

S3 Appendix. List of genome and transcriptome databases interrogated in this study, and the list of MCA genes included in the MCA phylogenetic analyses.

vernacular	clade	clade	clade	order	family	Taxon	database	note	gene ID	chromosome/Genome scaffolds	ID in matrix	ID in proteome analyses	MCA HMMsearch				MCAfunc HMMsearch				PLAC8 HMMsearch								
													length (AA)	E value	from	to	length	E value	from	to	length	E value	from	to	length	E value	from	to	length
Hornworts	-	-	-	Anthocerotales	Anthocerotaceae	Anthoceros angustus	NCBI Genome	GCA_010909165.1	MU008170.1	scaffold 21	HW.MU008170.ANTAN			789	2.50E-148	3	406	404	1.70E-75	1	141	141	9.10E-14	1	99	99			
Liverworts	-	-	-	Marchantiales	Marchantiaceae	Marchantia polymorpha	Phytozome v.12		Mapoly124s0009	scaffold_134	LW.0134s0009.MARPO	A0A2R6W7G4_MARPO		483	3.30E-155	4	421	418	3.90E-65	5	166	162	8.70E-19	1	99	99			
Bryophytes	-	-	-	Funariales	Funariaceae	Physcomitrella patens	Phytozome v.12	v3.3	Pp3c12_21520V3	Chromosome 12	MO.12_21520V3.PHYPA	A0A2K1JKR9_PHYPA		438	3.50E-172	4	421	418	5.80E-75	5	167	163	1.00E-17	1	98	98			
Bryophytes	-	-	-	Sphagnales	Sphagnaceae	Sphagnum fallax	Phytozome v.12	v0.5	Pp3c8_990V3	Chromosome 08	MO.8_990V3.PHYPA	A0A2K1K5M7_PHYPA		445	4.80E-170	5	421	417	1.50E-72	7	166	160	1.30E-16	1	96	96			
Bryophytes	-	-	-	Sphagnales	Sphagnaceae	Sphagnum fallax	Phytozome v.12	v0.5	Sphfalx0076S0017	super_76	MO.0076S0017.SPHFA		440	1.30E-164	4	420	417	2.50E-75	4	167	164	2.40E-17	1	98	98				
Lycophytes	-	-	-	Selaginellales	Selaginellaceae	Selaginella moellendorffii	Phytozome v.12	v1.0	Sm_93428	scaffold_14	LY.93428.SELML	D85S21/D8GG8		396	1.10E-163	8	406	399	5.40E-79	8	167	160	4.10E-21	1	99	99			
Monilophytes	-	-	-	Salviniales	Salviniaceae	Azolla filiculoides	FernBase		Sacu_0316.g064349	scaffold_0316	FN.S0316.g064349.AZOFI		606	6.20E-148	3	376	374	8.30E-78	4	166	163	9.00E-12	1	80	80				
Monilophytes	-	-	-	Salviniales	Salviniaceae	Salvinia cucullata	FernBase		Sacu.v1.1.s0057.g014785	scaffold_0057	FN.S0057.g014785.SALCU		771	2.60E-169	4	421	418	2.00E-78	4	167	164	9.10E-20	1	99	99				
Gymnosperms	-	-	-	Ginkgoales	Ginkgoaceae	Ginkgo biloba	IKP		SGTW_scaffold_2002341	unknown	GY.2002341.GBI		422	6.10E-173	1	421	421	2.30E-76	1	63	63	7.00E-16	1	99	99				
Gymnosperms	-	-	-	Cycadales	Cycadaceae	Cycas michollitzi	IKP		XZUY_scaffold_2011951	unknown	GY_2011951.CMI	CMI00009383		434	1.10E-202	1	421	421	1.90E-95	1	167	167	7.60E-17	1	99	99			
Gymnosperms	-	-	-	Welwitschiales	Welwitschiaceae	Welwitschia mirabilis	IKP		TOXE_scaffold_2008256	unknown	GY_2008256.WMI		376	1.50E-168	1	402	402	2.20E-88	2	167	166	2.5E-16	1	99	99				
Gymnosperms	-	-	-	Cupressales	Taxaceae	Taxus baccata	FLAZA	TBA	TBA00013714	unknown	GY_00013714.TBA		419	2.70E-195	3	421	419	5.80E-95	4	167	164	5.90E-17	1	99	99				
Angiosperms	-	-	-	Amborellales	Amborellaceae	Amborella trichopoda	Phytozome v.12	v1.0	evm_27.model.AmTr.v1.0_scaffo	scaffold_00152	AG.Amtr_00152.28.AMBTC	W1PMV8.AMBTC		422	9.60E-231	1	422	422	1.30E-103	1	167	167	3.60E-18	1	99	99			
Angiosperms	-	-	-	Nymphaeales	Nymphaeaceae	Nymphaea thermarum	NCBI Genome	GCA_011799795.1	JAANDH010000004.1	scaffold4	AG.JAANDH010000004.1.NYMTH		140	3.80E-165	1	407	407	1.80E-99	1	166	166	3.10E-06	1	99	99				
Angiosperms	-	-	magnoliids	Magnoliales	Magnoliaceae	Magnolia grandiflora	IKP		WBOD_scaffold_2018894	unknown	AG_2018894.MAGGR		446	1.20E-237	1	422	422	6.50E-105	1	167	167	6.40E-18	1	99	99				
Angiosperms	-	-	magnoliids	Laurales	Lauraceae	Cinnamomum camphora	IKP		WBOD_scaffold_2019688	unknown	AG_2019688.MAGGR		290	2.90E-106	7	242	236	7.40E-70	8	166	159	no hits							
Angiosperms	-	-	magnoliids	Laurales	Lauraceae	Cinnamomum camphora	IKP		BCBG_scaffold_2010188	unknown	AG_2010188.CINCA		413	1.60E-215	1	422	422	9.20E-85	1	167	167	7.00E-18	1	99	99				
Angiosperms	-	-	magnoliids	Laurales	Lauraceae	Cinnamomum camphora	IKP		BCBG_scaffold_2008909	unknown	AG_2008909.CINCA		438	1.80E-203	1	420	420	1.40E-103	1	167	167	8.40E-14	19	99	87				
Angiosperms	-	-	magnoliids	Laurales	Lauraceae	Cinnamomum camphora	IKP		BCBG_scaffold_2048332	unknown	AG_2048332.CINCA		308	1.40E-105	14	53	40	2.00E-24	14	53	40	8.60E-17	1	99	99				
Monocots	-	-	-	Alismatales	Araceae	Sipodola polytricha	Phytozome v.12	v2.0	Spijo1G0068000	pseudo1	AGM.1G0068000.SPIPO		401	5.30E-209	1	421	421	4.50E-104	1	167	167	4.80E-17	1	99	99				
Monocots	-	-	-	Alismatales	Araceae	Sipodola polytricha	Phytozome v.12	v2.0	Spijo1G0028800	pseudo17	AGM.1G0028800.SPIPO		362	9.60E-180	1	262	262	7.90E-101	1	167	167	4.90E-12	50	99	50				
Monocots	-	-	-	Alismatales	Araceae	Sipodola polytricha	Phytozome v.12	v2.0	Spijo1G0041200	pseudo11	AGM.1G0041200.SPIPO		416	5.00E-212	4	422	419	4.50E-103	4	167	164	1.50E-17	1	99	99				
Monocots	-	-	-	Alismatales	Zosteraceae	Zostera marina	Phytozome v.12	v2.2	Spijo0G0150600	pseudo0	AGM.0G0150600.SPIPO		312	2.90E-122	103	422	320	2.20E-32	103	165	63	2.30E-16	1	99	99				
Monocots	-	-	-	Asparagales	Asparagaceae	Asparagus officinalis	KEGG genome	T0543	Zosma1g03120.1	scaffold 1	AGM.1g03120.1.ZOSMR		403	1.70E-203	3	421	419	7.10E-100	3	166	164	3.70E-18	1	99	99				
Monocots	-	-	-	Asparagales	Asparagaceae	Asparagus officinalis	KEGG genome	T0543	aof:109847658	unknown	AGM.aof_109847658.ASPOF		419	5.90E-228	2	422	421	8.60E-102	1	167	167	4.50E-19	1	99	99				
Monocots	-	-	-	Asparagales	Asparagaceae	Asparagus officinalis	KEGG genome	T0543	aof:109837680	unknown	AGM.aof_109837680.ASPOF		414	5.30E-223	7	420	414	8.60E-102	7	167	161	2.90E-17	1	99	99				
Monocots	-	-	commelinids	Poales	Poaceae	Ananas comosus	Phytozome v.12	v3	Aco010382.1	LG03	AGM.Aco010382.1.ANACO		420	3.00E-237	2	422	421	7.40E-106	1	167	167	2.40E-17	1	99	99				
Monocots	-	-	commelinids	Poales	Poaceae	Oryza sativa	Phytozome v.12	v1.1	Os03g0157300	chromosome 3	AGM.Os03g0157300.ORYSI	Q10RJ5_ORYSI		418	2.90E-229	2	422	421	9.30E-101	1	167	167	1.60E-19	1	99	99			
Monocots	-	-	commelinids	Poales	Poaceae	Panicum hallii	Phytozome v.12	v2.0	Pahal300468.1	chromosome 9	AGM.Pahal300468.1.PANHA		419	9.20E-224	2	422	421	5.90E-101	1	167	167	5.80E-18	1	99	99				
Monocots	-	-	commelinids	Poales	Poaceae	Setaria viridis	Phytozome v.12	v1.1	Sevir_9539400.1	chromosome 9	AGM.9539400.1.SETVI		419	2.80E-223	2	422	421	7.00E-101	1	167	167	3.70E-18	1	99	99				
Monocots	-	-	commelinids	Poales	Poaceae	Sorghum bicolor	Phytozome v.12	v1.1	Sobic001G499200.1	chromosome 9	AGM.001G499200.1.SORBI	CSWAT4_SORBI		421	1.70E-225	2	422	421	8.00E-101	1	167	167	3.20E-19	1	99	99			
Monocots	-	-	commelinids	Poales	Poaceae	Brachypodium distachyon	Phytozome v.12	v3.1	Bradi1g74690.2	Bd1	AGM.1g74690.2.BRADI		413	3.40E-223	7	422	418	3.40E-223	7	167	161	1.10E-18	1	99	99				
Monocots	-	-	commelinids	Poales	Poaceae	Brachypodium distachyon	Phytozome v.12	v3.1	GSMLA_Achr1T26450_001	chromosome 7	AGM.1T26450_001.MUSAC	M0TEH5_MUSAM		415	1.20E-218	2	421	420	1.40E-102	1	167	167	2.50E-18	1	99	99			
Monocots	-	-	commelinids	Poales	Poaceae	Musa acuminata	Phytozome v.12	v1	GSMLA_Achr1T26450_001	chromosome 1	AGM.1T26450_001.MUSAC	M0S3A2_MUSAM		419	6.50E-224	2	421	422	6.30E-104	1	167	167	7.70E-19	1	99	99			
Eudicots	-	-	-	Ranunculales	Ranunculaceae	Azulégia cœrulea	Phytozome v.12	v3.1	Azcoe6G217900.1	chromosome 6	AGE.6G217900.1.AZUCA	A0A2G5C987_AZUCA		422	1.30E-233	1	422	422	5.30E-106	1	167	167	3.60E-18	1	99	99			
Eudicots	-	-	-	Proteales	Nelumbonaceae	Nelumbo nucifera	KEGG genome	T04133	nmu_104603638	unknown	AGE_104603638.NELNU		420	3.00E-241	1	421	421	6.40E-104	1	167	167	1.10E-17	1	99	99				
Eudicots	-	-	-	Proteales	Nelumbonaceae	Nelumbo nucifera	KEGG genome	T04133	nmu_104604258	unknown	AGE_104604258.NELNU		409	2.40E-234	1	421	421	6.20E-104	1	167	167	6.10E-19	1	99	99				
Eudicots	core eudicots	superrosids	-	Saxifragales	Crassulaceae	Kalanchoe fedtschenkoi	Phytozome v.12	v1.0	Kaladp0008r0106.1	scaffold 9	AGE.0008r0106.1.KALFE		419	2.40E-217	2	421	420	1.10E-103	1	167	167	2.30E-18	1	99	99				
Eudicots	core eudicots	superrosids	-	Saxifragales	Crassulaceae	Kalanchoe fedtschenkoi	Phytozome v.12	v1.0	Kaladp0067r0162.1	scaffold 67	AGE.0067r0162.1.KALFE		418	5.60E-227	2	422	421	1.40E-103	1	167	167	3.10E-16	1	99	99				
Eudicots	core eudicots	superrosids	rosids	Vitales	Vitaceae	Vitis vinifera	Phytozome v.12	v2.1	VIT_200u0349g0020.3_GSVNV70	unknown	AGE.200u0349g0020.3.VITVI	F6H5H_VITVI		319	5.60E-173	103	422	320	2.00E-105	1	167	167	3.30E-17	1	99	99			
Eudicots	core eudicots	superrosids	rosids	Malpighiales	Linaceae	Linum usitatissimum	Phytozome v.12	v1.0	Lus1002595	scaffold_319	AGR.1002595.LINUS		419	8.40E-229	2	422	421	1.30E-102	1	167	167	6.30E-18	1	99	99				
Eudicots	core eudicots	superrosids	rosids	Malpighiales	Linaceae	Linum usitatissimum	Phytozome v.12	v1.0	Lus10041875	scaffold_272	AGR.10041875.LINUS		477	2.00E-225	3	422	420	2.00E-102	3	167	165	2.30E-17	1	99	99				
Eudicots	core eudicots	superrosids	rosids	Malpighiales	Linaceae	Linum usitatissimum	Phytozome v.12	v1.0	Lus10028421	scaffold_413	AGR.10028421.LINUS		526	2.50E-226	3	422	420	2.40E-102	3	167	165	2.30E-18	1	99	99				
Eudicots	core eudicots	superrosids	rosids	Malpighiales	Linaceae	Linum usitatissimum	Phytozome v.12	v1.0	Lus10014256	scaffold_275	AGR.10014256.LINUS		490	1.10E-229	2	422	421	1.10E-101	1	167	167	2.40E-18	1	99					

vernacular	clade	clade	clade	order	family	Taxon	database	note	gene ID	chromosome/Genome scaffolds	ID in matrix	ID in proteome analyses	length (AA)	HMM		from	to	length	HMM		from	to	length	HMM		from	to	length		
														E value					E value					E value						
Eudicots	core eudicots	superrosids	rosids	Sapindales	Rutaceae	Citrus sinensis	Phytozome v.12	v.1.1	orange1.lg014734m	scaffold00017	AGR.lg014734m.CITSI		419	3.90E-236		2	422	421	9.00E-105	1	167	167	5.70E-17	1	99	99				
									orange1.lg020955m	scaffold00021	AGR.lg020955m.CITSI		329	2.10E-104	14	239	226	1.70E-61	14	167	154	no hits	na	na	na					
															291	340	50													
Eudicots	core eudicots	superrosids	rosids	Malvales	Malvaceae	Gossypium raimondii	Phytozome v.12	v2.1	Gorai.003G007400.1	chromosome 3	AGR.003G007400.1.GOSRA	A0A02MH18_GOSRA	418	2.10E-242	2	422	421	6.20E-105	1	167	167	1.00E-17	1	99	99					
									Gorai.007G192000.1	chromosome 7	AGR.007G192000.1.GOSRA	A0A0D2THW9_GOSRA	416	3.50E-239	1	422	422	2.30E-105	1	167	167	2.80E-17	1	99	99					
Eudicots	core eudicots	superrosids	rosids	Brassicales	Brassicaceae	Arabidopsis thaliana	Phytozome v.12	TAIR10	AT4G35920.1 (MCA1)	chromosome 4	AGR.AIMCA1.ARATH	MCAC1_ARATH	419	3.10E-224	1	422	422	5.40E-104	1	167	167	2.90E-20	1	99	99					
									AT2G11780.1 (MCA2)	chromosome 2	AGR.AIMCA2.ARATH	MCAC2_ARATH	417	1.10E-191	1	421	421	8.70E-95	1	167	167	2.30E-17	1	99	99					
Eudicots	core eudicots	superrosids	rosids	Brassicales	Brassicaceae	Brassica oleracea capitata	Phytozome v.12	v1.0	BoI018686	chromosome 7	AGR.BoI018686.BRAOC		421	4.70E-219	1	422	422	1.40E-102	1	167	167	8.00E-18	1	99	99					
									BoI029039	chromosome 1	AGR.BoI029039.BRAOC		419	4.40E-223	1	422	422	1.40E-105	1	167	167	5.20E-18	1	99	99					
Eudicots	core eudicots	superrosids	rosids	Brassicales	Brassicaceae	Brassica oleracea oleracea	KEGG genome	T04124	A0A0D3A1N3_BRAOL:boe_10631	chromosome 1	AGR.boe_106303054.BRAOL	A0A0D3A1N3_BRAOL	420	1.40E-224	1	422	422	2.00E-104	1	167	167	6.10E-20	1	99	99					
									A0A0D3DHX0_BRAOL:boe_10631	chromosome 1	AGR.boe_106301973.BRAOL	A0A0D3DHX0_BRAOL	412	2.20E-221	1	422	422	1.00E-102	1	167	167	9.10E-20	1	99	99					
									A0A0D3E374_BRAOL:boe_10631	chromosome 9	AGR.boe_106313387.BRAOL	A0A0D3E374_BRAOL	411	5.70E-190	1	242	242	5.70E-101	1	167	167	4.80E-20	1	99	99					
															293	406	114													
Eudicots	core eudicots	superrosids	rosids	Brassicales	Brassicaceae	Capsella rubella	Phytozome v.12	v1.0	Carubv10004901m	scaffold_7_5'end F	AGR.10004901m.CAPRU		421	9.20E-221	1	422	422	5.50E-104	1	167	167	3.60E-18	1	99	99					
									Carubv10013809m	scaffold_3_3'end R	AGR.10013809m.CAPRU		417	1.30E-201	1	421	421	4.90E-99	1	166	166	9.70E-18	1	99	99					
Eudicots	core eudicots	superrosids	rosids	Brassicales	Caricaceae	Carica papaya	Phytozome v.12	v0.4	evm_model.supercontig_6.294	supercontig_6	AGR.6.294.CARPA		420	1.90E-239	1	421	421	8.90E-109	1	167	167	7.20E-18	1	99	99					
									evm_model.supercontig_19.136	supercontig_19	AGR.19.136.CARPA		345	1.80E-104	11	235	225	1.00E-102	11	167	157	3.70E-04	1	37	37					
															295	341	47													
Eudicots	core eudicots	superasterids	-	Caryophyllales	Amaranthaceae	Amaranthus hypochondrioides	Phytozome v.12	v1.0	AHYPO_016156-RA	scaffold 297	AGA_016156.AMAHP		378	3.90E-185	6	421	416	3.70E-87	6	139	134	3.10E-15	1	99	99					
									AHYPO_016414-RA	scaffold 310	AGA_016414.AMAHP		375	1.50E-186	2	339	338	1.40E-100	6	167	162	7.80E-09	1	36	36					
									AHYPO_007217-RA	scaffold 56	AGA_007217.AMAHP		385	1.00E-175	3	314	312	8.00E-93	3	167	165	3.20E-09	2	99	98					
															338	421	84													
Eudicots	core eudicots	superasterids	-	Caryophyllales	Chenopodiaceae	Beta vulgaris	EnsemblPlants	RefBeet-1.2.2	KMT09333	chromosome 6	AGA.KMT09333.BETVU		407	3.00E-217	9	422	414	2.1E-99	9	167	159	4.1E-19	1	99	99					
									KMS99790	chromosome 1	AGA.KMS99790.BETVU		406	1.80E-190	3	421	419	1.7E-90	3	167	165	5.4E-21	1	99	99					
									KMT09333b	chromosome 6	AGA.KMT09333b.BETVU		407	3.00E-217	9	422	414	2.1E-99	9	167	159	4.1E-19	1	99	99					
									KMS99790b	chromosome 1	AGA.KMS99790b.BETVU		406	1.80E-190	3	421	419	1.7E-90	3	167	165	5.4E-21	1	99	99					
Eudicots	core eudicots	superasterids	asterids	Solanales	Solanaceae	Nicotiana tabacum	KEGG Genome	T04643	LOC107799659_NIMCA2	unknown	AGANIMCA2.TOBAC		419	3.60E-232	2	422	421	1.70E-104	1	167	167	3.30E-18	1	99	99					
									LOC107804487_NIMCA1	unknown	AGANIMCA1.TOBAC		419	3.60E-232	2	422	421	1.70E-102	1	167	167	5.60E-19	1	99	99					
									LOC107766330	unknown	AGA.L07766330.TOBAC		419	2.40E-233	2	422	421	8.20E-103	1	167	167	5.60E-19	1	99	99					
Eudicots	core eudicots	superasterids	asterids	Solanales	Solanaceae	Solanum lycopersicum	Phytozome v.12	ITAG2.4	Solyc02g083540.2.1	SL2.50ch02	AGA.02g083540.2.1.SOLLC	A0A3Q7F6L0_SOLLC	418	2.10E-228	4	422	419	5.60E-102	1	167	167	3.60E-18	1	99	99					
									Solyc03g095820.2.1 has two dom	SL2.50ch03	AGA.03g095820.2.1.SOLLC	A0A3Q7FPG3_SOLLC	390	1.80E-136	13	237	225	1.30E-56	13	167	155	1.60E-18	1	99	99					
															288	420	133													
Eudicots	core eudicots	superasterids	asterids	Solanales	Solanaceae	Solanum tuberosum	Phytozome v.12	v4.03	PGSC0003DMT400009236	ST4.03ch02	AGA.DMT400009236.SOLTU		418	9.70E-228	4	422	419	8.20E-102	1	167	167	4.30E-18	1	99	99					
									PGSC0003DMT400058105	ST4.03ch03	AGA.DMT400058105.SOLTU		432	1.70E-227	2	407	406	5.80E-102	1	167	167	8.70E-18	1	99	99					
									PGSC0003DMT400053095	ST4.03ch03	AGA.DMT400053095.SOLTU		389	1.70E-141	13	231	219	2.60E-62	13	167	159	2.30E-18	1	99	99					
															289	420	132													
Eudicots	core eudicots	superasterids	asterids	Lamiales	Phymaceae	Erythranthe guttata	Phytozome v.12	v2.0	Migut.N03178.1	scaffold 14	AGA.N03178.1.ERYGU	A0A022RAP2_ERYGU	389	1.60E-186	4	421	418	2.30E-95	3	164	162	5.90E-19	1	99	99					
									Migut.H02182.1	scaffold 9	AGA.H02182.1.ERYGU	A0A022PTL3_ERYGU	413	6.90E-217	6	421	416	6.70E-100	6	167	162	8.90E-17	1	99	99					
									Migut.C00882.1	scaffold 3	AGA.C00882.1.ERYGU	A0A022Q797_ERYGU	404	1.10E-195	2	421	420	5.30E-94	1	165	165	1.00E-16	1	99	99					
Eudicots	core eudicots	superasterids	asterids	Asterales	Asteraceae	Helianthus annuus	EnsemblPlants	HanXRQ1.0	OTF93336	chromosome 16	AGA.OTF93336.HELEN		413	1.80E-231	1	422	422	5.80E-105	1	167	167	5.20E-19	1	99	99					
									OTF96330	chromosome 15	AGA.OTF96330.HELEN		420	7.80E-236	1	422	422	9.90E-104	1	167	167	4.10E-19	1	99	99					
									OTF98085	chromosome 14	AGA.OTF98085.HELEN		428	2.10E-214	1	421	421	8.70E-103	1	166	166	1.50E-16	1	99	99					
									OTG15114	chromosome 9	AGA.OTG15114.HELEN		544	2.80E-197	1	398	398	2.70E-99	1	167	167	6.10E-06	1	47	47					
Eudicots	core eudicots	superasterids	asterids	Apiales	Apiaceae	Daucus carota	Phytozome v.12	v2.0	DCAR_011609	chromosome 3	AGA.011609.DAUCA		478	1.40E-220	1	407	407	3.60E-104	1	167	167	4.20E-15	1	99	99					
									DCAR_014040	chromosome 4	AGA.014040.DAUCA		315	2.10E-156	2	315	314	4.60E-100	1	167	167	no hits </								