Supplementary Material

Genome-wide identification and comparison of legume MLO gene family

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Supplementary Table S1. Characteristics of full length legume *MLO* genes.

Gene name	Contig name	Transcript	Exon	Chr.	Dir.	Lenght (kb/aa)			Protein characteristics	
						Genomic	CDS	Protein	pI	kDa
Medicago truncatula										
MtMLO1	Medtr6g033330		15	Chr6	-	5.91	1.73	574	9.18	66.01
MtMLO2	Medtr5g022400		15	Chr5	+	3.49	1.64	545	8.19	63.11
MtMLO3	Medtr2g093750		14	Chr2	+	3.24	1.78	593	9.19	67.83
MtMLO4	Medtr2g028470		14	Chr2	-	4.27	1.44	479	7.89	55.75
MtMLO5	Medtr3g115960		15	Chr3	+	3.97	1.61	537	7.41	60.75
MtMLO6	Medtr5g024700		15	Chr5	+	5.09	1.70	567	9.69	64.92
MtMLO7	Medtr2g006280		15	Chr2	+	4.44	1.66	551	8.15	63.60
MtMLO8	Medtr3g115940		14	Chr3	+	3.69	1.66	551	9.39	63.49
MtMLO9	Medtr3g118190		12	Chr3	+	4.12	1.55	517	9.35	58.43
MtMLO10	Medtr8g073130		15	Chr8	-	6.11	1.77	588	9.04	67.14
MtMLO11	Medtr4g079140		14	Chr4	-	5.63	1.71	568	7.26	65.31
MtMLO12	Medtr2g030020		5	Chr2		1.19	0.48	159		
MtMLO13	Medtr8g010500		14	Chr8	-	3.54	1.57	522	8.35	59.05
MtMLO14	Medtr8g010530		13	Chr8	-	3.11	1.56	520	9.12	59.41
MtMLO15	Medtr2g079500		15	Chr2	-	5.17	1.65	549	9.63	62.82
MtMLO16	Medtr5g009630		7	Chr5	-	5.60	0.654	217		
		mean	**14**			**4.41**	**1.65**	**547**	**8.70**	**62.69**
Cicer arietinum										
CaMLO1	Ca_04814 / LOC101504273	XM_004500787	14	Ca5	-	2.98	1.66	553	9.63	63.72
CaMLO2	Ca_23649 / LOC10500098	XM_004514937	15		+	7.96	1.68	559	9.57	64.53
CaMLO3	Ca_04697 / LOC101490933	XM_004500656, XM_004500657	13	Ca 5	-	3.94	1.60	533	9.44	60.54

Gene name	**Contig name**	**Transcript**	**Exon**	**Chr.**	**Dir.**	**Lenght (kb/aa)**			**Protein characteristics**	
						Genomic	**CDS**	**Protein**	**pI**	**kDa**
CaMLO4	Ca_01959 / LOC101505951		15	Ca 8	+	4.63	1.56	518	9.78	60.03
CaMLO5	Ca_04811 / LOC101503406	XM_004500784, XM_004500785	15	Ca5	-	3.40	1.75	481	6.78	65.76
CaMLO6	Ca_02517 / LOC101492588	XM_004487077	15	Ca1	-	3.40	1.77	590	9.28	67.44
CaMLO7	Ca_11758 / LOC101501959	XM_004510141	13	Ca7	-	4.33	1.54	513	8.26	58.71
CaMLO8	Ca_00046 / LOC101508058	XM_004485414, XM_004485415	15	Ca1	+	3.68	1.67	555	8.75	63.95
CaMLO9	Ca_11277 / LOC101495573	XM_004505476	14	Ca6	+	3.89	1.75	560	7.90	64.65
CaMLO10	Ca_10710 / LOC101494654	XM_004512376	15	Ca8	+	4.68	1.67	555	9.20	63.51
CaMLO11	Ca_06880 / LOC101511064	XM_004487635	15	Ca1	+	7.65	1.66	551	9.67	63.06
CaMLO12	Ca_09883 / LOC101496809	XM_004509404	15	Ca7	+	6.35	1.68	586	9.30	66.87
CaMLO13	Ca_07953 / LOC101510624	XM_004486357	14	Ca1	-	5.56	1.40	465	7.08	53.86
	Ca_15834	gnomon17445181	7	Ca7	-			178		
mean			**14**			**4.80**	**1.65**	**540**	**8.82**	**62.82**
Pisum sativum										
PsMLO1	FJ463618	GAMJ01003109					1.72	574	9.38	65.94
PsMLO2		GCMF01001473					1.56	518	9.30	58.58
PsMLO3		GAMJ01004855					1.76	581	7.87	66.81
PsMLO4		GAMJ01021849, GAMJ01018602,GAMJ01042925					1.65	550	9.65	62.73
Lupinus angustifolius										
LaMLO1	AOCW01137726_AOCW01137727	GBRP01032299, GBRP01057990, GBRP01055692	15		+	6.51	1.72	571	8.95	65.84
LaMLO2	AOCW01065981_AOCW01147792	GBRP0101286	15		-	5.98	1.72	572	8.66	65.82
LaMLO3	AOCW01159416		15		+	4.43	1.43	474	9.27	55.48
LaMLO4	AOCW01114694_AOCW01136624	GBRP01058592, GBRP01073743	15		+	8.19	1.79	597	10.22	68.80
LaMLO5	AOCW01127929	GBRP01087504	13		-	4.38	1.54	513	7.51	59.54
LaMLO6	AOCW01133085		15		-	3.91	1.55	514	9.72	58.16
LaMLO7	AOCW01138453	GBRP01046806, GBRP01061917	15		-	4.28	1.62	540	8.54	61.01
LaMLO8	AOCW01146534	GBRP01037926	15		-	6.26	1.78	591	9.34	66.85

Gene name	Contig name	Transcript	Exon	Chr.	Dir.	Lenght (kb/aa)			Protein characteristics	
						Genomic	CDS	Protein	pI	kDa
LaMLO9	AOCW01154130	GBRP01073792, GBRP01080451	15		-	5.49	1.67	554	9.99	63.21
LaMLO10	AOCW01039454_AOCW01039455		15		-	4.87	1.74	578	9.19	66.07
LaMLO11	AOCW01135152	GBRP01069086, GBRP01059884	15		-	5.95	1.75	581	8.88	66.05
LaMLO12	AOCW01152069	GBRP01084057, GBRP01089663	15		-	4.31	1.61	537	9.08	61.96
LaMLO13	AOCW01152789	GBRP01018422	13		-	3.80	1.49	497	9.37	56.89
LaMLO14	AOCW01138218	GBRP01077588	13		-	6.72	1.53	510	8.23	58.02
LaMLO15	AOCW01116641		15		+	5.83	1.66	552	8.85	62.69
mean			**15**			**5.39**	**1.64**	**545**	**9.05**	**62.43**
***Arachis* spp.**										
ArMLO1	ARADU.27DYI / ARAIP.PW5DF	GBIP01027541, GBIR01038206	15	Chr1/Chr10	-	5.53	1.71	569	9.00	63.96
ArMLO2	ARADU.5Y217/ARAIP.Y3LT4	GBJG01024432	13	Chr2/Chr9	-/ +	7.26	1.52	507	9.00	58.15
ArMLO3	ARADU.65SUF/ARAIP.0US16_7B80	GBIY01009746, GBJL01025099	14	Chr3	-	7.34	1.79	594	6.45	67.88
ArMLO4	ARADU.N8G7F/ARAIP.N905Y	GBJI01054888, GAIG01036165, GBJI01028580, GBIX01019295	14	Chr4	-	3.47	1.59	504	7.36	58.79
ArMLO5	ARADU.U7W18/ARAIP.Z8ALS	GBJI01008120	15	Chr4	-	3,45	1.69	563	8.30	64.59
ArMLO6	ARADU.EU0BW/ARAIP.HRR0E		15	Chr5	-	3.20	1.60	533	8.59	61.72
ArMLO7	ARADU.0YR51/ARAIP.SD8AP	GBJI01054216, GBJI01099636	14	Chr8/Chr7	+/ -	3.81	1.69	561	9.75	64.36
ArMLO8	ARADU.QG7T6/ARAIP.L2HMX	LN657014	15	Chr8/Chr7	+/ -	3.38	1.60	531	9.67	59.96
ArMLO9	ARADU.NF3XX_3QT4K/ ARAIP.CFV17	GAER01011659	14	Chr8	+	4.74	1.61	536	9.63	61.38
ArMLO10	ARADU.WJ2TG/ARAIP.N0DTV	GBJE01045697	13	Chr8/Chr7	-	5.20	1.55	515	9.08	58.72
ArMLO11	ARADU.AK182/ARAIP.SR8Z2	GBJE01048686	15	Chr8	+	5.64	1.68	558	9.12	63.30
ArMLO12	ARADU.18BQR/ARAIP.WMV74		13	Chr9	-	4.09	1.51	501	8.25	57.75
ArMLO13	ARADU.SSV2N_48N80	GBJE01033068, GBIY01021795	15	Chr4	-	28.05	1.68	559	9.38	63.91
ArMLO14	ARAIP.MQE1N	GBIX01058238,GBJI01167672	17	Chr9	+	5.29	1.54	512	8.69	58.50
mean			**14**			**6.46**	**1.63**	**539**	**8.73**	**61.64**
Cajanus cajan										
CcMLO1	C.cajan_46346	EZ668429, EZ666134	15		+	8.43	1.76	586	8.9	66.92
CcMLO2	C.cajan_07194	EZ630985.,EZ631564	15	CcLG02	-	4.69	1.76	586	9.1	67.34

Gene name	**Contig name**	**Transcript**	**Exon**	**Chr.**	**Dir.**	**Lenght (kb/aa)**			**Protein characteristics**	
						Genomic	**CDS**	**Protein**	**pI**	**kDa**
CcMLO3	C.cajan_32587		15		-	11.51	1.68	558	9.48	63.9
CcMLO4	C.cajan_12516	EZ676746	15	CcLG06	+	4.8	1.6	531	9.18	61.13
CcMLO5	C.cajan_34110		15		+	5.85	1.69	562	9.66	65.12
CcMLO6	C.cajan_34112	EZ634497	15		+	7.4	1.67	557	10.12	64.50
CcMLO7	C.cajan_21483	EZ636890	15	CcLG04	+	6.15	1.72	572	10.07	65.53
CcMLO8	C.cajan_16636	EZ668567,EZ666340, EZ676653	14	CcLG08	+	5.08	1.47	489	7.81	56.80
CcMLO9	C.cajan_01454	EZ623710, EZ653599, EZ647598, EZ680636, EZ680914	15	CcLG11	+	5.13	1.79	596	9.25	67.9
CcMLO10	C.cajan_18941		15	CcLG07	+	3.81	1.58	525	8.12	59.76
CcMLO11	C.cajan_18939		14	CcLG07	+	5.47	1.63	542	9.89	62.35
CcMLO12	C.cajan_36621	EZ682163, EZ633519	15		+	5.75	1.7	567	9.03	64.00
CcMLO13	C.cajan_17246		15	CcLG08	-	4.99	1.7	562	8.52	64.48
CcMLO14	C.cajan_23778	EZ632699, EZ680401	13		+	5.28	1.54	513	9.45	57.64
CcMLO15	C.cajan_47280	EZ658204, EZ65806, EZ675970	13		+	6.6	1.55	515	8.85	58.48
CcMLO16	C.cajan_13783	EZ671180	14	CcLG10	+	7.37	1.77	573	8.28	65.22
CcMLO17	C.cajan_37300	EZ666312, EZ641386, EZ645440	16		+	8.28	1.66	547	8.88	63.03
CcMLO18	C.cajan_37291		14		-	13.11	1.56	519	7.68	59.92
CcMLO19	C.cajan_09813	EZ665270	15	CcLG03	-	6.54	1.49	495	9.33	57.01
CcMLO20	C.cajan_24758		15		-	6.16	1.55	517	9.23	59.8
mean			**15**			**6.62**	**1.63**	**546**	**9.04**	**62.54**
Phaseolus vulgaris										
PvMLO1	Phvul.001G175900	GAMK01034684,GAMK01071155, GAMK01015455	15	Chr1	-	10.97	1.5	498	8.3	57.32
PvMLO2	Phvul.002G107600	GAMK01035468	15	Chr2	-	4.46	1.61	534	9.55	61.5
PvMLO3	Phvul.002G117900	GAMK01111725,GAMK01012053	15	Chr2	-	7.16	1.82	604	9.58	68.77
PvMLO4	Phvul.003G271300	GAMK01039073	15	Chr3	-	6.04	1.73	577	9.32	65.7
PvMLO5	Phvul.004G071700	GAMK01040872, GAMK01074602	15	Chr4	-	6.31	1.72	573	8.76	65.19

Gene name	Contig name	Transcript	Exon	Chr.	Dir.	Lenght (kb/aa)			Protein characteristics	
						Genomic	CDS	Protein	pI	kDa
PvMLO6	Phvul.004G071800	GAMK01030163,GAMK01023790, GAMK01048741, GAMK01043348	15	Chr4	-	10.48	1.62	539	10.09	61.5
PvMLO7	Phvul.005G082500	GAMK01116174, GAMK01040070, GAMK01095386	15	Chr5	-	16.62	1.64	544	8.98	62.21
PvMLO8	Phvul.005G136700	GAMK01048395, GAMK01056244	15	Chr5	-	4.21	1.66	551	9.67	64.03
PvMLO9	Phvul.005G136800	GAMK01065961, GAMK01098978, GAMK01018577	15	Chr5	-	6.1	1.68	560	10.06	65
PvMLO10	Phvul.006G133800	GAMK01046431, GAMK01056998	14	Chr6	+	4.64	1.43	474	7.11	55.79
PvMLO11	Phvul.006G216900	GAMK01044295, GAMK01053693, GAMK01061530, GAMK01054071	15	Chr6	-	4.11	1.54	512	9.1	59.07
PvMLO12	Phvul.007G093600	GAMK01033253	15	Chr7	+	4.95	1.67	556	8.7	63.35
PvMLO13	Phvul.009G006800		14	Chr9	+	3.03	1.66	551	9.85	63.24
PvMLO14	Phvul.009G007000	GAMK01055948,GAMK01088610	15	Chr9	+	4.33	1.65	550	8.62	61.7
PvMLO15	Phvul.009G117900	GAMK01045539, GAMK01119734, GAMK01064264	13	Chr9	-	5.57	1.54	513	9.34	58.01
PvMLO16	Phvul.010G034400	GAMK01051424, GAMK01041048, GAMK01109343, GAMK01017151	13	Chr10	+	5.97	1.52	507	8.71	57.98
PvMLO17	Phvul.011G073800	GAMK01113404	15	Chr11	+	6.42	1.7	566	9.82	64.85
PvMLO18	Phvul.011G122800	GAMK01050130, GAMK01040786, GAMK01049351, GAMK01050286	14	Chr11	+	5.15	1.72	571	8.57	65.85
PvMLO19	Phvul.011G172300		15	Chr11	-	9.14	1.64	545	8.98	62.33
	Phvul.009G193200		6	Chr9	+	4.38	0.3	99	10.15	22.59
mean			**15**			**6.61**	**1.63**	**543**	**9.11**	**62.28**
Vigna radiata										
VrMLO1	JJMO01000124	GBXO01007773	15	Chr1	+	6.97	1.73	577	9.15	65.93
VrMLO2	JJMO01000125	GBXO01030879	15	Chr2	+	4.7	1.71	568	9.74	65.08
VrMLO3	JJMO01000125	FF394677, FF398548	14	Chr2	+	6.3	1.81	603	8.52	69.19
VrMLO4	JJMO01000126	GBXO01029476	15	Chr3	-	4.78	1.48	493	8.75	56.44

Gene name	**Contig name**	**Transcript**	**Exon**	**Chr.**	**Dir.**	**Lenght (kb/aa)**			**Protein characteristics**	
						Genomic	**CDS**	**Protein**	**pI**	**kDa**
VrMLO5	JJMO01000120	GBXO01004030	15	Chr4	+	4.78	1.68	560	10.02	65.24
VrMLO6	JJMO01000120		15	Chr4	+	5.29	1.65	548	9.51	63.61
VrMLO7	JJMO01000121	GBX01064970	14	Chr5	+	3.11	1.67	554	9.74	63.6
VrMLO8	JJMO01000121		16	Chr5	+	3.42	1.57	522	9.41	58.77
VrMLO9	JJMO01000121	GBXO01028231, FF546578, FF546738	13	Chr5	+	5.35	1.55	515	8.57	63.75
VrMLO10	JJMO01000123		15	Chr7	+	5.29	1.72	573	9.2	65.04
VrMLO11	JJMO01000128	GBXO01035550,GBXO01044502	15	Chr8	-	4.79	1.67	554	8.25	63.63
VrMLO12	JJMO01000129	GBXO01048488, GBXO01048759	13	Chr9	-	5.53	1.55	514	9.13	58.32
VrMLO13	JJMO01000320	GBXO01033295, GBXO01073055. GBXO01013847	15	Chr10	-	3.97	1.68	559	8.82	63.98
VrMLO14	JJMO01000320	GBXO01075545	14	Chr10	+	4.57	1.41	469	7.62	54.5
VrMLO15	JJMO01000319	GBXO01055350, GBXO01035975	15	Chr11	+	3.96	1.71	569	9.03	64.74
VrMLO16	JJMO01000319	GBXO01055546, GBXO01069063	15	Chr11	+	4.18	1.59	528	9.49	60.93
VrMLO17	JJMO01000831	GBXO01053704, GBXO01009906	15		+	12.95	1.56	520	10.09	59.55
VrMLO18	JJMO01001841	GBXO01045250	15		-	5.96	1.64	546	9.12	62.52
mean			**15**			**5.33**	**1.63**	**543**	**9.12**	**62.49**

Supplementary Table S2. Online prediction servers and tools used for the analysis of legume *MLO* gene family.

Resources	**Characteristics and purpose**	**Web address**	**References**
Fgenesh	ab initio gene prediction program	http://www.softberry.com/berry.phtml?topic=index&group=programs&subgroup=gfind	Solovyev et al.[46]
SignalP	prediction of signal peptide	http://www.cbs.dtu.dk/services/SignalP/	Petersen et al.[59]
TMHMM	prediction of transmembrane domains	http://www.cbs.dtu.dk/services/TMHMM/	Krogh et al.[27]
Psort	prediction of protein subcellular localisation	http://psort.hgc.jp/form.html	Nakai and Horton[28]
Plant-mPloc	prediction of protein subcellular localisation	http://www.csbio.sjtu.edu.cn/bioinf/plant-multi/	Chou and Shen[60]
Interproscan5	Protein domain identification	http://www.ebi.ac.uk/interpro/search/sequence-search	Jones et al.[29]
IBS	Illustrator of biological sequences	http://ibs.biocuckoo.org/online.php#	Liu et al.[51]
MEME Suite	Identification of and Scanning for conserved motif	http://meme-suite.org/index.html	Bailey et al.[30]

Supplementary Table S3. Protein characteristics and identity score of legume *MLO* with its closest homologues in *M. truncatula* and *A. thaliana.*[a] Subcellular localization as predicted by the web server Psort[28] and Plant-mPloc[60]. mb and PM stand for membrane and Plasma membrane, respectively.[b] Prediction of Signal peptide (SP) as indicated by SignalP[59]. [c] Number of transmembrane domains (TM) as predicted by TMHMM[27] (T), Psort[28](P) and Interproscan5[29] (I) webservers.

Gene name	**Interproscan prediction**		**Subcellular localization**[a]		**SP**[b]	**TM domain**[c]			**Identity with *M. truncatula***					**Identity with *A. thaliana***				
									M. truncatula gene name	**Blastp hit**		**Pair-wise (%)**		**A. thaliana gene name**	**Blastp hit**		**Pair-wise (%)**	
	Pfam Ref.	**name**	**Psort**	**Plant-mPloc**		**T**	**P**	**I**		**Id.**	**E-value**	**Id.**	**Sim.**		**Id.**	**E-value**	**Id.**	**Sim.**
Medicago truncatula																		
MtMLO1	PF03094	MLO-related	mb	Cell mb	No	8	7	7	Medtr6g033330					*AtMLO6*	63	0.0	62.4	75.8
MtMLO2	PF03094	MLO-related	PM	Cell mb	No	6	6	7	Medtr5g022400					*AtMLO4*	51	$1e^{-131}$	45.0	62.7
MtMLO3	PF03094	MLO-related	mb	Cell mb	No	7	7	7	Medtr2g093750					*AtMLO6*	56	0.0	56.1	70.4
MtMLO4	PF03094	MLO-related	mb	Cell mb	No	7	6	7	Medtr2g028470					*AtMLO13*	60	$1e^{-144}$	55.9	68.2
MtMLO5	PF03094	MLO-related	mb	Cell mb	No	7	6	7	Medtr3g115960					*AtMLO5*	57	$1e^{-175}$	57.3	71.2
MtMLO6	PF03094	MLO-related	PM	Cell mb	Yes	8	7	7	Medtr5g024700					*AtMLO8*	58	0.0	55.6	70.4
MtMLO7	PF03094	MLO-related	PM	Cell mb	No	6	6	7	Medtr2g006280					*AtMLO4*	68	0.0	64.9	78.4
MtMLO8	PF03094	MLO-related	mb	Cell mb	No	7	7	7	Medtr3g115940					*AtMLO12*	50	$1e^{-150}$	46.5	62.0
MtMLO9	PF03094	MLO-related	PM	Cell mb	No	6	7	7	Medtr3g118190					*AtMLO1*	65	0.0	66.8	75.0
MtMLO10	PF03094	MLO-related	PM	Cell mb	Yes	8	7	7	Medtr8g073130					*AtMLO8*	56	0.0	59.9	72.7
MtMLO11	PF03094	MLO-related	mb	Cell mb	No	7	5	7	Medtr4g079140					*AtMLO12*	42	$1e^{-128}$	38.8	59.2
MtMLO13	PF03094	MLO-related	mb	Cell mb	No	7	8	7	Medtr8g010500					*AtMLO1*	60	0.0	59.9	71.1
MtMLO14	PF03094	MLO-related	mb	Cell mb	No	7	7	7	Medtr8g010530					*AtMLO1*	63	0.0	63.8	75.0
MtMLO15	PF03094	MLO-related	mb	Cell mb	No	7	7	7	Medtr2g079500					*AtMLO11*	68	0.0	67.4	78.3
Cicer arietinum																		
CaMLO1	PF03094	MLO-related	mb	Cell mb	No	7	7	7	Medtr3g115940	91.9	0.0	91.9	95.7	*AtMLO12*	49	$1e^{-150}$	47.0	62.1
CaMLO2	PF03094	MLO-related	mb	Cell mb	No	7	7	7	Medtr6g033330	82.7	0.0	82.3	89.4	*AtMLO6*	62	0.0	62.0	75.9
CaMLO3	PF03094	MLO-related	PM	Cell mb	No	6	7	7	Medtr3g118190	83.7	0.0	81.8	87.1	*AtMLO1*	71	0.0	65.0	73.5
CaMLO4	PF03094	MLO-related	mb	Cell mb	No	7	7	7	Medtr5g022400	83.8	0.0	79.5	86.7	*AtMLO4*	50	$1e^{-30}$	44.8	61.0
CaMLO5	PF03094	MLO-related	mb	Nucleus	No	7	6	7	Medtr3g115960	81.0	0.0	81.1	84.7	*AtMLO5*	54	$1e^{-173}$	54.1	66.3
CaMLO6	PF03094	MLO-related	mb	Cell mb	No	6	6	7	Medtr2g093750	83.4	0.0	83.4	88.1	*AtMLO6*	62	0.0	56.7	71.0
CaMLO7	PF03094	MLO-related	mb	Cell mb	No	6	8	7	Medtr8g010530	82.1	0.0	81.2	89.4	*AtMLO1*	65	0.0	64.5	74.7

Gene name	**Interproscan prediction**		**Subcellular localization[a]**		**SP[b]**	**TM domain[c]**			**Identity with *M. truncatula***					**Identity with *A. thaliana***				
									M. truncatula gene name	**Blastp hit**		**Pair-wise (%)**		**A. thaliana gene name**	**Blastp hit**		**Pair-wise (%)**	
	Pfam Ref.	**name**	**Psort**	**Plant-mPloc**		**T**	**P**	**I**		**Id.**	**E-value**	**Id.**	**Sim.**		**Id.**	**E-value**	**Id.**	**Sim.**
CaMLO8	PF03094	MLO-related	PM	cell mb	No	6	6	7	Medtr2g006280	88.7	0.0	88.3	92.3	*AtMLO4*	71	0.0	64.1	76.9
CaMLO9	PF03094	MLO-related	PM	Cell mb	No	8	6	7	Medtr4g079140	76.8	0.0	75.3	82.4	*AtMLO6*	44	$1e^{-123}$	38.6	58.9
CaMLO10	PF03094	MLO-related	PM	Cell mb	No	8	6	7	Medtr5g024700	83.7	0.0	80.8	87.0	*AtMLO8*	59	0.0	54.6	69.5
CaMLO11	PF03094	MLO-related	mb	Cell mb	No	7	7	7	Medtr2g079500	90.7	0.0	90.6	93.8	*AtMLO11*	69	0.0	68.5	78.9
CaMLO12	PF03094	MLO-related	PM	Cell mb	Yes	8	7	7	Medtr8g073130	80.8	0.0	76.9	85.3	*AtMLO8*	61	0.0	60.8	74.5
CaMLO13	PF03094	MLO-related	mb	Cell mb	No	7	6	7	Medtr2g028470	82.4	0.0	74.4	81.2	*AtMLO13*	57	$1e^{-146}$	56.9	69.4
Pisum sativum																		
PsMLO1	PF03094	MLO-related	mb	Cell mb	No	8	7	7	Medtr6g03330	83.3	0.0	83.3	91.0	*AtMLO12*	64	0.0	61.2	74.2
PsMLO2	PF03094	MLO-related	PM	Cell mb	No	7	7	7	Medtr3g118190	88.3	0.0	88.3	92.5	*AtMLO1*	70	0.0	66.4	74.5
PsMLO3	PF03094	MLO-related	mb	Cell mb	No	8	6	7	Medtr4g079140	82.5	0.0	78.9	84.1	*AtMLO6*	44	$1e^{-124}$	38.6	56.4
PsMLO4	PF03094	MLO-related	mb	Cell mb	No	7	7	7	Medtr2g079500	91.1	0.0	91.1	95.8	*AtMLO11*	69	0.0	68.6	79.6
Lupinus angustifolius																		
LaMLO1	PF03094	MLO-related	mb	Cell mb	No	6	7	7	Medtr6g03330	74.1	0.0	73.8	84.9	*AtMLO6*	63	0.0	62.3	76.4
LaMLO2	PF03094	MLO-related	mb	Cell mb	No	7	7	7	Medtr6g03330	73.2	0.0	72.9	84.1	*AtMLO6*	61	0.0	60.6	75.5
LaMLO3	PF03094	MLO-related	mb	Cell mb	No	7	6	7	Medtr5g022400	76.4	0.0	66.6	75.6	*AtMLO4*	50	$1e^{-124}$	40.8	55.7
LaMLO4	PF03094	MLO-related	mb	Cell mb	No	7	6	7	Medtr2g093750	68.2	0.0	63.9	75.5	*AtMLO6*	60	0.0	56.7	70.5
LaMLO5	PF03094	MLO-related	mb	Cell mb	No	7	6	7	Medtr2g028470	66.0	0.0	63.6	71.5	*AtMLO13*	55	$1e^{-142}$	52.0	64.8
LaMLO6	PF03094	MLO-related	PM	Cell mb	No	7	6	7	Medtr3g115960	75.4	0.0	73.1	80.1	*AtMLO5*	62	$1e^{-167}$	57.4	72.3
LaMLO7	PF03094	MLO-related	PM	Cell mb	No	7	7	7	Medtr3g115960	75.0	0.0	74.6	82.3	*AtMLO5*	57	$1e^{-171}$	57.2	70.9
LaMLO8	PF03094	MLO-related	PM	Cell mb	Yes	9	8	7	Medtr5g024700	70.7	0.0	68.0	79.0	*AtMLO8*	58	0.0	56.9	71.4
LaMLO9	PF03094	MLO-related	mb	Cell mb	Yes	9	7	7	Medtr8g073130	69.0	0.0	65.7	76.1	*AtMLO8*	60	0.0	55.4	69.0
LaMLO10	PF03094	MLO-related	mb	Cell mb	Yes	8	7	7	Medtr5g024700	69.1	0.0	67.2	77.4	*AtMLO8*	59	$1e^{-177}$	54.9	68.9
LaMLO11	PF03094	MLO-related	PM	Cell mb	Yes	8	7	7	Medtr8g073130	75.6	0.0	68.9	78.1	*AtMLO8*	61	0.0	57.6	71.8
LaMLO12	PF03094	MLO-related	PM	Cell mb	No	6	4	7	Medtr2g006280	79.4	0.0	78.4	85.3	*AtMLO4*	67	0.0	61.0	74.5
LaMLO13	PF03094	MLO-related	PM	Cell mb	No	7	7	7	Medtr3g118190	75.2	0.0	74.9	84.6	*AtMLO1*	71	0.0	66.9	76.5
LaMLO14	PF03094	MLO-related	mb	Cell mb	No	6	7	7	Medtr8g010530	73.0	0.0	72.2	83.7	*AtMLO1*	65	0.0	65.0	75.5

Gene name	Interproscan prediction		Subcellular localization[a]		SP[b]	TM domain[c]			Identity with *M. truncatula*					Identity with *A. thaliana*				
									M. truncatula gene name	Blastp hit		Pair-wise (%)		A. thaliana gene name	Blastp hit		Pair-wise (%)	
	Pfam Ref.	name	Psort	Plant-mPloc		T	P	I		Id.	E-value	Id.	Sim.		Id.	E-value	Id.	Sim.
LaMLO15	PF03094	MLO-related	mb	Cell mb	No	7	7	7	Medtr2g079500	82.6	0.0	82.4	89.6	*AtMLO11*	69	0.0	67.9	78.5
***Arachis* spp.**																		
ArMLO1	PF03094	MLO-related	PM	Cell mb	Yes	8	7	7	Medtr8g073130	73.0	0.0	66.9	77.3	*AtMLO8*	63	0.0	58.6	70.7
ArMLO2	PF03094	MLO-related	mb	Cell mb	No	7	7	7	Medtr8g010530	72.5	0.0	71.1	82.2	*AtMLO1*	69	0.0	65.9	74.5
ArMLO3	PF03094	MLO-related	mb	Cell mb	No	7	6	7	Medtr4g079140.	60.7	0.0	59.9	72.0	*AtMLO6*	41	$1e^{-124}$	39.3	57.1
ArMLO4	PF03094	MLO-related	mb	Cell mb	No	6	6	7	Medtr2g028470	67.4	0.0	63.9	73.8	*AtMLO13*	56	$1e^{-152}$	54.1	67.2
ArMLO5	PF03094	MLO-related	mb	Cell mb	No	6	7	7	Medtr2g006280	82.3	0.0	82.0	88.0	*AtMLO4*	66	0.0	66.6	80.0
ArMLO6	PF03094	MLO-related	PM	Cell mb	No	7	7	7	Medtr5g022400	73.5	0.0	73.7	84.0	*AtMLO4*	50	$1e^{-125}$	44.0	60.3
ArMLO7	PF03094	MLO-related	mb	Cell mb	No	7	6	7	Medtr3g115940	74.1	0.0	74.6	84.5	*AtMLO12*	51	$1e^{-155}$	47.5	65.0
ArMLO8	PF03094	MLO-related	mb	Cell mb	No	7	7	7	Medtr3g115960	72.6	0.0	72.7	80.3	*AtMLO5*	56	$1e^{-169}$	57.4	69.8
ArMLO9	PF03094	MLO-related	PM	Cell mb	No	7	7	7	Medtr2g093750	63.4	0.0	61.3	73.4	*AtMLO6*	56	$1e^{-177}$	54.4	68.3
ArMLO10	PF03094	MLO-related	mb	Cell mb	No	7	7	7	Medtr3g118190	79.6	0.0	79.0	85.9	*AtMLO1*	71	0.0	66.6	74.5
ArMLO11	PF03094	MLO-related	mb	Cell mb	No	6	7	7	Medtr2g079500	84.0	0.0	84.0	90.6	*AtMLO11*	71	0.0	69.2	79.6
ArMLO12	PF03094	MLO-related	mb	Cell mb	No	7	7	7	Medtr8g010530	63.5	0.0	62.4	76.8	*AtMLO1*	63	$1e^{-177}$	59.0	71.1
ArMLO13	PF03094	MLO-related	mb	Cell mb	No	5	6	7	Medtr6g033330	69.7	0.0	68.5	81.6	*AtMLO6*	60	0.0	59.6	74.2
ArMLO14	PF03094	MLO-related	mb	Cell mb	No	6	7	7	Medtr2g079500	80.6	0.0	74.7	82.3	*AtMLO11*	70	0.0	63.6	74.9
Cajanus cajan																		
CcMLO1	PF03094	MLO-related	mb	Cell Mb	No	6	7	7	Medtr6g033330	74.0	0.0	73.0	84.1	*AtMLO12*	62	0.0	61.1	72.8
CcMLO2	PF03094	MLO-related	PM	Cell Mb	No	7	7	7	Medtr6g033330	62.3	0.0	62.0	74.6	*AtMLO6*	56	0.0	56.0	68.9
CcMLO3	PF03094	MLO-related	mb	Cell Mb	No	7	6	7	Medtr6g033330	71.1	0.0	70.4	80.3	*AtMLO12*	60	0.0	59.8	71.9
CcMLO4	PF03094	MLO-related	PM	Cell Mb	No	7	7	7	Medtr5g022400	76.7	0.0	76.7	85.1	*AtMLO4*	51	$1e^{-132}$	44.1	60.8
CcMLO5	PF03094	MLO-related	mb	Cell Mb	No	7	6	7	Medtr2g093750	71.4	0.0	69.2	77.6	*AtMLO6*	59	0.0	55.1	68.5
CcMLO6	PF03094	MLO-related	mb	Cell Mb	No	7	7	7	Medtr2g093750	70.3	0.0	67.8	76.8	*AtMLO6*	57	0.0	57.8	71.5
CcMLO7	PF03094	MLO-related	mb	Cell Mb	No	7	7	7	Medtr2g093750	70.6	0.0	66.4	78.0	*AtMLO6*	61	0.0	58.3	73.3
CcMLO8	PF03094	MLO-related	mb	Cell Mb	No	7	7	7	Medtr2g028470	72.3	0.0	67.2	76.7	*AtMLO13*	57	$1e^{-145}$	53.7	67.5
CcMLO9	PF03094	MLO-related	PM	Cell Mb	Yes	9	7	7	Medtr5g024700	76.6	0.0	73.7	83.4	*AtMLO8*	59	0.0	58.3	72.3

Gene name	**Interproscan prediction**		**Subcellular localization**[a]		**SP**[b]	**TM domain**[c]			**Identity with *M. truncatula***					**Identity with *A. thaliana***				
									M. truncatula gene name	**Blastp hit**		**Pair-wise (%)**		**A. thaliana gene name**	**Blastp hit**		**Pair-wise (%)**	
	Pfam Ref.	**name**	**Psort**	**Plant-mPloc**		**T**	**P**	**I**		**Id.**	**E-value**	**Id.**	**Sim.**		**Id.**	**E-value**	**Id.**	**Sim.**
CcMLO10	PF03094	MLO-related	mb	Cell Mb	No	7	6	7	Medtr3g115960	80.6	0.0	80.7	87.2	*AtMLO5*	59	$1e^{-180}$	59.6	75.2
CcMLO11	PF03094	MLO-related	mb	Cell Mb	No	7	7	7	Medtr3g115940	79.5	0.0	79.5	88.4	*AtMLO6*	49	$1e^{-151}$	46.7	66.3
CcMLO12	PF03094	MLO-related	PM	Cell Mb	Yes	8	7	7	Medtr8g073130	77.3	0.0	69.1	77.2	*AtMLO8*	64	0.0	60.5	72.4
CcMLO13	PF03094	MLO-related	PM	Cell Mb	No	6	6	7	Medtr2g006280	83.6	0.0	83.4	89.2	*AtMLO4*	64	0.0	65.4	49.6
CcMLO14	PF03094	MLO-related	mb	Cell Mb	No	7	7	7	Medtr3g118190	78.1	0.0	78.8	87.2	*AtMLO1*	71	0.0	66.8	75.8
CcMLO15	PF03094	MLO-related	mb	Cell Mb	No	7	7	7	Medtr8g010530	76.6	0.0	76.2	84.8	*AtMLO1*	64	0.0	65.0	73.8
CcMLO16	PF03094	MLO-related	mb	Cell Mb	No	7	5	7	Medtr4g079140	69.0	0.0	68.2	77.9	*AtMLO12*	42	$1e^{-130}$	42.4	60.4
CcMLO17	PF03094	MLO-related	mb	Cell Mb	No	7	7	7	Medtr2g079500	86.7	0.0	86.8	92.3	*AtMLO11*	71	0.0	70.7	80.6
CcMLO18	PF03094	MLO-related	mb	Cell Mb	No	6	7	7	Medtr2g079500	60.4	0.0	59.9	71.0	*AtMLO11*	55	$1e^{-172}$	55.2	67.3
CcMLO19	PF03094	MLO-related	mb	Cell Mb	No	7	7	7	Medtr6g033330	47.4	$2e^{-257}$	41.6	59.2	*AtMLO3*	52	$1e^{-135}$	46.3	66.2
CcMLO20	PF03094	MLO-related	PM	Cell Mb	No	6	6	7	Medtr6g033330	50.4	$3e^{-164}$	42.8	58.9	*AtMLO6*	49	$1e^{-135}$	42.4	58.2
Phaseolus vulgaris																		
PvMLO1	PF03094	MLO-related	PM	Cell Mb	No	6	7	7	Medtr6g033330	48.3	$2e^{-156}$	40.6	59.0	*AtMLO3*	49	$1e^{-138}$	47.6	66.9
PvMLO2	PF03094	MLO-related	mb	Cell Mb	No	7	7	7	Medtr5g022400	78.4	0.0	78.6	87.4	*AtMLO4*	47	$1e^{-130}$	45.6	61.9
PvMLO3	PF03094	MLO-related	PM	Cell Mb	Yes	9	7	7	Medtr5g024700	71.2	0.0	68.4	78.8	*AtMLO8*	61	0.0	58.3	72.2
PvMLO4	PF03094	MLO-related	PM	Cell Mb	Yes	8	7	7	Medtr8g073130	78.7	0.0	71.7	79.3	*AtMLO8*	61	0.0	60.1	73.2
PvMLO5	PF03094	MLO-related	mb	Cell Mb	No	7	7	7	Medtr6g033330	74.3	0.0	73.9	85.7	*AtMLO12*	64	0.0	64.0	75.6
PvMLO6	PF03094	MLO-related	mb	Cell Mb	No	6	7	7	Medtr6g033330	71.3	0.0	67.7	80.6	*AtMLO12*	63	0.0	58.7	71.6
PvMLO7	PF03094	MLO-related	mb	Cell Mb	No	7	7	7	Medtr2g079500	84.3	0.0	84.1	90.3	*AtMLO11*	71	0.0	69.5	79.1
PvMLO8	PF03094	MLO-related	mb	Cell Mb	No	7	7	7	Medtr2g093750	69.0	0.0	67.9	76.1	*AtMLO6*	58	0.0	57.1	70.4
PvMLO9	PF03094	MLO-related	mb	Cell Mb	No	7	8	7	Medtr2g093750	67.2	0.0	66.4	76.6	*AtMo6*	59	0.0	56.1	69.1
PvMLO10	PF03094	MLO-related	mb	Cell Mb	No	7	6	7	Medtr2g028470	68.5	0.0	63.2	72.9	*AtMLO13*	59	$1e^{-142}$	53.3	67.3
PvMLO11	PF03094	MLO-related	mb	Cell Mb	No	6	7	7	Medtr2g006280	82.4	0.0	76.6	83.9	*AtMLO4*	71	0.0	62.3	73.8
PvMLO12	PF03094	MLO-related	PM	Cell Mb	No	6	7	7	Medtr6g033330	60.6	0.0	59.2	72.9	*AtMLO6*	55	0.0	53.3	69.3
PvMLO13	PF03094	MLO-related	mb	Cell Mb	No	7	7	7	Medtr3g115940	80.0	0.0	78.9	87.7	*AtMLO12*	48	$1e^{-151}$	45.9	62.9
PvMLO14	PF03094	MLO-related	mb	Cell Mb	No	7	6	7	Medtr3g115960	78.9	0.0	78.9	85.4	*AtMLO5*	56	$1e^{-176}$	57.2	69.9

Gene name	Interproscan prediction		Subcellular localization[a]		SP[b]	TM domain[c]			Identity with *M. truncatula*					Identity with *A. thaliana*				
									M. truncatula gene name	Blastp hit		Pair-wise (%)		A. thaliana gene name	Blastp hit		Pair-wise (%)	
	Pfam Ref.	name	Psort	Plant-mPloc		T	P	I		Id.	E-value	Id.	Sim.		Id.	E-value	Id.	Sim.
PvMLO15	PF03094	MLO-related	mb	Cell Mb	No	7	7	7	Medtr3g118190	78.8	0.0	78.5	86.0	*AtMLO1*	70	0.0	65.4	74.2
PvMLO16	PF03094	MLO-related	mb	Cell Mb	No	7	7	7	Medtr8g010530	75.6	0.0	74.6	84.5	*AtMLO1*	69	0.0	65.4	74.7
PvMLO17	PF03094	MLO-related	mb	Cell Mb	No	7	7	7	Medtr2g093750	70.6	0.0	66.3	76.7	*AtMLO6*	60	0.0	59.0	72.3
PvMLO18	PF03094	MLO-related	mb	Cell Mb	No	7	5	9	Medtr4g079140	68.7	0.0	67.0	76.9	*AtMLO12*	42	$1e^{-127}$	40.7	58.4
PvMLO19	PF03094	MLO-related	mb	Cell Mb	No	7	7	7	Medtr2g079500	84.7	0.0	84.5	90.3	*AtMLO11*	71	0.0	69.9	79.1
Vigna radiata																		
VrMLO1	PF03094	MLO-related	mb	Cell mb	No	7	7	7	Medtr6g033330	74.7	0.0	73.4	84.5	*AtMLO6*	64	0.0	62.9	76.4
VrMLO2	PF03094	MLO-related	mb	Cell mb	No	7	7	7	Medtr2g093750	69.8	0.0	66.4	76.7	*AtMLO6*	60	0.0	59.3	72.2
VrMLO3	PF03094	MLO-related	PM	Cell mb	No	8	5	9	Medtr4g079140	68.5	0.0	63.4	73.4	*AtMLO12*	42	$1e^{-127}$	38.3	55.7
VrMLO4	PF03094	MLO-related	mb	Cell mb	No	6	7	7	Medtr6g033330	47.8	$2e^{-160}$	42.5	59.4	*AtMLO3*	52	$1e^{-138}$	45.9	65.4
VrMLO5	PF03094	MLO-related	mb	Cell mb	No	7	8	9	Medtr2g093750	67.3	0.0	66.7	75.5	*AtMLO6*	58	0.0	57.5	71.4
VrMLO6	PF03094	MLO-related	mb	Cell mb	No	7	6	7	Medtr2g093750	69.1	0.0	67.9	76.8	*AtMLO6*	56	0.0	55.7	70.8
VrMLO7	PF03094	MLO-related	mb	Cell mb	No	7	6	7	Medtr3g115940	79.8	0.0	78.4	87.1	*AtMLO12*	49	$1e^{-152}$	46.9	62.4
VrMLO8	PF03094	MLO-related	mb	Cell mb	No	7	6	7	Medtr3g115960	81.0	0.0	81.3	86.9	*AtMLO5*	60	$1e^{-177}$	60.6	73.4
VrMLO9	PF03094	MLO-related	mb	Cell mb	No	7	6	6	Medtr3g118190	79.3	0.0	64.7	71.9	*AtMLO1*	70	0.0	53.5	60.9
VrMLO10	PF03094	MLO-related	PM	Cell mb	Yes	8	7	7	Medtr8g073130	79.3	0.0	76.7	84.0	*AtMLO8*	61	0.0	60.8	74.1
VrMLO11	PF03094	MLO-related	mb	Cell mb	No	7	7	7	Medtr6g033330	64.7	0.0	63.8	75.8	*AtMLO6*	56	0.0	55.1	70.9
VrMLO12	PF03094	MLO-related	mb	Cell mb	No	6	7	7	Medtr8g010530	74.8	0.0	74.1	83.7	*AtMLO1*	65	0.0	66.7	74.6
VrMLO13	PF03094	MLO-related	mb	Cell mb	No	6	6	7	Medtr2g006280	81.0	0.0	80.6	86.9	*AtMLO4*	71	0.0	42.1	61.4
VrMLO14	PF03094	MLO-related	mb	Cell mb	No	7	7	7	Medtr2g028470	69.2	0.0	63.4	73.6	*AtMLO13*	59	$1e^{-141}$	53.4	67.6
VrMLO15	PF03094	MLO-related	mb	Cell mb	No	8	6	7	Medtr5g024700	73.3	0.0	68.3	78.3	*AtMLO8*	60	0.0	56.2	69.9
VrMLO16	PF03094	MLO-related	PM	Cell mb	No	7	7	7	Medtr5g022400	78.4	0.0	78.5	87.0	*AtMLO4*	49	$1e^{-130}$	44.9	60.8
VrMLO17	PF03094	MLO-related	mb	Cell mb	No	7	7	7	Medtr6g033330	73.6	0.0	66.8	78.8	*AtMLO12*	65	0.0	58.9	70.6
VrMLO18	PF03094	MLO-related	mb	Cell mb	No	7	7	7	Medtr2g079500	83.8	0.0	83.8	89.9	*AtMLO11*	70	0.0	68.7	78.3

Supplementary Table S4. Conservation in legume sequences of the 73 amino acids previously found to discriminate between monocot and eudicot powdery mildew susceptibility proteins[18]. The comparison was performed by aligning the monocot and dicot powdery mildew susceptibility proteins as in Appiano *et al.*[18] with the corresponding legume MLO sequences from clades IV and V. Colored residues highlight residue varying between monocot and eudicot plant species (red), between clades (blue) or both (green), respectively.

Localization	**TM1**					**EC1**			**TM3**			**IC2**										
Position in *HvMLO1*	**13**	**25**	**27**	**28**	**32**	**91**	**96**	**125**	**143**	**145**	**146**	**197**	**198**	**178**	**183**	**184**	**185**	**188**	**189**	**194**	**195**	**197**
Monocot (Cl. IV)	**P**	**A**	**M/I**	V/I	**V**	A	**W/L/R**	**G**	T/L	**S**	V	**A/T**	S	**A/S**	T	**H**	**Q**	**V**	K	**G**	L	**S**
Legume Cl. IV	**Q/K/E**	**A/S**	**F**	V/I	**V**	A/L	**L**	**S**	F/L	**S**	V	**S/T**	S	**A/S**	T/A	**H**	**Q**	**V**	R/K	**G**	W/L	**R**
Eudicot (Cl. V)	**T/E/D**	**F**	L/M	L	**I**	V/I/L	**H**	Y	L/I/F	**C**	I	**K/R**	T	**E**	A/T	**R**	**D**	**G**	R	**S/N/H/**	W	Q/K
Legume Cl. V	**T/E/D/Q**	**F/L**	L/M	L/V/I	**I**	V/I/A	**H/N**	Y/E/D/G	L/I	**C**	I/V	**K/R**	T/S	**E**	A	**R/K**	**D/E**	**G**	R/Q	**S/N**	W	Q/K/R

Supplementary Table S4 (continued)

Localization	**IC2**										**TM4**				**EC2**				**TM5**		
Position in *HvMLO1*	**198**	**200**	**202**	**206**	**225**	**229**	**233**	**234**	**241**	**245**	**250**	**260**	**261**	**267**	**271**	**272**	**273**	**274**	**276**	**278**	**279**
Monocot (Cl. IV)	**T**	**G**	**R**	**A**	**A/Q**	**N**	S	**Q**	H	K	**D**	**L**	P	**I**	**F**	L	**D**	**I**	**G**	**G**	**T**
Legume Cl. IV	**M/K**	**G**	**R**	**A**	**H**	**N**	A	**P**	H/Q	K	**D**	**I/M**	P	**I**	**L**	L/M/V	**N**	**V**	**K**	**Y**	**T**
Eudicot (Cl. V)	S/N/T	**V/I/F**	**L/M/I**	**C**	**H**	**M/I**	A/T/P	**P**	R/Q	Q/S/N	**E/K/Q**	**P**	A/V/T/L	**V**	**L**	T	**N/T**	**T/S**	G	**Y/H**	**S**
Legume Cl. V	S/N/T	**V/I**	**L/M/I/V**	**C/S**	**H**	**M/T/V**	A/T/G/S	**P**	R/Q/H	E/Q/K	**E/K**	**P**	I/V/T/P	**V**	**L**	T/F/L	**N/H**	**T**	G	**Y/H**	**S**

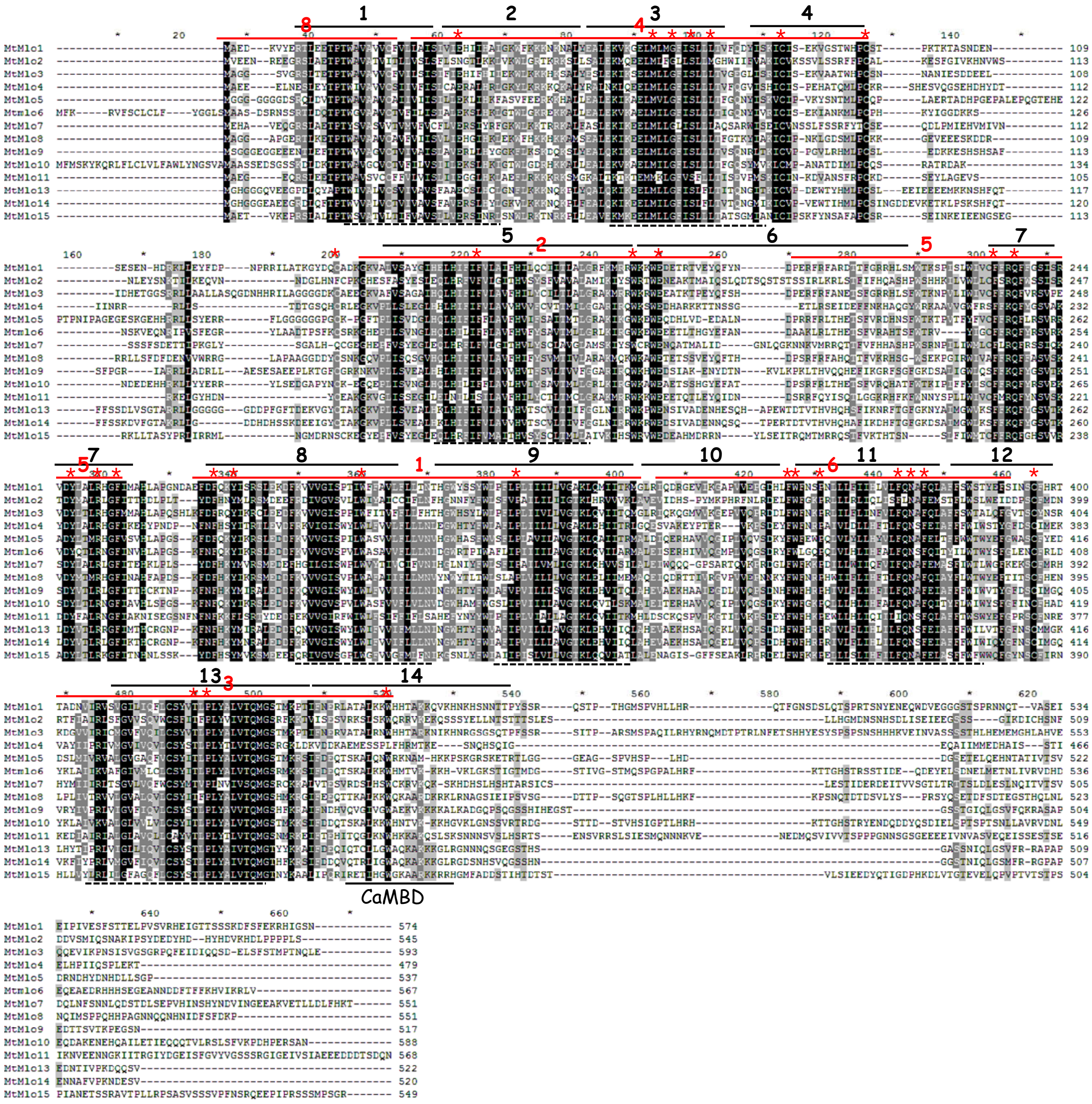
Supplementary Table S4 (continued)

Localization	**TM5**				**IC3**										**TM6**			**EC3**				
Position in *HvMLO1*	**280**	**284**	**285**	**291**	**303**	**306**	**308**	**313**	**314**	**325**	**326**	**327**	**335**	**336**	**344**	**352**	**354**	**358**	**360**	**361**	**362**	**366**
Monocot (Cl. IV)	**L**	**S**	**F**	**L**	**M**	A	**E**	**A**	**S/T**	**S**	**N**	**K**	D	**W**	**I/T**	M	H	T	**A**	**T**	**P**	**K/D**
Legume Cl. IV	**L**	**S**	**V**	**L**	**M**	A	**E/Q**	**A/T**	**T**	**N**	**N**	**K**	Q/H	**W**	**T/I**	I/M	F	T	**Y**	**E**	**F**	**S**
Eudicot (Cl. V)	**Y**	**P**	F	**I**	**T/S**	G	**R/K**	**G**	**D**	**G**	**D**	**D/H**	R/G	**F/L**	**V**	L/V	F	S	**W/Y/L**	E/K/D	**F**	**S/N**
Legume Cl. V	**Y**	**P**	F	**I/V**	**T**	G/A	**R/K**	**G**	**D/E**	**G**	**D**	**E/D/H**	R/G/D/H	**F/L**	**V**	L/V/M	F/H/Y	S/T/A	**L/Y/F**	E/Q/D	**F**	**S/N**

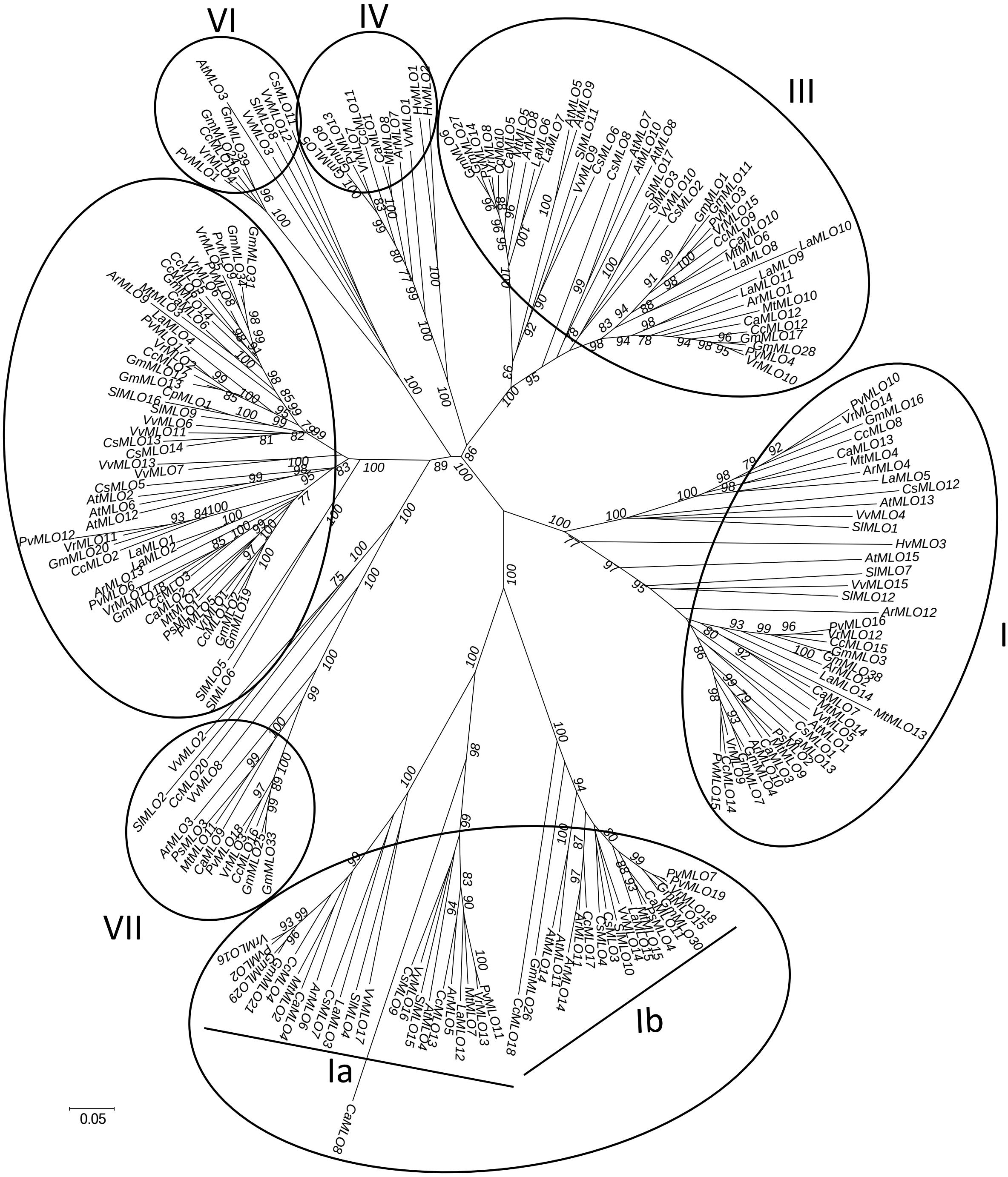
Supplementary Table S4 (continued)

Localization	**EC3**			**TM7**	**C-TERMINAL**					**CaMBD**							
Position in *HvMLO1*	**374**	**377**	**378**	**394**	**406**	**409**	**413**	**415**	**416**	**418**	**420**	**421**	**429**	**430**	**431**	**434**	**435**
Monocot (Cl. IV)	**L**	**M**	K	**F**	**N/H**	**R/K**	**E/D**	**Q**	**T**	K	**M/T**	**R**	E	K	K	R	D
Legume Cl. IV	**L**	**T/V**	R	**F**	**H**	**R/K**	**E**	**Q**	**T**	K	**K**	**Q**	D/E	K/R	K/R/T	R	K
Eudicot (Cl. V)	**D**	I	R	**L**	**T/S/K**	**P**	**G/N**	**N/R**	**V**	T	**K**	**H**	K	R/Q/H	V/T/I	G/N	R/K
Legume Cl. V	**D/E**	I/V	R/K	**L**	**T/S**	**P/A/H**	**N**	**N/R**	**V/I/L**	T/S/K/E	**K/R**	**H**	K/N/E	N/Q/H	V/K/I	G/N/S/K/R	R/K/D

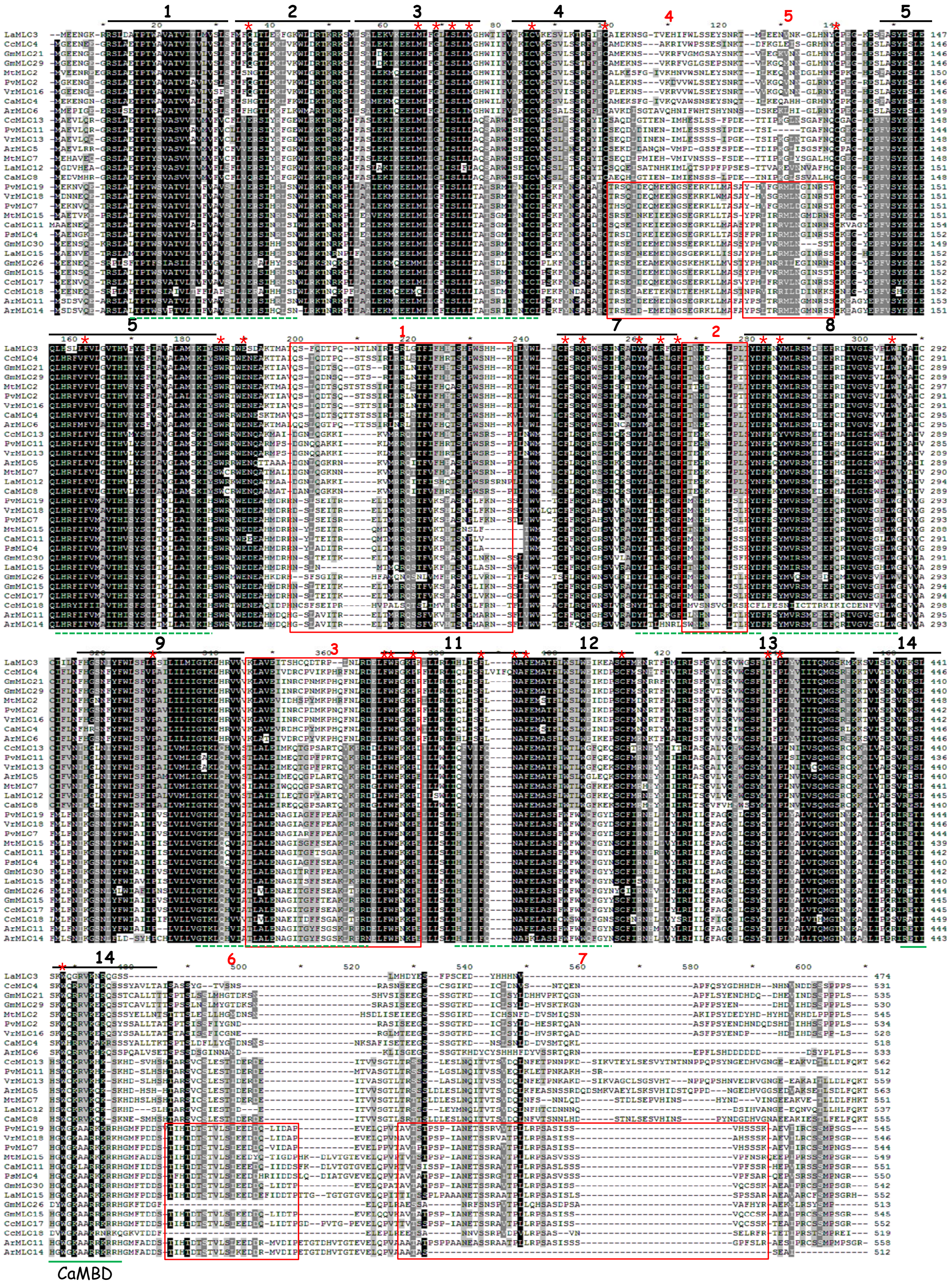
Supplementary Figure S1. Alignment *of M. truncatula* MLO protein sequences. Alignment was obtained with ClustalW[34]with default parameters. Shading represents amino acid conservation at 90%, 70% and 50% respectively. Red Asterisks on top of the alignment show the 30 highly conserved residues previously detected in MLO sequences[33]. MEME conserved motifs are indicated by numbered horizontal bars on top of the alignment while the transmembrane domains (dashed line) and the CaMBD motif are represented below the alignment. Numbered horizontal bar in red represent the localization of the most significant motifs identified previously by Deskmuth *et al.*[15].



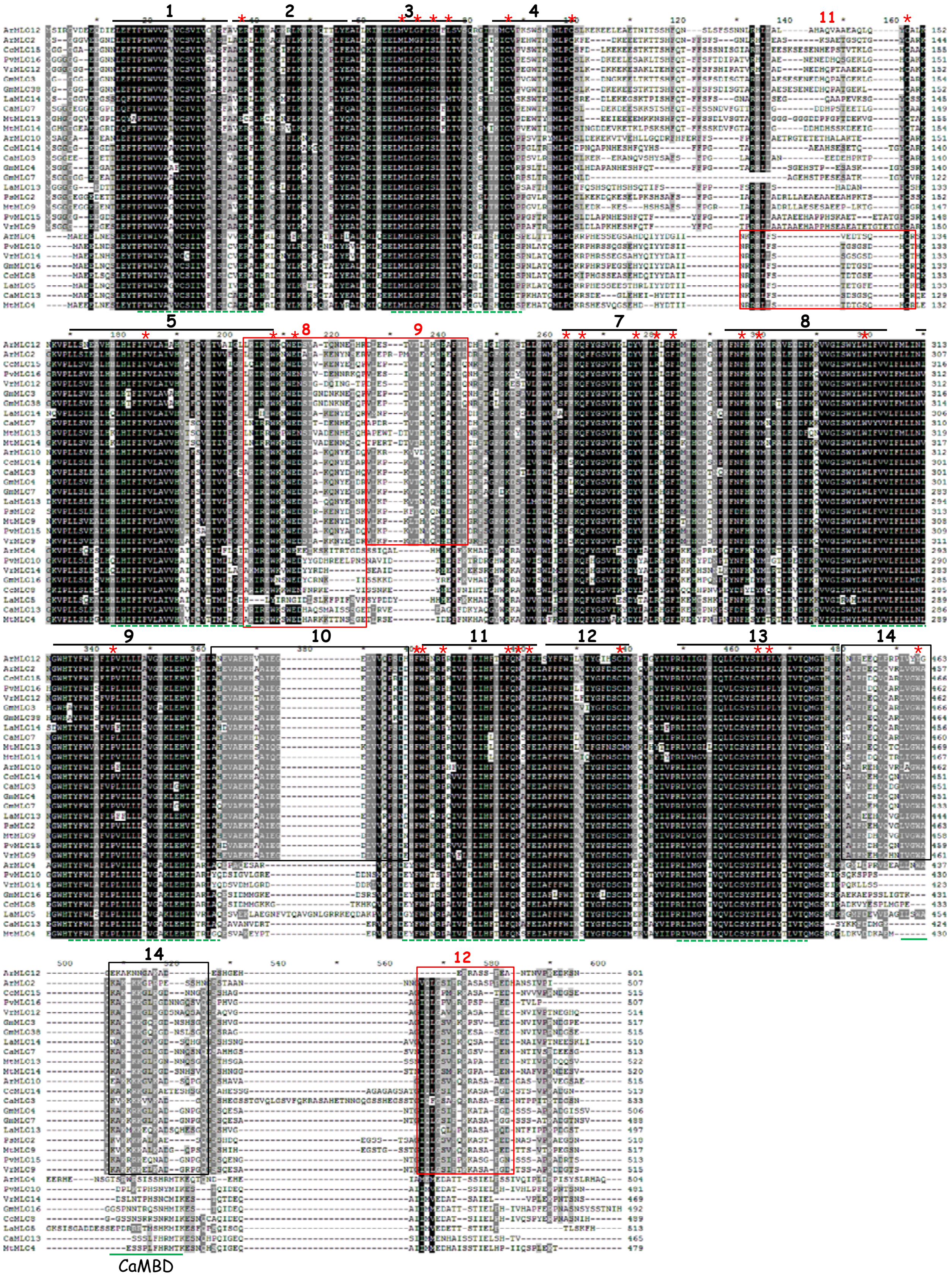
Supplementary Figure S2. Phylogenetic relationship of MLO protein sequences. The phylogenetic tree includes all MLO sequences identified in this study with those of *Arabidopsis thaliana, Cucumis sativus, Solanum lycopersicum, Vitis vinifera* and *Hordeum vulgare* (Table 1). The unrooted tree was built with the Neighbor-Joining method on MEGA 6 software[48] and reveals seven well-supported clades. Clade I MLO appears further subdivided in two distinct groups (Ia and Ib). Numbers above branches indicate the percentage of bootstrap replicates supporting this branch. Only bootstrap values higher than 75 are represented.



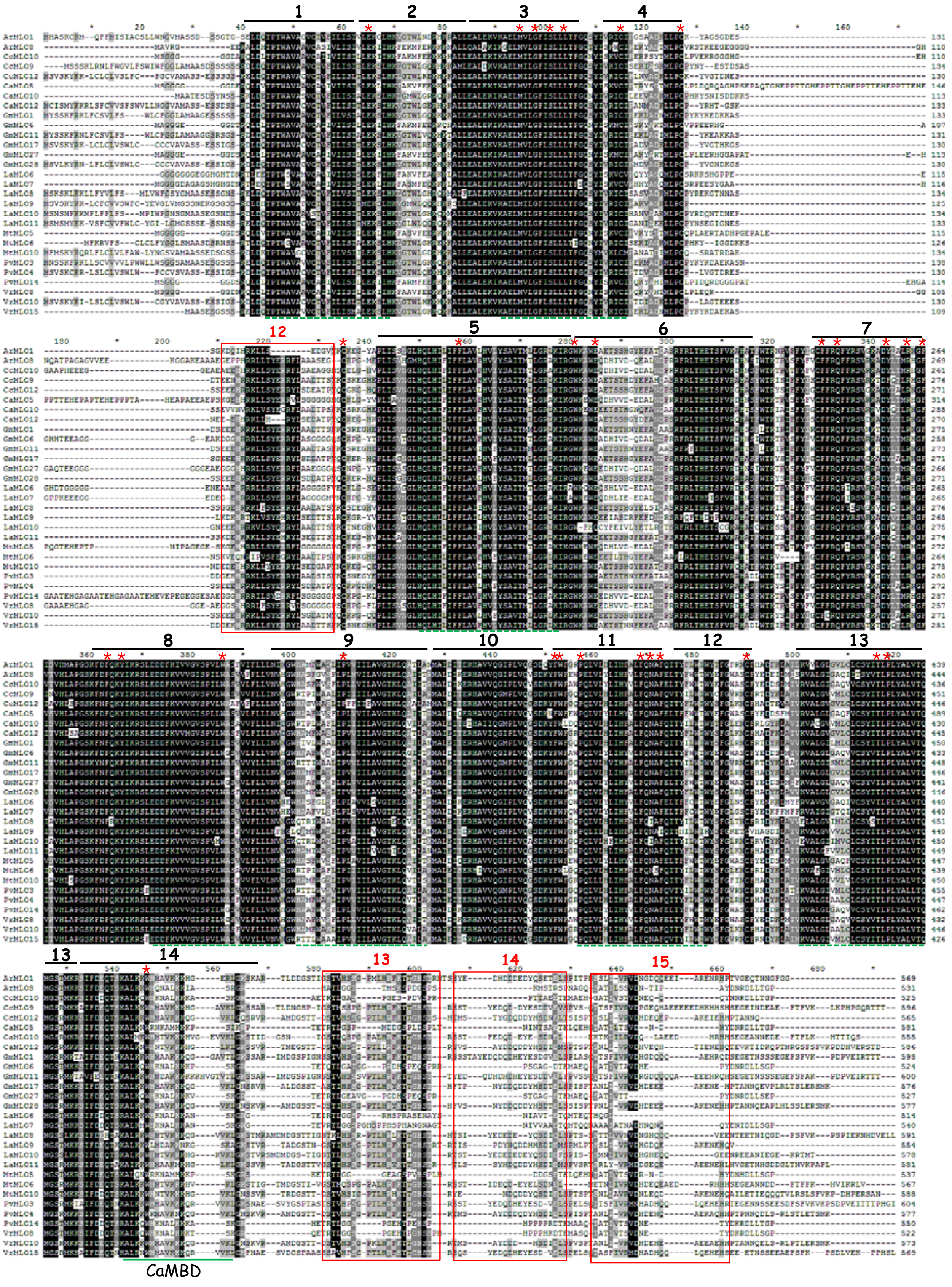
Supplementary Figure S3. Alignment of Clade I MLO protein sequences from legume species. Alignment was obtained with ClustalW[34] with default parameters. Shading represents amino acid conservation at 90%, 70% and 50% respectively. MLO-specific motifs are indicated by black horizontal lines. Clade I-specific MEME motifs are shown in red boxes. Transmembrane domains (green dashed lines) and the CaMBD domain (green line) are represented below the alignment. Red asterisks on top of the alignment show the 30 highly conserved residues previously detected in MLO sequences[33].



Supplementary Figure S4. Alignment of Clade II MLO protein sequences from legume species. Alignment was obtained with ClustalW[34] with default parameters. Shading represents amino acid conservation at 90%, 70% and 50% respectively. MLO-specific motifs are indicated by black horizontal lines. Clade II-specific MEME motifs are shown in red boxes. Transmembrane domains (green dashed lines) and the CaMBD domain (green line) are represented below the alignment. Red asterisks on top of the alignment show the 30 highly conserved residues previously detected in MLO sequences[33].



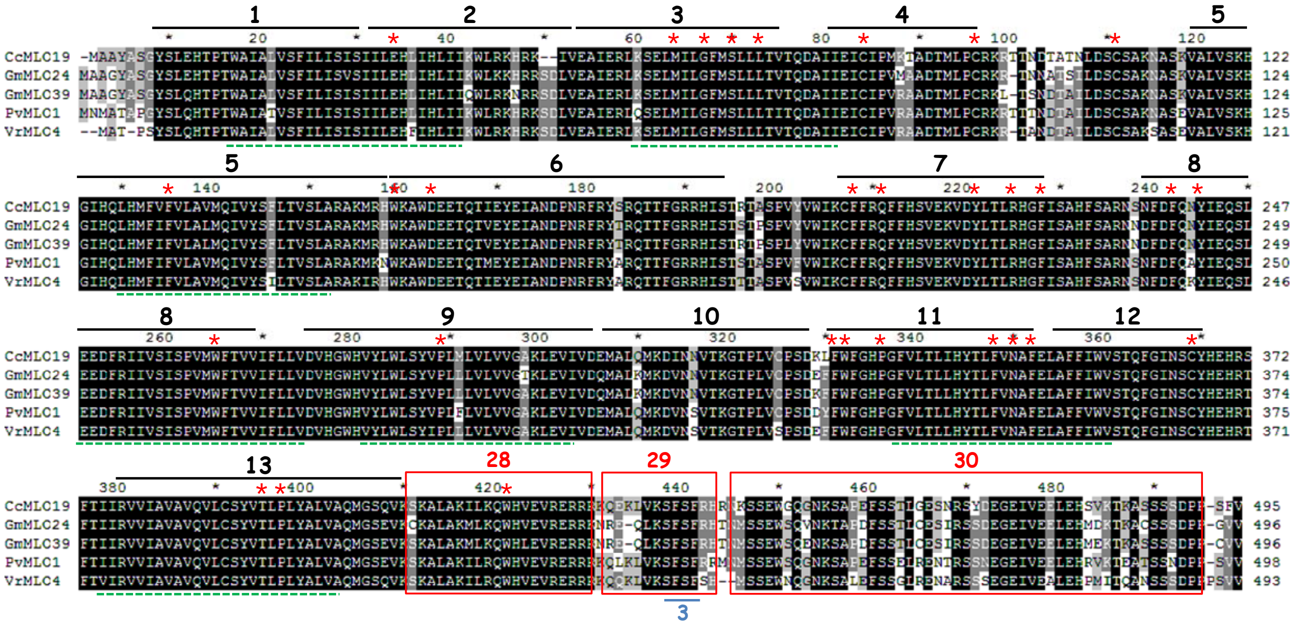
Supplementary Figure S5. Alignment of Clade III MLO protein sequences from legume species. Alignment was obtained with ClustalW[34] with default parameters. Shading represents amino acid conservation at 90%, 70% and 50% respectively. MLO-specific motifs are indicated by black horizontal lines. Clade III-specific MEME motifs are shown in red boxes. Transmembrane domains (green dashed lines) and the CaMBD domain (green line) are represented below the alignment. Red asterisks on top of the alignment show the 30 highly conserved residues previously detected in MLO sequences[33].



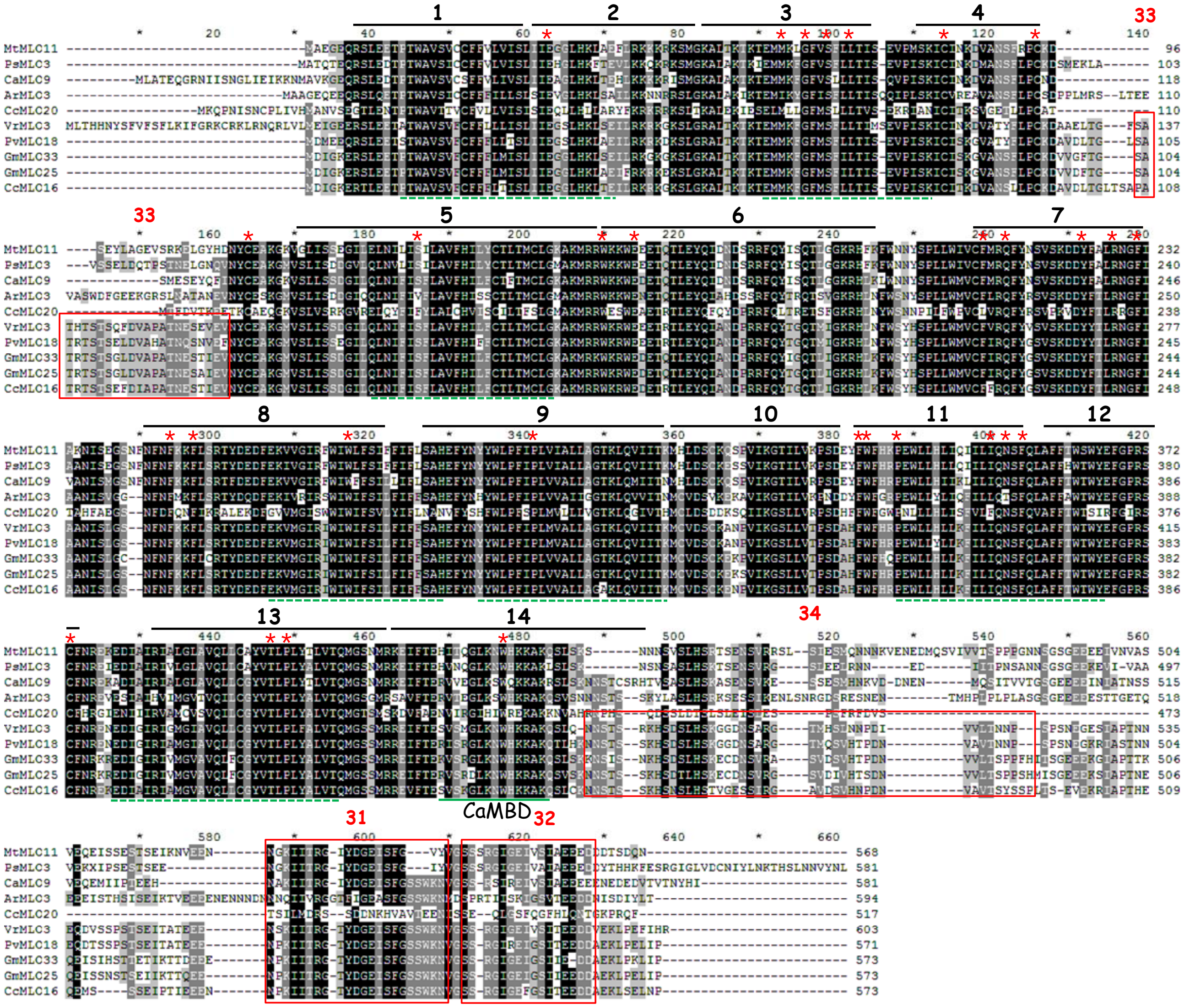
Supplementary Figure S6. Alignment of Clade IV MLO protein sequences from legume species. Alignment was obtained with ClustalW[34] with default parameters. Shading represents amino acid conservation at 90%, 70% and 50% respectively. MLO-specific motifs are indicated by black horizontal lines. Clade IV-specific MEME motifs are shown in red boxes. Transmembrane domains (green dashed lines) and the CaMBD domain (green line) are represented below the alignment. Red asterisks on top of the alignment show the 30 highly conserved residues previously detected in MLO sequences[33]. A motif similar to the [DE]FSF tetrad previously identified in Class V MLO sequences by Panstruga[35] is also shown in numbered blue horizontal line below the alignment.

Supplementary Figure S7. Alignment of Clade V MLO protein sequences from legume species. Alignment was obtained with ClustalW[34] with default parameters. Shading represents amino acid conservation at 90%, 70% and 50% respectively. MLO-specific motifs are indicated by black horizontal lines. Clade V-specific MEME motifs are shown in red boxes. Transmembrane domains (green dashed lines) and the CaMBD domain (green line) are represented below the alignment. Red asterisks on top of the alignment show the 30 highly conserved residues previously detected in MLO sequences[33]. Conserved motifs identified previously from clade V MLO sequences[16,35] are also indicated by blue lines below the alignment.

Supplementary Figure S8. Alignment of Clade VI MLO protein sequences from legume species. Alignment was obtained with ClustalW[34] with default parameters. Shading represents amino acid conservation at 90%, 70% and 50% respectively. MLO-specific motifs are indicated by black horizontal lines. Clade VI-specific MEME motifs are shown in red boxes. Transmembrane domains (green dashed lines) and the CaMBD domain (green line) are represented below the alignment. Red asterisks on top of the alignment show the 30 highly conserved residues previously detected in MLO sequences[33]. A motif similar to the [DE]FSF tetrad previously identified in Class V MLO sequences by Panstruga[35] is also shown in numbered blue horizontal line below the alignment.



Supplementary Figure S9. Alignment of Clade VII MLO protein sequences from legume species. Alignment was obtained with ClustalW[34] with default parameters. Shading represents amino acid conservation at 90%, 70% and 50% respectively. MLO-specific motifs are indicated by black horizontal lines. Clade VII-specific MEME motifs are shown in red boxes. Transmembrane domains (green dashed lines) and the CaMBD domain (green line) are represented below the alignment. Red asterisks on top of the alignment show the 30 highly conserved residues previously detected in MLO sequences[33].



Supplementary Figure S10. List of legume *MLO* CDS sequences.

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Supplementary Figure S11. List of legume MLO deduced protein sequences.

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