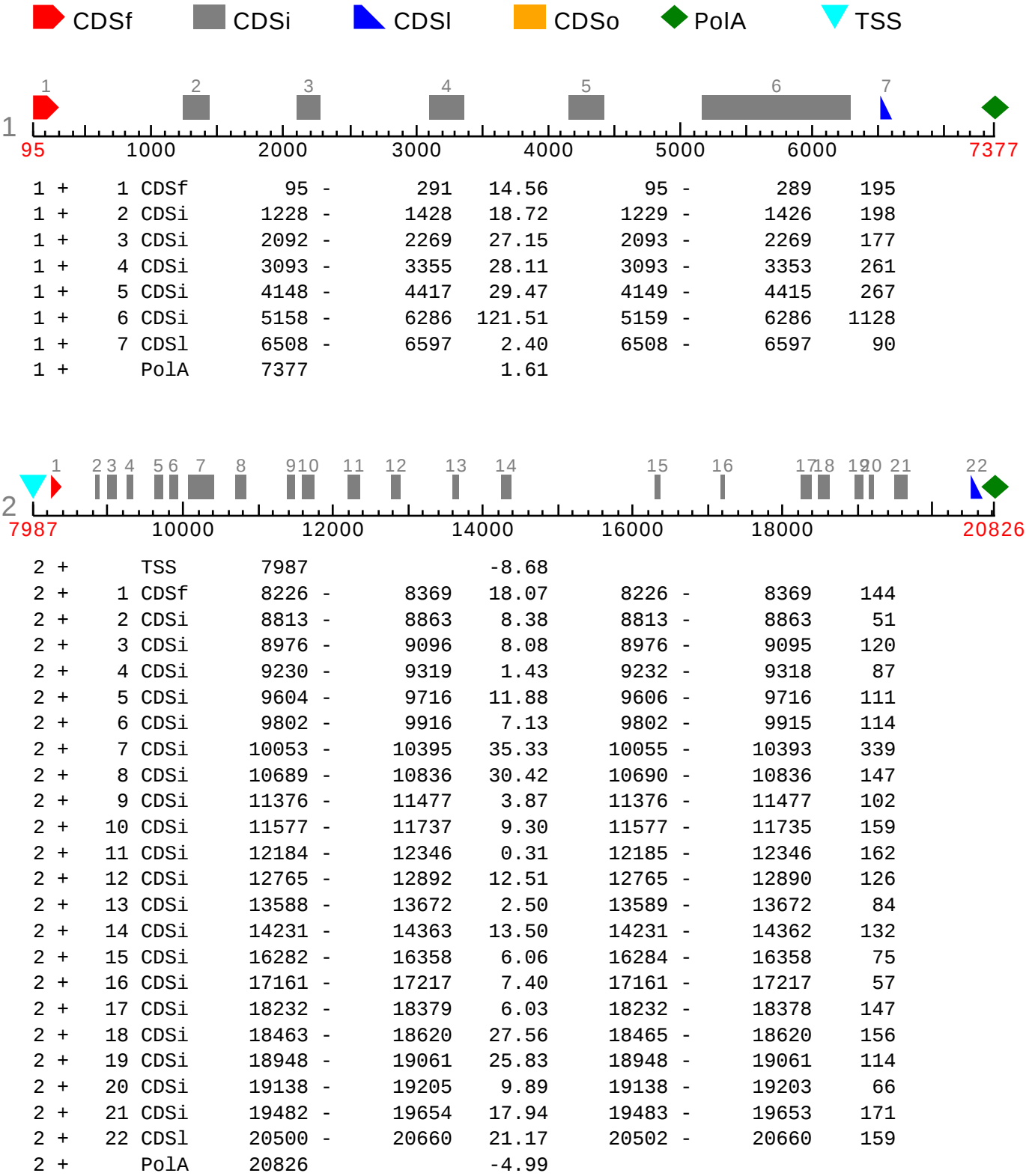


FGENESH 2.6 Prediction of potential genes in Tomato genomic DNA
Seq name: test sequence
Length of sequence: 20890
Number of predicted genes 2: in +chain 2, in -chain 0.
Number of predicted exons 29: in +chain 29, in -chain 0.
Positions of predicted genes and exons: Variant 1 from 1, Score:464.376855



Predicted protein(s):

>FGENESH:[mRNA] 1 7 exon (s) 95 - 6597 2328 bp, chain +
ATGAGAAAGCAAGAAGATATAGAAAATGAAGGAGTTGGGGTAATGGTAATGGAAGATGGG
AAGGATTTAGAGAGGAATATTTTCATCTGAGGGTGGTTTTAGAGAGCCATTGCTTAAATCA
AAGAGTAGAGTCAATAATACATCACAAATTGCTATTATTGGAGCCAATGTTTGCCTTATT
GAGAGTCTTGATTATGACATTGTTGAAAATGACCTATTCAAGCAAGATTGGAGATCAAGG
AAAAAGGTCCAGATATATCAATATATATTCCTTAAGTGGACACTCGTGCTTCTTATTGGA
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TTTGCAGGTTGCAATTTGGGTCTTGCAACTTGTGCTGCCATCCTATGTGCATGTATTGCA
CCTGCAGCTGCAGGGTCAGGAATTCCTGAAGTTAAAGCATATTTGAATGGTGTGGATGCT
CATTCCATTTTAGCTCCTAGTACTTTATTTGTAAAGATAATTGGTTCTGTTTTGGGTGTT
TCTGCTGGATTTGTTGTTGGTAAGGAAGGACCCATGGTCCACACTGGCGCTTGCATAGCT
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GCCGCTTTCCGTGCTCCAGTTGGTGGTGTCTTTTTGCTCTCGAAGAAGTAGCCTCATGG
TGGCGAAGTGCTCTACTTTGGAGGACTTTCTTCACAACTGCTATAGTAGCTATGGTGCTC
AGATCTTGCATTCAATTCTGTGCGAGTGGGAACTGTGGACTATTTGGTCAAGGAGGTTTG
ATAATGTTTGATGTGAATTCAGGATTTCTAATTATAACACTGTAGATGTACTGGCGGTA
TTGACAATTGGAGTTCTTGGAGGCCTTTTAGGAAGCCTTTATAATTATCTTGTGGACAAG
GTCCTGCGGACTTACAGCATCATTAATGAGAGAGGTCCTGCTTTCAAATCATGCTCGTA
ATGACCATTTTCGATCCTGACTTCTCTTTGTGCATATGGTCTTCCATGGTTTGCAAGTTGC
ACACCGTGCCCCGTAGGCTTGGAGGAAAAATGTCCTACTGTAGGTCGCTCTGGAAACTAT
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AATGATGACGCCATCCGCAATTTGTTTAGTGCAGAAAATTCAAGTGAATTCCACCTTTCT
ACACTTTTTGTCTTCTTCGCTGGGGTATACTGCCTTGGCATTATTACCTATGGAATTGCT
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GGAAGTGTCTTAGGTTCCGGTCTCTAATCTTAATAATGGCCTGTTTGCCTCCTTGGGGCT
GCCTCCTTCCCTTGGTGGTACTATGAGGATGACAGTATCACTCTGTGTCATACTACTTGAG
CTCACCAATAATCTGCTAATGCTTCCGTTGGTGATGCTTGTCTCCTTGTATCAAAAAT
GTGGCCGATAGTCTTAACAAGGGTATCTATGACCAGATTGTGCAAATGAAAGGCTTGCCT
TACTTGGAAGCACACGCCGAGCCTTACATGAGGCAATTGGCTGCAGGAGATGTTTGTCT
GGGCCTTTAGTAACATTTTCAGGTGTTGAGAAGGTAGGAAACATAGTACACGCTTTGAAG
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ATGTCTCTGGCCAAAGCTGCAATTCTTTCCGTGAACTCGGTCTCAGACATTTGTGTGTC
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CCAGAGCATATAAAGGGACTGTATCCACATTTGGTCCATCACAAGTAA
>FGENESH: 1 7 exon (s) 95 - 6597 775 aa, chain +
MRKQEDIENEGVGVMMEDGKDLERNISSEGGFREPLLKSKSRVNNTSQIAIIGANVCPI
ESLDYDIVENDLFKQDWRSRKKVQIYQYIFLKWTLVLLIGLFTGLVGFLLNIAVENIAGF
KLLLASDLMLEDKYFRAFAIFAGCNLGLATCAAILCACIAPAAAGSGIPEVKAYLNGVDA
HSILAPSTLKVKIIGSVLVGSAGFVVGKEGPMVHTGACIANLLGQGGSRKYHLTWKWLRY
FKNDRDRDLITCGAAAGVAAAFRAPVGGVLFALIEVASWWSALLWRTFFTTAIVAMVL
RSCIQFCRSGNCGLFQGGLIMFDVNSGFPNYNTVDVLAVLTIGVLGGLLGSLYNYLVDK

VLRTYSIINERGPAFKIMLVMTISILTSLCAYGLPWFASCTPCPVGLEEKPTVGRSGNY
KNFQCPAGHYNDLASLFMNTNDDAIRNLFSAENSSEFHLSTLFVFFAGVYCLGIITYGIA
IPSGLFIPVILAGASYGRLVGSVLGSVSNLNNGLFALLGAASFLGGTMRMTVSLCVILLE
LTNNLLMLPLVMLVLLVSKTVADSLNKGIIYDQIVQMKGLPYLEAHAEPYMRQLAAGDVCS
GPLVTFSGVEKVGNIHALKFTRHNGFPVVDLPFSDAPEFCGLVLRSHLVLLKGKTFT
KQNVLSGSNTLKKFHAFDFAKPGSGKGLKFEDLSFSPEEMEMYVDLHPITNTSPYTVVET
MSLAKAAILFRELGLRHLCVVPKTTKRNPVIGILTRHDFMPEHIKGLYPHLVHHK

>FGENESH:[mRNA] 2 22 exon (s) 8226 - 20660 2853 bp, chain +
ATGGAAGCGATCGAGGAATTGGAGCAGCTCGGCGATGCGATGAGGCAAGCCGCTGCGTTG
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AATGTAGTGGCGCTAGGCAATACTGGTGCTGGTAAATCAGCTGTATTGAACAGTCTTCTA
GGACATCCTGCTTTGCCAACTGGTGAAGGAGGTGCTACTCGTGCTCCTATATGTATTGAA
CTTAAAAAGGATAGTTCCTTAAACAGCAAGTCAATTATCTTGCAAATCGACAGTAAATCC
CAACAAGTCTCTGCAAGTGCTCTTCGCCATTCTTTACAGGATAGACTAAGCAAGATCTCA
AACAAAAGCCGAGACGAGATATATTTGAAGCTTCGAACTAGTACAGATAGTTTTCTACTT
ATCTTTGTTGTTTTTGTGGTTTTACCTTGCTGTACAGCTCCTCCATTGAAGTTGGTTGAT
CTACCTGGAGTGGATAAGGGACATATTGATGATGCATTGAGTACATATGTTGCGCGCAGT
GATGCCATATTACTAGTGGTTATTCCCGCTGCTCTAGCACCAGAAATTTCTCGTATAAA
GCACTTCGACTTGTGAAGGAGCATGATGGAGAATGTACAAGAACTATAGGTATTATTAGC
AAGGTAGATCAAGCAGCTTCAGATCCAAAAGTTCTTGCACTATCCATGCGCTTTTGCTA
AACCAGGGACCACCAAGCACATCCGATATCCCATGGGTTGCTTTGATTGGTCAATCTGTT
TCTATAGCTTCAGCCCAATCAGGAAATGTAGGCAATGATAATTCCTAGAAACAGCATGG
CGTGCTGAGAGTGAAAAGTCTTAAATCAATATTGACAAAGGCTCCTCAAAGCAAGCTTGGT
AGGGTAGCATTAGTGGAGGTCCTTGCTCAACAGATCCGTAATCGAATGAAAGTCAGACTT
CCAAATCTTCTCTCAGGGCTCCAGGGAAAATCTCAATCAGTAAAGGATGAACTGGTAAAG
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GTAATTGCAAGTTTTGAAGGCAAATTCCTGATAGGATTAAGCAGCTACCTATGGATAGA
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AAAAAAAGTGGCTGGAGCAAGCGATGGTTTGTGTTTAAATGACAAGACTGGAAAGCTTGGA
TATACCAAGAAGCAAGAAGAACGGCATTTCATGGTGTAATTACTTTGGAGGAATGTAAT
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ATGATGACTAGGAAACCAGCAGATCCAGAAGAAGAACTTCGATGGATGGCTCAAGAAGTA

CGTGGTTATGTTGAAGCTGTTCTCAACAGTCTTGCTGCTAACGTACCAAAGGCAGTTGTT
CTTTGCCAAGTAGAGAAGGCCAGAGAAGATATGCTTAATAAGTTGTACAGTTCTGTCAGC
GCACAAAGTAGAGCAAAGATCGAAGAGCTACTCCTGGAAGACCATAATGTGAAGCGTAGG
AGGGAGCACTTTTCAGAAACAGTCCTCTCTTCTTGCTAAGGTCACTCAGCAGCTTAGTGTT
CATGATAATCGAGCAGCTGCTGCGTCTAGCTACTCAAATAGTGATGGAGCGGAAAGCGTC
TCAAGATCTGGTGGACAGTCATCAGGTGATGAATGGCGATCTGCATTTGATGGTACTTCA
AGTGCCCCTCAAATGGTGATGCAGGGTCTAGAAGTCGTCGTACACCTAGCCGGATGCCA
CCTGCACCTCCTGGTTCTGGACAAAAATCCTAG

>FGENESH: 2 22 exon (s) 8226 - 20660 950 aa, chain +

MEAIEELEQLGDAMRQAAAALLADEDVNEAAASNKRPFSLNVVALGNTGAGKSAVLNSLL
GHPALPTGEGGATRAPIELKLDSSLNSKSIILQIDSKSQVVSASALRHSLQDRLSKIS
NKSRLDEIYLLKRLTSTDSEFLIFVVFVVLPCCTAPPLKLVLDLPGVDKGHIDDALSTYVARS
DAILLVVIPAALAPEISSYKALRLVKEHDGECTRTIGIISKVDQAASDPKVLAAIHALLL
NQGPPSTSDIPWVALIGQSVSIASAQSGNVGNDNSLETAWRAESESLSILTKAPQSKLG
RVALVEVLAQQIRNRMKVRLPNLLSGLQGKSQSVKDELVKFGDQMVNSGEGTKALALELC
REFEDKFLEHLTTGEGGGWKVIASFEGKFPDRIKQLPMDRHFELKNVKRVVLEADGYQPY
LISPEKGLRSLIKTVLELAKEPSTLCVEEVISIRCYALSRLNYAILAVHNCLSEAFCL
FLLLSIPWLAFGNTLMKNEPNLIRNVAFLALYSCLAEVIAIATTALDGFRTAKNMVIAL
VDMERVYVPPQHFIRLVQRRMDRQRRDDGLKNQSSKAAQAEQSMLTRATSSQAGDEKSS
SKSGKDKSAQQDKDSQEGPVLKTAGPDGEITAGFLLKSDKSGWSKRWFVLNDKTGKLG
YTKKQEERHFHGVITLEECNLEDASEEDEPSKSSKDKKATWPDGGKGPSLLFKLTNRVQY
KTILKGAQSTVILKAETLAEKTEWLNKLKNVISSKGGQVIAESSQPMRPSLSEGTPGTPD
MMTRKPADPEEELRWMAQEVRGYVEAVLNSLAANVPKAVVLCQVEKAREDMNLKLYSSVS
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SRSGGQSSGDEWRSAPQNGDAGSRSRRTPSRMPPAPPGSGQKS