

**BLASTn Search Outputs of the DNA Sequences at the Parental Locus of 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= DAS-40278-9\Original\Locus  
(2212 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 EF468501.1  Zea mays clone pBK118-2 retrotransposons GrandeB,...	1031	0.0
gb AC165175.2  Zea mays clone ZMMBBb-136N21, complete sequence	428	e-116
ref NM_001152615.1  Zea mays hypothetical protein LOC100279619 (...)	313	2e-81
gb AY883559.2  Zea mays cultivar inbred line B73 teosinte glume ...	196	4e-46
gb EU949251.1  Zea mays clone 400160 mRNA sequence	167	4e-37
gb AC209386.4  Zea mays BAC clone CH201-98J13 from chromosome 5,...	157	3e-34
gb EU940901.1  Zea mays clone 1168199 mRNA sequence	155	1e-33
gb AF546188.1  Contiguous genomic DNA sequence comprising the 19...	143	5e-30
gb EF190061.1  Zea mays clone FS2_19 chromosome B, genomic sequence	137	3e-28
emb AJ312478.1  Zea mays Grande retrotransposon DNA, partial LTR...	137	3e-28
gb DQ493649.1  Zea mays cultivar Coroico bz locus region	135	1e-27
gb AC194842.4  Zea mays BAC clone CH201-514N20 from chromosome 4...	127	3e-25
gb AF090447.2  Zea mays 22 kDa alpha zein gene cluster, complete...	127	3e-25
gb EF468504.1  Zea mays clone pBK118-5 LL repeat sequence	123	5e-24
gb EF468502.1  Zea mays clone pBK118-3 LL repeat sequence	123	5e-24
gb EU952187.1  Zea mays clone 1218827 hypothetical protein mRNA,...	119	7e-23
gb EF190066.1  Zea mays clone PS53 chromosome B, genomic sequence	119	7e-23
gb EF190062.1  Zea mays clone FS2_20 chromosome B, genomic sequence	119	7e-23
gb AC225631.3  Zea mays BAC clone CH201-111A2 from chromosome 8,...	117	3e-22
gb EF190051.1  Zea mays clone 46F3FF5Rm5 chromosome B, genomic s...	115	1e-21
gb AC229878.2  Zea mays BAC clone CH201-108P8 from chromosome 9,...	113	5e-21
gb DQ002407.1  Zea mays copia retrotransposon opiel, gypsy retro...	113	5e-21
gb AC196084.4  Zea mays BAC clone CH201-52A17 from chromosome 5,...	111	2e-20
gb AC194844.5  Zea mays BAC clone CH201-463C23 from chromosome 5...	111	2e-20
gb AC203533.4  Zea mays BAC clone CH201-452L5 from chromosome 5,...	111	2e-20
gb AC210997.6  Zea mays BAC clone CH201-545A13 from chromosome 5...	111	2e-20

gb	EF190053.1	Zea mays clone 46F3FF5Rs2 chromosome B, genomic s...	111	2e-20
gb	EF190052.1	Zea mays clone 46F3FF5Rs1 chromosome B, genomic s...	111	2e-20
gb	AC185486.5	Zea mays BAC clone CH201-162J17 from chromosome 5...	109	7e-20
gb	FJ386419.1	Zea mays clone R4-b StarkB element, partial sequence	109	7e-20
gb	AY555142.1	Zea mays BAC clone c573F08, complete sequence	109	7e-20
emb	AJ312473.1	Zea mays Grande retrotransposon DNA, partial LTR...	109	7e-20
gb	DQ493650.1	Zea mays cultivar A188 bz locus region	105	1e-18
gb	DQ493646.1	Zea mays cultivar CML258 bz locus region	105	1e-18
gb	AF448416.1	Zea mays B73 chromosome 9S bz genomic region	105	1e-18
gb	AY664416.1	Zea mays cultivar Mo17 locus bz, complete sequence	105	1e-18
gb	AY664415.1	Zea mays cultivar B73 locus 9009, complete sequence	105	1e-18
gb	EF468503.1	Zea mays clone pBK118-4 retrotransposon GrandeB, ...	103	4e-18
gb	AC209754.5	Zea mays BAC clone CH201-23E16 from chromosome 5,...	101	2e-17
gb	EF190049.1	Zea mays clone 46F3FF5Rm3 chromosome B, genomic s...	101	2e-17
gb	EF190050.1	Zea mays clone 46F3FF5Rm4 chromosome B, genomic s...	100	7e-17
gb	AC203284.4	Zea mays BAC clone CH201-504M1 from chromosome 5,...	98	3e-16
gb	AC203072.5	Zea mays BAC clone CH201-26J18 from chromosome 6,...	98	3e-16
gb	FJ386423.1	Zea mays clone R6-b StarkB element, partial sequence	98	3e-16
gb	AC230040.3	Zea mays BAC clone CH201-122P19 from chromosome 7...	98	3e-16
gb	AC217319.3	Zea mays BAC clone ZMMBBb-86E19 from chromosome 5...	98	3e-16
gb	AC198320.5	Zea mays BAC clone ZMMBBb-334D6 from chromosome 5...	98	3e-16
gb	AC229879.2	Zea mays BAC clone CH201-103M12 from chromosome 8...	96	1e-15
gb	AC206691.5	Zea mays BAC clone CH201-149B20 from chromosome 1...	96	1e-15
gb	EF468507.1	Zea mays clone pBK118-8 LL repeat sequence	96	1e-15
gb	DQ493647.1	Zea mays cultivar NalTel bz locus region	96	1e-15
gb	AC206303.5	Zea mays BAC clone CH201-328A17 from chromosome 5...	94	4e-15
gb	AC211313.4	Zea mays BAC clone CH201-9J2 from chromosome 5, c...	94	4e-15
gb	AC231746.2	Zea mays BAC clone CH201-98H14 from chromosome 6,...	94	4e-15
gb	AC165174.2	Zea mays clone ZMMBBb-127F19, complete sequence	94	4e-15
gb	AC152494.1	Zea mays BAC clone Z418K17, complete sequence	94	4e-15
gb	AC160211.1	Genomic sequeunce for Zea mays BAC clone ZMMBBb044...	94	4e-15
gb	AF466932.1	Zea mays clone BAC 206C17, complete sequence	94	4e-15
emb	X97604.1	Z. diploperennis DNA for Grandel-4 retrotransposon	94	4e-15
gb	EF190065.1	Zea mays clone PS52 chromosome B, genomic sequence	90	7e-14
gb	AY325816.1	Zea mays BAC clone Z013I05, complete sequence	90	7e-14
gb	EF468511.1	Zea mays clone pBS-2 LL repeat sequence	86	1e-12
gb	AY574035.1	Zea mays rust resistance protein rp3-1 (rp3-1) ge...	86	1e-12
emb	AJ312503.1	Zea mays subsp. mexicana Grande retrotransposon ...	86	1e-12
gb	AC226723.4	Zea mays BAC clone CH201-110I20 from chromosome 6...	82	2e-11
gb	AC204225.4	Zea mays BAC clone CH201-427P14 from chromosome 5...	80	6e-11
gb	U68403.1	ZMU68403 Zea mays retrotransposon Grande-Zm 5' LTR a...	80	6e-11
gb	EF190048.1	Zea mays clone 46F3FF5Rm1 chromosome B, genomic s...	78	3e-10
gb	EF468510.1	Zea mays clone pBS-1 LL repeat sequence	74	4e-09
gb	EF468508.1	Zea mays clone pB3-201 retrotransposon GrandeB, c...	74	4e-09
gb	EF190064.1	Zea mays clone pStark5.5 chromosome B, genomic se...	74	4e-09
emb	AJ312504.1	Zea mays subsp. mexicana Grande retrotransposon ...	74	4e-09
gb	AC204937.4	Zea mays BAC clone CH201-488A19 from chromosome 5...	70	6e-08
gb	AC205029.6	Zea mays BAC clone CH201-7M14 from chromosome 5, ...	70	6e-08
emb	X97605.1	Z. diploperennis DNA for Grandel-6 retrotransposon	70	6e-08

gb FJ386429.1	Zea mays clone R9-b StarkB element, partial sequence	66	1e-06
gb FJ386412.1	Zea mays clone L5-a StarkB element, partial sequence	66	1e-06
gb EF190063.1	Zea mays clone FS3_49 chromosome B, genomic sequence	66	1e-06
gb DQ183075.1	Zea mays clone A-RGA7 resistance gene analog-like...	66	1e-06
gb EF468505.1	Zea mays clone pBK118-6 LL repeat sequence	64	4e-06
gb AC210188.4	Zea mays BAC clone CH201-257L10 from chromosome 5...	58	2e-04
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
emb AJ312460.1	Zea mays Grande retrotransposon DNA, partial LTR...	58	2e-04
gb EZ064107.1	TSA: Zea mays contig65230, mRNA sequence	56	0.001
gb AC229874.3	Zea mays BAC clone CH201-314N3 from chromosome 3,...	54	0.004
gb GU235996.1	Coix lacryma-jobi 22-kDa prolamin gene cluster, c...	54	0.004
gb AC226722.2	Zea mays BAC clone CH201-146D18 from chromosome 1...	54	0.004
gb AC186565.4	Zea mays BAC clone ZMMBBb-610A7 from chromosome 5...	54	0.004
gb AC194974.4	Zea mays BAC clone CH201-115G11 from chromosome 5...	54	0.004
gb FJ386416.1	Zea mays clone L7-a StarkB element, partial sequence	54	0.004
gb FJ386414.1	Zea mays clone L6-a StarkB element, partial sequence	54	0.004
gb AC237090.1	Oryza granulata clone OG_ABa0119F03, complete seq...	54	0.004
gb AC231756.2	Zea mays BAC clone CH201-111G11 from chromosome 1...	54	0.004
gb AC233030.1	Oryza minuta clone OM_Ba0022H02, complete sequence	54	0.004
gb EU965848.1	Zea mays clone 289347 hypothetical protein mRNA, ...	54	0.004
gb AC231332.1	Oryza minuta clone OM_Ba0219N21, complete sequence	54	0.004
gb BT043326.1	Zea mays full-length cDNA clone ZM_BFc0158M15 mRN...	54	0.004
gb EU338354.1	Zea mays cultivar W22 bz gene locus, complete seq...	54	0.004
gb EF190044.1	Zea mays clone 46F3FF4R-4 chromosome B, genomic s...	54	0.004
gb AC196829.2	Sorghum bicolor clone SB_BBc0050H06, complete seq...	54	0.004
gb AC196818.2	Sorghum bicolor clone SB_BBc0005H14, complete seq...	54	0.004
gb AC165173.2	Zea mays clone ZMMBBb-125019, complete sequence	54	0.004
gb AY455286.1	Zea mays chloroplast phytoene synthase (Y1) gene,...	54	0.004
gb GU080322.1	Saccharum hybrid cultivar R570 clone BAC 086H20, ...	52	0.015
gb AC231130.2	Oryza minuta clone OM_Ba0135C17, complete sequence	52	0.015
gb AC229876.2	Zea mays BAC clone CH201-115J9 from chromosome 8,...	52	0.015
gb BT069726.1	Zea mays full-length cDNA clone ZM_BFb0216P01 mRN...	52	0.015
gb EU952061.1	Zea mays clone 1145983 hypothetical protein mRNA,...	52	0.015
gb AC213133.1	Oryza glaberrima clone OG_BBa0042C22, complete se...	52	0.015
gb EF659468.1	Zea mays clone BAC b0288K09 AP2 domain transcript...	52	0.015
gb EF659467.1	Zea mays clone BAC m.pk066.114 AP2 domain transcr...	52	0.015
emb CR855170.1	Oryza sativa genomic DNA, chromosome 4, BAC clon...	52	0.015
gb AC105320.2	Oryza sativa Japonica Group chromosome 5 clone OJ...	52	0.015
gb AC117264.2	Oryza sativa Japonica Group chromosome 5 clone OJ...	52	0.015
gb AC135924.2	Oryza sativa Japonica Group chromosome 5 clone PO...	52	0.015
gb AC130598.2	Oryza sativa Japonica Group chromosome 5 clone OS...	52	0.015
gb AC145127.1	Oryza sativa Japonica Group chromosome 10 clone P...	52	0.015
gb AC165267.2	Zea mays clone ZMMBBb-151F20, complete sequence	52	0.015
gb AC092388.5	Oryza sativa chromosome 10 BAC OSJNBa0011L09 geno...	52	0.015
gb AC068654.2	Genomic Sequence For Oryza sativa (japonica culti...	52	0.015
dbj AP006233.3	Oryza sativa Japonica Group genomic DNA, chromos...	52	0.015
dbj AP005460.3	Oryza sativa Japonica Group genomic DNA, chromos...	52	0.015

dbj	AP004729.3	Oryza sativa Japonica Group genomic DNA, chromos...	52	0.015
dbj	AP003458.4	Oryza sativa Japonica Group genomic DNA, chromos...	52	0.015
dbj	AP005684.3	Oryza sativa Japonica Group genomic DNA, chromos...	52	0.015
dbj	AP005834.4	Oryza sativa Japonica Group genomic DNA, chromos...	52	0.015
dbj	AP006556.2	Oryza sativa Japonica Group genomic DNA, chromos...	52	0.015
dbj	AP005414.3	Oryza sativa Japonica Group genomic DNA, chromos...	52	0.015
dbj	AP004229.3	Oryza sativa Japonica Group genomic DNA, chromos...	52	0.015
dbj	AP003988.3	Oryza sativa Japonica Group genomic DNA, chromos...	52	0.015
dbj	AP005563.3	Oryza sativa Japonica Group genomic DNA, chromos...	52	0.015
dbj	AP003525.2	Oryza sativa Japonica Group genomic DNA, chromos...	52	0.015
dbj	AP006062.2	Oryza sativa Japonica Group genomic DNA, chromos...	52	0.015
dbj	AP005795.3	Oryza sativa Japonica Group genomic DNA, chromos...	52	0.015
dbj	AP005512.3	Oryza sativa Japonica Group genomic DNA, chromos...	52	0.015
dbj	AP004645.3	Oryza sativa Japonica Group genomic DNA, chromos...	52	0.015
dbj	AP004375.3	Oryza sativa Japonica Group genomic DNA, chromos...	52	0.015
dbj	AP006237.3	Oryza sativa Japonica Group genomic DNA, chromos...	52	0.015
emb	AL731605.3	Oryza sativa genomic DNA, chromosome 4, BAC clon...	52	0.015
dbj	AP004611.3	Oryza sativa Japonica Group genomic DNA, chromos...	52	0.015
dbj	AP004821.4	Oryza sativa Japonica Group genomic DNA, chromos...	52	0.015
emb	AL606634.2	Oryza sativa genomic DNA, chromosome 4, BAC clon...	52	0.015
dbj	AP003760.4	Oryza sativa Japonica Group genomic DNA, chromos...	52	0.015
dbj	AP004194.3	Oryza sativa Japonica Group genomic DNA, chromos...	52	0.015
dbj	AP002482.1	Oryza sativa Japonica Group genomic DNA, chromos...	52	0.015
emb	AL713941.3	Oryza sativa chromosome 12, . BAC OSJNBa0006M08 ...	52	0.015
emb	AL731592.2	Oryza sativa genomic DNA, chromosome 4, BAC clon...	52	0.015
gb	GQ407104.1	Oryza granulata chromosome 6 clone BAC a0186L08/a...	50	0.057
gb	AC231811.1	Oryza minuta clone OM_Ba0091E17, complete sequence	50	0.057
gb	AF391808.3	Zea mays cultivar McC bz locus region	50	0.057
gb	EF190043.1	Zea mays clone 46F3FF4R-3 chromosome B, genomic s...	50	0.057
emb	CR855225.1	Oryza sativa genomic DNA, chromosome 4, BAC clon...	50	0.057
gb	AC083945.3	Oryza sativa Japonica Group chromosome X clone OS...	50	0.057
gb	AC135929.2	Oryza sativa Japonica Group chromosome 5 clone PO...	50	0.057
gb	AC136226.2	Oryza sativa Japonica Group chromosome 5 clone OS...	50	0.057
gb	AC108498.2	Oryza sativa Japonica Group chromosome 5 clone OJ...	50	0.057
gb	AC134348.2	Oryza sativa Japonica Group chromosome 5 clone PO...	50	0.057
emb	AL606649.4	Oryza sativa genomic DNA, chromosome 4, BAC clon...	50	0.057
gb	AY530950.1	Zea mays putative zinc finger protein (Z438D03.1)...	50	0.057
dbj	AP005866.2	Oryza sativa Japonica Group genomic DNA, chromos...	50	0.057
dbj	AP003435.2	Oryza sativa Japonica Group genomic DNA, chromos...	50	0.057
gb	AC207417.4	Zea mays BAC clone CH201-186N18 from chromosome 5...	48	0.23
gb	AC229780.2	Oryza minuta clone OM_Ba0081J07, complete sequence	48	0.23
gb	AC231887.2	Oryza minuta clone OM_Ba0018L21, complete sequence	48	0.23
gb	AC225222.3	Zea mays BAC clone CH201-123I12 from chromosome 1...	48	0.23
gb	FJ266023.1	Oryza granulata clone OG_ABa077F15_032P05, comple...	48	0.23
gb	AC231882.1	Oryza minuta clone OM_Ba0091G05, complete sequence	48	0.23
gb	AC229741.1	Oryza minuta clone OM_Ba0230E13, complete sequence	48	0.23
gb	AC223439.1	Oryza brachyantha, complete sequence	48	0.23
emb	AM489152.2	Vitis vinifera contig VV78X015348.8, whole genom...	48	0.23
gb	AC097176.3	Oryza sativa Japonica Group chromosome 5 clone OJ...	48	0.23

gb	AC078839.4	Oryza sativa Japonica Group chromosome X clone OS...	48	0.23
gb	AC130602.5	Oryza sativa Japonica Group chromosome 5 clone B1...	48	0.23
gb	AC087552.3	Oryza sativa Japonica Group chromosome 5 clone P0...	48	0.23
dbj	AP005458.3	Oryza sativa Japonica Group genomic DNA, chromos...	48	0.23
dbj	AP005456.3	Oryza sativa Japonica Group genomic DNA, chromos...	48	0.23
dbj	AP005570.3	Oryza sativa Japonica Group genomic DNA, chromos...	48	0.23
dbj	AP005424.3	Oryza sativa Japonica Group genomic DNA, chromos...	48	0.23
dbj	AP005774.5	Oryza sativa Japonica Group genomic DNA, chromos...	48	0.23
dbj	AP003991.3	Oryza sativa Japonica Group genomic DNA, chromos...	48	0.23
dbj	AP003977.3	Oryza sativa Japonica Group genomic DNA, chromos...	48	0.23
dbj	AP003974.3	Oryza sativa Japonica Group genomic DNA, chromos...	48	0.23
dbj	AP003724.2	Oryza sativa Japonica Group genomic DNA, chromos...	48	0.23
dbj	AP005628.3	Oryza sativa Japonica Group genomic DNA, chromos...	48	0.23
emb	AL606615.4	Oryza sativa genomic DNA, chromosome 4, BAC clon...	48	0.23
dbj	AP004030.2	Oryza sativa Japonica Group genomic DNA, chromos...	48	0.23
emb	AL731618.3	Oryza sativa genomic DNA, chromosome 4, BAC clon...	48	0.23
emb	AL663012.3	Oryza sativa genomic DNA, chromosome 4, BAC clon...	48	0.23
dbj	AP005464.3	Oryza sativa Japonica Group genomic DNA, chromos...	48	0.23
dbj	AP003204.3	Oryza sativa Japonica Group genomic DNA, chromos...	48	0.23
dbj	AP002968.2	Oryza sativa Japonica Group genomic DNA, chromos...	48	0.23
dbj	AP002525.1	Oryza sativa Japonica Group genomic DNA, chromos...	48	0.23
emb	X68678.1	Z.mays gene for cyclophilin	48	0.23
emb	X82087.1	Z.diploperennis Grandel gene	48	0.23
gb	AC208340.4	Zea mays BAC clone CH201-53J11 from chromosome 5,...	46	0.90
gb	AC216353.5	Zea mays BAC clone CH201-194K18 from chromosome 5...	46	0.90
gb	AC205514.6	Zea mays BAC clone CH201-227F5 from chromosome 5,...	46	0.90
gb	AC210260.5	Zea mays BAC clone CH201-44F4 from chromosome 5, ...	46	0.90
gb	AC190571.5	Zea mays BAC clone CH201-151G9 from chromosome 5,...	46	0.90
gb	AC216070.4	Zea mays BAC clone CH201-459P15 from chromosome 5...	46	0.90
gb	AC226721.2	Zea mays BAC clone CH201-150M20 from chromosome 1...	46	0.90
gb	AC213983.4	Zea mays BAC clone CH201-326E16 from chromosome 5...	46	0.90
gb	AC225944.3	Zea mays BAC clone CH201-127G5 from chromosome 10...	46	0.90
gb	AC214043.4	Zea mays BAC clone CH201-299G22 from chromosome 5...	46	0.90
gb	AC196472.3	Zea mays BAC clone ZMABBb-235B12 from chromosome ...	46	0.90
gb	AC185472.4	Zea mays BAC clone CH201-257N23 from chromosome 5...	46	0.90
gb	AC201762.5	Zea mays BAC clone CH201-479M22 from chromosome 5...	46	0.90
gb	AC203071.4	Zea mays BAC clone CH201-184N10 from chromosome 5...	46	0.90
gb	AC203365.4	Zea mays BAC clone ZMABBb-196K7 from chromosome 5...	46	0.90
gb	AC196774.5	Zea mays BAC clone CH201-435B12 from chromosome 5...	46	0.90
gb	AC203430.5	Zea mays BAC clone CH201-142M10 from chromosome 5...	46	0.90
gb	AC186011.4	Zea mays BAC clone CH201-417E17 from chromosome 5...	46	0.90
gb	AC195458.4	Zea mays BAC clone CH201-47808 from chromosome 5,...	46	0.90
gb	AC191361.5	Zea mays BAC clone CH201-21609 from chromosome 5,...	46	0.90
gb	AC190647.4	Zea mays BAC clone ZMABBb-216G14 from chromosome ...	46	0.90
gb	AC215174.5	Zea mays BAC clone CH201-70P8 from chromosome 5, ...	46	0.90
gb	AC211535.5	Zea mays BAC clone ZMABBb-223D21 from chromosome ...	46	0.90
gb	FJ386410.1	Zea mays clone L4-a StarkB element, partial sequence	46	0.90
gb	AC237089.1	Oryza granulata clone OG_ABa0096023, complete seq...	46	0.90
gb	AC237088.1	Oryza granulata clone OG_ABa0089G14, complete seq...	46	0.90

gb	AC237087.1	Oryza granulata clone OG_ABa0028G18, complete seq...	46	0.90
gb	AC229873.2	Zea mays BAC clone CH201-387D15 from chromosome 2...	46	0.90
ref	XM_002442558.1	Sorghum bicolor hypothetical protein, mRNA	46	0.90
ref	XM_002465520.1	Sorghum bicolor hypothetical protein, mRNA	46	0.90
gb	FJ614806.1	Zea mays cultivar B73 p cluster, complete sequence	46	0.90
gb	AC213848.4	Zea mays BAC clone CH201-495D12 from chromosome 5...	46	0.90
gb	AC232337.2	Oryza minuta clone OM_Ba0147P17, complete sequence	46	0.90
gb	AC213131.2	Oryza glaberrima clone OG_BBa0031E23, complete se...	46	0.90
gb	AC217961.4	Zea mays BAC clone ZMMBBb-353K3 from chromosome 6...	46	0.90
gb	AC187050.5	Zea mays BAC clone ZMMBBb-293C24 from chromosome ...	46	0.90
gb	AC231617.2	Zea mays BAC clone CH201-190G15 from chromosome 8...	46	0.90
gb	AC229877.2	Zea mays BAC clone CH201-11105 from chromosome 9,...	46	0.90
gb	FJ032637.1	Oryza ridleyi clone a0301G20 Monoculm1 and Mlo fa...	46	0.90
gb	EU940899.1	Zea mays clone 1168123 mRNA sequence	46	0.90
gb	AC229778.1	Oryza minuta clone OM_Ba0085P10, complete sequence	46	0.90
gb	CP001078.1	Clostridium botulinum E3 str. Alaska E43, complet...	46	0.90
gb	AC225785.1	Oryza granulata, complete sequence	46	0.90
gb	EF190046.1	Zea mays clone 46F3FF4R-H2 chromosome B, genomic ...	46	0.90
gb	EF190045.1	Zea mays clone 46F3FF4R-H1 chromosome B, genomic ...	46	0.90
gb	AC196850.2	Sorghum bicolor clone SB_BBc0140005, complete seq...	46	0.90
gb	AC196847.2	Sorghum bicolor clone SB_BBc0109L12, complete seq...	46	0.90
gb	AC196837.2	Sorghum bicolor clone SB_BBc0073F19, complete seq...	46	0.90
gb	DQ493648.1	Zea mays cultivar I137TN bz locus region	46	0.90
emb	CR855167.1	Oryza sativa genomic DNA, chromosome 4, BAC clon...	46	0.90
gb	DQ417752.1	Zea mays B73 pathogenesis-related protein 2 and G...	46	0.90
gb	AC169378.2	Sorghum bicolor clone SB_BBc0007L02, complete seq...	46	0.90
gb	AC165172.2	Zea mays clone CH201-171E16, complete sequence	46	0.90
gb	AC157319.2	Zea mays clone ZMMBBb-136E2, complete sequence	46	0.90
gb	AC152495.1	Zea mays BAC clone Z486N13, complete sequence	46	0.90
gb	AF528565.1	Zea mays cultivar BSS53 chromosome 4 clone BAC 0...	46	0.90
gb	AC147925.2	Oryza sativa Japonica Group chromosome 11 clone 0...	46	0.90
gb	AC108761.2	Oryza sativa (japonica cultivar-group) chromosome...	46	0.90
gb	BT018612.1	Zea mays clone ELO1N0501C03.d mRNA sequence	46	0.90
gb	BT017984.1	Zea mays clone ELO1N0525E01.c mRNA sequence	46	0.90
gb	AC135502.4	Oryza sativa chromosome 3 BAC OSJNBb0085A04 genom...	46	0.90
gb	AC121364.2	Oryza sativa Japonica Group chromosome 5 clone OS...	46	0.90
gb	AC135418.3	Oryza sativa Japonica Group chromosome 5 clone OS...	46	0.90
gb	AC120991.3	Oryza sativa Japonica Group chromosome 5 clone OS...	46	0.90
gb	AC112159.2	Oryza sativa Japonica Group chromosome 5 clone OJ...	46	0.90
gb	AY078063.2	Zea mays B transcriptional activator (b1) gene, b...	46	0.90
gb	DQ002408.1	Zea mays gypsy retrotransposon huck, and copia re...	46	0.90
gb	AC145386.1	Oryza sativa chromosome 3 BAC OSJNBb0028K20 genom...	46	0.90
gb	AC169373.2	Sorghum bicolor clone SB_BBc0188M08, complete seq...	46	0.90
gb	AC137992.2	Oryza sativa chromosome 3 BAC OSJNBb0056B16 genom...	46	0.90
gb	AC165171.2	Zea mays clone CH201-145P10, complete sequence	46	0.90
gb	AC165176.2	Zea mays clone ZMMBBb-177G21, complete sequence	46	0.90
gb	AC122147.1	Oryza sativa Japonica Group chromosome 10 clone 0...	46	0.90
gb	AC092553.4	Oryza sativa Japonica Group chromosome 10 clone 0...	46	0.90
gb	AC163004.1	Gap filling sequence from Zea mays clone ZMMBBb03...	46	0.90

dbj AP006849.2	Oryza sativa Japonica Group genomic DNA, chromos...	46	0.90
dbj AP003874.5	Oryza sativa Japonica Group genomic DNA, chromos...	46	0.90
dbj AP005820.3	Oryza sativa Japonica Group genomic DNA, chromos...	46	0.90
gb AY530951.1	Zea mays putative growth-regulating factor 1 (Z21...	46	0.90
gb AY555143.1	Zea may BAC clone c573L14, complete sequence	46	0.90
gb AF466202.2	Zea mays putative pol protein gene, partial cds; ...	46	0.90
dbj AP003911.3	Oryza sativa Japonica Group genomic DNA, chromos...	46	0.90
dbj AP004705.3	Oryza sativa Japonica Group genomic DNA, chromos...	46	0.90
emb BX842604.1	Oryza sativa genomic DNA, chromosome 4, BAC clon...	46	0.90
gb AY144442.1	Sorghum bicolor BAC 95A23/98N8.1 Rph region, part...	46	0.90
gb AC137696.2	Genomic sequence for Oryza sativa, Nipponbare str...	46	0.90
gb AC134229.2	Oryza sativa Japonica Group chromosome 3 clone OJ...	46	0.90
gb AF546189.1	Contiguous genomic DNA sequence comprising the 19...	46	0.90
dbj AP005244.3	Oryza sativa Japonica Group genomic DNA, chromos...	46	0.90
gb AF369906.1	Sorghum bicolor clone BAC10J22 Sbb3766 sequence	46	0.90
gb AF466204.1	Sorghum bicolor clone SBTXS_0045I19, partial sequ...	46	0.90
gb AF466203.1	Zea mays clone ZMBBb_0092E12, partial sequence	46	0.90
emb AJ312444.1	Zea mays Grande retrotransposon DNA, partial LTR...	46	0.90
gb AF050437.1	Zea mays retrotransposon Grande-Zm1 3' LTR, parti...	46	0.90
gb U68404.1	ZMU68404 Zea mays retrotransposon Huck-2 5' LTR and ...	46	0.90
gb AC157977.1	Genomic sequence for Zea mays chromosome 8 BAC cl...	46	0.90
gb AC157487.1	Genomic sequence for Zea mays clone ZMBBb0614J24...	46	0.90
gb AY664419.1	Zea mays cultivar Mo17 locus 9009, complete sequence	46	0.90
gb AY664418.1	Zea mays cultivar Mo17 locus 9008, complete sequence	46	0.90
gb AY664417.1	Zea mays cultivar Mo17 locus 9002, complete sequence	46	0.90
gb AY664414.1	Zea mays cultivar B73 locus 9008, complete sequence	46	0.90
gb AY691949.1	Zea mays alcohol dehydrogenase 1 (adh1A) gene, co...	46	0.90
emb AL732380.4	Oryza sativa chromosome 12, . BAC OSJNBb0119N22 ...	46	0.90
gb AF123535.1	Zea mays alcohol dehydrogenase 1 (adh1) gene, adh...	46	0.90
gb GU080321.1	Saccharum hybrid cultivar R570 clone BAC 095F04, ...	44	3.5
gb GQ845073.1	Zea mays chromosome 4 PCR sequence AGI.995 genomi...	44	3.5
gb AC226365.2	Oryza minuta clone OM_Ba0223P12, complete sequence	44	3.5
gb EZ077797.1	TSA: Zea mays contig13436, mRNA sequence	44	3.5
gb FJ032628.1	Oryza punctata clone a0082J04 subtilisin-like pro...	44	3.5
gb CP000932.1	Campylobacter lari RM2100, complete genome	44	3.5
gb CP001364.1	Chloroflexus sp. Y-400-fl, complete genome	44	3.5
gb FJ266020.1	Oryza australiensis clone OA_CBa062H21, complete ...	44	3.5
gb AC226816.1	Oryza minuta clone OM_Ba0145I21, complete sequence	44	3.5
gb AC226776.1	Oryza minuta clone OM_Ba0084A05, complete sequence	44	3.5
gb AC229748.1	Oryza minuta clone OM_Ba0197P05, complete sequence	44	3.5
gb AC223438.1	Oryza brachyantha, complete sequence	44	3.5
ref XM_001909862.1	Podospora anserina DSM 980 hypothetical prot...	44	3.5
emb CU638744.1	Podospora anserina genomic DNA chromosome 6, sup...	44	3.5
gb CP000909.1	Chloroflexus aurantiacus J-10-fl, complete genome	44	3.5
gb EF396164.1	Zea mays nitrilase 2 (NIT2) gene, complete cds	44	3.5
gb EF190047.1	Zea mays clone 46F3FF4R-H3 chromosome B, genomic ...	44	3.5
gb EF190042.1	Zea mays clone 46F3FF4R-2 chromosome B, genomic s...	44	3.5
gb EF059989.1	Brachypodium sylvaticum hypothetical protein (57h...	44	3.5
emb CR855106.1	Oryza sativa genomic DNA, chromosome 4, BAC clon...	44	3.5

gb	AC188446.2	Gallus gallus BAC clone CH261-122M13 from chromos...	44	3.5
gb	CP000393.1	Trichodesmium erythraeum IMS101, complete genome	44	3.5
gb	AC157320.2	Zea mays clone ZMMBBb-7C14, complete sequence	44	3.5
gb	CP000284.1	Methylobacillus flagellatus KT, complete genome	44	3.5
gb	AC115727.10	Mus musculus chromosome 3, clone RP23-30A13, com...	44	3.5
gb	AC110735.6	Mus musculus chromosome 1, clone RP24-123P22, com...	44	3.5
gb	AC107851.17	Mus musculus chromosome 9, clone RP23-451B4, com...	44	3.5
gb	AF488416.1	Zea mays chromosome 9 BAC 9C20 complete sequence	44	3.5
gb	AC135956.6	Oryza sativa Japonica Group chromosome 3 clone OS...	44	3.5
gb	AC092387.6	Oryza sativa Japonica Group chromosome 10 clone O...	44	3.5
gb	AC112971.8	Mus musculus chromosome 1, clone RP24-444M12, com...	44	3.5
gb	AC151537.1	Oryza sativa Japonica Group chromosome 3 clone OS...	44	3.5
gb	AC137002.2	Oryza sativa (japonica cultivar-group) chromosome...	44	3.5
gb	AC097175.2	Oryza sativa Japonica Group chromosome 5 clone OJ...	44	3.5
gb	AC137128.17	Mus musculus chromosome 3, clone RP24-271G16, co...	44	3.5
gb	AC093952.2	Oryza sativa Japonica Group chromosome 5 clone OJ...	44	3.5
gb	AC135919.2	Oryza sativa (japonica cultivar-group) chromosome...	44	3.5
gb	AC121523.6	Mus musculus chromosome 18, clone RP24-92N23, com...	44	3.5
gb	AC161177.4	Mus musculus chromosome 18, clone RP24-131H12, co...	44	3.5
gb	AC074327.6	Homo sapiens chromosome 10 clone RP11-556E13, com...	44	3.5
tpg	BK000854.1	TPA: TPA_inf: Oryza sativa transposon Rim2-M255,...	44	3.5
gb	AC119747.1	Genomic sequence for Oryza sativa, Nipponbare str...	44	3.5
gb	AC068924.11	Oryza sativa chromosome 10 BAC OSJNBa0026L12 gen...	44	3.5
gb	AC092172.3	Oryza sativa Japonica Group chromosome 10 clone O...	44	3.5
emb	AL606923.8	Human DNA sequence from clone RP11-361F19 on chr...	44	3.5
gb	AF331854.1	AF331854 Zea mays cultivar B 73 UDP-glucosyltransf...	44	3.5
emb	AL357873.17	Human DNA sequence from clone RP11-344F13 on ch...	44	3.5
emb	AL592043.7	Human DNA sequence from clone RP11-281B1 on chro...	44	3.5
emb	AL583825.8	Human DNA sequence from clone RP11-362H12 on chr...	44	3.5
gb	AC155725.3	Mus musculus 6 BAC RP24-231N5 (Roswell Park Cance...	44	3.5
emb	AL606658.5	Oryza sativa genomic DNA, chromosome 4, BAC clon...	44	3.5
dbj	AP005912.3	Oryza sativa Japonica Group genomic DNA, chromos...	44	3.5
dbj	AP003574.3	Oryza sativa Japonica Group genomic DNA, chromos...	44	3.5
dbj	AP005127.5	Oryza sativa Japonica Group genomic DNA, chromos...	44	3.5
dbj	AP005261.4	Oryza sativa Japonica Group genomic DNA, chromos...	44	3.5
dbj	AP005199.3	Oryza sativa Japonica Group genomic DNA, chromos...	44	3.5
dbj	AP005798.3	Oryza sativa Japonica Group genomic DNA, chromos...	44	3.5
dbj	AP005698.3	Oryza sativa Japonica Group genomic DNA, chromos...	44	3.5
dbj	AP004156.3	Oryza sativa Japonica Group genomic DNA, chromos...	44	3.5
dbj	AP004870.3	Oryza sativa Japonica Group genomic DNA, chromos...	44	3.5
dbj	AP004092.3	Oryza sativa Japonica Group genomic DNA, chromos...	44	3.5
gb	AY530952.1	Zea mays unknown (Z576C20.2), putative heme oxyge...	44	3.5
dbj	AP004023.3	Oryza sativa Japonica Group genomic DNA, chromos...	44	3.5
dbj	AP003528.2	Oryza sativa Japonica Group genomic DNA, chromos...	44	3.5
dbj	AP005319.3	Oryza sativa Japonica Group genomic DNA, chromos...	44	3.5
dbj	AP005312.2	Oryza sativa Japonica Group genomic DNA, chromos...	44	3.5
dbj	AP003877.3	Oryza sativa Japonica Group genomic DNA, chromos...	44	3.5
emb	BX842606.1	Oryza sativa genomic DNA, chromosome 4, BAC clon...	44	3.5
dbj	AP006523.2	Oryza sativa Japonica Group genomic DNA, chromos...	44	3.5

dbj AP005067.2	Oryza sativa Japonica Group genomic DNA, chromos...	44	3.5
dbj AP003846.2	Oryza sativa Japonica Group genomic DNA, chromos...	44	3.5
dbj AP004308.3	Oryza sativa Japonica Group genomic DNA, chromos...	44	3.5
dbj AP004309.3	Oryza sativa Japonica Group genomic DNA, chromos...	44	3.5
emb AL645990.14	Mouse DNA sequence from clone RP23-403C12 on ch...	44	3.5
dbj AP003253.3	Oryza sativa Japonica Group genomic DNA, chromos...	44	3.5
dbj AP004222.3	Oryza sativa Japonica Group genomic DNA, chromos...	44	3.5
gb AC097720.5	Homo sapiens BAC clone RP11-1422N15 from 2, compl...	44	3.5
dbj AP003563.3	Oryza sativa Japonica Group genomic DNA, chromos...	44	3.5
gb AF466199.1	Sorghum bicolor putative receptor protein kinase,...	44	3.5
gb AC084404.8	AC084404 Oryza sativa chromosome 3 BAC OSJNBa0026A...	44	3.5
emb AJ312483.1	Zea mays Grande retrotransposon DNA, partial LTR...	44	3.5
emb AJ312451.1	Zea mays Grande retrotransposon DNA, partial LTR...	44	3.5
dbj AP002855.2	Oryza sativa Japonica Group genomic DNA, chromos...	44	3.5
emb CT025562.10	Mouse DNA sequence from clone RP24-225012 on ch...	44	3.5
gb AC155715.24	Mus musculus 10 BAC RP24-118H2 (Roswell Park Can...	44	3.5
gb AC153847.7	Mus musculus 10 BAC RP23-286J11 (Roswell Park Can...	44	3.5
gb AC132599.3	Mus musculus BAC clone RP24-131015 from 3, comple...	44	3.5
gb AC131696.4	Mus musculus BAC clone RP23-403E5 from 1, complet...	44	3.5
gb AC110817.6	Mus musculus BAC clone RP23-155B20 from 13, compl...	44	3.5
emb AL844880.3	Oryza sativa chromosome 12, . BAC OSJNBb0049H14 ...	44	3.5
emb AL935152.9	Mouse DNA sequence from clone RP24-387M5 on chro...	44	3.5
dbj AP001359.4	Homo sapiens genomic DNA, chromosome 11q clone:R...	44	3.5
dbj AP000755.4	Homo sapiens genomic DNA, chromosome 11q clone:R...	44	3.5

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

Score = 1031 bits (520), Expect = 0.0  
Identities = 1197/1413 (84%), Gaps = 11/1413 (0%)  
Strand = Plus / Minus

Query: 788 ggcgtattaggatgagtcagtcagcgagattttcggaagattagttcagtttgttcgctatta 847  
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Sbjct: 5721 ggcggattaggatgagtcggtgggattttggggagatcagttcagtcggttcactatta 5662

Query: 848 tttaggagacatatgatcctcatgtacgtatggagtgccccacggctcgtgtatataaggt 907  
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Sbjct: 5661 gttaggagacatatgatcatcatgtacgtttggagtgccccacggctcagatataagtc 5602

Query: 908 ccagagggtaccccatcatttctatcgaccatctacctatctcatcagcttttctccatt 967  
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Sbjct: 5601 ctag-gggaaccccatcattt-tatt-accatctacctatctcattagcctctctccatt 5545

Query: 968 caggagacctgcttgttaaccaccacatatagatccatcccaagaagtagtgattacg 1027



Query: 1563 catctttccgacgccttcgccctcaaatgaggatggaaagaagagcgccatcgcgctggc 1622  
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Sbjct: 4945 cat-tttctgacgccttcgccctcaaatgagtagaatggaaataagagcgccatcacgccgc 4887

Query: 1623 tcctttctaccccagcgtcctcttcatcagggggagattggagttagcacccttcaa 1682  
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Sbjct: 4886 tcctttctaccccagcgtcctcttcatcagggggaaattggagtcatcacccatctccga 4827

Query: 1683 cgatgagccaacctgcaaggggaagagcctcccagcgtgaggcgcgacgacggaggaa 1742  
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Sbjct: 4826 tgatgaacctaccatgcaaggggaagaacctccc-agtgtgaagcgcgacaacggaggaa 4768

Query: 1743 tagaagccagaacgtcggcgacatcacgaggctggggaacgggatccggcgcaaccctg 1802  
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Sbjct: 4767 caaatgccgaaacatacggtgacatcacgaagctagggaaacgggatccgacatagcctgt 4708

Query: 1803 atccccggacgaagctttagaagtaggaaaaactcccagcagtggttacaccgagaaa 1862  
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Sbjct: 4707 atccaagacgaggcctcataagtgggaaaaactcccagcagcagtgaccgggaaat 4648

Query: 1863 gcggaactctcgcccgctgatcgccgacaagcttaggaccgagaacgagagcaagccga 1922  
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Sbjct: 4647 gtggaactctcaccaccgtgattgccgacaagctcaggaccaagagcaggaacaagccga 4588

Query: 1923 gcaaggtgcaaggctgcgccgagagaatgctctctttgctcggaacctgtacccgactt 1982  
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Sbjct: 4587 gcaaggtgcaaggctgtgccgagagaacctctcttctgctcggaacctgtatcccgactt 4528

Query: 1983 cgctcgtgcaatgaacacgccgagtgaaagtcggaggggtactggcccagatagctgacgg 2042  
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Sbjct: 4527 tgctcatgcaatgaacacgccgagtgaaatcggaggggtactgtcccagatagctgacag 4468

Query: 2043 cctcccgcgaaccctagacacggaaggctaccggcggctgcttactcgagcagttaatca 2102  
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Sbjct: 4467 catcctgcaaacccaagatgctgaaggctaccggcggctgcttactcgagcagttaatca 4408

Query: 2103 ccttctaccatcactaatctccaagcgacctacgccatgccatcaacagccggcgaga 2162  
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Sbjct: 4407 ccttctaccatcgtcatctgcaaacacctacgtcccaccatcaatagccggcgaga 4348

Query: 2163 cacgcgagctccatcaacgcttcgcgacccg 2195  
| || |||||  
Sbjct: 4347 cgctagagctccatcaacgcttcgcgacccg 4315

Score = 143 bits (72), Expect = 5e-30  
Identities = 105/116 (90%)  
Strand = Plus / Plus

Query: 1084 gcacgaaccattgagttacaatcaacagcaccgtcctacccaaaagcaccgcaaggggta 1143  
|||||  
Sbjct: 11406 gcacgaaccattgagttacaatcaacagcaccatcctactcaaatgcaccgaggggta 11465

Query: 1144 gccctgggtgtgacggactcctaacaccgacagctggcgccaggtaggggg 1199  
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Sbjct: 11466 accctaggtgtgacgtcgggctccaacaccgacagctggcgccaggttaggggg 11521

Score = 87.7 bits (44), Expect = 3e-13  
Identities = 95/111 (85%), Gaps = 2/111 (1%)  
Strand = Plus / Plus

Query: 1938 gcgccgagagaatgctctctttgctcggaacctgtaccccgacttcgctcgtgcaatgaa 1997  
|||||  
Sbjct: 12178 gcgccgagagaacctcttttactcgaacctgaacctgactttgctcgtgcaatgaa 12237

Query: 1998 cacgccgagtgaagtcggaggggtactggcccagatagctgacggcctccc 2048  
||| |  
Sbjct: 12238 cac--caagtgaagtcggagggagtattggctcagatagctgatggcctccc 12286

Score = 65.9 bits (33), Expect = 1e-06  
Identities = 171/217 (78%)  
Strand = Plus / Plus

Query: 1622 ctctttctaccccgacgtcctcttcatcagggggagattggagttagcaccgtettca 1681  
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Sbjct: 11920 ctctttctaccccgacatcgtctttatcaaaggagattggagtcgtttcccatctccg 11979







>gb|AY883559.2| Zea mays cultivar inbred line B73 teosinte glume architecture 1 (tg1)  
gene, complete cds  
Length = 169976

Score = 196 bits (99), Expect = 4e-46  
Identities = 306/371 (82%), Gaps = 3/371 (0%)  
Strand = Plus / Plus

Query: 982 tgtaaccaccacatatagatccatccaagaagtagtgattacgcctctctaagcggc 1041  
|||||  
Sbjct: 94023 tgtaaccaccacataaagatccacaccaggaagtaggtattacgcctctctaagcggc 94082

Query: 1042 ccaaacttgcaaaaaccgcctatccctctctctgctgctccagcacgaaccattgagtta 1101  
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Sbjct: 94083 ccgaacctatagaaaattatctatcg-tctctcgtgctgctccagcacgaaccatcgagcta 94141

Query: 1102 caatcaacagcaccgtcctacccaaaagcaccgcaagggtagccctgggtgtgcggacg 1161  
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Sbjct: 94142 cagttagcaacaccgtcctacccaaaagcactgaggggtaaccccggtgctgctgctg 94201

Query: 1162 gactctaaacaccgacagctggcgcgccaggtaggggtgtgtctttgatctgagctagc 1221  
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Sbjct: 94202 ggtcctaaacaccgacagctggcgcgctaggtaggggtgtgtcgtgatccaagctagc 94261

Query: 1222 tcaatgaccatta-ctcctcaaatgcaagatgcccttcgccccgggactatgttttgctt 1280  
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Sbjct: 94262 tcaatggccatcatctctcc-aacacaagattgctctcgcctggatctgtgttctggtt 94320

Query: 1281 tggaaccatctcatccatagcagatgaagaggaactctgcaccgatagcagatctatt 1340  
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Sbjct: 94321 cgggaccatctcgtccatggcagacgaagaaggaattctgcatcgtatagcggatccatc 94380

Query: 1341 ggagaagaagc 1351  
|||||  
Sbjct: 94381 ggagaagaagc 94391

Score = 91.7 bits (46), Expect = 2e-14  
Identities = 103/122 (84%)







Query: 2086 actcgagcagttaatcaccttctacccatcactaatcctccaagcgacctacgccatgcc 2145  
||||| ||||| || || ||||| || || | || || | ||||| || ||  
Sbjct: 161728 actcaagcagccaaccatcttctacctctcgcctcaccgccgaacgacctacgacacacc 161787

Query: 2146 atcaacagccggcgagacacgaggctccatcaacgcttcgcg 2189  
||||||| || ||| ||| ||||| ||||| |||||  
Sbjct: 161788 atcaacagccggcgagacacgaggctccatcaacgcttcgcg 161831

Score = 79.8 bits (40), Expect = 6e-11  
Identities = 83/96 (86%), Gaps = 1/96 (1%)  
Strand = Plus / Minus

Query: 562 ttgtgggggatagatatcccc-gggtccactagaaggcgagaaggcctcgcgtgtggcca 620  
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Sbjct: 112124 ttgtgggggacagatatccccgggtccactagaaggtagaaggcctcgcgaaaggcct 112065

Query: 621 cgggccagttaccccgcaaggccatcccttcgtggg 656  
||||| ||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 112064 cgggccattatttcgcaaggccatcccttcgtggg 112029

Score = 54.0 bits (27), Expect = 0.004  
Identities = 55/63 (87%), Gaps = 1/63 (1%)  
Strand = Plus / Minus

Query: 982 tgtaaccaccacatat-agatccatcccaagaagtagtgtattacgcctctctaagcgg 1040  
||||||| ||||| ||||| ||| ||||| || ||||| ||||| |||||  
Sbjct: 111697 tgtaacctaccacataagagatccacgccaggaagtaggtgttacgcctctctaagcgg 111638

Query: 1041 ccc 1043  
|||  
Sbjct: 111637 ccc 111635

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Minus





Score = 133 bits (67), Expect = 5e-27  
Identities = 196/239 (82%)  
Strand = Plus / Plus

Query: 1966 aacctgtaccccgacttcgctcgtgcaatgaacacgccgagtgagtcggagggtactg 2025  
||||| ||||||||| | | || ||||||||||||||||||||||||||||| |||  
Sbjct: 54934 aacctgaaccccgactttgcctgagccatgaacacgccgagtgagtcggagggtgctg 54993

Query: 2026 gccagatagctgacggcctcccgcaaccctagacacggaaggctaccggcggtgctt 2085  
|| | ||||||||| ||||||||| || || | ||| | || ||||| ||||||||| |  
Sbjct: 54994 gctcggatagctgatggcctccctcggactccggacgccgaggctatcggcggtgttc 55053

Query: 2086 actcgagcagttaatcaccttctaccatcactaatcctccaagcgacctacgccatgcc 2145  
|||| ||||| ||||||||||||||||| || || | | || | ||| ||||| || |||  
Sbjct: 55054 actcaagcagccaatcaccttctaccctcgtcacctgccgaacgatctacgacacgcc 55113

Query: 2146 atcaacagccggcgagacacgggagctccatcaacgcttcgcgcgaccgatgacacga 2204  
||||||| || || ||| ||||||||||||||||| ||||| || | || |||||||||  
Sbjct: 55114 atcaacagtgcgcgggacgcgggagctccatcaatgcttcacgtgaacgatgacacga 55172

Score = 99.6 bits (50), Expect = 7e-17  
Identities = 185/230 (80%)  
Strand = Plus / Plus

Query: 1138 gggtagccctgggtgtgcggacggactctaacaccgacagctggcgccaggtaggg 1197  
||||||| ||||||||| ||| ||||| | |||||||||||||||||||||||||||||  
Sbjct: 54142 ggggtaaccctgggtgcacggtcggacccgaaacaccgacagctggcgccaggtaggg 54201

Query: 1198 ggtgtgtctttgatctgagctagctcaatgaccattacctccaaatgcaagatcgccctt 1257  
||||||| | |||| | ||||| ||||||||| || | |||| | | ||||||||| |||  
Sbjct: 54202 ggtgtgtcatcgatccaagctatctcaatggccgtcaccttcagcgcaagatcatcctc 54261

Query: 1258 cgccccgggactatgttttgccttggaaacctctcatccatagcagatgaagagggaact 1317  
| |||||| | || || ||||| || || ||||||||| |||| ||||| |||||||||  
Sbjct: 54262 caccocggatccatattctgcttcggtactatctcatctgtagcggatgaggagggaact 54321

Query: 1318 ctgcaccgcatagcagatctattggagaagaagctttcctcagaaatctc 1367  
||||| ||| | || ||||| ||||| ||||| ||||| |||||  
Sbjct: 54322 ctgcatcgcccttgccgatccgccggagaaaaagccttcctcaggaatctc 54371

Score = 67.9 bits (34), Expect = 2e-07  
Identities = 109/134 (81%)  
Strand = Plus / Minus

Query: 1915 caagccgagcaaggtgcaaggctgcccagagagaatgctctctttgctcggaaacctgtac 1974  
||||||| ||||| | ||| ||||| | |||| | || ||||| |  
Sbjct: 28040 caagccgagcaagatgcaaggcaacaccgggagaaatccattcttcgggcgcaacctgaat 27981

Query: 1975 cccgacttcgctcgtgcaatgaacacgccgagtgaaagtcggagggtactggcccagata 2034  
||||||| || || ||||| ||||| ||||| ||||| || || |||||  
Sbjct: 27980 cccgacttcgcccagccatgaacacgccgagcgaagttggaggagtactagctcggata 27921

Query: 2035 gctgacggcctccc 2048  
||||| || |||||  
Sbjct: 27920 gctgatggactccc 27907

Score = 54.0 bits (27), Expect = 0.004  
Identities = 42/47 (89%)  
Strand = Plus / Minus

Query: 2143 gccatcaacagccggcgagacacgcggagctccatcaacgcttcgcg 2189  
||||||| || ||||| ||||| ||||| ||||| |||||  
Sbjct: 27812 gccatcaacagtcgccgagacgcggaagctccatcaatgcttcgcg 27766

Score = 50.1 bits (25), Expect = 0.057  
Identities = 28/29 (96%)  
Strand = Plus / Plus

Query: 1622 ctccctttctaccccagctcctcttcatc 1650  
|||| | ||||| ||||| ||||| |||||  
Sbjct: 54605 ctccattctaccccagctcctcttcatc 54633





Query: 621 cgggccagttaccccgaagccatcccttcgtgggtcgag 661  
||||| ||| ||||||||| ||||||||| ||||  
Sbjct: 8634 cgggccattatttcgaagccacccttcgtgggccgag 8674

Score = 63.9 bits (32), Expect = 4e-06  
Identities = 83/100 (83%)  
Strand = Plus / Plus

Query: 562 ttgtgggggatagatatccccgggtccactagaaggcgagaaggcctcgctgtggccac 621  
||||||||| ||||||||| || ||||||||||| ||||||||| || |||||  
Sbjct: 28412 ttgtgggggacagatatccccgggtccactagaaggcaagaaggcctcacgaaaggcctc 28471

Query: 622 gggccagttaccccgaagccatcccttcgtgggtcgag 661  
||||| ||| ||||||||| ||||||||| ||||  
Sbjct: 28472 gggccattatttcgaagccacccttcgtgggccgag 28511

Score = 48.1 bits (24), Expect = 0.23  
Identities = 30/32 (93%)  
Strand = Plus / Plus

Query: 1012 gaagtagtgattacgcctctctaagcgccc 1043  
||||||| || |||||||||||||||||||||  
Sbjct: 28869 gaagtaggtgttacgcctctctaagcgccc 28900

Score = 46.1 bits (23), Expect = 0.90  
Identities = 32/35 (91%)  
Strand = Plus / Plus

Query: 1966 aacctgtaccccgacttcgctcgatgaatgaacac 2000  
||||| ||||||||||||||||| || |||||||||  
Sbjct: 16694 aacctgaaccccgacttcgctcgagccatgaacac 16728

Score = 44.1 bits (22), Expect = 3.5  
Identities = 106/134 (79%)  
Strand = Plus / Plus

Query: 2068 ggctaccggggctgcttactcgagcagttaatcaccttctacccatcaactaatcctcca 2127  
||||| ||||||||| ||||| ||||| ||| ||| ||||| || || | |||||||  
Sbjct: 16796 ggctatcgggctgctcactcgggcagtaaccatcttctgcctctcggtcacctccg 16855

Query: 2128 agcgacctagccatgccatcaacagccggcgagacacgaggagctccatcaacgcttcg 2187  
||||| ||||| ||||||||| || | || ||| | ||||||| ||||||| |||||  
Sbjct: 16856 agcgatctacaacatgccatcaatagtcaacgggacgcacggagcccatcaatgcttca 16915

Query: 2188 cgcgaccgatgaca 2201  
||||| ||| |||||  
Sbjct: 16916 cgcgaacgacgaca 16929

>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: 881 agtgccccacggtcgtgtatataaggtccagagggtaccccatcatTT-ctatcgaccat 939  
||||| ||||||||| ||||||||| | || ||||||| ||||||||| | |||||||||  
Sbjct: 289 agtgccccacggtcggatataaggcctaggggtaccccatcatTTTccatcgaccat 348

Query: 940 ctacctatctcatcagcttttctccattcaggagacctcgttgtaaccaccacatata 999  
| ||||||||| ||||||||| ||||||||| || ||||||| ||||||||| |||  
Sbjct: 349 caacctatctcattagcttttcttccattcaggagacctcagttgtaaccaccacataaa 408

Query: 1000 gatccatccaagaagtagtgattacgc 1028  
||||| ||| ||||||| || |||||||  
Sbjct: 409 gatccacaccaggaagtaggtgttacgc 437

Score = 44.1 bits (22), Expect = 3.5  
Identities = 22/22 (100%)  
Strand = Plus / Plus

Query: 635 cgcaaggccatcccttcgtggg 656  
||||| ||||||||| |||||||||  
Sbjct: 43 cgcaaggccatcccttcgtggg 64



Score = 48.1 bits (24), Expect = 0.23  
Identities = 24/24 (100%)  
Strand = Plus / Plus

Query: 1627 ttctaccccgacgtcctcttcac 1650  
|||||  
Sbjct: 81094 ttctaccccgacgtcctcttcac 81117

Score = 48.1 bits (24), Expect = 0.23  
Identities = 31/32 (96%), Gaps = 1/32 (3%)  
Strand = Plus / Plus

Query: 562 ttgtgggggatagatatcccc-gggtccacta 592  
|||||  
Sbjct: 102517 ttgtgggggatagatatcccctgggtccacta 102548

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Plus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198  
||||  
Sbjct: 133339 aaacgccgacagttggcgcgccaggtagggg 133369

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

Score = 127 bits (64), Expect = 3e-25  
Identities = 306/384 (79%), Gaps = 2/384 (0%)  
Strand = Plus / Plus

Query: 984 taaccaccacatatagatccatccaagaagtagtgattacgcctctctaagcgccc 1043  
|||||  
Sbjct: 148845 taaccaccacataaagatccacatcaggaagtaggtgttacacctctctaagcgccct 148904

Query: 1044 aaacttgcagaaaaccgcctatccctctctctgctgcgtccagcagcgaaccattgagttaca 1103  
|||





Query: 1973 accccgacttcgctcgtgcaatgaacacgccgagtgaagtcggagggtactggcccaga 2032  
||||||| | || | |||||||||||||||||||||||| | ||| | ||  
Sbjct: 79768 accccgacttcaccgggcatgaacacgccgagtgaagtcggaggagtgttgctcgga 79709

Query: 2033 tagctgacggcctcccgcgaaccctagacacggaaggctaccggcggctgcttactcgag 2092  
|||||| | ||||| | | | | || | | | |||| | ||||| | ||| | ||  
Sbjct: 79708 tagctgatggcctccccggactcccagccgagggtatcggcggctgttactcaag 79649

Query: 2093 cagttaatcaccttctaccatcactaatcctccaagcgacctacgccatgccatcaaca 2152  
||| | |||||||||||| | || | | | | | || | |||| | | |||||||||  
Sbjct: 79648 cagccaaccaccttctaccctcgtcaccgccgaacgatctacgacagccatcaaca 79589

Query: 2153 gccggcgagacacgaggctccatcaacgcttcgcgaccgatgacacga 2204  
| |||| | || | |||||||||||||||||| |||| | || | |||||  
Sbjct: 79588 gtcggcgggacgcacggagctccatcaacgcttcacgcgaacgacgacacga 79537

Score = 79.8 bits (40), Expect = 6e-11  
Identities = 121/147 (82%), Gaps = 2/147 (1%)  
Strand = Plus / Minus

Query: 1083 agcacgaaccattgagttacaatcaacagcaccgtcctacc--aaaagcaccgcaagg 1140  
||||||| ||| ||| | | | |||||||||||| | |||||||| | |||  
Sbjct: 80636 agcacgaaccatcgagctacagtcgataaacaccgtcctacacaaaaagcacttgagg 80577

Query: 1141 gtagccctgggtgtgcgacggactctaaacaccgacagctggcgcgccaggtaggggt 1200  
| | | |||| | || | |||| | |||||||||||||| |||||| | |||  
Sbjct: 80576 gccacccgggtgcgcggtcgaccacaaaacaccgacagctggcgtgccaggtagcgggt 80517

Query: 1201 gtgtctttgatctgagctagctcaatg 1227  
|||| | ||| | |||||||||  
Sbjct: 80516 gtgtcgtcgatccaagctagctcaatg 80490

Score = 54.0 bits (27), Expect = 0.004  
Identities = 33/35 (94%)  
Strand = Plus / Minus

Query: 1621 gtcctttctaccccgacgtcctcttcatcagggg 1655  
||||| ||||||||||||||||||||||||||| ||||  
Sbjct: 80108 gtcctattctaccccgacgtcctcttcatcagggg 80074

Score = 52.0 bits (26), Expect = 0.015  
Identities = 47/54 (87%)  
Strand = Plus / Minus

Query: 1761 ggcacatcacgaggtggggaacgggatccggcgcaaccgatatccgggacga 1814  
||||||| || || ||||||||||| ||| ||||||||||| || |||||  
Sbjct: 79968 ggcacatcacgaagccggagaacgggatctggcacaaccgatatcgcgagacga 79915

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Plus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198  
||||| ||||||| |||||||||||||||||||  
Sbjct: 303154 aaacgccgacagttggcgcgccaggtagggg 303184

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

Score = 123 bits (62), Expect = 5e-24  
Identities = 137/161 (85%), Gaps = 2/161 (1%)  
Strand = Plus / Plus

Query: 1069 tctctcgtgcgtccagcacgaaccattgagttacaatcaacagcacctctacc--aa 1126  
||||||| || ||||||||||||||||||| |||| | | ||||||||||| | ||  
Sbjct: 2693 tctctcgtgcatttagcacgaaccattgagctacagtcgataaacacctctactccaaa 2752

Query: 1127 aagcaccgcaagggtagccctgggtgtgcggacggactctaacaccgacagctggcgc 1186  
||||||| | ||||| | || ||||| ||| ||||| ||||||| |||||||  
Sbjct: 2753 aagcacctcgaggggcaaccccggtgcgcggtcggacccaaaactgacagctggcgc 2812

Query: 1187 gccaggtagggggtgtgtctttgatctgagctagctcaatg 1227  
||||||| ||||||| ||||| |||||||  
Sbjct: 2813 gccaggtagggggtgtgtcactgatccaagctagctcaatg 2853

Score = 65.9 bits (33), Expect = 1e-06  
Identities = 46/49 (93%), Gaps = 1/49 (2%)  
Strand = Plus / Plus

Query: 562 ttgtgggggatagatatcc-ccggtccactagaaggcgagaaggcctc 609  
||||| ||||| ||||||||| ||||| |||||  
Sbjct: 2178 ttgtggggacagatatcctccggtccactagaaggcaagaaggcctc 2226

Score = 54.0 bits (27), Expect = 0.004  
Identities = 39/43 (90%)  
Strand = Plus / Plus

Query: 1622 ctcttttctaccccgactcctcttcatcaggggagattgga 1664  
|||| ||||||||| ||| ||||| |||  
Sbjct: 3211 ctccgttctaccccgactcctctttatcgggggagagtgga 3253

Score = 50.1 bits (25), Expect = 0.057  
Identities = 145/185 (78%)  
Strand = Plus / Plus

Query: 1966 aacctgtaccccgacttcgctcgtgcaatgaacacgccgagtgaagtcggagggtactg 2025  
||||| ||||||||| || | ||||||| ||||| || ||||| || || ||  
Sbjct: 3543 aacctgaaccccgacttcgctccgatccatgaacacaccgagcgaggtcggtggagtgtg 3602

Query: 2026 gccagatagctgacggcctcccgcaaccctagacacggaaggctaccggcggtgctt 2085  
|| | ||||| | ||||||| || || | |||| | || ||||| |||||||||  
Sbjct: 3603 gtcgcatagccaatggcctccccggactccagacgccgagggtatcggcggtgctc 3662

Query: 2086 actcgagcagttaatcaccttctacctatcactaatcctccaagcgacctacgccatgcc 2145  
||||| |||| ||| || ||||| || || || ||||||||| ||| | || |||  
Sbjct: 3663 actcgggcagctaaccatcttctgcctctcgtcatcctccaagcgatctatgacacgcc 3722

Query: 2146 atcaa 2150  
|||||  
Sbjct: 3723 atcaa 3727

Score = 48.1 bits (24), Expect = 0.23  
Identities = 45/52 (86%)  
Strand = Plus / Plus

Query: 1459 acccgaaaaactccgctgtccacttcgccacaaaaggagtggacacggatta 1510  
||||||| ||| ||| ||||||| || ||||||| ||||||||||||||||  
Sbjct: 3069 acccgaagaaccccggtgtccacctcatccacaaaaggagtggacacggatta 3120

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

Score = 123 bits (62), Expect = 5e-24  
Identities = 137/161 (85%), Gaps = 2/161 (1%)  
Strand = Plus / Plus

Query: 1069 tctctcgtgcgtccagcacgaaccattgagttacaatcaacagcaccgtcctacc--aa 1126  
||||||||| || ||||||||||||||||||| |||| || | | ||||||||||| | ||  
Sbjct: 10022 tctctcgtgcatctagcacgaaccattgagctacagtcgataacaccgtcctactccaaa 10081

Query: 1127 aagcaccgcaaggggtagccctgggtgtgcgacggactctaaacaccgacagctggcgc 1186  
||||||| | ||||| | ||| ||||| |||| | ||||| | ||||||| |||||||||||  
Sbjct: 10082 aagcacctcgaggggcaaccccggtgctcggtcggacccaaaactgacagctggcgc 10141

Query: 1187 gccaggtagggggtgtgtctttgatctgagctagctcaatg 1227  
||||||||||||||||||||| ||||| |||||||||||||||  
Sbjct: 10142 gccaggtagggggtgtgtcactgatccaagctagctcaatg 10182

Score = 65.9 bits (33), Expect = 1e-06  
Identities = 46/49 (93%), Gaps = 1/49 (2%)  
Strand = Plus / Plus

Query: 562 ttgtgggggatagatatcc-ccggtccactagaaggcgagaaggcctc 609  
||||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
Sbjct: 9507 ttgtggggacagatatcctccgggtccactagaaggcaagaaggcctc 9555

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



Query: 1459 acccgaaaaactccgctgtccacttcgccacaaaaggagtgacacggatta 1510  
||||||| ||| ||| ||||||| || ||||||| |||||||||||||||||  
Sbjct: 10398 acccgaagaaccccggttgtccacctcatccacaaaagagtgacacggatta 10449

Score = 46.1 bits (23), Expect = 0.90  
Identities = 54/63 (85%), Gaps = 1/63 (1%)  
Strand = Plus / Plus

Query: 982 tgtaaccaccacatata-gatccatcccaagaagtagtgattacgcctctctaagcgg 1040  
||||||||||||||||| | |||||| | | |||||| | | ||||||||||||||| |  
Sbjct: 1115 tgtaaccaccacataaaaagatccacacaaggaagtaggtgttacgcctctctaagcag 1174

Query: 1041 ccc 1043  
|||  
Sbjct: 1175 ccc 1177

>gb|EU952187.1| Zea mays clone 1218827 hypothetical protein mRNA, complete cds  
Length = 2277

Score = 119 bits (60), Expect = 7e-23  
Identities = 102/116 (87%)  
Strand = Plus / Minus

Query: 2097 taatcaccttctaccatcaactaatcctccaagcgacctagccatgccatcaacagccg 2156  
||||||||||||| ||||| || |||| | ||| |||||| | | |||||||||||||  
Sbjct: 2273 taatcaccttctgccatcgctcatccccgagcaacctacaccagccatcaacagccg 2214

Query: 2157 gcgagacacgaggctccatcaacgcttcgcgcgaccgatgacacgaaagtgaga 2212  
||||| ||||||||||||||| ||||||||||||||| | ||||||| |||  
Sbjct: 2213 acgagacgcgaggctccatcaatgcttcgcgcgaccgacggcacgaaagcgaga 2158

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

Score = 119 bits (60), Expect = 7e-23  
Identities = 293/367 (79%), Gaps = 4/367 (1%)  
Strand = Plus / Minus

Query: 982 tgtaaccaccacatata-gatccatcccaagaagtagtgattacgcctctctaagcgg 1040



Score = 56.0 bits (28), Expect = 0.001  
Identities = 184/236 (77%)  
Strand = Plus / Minus

Query: 1966 aacctgtaccccgacttcgctcgtgcaatgaacacgccgagtgaagtcggagggtactg 2025  
||||| ||||||||| | || ||||||| ||||| || ||||| || || ||  
Sbjct: 9121 aacctgaaccccgacttcgcctgagccatgaacacaccgagcgaggtcggtggagtgtg 9062

Query: 2026 gccagatagctgacggcctcccgcgaaccctagacacggaaggctaccggcggtgctt 2085  
|| | ||||| || ||||||| | || | |||| | || ||||| |||||||||  
Sbjct: 9061 gtcggatagccgatggcctcccctgactccagacgctgagggtatcggcggtgctc 9002

Query: 2086 actcgagcagttaatcaccttctaccatcactaatcctccaagcgacctacgccatgcc 2145  
||||| |||| ||| | ||||| || || || ||||||| ||||| ||| || ||  
Sbjct: 9001 actcgggcagctaacaattcttctgectctcgtcctcctccgagcgatctatgacacacc 8942

Query: 2146 atcaacagccggcgagacacgcggagctccatcaacgcttcgcgacccgatgaca 2201  
||||| || || || || || | | ||||||||| ||||||||| ||| ||||  
Sbjct: 8941 atcaatagtcgacgggacgcacagagctccatcaatgcttcgcggaacgacgaca 8886

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

Score = 119 bits (60), Expect = 7e-23  
Identities = 174/212 (82%)  
Strand = Plus / Minus

Query: 1125 aaaagcaccgcaagggtagccctgggtgtgctggacggactctaacaccgacagctggc 1184  
||||||| | ||||| | ||| ||||||||| ||||| | |||||||||  
Sbjct: 9408 aaaagcacctcgaggggcaaccccggtgtgctggacccaaacaccgacagctggt 9349

Query: 1185 gcgccaggtaggggtgtgtctttgatctgagctagctcaatgaccattacctcctcctc 1244  
||||||||| ||||||| ||||| ||||||||| || || || || || ||  
Sbjct: 9348 gcgccaggtaggggtgtgtcactgatccaagctagctcaatggccgtcactttccagca 9289

Query: 1245 caagatcgcccttcgccccgggactatgttttgccttggaaacctctcatccatagcaga 1304  
||||||| || ||||| || | |||| ||||||||| ||||||||| || |||||  
Sbjct: 9288 caagatcgctctccgccctggatccgtgttctgcttggaaacctctcatccgtggcaga 9229



Score = 65.9 bits (33), Expect = 1e-06  
Identities = 46/49 (93%), Gaps = 1/49 (2%)  
Strand = Plus / Minus

Query: 562 ttgtgggggatagatatcccc-gggtccactagaaggcgagaaggcctc 609  
|||||  
Sbjct: 19216 ttgtgggggacagatatccccgggtccactagaaggcaagaaggcctc 19168

Score = 54.0 bits (27), Expect = 0.004  
Identities = 55/63 (87%), Gaps = 1/63 (1%)  
Strand = Plus / Minus

Query: 982 tgtaaccaccacatata-gatccatcccaagaagtagtattacgcctctctaagcgg 1040  
|||||  
Sbjct: 18788 tgtaaccaccacataaaagatccacaccaggaagtagagggttacgcctctctaagcgg 18729

Query: 1041 ccc 1043  
|||  
Sbjct: 18728 ccc 18726

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

Score = 117 bits (59), Expect = 3e-22  
Identities = 286/358 (79%), Gaps = 4/358 (1%)  
Strand = Plus / Plus

Query: 982 tgtaaccaccacatata-gatccatcccaagaagtagtattacgcctctctaagcgg 1040  
|||||  
Sbjct: 178146 tgtaaccaccacataaaagatccacaccaggaagtaggggttacacctctctaagcgg 178205

Query: 1041 cccaaacttgcaaaaaccgcctatccctctctcgtgctccagcagcaaccattgagtt 1100  
|||  
Sbjct: 178206 cccgaacctgtacaaaattgtcca-ctgtttctcgtgcttctagcagcaaccatcgagct 178264

Query: 1101 acaatcaacagcaccgtcctaccc--aaaagcacgcgaaggggtagccctgggtgtgcgg 1158  
|||  
Sbjct: 178265 acagtcggtaacaccttctactccaaaagcacctcgaggggcaacccgggtgcacgg 178324



Length = 582

Score = 115 bits (58), Expect = 1e-21  
Identities = 204/249 (81%), Gaps = 4/249 (1%)  
Strand = Plus / Plus

Query: 982 tgtaacccaccacatata-gatccatccaagaagtagtgattacgcctctctaagcgg 1040  
||||| ||||||||| | |||||| | || |||||| | || ||||||||| |||||||  
Sbjct: 271 tgtaatccaccacataaaagatccacaccaggaagtaggggtttacgcctctttaagcgg 330

Query: 1041 cccaaacttgagaaaaccgcctatccctctctcgtgcgtccagcacgaaccattgagtt 1100  
||||||| || | |||| | | | ||||||||| || ||||||||| ||| |  
Sbjct: 331 cccaaacctgtataaaattgtcca-ctgtctctcgtgcatctagcacgaaccatcgagct 389

Query: 1101 acaatcaacagcaccgtcctaccc--aaaagcacgcgaagggtagccctgggtgtgcgg 1158  
||| || ||||||||| | |||||||| | |||| | ||| ||||| |||||  
Sbjct: 390 acagtcggtgacaccgtcctactcctcaaaaagcacctcgaggggcaaccccggtgtgcgg 449

Query: 1159 acggactctaaacaccgacagctggcgcgccaggtaggggtgtgtctttgatctgagct 1218  
||||| | ||||||||| ||||||||| ||||||||| ||||||| |||||  
Sbjct: 450 tcggacccaaaacaccgacagctggcgcgccaggtaggggtgtgtcactgatccaagct 509

Query: 1219 agctcaatg 1227  
|||||||  
Sbjct: 510 agctcaatg 518

>gb|AC229878.2| Zea mays BAC clone CH201-108P8 from chromosome 9, complete sequence  
Length = 171809

Score = 113 bits (57), Expect = 5e-21  
Identities = 210/260 (80%), Gaps = 2/260 (0%)  
Strand = Plus / Minus

Query: 1071 tctcgtgcgtccagcacgaaccattgagttacaatcaacagcaccgtcctaccc--aaaa 1128  
||||||| || ||||||||| ||||||| |||| | | ||||||||| | |||||  
Sbjct: 56170 tctcgtgcatctggcagcaactattgagctacagtcgataaacaccgtcctactcctcaaaaa 56111

Query: 1129 gcaccgcaagggtagccctgggtgtgcggacggactctaaacaccgacagctggcgcgc 1188  
||||| | ||||| ||| ||||| |||| ||||| | ||||||| |||||||||  
Sbjct: 56110 gcacctgaggggtaccccggtgtgcggctggacccaaaactgacagctggcgcgc 56051

Query: 1189 caggtagggggtgtgtctttgatctgagctagctcaatgaccattacctccaaatgcaag 1248  
|||||  
Sbjct: 56050 caggtagggggtgtgtcatcgatccaagctagctcaatgaccgtcaccttctgcacaag 55991

Query: 1249 atcgcccttcgccccgggactatgttttgctttggaaccatctcatccatagcagatgaa 1308  
|||||  
Sbjct: 55990 atcgcccttcgccccgggactatgttttgctttggaaccatctcatctgtagcggataag 55931

Query: 1309 gagggaactctgcaccgcat 1328  
|||||  
Sbjct: 55930 gagggaactctgcatcgcat 55911

Score = 101 bits (51), Expect = 2e-17  
Identities = 192/239 (80%)  
Strand = Plus / Minus

Query: 1966 aacctgtaccccgacttcgctcgtgcaatgaacacgccgagtgaagtcggaggggtactg 2025  
|||||  
Sbjct: 55299 aacctgaaccccgacttcgcccagccatgaacacgccgagtgaagtcggaggggtgctg 55240

Query: 2026 gccagatagctgacggcctcccggaaccctagacacggaaggctaccggcggctgctt 2085  
|||  
Sbjct: 55239 gctcggatagctgatgggctcctcggactcacgacgccgagggtatcgacggctgttc 55180

Query: 2086 actcgagcagttaatcaccttctaccatcactaatcctccaagcgacctacgcatgcc 2145  
|||||  
Sbjct: 55179 actcaggcagccaatcaccttctacctctcgctcaccgccgaacaatctacgacacacc 55120

Query: 2146 atcaacagccggcgagacacgaggctccatcaacgcttcgcgcgaccgatgacacga 2204  
|||||  
Sbjct: 55119 atcaacagtcgctgggacgcgaggctccatcaatgcctcgcgtgaacgacgacacga 55061

Score = 48.1 bits (24), Expect = 0.23  
Identities = 24/24 (100%)  
Strand = Plus / Minus

Query: 1627 ttctaccccgacgtcctcttcac 1650

|||||  
Sbjct: 55624 ttctaccccgacgtcctcttcac 55601

Score = 46.1 bits (23), Expect = 0.90  
Identities = 89/110 (80%), Gaps = 2/110 (1%)  
Strand = Plus / Minus

Query: 1071 tctcgtgctccagcacgaaccattgagttacaatcaacagcaccgtccta--cccaaaa 1128  
||||| | |||||  
Sbjct: 13343 tctcgtgcatctggcacgaaccattgagctacagtcgataaacaccgtcctactcctaaaa 13284

Query: 1129 gcaccgcaagggtagccctgggtgtcggacggactctaaacaccgaca 1178  
||||| | ||||| ||| ||||| ||||| ||||| | |||||  
Sbjct: 13283 gcacctcgaggggtaccccggtgcgcggtcggacccaaaacaccgaca 13234

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Minus

Query: 1168 aaacaccgacagctggcgccaggtagggg 1198  
|||| | ||||| |||||  
Sbjct: 36120 aaacgccgacagttggcgccaggtagggg 36090

Score = 44.1 bits (22), Expect = 3.5  
Identities = 46/54 (85%)  
Strand = Plus / Minus

Query: 1761 gcgacatcacgaggtggggaacgggatccggcgcaaccggtatcccgggacga 1814  
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 55492 gcgacatcacgagccggggagcaggacccggcgagcctgtatcgcgagacga 55439

>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 = 113 bits (57), Expect = 5e-21

Identities = 147/177 (83%)  
Strand = Plus / Minus

Query: 1149 ggggtgtcggacggactctaaacaccgacagctggcgcgccaggtaggggtgtgtcttt 1208  
||||||| | | ||||||||||||||||||||||||||||||||  
Sbjct: 89981 ggggtgtcggtcggacccaaacaccgacagctggcgcgccaggtaggggtgtgtcgac 89922

Query: 1209 gatctgagctagctcaatgaccattacctccaaatgcaagatcgccttcgccccgggac 1268  
|||| | ||||||||||| | | |||| | | ||||||| ||| ||||||| |  
Sbjct: 89921 gatccaagctagctcaatggccgtcaccttctacagcaagatcacctgcgccccggatc 89862

Query: 1269 tatgttttgctttggaacctctcatccatagcagatgaagaggaactctgcaccg 1325  
| || ||||| |||| | ||||||| |||| | |||||||||||||||| |||||  
Sbjct: 89861 cgtattctgcttcgaaaaatctcatctgtagcggatgaagaggaactctacaccg 89805

Score = 91.7 bits (46), Expect = 2e-14  
Identities = 112/134 (83%)  
Strand = Plus / Minus

Query: 1915 caagccgagcaaggtgcaaggctgcgccgagagaatgctctctttgctcggaacctgtac 1974  
||||||||| ||||||| ||||| ||||| | |||| | || ||||||| |  
Sbjct: 89265 caagccgagcaagatgcaaggcaacgccgggagaatccattcttcgggcgcaacctgaat 89206

Query: 1975 cccgacttcgctcgtgcaatgaacacgccgagtgcaagtcggaggggtactggccccagata 2034  
||||||||| || || ||||||||||||| ||||||||||||| |||| | ||||  
Sbjct: 89205 cccgacttcgccccgagctatgaacacgccgagcgaagtcggaggggtattggctcggata 89146

Query: 2035 gctgacggcctccc 2048  
||||| || |||||  
Sbjct: 89145 gctgatggactccc 89132

Score = 48.1 bits (24), Expect = 0.23  
Identities = 31/32 (96%), Gaps = 1/32 (3%)  
Strand = Plus / Minus

Query: 562 ttgtgggggatagatat-ccccgggtccacta 592  
||||||||| ||||||| |||||  
Sbjct: 66192 ttgtgggggatagatatccccgggtccacta 66161





Strand = Plus / Minus

Query: 1621 gtcctttctaccccgacgtccttcat 1649  
||||| ||||||||||||||||||||||||  
Sbjct: 92174 gtcctttctaccccgacgtccttcat 92146

Score = 48.1 bits (24), Expect = 0.23  
Identities = 45/52 (86%)  
Strand = Plus / Minus

Query: 1763 gacatcacgaggctggggaacgggatccggcgcaaccgtatccgggacga 1814  
||||||||||| ||||| ||||| || ||||||||| ||||| || |||||  
Sbjct: 92035 gacatcacgaggccgggagcgggaccagcgcaaccatatacagagacga 91984

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Plus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198  
|||| | ||||| |||||||||||||||||  
Sbjct: 110714 aaacgccgacagttggcgcgccaggtagggg 110744

Score = 44.1 bits (22), Expect = 3.5  
Identities = 28/30 (93%)  
Strand = Plus / Plus

Query: 298 atttgtttgatggatttagtaaaggttatg 327  
||||||| ||||||||| |||||  
Sbjct: 4582 atttgtttggtggatttagtagaggttatg 4611

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

Score = 111 bits (56), Expect = 2e-20  
Identities = 134/159 (84%), Gaps = 2/159 (1%)  
Strand = Plus / Plus

Query: 1071 tctcgtgcgtccagcacgaaccattgagttacaatcaacagcaccgtcctaccc--aaaa 1128  
||||||| ||||||||||||| ||| ||| | | ||||||||| | |||  
Sbjct: 46719 tctcgtgcgccagcacgaaccatcgagctacagtcggtaacaccgtcctactcctaaaa 46778

Query: 1129 gcaccgcaagggtagccctgggtgtgcggacggactctaaacaccgacagctggcgcg 1188  
||||| | ||||||| ||||||||| ||| ||||| | ||||||| |||||||||  
Sbjct: 46779 gcacctcgggggtaaacctgggtgcggtcggaccgaaacactgacagctggcgcg 46838

Query: 1189 caggtaggggtgtgtctttgatctgagctagctcaatg 1227  
||||||||||||||| | || | |||||||||  
Sbjct: 46839 caggtaggggtgtgtcatcgaccaagctagctcaatg 46877

Score = 101 bits (51), Expect = 2e-17  
Identities = 192/239 (80%)  
Strand = Plus / Plus

Query: 1966 aacctgtaccccgacttcgctcgtgcaatgaacacgccgagtgagtgagggtactg 2025  
||||| ||||||||||||| || || ||||||||||||||||||| ||||||| ||  
Sbjct: 57038 aacctgaaccccgacttcgcccagccatgaacacgccgagtgagttggagggtgtg 57097

Query: 2026 gccagatagctgacggcctcccgcgaaccctagacacggaaggctaccggcggtgctt 2085  
|| | || | || ||||||||| || || | ||||| || || || ||||||||| |  
Sbjct: 57098 gctcggatggatgatggcctccctcggactcccgacaccgagggtatcggcggtattc 57157

Query: 2086 actcgagcagttaatcaccttctaccatcaactcctccaagcgacctagccatgcc 2145  
||||| ||||| ||||||||||||||||| || || | || || | ||| ||| || ||  
Sbjct: 57158 actcaagcagccaatcaccttctaccctcgtcaccgccgaacgatctatgacacacc 57217

Query: 2146 atcaacagccggcgagacacgggagctccatcaacgcttcgcgacccgatgacacga 2204  
||||||| || ||||||| ||||||||||||||||| || ||||| || ||| |||||||  
Sbjct: 57218 atcaacagtgcggagacgcgaggctccatcaatgcctcgcgtgaacgacgacacga 57276

Score = 52.0 bits (26), Expect = 0.015  
Identities = 36/38 (94%), Gaps = 1/38 (2%)  
Strand = Plus / Plus

Query: 561 gttgtgggggatagatatcccc-gggtccactagaagg 597  
||||||||||| ||||||||| |||||||||

Sbjct: 46183 gttgtggggacagatatccccgggtccactagaagg 46220

Score = 50.1 bits (25), Expect = 0.057  
Identities = 28/29 (96%)  
Strand = Plus / Plus

Query: 1621 gtcctttctaccccgacgtccttcat 1649  
||||| ||||||||||||||||||||||||  
Sbjct: 56708 gtcctattctaccccgacgtccttcat 56736

Score = 48.1 bits (24), Expect = 0.23  
Identities = 45/52 (86%)  
Strand = Plus / Plus

Query: 1763 gacatcacgaggctggggaacgggatccggcgcaaccgtatccgggacga 1814  
||||||||||| ||||| ||||| || ||||||||| ||||| || |||||  
Sbjct: 56847 gacatcacgaggccggggagcgggaccagcgcgaaccatatacagagacga 56898

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Minus

Query: 1168 aaacaccgacagctggcgccaggtagggg 1198  
|||| ||||||| |||||||||||||||||  
Sbjct: 38168 aaacgccgacagttggcgccaggtagggg 38138

Score = 44.1 bits (22), Expect = 3.5  
Identities = 28/30 (93%)  
Strand = Plus / Minus

Query: 298 atttgtttgatggatttagtaaaggttatg 327  
||||||||| ||||||||||| |||||||||  
Sbjct: 144300 atttgtttgatggatttagtagaggttatg 144271

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

Score = 111 bits (56), Expect = 2e-20  
Identities = 155/188 (82%)  
Strand = Plus / Plus

Query: 1150 ggtgtgCGGACGGACTCTAAACACCGACAGCTGGCGGCCAGGTAGGGGGTGTGTCTTTG 1209  
||||||| ||||| | ||||||||||||||||||||||||||||||||||| |  
Sbjct: 164744 ggtgtgCGGTCCGACCCAAAACACCGACAGCTGGCGGCCAGGTAGGGGGTGTGTGCGACG 164803

Query: 1210 atctgagctagctcaatgaccattacctccaaatgcaagatcgcccttcgccccgggact 1269  
||| ||||||||||||| || | |||| | | ||||||||||| | || ||||| ||  
Sbjct: 164804 atccaagctagctcaatggccgtcaccttccacagcaagatcgccgtgCGTCCCgGATCT 164863

Query: 1270 atgttttGCTTTGGAACCATCTCATCCATAGCAGATGAAGAGGGAACCTCTGCACCGCATA 1329  
| || ||||| || || ||||||| |||| ||||||||||||||| || ||||| |  
Sbjct: 164864 gtattctGCTTCGGGACAATCTCATCTGTAGCGGATGAAGAGGGAATTCTACACCGCTC 164923

Query: 1330 gcagatct 1337  
|||||||  
Sbjct: 164924 gcagatct 164931

Score = 93.7 bits (47), Expect = 4e-15  
Identities = 110/131 (83%)  
Strand = Plus / Plus

Query: 1912 gagcaagccgagcaaggtgcaaggctgCGCCGAGAGAAATGCTCTCTTTGCTCGGAACCTG 1971  
||||||||||||||||| ||||||| || || ||||| | ||||| | || |||||  
Sbjct: 165458 gagcaagccgagcaagatgcaaggcaacgacgCGAGAAATCCGCTCTTCGGGCGAACCTG 165517

Query: 1972 taccccgacttcgctcgtgcaatgaacacgCGGAGTGAAGTCGGAGGGTACTGGCCAG 2031  
||||||||||||||| || || ||||||||||||||| ||||||||||||| || || || |  
Sbjct: 165518 aaccCGACTTCGCCGAGCTATGAACACGCGAGCGAAGTCGGAGGCGTTCTAGCTCGG 165577

Query: 2032 atagctgacgg 2042  
|||||||||||  
Sbjct: 165578 atagctgacgg 165588

Score = 48.1 bits (24), Expect = 0.23

Identities = 31/32 (96%), Gaps = 1/32 (3%)  
Strand = Plus / Plus

Query: 562 ttgtgggggatagatatcccc-gggtccacta 592  
|||||  
Sbjct: 177802 ttgtgggggatagatatcccctgggtccacta 177833

Score = 46.1 bits (23), Expect = 0.90  
Identities = 30/31 (96%), Gaps = 1/31 (3%)  
Strand = Plus / Plus

Query: 563 tgtgggggatagatatcccc-gggtccacta 592  
|||||  
Sbjct: 164160 tgtgggggatagatatcccctgggtccacta 164190

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Minus

Query: 1168 aaacaccgacagctggcgccaggtagggg 1198  
||||  
Sbjct: 187569 aaacgccgacagttggcgccaggtagggg 187539

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

Score = 111 bits (56), Expect = 2e-20  
Identities = 155/188 (82%)  
Strand = Plus / Minus

Query: 1150 ggtgtgcggacggactctaaacaccgacagctggcgccaggtagggggtgtgtctttg 1209  
|||||  
Sbjct: 156890 ggtgtgcggtcggaccctaaacaccgacagctggcgccaggtagggggtgtgtcgacg 156831

Query: 1210 atctgagctagctcaatgaccattacctccaaatgcaagatcgcccttcgccccgggact 1269  
|||  
Sbjct: 156830 atccaagctagctcaatggccgtcaccttccacagcaagatcgccgtgcgtcccggatct 156771



Identities = 91/107 (85%)  
Strand = Plus / Minus

Query: 1912 gagcaagccgagcaaggtgcaaggctgcccagagagaatgctctctttgctcggaacctg 1971  
|||||  
Sbjct: 22203 gagcaagccgagcaagatgcaaggcaacgacgcgagaatccgctcttcggcgcaacttg 22144

Query: 1972 taccgacttcgctcgtgcaatgaacacgccgagtgaagtcggagg 2018  
|||||  
Sbjct: 22143 aaccgacttcgctcgagctatgaacacgccgagcgaagtcggagg 22097

Score = 48.1 bits (24), Expect = 0.23  
Identities = 31/32 (96%), Gaps = 1/32 (3%)  
Strand = Plus / Minus

Query: 562 ttgtgggggatagatatcccc-gggtccacta 592  
|||||  
Sbjct: 10274 ttgtgggggatagatatcccctgggtccacta 10243

Score = 48.1 bits (24), Expect = 0.23  
Identities = 24/24 (100%)  
Strand = Plus / Minus

Query: 1627 ttctaccccgacgtcctcttcac 1650  
|||||  
Sbjct: 22473 ttctaccccgacgtcctcttcac 22450

Score = 48.1 bits (24), Expect = 0.23  
Identities = 31/32 (96%), Gaps = 1/32 (3%)  
Strand = Plus / Minus

Query: 562 ttgtgggggatagatatcccc-gggtccacta 592  
|||||  
Sbjct: 143832 ttgtgggggatagatatcccctgggtccacta 143801

Score = 46.1 bits (23), Expect = 0.90

Identities = 29/31 (93%)  
Strand = Plus / Plus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198  
||||| ||||||| ||||||||||||||||||  
Sbjct: 8539 aaacgccgacagttggcgcgccaggtagggg 8569

Score = 46.1 bits (23), Expect = 0.90  
Identities = 30/31 (96%), Gaps = 1/31 (3%)  
Strand = Plus / Minus

Query: 563 tgtgggggatagatatcccc-gggtccacta 592  
||||||||||||||||||||| |||||||||  
Sbjct: 23516 tgtgggggatagatatcccctgggtccacta 23486

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Plus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198  
||||| ||||||| ||||||||||||||||||  
Sbjct: 134065 aaacgccgacagttggcgcgccaggtagggg 134095

Score = 46.1 bits (23), Expect = 0.90  
Identities = 30/31 (96%), Gaps = 1/31 (3%)  
Strand = Plus / Minus

Query: 563 tgtgggggatagatatcccc-gggtccacta 592  
||||||||||||||||||||| |||||||||  
Sbjct: 157474 tgtgggggatagatatcccctgggtccacta 157444

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

Score = 111 bits (56), Expect = 2e-20  
Identities = 141/168 (83%), Gaps = 1/168 (0%)  
Strand = Plus / Plus



Sbjct: 111101 gggtaaccccggtgtgcggtcggaccacaaacaccgacagctggcgcgccaggtagggg 111042

Query: 1199 gtgtgtctttgatctgagctagctcaatgaccattacctccaaatgcaagatcgcccttc 1258

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

Sbjct: 111041 gtgtgtcgacgatccaagctagctcaatggccgtcaccttccacagcaagatcatcgtgc 110982

Query: 1259 gccccgggactatgttttgctttggaacatctcatccatagcagatgaagagggaaactc 1318

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

Sbjct: 110981 gtccccgatctgtattctgcttcgggacaatctcatctgtagcggatgaagagggaaattc 110922

Query: 1319 tgcaccgcatagcagatct 1337

| ||||| |||||

Sbjct: 110921 tacaccgcatcgcagatct 110903

Score = 87.7 bits (44), Expect = 3e-13

Identities = 107/128 (83%)

Strand = Plus / Minus

Query: 1912 gagcaagccgagcaaggtgcaaggtgcgccgagagaatgctctctttgctcggaacctg 1971

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

Sbjct: 110376 gagcaagccgagcaagatgagaggcaacgccgggagaatccgctcttcgggcgaacctg 110317

Query: 1972 taccgccacttcgctcgtgcaatgaacacgccgagtgcaagtcggaggggtactggccag 2031

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

Sbjct: 110316 aaccgccacttcgccgagctatgaacacgccgaagtcggaggggtacttagctcgg 110257

Query: 2032 atagctga 2039

|||||||

Sbjct: 110256 atagctga 110249

Score = 60.0 bits (30), Expect = 6e-05

Identities = 30/30 (100%)

Strand = Plus / Minus

Query: 563 tgtgggggatagatatccccgggtccacta 592

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

Sbjct: 111690 tgtgggggatagatatccccgggtccacta 111661



Sbjct: 1736 cccgaacatgtataaaattgtcca-ctgtctctcttgcacacgaaccatcgagtt 1794

Query: 1101 acaatcaacagcaccgtcctacc--aaaagcaccgcaagggtagccctgggtgtgcgg 1158  
||| || | ||||| |||| | ||||| |||| | ||| ||| ||||| ||||

Sbjct: 1795 acagtcggtaacaccgtgctactccaaaatcacctcgagcggcaaccccggtgcgcgg 1854

Query: 1159 acggactctaaacaccgacagctggcgcgccaggtaggggtgtgtctttgatctgagct 1218  
| ||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 1855 tcagacccaaaacaccgacagctggcgcgccaggtaggggtgtgtcactgatccaagct 1914

Query: 1219 agtcaatgaccattacctccaaatgcaagatcgcccttcgccccgggactatgttttgc 1278  
||| ||||| ||| || | | | ||||| || | ||| || | ||| |||

Sbjct: 1915 agtcaatggacatcactttccagcacaagatcgctctcctccctggatccgtgttctgc 1974

Query: 1279 tttggaaccatctcatccatagcagatgaagaggaactctgcaccgcatagcagatc 1336  
|| ||||| ||||| || ||||| ||||| ||||| || ||||| |||||

Sbjct: 1975 ttcggaaccatctcatccgtggcagacgaagaaggaactctacatcgcatagcggatc 2032

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

Query: 562 ttgtgggggatagatatcccc-gggtccactagaaggcgagaaggcctc 609  
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 1249 ttgtggggacagatatccccgggtccactagaaggcaagaaggcctc 1297

Score = 44.1 bits (22), Expect = 3.5  
Identities = 43/50 (86%)  
Strand = Plus / Plus

Query: 1966 aacctgtaccccgacttcgctcgtgcaatgaacacgccgagtgaagtcgg 2015  
||| ||||| ||||| ||||| || || ||||| ||||| || |||||

Sbjct: 2629 aacctgaaccccgacttcgcccagccatgaacacaccgagcggagtcgg 2678

Score = 44.1 bits (22), Expect = 3.5  
Identities = 31/34 (91%)  
Strand = Plus / Plus

Query: 2168 ggagctccatcaacgcttcgcgcgaccgatgaca 2201  
|||||  
Sbjct: 2831 ggagctccatcaatgcttcgcgcggaacgacgaca 2864

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

Score = 109 bits (55), Expect = 7e-20  
Identities = 184/227 (81%)  
Strand = Plus / Minus

Query: 1966 aacctgtaccccgacttcgctcgtgcaatgaacacgccgagtgaagtcggagggtactg 2025  
|||||  
Sbjct: 25162 aacctgaaccccgacttcgcccagccatgaagacgccgagtgaagtcggaggagtattg 25103

Query: 2026 gccagatagctgacggcctcccgcaacccctagacacggaaggctaccggcggtgctt 2085  
|||  
Sbjct: 25102 gtcggatagctgatggcctccccggactcccgacgctgagggtatcggcggtattc 25043

Query: 2086 actcgagcagttaatcaccttctaccataactaatcctccaagcgacctacgccatgcc 2145  
|||||  
Sbjct: 25042 actcaagcagccaatcatcttctaccctcgctcaccgccgaacgatctacgacacacc 24983

Query: 2146 atcaacagccggcgagacacgggagctccatcaacgcttcgcgca 2192  
|||||  
Sbjct: 24982 atcaacagtcggcgggagcacagagctccatcaacgcttcggtgca 24936

Score = 103 bits (52), Expect = 4e-18  
Identities = 133/159 (83%), Gaps = 2/159 (1%)  
Strand = Plus / Minus

Query: 1071 tctcgtgctccagcacgaaccattgagttacaatcaacagcaccgtcctacc--aaaa 1128  
|||||  
Sbjct: 26022 tctcgtgcccacacgaaccatcgagctacagtcggtaacaccgtcctactcctaaaa 25963

Query: 1129 gcaccgcaagggtagccctgggtgtcggacggactctaaacaccgacagctggcgcg 1188  
|||||  
Sbjct: 25962 gcaccttgagggtaacccgggtgctgggtcggacccaaaacaccgacagctggcgcg 25903

Query: 1189 caggtaggggtgtgtctttgatctgagctagctcaatg 1227  
||||||| ||||||||| | |||| | |||||||||  
Sbjct: 25902 caggtagcgggtgtgtcatcgatccaagctagctcaatg 25864

Score = 56.0 bits (28), Expect = 0.001  
Identities = 49/56 (87%)  
Strand = Plus / Minus

Query: 1759 cggcgacatcacgaggctggggaacgggatccggcgcaaccegtatcccggaaga 1814  
||||||||| || || ||||| ||||||||| ||||| || |||||  
Sbjct: 25357 cggcgacatcacgaggccggagagcgggacccggcgcaacctgtatcgcgagacga 25302

Score = 54.0 bits (27), Expect = 0.004  
Identities = 90/110 (81%), Gaps = 2/110 (1%)  
Strand = Plus / Minus

Query: 1071 tctcgtgctccagcacgaaccattgagttacaatcaacagcacctccta--cccaaaa 1128  
||||||||| ||||||||| ||| ||||| || | ||||||||| || |||||  
Sbjct: 3663 tctcgtgctcccagcacgaaccatcgagctacagtcggtaacaccgtcctactcctaaaa 3604

Query: 1129 gcaccgcaagggtagccctgggtgtgctggacggactctaaacaccgaca 1178  
||||| ||||||| ||| ||||| ||||| ||||| | |||||||||  
Sbjct: 3603 gcaccttgagggtaacccccgggtgctgctggacccaaaacaccgaca 3554

Score = 50.1 bits (25), Expect = 0.057  
Identities = 35/37 (94%), Gaps = 1/37 (2%)  
Strand = Plus / Minus

Query: 562 ttgtggggatagatatcccc-gggtccactagaagg 597  
||||||||| ||||||||| ||||||||| |||||||||  
Sbjct: 4181 ttgtggggacagatatccccgggtccactagaagg 4145

Score = 50.1 bits (25), Expect = 0.057  
Identities = 28/29 (96%)  
Strand = Plus / Minus

Query: 1622 ctcctttctaccccgacgtcctcttcatc 1650  
||||| ||||||||||||||||||||||||||||  
Sbjct: 25491 ctccattctaccccgacgtcctcttcatc 25463

Score = 50.1 bits (25), Expect = 0.057  
Identities = 35/37 (94%), Gaps = 1/37 (2%)  
Strand = Plus / Minus

Query: 562 ttgtgggggatagatatcccc-gggtccactagaagg 597  
||||||||| ||||||||||| ||||||||||||||||  
Sbjct: 26540 ttgtgggggacagatatccccgggtccactagaagg 26504

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Plus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198  
||||| ||||||| ||||||||||||||||||||  
Sbjct: 106752 aaacgccgacagttggcgcgccaggtagggg 106782

Score = 44.1 bits (22), Expect = 3.5  
Identities = 34/38 (89%)  
Strand = Plus / Minus

Query: 884 gccccacggtcgtgtatataaggtccagagggtacccc 921  
||||||||||||| ||||||||||| | ||||||| |||||  
Sbjct: 3860 gccccacggtcgagtatataaggcctagagggcacccc 3823

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

Score = 109 bits (55), Expect = 7e-20  
Identities = 112/131 (85%)  
Strand = Plus / Plus

Query: 798 ggatgagtcagcgagattttcggaagattagttcagtttgcgtattattaggagac 857

|||||  
Sbjct: 207 ggatgagtcagcatgattttcggtagattggttcagtcagttcactattagttaggagat 266

Query: 858 atatgatcctcatgtacgtatggagtgccccacggctcgtgtatataaggtccagaggta 917  
| |||||  
Sbjct: 267 acgtgatcatcatgtacgtatggagtgccctatggctcgtgtatataaggccaagaggaa 326

Query: 918 ccccatcattt 928  
|||||  
Sbjct: 327 ccccatcattt 337

Score = 44.1 bits (22), Expect = 3.5  
Identities = 37/42 (88%)  
Strand = Plus / Plus

Query: 964 cattcaggagacctcgttgtaacccaccacatatagatcca 1005  
|||||  
Sbjct: 393 cattcaggagaccacttgtaacacaccacatacagatcca 434

>gb|DQ493650.1| Zea mays cultivar A188 bz locus region  
Length = 54821

Score = 105 bits (53), Expect = 1e-18  
Identities = 215/268 (80%), Gaps = 2/268 (0%)  
Strand = Plus / Plus

Query: 1071 tctcgtgcgtccagcacgaaccattgagttacaatcaacagcaccgtcctacc--aaaa 1128  
|||||  
Sbjct: 32418 tctcgtgcgccaacacgaaccatcgagctacagtcggtaacatcgtcctactcctaaaa 32477

Query: 1129 gcaccgcaaggggtagccctgggtgtcggacggactctaaacaccgacagctggcgcgc 1188  
|||||  
Sbjct: 32478 acacctgaggggcaacccgggtgtcggtcggacccaaaacaccgacagccggcgcgc 32537

Query: 1189 caggtagggggtgtgtctttgatctgagctagctcaatgaccattacctccaaatgcaag 1248  
|||||  
Sbjct: 32538 caggtagggggtgtgtagccgatctaagctagctcaatggctcgtcaccttcagcgcaag 32597

Query: 1249 atcgcccttcgccccgggactatgttttgctttggaaccatctcatccatagcagatgaa 1308

```
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 32598 atcacccctccgccccgatccgtgttctgcttcggaactatctcatctgtagccgatgag 32657
```

Query: 1309 gaggaactctgcaccgcatagcagatc 1336

```
|| ||||| || ||||| |||||
Sbjct: 32658 gaaggaactctacatcgattgcagatc 32685
```

Score = 87.7 bits (44), Expect = 3e-13  
Identities = 179/224 (79%)  
Strand = Plus / Plus

Query: 1966 aacctgtacccccgacttcgctcgtgcaatgaacacgccgagtgaagtcggagggtactg 2025

```
||||| ||||||| ||||| || || ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 33289 aacctgaacccccgacttcgcccggagccatgaatacgccaagtgaagtcggaggagtactg 33348
```

Query: 2026 gccagatagctgacggcctcccgcaaccctagacacggaaggctaccggcggtgctt 2085

```
|| | ||||| || ||||| || || | ||| || ||||| || || |||||
Sbjct: 33349 gctcggatagctgatgggctccctcggactcccgcacgtcgagggtatcgacgactgttc 33408
```

Query: 2086 actcgagcagttaatcaccttctaccatactaatactccaagcgacctacgccatgcc 2145

```
||||| ||||| || || ||||| || || || | || | ||||| |||||
Sbjct: 33409 actcaagcagccaacatcttctacctctcgtcaccgccgaacgacctacgacatgcc 33468
```

Query: 2146 atcaacagccggcgagacacgaggactccatcaacgcttcgcg 2189

```
||||||| || || ||| ||||| ||||| || || |||||
Sbjct: 33469 atcaacagtgcgccggacgcggagctccatcaatgcctcgcg 33512
```

Score = 54.0 bits (27), Expect = 0.004  
Identities = 27/27 (100%)  
Strand = Plus / Plus

Query: 1627 ttctacccccgacgtcctcttcatcagg 1653

```
||||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 32965 ttctacccccgacgtcctcttcatcagg 32991
```

>gb|DQ493646.1| Zea mays cultivar CML258 bz locus region  
Length = 66062

Score = 105 bits (53), Expect = 1e-18  
Identities = 215/268 (80%), Gaps = 2/268 (0%)  
Strand = Plus / Plus

Query: 1071 tctcgtgcgtccagcacgaaccattgagttacaatcaacagcaccgtcctaccc--aaaa 1128  
||||||| ||| ||||||||| ||| |||| | | || ||||||||| | ||||  
Sbjct: 43660 tctcgtgcgcccacacgaaccatcgagctacagtcggttaacatcgctcctactcctaaaa 43719

Query: 1129 gcaccgcaagggtagccctgggtgtgcggacggactctaaacaccgacagctggcgcg 1188  
|||| | ||||| | ||| ||||||||| ||||| | ||||||||| |||||||  
Sbjct: 43720 acacctcgaggggcaaccccgggtgtgcggtcggacccaaaacaccgacagccggcgcg 43779

Query: 1189 caggtaggggtgtgtctttgatctgagctagctcaatgaccattacctcaaatacaag 1248  
||||||||||| ||||| ||||||||| ||| | ||||| | | |||||  
Sbjct: 43780 caggtaggggtgtgttagccgatctaagctagctcaatggctcgtcacctccagcgcaag 43839

Query: 1249 atcgcccttcgccccgggactatgttttgccttggaaacctctcatccatagcagatgaa 1308  
||| |||| ||||||| | |||| |||| |||| ||||||| |||| |||||  
Sbjct: 43840 atcacctccgccccgatccgtgtctctgcttcggaactatctcatctgtagccgatgag 43899

Query: 1309 gagggaaactctgcaccgcatagcagatc 1336  
|| |||||||| || ||||| |||||||  
Sbjct: 43900 gaaggaactctacatcgattgcagatc 43927

Score = 87.7 bits (44), Expect = 3e-13  
Identities = 179/224 (79%)  
Strand = Plus / Plus

Query: 1966 aacctgtaccccgacttcgctcgtgcaatgaacacgccgagtgagtcggaggggtactg 2025  
||||||| ||||||||| || || ||||| ||||| ||||||||| |||||||  
Sbjct: 44531 aacctgaaccccgacttcgcccagccatgaatacgccaagtgaagtcggaggagtactg 44590

Query: 2026 gccagatagctgacggcctcccgcgaaccctagacacggaaggctaccggcggtgctt 2085  
|| | ||||||||| || ||||| || || | ||| || ||||||| || |||||  
Sbjct: 44591 gctcggatagctgatgggtccctcggactcccgcagctcggaggctatcgacgactgttc 44650

Query: 2086 actcgagcagttaatcaccttctaccatcactaatcctccaagcgacctacgcatgcc 2145  
|||| ||||| || || ||||||||| || || | || || | ||||||||| |||||||  
Sbjct: 44651 actcaagcagccaaccatcttctacctctcgtcaccgccgaacgacctacgacatgcc 44710

Query: 2146 atcaacagccggcgagacacgaggctccatcaacgcttcgcg 2189  
||||||| || || ||| ||||||||||||||||| || |||||  
Sbjct: 44711 atcaacagtcgcccgggacgcgaggctccatcaatgcctcgcg 44754

Score = 54.0 bits (27), Expect = 0.004  
Identities = 27/27 (100%)  
Strand = Plus / Plus

Query: 1627 ttctaccccgacgtcctcttcatcagg 1653  
|||||||||||||||||||||||||||  
Sbjct: 44207 ttctaccccgacgtcctcttcatcagg 44233

>gb|AF448416.1| Zea mays B73 chromosome 9S bz genomic region  
Length = 106186

Score = 105 bits (53), Expect = 1e-18  
Identities = 215/268 (80%), Gaps = 2/268 (0%)  
Strand = Plus / Plus

Query: 1071 tctcgtgctccagcacgaaccattgagttacaatcaacagcaccgtcctacc--aaaa 1128  
||||||| ||| ||||||||| ||| |||| | | ||||||||| | ||||  
Sbjct: 82798 tctcgtgcccacacgaaccatcgagctacagtcgtaacatcgtcctactcctaaaa 82857

Query: 1129 gcaccgcaagggtagccctgggtgtgcgacggactctaaacaccgacagctggcgcg 1188  
|||| | |||| | ||| ||||||||| |||| | ||||||||| |||||  
Sbjct: 82858 acacctcgaggggaaccccggtgtgcggtcggacccaaaacaccgacagccggcgcg 82917

Query: 1189 caggtaggggtgtgtctttgatctgagctagctcaatgaccattacctccaatgcaag 1248  
||||||||||||||| |||| ||||||||||||| | | |||| | | |||||  
Sbjct: 82918 caggtaggggtgtgtagccgatctaagctagctcaatggctgcaccttccagcgaag 82977

Query: 1249 atcgcccttcgccccgggactatgttttgctttggaaccatctcatccatagcagatgaa 1308  
||| ||| ||||||| | ||| |||| |||| ||||||| |||| |||||  
Sbjct: 82978 atcacctccgccccgatccgtgttctgcttcggaactatctcatctgtagccgatgag 83037

Query: 1309 gaggaactctgcaccgcatagcagatc 1336  
|| |||||||| | |||| |||||||  
Sbjct: 83038 gaaggaactctacatgcattgcagatc 83065

Score = 87.7 bits (44), Expect = 3e-13  
Identities = 179/224 (79%)  
Strand = Plus / Plus

Query: 1966 aacctgtacccccgacttcgctcgtgcaatgaacacgccgagtggaagtcggaggggtactg 2025  
||||| ||||||||| || || ||||| ||||| ||||||||| |||||  
Sbjct: 83669 aacctgaacccccgacttcgcccagccatgaatacgcgaagtggaagtcggaggagtactg 83728

Query: 2026 gccagatagctgacggcctcccgcgaacctagacacggaaggtaccggcggtgctt 2085  
|| | ||||||||| || ||||| || || | ||| || ||||| || || ||| |  
Sbjct: 83729 gctcggatagctgatgggctccctcggactcccgacgtcggggctatcgacgactgttc 83788

Query: 2086 actcgagcagttaatcaccttctaccatcactaatcctccaagcgacctacgcatgcc 2145  
|||| ||||| || || ||||||||| || || | || | ||||||||| |||||  
Sbjct: 83789 actcaagcagccaaccatcttctacctctcgctcaccgccgaacgacctacgacatgcc 83848

Query: 2146 atcaacagccggcgagacacgcggagctccatcaacgcttcgcg 2189  
||||||| || || ||| ||||||||| || || |||||  
Sbjct: 83849 atcaacagtgcgggacgcggagctccatcaatgcctcgcg 83892

Score = 54.0 bits (27), Expect = 0.004  
Identities = 27/27 (100%)  
Strand = Plus / Plus

Query: 1627 ttctaccccgacgtcctcttcatcagg 1653  
||||||||||| |||||||||  
Sbjct: 83345 ttctaccccgacgtcctcttcatcagg 83371

>gb|AY664416.1| Zea mays cultivar Mo17 locus bz, complete sequence  
Length = 203581

Score = 105 bits (53), Expect = 1e-18  
Identities = 215/268 (80%), Gaps = 2/268 (0%)  
Strand = Plus / Plus

Query: 1071 tctcgtgcgtccagcacgaaccattgagttacaatcaacagcaccgtcctacc--aaaa 1128  
||||||| ||| ||||||||| ||| ||||| || | || ||||||||| | |||||

Sbjct: 71429 tctcgtgcgcccacacgaaccatcgagctacagtcggtaacatcgctcctactcctaaaa 71488

Query: 1129 gcaccgcaaggggtagccctgggtgtcggacggactctaaacaccgacagctggcgcgc 1188

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Sbjct: 71489 acacctcgaggggcaaccccggtgtcggtcggacccaaaacaccgacagccggcgcgc 71548

Query: 1189 caggtaggggtgtgtctttgatctgagctagctcaatgaccattacctcaaagcaag 1248

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

Sbjct: 71549 caggtaggggtgtgtagccgatctaagctagctcaatggctcgtcacctccagcgaag 71608

Query: 1249 atcgcccttcgccccgggactatgttttgctttggaaccatctcatccatagcagatgaa 1308

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

Sbjct: 71609 atcaccctccgccccggatccgtgttctgcttcggaactatctcatctgttagccgatgag 71668

Query: 1309 gagggaaactctgcaccgcatagcagatc 1336

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

Sbjct: 71669 gaaggaactctacatcgattgcagatc 71696

Score = 87.7 bits (44), Expect = 3e-13  
Identities = 179/224 (79%)  
Strand = Plus / Plus

Query: 1966 aacctgtaccccgaacttcgctcgtgcaatgaacacgccgagtggaagtcggaggggtactg 2025

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

Sbjct: 72300 aacctgaaccccgaacttcgcccagccatgaatacggcaagtggaagtcggaggggtactg 72359

Query: 2026 gccagatagctgacggcctcccgcgaaccctagacacggaaggctaccggcggtgctt 2085

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

Sbjct: 72360 gctcggatagctgatgggctccctcggactcccgcagctcggaggctatcgacgactgttc 72419

Query: 2086 actcgagcagttaatcaccttctaccatcactaatcctccaagcgacctacgccatgcc 2145

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

Sbjct: 72420 actcaagcagccaaccatcttctacctctcgtcaccgccgaacgacctacgacatgcc 72479

Query: 2146 atcaacagccggcgagacacgcggagctccatcaacgettcgcg 2189

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

Sbjct: 72480 atcaacagtcgccgggacgcgcggagctccatcaatgcctcgcg 72523

Score = 54.0 bits (27), Expect = 0.004  
Identities = 27/27 (100%)  
Strand = Plus / Plus

Query: 1627 ttctaccccgacgtcctcttcatcagg 1653  
|||||  
Sbjct: 71976 ttctaccccgacgtcctcttcatcagg 72002

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Minus

Query: 1168 aaacaccgacagctggcgccaggtagggg 1198  
|||| |  
Sbjct: 29682 aaacgccgacagttggcgccaggtagggg 29652

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Minus

Query: 1168 aaacaccgacagctggcgccaggtagggg 1198  
|||| |  
Sbjct: 121172 aaacgccgacagttggcgccaggtagggg 121142

>gb|AY664415.1| Zea mays cultivar B73 locus 9009, complete sequence  
Length = 323584

Score = 105 bits (53), Expect = 1e-18  
Identities = 224/281 (79%)  
Strand = Plus / Minus

Query: 1912 gagcaagccgagcaaggtgcaaggctgcccagagagaatgctctctttgctcggaacctg 1971  
|||||  
Sbjct: 109929 gagcaagccgagcaagatgcaaggcaacgacgagagaatccgctcttcgggcaacctg 109870

Query: 1972 taccggacttcgctcgtgcaatgaacacgccgagtgagtcggaggggtactggcccag 2031  
|||||  
Sbjct: 109869 aacccgacttcgcccagccatgaatacggcagcgaagtcggagggcgttctagcccag 109810

Query: 2032 atagctgacggcctcccgcgaaccctagacacggaaggctaccggcggtgcttactcga 2091  
|||||  
Sbjct: 109809 atagctgacggacttcctcggacccccgacgccgaggataccggcgctgttcaactcag 109750

Query: 2092 gcagttaatcaccttctaccatcaactaatcctccaagcgacctacgccatgccatcaac 2151  
|||||  
Sbjct: 109749 gcagccaaccatcttctaccgctcgtcatccgccgaacgacctgacgacgccatcaac 109690

Query: 2152 agccggcgagacacgaggagctccatcaacgcttcgcgga 2192  
|||  
Sbjct: 109689 agtcgtcgagacgcacgaagctctatcaatgcttcgcgga 109649

Score = 91.7 bits (46), Expect = 2e-14  
Identities = 70/78 (89%)  
Strand = Plus / Minus

Query: 1150 ggtgtgcgacggactcctaacaccgacagctggcgccaggtaggggtgtgtctttg 1209  
|||||  
Sbjct: 110643 ggtgtgcggtcggaccctaacaccgacagctggcgccaggtaggggtgtgtcgacg 110584

Query: 1210 atctgagctagctcaatg 1227  
|||  
Sbjct: 110583 atccaagctagctcaatg 110566

Score = 48.1 bits (24), Expect = 0.23  
Identities = 31/32 (96%), Gaps = 1/32 (3%)  
Strand = Plus / Minus

Query: 562 ttgtgggggatagatatcccc-gggtccacta 592  
|||||  
Sbjct: 97420 ttgtgggggatagatatcccctgggtccacta 97389

Score = 48.1 bits (24), Expect = 0.23  
Identities = 24/24 (100%)  
Strand = Plus / Minus





Query: 2086 actcgagcagttaatcaccttctacccatcactaatcctccaagcagcctacgccatgcc 2145  
||||| |||| ||| || ||||| || | || ||||| ||||| ||||| |||||  
Sbjct: 3584 actcgggcagctaaccatcttctgcctcttgcctcatcctccgagcgatctacgacatgcc 3643

Query: 2146 atcaacagccggcgagacacgcggagctccatcaacgcttcgcgc 2190  
||||| || || | ||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 3644 atcaatagtcgatgggacgcgcggagctccatcaatgcttcgcgc 3688

Score = 54.0 bits (27), Expect = 0.004  
Identities = 39/43 (90%)  
Strand = Plus / Plus

Query: 1622 ctcttttctaccccgacgtcctcttcatcagggggagattgga 1664  
|||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 3132 ctccattctaccctgacgtcctcttcatcggggggagagtgga 3174

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

Score = 101 bits (51), Expect = 2e-17  
Identities = 90/103 (87%)  
Strand = Plus / Minus

Query: 1125 aaaagcaccgcaagggtagccctgggtgtgcggacggactctaaacaccgacagctggc 1184  
||||| |||| | ||| ||||| ||||| | ||||| ||||| |||||  
Sbjct: 109028 aaaagcaccgtgaggggcaaccccggtgtgcggtcggacccaaaacaccgacagctggc 108969

Query: 1185 gcgccaggtaggggtgtgtctttgatctgagctagctcaatg 1227  
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 108968 gcgccaggtaggggtgtgtcgacgatccaagctagctcaatg 108926

Score = 48.1 bits (24), Expect = 0.23  
Identities = 31/32 (96%), Gaps = 1/32 (3%)  
Strand = Plus / Plus

Query: 562 ttgtggggatagatat-ccccgggtccacta 592  
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 3262 ttgtggggatagatatccccgggtccacta 3293

Score = 48.1 bits (24), Expect = 0.23  
Identities = 31/32 (96%), Gaps = 1/32 (3%)  
Strand = Plus / Minus

Query: 562 ttgtgggggatagatatcccc-gggtccacta 592  
|||||  
Sbjct: 99526 ttgtgggggatagatatcccctgggtccacta 99495

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Minus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198  
||||  
Sbjct: 30117 aaacgccgacagttggcgcgccaggtagggg 30087

Score = 46.1 bits (23), Expect = 0.90  
Identities = 23/23 (100%)  
Strand = Plus / Minus

Query: 1628 tctaccccgacgtcctcttcatc 1650  
|||||  
Sbjct: 108558 tctaccccgacgtcctcttcatc 108536

Score = 46.1 bits (23), Expect = 0.90  
Identities = 30/31 (96%), Gaps = 1/31 (3%)  
Strand = Plus / Minus

Query: 563 tgtgggggatagatatcccc-gggtccacta 592  
|||||  
Sbjct: 109596 tgtgggggatagatatcccctgggtccacta 109566

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

Score = 101 bits (51), Expect = 2e-17  
Identities = 90/103 (87%)  
Strand = Plus / Plus

Query: 1125 aaaagcaccgcaagggtagccctgggtgtgcggaaggactctaacaccgacagctggc 1184  
||||||| | ||||| | ||| ||||||||| ||||| | |||||||||  
Sbjct: 419 aaaagcacctcgaggggcaaccccggtgtgcggtcggacccaaaacaccgacagctggt 478

Query: 1185 gcgccaggtaggggtgtgtctttgatctgagctagctcaatg 1227  
||||||| ||||||| ||||| |||||||||  
Sbjct: 479 gcgccaggtaggggtgtgtcactgatccaagctagctcaatg 521

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

Score = 99.6 bits (50), Expect = 7e-17  
Identities = 202/249 (81%), Gaps = 4/249 (1%)  
Strand = Plus / Plus

Query: 982 tgtaaccaccacatata-gatccatccaagaagtagtgtattacgcctctctaagcgg 1040  
||||||| ||||| ||| ||||| | |||||||||  
Sbjct: 271 tgtaaccaccacataaaagatccataaccaggaagtagctgttacgcctctctaagcgg 330

Query: 1041 cccaaacttcagaaaaccgcctatccctctctcgtgcgtccagcacgaaccattgagtt 1100  
||||||| | ||||| | | ||||||||| || ||||||||| || |  
Sbjct: 331 cccaaacctatataaaattgtcca-ctgtctctcgtgcatctagcacgaaccatcgatct 389

Query: 1101 acaatcaacagcaccgtcctacc--aaaagcaccgcaagggtagccctgggtgtgcg 1158  
||| | ||||||||| | ||||||||| | ||||| | ||| ||||| |||||  
Sbjct: 390 acagttggtaacaccgtcctactccaaaagcacctctaggggcaaccccggtgcgcg 449

Query: 1159 acggactctaacaccgacagctggcgcgccaggtaggggtgtgtctttgatctgagct 1218  
||||| | ||||||||| ||||||||| ||||||||| ||||| |||||  
Sbjct: 450 tcggacccaaaacaccgacagctggcgcgccaggaaggggtgtgttactgatccaagct 509

Query: 1219 agctcaatg 1227  
|||||||  
Sbjct: 510 agctcaatg 518

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

Length = 179214

Score = 97.6 bits (49), Expect = 3e-16  
Identities = 163/201 (81%)  
Strand = Plus / Plus

Query: 1137 aggggtagccctgggtgtgcggacggactcctaacaccgacagctggcgcgccaggtagg 1196  
||||||| ||| ||||||||| ||||| | ||||||||| |||||||||  
Sbjct: 94728 aggggtaaccccaggtgtgcggtcggacccaaacaccgacagctggcacgccaggtagg 94787

Query: 1197 ggggtgtgtctttgatctgagctagctcaatgaccattacctccaaatgcaagatcgcct 1256  
||||||| |||| ||||||||| || | |||| | | ||||||| || |  
Sbjct: 94788 ggggtgtgtcgacgatccaagctagctcaatggccgtcacctccacagcaagatcacctg 94847

Query: 1257 tcgccccgggactatgttttgcctttggaacctctcatccatagcagatgaagagggaac 1316  
|| ||||| || | || ||||| || || ||||||| |||| |||||||||  
Sbjct: 94848 gcgtcccggatctgtattctgcttcgggacaatctcatctgtagcggatgaagagggaaat 94907

Query: 1317 tctgcaccgcatagcagatct 1337  
||| ||||| | |||||||  
Sbjct: 94908 tctacaccgctcgcagatct 94928

Score = 85.7 bits (43), Expect = 1e-12  
Identities = 109/131 (83%)  
Strand = Plus / Plus

Query: 1912 gagcaagccgagcaaggtgcaaggctgcgccgagagaatgctctctttgctcggaacctg 1971  
||||||||| ||||||| ||| | ||||| | ||||| | || |||||  
Sbjct: 95455 gagcaagccgagcaagatgcaaggcaacgctgggagaatccgctcttcgggcgcaaccta 95514

Query: 1972 taccocgacttgcctcgtgcaatgaacacgccgagtgcaagtcggagggtactggcccag 2031  
||||||||| || || || ||||||||| ||||||||| ||||| || | |  
Sbjct: 95515 aaccccgactttgcccgagctatgaacacgccgagcgaagtcggaggcgtactagctcgg 95574

Query: 2032 atagctgacgg 2042  
|||||||||  
Sbjct: 95575 atagctgacgg 95585

Score = 48.1 bits (24), Expect = 0.23  
Identities = 24/24 (100%)  
Strand = Plus / Plus

Query: 1627 ttctaccccgacgtcctcttcatc 1650  
|||||  
Sbjct: 95185 ttctaccccgacgtcctcttcatc 95208

Score = 46.1 bits (23), Expect = 0.90  
Identities = 30/31 (96%), Gaps = 1/31 (3%)  
Strand = Plus / Plus

Query: 563 tgtgggggatagatatcccc-gggtccacta 592  
|||||  
Sbjct: 94141 tgtgggggatagatatcccctgggtccacta 94171

Score = 44.1 bits (22), Expect = 3.5  
Identities = 43/50 (86%)  
Strand = Plus / Plus

Query: 1459 acccgaaaaactccgctgtcacttcgccacaaaggagtgacacggat 1508  
|||||  
Sbjct: 95038 acccggaagactccgctgtctacttccccaacaaaagaatggacacggat 95087

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

Score = 97.6 bits (49), Expect = 3e-16  
Identities = 145/177 (81%)  
Strand = Plus / Minus

Query: 1149 ggggtgtcggacggactctaaacaccgacagctggcgcgccaggtaggggtgtgtcttt 1208  
|||||  
Sbjct: 114818 ggggtgtcggcggaccctgacagctggcgcgccaggtaggggtgtgtcgcac 114759

Query: 1209 gatctgagctagctcaatgaccattacctccaaatgcaagatcgcccttcgccccgggac 1268  
|||||  
Sbjct: 114758 gatccaagctagctcaatggccgacaccttcaacagcaagatcacatgcgtcccggatc 114699



Score = 89.7 bits (45), Expect = 7e-14  
Identities = 69/77 (89%)  
Strand = Plus / Minus

Query: 1966 aacctgtaccccgacttcgctcgtgcaatgaacacgccgagtgagtcggaggggtactg 2025  
||||| | ||||||||| || || |||||||||||||||||||||||||||||  
Sbjct: 123323 aacctgaatcccgacttcgccgagctatgaacacgccgagtgagtcggaggggtacta 123264

Query: 2026 gccagatagctgacgg 2042  
|| | |||||||||  
Sbjct: 123263 gctcggatagctgacgg 123247

Score = 85.7 bits (43), Expect = 1e-12  
Identities = 70/79 (88%)  
Strand = Plus / Plus

Query: 1149 ggggtgtcggacggactcctaacaccgacagctggcgcgccaggtaggggtgtgtcttt 1208  
||||||||| |||| | ||||||||||||||||||| |||||||||||||||||  
Sbjct: 28062 ggggtgtcggtcggacccaaacaccgacagctggcgtgccaggtaggggtgtgtcgac 28121

Query: 1209 gatctgagctagctcaatg 1227  
|||| | |||||||||  
Sbjct: 28122 gatccaagctagctcaatg 28140

Score = 81.8 bits (41), Expect = 2e-11  
Identities = 104/125 (83%)  
Strand = Plus / Minus

Query: 1915 caagccgagcaagtgcaaggctgcgccgagagaatgctctctttgctcggaaacctgtac 1974  
||||||||||| ||||||| |||| ||||| | |||| | || ||||| |  
Sbjct: 114101 caagccgagcaagatgcaaggcaacgccgggagaatccgctcttcgggcgaaacctgaat 114042

Query: 1975 cccgacttcgctcgtgcaatgaacacgccgagtgagtcggaggggtactggcccagata 2034  
||||||||||| || || || ||||||||| || ||||||||||||||||| || | |||||  
Sbjct: 114041 cccgacttcgccgagctataaacacgccaaagcgaagtcggaggggtactagctcggata 113982

Query: 2035 gctga 2039  
|||||



Query: 2032 atagctgac 2040  
          |||||  
Sbjct: 61261 atagctgac 61253

Score = 48.1 bits (24), Expect = 0.23  
Identities = 24/24 (100%)  
Strand = Plus / Plus

Query: 1627 ttctaccccgacgtcctcttcac 1650  
          |||||  
Sbjct: 28507 ttctaccccgacgtcctcttcac 28530

Score = 48.1 bits (24), Expect = 0.23  
Identities = 31/32 (96%), Gaps = 1/32 (3%)  
Strand = Plus / Plus

Query: 562 ttgtgggggatagatat-ccccgggtccacta 592  
          |||||  
Sbjct: 41260 ttgtgggggatagatatccccgggtccacta 41291

Score = 48.1 bits (24), Expect = 0.23  
Identities = 24/24 (100%)  
Strand = Plus / Minus

Query: 1627 ttctaccccgacgtcctcttcac 1650  
          |||||  
Sbjct: 61651 ttctaccccgacgtcctcttcac 61628

Score = 48.1 bits (24), Expect = 0.23  
Identities = 31/32 (96%), Gaps = 1/32 (3%)  
Strand = Plus / Minus

Query: 562 ttgtgggggatagatat-ccccgggtccacta 592  
          |||||  
Sbjct: 94022 ttgtgggggatagatatccccgggtccacta 93991

Score = 48.1 bits (24), Expect = 0.23  
Identities = 24/24 (100%)  
Strand = Plus / Minus

Query: 1627 ttctaccccgacgtcctcttcac 1650  
|||||  
Sbjct: 114374 ttctaccccgacgtcctcttcac 114351

Score = 48.1 bits (24), Expect = 0.23  
Identities = 24/24 (100%)  
Strand = Plus / Minus

Query: 1627 ttctaccccgacgtcctcttcac 1650  
|||||  
Sbjct: 123647 ttctaccccgacgtcctcttcac 123624

Score = 46.1 bits (23), Expect = 0.90  
Identities = 30/31 (96%), Gaps = 1/31 (3%)  
Strand = Plus / Plus

Query: 563 tgtgggggatagatat-ccccgggtccacta 592  
|||||  
Sbjct: 27464 tgtgggggatagatatccccgggtccacta 27494

Score = 46.1 bits (23), Expect = 0.90  
Identities = 30/31 (96%), Gaps = 1/31 (3%)  
Strand = Plus / Minus

Query: 563 tgtgggggatagatatcccc-gggtccacta 592  
|||||  
Sbjct: 115417 tgtgggggatagatatcccctgggtccacta 115387

Score = 44.1 bits (22), Expect = 3.5  
Identities = 43/50 (86%)

Strand = Plus / Minus

Query: 1459 acccgaaaaactccgctgtccacttcgccacaaaaggagtggacacggat 1508  
||||| || |||||||||||| ||||| || ||||| || ||||||||||||  
Sbjct: 114521 acccggaagactccgctgtctacttccccgacaaaagaatggacacggat 114472

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

Score = 97.6 bits (49), Expect = 3e-16  
Identities = 139/169 (82%)  
Strand = Plus / Plus

Query: 1168 aaacaccgacagctggcgcgccaggtaggggtgtgtccttgatctgagctagctcaatg 1227  
|||||||||||||||||||||||||||||||| ||||| ||||||||||||||||  
Sbjct: 1920 aaacaccgacagctggcgcgccaggtaggggtgtgtcactgatccaagctagctcaatg 1979

Query: 1228 accattacctccaaatgcaagatcgcccttcgccccgggactatgttttgctttggaacc 1287  
||| || | | | |||||| | | | ||||| | | |||| ||||| |||||  
Sbjct: 1980 gtcacactttccagcacaagattgctctccgccctggatccgtgttctgcttcggaacc 2039

Query: 1288 atctcatccatagcagatgaagagggaactctgcaccgcatagcagatc 1336  
||||||||| | ||||| ||||| ||||||||| || |||||||||||||  
Sbjct: 2040 atctcatccgtggcagacgaagaagggaactctacatcgcatagcagatc 2088

Score = 73.8 bits (37), Expect = 4e-09  
Identities = 86/101 (85%), Gaps = 1/101 (0%)  
Strand = Plus / Plus

Query: 562 ttgtgggggatagatatcccc-gggtccactagaaggcgagaaggcctcgctgtggcca 620  
|||||||||| |||||||||| |||||||||||||| |||||||||| || |||||  
Sbjct: 1198 ttgtgggggacagatatccccgggtccactagaaggcaagaaggcctcacgaaaggcct 1257

Query: 621 cgggccagttaccccgcaaggccatcccttcgtgggtcgag 661  
|||||| ||| |||||||||| |||||||||| |||||  
Sbjct: 1258 cgggccattatttcgcaaggccacccttcgtgggcccag 1298

Score = 58.0 bits (29), Expect = 2e-04

Identities = 47/53 (88%)  
Strand = Plus / Plus

Query: 1149 gggtgtgCGGacggactctaaacaccgacagctggcgcgccaggtaggggtg 1201  
||||| ||| ||||| | ||||||| ||||||||||||||||||| |||||  
Sbjct: 1796 gggtgCGGggtcggacccaaacaccggcagctggcgcgccaggtaggtggtg 1848

Score = 58.0 bits (29), Expect = 2e-04  
Identities = 173/221 (78%)  
Strand = Plus / Plus

Query: 1966 aacctgtaccccgacttcgctcgtgcaatgaacacgccgagtgaagtcggaggggtactg 2025  
||||| ||||||||||||||| || ||||||| ||||| || ||||| || || ||  
Sbjct: 2685 aacctgaaccccgacttcgcccagccatgaacacaccgagcgggtcggtggagtgtg 2744

Query: 2026 gccagatagctgacggcctcccgcgaaccctagacacggaaggctaccggcggtgctt 2085  
|| | ||||| || ||||||| || || | ||| | || ||||| |||||||||  
Sbjct: 2745 gtcggatagccgatggcctccccggactccagatgccgagggtatcggcggtgctc 2804

Query: 2086 actcgagcagttaatcaccttctacccatcactaatctccaagegacctacgcatgcc 2145  
||||| ||| ||| || ||||| || | || ||||||||||||||| ||||| || |  
Sbjct: 2805 actcgggcaactaacatcttctgcctctagctcatcctccaagcgatctacgacacagc 2864

Query: 2146 atcaacagccggcgagacacgcggagctccatcaacgcttc 2186  
||||| || || || ||| | ||||||||||||||| |||||  
Sbjct: 2865 atcaatagtcgacgggacgcacggagctccatcaatgcttc 2905

Score = 54.0 bits (27), Expect = 0.004  
Identities = 39/43 (90%)  
Strand = Plus / Plus

Query: 1622 ctcttttctaccccgacgtcctcttcatcagggggagattgga 1664  
|||| ||||||||||||||||||| ||| ||||||| |||||  
Sbjct: 2353 ctccgttctaccccgacgtcctctttatcggggggagagtgga 2395

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

Score = 97.6 bits (49), Expect = 3e-16  
Identities = 154/189 (81%)  
Strand = Plus / Plus

Query: 1149 ggggtgtgcggacggactcctaacaccgacagctggcgccaggtagggggtgtgtcttt 1208  
|||||  
Sbjct: 18097 ggggtgtgcggtcggacccaaacaccgacagctggcgccaggtagggggtgtgtcgac 18156

Query: 1209 gatctgagctagctcaatgaccattacctccaaatgcaagatcgcccttcgccccgggac 1268  
|||||  
Sbjct: 18157 gatccaagctagctcaatggccgtcactttccacagcaagatcgccgtacgtcccggatc 18216

Query: 1269 tatgttttgctttggaacctctcatccatagcagatgaagaggaactctgcaccgcat 1328  
|||  
Sbjct: 18217 tgtattctgcttcgggacaatctcgtccgtagcggatgaagaaggaattctacaccgct 18276

Query: 1329 agcagatct 1337  
|||||  
Sbjct: 18277 cgcagatct 18285

Score = 93.7 bits (47), Expect = 4e-15  
Identities = 110/131 (83%)  
Strand = Plus / Minus

Query: 1912 gagcaagccgagcaaggtgcaaggctgcgccgagagaatgctctctttgctcggaacctg 1971  
|||||  
Sbjct: 97188 gagcaagccgagcaagatgcaaggcaacgacgcgagaatccgctcttcggcgcaacctg 97129

Query: 1972 tacccccgacttcgctcgtgcaatgaacacgccgagtgcaagtcggaggggtactggcccag 2031  
|||||  
Sbjct: 97128 aacccccgacttcgcccagctatgaatacggcgagcgaagtcggaggcgttctggcccgg 97069

Query: 2032 atagctgacgg 2042  
|||||  
Sbjct: 97068 atagccgacgg 97058

Score = 93.7 bits (47), Expect = 4e-15  
Identities = 71/79 (89%)



Query: 562 ttgtgggggatagatatcccc-gggtccacta 592  
|||||  
Sbjct: 31129 ttgtgggggatagatatcccctgggtccacta 31160

Score = 48.1 bits (24), Expect = 0.23  
Identities = 31/32 (96%), Gaps = 1/32 (3%)  
Strand = Plus / Minus

Query: 562 ttgtgggggatagatatcccc-gggtccacta 592  
|||||  
Sbjct: 85079 ttgtgggggatagatatcccctgggtccacta 85048

Score = 46.1 bits (23), Expect = 0.90  
Identities = 30/31 (96%), Gaps = 1/31 (3%)  
Strand = Plus / Plus

Query: 563 tgtgggggatagatatcccc-gggtccacta 592  
|||||  
Sbjct: 17495 tgtgggggatagatatcccctgggtccacta 17525

Score = 46.1 bits (23), Expect = 0.90  
Identities = 23/23 (100%)  
Strand = Plus / Minus

Query: 1627 ttctaccccgacgtccttctcat 1649  
|||||  
Sbjct: 97458 ttctaccccgacgtccttctcat 97436

Score = 46.1 bits (23), Expect = 0.90  
Identities = 30/31 (96%), Gaps = 1/31 (3%)  
Strand = Plus / Minus

Query: 563 tgtgggggatagatatcccc-gggtccacta 592  
|||||  
Sbjct: 98496 tgtgggggatagatatcccctgggtccacta 98466



Sbjct: 17182 gagcaagccgaacaagatgcaaggcaacgccgggagaatccgctcttcgggcgcaacctg 17123

Query: 1972 taccgccgacttcgctcgtgcaatgaacacgccgagtggaagtcggaggggtactggcccag 2031

|||||  
|||||

Sbjct: 17122 aaccccgacttcgcccgagctatgaacacgccgagcggagtcggaggcgttctagctcgg 17063

Query: 2032 atagctgac 2040

|||||

Sbjct: 17062 atagctgac 17054

Score = 52.0 bits (26), Expect = 0.015

Identities = 44/50 (88%)

Strand = Plus / Minus

Query: 2143 gccatcaacagccggcgagacacgccgagctccatcaacgcttcgcgga 2192

|||||  
|||||

Sbjct: 16951 gccatcaacagtcgccgagacgcggaagctctatcaatgcttcgcgga 16902

Score = 48.1 bits (24), Expect = 0.23

Identities = 57/68 (83%)

Strand = Plus / Minus

Query: 1732 cgacggaggaatagaagccagaacgtcggcgacatcacgaggtggggaacgggatccg 1791

|||||  
|||||

Sbjct: 17350 cgacggaggaatcgacgcaggaacgttcgacgacatcacgcagccggggagcgggatccg 17291

Query: 1792 gcgcaacc 1799

|  
|||||

Sbjct: 17290 gagcaacc 17283

Score = 46.1 bits (23), Expect = 0.90

Identities = 23/23 (100%)

Strand = Plus / Minus

Query: 1627 ttctaccgcgactcctcttcat 1649

|||||

Sbjct: 17452 ttctaccgcgactcctcttcat 17430

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Plus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198  
|||| ||||||| ||||||||||||||||  
Sbjct: 42263 aaacgccgacagttggcgcgccaggtagggg 42293

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Minus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198  
|||| ||||||| ||||||||||||||||  
Sbjct: 109561 aaacgccgacagttggcgcgccaggtagggg 109531

>gb|AC198320.5| Zea mays BAC clone ZMMBBb-334D6 from chromosome 5, complete sequence  
Length = 142632

Score = 97.6 bits (49), Expect = 3e-16  
Identities = 154/189 (81%)  
Strand = Plus / Plus

Query: 1149 ggggtgtgcggacggactctaacaccgacagctggcgcgccaggtagggggtgtgtcttt 1208  
||||||||| ||||| | || ||||||||||||||||||||||||||||||||  
Sbjct: 68045 ggggtgtcggtcggacccaaagcaccgacagctggcgcgccaggtagggggtgtgtcgac 68104

Query: 1209 gatctgagctagctcaatgaccattacctccaaatgcaagatcgcccttcgccccgggac 1268  
||| ||||||||||||| || | |||| | | ||||||||||| | || | ||| |  
Sbjct: 68105 aatccaagctagctcaatggccgtcaccttcacagcaagatcgccgtgctctcggatc 68164

Query: 1269 tatgttttgcctttggaacctctcatccatagcagatgaagaggggaactctgcaccgcat 1328  
||| || |||| || || || ||||||||||| ||||||||||||| ||| ||||| |  
Sbjct: 68165 tatattccgcttcgggacaatttcatccatagcggatgaagaggggaattctacaccgct 68224

Query: 1329 agcagatct 1337  
|||||||

Sbjct: 68225 cgcagatct 68233

Score = 81.8 bits (41), Expect = 2e-11  
Identities = 107/129 (82%)  
Strand = Plus / Plus

Query: 1912 gagcaagccgagcaaggtgcaaggctgcgccgagagaatgctctctttgctcggaacctg 1971  
|||||  
Sbjct: 68760 gagcaagccgaacaagatgcaaggcaagccgggagaatccgctcttcggcgcaacctg 68819

Query: 1972 taccccgacttcgctcgtgcaatgaacacgccgagtgagtcggaggggtactggcccag 2031  
|||||  
Sbjct: 68820 aaccgacttcgcccagctatgaacacgccgagcgaggtcggaggcgttctagctcgg 68879

Query: 2032 atagctgac 2040  
|||||  
Sbjct: 68880 atagctgac 68888

Score = 52.0 bits (26), Expect = 0.015  
Identities = 44/50 (88%)  
Strand = Plus / Plus

Query: 2143 gccatcaacagccggcgagacacgcggagctccatcaacgcttcgcgcga 2192  
|||||  
Sbjct: 68991 gccatcaacagtcgccgagacgcgcgaagctctatcaatgcttcgcgcga 69040

Score = 48.1 bits (24), Expect = 0.23  
Identities = 57/68 (83%)  
Strand = Plus / Plus

Query: 1732 cgacggaggaatagaagccagaacgtgcggcgacatcacgaggtggggaacgggatccg 1791  
|||||  
Sbjct: 68592 cgacggaggaatcgacgcaggaacgttcgacgacatcacgcagccgggagcgggatccg 68651

Query: 1792 gcgcaacc 1799  
|  
Sbjct: 68652 gagcaacc 68659



Identities = 110/131 (83%)  
Strand = Plus / Minus

Query: 1912 gagcaagccgagcaaggtgcaaggctgcgccgagagaatgctctctttgctcggaacctg 1971  
|||||  
Sbjct: 37812 gagcaagccgagcaagatgcaaggcaacgccgggagaatccgctcttcggcgcaacctg 37753

Query: 1972 taccgacttcgctcgtgcaatgaacacgccgagtgagtcggaggggtactggcccag 2031  
|||||  
Sbjct: 37752 aaccgacttcgccgagctatgaacacgccgagtcggaggtcgagggcgttctagctcgg 37693

Query: 2032 atagctgacgg 2042  
|||||  
Sbjct: 37692 atagctgacgg 37682

Score = 93.7 bits (47), Expect = 4e-15  
Identities = 71/79 (89%)  
Strand = Plus / Minus

Query: 1149 ggggtgtcggacggactcctaaacaccgacagctggcgccaggtaggggtgtgtcttt 1208  
|||||  
Sbjct: 38527 ggggtgtcggtcggacccaaacaccgacagctggcgccaggtaggggtgtgtcgac 38468

Query: 1209 gatctgagctagctcaatg 1227  
|||||  
Sbjct: 38467 gatccaagctagctcaatg 38449

Score = 50.1 bits (25), Expect = 0.057  
Identities = 35/37 (94%), Gaps = 1/37 (2%)  
Strand = Plus / Minus

Query: 562 ttgtggggatagatatcccc-gggtccactagaagg 597  
|||||  
Sbjct: 122894 ttgtggggacagatatccccgggtccactagaagg 122858

Score = 48.1 bits (24), Expect = 0.23  
Identities = 31/32 (96%), Gaps = 1/32 (3%)

Strand = Plus / Minus

Query: 562 ttgtgggggatagatat-ccccgggtccacta 592  
|||||  
Sbjct: 25568 ttgtgggggatagatatccccgggtccacta 25537

Score = 48.1 bits (24), Expect = 0.23  
Identities = 24/24 (100%)  
Strand = Plus / Minus

Query: 1627 ttctaccccgacgtcctcttcatc 1650  
|||||  
Sbjct: 38082 ttctaccccgacgtcctcttcatc 38059

Score = 46.1 bits (23), Expect = 0.90  
Identities = 30/31 (96%), Gaps = 1/31 (3%)  
Strand = Plus / Minus

Query: 563 tgtgggggatagatat-ccccgggtccacta 592  
|||||  
Sbjct: 39115 tgtgggggatagatatccccgggtccacta 39085

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Plus

Query: 1168 aaacaccgacagctggcgccaggtagggg 1198  
||||  
Sbjct: 68664 aaacaccgacagctggcgccaggtagggg 68694

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

Score = 95.6 bits (48), Expect = 1e-15  
Identities = 108/128 (84%)  
Strand = Plus / Plus

Query: 1912 gagcaagccgagcaaggtgcaaggctgcgccgagagaatgctctctttgctcggaacctg 1971  
|||||  
Sbjct: 25420 gagcaagccgagcaagatgcaaggcaacgccgggagaatccgctcttcgggcgcaacttg 25479

Query: 1972 taccccgaacttcgctcgtgcaatgaacacgccgagtgaaagtcggaggggtactggcccag 2031  
|||||  
Sbjct: 25480 aaccccgaacttcgctcgagctatgaacacgccgagcgaagtcggaggcgttctagctcgg 25539

Query: 2032 atagctga 2039  
|||||  
Sbjct: 25540 atagctga 25547

Score = 89.7 bits (45), Expect = 7e-14  
Identities = 153/189 (80%)  
Strand = Plus / Plus

Query: 1149 ggggtgtcggacggactcctaacaccgacagctggcgccaggtagggggtgtgtcttt 1208  
|||||  
Sbjct: 24704 ggggtgtcggtcggaccaagaccgacagctggcgccaggtagggggtgtgtcgac 24763

Query: 1209 gatctgagctagctcaatgaccattacctccaaatgcaagatcgcccttcgccccgggac 1268  
|||||  
Sbjct: 24764 gatccaagctagctcaatggccgtcaccttcacagcaaaatcgctgtgctcccggatc 24823

Query: 1269 tatgttttgctttggaacctctcatccatagcagatgaagaggggaactctgcaccgcat 1328  
|||  
Sbjct: 24824 tgtattctgcttcgggacgactctcgtccgtagcagatgaagaaggaattctacaccgct 24883

Query: 1329 agcagatct 1337  
|||||  
Sbjct: 24884 cgcagatct 24892

Score = 48.1 bits (24), Expect = 0.23  
Identities = 24/24 (100%)  
Strand = Plus / Plus

Query: 1627 ttctaccccgacgtcctcttcac 1650  
|||||

Sbjct: 25150 ttctacccccgacgtcctcttcatc 25173

Score = 48.1 bits (24), Expect = 0.23  
Identities = 31/32 (96%), Gaps = 1/32 (3%)  
Strand = Plus / Plus

Query: 562 ttgtgggggatagatatcccc-gggtccacta 592  
|||||  
Sbjct: 37611 ttgtgggggatagatatcccctgggtccacta 37642

Score = 46.1 bits (23), Expect = 0.90  
Identities = 30/31 (96%), Gaps = 1/31 (3%)  
Strand = Plus / Plus

Query: 563 tgtgggggatagatatcccc-gggtccacta 592  
|||||  
Sbjct: 24104 tgtgggggatagatatcccctgggtccacta 24134

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Plus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198  
||||  
Sbjct: 116116 aaacgccgacagttggcgcgccaggtagggg 116146

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

Score = 95.6 bits (48), Expect = 1e-15  
Identities = 207/260 (79%)  
Strand = Plus / Plus

Query: 1942 cgagagaatgctctctttgctcggaacctgtaccccgacttcgctcgtgcaatgaacacg 2001  
|||||  
Sbjct: 7909 cgagagaatcctctccttggacgaaacctgaaccccgacttcgcccgagccatgaacaca 7968

Query: 2002 ccgagtgaagtcggaggggtaactggcccagatagctgacggcctcccgcgaaccctagac 2061  
||||| | ||||| || | |||| | ||||| | ||||| | ||||| | ||||| | |||||  
Sbjct: 7969 ccgagcaaggtcggaggagtgtggctcggatagccgatggcctccccggactccagac 8028

Query: 2062 acggaaggctaccggcggtgcttactcgagcagttaatcaccttctaccatcactaat 2121  
|| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 8029 accaagggtatcggcggtgctcactcgggcagctaaccatcttctgcctctcactcat 8088

Query: 2122 cctccaagcgacctacgcatgccatcaacagccggcgagacacgggagctccatcaac 2181  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 8089 cctccgagcgatctatgacacgcatcaatagtcgacgggacgcacggagctccatcaat 8148

Query: 2182 gcttcgcgcgaccgatgaca 2201  
||||| ||||| ||||| |||||  
Sbjct: 8149 gcttcacggaacgacgaca 8168

Score = 81.8 bits (41), Expect = 2e-11  
Identities = 87/101 (86%), Gaps = 1/101 (0%)  
Strand = Plus / Plus

Query: 562 ttgtgggggatagatat-ccccgggtccactagaaggcgagaaggcctcgcggtggcca 620  
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 6737 ttgtgggggacagatattccccgggtccactagaaggcaagaaggcctcacgaaaggcct 6796

Query: 621 cgggccagttaccccgaaggccatcccttcgtgggtcgag 661  
||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 6797 cgggccattatttcgcaaggccacccttcgtgggtcgag 6837

Score = 54.0 bits (27), Expect = 0.004  
Identities = 151/190 (79%), Gaps = 3/190 (1%)  
Strand = Plus / Plus

Query: 999 agatccatccaagaagtagtgattacgcctctctaagcgcccaaacttcagaaaac 1058  
||||||| ||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 7182 agatccaaaccaggaagtagggtgttacgcctctctaagcgcccaaacctgtataaaat 7241

Query: 1059 cgccta-tcctctctcgctgcgtccagcacgaaccattgagttacaatcaacagcaccgt 1117  
| ||| | ||||| || ||||| || ||||| || ||||| || ||||| || ||||| || |||||  
Sbjct: 7182 agatccaaaccaggaagtagggtgttacgcctctctaagcgcccaaacctgtataaaat 7241

Sbjct: 7242 tgtctactgtctctctctctgcatctagcacgaaactatcaagctacagtcggtaacaccgt 7301

Query: 1118 ccta--ccaaaagcaccgcaagggtagccctgggtgtcggacggactcctaaacaccg 1175  
|||| | | ||||||||| | |||| | || |||| | || |||| | |||||||||

Sbjct: 7302 cctactccaaaagcactcgaggggaaccccggtgcacggtcggacccaaaacaccg 7361

Query: 1176 acagctggcg 1185  
|||||||

Sbjct: 7362 acagctggcg 7371

Score = 46.1 bits (23), Expect = 0.90  
Identities = 38/43 (88%)  
Strand = Plus / Plus

Query: 1622 ctcttttctaccccgacgtcctcttcatcaggggagattgga 1664  
|||| ||||||||||||||||||||| ||| ||||||| ||||

Sbjct: 7603 ctccgttctaccccgacgtcctctttatcgaggggagagtgga 7645

>gb|DQ493647.1| Zea mays cultivar NalTel bz locus region  
Length = 79183

Score = 95.6 bits (48), Expect = 1e-15  
Identities = 153/188 (81%)  
Strand = Plus / Plus

Query: 1149 ggggtgtcggacggactcctaaacaccgacagctggcgcgccaggtaggggtgtgtcttt 1208  
||||||| |||| | ||||||||||||| ||||| |||||||||||||

Sbjct: 46602 ggggtgtcggtcggacccaaaacaccgacagccggcgcgcaaggtaggggtgtgtagcc 46661

Query: 1209 gatctgagctagctcaatgaccattacctccaaatgcaagatcggccttcgccccgggac 1268  
|||| | ||||||||||||| | | |||| | | ||||||| |||| ||||||| |

Sbjct: 46662 gatctaagctagctcaatggctcgtcaccttcagcgcgaagatcacctccgccccggatc 46721

Query: 1269 tatgttttgcctttggaacctctcatccatagcagatgaagaggaactctgcaccgcat 1328  
|||| |||| | |||| | ||||| |||| | ||||| || ||||| || |||||

Sbjct: 46722 cgtgttctgcttcggaactatctcatctgttagccgatgaggaaggaactctacatcgcat 46781

Query: 1329 agcagatc 1336  
|||||||

Sbjct: 46782 tgcagatc 46789

Score = 87.7 bits (44), Expect = 3e-13  
Identities = 179/224 (79%)  
Strand = Plus / Plus

Query: 1966 aacctgtaccccgacttcgctcgtgcaatgaacacgccgagtgagtcggaggggtactg 2025  
||||| ||||||||||||| || || ||||| ||||| ||||||||||||| |||||  
Sbjct: 47393 aacctgaaccccgacttcgcccagccatgaatacggcaagtgaagtcggaggagtactg 47452

Query: 2026 gccagatagctgacggcctcccgcgaaccctagacacggaaggctaccggcggctgctt 2085  
|| | ||||||||| || ||||| || || | ||| || ||||| || || ||| |  
Sbjct: 47453 gctcggatagctgatgggctccctcggactcccgacgtcggaggctatcgacgactgttc 47512

Query: 2086 actcgagcagttaatcaccttctaccatcaactaatcctccaagcgacctacgccatgcc 2145  
|||| ||||| || || ||||||||| || || | || || | ||||||||| |||||  
Sbjct: 47513 actcaagcagccaaccatcttctacctctcgctcaccgccgaacgacctacgacatgcc 47572

Query: 2146 atcaacagccggcgagacacgcggagctccatcaacgcttcgcg 2189  
||||||| || || ||| ||||||||||||| || |||||  
Sbjct: 47573 atcaacagtcgccgggacgcgcggagctccatcaatgcctcgcg 47616

Score = 54.0 bits (27), Expect = 0.004  
Identities = 27/27 (100%)  
Strand = Plus / Plus

Query: 1627 ttctaccccgacgtcctcttcatcagg 1653  
|||||||||||||||||||||||||||  
Sbjct: 47069 ttctaccccgacgtcctcttcatcagg 47095

>gb|AC206303.5| Zea mays BAC clone CH201-328A17 from chromosome 5, complete sequence  
Length = 168620

Score = 93.7 bits (47), Expect = 4e-15  
Identities = 191/239 (79%)  
Strand = Plus / Minus

Query: 1966 aacctgtaccccgacttcgctcgtgcaatgaacacgccgagtgagtcggaggggtactg 2025

||||| ||| ||||||||| || || ||||||||| ||||| ||||| || || ||||| ||  
Sbjct: 166425 aacctgaacctcgacttcgccgagccatgaacacaccgagcgaagttggtggagtattg 166366

Query: 2026 gccagatagctgacggcctcccgcgaaccctagacacggaaggctaccggcggctgctt 2085

||||| ||||||||| ||||||||| ||||| | ||||||| || ||||||| ||||| || |  
Sbjct: 166365 gccggaatagctgatggcctccccgaactccagacaccgagggtattggcgactattc 166306

Query: 2086 actcgagcagttaatcaccttctaccatcactaatcctccaagcgacctacgccatgcc 2145

||||| || | || ||||||||||||| || || ||||| || ||||||||| || || |||||  
Sbjct: 166305 actcgggcggccaaccaccttctacctctcgtctcatccgccgagcgacctgcgacacgcc 166246

Query: 2146 atcaacagccggcgagacacgcggagctccatcaacgcttcgcgcgacctgatgacacga 2204

||||||||| ||||| | | | | ||||||||||||||||||||||||| ||| |||||||||  
Sbjct: 166245 atcaacagtcggcggggcgcaaaagctccatcaacgcttcgcgcgaacgacgacacga 166187

Score = 91.7 bits (46), Expect = 2e-14  
Identities = 107/126 (84%), Gaps = 1/126 (0%)  
Strand = Plus / Plus

Query: 271 tttgatggtatgttaaatttgtgtgtcatttgtttgatggatttagtaaagttatgggt 330

||||||||| ||||| ||||| ||| ||| ||||||||||| ||||||||||| |||||||||  
Sbjct: 97426 tttgatggtgtgttaagtttgagtcaatttgtttggtggatttagtgggagttatgggt 97485

Query: 331 ctagaggatgatttttgttgggtgggttttacagagtttaaactagcggattatatagtg 390

| | ||||||||| ||||||||||||||||| || | ||||||||| |||||||||||||  
Sbjct: 97486 gtgggggtgatttg-gttgggtgggttttgcaaaatttaaactagtgattatatagtg 97544

Query: 391 tataga 396

|||||  
Sbjct: 97545 tataga 97550

Score = 87.7 bits (44), Expect = 3e-13  
Identities = 77/88 (87%)  
Strand = Plus / Minus

Query: 1145 ccctgggtgtgcggacggactctaacaccgacagctggcgcgccaggtaggggtgtgt 1204

||||||||| ||||| ||||| | ||||||||||||||||| | |||||||||||||||||  
Sbjct: 167218 ccctgggtgcgcggtcggacccaaaaccgacagctagtgcgccaggtaggggtgtgt 167159

Query: 1205 ctttgatctgagctagctcaatgacat 1232  
| ||||| ||||||||||||||| ||||  
Sbjct: 167158 cactgatccaagctagctcaatggccat 167131

Score = 48.1 bits (24), Expect = 0.23  
Identities = 39/44 (88%)  
Strand = Plus / Minus

Query: 1762 cgacatcacgagctggggaacgggatccggcgcaaccgtatc 1805  
||||||||||||||| | ||||||||| |||| ||| |||||||||  
Sbjct: 166617 cgacatcacgagccgaggaacgggacccgggtgcagccgtatc 166574

Score = 48.1 bits (24), Expect = 0.23  
Identities = 24/24 (100%)  
Strand = Plus / Minus

Query: 1627 ttctaccccgacgtcctcttcatc 1650  
|||||||||||||||||||||||  
Sbjct: 166749 ttctaccccgacgtcctcttcatc 166726

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Plus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198  
|||| ||||||| |||||||||||||||||  
Sbjct: 2981 aaacgccgacagttggcgcgccaggtagggg 3011

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

Score = 93.7 bits (47), Expect = 4e-15  
Identities = 71/79 (89%)  
Strand = Plus / Minus

Query: 1149 ggggtgtcggacggactctaaacaccgacagctggcgcgccaggtagggggtgtgtcttt 1208



Identities = 29/31 (93%)  
Strand = Plus / Minus

Query: 1168 aaacaccgacagctggcgccaggtagggg 1198  
||||| ||||||| ||||||||||||||||  
Sbjct: 21334 aaacgccgacagttggcgccaggtagggg 21304

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Plus

Query: 1168 aaacaccgacagctggcgccaggtagggg 1198  
||||| ||||||| ||||||||||||||||  
Sbjct: 90226 aaacgccgacagttggcgccaggtagggg 90256

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Plus

Query: 1168 aaacaccgacagctggcgccaggtagggg 1198  
||||| ||||||| ||||||||||||||||  
Sbjct: 139072 aaacgccgacagttggcgccaggtagggg 139102

Score = 46.1 bits (23), Expect = 0.90  
Identities = 30/31 (96%), Gaps = 1/31 (3%)  
Strand = Plus / Minus

Query: 563 tgtgggggatagatatcccc-gggtccacta 592  
||||||||||||||||| ||||||||  
Sbjct: 154049 tgtgggggatagatatcccctgggtccacta 154019

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

Score = 93.7 bits (47), Expect = 4e-15  
Identities = 110/131 (83%)  
Strand = Plus / Plus

Query: 1912 gagcaagccgagcaaggtgcaaggctgcccagagagaatgctctctttgctcggaacctg 1971  
|||||  
Sbjct: 185684 gagcaagccgagcaagatgcaaggcaacccgggagaaatccgctcttcgggcgcaacctg 185743

Query: 1972 taccccgacttcgctcgtgcaatgaacacgccgagtgagtcggaggggtactggcccag 2031  
|||||  
Sbjct: 185744 aaccccgacttcgcccagctatgaacacgccgagtgaggtcagaggcgttctagctcgg 185803

Query: 2032 atagctgacgg 2042  
|||||  
Sbjct: 185804 atagctgacgg 185814

Score = 85.7 bits (43), Expect = 1e-12  
Identities = 70/79 (88%)  
Strand = Plus / Plus

Query: 1149 ggggtgtcggacggactctaaacaccgacagctggcgcgccaggtaggggtgtgtcttt 1208  
|||||  
Sbjct: 184969 ggggtgtcggtcggacccaaaacatcgacagctggcgcgccaggtaggggtgtgtcgac 185028

Query: 1209 gatctgagctagctcaatg 1227  
|||||  
Sbjct: 185029 gatccaagctagctcaatg 185047

Score = 50.1 bits (25), Expect = 0.057  
Identities = 52/61 (85%)  
Strand = Plus / Plus

Query: 1732 cgacggaggaatagaagccagaacgtgcccgcacatcacgagctggggaacgggatccg 1791  
|||||  
Sbjct: 185516 cgacggaggaaccgacgcaggaacgttcgacgacatcacgcgctggagaacgggatccg 185575

Query: 1792 g 1792  
|  
Sbjct: 185576 g 185576

Score = 48.1 bits (24), Expect = 0.23  
Identities = 24/24 (100%)  
Strand = Plus / Plus

Query: 1627 ttctaccccgacgtcctcttcac 1650  
|||||  
Sbjct: 185414 ttctaccccgacgtcctcttcac 185437

Score = 46.1 bits (23), Expect = 0.90  
Identities = 30/31 (96%), Gaps = 1/31 (3%)  
Strand = Plus / Plus

Query: 563 tgtgggggatagatatcccc-gggtccacta 592  
|||||  
Sbjct: 184382 tgtgggggatagatatcccctgggtccacta 184412

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

Score = 93.7 bits (47), Expect = 4e-15  
Identities = 71/79 (89%)  
Strand = Plus / Minus

Query: 1149 ggggtgtgcggacggactctaaacaccgacagctggcgccaggtaggggtgtgtcttt 1208  
|||||  
Sbjct: 160360 ggggtgtgcggacggacccaaaacaccgacagctggcgccaggtaggggtgtgtcgac 160301

Query: 1209 gatctgagctagctcaatg 1227  
|||||  
Sbjct: 160300 gatccaagctagctcaatg 160282

Score = 73.8 bits (37), Expect = 4e-09  
Identities = 220/281 (78%)  
Strand = Plus / Minus

Query: 1912 gagcaagccgagcaaggtgcaaggctgcccagagagaatgctctctttgctcggaacctg 1971  
|||||  
Sbjct: 159645 gagcaagccgagcaagacgcaaggcaacgacgagagaatccgctcttcgggcgcaactg 159586

Query: 1972 taccgccgacttcgctcgtgcaatgaacacgccgagtgaaagtcggaggggtactggcccag 2031  
||||| ||||||||| || || ||||||||||||||||| || ||||||||| || || ||||| |  
Sbjct: 159585 aaccctgacttcgcccagcgatgaacacgccgagcaggctcggagggcgttctagcccgg 159526

Query: 2032 atagctgacggcctcccgcgaaccctagacacggaaggctaccggcggtgcttactcga 2091  
||||||||||| || || || ||||| ||| | || || ||||||||| ||| | |||||  
Sbjct: 159525 atagctgacggacttcctcggacccccgacgccgaggataaccggcgctgttcactcag 159466

Query: 2092 gcagttaatcaccttctaccatcactaatcctccaagcgacctacgccatgccatcaac 2151  
||||| || || ||||||||| || || | || || | ||| || || || |||||||||  
Sbjct: 159465 gcagccaaccatcttctaccgctcgtcaccgccgaacgatctgcgacacgccatcaac 159406

Query: 2152 agccggcgagacacgccgagctccatcaacgcttcgcgca 2192  
|| || ||||||| |||| |||||| |||||| |||||||||  
Sbjct: 159405 agtcgccgagacgcgcaagctctatcaatgcttcgcgca 159365

Score = 69.9 bits (35), Expect = 6e-08  
Identities = 92/111 (82%)  
Strand = Plus / Minus

Query: 1069 tctctcgtgcgtccagcacgaaccattgagttacaatcaacagcaccgtcctaccacaaa 1128  
||||||||||| ||||||||||||||||| ||| ||||| || | || |||||||||||||  
Sbjct: 137188 tctctcgtgcgcccagcacgaaccatcgagctacagtcggtaacatcgtcctaccacaaa 137129

Query: 1129 gcaccgcaaggggtagccctgggtgtgcggacggactctaacaccgacag 1179  
||||| | ||||||| ||||||||| |||| ||| | |||||||||  
Sbjct: 137128 gcacctcgaggggtcaccctgggtgcgcggtcgggtcccaaacaccgacag 137078

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

Query: 562 ttgtgggggatagatatcccc-gggtccactagaaggcgagaaggcctc 609  
||||||||||| ||||||||||| ||||||||||||| |||||||||  
Sbjct: 137705 ttgtgggggacagatatcccccggtccactagaaggttagaaggcctc 137657

Score = 48.1 bits (24), Expect = 0.23  
Identities = 31/32 (96%), Gaps = 1/32 (3%)  
Strand = Plus / Minus

Query: 562 ttgtgggggatagatatcccc-gggtccacta 592  
|||||  
Sbjct: 147600 ttgtgggggatagatatcccctgggtccacta 147569

Score = 48.1 bits (24), Expect = 0.23  
Identities = 42/48 (87%)  
Strand = Plus / Minus

Query: 1752 gaacgtgcggcgacatcacgaggctggggaacgggatccggcgcaacc 1799  
||||| || |||||  
Sbjct: 159793 gaacgttcgacgacatcacgcagctggagaacgggatccggagcaacc 159746

Score = 48.1 bits (24), Expect = 0.23  
Identities = 24/24 (100%)  
Strand = Plus / Minus

Query: 1627 ttctaccccgacgtcctcttcate 1650  
|||||  
Sbjct: 159915 ttctaccccgacgtcctcttcate 159892

Score = 48.1 bits (24), Expect = 0.23  
Identities = 31/32 (96%), Gaps = 1/32 (3%)  
Strand = Plus / Minus

Query: 562 ttgtgggggatagatatcccc-gggtccacta 592  
|||||  
Sbjct: 160955 ttgtgggggatagatatcccctgggtccacta 160924

Score = 46.1 bits (23), Expect = 0.90  
Identities = 38/43 (88%)  
Strand = Plus / Minus

Query: 883 tgccccacggctggtatataaggtccagagggtaccccatca 925  
|||||  
Sbjct: 137385 tgccccacggctgagtatataaggcctagggggcaccccatca 137343

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

Score = 93.7 bits (47), Expect = 4e-15  
Identities = 71/79 (89%)  
Strand = Plus / Plus

Query: 1149 ggggtgtgcggacggactctaaacaccgacagctggcgcgccaggtagggggtgtgtcttt 1208  
|||||  
Sbjct: 111556 ggggtgtgcggctggacccaaaacaccgacagctggcgcgccaggtagggggtgtgtcgac 111615

Query: 1209 gatctgagctagctcaatg 1227  
|||||  
Sbjct: 111616 gatccaagctagctcaatg 111634

Score = 69.9 bits (35), Expect = 6e-08  
Identities = 107/131 (81%)  
Strand = Plus / Plus

Query: 1912 gagcaagccgagcaaggtgcaaggctgcgccgagagaatgctctctttgctcggaacctg 1971  
|||||  
Sbjct: 112271 gagcagccgagcaagatgcaaggcaacgacgcgagagaatccgctcttcgggcgcaacttg 112330

Query: 1972 taccgccacttcgctcgtgcaatgaacacgccgagtggaagtcggaggggtactggcccag 2031  
|||||  
Sbjct: 112331 aaccgccacttcgcccagccgtgaatacaccgagcgaagtcggagggcgttctggcccgg 112390

Query: 2032 atagctgacgg 2042  
|||||  
Sbjct: 112391 atagctgacgg 112401

Score = 48.1 bits (24), Expect = 0.23  
Identities = 24/24 (100%)  
Strand = Plus / Plus

Query: 1627 ttctacccccgacgtcctcttcatc 1650  
|||||  
Sbjct: 112001 ttctacccccgacgtcctcttcatc 112024

Score = 48.1 bits (24), Expect = 0.23  
Identities = 31/32 (96%), Gaps = 1/32 (3%)  
Strand = Plus / Plus

Query: 562 ttgtgggggatagatatcccc-gggtccacta 592  
|||||  
Sbjct: 121910 ttgtgggggatagatatcccctgggtccacta 121941

Score = 46.1 bits (23), Expect = 0.90  
Identities = 30/31 (96%), Gaps = 1/31 (3%)  
Strand = Plus / Plus

Query: 563 tgtgggggatagatatcccc-gggtccacta 592  
|||||  
Sbjct: 110963 tgtgggggatagatatcccctgggtccacta 110993

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

Score = 93.7 bits (47), Expect = 4e-15  
Identities = 110/131 (83%)  
Strand = Plus / Minus

Query: 1912 gagcaagccgagcaaggtgcaaggctgcccagagagaatgctctctttgctcggaacctg 1971  
|||||  
Sbjct: 114625 gagcaagccgagcaagatgcaaggcaacgacgcgagaaatccgctcttcgggagcaacctg 114566

Query: 1972 taccgccacttcgctcgtgcaatgaacacgccgagtggaagtcggagggtactggcccag 2031  
|||||  
Sbjct: 114565 aaccgccacttcgcccagctatgaatacggcgagcgaagtcggaggcgttctggcccag 114506

Query: 2032 atagctgacgg 2042  
|||||  
Sbjct: 114505 atagccgacgg 114495



Score = 61.9 bits (31), Expect = 2e-05  
Identities = 52/59 (88%)  
Strand = Plus / Plus

Query: 2134 ctacgccatgcatcaacagccggcgagacacgaggctccatcaacgcttcgcgga 2192  
||||| || |||||||||||| || |||||| |||| |||||||||||| ||||||||||||  
Sbjct: 128356 ctacgacagccatcaacagtcgccgagacgcggaagctccatcaatgcttcgcgga 128414

Score = 52.0 bits (26), Expect = 0.015  
Identities = 29/30 (96%)  
Strand = Plus / Plus

Query: 1621 gtcctttctaccccgacgtcctcttcac 1650  
||||| ||||||||||||||||||||||||  
Sbjct: 127858 gtcctattctaccccgacgtcctcttcac 127887

Score = 50.1 bits (25), Expect = 0.057  
Identities = 32/33 (96%), Gaps = 1/33 (3%)  
Strand = Plus / Minus

Query: 561 gttgtggggatagatatcccc-gggtccacta 592  
|||||||||||||||||||||||||| ||||||||||||  
Sbjct: 115935 gttgtggggatagatatcccctgggtccacta 115903

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Minus

Query: 1168 aaacaccgacagctggcgccaggtagggg 1198  
|||| |||||| ||||||||||||||||||||  
Sbjct: 85948 aaacgccgacagttggcgccaggtagggg 85918

Score = 46.1 bits (23), Expect = 0.90  
Identities = 23/23 (100%)  
Strand = Plus / Minus



Identities = 109/131 (83%)  
Strand = Plus / Plus

Query: 1912 gagcaagccgagcaaggtgcaaggctgcgccgagagaatgctctctttgctcggaacctg 1971  
||||| ||||||||| ||||||| || || ||||| | ||||||| || ||| ||  
Sbjct: 86537 gagcaggccgagcaagatgcaaggcaacgacgcgagaatccgctctttggcgcaactg 86596

Query: 1972 taccgacttcgctcgtgcaatgaacacgccgagtgagtcggaggggtactggcccag 2031  
||||||||||| || || ||| ||||||| ||||||||| || ||||||| |  
Sbjct: 86597 aaccgacttcgccgagccgtgaatacggcgaagtcggagggcgttctggcccag 86656

Query: 2032 atagctgacgg 2042  
|||||||||  
Sbjct: 86657 atagctgacgg 86667

Score = 48.1 bits (24), Expect = 0.23  
Identities = 24/24 (100%)  
Strand = Plus / Plus

Query: 1627 ttctacccgacgtcctcttcac 1650  
|||||||||||  
Sbjct: 86267 ttctacccgacgtcctcttcac 86290

Score = 48.1 bits (24), Expect = 0.23  
Identities = 31/32 (96%), Gaps = 1/32 (3%)  
Strand = Plus / Plus

Query: 562 ttgtggggatagatatcccc-gggtccacta 592  
||||||||||| |||||||||  
Sbjct: 96175 ttgtggggatagatatcccctgggtccacta 96206

Score = 46.1 bits (23), Expect = 0.90  
Identities = 30/31 (96%), Gaps = 1/31 (3%)  
Strand = Plus / Plus

Query: 563 tgtggggatagatatcccc-gggtccacta 592  
||||||||||| |||||||||

Sbjct: 85229 tgtggggatagatatccccctgggtccacta 85259

>emb|X97604.1| Z.diploperennis DNA for Grandel-4 retrotransposon  
Length = 13779

Score = 93.7 bits (47), Expect = 4e-15  
Identities = 71/79 (89%)  
Strand = Plus / Plus

Query: 1149 ggggtgtgcgacggactctaaacaccgacagctggcgccaggtagggggtgtgtcttt 1208  
||||||| |||| | ||||||||||||||||||||||||||||||||  
Sbjct: 607 ggggtgtgcggtcgaccacaaacaccgacagctggcgccaggtagggggtgtgtcgac 666

Query: 1209 gatctgagctagctcaatg 1227  
|||| ||||||||||||  
Sbjct: 667 gatccaagctagctcaatg 685

Score = 77.8 bits (39), Expect = 3e-10  
Identities = 106/126 (84%), Gaps = 3/126 (2%)  
Strand = Plus / Plus

Query: 1915 caagccgagcaaggtgcaaggctgcgccgagagaatgctctctttg-ctcggaacctgta 1973  
||||||||||| ||||||| |||| ||||| | |||| | ||| ||||| |  
Sbjct: 1328 caagccgagcaagatgcaaggcaacgccgggagaatccattcttcggctc--aacctgaa 1385

Query: 1974 ccccgacttcgctcgtgcaatgaacacgccgagtgaagtcggaggggtactggcccagat 2033  
||||||||||| || || ||||||||||||||| ||||||||||||||||| || | |||  
Sbjct: 1386 tcccgacttcgcccagctatgaacacgccgagcgaagtcggaggggtactagctcgat 1445

Query: 2034 agctga 2039  
|||||  
Sbjct: 1446 agctga 1451

Score = 48.1 bits (24), Expect = 0.23  
Identities = 24/24 (100%)  
Strand = Plus / Plus

Query: 1627 ttctaccccgacgtcctcttcatc 1650

|||||  
Sbjct: 1055 ttctaccccgacgtcctcttcatc 1078

>gb|EF190065.1| Zea mays clone PS52 chromosome B, genomic sequence  
Length = 14530

Score = 89.7 bits (45), Expect = 7e-14  
Identities = 183/229 (79%)  
Strand = Plus / Plus

Query: 1973 accccgacttcgctcgtgcaatgaacacgccgagtggaagtcggaggggtactggcccaga 2032  
|||||  
Sbjct: 3599 accccgacttcgcctgagccatgaacacaccgagcggaggtcggaggagtgttgctcaga 3658

Query: 2033 tagctgacggcctcccgcgaaccctagacacggaaggctaccggcggtgcttactcgag 2092  
|||||  
Sbjct: 3659 tagccgatggcctcccctggactctagacgccgagggtatcgggcggtgctcactcggg 3718

Query: 2093 cagttaatcaccttctaccatcactaatcctccaagcgacctacgccatgccatcaaca 2152  
|||||  
Sbjct: 3719 cagetaaccatcttctgcctctcgtcctccttcgagcgatctacgacacgccatcaata 3778

Query: 2153 gccggcgagacacgcggagctccatcaacgcttcgcgcgaccgatgaca 2201  
|||||  
Sbjct: 3779 gtcgacgggacgcacggagctccatcaatgcttcgcggaacgacgaca 3827

Score = 73.8 bits (37), Expect = 4e-09  
Identities = 195/244 (79%), Gaps = 4/244 (1%)  
Strand = Plus / Plus

Query: 982 tgtaaccaccacatata-gatccatcccaagaagtagtgattacgcctctctaagcgg 1040  
|||||  
Sbjct: 2641 tgtaaccaccacataaaagatccacaccaggaagtagggtgttacgcctctctaagcgg 2700

Query: 1041 cccaaacttgagaaaaccgcctatccctctctcgtgcgtccagcacgaaccattgagtt 1100  
|||||  
Sbjct: 2701 cctgaacctgtataaaattgtccattg-tctctcgtgcatctaacacgaaccatcgagct 2759

Query: 1101 acaatcaacagcaccgtcctacc--aaaagcaccgcaagggtagccctgggtgtgcgg 1158



Query: 1972 taccocgacttcgctcgtgcaatgaacacgccgagtggaagtcggagg 2018  
|||||  
Sbjct: 30522 aaccccgacttcgctcgcgagctatgaacacgccgagcgaagtcggagg 30476

Score = 48.1 bits (24), Expect = 0.23  
Identities = 24/24 (100%)  
Strand = Plus / Minus

Query: 1627 ttctaccccgacgtcctcttcatc 1650  
|||||  
Sbjct: 30852 ttctaccccgacgtcctcttcatc 30829

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

Score = 85.7 bits (43), Expect = 1e-12  
Identities = 282/358 (78%), Gaps = 4/358 (1%)  
Strand = Plus / Plus

Query: 982 tgtaaccaccacatata-gatccatcccaagaagtagtgattacgcctctctaagcgg 1040  
|||||  
Sbjct: 5793 tgtaaccaccacataaaaagatccacactaggaagtaggggtgttacgcctctctaagcgg 5852

Query: 1041 cccaaacttgcaaaaaccgcctatccctctctcgtgcgtccagcagcaaccattgagtt 1100  
||| ||| || | |||| | | | ||||| || | ||||| ||||| ||| |  
Sbjct: 5853 cccgaacctgtataaaattgtcca-ctatctctcgtgcatctagcagcaaccatcgagct 5911

Query: 1101 acaatcaacagcaccgtcctacc--aaaagcaccgcaagggtagccctgggtgtgcgg 1158  
||| || | || ||||| | ||||| | |||| | ||| ||| |||  
Sbjct: 5912 acagtcggtaacatcgtcctactccaaaagcaccaggggcaacccaggtgcgcgg 5971

Query: 1159 acggactctaaacaccgacagctggcgcgccaggtaggggtgtgtctttgatctgagct 1218  
|| || | ||||| || ||||| ||||| ||||| ||||| |||||  
Sbjct: 5972 tcgaacccaaaacaccgacaactagcgcgccaggtaggggtgtgtcactgatccaagct 6031

Query: 1219 agetcaatgaccattacctccaaatgcaagatcgcccttcgccccgggactatgttttgc 1278  
||| ||| || | || | | | ||||| || ||||| || | |||| |||  
Sbjct: 6032 agcttaatggccgtcactttctagcacaagatcgctctcgcctggatccgtgttctgc 6091



truncated rust resistance protein rp3-2t (rp3-2) gene,  
complete sequence  
Length = 276326

Score = 85.7 bits (43), Expect = 1e-12  
Identities = 148/183 (80%)  
Strand = Plus / Plus

Query: 1155 gcgacggactctaacaccgacagctggcgcgccaggtaggggtgtgtctttgatctg 1214  
||||| ||||| | ||||| ||||||||||||||||||||||||||||||||||| |||||  
Sbjct: 27626 gcggtcggacccaaacatcgacagctggcgcgccaggtaggggtgtgtcactgatcca 27685

Query: 1215 agctagctcaatgaccattacctccaaatgcaagatcgcccttcgccccgggactatgtt 1274  
|||||||||||||| || | || | | | ||||| || | || ||||| || | |||||  
Sbjct: 27686 agctagctcaatggccgtcactttccagcacaagattgctctccgcctggatccgtgt 27745

Query: 1275 ttgctttggaaccatctcatccatagcagatgaagaggaactctgcaccgcatagcaga 1334  
||||| || ||||||||||||| | ||||| ||||| ||||||||| || ||||||||| ||  
Sbjct: 27746 ctgcttcgggaccatctcatccgtggcagacgaagaaggaactctacatcgcatagcgga 27805

Query: 1335 tct 1337  
|||  
Sbjct: 27806 tct 27808

Score = 61.9 bits (31), Expect = 2e-05  
Identities = 47/51 (92%), Gaps = 1/51 (1%)  
Strand = Plus / Plus

Query: 563 tgtgggggatagatatccc-cgggtccactagaaggcgagaaggcctcgcg 612  
||||||||| ||||||||||| ||||||||||||||||||| ||||| |||||||  
Sbjct: 27029 tgtgggggacagatatccctcggtccactagaaggctagaagacctcgcg 27079

Score = 52.0 bits (26), Expect = 0.015  
Identities = 89/110 (80%)  
Strand = Plus / Plus

Query: 2068 ggctaccggcggctgcttactcgagcagttaatcaccttctaccatcactaatcctcca 2127  
||||| || |||||||||||||||| ||||| ||| ||||||||| || | || || || || ||  
Sbjct: 43987 ggctatcgacggctgcttactcgggcagctaaccaccttctgcctctcgctcatcgctcg 44046



||||| ||||||| ||||||| ||| ||||||| || |||||||  
Sbjct: 393 taacctaccacataaagatccatgccaggaagtaggggtgttacgc 437

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

Score = 81.8 bits (41), Expect = 2e-11  
Identities = 152/189 (80%)  
Strand = Plus / Plus

Query: 1149 ggggtgtcggacggactctaaacaccgacagctggcgcgccaggtaggggtgtgtcttt 1208  
||||| ||||| ||||||| | ||||||||||||| ||||||| ||||||||||||||||| |  
Sbjct: 151640 ggggtgcgcggtcggacccaaaacaccgacagttggcgcaccaggtaggggtgtgtcact 151699

Query: 1209 gatctgagctagctcaatgaccattacctccaaatgcaagatcgccttcgccccggac 1268  
||||| ||||||| ||||||| ||| ||| | | ||||||| ||| ||||| |||  
Sbjct: 151700 gatccaagctagatcaatggccgtcacttttcagcacaagatcttctctgccccaggtc 151759

Query: 1269 tatgttttgctttggaaccatctcatccatagcagatgaagaggaactctgcaccgcat 1328  
||||| ||||||| ||||||||||||||||| | ||||||| ||||||| ||||||||| |||||||||  
Sbjct: 151760 catgtttctgcttcggaaccatctcatccgtggcagacgaagaaggaactctacaccgcat 151819

Query: 1329 agcagatct 1337  
|| |||||  
Sbjct: 151820 cgcgatct 151828

Score = 77.8 bits (39), Expect = 3e-10  
Identities = 144/179 (80%)  
Strand = Plus / Plus

Query: 1930 gcaaggtcgcgccgagagaatgctctctttgctcggaaacctgtacccccgacttcgctcgt 1989  
||||||| ||||||||||||| ||||| | | ||||||||| ||||||||||||| ||  
Sbjct: 152394 gcaaggcaacgccgagagaatcctcttctcggcggaacctaaacccccgacttcgcccga 152453

Query: 1990 gcaatgaacacgccgagtgaagtcggaggggtactggcccagatagctgacggcctccc 2049  
|| ||||||||||||||||| ||||||| | || ||||| | ||||||| ||||| |||  
Sbjct: 152454 gccatgaacacgccgagtgaggtcgggtgaagtgttgctcggatagccgacggcttccc 152513

Query: 2050 cgaaccctagacacggaaggctaccggcggtgcttactcgagcagttaatcaccttct 2108

||||| | |||| | ||||||| ||||||||| |||| ||| || |||||  
Sbjct: 152514 cgaactccagacgctgaaggctatcggggctgctcactcgggcagctaaccatcttct 152572

Score = 56.0 bits (28), Expect = 0.001  
Identities = 31/32 (96%)  
Strand = Plus / Plus

Query: 1622 ctctttctaccccgacgtcctcttcatcagg 1653  
|||| ||||||||| ||||||||| |||||  
Sbjct: 152101 ctccattctaccccgacgtcctcttcatcagg 152132

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Plus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198  
|||| ||||||| ||||||||| |||||||  
Sbjct: 14604 aaacgccgacagttggcgcgccaggtagggg 14634

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Plus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198  
|||| ||||||| ||||||||| |||||||  
Sbjct: 134363 aaacgccgacagttggcgcgccaggtagggg 134393

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Plus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198  
|||| ||||||| ||||||||| |||||||  
Sbjct: 135467 aaacgccgacagttggcgcgccaggtagggg 135497

Score = 46.1 bits (23), Expect = 0.90  
Identities = 42/47 (89%), Gaps = 1/47 (2%)  
Strand = Plus / Plus

Query: 563 tgtgggggatagatatcccc-gggtccactagaaggcgagaaggcct 608  
||||||| | ||||| ||||||||| |||||  
Sbjct: 151044 tgtgggggacatatatccccgggtccactagaaggctaaaaggcct 151090

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

Score = 79.8 bits (40), Expect = 6e-11  
Identities = 184/232 (79%)  
Strand = Plus / Plus

Query: 1973 accccgacttcgctcgtgcaatgaacacgccgagtggaagtcggagggtactggcccaga 2032  
||||| |||| | | ||||||||| ||||||||| | | | | | | | |  
Sbjct: 55013 accccgatttcgcccagccatgaacacgccagtggaagtcggtggagtattggctcgga 55072

Query: 2033 tagctgacggcctcccgcaaccctagacacggaaggctaccggcggctgcttactcgag 2092  
|||| | ||||||||| | | | | | | | | | | | | | | | | |  
Sbjct: 55073 tagcagatggcctcccgtagactccgatgccagggtatcggtggctgttactcaag 55132

Query: 2093 cagttaatcaccttctaccatcactaatcctccaagcgacctagccatgccatcaaca 2152  
||| |||| | | |||| | | | | | | | | | | | | | | | | | |  
Sbjct: 55133 cagccaatcatctctaccctcgtcaccgccgaacgatctacgacagccatgaaca 55192

Query: 2153 gccggcgagacacgcggagctccatcaacgcttcgcgcgaccgatgacacga 2204  
| |||| | | | ||||||||| ||||||||| | | | | | | | |  
Sbjct: 55193 gtcggcgagacacgcggagctccatcaacgcttcgcgcaaacgacgacacga 55244

Score = 65.9 bits (33), Expect = 1e-06  
Identities = 129/161 (80%)  
Strand = Plus / Plus

Query: 1168 aaacaccgacagctggcgcgccaggtaggggtgtgtctttgatctgagctagctcaatg 1227  
||||| ||||||||| || | ||||||||| ||||| |||||||||  
Sbjct: 54235 aaacactgacagctggcagcctaggtaggggtgtgtcatcgatccaagctagctcaatg 54294



Score = 77.8 bits (39), Expect = 3e-10  
Identities = 204/254 (80%), Gaps = 5/254 (1%)  
Strand = Plus / Plus

Query: 982 tgtaaccaccacatata-gatccatccaagaagtagtgattacgcctctctaagcgg 1040  
|||||  
Sbjct: 271 tgtaaccaccacataaaaagatccataaccaggaagtaggggtttacggctctctaagcgg 330

Query: 1041 cccaaacttgcaaaaaccgcctatccctctctcgtgcgtccagcacgaaccattgagtt 1100  
|||  
Sbjct: 331 cccgaacctgtataaaattgtcca-ctatctctcgtgcatctggcacgaaccatcgacct 389

Query: 1101 acaatcaacagcacctcctacc--aaaagcaccgcaagggtagccctgggtgtgcgg 1158  
|||  
Sbjct: 390 acagtcggtaacaccgtcctacacaaaaagcacctcgaggggcaacccaggagcgcg 449

Query: 1159 acggactctaaacaccgacagctggcgcgccaggtaggggtgtgtctttgatctgagct 1218  
|||  
Sbjct: 450 tcggacccaaaacaccgacagctggcgcgccaggtagggtgtgtcactgatccaagtt 508

Query: 1219 agctcaatgacat 1232  
|||  
Sbjct: 509 agctcaatggccat 522

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

Score = 73.8 bits (37), Expect = 4e-09  
Identities = 86/101 (85%), Gaps = 1/101 (0%)  
Strand = Plus / Plus

Query: 562 ttgtgggggatagatatcccc-gggtccactagaaggcagaaggcctcgcgtgtggcca 620  
|||  
Sbjct: 13840 ttgtgggggacagatatccccgggtccactagaaggcaagaaggcctcacgaaaggcct 13899

Query: 621 cgggccagttaccccgaaggccatcccttcgtgggtcgag 661  
|||  
Sbjct: 13900 cgggccattatttcgaaggccaccccttcgtgggccgag 13940

Score = 61.9 bits (31), Expect = 2e-05  
Identities = 56/63 (88%), Gaps = 1/63 (1%)  
Strand = Plus / Plus

Query: 982 tgtaaccaccacatata-gatccatccaagaagtagtgattacgcctctctaagcgg 1040  
|||||  
Sbjct: 5047 tgtaaccaccacataaaagatccacaccaggaagtagggtgttacgcctctctaagcgg 5106

Query: 1041 ccc 1043  
|||  
Sbjct: 5107 ccc 5109

Score = 60.0 bits (30), Expect = 6e-05  
Identities = 43/46 (93%), Gaps = 1/46 (2%)  
Strand = Plus / Plus

Query: 565 tgggggatagatatccc-cgggtccactagaaggcgagaaggcctc 609  
|||||  
Sbjct: 4622 tgggggacagatatccctcgggtccactagaaggcaagaaggcctc 4667

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

Score = 73.8 bits (37), Expect = 4e-09  
Identities = 86/101 (85%), Gaps = 1/101 (0%)  
Strand = Plus / Plus

Query: 562 ttgtgggggatagatatcccc-gggtccactagaaggcgagaaggcctcgcgtgtggcca 620  
|||||  
Sbjct: 7923 ttgtgggggacagatatccccgggtccactagaaggcaagaaggcctcacgaaaggcct 7982

Query: 621 cgggccagttaccocgcaaggccatcccttcgtgggctcgag 661  
|||||  
Sbjct: 7983 cgggccattatttcgcaaggccacccttcgtgggctcgag 8023

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

Score = 73.8 bits (37), Expect = 4e-09  
Identities = 86/101 (85%), Gaps = 1/101 (0%)



Score = 73.8 bits (37), Expect = 4e-09  
Identities = 98/117 (83%), Gaps = 1/117 (0%)  
Strand = Plus / Plus

Query: 881 agtgccccacggtcgtgtatataaggtccagagggtaccccatcatttctatcgaccatc 940  
||||||| |||| | ||||| | | ||||| ||||| |||||  
Sbjct: 289 agtgccccatggtcaagtatataaggcctaggggtaccctgtcatttccatcgaccatc 348

Query: 941 tacctatctcatcagcttttctccattcaggagacctcgcttgtaaccaccacata 997  
||| | ||| | ||||| ||||| ||||| || ||||| ||||| |||||  
Sbjct: 349 tactcagctcactagcttttctccataaaggaga-ttcccttgtaaccaccacata 404

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

Score = 69.9 bits (35), Expect = 6e-08  
Identities = 47/51 (92%)  
Strand = Plus / Minus

Query: 346 gttgggtgggttttacagagtttaactagcggattatatagtggtataga 396  
||||||| |||| | ||||| | ||||| ||||| |||||  
Sbjct: 119042 gttgggtgggttttgcaaagtttaacttggtgattatatagtggtataga 118992

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Plus

Query: 1168 aaacaccgacagctggcgccaggtagggg 1198  
|||| | ||||| ||||| ||||| |||||  
Sbjct: 81522 aaacgccgacagttggcgccaggtagggg 81552

Score = 44.1 bits (22), Expect = 3.5  
Identities = 25/26 (96%)  
Strand = Plus / Plus

Query: 1173 ccgacagctggcgccaggtagggg 1198  
||||| | ||||| ||||| |||||  
Sbjct: 45119 ccgacagttggcgccaggtagggg 45144

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

Score = 69.9 bits (35), Expect = 6e-08  
Identities = 47/51 (92%)  
Strand = Plus / Plus

Query: 346 gttgggtgggttttacagagtttaactagcggattatatagtggataga 396  
|||||  
Sbjct: 171940 gttgggtgggttttgcaaagtttaacttggattatatagtggataga 171990

>emb|X97605.1| Z. diploperennis DNA for Grandel-6 retrotransposon  
Length = 2533

Score = 69.9 bits (35), Expect = 6e-08  
Identities = 71/83 (85%)  
Strand = Plus / Plus

Query: 1966 aacctgtaccccgacttcgctcgtgcaatgaacacgccgagtgagtcggaggggtactg 2025  
|||||  
Sbjct: 63 aacctgaaccccgacttcgcccggagccgtgaacacgccgagtcggagggagtagtactg 122

Query: 2026 gccagatagctgacggcctccc 2048  
|||  
Sbjct: 123 gctcggatagctgaggactccc 145

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

Score = 65.9 bits (33), Expect = 1e-06  
Identities = 46/49 (93%), Gaps = 1/49 (2%)  
Strand = Plus / Plus

Query: 562 ttgtgggggatagatatcccc-gggtccactagaaggcagaaggcctc 609  
|||||  
Sbjct: 1198 ttgtggggacagatatccccgggtccactagaaggcaagaaggcctc 1246

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

Score = 65.9 bits (33), Expect = 1e-06

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

Query: 562 ttgtgggggatagatatcccc-gggtccactagaaggcgagaaggcctc 609  
||||||| ||||||| ||||||||| |||||||  
Sbjct: 501 ttgtgggggacagatatccccgggtccactagaaggcaagaaggcctc 549

Score = 61.9 bits (31), Expect = 2e-05  
Identities = 59/67 (88%), Gaps = 1/67 (1%)  
Strand = Plus / Plus

Query: 982 tgtaaccaccacatata-gatccatcccaagaagtagtgtattacgcctctctaagcgg 1040  
||||| ||||||| | ||||| || ||||||| || ||||||||| |||||||  
Sbjct: 929 tgtaatccaccacataaaagatccacaccaggaagtaggtgttacgcctctctaagcgg 988

Query: 1041 cccaaac 1047  
|||||  
Sbjct: 989 cccaaac 995

>gb|EF190063.1| Zea mays clone FS3\_49 chromosome B, genomic sequence  
Length = 38116

Score = 65.9 bits (33), Expect = 1e-06  
Identities = 46/49 (93%), Gaps = 1/49 (2%)  
Strand = Plus / Plus

Query: 562 ttgtgggggatagatatcccc-gggtccactagaaggcgagaaggcctc 609  
||||||| ||||||| ||||||||| |||||||  
Sbjct: 32550 ttgtgggggacagatatccccgggtccactagaaggcaagaaggcctc 32598

Score = 50.1 bits (25), Expect = 0.057  
Identities = 50/57 (87%), Gaps = 1/57 (1%)  
Strand = Plus / Plus

Query: 982 tgtaaccaccacatata-gatccatcccaagaagtagtgtattacgcctctctaag 1037  
||||||||| ||||||| || ||||||| || ||||||||| |||||||  
Sbjct: 32977 tgtaaccaccacataaaagatccacaccaggaagtaggtgttacgcctctctaag 33033

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

Score = 65.9 bits (33), Expect = 1e-06  
Identities = 140/173 (80%), Gaps = 2/173 (1%)  
Strand = Plus / Minus

Query: 872 tacgtatggagtgcccca-cggtcgtgtatataaggtccagagggtaccccatcatttct 930  
|||| ||| ||||||||| ||||||| ||||||||| | || |||||||||  
Sbjct: 218 tacgcatgtagtgcccagcggtcgagtatataaggcctaggggtaccccatcatttca 159

Query: 931 atcgaccatctacctatctcatcagcttttctccattcaggagacctcgcttgt-aacct 989  
||| ||||| ||| | ||||| | | ||||||||| | ||||| || ||||| |||  
Sbjct: 158 atcaacctgtactcaactcattatcctttctccatactggagacttctcttgtaaactg 99

Query: 990 accacatatagatccatcccaagaagtagtgattacgcctctctaagcgcc 1042  
|||| ||| ||||||| ||| ||||||| ||||| | |||||||||  
Sbjct: 98 accatataagatccacaccaggaagtaggatattatgtatctctaagcgcc 46

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

Score = 63.9 bits (32), Expect = 4e-06  
Identities = 81/96 (84%), Gaps = 1/96 (1%)  
Strand = Plus / Plus

Query: 562 ttgtgggggatagatatcccc-gggtccactagaaggcgagaaggcctcgcgtgtggcca 620  
||||||||| ||||||||| ||||||||| ||||||||| ||| |||||  
Sbjct: 12021 ttgtgggggacagatatccccgggtccactagaagtaagaaggcctcacgaaaggcca 12080

Query: 621 cgggccagttaccccgcaaggccatcccttcgtggg 656  
||||| ||| ||||||||| |||||||||  
Sbjct: 12081 tgggccattatctcgcaaggccacccttcgtggg 12116

Score = 63.9 bits (32), Expect = 4e-06  
Identities = 61/68 (89%), Gaps = 2/68 (2%)  
Strand = Plus / Plus

Query: 982 tgtaaccaccacatata-gatccatcccaagaagtagtgattta-cgcctctctaagcg 1039

|||||  
Sbjct: 12449 tgtaaccaccacataaaaagatccacaccaagaagtagggtgtaaacgcctctctaagcg 12508

Query: 1040 gcccaaac 1047

|||||  
Sbjct: 12509 gcccaaac 12516

>gb|AC210188.4| Zea mays BAC clone CH201-257L10 from chromosome 5, complete sequence  
Length = 181384

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

Query: 1085 cacgaaccattgagttacaatcaacagcaccgtcctacccaaaagcacc 1133

|||||  
Sbjct: 115369 cacgaaccatcgagttacaatctacgacaccgtcctaaccaaaagcacc 115417

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Minus

Query: 1168 aaacaccgacagctggcgccaggtagggg 1198

|||||  
Sbjct: 87495 aaacgccgacagttggcgccaggtagggg 87465

>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: 562 ttgtgggggatagatatcccc-gggtccactagaaggcgagaaggcctc 609

|||||  
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: 566 ggggatagatatcccc-gggtccactagaaggcgagaaggcctc 609  
||||| ||||||||| ||||||||||||| |||||||||  
Sbjct: 7398 gggggacagatatccccgggtccactagaaggcaagaaggcctc 7442

Score = 50.1 bits (25), Expect = 0.057  
Identities = 53/61 (86%), Gaps = 1/61 (1%)  
Strand = Plus / Plus

Query: 982 tgtaaccaccacatata-gatccatccaagaagtagtgtattacgcctctctaagcgg 1040  
||||||||||||||| | ||||| || ||||||| || ||| |||||||||||||  
Sbjct: 7822 tgtaaccaccacataaaaagatccacaccaggaagtagggtgttatgcctctctaagcgg 7881

Query: 1041 c 1041  
|  
Sbjct: 7882 c 7882

Score = 44.1 bits (22), Expect = 3.5  
Identities = 91/113 (80%), Gaps = 2/113 (1%)  
Strand = Plus / Plus

Query: 1069 tctctcgtgcgtccagcacgaaccattgagttacaatcaacagcaccgtccta--cccaa 1126  
||||||||||| || ||||||||||||| ||| ||||| || | ||||||||||| || ||  
Sbjct: 7909 tctctcgtgcatttagcacgaaccatcgagctacattcggtaacaccgtcctactccaaa 7968

Query: 1127 aagcacgcgaagggtagccctgggtgtgcggacggactctaaacaccgacag 1179  
||||||| | ||||| | ||| ||||| ||||| ||||| | ||||||| |||||  
Sbjct: 7969 aagcacctcgaggggcaacccgggtgcgcggtcggacccaaaacaccaacag 8021

>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: 566 ggggatagatatcccc-gggtccactagaaggcgagaaggcctc 609  
||||||| ||||||||||| ||||||||||| ||||||||||| |||||||||||  
Sbjct: 4473 gggggacagatatccccgggtccactagaaggcaagaaggcctc 4517

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

Query: 982 tgtaaccaccacatatata-gatccatccaagaagtagtgattacgcctctctaagcgg 1040  
||||||||| ||||||| ||| ||||||| || ||||||||||| |||||||  
Sbjct: 4897 tgtaaccaccacataaaagatccacaccaggaagtagggtgttacgcctctctaagcgg 4956

Query: 1041 c 1041  
|  
Sbjct: 4957 c 4957

>emb|AJ312460.1| Zea mays Grande retrotransposon DNA, partial LTR, clone Mo14  
Length = 433

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

Query: 970 ggagacctcgcttgtaaccaccacatatagatccatccaagaagtag 1018  
||||||||| ||||||||||| ||||||| ||| |||||||  
Sbjct: 375 ggagacctcccttgtaaccaccacataaagatccacaccaggaagtag 423

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

Score = 56.0 bits (28), Expect = 0.001  
Identities = 46/52 (88%)  
Strand = Plus / Minus

Query: 269 attttgatggtatgttaaatttggtgtgcatttgtttgatggatttagtaaa 320  
||||||||| ||||||||||| || ||| ||||||||||| |||||||  
Sbjct: 138 attttgatgttatgttaaatatgagtgcaatttgtttgatggatttcgtaaa 87

>gb|AC229874.3| Zea mays BAC clone CH201-314N3 from chromosome 3, complete sequence  
Length = 159830

Score = 54.0 bits (27), Expect = 0.004  
Identities = 30/31 (96%)  
Strand = Plus / Minus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198  
|||||  
Sbjct: 129148 aaacaccgacagttggcgcgccaggtagggg 129118

Score = 44.1 bits (22), Expect = 3.5  
Identities = 25/26 (96%)  
Strand = Plus / Plus

Query: 1173 ccgacagctggcgcgccaggtagggg 1198  
|||||  
Sbjct: 103455 ccgacagttggcgcgccaggtagggg 103480

>gb|GU235996.1| Coix lacryma-jobi 22-kDa prolamin gene cluster, complete sequence  
Length = 283037

Score = 54.0 bits (27), Expect = 0.004  
Identities = 30/31 (96%)  
Strand = Plus / Plus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198  
|||||  
Sbjct: 189303 aaacaccgacagttggcgcgccaggtagggg 189333

>gb|AC226722.2| Zea mays BAC clone CH201-146D18 from chromosome 1, complete sequence  
Length = 194152

Score = 54.0 bits (27), Expect = 0.004  
Identities = 30/31 (96%)  
Strand = Plus / Minus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198  
|||||  
Sbjct: 29283 aaacaccgacagttggcgcgccaggtagggg 29253

Score = 44.1 bits (22), Expect = 3.5  
Identities = 25/26 (96%)  
Strand = Plus / Minus

Query: 1173 ccgacagctggcgcgccaggtaggg 1198  
          ||||||| |||||||||||||||||  
Sbjct: 165564 ccgacagttggcgcgccaggtaggg 165539

>gb|AC186565.4| Zea mays BAC clone ZMMBBb-610A7 from chromosome 5, complete sequence  
          Length = 160080

Score = 54.0 bits (27), Expect = 0.004  
Identities = 30/31 (96%)  
Strand = Plus / Plus

Query: 1168 aaacaccgacagctggcgcgccaggtaggg 1198  
          ||||||||||||| |||||||||||||||||  
Sbjct: 48261 aaacaccgacagttggcgcgccaggtaggg 48291

>gb|AC194974.4| Zea mays BAC clone CH201-115G11 from chromosome 5, complete sequence  
          Length = 152901

Score = 54.0 bits (27), Expect = 0.004  
Identities = 30/31 (96%)  
Strand = Plus / Minus

Query: 1168 aaacaccgacagctggcgcgccaggtaggg 1198  
          ||||||||||||| |||||||||||||||||  
Sbjct: 49821 aaacaccgacagttggcgcgccaggtaggg 49791

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

Score = 54.0 bits (27), Expect = 0.004  
Identities = 58/67 (86%), Gaps = 1/67 (1%)  
Strand = Plus / Plus

Query: 982 tgtaaccaccacatata-gatccatccaagaagtagtgattacgcctctctaagcgg 1040  
          ||||||||||||||||| | ||||||| | | ||||||| || ||||||||||||||||| |

Sbjct: 362 tgtaaccaccacataaaaagatccacacaaggaagtagggtgttacgcctctctaagcag 421

Query: 1041 cccaaac 1047

|||||||

Sbjct: 422 cccaaac 428

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

Score = 54.0 bits (27), Expect = 0.004  
Identities = 58/67 (86%), Gaps = 1/67 (1%)  
Strand = Plus / Plus

Query: 982 tgtaaccaccacatata-gatccatccaagaagtagtgtattacgcctctctaagcgg 1040

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

Sbjct: 362 tgtaatccaccacataaaaagatccacaccaggaagtagggtgttacgcctctctaagcgg 421

Query: 1041 cccaaac 1047

|||||||

Sbjct: 422 tccaaac 428

>gb|AC237090.1| Oryza granulata clone OG\_ABa0119F03, complete sequence  
Length = 162698

Score = 54.0 bits (27), Expect = 0.004  
Identities = 30/31 (96%)  
Strand = Plus / Plus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198

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

Sbjct: 91452 aaacatcgacagctggcgcgccaggtagggg 91482

>gb|AC231756.2| Zea mays BAC clone CH201-111G11 from chromosome 10, complete sequence  
Length = 195704

Score = 54.0 bits (27), Expect = 0.004  
Identities = 30/31 (96%)  
Strand = Plus / Minus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198

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

Sbjct: 168287 aaacaccgacagttggcgcgccaggtagggg 168257

>gb|AC233030.1| Oryza minuta clone OM\_Ba0022H02, complete sequence  
Length = 127011

Score = 54.0 bits (27), Expect = 0.004  
Identities = 27/27 (100%)  
Strand = Plus / Minus

Query: 1173 cgcacagctggcgcgccaggtagggg 1199  
|||||  
Sbjct: 53099 cgcacagctggcgcgccaggtagggg 53073

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

Score = 54.0 bits (27), Expect = 0.004  
Identities = 42/47 (89%)  
Strand = Plus / Plus

Query: 350 ggtgggttttacagagtttaactagcggattatatagtggtataga 396  
||||| | ||||| | |||||  
Sbjct: 1358 ggtgggtttttaaagtttaactggtggattatatagtggtataga 1404

>gb|AC231332.1| Oryza minuta clone OM\_Ba0219N21, complete sequence  
Length = 107464

Score = 54.0 bits (27), Expect = 0.004  
Identities = 27/27 (100%)  
Strand = Plus / Plus

Query: 1173 cgcacagctggcgcgccaggtagggg 1199  
|||||  
Sbjct: 77098 cgcacagctggcgcgccaggtagggg 77124

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

Score = 54.0 bits (27), Expect = 0.004  
Identities = 42/47 (89%)  
Strand = Plus / Plus

Query: 350 ggtgggttttacagagtttaactagcggattatagtggtataga 396  
||||||| | ||||| | |||||  
Sbjct: 1189 ggtgggtttttaaagtttaactggtggattatagtggtataga 1235

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

Score = 54.0 bits (27), Expect = 0.004  
Identities = 69/83 (83%)  
Strand = Plus / Plus

Query: 245 gttattcaactatccgaccgctgattttgatgggatgttaaatttgtgtgcatttggt 304  
||||||| ||| || |||| | ||||| | ||||| | || ||| |||||  
Sbjct: 111207 gttattcaaagatctgaaccgttgattttgatggttgttaagtatgagtgaatttggt 111266

Query: 305 tgatggatttagtaaaggttatg 327  
|| |||||  
Sbjct: 111267 tggatggatttagtaaagatttatg 111289

Score = 50.1 bits (25), Expect = 0.057  
Identities = 31/33 (93%)  
Strand = Plus / Minus

Query: 1168 aaacaccgacagctggcgcgccaggtaggggt 1200  
|||| | |||| | |||||  
Sbjct: 39149 aaacatcgacagttggcgcgccaggtaggggt 39117

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Plus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198  
|||| | |||| | |||||  
Sbjct: 58988 aaacgccgacagttggcgcgccaggtagggg 59018

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)

Strand = Plus / Minus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198  
|||||  
Sbjct: 179323 aaacaccgacagttggcgcgctaggtagggg 179293

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

Score = 54.0 bits (27), Expect = 0.004  
Identities = 55/63 (87%), Gaps = 1/63 (1%)  
Strand = Plus / Plus

Query: 982 tgtaaccaccacatata-gatccatccaagaagtagtgtattacgcctctctaagcgg 1040  
|||||  
Sbjct: 271 tgtaaccaccacataaaaagatccacaccaggaagtagggtgttactcctctctaagcgg 330

Query: 1041 ccc 1043  
|||  
Sbjct: 331 ccc 333

>gb|AC196829.2| Sorghum bicolor clone SB\_BBc0050H06, complete sequence  
Length = 115915

Score = 54.0 bits (27), Expect = 0.004  
Identities = 30/31 (96%)  
Strand = Plus / Minus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198  
|||||  
Sbjct: 115212 aaacaccgacagttggcgcgccaggtagggg 115182

Score = 46.1 bits (23), Expect = 0.90  
Identities = 23/23 (100%)  
Strand = Plus / Minus

Query: 1181 tggcgcgccaggtagggggtgtg 1203  
|||||  
Sbjct: 27029 tggcgcgccaggtagggggtgtg 27007

>gb|AC196818.2| Sorghum bicolor clone SB\_BBc0005H14, complete sequence  
Length = 123072

Score = 54.0 bits (27), Expect = 0.004  
Identities = 30/31 (96%)  
Strand = Plus / Plus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198  
|||||  
Sbjct: 23883 aaacaccgacagttggcgcgccaggtagggg 23913

Score = 46.1 bits (23), Expect = 0.90  
Identities = 23/23 (100%)  
Strand = Plus / Plus

Query: 1181 tggcgcgccaggtaggggtgtg 1203  
|||||  
Sbjct: 77890 tggcgcgccaggtaggggtgtg 77912

>gb|AC165173.2| Zea mays clone ZMMBBb-125019, complete sequence  
Length = 157660

Score = 54.0 bits (27), Expect = 0.004  
Identities = 30/31 (96%)  
Strand = Plus / Minus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198  
|||||  
Sbjct: 19157 aaacaccgacagttggcgcgccaggtagggg 19127

Score = 54.0 bits (27), Expect = 0.004  
Identities = 30/31 (96%)  
Strand = Plus / Plus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198  
|||||  
Sbjct: 141998 aaacaccgacagttggcgcgccaggtagggg 142028

>gb|AY455286.1| Zea mays chloroplast phytoene synthase (Y1) gene, complete cds; nuclear  
gene for chloroplast product  
Length = 94829

Score = 54.0 bits (27), Expect = 0.004  
Identities = 30/31 (96%)  
Strand = Plus / Plus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198  
|||||  
Sbjct: 61604 aaacaccgacagttggcgcgccaggtagggg 61634

Score = 48.1 bits (24), Expect = 0.23  
Identities = 30/32 (93%)  
Strand = Plus / Minus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1199  
||| |  
Sbjct: 3482 aaacgccgacagttggcgcgccaggtagggg 3451

Score = 48.1 bits (24), Expect = 0.23  
Identities = 30/32 (93%)  
Strand = Plus / Minus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1199  
||| |  
Sbjct: 22781 aaacgccgacagttggcgcgccaggtagggg 22750

>gb|GU080322.1| Saccharum hybrid cultivar R570 clone BAC 086H20, partial sequence  
Length = 143827

Score = 52.0 bits (26), Expect = 0.015  
Identities = 29/30 (96%)  
Strand = Plus / Plus

Query: 1169 aacaccgacagctggcgcgccaggtagggg 1198  
|||||  
Sbjct: 131948 aacaccgacagttggcgcgccaggtagggg 131977

Score = 46.1 bits (23), Expect = 0.90  
Identities = 26/27 (96%)  
Strand = Plus / Minus

Query: 1168 aaacaccgacagctggcgcgccaggta 1194  
          |||||          |||||  
Sbjct: 44092 aaacaccgatagctggcgcgccaggta 44066

>gb|AC231130.2| Oryza minuta clone OM\_Ba0135C17, complete sequence  
          Length = 89171

Score = 52.0 bits (26), Expect = 0.015  
Identities = 26/26 (100%)  
Strand = Plus / Minus

Query: 1173 ccgacagctggcgcgccaggtagggg 1198  
          |||||  
Sbjct: 44219 ccgacagctggcgcgccaggtagggg 44194

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

Score = 52.0 bits (26), Expect = 0.015  
Identities = 26/26 (100%)  
Strand = Plus / Plus

Query: 379 attatatagtggtatagaagatatag 404  
          |||||  
Sbjct: 173236 attatatagtggtatagaagatatag 173261

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Plus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198  
          |||| |          |||||  
Sbjct: 113138 aaacgccgacagttggcgcgccaggtagggg 113168

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Minus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198  
||||| ||||||| |||||||||||||||||||  
Sbjct: 144830 aaacgccgacagttggcgcgccaggtagggg 144800

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Minus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198  
||||| ||||||| |||||||||||||||||||  
Sbjct: 161365 aaacgccgacagttggcgcgccaggtagggg 161335

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

Score = 52.0 bits (26), Expect = 0.015  
Identities = 35/38 (92%)  
Strand = Plus / Plus

Query: 293 gtgtcatttgtttgatggatttagtaaaggttatgggt 330  
||||| ||||||| ||||||||||||||| |||||||  
Sbjct: 1454 gtgtaatttgtttgtggatttagtaaagattatgggt 1491

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

Score = 52.0 bits (26), Expect = 0.015  
Identities = 29/30 (96%)  
Strand = Plus / Plus

Query: 526 ctatattttaaaatagggtactgatttaaa 555  
||||||||| |||||||||||||||  
Sbjct: 1548 ctatattttaagatagggtactgatttaaa 1577

>gb|AC213133.1| Oryza glaberrima clone OG\_BB0042C22, complete sequence  
Length = 112632

Score = 52.0 bits (26), Expect = 0.015  
Identities = 26/26 (100%)  
Strand = Plus / Minus

Query: 1174 cgacagctggcgcgccaggtagggg 1199  
|||||  
Sbjct: 79649 cgacagctggcgcgccaggtagggg 79624

Score = 44.1 bits (22), Expect = 3.5  
Identities = 25/26 (96%)  
Strand = Plus / Plus

Query: 1174 cgacagctggcgcgccaggtagggg 1199  
|||||  
Sbjct: 67240 cgacagctggcgcgccaggtagggg 67265

>gb|EF659468.1| Zea mays clone BAC b0288K09 AP2 domain transcription factor (Rap2.7)  
gene, partial cds  
Length = 151668

Score = 52.0 bits (26), Expect = 0.015  
Identities = 32/34 (94%)  
Strand = Plus / Minus

Query: 1168 aaacaccgacagctggcgcgccaggtagggggtg 1201  
|||||  
Sbjct: 73626 aaacaccgacagctggcgcgccaggtagggggtg 73593

>gb|EF659467.1| Zea mays clone BAC m.pk066.114 AP2 domain transcription factor (Rap2.7)  
gene, partial cds  
Length = 133964

Score = 52.0 bits (26), Expect = 0.015  
Identities = 32/34 (94%)  
Strand = Plus / Minus

Query: 1168 aaacaccgacagctggcgcgccaggtagggggtg 1201  
|||||  
Sbjct: 61954 aaacaccgacagctggcgcgccaggtagggggtg 61921

>emb|CR855170.1| Oryza sativa genomic DNA, chromosome 4, BAC clone: H0818E04, complete  
sequence  
Length = 146307

Score = 52.0 bits (26), Expect = 0.015  
Identities = 26/26 (100%)  
Strand = Plus / Plus

Query: 1174 cgacagctggcgcgccaggtagggg 1199  
|||||  
Sbjct: 141993 cgacagctggcgcgccaggtagggg 142018

>gb|AC105320.2| Oryza sativa Japonica Group chromosome 5 clone OJ1675\_H07, complete  
sequence  
Length = 135294

Score = 52.0 bits (26), Expect = 0.015  
Identities = 26/26 (100%)  
Strand = Plus / Plus

Query: 1174 cgacagctggcgcgccaggtagggg 1199  
|||||  
Sbjct: 105195 cgacagctggcgcgccaggtagggg 105220

>gb|AC117264.2| Oryza sativa Japonica Group chromosome 5 clone OJ1005\_D04, complete  
sequence  
Length = 168424

Score = 52.0 bits (26), Expect = 0.015  
Identities = 26/26 (100%)  
Strand = Plus / Plus

Query: 1174 cgacagctggcgcgccaggtagggg 1199  
|||||  
Sbjct: 56260 cgacagctggcgcgccaggtagggg 56285

>gb|AC135924.2| Oryza sativa Japonica Group chromosome 5 clone P0486C01, complete  
sequence  
Length = 146432

Score = 52.0 bits (26), Expect = 0.015  
Identities = 26/26 (100%)

Strand = Plus / Minus

Query: 1174 cgacagctggcgcgccaggtagggg 1199  
|||||  
Sbjct: 55487 cgacagctggcgcgccaggtagggg 55462

>gb|AC130598.2| Oryza sativa Japonica Group chromosome 5 clone OSJNBa0056I11,  
complete sequence  
Length = 145796

Score = 52.0 bits (26), Expect = 0.015  
Identities = 26/26 (100%)  
Strand = Plus / Minus

Query: 1174 cgacagctggcgcgccaggtagggg 1199  
|||||  
Sbjct: 4119 cgacagctggcgcgccaggtagggg 4094

>gb|AC145127.1| Oryza sativa Japonica Group chromosome 10 clone Pseudo10p0.0-10p4.4,  
complete sequence  
Length = 2331000

Score = 52.0 bits (26), Expect = 0.015  
Identities = 26/26 (100%)  
Strand = Plus / Minus

Query: 1174 cgacagctggcgcgccaggtagggg 1199  
|||||  
Sbjct: 588003 cgacagctggcgcgccaggtagggg 587978

Score = 46.1 bits (23), Expect = 0.90  
Identities = 26/27 (96%)  
Strand = Plus / Plus

Query: 1173 cgcacagctggcgcgccaggtagggg 1199  
|||||  
Sbjct: 1793581 cgcacatctggcgcgccaggtagggg 1793607

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

Score = 52.0 bits (26), Expect = 0.015  
Identities = 44/50 (88%)  
Strand = Plus / Minus

Query: 347 ttgggtgggttttacagagtttaaactagcggattatatagtggtataga 396  
||||||| ||||| | ||||||||| ||||||||| |||||||||  
Sbjct: 90446 ttgggtgagttttgctaagtttaaactggcggattataaagtggtataga 90397

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Plus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198  
|||| ||||||| ||||||||| |||||||||  
Sbjct: 47433 aaacgccgacagttggcgcgccaggtagggg 47463

>gb|AC092388.5| Oryza sativa chromosome 10 BAC OSJNBa0011L09 genomic sequence, complete  
sequence  
Length = 177565

Score = 52.0 bits (26), Expect = 0.015  
Identities = 26/26 (100%)  
Strand = Plus / Minus

Query: 1174 cgacagctggcgcgccaggtagggg 1199  
||||||||| ||||||||| ||||||||| |||||||||  
Sbjct: 86800 cgacagctggcgcgccaggtagggg 86775

>gb|AC068654.2| Genomic Sequence For Oryza sativa (japonica cultivar-group) cultivar  
Nipponbare Clone OSJNBa0015022 From Chromosome 10,  
complete sequence  
Length = 189349

Score = 52.0 bits (26), Expect = 0.015  
Identities = 26/26 (100%)  
Strand = Plus / Minus

Query: 1174 cgacagctggcgcgccaggtagggg 1199  
||||||||| ||||||||| ||||||||| |||||||||  
Sbjct: 55611 cgacagctggcgcgccaggtagggg 55586

>dbj|AP006233.3| Oryza sativa Japonica Group genomic DNA, chromosome 1, BAC  
clone:B1249E06  
Length = 126534

Score = 52.0 bits (26), Expect = 0.015  
Identities = 26/26 (100%)  
Strand = Plus / Minus

Query: 1174 cgacagctggcgcgccaggtagggg 1199  
|||||  
Sbjct: 59441 cgacagctggcgcgccaggtagggg 59416

>dbj|AP005460.3| Oryza sativa Japonica Group genomic DNA, chromosome 6, PAC  
clone:P0610D01  
Length = 146418

Score = 52.0 bits (26), Expect = 0.015  
Identities = 26/26 (100%)  
Strand = Plus / Plus

Query: 1174 cgacagctggcgcgccaggtagggg 1199  
|||||  
Sbjct: 73246 cgacagctggcgcgccaggtagggg 73271

>dbj|AP004729.3| Oryza sativa Japonica Group genomic DNA, chromosome 6, BAC  
clone:OSJNBa0006A22  
Length = 190690

Score = 52.0 bits (26), Expect = 0.015  
Identities = 26/26 (100%)  
Strand = Plus / Plus

Query: 1174 cgacagctggcgcgccaggtagggg 1199  
|||||  
Sbjct: 37650 cgacagctggcgcgccaggtagggg 37675

>dbj|AP003458.4| Oryza sativa Japonica Group genomic DNA, chromosome 6, PAC clone:P0701E03  
Length = 183245

Score = 52.0 bits (26), Expect = 0.015  
Identities = 26/26 (100%)

Strand = Plus / Minus

```
Query: 1174  cgacagctggcgcgccaggtagggg 1199
            |||
Sbjct: 153905 cgacagctggcgcgccaggtagggg 153880
```

>dbj|AP005684.3| Oryza sativa Japonica Group genomic DNA, chromosome 9, BAC  
clone:0J1742\_G01  
Length = 154912

Score = 52.0 bits (26), Expect = 0.015  
Identities = 26/26 (100%)  
Strand = Plus / Plus

```
Query: 1174  cgacagctggcgcgccaggtagggg 1199
            |||
Sbjct: 81368  cgacagctggcgcgccaggtagggg 81393
```

>dbj|AP005834.4| Oryza sativa Japonica Group genomic DNA, chromosome 7, BAC  
clone:OSJNBa0005C24  
Length = 168151

Score = 52.0 bits (26), Expect = 0.015  
Identities = 26/26 (100%)  
Strand = Plus / Minus

```
Query: 1174  cgacagctggcgcgccaggtagggg 1199
            |||
Sbjct: 104930 cgacagctggcgcgccaggtagggg 104905
```

>dbj|AP006556.2| Oryza sativa Japonica Group genomic DNA, chromosome 7, BAC  
clone:B1010G04a  
Length = 61450

Score = 52.0 bits (26), Expect = 0.015  
Identities = 26/26 (100%)  
Strand = Plus / Plus

```
Query: 1174  cgacagctggcgcgccaggtagggg 1199
            |||
Sbjct: 25639  cgacagctggcgcgccaggtagggg 25664
```

>dbj|AP005414.3| Oryza sativa Japonica Group genomic DNA, chromosome 2, BAC  
clone:OSJNBa0073G17  
Length = 162391

Score = 52.0 bits (26), Expect = 0.015  
Identities = 26/26 (100%)  
Strand = Plus / Plus

Query: 1174 cgacagctggcgcgccaggtagggg 1199  
|||||  
Sbjct: 128075 cgacagctggcgcgccaggtagggg 128100

>dbj|AP004229.3| Oryza sativa Japonica Group genomic DNA, chromosome 2, BAC  
clone:OJ1124\_E11  
Length = 133524

Score = 52.0 bits (26), Expect = 0.015  
Identities = 26/26 (100%)  
Strand = Plus / Plus

Query: 1174 cgacagctggcgcgccaggtagggg 1199  
|||||  
Sbjct: 117613 cgacagctggcgcgccaggtagggg 117638

>dbj|AP003988.3| Oryza sativa Japonica Group genomic DNA, chromosome 2, BAC  
clone:OJ1057\_D08  
Length = 119557

Score = 52.0 bits (26), Expect = 0.015  
Identities = 26/26 (100%)  
Strand = Plus / Plus

Query: 1174 cgacagctggcgcgccaggtagggg 1199  
|||||  
Sbjct: 54098 cgacagctggcgcgccaggtagggg 54123

>dbj|AP005563.3| Oryza sativa Japonica Group genomic DNA, chromosome 9, BAC  
clone:OJ1227\_D07  
Length = 118358

Score = 52.0 bits (26), Expect = 0.015  
Identities = 26/26 (100%)

Strand = Plus / Plus

Query: 1174 cgacagctggcgcgccaggtagggg 1199  
|||||  
Sbjct: 16748 cgacagctggcgcgccaggtagggg 16773

>dbj|AP003525.2| Oryza sativa Japonica Group genomic DNA, chromosome 6, PAC  
clone:P0537F07  
Length = 147724

Score = 52.0 bits (26), Expect = 0.015  
Identities = 26/26 (100%)  
Strand = Plus / Minus

Query: 1174 cgacagctggcgcgccaggtagggg 1199  
|||||  
Sbjct: 39151 cgacagctggcgcgccaggtagggg 39126

>dbj|AP006062.2| Oryza sativa Japonica Group genomic DNA, chromosome 9, PAC clone:P0415D04  
Length = 176627

Score = 52.0 bits (26), Expect = 0.015  
Identities = 26/26 (100%)  
Strand = Plus / Plus

Query: 1174 cgacagctggcgcgccaggtagggg 1199  
|||||  
Sbjct: 164658 cgacagctggcgcgccaggtagggg 164683

>dbj|AP005795.3| Oryza sativa Japonica Group genomic DNA, chromosome 8, BAC  
clone:B1090H08  
Length = 200720

Score = 52.0 bits (26), Expect = 0.015  
Identities = 26/26 (100%)  
Strand = Plus / Minus

Query: 1174 cgacagctggcgcgccaggtagggg 1199  
|||||  
Sbjct: 75026 cgacagctggcgcgccaggtagggg 75001

>dbj|AP005512.3| Oryza sativa Japonica Group genomic DNA, chromosome 8, BAC  
clone:OSJNBa0012003  
Length = 141860

Score = 52.0 bits (26), Expect = 0.015  
Identities = 26/26 (100%)  
Strand = Plus / Plus

Query: 1174 cgacagctggcgcgccaggtagggg 1199  
|||||  
Sbjct: 134937 cgacagctggcgcgccaggtagggg 134962

>dbj|AP004645.3| Oryza sativa Japonica Group genomic DNA, chromosome 8, BAC  
clone:0J1119\_B10  
Length = 148508

Score = 52.0 bits (26), Expect = 0.015  
Identities = 26/26 (100%)  
Strand = Plus / Minus

Query: 1174 cgacagctggcgcgccaggtagggg 1199  
|||||  
Sbjct: 82803 cgacagctggcgcgccaggtagggg 82778

>dbj|AP004375.3| Oryza sativa Japonica Group genomic DNA, chromosome 8, PAC  
clone:P0475C12  
Length = 140863

Score = 52.0 bits (26), Expect = 0.015  
Identities = 26/26 (100%)  
Strand = Plus / Plus

Query: 1174 cgacagctggcgcgccaggtagggg 1199  
|||||  
Sbjct: 26933 cgacagctggcgcgccaggtagggg 26958

>dbj|AP006237.3| Oryza sativa Japonica Group genomic DNA, chromosome 1, BAC  
clone:OSJNBb0008D07  
Length = 156874

Score = 52.0 bits (26), Expect = 0.015  
Identities = 26/26 (100%)  
Strand = Plus / Plus

Query: 1174 cgacagctggcgcgccaggtagggg 1199  
|||||  
Sbjct: 1391 cgacagctggcgcgccaggtagggg 1416

>emb|AL731605.3| Oryza sativa genomic DNA, chromosome 4, BAC clone: OSJNBa0042F21,  
complete sequence  
Length = 167113

Score = 52.0 bits (26), Expect = 0.015  
Identities = 26/26 (100%)  
Strand = Plus / Minus

Query: 1174 cgacagctggcgcgccaggtagggg 1199  
|||||  
Sbjct: 110588 cgacagctggcgcgccaggtagggg 110563

>dbj|AP004611.3| Oryza sativa Japonica Group genomic DNA, chromosome 1, BAC  
clone:OJ1005\_B10  
Length = 142680

Score = 52.0 bits (26), Expect = 0.015  
Identities = 26/26 (100%)  
Strand = Plus / Minus

Query: 1174 cgacagctggcgcgccaggtagggg 1199  
|||||  
Sbjct: 125370 cgacagctggcgcgccaggtagggg 125345

>dbj|AP004821.4| Oryza sativa Japonica Group genomic DNA, chromosome 1, PAC clone:P0676G08  
Length = 153154

Score = 52.0 bits (26), Expect = 0.015  
Identities = 26/26 (100%)  
Strand = Plus / Plus

Query: 1174 cgacagctggcgcgccaggtagggg 1199  
|||||  
Sbjct: 115721 cgacagctggcgcgccaggtagggg 115746

>emb|AL606634.2| Oryza sativa genomic DNA, chromosome 4, BAC clone: OSJNBb0072N21,

complete sequence  
Length = 130433

Score = 52.0 bits (26), Expect = 0.015  
Identities = 26/26 (100%)  
Strand = Plus / Minus

Query: 1174 cgacagctggcgcgccaggtaggggg 1199  
|||||  
Sbjct: 127992 cgacagctggcgcgccaggtaggggg 127967

>dbj|AP003760.4| Oryza sativa Japonica Group genomic DNA, chromosome 1, BAC  
clone:OSJNBb0063G05  
Length = 182681

Score = 52.0 bits (26), Expect = 0.015  
Identities = 26/26 (100%)  
Strand = Plus / Plus

Query: 1174 cgacagctggcgcgccaggtaggggg 1199  
|||||  
Sbjct: 167523 cgacagctggcgcgccaggtaggggg 167548

>dbj|AP004194.3| Oryza sativa Japonica Group genomic DNA, chromosome 1, PAC  
clone:P0014E08  
Length = 144219

Score = 52.0 bits (26), Expect = 0.015  
Identities = 26/26 (100%)  
Strand = Plus / Plus

Query: 1174 cgacagctggcgcgccaggtaggggg 1199  
|||||  
Sbjct: 69901 cgacagctggcgcgccaggtaggggg 69926

>dbj|AP002482.1| Oryza sativa Japonica Group genomic DNA, chromosome 1, clone:P0706B05  
Length = 187835

Score = 52.0 bits (26), Expect = 0.015  
Identities = 26/26 (100%)  
Strand = Plus / Minus

Query: 1174 cgacagctggcgcgccaggtagggg 1199  
||||||||||||||||||||||||||||||  
Sbjct: 40167 cgacagctggcgcgccaggtagggg 40142

>emb|AL713941.3| Oryza sativa chromosome 12, . BAC OSJNBa0006M08 of library OSJNBa from  
chromosome 12 of cultivar Nipponbare of ssp. japonica of  
Oryza sativa (rice), complete sequence  
Length = 136254

Score = 52.0 bits (26), Expect = 0.015  
Identities = 26/26 (100%)  
Strand = Plus / Minus

Query: 1174 cgacagctggcgcgccaggtagggg 1199  
||||||||||||||||||||||||||||||  
Sbjct: 62956 cgacagctggcgcgccaggtagggg 62931

>emb|AL731592.2| Oryza sativa genomic DNA, chromosome 4, BAC clone: OSJNBa0036B17,  
complete sequence  
Length = 99093

Score = 52.0 bits (26), Expect = 0.015  
Identities = 26/26 (100%)  
Strand = Plus / Minus

Query: 1174 cgacagctggcgcgccaggtagggg 1199  
||||||||||||||||||||||||||||||  
Sbjct: 30047 cgacagctggcgcgccaggtagggg 30022

>gb|GQ407104.1| Oryza granulata chromosome 6 clone BAC a0186L08/a0076A15, complete  
sequence  
Length = 242758

Score = 50.1 bits (25), Expect = 0.057  
Identities = 25/25 (100%)  
Strand = Plus / Plus

Query: 1175 gacagctggcgcgccaggtagggg 1199  
||||||||||||||||||||||||||||||  
Sbjct: 182050 gacagctggcgcgccaggtagggg 182074

>gb|AC231811.1| Oryza minuta clone OM\_Ba0091E17, complete sequence

Length = 115162

Score = 50.1 bits (25), Expect = 0.057  
Identities = 25/25 (100%)  
Strand = Plus / Plus

Query: 1177 cagctggcgcgccaggtagggggtg 1201  
|||||  
Sbjct: 113939 cagctggcgcgccaggtagggggtg 113963

>gb|AF391808.3| Zea mays cultivar McC bz locus region  
Length = 225984

Score = 50.1 bits (25), Expect = 0.057  
Identities = 31/33 (93%)  
Strand = Plus / Minus

Query: 1168 aaacaccgacagctggcgcgccaggtaggggt 1200  
||||| ||||| |||||  
Sbjct: 38172 aaacatcgacagttggcgcgccaggtaggggt 38140

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Plus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198  
||||| ||||| |||||  
Sbjct: 58012 aaacgccgacagttggcgcgccaggtagggg 58042

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Minus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198  
||||| ||||| |||||  
Sbjct: 179665 aaacaccgacagttggcgcgctaggtagggg 179635

Score = 46.1 bits (23), Expect = 0.90

Identities = 29/31 (93%)  
Strand = Plus / Plus

Query: 1168 aaacaccgacagctggcgcgccaggtaggg 1198  
||||| ||||||| |||||||||||||||||||  
Sbjct: 202313 aaacgccgacagttggcgcgccaggtaggg 202343

>gb|EF190043.1| Zea mays clone 46F3FF4R-3 chromosome B, genomic sequence  
Length = 461

Score = 50.1 bits (25), Expect = 0.057  
Identities = 62/73 (84%), Gaps = 1/73 (1%)  
Strand = Plus / Plus

Query: 971 gagacctcgcttgtaaccaccacat-atagatccatccaagaagtagtgattacgcc 1029  
||||| ||| ||||||||||||||||||| | ||||||| ||| ||||||| || |||||||  
Sbjct: 260 gagaactcccttgtaaccaccacataaaagatccacaccaggaagtaggtgctacgct 319

Query: 1030 tctctaagcgcc 1042  
|||||||||||||||  
Sbjct: 320 tctctaagcgcc 332

>emb|CR855225.1| Oryza sativa genomic DNA, chromosome 4, BAC clone:  
OSIGBa0138H21-OSIGBa0138E01, complete sequence  
Length = 129321

Score = 50.1 bits (25), Expect = 0.057  
Identities = 25/25 (100%)  
Strand = Plus / Plus

Query: 1174 cgacagctggcgcgccaggtaggg 1198  
|||||||||||||||||||||||||||||  
Sbjct: 8725 cgacagctggcgcgccaggtaggg 8749

>gb|AC083945.3| Oryza sativa Japonica Group chromosome X clone OSJNBa0058E19, complete  
sequence  
Length = 147706

Score = 50.1 bits (25), Expect = 0.057  
Identities = 28/29 (96%)  
Strand = Plus / Minus

Query: 1173 cgcacagctggcgcgccaggtaggggtg 1201  
||||| ||||||||||||||||||||  
Sbjct: 28946 cgcacatctggcgcgccaggtaggggtg 28918

>gb|AC135929.2| Oryza sativa Japonica Group chromosome 5 clone P0692D12, complete  
sequence  
Length = 164064

Score = 50.1 bits (25), Expect = 0.057  
Identities = 25/25 (100%)  
Strand = Plus / Minus

Query: 1174 cgacagctggcgcgccaggtagggg 1198  
||||||||||||||||||||||  
Sbjct: 33780 cgacagctggcgcgccaggtagggg 33756

>gb|AC136226.2| Oryza sativa Japonica Group chromosome 5 clone OSJNBb0067H15, complete  
sequence  
Length = 184316

Score = 50.1 bits (25), Expect = 0.057  
Identities = 28/29 (96%)  
Strand = Plus / Plus

Query: 1170 acaccgacagctggcgcgccaggtagggg 1198  
||||||||| ||||||||||||||||  
Sbjct: 180861 acaccgacagttggcgcgccaggtagggg 180889

>gb|AC108498.2| Oryza sativa Japonica Group chromosome 5 clone OJ1076\_H08, complete  
sequence  
Length = 148348

Score = 50.1 bits (25), Expect = 0.057  
Identities = 28/29 (96%)  
Strand = Plus / Plus

Query: 1170 acaccgacagctggcgcgccaggtagggg 1198  
||||||||| ||||||||||||||||  
Sbjct: 10787 acaccgacagttggcgcgccaggtagggg 10815

>gb|AC134348.2| Oryza sativa Japonica Group chromosome 5 clone P0530H10, complete

sequence  
Length = 148373

Score = 50.1 bits (25), Expect = 0.057  
Identities = 25/25 (100%)  
Strand = Plus / Minus

Query: 1174 cgacagctggcgcgccaggtagggg 1198  
|||||  
Sbjct: 83012 cgacagctggcgcgccaggtagggg 82988

>emb|AL606649.4| Oryza sativa genomic DNA, chromosome 4, BAC clone: OSJNBb0003B01,  
complete sequence  
Length = 153643

Score = 50.1 bits (25), Expect = 0.057  
Identities = 25/25 (100%)  
Strand = Plus / Plus

Query: 1174 cgacagctggcgcgccaggtagggg 1198  
|||||  
Sbjct: 40302 cgacagctggcgcgccaggtagggg 40326

>gb|AY530950.1| Zea mays putative zinc finger protein (Z438D03.1), unknown (Z438D03.5),  
epsilon-COP (Z438D03.6), putative kinase (Z438D03.7),  
unknown (Z438D03.25), and C1-B73 (Z438D03.27) genes,  
complete cds  
Length = 185988

Score = 50.1 bits (25), Expect = 0.057  
Identities = 31/33 (93%)  
Strand = Plus / Minus

Query: 1168 aaacaccgacagctggcgcgccaggtagggggt 1200  
|||| |  
Sbjct: 111324 aaacccgacagtggcgcgccaggtagggggt 111292

>dbj|AP005866.2| Oryza sativa Japonica Group genomic DNA, chromosome 8, BAC  
clone:OSJNBb0076003  
Length = 140823

Score = 50.1 bits (25), Expect = 0.057  
Identities = 25/25 (100%)

Strand = Plus / Minus

Query: 1174 cgacagctggcgcgccaggtagggg 1198  
|||||  
Sbjct: 46297 cgacagctggcgcgccaggtagggg 46273

>dbj|AP003435.2| Oryza sativa Japonica Group genomic DNA, chromosome 1, PAC  
clone:P0455H03  
Length = 175947

Score = 50.1 bits (25), Expect = 0.057  
Identities = 25/25 (100%)  
Strand = Plus / Plus

Query: 1174 cgacagctggcgcgccaggtagggg 1198  
|||||  
Sbjct: 18120 cgacagctggcgcgccaggtagggg 18144

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

Score = 48.1 bits (24), Expect = 0.23  
Identities = 31/32 (96%), Gaps = 1/32 (3%)  
Strand = Plus / Minus

Query: 562 ttgtgggggatagatatcccc-gggtccacta 592  
|||||  
Sbjct: 172679 ttgtgggggatagatatcccctgggtccacta 172648

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Minus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198  
||||  
Sbjct: 27051 aaacgccgacagttggcgcgccaggtagggg 27021

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)

Strand = Plus / Minus

Query: 1168 aaacaccgacagctggcgccaggtaggg 1198  
|||| ||||||| |||||||||||||||||  
Sbjct: 97256 aaacgccgacagttggcgccaggtaggg 97226

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Minus

Query: 1168 aaacaccgacagctggcgccaggtaggg 1198  
|||| ||||||| |||||||||||||||||  
Sbjct: 103145 aaacgccgacagttggcgccaggtaggg 103115

>gb|AC229780.2| Oryza minuta clone OM\_Ba0081J07, complete sequence  
Length = 103110

Score = 48.1 bits (24), Expect = 0.23  
Identities = 27/28 (96%)  
Strand = Plus / Minus

Query: 1171 caccgacagctggcgccaggtaggg 1198  
||||||||||||||||| |||||  
Sbjct: 94501 caccgacagctggcgctaggtaggg 94474

>gb|AC231887.2| Oryza minuta clone OM\_Ba0018L21, complete sequence  
Length = 97902

Score = 48.1 bits (24), Expect = 0.23  
Identities = 24/24 (100%)  
Strand = Plus / Plus

Query: 1174 cgacagctggcgccaggtaggg 1197  
|||||||||||||||||  
Sbjct: 88007 cgacagctggcgccaggtaggg 88030

>gb|AC225222.3| Zea mays BAC clone CH201-123I12 from chromosome 1, complete sequence  
Length = 178957

Score = 48.1 bits (24), Expect = 0.23

Identities = 33/36 (91%)  
Strand = Plus / Minus

Query: 1166 ctaaacaccgacagctggcgcgccaggtaggggtg 1201  
||||||| ||||||||||| ||||| |||||||||||  
Sbjct: 83102 ctaaacatcgacagctggcgcgccaagtaggggtg 83067

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Plus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198  
||||| ||||||| |||||||||||||||||||  
Sbjct: 177040 aaacgccgacagttggcgcgccaggtagggg 177070

>gb|FJ266023.1| Oryza granulata clone OG\_ABa077F15\_032P05, complete sequence  
Length = 285707

Score = 48.1 bits (24), Expect = 0.23  
Identities = 24/24 (100%)  
Strand = Plus / Minus

Query: 1173 ccgacagctggcgcgccaggtagg 1196  
|||||||||||||||||||||||||  
Sbjct: 28434 ccgacagctggcgcgccaggtagg 28411

>gb|AC231882.1| Oryza minuta clone OM\_Ba0091G05, complete sequence  
Length = 123139

Score = 48.1 bits (24), Expect = 0.23  
Identities = 24/24 (100%)  
Strand = Plus / Plus

Query: 1174 cgacagctggcgcgccaggtagg 1197  
|||||||||||||||||||||||||  
Sbjct: 32770 cgacagctggcgcgccaggtagg 32793

>gb|AC229741.1| Oryza minuta clone OM\_Ba0230E13, complete sequence  
Length = 130811

Score = 48.1 bits (24), Expect = 0.23  
Identities = 27/28 (96%)  
Strand = Plus / Minus

Query: 1171 caccgacagctggcgcgccaggtagggg 1198  
|||||  
Sbjct: 37301 caccgacagctggcgcgctaggtagggg 37274

>gb|AC223439.1| Oryza brachyantha, complete sequence  
Length = 163153

Score = 48.1 bits (24), Expect = 0.23  
Identities = 27/28 (96%)  
Strand = Plus / Minus

Query: 1174 cgacagctggcgcgccaggtagggggtg 1201  
|||||  
Sbjct: 121233 cgacagttggcgcgccaggtagggggtg 121206

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

Score = 48.1 bits (24), Expect = 0.23  
Identities = 27/28 (96%)  
Strand = Plus / Plus

Query: 529 tattttaaaatagggtactgatttaaaa 556  
|||||  
Sbjct: 1545 tattttaaaatagggtattgatttaaaa 1572

>gb|AC097176.3| Oryza sativa Japonica Group chromosome 5 clone OJ1576\_F01, complete  
sequence  
Length = 119525

Score = 48.1 bits (24), Expect = 0.23  
Identities = 24/24 (100%)  
Strand = Plus / Minus

Query: 1176 acagctggcgcgccaggtaggggg 1199  
|||||  
Sbjct: 12190 acagctggcgcgccaggtaggggg 12167

>gb|AC078839.4| Oryza sativa Japonica Group chromosome X clone OSJNBa0094J09, complete  
sequence  
Length = 168192

Score = 48.1 bits (24), Expect = 0.23  
Identities = 30/32 (93%)  
Strand = Plus / Plus

Query: 1174 cgacagctggcgcgccaggtaggggtgtgtc 1205  
||||| ||||||||||||||||||| |||||  
Sbjct: 12916 cgacagttggcgcgccaggtaggggtgtgtc 12947

>gb|AC130602.5| Oryza sativa Japonica Group chromosome 5 clone B1122D01, complete  
sequence  
Length = 126532

Score = 48.1 bits (24), Expect = 0.23  
Identities = 24/24 (100%)  
Strand = Plus / Minus

Query: 1176 acagctggcgcgccaggtagggg 1199  
|||||||||||||||||||||  
Sbjct: 82918 acagctggcgcgccaggtagggg 82895

>gb|AC087552.3| Oryza sativa Japonica Group chromosome 5 clone P0519E07, complete  
sequence  
Length = 151399

Score = 48.1 bits (24), Expect = 0.23  
Identities = 27/28 (96%)  
Strand = Plus / Plus

Query: 1174 cgacagctggcgcgccaggtaggggtg 1201  
||||| |||||||||||||||||||  
Sbjct: 65303 cgacagttggcgcgccaggtaggggtg 65330

>dbj|AP005458.3| Oryza sativa Japonica Group genomic DNA, chromosome 6, PAC  
clone:P0567G03  
Length = 196834

Score = 48.1 bits (24), Expect = 0.23  
Identities = 27/28 (96%)

Strand = Plus / Minus

Query: 1174 cgacagctggcgcgccaggtagggggtg 1201  
||||||| ||||||||||||||||||||  
Sbjct: 6508 cgacagttggcgcgccaggtagggggtg 6481

>dbj|AP005456.3| Oryza sativa Japonica Group genomic DNA, chromosome 6, PAC  
clone:P0513E02  
Length = 141477

Score = 48.1 bits (24), Expect = 0.23  
Identities = 27/28 (96%)  
Strand = Plus / Minus

Query: 1174 cgacagctggcgcgccaggtagggggtg 1201  
||||||| ||||||||||||||||||||  
Sbjct: 83824 cgacagttggcgcgccaggtagggggtg 83797

>dbj|AP005570.3| Oryza sativa Japonica Group genomic DNA, chromosome 9, BAC  
clone:0J1344\_B01  
Length = 170912

Score = 48.1 bits (24), Expect = 0.23  
Identities = 30/32 (93%)  
Strand = Plus / Plus

Query: 1174 cgacagctggcgcgccaggtagggggtgtgtc 1205  
||||||| |||||||||||||||||||| |||||  
Sbjct: 3402 cgacagttggcgcgccaggtagggggtgtgtc 3433

>dbj|AP005424.3| Oryza sativa Japonica Group genomic DNA, chromosome 9, PAC  
clone:P0556H01  
Length = 149800

Score = 48.1 bits (24), Expect = 0.23  
Identities = 30/32 (93%)  
Strand = Plus / Plus

Query: 1174 cgacagctggcgcgccaggtagggggtgtgtc 1205  
||||||| |||||||||||||||||||| |||||  
Sbjct: 91487 cgacagttggcgcgccaggtagggggtgtgtc 91518

>dbj|AP005774.5| Oryza sativa Japonica Group genomic DNA, chromosome 7, BAC  
clone:OSJNBa0086N05  
Length = 163670

Score = 48.1 bits (24), Expect = 0.23  
Identities = 27/28 (96%)  
Strand = Plus / Plus

Query: 1174 cgacagctggcgcgccaggtagggggtg 1201  
||||||| ||||||||||||||||||||||||  
Sbjct: 36560 cgacagttggcgcgccaggtagggggtg 36587

>dbj|AP003991.3| Oryza sativa Japonica Group genomic DNA, chromosome 2, BAC  
clone:OJ1077\_A12  
Length = 149089

Score = 48.1 bits (24), Expect = 0.23  
Identities = 27/28 (96%)  
Strand = Plus / Plus

Query: 1174 cgacagctggcgcgccaggtagggggtg 1201  
||||||| ||||||||||||||||||||||||  
Sbjct: 3663 cgacagttggcgcgccaggtagggggtg 3690

Score = 44.1 bits (22), Expect = 3.5  
Identities = 25/26 (96%)  
Strand = Plus / Minus

Query: 1174 cgacagctggcgcgccaggtaggggg 1199  
||||||||| ||||||||||||||||||||  
Sbjct: 129955 cgacagctgggagcgccaggtaggggg 129930

>dbj|AP003977.3| Oryza sativa Japonica Group genomic DNA, chromosome 2, BAC  
clone:OJ1006\_A02  
Length = 175153

Score = 48.1 bits (24), Expect = 0.23  
Identities = 30/32 (93%)  
Strand = Plus / Minus

Query: 1173 cgcacagctggcgcgccaggtaggggtgtgt 1204  
||||| ||||||||||||||||||| |||||  
Sbjct: 66521 cgcacatctggcgcgccaggtaggggtgtgtgt 66490

>dbj|AP003974.3| Oryza sativa Japonica Group genomic DNA, chromosome 2, BAC  
clone:OJ1003\_F05  
Length = 147472

Score = 48.1 bits (24), Expect = 0.23  
Identities = 30/32 (93%)  
Strand = Plus / Minus

Query: 1173 cgcacagctggcgcgccaggtaggggtgtgt 1204  
||||| ||||||||||||||||||| |||||  
Sbjct: 121878 cgcacatctggcgcgccaggtaggggtgtgtgt 121847

>dbj|AP003724.2| Oryza sativa Japonica Group genomic DNA, chromosome 6, PAC  
clone:P0498C03  
Length = 146394

Score = 48.1 bits (24), Expect = 0.23  
Identities = 27/28 (96%)  
Strand = Plus / Minus

Query: 1174 cgcacagctggcgcgccaggtaggggtgtgt 1201  
||||| ||||||||||||||||||| |||||  
Sbjct: 54023 cgcacagttggcgcgccaggtaggggtgtgt 53996

>dbj|AP005628.3| Oryza sativa Japonica Group genomic DNA, chromosome 8, BAC  
clone:OJ1014\_E02  
Length = 159669

Score = 48.1 bits (24), Expect = 0.23  
Identities = 30/32 (93%)  
Strand = Plus / Minus

Query: 1174 cgcacagctggcgcgccaggtaggggtgtgtc 1205  
||||| ||||||||||||||||||| |||||  
Sbjct: 146215 cgcacagttggcgcgccaggtaggggtgtgtc 146184

>emb|AL606615.4| Oryza sativa genomic DNA, chromosome 4, BAC clone: OSJNBa0086B14,  
complete sequence

Length = 175698

Score = 48.1 bits (24), Expect = 0.23  
Identities = 24/24 (100%)  
Strand = Plus / Plus

Query: 1176 acagctggcgcgccaggtagggg 1199  
          |||||  
Sbjct: 66981 acagctggcgcgccaggtagggg 67004

>dbj|AP004030.2| Oryza sativa Japonica Group genomic DNA, chromosome 2, BAC  
          clone:OJ1145\_E05  
          Length = 101333

Score = 48.1 bits (24), Expect = 0.23  
Identities = 27/28 (96%)  
Strand = Plus / Plus

Query: 1174 cgacagctggcgcgccaggtaggggtg 1201  
          ||||| |||||  
Sbjct: 84158 cgacagttggcgcgccaggtaggggtg 84185

>emb|AL731618.3| Oryza sativa genomic DNA, chromosome 4, BAC clone: OSJNBb0012A12,  
          complete sequence  
          Length = 122766

Score = 48.1 bits (24), Expect = 0.23  
Identities = 27/28 (96%)  
Strand = Plus / Plus

Query: 1174 cgacagctggcgcgccaggtaggggtg 1201  
          ||||| |||||  
Sbjct: 8706 cgacagttggcgcgccaggtaggggtg 8733

>emb|AL663012.3| Oryza sativa genomic DNA, chromosome 4, BAC clone: OSJNBb0069N01,  
          complete sequence  
          Length = 180264

Score = 48.1 bits (24), Expect = 0.23  
Identities = 27/28 (96%)  
Strand = Plus / Plus

Query: 1174 cgacagctggcgcgccaggtagggggtg 1201  
||||| ||||||||||||||||||||  
Sbjct: 156114 cgacagttggcgcgccaggtagggggtg 156141

>dbj|AP005464.3| Oryza sativa Japonica Group genomic DNA, chromosome 8, BAC  
clone:B1027A11  
Length = 169506

Score = 48.1 bits (24), Expect = 0.23  
Identities = 30/32 (93%)  
Strand = Plus / Minus

Query: 1174 cgacagctggcgcgccaggtagggggtgtgtc 1205  
||||| |||||||||||||||||||| |||||  
Sbjct: 50301 cgacagttggcgcgccaggtagggggtgtgtc 50270

>dbj|AP003204.3| Oryza sativa Japonica Group genomic DNA, chromosome 1, BAC clone:B1111C09  
Length = 156393

Score = 48.1 bits (24), Expect = 0.23  
Identities = 27/28 (96%)  
Strand = Plus / Minus

Query: 1174 cgacagctggcgcgccaggtagggggtg 1201  
||||| ||||||||||||||||||||  
Sbjct: 144424 cgacagttggcgcgccaggtagggggtg 144397

>dbj|AP002968.2| Oryza sativa Japonica Group genomic DNA, chromosome 1, PAC  
clone:P0416G11  
Length = 138858

Score = 48.1 bits (24), Expect = 0.23  
Identities = 27/28 (96%)  
Strand = Plus / Minus

Query: 1174 cgacagctggcgcgccaggtagggggtg 1201  
||||| ||||||||||||||||||||  
Sbjct: 24812 cgacagttggcgcgccaggtagggggtg 24785

>dbj|AP002525.1| Oryza sativa Japonica Group genomic DNA, chromosome 1, PAC  
clone:P0462H08  
Length = 139152

Score = 48.1 bits (24), Expect = 0.23  
Identities = 27/28 (96%)  
Strand = Plus / Plus

Query: 1174 cgacagctggcgcgccaggtagggggtg 1201  
||||| ||||||||||||||||||||  
Sbjct: 35648 cgacagttggcgcgccaggtagggggtg 35675

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

Score = 48.1 bits (24), Expect = 0.23  
Identities = 42/48 (87%)  
Strand = Plus / Plus

Query: 270 ttttgatggtatgttaaatttgtgtgtcatttgtttgatggatttagt 317  
||||||| | ||||| ||| ||| ||||||||||||||||||||  
Sbjct: 558 ttttgatgatctgttaagtttaggtgtaatttgtttgatggatttagt 605

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

Score = 48.1 bits (24), Expect = 0.23  
Identities = 31/32 (96%), Gaps = 1/32 (3%)  
Strand = Plus / Minus

Query: 562 ttgtgggggatagatat-ccccgggtccacta 592  
||||||||||||||||| |||||||||||||||  
Sbjct: 992 ttgtgggggatagatatccccgggtccacta 961

>gb|AC208340.4| Zea mays BAC clone CH201-53J11 from chromosome 5, complete sequence  
Length = 187725

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Minus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198  
||| ||||| ||||||||||||||||  
Sbjct: 4170 aaacgccgacagttggcgcgccaggtagggg 4140

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Plus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198  
|||| |  
Sbjct: 49380 aaacgccgacagttggcgcgccaggtagggg 49410

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Plus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198  
|||| |  
Sbjct: 161929 aaacgccgacagttggcgcgccaggtagggg 161959

>gb|AC216353.5| Zea mays BAC clone CH201-194K18 from chromosome 5, complete sequence  
Length = 176200

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Minus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198  
|||| |  
Sbjct: 57575 aaacgccgacagttggcgcgccaggtagggg 57545

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Plus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198  
|||| |  
Sbjct: 82787 aaacgccgacagttggcgcgccaggtagggg 82817

Score = 44.1 bits (22), Expect = 3.5

Identities = 25/26 (96%)  
Strand = Plus / Minus

Query: 1173 cgcacagctggcgcgccaggtaggg 1198  
||||| ||||||||||||||||||  
Sbjct: 69916 cgcacagttggcgcgccaggtaggg 69891

>gb|AC205514.6| Zea mays BAC clone CH201-227F5 from chromosome 5, complete sequence  
Length = 168591

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Plus

Query: 1168 aaacaccgacagctggcgcgccaggtaggg 1198  
|||| ||||||| ||||||||||||||||||  
Sbjct: 52277 aaacgccgacagttggcgcgccaggtaggg 52307

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Minus

Query: 1168 aaacaccgacagctggcgcgccaggtaggg 1198  
|||| ||||||| ||||||||||||||||||  
Sbjct: 94136 aaacgccgacagttggcgcgccaggtaggg 94106

>gb|AC210260.5| Zea mays BAC clone CH201-44F4 from chromosome 5, complete sequence  
Length = 188949

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Plus

Query: 1168 aaacaccgacagctggcgcgccaggtaggg 1198  
|||| ||||||| ||||||||||||||||||  
Sbjct: 112762 aaacgccgacagttggcgcgccaggtaggg 112792

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)

Strand = Plus / Plus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198  
||||| ||||||| ||||||||||||||||||||  
Sbjct: 158316 aaacgccgacagttggcgcgccaggtagggg 158346

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

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Minus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198  
||||| ||||||| ||||||||||||||||||||  
Sbjct: 57140 aaacgccgacagttggcgcgccaggtagggg 57110

Score = 44.1 bits (22), Expect = 3.5  
Identities = 28/30 (93%)  
Strand = Plus / Plus

Query: 298 atttgtttgatggatttagtaaaggttatg 327  
||||||||| ||||||||||| |||||||||  
Sbjct: 182189 atttgtttggtggatttagtagaggttatg 182218

>gb|AC216070.4| Zea mays BAC clone CH201-459P15 from chromosome 5, complete sequence  
Length = 226532

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Minus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198  
||||| ||||||| ||||||||||||||||||||  
Sbjct: 77633 aaacgccgacagttggcgcgccaggtagggg 77603

>gb|AC226721.2| Zea mays BAC clone CH201-150M20 from chromosome 10, complete sequence  
Length = 207605

Score = 46.1 bits (23), Expect = 0.90

Identities = 29/31 (93%)  
Strand = Plus / Minus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198  
||||| ||||||| ||||||||||||||||  
Sbjct: 148376 aaacgccgacagttggcgcgccaggtagggg 148346

>gb|AC213983.4| Zea mays BAC clone CH201-326E16 from chromosome 5, complete sequence  
Length = 180103

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Minus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198  
||||| ||||||| ||||||||||||||||  
Sbjct: 6768 aaacgccgacagttggcgcgccaggtagggg 6738

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Minus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198  
||||| ||||||| ||||||||||||||||  
Sbjct: 126670 aaacgccgacagttggcgcgccaggtagggg 126640

>gb|AC225944.3| Zea mays BAC clone CH201-127G5 from chromosome 10, complete sequence  
Length = 216347

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Plus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198  
||||| ||||||| ||||||||||||||||  
Sbjct: 107278 aaacgccgacagttggcgcgccaggtagggg 107308

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)



Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198  
|||| | ||||| | ||||| ||||| |||||  
Sbjct: 81733 aaacgccgacagtggcgcgccaggtagggg 81703

>gb|AC196472.3| Zea mays BAC clone ZMMBBb-235B12 from chromosome 5, complete sequence  
Length = 126719

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Minus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198  
|||| | ||||| | ||||| ||||| |||||  
Sbjct: 107458 aaacgccgacagtggcgcgccaggtagggg 107428

>gb|AC185472.4| Zea mays BAC clone CH201-257N23 from chromosome 5, complete sequence  
Length = 185919

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Plus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198  
|||| | ||||| | ||||| ||||| |||||  
Sbjct: 19944 aaacgccgacagtggcgcgccaggtagggg 19974

>gb|AC201762.5| Zea mays BAC clone CH201-479M22 from chromosome 5, complete sequence  
Length = 179408

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Plus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198  
|||| | ||||| | ||||| ||||| |||||  
Sbjct: 95001 aaacgccgacagtggcgcgccaggtagggg 95031

>gb|AC203071.4| Zea mays BAC clone CH201-184N10 from chromosome 5, complete sequence  
Length = 194840

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)





Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198  
||||| ||||||| |||||||||||||||||||  
Sbjct: 156005 aaacgccgacagttggcgcgccaggtagggg 156035

>gb|AC195458.4| Zea mays BAC clone CH201-47808 from chromosome 5, complete sequence  
Length = 200301

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Plus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198  
||||| ||||||| |||||||||||||||||||  
Sbjct: 21244 aaacgccgacagttggcgcgccaggtagggg 21274

>gb|AC191361.5| Zea mays BAC clone CH201-21609 from chromosome 5, complete sequence  
Length = 182607

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Plus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198  
||||| ||||||| |||||||||||||||||||  
Sbjct: 73957 aaacgccgacagttggcgcgccaggtagggg 73987

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Plus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198  
||||| ||||||| |||||||||||||||||||  
Sbjct: 180691 aaacgccgacagttggcgcgccaggtagggg 180721

>gb|AC190647.4| Zea mays BAC clone ZMMBBb-216G14 from chromosome 5, complete sequence  
Length = 148198

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Minus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198  
||||| ||||||| |||||||||||||||||||  
Sbjct: 43908 aaacgccgacagttggcgcgccaggtagggg 43878

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Minus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198  
||||| ||||||| |||||||||||||||||||  
Sbjct: 98402 aaacgccgacagttggcgcgccaggtagggg 98372

>gb|AC215174.5| Zea mays BAC clone CH201-70P8 from chromosome 5, complete sequence  
Length = 184384

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Minus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198  
||||| ||||||| |||||||||||||||||||  
Sbjct: 28715 aaacgccgacagttggcgcgccaggtagggg 28685

>gb|AC211535.5| Zea mays BAC clone ZMMBBb-223D21 from chromosome 5, complete sequence  
Length = 175907

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Minus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198  
||||| ||||||| |||||||||||||||||||  
Sbjct: 156086 aaacgccgacagttggcgcgccaggtagggg 156056

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

Score = 46.1 bits (23), Expect = 0.90  
Identities = 57/67 (85%), Gaps = 1/67 (1%)

Strand = Plus / Plus

```
Query: 982  tgtaaccaccacatata-gatccatcccaagaagtagtgtattacgcctctctaagcgg 1040
          ||||| ||||||||| | |||||| | ||||||| | ||||||| ||||||| |||||||
Sbjct: 362  tgtaatccaccacataaaagatccacaccaggaagtaggtgttacgtctctctaagcgg 421
```

```
Query: 1041  cccaaac 1047
          |||||
Sbjct: 422  tccaaac 428
```

>gb|AC237089.1| Oryza granulata clone OG\_ABa0096023, complete sequence  
Length = 145921

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Plus

```
Query: 1168  aaacaccgacagctggcgcgccaggtagggg 1198
          ||||| |||||| | ||||||| ||||||| |||||||
Sbjct: 13212 aaacatcgacagttggcgcgccaggtagggg 13242
```

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Minus

```
Query: 1168  aaacaccgacagctggcgcgccaggtagggg 1198
          ||||| |||||| | ||||||| ||||||| |||||||
Sbjct: 19723 aaacatcgacagttggcgcgccaggtagggg 19693
```

>gb|AC237088.1| Oryza granulata clone OG\_ABa0089G14, complete sequence  
Length = 118754

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Plus

```
Query: 1168  aaacaccgacagctggcgcgccaggtagggg 1198
          ||||| |||||| | ||||||| ||||||| |||||||
Sbjct: 39396 aaacatcgacagttggcgcgccaggtagggg 39426
```

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Plus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198  
||||| ||||||| |||||||||||||||||||  
Sbjct: 97242 aaacatcgacagttggcgcgccaggtagggg 97272

>gb|AC237087.1| Oryza granulata clone OG\_ABa0028G18, complete sequence  
Length = 124143

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Minus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198  
||||| ||||||| |||||||||||||||||||  
Sbjct: 115132 aaacatcgacagttggcgcgccaggtagggg 115102

>gb|AC229873.2| Zea mays BAC clone CH201-387D15 from chromosome 2, complete sequence  
Length = 150685

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Plus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198  
||||| ||||||| |||||||||||||||||||  
Sbjct: 51769 aaacgccgacagttggcgcgccaggtagggg 51799

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Plus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198  
||||||||||||| ||||| |||||||||||||||  
Sbjct: 131072 aaacaccgacagttggcacgccaggtagggg 131102

>ref|XM\_002442558.1| Sorghum bicolor hypothetical protein, mRNA  
Length = 654

Score = 46.1 bits (23), Expect = 0.90  
Identities = 23/23 (100%)  
Strand = Plus / Plus

Query: 1181 tggcgcgccaggtagggggtgtg 1203  
          |||||  
Sbjct: 353 tggcgcgccaggtagggggtgtg 375

>ref|XM\_002465520.1| Sorghum bicolor hypothetical protein, mRNA  
Length = 3219

Score = 46.1 bits (23), Expect = 0.90  
Identities = 23/23 (100%)  
Strand = Plus / Plus

Query: 1181 tggcgcgccaggtagggggtgtg 1203  
          |||||  
Sbjct: 26 tggcgcgccaggtagggggtgtg 48

>gb|FJ614806.1| Zea mays cultivar B73 p cluster, complete sequence  
Length = 379557

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Minus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198  
          |||| |  
Sbjct: 317746 aaacgccgacagttggcgcgccaggtagggg 317716

>gb|AC213848.4| Zea mays BAC clone CH201-495D12 from chromosome 5, complete sequence  
Length = 170022

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Minus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198  
          |||| |

Sbjct: 114757 aaacgccgacagttggcgcgccaggtagggg 114727

>gb|AC232337.2| Oryza minuta clone OM\_Ba0147P17, complete sequence  
Length = 111380

Score = 46.1 bits (23), Expect = 0.90  
Identities = 26/27 (96%)  
Strand = Plus / Plus

Query: 1173 cgcacagctggcgcgccaggtagggg 1199  
||||||| |||||||||||||||||||||  
Sbjct: 16560 cgcacagttggcgcgccaggtagggg 16586

>gb|AC213131.2| Oryza glaberrima clone OG\_BB0031E23, complete sequence  
Length = 118417

Score = 46.1 bits (23), Expect = 0.90  
Identities = 26/27 (96%)  
Strand = Plus / Minus

Query: 1173 cgcacagctggcgcgccaggtagggg 1199  
||||||| |||||||||||||||||||||  
Sbjct: 39516 cgcacatctggcgcgccaggtagggg 39490

>gb|AC217961.4| Zea mays BAC clone ZMMBBb-353K3 from chromosome 6, complete sequence  
Length = 130360

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Plus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198  
|||| ||||||| |||||||||||||||||||||  
Sbjct: 52583 aaacgccgacagttggcgcgccaggtagggg 52613

>gb|AC187050.5| Zea mays BAC clone ZMMBBb-293C24 from chromosome 5, complete sequence  
Length = 137364

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Plus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198  
||||| ||||||| |||||||||||||||||||  
Sbjct: 43923 aaacgccgacagttggcgcgccaggtagggg 43953

>gb|AC231617.2| Zea mays BAC clone CH201-190G15 from chromosome 8, complete sequence  
Length = 166972

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Plus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198  
||||| ||||||| |||||||||||||||||||  
Sbjct: 19091 aaacgccgacagttggcgcgccaggtagggg 19121

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Minus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198  
||||| ||||||| |||||||||||||||||||  
Sbjct: 108951 aaacgccgacagttggcgcgccaggtagggg 108921

>gb|AC229877.2| Zea mays BAC clone CH201-11105 from chromosome 9, complete sequence  
Length = 167856

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Plus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198  
||||| ||||||| |||||||||||||||||||  
Sbjct: 57491 aaacgccgacagttggcgcgccaggtagggg 57521

>gb|FJ032637.1| Oryza ridleyi clone a0301G20 Monoculm1 and Mlo family protein genes,  
complete cds  
Length = 125771

Score = 46.1 bits (23), Expect = 0.90  
Identities = 26/27 (96%)

Strand = Plus / Minus

Query: 1174 cgacagctggcgcgccaggtaggggt 1200  
|||||  
Sbjct: 69320 cgacagctggcgcgccaggtaggggt 69294

>gb|EU940899.1| Zea mays clone 1168123 mRNA sequence  
Length = 3007

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Plus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198  
|||||  
Sbjct: 1968 aaacgccgacagttggcgcgccaggtagggg 1998

>gb|AC229778.1| Oryza minuta clone OM\_Ba0085P10, complete sequence  
Length = 103044

Score = 46.1 bits (23), Expect = 0.90  
Identities = 23/23 (100%)  
Strand = Plus / Plus

Query: 1177 cagctggcgcgccaggtaggggg 1199  
|||||  
Sbjct: 47518 cagctggcgcgccaggtaggggg 47540

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

Score = 46.1 bits (23), Expect = 0.90  
Identities = 23/23 (100%)  
Strand = Plus / Plus

Query: 471 tttgataaaaaaggtaaagtaga 493  
|||||  
Sbjct: 1648880 tttgataaaaaaggtaaagtaga 1648902

>gb|AC225785.1| Oryza granulata, complete sequence  
Length = 117123

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Minus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198  
||||| ||||| ||||||||||||||||  
Sbjct: 36202 aaacatcgacagttggcgcgccaggtagggg 36172

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

Score = 46.1 bits (23), Expect = 0.90  
Identities = 54/63 (85%), Gaps = 1/63 (1%)  
Strand = Plus / Plus

Query: 982 tgtaaccaccacatata-gatccatccaagaagtagtgattacgcctctctaagcgg 1040  
||||||||||||||| | |||| | ||| ||||||| || ||| |||||||||||||  
Sbjct: 270 tgtaaccaccacataaaagatctacaccaggaagtagggtgttatgcctctctaagcgg 329

Query: 1041 ccc 1043  
|||  
Sbjct: 330 ccc 332

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

Score = 46.1 bits (23), Expect = 0.90  
Identities = 54/63 (85%), Gaps = 1/63 (1%)  
Strand = Plus / Plus

Query: 982 tgtaaccaccacatata-gatccatccaagaagtagtgattacgcctctctaagcgg 1040  
||||||||||||||| | |||| | ||| ||||||| || ||| |||||||||||||  
Sbjct: 270 tgtaaccaccacataaaagatctacaccaggaagtagggtgttatgcctctctaagcgg 329

Query: 1041 ccc 1043  
|||  
Sbjct: 330 ccc 332

>gb|AC196850.2| Sorghum bicolor clone SB\_BBc0140005, complete sequence  
Length = 112839

Score = 46.1 bits (23), Expect = 0.90  
Identities = 23/23 (100%)  
Strand = Plus / Minus

Query: 1181 tggcgcgccaggtagggggtgtg 1203  
|||||  
Sbjct: 6943 tggcgcgccaggtagggggtgtg 6921

>gb|AC196847.2| Sorghum bicolor clone SB\_BBc0109L12, complete sequence  
Length = 112916

Score = 46.1 bits (23), Expect = 0.90  
Identities = 23/23 (100%)  
Strand = Plus / Minus

Query: 1181 tggcgcgccaggtagggggtgtg 1203  
|||||  
Sbjct: 20035 tggcgcgccaggtagggggtgtg 20013

>gb|AC196837.2| Sorghum bicolor clone SB\_BBc0073F19, complete sequence  
Length = 105211

Score = 46.1 bits (23), Expect = 0.90  
Identities = 23/23 (100%)  
Strand = Plus / Plus

Query: 1181 tggcgcgccaggtagggggtgtg 1203  
|||||  
Sbjct: 115 tggcgcgccaggtagggggtgtg 137

>gb|DQ493648.1| Zea mays cultivar I137TN bz locus region  
Length = 120751

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Plus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198  
||||| || ||  
Sbjct: 26152 aaacaccgatagttggcgcgccaggtagggg 26182





Score = 46.1 bits (23), Expect = 0.90  
Identities = 41/47 (87%)  
Strand = Plus / Plus

Query: 350 ggtgggttttacagagtttaactagcggattatatagtggataga 396  
|||| ||||| || |||||||||||| |||||||||||| ||||||||  
Sbjct: 88108 ggtgtgttttgcaaagtttaactagtagattatatagtagtataga 88154

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Minus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198  
|||| ||||| ||||||||||||||||||||  
Sbjct: 122060 aaacgccgacagttggcgcgccaggtagggg 122030

>gb|AC157319.2| Zea mays clone ZMMBBb-136E2, complete sequence  
Length = 138186

Score = 46.1 bits (23), Expect = 0.90  
Identities = 29/31 (93%)  
Strand = Plus / Plus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198  
|||| ||||| ||||||||||||||||||||  
Sbjct: 93286 aaacgccgacagttggcgcgccaggtagggg 93316

Score = 44.1 bits (22), Expect = 3.5  
Identities = 25/26 (96%)  
Strand = Plus / Plus

Query: 1173 ccgacagctggcgcgccaggtagggg 1198  
||||||| ||||||||||||||||||||  
Sbjct: 47153 ccgacagttggcgcgccaggtagggg 47178

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: 572,545,080  
Number of extensions: 29811019  
Number of successful extensions: 570449  
Number of sequences better than 10.0: 393  
Number of HSP's gapped: 570335  
Number of HSP's successfully gapped: 835  
Length of query: 2212  
Length of database: 30,878,341,354  
Length adjustment: 24  
Effective length of query: 2188  
Effective length of database: 30,605,918,290  
Effective search space: 66965749218520  
Effective search space used: 66965749218520  
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)