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## Supplementary Material

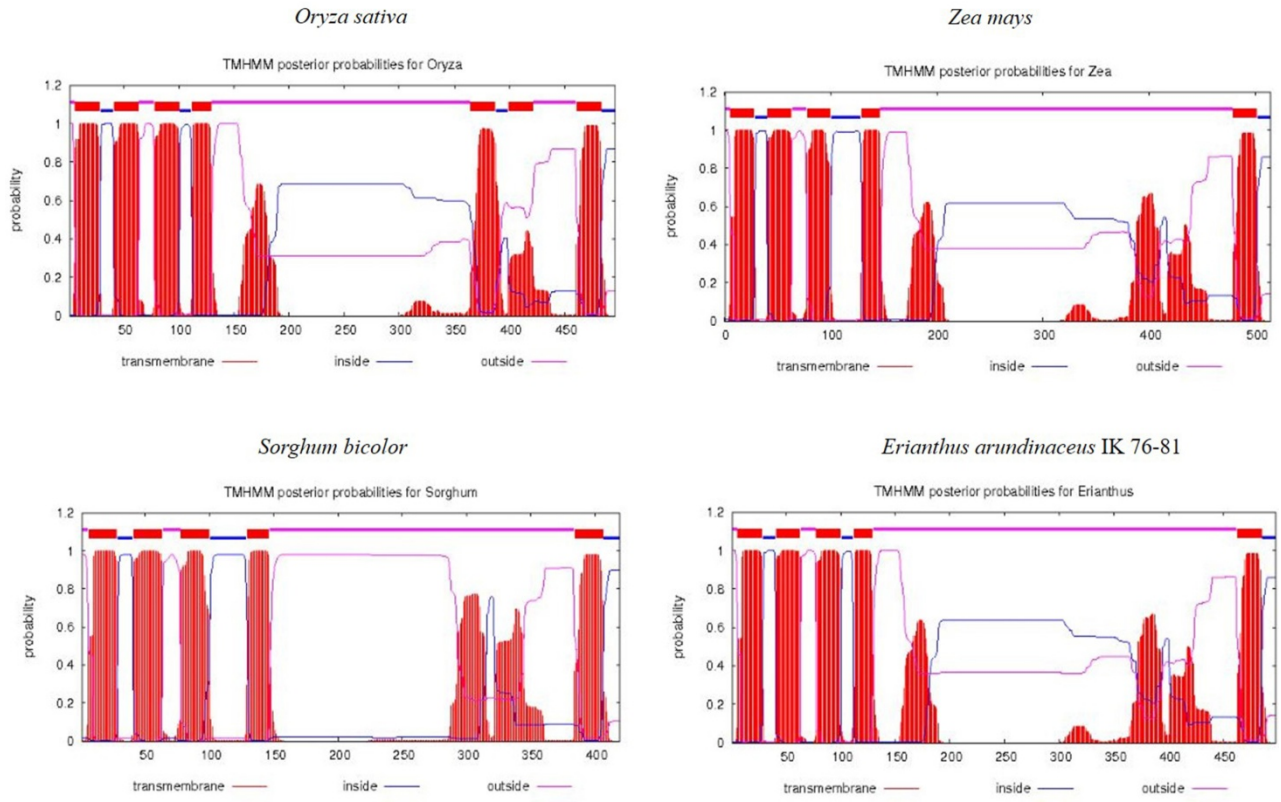
### ***In silico* characterisation and functional validation of chilling tolerant divergence 1 (COLD1) gene in monocots during abiotic stress**

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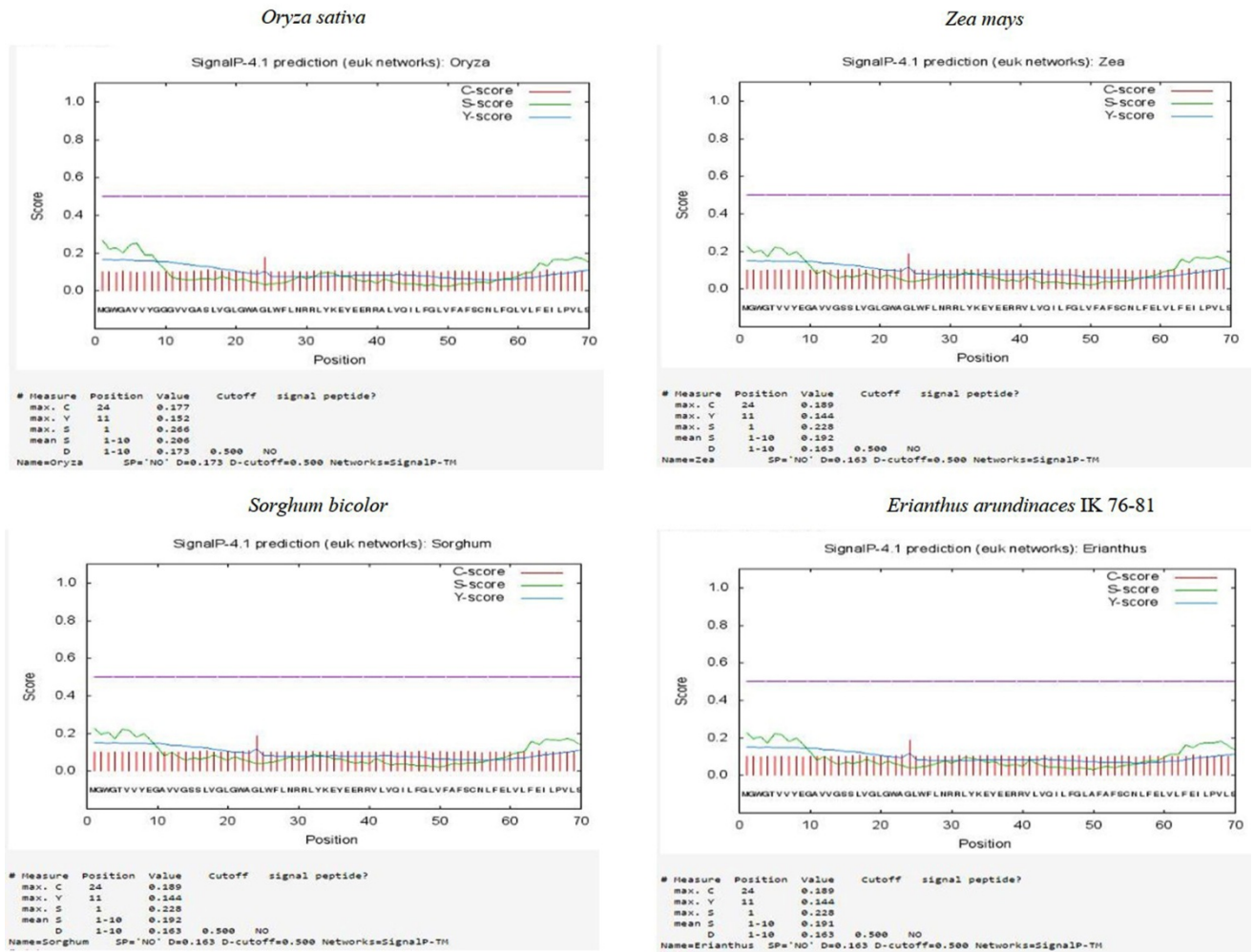
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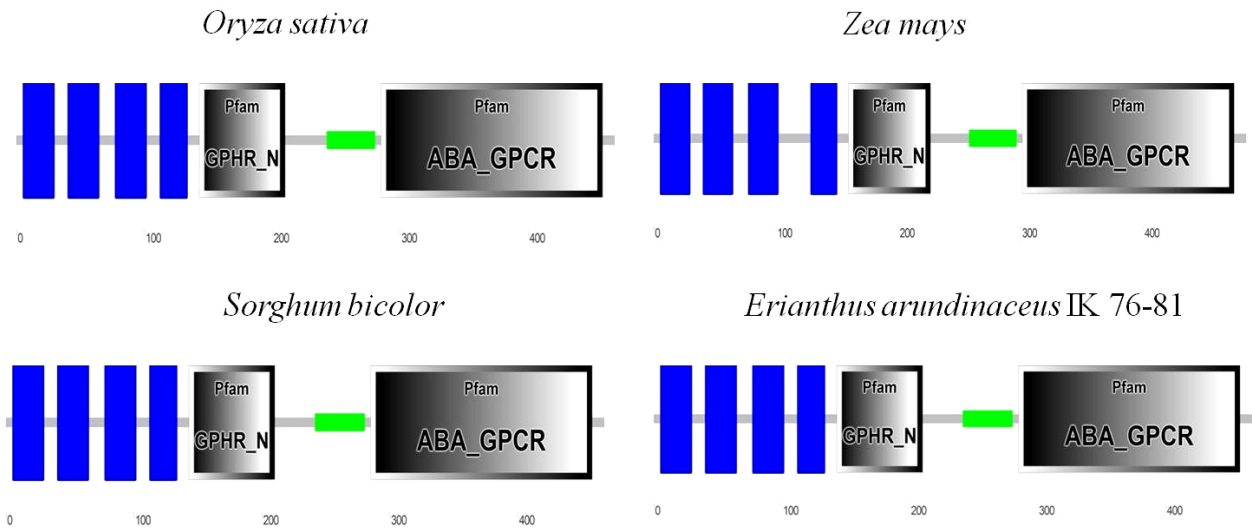
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**Fig. S1.** TMHMM topology for the studied monocot crops.



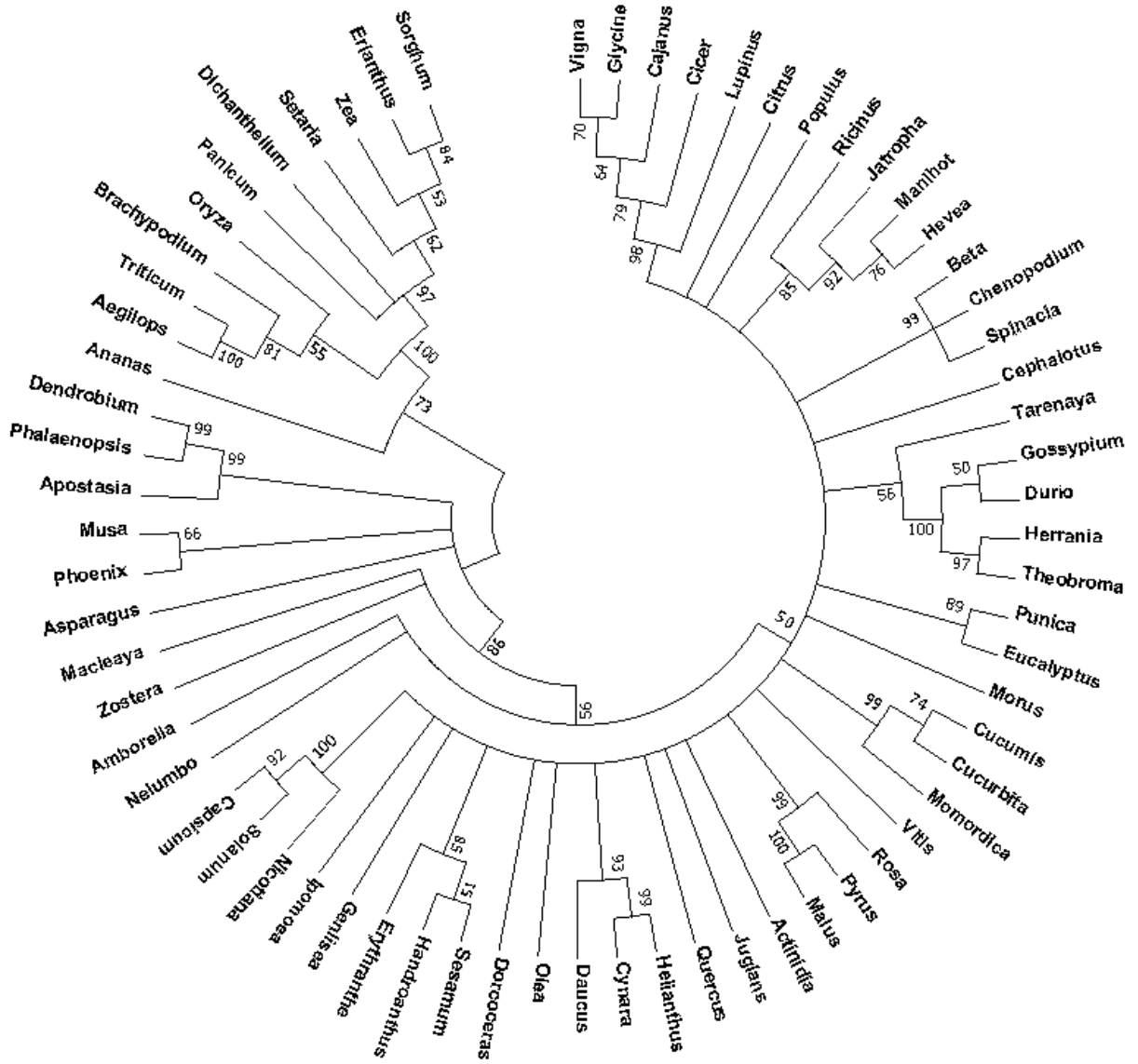
**Fig. S2.** Signal peptide analysis for the studied monocot crops using SignalP4.1 server. Outputs are in three different forms i.e. S, D and Y score. S-score, the average mean of the possible signal peptide; D-score (discrimination score) describes the weighted average of the mean S and the max; Y scores used to discriminate signal peptides from non-signal peptides.



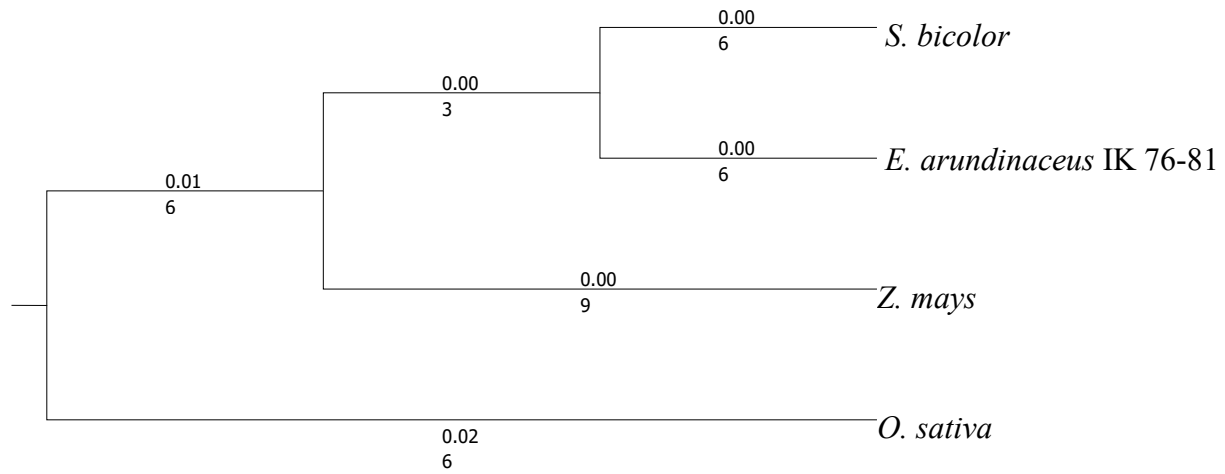
**Fig. S3.** Domain prediction using Pfam and SMART for the studied monocot crops.



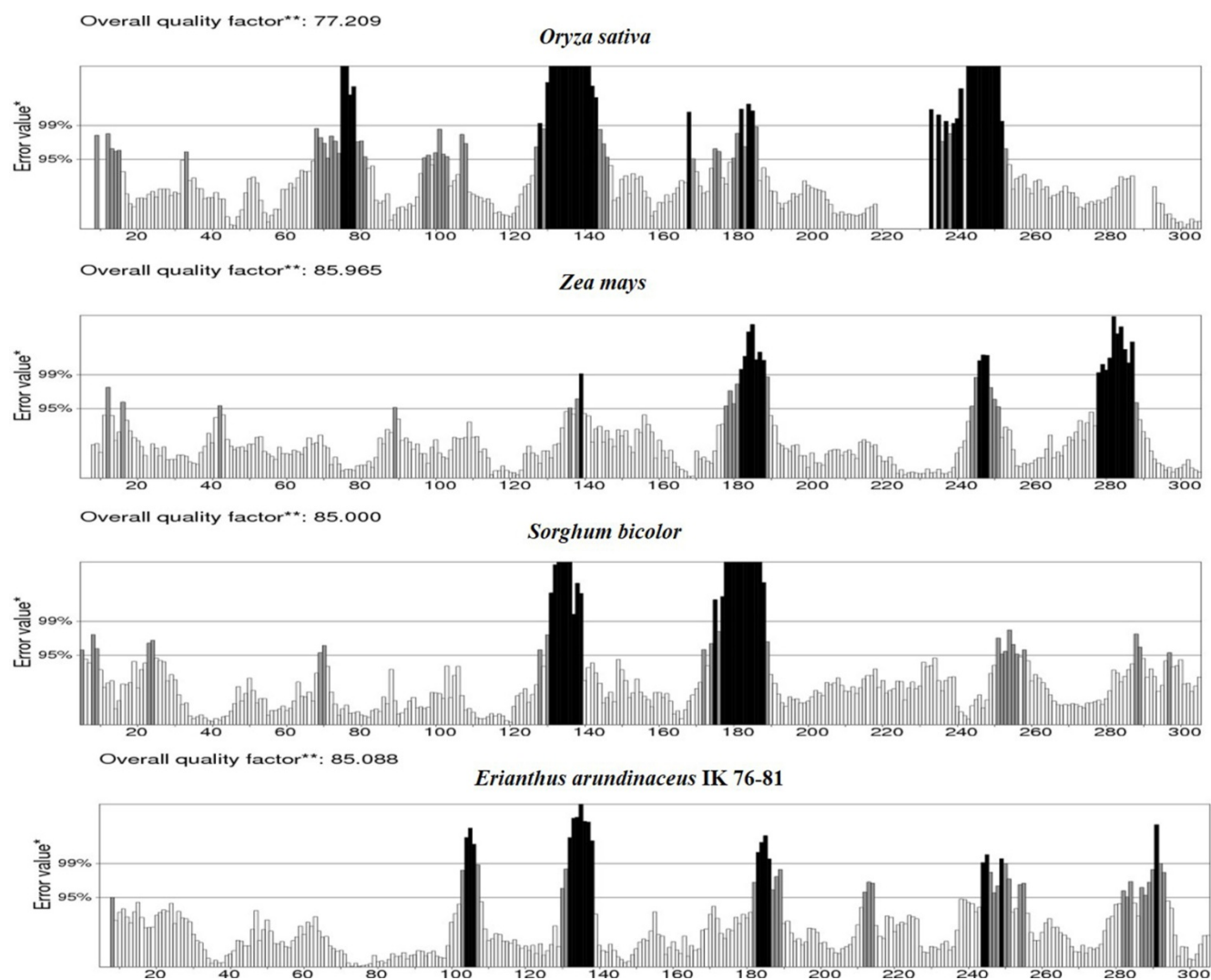
(a)



(b)

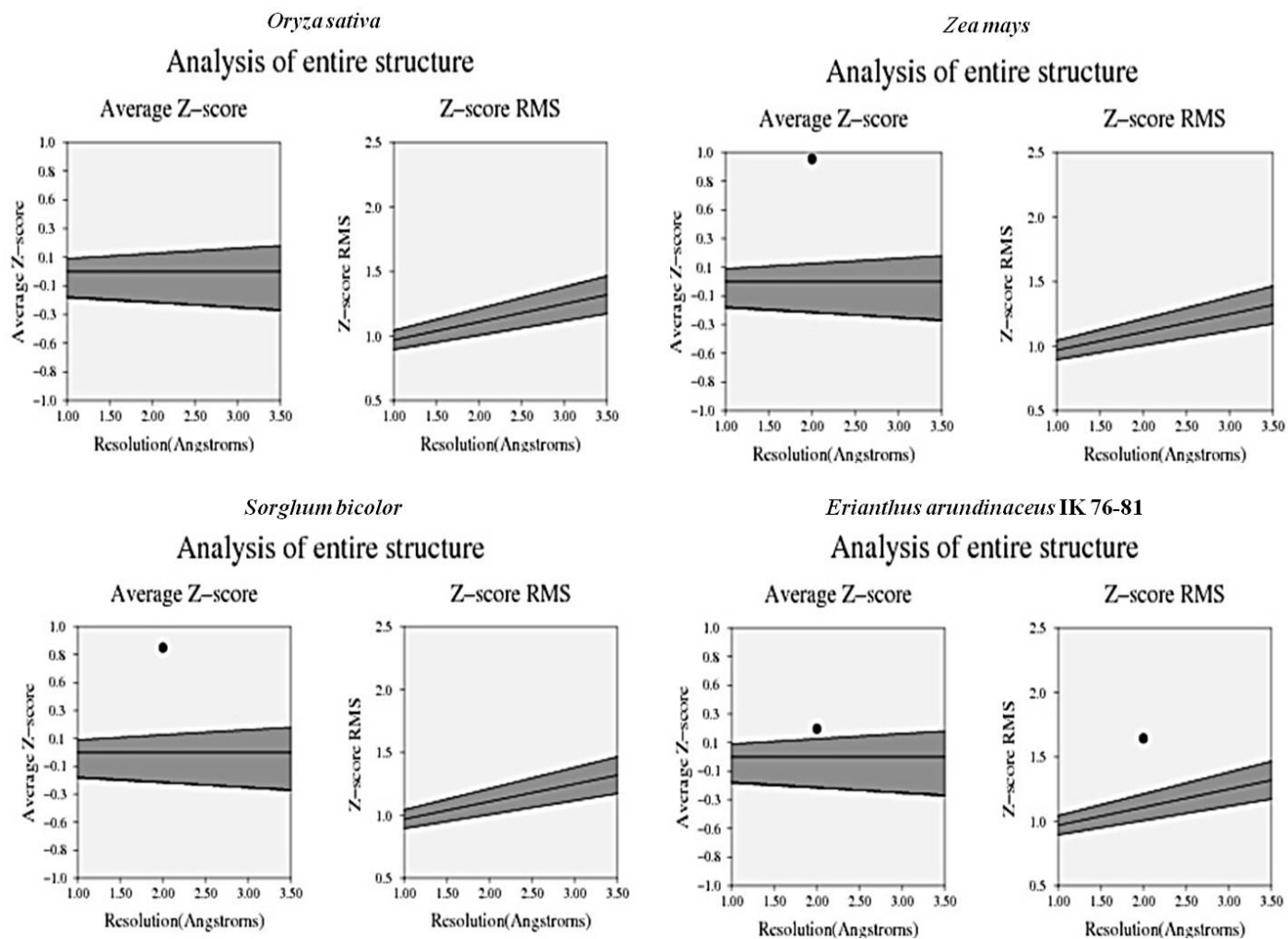


**Fig. S5.** (a) Phylogenetic analysis of COLD1 proteins using BLAST sequence (67 sequences); (b) Phylogenetic analysis of COLD1 proteins using MEGA7 software for the studied monocot crop species.



**Fig. S6.** ERRAT analysis of studied for the studied monocot crop species. Error value is represented on X axis, two lines drawn to indicate the confidence and possibility to reject regions that exceed error value. Overall quality factor is expressed as the percentage of the protein calculated. 95% or higher provide good high-resolution structures. For lower resolutions (2.5 to 3Å) the average overall quality factor is around 91%.





**Fig. S7.** PROVE analysis of studied COLD1 proteins. Output shows the level of Z score. 2.0 Å or better is highly resolved structures for the studied monocot crop species.

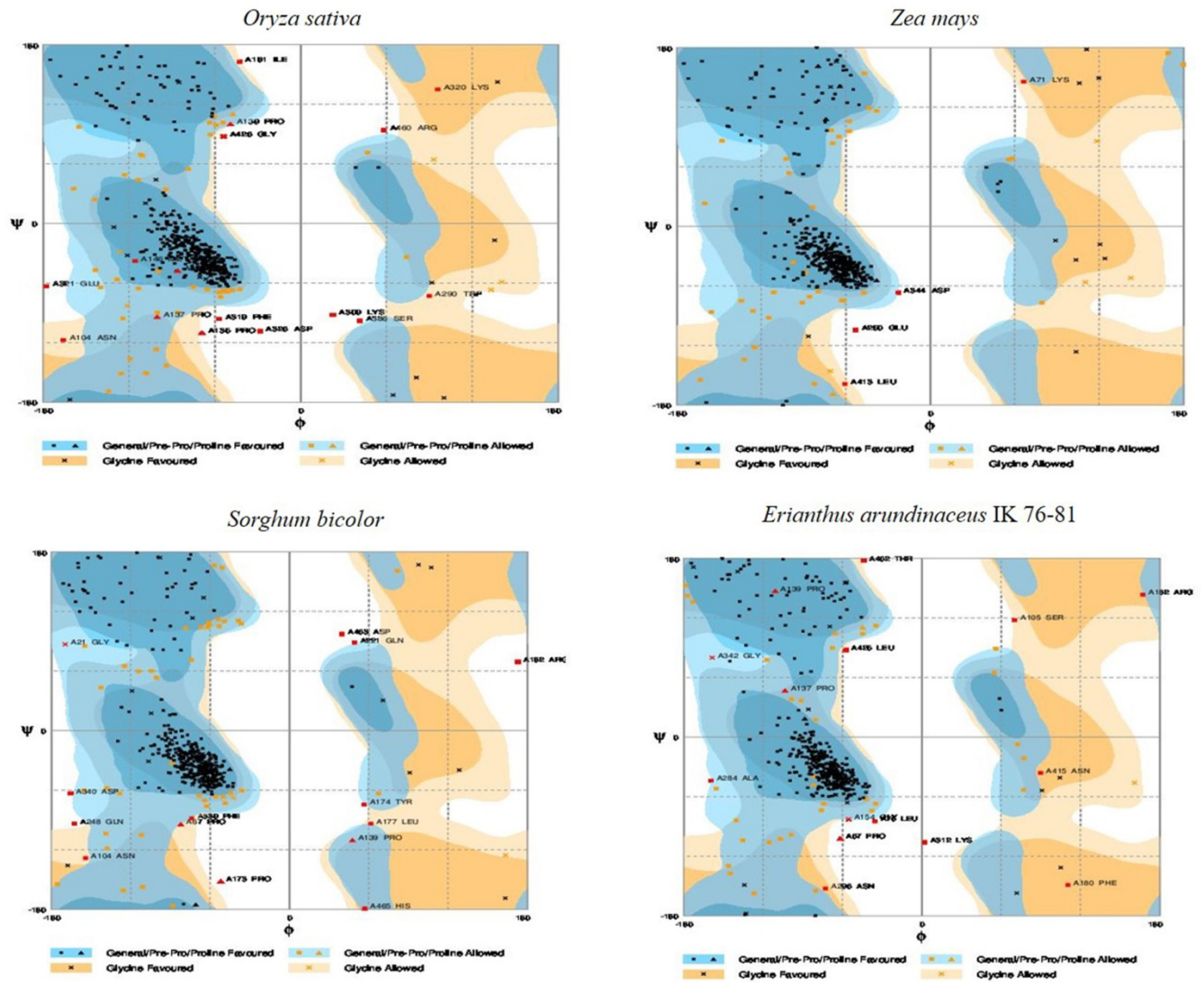
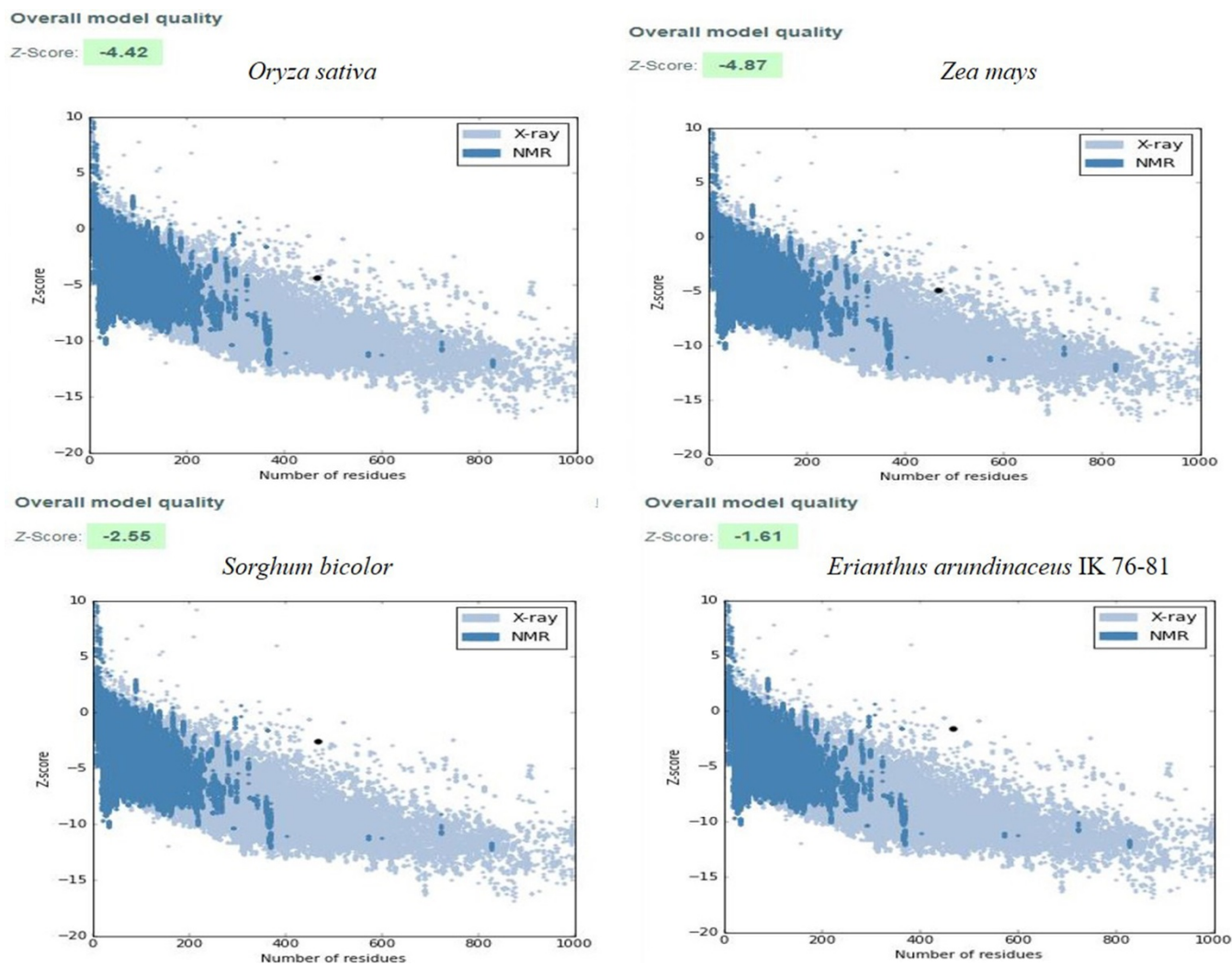


Fig. S8. Ramachandran plot using RAMPAGE for the studied COLD1 proteins.



**Fig. S9.** ProSA analysis for the studied monocot crop species. Output display Z-scores, which indicate the overall model quality represented by large black dot. All protein chains in PDB are determined from different sources by X-ray crystallography and NMR spectroscopy with respect to their length.

**Table S1. qRT-PCR primers designed for the studied monocot crop species using IDT software**

<b>S.NO</b>	<b>PLANT</b>	<b>Primers</b>	<b>Internal gene reference</b>
1	<i>Oryza sativa</i>	Cold1 Fw - TGGCGTGATTGGAGTAAGTG Cold1 Rv - CATGAGCTGCCTTTCCAATG UBQ5 Fw - ACCACTTCGACCGCCACTACT UBQ5 Rv - ACGCCTAAGCCTGCTGGTT	Jain et al (2006) Sakuraba et al (2017)
2	<i>Zea mays</i>	Cold1 Fw - TTCACTTCCCCATGCCTTC Cold1 Rv - CTCCAATCACCCCAATCCTAC Tubulin Fw - AGAACTGCGACTGCCTCCAAAG Tubulin Rv - AGATGAGCAGGGTGCCCATTC	Galli et al (2013) Lin et al (2014)
3	<i>Sorghum bicolor</i>	Cold1 Fw - CCGCTGGTTTGATGCTATATTTG Cold1 Rv - GATGCTTGTCTGTTTGCCTG PP2A Fw - AACCCGCAAAACCCAGACTA PP2A Rv - TACAGGTCGGGCTCATGGAAC	Reddy et al (2016)
4	<i>Erianthus arundinaceus</i> IK 76-81	Cold1 Fw - CGCAGTTGGTCAGTAGGATT Cold1 Rv - CCTGATGAAGAGCGACAGATAA GAPDH Fw - CACGGCCACTGGAAGCA GAPDH Rv - TCCTCAGGGTTCCTGATGCC	Iskandar et al 2012 Guo et al 2014 Ling et al 2014 Silva et al 2014 Andrade et al 2017

**Table S2. Similarity percentage of *Erianthus arundinaceus* IK 76-81 protein sequence with *Oryza sativa*, *Zea mays* and *Sorghum bicolor* obtained using Emboss needle tool**

<i>Erianthus arundinaceus</i> IK 76-81	<i>Oryza sativa</i> (%)		<i>Zea mays</i> (%)		<i>Sorghum bicolor</i> (%)	
	Similarity	Identity	Similarity	Identity	Similarity	Identity
	97.6	95.3	96.3	95.2	76.1	76.1