

Fire and Brimstone: Molecular Interactions between Sulfur and Glucosinolate Biosynthesis in Model and Crop Brassicaceae

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Supplementary Table 2

Candidate genes for GSLs synthesis and signalling in annotated brassica genomes. Summarised from Wang et al. (2011); Chalhoub et al. (2014); Liu et al. (2014)

Group name	AGI	B.rapa ID (Ar)	B.rapa ID (Ar) ro18	Blocks	specific chromo some of B.rapa	B.oleracea ID (Co)	B.napus (An sbugenome) ID	B.napus (Cn sbugenome) ID	Missing gene detailed analysis	status <i>B. napus</i> (after final validations)
Transcription factors										
Dof1.1	At1g07640	Bra031588	Bra031960-RA	A	(A09)	Bo8g112940				
		Bra030696	Bra005208-RA	A	(A08)	Bo8g010700	BnaA08g29080D	[NS]chrA08:18942871-18943761	Cn missing	not validated as lost
						Bo5g008360				
IQD1-1	At3g09710	Bra034081	Bra017665-RA	F	(A01)	Bo1g144340	BnaA01g32120D	BnaC01g39030D		
		Bra001299	Bra008263-RA	F	(A03)	Bo3g061890	BnaA03g30550D	BnaC03g35860D		
MYB28	At5g61420	Bra012961	Bra025143-RA	X	(A03)	Bo7g098590	BnaA03g40190D	[NS]chrCnn_random:42331702-42332506	Inside no syntenic model [NS] random	

		Bra035929	Bra000631-RA	X	(A09)	Bo9g014610	[NS]chrC09:3099350-3100161	BnaC09g05300D	An missing	LOST An
		Bra029311	Bra009052-RA	X	(A02)	Bo2g161590	[S]chrAnn_random:6899080-6899225	[NS]chrAnn_random:6898533-6898665		HE: 5DAn2+/5D Cn2-
MYB29	At5g07690	Bra009245	Bra034417-RA	R	(A10)	Bo9g175680				
		Bra005949	Bra005701-RA	R	(A03)	Bo3g004500	BnaA03g02170D	BnaC03g03210D		
MYB76	At5g07700									
MYB34	At5g60890	Bra013000	Bra009027-RA	X	(A03)	Bo7g098110	BnaA03g39790D	BnaCnng21270D		
		Bra035954	Bra000610-RA	X	(A09)	Bo9g014380	BnaA09g05480D	BnaC09g05060D		
		Bra029350		X	(A02)	Bo2g161170	BnaAnng06630D	BnaC02g41860D		
		Bra029349		X	(A02)	Bo2g161180	BnaAnng06640D	BnaC02g41860D		
MYB51	At1g18570	Bra025666	Bra031655-RA	A	(A06)	Bo5g025570	BnaA06g12690D	BnaC05g14250D		
		Bra031035	Bra023576-RA	A	(A09)	Bo8g104300	BnaA09g44500D	BnaC08g37160D		

		Bra016553	Bra021185-RA	A	(A08)	Bo8g067910	BnaA08g22580D	BnaC08g18090D
			Bra011642-RA					
			Bra004739-RA					
MYB122	At1g74080	Bra015939		E	(A07)	Bo6g008480	BnaA07g31220D	BnaC06g34910D
		Bra008131		E	(A02)	Bo2g080900	BnaA02g16690D	BnaC02g22630D
Side-chain elongation								
BCAT-4	At3g19710	Bra022448	Bra029343-RA	F	(A05)	Bo5g113720	BnaA05g36800D	BnaC05g33030D
		Bra001761	Bra027923-RA	F	(A03)	Bo3g073430	BnaA03g35400D	BnaC03g41100D
			Bra023142-RA					
			Bra010713-RA					
BAT5	At4g12030		Bra008649-RA					
		Bra029434	Bra009534-RA	P	(A09)	Bo9g094080	BnaA09g21170D	BnaC09g23550D

		Bra000760	Bra007801-RA	P	(A03)	Bo3g045530	BnaA03g24950D	BnaC03g73000D
		Bra019352	Bra002450-RA					
MAM1	At5g23010	Bra013007	Bra036842-RA	Q	(A03)	Bo7g098000	BnaA03g39720D	BnaCnng21190D
		Bra029355	Bra025109-RA	Q	(A02)	Bo2g161100	BnaA02g33040D	BnaC02g41790D
		Bra018524*	Bra024037-RA	O	(A02)	Bo2g102060	BnaA02g20830D	BnaC02g26810D
MAM3	At5g23020	Bra013009	Bra009023-RA	Q	(A03)	Bo7g098000	BnaA03g39710D	BnaCnng21190D
		Bra013011	Bra009021-RA	Q	(A03)	Bo7g098000	BnaA03g39680D	BnaCnng21190D
		Bra029356		Q	(A02)	Bo2g161100	BnaA02g33040D	BnaC02g41790D
		Bra021947*		J	(A04)	Bo4g183080	BnaA04g20510D	[NS]chrA03:19821938-19822196
IPMI LSU1	At4g13430	Bra032708	Bra035540-RA	T	(A04)	Bo4g131050	BnaA04g06890D	BnaCnng15040D
		Bra040341	Bra029915-RA	T	(A08)	Bo00805s020		

IPMI SSU2	At2g43100	Bra004744	Bra007416-RA	J	(A05)	Bo4g018590	[NS]chrA05_random:134636-135412	BnaC04g52970D	
IPMI SSU3	At3g58990	Bra004743				Bo4g018580.1			
						Bo3g036360.1			
IPMDH1	At5g14200	Bra023450		R	(A02)	Bo2g011730	BnaA02g02020D	[NS]chrCnn_random:64596419-64596639	inside-no_syntenic_model-[NS]-random
IPMDH3	At1g31180								
BCAT-3	At3g49680	Bra017964		M	(A06)	Bo8g078930	BnaA06g15650D	[NS]chrCnn_random:25107841-25108074	inside-no_syntenic_model-[NS]-random
		Bra029966		M	(A01)	Bo1g080200	BnaA01g20890D	[S]chrC01:22970928-22971059	inside-no_syntenic_model-[S]-complete
Core structure formation									
CYP79F1	At1g16410	Bra026058		A	(A06)	Bo5g021810	BnaA06g11010D	BnaC05g12520D	
CYP79F2	At1g16400								

CYP79A2	At5g05260	Bra009100	R	(A10)	Bo9g177260	BnaA10g25130D	BnaC09g50060D	
		Bra028764	R	(A02)	Bo2g006900	BnaAnng01260D	BnaC02g02390D	
CYP79B2	At4g39950	Bra011821	U	(A01)	Bo1g002970	BnaA01g34610D	BnaC01g00800D	
		Bra010644	U	(A08)	Bo3g152800	BnaA08g16100D	BnaC03g60820D	
		Bra017871*	U	(A03)	Bo7g118840	[S]chrA03:29024090-29025083	[NS]chrC07_random:2929352-2930345	Inside no syntenic model [S] complete
CYP79B3	At2g22330	Bra030246	I	(A04)	Bo4g149550	BnaA04g12790D	[S]chrC04:36225448-36226452	Inside no syntenic model [S] complete
CYP83A1	At4g13770	Bra032734	T	(A04)	Bo4g130780	BnaA04g06630D	BnaC04g29320D	
		Bra016908*	J	(A04)	Bo4g191120	BnaA04g24160D	BnaC04g47910D	
CYP83B1	At4g31500	Bra034941*	R	(A08)	Bo8g024390	BnaA08g04520D	BnaC08g05690D	

GSTF9	At2g30860	Bra021673	IJ	(A04)	Bo4g173610	BnaA04g17910D	BnaC04g41510D		
		Bra022815	IJ	(A03)	Bo3g024840	BnaA03g14140D	BnaC03g17110D		
GSTF10	At2g30870	Bra022816	IJ	(A03)	Bo3g024850	BnaA03g14150D	BnaC03g17120D		
GSTF11	At3g03190	Bra032010	F	(A05)	Bo5g150180	BnaA05g32420D	BnaCnng06300D		
GSTU20	At1g78370	Bra003645*	E	(A07)	Bo6g045200	BnaA07g20570D	BnaC06g20430D		
GGP1	At4g30530	Bra011201	U	(A01)	Bo1g012070	BnaA01g06540D	BnaC01g07810D		
		Bra024068	U	(A03)	Bo7g114570	BnaA03g50240D	BnaC07g42720D		
		Bra010282	U	(A08)					
		Bra010283	U	(A08)	Bo3g175530	BnaA08g13020D	[NS]chrA08:11366369-11366700	Cn missing	not validated as lost
SUR1	At2g20610	Bra036490	H	(A07)	Bo7g003330	BnaA07g00460D	[S]chrC07:490537-490603	Inside no syntenic model [S] complete	
		Bra036703	H	(A09)					

UGT74B1	At1g24100	Bra024634	B	(A09)	Bo5g041080	BnaA09g29790D	[NS]chrC05_rando m:1636643- 1637374	Inside no syntenic model [NS] random
UGT74C1	At2g31790	Bra005641	J	(A05)	Bo4g049480	BnaA05g11170D	BnaC04g12860D	
		Bra021743	J	(A04)	Bo4g177540	BnaA04g18440D	BnaC04g42530D	
ST5a	At1g74100	Bra015935	E	(A07)	Bo6g008450	BnaA07g31260D	BnaC06g35000D	
		Bra008132	E	(A02)	Bo2g080910	[NS]chrAnn_rand om:31132802- 31133821	BnaC02g22640D	
ST5b	At1g74090	Bra015938	E	(A07)	Bo6g008470	BnaA07g31230D	BnaC06g34930D	
		Bra015936	E	(A07)	Bo6g008460	BnaA07g31250D	BnaC06g34970D	
		Bra003817	E	(A07)				
		Bra003818	E	(A07)				
		Bra003726	E	(A07)				

		Bra027880*	D	(A09)			
		Bra027117*	D	(A09)			
		Bra027118*	D	(A09)			
		Bra027623*	D	(A09)			
		Bra031476*	D	(A01)			
ST5c	At1g18590	Bra025668	A	(A06)	Bo5g025610	BnaA06g12720D	BnaC05g14270D
Secondary modification							
FMOGS-OX1	At1g65860						
FMOGS-OX2	At1g62540	Bra027035*	D	(A09)	Bo9g037180	BnaA09g13190D	BnaC09g13360D
FMOGS-OX3	At1g62560						
FMOGS-OX4	At1g62570						
FMOGS-OX5	At1g12140	Bra026988	A	(A09)	Bo8g108390	BnaA09g47360D	BnaC08g41540D

AOP1	At4g03070	Bra016787	A	(A08)	Bo8g062610	BnaA08g24880D	BnaC08g15390D
		Bra034182	O	(A09)			
		Bra034181	O	(A09)			
AOP2	At4g03060	Bra000847	O	(A03)			
		Bra034180	O	(A09)	Bo9g006240	BnaA09g01260D	BnaC09g00410D
		Bra000848	O	(A03)	Bo3g052110	BnaA03g25870D	BnaC03g30450D
AOP3	At4g03050	Bra018521	O	(A02)	Bo2g102190	BnaA02g20860D	BnaC02g26740D
GSL-OH	At2g25450	Bra021670*	IJ	(A04)	Bo4g173530	BnaA04g17890D	BnaC04g41490D
		Bra021671*	IJ	(A04)	Bo4g173560	BnaA04g17890D	BnaC04g41490D
		Bra022920*	J	(A03)			
CYP81F2	At5g57220	Bra002747	W	(A10)	Bo9g131960	BnaA10g11290D	BnaC09g32980D

		Bra020459	W	(A02)	Bo2g032590	BnaA02g08270D	BnaC02g11750D	
		Bra006830	W	(A03)	Bo3g019420	BnaA03g10380D	BnaC03g13070D	
Co-substrate pathways								
BZO1p1	At1g65880	Bra004132	E	(A07)	Bo6g027260	BnaA07g25490D	BnaC06g27280D	
		Bra039743	E	(A02)				
APK1	At2g14750	Bra013120	GH	(A03)	Bo3g088400	BnaA03g38670D	[NS]chrC09:55684-20-5568717	Inside no syntenic model [NS] real ns
		Bra039818	GH	(S178)	Bo9g022580	BnaA09g08410D	BnaC09g08710D	
APK2	At4g39940	Bra011822	U	(A01)	Bo1g002960	BnaA01g34620D	BnaC01g00790D	
		Bra010645	U	(A08)	Bo3g152770	BnaA08g16110D	BnaC03g60800D	
		Bra017872*	U	(A03)	Bo7g118850	BnaA03g54400D	[NS]chrC07_random:2934264-2934567	Inside no syntenic model [NS] random

GSH1/PAD2	At4g23100	Bra013675	U	(A01)	Bo1g033120	BnaA01g12900D	[NS]chrC01_rando m:635625-635927	Inside no syntenic model [NS] random
		Bra019333	U	(A03)	Bo7g108480	BnaA03g45730D	BnaC07g37900D	
		Bra019332	U	(A03)	Bo7g108500	BnaA03g45730D	BnaC07g37950D	
CHY1	At5g65940	Bra031802	X	(A02)	Bo2g167570	BnaA02g34880D	BnaC02g45100D	
		Bra039968*	IJ	(A04)				
		Bra039975*	IJ	(A04)				
AAO4	At1g04580	Bra018392*	IJ	(A05)				
		Bra015330	A	(A10)	Bo5g004710	BnaA10g02720D	BnaC05g02700D	
		Bra011762			Bo1g003710	BnaA01g00510D	BnaC01g01500D	
		Bra011761			Bo1g003710	BnaA01g00520D	BnaC01g01500D	

Bra011759	Bo1g004730	BnaA01g00520D	BnaC01g01530D	
Bra011758	Bo1g004740	BnaA01g00570D	BnaC01g01540D	
Bra023629	Bo2g013840	[NS]chrAnn_random:16922504-16923140	[S]chrC02:3990264-3990915	
Bra006417	Bo3g012730	BnaA03g06690D	BnaC03g08560D	
Bra022816	Bo3g024850	BnaA03g14150D	BnaC03g17120D	
Bra004743	Bo4g018580	[NS]chrA05_random:130347-131105	BnaC04g52960D	Inside no syntenic model [NS] random
Bra012270	Bo7g059680	BnaA07g11060D	BnaC07g14650D	
Bra012269	Bo7g059670	BnaA07g11070D	BnaC07g14640D	
Bra012268	Bo7g059680	BnaA07g11080D	BnaC07g14650D	
Bra013958	Bo9g159960	BnaA10g17060D	BnaC09g40240D	
Bra010597	Bo3g153480	BnaA08g15650D	BnaC03g61420D	

Bra010598	Bo3g153450	BnaA08g15660D	BnaC03g61420D
Bra016432	Bo8g070660	BnaA08g21450D	BnaC08g19690D
Bra016433	Bo8g070650	BnaA08g21450D	BnaC08g19680D

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