

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 Mol7 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 (Yl) 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 P0...	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 P0...	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 P0...	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 ZMMBBb-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 ZMMBBb-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 ZMMBBb-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 ZMMBBb-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_BB0031E23, 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 BSSS53 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 EL01N0501C03.d mRNA sequence	46	0.90
gb	BT017984.1	Zea mays clone EL01N0525E01.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 ggcgattaggatgagtcggtgggattttggggagatcagttcagtcggttcactatta 5662

Query: 848 tttaggagacatatgatcctcatgtacgtatggagtgcacacggtcgtgtatataaggt 907
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Sbjct: 5661 gttaggagacatatgatcatcatgtacgtttggagtgcacacggtcaggtatataagtc 5602

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

Query: 968 caggagacctcgcttgtaacccaccacatatagatccatcccaagaagtagtgattacg 1027

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Sbjct: 5544 caggagacaccgcttgaacacccacatacagatccgccctaggaagtagggtaatac 5485

Query: 1028 cctctctaagcgcccaaaccttcagaaaaaccgctatccctctctcg----tgcgtcca 1083
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Sbjct: 5484 cctctccaagtgacccgaacttcagaaaaattgcatgtctctctctctctctctcttcttcca 5425

Query: 1084 gcacgaaccattgagttacaatcaacagcaccgtcctacccaaaagcaccgcaaggggta 1143
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Sbjct: 5424 gcatgaaccattgagctacagtcaacaacaccatcctacccaaaagcaccgcaaagg-ta 5366

Query: 1144 gccctgggtgtgcggtcgactctaaacaccgacagctggcgccaggtaggggggtgtg 1203
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Sbjct: 5365 accctaggtgtgcggtcgactctaaacaccgacagccggcacgccaggtaggggggtgtg 5306

Query: 1204 tctttgatctgagctagctcaatgaccattacctccaaatgaagatcgcccttcgcccc 1263
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Sbjct: 5305 tcgttgatcatagtaactcaatggccatcacctccaagtgaagatcgcccttcacccc 5246

Query: 1264 gggactatgttttgctttggaaccatctcatccatagcagatgaagaggggaactctgcac 1323
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Sbjct: 5245 ggaactatgttctgctttggaactatctcttccatagtggatgaagaggggactctgcac 5186

Query: 1324 cgcatagcagatctattggagaagaagctttcctcagaaaatctcgaggggagccaggga 1383
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Sbjct: 5185 cacgtggaagatccgactgagaagaagctttcctgagaaaatcctgaggaatccaaagca 5126

Query: 1384 gaacagcgggtggcaccatcacccgcacctcaagcgaagatgacctcttacaaccgaaa 1443
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Sbjct: 5125 gaatagcgggtggtgccaccacccgcactctcgagggaagatgacccctcataaaccgaag 5066

Query: 1444 gtcgggagctcacctacccgaa-aaactccgctgtccacttcgccacaaaaggagtggac 1502
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Sbjct: 5065 gttgggatctcacttacccgaagaaactccactgttcacctcgcccacaaaaggagtgcac 5006

Query: 1503 acggattactcgaaaagaaggaagcgagtgtcccgagtcaggggacgggaacacgcccaagc 1562
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Sbjct: 5005 acggatcactcgaaaagaagaagcaaatgtcccgagtcaggggacgagaacacgcccgagc 4946

Query: 1563 catcttttcgacgccttcgccctcaaagtaggatggaaagaagagcgccatcgcgctggc 1622
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 Sbjct: 4945 cat-tttctgacgccttcgccctcaaagtagaatggaaataagagcgccatcacgccggc 4887

Query: 2163 cacgcgagctccatcaacgcttcgcgcgaccg 2195
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Sbjct: 4347 cgctagagctccatcaacgcttcgcgcgaccg 4315

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

Query: 1084 gcacgaaccattgagttacaatcaacagcaccgtcctacccaaaagcaccgcaaggggta 1143
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Sbjct: 11406 gcacgaaccattgagttacaatcaacagcaccatcctactcaaatgcaccgcgaggggta 11465

Query: 1144 gccctgggtgtgcggacggactctaacaccgacagctggcgcgccaggtaggggg 1199
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Sbjct: 11466 accctaggtgtgcagtcgggctccaaacaccgacagctggcgcgccagttaggggg 11521

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

Query: 1938 gcgccgagagaatgctctctttgctcggaacctgtaccccgacttcgctcgtgcaatgaa 1997
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Sbjct: 12178 gcgccgagagaacctcttttcaactcgaaacctgaacctgactttgctcgtgcaatgaa 12237

Query: 1998 cacgccgagtgaagtcggaggggtactggcccagatagctgacggcctccc 2048
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Sbjct: 12238 cac--caagtgaagtcggaggagtattggctcagatagctgatggcctccc 12286

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

Query: 1622 ctcttttctaccccgacgtcctctttcatcagggggagattggagttagcaccgctttca 1681
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Sbjct: 11920 ctcttttctaccccgacatcgtctttatcaaagggagattggagtcgtttcccatctccg 11979

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Query: 1682  acgatgagccaaccatgcaaggggaagagcctccccagcgtgaggcgcgacgacggagga 1741
             | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct: 11980 atgacgagccaaccgtaccaggggaagaacctccccagcaggaagctcagcgacgaagga 12039
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Query: 1802  tatcccgggacgaagctttagaagtaggaaaaactcc 1838
           ||||| || ||||| | ||| ||||| |||||
Sbjct: 12100  tatccgcgatgaagcctcagatgtaggagaaactcc 12136
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Query: 881   agtgcacccacggctcgtgtatataaggtccagagggtaccccatcat 926
          |||||
Sbjct: 11194 agtgcacccacggctcgaatatataaggcctagggggtaccccatcat 11239
```

Score = 428 bits (216), Expect = e-116
Identities = 521/617 (84%), Gaps = 8/617 (1%)
Strand = Plus / Minus

```
Query: 622   gggccagttaccccgcaaggccatcccttcgtgggtcgagctagaattactggtagaatg 681
            |||||
Sbjct: 46751 gggccagttaccttgcaaggccatcccttctgtgggtcgggcaaaagctactggcagaatg 46692
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Query: 742 acagaaactacccgactttccggcgcatggcatcctagaatatcgggcggtattagggat 801
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Sbjct: 46631 aaagaaaccgtccgactttcccacgcatggcgccctcaaattgtcgtag---attagggat 46575

Query: 802 gaggcagcgagattttcggaagattagttcagtttggtcgtattattaggagacatat 861
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Sbjct: 46574 aagtcggcgaggattttcgggagatcagttcagtcattcactattattaggggacatgt 46515

Query: 862 gatcctcatgtacgtatggagtgccccacggctgtgtatataaggtccagagggtacccc 921
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Sbjct: 46514 gatcaatatgtacgtatggagtgccccactgtcgtgtatataaggccagggggaacccc 46455

Query: 922 atcattttctatcgaccatctacctatctcatcagcttttctccattcaggagacctcgct 981
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Sbjct: 46454 atcattttcattc--ccatctacttatctcattagcttttctccattcaggaaacaccgct 46396

Query: 982 tgtaaccaccacatatagatccatcccaagaagtagtgtattacgcctctctaagcggc 1041
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Sbjct: 46395 tgtaaccaccatatacagctccaccctaggaagtatggtattacacctctccaagcggc 46336

Query: 1042 ccaaacttgagaaaaccgcctatccctctctcgtgcgtccagcacgaaccattgagtta 1101
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Sbjct: 46335 ccaacatgcagaaaatcgctctgt--ctctctcgtgtgtccagcacgaaccattgagtta 46278

Query: 1102 caatcaacagcaccgtcctacccaaaagcaccgcaaggggtagccctgggtgtgcggacg 1161
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Sbjct: 46277 caatcaacagcattgtcctacccaatagcaccgcaa-gggtaaccctaggtgtgcgggtcg 46219

Query: 1162 gactctaaacaccgaca 1178
||||||| |||||
Sbjct: 46218 gactctaaacaccgaca 46202

>ref|NM_001152615.1| Zea mays hypothetical protein LOC100279619 (LOC100279619), mRNA
>gi|219885622|gb|BT054579.1| Zea mays full-length cDNA
clone ZM_BFc0162011 mRNA, complete cds
Length = 2299

Score = 313 bits (158), Expect = 2e-81
Identities = 467/567 (82%), Gaps = 11/567 (1%)
Strand = Plus / Minus

Query: 573 agatatccccgggtccactagaaggcgagaaggcctcgcggtgtggccacgggcccagttac 632
||||||| || ||||||||| ||||||||| ||||||||| ||||| ||||||| |||||
Sbjct: 1708 agatatccctggatccactagaatgcgagaaggctctcgcggtgggcccctcgggccggttac 1649

Query: 633 cccgcaaggccatcccttcgtgggtcgagctagaattactggtagaatgggctgaccgaa 692
| |||||| ||||| | ||||| | | || | | || ||| ||||||| ||| |
Sbjct: 1648 ctcgcaagaccatctccttcgtgagccaggcaaaagctaattggcgtaatgggcccgacttga 1589

Query: 693 gaaggcaacagactcgagcccaaacaatccatcggtcgtgcgctatccacagaaactac 752
||||||| | ||||| ||||| ||||||| ||| ||||||||||||||||||||| |||
Sbjct: 1588 gaaggcaacggcctcgaaccagacaatcc-tcgactcgtgcgctatccacagaaaccac 1530

Query: 753 ccgactttccggcgcatggcatcctagaatatcggggcgtattagggatgagtcagcgag 812
||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||| ||||| |||
Sbjct: 1529 ccgactttcccacgcatggcgtcctcgaatatcggggcgtgtaggattaagtcggctag 1470

Query: 813 attttcgaagattagttcagtttggtcgctattatttaggagacatatga-tcctcatg 871
|| | || ||| ||||||| |||| |||| |||||||||||| ||| |||||||
Sbjct: 1469 gttgtaggggatcagttcagtcggttcactataatttaggagacacgtgaatcctcatg 1410

Query: 872 tacgtatggagtgcgccacggtcgtgtatataagggtccagagggtaccccatcatttcta 931
|| |||| ||||||| ||||||| | ||||||||||||| ||||||| ||||||| |
Sbjct: 1409 tatgtattgagtgccttacggtcatatatataagggtcca-agggtacaccatcatttcta 1351

Query: 932 tcgaccatctacctatctcatcagcttttctccattcaggagacctcgcttgtaaccac 991
||||||| |||||||||||| ||||||||||||||||| || |||||||
Sbjct: 1350 tcgaccatttacctatctcatttagcttttctccattcaggaaacttcgcttg----- 1299

Query: 992 cacatatagatccatcccaagaagtagtgattacgcctctctaaagcgcccaaacctgc 1051
||| ||||||||| | ||||||||| ||||||||||||||||||||| ||||| |
Sbjct: 1298 cacttatagatccaccacaagaagtaggtattacgcctctctaaagcgcccaaacctac 1239

Query: 1052 agaaaaccgcctatccctctctcgtgcgtccagcacgaaccattgagttacaatcaacag 1111
||||||| | | ||||||||| ||||||||||||||||||||| || | |||||||
Sbjct: 1238 agaaaatcatttttacctctctcgtgcgtccagcacgaaccattgaggtagagtcaacaa 1179

Query: 1112 caccgtcctacccaaaagcaccgcaag 1138
| |||| || ||||||| |||||||
Sbjct: 1178 tatcgtcatagccaaaacaccgcaag 1152

```
>gb|AY883559.2| Zea mays cultivar inbred line B73 teosinte glume architecture 1 (tga1)
      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 tgtaaccaccacataaagatccacaccaggaagtagggtattacgcctctctaagcggc 94082
```

```
Query: 1042  ccaaacttgcagaaaaccgcctatccctctctcgtgcgtccagcacgaaccattgagtta 1101
           || ||| | ||||| |||| ||||| ||| | ||||| ||| ||
Sbjct: 94083  ccgaacctatagaaaattatctatcg-tctctcgtgcgcttagcacgaaccatcgagcta 94141
```

```
Query: 1102 caatcaacagcaccgtctaccctacccaaaagcaccgcaaggggtagccctgggtgtgcggacg 1161
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 94142 cagttagcaacaccgtctaccctacccaaaagcactgcgaggggtaaccccggggtgcgcgggtcg 94201
```

```
Query: 1162  gactctaaacaccgcagctggcgcgccaggtagggggtgtgtctttgatctgagctagc 1221
             |||||||||||||||||||||||||||||||||||||||||
Sbjct: 94202  ggtcctaaacaccgcagctggcgcgctaggtagggggtgtgtcgctgatccaagctagc 94261
```

Query: 1222 tcaatgaccatta-cctccaaatgaagatcgcccttcgccccgggactatgttttgctt 1280
 ||||| ||| | |||| | ||||| | | ||||| | | ||||| | |
 Sbjct: 94262 tcaatggccatcattctcc-aacacaagattgctctccgccctggatctgtgttctggtt 94320

Query: 1281 tggaaaccatctcatccatagcagatgaagagggaactctgcaccgcatagcagatctatt 1340
 || ||||| |||| |||| |||| |||| |||| || |||| |||| ||
 Sbjct: 94321 cgggaccatctcgtccatggcagacgaagaagggaattctgcatcgtatagcggatccatc 94380

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

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


```

Query: 2065   gaaggctaccggcggtgtcttactcgagcagttaatcacctttctaccatcataatcct 2124
             |||||
Sbjct: 110184 gaaggctatcgggcggtgtctactcgggcatctaatacatcttctaccctctgctcatccc 110125

```

```
Query: 2125   ccaagcgacctacgccatgccatcaacagccggcgagacacgcggagctccatcaacgct 2184
             || ||||| ||||| || ||||| ||||| ||||| ||||| |||||
Sbjct: 110124 ccgagcgatctacgacagccatcaacagttgggtgggacacgcagagctccatcaacgct 110065
```

```
Query: 2185      tc 2186
      ||
Sbjct: 110064    tc 110063
```

Score = 69.9 bits (35), Expect = 6e-08
Identities = 140/175 (80%)
Strand = Plus / Plus

Query: 1622 ctcctttctaccccgacgtcctcttcatcagggggagattggagttagcaccgctcttca 1681
 ||||||||||| ||||||| ||||| ||| || ||||| | | ||| ||| |
 Sbjct: 94650 ctcctttctacccgtacgtccttttcatcgagggaagagtggagtcatctcccatctccg 94709

```
Query: 1682  acgatgagccaaccatgcaagggaagagcctccccagcgtgaggcgcgacgacggagga 1741
            | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct: 94710 atgatgagccaaccatgcctggggaagaacctctctcagcgagaagctcgccgatggagga 94769
```

Query: 1742 atagaagccagaacgtgctggcgacatcacaggctgggaacgggatccggcgca 1796
| | ||| || | ||||| ||| ||||| ||| |||||
Sbjct: 94770 accaacgccgaatatctggcgacatcacaagcagggaacgggaactcggcgca 94824

Score = 60.0 bits (30), Expect = 6e-05
Identities = 46/50 (92%), Gaps = 1/50 (2%)
Strand = Plus / Plus

```
Query: 563   tgtgggggatagatatcccc-gggtccactagaaggcgagaaggcctcgc 611
            |||||  |||||  |||||  |||||  |||||  |||||
Sbjct: 93595 tgtgggggacagatatcccccggtccactagaaggttagaaggcctcgc 93644
```

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

Query: 1168 aaacaccgacagctggcgccaggtagggg 1198
|||| |||||| |||||||||
Sbjct: 67172 aaacgccgacagttggcgccaggtagggg 67202

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

Query: 1168 aaacaccgacagctggcgccaggtagggg 1198
|||| |||||| |||||||||
Sbjct: 131516 aaacgccgacagttggcgccaggtagggg 131546

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

Score = 167 bits (84), Expect = 4e-37
Identities = 172/200 (86%), Gaps = 1/200 (0%)
Strand = Plus / Minus

Query: 980 cttgtaaccaccacatatagatccatcccaagaagtagtgattacgcctctctaagcg 1039
||||||| ||||| | || ||||| ||||||||| |||
Sbjct: 528 cttgtaaccaccacataaagatccttaccaggaagtagggattacgcctctccaagtg 469

Query: 1040 gcccaaacttgcaaaaaccgcctatccctctctcgtgcgtccagcacgaaccattgagt 1099
|||| ||| || ||||| ||||| || ||||| ||| | |||||||||
Sbjct: 468 gcccgaaactgtagaaaatcgctgtcg-tctctcgtgcatctgttacgaaccattgagt 410

Query: 1100 tacaatcaacagcaccgtcctacccaaaagcaccgcaaggggtagccctgggtgtgcgga 1159
||||||| ||||| | ||||||||| || ||||| ||| |||||||||
Sbjct: 409 tacaatcaaaagcaccattctacccaaaagcactgcgaggggtaacccgggtgtgcggt 350

Query: 1160 cggactctaacaccgacag 1179
||| ||| |||||||||
Sbjct: 349 cgggctccaacaccgacag 330

>gb|AC209386.4| Zea mays BAC clone CH201-98J13 from chromosome 5, complete sequence
Length = 196028

Score = 157 bits (79), Expect = 3e-34
Identities = 222/269 (82%), Gaps = 3/269 (1%)
Strand = Plus / Plus

Query: 1071 tctcgtgcgtccagcacgaaccattgagttacaatcaacagcaccgtcctaccc---aaa 1127
||||||| ||||||||||||||||| |||| | | || || ||||| | |||
Sbjct: 160739 tctcgtgcgcccagcacgaaccattgagctacagtcggcaacatcgtcctactcttaaaa 160798

Query: 1128 agcaccgcaaggggtagccctgggtgtgcggacggactctaacaccgacagctggcgcg 1187
| |||| | |||| | || ||||||||||||||| |||||||||||||||
Sbjct: 160799 aacacctgaggggcaaccttgggtgtgcggtcggacccaaaacaccgacagctggcgcg 160858

Query: 1188 ccaggtagggggtgtgtctttgatctgagctagctcaatgaccattacctccaaatgcaa 1247
||||||| ||||| ||||||||||||| | | |||| | | |||
Sbjct: 160859 ccaggtagggggtgtgtcggcatctaagctagctcaatggctcgtcaccttcaccgcaa 160918

Query: 1248 gatcgcccttcgccccgggactatgttttgccttgggaaccatctcatccatagcagatga 1307
|||| |||| |||| | | || |||| |||| |||| ||||||||| |||||||||
Sbjct: 160919 gatcaccctccgccctggatctgtgttctgcttcggaactatctcatccgtagcagatga 160978

Query: 1308 agagggaactctgcaccgcatagcagatc 1336
||| |||||| | || |||| |||||||
Sbjct: 160979 agaaggaactctacatcgcatcgagatc 161007

Score = 95.6 bits (48), Expect = 1e-15
Identities = 180/224 (80%)
Strand = Plus / Plus

Query: 1966 aacctgtaccccgacttcgctcgtgcaatgaacacgccgagtgaagtcggaggggtactg 2025
||||| ||||||||||||| || || ||||||| |||||||||||||
Sbjct: 161608 aacctgaaccccgacttcgcccagccatgaacacaccgagtgaagtcggaggggtactg 161667

Query: 2026 gccagatagctgacggcctcccgcgaaccctagacacggaaggctaccggcggtgctt 2085
|| | |||||||| | || |||| | || | || | || |||| | || |
Sbjct: 161668 gctcggatagctgatggactccctcggactcccgcgagggtatcgacgattgttc 161727

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

Query: 2146 atcaacagccggcgagacacgaggagctccatcaacgcttcgcg 2189
||||||| || ||| ||| ||||| ||||| |||||
Sbjct: 161788 atcaacagccgccgggacgcggaagctccatcaacgcctcgcg 161831

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

Query: 562 ttgtgggggatagatatcccc-gggtccactagaaggcgagaaggcctcgcggtgtggcca 620
||||||| ||||| ||||| ||||| ||||| ||||| |||||
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

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198
|||| |||||| ||||||||||||||||
Sbjct: 89649 aaacgccgacagttggcgcgccaggtagggg 89619

>gb|EU940901.1| Zea mays clone 1168199 mRNA sequence
Length = 2718

Score = 155 bits (78), Expect = 1e-33
Identities = 160/186 (86%), Gaps = 1/186 (0%)
Strand = Plus / Plus

Query: 1149 ggggtgtcggacggactctaaacaccgacagctggcgcgccaggtagggggtgtgtcttt 1208
||||||| |||| | ||||||||||||||||||||||||||||
Sbjct: 1380 ggggtgtcgg-cggacccaaaacaccgacagctggcgcgccaggtagggggtgtgtcgcc 1438

Query: 1209 gatctgagctagctcaatgaccattacctccaaatgcaagatcgcccttcgccccgggac 1268
||||| ||||||||| || | |||| | | |||||| |||| ||||| |
Sbjct: 1439 gatctaagctagctcaatggccgtcaccttcaccgcaagatcacctccgccccggatc 1498

Query: 1269 tatgttttgccttggaaacctctcatccatagcagatgaagagggaactctgcaccgcat 1328
| |||| ||||||||| ||||||| ||||||||||||| ||||||| || |||||
Sbjct: 1499 tgtgttctgccttggaaactatctcatccgtagcagatgaagaagggaactctacatcgcat 1558

Query: 1329 agcaga 1334
|||||
Sbjct: 1559 cgcaga 1564

Score = 95.6 bits (48), Expect = 1e-15
Identities = 180/224 (80%)
Strand = Plus / Plus

Query: 1966 aacctgtaccccgacttcgctcgtgcaatgaacacgccgagtgaagtcggaggggtactg 2025
||||||| ||||||||| || || ||||||||||||||||||||
Sbjct: 2169 aacctgaaccccgacttcgcccagccatgaacacgccgagtgaagtcggaggggtacta 2228

Query: 2026 gccagatagctgacggcctcccgcaaccctagacacggaaggctaccggcggtgctt 2085
|| | ||||||| || ||||| || | | ||| | || ||||| || || |||
Sbjct: 2229 gtcggatagctgatggactcctcggaaatcccgacgccgagggtatcgacgactgttc 2288

```
Query: 2086 actcgagcagttaatcaccttctacccatcactaatctccaagcgacctacgccatgcc 2145
          ||| ||||| ||| || ||||| ||| ||| ||| ||||| ||| |||
Sbjct: 2289 acccaagcagccaaccatcttctacctatcgctacccgccgaacgacctacgacagcc 2348
```

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

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

Query: 1149 ggggtgtgcggacggactctaaacaccgacagctggcgcgccaggtagggggtgtgtcttt 1208
||||| |||| | ||||| ||||| ||||| ||||| |||||
Sbjct: 28758 ggggtgtgcggtcggacccaaaacaccgacagctggcgcgccaggtagggggtgtgtcgac 28699

Query: 1269 tatgttttgctttggaaccatctcatccatagcagatgaagagggaactctgcaccgcat 1328
 | ||| ||||| ||||||| ||||||| ||||||| ||||||| |||||||
Sbjct: 28638 cgtattctgcttcggaacaatctcatccgtagcagatgaagagggaactctacaccgcat 28579

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

Query: 1966 aacctgtaccccgacttcgctcgtgcaatgaacacgccgagtgagtcggaggggtactg 2025
||||| ||||||||| | | || ||||||||||||||||||||||||| |||
Sbjct: 54934 aacctgaaccccgactttgcctgagccatgaacacgccgagtgagtcggaggggtgctg 54993

Query: 2026 gccagatagctgacggcctcccgcaaccctagacacggaaggctaccggcggctgctt 2085
|| | ||||||||| ||||||| || || | ||| | || ||||| ||||||||| |
Sbjct: 54994 gtcgcatagctgatggcctccctcggactccggacgccgagggtatcgcggtgttc 55053

Query: 2086 actcgagcagttaatcaccttctacccatcactaatcctccaagcgacctacgccatgcc 2145
|||| ||||| |||||||||||||||| || || | || | ||| ||||| || |||
Sbjct: 55054 actcaagcagccaatcaccttctacccctcgctcacctgccgaacgatctacgacacgcc 55113

Query: 2146 atcaacagccggcgagacacgcggagctccatcaacgcttcgcgcgaccgatgacacga 2204
||||||| || || ||| |||||||||||||||| ||||| || || |||||||||
Sbjct: 55114 atcaacagtcgtcgggacgcgcggagctccatcaatgcttcacgtgaacgatgacacga 55172

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

Query: 1138 ggggtagccctgggtgtgcggacggactctaacaccgacagctggcgcgccaggtaggg 1197
||||| ||||||||| ||| ||||| | |||||||||||||||||||||||||
Sbjct: 54142 ggggtaaccctgggtgcacggtcggacccgaaacaccgacagctggcgcgccaggtaggg 54201

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

Query: 1258 cccccgggactatgttttgccttgaaccatctcatccatagcagatgaagagggaact 1317
| ||||| | || || ||||| || || ||||||||| |||| ||||| |||||||||
Sbjct: 54262 cccccggatccatattctgcttcggtactatctcatctgtagcggatgaggagggaact 54321

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

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

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

Query: 1975 cccgacttcgctcgtgcaatgaacacgccgagtgagtcggagggtactggcccagata 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 ctcttttctaccccgacgtcctcttcatc 1650
|||| | ||||| ||||| |||||
Sbjct: 54605 ctccattctaccccgacgtcctcttcatc 54633

Score = 48.1 bits (24), Expect = 0.23
Identities = 34/36 (94%), Gaps = 1/36 (2%)
Strand = Plus / Minus

Query: 562 ttgtgggggatagatatcccc-gggtccactagaag 596
||||||| ||||||| |||||||||
Sbjct: 15523 ttgtggggacagatatccccgggtccactagaag 15488

Score = 48.1 bits (24), Expect = 0.23
Identities = 34/36 (94%), Gaps = 1/36 (2%)
Strand = Plus / Plus

Query: 563 tgtgggggatagatatcccc-gggtccactagaagg 597
||||||| ||||||| |||||||||
Sbjct: 53541 tgtggggacagatatccctgggtccactagaagg 53576

Score = 46.1 bits (23), Expect = 0.90
Identities = 47/55 (85%)
Strand = Plus / Minus

Query: 1760 ggcgacatcacgaggctggggaacgggatccggcgcaacccgtatcccgggacga 1814
||||||| ||| | ||||||||| ||||| || || |||||
Sbjct: 28183 ggcgacatcacgcggccagagaacgggatccggagcaacctgtctcgcgggacga 28129

Score = 46.1 bits (23), Expect = 0.90
Identities = 33/35 (94%), Gaps = 1/35 (2%)
Strand = Plus / Minus

Query: 563 tgtgggggatagatatcccc-gggtccactagaag 596
||||||| ||||||| |||||||||
Sbjct: 29356 tgtggggacagatatccccgggtccactagaag 29322

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

Length = 39598

Score = 137 bits (69), Expect = 3e-28

Identities = 220/269 (81%), Gaps = 1/269 (0%)

Strand = Plus / Plus

Query: 1069 tctctcgtgcgtccagcacgaaccattgagttacaatcaacagcacccgtcctac-ccaaa 1127

Query: 1128 agcaccgcaaggggtagccctgggtgtgcggaaggactctaaacaccgacagctggcgcg 1187

Query: 1188 ccaggtagggggtgtgtctttgatctgagctagctcaatgaccattacctccaaatgcaa 1247

Query: 1248 gatcgcccttcgccccgggactatgttttgctttggaaccatctcatccatagcagatga 1307

Query: 1308 agagggaactctgcaccgcatagcagatc 1336

Score = 73.8 bits (37), Expect = 4e-09

Identities = 86/101 (85%), Gaps = 1/101 (0%)

Strand = Plus / Plus

Query: 562 ttgtgggggatatagatatcccc-gggtccactagaaggcgagaaggcctcgcgtgtggcca 620

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
---	---	---	---	---	---	---	---	---	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	-----

Subject: 8574 ttgtgggggacagatatccccgggtccactagaaggcaagaaggcctcacgaaaggcct 8633

Query: 621 cgggccagttaccccgcaaggccatcccttcgtgggtcgag 661
||||| ||| ||||||||| ||||||||| ||||
Sbjct: 8634 cgggccattatttcgcaaggccacccttcgtgggccgag 8674

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

Query: 562 ttgtgggggatagatatccccgggtccactagaaggcgagaaggcctcgcggtggtggccac 621
||||||||| ||||||||| || ||||||||||| ||||||||| || |||||
Sbjct: 28412 ttgtgggggacagatatccccgggtcactagaaggcaagaaggcctcacgaaaggcctc 28471

Query: 622 gggccagttaccccgcaaggccatcccttcgtgggtcgag 661
||||| ||| ||||||||| ||||||||| ||||
Sbjct: 28472 gggccattatttcgcaaggccacccttcgtgggccgag 28511

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

Query: 1012 gaagtagtgtattacgcctctctaagcgggcc 1043
||||||| || |||||||||||||||||
Sbjct: 28869 gaagtaggtgttacgcctctctaagcgggcc 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 ggctaccggcggtctgttactcgagcagttaatcaccttctacccatcactaatcctcca 2127
||||| ||||||||| ||||| ||||| || || ||||| || || || |||||
Sbjct: 16796 ggctatcgggcggtctgtcactcgggcagctaaccatcttctgcctctcggtcatcctccg 16855

Query: 2128 agcgacctagccatgccatcaacagccggcgagacacggagctccatcaacgcttcg 2187
||||| ||||| ||||||||| || || || ||| || ||||| ||||||| |||||
Sbjct: 16856 agcgatctacaacatgccatcaatagtcacgggacgcacggagcccatcaatgcttca 16915

Query: 2188 cgcgaccgatgaca 2201
||||| ||| |||
Sbjct: 16916 cggaacgacgaca 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 agtgcgccacggtcgtgtatataaggtccagagggtaccccatcatTT-ctatcgaccat 939
||||| ||||||||| ||||||||| || || ||||||| ||||||||| || |||||||||
Sbjct: 289 agtgcgccacggtcggatatataaggcctaggggtaccccatcatTTTccatcgaccat 348

Query: 940 ctacctatctcatcagcttttctccattcaggagacctcgcttgtaaccaccacatatata 999
| ||||||||| ||||||||| ||||||||| || || ||||||| ||||||||| ||
Sbjct: 349 caacctatctcattagcttttcttccattcaggagacttcagttgtaaccaccacataaa 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

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

Score = 135 bits (68), Expect = 1e-27
Identities = 152/180 (84%)
Strand = Plus / Plus

Query: 1149 ggggtgtgcggacggactctaaacaccgacagctggcgcgccaggtagggggtgtgtcttt 1208
||||||| ||||| | ||||||||||||||||||||||||||||
Sbjct: 80649 ggggtgtcggtcggacccaaacaccgacagctggcgcgccaggtagggggtgtgtcgac 80708

Query: 1209 gatctgagctagctcaatgaccattacctccaaatgcaagatcgcccttcgccccgggac 1268
|||| ||||||||||||| || | |||| | ||||||| ||| || ||||| |
Sbjct: 80709 gatccaagctagctcaatggccgtcacctttcacagcaagatcacctccgtcccggatc 80768

Query: 1269 tatgttttgcctttggaaccatctcatccatagcagatgaagaggggaactctgcaccgcat 1328
| || ||||| ||||| ||||||||| |||||||||||||||||||||||||
Sbjct: 80769 cgtattctgcttcggaacaatctcatccgtagcagatgaagaggggaactctgcaccgcat 80828

Score = 83.8 bits (42), Expect = 4e-12
Identities = 93/110 (84%)
Strand = Plus / Plus

Query: 1915 caagccgagcaaggtgcaaggtgcgccgagagaatgctctctttgctcggaaacctgtac 1974
||||||||||||| ||||||| |||| ||||| | |||| | || ||||| ||
Sbjct: 81367 caagccgagcaagatgcaaggcaacgccaggagaatccattcttcgggcgcaacctgaac 81426

Query: 1975 cccgacttcgctcgtgcaatgaacacgccgagtgaagtcggagggtact 2024
||||||||||| || || ||||||||||||||||||||||||| |||||
Sbjct: 81427 cccgacttcgcccagccatgaacacgccgagtgaagtcggaggagtact 81476

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

Query: 562 ttgtgggggatagatatcccc-gggtcacta 592
||||||||||||||||||| |||||||||
Sbjct: 80049 ttgtgggggatagatatcccctgggtcacta 80080

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 aaacaccgacagctggcgccaggtagggg 1198
||||
Sbjct: 133339 aaacgccgacagttggcgccaggtagggg 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 taaccaccacatatagatccatccaagaagtagtgattacgcctctctaagcggcc 1043
|||||
Sbjct: 148845 taaccaccacataaagatccacatcaggaagtaggtgttacacctctctaagcggcct 148904

Query: 1044 aaacttgcagaaaaccgcctatccctctctcgtgcgtccagcacgaaccattgagttaca 1103
|||

Sbjct: 148905 gaacctgtagaaatt-gtctatcg-tctctcatgcgcctagcatgaaccatcgagctaca 148962

Query: 1104 atcaacagcaccgtcctacccaaaagcaccgcaagggtagccctgggtgtgcggacgga 1163
|| || |||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 148963 gtcggcaacaccatcctacccgaaagcacctcgaggggtaaccctgggtgcatggtcggg 149022

Query: 1164 ctctaaacaccgacagctggcgcgccaggtaggggtgtgtctttgatctgagctagctc 1223
| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 149023 tcccaaacaccgacagctggcgcgccaggtaggggtgtgtcgtgatccaagttagctc 149082

Query: 1224 aatgaccattacctccaaatgcaagatcgcccttcgccccgggactatgttttgccttgg 1283
||||||| || || || ||||| || || ||||| || || ||||| || |||||

Sbjct: 149083 aatgaccatcactttccaacacaagattgctctccgcctggatccgtgttcttcttgg 149142

Query: 1284 aaccatctcatccatagcagatgaagagggaactctgcaccgcatagcagatctattgga 1343
||||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 149143 gaccatctcatccgtggcagacgaagaaggaattctacatcatatagcgatccaccgga 149202

Query: 1344 gaagaagctttcctcagaaatctc 1367
||||||| ||||| |||||

Sbjct: 149203 gaagaagccttcctcaaaaatctc 149226

Score = 85.7 bits (43), Expect = 1e-12
Identities = 106/127 (83%)
Strand = Plus / Plus

Query: 2066 aaggctaccggcggtgcttactcgagcagttaatcaccttctacccatcactaatcctc 2125
||||||| ||| ||||| ||||| || || ||||| ||||| || || |||||

Sbjct: 149902 aaggctatcggtggctgctcactcgggcgactaatcatcttctacctctcgtcctcctc 149961

Query: 2126 caagcgacctacgcatgccatcaacagccggcgagacacgggagctccatcaacgctt 2185
| ||||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 149962 cgagcgatctacggcacgccatcaacagtcggcgggacgcgcagagctccatcaacgctt 150021

Query: 2186 cgcgca 2192
| |||||

Sbjct: 150022 cacgca 150028

Score = 71.9 bits (36), Expect = 2e-08
Identities = 49/52 (94%), Gaps = 1/52 (1%)
Strand = Plus / Plus

Query: 562 ttgtgggggatagatatcccc-gggtccactagaaggcgagaaggcctcgcg 612
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 148416 ttgtgggggacagatatccccgggtccactagaaggcaagaaggcctcgcg 148467

Score = 50.1 bits (25), Expect = 0.057
Identities = 97/121 (80%)
Strand = Plus / Plus

Query: 1622 ctcttttctaccccgacgtcctcttcatcagggggagattggagtttagcaccgctcttca 1681
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 149470 ctccattctaccccgacgtcctcttcatcagggggaagagtggaatcatctcccatctcgg 149529

Query: 1682 acgatgagccaacccatgcaaggggaagagcctccccagcgtgaggcgcgacgacggagga 1741
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 149530 acgacgagccaaccgtgcctggggaagaacccctcagtgagaagctcgccgacggagga 149589

Query: 1742 a 1742
 |
Sbjct: 149590 a 149590

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

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 43416 aaacgccgacagttggcgcgccaggtagggg 43386

>gb|AF090447.2| Zea mays 22 kDa alpha zein gene cluster, complete sequence
Length = 346296

Score = 127 bits (64), Expect = 3e-25
Identities = 190/232 (81%)
Strand = Plus / Minus

Query: 1973 accccgacttcgctcgtgcaatgaacacgccgagtggaagtcggagggtactggcccaga 2032
||||||| | || | ||||| ||||| ||||| || |||| | ||
Sbjct: 79768 accccgacttcacccgggcatgaacacgccgagtggaagtcggaggagtgttgctcgga 79709

Query: 2033 tagctgacggcctcccggaaccctagacacggaaggctaccggcggtgcttactcgag 2092
||||| ||||| | || | || | || ||||| ||||| | |||| |
Sbjct: 79708 tagctgatggcctccccggactcccgacgccgagggtatcgcggtgttcactcaag 79649

Query: 2093 cagttaatcaccttctacccatcactaatcctccaagcgacctacgccatgccatcaaca 2152
||| | ||||| || || | || | || | || ||||| || ||||| ||
Sbjct: 79648 cagccaaccaccttctacccctcgctacccgccgaacgatctacgacacgccatcaaca 79589

Query: 2153 gccggcgagacacgaggagctccatcaacgcttcgcgcgaccgatgacacga 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 agcacgaaccattgagttacaatcaacagcacgcgtcctaccc--aaaagcaccgcaagg 1140
||||||| ||| |||| | | | ||||| || | ||||| ||||
Sbjct: 80636 agcacgaaccatcgagctacagtcgataacaccgtcctacacaaaaagcaccttgagg 80577

Query: 1141 gtagccctgggtgtgcggacggactctaaacaccgacagctggcgccaggtagggggt 1200
| ||| |||| |||| |||| | ||||| ||||| ||||| ||||
Sbjct: 80576 gccaccccggtgcgcggtcgacccaaaacaccgacagctggcgtgccaggtagcgggt 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 gctcctttctaccccgacgtcctcttcatcagggg 1655
||||| ||||||||||||||||||||| ||||
Sbjct: 80108 gctccattctaccccgacgtcctcttcatcggggg 80074

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

Query: 1761 gcgacatcacgaggtggggaacgggatccggcgcaaccggtatcccgggacga 1814
||||||| || || ||||||||| ||| ||||||||| || |||||
Sbjct: 79968 gcgacatcacgaagccggagaacgggatctggcacaaccggtatcgcgagacga 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 tctctcgtgcgtccagcacgaaccattgagttacaatcaacagcaccgctcctaccc--aa 1126
||||||| || ||||||||||||||||| |||| || | ||||||||| | ||
Sbjct: 2693 tctctcgtgcatctagcacgaaccattgagctacagtcgataaacccgctcctactccaaa 2752

Query: 1127 aagcaccgcaaggggtagccctgggtgtgcggacggactctaaacaccgacagctggcgc 1186
||||||| | ||||| | || ||||| |||| | ||||| |||||||||
Sbjct: 2753 aagcacctcgaggggcaaccccggtgcgcggtcggacccaaaacactgacagctggcgc 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-ccgggtccactagaaggcgagaaggcctc 609
||||||| ||||| ||||||||| |||||
Sbjct: 2178 ttgtgggggacagatatcctccgggtccactagaaggcaagaaggcctc 2226

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

Query: 1622 ctcctttctaccccgacgtcctcttcatcagggggagattgga 1664
||| ||||||||| ||| ||||| |||
Sbjct: 3211 ctccgttctaccccgacgtcctctttatcggggggagagtgga 3253

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

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

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

Query: 2086 actcgagcagttaatcaccttctacccatcactaatcctccaagcgacctacgccatgcc 2145
||||| |||| || | ||||| || || | ||||||||| || | || |||
Sbjct: 3663 actcgggcagctaaccatcttctgcctctcgtcatcctccaagcgatctatgacagcc 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 acccgaaaaactccgtgtccacttcgccacaaaggagtggacacggatta 1510
||||||| ||| ||| ||||||| || ||||||| ||||||||||||||||
Sbjct: 3069 acccgaagaaccccggtgtccacctcatccacaaaagagtggacacggatta 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 tctctcgtgcgtccagcacgaaccattgagttacaatcaacagcacgcgtcctaccc--aa 1126
||||||||| || ||||||||||||||||| |||| || | ||||||||||| | ||
Sbjct: 10022 tctctcgtgcatctagcacgaaccattgagctacagtcgataacaccgtcctactccaaa 10081

Query: 1127 aagcaccgcaaggggtagccctgggtgtgcggacggactctaaacaccgacagctggcgc 1186
||||||| | ||||| | ||| ||||| |||| ||||| | ||||||| |||||||||||||
Sbjct: 10082 aagcacctcgaggggcaaccccggtgcgcggtcggacccaaaacactgacagctggcgc 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 ttgtgggggacagatatcctccgggtccactagaaggcaagaaggcctc 9555

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

Query: 562 ttgtgggggatagatatccccg-ggtccactagaaggcgagaaggcctc 609
||||||| ||||||| ||||||||| |||||||
Sbjct: 687 ttgtgggggacagatatcccccggtccactagaaggcaagaaggcctc 735

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

Query: 1622 ctccctttctaccccgacgtcctcttcatcagggggagattgga 1664
|||| ||||||||| ||| ||||||| |||
Sbjct: 10540 ctccgttctaccccgacgtcctcttctatcggggggagagtgga 10582

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

Query: 1966 aacctgtaccccgacttcgctcgtgcaatgaacacgccgagtgaagtcggaggggtactg 2025
||||| ||||||||| || | ||||||| |||| | |||| | || ||
Sbjct: 10872 aacctgaaccccgacttcgtccgatccatgaacacaccgagcgaggtcggtggagtgtg 10931

Query: 2026 gcccagatagctgacggcctcccgcaaccctagacacggaaggctaccggcggtgctt 2085
|| | ||||| | ||||||| || | |||| | | ||||| |||||||||
Sbjct: 10932 gtcgagatagccaatggcctccccggactccagacgccgagggtatcggcggctgctc 10991

Query: 2086 actcgagcagttaatcaccttctacccatcactaatcctccaagcgacctacgccatgcc 2145
||||| |||| ||| || ||||||| || || || ||||||||| ||| | || |||
Sbjct: 10992 actcgggcagctaaccatcttctgcctctcgtcatcctccaagcgatctatgacacgcc 11051

Query: 2146 atcaa 2150
|||||
Sbjct: 11052 atcaa 11056

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

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

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

Query: 982 tgtaaccaccacatatata-gatccatcccaagaagtagtgtattacgcctctctaagcgg 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 taatcaccttctacccatcactaatcctccaagcgacctacgccatgccatcaacagccg 2156
||||||||||||| |||||| || |||| || ||| |||||| ||| |||||||||||||||
Sbjct: 2273 taatcaccttctgcccatcgctcatccccgagcaacctacaccagccatcaacagccg 2214

Query: 2157 gcgagacacgcggagctccatcaacgcttcgcgcgaccgatgacacgaaagtgaga 2212
|||||| | ||||||||||||||||| ||||||||||||||||| | |||||||| |||||
Sbjct: 2213 acgagacgcgcggagctccatcaatgcttcgcgcgaccgacggcacgaaagcgaga 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 tgtaaccaccacatatata-gatccatcccaagaagtagtgtattacgcctctctaagcgg 1040

||||| ||||||||| | ||||| ||| ||||||| || ||||||||| |||||||
Sbjct: 10074 tgtaatccaccacataaaagatccacaccaggaagtaggggtgttacgcctctttaagcgg 10015

Query: 1041 cccaaacttgcaaaaaccgctatccctctctcgtgcgtccagcacgaaccattgagtt 1100
||||||| || | |||| | | | ||||||||| || ||||||||| ||| |

Sbjct: 10014 cccaaacctgtataaaattgtcca-ctgtctctcgtgcatctagcacgaaccatcgagct 9956

Query: 1101 acaatcaacagcacgcgtcctaccc--aaaagcacgcgaagggtagccctgggtgtgcgg 1158
||| | | ||||||||| | ||||||||| | |||| | ||| ||||| |||

Sbjct: 9955 acagttggtaacaccgtcctactccaaaaagcacctcgaggggcaaccccggtgcgcgg 9896

Query: 1159 acggactctaaacaccgacagctggcgcgccaggtagggggtgtgtctttgatctgagct 1218
||||| | ||||||||| ||||||||| ||||||||| ||||| ||||

Sbjct: 9895 tcggacccaaaacaccgacagctggcgcgccaggtagggggtgtgtcactgatccaagct 9836

Query: 1219 agctcaatgaccattacctccaaatgcaagatcgcccttcgccccgggactatgttttgc 1278
||||||| || | || | | | |||||| | || |||| | | | |||| |

Sbjct: 9835 agctcaatggccgtcactttccagcacaagatcactctccgacctggatccgtgttctac 9776

Query: 1279 tttggaaccatctcatccatagcagatgaagaggaactctgcaccgcatagcagatcta 1338
|| ||||||||| |||||| |||| | |||||| | || || ||||||||| |

Sbjct: 9775 ttcggaaccatctcatccatggcagacgaagaagaactctacatcgcgtagcagatcca 9716

Query: 1339 ttggaga 1345
| |||||

Sbjct: 9715 tcggaga 9709

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

Query: 562 ttgtgggggtagatatcccc-gggtccactagaaggcgagaaggcctcgcgtgtggcca 620
||||||| ||||||||| ||||||||| ||||||||| || |||||

Sbjct: 10502 ttgtgggggacagatatccccgggtccactagaaggcaagaaggcctcacgaaaggcct 10443

Query: 621 cgggccagttaccccgcaaggccatcccttcgtgggtcgag 661
|||||| ||| ||||||||| ||||||||| |||||||

Sbjct: 10442 cgggccattatatcgcaaggccacccttcgtgggtcgag 10402

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

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

Query: 2026 gccagatagctgacggcctcccggaaccctagacacggaaggctaccggcggtgctt 2085
|| | ||||| || ||||||| | || | |||| | | ||||| |||||||||
Sbjct: 9061 gctcggatagccgatggcctccccctgactccagacgctgagggtatcggcggctgctc 9002

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

Query: 2146 atcaacagccggcgagacacgcggagctccatcaacgcttcgcgcgaccgatgaca 2201
||||| || | || || || | || ||||||||| ||||||||| || ||||
Sbjct: 8941 atcaatagtcgacgggacgcacagagctccatcaatgcttcgcgcgaacgacgaca 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 aaaagcaccgcaaggggtagccctgggtgtgcggacggactctaaacaccgacagctggc 1184
||||||| | ||||| | ||| ||||||||| |||| | |||||||||
Sbjct: 9408 aaaagcacctcgaggggcaaccccggtgtgcggtcggacccaaacaccgacagctggt 9349

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

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

Query: 1305 tgaagagggaactctgcaccgcatagcagatc 1336
||||| ||||||| || ||||||| |||
Sbjct: 9228 cgaagaagggaactctacattgcatagcggatc 9197

Score = 71.9 bits (36), Expect = 2e-08
Identities = 82/96 (85%), Gaps = 1/96 (1%)
Strand = Plus / Minus

Query: 562 ttgtgggggatagatatcccc-gggtccactagaaggcgagaaggcctcgctgtggcca 620
||||||| ||||||| ||||||||| ||||||| || |||
Sbjct: 9984 ttgtgggggacagatatccccgggtccactagaaggcaagaaggcctcacgaaaggcct 9925

Query: 621 cgggccagttaccccgcaaggccatcccttcgtggg 656
||||| ||| ||||||| |||||||
Sbjct: 9924 cgggccattatttcgcaaggccacccttcgtggg 9889

Score = 67.9 bits (34), Expect = 2e-07
Identities = 184/234 (78%)
Strand = Plus / Minus

Query: 1966 aacctgtaccccgacttcgctcgtgcaatgaacacgccgagtgaagtcggaggggtactg 2025
||||| | ||||||||| || ||||||| ||||| || | || || ||
Sbjct: 8600 aacctgaatcccgacttcgctcgagccatgaacacaccgagcgaggttgatggagtgtg 8541

Query: 2026 gccagatagctgacggcctcccgcaaccctagacacggaaggctaccggcggctgctt 2085
|| | ||||| || ||||||| || || ||||| | || ||||| || |||||
Sbjct: 8540 gtcgगतagccgatggcctcccgactctagacgccgagggtatcggtggctgctc 8481

Query: 2086 actcgagcagttaatcaccttctacccatcactaatcctccaagcgacctacgccatgcc 2145
||||| |||| ||| || ||||| || | || ||||||| ||||| |||| || |||
Sbjct: 8480 actcgggcagctaaccatcttctgcctcccgctcatcctccgagcgatctacaacagcc 8421

Query: 2146 atcaacagccggcgagacacgcggagctccatcaacgcttcgcgcgaccgatga 2199
||||| || || || ||| || || ||||||||| ||||||||| |||||
Sbjct: 8420 atcaatagtcgacgggacgcacagagctccatcaatgcttcgcgcgaacgatga 8367

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-gatccatcccaagaagtagtgtattacgcctctctaagcgg 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-gatccatcccaagaagtagtgtattacgcctctctaagcgg 1040
||||||| ||||| || ||||||| | ||||| |||||||||
Sbjct: 178146 tgtaaccaccacataaaagatccacaccaggaagtaggggttacacctctctaagcgg 178205

Query: 1041 cccaaacttgcagaaaaccgcctatccctctctcgtgcgtccagcacgaaccattgagtt 1100
||| || | ||| | | | | ||||||| || ||||||||| ||| |
Sbjct: 178206 cccgaacctgtacaaaattgtcca-ctgtttctcgtgcttctagcacgaaccatcgagct 178264

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

Query: 1159 acggactctaaacaccgacagctggcgcgccaggtagggggtgtgtctttgatctgagct 1218
| ||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 178325 tcagacccaaaacaccgacagctggcgcgccaggtagggggtgtgtcactgatccaagct 178384

Query: 1219 agctcaatgaccattacctccaaatgcaagatcgcccttcgccccgggactatgttttgc 1278
||||||| |||| | | | | ||||| || |||| | | ||||| ||
Sbjct: 178385 agctcaatggccatcactttccagcacaagatcgctctccgccctagatctgtgttctgc 178444

Query: 1279 tttggaaccatctcatccatagcagatgaagaggaactctgcaccgcatagcagatc 1336
|| ||||| ||||| ||||| ||||| ||||| || ||||| ||||| |||||
Sbjct: 178445 ttcagaaccatctcatccatggcagatgaagaaggaactctacatcgcatagcggatc 178502

Score = 60.0 bits (30), Expect = 6e-05
Identities = 46/50 (92%), Gaps = 1/50 (2%)
Strand = Plus / Plus

Query: 564 gtgggggatagatatccc-cgggtccactagaaggcgagaaggcctcgcg 612
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 177721 gtgggggacagatatccctcggtccactagaaggctagaagacctcgcg 177770

Score = 52.0 bits (26), Expect = 0.015
Identities = 35/38 (92%)
Strand = Plus / Plus

Query: 1627 ttctaccccgacgtcctcttcatcagggggagattgga 1664
||||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 178772 ttctaccccgacgtcctctttatcggggggagagtgga 178809

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

Query: 1173 ccgacagctggcgcgccaggtagggg 1198
|||||| | ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 56887 ccgacagttggcgcgccaggtagggg 56912

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

Length = 582

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

Query: 982 tgtaacccaccacatata-gatccatcccaagaagtagtgtattacgcctctctaagcgg 1040
||||| ||||||||| | ||||| ||| ||||||| | ||||||||| |||||||
Sbjct: 271 tgtaatccaccacataaaagatccacaccaggaagtaggggtgttacgcctctttaagcgg 330

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

Query: 1101 acaatcaacagcacgcctctacc--aaaagcacgcgaaggggtagccctgggtgtgcgg 1158
||| || ||||||||| | ||||||||| | |||| | ||| ||||| |||||
Sbjct: 390 acagtcggtgacacgcctactccaaaagcacctcgaggggcaacccgggtgcgcgg 449

Query: 1159 acggactctaaacaccgacagctggcgccaggtagggggtgtgtctttgatctgagct 1218
||||| | ||||||||||||||||||||||||||||||||||| ||||| |||||
Sbjct: 450 tcggacccaaaacaccgacagctggcgccaggtagggggtgtgtcactgatccaagct 509

Query: 1219 agtcaatg 1227
|||||||
Sbjct: 510 agtcaatg 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 tctcgtgcgtccagcacgaaccattgagttacaatcaacagcacgcctctacc--aaaa 1128
||||||| || ||||||||| ||||| ||| | ||||||||| | |||||
Sbjct: 56170 tctcgtgcatctggcacgaactattgagctacagtcgataacaccgtctactccaaaaa 56111

Query: 1129 gcaccgcaaggggtagccctgggtgtgcggacggactctaaacaccgacagctggcgcg 1188
||||| | |||| | ||| |||| | ||| |||| | ||||||| |||||||||
Sbjct: 56110 gcacctcgaggggtaccccggtgcgcggtcgacccaaaacactgacagctggcgcg 56051

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

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

Query: 1309 gagggaaactctgcaccgcat 1328
|||||
Sbjct: 55930 gagggaaactctgcatcgcat 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 gctcggatagctgatgggctccctcggactcacgacgccgagggtatcgacggctgttc 55180

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

Query: 2146 atcaacagccggcgagacacgcggagctccatcaacgcttcgcgcgaccgatgacacga 2204
|||||
Sbjct: 55119 atcaacagtcgtcgggacgcgcggagctccatcaatgcctcgcgtgaacgacgacacga 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 tctcgtgcgtccagcacgaaccattgagttacaatcaacagcacgcgtccta--cccaaaa 1128
||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 13343 tctcgtgcatctggcacgaaccattgagctacagtcgataaacaccgtcctactcctaaaa 13284

Query: 1129 gcaccgcaaggggtagccctgggtgtcggacggactctaaacaccgaca 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 gcgacatcacgaggtggggaacgggatccggcgcaaccgatatcccgggacga 1814
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 55492 gcgacatcacgagccgggggagcaggacccggcgagcctgtatcgcgagacga 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 ggggtgtgcggacggactctaaacaccgacagctggcgcgccaggtaggggggtgtgtcttt 1208
||||||| ||||| | ||||||||||||||||||||||||||||
Sbjct: 89981 ggggtgtgcggtcggacccaaacaccgacagctggcgcgccaggtaggggggtgtgtcgac 89922

Query: 1209 gatctgagctagctcaatgaccattacctccaaatgcaagatcgcccttcgccccgggac 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 cccgacttcgctcgtgcaatgaacacgccgagtgagtcggaggggtactggcccagata 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

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

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198
|||| ||||||| |||||||||||||||||
Sbjct: 17151 aaacgccgacagttggcgcgccaggtagggg 17121

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

Query: 563 tgtgggggatagatatcc-cgggtccacta 592
||||||||||||||||| |||||||||||
Sbjct: 90582 tgtgggggatagatatcctcgggtccacta 90552

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

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198
|||| ||||||| |||||||||||||||||
Sbjct: 111035 aaacgccgacagttggcgcgccaggtagggg 111065

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

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

Query: 1071 tctcgtgcgtccagcacgaaccattgagttacaatcaacagcacccgtcctaccc--aaaa 1128
||||||||| ||||||||||||||| ||| |||| | | ||||||||||| | ||||
Sbjct: 102163 tctcgtgcgcccagcacgaaccatcgagctacagtcggtaacaccgtcctactcctaaaa 102104

Query: 1129 gcaccgcaaggggtagccctgggtgtgcggacggactctaaacaccgacagctggcgcg 1188

Strand = Plus / Minus

Query: 1621 gtccttttctaccccgacgtccttcat 1649
||||| ||||||||||||||||||||
Sbjct: 92174 gtcctattctaccccgacgtccttcat 92146

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

Query: 1763 gacatcacgaggctggggaacgggatccggcgcaaccgtatcccgggacga 1814
||||||| ||||| ||||| || ||||||||| ||||| || |||||
Sbjct: 92035 gacatcacgaggccggggagcgggaccagcgcaaccatattcacgagacga 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 gcaccgcaaggggtagccctgggtgtgcggacggactctaaacaccgacagctggcgcg 1188
||||| | ||||||| ||||||||| ||| ||||| | ||||||| |||||||||
Sbjct: 46779 gcacctcgggggtaaacctgggtgcgcggtcggaccgaaacactgacagctggcgcg 46838

Query: 1189 caggtagggggtgtgtctttgatctgagctagctcaatg 1227
||||||||||| ||| | |||||||||
Sbjct: 46839 caggtagggggtgtgtcatcgacccaagctagctcaatg 46877

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

Query: 1966 aacctgtaccccgacttcgctcgtgcaatgaacacgccgagtgagtcggaggggtactg 2025
||||| ||||||||| || || ||||||||| ||||||||| |||
Sbjct: 57038 aacctgaaccccgacttcgcccagccatgaacacgccgagtgagttggaggggtgttg 57097

Query: 2026 gcccgatagctgacggcctcccgcaaccctagacacggaaggctaccggcggtgctt 2085
|| | || | || ||||||| || || | ||||| || || || ||||||| |
Sbjct: 57098 gtcggtatgatgatggcctccctcgactcccgacaccgaggggtatcgcggtattc 57157

Query: 2086 actcgagcagttaatcaccttctacccatcactaatcctccaagcgacctacgccatgcc 2145
|||| ||||| ||||||||| || || | || | || || || ||
Sbjct: 57158 actcaagcagccaatcaccttctaccctcgctcaccgcggaacgatctatgacacacc 57217

Query: 2146 atcaacagccggcgagacacgcggagctccatcaacgcttcgcgcgaccgatgacacga 2204
||||||| || ||||||| ||||||||| || ||||||| || || |||||||
Sbjct: 57218 atcaacagtcgccgagacgcgcggagctccatcaatgcctcgcgtgaacgacgacacga 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 gtccttttctaccccgacgtccttcat 1649
||||| ||||||||||||||||||||
Sbjct: 56708 gtcctattctaccccgacgtccttcat 56736

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

Query: 1763 gacatcacgaggctggggaacgggatccggcgcaaccgtatcccgggacga 1814
||||||| ||||| ||||| || ||||||||| ||||| || |||||
Sbjct: 56847 gacatcacgaggccggggagcgggaccagcgcaaccatatacacgagacga 56898

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

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198
||||| ||||||| |||||||||||||||||
Sbjct: 38168 aaacgccgacagttagcgcgccaggtagggg 38138

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

Query: 298 atttgtttgatggatttagtaaaggttatg 327
||||||| ||||||||| |||||||
Sbjct: 144300 atttgtttggtggatttagtagaggttatg 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 ggtgtgcggacggactctaacaccgacagctggcgcgccaggtaggggtgtgtctttg 1209
||||||| ||||| | ||||||||||||||||||||||||||||||| |
Sbjct: 164744 ggtgtgcggtcggacccaaaacaccgacagctggcgcgccaggtaggggtgtgtcgacg 164803

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

Query: 1270 atgttttgctttggaaccatctcatccatagcagatgaagagggaaactctgcaccgcata 1329
| || ||||| || || ||||||| |||| ||||||||||||| ||| ||||||| |
Sbjct: 164864 gtattctgcttcgggacaatctcatctgtagcggatgaagaggggaattctacaccgcctc 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 gagcaagccgagcaaggtgcaaggctgcgccgagagaatgctctctttgctcggaacctg 1971
||||||||||||||| ||||||| || || ||||| | ||||| | || |||||
Sbjct: 165458 gagcaagccgagcaagatgcaaggcaacgacgcgagaatccgctcttcgggcgcaacctg 165517

Query: 1972 taccccgacttcgctcgtgcaatgaacacgccgagtgaaagtcggaggggtactggcccag 2031
||||||||||| || || ||||||||||||| ||||||||| || || || || |
Sbjct: 165518 aaccgacttcgcccagctatgaacacgccgagcgaagtcggagcggttctagctcgg 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 aaacgccgacagtggcgccaggtagggg 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 ggtgtgcggacggactctaacaccgacagctggcgccaggtagggggtgtgtctttg 1209
 ||||| ||||| |
Sbjct: 156890 ggtgtgcggtcggacccaaacaccgacagctggcgccaggtagggggtgtgtcgacg 156831

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

```
Query: 1270   atgttttgctttggaaccatctcatccatagcagatgaagagggaactctgcaccgcata 1329
             | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct: 156770 gtattctgcttcgggacaatctcatctgtagcggatgaagagggaattctacaccgcctc 156711
```

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

Query: 1209 gatctgagctagctcaatg 1227
 ||| |||||
 Sbjct: 22858 gatccaagctagctcaatg 22840

```
Query: 1912   gagcaagccgagcaaggtgcaaggctgcgccgagagaatgctctctttgctcggaacctg 1971
             |||||
Sbjct: 156176 gagcaagccgagcaagatgcaaggcaacgacgcgagaatccgctcttcgggcgcaacctg 156117
```

```

Query: 2032   atagctgacgg 2042
          |||||
Sbjct: 156056 atagctgacgg 156046

```

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

Query: 1912 gagcaagccgagcaaggtgcaaggctgcgccgagagaatgctctctttgctcggaacctg 1971
|||||
Sbjct: 22203 gagcaagccgagcaagatgcaaggcaacgacgcgagaatccgctcttcgggcgcaacttg 22144

Query: 1972 taccgccacttcgctcgtgcaatgaacacgccgagtgaagtcggagg 2018
|||||
Sbjct: 22143 aaccgccacttcgctcgagctatgaacacgccgagcgaagtcggagg 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

Query: 1139 gggtagccctgggtgtgcggacggactctaaacaccgacagctggcgcgccaggtagggg 1198

Sbjct: 111101 gggtaaccccggtgtgcggtcggacccaaaacaccgacagctggcgcgccaggtagggg 111042

Query: 1199 gtgtgtctttgatctgagctagctcaatgaccattacctccaaatgcaagatcgcccttc 1258
||||||| ||||| ||||||||||||| || | ||||| | | ||||||||| | | |

Sbjct: 111041 gtgtgtcgacgatccaagctagctcaatggccgtcaccttcacagcaagatcatcgtgc 110982

Query: 1259 gccccgggactatgttttgctttggaaccatctcatccatagcagatgaagagggaactc 1318
| ||||| || | || ||||| || | ||||||||| ||||| ||||||||||||| ||

Sbjct: 110981 gtcccggatctgtattctgcttcgggacaatctcatctgtagcggatgaagagggaattc 110922

Query: 1319 tgcaccgcatagcagatct 1337
| ||||||||| |||||||||

Sbjct: 110921 tacaccgcatcgagatct 110903

Score = 87.7 bits (44), Expect = 3e-13
Identities = 107/128 (83%)
Strand = Plus / Minus

Query: 1912 gagcaagccgagcaaggtgcaaggctgcgccgagagaatgctctctttgctcggaacctg 1971
||||||||||||||||| ||| |||| | ||||| ||||||| | ||||| | || |||||||

Sbjct: 110376 gagcaagccgagcaagatgcgaggcaacgccgggagaatccgctcttcgggcgaacctg 110317

Query: 1972 tacccccgacttcgctcgtgcaatgaacacgccgagtggaagtcggaggggtactggcccg 2031
||||||||||||||| || || ||||||||||||| || ||||||||||||| ||||| || | |

Sbjct: 110316 aacccccgacttcgcccagctatgaacacgccaagcgaagtcggaggcgtactagctcgg 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

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: 98092 ttgtgggggatagatatccccgggtccacta 98061

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

Query: 1627 ttctaccccgacgtcctcttcac 1650
|||||
Sbjct: 110646 ttctaccccgacgtcctcttcac 110623

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

Query: 1137 aggggtagccctgggtgtgcggacggactctaaacaccgacag 1179
||||| ||| ||||| ||||| | |||||
Sbjct: 97503 aggggtaacccgggtgtgcggtcggacccaaacaccgacag 97461

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

Score = 109 bits (55), Expect = 7e-20
Identities = 285/358 (79%), Gaps = 4/358 (1%)
Strand = Plus / Plus

Query: 982 tgtaaccaccacatatata-gatccatcccaagaagtagtgtattacgcctctctaagcgg 1040
||||| ||||| ||| ||||| || |||||
Sbjct: 1676 tgtaaccaccacataaaaagatccacaccaggaagtagggtgttacgcctctctaagcgg 1735

Query: 1041 cccaaacttgcagaaaaccgcctatccctctctcgtgcgtccagcacgaaccattgagtt 1100
||| ||| || | |||| | | | | ||||| || | | ||||| |||||

Sbjct: 1736 cccgaacatgtataaaattgtcca-ctgtctctcttgcatctagcacgaaccatcgagtt 1794

Query: 1101 acaatcaacagcacccgtcctaccc--aaaagcacgcgaaggggtagccctgggtgtgcgg 1158
||| || | ||||| |||| | ||||| ||| ||| ||||| ||||

Sbjct: 1795 acagtcggtaacaccgtgctactccaaaatcacctcgagcggcaaccccggtgcgcgg 1854

Query: 1159 acggactctaaacaccgacagctggcgcgccaggtagggggtgtgtctttgatctgagct 1218
| ||| | ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 1855 tcagacccaaaacaccgacagctggcgcgccaggtagggggtgtgtcactgatccaagct 1914

Query: 1219 agctcaatgaccattacctccaaatgcaagatcgcccttcgccccgggactatgttttgc 1278
||||||| ||| ||| | | ||||| ||| | ||| || | ||| |||

Sbjct: 1915 agctcaatggacatcactttccagcacagaagatcgctctcctccctggatccgtgttctgc 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 ttgttggggacagatatcccccggtccactagaaggcaagaaggcctc 1297

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

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

Sbjct: 2629 aacctgaaccccgacttcgcccagccatgaacacaccgagcgaggtcgg 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 aacctgtaccccgacttcgctcgtgcaatgaacacgccgagtgaagtcggaggggtactg 2025
|||||||
Sbjct: 25162 aacctgaaccccgacttcgcccagccatgaagacgccgagtgaagtcggaggagtattg 25103

Query: 2026 gccagatagctgacggcctcccgcgaaacctagacacggaaggctaccggcggtgctt 2085
|||
Sbjct: 25102 gtcggtatagctgatggcctccccggactcccgacgctgagggtatcggcggtattc 25043

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

Query: 2146 atcaacagccggcgagacacgcgagctccatcaacgcttcgcgca 2192
|||||||
Sbjct: 24982 atcaacagtcggcgggacgcacagactccatcaacgcttcgtgca 24936

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

Query: 1071 tctcgtgcgtccagcacgaaccattgagttacaatcaacagcaccgtcctaccc--aaaa 1128
|||||||
Sbjct: 26022 tctcgtgcgcccacacgaaccatcgagctacagtcggtaacaccgtcctactcctaaaa 25963

Query: 1129 gcaccgcaaggggtagccctgggtgtgcggacggactctaaacaccgacagctggcgcg 1188
|||||
Sbjct: 25962 gcaccttgaggggtaaccccggtgcgcggtcgacccaaaacaccgacagctggcgcg 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 cggcgacatcacgaggctggggaacgggatccggcgcaacccgtatcccgggacga 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 tctcgtgcgtccagcacgaaccattgagttacaatcaacagcaccgtccta--cccaaaa 1128
||||||||| ||||||||| || |||| | | ||||||||| || |||||
Sbjct: 3663 tctcgtgcgcccagcacgaaccatcgagctacagtcggtaacaccgtcctactcctaaaa 3604

Query: 1129 gcaccgcaaggggtagccctgggtgtgcggacggactctaaacaccgaca 1178
||||| ||||||| || ||||| ||||| ||||| | |||||||||
Sbjct: 3603 gcaccttgagggtaaccccggtgcgcggtcggacccaaaacaccgaca 3554

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: 4181 ttgtgggggacagatatcccccggtccactagaagg 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 ggatgagtcagcgagattttcggaagattagttcagtttctcgtattattaggagac 857

|||||
Sbjct: 207 ggatgagtcagcatgattttcggtagattggttcagtcagttcactattagttaggagat 266

Query: 858 atatgatcctcatgtacgtatggagtgccccacggtcgtgtatataaggtccagaggta 917
|
Sbjct: 267 acgtgatcatcatgtacgtatggagtgccctatggtcgtgtatataaggccaagaggaa 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 cattcaggagacctcgcttgtaacccaccacatatagatcca 1005
|||
Sbjct: 393 cattcaggagacaccacttgtaacacaccacatacagatcca 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 tctcgtgcgccaacacgaaccatcgagctacagtcggtacatcgtcctactcctaaaa 32477

Query: 1129 gcaccgcaaggggtagccctgggtgtcggtcggtacgactctaaacaccgacagctggcgcg 1188
|||
Sbjct: 32478 acacctcgaggggaaccccggtgtcggtcggtacccaaaacaccgacagccggcgcg 32537

Query: 1189 caggtaggggtgtgtctttgatctgagctagctcaatgaccattacctccaaatgcaag 1248
|||
Sbjct: 32538 caggtaggggtgtgttagccgatctaagctagctcaatggtcgtcaccttcagcgcaag 32597

Query: 1249 atcgcccttcgccccgggactatgttttgctttggaaccatctcatccatagcagatgaa 1308

Sbjct: 32598 atcacccctccgccccggatccgtgttctgcttcggaactatctctatctgtagccgatgag 32657

Query: 1309 gagggaaactctgcaccgcatagcagatc 1336

Sbjct: 32658 gaaggaactctacatcgcatcgcagatc 32685

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

Identities = 179/224 (79%)

Strand = Plus / Plus

Query: 1966 aacctgtaccccgacttcgctcgtgcaatgaacacgccgagtgaagtcggaggggtactg 2025

Sbjct: 33289 aacctgaaccccgacttcgcccagccatgaatacgcgaagtgaagtcggaggagtactg 33348

Query: 2026 gccagatagctgacggcctcccgcaaccctagacacggaaggctaccggcggctgctt 2085

Sbjct: 33349 gctcggatagctgatgggctccctcggactcccgcagctcgagggctatcgacgactgttc 33408

Query: 2086 actcgagcagttaatcaccttctacccatcactaatcctccaagcgacctacgccatgcc 2145

Sbjct: 33409 actcaagcagccaaccatcttctacctctcgtcacccgcgcgaacgacctacgacatgcc 33468

Query: 2146 atcaacagccggcgagacacgcggagctccatcaacgcttcgcg 2189

||||| || ||| ||||||||| || ||||
 Sbjct: 33469 atcaacagtcgccgggacgcgcggagctccatcaatgcctcgcg 33512

Score = 54.0 bits (27), Expect = 0.004

Identities = 27/27 (100%)

Strand = Plus / Plus

Query: 1627 ttctaccccgacgtcctcttcacagg 1653

|||||
Sbjct: 32965 ttctaccccgacgtcctctttcatcagg 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 tctcgtgcgcccacacgaaccatcgagctacagtcggtaacatcgctcctactcctaaaa 43719

Query: 1129 gcaccgcaaggggtagccctgggtgtgcggacggactctaaacaccgacagctggcgcg 1188
|||| | |||| | ||| ||||||||| |||| | ||||||||| |||||||
Sbjct: 43720 acacctcgaggggcaaccccggtgtgcggtcggacccaaaacaccgacagccggcgcg 43779

Query: 1189 caggtaggggtgtgtctttgatctgagctagctcaatgaccattacctccaaatgcaag 1248
||||||| |||| | |||| ||||||||| |||| | |||| | |||||
Sbjct: 43780 caggtaggggtgtgttagccgatctaagctagctcaatggtcgtcacctccagcgcaag 43839

Query: 1249 atcgcccttcgccccgggactatgttttgctttggaaccatctcatccatagcagatgaa 1308
||| |||| ||||||| | |||| |||| |||| ||||||| |||| |||||
Sbjct: 43840 atcacctccgccccggatccgtgttctgcttcggaactatctcatctgtagccgatgag 43899

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

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

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

Query: 2026 gccagatagctgacggcctcccgcaaccctagacacggaaggctaccggcggtgctt 2085
|| | ||||||||| || |||| | || | ||| || ||||| || |||||
Sbjct: 44591 gctcggatagctgatgggtccctcggactcccgacgtcgagggtatcgacgactgttc 44650

Query: 2086 actcgagcagttaatcaccttctacccatcactaatcctccaagcgacctacgccatgcc 2145
|||| |||| | || || ||||||| || || | || | || ||||||| |||||
Sbjct: 44651 actcaagcagccaaccatcttctacctctcgtccacccgccgaacgacctacgacatgcc 44710

Query: 2146 atcaacagccggcgagacacgcggagctccatcaacgcttcgcg 2189
 ||||| | | | | ||||| | | | | |
 Sbjct: 44711 atcaacagtcgccgggacgcgcggagctccatcaatgccttcgcg 44754

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

```
Query: 1627  ttctaccccgacgtctctttcatcagg 1653
          |||||
Sbjct: 44207  ttctaccccgacgtctctttcatcagg 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 tctcgtgcgtccagcagcaaccattgagttacaatcaacagcaccgtcctacc--aaaa 1128
 ||||| ||| ||||| ||| ||| | | ||||| | |||
 Sbjct: 82798 tctcgtgcgccaacagcaaccatcgagctacagtcggttaacatcgctcctactcctaaaa 82857

Query: 1129 gcaccgcaaggggtagccctgggtgtgcggacggactctaaacaccgacagctggcgcg 1188
 |||| | |||| | || |||| |||| | |||| |||| |||| |||| ||||
 Sbjct: 82858 acacctcgaggggcaaccccggtgtgcggtcggaccaaaccgacagccggcgcg 82917

Query: 1189 caggtagggggtgtgtctttgatctgagctagctcaatgaccattacctccaaatgcaag 1248
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Sbjct: 82918 caggtagggggtgtgtagccgatctaagctagctcaatggctgctcaccttcagcgcaag 82977

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

```
Query: 1309   gagggaactctgcaccgcatagcagatc 1336
              || ||||| || ||||| |||||
Sbjct: 83038  gaaggaactctacatcgattgcagatc 83065
```

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

Query: 1966 aacctgtaccccgacttcgctcgtgcaatgaacacgccgagtgagtcggaggggtactg 2025
||||| |||||||||||| || || ||||| ||||| ||||||||||||| |||||
Sbjct: 83669 aacctgaaccccgacttcgcccagccatgaatacgccaagtgaagtcggaggagtactg 83728

Query: 2026 gccagatagctgacggcctcccgcaaccctagacacggaaggctaccggcggtgctt 2085
|| | ||||||||| || ||||| || || | ||| || ||||| || || ||| |
Sbjct: 83729 gctcggatagctgatgggctccctcgactcccgacgtcagggctatcgacgactgttc 83788

Query: 2086 actcgagcagttaatcaccttctacccatcactaatcctccaagcgacctacgccatgcc 2145
|||| ||||| || || ||||||||| || || | || | ||||||||| |||||
Sbjct: 83789 actcaagcagccaaccatcttctacctctcgctcaccgcggaacgacctacgacatgcc 83848

Query: 2146 atcaacagccggcgagacacgcggagctccatcaacgcttcgcg 2189
||||||| || || ||| ||||||||||||||||| || |||||
Sbjct: 83849 atcaacagtcgccgggacgcgcggagctccatcaatgcctcgcg 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 tctcgtgcgtccagcacgaaccattgagttacaatcaacagcaccgtcctaccc--aaaa 1128
||||||| ||| ||||||||| ||| |||| || | || ||||||||| | ||||

Sbjct: 71429 tctcgtgcgccccaacacgaaccatcgagctacagtcggtaacatcgctcctactcctaaaa 71488

Query: 1129 gcaccgcaaggggtagccctgggtgtgcgacggactctaaacaccgacagctggcgcg 1188

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

Sbjct: 71489 acacctcgaggggcaaccccggtgtgcggtcggacccaaaacaccgacagccggcgcg 71548

Query: 1189 caggtaggggtgtgtctttgatctgagctagctcaatgaccattacctccaaatgcaag 1248

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

Sbjct: 71549 caggtaggggtgtgtagccgatctaagctagctcaatggtcgtcacctccagcgcaag 71608

Query: 1249 atcgcccttcgccccgggactatgttttgctttggaaccatctcatccatagcagatgaa 1308

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

Sbjct: 71609 atcaccctccgccccgatccgtgttctgcttcggaactatctcatctgtagccgatgag 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 aacctgtaccccgacttcgctcgtgcaatgaacacgccgagtgaaagtcggaggggtactg 2025

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

Sbjct: 72300 aacctgaaccccgacttcgcccagccatgaatacgccaagtgaagtcggaggagtactg 72359

Query: 2026 gccagatagctgacggcctcccggaaccctagacacggaaggctaccggcggtgctt 2085

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

Sbjct: 72360 gctcggatagctgatgggtccctcggactcccgacgtcgagggtatcgacgactgttc 72419

Query: 2086 actcgagcagttaatcaccttctacccatcactaatcctccaagcgacctacgccatgcc 2145

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

Sbjct: 72420 actcaagcagccaacctcttctacctctcgctcaccgcccgaacgacctacgacatgcc 72479

Query: 2146 atcaacagccggcgagacacgcgagctccatcaacgcttcgcg 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 gagcaagccgagcaaggtgcaaggctgcgccgagagaatgctctctttgctcggaacctg 1971
|||||
Sbjct: 109929 gagcaagccgagcaagatgcaaggcaacgacgcgagaaatccgctcttcgggcgcaacctg 109870

Query: 1972 taccgccacttcgctcgtgcaatgaacacgccgagtggaagtcggaggggtactggcccag 2031
|||||
Sbjct: 109869 aaccccgacttcgcccagccatgaatacgccgagcgaagtcggagggcgttctagcccgg 109810

```
Query: 2032   atagctgacggcctcccgcaaccctagacacggaaggctaccggcggtgcttactcga 2091
              ||||| ||||| || || ||||| ||| | || ||||| ||| |||||
Sbjct: 109809 atagctgacggacttctcggaccccgacgccgagggataccggcgctgttcactcag 109750
```

```
Query: 2092   gcagttaatcaccttctacccatcactaatcctccaagcgacctagccatgccatcaac 2151
             |||  ||  ||  |||||  ||  |||||  ||  ||  |||||  ||  |||||  ||
Sbjct: 109749 gcagccaaccatcttctaccgctcgctcatccgccaagcgacctgcgacacgccatcaac 109690
```

```
Query: 2152   agccggcgagacacgcggaggtccatcaacgcttcgcgcga 2192
             || || ||||| | || |||| |||| |||||
Sbjct: 109689 agtcgtcgagacgcacgaagctctatcaatgcttcgcgcga 109649
```

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

```
Query: 1150      ggtgtgcggacggactctaaacaccgacagctggcgcgccaggtagggggtgtgtctttg 1209
                ||||| |||| | ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 110643    ggtgtgcggtcgacccaaacaccgacagctggcgcgccaggtagggggtgtgtcgacg 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

Score = 46.1 bits (23), Expect = 0.90

Query: 1753 aacgtgcggcgacatcacgaggctggggaacgggatccggcgcaacc 1799

Score = 46.1 bits (23), Expect = 0.90

Query: 563 tgtgggggatagatatcccc-gggtccacta 592

Score = 46.1 bits (23), Expect = 0.90

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198

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

Score = 103 bits (52), Expect = 4e-18

Query: 1150 ggtgtgcggacggactctaaacaccgacagctggcgcgccaggtaggggggtgtgtctttg 1209

Sbjct: 2672 ggtgcgcggtcggacccaaaacaccgacagctggcgcaccaggtagggggtgtgtcactg 2731

Query: 1210 atctgagctagctcaatgaccattacctccaaatgcaagatcgcccttcgccccgggact 1269
||| ||||| ||||| ||||| ||| | ||||| ||| ||||| |||

Sbjct: 2732 atccaagctagctcaatggccatcacttttcagcacaagatcgctctctgacctggatcc 2791

Query: 1270 atgttttgctttggaaccatctcatccatagcagatgaagagggaaactctgcaccgcata 1329
||||| ||||| ||||| ||||| ||| ||||| ||||| ||| ||||| |||||

Sbjct: 2792 atgttctgcttcggaaccatctcatccgtggcagacgaagaagggactctgcatcgcata 2851

Query: 1330 gcagatct 1337
|| |||||

Sbjct: 2852 gcggatct 2859

Score = 91.7 bits (46), Expect = 2e-14
Identities = 82/94 (87%)
Strand = Plus / Plus

Query: 563 tgtgggggatagatatccccgggtccactagaaggcgagaaggcctcgctgtggccacg 622
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 2078 tgtgggggacagatatccccgggtccactagaaggcaagaaggcgtcgcgaaaggcctcg 2137

Query: 623 ggccagttaccccgcaaggccatcccttcgtggg 656
||||| ||| ||||| ||||| ||||| ||||| |||||

Sbjct: 2138 ggcccattatttcgaaggccatcccttcgtggg 2171

Score = 65.9 bits (33), Expect = 1e-06
Identities = 177/225 (78%)
Strand = Plus / Plus

Query: 1966 aacctgtaccccgacttcgctcgtgcaatgaacacgccgagtgaagtcggaggggtactg 2025
||||||| ||||| ||||| ||| ||| ||||| ||| ||| ||||| ||| ||| |||

Sbjct: 3464 aacctgaaccccgacttcgcccagccatgaaaacactgagcgaggtcggtggagtgtg 3523

Query: 2026 gccagatagctgacggcctcccgcaaccctagacacggaaggctaccggcggtgctt 2085
||| ||||| || ||||| || ||| ||||| || ||||| ||| ||||| |||

Sbjct: 3524 ccccgatagccgatggcctcccggaactccagacgccgagggtatcggtgggtactc 3583

Query: 2086 actcgagcagtttaatcaccttctacccatcactaatcctccaagcgacctacgccatgcc 2145
||||| |||| ||| || ||||| || | || ||||| ||||| ||||| |||||
Sbjct: 3584 actcgggcagctaaccatcttctgcctcttgctcatcctccgagcgatctacgacatgcc 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 ctccctttctaccccgacgtcctcttcatcagggggagattgga 1664
|||| | ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 3132 ctccattctaccctgacgtcctcttcatcagggggagagtgga 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 aaaagcacccgcaaggggtagccctgggtgtgcggacggactctaaacaccgacagctggc 1184
||||||| |||| | ||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 109028 aaaagcacccgtgaggggcaaccccggtgtgcggtcggacccaaaacaccgacagctggc 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 ttgtgggggatagatat-ccccgggtccacta 592
||||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 3262 ttgtgggggatagatatccccgggtccacta 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 aaacgccgacagtggcgcgccaggtagggg 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 aaaagcaccgcaaggggtagccctgggtgtgcggacggactctaaacaccgacagctggc 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 tgtaaccaccacataaaagatccataaccaggaagtaggtgttacgcctctctaagcgg 330

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

Query: 1101 acaatcaacagcacgcctacc--aaaagcaccgcaaggggtagccctgggtgtgcgg 1158
||| | ||||||||| | ||||||| | |||| | ||| |||||
Sbjct: 390 acagttggtaacacgcctactccaaaagcacctctaggggcaaccccggtgcgcgg 449

Query: 1159 acggactctaaacaccgacagctggcgcgccaggtaggggtgtgtctttgatctgagct 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 aggggtagccctgggtgtgcggacggactctaaacaccgacagctggcgccaggtagg 1196
||||||| ||| ||||||||| ||||| | ||||||||| |||||||||
Sbjct: 94728 aggggtaacccaggtgtgcggtcggacccaaacaccgacagctggcacgccaggtagg 94787

Query: 1197 ggggtgtgtctttgatctgagctagctcaatgaccattacctccaaatgcaagatcgccct 1256
||||||| |||| ||||||||| || | |||| | | ||||||| |||
Sbjct: 94788 ggggtgtgtcgacgatccaagctagctcaatggccgtcaccttcacagcaagatcacctg 94847

Query: 1257 tcgccccgggactatgttttgctttggaaccatctcatccatagcagatgaagaggggaac 1316
|| ||||| || | || ||||| || || ||||||| |||| |||||||||
Sbjct: 94848 gcgtcccggatctgtattctgcttcgggacaatctcatctgtagcggatgaagaggggaat 94907

Query: 1317 tctgcaccgcatagcagatct 1337
||| ||||| | |||||||
Sbjct: 94908 tctacaccgcctcgcagatct 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 tacccegaacttcgctcgtgcaatgaacacgccgagtgaaagtcggaggggtactggcccag 2031
||||||||| || || | ||||||||| ||||||||| ||||| || |
Sbjct: 95515 aacccegaactttgcccgagctatgaacacgccgagcgaagtcggaggcgtactagctcgg 95574

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

```

Query: 1627  ttctaccccgacgtcctcttcac 1650
          |||||
Sbjct: 95185 ttctaccccgacgtcctcttcac 9520

```

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

```
Query: 1459  acccgaaaaactccgctgtccacttcgccacaaaggagtggacacggat 1508
              |||||  ||  |||||gttctacttccccaacaaagaatggacacggat
Sbjct: 95038 acccggaagactccgctgtctacttccccaacaaagaatggacacggat 95087
```

```
Query: 1149   gggtgtgcggacggactctaaacaccgacagctggcgcgccaggtaggggggtgtgtcttt 1208
             ||||| |||| | |||| ||||| ||||| ||||| ||||| |||||
Sbjct: 114818 gggtgtgcggtcggacccaaaacactgacagctggcgcgccaggtaggggggtgtgtcgac 114759
```

```
Query: 1209   gatctgagctagctcaatgaccattacctccaaatgaagatcgcccttcgccccgggac 1268
             |||  ||||| ||||| ||  ||| ||  ||||| ||  ||  ||||| |
Sbjct: 114758 gatccaagctagctcaatggccgacaccttaacagcaagatcaccatgcgtcccgatc 114699
```

```
Query: 1269   tatgttttgctttggaaccatctcatccatagcagatgaagagggaactctgcaccg 1325
              ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 114698 cgtattctgctttgggacaatctcatccgtagcggatgaagagggaattctacaccg 114642
```

Score = 93.7 bits (47), Expect = 4e-15
Identities = 182/227 (80%)
Strand = Plus / Plus

Query: 1966 aacctgtaccccgacttcgctcgtgcaatgaacacgccgagtggaagtcggaggggtactg 2025
 ||||| | ||||||| | | || ||||| |||||
 Sbjct: 28831 aacctaatacccgacttcgcccagctatgaacacgccgagtggaagtcggaggggtacta 28890

Query: 2026 gccagatagctgacggcctcccgcaaccctagacacggaaggctaccggcggtgctt 2085
||| ||||||||| ||| |||| | ||| ||| ||| ||| ||| |||
Sbjct: 28891 gctcggatagctgacggacttcctcgaactcccgcgccgaggataccgcacctgttc 28950

```
Query: 2086  actcgagcagttaatcaccttctaccatcactaatcctccaagcgacctagccatgcc 2145
              ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 28951  acccaggcagccaaccatcttctaccgctcgtcaccgcgcgaacgatctacgacacgcc 29010
```

```
Query: 2146  atcaacagccggcgagacacgcggagctccatcaacgcttcgcgcga 2192
            ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 29011 atcaacagtcgccgagacgcgcgaagctccatcaatgcttcgcgcga 29057
```

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

Query: 1149 ggggtgtgcggacggactctaaacaccgacagctggcgcgccaggtagggggtgtgtcttt 1208
||||| |||| | ||||||||| |||||||||
Sbjct: 62096 ggggtgtcgggtcggaacaaaacaccgacagctggcgcgccaggtagggggtgtgtcgac 62037

Query: 1209 gatctgagctagctcaatg 1227
 |||| |||||||||
 Sbjct: 62036 gatccaagctagctcaatg 62018

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

Query: 1966 aacctgtaccccgacttcgctcgtgcaatgaacacgccgagtgaagtcggaggggtactg 2025
||||| | ||||||||| || || ||||||||||||||||||||||||||||
Sbjct: 123323 aacctgaatcccgacttcgcccagctatgaacacgccgagtgaagtcggaggggtacta 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 ggggtgtcggacggactctaacaccgacagctggcgccaggtagggggtgtgtcttt 1208
||||||| |||| | ||||||||||||||||| |||||||||||||||||
Sbjct: 28062 ggggtgtcggtcggacccaaacaccgacagctggcgtgccaggtagggggtgtgtcgac 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 caagccgagcaaggtgcaaggctgcgccgagagaatgctctctttgctcggaacctgtac 1974
||||||||||| ||||| |||| ||||| | |||| | || ||||| |
Sbjct: 114101 caagccgagcaagatgcaaggcaacgccgggagaatccgctcttcgggcgcaacctgaat 114042

Query: 1975 cccgacttcgctcgtgcaatgaacacgccgagtgaagtcggaggggtactggcccagata 2034
||||||||||| || || || ||||||||| || ||||||||||||||||| || | ||||
Sbjct: 114041 cccgacttcgcccagctataaacacgccaagcgaagtcggaggggtactagctcgata 113982

Query: 2035 gctga 2039
|||||

Sbjct: 113981 gctga 113977

Score = 81.8 bits (41), Expect = 2e-11
Identities = 143/177 (80%)
Strand = Plus / Minus

Query: 1149 ggggtgtcggacggactctaaacaccgacagctggcgcgccaggtagggggtgtgtcttt 1208
||||||| ||||| | ||||||||||||||| ||||||||||||||| ||
Sbjct: 124092 ggggtgtcggtcggacccaaaacaccgacagctggcacgccaggtagggggtgtatcgac 124033

Query: 1209 gatctgagctagctcaatgaccattacctccaaatgcaagatcgcccttcgccccgggac 1268
|||| |||||||||||| || | ||| ||| ||||||| || | || ||||| |
Sbjct: 124032 gatccaagctagctcaatggccgtcaccttcaacagcaagatcaccatgcgtcccggatc 123973

Query: 1269 tatgttttgctttggaaccatctcatccatagcagatgaagagggaaactctgcaccg 1325
| || ||||||| || ||||||| |||| ||||||| |||| || |||||
Sbjct: 123972 cgtattctgctttgggacaatctcatctgtagcggatgaagggggaattctacaccg 123916

Score = 60.0 bits (30), Expect = 6e-05
Identities = 45/50 (90%)
Strand = Plus / Minus

Query: 2143 gccatcaacagccggcgagacacgcggagctccatcaacgcttcgcgcga 2192
|||||||||| || |||||| |||||||||| |||| |||||||||||
Sbjct: 61150 gccatcaacagtcgccgagacgcgcggagctctatcaatgcttcgcgcga 61101

Score = 58.0 bits (29), Expect = 2e-04
Identities = 104/129 (80%)
Strand = Plus / Minus

Query: 1912 gagcaagccgagcaaggtgcaaggctgcgccgagagaatgctctctttgctcggaacctg 1971
|||||||||| |||| |||||||| || || ||||||| |||||| | |||||
Sbjct: 61381 gagcaagccgaacaagatgcaaggcaacgacgcgagaaatccgctcttcgggtgtaacttg 61322

Query: 1972 taccctgacttcgctcgtgcaatgaacacgccgagtgagtcggaggggtactggcccag 2031
|||| |||||||| || || |||||||||||||| || |||||||| || || |||||
Sbjct: 61321 aacctgacttcgccgagctatgaacacgccgagtcgaggtcggagggcgttctagcccg 61262

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 acccgaaaaactccgctgtccacttcgccacaaaggagtggacacggat 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 aaacaccgacagctggcgcgccaggtaggggtgtgtctttgatctgagctagctcaatg 1227
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 1920 aaacaccgacagctggcgcgccaggtaggggtgtgtcactgatccaagctagctcaatg 1979

Query: 1228 accattacctccaaatgcaagatcgcccttcgccccgggactatgttttgctttggaacc 1287
||| || || || ||||| || || ||||| || | ||||| ||||| |||||

Sbjct: 1980 gtcacacatttccagcacaagattgctctccgccctggatccgtgttctgcttcggaacc 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-gggtccactagaaggcgagaaggcctcgcggtgtggcca 620
||||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 1198 ttgtgggggacagatatccccgggtccactagaaggcaagaaggcctcacgaaaggcct 1257

Query: 621 cgggccagttaccccgcaaggccatcccttcgtgggtcgag 661
||||| ||| ||||| ||||| ||||| |||||

Sbjct: 1258 cgggccattatttcgcaaggccacccttcgtgggccgag 1298

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

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

Query: 1149 ggggtgtcggacggactctaaacaccgacagctggcgcgccaggtagggggtg 1201
||||| |||| ||||| | ||||| ||||| ||||| ||||| |||||
Sbjct: 1796 ggggtgcgcggtcggacccaaaacaccggcagctggcgcgccaggtaggtggtg 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 gcccgatagctgacggcctcccgcaaccctagacacggaaggctaccggcggtgctt 2085
|| | ||||| || ||||| || || | || | || | ||||| ||||| |||||
Sbjct: 2745 gtcggatagccgatggcctcccccggactccagatgccgagggtatcggcggctgctc 2804

Query: 2086 actcgagcagttaatcaccttctacccatcactaatctccaagcgacctacgcatgcc 2145
||||| || | || | || ||||| || | || ||||| ||||| ||||| || |
Sbjct: 2805 actcgggcaactaaccatcttctgcctctagctcatcctccaagcgatctacgacacagc 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 ctccgttctaccccgacgtcctcttctatcggggggagagtga 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 ggggtgtgcggacggactctaacaccgacagctggcgcgccaggtagggggtgtgtcttt 1208
||||||| ||||| | ||||||||||||||||||||||||||||
Sbjct: 18097 ggggtgtgcggtcggacccaaaacaccgacagctggcgcgccaggtagggggtgtgtcgac 18156

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

Query: 1269 tatgttttgctttggaaccatctcatccatagcagatgaagagggaactctgcaccgcat 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 gagcaagccgagcaagatgcaaggcaacgacgcgagaatccgctcttcgggcgcaacctg 97129

Query: 1972 taccccgacttcgctcgtgcaatgaacacgccgagtgaagtcggaggggtactggcccag 2031
|||||||||||||| | | ||||| ||||||||| ||||||||| || ||||| |
Sbjct: 97128 aaccgacttcgcccagctatgaatacgccgagcgaagtcggaggcgttctggcccgg 97069

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

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

Strand = Plus / Minus

```
Query: 1149  ggggtgtgcggacggactctaaacaccgacagctggcgcgccaggtaggggggtgtgtcttt 1208
             ||||| ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 97903  ggggtgtgcggtcggacccaaaacaccgacagctggcgcgccaggtaggggggtgtgtcgac 97844
```

```
Query: 1209  gatctgagctagctcaatg 1227
             ||| | ||||| |||||
Sbjct: 97843  gatccaagctagctcaatg 97825
```

Score = 77.8 bits (39), Expect = 3e-10
Identities = 108/131 (82%)
Strand = Plus / Plus

```
Query: 1912  gagcaagccgagcaaggtgcaaggctgcgccgagagaatgctctctttgctcggaacctg 1971
             ||||| ||||| ||||| || || ||||| | ||||| | || |||||
Sbjct: 18812  gagcaggccgagcaagatgcaaggcaacgacgcgagaatccgctcttcgggcgcaacctg 18871
```

```
Query: 1972  taccccgacttcgctcgtgcaatgaacacgccgagtgaaagtcggaggggtactggcccag 2031
             ||||| || || || ||||| ||||| ||||| || || || || |
Sbjct: 18872  aaccctcgactttgcccgagctatgaacacgccgagcgaagtcggaggcgttctagctcgg 18931
```

```
Query: 2032  atagctgacgg 2042
             ||||| |||||
Sbjct: 18932  atagctgacgg 18942
```

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

```
Query: 1627  ttctaccccgacgtcctcttcatc 1650
             ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 18542  ttctaccccgacgtcctcttcatc 18565
```

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: 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 ttctaccccgacgtcctcttcat 1649
|||||||
Sbjct: 97458 ttctaccccgacgtcctcttcat 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

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

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198
|||| ||||| |||||
Sbjct: 120842 aaacgccgacagttggcgcgccaggtagggg 120812

>gb|AC217319.3| Zea mays BAC clone ZMMBBb-86E19 from chromosome 5, complete sequence
Length = 118973

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

Query: 1149 ggggtgtgcggacggactctaaacaccgacagctggcgcgccaggtagggggtgtgtcttt 1208
||||| ||||| | || |||||
Sbjct: 17897 ggggtgtgcggtcggacccaaagcaccgacagctggcgcgccaggtagggggtgtgtcgac 17838

Query: 1209 gatctgagctagctcaatgaccattacctccaaatgcaagatcgcccttcgccccgggac 1268
||| ||||| || | ||| | | ||||| | || | ||| |
Sbjct: 17837 aatccaagctagctcaatggccgtcaccttcacagcaagatcgccgtgcgtctcggtac 17778

Query: 1269 tatgttttgcctttggaaccatctcatccatagcagatgaagaggggaactctgcaccgcat 1328
||| || ||| || || || ||||| ||||| ||| ||||| |
Sbjct: 17777 tatattccgcttcgggacaatttcatccatagcggatgaagaggggaattctacaccgcct 17718

Query: 1329 agcagatct 1337
|||||
Sbjct: 17717 cgcagatct 17709

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

Query: 1912 gagcaagccgagcaaggtgcaaggctgcgccgagagaatgctctctttgctcggaacctg 1971
||||| |||| | ||||| ||||| | ||||| | || |||||

Sbjct: 17182 gagcaagccgaacaagatgcaaggcaacgccgggagaaatccgctcttcgggcgcaacctg 17123

Query: 1972 taccctgacttcgctcgtgcaatgaacacgccgagtggaagtcggaggggtactggcccag 2031
|||||||

Sbjct: 17122 aaccccgacttcgcccagctatgaacacgccgagcgaggtcggaggcgttctagctcgg 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 gccatcaacagccggcgagacacgccgagctccatcaacgcttcgcgcga 2192
||||||| || ||||| |||| |||| |||| |||||
Sbjct: 16951 gccatcaacagtcgccgagacgcgcgaagctctatcaatgcttcgcgcga 16902

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

Query: 1732 cgacggaggaatagaagccagaaacgtgcggcgacatcacgaggtggggaacgggatccg 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 ttctaccccgacgtcctcttcat 1649
|||||||
Sbjct: 17452 ttctaccccgacgtcctcttcat 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 ggggtgtgcggacggactctaacaccgacagctggcgcgccaggtaggggggtgtgtcttt 1208
|||||||| |||| | || ||||||||||||||||||||||||||||
Sbjct: 68045 ggggtgtgcggtcggacccaaagcaccgacagctggcgcgccaggtaggggggtgtgtcgac 68104

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

Query: 1269 tatgttttgcctttggaacctctcatccatagcagatgaagagggaactctgcaccgcat 1328
||| || ||| || || || |||||||||| |||||||||| ||| ||||| |
Sbjct: 68165 tatattccgcttcgggacaatttcacatagcggatgaagagggaattctacaccgcct 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 gagcaagccgaacaagatgcaaggcaacgccgggagaatccgctcttcgggcgcaacctg 68819

Query: 1972 taccgccacttcgctcgtgcaatgaacacgccgagtggaagtcggaggggtactggcccag 2031
||||||| || || ||||| ||||| || ||||| || || || || ||
Sbjct: 68820 aaccgccacttcgccgagctatgaacacgccgagcgaggtcggagcggttctagctcgg 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 gccatcaacagccggcgagacgcggagctccatcaacgcttcgcgcga 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 cgacggaggaatcgacgcaggaacgttcgacgacatcacgcagccggggagcgggatccg 68651

Query: 1792 gcgcaacc 1799
| |||||
Sbjct: 68652 gagcaacc 68659

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

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198
|||| ||||||| ||||||||||||||||
Sbjct: 43679 aaacgccgacagttggcgcgccaggtagggg 43649

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

Query: 1627 ttctaccccgacgtcctcttcat 1649
||||||||||||||||||
Sbjct: 68490 ttctaccccgacgtcctcttcat 68512

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

Score = 95.6 bits (48), Expect = 1e-15
Identities = 142/172 (82%), Gaps = 1/172 (0%)
Strand = Plus / Minus

Query: 982 tgtaaccaccacatatagatccatcccaagaagtagtgtattacgcctctctaagcggc 1041
||||||||||||||| ||||||| ||| ||||||| ||||||||||||||| |||||||
Sbjct: 122467 tgtaaccaccacataaagatccacaccaggaagtaggggtattacgcctctcaaagcggc 122408

Query: 1042 ccaaacttgcaaaaaccgcctatccctctctcgtgcgtccagcacgaaccattgagtta 1101
| ||| || ||||||| | |||| | |||||| |||| | ||||||||||||| ||| ||
Sbjct: 122407 tcgaacctgtagaaaattgtctat-cgtctctcatgcgcctagcacgaaccatcgaggta 122349

Query: 1102 caatcaacagcaccgtcctacccaaaagcaccgcaaggggtagccctgggtg 1153
|| || ||||||||||||||||||||| | ||||||| ||| |||||
Sbjct: 122348 cagtcgggttacaccgtcctacccaaaagcacctcgaggggtaaccccggtg 122297

Score = 93.7 bits (47), Expect = 4e-15

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

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

Query: 1972 taccctgacttcgctcgtgcaatgaacacgccgagtgagtcggaggggtactggcccag 2031
|||||
Sbjct: 37752 aaccctgacttcgcccagctatgaacacgccgagtcgaggtcggagggcgttctagctcgg 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 gggtgtgcggacggactcctaaacaccgacagctggcgccaggtagggggtgtgtcttt 1208
|||||
Sbjct: 38527 gggtgtgcggtcggacccaaacaccgacagctggcgccaggtagggggtgtgtcgac 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 ttgtgggggatagatatcccc-gggtccactagaagg 597
|||||
Sbjct: 122894 ttgtgggggacagatatccccgggtccactagaagg 122858

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

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

```
Query: 1627  ttctaccccgacgtcctcttcac 1650
          |||||
Sbjct: 38082 ttctaccccgacgtcctcttcac 38059
```

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

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198
 ||| ||||| |||||||||
 Sbjct: 68664 aaacgccgacagttggcgcgccaggtagggg 68694

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

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

Query: 1972 taccccgacttcgctcgtgcaatgaacacgccgagtgaaagtcggaggggtactggcccag 2031
|||||||
Sbjct: 25480 aaccccgacttcgctcgagctatgaacacgccgagcgaagtcggaggcgttctagctcgg 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 ggggtgtgcggacggactctaacaccgacagctggcgcgccaggtagggggtgtgtcttt 1208
|||||||
Sbjct: 24704 ggggtgtgcggtcggaccgaagacaccgacagctggcgcgccaggtagggggtgtgtcgac 24763

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

Query: 1269 tatgttttgcctttggaaccatctcatccatagcagatgaagaggaactctgcaccgcat 1328
|||
Sbjct: 24824 tgtattctgcttcgggacgatctcgtccgtagcagatgaagaaggaattctacaccgcct 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 ttctaccccgacgtcctcttcac 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 aaacaccgacagctggcgccaggtagggg 1198
||||
Sbjct: 116116 aaacgccgacagttggcgccaggtagggg 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 ccgagtgaagtcggagggtactggcccagatagctgacggcctcccgcgaaccctagac 2061
||||| | ||||| || | |||| | ||||| | ||||| | || | ||||
Sbjct: 7969 ccgagcaaggtcgggtggagtgttggtcggatagccgatggcctccccggactccagac 8028

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

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

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

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

Query: 562 ttgtggggatagatat-ccccgggtccactagaaggcgagaaggcctcgcggtggcca 620
||||||| ||||| ||||| ||||| ||||| ||||| ||||| || ||||
Sbjct: 6737 ttgtggggacagatattccccgggtccactagaaggcaagaaggcctcacgaaaggcct 6796

Query: 621 cgggccagttaccccgcaaggccatcccttcgtgggtcgag 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 agatccatcccaagaagtagtgattacgcctctctaagcgcccaaacttcagaaaaac 1058
|||||| | || ||||| || ||||| ||||| ||||| || || || ||||
Sbjct: 7182 agatccaaaccaggaagtaggtgttacgcctctctaagcgcccgaaacctgtataaaat 7241

Query: 1059 cgccta-tccctctctcgctgcgtccagcacgaaccattgagttacaatcaacagaccgt 1117
| ||| | ||||| || ||||| || | || |||| | |||||

Sbjct: 7242 tgtctactgtctctctctgtgcatctagcacgaactatcaagctacagtcggtaacaccgt 7301

Query: 1118 ccta--cccaaaagcaccgcaagggtagccctgggtgtgctggacggactctaaacaccg 1175
|||| || ||||| || |||| || |||| || |||| || |||| ||

Sbjct: 7302 cctactccaaaagcacctcgaggggcaacccgggtgcacggtcggacccaaaacaccg 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 ctccctttctaccccgacgtcctcttcatcaggggagattgga 1664
|||| ||||| ||||| ||| ||||| |||

Sbjct: 7603 ctccgttctaccccgacgtcctctttatcgaggggagagtga 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 ggggtgtgctggacggactctaaacaccgacagctggcgccaggtaggggtgtgtcttt 1208
||||||| |||| | ||||| ||||| ||||| ||||| |||||

Sbjct: 46602 ggggtgtcggtcggacccaaaacaccgacagccggcgcaaggtaggggtgtgtagcc 46661

Query: 1209 gatctgagctagctcaatgaccattacctccaaatgcaagatcgcccttcgccccgggac 1268
|||| ||||| |||| | |||| | | ||||| ||| ||||| |

Sbjct: 46662 gatctaagctagctcaatggtcgtcaccttcagcgcaagatcacctccgccccggatc 46721

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

Sbjct: 46722 cgtgttctgcttcggaactatctcatctgtagccgatgaggaaggaactctacatcgcat 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 aacctgtaccccgacttcgctcgtgcaatgaacacgccgagtgaagtcggaggggtactg 2025
||||| ||||||||| || || ||||| ||||| ||||||||| |||||
Sbjct: 47393 aacctgaaccccgacttcgcccagccatgaatacgccaagtgaagtcggaggagtactg 47452

Query: 2026 gccagatagctgacggcctcccgcaaccctagacacggaaggctaccggcggctgctt 2085
|| | ||||||| || ||||| || || | ||| || ||||| || || ||| |
Sbjct: 47453 gctcggatagctgatgggctccctcggactcccgacgtcgagggtatcgacgactgttc 47512

Query: 2086 actcgagcagttaatcaccttctacccatcactaatcctccaagcgacctacgccatgcc 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 aacctgtaccccgacttcgctcgtgcaatgaacacgccgagtgaagtcggaggggtactg 2025

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

Query: 2026 gccagatagctgacggcctcccgcgaaccctagacacggaaggctaccggcggctgctt 2085
|||| |||||||| |||||||| |||| | |||||| || |||| || ||
Sbjct: 166365 gccgaatagctgatggcctccccgaactccagacaccgagggtattggcgactattc 166306

Query: 2086 actcgagcagttaatcaccttctacccatcactaatcctccaagcgacctacgcatgcc 2145
|||| || | || |||||||||| || || |||| || |||||||| || || |||
Sbjct: 166305 actcgggcggccaaccaccttctacctctcgtcatccgccgagcgacctgcgacagcc 166246

Query: 2146 atcaacagccggcgagacacgcggagctccatcaacgcttcgcgcgaccgatgacacga 2204
||||||| |||| | | | ||||||||||||||||||||| || |||||||
Sbjct: 166245 atcaacagtcggcggggcgcaaaagctccatcaacgcttcgcgcgaacgacgacga 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 ctagaggatgtttttgttgggtgggttttacagagtttaaactagcggattatatagtg 390
| | ||||||| |||||||||||| || | |||||||| |||||||||||||
Sbjct: 97486 gtgggggtgatttg-gttgggtgggttttgcaaaatttaaactagtggttatatatagtg 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 ccctgggtgtgcggacggactctaacaccgacagctggcgcgccaggtagggggtgtgt 1204
||||||| |||| |||| | |||||||||||| | |||||||||||||||||
Sbjct: 167218 ccctgggtgcgcggtcggacccaaaaaccgacagctagtgcgccaggtagggggtgtgt 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 cgacatcacgagccgaggaacgggacccggtgcagcccgatc 166574

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

Query: 1627 ttctaccccgacgtcctcttcac 1650
||||| ||||| |||||
Sbjct: 166749 ttctaccccgacgtcctcttcac 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 ggggtgtgcggacggactctaaacaccgacagctggcgcgccaggtaggggtgtgtcttt 1208

```
Query: 1209   gatctgagctagctcaatg 1227
          |||  |||||
Sbjct: 153391 gatccaagctagctcaatg 153373
```

Query: 1912 gagcaagccgagcaaggtgcaaggctgcgccgagagaatgctctctttgctcggaacctg 1971
 |||||
 Sbjct: 152736 gagcaagccgagcaagatgcaaggcaacgacgcgagaatccgctcttcgggcgcaacttg 152677

```
Query: 1972      taccgacgttcgctcgtgcaatgaacacgccgagtgagtcggagg 2018
              |||||
Sbjct: 152676    aaccgacgttcgctcgtgagctatgaacacgccgagtcgagtcggagg 152630
```

```
Query: 562      ttgtgggggatagatatcccc-gggtccacta 592
               |||
Sbjct: 140807  ttgtgggggatagatatccccctgggtccacta 140776
```

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

```
Query: 1627      ttctaccccgacgtcctcttcac 1650
              |||||
Sbjct: 153006    ttctaccccgacgtcctcttcac 152983
```

Score = 46.1 bits (23), Expect = 0.90

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

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198
|||| |||||| |||||||||
Sbjct: 21334 aaacgccgacagttggcgcgccaggtagggg 21304

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

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198
|||| |||||| |||||||||
Sbjct: 90226 aaacgccgacagttggcgcgccaggtagggg 90256

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

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198
|||| |||||| |||||||||
Sbjct: 139072 aaacgccgacagttggcgcgccaggtagggg 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 gagcaagccgagcaaggtgcaaggctgcgccgagagaatgctctctttgctcggaacctg 1971
|||||||
Sbjct: 185684 gagcaagccgagcaagatgcaaggcaacgccgggagaaatccgctcttcgggcgcaacctg 185743

Query: 1972 tacccccgacttcgctcgtgcaatgaacacgccgagtgagtcggaggggtactggcccag 2031
|||||||
Sbjct: 185744 aacccccgacttcgcccagctatgaacacgccgagtgaggtcagaggcgttctagctcgg 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 ggggtgtgcggacggactctaaacaccgacagctggcgccaggtagggggtgtgtcttt 1208
|||||||
Sbjct: 184969 ggggtgtgcggtcggacccaaaacatcgacagctggcgccaggtagggggtgtgtcgac 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 cgacggaggaatagaagccagaacgtgcggcgacatcacgaggtggggaacgggatccg 1791
|||||||
Sbjct: 185516 cgacggaggaaccgacgcaggaacgttcgacgacatcacgcggtggagaacgggatccg 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 ggggtgtgcggacggactctaaacaccgacagctggcgcgccaggtaggggtgtgtcttt 1208
 |||||
Sbjct: 160360 ggggtgtgcggtcggacccaaaacaccgacagctggcgcgccaggtaggggtgtgtcgac 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 gagcaagccgagcaaggtgcaaggctgcgccgagagaatgctctctttgctcggaacctg 1971
 |||||
Sbjct: 159645 gagcaagccgagcaagacgcaaggcaacgacgcgagaatccgctcttcgggcgcaacttg 159586

Query: 1972 taccctgacttcgctcgtgcaatgaacacgccgagtgagtcggaggggtactggcccag 2031
 ||||| ||||| || || ||||| ||||| || ||||| || || |||||
Sbjct: 159585 aacctgacttcgcccagcgatgaacacgccgagtcggaggtcggagggcgttctagcccag 159526

Query: 2032 atagctgacggcctcccgcaaccctagacacggaaggctaccggcggtgcttactcga 2091
 ||||| || || || ||||| ||||| || || || ||||| ||||| |||||
Sbjct: 159525 atagctgacggacttcctcgaccccgacgccgaggataccggcgctgttcactcag 159466

Query: 2092 gcagttaatcaccttctacccatcactaatcctccaagcgacctacgccatgccatcaac 2151
 ||||| || || ||||| || || || || || || || || || || || || |||||
Sbjct: 159465 gcagccaaccatcttctacgctcgtcaccgcggaacgatctgcgacagccatcaac 159406

Query: 2152 agccggcgagacacgcggagctccatcaacgcttcgcgcga 2192
 || || ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 159405 agtcgccgagacgcgcgaagctctatcaatgcttcgcgcga 159365

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

Query: 1069 tctctcgtgcgtccagcacgaaccattgagttacaatcaacagcaccgtcctacccaaaa 1128
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 137188 tctctcgtgcgcccagcacgaaccatcgagctacagtcggtaacatcgtcctacccaaaa 137129

Query: 1129 gcaccgcaaggggtagccctgggtgtgcggacggactctaaacaccgacag 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 ttgtgggggacagatatccccgggtccactagaaggttagaaggcctc 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 ttctaccccgacgtcctcttcatc 1650
 |||||
Sbjct: 159915 ttctaccccgacgtcctcttcatc 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      tgcccccacggctcgtgtatataaggtccagagggtaccccatca 925
              ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 137385  tgcccccacggctcgagtatataaggcctagggggcaccatca 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 gggtgtgctggacggactctaacaaccgacagctggcgcgccaggtaggggggtgtgtcttt 1208
 ||||| | |||| | ||||||||| |||||

Sbjct: 111556 gggtgtgcggtcggacccaacacggacagctggcgcgccaggtaggggggtgtgtcgac 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 gagcaggccgagcaagatgcaaggcaacgacgcgagaatccgctcttcgggcgcaacttg 112330
```

```
Query: 1972   taccgcgacttcgctcgtgcaatgaacacgccgagtgaagtcggaggggtactggcccag 2031
             |||||
Sbjct: 112331 aaccgcgacttcgcccagccgtgaatacaccgagcgaagtcggaggcgttctggcccgg 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 ttctaccccgacgtcctcttcac 1650
|||||||
Sbjct: 112001 ttctaccccgacgtcctcttcac 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 sequeunce 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 gagcaagccgagcaaggtgcaaggctgcgccgagagaatgctctctttgctcggaacctg 1971
|||||||
Sbjct: 114625 gagcaagccgagcaagatgcaaggcaacgacgcgagaatccgctcttcgggcgcaacctg 114566

Query: 1972 taccccgacttcgctcgtgcaatgaacacgccgagtggaagtcggaggggtactggcccag 2031
|||||||
Sbjct: 114565 aaccccgacttcgcccagctatgaatacgccgagcgaagtcggagggcgttcttgcccgg 114506

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

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

Query: 1149 ggggtgtgcggacggactctaaacaccgacagctggcgcgccaggtagggggtgtgtcttt 1208
||||||| |||| | |||||||||||||||||||||||||||||
Sbjct: 115340 ggggtgtgcggtcggacccaaaacaccgacagctggcgcgccaggtagggggtgtgtcgac 115281

Query: 1209 gatctgagctagctcaatg 1227
|||| |||||||||||||
Sbjct: 115280 gatccaagctagctcaatg 115262

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

Query: 1149 ggggtgtgcggacggactctaaacaccgacagctggcgcgccaggtagggggtgtgtcttt 1208
||||||| |||| | |||||||||||||||||||||| |||||||||||||||||
Sbjct: 127419 ggggtgtgcggtcggacccaaaacaccgacagctggcgcgctaggtagggggtgtgtcgac 127478

Query: 1209 gatctgagctagctcaatg 1227
|||| |||||||||||||
Sbjct: 127479 gatccaagctagctcaatg 127497

Score = 67.9 bits (34), Expect = 2e-07
Identities = 64/74 (86%)
Strand = Plus / Plus

Query: 1966 aacctgtaccccgacttcgctcgtgcaatgaacacgccgagtgaagtcggaggggtactg 2025
||||| | ||||||||| || || ||||||||| || |||||||||
Sbjct: 128188 aacctgaatcccgacttcgcccgagctatgaacacgccaagcgaagtcggaggggtacta 128247

Query: 2026 gcccagatagctga 2039
|| | |||||||
Sbjct: 128248 gctcggatagctga 128261

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

Query: 2134 ctacgccatgccatcaacagccggcgagacacgaggctccatcaacgcttcgcgcga 2192
||||| || |||||||||||| || |||||| |||| |||||||||||| ||||||||||||
Sbjct: 128356 ctacgacagccatcaacagtcgccgagacgcgcgaagctccatcaatgcttcgcgcga 128414

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

Query: 1621 gctcctttctaccccgacgtcctcttcatc 1650
||||| ||||||||||||||||||||||||
Sbjct: 127858 gctccattctaccccgacgtcctcttcatc 127887

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

Query: 561 gttgtgggggatagatatcccc-gggtccacta 592
|||||||||||||||||||||||||| |||||||||
Sbjct: 115935 gttgtgggggatagatatcccctgggtccacta 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

Query: 1627 ttctaccccgacgtcctcttcat 1649
|||||||
Sbjct: 114895 ttctaccccgacgtcctcttcat 114873

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

Query: 1173 ccgacagctggcgcgccaggtagggg 1198
|||||||
Sbjct: 24644 ccgacagctggcgcgccaggtagggg 24619

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

Query: 1459 acccgaaaaactccgctgtccacttcgccacaaaggagtggacacggat 1508
||||| || ||||| ||||| || ||||| || |||||
Sbjct: 127717 acccggaagactccgctgtctacttccccgacaaaagaatggacacggat 127766

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

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

Query: 1149 ggggtgtgcggacggactctaaacaccgacagctggcgcgccaggtaggggtgtgtcttt 1208
||||||| ||||| | |||||
Sbjct: 85822 ggggtgtgcggtcggacccaaaacaccgacagctggcgcgccaggtaggggtgtgtcgac 85881

Query: 1209 gatctgagctagctcaatg 1227
|||||
Sbjct: 85882 gatccaagctagctcaatg 85900

Score = 85.7 bits (43), Expect = 1e-12

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

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

Query: 1972 taccgccacttcgctcgtgcaatgaacacgccgagtgaagtcggaggggtactggcccag 2031
||||| ||||||| || || |||| ||||||| ||||||||| || ||||||| |
Sbjct: 86597 aaccgccacttcgccgagccgtgaatacgccgagcgaagtcggaggcgttctggcccgg 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 ttctaccccgacgtcctcttcac 1650
||||| ||||||| ||||||| |||||
Sbjct: 86267 ttctaccccgacgtcctcttcac 86290

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: 96175 ttgtgggggatagatatcccctgggtccacta 96206

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: 85229 tgtggggatagatatcccctgggtccacta 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 ggggtgtgcggacggactctaaacaccgacagctggcgcgccaggtaggggggtgtgtcttt 1208
||||||| ||||| | ||||||||||||||||||||||||||||||||
Sbjct: 607 ggggtgtgcggtcggacccaaaacaccgacagctggcgcgccaggtaggggggtgtgtcgac 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 caagccgagcaagatgcaaggcaacgccgggagaaatccattcttcggctc--aacctgaa 1385

Query: 1974 ccccgacttcgctcgtgcaatgaacacgccgagtgagtcggaggggtactggcccagat 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 ttctaccccgacgtcctcttcac 1650

|||||
Sbjct: 1055 ttctaccccgacgtcctctttcatc 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 accccgacttcgctcgtgcaatgaacacgccgagtgaagtcggaggggtactggcccaga 2032
|||||
Sbjct: 3599 accccgacttcgcctgagccatgaacacaccgagcgaggtcggtggagtgttggtcaga 3658

Query: 2033 tagctgacggcctcccgcaaccctagacacggaaggctaccggcggtgcttactcgag 2092
|||||
Sbjct: 3659 tagccgatggcctcccttgactctagacgccgagggctatcggcggctgctcactcggg 3718

Query: 2093 cagttaatcaccttctacccatcactaatcctccaagcgacctacgccatgccatcaaca 2152
|||||
Sbjct: 3719 cagctaaccatcttctgcctctcgtcctccttcgagcgatctacgacgccatcaata 3778

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

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

Query: 982 tgtaaccacccacatata-gatccatcccaagaagtagtgtattacgcctctctaagcgg 1040
|||||
Sbjct: 2641 tgtaaccacccacataaaagatccacaccaggaagtaggtgttacgcctctctaagcgg 2700

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

Query: 1101 acaatcaacagcaccgtcctaccc--aaaagcaccgcaaggggtagccctgggtgtgcgg 1158

|||||
Sbjct: 2760 acagttggtaacaccgtcctactccaaaaagcacctcgaggggcaacccgggtgcgcgg 2819

Query: 1159 acggactctaaacaccgacagctggcgcgccaggtaggggtgtgtctttgatctgagct 1218

|||||
Sbjct: 2820 tcagacccaaaacaccgaaagccggcgcgccaggtaggggtgtgtcactaatctaagct 2879

Query: 1219 agct 1222

|||||
Sbjct: 2880 agct 2883

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: 2213 ttgtggggacagatatccccgggtccactagaaggcaagaaggcctc 2261

>gb|AY325816.1| Zea mays BAC clone Z013I05, complete sequence
Length = 152337

Score = 89.7 bits (45), Expect = 7e-14
Identities = 54/57 (94%)
Strand = Plus / Minus

Query: 1149 gggtgtgcggacggactctaaacaccgacagctggcgcgccaggtaggggtgtgtc 1205

|||||
Sbjct: 31297 gggtgtgcggtcggacccaaaacaccgacagctggcgcgccaggtaggggtgtgtc 31241

Score = 77.8 bits (39), Expect = 3e-10
Identities = 90/107 (84%)
Strand = Plus / Minus

Query: 1912 gagcaagccgagcaaggtgcaaggctgcgccagagaatgctctctttgctcggaacctg 1971

|||||
Sbjct: 30582 gagcaagccgagcaagatgagaggcaacgacgcgagaatccgctcttcgggcgcaacttg 30523

Query: 1972 taccgccgacttcgctcgtgcaatgaacacgccgagtggaagtcggagg 2018
|||||
Sbjct: 30522 aaccgccgacttcgctcgagctatgaacacgccgagcggaagtcggagg 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 tgtaaccaccacatatata-gatccatcccaagaagtagtgattacgcctctctaagcgg 1040
|||||
Sbjct: 5793 tgtaaccaccacataaaaagatccacactaggaagtaggggtgttacgcctctctaagcgg 5852

Query: 1041 cccaaacttgcaaaaaccgcctatccctctctcgtgcgtccagcacgaaccattgagtt 1100
||| ||| || ||||| || || || ||||| || ||||| ||||| |||||
Sbjct: 5853 cccgaacctgtataaaattgtcca-ctatctctcgtgcatctagcacgaaccatcgagct 5911

Query: 1101 acaatcaacagcacgcgtcctaccc--aaaagcaccgcaaggggtagccctgggtgtgcgg 1158
||| || || ||||| || ||||| || ||||| ||||| ||||| |||||
Sbjct: 5912 acagtcggtaacatcgtcctactccaaaagcaccagaggggcaacccaggtgcgcgg 5971

Query: 1159 acggactctaaacaccgacagctggcgccaggtagggggtgtgtctttgatctgagct 1218
|| || | ||||| || ||||| ||||| ||||| ||||| |||||
Sbjct: 5972 tcgaacccaaaacaccgacaactagcgccaggtagggggtgtgtcactgatccaagct 6031

Query: 1219 agctcaatgaccattacctccaaatgcaagatcgcccttcgccccgggactatgttttgc 1278
|||| |||| || || || || || ||||| || ||||| || ||||| |||||
Sbjct: 6032 agcttaatggccgctactttctagcacaagatcgctctccgccctggatccgtgttctgc 6091

Query: 1279 tttggaaccatctcatccatagcagatgaagaggaactctgcaccgcatagcagatc 1336
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 6092 ttcagaaccatctcatccatggcagacgaagaaggaactctacatctcatagcggatc 6149

Score = 61.9 bits (31), Expect = 2e-05
Identities = 136/171 (79%)
Strand = Plus / Plus

Query: 2031 gatagctgacggcctcccggaaccctagacacggaaggtaccggcggctgcttactcg 2090
||||| || ||||| || || || ||||| || ||||| ||||| ||||| |||||
Sbjct: 6811 gatagccgatggcctcccggaactccagacgagggctatcggcggctgcttactcg 6870

Query: 2091 agcagttaatcaccttctacccatcactaatcctccaagcgacctacgccatgccatcaa 2150
||||| || || ||||| || || || ||||| ||||| ||||| || ||||| ||
Sbjct: 6871 ggcagctaaccatattctgcctctcgctcatctccgagcgatctacgacacgccattaa 6930

Query: 2151 cagccggcgagacacgcggagctccatcaacgcttcgcgcgaccgatgaca 2201
|| || || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 6931 tagtcgacgggacgcacggagctccatcaatgtcttcgctcgaacgatgaca 6981

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

Query: 579 ccccggtccactagaaggcgagaaggcctc 609
|||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 5441 ccccggtccactagaaggcaagaaggcctc 5471

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

Query: 1622 ctcttttctaccccgacgtcctcttcatcagggggagattgga 1664
|||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 6414 ctccgttctaccccgacgtcctcttctatcgaggggagagtga 6456

>gb|AY574035.1| Zea mays rust resistance protein rp3-1 (rp3-1) gene, complete cds; and

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

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

Query: 1155 gcggacggactctaaacaccgacagctggcgccaggtagggggtgtgtctttgatctg 1214
||||| ||||| | ||||| ||||||||||||||||||||||||||||| |||||
Sbjct: 27626 gcggtcggacccaaacatcgacagctggcgccaggtagggggtgtgtcactgatcca 27685

Query: 1215 agctagctcaatgaccattacctccaaatgcaagatcgcccttcgccccgggactatggt 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 ggctaccggcggctgcttactcgagcagttaatcaccttctacccatcactaatcctcca 2127
||||| || ||||||||||||||| ||||| ||| ||||||| || || || || || ||
Sbjct: 43987 ggctatcgacggctgcttactcgggcagctaaccacctctgcctctcgctcatcgtcgg 44046

Query: 2128 agcgacctacgccaatgccatcaacagccggcgagacacgaggctccat 2177
||||| ||||| || ||||| || || | ||||| |||||
Sbjct: 44047 agcgatctacgacacgccaatcaatagtcgatgggacacgaggctccat 44096

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

Query: 1168 aaacaccgacagctggcgccaggtagggg 1198
|||| | ||||| ||||| |||||
Sbjct: 249165 aaacgccgacagttggcgccaggtagggg 249135

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

Query: 884 gccccacggtcgtgtatataaggtccagagggtaccccatca 925
||||| ||||| ||||| || || || |||||
Sbjct: 27347 gccccacggtcgagtatataaggcctaggggaccccatca 27388

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

Score = 85.7 bits (43), Expect = 1e-12
Identities = 135/165 (81%), Gaps = 3/165 (1%)
Strand = Plus / Plus

Query: 867 tcatgtacgtatggagtgccccacggtcgtgtatataaggtccagagggtaccccatcat 926
|||| |||| ||| ||||| ||||| ||||| || || || |||||
Sbjct: 273 tcatatacgcatgtagtgccccacggtaagtatataaggcctaggggaccccatcaa 332

Query: 927 ttc---tatcgaccatctacctatctcatcagcttttctccattcaggagacctcgttg 983
| ||||| ||||| || ||| ||||| || |||||
Sbjct: 333 aacatatatcgaccatctactcagctcactagcttttctccataccggagacttccttg 392

Query: 984 taaccaccacatatagatccatcccaagaagtagtgtattacgc 1028

||||| ||||||| ||||||| ||| ||||||| || |||||||
Sbjct: 393 taacctaccacataaagatccatgccaggaagtagggtgttacgc 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 ggggtgtgcggacggactctaaacaccgacagctggcgcgccaggtagggggtgtgtcttt 1208
||||| ||||| ||||||| | ||||||||||||| ||||||| ||||||||||||||||| |
Sbjct: 151640 ggggtgcgcggtcggacccaaaacaccgacagttggcgcaccaggtagggggtgtgtcact 151699

Query: 1209 gatctgagctagctcaatgaccattacctccaaatgcaagatcgcccttcgccccgggac 1268
||||| ||||||| ||||||| ||| ||| | | ||||||| ||| ||||| |||
Sbjct: 151700 gatccaagctagatcaatggccgtcacttttcagcacaagatcttcctctgccccaggtc 151759

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

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

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

Query: 1930 gcaaggctgcgccgagagaatgctctctttgctcggaacctgtaccccgacttcgctcgt 1989
||||||| ||||||||||||| ||||| | | ||||||| ||||||||||||| ||
Sbjct: 152394 gcaaggcaacgccgagagaatcctcttctcgggcggaacctaaaccccgacttcgcccga 152453

Query: 1990 gcaatgaacacgccgagtgaggtcggagggtactggcccagatagctgacggcctccc 2049
|| ||||||||||||||||| ||||| | || ||||| ||||| ||||| ||
Sbjct: 152454 gccatgaacacgccgagtgaggtcgggtgaagtgttggtcggatagccgacggtcttccc 152513

Query: 2050 cgaaccctagacacggaaggctaccggcggtgcttactcgagcagttaatcaccttct 2108

||||| | |||| | ||||||| ||||||||| |||| ||| || |||||
Sbjct: 152514 cgaactccagacgctgaaggctatcggcggctgctcactcgggcagctaaccatcttct 152572

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

Query: 1622 ctcctttctaccccgacgtcctcttcatcagg 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 accccgatttcgcccagccatgaacacgcccgagtggaagtcggtggagtattggctcgga 55072

Query: 2033 tagctgacggcctcccggaaccctagacacggaaggctaccggcggctgcttactcgag 2092
|||| | |||||||| | || | || | || |||| | |||| | ||||
Sbjct: 55073 tagcagatggcctcccgtaggactcccgatgccgagggtatcggtggctgttactcaag 55132

Query: 2093 cagttaatcaccttctaccatcactaatcctccaagcgacctacgccatgccatcaaca 2152
||| |||| | |||| | || | || | || |||| | |||| ||||
Sbjct: 55133 cagccaatcatctcctaccctcgctcacccgccgaacgatctacgacagccatgaaca 55192

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

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

Query: 1168 aaacaccgacagctggcgccaggtaggggtgtgtctttgatctgagctagctcaatg 1227
||||| |||||||| | || ||||||||| |||| | |||| | |||||||||
Sbjct: 54235 aaacactgacagctggcacgctaggtaggggtgtgtcatcgatccaagctagctcaatg 54294

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

Query: 982 tgtaaccaccacatatata-gatccatcccaagaagtagtgtattacgcctctctaagcgg 1040
|||||
Sbjct: 271 tgtaaccaccacataaaaagatccataaccaggaagtaggggtgttacggctctctaagcgg 330

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

Query: 1101 acaatcaacagcacccgtcctaccc--aaaagcacgcgaaggggtagccctgggtgtgcgg 1158
|||
Sbjct: 390 acagtcggtaacaccgtcctacacaaaaagcacctcgaggggcaacccaggagcgcg 449

Query: 1159 acggactctaaacaccgacagctggcgccaggtagggggtgtgtctttgatctgagct 1218
|||
Sbjct: 450 tcggacccaaaacaccgacagctggcgccaggtgta-ggggtgtgtcactgatccaagtt 508

Query: 1219 agctcaatgacccat 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-ggggtccactagaaggcgagaaggcctcgcgtgtggcca 620
|||
Sbjct: 13840 ttgtgggggacagatatccccgggtccactagaaggcaagaaggcctcacgaaaggcct 13899

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

```
Query: 982   tgtaaccacccacatatata-gatccatcccagaagtagtgatttacgcctctctaagcgg 1040
          |||.....|...||..||..||||..||..||||..||..||||..||..||
Sbjct: 5047  tgtaaccacccacataaaagatccacaccagggaagttagggtgtttacgcctctctaagcgg 5106
```

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

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

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

>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%)

Strand = Plus / Plus

Query: 562 ttgtggggatagatatcccc-gggtccactagaaggcgagaaggcctcgcggtgtggcca 620
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 4653 ttgtggggacagatatccccgggtccactagaaggcaagaaggcctcacgaaaggcct 4712

Query: 621 cgggccagttaccccgcaaggccatcccttcgtgggtcgag 661
||||| ||| ||||| ||||| ||||| ||||| |||||
Sbjct: 4713 cgggccattatttcgcaaggccacccttcgtgggccgag 4753

Score = 61.9 bits (31), Expect = 2e-05
Identities = 85/103 (82%)
Strand = Plus / Plus

Query: 1125 aaaagcacgcgaagggtagccctgggtgtgcggaaggactctaaacaccgacagctggc 1184
||||||| | ||||| | ||| | ||||| | ||||| | ||||| ||||| |||||
Sbjct: 5330 aaaagcacctcgaggggcaaccccgagtgtgcagtcggacccaaaacaccgacagcttgt 5389

Query: 1185 gcgccaggtaggggtgtgtctttgatctgagctagctcaatg 1227
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 5390 gcgccaagtaggtgtgtgtcactgatccaagctagctcaatg 5432

Score = 61.9 bits (31), Expect = 2e-05
Identities = 58/67 (86%)
Strand = Plus / Plus

Query: 1270 atgttttgctttggaaccatctcatccatagcagatgaagagggaactctgcaccgcata 1329
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 5475 atgttctgcttcggaaccatctcatccgtggcagacgaagaagggaactctacatcgcata 5534

Query: 1330 gcagatc 1336
|| ||||
Sbjct: 5535 gcggatc 5541

>emb|AJ312504.1| Zea mays subsp. mexicana Grande retrotransposon DNA, partial LTR,
clone ZMM16
Length = 434

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 agtgccccatgggtcaagtatataaggcctaggggtaccctgtcatttccatcgaccatc 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 gttgggtgggttttgcaaagtttaacttgtggattatatagtggtataga 118992

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

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198
|||| ||||| ||||||||| |||||
Sbjct: 81522 aaacgccgacagttggcgcgccaggtagggg 81552

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

Query: 1173 ccgacagctggcgcgccaggtagggg 1198
||||| ||||||||| |||||
Sbjct: 45119 ccgacagttggcgcgccaggtagggg 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 gttgggtgggttttacagagtttaactagcggattatatagtggtataga 396
|||||
Sbjct: 171940 gttgggtgggttttgcaaagtttaacttgtggattatatagtggtataga 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 aacctgaaccccgacttcgcccagccgtgaacacgccgagcgaggtcggaggagtactg 122

Query: 2026 gccagatagctgacggcctccc 2048
||
Sbjct: 123 gctcggatagctgagggactccc 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-gggtccactagaaggcgagaaggcctc 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 tgtaaccaccacatatata-gatccatcccaagaagtagtgattacgcctctctaagcgg 1040
||||| ||||||| | ||||| ||| ||||||| || ||||||||| |||||
Sbjct: 929 tgtaatccaccacataaaagatccacaccaggaagtagggtgttacgcctctctaagcgg 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 tgtaaccaccacatatata-gatccatcccaagaagtagtgattacgcctctctaag 1037
||||||| ||||||| | ||||| ||| ||||||| || ||||||||| |||||
Sbjct: 32977 tgtaaccaccacataaaagatccacaccaggaagtagggtgttacgcctctctaag 33033

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

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

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

Query: 931 atcgaccatctacctatctcatcagcttttctccattcaggagacctcgcttgt-aaccc 989
||| ||||| ||| | ||||| | | ||||||||| | ||||| || ||||| |||
Sbjct: 158 atcaacatgtactcaactcattatcctttctccatactggagacttctcttgtaaactg 99

Query: 990 accacatatagatccatcccaagaagtagtgattacgcctctctaagcggcc 1042
|||| ||| ||||||| ||| ||||||| ||||| | |||||||||
Sbjct: 98 accatataaagatccacaccaggaagtaggatattatgtatctctaagcggcc 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-gggtccactagaaggcgagaaggcctcgcggtgtggcca 620
||||||||| ||||||||| ||||||||| ||||||||| ||| |||||
Sbjct: 12021 ttgtgggggacagatatccccgggtccactagaaggtaagaaggcctcacgaaaggcca 12080

Query: 621 cgggccagttaccccgcaaggccatcccttcgtggg 656
||||| ||| ||||||||| |||||||||
Sbjct: 12081 tgggccattatttcgcaaggccaccccttcgtggg 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 tgtaaccaccacataaaaagatccacaccaagaagtaggggtgtaacgcctctctaagcg 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 cacgaaccattgagttacaatcaacagcacccgtcctacccaaaagcacc 1133
|||||
Sbjct: 115369 cacgaaccatcgagttacaatctacgacaccgtcctaaccaaaagcacc 115417

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

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198
||||
Sbjct: 87495 aaacgccgacagttggcgcgccaggtagggg 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 ggggtagatatacccc-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 tgtaaccaccacatatata-gatccatcccaagaagtagtgtattacgcctctctaagcgg 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 aagcacgcgaaggggtagccctgggtgtgcggacggactctaaacaccgacag 1179
||||||| | ||||| | ||| ||||| ||||| ||||| | ||||||| |||||
Sbjct: 7969 aagcacctcgaggggcaaccccggtgcgcggtcggacccaaaacaccaacag 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-gatccatcccaagaagtagtgattacgcctctctaagcgg 1040
||||| ||||||| | ||||| ||| ||||||| || ||||||| |||||||
Sbjct: 4897 tgtaaccaccacataaaagatccacaccaggaagtaggggtgttacgcctctctaagcgg 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 ggagacctcgcttgtaaccaccacatatagatccatcccaagaagtag 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 attttgatggtatgttaaatttgtgtgtcatttgtttgatggatttagtaaa 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 ccgacagctggcgcgccaggtagggg 1198
 ||||||| |||||||||||||||||
Sbjct: 165564 ccgacagttggcgcgccaggtagggg 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 aaacaccgacagctggcgcgccaggtagggg 1198
 ||||||||||| |||||||||||||||||
Sbjct: 48261 aaacaccgacagttggcgcgccaggtagggg 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 aaacaccgacagctggcgcgccaggtagggg 1198
 ||||||||||| |||||||||||||||||
Sbjct: 49821 aaacaccgacagttggcgcgccaggtagggg 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 tgtaaccacccacatata-gatccatcccaagaagtagtgtattacgcctctctaagcgg 1040
 ||||||||||||||| | ||||| | | ||||| | | ||||||||||||| |

Sbjct: 362 tgtaaccaccacataaaagatccacacaaggaagtagggtgttacgcctctctaagcag 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-gatccatcccaagaagtagtgtattacgcctctctaagcgg 1040

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

Sbjct: 362 tgtaatccaccacataaaagatccacaccaggaagtagggtgttacgcctctctaagcgg 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

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

Sbjet: 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 ccgacagctggcgcgccaggtaggggg 1199
|||||
Sbjet: 53099 ccgacagctggcgcgccaggtaggggg 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 ggtgggttttacagagtttaactagcgattatatagtggatataga 396
||||| | ||||| | |||||
Sbjet: 1358 ggtgggttttttaaagtttaactggtggattatatagtggatataga 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 ccgacagctggcgcgccaggtaggggg 1199
|||||
Sbjet: 77098 ccgacagctggcgcgccaggtaggggg 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 ggtgggttttacagagtttaactagcggattatatagtggatataga 396
||||||| | ||||| | |||||
Sbjct: 1189 ggtgggtttttaagtttaactggtggattatatagtggatataga 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 gttattcaactatccgacccgtcgattttgatggatgttaaatttgtgtgcatttggt 304
||||||| ||| | ||| ||||| | ||||| | | ||| |||||
Sbjct: 111207 gttattcaaagatctgaaccgttgattttgatgttggttaagtatgagtgaatttggt 111266

Query: 305 tgatggatttagtaaaggttatg 327
|| |||||
Sbjct: 111267 tggatggatttagtaaagattatg 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%)

```

Query: 1168      aaacaccgacagctggcgcgccaggtagggg 1198
              ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 179323    aaacaccgacagttaggcgcgctaggtagggg 179293

```

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

Query: 1041 ccc 1043
 |||
 Sbjct: 331 ccc 333

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  tggcgccaggtaggggtgtg 1203
          |||||
Sbjct: 27029 tggcgccaggtaggggtgtg 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 tggcgcgccaggtagggggtgtg 1203
|||||||
Sbjct: 77890 tggcgcgccaggtagggggtgtg 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 (Yl) 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

```

Query: 1168    aaacaccgacagctggcgcgccaggtagggg 1198
             |||| ||||| ||||| |||||
Sbjct: 144830 aaacgccgacagttggcgcgccaggtagggg 144800

```

```
Query: 1168    aaacaccgacagctggcgcgccaggtagggg 1198
           ||| ||||| ||||| ||||| |||||
Sbjct: 161365 aaacgccgacagttggcgcgccaggtagggg 161335
```

```
Query: 293  gtgtcatttgtttgatggattagtaaaggttatgggt 330
          ||| ||||| ||||| ||||| ||||| |||||
Sbjct: 1454 gtgtaatttgtttggtggattagtaaagattatgggt 1491
```

```

Query: 526  ctatatattttaaaatagggtactgatttaa 555
          |||||
Sbjct: 1548 ctatatattttaagatagggtactgatttaa 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  cgacagctggcgcgccaggtaggggg 1199
          ||||||||||||||||||||||||
Sbjct: 55487 cgacagctggcgcgccaggtaggggg 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 cgacagctggcgcgccaggtaggggg 1199
          ||||||||||||||||||||||||
Sbjct: 4119 cgacagctggcgcgccaggtaggggg 4094
```

>gb|AC145127.1| Oryza sativa Japonica Group chromosome 10 clone Pseudol10p0.0-10p4.4,
complete sequence
Length = 2331000

Score = 52.0 bits (26), Expect = 0.015
Identities = 26/26 (100%)
Strand = Plus / Minus

```
Query: 1174  cgacagctggcgcgccaggtaggggg 1199
          ||||||||||||||||||||||||
Sbjct: 588003 cgacagctggcgcgccaggtaggggg 587978
```

Score = 46.1 bits (23), Expect = 0.90
Identities = 26/27 (96%)
Strand = Plus / Plus

```
Query: 1173  ccgacagctggcgcgccaggtaggggg 1199
          ||||| ||||||||||||||||||||
Sbjct: 1793581 ccgacatctggcgcgccaggtaggggg 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 cgacagctggcgcgccaggtaggggg 1199
|||||||
Sbjct: 59441 cgacagctggcgcgccaggtaggggg 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 cgacagctggcgcgccaggtaggggg 1199
|||||||
Sbjct: 73246 cgacagctggcgcgccaggtaggggg 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 cgacagctggcgcgccaggtaggggg 1199
|||||||
Sbjct: 37650 cgacagctggcgcgccaggtaggggg 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   cgacagctggcgcgccaggtaggggg 1199
          |||||||||||||||||||||||||
Sbjct: 153905 cgacagctggcgcgccaggtaggggg 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   cgacagctggcgcgccaggtaggggg 1199
          |||||||||||||||||||||||||
Sbjct: 81368   cgacagctggcgcgccaggtaggggg 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   cgacagctggcgcgccaggtaggggg 1199
          |||||||||||||||||||||||||
Sbjct: 104930 cgacagctggcgcgccaggtaggggg 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   cgacagctggcgcgccaggtaggggg 1199
          |||||||||||||||||||||||||
Sbjct: 25639   cgacagctggcgcgccaggtaggggg 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  cgacagctggcgcgccaggtaggggg 1199
          |||||||||||||||||||||||||
Sbjct: 16748 cgacagctggcgcgccaggtaggggg 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  cgacagctggcgcgccaggtaggggg 1199
          |||||||||||||||||||||||||
Sbjct: 39151 cgacagctggcgcgccaggtaggggg 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  cgacagctggcgcgccaggtaggggg 1199
          |||||||||||||||||||||||||
Sbjct: 164658 cgacagctggcgcgccaggtaggggg 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  cgacagctggcgcgccaggtaggggg 1199
          |||||||||||||||||||||||||
Sbjct: 75026 cgacagctggcgcgccaggtaggggg 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 cgacagctggcgcgccaggtaggggg 1199
|||||||
Sbjct: 134937 cgacagctggcgcgccaggtaggggg 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 cgacagctggcgcgccaggtaggggg 1199
|||||||
Sbjct: 82803 cgacagctggcgcgccaggtaggggg 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 cgacagctggcgcgccaggtaggggg 1199
|||||||
Sbjct: 26933 cgacagctggcgcgccaggtaggggg 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 cgacagctggcgcgccaggtaggggg 1199
|||||||
Sbjct: 1391 cgacagctggcgcgccaggtaggggg 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 cgacagctggcgcgccaggtaggggg 1199
|||||||
Sbjct: 110588 cgacagctggcgcgccaggtaggggg 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 cgacagctggcgcgccaggtaggggg 1199
|||||||
Sbjct: 125370 cgacagctggcgcgccaggtaggggg 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 cgacagctggcgcgccaggtaggggg 1199
|||||||
Sbjct: 115721 cgacagctggcgcgccaggtaggggg 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 cgacagctggcgcgccaggtagggg 1199
|||||||
Sbjct: 127992 cgacagctggcgcgccaggtagggg 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 cgacagctggcgcgccaggtagggg 1199
|||||||
Sbjct: 167523 cgacagctggcgcgccaggtagggg 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 cgacagctggcgcgccaggtagggg 1199
|||||||
Sbjct: 69901 cgacagctggcgcgccaggtagggg 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      aaacaccgacagctggcgcgccaggtagggg 1198
              |||| ||||| ||||| ||||| |||||
Sbjct: 202313    aaacgccgacagttggcgcgccaggtagggg 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 gagaactcccttgtaaccaccacataaaagatccacaccaggaagtaggggtgctacgct 319
```

```
Query: 1030 tctctaagcggcc 1042
          |||||
Sbjct: 320 tctctaagcggcc 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 cgacagctggcgccaggtagggg 1198
      |||||
Sbjct: 8725 cgacagctggcgccaggtagggg 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 ccgacagctggcgcgccaggtaggggtg 1201
||||| ||||||||||||||||||||
Sbjct: 28946 ccgacatctggcgcgccaggtaggggtg 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 cgacagctggcgccaggtagggg 1198
|||||
Sbjct: 83012 cgacagctggcgccaggtagggg 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 cgacagctggcgccaggtagggg 1198
|||||
Sbjct: 40302 cgacagctggcgccaggtagggg 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 aaacaccgacagctggcgccaggtagggggt 1200
||||
Sbjct: 111324 aaacgccgacagtggcgccaggtagggggt 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 aaacaccgacagctggcgcgccaggtagggg 1198
||||| ||||||| ||||||| ||||||| |||||||
Sbjct: 97256 aaacgccgacagtggcgcgccaggtagggg 97226

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

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198
||||| ||||||| ||||||| ||||||| |||||||
Sbjct: 103145 aaacgccgacagtggcgcgccaggtagggg 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 caccgacagctggcgcgccaggtagggg 1198
||||| ||||||| ||||||| ||||||| |||||||
Sbjct: 94501 caccgacagctggcgcgctaggtagggg 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 cgacagctggcgcgccaggtaggg 1197
||||| ||||||| ||||||| ||||||| |||||||
Sbjct: 88007 cgacagctggcgcgccaggtaggg 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 cgacagctggcgcgccaggtaggg 1197
|||||||||||||||||||||||||
Sbjct: 32770 cgacagctggcgcgccaggtaggg 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 acagctggcgcgccaggtagggg 1199
|||||
Sbjct: 12190 acagctggcgcgccaggtagggg 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 acagctggcgcgccaggtaggggg 1199
|||||||||||||||||||
Sbjct: 82918 acagctggcgcgccaggtaggggg 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:OJ1344_B01
Length = 170912

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

```
Query: 1174 cgacagctggcgcgccaggtaggggtgtgtc 1205
      ||||| |||||
Sbjct: 3402 cgacagttggcgcgccaggtaggggtgtgtc 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 cgacagctggcgcgccaggtaggggtgtgtc 1205
      ||||| |||||
Sbjct: 91487 cgacagttggcgcgccaggtaggggtgtgtc 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 cgacagctggagcgccaggtaggggg 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 cgcacagctggcgcgccaggtagggggtgtgt 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 cgcacagctggcgcgccaggtagggggtgtgt 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 cgacagctggcgcgccaggtagggggtg 1201
||||| |||||||||||||||| |||||
Sbjct: 54023 cgacagttggcgcgccaggtagggggtg 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 cgacagctggcgcgccaggtagggggtgtgtc 1205
||||| |||||||||||||||| |||||
Sbjct: 146215 cgacagttggcgcgccaggtaggggtgtgtgtc 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 acagctggcgcgccaggtaggggg 1199

|||||

Sbjct: 66981 acagctggcgcgccaggtaggggg 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 cgacagctggcgcgccaggtaggggggtg 1201

|||||

Sbjct: 84158 cgacagttggcgcgccaggtaggggggtg 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 cgacagctggcgcgccaggtaggggggtg 1201

|||||

Sbjct: 8706 cgacagttggcgcgccaggtaggggggtg 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 ccgacagctggcgcgccaggtagggg 1198
||||||| |||||||||||||||||
Sbjct: 69916 ccgacagttggcgcgccaggtagggg 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 aaacaccgacagctggcgcgccaggtagggg 1198
|||| ||||||| |||||||||||||||||
Sbjct: 52277 aaacgccgacagttggcgcgccaggtagggg 52307

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

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198
|||| ||||||| |||||||||||||||||
Sbjct: 94136 aaacgccgacagttggcgcgccaggtagggg 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 aaacaccgacagctggcgcgccaggtagggg 1198
|||| ||||||| |||||||||||||||||
Sbjct: 112762 aaacgccgacagttggcgcgccaggtagggg 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%)

Strand = Plus / Minus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198
||||| ||||||| ||||||| ||||||| |||||||
Sbjct: 160565 aaacgccgacagttggcgcgccaggtagggg 160535

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

Query: 1173 ccgacagctggcgcgccaggtagggg 1198
||||||| ||||||| ||||||| ||||||| |||||||
Sbjct: 26505 ccgacagttggcgcgccaggtagggg 26480

>gb|AC214043.4| Zea mays BAC clone CH201-299G22 from chromosome 5, complete sequence
Length = 166124

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

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198
||||| ||||||| ||||||| ||||||| |||||||
Sbjct: 23565 aaacgccgacagttggcgcgccaggtagggg 23595

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

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198
||||| ||||||| ||||||| ||||||| |||||||
Sbjct: 58049 aaacgccgacagttggcgcgccaggtagggg 58079

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

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198
|||| |||||| ||||||||||||||||
Sbjct: 81733 aaacgccgacagttggcgcgccaggtagggg 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 aaacgccgacagttggcgcgccaggtagggg 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 aaacgccgacagttggcgcgccaggtagggg 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 aaacgccgacagttggcgcgccaggtagggg 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%)

Strand = Plus / Plus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198
|||| ||||||| ||||||||||||||||
Sbjct: 21578 aaacgccgacagttggcgcgccaggtagggg 21608

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

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198
|||| ||||||| ||||||||||||||||
Sbjct: 45262 aaacgccgacagttggcgcgccaggtagggg 45232

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

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198
|||| ||||||| ||||||||||||||||
Sbjct: 79745 aaacgccgacagttggcgcgccaggtagggg 79715

>gb|AC203365.4| Zea mays BAC clone ZMMBBb-196K7 from chromosome 5, complete sequence
Length = 138785

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

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198
|||| ||||||| ||||||||||||||||
Sbjct: 31631 aaacgccgacagttggcgcgccaggtagggg 31601

>gb|AC196774.5| Zea mays BAC clone CH201-435B12 from chromosome 5, complete sequence
Length = 208481

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

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198
|||| |||||| ||||||||||||||||
Sbjct: 42913 aaacgccgacagttggcgcgccaggtagggg 42943

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

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198
|||| |||||| ||||||||||||||||
Sbjct: 149647 aaacgccgacagttggcgcgccaggtagggg 149677

>gb|AC203430.5| Zea mays BAC clone CH201-142M10 from chromosome 5, complete sequence
Length = 195985

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

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198
|||| |||||| ||||||||||||||||
Sbjct: 56936 aaacgccgacagttggcgcgccaggtagggg 56906

>gb|AC186011.4| Zea mays BAC clone CH201-417E17 from chromosome 5, complete sequence
Length = 174321

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

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198
|||| |||||| ||||||||||||||||
Sbjct: 1307 aaacgccgacagttggcgcgccaggtagggg 1277

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

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 tgtaaccacacatatata-gatccatcccaagaagtagtgtattacgcctctctaagcgg 1040
||||| ||||||||| | |||||| | || ||||||| || ||||||| |||||||

Sbjct: 362 tgtaatccaccacataaaaagatccacaccaggaagtagggtgttacgtctctctaagcgg 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 tggcgcgccaggtaggggtgtg 1203
 |||||
Sbjct: 353 tggcgcgccaggtaggggtgtg 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 tggcgcgccaggtaggggtgtg 1203
 |||||
Sbjct: 26 tggcgcgccaggtaggggtgtg 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 ccgacagctggcgcgccaggtagggg 1199
||||| ||||||||||||||||
Sbjct: 16560 ccgacagttggcgcgccaggtagggg 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 ccgacagctggcgcgccaggtagggg 1199
||||| ||||||||||||||||
Sbjct: 39516 ccgacatctggcgcgccaggtagggg 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 cgacagctggcgcgccaggtaaaggggt 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 tgtaaccaccacatatata-gatccatccaagaagtagtgtattacgcctctctaagcgg 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 tgtaaccaccacatatata-gatccatccaagaagtagtgtattacgcctctctaagcgg 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 = 29/31 (93%)
Strand = Plus / Plus

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198
|||| ||||||| |||||||||||||||||
Sbjct: 94738 aaacgccgacagttggcgcgccaggtagggg 94768

>emb|CR855167.1| Oryza sativa genomic DNA, chromosome 4, BAC clone: OSIGBa0127A14,
complete sequence
Length = 81442

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

Query: 1180 ctggcgcgccaggtaggggggtgt 1202
|||||||||||||||||||||
Sbjct: 29831 ctggcgcgccaggtaggggggtgt 29809

>gb|DQ417752.1| Zea mays B73 pathogenesis-related protein 2 and GASA-like protein
genes, complete cds
Length = 156772

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

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198
|||| ||||||| |||||||||||||||||
Sbjct: 73780 aaacgccgacagttggcgcgccaggtagggg 73810

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

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198
|||| ||||||| |||||||||||||||||
Sbjct: 109963 aaacgccgacagttggcgcgccaggtagggg 109933

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

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198
|||| ||||||| ||||||||||||||||
Sbjct: 136436 aaacgccgacagttggcgcgccaggtagggg 136406

>gb|AC169378.2| Sorghum bicolor clone SB_BBc0007L02, complete sequence
Length = 138518

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

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198
||||||||||| ||||||||||| |||||
Sbjct: 3582 aaacaccgacagttggcgcgccagatagggg 3612

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

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

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198
|||| ||||||| ||||||||||||||||
Sbjct: 16033 aaacgccgacagttggcgcgccaggtagggg 16003

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

Query: 1168 aaacaccgacagctggcgcgccaggtagggg 1198
||||||| ||| ||||||||||||||||
Sbjct: 72192 aaacaccaacagttggcgcgccaggtagggg 72222

Score = 46.1 bits (23), Expect = 0.90
Identities = 41/47 (87%)
Strand = Plus / Plus

Query: 350 ggtgggttttacagagtttaactagcggattatatagtggtataga 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)