

Table S4 BLASTP analysis of two *B. rapa* BAC clones, KBrB003A10 and KBrB069I05, and the putative syntenic counterpart regions in *A. thaliana*

<i>A. thaliana</i> gene	<i>B. rapa</i> gene	% identity	BLASTP E value	Description
AT3G05580	KBrB003A10.1	93%	e-112	serine/threonine protein phosphatase, putative
AT3G05590	KBrB003A10.2	97%	e-102	RPL18 (RIBOSOMAL PROTEIN L18); structural constituent of ribosome
AT3G05610	KBrB003A10.3	76%	0	pectinesterase family protein
AT3G05620	KBrB003A10.3	40%	e-109	pectinesterase family protein
AT3G05625	KBrB003A10.4	88%	e-135	binding
AT3G05670	KBrB003A10.5	72%	0	PHD finger family protein
AT3G05675	KBrB003A10.10	81%	0	protein binding
AT3G05680	KBrB003A10.11	83%	0	EMB2016 (EMBRYO DEFECTIVE 2016)
AT3G05690	KBrB003A10.13	78%	e-127	ATHAP2B/HAP2B/UNE8 (HEME ACTIVATOR PROTEIN (YEAST) HOMOLOG 2B); transcription factor
AT3G05770	KBrB003A10.16	48%	1E-26	catalytic/ cobalamin binding
AT3G05800	KBrB003A10.19	71%	3E-71	transcription factor
AT3G05840	KBrB003A10.21	96%	0	ATSK12 (Arabidopsis thaliana SHAGGY-like kinase 12); protein kinase
AT3G05900	KBrB003A10.28	47%	6E-95	neurofilament protein-related
AT3G05910	KBrB003A10.29	94%	0	pectinacylesterase, putative
AT3G05930	KBrB003A10.31	78%	e-100	GLP8 (GERMIN-LIKE PROTEIN 8); manganese ion binding / metal ion binding / nutrient reservoir
AT3G05950	KBrB003A10.31	44%	1E-48	germin-like protein, putative
AT3G05937	KBrB003A10.33	84%	2E-47	unknown protein
AT3G05960	KBrB003A10.35	88%	9E-68	sugar transporter, putative
AT5G18910	KBrB069I05.2	85%	0	protein kinase family protein
AT5G18500	KBrB069I05.2	41%	3E-59	protein kinase family protein
AT5G18900	KBrB069I05.3	89%	e-157	oxidoreductase, 2OG-Fe(II) oxygenase family protein
AT5G18890	KBrB069I05.4	74%	e-151	inosine-uridine preferring nucleoside hydrolase family protein
AT5G18860	KBrB069I05.4	72%	e-146	inosine-uridine preferring nucleoside hydrolase family protein
AT5G18830	KBrB069I05.5	83%	0	SPL7 (SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 7); DNA binding / transcription factor
AT5G18820	KBrB069I05.6	92%	0	EMB3007 (EMBRYO DEFECTIVE 3007); ATP binding / protein binding / unfolded protein binding
AT5G18800	KBrB069I05.7	99%	9E-63	NADH-ubiquinone oxidoreductase 19 kDa subunit (NDUFA8) family protein
AT5G18760	KBrB069I05.8	78%	e-167	zinc finger (C3HC4-type RING finger) family protein
AT5G18640	KBrB069I05.10	83%	e-163	lipase class 3 family protein
AT5G18630	KBrB069I05.10	79%	e-156	lipase class 3 family protein
AT5G18650	KBrB069I05.10	89%	e-151	zinc finger (C3HC4-type RING finger) family protein
AT5G18630	KBrB069I05.11	79%	e-173	lipase class 3 family protein

AT5G18640	KBrB069I05.11	81%	e-173	lipase class 3 family protein
AT5G18620	KBrB069I05.12	88%	0	CHR17 (CHROMATIN REMODELING FACTOR17); DNA-dependent ATPase
AT5G18600	KBrB069I05.13	91%	2E-53	glutaredoxin family protein
AT5G18370	KBrB069I05.14	63%	1E-59	disease resistance protein (TIR-NBS-LRR class), putative
AT5G18350	KBrB069I05.14	68%	2E-58	disease resistance protein (TIR-NBS-LRR class), putative
AT5G18360	KBrB069I05.14	54%	7E-46	disease resistance protein (TIR-NBS-LRR class), putative
AT5G18580	KBrB069I05.15	95%	0	FASS (FASS 1)
AT5G18570	KBrB069I05.16	87%	0	GTP1/OBG family protein
AT5G18560	KBrB069I05.18	83%	e-155	PUCHI; DNA binding / transcription factor
AT5G18550	KBrB069I05.19	75%	0	nucleic acid binding
AT5G18540	KBrB069I05.20	91%	8E-84	
AT5G18520	KBrB069I05.21	92%	0	
AT5G18500	KBrB069I05.22	89%	0	protein kinase family protein
AT5G18610	KBrB069I05.22	41%	4E-66	protein kinase family protein
AT5G18480	KBrB069I05.23	84%	0	PGSIP6 (PLANT GLYCOGENIN-LIKE STARCH INITIATION PROTEIN 6); transferase, transferring glycosyl groups / transferase, transferring hexosyl groups
AT5G18475	KBrB069I05.24	80%	0	pentatricopeptide (PPR) repeat-containing protein
AT5G18470	KBrB069I05.25	76%	0	curculin-like (mannose-binding) lectin family protein
AT5G18460	KBrB069I05.26	90%	0	
AT5G18450	KBrB069I05.27	76%	e-130	AP2 domain-containing transcription factor, putative
AT5G18430	KBrB069I05.28	89%	0	GDSL-motif lipase/hydrolase family protein
AT5G18350	KBrB069I05.30	49%	0	disease resistance protein (TIR-NBS-LRR class), putative
AT5G18370	KBrB069I05.30	48%	0	disease resistance protein (TIR-NBS-LRR class), putative
AT5G18360	KBrB069I05.30	52%	e-110	disease resistance protein (TIR-NBS-LRR class), putative
AT5G18350	KBrB069I05.32	49%	0	disease resistance protein (TIR-NBS-LRR class), putative
AT5G18370	KBrB069I05.32	49%	0	disease resistance protein (TIR-NBS-LRR class), putative
AT5G18360	KBrB069I05.32	46%	0	disease resistance protein (TIR-NBS-LRR class), putative
AT5G18930	KBrB069I05.1	88%	e-176	BUD2/SAMDC4 (BUSHY AND DWARF 2); adenosylmethionine decarboxylase
