

BLASTn Search Outputs of the 3' Border Sequences in Maize Event DAS-40278-9 against GenBank Nucleotide Collection (nt/nr)

BLASTN 2.2.21 [Jun-14-2009]

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

Query= Region 4
(1868 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,...		912	0.0
gb EU952187.1	Zea mays clone 1218827 hypothetical protein mRNA,...		648	0.0
gb AC152494.1	Zea mays BAC clone Z418K17, complete sequence		240	2e-59
gb AC160211.1	Genomic sequeunce for Zea mays BAC clone ZMMBBb044...		240	2e-59
gb AF466932.1	Zea mays clone BAC 206C17, complete sequence		240	2e-59
gb AC230040.3	Zea mays BAC clone CH201-122P19 from chromosome 7...		232	6e-57
gb AC211313.4	Zea mays BAC clone CH201-9J2 from chromosome 5, c...		224	1e-54
gb AC210997.6	Zea mays BAC clone CH201-545A13 from chromosome 5...		224	1e-54
gb AY325816.1	Zea mays BAC clone Z013I05, complete sequence		224	1e-54
gb AF546188.1	Contiguous genomic DNA sequence comprising the 19...		224	1e-54
gb AC206303.5	Zea mays BAC clone CH201-328A17 from chromosome 5...		220	2e-53
gb AC185486.5	Zea mays BAC clone CH201-162J17 from chromosome 5...		216	4e-52
gb AC229879.2	Zea mays BAC clone CH201-103M12 from chromosome 8...		216	4e-52
gb AC203072.5	Zea mays BAC clone CH201-26J18 from chromosome 6,...		216	4e-52
gb EU952110.1	Zea mays clone 1165529 hypothetical protein mRNA,...		216	4e-52
gb AC165174.2	Zea mays clone ZMMBBb-127F19, complete sequence		214	1e-51
gb AC231746.2	Zea mays BAC clone CH201-98H14 from chromosome 6,...		208	9e-50
gb EF190061.1	Zea mays clone FS2_19 chromosome B, genomic sequence		208	9e-50
gb DQ493649.1	Zea mays cultivar Coroico bz locus region		208	9e-50
gb AY664415.1	Zea mays cultivar B73 locus 9009, complete sequence		208	9e-50
gb AC217319.3	Zea mays BAC clone ZMMBBb-86E19 from chromosome 5...		206	3e-49
gb AC198320.5	Zea mays BAC clone ZMMBBb-334D6 from chromosome 5...		206	3e-49
emb X97605.1	Z.diploperennis DNA for Grandel-6 retrotransposon		206	3e-49
gb DQ493647.1	Zea mays cultivar NalTel bz locus region		204	1e-48
gb AC203284.4	Zea mays BAC clone CH201-504M1 from chromosome 5,...		200	2e-47
gb DQ002407.1	Zea mays copia retrotransposon opiel, gypsy retro...		200	2e-47

gb	AC206691.5	Zea mays BAC clone CH201-149B20 from chromosome 1...	198	8e-47
gb	DQ493650.1	Zea mays cultivar A188 bz locus region	196	3e-46
gb	DQ493646.1	Zea mays cultivar CML258 bz locus region	196	3e-46
gb	AF448416.1	Zea mays B73 chromosome 9S bz genomic region	196	3e-46
gb	AY664416.1	Zea mays cultivar Mo17 locus bz, complete sequence	196	3e-46
gb	AC209386.4	Zea mays BAC clone CH201-98J13 from chromosome 5,...	194	1e-45
emb	X97604.1	Z. diploperennis DNA for Grandel-4 retrotransposon	192	5e-45
gb	AC203533.4	Zea mays BAC clone CH201-452L5 from chromosome 5,...	184	1e-42
gb	AY883559.2	Zea mays cultivar inbred line B73 teosinte glume ...	180	2e-41
gb	AC225631.3	Zea mays BAC clone CH201-111A2 from chromosome 8,...	178	8e-41
gb	EF190062.1	Zea mays clone FS2_20 chromosome B, genomic sequence	176	3e-40
gb	AC196084.4	Zea mays BAC clone CH201-52A17 from chromosome 5,...	174	1e-39
gb	AC194844.5	Zea mays BAC clone CH201-463C23 from chromosome 5...	174	1e-39
gb	AC226723.4	Zea mays BAC clone CH201-110I20 from chromosome 6...	170	2e-38
gb	AC194842.4	Zea mays BAC clone CH201-514N20 from chromosome 4...	165	1e-36
gb	EF468511.1	Zea mays clone pBS-2 LL repeat sequence	159	7e-35
gb	AC229878.2	Zea mays BAC clone CH201-108P8 from chromosome 9,...	157	3e-34
gb	EF468503.1	Zea mays clone pBK118-4 retrotransposon GrandeB, ...	157	3e-34
gb	EU940901.1	Zea mays clone 1168199 mRNA sequence	155	1e-33
gb	AF090447.2	Zea mays 22 kDa alpha zein gene cluster, complete...	151	2e-32
gb	AC204225.4	Zea mays BAC clone CH201-427P14 from chromosome 5...	145	1e-30
gb	AY574035.1	Zea mays rust resistance protein rp3-1 (rp3-1) ge...	145	1e-30
gb	AY555142.1	Zea mays BAC clone c573F08, complete sequence	145	1e-30
gb	EF468504.1	Zea mays clone pBK118-5 LL repeat sequence	135	1e-27
gb	EF468502.1	Zea mays clone pBK118-3 LL repeat sequence	135	1e-27
gb	FJ386419.1	Zea mays clone R4-b StarkB element, partial sequence	129	7e-26
gb	EF190065.1	Zea mays clone PS52 chromosome B, genomic sequence	129	7e-26
gb	EF190066.1	Zea mays clone PS53 chromosome B, genomic sequence	127	3e-25
gb	DQ183073.1	Zea mays clone A-RGA5 resistance gene analog-like...	121	2e-23
gb	EF468507.1	Zea mays clone pBK118-8 LL repeat sequence	111	2e-20
gb	AC209754.5	Zea mays BAC clone CH201-23E16 from chromosome 5,...	101	1e-17
gb	EF190051.1	Zea mays clone 46F3FF5Rm5 chromosome B, genomic s...	101	1e-17
gb	EF190049.1	Zea mays clone 46F3FF5Rm3 chromosome B, genomic s...	101	1e-17
gb	FJ386423.1	Zea mays clone R6-b StarkB element, partial sequence	98	2e-16
gb	EF190053.1	Zea mays clone 46F3FF5Rs2 chromosome B, genomic s...	90	6e-14
gb	EF190052.1	Zea mays clone 46F3FF5Rs1 chromosome B, genomic s...	90	6e-14
gb	EF190050.1	Zea mays clone 46F3FF5Rm4 chromosome B, genomic s...	86	9e-13
gb	U68403.1	ZMU68403 Zea mays retrotransposon Grande-Zm 5' LTR a...	80	5e-11
gb	DQ183088.1	Zea mays clone A-RGA20 resistance gene analog-lik...	78	2e-10
gb	AC165175.2	Zea mays clone ZMMBBb-136N21, complete sequence	70	5e-08
gb	EF190048.1	Zea mays clone 46F3FF5Rm1 chromosome B, genomic s...	68	2e-07
gb	EU949251.1	Zea mays clone 400160 mRNA sequence	64	3e-06
gb	EF190064.1	Zea mays clone pStark5.5 chromosome B, genomic se...	62	1e-05
gb	AC229874.3	Zea mays BAC clone CH201-314N3 from chromosome 3,...	54	0.003
gb	GU235996.1	Coix lacryma-jobi 22-kDa prolamin gene cluster, c...	54	0.003
gb	AC226722.2	Zea mays BAC clone CH201-146D18 from chromosome 1...	54	0.003
gb	AC186565.4	Zea mays BAC clone ZMMBBb-610A7 from chromosome 5...	54	0.003
gb	AC194974.4	Zea mays BAC clone CH201-115G11 from chromosome 5...	54	0.003
gb	AC237090.1	Oryza granulata clone OG_ABa0119F03, complete seq...	54	0.003

gb	AC231756.2	Zea mays BAC clone CH201-111G11 from chromosome 1...	54	0.003
gb	AC233030.1	Oryza minuta clone OM_Ba0022H02, complete sequence	54	0.003
gb	AC231332.1	Oryza minuta clone OM_Ba0219N21, complete sequence	54	0.003
gb	AC196829.2	Sorghum bicolor clone SB_BBc0050H06, complete seq...	54	0.003
gb	AC196818.2	Sorghum bicolor clone SB_BBc0005H14, complete seq...	54	0.003
gb	AC165173.2	Zea mays clone ZMMBBb-125019, complete sequence	54	0.003
gb	AY455286.1	Zea mays chloroplast phytoene synthase (Y1) gene,...	54	0.003
gb	GU080322.1	Saccharum hybrid cultivar R570 clone BAC 086H20, ...	52	0.012
gb	AC231130.2	Oryza minuta clone OM_Ba0135C17, complete sequence	52	0.012
gb	AC213133.1	Oryza glaberrima clone OG_BBa0042C22, complete se...	52	0.012
gb	EF659468.1	Zea mays clone BAC b0288K09 AP2 domain transcript...	52	0.012
gb	EF659467.1	Zea mays clone BAC m.pk066.114 AP2 domain transcr...	52	0.012
emb	CR855170.1	Oryza sativa genomic DNA, chromosome 4, BAC clon...	52	0.012
gb	AC105320.2	Oryza sativa Japonica Group chromosome 5 clone OJ...	52	0.012
gb	AC117264.2	Oryza sativa Japonica Group chromosome 5 clone OJ...	52	0.012
gb	AC135924.2	Oryza sativa Japonica Group chromosome 5 clone P0...	52	0.012
gb	AC130598.2	Oryza sativa Japonica Group chromosome 5 clone OS...	52	0.012
gb	AC145127.1	Oryza sativa Japonica Group chromosome 10 clone P...	52	0.012
gb	AC092388.5	Oryza sativa chromosome 10 BAC OSJNBa0011L09 geno...	52	0.012
gb	AC068654.2	Genomic Sequence For Oryza sativa (japonica culti...	52	0.012
dbj	AP006233.3	Oryza sativa Japonica Group genomic DNA, chromos...	52	0.012
dbj	AP005460.3	Oryza sativa Japonica Group genomic DNA, chromos...	52	0.012
dbj	AP004729.3	Oryza sativa Japonica Group genomic DNA, chromos...	52	0.012
dbj	AP003458.4	Oryza sativa Japonica Group genomic DNA, chromos...	52	0.012
dbj	AP005684.3	Oryza sativa Japonica Group genomic DNA, chromos...	52	0.012
dbj	AP005834.4	Oryza sativa Japonica Group genomic DNA, chromos...	52	0.012
dbj	AP006556.2	Oryza sativa Japonica Group genomic DNA, chromos...	52	0.012
dbj	AP005414.3	Oryza sativa Japonica Group genomic DNA, chromos...	52	0.012
dbj	AP004229.3	Oryza sativa Japonica Group genomic DNA, chromos...	52	0.012
dbj	AP003988.3	Oryza sativa Japonica Group genomic DNA, chromos...	52	0.012
dbj	AP005563.3	Oryza sativa Japonica Group genomic DNA, chromos...	52	0.012
dbj	AP003525.2	Oryza sativa Japonica Group genomic DNA, chromos...	52	0.012
dbj	AP006062.2	Oryza sativa Japonica Group genomic DNA, chromos...	52	0.012
dbj	AP005795.3	Oryza sativa Japonica Group genomic DNA, chromos...	52	0.012
dbj	AP005512.3	Oryza sativa Japonica Group genomic DNA, chromos...	52	0.012
dbj	AP004645.3	Oryza sativa Japonica Group genomic DNA, chromos...	52	0.012
dbj	AP004375.3	Oryza sativa Japonica Group genomic DNA, chromos...	52	0.012
dbj	AP006237.3	Oryza sativa Japonica Group genomic DNA, chromos...	52	0.012
emb	AL731605.3	Oryza sativa genomic DNA, chromosome 4, BAC clon...	52	0.012
dbj	AP004611.3	Oryza sativa Japonica Group genomic DNA, chromos...	52	0.012
dbj	AP004821.4	Oryza sativa Japonica Group genomic DNA, chromos...	52	0.012
emb	AL606634.2	Oryza sativa genomic DNA, chromosome 4, BAC clon...	52	0.012
dbj	AP003760.4	Oryza sativa Japonica Group genomic DNA, chromos...	52	0.012
dbj	AP004194.3	Oryza sativa Japonica Group genomic DNA, chromos...	52	0.012
dbj	AP002482.1	Oryza sativa Japonica Group genomic DNA, chromos...	52	0.012
emb	AL713941.3	Oryza sativa chromosome 12, . BAC OSJNBa0006M08 ...	52	0.012
emb	AL731592.2	Oryza sativa genomic DNA, chromosome 4, BAC clon...	52	0.012
gb	GQ407104.1	Oryza granulata chromosome 6 clone BAC a0186L08/a...	50	0.048
gb	AC231811.1	Oryza minuta clone OM_Ba0091E17, complete sequence	50	0.048

gb	EU338354.1	Zea mays cultivar W22 bz gene locus, complete seq...	50	0.048
gb	AF391808.3	Zea mays cultivar McC bz locus region	50	0.048
emb	CR855225.1	Oryza sativa genomic DNA, chromosome 4, BAC clon...	50	0.048
gb	AC083945.3	Oryza sativa Japonica Group chromosome X clone OS...	50	0.048
gb	AC135929.2	Oryza sativa Japonica Group chromosome 5 clone P0...	50	0.048
gb	AC136226.2	Oryza sativa Japonica Group chromosome 5 clone OS...	50	0.048
gb	AC108498.2	Oryza sativa Japonica Group chromosome 5 clone OJ...	50	0.048
gb	AC134348.2	Oryza sativa Japonica Group chromosome 5 clone P0...	50	0.048
emb	AL606649.4	Oryza sativa genomic DNA, chromosome 4, BAC clon...	50	0.048
gb	AY530950.1	Zea mays putative zinc finger protein (Z438D03.1)...	50	0.048
dbj	AP005866.2	Oryza sativa Japonica Group genomic DNA, chromos...	50	0.048
dbj	AP003435.2	Oryza sativa Japonica Group genomic DNA, chromos...	50	0.048
gb	AC229780.2	Oryza minuta clone OM_Ba0081J07, complete sequence	48	0.19
gb	AC231887.2	Oryza minuta clone OM_Ba0018L21, complete sequence	48	0.19
gb	AC225222.3	Zea mays BAC clone CH201-123I12 from chromosome 1...	48	0.19
gb	FJ266023.1	Oryza granulata clone OG_ABa077F15_032P05, comple...	48	0.19
gb	AC231882.1	Oryza minuta clone OM_Ba0091G05, complete sequence	48	0.19
gb	AC229741.1	Oryza minuta clone OM_Ba0230E13, complete sequence	48	0.19
gb	AC223439.1	Oryza brachyantha, complete sequence	48	0.19
gb	AC097176.3	Oryza sativa Japonica Group chromosome 5 clone OJ...	48	0.19
gb	AC078839.4	Oryza sativa Japonica Group chromosome X clone OS...	48	0.19
gb	AC130602.5	Oryza sativa Japonica Group chromosome 5 clone B1...	48	0.19
gb	AC087552.3	Oryza sativa Japonica Group chromosome 5 clone P0...	48	0.19
dbj	AP005458.3	Oryza sativa Japonica Group genomic DNA, chromos...	48	0.19
dbj	AP005456.3	Oryza sativa Japonica Group genomic DNA, chromos...	48	0.19
dbj	AP005570.3	Oryza sativa Japonica Group genomic DNA, chromos...	48	0.19
dbj	AP005424.3	Oryza sativa Japonica Group genomic DNA, chromos...	48	0.19
dbj	AP005774.5	Oryza sativa Japonica Group genomic DNA, chromos...	48	0.19
dbj	AP003991.3	Oryza sativa Japonica Group genomic DNA, chromos...	48	0.19
dbj	AP003977.3	Oryza sativa Japonica Group genomic DNA, chromos...	48	0.19
dbj	AP003974.3	Oryza sativa Japonica Group genomic DNA, chromos...	48	0.19
dbj	AP003724.2	Oryza sativa Japonica Group genomic DNA, chromos...	48	0.19
dbj	AP005628.3	Oryza sativa Japonica Group genomic DNA, chromos...	48	0.19
emb	AL606615.4	Oryza sativa genomic DNA, chromosome 4, BAC clon...	48	0.19
dbj	AP004030.2	Oryza sativa Japonica Group genomic DNA, chromos...	48	0.19
emb	AL731618.3	Oryza sativa genomic DNA, chromosome 4, BAC clon...	48	0.19
emb	AL663012.3	Oryza sativa genomic DNA, chromosome 4, BAC clon...	48	0.19
dbj	AP005464.3	Oryza sativa Japonica Group genomic DNA, chromos...	48	0.19
dbj	AP003204.3	Oryza sativa Japonica Group genomic DNA, chromos...	48	0.19
dbj	AP002968.2	Oryza sativa Japonica Group genomic DNA, chromos...	48	0.19
dbj	AP002525.1	Oryza sativa Japonica Group genomic DNA, chromos...	48	0.19
gb	AC208340.4	Zea mays BAC clone CH201-53J11 from chromosome 5,...	46	0.76
gb	AC216353.5	Zea mays BAC clone CH201-194K18 from chromosome 5...	46	0.76
gb	AC205514.6	Zea mays BAC clone CH201-227F5 from chromosome 5,...	46	0.76
gb	AC207417.4	Zea mays BAC clone CH201-186N18 from chromosome 5...	46	0.76
gb	AC204937.4	Zea mays BAC clone CH201-488A19 from chromosome 5...	46	0.76
gb	AC210260.5	Zea mays BAC clone CH201-44F4 from chromosome 5, ...	46	0.76
gb	AC190571.5	Zea mays BAC clone CH201-151G9 from chromosome 5,...	46	0.76
gb	AC216070.4	Zea mays BAC clone CH201-459P15 from chromosome 5...	46	0.76

gb	AC226721.2	Zea mays BAC clone CH201-150M20 from chromosome 1...	46	0.76
gb	AC213983.4	Zea mays BAC clone CH201-326E16 from chromosome 5...	46	0.76
gb	AC225944.3	Zea mays BAC clone CH201-127G5 from chromosome 10...	46	0.76
gb	AC214043.4	Zea mays BAC clone CH201-299G22 from chromosome 5...	46	0.76
gb	AC196472.3	Zea mays BAC clone ZMMBBb-235B12 from chromosome ...	46	0.76
gb	AC185472.4	Zea mays BAC clone CH201-257N23 from chromosome 5...	46	0.76
gb	AC201762.5	Zea mays BAC clone CH201-479M22 from chromosome 5...	46	0.76
gb	AC203071.4	Zea mays BAC clone CH201-184N10 from chromosome 5...	46	0.76
gb	AC203365.4	Zea mays BAC clone ZMMBBb-196K7 from chromosome 5...	46	0.76
gb	AC196774.5	Zea mays BAC clone CH201-435B12 from chromosome 5...	46	0.76
gb	AC203430.5	Zea mays BAC clone CH201-142M10 from chromosome 5...	46	0.76
gb	AC186011.4	Zea mays BAC clone CH201-417E17 from chromosome 5...	46	0.76
gb	AC210188.4	Zea mays BAC clone CH201-257L10 from chromosome 5...	46	0.76
gb	AC195458.4	Zea mays BAC clone CH201-47808 from chromosome 5,...	46	0.76
gb	AC191361.5	Zea mays BAC clone CH201-21609 from chromosome 5,...	46	0.76
gb	AC190647.4	Zea mays BAC clone ZMMBBb-216G14 from chromosome ...	46	0.76
gb	AC215174.5	Zea mays BAC clone CH201-70P8 from chromosome 5, ...	46	0.76
gb	AC211535.5	Zea mays BAC clone ZMMBBb-223D21 from chromosome ...	46	0.76
gb	AC237089.1	Oryza granulata clone OG_ABa0096023, complete seq...	46	0.76
gb	AC237088.1	Oryza granulata clone OG_ABa0089G14, complete seq...	46	0.76
gb	AC237087.1	Oryza granulata clone OG_ABa0028G18, complete seq...	46	0.76
gb	AC229873.2	Zea mays BAC clone CH201-387D15 from chromosome 2...	46	0.76
ref	XM_002442558.1	Sorghum bicolor hypothetical protein, mRNA	46	0.76
ref	XM_002465520.1	Sorghum bicolor hypothetical protein, mRNA	46	0.76
gb	FJ614806.1	Zea mays cultivar B73 p cluster, complete sequence	46	0.76
gb	AC213848.4	Zea mays BAC clone CH201-495D12 from chromosome 5...	46	0.76
gb	AC232337.2	Oryza minuta clone OM_Ba0147P17, complete sequence	46	0.76
gb	AC213131.2	Oryza glaberrima clone OG_BB0031E23, complete se...	46	0.76
gb	AC229876.2	Zea mays BAC clone CH201-115J9 from chromosome 8,...	46	0.76
gb	AC217961.4	Zea mays BAC clone ZMMBBb-353K3 from chromosome 6...	46	0.76
gb	AC187050.5	Zea mays BAC clone ZMMBBb-293C24 from chromosome ...	46	0.76
gb	AC231617.2	Zea mays BAC clone CH201-190G15 from chromosome 8...	46	0.76
gb	AC229877.2	Zea mays BAC clone CH201-11105 from chromosome 9,...	46	0.76
gb	FJ032637.1	Oryza ridleyi clone a0301G20 Monoculm1 and Mlo fa...	46	0.76
gb	EU940899.1	Zea mays clone 1168123 mRNA sequence	46	0.76
gb	AC229778.1	Oryza minuta clone OM_Ba0085P10, complete sequence	46	0.76
gb	AC225785.1	Oryza granulata, complete sequence	46	0.76
gb	AC196850.2	Sorghum bicolor clone SB_BB0140005, complete seq...	46	0.76
gb	AC196847.2	Sorghum bicolor clone SB_BB0109L12, complete seq...	46	0.76
gb	AC196837.2	Sorghum bicolor clone SB_BB0073F19, complete seq...	46	0.76
gb	DQ493648.1	Zea mays cultivar I137TN bz locus region	46	0.76
emb	CR855167.1	Oryza sativa genomic DNA, chromosome 4, BAC clon...	46	0.76
gb	DQ417752.1	Zea mays B73 pathogenesis-related protein 2 and G...	46	0.76
gb	AC169378.2	Sorghum bicolor clone SB_BB0007L02, complete seq...	46	0.76
gb	AC165172.2	Zea mays clone CH201-171E16, complete sequence	46	0.76
gb	AC157319.2	Zea mays clone ZMMBBb-136E2, complete sequence	46	0.76
gb	AC152495.1	Zea mays BAC clone Z486N13, complete sequence	46	0.76
gb	AF528565.1	Zea mays cultivar BSSS53 chromosome 4 clone BAC 0...	46	0.76
gb	AC147925.2	Oryza sativa Japonica Group chromosome 11 clone 0...	46	0.76

gb	AC108761.2	Oryza sativa (japonica cultivar-group) chromosome...	46	0.76
gb	BT018612.1	Zea mays clone EL01N0501C03.d mRNA sequence	46	0.76
gb	BT017984.1	Zea mays clone EL01N0525E01.c mRNA sequence	46	0.76
gb	AC135502.4	Oryza sativa chromosome 3 BAC OSJNBb0085A04 genom...	46	0.76
gb	AC121364.2	Oryza sativa Japonica Group chromosome 5 clone OS...	46	0.76
gb	AC135418.3	Oryza sativa Japonica Group chromosome 5 clone OS...	46	0.76
gb	AC120991.3	Oryza sativa Japonica Group chromosome 5 clone OS...	46	0.76
gb	AC112159.2	Oryza sativa Japonica Group chromosome 5 clone OJ...	46	0.76
gb	AY078063.2	Zea mays B transcriptional activator (b1) gene, b...	46	0.76
gb	DQ002408.1	Zea mays gypsy retrotransposon huck, and copia re...	46	0.76
gb	AC145386.1	Oryza sativa chromosome 3 BAC OSJNBb0028K20 genom...	46	0.76
gb	AC169373.2	Sorghum bicolor clone SB_BBc0188M08, complete seq...	46	0.76
gb	AC165267.2	Zea mays clone ZMMBBb-151F20, complete sequence	46	0.76
gb	AC137992.2	Oryza sativa chromosome 3 BAC OSJNBb0056B16 genom...	46	0.76
gb	AC165171.2	Zea mays clone CH201-145P10, complete sequence	46	0.76
gb	AC165176.2	Zea mays clone ZMMBBb-177G21, complete sequence	46	0.76
gb	AC122147.1	Oryza sativa Japonica Group chromosome 10 clone O...	46	0.76
gb	AC092553.4	Oryza sativa Japonica Group chromosome 10 clone O...	46	0.76
gb	AC163004.1	Gap filling sequence from Zea mays clone ZMMBBb03...	46	0.76
dbj	AP006849.2	Oryza sativa Japonica Group genomic DNA, chromos...	46	0.76
dbj	AP003874.5	Oryza sativa Japonica Group genomic DNA, chromos...	46	0.76
dbj	AP005820.3	Oryza sativa Japonica Group genomic DNA, chromos...	46	0.76
gb	AY530951.1	Zea mays putative growth-regulating factor 1 (Z21...	46	0.76
gb	AY555143.1	Zea may BAC clone c573L14, complete sequence	46	0.76
gb	AF466202.2	Zea mays putative pol protein gene, partial cds; ...	46	0.76
dbj	AP003911.3	Oryza sativa Japonica Group genomic DNA, chromos...	46	0.76
dbj	AP004705.3	Oryza sativa Japonica Group genomic DNA, chromos...	46	0.76
emb	BX842604.1	Oryza sativa genomic DNA, chromosome 4, BAC clon...	46	0.76
gb	AY144442.1	Sorghum bicolor BAC 95A23/98N8.1 Rph region, part...	46	0.76
gb	AC137696.2	Genomic sequence for Oryza sativa, Nipponbare str...	46	0.76
gb	AC134229.2	Oryza sativa Japonica Group chromosome 3 clone OJ...	46	0.76
gb	AF546189.1	Contiguous genomic DNA sequence comprising the 19...	46	0.76
dbj	AP005244.3	Oryza sativa Japonica Group genomic DNA, chromos...	46	0.76
gb	AF369906.1	Sorghum bicolor clone BAC10J22 Sbb3766 sequence	46	0.76
gb	AF466204.1	Sorghum bicolor clone SBTXS_0045I19, partial sequ...	46	0.76
gb	AF466203.1	Zea mays clone ZMBBb_0092E12, partial sequence	46	0.76
gb	U68404.1	ZMU68404 Zea mays retrotransposon Huck-2 5' LTR and ...	46	0.76
gb	AC157977.1	Genomic sequence for Zea mays chromosome 8 BAC cl...	46	0.76
gb	AC157487.1	Genomic sequence for Zea mays clone ZMMBBb0614J24...	46	0.76
gb	AY664419.1	Zea mays cultivar Mo17 locus 9009, complete sequence	46	0.76
gb	AY664418.1	Zea mays cultivar Mo17 locus 9008, complete sequence	46	0.76
gb	AY664417.1	Zea mays cultivar Mo17 locus 9002, complete sequence	46	0.76
gb	AY664414.1	Zea mays cultivar B73 locus 9008, complete sequence	46	0.76
gb	AY691949.1	Zea mays alcohol dehydrogenase 1 (adh1A) gene, co...	46	0.76
emb	AL732380.4	Oryza sativa chromosome 12, . BAC OSJNBb0119N22 ...	46	0.76
gb	AF123535.1	Zea mays alcohol dehydrogenase 1 (adh1) gene, adh...	46	0.76
gb	GU080321.1	Saccharum hybrid cultivar R570 clone BAC 095F04, ...	44	3.0
gb	GQ845073.1	Zea mays chromosome 4 PCR sequence AGI.995 genom...	44	3.0
gb	AC226365.2	Oryza minuta clone OM_Ba0223P12, complete sequence	44	3.0

gb FJ032628.1	Oryza punctata clone a0082J04 subtilisin-like pro...	44	3.0
gb CP000932.1	Campylobacter lari RM2100, complete genome	44	3.0
gb CP001364.1	Chloroflexus sp. Y-400-fl, complete genome	44	3.0
gb FJ266020.1	Oryza australiensis clone OA_CBa062H21, complete ...	44	3.0
gb AC226816.1	Oryza minuta clone OM_Ba0145I21, complete sequence	44	3.0
gb AC226776.1	Oryza minuta clone OM_Ba0084A05, complete sequence	44	3.0
gb AC229748.1	Oryza minuta clone OM_Ba0197P05, complete sequence	44	3.0
gb AC223438.1	Oryza brachyantha, complete sequence	44	3.0
gb CP000909.1	Chloroflexus aurantiacus J-10-fl, complete genome	44	3.0
gb EF059989.1	Brachypodium sylvaticum hypothetical protein (57h...	44	3.0
emb CR855106.1	Oryza sativa genomic DNA, chromosome 4, BAC clon...	44	3.0
gb AC157320.2	Zea mays clone ZMMBBb-7C14, complete sequence	44	3.0
gb CP000284.1	Methylobacillus flagellatus KT, complete genome	44	3.0
gb AF488416.1	Zea mays chromosome 9 BAC 9C20 complete sequence	44	3.0
gb AC135956.6	Oryza sativa Japonica Group chromosome 3 clone OS...	44	3.0
gb AC092387.6	Oryza sativa Japonica Group chromosome 10 clone O...	44	3.0
gb AC151537.1	Oryza sativa Japonica Group chromosome 3 clone OS...	44	3.0
gb AC097175.2	Oryza sativa Japonica Group chromosome 5 clone OJ...	44	3.0
gb AC093952.2	Oryza sativa Japonica Group chromosome 5 clone OJ...	44	3.0
gb AC135919.2	Oryza sativa (japonica cultivar-group) chromosome...	44	3.0
gb AC119747.1	Genomic sequence for Oryza sativa, Nipponbare str...	44	3.0
gb AC068924.11	Oryza sativa chromosome 10 BAC OSJNBa0026L12 gen...	44	3.0
gb AC092172.3	Oryza sativa Japonica Group chromosome 10 clone O...	44	3.0
emb AL606658.5	Oryza sativa genomic DNA, chromosome 4, BAC clon...	44	3.0
dbj AP005912.3	Oryza sativa Japonica Group genomic DNA, chromos...	44	3.0
dbj AP003574.3	Oryza sativa Japonica Group genomic DNA, chromos...	44	3.0
dbj AP005127.5	Oryza sativa Japonica Group genomic DNA, chromos...	44	3.0
dbj AP005261.4	Oryza sativa Japonica Group genomic DNA, chromos...	44	3.0
dbj AP005199.3	Oryza sativa Japonica Group genomic DNA, chromos...	44	3.0
dbj AP005798.3	Oryza sativa Japonica Group genomic DNA, chromos...	44	3.0
dbj AP005698.3	Oryza sativa Japonica Group genomic DNA, chromos...	44	3.0
dbj AP004156.3	Oryza sativa Japonica Group genomic DNA, chromos...	44	3.0
dbj AP004870.3	Oryza sativa Japonica Group genomic DNA, chromos...	44	3.0
dbj AP004092.3	Oryza sativa Japonica Group genomic DNA, chromos...	44	3.0
gb AY530952.1	Zea mays unknown (Z576C20.2), putative heme oxyge...	44	3.0
dbj AP004023.3	Oryza sativa Japonica Group genomic DNA, chromos...	44	3.0
dbj AP003528.2	Oryza sativa Japonica Group genomic DNA, chromos...	44	3.0
dbj AP005319.3	Oryza sativa Japonica Group genomic DNA, chromos...	44	3.0
dbj AP005312.2	Oryza sativa Japonica Group genomic DNA, chromos...	44	3.0
dbj AP003877.3	Oryza sativa Japonica Group genomic DNA, chromos...	44	3.0
emb BX842606.1	Oryza sativa genomic DNA, chromosome 4, BAC clon...	44	3.0
dbj AP006523.2	Oryza sativa Japonica Group genomic DNA, chromos...	44	3.0
dbj AP005067.2	Oryza sativa Japonica Group genomic DNA, chromos...	44	3.0
dbj AP003846.2	Oryza sativa Japonica Group genomic DNA, chromos...	44	3.0
dbj AP004308.3	Oryza sativa Japonica Group genomic DNA, chromos...	44	3.0
dbj AP004309.3	Oryza sativa Japonica Group genomic DNA, chromos...	44	3.0
dbj AP003253.3	Oryza sativa Japonica Group genomic DNA, chromos...	44	3.0
gb AF466199.1	Sorghum bicolor putative receptor protein kinase,...	44	3.0
gb AC084404.8	AC084404 Oryza sativa chromosome 3 BAC OSJNBa0026A...	44	3.0

dbj|AP002855.2| Oryza sativa Japonica Group genomic DNA, chromos... 44 3.0
emb|AL844880.3| Oryza sativa chromosome 12, . BAC OSJNBb0049H14 ... 44 3.0

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

Score = 912 bits (460), Expect = 0.0
Identities = 1161/1388 (83%), Gaps = 5/1388 (0%)
Strand = Plus / Minus

Query: 2 taccctaaagcaccgcaagggttagccctgggtgtgcggacggactctaaacaccgacag 61
|||||
Sbjct: 5388 taccctaaagcaccgcaagg-taacctaggtgtgcggacggactctaaacaccgacag 5330

Query: 62 ctggcgcgccaggtaggggtgtgtctttgatctgagctagctcaatgaccattacctcc 121
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Sbjct: 5329 ccggcagccaggtaggggtgtgtcgttgatcatagctaactcaatggccatcacctcc 5270

Query: 122 aaatgcaagatcgcccttcgccccgggactatgttttgctttggaacctatctcatccata 181
||
Sbjct: 5269 aagtgaagatcgcccttcaccccggaactatgttctgctttggaactatctcttccata 5210

Query: 182 gcagatgaagaggggaactctgcaccgcatagcagatctattggagaagaagctttcctca 241
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Sbjct: 5209 gtgatgaagaggggactctgcaccacgtggaagatccgactgagaagaagctttcctga 5150

Query: 242 gaaatctcgaggggagccagggcagaacagcgggtggcaccatcacccgcacctcaagcg 301
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Sbjct: 5149 gaaatcctgaggggaatccaaagcagaatagcgggtggtgccaccacccgcatctcgaggg 5090

Query: 302 aagatgacctcttacaaccgaaagtcgggagctcacctacccgaa-aaactccgctgtc 360
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Sbjct: 5089 aagatgacccctcataaaccgaaggttgggatctcacttaccgaaagaaactccactgtt 5030

Query: 361 cacttcgccacaaaggagtggacacggattactcgaaagaaggaagcgagtgtcccgag 420
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Sbjct: 5029 cacctcgccacaaaggagtgcacacggatcactcgaaagaaggaagcaaatgtcccgag 4970

Query: 421 tcaggggacgggaacacgcccaagccatctttccgacgccttcgccttcaaatgaggatgg 480
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Sbjct: 4969 tcaggggacgagaacacgccgagccat-tttctgacgccttcgccttcaagtagaatgg 4911

Query: 481 aaagaagagcgccatcgcgctggctcctttctaccccgacgtcctcttcatcagggggag 540
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Sbjct: 4910 aaataagagcgccatcacgccggctcctttctaccccgacgtcctcttcatcgggggaa 4851

Query: 541 attggagttagcaccgcttccaacgatgagccaacctgcaaggggaagagcctcccca 600
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Sbjct: 4850 attggagtcacccatctccgatgatgaacctaccatgcaaggggaagaacctccc-a 4792

Query: 601 gcgtgaggcgcgacgacggaggaatagaagccagaacgtcggcgacatcacgaggctgg 660
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Sbjct: 4791 gtgtgaagcgcgacaacggaggaacaaatgccgaaacatacggtgacatcacgaagctag 4732

Query: 661 ggaacgggatccggcgcaaccgctatcccgggacgaagctttagaagtaggaaaaactcc 720
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Sbjct: 4731 ggaacgggatccgacatagcctgtatcccaagacgaggcctcataagtgggagaaactcc 4672

Query: 721 cgacgagtgggtacaccgagaaaggcggaactctcgccgccgtgatcgccgacaagctta 780
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Sbjct: 4671 cgacgagcgagtgcaccgggaaatgtggaactctcaccaccgtgattgccgacaagctca 4612

Query: 781 ggaccgagaacgagagcaagccgagcaaggtgcaaggctgcgccgagagaatgctctctt 840
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Sbjct: 4611 ggaccaagagcaggaacaagccgagcaaggtgcaaggctgtgccgagagaacctctctt 4552

Query: 841 tgctcggaacctgtaccccgacttcgctcgtgcaatgaacacgccgagtgaagtcggagg 900
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Sbjct: 4551 cgctcggaacctgtatcccgactttgctcatgcaatgaacacgccgagtgaattcggagg 4492

Query: 901 ggtactggcccagatagctgacggcctcccgcaaccctagacacggaaggtaccggcg 960
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Sbjct: 4491 ggtactgtcccagatagctgacagcatcctgcaaaccgaagatgctgaaggctaccggcg 4432

Query: 961 gctgcttactcgagcagttaatcaccttctacccatcactaatcctccaagcgacctacg 1020
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Sbjct: 4431 actgcttgctcaagtagctaatcaccttctacccatcgtcatcctgcaaacaacctacg 4372

Query: 1021 ccatgccatcaacagccggcgagacacgcggagctccatcaacgcttcgcgcgaccgatg 1080
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Sbjct: 4431 actgcttgctcaagtagctaatcaccttctacccatcgtcatcctgcaaacaacctacg 4372

Sbjct: 4371 tcccaccatcaatagccggcgagacgcgtagagctccatcaacgcttcgcgcgaccggcg 4312

Query: 1081 acacgaaagtgagataggggaaccgagaggagtatgtccgagatcatgccatcctggcatg 1140
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Sbjct: 4311 gcacaaaaatgagataaggcgccgggaggagtatgaccgagatcactatgtatcggcacg 4252

Query: 1141 aagtcatgccacccgagctgagtcggttgccgcctcgaccagtgctccggtccaggacg 1200
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Sbjct: 4251 aagtcgcacgaccgtgttgagtcggccgaacctcgactagtggccattctaggacg 4192

Query: 1201 atcaagatgacacacaactggctccctccttgggaccgacctcacgaacgccgacatga 1260
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Sbjct: 4191 gtcgagatggcatactaccgactccctccttgggaccgacaacacgaacaccgactgga 4132

Query: 1261 agacacgtgccgagttcttcgcacttactccgtgtctccgggccatccagtg-gccccaa 1319
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Sbjct: 4131 acacacatgtggagtctctgtgttggtactccgcgtctccgggccatccagtgcccccaa 4072

Query: 1320 cttcaaggtctccaacgtcagcaagtatgagcgcaagcaggacctgggtggctggttagc 1379
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Sbjct: 4071 cttcaaggtctccaacgtcgacaagtacgagcccaagcaggacccggcggtggttggc 4012

Query: 1380 catctaca 1387

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Sbjct: 4011 cgtctaca 4004

Score = 244 bits (123), Expect = 2e-60
Identities = 459/567 (80%), Gaps = 3/567 (0%)
Strand = Plus / Plus

Query: 1259 gaagacacgtgccgagttcttcgcacttactccgtgtctccgggccatccagtggcc-cct 1317
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Sbjct: 12615 gaagacacatgtggagtatccgcacttacttcgcgtcttagggccgtccagtggcatcca 12674

Query: 1318 aacttcaaggtctccaacgtcagcaagtatgagcgcaagcaggacctgggtggctggtta 1377
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Sbjct: 12675 aacttcaaggtctccaacgtcaacaatacagccaaagcaggacccgagaggctggttg 12734

Query: 1378 gccatctacacgattgtcacatgggccgcccggagcgacggaggacgtgatgacagtgtat 1437
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Sbjct: 12735 gccgtctatacaactgccgcttgggccgctagggaactgaagatgtgatgactgcatat 12794

Query: 1438 tttccattgtcctagggaagacgcaatgcagtggtccgacatctacccaacattgc 1497
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Sbjct: 12795 ttgccgatcatc-tcgggcaagatgcgttgcaatggctttgacacctacctcagcactgc 12853

Query: 1498 atagacaattggagcgacttcagttggtgcttcacgccaaactccagtcctctttgac 1557
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Sbjct: 12854 atcgacgattggaacgacttcagtcggcgcttcacgccaaactccaatccctctccgac 12913

Query: 1558 aagccggcgagccatgggacctaaaatccattgggcatcagggcgatgaaacgctccgg 1617
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Sbjct: 12914 aaactggcgagccatgggacctcaaatccattaggcgccggggggacgaaacacttcgg 12973

Query: 1618 ttgtacctcaagaggttttagacctagaggaaccacacccccgaagtcgccgaggcggg 1677
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Sbjct: 12974 tcgtacctcaaaaggttttagacctagaggaactggatcccaaagtcattgaggcggca 13033

Query: 1678 gtgattgaagacttctaccgaggatccaatgactcggtttcgtccgagccatactccag 1737
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Sbjct: 13034 gtgaatgaggacttctaccgggggtctaatactcggtttcgtccgagccatactacag 13093

Query: 1738 aaaagcgtcgccacctccgaacacttgttccgggaggcagacctctacatcaccacgga 1797
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Sbjct: 13094 -aaagtgcgaccacctccgagcaactgtttcgagaagcagacctctacattaccattga 13152

Query: 1798 ttaacgggcccaggacctcatcgagg 1824
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Sbjct: 13153 cgagcgggcccaggacctcatcgagg 13179

Score = 228 bits (115), Expect = 9e-56
Identities = 302/363 (83%), Gaps = 1/363 (0%)
Strand = Plus / Minus

Query: 1505 attggagcgacttcagttggtgcttcacgccaaactccagtcctctttgacaagccgg 1564
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Sbjct: 3920 attggagcgacttttagtcggcggtttcatccccaatttcagtcctctcttaacaagccgg 3861

Query: 1565 cgcagccatgggacctaataatccattgggcatcagggcgatgaaacgctccggttgacc 1624
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Sbjct: 3860 cgcagccgtgggacctcaatccatcaggcgctagaacaatgaaacacctccggtcgtacc 3801

Query: 1625 tcaagaggttttagaccatgaggaaccacacccccgaagtcgccgaggcggggtgattg 1684
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Sbjct: 3800 tcaagagttttcagatagtgaggaaccgcatccccaagtcgttgaggtggaggcgattg 3741

Query: 1685 aagacttctaccgaggatccaatgactcggctttcgtccgagccatactccagaaaagcg 1744
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Sbjct: 3740 aagacgtctacctagatccaatgactcggacttcatctgagccatacatcagaaa-gca 3682

Query: 1745 tcggccacctccgaacacttgttcgggaggcagacctctacatcaccacggattaacgg 1804
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Sbjct: 3681 ccggccacctctgaataattatttcggaaggcagacctctacatcactgcggatgaacgg 3622

Query: 1805 gcccgagacctcatcgaggcacgaaagccgcgccacacgcgccacggtgtgacacgaac 1864
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Sbjct: 3621 gcccatgacctcttcggaggcacgaaaaccacgccacacgcgccatggcgagacgcgaac 3562

Query: 1865 cag 1867
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Sbjct: 3561 cag 3559

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

Query: 820 gcgccgagagaatgctctctttgctcggaacctgtaccccgacttcgctcgtgcaatgaa 879
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Sbjct: 12178 gcgccgagagaacctctttcactcgaaacctgaacctgactttgctcgtgcaatgaa 12237

Query: 880 caccgcgagtgaagtcggaggggtactggcccagatagctgacggcctccc 930
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Sbjct: 12238 cac--caagtgaagtcggagggagtattggctcagatagctgatggcctccc 12286

Strand = Plus / Plus

Sbjct: 11446 caaatgcaccgcgaggggtaaccctaggtgtgcagtcgggctccaaacaccgacagctgg 11505

Sbjct: 11506 cgcgccagttaggggg 11521

Strand = Plus / Plus

Sbjct: 11920 ctcctttctaccccgacatcgtctttatcaaaggagattggagtcgtttcccatctccg 11979

Sbjct: 11980 atgacgagccaaccgtaccaggggaagaacctccccagcaggaagctcagcgacgaagga 12039

Sbjct: 12040 atagaagccgaaatatctggcgacatcacgaagcaggggaataggacccgacacagcccg 12099

Sbjct: 12100 tatcccgcgatgaagcctcagatgtaggagaaactcc 12136

Strand = Plus / Plus

Sbjct: 12407 gagctctatcaatgcttcgcacgaacgacgacatgaaagtgagataaggagccgagaaga 12466

Query: 1111 gtatg 1115

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Sbjct: 12467 gtatg 12471

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

Score = 648 bits (327), Expect = 0.0
Identities = 752/891 (84%), Gaps = 2/891 (0%)
Strand = Plus / Minus

Query: 979 taatcaccttctacccatcactaatcctccaagcgacctacgccatgccatcaacagccg 1038

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Sbjct: 2273 taatcaccttctgcccatcgctcatccccgagcaacctacaccagccatcaacagccg 2214

Query: 1039 gcgagacacgcggagctccatcaacgcttcgcgcgaccgatgacacgaaagtgagatagg 1098

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Sbjct: 2213 acgagacgcgcggagctccatcaatgcttcgcgcgaccgacggcacgaaagcgagataag 2154

Query: 1099 gaaccgagaggagtatgtccgagatcatgccatcctggcatgaagtcatgccacccgagc 1158

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Sbjct: 2153 gcgccgggaggagtatgaccgggatcatggtgtcccagcttgaagttgcgccacccgagt 2094

Query: 1159 tgagtcggttgcggcctcgaccagtgctccggttcaggacgatcaagatgacacacaac 1218

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Sbjct: 2093 tgagtcggttgcggcctcgaccagtggtcccgacccggggacggtcgagacgacacaccac 2034

Query: 1219 tggtccctccttgggaccgacctcacgaacgccgacatgaagacagtcgaggagtctt 1278

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Sbjct: 2033 cagctccctccccgggaccgacctcacgaacgccgacaggaagacacatgcggggtctc 1974

Query: 1279 cgcacttactccgtgtctccgggccatccagtggtccct-aacttcaaggtctccaacgt 1337

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Sbjct: 1973 tgcgttactccgctctccgggccatccagtggtccccaacttcaaagttctcaaacgt 1914

Query: 1338 cagcaagtatgagcgcaagcaggacctgggtggctggttagccatctacacgattgtcac 1397

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Sbjct: 1913 cgacaagtacgagcccaagcagcaccagggggctagttggcgtctacacgaccgccgc 1854

Query: 1398 atgggccgcccggagcgacggaggacgtgatgacagtgtatTTTccattgtcctaggga 1457
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Sbjct: 1853 tcgggtcgtctggggcgacggaagacgtaatgacagcgtatttggccatcgtcctaggga 1794

Query: 1458 agacgcaatgcagtggctccgacatctaccccaacattgcatagacaattggagcgactt 1517
||||| ||||| ||||| ||| | ||| ||||| ||| ||| |||||

Sbjct: 1793 agacgcactgcagtggcttcgacatctgccacgacactgcatcgacggttggggcgactt 1734

Query: 1518 cagttggtgcttcacgcgaacttcagtcctctttgacaagccggcgagccatggga 1577
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Sbjct: 1733 tagtcggcgctttcatcgccaacttcagtcctctctgacaagccggcgagccatggta 1674

Query: 1578 cctaaaatccattgggcatcagggcgatgaaacgctccggttgtaacctcaagaggtttta 1637
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Sbjct: 1673 cctcaaatccatcaggcgccagggcgatgaaacactctggtcataacctcaagaggtttca 1614

Query: 1638 gaccatgaggaaccacacccccgaagtcgccgaggcggggtgattgaagacttctaccg 1697
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Sbjct: 1613 gaccatgaggaaccgcatccccgaagtcgtcaaggcagcgatgattgaagatttctaccg 1554

Query: 1698 aggatccaatgactcggctttcgtccgagccatactccagaaaagcgtcggccacctccg 1757
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Sbjct: 1553 gggatccaatgactcggccttcgtcggagccatactacag-aaagcgtcggccacctccg 1495

Query: 1758 aacacttggtccgggaggcagacctctacatcaccacggattaacgggccaggacctca 1817
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Sbjct: 1494 agcaactgtttcgagaggcagacctctacatcaccatagatgagcgggccaggacctca 1435

Query: 1818 tcggaggcacgaaagccgcgccacacgcgccacggtgtgacacgaaccagc 1868
||||| || ||| |||| |||| |||| |||| | || ||||| |||||

Sbjct: 1434 tcggagggtactaaacccgcaccacccgcaccacgacgcgatacgaaccagc 1384

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

Score = 240 bits (121), Expect = 2e-59
Identities = 462/573 (80%), Gaps = 2/573 (0%)
Strand = Plus / Plus

Query: 1253 cgacatgaagacacgtgcgaggagtcttcgcacttactccgtgtctccgggccatccagtgg 1312
||||| || ||||||||||||||| | ||| ||||||||||| | || ||||||||||| |||
Sbjct: 112730 cgacaggaggacacgtgcgaggatatccgcccttactccgcgccttagggccatccaatgg 112789

Query: 1313 cc-cctaacttcaaggtctccaacgtcagcaagtatgagcgcaagcaggacctgggtggc 1371
|| || ||||||||||| ||||| ||| ||| ||||| | ||||||| | ||| |||
Sbjct: 112790 cctcccaacttcaaggtatccaatgtcgacaaatatgaacctaagcaggatccggggggc 112849

Query: 1372 tggttagccatctacacgattgtcacatgggccgccggagcgacggaggacgtgatgaca 1431
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Sbjct: 112850 tggttagccgtctacaccaccgtgctcgggccgtggggcatctgaggacgtcatgact 112909

Query: 1432 gtgtattttccattgtcctagggcaagacgcaatgcagtggctccgacatctaccccaa 1491
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Sbjct: 112910 gcgtatctgcccacgtcctcgggcaagacgcgtgcagtggctacgacatctacccca 112969

Query: 1492 cattgcatagacaattggagcgacttcagttggtgcttcacgccaacttccagtcctc 1551
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Sbjct: 112970 cactgcatcgacgactggggagacttcagtcgacgtttaccgccaacttccagtcctc 113029

Query: 1552 tttgacaagccggcgcagccatgggacctaataatccattgggcatcagggcgatgaaacg 1611
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Sbjct: 113030 tccgacaagccggcgcaaccatgggacctcaatccatcaagcgccggggggatgagact 113089

Query: 1612 ctccggttgctacctaagaggtttttagaccatgaggaaccacacccccgaagtcgccgag 1671
||| ||| ||||| || ||||| ||||||||| |||| || ||||||| ||| | |||
Sbjct: 113090 ctcaggctgtaccttaaaaggttccagaccatgagaaccgcatccccgaggtcacggag 113149

Query: 1672 gcgggggtgattgaagacttctaccgaggatccaatgactcggttttcgtccgagccata 1731
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Sbjct: 113150 gcggccgtaatcgaggacttctacagaggatctaacgactcggttttcgtccgagccata 113209

Query: 1732 ctccagaaaagcgtcggccacctccgaacacttggtccgggaggcagacctctacatcac 1791
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Sbjct: 113210 ctgca-aaaggcgccgactacctccgaggagctgttccgggaagccgacctctacatcac 113268

Query: 1792 cacggattaacgggcccaggacctcatcggagg 1824
| | | | | |||||||||||||||||
Sbjct: 113269 cgctgacgagcgagcccaggacctcatcggagg 113301

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

Query: 31 ggggtgtgcggacggactctaaacaccgacagctggcgcgccaggtaggggggtgtgtcttt 90
||||| |||| | ||||||||||||||||||||||||||||
Sbjct: 111556 ggggtgtgcggtcggacccaaaacaccgacagctggcgcgccaggtaggggggtgtgtcgac 111615

Query: 91 gatctgagctagctcaatg 109
|||| ||||||||||||
Sbjct: 111616 gatccaagctagctcaatg 111634

Score = 69.9 bits (35), Expect = 5e-08
Identities = 107/131 (81%)
Strand = Plus / Plus

Query: 794 gagcaagccgagcaaggtgcaaggctgcgccgagagaatgctctctttgctcggaacctg 853
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Sbjct: 112271 gagcaggccgagcaagatgcaaggcaacgacgcgagaatccgctcttcgggcgcaacttg 112330

Query: 854 taccccgacttcgctcgtgcaatgaacacgccgagtgaagtcggaggggtactggcccag 913
||||| |||| | || || |||| |||||| || ||||| |
Sbjct: 112331 aaccccgacttcgcccagccgtgaatacaccgagcgaagtcggaggcgttctggcccgg 112390

Query: 914 atagctgacgg 924
||||| ||||
Sbjct: 112391 atagctgacgg 112401

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

Query: 509 ttctaccccgacgtcctcttcac 532
||||| |||||| |||||
Sbjct: 112001 ttctaccccgacgtcctcttcac 112024

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

Score = 240 bits (121), Expect = 2e-59
Identities = 462/573 (80%), Gaps = 2/573 (0%)
Strand = Plus / Minus

Query: 1253 cgacatgaagacacgtgcggagtcttcgcacttactccgtgtctccgggccatccagtgg 1312
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Sbjct: 114166 cgacaggaggacacgtgcggagtatctgctcttactccgcgccttagggccatccaatgg 114107

Query: 1313 cc-cctaacttcaaggtctccaacgtcagcaagtatgagcgcaagcaggacctgggtggc 1371
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Sbjct: 114106 cctccaaacttcaaggtatccaatgtcgacaaatatgaacctaagcaggaccagggggc 114047

Query: 1372 tggttagccatctacacgattgtcacatgggccgccggagcgacggaggacgtgatgaca 1431
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Sbjct: 114046 tggttagccgtctacaccaccgccgctcgggctgccggggcatctgaggacgtcatgact 113987

Query: 1432 gtgtattttccattgtcctagggcaagacgcaatgcagtggctccgacatctaccccaa 1491
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Sbjct: 113986 gcgtatctgcccatcgctcctcgggcaagacgcactgcagtggctacggcatctaccccgaa 113927

Query: 1492 cattgcatagacaattggagcgacttcagttggtgcttcacgccaaacttccagtccectc 1551
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Sbjct: 113926 cactgcatcgacgactggggagacttcagccgacgattcaccgccaaacttccagtcctctc 113867

Query: 1552 tttgacaagccggcgcagccatgggacctaataatccattgggcatcagggcgatgaaacg 1611
| ||||||||| ||||| ||||||||||||| ||||||||| || | ||| ||||| |||
Sbjct: 113866 tccgacaagccagcgcaaccatgggacctcaaatccatcaagcgccggggagatgagact 113807

Query: 1612 ctccggttgtagctcaagagggttttagaccatgaggaaccacacccccgaagtgcggag 1671
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Sbjct: 113806 ctccggtcataccttaaaagggttcagaccatgagaaaccgcatccccgaggtcacggag 113747

Query: 1672 gcgggggtgattgaagacttctaccgaggatccaatgactcggttttcgtccgagccata 1731
||||| ||||| || ||||||||| ||||||| ||||||||||||||||||| |||||
Sbjct: 113746 gcggccgtgatcgaggacttctacagaggatctaatactcggttttcgtccgaaccata 113687

Query: 1732 ctccagaaaagcgtcggccacctccgaacacttggtccgggaggcagacctctacatcac 1791
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Sbjct: 113686 ctgca-aaaggcgccaaccacctccgaggagctggtccgggaagccgacctctacatcac 113628

Query: 1792 cacggattaacgggcccaggacctcatcggagg 1824
| | | | | ||||| ||||| ||||| |||||
Sbjct: 113627 cgctgacgagcgggcccaggacctcatcggagg 113595

Score = 200 bits (101), Expect = 2e-47
Identities = 457/573 (79%), Gaps = 2/573 (0%)
Strand = Plus / Plus

Query: 1253 cgacatgaagacacgtgcggagtcttcgcacttactccgtgtctccgggccatccagtgg 1312
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Sbjct: 128593 cgacaggaagacacgtgcggagtgtccgctcttactccgcgccttagggccatccagtgg 128652

Query: 1313 cc-cctaacttcaaggtctccaacgtcagcaagtatgagcgcaagcaggacctgggtggc 1371
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Sbjct: 128653 cctcccaacttcaaggtatccaatgtcgacaaatgaacctaagcaggatccagggggt 128712

Query: 1372 tggttagccatctacacgattgtcacatgggccgccggagcgacggaggacgtgatgaca 1431
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Sbjct: 128713 tggctagccgtctacaccaccgtgctcgagctgccggggcatctgaggacgttatgacc 128772

Query: 1432 gtgtattttcccatgtcttagggcaagacgaatgcagtggctccgacatctaccccaa 1491
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Sbjct: 128773 gcgtatttgcccatcgctccttgggcaagatgcgctacagtggctacgacatctaccccg 128832

Query: 1492 cattgcatagacaattggagcgacttcagttggtgcttcacgccaacttcagtcctc 1551
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Sbjct: 128833 cactgcatcgacgactggggagacttcagtcgacgtttcaccgccaacttcagtcctc 128892

Query: 1552 tttgacaagccggcgcagccatgggacctaaaatccattgggcatcagggcgatgaaacg 1611
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Sbjct: 128893 tccgacaagccagcgcaaccgtgggacctcaaatccatcaagcgccgggggatgagact 128952

Query: 1612 ctccggttgctacctcaagaggttttagacctgaggaaccacaccccgaaagtcgccgag 1671
||||||| ||||| ||||| ||||| ||||| ||| ||| ||||| ||| |||
Sbjct: 128953 ctccggttgctacctcaaaaggttccagacctgagaaatcgcatcccgaggtcacggag 129012

Query: 1672 gcgggggtgattgaagacttctaccgaggatccaatgactcggctttcgtccgagccata 1731
||||| ||||| || ||||| || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 129013 gcggccgtgatcgaggacttctacaggggatccaacgactcggcttttgcgagccata 129072

Query: 1732 ctccagaaaagcgtcggccacctccgaacacttggtccgggaggcagacctctacatcac 1791
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Sbjct: 129073 ctacagaaa-gcggcgactacttccgaggagctgttccgggaagccgacctctacatcac 129131

Query: 1792 cacggattaacgggccaggacctcatcgagg 1824
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Sbjct: 129132 cgccgacgagcgagctcaggacctcatcgagg 129164

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

Query: 794 gagcaagccgagcaaggtgcaaggctgcgccgagagaatgctctctttgctcggaacctg 853
||||| ||||| ||||| || || ||||| | ||||| | || |||||
Sbjct: 114625 gagcaagccgagcaagatgcaaggcaacgacgcgagaatccgctcttcgggcgaacctg 114566

Query: 854 taccgccacttcgctcgtgcaatgaacacgccgagtgaaagtcggaggggtactggcccag 913
||||| ||||| || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 114565 aaccgccacttcgcccagctatgaatacgcgcgagcgaagtcggaggcgttctggcccag 114506

Query: 914 atagctgacgg 924
||||| |||||
Sbjct: 114505 atagccgacgg 114495

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

Query: 31 ggggtgtgcggacggactctaaacaccgacagctggcgccaggtagggggtgtgtcttt 90
||||| ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 115340 ggggtgtgcggtcggacccaaaacaccgacagctggcgccaggtagggggtgtgtcgac 115281

Query: 91 gatctgagctagctcaatg 109
|||| ||||||||||||
Sbjct: 115280 gatccaagctagctcaatg 115262

Score = 85.7 bits (43), Expect = 9e-13
Identities = 70/79 (88%)
Strand = Plus / Plus

Query: 31 ggggtgtgcggacggactctaaacaccgacagctggcgcgccaggtagggggtgtgtcttt 90
||||||| ||||| | ||||||||||||||||||| |||||||||||||||
Sbjct: 127419 ggggtgtgcggtcggacccaaaacaccgacagctggcgcgctaggtagggggtgtgtcgac 127478

Query: 91 gatctgagctagctcaatg 109
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Sbjct: 127479 gatccaagctagctcaatg 127497

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

Query: 848 aacctgtaccccgacttcgctcgtgcaatgaacacgccgagtgaaagtcggaggggtactg 907
||||| | ||||||||||| || || ||||||||||| || |||||||||||||||
Sbjct: 128188 aacctgaatcccgacttcgcccgagctatgaacacgccaagcgaagtcggaggggtacta 128247

Query: 908 gcccagatagctga 921
|| | ||||||||
Sbjct: 128248 gctcggatagctga 128261

Score = 61.9 bits (31), Expect = 1e-05
Identities = 52/59 (88%)
Strand = Plus / Plus

Query: 1016 ctacgccatgccatcaacagccggcgagacacgcggagctccatcaacgcttcgcgcga 1074
||||| || ||||||||||| || |||||| |||| ||||||||||| |||||||||
Sbjct: 128356 ctacgacacgccatcaacagtcgccgagacgcgcgaagctccatcaatgcttcgcgcga 128414

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

Query: 503 gctcctttctaccccgacgtcctcttcac 532
||||| ||||||||||||||||||||
Sbjct: 127858 gctccattctaccccgacgtcctcttcac 127887

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Minus

Query: 50 aaacaccgacagctggcgccaggtagggg 80
||||| ||||||| ||||||||||||||||
Sbjct: 85948 aaacgccgacagttggcgccaggtagggg 85918

Score = 46.1 bits (23), Expect = 0.76
Identities = 23/23 (100%)
Strand = Plus / Minus

Query: 509 ttctaccccgacgtcctcttcac 531
||||||||||||||||||
Sbjct: 114895 ttctaccccgacgtcctcttcac 114873

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

Query: 55 ccgacagctggcgccaggtagggg 80
||||||| ||||||||||||||||
Sbjct: 24644 ccgacagttggcgccaggtagggg 24619

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

Query: 341 acccgaaaaactccgctgtccacttcgcccacaaaggagtggacacggat 390
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Sbjct: 127717 acccggaagactccgctgtctacttccccgacaaaagaatggacacggat 127766

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

Score = 240 bits (121), Expect = 2e-59
Identities = 462/573 (80%), Gaps = 2/573 (0%)
Strand = Plus / Plus

Query: 1253 cgacatgaagacacgtgcgagagtcttcgcacttactccgtgtctccgggccatccagtgg 1312
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Sbjct: 86996 cgacaggaggacacgtgcgagtatccgcccttactccgcgccttagggccatccaatgg 87055

Query: 1313 cc-cctaacttcaaggtctccaacgtcagcaagtatgagcgcaagcaggacctgggtggc 1371
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Sbjct: 87056 cctcccaacttcaaggtatccaatgtcgacaaatatgaacctaacgaggatccggggggc 87115

Query: 1372 tggttagccatctacacgattgtcacatgggccgcccggagcgacggaggacgtgatgaca 1431
||||||| ||||| || || || ||||| || || || ||||| |||||
Sbjct: 87116 tggttagccgtctacaccaccgctgctcgggccgctggggcatctgaggacgtcatgact 87175

Query: 1432 gtgtattttccattgtcctagggcaagacgcaatgcagtggtccgacatctaccccaa 1491
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Sbjct: 87176 gcgtatctgccatcgtcctcgggcaagacgcgctgcagtggttacgacatctaccccca 87235

Query: 1492 cattgcatagacaattggagcgacttcagttggtgcttcacgccaacttccagtccttc 1551
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Sbjct: 87236 cactgcatcgacgactggggagacttcagtcgacgtttcaccgccaacttccagtccttc 87295

Query: 1552 tttgacaagccggcgcagccatgggacctaaaatccattgggcatcagggcgatgaaacg 1611
| ||||| ||||| ||||| ||||| || || | || | ||||| ||
Sbjct: 87296 tccgacaagccggcgaaccatgggacctcaaatccatcaagcgccgggggatgagact 87355

Query: 1612 ctccggttgtagctcaagaggttttagacatgaggaaccacacccccgaagtcgccgag 1671
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Sbjct: 87356 ctccaggtcgtaccttaaaaggttccagacatgagaaaccgcatccccgaggtcacggag 87415

Query: 1672 gcgggggtgattgaagacttctaccgaggatccaatgactcggctttcgtccgagccata 1731

```
Query: 914   atagctgacgg 924
        |||||
Sbjct: 86657 atagctgacgg 86667
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Score = 48.1 bits (24), Expect = 0.19
Identities = 24/24 (100%)
Strand = Plus / Plus

Query: 509 ttctaccccgacgtcctcttcac 532
|||||||
Sbjct: 86267 ttctaccccgacgtcctcttcac 86290

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

Score = 232 bits (117), Expect = 6e-57
Identities = 461/573 (80%), Gaps = 2/573 (0%)
Strand = Plus / Plus

Query: 1253 cgacatgaagacacgtgcggagtcttcgcacttactccgtgtctccgggccatccagtgg 1312
||||| || ||||| ||||| || ||| ||||| || || ||||| |||||
Sbjct: 19271 cgacaggaggacacgtgcggagtatccgctcttactccgcgccttagggccatccaatgg 19330

Query: 1313 cc-cctaacttcaaggtctccaacgtcagcaagtatgagcgcaagcaggacctgggtggc 1371
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Sbjct: 19331 cctcccaacttcaaggtatccaatgtcgacaaatatgaacctaacgaggatccaggggg 19390

Query: 1372 tggtagccatctacacgattgtcacatgggcccggagcgacggaggacgtgatgaca 1431
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Sbjct: 19391 tggtagccgtctacaccacgctgctcggggtgccggagcatccgaagacgtcatgacc 19450

Query: 1432 gtgtattttccattgtcctagggcaagacgcaatgcagtggctccgacatctaccccaa 1491
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Sbjct: 19451 gcgtatctgccatcgctccttgggcaagacgtgctgcagtggctacgacatctacccga 19510

Query: 1492 cattgcatagacaattggagcgacttcagttggtgcttcacgccaacttcagtcctc 1551
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Sbjct: 19511 cactgcatcgacgactaggagacttcagtcgacgtttcacgccaacttcagtcctc 19570

Query: 1552 ttgacaagccggcgcagccatgggacctaaatccattgggcatcaggcgcatgaaacg 1611
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Sbjct: 19571 tccgacaagccagcgcaaccatgggacctcaatccatcaagcgggggggatgagact 19630

Query: 1612 ctccggttgtacctcaagaggttttagaccatgaggaaccacacccccgaagtcgccgag 1671
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 Sbjct: 19631 cttcggtcataacctcaaaaggttcagaccatgagaaaccgcacccccgaagtcacggag 19690

Query: 1732 ctccagaaaagcgtcgccacctccgaacattgttcgggaggcagacctctacatcac 1791
 ||| ||| ||| | ||||| | ||||| ||| ||||| |||||
 Sbjct: 19751 ctgca-aaaggcgccaactacctccgaggagctgttcgggaagccgacctctacatcac 19809

Score = 232 bits (117), Expect = 6e-57
Identities = 461/573 (80%), Gaps = 2/573 (0%)
Strand = Plus / Minus

Query: 1313 cc-cctaacttcaaggtctccaacgtcagcaagtatgagcgaagcaggacctgggtggc 1371
 || || ||||| |||| || || |||| | ||||| || || ||
 Sbict: 96669 cctccaaacttcaaggtatccaatgtcgacaaatatgaacctaaagcaggacccagggggc 96610

Query: 1432 gtgtattttccattgtcctagggaagacgcaatgcagtggctccgacatctacccaa 1491
| | | | | | | | | | | | | | | | | | | | | | | |
Sbjct: 96549 gcgtatctgcccatcgctcctcgggcaagacgcaactgcagtggctaccgcacatcacccga 96490

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Sbjct: 96489 cactgcatcgacgactggggagacttcagccgacgattcacgccaacttccagtctctc 96430

Query: 1552 ttgacaagccggcgcgccatgggacctaaaatccattgggcatcagggcgatgaaacg 1611
| ||||| ||||| ||||| ||||| ||||| || || ||| ||||| ||
Sbjct: 96429 tccgacaagccagcgcaaccatgggacctcaaatccatcaagcgccggggagatgagact 96370

Query: 1612 ctccggttgtagctcaagaggttttagacctgaggaaccacacccccgaagtcgccgag 1671
||||| ||||| || ||||| ||||| ||||| || ||||| ||| | |||
Sbjct: 96369 ctccggtcataccttaaaaggttcagacctgagaaaccgcatccccgaggtcacggag 96310

Query: 1672 gcgggggtgattgaagacttctaccgaggatccaatgactcggctttcgtccgagccata 1731
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Sbjct: 96309 gcggccgtgatcgaggacttctacagaggatctaatactcggctttcgtccgaaccata 96250

Query: 1732 ctccagaaaagcgtcgccacctccgaacacttggtccgggagcgacctctacatcac 1791
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Sbjct: 96249 ctgca-aaaggcgccaaccacctccgaggagctggtccgggaagccgacctctacatcac 96191

Query: 1792 cacggattaacggggccaggacctcatcgagg 1824
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Sbjct: 96190 cgctgacgagcggggccaggacctcatcgagg 96158

Score = 97.6 bits (49), Expect = 2e-16
Identities = 154/189 (81%)
Strand = Plus / Plus

Query: 31 ggggtgtcggacggactctaaacaccgacagctggcgcgccaggtagggggtgtgtcttt 90
||||||| |||| | ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 18097 ggggtgtcggtcggacccaaaacaccgacagctggcgcgccaggtagggggtgtgtcgac 18156

Query: 91 gatctgagctagctcaatgaccattacctccaaatgcaagatcgcccttcgccccgggac 150
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Sbjct: 18157 gatccaagctagctcaatggccgtcactttccacagcaagatcgccgtacgtcccggatc 18216

Query: 151 tatgttttgctttggaacctctcatccatagcagatgaagagggaactctgcaccgcat 210
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Sbjct: 18217 tgtattctgcttcgggacaatctctgcgtcgtagcggatgaagaaggaattctacaccgcct 18276

Query: 211 agcagatct 219
|||||||
Sbjct: 18277 cgcagatct 18285

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

Query: 794 gagcaagccgagcaaggtgcaaggctgcgccgagagaatgctctctttgctcggaacctg 853
|||||||
Sbjct: 97188 gagcaagccgagcaagatgcaaggcaacgacgcgagaatccgctcttcgggcgcaacctg 97129

Query: 854 tacccecgacttcgctcgtgcaatgaacacgccgagtgaagtcggaggggtactggcccag 913
|||||||
Sbjct: 97128 aacccecgacttcgccgagctatgaatacgccgagcgaagtcggagcgcttctggcccgg 97069

Query: 914 atagctgacgg 924
|||||
Sbjct: 97068 atagccgacgg 97058

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

Query: 31 ggggtgtgcggacggactctaaacaccgacagctggcgcgccaggtagggggtgtgtcttt 90
|||||||
Sbjct: 97903 ggggtgtcggtcggacccaaacaccgacagctggcgcgccaggtagggggtgtgtcgac 97844

Query: 91 gatctgagctagctcaatg 109
|||||
Sbjct: 97843 gatccaagctagctcaatg 97825

Score = 77.8 bits (39), Expect = 2e-10
Identities = 108/131 (82%)
Strand = Plus / Plus

Query: 794 gagcaagccgagcaaggtgcaaggctgcgccgagagaatgctctctttgctcggaacctg 853
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Sbjct: 18812 gaggcaggccgagcaagatgcaaggcaacgacgcgagaatccgctcttcgggcgcaacctg 18871

Query: 854 taccgccacttcgctcgtgcaatgaacacgccgagtgaagtcggaggggtactggcccag 913
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Sbjct: 18872 aaccgccactttgccgagctatgaacacgccgagcgaagtcggaggcgttctagctcgg 18931

Query: 914 atagctgacgg 924
|||||||
Sbjct: 18932 atagctgacgg 18942

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

Query: 509 ttctaccccgacgtcctcttcatc 532
|||||||||||||||||
Sbjct: 18542 ttctaccccgacgtcctcttcatc 18565

Score = 46.1 bits (23), Expect = 0.76
Identities = 23/23 (100%)
Strand = Plus / Minus

Query: 509 ttctaccccgacgtcctcttcat 531
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Sbjct: 97458 ttctaccccgacgtcctcttcat 97436

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Minus

Query: 50 aaacaccgacagctggcgccaggtagggg 80
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Sbjct: 120842 aaacgccgacagttggcgccaggtagggg 120812

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

Length = 202568

Score = 224 bits (113), Expect = 1e-54
Identities = 460/573 (80%), Gaps = 2/573 (0%)
Strand = Plus / Minus

Query: 1253 cgacatgaagacacgtgctggagtcttcgcacttactccgtgtctccgggccatccagtgg 1312
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Sbjct: 152277 cgacaggaggacacgtgctggagtatctgcacttactccgcgccttagggccatccaatgg 152218

Query: 1313 cc-cctaacttcaaggtctccaacgtcagcaagtatgagcgcaagcaggacctgggtggc 1371
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Sbjct: 152217 cctcccaacttcaaggtatccaatgtcgacaaatatgaacctaagcaggatccaggggt 152158

Query: 1372 tggttagccatctacacgattgtcacatgggccgccggagcgacggaggacgtgatgaca 1431
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Sbjct: 152157 tggttagccgtctacaccactgccgtcgagctgccggagcatccgaagatgtcatgacc 152098

Query: 1432 gtgtattttccattgtcctagggcaagacgcaatgcagtggtctccgacatctacccaa 1491
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Sbjct: 152097 gcatactgcccacgtccttgggcaagatgcgctgcagtggtctcgacatctacccga 152038

Query: 1492 cattgcatagacaattggagcgacttcagttggtgcttcacgccaacttccagtcctc 1551
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Sbjct: 152037 cactgcatcgacgactggggagacttcagtcgacgtttcactgccaacttccagtcctc 151978

Query: 1552 tttgacaagccggcgcagccatgggacctaaatccattgggcatcagggcgatgaaacg 1611
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Sbjct: 151977 tccgacaagccggcgaaccatgggacctcaatccatcaagcgccgggggatgagact 151918

Query: 1612 ctccggttgtagctcaagaggtttttagaccatgaggaaccacacccccgaagtcgccgag 1671
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Sbjct: 151917 ctccggtcataccttaaaaggttccagaccatgagaaaccgcatccccgaggtcatggag 151858

Query: 1672 gcgggggtgattgaagacttctaccgaggatccaatgactcggttttcgtccgagccata 1731
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Sbjct: 151857 gcggcgtgatcgaggacttctacagaggatccaatgactcggttttcgtccgagccata 151798

Query: 1732 ctccagaaaagcgtcggccacctccgaacacttggtccgggaggcagacctctacatcac 1791
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Sbjct: 151797 ctaca-aaaggcgccgactacttccgaggagctgttccgggaagccgacctctacatcac 151739

Query: 1792 cacggattaacggggcccaggacctcatcggagg 1824

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Sbjct: 151738 cgccgacgagcggggcccaggatctcatcggagg 151706

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

Identities = 71/79 (89%)

Strand = Plus / Minus

Query: 31 ggggtgtcggacggactctaaacaccgacagctggcgcgccaggtaggggggtgtgtcttt 90

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Sbjct: 153451 ggggtgtcgggtcggacccaaaacaccgacagctggcgcgccaggtaggggggtgtgtcgac 153392

Query: 91 gatctgagctagctcaatg 109

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Sbjct: 153391 gatccaagctagctcaatg 153373

Score = 85.7 bits (43), Expect = 9e-13

Identities = 91/107 (85%)

Strand = Plus / Minus

Query: 794 gagcaagccgagcaaggtgcaaggctgcgccgagagaatgctctctttgctcggaacctg 853

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Sbjct: 152736 gagcaagccgagcaagatgcaaggcaacgacgcgagaaatccgctcttcgggcgcaacttg 152677

Query: 854 taccgccacttcgctcgtgcaatgaacacgccgagtgagtcggagg 900

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Sbjct: 152676 aaccgccacttcgctcgagctatgaacacgccgagcgaagtcggagg 152630

Score = 48.1 bits (24), Expect = 0.19

Identities = 24/24 (100%)

Strand = Plus / Minus

Query: 509 ttctaccccgacgtcctcttcac 532

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Sbjct: 153006 ttctaccccgacgtcctcttcac 152983

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Minus

Query: 50 aaacaccgacagctggcgccaggtagggg 80
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Sbjct: 21334 aaacgccgacagttggcgccaggtagggg 21304

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgccaggtagggg 80
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Sbjct: 90226 aaacgccgacagttggcgccaggtagggg 90256

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgccaggtagggg 80
|||| |||||| ||||||||||||||||
Sbjct: 139072 aaacgccgacagttggcgccaggtagggg 139102

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

Score = 224 bits (113), Expect = 1e-54
Identities = 460/573 (80%), Gaps = 2/573 (0%)
Strand = Plus / Minus

Query: 1253 cgacatgaagacagtgcgagtgcttcgcacttactccgtgtctccgggccatccagtgg 1312
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Sbjct: 21744 cgacaggaggacagtgcgagtgcttcgcacttactccgcgccttagggccatccaatgg 21685

Query: 1313 cc-cctaacttcaaggtctccaacgtcagcaagtatgagcgcaagcaggacctgggtggc 1371

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Sbjct: 21684 cctcccaacttcaaggtatccaatgtcgacaaatatgaacctaacgaggatccaggggt 21625

Query: 1372 tggttagccatctacacgattgtcacatgggccgccgagcgacggaggacgtgatgaca 1431
||||||| ||||| | || | | || ||||| | || || || |||||

Sbjct: 21624 tggttagccgtctacaccactgccgtctgagctgccggagcatccgaagatgtcatgacc 21565

Query: 1432 gtgtattttccattgtcctagggcaagacgcaatgcagtggctccgacatctacccaa 1491
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Sbjct: 21564 gcatacttgcctcgtccttgggcaagatgcgtgcagtggctgcgacatctacccga 21505

Query: 1492 cattgcatagacaattggagcgacttcagttggtgcttcacgccaacttccagtcctc 1551
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Sbjct: 21504 cactgcatcgacgactggggagacttcagtcgacgtttcatcgccaacttccagtcctc 21445

Query: 1552 ttgacaagccggcgagccatgggacctaaatccattgggcatcaggcgatgaaacg 1611
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Sbjct: 21444 tccgacaagccggcgcaacctgggacctcaatccatcaagcgccgggggatgagact 21385

Query: 1612 ctccggttgtagctcaagaggttttagaccatgaggaaccacacccccgaagtcgccgag 1671
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Sbjct: 21384 ctccggtcataccttaaaagggttcagaccatgagaaaccgcatccccgaggtcatggag 21325

Query: 1672 gcgggggtgattgaagacttctaccgaggatccaatgactcggttttcgtccgagccata 1731
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Sbjct: 21324 gcggcgtgatcgaggacttctacagaggatccaatgactcggttttcgtccgagccata 21265

Query: 1732 ctccagaaaagcgtcgccacctccgaacacttggtccgggaggcagacctctacatcac 1791
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Sbjct: 21264 ctaca-aaaggcgccgactacttccgaggagctgttccgggaagccgacctctacatcac 21206

Query: 1792 cacggattaacggggccaggacctcatcgagg 1824
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Sbjct: 21205 cgccgacgagcggggccaggatctcatcgagg 21173

Score = 184 bits (93), Expect = 1e-42
Identities = 455/573 (79%), Gaps = 2/573 (0%)
Strand = Plus / Minus

Query: 1253 cgacatgaagacacgtgcgagagtcttcgcacttactccgtgtctccgggccatccagtgg 1312
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Sbjct: 155717 cgacaggaggacacgtgcgaggtatccgcccttactccgcgccttagggccatccaatgg 155658

Query: 1313 cccct-aacttcaaggtctccaacgtcagcaagtatgagcgcaagcaggacctgggtggc 1371
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Sbjct: 155657 cctctcaacttcaaggtatccaatgtcgacaaatatgaaccaagcaggatccaggggt 155598

Query: 1372 tggttagccatctacacgattgtcacatgggccgccggagcgacggaggacgtgatgaca 1431
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Sbjct: 155597 tggttagccgtctacaccaccgtgctcgggctgccgggcatccgaagacgtcatgacc 155538

Query: 1432 gtgtattttccattgtcctagggcaagacgcaatgcagtggtccgacatctaccccaa 1491
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Sbjct: 155537 gcgtatctgtcatcgtccttggacaagatgcgctgcagtggttacgacatctacccga 155478

Query: 1492 cattgcatagacaattggagcgacttcagttggtgcttcacgccaacttccagtcctc 1551
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Sbjct: 155477 cactgcatcaacaactggggagacttcagtcgacgtttaccgccaacttccagtcctc 155418

Query: 1552 tttgacaagccggcgcagccatgggacctaataatccattgggcatcagggcgatgaaacg 1611
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Sbjct: 155417 ttcgacaagccagcgcacccatgggacctcaatccatcaagcgcgggggatgagact 155358

Query: 1612 ctccggttgtagctcaagaggttttagaccatgaggaaccacacccccgaagtcgccgag 1671
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Sbjct: 155357 ctccggtcataccttaaaaggttccagaccatgagaaccgcatccccgaggtcacagag 155298

Query: 1672 gcgggggtgattgaagacttctaccgaggatccaatgactcggttttcgtccgagccata 1731
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Sbjct: 155297 gcggccgtggtctaggacttctacagaggatctaacgactcggttttcgtccgagccata 155238

Query: 1732 ctccagaaaagcgtcggccacctccgaacacttgttccgggaggcagacctctacatcac 1791
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Sbjct: 155237 ctaca-aaaggcgcgactacctccgaggagctgttccgggaagccgacctctacattac 155179

Query: 1792 cacggattaacgggccagacctcatcggagg 1824
| | | | | ||||||||| |||||||||
Sbjct: 155178 cgccgacgagcgggccaggatctcatcggagg 155146

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

Query: 32 ggtgtgctggacggactctaaacaccgacagctggcgcgccaggtaggggtgtgtctttg 91
||||||| ||||| | |||||||||||||||||||||||||||||||
Sbjct: 156890 ggtgtgctggacggacccaaacaccgacagctggcgcgccaggtaggggtgtgtcgacg 156831

Query: 92 atctgagctagctcaatgaccattacctccaaatgcaagatcgcccttcgccccgggact 151
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Sbjct: 156830 atccaagctagctcaatggccgtcaccttcacagcaagatcgccgtgctcccggatct 156771

Query: 152 atgttttgctttggaaccatctcatccatagcagatgaagaggggaactctgcaccgcata 211
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Sbjct: 156770 gtattctgcttcgggacaatctcatctgttagcgatgaagaggggaattctacaccgcctc 156711

Query: 212 gcagatct 219
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Sbjct: 156710 gcagatct 156703

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

Query: 31 ggtgtgctggacggactctaaacaccgacagctggcgcgccaggtaggggtgtgtcttt 90
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Sbjct: 22918 ggtgtgctggacggacccaaacaccgacagctggcgcgccaggtaggggtgtgtcgac 22859

Query: 91 gatctgagctagctcaatg 109
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Sbjct: 22858 gatccaagctagctcaatg 22840

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

Query: 794 gagcaagccgagcaaggtgcaaggctgcgccgagagaatgctctctttgctcggaacctg 853
|||||
Sbjct: 156176 gagcaagccgagcaagatgcaaggcaacgacgcgagaatccgctcttcgggcgcaacctg 156117

Query: 854 taccccgacttcgctcgtgcaatgaacacgccgagtgaagtcggagggtactggccag 913
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Sbjct: 156116 aaccccgacttcgcccagctatgaacacgccgagcgaagtcggaggcgttctagctcgg 156057

Query: 914 atagctgacgg 924
|||||
Sbjct: 156056 atagctgacgg 156046

Score = 85.7 bits (43), Expect = 9e-13
Identities = 91/107 (85%)
Strand = Plus / Minus

Query: 794 gagcaagccgagcaaggtgcaaggctgcgccgagagaatgctctctttgctcggaacctg 853
|||||
Sbjct: 22203 gagcaagccgagcaagatgcaaggcaacgacgcgagaatccgctcttcgggcgcaacttg 22144

Query: 854 taccccgacttcgctcgtgcaatgaacacgccgagtgaagtcggagg 900
|||||
Sbjct: 22143 aaccccgacttcgctcgagctatgaacacgccgagcgaagtcggagg 22097

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

Query: 509 ttctaccccgacgtcctcttcac 532
|||||
Sbjct: 22473 ttctaccccgacgtcctcttcac 22450

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
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Sbjct: 8539 aaacgccgacagttggcgcgccaggtagggg 8569

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
|||| |||||| |||||||||
Sbjct: 134065 aaacgccgacagttggcgcgccaggtagggg 134095

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

Score = 224 bits (113), Expect = 1e-54
Identities = 309/373 (82%), Gaps = 1/373 (0%)
Strand = Plus / Minus

Query: 1420 gacgtgatgacagtgtattttccattgtcctagggaagacgcaatgcagtggctccga 1479
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Sbjct: 29955 gacgtcatgaccgcgtatctacctatcgctcctcgggcaagacgcgtgcagtggctacga 29896

Query: 1480 catctaccccaacattgcatagacaattggagcgacttcagttggtgcttcacgccaac 1539
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Sbjct: 29895 catctaccccgacactgcatcgacgactggggagacttcagtcgacgtttcatcgccaac 29836

Query: 1540 ttccagtcctcttttgacaagccggcgagccatgggacctaaaatccattgggcatcag 1599
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Sbjct: 29835 ttccagtcctcttcgcacaagccggcgcaaccatgggacctcaaatccatcaagcgccg 29776

Query: 1600 ggcgatgaaacgctccggttgacctcaagaggttttagaccatgaggaaccacaccccc 1659
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Sbjct: 29775 ggggatgagactctccggtcataccttaaaaggttcagaccatgagaaaccgcatcccc 29716

Query: 1660 gaagtcgccgaggcggggtgattgaagacttctaccgaggatccaatgactcggtttc 1719
|| || | |||||| |||| | ||||||||| |||||||||||||
Sbjct: 29715 gaggtcacggaggcgccgtgatcgaggacttctacagaggatccaatgactcggtttc 29656

Query: 1720 gtccgagccatactccagaaaagcgtcggccacctccgaacacttgttccgggaggcaga 1779
|||||||
Sbjct: 29655 gtccgagccatactaca-aaaggggcccgactacctccgaggagctgttccgggaagccga 29597

Query: 1780 cctctacatcacc 1792
|||||||
Sbjct: 29596 cctctacatcacc 29584

Score = 89.7 bits (45), Expect = 6e-14
Identities = 54/57 (94%)
Strand = Plus / Minus

Query: 31 ggggtgtgcggacggactctaacaccgacagctggcgcgccaggtaggggggtgtgtc 87
|||||||
Sbjct: 31297 ggggtgtgcggtcggacccaaacaccgacagctggcgcgccaggtaggggggtgtgtc 31241

Score = 77.8 bits (39), Expect = 2e-10
Identities = 90/107 (84%)
Strand = Plus / Minus

Query: 794 gagcaagccgagcaaggtgcaaggctgcgccgagagaatgctctctttgctcggaacctg 853
|||||||
Sbjct: 30582 gagcaagccgagcaagatgcgaggcaacgacgcgagaatccgctcttcgggcgcaacttg 30523

Query: 854 tacccecgacttcgctcgtagaatgaacacgccgagtgagtcggagg 900
|||||||
Sbjct: 30522 aacccecgacttcgctcgtagaatgaacacgccgagtcgagtcggagg 30476

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

Query: 509 ttctaccccgacgtcctcttcac 532
|||||||
Sbjct: 30852 ttctaccccgacgtcctcttcac 30829

>gb|AF546188.1| Contiguous genomic DNA sequence comprising the 19-kDa-zein gene family

from Zea mays, complete sequence
Length = 203363

Score = 224 bits (113), Expect = 1e-54
Identities = 330/401 (82%), Gaps = 1/401 (0%)
Strand = Plus / Minus

Query: 1424 tgatgacagtgtattttccattgtcctagggcaagacgcaatgcagtggctccgacatc 1483
||||||| | ||| || ||||| ||||| ||||| || ||||| ||||| |||||
Sbjct: 27412 tgatgaccgcgtacttacccattgtcctcgggcaagacacgctgcaatggctgcgacatc 27353

Query: 1484 taccccaacattgcatagacaattggagcgacttcagttggtgcttcacgccaacttcc 1543
||||||| ||| ||||| ||| | ||| ||||| ||||| | ||||| ||| ||||| |||||
Sbjct: 27352 taccctgacactgcatcgacgactggggcgacttcagtcgatgcttcaccaccaatttcc 27293

Query: 1544 agtcctctcttgacaagccggcgagccatgggacctaataatccattgggcatcagggcg 1603
||||||| ||||| ||||| || ||||| ||||| ||||| || ||||| |||||
Sbjct: 27292 agtcctctcctcgacaacccggcgcaaccgtgggacctaataatccatcaagcgtcggggg 27233

Query: 1604 atgaaacgctccggttgctacctaagaggttttagaccatgaggaaccacacccccgaag 1663
| ||||| ||||| ||||| ||||| ||||| ||||| || ||| ||||| |||||
Sbjct: 27232 acgaaactctccggtcgctacctaagaggttcagaccatgagaaatcgtatccccgagg 27173

Query: 1664 tcgccgaggcgggggtgattgaagacttctaccgaggatccaatgactcggctttcgtcc 1723
|| | ||||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 27172 tcacggaggcggccgtgatcgaggacttctacagaggatccaatgactcggctttcgtcc 27113

Query: 1724 gagccatactccagaaaagcgtcggccacctccgaacacttggtccgggaggcagacctc 1783
||||||| | ||| || ||| || | ||||| || | ||||| ||||| || |||||
Sbjct: 27112 gagccatattacag-aaggcggcgactacctccgaggagctggtccgggaagccgacctc 27054

Query: 1784 tacatcaccacggattaacggggcccaggacctcatcgagg 1824
||||||| || | ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 27053 tacatcacgtcgacgagcggggcccaggacctcatcgagg 27013

Score = 143 bits (72), Expect = 4e-30
Identities = 159/188 (84%)
Strand = Plus / Minus

Query: 31 ggggtgtgcggacggactctaaacaccgacagctggcgcgccaggtagggggtgtgtcttt 90
|||||
Sbjct: 28758 ggggtgtcggtcggacccaaaacaccgacagctggcgcgccaggtagggggtgtgtcgac 28699

```
Query: 91      gatctgagctagctcaatgaccattacctc caaatgcaagatcgcccttcgccccgggac 150
             ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 28698  gatccaagctagctcaatggccgtcaccttccacagcaagatcacccctccgtcccggatc 28639
```

Query: 151 tatgttttgcttgggaaccatctcatccatagcagatgaagagggaactctgcaccgcat 210
 | ||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 28638 cgtattctgcttcggaacaatctcatccgtagcagatgaagagggaactctacaccgcat 28579

```
Query: 211   agcagatc 218
          |||||
Sbjct: 28578 tgcagatc 28571
```

Score = 133 bits (67), Expect = 4e-27
Identities = 196/239 (82%)
Strand = Plus / Plus

Query: 848 aacctgtaccccgacttcgctcgtgcaatgaacacgccgagtggaagtcggaggggtactg 907
 ||||| ||||||||| || | || ||||||||| |||||
 Sbjct: 54934 aacctgaaccccgactttgcctgagccatgaacacgccgagtggaagtcggaggggtctg 54993

Query: 908 gccagatagctgacggcctcccgcaaccctagacacggaaggctaccggcggtgctt 967
||| ||||||| ||||||| || | ||| | || ||||| |||||
Sbjct: 54994 gctcggatagctgatggcctccctcggaactccggacgccgagggctatcggcggtgttc 55053

Query: 968 actcgagcagttaatcaccttctacccatcactaatcctccaagcgacctacgccatgcc 1027
 ||| |||| |||||||||||| | | | | || | ||| ||| |||
 Sbjct: 55054 actcaagcagccaatcaccttctacccctcgtcacctgccgaacgatctacgacacgcc 55113

Query: 1028 atcaacagccggcgagacacgcggagctccatcaacgcttcgcgcgaccgatgacacga 1086
||||||| || | ||| ||||| ||| ||| ||| ||| |||
Sbjct: 55114 atcaacagtctgtcgggacgcgcggagctccatcaatgcttcacgtgaacgatgacacga 55172

Score = 127 bits (64), Expect = 3e-25
Identities = 217/268 (80%)

Strand = Plus / Plus

Query: 1447 gtcctagggcaagacgcaatgcagtggtccgacatctaccccaacattgcatagacaat 1506
||||| ||||||| ||| ||||| ||||| ||| ||| |||

Sbjct: 55534 gtcctcgggcaagacgcgtgcaatggctgcgacacctaccccgacactgcatcaacgac 55593

Query: 1507 tggagcgacttcagttggtgcttcacgccaacttcagtcctctttgacaagccggcg 1566
||||| ||||||| || ||||||| ||||| |||| || ||| |||||

Sbjct: 55594 tggagcgacttcagtcggcgcttcaccgccaactttcagtcctctctccgataagtcggcg 55653

Query: 1567 cagccatgggacctaataatccattgggcatcaggcgatgaaacgctccggttgtacctc 1626
|| ||||||| ||||||| || | || | ||| ||||||| |||||

Sbjct: 55654 caaccatgggacctaataatccatcaaacaccgaggggactaaactctccggtcatactc 55713

Query: 1627 aagaggttttagacatgaggaaccacacccccgaagtcgccgaggcggggtgattgaa 1686
|| ||||| ||||||| || | | ||||| ||||| ||||| ||||| ||

Sbjct: 55714 aaaaggttccagacatgagaaatcgatatccccgaggtcgccaaggcggcagtgatcgag 55773

Query: 1687 gacttctaccgaggatccaatgactcgg 1714
||||||| ||||||| |||||

Sbjct: 55774 gacttctacagaggatccaatgactcgg 55801

Score = 99.6 bits (50), Expect = 6e-17

Identities = 185/230 (80%)

Strand = Plus / Plus

Query: 20 ggggtagccctgggtgtgcggacggactctaacaccgacagctggcgccaggtaggg 79
||||| ||||||| ||| ||||| | ||||||| ||||||| |||||||

Sbjct: 54142 ggggtaaccctgggtgcacggtcggacccgaaacaccgacagctggcgccaggtaggg 54201

Query: 80 ggtgtgtctttgatctgagctagctcaatgaccattacctccaaatgcaagatcgccctt 139
||||||| | |||| ||||| ||||||| || | |||| | | ||||||| |||

Sbjct: 54202 ggtgtgtcatcgatccaagctatctcaatggccgtcaccttcagcgcaagatcatcctc 54261

Query: 140 cgccccgggactatgttttgccttgaaccatctcatccatagcagatgaagagggaact 199
| |||||| | || | ||||| || | ||||||| ||||| ||||| |||||||

Sbjct: 54262 caccgccgatccatattctgcttcggtactatctcatctgtagcggatgaggagggaact 54321

Query: 200 ctgcaccgcatagcagatctattggagaagaagctttcctcagaaatctc 249
||||| ||| | || |||| | ||||| |||| | ||||| |||||
Sbjct: 54322 ctgcatcgcccttgccgatccgccggagaaaaagccttcctcaggaatctc 54371

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

Query: 797 caagccgagcaaggtgcaaggctgcgccgagagaatgctctctttgctcggaaacctgtac 856
||||||| ||||| | ||| ||||| | |||| | || ||||| |
Sbjct: 28040 caagccgagcaagatgcaaggcaacaccgggagaaatccattcttcgggcgcaacctgaat 27981

Query: 857 cccgacttcgctcgtgcaatgaacacgccgagtgagtcggagggtactggcccagata 916
||||||| || || ||||| ||||| ||||| ||||| || || ||||
Sbjct: 27980 cccgacttcgcccagccatgaacacgccgagcgaagttggaggagtactagctcggata 27921

Query: 917 gctgacggcctccc 930
||||| || |||||
Sbjct: 27920 gctgatggactccc 27907

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

Query: 1025 gccatcaacagccggcgagacacgcggagctccatcaacgcttcgcg 1071
||||||| || ||||| |||| | ||||| ||||| |||||
Sbjct: 27812 gccatcaacagtcgccgagacgcggaagctccatcaatgcttcgcg 27766

Score = 50.1 bits (25), Expect = 0.048
Identities = 28/29 (96%)
Strand = Plus / Plus

Query: 504 ctccctttctaccccgacgtcctcttcatc 532
|||| | ||||| ||||| ||||| |||||
Sbjct: 54605 ctccattctaccccgacgtcctcttcatc 54633

Score = 46.1 bits (23), Expect = 0.76
Identities = 47/55 (85%)
Strand = Plus / Minus

Query: 642 ggcgacatcacgaggctggggaacgggatccggcgcaacccgtatcccgggacga 696
|||||
Sbjct: 28183 ggcgacatcacgcggccagagaacgggatccggagcaacctgtctcgcgggacga 28129

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Minus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
||||
Sbjct: 131970 aaacgccgacagttggcgcgccaggtagggg 131940

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

Score = 220 bits (111), Expect = 2e-53
Identities = 425/527 (80%), Gaps = 2/527 (0%)
Strand = Plus / Minus

Query: 1299 gggccatccagtggcccc-taacttcaaggtctccaacgtcagcaagtatgagcgcaagc 1357
|||||
Sbjct: 165974 gggccattcagtggccccctaacttcaaggtctccaacatcgacaaatatgaacctaacg 165915

Query: 1358 aggacctgggtggctggttagccatctacacgattgtcacatgggcccgggagcgacgg 1417
||
Sbjct: 165914 aagatctgggaggtggctggccatctacaccactgctgcccagccgctggggcaaccg 165855

Query: 1418 aggacgtgatgacagtgtattttccattgtcctagggaagacgcaatgcagtggctcc 1477
||
Sbjct: 165854 aagacgtgatgaccgcgtacttgccatctcgtccttgggcaggacgcactgcaatggctgc 165795

Query: 1478 gacatctaccccaacattgcatagacaattggagcgacttcagttggtgcttcacgcca 1537
||||
Sbjct: 165794 gacacctaccccgacactgcatcgacgactggagcgacttcagtcgacgcttcaccgcca 165735

Query: 1538 acttcagtcctctcttgacaagccggcgagccatgggacctaaaatccattggggcatc 1597

Query: 1598 agggcgatgaaacgctccggttgtagacctcaagaggttttagaccatgaggaaccacaccc 1657

Query: 1658 ccgaagtcgcccaggcggggtgattgaagacttctaccgaggatccaatgactcggctt 1717
||| ||| | | | | | | | | | | | | | | | | | | |

Query: 1718 tcgtccgagccatactccagaaaagcgtcgccacctccgaacacttgttccgggaggca 1777

Query: 1778 gacctctacatcaccacggattaacggggcccaggacctcatcggagg 1824

Score = 87.7 bits (44), Expect = 2e-13
Identities = 77/88 (87%)
Strand = Plus / Minus

Query: 27 ccctgggtgtgcggacggactctaaacaccgacagctggcgccaggtagggggtgtgt 86

Query: 87 ctttgatctgagctagctcaatgaccat 114
 | | | | | | | | | | | | | | | | |

Score = 48.1 bits (24), Expect = 0.19
Identities = 39/44 (88%)
Strand = Plus / Minus

Query: 644 cgacatcacgaggctggggaacgggatccggcgcaaccgcgtatc 687
|||

Sbjct: 166617 cgacatcacgaggccgaggaacgggacccggtgcagcccgtatc 166574

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

Query: 509 ttctaccccgacgtcctcttcatc 532
|||||
Sbjct: 166749 ttctaccccgacgtcctcttcatc 166726

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgccaggtagggg 80
||| |||||
Sbjct: 2981 aaacgccgacagttggcgccaggtagggg 3011

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

Score = 216 bits (109), Expect = 4e-52
Identities = 332/405 (81%), Gaps = 1/405 (0%)
Strand = Plus / Minus

Query: 1417 gaggacgtgatgacagtgtatccccattgtcctagggaagacgcaatgcagtggctc 1476
||||| |||| | |||| | |||| |||| ||||| || |||||
Sbjct: 109752 gaggacgtcatgaccgcgtatctgcccatcgtccttgggaagatgcgctgcagtggcta 109693

Query: 1477 cgacatctaccccaacattgcatagacaattggagcgacttcagttggtgcttcacgcc 1536
||||| |||| || |||| || | || | ||||| || | |||| |||
Sbjct: 109692 cgacatctaccccgacactgcatcgacgactggggagacttcagtcgacgtttcaccgcc 109633

Query: 1537 aacttcagtcctctcttgacaagccggcgagccatgggacctaaaatccattgggcat 1596
||||| |||| || |||| ||||| ||||| ||||| ||
Sbjct: 109632 aacttcagtcctctccgacaaaccagcgcaacctgggacctcaaatccatcaagcgc 109573

Query: 1597 cagggcgatgaaacgctccggttgctacctcaagaggttttagacctgaggaaccacacc 1656

Sbjct: 109572 cggggggacgagactctccggtcgtagctcaaaagggttcagaccatgagaaaccgtatc 109513

Query: 1657 cccgaagtcgccgaggcgggggtgattgaagacttctaccgaggatccaatgactcggt 1716

Sbjct: 109512 cccgaggtcacggaggcggccgtgatcgaggacttctacagaggatccaatgactcggct 109453

Query: 1717 ttcgtccgagccataactccagaaaagcgtcggccacctccgaacacttgttccgggaggc 1776

Sbjct: 109452 ttcgtccgagccatactaca-aaaggcgccgactacctccgaggagctgttccgggaagc 109394

Query: 1777 agacctctacatcaccacggattaacggggccaggacctcatcg 1821

Objet: 109393 cgacctetacatcaccgccgacgagcggggcccaggatctcatcgg 109349

Score = 109 bits (55), Expect = 6e-20

Identities = 163/199 (81%)

Strand = Plus / Minus

Query: 21 gggtagccctgggtgtgcggacggactctaaacaccgacagctggcgcgccaggtagggg 80

Sbjct: 111101 gggtaaccccggggtgtgcggtcggacccaaaacaccgacagctggcgcgccaggtagggg 111042

Query: 81 gtgtgtctttgatctgagctagctcaatgaccattacctccaaatgcaagatcgcccttc 140

Sbjct: 111041 gtgtgtcgacgatccaagctagctcaatggccgtcaccttccacagcaagatcatcgtgc 110982

Query: 141 gccccgggactatgttttgctttggaaccatctcatccatagcagatgaagagggaactc 200

Sbjct: 110981 gtcccgatctgtattctgcttcgggacaatctcatctgtagcggatgaagagggaattc 110922

Query: 201 tgcaccgcatagcagatct 219

Sbjct: 110921 tacaccgcatcgcagatct 110903

Score = 87.7 bits (44), Expect = 2e-13

Identities = 107/128 (83%)

Strand = Plus / Minus

Query: 794 gagcaagccgagcaaggtgcaaggctgcgccgagagaatgctctctttgctcggaacctg 853
|||||
Sbjct: 110376 gagcaagccgagcaagatgcgaggcaacgccgggagaatccgctcttcgggcgcaacctg 110317

Query: 854 taccctcgacttcgctcgtgcaatgaacacgccgagtggaagtcggagggtactggccag 913
|||||
Sbjct: 110316 aaccctcgacttcgcccagctatgaacacgcccaagcgaagtcggaggcgtactagctcgg 110257

Query: 914 atagctga 921
|||||
Sbjct: 110256 atagctga 110249

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

Query: 509 ttctaccccgacgtcctcttcac 532
|||||
Sbjct: 110646 ttctaccccgacgtcctcttcac 110623

Score = 46.1 bits (23), Expect = 0.76
Identities = 38/43 (88%)
Strand = Plus / Minus

Query: 19 aggggtagccctgggtgtgcggacggactctaaacaccgacag 61
|||||
Sbjct: 97503 aggggtaacccgggtgtgcggacggacccaaaacaccgacag 97461

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

Score = 216 bits (109), Expect = 4e-52
Identities = 450/561 (80%), Gaps = 2/561 (0%)
Strand = Plus / Minus

Query: 1265 acgtgcggagtcttcgcacttactccgtgtctccgggccatccagtggcc-cctaacttc 1323
|||||

Sbjct: 37341 acgtgcggagtatccgctcttactccgcgccttagggccatccaatggcctcccaacttc 37282

Query: 1324 aaggtctccaacgtcagcaagtatgagcgcgaagcaggacctgggtggctggttagccatc 1383
||||| ||||| ||| ||| ||||| | ||| ||||| |||

Sbjct: 37281 aaggtatccaatgtcgacaaatatgaacctaaagcaggatccaggggttggttagccgtc 37222

Query: 1384 tacacgattgtcacatgggcccggagcgacggaggacgtgatgacagtgtattttccc 1443
||||| | | | ||||| ||||| | ||| ||||| ||||| | ||| | |||

Sbjct: 37221 tacaccaccgctgctcgggtgccggagcatccgaagacgtcatgaccgcgtatctgccc 37162

Query: 1444 attgtcctagggcaagacgcaatgcagtggtccgacatctaccccaacattgcatagac 1503
|| ||||| ||||| ||||| ||||| ||||| ||||| ||| ||||| |||

Sbjct: 37161 atcgtccttgggcaagacgcgctgcagtggttacgacatctaccccgacactgcatcgac 37102

Query: 1504 aattggagcgacttcagttggtgcttcacgcccaacttccagtcctctcttgacaagccg 1563
| ||| | ||||| ||| | ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 37101 gactgggggagacttcagtcgacgtttcacgcccaacttccagtcctctctccgacaagcca 37042

Query: 1564 gcgcagccatgggacctaaaatccattgggcatcaggcgcatgaaacgctccggttgtagc 1623
||||| ||||| ||||| ||||| ||| ||| ||||| ||| ||||| |||

Sbjct: 37041 gcgcaaccatgggacctcaaatccatcaagcgcgggggggatgagactctccggtcatac 36982

Query: 1624 ctcaagaggttttagaccatgaggaaccacacccccgaagtcgccgaggcgggggtgatt 1683
||||| ||||| ||||| ||||| ||||| ||| ||| ||||| |||||

Sbjct: 36981 ctcaaaaggttccagaccatgagaaaccgcatccccgaggtcacggaggcggccgtgatc 36922

Query: 1684 gaagacttctaccgaggatccaatgactcggctttcgtccgagccatactccagaaaagc 1743
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||| ||| |||

Sbjct: 36921 gaggacttctacagaggatccaatgactcggctttcgtccgagccatactaca-aaaggc 36863

Query: 1744 gtcggccacctccgaacacttgttccgggaggcagacctctacatcaccacggattaacg 1803
| || ||||| | ||||| ||| ||| ||||| ||| ||| |||

Sbjct: 36862 gccgattacctccgaggagctgttccgggaagccgacatctacatcaccgccgacgagcg 36803

Query: 1804 ggcccaggacctcatcgagg 1824
||||||| |||||

Sbjct: 36802 ggcccaggatctcatcgagg 36782

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

Query: 794 gagcaagccgagcaaggtgcaaggctgcgccgagagaatgctctctttgctcggaacctg 853
|||||
Sbjct: 37812 gagcaagccgagcaagatgcaaggcaacgccgggagaaatccgctcttcgggcgcaacctg 37753

Query: 854 taccctcgacttcgctcgtgcaatgaacacgccgagtgaaagtcggaggggtactggcccag 913
|||||
Sbjct: 37752 aaccctcgacttcgcccagctatgaacacgccgagtcgaggtcggaggcgttctagctcgg 37693

Query: 914 atagctgacgg 924
|||||
Sbjct: 37692 atagctgacgg 37682

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

Query: 31 ggggtgtgcggacggactctaaacaccgacagctggcgcgccaggtagggggtgtgtcttt 90
|||||
Sbjct: 38527 ggggtgtgcggtcggacccaaacaccgacagctggcgcgccaggtagggggtgtgtcgac 38468

Query: 91 gatctgagctagctcaatg 109
|||||
Sbjct: 38467 gatccaagctagctcaatg 38449

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

Query: 509 ttctaccccgacgtcctcttcac 532
|||||
Sbjct: 38082 ttctaccccgacgtcctcttcac 38059

Score = 46.1 bits (23), Expect = 0.76

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

Query: 50 aaacaccgacagctggcgccaggtagggg 80
|||| ||||| |||||
Sbjct: 68664 aaacgccgacagttggcgccaggtagggg 68694

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

Score = 216 bits (109), Expect = 4e-52
Identities = 459/573 (80%), Gaps = 2/573 (0%)
Strand = Plus / Minus

Query: 1253 cgacatgaagacacgtgcgagtgcttcgcacttactccgtgtctccgggccatccagtgg 1312
|||| | ||||| ||||| | || ||||| | || |||||
Sbjct: 60922 cgacaggaggacacgtgcgagttatctgccttactccgccttagggccatccaatgg 60863

Query: 1313 cc-cctaacttcaaggtctccaacgtcagcaagtatgagcgcaagcaggacctgggtggc 1371
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Sbjct: 60862 cctcccaacttcaaggtatccaatgtcgacaaatatgaacctaacgaggatccagggggc 60803

Query: 1372 tggttagccatctacacgattgtcacatgggcccgggagcgacggaggacgtgatgaca 1431
|||| ||| ||||| | | | ||| |||| | ||||| |||||
Sbjct: 60802 tggttggccgtctacaccaccgtgtctgggctgccggggcatccgaggacatcatgact 60743

Query: 1432 gtgtattttccattgtccttagggcaagacgcaatgcagtggctccgacatctaccccaa 1491
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Sbjct: 60742 gcgtatttgcccatcgtcctcgggcaagacgcgtacagtggctacgacatctaccccca 60683

Query: 1492 cattgcatagacaattggagcgacttcagttggtgcttcacgccaacttccagtccttc 1551
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Sbjct: 60682 cactgcatcgacgactggggagacttcagtcgacgtttcaccgccaacttccagtccttc 60623

Query: 1552 ttgacaagccggcgccagccatgggacctaaatccattgggcatcaggcgcatgaaacg 1611
| ||||| |||| | ||||| ||||| ||||| || | ||| ||||| |||
Sbjct: 60622 tccgacaagccagcgcaaccatgggacctcaatccatcaagcgggggggatgagact 60563

Query: 1612 ctccggttgtagctcaagaggttttagaccatgaggaaccacacccccgaagtcgccgag 1671
|||||| | |||| | |||| | ||||| |||| | ||||| ||| | |||

Sbjct: 60562 ctccgggtcataccttaaaaggttccagaccatgagaaaccgcatccccgaggtcacggag 60503

Query: 1672 gcgggggtgattgaagacttctaccgaggatccaatgactcggctttcgtccgagccata 1731
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Sbjct: 60502 gcggccgtgatcaggacttctacagaggatctaacgactcggctttcgtccgagccata 60443

Query: 1732 ctccagaaaagcgtcggccacctccgaacacttgttccgggaggcagacctctacatcac 1791
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Sbjct: 60442 ctaca-aaaggcgccgactacctccgaggagctggtccggaagccgacctctacatcac 60384

Query: 1792 cacggattaacggggccaggacctcatcgagg 1824
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Sbjct: 60383 cgctgacgagcggggccaggacctcatcgagg 60351

Score = 200 bits (101), Expect = 2e-47
Identities = 457/573 (79%), Gaps = 2/573 (0%)
Strand = Plus / Minus

Query: 1253 cgacatgaagacacgtgcggagtcttcgcacttactccgtgtctccgggccatccagtgg 1312
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Sbjct: 113645 cgacaggaggacacgtgcggagtgtccgctcttactccgcgccttagggccatccaatgg 113586

Query: 1313 cc-cctaacttcaaggtctccaacgtcagcaagtatgagcgcaagcaggacctgggtggc 1371
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Sbjct: 113585 cctcccaacttcaaggtatccaatgtcgacaaatatgaacctaaagcaggatccagggggt 113526

Query: 1372 tggttagccatctacacgattgtcacatgggccgaggagcgacggaggacgtgatgaca 1431
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Sbjct: 113525 tggctagccgtctacaccacgctgctcgggctgccggagcatctgaggacgttatgacc 113466

Query: 1432 gtgtattttccattgtcctagggcaagacgcaatgcagtggctccgacatctaccccaa 1491
| |||| | |||| | |||| | |||| | || ||||| ||||| ||||| ||||| |||||

Sbjct: 113465 gcgtatctgcccacgtccttgggcaagatgcgctacagtggctacgacatctacccca 113406

Query: 1492 cattgcatagacaattggagcgacttcagttggtgcttcacgccaacttccagtcctc 1551
|| ||||| ||| | ||| | ||||| || | |||| | ||||| ||||| ||||| |||||

Sbjct: 113405 cactgcatcgacgactggggagacttcagtcgacgtttcaccgccaacttccagtcctc 113346

Query: 1552 tttgacaagccggcgcagccatgggacctaaaatccattgggcatcagggcgatgaaacg 1611
 | ||||| ||||| ||||| ||||| || | || ||||| ||
Sbjct: 113345 tccgacaagccagcgcacccatgggacctcaaatccatcaagcgccgggggatgagact 113286

Query: 1612 ctccggtgtacctcaagaggttttagacctgaggaaccacacccccgaagtcgccgag 1671
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Sbjct: 113285 ctccggtcgtacctcaaaaggttccagacctgagaaatcgcatccccgaggtcatggag 113226

Query: 1672 gcgggggtgattgaagacttctaccgaggatccaatgactcggtttctccgagccata 1731
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Sbjct: 113225 gcggtcgtgattgaggacttctacagaggatccaacgactcggtttttgtccgagccata 113166

Query: 1732 ctccagaaaagcgtcggccacctccgaacattgttccgggaggcagacctctacatcac 1791
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Sbjct: 113165 ctacag-aaggcgccgactacttccgaggagctgttccgggaagccgacctctacatcac 113107

Query: 1792 cacggattaacgggcccaggacctcatcggagg 1824
 | | | | | | ||||| ||||| |||||
Sbjct: 113106 cgccgacgagcgagctcaggacctcatcggagg 113074

Score = 167 bits (84), Expect = 3e-37
Identities = 328/408 (80%), Gaps = 1/408 (0%)
Strand = Plus / Plus

Query: 1417 gaggacgtgatgacagtgtattttccattgtcctagggcaagacgcaatgcagtggctc 1476
 ||||| ||||| | ||||| ||||| ||||| ||||| || | ||||| ||
Sbjct: 29401 gaggacgttatgaccgcgtatttgcccatcgtccttgggcaagatgcgctacagtggcta 29460

Query: 1477 cgacatctacccaacattgcatagacaattggagcgacttcagttggtgcttcacgcc 1536
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Sbjct: 29461 cgacatctaccccgacactgcatcgacgactggggagacttcagtcgacgtttcacgcc 29520

Query: 1537 aacttcagtcacctctttgacaagccggcgcagccatgggacctaaaatccattgggcat 1596
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Sbjct: 29521 aacttcagtcacctctccgacaagtgcgcgaaccgtgggacctcaaatccatcaagcgc 29580

Query: 1597 cagggcgatgaaacgctccggtgtacctcaagaggttttagacctgaggaaccacacc 1656
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Sbjct: 29581 cggggggatgagactctccgatcgtacctcaaaaggttccagacctgagaaatcgcatc 29640

Query: 1657 cccgaagtcgccgaggcgggggtgattgaagacttctaccgaggatccaatgactcggct 1716
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Sbjct: 29641 cctgaggtcacggaggcagccgtgatcgaggacttctacagaggatccaacgactcggct 29700

Query: 1717 ttcgtccgagccatactccagaaaagcgtcggccacctccgaacacttggtccgggaggc 1776
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Sbjct: 29701 tttgtccgagccatactgcag-aaggcggcgactacttccgaggagctgttccgggaagc 29759

Query: 1777 agacctctacatcaccacggattaacgggccaggacctcatcggagg 1824
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Sbjct: 29760 cgacctctacatcaccggccgacgagcgagctcaggacctcatcggagg 29807

Score = 165 bits (83), Expect = 1e-36
Identities = 264/323 (81%), Gaps = 1/323 (0%)
Strand = Plus / Minus

Query: 1417 gaggacgtgatgacagtgtattttccattgtcctagggcaagacgcaatgcagtggctc 1476
 ||||||| |||| | ||||| |||| | |||| | ||||| || || | ||||| ||
Sbjct: 122753 gaggacgttatgaccgcgtatttgccatcgtccttgggcaagatgcgctacagtggcta 122694

Query: 1477 cgacatctacccaacattgcatagacaattggagcgacttcagttggtgcttcacgcc 1536
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Sbjct: 122693 cgacatctacccgacactgcatcgacgactggggagacttcagtcgacgtttcaccgcc 122634

Query: 1537 aacttcagtcacctctttgacaagccggcgagccatgggacctaaaatccattgggcat 1596
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Sbjct: 122633 aacttcagtcacctctccgacaagccagcgcaaccgtgggacctcaaatccatcaagc-g 122575

Query: 1597 cagggcgatgaaacgctccggttgctacctcaagaggttttagaccatgaggaaccacacc 1656
 | || | |||| | || |||| | ||||| |||| | ||||| || || | || |
Sbjct: 122574 ccgggggatgagactctccgatcgtacctcaaaaggttcagaccatgagaaatcgcac 122515

Query: 1657 cccgaagtcgccgaggcgggggtgattgaagacttctaccgaggatccaatgactcggct 1716
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Sbjct: 122514 cccgaggtcacggaggcggccatgatcgaggacttctacagaggatccaacgactcggct 122455

Query: 1717 ttcgtccgagccatactccagaa 1739

|| |||||
Sbjct: 122454 tttgtccgagccatactgcagaa 122432

Score = 97.6 bits (49), Expect = 2e-16
Identities = 145/177 (81%)
Strand = Plus / Minus

Query: 31 ggggtgtcggacggactctaaacaccgacagctggcgcgccaggtagggggtgtgtcttt 90
||||||| ||||| | ||||| |||||
Sbjct: 114818 ggggtgtcggtcggacccaaaacactgacagctggcgcgccaggtagggggtgtgtcgac 114759

Query: 91 gatctgagctagctcaatgaccattacctccaaatgcaagatcgcccttcgccccgggac 150
|||| | ||||| || || ||| || ||||| || | ||||| |
Sbjct: 114758 gatccaagctagctcaatggccgacaccttcaacagcaagatcaccatgcgtcccggatc 114699

Query: 151 tatgttttgctttggaaccatctcatccatagcagatgaagagggaaactctgcaccg 207
| || ||||| || ||||| ||| ||||| ||| |||||
Sbjct: 114698 cgtattctgctttgggacaatctcatccgtagcggatgaagagggaaattctacaccg 114642

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

Query: 848 aacctgtaccccgacttcgctcgtgcaatgaacacgccgagtgaaagtcggaggggtactg 907
||||| | ||||| || || ||||| |||||
Sbjct: 28831 aacctgaatcccgacttcgcccagctatgaacacgccgagtgaaagtcggaggggtacta 28890

Query: 908 gccagatagctgacggcctcccgcaaccctagacacggaaggtaccggcggtgctt 967
|| | ||||| || || ||||| | ||| | || ||||| || ||| |
Sbjct: 28891 gctcggatagctgacggacttcctcgaactcccgacgccgagggataccgacgcctgttc 28950

Query: 968 actcgagcagttaatcaccttctacccatcactaatcctccaagcgacctacgccatgcc 1027
|| | |||| || || ||||| || || | || ||||| || |||
Sbjct: 28951 acccaggcagccaaccatcttctaccgctcgtcaccgccgaacgatctacgacacgcc 29010

Query: 1028 atcaacagccggcgagacacgcggagctccatcaacgcttcgcgcga 1074
|||||| | ||||| |||| ||||| |||||
Sbjct: 29011 atcaacagtcgccgagacgcgcgaagctccatcaatgcttcgcgcga 29057

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

Query: 31 ggggtgtgcggacggactctaaacaccgacagctggcgcgccaggtagggggtgtgtcttt 90
||||| |||| | ||||||||||||||||||||||||||||
Sbjct: 62096 ggggtgtgcggtcggacccaaaacaccgacagctggcgcgccaggtagggggtgtgtcgac 62037

Query: 91 gatctgagctagctcaatg 109
|||| ||||||||||||
Sbjct: 62036 gatccaagctagctcaatg 62018

Score = 89.7 bits (45), Expect = 6e-14
Identities = 69/77 (89%)
Strand = Plus / Minus

Query: 848 aacctgtaccccgacttcgctcgtgcaatgaacacgccgagtgaagtcggaggggtactg 907
||||| | |||||||||| || || ||||||||||||||||||||||||
Sbjct: 123323 aacctgaatcccgacttcgcccagctatgaacacgccgagtgaagtcggaggggtacta 123264

Query: 908 gcccagatagctgacgg 924
|| | ||||||||||||
Sbjct: 123263 gctcggatagctgacgg 123247

Score = 85.7 bits (43), Expect = 9e-13
Identities = 70/79 (88%)
Strand = Plus / Plus

Query: 31 ggggtgtgcggacggactctaaacaccgacagctggcgcgccaggtagggggtgtgtcttt 90
||||| |||| | ||||||||||||||||||||||||||||
Sbjct: 28062 ggggtgtgcggtcggacccaaaacaccgacagctggcgtgccaggtagggggtgtgtcgac 28121

Query: 91 gatctgagctagctcaatg 109
|||| ||||||||||||
Sbjct: 28122 gatccaagctagctcaatg 28140

Score = 81.8 bits (41), Expect = 1e-11
Identities = 104/125 (83%)
Strand = Plus / Minus

Query: 797 caagccgagcaaggtgcaaggctgcgccgagagaatgctctctttgctcggaacctgtac 856
|||||
Sbjct: 114101 caagccgagcaagatgcaaggcaacgccgggagaatccgctcttcgggcgcaacctgaat 114042

Query: 857 cccgacttcgctcgtgcaatgaacacgccgagtgaagtcggaggggtactggcccagata 916
|||||
Sbjct: 114041 cccgacttcgcccagctataaacacgccgaagtcggaggggtactagctcggata 113982

Query: 917 gctga 921
|||||
Sbjct: 113981 gctga 113977

Score = 81.8 bits (41), Expect = 1e-11
Identities = 143/177 (80%)
Strand = Plus / Minus

Query: 31 ggggtgtgcggacggactctaaacaccgacagctggcgcgccaggtagggggtgtgtcttt 90
|||||
Sbjct: 124092 ggggtgtcggtcggacccaaaacaccgacagctggcgcgccaggtagggggtgtatcgac 124033

Query: 91 gatctgagctagctcaatgaccattacctccaaatgcaagatcgcccttcgccccgggac 150
|||||
Sbjct: 124032 gatccaagctagctcaatggccgtcaccttcaacagcaagatcaccatgcgtcccggatc 123973

Query: 151 tatgttttgctttggaaccatctcatccatagcagatgaagagggaactctgcaccg 207
| || |||||
Sbjct: 123972 cgtattctgctttgggacaatctcatctgtagcggatgaagggggaattctacaccg 123916

Score = 60.0 bits (30), Expect = 5e-05
Identities = 45/50 (90%)
Strand = Plus / Minus

Query: 1025 gccatcaacagccggcgagacacgcggagctccatcaacgcttcgcgcga 1074
||||||| || ||||| ||||| ||||| ||||| |||||
Sbjct: 61150 gccatcaacagtcgccgagacgcgcggagctctatcaatgcttcgcgcga 61101

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

Query: 794 gagcaagccgagcaaggtgcaaggctgcgccgagagaatgctctctttgctcggaacctg 853
||||||| ||||| ||||| || || ||||| | ||||| | |||||
Sbjct: 61381 gagcaagccgaacaagatgcaaggcaacgacgcgagaatccgctcttcgggtgtaacttg 61322

Query: 854 taccctgacttcgctcgtgcaatgaacacgccgagtgaaagtcggaggggtactggcccag 913
|||| ||||| || || ||||| ||||| || ||||| || || |||||
Sbjct: 61321 aacctgacttcgccgagctatgaacacgccgagcgaggtcggaggcgttctagcccgg 61262

Query: 914 atagctgac 922
|||||||
Sbjct: 61261 atagctgac 61253

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

Query: 509 ttctaccccgacgtcctcttcac 532
||||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 28507 ttctaccccgacgtcctcttcac 28530

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

Query: 509 ttctaccccgacgtcctcttcac 532
||||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 61651 ttctaccccgacgtcctcttcac 61628

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

Query: 509 ttctaccccgacgtcctcttcac 532
 |||||
Sbjct: 114374 ttctaccccgacgtcctcttcac 114351

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

Query: 509 ttctaccccgacgtcctcttcac 532
 |||||
Sbjct: 123647 ttctaccccgacgtcctcttcac 123624

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

Query: 341 acccgaaaaactccgctgtccacttcgccacaaaggagtggacacggat 390
 ||||| || ||||| ||||| ||||| || ||||| || |||||
Sbjct: 114521 acccggaagactccgctgtctacttccccgacaaaagaatggacacggat 114472

>gb|EU952110.1| Zea mays clone 1165529 hypothetical protein mRNA, complete cds
Length = 1837

Score = 216 bits (109), Expect = 4e-52
Identities = 332/405 (81%), Gaps = 1/405 (0%)
Strand = Plus / Minus

Query: 1420 gacgtgatgacagtgtattttccattgtcctagggaagacgcaatgcagtggctccga 1479
 ||||| || ||||| ||||| ||||| || ||||| || |||||
Sbjct: 1820 gacgtgatgaccgcgtatttaccattgtccttgggaagatgcgttgcaatggctccga 1761

Query: 1480 catctaccccaacattgcatagacaattggagcgacttcagttggtgcttcacgccaac 1539
 ||||| ||||| ||| || ||||| || ||||| |||||
Sbjct: 1760 catctaccccgacattgcatcgacgactggggcgacttcagtcgacgcttcaccgccaat 1701

```
Query: 1540 ttccagtcacctctttgacaagccggcgcagccatgggacctaaaatccattgggcatcag 1599
          ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 1700 ttctagtcacctctccgacaaaccggcacaaccatgggacctcaaatccatcaagcgccgg 1641
```

```
Query: 1600  ggcgatgaaacgctccggttgacctcaagaggttttagaccatgaggaaccacaccccc 1659
           ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||| | |||||
Sbjct: 1640  ggggacaaaactctccggtcatacctcaaaaggttcagaccatgagaaatcgatcccc 1581
```

```
Query: 1660 gaagtcgccgaggcgggggtgattgaagacttctaccgaggatccaatgactcggctttc 1719
          || || | ||||| |||| | ||||| ||||| ||||| ||||| |||||
Sbjct: 1580 gaggtcacggaggcggccgtgatcgaggacttctacagaggatccaacgactcggctttc 1521
```

```
Query: 1720 gtccgagccataactccagaaaagcgtcgccacactccgaacacttgttcgggaggcaga 1779
          |||||
Sbjct: 1520 gtccgagccatattaca-aaagcgccgactacctccgaggagctgttcgggaagccga 1462
```

```
Query: 1780 cctctacatcaccacggattaacgggccaggacctcatcgagg 1824
          |||||
Sbjct: 1461 cctctacatcaccgccgacgagcggggcccaggacctcatcgagg 1417
```

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

Score = 214 bits (108), Expect = 1e-51
Identities = 316/384 (82%), Gaps = 1/384 (0%)
Strand = Plus / Minus

Identities = 316/384 (82%), Gaps = 1/384 (0%)

Strand = Plus / Minus

```
Query: 1441   cccattgtcctagggcaagacgcaatgcagtggtccgacatctacccaacattgcata 1500
             ||||| ||||| |||||||||  ||||||| ||||||||| ||| |||||
Sbjct: 158997 cccatcgctctgggcaagacgcgtgcagtggtctacgacatctacccgacactgcac 158938
```

```
Query: 1501   gacaattggagcgcattcagttggtgcttcacgcgccaacttcagtcctctttgacaag 1560
             ||| | ||| ||||| ||| | ||| ||||| ||||| ||||| |||||
Sbjct: 158937 gagcactggggagacttcagtcgacgtttaccgcgccaacttcagtcctctctccgacaag 158878
```

Query: 1561 cggcgccagccatgggacctaaaatccattgggcatcaggcgatgaaacgctccggttg 1620
 ||||||| ||||||| || || ||| ||||| || ||| ||| |
 Sbjct: 158877 ccagcgcaaccatgggacctcaaatccatcaagcgccgggggggatgagactctcaggtcg 158818

Subjct: 158877 ccagcgcaaccatgggacctcaaatccatcaagcgccgggggggatgagactctcaggtcg 158818

Query: 1621 tacctcaagaggttttagaccatgaggaaccacacccccgaagtcgccgaggcgggggtg 1680
 ||||| ||||||| ||||||||| |||| | | |||||| | || | ||||||| ||
Sbjct: 158817 taccttaagaggttcagaccatgagaaaccgcatccccgaggtcacggaggcgccgta 158758

Query: 1681 attgaagacttctaccgaggatccaatgactcggcttttcgtccgagccatactccagaaa 1740
 || | ||||||||| ||||||| || ||||||||||||||||||||||||| || |||
Sbjct: 158757 atcgaggacttctacagaggatctaacgactcggcttttcgtccgagccatactgca-aaa 158699

Query: 1741 agcgtcggccacctccgaacacttgttcgggaggcagacctctacatcaccacggatta 1800
 ||| || | ||||||| | ||||||||| || ||||||||||||||||| || | |
Sbjct: 158698 ggcgccgactacctccgaggagttgttcgggaagccgacctctacatcaccgctgacga 158639

Query: 1801 acgggccaggacctcatcggagg 1824
 || |||||||||||||||||
Sbjct: 158638 gcgagcccaggacctcatcggagg 158615

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

Query: 31 ggggtgtcggacggactctaaacaccgacagctggcgcgccaggtagggggtgtgtcttt 90
 ||||||||| |||| | |||||||||||||||||||||||||||||||||
Sbjct: 160360 ggggtgtcgggtcgacccaaaacaccgacagctggcgcgccaggtagggggtgtgtcgac 160301

Query: 91 gatctgagctagctcaatg 109
 |||| | |||||||||
Sbjct: 160300 gatccaagctagctcaatg 160282

Score = 73.8 bits (37), Expect = 3e-09
Identities = 220/281 (78%)
Strand = Plus / Minus

Query: 794 gagcaagccgagcaaggtgcaaggctgcgccgagagaatgctctctttgctcggaacctg 853
 ||||||||||||||| |||||| | || || |||||| | |||| | || |||||
Sbjct: 159645 gagcaagccgagcaagacgaaggcaacgacgcgagaaatccgctcttcgggcgcaacttg 159586

Query: 854 taccgccacttcgctcgtgcaatgaacacgccgagtgaaagtcggaggggtactggcccag 913
 |||| | ||||||| || || ||||||||||||| || ||||||||| || || |||||

||||| ||||| || ||||| ||||| || ||||| ||||| ||||| ||||| |||||
Sbjct: 186291 gggctgccggagcatccgaggacgtcatgaccgcgtatctgcccacgtccttgggcaag 186350

Query: 1460 acgcaatgcagtggtccgacatctaccccaacattgcatagacaattggagcgacttca 1519
| | | ||||| ||||| ||||| || ||||| || || ||||| |||||
Sbjct: 186351 atgcgctgcagtggttacgacatctaccccgacactgcatcgacgactggggagacttca 186410

Query: 1520 gttggtgcttcacgcgaacttcagtcaccttttgacaagccggcgagccatgggacc 1579
|| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 186411 gtcgacgcttcaccgccaacttcagtcctctctccgacaagccagcgcaaccatgggacc 186470

Query: 1580 taaaatccattgggcatcaggcgcatgaaacgctccggttgacctcaagaggttttaga 1639
| ||||| || | || | || | || ||||| ||||| || ||||| |||
Sbjct: 186471 tcaaatccatcaagcgccgggagacgagactctccggtcataccttaaaggttccaga 186530

Query: 1640 ccatgaggaaccacacccccgaagtcgcgaggcgggggtgattgaagacttctaccgag 1699
||||| |||| | ||||| || | ||||| |||| | ||||| ||||| |||
Sbjct: 186531 ccatgagaaaccgcatccccgaggtcacggaggcgccggtgatcgaggacttctacagag 186590

Query: 1700 gatccaatgactcggttttcgtccgagccatactccagaaaagcgtcggccacctccgaa 1759
|||| | ||||| ||||| ||||| ||||| || || || || || |||||
Sbjct: 186591 gatctaacgactcggttttcgtccgagccatactaca-aaaggcgccgactacctccgag 186649

Query: 1760 cacttgttccgggaggcagacctctacatcaccacggattaacgggccaggacctcatc 1819
| ||||| || ||||| ||||| || || ||||| ||||| ||||| |||||
Sbjct: 186650 gagctgttccgggaagccgacctctacatcaccgccgacgagcgggcccaggacctcatc 186709

Query: 1820 ggagg 1824
|||||
Sbjct: 186710 ggagg 186714

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

Query: 794 gagcaagccgagcaaggtgcaaggctgcgccgagagaatgctctctttgctcggaacctg 853
||||| ||||| ||||| ||||| || ||||| || || |||||
Sbjct: 185684 gagcaagccgagcaagatgcaaggcaacgccgggagaatccgctcttcgggcgcaacctg 185743

```
Query: 914      atagctgacgg 924
          |||||
Sbjct: 185804 atagctgacgg 185814
```

Score = 85.7 bits (43), Expect = 9e-13
Identities = 70/79 (88%)
Strand = Plus / Plus

Query: 31 gggtgtgcggacggactctaaacaccgacagctggcgcgccaggtaggggggtgtgtcttt 90
 |||||
 Sbjct: 184969 gggtgtgcggtcggacccaaaacatcgacagctggcgcgccaggtaggggggtgtgtcgac 185028

```

Query: 91      gatctgagctagctcaatg 109
          |||  |||||
Sbjct: 185029  gatccaagctagctcaatg 185047

```

Score = 50.1 bits (25), Expect = 0.048
Identities = 52/61 (85%)
Strand = Plus / Plus

```
Query: 614      cgacggaggaatagaagccagaacgtgcggcgacatcacgaggctggggaacgggatccg 673
               ||||| ||| || ||||| || ||||| ||||| ||||| |||||
Sbjct: 185516   cgacggaggaaccgacgcaggaacgttcgacgacatcacgcggctggagaacgggatccg 185575
```

```
Query: 674      g 674
      |
Sbjct: 185576   g 185576
```

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

Query: 509 ttctaccccgacgtcctcttcac 532
 |||||
Sbjct: 185414 ttctaccccgacgtcctcttcac 185437

>gb|EF190061.1| Zea mays clone FS2_19 chromosome B, genomic sequence
Length = 39598

Score = 208 bits (105), Expect = 9e-50
Identities = 458/573 (79%), Gaps = 2/573 (0%)
Strand = Plus / Plus

Query: 1253 cgacatgaagacacgtgcgagtgcttcgcacttactccgtgtctccgggccatccagtgg 1312
 ||||| || ||||| || ||||| || ||||| ||||| ||||| |||||
Sbjct: 17079 cgacaggaggacacgtctggagtattggcgcttactccatgtctcagggccattcagtgg 17138

Query: 1313 cccc-taacttcaaggtctccaacgtcagcaagtatgagcgcaagcaggacctgggtggc 1371
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 17139 ccccctaacttcaaggtctccaacgtcgacaagtacgagcccaagcaggacccaggaggc 17198

Query: 1372 tggttagccatctacacgattgtcacatgggcccgcgagcgacggaggacgtgatgaca 1431
 ||||| || ||||| || ||||| || ||||| || ||||| || |||||
Sbjct: 17199 tggttggtgtctataccactactgcccggcgctggggcaactgaatatgtgatgact 17258

Query: 1432 gtgtattttccattgtcctagggcaagacgcaatgcagtggtccgacatctaccccaa 1491
 | ||||| || || ||||| ||||| || || ||||| ||||| || |||||
Sbjct: 17259 gcgattttgcctatcgctcttcggcacgatgcgctgcaatggctacgacacctgccccga 17318

Query: 1492 cattgcatagacaattggagcgacttcagttggtgcttcacgccaacttcagtccttc 1551
 || ||||| || ||||| ||||| ||||| || ||||| ||||| |||||
Sbjct: 17319 cactgcatcgacgattggagcgatttcagtcggtgttttatcgccaacttccaatccttc 17378

Query: 1552 tttgacaagccggcgagccatgggacctaaaatccattgggcatcaggcgatgaaacg 1611
 | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 17379 tctgacaagccggcgcaaccatgggacctcaaatccatcaggcgccgaggggatgaaact 17438

Query: 1612 ctccggttgtagctcaagaggttttagacatgaggaaccacacccccgaagtcgccgag 1671
 ||||| ||||| || ||||| ||||| || ||||| || |||||
Sbjct: 17439 ctccggtcataacctcaaaagatttcagacatgagaaatcgatatccccgaggttggtgaa 17498

Query: 1672 gcgggggtgattgaagacttctaccgaggatccaatgactcggctttcgtccgagccata 1731


```
Query: 848   aacctgtaccccgacttcgctcgtgcaatgaacac 882
           ||||| ||||||||| || |||||||
Sbjct: 16694 aacctgaaccccgacttcgctcgagccatgaacac 16728
```

Score = 44.1 bits (22), Expect = 3.0
Identities = 106/134 (79%)
Strand = Plus / Plus

Query: 950 ggctaccggcggtgcttactcgagcagttaatcaccttctacccatcactaatcctcca 1009
||||| ||||||||| ||||| ||| || ||||| || || | |||||
Sbjct: 16796 ggctatcggcggtgctcactcgggcagctaaccatcttctgcctctcggtcacacctccg 16855

Query: 1010 agcgacctacgccatgccatcaacagccggcgagacacgggagctccatcaacgcttcg 1069
||||| |||| | ||||||||| || | || ||| | ||||| ||||| |||||
Sbjct: 16856 agcgatctacaacatgccatcaatagtcaacgggacgcacggagcccatcaatgcttca 16915

Query: 1070 cgcgaccgatgaca 1083
||||| ||| ||||
Sbjct: 16916 cggaacgacgaca 16929

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

Score = 208 bits (105), Expect = 9e-50
Identities = 332/405 (81%), Gaps = 2/405 (0%)
Strand = Plus / Plus

Query: 1420 gacgtgatgacagtgtatccccattgtcctagggcaagacgcaatgcagtggctccga 1479
||||||| ||||| || ||||| ||||| ||||||||| ||||| ||| |||
Sbjct: 81990 gacgtgatgaccgtgtacttaccatcgctccttgggcaagacgcgctgcaatggatgcga 82049

Query: 1480 catctaccccaacattgcatagacaattggagcgacttcagttggtgcttcacgccaac 1539
||||||| ||||| |||| | ||| | ||||||| | ||||| |||||
Sbjct: 82050 catctaccccaacactgcatcgacgactggggtgacttcagtcgacgcttcaccgccaat 82109

Query: 1540 ttccagtcctcttttgacaagccggcgagccatgggacctaaaatccattgggcatcag 1599
||||||| ||||| |||| ||| || ||||| || ||||| || |||
Sbjct: 82110 ttccagtcctctccgacaaaccggtgcaaccgtgggatctcaatccatcaagcgtc-g 82168

Query: 1600 ggcgatgaaacgctccggtgtacctcaagaggttttagaccatgaggaaccacaccccc 1659
|| | ||||| ||||| ||||||||| ||||| ||||||||| || | |||||
Sbjct: 82169 ggggaagaaactctccggtcgtacctcaaaaggttcagaccatgagaaatcgtatcccc 82228

Query: 1660 gaagtcgccgaggcggggtgattgaagacttctaccgaggatccaatgactcggctttc 1719
|| ||| | |||||| | ||| | ||||| |||||
Sbjct: 82229 gaggtcacggaggcgcccatgatcgaggacttctaccgaggatccaatgactcggctttc 82288

Query: 1780 cctctacatcaccacggattaacgggccaggacctcatcgagg 1824
|||||
Sbjct: 82348 cctctacatcacccgcgacgagcgggccaggacctcatcgagg 82392

Query: 31 ggggtgtgcggacggactctaaacaccgacagctggcgcgccaggtagggggtgtgtcttt 90
||||||| |||| | |||||||||||||||||||||
Sbjct: 80649 ggggtgtgcggtcgacccaaaacaccgacagctggcgcgccaggtagggggtgtgtcgac 80708

Query: 151 tatgttttgcttggcaaccatctcatccatagcagatgaagagggaactctgcaccgcat 210
 | || ||||| ||||| ||||||| ||||||| ||||||| ||||||| |||||||
Sbjct: 80769 cgtattctgcttcggaacaatctcatccgtagcagatgaagagggaactctgcaccgcat 80828

Query: 797 caagccgagcaaggtgcaaggctgcgccgagagaatgctctctttgctcggaacctgtac 856
 ||||||||||| ||||||| ||| ||||| | ||| | || ||||||| ||
 Sbjct: 81367 caagccgagcaagatgcaaggcaagccaggagaatccattcttcgggcgcaacctgaac 81426

Query: 857 cccgacttcgctcgtgcaatgaacacgccgagtgaagtcggaggggtact 906
 ||||| || || ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 81427 cccgacttcgcccagccatgaacacgccgagtgaagtcggaggagtact 81476

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

Query: 509 ttctaccccgacgtcctcttcatc 532
 ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 81094 ttctaccccgacgtcctcttcatc 81117

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgccaggtagggg 80
 |||| | ||||| | ||||| ||||| ||||| |||||
Sbjct: 133339 aaacgccgacagttggcgccaggtagggg 133369

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

Score = 208 bits (105), Expect = 9e-50
Identities = 458/573 (79%), Gaps = 2/573 (0%)
Strand = Plus / Minus

Query: 1253 cgacatgaagacacgtgcggagtcttcgcacttactccgtgtctccgggccatccagtgg 1312
 ||||| || ||||| ||||| || || ||||| || || ||||| ||||| |||||
Sbjct: 109470 cgacaggaggacacgtgcggagtatccgcccttactccgcgccttagggccatccaatgg 109411

Query: 1313 cc-cctaacttcaaggtctccaacgtcagcaagtatgagcgcaagcaggacctgggtggc 1371
 || || ||||| ||||| ||||| ||||| ||||| || ||||| || |||||
Sbjct: 109410 cctcccaacttcaaggtatccaatgtcgacaaatatgaacctaagcaggatccagggggc 109351

Query: 1372 tggttagccatctacacgattgtcacatgggccgccggagcgacggaggacgtgatgaca 1431
 ||||| ||||| || || || ||||| ||||| || || ||||| |||||
Sbjct: 109350 tggttagccgtctacaccacgctgctcgggctgccggggcatccgaagacgtcatgact 109291

```
Query: 1432   gtgtattttccattgtctctagggaagacgcaatgcagtggctccgacatctacccaa 1491
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 109290 gcgtatctgcccacgtctctgggaagacgcgtgcagtggctacgacatctacccga 109231
```

Query: 1552 tttgacaagccggcgcagccatgggacctaaaatccattgggcatcagggcgatgaaacg 1611
 | ||||| |||| ||||| ||||| ||||| || | || ||||| ||
Sbjct: 109170 tccgacaagccagcgaaccatgggacctcaaatccatcaagcgccgaggggatgagact 109111

```
Query: 1672   gcgggggtgattgaagacttctaccgaggatccaatgactcggctttcgtccgagccata 1731
             |||  ||||  ||  ||||||||  ||||||  ||  |||||||||
Sbjct: 109050 gcggccgtgatcgaggacttctacagaggatctaacgactcggctttcgtccgagccata 108991
```

```
Query: 1792   cacggattaacgggccaggacctcatcggagg 1824
            | | | | | | | | | | | | | | | | | |
Sbjct: 108931 cgctgacgagcggggcccaggacctcatcggagg 108899
```

Query: 794 gagcaagccgagcaaggtgcaaggctgcgccgagagaatgctctctttgctcggaacctg 853
 ||||||||||||||| ||||||| || || ||||||| | ||||| | || |||||||
 Sbjct: 109929 gagcaagccgagcaagatgcaaggcaacgacgcgagaatccgctcttcgggcgcaacctg 109870

Sbjct: 109869 aaccccgacttcgcccgagccatgaatacgccgagcgaagtcggaggcgttctagcccg 109810

```
Query: 974      gcagttaatcaccttctacccatcactaatcctccaagcgacctacgccatgccatcaac 1033
               ||||  ||  ||||| ||  ||||| ||  ||||| ||  ||||| ||  ||||| ||
Sbjct: 109749   gcagccaaccatcttctaccgctcgctcatccgccgaacgacctgcgacacgccatcaac 109690
```

```
Query: 1034      agccggcgagacacgcggagctccatcaacgcttcgcgcga 1074
                || || ||||| | || |||| | |||| |||||
Sbjct: 109689    agtcgtcgagacgcacgaagctctatcaatgcttcgcgcga 109649
```

Score = 91.7 bits (46), Expect = 1e-14
Identities = 70/78 (89%)
Strand = Plus / Minus

```
Query: 32      ggtgtgcggacggactctaaacaccgacagctggcgcgccaggtagggggtgtgtctttg 91
              |||||
Sbjct: 110643  ggtgtgcggtcgaccctaaacaccgacagctggcgcgccaggtagggggtgtgtcgacg 110584
```

```

Query: 92      atctgagctagctcaatg 109
             ||| |||||
Sbjct: 110583 atccaagctagctcaatg 110566

```

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

```

Query: 509      ttctaccccgacgtcctcttcac 532
              |||||
Sbjct: 110199  ttctaccccgacgtcctcttcac 110176

```

Score = 46.1 bits (23), Expect = 0.76
Identities = 41/47 (87%)
Strand = Plus / Minus

Query: 635 aacgtgcggcgacatcacgaggctggggaacgggatccggcgcaacc 681
||||| || ||||||||| ||||| ||||||||||||| |||||
Sbjct: 110076 aacgttcgacgacatcacgcagctggagaacgggatccggagcaacc 110030

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Minus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
|||| | ||||| | |||||||||||||||||
Sbjct: 196004 aaacgccgacagttggcgcgccaggtagggg 195974

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

Score = 206 bits (104), Expect = 3e-49
Identities = 291/352 (82%), Gaps = 1/352 (0%)
Strand = Plus / Minus

Query: 1441 cccattgtcctagggaagacgcaatgcagtggctccgacatctaccccaacattgcata 1500
||||| ||||| ||||||||| ||||||||| ||||||||| ||| |||||
Sbjct: 16534 cccatcgtccttgggaagacgcgctgcagtggctacgacatctaccccgacactgcata 16475

Query: 1501 gacaattggagcgacttcagttggtgcttcacgccaacttcagtcctctttgacaag 1560
||| | ||| | ||||||| | | |||| | ||||||||| |||| | |||||
Sbjct: 16474 gacgactggggagacttcagtcgacgtttcaccgccaacttcagtcctctctccgacaag 16415

Query: 1561 ccggcgcgagccatgggacctaataatccattgggcatcaggcgatgaaacgctccggttg 1620
|| ||||| ||||||||| ||||||| || | || ||||||| ||||||| |
Sbjct: 16414 ccagcgcaaccatgggacctaataatccatcaagcgccgaggggatgaaactctccggtcg 16355

Query: 1621 tacctcaagaggttttagaccatgaggaaccacacccccgaagtcgccgaggcgggggtg 1680
||||||| ||||| ||||||||| |||| | |||||| | ||| | ||||||| |||
Sbjct: 16354 tacctcaaaaggttcagaccatgagaaacgcacatccccgaggtcacggaggcgccgtg 16295

Query: 1681 attgaagacttctaccgaggatccaatgactcggttttcgtccgagccatactccagaaa 1740
|| | ||||||| ||||||| ||||||||| ||||||||| ||||||||| || |||
Sbjct: 16294 atcgaggacttctacagaggatctaatactcggttttcgtccgagccatactaca-aaa 16236

Query: 1741 agcgtcggccacctccgaacacttggtccgggaggcagacctctacatcacc 1792
||| || | ||||| | | ||||| || | ||||| |||||
Sbjct: 16235 ggcgccgactacctccgaggagctggtccgagaagccgacctctacatcacc 16184

Score = 97.6 bits (49), Expect = 2e-16
Identities = 154/189 (81%)
Strand = Plus / Minus

Query: 31 ggggtgtgcggacggactctaaacaccgacagctggcgcgccaggtaggggggtgtgtcttt 90
||||||| |||| | || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 17897 ggggtgtgcggtcggacccaaagcaccgacagctggcgcgccaggtaggggggtgtgtcgac 17838

Query: 91 gatctgagctagctcaatgaccattacctccaaatgcaagatcgcccttcgccccgggac 150
||| ||||| |||| | || | |||| | | ||||| |||| | ||| | ||| |
Sbjct: 17837 aatccaagctagctcaatggccgtcaccttccacagcaagatcgccgtgcgtctcggatc 17778

Query: 151 tatgttttgccttgaaccatctcatccatagcagatgaagaggggaactctgcaccgcat 210
||| || |||| | || | || ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 17777 tatattccgcttcgggacaatttcacatagcggatgaagaggggaattctacaccgcct 17718

Query: 211 agcagatct 219
|||||||
Sbjct: 17717 cgcagatct 17709

Score = 81.8 bits (41), Expect = 1e-11
Identities = 107/129 (82%)
Strand = Plus / Minus

Query: 794 gagcaagccgagcaaggtgcaaggctgcgccgagagaatgctctctttgctcggaacctg 853
||||||| |||| | ||||| |||| | |||| | |||| | |||||
Sbjct: 17182 gagcaagccgaacaagatgcaaggcaacgccgggagaatccgctcttcgggcgcaacctg 17123

Query: 854 tacccegaacttcgctcgtgcaatgaacacgccgagtgagtcggaggggtactggcccag 913
||||||| || | ||||| |||| | ||||| || || | ||| |
Sbjct: 17122 aaccccgacttcgcccagctatgaacacgccgagtcggaggtcggagcggttctagctcgg 17063

Query: 914 atagctgac 922
|||||
Sbjct: 17062 atagctgac 17054

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

Query: 1025 gccatcaacagccggcgagacacgcggagctccatcaacgcttcgcgcga 1074
||||| || ||||| |||| |||| |||| |||||
Sbjct: 16951 gccatcaacagtcgccgagacgcgcgaagctctatcaatgcttcgcgcga 16902

Score = 48.1 bits (24), Expect = 0.19
Identities = 57/68 (83%)
Strand = Plus / Minus

Query: 614 cgacggaggaatagaagccagaaacgtgcggcgacatcacgaggctggggaacgggatccg 673
||||| || || ||||| || ||||| || ||||| |||||
Sbjct: 17350 cgacggaggaatcgacgcaggaacgttcgacgacatcacgcagccggggagcgggatccg 17291

Query: 674 gcgcaacc 681
| |||||
Sbjct: 17290 gagcaacc 17283

Score = 46.1 bits (23), Expect = 0.76
Identities = 23/23 (100%)
Strand = Plus / Minus

Query: 509 ttctaccccgacgtcctcttcat 531
|||||
Sbjct: 17452 ttctaccccgacgtcctcttcat 17430

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
|||| |||||| ||||||||||||||||
Sbjct: 42263 aaacgccgacagttggcgcgccaggtagggg 42293

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Minus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
|||| |||||| ||||||||||||||||
Sbjct: 109561 aaacgccgacagttggcgcgccaggtagggg 109531

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

Score = 206 bits (104), Expect = 3e-49
Identities = 291/352 (82%), Gaps = 1/352 (0%)
Strand = Plus / Plus

Query: 1441 cccattgtcctagggcaagacgcaatgcagtggctccgacatctaccccaacattgcata 1500
|||| |||||| |||||||||| |||||||||| |||||||||| ||| |||||
Sbjct: 69408 cccatcgctccttgggcaagacgcgctgcagtggctacgacatctaccccgacactgcatac 69467

Query: 1501 gacaattggagcgacttcagttggtgcttcacgcgaacttccagtcctctttgacaag 1560
||| | ||| | |||||||| | | ||| |||||||||||||| |||| |||||
Sbjct: 69468 gacgactggggagacttcagtcgacgtttcaccgccaacttccagtcctctctccgacaag 69527

Query: 1561 ccggcgagccatgggacctaataatccattgggcatcagggcgatgaaacgctccggttg 1620
|| ||||| |||||||||| |||||||| || | || |||||||| |||||||| |
Sbjct: 69528 ccagcgcaaccatgggacctaataatccatcaagcgccgaggggatgaaactctccggtcg 69587

Query: 1621 tacctcaagaggttttagaccatgaggaaccacacccccgaagtcgcccaggcgggggtg 1680
||||||| ||||| |||||||||| |||| | |||||| ||| | |||||| |||
Sbjct: 69588 tacctcaaaaggttccagaccatgagaaaccgcatccccgaggtcacggaggcggccgtg 69647

Query: 1681 attgaagacttctaccgaggatccaatgactcggttttcgtccgagccatactccagaaa 1740
|| | |||||||| |||||| |||||||||||||||||||||||| || |||
Sbjct: 69648 atcgaggacttctacagaggatctaataatgactcggttttcgtccgagccatactaca-aaa 69706

Query: 1741 agcgtcgccacctccgaacacttgttcgggaggcagacctctacatcacc 1792
||| || | ||||| | | ||||| || | ||||| |||||
Sbjct: 69707 ggccgactacctccgaggagctgttcgagaagccgacctctacatcacc 69758

Score = 97.6 bits (49), Expect = 2e-16
Identities = 154/189 (81%)
Strand = Plus / Plus

Query: 31 ggggtgtcggacggactctaaacaccgacagctggcgcgccaggtaggggtgtgtcttt 90
||||||| |||| | || ||||| ||||| ||||| ||||| |||||
Sbjct: 68045 ggggtgtcggtcggacccaaagcaccgacagctggcgcgccaggtaggggtgtgtcgac 68104

Query: 91 gatctgagctagctcaatgaccattacctccaaatgcaagatcgcccttcgccccgggac 150
||| ||||| |||| | || |||| | || ||||| || || |||
Sbjct: 68105 aatccaagctagctcaatggccgtcaccttccacagcaagatcgccgtgcgtctcggatc 68164

Query: 151 tatgttttgcctttggaacctctcatccatagcagatgaagaggaactctgcaccgcat 210
||| || |||| || || || ||||| ||||| ||||| ||||| |||||
Sbjct: 68165 tatattccgcttcgggacaatttcatccatagcggatgaagaggaattctacaccgct 68224

Query: 211 agcagatct 219
|||||||
Sbjct: 68225 cgcagatct 68233

Score = 81.8 bits (41), Expect = 1e-11
Identities = 107/129 (82%)
Strand = Plus / Plus

Query: 794 gagcaagccgagcaaggtgcaaggctgcgccgagagaatgctctctttgctcggaacctg 853
||||||| |||| ||||| |||| ||||| | |||| | || |||||
Sbjct: 68760 gagcaagccgaacaagatgcaaggcaacgccgggagaatccgctcttcggcgcaacctg 68819

Query: 854 taccgccacttcgctcgtgcaatgaacacgccgagtgaagtcggaggggtactggcccag 913
||||||| || || ||||| |||| | ||||| || || |||
Sbjct: 68820 aaccgccacttcgccgagctatgaacacgccgagcgaggtcggagcggttctagctcgg 68879

Query: 914 atagctgac 922
|||||||

Sbjct: 68880 atagctgac 68888

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

Query: 1025 gccatcaacagccggcgagacacgcggagctccatcaacgcttcgcgcga 1074
||||| ||| ||||| |||| |||| |||| ||||| |||||
Sbjct: 68991 gccatcaacagtcgccgagacgcgcgaagctctatcaatgcttcgcgcga 69040

Score = 48.1 bits (24), Expect = 0.19
Identities = 57/68 (83%)
Strand = Plus / Plus

Query: 614 cgacggaggaatagaagccagaacgtgcggcgacatcacgaggctggggaacgggatccg 673
||||| ||| || ||||| || ||||| ||| ||||| |||||
Sbjct: 68592 cgacggaggaatcgacgcaggaacgttcgacgacatcacgcagccggggagcgggatccg 68651

Query: 674 gcgcaacc 681
| |||||
Sbjct: 68652 gagcaacc 68659

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Minus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
|||| ||||| ||||| ||||| |||||
Sbjct: 43679 aaacgccgacagttggcgcgccaggtagggg 43649

Score = 46.1 bits (23), Expect = 0.76
Identities = 23/23 (100%)
Strand = Plus / Plus

Query: 509 ttctaccccgacgtcctcttcat 531
||||| ||||| ||||| ||||| |||||

Score = 69.9 bits (35), Expect = 5e-08
Identities = 71/83 (85%)

Strand = Plus / Plus

Query: 848 aacctgtaccccgacttcgctcgtgcaatgaacacgccgagtgaagtcggaggggtactg 907
||||| ||||| ||||| || || ||||| ||||| || ||||| |||||

Sbjct: 63 aacctgaaccccgacttcgcccagccgtgaacacgccgagcgaggtcggaggagtactg 122

Query: 908 gcccagatagctgacggcctccc 930
|| | ||||| || |||||

Sbjct: 123 gctcggatagctgagggactccc 145

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

Score = 204 bits (103), Expect = 1e-48
Identities = 332/407 (81%), Gaps = 1/407 (0%)
Strand = Plus / Plus

Query: 1418 aggacgtgatgacagtgtattttccattgtcctagggaagacgcaatgcagtggctcc 1477
||||| ||||| || || || ||||| ||||| ||||| ||||| |||||

Sbjct: 47964 aggacgtgatgaccgcatacttgcccattgtcctcgggaagacgcgctgcaatggctgc 48023

Query: 1478 gacatctaccccaacattgcatagacaattggagcgacttcagttggtgcttcacgcga 1537
||||| ||||| || ||||| || || ||||| ||||| || || |||||

Sbjct: 48024 gacatctaccccgacactgcatcgacgactggagcgacttcagtcgacgtttcaccgcca 48083

Query: 1538 acttccagtcacctctttgacaagccggcgagccatgggacctaaaatccattgggcac 1597
|||| ||||| ||||| || ||||| ||||| || ||||| || || ||

Sbjct: 48084 actttcagtcacctctccgacaaaccagcgcaaccatgggacctcaagtcacatcaagcgcc 48143

Query: 1598 agggcgatgaaacgctccggtgtacctcaagaggttttagaccatgaggaaccacaccc 1657
|||| || ||||| ||||| ||||| ||||| ||||| || || || ||

Sbjct: 48144 agggggacgaaactctccggtcgtacctcaaaaggttcagaccatgagaaatcgtatcc 48203

Query: 1658 ccgaagtcgccgaggcgggggtgattgaagacttctaccgaggatccaatgactcggtt 1717
|||| ||| | ||||| ||||| || || ||||| ||||| ||||| |||||

Sbjct: 48204 ccgaggtcacggaggcgccgtgatcgaggatttctacagaggatccaacgactcggtt 48263

Query: 1718 tcgtccgagccatactccagaaaagcgctcgccacctccgaacacttgttccgggaggca 1777
|||| | ||||| || || || || || ||||| || ||||| |||||

Sbjct: 48264 tcgtctgagccatattacag-aaggcgccgactacctccgagcaactgttccgggaagcc 48322

Query: 1778 gacctctacatcaccacggattaacgggccaggacctcatcgagg 1824
 ||||| | | | | |
Sbjct: 48323 gacctctacatcaccgccgagcgcagctcaggacctcatcgagg 48369

Score = 95.6 bits (48), Expect = 9e-16
Identities = 153/188 (81%)
Strand = Plus / Plus

Query: 31 ggggtgtgcggacggactctaaacaccgacagctggcgcgccaggtagggggtgtgtcttt 90
|||||
Sbjct: 46602 ggggtgtcggtcgaccctaaacaccgacagcgggcgcgcaaggtagggggtgtgtagcc 46661

Query: 91 gatctgagctagctcaatgaccattacctccaaatgcaagatcgcccttcgccccgggac 150
 ||||| ||||| ||||| | |||| | ||||| ||||| ||||| |||||
 Sbjct: 46662 gatctaagctagctcaatggctgcaccttcagcgcaagatcacccctcgccccggatc 46721

Query: 151 tatgttttgctttggaaccatctcatccatagcagatgaagagggaactctgcaccgcat 210
 ||| |||| |||| ||||| ||| |||| | ||||| || |||||
Sbjct: 46722 cgtgttctgcttcggaactatctcatctgtagccgatgaggaaggaactctacatcgcat 46781

```
Query: 211   agcagatc 218
          |||||
Sbjct: 46782 tgcagatc 46789
```

Score = 87.7 bits (44), Expect = 2e-13
Identities = 179/224 (79%)
Strand = Plus / Plus

Query: 848 aacctgtaccccgacttcgctcgtgcaatgaacacgccgagtgaagtcggaggggtactg 907
 ||||| |||||||||||| || || ||||| ||||| ||||||| |||||||
 Sbjct: 47393 aacctgaaccccgacttcgcccagccatgaatacgcgaagtgaagtcggaggagtactg 47452

Query: 908 gccagatagctgacggcctcccgcaaccctagacacggaaggctaccggcggtgctt 967
 ||| ||||| || |||| || || | ||| || ||||| || || ||| |
 Sbjct: 47453 gctcggatagctgatgggctccctcggaactcccgacgtcgagggtatcgacgactgttc 47512

```
Query: 968   actcgagcagttaatcaccttctacccatcactaatcctccaagcgacctaagccatgcc 1027
           ||||| ||||| || ||||| || || ||||| ||||| |||||
Sbjct: 47513 actcaagcagccaaccatcttctacctctcgtcaccgcgcgaacgacctacgacatgcc 47572
```

Score = 54.0 bits (27), Expect = 0.003
Identities = 27/27 (100%)
Strand = Plus / Plus

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

```
Query: 1420  gacgtgatgacagtgtattttccattgtcctagggaagacgcaatgcagtggtccga 1479
              ||||| ||||| | |||| | ||||| ||||| | ||||| ||||| |||
Sbjct: 96082  gacgtcatgaccgcgtatctgcccattgtcattgggaagatgcgctgcagtggtacga 96141
```

Query: 1540 ttccagtcctctttgacaagccggcgcagccatgggacctaaaatccattgggcatcag 1599
||||| | |||| | |||| | |||| | |||| | ||
Sbjct: 96202 ttccagtcctctccgacaaaccagcgcaaccatgggacctcaaatccatcaagcgccgg 96261


```
Query: 1660   gaagtcgccgaggcgggggtgattgaagacttctaccaggatccaatgactcggctttc 1719
              ||||| | ||||| | ||||| | ||||| | ||||| | ||||| | ||||| |
Sbjct: 96322 gaggtcacagaggcggccgtgatcgaggacttctacagaggatccaatgactcggctttc 96381
```

```
Query: 1720  gtccgagccataactccagaaaagcgtcggccacctccgaacacttgttccgggaggcaga 1779
              |||||
Sbjct: 96382  gtccgagccataactaca-aaaggcaccgactacctccgaggagctgttcgggaagccga 96440
```

```
Query: 1780  cctctacatcaccacggattaacgggccaggacctcatcggagg 1824
              ||||| | | | | | | | | | | | | | |
Sbjct: 96441  cctctacatcaccgccgacgagcgggcccaggatctcattggagg 96485
```

Score = 97.6 bits (49), Expect = 2e-16
Identities = 163/201 (81%)
Strand = Plus / Plus

Query: 19 aggggtagccctgggtgtgcggacggactctaaacaccgacagctggcgcgccaggtagg 78
 ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Sbjct: 94728 aggggtaaccccaggtgtgcggtcgacccaaaacaccgacagctggcacgccaggtagg 94787

Query: 79 ggggtgtgtctttgatctgagctagctcaatgaccattacctccaaatgaagatcgccct 138
 ||||| ||| ||||| || | ||| | ||||| || |
 Sbjct: 94788 ggggtgtgtcgacgatccaagctagctcaatggccgtcaccttcacagcaagatcacggt 94847

```
Query: 139   tcgcccgggactatgttttgccttggaaccatctcatccatagcagatgaagagggaac 198
            |||||  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 94848 gcgtcccgatctgtattctgcttcgggacaatctcatctgtagcggatgaagagggaat 94907
```

```
Query: 199      tctgcaccgcatagcagatct 219
              ||| ||||| | |||||
Sbjct: 94908    tctacaccgcctgcagatct 94928
```

Score = 85.7 bits (43), Expect = 9e-13
Identities = 109/131 (83%)
Strand = Plus / Plus

Query: 794 gagcaagccgagcaaggtgcaaggctgcgccgagagaatgctctctttgctcggaaacctg 853

Sbjct: 95455 gagcaagccgagcaagatgcaaggcaacgctgggagaatccgctcttcgggcgcaaccta 95514

```
Query: 914      atagctgacgg 924
          |||||
Sbjct: 95575 atagctgacgg 95585
```

```

Query: 509      ttctaccccgacgtcctcttcac 532
                |||||
Sbjct: 95185    ttctaccccgacgtcctcttcac 95208

```

```
Query: 341   acccgaaaaactccgctgtccacttcgccacaaaggagtggacacggat 390
           ||||| || ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 95038 acccggaagactccgctgtctacttccccaacaaaagaatggacacggat 95087
```

Score = 200 bits (101), Expect = 2e-47
Identities = 331/405 (81%), Gaps = 2/405 (0%)
Strand = Plus / Minus

Query: 1480 catctaccccaacattgcatagacaattggagcgacttcagttggtgcttcacgccaac 1539
||||||| ||| |||| | | ||| | ||||| | ||||| |||||
Sbjct: 88581 catctaccccgacactgcatcgacgactgggggacttcagtcgacgcttcaccgccaac 88522

Query: 1540 ttccagtcctcttttgacaagccggcgagccatgggacctaaaatccattgggcatcag 1599
||||||| ||||| ||| | ||||| ||||| | | |
Sbjct: 88521 ttccagtcctctccgacaagccgacgcaaccgtgggacctcaaatccatcaagc-gctg 88463

Query: 1600 ggcgatgaaacgctccggttgatctcaagaggttttagaccatgaggaaccacaccccc 1659
|| |||| | ||||| ||||| ||||| ||||| || | | |||
Sbjct: 88462 ggggatgagactctccggtcgatctcaaaaggttcagaccatgagaaatcgattccc 88403

Query: 1660 gaagtcgccgaggcggggtgattgaagacttctaccgaggatccaatgactcggctttc 1719
|| || | ||||| |||| | | ||||| ||||| ||||| |||||
Sbjct: 88402 gaggtcacggaggcgccgtgatcgaggaattctacagaggatccaacgactcggctttt 88343

Query: 1720 gtccgagccatactccagaaaagcgctggccacctccgaacacttgttccgggaggcaga 1779
||||||| |||| | ||| | | ||||| | ||||| ||||| |||
Sbjct: 88342 gtccgagccatactacag-aaggcgccgactacctccgaggagctgttccgggaagccga 88284

Query: 1780 cctctacatcaccacggattaacgggcccaggacctcatcgagg 1824
||||||| || | | | ||||| |||||
Sbjct: 88283 cctctacatcaccgccgacgagcgagctcaggacctcatcgagg 88239

Score = 113 bits (57), Expect = 4e-21
Identities = 147/177 (83%)
Strand = Plus / Minus

Query: 31 ggggtgtgcggacggactctaaacaccgacagctggcgcgccaggtagggggtgtgtcttt 90
||||||| |||| | ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 89981 ggggtgtgcggtcggacccaaaacaccgacagctggcgcgccaggtagggggtgtgtcgac 89922

Query: 91 gatctgagctagctcaatgaccattacctccaaatgcaagatcgcccttcgccccgggac 150
|||| | ||||| || | ||| | | ||||| |||| | ||||| |
Sbjct: 89921 gatccaagctagctcaatggccgtcaccttctacagcaagatcacctcgccccgggac 89862

Query: 151 tatgttttgcctttggaacctctcatccatagcagatgaagagggaactctgcaccg 207

| || ||||| |||| | ||||| || ||| ||||| ||||| |||||
Sbjct: 89861 cgtattctgcttcggaaaaatctcatctgtagcggatgaagagggaaactctacaccg 89805

Score = 91.7 bits (46), Expect = 1e-14
Identities = 112/134 (83%)
Strand = Plus / Minus

Query: 797 caagccgagcaaggtgcaaggctgcgccgagagaatgctctctttgctcggaacctgtac 856
 ||||| ||||| ||||| ||||| | ||| | || ||||| |
Sbjct: 89265 caagccgagcaagatgcaaggcaacgccgggagaatccattcttcgggcgcaacctgaat 89206

Query: 857 cccgacttcgctcgtgcaatgaacacgccgagtgaaagtcggaggggtactggcccagata 916
 ||||| || || || ||||| ||||| ||||| ||||| ||||| | ||||
Sbjct: 89205 ccgacttcgcccagctatgaacacgccgagcgaagtcggaggggtattggctcggata 89146

Query: 917 gctgacggcctccc 930
 |||| | |||||
Sbjct: 89145 gctgatggactccc 89132

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Minus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
 |||| ||||| ||||| ||||| |||||
Sbjct: 17151 aaacgccgacagttggcgcgccaggtagggg 17121

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
 |||| ||||| ||||| ||||| |||||
Sbjct: 111035 aaacgccgacagttggcgcgccaggtagggg 111065

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

Score = 198 bits (100), Expect = 8e-47
Identities = 314/384 (81%), Gaps = 1/384 (0%)
Strand = Plus / Plus

Query: 1441 cccattgtcctagggcaagacgcaatgcagtggctccgacatctaccccaacattgcata 1500
||||| ||||| ||||| || || ||||| ||||| ||||| ||||| |||||
Sbjct: 26067 cccatcgctccttgggcaagatgcgctgcagtggctgcgacatctacccgacactgcatc 26126

Query: 1501 gacaattggagcgacttcagttggtgcttcacgcgcaacttcagtcctctttgacaag 1560
||| | ||| | ||||| || | ||||| ||||| ||||| ||||| |||||
Sbjct: 26127 gacgactggggagacttcagtcgacgtttcgcgcaacttcagtcctctccgacaag 26186

Query: 1561 ccggcgcagccatgggacctaaaatccattgggcatcagggcgatgaaacgctccggttg 1620
||||||| ||||| ||||| || || | ||||| || |||||
Sbjct: 26187 ccggcgcaaccatgggacctcaaatccatcaagcgccgggaggatgagactctccggtca 26246

Query: 1621 tacctcaagaggttttagaccatgaggaaccacacccccgaagtcgccgaggcgggggtg 1680
||||| || ||||| ||||| || || ||||| ||| | ||||| |||
Sbjct: 26247 taccttaaaaggttccagaccatgagaaactgcacccccgaggtcacggaggcggccgtg 26306

Query: 1681 attgaagacttctaccgaggatccaatgactcggctttcgtccgagccatactccagaaa 1740
|| || ||||| ||||| ||||| ||||| ||||| ||||| || |||
Sbjct: 26307 atcgaggacttctacagaggatccaacgactcggctttcgtccgagccatactaca-aaa 26365

Query: 1741 agcgtcgccacctccgaacacttggtccgggagcgacctctacatcaccacggatta 1800
||| || | ||||| | ||||| || ||||| ||||| || |||
Sbjct: 26366 ggcgcgactacctccgaggagctggtccgggaagccgacctctacatcaccgccgacga 26425

Query: 1801 acgggcccaggacctcatcggagg 1824
|| ||||| |||||
Sbjct: 26426 gcgagcccaggatctcatcggagg 26449

Score = 95.6 bits (48), Expect = 9e-16
Identities = 108/128 (84%)
Strand = Plus / Plus

Query: 794 gagcaagccgagcaaggtgcaaggctgcgccgagagaatgctctctttgctcggaacctg 853
||||||| ||||| ||||| ||||| | ||||| | || |||||

Sbjct: 25420 gagcaagccgagcaagatgcaaggcaacgccgggagaatccgctcttcgggcgcaacttg 25479

Query: 854 taccctgacttcgctcgtgcaatgaacacgccgagtgaaagtcggaggggtactggcccag 913

|||||

Sbjct: 25480 aaccccgacttcgctcgagctatgaacacgccgagcgaagtcggaggcgttctagctcgg 25539

Query: 914 atagctga 921

|||||

Sbjct: 25540 atagctga 25547

Score = 89.7 bits (45), Expect = 6e-14

Identities = 153/189 (80%)

Strand = Plus / Plus

Query: 31 ggggtgtgcggacggactctaaacaccgacagctggcgcgccaggtaggggggtgtgtcttt 90

|||||

Sbjct: 24704 ggggtgtgcggtcggaccaagacaccgacagctggcgcgccaggtaggggggtgtgtcgac 24763

Query: 91 gatctgagctagctcaatgaccattacctccaaatgcaagatcgcccttcgccccgggac 150

|||||

Sbjct: 24764 gatccaagctagctcaatggccgtcaccttcacagcaaaatcgctgtgcgtcccggatc 24823

Query: 151 tatgttttgccttgaaccatctcatccatagcagatgaagaggaactctgcaccgcat 210

| | | | |

Sbjct: 24824 tgtattctgcttcgggacgatctcgtccgtagcagatgaagaaggaattctacaccgcct 24883

Query: 211 agcagatct 219

|||||

Sbjct: 24884 cgcagatct 24892

Score = 48.1 bits (24), Expect = 0.19

Identities = 24/24 (100%)

Strand = Plus / Plus

Query: 509 ttctaccccgacgtcctcttcac 532

|||||

Sbjct: 25150 ttctaccccgacgtcctcttcac 25173

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgccaggtagggg 80
|||| ||||| |||||
Sbjct: 116116 aaacgccgacagttggcgccaggtagggg 116146

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

Score = 196 bits (99), Expect = 3e-46
Identities = 331/407 (81%), Gaps = 1/407 (0%)
Strand = Plus / Plus

Query: 1418 aggacgtgatgacagtgtattttccattgtcctagggaagacgcaatgcagtggctcc 1477
||||| ||||| | || || ||||| ||||| ||||| ||||| |||||
Sbjct: 33860 aggacgtgatgaccgcatacttgcccattgtcctcgggcaagacgcgctgcaatggctgc 33919

Query: 1478 gacatctaccccaacattgcatagacaattggagcgacttcagttggtgcttcacgcga 1537
||||| ||||| || ||||| || | ||||| ||||| | | ||||| |||||
Sbjct: 33920 gacatctaccccgacactgcatcgacgactggagcgacttcagtcgacgtttcaccgcga 33979

Query: 1538 acttccagtcacctctttgacaagccggcgagccatgggacctaaaatccattgggcac 1597
|||| ||||| ||||| || ||||| ||||| || ||||| || || || || ||
Sbjct: 33980 actttcagtcacctctccgacaaaccagcgcaaccatgggacctcaagtccatcaagcgcc 34039

Query: 1598 agggcgatgaaacgctccggtgtacctcaagaggttttagaccatgaggaaccacaccc 1657
|||| || ||||| ||||| ||||| ||||| ||||| ||||| || || || || ||
Sbjct: 34040 agggggacgaaactctccggtcgtacctcaaaaggttcagaccatgagaaatcgatatcc 34099

Query: 1658 ccgaagtcgccgaggcgggggtgattgaagacttctaccgaggatccaatgactcggctt 1717
|||| || | ||||| ||||| || || || ||||| ||||| ||||| || || || || ||
Sbjct: 34100 ccgaggtcacggaggcggccgtgatcgaggatttctacagaggatccaacgactcggcct 34159

Query: 1718 tcgtccgagccatactccagaaaagcgctcggccacctccgaacacttgttccgggaggca 1777
|||| ||||| || || || || || || ||||| || || ||||| || || || || ||
Sbjct: 34160 tcgtctgagccatattacag-aaggcgccgactacctccgagcaactgttccgggaagcc 34218

Query: 1778 gacctctacatcaccacggattaacgggccaggacatcgagg 1824
|||||
Sbjct: 34219 gacctctacatcaccgccgacgagcagctcaggacatcgagg 34265

Score = 103 bits (52), Expect = 4e-18
Identities = 154/188 (81%)
Strand = Plus / Plus

Query: 31 ggggtgtgcggacggactctaaacaccgacagctggcgcgccaggtaggggtgtgtcttt 90
|||||
Sbjct: 32498 ggggtgtgcggtcggacccaaaacaccgacagccggcgcgccaggtaggggtgtgtagcc 32557

Query: 91 gatctgagctagctcaatgaccattacctccaaatgcaagatcgcccttcgccccgggac 150
|||||
Sbjct: 32558 gatctaagctagctcaatggtcgtcaccttcagcgcaagatcaccttcgccccgggac 32617

Query: 151 tatgttttgcctttggaaccatctcatccatagcagatgaagagggaactctgcaccgcat 210
|||||
Sbjct: 32618 cgtgttctgcttcggaactatctcatctgtagccgatgaggaaggaactctacatcgcat 32677

Query: 211 agcagatc 218
|||||
Sbjct: 32678 tgcagatc 32685

Score = 87.7 bits (44), Expect = 2e-13
Identities = 179/224 (79%)
Strand = Plus / Plus

Query: 848 aacctgtaccccgacttcgctcgtgcaatgaacacgccgagtgaaagtcggagggtactg 907
|||||
Sbjct: 33289 aacctgaaccccgacttcgcccagccatgaatacgccaagtgaagtcggaggagtactg 33348

Query: 908 gccagatagctgacggcctcccgcaaccctagacacggaaggtaccggcggtgctt 967
|||
Sbjct: 33349 gctcggatagctgatgggctccctcggactcccgacgtcgagggtatcgacgactgttc 33408

Query: 968 actcgagcagttaatcaccttctacccatcactaatcctccaagcgacctacgccatgcc 1027

||||| ||||| || || ||||| || || || || || ||||| |||||
Sbjct: 33409 actcaagcagccaaccatcttctacctctcgctcaccgccgaacgacctacgacatgcc 33468

Query: 1028 atcaacagccggcgagacacgcggagctccatcaacgcttcgcg 1071

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

Score = 54.0 bits (27), Expect = 0.003
Identities = 27/27 (100%)
Strand = Plus / Plus

Query: 509 ttctaccccgacgtcctcttcatcagg 535

||||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 32965 ttctaccccgacgtcctcttcatcagg 32991

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

Score = 196 bits (99), Expect = 3e-46
Identities = 331/407 (81%), Gaps = 1/407 (0%)
Strand = Plus / Plus

Query: 1418 aggacgtgatgacagtgtattttccattgtcctagggaagacgcaatgcagtggctcc 1477

||||||| ||||| || || || || ||||| ||||| ||||| ||||| |||||
Sbjct: 45102 aggacgtgatgaccgcatacttgcccattgtcctcgggaagacgcgctgcaatggctgc 45161

Query: 1478 gacatctaccccaacattgcatagacaattggagcgacttcagttggtgcttcatcgcca 1537

||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 45162 gacatctaccccgacactgcatcgacgactggagcgacttcagtcgacgtttcaccgcca 45221

Query: 1538 acttccagtcacctctttgacaagccggcgagccatgggacctaaaatccattgggcac 1597

|||| ||||| ||||| || ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 45222 actttcagtcacctctccgacaaaccagcgcaaccatgggacctcaagtccatcaagcgcc 45281

Query: 1598 agggcgatgaaacgctccggtgtacctcaagaggttttagaccatgaggaaccacacc 1657

|||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 45282 agggggacgaaactctccggtcgtacctcaaaaggttcagaccatgagaaatcgatatcc 45341

Query: 1658 ccgaagtcgccgaggcgggggtgattgaagacttctaccgaggatccaatgactcggett 1717

||||| ||| | ||||| ||||| || || ||||| ||||| ||||| ||||| ||
Sbjct: 45342 ccgaggtcacggaggcgccgtgatcgaggatttctacagaggatccaacgactcggcct 45401

Query: 1718 tcgtccgagccatactccagaaaagcgtcggccacctccgaacacttggtccgggaggca 1777
||||| ||||| || ||| || ||| || || ||||| || || ||||| || ||
Sbjct: 45402 tcgtctgagccatattacag-aaggcgccgactacctccgagcaactgttccgggaagcc 45460

Query: 1778 gacctctacatcaccacggattaacgggccaggacctcatcgagg 1824
||||| ||||| || || | || || || ||||| ||||| ||||| ||||| ||
Sbjct: 45461 gacctctacatcaccgccgacgagcgagctcaggacctcatcgagg 45507

Score = 103 bits (52), Expect = 4e-18
Identities = 154/188 (81%)
Strand = Plus / Plus

Query: 31 ggggtgtgcggacggactctaaacaccgacagctggcgcgccaggtagggggtgtgtcttt 90
||||| ||||| || || ||||| ||||| ||||| ||||| ||||| ||||| ||
Sbjct: 43740 ggggtgtgcggtcggacccaaaacaccgacagccggcgcgccaggtagggggtgtgtagcc 43799

Query: 91 gatctgagctagctcaatgaccattacctccaaatgcaagatcgcccttcgccccgggac 150
||||| ||||| ||||| || || ||||| || || ||||| || || ||||| ||
Sbjct: 43800 gatctaagctagctcaatggtcgtcaccttcagcgcaagatcaccttcgccccggatc 43859

Query: 151 tatgttttgccttgaaccatctcatccatagcagatgaagaggaactctgcaccgcat 210
||| ||||| ||||| ||||| ||||| ||||| || ||||| || ||||| ||
Sbjct: 43860 cgtgttctgcttcggaactatctcatctgtagccgatgaggaaggaactctacatcgcat 43919

Query: 211 agcagatc 218
|||||
Sbjct: 43920 tgcagatc 43927

Score = 87.7 bits (44), Expect = 2e-13
Identities = 179/224 (79%)
Strand = Plus / Plus

Query: 848 aacctgtaccccgacttcgctcgtgcaatgaacacgccgagtgaagtcggagggtactg 907
||||| ||||| ||||| || || ||||| ||||| ||||| ||||| ||||| ||
Sbjct: 44531 aacctgaaccccgacttcgcccagccatgaatacgccaagtgaagtcggaggagtactg 44590

```
Query: 908   gccagatagctgacggcctcccgcgaaaccctagacacggaaggctaccggcggtgctt 967
           ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 44591 gctcggatagctgatgggctccctcggactcccgacgtcgagggctatcgacgactgttc 44650
```

Query: 1028 atcaacagccggcgagacacgcggagctccatcaacgcttcgcg 1071
 ||||| | | | | | | | | | | | | | | | | | |
 Sbjct: 44711 atcaacagtcgccgggacgcgcggagctccatcaatgccttcgcg 44754

```
Query: 509   ttctaccccgacgtcctcttcatcagg 535
           |||||
Sbjct: 44207 ttctaccccgacgtcctcttcatcagg 44233
```

Score = 196 bits (99), Expect = 3e-46
Identities = 331/407 (81%), Gaps = 1/407 (0%)
Strand = Plus / Plus

Query: 1478 gacatctaccccaacattgcatagacaattggagcgacttcagttggtgcttcacgcga 1537
 |||||
 Sbjct: 84300 gacatctaccccgacaactgcatcgacgaactggagcgacttcagtcgacgtttaccgcga 84359

Query: 1598 agggcgatgaaacgctccggttgctacctcaagaggttttagaccatgaggaaccacacc 1657
 ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Sbjct: 84420 agggggacgaaactctccggtcgtacctcaaaaggttccagaccatgagaaatcgatatcc 84479

Query: 1658 ccgaagtcgccgaggcgggggtgattgaagacttctaccgaggatccaatgactcggcct 1717
||||| |||| | ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 84480 ccgaggtcacggaggcgccgtgatcgaggatttctacagaggatccaacgactcggcct 84539

```
Query: 1718  tcgtccgagccatactccagaaaagcgtcgccacctccgaacacttgttccgggaggca 1777
             ||||| ||||| || ||| || ||| || ||| ||||| || ||| ||||| ||
Sbjct: 84540  tcgtctgagccatattacag-aaggcgccgactacctccgagcaactgttccgggaagcc 84598
```

```
Query: 1778  gacctctacatcaccacggattaacgggccaggacctcatcgagg 1824
             |||||
Sbjct: 84599  gacctctacatcaccgccgacgagcgagctcaggacctcatcgagg 84645
```

Score = 103 bits (52), Expect = 4e-18
Identities = 154/188 (81%)
Strand = Plus / Plus

Query: 31 ggggtgtgcggacggactctaaacaccgacagctggcgcgccaggtaggggggtgtgtcttt 90
||||||| |||| | ||||||||| |||||||||
Sbjct: 82878 ggggtgtcggtcggacccaaaacaccgacagcggcgcgccaggtaggggggtgtgtagcc 82937

```
Query: 91      gatctgagctagctcaatgaccattacctccaaatgaagatcgcccttcgccccgggac 150
              ||||| ||||||||||||| | |||| | | ||||||| ||| ||||||| |
Sbjct: 82938  gatctaagctagctcaatggctcgtcaccttccagcgcaagatcacccctcgccccggatc 82997
```

Query: 151 tatgttttgctttggaaccatctcatccatagcagatgaagagggaactctgcaccgcat 210
 ||| |||| |||| ||||| ||| |||| | ||||| || |||||
 Sbjct: 82998 cgtgttctgcttggaaactatctcatctgtagccgatgaggaaggaactctacatcgcat 83057

```
Query: 211   agcagatc 218
          |||||
Sbjct: 83058 tgcagatc 83065
```

Score = 87.7 bits (44), Expect = 2e-13
Identities = 179/224 (79%)
Strand = Plus / Plus

Query: 848 aacctgtaccccgacttcgctcgtgcaatgaacacgccgagtgaagtcggaggggtactg 907
||||| ||||||||| || || ||||| ||||| ||||||||| |||||
Sbjct: 83669 aacctgaaccccgacttcgcccagccatgaatacgcgaagtgaagtcggaggagtactg 83728

Query: 908 gccagatagctgacggcctcccgcaaccctagacacggaaggctaccggcggtgctt 967
|| | ||||||| || ||||| || || | ||| || ||||| || || |||
Sbjct: 83729 gctcggatagctgatgggtccctcggactcccgacgtcgagggtatcgacgactgttc 83788

Query: 968 actcgagcagttaatcaccttctacccatcactaatcctccaagcgacctacgccatgcc 1027
|||| ||||| || || ||||||| || || | || || ||||||||| |||||
Sbjct: 83789 actcaagcagccaaccatcttctacctctcgtcacccgccgaacgacctacgacatgcc 83848

Query: 1028 atcaacagccggcgagacacgcggagctccatcaacgcttcgcg 1071
||||||| || || || || ||||||||| || || |||||
Sbjct: 83849 atcaacagtgcgccggagcgcggagctccatcaatgcctcgcg 83892

Score = 54.0 bits (27), Expect = 0.003
Identities = 27/27 (100%)
Strand = Plus / Plus

Query: 509 ttctaccccgacgtcctcttcatcagg 535
|||||||||||||||||||
Sbjct: 83345 ttctaccccgacgtcctcttcatcagg 83371

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

Score = 196 bits (99), Expect = 3e-46
Identities = 331/407 (81%), Gaps = 1/407 (0%)
Strand = Plus / Plus

Query: 1418 aggacgtgatgacagtgtattttccattgtcctagggaagacgcaatgcagtggctcc 1477
||||||||||| | || || ||||||||| ||||||||| |||| |||||
Sbjct: 72871 aggacgtgatgaccgcatacttgccattgtcctcgggcaagacgcgctgcaatggctgc 72930

Query: 31 ggggtgtgcggacggactctaaacaccgacagctggcgcgccaggtaggggggtgtgtcttt 90
||||||| |||| | ||||||||| |||||||||
Sbjct: 71509 ggggtgtgcggtcgacccaaaacaccgacagcggcgcgccaggtaggggggtgtgtagcc 71568

Query: 211 agcagatc 218
||||||
Sbjct: 71689 tgcagatc 71696

Score = 87.7 bits (44), Expect = 2e-13
Identities = 179/224 (79%)
Strand = Plus / Plus

Query: 848 aacctgtaccccgacttcgctcgtgcaatgaacacgccgagtggaagtcggaggggtactg 907
||||| |||||||||||| || || ||||| ||||| ||||||||||||||| |||||
Sbjct: 72300 aacctgaaccccgacttcgcccagccatgaatacgccaagtgaagtcggaggagtactg 72359

Query: 908 gcccagatagctgacggcctcccgcgaaacctagacacggaaggctaccggcggtgctt 967
|| | |||||||| || ||||| || || | ||| || ||||| || || |||||
Sbjct: 72360 gctcggatagctgatgggctccctcggactcccgacgtcgagggtatcgacgactgttc 72419

Query: 968 actcgagcagttaatcaccttctacccatcactaatcctccaagcgacctacgccatgcc 1027
|||| ||||| || || |||||||| || || | || | || ||||||||| |||||
Sbjct: 72420 actcaagcagccaacctcttctacctctcgtcacccgccgaacgacctacgacatgcc 72479

Query: 1028 atcaacagccggcgagacacgcggagctccatcaacgcttcgcg 1071
||||||| || || || || |||||||||||| || |||||
Sbjct: 72480 atcaacagtcgccgggacgcgcggagctccatcaatgcctcgcg 72523

Score = 54.0 bits (27), Expect = 0.003
Identities = 27/27 (100%)
Strand = Plus / Plus

Query: 509 ttctaccccgacgtcctcttcatcagg 535
|||||||||||||||||||||||
Sbjct: 71976 ttctaccccgacgtcctcttcatcagg 72002

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Minus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
|||| |||||| ||||||||||||||||
Sbjct: 29682 aaacgccgacagttggcgcgccaggtagggg 29652

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Minus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
|||| |||||| ||||||||||||||||
Sbjct: 121172 aaacgccgacagttggcgcgccaggtagggg 121142

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

Score = 194 bits (98), Expect = 1e-45
Identities = 318/390 (81%), Gaps = 1/390 (0%)
Strand = Plus / Plus

Query: 1441 cccattgtcctagggaagacgcaatgcagtggctccgacatctacccaacattgcata 1500
|||| |||||| |||||||||| ||| |||| |||||||||| ||| ||||
Sbjct: 162198 cccatcgtcctcgggaagacgcgctgcaatggctgcgacatctacccgacactgcatc 162257

Query: 1501 gacaattggagcgacttcagttggtgcttcacgccaaacttcagtcctctttgacaag 1560
|| | |||||||||| || |||| |||||| |||||| ||||
Sbjct: 162258 gaagactggagcgacttcagtcgacgcttcaccgcaactttcagtcctctccgacaaa 162317

Query: 1561 ccggcgagccatgggacctaaaatccattgggcatcaggcgatgaaacgctccggttg 1620
|| |||| |||||||||| |||||| || | || || || || |||| ||||
Sbjct: 162318 ccagcgcaacctgggacctcaaatccatcaagcgccgggggacaaaactctccggtcg 162377

Query: 1621 tacctcaagaggttttagaccatgaggaaccacacccccgaagtcgccgaggcggggtg 1680
|||| |||| |||||| || | |||| ||| || |||| |||
Sbjct: 162378 tacctcaaaaggttcagaccatgagaaatcgatccccgaggtcacagaggcgccgtg 162437

Query: 1681 attgaagacttctaccgaggatccaatgactcggctttcgtccgagccatactccagaaa 1740
|| | |||||| |||||| |||||| |||||| |||| |||
Sbjct: 162438 atcgaggacttctacagaggatccaacgactcggccttcgtccgagccatattacag-aa 162496


```
Query: 1741   agcgtcgccacctccgaacctgtgtccgggaggcagacctctacatcaccacggatta 1800
             ||| || | ||||| ||||| ||||| ||||| ||||| ||||| ||| |
Sbjct: 162497 ggcgacgactacctccgaacaactgttccgggaagccgacctctacatcaccgccgacga 162556
```

Score = 145 bits (73), Expect = 1e-30
Identities = 160/189 (84%)
Strand = Plus / Plus

```
Query: 90      tgatctgagctagctcaatgaccattacctccaaatgcaagatcgcccttcgccccggga 149
              ||||| ||||| ||||| | ||||| | ||||| ||||| ||||| ||
Sbjct: 160879 cgatctaagctagctcaatggctcgtcaccttcaccgcgaagatcaccttcgccttgga 160938
```

```
Query: 210      tagcagatc 218
           | | | | |
Sbjct: 160999  tcgcagatc 161007
```

Query: 848 aacctgtaccccgacttcgctcgtgcaatgaacacgccgagtgaagtcggagggggtactg 907
 ||||| ||||| ||||| || || ||||| ||||| ||||| |||||
 Sbjct: 161608 aacctgaaccccgacttcgcccagccatgaacacaccgagtgaagtcggagggggtactg 161667

|| | ||||| || ||||| || || | ||| | || ||||| || || || |
Sbjct: 161668 gctcggatagctgatggactccctcggactcccgacgccgagggtatcgacgattgttc 161727

Query: 968 actcgagcagttaatcaccttctacccatcactaatcctccaagcgacctacgccatgcc 1027
|||| ||||| || || ||||| || || | || || | ||||| || || ||
Sbjct: 161728 actcaagcagccaaccatcttctacctctcgtcaccgccgaacgacctacgacacacc 161787

Query: 1028 atcaacagccggcgagacacgcggagctccatcaacgcttcgcg 1071
||||||| || || | ||| ||||| ||||| |||||
Sbjct: 161788 atcaacagccggcgagcgcgaagctccatcaacgcctcgcg 161831

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Minus

Query: 50 aaacaccgacagctggcgccaggtagggg 80
|||| ||||| ||||| ||||| |||||
Sbjct: 89649 aaacgccgacagttggcgccaggtagggg 89619

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

Score = 192 bits (97), Expect = 5e-45
Identities = 329/405 (81%), Gaps = 1/405 (0%)
Strand = Plus / Plus

Query: 1420 gacgtgatgacagtgtattttccattgtcctagggaagacgcaatgcagtggctccga 1479
||||||| || ||||| |||| | |||| | ||||| || || ||||| |||
Sbjct: 1949 gacgtgatgaccgcgtatttaccatcgctccttgggaagacgcgctgtagtggctgcga 2008

Query: 1480 catctaccccaacattgcatagacaattggagcgacttcagttggtgcttcacgccaac 1539
||||||| || | || | || | || | ||||| || | ||||| |||||
Sbjct: 2009 gatctaccccgacacaacatcgacgactggggagacttcagtcgacgcttcaccgccaac 2068

Query: 1540 ttccagtcctctttgacaagccggcgagccatgggacctaaaatccattgggcatcag 1599
||||| |||| | ||||| || || ||||| ||||| || || |
Sbjct: 2069 ttccagtacctctccgacaagccggcgcaaccgtgggacctcaaatccatcaagcgccgg 2128

Query: 1600 ggcgatgaaacgctccggttgctacctcaagaggttttagacctgaggaaccacaccccc 1659

Query: 916 agctga 921
|||||
Sbjct: 1446 agctga 1451

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

Query: 509 ttctaccccgacgtcctcttcac 532
|||||||
Sbjct: 1055 ttctaccccgacgtcctcttcac 1078

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

Score = 184 bits (93), Expect = 1e-42
Identities = 455/573 (79%), Gaps = 2/573 (0%)
Strand = Plus / Plus

Query: 1253 cgacatgaagacacgtgcggagtcttcgcacttactccgtgtctccgggccatccagtgg 1312
||||| || ||||| ||||| || ||| ||||| || || ||||| |||||
Sbjct: 165917 cgacaggaggacacgtgcggagtatccgcccttactccgcgccttagggccatccaatgg 165976

Query: 1313 cccct-aacttcaaggtctccaacgtcagcaagtatgagcgcaagcaggacctgggtggc 1371
|| || ||||| ||||| ||| ||| ||||| || ||||| || || ||
Sbjct: 165977 cctctcaacttcaaggtatccaatgtcgacaaatatgaaccaagcaggatccaggggt 166036

Query: 1372 tggttagccatctacacgattgtcacatgggccgccggagcgacggaggacgtgatgaca 1431
||||||| ||||| || || ||| ||||| || || ||||| |||||
Sbjct: 166037 tggttagccgtctacaccaccgtgctcgggctgccgggcatccgaagacgtcatgacc 166096

Query: 1432 gtgtattttccattgtcctagggaagacgcaatgcagtggtctccgacatctaccccaa 1491
| |||| | ||| ||||| || ||||| || ||||| ||||| |||||
Sbjct: 166097 gcgtatctgctcatcgtccttggacaagatgcgctgcagtggtctacgacatctacccga 166156

Query: 1492 cattgcatagacaattggagcgacttcagttggtgcttcacgccaacttccagtcctc 1551
|| ||||| |||| ||| ||||| || || ||||| ||||| ||||| |||||
Sbjct: 166157 cactgcatcaacaactggggagacttcagtcgacgtttaccgccaacttccagtcctc 166216

```
Query: 1552   ttgacaagccggcgcagccatgggacctaaaatccattgggcatcagggcgatgaaacg 1611
              || ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 166217 ttcgacaagccagcgcgaacctgggacctcaaatccatcaagcgccgggggatgagact 166276
```

Query: 1612 ctccggttgtaacctcaagaggttttagaccatgaggaaccacacccccgaagtcgccgag 1671
 ||||| ||||| || ||||| ||||| || || || || || ||
 Sbjct: 166277 ctccggtcataaccttaaaaggttcagaccatgagaaaccgcatccccgaggtcacagag 166336

```
Query: 1672   gcgggggtgattgaagacttctaccgaggatccaatgactcggctttcgtccgagccata 1731
             |||  |||  |  | ||||| ||||| || ||||| ||||| |||||
Sbjct: 166337 gcggccgtggtctaggacttctacagaggatctaacgactcggctttcgtccgagccata 166396
```

Query: 1732 ctccagaaaagcgctcgggccacctccgaacacttggtccgggaggcagacctctacatcac 1791
 || || ||| ||| || | ||||| | ||||| ||| ||| ||| ||| ||
 Sbjct: 166397 ctaca-aaaggcgccgactacctccgaggagctgttcgggaagccgacctctacattac 166455

```
Query: 1792   cacggattaacggggccaggacctcatcggagg 1824
           ||||| ||||||||| |||||||||
Sbjct: 166456 cgccgacgagcggggccaggatctcatcggagg 166488
```

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

```
Query: 32      ggtgtgcggacggactctaaacaccgacagctggcgcgccaggtagggggtgtgtctttg 91
              ||||| |||| | ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 164744 ggtgtgcggtcgacccaaaacaccgacagctggcgcgccaggtagggggtgtgtcgacg 164803
```

Query: 92 atctgagctagctcaatgaccattacctccaaatgcaagatcgcccttcgccccgggact 151
||| ||||| ||| ||| | ||||| ||| ||| ||| |||
Sbjct: 164804 atccaagctagctcaatggccgtcaccttcacagcaagatcgccgtcggtcccggatct 164863

```
Query: 152      atgttttgctttggaaccatctcatccatagcagatgaagagggaactctgcaccgcata 211
               | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct: 164864  gtattctgcttcgggacaatctcatctgtagcggatgaagagggaattctacaccgcctc 164923
```

Query: 212 gcagatct 219

|||||||
Sbjct: 164924 gcagatct 164931

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

Query: 794 gagcaagccgagcaaggtgcaaggctgcgccgagagaatgctctctttgctcggaacctg 853
|||||||
Sbjct: 165458 gagcaagccgagcaagatgcaaggcaacgacgcgagaatccgctcttcgggcgcaacctg 165517

Query: 854 taccccgacttcgctcgtgcaatgaacacgccgagtgaaagtcggaggggtactggcccag 913
|||||||
Sbjct: 165518 aaccccgacttcgcccagctatgaacacgccgagcgaagtcggaggcgttctagctcgg 165577

Query: 914 atagctgacgg 924
|||||||
Sbjct: 165578 atagctgacgg 165588

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Minus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
||||
Sbjct: 187569 aaacgccgacagttggcgcgccaggtagggg 187539

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

Score = 180 bits (91), Expect = 2e-41
Identities = 454/571 (79%), Gaps = 3/571 (0%)
Strand = Plus / Minus

Query: 1252 ccgacatgaagacacgtgcggagtcttcgcacttactccgtgtctccgggccatccagtg 1311
|||||
Sbjct: 109879 ccgacaggaagacacgtgtggagtatctgcgctcactccgtgtctcagggccattcaatg 109820

Query: 1312 gcccctaa-cttcaaggtctccaacgtcagcaagtatgagcgcgaagcaggacctgggtgg 1370
||||| || ||||||||||||||||||||| || | ||| ||||||||| ||| ||
Sbjct: 109819 gcccccaaacttcaaggtctccaacgtcaacaaatacagcctaagcaggacccgggagg 109760

Query: 1371 ctggttagccatctacacgattgtcacatgggcccggagcgacggaggacgtgatgac 1430
||||| ||| ||||| || | | | | ||| | ||| || | ||| |||||||
Sbjct: 109759 ctggttggccgtctatacaaccgctgccccggccactggggcaactaaagatgtgatgac 109700

Query: 1431 agtgtattttccattgtcctagggcaagacgcaatgcagtggctccgacatctacccca 1490
||||||| ||||| ||||| ||||||||| || | | ||||| ||||||||| ||
Sbjct: 109699 tgtgtatttacctcatccttgggcaagacacatttcaatggctacgacatctaccgca 109640

Query: 1491 acattgcatagacaattggagcgacttcagttggtgcttcacgccaacttccagtcct 1550
|| ||||| || ||||||| ||||||||| | || ||||||||| |||||
Sbjct: 109639 gcactgcattgatgattggagtgacttcagtcgacatttt-tcgccaacttccaatccct 109581

Query: 1551 ctttgacaagccggcgcagccatgggacctaaaatccattgggcatcaggcgatgaaac 1610
|| ||||||| || ||||| ||||||||| ||||||||| ||||| | || ||||| ||
Sbjct: 109580 ctccgacaagccagcatagccgtgggacctcaaatccatcaggcaccgaggggatgagac 109521

Query: 1611 gtcctcggttgtagctcaagaggtttttagaccatgaggaaccacacccccgaagtgcgcca 1670
|| ||||| ||||||||| ||||||| ||||||||| || | || ||||| | | ||
Sbjct: 109520 tcttcggtcgtacctcaagtggtttcagaccatgagaaatcgcatctccgaggccactga 109461

Query: 1671 ggcgggggtgattgaagacttctaccgaggatccaatgactcggctttcgtccgagccat 1730
|| | ||||| || ||||||||| ||||||||| ||||| |||||||||
Sbjct: 109460 agcagcagtgatcgaggacttctaccgggatccaatgactcggccttcatccgagccat 109401

Query: 1731 actccagaaaagcgtcggccacctccgaacacttgttccgggaggcagacctctacatca 1790
||| || ||| || || ||||| ||||| || ||||| ||||||| |||||||||
Sbjct: 109400 actaca-aaaggcaccgaccacttccgagcagctgttcagggaggcggacctctacatca 109342

Query: 1791 ccacggattaacgggccaggacctcatcgg 1821
|| |||| ||||||| ||||||||| |||||
Sbjct: 109341 ccgcggacgaacgggctcaggacctcatcgg 109311

Score = 113 bits (57), Expect = 4e-21
Identities = 191/233 (81%), Gaps = 2/233 (0%)

Strand = Plus / Plus

Query: 2 taccctaaagcaccgcaagggtagccctgggtgtgcggacggactctaacaccgacag 61
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 94160 taccctaaagcactgcgaggggtaaccccggtgcgcggtcgggtcctaacaccgacag 94219

Query: 62 ctggcgcgccaggtaggggtgtgtctttgatctgagctagctcaatgaccatta-cctc 120
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 94220 ctggcgcgctaggtaggggtgtgtcgtgatccaagctagctcaatggccatcattctc 94279

Query: 121 caaatgcaagatcgcccttcgccccgggactatgttttgctttggaaccatctcatccat 180
 || || ||||| || || ||||| || || ||||| || || || ||||| |||||
Sbjct: 94280 c-aacacaagattgctctccgccctggatctgtgttctggttcgggaccatctcgtccat 94338

Query: 181 agcagatgaagaggaactctgcaccgcatagcagatctattggagaagaagc 233
 ||||| ||||| ||||| ||||| || ||||| ||||| || ||||| |||||
Sbjct: 94339 ggacagacgaagaaggaattctgcatcgtatagcgatccatcggaagaagaagc 94391

Score = 91.7 bits (46), Expect = 1e-14
Identities = 103/122 (84%)
Strand = Plus / Minus

Query: 947 gaaggctaccggcggtgtcttactcgagcagttaatcaccttctaccatcactaatcct 1006
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 110184 gaaggctatcgggcggtgtcactcgggcatctaatacatcttctaccctcgtcatccc 110125

Query: 1007 ccaagcgacctagccatgccatcaacagccggcgagacacgcggagctccatcaacgct 1066
 || ||||| ||||| || ||||| ||||| || || ||||| ||||| ||||| |||||
Sbjct: 110124 ccgagcgatctacgacagccatcaacagttggtgggacacgcagagctccatcaacgct 110065

Query: 1067 tc 1068
 ||
Sbjct: 110064 tc 110063

Score = 69.9 bits (35), Expect = 5e-08
Identities = 140/175 (80%)
Strand = Plus / Plus

Query: 504 ctcctttctaccccgacgtcctctttcatcagggggagattggagtttagcaccgcttca 563
||||| ||||| ||||| ||| || ||||| | | ||| |||
Sbjct: 94650 ctcctttctaccctgacgtccttttcatcgagggaagagtggagtcattctccatctccg 94709

Query: 564 acgatgagccaacatgcaaggggaagagcctcccagcgtgaggcgcgacgacggagga 623
| ||||| ||||| ||||| ||||| ||| ||| ||| |||||
Sbjct: 94710 atgatgagccaacatgcctggggaagaacctcctcagcgagaagctcgccgatggagga 94769

Query: 624 atagaagccagaacgtgcggcgacatcacgaggtggggaacgggatccggcgca 678
| | ||| || | ||||| ||||| || ||||| ||||| |||||
Sbjct: 94770 accaacgccgaaatattcggcgacatcacgaagcaggggaacgggactcggcgca 94824

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
|||| ||||| ||||| ||||| |||||
Sbjct: 67172 aaacgccgacagttggcgcgccaggtagggg 67202

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
|||| ||||| ||||| ||||| |||||
Sbjct: 131516 aaacgccgacagttggcgcgccaggtagggg 131546

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

Score = 178 bits (90), Expect = 8e-41
Identities = 325/402 (80%), Gaps = 1/402 (0%)
Strand = Plus / Plus

Query: 1423 gtgatgacagtgtattttccattgtcctagggcaagacgcaatgcagtggctccgacat 1482
||||| ||||| ||||| ||||| ||||| ||| ||| ||||| |||||
Sbjct: 179623 gtgatgactgtgtatttgccatcgtccttgggcaggatgcgctgcaatggctacgacac 179682

Query: 1483 ctaccccaacattgcatagacaattggagcgacttcagttggtgcttcacgccaacttc 1542
|| || | ||| |||| ||| |||||||||||||||| || || ||||||||||||
Sbjct: 179683 ctgcctcgacactgcatcgacgattggagcgacttcagtcggcattttatcgccaacttc 179742

Query: 1543 cagtcacctctttgacaagccggcgagccatgggacctaataatccattgggcatcagggc 1602
|| ||||||| |||||||||||||||||| |||| ||||||| | | | ||
Sbjct: 179743 caatccctctccgacaagccggcgagccatgagacctcaatccatcagacgccgaggg 179802

Query: 1603 gatgaaacgctccggttgtaacctcaagaggttttagaccatgaggaaccacacccccgaa 1662
||||| || ||||||| ||||||| |||||||||||||||| | | | |||||||
Sbjct: 179803 gatgagactctccggtcataacctcaaaaggttttagaccatgagacatcgatatccccgag 179862

Query: 1663 gtgcgccgaggcggggtgattgaagacttctaccgaggatccaatgactcggctttcgtc 1722
|| || || || | |||||| |||||||||||||||| |||| |||||||||||| ||| ||
Sbjct: 179863 gttgcggaagcagcggtgatcgaagacttctaccgggatctaatactcgcccttcac 179922

Query: 1723 cgagccatactccagaaaagcgctcgccacctccgaacacttggtccgggaggcagacct 1782
|||||||||| || ||| | | || | |||||||| || | ||| ||||| ||||||||
Sbjct: 179923 cgagccatactgca-aaaggtgccgacaacctccgagcagctattcaggaagcagacct 179981

Query: 1783 ctacatcaccacggattaacgggccagacctcatcgagg 1824
|||||||||| || |||||||| || ||||||||||||
Sbjct: 179982 ctacatcaccggcgacgaacgggctcagaacctcatcgagg 180023

Score = 113 bits (57), Expect = 4e-21
Identities = 141/169 (83%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgccaggtaggggtgtgtctttgatctgagctagctcaatg 109
|||||||||||||||| |||||||||||||||||| ||||| ||||||||||||
Sbjct: 178334 aaacaccgacagctggcgccaggtaggggtgtgtcactgatccaagctagctcaatg 178393

Query: 110 accattacctccaaatgcaagatcgcccttcgccccgggactatgttttgctttggaacc 169
||| || | | | |||||||| || |||| | || |||| ||||| |||||
Sbjct: 178394 gccatcactttccagcacaagatcgctctccgccctagatctgtgttctgcttcagaacc 178453

Query: 170 atctcatccatagcagatgaagagggaactctgcaccgcatagcagatc 218

|||||
Sbjct: 178454 atctcatccatggcagatgaagaaggaactctacatcgcatagcggatc 178502

Score = 85.7 bits (43), Expect = 9e-13
Identities = 119/143 (83%), Gaps = 1/143 (0%)
Strand = Plus / Plus

Query: 1222 ctccccctccttgggaccgacctcacgaacgccgacatgaagacacgtgcggagtcttcgc 1281
|||||
Sbjct: 179472 ctccccctccccgggaccgacaccacaaccgtcgacaggaagacacgtgtggagtatcggc 179531

Query: 1282 acttactccgtgtctccgggccatccagtgg-cccctaacttcaaggtctccaacgtcag 1340
|||||
Sbjct: 179532 gcttactccacgtctcagggccatccagtggccccctaacttcaaggtctctaacatcga 179591

Query: 1341 caagtatgagcgcaagcaggacc 1363
|||||
Sbjct: 179592 caagtacgagcctaagcaggacc 179614

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

Query: 509 ttctaccccgacgtcctcttcatcagggggagattgga 546
|||||
Sbjct: 178772 ttctaccccgacgtcctctttatcggggggagagtgga 178809

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

Query: 55 ccgacagctggcgcgccaggtagggg 80
|||||
Sbjct: 56887 ccgacagttggcgcgccaggtagggg 56912

>gb|EF190062.1| Zea mays clone FS2_20 chromosome B, genomic sequence
Length = 39210

Score = 176 bits (89), Expect = 3e-40
Identities = 450/569 (79%), Gaps = 1/569 (0%)
Strand = Plus / Minus

Query: 1262 gacacgtgcggagtcttcgcacttactccgtgtctccggccatccagtggcccctaact 1321
||||||| ||||| || || ||||| ||||| ||||| ||||| |||||
Sbjct: 8187 gacacgtgtggagtattggcgcttactccacgtcttagggccattcagtggcccctaact 8128

Query: 1322 tcaaggtctccaacgtcagcaagtatgagcgcaagcaggacctgggtggctggttagcca 1381
||||||| ||||| || ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 8127 tcaaggtctccaacatcgacaagtacgagcccaagcagaacccgggaggctggttgctg 8068

Query: 1382 tctacacgattgtcacatgggccgccggagcgacggaggacgtgatgacagtgtattttc 1441
|||| | | || | ||||| || || || || || ||||| | |||||
Sbjct: 8067 tctataccactgctgcctgggccgctggggcaactgaagatttgatgactgcgtatttgc 8008

Query: 1442 ccattgtcctagggcaagacgcaatgcagtggctccgacatctacccaacattgcatag 1501
|||| ||||| ||||| || ||||| ||||| ||||| ||||| |||||
Sbjct: 8007 ccatcgctcctaagcaagatgcgctgcaatggctacgacacctgccccgacactacatcg 7948

Query: 1502 acaattggagcgacttcagttggtgcttcacgccaacttccagtcacctctttgacaagc 1561
|| ||||| ||||| || || ||||| ||||| ||||| |||||
Sbjct: 7947 acgattggagcgatttcagtcgatgttttatcgccaacttccaatccctctccgacaagc 7888

Query: 1562 cggcgcagccatgggacctaaaatccattgggcatcaggcgatgaaacgctccggttgt 1621
||||||| ||||| ||||| ||||| || || || ||||| ||||| |||||
Sbjct: 7887 cggcgcaaccatgggacctcaatccatcaggcgccgaggggatgaaactcacggtcat 7828

Query: 1622 acctcaagaggttttagaccatgaggaaccacacccccgaagtcgccgaggcgggggtga 1681
||||||| || |||| | |||| |||| || || ||||| || || || || |||||
Sbjct: 7827 acctcaaaagatttcaaaccttgagaaatcatatccccgaggttgctgaagcagcgatga 7768

Query: 1682 ttgaagacttctaccgaggatccaatgactcggtttcgtccgagccatactccagaaaa 1741
| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 7767 tcgaggacttctaccgggatctaatactcgcccttcgtccgagccatactgca-aaag 7709

Query: 1742 gcgtcggccacctccgaacacttggtccgggaggcagacctctacatcaccacggattaa 1801
||| | | ||||| || | |||| |||| | ||||| ||||| |||||
Sbjct: 7708 gcgccaactacctccgagcagctattcagggaagcgaacctctacatcaccgccgacgaa 7649

Query: 1802 cgggccaggacatcatcgaggcacgaa 1830
|||| |||||||||| |||| ||||
Sbjct: 7648 tgggctcaggacctattggaggaacgaa 7620

Score = 119 bits (60), Expect = 6e-23
Identities = 174/212 (82%)
Strand = Plus / Minus

Query: 7 aaaagcacgcgaagggtagccctgggtgtgcggacggactctaaacaccgacagctggc 66
||||||| | ||||| | || ||||||||| |||| | |||||||||||||
Sbjct: 9408 aaaagcacctcgaggggaaccccggtgtgcggtcggacccaaacaccgacagctggt 9349

Query: 67 gcgccaggtaggggtgtgtctttgatctgagctagctcaatgaccattacctccaaatg 126
|||||||||||||||||| |||| |||||||||||| || || || ||
Sbjct: 9348 gcgccaggtaggggtgtgtcactgatccaagctagctcaatggccgtcactttccagca 9289

Query: 127 caagatcgcccttcgccccgggactatgttttgctttggaaccatctcatccatagcaga 186
||||||| || ||||| || | |||| ||||||||||||||||||| |||||
Sbjct: 9288 caagatcgctctccgccctggatcgtgttctgctttggaaccatctcatccgtggcaga 9229

Query: 187 tgaagagggaactctgcaccgcatagcagatc 218
||||| |||||||| || ||||||| ||||
Sbjct: 9228 cgaagaaggaaactctacattgcatagcggatc 9197

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

Query: 848 aacctgtaccccgacttcgctcgtgcaatgaacacgccgagtgaagtcggaggggtactg 907
||||| | |||||||||||| || ||||||| |||| | || | || ||
Sbjct: 8600 aacctgaatcccgacttcgctcgagccatgaacacaccgagcgaggttgatggagtgtg 8541

Query: 908 gccagatagctgacggcctcccggaaccctagacacggaaggetaccggcggtgctt 967
|| | ||||| || ||||||| || || ||||| | || ||||| || |||||
Sbjct: 8540 gtcgcatagccgatggcctccccggactctagacgccgagggtatcggtggctgctc 8481

Query: 968 actcgagcagtttaatcaccttctacccatcactaatcctccaagcgacctacgccatgcc 1027
||||| |||| ||| || ||||| || | || ||||| ||||| |||| || |||
Sbjct: 8480 actcgggcagctaaccatcttctgcctcccgtcatcctccgagcgatctacaacacgcc 8421

Query: 1028 atcaacagccggcgagacacgcggagctccatcaacgcttcgcgcgaccgatga 1081
||||| || || || ||| || | ||||| ||||| ||||| ||||| |||||
Sbjct: 8420 atcaatagtcgacgggacgcacagagctccatcaatgcttcgcgcgaacgatga 8367

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

Score = 174 bits (88), Expect = 1e-39
Identities = 305/376 (81%), Gaps = 1/376 (0%)
Strand = Plus / Minus

Query: 1417 gaggacgtgatgacagtgtattttccattgtcctagggcaagacgcaatgcagtggctc 1476
||||||| ||||| ||||| || || || ||||| ||||| ||||| ||||| |||||
Sbjct: 91274 gaggacgtaatgaccgtgtacttgcctatcgtcctcgggcaagacgcgctgcaatggctg 91215

Query: 1477 cgacatctaccccaacattgcatagacaattggagcgacttcagttggtgcttcacgcc 1536
||||| ||||| || | ||||| ||| | ||||| ||||| || ||||| |||||
Sbjct: 91214 cgacacctaccctgagactgcacgcactggagccacttcagtcggcgcttcaccgcc 91155

Query: 1537 aacttccagtcctcttttgacaagccggcgcgacccatgggacctaaaatccattgggcat 1596
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 91154 aactttcagtctctctccgacaaaccggcgcaaccatgggacctcaaatccatcaagcgt 91095

Query: 1597 cagggcgatgaaacgctccggttgctacctaagaggttttagacatgaggaaccacacc 1656
| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 91094 cgggggatgaaactctccggtcatacctcaaaaggttcagacctgagaaatcatatc 91035

Query: 1657 cccgaagtcgcgcgaggcgggggtgattgaagacttctaccgaggatccaatgactcggct 1716
||||| ||||| || ||||| ||||| || ||||| ||||| ||||| ||||| |||||
Sbjct: 91034 cccgaggtcgcagatgcggcagtgatcgaggacttctacagaggatccaatgactcgacc 90975

Query: 1717 ttcgtccgagccatactccagaaaagcgctcgccacctccgaacacttggtccgggaggc 1776
|| ||||| ||||| || || ||| || || || ||||| || || ||||| |||||
Sbjct: 90974 tttgtccgaacctattaca-aaaggtgccgactacctccgagcaactgttccgggaagc 90916

Query: 1777 agacctctacatcacc 1792

|||||
Sbjct: 90915 cgacctctacatcacc 90900

Score = 101 bits (51), Expect = 1e-17
Identities = 192/239 (80%)
Strand = Plus / Minus

Query: 848 aacctgtaccccgacttcgctcgtgcaatgaacacgccgagtgaagtcggaggggtactg 907
||||| ||||||| || || ||||||| ||||||| ||||||| ||
Sbjct: 91844 aacctgaaccccgacttcgcccagccatgaacacgccgagtgaagttggaggggtgttg 91785

Query: 908 gccagatagctgacggcctcccggaaccctagacacggaaggctaccggcggctgctt 967
|| | || | || ||||||| || || | ||||| || || ||||||| |
Sbjct: 91784 gctcggtatgatgatggcctccctcggactcccgacaccgaggggtatcggcggctattc 91725

Query: 968 actcgagcagttaatcaccttctacccatcactaatcctccaagcgacctacgccatgcc 1027
|||| |||| | ||||||| || || | || | || || || || ||
Sbjct: 91724 actcaagcagccaatcaccttctaccctcgtcaccgccgaacgatctatgacacacc 91665

Query: 1028 atcaacagccggcgagacacgcggagctccatcaacgcttcgcgcgaccgatgacacga 1086
||||||| || |||||| | ||||||| || || |||| | || || |||||
Sbjct: 91664 atcaacagtcgccgagacgcgcggagctccatcaatgcctcgcgtgaacgacgacacga 91606

Score = 93.7 bits (47), Expect = 4e-15
Identities = 89/103 (86%)
Strand = Plus / Minus

Query: 7 aaaagcacccgaaggggtagccctgggtgtgcggacggactctaaacaccgacagctggc 66
||||||| | |||||| | |||||| | || |||| | ||||| |||||||
Sbjct: 102107 aaaagcacctcgggggtaaccctgggtgcgcggtcggacccgaaacactgacagctggc 102048

Query: 67 gcgccaggtaggggtgtgtctttgatctgagctagctcaatg 109
||||||| ||||||| || || | ||||||| |||||
Sbjct: 102047 gcgccaggtaggggtgtgtcatcgacccaagctagctcaatg 102005

Score = 50.1 bits (25), Expect = 0.048
Identities = 28/29 (96%)

Strand = Plus / Minus

Query: 503 gtccttttctaccccgacgtccttctcat 531
||||| ||||||||||||||||||||
Sbjct: 92174 gtcctattctaccccgacgtccttctcat 92146

Score = 48.1 bits (24), Expect = 0.19
Identities = 45/52 (86%)
Strand = Plus / Minus

Query: 645 gacatcacgaggctggggaacgggatccggcgcaaccgtatcccgggacga 696
||||| |||||| |||| | |||||| |||| | ||||
Sbjct: 92035 gacatcacgaggccggggagcgggaccagcgcaaccatattcacgagacga 91984

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
|||| |||||| ||||||||||||||||
Sbjct: 110714 aaacgccgacagtggcgcgccaggtagggg 110744

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

Score = 174 bits (88), Expect = 1e-39
Identities = 305/376 (81%), Gaps = 1/376 (0%)
Strand = Plus / Plus

Query: 1417 gaggacgtgatgacagtgtattttccattgtcctagggcaagacgcaatgcagtggctc 1476
|||||| |||| |||| | || | |||| |||||||| |||| ||||
Sbjct: 57608 gaggacgtaatgaccgtgtacttgccatcgtcctcgggcaagacgcgctgcaatggctg 57667

Query: 1477 cgacatctacccaacattgcatagacaattggagcgacttcagttggtgcttcacgcgc 1536
||||| |||||| | | |||| || | |||||| |||||||| || |||||| ||||
Sbjct: 57668 cgacacctaccctgagactgcatcgacgactggagccacttcagtcggcgcttcaccgcc 57727

Query: 1537 aacttcagtcctcttttgacaagccggcgagccatgggacctaaaatccattgggcat 1596

Query: 1028 atcaacagccggcgagacacgcggagctccatcaacgcttcgcgcgaccgatgacacga 1086
 ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Sbjct: 57218 atcaacagtgcggagacgcgcggagctccatcaatgcctcgctgaacgacgacacga 57276

Score = 93.7 bits (47), Expect = 4e-15
Identities = 89/103 (86%)
Strand = Plus / Plus

Query: 7 aaaagcaccgcaaggggtagccctgggtgtgcggacggactctaaacaccgacagctggc 66
 ||||| ||| ||||| ||||| ||| ||| ||| ||||| ||||| |||||
Sbjct: 46775 aaaagcacctcgggggtaaccctgggtgcgcggtcggacccgaaacactgacagctggc 46834

Query: 67 gcgccaggtaggggtgtgtctttgatctgagctagctcaatg 109
 ||||| ||||| ||||| ||| ||| ||| ||||| ||||| |||||
Sbjct: 46835 gcgccaggtaggggtgtgtcatcgacccaagctagctcaatg 46877

Score = 50.1 bits (25), Expect = 0.048
Identities = 28/29 (96%)
Strand = Plus / Plus

Query: 503 gctcctttctaccccgacgtcctcttcat 531
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 56708 gctccattctaccccgacgtcctcttcat 56736

Score = 48.1 bits (24), Expect = 0.19
Identities = 45/52 (86%)
Strand = Plus / Plus

Query: 645 gacatcacgaggctggggaacgggatccggcgcaaccgtatcccgggacga 696
 ||||| ||||| ||||| ||| ||||| ||||| ||||| |||||
Sbjct: 56847 gacatcacgaggccggggagcgggaccagcgcaaccatatacacgagacga 56898

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Minus

Query: 50 aaacaccgacagctggcgccaggtagggg 80
 |||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 38168 aaacgccgacagttggcgccaggtagggg 38138

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

Score = 170 bits (86), Expect = 2e-38
Identities = 288/354 (81%), Gaps = 1/354 (0%)
Strand = Plus / Plus

Query: 1471 tggctccgacatctaccccaacattgcatagacaattggagcgacttcagttggtgcttc 1530
||||| ||||| ||||| || ||||| ||| | ||||| ||||| ||||| |||||
Sbjct: 153054 tggctacgacacctaccccgacctgcatcgacgactggagcgacttcagtcggtgcttc 153113

Query: 1531 atcgccaacttccagtcacctctttgacaagccggcgagccatgggacctaaaatccatt 1590
| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 153114 accgccaacttccaatccctctccgacaagccggcgagccatgggacctcaaatccatc 153173

Query: 1591 gggcatcagggcgatgaaacgctccggttgctacctaagaggttttagaccatgaggaac 1650
|| || || ||||| || ||||| ||||| || || || || || |||||
Sbjct: 153174 aagcgccaaggggatgagactctccggtcgtacctaagagatttcagacaatgaggaat 153233

Query: 1651 cacacccccgaagtcgccgaggcggggtgattgaagacttctaccgaggatccaatgac 1710
| | ||||| |||| || || | ||||| || ||||| ||||| ||||| |||||
Sbjct: 153234 cgaatccccgaggtcgtggaagcatcgatgatcgaggacttctaccgggatccaatgac 153293

Query: 1711 tcggctttcgtccgagccatactccagaaaagcgtcggccacctccgaacacttgttccg 1770
||||| ||||| ||||| ||||| ||||| || || | ||||| || || |||||
Sbjct: 153294 tcggccttcgtccgagccatactcgagaaga-cgccatctacctccgagcagctgttccg 153352

Query: 1771 ggaggcagacctctacatcaccacggattaacggggccaggacctcatcgagg 1824
||| || ||||| |||| || || || || || || || || || ||||| |||||
Sbjct: 153353 ggaagccgacctctacaacactactgatgaacgagctcaagacctcattggagg 153406

Score = 81.8 bits (41), Expect = 1e-11
Identities = 152/189 (80%)
Strand = Plus / Plus

Query: 31 ggggtgtgcggacggactctaaacaccgacagctggcgccaggtagggggtgtgtcttt 90
||||| ||||| ||||| | ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 151640 ggggtgcggtcggacccaaaacaccgacagttggcgccaggtagggggtgtgtcact 151699

```
Query: 91      gatctgagctagctcaatgaccattacctccaaatgcaagatcgcccttcgccccgggac 150
              |||  ||||  ||||  ||  ||  ||  ||  ||  ||||  ||  ||||  ||  |
Sbjct: 151700 gatccaagctagatcaatggccgtcacatttcagcacagaatcttctctgccccaggtc 151759
```

```

Query: 211      agcagatct 219
           || |||||
Sbjct: 151820   cgcgatct 151828

```

Query: 812 gcaaggctgcgccgagagaatgctctctttgctcggaacctgtaccccgacttcgctcgt 871
 ||||| ||||| ||||| ||| | ||||| ||||| ||||| ||
 Sbjct: 152394 gcaaggcaacgccgagagaatcctcttctcgggcggaacctaaaccccgacttcgcccg 152453

Query: 932 cgaaccctagacacggaaggctaccggcggtgcttactcgagcagttaatcaccttct 990
 ||||| | |||| | ||||| ||||| ||||| ||||| ||||| |||||
 Sbjct: 152514 cgaactccagacgtgaaggctatcgggcggtgctcactcgggcagetaaccatcttct 152572

```
Query: 504      ctcctttctaccccgacgtcctcttcatcagg 535
               |||| |||||||||||||||||||||
Sbjct: 152101  ctccattctaccccgacgtcctcttcatcagg 152132
```

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
|||| |||||| |||||||||
Sbjct: 14604 aaacgccgacagttggcgcgccaggtagggg 14634

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
|||| |||||| |||||||||
Sbjct: 134363 aaacgccgacagttggcgcgccaggtagggg 134393

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
|||| |||||| |||||||||
Sbjct: 135467 aaacgccgacagttggcgcgccaggtagggg 135497

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

Score = 165 bits (83), Expect = 1e-36
Identities = 314/390 (80%), Gaps = 2/390 (0%)
Strand = Plus / Plus

Query: 1441 cccattgtcctagggcaagacgcaatgcagtggctccgacatctacccaacattgcata 1500
||||||| ||||||| || ||| ||| ||||| ||||| || |||||
Sbjct: 150396 cccattgtcctcgggcaagatgcactgcaatggctacgacacctacccggcactgcatac 150455

Query: 1501 gacaattggagcgacttcagttggtgcttcacgcgcaacttcagtcacctctttgacaag 1560
||| ||||||||| ||||||| || ||||||| ||||| ||||||| |||||
Sbjct: 150456 gacgattggagcgatttcagttggcattttatcgccaaattccaatccctctccgacaag 150515

Query: 1561 ccggcgcagccatgggacctaataatccattgggcatcaggcgcatgaaacgctccggttg 1620
|| ||||| || || || ||||| | | | ||||| || || |||||
Sbjct: 150516 ccagcgcagccgtgagatctccgatccattagacgccgaggggatgagactcttcggtca 150575

Query: 1621 tacctcaagaggttttagaccatgaggaaccacacccccgaagtcgccgaggcgggggtg 1680
||||| ||||| || ||||| || || | ||||| ||||| || || | |||
Sbjct: 150576 tacctcaagaggtttcaggccatgagaaatcatattcccagagtcgctgaagcagcagt 150635

Query: 1681 attgaagacttctaccgaggatccaatgactcggctttcgtccgagccatactccagaaa 1740
|| || ||||| ||||| ||||| || ||||| ||||| ||||| || || ||
Sbjct: 150636 atcgatgacttctaccgggatccaatgacttagccttcgtccgagccatactaca--aa 150693

Query: 1741 agcgtcggccacctccgaacacttgttcgggaggcagacctctacatcaccacggatta 1800
||| || |||| |||| || ||||| ||||| ||||| ||||| || || |
Sbjct: 150694 ggcgccgaccacttccgagcagctgttcaaggaggcagacctctacatcaccaccgacaa 150753

Query: 1801 acgggccaggacctcatcggaggcacgaa 1830
||||| ||||| ||||| || |||||
Sbjct: 150754 acgggctcaggacctcatcgggggaacgaa 150783

Score = 103 bits (52), Expect = 4e-18
Identities = 163/200 (81%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgcgccaggtaggggtgtgtctttgatctgagctagctcaatg 109
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 149027 aaacaccgacagctggcgcgccaggtaggggtgtgtcgtgatccaagttagctcaatg 149086

Query: 110 accattacctccaaatgcaagatcgcccttcgccccgggactatgttttgctttggaacc 169
||||| || | | || ||||| || || ||||| || | ||||| ||||| |||||
Sbjct: 149087 accatcactttccaacacaagattgctctccgccctggatccgtgttcttctttgggacc 149146

Query: 170 atctcatccatagcagatgaagagggaactctgcaccgcatagcagatctattggagaag 229
||||||| | ||||| ||||| ||||| || || | ||||| ||||| | |||||
Sbjct: 149147 atctcatccgtggcagacgaagaaggaattctacatcatatagcggatccaccggagaag 149206

Query: 230 aagctttcctcagaaatctc 249
||||| ||||| ||||| |||||

Sbjct: 149207 aagccttcctcaaaaatctc 149226

Score = 85.7 bits (43), Expect = 9e-13
Identities = 106/127 (83%)
Strand = Plus / Plus

Query: 948 aaggctaccggcggtgcttactcgagcagttaatcaccttctacccatcactaatcctc 1007
||||| ||| ||||| ||||| || ||||| ||||| || |||||
Sbjct: 149902 aaggctatcggtggctgctcactcgggcgactaatcatcttctacctctcgctcactc 149961

Query: 1008 caagcgacctacgccatgccatcaacagccggcgagacacgaggagctccatcaacgctt 1067
| |||| |||| | ||||||||| |||| | || |||||||||||||
Sbjct: 149962 cgagcgatctacggcacgccatcaacagtcggcgggacgcgagagctccatcaacgctt 150021

Query: 1068 cgcgca 1074
| ||||
Sbjct: 150022 cacgca 150028

Score = 50.1 bits (25), Expect = 0.048
Identities = 97/121 (80%)
Strand = Plus / Plus

Query: 504 ctcttttctaccccgagctcctcttcatcagggggagattggagttagcaccgtcttca 563
|||| ||||||||||||||||||| |||| || |||| | | || ||||
Sbjct: 149470 ctccattctaccccgagctcctcttattgggggaagagtggaatcatctccatctcgg 149529

Query: 564 acgatgagccaaccatgcaaggggaagagcctccccagcgtgaggcgcgacgacggagga 623
|||| ||||||||| ||| |||||||| | || ||| | || || |||||
Sbjct: 149530 acgacgagccaaccgtgcctggggaagaaccccctcagtgagaagctcgccgacggagga 149589

Query: 624 a 624
|
Sbjct: 149590 a 149590

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Minus

Query: 50 aaacaccgacagctggcgccaggtagggg 80
|||| |||||| |||||||||
Sbjct: 43416 aaacgccgacagttggcgccaggtagggg 43386

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

Score = 159 bits (80), Expect = 7e-35
Identities = 360/452 (79%), Gaps = 1/452 (0%)
Strand = Plus / Plus

Query: 1283 cttactccgtgtctccgggcatccagtggcccc-taacttcaaggtctccaacgtcagc 1341
||||||| ||||| ||||||||| ||||||||| ||||||||| || ||
Sbjct: 7181 cttactccatgtcttagggcatccagtggccccgtaacttcaaggtctccaacatcgac 7240

Query: 1342 aagtatgagcgcaagcaggacctgggtggctggttagccatctacacgattgtcacatgg 1401
||||| |||| ||||||||| || || ||||||||| || ||||| || || || || ||
Sbjct: 7241 aagtacgagcccaagcaggatctaggaggctggttggctgtctataccactgctgcctcg 7300

Query: 1402 gccgccggagcgacaggagacgtgatgacagtgtattttccattgtcctagggaagac 1461
||||| || || || || || || ||||| || || ||||| ||||| ||||| |||||||
Sbjct: 7301 gccgctggggcaactgaagatgtgattactgcataatttggccatcgtccttaggcaagat 7360

Query: 1462 gcaatgcagtggctccgacatctaccccaacattgcatagacaattggagcgacttcagt 1521
| ||||| ||||| ||||| || ||||| || || || || ||||| || || ||
Sbjct: 7361 gtgttgcaatggctacgacacctgccccgacacttcacgactattggagcgattttagt 7420

Query: 1522 tggtgcttcacgccaacttccagtcacctctttgacaagccggcgagccatgggacctc 1581
|| || || ||||||||| ||||| ||||||||| ||||||||| |||||||||
Sbjct: 7421 cggcgttttatcgccaacttccaatccctctccgacaagccggcgcaaccatgggacctc 7480

Query: 1582 aaatccattgggcatcagggcgatgaaacgctccggtgtacctcaagaggttttagacc 1641
||||||| || || || ||||||||| ||||||| ||||||| || || |||||
Sbjct: 7481 aaatccatcacgcgccgaggggatgaaactctccggtcatacctcaaaggatttcagacc 7540

Query: 1642 atgaggaaccacacccccgaagtgcgccaggcggggtgattgaagacttctaccgagga 1701
||||| || | ||||||| || || || || || ||||| || ||||||||| ||
Sbjct: 7541 atgagaaatcgatccccgaggttgcggaagcagcggtgatcgaggacttctaccgggga 7600

Identities = 136/169 (80%)

[illegible]

Identities = 136/171 (79%)

Score = 46.1 bits (23), Expect = 0.76
Identities = 38/43 (88%)
Strand = Plus / Plus

Query: 504 ctcctttctaccccgacgtcctctttcatcaggggagattgga 546
||||| ||||||| ||||||| ||| ||||||| |||||
Sbjct: 6414 ctccgttctaccccgacgtcctctttatcgagggagagtga 6456

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

Score = 157 bits (79), Expect = 3e-34
Identities = 154/179 (86%)
Strand = Plus / Minus

Query: 1411 gcgacggaggacgtgatgacagtgtatttccattgtcctagggcaagacgcaatgcag 1470
||||| ||||||| ||||| | ||| || ||||||| ||||||| |||||
Sbjct: 54735 gcgaccgaggacgtaatgaccgcgtacttaccattgtcctcgggcaagacgtgctgcaa 54676

Query: 1471 tggctccgacatctacccaacattgcatagacaattggagcgacttcagttggtgcttc 1530
||||| ||||||| ||| ||| ||||| ||| | ||||||| ||||||| |||||||
Sbjct: 54675 tggctgcgacatctacctcgacactgcatcgacgactggagcgacttcagtcggtgcttc 54616

Query: 1531 atcgccaacttccagtcacctctttgacaagccggcgagccatgggacctaaaatccat 1589
| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Sbjct: 54615 accgccaactttcagtcacctctctgacaaaccggcgcaacctgggacctcaaatccat 54557

Score = 103 bits (52), Expect = 4e-18
Identities = 148/180 (82%)
Strand = Plus / Minus

Query: 31 ggggtgtgcggacggactctaaacaccgacagctggcgcgccaggtagggggtgtgtcttt 90
||||| ||||| ||||| | ||||| ||||||| ||||||| ||||||| |||||||
Sbjct: 56090 ggggtgcgcggtcggacccaaaacactgacagctggcgcgccaggtagggggtgtgtcatc 56031

Query: 91 gatctgagctagctcaatgaccattacctccaaatgcaagatcgcccttcgccccgggac 150
||||| ||||||| ||||||| ||||| | ||||||| | ||||| ||| |
Sbjct: 56030 gatccaagctagctcaatgaccgtcaccttctgcacaagatcgcccttcgcccctgggtc 55971

Query: 151 tatgttttgc ttttgaaccatctcatccatagcagatgaagaggggaactctgcaccgcat 210
 | || ||||| ||||||||||||| |||| || | ||||||||||||| |||||
Sbjct: 55970 cacattatgcttcggaaccatctcatctgtagcggataagaggggaactctgcatcgcat 55911

Score = 101 bits (51), Expect = 1e-17
Identities = 192/239 (80%)
Strand = Plus / Minus

Query: 848 aacctgtaccccgacttcgctcgtgcaatgaacacgccgagtgagtcggaggggtactg 907
 ||||| ||||||||||||| || || ||||||||||||||||||||||||||| |||
Sbjct: 55299 aacctgaaccccgacttcgcccagccatgaacacgccgagtgagtcggaggggtgctg 55240

Query: 908 gcccagatagctgacggcctcccgcaaccctagacacggaaggctaccggcggtgctt 967
 || | ||||||||| || ||||| || || | ||| | || ||||| || ||||| |
Sbjct: 55239 gctcggatagctgatgggtccctcggactcacgacgccgagggtatcgacggctgttc 55180

Query: 968 actcgagcagttaatcaccttctacccatcactaatcctccaagcgacctacgccatgcc 1027
 |||| ||||| ||||||||||||| || || | || || | || ||||| || ||
Sbjct: 55179 actcaggcagccaatcaccttctacctctcgctcaccgcggaacaatctacgacacacc 55120

Query: 1028 atcaacagccggcgagacacgcggagctccatcaacgcttcgcgcgaccgatgacacga 1086
 ||||||| || || ||| ||||||||||||||||| || ||||| || ||| ||||| |
Sbjct: 55119 atcaacagtcgtcgggacgcgcggagctccatcaatgcctcgcgtgaacgacgacacga 55061

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

Query: 509 ttctaccccgacgtcctcttcatc 532
 |||||||||||||||||
Sbjct: 55624 ttctaccccgacgtcctcttcatc 55601

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Minus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80

|||| |||||| |||||||||
Sbjct: 36120 aaacgccgacagttggcgccaggtagggg 36090

Score = 44.1 bits (22), Expect = 3.0
Identities = 46/54 (85%)
Strand = Plus / Minus

Query: 643 gcgacatcacgaggtggggaacgggatccggcgcaaccggtatcccgggacga 696
||||||| ||||| | ||| ||||||| || ||||| || |||||
Sbjct: 55492 gcgacatcacgagggccggggagcaggaccggcgcgagcctgtatcgcgagacga 55439

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

Score = 157 bits (79), Expect = 3e-34
Identities = 426/539 (79%), Gaps = 2/539 (0%)
Strand = Plus / Plus

Query: 1293 gtctccgggccatccagtggccct-aacttcaaggtctccaacgtcagcaagtatgagc 1351
||||| ||||||| ||||||||| ||||||||| ||||||||| ||||| |||
Sbjct: 3909 gtctcagggccattcagtggcccccaacttcaaggtctccaacgtcgacaagtacgaac 3968

Query: 1352 gcaagcaggacctgggtggctggttagccatctacacgattgtcacatgggccgccggag 1411
||||||| ||| ||||||| ||| ||||| || | | | ||||||| |||
Sbjct: 3969 ctaagcaggaccgggaggtggttgccgtctataaccacgctgcccgggccgctgggg 4028

Query: 1412 cgacggaggacgtgatgacagtgtattttccattgtcctagggaagacgcaatgcagt 1471
|| | || || ||||||| ||||||| ||||| ||||| ||||||| || |||||
Sbjct: 4029 caattgaagatgtgatgactatgtatttgcccatcgtccttgggcaagatgctctgcaat 4088

Query: 1472 ggctccgacatctaccccaacattgcatagacaattggagcgacttcagttggtgcttca 1531
|||| | ||||| || ||| ||| ||||| ||| ||||||||| ||||| || |||||
Sbjct: 4089 ggctacgacacctttcccgacactgcatcgacgattggagcgacttcagtcagcgtttta 4148

Query: 1532 tcgccaacttcagtcctctcttgacaagccggcgagccatgggacctaaatccattg 1591
||| ||||||| ||||| ||||||||| ||||||||| |||||||
Sbjct: 4149 tcgtcaacttcaacccctctccgacaagccggcacagccatgggacctcaaatccatca 4208

Query: 1592 ggcatcaggcgatgaaacgctccggtgtacctcaagaggttttagacctgaggaacc 1651

|||| | || ||||| || || |||| | ||||| ||||| ||||| ||||| ||
Sbjct: 4209 ggcaccgaggggatgagactcttcggtcatacctcaaaaggtttcagaccatgagaaatt 4268

Query: 1652 acacccccgaagtcgccgaggcgggggtgattgaagacttctaccgaggatccaatgact 1711
| ||||| || || || || | ||||| || ||||| ||||| ||||| ||||| ||

Sbjct: 4269 gtatccccgaggttcggaagcagcagtgatcgaggacttctaccgggatctaatactgact 4328

Query: 1712 cggttttcgtccgagccatactccagaaaagcgtcggccacctccgaacacttgttccgg 1771
|||| ||||| ||||| || || || || || || || || || || || || ||

Sbjct: 4329 cggtcttcgtccgagccatactgca-aaaggcaccgactacctctgagcagctattcagg 4387

Query: 1772 gagcagacctctacatcaccacggattaacgggccaggacctcatcgaggacacgaa 1830
|| || ||||| ||||| || || ||||| || || ||||| ||||| ||||| |||||

Sbjct: 4388 gaagcggacctctatatcaccaccgacaaacgggctcagaacctcatgggaggaacgaa 4446

Score = 103 bits (52), Expect = 4e-18
Identities = 154/188 (81%)
Strand = Plus / Plus

Query: 32 ggtgtgcggacggactctaaacaccgacagctggcgcgccaggtagggggtgtgtctttg 91
|||| |||| |||| | ||||| ||||| ||||| ||||| ||||| ||||| ||

Sbjct: 2672 ggtgcgcggtcggacccaaaacaccgacagctggcgccaccaggtagggggtgtgtcactg 2731

Query: 92 atctgagctagctcaatgaccattacctccaaatgcaagatcgcccttcgccccgggact 151
||| ||||| ||||| |||| || | | ||||| || |||| || ||

Sbjct: 2732 atccaagctagctcaatggccatcacttttcagcacaagatcgctctctgacctggatcc 2791

Query: 152 atgttttgctttggaacctctcatccatagcagatgaagagggaactctgcaccgcata 211
|||| | |||| | ||||| ||||| || |||| | |||| | |||| | |||| |

Sbjct: 2792 atgttctgcttcggaacctctcatccgtggcagacgaagaagggactctgcatcgcata 2851

Query: 212 gcagatct 219
|| |||||

Sbjct: 2852 gcggatct 2859

Score = 65.9 bits (33), Expect = 8e-07
Identities = 177/225 (78%)
Strand = Plus / Plus

Query: 848 aacctgtaccccgacttcgctcgtgcaatgaacacgccgagtgaagtcggaggggtactg 907
||||| ||||||||||||| || || ||||| || | ||| || ||||| || || ||
Sbjct: 3464 aacctgaaccccgacttcgcccagccatgaaaacactgagcgaggtcggaggagtgtg 3523

Query: 908 gcccgatagctgacggcctcccggaaccctagacacggaaggctaccggcggtgctt 967
||| ||||| || ||||||| || || | |||| | || ||||| || || ||||| ||
Sbjct: 3524 ccccgatagccgatggcctcccccggactccagacgccgagggtatcggtggctactc 3583

Query: 968 actcgagcagttaatcaccttctacccatcactaatcctccaagcgacctacgccatgcc 1027
||||| |||| ||| || ||||||| || | || ||||||| ||||| ||||| ||||| ||
Sbjct: 3584 actcgggcagctaaccatcttctgcctcttgctcatcctccgagcgatctacgacatgcc 3643

Query: 1028 atcaacagccggcgagacacgcggagctccatcaacgcttcgcgc 1072
||||| || || | ||| ||||||||||||||| |||||||||
Sbjct: 3644 atcaatagtcgatgggacgcgcggagctccatcaatgcttcgcgc 3688

Score = 54.0 bits (27), Expect = 0.003
Identities = 39/43 (90%)
Strand = Plus / Plus

Query: 504 ctcttttctaccccgacgtcctcttcatcagggggagattgga 546
|||| ||||||| ||||||||||||||| ||||||| ||||
Sbjct: 3132 ctccattctaccctgacgtcctcttcatcggggggagagtga 3174

>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: 31 ggggtgtgcggacggactctaaacaccgacagctggcgccaggtagggggtgtgtcttt 90
||||||||| |||| | ||||||||||||||| |||||||||||
Sbjct: 1380 ggggtgtgcgg-cggacccaaaacaccgacagctggcgccaggtagggggtgtgtcgcc 1438

Query: 91 gatctgagctagctcaatgaccattacctccaaatgcaagatcgcccttcgccccgggac 150
||||| ||||||||||||| || | |||| | | ||||||| ||||| ||||||| ||
Sbjct: 1439 gatctaagctagctcaatggccgtcaccttcaccgcaagatcacctccgccccggatc 1498

Query: 151 tatgttttgctttggaaccatctcatccatagcagatgaagagggaactctgcaccgcat 210
| |||| |||||||||| |||||||| |||||||||| |||||||| || |||||
Sbjct: 1499 tgtgttctgctttggaactatctcatccgtagcagatgaagaagggaactctacatcgcat 1558

Query: 211 agcaga 216
|||||
Sbjct: 1559 cgcaga 1564

Score = 95.6 bits (48), Expect = 9e-16
Identities = 180/224 (80%)
Strand = Plus / Plus

Query: 848 aacctgtaccccgacttcgctcgtgcaatgaacacgccgagtgaagtcggaggggtactg 907
|||||| |||||||||| || || |||||||||||||||||||||||||||||
Sbjct: 2169 aacctgaaccccgacttcgcccagagccatgaacacgccgagtgaagtcggaggggtacta 2228

Query: 908 gccagatagctgacggcctcccggaaccctagacacggaaggctaccggcggctgctt 967
|| | |||||| || |||| || | | ||| | || |||| || || || |
Sbjct: 2229 gctcggatagctgatggactccctcggaatcccgacgccgagggtatcgacgactgttc 2288

Query: 968 actcgagcagttaatcaccttctacccatcactaatcctccaagcgacctacgccatgcc 1027
|| | |||| || || |||||| || || || || || || || || || ||
Sbjct: 2289 acccaagcagccaaccatcttctacctatcgctcacccgccgaacgacctacgacacgcc 2348

Query: 1028 atcaacagccggcgagacacgcggagctccatcaacgcttcgcg 1071
|||||||| || |||| | |||||| || |||||||
Sbjct: 2349 atcaacagccgtcgggacacgtgaagctccataaatgcttcgcg 2392

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

Query: 509 ttetaccccgacgtcctcttcac 532
|||||||||||||||||
Sbjct: 1845 ttetaccccgacgtcctcttcac 1868

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

Score = 151 bits (76), Expect = 2e-32
Identities = 426/540 (78%), Gaps = 2/540 (0%)
Strand = Plus / Minus

Query: 1283 cttactccgtgtctccgggccatccagtggccct-aacttcaaggctccaacgtcagc 1341
||||||| || ||| ||||||| || ||||||| ||||||||| |||||
Sbjct: 79340 cttactccatgcctcagggccattcaatggccccgaacttcaaggctccaatgtcgac 79281

Query: 1342 aagtatgagcgcaagcaggacctgggtggctggtagccatctacacgattgtcatgg 1401
|| ||||| | ||||||| ||||| ||||||| ||| ||||||| | | | |
Sbjct: 79280 aaatatgaacctaagcaggatctgggaggctgggtggccgtctacaccacgccccga 79221

Query: 1402 gccgccggagcgacggaggacgtgatgacagtgtatttccattgtcctagggaagac 1461
||| | ||||| || ||||| ||||||| | ||| || ||| ||||| |||||||
Sbjct: 79220 gccactggagcaaccgaggatgtgatgaccgcgtacttgccctatcgctccttgggaagac 79161

Query: 1462 gcaatgcagtggctccgacatctacccaacattgcatagacaattggagcgacttcagt 1521
|| |||| ||||| ||||| ||||| | ||| ||||| ||| | ||||||| || |||
Sbjct: 79160 gcgctgcaatggctacgacacctaccacgacactgcatcgacgactggagcgattttagt 79101

Query: 1522 tgggtgcttcacgccaacttccagtcctctttgacaagccggcgagccatgggaccta 1581
|| |||| | ||||| ||||| ||||| ||||| || ||||| |||||||
Sbjct: 79100 cggcgctttactgccaatttccagtcctctctccgacaaaccagcgcaaccatgggacctc 79041

Query: 1582 aaatccattgggcatcaggcgatgaaacgctccggtgtacctcaagaggttttagacc 1641
||||||| || | ||| || ||||| ||||||| ||||||| || || |||||
Sbjct: 79040 aaatccatcaagcgccgggggacgaaactctccggtcgacctcaaaagattccagacc 78981

Query: 1642 atgaggaaccacacccccgaagtgcgcgaggcgggggtgattgaagacttctaccagga 1701
||||| || | | ||||| ||||| ||||| | ||||| || ||||||| |||
Sbjct: 78980 atgagaaatcgatccccgaggtcgcgaggcagcagtgatcgaggacttctaccagga 78921

Query: 1702 tccaatgactcggtttctgctccgagccatactccagaaaagcgctcgccacctccgaaca 1761
||||||||| || ||| ||||||||| || ||| ||| | ||||| || |||
Sbjct: 78920 tccaatgactcagccttcatccgagccatactaca-aaaggcgccaaccacttcggaata 78862

Query: 1762 cttgttccgggaggcagacctctacatcaccacggattaacgggccaggacctcatcgg 1821

Sbjct: 78861 gctattccgggaagccgacctctacatcaccgccgatgaacggggccctagacctcatcg 78802

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

Query: 855 accccgacttcgctcgtgcaatgaacacgccgagtgaagtcggaggggtactggcccaga 914
 |||||
 Sbjct: 79768 accccgacttcacccgggccatgaacacgccgagtgaagtcggaggagtgttggtcgcga 79709

```
Query: 915   tagctgacggcctcccggaaccctagacacggaaggctaccggcggtgcttactcgag 974
            ||||| ||||| ||| | ||| ||| ||||| ||||| ||||| ||
Sbjct: 79708 tagctgatggcctccccggactcccgacgcgagggtatcggcggtgttactcaag 79649
```

```
Query: 975   cagttaatcaccttctacccatcactaatcctccaagcgacctacgccatgccatcaaca 1034
           |||  || ||||| ||||| || || | || | || ||||| || ||||| |||||
Sbjct: 79648 cagccaaccaccttctacccctcgctcacccgcggaacgatctacgacagccatcaaca 79589
```

Query: 1035 gccggcgagacacgcggagctccatcaacgcttcgcgcgaccgatgacacga 1086
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Sbjct: 79588 gtcggcgggacgcacggagctccatcaacgcttcacgcgaacgacgacacga 79537

Score = 77.8 bits (39), Expect = 2e-10
Identities = 69/79 (87%)
Strand = Plus / Minus

Query: 31 ggggtgtgcggacggactctaaacaccgacagctggcgccgaggtagggggtgtgtcttt 90
||||| |||| | ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 80568 ggggtgcgggtcggacccaaaacaccgacagctggcgtgccaggtagcgggtgtgtcgtc 80509

```
Query: 91      gatctgagctagctcaatg 109
             |||| |||||
Sbjct: 80508  gatccaagctagctcaatg 80490
```

Score = 54.0 bits (27), Expect = 0.003
Identities = 33/35 (94%)

Strand = Plus / Minus

Query: 503 gtccttttctaccccgacgtcctcttcatcagggg 537
||||| |||||||||||||||||||||||||
Sbjct: 80108 gtcctattctaccccgacgtcctcttcatcggggg 80074

Score = 52.0 bits (26), Expect = 0.012
Identities = 47/54 (87%)
Strand = Plus / Minus

Query: 643 gcgacatcacgaggtggggaacgggatccggcgcaaccgatatccggggacga 696
||||||| || || ||||||||| || ||||||||| || |||||
Sbjct: 79968 gcgacatcacgaagccgggagaacgggatctggcacaaccgatatcgcgagacga 79915

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
|||| ||||| |||||||||||||||||
Sbjct: 303154 aaacgccgacagtggcgcgccaggtagggg 303184

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

Score = 145 bits (73), Expect = 1e-30
Identities = 450/573 (78%), Gaps = 2/573 (0%)
Strand = Plus / Plus

Query: 1253 cgacatgaagacacgtgcgaggtcttcgcacttactccgtgtctccgggccatccagtgg 1312
||||| || ||| ||||||||| | ||||| ||||| || ||| ||||||| || |||
Sbjct: 55410 cgacaggaggacatgtgcgaggtatcggcactcactccatgcctcagggccattcaatgg 55469

Query: 1313 cccc-taacttcaaggtctccaacgtcagcaagtatgagcgcaagcaggacctgggtggc 1371
||||| ||||||||||||||||||||| ||||| || | ||||||| || || |||
Sbjct: 55470 ccccctaacttcaaggtctccaacgtcgataagtagaacctaagcaggatccggaaggc 55529

Query: 1372 tggttagccatctacacgattgtcacatgggccgccggagcgacggaggacgtgatgaca 1431

Query: 915 tagctgacggcctcccgcgaaccctagacacggaaggctaccggcggtgcttactcgag 974
|||| | ||||| | | | | | | | | | | | | | |
Sbjct: 55073 tagcagatggcctcccgtaggactcccgatgccgagggctatcggtggctgttactcaag 55132

Query: 975 cagttaatcaccttctacccatcactaatcctccaagcgacctacgcatgccatcaaca 1034
||| |||| | | |||| | | | | | | | | | | | |
Sbjct: 55133 cagccaatcatctcctaccctcgctacccgccaacgatctacgacacgcatgaaca 55192

Query: 1035 gccggcgagacacgcggagctccatcaacgcttcgcgcgaccgatgacacga 1086
| |||| | | | ||||| ||||| ||||| | | | |||||
Sbjct: 55193 gtcggcgaggacgcacggagctccatcaacgcttcgcgcaaacgacgacacga 55244

Score = 65.9 bits (33), Expect = 8e-07
Identities = 129/161 (80%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgcgccaggtaggggtgtgtctttgatctgagctagctcaatg 109
|||| | ||||| | | | ||||| ||||| | | | |||||
Sbjct: 54235 aaacactgacagctggcacgctaggtaggggtgtgtcatcgatccaagctagctcaatg 54294

Query: 110 accattacctccaaatgcaagatcgcccttcgccccgggactatgttttgctttggaacc 169
|| | |||| | | |||| | | | | | | | | | | | |
Sbjct: 54295 gccgtcaccttcagcacaagatcatcctccgtcctgggtccactttctgctttggaact 54354

Query: 170 atctcatccatagcagatgaagaggaactctgcaccgcat 210
|||||| | ||||| | | ||||| | | |||||
Sbjct: 54355 atctcatctgtagcagatgaggaaggaactctacatcgcat 54395

>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 = 145 bits (73), Expect = 1e-30
Identities = 405/513 (78%), Gaps = 2/513 (0%)
Strand = Plus / Plus

Query: 1222 ctcccctccttgggaccgacctcacgaacgccgacatgaagacacgtgcggagtcttcgc 1281
||||||| ||||| | | | | | | | | ||||| ||||| | |

Sbjct: 44259 ctcccctccctgggaccgacaccacaatcgctcgacaggaggacacgtgtggagtatcggc 44318

Query: 1282 acttactccgtgtctccggccatccagtggcccc-taacttcaaggtctccaacgtcag 1340
|| ||||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 44319 gctcactccacgtctcaggtccattcagtgccccctaacttcaaggtctccaacattga 44378

Query: 1341 caagtatgagcgcaagcaggacctgggtggctggttagccatctacacgattgtcacatg 1400
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 44379 caagtacgagcctaagcaggacccgggaggctggttgccgtctataccaccgctgcca 44438

Query: 1401 ggccgccggagcgacggaggacgtgatgacagtgtattttccattgtcctagggcaaga 1460
||||| || || || || || || ||||| || ||||| ||||| ||||| ||||| |||||

Sbjct: 44439 agccgttggggcaactgaagatgtgatgactgcgtatttgcccatcgctccttgggcaaga 44498

Query: 1461 cgcaatgcagtggctccgacatctaccccaacattgcatagacaattggagcgacttcag 1520
||| ||||| ||||| ||||| || ||||| || ||||| || || ||||| ||||| |||||

Sbjct: 44499 tgcactgcaatggctacgacacctgccccgacactgcatcaacgat-ggagcgacttcag 44557

Query: 1521 ttggtgcttcacgcccaacttccagtcctctttgacaagccggcgcagccatgggacct 1580
| || | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 44558 tcggcggttcacgcccaacttccaatccctctccgacaagttggcgcagccatgggacct 44617

Query: 1581 aaaatccattgggcatcagggcgatgaaacgctccggtgtacctcaagaggttttagac 1640
||||| || || | || ||||| || || || || || ||||| || ||||| || || || ||

Sbjct: 44618 caaatctatcaagcgccgaggggatgaaactctccggtcatacctcaaaagatttcaggc 44677

Query: 1641 catgaggaaccacacccccgaagtcgccgaggcgggggtgattgaagacttctaccgagg 1700
||||| || | | ||||| || || || || || ||||| || ||||| ||||| |||||

Sbjct: 44678 catgagaaatcgatatccccgaggttcggaagcagcggtgatcaggacttctaccgagg 44737

Query: 1701 atccaatgactcggttttctcgagccatact 1733
| | ||||| ||||| || ||||| |||||

Sbjct: 44738 acctaatactcggcctttgtccgagccatact 44770

Score = 85.7 bits (43), Expect = 9e-13
Identities = 148/183 (80%)
Strand = Plus / Plus

Query: 37 gcggacggactctaaacaccgacagctggcgcgccaggtagggggtgtgtctttgatctg 96
|||| |||| | |||| |||||||||||||||||||||||||| ||||
Sbjct: 27626 gcggtcggacccaaaacatcgacagctggcgcgccaggtagggggtgtgtcactgatcca 27685

Query: 97 agctagctcaatgaccattacctccaaatgcaagatcgcccttcgccccgggactatgtt 156
|||||||||| | | | | | |||| | | |||| | | ||||
Sbjct: 27686 agctagctcaatggccgtcactttccagcacagaagattgctctccgccctggatccgtgtt 27745

Query: 157 ttgctttggaaccatctcatccatagcagatgaagaggaactctgcaccgcatagcaga 216
|||| | |||||||||| | |||| |||| |||||| | |||||| ||
Sbjct: 27746 ctgcttcgggaccatctcatccgtggcagacgaagaaggaactctacatcgcatagcgga 27805

Query: 217 tct 219
|||
Sbjct: 27806 tct 27808

Score = 52.0 bits (26), Expect = 0.012
Identities = 89/110 (80%)
Strand = Plus / Plus

Query: 950 ggctaccggcggtgcttactcgagcagttaatcaccttctacccatcactaatcctcca 1009
|||| | |||||||||||||| |||| | |||||| | | || || || ||
Sbjct: 43987 ggctatcgacggctgcttactcgggcagctaaccaccttctgcctctcgctcatcgctccg 44046

Query: 1010 agcgacctagccatgccatcaacagccggcgagacacgaggagctccat 1059
|||| |||| | |||||| || || | |||| ||||||||
Sbjct: 44047 agcgatctacgacacgccatcaatagtcgatgggacacacggagctccat 44096

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Minus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
|||| |||| | ||||||||||||||||
Sbjct: 249165 aaacgccgacagttggcgcgccaggtagggg 249135

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

```
Query: 1417  gaggacgtgatgacagtgtattttccattgtcctagggcaagacgcaatgcagtggctc 1476
            ||||| |||| | || | | | ||||| ||||| ||||| |||||
Sbjct: 15503  gaggacgtaatgaccgcgtacttgccatcgtcctcgggcaagacgcgtgcaatggctg 15444
```

Query: 1537 aacttccagtccctctttgacaagccggcgagccatgggacctaaaatccattgggcac 1596
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Sbjct: 15383 aactttcagtctctctctgacaaaccggcgcaaccatgggacctcaaatccatcaagcac 15324

Query: 1657 cccgaagtcgccgaggcgggggtgattgaagacttctaccgaggatccaatgactcggct 1716
 ||||| ||||| ||||| | ||||| || || || || || || ||||| |||||
 Sbjct: 15263 cccgaggtcgcggaggcagcagtgatcgaggatttttacaggggatccaatgactcggcc 15204

Query: 1777 agacctctacatcaccacggattaacggggccaggacctcatcg 1821
 |||||||||||| || ||| || ||||||||||||
 Sbjct: 15144 cgatctctacatcaccatcgacgaacgagctcaggacctcatcg 15100

Query: 848 aacctgtaccccgacttcgctcgtgcaatgaacacgccgagtgaagtgcggaggggtactg 907

Sbjct: 25162 aacctgaaccccgacttcgcccagccatgaagacgccgagtgaagtcggaggagtattg 25103

Query: 908 gcccagatagctgacggcctcccgcgaaaccctagacacggaaggctaccggcggctgctt 967
|| | ||||||| ||||||| || | | || | ||||||| ||||||| |

Sbjct: 25102 gctcggatagctgatggcctccccggactcccgacgctgagggtatcggcggctattc 25043

Query: 968 actcgagcagttaatcaccttctacccatcactaatcctccaagcgacctacgccatgcc 1027
|||| |||| | |||| | |||||| | || | | || | |||| | ||

Sbjct: 25042 actcaagcagccaatcatcttctacccctcgctcaccgccgaacgatctacgacacacc 24983

Query: 1028 atcaacagccggcgagacacgaggactccatcaacgcttcgcgca 1074
|||||| | |||| | | | ||||||||| |||| | ||||

Sbjct: 24982 atcaacagtcggcgggacgcacagagctccatcaacgcttcgtgcga 24936

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

Identities = 80/91 (87%)

Strand = Plus / Minus

Query: 19 aggggtagccctgggtgtgcggacggactctaaacaccgacagctggcgcgccaggtagg 78
|||||| | || |||| | || | |||| | | ||||||||| |||||||||

Sbjct: 25954 aggggtaaccccggtgctgcggctggacccaaaacaccgacagctggcgcgccaggtagg 25895

Query: 79 ggggtgtgtctttgatctgagctagctcaatg 109
||||||| | |||| | |||||||||

Sbjct: 25894 ggggtgtgtcatcgatccaagctagctcaatg 25864

Score = 56.0 bits (28), Expect = 8e-04

Identities = 49/56 (87%)

Strand = Plus / Minus

Query: 641 cggcgacatcacgaggctggggaacgggatccggcgcaacccgtatcccgggacga 696
||||||||||| || | |||| | ||||||||| |||| | ||||

Sbjct: 25357 cggcgacatcacgaggccggagagcgggacccggcgcaacctgtatcgcgagacga 25302

Score = 50.1 bits (25), Expect = 0.048

Identities = 28/29 (96%)

Strand = Plus / Minus

Query: 504 ctcctttctaccccgacgtcctcttcatc 532
|||| |||||||||
Sbjct: 25491 ctccattctaccccgacgtcctcttcatc 25463

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgccaggtagggg 80
|||| |||||||
Sbjct: 106752 aaacgccgacagttggcgccaggtagggg 106782

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

Score = 135 bits (68), Expect = 1e-27
Identities = 324/408 (79%), Gaps = 1/408 (0%)
Strand = Plus / Plus

Query: 1423 gtgatgacagtgtattttccattgtcctagggaagacgcaatgcagtggctccgacat 1482
||||||| | ||||| ||||| ||||| ||||| || || || ||||| |||||
Sbjct: 4118 gtgatgactgcgtatttggccatcatccttgggaagatgcgctacaatggctacgacac 4177

Query: 1483 ctaccccaacattgcatagacaattggagcgacttcagttggtgcttcacgccaacttc 1542
|| ||||| || ||||| || ||||| ||||| || || || ||||| ||
Sbjct: 4178 ctgccccgacactgcatcgacgattggagcgatttcagtcggcggttttatcgccaacatc 4237

Query: 1543 cagtcctcttttgacaagccggcgagccatgggacctaaaatccattgggcatcagggc 1602
|| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||
Sbjct: 4238 caatccctctccgacaagccggcgcaaccatgggacctcaaatccatcaggcgccgaggg 4297

Query: 1603 gatgaaacgctccggtgtacctcaagaggttttagaccatgaggaaccacaccccgaa 1662
||||||| ||||| || ||||| ||||| ||||| ||||| ||||| ||
Sbjct: 4298 gatgaaactttccgatcatacctcaaaagatttttagaccatgagaaatcgtatccttgag 4357

Query: 1663 gtcgccgaggcgggggtgattgaagacttctaccgaggatccaatgactcggctttcgtc 1722
|| | || || || ||||| || ||||| ||||| ||||| ||||| |||||
Sbjct: 4358 gttgtggaagcagcggtgatcgaggacttctaccgggatctaatactcggccttcgtc 4417

Query: 1723 cgagccatactccagaaaagcgtcggccacctccgaacacttggtccgggaggcagacct 1782
||||||| || ||| || || | ||||| || | ||| ||| | |||||
Sbjct: 4418 cgagccatactgca-aaagccaccgactacctccgagcagctattcaggaagtggacct 4476

Query: 1783 ctacatcaccacggattaacggggccaggacctcatcgaggcacgaa 1830
||||||| | || ||||| ||||| ||||| |||||
Sbjct: 4477 ctacatcacgctgacgaacgggctcaggacctcattggaggaaacgaa 4524

Score = 93.7 bits (47), Expect = 4e-15
Identities = 89/103 (86%)
Strand = Plus / Plus

Query: 7 aaaagcaccgcaaggggtagccctgggtgtgcggacggactctaaacaccgacagctggc 66
||||||| | ||||| | ||| ||||| ||||| ||||| | ||||| |||||
Sbjct: 2751 aaaagcacctcgaggggcaaccccgggtgcgcggtcggacccaaaacactgacagctggc 2810

Query: 67 gcgccaggtaggggtgtgtctttgatctgagctagctcaatg 109
||||||| ||||| ||||| ||||| |||||
Sbjct: 2811 gcgccaggtaggggtgtgtcactgatccaagctagctcaatg 2853

Score = 54.0 bits (27), Expect = 0.003
Identities = 39/43 (90%)
Strand = Plus / Plus

Query: 504 ctcttttctaccccgacgtcctcttcatcagggggagattgga 546
|||| | ||||| ||||| ||||| ||||| |||||
Sbjct: 3211 ctccgttctaccccgacgtcctctttatcggggggagagtgga 3253

Score = 50.1 bits (25), Expect = 0.048
Identities = 145/185 (78%)
Strand = Plus / Plus

Query: 848 aacctgtaccccgacttcgctcgtgcaatgaacacgccgagtgaagtcggaggggtactg 907
||||| ||||| ||||| || | ||||| ||||| || ||||| || || ||
Sbjct: 3543 aacctgaaccccgacttcgtccgatccatgaacacaccgagcgaggtcggtggagtgtg 3602

Query: 908 gccagatagctgacggcctcccggaaccctagacacggaaggctaccggcggtgctt 967
||| ||||| | ||||| || | ||| | | ||||| |||||
Sbjct: 3603 gctcggatagccaatggcctccccggactccagacgccgagggtatcggcggtgctc 3662

Query: 968 actcgagcagttaatcaccttctacccatcactaatcctccaagcgacctacgcatgcc 1027
||||| |||| | | ||||| | | ||| ||||| ||||| ||| | | |||
Sbjct: 3663 actcgggcagctaaccatcttctgcctctcgtcatcctccaagcgatctatgacagcc 3722

Query: 1028 atcaa 1032
|||||
Sbjct: 3723 atcaa 3727

Score = 48.1 bits (24), Expect = 0.19
Identities = 45/52 (86%)
Strand = Plus / Plus

Query: 341 acccgaaaaactccgctgtccacttcgccacaaaaggagtggacacggatta 392
||||||| ||| ||| ||||| || | ||||| ||||| |||||
Sbjct: 3069 acccgagaacccgttgtccacctcatccacaaaaggagtggacacggatta 3120

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

Score = 135 bits (68), Expect = 1e-27
Identities = 324/408 (79%), Gaps = 1/408 (0%)
Strand = Plus / Plus

Query: 1423 gtgatgacagtgtattttccattgtcctagggcaagacgcaatgcagtggctccgacat 1482
||||||| | ||||| ||||| ||||| ||||| || | ||| |||||
Sbjct: 11447 gtgatgactgcgtatttgcccatcatccttgggcaagatgcgctacaatggctacgacac 11506

Query: 1483 ctaccccaacattgcatagacaattggagcgacttcagttggtgcttcacgccaacttc 1542
|| |||| | ||||| ||| ||||| ||||| ||| ||| ||||| |||
Sbjct: 11507 ctgccccgacactgcatcgacgattggagcgatttcagtcggcggttttatcgccaacatc 11566

Query: 1543 cagtcctcttttgacaagccggcgagccatgggacctaaaatccattgggcatcagggc 1602
|| ||||| ||||| ||||| ||||| ||||| ||| | |||
Sbjct: 11567 caatcctctccgacaagccggcgcaaccatgggacctaaaatccatcaggcgccgaggg 11626

Query: 1603 gatgaaacgctccggttgtagctcaagaggttttagaccatgaggaaccacacccccgaa 1662
||||||| |||| | ||||||| || |||||||||||||| || | || ||
Sbjct: 11627 gatgaaactttccgatcatactcaaaagatttttagaccatgagaaatcgtatccttgag 11686

Query: 1663 gtcgccgaggcgggggtgattgaagacttctaccgaggatccaatgactcggttttcgtc 1722
|| | || || | ||||| || |||||||||||||| ||||| ||||||||||| |||||
Sbjct: 11687 gttgtggaagcagcggtgatcgaggacttctaccgggatctaatactcggttcgtc 11746

Query: 1723 cgagccatactccagaaaagcgtcgccacctccgaacacttggtccgggaggcagacct 1782
|||||||||| || ||| || || | |||||||| || | ||| |||| | |||||
Sbjct: 11747 cgagccatactgca-aaaggcacgcactacctccgagcagctattcagggaagtggacct 11805

Query: 1783 ctacatcaccacggattaacgggccaggacctcatcgaggcacgaa 1830
|||||||||| | || ||||||| ||||||||||| ||||| |||||
Sbjct: 11806 ctacatcacgcgtgacgaacgggctcaggacctcattggaggaacgaa 11853

Score = 93.7 bits (47), Expect = 4e-15
Identities = 89/103 (86%)
Strand = Plus / Plus

Query: 7 aaaagcacgcgaaggggtagccctgggtgtgcggacggactctaaccacgcagctggc 66
||||||| | ||||| || ||||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 10080 aaaagcacctcgaggggcaaccccggtgcgcggtcggacccaaacactgacagctggc 10139

Query: 67 gcgccaggtaggggtgtgtctttgatctgagctagctcaatg 109
|||||||||||||||| |||| |||||||||||
Sbjct: 10140 gcgccaggtaggggtgtgtcactgatccaagctagctcaatg 10182

Score = 54.0 bits (27), Expect = 0.003
Identities = 39/43 (90%)
Strand = Plus / Plus

Query: 504 ctccctttctaccccgacgtcctctttcatcagggggagattgga 546
|||| |||||||||||||| || ||||||| |||||
Sbjct: 10540 ctccgtttctaccccgacgtcctctttatcgggggagagtgga 10582

Score = 50.1 bits (25), Expect = 0.048
Identities = 145/185 (78%)
Strand = Plus / Plus

Query: 848 aacctgtaccccgacttcgctcgtgcaatgaacacgccgagtgaagtcggaggggtactg 907
||||| ||||||||| || | ||||||| ||||| || ||||| || ||
Sbjct: 10872 aacctgaaccccgacttcgtccgatccatgaacacaccgagcgaggtcggtggagtgtg 10931

Query: 908 gccagatagctgacggcctcccgcaaccctagacacggaaggctaccggcggtgctt 967
|| | ||||| | ||||||| || || | |||| | || ||||| |||||||||
Sbjct: 10932 gtcgggatagccaatggcctcccccggactccagacgccgagggtatcgggcggtgctc 10991

Query: 968 actcgagcagttaatcaccttctaccatcactaatcctccaagcgacctacgccatgcc 1027
||||| |||| ||| || ||||| || || || ||||||||| |||| | || ||
Sbjct: 10992 actcgggcagctaaccatcttctgcctctcgtcctcctccaagcgatctatgacacgcc 11051

Query: 1028 atcaa 1032
|||||
Sbjct: 11052 atcaa 11056

Score = 48.1 bits (24), Expect = 0.19
Identities = 45/52 (86%)
Strand = Plus / Plus

Query: 341 acccgaaaaactccgctgtccacttcgccacaaaaggagtggacacggatta 392
||||||| ||| ||| ||||||| || ||||||| |||||||||
Sbjct: 10398 acccgaagaaccccggttgccacctcatccacaaaagagtggacacggatta 10449

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

Score = 129 bits (65), Expect = 7e-26
Identities = 418/533 (78%), Gaps = 2/533 (0%)
Strand = Plus / Plus

Query: 1293 gtctccgggccatccagtggcccc-taacttcaaggtctccaacgtcagcaagtatgagc 1351
||||| ||||||| || ||||||| ||||||||| ||||||||| ||||| || |
Sbjct: 3074 gtctcagggccattcattggccccctaacttcaaggtctccaacgtcgacaagtacgaac 3133

Query: 1352 gcaagcaggacctgggtggctggttagccatctacacgattgtcacatgggccgccggag 1411
|||||
Sbjct: 3134 ccaagcaggacccgagaggctggttggctgtctataccactactgcccgccggttgggg 3193

Query: 1412 cgacggaggacgtgatgacagtgtattttccattgtcctagggcaagacgcaatgcagt 1471
|||
Sbjct: 3194 caactgaagatgtgatgactgcgaatttgccaatcgctcttgggcaagatgcactgcaat 3253

Query: 1472 ggctccgacatctaccccaacattgcatagacaattggagcgacttcagttggtgcttca 1531
|||||
Sbjct: 3254 ggctacgacacatgccccgacactgcatgacgattggagcgatttcagtcggcgttttg 3313

Query: 1532 tcgccaacttcagtcctctttgacaagccggcgcagccatgggacctaaatccattg 1591
|||||
Sbjct: 3314 tcgctaactccaatccctctctgacaagccagcgcaaccatgggacctcaaatccatca 3373

Query: 1592 ggcatcaggcgcatgaaacgctccggtgtacctcaagaggttttagacctgaggaacc 1651
|||
Sbjct: 3374 ggcgccgaggggatgaaactctctgtgcataacctcaaaagatttcagacctgagaaatc 3433

Query: 1652 acacccccgaagtcgccgaggcggggtgattgaagacttctaccgaggatccaatgact 1711
|
Sbjct: 3434 gtatccccaaggttgcaagcagcagtgatcaaggacttctaccgggatctaagact 3493

Query: 1712 cggttttcgtccgagccatactccagaaaagcgtcgccacctccgaacacttgttccgg 1771
|||||
Sbjct: 3494 cggccttcgttcgagccatactgca-aaaggcgccaactacctccgagcagctattcagg 3552

Query: 1772 gaggcagacctctacatcaccacggattaacgggccaggacctcatcgagg 1824
|||
Sbjct: 3553 gaagcggacctctacatcaccgccgacgaacgggctcaggacctcattggagg 3605

Score = 97.6 bits (49), Expect = 2e-16
Identities = 139/169 (82%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgcgccaggtagggggtgtgtctttgatctgagctagctcaatg 109
|||||
Sbjct: 1864 aaacaccgacagctggcgcgccaggtagggggtgtgtcactgatccaagctagctcaatg 1923

```
Query: 110  accattacctccaaatgcaagatgcaccttcgccccgggactatgttttgccttgggaacc 169
           ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 1924  gacatacctttccagcacagaatcgctctcctcctggatccgtgttctgcttcggaacc 1983
```

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

Score = 44.1 bits (22), Expect = 3.0
Identities = 31/34 (91%)
Strand = Plus / Plus

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

```
Query: 1283 cttactccgtgtctccgggccatccagtggcccc-taacttcaaggtctccaacgtcagc 1341
          |||||  ||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct: 4027 cttactccacgtctcaggggccattcagtgggcccctaacttcaaggtctccaacatcgac 4086
```

Sbjct: 4087 aagtatgagcccaagcaaaacctgggaggctggttgactgtctataaccactgctgcctat 4146

Sbjct: 4147 gccgctggggcaactgaagatgtgatgactgcgtat ttgcccatcgtccttgggcaagat 4206

Sbjct: 4207 gcgttgcaatggctacgacacctgccccgacacaacatcgatgactggagcgatttcagt 4266

Sbjct: 4267 cgggtgttttatcgccaacttcccatccctctccgacaagtcggcgcaaccatgggacctc 4326

Sbjct: 4327 aaatccatcaggcgccgagggggtgaaactcatcggtcatacctcaaaagatttcagacc 4386

Sbjct: 4387 atgagaaatcgtatcctcgaggttgcagaagcagcggatgatcgaggacttctatcgggga 4446

Sbjct: 4447 tctaatagactcggccttcgtccgagccataactgca-aaaggcgccaaatacctccgagca 4505

Sbjct: 4506 gctattcaggggaagcagacctctacttcaccgccgatgaatgggctcaggacctcat 4562

Query: 855 a c c c c g a c t t c g c t c g t g c a a t g a a c a c g c c g a g t g a a g t c g g a g g g g t a c t g g c c c a g a 914

Query: 915 tagctgacggcctcccggaaccctagacacggaaggctaccggcggtgcttactcgag 974
|||| || ||||| | || |||| | || |||| ||||| ||||| |
Sbjct: 3659 tagccgatggcctccctggactctagacgccgagggtatcgggcggtgctcactcggg 3718

Query: 975 cagttaatcaccttctacccatcactaatcctccaagcgacctacgcatgccatcaaca 1034
||| ||| || |||| | | || |||| | |||| |||| | ||||| ||
Sbjct: 3719 cagctaaccatcttctgcctctcgctcatcctcgagcgatctacgacagccatcaata 3778

Query: 1035 gccggcgagacacgcggagctccatcaacgcttcgcgcgaccgatgaca 1083
| || || ||| | ||||| ||||| ||||| ||||| ||| ||||
Sbjct: 3779 gtcgacgggacgcacggagctccatcaatgcttcgcgcgaacgacgaca 3827

Score = 67.9 bits (34), Expect = 2e-07
Identities = 82/98 (83%)
Strand = Plus / Plus

Query: 7 aaaagcaccgcaaggggtagccctgggtgtgcgacggactctaacaccgacagctggc 66
||||||| | |||| | ||| |||| |||| | ||| | ||||| ||| |||
Sbjct: 2786 aaaagcacctcgaggggcaacccgggtgcgcggtcagacccaaacaccgaaagccggc 2845

Query: 67 gcgccaggtaggggtgtgtctttgatctgagctagct 104
||||||| ||||| |||| | |||| |||||
Sbjct: 2846 gcgccaggtaggggtgtgtcactaatctaagctagct 2883

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

Score = 127 bits (64), Expect = 3e-25
Identities = 323/408 (79%), Gaps = 1/408 (0%)
Strand = Plus / Minus

Query: 1423 gtgatgacagtgtattttccattgtcctagggaagacgcaatgcagtggctccgacat 1482
||||||| ||||| |||| |||| ||||| || | || ||||| |||||
Sbjct: 8545 gtgatgactgtgtatttgccatcgctcttgggcaagatgcgctccaatggctacgacac 8486

Query: 1483 ctaccccaacattgcatagacaattggagcgacttcagttggtgcttcacgccaacttc 1542
|| |||| ||| | ||| || ||||| ||||| |||| | ||| ||||| ||
Sbjct: 8485 ctgccccgacactacatcgatgattggagcgatttcagtcggtgttttatcaccaacttc 8426

```
Query: 1543 cagtccctctttgacaagccggcgagccatgggacctaaatccattgggcatcagggc 1602
          || ||||| | ||||| ||||| ||||| ||||| ||||| ||| | ||
Sbjct: 8425 caatccctctccgacaagccggcgcaaccataggacctcaaatccatcaggcgccgaggg 8366
```

```
Query: 1663 gtcgccgaggcgggggtgattgaagacttctaccgaggatccaatgactcggcttttcgtc 1722
          ||| ||| | ||||| ||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 8305 gtttgtgaagttagcggtgatcaggacttataccagggatctaatgactcggccttcgtc 8246
```

Query: 1783 ctacatcaccacgattaacggggccaggacctcatcgaggcacgaa 1830
 ||||| | || ||||| ||||| ||||| |||||
 Sbjct: 8186 ctacatcaccgccgacaaacgggctcaggacctcattggaggaaacgaa 8139

Query: 7 aaaagcaccgcaaggggtagccctgggtgtgcggacggactctaaacaccgacagctggc 66
 ||||||| | |||| | || |||| |||| |||| |||| |||| |||| |||| |||| ||||
 Sbjct: 9929 aaaagcacctcgaggggcaaccccggtgcgcggtcggacccaaaacaccgacagctggc 9870

Query: 127 caagatcgcccttcgccccgggactatgttttgctttggaaccatctcatccatagcaga 186
 ||||| | || ||||| || | ||||| ||| ||||| ||||| ||||| |||||
 Sbjct: 9809 caagatcactctccgccttggaatcggtgttctacttcggaaccatctcatccatggcaga 9750

Score = 56.0 bits (28), Expect = 8e-04
Identities = 184/236 (77%)
Strand = Plus / Minus

Query: 848 aacctgtaccccgacttcgctcgtgcaatgaacacgccgagtgaagtcggaggggtactg 907
||||| ||||||||| | || ||||||| ||||| || ||||| || ||
Sbjct: 9121 aacctgaaccccgacttcgcctgagccatgaacacaccgagcgaggtcggtggagtgtg 9062

Query: 908 gccagatagctgacggcctcccggaaccctagacacggaaggctaccggcggtgctt 967
|| | ||||| || ||||||| | || | |||| | || ||||| |||||||||
Sbjct: 9061 gctcggatagccgatggcctccccctgactccagacgctgagggtatcggcggctgctc 9002

Query: 968 actcgagcagttaatcaccttctacccatcactaatcctccaagcgacctacgccatgcc 1027
||||| |||| ||| | ||||| || || || ||||||| ||||| ||| || ||
Sbjct: 9001 actcgggcagctaacaatcttctgcctctcgtcatcctccgagcgatctatgacacacc 8942

Query: 1028 atcaacagccggcgagacacgcggagctccatcaacgcttcgcgcgaccgatgaca 1083
||||| || || || ||| | | ||||||||| ||||||||| ||| ||||
Sbjct: 8941 atcaatagtcgacgggacgcacagagctccatcaatgcttcgcgcgaacgacgaca 8886

>gb|DQ183073.1| Zea mays clone A-RGA5 resistance gene analog-like gene, partial
sequence
Length = 489

Score = 121 bits (61), Expect = 2e-23
Identities = 290/365 (79%), Gaps = 1/365 (0%)
Strand = Plus / Minus

Query: 1283 cttactccgtgtctccgggcatccagtggcc-cctaacttcaaggtctccaacgtcagc 1341
||||||| |||| ||||||||| || || ||||||| ||||||| ||||| |
Sbjct: 470 cttactccgcatctcagggcatccagtggcctccaaacttcaaagttccaatgtcaac 411

Query: 1342 aagtatgagcgcaagcaggacctgggtggtggttagccatctacacgattgtcacatgg 1401
|| || |||| ||||| |||| || ||||||| | | |||| |||| | |||||
Sbjct: 410 aaatacgagcctaagcaagacccgggaggtggttggtcgtctatacgaccgccacacag 351

Query: 1402 gccgccggagcgacggaggacgtgatgacagtgtattttccattgtcctagggcaagac 1461
||||| || || | || ||||||||| || || || ||||| ||||| |||||||

Sbjct: 350 gccgctggggcaatcgaagacgtgatgacagcatagttgcccatcgctccttaggcaagat 291

Query: 1462 gcaatgcagtggtccgacatctaccccaacattgcatagacaattggagcgacttcagt 1521
||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 290 gcattacagtggtcgacatctgccgtggcactgcatcgatgattggagcgacttcagt 231

Query: 1522 tgggtgcttcatcgccaacttccagtcctctttgacaagccggcgagccatgggaccta 1581
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 230 cggcatttcattgccaaacttctagtcctctcgcgacaagccagcgcatccatgggacctc 171

Query: 1582 aaatccattgggcatcagggcgatgaaacgctccggttgacctcaagaggttttagacc 1641
||| |||| ||| | ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 170 aaaccataaggcgccgagggcgatgaaagccttcggtcatatctcaagaggtttcagacc 111

Query: 1642 atgag 1646
|||||

Sbjct: 110 atgag 106

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

Score = 111 bits (56), Expect = 2e-20
Identities = 182/224 (81%)
Strand = Plus / Plus

Query: 1423 gtgatgacagtgtattttccattgtcctagggaagacgcaatgcagtggtccgacat 1482
||||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 8417 gtgatgactgcgtattttgcccatcgctccttgggcaagatgcgctgcaatggctacgacac 8476

Query: 1483 ctaccccaacattgcatagacaattggagcgacttcagttggtgcttcatcgccaacttc 1542
|| |||| ||| ||||| ||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 8477 ctgccccgacactgcattgacgattggagcgatttcagtcgccgttttgtcgccaacttc 8536

Query: 1543 cagtcctctttgacaagccggcgagccatgggacctaaaatccattgggcatcagggc 1602
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 8537 caatccctctccgacaagccggcgcaacatgggacctcaaatccataaggcgccgaggg 8596

Query: 1603 gatgaaacgctccggttgacctcaagaggttttagaccatgag 1646
||||||| ||||| | ||||| ||||| ||||| ||||| |||||

Sbjct: 8597 gatgaaactctccgatcatacctcaaaagatttcagaccatgag 8640

Score = 95.6 bits (48), Expect = 9e-16
Identities = 207/260 (79%)
Strand = Plus / Plus

Query: 824 cgagagaatgctctctttgctcggaacctgtaccccgacttcgctcgtgcaatgaacacg 883
||||||| ||||| || | ||||| ||||| ||||| || || |||||
Sbjct: 7909 cgagagaatcctctccttgacgaaacctgaaccccgacttcgcccagccatgaacaca 7968

Query: 884 ccgagtgaagtcggaggggtactggcccagatagctgacggcctcccggaaccctagac 943
||||| | ||||| || | ||||| | ||||| || || || |||||
Sbjct: 7969 ccgagcaaggtcggaggagtgtggctcggatagccgatggcctcccccggactccagac 8028

Query: 944 acggaaggctaccggcggtgcttactcgagcagttaatcaccttctaccatcactaat 1003
|| | ||||| ||||| ||||| ||||| || || ||||| || ||||| ||
Sbjct: 8029 accaagggtatcggcggtgctcactcgggcagctaaccatcttctgcctctcactcat 8088

Query: 1004 cctccaagcgacctacgccatgccatcaacagccggcgagacacgcggagctccatcaac 1063
||||| ||||| ||| | || ||||| || || || ||||| || ||||| |||||
Sbjct: 8089 cctccgagcgatctatgacacgccatcaatagtcgacgggacgcacggagctccatcaat 8148

Query: 1064 gcttcgcgcgaccgatgaca 1083
||||| ||||| ||| |||||
Sbjct: 8149 gcttcacggaacgacgaca 8168

Score = 46.1 bits (23), Expect = 0.76
Identities = 38/43 (88%)
Strand = Plus / Plus

Query: 504 ctcttttctaccccgacgtcctctttcatcagggggagattgga 546
|||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 7603 ctccgttctaccccgacgtcctctttatcgaggggagagtgga 7645

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

Score = 101 bits (51), Expect = 1e-17
Identities = 90/103 (87%)

Strand = Plus / Minus

```
Query: 7      aaaagcaccgcaaggggtagccctgggtgtgcggacggactctaaacaccgacagctggc 66
          ||||| ||||| | ||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 109028 aaaagcaccgtgaggggcaaccccggtgtgcggtcggacccaaaacaccgacagctggc 108969
```

```
Query: 67      gcgccaggtagggggtgtgtctttgatctgagctagctcaatg 109
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 108968 gcgccaggtagggggtgtgtcgcgatccaagctagctcaatg 108926
```

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Minus

```
Query: 50      aaacaccgacagctggcgccaggtagggg 80
          |||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 30117 aaacgccgacagtggcgccaggtagggg 30087
```

Score = 46.1 bits (23), Expect = 0.76
Identities = 23/23 (100%)
Strand = Plus / Minus

```
Query: 510     tctaccccgacgtcctctttcatc 532
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 108558 tctaccccgacgtcctctttcatc 108536
```

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

Score = 101 bits (51), Expect = 1e-17
Identities = 90/103 (87%)
Strand = Plus / Plus

```
Query: 7      aaaagcaccgcaaggggtagccctgggtgtgcggacggactctaaacaccgacagctggc 66
          ||||| ||||| | ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 416 aaaagcacctcgaggggcaaccccggtgtgcggtcggacccaaaacaccgacagctggc 475
```

```
Query: 67      gcgccaggtagggggtgtgtctttgatctgagctagctcaatg 109
```

|||||
Sbjct: 476 gcgccaggtagggggtgtgtcactgatccaagctagctcaatg 518

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

Score = 101 bits (51), Expect = 1e-17
Identities = 90/103 (87%)
Strand = Plus / Plus

Query: 7 aaaagcaccgcaagggtagccctgggtgtgcggacggactctaaacaccgacagctggc 66
|||||
Sbjct: 419 aaaagcacctcgaggggcaaccccggtgtgcggtcggacccaaaacaccgacagctggt 478

Query: 67 gcgccaggtagggggtgtgtctttgatctgagctagctcaatg 109
|||||
Sbjct: 479 gcgccaggtagggggtgtgtcactgatccaagctagctcaatg 521

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

Score = 97.6 bits (49), Expect = 2e-16
Identities = 139/169 (82%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgccaggtagggggtgtgtctttgatctgagctagctcaatg 109
|||||
Sbjct: 1920 aaacaccgacagctggcgccaggtagggggtgtgtcactgatccaagctagctcaatg 1979

Query: 110 accattacctccaaatgcaagatcgcccttcgccccgggactatgttttgctttggaacc 169
|||
Sbjct: 1980 gtcatcactttccagcacaagattgctctccgacctggatccgtgttctgcttcggaacc 2039

Query: 170 atctcatccatagcagatgaagagggaactctgcaccgcatagcagatc 218
|||||
Sbjct: 2040 atctcatccgtggcagacgaagaaggaaactctacatcgcatagcagatc 2088

Score = 58.0 bits (29), Expect = 2e-04
Identities = 47/53 (88%)
Strand = Plus / Plus

Query: 31 ggggtgtgcggacggactctaaacaccgacagctggcgcgccaggtagggggtg 83
||||| |||| ||||| | |||||||| |||||||||||||||| |||||
Sbjct: 1796 ggggtgcgcggtcggacccaaacaccggcagctggcgcgccaggtaggtggtg 1848

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

Query: 848 aacctgtaccccgacttcgctcgtgcaatgaacacgccgagtgaagtcggaggggtactg 907
||||| ||||||||||||| || || |||||||| ||||| || ||||| || || ||
Sbjct: 2685 aacctgaaccccgacttcgcccagccatgaacacaccgagcgaggtcggtggagtgtg 2744

Query: 908 gccagatagctgacggcctcccgcaaccctagacacggaaggctaccggcggtgctt 967
|| | ||||| || |||||||| || || | ||| | || ||||| |||||||||
Sbjct: 2745 gtcctgatagccgatggcctccccggactccagatgccgagggctatcggcggtgctc 2804

Query: 968 actcgagcagttaatcaccttctaccatcactaatcctccaagcgacctacgcatgcc 1027
||||| ||| ||| || ||||| || | || ||||||||||||| ||||| || |
Sbjct: 2805 actcgggcaactaaccatcttctgectctagctcactcctccaagcgatctacgacacagc 2864

Query: 1028 atcaacagccggcgagacacgcggagctccatcaacgcttc 1068
||||| || || || ||| | ||||||||||||| |||||
Sbjct: 2865 atcaatagtgcagggagcgacggagctccatcaatgcttc 2905

Score = 54.0 bits (27), Expect = 0.003
Identities = 39/43 (90%)
Strand = Plus / Plus

Query: 504 ctcttttctaccccgacgtcctctttcatcagggggagattgga 546
|||| ||||||||||||||||||||| ||| |||||||| |||||
Sbjct: 2353 ctccgttctaccccgacgtcctctttatcggggggagagtgga 2395

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

Score = 89.7 bits (45), Expect = 6e-14
Identities = 96/113 (84%)

Strand = Plus / Plus

```
Query: 5   ccaaaagcacgcgaaggggtagccctgggtgtgctggacggactctaaacaccgacagctg 64
          ||||| ||| ||||| | || ||||| | || ||||| |||||
Sbjct: 284 ccaaaacacctcaaggggcaaccccggtgcgtggcgacccaaacaccgacagctg 343
```

```
Query: 65   gcgcgccaggtaggggtgtgtctttgatctgagctagctcaatgaccattac 117
          ||||| ||||| ||||| || || || ||||| |||||
Sbjct: 344 gcgcgccaagtaggggtgtgtcactggtccaagctagctcaatggccattac 396
```

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

Score = 89.7 bits (45), Expect = 6e-14
Identities = 96/113 (84%)
Strand = Plus / Plus

```
Query: 5   ccaaaagcacgcgaaggggtagccctgggtgtgctggacggactctaaacaccgacagctg 64
          ||||| ||| ||||| | || ||||| | || ||||| |||||
Sbjct: 284 ccaaaacacctcaaggggcaaccccggtgcgtggcgacccaaacaccgacagctg 343
```

```
Query: 65   gcgcgccaggtaggggtgtgtctttgatctgagctagctcaatgaccattac 117
          ||||| ||||| ||||| || || || ||||| |||||
Sbjct: 344 gcgcgccaagtaggggtgtgtcactggtccaagctagctcaatggccattac 396
```

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

Score = 85.7 bits (43), Expect = 9e-13
Identities = 88/103 (85%)
Strand = Plus / Plus

```
Query: 7   aaaagcacgcgaaggggtagccctgggtgtgctggacggactctaaacaccgacagctggc 66
          ||||| ||| ||||| | || ||||| || ||||| |||||
Sbjct: 416 aaaagcacctctaggggcaaccccggtgcgcggtcgacccaaacaccgacagctggc 475
```

```
Query: 67   gcgccaggtaggggtgtgtctttgatctgagctagctcaatg 109
          ||||| ||||| ||||| || || ||||| |||||
Sbjct: 476 gcgccaggaaggggtgtgttactgatccaagctagctcaatg 518
```

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

Score = 79.8 bits (40), Expect = 5e-11
Identities = 49/52 (94%)
Strand = Plus / Plus

Query: 31 ggggtgtgcggacggactctaaacaccgacagctggcgcgccaggtagggggt 82
||||| ||||| | ||||||||||||||||||||||||
Sbjct: 594 ggggtgtgcggtcggacccaaaacaccgacagctggcgcgccaggtagggggt 645

>gb|DQ183088.1| Zea mays clone A-RGA20 resistance gene analog-like gene, partial
sequence
Length = 433

Score = 77.8 bits (39), Expect = 2e-10
Identities = 93/111 (83%)
Strand = Plus / Minus

Query: 1614 ccggttgtagctcaagaggttttagaccatgaggaaccacacccccgaagtcgccgaggc 1673
||||| ||||||||| ||||| ||||||||| || | | ||||||| ||||| |||||
Sbjct: 433 ccggtcgtacctcaaaaggttcagaccatgagaaatcgtatccccgaggtcgcgaggc 374

Query: 1674 gggggtgattgaagacttctaccgaggatccaatgactcggcttttcgtccg 1724
|| ||||| || ||||||||| ||||||||||||||||||| |||||||||
Sbjct: 373 ggcagtgatcgaggacttctatagaggatccaatgactcggccttcgtccg 323

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

Score = 69.9 bits (35), Expect = 5e-08
Identities = 54/59 (91%), Gaps = 1/59 (1%)
Strand = Plus / Minus

Query: 2 taccctaaagcaccgcaagggtagccctgggtgtgcggacggactctaaacaccgaca 60
||||||| ||||||||||||| || ||||| ||||||| ||||||||| |||||
Sbjct: 46259 taccctaatagcaccgcaaggg-taacctaggtgtgcggtcggactctaaacaccgaca 46202

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

Score = 67.9 bits (34), Expect = 2e-07
Identities = 68/78 (87%), Gaps = 1/78 (1%)
Strand = Plus / Plus

Query: 37 gcggacggactctaaacaccgacagctggcgcgccaggtaggggtgtgtctttgatctg 96
|||| |||| | |||||||||||||||||||||| |||||| ||||
Sbjct: 446 gcggtcggacccaaaacaccgacagctggcgcgccaggtg-ggggtgtgtcactgatcca 504

Query: 97 agctagctcaatgacat 114
|| ||||||||| ||||
Sbjct: 505 agttagctcaatggccat 522

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

Score = 63.9 bits (32), Expect = 3e-06
Identities = 53/60 (88%)
Strand = Plus / Minus

Query: 2 tacccaaaagcaccgcaagggtagccctgggtgtgcgacggactctaaacaccgacag 61
||||||||||| || ||||||| ||| ||||||||| ||| ||| |||||||||
Sbjct: 389 tacccaaaagcactgcgaggggtaaccccggtgtgcggtcgggtccaaacaccgacag 330

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

Score = 61.9 bits (31), Expect = 1e-05
Identities = 85/103 (82%)
Strand = Plus / Plus

Query: 7 aaaagcaccgcaagggtagccctgggtgtgcgacggactctaaacaccgacagctggc 66
||||||| | |||| | ||| | ||||| | |||| | ||||||||| |
Sbjct: 5330 aaaagcacctcgaggggcaaccccgagtgtgcagtcggacccaaaacaccgacagcttgt 5389

Query: 67 gcgccaggtaggggtgtgtctttgatctgagctagctcaatg 109
||||| |||| ||||| |||| ||||| |||||
Sbjct: 5390 gcgccaagtaggtgtgtgtcactgatccaagctagctcaatg 5432

Score = 61.9 bits (31), Expect = 1e-05
Identities = 58/67 (86%)

Strand = Plus / Plus

```
Query: 152  atgttttgctttggaaccatctcatccatagcagatgaagaggaactctgcaccgcata 211
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 5475 atgttctgcttcggaaccatctcatccgtggcagacgaagaaggaactctacatcgcata 5534
```

```
Query: 212  gcagatc 218
          || ||||
Sbjct: 5535  gcgcatc 5541
```

>gb|AC229874.3| Zea mays BAC clone CH201-314N3 from chromosome 3, complete sequence
Length = 159830

Score = 54.0 bits (27), Expect = 0.003
Identities = 30/31 (96%)
Strand = Plus / Minus

```
Query: 50      aaacaccgacagctggcgcgccaggtagggg 80
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 129148 aaacaccgacagttggcgcgccaggtagggg 129118
```

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

```
Query: 55      ccgacagctggcgcgccaggtagggg 80
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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 = 0.003
Identities = 30/31 (96%)
Strand = Plus / Plus

```
Query: 50      aaacaccgacagctggcgcgccaggtagggg 80
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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 = 0.003
Identities = 30/31 (96%)
Strand = Plus / Minus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
||||||| |||||||
Sbjct: 29283 aaacaccgacagttggcgcgccaggtagggg 29253

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

Query: 55 ccgacagctggcgcgccaggtagggg 80
||||| |||||||
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 = 0.003
Identities = 30/31 (96%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
||||||| |||||||
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 = 0.003
Identities = 30/31 (96%)
Strand = Plus / Minus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
||||||| |||||||
Sbjct: 49821 aaacaccgacagttggcgcgccaggtagggg 49791

>gb|AC237090.1| Oryza granulata clone OG_ABa0119F03, complete sequence
Length = 162698

Score = 54.0 bits (27), Expect = 0.003
Identities = 30/31 (96%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
||||| ||||||||||||||||||||
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 = 0.003
Identities = 30/31 (96%)
Strand = Plus / Minus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
||||||| |||||||||||||||||||
Sbjct: 168287 aaacaccgacagttggcgcgccaggtagggg 168257

>gb|AC233030.1| Oryza minuta clone OM_Ba0022H02, complete sequence
Length = 127011

Score = 54.0 bits (27), Expect = 0.003
Identities = 27/27 (100%)
Strand = Plus / Minus

Query: 55 ccgacagctggcgcgccaggtagggg 81
|||||||||||||||||||||||
Sbjct: 53099 ccgacagctggcgcgccaggtagggg 53073

>gb|AC231332.1| Oryza minuta clone OM_Ba0219N21, complete sequence
Length = 107464

Score = 54.0 bits (27), Expect = 0.003
Identities = 27/27 (100%)
Strand = Plus / Plus

Query: 55 ccgacagctggcgcgccaggtagggg 81
 |||||
Sbjct: 77098 ccgacagctggcgcgccaggtagggg 77124

>gb|AC196829.2| Sorghum bicolor clone SB_BBc0050H06, complete sequence
 Length = 115915

Score = 54.0 bits (27), Expect = 0.003
Identities = 30/31 (96%)
Strand = Plus / Minus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
 |||||
Sbjct: 115212 aaacaccgacagctggcgcgccaggtagggg 115182

Score = 46.1 bits (23), Expect = 0.76
Identities = 23/23 (100%)
Strand = Plus / Minus

Query: 63 tggcgcgccaggtagggggtgtg 85
 |||||
Sbjct: 27029 tggcgcgccaggtagggggtgtg 27007

>gb|AC196818.2| Sorghum bicolor clone SB_BBc0005H14, complete sequence
 Length = 123072

Score = 54.0 bits (27), Expect = 0.003
Identities = 30/31 (96%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
 |||||
Sbjct: 23883 aaacaccgacagctggcgcgccaggtagggg 23913

Score = 46.1 bits (23), Expect = 0.76
Identities = 23/23 (100%)
Strand = Plus / Plus

Query: 63 tggcgcgccaggtagggggtgtg 85

|||||
Sbjct: 77890 tggcgcgccaggtaggggtgtg 77912

>gb|AC165173.2| Zea mays clone ZMMBBb-125019, complete sequence
Length = 157660

Score = 54.0 bits (27), Expect = 0.003
Identities = 30/31 (96%)
Strand = Plus / Minus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
|||||
Sbjct: 19157 aaacaccgacagttggcgcgccaggtagggg 19127

Score = 54.0 bits (27), Expect = 0.003
Identities = 30/31 (96%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
|||||
Sbjct: 141998 aaacaccgacagttggcgcgccaggtagggg 142028

>gb|AY455286.1| Zea mays chloroplast phytoene synthase (Y1) gene, complete cds; nuclear
gene for chloroplast product
Length = 94829

Score = 54.0 bits (27), Expect = 0.003
Identities = 30/31 (96%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
|||||
Sbjct: 61604 aaacaccgacagttggcgcgccaggtagggg 61634

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

Query: 50 aaacaccgacagctggcgcgccaggtagggg 81

|||| ||||||| ||||||||||||||||
Sbjct: 3482 aaacgccgacagttggcgcgccaggtagggg 3451

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

Query: 50 aaacaccgacagctggcgcgccaggtagggg 81
|||| ||||||| ||||||||||||||||
Sbjct: 22781 aaacgccgacagttggcgcgccaggtagggg 22750

>gb|GU080322.1| Saccharum hybrid cultivar R570 clone BAC 086H20, partial sequence
Length = 143827

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

Query: 51 aacaccgacagctggcgcgccaggtagggg 80
||||||||||| ||||||||||||||||
Sbjct: 131948 aacaccgacagttggcgcgccaggtagggg 131977

Score = 46.1 bits (23), Expect = 0.76
Identities = 26/27 (96%)
Strand = Plus / Minus

Query: 50 aaacaccgacagctggcgcgccaggtag 76
||||||||| ||||||||||||||||
Sbjct: 44092 aaacaccgatagctggcgcgccaggtag 44066

>gb|AC231130.2| Oryza minuta clone OM__Ba0135C17, complete sequence
Length = 89171

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

Query: 55 ccgacagctggcgcgccaggtagggg 80
|||||||||||||||||||||||

Sbjct: 44219 ccgacagctggcgcgccaggtagggg 44194

>gb|AC213133.1| Oryza glaberrima clone OG_BB0042C22, complete sequence
Length = 112632

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

Query: 56 cgacagctggcgcgccaggtagggg 81
|||||
Sbjct: 79649 cgacagctggcgcgccaggtagggg 79624

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

Query: 56 cgacagctggcgcgccaggtagggg 81
|||||
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 = 0.012
Identities = 32/34 (94%)
Strand = Plus / Minus

Query: 50 aaacaccgacagctggcgcgccaggtaggggtg 83
|||||
Sbjct: 73626 aaacaccgacagctggcgcgccaggtaggggtg 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 = 0.012
Identities = 32/34 (94%)
Strand = Plus / Minus

Query: 50 aaacaccgacagctggcgcgccaggtaggggtg 83
 |||||
Sbjct: 61954 aaacaccgacagctggcgcgccaggtaggggtg 61921

>emb|CR855170.1| Oryza sativa genomic DNA, chromosome 4, BAC clone: H0818E04, complete
 sequence
 Length = 146307

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

Query: 56 cgacagctggcgcgccaggtaggggg 81
 |||||
Sbjct: 141993 cgacagctggcgcgccaggtaggggg 142018

>gb|AC105320.2| Oryza sativa Japonica Group chromosome 5 clone OJ1675_H07, complete
 sequence
 Length = 135294

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

Query: 56 cgacagctggcgcgccaggtaggggg 81
 |||||
Sbjct: 105195 cgacagctggcgcgccaggtaggggg 105220

>gb|AC117264.2| Oryza sativa Japonica Group chromosome 5 clone OJ1005_D04, complete
 sequence
 Length = 168424

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

Query: 56 cgacagctggcgcgccaggtaggggg 81
 |||||
Sbjct: 56260 cgacagctggcgcgccaggtaggggg 56285

>gb|AC135924.2| Oryza sativa Japonica Group chromosome 5 clone P0486C01, complete

sequence
Length = 146432

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

Query: 56 cgacagctggcgccaggtagggg 81
|||||||
Sbjct: 55487 cgacagctggcgccaggtagggg 55462

>gb|AC130598.2| Oryza sativa Japonica Group chromosome 5 clone OSJNBa0056I11,
complete sequence
Length = 145796

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

Query: 56 cgacagctggcgccaggtagggg 81
|||||||
Sbjct: 4119 cgacagctggcgccaggtagggg 4094

>gb|AC145127.1| Oryza sativa Japonica Group chromosome 10 clone Pseudo10p0.0-10p4.4,
complete sequence
Length = 2331000

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

Query: 56 cgacagctggcgccaggtagggg 81
|||||||
Sbjct: 588003 cgacagctggcgccaggtagggg 587978

Score = 46.1 bits (23), Expect = 0.76
Identities = 26/27 (96%)
Strand = Plus / Plus

Query: 55 ccgacagctggcgccaggtagggg 81
||||| |||||

Sbjct: 1793581 ccgacatctggcgcgccaggtaggggg 1793607

>gb|AC092388.5| Oryza sativa chromosome 10 BAC OSJNBa0011L09 genomic sequence, complete
sequence

Length = 177565

Score = 52.0 bits (26), Expect = 0.012

Identities = 26/26 (100%)

Strand = Plus / Minus

Query: 56 cgacagctggcgcgccaggtaggggg 81

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

Sbjct: 86800 cgacagctggcgcgccaggtaggggg 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 = 0.012

Identities = 26/26 (100%)

Strand = Plus / Minus

Query: 56 cgacagctggcgcgccaggtaggggg 81

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

Sbjct: 55611 cgacagctggcgcgccaggtaggggg 55586

>dbj|AP006233.3| Oryza sativa Japonica Group genomic DNA, chromosome 1, BAC
clone:B1249E06

Length = 126534

Score = 52.0 bits (26), Expect = 0.012

Identities = 26/26 (100%)

Strand = Plus / Minus

Query: 56 cgacagctggcgcgccaggtaggggg 81

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

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 = 0.012
Identities = 26/26 (100%)
Strand = Plus / Plus

Query: 56 cgacagctggcgccaggtagggg 81
|||||
Sbjct: 73246 cgacagctggcgccaggtagggg 73271

>dbj|AP004729.3| Oryza sativa Japonica Group genomic DNA, chromosome 6, BAC
clone:OSJNBa0006A22
Length = 190690

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

Query: 56 cgacagctggcgccaggtagggg 81
|||||
Sbjct: 37650 cgacagctggcgccaggtagggg 37675

>dbj|AP003458.4| Oryza sativa Japonica Group genomic DNA, chromosome 6, PAC clone:P0701E03
Length = 183245

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

Query: 56 cgacagctggcgccaggtagggg 81
|||||
Sbjct: 153905 cgacagctggcgccaggtagggg 153880

>dbj|AP005684.3| Oryza sativa Japonica Group genomic DNA, chromosome 9, BAC
clone:OJ1742_G01
Length = 154912

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

Query: 56 cgacagctggcgccaggtagggg 81
|||||

Sbjct: 81368 cgacagctggcgcgccaggtagggg 81393

>dbj|AP005834.4| Oryza sativa Japonica Group genomic DNA, chromosome 7, BAC
clone:OSJNBa0005C24
Length = 168151

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

Query: 56 cgacagctggcgcgccaggtagggg 81
|||||
Sbjct: 104930 cgacagctggcgcgccaggtagggg 104905

>dbj|AP006556.2| Oryza sativa Japonica Group genomic DNA, chromosome 7, BAC
clone:B1010G04a
Length = 61450

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

Query: 56 cgacagctggcgcgccaggtagggg 81
|||||
Sbjct: 25639 cgacagctggcgcgccaggtagggg 25664

>dbj|AP005414.3| Oryza sativa Japonica Group genomic DNA, chromosome 2, BAC
clone:OSJNBa0073G17
Length = 162391

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

Query: 56 cgacagctggcgcgccaggtagggg 81
|||||
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 = 0.012
Identities = 26/26 (100%)
Strand = Plus / Plus

Query: 56 cgacagctggcgcgccaggtaggggg 81
|||||||
Sbjct: 117613 cgacagctggcgcgccaggtaggggg 117638

>dbj|AP003988.3| Oryza sativa Japonica Group genomic DNA, chromosome 2, BAC
clone:OJ1057_D08
Length = 119557

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

Query: 56 cgacagctggcgcgccaggtaggggg 81
|||||||
Sbjct: 54098 cgacagctggcgcgccaggtaggggg 54123

>dbj|AP005563.3| Oryza sativa Japonica Group genomic DNA, chromosome 9, BAC
clone:OJ1227_D07
Length = 118358

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

Query: 56 cgacagctggcgcgccaggtaggggg 81
|||||||
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 = 0.012
Identities = 26/26 (100%)
Strand = Plus / Minus

Query: 56 cgacagctggcgcgccaggtaggggg 81
|||||||

Sbjct: 39151 cgacagctggcgcgccaggtagggg 39126

>dbj|AP006062.2| Oryza sativa Japonica Group genomic DNA, chromosome 9, PAC clone:P0415D04
Length = 176627

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

Query: 56 cgacagctggcgcgccaggtagggg 81
|||||||
Sbjct: 164658 cgacagctggcgcgccaggtagggg 164683

>dbj|AP005795.3| Oryza sativa Japonica Group genomic DNA, chromosome 8, BAC
clone:B1090H08
Length = 200720

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

Query: 56 cgacagctggcgcgccaggtagggg 81
|||||||
Sbjct: 75026 cgacagctggcgcgccaggtagggg 75001

>dbj|AP005512.3| Oryza sativa Japonica Group genomic DNA, chromosome 8, BAC
clone:OSJNBa0012003
Length = 141860

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

Query: 56 cgacagctggcgcgccaggtagggg 81
|||||||
Sbjct: 134937 cgacagctggcgcgccaggtagggg 134962

>dbj|AP004645.3| Oryza sativa Japonica Group genomic DNA, chromosome 8, BAC
clone:OJ1119_B10
Length = 148508

Score = 52.0 bits (26), Expect = 0.012

Identities = 26/26 (100%)
Strand = Plus / Minus

Query: 56 cgacagctggcgcgccaggtagggg 81
|||||||
Sbjct: 82803 cgacagctggcgcgccaggtagggg 82778

>dbj|AP004375.3| Oryza sativa Japonica Group genomic DNA, chromosome 8, PAC
clone:P0475C12
Length = 140863

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

Query: 56 cgacagctggcgcgccaggtagggg 81
|||||||
Sbjct: 26933 cgacagctggcgcgccaggtagggg 26958

>dbj|AP006237.3| Oryza sativa Japonica Group genomic DNA, chromosome 1, BAC
clone:OSJNBb0008D07
Length = 156874

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

Query: 56 cgacagctggcgcgccaggtagggg 81
|||||||
Sbjct: 1391 cgacagctggcgcgccaggtagggg 1416

>emb|AL731605.3| Oryza sativa genomic DNA, chromosome 4, BAC clone: OSJNBa0042F21,
complete sequence
Length = 167113

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

Query: 56 cgacagctggcgcgccaggtagggg 81
|||||||
Sbjct: 110588 cgacagctggcgcgccaggtagggg 110563

>dbj|AP004611.3| Oryza sativa Japonica Group genomic DNA, chromosome 1, BAC
clone:OJ1005_B10
Length = 142680

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

Query: 56 cgacagctggcgcgccaggtaggggg 81
|||||
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 = 0.012
Identities = 26/26 (100%)
Strand = Plus / Plus

Query: 56 cgacagctggcgcgccaggtaggggg 81
|||||
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 = 0.012
Identities = 26/26 (100%)
Strand = Plus / Minus

Query: 56 cgacagctggcgcgccaggtaggggg 81
|||||
Sbjct: 127992 cgacagctggcgcgccaggtaggggg 127967

>dbj|AP003760.4| Oryza sativa Japonica Group genomic DNA, chromosome 1, BAC
clone:OSJNBb0063G05
Length = 182681

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

Strand = Plus / Plus

```
Query: 56      cgacagctggcgcgccaggtaggggg 81
             |||||
Sbjct: 167523 cgacagctggcgcgccaggtaggggg 167548
```

>dbj|AP004194.3| Oryza sativa Japonica Group genomic DNA, chromosome 1, PAC
clone:P0014E08
Length = 144219

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

```
Query: 56      cgacagctggcgcgccaggtaggggg 81
             |||||
Sbjct: 69901 cgacagctggcgcgccaggtaggggg 69926
```

>dbj|AP002482.1| Oryza sativa Japonica Group genomic DNA, chromosome 1, clone:P0706B05
Length = 187835

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

```
Query: 56      cgacagctggcgcgccaggtaggggg 81
             |||||
Sbjct: 40167 cgacagctggcgcgccaggtaggggg 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 = 0.012
Identities = 26/26 (100%)
Strand = Plus / Minus

```
Query: 56      cgacagctggcgcgccaggtaggggg 81
             |||||
Sbjct: 62956 cgacagctggcgcgccaggtaggggg 62931
```

>emb|AL731592.2| Oryza sativa genomic DNA, chromosome 4, BAC clone: OSJNBa0036B17,
complete sequence
Length = 99093

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

Query: 56 cgacagctggcgcgccaggtaggggg 81
|||||||
Sbjct: 30047 cgacagctggcgcgccaggtaggggg 30022

>gb|GQ407104.1| Oryza granulata chromosome 6 clone BAC a0186L08/a0076A15, complete
sequence
Length = 242758

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

Query: 57 gacagctggcgcgccaggtaggggg 81
|||||||
Sbjct: 182050 gacagctggcgcgccaggtaggggg 182074

>gb|AC231811.1| Oryza minuta clone OM__Ba0091E17, complete sequence
Length = 115162

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

Query: 59 cagctggcgcgccaggtagggggtg 83
|||||||
Sbjct: 113939 cagctggcgcgccaggtagggggtg 113963

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

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

Query: 50 aaacaccgacagctggcgcgccaggtaggggt 82
||||| ||||| ||||||||||||||||
Sbjct: 39149 aaacatcgacagttggcgcgccaggtaggggt 39117

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
||||| ||||| ||||||||||||||||
Sbjct: 58988 aaacgccgacagttggcgcgccaggtagggg 59018

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Minus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
||||||||||| ||||||| |||||||
Sbjct: 179323 aaacaccgacagttggcgcgctaggtagggg 179293

>gb|AF391808.3| Zea mays cultivar McC bz locus region
Length = 225984

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

Query: 50 aaacaccgacagctggcgcgccaggtaggggt 82
||||| ||||| ||||||||||||||||
Sbjct: 38172 aaacatcgacagttggcgcgccaggtaggggt 38140

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
||||| ||||| ||||||||||||||||

Sbjct: 58012 aaacgccgacagttggcgcgccaggtagggg 58042

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Minus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
|||||
Sbjct: 179665 aaacaccgacagttggcgcgctaggtagggg 179635

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
||||
Sbjct: 202313 aaacgccgacagttggcgcgccaggtagggg 202343

>emb|CR855225.1| Oryza sativa genomic DNA, chromosome 4, BAC clone:
OSIGBa0138H21-OSIGBa0138E01, complete sequence
Length = 129321

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

Query: 56 cgacagctggcgcgccaggtagggg 80
|||||
Sbjct: 8725 cgacagctggcgcgccaggtagggg 8749

>gb|AC083945.3| Oryza sativa Japonica Group chromosome X clone OSJNBa0058E19, complete
sequence
Length = 147706

Score = 50.1 bits (25), Expect = 0.048
Identities = 28/29 (96%)
Strand = Plus / Minus

Query: 55 ccgacagctggcgcgccaggtagggggtg 83

||||| ||||||||||||||||||
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 = 0.048
Identities = 25/25 (100%)
Strand = Plus / Minus

Query: 56 cgacagctggcgcgccaggtagggg 80
||||||||||||||||
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 = 0.048
Identities = 28/29 (96%)
Strand = Plus / Plus

Query: 52 acaccgacagctggcgcgccaggtagggg 80
||||||||| ||||||||||||||
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 = 0.048
Identities = 28/29 (96%)
Strand = Plus / Plus

Query: 52 acaccgacagctggcgcgccaggtagggg 80
||||||||| ||||||||||||||
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 = 0.048
Identities = 25/25 (100%)
Strand = Plus / Minus

Query: 56 cgacagctggcgcgccaggtagggg 80
|||||
Sbjct: 83012 cgacagctggcgcgccaggtagggg 82988

>emb|AL606649.4| Oryza sativa genomic DNA, chromosome 4, BAC clone: OSJNBb0003B01,
complete sequence
Length = 153643

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

Query: 56 cgacagctggcgcgccaggtagggg 80
|||||
Sbjct: 40302 cgacagctggcgcgccaggtagggg 40326

>gb|AY530950.1| Zea mays putative zinc finger protein (Z438D03.1), unknown (Z438D03.5),
epsilon-COP (Z438D03.6), putative kinase (Z438D03.7),
unknown (Z438D03.25), and C1-B73 (Z438D03.27) genes,
complete cds
Length = 185988

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

Query: 50 aaacaccgacagctggcgcgccaggtagggggt 82
|||| |||||
Sbjct: 111324 aaacgccgacagttggcgcgccaggtagggggt 111292

>dbj|AP005866.2| Oryza sativa Japonica Group genomic DNA, chromosome 8, BAC
clone:OSJNBb0076003
Length = 140823

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

Query: 56 cgacagctggcgcgccaggtaggg 80
||||||||||||||||||||
Sbjct: 46297 cgacagctggcgcgccaggtaggg 46273

>dbj|AP003435.2| Oryza sativa Japonica Group genomic DNA, chromosome 1, PAC
clone:P0455H03
Length = 175947

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

Query: 56 cgacagctggcgcgccaggtaggg 80
||||||||||||||||||||
Sbjct: 18120 cgacagctggcgcgccaggtaggg 18144

>gb|AC229780.2| Oryza minuta clone OM__Ba0081J07, complete sequence
Length = 103110

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

Query: 53 caccgacagctggcgcgccaggtaggg 80
|||||||||||||||||||
Sbjct: 94501 caccgacagctggcgcgctaggtaggg 94474

>gb|AC231887.2| Oryza minuta clone OM__Ba0018L21, complete sequence
Length = 97902

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

Query: 56 cgacagctggcgcgccaggtaggg 79
|||||||||||||||||||
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 = 0.19
Identities = 33/36 (91%)
Strand = Plus / Minus

Query: 48 ctaaacaccgacagctggcgcgccaggtaggggtg 83
 ||||||| ||||||||| ||||| |||||||||
Sbjct: 83102 ctaaacatcgacagctggcacgccaagtaggggtg 83067

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
 ||||| ||||||| |||||||||||||||||
Sbjct: 177040 aaacgccgacagttggcgcgccaggtagggg 177070

>gb|FJ266023.1| Oryza granulata clone OG_ABa077F15_032P05, complete sequence
Length = 285707

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

Query: 55 ccgacagctggcgcgccaggtagg 78
 |||||||||||||||||||||
Sbjct: 28434 ccgacagctggcgcgccaggtagg 28411

>gb|AC231882.1| Oryza minuta clone OM__Ba0091G05, complete sequence
Length = 123139

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

Query: 56 cgacagctggcgcgccaggtaggg 79
 |||||||||||||||||||||
Sbjct: 32770 cgacagctggcgcgccaggtaggg 32793

>gb|AC229741.1| Oryza minuta clone OM__Ba0230E13, complete sequence
Length = 130811

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

Query: 53 caccgacagctggcgcgccaggtagggg 80
|||||||
Sbjct: 37301 caccgacagctggcgcgctaggtagggg 37274

>gb|AC223439.1| Oryza brachyantha, complete sequence
Length = 163153

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

Query: 56 cgacagctggcgcgccaggtagggggtg 83
|||||
Sbjct: 121233 cgacagtggcgcgccaggtagggggtg 121206

>gb|AC097176.3| Oryza sativa Japonica Group chromosome 5 clone OJ1576_F01, complete
sequence
Length = 119525

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

Query: 58 acagctggcgcgccaggtagggg 81
|||||||
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 = 0.19
Identities = 30/32 (93%)
Strand = Plus / Plus

Query: 56 cgacagctggcgcgccaggtagggggtgtgtc 87
|||||

Sbjct: 12916 cgacagttggcgcgccaggtaggggttggtc 12947

>gb|AC130602.5| Oryza sativa Japonica Group chromosome 5 clone B1122D01, complete
sequence
Length = 126532

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

Query: 58 acagctggcgcgccaggtaggggg 81
|||||||
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 = 0.19
Identities = 27/28 (96%)
Strand = Plus / Plus

Query: 56 cgacagctggcgcgccaggtaggggggtg 83
||||| |||||||
Sbjct: 65303 cgacagttggcgcgccaggtaggggggtg 65330

>dbj|AP005458.3| Oryza sativa Japonica Group genomic DNA, chromosome 6, PAC
clone:P0567G03
Length = 196834

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

Query: 56 cgacagctggcgcgccaggtaggggggtg 83
||||| |||||||
Sbjct: 6508 cgacagttggcgcgccaggtaggggggtg 6481

>dbj|AP005456.3| Oryza sativa Japonica Group genomic DNA, chromosome 6, PAC
clone:P0513E02
Length = 141477

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

Query: 56 cgacagctggcgcgccaggtagggggtg 83
||||| ||||||||||||||||||
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 = 0.19
Identities = 30/32 (93%)
Strand = Plus / Plus

Query: 56 cgacagctggcgcgccaggtagggggtgtgtc 87
||||| |||||||||||||||||| |||||
Sbjct: 3402 cgacagttggcgcgccaggtagggggtgtgtc 3433

>dbj|AP005424.3| Oryza sativa Japonica Group genomic DNA, chromosome 9, PAC
clone:P0556H01
Length = 149800

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

Query: 56 cgacagctggcgcgccaggtagggggtgtgtc 87
||||| |||||||||||||||||| |||||
Sbjct: 91487 cgacagttggcgcgccaggtagggggtgtgtc 91518

>dbj|AP005774.5| Oryza sativa Japonica Group genomic DNA, chromosome 7, BAC
clone:OSJNBa0086N05
Length = 163670

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

Query: 56 cgacagctggcgcgccaggtagggggtg 83
||||| ||||||||||||||||||

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 = 0.19
Identities = 27/28 (96%)
Strand = Plus / Plus

Query: 56 cgacagctggcgcgccaggtagggggtg 83
||||| ||||||||||||||||||||
Sbjct: 3663 cgacagttggcgcgccaggtagggggtg 3690

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

Query: 56 cgacagctggcgcgccaggtaggggg 81
||||||| ||||||||||||||||
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 = 0.19
Identities = 30/32 (93%)
Strand = Plus / Minus

Query: 55 ccgacagctggcgcgccaggtagggggtgtgt 86
||||| |||||||||||||||||| |||||
Sbjct: 66521 ccgacatctggcgcgccaggtaggggtgtgtgt 66490

>dbj|AP003974.3| Oryza sativa Japonica Group genomic DNA, chromosome 2, BAC
clone:OJ1003_F05
Length = 147472

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

Query: 55 cgcacagctggcgcgccaggtagggggtgtgt 86
 ||||| |||||||||||||||| |||||
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 = 0.19
Identities = 27/28 (96%)
Strand = Plus / Minus

Query: 56 cgacagctggcgcgccaggtagggggtg 83
 ||||| |||||||||||||||| |||||
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 = 0.19
Identities = 30/32 (93%)
Strand = Plus / Minus

Query: 56 cgacagctggcgcgccaggtagggggtgtgtc 87
 ||||| |||||||||||||||| |||||
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 = 0.19
Identities = 24/24 (100%)
Strand = Plus / Plus

Query: 58 acagctggcgcgccaggtaggggg 81
 |||||||||||||||| |||||
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 = 0.19
Identities = 27/28 (96%)
Strand = Plus / Plus

Query: 56 cgacagctggcgcgccaggtagggggtg 83
||||| ||||||||||||||||||||
Sbjct: 84158 cgacagttggcgcgccaggtagggggtg 84185

>emb|AL731618.3| Oryza sativa genomic DNA, chromosome 4, BAC clone: OSJNBb0012A12,
complete sequence
Length = 122766

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

Query: 56 cgacagctggcgcgccaggtagggggtg 83
||||| ||||||||||||||||||||
Sbjct: 8706 cgacagttggcgcgccaggtagggggtg 8733

>emb|AL663012.3| Oryza sativa genomic DNA, chromosome 4, BAC clone: OSJNBb0069N01,
complete sequence
Length = 180264

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

Query: 56 cgacagctggcgcgccaggtagggggtg 83
||||| ||||||||||||||||||||
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 = 0.19
Identities = 30/32 (93%)
Strand = Plus / Minus

Query: 56 cgacagctggcgcgccaggtagggggtgtgtc 87
||||| ||||||||||||||| |||||
Sbjct: 50301 cgacagttggcgcgccaggtaggggtgtgtc 50270

>dbj|AP003204.3| Oryza sativa Japonica Group genomic DNA, chromosome 1, BAC clone:B1111C09
Length = 156393

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

Query: 56 cgacagctggcgcgccaggtagggggtg 83
||||| ||||||||||||||| |||||
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 = 0.19
Identities = 27/28 (96%)
Strand = Plus / Minus

Query: 56 cgacagctggcgcgccaggtagggggtg 83
||||| ||||||||||||||| |||||
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 = 0.19
Identities = 27/28 (96%)
Strand = Plus / Plus

Query: 56 cgacagctggcgcgccaggtagggggtg 83
||||| ||||||||||||||| |||||
Sbjct: 35648 cgacagttggcgcgccaggtagggggtg 35675

>gb|AC208340.4| Zea mays BAC clone CH201-53J11 from chromosome 5, complete sequence

Length = 187725

Score = 46.1 bits (23), Expect = 0.76

Identities = 29/31 (93%)

Strand = Plus / Minus

```
Query: 50    aaacaccgacagctggcgcgccaggtagggg 80
           |||| | |||| |||| |||| |||| |||| |||| ||||
Sbjct: 4170 aaacgccgacagttggcgcgccaggtagggg 4140
```

Score = 46.1 bits (23), Expect = 0.76

Identities = 29/31 (93%)

Strand = Plus / Plus

```
Query: 50    aaacaccgacagctggcgcgccaggtagggg 80
           |||| | |||| |||| |||| |||| |||| |||| ||||
Sbjct: 49380 aaacgccgacagttggcgcgccaggtagggg 49410
```

Score = 46.1 bits (23), Expect = 0.76

Identities = 29/31 (93%)

Strand = Plus / Plus

```
Query: 50    aaacaccgacagctggcgcgccaggtagggg 80
           |||| | |||| |||| |||| |||| |||| |||| ||||
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 = 0.76

Identities = 29/31 (93%)

Strand = Plus / Minus

```
Query: 50    aaacaccgacagctggcgcgccaggtagggg 80
           |||| | |||| |||| |||| |||| |||| |||| ||||
Sbjct: 57575 aaacgccgacagttggcgcgccaggtagggg 57545
```

Score = 46.1 bits (23), Expect = 0.76

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

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
 |||| | ||||| | ||||| ||||| |||||
Sbjct: 82787 aaacgccgacagttggcgcgccaggtagggg 82817

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

Query: 55 ccgacagctggcgcgccaggtagggg 80
 ||||| | ||||| ||||| ||||| |||||
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 = 0.76
Identities = 29/31 (93%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
 |||| | ||||| | ||||| ||||| |||||
Sbjct: 52277 aaacgccgacagttggcgcgccaggtagggg 52307

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Minus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
 |||| | ||||| | ||||| ||||| |||||
Sbjct: 94136 aaacgccgacagttggcgcgccaggtagggg 94106

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

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)

Strand = Plus / Minus

```
Query: 50      aaacaccgacagctggcgcgccaggtagggg 80
          |||| | ||||| | ||||| ||||| |||||
Sbjct: 27051 aaacgccgacagttggcgcgccaggtagggg 27021
```

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Minus

```
Query: 50      aaacaccgacagctggcgcgccaggtagggg 80
          |||| | ||||| | ||||| ||||| |||||
Sbjct: 97256 aaacgccgacagttggcgcgccaggtagggg 97226
```

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Minus

```
Query: 50      aaacaccgacagctggcgcgccaggtagggg 80
          |||| | ||||| | ||||| ||||| |||||
Sbjct: 103145 aaacgccgacagttggcgcgccaggtagggg 103115
```

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

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Plus

```
Query: 50      aaacaccgacagctggcgcgccaggtagggg 80
          |||| | ||||| | ||||| ||||| |||||
Sbjct: 81522 aaacgccgacagttggcgcgccaggtagggg 81552
```

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

Query: 55 ccgacagctggcgcgccaggtagggg 80
 ||||| ||||||||||||||||
Sbjct: 45119 ccgacagttggcgcgccaggtagggg 45144

>gb|AC210260.5| Zea mays BAC clone CH201-44F4 from chromosome 5, complete sequence
 Length = 188949

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
 |||| |||||| ||||||||||||||||
Sbjct: 112762 aaacgccgacagttggcgcgccaggtagggg 112792

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
 |||| |||||| ||||||||||||||||
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 = 0.76
Identities = 29/31 (93%)
Strand = Plus / Minus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
 |||| |||||| ||||||||||||||||
Sbjct: 57140 aaacgccgacagttggcgcgccaggtagggg 57110

>gb|AC216070.4| Zea mays BAC clone CH201-459P15 from chromosome 5, complete sequence
 Length = 226532

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Minus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
 |||| | ||||| | ||||| ||||| ||||| |||||
Sbjct: 77633 aaacgccgacagtggcgcgccaggtagggg 77603

>gb|AC226721.2| Zea mays BAC clone CH201-150M20 from chromosome 10, complete sequence
Length = 207605

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Minus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
 |||| | ||||| | ||||| ||||| ||||| |||||
Sbjct: 148376 aaacgccgacagtggcgcgccaggtagggg 148346

>gb|AC213983.4| Zea mays BAC clone CH201-326E16 from chromosome 5, complete sequence
Length = 180103

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Minus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
 |||| | ||||| | ||||| ||||| ||||| |||||
Sbjct: 6768 aaacgccgacagtggcgcgccaggtagggg 6738

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Minus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
 |||| | ||||| | ||||| ||||| ||||| |||||
Sbjct: 126670 aaacgccgacagtggcgcgccaggtagggg 126640

>gb|AC225944.3| Zea mays BAC clone CH201-127G5 from chromosome 10, complete sequence
Length = 216347

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
 |||| | ||||| | ||||| ||||| |||||
Sbjct: 107278 aaacgccgacagttggcgcgccaggtagggg 107308

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Minus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
 |||| | ||||| | ||||| ||||| |||||
Sbjct: 160565 aaacgccgacagttggcgcgccaggtagggg 160535

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

Query: 55 ccgacagctggcgcgccaggtagggg 80
 ||||| | ||||| ||||| ||||| |||||
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 = 0.76
Identities = 29/31 (93%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
 |||| | ||||| | ||||| ||||| |||||
Sbjct: 23565 aaacgccgacagttggcgcgccaggtagggg 23595

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80

|||| ||||||| ||||||||||||||||
Sbjct: 58049 aaacgccgacagttggcgcgccaggtagggg 58079

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Minus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
|||| ||||||| ||||||||||||||||
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 = 0.76
Identities = 29/31 (93%)
Strand = Plus / Minus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
|||| ||||||| ||||||||||||||||
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 = 0.76
Identities = 29/31 (93%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
|||| ||||||| ||||||||||||||||
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 = 0.76
Identities = 29/31 (93%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgccaggtagggg 80

|||| ||||||| ||||||||||||||||
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 = 0.76
Identities = 29/31 (93%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
|||| ||||||| ||||||||||||||||
Sbjct: 42913 aaacgccgacagttggcgcgccaggtagggg 42943

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
|||| ||||||| ||||||||||||||||
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 = 0.76
Identities = 29/31 (93%)
Strand = Plus / Minus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
|||| ||||||| ||||||||||||||||
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 = 0.76
Identities = 29/31 (93%)
Strand = Plus / Minus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
|||| |||||| ||||||||||||||||
Sbjct: 1307 aaacgccgacagttggcgcgccaggtagggg 1277

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
|||| |||||| ||||||||||||||||
Sbjct: 156005 aaacgccgacagttggcgcgccaggtagggg 156035

>gb|AC210188.4| Zea mays BAC clone CH201-257L10 from chromosome 5, complete sequence
Length = 181384

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Minus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
|||| |||||| ||||||||||||||||
Sbjct: 87495 aaacgccgacagttggcgcgccaggtagggg 87465

>gb|AC195458.4| Zea mays BAC clone CH201-47808 from chromosome 5, complete sequence
Length = 200301

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
|||| |||||| ||||||||||||||||
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 = 0.76
Identities = 29/31 (93%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
 |||| | ||||| | ||||| ||||| |||||
Sbjct: 73957 aaacgccgacagttggcgcgccaggtagggg 73987

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
 |||| | ||||| | ||||| ||||| |||||
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 = 0.76
Identities = 29/31 (93%)
Strand = Plus / Minus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
 |||| | ||||| | ||||| ||||| |||||
Sbjct: 43908 aaacgccgacagttggcgcgccaggtagggg 43878

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Minus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
 |||| | ||||| | ||||| ||||| |||||
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 = 0.76
Identities = 29/31 (93%)
Strand = Plus / Minus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
 ||||| ||||||| |||||||||||||||||
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 = 0.76
Identities = 29/31 (93%)
Strand = Plus / Minus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
 ||||| ||||||| |||||||||||||||||
Sbjct: 156086 aaacgccgacagttggcgcgccaggtagggg 156056

>gb|AC237089.1| Oryza granulata clone OG_ABa0096023, complete sequence
Length = 145921

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
 ||||| ||||||| |||||||||||||||||
Sbjct: 13212 aaacatcgacagttggcgcgccaggtagggg 13242

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Minus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
 ||||| ||||||| |||||||||||||||||
Sbjct: 19723 aaacatcgacagttggcgcgccaggtagggg 19693

>gb|AC237088.1| Oryza granulata clone OG_ABa0089G14, complete sequence
Length = 118754

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
||||| ||||| ||||||||||||||||
Sbjct: 39396 aaacatcgacagttggcgcgccaggtagggg 39426

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
||||| ||||| ||||||||||||||||
Sbjct: 97242 aaacatcgacagttggcgcgccaggtagggg 97272

>gb|AC237087.1| Oryza granulata clone OG_ABa0028G18, complete sequence
Length = 124143

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Minus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
||||| ||||| ||||||||||||||||
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 = 0.76
Identities = 29/31 (93%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
||||| ||||| ||||||||||||||||
Sbjct: 51769 aaacgcccagagttggcgcgccaggtagggg 51799

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
 ||||| |||| | ||||| |||||
Sbjct: 131072 aaacaccgacagttggcacgccaggtagggg 131102

>ref|XM_002442558.1| Sorghum bicolor hypothetical protein, mRNA
 Length = 654

Score = 46.1 bits (23), Expect = 0.76
Identities = 23/23 (100%)
Strand = Plus / Plus

Query: 63 tggcgcgccaggtagggggtgtg 85
 ||||| ||||| ||||| |||||
Sbjct: 353 tggcgcgccaggtagggggtgtg 375

>ref|XM_002465520.1| Sorghum bicolor hypothetical protein, mRNA
 Length = 3219

Score = 46.1 bits (23), Expect = 0.76
Identities = 23/23 (100%)
Strand = Plus / Plus

Query: 63 tggcgcgccaggtagggggtgtg 85
 ||||| ||||| ||||| |||||
Sbjct: 26 tggcgcgccaggtagggggtgtg 48

>gb|FJ614806.1| Zea mays cultivar B73 p cluster, complete sequence
 Length = 379557

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Minus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
 |||| | ||||| ||||| ||||| |||||
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 = 0.76
Identities = 29/31 (93%)

Strand = Plus / Minus

```
Query: 50      aaacaccgacagctggcgcgccaggtagggg 80
          |||| | ||||| | ||||| ||||| |||||
Sbjct: 114757 aaacgccgacagttggcgcgccaggtagggg 114727
```

>gb|AC232337.2| Oryza minuta clone OM__Ba0147P17, complete sequence
Length = 111380

Score = 46.1 bits (23), Expect = 0.76
Identities = 26/27 (96%)
Strand = Plus / Plus

```
Query: 55      ccgacagctggcgcgccaggtaggggg 81
          ||||| | ||||| ||||| ||||| |||||
Sbjct: 16560 ccgacagttggcgcgccaggtaggggg 16586
```

>gb|AC213131.2| Oryza glaberrima clone OG_BB0031E23, complete sequence
Length = 118417

Score = 46.1 bits (23), Expect = 0.76
Identities = 26/27 (96%)
Strand = Plus / Minus

```
Query: 55      ccgacagctggcgcgccaggtaggggg 81
          ||||| | ||||| ||||| ||||| |||||
Sbjct: 39516 ccgacatctggcgcgccaggtaggggg 39490
```

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

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Plus

```
Query: 50      aaacaccgacagctggcgcgccaggtagggg 80
          |||| | ||||| | ||||| ||||| |||||
Sbjct: 113138 aaacgccgacagttggcgcgccaggtagggg 113168
```

Score = 46.1 bits (23), Expect = 0.76

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

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
|||| |||||| |||||||||
Sbjct: 144830 aaacgccgacagttggcgcgccaggtagggg 144800

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Minus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
|||| |||||| |||||||||
Sbjct: 161365 aaacgccgacagttggcgcgccaggtagggg 161335

>gb|AC217961.4| Zea mays BAC clone ZMMBBb-353K3 from chromosome 6, complete sequence
Length = 130360

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
|||| |||||| |||||||||
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 = 0.76
Identities = 29/31 (93%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
|||| |||||| |||||||||
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 = 0.76
Identities = 29/31 (93%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
||||| ||||||| ||||||||||||||||
Sbjct: 19091 aaacgccgacagttggcgcgccaggtagggg 19121

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Minus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
||||| ||||||| ||||||||||||||||
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 = 0.76
Identities = 29/31 (93%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
||||| ||||||| ||||||||||||||||
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 = 0.76
Identities = 26/27 (96%)
Strand = Plus / Minus

Query: 56 cgacagctggcgcgccaggtagggggt 82
||||||||||||||||| |||||
Sbjct: 69320 cgacagctggcgcgccaggtaaagggt 69294

>gb|EU940899.1| Zea mays clone 1168123 mRNA sequence

Length = 3007

Score = 46.1 bits (23), Expect = 0.76

Identities = 29/31 (93%)

Strand = Plus / Plus

```
Query: 50   aaacaccgacagctggcgcgccaggtagggg 80
          |||| ||||| ||||| ||||| |||||
Sbjct: 1968 aaacgccgacagttggcgcgccaggtagggg 1998
```

>gb|AC229778.1| Oryza minuta clone OM_Ba0085P10, complete sequence
Length = 103044

Score = 46.1 bits (23), Expect = 0.76

Identities = 23/23 (100%)

Strand = Plus / Plus

```
Query: 59   cagctggcgcgccaggtagggg 81
          ||||| ||||| ||||| |||||
Sbjct: 47518 cagctggcgcgccaggtagggg 47540
```

>gb|AC225785.1| Oryza granulata, complete sequence
Length = 117123

Score = 46.1 bits (23), Expect = 0.76

Identities = 29/31 (93%)

Strand = Plus / Minus

```
Query: 50   aaacaccgacagctggcgcgccaggtagggg 80
          |||| ||||| ||||| ||||| |||||
Sbjct: 36202 aaacatcgacagttggcgcgccaggtagggg 36172
```

>gb|AC196850.2| Sorghum bicolor clone SB_BBc0140005, complete sequence
Length = 112839

Score = 46.1 bits (23), Expect = 0.76

Identities = 23/23 (100%)

Strand = Plus / Minus

```
Query: 63   tggcgcgccaggtagggggtgtg 85
          ||||| ||||| ||||| |||||
Sbjct: 6943 tggcgcgccaggtagggggtgtg 6921
```

>gb|AC196847.2| Sorghum bicolor clone SB_BBc0109L12, complete sequence
Length = 112916

Score = 46.1 bits (23), Expect = 0.76
Identities = 23/23 (100%)
Strand = Plus / Minus

Query: 63 tggcgcgccaggtaggggtgtg 85
 |||||
Sbjct: 20035 tggcgcgccaggtaggggtgtg 20013

>gb|AC196837.2| Sorghum bicolor clone SB_BBc0073F19, complete sequence
Length = 105211

Score = 46.1 bits (23), Expect = 0.76
Identities = 23/23 (100%)
Strand = Plus / Plus

Query: 63 tggcgcgccaggtaggggtgtg 85
 |||||
Sbjct: 115 tggcgcgccaggtaggggtgtg 137

>gb|DQ493648.1| Zea mays cultivar I137TN bz locus region
Length = 120751

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
 ||||| || |||||
Sbjct: 26152 aaacaccgatagttggcgcgccaggtagggg 26182

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
 ||||| |||||

Sbjct: 94738 aaacgccgacagttggcgccaggtagggg 94768

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

Score = 46.1 bits (23), Expect = 0.76
Identities = 23/23 (100%)
Strand = Plus / Minus

Query: 62 ctggcgccaggtaggggtgt 84
|||||
Sbjct: 29831 ctggcgccaggtaggggtgt 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 = 0.76
Identities = 29/31 (93%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgccaggtagggg 80
|||| |||||
Sbjct: 73780 aaacgccgacagttggcgccaggtagggg 73810

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Minus

Query: 50 aaacaccgacagctggcgccaggtagggg 80
|||| |||||
Sbjct: 109963 aaacgccgacagttggcgccaggtagggg 109933

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Minus

Query: 50 aaacaccgacagctggcgccaggtagggg 80

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

Sbjct: 136436 aaacgccgacattggcgccaggtagggg 136406

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

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Plus

Identities = 29/31 (93%)

Strand = Plus / Plus

```
Query: 50    aaacaccgacagctggcgcgccaggtagggg 80
           |||||
Sbjct: 3582 aaacaccgacagttggcgcgccagatagggg 3612
```

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

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Minus

Identities = 29/31 (93%)

Strand = Plus / Minus

```
Query: 50      aaacaccgacagctggcgcgccaggtagggg 80
             ||||| ||||| ||||| ||||| |||||
Sbjct: 16033  aaacgccgacagttggcgcgccaggtagggg 16003
```

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Plus

Identities = 29/31 (93%)

Strand = Plus / Plus

```
Query: 50      aaacaccgacagctggcgcgccaggtagggg 80
             ||||| ||| |||||
Sbjct: 72192  aaacaccaacagttggcgcgccaggtagggg 72222
```

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Minus

Identities = 29/31 (93%)

Strand = Plus / Minus

Query: 50 aaacaccgacagctggcgccaggtagggg 80
 ||| ||| |

Sbjct: 122060 aaacgccgacagttggcgcgccaggtagggg 122030

>gb|AC157319.2| Zea mays clone ZMMBBb-136E2, complete sequence
Length = 138186

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
|||| ||||||| |||||||||||||||||
Sbjct: 93286 aaacgccgacagttggcgcgccaggtagggg 93316

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

Query: 55 ccgacagctggcgcgccaggtagggg 80
||||||| |||||||||||||||||
Sbjct: 47153 ccgacagttggcgcgccaggtagggg 47178

>gb|AC152495.1| Zea mays BAC clone Z486N13, complete sequence
Length = 169348

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Minus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
|||| ||||||| |||||||||||||||||
Sbjct: 152458 aaacgccgacagttggcgcgccaggtagggg 152428

>gb|AF528565.1| Zea mays cultivar BSSS53 chromosome 4 clone BAC 072, complete sequence
Length = 106246

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Minus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80

|||| ||||||| ||||||||||||||||
Sbjct: 86878 aaacgccgacagttggcgcgccaggtagggg 86848

>gb|AC147925.2| Oryza sativa Japonica Group chromosome 11 clone OSJNBa0032N11 map near
50283S, complete sequence
Length = 139217

Score = 46.1 bits (23), Expect = 0.76
Identities = 26/27 (96%)
Strand = Plus / Plus

Query: 55 ccgacagctggcgcgccaggtagggg 81
|||||||||||||||||||||||
Sbjct: 96546 ccgacagctggcgcgccaggtagggg 96572

>gb|AC108761.2| Oryza sativa (japonica cultivar-group) chromosome 9 BAC clone
OSJNBa0087J09, complete sequence
Length = 153351

Score = 46.1 bits (23), Expect = 0.76
Identities = 26/27 (96%)
Strand = Plus / Minus

Query: 55 ccgacagctggcgcgccaggtagggg 81
||||| |||||||||||||||||
Sbjct: 66360 ccgacatctggcgcgccaggtagggg 66334

>gb|BT018612.1| Zea mays clone EL01N0501C03.d mRNA sequence
Length = 1338

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
|||| ||||||| |||||||||||||||||
Sbjct: 371 aaacgccgacagttggcgcgccaggtagggg 401

>gb|BT017984.1| Zea mays clone EL01N0525E01.c mRNA sequence
Length = 1414

Score = 46.1 bits (23), Expect = 0.76

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

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
||||| ||||||| |||||||||||||||||
Sbjct: 374 aaacgccgacagttggcgcgccaggtagggg 404

>gb|AC135502.4| Oryza sativa chromosome 3 BAC OSJNBb0085A04 genomic sequence, complete
sequence
Length = 132292

Score = 46.1 bits (23), Expect = 0.76
Identities = 26/27 (96%)
Strand = Plus / Plus

Query: 55 ccgacagctggcgcgccaggtagggg 81
||||| |||||||||||||||||||
Sbjct: 109246 ccgacatctggcgcgccaggtagggg 109272

>gb|AC121364.2| Oryza sativa Japonica Group chromosome 5 clone OSJNBa0052E20,
complete sequence
Length = 162434

Score = 46.1 bits (23), Expect = 0.76
Identities = 23/23 (100%)
Strand = Plus / Minus

Query: 56 cgacagctggcgcgccaggtagg 78
|||||||||||||||||
Sbjct: 541 cgacagctggcgcgccaggtagg 519

>gb|AC135418.3| Oryza sativa Japonica Group chromosome 5 clone OSJNBa0035J16, complete
sequence
Length = 170233

Score = 46.1 bits (23), Expect = 0.76
Identities = 26/27 (96%)
Strand = Plus / Minus

Query: 55 ccgacagctggcgcgccaggtagggg 81
||||| |||||||||||||||||||
Sbjct: 134285 ccgacatctggcgcgccaggtagggg 134259

>gb|AC120991.3| Oryza sativa Japonica Group chromosome 5 clone OSJNBb0006J12, complete
sequence
Length = 157069

Score = 46.1 bits (23), Expect = 0.76
Identities = 26/27 (96%)
Strand = Plus / Minus

Query: 55 ccgacagctggcgcgccaggtagggg 81
 ||||| |||||||||||||||||
Sbjct: 31648 ccgacatctggcgcgccaggtagggg 31622

>gb|AC112159.2| Oryza sativa Japonica Group chromosome 5 clone OJ1058_C01, complete
sequence
Length = 114236

Score = 46.1 bits (23), Expect = 0.76
Identities = 23/23 (100%)
Strand = Plus / Minus

Query: 56 cgacagctggcgcgccaggtagg 78
 |||||||||||||||||||
Sbjct: 95232 cgacagctggcgcgccaggtagg 95210

>gb|AY078063.2| Zea mays B transcriptional activator (b1) gene, b1-B' allele, exons 1
through 3 and partial cds
Length = 107840

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Minus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
 |||| ||||||| |||||||||||||||||
Sbjct: 30047 aaacgccgacagttggcgcgccaggtagggg 30017

>gb|DQ002408.1| Zea mays gypsy retrotransposon huck, and copia retrotransposon ji,
complete sequence; and helitron Mo17_14594, complete
sequence
Length = 57607

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Minus

Query: 50 aaacaccgacagctggcgccaggtagggg 80
 ||| | ||||| |||||||||
Sbjct: 45031 aaacgccgacagtggcgccaggtagggg 45001

```
>gb|AC145386.1| Oryza sativa chromosome 3 BAC OSJNBb0028K20 genomic sequence, complete
sequence
Length = 115326
```

Score = 46.1 bits (23), Expect = 0.76
Identities = 26/27 (96%)
Strand = Plus / Minus

Query: 55 cgcacagctggcgcgccaggtagggg 81
 ||||| |||||||||
 Sbjct: 91750 cgcacatctggcgcgccaggtagggg 91724

>gb|AC169373.2| Sorghum bicolor clone SB_BBc0188M08, complete sequence
Length = 137889

Score = 46.1 bits (23), Expect = 0.76
Identities = 23/23 (100%)
Strand = Plus / Minus

```
Query: 63      tggcgccaggtaggggtgtg 85
             |||||
Sbjct: 80721   tggcgccaggtaggggtgtg 80699
```

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

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Plus

```
Query: 50      aaacaccgacagctggcgcgccaggtagggg 80
             ||| ||||| |||||||||
Sbjct: 47433  aaacgccgacagttggcgcgccaggtagggg 47463
```

>gb|AC137992.2| Oryza sativa chromosome 3 BAC OSJNBb0056B16 genomic sequence, complete
sequence
Length = 153247

Score = 46.1 bits (23), Expect = 0.76
Identities = 26/27 (96%)
Strand = Plus / Minus

Query: 55 ccgacagctggcgcgccaggtagggg 81
 ||||| |||||||||||||||||
Sbjct: 150371 ccgacatctggcgcgccaggtagggg 150345

>gb|AC165171.2| Zea mays clone CH201-145P10, complete sequence
Length = 233369

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
 |||| ||||||| |||||||||||||||||
Sbjct: 54647 aaacgccgacagttaggcgcgccaggtagggg 54677

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
 |||| ||||||| |||||||||||||||||
Sbjct: 86382 aaacgccgacagttaggcgcgccaggtagggg 86412

>gb|AC165176.2| Zea mays clone ZMMBBb-177G21, complete sequence
Length = 176679

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
 |||| ||||||| |||||||||||||||||

Sbjct: 56859 aaacgccgacagttggcgcgccaggtagggg 56889

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Minus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
||||| ||||||| |||||||||||||||||
Sbjct: 128798 aaacgccgacagttggcgcgccaggtagggg 128768

>gb|AC122147.1| Oryza sativa Japonica Group chromosome 10 clone OSJNAb0072F04, complete
sequence
Length = 137724

Score = 46.1 bits (23), Expect = 0.76
Identities = 26/27 (96%)
Strand = Plus / Plus

Query: 55 ccgacagctggcgcgccaggtagggg 81
||||| |||||||||||||||||||
Sbjct: 12034 ccgacatctggcgcgccaggtagggg 12060

>gb|AC092553.4| Oryza sativa Japonica Group chromosome 10 clone OSJNBb0072F04, complete
sequence
Length = 133121

Score = 46.1 bits (23), Expect = 0.76
Identities = 26/27 (96%)
Strand = Plus / Plus

Query: 55 ccgacagctggcgcgccaggtagggg 81
||||| |||||||||||||||||||
Sbjct: 45155 ccgacatctggcgcgccaggtagggg 45181

>gb|AC163004.1| Gap filling sequence from Zea mays clone ZMMBBb0382K21, from chromosome
8, complete sequence
Length = 21864

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Plus

```
Query: 50      aaacaccgacagctggcgcgccaggtagggg 80
             ||||| ||||| ||||| |||||
Sbjct: 21321  aaacgccgacagttggcgcgccaggtagggg 21351
```

>dbj|AP006849.2| *Oryza sativa* Japonica Group genomic DNA, chromosome 9, BAC
clone:OSJNBa0054F02
Length = 180651

Score = 46.1 bits (23), Expect = 0.76
Identities = 26/27 (96%)
Strand = Plus / Plus

```
Query: 55      ccgacagctggcgcgccaggtaggggg 81
          ||||| |||||||||
Sbjct: 154412 ccgacatctggcgcgccaggtaggggg 154438
```

```
>dbj|AP003874.5| Oryza sativa Japonica Group genomic DNA, chromosome 7, BAC
clone:0J1118_G09
Length = 115815
```

Score = 46.1 bits (23), Expect = 0.76
Identities = 26/27 (96%)
Strand = Plus / Plus

```
Query: 55      ccgacagctggcgcgccaggtaggggg 81
           ||||| |||||||||
Sbjct: 103798 ccgacatctggcgcgccaggtaggggg 103824
```

```
>dbj|AP005820.3| Oryza sativa Japonica Group genomic DNA, chromosome 2, BAC
clone:OSJNBa0091C16
Length = 162527
```

Score = 46.1 bits (23), Expect = 0.76
Identities = 26/27 (96%)
Strand = Plus / Minus

```
Query: 55      cgcacagctggcgcgccaggtaggggg 81
          ||||| |||||||||
Sbjct: 122622 cgcacatctggcgcgccaggtaggggg 122596
```

>gb|AY530951.1| Zea mays putative growth-regulating factor 1 (Z214A02.12), putative 40S ribosomal protein S8 (Z214A02.25), and putative casein kinase I (Z214A02.27) genes, complete cds
Length = 158797

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Minus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
|||| ||||||| ||||||||||||||||
Sbjct: 101631 aaacgccgacagttggcgcgccaggtagggg 101601

>gb|AY555143.1| Zea may BAC clone c573L14, complete sequence
Length = 144792

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Minus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
|||| ||||||| ||||||||||||||||
Sbjct: 51623 aaacgccgacagttggcgcgccaggtagggg 51593

>gb|AF466202.2| Zea mays putative pol protein gene, partial cds; and putative gag-pol precursor -orf2, putative Fourf gag/pol protein, putative NADP-dependent malic enzyme, putative argonaute protein, putative pinhead protein, putative pol protein, putative gag protein, putative TNP2, r1-B73 proteins, putative genetic modifier, putative S-receptor kinase, putative aldose reductase-related protein, putative glutathione peroxidase, putative glycerol 3-phosphate permease, putative response regulator, and putative 4-coumarate-CoA ligase-like protein genes, complete cds
Length = 290350

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Minus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
|||| ||||||| ||||||||||||||||
Sbjct: 8650 aaacgccgacagttggcgcgccaggtagggg 8620

Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
 |||| | ||||| | ||||| ||||| |||||
Sbjct: 149217 aaacgccgacagttggcgcgccaggtagggg 149247

>dbj|AP003911.3| Oryza sativa Japonica Group genomic DNA, chromosome 8, BAC
 clone:OJ1368_G08
 Length = 107074

Score = 46.1 bits (23), Expect = 0.76
Identities = 26/27 (96%)
Strand = Plus / Minus

Query: 55 ccgacagctggcgcgccaggtaggggg 81
 ||||| | ||||| ||||| ||||| |||||
Sbjct: 42085 ccgacatctggcgcgccaggtaggggg 42059

>dbj|AP004705.3| Oryza sativa Japonica Group genomic DNA, chromosome 8, PAC clone:P0682A06
 Length = 142023

Score = 46.1 bits (23), Expect = 0.76
Identities = 26/27 (96%)
Strand = Plus / Plus

Query: 55 ccgacagctggcgcgccaggtaggggg 81
 ||||| | ||||| ||||| ||||| |||||
Sbjct: 109345 ccgacatctggcgcgccaggtaggggg 109371

>emb|BX842604.1| Oryza sativa genomic DNA, chromosome 4, BAC clone: B1160F02, complete
 sequence
 Length = 139971

Score = 46.1 bits (23), Expect = 0.76
Identities = 23/23 (100%)
Strand = Plus / Plus

Query: 58 acagctggcgcgccaggtagggg 80

|||||
Sbjct: 1009 acagctggcgcgccaggtagggg 1031

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: 422,762,834
Number of extensions: 20547858
Number of successful extensions: 370465
Number of sequences better than 10.0: 322
Number of HSP's gapped: 370327
Number of HSP's successfully gapped: 789
Length of query: 1868
Length of database: 30,878,341,354
Length adjustment: 23
Effective length of query: 1845
Effective length of database: 30,617,269,251
Effective search space: 56488861768095
Effective search space used: 56488861768095
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)