	Logo	E-value	Sites	Width
1.	#BRXWLGTFRTAERAAHAYDRAAEK+BG=KAFLNFP	7.6e-820	34	35
2.	a sa	1.4e-574	33	26
3.	#MTAEGSGIGES VSGSSELVWGDMAESWFNAIPAGWGPGSPVWDDLDTTNN	6.6e-086	4	50
4.	#JKW&V&DETEKMTIGQDWETYKGWPLD+GFERROWKPVFDEASMSQFPLKK	2.2e-074	4	50
5.	#ASLPSSRLxFPFAEDAS9QPIYEPQQYBNTPTLMPMFEPSeQNQQY#ISF	1.6e-072	4	50
6.	TEHESSKPNQNQNLPK&EQEGLNLQS&KMEMMPPPAQPQG&NPDSDSGMG	1.7e-067	4	50
7.	######################################	1.3e-036	4	24
8.	#ES#FELTERWGDLPLK#DDSEDMLYY8#LRDALN&GW&PSB	4.8e-039	4	41
9.	DAF I DLPDL + DMN + QUDEFWGS + SWQL + ATDDP VENGF & YEEP BLWEYE	5.4e-050	3	50
10.	#JELANQNQQEESQESDLEKQQDSSASSSASCPWKBFFWKDQD	1.5e-037	4	41

S3 Fig. Multilevel consensus sequences identified by MEME. Protein sequences of ripening-associated DzERFs were used to identify conserved motifs. Ten conserved motifs were identified. Motifs 1 and 2 represent the conserved DNA binding domain (AP2/ERF domain) always observed at the N-terminus.