



S11 Fig. Sequence logos for plant Cesa/CsIF proteins. Sequence logos that highlight the frequency with which amino acids are found at particular positions for Cesa from *Arabidopsis thaliana* and *Oryza sativa*; and CsIF from *Brachypodium distachyon*, *Oryza sativa*, *Hordeum vulgare*, *Sorghum bicolor*, with additional CsIF6 from *Zea mays*, *Avena sativa*, *Triticum aestivum*, *Lolium multiflorum*. The font size of an amino acid represents the frequency with which that amino acid is found at that position, with the greater the size the greater the conservation. Amino acids are coloured by residue type: red, acidic; blue, basic; green, polar; neutral, purple; black, hydrophobic. Gaps were inserted into each sequence logo, based on the multiple sequence alignment of all proteins such that when stacked with the other logos, key conserved residues would align. Secondary structures based on the crystal structure of BcsA, and sites of key mutations (**S15 Table**) are also displayed.

Uniprot accession numbers used were: AtCesA1: O48946, AtCesA2: O48947, AtCesA3: Q941L0, AtCesA4: Q84JA6, AtCesA5: Q8L778, AtCesA6: Q94JQ6, AtCesA7: Q9SWW6, AtCesA8: Q8LPK5, AtCesA9: Q9SJ22, AtCesA10: Q9SKJ5, OsCesA1: Q6AT26, OsCesA2: Q84M43, OsCesA3: Q69V23, OsCesA4: Q5JN63, OsCesA5: Q851L8, OsCesA6: Q6YVM4, OsCesA7: Q9AV71, OsCesA8: Q84ZN6, ZmCsIF6: K7UFI6, AsCsIF6: A0A0R6UQB6, HvCsIF6: F2DMH9 TaCsIF6: A0A1D6C5K7, BdCsIF6: I1I1D2, OsCsIF6: A0A0R6UPD3, SbCsIF6: C5YHD7, LmCsIF6: (Wilson et al., 2015), OsCsIF8: Q84S18, HvCsIF8: B1P2T6, BdCsIF8: I1GTL1, OsCsIF9: Q7XHV0, HvCsIF9: B1P2T7, BdCsIF9: I1IAF2 SbCsIF4: A0A1W0W6N3, OsCsIF4: Q6ZF86, HvCsIF4: F2DP95, BdCsIF4: I1GTL2, OsCsIF1: Q6ZF89, OsCsIF2: Q84S11, OsCsIF3: Q6ZF85, HvCsIF3: B1P2T2, SbCsIF3: A0A1B6QEW4, BdCsIF3: I1GTL3, SbCsIF7: C5XAX7, SbCsIF1: A0A1B6QEV1, HvCsIF10: B1P2T8, BdCsIF10: I1GTL5, BdCsIF11: I1GTL9, SbCsIF2: A0A1B6QEU7, SbCsIF5: A0A1W0W4H7, SbCsIF10: A0A1B6QEV0