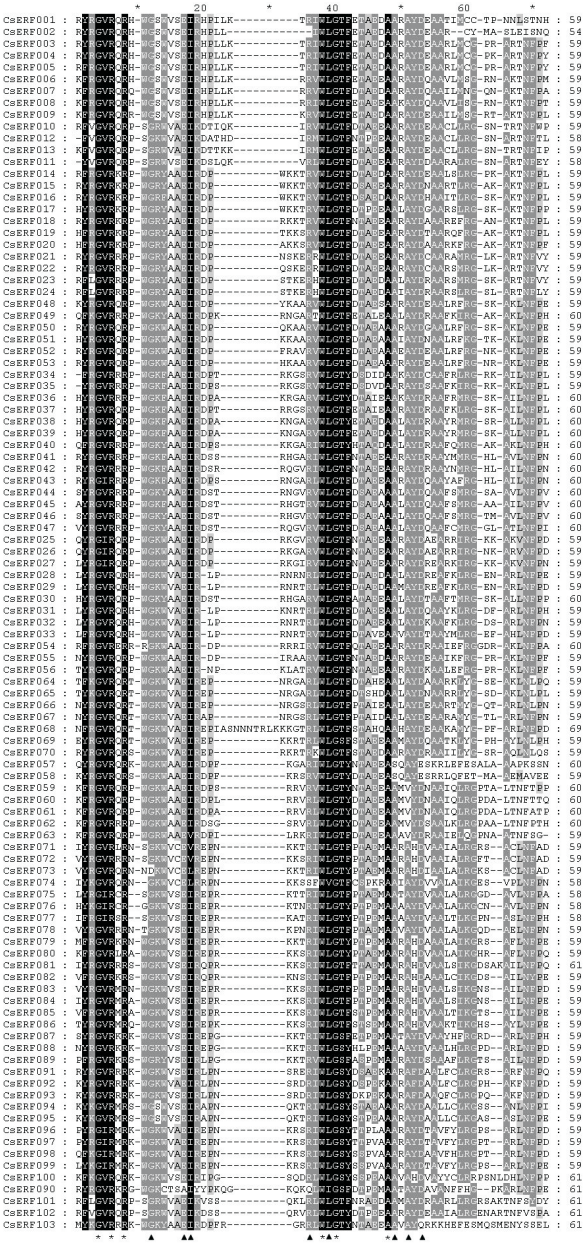

Figure S2 - Multiple sequence alignment of the AP2/ERF domains in 103 cucumber ERF proteins. The protein sequences were aligned using Clustal X software. Completely conserved residues among these proteins are marked with asterisks. Conserved residues among more than > 95% of the proteins are marked with filled-in triangles.