

Table S4. Funcional classification of methylated fragments. BLAST based alignments for chromosome association and functional annotation were performed versus both *Brassica* and *Arabidopsis* genomes. For the fragment aligning a *B. rapa* chromosome sequence, the annotation of the putative overlapping gene and of the flanking genes (Gene on the left/right) are reported.

<i>Brassica rapa</i>										<i>Brassica oleracea</i>						Sequence Read Archive (SRA)						<i>Arabidopsis thaliana</i>																	
BLASTn					tBLASTx					Overlapping gene			Gene on the left			Gene on the right			blastn			<i>B. Rapa</i>			<i>B. Rapa subp. pekinensis</i>			<i>B. rapa cultivar Chiifu-401-42</i>			BLASTn			tBLASTx			blast2GO		
IDs	length	chromosome	score	evalue	genomic region	chromosome	score	evalue	genomic region	Gene ID	Gene Annotation	Transposon	dist(Kb)	strand	Gene ID	Gene Annotation	dist(Kb)	strand	Gene ID	Gene Annotation	chromosome	score	evalue	query coverage (max)	evalue (max)	query coverage (max)	evalue (max)	query coverage (max)	evalue (max)	chromosome	score	evalue	Gene_ID Annotation	score	evalue	GeneOntology			
Bn_01	134	V	359	4E-98	2619297 - 2619525	V	194	1E-49	2619523 - 2619293	Bra004951	similar to AT2G45970 - fatty acid (omega-1)-hydroxylase/oxygen binding GO:0006631:fatty acid metabolic		1,96	+	Bra004950	similar to AT2G45960 water channel	15,99	-	Bra004952	similar to AT2G45980 - unknown protein	IV	454	1,00E-126	99%	1E-51	99%	2E-53	100%	4E-99	II	297	5,00E-80	AT2G45970 - CYP86A8, Lacerata (LCR)	103	3,E-23	GO:0006631 (fatty acid metabolic process)			
Bn_02	363	IX	507	1E-142	7773082 - 7773447	IX	138	2E-62	7773445 - 7773272			yes	1,14	-	Bra027033	similar to AT1G62600 - flavin-containing monooxygenase family protein	2,90	+	Bra027034	similar to AT3G02340 - zinc finger (C3HC4-type RING finger) family protein	VI	720	0	33%	6,E-05	12%	0,69	100%	8E-152				AT4G22505 - Bifunctional inhibitor/lipid-transfer	41	5,E-07	GO:0006869 (lipid transport)			
Bn_03	300	VIII	186	5E-46	5337782 - 5337513	VIII	157	3E-38	5337483 - 5337782			yes	4,68	-	Bra034913	similar to AT1G35490 - bZIP family transcription factor	1,16	+	Bra034912	similar to AT4G12760 - unknown protein		595	1,00E-168	28%	4,E-08		100%	3E-81				AT3G18810 - Protein kinase superfamily	35	7,E-02					
Bn_04	168	chloroplast	296	1E-46	75643 - 75543	chloroplast	517	3E-18	75380 - 75280															60%	2E-43	60%	9E-44	56%	2E-14	chloroplast	168	2,00E-41	ATCG00730 - Photosynthetic electron transfer D (chloroplast)	58	3,E-09	GO:0006355 (regulation of transcription, DNA-dependent)			
Bn_05	120	III	208	5E-53	8707996 - 8707876	III	68	3E-16	8707878 - 8707961				0,25	+	Bra023103	similar to AT2G37170 - water channel	0,58	-	Bra023104	similar to AT3G53430 - 60S ribosomal protein L12 (RPL12B)	III	167	3,E-40	32%	1,4		100%	7E-51	V	41	0,007								
Bn_06	113	VIII	192	2E-48	6744377 - 6744281	VIII	82	3E-16	6744281 - 6744382				2,57	+	Bra038074	n/a	6,67	-	Bra038073	similar to AT4G15740 - C2 domain-containing protein	VIII	131	1,E-29	85%	6E-43	15%	8,3	85%	3E-43	II	39,2	0,023							
Bn_07	266					III	47	1E-08	19385783 - 19385691												IV	38	0,42			83%	5E-53	8%	2,2	I	37,4	0,081	AT3G24090 - Glutamine-fructose-6-phosphate transaminase	47	7,E-09	GO:0006040 (amino sugar metabolic process)			
Bn_08	325					II	47	0,00006	21750725 - 21750955																		16%	2,2											
Bn_09	99																				VII	34	2,1			18%	2,4	26%	0,64	IV	35,6	0,28	AT4G27550 - Trehalose-6-phosphatase/synthetase 4(TPS4)	35	1,E-04	GO:0005992 (trehalose biosynthetic process)			