

The control of seed oil polyunsaturate content in the polyploid crop species *Brassica napus*

Molecular Breeding

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Primer No.	Sequence (5'-3')	Length (bp)	GC %	Tm
1	GTCTCCTCCCTCCAAAAAGT	20	50.0	54.9
2	GTGTCTCCTCCCTCCAAA	18	55.6	51.9
3	CTACAGAAACAAACATGGGC	20	45.0	53.1
4	CTCTCCTCCCTCCAGCTCCC	20	70.0	62.4
5	CTCTTCGACATCCTCCTCTC	20	55.0	53.3
6	CCTCGTCCCTTACTTCTCCTG	21	57.1	58.2
7	CCTCATAACTTATTGTTGTACCAG	24	37.5	53.9
8	CAAGACGACCAGAGACAGC	20	55.3	55.0
9	GAACTCGACAAATTTGCCTG	20	55.7	45.0

Supplemental Table 1. Primers used for the amplification of *BnaFAD2*.

Homologue	F primer	R primer	Amplicon size (bp)	Notes
<i>BnaC.FAD2.a</i>	1	8	1212	
<i>BnaA.FAD2.a</i>	2	7	1133	
<i>BnaC.FAD2.b</i>	5	7	991	Will not amplify in Cabriolet
<i>BnaA.FAD2.b</i>	6	9	966	
<i>BnaA.FAD2.b</i>	3	7	1173	<i>BnaA.FAD2.a</i> -specific in Cabriolet. Will also amplify <i>BnaC.FAD2.a</i> in other genotypes.
<i>BnaA.FAD2.b</i>	4	7	1133	<i>BnaA.FAD2.a</i> -specific in Cabriolet. Will also amplify <i>BnaC.FAD2.a</i> in other genotypes.

Supplemental Table 2. Primer combinations required for the homologue specific amplification of *BnaFAD2*.

Treatment	Total sown	Establishment %	No. grown on	% plants with >20seed	Fertile plants %
0	1000	86.0	42	73.2	97.6
0.2	6000	77.0	42	88.1	100.0
0.4	6000	76.9	4130	91.6	90.2
0.6	6000	73.5	4352	92.0	98.7
0.8	6000	60.7	1148	93.7	100.0
1	6000	70.0	42	63.3	71.4
2	1000	0.0	0	N/A	N/A
0	1000	86.0	42	73.2	97.6

Supplemental Table 3. Emergence, fertility and seed number of *B. napus* Cabriolet seeds subjected to EMS treatment.

Line	EMS %	Mutation	Status	Position relative to first coding base	Amino acid number	Amino acid	Amino acid classification	New amino acid	New amino acid classification	
S	713	0.6	C>CT	HET	224	75	Pro	Non-polar	Leu	Non-polar
M	77	0.4	C>CT	HET	228	76	Leu	Silent		
S	595	0.6	C>CT	HET	228	76	Leu	Silent		
K	28	0.8	C>CT	HET	239	80	Pro	Non-polar	Leu	Non-polar
M	529	0.6	C>T	HOM	241	81	Leu	Non-polar	Phe	Non-polar
S	388	0.8	C>CT	HET	245	82	Ser	Polar	Phe	Non-polar
S	314	0.8	G>AG	HET	257	86	Trp		STOP	
M	2505	0.8	G>AG	HET	258	86	Trp		STOP	
K	722	0.6	C>CT	HET	264	88	Leu	Silent		
M	2419	0.8	C>CT	HET	264	88	Leu	Silent		
S	732	0.6	G>AG	HET	270	90	Trp		STOP	
K	472	0.8	G>GA	HET	284	95	Cys	Polar	Tyr	Polar
M	2464	0.8	G>A	HOM	286	96	Val	Non-polar	Ile	Non-polar
M	1069	0.6	G>AG	HET	296	99	Gly	Polar	Asp	Acidic
S	127	0.8	C>CT	HET	297	99	Gly	Silent		
M	814	0.6	G>A	HOM	310	104	Ala	Non-polar	Thr	Polar
K	164	0.6	C>CT	HET	312	104	Ala	Silent		
S	635	0.6	C>CT	HET	315	105	His	Silent		
S	1021	0.6	G>AG	HET	316	106	Glu	Acidic	Lys	Basic
S	135	0.8	C>CT	HET	321	107	Cys	Silent		
M	2234	0.8	G>GA	HET	322	108	Gly	Polar	Ser	Polar
S	418	0.8	C>CT	HET	328	110	His	Basic	Tyr	Polar
M	951	0.6	C>T	HOM	330	110	His	Silent		
S	422	0.8	C>CT	HET	333	111	Ala	Silent		
M	888	0.6	C>CT	HET	345	115	Tyr	Silent		
M	643	0.6	G>AG	HET	350	117	Trp		STOP	
S	17	0.8	G>AG	HET	355	119	Asp	Acidic	Asn	Polar
S	57	0.8	C>CT	HET	366	122	Val	Silent		
K	692	0.6	G>GA	HET	367	123	Gly	Polar	Ser	Polar
S	149	0.8	G>AG	HET	367	123	Gly	Polar	Ser	Polar
K	647	0.4	G>GA	HET	368	123	Gly	Polar	Asp	Polar
S	740	0.6	C>CT	HET	375	125	Ile	Silent		
M	2326	0.8	C>CT	HET	388	130	Leu	Non-polar	Phe	Non-polar
M	830	0.6	C>CT	HET	390	130	Leu	Silent		
K	71	0.8	C>CT	HET	405	135	Phe	Silent		
S	131	0.8	C>T	HOM	408	136	Ser	Silent		
S	689	0.6	C>CT	HET	408	136	Ser	Silent		
S	1015	0.6	C>CT	HET	408	136	Ser	Silent		
K	60	0.8	C>CT	HET	417	139	Tyr	Silent		
K	350	0.6	C>CT	HET	421	141	His	Basic	Tyr	Polar
K	143	0.6	G>A	HOM	425	142	Arg	Basic	Gln	Polar
M	2179	0.8	G>A	HOM	428	143	Arg	Basic	His	Basic
M	1112	0.6	C>CT	HET	432	144	His	Silent		
S	322	0.8	C>CT	HET	437	146	Ser	Polar	Phe	Non-polar
M	1083	0.6	C>CT	HET	438	146	Ser	Silent		
M	962	0.6	G>GA	HET	458	153	Arg	Basic	Lys	Basic
M	1069	0.6	G>AG	HET	458	153	Arg	Basic	Lys	Basic
M	1070	0.6	G>AG	HET	458	153	Arg	Basic	Lys	Basic
M	635	0.6	C>CT	HET	475	159	Pro	Non-polar	Ser	Polar
M	611	0.6	G>A	HOM	480	160	Lys	Silent		
K	430	0.8	G>GA	HET	490	164	Asp	Acidic	Asn	Polar
K	750	0.6	G>GA	HET	498	166	Lys	Silent		
M	2345	0.8	G>AG	HET	510	170	Lys	Silent		
K	325	0.6	G>A	HOM	543	181	Met	Non-polar	Ile	Non-polar
M	14	0.4	C>CT	HET	560	187	Thr	Polar	Asn	Polar
M	2466	0.8	G>AG	HET	566	189	Gly	Polar	Asp	Acidic
S	108	0.8	G>AG	HET	566	189	Gly	Polar	Asp	Acidic
M	362	0.6	G>GA	HET	570	190	Trp		STOP	
K	420	0.8	C>CT	HET	579	193	Tyr	Silent		
S	92	0.8	G>AG	HET	598	200	Gly	Polar	Arg	Basic
M	965	0.6	C>CT	HET	615	205	Gly	Silent		
M	2515	0.8	G>AG	HET	616	206	Gly	Polar	Tyr	Polar
S	32	0.8	G>AG	HET	617	206	Gly	Polar	Asp	Acidic
M	2127	0.8	C>CT	HET	623	208	Ala	Non-polar	Val	Non-polar
S	305	0.8	C>CT	HET	623	208	Ala	Non-polar	Val	Non-polar
M	2287	0.8	C>CT	HET	627	209	Cys	Silent		
M	967	0.6	C>CT	HET	633	211	Phe	Silent		

M	1136	0.6	C>CT	HET	633	211	Phe	Silent		
S	350	0.8	C>CT	HET	634	212	His	Basic	Tyr	Polar
M	2444	0.8	C>CT	HET	637	213	Pro	Non-polar	Ser	Polar
K	497	0.4	C>CT	HET	642	214	Asn	Silent		
S	265	0.8	C>A	HOM	642	214	Asn	Polar	Lys	Basic
M	2547	0.8	G>AG	HET	643	215	Ala	Non-polar	Thr	Polar
S	770	0.6	C>CT	HET	657	219	Asn	Silent		
S	1154	0.6	C>CT	HET	657	219	Asn	Silent		
S	354	0.8	G>A	HOM	662	221	Arg	Basic	His	Basic
M	2481	0.8	C>CT	HET	684	228	Ile	Silent		
S	405	0.8	C>CT	HET	686	229	Ser	Polar	Phe	Non-polar
K	938	0.6	C>CT	HET	687	229	Ser	Silent		
S	585	0.6	C>T	HOM	687	229	Ser	Silent		
S	336	0.8	C>CT	HET	702	234	Leu	Silent		
M	405	0.6	C>T	HOM	704	235	Ala	Non-polar	Val	Non-polar
M	2552	0.8	G>AG	HET	710	237	Cys	Polar	Tyr	Polar
M	2381	0.8	G>AG	HET	715	239	Gly	Polar	Ser	Polar
K	47	0.8	G>AG	HET	716	239	Gly	Polar	Asp	Acidic
S	389	0.8	C>CT	HET	729	243	Tyr	Silent		
K	411	0.8	C>CT	HET	732	244	Ala	Silent		
M	2210	0.8	C>CT	HET	737	246	Ala	Non-polar	Val	Non-polar
M	2248	0.8	C>TC	HOM	737	246	Ala	Non-polar	Val	Non-polar
S	619	0.6	G>A	HOM	743	248	Gly	Polar	Glu	Acidic
M	2349	0.8	G>A	HOM	772	258	Val	Non-polar	Ile	Non-polar
M	830	0.6	C>CT	HET	776	259	Pro	Non-polar	Leu	Non-polar
S	244	0.8	C>CT	HET	776	259	Pro	Non-polar	Leu	Non-polar
S	243	0.8	G>AG	HET	777	259	Pro	Silent		
M	2147	0.8	C>CT	HET	778	260	Leu	Non-polar	Phe	Non-polar
M	2135	0.8	G>GA	HET	807	269	Leu	Silent		
M	2170	0.8	G>GA	HET	807	269	Leu	Silent		
S	1154	0.6	C>CT	HET	816	272	Tyr	Silent		
M	1085	0.6	G>AG	HET	876	292	Arg	Silent		
S	329	0.8	C>CT	HET	890	297	Thr	Polar	Ile	Non-polar
M	1020	0.6	C>CT	HET	924	308	Val	Silent		
M	2230	0.8	C>CT	HET	939	313	Thr	Silent		

Supplemental Table 4. Mutations in *BnaC.FAD2.a* identified in the JBnaCAB_E population.

Supplemental Figure 1. BnaFAD2 sequence alignment

		Section 1										
		(1)	1	10	20	30	40	50	55			
Tap_BnaC.FAD2.a	(1)	ATGGG	TGCAGGTGGAAGAATGCAAGT	GTCTCCTCCCTCCA	AGAAAGTCTGAAACC	G						
Cab_BnaC.FAD2.a	(1)	ATGGG	TGCAGGTGGAAGAATGCAAGT	GTCTCCTCCCTCCA	AGAAAGTCTGAAACC	G						
Tap_BnaA.FAD2.a	(1)	ATGGG	TGCAGGTGGAAGAATGCAAGT	GTCTCCTCCCTCCA	AAAGTCTGAAACC	G						
Cab_BnaA.FAD2.a	(1)	ATGGG	TGCAGGTGGAAGAATGCAAGT	GTCTCCTCCCTCCA	AAAGTCTGAAACC	G						
Tap_BnaC.FAD2.b	(1)	ATGGG	GCAGGTGGAAGAATGCAAGT	C	TCTCCTCCCTCCA	GCTCCC	C	GAAACC	A			
Tap_BnaA.FAD2.b	(1)	ATGGG	GCAGGTGGAAGAATGCAAGT	C	TCTCCTCCCTCCA	GCTCCC	C	GAAACC	A			
Cab_BnaA.FAD2.b	(1)	ATGGG	GCAGGTGGAAGAATGCAAGT	C	TCTCCTCCCTCCA	GCTCCC	C	GAAACC	A			
		Section 2										
		(56)	56	70	80	90	100	110				
Tap_BnaC.FAD2.a	(56)	ACAAC	ATCAAGCGCGTA	CCCTGCGAGACACC	GCC	CTTCACT	GTCGGAGA	ACTCAA				
Cab_BnaC.FAD2.a	(56)	ACAAC	ATCAAGCGCGTA	CCCTGCGAGACACC	GCC	CTTCACT	GTCGGAGA	ACTCAA				
Tap_BnaA.FAD2.a	(56)	ACAAC	ATCAAGCGCGTA	CCCTGCGAGACACC	GCC	CTTCACT	GTCGGAGA	ACTCAA				
Cab_BnaA.FAD2.a	(56)	ACAAC	ATCAAGCGCGTA	CCCTGCGAGACACC	GCC	CTTCACT	GTCGGAGA	ACTCAA				
Tap_BnaC.FAD2.b	(56)	AAAC	CTCAAACGCGT	C	CCCTGCGAGACACC	ACC	CTTCACT	C	T	CGGAGA	C	CTCAA
Tap_BnaA.FAD2.b	(56)	ACAAC	CTCAAACGCGT	C	CCCTGCGAGACACC	ACC	ATTCACT	C	T	CGGAGA	C	CTCAA
Cab_BnaA.FAD2.b	(56)	ACAAC	CTCAAACGCGT	C	CCCTGCGAGACACC	ACC	ATTCACT	C	T	CGGAGA	C	CTCAA
		Section 3										
		(111)	111	120	130	140	150	165				
Tap_BnaC.FAD2.a	(111)	GAAAGCAATCCCACC	G	CACTG	TTCAAACGCTC	GATCCC	TCGCTC	TTCTCCT	AC			
Cab_BnaC.FAD2.a	(111)	GAAAGCAATCCCACC	G	CACTG	TTCAAACGCTC	GATCCC	TCGCTC	TTCTCCT	AC			
Tap_BnaA.FAD2.a	(111)	GAAAGCAATCCCACC	G	CACTG	TTCAAACGCTC	GATCCC	TCGCTC	TTCTCCT	AC			
Cab_BnaA.FAD2.a	(111)	GAAAGCAATCCCACC	G	CACTG	TTCAAACGCTC	GATCCC	TCGCTC	TTCTCCT	AC			
Tap_BnaC.FAD2.b	(111)	GAAAGCAATCCCACC	T	CACTG	TTCAAACGCTC	CATCCC	TCGCTC	TTCTCCT	AC			
Tap_BnaA.FAD2.b	(111)	GAAAGCAATCCCACC	T	CACTG	TTCAAACGCTC	CATCCC	ACGCTC	TTCTCCT	-	C		
Cab_BnaA.FAD2.b	(111)	GAAAGCAATCCCACC	T	CACTG	TTCAAACGCTC	CATCCC	ACGCTC	TTCTCCT	-	C		
		Section 4										
		(166)	166	180	190	200	210	220				
Tap_BnaC.FAD2.a	(166)	CTCATCTGGGACATC	--	ATCATAGC	CTCCTGCT	TCTACT	TACGTC	CGCCAC	CACTTA			
Cab_BnaC.FAD2.a	(166)	CTCATCTGGGACATC	--	ATCATAGC	CTCCTGCT	TCTACT	TACGTC	CGCCAC	CACTTA			
Tap_BnaA.FAD2.a	(166)	CTCATCTGGGACATC	--	ATCATAGC	CTCCTGCT	TCTACT	TACGTC	CGCCAC	CACTTA			
Cab_BnaA.FAD2.a	(166)	CTCATCTGGGACATC	--	ATCATAGC	CTCCTGCT	TCTACT	TACGTC	CGCCAC	CA	-	ITA	
Tap_BnaC.FAD2.b	(166)	CTCCTCTTCGACATC	--	CTGTC	CTCCTC	CTTACT	CACCTC	TCCAC	AG	C	TA	
Tap_BnaA.FAD2.b	(165)	TTGACATCATCATCTCC	TC	CTCG	GCTCCT	CTTACT	CACCTC	TCCAC	AG	C	TA	
Cab_BnaA.FAD2.b	(165)	TTGACATCATCATCTCC	TC	CTCG	GCTCCT	CTTACT	CACCTC	TCCAC	AG	C	TA	
		Section 5										
		(221)	221	230	240	250	260	275				
Tap_BnaC.FAD2.a	(219)	CTTCCCTCTCC	TCCCTCACCCCTCTCT	CTTACT	TCGCCTG	GCCT	CTCTACT	GGGCC				
Cab_BnaC.FAD2.a	(219)	CTTCCCTCTCC	TCCCTCACCCCTCTCT	CTTACT	TCGCCTG	GCCT	CTCTACT	GGGCC				
Tap_BnaA.FAD2.a	(219)	CTTCCCTCTCC	TCCCTCACCCCTCTCT	CTTACT	TCGCCTG	GCCT	CTCTACT	GGGCC				
Cab_BnaA.FAD2.a	(218)	CTTCCCTCTCC	TCCCTCACCCCTCTCT	CTTACT	TCGCCTG	GCCT	CTCTACT	GGGCC				
Tap_BnaC.FAD2.b	(219)	CTTCCCTCTCC	TCCCTCACCCCTCTCT	CTTACT	TCGCCTG	GCCT	CTCTACT	GGGCC				
Tap_BnaA.FAD2.b	(220)	CTTCCCTCTCC	-----	CTTACT	TCGCCTG	ACC	CTCTACT	GGGCC				
Cab_BnaA.FAD2.b	(220)	CTTCCCTCTCC	-----	CTTACT	TCGCCTG	ACC	CTCTACT	GGGCC				

Supplemental Figure 1. BnaFAD2 sequence alignment

		Section 6														
		276	290			300	310		320		330					
Tap_BnaC.FAD2.a	(276)	TGCCA	AGG	G	TGCGT	CCTAAC	C	GGC	G	TCTGGG	TCAT	AGCCC	CACGA	GTGCGG	CACC	
Cab_BnaC.FAD2.a	(274)	TGCCA	AGG	G	TGCGT	CCTAAC	C	GGC	G	TCTGGG	TCAT	AGCCC	CACGA	GTGCGG	CACC	
Tap_BnaA.FAD2.a	(274)	TGCCA	G	GGC	TGCGT	CCTAAC	C	GGC	G	TCTGGG	TCAT	AGCCC	CACGA	GTGCGG	CACC	
Cab_BnaA.FAD2.a	(273)	TGCCA	G	GGC	TGCGT	CCTAAC	C	GGC	G	TCTGGG	TCAT	AGCCC	CACGA	GTGCGG	CACC	
Tap_BnaC.FAD2.b	(274)	TGCCA	AGG	C	TGCGT	CCTAAC	G	GGC	C	TCTGGG	TCAT	C	GCCC	CACGA	ATGCGG	CACC
Tap_BnaA.FAD2.b	(260)	TGCCA	AGG	C	TGCGT	CCTAAC	G	GGC	C	TCTGGG	TCAT	AGCCC	CACGA	GTGCGG	CACC	
Cab_BnaA.FAD2.b	(260)	TGCCA	AGG	C	TGCGT	CCTAAC	G	GGC	C	TCTGGG	TCAT	AGCCC	CACGA	GTGCGG	CACC	

		Section 7														
		331	340			350	360		370		385					
Tap_BnaC.FAD2.a	(329)	ACGCCT	TCAGCGAC	T	ACCAGT	TGGCT	T	GACGAC	A	CCGT	C	GGT	C	TCA	TCTT	CACTC
Cab_BnaC.FAD2.a	(329)	ACGCCT	TCAGCGAC	T	ACCAGT	TGGCT	T	GACGAC	A	CCGT	C	GGT	C	TCA	TCTT	CACTC
Tap_BnaA.FAD2.a	(329)	ACGCCT	TCAGCGAC	T	ACCAGT	TGGCT	G	GACGAC	A	CCGT	C	GGC	C	TCA	TCTT	CACTC
Cab_BnaA.FAD2.a	(328)	ACGCCT	TCAGCGAC	T	ACCAGT	TGGCT	G	GACGAC	A	CCGT	C	GGC	C	TCA	TCTT	CACTC
Tap_BnaC.FAD2.b	(329)	ACGCCT	TCAGCGAC	C	ACCAGT	TGGCT	G	GACGAC	G	CCGT	G	GGC	C	TCA	TCTT	CACTC
Tap_BnaA.FAD2.b	(315)	ACGCCT	TCAGCGAC	C	ACCAGT	TGGCT	G	GACGAC	G	CCGT	C	GGC	C	TCA	TCTT	CACTC
Cab_BnaA.FAD2.b	(315)	ACGCCT	TCAGCGAC	C	ACCAGT	TGGCT	G	GACGAC	G	CCGT	C	GGC	C	TCA	TCTT	CACTC

		Section 8												
		386	400			410	420		430		440			
Tap_BnaC.FAD2.a	(384)	CTTCCT	CCTCGTCCC	T	TACTT	TCTCCT	GGAAGT	TACA	GT	CAT	C	GACGCC	ACCATT	TCC
Cab_BnaC.FAD2.a	(384)	CTTCCT	CCTCGTCCC	T	TACTT	TCTCCT	GGAAGT	TACA	GT	CAT	C	GACGCC	ACCATT	TCC
Tap_BnaA.FAD2.a	(384)	CTTCCT	CCTCGTCCC	T	TACTT	TCTCCT	GGAAGT	TACA	GT	CAT	C	GACGCC	ACCATT	TCC
Cab_BnaA.FAD2.a	(383)	CTTCCT	CCTCGTCCC	T	TACTT	TCTCCT	GGAAGT	TACA	GT	CAT	C	GACGCC	ACCATT	TCC
Tap_BnaC.FAD2.b	(384)	CTTCCT	CCTCGTCCC	T	TACTT	TCTCCT	GGAAGT	TACA	GC	CAT	C	GACGCC	ACCATT	TCC
Tap_BnaA.FAD2.b	(370)	CTTCCT	CCTCGTCCC	G	TACTT	TCTCCT	GGAAGT	TACA	TC	CAT	-	GACGCC	ACCATT	TCC
Cab_BnaA.FAD2.b	(370)	CTTCCT	CCTCGTCCC	G	TACTT	TCTCCT	GGAAGT	TACA	TC	CAT	-	GACGCC	ACCATT	TCC

		Section 9																		
		441	450			460	470		480		495									
Tap_BnaC.FAD2.a	(439)	AACAC	TGG	C	TCCCT	CGAGAG	A	GAC	GAAGT	GTT	T	GTCCCC	AAGAAGAA	GTCA	GACA					
Cab_BnaC.FAD2.a	(439)	AACAC	TGG	C	TCCCT	CGAGAG	A	GAC	GAAGT	GTT	T	GTCCCC	AAGAAGAA	GTCA	GACA					
Tap_BnaA.FAD2.a	(439)	AACAC	TGG	C	TCCCT	CGAGAG	A	GAC	GAAGT	GTT	T	GTCCCC	AAGAAGAA	GTCA	GACA					
Cab_BnaA.FAD2.a	(438)	AACAC	TGG	C	TCCCT	CGAGAG	A	GAC	GAAGT	GTT	T	GTCCCC	AAGAAGAA	GTCA	GACA					
Tap_BnaC.FAD2.b	(439)	AACAC	C	GG	A	TCCCT	CGAGAG	G	GAT	GAAGT	GTT	C	GTCCCC	AAGAAGAA	A	TCC	GACA			
Tap_BnaA.FAD2.b	(424)	AACAC	C	GG	A	TCCCT	CGA	T	AG	G	GAC	C	GAAGT	GTT	C	GTCCCC	AAGAAGAA	A	TCC	GACA
Cab_BnaA.FAD2.b	(424)	AACAC	C	GG	A	TCCCT	CGA	T	AG	G	GAC	C	GAAGT	GTT	C	GTCCCC	AAGAAGAA	A	TCC	GACA

		Section 10													
		496	510			520	530		540		550				
Tap_BnaC.FAD2.a	(494)	TCAAGT	TGGTACGG	C	AAGTAC	CTCAACA	A	CCCTTT	T	GGGAC	GCAC	C	GTGATG	T	TAAC
Cab_BnaC.FAD2.a	(494)	TCAAGT	TGGTACGG	C	AAGTAC	CTCAACA	A	CCCTTT	T	GGGAC	GCAC	C	GTGATG	T	TAAC
Tap_BnaA.FAD2.a	(494)	TCAAGT	TGGTACGG	C	AAGTAC	CTCAACA	A	CCCTTT	T	GGGAC	GCAC	C	GTGATG	T	TAAC
Cab_BnaA.FAD2.a	(493)	TCAAGT	TGGTACGG	C	AAGTAC	CTCAACA	A	CCCTTT	T	GGGAC	GCAC	C	GTGATG	T	TAAC
Tap_BnaC.FAD2.b	(494)	TCAAGT	TGGTACGG	A	AAGTAC	CTCAACA	A	CCCGC	T	AGGAC	GCAC	G	GTGATG	C	TAAC
Tap_BnaA.FAD2.b	(479)	TCAAGT	TGGTACGG	C	AAGTAC	CTCAACA	A	CCCGC	T	AGGAC	GCAC	G	GTGATG	C	TAAC
Cab_BnaA.FAD2.b	(479)	TCAAGT	TGGTACGG	C	AAGTAC	CTCAACA	A	CCCGC	T	AGGAC	GCAC	G	GTGATG	C	TAAC

Supplemental Figure 1. BnaFAD2 sequence alignment

		Section 11																																																					
		(551)	551	560	570	580	590	605																																															
Tap_BnaC.FAD2.a	(549)	G	G	T	T	C	A	G	T	T	C	A	C	T	C	T	C	T	C	G	G	A	A	G	A																														
Cab_BnaC.FAD2.a	(549)	G	G	T	T	C	A	G	T	T	C	A	C	T	C	T	C	T	C	G	G	A	A	G	A																														
Tap_BnaA.FAD2.a	(549)	G	G	T	T	C	A	G	T	T	C	A	C	T	C	T	C	T	C	G	G	A	A	G	A																														
Cab_BnaA.FAD2.a	(548)	G	G	T	T	C	A	G	T	T	C	A	C	T	C	T	C	T	C	G	G	A	A	G	A																														
Tap_BnaC.FAD2.b	(549)	C	G	T	T	C	A	G	T	T	C	A	C	T	C	T	C	T	C	G	G	A	A	G	A																														
Tap_BnaA.FAD2.b	(534)	C	G	T	T	C	A	G	T	T	C	A	C	T	C	T	C	T	C	G	G	A	A	G	A																														
Cab_BnaA.FAD2.b	(534)	C	G	T	T	C	A	G	T	T	C	A	C	T	C	T	C	T	C	G	G	A	A	G	A																														
		Section 12																																																					
		(606)	606	620	630	640	650	660																																															
Tap_BnaC.FAD2.a	(604)	C	C	T	T	A	C	G	A	C	G	G	C	T	T	C	G	C	T	T	G	C	A	T	T	T	C	C	A	C	C	C	A	A	C	G																			
Cab_BnaC.FAD2.a	(604)	C	C	T	T	A	C	G	A	C	G	G	C	T	T	C	G	C	T	T	G	C	A	T	T	T	C	C	A	C	C	C	A	A	C	G																			
Tap_BnaA.FAD2.a	(604)	C	C	T	T	A	C	G	A	C	G	G	C	T	T	C	G	C	T	T	G	C	A	T	T	T	C	C	A	C	C	C	A	A	C	G																			
Cab_BnaA.FAD2.a	(603)	C	C	T	T	A	C	G	A	C	G	G	C	T	T	C	G	C	T	T	G	C	A	T	T	T	C	C	A	C	C	C	A	A	C	G																			
Tap_BnaC.FAD2.b	(604)	C	C	T	T	A	C	A	G	C	G	G	T	T	T	C	G	C	T	T	G	C	A	T	T	T	C	C	A	C	C	C	A	A	C	G																			
Tap_BnaA.FAD2.b	(589)	C	C	T	T	A	C	A	G	C	G	G	T	T	T	C	G	C	T	T	G	C	A	T	T	T	C	C	A	C	C	C	A	A	C	G																			
Cab_BnaA.FAD2.b	(589)	C	C	T	T	A	C	A	G	C	G	G	T	T	T	C	G	C	T	T	G	C	A	T	T	T	C	C	A	C	C	C	A	A	C	G																			
		Section 13																																																					
		(661)	661	670	680	690	700	715																																															
Tap_BnaC.FAD2.a	(659)	A	C	C	G	T	C	T	C	C	A	G	A	T	A	C	A	T	C	T	C	G	A	C	G	T	G	G	C	A	T	C	C	T	C	G	T	A																	
Cab_BnaC.FAD2.a	(659)	A	C	C	G	T	C	T	C	C	A	G	A	T	A	C	A	T	C	T	C	G	A	C	G	T	G	G	C	A	T	C	C	T	C	G	T	A																	
Tap_BnaA.FAD2.a	(659)	A	C	C	G	T	C	T	C	C	A	G	A	T	A	C	A	T	C	T	C	G	A	C	G	T	G	G	C	A	T	C	C	T	C	G	T	A																	
Cab_BnaA.FAD2.a	(658)	A	C	C	G	T	C	T	C	C	A	G	A	T	A	C	A	T	C	T	C	G	A	C	G	T	G	G	C	A	T	C	C	T	C	G	T	A																	
Tap_BnaC.FAD2.b	(659)	A	C	C	G	T	C	T	C	C	A	G	A	T	A	C	A	T	C	T	C	T	G	A	C	G	T	G	G	C	A	T	C	C	T	C	G	T	A																
Tap_BnaA.FAD2.b	(644)	A	C	C	G	T	C	T	C	C	A	G	A	T	A	C	A	T	C	T	C	T	G	A	C	G	T	G	G	C	A	T	C	C	T	C	G	T	A																
Cab_BnaA.FAD2.b	(644)	A	C	C	G	T	C	T	C	C	A	G	A	T	A	C	A	T	C	T	C	T	G	A	C	G	T	G	G	C	A	T	C	C	T	C	G	T	A																
		Section 14																																																					
		(716)	716	730	740	750	760	770																																															
Tap_BnaC.FAD2.a	(714)	C	G	G	T	C	T	C	T	C	C	G	T	T	A	C	G	C	C	G	C	G	C	A	G	G	A	G	T	G	C	C	T	C	G	A	T	G	G	T	C	T	G	C	T	T	C	T	A	C					
Cab_BnaC.FAD2.a	(714)	C	G	G	T	C	T	C	T	C	C	G	T	T	A	C	G	C	C	G	C	G	C	A	G	G	A	G	T	G	C	C	T	C	G	A	T	G	G	T	C	T	G	C	T	T	C	T	A	C					
Tap_BnaA.FAD2.a	(714)	C	G	G	T	C	T	C	T	A	C	C	G	T	T	A	C	G	T	G	C	T	G	T	C	A	A	G	A	G	T	G	C	C	T	C	G	A	T	G	G	T	C	T	G	C	T	T	C	T	A	C			
Cab_BnaA.FAD2.a	(713)	C	G	G	T	C	T	C	T	A	C	C	G	T	T	A	C	G	T	G	C	T	G	T	C	A	A	G	A	G	T	G	C	C	T	C	G	A	T	G	G	T	C	T	G	C	T	T	C	T	A	C			
Tap_BnaC.FAD2.b	(714)	C	G	G	T	C	T	C	T	A	C	C	G	T	T	A	C	G	T	G	C	T	G	T	C	A	A	G	A	G	T	G	C	C	T	C	G	A	T	G	G	T	C	T	G	C	T	T	C	T	A	C			
Tap_BnaA.FAD2.b	(699)	C	G	G	T	C	T	C	T	A	C	C	G	T	T	A	C	G	T	G	C	T	G	T	C	A	A	G	A	G	T	A	G	C	C	T	C	G	A	T	G	G	T	C	T	G	C	T	T	C	T	A	C		
Cab_BnaA.FAD2.b	(699)	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N
		Section 15																																																					
		(771)	771	780	790	800	810	825																																															
Tap_BnaC.FAD2.a	(769)	G	G	A	G	T	C	C	G	C	T	T	C	T	G	A	T	T	G	T	C	A	A	T	G	G	T	T	T	C	T	C	G	T	G	T	T	G	A	T	C	A	C	T	T	A	C	T	T	G	C	A	G	C	
Cab_BnaC.FAD2.a	(769)	G	G	A	G	T	C	C	G	C	T	T	C	T	G	A	T	T	G	T	C	A	A	T	G	G	T	T	T	C	T	C	G	T	G	T	T	G	A	T	C	A	C	T	T	A	C	T	T	G	C	A	G	C	
Tap_BnaA.FAD2.a	(769)	G	G	A	G	T	C	C	G	C	T	T	C	T	G	A	T	T	G	T	C	A	A	T	G	G	T	T	T	C	T	C	G	T	G	T	T	G	A	T	C	A	C	T	T	A	C	T	T	G	C	A	G	C	
Cab_BnaA.FAD2.a	(768)	G	G	A	G	T	C	C	G	C	T	T	C	T	G	A	T	T	G	T	C	A	A	T	G	G	T	T	T	C	T	C	G	T	G	T	T	G	A	T	C	A	C	T	T	A	C	T	T	G	C	A	G	C	
Tap_BnaC.FAD2.b	(769)	G	G	A	G	T	C	C	G	C	T	T	C	T	G	A	T	T	G	T	C	A	A	T	G	G	T	T	T	C	T	C	G	T	G	T	T	G	A	T	C	A	C	T	T	A	C	T	T	G	C	A	G	C	
Tap_BnaA.FAD2.b	(754)	G	G	A	G	T	C	C	G	C	T	T	C	T	G	A	T	T	G	T	C	A	A	T	G	G	T	T	T	C	T	C	G	T	G	T	T	G	A	T	C	A	C	T	T	A	C	T	T	G	C	A	G	C	
Cab_BnaA.FAD2.b	(754)	G	G	A	G	T	C	C	G	C	T	T	C	T	G	A	T	T	G	T	C	A	A	T	G	G	T	T	T	C	T	C	G	T	G	T	T	G	A	T	C	A	C	T	T	A	C	T	T	G	C	A	G	C	

Supplemental Figure 1. BnaFAD2 sequence alignment

		Section 16					
		826	840	850	860	870	880
Tap_BnaC.FAD2.a	(826)	ACACGCATCCTTGCCTGCCTCACTACGATTCGTCCGAGTGGGATTGGTTGAGGGG					
Cab_BnaC.FAD2.a	(824)	ACACGCATCCTTGCCTGCCTCACTACGATTCGTCCGAGTGGGATTGGTTGAGGGG					
Tap_BnaA.FAD2.a	(824)	ACACGCATCCTTGCCTGCCTCACTATGATTCGTTCGAGTGGGATTGGTTGAGGGG					
Cab_BnaA.FAD2.a	(823)	ACACGCATCCTTGCCTGCCTCACTATGATTCGTTCGAGTGGGATTGGTTGAGGGG					
Tap_BnaC.FAD2.b	(824)	ACACGCACCCTTGCCTGCCTCACTATGATTCCTTCGAGTGGGATTGGTTGAGAGG					
Tap_BnaA.FAD2.b	(809)	ACACGCACCCTTGCCTGCCTCACTATGATTCCTTCGAGTGGGATTGGTTGAGAGG					
Cab_BnaA.FAD2.b	(809)	ACACGCANNCTNCTGCCTCACTATGATTCCTTCGAGTGGGATTGGTTGAGAGG					
		Section 17					
		881	890	900	910	920	935
Tap_BnaC.FAD2.a	(879)	AGCTTTGGCTACCGTTGACAGAGACTACGGAATCTTGAACAAGGTCFTCCACAAT					
Cab_BnaC.FAD2.a	(879)	AGCTTTGGCTACCGTTGACAGAGACTACGGAATCTTGAACAAGGTCFTCCACAAT					
Tap_BnaA.FAD2.a	(879)	AGCTTTGGCTACCGTTGACAGAGACTACGGAATCTTGAACAAGGTCFTCCACAAT					
Cab_BnaA.FAD2.a	(878)	AGCTTTGGCTACCGTTGACAGAGACTACGGAATCTTGAACAAGGTCFTCCACAAT					
Tap_BnaC.FAD2.b	(879)	AGCTTTGGCTACTGTGTGATAGAGACTATGGAATCTTGAACAAGGTGTTTCAATAAC					
Tap_BnaA.FAD2.b	(864)	AGCTTTGGCTACTGTGTGATAGAGACTATGGAATCTTGAACAAGGTGTTTCAATAAC					
Cab_BnaA.FAD2.b	(864)	AGCTTTGGCTACTGTGTGATAGAGACTATGGAATCTTGAACAAGGTGTTTCAATAAC					
		Section 18					
		936	950	960	970	980	990
Tap_BnaC.FAD2.a	(934)	ATTACCGACACGCACGTGGCGCATCATCTGTTCTCCACGATGCCGCATTATCAC					
Cab_BnaC.FAD2.a	(934)	ATTACCGACACGCACGTGGCGCATCATCTGTTCTCCACGATGCCGCATTATCAC					
Tap_BnaA.FAD2.a	(934)	ATTACGGACACGCACGTGGCGCATCATCTGTTCTCCACGATGCCGCATTATCAT					
Cab_BnaA.FAD2.a	(933)	ATTACGGACACGCACGTGGCGCATCATCTGTTCTCCACGATGCCGCATTATCAT					
Tap_BnaC.FAD2.b	(934)	ATTACGGACACGCACGTGGCGCATCATCTGTTCTCCACGATGCCGCATTATAAC					
Tap_BnaA.FAD2.b	(919)	ATTACGGACACGCACGTGGCGCATCATCTGTTCTCCACGATGCCGCATTATAAC					
Cab_BnaA.FAD2.b	(919)	ATTACGGACACGCACGTGGCGCATCATCTGTTCTCCACGATGCCGCATTATAAC					
		Section 19					
		991	1000	1010	1020	1030	1045
Tap_BnaC.FAD2.a	(988)	GCGATGGAAGCTTACCAAGGCGATAAAGCCGATACTGGGGAGAGTATTATCAGTTT					
Cab_BnaC.FAD2.a	(988)	GCGATGGAAGCTTACCAAGGCGATAAAGCCGATACTGGGGAGAGTATTATCAGTTT					
Tap_BnaA.FAD2.a	(988)	GCGATGGAAGCTTACGAAGGCGATAAAGCCGATACTGGGGAGAGTATTATCAGTTT					
Cab_BnaA.FAD2.a	(987)	GCGATGGAAGCTTACGAAGGCGATAAAGCCGATACTGGGGAGAGTATTATCAGTTT					
Tap_BnaC.FAD2.b	(988)	GCGATGGAAGCGACCAAGGCGATAAAGCCGATACTTGGGGAGAGTATTATCAGTTT					
Tap_BnaA.FAD2.b	(973)	GCGATGGAAGCGACCAAGGCGATAAAGCCGATACTTGGGGAGAGTATTATCAGTTT					
Cab_BnaA.FAD2.b	(973)	GCGATGGAAGCGACCAAGGCGATAAAGCCGATACTTGGGGAGAGTATTATCAGTTT					
		Section 20					
		1046	1060	1070	1080	1090	1100
Tap_BnaC.FAD2.a	(1042)	GATGGGACGCCGGTGGTTAAGGCGATGTGGAGGGAGGCGAAGGAGTGTATCTATG					
Cab_BnaC.FAD2.a	(1042)	GATGGGACGCCGGTGGTTAAGGCGATGTGGAGGGAGGCGAAGGAGTGTATCTATG					
Tap_BnaA.FAD2.a	(1042)	GATGGGACGCCGGTGGTTAAGGCGATGTGGAGGGAGGCGAAGGAGTGTATCTATG					
Cab_BnaA.FAD2.a	(1041)	GATGGGACGCCGGTGGTTAAGGCGATGTGGAGGGAGGCGAAGGAGTGTATCTATG					
Tap_BnaC.FAD2.b	(1042)	GATGGAACGCCGGTGGTTAAGGCGATGTGGAGGGAGGCGAAGGAGTGTATCTATG					
Tap_BnaA.FAD2.b	(1028)	GATGGAACGCCGGCGGTTAAGGCGATGTGGAGGGAGGCGAAGGAGTGTATCTATG					
Cab_BnaA.FAD2.b	(1028)	GATGGAACGCCGGCGGTTAAGGCGATGTGGAGGGAGGCGAAGGAGTGTATCTATG					

Supplemental Figure 1. BnaFAD2 sequence alignment

	(1101)	1101	1110	1120	1130	1140	1155	Section 21
Tap_BnaC.FAD2.a (1097)	T	GGAACCGGA	CAGGCAAGGT	GAGAAGAAAGGT	TGTGTTCT	GGTACAACAATAAGTT		
Cab_BnaC.FAD2.a (1097)	T	GGAACCGGA	CAGGCAAGGT	GAGAAGAAAGGT	TGTGTTCT	GGTACAACAATAAGTT		
Tap_BnaA.FAD2.a (1097)	T	GGAACCGGA	CAGGCAAGGT	GAGAAGAAAGGT	TGTGTTCT	GGTACAACAATAAGTT		
Cab_BnaA.FAD2.a (1096)	T	GGAACCGGA	CAGGCAAGGT	GAGAAGAAAGGT	TGTGTTCT	GGTACAACAATAAGTT		
Tap_BnaC.FAD2.b (1097)	T	GAACCGGA	TAGGCAAGGT	GAGAAGAAAGGT	TGTGTTCT	GGTACAACAATAAGTT		
Tap_BnaA.FAD2.b (1083)	T	GAACCGGA	TAGGCAAGGT	GAGAAGAAAGGT	TGTGTTCT	GGTACAACAATAAGTT		
Cab_BnaA.FAD2.b (1083)	T	GAACCGGA	TAGGCAAGGT	GAGAAGAAAGGT	TGTGTTCT	GGTACAACAATAAGTT		

	(1156)	1156	1159	Section 22
Tap_BnaC.FAD2.a (1152)	ATGA			
Cab_BnaC.FAD2.a (1152)	ATGA			
Tap_BnaA.FAD2.a (1152)	ATGA			
Cab_BnaA.FAD2.a (1151)	ATGA			
Tap_BnaC.FAD2.b (1152)	ATGA			
Tap_BnaA.FAD2.b (1138)	ATGA			
Cab_BnaA.FAD2.b (1138)	ATGA			

Supplemental Figure 2. BnaFAD2 amino acid alignment

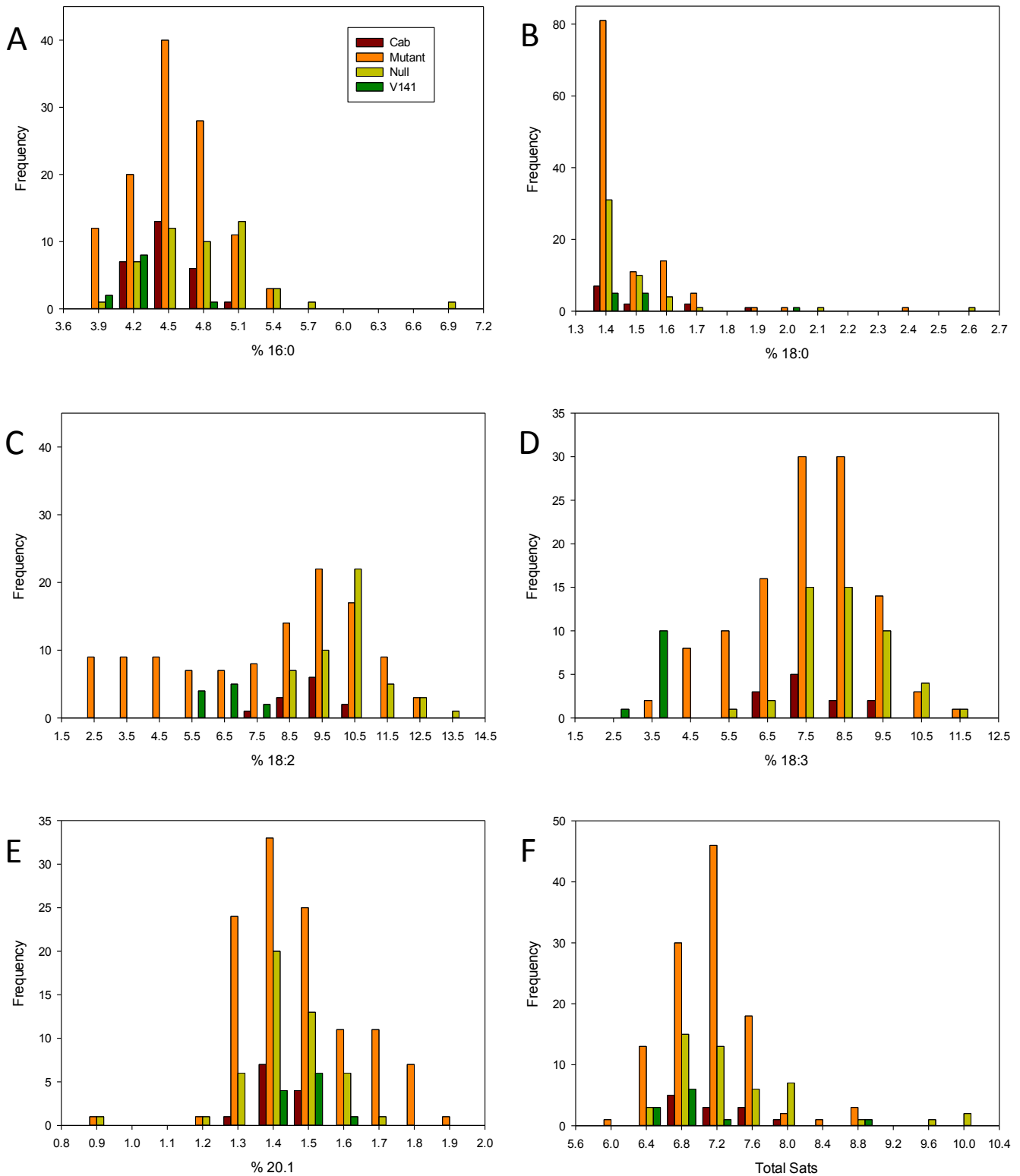
		Section 1									
		(1)	1	10	20	30	40	50	60	70	56
Tap_BnaC.FAD2.a	(1)	MGAGGRMQVSPPS	KKSE	TDTI	KRVPCETPPFT	VG	ELKKAIPPHCFKRSIPRSFS	YL			
Cab_BnaC.FAD2.a	(1)	MGAGGRMQVSPPS	KKSE	TDTI	KRVPCETPPFT	VG	ELKKAIPPHCFKRSIPRSFS	YL			
Tap_BnaA.FAD2.a	(1)	MGAGGRMQVSPPS	KKSE	TDNI	KRVPCETPPFT	VG	ELKKAIPPHCFKRSIPRSFS	YL			
Cab_BnaA.FAD2.a	(1)	MGAGGRMQVSPPS	KKSE	TDNI	KRVPCETPPFT	VG	ELKKAIPPHCFKRSIPRSFS	YL			
Tap_BnaC.FAD2.b	(1)	MGAGGRMQVSPPS	SSPE	TKTL	KRVPCETPPFT	LG	DLKKAIPPHCFKRSIPRSFS	YL			
Tap_BnaA.FAD2.b	(1)	MGAGGRMQVSPPS	SSPG	TNTL	KRVPCETPPFT	LG	DLKKAIPPHCFKRSIPRSFS	SS			
Cab_BnaA.FAD2.b	(1)	MGAGGRMQVSPPS	SSPG	TNTL	KRVPCETPPFT	LG	DLKKAIPPHCFKRSIPRSFS	SS			
		Section 2									
		(57)	57	70	80	90	100	110	120	112	
Tap_BnaC.FAD2.a	(57)	IWDIIIASC	FYYVAT	TYFPLLPHPL	SYF	AWPLYWACQGC	VLTVGV	VWVIAHECGH	HAF		
Cab_BnaC.FAD2.a	(57)	IWDIIIASC	FYYVAT	TYFPLLPHPL	SYF	AWPLYWACQGC	VLTVGV	VWVIAHECGH	HAF		
Tap_BnaA.FAD2.a	(57)	IWDIIIASC	FYYVAT	TYFPLLPHPL	SYF	AWPLYWACQGC	VLTVGV	VWVIAHECGH	HAF		
Cab_BnaA.FAD2.a	(57)	IWDIIIASC	FYYVAT	ITSLSSLT	LSPTSP	GLSTGPARA	ASPASGSPT	SAATTPSA	T		
Tap_BnaC.FAD2.b	(57)	LFDI	LVSS	SLYHLSTA	YFPLLPHPL	PYL	AWPLYWACQGC	VLTVGL	LWVIAHECGH	HAF	
Tap_BnaA.FAD2.b	(57)	TSSSPRLL	LPLPPLHS	LL	PSPLPRLT	PLLGLPRLRP	NGPL	LGHSPRV	RPPRLQRPPV		
Cab_BnaA.FAD2.b	(57)	TSSSPRLL	LPLPPLHS	LL	PSPLPRLT	PLLGLPRLRP	NGPL	LGHSPRV	RPPRLQRPPV		
		Section 3									
		(113)	113	120	130	140	150	160	170	168	
Tap_BnaC.FAD2.a	(113)	SDYQWLDD	TVGLIFHSFL	LVPYFSWKYSHRRHNS	TGSLER	DEVFVPKKS	SDIKWY				
Cab_BnaC.FAD2.a	(113)	SDYQWLDD	TVGLIFHSFL	LVPYFSWKYSHRRHNS	TGSLER	DEVFVPKKS	SDIKWY				
Tap_BnaA.FAD2.a	(113)	SDYQWLDD	TVGLIFHSFL	LVPYFSWKYSHRRHNS	TGSLER	DEVFVPKKS	SDIKWY				
Cab_BnaA.FAD2.a	(113)	TSGWTT	PSASSSTPS	SSLT	TSPGS---	TVIDATIP	TLA	PSRETKCL	SPRRS	QTSSG	
Tap_BnaC.FAD2.b	(113)	SDH	QWLDD	AVGLV	FHSFL	LVPYFSWKYSHRRHNS	TGSLER	DEVFVPKKS	SDIKWY		
Tap_BnaA.FAD2.b	(113)	AGR	RRRRLPL	LPPRPV	LL	LEVHP-----	RHNS	TGSLDR	DEVFVPKKS	SDIKWY	
Cab_BnaA.FAD2.b	(113)	AGR	RRRRLPL	LPPRPV	LL	LEVHP-----	RHNS	TGSLDR	DEVFVPKKS	SDIKWY	
		Section 4									
		(169)	169	180	190	200	210	220	230	224	
Tap_BnaC.FAD2.a	(169)	GKYLNNP	LGRIVMLTVQFT	LLGWPL	YLAFNV	SGRPY	DG	GFACHFHPNAPI	YNDRERL		
Cab_BnaC.FAD2.a	(169)	GKYLNNP	LGRIVMLTVQFT	LLGWPL	YLAFNV	SGRPY	DG	GFACHFHPNAPI	YNDRERL		
Tap_BnaA.FAD2.a	(169)	GKYLNNP	LGRIVMLTVQFT	LLGWPL	YLAFNV	SGRPY	DG	GFACHFHPNAPI	YNDRERL		
Cab_BnaA.FAD2.a	(166)	TASTSTT	LWDAP-C-RFS	SL	SAGLCT-PST	SRGDLT	TAAS	LAISTPTLPSTTT	TVSV	V	
Tap_BnaC.FAD2.b	(169)	GKYLNNP	LGRIVMLTVQFT	LLGWPL	YLAFNV	SGRPY	SD	GFACHFHPNAPI	YNDRERL		
Tap_BnaA.FAD2.b	(163)	GKYLNNP	LGRIVMLTVQF	KL	GWPL	YLAFNV	SGRPY	SD	GFACHFHPNAPI	YNDRERL	
Cab_BnaA.FAD2.b	(163)	GKYLNNP	LGRIVMLTVQF	KL	GWPL	YLAFNV	SGRPY	SD	GFACHFHPNAPI	YNDRERL	
		Section 5									
		(225)	225	230	240	250	260	270	280		
Tap_BnaC.FAD2.a	(225)	QIYIS	DAGILAVCYGL	FRYAAA	-----	QGVAS	MVCFY	---	GVPLLI	VNGFLV	
Cab_BnaC.FAD2.a	(225)	QIYIS	DAGILAVCYGL	FRYAAA	-----	QGVAS	MVCFY	---	GVPLLI	VNGFLV	
Tap_BnaA.FAD2.a	(225)	QIYIS	DAGILAVCYGL	RYAAV	-----	QGVAS	MVCFY	---	GVPLLI	VNGFLV	
Cab_BnaA.FAD2.a	(219)	SRYTS	PPTLAS	SPSATV	STATLLS	SKELP	RWSAS	TEFL	LSTGS	-F-SLTC	
Tap_BnaC.FAD2.b	(225)	QIYIS	DAGVLSVCYGL	RYAGS	-----	RGVAS	MVCVY	---	GVPLM	IVNCFV	
Tap_BnaA.FAD2.b	(219)	QIYIS	DAGVLSVCYGL	RYAAS	-----	RGVAS	VVCVY	---	GVPLLI	VNCFV	
Cab_BnaA.FAD2.b	(219)	QIYIS	DAGVLSVC	XXXXXXXXXX	-----	RGVAS	VVCVY	---	GVPLLI	VNCFV	

Supplemental Figure 2. BnaFAD2 amino acid alignment

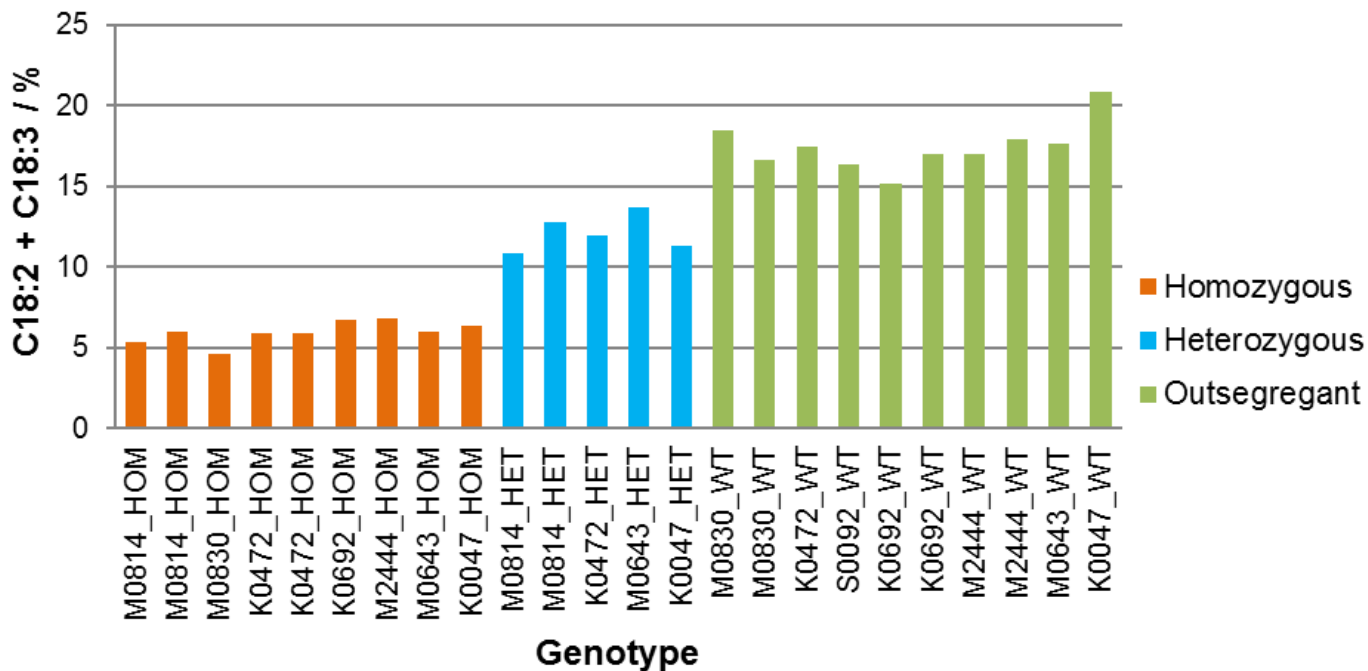
		Section 6																																																					
		(281)	281	290	300	310	320	330	340	350	336																																												
Tap_BnaC.FAD2.a	(273)	L	Q	H	T	H	P	S	L	P	H	Y	D	S	S	E	W	D	L	R	G	A	L	T	V	D	R	D	Y	G	I	L	N	K	V	F	H	N	I	T	D	T	H	V	A	H	H	L	F	S	T	M	P	H	Y
Cab_BnaC.FAD2.a	(273)	L	Q	H	T	H	P	S	L	P	H	Y	D	S	S	E	W	D	L	R	G	A	L	T	V	D	R	D	Y	G	I	L	N	K	V	F	H	N	I	T	D	T	H	V	A	H	H	L	F	S	T	M	P	H	Y
Tap_BnaA.FAD2.a	(273)	L	Q	H	T	H	P	S	L	P	H	Y	D	S	S	E	W	D	L	R	G	A	L	T	V	D	R	D	Y	G	I	L	N	K	V	F	H	N	I	T	D	T	H	V	A	H	H	L	F	S	T	M	P	H	Y
Cab_BnaA.FAD2.a	(273)	L	T	M	T	R	L	S	G	I	G	--	G	E	L	W	P	P	L	T	E	T	E	S	-	T	R	S	S	T	I	S	R	T	R	T	W	R	I	T	C	S	R	P	C	R	I	T	M	R	W	K	L	R	R
Tap_BnaC.FAD2.b	(273)	L	Q	H	T	H	P	S	L	P	H	Y	D	S	S	E	W	D	L	R	G	A	L	T	V	D	R	D	Y	G	I	L	N	K	V	F	H	N	I	T	D	T	H	V	A	H	H	L	F	S	T	M	P	H	Y
Tap_BnaA.FAD2.b	(267)	L	Q	H	T	H	P	S	L	P	H	Y	D	S	S	E	W	D	L	R	G	A	L	T	V	D	R	D	Y	G	I	L	N	K	V	F	H	N	I	T	D	T	H	V	A	H	H	L	F	S	T	M	P	H	Y
Cab_BnaA.FAD2.b	(267)	L	Q	H	T	X	X	X	L	P	H	Y	D	S	S	E	W	D	L	R	G	A	L	T	V	D	R	D	Y	G	I	L	N	K	V	F	H	N	I	T	D	T	H	V	A	H	H	L	F	S	T	M	P	H	Y

		Section 7																																																						
		(337)	337	350	360	370	380	390	392																																															
Tap_BnaC.FAD2.a	(329)	H	A	M	E	A	T	K	A	I	K	P	I	L	G	E	Y	Y	Q	F	D	G	T	P	V	V	K	A	M	W	R	E	A	K	E	C	I	Y	V	E	P	D	R	--	Q	G	E	K	K	G	V	F	W	Y	N	N
Cab_BnaC.FAD2.a	(329)	H	A	M	E	A	T	K	A	I	K	P	I	L	G	E	Y	Y	Q	F	D	G	T	P	V	V	K	A	M	W	R	E	A	K	E	C	I	Y	V	E	P	D	R	--	Q	G	E	K	K	G	V	F	W	Y	N	N
Tap_BnaA.FAD2.a	(329)	H	A	M	E	A	T	K	A	I	K	P	I	L	G	E	Y	Y	Q	F	D	G	T	P	V	V	K	A	M	W	R	E	A	K	E	C	I	Y	V	E	P	D	R	--	Q	G	E	K	K	G	V	F	W	Y	N	N
Cab_BnaA.FAD2.a	(326)	R	--	S	R	Y	W	E	S	I	S	S	M	G	R	R	W	L	R	--	--	R	C	G	G	--	--	R	R	S	V	S	M	W	N	R	T	G	K	V	R	R	K	V	C	S	G	T	T	I	S	Y	--			
Tap_BnaC.FAD2.b	(329)	N	A	M	E	A	T	K	A	I	K	P	I	L	G	E	Y	Y	Q	F	D	G	T	P	V	V	K	A	M	W	R	E	A	K	E	C	I	Y	V	E	P	D	R	--	Q	G	E	K	K	G	V	F	W	Y	N	N
Tap_BnaA.FAD2.b	(323)	N	A	M	E	A	T	K	A	I	K	P	I	L	W	R	V	L	P	V	--	W	N	A	G	G	-	G	D	V	E	G	E	G	V	Y	L	C	-	T	G	-	A	R	-	E	E	R	C	V	L	V	Q	Q	--	
Cab_BnaA.FAD2.b	(323)	N	A	M	E	A	T	K	A	I	K	P	I	L	W	R	V	L	P	V	--	W	N	A	G	G	-	G	D	V	E	G	E	G	V	Y	L	C	-	T	G	-	A	R	-	E	E	R	C	V	L	V	Q	Q	--	

		Section 8									
		(393)	393								
Tap_BnaC.FAD2.a	(383)	K	L								
Cab_BnaC.FAD2.a	(383)	K	L								
Tap_BnaA.FAD2.a	(383)	K	L								
Cab_BnaA.FAD2.a	(374)	--	--								
Tap_BnaC.FAD2.b	(383)	K	L								
Tap_BnaA.FAD2.b	(372)	V	M								
Cab_BnaA.FAD2.b	(372)	V	M								



Supplemental Figure 3. Distribution of fatty acid composition of seeds in mutant and control lines. A) Palmitic acid (C16:0), B) Stearic acid (C18:0), C) Linoleic acid (C18:2), D) Linolenic acid (C18:3), E) 9-Eicosenoic acid (C20:1) and F) total saturated fatty acids in seeds of *B. napus* variety Cabriolet (Cab), *BnaA.FAD2.a* mutated lines (Mutant), outsegregant lines (Null) and a commercial high oleic, low linolenic line (V141).



Supplemental Figure 4. Polyunsaturated fatty acid content of seeds from plants segregating for mutations in *BnaC.FAD2.a* that have major effects on oil composition