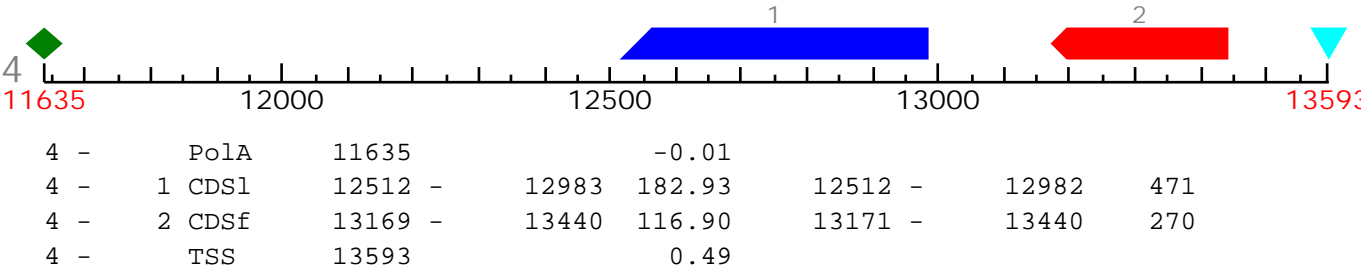
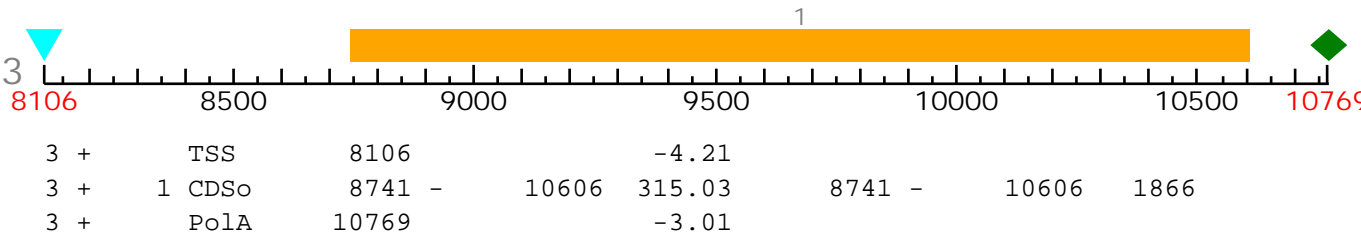
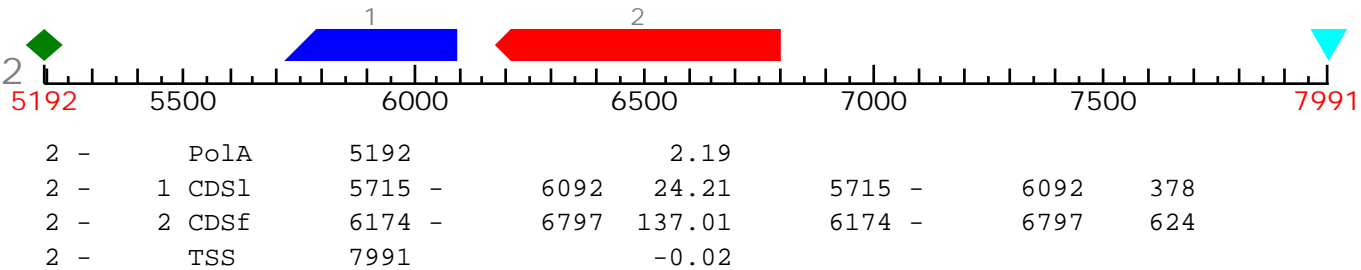
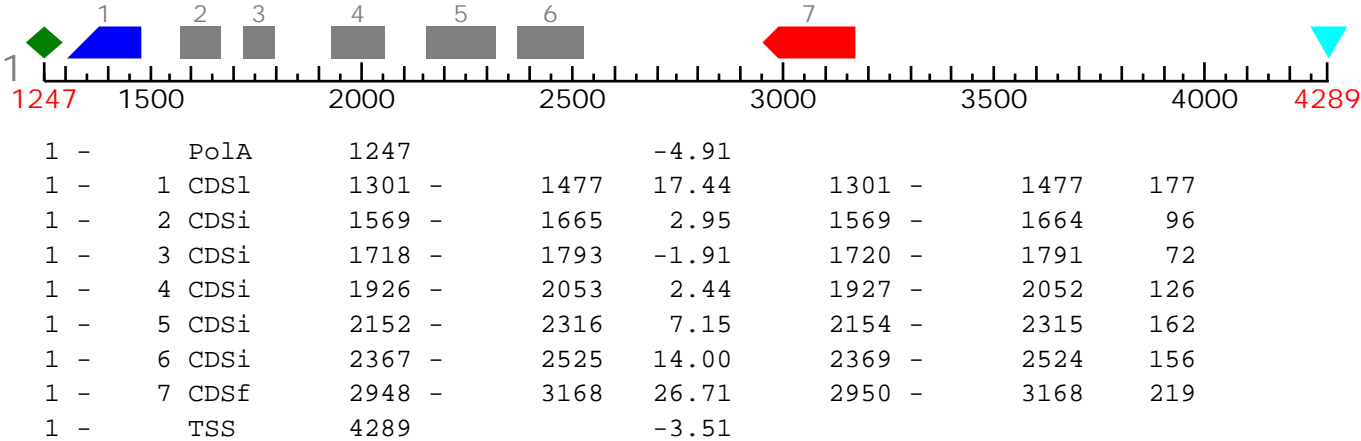


FGENESH 2.6 Prediction of potential genes in Triticum genomic DNA  
Seq name: test sequence  
Length of sequence: 14001  
Number of predicted genes 4: in +chain 1, in -chain 3.  
Number of predicted exons 12: in +chain 1, in -chain 11.  
Positions of predicted genes and exons: Variant 1 from 1, Score:813.705811

CDSf CDSi CDSl CDSo PoIA TSS



Predicted protein(s):

>FGENESH:[mRNA] 1 7 exon (s) 1301 - 3168 1023 bp, chain -  
ATGTCGCTTCTGGTCAATGTTTTGGTGCCGAAGAGAGAACACACGCGAGTGTACGTGTGG  
ATGTACAGGAACGGGATCAATAACAGAGCTGGAGCGCACCCCCGCCAGGAACGGGATCA  
ATAACAGATCCGGCCGGGCCGGGAGAACCGGACAAGGTTGAACAGAGCCGGAAGAGACGA  
ACGAGGCTAGGTGCAGATCACTGTCACGTAGCACGTCAAAGGAAAGATTCAGAAGGCCGG  
CGTTCGTCCAGCTCTAGCCGCATGCATGCATGCGCATGTGCCGGCCATGTTCTTGCCCTGC  
TTCGGATCAAACGGCGCGGTTAATGGTGCTACGAAGGACCTGCGGTTCAAGTCCGGCGGC  
TCGATCTGGCGCTCAAGAGAGAAAAAGAAGGCCTGCCGGCCGGCCGGAGTCTCGCATGCG  
GCGCGCCGTCCGAACCACATGTTTCGGCGGCGCGCGGTTGGTGGGGGTTGGACTCGCACCG  
GACATGAAGGCGTCTCGCTCGTCTGCTTTCGCACTTCGCCGTCGCCTCCGTCTGCACTTTTTT  
TTCGGGAGTAGCGGAGACTCAGAGCGATCGATTGCGTGGATAGCCAGGTGCGTGGGCGTG  
TATCGTGACCAGTGTACCGCGACGACGCGAGCGTCTCGGGACGCGTTTGGTACCCTGCAT  
CCCGCCCAAGCAGCGGGTCAAGCCCGAGCGATGCTCTCGAGCCCACAACACGTGGATTGG  
CTCTCACGAGACGTGTACTTGGTTTGTAGGAGTAGATCAGTGGGATATTGTCTGTATTCTG  
GGTGTTTACCTTAGCGTTCCGGCCATTGCTGGTTTCGTTCGATGGAGGACTGCGCCCCGGGCA  
GCGACGGAGTGGGGAACAGTGGCGGTGACGAACCTCGTACTCCGTGCCCCTGGTCCCCAC  
CTCCTCTTTATAGCACTGCGCGACAGGGGCCCACCAGCCTTGCTTGGGCTGGACGCCCCC  
GATCAGGGCGTGGGTCAAGTGCCCAATGAGCCGTTGGGCCCATTTGGTGGAGAGATCAACC  
TAA

>FGENESH: 1 7 exon (s) 1301 - 3168 340 aa, chain -  
MSLLVNVLPKREHTRVYVWMYRNGINNRAHAHPRPGTGSITDPAGPGEPAKVEQSRKRR  
TRLGADHCHVARQRKDSEGRSSSSSRMHACACAGHVLACFGSNGAVNGATKDLRFKSGG  
SIWRSREKKKACRPAGVSHAARRPNHMFGGARLVGVGLAPDMKASRSSFALRRRLRLHFF  
FGSSGDSERSIAWIARCVGVYRDQCTATTRASRDAFGTLHPAQAAQARAMLSSPQHVDW  
LSRDVYLVCRSRVGYCLYSGVYLSVPAIAGSSMEDCARAATEWGTVAVTNLVLRAPGPH  
LLFIALRDRGPPALLGLDAPDQGVGVQVNEPLGLVERST

>FGENESH:[mRNA] 2 2 exon (s) 5715 - 6797 1002 bp, chain -  
ATGGATGGAATGGCCAAGAAGATGGAGCCCTCACCTTGGAGCCCCGGCTGCCGGAGCTG  
GAGAGCCGCCGCGAGGACACGGACGGCGACCTCGCCTTCTCCTCCCCCGTCGCCGGGCCG  
GCCTCCACCGCCGTCGTTGGATGGTGCGCCTCGCGTCCCGGCGGCGGGCGGCGGGGCG  
TCCTCGAGGGCCCTCTGGCGGTCCGGCAGGCGGATGCAGAGCTTGGTGGCGAGCGCGCGC  
TTGGCCCCGGCCCCAGGCGTCCGCCATTGCTAGCTCCTCCCGACGCGACGCGACCCGACCC  
GGCCCCGGCCCCCTCTCTCGCGCACACAGAGCTGGGAGCGGGAGTGGGATCGCTCGGCGGAG  
GAAGCGGATCAGGAAGGAGCGCCGGAGGGAGGGAGAGGGAGGGAGTTGGTTGGCTCGGGT  
CCCGGCTTCTCTCGTTCGCGCGTTCGCCGCGGGCGTCCGTTTCTTGGTTTACGTGGAGCG  
TCGCGGCGAATAAAACAACGGGGGAGGGGAACTCGTTCGTGCTTGGCTTCCCCGTTTTT  
GCCCTCGGGCCAGAGGGTGTGGACGCGCCGGGATCCCCGGTCAGCGCGGGGCGTTTCGGG  
GCTTTCGCGTCCCTGAGTTACTTGTTCAGCTGTTTCGACGCGAGGAATGTTGAAGCTTTT  
TTGGGTTTGGCTCGGATTCAGTTTCGGAGACGCGGCGGCTGCGTCTCGATCGTGTGGCCGG  
CGGCCAACGGCGAACGAGTTTTTGGTCACAACATTGGCGTGAATTGATCACATATCACATT  
AAGGTAACGGCTGCTTTGAAGATGCTTGCATATGGCGCGACCGTAGATTTGTGGGACGAG  
TACCTCCGAATATCTGAAAGCACATGTGTTGAAGTCATGGTTAATTTTTCAACTGCGATG  
ATCAAGTTGTTTGGACCGGAGTACTTGAGGGAACCAACTATCGTAAACACCACAAGGCTA  
ATACCACTGTTGAAAGCAAGAGGGTGCCCAGATACGCTCTGA

>FGENESH: 2 2 exon (s) 5715 - 6797 333 aa, chain -  
MDGNGQEDGALTLEPRLPELESRRDDTDGDLAFSSPVAGPASTAVVGWCASRPGGGGGGA  
SSRALWRSGRMQSLVASARLARPAQASAIASSSRDATRPGPAPLSRTQSWEREWDRSAE

EADQEGAPEGGRGRELVGSGPGFLSSRVRRGRPFLGLRGASRRIKQRGQGKLVRAWLPRF  
ALGPEGVDAPGSPVSAGRFGAFASLSYLFQLFDARNVEAFLGLLGFSFGDAAAASRSCGR  
RPTANEFWSQHWRELITYHIKVTAAKMLAYGATVDLWDEYLRISESTCVEVMVNFSTAM  
IKLFGPEYLREPTIVNTTRLIPLLKARGCPDTL

>FGENESH:[mRNA] 3 1 exon (s) 8741 - 10606 1866 bp, chain +  
ATGAGGACAGGGCACGGACAGGCCCTGTTTACTGCTGAATGCTCCCATAAGTTCCATTTT  
CATTGCATCACCTCAAATGTTAGGCATGGCAACCATATCTGCCCAATATGCCGTGCCGAC  
TGGAAAGAACTGCCCTTCCAGGGACCTCAACTTGCAGATGCCACTCATGGGAGAGCTAGA  
GTAAGCCCCGGTAAATTTGGCCCCAAGACGACGGACACATGGCTGTTATCCGCAGGCTTTCC  
AACTCATACAGTGGAAATCTGCTGGAGCAATTTCTGTCTTCCGTACTCCCGAGGCAGAC  
ATTTTCAATGACGACGAGCAAATAGATATTCAGTCTGAAACTGTGGAGGACAGCAATGCA  
GTTACTGGTTTCGGTTGAAATCAAGACATATGCAGAAGTGCAAGCCATACAGCAATCAGTG  
ACCCAGAAGGTCTTCTCTATCTTGATCCATCTCAAGGCTCCGAAGTCCTTGAGTCCGTG  
AGCTCCCGTGACCTCTTGACCTTGTGACCGTGCTTGATGTCAGTGGCAGCATGAAAGGG  
GCAAACTTGCACCTTCTCAAGAAGGCAATGGGCTTTGTCATCCAGACGCTTGGGCCCAAT  
GACCGGCTGTCTGTCAATTGCCTTCTCATCTACGGCACGGAGGCTCTTTCCCTTCGCCAA  
ATGAACGTCAACGGACGAATGCAAGCCATGCATGCTGTGAATTCCCTTGTTGATGGCGGT  
GGCACAAACATTTCTGATGGGCTAAAGAAGGGTGCTAAAGTCATTGAGCACCGTCGGCTG  
AAGAATCCTGTTTGCAGCATCATTCTTCTGTGCGATGGTCAAGACACATATTCGGTGCCA  
ACCTTTGACGACGGGGTTTCAGACAAACCACAGCATGCTTGTTCTCCTCAATCCTGCCT  
GGAACAGGTAATCATGTGCAAATCCACACCTTTGGTTTCGGCGCAGATCATGACTCGGCG  
GCGATGCATGCTATTGCGGAGACATCTAGCGGCACATTCTCATTTATTGATGCTGAAGGC  
TCAATCCAGAACGGATTTGCTCAGTGTATTGGTGGCCTCCTCAGTGTGTGGTCAAGGAG  
ATGCGGCTGGGCGTCGAGTGTGTGGACGAAGGCGTGGTACTCACCTCCATCAAGTCAGGC  
GGCTATGCAAGTGAAGTAGCCGTGGATGGACGTAACGGGTGAGTCGATATCGGCGACCTG  
TATGCAGATGAAGAGAGGGGGTTTCTGATCACCTACATGTCCCAGCTGCACAGGGGCAG  
CAGACTGTACTGATCAAACCAAGCTGTACATACCAAGATGCAGTTACAACAGAGAGCATT  
CAGGTACATGGTTTCAAGAGTGAGTGTGAGCGTCCTGCATACTCTGTGGACTGCAAAATG  
TCTCCCGAGGTTGAGCGTGAGTGGCACCGCGTTCAAGCCATGGAGGACATGTCTGCTGCG  
CGGGCTGCAGCCGACGGAGGCGATTTCTCCAGGCCGTGTCGATCCTCGAAGGCCGCACG  
AGGATCCTGGAGTCACAGGCAGCGCAATCTTCAGACAGCCAGTGCCTGGCGCTGATCACG  
GAGCTGAGGGAGATGCAGGAGAGGGTGGAAAGCCGGAGGAGGTACGACGAATCAGGCAGG  
GCCTTCATGCTGGCAGGCCTGAGCTCGCACTCGTGGCAGAGGGCCACGGCGCGCGGCGAC  
TCGACGGAGCTCAACACCCAAATCCACACCTACCAGACGCCGTCGATGGTCGACATGCTG  
CACCGCTCGCAGACTCTCGTGCCCGCCGTCGTCGAGATGCTGAACCGCTCCCCGACCGTT  
GCTCCTTACACGCGGCTCCGGCCGGTCGGTGAGGTCGACAAAATCCTTCTCCGAGCGGCTG  
GCGTGA

>FGENESH: 3 1 exon (s) 8741 - 10606 621 aa, chain +  
MRTGHGQALFTAECCHKFHFHCITSNVRHGNHICPICRADWKELPFQGPQLADATHGRAR  
VSPVNWPDQDDGHMAVIRRLSNSYSGNLLEQFPVFRTPHADIFNDDEQIDIQSETVEDSNA  
VTGSVEIKTYAEVQAIQQSVTQKVFSILIHLLKAPKSLESVSSRAPLDLTVLVDVSGSMKG  
AKLALLKKAMGFVIQTLGPNDRLSVIAFSSTARRLFPLRQMNVNMRMQAMHAVNSLVDGG  
GTNISDGLKKGAKVIEHRLKNPVCIIILLSDGQDTYSVPTFDDGVQTNHSMVPPSILP  
GTGNHVQIHTFGFGADHDSAAMHAIETSSGTFSSFIDAEGSIQNGFAQCIGLLSVVKE  
MRLGVECVDEGVVLTSIKSGGYASEVAVDGRNGSVDIGDLYADEERGFLITLHVPAAQGQ  
QTVLIKPSCTYQDAVTTESIQVHGSEVSVERPAYSVDCKMSPEVEREWHRVQAMEDMSAA  
RAAADGGDFSQAVSILEGRTRILESQAQSSDSQCLALITELREMQRERVESRRRYDESGR  
AFMLAGLSSHSWQRATARGDSTELNTQIHTYQTPSMVDMLHRSQTLVPAVVEMLNRSPTV

APSRGSGRSVRSTKSFSERLA

>FGENESH:[mRNA] 4 2 exon (s) 12512 - 13440 744 bp, chain -  
ATGGCCATGGACGCGATGAGCAGCGCGGTGTTGCAGGGGGCGTGGAGGAAGGGGCCATGG  
ACGGCGCTGGAGGACCGGCTGCTGACCGAGTACGTGCAGCAGCAGGGCGAGGGCAGCTGG  
AACTCCGTCGCCAAGCTCACCGGGCTGCGGCGGAGCGGCAAGAGCTGCCGGCTGCGGTGG  
GTGAACTACCTCCGGCCGGACCTGAAGCGGGGCAAGATCACCGCCGACGAGGAGACCGTC  
ATCCTCCAGCTCCACGCCATGCTCGGCAACAGGTGGTCGGCGATCGCGCGGTGCCTGCCG  
GGGAGGACGGACAACGAGATCAAGAACTACTGGCGGACGCACTTCAAGAAGGCGCGGCCG  
TCCAGGCGGGGCCAGGGCGCAGCTGCTGCACCAGTACCAGCTCCAGCAGCAGCAGCAGCAC  
CGCCAGTACCTCCACGCGCTGCACCTCCTCCAGCAGCAGCAGCAGGAGATGCAGATGCAG  
CTGCAGATGGAGCAGCAGACCCACCAGCCGCAGGTGATGATGATGCAGCAGCAGAGCCCG  
CCGGAGGAGGACCAGGCCGTGATCACCAACGTCGGCAACATGAACAGCATGGAGGCTGCG  
GAGTGCTACTGCCCCTGCCCGGCGGCGTCGGCGGTGCTCGACCTTCCGCTCCCGGCCGAC  
GACGAGGACGCGCTCTGGGACAGCCTCTGGCGGCTCGTCGACGGCGAGGACGGCTCCAGC  
GGAGGCGACTCAGGCGAGTACTAG

>FGENESH: 4 2 exon (s) 12512 - 13440 247 aa, chain -  
MAMDAMSSAVLQGAWRKGPWTALEDRLLEIYVQQQGEQSWNSVAKLTGLRRSGKSCRLRW  
VNYLRPDLKRKITADEETVILQLHAMLGNRWSAIARCLPGRTDNEIKNYWRTHFKKARP  
SRRARAQLLHQYQLQQQQQHRQYLHALHLLQQQQQEMQMLQMEQQTHQPQVMMMQQQSP  
PEEDQAVITTVGNMNSMEAAECYCPCPAASAVLDLPLPADDEDALWDSLWRLVDGEDGSS  
GGDSGEY