Table S4. Consistent sequences of the predicted AP2/ERF motifs in *L. cylindrica.*

Motif	E-value	Sites	Width	Best possible match
Motif1	5.8E-1922	131	21	RVWLGTFDTAEEAARAYDRAA
Motif2	1.9E-771	129	10	GKWVAEIRDP
Motif3	2.2E-790	124	11	KHYRGVRQRPW
Motif4	2.3E-679	121	15	IKMRGHKAKLNFPYL
Motif5	1.7E-329	12	41	VAHLRRKSSGFSRGVSIYRGVTRHHHHGRWQARIGRVFGNK
Motif6	6.6E-303	12	50	KQVYLGGYDKEEKAARAYDLAALKYWGPTTHTNFPISNYEKELEEMKHMT
Motif7	6.3E-83	19	26	ANSLPRPASMSPKDIQAAAAKAAAMT
Motif8	3.5E-53	9	21	RKVRIICYDPDATDSSSSEDE
Motif9	3.3E-47	4	45	PKGLSEILHAKLRKCCKTPSPSMTCLRLDTENCHIGVWQKRAGQR
Motif10	2.5E-40	5	29	FVDEEMIFDMPNLLMDMAEGMLLSPPRMN
Motif11	4.3E-40	7	29	EEDLKQMQNFSKEEFVHILRRQITGFKRG
Motif12	2.0E-35	4	29	CWNEGQNKKGRQVYLGAYDDEEAAAHAYD
Motif13	2.9E-31	9	16	VIVFEYLGDEYLEELL
Motif14	9.3E-30	4	26	QPVKKSRRGPRSRSSQYRGVTFYRRT
Motif15	1.0E-29	4	18	FDTCHVCRISGCLGCNFF
Motif16	1.6E-38	3	50	TFLEDFASLDDTQMFEFADDEPSGLLDWDFGDFGNDDISYWLDEPINIPC