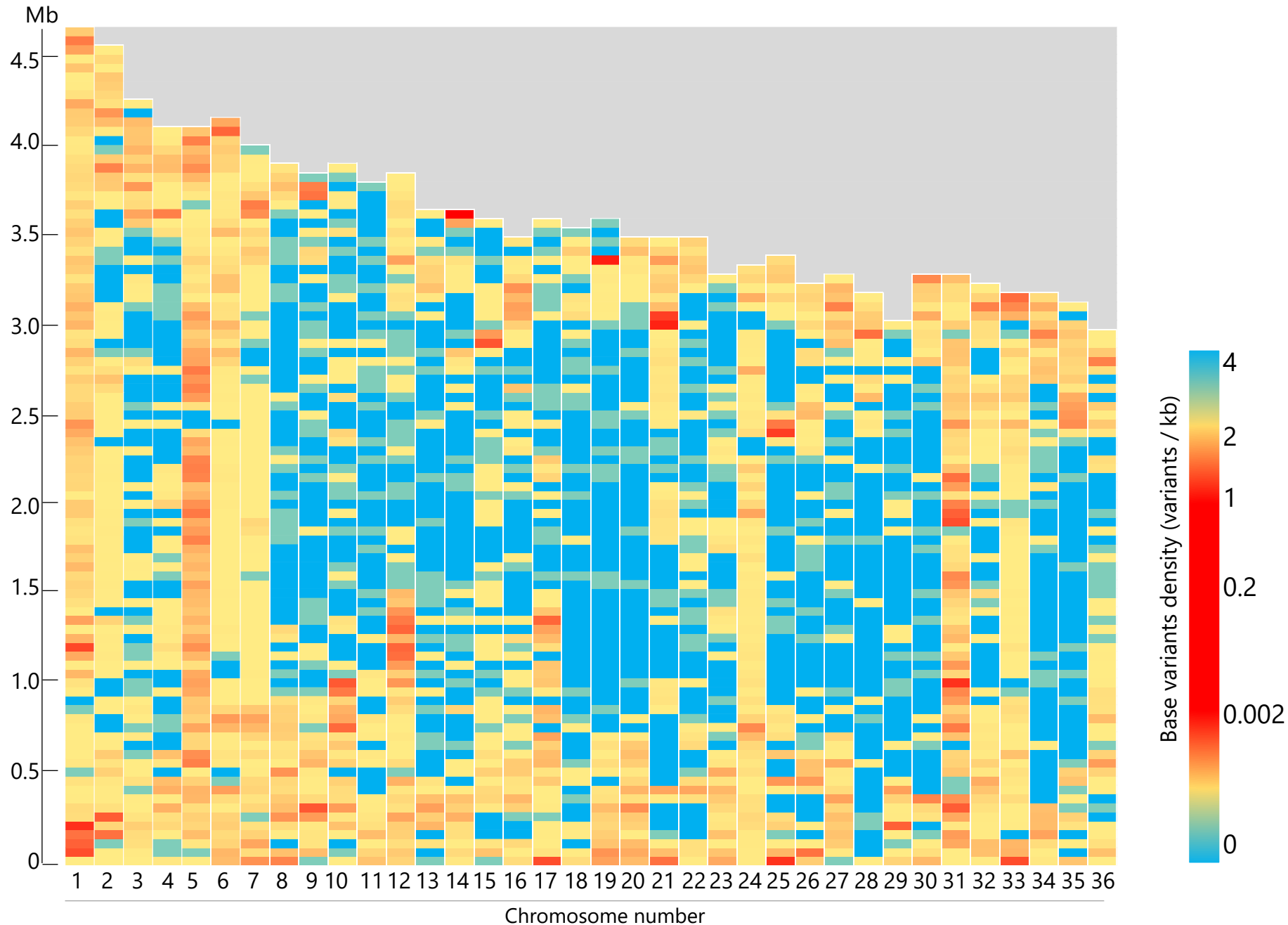


**Fig. S5.** Graphical view of syntenic relationships between *E. grandiflorum* and *G. dahurica*.

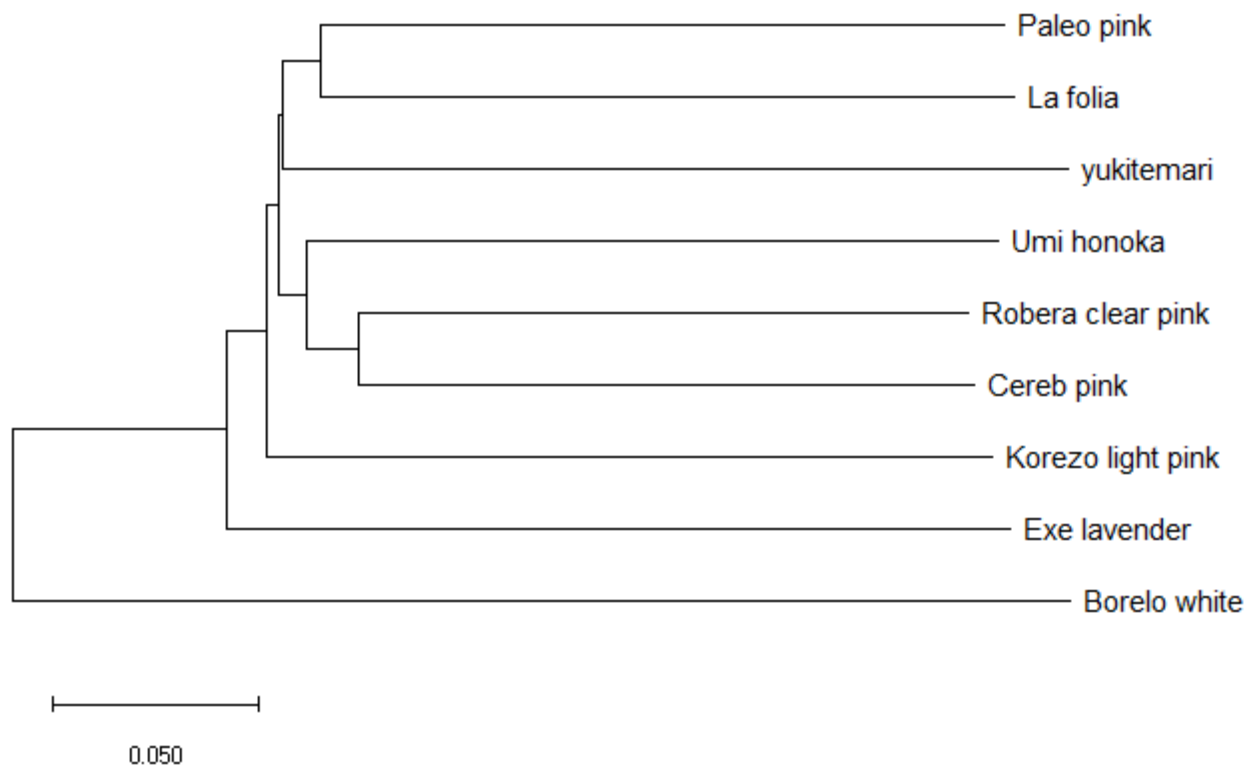




**Fig. S6.** Graphical view of syntenic relationships between *E. grandiflorum* and *C. canephora* (left) or *O. pumila* (right).



**Fig. S7.** Base variants density on the Eustoma genome. The variants were identified with nine Eustoma varieties, and the density (variants /kb) was calculated in each 500kb windows.



**Fig. S8.** A phylogenetic tree of nine *Eustoma* varieties based on 254,205 variants.