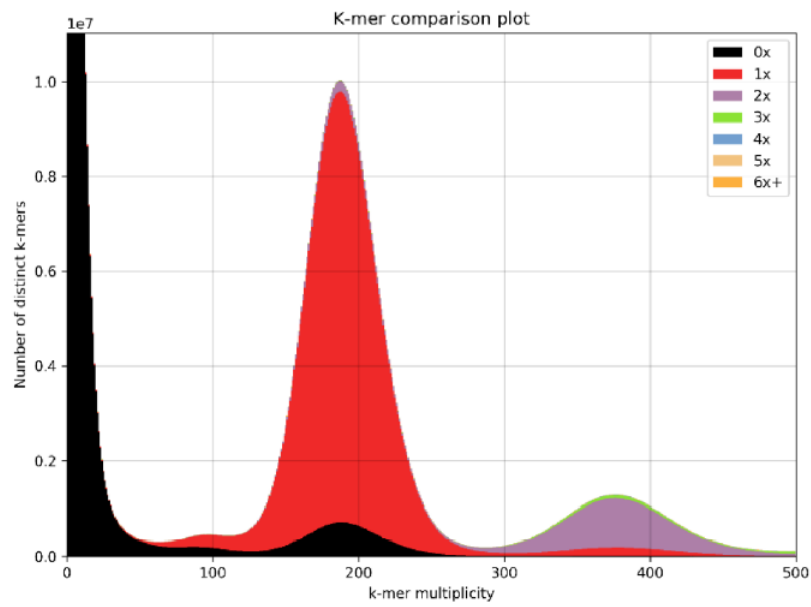
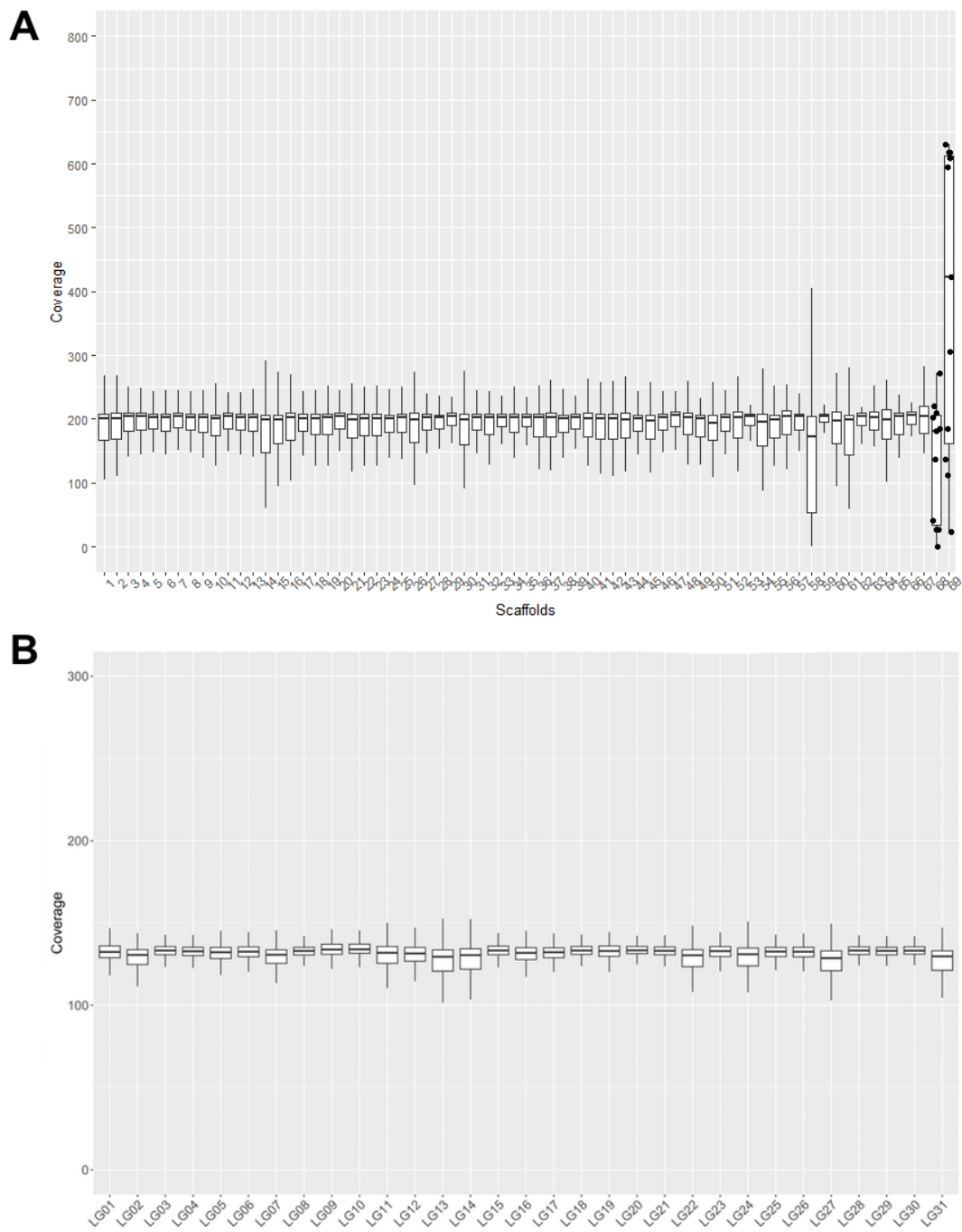


**On the way to diploidization and unexpected ploidy in the grass *Sporobolus*
section *Spartina* mesopolyploids**

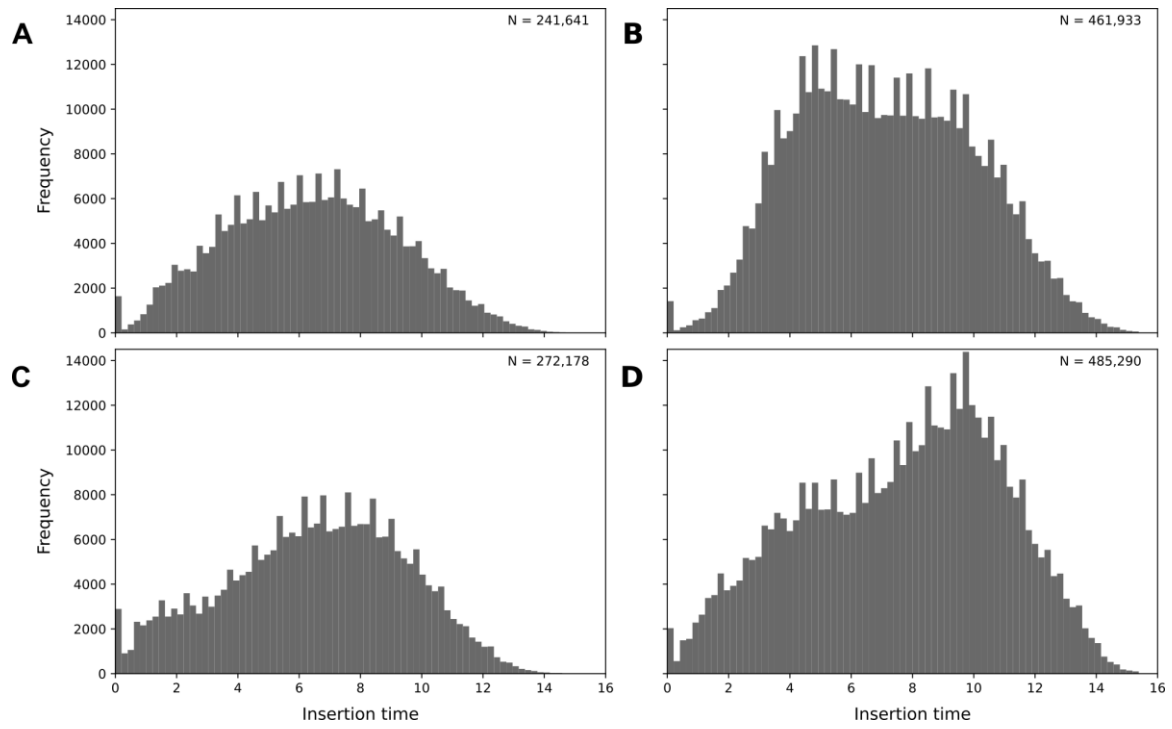
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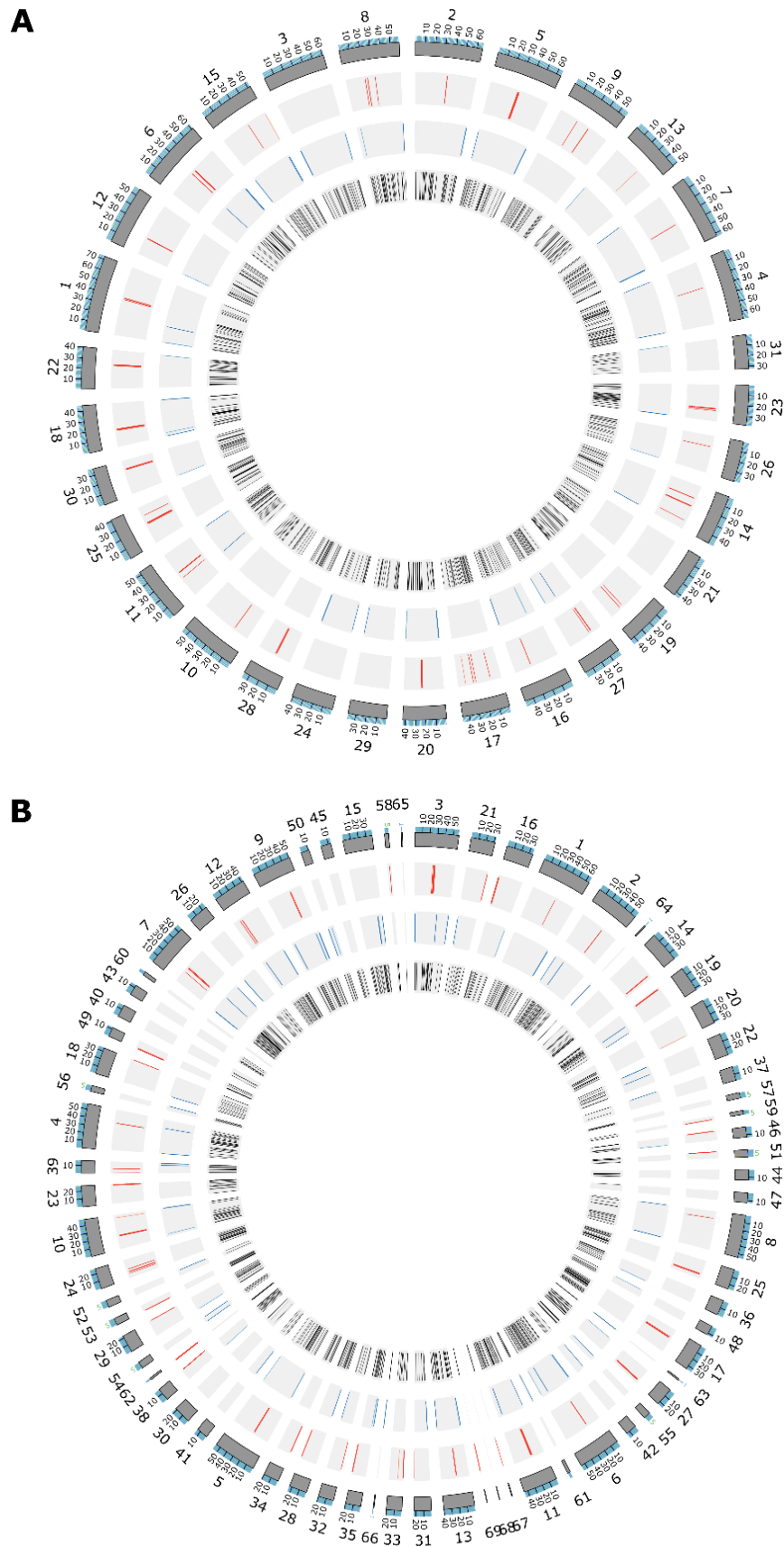
Supplementary Figure 1. K-mer (31-mers) distribution in the *S. maritimus* genome.



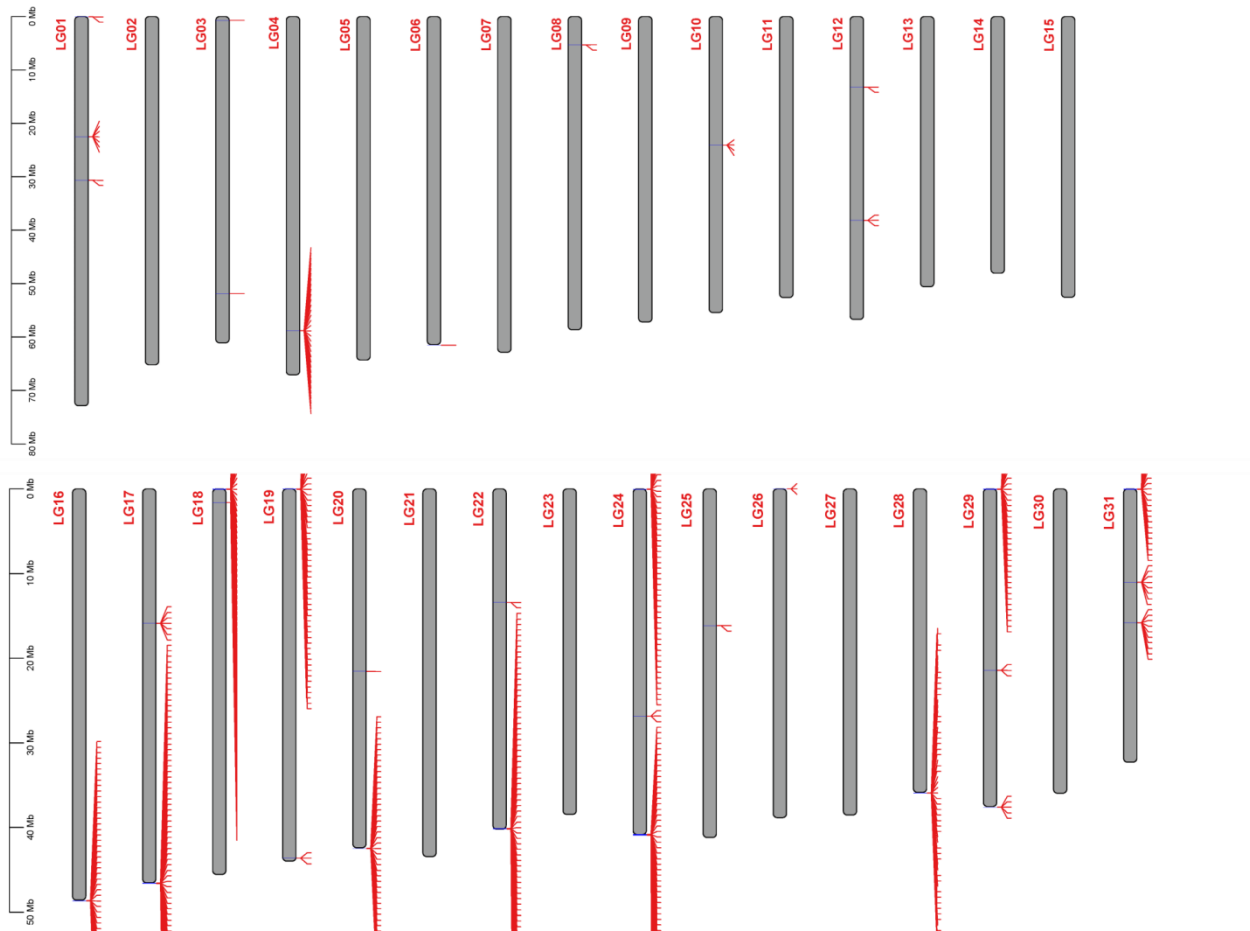
Supplementary Figure 2. Illumina reads mapping and coverage across genomes within 50kb sliding windows. (A) *S. maritimus* and (B) *S. alterniflorus*.



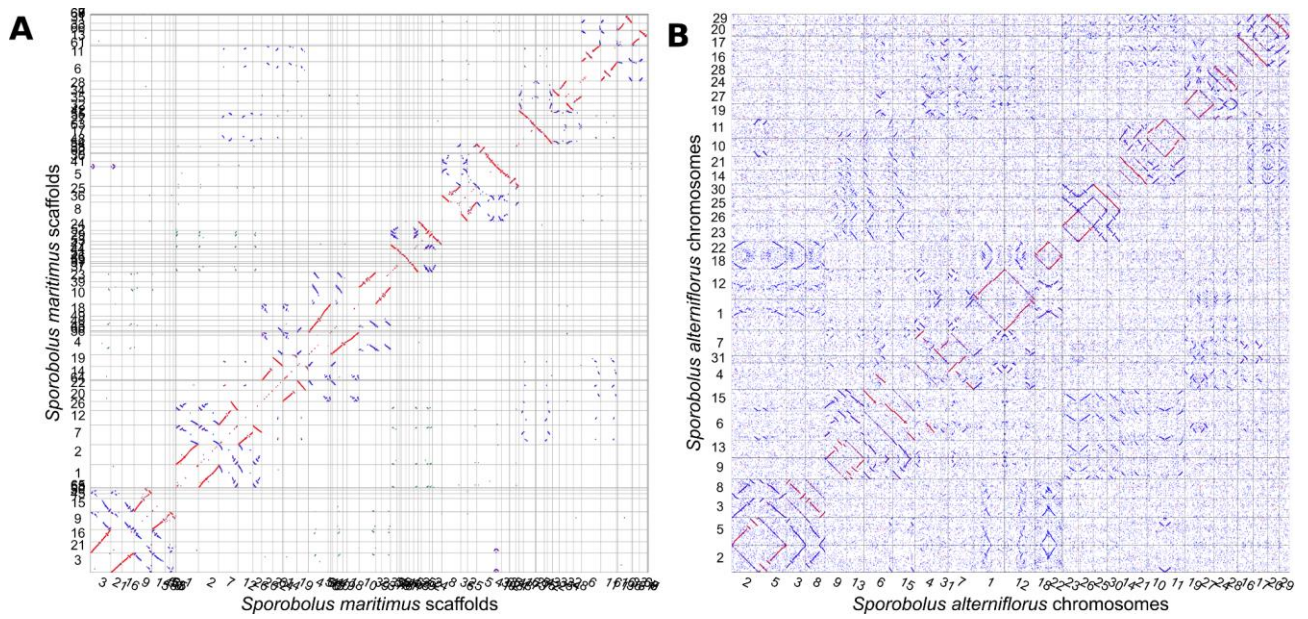
Supplementary Figure 3. Distribution of Class I-LTR retrotransposon insertions. (A) *S. maritimus* Copia; (B) *S. maritimus* Gypsy; (C) *S. alterniflorus* Copia; (D) *S. alterniflorus* Gypsy.



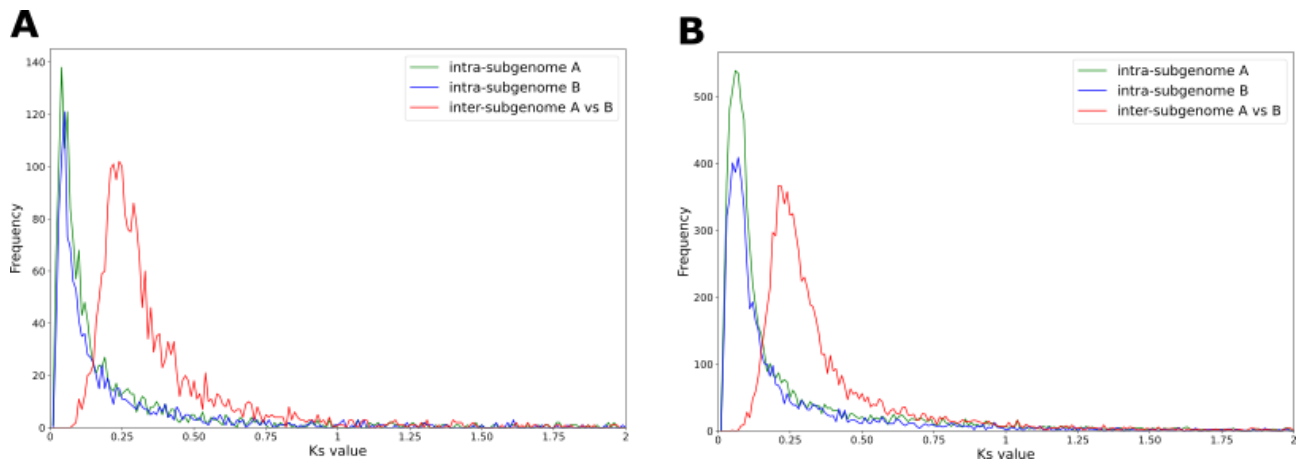
Supplementary Figure 4. Distribution of High Order Repeats (HORs). (A) *S. alterniflorus* and (B) *S. maritimus*. The two most represented HORs are illustrated in external circles (the 146-147bp HOR is represented as red tiles, the 168-169bp as blue tiles), all detected HORs are represented as black tiles in internal circles.



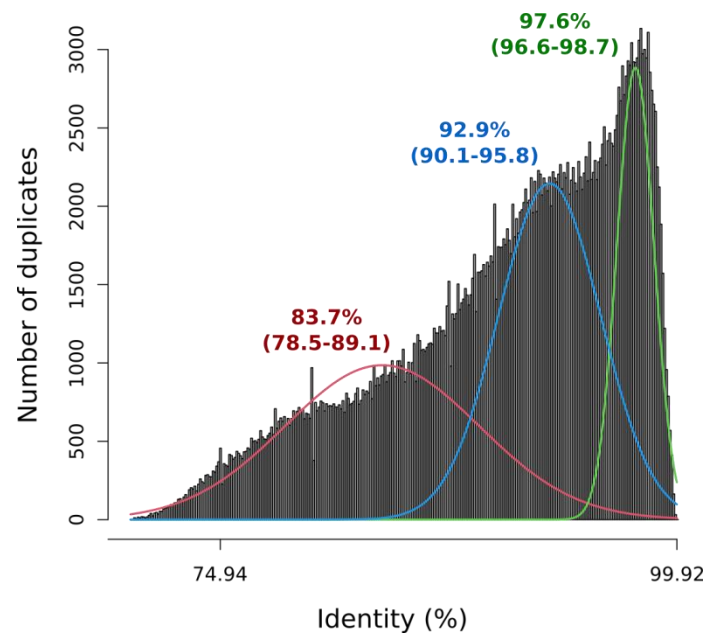
Supplementary Figure 5. Distribution of the 370-bp satellite repeat across the *S. alterniflorus* genome.



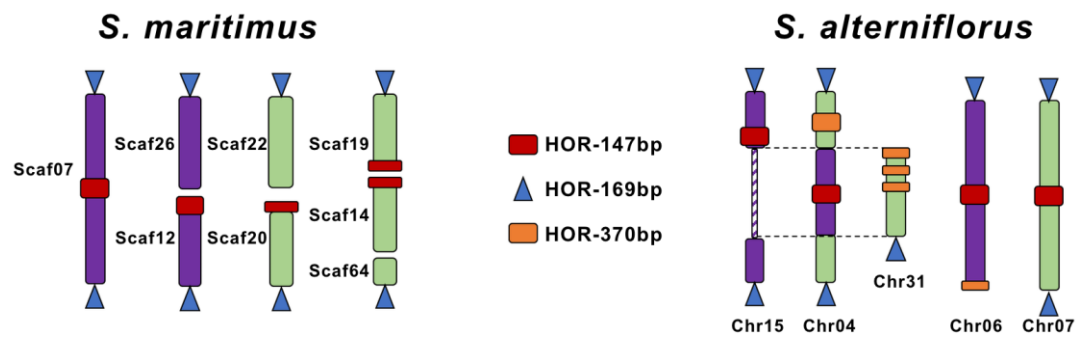
Supplementary Figure 6. Dotplot comparisons within *S. maritimus* and *S. alterniflorus* assembled genomes. (A) *S. maritimus* x *S. maritimus* (B) *S. alterniflorus* x *S. alterniflorus*. Ks values were used to color the dots, in (A): red (0.01-0.1), blue (0.1-0.3) and green (0.3-3); in (B): red (0.01-0.1) and blue (0.1-3). *S. maritimus* scaffolds are ordered as following: 3, 21, 16, 9, 15, 45, 50, 58, 65, 1, 2, 7, 12, 26, 20, 22, 64, 14, 19, 4, 56, 60, 43, 40, 49, 18, 10, 39, 23, 37, 57, 59, 46, 51, 44, 47, 53, 29, 52, 24, 8, 36, 25, 5, 41, 30, 62, 38, 54, 48, 17, 63, 27, 55, 42, 32, 35, 34, 28, 6, 11, 61, 13, 66, 33, 31, 67, 68, 69.



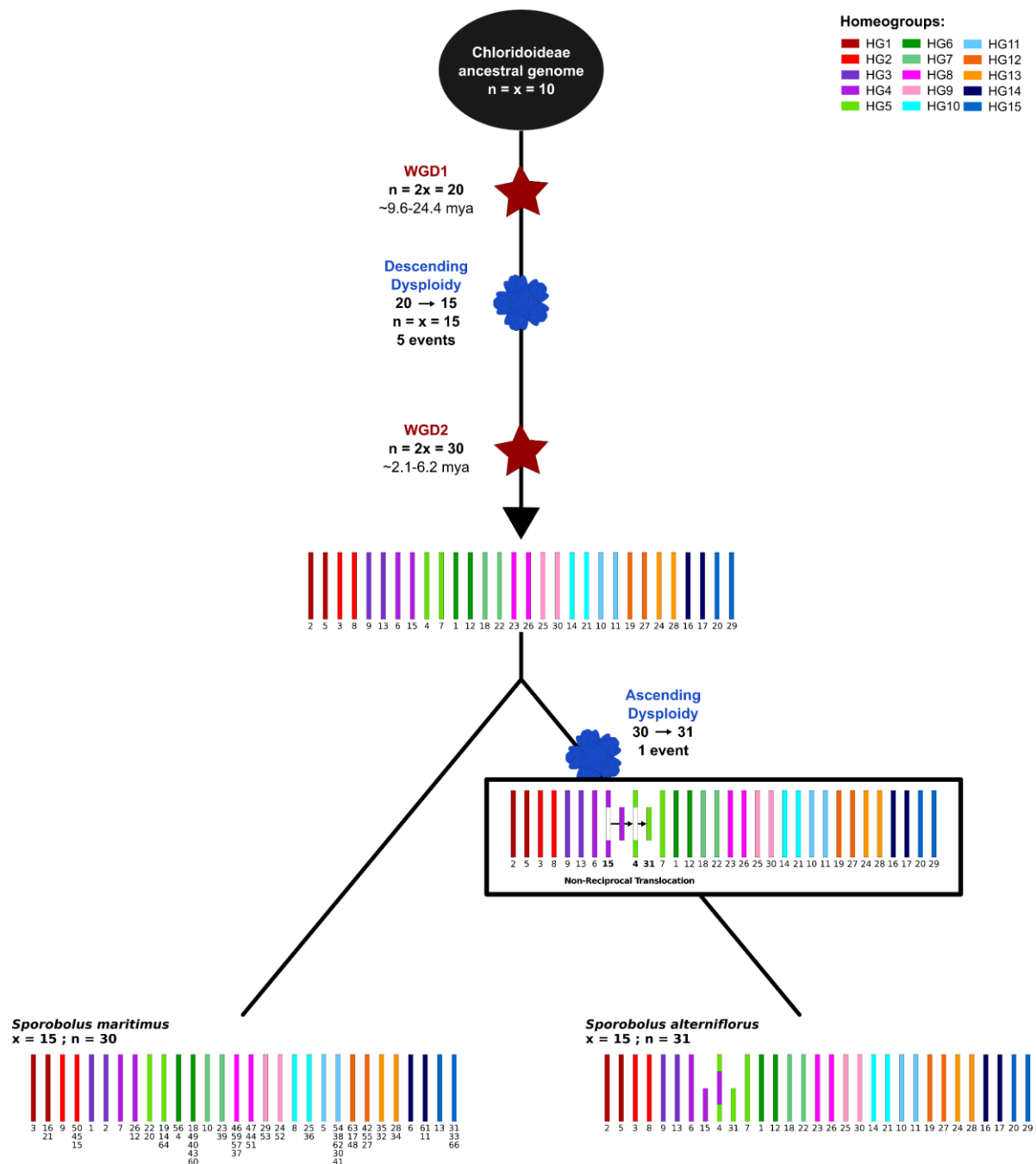
Supplementary Figure 7. Ks distributions between homeogroups 8 (A subgenome) and 9 (B subgenome). (A) comparisons of homeologous gene pairs within *S. maritimus* and (B) orthologous gene pairs between *S. maritimus* and *S. alterniflorus*. A versus B subgenomes in red; A1 vs A2 subgenomes in green and B1 vs B2 subgenomes in blue.



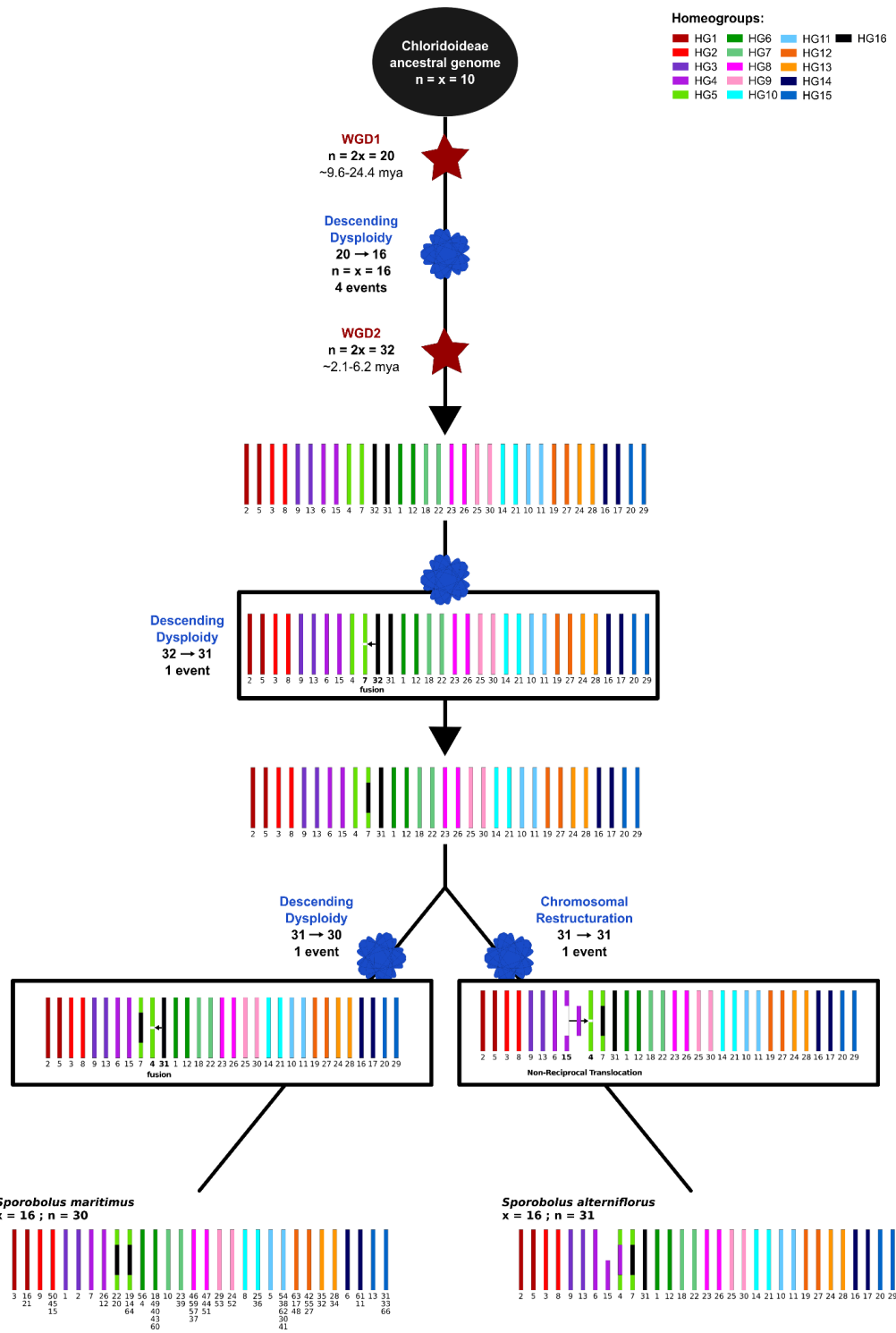
Supplementary Figure 8. Distribution of genetic identities between *S. maritimus* and *S. alterniflorus* genes (RBH dataset, N=356,305). Peak modes and range values were estimated by mixtools.



Supplementary Figure 9. Distribution of high order repeats (HORs) in chromosomal regions restructured between *S. maritimus* and *S. alterniflorus*.



Supplementary Figure 10. First hypothesis regarding karyotype evolution in *S. maritimus* ($n=30$) and *S. alterniflorus* ($n=31$) species. Chromosomes are numbered using *S. alterniflorus* as a reference, and corresponding scaffold numbers are indicated for *S. maritimus*: Evolution from $n=30$ (ancestral) to $n=31$ (derived): this could be achieved by base chromosome number reduction from $n=20$ to $n=15$ between WGD1 and WGD2, followed by non-reciprocal translocation (between chromosomes 15 and 4) leading to an additional chromosome pair (31) which accompanied speciation. Total: 6 evolutionary events.



Supplementary Figure 11. Second hypothesis regarding karyotype evolution in *S. maritimus* ($n=30$) and *S. alterniflorus* ($n=31$) species. Chromosomes are numbered using *S. alterniflorus* as a reference, and corresponding scaffold numbers are indicated for *S. maritimus*: Evolution from $n=31$ (ancestral) to $n=30$ (derived): this could be achieved by chromosome number reduction from $n=20$ to $n=16$ between WGD1 and WGD2, followed by fusion of chromosomes (32 and 7) in the ancestral genome of *S. maritimus* and *S. alterniflorus*. An additional chromosome fusion (involving chromosomes 31 and 4) would result in $n=30$ observed in *S. maritimus*. However, as synteny analysis shows chromosomal restructuring in *S. alterniflorus*, this scenario requires an additional translocation compared to the first hypothesis presented in the supplementary figure 10 (between chromosomes 15 and 4) occurring independently in this species. Total: 7 evolutionary events, affecting recurrently the same ancestral 4-7 (in both species) and 31-32 (in *S. maritimus*) chromosomes.

Supplementary Table 1. Summary of *S. maritimus* genome assembly.

	Final assembly (scaffolds)	Final assembly (contigs)
Cumulative size (bp)	1,594,960,029	1,562,213,943
# sequences	69	2,396
N50 (L50)	34,729,896 bp (17)	1,097,494 bp (421)
N90 (L90)	13,196,519 bp (45)	297,550 bp (1,456)
N's (bp)	32,746,086 (2.05%)	
BUSCO	Complete	1,381 (95.9%)
	Dup.	775 (53.8%)
	Frag.	17 (1.2%)
	Missing	42 (2.9%)

Supplementary Table 2. Repeated sequences in the *S. alterniflorus* and *S. maritimus* genomes.

Type of repeat	<i>S. alterniflorus</i>		<i>S. maritimus</i>	
	Total length (bp)	Genome coverage (%)	Total length (bp)	Genome coverage (%)
Class I	1,028,605,270	63.06	716,658,281	44.94
Class I <i>LINE-RTE</i>	37,430,641	2.29	19,219,557	1.21
Class I LTR <i>Copia</i>	273,425,343	16.76	180,343,329	11.31
Class I LTR <i>Gypsy</i>	571,349,199	35.03	512,017,552	32.11
Class I SINE	101,508	0.01	2,091,767	0.14
Class II	124,255,447	7.62	101,389,039	6.36
Class II <i>Helitron</i>	8,676,297	0.53	3,660,732	0.23
Class II TIR	110,532,681	6.78	74,212,614	4.66
Class II Unknown	3,356,105	0.21	9,277,364	0.59
Potential Host Gene	2,373,395	0.15	21,022	0.01
370-bp satellite	29,358,629	1.80	351,385	0.03
SSR	780,298	0.05	36,549,738	2.30
Unknown	95,966,815	5.88	79,398,167	4.98
Total	1,192,775,858	73.13	946,021,093	59.31