

FGENESH 2.6 Prediction of potential genes in Triticum genomic DNA

Seq name: region7

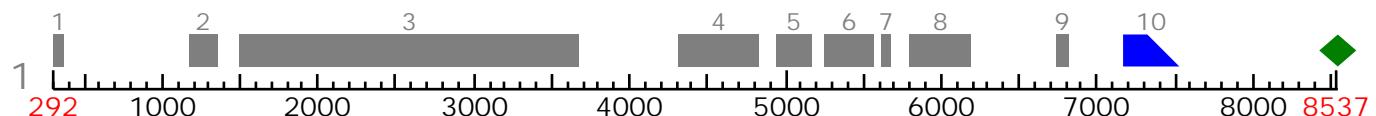
Length of sequence: 15001

Number of predicted genes 3: in +chain 3, in -chain 0.

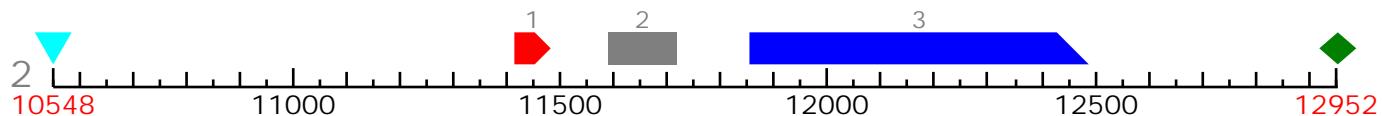
Number of predicted exons 15: in +chain 15, in -chain 0.

Positions of predicted genes and exons: Variant 1 from 1, Score: 1114.543750

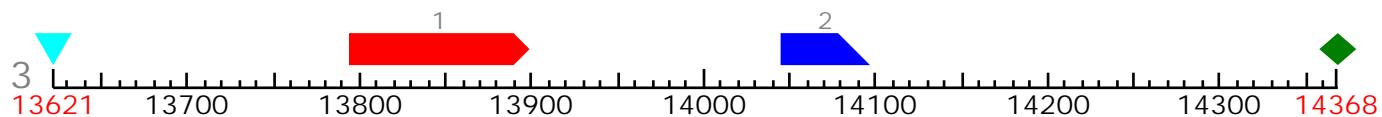




1	+	1	CDSi	292	-	360	0.05	292	-	360	69
1	+	2	CDSi	1161	-	1346	13.98	1161	-	1346	186
1	+	3	CDSi	1487	-	3664	722.04	1487	-	3664	2178
1	+	4	CDSi	4306	-	4824	56.32	4306	-	4824	519
1	+	5	CDSi	4933	-	5159	26.79	4933	-	5157	225
1	+	6	CDSi	5240	-	5559	57.52	5241	-	5558	318
1	+	7	CDSi	5610	-	5668	-0.94	5612	-	5668	57
1	+	8	CDSi	5788	-	6185	59.90	5788	-	6183	396
1	+	9	CDSi	6727	-	6809	9.60	6728	-	6808	81
1	+	10	CDS1	7159	-	7520	75.00	7161	-	7520	360
1	+		PolA	8537			2.19				



2	+	TSS	10548		-2.11						
2	+	1	CDSf	11411	-	11479	0.36	11411	-	11479	69
2	+	2	CDSi	11587	-	11715	18.76	11587	-	11715	129
2	+	3	CDS1	11851	-	12486	96.54	11851	-	12486	636
2	+		PolA	12952			2.19				



3	+	TSS	13621		1.09						
3	+	1	CDSf	13793	-	13898	-1.27	13793	-	13897	105
3	+	2	CDS1	14044	-	14096	4.58	14046	-	14096	51
3	+		PolA	14368			2.19				

Predicted protein(s):

>FGENESH:[mRNA] 1 10 exon (s) 292 - 7520 4401 bp, chain +

AAGCAGCAGCAGGCTGATCAACATGTTGCACATTGGCATAGTATGCTTCCAGACCAAGT
GGCCCCATGGCATTGGTCGGGTCAAGCACGACGAACGTGACCTCCACGGCGAAAATT
AACAGCGCTAGAATTATTTCCCGCACGAAGCATCTGCCTCGTTTATGTCGCTGAT

GCCCTGCTAACTTGTTCGTACCAATTTCACAGCAGCCTGCAGTCGAGAGATG
GAAGCCCCCTGACCAGGAGAATCCTTGCAGGCCATCTGCCTCGCCGGCATGGCCGCCGGCG
GGGCAGGCCACCTTCACGGCGGAGTGCTCCCACACCTTCAACTGCATCTCCGCC
AGCGTCGCGCACGGCACCTCGTCTGCCCCTGCAACGCGCTGGCGAGAGCTGCC
TTCCTGCGACCCACCGCGCCGGTGCCAGCCGCCTACGCTGCCTAGGCTGGTGTCCC
GTTCCCATGCACGGCGTGCAGCCTCCAGCGCAGGCCACCGCCGCCGGCATATCATGCAG
GGCGGGATGCCTCCGTTCCCAGCGCAGGCCACCGCCGCCGGCATATCATGCAG
CATCACCAGCCGCCGCCGAACGTGCATGTCGTGCAGCATCATCAGCCGCCGCC
GTGCATACCGTGCAGCATCATCAGCCCCGCCGGCAGCCTACGGTGTCTTCGACGAC
GACGAGCAGGTGGAGCCGGCTCCAGGCCAGCTGACAGCACACCGCAGCTGCATCG
AACGGGCAGTGGTGTCAACACGCACGCCGAGTACTCGGCCGTGCCAGGGACTCGTCC
AGCGACAACCTCGCCGTCTCGTGCACGTCAAGGCTCCCGCATGGCCGACACCGTGGCG
GCCGGCAGCGACAAGCCGCCCGCGCGCCGCTGGACCTCGTACCGTGTGACGTC
AGCGGCAGCATGAGCCGCCACAAACTGGCGCTCCTGAAGCAGGCCATGCGGTTGTCATC
GACAACCTCGGCCCAACGACCGCCTCCGTGTGTCCTCTCCTCCGAGGCCGCCGG
CTGACCAGGCTCACGCGCATGTCGGACGCCGGAAAGGCACTGGCGTGANCGCCGTGGAG
TCCCTCGCGCGCGCGCGGACCAACATGCCGAGGGCTCCGCACGCCGCCAAGGTG
CTCGACGAGCGCCGGCACAGGAACGCCGTCTCCAGCGTGTGTCCTCTCCGACGGTCAG
GATACTATACCATGATGAGGCCGCCGGGACCGTCCGGCGTCAAGGCCAACAACTACGAG
GAGCTCGTCCGCCCTCCTCGCACGCACGGCGCTGACGGCGAGTGGTCCGCCGATC
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ACGGCGGCACGTTCTCGTCATCGAGAACGAGGCTGTGATACAGGACGCCGTTCGCGCAG
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CACCCCGGGGTCCGTGTGTCCTCCGTCAAGTCCGCCGTTACGAGAGGCCGTCAGCAG
GACGGCTGCCGCATCTGTCGAGTCGGGAGCTCTACGCCACGCCAGGAGAGGCCGTTTC
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AGAGTGGTCTTCAGCTACAGAAACGCCGAGCGGCCGGAGGTGAGCGTGACGCCGAG
GACACGGTGGTGGCGAGGCCGGAGCACGCCGAGCGCGTGGAGCGCTAGTGGAGGTG
GAGCGGGAGCGCGTCCGGTGGAGGCCGGAGAGACATGCCGCCGGCGAGGGCAGCGCG
GAGCGGGCGAGCACAGGAAGCGGTGGAGATCCTCGACAACCGTCAGCGGCCGTGGAG
CAGTCGGAGGCCGCAGGGACGGCGACCCATGATCGTGGCGCTGGGGCGGAGCTGCAG
GAGATGCCGGCGCGTGTGCAACCGGCAGAGCTACATGCCGTGGGGCGGCGTACATG
CTGCCGGCATGAGGCCGCCACAGCACGCCACCTCCAGGCAGATGCTGGAGGCC
GAGGAGCAGCAGCTCGATGATGGCGAGGAATAGTGGAGTGAGGAGGATGATCAGAAGA
GGAGTGGGTCGAGCGGGGGGATATATGGCGGCAGCGGCCCGTGGCGAGGCCGTC
AACGAGGCCGACGATGTCGTACCGCACGCCGGCATGCCGCTGCTGCCGCTCGCG
GAGGCCGTGGGGCGTGGCCGAGCAAGGGCAGCAGGAGGAGCAGGCCATGCCGGA
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GCTACCCAGCACCGCTGGATACATTACGTCTCGCTTTCGTTGTGAATCTGGTGTG
CGGGGTGCGGGGCCGCCGACGCCAGCTGGCGAGGCCGGGGAGCTCGAGCGTGAGGCT
ACAATGCTGCAATCGCGAGATGCCGGCGACCGAGCTGCCGCCGAGGTGCCGGTGTG
CAACCGCTATGCGTGGAGCTGGAACCGGCACGCCGGCTGCCAGCGACGCCATAGCG
GTACTGCTACCGACGCCGTGGCGCTACGACCAGCGCGGCCGACGCCACCGTCGGC
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CGTCCTCGGCACTGTGGCGACATGCCACGCCGGCATGCTACGACGGCAAGACAAGGTGCT
ACTACCGACAAGTTTTGCTGGAACCGATGCCAATCTGCTGGAACCTAGCCGACACA
GAAGCTGCAATGGACGGTGGAGCGGCCAGCTACAACCATTGTTCCGGCGACGCCGTG
ATTGGCTACAACCGACAATGAGAAAGCTACAACCGGCCCTGGATTGCTGCATCCGGT

GAAGTGCAGCGGCGACGGCAGCTCTGCCTTTGCTGCAAACGGCAACCAGAAAGCTTCC
ACTGGCGACCGCATATGCTACAGCCAGGGATGACGGTAAGTGTGGCCGGCAACGC
GTACTCCGGAGCCGACGGGGCGGAGACGACGTGCAGGCATCGAGGCGAGATGGAAGCAG
GGCTACTCGGGAGCGAAGGCGATGAGCCGACGGGGCGGAGCCCACGTGCGGGCACCAA
GGTAGATGGAAGCGGGCTGCTCGGTCTCGGAGCGAAGGCAGCAAGCCGGCGGGGG
GCGAAGACGACGTGCGGGCACCAGGGCAAGATGGAAGTGGGCTGCTCGGAGGGAAAGC
GGCGAGCCGGCAAGGGCGGAGATGCGCGAGCGTGGCGAGCAAGGAAGGGCGGAGAT
CCGGCAGCTCGACGCCATTACGGGAAAAGCAGTACAACGGGAC
ATTGGATCAGATCTGACGACTCCTCTTCCCCACGCCTGCCATGAATTGAAACGACCA
GGGTGCCATTCCATCACCGCCGAGGAGCCGCACCTCTGCCGTCAGGCTGCTTCCCCAT
CCGTCGCGGAGAACCTCTCGACGCCGGCACAAGCACGCGCTCTCCCGCCGGCGATG
CCATGGTCCTTGACGCCGGCACATCTGCTGCTGCCGGCGTAACCTCACTGCTCGC
CGGCTCTCTCGTTTCTGCAACCAGATCAGTCTGGAAAATCCATCAGTCATGACGTA
CAACAATGTTGGCTGCCGTTGGATGTCACCGCCGTCTGCCGTATGCCGT
CATCGTCGGAACGAGCGCACCGAGCTGGAAATCGAGATTGGCAAAGGAAATCCGCATC
ACCAGCCGCCCGGAACGTCATGTCGTGCAGCATTGTTACAAGCTGTTGGGACTAT
ATTATGAGATGGATGGACAACACTCCTCGCCGAGTCGTTGTCGAGTCGCC
GTTGCAGGGTGGGGCTCGTGCCTGGAGGGTATGGTAGATGAGCGTGTGGAGAGGGT
CGAACGCACTGGTACTCCTCCGGAGCGCCGGCAGGTGCGCAGCCGAGCTGCATCT
GGCAGCGCCGGCTTCCTCGCCTCCAGCATGCGCCTCGGCCAGAGGGCGTGGATG
GAAGGATCGAAGATCCCCTGAGGCCTGGAAAGTAGCCCATGCCACAAGCCAGCGTTG
GAGGACTTCGTGCCGGTGCCTGCTCCCTGCGCTTCCGACGCCGGAGGGCAG
AGGGAGGAACGTCAAGCCTAA

>FGENESH: 1 10 exon (s) 292 - 7520 1466 aa, chain +

KQQQADQHVAWHMSLPRPSGPMAFGSGSSTTNVTSTAKINSARIIFLPHEASASFYVAD
ALLTCSYQFSQQPAVAVAEMEAPDQENPCAICLGGMAAGGGQATFTAEC SHTFHFNCISA
SVAHGLVCPCLCNARWELPFLRPTAPVPQPPTLPRLGRPVPMHGVPQPSEPTASPLMH
GGMPPFPQA PPPRGHIMQHHQPPPNVVVQHHQPPP VHTVQHHQPPPPEPTVFDD
DEQVEPASRPPADSTPAAASNGAVVNTHAEYSAVARDSSDNFAVLHVKA PAMADTV
AGSDKPPPRAPLDLTVLDVSGSMSGHKLALLKQAMRFVIDNLGPNDRLSVVSFSSEARR
LTRLTRMSDAGKALAVSAVESLAARGGTNIAEGLRTAAKVLDERRRNAVSSVLLSDGQ
DTYTMMRRRGPSGVQANNYEELVPPSFARTGADGEWSAPIHTFGFGNDHAAAMHVI
TGGTFSFIENEAVI QDAFAQCIGLLS VVVQEARI AVACVHPGVRVSVKSGRYESRVDE
DGCAASVRVGELYADEERRFLFLTVPRVEATDGD T TALARVVFSYRNAASGAEV
DTVVARPEHAPSASERSVEVERERVRVEAAEDIAAARAAAERGEHQEA
EVRLNRQALE QSEAAGDGDPMIVALGAELQEMRGRVSNRQSYMRSGRAYMLAGMSAHQQRATSRQM
EEQQTSMMARNSGVRRMIRRGVGSSGGYMAAAAPVAEASNEATMSYATPAMRAM
LRLRSR EARGASAEQQQEEQQPMAGKDDAGSSGPKDVRSWPPLDTATQH
RGAGPPTAACRSRGSFEREATMLQSARCGATSCAARCRVLQPPMRGAGTGT
RPCSDQHIA VLLPTRRGATTSAAATATVGQKGTTIYVDGCNQRLPMLQPRPRH
CGDMHTGDATTARQGA TTDKFFCWNRWPILLELADTEAAMDGG
AASYNHCSGDGVVILLQPTMRKLQPAPGFAASG EVRRRRQLCVFAANGNQ
KASTGDRICYSQGMTVKCGRRQRVLSRRR RAGIEARWKQ GYSGAKAMS
RRGAEP TCGHQGEMEAGL LGSRERRQQAGGGAKTT
CGHRGKMEVGLLREG GEPARGGDAASGG
EQRG DGPASFDADSRAKAKKKQYNG
DIGSDLTTSFFPTPCHELKR
GC HSITAEEPHLWPSGCLPHPSRQN
FSTPAQARGSPRRPMPWSLTPGTSAARRRN
STAR RLSRFSCNQISLGKSI
SHDVQQCWLPLSGC
VTAVLPSCRHRRERA
H RAGNRD
WAKE IRI TSRRGTSMSCSIVLQAVWDYI
YEMGWTT
PRRVVV
RVAVAGWGL
VAEGMV
DERVGEG
RSDLVLLPERRQ
VRSRSCISGSGFLRLQ
HASAAQRRWM
EGSKIPSRR
WKVA
AHKPAL

EDFVPRVRACSLRFSAGGQREELSA

>FGENESH: [mRNA] 2 3 exon (s) 11411 - 12486 834 bp, chain +
ATGGGCCAACGGCTCATTGGCACTTGACCCACGCCCTGATCGGGGCGTCCAGCCAA
GCAAGGCTGAGGGAGGCACTGAAGCGATGGAAAGCTCCACCGCTGCCACTCATGCACCTC
ACCGTCGACCTCTACACCGACCGTCGCTGCCCGGGCGCAGTCCTCCATGACGAACCAGC
AATGGCCGGAACGCTAAGAAAAGAAAACGAACACAAATACGATTCGATCTGGATCGAA
GCAGATAGAGAGAAAAGAACTCCTCGTGGAAAAGTTGCGCCGCCAACGGCCGCCG
TTCCTCTCGATCCGGACGGCATCGGCAAGCCAGGCCGTTCGGAAGAAGAACTCACCCA
CAGGGCAAAGGGCACCACCAAGAGCCATTTGACGGCGACCGCTCACCGTCAAGGTGC
TCGCGCACGCCGCAAAGGGTCAGCGGGGCCGCATCTGAAACCGCCGTCGCTCG
GCGAAGGGGAGCAGAGGAGGCTCTGCTCGCGCTCGCGTCCCTCTCGCGCTGGGTGG
TGGTGGAAAGAAGAGAGGGAAAGGGAACGGCTCGCGCGCAGTGGCCCTGCCGCCAG
CACGGGGCCGGAGCGGCCTACCAAGGGCCTGCCCCCTTACCTTGACAGAGAGGGAGCC
GACGGGACAGAAGAAGAGAAAGAAGAAGGGAAAGGGAAAGAAAGAGAACGGCCAGGCTC
GCGCGTGGTGGACGCCGTCGCCGGCTCGACCGGACAGGCACGGCGCCGCCAG
CACGGCGCGTCGCCGGCACCAGGACATCGTCGGCGAGAGACGAGAGGATGA

>FGENESH: 2 3 exon (s) 11411 - 12486 277 aa, chain +
MGPTAHWALDPRPDRGRPAQARLREALKRWEAPPLPLMHFTVDLYTDRRCPGAVLHRRTS
NGRNAKKRKRTQIRFRSRIEADREKRTPRRKSCAATAAPFLSIRTGIGKPSRSEELTP
QGQRAPPQSHLTATRSPSRCRTPAKGSAGAPHLETAVARAKGSRGGSARAARVPLALGW
WWKKRGKGNGSRGAVALAAEHGGRSGLPGRCFPFYLDREGADGTEEEKEEGKGRKRTARL
ARWWTPSPAARPDRHGAAAEGAVAGDRDIVGRETRG

>FGENESH: [mRNA] 3 2 exon (s) 13793 - 14096 159 bp, chain +
ATGACCAAGAAAGGTCTAACGTGAGGGAGTATGTGCTCTAAAGGATGGCTTCAAAAG
AAAAGAGAAAGATCATTGAGAGTCTTGGTGACGAATGTCTTCATTCAAAAGAGCCAAT
TTTGGCATTATGTCCCTTACAGGAATTACCTGCATAG

>FGENESH: 3 2 exon (s) 13793 - 14096 52 aa, chain +
MTKKGHNVREYVLSKGWLQKKRERSLRVLVDECLSFKRANFGIYVPYRELPA