

Symbol	Motif	Logo	Consensus sequence	Width (aa)	E-value
	Motif 1		SSSSSYTCGYCKREFRSAQALGGHMNVHRRDRARLRHGQSP	41	9.9e-1061
	Motif 2		GDGAEEGLDLELR LG	15	1.2e-282
	Motif 3		ARAPJPNLNYSPPHPA	16	1.5e-134
	Motif 4		APPVVYSFFSLAASA	15	1.3e-080
	Motif 5		MERESDKQQQQ	11	6.2e-032
	Motif 6		IHLPNILATVAKQCALEKQEIEETSHANYTGHHSTTPAGHPPTMEGRDH	50	2.7e021
	Motif 7		WPPQVRS	8	2.3e-014
	Motif 8		PPPNPNPSCTVLDL	14	1.5e-009
	Motif 9		WYYS CSF	7	3.2e-005
	Motif 10		LKPLQPWTTT	11	1.3e-004
	Motif 11		FPWPPQ	6	1.6e-004
	Motif 12		VVCSSST	8	6.2e-003
	Motif 13		MESRSAARAGDQQH	14	9.6e-004
	Motif 14		MAVTKGLEVDLELV	15	4.6e-001
	Motif 15		AASDGGLAVP	10	6.4e+000

Figure S8. Motif consensus sequences identified by MEME based on 35 RA1 and RA1-like sequences identified for 16 grass species. Motif 1 represents the conserved zinc finger domain. Motif 2 represents the conserved EAR motif. Motifs presence and distribution along each of the sequences is presented in Figure S7.