

Symbol	Motif	Logo	Consensus sequence	Width (aa)	E-value
	Motif 1		SSSSSYTCGYCKREFRSQAQLGGHMNVHRRDRARLRHQSP	41	9.9e-1061
	Motif 2		GDGAEEGLDLELRIG	15	1.2e-282
	Motif 3		ARAPJPNLNYSPHPA	16	1.5e-134
	Motif 4		APPVVYSFFSLAASA	15	1.3e-080
	Motif 5		MERESDKQQQQ	11	6.2e-032
	Motif 6		IHLPNILATVAKQCALEKQEQIETSHANYTGHHSTTPAGHPPTMEGRDH	50	2.7e021
	Motif 7		WPPQVRS	8	2.3e-014
	Motif 8		PPNPNPSCVTLDL	14	1.5e-009
	Motif 9		WYYSCSF	7	3.2e-005
	Motif 10		LKPLQPWTTTT	11	1.3e-004
	Motif 11		FWPPQ	6	1.6e-004
	Motif 12		VVCSCST	8	6.2e-003
	Motif 13		MESRSAARAGDQQH	14	9.6e-004
	Motif 14		MAVTKGLEVDLELEV	15	4.6e-001
	Motif 15		AASDGGGLAVP	10	6.4e+000

**Figure S8.** Motif consensus sequences identified by MEME. The 35 amino acid C2H2 sequences from 16 grass species were used to identify conserved motifs among them. Fifteen motifs were identified. Motif 1 represents the conserved zinc finger domain. Motif 2 represents the conserved EAR motif.