**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**