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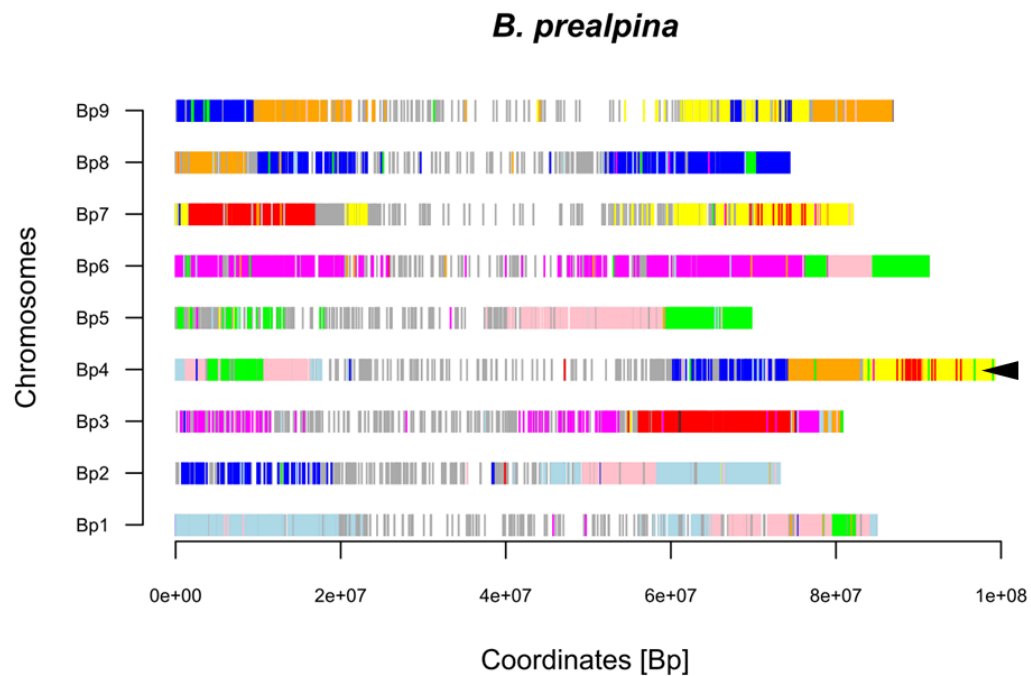
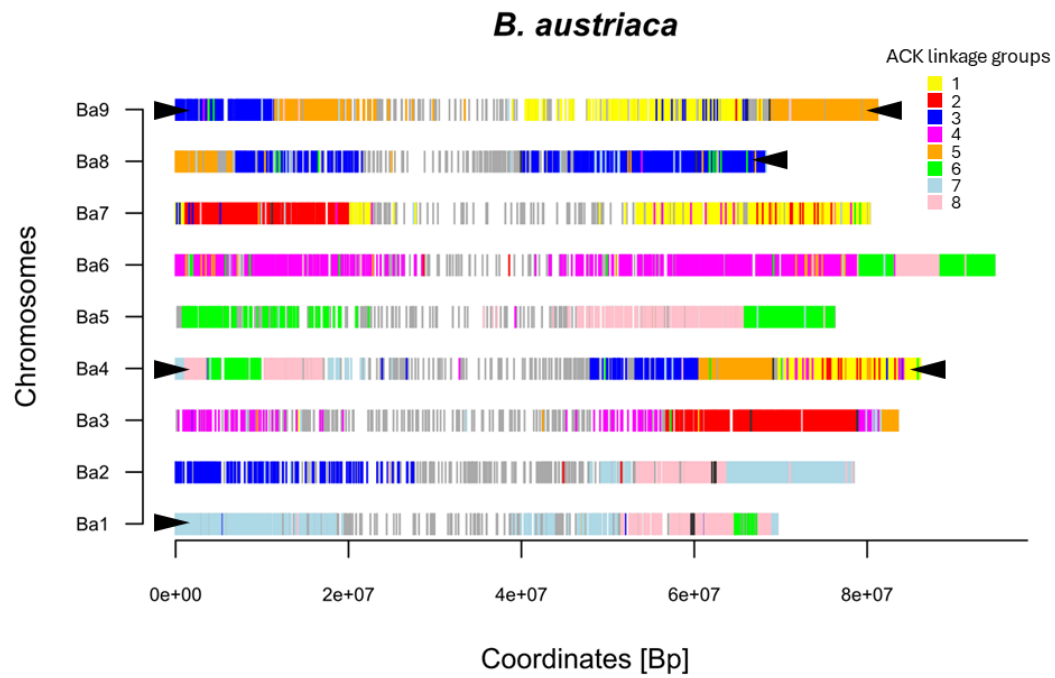
Supplementary Table S6. Abundance of LTR retrotransposons clades.

Supplementary Table S7. Abundance and distribution of the 20% most abundant CRM families.

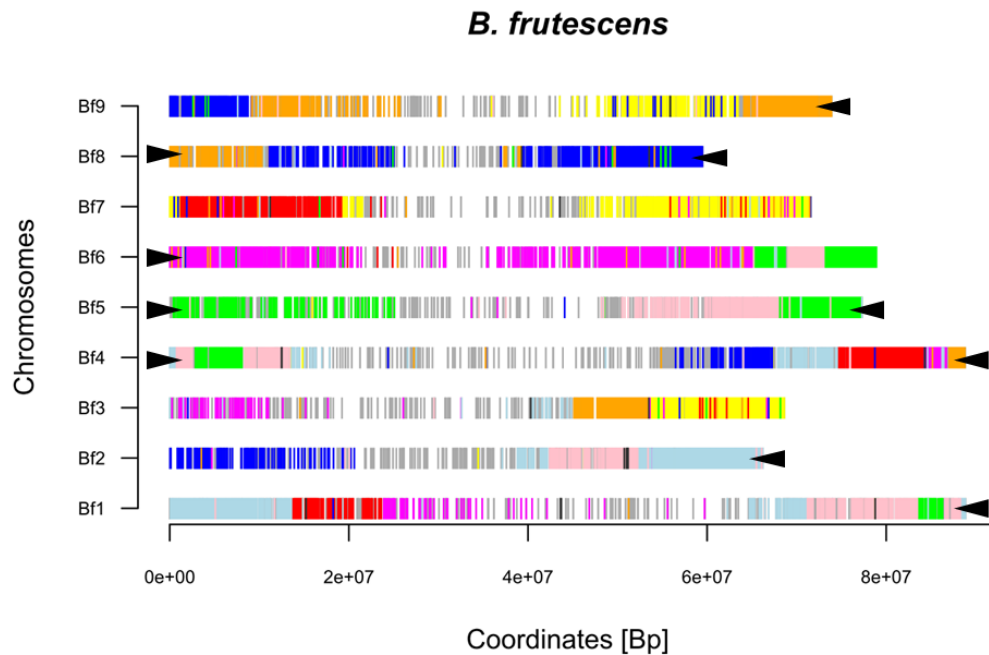
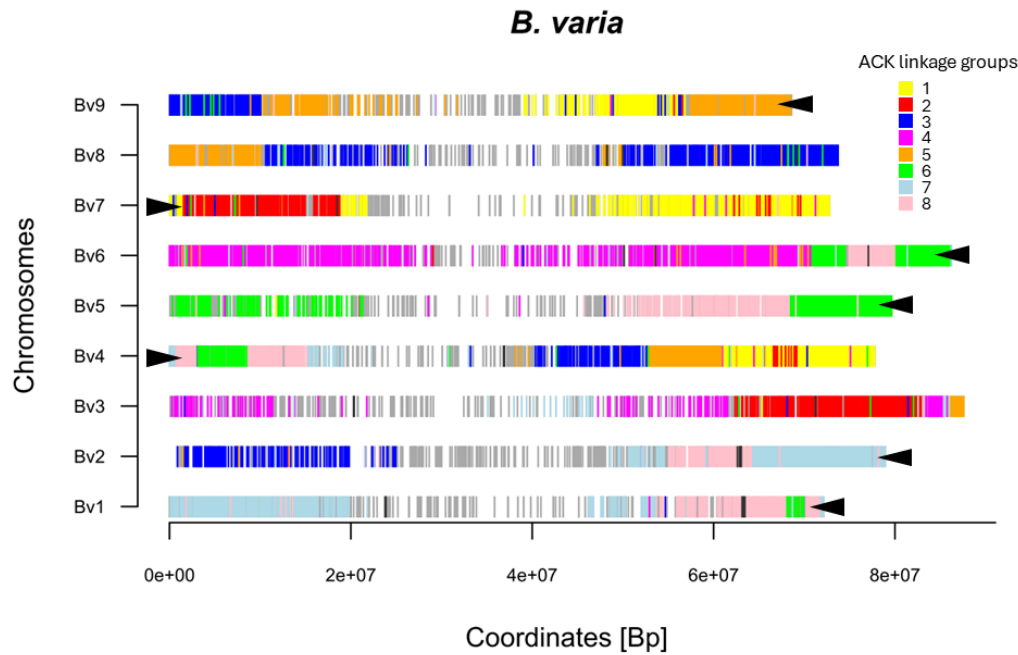
Supplementary Table S8. Abundance and distribution of the 20% most abundant Athila families.

Supplementary Table S9. Abundance and distribution of 20% most abundant pericentromeric TE families.

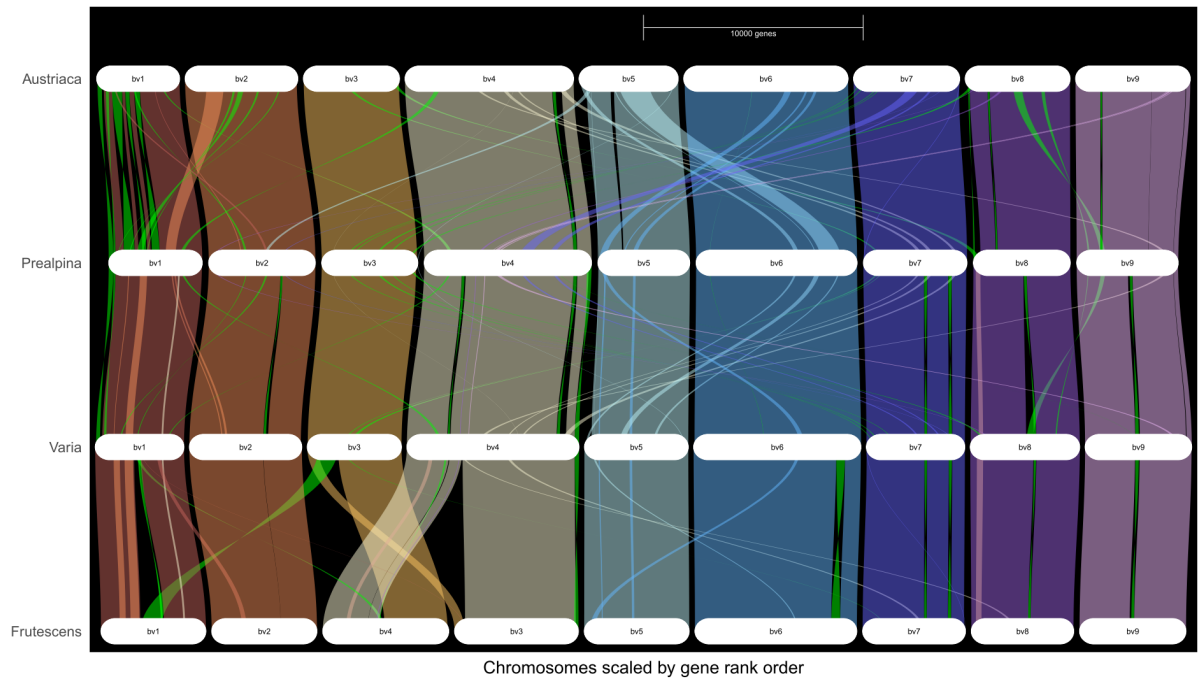
Supplementary figures



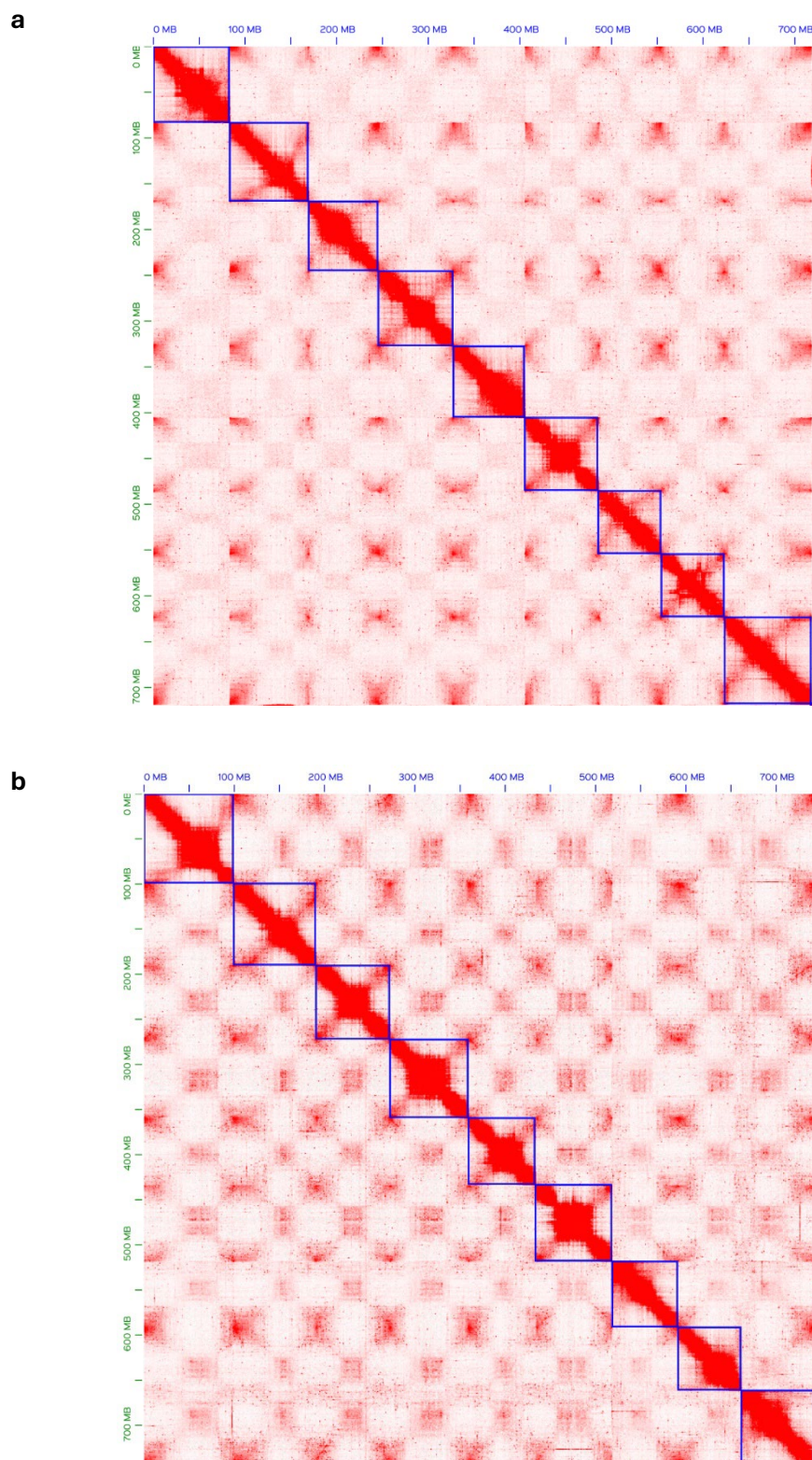
Supplementary Figure S1. See complete legend on the next page.



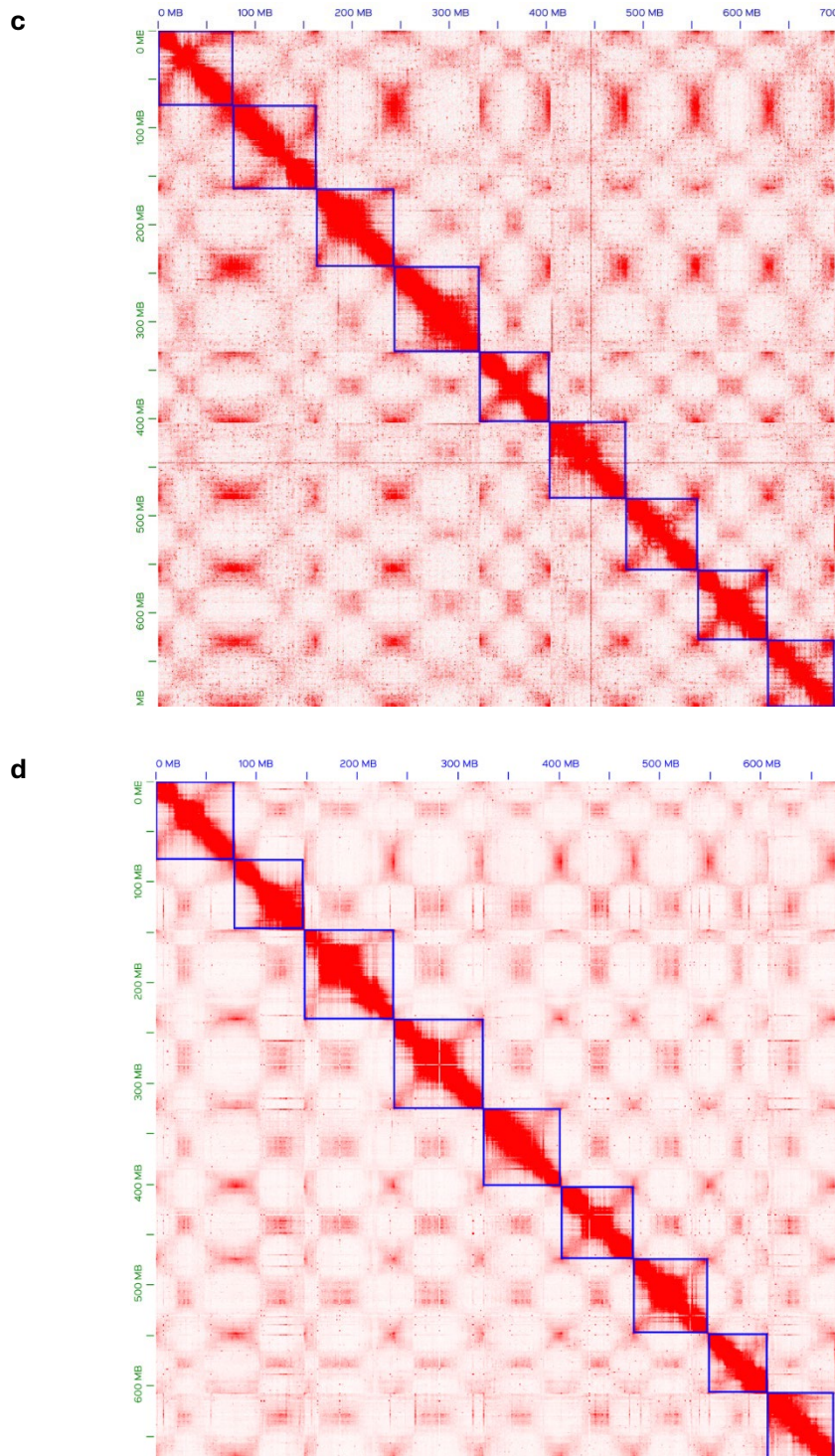
Supplementary Figure S1. *In-silico* chromosome painting. Genes are plotted along the chromosome length and coloured based on syntenic analysis against *Arabidopsis thaliana* and according to their positions in the ancestral crucifer karyotype (ACK) linkage groups. Non-syntenic genes (indicated in grey) mark the boundaries between pericentromeres and chromosome arms. *B. laevigata* species (*B. varia*, *B. austriaca*, *B. prealpina*) share the same chromosomal structure. Large scale chromosomal rearrangements are found between chromosomes 1,3 and 4 of *B. laevigata* species and *B. frutescens*. Triangles indicate the presence of telomeric repeats.



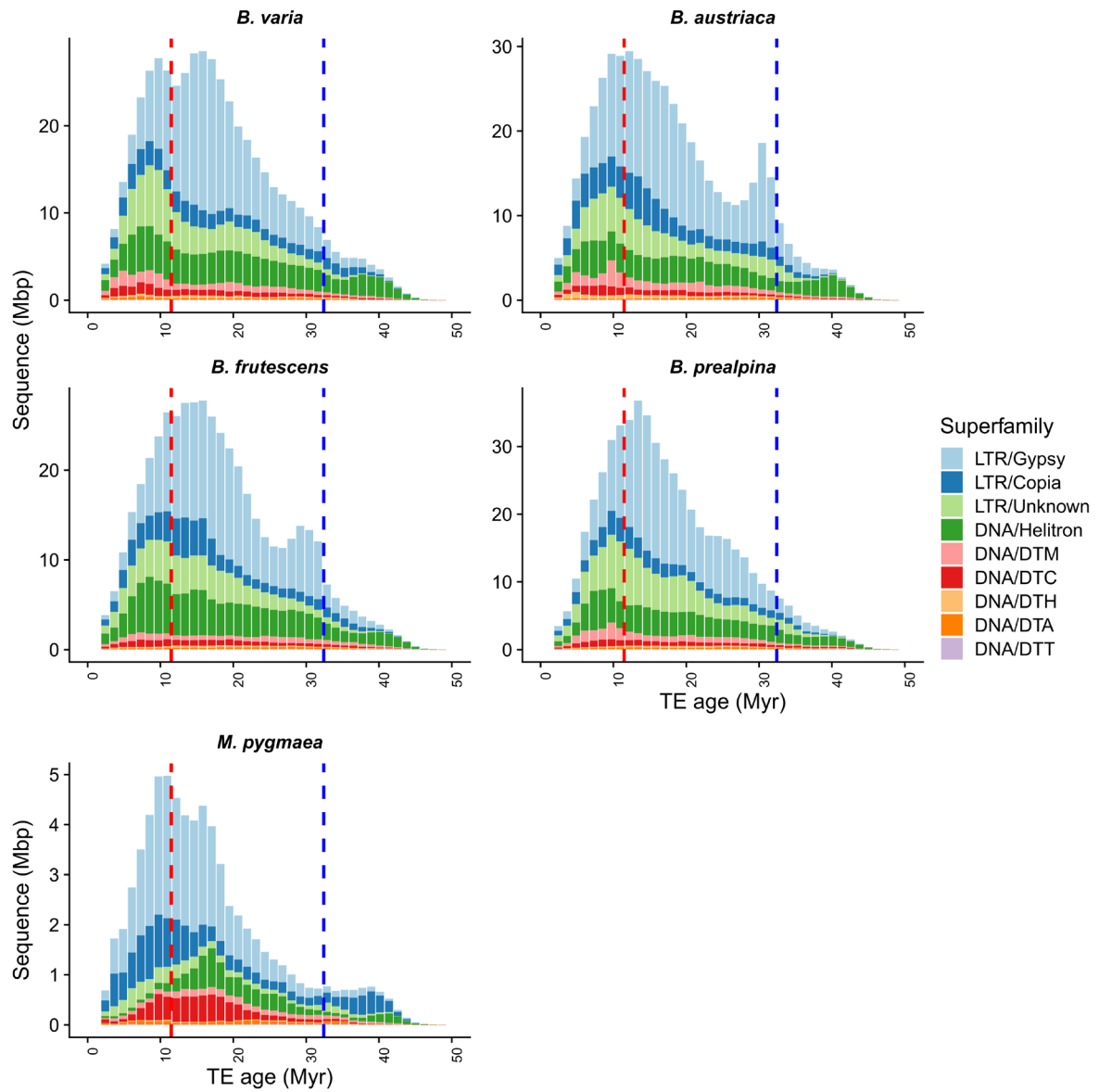
Supplementary Figure S2. Analysis of syntenic orthologous genes across *Biscutella* species. The GENESPACE pipeline was used for the analysis. The plot shows syntenic relationships between chromosomes and large-scale rearrangements between chromosomes 1,3, and 4 of *B. laevigata* species and *B. frutescens*. Inversions are highlighted in green.



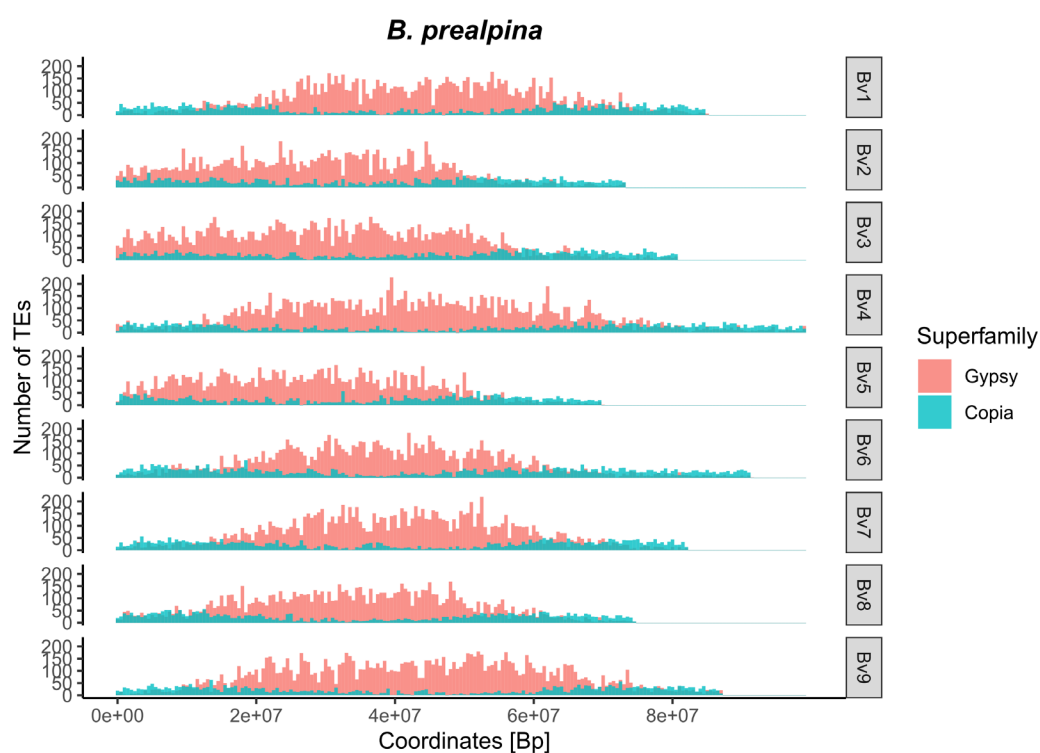
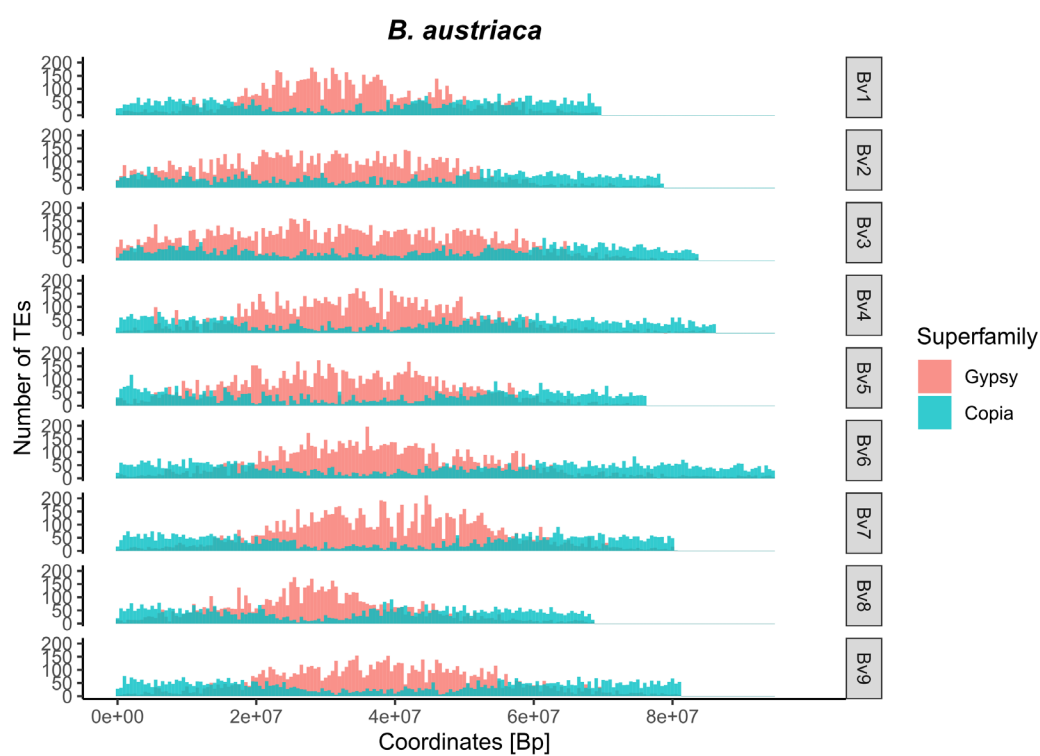
Supplementary Figure S3. See complete legend on the next page.



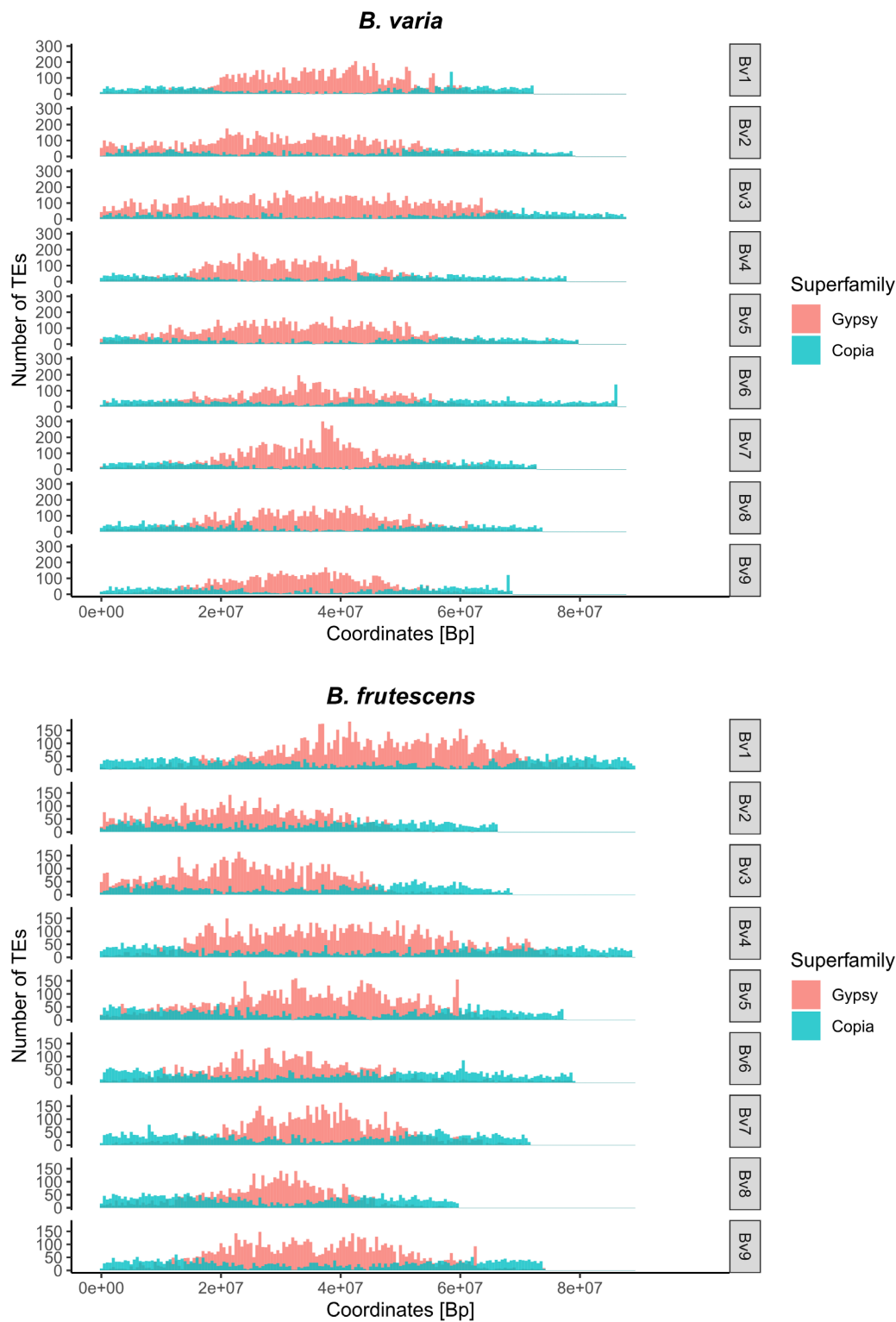
Supplementary Figure S3. Manually curated Hi-C interaction matrix of **(a)** *B. austriaca*, **(b)** *B. prealpina*, **(c)** *B. varia*, and **(d)** *B. frutescens*. Blue boxes indicate the nine main scaffolds (i.e. chromosomes). Anti-diagonal interactions, as well as inter-chromosomal interactions within telomeres and centromeres, suggest a Rabl organization of the chromosomes. Short arms of nucleolar chromosomes 2 and 3 are heterochromatic, a phenomenon probably explained by the presence of nucleolar organizer region (NOR). NOR is known to induce the association of the proximal telomere and centromere with the nucleolus.



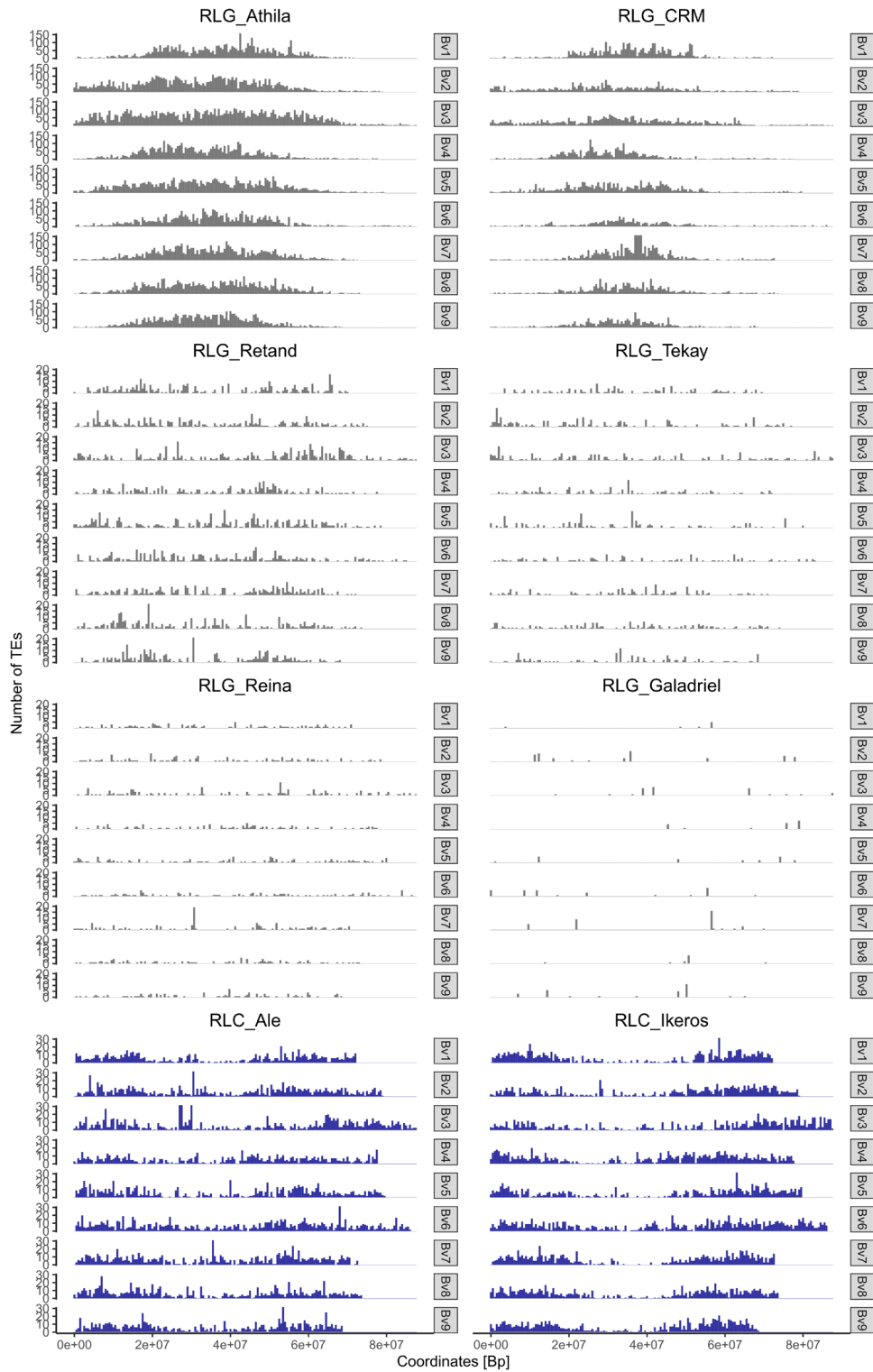
Supplementary Figure S4. Dynamics of transposable element (TE) superfamilies in *Biscutella laevigata* species (*B. varia*, *B. austriaca*, *B. prealpina*), *B. frutescens*, and the outgroup species *Megadenia pygmaea*. The sequence divergence between TE copies and the family consensus sequence was utilized to date the insertion time (age) in million years. The Y-axis represents the amount of genome space (Mb) covered by TE superfamilies of different ages, indicating potential peaks of activity. Dotted lines denote the α (~32.5 mya; blue) and the BL-m (~11.5 mya; red) whole genome duplication events (WGDs). Compared to *Biscutella* species, *M. pygmaea* did not undergo BL-m-WGD event and is therefore considered as the “true” diploid outgroup species of the *Biscutella* genus. WGD events are believed to activate TEs transposition. Indeed, in *Biscutella* species we observe a peak of TE activity following BL-m-WGD, which is not observed in *M. pygmaea*.



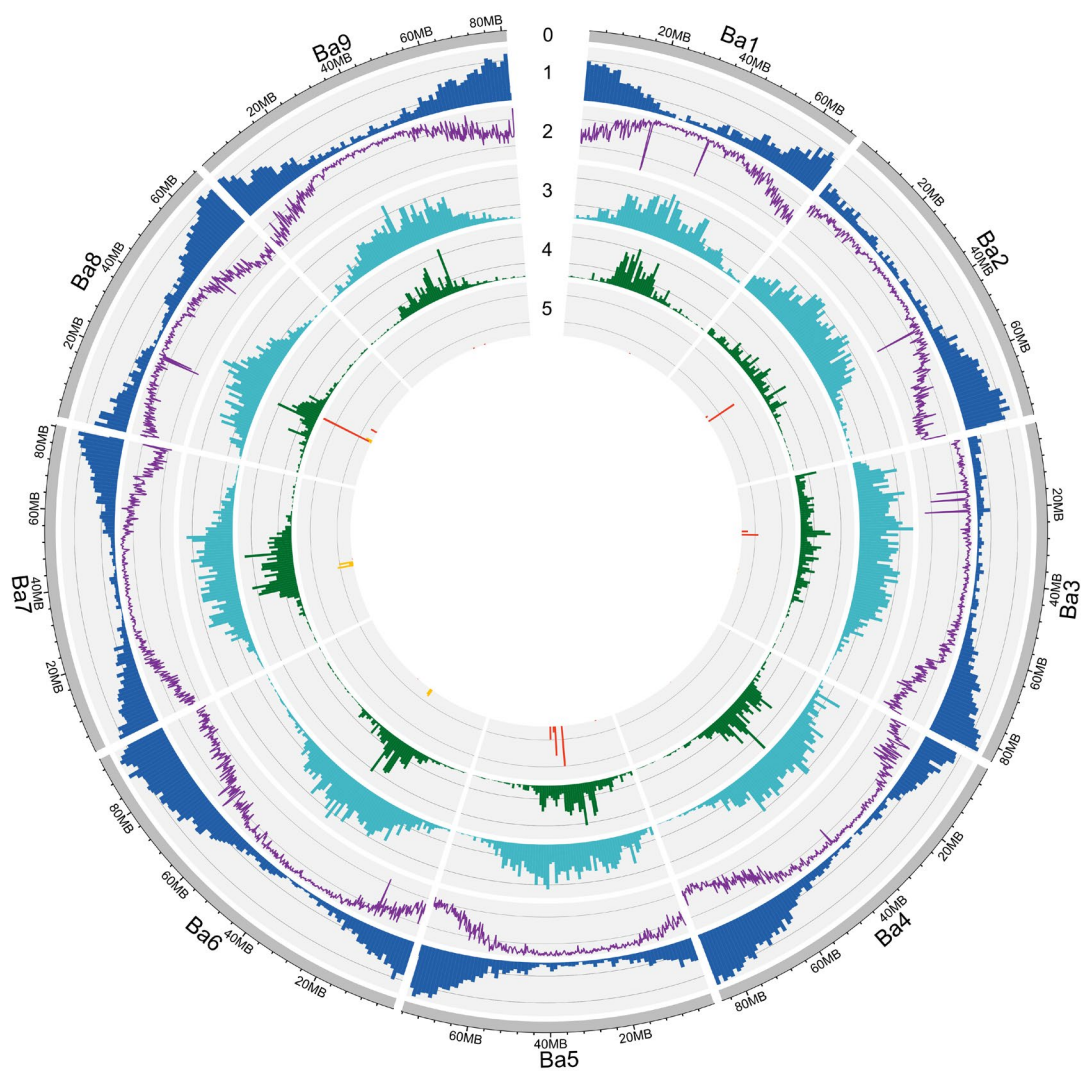
Supplementary Figure S5. See complete legend on the next page.



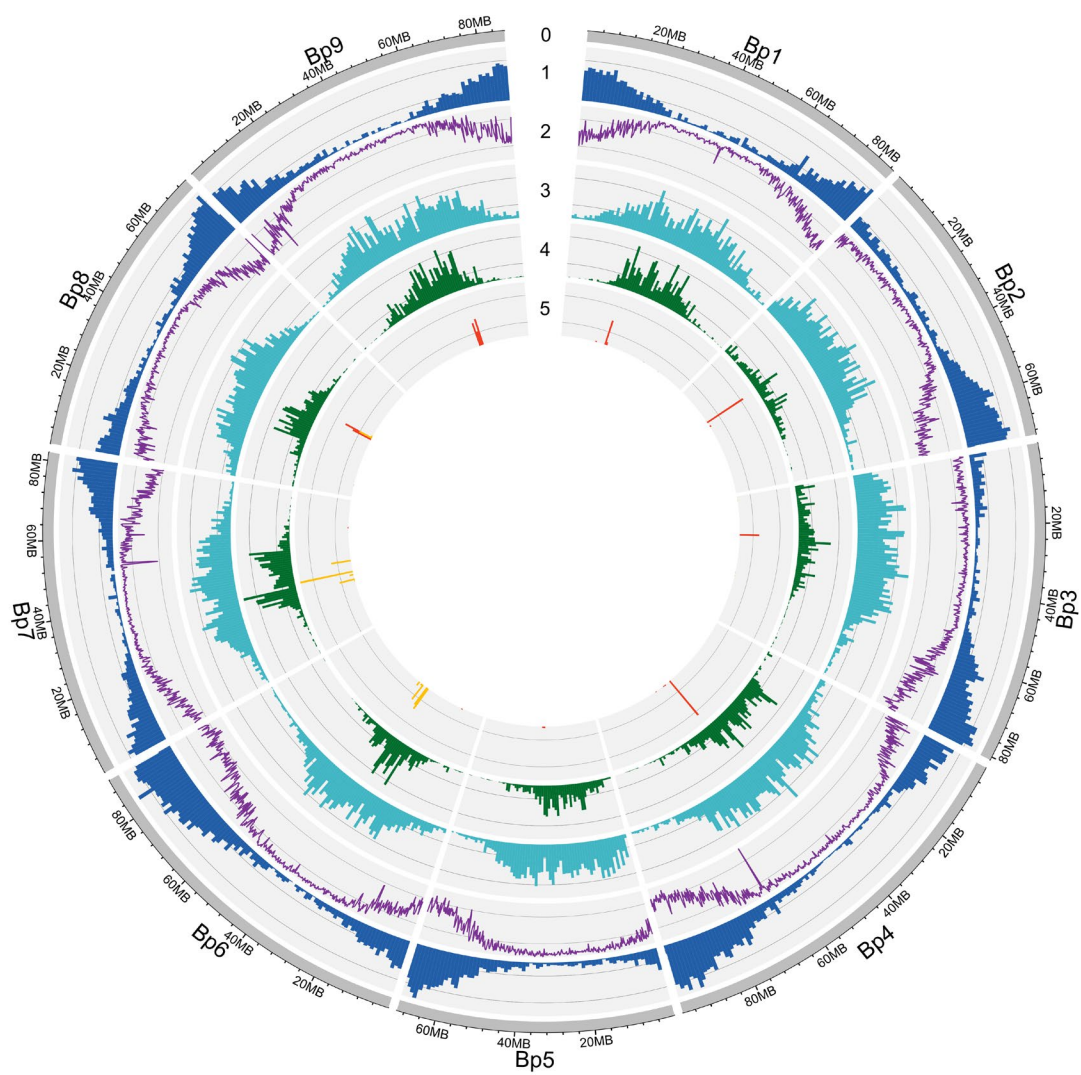
Supplementary Figure S5. Abundance and distribution of long terminal repeat retrotransposons. The two retrotransposon superfamilies show very different patterns, with Gypsy being more abundant and mostly localized in the pericentromeric regions and Copia being more distributed within gene-rich chromosome arms. Only exceptions are nucleolar chromosome arms 2 and 3, where Gypsy elements are evenly distributed between the centromere and the NOR-bearing telomere.



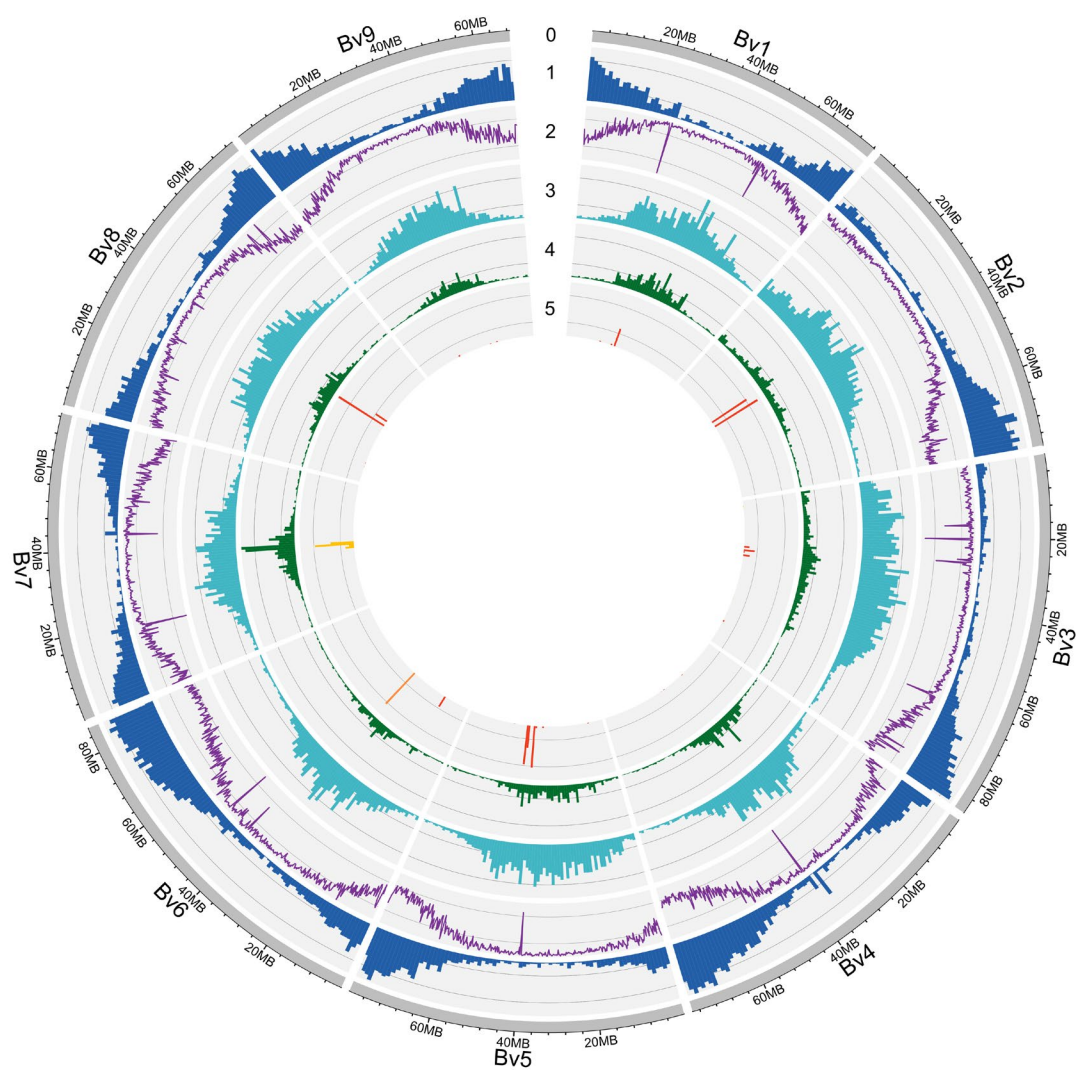
Supplementary Figure S6. Abundance and distribution of TE clades. LTR retrotransposons were assigned to clades using TEsor and the number of TE copies were plotted against the chromosome length. Athila and CRM clades are the most abundant ones (notice difference between y-axis lengths), and also the only TE clades to clearly localize within pericentromeric regions. The two most abundant clades from the Copia superfamily (RLC; depicted in blue) are shown to highlight their contrasting distribution compared to clades from the Gypsy superfamily (RLG).



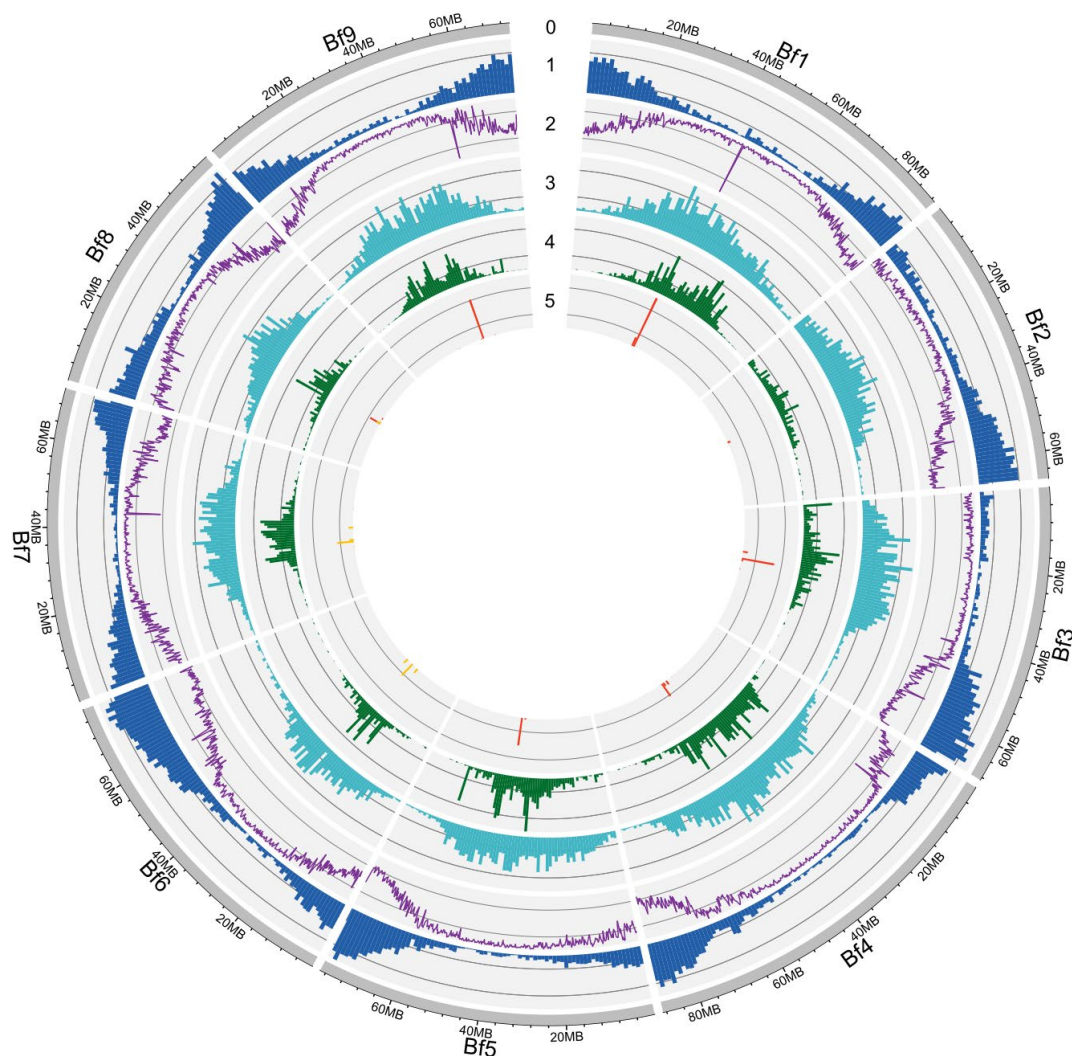
Supplementary Figure S7a. Circos plot of *B. austriaca*. See figure S8d for the complete legend.



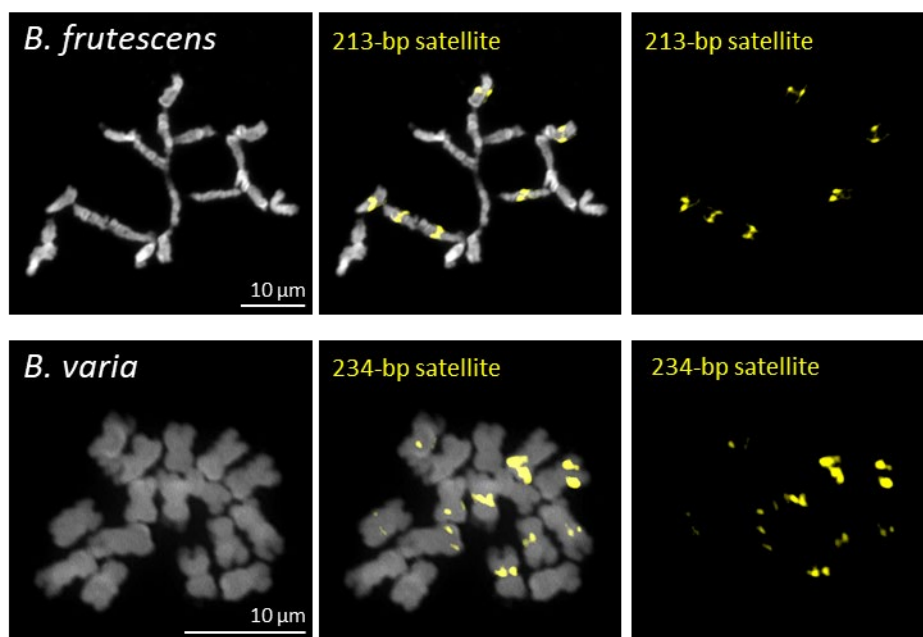
Supplementary Figure S7b. Circos plot of *B. prealpina*. See figure S8d for the complete legend.



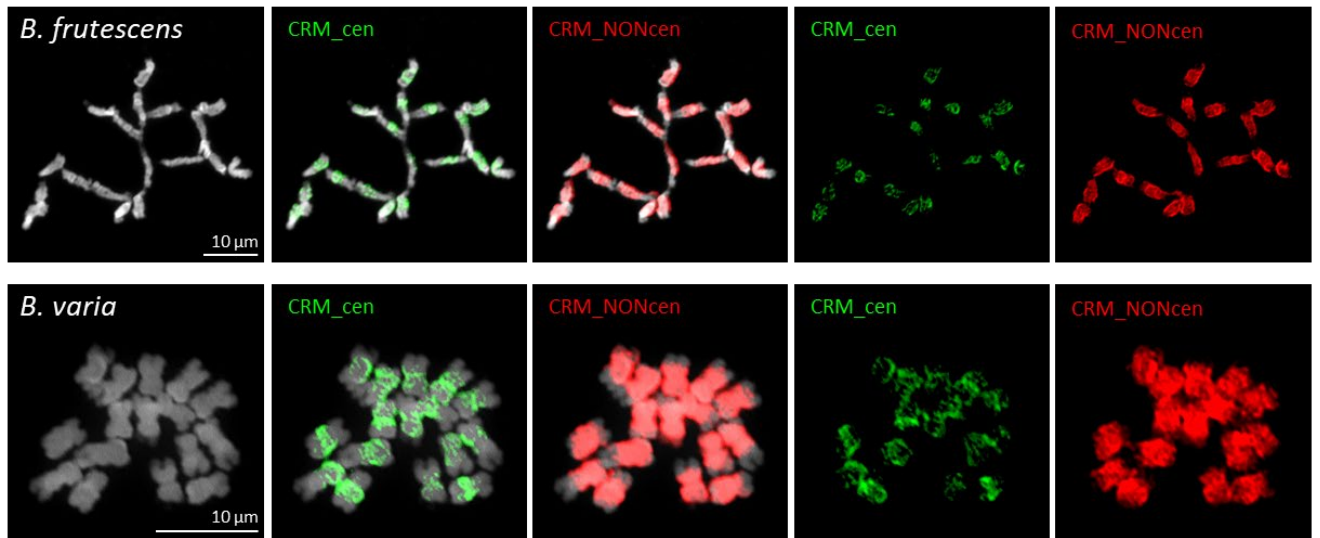
Supplementary Figure S7c. Circos plot of *B. varia*. See figure S8d for the complete legend.



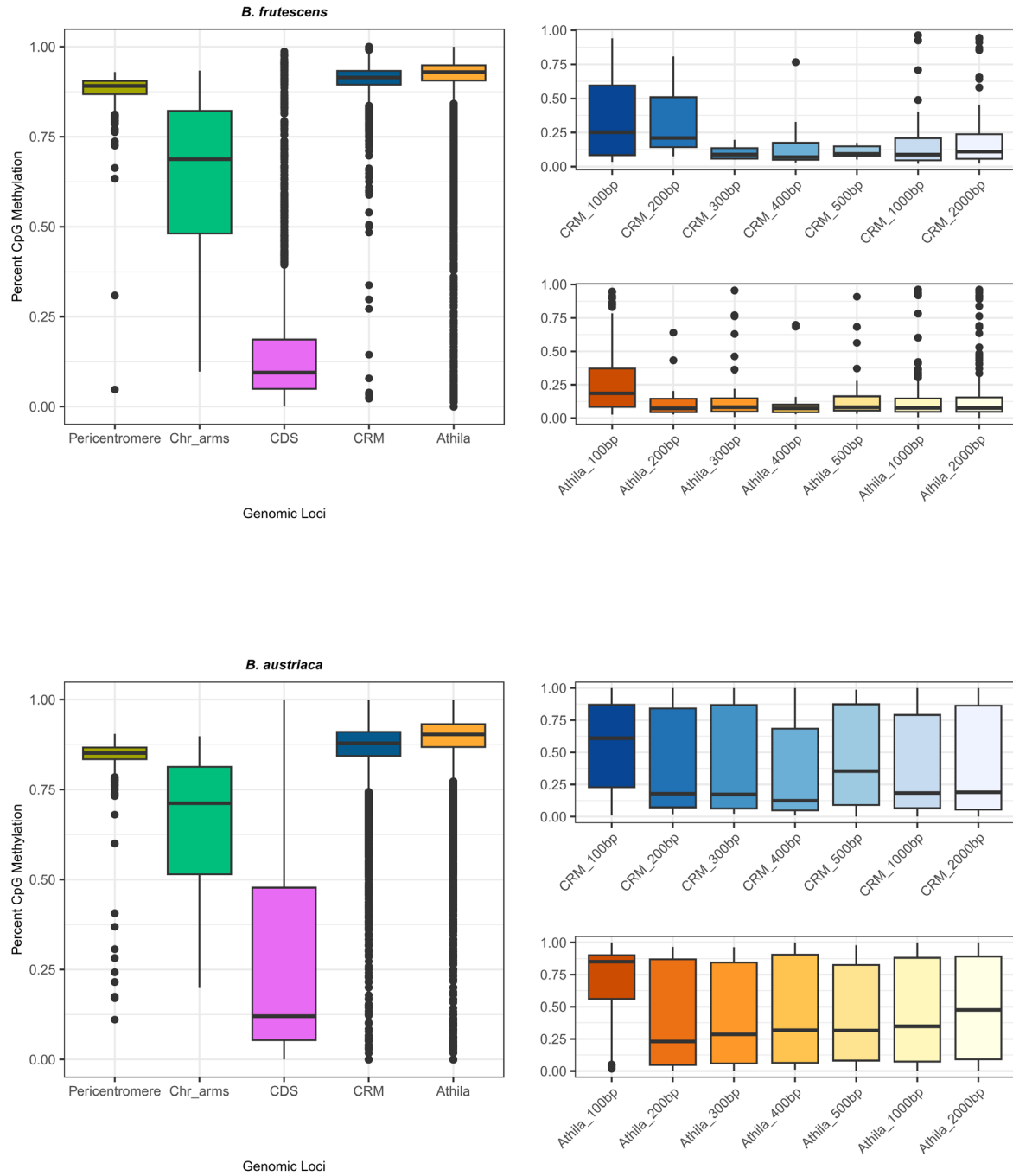
Supplementary Figure S7d. Circos plot of *B. frutescens*. The R/Shiny application shinyCircos was used for generating circos plots of *Biscutella* species. Following features are shown: Genes (track 1), CpG methylation (track 2), pericentromeric retrotransposons from the Athila (track 3) and CRM clades (track 4), and three centromeric satellite DNA sequences (track 5; red: Cent213; yellow: Cent234; orange: Cent405).



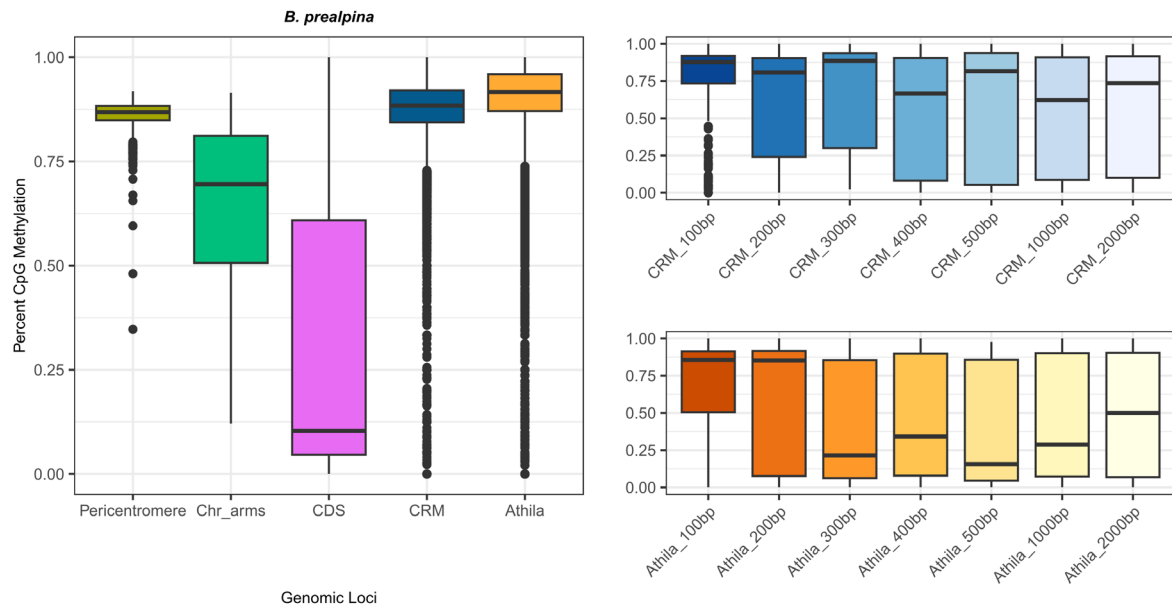
Supplementary Figure S8. *In situ* localization of centromeric satellites. *In-silico* identified satellites Cen213 and Cen234 were localized on mitotic chromosomes ($2n = 18$) of *B. frutescens* and *B. varia*, respectively. While Cen213 was found on most chromosomes across all *Biscutella* species investigated in this study, Cen234 was only observed in *B. varia*. *In situ* hybridization analysis confirms the centromeric nature of Cen213 and Cen234.



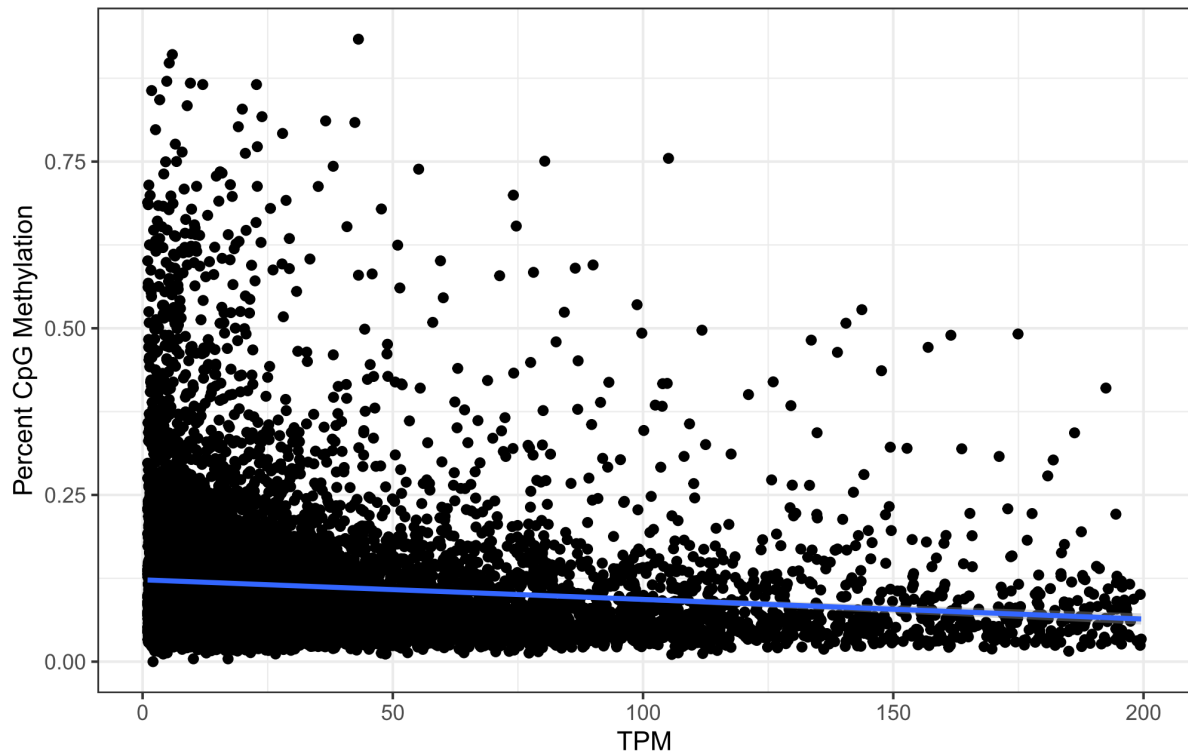
Supplementary Figure S9. *In situ* localization of CRM families. *In-silico* annotated CRM families were localized on mitotic chromosomes ($2n = 18$) of *B. frutescens* and *B. varia*. CRM families TE_00005474 (in *B. varia*) and TE_00003221 (in *B. frutescens*) show a pericentromeric localization (CRM_cen; highlighted in green), while TE_00005833 (*B. varia*) and TE_00003812 (*B. frutescens*) are dispersed widely throughout the chromosome (CRM_NONcen; highlighted in red). Validation through *in situ* hybridization experiments confirms the computational predictions of TEs distribution. This experiment highlights the distinct insertion biases observed among different CRM families.



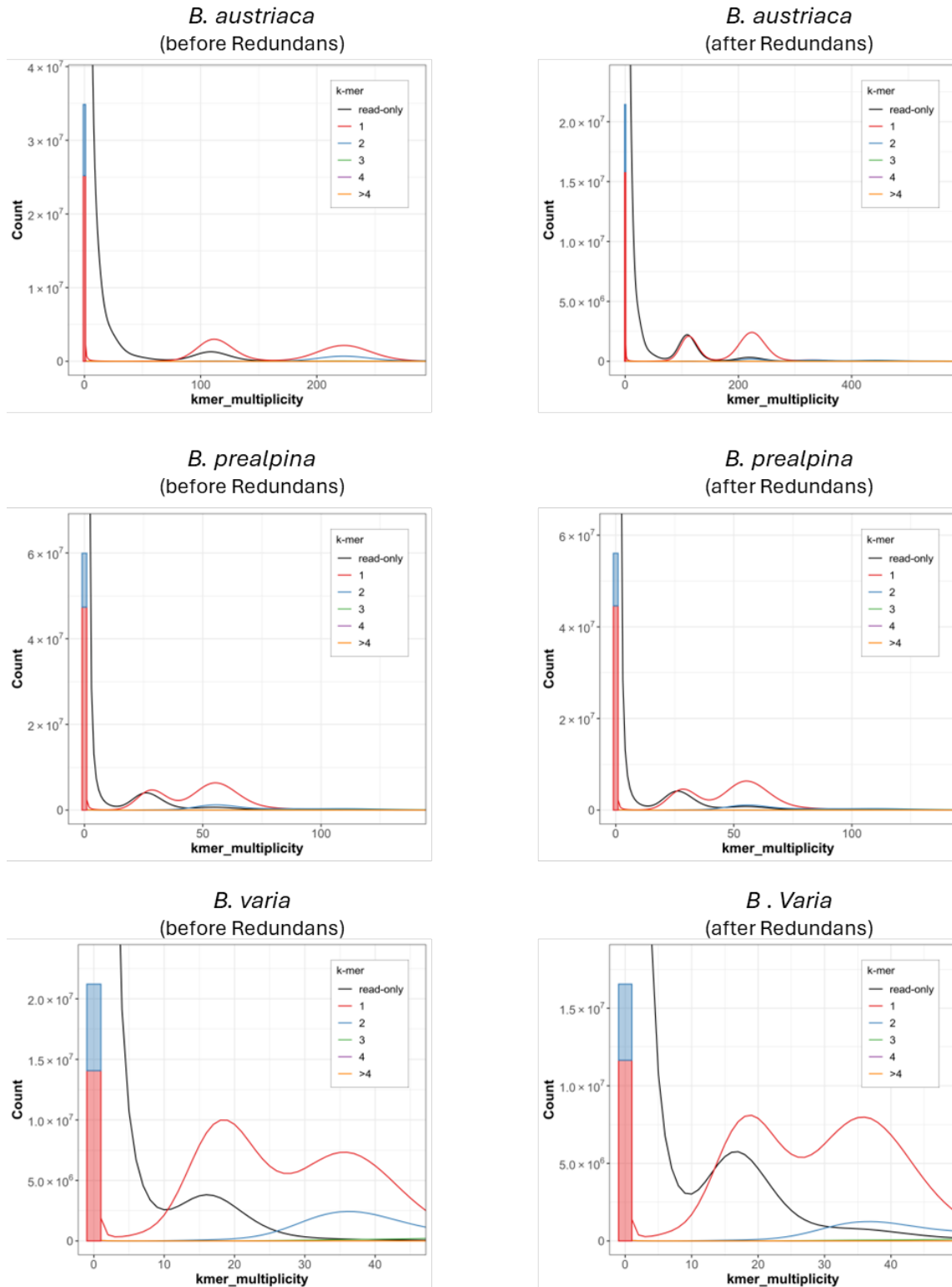
Supplementary Figure S10a. DNA methylation analysis of *B. frutescens* and *B. austriaca*. See complete legend on the next page.



Supplementary Figure S10b. DNA methylation analysis of *B. prealpina*. (left) Average frequency of CpG DNA methylation (percentage of methylated cytosines) across various genomic features, including pericentromeres, chromosome arms, gene coding sequences (CDS), and pericentromeric transposable elements (TEs) from the Athila and CRM clades. (right) CpG methylation levels of genes with CRM (blue) or Athila (orange) insertions within 100-2000bp, often showing significantly increased gene methylation when a TE is in close proximity. In *B. prealpina*, CRM elements show increased spread of DNA methylation.



Supplementary Figure S11. Correlation between expression and DNA methylation in genes. CpG DNA methylation was calculated as average percent of methylated Cytosines within CDS (from ONT data), while transcripts per million (TPM) was used as a proxy for gene expression. As expected, we found a negative correlation between DNA methylation and expression with highly methylated genes (median gene methylation level: 10%) being less expressed than low methylated ones.



Supplementary Figure S12. Merqury copy number spectrum plots. K-mer (size19) analysis was used for evaluating single haplotype genome assemblies (from diploid genomes) before and after heterozygosity reduction. After reduction, the first peak (representing heterozygous k-mers) shows a better overlap between assembled (red) and missing k-mers (black) that belong to the other haplotype, indicating efficient removal of redundant contigs.

Supplementary tables

Supplementary Table S1. Genome assemblies statistics. Comparison of four chromosome-scale *Biscutella* genomes assembled in this study. As expected, all genomes were successfully scaffolded into nine main scaffolds, corresponding to the nine chromosomes. Based on statistics such as the number of scaffolds and N90, *B. varia* and *B. frutescens* show the highest assembly quality, while *B. prealpina* shows indications of missing genomic regions, as evidenced by its low BUSCO score. Additionally, in accordance with genome size estimates from flow cytometry analysis (FCM), *B. frutescens* displays the smallest genome size, suggesting extensive diploidization following WGD event.

	<i>B. austriaca</i>	<i>B. prealpina</i>	<i>B. varia</i>	<i>B. frutescens</i>
FCM Estimated genome size (Mb)	904	936	916	814
Assembly size (Mb)	1001	866	832	710
Number of scaffolds	591	491	267	101
Number of chromosomes	9	9	9	9
Average scaffold length (Mb)	1.7	1.8	3	7
Longest scaffold (Mb)	95	99	88	89
N50 (Mb)	78	82	74	74
N90 (Mb)	0.7	0.8	2	60
Complete BUSCO (n=1,614)	99.1%	92.0%	98.7%	98.9%

Supplementary Table S2. Gene annotation statistics. This table compares the predicted number of gene models in various *Biscutella* species. Gene models were predicted using both extrinsic evidence (homology-based, incorporating RNA-Seq data and reference protein sequences) and *ab-initio* prediction tools (SNAP and AUGUSTUS), through the MAKER and BRAKER pipelines. The final gene predictions were consolidated using MAKER, retaining only models supported by extrinsic evidence (minimum AED score of 1). The reported numbers represent gene models predicted at each step and validated by sequence homology with RNA or protein sequences. Notably, for *B. austriaca* we used Illumina RNA-Seq data from seven tissues, while for other species we used PacBio IsoSeq from three tissues, potentially explaining the increased number of gene models predicted from RNA evidence and SNAP. The low complete BUSCO score in *B. prealpina* reflects the one shown in Table S1.

	Evidence	<i>B. austriaca</i>	<i>B. prealpina</i>	<i>B. varia</i>	<i>B. frutescens</i>
homology-based	Protein	15,670	12,269	15,051	14,189
	RNA	12,541	803	3,500	4,395
<i>ab-initio</i>	SNAP	23,267	15,540	11,627	7,874
	AUGUSTUS	3,003	10,876	8,705	5,747
	BRAKER	3,211	14,319	8,137	9,450
	Total	57,692	53,807	47,020	41,655
	complete BUSCO	94.0%	89.3%	93.9%	95.2%

Supplementary Table S3. Detailed BUSCO summary. Here, we compare full BUSCO reports derived from genome assemblies (genome based) and annotations (protein based). Note that compared to *B. laevigata* species, *B. frutescens* show a lower duplicated BUSCO score, further suggesting extensive reduction of duplicated loci in its genome. *B. prealpina* show higher percentage of missing BUSCO genes, indicating incomplete assembly in certain genomic regions.

	Species	complete	single-copy	duplicated	fragmented	missing
Genome based	<i>B. austriaca</i>	99.1 %	70.3 %	28.8 %	0.2 %	0.7 %
	<i>B. prealpina</i>	92.0 %	69.9 %	22.1 %	0.9 %	7.1 %
	<i>B. varia</i>	98.7 %	76.6 %	22.1 %	0.2 %	1.1 %
	<i>B. frutescens</i>	98.9 %	84.4 %	14.5 %	0.4 %	0.7 %
Protein based	<i>B. austriaca</i>	94.0 %	69.1 %	24.9 %	2.7 %	3.3 %
	<i>B. prealpina</i>	89.3 %	68.8 %	20.5 %	2.2 %	8.5 %
	<i>B. varia</i>	93.9 %	73.4 %	20.5 %	1.6 %	4.5 %
	<i>B. frutescens</i>	95.2 %	80.9 %	14.3 %	1.2 %	3.6 %

Supplementary Table S4. Pericentromeric boundaries. Through synteny analysis with *Arabidopsis thaliana*, we mapped *Biscutella* genes onto crucifer genomic blocks (GBs) and linkage groups (LGs). Subsequently, we delineated pericentromeric regions by identifying the boundaries between pericentromeres and chromosome arms, utilizing the flanking GBs at the chromosome centre. These tables summarize the gene positions (utilizing *A. thaliana* identifiers) delineating these boundaries downstream and upstream of the pericentromeres.

B. austriaca

Ath_Gene	Chromosome	Start	End	GB	LG
--	--	--	--	--	--
AT4G15560.1	Ba1	19353075	19356174	T	7
AT4G14030.1	Ba1	38930943	38933134	T	7
--	--	--	--	--	--
AT2G15290.1	Ba2	26845912	26847784	H	3
AT5G38070.1	Ba2	47977261	47978529	S	7
--	--	--	--	--	--
AT2G24530.1	Ba3	12671527	12672747	I	4
AT2G27180.1	Ba3	45218455	45218796	I	4
--	--	--	--	--	--
AT4G14368.1	Ba4	21821591	21825444	T	7
AT3G25520.1	Ba4	48000956	48002288	F	3
--	--	--	--	--	--
AT4G09600.1	Ba5	22323091	22323205	P	6
AT5G50320.1	Ba5	43675038	43678741	W	8
--	--	--	--	--	--
AT2G28260.1	Ba6	28492182	28494628	I	4
AT2G27050.1	Ba6	41647754	41649355	I	4
--	--	--	--	--	--
AT1G54380.1	Ba7	22691946	22693896	C	1
AT1G34010.1	Ba7	49059903	49061237	B	1
--	--	--	--	--	--
AT2G17260.1	Ba8	21541509	21544552	H	3
AT3G25520.1	Ba8	39949925	39951278	F	3
--	--	--	--	--	--
AT3G44900.1	Ba9	33439867	33475056	MN	5
AT1G43245.1	Ba9	38976273	38978688	C	1

B. prealpina

Ath_Gene	Chromosome	Start	End	GB	LG
--	--	--	--	--	--
AT4G14480.1	Bp1	22557117	22558528	T	7
AT5G37290.1	Bp1	56285075	56286621	S	7
--	--	--	--	--	--
AT2G15480.1	Bp2	18887756	18889386	H	3
AT5G37600.1	Bp2	40989055	40991708	S	7
--	--	--	--	--	--
AT2G24590.1	Bp3	11011513	11012563	I	4
AT2G26700.1	Bp3	41666576	41669380	I	4
--	--	--	--	--	--
AT4G14620.1	Bp4	17661617	17662578	T	7
AT3G25520.1	Bp4	60254873	60256205	F	3
# Bv5:					
AT4G09600.1	Bp5	17903579	17903739	P	6
AT5G50920.1	Bp5	40277698	40281544	W	8
--	--	--	--	--	--
AT2G28260.1	Bp6	25567387	25569833	I	4
AT2G27060.1	Bp6	46356547	46359750	I	4
--	--	--	--	--	--
AT1G54380.1	Bp7	23153210	23154836	C	1
AT1G33800.1	Bp7	55297998	55299489	B	1
--	--	--	--	--	--
AT2G15080.1	Bp8	24907175	25016167	H	3
AT3G25470.1	Bp8	52098427	52098593	F	3
--	--	--	--	--	--
AT3G46290.1	Bp9	21209389	21211884	MN	5
AT1G47480.1	Bp9	54448964	54451718	C	1

B. varia

Ath_Gene	Chromosome	Start	End	GB	LG
--	--	--	--	--	--
AT4G15520.1	Bv1	19795668	19797010	T	7
AT5G37740.1	Bv1	46190952	46192132	S	7
--	--	--	--	--	--
AT2G15890.1	Bv2	19812964	19813724	H	3
AT5G38130.1	Bv2	48577150	48578484	S	7
--	--	--	--	--	--
AT2G23940.1	Bv3	11358825	11360027	I	4
AT4G13260.1	Bv3	38847623	38849338	T	7
--	--	--	--	--	--
AT4G14310.1	Bv4	19134898	19137398	T	7
AT3G25520.1	Bv4	40369053	40370367	F	3
--	--	--	--	--	--
AT4G09820.1	Bv5	20101283	20126016	P	6
AT5G50920.1	Bv5	48257951	48261858	W	8
--	--	--	--	--	--
AT2G28260.1	Bv6	28844010	28846556	I	4
AT2G27060.1	Bv6	36655181	36658404	I	4
--	--	--	--	--	--
AT1G54380.1	Bv7	21716153	21745279	C	1
AT1G34180.1	Bv7	46353267	46353947	B	1
--	--	--	--	--	--
AT2G15130.2	Bv8	26272446	26272880	H	3
AT2G05120.2	Bv8	47849886	47854645	KL1	5
--	--	--	--	--	--
AT3G46180.1	Bv9	25106384	25108873	MN	5
AT1G47640.1	Bv9	39133902	39135619	C	1

B. frutescens

Ath_Gene	Chromosome	Start	End	GB	LG
--	--	--	--	--	--
AT2G26440.1	Bf1	42123024	42127348	I	4
AT5G37710.1	Bf1	64727516	64729715	S	7
--	--	--	--	--	--
AT2G15695.1	Bf2	19382974	19385158	H	3
AT5G38210.1	Bf2	38819176	38819836	S	7
--	--	--	--	--	--
AT2G24590.1	Bf3	10992385	10993435	I	4
AT4G13510.1	Bf3	40501284	40502786	T	7
--	--	--	--	--	--
AT4G14290.1	Bf4	17867070	17871447	T	7
AT3G24620.1	Bf4	57175319	57177362	F	3
--	--	--	--	--	--
AT4G09570.1	Bf5	25071685	25074241	P	6
AT5G50920.1	Bf5	50497042	50500978	W	8
--	--	--	--	--	--
AT2G28520.1	Bf6	21369205	21374752	I	4
AT2G27060.1	Bf6	35393642	35396848	I	4
--	--	--	--	--	--
AT1G54390.3	Bf7	21515224	21517037	C	1
AT1G33680.1	Bf7	46179018	46183205	B	1
--	--	--	--	--	--
AT2G15230.1	Bf8	24719113	24721240	H	3
AT3G25500.1	Bf8	39456899	39460413	F	3
--	--	--	--	--	--
AT3G46040.1	Bf9	22072296	22073145	MN	5
AT1G47610.1	Bf9	45001810	45002865	C	1

Supplementary Table S5. Transposable elements annotation summary. For each TE superfamily, we provide the total count of TE copies, occupied base pairs (bp), and the corresponding percentage of the genome covered.

	<i>B. austriaca</i>			<i>B. prealpina</i>		
Class	Count	bpMasked	%masked	Count	bpMasked	%masked
LTR	--	--	--	--	--	--
Copia	81601	70570689	9.82%	52928	52739587	7.10%
Gypsy	205296	222659365	30.99%	200054	236147270	31.81%
unknown	126786	81165854	11.30%	199466	102928363	13.86%
TIR	--	--	--	--	--	--
DTC	28905	15590274	2.17%	32255	16832981	2.27%
DTM	52744	27386626	3.81%	54356	25674780	3.46%
DTH	19227	8698120	1.21%	15018	5332246	0.72%
DTT	3905	1225444	0.17%	3908	1226478	0.17%
DTA	15420	5451805	0.76%	17970	6482809	0.87%
nonTIR	--	--	--	--	--	--
helitron	187618	74560867	10.38%	212775	86374750	11.63%
Total_interspersed	721502	507309044	70.61%	788730	533739264	71.89%

	<i>B. varia</i>			<i>B. frutescens</i>		
Class	Count	bpMasked	%masked	Count	bpMasked	%masked
LTR	--	--	--	--	--	--
Copia	62449	53283801	7.64%	51791	53974208	8.01%
Gypsy	170781	212971678	30.54%	169618	197968623	29.38%
unknown	133420	79971159	11.47%	123759	78442880	11.64%
TIR	--	--	--	--	--	--
DTC	32435	17627313	2.53%	27927	14489934	2.15%
DTM	40231	23432333	3.36%	36210	15897818	2.36%
DTH	14669	6108902	0.88%	11017	4635701	0.69%
DTT	2958	1084361	0.16%	3963	1188640	0.18%
DTA	14275	5530986	0.79%	14814	4971120	0.74%
nonTIR	--	--	--	--	--	--
helitron	221749	91193077	13.08%	217676	99284170	14.73%
Total_interspersed	692967	491203610	70.43%	656775	470853094	69.88%

Supplementary Table S6. Abundance of LTR retrotransposons clades. Long terminal repeat (LTR) retrotransposons were categorized into distinct clades using TEsorter. Here, we compare the count of TE families and the respective percentage of occupied genome for each retrotransposon clade across different *Biscutella* species. Notably, pericentromeric clades (Athila and CRM) show higher abundance in *B. varia* and *B. prealpina*.

Superfam.	Clade	Number of families				Genome content %			
		<i>B. varia</i>	<i>B. prealpina</i>	<i>B. frutescens</i>	<i>B. austriaca</i>	<i>B. varia</i>	<i>B. prealpina</i>	<i>B. frutescens</i>	<i>B. austriaca</i>
Gypsy	Athila	226	274	207	160	10.70	11.05	7.51	7.98
	CRM	212	99	78	75	5.15	7.51	4.14	4.17
	Galadriel	5	4	6	5	0.04	0.01	0.08	0.04
	Reina	139	142	140	155	0.23	0.28	0.25	0.33
	Retand	69	60	42	53	1.28	1.22	0.98	1.32
	Tekay	21	31	21	20	0.57	0.65	0.32	0.61
Copia	Ale	482	489	498	527	1.83	1.89	1.77	2.03
	Alesia	1	1	6	1	0.02	0.02	0.09	0.04
	Angela	1	1	1	1	0.01	0.01	0.01	0.01
	Bianca	20	94	103	110	0.59	1.81	2.25	2.93
	Ikeros	17	13	18	7	0.74	0.36	0.33	0.32
	Ivana	168	164	172	148	0.68	0.69	0.75	1.02
	SIRE	92	92	63	88	0.61	0.59	0.70	0.53
	TAR	15	14	15	21	0.23	0.22	0.22	0.26
	Tork	138	133	131	131	0.63	0.80	1.05	1.13

Supplementary Table S7. Abundance and distribution of the 20% most abundant CRM families. After defining boundaries between pericentromere and chromosome arms for each chromosome, we quantified the number of TE copies present in the respective regions. We assessed whether a TE family showed an insertion bias or was uniformly dispersed (randomly) along the chromosomes.

B. austriaca

TE_family	Pericent.	Chr.arms	Total	Type
TE_00002994	4845	1351	6196	Cent
TE_00006634	3054	972	4026	Cent
TE_00006908	997	346	1343	Cent
TE_00006767	238	472	710	Distal
TE_00002149	477	106	583	Cent
TE_00004891	125	363	488	Distal
TE_00002392	25	454	479	Distal
TE_00005978	344	96	440	Cent
TE_00001570	273	89	362	Cent
TE_00002551	258	89	347	Cent
TE_00005438	243	77	320	Cent
TE_00000819	242	61	303	Cent
TE_00003364	254	44	298	Cent
TE_00005900	216	56	272	Cent
TE_00001811	210	53	263	Cent

B. prealpina

TE_family	Pericent.	Chr.arms	Total	Type
TE_00005306	6786	1574	8360	Cent
TE_00002599	1207	281	1488	Cent
TE_00001465	1003	207	1210	Cent
TE_00000687	843	304	1147	Cent
TE_00005919	534	173	707	Cent
TE_00001268	192	390	582	Dispersed
TE_00002313	440	96	536	Cent
TE_00003401	366	107	473	Cent
TE_00005110	319	134	453	Cent
TE_00002068	294	73	367	Cent
TE_00001954	270	65	335	Cent
TE_00007186	275	54	329	Cent
TE_00002211	221	82	303	Cent
TE_00002206	232	41	273	Cent
TE_00002140	208	34	242	Cent
TE_00003325	96	142	238	Dispersed
TE_00004059	206	27	233	Cent
TE_00001264	197	35	232	Cent
TE_00007172	204	25	229	Cent

B. varia

TE_family	Pericent.	Chr.arms	Total	Type
TE_00005105	2811	930	3741	Cent
TE_00005474	1106	342	1448	Cent
TE_00003631	893	507	1400	Dispersed
TE_00003875	799	239	1038	Cent
TE_00002887	59	766	825	Distal
TE_00005833	113	576	689	Distal
TE_00001407	72	566	638	Distal
TE_00002954	586	17	603	Cent
TE_00005878	472	109	581	Cent
TE_00003885	461	112	573	Cent
TE_00006563	434	93	527	Cent
TE_00002081	418	60	478	Cent
TE_00006049	359	87	446	Cent
TE_00002644	335	89	424	Cent
TE_00004628	317	97	414	Cent
TE_00001716	318	76	394	Cent
TE_00003596	330	64	394	Cent
TE_00002787	266	61	327	Cent
TE_00006458	266	60	326	Cent
TE_00005458	242	71	313	Cent
TE_00000831	233	77	310	Cent
TE_00002209	207	103	310	Cent
TE_00002283	100	205	305	Distal
TE_00002696	205	87	292	Cent
TE_00005575	97	189	286	Distal
TE_00003863	186	65	251	Cent
TE_00004324	200	48	248	Cent
TE_00004444	191	50	241	Cent
TE_00007036	173	56	229	Cent
TE_00002978	106	121	227	Dispersed
TE_00000832	184	36	220	Cent
TE_00002866	171	40	211	Cent
TE_00005646	149	38	187	Cent
TE_00002345	149	36	185	Cent
TE_00001414	118	63	181	Cent
TE_00004123	141	39	180	Cent
TE_00002758	93	73	166	Dispersed
TE_00002082	110	53	163	Cent
TE_00001902	95	64	159	Dispersed
TE_00005774	69	85	154	Dispersed
TE_00002470	121	32	153	Cent
TE_00005078	125	23	148	Cent
TE_00007132	113	27	140	Cent

B. frutescens

TE_family	Pericent.	Chr.arms	Total	Type
TE_00004597	4641	1167	5808	Cent
TE_00003221	3758	1020	4778	Cent
TE_00003445	1233	262	1495	Cent
TE_00002100	627	173	800	Cent
TE_00003812	305	369	674	Dispersed
TE_00005661	542	94	636	Cent
TE_00005338	496	117	613	Cent
TE_00005402	324	73	397	Cent
TE_00003585	312	72	384	Cent
TE_00002318	317	38	355	Cent
TE_00006069	255	46	301	Cent
TE_00002978	242	52	294	Cent
TE_00004943	211	66	277	Cent
TE_00003759	202	40	242	Cent
TE_00000825	202	22	224	Cent
TE_00004579	181	39	220	Cent

Supplementary Table S8. Abundance and distribution of the 20% most abundant Athila families. Refer to Table S7 for the complete legend. As expected, we observe an increase in dispersed Athila TE families compared to CRM, suggesting that Athila retrotransposons are not biased towards the centromeric environment.

B. austriaca

TE_family	Pericent.	Chr.arms	Total	Type
TE_00006745	2446	1834	4280	Dispersed
TE_00002966	1583	2231	3814	Distal
TE_00002152	1423	1402	2825	Dispersed
TE_00002643	1036	1171	2207	Dispersed
TE_00007028	1410	633	2043	Cent
TE_00002635	982	902	1884	Dispersed
TE_00004574	902	687	1589	Dispersed
TE_00006840	847	652	1499	Dispersed
TE_00005089	719	581	1300	Dispersed
TE_00006842	640	540	1180	Dispersed
TE_00003876	605	449	1054	Dispersed
TE_00003104	227	770	997	Distal
TE_00004005	740	225	965	Cent
TE_00000669	506	450	956	Dispersed
TE_00000698	412	515	927	Dispersed
TE_00004201	355	406	761	Dispersed
TE_00003319	431	325	756	Dispersed
TE_00005661	83	606	689	Distal
TE_00004170	485	169	654	Cent
TE_00003122	345	304	649	Dispersed
TE_00003726	344	298	642	Dispersed
TE_00001330	314	327	641	Dispersed
TE_00001357	145	463	608	Distal
TE_00002668	316	292	608	Dispersed
TE_00005840	321	269	590	Dispersed
TE_00005828	316	271	587	Dispersed
TE_00004942	342	235	577	Dispersed
TE_00004429	154	420	574	Distal
TE_00002511	83	481	564	Distal
TE_00006047	63	489	552	Distal
TE_00006375	373	153	526	Cent
TE_00005021	250	222	472	Dispersed

B. prealpina

TE_family	Pericent.	Chr.arms	Total	Type
TE_00002612	3387	2923	6310	Dispersed
TE_00005940	2046	1711	3757	Dispersed
TE_00005437	564	1442	2006	Distal
TE_00003183	1545	354	1899	Cent
TE_00003582	1060	782	1842	Dispersed
TE_00005355	611	1124	1735	Distal
TE_00002667	877	718	1595	Dispersed
TE_00005567	835	739	1574	Dispersed
TE_00003656	234	1311	1545	Distal
TE_00001886	900	625	1525	Dispersed
TE_00003253	781	652	1433	Dispersed
TE_00001689	921	339	1260	Cent
TE_00003112	641	582	1223	Dispersed
TE_00000568	620	511	1131	Dispersed
TE_00006272	555	541	1096	Dispersed
TE_00006558	572	463	1035	Dispersed
TE_00002816	691	343	1034	Cent
TE_00002925	550	466	1016	Dispersed
TE_00006203	522	402	924	Dispersed
TE_00005696	124	789	913	Distal
TE_00002186	286	616	902	Distal
TE_00006427	429	428	857	Dispersed
TE_00000954	392	393	785	Dispersed
TE_00001896	340	402	742	Dispersed
TE_00003302	517	196	713	Cent
TE_00007135	533	171	704	Cent
TE_00006769	233	469	702	Distal
TE_00003922	134	566	700	Distal
TE_00006735	509	172	681	Cent
TE_00005086	404	275	679	Dispersed
TE_00001304	366	299	665	Dispersed
TE_00000861	335	288	623	Dispersed
TE_00002747	428	170	598	Cent
TE_00004388	313	253	566	Dispersed
TE_00005287	262	260	522	Dispersed
TE_00000829	309	201	510	Dispersed
TE_00003356	221	288	509	Dispersed
TE_00005645	352	123	475	Cent
TE_00005836	346	128	474	Cent
TE_00000718	151	313	464	Distal
TE_00004833	77	371	448	Distal
TE_00006594	141	286	427	Distal
TE_00002488	301	125	426	Cent

TE_00003710	303	105	408	Cent
TE_00006702	238	146	384	Dispersed
TE_00001505	231	148	379	Dispersed
TE_00004041	264	115	379	Cent
TE_00000750	225	148	373	Dispersed
TE_00006876	261	110	371	Cent
TE_00006206	281	84	365	Cent
TE_00000646	242	118	360	Cent
TE_00003508	149	204	353	Dispersed
TE_00004066	174	177	351	Dispersed
TE_00002718	188	160	348	Dispersed
TE_00001566	270	64	334	Cent

B. varia

TE_family	Pericent.	Chr.arms	Total	Type
TE_00004761	6486	2184	8670	Cent
TE_00006108	2270	1558	3828	Dispersed
TE_00003772	1738	1866	3604	Dispersed
TE_00006123	1328	1387	2715	Dispersed
TE_00002760	523	1527	2050	Distal
TE_00001054	764	523	1287	Dispersed
TE_00006275	712	482	1194	Dispersed
TE_00006906	664	455	1119	Dispersed
TE_00002762	441	620	1061	Dispersed
TE_00004566	620	437	1057	Dispersed
TE_00002952	615	420	1035	Dispersed
TE_00004477	509	399	908	Dispersed
TE_00001883	475	314	789	Dispersed
TE_00006160	147	493	640	Distal
TE_00005671	314	246	560	Dispersed
TE_00003483	177	382	559	Distal
TE_00004328	171	358	529	Distal
TE_00005359	250	253	503	Dispersed
TE_00005677	384	117	501	Cent
TE_00001714	314	181	495	Dispersed
TE_00005945	300	193	493	Dispersed
TE_00005027	317	141	458	Cent
TE_00001689	276	162	438	Dispersed
TE_00004498	247	184	431	Dispersed
TE_00000991	272	158	430	Dispersed
TE_00004884	216	211	427	Dispersed
TE_00006663	219	181	400	Dispersed
TE_00004784	55	326	381	Distal
TE_00002035	224	136	360	Dispersed
TE_00004662	221	125	346	Dispersed

TE_00003897	218	123	341	Dispersed
TE_00004152	210	124	334	Dispersed
TE_00001624	194	131	325	Dispersed
TE_00003046	239	82	321	Cent
TE_00001923	190	126	316	Dispersed
TE_00004076	182	116	298	Dispersed
TE_00004590	215	79	294	Cent
TE_00006555	74	213	287	Distal
TE_00006770	204	82	286	Cent
TE_00002900	184	88	272	Cent
TE_00001305	148	116	264	Dispersed
TE_00003705	202	61	263	Cent
TE_00005989	33	213	246	Distal
TE_00002947	181	63	244	Cent
TE_00006196	147	93	240	Dispersed
TE_00006389	147	92	239	Dispersed

B. frutescens

TE_family	Pericent.	Chr.arms	Total	Type
TE_00002321	1641	1107	2748	Dispersed
TE_00002783	1733	592	2325	Cent
TE_00002238	912	841	1753	Dispersed
TE_00002806	723	894	1617	Dispersed
TE_00001485	1066	237	1303	Cent
TE_00004449	616	673	1289	Dispersed
TE_00002894	739	401	1140	Dispersed
TE_00004697	811	310	1121	Cent
TE_00005965	772	253	1025	Cent
TE_00005918	653	363	1016	Dispersed
TE_00005381	613	400	1013	Dispersed
TE_00000901	719	245	964	Cent
TE_00005793	554	356	910	Dispersed
TE_00001915	53	759	812	Distal
TE_00004548	453	258	711	Dispersed
TE_00001407	437	270	707	Dispersed
TE_00003940	411	234	645	Dispersed
TE_00003158	391	253	644	Dispersed
TE_00001823	302	333	635	Dispersed
TE_00000938	110	485	595	Distal
TE_00001167	385	198	583	Dispersed
TE_00005181	307	196	503	Dispersed
TE_00001327	149	319	468	Distal
TE_00003818	367	92	459	Cent
TE_00005245	331	124	455	Cent
TE_00005004	183	269	452	Dispersed

TE_00004758	317	117	434	Cent
TE_00003204	316	90	406	Cent
TE_00001797	131	272	403	Distal
TE_00006142	259	112	371	Cent
TE_00006976	131	218	349	Dispersed
TE_00002572	172	173	345	Dispersed
TE_00000989	77	263	340	Distal
TE_00004614	154	179	333	Dispersed
TE_00006983	209	115	324	Dispersed
TE_00000830	198	112	310	Dispersed
TE_00007223	180	102	282	Dispersed
TE_00002738	195	85	280	Cent
TE_00001412	91	177	268	Distal
TE_00001415	56	193	249	Distal
TE_00007030	190	59	249	Cent
TE_00002681	154	91	245	Dispersed
TE_00002239	52	189	241	Distal

Supplementary Table S9. Abundance and distribution of 20% most abundant pericentromeric TE families. Based on the results reported in Tables S7 and S8, we compiled the number of CRM and Athila families showing random distribution (dispersed) or insertion bias towards the pericentromere or chromosome arms (distal), together with their total count of TE copies.

	Species	Families			Elements			Total
		Pericen.	Distal	Dispersed	Pericen.	Distal	Dispersed	
CRM	<i>B. varia</i>	33	5	5	20525 (74%)	4262 (15%)	2815 (10%)	27602
	<i>B. prealpina</i>	18	0	2	17737 (94%)	0	1037 (6%)	18774
	<i>B. frutescens</i>	15	0	1	17498 (95%)	0	878 (5%)	18376
	<i>B. austriaca</i>	12	3	0	16430 (89%)	2117 (11%)	0	18547
Athila	<i>B. varia</i>	9	7	30	19880 (32%)	6435 (11%)	34916 (57%)	61231
	<i>B. prealpina</i>	16	10	29	16393 (23%)	14275 (20%)	40304 (57%)	70972
	<i>B. frutescens</i>	12	8	23	15079 (32%)	4312 (9%)	27158 (58%)	46549
	<i>B. austriaca</i>	7	4	21	6348 (13%)	10215 (21%)	32602 (66%)	49165