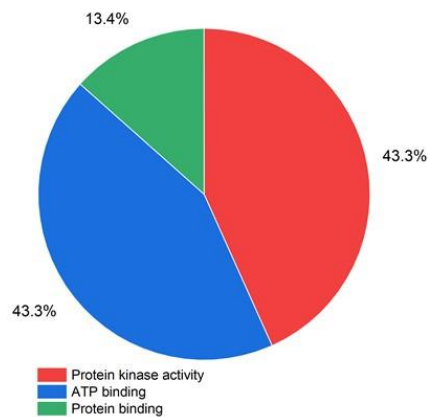
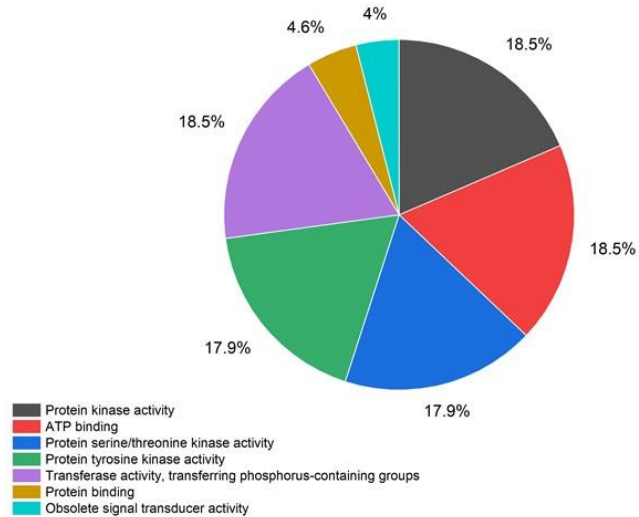


a



b



c

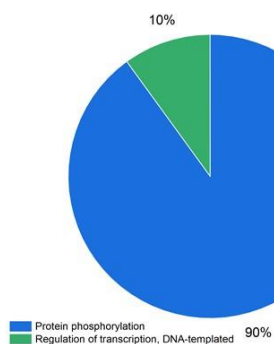
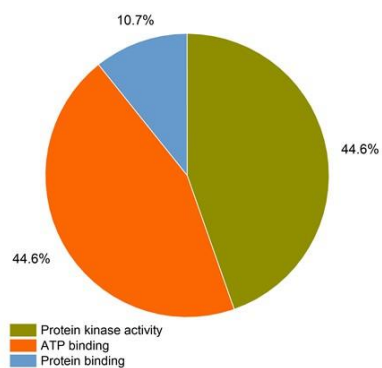
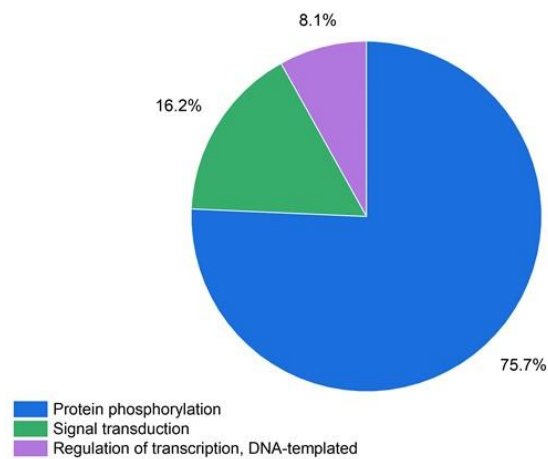
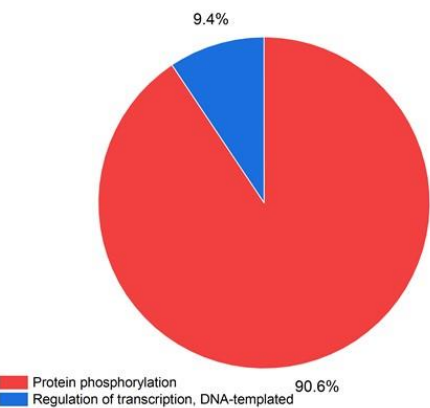


Figure S1. Analysis of RAF gene ontology to study molecular and biological functions (A) *G. arboreum* (B) *G. raimondii* (C) *G. barbadense*:

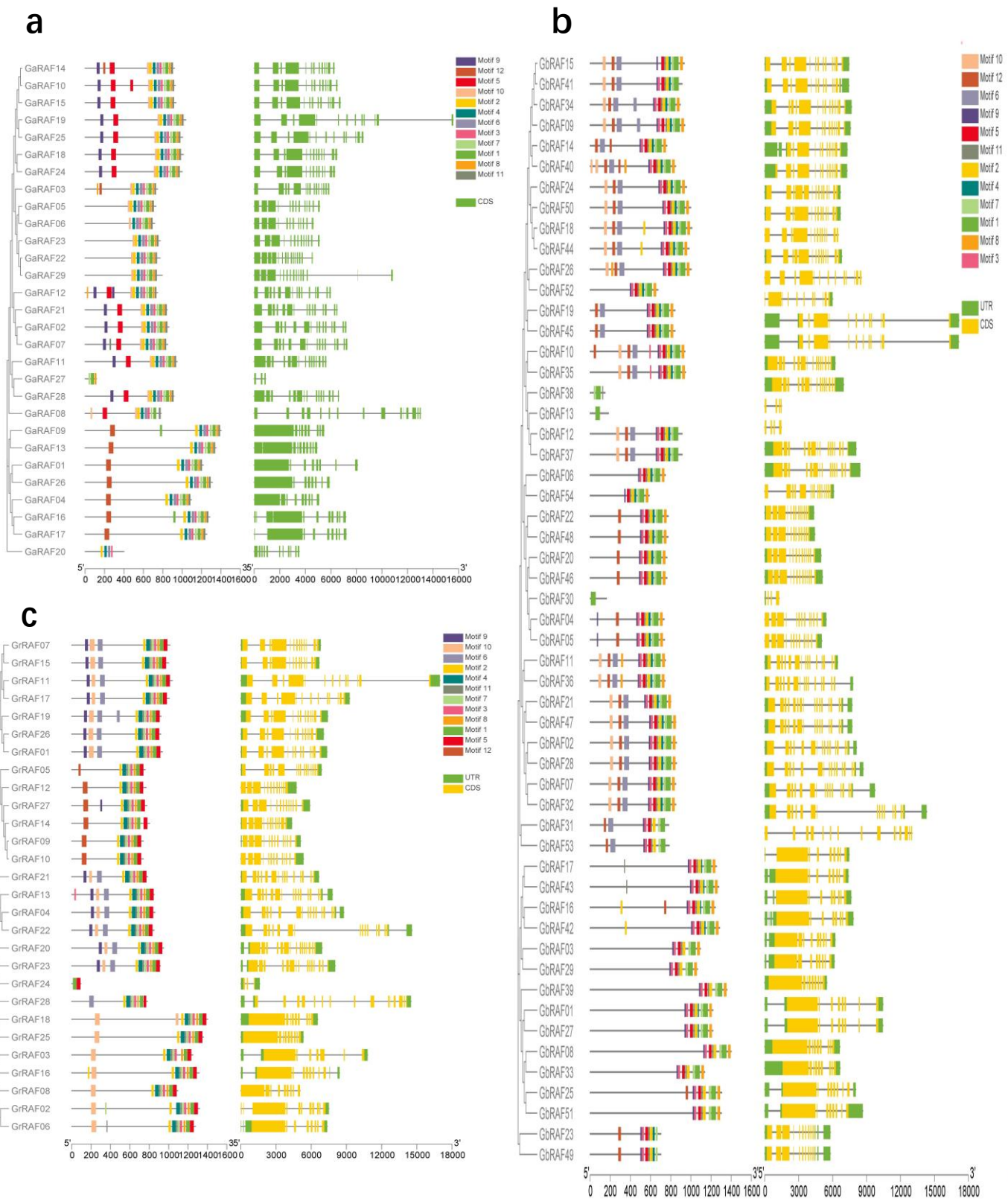


Figure S2: Phylogenetic tree, Motif and Gene structure of RAF gene Family of cotton (A) *G. arboreum* (b) *G. barbadense* (c) *G. raimondii*

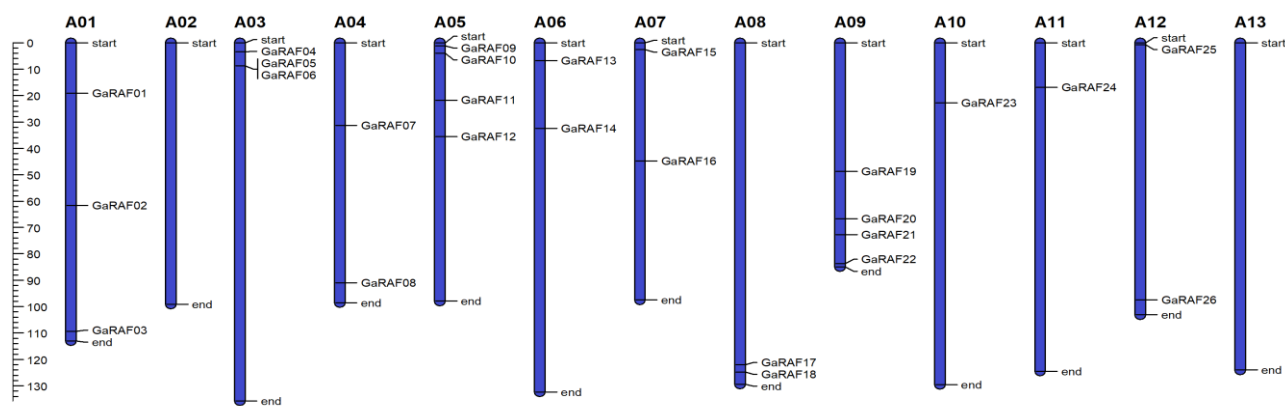
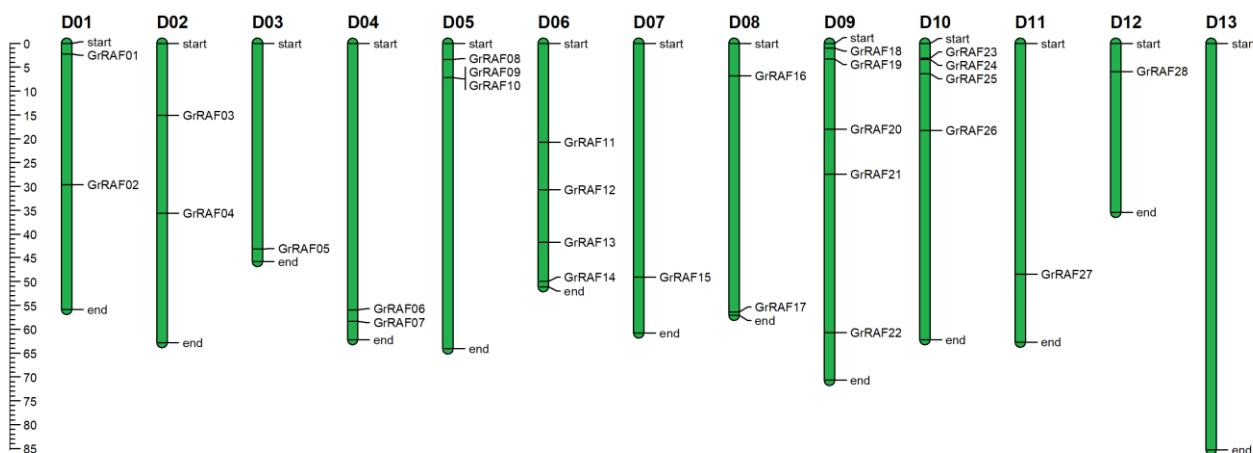
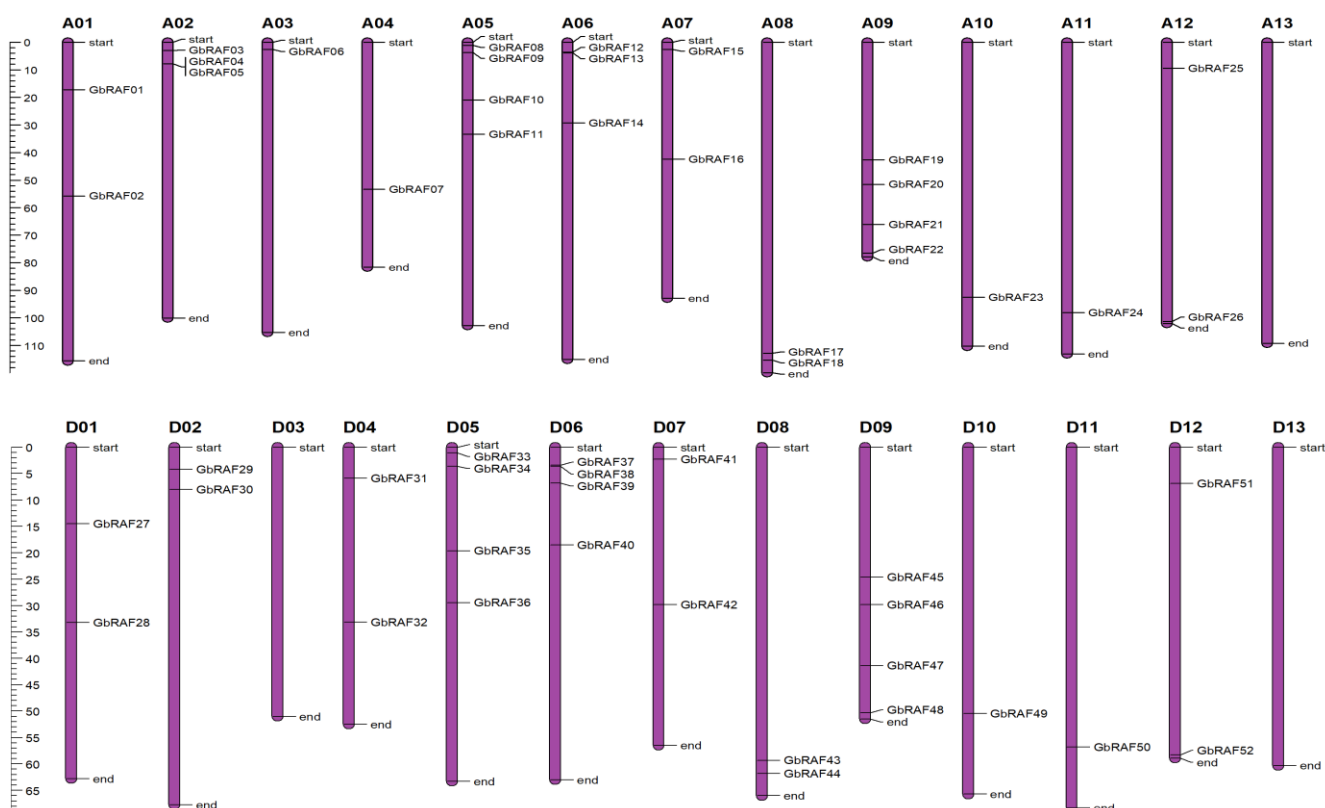
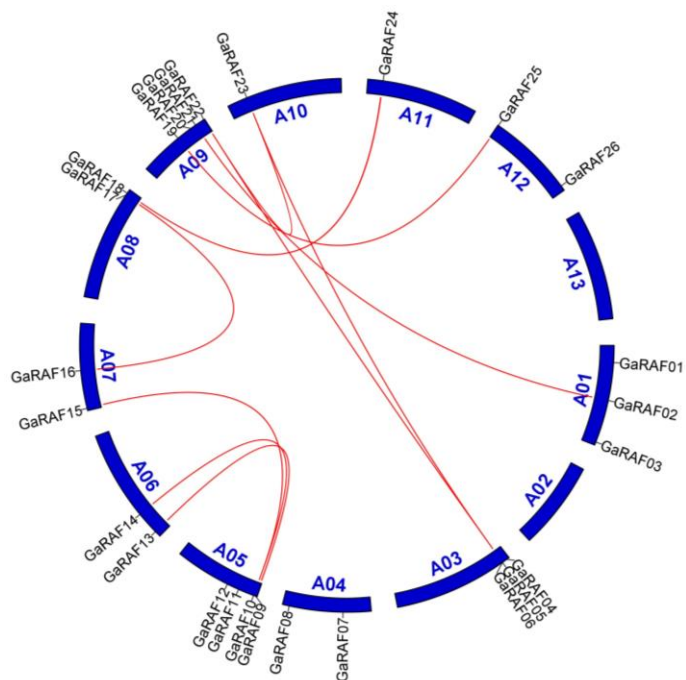
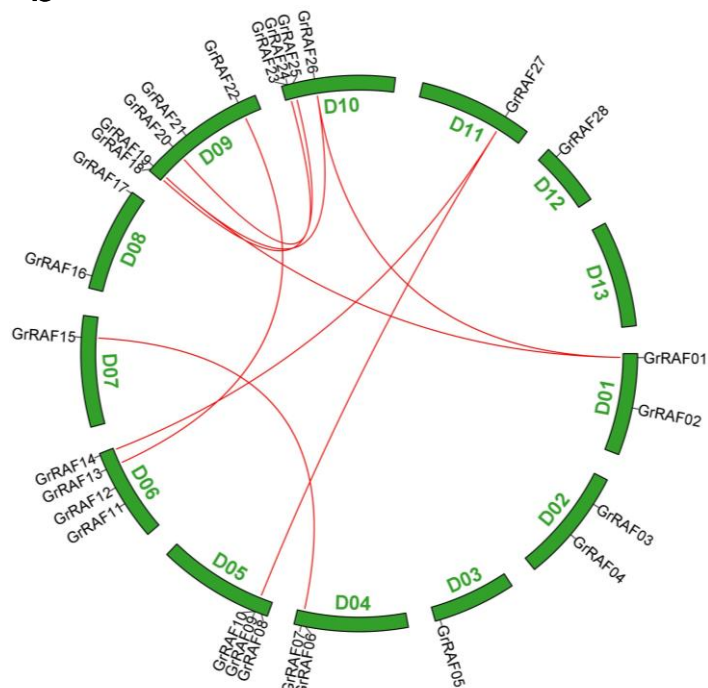
a**b****c**

Figure S3. Chromosomal map of RAF gene family of cotton (A) *G. arboreum* (B) *G. raimondii* (c) *G. barbadense*

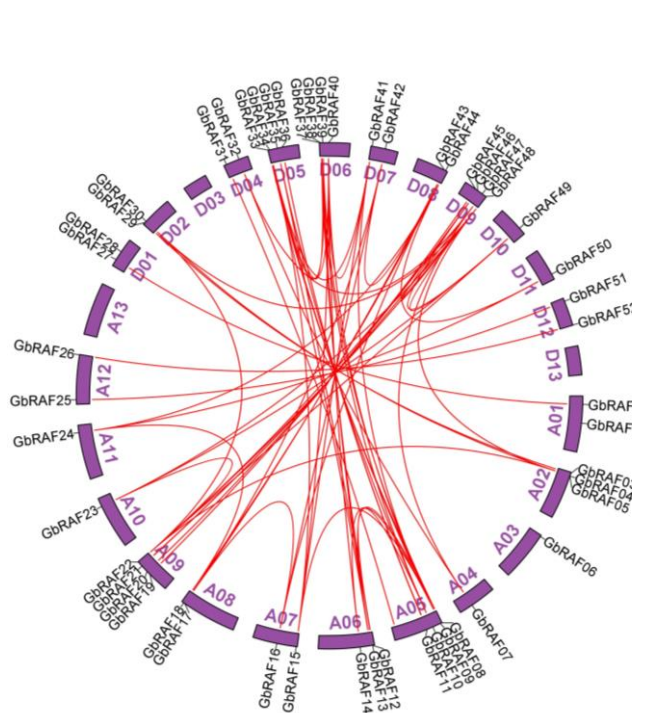
a



b



c



d

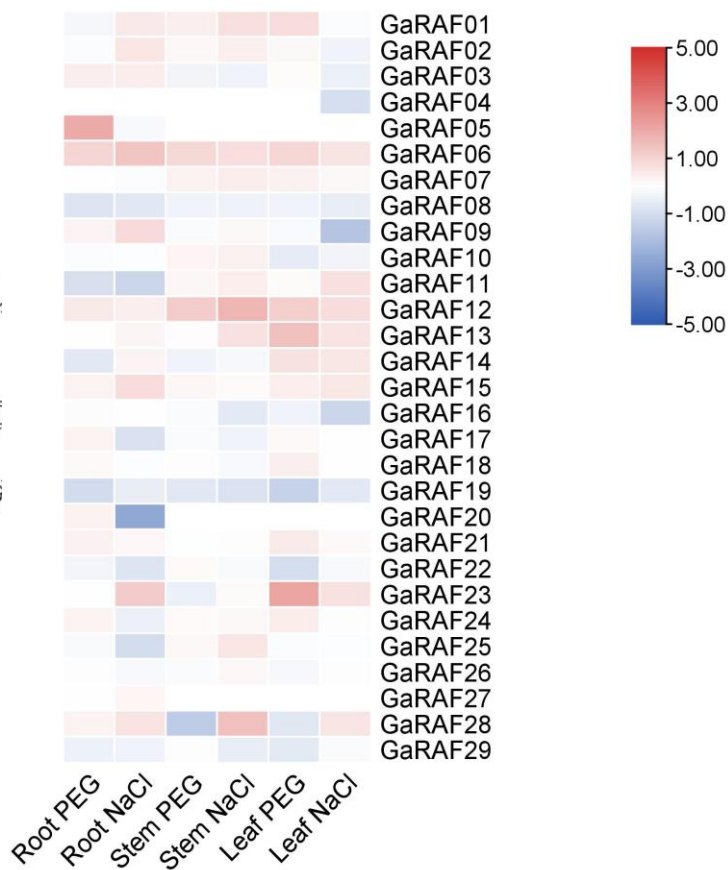


Figure S4: Collinearity and expression analysis of RAF gene family in cotton (a) *G. arboreum* (b) *G. raimondii* (c) *G. barbadense* (d) Expression analysis of *G. arboreum*

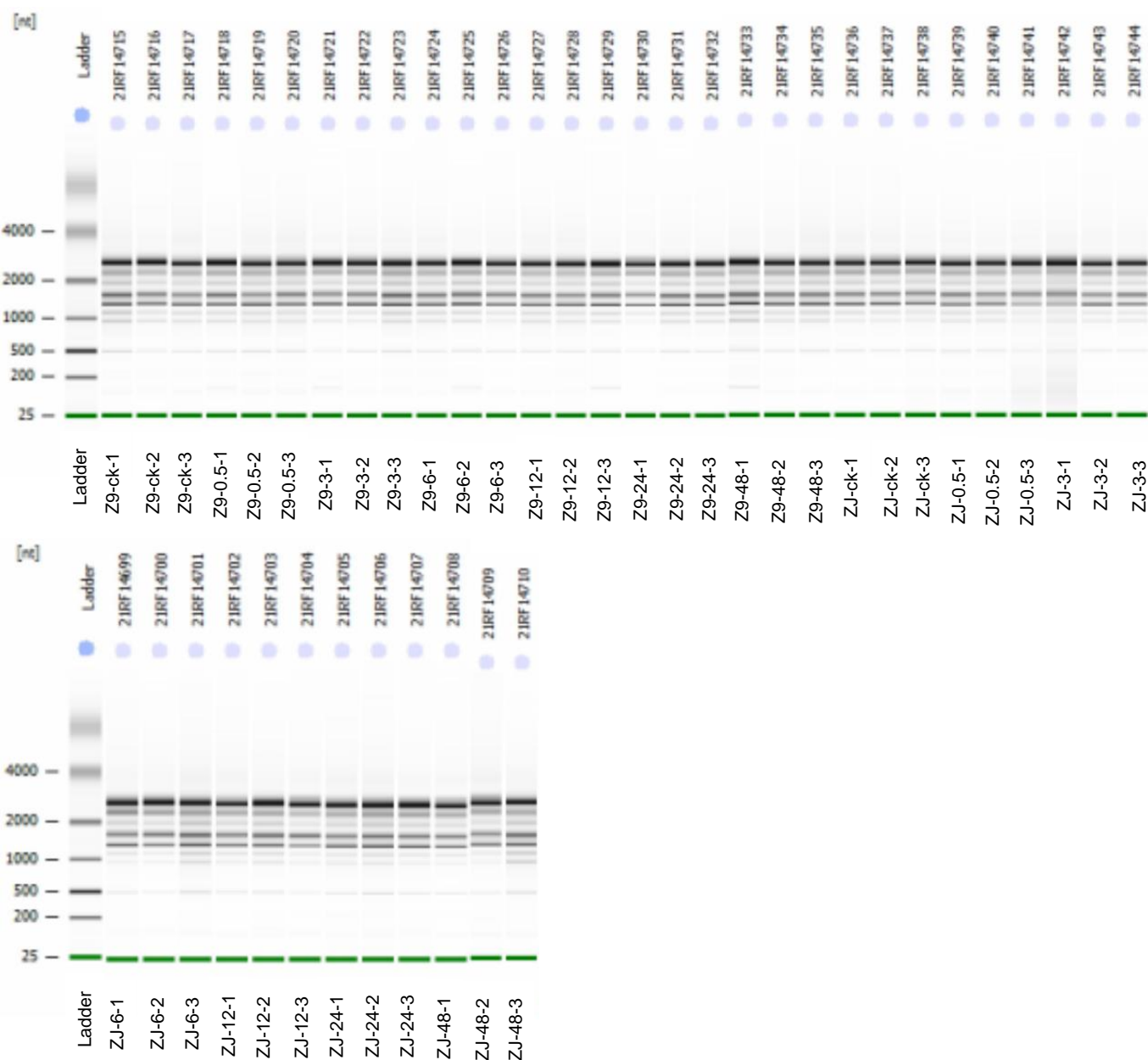
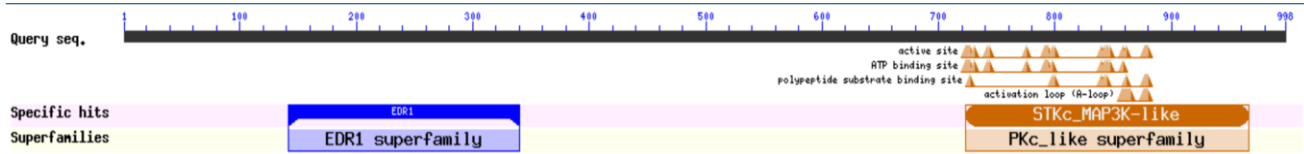


Figure S5: Analysis of the quantity, integrity and purity of total RNA for 42 leaf samples with the Agilent 2100 Bioanalyzer for qRT-PCR and RNA-seq. CK means NaCl-untreated as control.0.5h-48h means different time points after NaCl stress. Z9:Z9807;ZJ:ZJ0102.

a



b

AT1G08720.1	POVLLFADVGE....CEIPWNDIV...IAERIGIGSYGEV	683
GbRAF24	HQLFDDVDVGE....CEIPWEDLD...ICERIGIGSYGEV	693
GaRAF24	HQLFDDVDVGE....CEIPWEDLD...ICERIGIGSYGEV	733
GhRAF25	HQLFDDVDVGE....CEIPWEDLD...ICERIGIGSYGEV	731
GhRAF42	HQLFDDVDVGE....CEIPWEDLD...ICERIGIGSYGEV	731
GbRAF50	HQLFDDVDVGE....CEIPWEDLD...ICERIGIGSYGEV	733
GhRAF02	HQLFDDVDVGE....CEIPWEDLD...ICERIGIGSYGEV	733
GrRAF15	HQLFDDVDVGE....CEIPWEDLD...ICERIGIGSYGEV	733
GaRAF18	EQLFDDVDVGE....CEIPWEDLD...ICERIGIGSYGEV	745
GbRAF18	EQLFDDVDVGE....CEIPWEDLD...ICERIGIGSYGEV	745
GhRAF10	EQLFDDVDVGE....CEIPWEDLD...ICERIGIGSYGEV	745
GrRAF07	EQLFDDVDVGE....CEIPWEDLD...ICERIGIGSYGEV	746
GbRAF44	EQLFDDVDVGE....CEIPWEDLD...ICERIGIGSYGEV	717
GhRAF24	EQLFDDVDVGE....CEIPWEDLD...ICERIGIGSYGEV	746
AT5G49470.2	NKVDMSDCLD...YEILWEDLT...ICEQIGGSGCGTV	502
AT1G67890.1	NKVDMSDCLD...YEILWEDLT...ICEQIGGSGCGTV	501
AT3G06620.1	NKVDTSSEGLE....YEILWEDLT...ICEQIGGSGCGTV	508
Consensus	d ei w dl i e g g s g v	
AT1G08720.1	RRLRHPNVVFLFMGAVTRPP...NLSIIITEFLP.....	747
GbRAF24	RRLRHPNVVFLFMGAVTRPP...NLSIIITEFLP.....	757
GaRAF24	RRLRHPNVVFLFMGAVTRPP...NLSIIITEFLP.....	797
GhRAF25	RRLRHPNVVFLFMGAVTRPP...NLSIIITEFLP.....	795
GhRAF42	RRLRHPNVVFLFMGAVTRPP...NLSIIITEFLP.....	795
GbRAF50	RRLRHPNVVFLFMGAVTRPP...NLSIIITEFLP.....	797
GhRAF02	RRLRHPNVVFLFMGAVTRPP...NLSIIITEFLP.....	797
GrRAF15	RRLRHPNVVFLFMGAVTRPP...NLSIIITEFLP.....	797
GaRAF18	RRLRHPNVVFLFMGAVTRPP...NLSIIITEFLP.....	809
GbRAF18	RRLRHPNVVFLFMGAVTRPP...NLSIIITEFLP.....	809
GhRAF10	RRLRHPNVVFLFMGAVTRPP...NLSIIITEFLP.....	809
GrRAF07	RRLRHPNVVFLFMGAVTRPP...NLSIIITEFLP.....	810
GbRAF44	RRLRHPNVVFLFMGAVTRPP...NLSIIITEFLP.....	781
GhRAF24	RRLRHPNVVFLFMGAVTRPP...NLSIIITEFLP.....	810
AT5G49470.2	KRLRHPNVLLFMGAVTSPQ...RLCIVTEFLP.....	566
AT1G67890.1	KRLRHPNVLLFMGAVTSPQ...RLCIVTEFLP.....	565
AT3G06620.1	KRLRHPNVLLFMGAVTSPQ...RLCIVSEFLP.....	572
Consensus	rlrhpnv f gav p l i eflp	
AT1G08720.1RIKMALDVARGMNCNLTSTP...TIVHRDLKTFENLLVD	801
GbRAF24RIKMALDVARGMNCNLTSTP...TIVHRDLKTFENLLVD	811
GaRAF24RIKMALDVARGMNCNLTSTP...TIVHRDLKTFENLLVD	851
GhRAF25RIKMALDVARGMNCNLTSTP...TIVHRDLKTFENLLVD	849
GhRAF42RIKMALDVARGMNCNLTSTP...TIVHRDLKTFENLLVD	849
GbRAF50RIKMALDVARGMNCNLTSTP...TIVHRDLKTFENLLVD	851
GhRAF02RIKMALDVARGMNCNLTSTP...TIVHRDLKTFENLLVD	851
GrRAF15RIKMALDVARGMNCNLTSTP...TIVHRDLKTFENLLVD	851
GaRAF18RIKMALDVARGMNCNLTSTP...TIVHRDLKTFENLLVD	863
GbRAF18RIKMALDVARGMNCNLTSTP...TIVHRDLKTFENLLVD	863
GhRAF10RIKMALDVARGMNCNLTSTP...TIVHRDLKTFENLLVD	863
GrRAF07RIKMALDVARGMNCNLTSTP...TIVHRDLKTFENLLVD	864
GbRAF44RIKMALDVARGMNCNLTSTP...TIVHRDLKTFENLLVD	835
GhRAF24RIKMALDVARGMNCNLTSTP...TIVHRDLKTFENLLVD	864
AT5G49470.2	MLHIFLTYYFAQARGMNYLHHCSP...PIIHRDLKSSNLLVD	684
AT1G67890.1RIHMASDIARGMNYLHHCSP...PIIHRDLKSSNLLVD	619
AT3G06620.1RIHMALDIARGMNYLHHCSP...PIIHRDLKSSNLLVD	626
Consensus	a gmn lh p i hrdlk nllvd	
AT1G08720.1	APEVLRNEP...SNEKCDVYSFGVILWEIATLRLPWSGMN	871
GbRAF24	APEVLRNEP...SNEKCDVYSFGVILWEIATLRLPWSGMN	881
GaRAF24	APEVLRNEP...SNEKCDVYSFGVILWEIATLRLPWSGMN	921
GhRAF25	APEVLRNEP...SNEKCDVYSFGVILWEIATLRLPWSGMN	919
GhRAF42	APEVLRNEP...SNEKCDVYSFGVILWEIATLRLPWSGMN	919
GbRAF50	APEVLRNEP...SNEKCDVYSFGVILWEIATLRLPWSGMN	921
GhRAF02	APEVLRNEP...SNEKCDVYSFGVILWEIATLRLPWSGMN	921
GrRAF15	APEVLRNEP...SNEKCDVYSFGVILWEIATLRLPWSGMN	921
GaRAF18	APEVLRNEP...SNEKCDVYSFGVILWEIATLRLPWSGMN	933
GbRAF18	APEVLRNEP...SNEKCDVYSFGVILWEIATLRLPWSGMN	933
GhRAF10	APEVLRNEP...SNEKCDVYSFGVILWEIATLRLPWSGMN	933
GrRAF07	APEVLRNEP...SNEKCDVYSFGVILWEIATLRLPWSGMN	934
GbRAF44	APEVLRNEP...SNEKCDVYSFGVILWEIATLRLPWSGMN	905
GhRAF24	APEVLRNEP...SNEKCDVYSFGVILWEIATLRLPWSGMN	934
AT5G49470.2	APEVLRNEA...ADEKSDVYSFGVILWEIATLRLPWESLN	754
AT1G67890.1	APEVLRNEA...ADEKSDVYSFGVILWEIATLRLPWENLN	688
AT3G06620.1	APEVLRNES...ADEKSDVYSFGVILWEIATLRLPWETLN	696
Consensus	apevlrne ek d ysfg lwe t pw n	

Figure S6: *GhRAF* gene cloning, conserved domain database and sequence alignment analysis (A) Conserved domain database analysis of GhRAF42 (E) Multiple sequence alignment of GhRAF42