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PHYTOMORPHOLOGY

Isolation, genetic mapping and expression studies of a peptide deformylase gene, *DEF2*, from bold-seeded and small-seeded varieties of the oilseed crop, *Brassica juncea* (Indian mustard) and analysis of its over-expression and down-regulation on seed size of transgenic plants

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## Supplementary data

Supplementary Table 1. Primers for amplification of full-length sequences of DEF2

Primer Name	Primer sequence (5'-3')
DEF2- FP	GTCCATGGTCTAGCCATGGCCGTATGTA
DEF2- RP	CGTCTAGATCAACGTTTGCCAAAACCAA

Construct	Primer name	Primer sequence $(5' - 3')$
pDEF2 (over-	DEF2 SO-1	TCGACTAGTTCTCATCCCCTTTTAAACCAA
expression	DEF2 SO-2	TACATACGGCCATGGCTAGACCATGTGTATGTT
cassette)		TTTAATCTTGTTTGTATTG
	DEF2 SO-3	CAATACAAACAAGATTAAAAAACATACACATGG
		TCTAGCCATGGCCGTATGTA
	DEF2 SO-4	CGGGTACCGAGCTCGAATTCTCAACGTTTGCCA
		AAACCAA
	DEF2 SO-5	TTGGTTTTGGCAAACGTTGAGAATTCGAGCTCG
		GTACCCG
	DEF2 SO-6	ACGTCTAGAAAGCTTGGTACAATCAGTAAA TTG
pASDEF2	ASDEF2 SO-1	TCGACTAGTTCTCATCCCCTTTTAAACCAA
(antisense	ASDEF2 SO-2	TTGGTTTTGGCAAACGTTGAGTGTATGTTTTTA
cassette)		ATCTTGTTTGTATTG
	ASDEF2 SO-3	CAATACAAACAAGATTAAAAAACATACACTCAAC
		GTTTGCCAAAACCAA
	ASDEF2 SO-4	CGGGTACCGAGCTCGAATTCATGGTCTAGCCA
		TGGCCGTATGTA
	ASDEF2 SO-5	TACATACGGCCATGGCTAGACCATGAATTCGAG
		CTCGGTACCCG
	ASDEF2 SO-6	ACGTCTAGAAAGCTTGGTACAATCAGTAAATTG

Supplementary Table 2. SOE-ing primers utilized for development of transgene cassettes

Homolog a Varuna Homolog b Varuna	ATGGCCGTATGTAACTGTTTCCTCCAAGCTCCACCGTTCTCTCGCTTCTTATCACCGGTT ATGGCCGTATGTAACTGTTTCCTCCAAGCTCCACCTCTCTCGCTTCTTATCCCCCGGTT	60 60
Homolog a Varuna	TTCTCCCGCCGCGCTCCGAATCTCTTCCCCCGGCTATGGTCAGCTCAAATCCACCGTCATG	120
Homolog b Varuna	TTCTCCCGCCG <mark>TC</mark> CT <mark>A</mark> CAAAT <mark>T</mark> TCTTC <mark>G</mark> CCGGCTAT <mark>AA</mark> TCAGCTCAAATCCACCGTCATG	120
Homolog a Varuna Homolog b Varuna	TTCTCCTCCTCCTCCCCCCCCCCCCCCCCCCCCCCCCC	180 174
Homolog a Varuna	GCTGAAGTAAAGCGCGTCTCGCGCAAGGAATCCTGAAATAGCTTCCGCATCCGATCTTCAA	240
Homolog b Varuna	GCTGAAGTAAAGCGCGTCTCGCGCAAGGAA <mark>GA</mark> TGAAATAGCTTCCGC <mark>T</mark> TC <mark>T</mark> GATCTTCAA	234
Homolog a Varuna	TTCGAGACGCCGTTGAAGATTGTTGAGTATCC <mark>G</mark> GATCCTATCTTACG <mark>C</mark> GCTAAG <mark>A</mark> GCAAG	
Homolog b Varuna	TTCGAGACGCCGTTGAAGATTGTTGAGTATCC <mark>A</mark> GATCCTATCTTACG <mark>G</mark> GCTAAG <mark>T</mark> GCAAG	294
Homolog a Varuna Homolog b Varuna	AGGATTGGTGTTTTTGACGAGAATTTGAAGAACTTGGCCGATGCTATGTTCGATGTTATG AGGATTGGTGTTTTTGACGAGCATTTGAAGAACTTGGCCGATGCTATGTTTGATGTTATG	360 354
Homolog a Varuna Homolog b Varuna	TACAAAACGGATGGCATCGGGCTCTCAGCACCACAAGTGGGGCTCAATGTTCAACTCATG TACAAGACGGATGGCATCGGCCTCTCAGCACCACAAGTGGGGCTCAATGTTCAACTCATG	420 414
Homolog a Varuna	GTGTTTAATCCAGCTGGGGAGTCTGGTGAAGGAGAAGAGATTGTTCTTGTTAATCCGAAA	480
Homolog b Varuna	GTGTTTAATCCAGCTGGGGAGTCTGGTGAAGGAGAAGAGATTGTTCTTGT <mark>G</mark> AA <mark>C</mark> CCGAAA	474
Homolog a Varuna	ATCAATAA <mark>G</mark> TATTCTGATAAATT <mark>A</mark> GTACCATTCAACGAAGGATGC <mark>T</mark> TATCCTTCCCTGGG	540
Homolog b Varuna	ATCAATAA <mark>A</mark> TATTCTGATAAATT <mark>G</mark> GTACCATTCAACGAAGGATGC <mark>C</mark> TATCCTTCCCTGGG	534
Homolog a Varuna Homolog b Varuna	ATCTATGCTGATGTAGTTCGACCACAATCTGTCAAGATTGACGCAAGAGACATTACTGGC ATCTATGCTGATCGACCACAATCGGTCAAGATTGACGCAAGAGACATTACTGGT	600 588
Homolog a Varuna	GCTAGATTTTCGATCAGTCTATCACGTTTACCTGCACGAATCTTTCAGCACGAATACGAC	660
Homolog b Varuna	GCTAGATTTTCGATCAGTCTATCACGTTTACCTGCACGAATCTTTCAGCACGAATACGAC	648
Homolog a Varuna	CACTTAGAGGGAGTTCTCTTCTCGACAGAATGACGGATGACGTTCTTGACACCATTCGT	720
Homolog b Varuna	CAC <mark>C</mark> TAGAGGGAGTTCTCTTCTTCGACAGAATGACGGATGACGTTCTTGACACCATTCGT	708
Homolog a Varuna	GAAGAGCTAGAGGCCCTGGAAAAGAAGTACGAAGAGAGAAAAACTGGACTGCCAAGCCCTGAA	
Homolog b Varuna	GAAGAG <mark>T</mark> TAGAGGC <mark>AT</mark> TGGAAAAGAAGTACGAAGA <mark>A</mark> AAAA <mark>A</mark> TGGA <mark>T</mark> TGCCAAGCCCTGAA	Children
Homolog a Varuna Homolog b Varuna	AAAGTACAAGCACGACAAAAAAA <mark>G</mark> GAAAGCAGGAGTTGGTTTTGGCAAACGTTGA AAAGTACAAGCACGACAAAAAAAAAA	834 822

**Supplementary Fig. 1.** cDNA sequence alignment of *DEF2* homologs 'a' and 'b' from *Brassica juncea* var. Varuna. Polymorphisms are highlighted in yellow boxes

Homolog a Varuna	MAVCNCFLQAPP <mark>F</mark> SRFLSPVFSRR <mark>APNLFP</mark> GYGQLKSTVMFSSS <mark>SS</mark> SAANR <mark>I</mark> GPLTSPVR	60
Homolog b Varuna	MAVCNCFLQAPP <mark>L</mark> SRFLSPVFSRR <mark>PT</mark> N <mark>FFA</mark> GYNQLKSTVMFSSS <mark></mark> SAANR <mark>T</mark> GPLTSPVR	58
Homolog a Varuna	AEVKRVSRKE <mark>S</mark> EIASASDLQFETPLKIVEYPDPILRAK <mark>S</mark> KRIGVFDE <mark>N</mark> LKNLADAMFDVM	120
Homolog b Varuna	AEVKRVSRKE <mark>D</mark> EIASASDLQFETPLKIVEYPDPILRAK <mark>C</mark> KRIGVFDE <mark>H</mark> LKNLADAMFDVM	118
Homolog a Varuna	YKTDGIGLSAPQVGLNVQLMVFNPAGESGEGEEIVLVNPKINKYSDKLVPFNEGCLSFPG	180
Homolog b Varuna	YKTDGIGLSAPQVGLNVQLMVFNPAGESGEGEEIVLVNPKINKYSDKLVPFNEGCLSFPG	178
Homolog a Varuna	IYAD <mark>VV</mark> RPQSVKIDARDITGARFSISLSRLPARIFQHEYDHLEGVLFFDRMTDDVLDTIR	240
Homolog b Varuna	IYAD <mark></mark> RPQSVKIDARDITGARFSISLSRLPARIFQHEYDHLEGVLFFDRMTDDVLDTIR	236
Homolog a Varuna Homolog b Varuna	EELEALEKKYEEK <mark>T</mark> GLPSPEKVQARQK <mark>R</mark> KAGVGFGKR 277 EELEALEKKYEEK <mark>N</mark> GLPSPEKVQARQK <mark>K</mark> KAGVGFGKR 273	

**Supplementary Fig. 2.** Amino acid sequence alignment of *DEF2* homologs 'a' and 'b' from *Brassica juncea* var. Varuna. Polymorphisms are highlighted in yellow boxes

Homolog a Heera	ATGGCCGTATGTA <mark>G</mark> CTGTTTCCTCCAAGCTCCACC <mark>GT</mark> T <mark>T</mark> CTCGCTTCTTATC <mark>A</mark> CCGGTT	60
Homolog b Heera	ATGGCCGTATGTA <mark>A</mark> CTGTTTCCTCCAAGCTCCACC <mark>TC</mark> TCTCGCTTCTTATC <mark>C</mark> CCGGTT	60
Homolog a Heera	TTCTCCCGCCG <mark>CG</mark> CT <mark>CCG</mark> AATCTCTTCCCCGGCTATGGTCAGCTCAAATCCACCGTCATG	120
Homolog b Heera	TTCTCCCGCCG <mark>TC</mark> CT <mark>ACA</mark> AAT <mark>T</mark> TCTTC <mark>G</mark> CCGGCTAT <mark>AA</mark> TCAGCTCAAATCCACCGTCATG	120
Homolog a Heera	TTCTCCTCCTCCTCCTCCCCCCCCCCCCCCCCCCCCCC	180
Homolog b Heera	TTCTCCTCCTCCTCC <mark>G</mark> CCGC <mark>GAACCGCAC</mark> C <mark>G</mark> ACatCATCTCCGGTC <mark>C</mark> GAGCT	173
Homolog a Heera	GAAGTAAAGCGCGTCTCGCGCAAGGAA <mark>TC</mark> TGAAATAGCTTCCGCTTCTGATCT <mark>A</mark> CAATTC	240
Homolog b Heera	GAAGTAAAGCGCGTCTCGCGCAAGGAA <mark>GA</mark> TGAAATAGCTTCCGCTTCTGATCT <mark>T</mark> CAATTC	233
Homolog a Heera	GAGACGCCGTTGAAGATTGTTGAGTATCC <mark>G</mark> GATCCTATCTTACG <mark>C</mark> GCTAAG <mark>A</mark> GCAAGAGG	300
Homolog b Heera	GAGACGCCGTTGAAGATTGTTGAGTATCC <mark>A</mark> GATCCTATCTTACG <mark>G</mark> GCTAAG <mark>T</mark> GCAAGAGG	293
Homolog a Heera	ATTGGTGTTTTTGACGAG <mark>A</mark> ATTTGAAGAACTTGGCCGATGCTATGTT <mark>C</mark> GATGTTATGTAC	360
Homolog b Heera	ATTGGTGTTTTTGACGAG <mark>C</mark> ATTTGAAGAACTTGGCCGATGCTATGTT <mark>T</mark> GATGTTATGTAC	353
Homolog a Heera	AA <mark>A</mark> ACGGATGGCAT <mark>T</mark> GG <mark>G</mark> CTCTCAGCACCACAAGTGGGGCTCAATGTTCAACTCATGGTG	420
Homolog b Heera	AA <mark>G</mark> ACGGATGGCAT <mark>C</mark> GG <mark>C</mark> CTCTCAGCACCACAAGTGGGGCTCAATGTTCAACTCATGGTG	413
Homolog a Heera	TTTAATCC <mark>G</mark> GCTGGGGAGTCTGGTGAAGGAGAGAGAGATTGTTCTTGTGAA <mark>T</mark> CCGAAAATC	480
Homolog b Heera	TTTAATCC <mark>A</mark> GCTGGGGAGTCTGGTGAAGGAGAAGAGATTGTTCTTGTGAA <mark>C</mark> CCGAAAATC	473
Homolog a Heera	AATAA <mark>G</mark> TATTCTGATAAATT <mark>A</mark> GTACCATTCAACGAAGGATGC <mark>T</mark> TATCCTTCCCTGGGATC	540
Homolog b Heera	AATAA <mark>A</mark> TATTCTGATAAATT <mark>G</mark> GTACCATTCAACGAAGGATGC <mark>C</mark> TATCCTTCCCTGGGATC	533
Homolog a Heera	TATGCTGAT <mark>GTAGTT</mark> CGACCACAATC <mark>T</mark> GTCAAGATTGACGCAAG <mark>G</mark> GACATTACTGG <mark>C</mark> GCT	600
Homolog b Heera	TATGCTGAT <mark></mark> CGACCACAATC <mark>G</mark> GTCAAGATTGACGCAAG <mark>A</mark> GACATTACTGG <mark>T</mark> GCT	587
Homolog a Heera	AGATTTTCGATCAGTCTATCACGTTTACCTGCACGAATCTTTCAGCACGAATACGACCAC	660
Homolog b Heera	AGATTTTCGATCAGTCTATCACGTTTACCTGCACGAATCTTTCAGCA <mark>T</mark> GAATACGA <mark>T</mark> CAC	647
Homolog a Heera	TTAGAGGGAGTTCTCTTCTTCGACAGAATGACGGATGACGTTCTTGACACCATTCGTGAA	720
Homolog b Heera	CTAGAGGGAGTTCTCTTCTTCGACAGAATGACGGATGACGTTCTTGACACCATTCGTGAA	707
Homolog a Heera	GAG <mark>C</mark> TAGAGGC <mark>CC</mark> TGGAAAAGAAGTACGAAGA <mark>G</mark> AAAA <mark>C</mark> TGGA <mark>C</mark> TGCCAAGCCCTGAAAAA	780
Homolog b Heera	GAG <mark>T</mark> TAGAGGC <mark>AT</mark> TGGAAAAGAAGTACGAAGA <mark>A</mark> AAAA <mark>A</mark> TGGA <mark>T</mark> TGCCAAGCCCTGAAAAA	767
Homolog a Heera	GTACAAGCACGACAAAAAA <mark>G</mark> GAAAGCAGGAGTTGGTTTTGGCAAACGTTGA 831	
Homolog b Heera	GTACAAGCACGACAAAAAAAAGCAGGAGTTGGTTTTGGCAAACGTTGA 818	

**Supplementary Fig. 3.** cDNA sequence alignment of *DEF2* homologs 'a' and 'b' from *Brassica juncea* var. Heera. Polymorphisms are highlighted in yellow boxes.

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Heera homolo	ga M	AVC <mark>S</mark> CFLQAPP <mark>F</mark> SRFLSPVFSRR <mark>AP</mark> NLF <mark>P</mark> GY <mark>G</mark> QLKSTVMFSSS <mark>S</mark> SAANRTGPLTSPVRA	60
Heera homolo	gb M	AVC <mark>N</mark> CFLQAPP <mark>L</mark> SRFLSPVFSRR <mark>PT</mark> NFF <mark>A</mark> GY <mark>N</mark> QLKSTVMFSSS <mark>-</mark> SAANRTGPLTSPVRA	59
Heera homolo	g <u>a</u> E	VKRVSRKE <mark>S</mark> EIASASDLQFETPLKIVEYPDPILRAK <mark>S</mark> KRIGVFDE <mark>N</mark> LKNLADAMFDVMY	120
Heera homolo	gb E	VKRVSRKE <mark>D</mark> EIASASDLQFETPLKIVEYPDPILRAK <mark>C</mark> KRIGVFDE <mark>H</mark> LKNLADAMFDVMY	119
Heera homolo	ga K	TDGIGLSAPQVGLNVQLMVFNPAGESGEGEEIVLVNPKINKYSDKLVPFNEGCLSFPGI	180
Heera homolo	gb K	TDGIGLSAPQVGLNVQLMVFNPAGESGEGEEIVLVNPKINKYSDKLVPFNEGCLSFPGI	179
Heera homolo	ga Y	AD <mark>VV</mark> RPQSVKIDARDITGARFSISLSRLPARIFQHEYDHLEGVLFFDRMTDDVLDTIRE	240
Heera homolo	gb Y	AD <mark></mark> RPQSVKIDARDITGARFSISLSRLPARIFQHEYDHLEGVLFFDRMTDDVLDTIRE	237
Heera homolo	ga E	LEALEKKYEEK <mark>T</mark> GLPSPEKVQARQK <mark>R</mark> KAGVGFGKR 276	
Heera homolo	g b E	LEALEKKYEEK <mark>N</mark> GLPSPEKVQARQK <mark>K</mark> KAGVGFGKR 273	

**Supplementary Fig. 4.** Amino acid sequence alignment of *DEF2* homologs 'a' and 'b' from *Brassica juncea* var. Heera. Polymorphisms are highlighted in yellow boxes

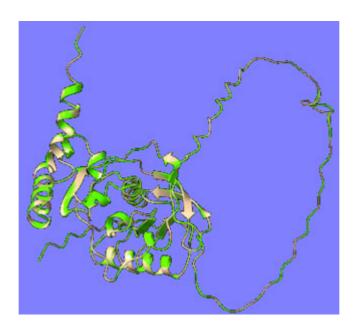
Homolog a		ATGGCCGTATGTA <mark>A</mark> CTGTTTCCTCCAAGCTCCACCGTT <mark>C</mark> TCTCGCTTCTTATCACCGGTT	60
Homolog a	Heera	ATGGCCGTATGTAGCTGTTTCCTCCAAGCTCCACCGTTTTCTCGCTTCTTATCACCGGTT	60
Homolog a	Varuna	TTCTCCCGCCGCGCTCCGAATCTCTTCCCCGGCTATGGTCAGCTCAAATCCACCGTCATG	120
Homolog a	Heera	TTCTCCCGCCGCGCTCCGAATCTCTTCCCCGGCTATGGTCAGCTCAAATCCACCGTCATG	120
Homolog a		TTctcctcctcctcccccccccccccccaAttGGACCGTTGACATCTCCGGTCCGA	
Homolog a	Heera	TTCTCCTCCTC <mark></mark> CTCCTCCGCCGCGAACCGAA <mark>CC</mark> GGACCGTTGACATCTCCGGTC <mark>A</mark> GA	177
Homolog a		GCTGAAGTAAAGCGCGTCTCGCGCAAGGAATCTGAAATAGCTTCCGC <mark>A</mark> TC <mark>C</mark> GATCT <mark>T</mark> CAA	
Homolog a	Heera	GCTGAAGTAAAGCGCGTCTCGCGCAAGGAATCTGAAATAGCTTCCGC <mark>T</mark> TC <mark>T</mark> GATCT <mark>A</mark> CAA	237
Homolog a	Varuna	TTCGAGACGCCGTTGAAGATTGTTGAGTATCCGGATCCTATCTTACGCGCTAAGAGCAAG	300
Homolog a	Heera	TTCGAGACGCCGTTGAAGATTGTTGAGTATCCGGATCCTATCTTACGCGCTAAGAGCAAG	297
Homolog a		AGGATTGGTGTTTTTGACGAGAATTTGAAGAACTTGGCCGATGCTATGTTCGATGTTATG	360
Homolog a	Heera	AGGATTGGTGTTTTTGACGAGAATTTGAAGAACTTGGCCGATGCTATGTTCGATGTTATG	357
Homolog a		TACAAAACGGATGGCATCGGGCTCTCAGCACCACAAGTGGGGCTCAATGTTCAACTCATG	
Homolog a	Heera	TACAAAACGGATGGCATTGGGCTCTCAGCACCACAAGTGGGGCTCAATGTTCAACTCATG	417
Homolog a		GTGTTTAATCC <mark>A</mark> GCTGGGGAGTCTGGTGAAGGAGAAGAGATTGTTCTTGT <mark>T</mark> AATCCGAAA	
Homolog a	Heera	GTGTTTAATCC <mark>G</mark> GCTGGGGAGTCTGGTGAAGGAGAAGAGATTGTTCTTGT <mark>G</mark> AATCCGAAA	477
Homolog a		ATCAATAAGTATTCTGATAAATTAGTACCATTCAACGAAGGATGCTTATCCTTCCCTGGG	540
Homolog a	Heera	ATCAATAAGTATTCTGATAAATTAGTACCATTCAACGAAGGATGCTTATCCTTCCCTGGG	537
Homolog a		ATCTATGCTGATGTAGTTCGACCACAATCTGTCAAGATTGACGCAAG <mark>A</mark> GACATTACTGGC	
Homolog a	Heera	ATCTATGCTGATGTAGTTCGACCACAATCTGTCAAGATTGACGCAAG <mark>G</mark> GACATTACTGGC	597
Homolog a		GCTAGATTTTCGATCAGTCTATCACGTTTACCTGCACGAATCTTTCAGCACGAATACGAC	
Homolog a	Heera	GCTAGATTTTCGATCAGTCTATCACGTTTACCTGCACGAATCTTTCAGCACGAATACGAC	657
Homolog a	Varuna	CACTTAGAGGGAGTTCTCTTCTCGACAGAATGACGGATGACGTTCTTGACACCATTCGT	720
Homolog a	Heera	CACTTAGAGGGAGTTCTCTTCTCGACAGAATGACGGATGACGTTCTTGACACCATTCGT	717
Homolog a		GAAGAGCTAGAGGCCCTGGAAAAGAAGTACGAAGAAAACTGGACTGCCAAGCCCTGAA	
Homolog a	Heera	GAAGAGCTAGAGGCCCTGGAAAAGAAGTACGAAGAGAAAACTGGACTGCCAAGCCCTGAA	777
Homolog a		AAAGTACAAGCACGACAAAAAAAGGAAAGCAGGAGTTGGTTTTGGCAAACGTTGA	834
Homolog a	Heera	AAAGTACAAGCACGACAAAAAAGGAAAGCAGGAGTTGGTTTTGGCAAACGTTGA	831

**Supplementary Fig. 5.** Comparative alignment of cDNA sequences for *DEF2* homolog 'a' in *Brassica juncea* vars. Varuna and Heera. Polymorphisms are highlighted in yellow boxes

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Homolog a Varuna Homolog a Heera	MAVC <mark>N</mark> CFLQAPPFSRFLSPVFSRRAPNLFPGYGQLKSTVMFSSS <mark>S</mark> SSAANR <mark>I</mark> GPLTSPVR MAVC <mark>S</mark> CFLQAPPFSRFLSPVFSRRAPNLFPGYGQLKSTVMFSSS <mark>-</mark> SSAANR <mark>I</mark> GPLTSPVR	
Homolog a Varuna Homolog a Heera	AEVKRVSRKESEIASASDLQFETPLKIVEYPDPILRAKSKRIGVFDENLKNLADAMFDVM AEVKRVSRKESEIASASDLQFETPLKIVEYPDPILRAKSKRIGVFDENLKNLADAMFDVM	
Homolog a Varuna Homolog a Heera	YKTDGIGLSAPQVGLNVQLMVFNPAGESGEGEEIVLVNPKINKYSDKLVPFNEGCLSFPG YKTDGIGLSAPQVGLNVQLMVFNPAGESGEGEEIVLVNPKINKYSDKLVPFNEGCLSFPG	
Homolog a Varuna Homolog a Heera	IYADVVRPQSVKIDARDITGARFSISLSRLPARIFQHEYDHLEGVLFFDRMTDDVLDTIR IYADVVRPQSVKIDARDITGARFSISLSRLPARIFQHEYDHLEGVLFFDRMTDDVLDTIR	
Homolog a Varuna Homolog a Heera	EELEALEKKYEEKTGLPSPEKVQARQKRKAGVGFGKR 277 EELEALEKKYEEKTGLPSPEKVQARQKRKAGVGFGKR 276	

**Supplementary Fig. 6.** Comparative alignment of amino acid sequences for *DEF2* homolog 'a' in *Brassica juncea* vars. Varuna and Heera. Polymorphisms are highlighted in yellow boxes.



**Supplementary Fig. 7.** Superimposed structure of DEF2 homolog 'a' protein from Varuna (beige) vs Heera (green). The models were generated using SWISS-MODEL and superimposed using ChimeraX

Homolog b HeeraATGGCCGTATGTAACTGTTTCCTCCAAGCTCCACCTCTCTCT	_			
Homolog b HeeraTTCTCCCGCCGTCTACAAATTTCTTCGCCGGCTATAATCAGCTCAAATCCACCGTCAG11Homolog b Varuna Homolog b HeeraTTCTCCTCCTCCGCGCGGAACCGGCACCGGACCGGACCG				60 60
Homolog b Varuna Homolog b Varuna Homolog b Varuna Homolog b Varuna 		-		120 120
Homolog b Varuna Homolog b HeeraGTAAAGCGCGTCTCGCGCAAGGAAGATGAAATAGCTTCCGCTTCTGATCTTCAATTCGAG GTAAAGCGCGTCTCGGCGCAAGGAAGATGAAATAGCTTCCGCTTCTGATCTTCAATTCGAG ACGCCGTTGAAGATTGTTGAGTATCCAGGATCCTATCTTACGGGCTAAGTGCAAGAGGATT 		Homolog b Varuna	TTCTCCTCCTCCGCCGCGAACCGCACCGGACCGTTGACATCTCCGGTCCGAGCTGAA	180
Homolog b HeeraGTAAAGCGCGTCTCGCGCAAGGAAGATGAAATAGCTTCCGCTTCTGATCTTCAATTCGAG24Homolog b VarunaACGCCGTTGAAGATTGTTGAGTATCCAGATCCTATCTTACGGGCTAAGTGCAAGAGGGATT33Homolog b VarunaGGTGTTTTTGACGAGCATTTGAAGAACTTGGCCGATGCTATGTTTGATGTTATGTACAAG34Homolog b VarunaGGTGTTTTTGACGAGCATTTGAAGAACTTGGCCGATGCTATGTTTGATGTTATGTACAAG34Homolog b VarunaACGGATGGCATCGGCCTCTCAGCACCACAAGTGGGGGCTCAATGTTGATGTATGT				180 240
Homolog b HeeraACGCCGTTGAAGATTGTTGAGTATCCAGATCCTATCTTACGGGCTAAGTGCAAGAGGATTHomolog b Varuna Homolog b HeeraGGTGTTTTTGACGAGCATTTGAAGAACTTGGCCGATGCTATGTTTGATGTTATGTACAAGHomolog b Varuna Homolog b Varuna Homolog b HeeraACGGATGGCATCGGCCTCTCAGCACCACAAGTGGGGCTCAATGTTCAACTCATGGTGTTTHomolog b Varuna 		Homolog b Heera	GTAAAGCGCGTCTCGCGCAAGGAAGATGAAATAGCTTCCGCTTCTGATCTTCAATTCGAG	240
Homolog b HeeraGGTGTTTTTGACGAGCATTTGAAGAACTTGGCCGATGCTATGTTTGATGTTATGTACAAG34Homolog b Varuna Homolog b HeeraACGGATGGCATCGGCCTCTCAGCACCACAAGTGGGGCTCAATGTTCAACTCATGGTGTTT44Homolog b Varuna Homolog b Varuna Homolog b HeeraAATCCAGCTGGGGAGTCTGGTGAAGGAGAAGAAGAGATTGTTCTTGTGAACCCGAAAATCAAT44Homolog b Varuna Homolog b HeeraAATCCAGCTGGGGAGTCTGGTGAAGGAGAAGAAGAGATTGTTCTTGTGAACCCGAAAATCAAT44Homolog b Varuna Homolog b HeeraAAATATTCTGATAAATTGGTACCATTCAACGAAGGATGCCTATCTTCCTGGGATCTAT AAATATTCTGATAAATTGGTACCATTCAACGAAGGATGCCTATCCTTCCCTGGGATCTAT54Homolog b Varuna Homolog b HeeraGCTGATCGACCACAATCGGTCAAGATTGACGCAAGGAGACATTACTGGTGCTAGATTTCG GCTGATCGACCACAATCGGTCAAGATTGACGCAAGAGACATTACTGGTGCTAGATTTCG GCTGATCGACCACAATCGGTCAAGATTGACGCAAGAGAACATTACTGGTGCTAGATTTTCG GCTGATCGACCACAATCGGTCAAGATTGACGCAAGAGAACATTACTGGTGCTAGATTTTCG GCTGATCGACCACAATCGGTCAAGATTGACGCAAGAGAACATTACTGGTGCTAGAGTAGCGAAGGGA GCTGATCGACCACAATCGGTTTACCTGCACGAATCTTTCAGCATGAATACGATCACCTAGAGGGA ATCAGTCTATCACGTTTACCTGCACGAATGACGTTCTTCAGCATGAATACGATCACCTAGAGGGA GCTGATCGACCACGAATGACGACGATGACGTTCTTGACACCATTCGGAGAGGATGACGTTAGAGGGAA GCTCTCTTCTCCGGCACGAATGACGGATGACGTTCTTGACACCATTCGGAGAGAGTTAGCG TCAGTCTATCACGTTTACCTGCACGAATGACGATCATCTGGAAGAGTTAGCGATGACGATCACCTAGAGGGA GCTCTCTTCTCCGCACGAATGCTCTTCAGCGATGACGTTCTGGAAGAGTTAGCG TCAGTCTATCACGTTTACCTGCACGAATGACGATCTTTCAGCATTGACCATTCGGAAGAGTTAGAG TCAGTCTATCACGTTTACCTGCACGAATGACGATCACCATTGACGATGAAGAGTTAGAG GCTCTCTTCTCCGCACGAATGACGATGACGTTCTTGACACCATTCGTGAAGAGGTTAGAG Homolog b VarunaGTTCTCTTCTTCGGACGAATGACGGATGACGTTCTTGACACCATTCGTGAAGAGTTAGAG TCAGTCTATCACGTTTACCTGCACGATGACGTTCTTGACACCATTCGTGAAGAGTTAGAG TCAGTCTATCACGTTTACCTGCACGAATGACGGATGACGTTCTTGACACCATTCGTGAAGAGTTAGAG TCTCTTCTTCGACACAAATGACGATGACGTTCTTGACACCATTCGTGAAGAGTTAGAG TCAGTCT				300 300
Homolog b HeeraACGGATGGCATCGGCCTCTCAGCACCACAAGTGGGGCTCAATGTTCAACTCATGGTGTTT42Homolog b VarunaAATCCAGCTGGGGAGTCTGGTGAAGGAAGAAGAGAGATTGTTCTTGTGAACCCGAAAATCAAT44Homolog b HeeraAATCCAGCTGGGGAGTCTGGTGAAGGAGAGAGAGAGAGAG		•		360 360
Homolog b HeeraAATCCAGCTGGGGAGTCTGGTGAAGGAGAGAGAGAGAGATTGTTCTTGTGAACCCGAAAATCAAT44Homolog b VarunaAAATATTCTGATAAATTGGTACCATTCAACGAAGGATGCCTATCCTTCCCTGGGATCTAT54Homolog b HeeraAAATATTCTGATAAATTGGTACCATTCAACGAAGGATGCCTATCCTTCCCTGGGATCTAT54Homolog b VarunaGCTGATCGACCACAATCGGTCAAGATTGACGCAAGAGACATTACTGGTGCTAGATTTTCG64Homolog b HeeraGCTGATCGACCACAATCGGTCAAGATTGACGCAAGAGACATTACTGGTGCTAGATTTTCG64Homolog b VarunaGCTGATCGACCACAATCGGTCAAGATTGACGCAAGAGAGACATTACTGGTGCTAGATTTTCG64Homolog b VarunaATCAGTCTATCACGTTTACCTGCACGAATCTTTCAGCATGAATACGATCACCTAGAGGGAA64Homolog b VarunaATCAGTCTATCACGTTTACCTGCACGAATCTTTCAGCATGAATACGATCACCTAGAGGGAA64Homolog b VarunaGTTCTCTTCTCGACAGAATGACGGATGACGTTCTTGACACCATTCGTGAAGAGTTAGAG72				420 420
Homolog b Varuna Homolog b Heera AAATATTCTGATAAATTGGTACCATTCAACGAAGGATGCCTATCCTTCCCTGGGATCTAT AAATATTCTGATAAATTGGTACCATTCAACGAAGGATGCCTATCCTTCCCTGGGATCTAT 54   Homolog b Heera GCTGATCGACCACAATCGGTCAAGATTGACGCAAGAGGACGTTACTGGTGCTAGATTTTCG 64   Homolog b Varuna Homolog b Heera GCTGATCGACCACAATCGGTCAAGATTGACGCAAGAGACATTACTGGTGCTAGATTTTCG 64   Homolog b Varuna Homolog b Varuna Homolog b Varuna ATCAGTCTATCACGTTTACCTGCACGAATCTTTCAGCATGAATACGATCACCTAGAGGGAA 64   Homolog b Varuna Homolog b Heera ATCAGTCTATCACGTTTACCTGCACGAATCTTTCAGCATGAATACGATCACCTAGAGGGAA 64   Homolog b Varuna GTTCTCTTCTGCACAGAATGACGGATGACGTTCTTGACACCATTCGTGAAGAGTTAGAG 72		0		480 480
Homolog b Varuna Homolog b Heera GCTGATCGACCACAATCGGTCAAGATTGACGCAAGAGAGACATTACTGGTGCTAGATTTTCG 64   Homolog b Heera GCTGATCGACCACAATCGGTCAAGATTGACGCAAGAGAGACATTACTGGTGCTAGATTTTCG 64   Homolog b Varuna Homolog b Heera ATCAGTCTATCACGTTTACCTGCACGAATCTTTCAGCATGAATACGATCACCTAGAGGGA 64   Homolog b Varuna ATCAGTCTATCACGTTTACCTGCACGAATCTTTCAGCATGAATACGATCACCTAGAGGGA 64   Homolog b Varuna ATCAGTCTATCACGTTTACCTGCACGAATCTTTCAGCATGAATACGATCACCTAGAGGGA 64   Homolog b Varuna GTTCTCTTCTGACAGAATGACGGATGACGTTCTTGACACCATTCGTGAAGAGGTTAGAG 72		Homolog b Varuna	AAATATTCTGATAAATTGGTACCATTCAACGAAGGATGCCTATCCTTCCCTGGGATCTAT	540
Homolog b Heera GCTGATCGACCACAATCGGTCAAGATTGACGCAAGAGACATTACTGGTGCTAGATTTTCG 64   Homolog b Varuna ATCAGTCTATCACGTTTACCTGCACGAATCTTTCAGCATGAATACGATCACCTAGAGGGA 64   Homolog b Heera ATCAGTCTATCACGTTTACCTGCACGAATCTTTCAGCATGAATACGATCACCTAGAGGGA 64   Homolog b Varuna GTTCTCTTCTGCACGAATGACGATGACGTTCTTGACACCATTCGTGAAGAGGTAGAG 64   Homolog b Varuna GTTCTCTTCTGACAGAATGACGGATGACGTTCTTGACACCATTCGTGAAGAGTTAGAG 72		Contraction of the second second		540 600
Homolog b Heera ATCAGTCTATCACGTTTACCTGCACGAATCTTTCAGCATGAATACGATCACCTAGAGGGA 6 Homolog b Varuna GTTCTCTTCCGACAGAATGACGGATGACGTTCTTGACACCATTCGTGAAGAGTTAGAG 72		Homolog b Heera	GCTGATCGACCACAATCGGTCAAGATTGACGCAAGAGACATTACTGGTGCTAGATTTTCG	600
				660 660
				720 720
0				780 780
Homolog b Varuna CGACAAAAAAAAAAAAAAAAGAAAGCAGGAGTTGGTTTTGGCAAACGTTGA 822 Homolog b Heera CGACAAAAAAAAAAAAAAAAAAAAAAGAAAGCAAGGAGTTGGTTTTGGCAAAACGTTGA 822		0		

**Supplementary Fig. 8.** Comparative alignment of cDNA sequences for *DEF2* homolog 'b' in *Brassica juncea* vars. Varuna and Heera.

Homolog b Varuna Homolog b Heera	MAVCNCFLQAPPLSRFLSPVFSRRPTNFFAGYNQLKSTVMFSSSSAANRTGPLTSPVRAE MAVCNCFLQAPPLSRFLSPVFSRRPTNFFAGYNQLKSTVMFSSSSAANRTGPLTSPVRAE	60 60
Homolog b Varuna Homolog b Heera	VKRVSRKEDEIASASDLQFETPLKIVEYPDPILRAKCKRIGVFDEHLKNLADAMFDVMYK VKRVSRKEDEIASASDLQFETPLKIVEYPDPILRAKCKRIGVFDEHLKNLADAMFDVMYK	
Homolog b Varuna Homolog b Heera	TDGIGLSAPQVGLNVQLMVFNPAGESGEGEEIVLVNPKINKYSDKLVPFNEGCLSFPGIY TDGIGLSAPQVGLNVQLMVFNPAGESGEGEEIVLVNPKINKYSDKLVPFNEGCLSFPGIY	
Homolog b Varuna Homolog b Heera	ADRPQSVKIDARDITGARFSISLSRLPARIFQHEYDHLEGVLFFDRMTDDVLDTIREELE ADRPQSVKIDARDITGARFSISLSRLPARIFQHEYDHLEGVLFFDRMTDDVLDTIREELE	240 240
Homolog b Varuna Homolog b Heera	ALEKKYEEKNGLPSPEKVQARQKKKAGVGFGKR 273 ALEKKYEEKNGLPSPEKVQARQKKKAGVGFGKR 273	

**Supplementary Fig. 9.** Comparative alignment of amino acid sequences for *DEF2* homolog 'b' in *Brassica juncea* vars. Varuna and Heera.