Table 1 Suppl. GenBank accession numbers for sequences used in phylogenetic analyses.

Taxon	Gene	GenBank accession number
AGMOUS-like genes accession number (see Fig. 2*A* Suppl.)		
*Arabidopsis thaliana*L.	*AGAMOUS*	NM_001203837
*Arabidopsis halleri*subsp.*halleri* L.	*AG*	JQ180296
*Arabidopsis lyrata*subsp. *kamchatica* L.	*AG*	JQ180294
Brassica napus L.	*BAG1*	M99415
Brassica rapa subsp.*pekinensis* L.	*KBrB060L22*	AC232508
Arabidopsis thaliana L.	*SHP1/AGL1*	NM_115740
Brassica napus L.	*BnSHP1*	AY036062
*Arabidopsis lyrata*subsp.*lyrata* L.		XM_002876433
Capsella bursa-pastoris L.	*SHP1b*	EU551771
Cakilelanceolata L.	*SHP1*	JX292963
Lepidiumappelianum L.	*SHP1*	FR727229
Lepidiumcampestre L.	*SHP1*	FR727235
Arabidopsis thaliana L.	*SHP2*	NM-180046
Brassica napus L.	*BnSHP2a*	EU424342
	BnSHP2b	EU424343
*Brassica rapa*subsp.*pekinensis* L.	*KBrH012N11*	AC189588
Capsella bursa-pastoris L.	*SHP2a*	EU551768
Cakilelanceolata L.	*SHP2*	JX292964
*Erucariaerucarioides*L.	*SHP2*	JX292970
Arabidopsis thaliana L.	*STK/AGL11*	NM_001203767
Capsella bursa-pastoris L.	*STK b*	EU551767
*Arabidopsis lyrata*subsp.*lyrata*L.		XM_002874550
NST1-like genes accession number (see Fig. 2*B* Suppl.)		
Arabidopsis thaliana L.	*NST1*	NM_130243
	NST2	NM_116056
	SND1	EF101892
*Arabidopsis lyrata*L.		XM_002882043
Cucumissativus L.	*NAC domain-containing protein 43-like*	XM_004140571
*Medicagotruncatula*L.	*NST1*	GU144511
Gossypiumhirsutum L.	*NST1*	HM565137
BHLH-like genes accession number (see Fig. 2*C* Suppl.)		
Arabidopsis thaliana L.	*IND*	NP_116229
	HEC3	M55553
*Brassica rapa*subsp. *pekinensis* L.	*BraA.IND.a*	GU386357
Brassica oleracea L.	*BolC.IND.a*	GU386356
Lepidiumcampestre L.	*IND*	FR727239
Lepidiumappelianum L.	*IND*	FR727233
Arabidopsis thaliana L.	*ALC*	NM_126111
*Arabidopsis lyrata*subsp.*lyrata*L.		XM_002864981
Brassica napus L.	*BnaA.ALC*	Hua *et al*. 2009*
	BnaC.ALC	Hua *et al*. 2009*
Lepidiumcampestre L.	*ALC*	FR727240
FRUITFULL-like genes accession number (see Fig. 2*D* Suppl.)		
Arabidopsis thaliana L.	*FUL/AGL8*	NM_125484
*Arabidopsis lyrata*subsp.*lyrata* L.		XM_002866356
Brassica oleracea L. var. *botrytis* L.	*FUL-a*	AJ505841
	FUL-b	AJ505842
	FUL-c	AJ505843
	FUL-d	AJ505844
Brassica napus L.	*Bn.FUL*	DQ414534
*Cakilelanceolata*L.	*FUL1*	JX292960
Cakilelanceolata L.	*FUL2*	JX292961
Lepidiumappelianum L.	*FUL*	FR727231
Lepidiumcampestre L.	*FUL*	FR727237
Erucariaerucarioides L.	*FUL*	JX292966
Sinapis alba L.	*SaMADS*	U25695

* Hua, S., Shamsi, I.H., Guo, Y., Pak, H, Chen, M., Shi, C., Meng, H., Jiang, L.: Sequence, expression divergence, and complementation of homologous *ALCATRAZ* loci in *Brassica napus*. - Planta **230**: 459-503, 2009.

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BraA.SHP1   CTGAATGTCCCGAATCTGCCTCCGAAGCTTAGAGGCTTCTTGCTGATAGTACTGAGTATT
SalS.SHP1   --GAATGTCCCGAATCTGCCTCCGAAGCTTAGAGGCTTCTTGCTGATAGTACTGAGTATT
Bca.SHP1    CTGAATGTCCCGAATCTGCCTCCGAAGCTTAGAGGCTTCTTGCTGATAGTACTGAGTATT
Bna.SHP1    CTGAATGTCCCGAATCTGCCTCCGAAGCTTAGAGGCTTCTTGCTGATAGTGCTTGGTATT
            ************************************************** **  *****

BraA.SHP1   AGCTTCGGTGACAGTAGGAGGGTTAACGGCATCGGAACAAGCTTTCTTATACCTTTCAAT
SalS.SHP1   AGCTTCGGTGACAGTAGGAGGGTTAACGGCATCGGAACAAGCTTTCTTATACCTTTCAAT
Bca.SHP1    AGCTTCGGTGACAGTAGGAGGGTTAACGGCATCGGAACAAGCTTTCTTATACCTTTCAAT
Bna.SHP1    AGCTTCAGTGACAGTAGGAGGGTTAACGGCATCGGAACAAGCTTTCTTGTACCTTTCAAT
            ****** ****************************************** ***********

BraA.SHP1   TGTACCCTTCACACTGTTGCTGGCGTATTCATAGAGACGGCCACGAGTGGAGAAGATAAC
SalS.SHP1   TGTACCCTTCACACTGTTGCTGGCGTATTCATAGAGACGGCCACGAGTGGAGAAGATAAC
Bca.SHP1    TGTACCCTTCACACTGTTGCTGGCGTATTCATAGAGACGGCCACGAGTGGAGAAGATAAC
Bna.SHP1    TGTACCCTTCACACTGTTGCTGGCGTACTCATAAAGAAGGCCACGAGTGGAGAAGATAAC
            ***************************** ***** *** **********************

BraA.SHP1   GAGGGCAACTTCAGCATCACAC
SalS.SHP1   GAGGGCAACTTCAGCATCACAC
Bca.SHP1    GAGGGCAACTTCAGCATCACAC
Bna.SHP1    GAGGGCAACTTCAGCATCACAC
            **********************

Bca.SHP2    -CAGGAAGCGAGTGTGATACATCAACAAGGGACGGTTTACGAGTCGTCTTCCCATCAGTC
BraA.SHP2   GCAGGAAGCGAGTGTGATACATCAACAAGGGACGGTTTACGAGTCATCTTCTCATCAGTC
Bna.SHP2    GCAGGAAGCGAGTGTGATACATCAACAAGGGACGGTTTACGAGTCATCTTCTCATCAGTC
SalS.SHP2   GCAGGAAGCGAGTGTGATACATCAA---GGGACGGTTTACGAGTCATCTTCACATCAGTC
             ************************   ****************** ***** ********

Bca.SHP2    GGAGCAGTACAACCGGAACTATATTCCGGTTAACCTTCTTGAACCAAATCAGAACTCCTC
BraA.SHP2   GGAGCAGTACAACCGGAACTATATTCCGGTTAACCTTCTTGAACCAAATCAGAACTCCTC
Bna.SHP2    GGAGCAGTACAACCGGAACTATATTCCGGTTAACCTTCTTGAACCAAATCAGAACTCCTC
SalS.SHP2   GGAGCAGTATAACCGGAATTATATTCCGGTTAACCTTCTTGAACCAAATCAGAACTCCTC
            ********* ******** ****************************************

Bca.SHP2    CGACCAAAAC
BraA.SHP2   CGACCAAAAC
Bna.SHP2    CGACCAAAAC
SalS.SHP2   CGACCAAAAC
            **********

BraA.IND    TTCAAGAACTTGGTGTAGCGGATGGCTTCGTCGAGCATGGAGGCAGTGTCCATCTTTGCA
Bca.IND     TTCAAGAACTTGGTGTAGCGGATGGCTTCGTCGAGCATGGAGGCAGTGTCCATCTTTGCA
SalS.IND    TTCAAGAACTTGGTGTAGCGGATGGCTTCGTCGAGCATGGAGGCAGTGTCCGTCTTTGCA
Bna.IND     TTCAAGAACTTGGTGTAGCGGATGGCTTCGTCAAGCATGGAGGCAGTGACCATCTTTGCA
            ********************************** ********** ** ********

BraA.IND    CCGCCTGGCACCATCCTCTTCAATATCCGGATCTTCTCGCTTATCCTTTCTCTACGCCGA
Bca.IND     CCGCCTGGCACCATCCTCTTCAATATCCGGATCTTCTCGCTTATCCTTTCTCTACGCCGA
SalS.IND    CCGCCTGGCACCATCCTCTTCAATATCCGGATCTTCTCGCTTATCCTTTCTCTACGCCGA
Bna.IND     CCGCCTGGCACCATCCTCTTCAATATCCGGATCTTCTCGCTTATCCTTTCTCTACGCCGA
            ************************************************************

BraA.ALC    GTTTCTTACGCCGCTTGTGCAGCCGCTGAAACTGGGGAAGGCAAATGTGGTTTCGAAAAC
Bna.ALC     GTTTCTTACGCCGCTTGTGCAGTCGCTGAAACTGGGGAAGGCAAATGTGGTTTCGAAAAC
Bca.ALC     GTTTCTTACGCCGCTTGTGCAGTCGCTGAAACCGGGGAAGGCAAATGTGGTTTCGAAAAC
SalS.ALC    GTTTCTTACGCCGCTTGTGCAGTCGCTGAAACTGGGGAAGGCAAATGTGATTTCGAAAAC
            ********************** ********* ********** ********** **********

BraA.ALC    AAGAGAAATGGAGCTAAACAGCGAAATTCATTGAAGAGAAACATTGATGCACAGTTCCAC
Bna.ALC     AAGAGAAATGGAGCTAGACAGCGAAATTCATTGAAGAGAAACATTGATGCACAGTTCCAC
Bca.ALC     AAGAGAAATGGAGCTAGACAGCGAAAATCATTGAAGAGAAACATTGATGCACAGTTCCAC
SalS.ALC    AAGAGAAATGGAGCTAGACAGAGAAATTCGTTGAAGAGAAACATTGATGCACAGTTCCAC
            ***************** **** **** ** ********************************

BraA.ALC    ACCTTGTCTGAAAAGGTAGGAGGAGGAGCAAGATCAACGAGAA
Bna.ALC     ACCTTGTCTGAAAAGGTAGGAGGAGGAGCAAGATCAACGAGAA
Bca.ALC     ACCTTGTCTGAAAAG--AGGAGGAGGAGCAAGATCAACGAGAA
SalS.ALC    AACTTGTCTGAAAAG--AGGAGGAGGAGCAAGATCAACGAGAA
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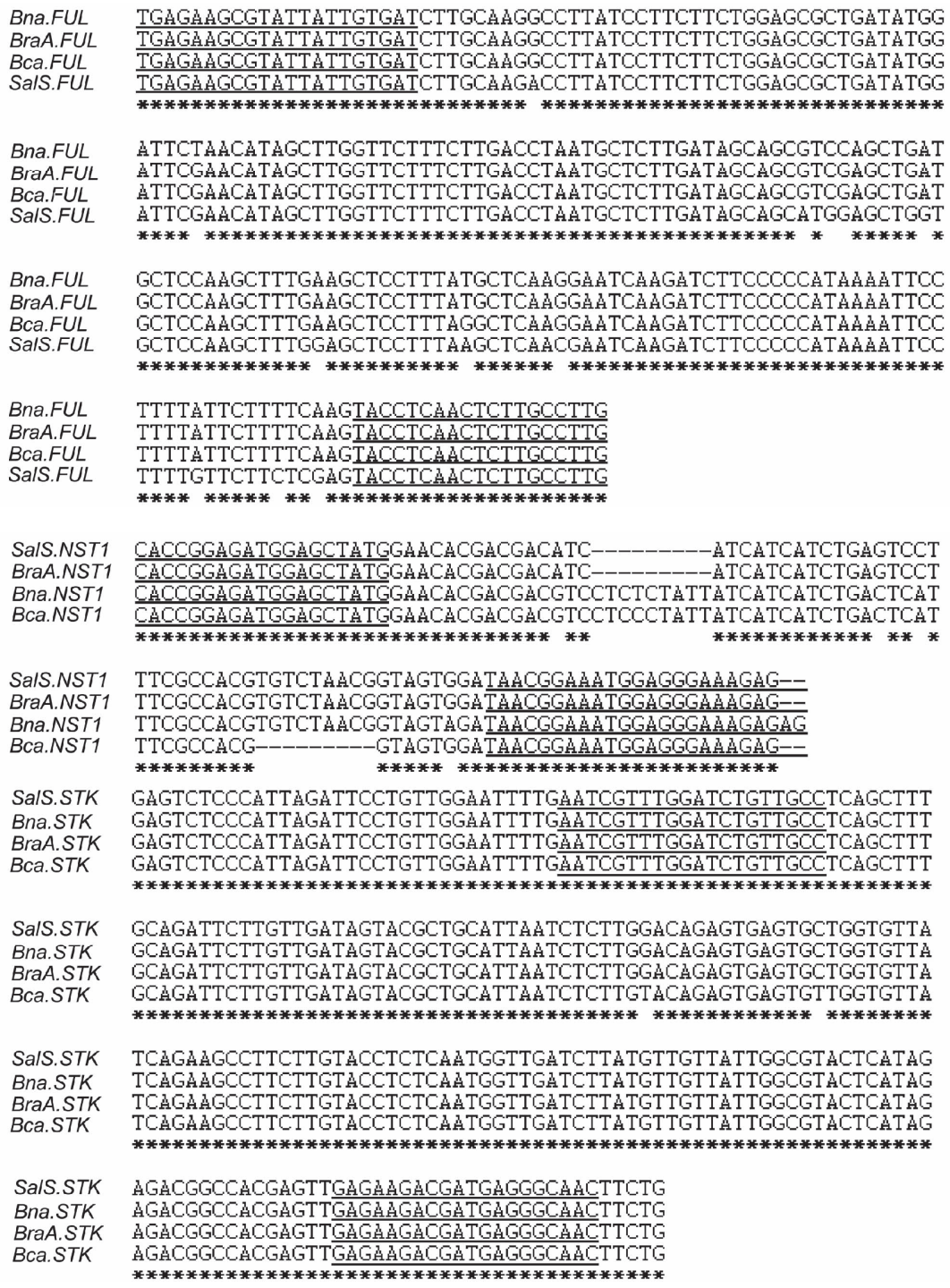

Fig. 1. Suppl. Alignments of *SHP1*, *SHP2*, *IND*, *ALC*, *FUL*, *AG*, *NST1*, and *STK* homolog sequences identified from *Sinapis alba* (*SalS*-), *Brassica napus* (*Bna*-), *B. rapa* (*BraA*-), and *B. carinata* (*Bca*-). *Stars* represent the same nucleotides of multiple sequences. Primers for real-time qPCR are denoted by single underline.

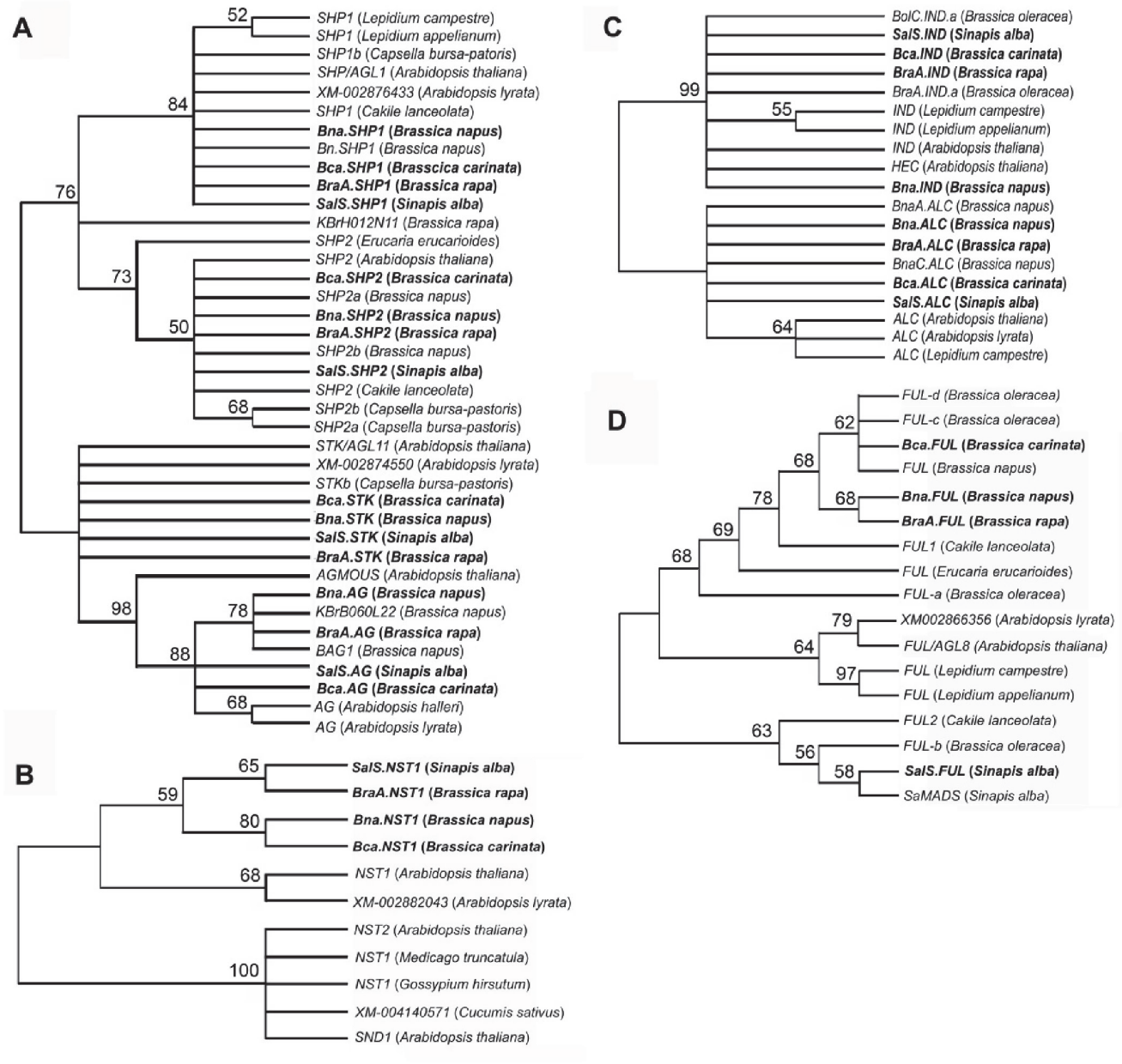

Fig. 2. Suppl. Neighbor-joining trees of pod shattering-related genes. *A* - Neighbour-joining tree of *AGAMOUS*-like genes including *SHATTERPROOF1*, *SHATTERPROOF2*, *AGAMOUS*, and *SEEDSTICK* homologs identified from *Sinapis alba* (*SalS.SHP1, SalS.SHP2*, *SalS.AG*, and *SalS.STK*, *in bold*), *Brassica napus* (*Bna.SHP1*, *Bna.SHP2*, *Bna.AG*, and *Bna.STK*, *in bold*), *B. rapa* (*BraA.SHP1*, *BraA.SHP2*, *BraA.AG*, and *BraA.STK*, *in bold*), and *B. carinata* (*Bca.SHP1, Bca.SHP2*, *Bca.AG*, and *Bca.STK*, *in bold*). *B* - Neighbor joining tree of *NST1*-like genes including *NST1* homologs identified from *S. alba*, *B. napus*, *B. rapa*, and *B. carinata* (*SalS.NST1*, *BnaNST1*, *BraA.NST1*, and *Bca.NST1*, *in bold*). *C* - Neighbor joining tree of bHLH-like genes (*IND* and *ALC*) including homologs identified from *S. alba* (*SalS.IND* and *SalS.ALC*, *in bold*), *B. napus* (*Bna.IND* and *Bna.ALC*, *in bold*), *B. rapa* (*BraA.IND* and *BraA.ALC*, *in bold*), and *B. carinata* (*Bca.IND* and *Bca.ALC*, *in bold*). *D* - Neighbor joining tree of *FRUITFULL*(*FUL*)-like genes including *FUL* homologs identified from *S. alba*, *B. napus*, *B. rapa*, and *B. carinata* (*SalS.FUL*, *Bna.FUL*, *BraA.FUL*, and *Bca.FUL*, *in bold*). Taxon names and GenBank accession numbers are provided in Table 1 Suppl. The *numbers* above the major branches indicate bootstrap values ≥ 50 %.

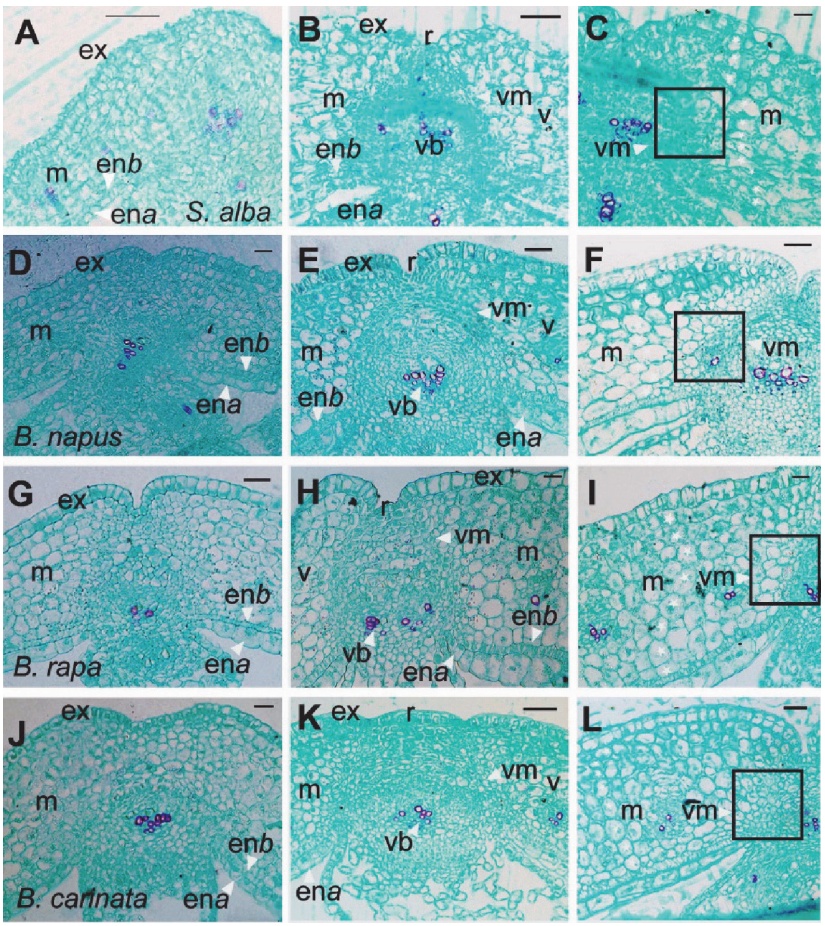

Fig. 3. Suppl. Transverse sections showing fruit development at pre-fertilization (stage 13, *A*, *D*, *G*, *J*) or just post-fertilization (stage16, *B*, *C*, *E*, *F*, *H*, *I*, *K*, *L*) stages in *Sinapis alba* (*A-C*), *Brassica napus* (*D-F*), *B. rapa* (*G-I*), and *B. carinata* (*J-L*). Staining with Safranin *O* and Fast Green reveals the light blue separation layer on the replum side of the valve margin. v - valve, r - replum, vm - valve margin, sl - separation layer, lm - lignified layer at the valve margin, en*b* - endocarp *b* layer, en*a* - endocarp *a* layer, m - mesocarp, ex - exocarp, vb - vascular bundle. *Stars*- cells of the mesocarp layer, *square frames* - valve margin cells, *scalebars* in *B*, *E*, *F*, *K* = 50 µm, in *A*, *C*, *D*, *F*, *G-J*, *L* = 20 µm.