**Supplementary Figure S1.** Genomic sequences of the *Brassica napus DOG1* homologues. Predicted exons are indicated with black letters in a white background, predicted introns are indicated with white letters in a grey background.

BAC3 (*BnaA.DOG1.a*)

**1 ATGGAGGACA AAGGGAAAAA CATCGAACAA GCTCAACAAA GTTGTTACCT**

**51 AGGGTGGATG AGTTTACAAT CCCAACGTGT CCTTGACCTT AAACAAGCCT**

**101 TAGCTCAACG ACGATCTCAC GAAGGCACAG CCGACGCTGC CGCGGATGAT**

**151 AAGAAACTCC GTGAATTAAC ACAAAAGATC ATTGGAGACT TCAAAGATTA**

**201 CGCCCGAAAA AGAGCCGATC TTTCACACCG ATGTAGCTCG AGCTATTATG**

**251 CGCCGTCGTG GAACACTCCT TTGGAGAACG CTCTCATTTG GATGGGTGGC**

**301 TGCAGACCAT CTTCTTTCTT TAGGCTTGTT TATGCTCTGT GTGGGTCCCA**

**351 AACTGAGATC CGTGTGACTC AGTTTCTCCG CAACATCGAT GGTTACGATG**

**401 CTTCAGGTAA CTTAAGGGTT TGGACATTAT CAGTTATTTG GAATTTTACT**

**451 TCTTATTTTC ACTTAGTTTG GTCAGCTCCG GTTCCAACAT CCGAATAAAA**

**501 CATTCTTCTT GGTTCCAAAA TTAAAAGTTA TTATACATAC ATTTTATTGC**

**551 TTTTAAACTG TCAATATTTT ATTAAAATTA ATTTAACACT GTTTATGGTC**

**601 TTTTGGATCT GGCCGGTCCT TGTTTAGTTT GGTTTCAATT TAAAAAATTT**

**651 GTTTTTGGTT TAAGAATTTT TAGGTCTAGT TTAGTACAAT TCGGTTTGAT**

**701 TCAACAGGTA GTGGTGGCGC ATCGCTCAGC GATCTAACGG CGGAGCAGCT**

**751 GGCGAAGATC AACGTCTTGC ATGTGAAGAT CATAGACGAA GAAGAGAAGA**

**801 TGACCAAGAA AGTCTCCAGT CTGCAAGAAG ACGCGGCTGA TATTCCTATC**

**851 TCCACCGTGG CTTACGCGGA GGAGCACGTT GGAGAGCCTA ACTTGGCGGT**

**901 AGATCAAGCT CTCGACAAGC AAGAAGAAGC TATGGCCACT TTATTAGCCG**

**951 AGGCCGATAA TCTGAGGGTA TATACTTTGA GTAAGATCAT AGAGGTTCTG**

**1001 GCGCCGATGC AAGCCGCGGA TTTTTTGCTG GCCGGGAAAA AACTTCATCT**

**1051 TTCAATGCAT GCGTGGGGAG CGCTAAGGGA TCGCCGCCGT CGTGAATGTA**

**1101 TAATAGACGC CGCAGATGAT GCCGGAGGGA AGGAGGGGAA GTAG**

BAC1(*BnaC.DOG1.a*)

**1 ATGGAGGACA AAGGGAAAAA CATCGAACAA GCTCAACAAA GTTGTTACCT**

**51 AGGGTGGATG AGTTTACAAT CCCAACGCGT CCTTGACCTT AAACAAGCCT**

**101 TAGCTCAACG ACGATCTCAC GAAGGCACAG CCGACGCTGC CACGGATGAG**

**151 AAGAAACTCC GTGAATTAAC ACAAAAGATC ATTGGAGACT TCAAAGATTA**

**201 CGCCCGAAAA AGAGCCGATC TCTCACACCG ATGTAGCTCG AACTATTATG**

**251 CGCCGTCGTG GAACACTCCT TTGGAGAACG CTCTGATTTG GATGGGTGGC**

**301 TGCAGACCAT CTTCTTTCTT TAGGCTTGTT TATGCTCTGT GTGGGTCCCA**

**351 AACTGAGATC CGTGTGACTC AGTTTCTCCG CAACGTCGAT GGTTACGATA**

**401 CTTCAGGTAA TTTAAGGGTT TGGACATTAT CAGTTATTTG GGATTTTACT**

**451 TCTTTTCACT TCTTAGTTTG GTCAGCTCCG GTTCCAAACA TCCGAATAAA**

**501 ACATTCTTCT TTGTTCCAAA ATTTAAAGTT ATTATACATA CATTTTATTG**

**551 CTTTTAAATT GTCAATATTT TATCAAAATT AATTTAAAAA TGTTTATGGT**

**601 CTTTTAGATC TGGCCGGTCC TGGATTTAGT TTGGTTTCAG TTTAAAATTT**

**651 TGTTTTTTTG GTTTAAGAAT TTTTAGGTCT GAGTTTAGTT CAATTCGGTT**

**701 TGATTCAACA GGTAGTGGTG GCGCATCACT CAGCGATCTA ACGGCGGAGC**

**751 AGCTGGCGAA GATCAACGTC TTGCATGTGA AGATCATAGA CGAAGAAGAG**

**801 AAGATGACCA AGAAAGTCTC CAGTCTGCAA GAAGACGCCG CTGATATTCC**

**851 TATCTCCACC GTGGCTTACG CGGAGGAGCA CGTAGGAGAG CCTAACTTGG**

**901 CAGTAGATCA AGCTCTCGAC AAGCAAGAAG AAGCTATGGC CACTTTATTG**

**951 GCCGAGGCCG ATAATCTGAG GGTATATACG TTGAGTAAAA TCATAGAGGT**

**1001 TCTGGCGCCG ATGCAAGCCG CGGATTTTTT GCTAGCCGGG ATAAAACTTC**

**1051 ATCTTTCAAT GCATTCTTGG GGAGCGCTAA GGGATCGCCG CCGTCGTGAA**

**1101 TGTATAATAG AGGCCGCAGA TGATGCCGGA GGGAAGGAAG GGAAGTAG**

BAC4 (*BnaC.DOG1.b*)

**1 ATGGAGAACA AAGGGAAGAA CATCGAACAA GCTCAAGAAA GTTGTTATCA**

**51 ACAGTGGATG AGTTTACAAT CCCAACGCGT CCCTGAGCTT AAACAAGCCT**

**101 TAGCTCAACG GCGCACTCAC GAAGGCACCG CCGACGCTGC CGCCGATGAT**

**151 AACAAGCTCC GTGAATTAAC ACAAAACATC ATTGGAGATT TCAAAAATTA**

**201 CGCTGGAAAA AGAGCTGATT TATCTCACCG ATGTAGCTCG AACTATTATG**

**251 CGCCGTCGTG GAACACTCCT TTAGAGAACG CTCTTCTTTG GATGGGTGGT**

**301 TGTAGACCTT CTTCTTTCTC GAGGCTCGTT TATGCTTTGT GTGGGTCCCA**

**351 AACCGATATT CTTGTTACTC AGTTTCTCCG TAACATCGAC GGCTACAATT**

**401 ATTCAGGTAA GGGTTTGGAC GTTTTCGGTT TTCTCAAAAG AGGTTTAAGA**

**451 ATCACTTAAC AAAAAAATAC TTTTCTATTC GGTTAACCAA AATTTTGGAT**

**501 TGGTTTGGAC AGGCACATCT AACTCGATGT TAAAATTTAC AATTATATCT**

**551 GTAAAAATCA ATAATATTAA TATATATATA TATATATATA TATATATATT**

**601 ATGATTTTTT TTGAAAAATA TATATAATAT GGTTTAACAT ATTACAGTTT**

**651 ATGTAGTAAG ATTTTCTGAC CATTTTGAAT TCTGCTGGGA TCTAACCTGA**

**701 GACTTGGTTT TTGGTTTCAG TTTAAGAGGT GTGAAAGATG AACTTTAGTT**

**751 AGGTTTGTTG TTTGGTTTAG TTTGTTCGAT ATAAACACCC GGTTTAGTTT**

**801 TTAATAATCT GGTCCAGGTT TATTATAACA TAATTCCATC TCGTTTATTA**

**851 ATACAGAAAA TATTTGGCTT ATTTTTTGTC ATAATCAAAA TGATGTAACG**

**901 CATAGATTTA TACATATCTT GGTTGTGGTT AAAAATTATG TTTTTGATTA**

**951 AAGAATTTTA GTTGGTATTT AATCCAATTT GGTCTGGTTC AACAGGTAGT**

**1001 GGTGGCGCAT CACTCAGCGA TCTAACGGCG GAGCAACTAG CAGAGATCAA**

**1051 CGTGTTGCAT GTAAAAATCA TAGACGAAGA AGAGAAGATG ACAAAGAAAG**

**1101 TTTCGAGCCT GCAAGAAGAC GCGGCGGATA TCCCCATCTC CACCGTGGCT**

**1151 TACGCAGAGG AGCACGTGGG AGAGCCTAAC GCAATGGTGG ATCAAGCTCT**

**1201 CGACAAGCAG GAAGAAGCTA TGGCCACTTT ATTGGCCGAG GCCGATAATC**

**1251 TGAGGGTAGA TACTTTGACC AAGATCATAG AGATTCTGAC GCCAGTGCAA**

**1301 GCGGGGGATT TTTTTATGGC CGGAAAAAAG CTTCATCTTT CAATGCATCA**

**1351 GTGGGGAGCG TTAAGAGATC GGCGCCGTCG TGAATGCATA ATTGACGCTG**

**1401 GAAACGATGC CGGAGGAGAG GAGGAGAAGT AG**