

# 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 sequeunce 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-ggtccactagaaggcgagaaggcctcgcggtggtggccac 1356  
||||||| ||||||| ||||||||| ||| ||||| |||||  
Sbjct: 46811 tgtgggggacagatatccccaggtccactagaaggcgaaaggtcctcgcggggctc 46752

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

Query: 1417 ggctgaccgaagaaggcaacagactcgagcccaacaatccatcggtcgtgctatcc 1476  
||| ||| ||||||| || ||||||||| || ||||| |||||





Strand = Plus / Minus

Query: 1523 ggcgtattaggatgagtcagcgagattttcggaagattagttcagtttgctcgtatta 1582  
||||| ||||||| ||||||| | | ||||||| || ||||||| ||||||| ||||||| |||||||

Sbjct: 5721 ggcggattaggatgagtcggtgggattttggggagatcagttcagtcggtcactatta 5662

Query: 1583 tttaggagacatatgatcctcatgtacgtatggagtgccccacggtcgtgtatataagg 1642  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||

Sbjct: 5661 gttaggagacatatgatcatcatgtacgtttggagtgccccacggtcaggtatataa-gt 5603

Query: 1643 ccagagggtaccccatcatttctatcgaccatctacctatctcatcagcttttctccatt 1702  
|| ||| ||||||| ||| ||||||| ||||||| ||| | |||||||

Sbjct: 5602 cctagggaaccccatcattt-tat-taccatctacctatctcattagcctctctccatt 5545

Query: 1703 caggagacctcgcttgtaaccaccacatatagatccatcccaagaagtagtgattacg 1762  
||||| ||||||| | ||||||| ||||||| || | ||||||| ||| |||

Sbjct: 5544 caggagaccgcttgtaacacccacatacagatccgcccctaggaagtaggtaatac 5485

Query: 1763 cctctctaagggcccaacttgcaaaaaccgc----ctatccctctctcgtgcgtcca 1818  
||||| ||| | ||| ||||||| || || || || ||||||| ||| |||

Sbjct: 5484 cctctccaagtgaccgaacttgcaaaaattgcatgtctctctctctctctctctc 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 agtgccccacggtcgtgtatataaggtccagagggtaccccatcat 1661  
|||||  
Sbjct: 11194 agtgccccacggtcgaatatataaggcctaggggtaccctatcat 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 agtgccccacggtcgtgtatataaggtccagagggtaccccatcattt-ctatcgaccat 1674  
|||||  
Sbjct: 289 agtgccccacggtcggatatataaggcctaggggtaccccatcattttccatcgaccat 348

Query: 1675 ctacctatctcatcagcttttctcattcaggagacctcgcttgtaaccaccacatatata 1734  
|  
Sbjct: 349 caacctatctcattagcttttcttattcaggagacttcagttgtaaccaccacataaa 408

Query: 1735 gatccatccaagaagtagtgattacgc 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 cttgtaaccaccacatatagatccatccaagaagtagtgattacgcctctctaagcg 1774

|||||  
Sbjct: 528 cttgtaaccaccacataaagatccttaccaggaagtagggtattacgcctctccaagt 469

Query: 1775 gcccaaacttgcagaaaaccgctatccctctctcgtgcgtccagcacgaaccattgagt 1834

|||||  
Sbjct: 468 gcccgaaacctgtagaaaatcgctgt-cgtctctcgtgcatcttgtacgaaccattgagt 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 ggatgagtcagcgagatnttcggaagattagttcagtttgttcgctattatttaggagac 1592

|||||  
Sbjct: 207 ggatgagtcagcatgatnttcggtagattggttcagtcagttcactattagttaggagat 266

Query: 1593 atatgatcctcatgtacgtatggagtgccccacggtcgtgtatataaggtccagaggta 1652

|  
Sbjct: 267 acgtgatcatcatgtacgtatggagtgcctatggtcgtgtatataaggcccaagaggaa 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 cattcaggagacctcgttgaaccaccacatatagatcca 1740

|||||  
Sbjct: 393 cattcaggagaccacttgaacacaccacatacatagatcca 434

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



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 tcatgtacgtatggagtgccccacggctcgtgtatataaggccagagggtaccccatcat 1661  
|||| |||| ||| ||||||||||||||| ||||||||||| | || ||| |||||||||  
Sbjct: 273 tcatatagcagatgtagtgccccacggtaagtatataaggcctagggggcaccatcaa 332

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

Query: 1719 taaccaccacatatagatccatcccaagaagtagtgattacgc 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 tgtaaccaccacatatagatccatcccaagaagtagtgattacgcctctctaagcggc 1776  
||||||||||||||||| ||||||||| ||| ||||||||| |||||||||||||||||||  
Sbjct: 94023 tgtaaccaccacataaagatccacaccaggaagtagggtattacgcctctctaagcggc 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 ttgtgggggacagatattccccgggtccactagaaggcaagaaggcctcacgaaaggcct 6796

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

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

Query: 1734 agatccatccaagaagtagtgattacgcctctctaagcggcc 1778  
||||||| ||| ||||||| || ||||||||| ||||||||| |||||||||  
Sbjct: 7182 agatccaaaccaggaagtaggtgttacgcctctctaagcggcc 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: 1717 tgtaaccaccacatat-agatccatcccaagaagtagtgattacgcctctctaagcgg 1775  
||||||| ||||||||| ||||||| ||| ||||||| || |||||||||||||||||||||  
Sbjct: 111697 tgtaacctaccacataagagatccacgccaggaagtaggggttacgcctctctaagcgg 111638

Query: 1776 ccc 1778  
|||  
Sbjct: 111637 ccc 111635

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

Query: 1806 tctcgtgcgtccagcacgaaccattgagttaca 1838  
||||||||| ||||||||||||||||||| |||||  
Sbjct: 160739 tctcgtgcgcccagcacgaaccattgagctaca 160771

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

Score = 75.8 bits (38), Expect = 8e-10  
Identities = 102/122 (83%), Gaps = 1/122 (0%)  
Strand = Plus / Minus

Query: 1717 tgtaaccaccacatatagatccatcccaagaagtagtgattacgcctctctaagcggc 1776  
||||||||||||||||| ||||||| ||| ||||||| ||||||||||||||| |||||||  
Sbjct: 122467 tgtaaccaccacataaagatccacaccaggaagtaggggtattacgcctctcaaagcggc 122408

Query: 1777 ccaaactgcagaaaaccgctatccctctctcgtgcgtccagcacgaaccattgagtta 1836  
| ||| || ||||||| | |||| | |||||| | ||| | ||||||||||||| ||| ||  
Sbjct: 122407 tcgaacctgtagaaaattgtctat-cgtctctcatgcgcttagcacgaaccatcgaggta 122349

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

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



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

Query: 1297 ttgtgggggatagatatcccc-gggtccactagaaggcgagaaggcctcgcggtgtggcca 1355  
||||||| ||||||| ||||||||| ||||||||| ||||||||| || |||  
Sbjct: 13840 ttgtgggggacagatatccccgggtccactagaaggcaagaaggcctcacgaaaggcct 13899

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

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

Query: 1717 tgtaaccaccacatata-gatccatccaagaagtagtgtattacgcctctctaagcgg 1775  
||||||| ||||| ||| ||||||| || ||||||||| |||||||||  
Sbjct: 5047 tgtaaccaccacataaaagatccacaccaggaagtagggtgttacgcctctctaagcgg 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





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 agtgccccacggctgtgtatataagggtccagagggtaccccatcatttctatcgaccatc 1675  
||||||| ||| ||||||||| | || ||||||| ||||| |||||||||  
Sbjct: 289 agtgcccatggtcaagtatataaggcctaggggtaccctgtcatttccatcgaccatc 348

Query: 1676 tacctatctcatcagctttttctccattcaggagacctcgttgttaaccaccacata 1732  
||| | |||| ||||||||| ||||| | |||||||||  
Sbjct: 349 tactcagctcactagcttttctccataaaggaga-ttcccttgttaaccaccacata 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 taaccaccacatatagatccatccaagaagtagtattacgcctctctaagcggcc 1777  
||||||| ||||| | ||||| || ||||| |||||||||  
Sbjct: 148845 taaccaccacataaagatccacatcaggaagtaggtgttacacctctctaagcggcc 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-gggtccactagaaggcgagaaggcctcgcgtgtggcca 1355  
||||||| ||||||| ||||||||| ||||||| || ||||  
Sbjct: 9984 ttgtggggacagatatccccgggtccactagaaggcaagaaggcctcacgaaaggcct 9925

Query: 1356 cgggccagttaccccgaaggccatcccttcgtggg 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 tgtaaccaccacatata-gatccatccaagaagtagtattacgcctctctaagcgg 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 tgtaaccaccacatata-gatccatccaagaagtagtattacgcctctctaagcgg 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-gatccatccaagaagtagtgattacgcctctctaagcgg 1775  
|||||  
Sbjct: 271 tgtaaccaccacataaaagatccataaccaggaagtaggctgttacgcctctctaagcgg 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 tgtaaccaccacatata-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-ccggtccactagaaggcgagaaggcctc 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-ccggtccactagaaggcgagaaggcctc 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 tgtaaccaccacataaaaagatccacacaaggaagtagggtggttacgcctctctaagcag 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 ttgtgggggacagatatccccgggtccactagaaggcaagaaggcctc 2261

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

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

Strand = Plus / Plus

Query: 1717 tgtaaccaccacatata-gatccatcccaagaagtagtgattacgcctctctaagcgg 1775

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

Sbjct: 2641 tgtaaccaccacataaaaagatccacaccaggaagtagggtggttacgcctctctaagcgg 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 tgtaaccaccacatata-gatccatcccaagaagtagtgattacgcctctctaag 1772  
|||||  
Sbjct: 32977 tgtaaccaccacataaaagatccacaccaggaagtagggtgttacgcctctctaag 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-cggtcgtgtatataagggtccagagggtaccccatcatttct 1665  
|||  
Sbjct: 218 tacgcatgtagtgccccagcggtcgagtatataaggcctaggggtaccccatcatttca 159

Query: 1666 atcgaccatctacctatctcatcagcttttctccattcaggagacctcgcttgt-aacc 1724  
|||  
Sbjct: 158 atcaacctgtactcaactcattatcctttctccatactggagacttctcttgtaaactg 99

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

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

Score = 63.9 bits (32), Expect = 3e-06  
Identities = 81/96 (84%), Gaps = 1/96 (1%)  
Strand = Plus / Plus

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

Query: 1356 cgggccagttaccccgaaggccatcccttcgtggg 1391  
||||| ||| ||||||| |||||||  
Sbjct: 12081 tgggccattatttcgcaaggccacccttcgtggg 12116

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

Query: 1717 tgtaaccaccacatata-gatccatcccaagaagtagtgattacgcctctctaagcg 1774  
||||||| ||||| ||||||| || ||| |||||||  
Sbjct: 12449 tgtaaccaccacataaaagatccacaccaagaagtagggtgtaacgcctctctaagcg 12508

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

>gb|FJ386419.1| Zea mays clone R4-b StarkB element, partial sequence  
Length = 6783

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

Query: 1717 tgtaaccaccacatata-gatccatcccaagaagtagtgattacgcctctctaagcgg 1775  
||||||| ||||| ||||||| || ||| |||||||  
Sbjct: 1676 tgtaaccaccacataaaagatccacaccaggaagtagggtgttacgcctctctaagcgg 1735

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 ttgtggggacagatatccccgggtccactagaaggcaagaaggcctc 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 tgtaaccaccacatata-gatccatccaagaagtagtgattacgcctctctaagcgg 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 tgtggggacagatatccctcgggtccactagaaggctagaagacctcgcg 27079

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

Query: 1706 gagacctcgcttgtaaccaccacat-atagatccatcccaagaagtagtgattacgcc 1764  
||||| ||| ||||||||||||||||||| | ||||||| ||| ||||||| | |||||||  
Sbjct: 27440 gagaactcccttgtaaccaccacataaaagatccacaccaggaagtaggggttacgct 27499

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

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

Query: 1619 gccccacggctcgtgtatataaggtccagagggtaccccatca 1660  
||||||||||||| ||||||||||| | || ||| |||||||||  
Sbjct: 27347 gccccacggctcgtgtatataaggcctagggggcaccatca 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 tgtaaccaccacatata-gatccatcccaagaagtagtgattacgcctctctaagcgg 1775  
||||||| ||||||| | ||||| ||| ||||||| || ||||| |||||||||  
Sbjct: 178146 tgtaaccaccacataaaagatccacaccaggaagtagggtgttacacctctctaagcgg 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 ttgtgggggacagatatccccgggcccactagaaggcaagaaggcctc 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 ggggacagatatccccgggtccactagaaggcaagaaggcctc 7442

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

Query: 1717 tgtaaccaccacatatata-gatccatccaagaagtagtgattacgcctctctaagcgg 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 ggggacagatatccccgggtccactagaaggcaagaaggcctc 4517

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

Query: 1717 tgtaaccaccacatatata-gatccatccaagaagtagtgattacgcctctctaagcgg 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 tctctcgtgcgccagcacgaaccatcgagctaca 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 ggagacctcgcttgtaaccaccacatatagatccatccaagaagtag 1753  
|||||  
Sbjct: 375 ggagacctcccttgtaaccaccacataaagatccacaccaggaagtag 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 attttgatggtatgttaaatttggtgtcatttgttgatggatttagtaaa 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 tgtaaccaccacatata-gatccatccaagaagtagtgattacgcctctctaagcgg 1775  
|||||  
Sbjct: 362 tgtaaccaccacataaaagatccacacaaggaagtagggtgttacgcctctctaagcag 421



>gb|EF468511.1| Zea mays clone pBS-2 LL repeat sequence  
Length = 13423

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

Query: 1717 tgtaaccaccacatatata-gatccatccaagaagtagtgattacgcctctctaagcgg 1775  
|||||  
Sbjct: 5793 tgtaaccaccacataaaagatccacactaggaagtagggtgttacgcctctctaagcgg 5852

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

Score = 46.1 bits (23), Expect = 0.75  
Identities = 29/31 (93%)  
Strand = Plus / Plus

Query: 1314 ccccggtccactagaaggcgagaaggcctc 1344  
||||  
Sbjct: 5441 cccaggtccactagaaggcaagaaggcctc 5471

>gb|EU338354.1| Zea mays cultivar W22 bz gene locus, complete sequence  
Length = 238141

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

Query: 980 gttattcaactatccgaccgctgattttgatggtatgttaaatttgtgtgcatttggt 1039  
|||||  
Sbjct: 111207 gttattcaaagatctgaaccgctgattttgatggttgttaagtatgagtgcaatttggt 111266

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-gatccatccaagaagtagtgattacgcctctctaagcgg 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-gatccatccaagaagtagtgattacgcctctctaagcgg 1774  
||||||||||||||||| | |||||| | || |||||| | | ||||| |||||||||  
Sbjct: 271 tgtaaccaccacataaaagatccataccaggaagtagggtgttacgcgctctctaagcgg 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-gatccatccaagaagtagtgattacgcctctctaagcgg 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 gttgtgggggacagatatccccgggtccactagaagg 102662

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

Query: 1033 atttgtttgatggatttagtaaaggttatg 1062  
|||||  
Sbjct: 4582 atttgtttggtggatttagtagaggttatg 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 gttgtgggggacagatatccccgggtccactagaagg 46220

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

Query: 1033 atttgtttgatggatttagtaaaggttatg 1062  
|||||  
Sbjct: 144300 atttgtttggtggatttagtagaggttatg 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 ctatattttaaataagggtactgatttaa 1290  
|||||  
Sbjct: 1548 ctatattttaaagatagggtactgatttaa 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 ttgggtgggttttacagagtttaaactagcggattatatagtggtataga 1131  
||||| |||| | |||||  
Sbjct: 90446 ttgggtgagttttgctaagtttaaactggcggattataaagtggataga 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 ttacgcctctctaagcggcccaaac 1782  
|||||  
Sbjct: 184 ttacgcctctctaagcggcccaaac 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 ttacgcctctctaagcggcccaaac 1782  
|||||  
Sbjct: 184 ttacgcctctctaagcggcccaaac 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-atagatccatccaagaagtagtgattacgcc 1764  
||||| ||| ||||||||||||||||||| | ||||||| ||| ||||||| || |||||  
Sbjct: 260 gagaactcccttgtaacccaccacataaaagatccacaccaggaagtagggtgctacgct 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-gggtccaacta 1327  
||||||||||||||||||||| |||||||  
Sbjct: 115935 gttgtgggggatagatatcccctgggtccaacta 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 ttgtggggacagatatccccgggtccactagaagg 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 tgtgggggatagatatccccctgggtccacta 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 ttgtgggggatagatatccccctgggtccacta 140776

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: 154049 tgtgggggatagatatccccctgggtccacta 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 ttgtgggggatagatatccccgggtccacta 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 ttgtgggggatagatatccccgggtccacta 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 ttgtgggggatagatatccccgggtccacta 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 ttgtgggggatagatatccccgggtccacta 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 acattaccatgtccaactgatttaaac 442  
|||||  
Sbjct: 183367 acattaccatgtccaactgacttaaac 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 acattaccatgtccaactgatttaaac 442  
|||||  
Sbjct: 147812 acattaccatgtccaactgacttaaac 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 acattaccatgtccaactgatttaaacc 442  
|||||  
Sbjct: 11423 acattaccatgtccaactgacttaaacc 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 ttaataatactttaataaatatta 31  
|||||  
Sbjct: 60907 ttaataatactttaataaatatta 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 tgtaaccaccacatatata-gatccatccaagaagtagtgattacgcctctctaagcgg 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 tgtgggggacatatatccccgggtccactagaaggctaaaaggcct 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 tttgataaaaaaggtaaagtaga 1228  
|||||  
Sbjct: 1648880 tttgataaaaaaggtaaagtaga 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-gatccatccaagaagtagtgattacgcctctctaagcgg 1775  
|||||  
Sbjct: 270 tgtaaccaccacataaaagatctacaccaggaagtagggtgttatgcctctctaagcgg 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 tgtaaccaccacatata-gatccatccaagaagtagtgattacgcctctctaagcgg 1775  
|||||  
Sbjct: 270 tgtaaccaccacataaaagatctacaccaggaagtagggtgttatgcctctctaagcgg 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 gttgggtgggttttacagagtttaaactagcggattatatagtggtataga 1131  
||||| ||| ||||| || ||||||||||||| | ||||||| |||||||  
Sbjct: 90789 gttgagtgagttttgcaaagtttaaactagtgattatataatggtataga 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 tgccccacggtcggtatataaggtccagagggtacccc 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 tgccccacggtcggtatataaggtccagagggtacccc 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-gggtccacta 1327  
||||||||||||| |||||||||||

Sbjct: 1 tgtgggggatagatatcccctgggtccacta 31

>gb|U68403.1|ZMU68403 Zea mays retrotransposon Grande-Zm 5' LTR and primer binding site  
DNA sequence  
Length = 645

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: 1 tgtgggggatagatatcccctgggtccacta 31

>gb|AE000666.1|Methanothermobacter thermautotrophicus str. Delta H, complete genome  
Length = 1751377

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

Query: 685 taaatggctttgatgttgaagac 707  
|||||  
Sbjct: 214894 taaatggctttgatgttgaagac 214872

>gb|AC204225.4|Zea mays BAC clone CH201-427P14 from chromosome 5, complete sequence  
Length = 203705

Score = 44.1 bits (22), Expect = 3.0  
Identities = 35/38 (92%), Gaps = 1/38 (2%)  
Strand = Plus / Plus

Query: 1296 gttgtgggggatagatatcccc-gggtccactagaagg 1332  
|||||  
Sbjct: 53615 gttgtgggggacagatatcccctgggtccacgagaagg 53652

>gb|AC190571.5|Zea mays BAC clone CH201-151G9 from chromosome 5, complete sequence  
Length = 190522

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

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 tttaataactttaataaatat 29  
          |||||          |||||  
Sbjct: 110942 tttaataactttaataaatat 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 ttgggtgggttttacagagtttaactagcggattatatagtggtataga 1131  
          |||||          |          |||||          |||||  
Sbjct: 66 ttgggtgggttttgtaaagtttaactatgaaattatatagtggtataga 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 gatgcgagtgaggaggagagg 866  
          |||||  
Sbjct: 1633 gatgcgagtgaggaggagagg 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 gatgcgagtgaggaggagagg 866  
|||||  
Sbjct: 150414 gatgcgagtgaggaggagagg 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 ttacagagtttaaactagcggattatatagtg 1125  
||||| ||||| | |||||  
Sbjct: 576 ttacaaagtttaaactggtggattatatagtg 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-atagatccatccaagaagtagtgattacgcctctctaagcgg 1775  
|||||  
Sbjct: 271 tgtaaccaccacataaaagatccacaccaggaagtaggtgctacgcttctctaagcgg 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 ctcatcagcttttctccattca 1704  
|||||  
Sbjct: 5139177 ctcatcagcttttctccattca 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 tgaaggggaggaaggggagg 803  
|||||  
Sbjct: 138782 tgaaggggaggaaggggagg 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 ggaaggggaggaaggggagga 804  
|||||  
Sbjct: 115727 ggaaggggaggaaggggagga 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 ggaaggggaggaaggggagga 804  
|||||  
Sbjct: 93065 ggaaggggaggaaggggagga 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 ggaaggggaggaaggggagga 804  
|||||  
Sbjct: 95586 ggaaggggaggaaggggagga 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   ggaaggggaggaaggggagga 804
           |||
Sbjct: 135529 ggaaggggaggaaggggagga 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   ggaaggggaggaaggggagga 804
           |||
Sbjct: 71045 ggaaggggaggaaggggagga 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 ggaaggggaggggaaggggagga 804  
|||||  
Sbjct: 40460 ggaaggggaggggaaggggagga 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 ggaaggggaggggaaggggagga 804  
|||||  
Sbjct: 19328 ggaaggggaggggaaggggagga 19307

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

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

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

Query: 783 ggaaggggaggggaaggggagga 804  
|||||  
Sbjct: 19707 ggaaggggaggggaaggggagga 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 attttaaaatagggtactgatttaa 1290

|||||  
Sbjct: 24592 attttaaataagggtacagatttaa 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 agcttttctcattcaggagac 1710  
|||||  
Sbjct: 62338 agcttttctcattcaggagac 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)