

**Supplementary Data****Identification and promoter analysis of some important storage protein genes from wheat (*Triticum aestivum* L.)**Jiarui Li<sup>1,2\*</sup>, Baoyan An<sup>3</sup> and Xiansheng zhang<sup>1</sup>**1. 6A4 (Genbank accession No. AF469489)****Sequence:**

GGGAGCAAAGCAAACCTTGAGGCTAGCCACCATGAAGGTCTTCATCCTGGCTCTCCTCG  
CCCTCACAGCAACCACCGCCATTGCCAGTTGGAAACCACATGTAGCCAGGGCTTCGG  
ACAATACCAACAACAGCAACAACCTGGGCAACGACAGTTGCTGGAGCAGATGAAGCC  
GTGTGTGGCATTCTCTGCAACAACAGTGTAGGCCACTGAGAATGCCATTCTCCAGACA  
CAGGTGGAGCAGCTTAGCAGCTGCCAGATCGTGCAACACCAATGCTGCCAGCAGCTAG  
CGCAGATCCCAGAGCGAATCCGGTGCCATGCCATCCACAGCGTGGTAGAGGCTATCAT  
GCAACAACAATCCCAACAACAATGGCAGGAGCGCCAACAGCAAGCACAACATAAGAG  
CATGAGGATGTTGCTTGAGAACCTATCATTGATGTGCAACATCTATGTCCCGGTACAAT  
GCCAGCAGCAACAACAATGGGGCAACAACAACAACAACAACAGTTGCAGGAGCAGT  
TGACACCGTGTGCGACATTCTCCAACATCAGTGTAGCCCAGTGACAGTGCCATTCCCC  
CAGATACCGGTGGATCAAGCCTACCAGCTGCCAGAATGTGCAGCACCAATGTTGCCGA  
CAGCTATCACAGATCCCGGAGCAATTTTCGTTGCCAAGCCATCCATAACGTGGCTGAGG  
CTATCAGGCAACAACAACCCCAACAACAATGGCAGGGTATGTACCAGCCCGCAGCA  
AGCCAGCACAACATGAGAGCATTTCGGATGTTCGCTTCAGGCCCTGCGGTCGATGTGCAAC  
ATCTACATACCGGTACAATGCCCCGCCCCACCGCCTACAACATTCCCATGGTGGCTACC  
TGCACTAGTGGTGCATGCTAGATGATCAATGTAGCGGCCGAAAAATAAAAATGCCATGCA  
TCATCATGTGTGGCAAATACTAGTTGCAATATGGAAATGATGAATAAACGTTCTGAATA  
AAGCATTTCCTGAATAAAACTACATATTTCAAAAAAAAAAAAAAAAAAAAAA

**Note:** Underlined sequence (482-bp) was used as template for synthesizing probes for Northern blot and Southern blot.

AF469489	GSKANLRLATMKVFILALIALTATTATAIAQIETTCSQGFQQ	40
AM087941	.....MKVFILALIALTATTATAIAQIETTCSQGFQQ	30
Consensus	mkvfilalialtattataiaqlettcsqgfgq	
AF469489	YQQQQQPGQRQLLEQMKPCVAFLQQCRPIRMPFLQTQVE	80
AM087941	YQQQQQPGQRQLLEQMKPCVAFLQQCRPIRMPFLQTQVE	70
Consensus	yqqqqqpgqrqlleqrkpcvafllqqqcrplrmpflqtqve	
AF469489	QLSSCQIVQHQQCCQQLAQIPERIRCHAIHSVVEAIMQQQS	120
AM087941	QLSSCQIVQHQQCCQQLAQIPERIRCHAIHSVVEAIMQQQS	110
Consensus	qlsscqivqhqqccqqlaqiperirchaihsvveaimqqqs	
AF469489	QQQWQERQQQACHKSMRMLLENISLMCNIYVPVQCCQQQQ	160
AM087941	QQQWQERQQQACHKSMRMLLENISLMCNIYVPVQCCQQQQ	150
Consensus	qqqwqerqqqaghksrmlllenlslrcniyvpvqcqqqqq	
AF469489	MGQQQQQQQLQEQLTFCATFLQHQCSPVTVPFQIPVD	198
AM087941	MGQQQQQQQLQEQLTFCATFLQHQCSPVTVPFQIPVD	188
Consensus	rgqqqqqqqlqeqltfcatflqhqcspvtvpfpqipvd	

**Note:** The putative amino acid sequence of 6A4 was blasted with amino acid sequence of a putative avenin-like b precursor (AM087941) using DNAMAN software. The sequence similarity between the two sequences is 95% similarity (189/199).

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## 2.8G17 (Genbank accession No. HQ833341)

### Sequence:

AAAAGTACGCTTGTAGCTAGTGCAACCTAACACAATGTACCAAAAATCCATTTCAGAA  
ACATCCAAACATAATTATTAAGCTGATGGAAAGAAGGAAAGAGATGGTGCCCGGGC  
TACTATAAATAGGCATGAAGTATCAAGATCATCACAGGCACAATCATCAAACCAAGC  
AATACTAGTTAACACCAATCCACCATGAAGACCTTCTCATCTTTGCTCTCCTTGCCATT  
GCGGCGACAAGTGCCATTGCACAAATGGAGACTAGCCGCGTCCCTGGTTTGGAGAAAC  
CATGGCAGCAACAACCATTACCACCACAACAACCACCATGTTACAGCAACAACA  
ACCATTTCCACAGCAACAACAACCAATTATTATACTGCAACAATCACCATTTTCGCAGC  
AACAACAACCAGTTCTGCCGCAACAGCAACCAGTTATTATACTGCAACAACCACCATT  
TTCGCAGCAACAACAACCAGTTCTACCACAACAACCACCATTTTCACAACAACAACA  
CCACCATTTTCGCAGCAGCACACATTCTTACAACAACCACCTTTTCCACAACAACCA  
ACAGTTTCCACAACAACAATCCCTGTTGTTCAACCATCCGTTTTGTCAGCAGCTAAACC  
CATGCAAGGTGTTCCCTCAACAGCAGTGTAGCCATGTGGCAATGTCGCAACGTCTTGCT  
AGGTCACAAATGTGGCAACAGAGTAGTTGCCATGTGATGCAACAACAATGTTGCCAAC  
AGCTGCCGCAAATCCCCGAACAATCCCGCTCTGAGGCAATCCGTGCCATCGTCTACTCC  
ATCATCCTGCAAGAACAACAACAGGGTTTTGTCCAACCTCAGCAGCAACAACCCCAAC  
AGTCGGGCCAAGGCGTCTCCCAACACCAACAGCAGTCGCAGCAGCAGCAGCAACTCG  
GACAGTGTCTTTCCAACAACCTCAACAACACTACAACAATTGGGTCAGCAGCCTCAACA  
ACAACAGATACCACAGGGTATATTCTTGCAGCCACACCAGATATCTCAACTTGAGGTG  
ATGACTTCCATTGCACTCCGTACCTTGCCAACGATGTGCGGTGTCAACGTGCCGTTGTA  
CAGCTCGACCACTATTATGCCATTCAGCATTGGCACTGGAGTTGGTGGCTACTGATAAG  
AAAAGATTCTAGTAATAT

**Note:** Underlined sequence (436-bp) was used as template for synthesizing probes for Northern blot.

HQ833341	MKTFLIFALLAIAATSIAIQMETSrvpGLEKpwQQQPLPP	40
AB062867	MKTFLIFALLAIAATSIAIQMETSrvpGLEKpwQQQPLPP	40
Consensus	mktflifallaiiaatsaiiqmetsrvpglekpwqqqplpp	
HQ833341	QQQPpCSQQQQPFpQQQQPIIILQQSPFSQQQQPVLpQQQ	80
AB062867	QQQPpCSQQQQPFpQQQQPIIILQQSPFSQQQQPVLpQQQ	80
Consensus	qqqppcsqqqqpfpqqqqpiiilqqspfsqqqqpvlpqqq	
HQ833341	PViiLQQPPFSQQQQPVLpQQPPFSQQQQPPFRSSTHSSQ	120
AB062867	PViiLQQPPFSQQQQPVLpQQPPFSQQQQPPFRSSTHSSQ	120
Consensus	pviilqqppfsqqqqpvlpqqppfsqqqqppfrssthssq	
HQ833341	QPPFPQQHQQFpQQQIPVVQPSVLQQLNpCKVfLQQQCSH	160
AB062867	QPPFPQQHQQFpQQQIPVVQPSVLQQLNpCKVfLQQQCSH	160
Consensus	qppfpqqhqfqfpqqqipvvqpsvlqqlnpckvflqqqcs	
HQ833341	VAMSQRlARSQmWQQSSCHVMQQQCCQQLPQIPEQSRSEA	200
AB062867	VAMSQRlARSQmWQQSSCHVMQQQCCQQLPQIPEQSRSEA	200
Consensus	vamsqrlarsqmwwqqsschvmqqqccqqlpqipeqsrsea	
HQ833341	IRAIvYSiiLQEQQQGFVQpQQQQPQQSGQGVsQHQQQSQ	240
AB062867	IRAIvYSiiLQEQQQGFVQpQQQQPQQSGQGVsQHQQQSQ	240
Consensus	iraiivysiilqeqqqgfvpqqqqppqqsgqgvsqhqqqsq	
HQ833341	QQQQLGQCSFQQPQQLQQLGQQPQQQQIPQGIFLQPHQIS	280
AB062867	QQQQLGQCSFQQPQQLQQLGQQPQQQQIPQGIFLQPHQIS	280
Consensus	qqqqlgqcsfqqpqqllqqlgqqppqqqipqgiflqphqis	
HQ833341	QLEVMTSIALRtlPTMCGVNVPLYSSTTimpFSIGTGVGG	320
AB062867	QLEVMTSIALRtlPTMCGVNVPLYSSTTimpFSIGTGVGG	320
Consensus	qlevmtsialrtlptmcgvnvplyssttimpfsigtgvvgg	

**Note:** The putative amino acid sequence of 8G17 was blasted with amino acid sequence of LMW-GS group 5 type III (AB062867) using DNAMAN software. The sequence similarity between the two sequences is 100% (320/320).

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### 3.6H11 (Submission No. 1503702)

#### Sequence:

CCCAGGCGGTGTCCCGGCAACTATAAATAGGCATGAAGTATAAAGATCATCACAAGCA  
CAAGCATCAAAGCCAAACAACACTAGTTAACACCAATCCACAATGAAGACCTTCCTCG  
TCTTTGCCCTCCTCGCTCTTGCGGCGGCAAGTGCCGTTGCGCAAATTCACAGCAACAA  
CAACAACCACCATTTTCACAGCAACAACAACCACAATTTTCACAACAGCCACCATTTTC  
CCAGCAGCAACAACCACCATTTTCGCAACAACAACAACAACCACCATTTGCGCAGCAA  
CAACAACCACCGTTTTTCACAACAACCACCAATTTTCACAGCAGCAACAACCACCATTTTC  
ACAGCAACAACAACCACAATTTTCACAGCAACAACAACCACCATATTCGCAGCAACAA  
CAGCCACCATATTCGCAGCAACAACAACCACCATTTTCGCAGCAACAACAACCACCAT  
TTTCGCAGCAACAACAACAACCACCATTTACACAGCAGCAGCAGCAGCAACAACAACA  
ACAACCATTTACACAGCAACAACAACCACCATTTTCACAACAGCCACCAATTTTCACAG  
CAGCAACAACCACCATTTTCGCAGCAACAACAACCACAATTTTCACAGCAACAACAAA  
TACCAGTTATTCATCCATCTGTTTTGCAGCAGCTAAACCCATGCAAGGTATTCCTCCAG

CAGCAGTGCATCCCTGTGGCAATGCAGCGATGTCTTGCTAGGTCACAAATGTTGCAGC  
 AGAGCATTTGCCATGTGATGCAGCAACAATGTTGCCAGCAGTTGCGGCAAATCCCCGA  
 GCAATCCCGCCATGAGTCAATCCGTGCTATCATCTACTCTATCATCCTGCAGCAGCAGC  
 AGCAGCAACAACAACAACAACAACAGGGTTCAGAGTATCATCCAATATCAGCAACAAC  
 AACCCCAACAGTTGGGCCAATGTGTCTCCCAACCCCAACAGCAGTTGCAGCAGCAACT  
 CGGGCAACAACCTCAACAACAACAATTGGCACATGGTACCTTTTTTGCAGCCACACCAG  
 ATAGCTCAGCTTGAGGTGATGACTTCCATTGCACCCCGTACCCTGCCAACAATGTGCAG  
 TGTC AATGTGCCGTTGTACGAAACCACCCTAGTGTGCCATTAGGCGTTGGCATCGGA  
 GTTGGTGTCTACTGATAAGAAAAGATCTCTAGTAATATATAGTTGGATCACCGTTGTTT  
 AGTCGATGGATATGTCAATGTAGCGGTGACAAATAAAGTGTACACAACGTCATGTGT  
 GACCCGCTCAAACCTAGTTGTTTAAATTCTGAAATAAAATACAAATAAAGTTGTATCAA  
 AAAAAAAAAAAAAAAAAA

**Note:** Underlined sequence (380-bp) was used as template for synthesizing probes for Northern blot.

6H11	<u>MKTFLV FALL LALAA SAVAQISQQQQQPPFSQQQQPQFSQ</u>	40
FJ549930	<u>MKTFLV FALL LALAA SAVAQISQQQQQPPFSQQ</u> .....Q	34
Consensus	mktflvfallalaaasavaqisqqqqppfsqq	q
6H11	<u>QPPFSQQQQP PFSQQQQQPPFAQQQQPPFSQQPPISQQQQ</u>	80
FJ549930	<u>QPPFSQQQQS PFSQQQQQPPFLQQQQPPFSQQPPISQQQQ</u>	74
Consensus	qppfsqqqq pfsqqqqppf qqqppfsqqppisqqqq	
6H11	<u>PPFSQQQQPQFSQQQQPPYSQQQQPPY</u> .....SQQQQ	112
FJ549930	<u>PPFSQQQQPQFSQQQQPPYSQQQQPPYSQQQQPPFSQQQQ</u>	114
Consensus	ppfsqqqqp qfsqqqqppysqqqqppy	sqqqq
6H11	<u>PPFSQQQQPPFSQQQQPPFT</u> .....QQQQ	137
FJ549930	<u>PPFSQQQQPPFSQQQQPPFTQQQQPSFSQQPPISQ</u> QQQQ	154
Consensus	ppfsqqqqppfsqqqqppft	qqqq
6H11	<u>QQQQQQPFTQQQQPPFSQQPPISQQQQPPFSQQQQPQFSQ</u>	177
FJ549930	<u>QQQQQQPFTQQQQPPFSQQPPISQQQQPPFSQQQQPQFSQ</u>	194
Consensus	qqqqqqpftqqqqppfsqqppisqqqqppfsqqqqp fsq	
6H11	<u>QQQIPVIHPSVLQQLNPCKVFLQQQCPVAMQRCLARSQM</u>	217
FJ549930	<u>QQQIPVIHPSVLQQLNPCKVFLQQQCPVAMQRCLARSQM</u>	234
Consensus	qqqipvihpsvllqqlnpckvflqqqcpvamqrclarsqm	
6H11	<u>LQQSICHVMQQQCCQQLRQIPEQSRHESIRAIYSIILQQ</u>	257
FJ549930	<u>LQQSICHVMQQQCCQQLRQIPEQSRHESIRAIYSIILQQ</u>	274
Consensus	lqqsihvmqqqccqqlrqipeqsrhesiraiiysiilqq	
6H11	<u>QQQQQQQQQQGQSI IQYQQQQPQQLGQCVSQPQQQLQQQL</u>	297
FJ549930	<u>QQQQQQQQQQGQSI IQYQQQQPQQLGQCVSQPQQQLQQQL</u>	314
Consensus	qqqqqqqqqqgqsi iqyqqqqpqqlgqcvsqppqqqlqqql	
6H11	<u>GQQPQQQQLAHGTF LQPHQIAQLEVMTSIA</u> RTLPTMCSV	337
FJ549930	<u>GQQPQQQQLAHGTF LQPHQIAQLEVMTSIA</u> RTLPTMCSV	354
Consensus	gqqppqqqqlahgtflqphqiaqlevmtsia rtlptmcsv	
6H11	<u>NVPLYETTTSVPLGVGIGVGV</u>	358
FJ549930	<u>NVPLYETTTSVPLGVGIGVGV</u>	375
Consensus	nvplyetttsvplgvigvgv	

**Note:** The putative amino acid sequence of 6H11 was blasted with amino acid sequence of LMW-GS GluA3-13 (FJ549930) using DNAMAN software. The sequence similarity between the two sequences is 91% (349/382).