燕麦盐碱响应基因 *AsGolS2* 的克隆及互作蛋白的筛选

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Cloning of the Saline-Alkali Response Gene *AsGolS2* and Screening of Interacting Proteins in Oat

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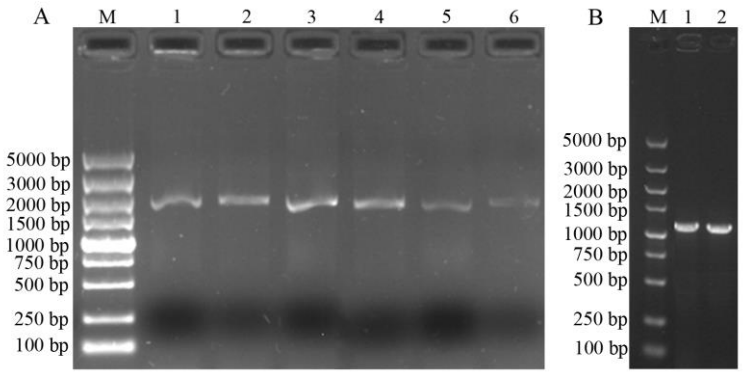
附表 1 本研究所用的引物序列
Table S1 Primer sequences used in this study

引物名称 Primer name	引物序列 Primer sequence (5′-3′)	用途 Usage
AsGolS2-F1	CCAACGAATCGCGTGACTG	gDNA 扩增
AsGolS2-R1	TGCTGGTGCGGGTAATCTG	
AsGolS2-F2	CATATGGCCATGGAGGCCGAATTCatggcacccatggcgctcaagggtgt	cDNA 扩增；
AsGolS2-R2	GGCCGCTGCAGGTCGACGGATCCCctatgcggcggagggcgcggggtagtactt	载体构建
AsGolS2-F3	AGTCGGCGTACCCGTTAGTG	qPCR
AsGolS2-R3	CATGGCGAACTGGGTCTGAC	
AsGAPDH-F	TTCTTCCTGAGTTGAACGGC	内参基因
AsGAPDH-R	ATGCAGCCTTCTCGATTCTG	
T7	TAATACGACTCACTATAGGG	载体测序
3-BD	TAAGAGTCACTTTAAAATTTGTATAC	

附表 2 生物信息学分析工具
Table S2 Bioinformatics tool

软件 Software	网址 Website	用途 Usage
Plant CARE	https://bioinformatics.psb.ugent.be/webtools/plantcare/html/	启动子顺式作用元件分析
Expasy	https://web.expasy.org/protparam/	理化性质分析
ProtScale	https://web.expasy.org/protscale/	亲疏水性分析
TMHMM-2.0	https:// services.healthtech.dtu.dk/services/TMHMM-2.0/	跨膜结构域预测
NetPhos	https://services.healthtech.dtu.dk/services/NetPhos-3.1/	磷酸化位点预测
Smart	https://smart.embl.de/	结构域分析
SOPMA	https://npsa.lyon.inserm.fr/cgi-bin/npsa_automat.pl page=/NPSA/npsa_sopma.html	二级结构预测
SignalP 6.0	https://services.healthtech.dtu.dk/services/SignalP-6.0/	信号肽预测
GSDS 2.0	https://gsds.gao-lab.org/	基因结构分析
MEGA 11		系统发育树构建

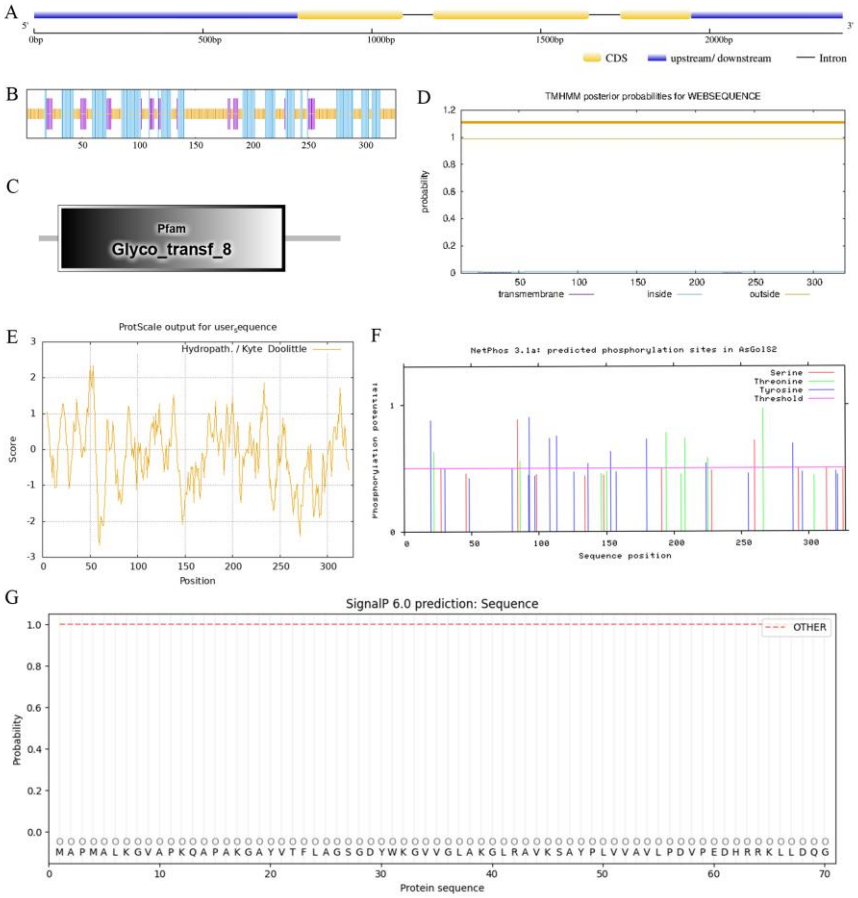


A：*AsGolS2* 基因 gDNA 扩增。M：DL5000，1–6 分别为加燕 2 号、定莜 2 号、晋燕 17 号、白燕 2 号、白燕 5 号和草莜 1 号；
B：*AsGolS2* 基因 cDNA 扩增。M：DL 5000，1–2：品种定莜 2 号

A: Amplification of gDNA for the *AsGolS2* gene. M: DL5000; 1-6 correspond to the following oat cultivars: Jiayan 2, Dingyou 2, Jinyan 17, Baiyan 2, Baiyan 5, and Caoyou 1, respectively. B: Amplification of cDNA for the *AsGolS2* gene. M: DL5000; 1 and 2 both represent the cultivar Dingyou 2

附图 1 燕麦 *AsGolS2* 基因的扩增

Fig. S1 Amplification of the *AsGolS2* gene in oat (*Avena sativa* L.)



A：基因结构图；B：二级结构预测；C：蛋白结构域预测；D:跨膜结构预测；E：亲疏水性预测；F：磷酸化位点预测；G：信号肽预测

A: Gene structure diagram. B: Secondary structure prediction. C: Protein domain prediction. D: Transmembrane structure prediction E: Hydrophilicity and Hydrophobicity prediction. F: Phosphorylation sites prediction. G: Signal peptide prediction

附图 2 *AsGolS2* 的生物信息学分析

Fig. S2 Bioinformatics analysis of *AsGolS2*