

FGENESH 2.6 Prediction of potential genes in Triticum genomic DNA

Seq name: region7

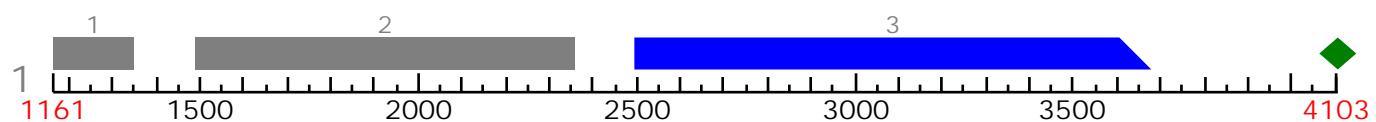
Length of sequence: 15001

Number of predicted genes 4: in +chain 3, in -chain 1.

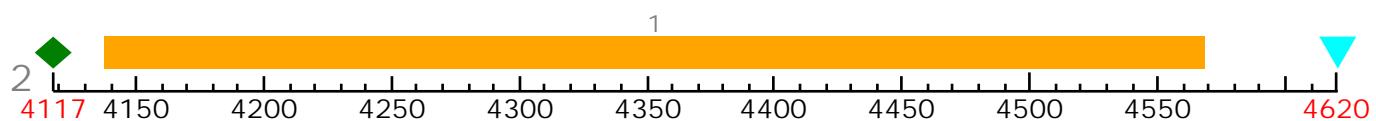
Number of predicted exons 12: in +chain 11, in -chain 1.

Positions of predicted genes and exons: Variant 1 from 1, Score: 853.606641

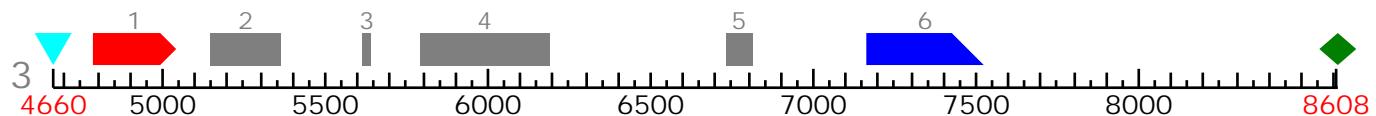




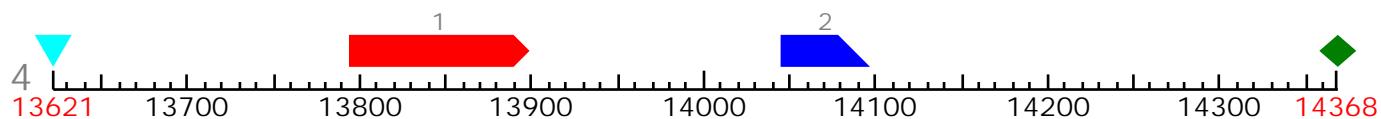
1	+	1	CDSi	1161	-	1346	13.98	1161	-	1346	186
1	+	2	CDSi	1487	-	2356	283.42	1487	-	2356	870
1	+	3	CDSi	2492	-	3676	366.34	2492	-	3676	1185
1	+		PolA	4103			-3.01				



2	-		PolA	4117			-6.61				
2	-	1	CDSo	4137	-	4568	61.58	4137	-	4568	432
2	-		TSS	4620			-13.31				



3	+		TSS	4660			-11.21				
3	+	1	CDSf	4782	-	5038	32.46	4782	-	5036	255
3	+	2	CDSi	5143	-	5361	30.83	5144	-	5359	216
3	+	3	CDSi	5610	-	5637	-9.59	5611	-	5637	27
3	+	4	CDSi	5788	-	6185	59.90	5788	-	6183	396
3	+	5	CDSi	6727	-	6809	-7.70	6728	-	6808	81
3	+	6	CDSi	7159	-	7520	75.00	7161	-	7520	360
3	+		PolA	8608			2.19				



4	+		TSS	13621			1.09				
4	+	1	CDSf	13793	-	13898	-1.27	13793	-	13897	105
4	+	2	CDSi	14044	-	14096	4.58	14046	-	14096	51
4	+		PolA	14368			2.19				

Predicted protein(s):

>FGENESH:[mRNA] 1 3 exon (s) 1161 - 3676 2241 bp, chain +
GCATTTGGGTCAAGCACGACAAACGTGACCTCCACGGCGAAAATTAAACAGCGCT
AGAATTATTTCTCCGCACGAAGCATCTGCCTCGTTTATGTCGCTGATGCCCTGCTA
ACTTGTCGTACCAATTTCACAGCAGCCTGCGGTGCGAGTCGAGAGATGGAAGCCCCT
GACCAGGAGAATCCTGCGCCATCTGCCTCGCGGCATGGCCGCCGGCGGGCAGGCC
ACCTTCACGGCGAGTGCTCCCACACCTTCACTTCAACTGCATCTCCGCCAGCGTCGCG
CACGGCCACCTCGTCTGCCCGCTCTGCAACCGCGCTGGCGAGAGCTGCCCTTGC
CCCACCGCGCCGGTGCCGCAGCCGCCTACGCTGCCTAGGCTGGGCGTCCCGTTCC
CACGGCGTGCAGCCTCCGAGCGAGCCGACAGCATTGCCTCTCATGCATGGCGGGATG
CCTCCGTTCCCAGCGCAGGCCACCGCCGCCGGCATATCATGCAGCATTACAG
CCGCCGCCCGAACGTGCATGTCGTGCAGCATTACAGCCGCCGCCGTGCATACC
GTGCAGCATTACAGCCCCCGCCGCCGGAGCCTACGGTGTCTCGACGACGAGCAG
GTGGAGCCGCCCTCAGGCCAGCTGACAGCACACGGCAGCTGCATCGAACGGGCA
GTGGTCGTCAACACGACGCCAGTACTCGGCCGTGCCAGGGACTCGTCAGCGACA
TTCGCCGTGCTCGTGCACGTCAAGGCTCCCGCATGGCCGACACCGTGGCGGCC
GACAAGCCGCCCGCGCGCCGCTGGACCTCGTGACCGTGCTCGACGTCAGCGCAGC
ATGAGCGGCCACAAACTGGCGCTCCTGAAGCAGGCCATCGGTTCGTCATCGACA
GGCCCCAACGACCGCCTCTCCGTGTCCTCTCCGAGGCGGCCGGCTGACCA
CTCACGCGCATGTCGGACGCCGGAAAGGCACTGGCGATACTACCATGATGAGGC
CGGGGACCGTCCGGCGTCCAGGCCAACAAACTACGAGGAGCTCGTCCGCC
CGCACGGCGCTGACGGCGAGTGGTCCGCCGATCCACACCTCGGCTCGGGAAC
CACGACGCCCGCGCATGTCACGTCACTGCCGAGGCGACGGCGGCCAC
GAGAACGAGGCTGTGATACTACGGACGCGTTCGCGAGTCATCGGCC
GTGGTCCAGGAGGCGCGCATGCCGTGCGTGCACCCCGGGTCCGTGTC
GTCAAGTCCGGCGTTACGAGAGGCCGTCGACGAGGACGGCTGCC
GTCGGGGAGCTTACGCCGACGGAGAGGCGTTCTGCTCTTCTGACCGT
GTCGAAGCGACGGACGGCGACACCACTGCTCTGCGAGAGTGGTCTTC
GCGCGAGCGCGCGGGAGGTGAGCGTGCAGGCCGAGGACACGGTGG
CACGCCGAGCGCGCTGGAGCGCTCAGTGGAGGTGGAGCGGGAGCG
GCGGCAGAGGACATCGCGCGGCCGAGGGCAGCGGGAGCGGGCGAG
GTGGAGATCCTCGACAACCGTCAGCGGCCGCTGGAGCGAGTC
GACCGGGAGGCGAGGCGACGGGAGCG
GACCCCATGATCGTGGCGCTGGGGCGAGCTGCAGGAGAT
GCGAGGAGCTACATCGGGTCGGCGGCCGTA
CAGCAACCGGCCACCTCCAGGCAGATGCTGGAGGCC
GAGGAGCAGACGAGTCGATGAT
GCGAGGAATAGTGGAGT
GAGGAGGATGATCAGAACAGAGGAGTGGGTC
GAGCGGGCGGGGG
TATATGGCGGCAGCGCGCCCGTGGCGAGGCGTC
ACGCCGGCCATCGCGCCATGCTGCGCTCG
CAAGGGCAGCAGGAGGAGCAGCAGCC
CCGAAGGACGTGAACCAATAG

>FGENESH: 1 3 exon (s) 1161 - 3676 746 aa, chain +
AFGSGSSTTNVTSTAKINSARIIFLPHEASASFYVADALLTCSYQFSQQPAVAVAEMEAP
DQEENPCAICLGGMAAGGGQATFTAEC
SHTFHNCISASVAHGLVCPLCNARWELPFLR
PTAPVPQPPTLPRLRPVPMHGVQPPSEPTAS
PPLMHGMPPFPAQAPP
PRGHIMQHQ
PPPPNVHVVQHHQPPP
VHTVQHHQPPP
PEPTVVFDDDE
QVEPASRPPAD
STPAA
ASNGA
VVVNTHAEY
SAVARDSSDN
FAVLHV
KAPAMADT
VAAGSDK
PPP
RAPLD
LTV
LVD
VSGS
MSGHKL
ALLKQAMRF
VIDNLGP
NDRLS
VVSFS
SEARRL
TRLTRMS
DAGKALADTY
TMMRR
RGPSGVQANN
YEELV
PPSFART
GADGEWS
SAPI
HTFG
FNDH
AAAMHV
IAEATGGTFSFI

ENEAVIQDAFAQCIGGLLSVVVQEARIAVACVHPGVRVSVKSGRYESRVDEDGCAASVR
VGELYADEERRFLLFLTVPRVEATDGDTTALARVVFSYRNAASGAEVSVTAEDTVVARPE
HAPSASERSVERERVRVEAAEDIAAARAAAERGEHQEAVEILDNRQRALLEQSEAAGDG
DPMIVALGAELQEMRGRVSNRQSYMRSGRAYMLAGMSAHQQQRATSRQMLEPEEQQTSMM
ARNSGVRRMIRRGVGSSGGYMAAAAPVAEASNEATMSYATPAMRAMLLRSREARGASAE
QGQQEEQQPMAGKDDAGSSGPKDVNQ

>FGENESH: [mRNA] 2 1 exon (s) 4137 - 4568 432 bp, chain -
ATGTGCTGGTCGCTGCACGGCCGCGTGCCGGTTCCAGCTCCACGCATAGCGGTTGCAGC
ACCCGGCACCTCGCCCGCAGCTGGTCGCCCCGCATCTCGCCGATTGCAGCATTGTAGCC
TCACGCTCGAAGCTCCCCGGCTCCGCCAGCTGCCGTGGCGGGCCGCACCCGCAAC
ACCAGATTACAACGAAAAACCGAGACGTAAATGTATCCAGCGGTGCTGGTAGCTGTG
TCCAGCGGTGGCCATGAACGCACCTGCTTGAGGAGATGAGGAGATAAGAGGAAGG
TATGGGCATAGTGGCTAGTCAACGACAATGGACAAGCAAAGGAAGCAGTGACACACGA
GGCGTATATGTGGCGAGCGCGAACACACGTGGGCCAGGGCCATGTGCGGGAGCGACCG
GCTCAAAGTTAA

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

>FGENESH: [mRNA] 3 6 exon (s) 4782 - 7520 1347 bp, chain +
ATGGCCAATCTGCTGGAACTAGCCGACACAGAACGCTGCAATGGTGATTGCCGGATGCT
GCGTGCACGCGCATCATGTGCTGGAAGCGACGAGCAATTGCTGGAAGCCGCTGGCCAT
TTTGCTGGAACAGCAAGCCTTTTGCTAGGACGGTGGAGCGGGAGCTACAACCATTG
TTCCGGCGACGGCGTTGTGATTTGCTACAACCGACAATGAGAAAGCTACAACCGCGCC
TGGATTGCTGCATCCGTGTGGCGGGCAACGGTGAGCTACAACCACCTTATTCTTG
CTGCAACCAGGTGATCTGGATTGCTGGATCCGGTGAATTGGTTGCTGGAACCAGCGTACT
CCGGAGCCGACGGGGCGGGAGACGACGTGCAGGCATCGAGGCAGATGGAAGCAGGGCTA
CTCGGGAGCGAAGCGATGAGCCGACGGGGGGGGAGCCCACGTGCGGGCACCAAGATTG
ACGGGCAAAAGCGAAAAAGAAACAACCTCCTTCTTCCCACGCCTGCCATGAATTGAAA
CGACCAGGGTGCCATTCCATCACCGCCGAGGAGGCCACCTCTGCCGTAGGCTGCTTG
CCCCATCCGTGCGGCCAGAACCTCTCGACGCCGGCACAGCACGCCCTCTCCCGCCGG
CCGATGCCATGGTCCTTGACGCCGGCACATCTGCTGCTGCCGCCGGTAACCTCCACT
GCTGCCGGCTCTCGTTCTTGCAACCAGATCAGTCTGGAAAATCCATCAGTCAT
GACGTACAACAATGTTGTTGGCTGCCGGTGTGTCACCGCCGTCTGCCGTCA
TGCCGTACCGTCGGAACGAGCGCACCGAGCTGGAATCGAGATTGGCAAAGGAAATC
CGCATCACCAGCCGCCGGAACGTCCATGTCGTGCAGCATTGTTACAAGCTGTTGG
GACTATATTATGAGATGGATGGACAACACTACTCCTCGCCGAGTCGTTGTGTCGCCGA
GTCGCCGGTGCAGGGTGGGGCTGTTGCCGTGGAGGGTATGGTAGATGAGCGTGTGCGGA
GAGGGTGAAGCGACTTGGTACTCCTCCGGAGCGCCGGCAGGTGCGCAGCCGCAGCTGC
ATCTCTGGCAGCGGGCTTCCTCGCCTCCAGCATGCGCCTCGGCCGCCAGAGGCC
TGGATGGAAGGATCGAAGATCCCCTCGAGGCCTGGAAAGTAGCCCATGCCACAAGCCA
GCGTTGGAGGACTTCGTGCCGGTGCAGCCTGCTCCCTGCGCTTCTCCGACGCCGG
GGGCAGAGGGAGGAAGTGTCAAGCCTAA

>FGENESH: 3 6 exon (s) 4782 - 7520 448 aa, chain +
MANLAGTSRHRSCNGDSPDAACTRIMCWKRRAILLEAAGHFAGNSKPFLGRWSGELQPL
FRRRRCDFATTNEKATTGAWICCIRVAGGNELQPPYFLLQPVIWIAGSGDLVCWNQRT
PEPTGAETTCRHRGEMEAGLLGSEGDEPTGGGAHVAPRFTGKSEKETTSFFPTPCHELK
RPGCHSITAEELWPSGCLPHPSRQNFPSTAQARGSPRRMPWSLPGTSAARRRNST

ARRLSRFSCNQISLGKSISHDVQQCCWLPLSGCVTAVLPSCHRERRAHRAGNRDWAKEI
RITSRRGTSMSCSIVLQAVWDYIYEMGWTTTPRRVVVVRVAVAGWGLVAVEGMVDERVG
EGRSDLVLLPERRQVRSRSCI SGSGFLRLQHASSAAQRRWMEGSKIPSRRWKVAHAHKP
ALEDFVPRVRACSLRFSDAGGQREELSA

>FGENESH: [mRNA] 4 2 exon (s) 13793 - 14096 159 bp, chain +
ATGACCAAGAAAGGTATAACGTGAGGGAGTATGTGCTCTAAAGGATGGCTTCAAAAG
AAAAGAGAAAGATCATTGAGAGTCTTGTTGACGAATGTCTTCATTCAAAAGAGCCAAT
TTTGGCATTATGTCCTTACAGGAATTACCTGCATAG

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