**Fig. 1. Supplementary data.** ProSA-web Z-score plot for the 3D structure of LHN2F fusion construct. The Z-score of the best model is –2.81 (A). The estimated normalized B-factor of LHN2F based on a Z-score (B).

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**Fig. 2. Supplementary data.** Evaluation of A/D) percentage of CAI (codon adaptation index), B/E) FOP (frequency of optimized codons) and C/F) C.G. percentage of protein fusion sequence after gene optimization for expression in *E. coli* (A-B-C) and maize (D-E-F) hosts. The codons changed, so G.C. percentage and CAI increased in the sequence in optimizing the gene for expression in both hosts.

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**Fig. 3. Supplementary data.** Prediction of mRNA structure using Mfold server. The area in the red box displays the structure at a higher magnification—mRNA structure of *E.coli* (A) and maize (B) constructs.



