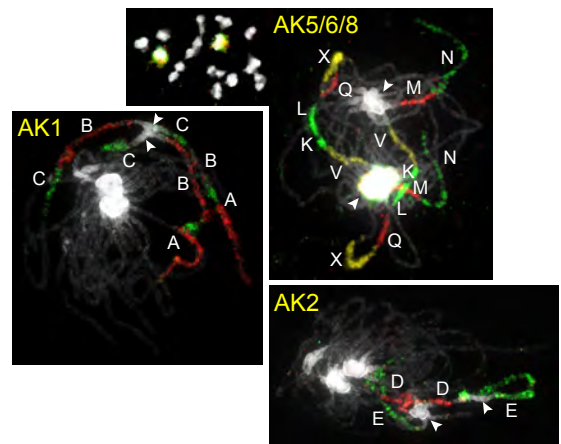
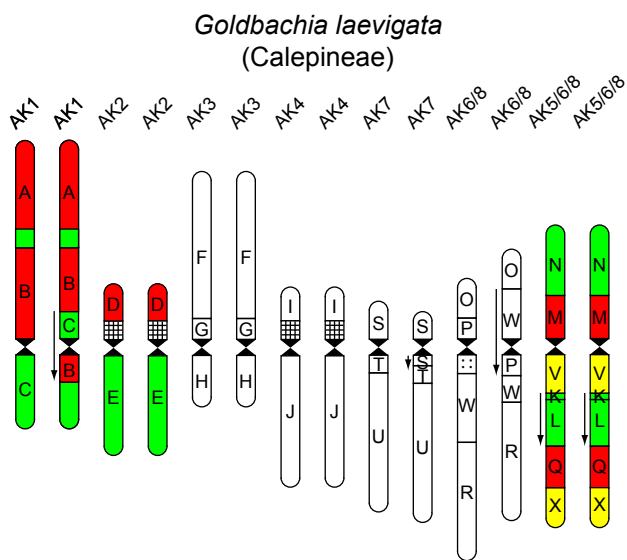
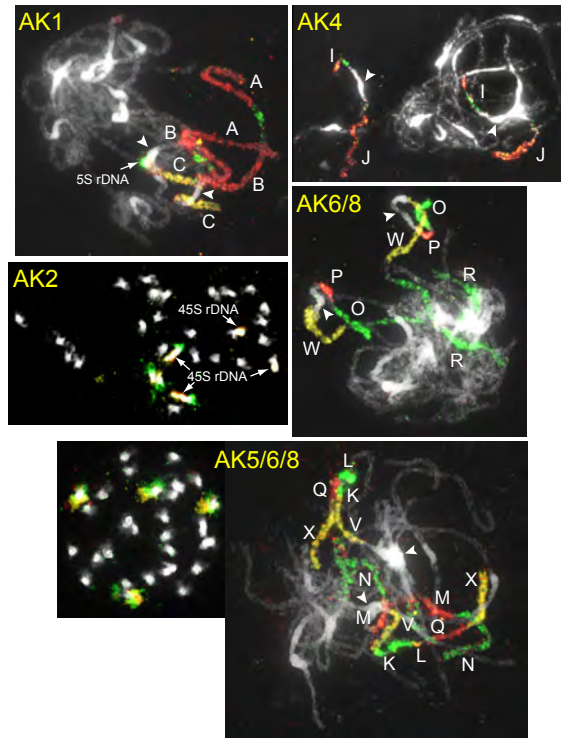
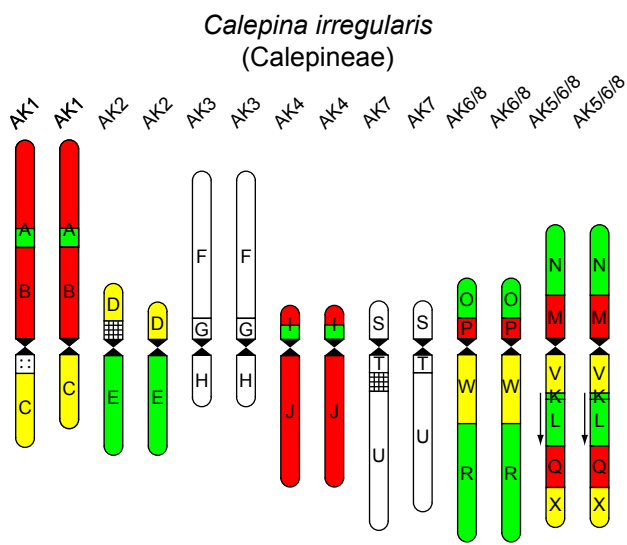
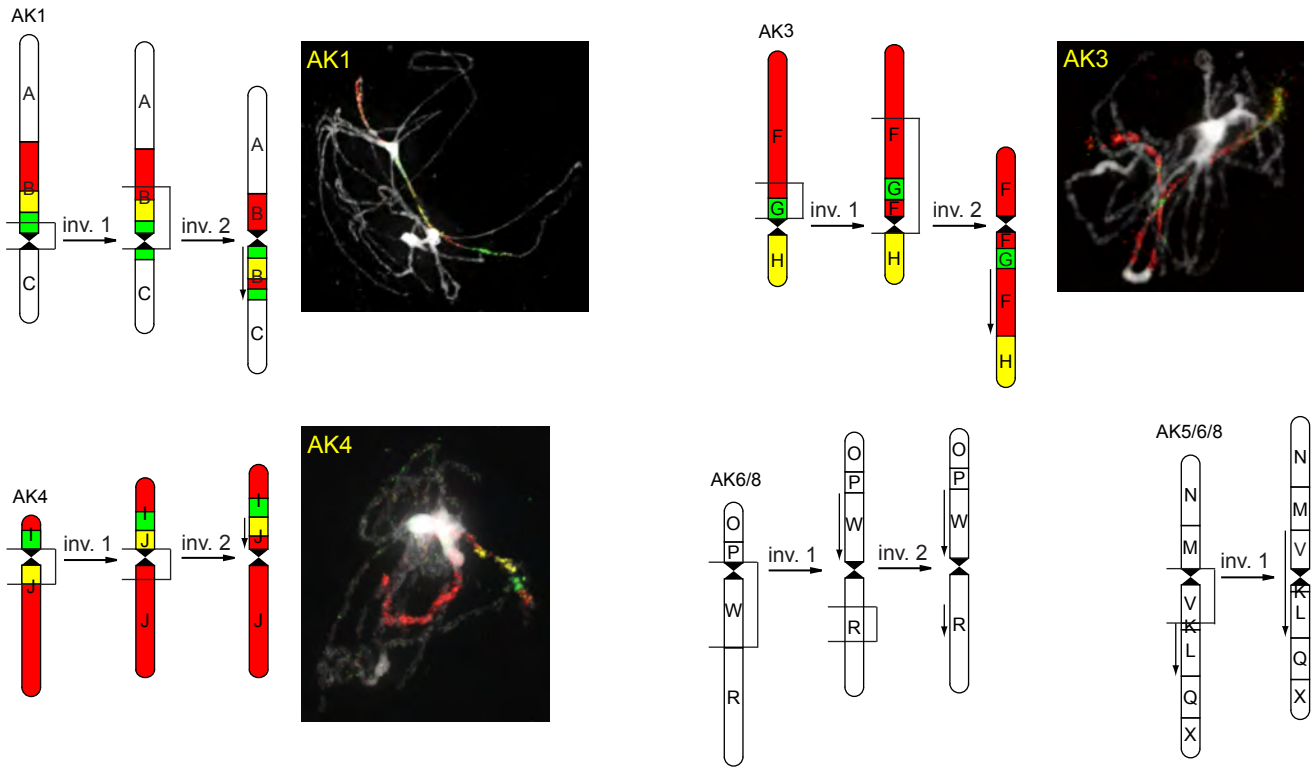


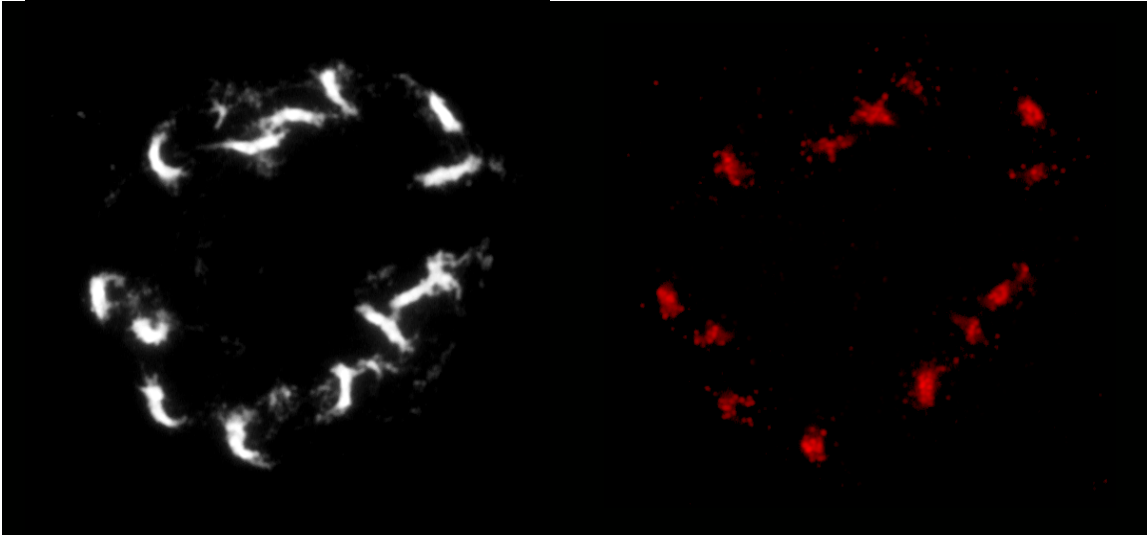
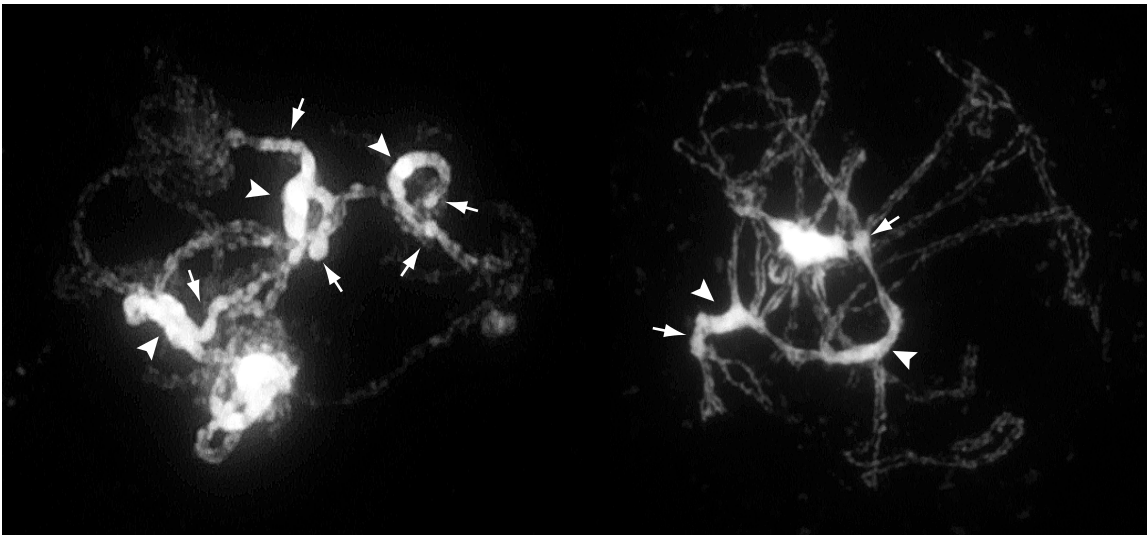
Supplemental Data. Mandáková and Lysak (2008).
 Chromosomal phylogeny and karyotype evolution in $x=7$ crucifer species (*Brassicaceae*).



Supplemental Figure 1. Examples of Comparative Chromosome Painting in Tetraploid Calepineae Species ($2n=4x=28$). 24 genomic blocks of the ACK are indicated by capital letters (A-X), and colored according to the experimental design used (green, yellow and red pseudocolors correspond to the fluorescence of AlexaFluor 488, Cy3 and Texas Red, respectively). Downward-pointing arrows indicate the opposite orientation of genomic blocks as compared to the position in the ACK. 5S rDNA and 45S rDNA loci are shown as dotted and cross-hatched boxes, respectively. Arrowheads point to the centromere position(s) on pachytene chromosomes.



Supplemental Figure 2. Species-specific Chromosome Rearrangements (Inversion Events) in *Nocca caerulea*. 24 genomic blocks of the ACK are indicated by capital letters (A-X), and colored according to the experimental design used (green, yellow and red pseudocolors correspond to the fluorescence of AlexaFluor 488, Cy3 and Texas Red, respectively). Downward-pointing arrows indicate the opposite orientation of genomic blocks as compared to the position in the ACK. Painted chromosomes AK6/8 and AK5/6/8 shown in Figure 2D.

A**B**

Supplemental Figure 3. Heterochromatic Landmarks in *Ochthodium aegyptiacum* and *Thellungiella halophila*. (A) Fourteen 5S rDNA loci (red) localized on mitotic chromosomes of *O. aegyptiacum* ($2n=14$). (B) DAPI-stained pachytene chromosomes of *T. halophila* ($2n=14$) with large arrays of pericentromeric and interstitial heterochromatin. Arrowheads and arrows point to the position of centromeres and prominent heterochromatic arrays, respectively.

Supplemental Table 1. Genomic Blocks of the Ancestral Crucifer Karyotype and Corresponding *Arabidopsis thaliana* BAC Contigs Used as Painting Probes in the Present Study.

Ancestral Chromosome ^a	Genomic Block ^a	Size (Mb) ^b	Boundary <i>A. thaliana</i> BAC Clones ^b (inc. GeneBank Accession Nos.)	<i>A. thaliana</i> Chromosome ^b
AK1	A	6.7	T25K16 (AC007323) - T29M8 (AC069143)	At1
AK1	B	5.7	F5M15 (AC027665) - F12K21 (AC023279)	At1
AK1	C	4.6	F2J6 (AC009526) T6H22 (AC009894)	At1
AK2	D	2.3	F12K22 (AC079732) - T12P18 (AC010852)	At1
AK2	E	6.2	T23K8 (AC007230) - F23A5 (AC011713)	At1
AK3	F	9.2	T4P13 (AC008261) - MWL2 (AB025629)	At3
AK3	G	1.3	F1O13 (AC007211) -T25N22 (AC005693)	At2
AK3	H	3.2	T10F5 (AC007063) - F11A3 (AC006569)	At2
AK4	I	2.1	F3K23 (AC006841) - T19L18 (AC004747)	At2
AK4	J	8.2	F18A8 (AC003105) - T8I3 (AC002337)	At2
AK5	K	0.4	F2I9 (AC005560) - F3C11 (AC007167)	At2
AK5	L	2.9	MJL14 (AP000601) - T4A2 (AP002066)	At2
AK5	M	2.7	T10D17 (AL353865) - F3A4 (AL132978)	At2
AK5	N	4.4	F24M12 (AL132980) - F16M2 (AL138648)	At2
AK6	O	2.5	F6N15 (AF069299) - T1J1 (AF128393)	At4
AK6	P	1.3	T3H13 (AF128396) - F8L21 (AL096882)	At4
AK6	Q	2.6	T20O7 (AB026660) - T8M17 (AF296835)	At5
AK6	R	7.4	F7J8 (AL137189) - T6G21 (AL090689)	At5
AK7	S	2.4	F5H8 (AB025605) - MJC20 (AB017067)	At5
AK7	T	1.1	F25E4 (AL050399) - F18A5 (AL035528)	At4
AK7	U	8.7	T6K21 (AL021889) - T5J17 (AL035708)	At4
AK8	V	2.4	MBD2 (AB008264) - K23F3 (AP000372)	At5
AK8	W	4.3	K21P3 (AB016872) - MMN10 (AB015475)	At5
AK8	X	2.5	MSL3 (AB008269) - K9I9 (AB013390)	At5

^a Ancestral chromosomes (AK1-8) and 24 genomic blocks (A-X) of the Ancestral Crucifer Karyotype (Schranz et al., Trends Plant Sci. 11: 535–542, 2006).

^b <http://www.arabidopsis.org>

Supplemental Table 2. Relative Length of Genomic Blocks (GBs) in the Eight x=7 Analyzed Species.

Relative length of GBs is given as a ratio between the measured length of a GB and the sum of all GB lengths in a given species.

Genomic ^a Block	<i>Myagrurn perfoliatum</i>	<i>Thellungiella halophila</i>	<i>Ochthodium aegyptiacum</i>	<i>Glastaria glastifolia</i>	<i>Noccaea caerulescens</i>	<i>Conringia orientalis</i>	<i>Calepina irregularis</i>	<i>Goldbachia laevigata</i>
A	0.068	0.065	0.059	0.066	0.064	0.089	0.091	0.073
B	0.055	0.065	0.049	0.053	0.052	0.073	0.072	0.055
C	0.034	0.032	0.034	0.029	0.031	0.047	0.038	0.027
D	0.027	0.025	0.029	0.025	0.040	0.035	0.034	0.064
E	0.072	0.058	0.107	0.066	0.076	0.079	0.098	0.109
F	0.106	0.104	0.117	0.127	0.116	0.104	0.140	0.136
G	0.007	0.004	0.010	0.008	0.006	0.006	0.004	0.005
H	0.027	0.025	0.029	0.029	0.024	0.032	0.045	0.032
I	0.017	0.022	0.020	0.037	0.012	0.028	0.030	0.023
J	0.079	0.090	0.068	0.094	0.080	0.066	0.091	0.100
K	0.007	0.011	0.010	0.016	0.018	0.009	0.008	0.009
L	0.017	0.014	0.020	0.012	0.015	0.019	0.019	0.023
M	0.041	0.025	0.029	0.029	0.031	0.025	0.027	0.023
N	0.065	0.058	0.059	0.053	0.058	0.047	0.049	0.064
O	0.021	0.022	0.024	0.025	0.015	0.019	0.023	0.027
P	0.017	0.018	0.015	0.012	0.021	0.016	0.015	0.014
Q	0.021	0.014	0.020	0.016	0.021	0.032	0.023	0.023
R	0.079	0.112	0.083	0.078	0.092	0.057	0.091	0.091
S	0.031	0.036	0.024	0.025	0.028	0.019	n.a. ^b	n.a.
T	0.007	0.004	0.005	0.012	0.006	0.006	n.a.	n.a.
U	0.096	0.097	0.088	0.098	0.110	0.082	n.a.	n.a.
V	0.024	0.022	0.029	0.025	0.021	0.032	0.027	0.027
W	0.055	0.054	0.044	0.041	0.040	0.041	0.045	0.045
X	0.027	0.025	0.029	0.025	0.021	0.035	0.030	0.032

^a 24 GBs (A-X) of the Ancestral Crucifer Karyotype (Schranz et al., Trends Plant Sci. 11: 535–542, 2006).

^b n.a. (= not analyzed).