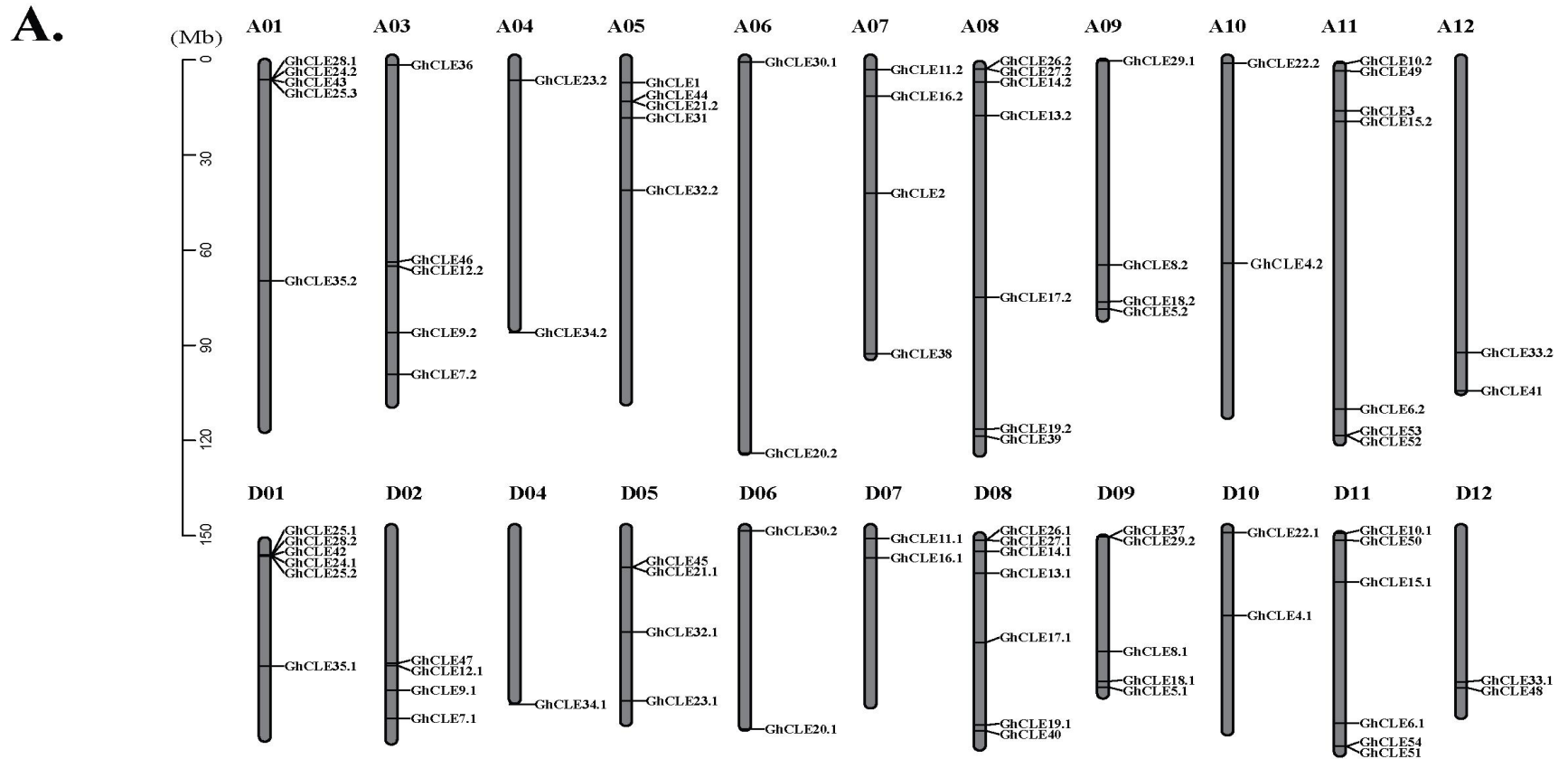
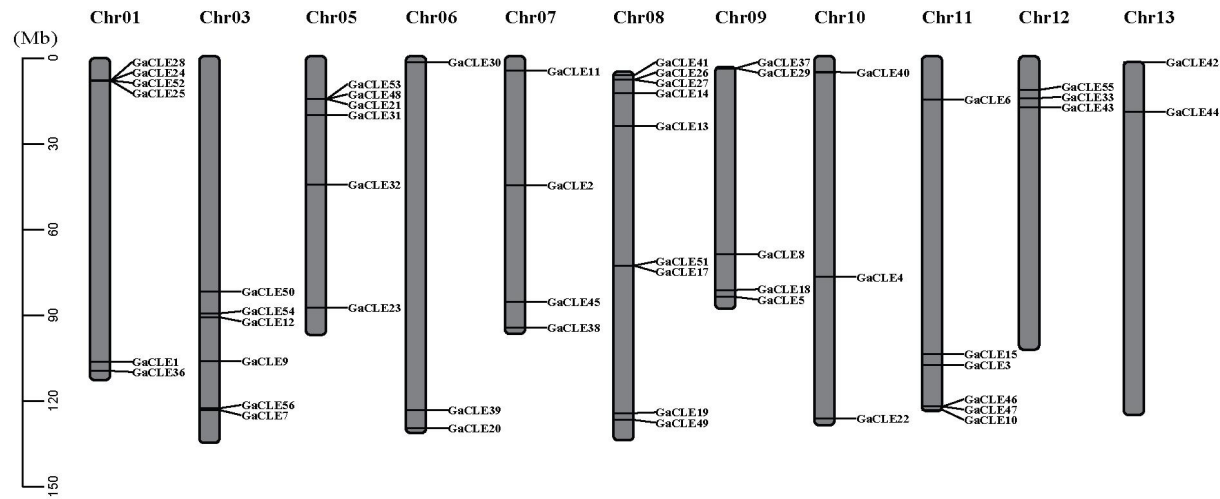


Supplementary Material

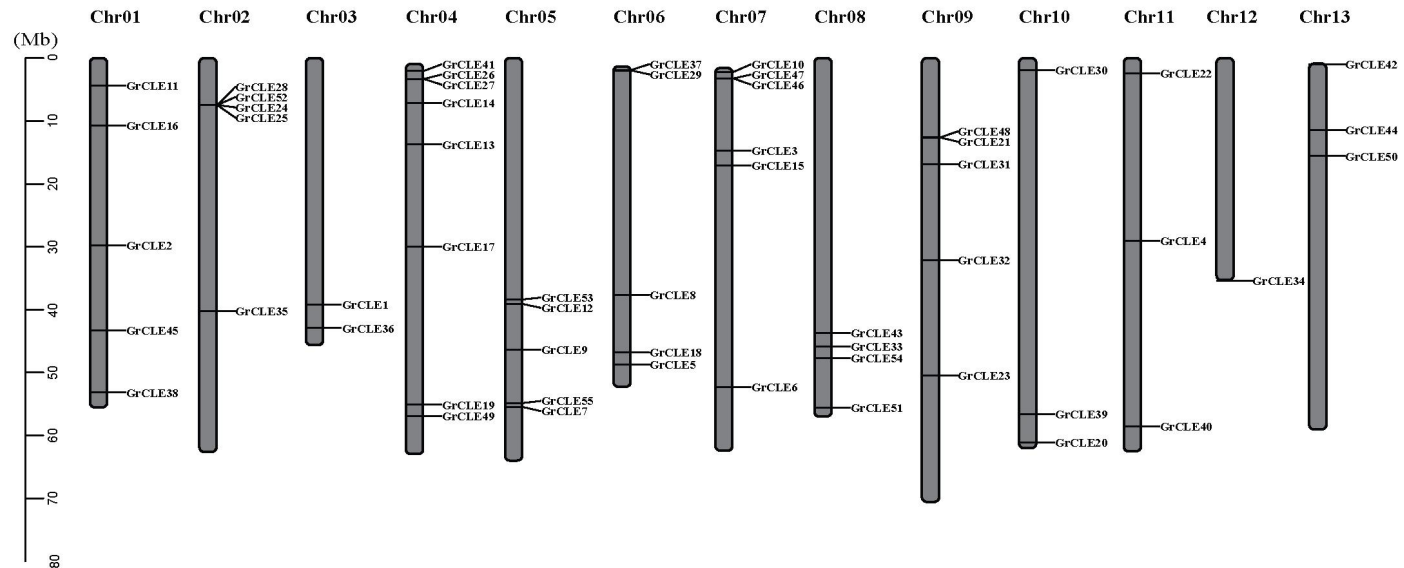
Supplementary Figures



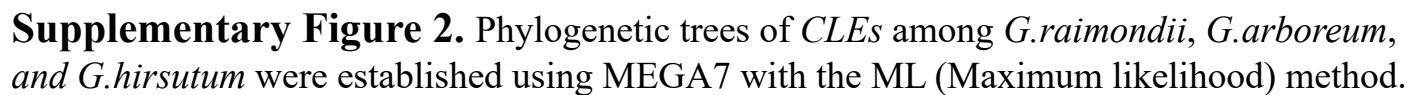
B.



C.



Supplementary Figure 1. A, B and C represent the chromosomal location of CLE gene on the chromosomes of *G. hirsutum*, *G. arboreum*, and *G. raimondii*, respectively. Above each gray bar are the names of chromosomes. The black line indicates the location of the corresponding gene. The vertical scale on the left indicates the size of the chromosome, and the scale represents the Mega Base (MB). The gene names correspond to Table 1-3.



Supplementary Figure 2. Phylogenetic trees of *CLEs* among *G.raimondii*, *G.arboreum*, and *G.hirsutum* were established using MEGA7 with the ML (Maximum likelihood) method.

VII

	signal peptide															CLE motif																																																																								
	10					20					30					40					50					60					70					80																																																				
GhCLE24.2	M	A	S	F	K	V	L	F	Y	L	S	L	Q	V	L	F	L	V	S	S	C	G	T	R	L	F	G	T	D	Q	L	A	L	A	V	A	G	K	Q	H	S	K	A	N	I	I	E	A	K	R	P	L	I	E	E	G	R	E	A	I	K	A	S	I	Q	R	N	G	G	I	P	F	E	S	K	R	L	S	P	G	G	P	D	P	H	H	H	K
GaCLE24	M	A	S	F	K	V	L	F	Y	L	S	L	Q	V	L	F	L	V	S	S	C	G	T	R	L	F	G	T	D	Q	L	A	L	A	V	A	G	K	Q	H	S	K	A	N	I	I	E	A	K	R	P	L	I	E	E	G	R	E	A	I	K	A	S	I	Q	R	N	G	G	I	P	F	E	S	K	R	L	S	P	G	G	P	D	P	H	H	H	K
MASFKLVLFYLSLQVLFVLS	S	G	A	R	L	F	G	T	D	Q	L	A	L	A	V	A	G	K	Q	H	S	K	A	T	I	I	E	A	N	R	P	L	I	E	E	G	R	E	A	I	K	A	S	I	Q	R	N	G	G	I	P	F	E	S	K	R	L	S	P	G	G	P	D	P	H	H	H	K																				
GrCLE52	M	A	S	F	K	V	L	F	Y	L	S	L	Q	V	L	F	L	V	S	S	S	G	A	R	L	F	G	T	D	Q	L	A	L	A	V	A	G	K	Q	H	S	K	A	T	I	I	E	A	N	R	P	L	I	E	E	G	R	E	A	I	K	A	S	I	Q	R	N	G	G	I	P	F	E	S	K	R	L	S	P	G	G	P	D	P	H	H	H	K
GhCLE24.1	M	A	S	F	K	V	L	F	Y	L	S	L	Q	V	L	F	L	V	S	S	S	G	T	R	L	F	G	T	D	Q	L	A	L	A	V	A	G	K	Q	H	S	K	A	T	I	I	E	A	K	R	P	L	I	E	E	G	R	E	A	I	K	A	S	I	Q	R	N	G	G	I	P	F	E	S	K	R	L	S	P	G	G	P	D	P	H	H	H	K
GrCLE24	M	A	S	F	K	V	L	F	Y	L	S	L	Q	V	L	F	L	V	S	S	S	G	T	R	L	F	G	T	D	Q	L	A	L	A	V	A	G	K	Q	H	S	K	A	T	I	I	E	A	N	R	P	L	I	E	E	G	R	E	A	I	K	A	S	I	Q	R	N	G	G	I	P	F	E	S	K	R	L	S	P	G	G	P	D	P	H	H	H	K
GhCLE43	M	A	S	F	K	V	L	F	Y	L	S	L	Q	V	L	F	L	V	S	S	S	G	T	R	L	F	G	T	D	Q	L	A	L	A	V	A	G	K	Q	H	S	K	A	T	I	I	E	A	K	R	P	L	I	E	E	G	R	E	A	I	K	A	S	I	Q	R	N	A	G	I	P	F	E	S	K	R	L	S	P	G	G	P	D	P	H	H	H	K
GaCLE52	M	A	S	F	K	V	L	F	Y	L	S	L	Q	V	L	F	L	V	S	S	S	G	T	R	L	F	G	T	D	Q	L	A	L	A	V	A	G	K	Q	H	S	K	A	T	I	I	E	A	K	R	P	L	I	E	E	G	R	E	A	I	K	A	S	I	Q	R	N	A	G	I	P	F	E	S	K	R	L	S	P	G	G	P	D	P	H	H	H	K
GhCLE25.3	M	A	S	F	K	V	L	F	C	L	S	L	H	V	L	F	L	V	S	S	S	G	T	R	L	F	G	I	D	Q	L	A	L	A	V	A	D	K	Q	H	P	E	A	A	I	I	E	S	K	R	A	L	I	E	E	G	R	E	A	I	K	A	S	I	E	R	N	G	G	I	P	Y	E	T	K	R	R	S	P	G	G	P	D	P	H	H	H	-
GaCLE25	M	A	S	F	K	V	L	F	C	L	S	L	H	V	L	F	L	V	S	S	S	G	T	R	L	F	G	I	D	Q	L	A	L	A	V	A	D	K	Q	H	P	E	A	A	I	I	E	S	K	R	A	L	I	E	E	G	R	E	A	I	K	A	S	I	E	R	N	G	G	I	P	Y	E	T	K	R	R	S	P	G	G	P	D	P	H	H	H	-
GhCLE25.1	M	A	S	F	K	V	L	F	C	L	S	L	H	V	L	F	L	V	S	S	S	G	T	R	L	F	G	I	D	Q	L	A	L	A	V	A	D	K	Q	H	P	E	A	A	I	I	E	S	K	R	A	L	I	E	E	G	R	E	A	I	K	A	S	I	E	R	N	G	G	I	P	Y	E	T	K	R	R	S	P	G	G	P	D	P	H	H	H	-
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GhCLE23.2	A	T	T	F	K	L	F	F	T	L	C	L	P	A	F	F	L	I	P	S	S	G	T	R	L	F	Q	L	S	L	A	V	A	G	A	N	-	G	A	E	S	E	Q	F	Q	S	N	S	K	H	T	M	K	E	A	R	E	A	I	K	A	S	I	E	R	N	A	G	N	P	L	E	S	K	R	L	S	P	G	G	P	D	P	H	H	H	-	
GaCLE23	A	T	T	F	K	L	F	F	T	L	C	L	P	A	F	F	L	I	P	S	T	G	T	R	L	F	Q	L	S	L	A	V	A	G	A	N	-	G	A	E	S	E	Q	F	Q	S	N	S	K	H	T	M	K	E	A	R	E	A	I	K	A	S	I	E	R	N	A	G	N	P	L	E	S	K	R	L	S	P	G	G	P	D	P	H	H	H	-	
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GrCLE23	M	A	T	F	K	L	F	F	T	L	C	L	H	A	F	F	L	I	P	S	S	G	I	R	L	F	Q	L	S	L	A	V	R	N	E	G	A	E	S	E	Q	F	R	S	N	S	K	H	T	M	K	E	A	R	E	A	I	K	A	S	I	E	R	N	A	G	N	P	L	E	S	K	R	L	S	P	G	G	P	D	P	H	H	H	-			
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GaCLE26	M	A	T	F	N	V	S	F	I	L	S	L	Y	A	L	L	I	S	S	S	A	S	R	L	P	V	D	K	Q	E	V	S	E	T	-	N	G	K	S	E	I	F	G	G	T	N	K	R	A	L	I	E	E	G	R	E	A	I	Q	A	S	L	K	R	N	A	G	N	P	L	E	S	K	R	R	S	P	G	G	P	D	P	H	H	H	-		
GhCLE26.1	M	A	T	F	N	V	S	F	I	L	S	L	Y	A	L	L	I	S	S	A	T	R	L	P	V	D	K	Q	E	V	S	E	T	-	N	G	K	S	E	I	F	G	G	T	N	K	R	A	L	I	E	E	G	R	E	A	I	Q	A	S	L	K	R	N	A	G	N	P	L	E	S	K	R	R	S	P	G	G	P	D	P	H	H	H	-			
GrCLE26	M	A	T	F	N	V	S	F	I	L	S	L	Y	A	L	L	I	S	S	A	T	R	L	P	V	D	K	Q	E	V	S	E	T	-	N	G	K	S	E	I	F	G	G	T	N	K	C	A	L	I	E	E	G	R	K	A	I	Q	A	S	L	K	R	N	A	G	N	P	L	E	S	K	R	R	S	P	G	G	P	D	P	H	H	H	-			
GhCLE27.2	M	A	T	F	N	L	F	F	I	L	S	L	Y	A	L	L	V	S	C	S	A	T	R	L	P	V	E	K	Q	V	R	E	T	-	N	G	S	E	Q	Y	G	S	T	I	K	R	A	L	I	E	E	G	R	E	A	I	K	A	S	L	K	R	N	A	G	N	P	L	E	S	K	R	Q	S	P	G	G	P	D	P	H	H	H	-				
GaCLE27	M	A	T	F	N	L	F	F	I	L	S	L	Y	A	L	L	V	S	C	S	A	T	R	L	P	V	E	K	Q	V	R	E	T	-	N	G	S	E	Q	Y	G	S	T	I	K	R	A	L	I	E	E	G	R	E	A	I	K	A	S	L	K	R	N	A	G	N	P	L	E	S	K	R	Q	S	P	G	G	P	D	P	H	H	H	-				
GhCLE27.1	M	A	T	F	N	L	F	F	I	L	S	L	Y	A	L	L	V	S	C	S	A	T	R	L	P	V	E	K	Q	V	R	E	T	-	N	G	S	E	Q	Y	G	S	T	I	K	R	A	L	I	E	E	G	R	E	A	I	K	A	S	L	K	R	N	A	G	N	P	L	E	S	K	R	R	S	P	G	G	P	D	P	H	H	H	-				
GrCLE27	M	A	T	F	N	F	F	I	L	S																																																																														

V

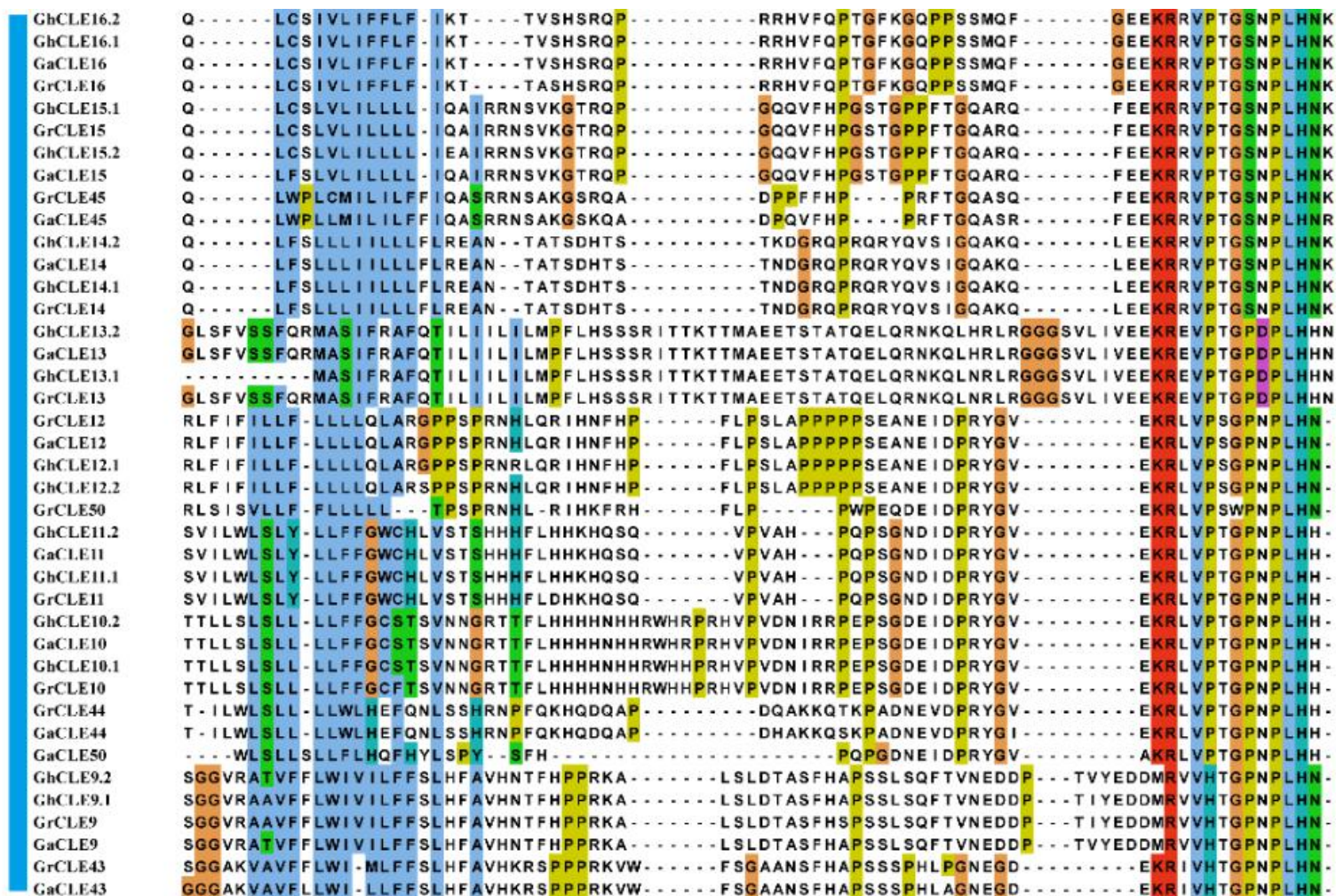
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GhCLE28.2	SSSRLVVMLSFIIIVLMLVMNTEARP	---YGHGPHGNPTMAEKIDGMTMLEKL	-GYDLSKIDYYRR-	-MLSSSPERI	SPGGDPQHYY
GaCLE28	SSSRLVVMLSFIIIVLMLVMNTEARP	---YGHGPHGNPTMAEKIDGMTMLEKL	-GYDLSKIDYYRR-	-MLSSSPERI	SPGGDPQHYY
GrCLE28	SSSRLVVMLSFIIIVLMLVTNTEARP	---YGHGPHGNPTMAEKIDGMTMLEKL	-GYDLSKIDYYRR-	-MLSSSPERI	SPGGDPQHYY
GhCLE44	-MPNSTIIQASLVIFLILSGNAINIL	---EAKSYGGRKTMQKRIDSRSI	IKALTGYDLSAMKHDGR-	-RVLTDVSR	SPGGDPQHD-
GaCLE53	-MPNSTIIQASLVIFLILSGNAINIL	---EAKSYGGRKTMQKRIDSRSI	IKALTGYDLSAMKHDGR-	-RVLTDVSR	SPGGDPQHD-
GhCLE45	-MPNSTVIQASLVIFLILSGNAISIL	---EAKSYGGRKTMQKRIDSRSI	IKALTGYDLSAMKHDGR-	-RVLTDVSR	SPGGDPQHD-
GhCLE29.1	ISTATTSSSLTMARLSFLAFAFFVVL	---LMSSSQAQSLVQKKISSRLLREL	-GYDRNKLEHYRQVFALKAD	SDRV	SPGGPDHEHA
GhCLE29.2	ISTATTSSSLTMARLSFLAFAFFVVL	---LMSSSQAQSLVQKKISSRLLREL	-GYDRNKLEHYRQVFALKAD	SDRV	SPGGPDHEHA
GrCLE29	-----MARLSFLAFAFFVVL	---LMSSSQAQSLVQKKISSRLLREL	-GYDRNKLEHYRQVFALKAD	SDRV	SPGGPDHEHA
GaCLE29	-----MARLSFLAFAFFVVL	---LMSSSQAQSLVQKKISSRLLREL	-GYDRNKLEHYRQVFALKAD	SDRV	SPGGPDHEHA
GhCLE37	MPKSSITLPSTSI AFLIL	---FFMLH---	MSCDARILKI	PETHMHKQFLHLKLGFDLHQLKRYENNSTHVP	ISDRVSPGGDPQHFF
GrCLE37	MPKSSITLPSTSI AFLIL	---FFMLH---	MSCDARILKI	PETHMHKQFLHLKLGFDLHQLKRYENNSTHVP	ISDRVSPGGDPQHFF
GaCLE37	MPKSSITLPSTSI AFLIL	---FFMLH---	MSCDARILKI	PETHMHKQFLHLKLGFDLHQLKRYENNSTHVS	ASDRVSPGGDPQHFF
GhCLE36	-----MF-----LIILASITLSSCHF	-AEERSNTEFHT-	-WHLP	AKSPSSRAEK-DQPVYQV	-----SYRTVPGGPNPLHN
GaCLE36	NPKSSFMF-----LMIIILASITLSSCHF	-AEERSNTEFHT-	-WHLP	AKSPSSRAEK-DQPVYQV	-----SYRTVPGGPNPLHN
GrCLE36	NPKSSFMF-----LMIIILASITLSSCHF	-AEERSNTEFHT-	-WHLP	AKSPSSRAEK-DQPVYQV	-----SYRTVPGGPNPLHN
GhCLE19.2	NPKFSFLLFIIIIILSSTIFSSCRYI	-DEQPSKTDFFA-	-WHFPTKSSE-	ESKAEK-SRPIHEV	-----SYRTVPGGPNPLHN
GaCLE19	NPKFSFLLFIIIIILSSTIFSSCRYI	-DEQPSKTDFFA-	-WHFPTKSSE-	ESKAEK-SRPIHEV	-----SYRTVPGGPNPLHN
GrCLE19	NPKFSFLLFIIIIILSSTIFSSCRYI	-DEQPSKTDFFA-	-WHFPTKSSE-	ESKAEK-SRPIHEV	-----SYRTVPGGPNPLHN
GhCLE19.1	NPKFSFLLFIIIIILSSTIFSSCRYI	-DEQPSKTDFFA-	-WHFPTKSSE-	ESKAEK-SRPIHEV	-----SYRTVPGGPNPLHN
GrCLE46	NPKFIFIF-----FTIIFSTILSSCRRY	-EPTTMAAELSTTWFFH	PAKSPQPSVAEKISRPIYEV	-----SYRTVPGGPNPLHN	
GaCLE46	NPKFIFIF-----FTIIFSTILSSCRRY	-EPTTMAAELSTTWFFH	PAKSPQPSVAEKSSRPIYEV	-----SYRTVPGGPNPLHN	
GrCLE47	TPKFLFIF-----FTIILSNILSSCRRH	-EPTPMAAAEQ---	-HFP-----RPSVAEK-GQPIYEV	-----SYRAVPGGPDPLHN	
GaCLE47	SPKFLFIF-----FTIILSNILSSCRRY	-EPTPMAAAEQ---	-HFP-----QPSVAEK-GQPIYEV	-----SYRTVPGGPDPLHN	
GhCLE17.2	SSYISQFI---VVLIIILGFVVTSSRYVRLDKYSP	IFLT---	SLSAIRSLGKSPASDKIRA-VHAV	-----SHRVVPGGPNQLHN	
GaCLE17	SSYISQFI---VVLIIILGFVVTSSRYVRLDKYSP	IFLT---	SLSAIRSLGKSPASDKIRA-VHAV	-----SHRVVPGGPNQLHN	
GhCLE17.1	PSYLSQFL---VVLIIILGFVVASSRYVRLDKYSP	IFLT---	SLSAIRSLGKSPASDKIRA-VHAV	-----SHRVVPSGPNQLHN	
GrCLE17	PSYISQFL---VVLIIILGFVVASSRYVRLDKYSP	IFLT---	SLSAIRSLGKSPASDKIRA-VHAV	-----SHRVVPSGPNQLHN	
GhCLE41	KNTLVMFL---VFLIIILGFVVTSCRHRLDRYSP	MFRL---	SFTVIHGRGPIRKPTSSSVHVV	-----SRLLVPGGPNPLHN	
GrCLE51	ENTLVMFL---VFLIIILGLMVTSCRHRLDRYSP	MFRL---	TFTVIHGRGPIGKPTSSSVHVV	-----SHRLVPGGPNPLHN	
GhCLE18.2	PSPFLLLL---ILAVMLATVLSSCRQL---	-YQQTKFSAH---	-HFSSSYYASVSGNSNKYTAADV	-----SHKVVPGGPNPLHN	
GaCLE18	HSPFLPLL---ILAVMLATVLSSCRQL---	-YQQTKFSAH---	-HFSSSYYASVSGNSNKYTAADV	-----SHKVVPGGPNPLHN	
GhCLE18.1	PSPFLPLL---ILAVMLATVLSSCRQL---	-YQQTKFSAH---	-HFTSSYYASVSGNNNKYTAADV	-----SHKVVPGGPNPLHN	
GrCLE18	PSPFLPLL---ILAVMLATVLSSCRQL---	-YQQTKFSAH---	-HFTSSYYASVSGNNNKYTAADV	-----SHKVVPGGPNPLHN	
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IV

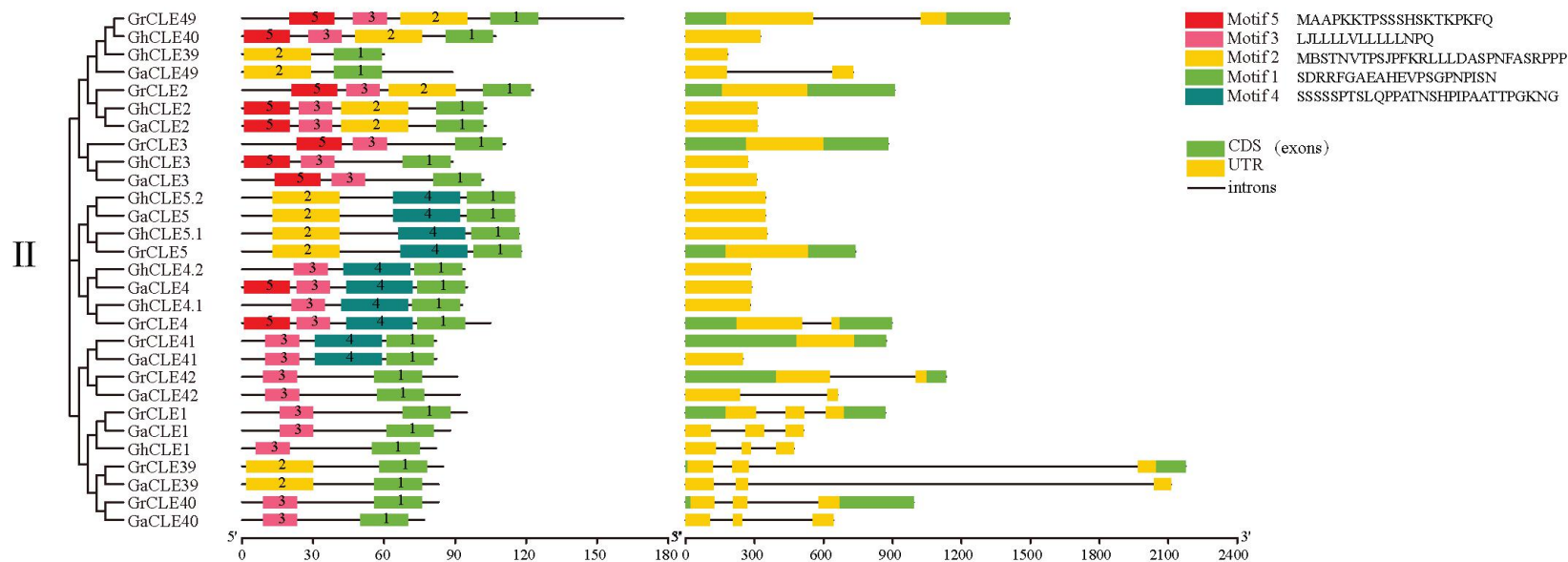
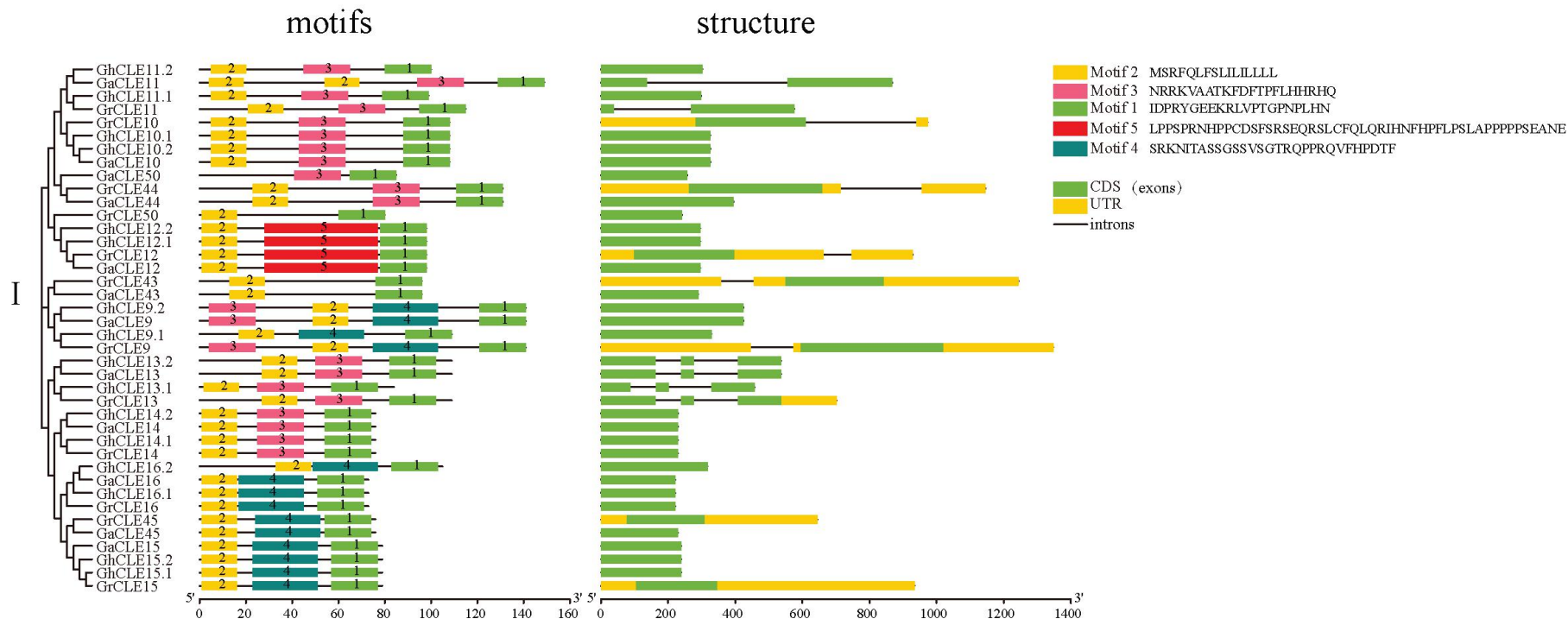
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GhCLE53	NSNPPLALSGFNVIVKREAPRGPNSL--IIRETPGDPNPLHNSNPPLAPSGGLNIIMKRETLGGSNAPSGGFNVIVKRETPGGPNPLHNS
GhCLE54	NSNPLLASTGFNIIVKREAPGGPNPLIIVKREAPGGPNPIQNSNPLLALSGGFNVIVKRETPGGPNAPSGGFNVIVKRETPRGPNPLHNS
GhCLE35.2	GSSLLFRTLFGTLIVLGFILGIVSGF--HQSSTTTAKVQHEEEQVKVLGQRKSNVAH-----PKQDLNYSKRRVPNGPDP IHNH
GaCLE35	GSSLLFRTLFGTLIVLGFILGIVSGF--HQSSTTTAKVQHEEEQVKVLGQRKSNVAH-----PKQDLNYSKRRVPNGPDP IHNH
GhCLE35.1	GSSLLFRTLFGTLIVLGFILGIVSGF--HQSSTTTAKVQHEEEQVKVLGQGVKSNVAH-----PKQDLNYSKRRVPNGPDP IHNH
GrCLE35	GSSLLFRTLFGTLIVLGFILGIVSGF--HQSSTTTAKVQHEEEQVKVLGQGVKSNVAH-----PKQDLNYSKRRVPNGPDP IHNH
GrCLE55	GVSLSFKTLFRTLIVLGFII---VGT-----QVKDLGKGKSTLVH-----QRLDLNYSKRRVPNGPDP IHNH
GaCLE56	GGSLSFKTLFRTLIVLGFII---VGT-----QVKDLGKGKSTLVH-----QRLDLNYSKRRVPNGPDP IHNH
GhCLE38	KSGRALRCFFAVAVLVGVVWLLFVSI-----VSSTEDLKHWEFVV-----DDFHNYSKRRVPNGPDP IHNH
GaCLE38	KSGKALRCFFAVAVLVGVVWLLFVSI-----VSSTEDLKHWEFVV-----DDFHNYSKRRVPNGPDP IHNH
GrCLE38	KSGRALRCFFAVAVLVGVVWLLFVSI-----VSSTEDLKHWEFVV-----DDFHNYSKRRVPNGPDP IHNH
GhCLE46	CSSQRVLLFLIFFGLLAIQADKVCGL-----TRKAV-EMKEMRTEQK-PLPVN-----NKTDPNESKRRVRRGSDP IHNH
GhCLE47	CSSQRVLLFLIFFGLLAIQADKVCGL-----GKGIVTRKAV-EMKEMRTEQK-PLPVN-----NKTDPNESKRRVRRGSDP IHNH
GrCLE53	CSSQRVLLFLIFFGLLAIQADKVCGL-----GKGIVTRKAV-EMKEMRTEQK-PLPVN-----NKTDPNESKRRVRRGSDP IHNH
GaCLE54	CSSQRVLLFLIFFGLLAIQADKVCGL-----TRKAV-EMKEMRTEQK-PLPVN-----NKTDPNESKRRVRRGSDP IHNH
GhCLE32.2	CSAQRFLMFLICFGLLAVAPDKASGL--AIRTNQRIKAA-DMKGTRIEKKLPEVVN-----NTFDPNRSKRRVRRGSDP IHNH
GaCLE32	CSAQRFLMFLICFGLLAVAPDKASGL--AIRTNQRIKAA-DMKGTRIEKKLPEVVN-----NTFDPNRSKRRVRRGSDP IHNH
GhCLE32.1	SSAQRFLMFLICFGLLAVAPDKAYGL--AIRTNQRIKAA-DMKGMSTENKLPEVVN-----NTFDPNRSKRRVRRGSDP IHNH
GrCLE32	SSAQRFLMFLICFGLLAVAPDKAYGL--AIRTNQRIKAA-DMKGMSTENKLPEVVN-----NTFDPNRSKRRVRRGSDP IHNH
GhCLE33.2	CSAQRVILLIFLGLLALQPVESVSGL-----SQRVLKAV-DTKGMSTEKK-PAFVN-----NKFDPNRSTKRRVRRGSDP IHNH
GaCLE33	CSAQRVILLIFLGLLALQPVESVSGL-----SQRVLKAV-DTKGMSTEKK-PAFVN-----NKFDPNRSTKRRVRRGSDP IHNH
GhCLE33.1	CSAQRVILLIFLGLLALQPVESVSGL-----SQRVLKAV-DTKGMSTEKK-PAFVN-----NKFDPNRSTKRRVRRGSDP IHNH
GrCLE33	CSAQRVILLIFLGLLALQPVESVSGL-----SQRVLKAV-DTKGMSTEKK-PAFVN-----NKFDPNRSTKRRVRRGSDP IHNH
GhCLE34.2	CSRQRVVMFLIFFGLLT IQPCRVCGL---SKNGRVLKAVVDMKG INTEKK-ASAVN-----NRFDPNQSSKRRFRRGSDP IHNH
GaCLE34	CSRQRVVMFLIFFGLLT IQPCRVCGL---SKNGRVLKAVVDMKG INTEKK-ASAVN-----NRFDPNQSSKRRFRRGSDP IHNH
GhCLE34.1	CSRQRVVMFLIFFGLLT IQPCRVCGL---SRNERVLKAVDMKG INTEKK-ASAVN-----NRFDPNQSSKRRFRRGSDP IHNH
GrCLE34	CSRQRVVMFLIFFGLLT IQPCRVCGL---SRNERVLKAVDMKG INTEKK-ASAVN-----NRFDPNQSSKRRFRRGSDP IHNH
GhCLE49	GGNSRGFIV I-----V IACC-AFVGRSGIVKAVVTVEALQTRQDLGPVSSSSSSSS--VMFDPNRSNKRKIKRGSDP IHDR
GhCLE50	GGNSRGFIV I-----V IACC-AFVGRSGIVKAVVTVEALQTRQDLGPVSSSSSSSSSS--VMFDPNRSNKRKIKRGSDP IHDR
GhCLE48	-----M-PLVENSRIIRAVGSVDSLQTPPSLAPAPS-----IMFDPNRSNKRKSVKKGSDP IHNH
GrCLE54	SVNTRGFILVSCIALLVFQTEIVSAM-PLVENSRIIRAVGSVDSLQTPPSLAPAPS-----IMFDPNRSNKRKSVKKGSDP IHNH
GaCLE55	SVNTRGFILVSCIALLVFQTEIVSAM-PLVENSRIIRAVGSVDSLQTPPSLAPAPS-----IMFDPNRSNKRKSVKKGSDP IHNH
GhCLE7.2	VLNSSMVVMLIISVLQIWIICSDCRAG---EMRKMIERKELFQTYFNGTS--FSFKGGDKGFED-----SKRRVPSCDP LHN-
GaCLE7	VLNSSMVVMLIISVLQIWIICSDCRAG---EMRKMIERKELFQTYFNGTS--FSFKGGDKGFED-----SKRRVPSCDP LHN-
GhCLE7.1	VLNSSMVVMLIISVLQIWIICSDCRAG---EMRKMIAQELFQTYFNGTS--FSFKGSDKGFED-----SKRRVPSCDP LHN-
GrCLE7	VLNSSMVVMLIISVLQIWIICSDCRAG---EMRKMIERQELFQTYFNGTS--FSFKGSDKGFED-----SKRRVPSCDP LHN-
GhCLE6.2	MVSKGLIGYVLLIMLSISALKNGVMG----EKVEDEEKT-ERSWKDQN--LDNGS-DGFFAT-----INREVPSCDP LHNK
GaCLE6	MVSKGLIGYVLLIMLSISALKNGVMG----EKVEDEEKT-ERSWKDQN--LDNGS-DGFFAT-----INREVPSCDP LHNK
GrCLE6	MVSKGLIGYVLLIMLSISALKNGVVG----EKVEDEEKT-ERSWKDQN--LDNGS-DGFFAT-----INREVPSCDP LHNK
GhCLE6.1	MVSKGLIGYVLLIMLSISALKNGVVG----EKVEDEEKT-ERSWKDQN--LENGS-DGFFAT-----INREVPSCDP LHNK
GhCLE8.2	---MSISLSFWCFGLWNFLTGCVSIG---EKPAQNRKILHADLKENNGSTTGAGNMENFVGW-----ELRAVPSGDP LHHN
GhCLE8.1	---MSISLSFWCFGLWNFLTGCVSIG---EKPAQNRKILHADLKENNGSTTGAGNMENFVGW-----ELRAVPSGDP LHHN
GrCLE8	LVTTRALVLALLYLLVLQGVCGCVSG---EKPAQNRKILHADLKENNGSTTGAGNMENFVGW-----ELRAVPSGDP LHHN
GaCLE8	LVTTRALVLALLYLLVLQGVCGCVSG---EKPAQNRKILHADLKENNGSTTGAGNMENFVGW-----ELRAVPSGDP LHHN
GhCLE31	SLQVGLLQTLMMGMVLVSVFVSVSGY-----KGHNPPHDKHKQPVKVKQHHQRFR-----HSFDVFYSKREVPNASDPLHNH
GaCLE31	-----MMQMLVLVSVFVSVSGY-----KGHNPPHDKHKQPVKVKQHHQRFR-----HSFDVFYSKREVPNASDPLHNH
GrCLE31	-----MMRILVLVSVFVSVSGY-----KGHNPPHDKHKQPVKVKQHHQRFR-----HSFDVFYSKREIPNALAPLHNH
GhCLE30.1	--MLRLLRILMVVMLLSSMLISAD-----TTNAHSPVSNEKIPMDKQQQPQSLR-----GSFGVFFSSKRRKVPNAADPLHNH
GaCLE30	--MLRLLRILMVVMLLSSMLISAD-----TTNAHSPVSNEKIPMDKQQQPQSLR-----GSFGVFFSSKRRKVPNAADPLHNH
GhCLE30.2	--MLRLLRILMVVMLLSSMLISAD-----TTNAHSPVSNEKIPMDKQQQPQSLR-----GSFGVFFSSKRRKVPNAADPLHNH
GrCLE30	--MLRLLRILMVVMLLSSMLISAD-----TTNAHSPVSNEKIPMDKQQQPQSLR-----GSFGVFFSSKRRKVPNAADPLHNH

III

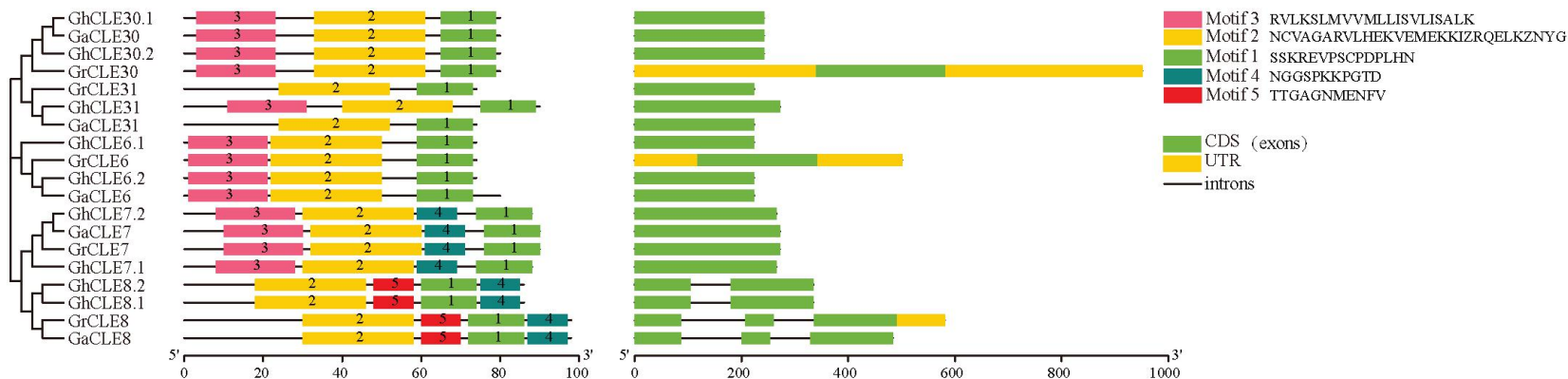
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GaCLE41	K----	LICFYLLLLLYFQFSSCSFQLMPVESH-----	GGFEANDDDDHGDEGEDFGD-----	EKRKVYTGPNPLHNR
GrCLE42	S----	LLLLLLLLLL-QFEYAGG--GGSNGEQK-----	SPKF IKSQKNGDD--IFAA-----	QQRKVYTGPNPLHNR
GaCLE42	S----	LLLLLLLLLLQFEYAGG--GGSNGEQK-----	SPKF IKSQKNGDD--IFAA-----	QQRKVYTGPNPLHNR
GrCLE1	MRDHVLIYLLLAWLLLIHYRAIDSV-----	FSTR-----	RSLMPRSRVRNALPTWVEMK-----	KIHKSPSSPNPVKNR
GaCLE1	MRDHVLIYLLLAWLLLIHY-----	M-----FSTR-----	RSLMPRSRVRNALPTWVEMK-----	KIHKSPSSPNPVKNL
GbCLE1	MREQLLICLLLAWLLAVSVQAIESG-----	YFLS-----	RSPMPRPR-----LPNWVEMK-----	KIHKSPSGPNPVGNH
GrCLE39	NIQV-LAYMIFAFLLLSAS-LRIPAI-----	LKIS-----	TARQTQNP SNRFSLAWVKDD-----	NMRKVPSAPNP SGNR
GaCLE39	NIQV-LAYMIFAFLLLSAS-LRIPAI-----	FSIS-----	TARQTQNP SNRFSLAWVKD-----	NMRKVPSAPNP I GNR
GrCLE40	KVQVMLAYLLIVFLLLPSS--SIPMQ-----	MKTR-----	PPKPNRFLLAAWEHGTNVKG-----	NMKKVPSAPNP KGNL
GaCLE40	KVQVMLAYLLIVFLLLPSS--SIPMQ-----	GK-----	LPKPNRFLLAAWEHGTNVKG-----	NMKKVPSAPNP KGNR
GbCLE2	KPHFFLLFLTIVFLVFLLL INSSNVTSSSSTMNL-----	PPKQRRHPRTSASS--FGA-----	EAHEVPSGPNP ISNR	
GaCLE2	KPHFFLLFLTIVFLVFLLL INSSNVTSSSSTMNL-----	PPKQRRHPRTSASS--FGA-----	EAHEVPSGPNP ISNR	
GrCLE2	KPHFFPLFLTIVFLVFLLL INSSNVTSSSSTMNL-----	PPKQRRHPRTSASS--FGA-----	EAHEVPSGPNP ISNR	
GbCLE39	-----	MDSPNGTDASSNMNL-----	HPKQTRTLGTSSSSSRREFGA-----	EAHEVPSGPNP ISNR
GaCLE49	-----	MDSPNGTDASSNMNL-----	HPKQTRTLGTSSSSSRREFGA-----	EAHEVPSGPNP ISNR
GrCLE49	KSHSLFLLTLFFIFLLLLMDSPNGTDASSNMNL-----	HPKQTRTLGTSSSSSRREFGA-----	EAHEVPSGPNP ISNR	
GbCLE40	KSHSLFLLTLFFIFLLLLMDSPNGTDASSNMNL-----	HPKQTRTLGTSSSSSRREFGA-----	EAHEVPSGPNP ISNR	
GbCLE3	KSQFFIVFLTTLFFISLLIFINSS--PTSSTMEI-----	NQSPNPHTSSSSSSRGQFGG-----	EAHEVPSGPNP ISNR	
GaCLE3	KSQFFIVFLTTLFFISLLIFINSS--PTSSTMEI-----	NQSPNPHTSSSSSSRGQFGG-----	EAHEVPSGPNP ISNR	
GrCLE3	KSQFFIIFLTTLFFISLLIFINSS--PTSSTMEI-----	NQSPNPHTSSSSSSRRQIGG-----	EAHEVPSGPNP ISNR	
GbCLE5.2	NTHFTLLFILLLLLVSPVFSSSCYGQKPPASNSHP-----	FPAPTTAAAEQSPRDRRFKG-----	AAHEVPSGPNP ESN-	
GaCLE5	NTHFTLLFILLLLLVSPVFSSSCYGQKPPASNSHP-----	FPAPTTAAAEQSPRDRRFKG-----	AAHEVPSGPNP ESN-	
GbCLE5.1	NTHFTLLFILLLLLVSPAFSSCYDQKPPASNSHP-----	FPAPTTAAAEQSPRDRRFKG-----	AAHEVPSGPNP ESN-	
GrCLE5	NTHFTLLFILLLLLVSPVFSSSCYDQKPPASNSHP-----	FQAPTIAAAEQSPRDRRFKG-----	AAHEVPSGPNP ESN-	
GbCLE4.2	SCALLQLFLLLLLLISPLFSSSSTTR-----	IPAAQTPGKNGAT-DGRFEA-----	DVHEVPSGPNP ESNK	
GaCLE4	SCALLQLFLLLLLLISPLFSSSSTTR-----	IPAAQTPGKNGAT-DGRFEA-----	DVHEVPSGPNP ESNK	
GbCLE4.1	SCALLQLLVLLLLLLISPLFSSSSTTR-----	IPAAQSPGKNGAT-DGRFEA-----	DVHEVPSGPNP ESNK	
GrCLE4	SYALLRLFVLLLLLLISPLFSSSSTTR-----	IPAAQSPGKNGAT-DGRFEA-----	DVHEVPSGPNP ESNK	



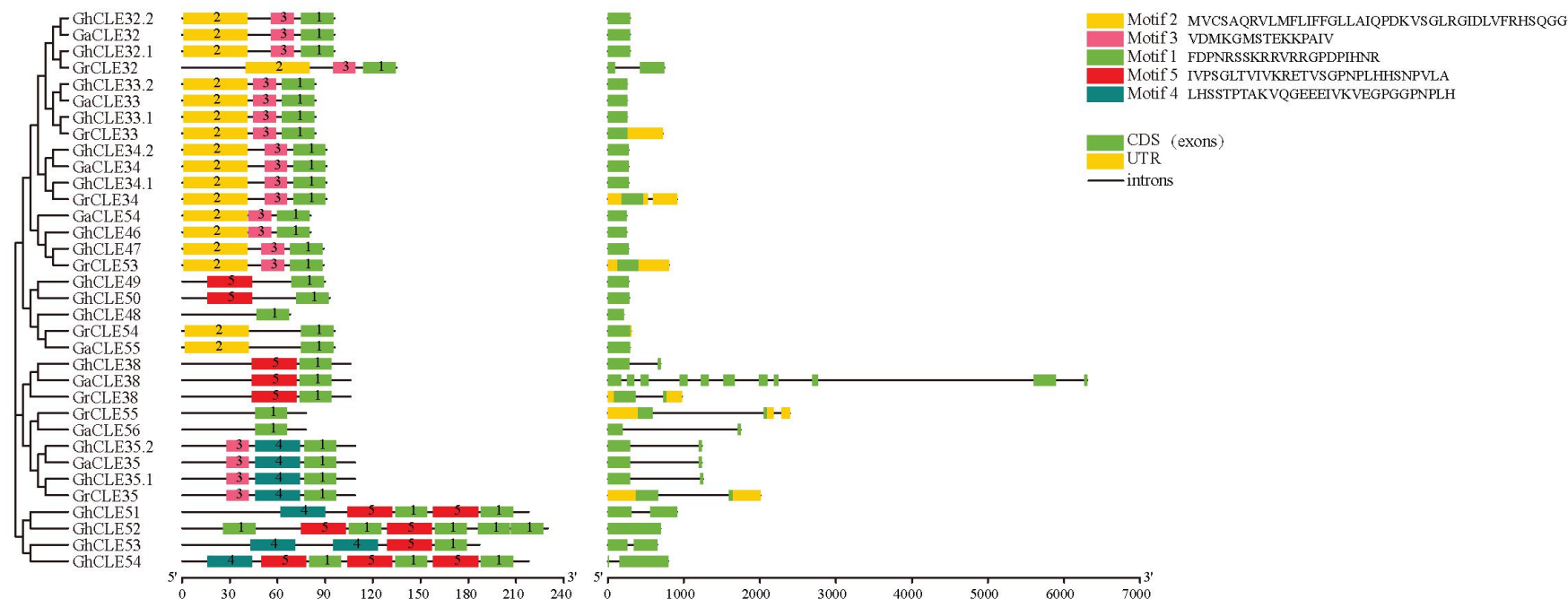
Supplementary Figure 3. Multiple sequence alignment of *G.hirsutum*, *G.arboreum*, and *G.raimondii* CLE pre-propeptides was performed using the ClustalX program. The CLE domain contains 14 amino acids, and the leucine-rich region in the signal peptide region is the most conserved in the whole pre-propeptide family.



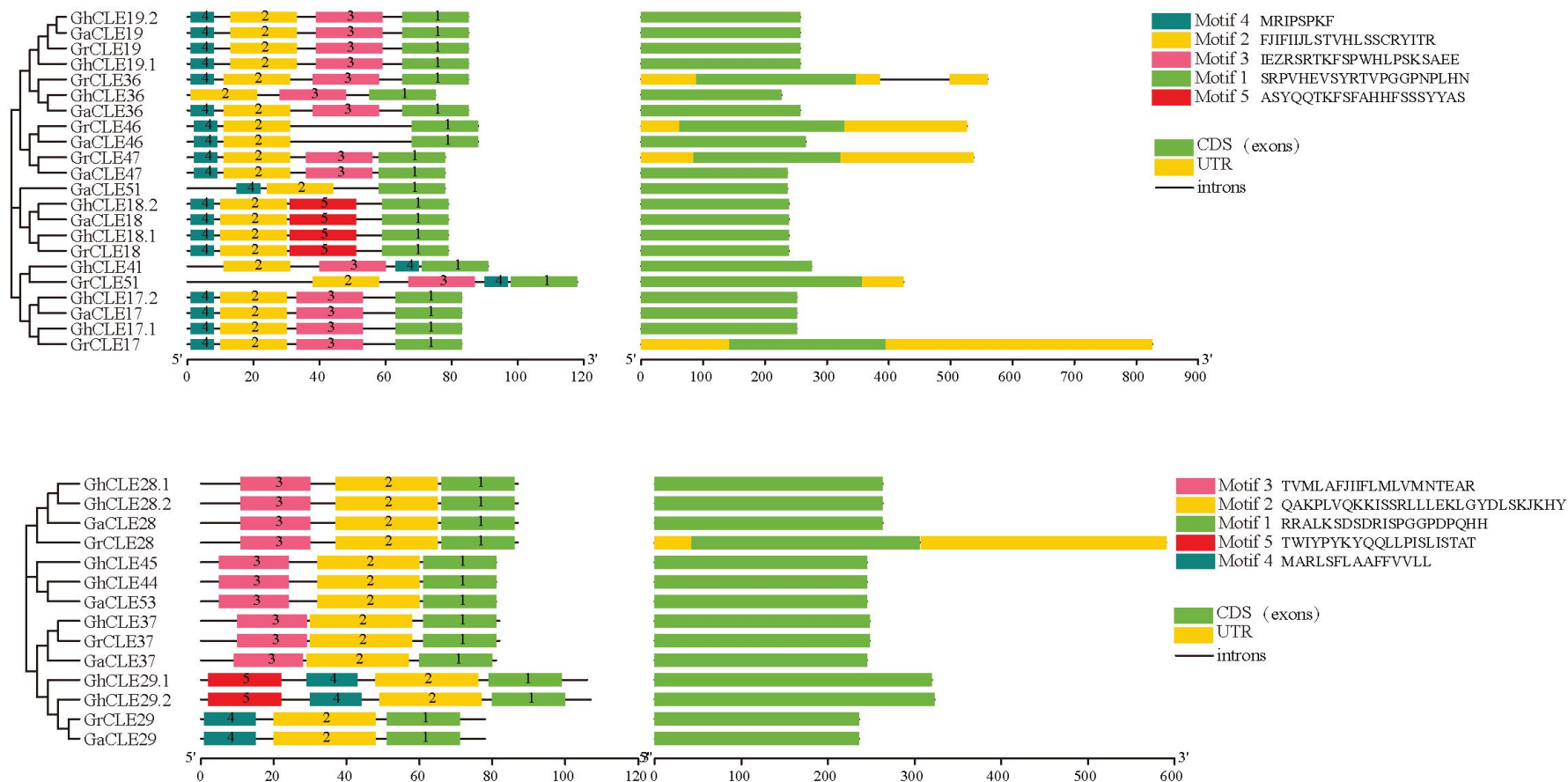
III



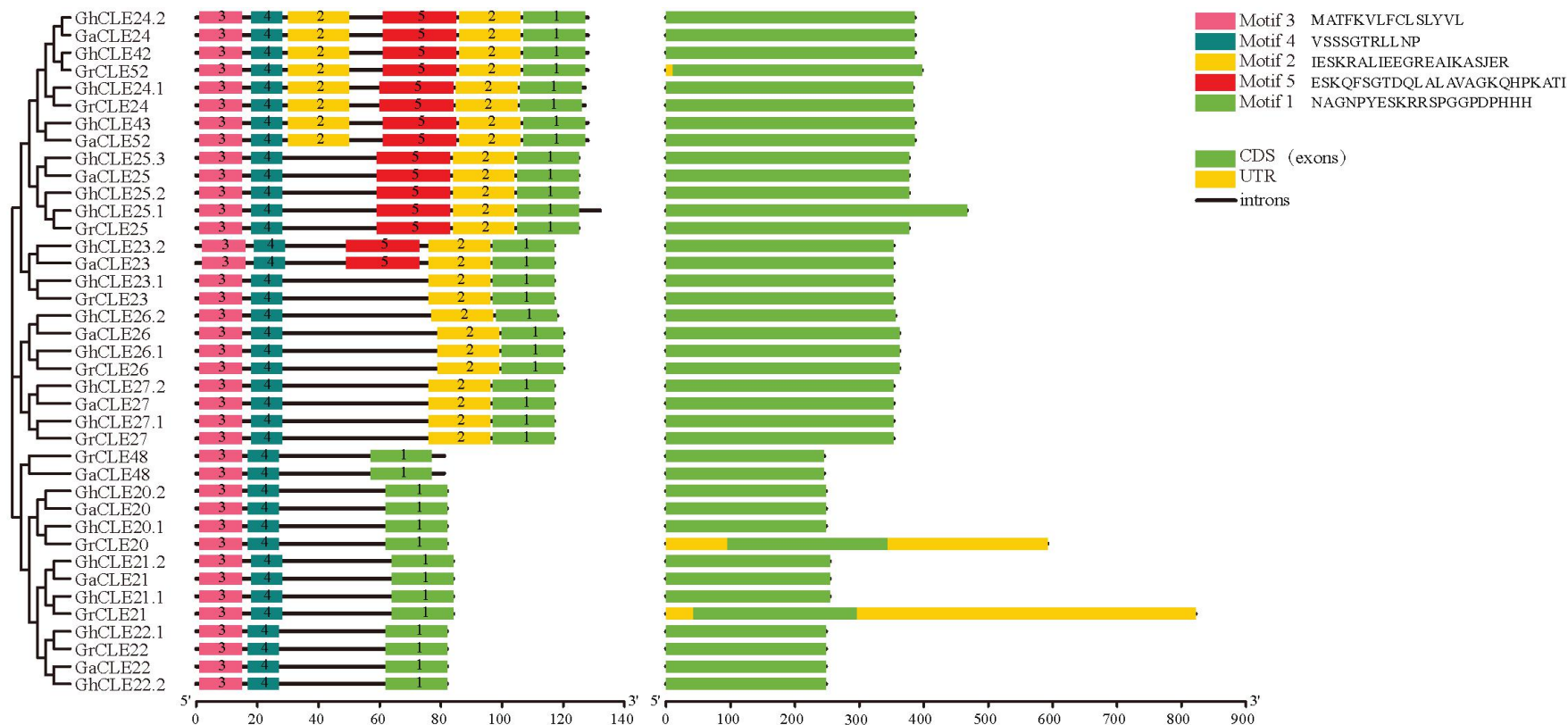
IV



VI



VII



Supplementary Figure 4. Gene structure and conserved motifs of seven groups in *G.hirsutum*, *G.arboreum*, and *G.raimondii* were illustrated by GSDS 2.0 and MEME. In gene structure diagrams, green boxes stand for exons; black lines for introns; yellow boxes for UTR. Five conserved motifs of each group were identified. Different color boxes with number represented different motifs.