

## Supplementary Data

# Analysis of structure variations and expression characteristics of *DMP8* and *DMP9* genes in Brassicaceae

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**Table S1.** List of DMP8 and DMP9 homologous genes in the 26 Brassicaceae species.

Species	Gene ID	Gene Name	Score	Query Cover	E value	Identity	Genomic Block	Reference
<i>Arabidopsis thaliana</i>	AT1G09157	AtDMP8	732	100%	0	100%	A	[44]
<i>Arabidopsis lyrata</i>	AL1G19610	AralyDMP8	592	94%	0	93.60%	A	[45]
<i>Arabidopsis thaliana</i>	AT5G39650	AtDMP9	1069	100%	0	100%	S	[44]
<i>Boechera retrofracta</i>	BOERETT00014525	BoereDMP9.1	558	99%	0	94%	S	[46]
<i>Boechera retrofracta</i>	segment	BoereDMP9.2*	425	95%	$9.88 \times 10^{-163}$	88%	unknown	[46]
<i>Boechera stricta</i>	Bostr.10058s0037	BoestDMP9	562	99%	0	94.20%	S	[47]
<i>Crucihimalaya himaliaca</i>	Crahi.1009s0009	CruhiDMP9.1	379	99%	0	87.90%	S	[48]
<i>Crucihimalaya himaliaca</i>	Crahi.0009s0062	CruhiDMP9.2	327	97%	$7.53 \times 10^{-85}$	86%	R	[48]
<i>Capsella grandiflora</i>	Cagra.5525s0001	CapgrDMP9.1	443	92%	0	91.30%	S	(phytozome V12)
<i>Capsella grandiflora</i>	Cagra.0003s0010	CapgrDMP9.2*	402	98%	0	88.50%	unknown	(phytozome V12)
<i>Capsella rubella</i>	Carubv10007365m.g	CapruDMP9.1	533	92%	0	90.60%	S	[49]
<i>Capsella rubella</i>	Carubv10019490m.g	CapruDMP9.2*	399	99%	0	86.30%	unknown	[49]
<i>Camelina sativa</i>	Csa10g046920.1	CamsaDMP9.1	559	99%	0	92.20%	S	[50]
<i>Camelina sativa</i>	Csa12g081800.1	CamsaDMP9.2	584	99%	0	91.90%	S	[50]
<i>Arabidopsis lyrata</i>	AL7G50660	AralyDMP9	846	99%	0	96.60%	S	[45]
<i>Arabidopsis halleri</i>	Araha.5030s0001	ArahaDMP9*	633	99%	0	96.60%	unknown	[51]
<i>Descurainia sophia</i>	Desop.0231s0593	DessoDMP9.1	558	99%	0	93.50%	S	(phytozome V12)
<i>Descurainia sophia</i>	Desop.0229s0263	DessoDMP9.2*	444	96%	$5.93 \times 10^{-129}$	89.40%	unknown	(phytozome V12)
<i>Cardamine hirsuta</i>	CARHR262660.1	CarhiDMP9.1	609	100%	0	91.60%	S	[52]
<i>Cardamine hirsuta</i>	CARHR017530	CarhiDMP9.2*	728	99%	0	90.20%	unknown	[52]
<i>Leavenworthia</i>	LA_scaffold3215_7.Mrna 1 alabamica	LeaalDMP9	413	99%	0	89.10%	S	[53]
<i>Brassica rapa</i>	BraA04g012030.3C	BraDMP9.1	523	99%	0	91.80%	S	[54]
<i>Brassica rapa</i>	BraA03g003970.3C	BraDMP9.2	458	99%	0	86.10%	R	[54]
<i>Brassica oleracea</i>	BolC04g044930.2J	BraolDMP9.1	442	99%	0	89.80%	S	[55]
<i>Brassica oleracea</i>	BolC03g004320.2J	BraolDMP9.2	428	99%	$1.24 \times 10^{-179}$	85.90%	R	[55]
<i>Brassica nigra</i>	BniB006273	BraniDMP9.1	518	99%	0	90.40%	S	[56]
<i>Brassica nigra</i>	BniB028978	BraniDMP9.2	453	99%	0	87.40%	R	[56]
<i>Brassica juncea</i>	BjuVA04G12740	BrajuDMP9.1	515	99%	0	91.50%	S	[57]
<i>Brassica juncea</i>	BjuVA03G03890	BrajuDMP9.3	532	99%	0	91%	R	[57]
<i>Brassica juncea</i>	BjuVB01G23230	BrajuDMP9.2	457	99%	0	87.50%	S	[57]
<i>Brassica juncea</i>	BjuVB08G02530	BrajuDMP9.4	444	99%	$7.04 \times 10^{-170}$	86.30%	R	[57]
<i>Brassica napus</i>	A04p12360.1_BnaDAR	BranaDMP9.1	513	99%	0	91.50%	S	[58]
<i>Brassica napus</i>	C04p46030.1_BnaDAR	BranaDMP9.2	482	99%	0	89.90%	S	[58]
<i>Brassica napus</i>	A03p04210.1_BnaDAR	BranaDMP9.3	420	99%	0	86.10%	R	[58]
<i>Brassica napus</i>	segment	BranaDMP9.4*	463	99%	$4.96 \times 10^{-177}$	85.70%	R	[58]
<i>Brassica carinata</i>	BcaB06g27350	BracaDMP9.1	477	99%	0	91%	S	[59]
<i>Brassica carinata</i>	BcaB01g05665	BracaDMP9.2	680.4	99%	0	86.80%	R	[59]

<i>Brassica carinata</i>	<i>BcaB01g05567</i>	<i>BracaDMP9.4*</i>	632.9	99%	$2.40 \times 10^{-179}$	85.90%	unknown	[59]
<i>Brassica carinata</i>	<i>BcaB01g05666</i>	<i>BracaDMP9.3</i>	535.7	99%	$4.17 \times 10^{-150}$	87.90%	R	[59]
<i>Raphanus sativus</i>	<i>Rsa10036334</i>	<i>RapsaDMP9</i>	391	99%	0	87%	R	[60]
<i>Sisymbrium irio</i>	<i>SI_scaffold522_13.mRNA</i>	<i>SisirDMP9.1</i>	417	99%	0	88.70%	S	[53]
	<i>1</i>							
<i>Sisymbrium irio</i>	<i>SI_scaffold2429_21.CDS</i>	<i>SisirDMP9.2*</i>	414	96%	0	89.70%	unknown	[53]
	<i>1</i>							
<i>Isatis indigotica</i>	<i>Iin20258</i>	<i>IsainDMP9.1</i>	682	99%	s	91.10%	S	[61]
<i>Isatis indigotica</i>	<i>Iin04615</i>	<i>IsainDMP9.2</i>	594	99%	0	90.60%	unknown	[61]
<i>Arabis alpina</i>	<i>AALP_AA8G309600</i>	<i>AraalDMP9.1</i>	918.3	99%	0	90.90%	unknown	[62]
<i>Arabis alpina</i>	<i>AALP_AA8G092900</i>	<i>AraalDMP9.2</i>	749.8	99%	0	87.70%	unknown	[62]
<i>Schrenkiella parvula</i>	segment	<i>SchpaDMP9.1*</i>	1227	99%	0	91.80%	unknown	<a href="http://thellungiella.org/data/">http://thellungiella.org/data/</a>
<i>Schrenkiella parvula</i>	segment	<i>SchpaDMP9.2*</i>	1146	95%	0	89.80%	unknown	<a href="http://thellungiella.org/data/">http://thellungiella.org/data/</a>
<i>Thlaspi arvense</i>	<i>Thlar.0083s0037</i>	<i>ThlarDMP9.1</i>	473	99%	0	91.40%	S	[63]
<i>Thlaspi arvense</i>	<i>Thlar.0017s0278</i>	<i>ThlarDMP9.2</i>	440	99%	0	89.50%	unknown	[63]
<i>Thellungiella halophila</i>	<i>Thhalv10027899m.g</i>	<i>ThehaDMP9.1</i>	738	99%	0	91.20%	S	[64]
<i>Thellungiella halophila</i>	<i>Thhalv10014525m.g</i>	<i>ThehaDMP9.2</i>	921	97%	0	89.60%	unknown	[64]
<i>Aethionema arabicum</i>	<i>AA_scaffold5916_18</i>	<i>AetarDMP9</i>	448.4	83%	$1.38 \times 10^{-124}$	85.30%	S	[53]

Notes: Asterisk (\*) indicates non-syntenic genes or segments.