

# BLASTn Search Outputs of the 5' Border Sequences in Maize Event DAS-40278-9 against GenBank Nucleotide Collection (nt/nr)

BLASTN 2.2.21 [Jun-14-2009]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= Region\_1  
(1852 letters)

Database: /usr/local/blast/db/blastlibs/nt  
11,350,961 sequences; 30,878,341,354 total letters

Searching.....done

Sequences producing significant alignments:		Score	E
		(bits)	Value
gb AC165175.2	Zea mays clone ZMMBBb-136N21, complete sequence	363	2e-96
ref NM_001152615.1	Zea mays hypothetical protein LOC100279619 (...)	305	5e-79
gb EF468501.1	Zea mays clone pBK118-2 retrotransposons GrandeB,...	196	3e-46
emb AJ312478.1	Zea mays Grande retrotransposon DNA, partial LTR...	137	3e-28
gb EU949251.1	Zea mays clone 400160 mRNA sequence	111	2e-20
emb AJ312473.1	Zea mays Grande retrotransposon DNA, partial LTR...	109	6e-20
gb AC206303.5	Zea mays BAC clone CH201-328A17 from chromosome 5...	92	1e-14
gb EF468503.1	Zea mays clone pBK118-4 retrotransposon GrandeB, ...	92	1e-14
emb AJ312503.1	Zea mays subsp. mexicana Grande retrotransposon ...	86	9e-13
gb AY883559.2	Zea mays cultivar inbred line B73 teosinte glume ...	84	3e-12
gb EF468507.1	Zea mays clone pBK118-8 LL repeat sequence	82	1e-11
gb EF190066.1	Zea mays clone PS53 chromosome B, genomic sequence	82	1e-11
gb AC209386.4	Zea mays BAC clone CH201-98J13 from chromosome 5,...	80	5e-11
gb AC229879.2	Zea mays BAC clone CH201-103M12 from chromosome 8...	76	8e-10
gb FJ386423.1	Zea mays clone R6-b StarkB element, partial sequence	74	3e-09
gb EF468510.1	Zea mays clone pBS-1 LL repeat sequence	74	3e-09
gb EF468508.1	Zea mays clone pB3-201 retrotransposon GrandeB, c...	74	3e-09
gb EF190064.1	Zea mays clone pStark5.5 chromosome B, genomic se...	74	3e-09
gb EF190061.1	Zea mays clone FS2_19 chromosome B, genomic sequence	74	3e-09
emb AJ312504.1	Zea mays subsp. mexicana Grande retrotransposon ...	74	3e-09
gb AC194842.4	Zea mays BAC clone CH201-514N20 from chromosome 4...	72	1e-08
gb EF190062.1	Zea mays clone FS2_20 chromosome B, genomic sequence	72	1e-08
gb AC204937.4	Zea mays BAC clone CH201-488A19 from chromosome 5...	70	5e-08
gb AC205029.6	Zea mays BAC clone CH201-7M14 from chromosome 5, ...	70	5e-08
gb EF190050.1	Zea mays clone 46F3FF5Rm4 chromosome B, genomic s...	70	5e-08
gb FJ386429.1	Zea mays clone R9-b StarkB element, partial sequence	66	8e-07

gb	FJ386412.1	Zea mays clone L5-a StarkB element, partial sequence	66	8e-07
gb	EF468504.1	Zea mays clone pBK118-5 LL repeat sequence	66	8e-07
gb	EF468502.1	Zea mays clone pBK118-3 LL repeat sequence	66	8e-07
gb	EF190065.1	Zea mays clone PS52 chromosome B, genomic sequence	66	8e-07
gb	EF190063.1	Zea mays clone FS3_49 chromosome B, genomic sequence	66	8e-07
gb	DQ183075.1	Zea mays clone A-RGA7 resistance gene analog-like...	66	8e-07
gb	EF468505.1	Zea mays clone pBK118-6 LL repeat sequence	64	3e-06
gb	FJ386419.1	Zea mays clone R4-b StarkB element, partial sequence	62	1e-05
gb	EF190048.1	Zea mays clone 46F3FF5Rm1 chromosome B, genomic s...	62	1e-05
gb	AY574035.1	Zea mays rust resistance protein rp3-1 (rp3-1) ge...	62	1e-05
gb	AC185486.5	Zea mays BAC clone CH201-162J17 from chromosome 5...	60	5e-05
gb	AC225631.3	Zea mays BAC clone CH201-111A2 from chromosome 8,...	60	5e-05
gb	FJ386425.1	Zea mays clone R7-b StarkB element, partial sequence	58	2e-04
gb	EF468506.1	Zea mays clone pBK118-7 LL repeat sequence and re...	58	2e-04
gb	EF468500.1	Zea mays clone pBK118-1 LL repeat sequence and re...	58	2e-04
gb	AC165174.2	Zea mays clone ZMMBBb-127F19, complete sequence	58	2e-04
emb	AJ312460.1	Zea mays Grande retrotransposon DNA, partial LTR...	58	2e-04
gb	EZ064107.1	TSA: Zea mays contig65230, mRNA sequence	56	8e-04
gb	FJ386416.1	Zea mays clone L7-a StarkB element, partial sequence	54	0.003
gb	FJ386414.1	Zea mays clone L6-a StarkB element, partial sequence	54	0.003
gb	EU965848.1	Zea mays clone 289347 hypothetical protein mRNA, ...	54	0.003
gb	BT043326.1	Zea mays full-length cDNA clone ZM_BFc0158M15 mRN...	54	0.003
gb	EF468511.1	Zea mays clone pBS-2 LL repeat sequence	54	0.003
gb	EU338354.1	Zea mays cultivar W22 bz gene locus, complete seq...	54	0.003
gb	EF190051.1	Zea mays clone 46F3FF5Rm5 chromosome B, genomic s...	54	0.003
gb	EF190049.1	Zea mays clone 46F3FF5Rm3 chromosome B, genomic s...	54	0.003
gb	EF190044.1	Zea mays clone 46F3FF4R-4 chromosome B, genomic s...	54	0.003
gb	AC196084.4	Zea mays BAC clone CH201-52A17 from chromosome 5,...	52	0.012
gb	AC194844.5	Zea mays BAC clone CH201-463C23 from chromosome 5...	52	0.012
gb	AC229876.2	Zea mays BAC clone CH201-115J9 from chromosome 8,...	52	0.012
gb	BT069726.1	Zea mays full-length cDNA clone ZM_BFb0216P01 mRN...	52	0.012
gb	EU952061.1	Zea mays clone 1145983 hypothetical protein mRNA,...	52	0.012
gb	AC165267.2	Zea mays clone ZMMBBb-151F20, complete sequence	52	0.012
gb	EF190053.1	Zea mays clone 46F3FF5Rs2 chromosome B, genomic s...	50	0.048
gb	EF190052.1	Zea mays clone 46F3FF5Rs1 chromosome B, genomic s...	50	0.048
gb	EF190043.1	Zea mays clone 46F3FF4R-3 chromosome B, genomic s...	50	0.048
gb	AC160211.1	Genomic sequence for Zea mays BAC clone ZMMBBb044...	50	0.048
gb	AY555142.1	Zea mays BAC clone c573F08, complete sequence	50	0.048
gb	AC207417.4	Zea mays BAC clone CH201-186N18 from chromosome 5...	48	0.19
gb	AC206691.5	Zea mays BAC clone CH201-149B20 from chromosome 1...	48	0.19
gb	AC211313.4	Zea mays BAC clone CH201-9J2 from chromosome 5, c...	48	0.19
gb	AC203072.5	Zea mays BAC clone CH201-26J18 from chromosome 6,...	48	0.19
gb	AC230040.3	Zea mays BAC clone CH201-122P19 from chromosome 7...	48	0.19
gb	AC203533.4	Zea mays BAC clone CH201-452L5 from chromosome 5,...	48	0.19
gb	AC210997.6	Zea mays BAC clone CH201-545A13 from chromosome 5...	48	0.19
gb	AC209754.5	Zea mays BAC clone CH201-23E16 from chromosome 5,...	48	0.19
emb	AM489152.2	Vitis vinifera contig VV78X015348.8, whole genom...	48	0.19
gb	DQ493649.1	Zea mays cultivar Coroico bz locus region	48	0.19
gb	AC152494.1	Zea mays BAC clone Z418K17, complete sequence	48	0.19

gb DQ002407.1	Zea mays copia retrotransposon opiel, gypsy retro...	48	0.19
gb AC124722.3	Mus musculus BAC clone RP23-389E7 from chromosome...	48	0.19
gb AC159713.6	Mus musculus 6 BAC RP24-317F6 (Roswell Park Cance...	48	0.19
gb AC090648.5	Genomic sequence for Mus musculus, clone RP23-331...	48	0.19
emb AL772329.14	Zebrafish DNA sequence from clone CH211-150D5 i...	48	0.19
gb AF546188.1	Contiguous genomic DNA sequence comprising the 19...	48	0.19
gb AF466932.1	Zea mays clone BAC 206C17, complete sequence	48	0.19
emb X68678.1	Z.mays gene for cyclophilin	48	0.19
gb AY664415.1	Zea mays cultivar B73 locus 9009, complete sequence	48	0.19
emb X82087.1	Z.diploperennis Grandel gene	48	0.19
gb AC203284.4	Zea mays BAC clone CH201-504M1 from chromosome 5,...	46	0.75
gb FJ386410.1	Zea mays clone L4-a StarkB element, partial sequence	46	0.75
gb AC226723.4	Zea mays BAC clone CH201-110I20 from chromosome 6...	46	0.75
gb AC231746.2	Zea mays BAC clone CH201-98H14 from chromosome 6,...	46	0.75
gb CP001078.1	Clostridium botulinum E3 str. Alaska E43, complet...	46	0.75
gb AC205914.3	Pongo abelii BAC clone CH276-7K14 from chromosome...	46	0.75
dbj AP009179.1	Sulfurovum sp. NBC37-1 genomic DNA, complete genome	46	0.75
gb EF190046.1	Zea mays clone 46F3FF4R-H2 chromosome B, genomic ...	46	0.75
gb EF190045.1	Zea mays clone 46F3FF4R-H1 chromosome B, genomic ...	46	0.75
gb AC187724.2	Pan troglodytes BAC clone CH251-318015 from chrom...	46	0.75
gb AC183623.3	Pan troglodytes BAC clone CH251-49H23 from chromo...	46	0.75
gb AC165172.2	Zea mays clone CH201-171E16, complete sequence	46	0.75
gb AC134822.19	Medicago truncatula clone mth2-15j20, complete s...	46	0.75
gb AC147708.7	Canis Familiaris, clone XX-25G10, complete sequence	46	0.75
gb AF466202.2	Zea mays putative pol protein gene, partial cds; ...	46	0.75
gb AF466203.1	Zea mays clone ZMBBb_0092E12, partial sequence	46	0.75
emb AJ312444.1	Zea mays Grande retrotransposon DNA, partial LTR...	46	0.75
gb AF050437.1	Zea mays retrotransposon Grande-Zm1 3' LTR, parti...	46	0.75
gb U68403.1	ZMU68403 Zea mays retrotransposon Grande-Zm 5' LTR a...	46	0.75
gb AE000666.1	Methanothermobacter thermautotrophicus str. Delta...	46	0.75
gb AC204225.4	Zea mays BAC clone CH201-427P14 from chromosome 5...	44	3.0
gb AC190571.5	Zea mays BAC clone CH201-151G9 from chromosome 5,...	44	3.0
emb CU207403.3	Pig DNA sequence from clone CH242-522I21 on chro...	44	3.0
gb EZ077797.1	TSA: Zea mays contig13436, mRNA sequence	44	3.0
ref XM_001909862.1	Podospora anserina DSM 980 hypothetical prot...	44	3.0
emb CU638744.1	Podospora anserina genomic DNA chromosome 6, sup...	44	3.0
gb EF396164.1	Zea mays nitrilase 2 (NIT2) gene, complete cds	44	3.0
gb EF190047.1	Zea mays clone 46F3FF4R-H3 chromosome B, genomic ...	44	3.0
gb EF190042.1	Zea mays clone 46F3FF4R-2 chromosome B, genomic s...	44	3.0
gb AC182574.2	Mimulus guttatus clone MGBa-83E5, complete sequence	44	3.0
gb AC188446.2	Gallus gallus BAC clone CH261-122M13 from chromos...	44	3.0
gb CP000393.1	Trichodesmium erythraeum IMS101, complete genome	44	3.0
gb AC115727.10	Mus musculus chromosome 3, clone RP23-30A13, com...	44	3.0
gb AC110735.6	Mus musculus chromosome 1, clone RP24-123P22, com...	44	3.0
gb AC107851.17	Mus musculus chromosome 9, clone RP23-451B4, com...	44	3.0
gb AC112971.8	Mus musculus chromosome 1, clone RP24-444M12, com...	44	3.0
gb AC137002.2	Oryza sativa (japonica cultivar-group) chromosome...	44	3.0
gb AC137128.17	Mus musculus chromosome 3, clone RP24-271G16, co...	44	3.0
gb AF394561.1	Oryza sativa alpha-expansin OsEXPA26 (EXPA26) gen...	44	3.0

gb AC121523.6	Mus musculus chromosome 18, clone RP24-92N23, com...	44	3.0
gb AC161177.4	Mus musculus chromosome 18, clone RP24-131H12, co...	44	3.0
gb AC074327.6	Homo sapiens chromosome 10 clone RP11-556E13, com...	44	3.0
tpg BK000854.1	TPA: TPA_inf: Oryza sativa transposon Rim2-M255,...	44	3.0
gb AC113420.2	Homo sapiens chromosome 5 clone RP11-586E1, compl...	44	3.0
emb AL513013.12	Human DNA sequence from clone RP5-990P15 on chr...	44	3.0
emb AL606923.8	Human DNA sequence from clone RP11-361F19 on chr...	44	3.0
emb AL357873.17	Human DNA sequence from clone RP11-344F13 on ch...	44	3.0
gb AC093256.2	Homo sapiens chromosome 5 clone RP11-182I24, comp...	44	3.0
emb AL592043.7	Human DNA sequence from clone RP11-281B1 on chro...	44	3.0
emb AL583825.8	Human DNA sequence from clone RP11-362H12 on chr...	44	3.0
gb AC155725.3	Mus musculus 6 BAC RP24-231N5 (Roswell Park Cance...	44	3.0
emb AL645990.14	Mouse DNA sequence from clone RP23-403C12 on ch...	44	3.0
dbj AP004222.3	Oryza sativa Japonica Group genomic DNA, chromos...	44	3.0
gb AC097720.5	Homo sapiens BAC clone RP11-1422N15 from 2, compl...	44	3.0
dbj AP003563.3	Oryza sativa Japonica Group genomic DNA, chromos...	44	3.0
emb AJ312483.1	Zea mays Grande retrotransposon DNA, partial LTR...	44	3.0
emb AJ312451.1	Zea mays Grande retrotransposon DNA, partial LTR...	44	3.0
emb CT025562.10	Mouse DNA sequence from clone RP24-225012 on ch...	44	3.0
gb AC155715.24	Mus musculus 10 BAC RP24-118H2 (Roswell Park Can...	44	3.0
gb AC153847.7	Mus musculus 10 BAC RP23-286J11 (Roswell Park Can...	44	3.0
gb AC132599.3	Mus musculus BAC clone RP24-131015 from 3, comple...	44	3.0
gb AC131696.4	Mus musculus BAC clone RP23-403E5 from 1, complet...	44	3.0
gb AC110817.6	Mus musculus BAC clone RP23-155B20 from 13, compl...	44	3.0
emb AL935152.9	Mouse DNA sequence from clone RP24-387M5 on chro...	44	3.0
emb AL731742.3	Oryza sativa chromosome 12, . BAC OJ1123_B09 of ...	44	3.0
dbj AP001359.4	Homo sapiens genomic DNA, chromosome 11q clone:R...	44	3.0
dbj AP000755.4	Homo sapiens genomic DNA, chromosome 11q clone:R...	44	3.0

>gb|AC165175.2| Zea mays clone ZMMBBb-136N21, complete sequence  
Length = 129274

Score = 363 bits (183), Expect = 2e-96  
Identities = 463/552 (83%), Gaps = 7/552 (1%)  
Strand = Plus / Minus

Query: 1298 tgtgggggatagatatccccg-ggtccactagaaggcgagaaggcctcgcggtgtggccac 1356  
||||||| ||||||| ||||||||| ||| ||||| |||||  
Sbjct: 46811 tgtgggggacagatatccccaggtccactagaaggcgaaaggtcctcgcgcggggcctc 46752

Query: 1357 gggccagttaccccgcaaggccatcccttcgtgggtcgagctagaattactggtagaatg 1416  
||||||| ||||||||| ||||||| ||| ||||| |||||  
Sbjct: 46751 gggccagttacctgcaaggccatccctttgtgggtcgggcaaaagctactggcagaatg 46692

Query: 1417 ggctgaccgaagaaggcaacagactcgagcccaacaatccatcggtcgtgcgctatcc 1476  
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Sbjct: 46691 ggccgacctagaaggcgacggactcgagcccaatcagtcacatcaaattgtgcactatcc 46632

Query: 1477 acagaaactacccgactttccggcgcatggcatcctagaatatcggggcgtattagggat 1536  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Sbjct: 46631 aaagaaaccgtccgactttccacgcatggcgccctcaaattgtcgtag---attagggat 46575

Query: 1537 gagtcaagcagattttcggaagattagttcagtttggtcgctattatattaggagacatat 1596  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Sbjct: 46574 aagtcggcgggattttcgggagatcagttcagtcattcactattatattaggggacatgt 46515

Query: 1597 gatcctcatgtacgtatggagtgcacacggtcgtgtatataaggtccagagggtacccc 1656  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Sbjct: 46514 gatcaatatgtacgtatggagtgcacacactgtcgtgtatataaggcccagggggaacccc 46455

Query: 1657 atcattttctatcgaccatctacctatctcatcagctttttctccattcaggagacctcgct 1716  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Sbjct: 46454 atcattttcattc--ccatctacttatctcattagctttttctccattcaggaaacaccgct 46396

Query: 1717 tgtaaccaccacatatagatccatcccaagaagtagtgattacgcctctctaagcggc 1776  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Sbjct: 46395 tgtaaccaccatatacagctccaccctaggaagtatggtattacacctctccaagcggc 46336

Query: 1777 ccaaacttgagaaaaccgcctatccctctctcgtgcgtccagcacgaaccattgagtta 1836  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Sbjct: 46335 ccaaacatgcagaaaatcgtctgt--ctctctcgtgtgtccagcacgaaccattgagtta 46278

Query: 1837 caatcaacagca 1848  
| | | | | | | | | |

Sbjct: 46277 caatcaacagca 46266

>ref|NM\_001152615.1| Zea mays hypothetical protein LOC100279619 (LOC100279619), mRNA  
>gi|219885622|gb|BT054579.1| Zea mays full-length cDNA  
clone ZM\_BFc0162011 mRNA, complete cds  
Length = 2299

Score = 305 bits (154), Expect = 5e-79  
Identities = 436/527 (82%), Gaps = 11/527 (2%)  
Strand = Plus / Minus

Query: 1308 agatatccccgggtccactagaaggcgagaaggcctcgcgtgtgcccacgggccagttac 1367

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Sbjct: 1708 agatatccctggatccactagaaatgcgagaaggctcgcgtggggcctcgggccggttac 1649

Query: 1368 cccgcaaggccatcccttcgtgggtcgagctagaattactggtagaatgggctgaccgaa 1427  
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Sbjct: 1648 ctcgcaagaccatctcctcgtgagccaggcaaaagctaataaggcgtaatgggccgacttga 1589

Query: 1428 gaaggcaacagactcgagcccaaacaatccatcggtcgtgcgctatccacagaaactac 1487  
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Sbjct: 1588 gaaggcaacggcctcgaaccagacaatcc-tcgactcgtgcgctatccacagaaaccac 1530

Query: 1488 ccgactttccggcgcgatggcatcctagaatatcgggcgctattagggatgagtcagcgag 1547  
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Sbjct: 1529 ccgactttcccacgcgatggcgtcctcgaatatcgggcgatgttaggattaagtcggctag 1470

Query: 1548 attttcgggaagattagttcagtttggtcgtattatttaggagacatatga-tcctcatg 1606  
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Sbjct: 1469 gttgtagggggatcagttcagtcggttcactataatttaggagacacgtgaatcctcatg 1410

Query: 1607 tacgtatggagtgccccacggtcgtgtatataaggtccagagggtaccccatcatttcta 1666  
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Sbjct: 1409 tatgtattgagtgccctacggtcatatatataaggtcca-agggtaaccatcattttca 1351

Query: 1667 tcgaccatctacctatctcatcagcttttctccattcaggagacctcgcttgtaaccac 1726  
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Sbjct: 1350 tcgaccatttacctatctcattagcttttctccattcaggaaacttcgcttg----- 1299

Query: 1727 cacatatagatccatcccaagaagtagtgattacgcctctctaagcgggcccaaacttgc 1786  
||| ||||||||||| | ||||||||||| ||||||||||||||||||||||||| |||

Sbjct: 1298 cacttatagatccaccacaagaagtagggtattacgcctctctaagcgggcccaaacttac 1239

Query: 1787 agaaaaccgcctatccctctctcgtgcgtccagcacgaaccattgag 1833  
||||||| | | |||||||||||||||||||||||||||||||||||

Sbjct: 1238 agaaaatcatttttacctctctcgtgcgtccagcacgaaccattgag 1192

>gb|EF468501.1| Zea mays clone pBK118-2 retrotransposons GrandeB, complete sequence  
Length = 15217

Score = 196 bits (99), Expect = 3e-46  
Identities = 277/332 (83%), Gaps = 7/332 (2%)

Strand = Plus / Minus

Query: 1523 ggcgatttagggatgagtcagcgagattttcggaagattagttcagtttgctgctatta 1582  
||||| ||||||| ||||| || ||||| ||||||| ||||| |||||

Sbjct: 5721 ggcgatttagggatgagtcggtgggattttggggagatcagttcagtcggttcactatta 5662

Query: 1583 tttaggagacatatgatcctcatgtacgtatggagtgtcccggtcggtatataaggt 1642  
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Sbjct: 5661 gttaggagacatatgatcatcatgtacgtttggagtgtcccggtcgagtatataa-gt 5603

Query: 1643 ccagagggtaccccatcatttctatcgaccatctacctatctcatcagcttttctccatt 1702  
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Sbjct: 5602 cctagggaaccccatcattt-tat-taccatctacctatctcattagcctctctccatt 5545

Query: 1703 caggagacctcgcttgtaaccaccacatatagatccatcccaagaagtagtgattacg 1762  
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Sbjct: 5544 caggagacaccgcttgtaacacccacatacagatccgccctaggaagtagggtaatacg 5485

Query: 1763 cctctctaagcgcccaacttgagaaaaccgc---ctatccctctctcggtcggtcca 1818  
|||||| ||| | ||| ||||||| || || || || ||||| ||| |||||

Sbjct: 5484 cctctccaagtgacccgaacttgagaaaattgcatgtctctctctctctctctcttcttcca 5425

Query: 1819 gcacgaaccattgagttacaatcaacagcacc 1850  
||| ||||||| |||| ||||| |||||

Sbjct: 5424 gcatgaaccattgagctacagtcaacaacacc 5393

Score = 63.9 bits (32), Expect = 3e-06

Identities = 32/32 (100%)

Strand = Plus / Plus

Query: 1819 gcacgaaccattgagttacaatcaacagcacc 1850  
||||| ||||||| ||||||| ||||||| |||||||

Sbjct: 11406 gcacgaaccattgagttacaatcaacagcacc 11437

Score = 44.1 bits (22), Expect = 3.0

Identities = 40/46 (86%)

Strand = Plus / Plus

Query: 1616 agtgcacccacggtcgtgtatataagggtccagagggtaccccatcat 1661  
|||||||  
Sbjct: 11194 agtgcacccacggtcgaatatataaggcctaggggtaccctatcat 11239

>emb|AJ312478.1| Zea mays Grande retrotransposon DNA, partial LTR, clone W12  
Length = 437

Score = 137 bits (69), Expect = 3e-28  
Identities = 130/149 (87%), Gaps = 1/149 (0%)  
Strand = Plus / Plus

Query: 1616 agtgcacccacggtcgtgtatataagggtccagagggtaccccatcatctt-ctatcgaccat 1674  
|||||||  
Sbjct: 289 agtgcacccacggtcggatatataaggcctaggggtaccccatcatctttccatcgaccat 348

Query: 1675 ctacctatctcatcagcttttctccattcaggagacctcgcttgtaaccaccacatatata 1734  
|  
Sbjct: 349 caacctatctcattagcttttcttcatcaggagacttcagttgtaaccaccacataaaa 408

Query: 1735 gatccatcccaagaagtagtgattacgc 1763  
|||||  
Sbjct: 409 gatccacaccaggaagtaggtgttacgc 437

Score = 44.1 bits (22), Expect = 3.0  
Identities = 22/22 (100%)  
Strand = Plus / Plus

Query: 1370 cgcaaggccatcccttcgtggg 1391  
|||||||  
Sbjct: 43 cgcaaggccatcccttcgtggg 64

>gb|EU949251.1| Zea mays clone 400160 mRNA sequence  
Length = 709

Score = 111 bits (56), Expect = 2e-20  
Identities = 117/136 (86%), Gaps = 1/136 (0%)  
Strand = Plus / Minus

Query: 1715 cttgtaaccaccacatatagatccatcccaagaagtagtgattacgcctctctaagcg 1774



|||||  
Sbjct: 528 cttgtaaccacacataaagatccttaccaggaagtagggtattacgcctctccaagt 469

Query: 1775 gcccaaacttgcaaaaaccgcctatccctctctcgtgcgtccagcacgaaccattgagt 1834  
|||||

Sbjct: 468 gcccgaaacctgtagaaaatcgctgt-cgtctctcgtgcatcttgtagaaccattgagt 410

Query: 1835 tacaatcaacagcacc 1850

|||||  
Sbjct: 409 tacaatcaaaagcacc 394

>emb|AJ312473.1| Zea mays Grande retrotransposon DNA, partial LTR, clone PT17  
Length = 457

Score = 109 bits (55), Expect = 6e-20  
Identities = 112/131 (85%)  
Strand = Plus / Plus

Query: 1533 ggatgagtcagcgagattttcggaagattagttcagtttgttcgctattatttaggagac 1592  
|||||

Sbjct: 207 ggatgagtcagcatgattttcggtagattggttcagtcagttcactattagttaggagat 266

Query: 1593 atatgatcctcatgtacgtatggagtgccccacggtcgtgtatataaggtccagagggt 1652  
|

Sbjct: 267 acgtgatcatcatgtacgtatggagtgccctatggtcgtgtatataaggcccaagaggaa 326

Query: 1653 ccccatcattt 1663

|||||  
Sbjct: 327 ccccatcattt 337

Score = 44.1 bits (22), Expect = 3.0  
Identities = 37/42 (88%)  
Strand = Plus / Plus

Query: 1699 cattcaggagacctcgttgtaaccacacatatagatcca 1740  
|||||

Sbjct: 393 cattcaggagacaccacttgtaacacacacatacatagatcca 434

>gb|AC206303.5| Zea mays BAC clone CH201-328A17 from chromosome 5, complete sequence

Length = 168620

Score = 91.7 bits (46), Expect = 1e-14  
Identities = 107/126 (84%), Gaps = 1/126 (0%)  
Strand = Plus / Plus

Query: 1006 tttgatggatgttaaatttgtgtgtcatttgtttgatggatttagtaaaggttatgggt 1065  
||||||| ||||| ||| || | ||||| ||||| |||||  
Sbjct: 97426 tttgatgggtgtttaagtttgagtgcatttgtttgggtggatttagtgggagttatgggt 97485

Query: 1066 ctagaggtgatttttgttgggtgggttttacagagtttaaactagcggattatatagtg 1125  
| | ||||| ||||| ||||| || | ||||| ||||| |||||  
Sbjct: 97486 gtgggggtgatttg-gttgggtgggttttgcaaaatttaaactagtgattatatagtg 97544

Query: 1126 tataga 1131  
|||||  
Sbjct: 97545 tataga 97550

>gb|EF468503.1| Zea mays clone pBK118-4 retrotransposon GrandeB, complete sequence  
Length = 13396

Score = 91.7 bits (46), Expect = 1e-14  
Identities = 82/94 (87%)  
Strand = Plus / Plus

Query: 1298 tgtgggggatagatatccccgggtccactagaaggcgagaaggcctcgcgtgtggccacg 1357  
||||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 2078 tgtgggggacagatatccccgggtccactagaaggcaagaaggcgtcgcgaaaggcctcg 2137

Query: 1358 ggccagttaccccgcaaggccatcccttcgtggg 1391  
|||| ||| ||||| ||||| ||||| |||||  
Sbjct: 2138 ggcccattatttcgaaggccatcccttcgtggg 2171

Score = 54.0 bits (27), Expect = 0.003  
Identities = 55/63 (87%), Gaps = 1/63 (1%)  
Strand = Plus / Plus

Query: 1717 tgtaaccaccacatata-gatccatccaagaagtagtgtattacgcctctctaagcgg 1775  
||||||| ||||| || | ||||| || | ||||| |||||  
Sbjct: 2503 tgtaaccaccacataaaagatccacactaggaagtaggtgttacgcctctctaagcgg 2562

Query: 1776 ccc 1778  
|||  
Sbjct: 2563 ccc 2565

>emb|AJ312503.1| Zea mays subsp. mexicana Grande retrotransposon DNA, partial LTR,  
clone ZMM15  
Length = 437

Score = 85.7 bits (43), Expect = 9e-13  
Identities = 135/165 (81%), Gaps = 3/165 (1%)  
Strand = Plus / Plus

Query: 1602 tcatgtacgtatggagtgccccacggtcgtgtatataaggtccagagggtaccccatcat 1661  
||||| ||||| ||| ||||||||||||||| ||||||||||| | || ||| |||||||||  
Sbjct: 273 tcatatacgcatgtagtgccccacggtaagtatataaggcctagggggcaccatcaa 332

Query: 1662 ttc---tatcgaccatctacctatctcatcagcttttctccattcaggagacctcgcttg 1718  
| ||||||||||||||| | |||| ||||||||||||| | |||||| || |||||  
Sbjct: 333 aacatatatcgaccatctactcagctcactagcttttctccataccggagacttcccttg 392

Query: 1719 taaccacccacatatagatccatcccaagaagtagtgtattacgc 1763  
||||| |||||||| |||||||| ||| |||||||| | |||||||  
Sbjct: 393 taacctaccacataaagatccatgccaggaagtagggtgttacgc 437

>gb|AY883559.2| Zea mays cultivar inbred line B73 teosinte glume architecture 1 (tga1)  
gene, complete cds  
Length = 169976

Score = 83.8 bits (42), Expect = 3e-12  
Identities = 57/62 (91%)  
Strand = Plus / Plus

Query: 1717 tgtaaccacccacatatagatccatcccaagaagtagtgtattacgcctctctaagcggc 1776  
||||||||||||||||| ||||||| ||| |||||||| |||||||||||||||  
Sbjct: 94023 tgtaaccacccacataaagatccacaccaggaagtaggtattacgcctctctaagcggc 94082

Query: 1777 cc 1778  
||  
Sbjct: 94083 cc 94084

Score = 60.0 bits (30), Expect = 5e-05  
Identities = 46/50 (92%), Gaps = 1/50 (2%)  
Strand = Plus / Plus

Query: 1298 tgtgggggatagatatcccc-gggtccactagaaggcgagaaggcctcgc 1346  
||||||| ||||||| ||||||||| |||||||  
Sbjct: 93595 tgtgggggacagatatccccgggtccactagaaggttagaaggcctcgc 93644

>gb|EF468507.1| Zea mays clone pBK118-8 LL repeat sequence  
Length = 13598

Score = 81.8 bits (41), Expect = 1e-11  
Identities = 87/101 (86%), Gaps = 1/101 (0%)  
Strand = Plus / Plus

Query: 1297 ttgtgggggatagatat-ccccgggtccactagaaggcgagaaggcctcgcgtgtggcca 1355  
||||||| ||||| ||||||||| ||||||| || |||||  
Sbjct: 6737 ttgtgggggacagatatccccgggtccactagaaggcaagaaggcctcacgaaaggcct 6796

Query: 1356 cgggccagttaccccgcaaggccatcccttcgtgggtcgag 1396  
||||| ||| ||||||| |||||||||  
Sbjct: 6797 cgggcccattatttcgcaaggccacccttcgtgggtcgag 6837

Score = 50.1 bits (25), Expect = 0.048  
Identities = 40/45 (88%)  
Strand = Plus / Plus

Query: 1734 agatccatcccaagaagtagtgtattacgcctctctaagcgggcc 1778  
|||||| ||| |||||| || ||||||||| |||||||  
Sbjct: 7182 agatccaaaccaggaagtaggtgttacgcctctctaagcgggcc 7226

>gb|EF190066.1| Zea mays clone PS53 chromosome B, genomic sequence  
Length = 16207

Score = 81.8 bits (41), Expect = 1e-11  
Identities = 87/101 (86%), Gaps = 1/101 (0%)  
Strand = Plus / Minus

Query: 1297 ttgtgggggtagatatacccc-gggtccactagaaggcgagaaggcctcgctgtggcca 1355  
 ||||||| ||||||| ||||||| ||||||| ||||||| || || |||||  
 Sbjct: 10502 ttgtgggggacagatatcccccggtccactagaaggcaagaaggcctcacgaaaggcct 10443

Score = 54.0 bits (27), Expect = 0.003  
Identities = 58/67 (86%), Gaps = 1/67 (1%)  
Strand = Plus / Minus

```

Query: 1776  cccaaac  1782
          |||||
Sbjct: 10014 cccaaac  10008

```

Score = 79.8 bits (40), Expect = 5e-11  
Identities = 83/96 (86%), Gaps = 1/96 (1%)  
Strand = Plus / Minus

```
Query: 1356   cgggccagttacccgcaggccatcccttcgtggg 1391
           |||||  |||  |||||||||||||||||
Sbjct: 112064 cggggccattatttcgcaaggccatcccttcgtggg 112029
```

```
Query: 1717      tgtaaccaccacatat-agatccatccaagaagtagtgtattacgcctctctaagcgg 1775
                ||||| ||||| ||||| ||| ||||| || ||||| ||||| |||||
Sbjct: 111697    tgtaacctaccacataagagatccacgccaggaagtaggtgttacgcctctctaagcgg 111638
```

Score = 50.1 bits (25), Expect = 0.048  
Identities = 31/33 (93%)  
Strand = Plus / Plus

>gb|AC229879.2| Zea mays BAC clone CH201-103M12 from chromosome 8, complete sequence  
Length = 175468

```
Query: 1717      tgtaaccaccacatatagatccatccaagaagtagtgtattacgctctctaagcggc 1776
                |||||
Sbjct: 122467    tgtaaccaccacataaagatccacaccaggaagtaggggtattacgctctcaaagcggc 122408
```

```
Query: 1837    ca 1838
      ||
Sbjct: 122348 ca 122347
```

Query: 1297 ttgtgggggatagatatcccc-gggtccactagaagg 1332  
||||||| ||||||| |||||||  
Sbjct: 122894 ttgtgggggacagatatccccgggtccactagaagg 122858

Score = 48.1 bits (24), Expect = 0.19  
Identities = 31/32 (96%), Gaps = 1/32 (3%)  
Strand = Plus / Minus

Query: 1297 ttgtgggggatagatat-ccccgggtccacta 1327  
||||||| ||||||| |||||||  
Sbjct: 25568 ttgtgggggatagatatccccgggtccacta 25537

Score = 46.1 bits (23), Expect = 0.75  
Identities = 30/31 (96%), Gaps = 1/31 (3%)  
Strand = Plus / Minus

Query: 1298 tgtgggggatagatat-ccccgggtccacta 1327  
||||||| ||||||| |||||||  
Sbjct: 39115 tgtgggggatagatatccccgggtccacta 39085

>gb|FJ386423.1| Zea mays clone R6-b StarkB element, partial sequence  
Length = 3194

Score = 73.8 bits (37), Expect = 3e-09  
Identities = 86/101 (85%), Gaps = 1/101 (0%)  
Strand = Plus / Plus

Query: 1297 ttgtgggggatagatatcccc-gggtccactagaaggcgagaaggcctcgcggtggcca 1355  
||||||| ||||||| ||||||| ||||||| || ||||  
Sbjct: 1198 ttgtgggggacagatatccccgggtccactagaaggcaagaaggcctcacgaaaggcct 1257

Query: 1356 cgggccagttaccccgcaaggccatcccttcgtgggtcgag 1396  
||||| || ||||||| ||||||| ||||  
Sbjct: 1258 cggggccattatttcgcaaggccacccttcgtgggccgag 1298

>gb|EF468510.1| Zea mays clone pBS-1 LL repeat sequence  
Length = 14009

Score = 73.8 bits (37), Expect = 3e-09  
Identities = 86/101 (85%), Gaps = 1/101 (0%)  
Strand = Plus / Plus

Query: 1297 ttgtgggggatagatatcccc-gggtccactagaaggcgagaaggcctcgcgtgtggcca 1355  
||||||| ||||||| ||||||||| ||||||| || ||||  
Sbjct: 13840 ttgtgggggacagatatccccgggtccactagaaggcaagaaggcctcacgaaagcct 13899

Query: 1356 cgggccagttaccccgcaaggccatcccttcgtgggtcgag 1396  
||||| || ||||||||| ||||||||| ||||  
Sbjct: 13900 cggggccattatttcgcaaggccaccccttcgtgggccgag 13940

Score = 61.9 bits (31), Expect = 1e-05  
Identities = 56/63 (88%), Gaps = 1/63 (1%)  
Strand = Plus / Plus

Query: 1717 tgtaaccaccacatatata-gatccatcccaagaagtagtgtattacgcctctctaagcgg 1775  
||||||| ||||| || ||||||| || ||||||||| |||||  
Sbjct: 5047 tgtaaccaccacataaaagatccacaccaggaagtaggtgttacgcctctctaagcgg 5106

Query: 1776 ccc 1778  
|||  
Sbjct: 5107 ccc 5109

Score = 60.0 bits (30), Expect = 5e-05  
Identities = 43/46 (93%), Gaps = 1/46 (2%)  
Strand = Plus / Plus

Query: 1300 tgggggatagatatccc-cgggtccactagaaggcgagaaggcctc 1344  
||||| ||||||||| ||||||||| |||||||  
Sbjct: 4622 tgggggacagatatccctcggtccactagaaggcaagaaggcctc 4667

>gb|EF468508.1| Zea mays clone pB3-201 retrotransposon GrandeB, complete sequence  
Length = 13066

Score = 73.8 bits (37), Expect = 3e-09  
Identities = 86/101 (85%), Gaps = 1/101 (0%)  
Strand = Plus / Plus



Query: 1297 ttgtgggggatagatatcccc-gggtccactagaaggcgagaaggcctcgcggtggcca 1355  
||||||| ||||||| ||||||||| ||||||| || ||||  
Sbjct: 7923 ttgtggggacagatatccccgggtccactagaaggcaagaaggcctcacgaaaggcct 7982

Query: 1356 cgggccagttaccccgcaaggccatcccttcgtgggtcgag 1396  
||||| ||| ||||||| ||||||| ||||  
Sbjct: 7983 cgggccattatttcgcaaggccacccttcgtgggccgag 8023

>gb|EF190064.1| Zea mays clone pStark5.5 chromosome B, genomic sequence  
Length = 5542

Score = 73.8 bits (37), Expect = 3e-09  
Identities = 86/101 (85%), Gaps = 1/101 (0%)  
Strand = Plus / Plus

Query: 1297 ttgtgggggatagatatcccc-gggtccactagaaggcgagaaggcctcgcggtggcca 1355  
||||||| ||||||| ||||||||| ||||||| || ||||  
Sbjct: 4653 ttgtggggacagatatccccgggtccactagaaggcaagaaggcctcacgaaaggcct 4712

Query: 1356 cgggccagttaccccgcaaggccatcccttcgtgggtcgag 1396  
||||| ||| ||||||| ||||||| ||||  
Sbjct: 4713 cgggccattatttcgcaaggccacccttcgtgggccgag 4753

>gb|EF190061.1| Zea mays clone FS2\_19 chromosome B, genomic sequence  
Length = 39598

Score = 73.8 bits (37), Expect = 3e-09  
Identities = 86/101 (85%), Gaps = 1/101 (0%)  
Strand = Plus / Plus

Query: 1297 ttgtgggggatagatatcccc-gggtccactagaaggcgagaaggcctcgcggtggcca 1355  
||||||| ||||||| ||||||||| ||||||| || ||||  
Sbjct: 8574 ttgtggggacagatatccccgggtccactagaaggcaagaaggcctcacgaaaggcct 8633

Query: 1356 cgggccagttaccccgcaaggccatcccttcgtgggtcgag 1396  
||||| ||| ||||||| ||||||| ||||  
Sbjct: 8634 cgggccattatttcgcaaggccacccttcgtgggccgag 8674

Score = 63.9 bits (32), Expect = 3e-06  
Identities = 83/100 (83%)  
Strand = Plus / Plus

Query: 1297 ttgtgggggatagatatccccgggtccactagaaggcgagaaggcctcgcgtgtggccac 1356  
||||||| ||||||| || ||||||||| ||||||||| || |||||  
Sbjct: 28412 ttgtgggggacagatatccccgggtcactagaaggcaagaaggcctcacgaaaggcctc 28471

Query: 1357 gggccagttaccccgcaaggccatcccttcgtgggtcgag 1396  
||||| ||| ||||||||| ||||||||| |||||  
Sbjct: 28472 gggccattattttcgcaaggccacccttcgtgggccgag 28511

Score = 50.1 bits (25), Expect = 0.048  
Identities = 25/25 (100%)  
Strand = Plus / Plus

Query: 1758 ttacgcctctctaagcgcccaaac 1782  
|||||||||||||||||||  
Sbjct: 8915 ttacgcctctctaagcgcccaaac 8939

Score = 48.1 bits (24), Expect = 0.19  
Identities = 30/32 (93%)  
Strand = Plus / Plus

Query: 1747 gaagtagtgtattacgcctctctaagcggcc 1778  
|||||| || |||||||||||||||||  
Sbjct: 28869 gaagtaggtgttacgcctctctaagcggcc 28900

Score = 46.1 bits (23), Expect = 0.75  
Identities = 32/35 (91%)  
Strand = Plus / Plus

Query: 1804 tctctcgtgcgtccagcacgaaccattgagttaca 1838  
||||||| ||||||||||||| ||| |||||  
Sbjct: 8960 tctctcgtgcatccagcacgaaccatcgagttaca 8994

>emb|AJ312504.1| Zea mays subsp. mexicana Grande retrotransposon DNA, partial LTR,

clone ZMM16  
Length = 434

Score = 73.8 bits (37), Expect = 3e-09  
Identities = 98/117 (83%), Gaps = 1/117 (0%)  
Strand = Plus / Plus

Query: 1616 agtgccccacggctcgtgtatataaggtccagagggtaccccatcatttctatcgaccatc 1675  
||||||| ||| ||||||||| | || ||||||| ||||||| |||||||||  
Sbjct: 289 agtgccccatggcgaagtatataaggcctaggggtaccctgtcatttccatcgaccatc 348

Query: 1676 tacctatctcatcagctttttctccattcaggagacctcgcttgtaaccaccacata 1732  
||| | |||| ||||||||| ||||| || ||||||||| |||||||  
Sbjct: 349 tactcagctcactagctttttctccataaaggaga-ttcccttgtaaccaccacata 404

>gb|AC194842.4| Zea mays BAC clone CH201-514N20 from chromosome 4, complete sequence  
Length = 156840

Score = 71.9 bits (36), Expect = 1e-08  
Identities = 49/52 (94%), Gaps = 1/52 (1%)  
Strand = Plus / Plus

Query: 1297 ttgtggggatagatatcccc-gggtccactagaaggcgagaaggcctcgcg 1347  
||||||| ||||||||| ||||||||| ||||||||| |||||||||  
Sbjct: 148416 ttgtggggacagatatccccgggtccactagaaggcaagaaggcctcgcg 148467

Score = 54.0 bits (27), Expect = 0.003  
Identities = 51/59 (86%)  
Strand = Plus / Plus

Query: 1719 taaccaccacatatagatccatcccaagaagtagtgattacgcctctctaagcggcc 1777  
||||||| ||||||| || ||||||| || ||||| |||||||||  
Sbjct: 148845 taaccaccacataaagatccacatcaggaagtagggtgttacacctctctaagcggcc 148903

>gb|EF190062.1| Zea mays clone FS2\_20 chromosome B, genomic sequence  
Length = 39210

Score = 71.9 bits (36), Expect = 1e-08  
Identities = 82/96 (85%), Gaps = 1/96 (1%)  
Strand = Plus / Minus

Query: 1297 ttgtgggggatagatatcccc-gggtccactagaaggcgagaaggcctcgcggtgtggcca 1355  
||||||| ||||| ||||||||| ||||| || ||||  
Sbjct: 9984 ttgtggggacagatatccccgggtccactagaaggcaagaaggcctcacgaaaggcct 9925

Query: 1356 cgggccagttaccccgcaaggccatcccttcgtggg 1391  
||||| || ||||||| |||||||  
Sbjct: 9924 cgggccattatttcgcaaggccacccttcgtggg 9889

Score = 65.9 bits (33), Expect = 8e-07  
Identities = 46/49 (93%), Gaps = 1/49 (2%)  
Strand = Plus / Minus

Query: 1297 ttgtgggggatagatatcccc-gggtccactagaaggcgagaaggcctc 1344  
||||||| ||||| ||||||||| ||||| |||||  
Sbjct: 19216 ttgtggggacagatatccccgggtccactagaaggcaagaaggcctc 19168

Score = 54.0 bits (27), Expect = 0.003  
Identities = 55/63 (87%), Gaps = 1/63 (1%)  
Strand = Plus / Minus

Query: 1717 tgtaaccaccacatatata-gatccatcccaagaagtagtgtattacgcctctctaagcgg 1775  
||||||| ||||| || ||||| | |||||||||  
Sbjct: 18788 tgtaaccaccacataaaagatccacaccaggaagtagagggttacgcctctctaagcgg 18729

Query: 1776 ccc 1778  
|||  
Sbjct: 18728 ccc 18726

Score = 44.1 bits (22), Expect = 3.0  
Identities = 53/62 (85%), Gaps = 1/62 (1%)  
Strand = Plus / Minus

Query: 1717 tgtaaccaccacatatata-gatccatcccaagaagtagtgtattacgcctctctaagcgg 1775  
||||||| ||||| || ||||| || ||||| |||||  
Sbjct: 9556 tgtaaccaccacataaaagatccacaccaggaagtagggtgctacgcttctctaagcgg 9497

Query: 1776 cc 1777  
||  
Sbjct: 9496 cc 9495

>gb|AC204937.4| Zea mays BAC clone CH201-488A19 from chromosome 5, complete sequence  
Length = 152162

Score = 69.9 bits (35), Expect = 5e-08  
Identities = 47/51 (92%)  
Strand = Plus / Minus

Query: 1081 gttgggtgggttttacagagtttaactagcggattatatagtggtataga 1131  
||||||| || ||||| | |||||  
Sbjct: 119042 gttgggtgggttttgc aaagtttaacttggattatatagtggtataga 118992

>gb|AC205029.6| Zea mays BAC clone CH201-7M14 from chromosome 5, complete sequence  
Length = 187257

Score = 69.9 bits (35), Expect = 5e-08  
Identities = 47/51 (92%)  
Strand = Plus / Plus

Query: 1081 gttgggtgggttttacagagtttaactagcggattatatagtggtataga 1131  
||||||| || ||||| | |||||  
Sbjct: 171940 gttgggtgggttttgc aaagtttaacttggattatatagtggtataga 171990

>gb|EF190050.1| Zea mays clone 46F3FF5Rm4 chromosome B, genomic sequence  
Length = 582

Score = 69.9 bits (35), Expect = 5e-08  
Identities = 60/67 (89%), Gaps = 1/67 (1%)  
Strand = Plus / Plus

Query: 1717 tgtaaccaccacatata-gatccatcccaagaagtagtgattacgcctctctaagcgg 1775  
||||||| | ||||| || ||||| | |||||  
Sbjct: 271 tgtaaccaccacataaaagatccataccaggaagtaggctgttacgcctctctaagcgg 330

Query: 1776 cccaaac 1782  
|||||  
Sbjct: 331 cccaaac 337

>gb|FJ386429.1| Zea mays clone R9-b StarkB element, partial sequence  
Length = 1264

Score = 65.9 bits (33), Expect = 8e-07  
Identities = 46/49 (93%), Gaps = 1/49 (2%)  
Strand = Plus / Plus

Query: 1297 ttgtgggggatagatatcccc-gggtccactagaaggcgagaaggcctc 1344  
||||||| ||||||| ||||||||| |||||||  
Sbjct: 1198 ttgtggggacagatatccccgggtccactagaaggcaagaaggcctc 1246

>gb|FJ386412.1| Zea mays clone L5-a StarkB element, partial sequence  
Length = 1477

Score = 65.9 bits (33), Expect = 8e-07  
Identities = 46/49 (93%), Gaps = 1/49 (2%)  
Strand = Plus / Plus

Query: 1297 ttgtgggggatagatatcccc-gggtccactagaaggcgagaaggcctc 1344  
||||||| ||||||| ||||||||| |||||||  
Sbjct: 501 ttgtggggacagatatccccgggtccactagaaggcaagaaggcctc 549

Score = 61.9 bits (31), Expect = 1e-05  
Identities = 59/67 (88%), Gaps = 1/67 (1%)  
Strand = Plus / Plus

Query: 1717 tgtaaccacacacatata-gatccatccaagaagtagtgattacgcctctctaagcgg 1775  
|||| ||||||| | ||||| || |||||| | |||||||||  
Sbjct: 929 tgtaatccaccacataaaagatccacaccaggaagtagggtgttacgcctctctaagcgg 988

Query: 1776 cccaaac 1782  
|||||  
Sbjct: 989 cccaaac 995

>gb|EF468504.1| Zea mays clone pBK118-5 LL repeat sequence  
Length = 14585

Score = 65.9 bits (33), Expect = 8e-07  
Identities = 46/49 (93%), Gaps = 1/49 (2%)  
Strand = Plus / Plus

Query: 1297 ttgtgggggatagatatcc-ccgggtccactagaaggcgagaaggcctc 1344  
||||||| ||||| ||||||||| |||||  
Sbjct: 2178 ttgtggggacagatatcctccgggtccactagaaggcaagaaggcctc 2226

Score = 46.1 bits (23), Expect = 0.75  
Identities = 32/35 (91%)  
Strand = Plus / Plus

Query: 1804 tctctcgtgcgtccagcacgaaccattgagttaca 1838  
||||||| || ||||||||| |||||  
Sbjct: 2693 tctctcgtgcatctagcacgaaccattgagctaca 2727

>gb|EF468502.1| Zea mays clone pBK118-3 LL repeat sequence  
Length = 14929

Score = 65.9 bits (33), Expect = 8e-07  
Identities = 46/49 (93%), Gaps = 1/49 (2%)  
Strand = Plus / Plus

Query: 1297 ttgtgggggatagatatcc-ccgggtccactagaaggcgagaaggcctc 1344  
||||||| ||||| ||||||||| |||||  
Sbjct: 9507 ttgtggggacagatatcctccgggtccactagaaggcaagaaggcctc 9555

Score = 58.0 bits (29), Expect = 2e-04  
Identities = 45/49 (91%), Gaps = 1/49 (2%)  
Strand = Plus / Plus

Query: 1297 ttgtgggggatagatatcccg-ggtccactagaaggcgagaaggcctc 1344  
||||||| ||||| ||||||||| |||||  
Sbjct: 687 ttgtggggacagatatcccccggtccactagaaggcaagaaggcctc 735

Score = 46.1 bits (23), Expect = 0.75  
Identities = 54/63 (85%), Gaps = 1/63 (1%)  
Strand = Plus / Plus

Query: 1717 tgtaaccaccacatata-gatccatccaagaagtagtgattacgcctctctaagcgg 1775  
||||||| ||||| | ||||| || ||||||||| |||||

Sbjct: 1115 tgtaaccacacataaaagatccacacaaggaagtaggggtgttacgcctctctaagcag 1174

Query: 1776 ccc 1778

|||

Sbjct: 1175 ccc 1177

Score = 46.1 bits (23), Expect = 0.75

Identities = 32/35 (91%)

Strand = Plus / Plus

Query: 1804 tctctcgtgcgtccagcacgaaccattgagttaca 1838

|||||||||| || |||||||||||||||||| ||||

Sbjct: 10022 tctctcgtgcatctagcacgaaccattgagctaca 10056

>gb|EF190065.1| Zea mays clone PS52 chromosome B, genomic sequence

Length = 14530

Score = 65.9 bits (33), Expect = 8e-07

Identities = 46/49 (93%), Gaps = 1/49 (2%)

Strand = Plus / Plus

Query: 1297 ttgtgggggatagatatcccc-gggtccactagaaggcgagaaggcctc 1344

|||||||||| |||||||||| |||||||||||||| ||||||||||

Sbjct: 2213 ttgtgggggacagatatcccccggtccactagaaggcaagaaggcctc 2261

Score = 60.0 bits (30), Expect = 5e-05

Identities = 55/62 (88%), Gaps = 1/62 (1%)

Strand = Plus / Plus

Query: 1717 tgtaaccacacatata-gatccatcccaagaagtagtgtattacgcctctctaagcgg 1775

|||||||||||||||| | ||||| || |||||| | ||||||||||||||||

Sbjct: 2641 tgtaaccacacataaaagatccacaccaggaagtaggggtgttacgcctctctaagcgg 2700

Query: 1776 cc 1777

||

Sbjct: 2701 cc 2702

>gb|EF190063.1| Zea mays clone FS3\_49 chromosome B, genomic sequence



Length = 38116

Score = 65.9 bits (33), Expect = 8e-07  
Identities = 46/49 (93%), Gaps = 1/49 (2%)  
Strand = Plus / Plus

Query: 1297 ttgtgggggatagatatcccc-gggtccactagaaggcgagaaggcctc 1344  
||||||| ||||||| ||||||||| |||||||  
Sbjct: 32550 ttgtgggggacagatatccccgggtccactagaaggcaagaaggcctc 32598

Score = 50.1 bits (25), Expect = 0.048  
Identities = 50/57 (87%), Gaps = 1/57 (1%)  
Strand = Plus / Plus

Query: 1717 tgtaaccaccacatatata-gatccatcccaagaagtagtgtattacgcctctctaag 1772  
||||||| ||||| || ||||| || |||||||||  
Sbjct: 32977 tgtaaccaccacataaaagatccacaccaggaagtaggggtgttacgcctctctaag 33033

>gb|DQ183075.1| Zea mays clone A-RGA7 resistance gene analog-like gene, partial  
sequence  
Length = 319

Score = 65.9 bits (33), Expect = 8e-07  
Identities = 140/173 (80%), Gaps = 2/173 (1%)  
Strand = Plus / Minus

Query: 1607 tacgtatggagtgcccca-cggtcgtgtatataaggtccagagggtaccccatcatttct 1665  
||| || ||||||| ||||| ||||||| | || |||||||||  
Sbjct: 218 tacgcatgtagtgcgccagcggtcgagtatataaggcctaggggtaccccatcatttca 159

Query: 1666 atcgaccatctacatatctcatcagcttttctccattcaggagacctcgcttgt-aaccc 1724  
||| ||||| ||| | ||||| | ||||||| | ||||| || ||||| |||  
Sbjct: 158 atcaaccatgtactcaactcattatcctttctccatactggagacttctcttgtaaactg 99

Query: 1725 accacatatagatccatcccaagaagtagtgtattacgcctctctaagcgcc 1777  
||||| || ||||||| || ||||||| ||||| | |||||||||  
Sbjct: 98 accatataaagatccacaccaggaagtaggatattatgtatctctaagcgcc 46

>gb|EF468505.1| Zea mays clone pBK118-6 LL repeat sequence  
Length = 14830

Query: 1297 ttgtgggggatagatatcccc-gggtccactagaaggcgagaaggcctcgctgtggcca 1355  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Sbjct: 12021 ttgtgggggacagatatccccgggtccactagaaggtaagaaggcctcacgaaaggcca 12080

Score = 63.9 bits (32), Expect = 3e-06  
Identities = 61/68 (89%), Gaps = 2/68 (2%)  
Strand = Plus / Plus

```

Query: 1775  gcccaaac 1782
          |||||
Sbjct: 12509 gcccaaac 12516

```

Score = 61.9 bits (31), Expect = 1e-05  
Identities = 56/63 (88%), Gaps = 1/63 (1%)  
Strand = Plus / Plus

Query: 1776 ccc 1778  
 |||  
 Sbjct: 1736 ccc 1738

Score = 58.0 bits (29), Expect = 2e-04  
Identities = 45/49 (91%), Gaps = 1/49 (2%)  
Strand = Plus / Plus

Query: 1297 ttgtgggggatagatatcccc-gggtccactagaaggcgagaaggcctc 1344  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 1249 ttgttggggacagatatcccccggtccactagaaggcaagaaggcctc 1297

>gb|EF190048.1| Zea mays clone 46F3FF5Rm1 chromosome B, genomic sequence  
Length = 581

Score = 61.9 bits (31), Expect = 1e-05  
Identities = 56/63 (88%), Gaps = 1/63 (1%)  
Strand = Plus / Plus

Query: 1717 tgtaaccaccacatatata-gatccatcccaagaagtagtgtattacgcctctctaagcgg 1775  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 271 tgtaaccaccacataaaagatccataaccaggaagtagggtgttacggctctctaagcgg 330

Query: 1776 ccc 1778  
|||  
Sbjct: 331 ccc 333

>gb|AY574035.1| Zea mays rust resistance protein rp3-1 (rp3-1) gene, complete cds; and  
truncated rust resistance protein rp3-2t (rp3-2) gene,  
complete sequence  
Length = 276326

Score = 61.9 bits (31), Expect = 1e-05  
Identities = 47/51 (92%), Gaps = 1/51 (1%)  
Strand = Plus / Plus

Query: 1298 tgtgggggatagatatccc-cgggtccactagaaggcgagaaggcctcgcg 1347  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 27029 tgtgggggacagatatccctcggtccactagaaggctagaagacctcgcg 27079

Score = 52.0 bits (26), Expect = 0.012  
Identities = 63/74 (85%), Gaps = 1/74 (1%)  
Strand = Plus / Plus

Query: 1706 gagacctcgcttgtaacccaccacat-atagatccatcccaagaagtagtgattacgcc 1764  
|||| ||| |||||||||||||||| | |||||| | || |||||| | |||||  
Sbjct: 27440 gagaactcccttgtaacccaccacataaaagatccacaccaggaagtaggggttacgct 27499

Query: 1765 tctctaagcggccc 1778  
|||||||||||||  
Sbjct: 27500 tctctaagcggccc 27513

Score = 44.1 bits (22), Expect = 3.0  
Identities = 37/42 (88%)  
Strand = Plus / Plus

Query: 1619 gccccacggtcgtgtatataaggtccagagggtaccccatca 1660  
||||||||||| ||||||||| | || ||| |||||||||  
Sbjct: 27347 gccccacggtcgagtatataaggcctagggggcaccccatca 27388

>gb|AC185486.5| Zea mays BAC clone CH201-162J17 from chromosome 5, complete sequence  
Length = 151524

Score = 60.0 bits (30), Expect = 5e-05  
Identities = 30/30 (100%)  
Strand = Plus / Minus

Query: 1298 tgtgggggatagatatccccgggtccacta 1327  
|||||||||||||||||||||||||||  
Sbjct: 111690 tgtgggggatagatatccccgggtccacta 111661

Score = 48.1 bits (24), Expect = 0.19  
Identities = 31/32 (96%), Gaps = 1/32 (3%)  
Strand = Plus / Minus

Query: 1297 ttgtgggggatagatat-ccccgggtccacta 1327  
||||||||||||||||| |||||||||||||  
Sbjct: 98092 ttgtgggggatagatatccccgggtccacta 98061

>gb|AC225631.3| Zea mays BAC clone CH201-111A2 from chromosome 8, complete sequence  
Length = 200661

Score = 60.0 bits (30), Expect = 5e-05  
Identities = 46/50 (92%), Gaps = 1/50 (2%)  
Strand = Plus / Plus

Query: 1299 gtgggggatagatatccc-cgggtccactagaaggcgagaaggcctcgcg 1347  
||||||| ||||||| ||||||||||||||| ||||| |||||||  
Sbjct: 177721 gtgggggacagatatccctcgggtccactagaaggctagaagacctcgcg 177770

Score = 54.0 bits (27), Expect = 0.003  
Identities = 55/63 (87%), Gaps = 1/63 (1%)  
Strand = Plus / Plus

Query: 1717 tgtaaccaccacatatata-gatccatcccaagaagtagtgtattacgcctctctaagcgg 1775  
||||||||||||||| | ||||| ||| ||||||| | ||||| |||||||||||||  
Sbjct: 178146 tgtaaccaccacataaaagatccacaccaggaagtaggggttacacctctctaagcgg 178205

Query: 1776 ccc 1778  
|||  
Sbjct: 178206 ccc 178208

>gb|FJ386425.1| Zea mays clone R7-b StarkB element, partial sequence  
Length = 1314

Score = 58.0 bits (29), Expect = 2e-04  
Identities = 45/49 (91%), Gaps = 1/49 (2%)  
Strand = Plus / Plus

Query: 1297 ttgtgggggatagatatcccc-gggtccactagaaggcgagaaggcctc 1344  
||||||||| ||||||||| ||| ||||||||||||| |||||||||  
Sbjct: 1248 ttgtgggggacagatatccccggggccactagaaggcaagaaggcctc 1296

>gb|EF468506.1| Zea mays clone pBK118-7 LL repeat sequence and retrotransposon zeon1,  
complete sequence  
Length = 15596

Score = 58.0 bits (29), Expect = 2e-04  
Identities = 42/45 (93%), Gaps = 1/45 (2%)  
Strand = Plus / Plus

Query: 1301 ggggatagatatcccc-gggtccactagaaggcgagaaggcctc 1344  
||||| ||||||||| ||||||||||||| |||||||||  
Sbjct: 7398 gggggacagatatccccgggtccactagaaggcaagaaggcctc 7442

Score = 50.1 bits (25), Expect = 0.048  
Identities = 53/61 (86%), Gaps = 1/61 (1%)  
Strand = Plus / Plus

Query: 1717 tgtaaccaccacatatata-gatccatcccaagaagtagtgtattacgcctctctaagcgg 1775  
||||||||||||||| | ||||| ||| ||||||| || ||| |||||||||||||  
Sbjct: 7822 tgtaaccaccacataaaagatccacaccaggaagtagggtgttatgcctctctaagcgg 7881

Query: 1776 c 1776  
|  
Sbjct: 7882 c 7882

>gb|EF468500.1| Zea mays clone pBK118-1 LL repeat sequence and retrotransposon zeon1,  
complete sequence  
Length = 13824

Score = 58.0 bits (29), Expect = 2e-04  
Identities = 42/45 (93%), Gaps = 1/45 (2%)  
Strand = Plus / Plus

Query: 1301 ggggatagatatcccc-gggtccactagaaggcgagaaggcctc 1344  
||||| ||||||||| ||||||||||||| |||||||||  
Sbjct: 4473 gggggacagatatccccgggtccactagaaggcaagaaggcctc 4517

Score = 58.0 bits (29), Expect = 2e-04  
Identities = 54/61 (88%), Gaps = 1/61 (1%)  
Strand = Plus / Plus

Query: 1717 tgtaaccaccacatatata-gatccatcccaagaagtagtgtattacgcctctctaagcgg 1775  
||||||||||||||| | ||||| ||| ||||||| || ||| |||||||||||||  
Sbjct: 4897 tgtaaccaccacataaaagatccacaccaggaagtagggtgttacgcctctctaagcgg 4956

Query: 1776 c 1776  
|  
Sbjct: 4957 c 4957

>gb|AC165174.2| Zea mays clone ZMMBBb-127F19, complete sequence  
Length = 187659

Score = 58.0 bits (29), Expect = 2e-04  
Identities = 45/49 (91%), Gaps = 1/49 (2%)  
Strand = Plus / Minus

Query: 1297 ttgtgggggatagatatcccc-gggtccactagaaggcgagaaggcctc 1344  
||||||| ||||||| ||||||| |||||||  
Sbjct: 137705 ttgtgggggacagatatccccgggtccactagaaggttagaaggcctc 137657

Score = 48.1 bits (24), Expect = 0.19  
Identities = 31/32 (96%), Gaps = 1/32 (3%)  
Strand = Plus / Minus

Query: 1297 ttgtgggggatagatatcccc-gggtccacta 1327  
||||||| ||||||| ||||||| |||||||  
Sbjct: 147600 ttgtgggggatagatatcccctgggtccacta 147569

Score = 48.1 bits (24), Expect = 0.19  
Identities = 31/32 (96%), Gaps = 1/32 (3%)  
Strand = Plus / Minus

Query: 1297 ttgtgggggatagatatcccc-gggtccacta 1327  
||||||| ||||||| ||||||| |||||||  
Sbjct: 160955 ttgtgggggatagatatcccctgggtccacta 160924

Score = 46.1 bits (23), Expect = 0.75  
Identities = 32/35 (91%)  
Strand = Plus / Minus

Query: 1804 tctctcgtgcgtccagcacgaaccattgagttaca 1838  
||||||| ||||||| ||| |||  
Sbjct: 137188 tctctcgtgcgcccagcacgaaccatcgagctaca 137154

Score = 46.1 bits (23), Expect = 0.75  
Identities = 38/43 (88%)  
Strand = Plus / Minus

Query: 1618 tgccccacggtcgtgtatataaggtccagagggtaccccatca 1660  
|||||  
Sbjct: 137385 tgccccacggtcgagtatataaggcctaggggcaccccatca 137343

>emb|AJ312460.1| Zea mays Grande retrotransposon DNA, partial LTR, clone Mol4  
Length = 433

Score = 58.0 bits (29), Expect = 2e-04  
Identities = 44/49 (89%)  
Strand = Plus / Plus

Query: 1705 ggagacctcgcttgtaacccaccacatatagatccatccaagaagtag 1753  
|||||  
Sbjct: 375 ggagacctcccttgtaacccaccacataaagatccacaccaggaagtag 423

>gb|EZ064107.1| TSA: Zea mays contig65230, mRNA sequence  
Length = 723

Score = 56.0 bits (28), Expect = 8e-04  
Identities = 46/52 (88%)  
Strand = Plus / Minus

Query: 1004 attttgatggtatgttaaatttgtgtgtcatttgttgatggatttagtaaa 1055  
|||||  
Sbjct: 138 attttgatgttatgttaaatatgagtgcaatttgttgatggatttcgtaaa 87

>gb|FJ386416.1| Zea mays clone L7-a StarkB element, partial sequence  
Length = 909

Score = 54.0 bits (27), Expect = 0.003  
Identities = 58/67 (86%), Gaps = 1/67 (1%)  
Strand = Plus / Plus

Query: 1717 tgtaaccaccacatatata-gatccatccaagaagtagtgattacgcctctctaagcgg 1775  
|||||  
Sbjct: 362 tgtaaccaccacataaaaagatccacacaaggaagtagggtgttacgcctctctaagcag 421



Query: 1776 cccaaac 1782  
|||||||  
Sbjct: 422 cccaaac 428

>gb|FJ386414.1| Zea mays clone L6-a StarkB element, partial sequence  
Length = 890

Score = 54.0 bits (27), Expect = 0.003  
Identities = 58/67 (86%), Gaps = 1/67 (1%)  
Strand = Plus / Plus

Query: 1717 tgtaaccacacacatata-gatccatccaagaagtagtgattacgcctctctaagcgg 1775  
||||| ||||||||| | |||||| | || |||||| | || |||||||||  
Sbjct: 362 tgtaatccaccacataaaagatccacaccaggaagtaggggtgttacgcctctctaagcgg 421

Query: 1776 cccaaac 1782  
|||||||  
Sbjct: 422 tccaaac 428

>gb|EU965848.1| Zea mays clone 289347 hypothetical protein mRNA, complete cds  
Length = 1436

Score = 54.0 bits (27), Expect = 0.003  
Identities = 42/47 (89%)  
Strand = Plus / Plus

Query: 1085 ggtgggttttacagagtttaactagcggattatatagtggatataga 1131  
||||||| | ||||||| | |||||||||  
Sbjct: 1358 ggtgggttttttaaagtttaactggtggattatatagtggatataga 1404

>gb|BT043326.1| Zea mays full-length cDNA clone ZM\_BFc0158M15 mRNA, complete cds  
Length = 1309

Score = 54.0 bits (27), Expect = 0.003  
Identities = 42/47 (89%)  
Strand = Plus / Plus

Query: 1085 ggtgggttttacagagtttaactagcggattatatagtggatataga 1131  
||||||| | ||||||| | |||||||||  
Sbjct: 1189 ggtgggttttttaaagtttaactggtggattatatagtggatataga 1235

Score = 54.0 bits (27), Expect = 0.003  
Identities = 55/63 (87%), Gaps = 1/63 (1%)  
Strand = Plus / Plus

```
Query: 1776 ccc 1778
      |||
Sbjct: 5853 ccc 5855
```

Query: 1314 ccccggttcactagaaggcgagaaggcctc 1344  
 ||| ||||| ||||| ||||| ||||| |||||  
 Sbjct: 5441 cccaggttcactagaaggcaagaaggcctc 5471

Score = 54.0 bits (27), Expect = 0.003  
Identities = 69/83 (83%)  
Strand = Plus / Plus

```
Query: 1040      tgatggatttagtaaaggttatg 1062
                || ||||| ||||| |||||
Sbjct: 111267    tggatggatttagtaaagattatg 111289
```

>gb|EF190051.1| Zea mays clone 46F3FF5Rm5 chromosome B, genomic sequence  
Length = 582

Score = 54.0 bits (27), Expect = 0.003  
Identities = 58/67 (86%), Gaps = 1/67 (1%)  
Strand = Plus / Plus

Query: 1717 tgtaaccaccacatatata-gatccatcccaagaagtagtgtattacgcctctctaagcgg 1775  
||||| ||||||||| | ||||| ||| ||||||| || ||||||||| |||||||  
Sbjct: 271 tgtaatccaccacataaaagatccacaccaggaagtagggtgttacgcctctttaagcgg 330

Query: 1776 cccaaac 1782  
|||||||  
Sbjct: 331 cccaaac 337

>gb|EF190049.1| Zea mays clone 46F3FF5Rm3 chromosome B, genomic sequence  
Length = 585

Score = 54.0 bits (27), Expect = 0.003  
Identities = 52/59 (88%), Gaps = 1/59 (1%)  
Strand = Plus / Plus

Query: 1717 tgtaaccaccacatatata-gatccatcccaagaagtagtgtattacgcctctctaagcg 1774  
||||||| ||||||||| | ||||||| ||| ||||||| || ||||||| |||||||||  
Sbjct: 271 tgtaaccaccacataaaagatccataaccaggaagtagggtgttacggctctctaagcg 329

>gb|EF190044.1| Zea mays clone 46F3FF4R-4 chromosome B, genomic sequence  
Length = 458

Score = 54.0 bits (27), Expect = 0.003  
Identities = 55/63 (87%), Gaps = 1/63 (1%)  
Strand = Plus / Plus

Query: 1717 tgtaaccaccacatatata-gatccatcccaagaagtagtgtattacgcctctctaagcgg 1775  
||||||| ||||||||| | ||||||| ||| ||||||| || ||||||| |||||||||  
Sbjct: 271 tgtaaccaccacataaaagatccacaccaggaagtagggtgttactcctctctaagcgg 330

Query: 1776 ccc 1778  
|||  
Sbjct: 331 ccc 333

>gb|AC196084.4| Zea mays BAC clone CH201-52A17 from chromosome 5, complete sequence  
Length = 187208

Score = 52.0 bits (26), Expect = 0.012  
Identities = 36/38 (94%), Gaps = 1/38 (2%)  
Strand = Plus / Minus

Query: 1296 gttgtgggggatagatatcccc-gggtccactagaagg 1332  
||||||| ||||||| |||||||  
Sbjct: 102699 gttgtggggacagatatccccgggtccactagaagg 102662

Score = 44.1 bits (22), Expect = 3.0  
Identities = 28/30 (93%)  
Strand = Plus / Plus

Query: 1033 atttgtttgatggatttagtaaaggttatg 1062  
||||||| ||||||| |||||||  
Sbjct: 4582 atttgtttgatggatttagtagaggttatg 4611

>gb|AC194844.5| Zea mays BAC clone CH201-463C23 from chromosome 5, complete sequence  
Length = 153983

Score = 52.0 bits (26), Expect = 0.012  
Identities = 36/38 (94%), Gaps = 1/38 (2%)  
Strand = Plus / Plus

Query: 1296 gttgtgggggatagatatcccc-gggtccactagaagg 1332  
||||||| ||||||| |||||||  
Sbjct: 46183 gttgtggggacagatatccccgggtccactagaagg 46220

Score = 44.1 bits (22), Expect = 3.0  
Identities = 28/30 (93%)  
Strand = Plus / Minus

Query: 1033 atttgtttgatggatttagtaaaggttatg 1062  
||||||| ||||||| |||||||  
Sbjct: 144300 atttgtttgatggatttagtagaggttatg 144271

>gb|AC229876.2| Zea mays BAC clone CH201-115J9 from chromosome 8, complete sequence  
Length = 177725

Score = 52.0 bits (26), Expect = 0.012  
Identities = 26/26 (100%)  
Strand = Plus / Plus

Query: 1114 attatatagtggtatagaagatatag 1139  
|||||  
Sbjct: 173236 attatatagtggtatagaagatatag 173261

>gb|BT069726.1| Zea mays full-length cDNA clone ZM\_BFb0216P01 mRNA, complete cds  
Length = 1566

Score = 52.0 bits (26), Expect = 0.012  
Identities = 35/38 (92%)  
Strand = Plus / Plus

Query: 1028 gtgtcatttgtttgatggatttagtaaaggttatgggt 1065  
|||| |||||  
Sbjct: 1454 gtgtaatttgtttgtggatttagtaaagattatgggt 1491

>gb|EU952061.1| Zea mays clone 1145983 hypothetical protein mRNA, complete cds  
Length = 2110

Score = 52.0 bits (26), Expect = 0.012  
Identities = 29/30 (96%)  
Strand = Plus / Plus

Query: 1261 ctatatatttaaaatagggtactgatttaaa 1290  
|||||  
Sbjct: 1548 ctatatatttaagatagggtactgatttaaa 1577

>gb|AC165267.2| Zea mays clone ZMMBBb-151F20, complete sequence  
Length = 115478

Score = 52.0 bits (26), Expect = 0.012  
Identities = 44/50 (88%)  
Strand = Plus / Minus

Query: 1082 ttgggtgggttttacagagtttaaactagcgattatatagtggtataga 1131  
|||||  
Sbjct: 90446 ttgggtgagttttgctaagtttaaactggcgattataaagtgggtataga 90397

>gb|EF190053.1| Zea mays clone 46F3FF5Rs2 chromosome B, genomic sequence  
Length = 452

Score = 50.1 bits (25), Expect = 0.048  
Identities = 25/25 (100%)  
Strand = Plus / Plus

Query: 1758 ttacgcctctcttaagcgcccaaac 1782  
|||||||  
Sbjct: 184 ttacgcctctcttaagcgcccaaac 208

Score = 46.1 bits (23), Expect = 0.75  
Identities = 32/35 (91%)  
Strand = Plus / Plus

Query: 1804 tctctcgtgcgtccagcacgaaccattgagttaca 1838  
||||||| ||||| |||  
Sbjct: 229 tctctcgtgcatccagcacgaaccatcgagctaca 263

>gb|EF190052.1| Zea mays clone 46F3FF5Rs1 chromosome B, genomic sequence  
Length = 452

Score = 50.1 bits (25), Expect = 0.048  
Identities = 25/25 (100%)  
Strand = Plus / Plus

Query: 1758 ttacgcctctcttaagcgcccaaac 1782  
|||||||  
Sbjct: 184 ttacgcctctcttaagcgcccaaac 208

Score = 46.1 bits (23), Expect = 0.75  
Identities = 32/35 (91%)  
Strand = Plus / Plus

Query: 1804 tctctcgtgcgtccagcacgaaccattgagttaca 1838  
||||||| ||||| |||  
Sbjct: 229 tctctcgtgcatccagcacgaaccatcgagctaca 263

>gb|EF190043.1| Zea mays clone 46F3FF4R-3 chromosome B, genomic sequence

Length = 461

Score = 50.1 bits (25), Expect = 0.048  
Identities = 62/73 (84%), Gaps = 1/73 (1%)  
Strand = Plus / Plus

Query: 1706 gagacctcgcttgtaacccaccacat-atagatccatcccaagaagtagtgattacgcc 1764  
||||| ||| ||||||||||||||||| | ||||||| ||| ||||||| || |||||  
Sbjct: 260 gagaactcccttgtaacccaccacataaaagatccacaccaggaagtaggggtgctacgct 319

Query: 1765 tctctaagcggcc 1777  
|||||||||||||  
Sbjct: 320 tctctaagcggcc 332

>gb|AC160211.1| Genomic sequence for Zea mays BAC clone ZMMBBb0448F23, complete sequence  
Length = 132549

Score = 50.1 bits (25), Expect = 0.048  
Identities = 32/33 (96%), Gaps = 1/33 (3%)  
Strand = Plus / Minus

Query: 1296 gttgtgggggatagatatcccc-gggtccacta 1327  
||||||||||||||||||||| |||||||||  
Sbjct: 115935 gttgtgggggatagatatcccctgggtccacta 115903

>gb|AY555142.1| Zea mays BAC clone c573F08, complete sequence  
Length = 181627

Score = 50.1 bits (25), Expect = 0.048  
Identities = 35/37 (94%), Gaps = 1/37 (2%)  
Strand = Plus / Minus

Query: 1297 ttgtgggggatagatatcccc-gggtccactagaagg 1332  
||||||||| ||||||||| |||||||||||||  
Sbjct: 4181 ttgtgggggacagatatccccgggtccactagaagg 4145

Score = 50.1 bits (25), Expect = 0.048  
Identities = 35/37 (94%), Gaps = 1/37 (2%)  
Strand = Plus / Minus

Query: 1297 ttgtgggggatagatatcccc-gggtccactagaagg 1332  
||||||| ||||| |||||  
Sbjct: 26540 ttgtgggggacagatatccccgggtccactagaagg 26504

Score = 44.1 bits (22), Expect = 3.0  
Identities = 34/38 (89%)  
Strand = Plus / Minus

Query: 1619 gccccacggtcgtgtatataaggtccagagggtacccc 1656  
||||||| ||||| | |||||  
Sbjct: 3860 gccccacggtcgagtatataaggcctagagggcacccc 3823

>gb|AC207417.4| Zea mays BAC clone CH201-186N18 from chromosome 5, complete sequence  
Length = 180967

Score = 48.1 bits (24), Expect = 0.19  
Identities = 31/32 (96%), Gaps = 1/32 (3%)  
Strand = Plus / Minus

Query: 1297 ttgtgggggatagatatcccc-gggtccacta 1327  
||||||| |||||  
Sbjct: 172679 ttgtgggggatagatatcccctgggtccacta 172648

>gb|AC206691.5| Zea mays BAC clone CH201-149B20 from chromosome 10, complete sequence  
Length = 174429

Score = 48.1 bits (24), Expect = 0.19  
Identities = 31/32 (96%), Gaps = 1/32 (3%)  
Strand = Plus / Plus

Query: 1297 ttgtgggggatagatatcccc-gggtccacta 1327  
||||||| |||||  
Sbjct: 37611 ttgtgggggatagatatcccctgggtccacta 37642

Score = 46.1 bits (23), Expect = 0.75  
Identities = 30/31 (96%), Gaps = 1/31 (3%)  
Strand = Plus / Plus

Query: 1298 ttgtgggggatagatatcccc-gggtccacta 1327



|||||  
Sbjct: 24104 ttgtgggggatagatatcccctgggtccacta 24134

>gb|AC211313.4| Zea mays BAC clone CH201-9J2 from chromosome 5, complete sequence  
Length = 202568

Score = 48.1 bits (24), Expect = 0.19  
Identities = 31/32 (96%), Gaps = 1/32 (3%)  
Strand = Plus / Minus

Query: 1297 ttgtgggggatagatatcccc-gggtccacta 1327  
|||||  
Sbjct: 140807 ttgtgggggatagatatcccctgggtccacta 140776

Score = 46.1 bits (23), Expect = 0.75  
Identities = 30/31 (96%), Gaps = 1/31 (3%)  
Strand = Plus / Minus

Query: 1298 ttgtgggggatagatatcccc-gggtccacta 1327  
|||||  
Sbjct: 154049 ttgtgggggatagatatcccctgggtccacta 154019

>gb|AC203072.5| Zea mays BAC clone CH201-26J18 from chromosome 6, complete sequence  
Length = 184681

Score = 48.1 bits (24), Expect = 0.19  
Identities = 31/32 (96%), Gaps = 1/32 (3%)  
Strand = Plus / Plus

Query: 1297 ttgtgggggatagatat-ccccgggtccacta 1327  
|||||  
Sbjct: 41260 ttgtgggggatagatatccccgggtccacta 41291

Score = 48.1 bits (24), Expect = 0.19  
Identities = 31/32 (96%), Gaps = 1/32 (3%)  
Strand = Plus / Minus

Query: 1297 ttgtgggggatagatat-ccccgggtccacta 1327  
|||||

Sbjct: 94022 ttgtgggggatagatatccccgggtccacta 93991

Score = 46.1 bits (23), Expect = 0.75  
Identities = 30/31 (96%), Gaps = 1/31 (3%)  
Strand = Plus / Plus

Query: 1298 ttgtgggggatagatat-c-c-c-gggtccacta 1327  
|||||||  
Sbjct: 27464 ttgtgggggatagatatccccgggtccacta 27494

Score = 46.1 bits (23), Expect = 0.75  
Identities = 30/31 (96%), Gaps = 1/31 (3%)  
Strand = Plus / Minus

Query: 1298 ttgtgggggatagatatcccc-gggtccacta 1327  
|||||||  
Sbjct: 115417 ttgtgggggatagatatcccctgggtccacta 115387

>gb|AC230040.3| Zea mays BAC clone CH201-122P19 from chromosome 7, complete sequence  
Length = 173182

Score = 48.1 bits (24), Expect = 0.19  
Identities = 31/32 (96%), Gaps = 1/32 (3%)  
Strand = Plus / Plus

Query: 1297 ttgtgggggatagatatcccc-gggtccacta 1327  
|||||||  
Sbjct: 31129 ttgtgggggatagatatcccctgggtccacta 31160

Score = 48.1 bits (24), Expect = 0.19  
Identities = 31/32 (96%), Gaps = 1/32 (3%)  
Strand = Plus / Minus

Query: 1297 ttgtgggggatagatatcccc-gggtccacta 1327  
|||||||  
Sbjct: 85079 ttgtgggggatagatatcccctgggtccacta 85048

Score = 46.1 bits (23), Expect = 0.75  
Identities = 30/31 (96%), Gaps = 1/31 (3%)  
Strand = Plus / Plus

Query: 1298 tgtgggggatagatatcccc-gggtccacta 1327  
|||||  
Sbjct: 17495 tgtgggggatagatatcccctgggtccacta 17525

Score = 46.1 bits (23), Expect = 0.75  
Identities = 30/31 (96%), Gaps = 1/31 (3%)  
Strand = Plus / Minus

Query: 1298 tgtgggggatagatatcccc-gggtccacta 1327  
|||||  
Sbjct: 98496 tgtgggggatagatatcccctgggtccacta 98466

>gb|AC203533.4| Zea mays BAC clone CH201-452L5 from chromosome 5, complete sequence  
Length = 196401

Score = 48.1 bits (24), Expect = 0.19  
Identities = 31/32 (96%), Gaps = 1/32 (3%)  
Strand = Plus / Plus

Query: 1297 ttgtgggggatagatatcccc-gggtccacta 1327  
|||||  
Sbjct: 177802 ttgtgggggatagatatcccctgggtccacta 177833

Score = 46.1 bits (23), Expect = 0.75  
Identities = 30/31 (96%), Gaps = 1/31 (3%)  
Strand = Plus / Plus

Query: 1298 tgtgggggatagatatcccc-gggtccacta 1327  
|||||  
Sbjct: 164160 tgtgggggatagatatcccctgggtccacta 164190

>gb|AC210997.6| Zea mays BAC clone CH201-545A13 from chromosome 5, complete sequence  
Length = 157790

Score = 48.1 bits (24), Expect = 0.19  
Identities = 31/32 (96%), Gaps = 1/32 (3%)  
Strand = Plus / Minus

Query: 1297 ttgtgggggatagatatcccc-gggtccacta 1327  
|||||  
Sbjct: 10274 ttgtgggggatagatatcccctgggtccacta 10243

Score = 48.1 bits (24), Expect = 0.19  
Identities = 31/32 (96%), Gaps = 1/32 (3%)  
Strand = Plus / Minus

Query: 1297 ttgtgggggatagatatcccc-gggtccacta 1327  
|||||  
Sbjct: 143832 ttgtgggggatagatatcccctgggtccacta 143801

Score = 46.1 bits (23), Expect = 0.75  
Identities = 30/31 (96%), Gaps = 1/31 (3%)  
Strand = Plus / Minus

Query: 1298 tgtgggggatagatatcccc-gggtccacta 1327  
|||||  
Sbjct: 23516 tgtgggggatagatatcccctgggtccacta 23486

Score = 46.1 bits (23), Expect = 0.75  
Identities = 30/31 (96%), Gaps = 1/31 (3%)  
Strand = Plus / Minus

Query: 1298 tgtgggggatagatatcccc-gggtccacta 1327  
|||||  
Sbjct: 157474 tgtgggggatagatatcccctgggtccacta 157444

>gb|AC209754.5| Zea mays BAC clone CH201-23E16 from chromosome 5, complete sequence  
Length = 188133

Score = 48.1 bits (24), Expect = 0.19  
Identities = 31/32 (96%), Gaps = 1/32 (3%)  
Strand = Plus / Plus

Query: 1297 ttgtgggggatagatat-ccccgggtccacta 1327  
|||||||  
Sbjct: 3262 ttgtgggggatagatatccccgggtccacta 3293

Score = 48.1 bits (24), Expect = 0.19  
Identities = 31/32 (96%), Gaps = 1/32 (3%)  
Strand = Plus / Minus

Query: 1297 ttgtgggggatagatatcccc-gggtccacta 1327  
|||||||  
Sbjct: 99526 ttgtgggggatagatatcccctgggtccacta 99495

Score = 46.1 bits (23), Expect = 0.75  
Identities = 30/31 (96%), Gaps = 1/31 (3%)  
Strand = Plus / Minus

Query: 1298 tgtgggggatagatatcccc-gggtccacta 1327  
|||||||  
Sbjct: 109596 tgtgggggatagatatcccctgggtccacta 109566

>emb|AM489152.2| Vitis vinifera contig VV78X015348.8, whole genome shotgun sequence  
Length = 1652

Score = 48.1 bits (24), Expect = 0.19  
Identities = 27/28 (96%)  
Strand = Plus / Plus

Query: 1264 tattttaaaatagggtactgatttaaaa 1291  
|||||||  
Sbjct: 1545 tattttaaaatagggtattgatttaaaa 1572

>gb|DQ493649.1| Zea mays cultivar Coroico bz locus region  
Length = 159340

Score = 48.1 bits (24), Expect = 0.19  
Identities = 31/32 (96%), Gaps = 1/32 (3%)  
Strand = Plus / Plus

Query: 1297 ttgtgggggatagatatcccc-gggtccacta 1327  
|||||  
Sbjct: 80049 ttgtgggggatagatatcccctgggtccacta 80080

Score = 48.1 bits (24), Expect = 0.19  
Identities = 31/32 (96%), Gaps = 1/32 (3%)  
Strand = Plus / Plus

Query: 1297 ttgtgggggatagatatcccc-gggtccacta 1327  
|||||  
Sbjct: 102517 ttgtgggggatagatatcccctgggtccacta 102548

>gb|AC152494.1| Zea mays BAC clone Z418K17, complete sequence  
Length = 195448

Score = 48.1 bits (24), Expect = 0.19  
Identities = 31/32 (96%), Gaps = 1/32 (3%)  
Strand = Plus / Plus

Query: 1297 ttgtgggggatagatatcccc-gggtccacta 1327  
|||||  
Sbjct: 121910 ttgtgggggatagatatcccctgggtccacta 121941

Score = 46.1 bits (23), Expect = 0.75  
Identities = 30/31 (96%), Gaps = 1/31 (3%)  
Strand = Plus / Plus

Query: 1298 tgtgggggatagatatcccc-gggtccacta 1327  
|||||  
Sbjct: 110963 tgtgggggatagatatcccctgggtccacta 110993

>gb|DQ002407.1| Zea mays copia retrotransposon opiel, gypsy retrotransposon grandel,  
xilon1 retrotransposon, helitron B73\_14578, gypsy  
retrotransposon huck1 and ruda retrotransposon, complete  
sequence  
Length = 152384

Score = 48.1 bits (24), Expect = 0.19  
Identities = 31/32 (96%), Gaps = 1/32 (3%)

Strand = Plus / Minus

Query: 1297 ttgtgggggatagatat-ccccgggtccacta 1327  
|||||  
Sbjct: 66192 ttgtgggggatagatatccccgggtccacta 66161

Score = 46.1 bits (23), Expect = 0.75  
Identities = 30/31 (96%), Gaps = 1/31 (3%)  
Strand = Plus / Minus

Query: 1298 tgtgggggatagatatcc-ccgggtccacta 1327  
|||||  
Sbjct: 90582 tgtgggggatagatatcctccgggtccacta 90552

>gb|AC124722.3| Mus musculus BAC clone RP23-389E7 from chromosome 6, complete sequence  
Length = 193830

Score = 48.1 bits (24), Expect = 0.19  
Identities = 27/28 (96%)  
Strand = Plus / Plus

Query: 415 acattaccatgtccaactgatttaaaac 442  
|||||  
Sbjct: 183367 acattaccatgtccaactgacttaaaac 183394

>gb|AC159713.6| Mus musculus 6 BAC RP24-317F6 (Roswell Park Cancer Institute (C57BL/6J  
Male) Mouse BAC Library) complete sequence  
Length = 200130

Score = 48.1 bits (24), Expect = 0.19  
Identities = 27/28 (96%)  
Strand = Plus / Minus

Query: 415 acattaccatgtccaactgatttaaaac 442  
|||||  
Sbjct: 147812 acattaccatgtccaactgacttaaaac 147785

>gb|AC090648.5| Genomic sequence for Mus musculus, clone RP23-331I23, complete sequence  
Length = 198695

Score = 48.1 bits (24), Expect = 0.19  
Identities = 27/28 (96%)  
Strand = Plus / Minus

Query: 415 acattaccatgtccaactgatttaaac 442  
|||||||  
Sbjct: 11423 acattaccatgtccaactgacttaaac 11396

>emb|AL772329.14| Zebrafish DNA sequence from clone CH211-150D5 in linkage group 3,  
complete sequence  
Length = 163559

Score = 48.1 bits (24), Expect = 0.19  
Identities = 24/24 (100%)  
Strand = Plus / Plus

Query: 8 tttaatatactttaataaatatta 31  
|||||||  
Sbjct: 60907 tttaatatactttaataaatatta 60930

>gb|AF546188.1| Contiguous genomic DNA sequence comprising the 19-kDa-zein gene family  
from Zea mays, complete sequence  
Length = 203363

Score = 48.1 bits (24), Expect = 0.19  
Identities = 34/36 (94%), Gaps = 1/36 (2%)  
Strand = Plus / Minus

Query: 1297 ttgtgggggatagatatcccc-gggtccactagaag 1331  
|||||||  
Sbjct: 15523 ttgtgggggacagatatccccgggtccactagaag 15488

Score = 48.1 bits (24), Expect = 0.19  
Identities = 34/36 (94%), Gaps = 1/36 (2%)  
Strand = Plus / Plus

Query: 1298 tgtgggggatagatatcccc-gggtccactagaagg 1332  
|||||||  
Sbjct: 53541 tgtgggggacagatatcccctgggtccactagaagg 53576



Score = 46.1 bits (23), Expect = 0.75  
Identities = 33/35 (94%), Gaps = 1/35 (2%)  
Strand = Plus / Minus

Query: 1298 tgtgggggatagatatcccc-gggtccactagaag 1331  
||||||| ||||||| |||||||||  
Sbjct: 29356 tgtgggggacagatatccccgggtccactagaag 29322

>gb|AF466932.1| Zea mays clone BAC 206C17, complete sequence  
Length = 99156

Score = 48.1 bits (24), Expect = 0.19  
Identities = 31/32 (96%), Gaps = 1/32 (3%)  
Strand = Plus / Plus

Query: 1297 ttgtgggggatagatatcccc-gggtccacta 1327  
||||||||| |||||||  
Sbjct: 96175 ttgtgggggatagatatcccctgggtccacta 96206

Score = 46.1 bits (23), Expect = 0.75  
Identities = 30/31 (96%), Gaps = 1/31 (3%)  
Strand = Plus / Plus

Query: 1298 tgtgggggatagatatcccc-gggtccacta 1327  
||||||||| |||||||  
Sbjct: 85229 tgtgggggatagatatcccctgggtccacta 85259

>emb|X68678.1| Z.mays gene for cyclophilin  
Length = 2598

Score = 48.1 bits (24), Expect = 0.19  
Identities = 42/48 (87%)  
Strand = Plus / Plus

Query: 1005 ttttgatggtatgttaaatttgtgtgtcatttgtttgatggatttagt 1052  
||||||| | ||||| || |||| |||||||||  
Sbjct: 558 ttttgatgatctgttaagtttaggtgtaatttgtttgatggatttagt 605

>gb|AY664415.1| Zea mays cultivar B73 locus 9009, complete sequence

Length = 323584

Score = 48.1 bits (24), Expect = 0.19  
Identities = 31/32 (96%), Gaps = 1/32 (3%)  
Strand = Plus / Minus

Query: 1297 ttgtgggggatagatatcccc-gggtccacta 1327  
|||||||  
Sbjct: 97420 ttgtgggggatagatatcccctgggtccacta 97389

Score = 46.1 bits (23), Expect = 0.75  
Identities = 30/31 (96%), Gaps = 1/31 (3%)  
Strand = Plus / Minus

Query: 1298 tgtgggggatagatatcccc-gggtccacta 1327  
|||||||  
Sbjct: 111237 tgtgggggatagatatcccctgggtccacta 111207

>emb|X82087.1| Z.diploperennis Grandel gene  
Length = 8449

Score = 48.1 bits (24), Expect = 0.19  
Identities = 31/32 (96%), Gaps = 1/32 (3%)  
Strand = Plus / Minus

Query: 1297 ttgtgggggatagatat-ccccgggtccacta 1327  
|||||||  
Sbjct: 992 ttgtgggggatagatatccccgggtccacta 961

>gb|AC203284.4| Zea mays BAC clone CH201-504M1 from chromosome 5, complete sequence  
Length = 179214

Score = 46.1 bits (23), Expect = 0.75  
Identities = 30/31 (96%), Gaps = 1/31 (3%)  
Strand = Plus / Plus

Query: 1298 tgtgggggatagatatcccc-gggtccacta 1327  
|||||||  
Sbjct: 94141 tgtgggggatagatatcccctgggtccacta 94171

>gb|FJ386410.1| Zea mays clone L4-a StarkB element, partial sequence  
Length = 890

Score = 46.1 bits (23), Expect = 0.75  
Identities = 57/67 (85%), Gaps = 1/67 (1%)  
Strand = Plus / Plus

Query: 1717 tgtaacccaccacatata-gatccatcccaagaagtagtgattacgcctctctaagcgg 1775  
||||| ||||||||| | ||||| ||| ||||||| || ||||| |||||||||  
Sbjct: 362 tgtaatccaccacataaaagatccacaccaggaagtagggtgttacgtctctctaagcgg 421

Query: 1776 cccaaac 1782  
|||||  
Sbjct: 422 tccaaac 428

>gb|AC226723.4| Zea mays BAC clone CH201-110I20 from chromosome 6, complete sequence  
Length = 190394

Score = 46.1 bits (23), Expect = 0.75  
Identities = 42/47 (89%), Gaps = 1/47 (2%)  
Strand = Plus / Plus

Query: 1298 tgtgggggatagatatcccc-gggtccactagaaggcgagaaggcct 1343  
||||||| | ||||||| ||||||||| |||||  
Sbjct: 151044 tgtgggggacatatatcccccggtccactagaaggctaaaaggcct 151090

>gb|AC231746.2| Zea mays BAC clone CH201-98H14 from chromosome 6, complete sequence  
Length = 189380

Score = 46.1 bits (23), Expect = 0.75  
Identities = 30/31 (96%), Gaps = 1/31 (3%)  
Strand = Plus / Plus

Query: 1298 tgtgggggatagatatcccc-gggtccacta 1327  
||||||| |||||||  
Sbjct: 184382 tgtgggggatagatatcccctgggtccacta 184412

>gb|CP001078.1| Clostridium botulinum E3 str. Alaska E43, complete genome  
Length = 3659644

Score = 46.1 bits (23), Expect = 0.75  
Identities = 23/23 (100%)

Strand = Plus / Plus

Query: 1206     ttgataaaaaaggtaaagtaga 1228  
                 ||||||||||||||||||||  
Sbjct: 1648880 ttgataaaaaaggtaaagtaga 1648902

>gb|AC205914.3| Pongo abelii BAC clone CH276-7K14 from chromosome unknown, complete  
                 sequence  
                 Length = 203364

Score = 46.1 bits (23), Expect = 0.75  
Identities = 23/23 (100%)  
Strand = Plus / Plus

Query: 650     ctttcatatatcttcccatcctt 672  
                 ||||||||||||||||||||  
Sbjct: 175329 ctttcatatatcttcccatcctt 175351

>dbj|AP009179.1| Sulfurovum sp. NBC37-1 genomic DNA, complete genome  
                 Length = 2562277

Score = 46.1 bits (23), Expect = 0.75  
Identities = 26/27 (96%)  
Strand = Plus / Minus

Query: 437     taaaacacaaactcttcttgaaccata 463  
                 ||||| ||||||||||||||||||||  
Sbjct: 839439 taaaacacaaactcttcttgaaccata 839413

>gb|EF190046.1| Zea mays clone 46F3FF4R-H2 chromosome B, genomic sequence  
                 Length = 578

Score = 46.1 bits (23), Expect = 0.75  
Identities = 54/63 (85%), Gaps = 1/63 (1%)  
Strand = Plus / Plus

Query: 1717 tgtaaccaccacatata-gatccatcccaagaagtagtgattacgcctctctaagcgg 1775  
                 |||||||||||||||| | |||| | ||| |||||| | || || ||||||||||||  
Sbjct: 270 tgtaaccaccacataaaagatctacaccaggaagtaggtgttatgcctctctaagcgg 329

Query: 1776 ccc 1778

|||  
Sbjct: 330 ccc 332

>gb|EF190045.1| Zea mays clone 46F3FF4R-H1 chromosome B, genomic sequence  
Length = 577

Score = 46.1 bits (23), Expect = 0.75  
Identities = 54/63 (85%), Gaps = 1/63 (1%)  
Strand = Plus / Plus

Query: 1717 tgtaaccaccacatatata-gatccatcccaagaagtagtgtattacgcctctctaagcgg 1775  
|||||  
Sbjct: 270 tgtaaccaccacataaaagatctacaccaggaagtaggtgttatgcctctctaagcgg 329

Query: 1776 ccc 1778  
|||  
Sbjct: 330 ccc 332

>gb|AC187724.2| Pan troglodytes BAC clone CH251-318015 from chromosome 7, complete  
sequence  
Length = 188968

Score = 46.1 bits (23), Expect = 0.75  
Identities = 23/23 (100%)  
Strand = Plus / Minus

Query: 650 ctttcatatatcttcccatcctt 672  
|||||  
Sbjct: 158580 ctttcatatatcttcccatcctt 158558

>gb|AC183623.3| Pan troglodytes BAC clone CH251-49H23 from chromosome 5, complete  
sequence  
Length = 184771

Score = 46.1 bits (23), Expect = 0.75  
Identities = 23/23 (100%)  
Strand = Plus / Plus

Query: 373 aatcatgtgccacataatcacgt 395  
|||||  
Sbjct: 82076 aatcatgtgccacataatcacgt 82098

>gb|AC165172.2| Zea mays clone CH201-171E16, complete sequence  
Length = 180971

Score = 46.1 bits (23), Expect = 0.75  
Identities = 41/47 (87%)  
Strand = Plus / Plus

Query: 1085 ggtgggttttacagagtttaactagcggattatatagtggtataga 1131  
||||| ||||| || ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 88108 ggtgtgttttgcaaagtttaactagtagattatatagtagtataga 88154

>gb|AC134822.19| Medicago truncatula clone mth2-15j20, complete sequence  
Length = 106152

Score = 46.1 bits (23), Expect = 0.75  
Identities = 23/23 (100%)  
Strand = Plus / Plus

Query: 513 attaaaaattactttgaagattc 535  
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 63022 attaaaaattactttgaagattc 63044

>gb|AC147708.7| Canis Familiaris, clone XX-25G10, complete sequence  
Length = 185084

Score = 46.1 bits (23), Expect = 0.75  
Identities = 23/23 (100%)  
Strand = Plus / Plus

Query: 7 atttaatatactttaataaatat 29  
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 177697 atttaatatactttaataaatat 177719

>gb|AF466202.2| Zea mays putative pol protein gene, partial cds; and putative gag-pol precursor -orf2, putative Fourf gag/pol protein, putative NADP-dependent malic enzyme, putative argonaute protein, putative pinhead protein, putative pol protein, putative gag protein, putative TNP2, r1-B73 proteins, putative genetic modifier, putative S-receptor kinase, putative aldose reductase-related protein, putative glutathione peroxidase, putative glycerol 3-phosphate permease, putative response regulator, and putative 4-coumarate-CoA

ligase-like protein genes, complete cds  
Length = 290350

Score = 46.1 bits (23), Expect = 0.75  
Identities = 44/51 (86%)  
Strand = Plus / Minus

Query: 1081 gttgggtgggttttacagagtttaactagcggattatatagtggatataga 1131  
||||| ||| ||||| || |||||||||||| | ||||||| |||||||  
Sbjct: 90789 gttgagtgagttttgcaaagtttaactagtgaattatataatggatataga 90739

>gb|AF466203.1| Zea mays clone ZMBBb\_0092E12, partial sequence  
Length = 147198

Score = 46.1 bits (23), Expect = 0.75  
Identities = 35/39 (89%)  
Strand = Plus / Plus

Query: 1618 tgccccacggtcgtgtatataaggtccagagggtacccc 1656  
||||||||||||| ||||||||||| | ||||||| |||||  
Sbjct: 21097 tgccccacggtcgagtatataaggcctagagggcacccc 21135

>emb|AJ312444.1| Zea mays Grande retrotransposon DNA, partial LTR, clone B13  
Length = 436

Score = 46.1 bits (23), Expect = 0.75  
Identities = 35/39 (89%)  
Strand = Plus / Plus

Query: 1618 tgccccacggtcgtgtatataaggtccagagggtacccc 1656  
||||||||||||| ||||||||||| | ||||||| |||||  
Sbjct: 291 tgccccacggtcgagtatataaggcctagagggcacccc 329

>gb|AF050437.1| Zea mays retrotransposon Grande-Zm1 3' LTR, partial sequence  
Length = 623

Score = 46.1 bits (23), Expect = 0.75  
Identities = 30/31 (96%), Gaps = 1/31 (3%)  
Strand = Plus / Plus

Query: 1298 tgtgggggatagatatcccc-ggggtccacta 1327  
||||||||||||||||||| |||||||||





Query: 1033    atttgtttgatggatttagtaaaggttatg 1062  
                 |||||    |||||    |||||  
Sbjct: 182189 atttgtttggtggatttagtagaggttatg 182218

>emb|CU207403.3| Pig DNA sequence from clone CH242-522I21 on chromosome X, complete  
                 sequence  
                 Length = 196911

Score = 44.1 bits (22), Expect = 3.0  
Identities = 22/22 (100%)  
Strand = Plus / Minus

Query: 8            tttaatatactttaataaatat 29  
                 |||||    |||||    |||||  
Sbjct: 110942 tttaatatactttaataaatat 110921

>gb|EZ077797.1| TSA: Zea mays contig13436, mRNA sequence  
                 Length = 117

Score = 44.1 bits (22), Expect = 3.0  
Identities = 43/50 (86%)  
Strand = Plus / Minus

Query: 1082 ttgggtgggttttacagagtttaactagcggattatagtggtataga 1131  
                 |||||    ||    |||||    |||||    |||||  
Sbjct: 66    ttgggtgggtttgtaaagtttaactatgaaattatagtggtataga 17

>ref|XM\_001909862.1| Podospora anserina DSM 980 hypothetical protein (PODANSg6934) partial  
                 mRNA  
                 Length = 1656

Score = 44.1 bits (22), Expect = 3.0  
Identities = 22/22 (100%)  
Strand = Plus / Plus

Query: 845    gatgcgagtgaggaggagaggg 866  
                 |||||    |||||    |||||  
Sbjct: 1633 gatgcgagtgaggaggagaggg 1654

>emb|CU638744.1| Podospora anserina genomic DNA chromosome 6, supercontig 2

Length = 2996286

Score = 44.1 bits (22), Expect = 3.0

Identities = 22/22 (100%)

Strand = Plus / Minus

Query: 845 gatgcgagtgaggaggagaggg 866

||||||||||||||||

Sbjct: 150414 gatgcgagtgaggaggagaggg 150393

>gb|EF396164.1| Zea mays nitrilase 2 (NIT2) gene, complete cds

Length = 7505

Score = 44.1 bits (22), Expect = 3.0

Identities = 31/34 (91%)

Strand = Plus / Minus

Query: 1092 ttacagagtttaaactagcggattatatagtgg 1125

||||| ||||||||| | |||||||||||||

Sbjct: 576 ttacaaagtttaaactggtggattatatagtgg 543

>gb|EF190047.1| Zea mays clone 46F3FF4R-H3 chromosome B, genomic sequence

Length = 477

Score = 44.1 bits (22), Expect = 3.0

Identities = 53/62 (85%), Gaps = 1/62 (1%)

Strand = Plus / Plus

Query: 1717 tgtaaccaccacat-atagatccatccaagaagtagtgattacgcctctctaagcgg 1775

||||||||||||||| | ||||||| ||| ||||||| || ||||| |||||||||||||

Sbjct: 270 tgtaaccaccacataaaagatccacaccaggaagtagggtgctacgcttctctaagcgg 329

Query: 1776 cc 1777

||

Sbjct: 330 cc 331

>gb|EF190042.1| Zea mays clone 46F3FF4R-2 chromosome B, genomic sequence

Length = 461

Score = 44.1 bits (22), Expect = 3.0

Identities = 53/62 (85%), Gaps = 1/62 (1%)

Strand = Plus / Plus

Query: 1717 tgtaaccaccacat-atagatccatcccaagaagtagtgattacgcctctctaagcgg 1775  
|||||||  
Sbjct: 271 tgtaaccaccacataaaagatccacaccaggaagtaggtgctacgttctctaagcgg 330

Query: 1776 cc 1777  
||  
Sbjct: 331 cc 332

>gb|AC182574.2| Mimulus guttatus clone MGBa-83E5, complete sequence  
Length = 139993

Score = 44.1 bits (22), Expect = 3.0  
Identities = 22/22 (100%)  
Strand = Plus / Minus

Query: 12 atatactttaataaatattatt 33  
|||||||  
Sbjct: 31941 atatactttaataaatattatt 31920

>gb|AC188446.2| Gallus gallus BAC clone CH261-122M13 from chromosome z, complete sequence  
Length = 193200

Score = 44.1 bits (22), Expect = 3.0  
Identities = 22/22 (100%)  
Strand = Plus / Plus

Query: 783 ggaaggggaggggaaggggagga 804  
|||||||  
Sbjct: 161989 ggaaggggaggggaaggggagga 162010

>gb|CP000393.1| Trichodesmium erythraeum IMS101, complete genome  
Length = 7750108

Score = 44.1 bits (22), Expect = 3.0  
Identities = 22/22 (100%)  
Strand = Plus / Minus

Query: 1683 ctcacagcttttctccattca 1704  
|||||||  
Sbjct: 5139177 ctcacagcttttctccattca 5139156

>gb|AC115727.10| Mus musculus chromosome 3, clone RP23-30A13, complete sequence  
Length = 183826

Score = 44.1 bits (22), Expect = 3.0  
Identities = 22/22 (100%)  
Strand = Plus / Minus

Query: 783 ggaaggggaggggaaggggagga 804  
|||||||  
Sbjct: 125838 ggaaggggaggggaaggggagga 125817

>gb|AC110735.6| Mus musculus chromosome 1, clone RP24-123P22, complete sequence  
Length = 187303

Score = 44.1 bits (22), Expect = 3.0  
Identities = 22/22 (100%)  
Strand = Plus / Minus

Query: 1036 tgtttgatggatttagtaaagg 1057  
|||||||  
Sbjct: 12801 tgtttgatggatttagtaaagg 12780

>gb|AC107851.17| Mus musculus chromosome 9, clone RP23-451B4, complete sequence  
Length = 190253

Score = 44.1 bits (22), Expect = 3.0  
Identities = 22/22 (100%)  
Strand = Plus / Minus

Query: 783 ggaaggggaggggaaggggagga 804  
|||||||  
Sbjct: 94906 ggaaggggaggggaaggggagga 94885

>gb|AC112971.8| Mus musculus chromosome 1, clone RP24-444M12, complete sequence  
Length = 161310

Score = 44.1 bits (22), Expect = 3.0  
Identities = 22/22 (100%)  
Strand = Plus / Minus

Query: 1036    tgtttgatggatttagtaaagg 1057  
                 |||||  
Sbjct: 157955 tgtttgatggatttagtaaagg 157934

>gb|AC137002.2| Oryza sativa (japonica cultivar-group) chromosome 5 BAC clone  
                 OSJNBb0061M13, complete sequence  
                 Length = 174910

Score = 44.1 bits (22), Expect = 3.0  
Identities = 22/22 (100%)  
Strand = Plus / Minus

Query: 783      ggaagggaggggaagggagga 804  
                 |||||  
Sbjct: 110516 ggaagggaggggaagggagga 110495

>gb|AC137128.17| Mus musculus chromosome 3, clone RP24-271G16, complete sequence  
                 Length = 182140

Score = 44.1 bits (22), Expect = 3.0  
Identities = 22/22 (100%)  
Strand = Plus / Plus

Query: 783      ggaagggaggggaagggagga 804  
                 |||||  
Sbjct: 59258 ggaagggaggggaagggagga 59279

>gb|AF394561.1| Oryza sativa alpha-expansin OsEXPA26 (EXPA26) gene, complete cds  
                 Length = 6312

Score = 44.1 bits (22), Expect = 3.0  
Identities = 22/22 (100%)  
Strand = Plus / Plus

Query: 458    accatatagtttgacaaaccaa 479  
                 |||||  
Sbjct: 4935 accatatagtttgacaaaccaa 4956

>gb|AC121523.6| Mus musculus chromosome 18, clone RP24-92N23, complete sequence  
                 Length = 202346

Score = 44.1 bits (22), Expect = 3.0

Identities = 22/22 (100%)  
Strand = Plus / Plus

Query: 783 ggaaggggaggaaggggagga 804  
|||||||  
Sbjct: 76087 ggaaggggaggaaggggagga 76108

>gb|AC161177.4| Mus musculus chromosome 18, clone RP24-131H12, complete sequence  
Length = 189231

Score = 44.1 bits (22), Expect = 3.0  
Identities = 22/22 (100%)  
Strand = Plus / Plus

Query: 783 ggaaggggaggaaggggagga 804  
|||||||  
Sbjct: 129914 ggaaggggaggaaggggagga 129935

>gb|AC074327.6| Homo sapiens chromosome 10 clone RP11-556E13, complete sequence  
Length = 189250

Score = 44.1 bits (22), Expect = 3.0  
Identities = 22/22 (100%)  
Strand = Plus / Plus

Query: 782 tggaagggaggaaggggagg 803  
|||||||  
Sbjct: 138782 tggaagggaggaaggggagg 138803

>tpg|BK000854.1| TPA: TPA\_inf: Oryza sativa transposon Rim2-M255, complete sequence  
Length = 4415

Score = 44.1 bits (22), Expect = 3.0  
Identities = 22/22 (100%)  
Strand = Plus / Plus

Query: 783 ggaaggggaggaaggggagga 804  
|||||||  
Sbjct: 713 ggaaggggaggaaggggagga 734

>gb|AC113420.2| Homo sapiens chromosome 5 clone RP11-586E1, complete sequence

Length = 176267

Score = 44.1 bits (22), Expect = 3.0  
Identities = 22/22 (100%)  
Strand = Plus / Plus

Query: 209 aaatttctaaagcagtatatat 230  
|||||||  
Sbjct: 89249 aaatttctaaagcagtatatat 89270

>emb|AL513013.12| Human DNA sequence from clone RP5-990P15 on chromosome 1 Contains the  
5' end of a novel gene, a novel gene (DKFZp564J047), two  
novel genes and a CpG island, complete sequence  
Length = 77001

Score = 44.1 bits (22), Expect = 3.0  
Identities = 25/26 (96%)  
Strand = Plus / Plus

Query: 560 cacatctaaccagaagggctaaggct 585  
||||||| |||||  
Sbjct: 18114 cacatctaaccagcagggctaaggct 18139

>emb|AL606923.8| Human DNA sequence from clone RP11-361F19 on chromosome 6 Contains a C2H2  
zinc finger protein pseudogene, complete sequence  
Length = 154285

Score = 44.1 bits (22), Expect = 3.0  
Identities = 22/22 (100%)  
Strand = Plus / Plus

Query: 783 ggaaggggaggggaaggggagga 804  
|||||||  
Sbjct: 132096 ggaaggggaggggaaggggagga 132117

>emb|AL357873.17| Human DNA sequence from clone RP11-344F13 on chromosome 1 Contains a  
novel gene, complete sequence  
Length = 143508

Score = 44.1 bits (22), Expect = 3.0  
Identities = 22/22 (100%)  
Strand = Plus / Minus

Query: 1067 tagaggtgatttttgttgggtg 1088  
|||||||  
Sbjct: 113435 tagaggtgatttttgttgggtg 113414

>gb|AC093256.2| Homo sapiens chromosome 5 clone RP11-182I24, complete sequence  
Length = 163807

Score = 44.1 bits (22), Expect = 3.0  
Identities = 22/22 (100%)  
Strand = Plus / Plus

Query: 209 aaatttctaaagcagtatatat 230  
|||||||  
Sbjct: 17971 aaatttctaaagcagtatatat 17992

>emb|AL592043.7| Human DNA sequence from clone RP11-281B1 on chromosome Xp21.3-22.12  
Contains part of a novel gene, an arginine/serine-rich  
splicing factor 2 ( SFRS2) pseudogene and a CpG island,  
complete sequence  
Length = 184391

Score = 44.1 bits (22), Expect = 3.0  
Identities = 22/22 (100%)  
Strand = Plus / Plus

Query: 783 ggaaggggaggggaaggggagga 804  
|||||||  
Sbjct: 139346 ggaaggggaggggaaggggagga 139367

>emb|AL583825.8| Human DNA sequence from clone RP11-362H12 on chromosome 1 Contains a  
mitochondrial intermediate peptidase (MIPEP) pseudogene  
and a CpG island, complete sequence  
Length = 198794

Score = 44.1 bits (22), Expect = 3.0  
Identities = 22/22 (100%)  
Strand = Plus / Plus

Query: 783 ggaaggggaggggaaggggagga 804  
|||||||  
Sbjct: 86906 ggaaggggaggggaaggggagga 86927



>gb|AC155725.3| Mus musculus 6 BAC RP24-231N5 (Roswell Park Cancer Institute (C57BL/6J  
Male) Mouse BAC Library) complete sequence  
Length = 167534

Score = 44.1 bits (22), Expect = 3.0  
Identities = 22/22 (100%)  
Strand = Plus / Plus

Query: 783 ggaaggggaggggaaggggagga 804  
|||||||  
Sbjct: 115727 ggaaggggaggggaaggggagga 115748

>emb|AL645990.14| Mouse DNA sequence from clone RP23-403C12 on chromosome 11 Contains a  
novel gene and the 5' end of the Mmd gene for monocyte to  
macrophage differentiation-associated, complete sequence  
Length = 134303

Score = 44.1 bits (22), Expect = 3.0  
Identities = 22/22 (100%)  
Strand = Plus / Minus

Query: 783 ggaaggggaggggaaggggagga 804  
|||||||  
Sbjct: 93065 ggaaggggaggggaaggggagga 93044

>dbj|AP004222.3| Oryza sativa Japonica Group genomic DNA, chromosome 1, BAC  
clone:B1003B09  
Length = 155263

Score = 44.1 bits (22), Expect = 3.0  
Identities = 22/22 (100%)  
Strand = Plus / Plus

Query: 783 ggaaggggaggggaaggggagga 804  
|||||||  
Sbjct: 95586 ggaaggggaggggaaggggagga 95607

>gb|AC097720.5| Homo sapiens BAC clone RP11-1422N15 from 2, complete sequence  
Length = 137856

Score = 44.1 bits (22), Expect = 3.0  
Identities = 22/22 (100%)

Strand = Plus / Minus

```
Query: 783      ggaaggggaggggaaggggagga 804
          |||||
Sbjct: 135529 ggaaggggaggggaaggggagga 135508
```

>dbj|AP003563.3| Oryza sativa Japonica Group genomic DNA, chromosome 1, BAC  
clone:B1168H06  
Length = 185600

Score = 44.1 bits (22), Expect = 3.0  
Identities = 22/22 (100%)  
Strand = Plus / Plus

```
Query: 783      ggaaggggaggggaaggggagga 804
          |||||
Sbjct: 71045 ggaaggggaggggaaggggagga 71066
```

>emb|AJ312483.1| Zea mays Grande retrotransposon DNA, partial LTR, clone W17  
Length = 442

Score = 44.1 bits (22), Expect = 3.0  
Identities = 22/22 (100%)  
Strand = Plus / Plus

```
Query: 1370 cgcaaggccatcccttcgtggg 1391
          |||||
Sbjct: 43   cgcaaggccatcccttcgtggg 64
```

>emb|AJ312451.1| Zea mays Grande retrotransposon DNA, partial LTR, clone B20  
Length = 446

Score = 44.1 bits (22), Expect = 3.0  
Identities = 22/22 (100%)  
Strand = Plus / Plus

```
Query: 1370 cgcaaggccatcccttcgtggg 1391
          |||||
Sbjct: 43   cgcaaggccatcccttcgtggg 64
```

>emb|CT025562.10| Mouse DNA sequence from clone RP24-225012 on chromosome 14, complete

sequence  
Length = 194430

Score = 44.1 bits (22), Expect = 3.0  
Identities = 22/22 (100%)  
Strand = Plus / Plus

Query: 783 ggaaggggaggaaggggagga 804  
|||||||  
Sbjct: 40460 ggaaggggaggaaggggagga 40481

>gb|AC155715.24| Mus musculus 10 BAC RP24-118H2 (Roswell Park Cancer Institute (C57BL/6J  
Male) Mouse BAC Library) complete sequence  
Length = 174860

Score = 44.1 bits (22), Expect = 3.0  
Identities = 22/22 (100%)  
Strand = Plus / Minus

Query: 783 ggaaggggaggaaggggagga 804  
|||||||  
Sbjct: 19328 ggaaggggaggaaggggagga 19307

Score = 44.1 bits (22), Expect = 3.0  
Identities = 22/22 (100%)  
Strand = Plus / Minus

Query: 783 ggaaggggaggaaggggagga 804  
|||||||  
Sbjct: 19610 ggaaggggaggaaggggagga 19589

Score = 44.1 bits (22), Expect = 3.0  
Identities = 22/22 (100%)  
Strand = Plus / Minus

Query: 783 ggaaggggaggaaggggagga 804  
|||||||  
Sbjct: 19707 ggaaggggaggaaggggagga 19686

>gb|AC153847.7| Mus musculus 10 BAC RP23-286J11 (Roswell Park Cancer Institute (C57BL/6J  
Female) Mouse BAC Library) complete sequence  
Length = 187753

Score = 44.1 bits (22), Expect = 3.0  
Identities = 22/22 (100%)  
Strand = Plus / Minus

Query: 783 ggaaggggaggggaaggggagga 804  
|||||||  
Sbjct: 163458 ggaaggggaggggaaggggagga 163437

>gb|AC132599.3| Mus musculus BAC clone RP24-131015 from 3, complete sequence  
Length = 153352

Score = 44.1 bits (22), Expect = 3.0  
Identities = 22/22 (100%)  
Strand = Plus / Minus

Query: 783 ggaaggggaggggaaggggagga 804  
|||||||  
Sbjct: 28043 ggaaggggaggggaaggggagga 28022

>gb|AC131696.4| Mus musculus BAC clone RP23-403E5 from 1, complete sequence  
Length = 214068

Score = 44.1 bits (22), Expect = 3.0  
Identities = 22/22 (100%)  
Strand = Plus / Minus

Query: 783 ggaaggggaggggaaggggagga 804  
|||||||  
Sbjct: 27805 ggaaggggaggggaaggggagga 27784

>gb|AC110817.6| Mus musculus BAC clone RP23-155B20 from 13, complete sequence  
Length = 200362

Score = 44.1 bits (22), Expect = 3.0  
Identities = 25/26 (96%)  
Strand = Plus / Plus

Query: 1265 attttaaaatagggtactgattttaaa 1290

|||||  
Sbjct: 24592 attttaaaatagggtacagatttaaa 24617

>emb|AL935152.9| Mouse DNA sequence from clone RP24-387M5 on chromosome 2, complete  
sequence  
Length = 98020

Score = 44.1 bits (22), Expect = 3.0  
Identities = 22/22 (100%)  
Strand = Plus / Plus

Query: 1689 agctttttctccattcaggagac 1710  
|||||  
Sbjct: 62338 agctttttctccattcaggagac 62359

>emb|AL731742.3| Oryza sativa chromosome 12, . BAC OJ1123\_B09 of library Monsanto from  
chromosome 12 of cultivar Nipponbare of ssp. japonica of  
Oryza sativa (rice), complete sequence  
Length = 155585

Score = 44.1 bits (22), Expect = 3.0  
Identities = 22/22 (100%)  
Strand = Plus / Minus

Query: 458 accatatagtttgacaaaccaa 479  
|||||  
Sbjct: 128797 accatatagtttgacaaaccaa 128776

>dbj|AP001359.4| Homo sapiens genomic DNA, chromosome 11q clone:RP11-820L6, complete  
sequences  
Length = 221535

Score = 44.1 bits (22), Expect = 3.0  
Identities = 22/22 (100%)  
Strand = Plus / Plus

Query: 783 ggaaggggaggggaaggggagga 804  
|||||  
Sbjct: 179801 ggaaggggaggggaaggggagga 179822

>dbj|AP000755.4| Homo sapiens genomic DNA, chromosome 11q clone:RP11-716H6, complete  
sequences

Length = 152306

Score = 44.1 bits (22), Expect = 3.0

Identities = 22/22 (100%)

Strand = Plus / Plus

Query: 783 ggaaggggaggggaaggggagga 804

||||||||||||||||||||

Sbjct: 9513 ggaaggggaggggaaggggagga 9534

Database: /usr/local/blast/db/blastlibs/nt

Posted date: Apr 19, 2010 12:09 PM

Number of letters in database: 30,878,341,354

Number of sequences in database: 11,350,961

Lambda	K	H
1.37	0.711	1.31

Gapped

Lambda	K	H
1.37	0.711	1.31

Matrix: blastn matrix:1 -3

Gap Penalties: Existence: 5, Extension: 2

Number of Sequences: 11350961

Number of Hits to DB: 610,081,806

Number of extensions: 34314732

Number of successful extensions: 731393

Number of sequences better than 10.0: 153

Number of HSP's gapped: 731334

Number of HSP's successfully gapped: 234

Length of query: 1852

Length of database: 30,878,341,354

Length adjustment: 23

Effective length of query: 1829

Effective length of database: 30,617,269,251

Effective search space: 55998985460079

Effective search space used: 55998985460079

X1: 11 (21.8 bits)

X2: 15 (29.7 bits)

X3: 50 (99.1 bits)

S1: 14 (28.2 bits)

S2: 22 (44.1 bits)