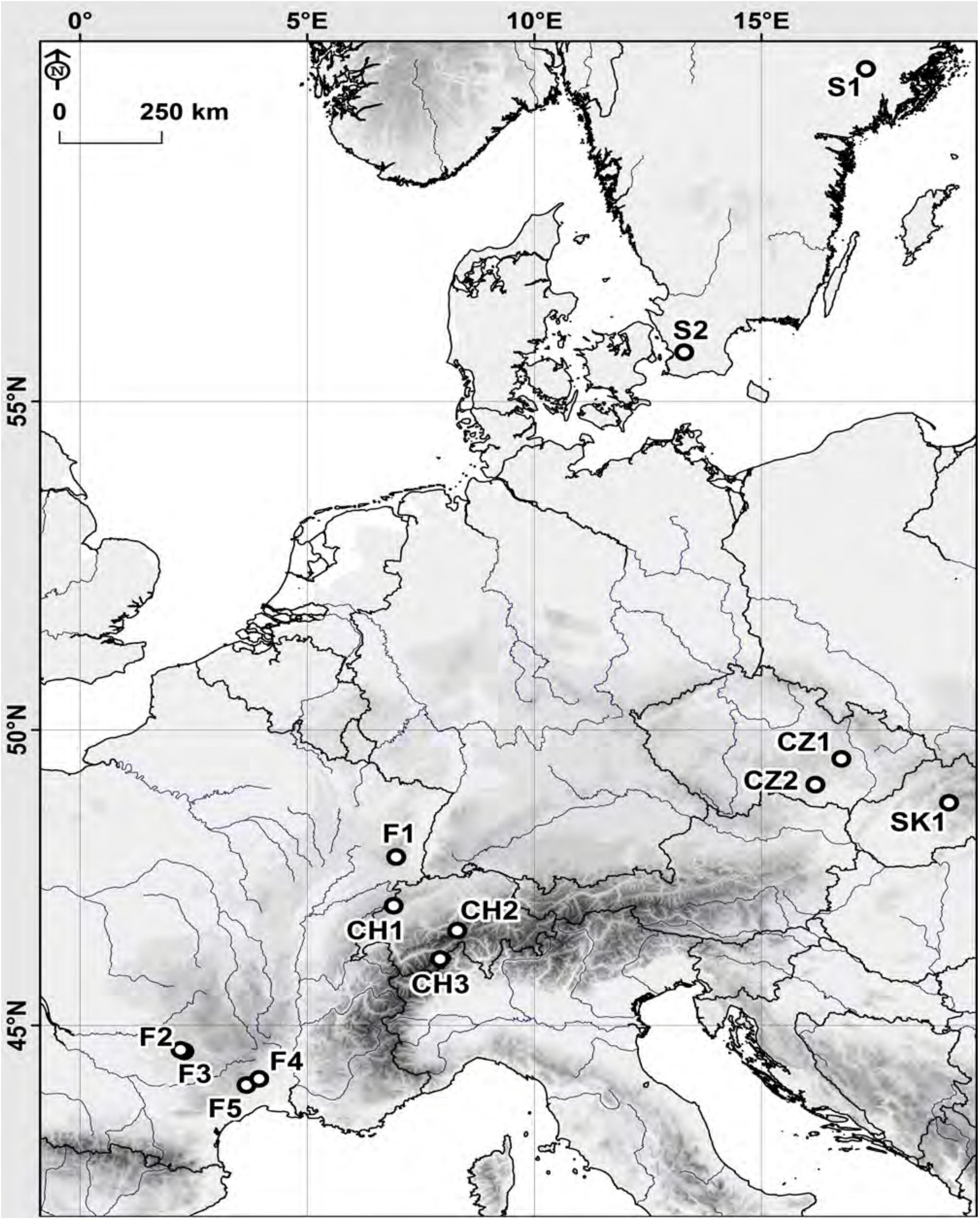
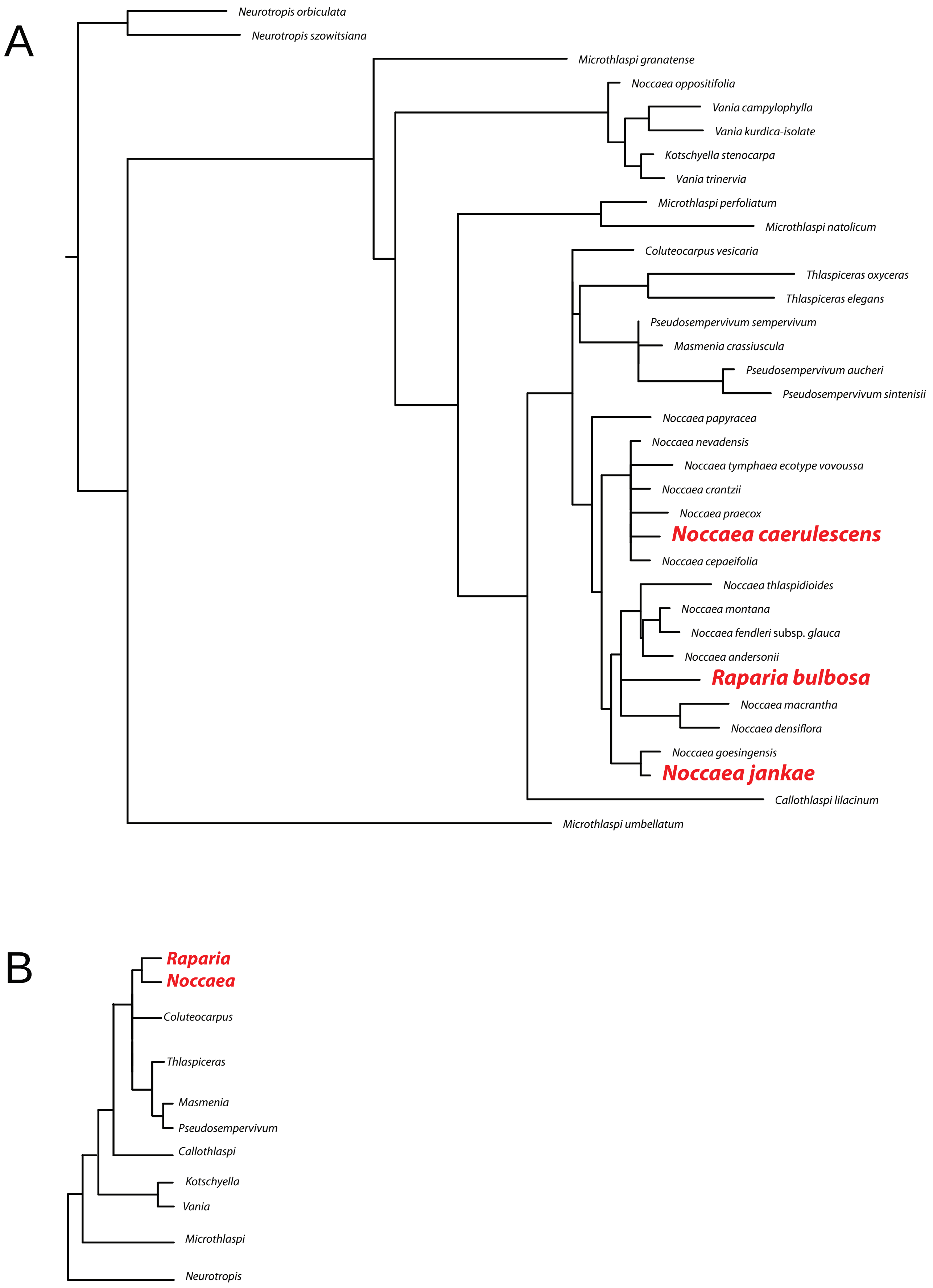
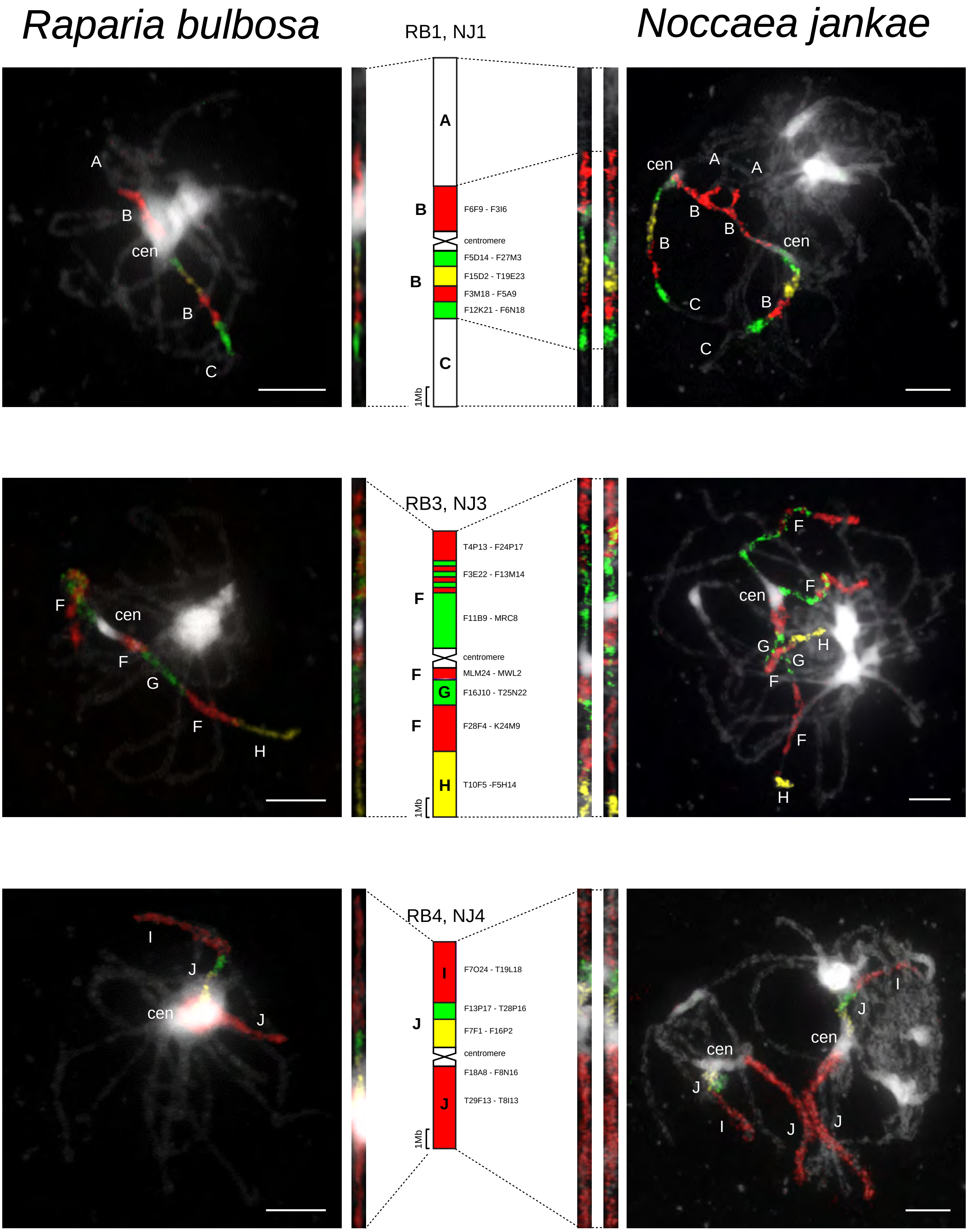


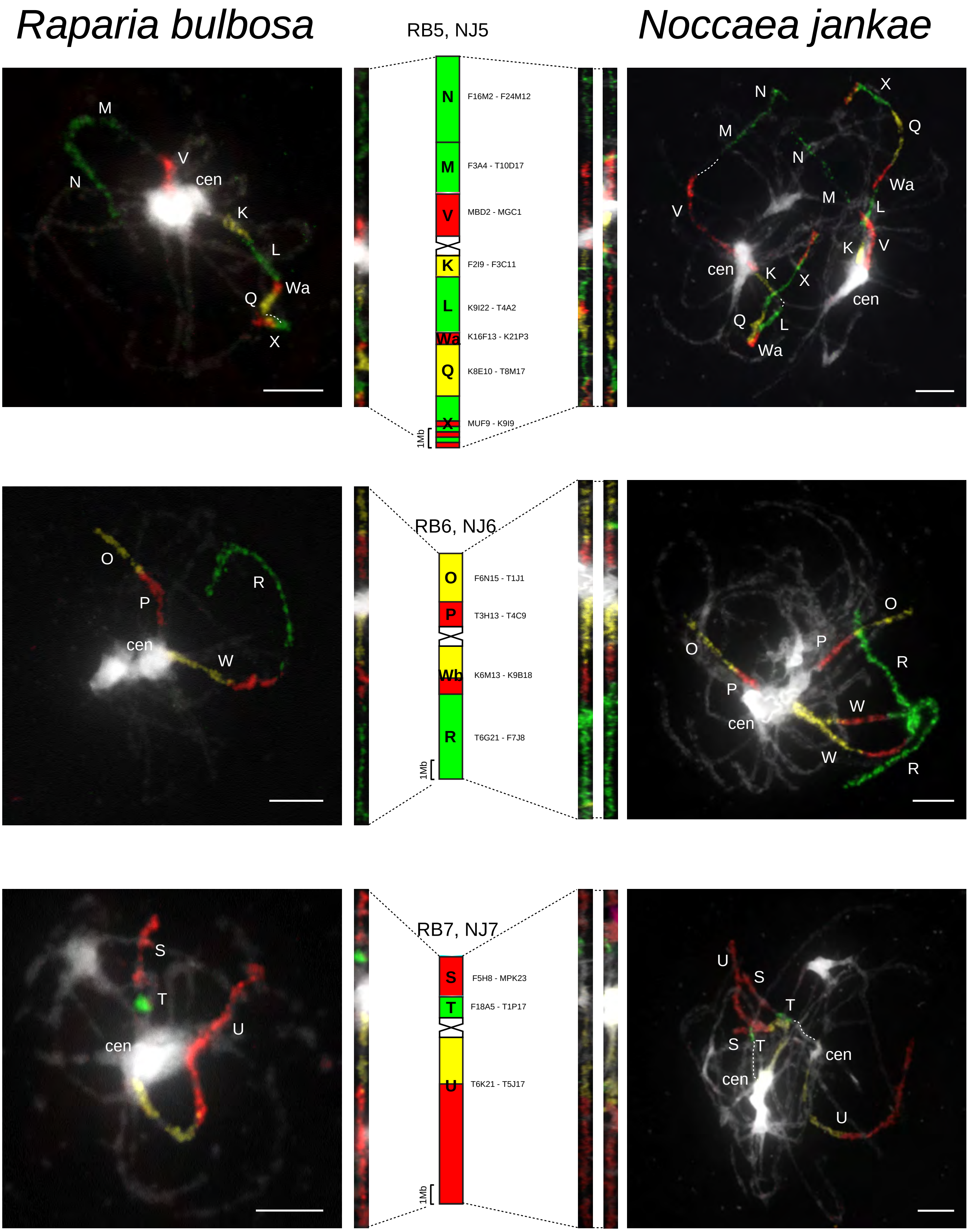
Supplementa Figure 1. Location of *Noccaea caerulescens* populations analyzed in the present study. S1: Kungs-Husby, S2: Sularp, CH1: Mont d´Amin, CH2: Haslital, CH3: Vallée de Saas, CZ1: Kořenec, CZ2: Mohelno, SK1: Špania dolina, F1: Bergenbach, F2: Viviez, F3: Puy de Wolf, F4: St. Felix de Pallières, and F5: St. Laurent le Minier.

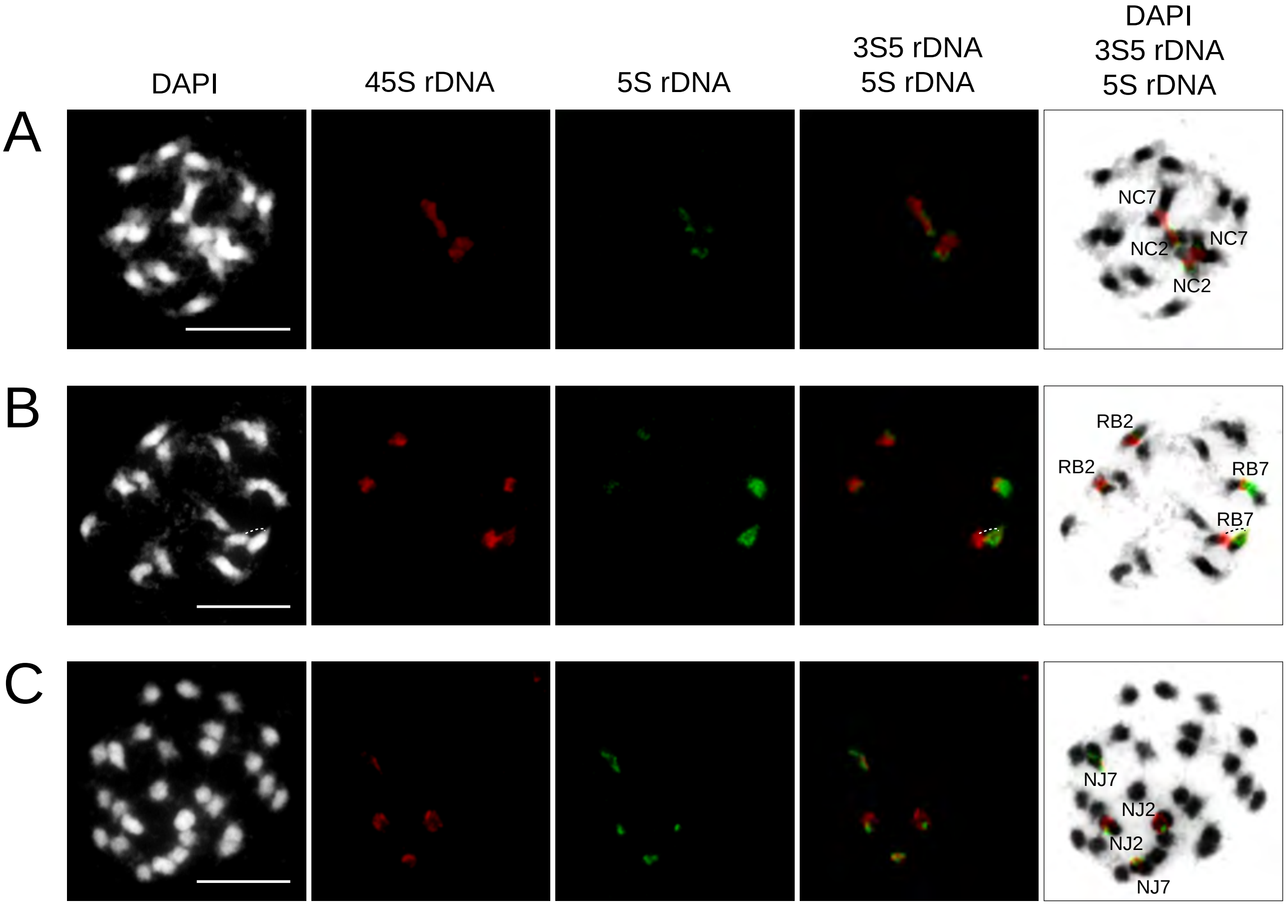


Supplemental Figure 2. Phylogenetic ralationships between Coluteocarpeae taxa analyzed in this study. (A) Phylogenetic tree of Coluteocarpeae based on ITS 1 and 2 sequences at the Brassibase website (http://brassibase.cos.uni-heidelberg.de/; Kiefer et al. 2014). Here the genus *Raparia* is embedded within the genus *Noccaea*. (B) The same phylogeny showing *Raparia* as a sister genus to *Noccaea* (redrawn from Koch and German 2013).

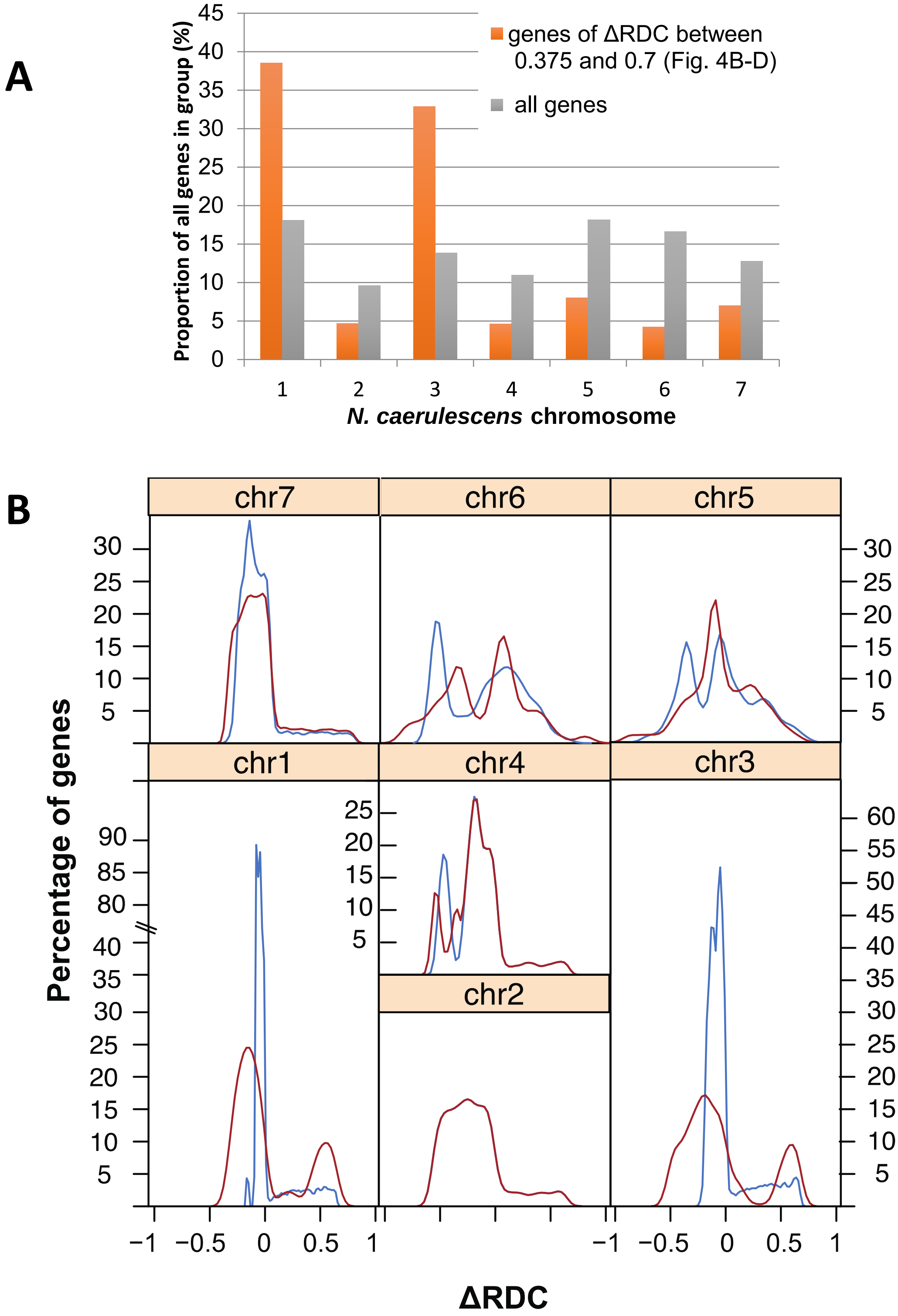


Supplemental Figure 3. Comparative structure of *R. bulbosa* and *N. jankae* chromosomes as inferred by CCP (see Figure 3 for complete karyotypes of both species). Chromosomes were painted with *A. thaliana* BAC contigs labelled by biotin-dUTP (red), digoxigenin-dUTP (green), and Cy3-dUTP (yellow); BAC clone coordinates of each contig used are given. Chromosomes counterstained by DAPI. All scales, 5 µm.


Raparia bulbosa
Noccaea jankae
RB5, NJ5
N
M
V
K
L
Wa
Q
X
F16M2 - F24M12
F3A4 - T10D17
MBD2 - MGC1
F2I9 - F3C11
K9I22 - T4A2
K16F13 - K21P3
K8E10 - T8M17
MUF9 - K9I9
1Mb
M
N
V
cen
K
L
Wa
Q
X
N
X
M
Q
N
Wa
M
V
L
K
V
cen
K
X
cen
Q
L
Wa
RB6, NJ6
O
P
Wb
R
F6N15 - T1J1
T3H13 - T4C9
K6M13 - K9B18
T6G21 - F7J8
1Mb
O
P
R
cen
W
O
O
P
R
P
W
cen
W
R
RB7, NJ7
S
T
U
F5H8 - MPK23
F18A5 - T1P17
T6K21 - T5J17
1Mb
S
T
U
cen
U
S
T
S
T
cen
cen
U



Supplemental Figure 4. Fluorescence *in situ* localization of 5S (green) and 35S (red) rDNA loci on chromosomes in *N. caerulescens* (A), *N. jankae* (B) and *R. bulbosa* (C). Chromosomes were indentified by CCP (see Figure 1, 2, and S3) and counterstained by DAPI. All scales, 5 µm.



Supplemental Figure 5. Distribution of genes and chromosome position differences with respect to *A. thaliana* along chromosomes of *N. caerulescens* and the ancestral PCK genome. A, Distribution of genes on *N. caerulescens* chromosomes for all genes and genes exhibiting ΔRDC between 0.375 and 0.7 (see Fig. 4). B, ΔRDC profiles of all genes shown for each *N. caerulescens* chromosome (red) and PCK chromosme (blue) (cf. Fig. 4). The secondary peak in Fig. 4 is primarily attributable to changes in RDC on chromosomes NC1 and NC3 relative to the homeologous PCK chromosomes (and also in comparison to *A. thaliana*; see Fig. 4), thus causing major changes in the lengths of the bottom arms of these two chromosomes (see Figs. 2A-B).