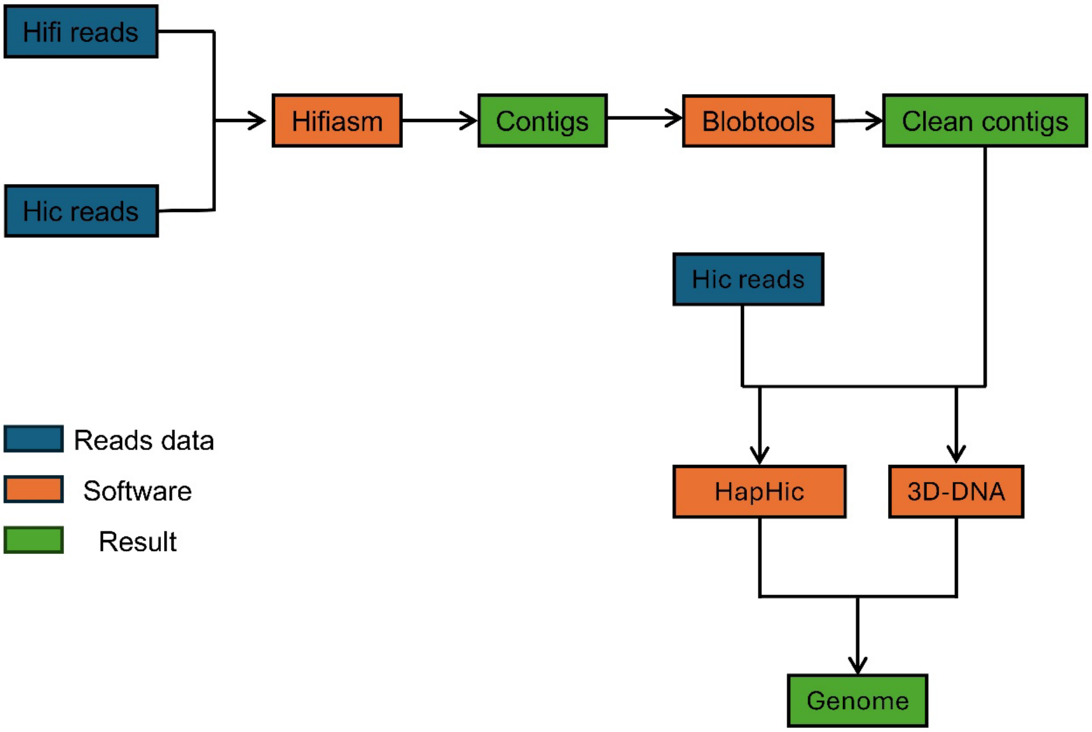
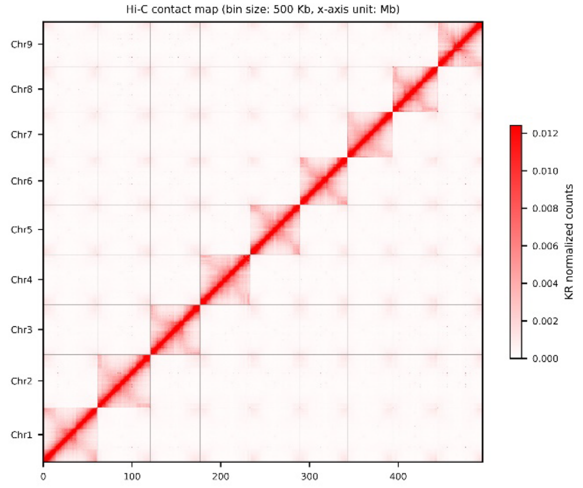
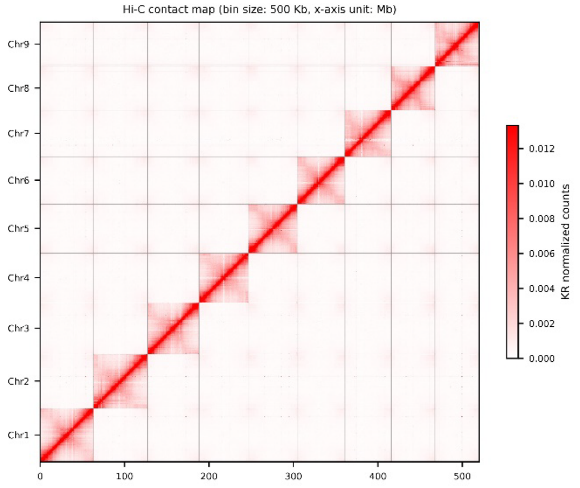


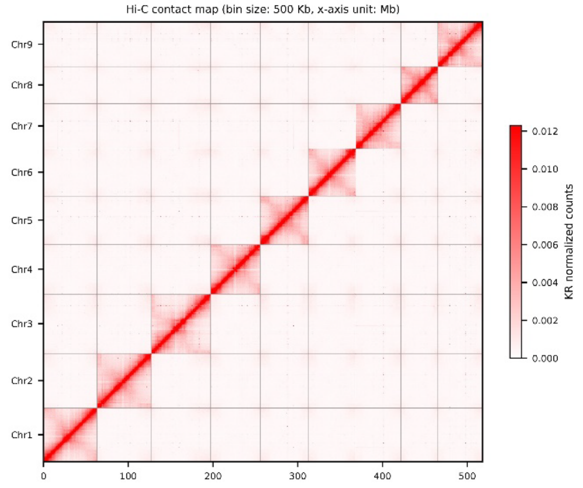
Extended Data Fig. 1. The genome assembly pipeline used in this study.



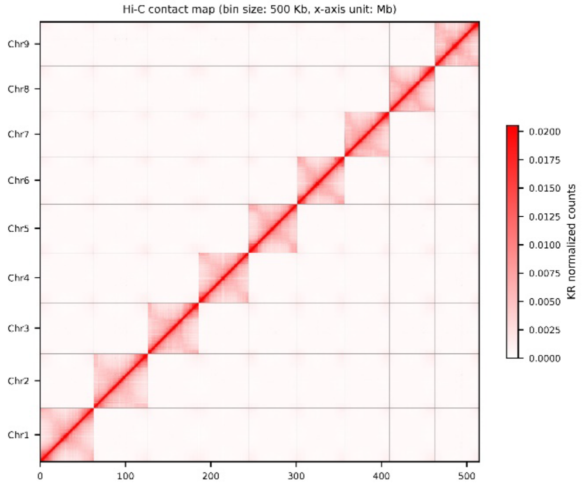
S. brachiata



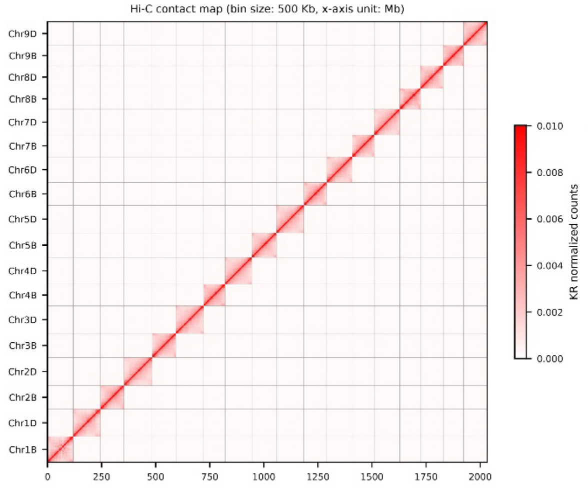
S. sinus-persica



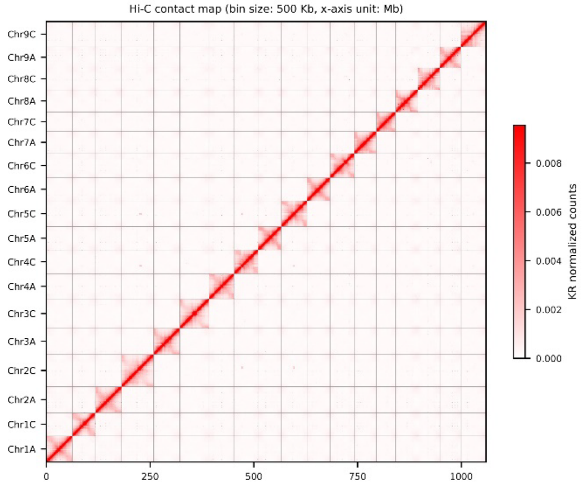
S. persica ssp. iranica



S. europaea (Israel)

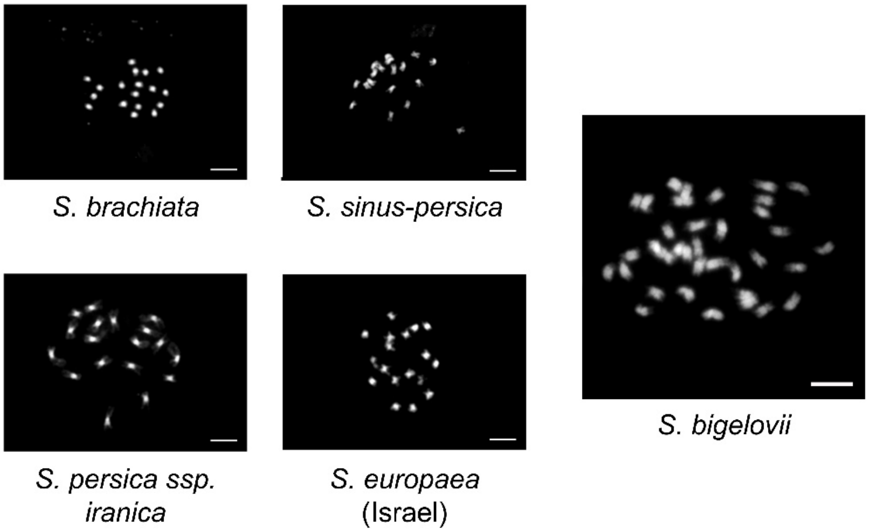


S. bigelovii



S. europaea (France)

Extended Data Fig. 2. The Omni-C heatmap of six pseudo chromosome-scale assembled genomes of *Salicornia*.



S. brachiata

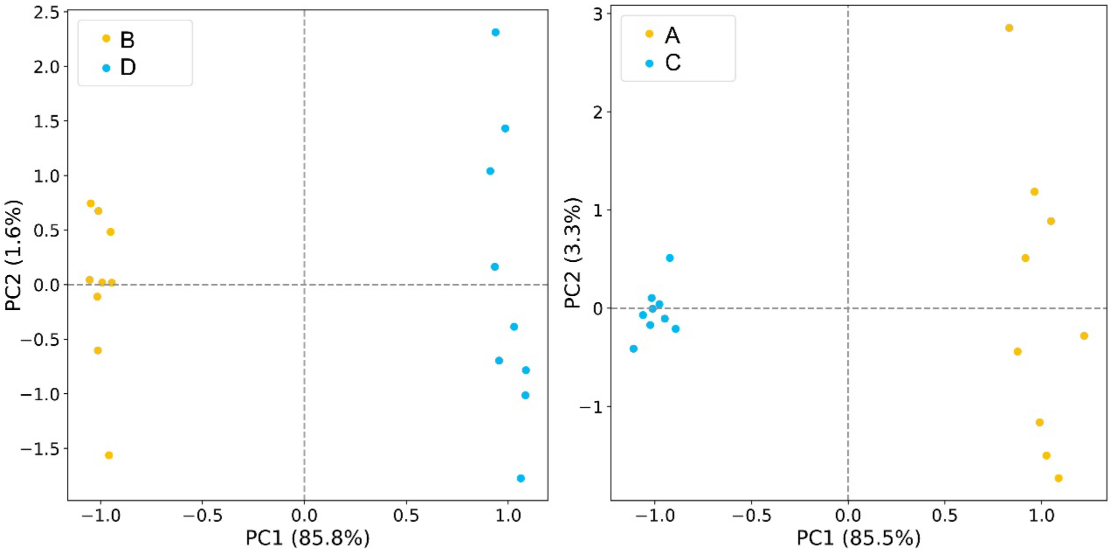
S. sinus-persica

S. persica ssp. iranica

S. europaea (Israel)

S. bigelovii

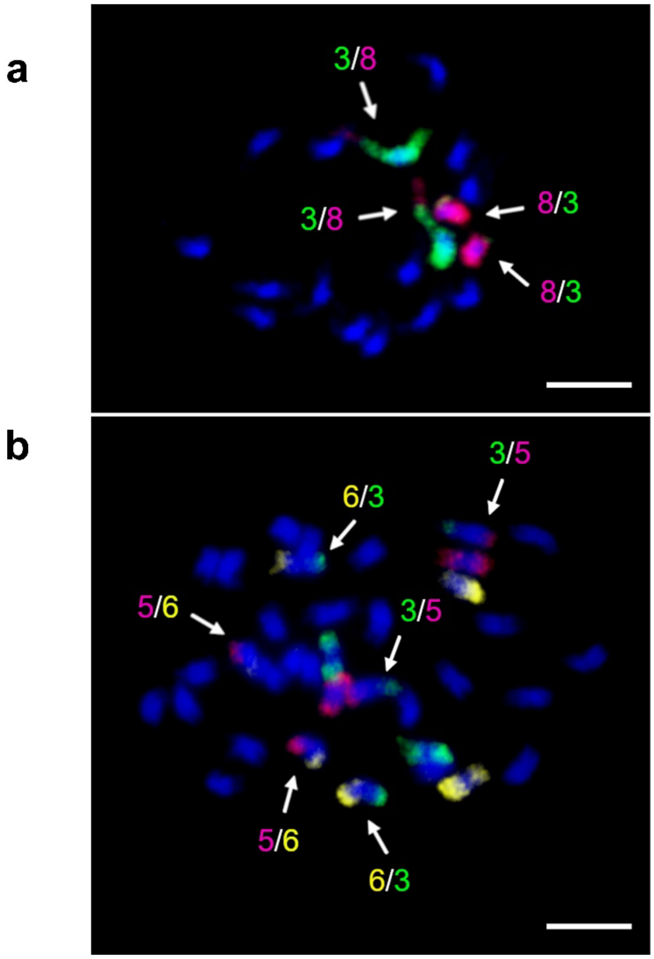
Extended Data Fig. 3. Chromosome counts on metaphase chromosomes in *S. brachiata*, *S. sinus-persica, S. europaea* (Israel) and *S. persica ssp. iranica*, and *S. bigelovii*. Chromosomes were stained with DAPI. Scale bars, 5 μm.



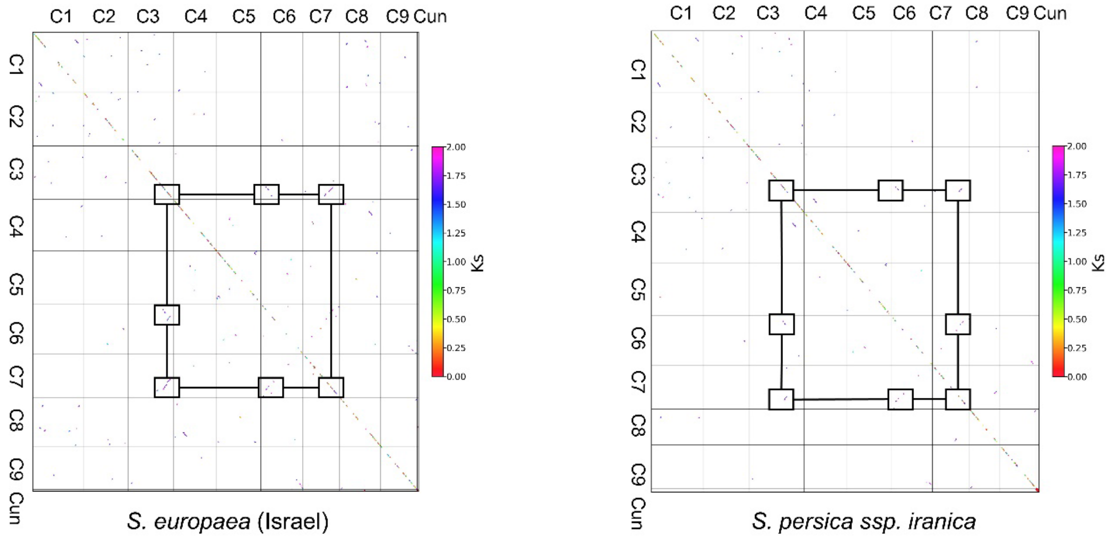
S. bigelovii

S. europaea (France)

Extended Data Fig. 4. Principal component analysis of differential *k-mers*. Points indicate chromosomes of the subgenome represented by colors.

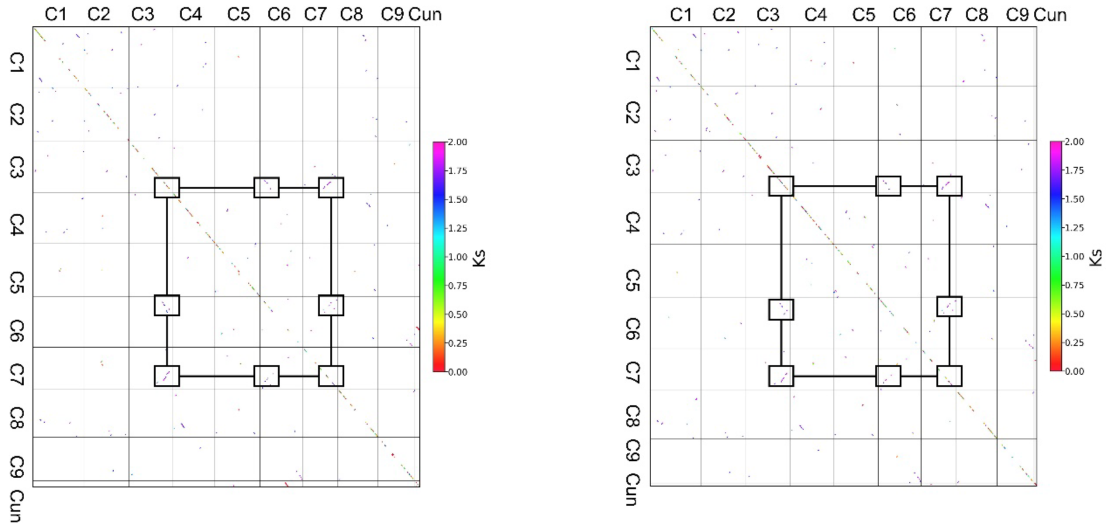


Extended Data Fig. 5. Reciprocal translocations revealed by oligo-FISH on mitotic metaphase chromosomes of *Salicornia* species. a: Reciprocal translocation between chromosomes three and eight in *S. persica ssp. iranica*. Oligo-FISH probes SEUR3 (green) and SEUR8 (pink); b: Reciprocal translocations between chromosomes three and five, chromosomes five and six, and chromosomes six and three in *S. bigelovii*. Oligo-painting probes SEUR3 (green), SEUR5 (pink) and SEUR6 (yellow). Translocated chromosomes are indicated by white arrows. Chromosomes were stained with DAPI (blue). Scale bars, 5 μm.



S. europaea (Israel)

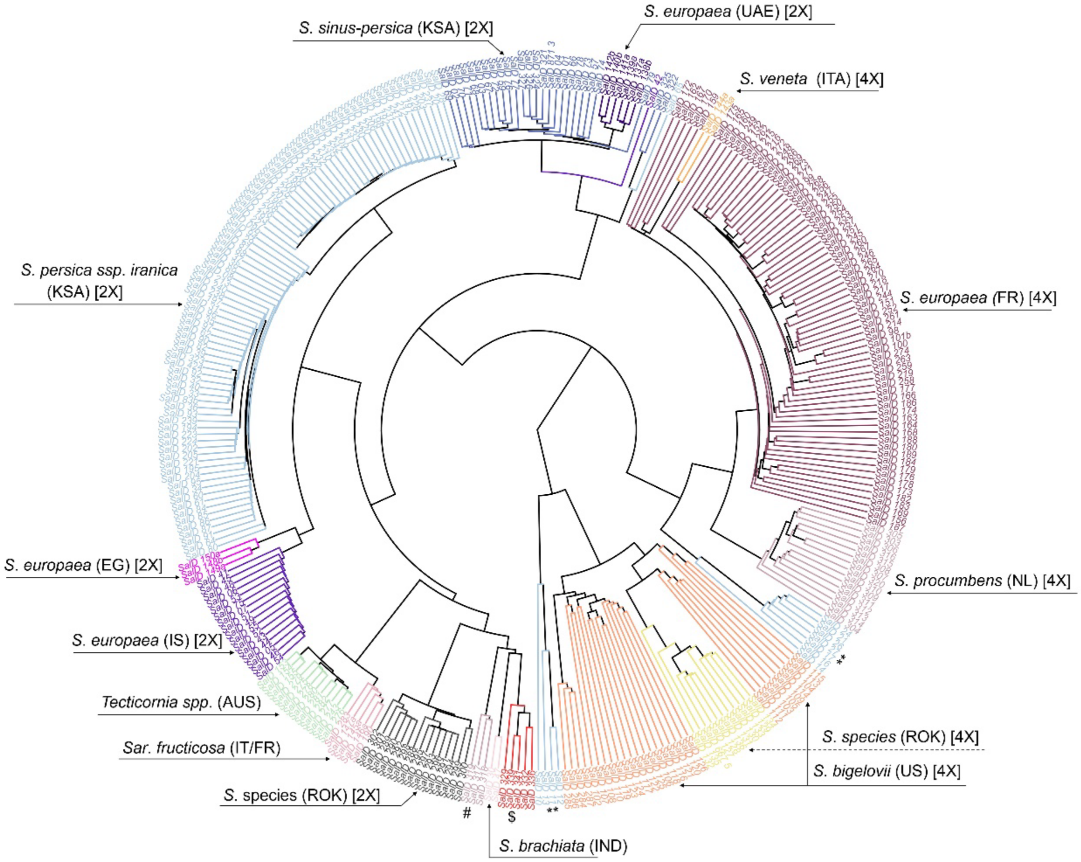
S. persica ssp. iranica



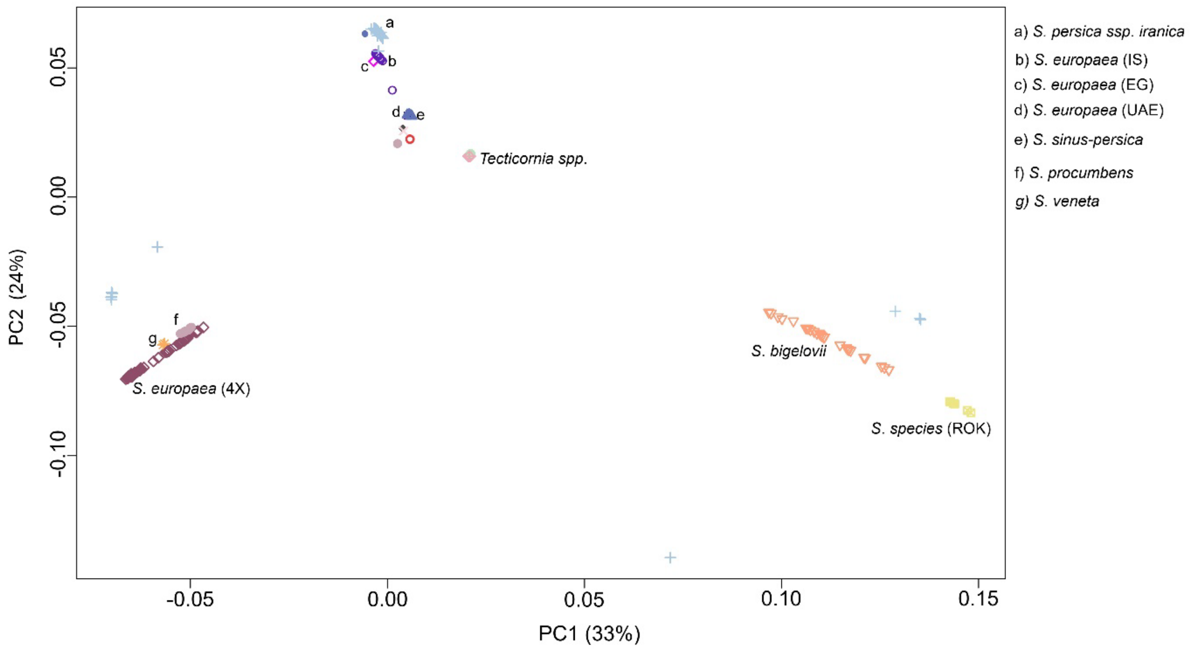
S. brachiata

S. sinus-persica

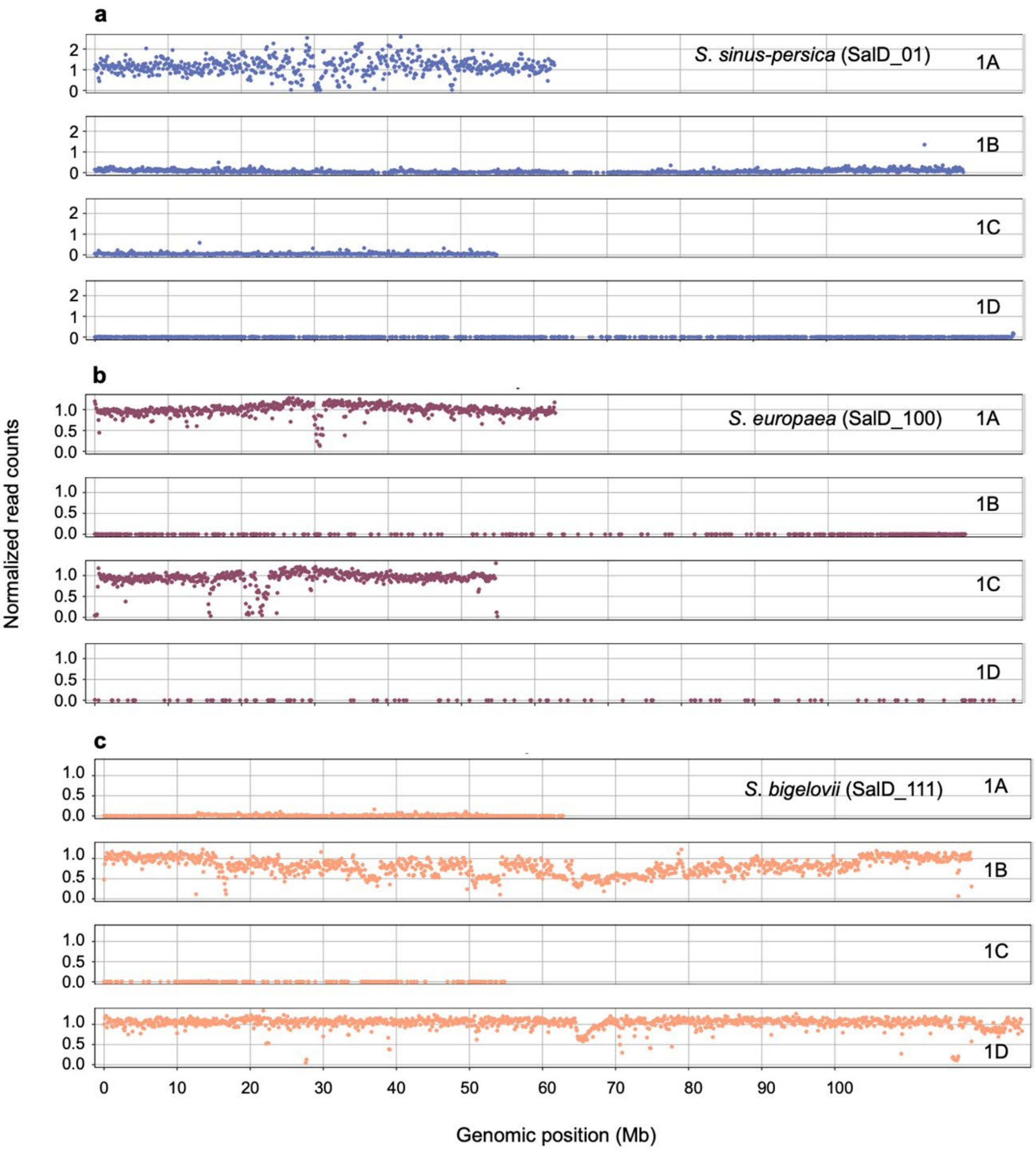
Extended Data Fig. 6. Dot plots of paralogues in the genomes of *S. europaea* (Israel), *S. persica ssp. iranica*, *S. brachiata* and *S. sinus-persica*, highlighted WGT-γ (1:3 relationships shown in black boxes). C denotes chromosome.



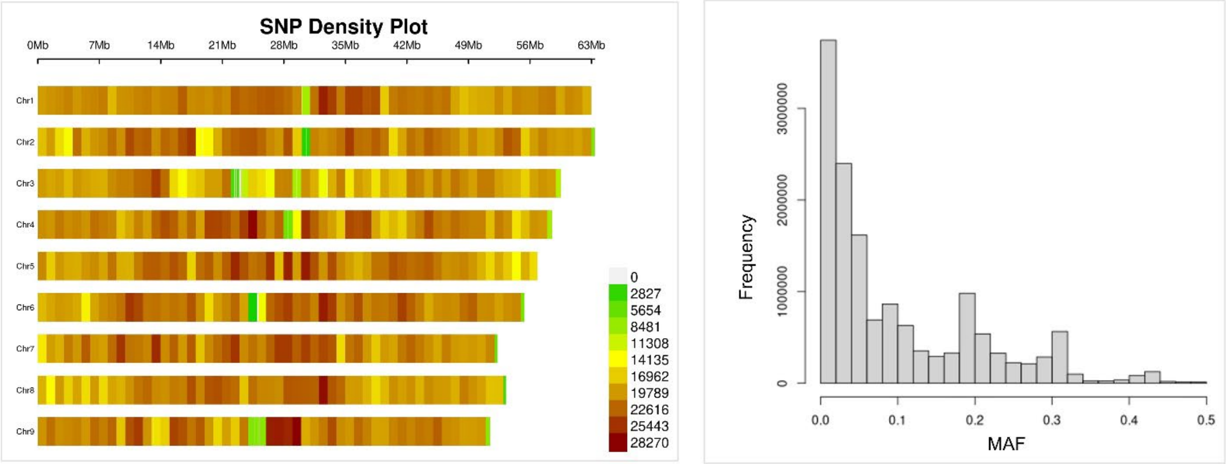
Extended Data Fig. 7. Unrooted Neighbor-joining (NJ) tree of *Salicornia* and related species based on *k-mer* analysis. Branch tips are labeled with the corresponding SalD_# accession identifiers. Distinct clades and subclades are highlighted and annotated according to species. Accessions marked with () represent putative *S. persica iranica* that were genetically distinct from the rest of the group. Accessions labeled with # represent putative diploid *S. europaea* or *S. procumbens* from the Netherlands, while those marked with ($) represent putative *S. europaea* from China. 'Sar.' refers to the genus Sarcocornia.



Extended Data Fig. 8. Principal component analysis (PCA) of *Salicornia* species based on *k-mer* data, showing the first two principal components (PC1 and PC2). Individual accessions are represented by colored shapes grouped according to species designation and genome composition.



Extended Data Fig. 9. Normalized read counts of different *Salicornia* species mapped to a combined reference genome of two tetraploids, *S. europaea* and *S. bigelovii*, showing chromosome 1 of different subgenomes. Normalized read count of 1 indicates two normal copies of the chromosome; 0.5 indicates a single copy; and 0 indicates a nullisomic condition. a: SalD-01, a diploid *S. sinus-persica* from KSA. b: SalD_100, a tetraploid *S. europaea* from France. c: SalD_111, a tetraploid *S. bigelovii* from the USA.



Extended Data Fig. 10. The genome-wide distribution of SNPs among diploid *Salicornia* species, measured using 1 Mb bins (left panel), and the distribution of minor allele frequency (MAF) across the same diploid species (right panel).