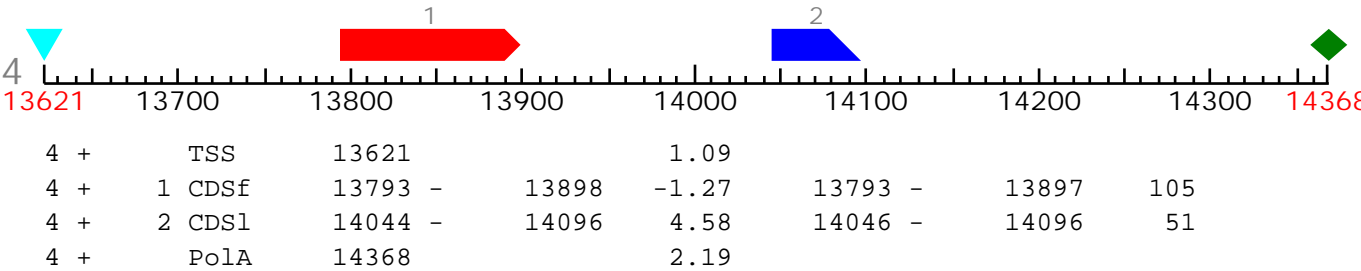
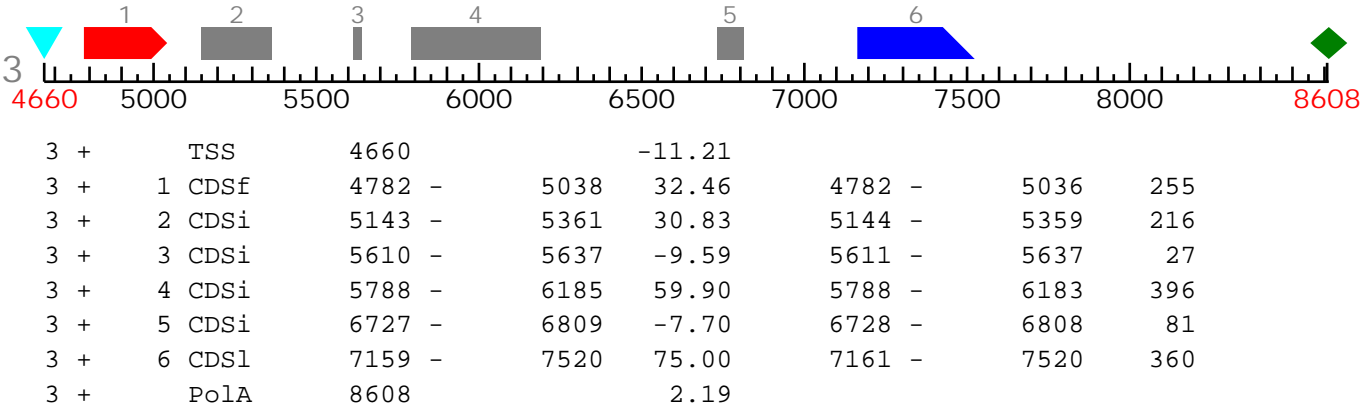
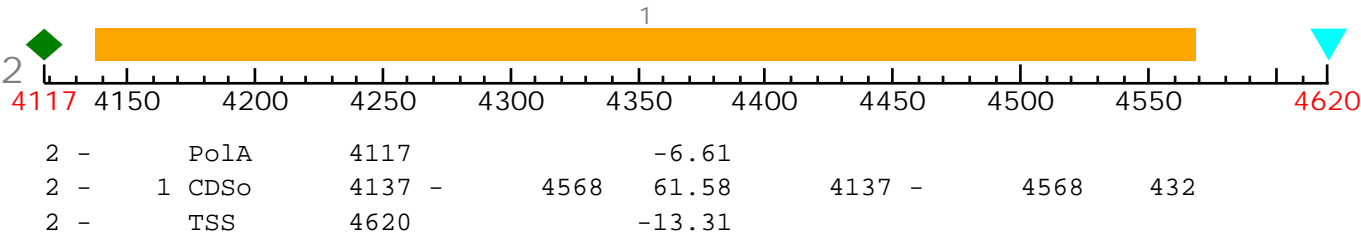
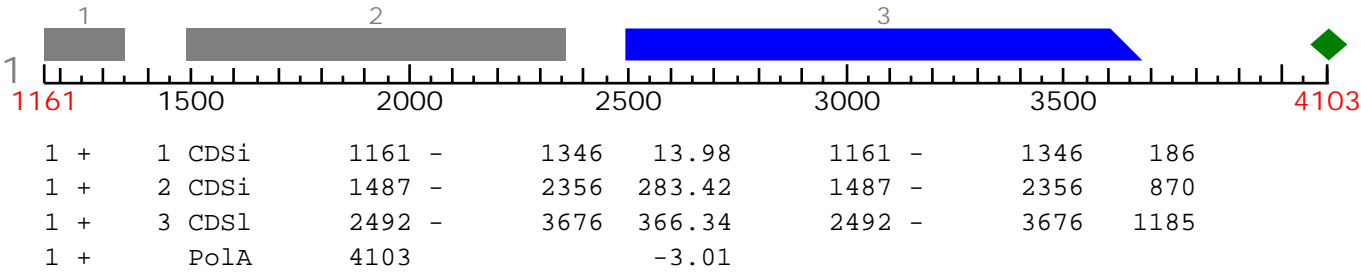


FGENESH 2.6 Prediction of potential genes in Triticum genomic DNA  
Seq name: region7  
Length of sequence: 15001  
Number of predicted genes 4: in +chain 3, in -chain 1.  
Number of predicted exons 12: in +chain 11, in -chain 1.  
Positions of predicted genes and exons: Variant 1 from 1, Score:853.606641

CDSf CDSi CDSl CDSo PoIA TSS



Predicted protein(s):

>FGENESH:[mRNA] 1 3 exon (s) 1161 - 3676 2241 bp, chain +  
GCATTTGGGTCGGGGTCAAGCACGACGAACGTGACCTCCACGGCGAAAATTAACAGCGCT  
AGAATTATTTTTCCTTCCGCACGAAGCATCTGCCTCGTTTTATGTCGCTGATGCCCTGCTA  
ACTTGTTCTGTACCAATTTTTCACAGCAGCCTGCGGTTCGAGTCGCAGAGATGGAAGCCCCT  
GACCAGGAGAATCCTTGCGCCATCTGCCTCGGCGGCATGGCCGCCGGCGGGCAGGCC  
ACCTTCACGGCGGAGTGCTCCCACACCTTCCACTTCAACTGCATCTCCGCCAGCGTCGCG  
CACGGCCACCTCGTCTGCCCGCTCTGCAACGCGCGCTGGCGAGAGCTGCCCTTCTTGCGA  
CCCACCGCGCCGGTGCCGCAGCCGCCTACGCTGCCTAGGCTGGGTCTCCCGTTCCCATG  
CACGGCGTGCAGCCTCCGAGCGAGCCGACAGCATCGCCTCCTCTCATGCATGGCGGGATG  
CCTCCGTTCCCGAGCGCAGGCGCCACCGCCGCCGCGCGGGCATATCATGCAGCATCACCAG  
CCGCCGCCGCCGAACGTGCATGTCGTGCAGCATCATCAGCCGCCGCCGCCCGTGCATACC  
GTGCAGCATCATCAGCCCCGCCGCCCGAGCCTACGGTCGTCTTCGACGACGACGAGCAG  
GTGGAGCCGGCCTCCAGGCCGCCAGCTGACAGCACACCGGCAGCTGCATCGAACGGGGCA  
GTGGTCGTCAACACGCACGCCGAGTACTCGGCCGTTCGCCAGGGACTCGTCCAGCGACAAC  
TTCGCCGTGCTCGTGCACGTCAAGGCTCCCGCGATGGCCGACACCGTGCGGCCCGGCAGC  
GACAAGCCGCCCGCGCGCGCCGCTGGACCTCGTGACCGTGCTCGACGTGACGGCAGC  
ATGAGCGGCCACAACTGGCGCTCCTGAAGCAGGCCATGCGGTTCTGTCATCGACAACCTC  
GGCCCCAACGACCGCCTCTCCGTCTGTCTTCTCCTCCGAGGCGCGCCGGCTGACCAGG  
CTCACGCGCATGTTCGACGCCGGGAAGGCACTGGCCGATACCTATAACCATGATGAGGCGC  
CGGGGACCGTCCGGCGTCCAGGCCAACAACTACGAGGAGCTCGTCCCGCCCTCCTTCGCA  
CGCACGGGCGCTGACGGCGAGTGGTCCGCGCCGATCCACACCTTCGGCTTCGGGAACGAC  
CACGACGCGGCCGCGATGCACGTTCATCGCCGAGGCGACGGGCGGCACGTTCTCGTTTCATC  
GAGAACGAGGCTGTGATACAGGACGCGTTTCGCGCAGTGCATCGGCGGCCTGCTCTCCGTC  
GTGGTCCAGGAGGCGCGCATCGCCGTTCGCGTGCCTGACCCCGGGGTCCGTGTCGTCTCC  
GTCAAGTCCGGCCGTTACGAGAGCCGCGTCGACGAGGACGGCTGCGCCGCATCTGTCCGA  
GTCGGGGAGCTCTACGCCGACGAGGAGAGGCGTTTCTTGCTCTTTCTGACCGTGCCAAGA  
GTCGAAGCGACGGACGGCGACACCACTGCTCTTGCGAGAGTGGTCTTCAGCTACAGAAAC  
GCGGCGAGCGGCGCGGAGGTGAGCGTGACGGCCGAGGACACGGTGGTGGCGAGGCGGAG  
CACGCGCCGAGCGCGTTCGAGCGCTCAGTGGAGGTGGAGCGGGAGCGCGTCCGGGTGGAG  
GCGGCAGAGGACATCGCGGCGGCGAGGGCAGCGGCGGAGCGGGGCGAGCACCAGGAAGCG  
GTGGAGATCCTCGACAACCGTCAGCGGGCGCTGGAGCAGTCGGAGGCGGCAGGGGACGGC  
GACCCCATGATCGTGGCGCTGGGGCGGAGCTGCAGGAGATGCGCGGGCGCGTGTCTGAAC  
CGGCAGAGCTACATGCGGTTCGGGGCGGGCGTACATGCTGGCCGGCATGAGCGCGCACAG  
CAGCAACGCGCCACCTCCAGGCAGATGCTGGAGCCGGAGGAGCAGCAGACGTTCGATGATG  
GCGAGGAATAGTGGAGTGAGGAGGATGATCAGAAGAGGAGTGGGGTTCGAGCGGCGGGGA  
TATATGGCGGCAGCGGCGCCCGTGGCCGAGGCGTCGAACGAGGCGACGATGTCGTACGCG  
ACGCCGGCCATGCGCGCCATGCTGCTGCGCTCGCGGGAGGCGCGTGGGGCGTTCGGCCGAG  
CAAGGGCAGCAGGAGGAGCAGCAGCCCATGGCCGGAAGACGATGCCGGGAGCTCGGGC  
CCGAAGGACGTGAACCAATAG

>FGENESH: 1 3 exon (s) 1161 - 3676 746 aa, chain +  
AFSGSSTTNVTSTAKINSARIIFLPHEASASFYVADALLTCSYQFSQQPAVAVAEMEAP  
DQENPCAICLGGMAAGGGQATFTAECSTHFHNCISASVAHGHLVCPLCNARWRELFPFLR  
PTAPVPQPPTLPRLGRPVPMHGVQPPSEPTASPLMHGGMPPFPAPQAPPPPRGHIMQHHQ  
PPPPNVHVQHHQPPPPVHTVQHHQPPPEPTVVFDDDEQVEPASRPPADSTPAAASNGA  
VVVNTHAEYSAVARDSSDNFAVLVHVKAPAMADTVAAGSDKPPPRAPLDLVTVLDSVSGS  
MSGHKLALLKQAMRFVIDNLGPNDRLSVVSFSSEARRLTRLTRMSDAGKALADTYTMMRR  
RGPSGVQANNYEELVPPSFARTGADGEWSAPIHTFGFGNDHDAAAMHVIAEATGGTFSFI

ENEAVIQDAFAQCIGGLLSVVVQEARIAVACVHPGVRVSVKSGRYESRVDEEDGCAASVR  
VGELYADEERRFLFLFTVPRVEATDGDTTALARVVFSYRNAASGAEVSVTAEDTVVARPE  
HAPSASERSVEVERERVVEAAEDIAAARAAAERGEHQEAVEILDNRQRALEQSEAAGDG  
DPMIVALGAELQEMRGRVSNRQSYMRSGRAYMLAGMSAHQQQRATSRQMLEPEEQQTSM  
ARNSGVRRMIRRGVGSSSGGGYMAAAAPVAEASNEATMSYATPAMRAMLLRSREARGASAE  
QGQQEEQQPMAGKDDAGSSGPKDVNQ

>FGENESH:[mRNA] 2 1 exon (s) 4137 - 4568 432 bp, chain -  
ATGTGCTGGTCGCTGCACGGCCGCGTGCCGGTTCCAGCTCCACGCATAGGCGGTTGCAGC  
ACCCGGCACCTCGCCGCGCAGCTGGTCGCCCCGCATCTCGCCGATTGCAGCATTTGTAGCC  
TCACGCTCGAAGCTCCCCCGGCTCCGGCCAGCTGCCGTCGGCGGCCCCCGCACCCCGCAAC  
ACCAGATTCAACGAAAAACGCGAGACGTAAATGTATCCAGCGGTGCTGGGTAGCTGTG  
TCCAGCGGTGGCCATGAACGCACCTTTGCTTTGTGGAGGAGATGAGGAGATAAGAGGAAGG  
TATGGGCATAGTGGCCTAGTCAACGACGAATGGACAAGCAAAGGAAGCAGTGACACACGA  
GGCGTATATGTGGCGAGCGCGCAACACACGTGGGCCAGGGCCATGTGCGGGAGCGACCG  
GCTCAAAGTTAA

>FGENESH: 2 1 exon (s) 4137 - 4568 143 aa, chain -  
MCWSLHGRVPVPAPRIGGCSTRHLAAQLVAPHLADCSIVASRSKLPRLRPAAVGGPAPRN  
TRFTTKNARRKCIQRCWVAVSSGGHERTLLCGGDEEIRGRYGHSGLVNDEWTSKGSSDTR  
GVYVASAQHTWAQGHVRERPAQS

>FGENESH:[mRNA] 3 6 exon (s) 4782 - 7520 1347 bp, chain +  
ATGGCCAATCTTGCTGGAAGTACCGACACAGAAGCTGCAATGGTGATTCGCCGGATGCT  
GCGTGACGCGCATCATGTGCTGGAAGCGACGAGCAATTTTGCTGGAAGCCGCTGGCCAT  
TTTGCTGGGAACAGCAAGCCTTTTTTGCTAGGACGGTGAGCGGCGAGCTACAACCATTG  
TTCCGGCGACGGCGTTGTGATTTTGCTACAACCGACAATGAGAAAGCTACAACCGGCGCC  
TGGATTTGCTGCATCCGTGTGGCCGGCGGCAACGGTGAGCTACAACCACCTTATTTCTTG  
CTGCAACCGGTGATCTGGATTGCTGGATCCGGTGACTTGGTTTGCTGGAACCAGCGTACT  
CCGGAGCCGACGGGGGCGGAGACGACGTGCAGGCATCGAGGCGAGATGGAAGCAGGGCTA  
CTCGGGAGCGAAGGCGATGAGCCGACGGGGGGCGGAGCCCACGTGCGGGCACCAAGATTC  
ACGGGCAAAAGCGAAAAAGAAACAACCTTCTTCTTCCCCACGCCTTGCCATGAATTGAAA  
CGACCAGGGTGCCATTCCATCACCGCCGAGGAGCCGCACCTCTGGCCGTCAGGCTGCTTG  
CCCCATCCGTCGCGGCAGAACTTCTCGACGCCGGCACAAGCACGCGGCTCTCCCCGCCGG  
CCGATGCCATGGTCCTTGACGCCGGGCACATCTGCTGCTCGCCGCCGGCGTAACCTCCACT  
GCTCGCCGGCTCTCTCGTTTTTCTTGCAACCAGATCAGTCTTGGAATCCATCAGTCAT  
GACGTACAACAATGTTGTTGGCTGCCGTTGTCCGGATGTGTACCGCCGTCTTGCCGTCA  
TGCCGTCATCGTCGGGAACGAGCGCACCGAGCTGGAATCGAGATTGGGCAAAGGAAATC  
CGCATCACCAGCCGCCGCGGAACGTCCATGTCTGTCAGCATTGTTTTACAAGCTGTTTGG  
GACTATATTTATGAGATGGGATGGACAACTACTCCTCGCCGAGTCGTTGTTGTCGTCCGA  
GTCGCCGTTGCAGGGTGGGGGCTCGTTGCCGTGGAGGGTATGGTAGATGAGCGTGTCCGA  
GAGGGTCGAAGCGACTTGGTACTCCTCCCGAGCGCCGGCAGGTGCGCAGCCGCAGCTGC  
ATCTCTGGCAGCGGCGGCTTCTTCTGCCTCCAGCATGCGTCCTCGGCCGCCAGAGGCGC  
TGGATGGAAGGATCGAAGATCCCCTCGAGGCGCTGGAAGTAGCCCATGCCACAAGCCA  
GCGTTGGAGGACTTCGTGCCGCGGGTGCGCGCCTGCTCCCTGCGCTTCTCCGACGCGGGA  
GGGCAGAGGGAGGAACTGTCAGCCTAA

>FGENESH: 3 6 exon (s) 4782 - 7520 448 aa, chain +  
MANLAGTSRHRSCNGDSPDAACTRIMCWKRRAILLEAAGHFAGNSKPFLLGRWSGELQPL  
FRRRRCDFATTDNEKATTGAWICIRVAGGNGELQPPYFLLQPVIWIAGSGDLVCWNQRT  
PEPTGAETTCRHRGEMEAGLLGSEGDEPTGGGAHVRAPRFTGKSEKETTSFFPTPCHELK  
RPGCHSITAEPHLWPSGCLPHPSRQNFSTPAQARGSPRRPMPWSLTPGTSAARRRRNST

ARRLSRFSCNQISLGKSISHDVQQCCWLPLSGCVTAVLPSCRHRRERAHNRDWAKEI  
RITSRRGTSMSCSIVLQAVWDYIYEMGWTTTPRRVVVVVRVAVAGWGLVAVEGMVDERVG  
EGRSDLVLLPERRQVRSRSCISGSGGFLRLQHASSAAQRRWMEGSKIPSRRWKVAHAHKP  
ALEDVPRVRACSLRFS DAGGQREELSA

>FGENESH:[mRNA] 4 2 exon (s) 13793 - 14096 159 bp, chain +  
ATGACCAAGAAAGGTCATAACGTGAGGGAGTATGTGCTCTCTAAAGGATGGCTTCAAAG  
AAAAGAGAAAGATCATTGAGAGTCTTGGTTGACGAATGTCTTTCATTCAAAGAGCCAAT  
TTTGGCATTTATGTCCCTTACAGGGAATTACCTGCATAG

>FGENESH: 4 2 exon (s) 13793 - 14096 52 aa, chain +  
MTKKGHNVREYVLSKGWLQKKRERSLRVLVDECLSFKRANFGIYVPYRELPA