

Functional Analysis of Maize Silk-Specific *ZmbZIP25* Promoter

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>GRMZM2G080731 | 8:119662868..119665630 forward
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TGTCATTTGTGCTCTTGTGCTGGCAACGAAATCAAGCTGAATCATAAGAAACCAANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
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TACTGAATGCGCGTTGTGCTGCGTAGGACACGTATGGCGAGCTAGCCTACAGATAAGCCTGGGGAATGGTTTCATATGCATCCGGCTCGCGCAGGTTTCT
GGCATCGAGCAGTCTGCGAGATCTCGATTCTGCTGGAAGACATCGCTACTACCCCAAGCCACAGGTATGCTGTGCTGCTAAGTTGCTCCAGGCAACCTTGT
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Figure S1. The region with a green background represents the 5' UTR of *ZmbZIP25* in Phytozome.

-2083 TGCTGAGGAGGAGGAAGTTCTCGGGCTTGAGGTCCGGTGGATGACGCCCATGGAGTGGC
 -2023 AGGTGTGACGATCTCGACGATGGTGCAGGAGCAGCGAGGCGGCGCGCTCGGTGTAGT
 -1963 GGCCCTGGCGATGATGCGGTCTGAAGAGCTCGCCGCCGCGCAGAGCTCCATGACGAGGT
 -1903 GCACGGAGCTTTTGTCTCGTACGCGCCCTTGAGCTCCACCACGCCCGGTGGCCGGACA
 -1843 GGTGGTACATGATCTGTACCTCGCGCCGACGTCCTCCACGTCCTCCTTGGTGGACAGCT
 -1783 TCCGCTTGCTGATGGTCTTGACGCGAACCTGTGCCCCGTGGCCTTGTGCGTGCACAGCG
 -1723 ACGTGACGCCGAACCTGCCCGCGCCCGAGCTCCTTGCCACGGCGTAGGTGGCCCTCACGT
 -1663 CCTCCATGGGCCGGCCAGCACGGGGCCGATGGGGGCCGGGGCCCTGGCGGGCGCGGGCG
 -1603 CCGCGGTCCGGCAGACCGAGGCAAGGCCACGGGGCGCGACGAGCCGGAGGGGTCCG
 -1543 GCGGCTGCGGCGGCGGGCTCCGCGGACGACGACGACCCCGGGCAGCAGTTGCCCATGT
 -1483 CGGCGACGGCGAGGGGGCGACGAGACGCGGGGGCCTCGCGCGCCGGGACGCGGACGC
 -1423 GCAGGCGCGGCGCAGCGAACCGGGGAGGTGTCCGGGCGAGCGGTGGGGCGCGCGGGGGA
 -1363 ACCTTTCTCGGACGGGTGGGAGCGCTGGCCATGAAAGGAAGGCTGGGAGGAAATGGCGG
 -1303 GAACGTAACGGCTGCTTGTCTTTGCCCTTCTGTTGCCCTGTTTATGCTCAACAGAGAAAAA
 -1243 CAACAGAAGCTTGCGTCCAACCTCTCTATTTTAGCACCAGGCCATAAATCATAGACACA
 -1183 GATGGTCTCATAAGTCATAAACAGAGGATCACATAATAAGCATTTAGCCACATTAATAAGG
 -1123 GCTAAAAATAGCAAAATTTTCCCTGCGTCCGTGCACCCACGCCGAGCTTGCCGCTGCGACC
 -1063 GTGGCCGAGCAGATCACGCACACGACATGCATTGCTTTGTTGCTCTTCAAAACAAACCCA
 -1003 AAAAAATAGTTTGGCGTTTGGCCGACCAAGCCTGGAGCACGGTGGTGGCTCAGCCAGAC
 -943 AGCCAATAGGACATTCTTGATTCTTGATGTTGTATTGTATTGTTGAGTTTGTGATCTAA
 -883 ATTTTGTATAGGACATATTAGCAAGTAAAGCGGAGGCTTGTATAGGTTTGGGCCGGA
 -823 GTATATTGCTGACTCTAATTAGGGTTTCTGTTGCGTCATAATTTTACTCCTCTATAAG
 -763 CCGTCGTACAAAGACGGCGTTATGTAAACATTTCTACATATAGTGAAGGTTTTCGTAATT
 -703 TTTCTCTTGCATTAAGGACCTGTTTGGTTAGAGGTCTCTCAGGCACTTGCCGCAAGT
 -643 AAGGAATCCTAGCCCATGTATTCAAAATCTAACGCCTGAGATCTGTGCAACTTTGGCCGG
 -583 CTCCAAACTAAATAAGCCTTAAAGAATTTCTATGTAAATCTATGTATGGTGTCTGTGG
 -523 TTTGTTGTTGATCTTCCCTGTTTGTCTGCTAACGGTATCCATCCGTCCATTGATGCTC
 -463 CGGCCCTTTCCCAATGTCCTGTGCTGGAATCTTGATAGCTTGGGGCAGTTGAGTTTGGCG
 -403 TGTGAAGTGGACGTGGACTTGGCGTTGGATAGATTCTGCAAGCTTTCGTGGATAGATTTT
 -343 TCGAGATTCTGAGCTTGCATCCGATCCAGCAAGCTCTCAGTTCCGTTTAGGCCCCCACA
 -283 AATGACTAAAAAGTAGACTGAAAAAGTTGAGACGCACGCACATGCAGCTACGCCGCTACGCT
 -223 ATGGCTGGTTCACCCACCGAGCCTGCAACGCGCTCCCTGTGGAGAGAGAAAAAGAAGCTC
 -163 TGCCACCCGTCACACATTCCTGTGATAGATCGCATTCTGCAGCTGGCTACTGAATGCG
 -103 CGTTGTGCTGCGTAGGACACGTATGGCAAGCCTGGGGAATGGTTTCATGTGCTCTGTTCT
 -43 ACAATGTACATACATATGCATCCGGCTCGCGCAGGGGCGTGGCTCGAGTAGTCTGCGAG
 +18 ATCTCGATTCTGTAAGACATCGCTACTATCCCATTCACAGCCACAGGTATGCTGTGC
 +78 TGCTAAATTGCTCCAGGCAACCTTGTTTTGAACCTGTTTTGCTGAACAATACTAGCT
 +138 GCTTCGATTTTTTGAAGTGTGAGTGCCCATTTGGGTATTTATCTGCTCCTTTGTGCTGAAG
 +198 CTGGAATGTGAGCTCGATCGGTTAGCGCTACGAGTCCTCGCTGAATCCAGCCAAATGAT
 +258 CCCCTTGAAGCTTGCAGTTAGAGCAGGTGAGCCTATTGTACTCTGATCATATCCGGTGA
 +318 GCCGATGATTTCTTAGAGCAAGATTAAATAGCCTCACCCCTCACAGCAGGCTTTTATATG
 +378 GTTCAGATCTGCAGATCTGTCTGTCTCCCATTCATTCTCTTTGCTTTTTTTTTTTGGGA
 +438 AGCGCAGCACCTAATATAATGCTGGCCTTCCGTCAGAAGTAACAACAGCTAGCTAAGAGA
 +498 AGCACAAGAAAATCTGGTGGTAGCTTGAGTTCTGACTCCAAGTGAAGAGTCAGAGATG

Figure S2. Sequences analysis of the 5'-flanking region of *ZmbZIP25*. The transcription start site identified by 5' RACE is represented by a bold red "A" at +1. The translation initiation codon is boxed in black. Two intron sequences are denoted with a gray background. The first intron is the region from +67 to +160. The second intron is the region from +285 to +444. Putative TATA and CAAT boxes in the promoter region are in blue letters.