

Additional file 2: Table S1. Characterization of ten conserved motifs in GmGRF sequences.

Motif	Width	E-value	Best possible match
1	41	1.3e-561	MRSPFTPSQWQELEHQALIYKYMVAGLPVPPDLLLPIKKSL
2	50	1.9e-940	GKKVDPEPGRCRRTDGKKWRCSKDAYPDSKYCERHMHARG RNRSRKPVEVQ
3	29	2.2e-096	RYVYGLKSEVDEHAFFTEPLGSMKVLSAE
4	20	1.8e-123	LKZEQHSLRHFFDEWPCKSR
5	21	1.1e-085	KSSTTQLSISIPISSEDFATF
6	21	2.7e-060	IPITWESSMGGPLAEVLRST
7	29	4.7e-051	GLEGVVGSESGCVFGSSLASDPETKHKWY
8	29	1.5e-040	AKTDHDMSSASKAMLFQQRNNSLLRSNNA
9	50	7.3e-061	LSFSSPKSESLLVDKASSNATLPFSYHQLSSYSRNTGYNSG SISMHGALA
10	31	2.1e-041	FAHNNVHHPLPPHSSPANTINRMFTSNKNN