

FGENESH 2.6 Prediction of potential genes in Triticum genomic DNA

Seq name: region7

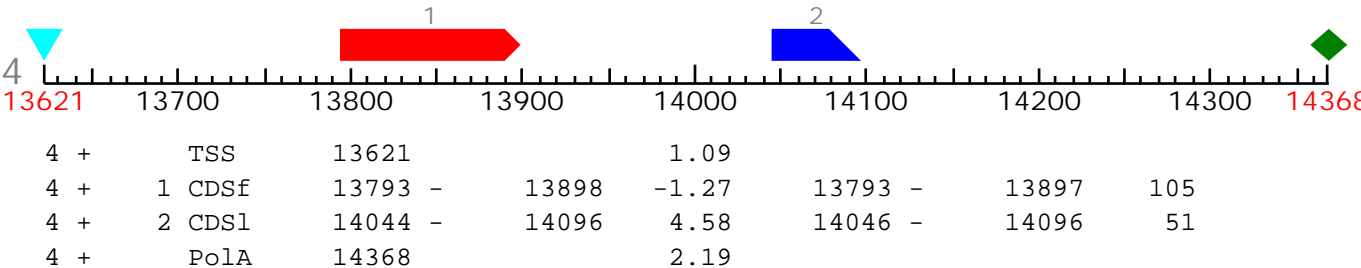
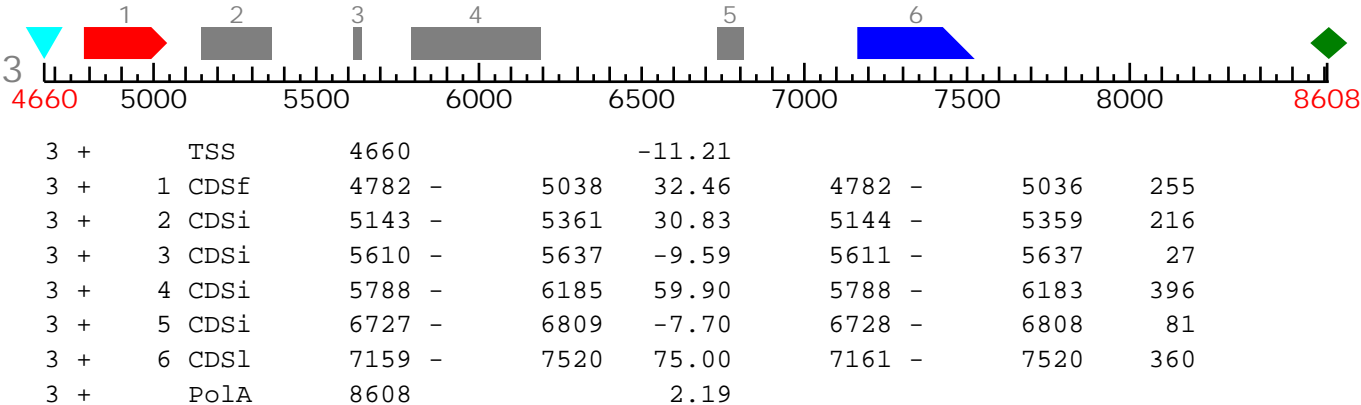
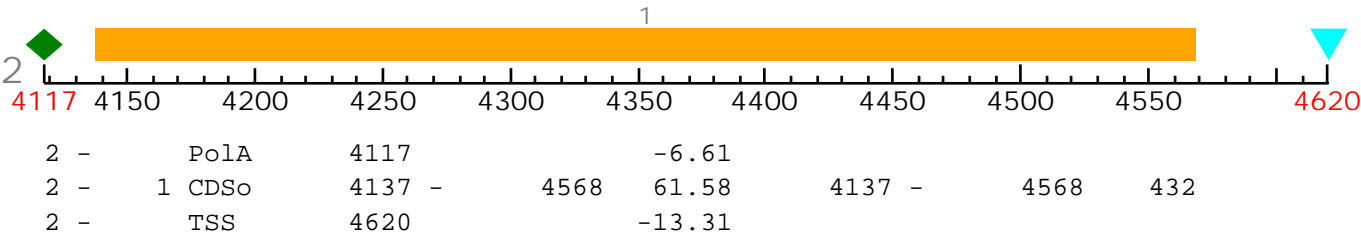
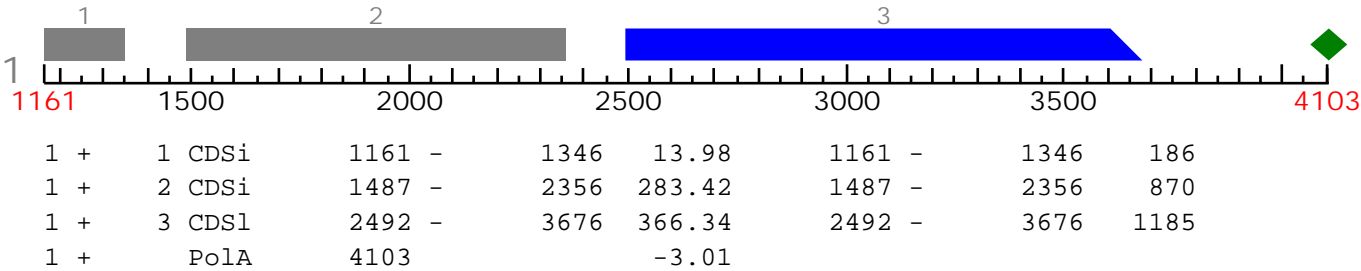
Length of sequence: 15001

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
CGCACGGGCGCTGACGGCGAGTGGTCCCGCGCCGATCCACACCTTCGGCTTCGGGAACGAC
CACGACGCGGCCGCGATGCACGTTCATCGCCGAGGCGACGGGCGGCACGTTCTCGTTTCATC
GAGAACGAGGCTGTGATACAGGACGCGTTCGCGCAGTGCATCGGCGGCCTGCTCTCCGTC
GTGGTCCAGGAGGCGCGCATCGCCGTGCGGTGCGTGACCCCGGGGTCCGTGTCGTCTCC
GTCAAGTCCGGCCGTTACGAGAGCCGCGTCGACGAGGACGGCTGCGCCGCATCTGTCCGA
GTCGGGGAGCTCTACGCCGACGAGGAGAGGCGTTTCTTGCTCTTTCTGACCGTGCCAAGA
GTCGAAGCGACGGACGGCGACACCACTGCTCTTGCGAGAGTGGTCTTCAGCTACAGAAAC
GCGGCGAGCGGCGCGGAGGTGAGCGTGACGGCCGAGGACACGGTGGTGGCGAGGCCGGAG
CACGCGCCGAGCGCGTTCGAGCGCTCAGTGGAGGTGGAGCGGGAGCGCGTCCGGGTGGAG
GCGGCAGAGGACATCGCGGCGGCGAGGGCAGCGGCGGAGCGGGGCGAGCACCAGGAAGCG
GTGGAGATCCTCGACAACCGTCAGCGGGCGCTGGAGCAGTCGGAGGCGGCAGGGGACGGC
GACCCCATGATCGTGGCGCTGGGGCGGAGCTGCAGGAGATGCGCGGGCGCGTGTCTGAAC
CGGCAGAGCTACATGCGGTTCGGGGCGGGCGTACATGCTGGCCGGCATGAGCGCGCACCAG
CAGCAACGCGCCACCTCCAGGCAGATGCTGGAGCCGGAGGAGCAGCAGACGTTCGATGATG
GCGAGGAATAGTGGAGTGAGGAGGATGATCAGAAGAGGAGTGGGGTTCGAGCGGCGGGGGA
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
ACCCGGCACCTCGCCGCGCAGCTGGTCGCCCCGCATCTCGCCGATTGCAGCATTGTAGCC
TCACGCTCGAAGCTCCCCCGGCTCCGGCCAGCTGCCGTCGGCGGCCCCCGCACCCCGCAAC
ACCAGATTCAACAACGAAAAACGCGAGACGTAAATGTATCCAGCGGTGCTGGGTAGCTGTG
TCCAGCGGTGGCCATGAACGCACCTTGCTTTGTGGAGGAGATGAGGAGATAAGAGGAAGG
TATGGGCATAGTGGCCTAGTCAACGACGAATGGACAAGCAAAGGAAGCAGTGACACACGA
GGCGTATATGTGGCGAGCGCGCAACACACGTGGGCCCAGGGCCATGTGCGGGAGCGACCG
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
ACGGGCAAAAGCGAAAAAGAAACAACCTTCCTTCTTCCCCACGCCTTGCCATGAATTGAAA
CGACCAGGGTGCCATTCCATCACCGCCGAGGAGCCGCACCTCTGGCCGTCAGGCTGCTTG
CCCCATCCGTCGCGGCAGAACTTCTCGACGCCGGCACAAGCACGCGGCTCTCCCCGCCGG
CCGATGCCATGGTCCTTGACGCCGGGCACATCTGCTGCTCGCCGCCGGCGTAACCTCCACT
GCTCGCCGGCTCTCTCGTTTTTCTTGCAACCAGATCAGTCTTGGAATCCATCAGTCAT
GACGTACAACAATGTTGTTGGCTGCCGTTGTCCGGATGTGTACCGCCGTCTTGCCGTCA
TGCCGTCATCGTCGGGAACGAGCGCACCGAGCTGGAATCGAGATTGGGCAAAGGAAATC
CGCATCACCAGCCGCCGCGGAACGTCCATGTCTGTCAGCATTGTTTTACAAGCTGTTTGG
GACTATATTTATGAGATGGGATGGACAACTACTCCTCGCCGAGTCGTTGTTGTCGTCCGA
GTCGCCGTTGCAGGGTGGGGGCTCGTTGCCGTGGAGGGTATGGTAGATGAGCGTGTCCGA
GAGGGTCAAGCGACTTGGTACTCCTCCCGGAGCGCCGGCAGGTGCGCAGCCGCAGCTGC
ATCTCTGGCAGCGGCGGCTTCCTTCGCCTCCAGCATGCGTCCTCGGCCGCCAGAGGCGC
TGGATGGAAGGATCGAAGATCCCCTCGAGGCGCTGGAAAGTAGCCCATGCCACAAGCCA
GCGTTGGAGGACTTCGTGCCGCGGGTGCGCGCCTGCTCCCTGCGCTTCTCCGACGCGGGA
GGGCAGAGGGAGGAACTGTCAGCCTAA

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

ARRLSRFSCNQISLGKSISHDVQQCCWLPLSGCVTAVLPSCRHRRERAHHRAGNRDWAKEI
RITSRRGTSMSCSIVLQAVWDYIYEMGWTTTTPRRVVVVVRVAVAGWGLVAVEGMVDERVG
EGRSDLVLLPERRQVRSRSCISGSGGFLRLQHASSAAQRRWMEGSKIPSRRWKVAHAHKP
ALEDVPRVRACSLRFSDAGGQREELSA

>FGENESH:[mRNA] 4 2 exon (s) 13793 - 14096 159 bp, chain +
ATGACCAAGAAAGGTCATAACGTGAGGGAGTATGTGCTCTCTAAAGGATGGCTTCAAAAG
AAAAGAGAAAGATCATTGAGAGTCTTGGTTGACGAATGTCTTTCATTCAAAAGAGCCAAT
TTTGGCATTATGTCCCTTACAGGGAATTACCTGCATAG

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