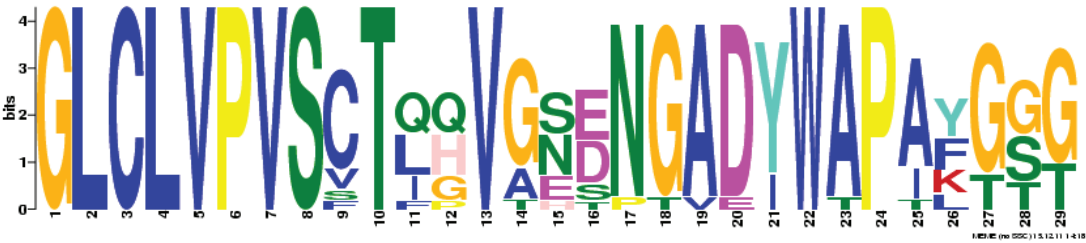


Additional File 8. New bHLH motif (Motif 40).

A: Sequence logo representation of consensus motif



B. MEME alignment of sequences used to discover motif

Name	Start	p-value	Sites
Glyma08g21770.2:(Glyma08g21770.2 PACid:16272011	287	5.24e-38	KDKPSDLKSR GLCLV F V S CT Q H V GN E NGAD Y WAP A Y G S G F
Glyma08g21770.1:(Glyma08g21770.1 PACid:16272010	289	5.24e-38	KDKPSDLKSR GLCLV F V S CT Q H V GN E NGAD Y WAP A Y G S G F
Glyma07g02120.3:(Glyma07g02120.3 PACid:16265869	289	5.24e-38	KDKPRDLKSR GLCLV F V S CT Q H V GN E NGAD Y WAP A Y G S G F
Glyma07g02120.2:(Glyma07g02120.2 PACid:16265868	287	5.24e-38	KDKPRDLKSR GLCLV F V S CT Q H V GN E NGAD Y WAP A Y G S G F
Glyma07g02120.1:(Glyma07g02120.1 PACid:16265867	289	5.24e-38	KDKPRDLKSR GLCLV F V S CT Q H V GN E NGAD Y WAP A Y G S G F
Glyma08g04110.3:(Glyma08g04110.3 PACid:16269892	316	2.62e-36	EEANKDLRSR GLCLV F V S CT L Q V GS D NGAD Y WAP A F G G G FR
Glyma08g04110.1:(Glyma08g04110.1 PACid:16269890	343	2.62e-36	EEANKDLRSR GLCLV F V S CT L Q V GS D NGAD Y WAP A F G G G FR
Glyma05g35610.1:(Glyma05g35610.1 PACid:16260811	325	2.62e-36	EEPKKDLRSR GLCLV F V S CT L Q V GS D NGAD Y WAP A F G G G FR
Glyma07g09180.3:(Glyma07g09180.3 PACid:16266721	220	2.57e-35	EEPKKGLRSR GLCLV F V S CT L Q V GS D NGAD Y WAP A L G G G FR
Glyma07g09180.1:(Glyma07g09180.1 PACid:16266719	303	2.57e-35	EEPKKGLRSR GLCLV F V S CT L Q V GS D NGAD Y WAP A L G G G FR
Glyma02g15520.3:(Glyma02g15520.3 PACid:16248175	124	5.33e-29	GVEPCSLRSR GLCLV F V S VT I G V A E S N GAD I WAP I K T T T SPKFEKDVSQ
Glyma02g15520.1:(Glyma02g15520.1 PACid:16248173	126	5.33e-29	GVEPCSLRSR GLCLV F V S VT I G V A E S N GAD I WAP I K T T T SPKFEKDVSQ
Glyma07g32980.1:(Glyma07g32980.1 PACid:16268553	126	5.83e-29	GMEPCSLRSR GLCLV F V S FT I G V A E T N GAD I WAP I K T T T SPKFEKDVSQ
Glyma06g40760.1:(Glyma06g40760.1 PACid:16264777	458	6.22e-24	EGPKQDLRSR GLCLV F V S ST F V T H E P T V E Y W T P T F G G T YR