

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 PO...	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 PO...	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 PO...	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 Bl...	48	0.19
gb	AC087552.3	Oryza sativa Japonica Group chromosome 5 clone PO...	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_BBa0031E23, 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_BBc0140005, complete seq...	46	0.76
gb	AC196847.2	Sorghum bicolor clone SB_BBc0109L12, complete seq...	46	0.76
gb	AC196837.2	Sorghum bicolor clone SB_BBc0073F19, 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_BBc0007L02, 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 BSS53 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 genomi...	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 taccctaaagcaccgcaagggtagccctgggtgtgcggacggactctaaacaccgacag 61
|||||
Sbjct: 5388 taccctaaagcaccgcaagggtagccctgggtgtgcggacggactctaaacaccgacag 5330

Query: 62 ctggcgcgccaggtaggggtgtgtctttgatctgagctagctcaatgaccattacctc 121
| |||
Sbjct: 5329 ccggcgcgccaggtaggggtgtgtctttgatctgagctagctcaatgaccattacctc 5270

Query: 122 aaatgcaagatcgcccttcgccccgggactatgttttgctttggaacctctcatccata 181
||
Sbjct: 5269 aaatgcaagatcgcccttcgccccgggactatgttttgctttggaacctctctccata 5210

Query: 182 gcagatgaagagggaactctgcaccgcatagcagatctattggagaagaagctttcctca 241
|
Sbjct: 5209 gtgatgaagagggactctgcaccagtggaagatccgactgagaagaagctttcctga 5150

Query: 242 gaaatctcaggggagccagggcagaacagcgggtggcaccatcaccgcacctcaagcg 301
|||||
Sbjct: 5149 gaaatctcaggggaatcacaagcagaatagcgggtggcaccaccgcacctcagggg 5090

Query: 302 aagatgacctcttacaaccgaaagtgcggagctcacctaccgaa-aaactccgctgtc 360
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Sbjct: 5089 aagatgacctcttacaaccgaaaggtgggatctcacttaccgaaagaaactccactgtt 5030

Query: 361 cacttcgccacaaaggagtggacacggattactcgaagaaggaagcagtggtcccgag 420
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Sbjct: 5029 cacttcgccacaaaggagtggacacggatcactcgaagaagaagcgaatgtcccgag 4970

Query: 421 tcaggggacgggaacacgccaagccatctttccgacgccttcgcctcaaatgaggatgg 480
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Sbjct: 4969 tcaggggacgagaacacgccaagccat-cttctgacgccttcgcctcaaatgagaatgg 4911

Query: 481 aaagaagagcgccatcgcgctggctcctttctaccccgacgtcctcttcatcagggggag 540
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Sbjct: 4910 aaataagagcgccatcacgccggctcctttctaccccgacgtcctcttcatcggggggaa 4851

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

Query: 601 gcgtgaggcgcgacgacggaggaatagaagccagaacgtcggcgacatcacgaggtgg 660
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Sbjct: 4791 gtgtgaagcgcgacaacggaggaacaaatgccgaaacatacggtgacatcacgaagctag 4732

Query: 661 ggaacgggatccggcgcaaccgctatcccgggacgaagctttagaagtaggaaaaactcc 720
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Sbjct: 4731 ggaacgggatccgacatagcctgtatcccaagacgaggcctcataagtgggagaaactcc 4672

Query: 721 cgacgagtggttacaccgagaaaggcgaactctcgcccgctgatcgccgacaagctta 780
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Sbjct: 4671 cgacgagcagtgaccgggaaatgtggaactctcaccacgctgattgccgacaagctca 4612

Query: 781 ggaccgagaacgagagcaagccgagcaaggtgcaaggctgcgccgagagaatgctctctt 840
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Sbjct: 4611 ggaccaagagcaggaacaagccgagcaaggtgcaaggctgtgccgagagaacctctctt 4552

Query: 841 tgctcggaacctgtacccgacttgcctcgtgcaatgaacacgccgagtggaagtcggagg 900
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Sbjct: 4551 cgctcggaacctgtatcccgacttgcctcatgcaatgaacacgccgagtggaattcggagg 4492

Query: 901 ggtactggcccagatagctgacggcctcccgcgaaccctagacacggaaggctaccggcg 960
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Sbjct: 4491 ggtactgtcccagatagctgacagcatcctgcaaaccaagatgctgaaggctaccggcg 4432

Query: 961 gctgcttactcgagcagttaatcaccttctacccatcactaatcctccaagcgacctacg 1020
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Sbjct: 4431 actgcttgetcaagtagctaatcaccttctacccatcactcctcctgcaaaacacctacg 4372

Query: 1021 ccatgccatcaacagccggcgagacacgggagctccatcaacgcttcgcgcgaccgatg 1080
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Sbjct: 4371 tcccacatcaatagccggcgagacgcgtagagctccatcaacgcttcgcgcgaccggcg 4312

Query: 1081 acacgaaagtgagataggggaaccgagaggagtatgtccgagatcatgccatcctggcatg 1140
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Sbjct: 4311 gcacaaaaatgagataaggcgccgggaggagtatgaccgagatcactatgtatcggcagc 4252

Query: 1141 aagtcatgccacccgagctgagtcggttgccgctcgaccagtgtcccgttcaggagc 1200
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Sbjct: 4251 aagtcgacgaccctgttgagtcggccgaacctcgactagtggccattctaggagc 4192

Query: 1201 atcaagatgacacacaactggctcccctccttgggaccgacctcacgaacgccgacatga 1260
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Sbjct: 4191 gtcgagatggcactactaccgactcccctccttgggaccgacaacacgaacaccgactgga 4132

Query: 1261 agacacgtgaggagtcttcgcacttactccgtgtctccgggcatccagtg-gcccctaa 1319
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Sbjct: 4131 acacacatgtggagtctctgtggttactccgcgtctccgggcatccagtgccccccaa 4072

Query: 1320 cttcaaggtctccaacgtcagcaagtatgagcgcaagcaggacctgggtggtggttagc 1379
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Sbjct: 4071 cttcaaggtctccaacgtcgacaagtagcagccaagcaggaccggcggtggttggc 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 gaagacacgtgaggagtcttcgcacttactccgtgtctccgggcatccagtggcc-cct 1317
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Sbjct: 12615 gaagacacatgtggagtatccgcacttacttcgcgtcttagggcctccagtggcatcca 12674

Query: 1318 aacttcaaggtctccaacgtcagcaagtatgagcgcaagcaggacctgggtggtggtta 1377
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Sbjct: 12675 aacttcaaggtctccaacgtcaacaaatagcagccaagcaggaccggagaggctggttg 12734

Sbjct: 12407 gagctctatcaatgcttcgcacgaacgacgacatgaaagtgagataaggagccgagaaga 12466

Query: 1111 gtagt 1115

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Sbjct: 12467 gtagt 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 taatcaccttctaccatcactaatcctccaagcgacctacgcatgccatcaacagccg 1038

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Sbjct: 2273 taatcaccttctgcccacgctcatccccgagcaacctacaccagccatcaacagccg 2214

Query: 1039 gcgagacacgaggagctccatcaacgcttcgcgaccgatgacacgaaagtgagatagg 1098

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Sbjct: 2213 acgagacgaggagctccatcaatgcttcgcgaccgatgacacgaaagtgagataag 2154

Query: 1099 gaaccgagaggagtatgtccgagatcatgccatcctggcatgaagtcattgccacccgagc 1158

| |||

Sbjct: 2153 ggcggggaggagtatgaccgggatcatgggtgtcccagctgaagttgcccacccgagt 2094

Query: 1159 tgagtcggttgccgctcgaccagtgtcccgttcaggacgatcaagatgacacacaac 1218

|||||

Sbjct: 2093 tgagtcggttgccgctcgaccagtggcccagccgggacggtcgagacgacacaccac 2034

Query: 1219 tggtccccctccttgggaccgacctcacgaacgccgacatgaagacacgtgaggagtctt 1278

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Sbjct: 2033 cagctccccctccccgggaccgacctcacgaacgccgacaggaagacacatgagggtctc 1974

Query: 1279 cgcacttactccgtgtctccgggcatccagtggcccct-aacttcaaggtctcaacgt 1337

| |

Sbjct: 1973 tgcgcttactccggtctccgggcatccagtggcccccaacttcaaagttctcaacgt 1914

Query: 1338 cagcaagtatgagcgaagcaggacctgggtggctggtagccatctacacgattgtcac 1397

| |

Sbjct: 1913 cgacaagtacgagcccaagcagcaccaggggctagttggcgtctacacgaccgccg 1854

Query: 1398 atgggccgcccggagcgacggaggacgtgatgacagtgtatccccattgtcctaggga 1457
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Sbjct: 1853 tcgggtcgctggggcgacggaagacgtaatgacagcgtatcccatcgtcctaggga 1794

Query: 1458 agacgcaatgcagtggtccgacatctacccaacattgcatagacaattggagcgactt 1517
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Sbjct: 1793 agacgcactgcagtggtccgacatctgccacgacactgcatcgacggttggggcgactt 1734

Query: 1518 cagttggtgcttcacgccaactccagtcctctttgacaagccggcgagccatggga 1577
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Sbjct: 1733 tagtcggcgcttcacgccaactccagtcctctctgacaagccgccgagccatggta 1674

Query: 1578 cctaaaatccattgggcatcaggcgcatgaaacgctccggttgacctcaagaggttta 1637
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Sbjct: 1673 cctcaaatccatcaggcgccaggcgcatgaaacactctggtcataacctcaagaggttta 1614

Query: 1638 gaccatgaggaaccacacccccgaagtcgccgaggcgggggtgattgaagacttctaccg 1697
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Sbjct: 1613 gaccatgaggaaccgcatccccgaagtcgtcaaggcagcagatgattgaagatttctaccg 1554

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

Query: 1758 aacacttggtccgggagggcagacctctacatcaccacggattaacgggccaggacctca 1817
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Sbjct: 1494 agcaactgtttcgagaggcagacctctacatcaccatagatgagcgggccaggacctca 1435

Query: 1818 tcggaggcacgaaagccgcccacacgcgccacgggtgtgacacgaaccagc 1868
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Sbjct: 1434 tcggaggtaactaaacccgaccacccgaccacgacgcgatacgaaccagc 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 cgacatgaagacacgtgaggagtcttcgcacttactccgtgtctccgggccatccagtgg 1312
||||| || ||||||||||||||| | ||| ||||||||||| | || | ||||||||||| |||
Sbjct: 112730 cgacaggaggacacgtgaggagtatccgcccttactccgcgccttagggccatccaatgg 112789

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

Query: 1372 tggttagccatctacacgattgtcacatgggccgaggagcgacggaggacgtgatgaca 1431
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Sbjct: 112850 tggttagccgtctacaccaccgtctcgggccgctggggcatctgaggacgtcatgact 112909

Query: 1432 gtgtatittccattgtcctagggcaagacgcaatgcagtggctccgacatctaccccaa 1491
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Sbjct: 112910 gcgatctgcccacgtcctcgggcaagacgcgctgcagtggctacgacatctacccca 112969

Query: 1492 cattgcatagacaattggagcgacttcagttggtgcttcatcgccaacttccagtcctc 1551
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Sbjct: 112970 cactgcatcgacgactggggagacttcagtcgacgtttaccgccaacttccagtcctc 113029

Query: 1552 tttgacaagccggcgagccatgggacctaaaatccattgggcatcaggcgatgaaacg 1611
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Sbjct: 113030 tccgacaagccggcgcaaccatgggacctcaatccatcaagcggggggatgagact 113089

Query: 1612 ctccggttgacctcaagaggtttagacctgaggaaccacacccccgaagtcgccgag 1671
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Sbjct: 113090 ctccaggtcgtaccttaaaaggttccagacctgagaaccgcatccccgaggtcaccgag 113149

Query: 1672 gcgggggtgattgaagacttctaccgaggatccaatgactcggtttcgtccgagccata 1731
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Sbjct: 113150 gcggccgtaatcgaggacttctacagaggatctaacgactcggtttcgtccgagccata 113209

Query: 1732 ctccagaaaagcgtcggccacctccgaacacttgttccgggaggcagacctctacatcac 1791
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Sbjct: 113210 ctgca-aaaggcggcactacctccgaggagctgttccgggaagccgacctctacatcac 113268

Query: 1792 cacggattaacgggccaggacctcatcggagg 1824
| | | | | |||||||||||||||
Sbjct: 113269 cgctgacgagcgagccaggacctcatcggagg 113301

>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 cgacatgaagacacgtgCGGAGTcttcgcaacttactccgtgtctccgggccatccagtgg 1312
||||| || ||||||||||||||| | || ||||||||||| | || ||||||||||| |||
Sbjct: 114166 cgacaggaggacacgtgCGGAGTatctgctcttactccgccttagggccatccaatgg 114107

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

Query: 1372 tggtagccatctacacgattgtcacaatggccgccggagcgacggaggacgtgatgaca 1431
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Sbjct: 114046 tggtagccgtctacaccaccgccgctcgggctgccggggcatctgaggacgtcatgact 113987

Query: 1432 gtgtattttccattgtcctagggcaagacgcaatgcagtggctccgacatctaccccaa 1491
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Sbjct: 113986 gcgtatctgcccatcgtcctcgggcaagacgcaatgcagtggctacggcatctaccccca 113927

Query: 1492 cattgcatagacaattggagcgacttcagttgggtgcttcacgccaaactccagtcctc 1551
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Sbjct: 113926 cactgcatcgacgactggggagacttcagccgacgattcaccgccaaactccagtcctc 113867

Query: 1552 tttgacaagccggcgcagccatgggacctaaaatccattgggcatcagggcgatgaaacg 1611
| ||||||||| ||||| ||||||||||||| ||||||||| || | ||| ||||| |||
Sbjct: 113866 tccgacaagccagcgaaccatgggacctaaaatccatcaagcgggggagatgagact 113807

Query: 1612 ctccggtgttacctcaagaggttttagacctgaggaaccacacccccgaagtcgccgag 1671
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Sbjct: 113806 ctccggtcataccttaaaaggttccagacctgagaaaccgcatccccgaggtcacggag 113747

Query: 1672 gcgggggtgattgaagacttctaccgaggatccaatgactcggtttcgtccgagccata 1731
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Sbjct: 113746 gcggccgtgatcgaggacttctacagaggatctaatactcggtttcgtccgaaccata 113687

Query: 1732 ctccagaaaagcgtcggccacctccgaacacttgttccgggaggcagacctctacatcac 1791
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Sbjct: 113686 ctgca-aaaggcgccaaccacctccgaggagctgttccgggaagccgacctctacatcac 113628

Query: 1792 caccgattaacgggccaggacctcatcggagg 1824
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Sbjct: 113627 cgctgacgagcgggccaggacctcatcggagg 113595

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

Query: 1253 cgacatgaagacacgtgaggagtcttcgcacttactccgtgtctccggccatccagtgg 1312
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Sbjct: 128593 cgacaggaagacacgtgaggagtgtccgctcttactccgccttagggccatccagtgg 128652

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

Query: 1372 tggtagccatctacacgattgtcacatgggccgccggagcgacggaggacgtgatgaca 1431
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Sbjct: 128713 tggtagccgtctacaccaccgtgctcgagctgccggggcatctgaggacgttatgacc 128772

Query: 1432 gtgtattttcccatgtcctagggcaagacgcaatgcagtggctccgacatctaccccaa 1491
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Sbjct: 128773 gcgtatttgccatcgctccttgggcaagatgcgctacagtggctacgacatctacccca 128832

Query: 1492 cattgcatagacaattggagcgacttcagttggtgcttcatgcccaacttccagtcctc 1551
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Sbjct: 128833 cactgcatcgacgactggggagacttcagtcgacgtttcaccgccaacttccagtcctc 128892

Query: 1552 tttgacaagccggcgcagccatgggacctaaaatccattgggcatcagggcgatgaaacg 1611
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Sbjct: 128893 tccgacaagccagcgaaccgtgggacctcaaatccatcaagcgcgggggatgagact 128952

Query: 1612 ctccggtgtacctcaagaggttttagaccatgaggaaccacacccccgaagtcgccgag 1671
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Sbjct: 128953 ctccggtgtacctcaaaaggttccagaccatgagaaatcgattcccagggtcacggag 129012

Query: 1672 gcgggggtgattgaagacttctaccgaggatccaatgactcggctttcgtccgagccata 1731
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Sbjct: 129013 gcggccgtgatcaggacttctacaggggatccaacactcggcttttgcgagccata 129072

Query: 1732 ctccagaaaagcgtcggccacctccgaacacttgttccgggaggcagacctctacatcac 1791
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Sbjct: 129073 ctacagaaa-gcggcgactacttccgaggagctggtccgggaagccgacctctacatcac 129131

Query: 1792 cacggattaacgggcccaggacctcatcggagg 1824
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Sbjct: 129132 cgccgacgagcgagctcaggacctcatcggagg 129164

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

Query: 794 gagcaagccgagcaaggtgcaaggctgcccagagagaatgctctctttgctcggaaactg 853
||||| ||||| ||||| || || ||||| | ||||| | || |||||
Sbjct: 114625 gagcaagccgagcaagatgcaaggcaacgacgcgagaaatccgctcttcgggcgaaactg 114566

Query: 854 taccgacttcgctcgtgcaatgaacacgccgagtgaaagtcgggggtactggcccag 913
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Sbjct: 114565 aaccgacttcgcccagctatgaatacggcgagcgaagtcggaggcgttctggcccag 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 ggggtgtcggcaggactctaaacaccgacagctggcgcgccaggtaggggtgtgtcttt 90
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Sbjct: 115340 ggggtgtcggcggaccctaaacaccgacagctggcgcgccaggtaggggtgtgtctgac 115281

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

Query: 503 gctcctttctaccccgacgtcctcttcatc 532
||||| ||||||||||||||||||||||||
Sbjct: 127858 gctccattctaccccgacgtcctcttcatc 127887

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

Query: 50 aaacaccgacagctggcgccaggtagggg 80
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Sbjct: 85948 aaacgccgacagttggcgccaggtagggg 85918

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

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

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

Query: 55 cgcacagctggcgccaggtagggg 80
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Sbjct: 24644 cgcacagttggcgccaggtagggg 24619

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

Query: 341 acccgaaaaactccgctgtccacttcgcccacaaaggagtggacacggat 390
||||| || ||||||||||| ||||| || ||||| || |||||||||||
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 cgacatgaagacacgtgcgagtgcttcgacttactccgtgtctccgggcatccagtgg 1312
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Sbjct: 86996 cgacaggaggacacgtgcgagtgcttcgacttactccgcttagggcatccaatgg 87055

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

Query: 1372 tggttagccatctacacgattgtcacatgggcccggagcgacggaggacgtgatgaca 1431
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Sbjct: 87116 tggttagcgtctacaccacgctgctcgggcgctggggcatctgaggacgtcatgact 87175

Query: 1432 gtgtatthttccattgtcctagggcaagacgcaatgcagtggtccgacatctaccccaa 1491
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Sbjct: 87176 gctatctgcccacgtcctcgggcaagacgcgctgcagtggttacgacatctaccccca 87235

Query: 1492 cattgcatagacaattggagcgacttcagttggtgcttcatcgccaacttccagtccctc 1551
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Sbjct: 87236 cactgcatcgacgactggggagacttcagtcgacgtttcaccgccaacttccagtctctc 87295

Query: 1552 tttgacaagccggcgagccatgggacctaaaatccattgggcatcagggcgatgaaacg 1611
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Sbjct: 87296 tccgacaagccggcgcaaccatgggacctcaatccatcaagcgggggggatgagact 87355

Query: 1612 ctccggttgatctcaagaggttttagacatgaggaaccacacccccgaagtgcggag 1671
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Sbjct: 87356 ctccaggtgatctcaagaggttttagacatgaggaaccacacccccgaagtgcggag 87415

Query: 1672 ggggggtgattgaagacttctaccaggatccaatgactcggctttcgtccgagccata 1731

Sbjct: 96489 cactgcatcgacgactggggagacttcagccgacgattcaccgccaacttccagtctctc 96430

Query: 1552 tttgacaagccggcgcagccatgggacctaaaatccattgggcatcagggcgatgaaacg 1611

Sbjct: 96429 tccgacaagccagcgcgaacctgggacctcaaaccatcaagcgggggagatgagact 96370

Query: 1612 ctccggttgtacctcaagaggttttagacatgaggaaccacacccccgaagtcgccgag 1671

Sbjct: 96369 ctccggtcataccttaaaggttcagacatgagaaaccgcatccccgaggtcacggag 96310

Query: 1672 gcgggggtgattgaagacttctaccgaggatccaatgactcggctttcgtccgagccata 1731

Sbjct: 96309 gcggccgtgatcaggacttctacagaggatctaagactcggctttcgtccgaaccata 96250

Query: 1732 ctccagaaaagegtcgccacctccgaacacttgttccgggaggcagacctctacatcac 1791

Sbjct: 96249 ctgca-aaaggcgccaaccacctccgaggagctggtccgggaagccgacctctacatcac 96191

Query: 1792 cacggattaacgggcccaggacctcatcggagg 1824

Sbjct: 96190 cgctgacgagcgggcccaggacctcatcggagg 96158

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

Query: 31 ggggtgtcggacggactcctaacaccgacagctggcgcgccaggtagggggtgtgtcttt 90

Sbjct: 18097 ggggtgtcggtcggacccaaaaccgacagctggcgcgccaggtagggggtgtgtcgac 18156

Query: 91 gatctgagctagctcaatgaccattacctccaaatgcaagatcgcccttcggccgggac 150

Sbjct: 18157 gatccaagctagctcaatggccgtcactttccacagcaagatcgccgtacgtcccggatc 18216

Query: 151 tatgttttgctttggaacctctcatccatagcagatgaagaggaactctgcaccgcat 210

Sbjct: 18217 tgtattctgcttcgggacaatctcgtccgtagcggatgaagaaggaattctacaccgct 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
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Sbjct: 97188 gagcaagccgagcaagatgcaaggcaacgacgcgagaatccgctcttcggcgcaacctg 97129

Query: 854 taccccgaacttcgctcgtgcaatgaacacgccgagtgaagtcggaggggtactggcccag 913
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Sbjct: 97128 aaccccgaacttcgcccgaactatgaatacgcgagcgaagtcggaggggttctggcccag 97069

Query: 914 atagctgacgg 924
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Sbjct: 97068 atagccgacgg 97058

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

Query: 31 ggggtgtcggacggactcctaaacaccgacagctggcgccaggtaggggtgtgtcttt 90
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Sbjct: 97903 ggggtgtcggtcggacccaaacaccgacagctggcgccaggtaggggtgtgtcgac 97844

Query: 91 gatctgagctagctcaatg 109
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Sbjct: 97843 gatccaagctagctcaatg 97825

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

Query: 794 gagcaagccgagcaaggtgcaaggctgcccagagagaatgctctctttgctcggaacctg 853
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Sbjct: 18812 gaggcaggccgagcaagatgcaaggcaacgacgcgagaatccgctcttcggcgcaacctg 18871

Query: 854 taccgccacttcgctcgtgcaatgaacacgccgagtgaagtcggaggggtactggcccag 913
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Sbjct: 18872 aaccccgactttgcccgagctatgaacacgccgagcgaagtcggaggcgttctagctcgg 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 ttctaccgacgtcctcttcatc 532
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Sbjct: 18542 ttctaccgacgtcctcttcatc 18565

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

Query: 509 ttctaccgacgtcctcttcat 531
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Sbjct: 97458 ttctaccgacgtcctcttcat 97436

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

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
|||| | |||||| | |||||||||||||||||
Sbjct: 120842 aaacgccgacagttggcgcgccaggtagggg 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 cgacatgaagacacgtgCGGAGTcttcgcaCtactccgTgtctccggGCCatccagTgg 1312
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Sbjct: 152277 cgacaggaggacacgtgCGGAGTatctgcaCtactccgCGcCttagggCCatccaatgg 152218

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

Query: 1372 tggttagccatctacacgattgtcacatgggCGCGCGGagcGacggaggacgtgatgaca 1431
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Sbjct: 152157 tggttagccgtctacaccactgCGcctcgagctgCGGagcatccgaagatgtcatgacc 152098

Query: 1432 gtgtatTTTccattgtcctagggcaagacGcaatgcagTggctccgacatctacCCcaa 1491
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Sbjct: 152097 gcatatctGCCcatcgtcctTgggcaagatgcgctgcagTggctgcgacatctacCCcga 152038

Query: 1492 cattgcatagacaattggagcGacttcagTtggTgcttcacGccaacttccagTccctc 1551
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Sbjct: 152037 cactgcatcgacGactggggagacttcagTcgacgttTcactGccaacttccagTccctc 151978

Query: 1552 tttgacaagccggCGcagccatgggacctaaatccattgggcatcagggcgatgaaacg 1611
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Sbjct: 151977 tccgacaagccggCGcaaccatgggacctcaatccatcaagCGCGGGGGatgagact 151918

Query: 1612 ctccggttgTacetcaagaggttttagaccatgaggaaccacacCCCCgaagtcGCCgag 1671
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Sbjct: 151917 ctccggtcataccttaaaggttccagaccatgagaaccgcatccccgaggtcatggag 151858

Query: 1672 gCGGGGgtgattgaagacttctaccgaggatccaatgactCGGctttcgtccgagccata 1731
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Sbjct: 151857 gCGGCGgtgatcGaggacttctacagaggatccaatgactCGGttttcgtccgagccata 151798

Query: 1732 ctccagaaaagcgtCGGCCacctccgaacactTgttccGGGaggcagacctctacatcac 1791
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Score = 46.1 bits (23), Expect = 0.76
Identities = 29/31 (93%)
Strand = Plus / Minus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
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Sbjct: 21334 aaacgccgacagttggcgcgccaggtagggg 21304

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

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
|||| ||||||| ||||||||||||||||
Sbjct: 90226 aaacgccgacagttggcgcgccaggtagggg 90256

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

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
|||| ||||||| ||||||||||||||||
Sbjct: 139072 aaacgccgacagttggcgcgccaggtagggg 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 cgacatgaagacagctgcgagtgcttgcacttactccgtgtctccgggccatccagtgg 1312
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Sbjct: 21744 cgacaggaggacagctgcgagttatctgcacttactccgccttagggccatccaatgg 21685

Query: 1313 cc-cctaacttcaaggtctccaacgtcagcaagtatgagcgcaagcaggacctgggtggc 1371

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Sbjct: 21684 cctcccaacttcaaggtatccaatgtcgcacaaatgatgaacctaacgaggatccaggggt 21625

Query: 1372 tggtagccatctacacgattgtcacatgggcccggagcgacggaggacgtgatgaca 1431

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Sbjct: 21624 tggtagccgtctacaccaactgccgctcgagctgccggagcatccgaagatgtcatgacc 21565

Query: 1432 gtgtatthtccattgtccttagggcaagacgcaatgcagtggtccgacatctacccaa 1491

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Sbjct: 21564 gcatactgcccatcgtccttgggcaagatgcgctgcagtggtccgacatctacccga 21505

Query: 1492 cattgcatagacaattggagcgaacttcagttggtgcttcacgccaactccagtcctc 1551

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Sbjct: 21504 cactgcatcgaactgggagacttcagtcgacgttcacgccaactccagtcctc 21445

Query: 1552 ttgacaagccggcgcagccatgggacctaaatccattgggcatcaggcgatgaaacg 1611

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Sbjct: 21444 tccgacaagccggcgaacctgggacctaaatccatcaagcgggggggatgagact 21385

Query: 1612 ctccggtgtacctaagaggttttagaccatgaggaaccacacccccgaagtcgccgag 1671

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Sbjct: 21384 ctccggtcataccttaaaggttcagaccatgagaaaccgcatccccgaggtcatggag 21325

Query: 1672 gcgggggtgattgaagacttctaccaggatccaatgactcggctttcgtccgagccata 1731

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Sbjct: 21324 gcggcctgatcaggacttctacagaggatccaatgactcggctttcgtccgagccata 21265

Query: 1732 ctccagaaaagcgtcggccacctccgaacacttgttccgggagcagacctctacatcac 1791

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Sbjct: 21264 ctaca-aaagcgcgactacttccgaggagctgttccgggaagccgacctctacatcac 21206

Query: 1792 cacgattaacgggccaggacctcatcgagg 1824

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Sbjct: 21205 cgccgacgagcgggccaggacctcatcgagg 21173

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

Query: 1253 cgacatgaagacacgtgaggagtcttcgcacttactccgtgtctccgggccatccagtgg 1312
||||| || ||||||||||||||| | ||| ||||||||||| | || ||||||||||| |||
Sbjct: 155717 cgacaggaggacacgtgaggagtatccgcccttactccgcgccttagggccatccaatgg 155658

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

Query: 1372 tggttagccatctacacgattgtcacatgggccgccggagcgacggaggacgtgatgaca 1431
||||||||| ||||||| | | | |||| ||||| || | || ||||||| |||||
Sbjct: 155597 tggttagccgtctacaccaccgtctcgggctgccggggcatccgaagacgtcatgacc 155538

Query: 1432 gtgtatittccattgtcctagggcaagacgcaatgcagtggctccgacatctaccccaa 1491
| |||| | | ||| ||||| || ||||| || ||||||||||| ||||||||||| |||
Sbjct: 155537 gcgtatctgctcatcgtccttggacaagatgcgctgcagtggctacgacatctacccca 155478

Query: 1492 cattgcatagacaattggagcgacttcagttggtgcttcatcgccaacttccagtcctc 1551
|| ||||| |||| ||| | ||||||||||| | | ||||| ||||||||||||||| |||
Sbjct: 155477 cactgcatcaacaactggggagacttcagtcgacgtttaccgccaacttccagtcctc 155418

Query: 1552 tttgacaagccggcgcagccatgggacctaaaatccattgggcatcaggcgatgaaacg 1611
|| ||||||||||| ||||| ||||||||||| ||||||||| || | ||| ||||| |||
Sbjct: 155417 ttcgacaagccagcgaaccatgggacctcaatccatcaagcgggggggatgagact 155358

Query: 1612 ctccggttgacctcaagaggtttagacctgaggaaccacacccccgaagtcgccgag 1671
||||||| ||||| || ||||| ||||||||||| ||||| || ||||||| ||| | |||
Sbjct: 155357 ctccggtcataccttaaaaggttccagacctgagaaaccgcatccccgaggtcacagag 155298

Query: 1672 gcgggggtgattgaagacttctaccgaggatccaatgactcggttttctccgagccata 1731
||||| ||| | | ||||||||||| ||||||| || ||||||||||| |||||||||||
Sbjct: 155297 gcggccgtggtctaggacttctacagaggatctaacgactcggttttctccgagccata 155238

Query: 1732 ctccagaaaagcgtcgccacctccgaacacttgttccgggaggcagacctctacatcac 1791
|| || ||| ||| | ||||||||||| | ||||||||||| ||||||||||| |||
Sbjct: 155237 ctaca-aaaggcggcactacctccgaggagctgttccgggaagccgacctctacattac 155179

Query: 1792 cacggattaacgggccaggacctcatcggagg 1824
| | | | ||||||||||| |||||||||||
Sbjct: 155178 cgccgacgagcgggccaggacctcatcggagg 155146

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

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

Query: 92 atctgagctagctcaatgaccattacctccaaatgcaagatgcccttcgccccgggact 151
||| ||||||||||||| || | |||| | | ||||||||||| | || ||||| ||
Sbjct: 156830 atccaagctagctcaatggccgtcaccttcacagcaagatgccctgcgtcccggatct 156771

Query: 152 atgttttgctttggaacctctcatccatagcagatgaagaggaactctgcaccgcata 211
| || ||||| || || ||||||||| |||| ||||||||||||||||| || ||||||| |
Sbjct: 156770 gtattctgcttcgggacaatctcatctgtagcggatgaagaggaattctacaccgcctc 156711

Query: 212 gcagatct 219
|||||||
Sbjct: 156710 gcagatct 156703

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

Query: 31 ggtgtgctggacggactctaaacaccgacagctggcgcgccaggtaggggtgtgtcttt 90
||||||| ||||| | ||||||||||||||||||||||||||||||||||| |
Sbjct: 22918 ggtgtgctggacggacccaaacaccgacagctggcgcgccaggtaggggtgtgtcgac 22859

Query: 91 gatctgagctagctcaatg 109
||| |||||||||||||
Sbjct: 22858 gatccaagctagctcaatg 22840

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

Query: 794 gagcaagccgagcaaggtgcaaggctgcccagagagaatgctctctttgctcggaacctg 853
|||||
Sbjct: 156176 gagcaagccgagcaagatgcaaggcaacgacgcgagaaatccgctcttcgggcgcaacctg 156117

Query: 854 taccgccacttcgctcgtgcaatgaacacgccgagtgagtcggagggtactggcccag 913
|||||
Sbjct: 156116 aaccgccacttcgcccagctatgaacacgccgagcgaagtcggaggcgttctagctcgg 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 gagcaagccgagcaaggtgcaaggctgcccagagagaatgctctctttgctcggaacctg 853
|||||
Sbjct: 22203 gagcaagccgagcaagatgcaaggcaacgacgcgagaaatccgctcttcgggcgcaacctg 22144

Query: 854 taccgccacttcgctcgtgcaatgaacacgccgagtgagtcggagg 900
|||||
Sbjct: 22143 aaccgccacttcgctcgagctatgaacacgccgagcgaagtcggagg 22097

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

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

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

Query: 1720 gtccgagccatactccagaaaagcgtcgccacctccgaacacttgttccgggaggcaga 1779
|||||
Sbjct: 29655 gtccgagccatactaca-aaagggccgactacctccgaggagctggtccggaagccga 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 ggggtgtcggacggactctaaacaccgacagctggcgcgccaggtaggggtgtgtc 87
|||||
Sbjct: 31297 ggggtgtcggacggacccaaacaccgacagctggcgcgccaggtaggggtgtgtc 31241

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

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

Query: 854 taccgccacttcgctcgtgcaatgaacacgccgagtggaagtcggagg 900
|||||
Sbjct: 30522 aaccgccacttcgctcgtgcaatgaacacgccgagtcgaagtcggagg 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 tgatgacagtgtatTTTCCcattgtcctagggcaagacgcaatgcagtggctccgacatc 1483
||||||| | ||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 27412 tgatgaccgcgtacttaccattgtcctcgggcaagacacgctgcaatggctgcgacatc 27353

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

Query: 1544 agtcctctttgacaagccggcgcagccatgggacctaaaatccattgggcatcagggcg 1603
||||||| ||||| ||||| || ||||| ||||| ||||| || || ||| |
Sbjct: 27292 agtcctctccgacaaaaccggcgcaaccgtgggacctcaaatccatcaagcgtcggggcg 27233

Query: 1604 atgaaacgctccggttgctacctcaagaggttttagaccatgaggaaccacacccccgaag 1663
| ||||| ||||| ||||| ||||| ||||| ||||| || | | ||||| |
Sbjct: 27232 acgaaactctccggtcgtacctcaaaaggttcagaccatgagaaatcgtatccccgagg 27173

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

Query: 1724 gagccatactccagaaaagcgtcggccacctccgaacacttgttccgggaggcagacctc 1783
||||||| | ||| || ||| || | ||||| | ||||| || |||||
Sbjct: 27112 gagccatattacag-aaggcggcactacctccgaggagctgttccgggaagccgacctc 27054

Query: 1784 tacatcaccacggattaacgggcccaggacctcatcgagg 1824
||||||| || | ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 27053 tacatcacgctcgacgagcgggcccaggacctcatcgagg 27013

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

Strand = Plus / Plus

Query: 1447 gtcttagggcaagacgcaatgcagtggtccgacatctacccaacattgcatagacaat 1506
||||| ||||||| ||| ||||| | ||||||| ||| ||||| |||

Sbjct: 55534 gtctcgggcaagacgcgctgcaatggctgacacctaccccgacactgcatcaacgac 55593

Query: 1507 tggagcgacttcagttggtgcttcacgcaacttcagtcctctttgacaagccggcg 1566
||||| ||||||| || ||||||| ||||||| ||||| ||||| || ||| |||||

Sbjct: 55594 tggagcgacttcagtcggcgcttcaccgcaactttcagtcctctctccgataagtcggcg 55653

Query: 1567 cagccatgggacctaataatccattgggcatcaggcgatgaaacgctccggtgtacctc 1626
|| ||||||| ||||||| || | || || || ||| ||||||| |||||

Sbjct: 55654 caacatgggacctaataatccatcaaacaccgagggactaaactctccggtcataacctc 55713

Query: 1627 aagaggttttagaccatgaggaaccacacccccgaagtcgccgaggcgggggtgattgaa 1686
|| ||||| ||||||| || | | ||||||| ||||||| ||||||| ||||| ||

Sbjct: 55714 aaaaggttccagaccatgagaaatcgtatccccgaggtcgccaaggcggcagtgatcgag 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 gggtagccctgggtgtgacggcggactctaacaccgacagctggcgcgccaggtaggg 79
||||||| ||||||| ||| ||||| | ||||||| ||||||| |||||||

Sbjct: 54142 ggggtaaccctgggtgcacggtcggacccgaaacaccgacagctggcgcgccaggtaggg 54201

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

Sbjct: 54202 ggtgtgtcatcgatccaagctatctcaatggccgtcaccttcagcgcaagatcatcctc 54261

Query: 140 cgccccgggactatgttttgccttggaaacctctcatccatagcagatgaagagggaact 199
| |||||| | || || ||||| || || ||||||| ||||| ||||| |||||||

Sbjct: 54262 caccgccgatccatattctgcttcggtactatctcatctgtagcggatgaggagggaact 54321

Query: 200 ctgaccgcatagcagatctattggagaagaagctttcctcagaaatctc 249
||||| ||| | || ||||| ||||| ||||| ||||| |||||
Sbjct: 54322 ctgcatcgcttgcggatccgccggagaaaaagccttcctcaggaatctc 54371

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

Query: 797 caagccgagcaagtgcaaggctgcccagagagaatgctctctttgctcggaacctgtac 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 ctccctttctaccccagctcctcttcatc 532
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 54605 ctccattctaccccagctcctcttcatc 54633

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

Query: 642 ggcgacatcacgaggctggggaacgggatccggcgcaaccgtatcccgggacga 696
|||||
Sbjct: 28183 ggcgacatcacgcgccagagaacgggatccggagcaacctgtctcggggacga 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 gggccatccagtggeccc-taacttcaaggtctccaacgtcagcaagtatgagcgcaagc 1357
|||||
Sbjct: 165974 gggccattcagtggecccc-taacttcaaggtctccaacatcgacaaatatgaacctaacg 165915

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

Query: 1418 aggacgtgatgacagtgatattttccattgtcctagggaagacgcaatgcagtggtctcc 1477
|||
Sbjct: 165854 aagacgtgatgaccgcgtacttgccatctcgtccttgggcaggacgcaatgcagtggtctcc 165795

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

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

Query: 854 taccgccacttcgctcgtgcaatgaacacgccgagtggaagtcggagggtactggcccag 913
|||||
Sbjct: 110316 aaccgccacttcgccgagctatgaacacgcccaagcgaagtcggaggcgtactagctcgg 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 agggtagccctgggtgtgcggacggactctaacaccgacag 61
|||||
Sbjct: 97503 agggtaacccgggtgtgcggtcggacccaaacaccgacag 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 acgtgcggagtcttcgacttactccgtgtctccggccatccagtggcc-cctaacttc 1323
|||||

Sbjct: 37341 acgtgcggagtatccgctcttactccgcgcttagggccatccaatggcctcccaacttc 37282

Query: 1324 aaggtctccaacgtcagcaagtatgagcgcaagcaggacctgggtggctggttagccatc 1383

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

Sbjct: 37281 aaggtatccaatgtcgacaaatatgaacctaaagcaggatccaggggttggttagccgtc 37222

Query: 1384 tacacgattgtcacatgggcccggagcgacggaggacgtgatgacagtgtatccc 1443

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

Sbjct: 37221 tacaccaccgctgctcgggctgccggagcatccaagacgtcatgaccgctatctgcc 37162

Query: 1444 attgtcctagggcaagacgcaatgcagtggtccgacatctacccaacattgcatagac 1503

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

Sbjct: 37161 atcgtccttgggcaagacgcgctgcagtggttacgacatctaccccgacactgcatcgac 37102

Query: 1504 aattggagcgacttcagttggtgcttcatcgccaacttccagtcctctttgacaagccg 1563

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

Sbjct: 37101 gactggggagacttcagtcgacgtttcaccgccaacttccagtcctcttccgacaagcca 37042

Query: 1564 ggcagccatgggacctaaaatccattgggcatcagggcgatgaaacgctccggtgtac 1623

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

Sbjct: 37041 ggcgaaccatgggacctcaaatccatcaagcgcgggggggatgagacttccggtcatac 36982

Query: 1624 ctcaagaggttttagaccatgaggaaccacacccccgaagtcgccgaggcgggggtgatt 1683

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

Sbjct: 36981 ctcaaaaggttccagaccatgagaaaccgcatccccgaggtcacggaggcggccgtgatc 36922

Query: 1684 gaagacttctaccgaggatccaatgactcggctttcgtccgagccatactccagaaaagc 1743

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

Sbjct: 36921 gaggacttctacagaggatccaatgactcggctttcgtccgagccatactaca-aaagc 36863

Query: 1744 gtcggccacctccgaacacttgttccgggaggcagacctctacatcaccacggattaacg 1803

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

Sbjct: 36862 gccgattacctccgaggagctggtccgggaagccgacatctacatcaccgccgacgagcg 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 gagcaagccgagcaaggtgcaaggctgcccagagagaatgctctctttgctcggaacctg 853
|||||
Sbjct: 37812 gagcaagccgagcaagatgcaaggcaacgccgggagaatccgctcttcggcgcaacctg 37753

Query: 854 taccgacttcgctcgtgcaatgaacacgccgagtggaagtcggaggggtactggcccag 913
|||||
Sbjct: 37752 aaccgacttcgcccagctatgaacacgccgagcggagtcggagcgttctagctcgg 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 ggggtgtgcccagcactcctaaacaccgacagctggcgcccaggtaggggtgtgtcttt 90
|||||
Sbjct: 38527 ggggtgtgcccagcaccctaaacaccgacagctggcgcccaggtaggggtgtgtcgc 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 aaacaccgacagctggcgcgccaggtagggg 80
|||| |
Sbjct: 68664 aaacgccgacagttggcgcgccaggtagggg 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 cgacatgaagacacgtgcgagctcttcgcacttactccgtgtctccgggccatccagtgg 1312
|||| |
Sbjct: 60922 cgacaggaggacacgtgcgagctcttcgcacttactccgcgcttagggccatccaatgg 60863

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

Query: 1372 tggttagccatctacacgattgtcacatgggcccggagcgacggaggacgtgatgaca 1431
|||| |
Sbjct: 60802 tggttggccgtctacaccaccgctgctcgggctgccggggcatccgaggacatcatgact 60743

Query: 1432 ggtatatttcccattgtcctagggaagacgcaatgcagtggctccgacatctaccccaa 1491
| |
Sbjct: 60742 gcgtatattgccatcgtcctcgggcaagacgcgctacagtggctacgacatctaccccca 60683

Query: 1492 cattgcatagacaattggagcgacttcagttggtgcttcatcgccaacttccagtccctc 1551
|| |
Sbjct: 60682 cactgcatcgacgactggggagacttcagtcgacgtttcaccgccaacttccagtctctc 60623

Query: 1552 ttgacaagccggcgagccatgggacctaaatccattgggcatcagggcgatgaaacg 1611
| |
Sbjct: 60622 tccgacaagccagcgcaacctgggacctaaatccatcaagcgggggggatgagact 60563

Query: 1612 ctccggtgtacctcaagaggttttagaccatgaggaaccacacccccgaagtcgcccag 1671
|||| |

Sbjct: 60562 ctccgggtcataccttaaaggttccagaccatgagaaaccgcatccccgaggtcacggag 60503

Query: 1672 gcgggggtgattgaagacttctaccgaggatccaatgactcggctttcgtccgagccata 1731
||||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 60502 gggccgtgatcgaggacttctacagaggatctaacgactcggctttcgtccgagccata 60443

Query: 1732 ctccagaaaagcgtcggccacctccgaacacttgttccgggaggcagacctctacatcac 1791
|| || ||| ||| || | ||||| || | ||||| || || ||||| |||||

Sbjct: 60442 ctaca-aaagcgccgactacctccgaggagctggtccgggaagccgacctctacatcac 60384

Query: 1792 cacggattaacgggcccaggacctcatcgagg 1824
| | || | ||||| ||||| ||||| |||||

Sbjct: 60383 cgctgacgagcgggcccaggacctcatcgagg 60351

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

Query: 1253 cgacatgaagacacgtgaggagtcttcgcaacttactccgtgtctccgggccatccagtgg 1312
||||| || ||||| ||||| || ||| ||||| || || ||||| ||||| |||||

Sbjct: 113645 cgacaggaggacacgtgaggagtgtccgctcttactccgccttagggccatccaatgg 113586

Query: 1313 cc-cctaacttcaaggtctccaacgtcagcaagtatgagcgcaagcaggacctgggtggc 1371
|| || ||||| ||||| ||||| ||| ||||| | ||||| || || ||

Sbjct: 113585 cctcccaacttcaaggtatccaatgtcgacaaatgatgaacctaagcaggatccaggggt 113526

Query: 1372 tggtagccatctacacgattgtcacatggccgaggagcgacggaggacgtgatgaca 1431
||| ||||| ||||| | | ||| ||||| | ||||| |||||

Sbjct: 113525 tggctagccgtctacaccacgctgctcgggctgccggagcatctgaggacgttatgacc 113466

Query: 1432 gtgtattttccattgtcctagggaagacgcaatgcagtggctccgacatctaccccaa 1491
| |||| | |||| |||| ||||| || || | ||||| ||||| |||||

Sbjct: 113465 gcgtatctgccatcgctccttgggcaagatgcgctacagtggctacgacatctacccca 113406

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

Sbjct: 113405 cactgcatcgacgactgggagacttcagtcgacgtttcaccgccaacttccagtcctc 113346

|| |||||
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 ggggtgtcggtcggacccaaaactgacagctggcgcgccaggtagggggtgtgtcgac 114759

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

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

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

Query: 848 aacctgtaccccgacttcgctcgtgcaatgaacacgccgagtggaagtcggaggggtactg 907
|||||
Sbjct: 28831 aacctgaatcccgacttcgcccagctatgaacacgccgagtggaagtcggaggggtacta 28890

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

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

Query: 1028 atcaacagccggcgagacacgcggagctccatcaacgcttcgcgca 1074
|||||
Sbjct: 29011 atcaacagtcgccgagacgcggaagctccatcaatgcttcgcgca 29057

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

Query: 797 caagccgagcaaggtgcaaggctgcgccgagagaatgctctctttgctcggaacctgtac 856
|||||
Sbjct: 114101 caagccgagcaagatgcaaggcaacgccgggagaatccgctcttcgggcgaacctgaat 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 ggtgtgctggacggactctaaacaccgacagctggcgcgccaggtaggggtgtgtcttt 90
|||||
Sbjct: 124092 ggtgtgctggacggacccaaaacaccgacagctggcgcgccaggtaggggtgtatcgac 124033

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

Query: 151 tatgttttgctttggaacctctcatccatagcagatgaagaggggaactctgcaccg 207
| || |||||
Sbjct: 123972 cgtattctgctttgggacaatctcatctgtagcggatgaaggggaattctacaccg 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 gagcaagccgaacaagatgcaaggcaacgacgcgagagaatccgctcttcgggtgtaactg 61322

Query: 854 taccctgacttcgctcgtgcaatgaacacgccgagtgaaagtcggaggggtactggcccag 913
|||||
Sbjct: 61321 aaccctgacttcgcccagactatgaacacgccgagcgcgaggtcggagggcgttctagcccgg 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 acccgaaaaactccgctgtccacttcgcccaaaaggagtgacacggat 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 gacgtgatgacagtgtatccccattgtccttagggcaagacgcaatgcagtggctccga 1479
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 1820 gacgtgatgaccgcgtatccaccattgtccttgggcaagatgcgttgcaatggctccga 1761

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

Sbjct: 159585 aaccctgacttcgcccgagcgatgaacacgccgagcgaggctcggaggcgttctagcccgg 159526

Query: 914 atagctgacggcctcccggaaccctagacacggaaggctaccggcggtgcttactcga 973
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Sbjct: 159525 atagctgacggacttctcggacccccgacgccgaggataaccggcgctgttactcag 159466

Query: 974 gcagttaatcaccttctacccatcactaatcctccaagcgacctacgccatgccatcaac 1033
|||| || || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Sbjct: 159465 gcagccaaccatcttctaccgctcgtcaccgccgaacgatctgcgacacgccatcaac 159406

Query: 1034 agccggcgagacacgaggctccatcaacgcttcgcgga 1074
|| || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Sbjct: 159405 agtcgccgagacgcggaagctctatcaatgcttcgcgga 159365

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

Query: 634 gaacgtgcgcgacatcacgaggctggggaacgggatccggcgcaacc 681
||||| || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Sbjct: 159793 gaacgttcgacgacatcacgcagctggagaacgggatccggcgcaacc 159746

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

Query: 509 ttctaccccgacgtccttctc 532
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Sbjct: 159915 ttctaccccgacgtccttctc 159892

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

Score = 208 bits (105), Expect = 9e-50
Identities = 346/425 (81%), Gaps = 1/425 (0%)
Strand = Plus / Plus

Query: 1400 gggccgccgagcgacggaggacgtgatgacagtgtatccccattgtcctagggaag 1459

Sbjct: 186291 gggctgccggagcatccgaggacgtcatgaccgcgtatctgcccatcgtccttgggcaag 186350
||||| ||||||| | ||||||| ||||| | |||| | ||||||| ||||||| |||||||

Query: 1460 acgcaatgcagtggtccgacatctaccccaacattgcatagacaattggagcgacttca 1519

Sbjct: 186351 atgcgctgcagtggttacgacatctaccccgacactgcatcgacgactggggagacttca 186410
| | | ||||||| ||||||| ||||| ||||| ||||| ||||| |||||

Query: 1520 gttggtgcttcacgccaaacttcagtcctctttgacaagccggcgagccatgggacc 1579

Sbjct: 186411 gtcgacgcttcaccgccaaacttcagtcctctctccgacaagccagcgcaacctgggacc 186470
|| | ||||||| ||||||| ||||||| ||||| ||||||| ||||||| |||||||

Query: 1580 taaaatccattgggcatcagggcgatgaaacgctccggttgacctcaagaggttttaga 1639

Sbjct: 186471 tcaaatccatcaagcgccgggagacgagactctccggtcatacttaaaggtccaga 186530
| ||||||| | | | ||||| ||||| ||||| ||||| ||||| |||||

Query: 1640 ccatgaggaaccacacccccgaagtcgccgagggcggggtgattgaagacttctaccgag 1699

Sbjct: 186531 ccatgagaaaccgatccccgaggtcacggaggcgccgctgatcgaggacttctacagag 186590
||||||| ||||| || ||||||| ||||| ||||| ||||| ||||| ||||| |||||

Query: 1700 gatccaatgactcggttttcgtccgagccatactccagaaaagcgtcggccacctccgaa 1759

Sbjct: 186591 gatctaacgactcggttttcgtccgagccatactaca-aaaggcgcgactacctccgag 186649
||||| || ||||||| ||||||| ||||||| ||||| ||||| ||||| ||||| |||||

Query: 1760 cacttgttccgggagggcagacctctacatcaccacggattaacgggcccaggacctcatc 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 gagcaagccgagcaaggtgcaaggctgcccagagagaatgctctctttgctcggaacctg 853

Sbjct: 185684 gagcaagccgagcaagatgcaaggcaacgccgggagaaatccgctcttcgggcaaacctg 185743
||||||||| ||||||| ||||| ||||||| ||||| ||||| ||||| |||||

Query: 854 taccgccacttcgctcgtgcaatgaacacgccgagtgaggagggtactggcccag 913
|||||
Sbjct: 185744 aaccgccacttcgccgagctatgaacacgccgagtgagggtcagaggcgttctagctcgg 185803

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 ggggtgtgcggacggactctaaacaccgacagctggcgccaggtaggggtgtgtcttt 90
|||||
Sbjct: 184969 ggggtgtgcggtcggacccaaaacatcgacagctggcgccaggtaggggtgtgtcgac 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 cgacggaggaaccgacgcaggaacgttcgacgacatcacgaggctggggaacgggatccg 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 cgacatgaagacacgtgceggagtcttcgcacttactccgtgtctccgggccatccagtgg 1312
||||| || ||||| || ||| ||||| ||||| ||||| ||||| |||||
Sbjct: 17079 cgacaggaggacacgtctggagtattggcgcttactccatgtctcagggccattcagtgg 17138

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

Query: 1372 tggttagccatctacacgattgtcacatgggccgccggagcgacggaggacgtgatgaca 1431
||||| || ||||| || | | | ||||| || || || || | |||||
Sbjct: 17199 tggttggtgtctataccactactgccggccgctggggcaactgaatatgtgatgact 17258

Query: 1432 gtgtatthttccattgtccttagggcaagacgcaatgcagtggtccgacatctacccaa 1491
| ||||| || || ||||| ||||| || || ||||| ||||| || |||||
Sbjct: 17259 gctgtatthttccattgtccttagggcacgatgcgctgcaatggctacgacacctgccccga 17318

Query: 1492 cattgcatagacaattggagcgacttcagttggtgcttcacgccaacttccagtcctc 1551
|| ||||| || ||||| ||||| ||||| || ||||| ||||| |||||
Sbjct: 17319 cactgcatcgacgattggagcgatttcagtcggtgttttatcgccaacttccaatcctc 17378

Query: 1552 tttgacaagccggcgcagccatgggacctaaaatccattgggcatcaggcgatgaaacg 1611
| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 17379 tctgacaagccggcgaaccatgggacctcaaatccatcaggcgccgagggatgaaact 17438

Query: 1612 ctccggttgatctcaagaggttttagaccatgaggaaccacacccccgaagtgcggag 1671
||||| ||||| || ||||| ||||| || || ||||| || || ||
Sbjct: 17439 ctccggtcatacctcaaaagatttcagaccatgagaaatcgatccccgaggttgaggaa 17498

Query: 1672 gcgggggtgattgaagacttctaccaggatccaatgactcggctttcgtccgagccata 1731

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

Query: 950 ggctaccggcggctgcttactcgagcagttaatcaccttctacccatcactaatcctcca 1009
||||| ||||||||||| ||||| ||||| ||| || ||||| || || || |||||
Sbjct: 16796 ggctatcggcggctgctcactcgggcagctaaccatcttctgcctctcggtcatectccg 16855

Query: 1010 agcgacctacgccatgccatcaacagccggcgagacacgaggctccatcaacgcttcg 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 gacgtgatgaccgtgtacttaccatcgctccttgggcaagacgcgctgcaatggatgca 82049

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

Query: 1540 ttccagtcctctttgacaagccggcgagccatgggacctaaaatccattgggcatcag 1599
||||||||||||| ||||| ||||| ||| || ||||| || ||||||||| || ||| |
Sbjct: 82110 ttccagtcctctccgacaaaccggtgcaaccgtgggatctcaaatccatcaagcgtc-g 82168

Query: 1600 ggcgatgaaacgctccggttgctacctaagaggttttagaccatgaggaaccacacccc 1659
|| || ||||| ||||||| ||||||||| ||||| ||||||||| || | |||||
Sbjct: 82169 gggaagaactctccggtcgtacctaagaggttccagaccatgagaaatcgtatcccc 82228

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 ttctaccccagctcctcttcatc 532
|||||
Sbjct: 81094 ttctaccccagctcctcttcatc 81117

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

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
|||||
Sbjct: 133339 aaacgccgacagttggcgcgccaggtagggg 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 cgacatgaagacacgtgaggagtcttcgacttactccgtgtctccggccatccagtgg 1312
|||||
Sbjct: 109470 cgacaggaggacacgtgaggagtatccgcccttactccgcgcttagggccatccaatgg 109411

Query: 1313 cc-cctaacttcaaggtctccaacgtcagcaagtatgagcgcgaagcaggacctgggtggc 1371
||
Sbjct: 109410 cctcccaacttcaaggtatccaatgtcgacaatatgaacctaagcaggatccagggggc 109351

Query: 1372 tggttagccatctacacgattgtcacatgggccggagcgacggaggacgtgatgaca 1431
|||||
Sbjct: 109350 tggttagccgtctacaccacgctgctcgggctgcccgggcatccgaagacgtcatgact 109291

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 aaacccgacagtggcgcgccaggtagggg 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 cccattgtcctagggaagacgcaatgcagtggtccgacatctaccccaacattgcata 1500
||||| ||||| ||||||||||| ||||||||||| ||||||||||||||| ||| |||||
Sbjct: 16534 cccatcgtccttgggaagacgcgctgcagtggtacgacatctaccccgacactgcatc 16475

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

Query: 1561 ccggcgcagccatgggacctaaaatccattgggcatcagggcgatgaaacgctccggttg 1620
|| ||||| ||||||||||| ||||||||| || | || ||||||||| ||||||| |
Sbjct: 16414 ccagcgaaccatgggacctcaaatccatcaagcgcgaggggatgaaactctccggtcg 16355

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

Query: 1681 attgaagacttctaccgaggatccaatgactcggctttcgtccgagccatactccagaaa 1740
|| | ||||||||| ||||||| ||||||||||||||||||| || |||||
Sbjct: 16294 atcgaggacttctacagaggatctaagactcggctttcgtccgagccatactaca-aaa 16236

Query: 50 aacaccgacagctggcgcgccaggtagggg 80
 |||| | ||||| | ||||| ||||| |||||
Sbjct: 42263 aacgccgacagttggcgcgccaggtagggg 42293

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

Query: 50 aacaccgacagctggcgcgccaggtagggg 80
 |||| | ||||| | ||||| ||||| |||||
Sbjct: 109561 aacgccgacagttggcgcgccaggtagggg 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 cccattgtcctagggcaagacgcaatgcagtggtccgacatctaccccaacattgcata 1500
 |||| | ||||| | ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 69408 cccacgtccttgggcaagacgcgctgcagtggttacgacatctaccccgacactgcatc 69467

Query: 1501 gacaattggagcgacttcagttggtgcttcacgccaacttcagtcctctttgacaag 1560
 ||| | ||| | ||||| ||| | ||| | ||||| ||||| ||||| ||||| |||||
Sbjct: 69468 gacgactgggggagacttcagtcgacgtttcaccgccaacttcagtcctctctccgacaag 69527

Query: 1561 ccggcgagccatgggacctaaaatccattgggcatcaggcgatgaaacgctccggttg 1620
 || ||||| | ||||| ||||| ||| | ||| | ||||| ||||| ||||| |||||
Sbjct: 69528 ccagcgcaaccatgggacctcaatccatcaagcgccgaggggatgaaactctccggtcg 69587

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

Query: 1681 attgaagacttctaccgaggatccaatgactcggctttcgtccgagccatactccagaaa 1740
 || | ||||| | ||||| | ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 69648 atcgaggacttctacagaggatctaatactcggctttcgtccgagccatactaca-aaa 69706

Sbjct: 68880 atagctgac 68888

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

Query: 1025 gccatcaacagccggcgagacacgcggagctccatcaacgcttcgcgca 1074
|||||
Sbjct: 68991 gccatcaacagtcgccgagacgcgcaagctctatcaatgcttcgcgca 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 aaacaccgacagctggcgccaggtagggg 80
|||||
Sbjct: 43679 aaacgccgacagttggcgccaggtagggg 43649

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

Query: 509 ttctaccccgacgtccttcat 531
|||||

Strand = Plus / Plus

Query: 848 aacctgtaccccgacttcgctcgtgcaatgaacacgccgagtgagtcggagggtactg 907
||||| ||||||| || || ||||||| || ||||||| |||||
Sbjct: 63 aacctgaaccccgacttcgcccagccgtgaacacgccgagtcggaggagtactg 122

Query: 908 gccagatagctgacggcctccc 930
|| | ||||||| || |||||
Sbjct: 123 gctcggatagctgaggactccc 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 aggacgtgatgacagtgtatTTCCATTGTCCTAGGGCAAGACGCAATGCAGTGGCTCC 1477
||||| ||||| | || || ||||||| ||||||| ||||| ||||| |
Sbjct: 47964 aggacgtgatgaccgcatacttgcccattgtcctcgggcaagacgcgctgcaatggctgc 48023

Query: 1478 gacatctaccccaacattgcatagacaattggagcgacttcagttggtgcttcacgcca 1537
||||| ||||| ||| ||||| ||| | ||||||| ||||| | ||||| |||||
Sbjct: 48024 gacatctaccccgacactgcatcgacgactggagcgacttcagtcgacgttcaccgcca 48083

Query: 1538 acttccagtcctctttgacaagccggcgagccatgggacctaaaatccattgggcatc 1597
|||| | ||||||| ||||| || ||||| ||||||| || ||||| || |
Sbjct: 48084 actttcagtcctctccgacaaaccagcgcaaccatgggacctcaagtcacatcaagcgcc 48143

Query: 1598 agggcgatgaaacgctccggtgtacctcaagagtttttagaccatgaggaaccacacc 1657
|||| | ||||| ||||||| ||||||| ||||| ||||||| || | |||
Sbjct: 48144 agggggacgaaactctccggtcgtacctcaaaagttccagaccatgagaaatcgtatcc 48203

Query: 1658 ccgaagtcgccgaggcgggggtgattgaagacttctaccgaggatccaatgactcggctt 1717
|||| | | ||||||| ||||| || || ||||||| ||||||| |||||||
Sbjct: 48204 ccgaggtcacggaggcggcgtgatcgaggatttctacagaggatccaacgactcggctt 48263

Query: 1718 tcgtccgagccatactccagaaaagcgtcggccacctccgaacacttgttccgggaggca 1777
||||| ||||||| | ||| || ||| || ||||||| || ||||||| |||
Sbjct: 48264 tcgtctgagccatattacag-aaggcggcactacctccgagcaactgttccgggaagcc 48322

Query: 1778 gacctctacatcaccacggattaacgggccaggacctcatcggagg 1824
|||||
Sbjct: 48323 gacctctacatcaccgccgacgagcagctcaggacctcatcggagg 48369

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

Query: 31 gggtgtgcggacggactcctaaacaccgacagctggcgccaggtaggggtgtgtcttt 90
|||||
Sbjct: 46602 gggtgtgcggtcggaccctaaacaccgacagccggcgcaaggtaggggtgtgtagcc 46661

Query: 91 gatctgagctagctcaatgaccattacctccaatgcaagatcgcccttcgccccgggac 150
|||||
Sbjct: 46662 gatctaagctagctcaatggtcgtcaccttcagcgcaagatcaccttcgccccgggatc 46721

Query: 151 tatgttttgctttggaacctctcatccatagcagatgaagaggggaactctgcaccgat 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 aacctgtacccccgacttcgctcgtgcaatgaacacgccgagtggaagtcggagggtactg 907
|||||
Sbjct: 47393 aacctgaacccccgacttcgcccagccatgaatacgccaagtgaagtcggaggagtactg 47452

Query: 908 gccagatagctgacggcctcccgcgaacctagacacggaaggetaccggcggtgctt 967
|||
Sbjct: 47453 gtcgcatagctgatgggctccctcggactcccgacgtcagggctatcgacgactgttc 47512

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

Query: 1441 cccattgtcctagggcaagacgcaatgcagtggtccgacatctaccccaacattgcata 1500
||||| ||||| ||||| || | ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 26067 cccatcgtccttgggcaagatgcgctgcagtggtcgacatctacccgacactgcatc 26126

Query: 1501 gacaattggagcgacttcagttggtgcttcatcgccaacttcagtcctctttgacaag 1560
||| | ||| | ||||| || | ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 26127 gacgactggggagacttcagtcgacgttcatcgccaacttcagtcctctcgcacaag 26186

Query: 1561 ccggcgcagccatgggacctaaatccattgggcatcagggcgatgaaacgctccggttg 1620
||||| ||||| ||||| ||||| || | || | ||||| ||||| ||||| |||||
Sbjct: 26187 ccggcgcaaccatgggacctcaatccatcaagcgggaggatgagactctccggtca 26246

Query: 1621 tacctcaagaggttttagaccatgaggaaccacaccccgaagtcgccgaggcgggggtg 1680
||||| || ||||| ||||| ||||| || || ||||| ||| | ||||| |||||
Sbjct: 26247 taccttaaaggttcagaccatgagaaactgcacccccgaggtcacggaggcggccgtg 26306

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

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

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

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

Query: 794 gagcaagccgagcaaggtgcaaggctcgcgccgagagaatgctctctttgctcggaacctg 853
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 25420 gagcaagccgagcaagatgcaaggcaacgccgggagaatccgctcttcgggcgcaacttg 25479

Query: 854 taccctgacttcgctcgtgcaatgaacacgccgagtgaaagtcggaggggtactggcccag 913

|||||
|||||

Sbjct: 25480 aaccctgacttcgctcgtgcaatgaacacgccgagtgaaagtcggaggggttctagctcgg 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 ggggtgtcggacggactcctaaacaccgacagctggcgcgccaggtaggggggtgtgtcttt 90

|||||
|||||

Sbjct: 24704 ggggtgtcggtcggaccaagacaccgacagctggcgcgccaggtaggggggtgtgtcgac 24763

Query: 91 gatctgagctagctcaatgaccattacctccaaatgcaagatcgccttcgccccgggac 150

||||
|||||

Sbjct: 24764 gatccaagctagctcaatggccgtcaccttccacagcaaaatcgtgtgctcccggatc 24823

Query: 151 tatgttttgcctttggaacctctcatccatagcagatgaagaggggaactctgcaccgcat 210

||
|||||

Sbjct: 24824 tgtattctgcttcgggacgatctcgtccgtagcagatgaagaaggaattctacaccgct 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

Query: 1778 gacctctacatcaccacggattaacgggccaggacctcatcggagg 1824
|||||
Sbjct: 34219 gacctctacatcaccgccgacgagcagctcaggacctcatcggagg 34265

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

Query: 31 ggggtgtcggacggactcctaacaccgacagctggcgccaggtaggggtgtgtcttt 90
|||||
Sbjct: 32498 ggggtgtcggtcggaccctaacaccgacagccggcgccaggtaggggtgtgtagcc 32557

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

Query: 151 tatgttttctttggaacctctcatccatagcagatgaagaggaactctgcaccgcat 210
|||||
Sbjct: 32618 cgtgttctcttcggaactatctctctgtagccgatgaggaaggaactctacatcgcat 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 aaacctgtacccccgacttcgctcgtgcaatgaacacgccgagtggaagtcggagggtactg 907
|||||
Sbjct: 33289 aaacctgaacccccgacttcgcccagccatgaatacgccaagtgaagtcggaggagtactg 33348

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

Query: 968 actcgagcagttaatcaccttctaccatcactaatctccaagcgacctacgcatgcc 1027

Query: 1598 agggcgatgaaacgctccggttgctacctaagaggttttagacatgaggaaccacacc 1657
|||| | | |||| | |||| | |||| | |||| | |||| | |||| | |||| | ||||
Sbjct: 84420 agggggacgaaactctccggtcgtacctaagaggttccagaccatgagaaatcgtatcc 84479

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

Query: 1718 tcgtccgagccatactccagaaaagcgtcggccacctccgaacacttgttccgggaggca 1777
|||| | |||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct: 84540 tcgtctgagccatattacag-aaggcggcactacctccgagcaactggtccgggaagcc 84598

Query: 1778 gacctctacatcaccacggattaacgggccaggacctcatcggagg 1824
|||| | |||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct: 84599 gacctctacatcaccgcgacgagcgagctcaggacctcatcggagg 84645

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

Query: 31 ggggtgtcggacggactctaaacaccgacagctggcgcgccaggtagggggtgtgtcttt 90
|||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | ||||
Sbjct: 82878 ggggtgtcggtcggacccaaaacaccgacagccggcgcgccaggtagggggtgtgtagcc 82937

Query: 91 gatctgagctagctcaatgaccattacctccaaatgcaagatgcccttcgccccgggac 150
|||| | |||| | |||| | | | |||| | | | |||| | |||| | |||| | ||||
Sbjct: 82938 gatctaagctagctcaatggtcgtcaccttccagcgcaagatcaccttcgccccgggac 82997

Query: 151 tatgttttgctttggaacctctcatccatagcagatgaagagggaaactctgcaccgcat 210
|||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | ||||
Sbjct: 82998 cgtgttctgcttcggaactatctcatctgtagccgatgaggaaggaactctacatcgcac 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 aacctgtacccccgacttcgctcgtgcaatgaacacgccgagtgaagtcggaggggtactg 907
||||| |||||||||||| | | |||| | |||| | |||||||||||| | |||||
Sbjct: 83669 aacctgaacccccgacttcgcccagccatgaatacggcaagtgaagtcggaggagtactg 83728

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

Query: 968 actcgagcagttaatcaccttctaccatcactaatcctccaagcgacctacgccatgcc 1027
|||| | |||| | | | |||||| | | | | | | | |||||| | |||||
Sbjct: 83789 actcaagcagccaaccatcttctacctctcgtcaccgccgaacgacctacgacatgcc 83848

Query: 1028 atcaacagccggcgagacacgaggctccatcaacgcttcgcg 1071
|||||| | | | |||||||||||||| | | |||||
Sbjct: 83849 atcaacagtcgccgggacgcgaggctccatcaatgcctcgcg 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 aggacgtgatgacagtgatatttccattgtcctagggcaagacgcaatgcagtggtcc 1477
|||||||||| | | | |||||||| | |||||||| | |||| | |||||
Sbjct: 72871 aggacgtgatgaccgcatacttgcccattgtcctcgggcaagacgcgctgcaatggctgc 72930

Query: 1478 gacatctaccccaacattgcatagacaattggagcgacttcagttggtgcttcacgcca 1537
|||||
Sbjct: 72931 gacatctaccccgacactgcatcgacgactggagcgacttcagtcgacgtttcaccgcca 72990

Query: 1538 acttccagtcacctctttgacaagccggcgagccatgggacctaaaatccattgggcatc 1597
|||||
Sbjct: 72991 actttcagtcacctctccgacaaaccagcgcaacctatgggacctcaagtcacatcaagcgcc 73050

Query: 1598 agggcgatgaaacgctccggtgtacctcaagaggttttagacctgaggaaccacacc 1657
|||||
Sbjct: 73051 agggggacgaaactctccggtcgtacctcaaaaggttcagacctgagaaatcgtatcc 73110

Query: 1658 ccgaagtcgccgaggcgggggtgattgaagacttctaccgaggatccaatgactcggctt 1717
|||||
Sbjct: 73111 ccgaggtcacggaggcggccgtgatcgaggatttctacagaggatccaacgactcggcct 73170

Query: 1718 tcgtccgagccatactccagaaaagcgtcggccacctccgaacacttgttccgggaggca 1777
|||||
Sbjct: 73171 tcgtctgagccatattacag-aaggcggcactacctccgagcaactgttccgggaagcc 73229

Query: 1778 gacctctacatcaccacggattaacgggcccaggacctcatcggagg 1824
|||||
Sbjct: 73230 gacctctacatcaccgccgacgagcagctcaggacctcatcggagg 73276

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

Query: 31 ggggtgtcggacggactcctaaacaccgacagctggcgccaggtagggggtgtgtcttt 90
|||||
Sbjct: 71509 ggggtgtcggtcggaccctaaacaccgacagcggcgccaggtagggggtgtgtagcc 71568

Query: 91 gatctgagctagctcaatgaccattacctccaaatgcaagatcgcccttcgccccgggac 150
|||||
Sbjct: 71569 gatctaagctagctcaatggctcgtcaccttccagcgcaagatcaccttcgccccgggac 71628

Query: 151 tatgttttgctttggaacctctcatccatagcagatgaagaggaactctgcaccgcat 210
|||||
Sbjct: 71629 cgtgttctgcttcggaactatctcatctgttagccgatgaggaaggaactctacatcgcat 71688

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 aacctgtaccccgacttgcctcgtgcaatgaacacgccgagtggaagtcggaggggtactg 907
||||||| ||||||||||||||| || || ||||| ||||| ||||||||||||||| |||||
Sbjct: 72300 aacctgaaccccgacttgcgccgagccatgaatacgccaagtgaagtcggaggagtactg 72359

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

Query: 968 actcgagcagttaatcaccttctaccatcactaatcctccaagcgacctacgccatgcc 1027
||||| ||||| || || ||||||||| || || | || | || ||||||||| |||||
Sbjct: 72420 actcaagcagccaaccatcttctacctctcgtcaccgccgaacgacctacgacatgcc 72479

Query: 1028 atcaacagccggcgagacacgggagctccatcaacgcttcgcg 1071
||||||| || || || ||||||||||||||||| || |||||
Sbjct: 72480 atcaacagtcgccgggacgcgggagctccatcaatgcctcgcg 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: 916 agctga 921
 |||||
Sbjct: 1446 agctga 1451

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

Query: 509 ttetaccccgacgtcctcttcac 532
 |||||||||||||||||||||||
Sbjct: 1055 ttetaccccgacgtcctcttcac 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 cgacatgaagacacgtgaggagtcttcgcacttactccgtgtctccgggccatccagtgg 1312
 |||| | | ||||||||||||| | || | |||||||| | || | ||||||||| |||
Sbjct: 165917 cgacaggaggacacgtgaggagtatccgcccttactccgcgccttagggccatccaatgg 165976

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

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

Query: 1432 gtgtattttccattgtcctagggcaagacgcaatgcagtggtctccgacatctaccccaa 1491
 | |||| | | || | |||| | || |||| | || ||||||| ||||||||| |||||
Sbjct: 166097 gcgtatctgctcatcgtccttggacaagatgcgctgcagtggttacgacatctacccca 166156

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

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

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

Query: 794 gagcaagccgagcaaggtgcaaggctgcccagagagaatgctctctttgctcggaacctg 853
|||||||
Sbjct: 165458 gagcaagccgagcaagatgcaaggcaacgacgagagaatccgctcttcgggcaacctg 165517

Query: 854 taccgccacttcgctcgtgcaatgaacacgccgagtgaaagtcggagggtactggcccag 913
|||||||
Sbjct: 165518 aaccgccacttcgccgagctatgaacacgccgagtgaaagtcggaggcgttctagctcgg 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 aaacaccgacagctggcgccaggtagggg 80
||||
Sbjct: 187569 aaacgccgacagttggcgccaggtagggg 187539

>gb|AY883559.2| Zea mays cultivar inbred line B73 teosinte glume architecture 1 (tg1)
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 ccgacatgaagacacgtgaggagctctgcacttactccgtgtctccggccatccagtg 1311
|||||
Sbjct: 109879 ccgacaggaagacacgtgtggagtatctgcgctcactccgtgtctcaggccattcaatg 109820

Query: 1312 gccctaa-cttcaaggtctccaacgtcagcaagtatgagcgcaagcaggacctgggtgg 1370
||||| || ||||||||||||||||||||||| ||| || |||| | ||||||||| ||| ||
Sbjct: 109819 gccccaaacttcaaggtctccaacgtcaacaatacagcctaagcaggacccgggagg 109760

Query: 1371 ctggttagccatctacacgattgtcacatgggccgcccggagcgacggaggacgtgatgac 1430
||||||| ||| ||||| || | | | ||||| | ||| ||| | ||| |||||||||
Sbjct: 109759 ctggttgccgtctatacaaccgctgccccggccactggggcaactaaagatgtgatgac 109700

Query: 1431 agtgtattttccattgtcctagggaagacgcaatgcagtggctccgacatctaccca 1490
||||||| ||||| ||||| ||||||||| ||| | | ||||| | ||||||||| |||
Sbjct: 109699 tgtgtatttaccatcatccttgggcaagacacatttcaatggctacgacatctaccga 109640

Query: 1491 acattgcatagacaattggagcgacttcagttggtgcttcacgccaacttcagtcct 1550
|| ||||| || ||||||| ||||||||| | || ||||||||| |||||||
Sbjct: 109639 gcaactgcattgatgattggagtgacttcagtcgacatttt-tcgccaacttccaatcct 109581

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

Query: 1611 gtcctcggttgctacctcaagaggttttagaccatgaggaaccacacccccgaagtgcgga 1670
|| ||||| ||||||||| ||||| ||||||||| || | || ||||| | | |||
Sbjct: 109520 tcttcggtcgtacctcaagtggtttcagaccatgagaaatcgattcccaggccactga 109461

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

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

Query: 1791 ccacggattaacgggcccaggacctcatcgg 1821
|| ||||| ||||||||| ||||||||| |||||
Sbjct: 109341 ccgcgacgaacgggctcaggacctcatcgg 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 taccctaaagcactgcgaggggtaacccgggtgcgcggtcgggtcctaacaccgacag 94219

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

Query: 121 caaatgcaagatgcccttcgccccgggactatgttttgctttggaaccatctcatccat 180
|||
Sbjct: 94280 c-aacacaagattgctctccgccctggatctgtgttctggttcggaccatctcgtccat 94338

Query: 181 agcagatgaagaggggaactctgcaccgcatagcagatctattggagaagaagc 233
|||||
Sbjct: 94339 ggcagacgaagaaggaattctgcatcgtatagcggatccatcggagaagaagc 94391

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

Query: 947 gaaggctaccggcggtgcttactcgagcagttaatcaccttctaccatcactaatcct 1006
|||||
Sbjct: 110184 gaaggctatcggcggtgctcactcgggcatctaataatccttctaccctcgtcatccc 110125

Query: 1007 ccaagcgacctacgccatgccatcaacagccggcgagacacgcggagctccatcaacgct 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 ctcttttctaccccacgtcctctttcatcaggggagattggagttagcacccttca 563
||||| ||||| ||||| ||| ||| ||||| | | ||| ||| |
Sbjct: 94650 ctcttttctaccctgacgtccttttcatcgaggaagagtggagtcattcccatctccg 94709

Query: 564 acgatgagccaacatgcaaggggaagagcctcccagcgtgaggcgcgacgagga 623
| ||||| ||||| ||||| ||||| ||| ||| ||| ||| |||||
Sbjct: 94710 atgatgagccaacatgcctggggaagaacctctcagcgagaagctcgccgatggagga 94769

Query: 624 atagaagccagaacgtgcgcgacatcacgaggtggggaacgggatccggcgca 678
| | ||| || | ||||| ||||| || ||||| ||||| |||||
Sbjct: 94770 accaacgccgaaatattcgcgacatcacgaagcaggggaacgggactcggcgca 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 gtgatgactgtgtattttgccatcgtccttgggcaggatgctgcaatggctacgacac 179682

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

Query: 1543 cagtcctctttgacaagccggcgcagccatgggacctaataatccattgggcatcagggc 1602
|| ||||||| |||||||||||||||||| ||||| ||||||| | | | ||
Sbjct: 179743 caatccctctccgacaagccggcgcagccatgagacctcaatccatcagacgccgaggg 179802

Query: 1603 gatgaaacgctccggtgtacctcaagaggttttagaccatgaggaaccacacccccgaa 1662
||||| || ||||||| ||||||||| |||||||||||||||| | | | |||||||
Sbjct: 179803 gatgagactctccggtcataacctcaaaaggttttagaccatgagacatcgtatccccgag 179862

Query: 1663 gtgcgccgagcggggtgattgaagacttctaccgaggatccaatgactcggctttcgtc 1722
|| || || | ||||||| |||||||||||||||| ||||| |||||||||||| ||| ||
Sbjct: 179863 gttgcggaagcagcggtgatcgaagacttctaccgggatcctaatgactcggccttcac 179922

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

Query: 1783 ctacatcaccacggattaacgggccagacctcatcggagg 1824
|||||||||| || |||||||| ||| |||||||||||||
Sbjct: 179982 ctacatcaccggcgacgaacgggctcagaacctcatcggagg 180023

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

Query: 50 aaacaccgacagctggcgcgccaggtaggggtgtgtctttgatctgagctagctcaatg 109
|||||||||||||||| |||||||||||||||||| ||||| |||||||||||||
Sbjct: 178334 aaacaccgacagctggcgcgccaggtaggggtgtgtcactgatccaagctagctcaatg 178393

Query: 110 accattacctcaaatgcaagatcgcccttcgccccgggactatgttttgctttggaacc 169
|||| | | | |||||||| || ||||| | || |||| ||||| |||||
Sbjct: 178394 gccatcactttccagcacaagatcgctctccgccctagatctgtttctgcttcagaacc 178453

Query: 170 atctcatccatagcagatgaagaggggaactctgcaccgcatagcagatc 218

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

Query: 1262 gacacgtgctggagctcttcgcaacttactccgtgtctccggccatccagtggcccctaact 1321
||||||| ||||| || || ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 8187 gacacgtgtggagtattggcgcttactccacgtcttagggcattcagtgccccctaact 8128

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

Query: 1382 tctacacgattgtcacatgggccgccggagcgacggaggacgtgatgacagtgtatttc 1441
|||| | | | | | ||||| || | | | | | ||||| || ||||| | ||||| |
Sbjct: 8067 tctataccactgctgctgggccgctggggcaactgaagatttgatgactgcgtatttc 8008

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

Query: 1502 acaattggagcgacttcagttggtgcttcacgccaacttccagtcctctttgacaagc 1561
|| ||||| ||||| || || ||||| ||||| ||||| ||||| |||||
Sbjct: 7947 acgattggagcgatttcagtcgatgtttatcgccaacttccaatccctctccgacaagc 7888

Query: 1562 cggcgcagccatgggacctaaaatccattgggcatcaggggatgaaacgctccggttg 1621
||||||| ||||| ||||| ||||| || | || ||||| || ||||| |
Sbjct: 7887 cggcgaacatgggacctcaatccatcaggcgccgaggggatgaaactcaccggtcat 7828

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

Query: 1682 ttgaagacttctaccgaggatccaatgactcggctttcgtccgagccatactccagaaaa 1741
| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| || |||||
Sbjct: 7767 tcgaggacttctaccgggatcctaatgactcggccttcgtccgagccatactgca-aaag 7709

Query: 1742 gcgtcggccacctccgaacacttgttccgggaggcagacctctacatcaccacggattaa 1801
||| | | ||||| || | ||| ||||| || ||||| ||||| || || ||
Sbjct: 7708 gcgccaactacctccgagcagctattcaggaagcgaacctctacatcaccgccgacgaa 7649

Query: 1802 cgggccaggacctcatcggaggcacgaa 1830
||||| ||||||||||||| ||||| |||||
Sbjct: 7648 tgggctcaggacctcattggaggaacgaa 7620

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

Query: 7 aaaagcaccgcaaggggtagccctgggtgtgaggacggactctaacaccgacagctggc 66
||||||| | ||||| | ||| ||||||||| ||||| | |||||||||||||
Sbjct: 9408 aaaagcacctcgaggggaaccccgggtgtgaggcggacccaaacaccgacagctggt 9349

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

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

Query: 187 tgaagaggaactctgcaccgcatagcagatc 218
||||||| ||||||||| || ||||||||| |||||
Sbjct: 9228 cgaagaaggaactctacattgcatagcggatc 9197

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

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

Query: 908 gccagatagctgacggcctcccgcgaaccctagacacggaaggetaccggcggtgctt 967
|| | ||||| || ||||||||| || || ||||||| | || ||||| ||| |||||||
Sbjct: 8540 gctcggatagccgatggcctccccggactctagacgccgagggctatcggtggctgctc 8481

Query: 968 actcgagcagttaatcaccttctacccatcactaatctccaagcgacctacgccaatgcc 1027
||||| |||| | | ||||| | | | ||||| ||||| |||| | | |||
Sbjct: 8480 actcgggcagctaaccatcttctgcctcccgcctcatcctccgagcgatctacaacacgcc 8421

Query: 1028 atcaacagccggcgagacacgcggagctccatcaacgcttcgcgcgaccgatga 1081
||||| | | | | | | | | ||||| ||||| ||||| |||||
Sbjct: 8420 atcaatagtcgacgggacgcacagagctccatcaatgcttcgcgcgaaacgatga 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 gaggacgtgatgacagtgtatTTTCCcattgtcctagggcaagacgcaatgcagtggctc 1476
||||||| ||||| ||||| | | | | | ||||| ||||| ||||| |||||
Sbjct: 91274 gaggacgtaatgaccgtgtacttgcctatcgtcctcgggcaagacgcgctgcaatggctg 91215

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

Query: 1537 aacttcagtcctctttgacaagccggcgagccatgggacctaaatccattgggcat 1596
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 91154 aactttcagtctctctccgacaaaccggcgcaacatgggacctcaatccatcaagcgt 91095

Query: 1597 cagggcgatgaaacgctccggttgacctcaagaggttttagaccatgaggaaccacacc 1656
| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 91094 cgggggatgaaactctccggtcatacctcaaaggttccagaccatgagaaatcatatc 91035

Query: 1657 cccgaagtcgcccaggcgggggtgattgaagacttctaccgaggatccaatgactcggct 1716
||||| ||||| || ||||| ||||| || ||||| ||||| ||||| ||||| |||||
Sbjct: 91034 cccgaggtcgagatgcggcagtgatcgaggacttctacagaggatccaatgactcgacc 90975

Query: 1717 ttcgtccgagccatactccagaaaagcgtcgccacctccgaacacttgttccgggaggc 1776
|| ||||| ||||| | || | | | | ||||| || ||||| |||||
Sbjct: 90974 tttgtccgaacctatattaca-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 aacctgaaccccgacttcgcccagccatgaacacgccgagtgaagttggaggggtgtg 91785

Query: 908 gccagatagctgacggcctcccgcgaaccctagacacggaaggctaccggcggctgctt 967
|| | || | || ||||||| || || | ||||| || || ||||||| |
Sbjct: 91784 gctcggatggatgatggcctccctcggactcccacaccgaggggtatcggcggctattc 91725

Query: 968 actcgagcagttaatcaccttctaccatcactaatcctccaagcgacctacgccatgcc 1027
|||| ||||| ||||||| || || | || | ||| ||| || ||
Sbjct: 91724 actcaagcagccaatcaccttctaccctcgtccaccgccgaacgatctatgacacacc 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 aaaagcacccgaagggtagccctgggtgtgcggacggactctaacaccgacagctggc 66
||||||| | ||||| ||||||| |||| ||||| | ||||| |||||||
Sbjct: 102107 aaaagcacctcgggggtaaccctgggtgcgcggtcggacccgaaactgacagctggc 102048

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

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

Strand = Plus / Minus

Query: 503 gtcctttctaccccgacgtccttcat 531
||||| ||||||||||||||||||||
Sbjct: 92174 gtcctttctaccccgacgtccttcat 92146

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

Query: 645 gacatcacaggctggggaacgggatccggcgcaaccgtatcccgggacga 696
||||| ||||| ||||| || ||||| ||||| ||||| |||||
Sbjct: 92035 gacatcacaggccggggagcgggaccagcgcgaaccatatacagagacga 91984

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

Query: 50 aaacaccgacagctggcgcgccaggtaggg 80
|||| | ||||| ||||||||||||||||
Sbjct: 110714 aaacccgacagttggcgcgccaggtaggg 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 gaggacgtaatgaccgtgtacttgccctatcgtcctcgggcaagacgcgctgcaatggctg 57667

Query: 1477 cgacatctacccaacattgcatagacaattggagcgaacttcagttggtgcttcacgcc 1536
||||| ||||| | | ||||| ||| | ||||| ||||||||| || ||||| |||||
Sbjct: 57668 cgacacctaccctgagactgcatcgacgactggagccacttcagtcggcgttcaccgcc 57727

Query: 1537 aacttcagtcctctttgacaagccggcgcagccatgggacctaaaatccattgggcat 1596

Sbjct: 57728 aactttcagtcctctcctccgacaaaccggcgcaaccatgggacctcaaatccatcaagcgt 57787

Query: 1597 cagggcgatgaaacgctccggtgtacctcaagaggttttagacctgaggaaccacacc 1656

Sbjct: 57788 cgggggatgaaactctccggtcatacctcaaaggttcagacctgagaaatcatatc 57847

Query: 1657 cccgaagtcgccgaggcgggggtgattgaagacttctaccgaggatccaatgactcggct 1716

Sbjct: 57848 cccgaggtcgcagatgccgagtgatcgaggacttctacagaggatccaatgactcgacc 57907

Query: 1717 ttcgtccgagccatactccagaaaagcgtcggccacctccgaacacttgttccgggaggc 1776

Sbjct: 57908 tttgtccgaacctattaca-aaagtgccgactacctccgagcaactgttccgggaagc 57966

Query: 1777 agacctctacatcacc 1792

Sbjct: 57967 cgacctctacatcacc 57982

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

Query: 848 aacctgtaccccgaacttcgctcgtgcaatgaacacgccgagtgagtcggaggggtactg 907

Sbjct: 57038 aacctgaaccccgaacttcgcccagccatgaacacgccgagtgagttggaggggtgttg 57097

Query: 908 gccagatagctgacggcctcccgcgaaccctagacacggaaggctaccggcggtgctt 967

Sbjct: 57098 gctcggatggatgatggcctccctcggactcccgcacaccgaggggtatcggcggtattc 57157

Query: 968 actcgagcagttaatcaccttctaccatcactaatcctccaagcgacctacgccatgcc 1027

Sbjct: 57158 actcaagcagccaatcaccttctaccctcgtcaccgccgaacgatctatgacacacc 57217

Query: 1028 atcaacagccggcgagacacgccgagctccatcaacgcttcgcgcgacctgacacga 1086

Sbjct: 57218 atcaacagtcgccgagacgcgcgagctccatcaatgcctcgcgtgaacgacgacacga 57276

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

Query: 7 aaaagcaccgcaaggggtagccctgggtgtgcggacggactctaaacaccgacagctggc 66
 ||||| | ||||| ||||| ||| ||| | ||||| |||||
Sbjct: 46775 aaaagcacctcgggggtaaccctgggtgcgcggtcggacccgaacactgacagctggc 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 gctcctttctaccccgacgtccttcat 531
 |||| | ||||| ||||| |||||
Sbjct: 56708 gctccattctaccccgacgtccttcat 56736

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

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

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

Query: 50 aacaccgacagctggcgccaggtagggg 80
 |||| | ||||| ||||| |||||
Sbjct: 38168 aacgccgacagtggcgccaggtagggg 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 tggctccgacatctacccaacattgcatagacaattggagcgacttcagttggtgcttc 1530
||||| ||||| ||||| || ||||| ||| | ||||| ||||| ||||| ||||| |||||
Sbjct: 153054 tggctacgacacctaccccgacctgcatcgacgactggagcgacttcagtcggtgcttc 153113

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

Query: 1591 gggcatcagggcgatgaaacgctccggttgacctcaagaggttttagaccatgaggaac 1650
|| || || ||||| || ||||| ||||| || || || || || |||||
Sbjct: 153174 aagcgccaaggggatgagactctccggtcgtacctcaaagatttcagacaatgaggaat 153233

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

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

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

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

Query: 31 ggggtgtcggcagcactctaaacaccgacagctggcgcgccaggtaggggtgtgtcttt 90
||||| ||||| ||||| | ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 151640 ggggtgcggtcggacccaaaacaccgacagctggcgcaccaggtaggggtgtgtcact 151699

Query: 91 gatctgagctagctcaatgaccattacctccaaatgcaagatcgcccttcgccccgggac 150
||||| ||||||| ||||||| || | || | | | ||||||| ||| ||||||| || |
Sbjct: 151700 gatccaagctagatcaatggccgtcacttttcagcacaagatcttcctctgccccaggtc 151759

Query: 151 tatgttttgctttggaaccatctcatccatagcagatgaagagggaaactctgcaccgcat 210
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Sbjct: 151760 catgttctgcttcggaaccatctcatccgtggcagacgaagaaggaactctacaccgcat 151819

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

Score = 77.8 bits (39), Expect = 2e-10
Identities = 144/179 (80%)
Strand = Plus / Plus

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

Query: 872 gcaatgaacacgccgagtgaggtcggagggtactggcccagatagctgacggcctccc 931
|| ||||||| ||||||| ||||||| ||||| | || ||||| | ||||||| ||||| || ||
Sbjct: 152454 gccatgaacacgccgagtgaggtcgggtgaagtgttgctcggatagccgacggtcttccc 152513

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

Score = 56.0 bits (28), Expect = 8e-04
Identities = 31/32 (96%)
Strand = Plus / Plus

Query: 504 ctctttctaccccgacgtcctcttcatcagg 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 cccattgtcctcgggcaagatgcaactggctacgacacctacccggcactgcac 150455

Query: 1501 gacaattggagcgacttcagttggtgcttcacgcgcaacttcagtcctctttgacaag 1560
||| ||||||||| ||||||||| || ||||||||| ||||| ||||||| |||||
Sbjct: 150456 gacgattggagcgatttcagttggtcattttatcgcaaatccaatcctctccgacaag 150515

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 aaggctatcggtggctgctcactcgggcgactaatcatcttctacctctcgtcctcctc 149961

Query: 1008 caagcgacctacgccatgccatcaacagccggcgagacacgaggctccatcaacgctt 1067
| ||||| ||||| || ||||||||||| ||||| ||| ||| |||||||||||||||||
Sbjct: 149962 cgagcgatctacggcacgccatcaacagtcggcgggacgcgcagagctccatcaacgctt 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 ctctttctaccccgagctcctcttcatcagggggagattggagttagcaccgtcttca 563
|||| ||||||||||||||||||||||||| |||| ||| |||| | | | ||| ||| |
Sbjct: 149470 ctccattctaccccgagctcctcttattgggggaagagtggaatcatctcccatctccg 149529

Query: 564 acgatgagccaacctatgcaaggggaagagcctccccagcgtgaggcgcgacgagggagga 623
|||| ||||||||| ||| ||||||||| || || ||| | || ||| ||| |||||||||
Sbjct: 149530 acgacgagccaaccgtgctggggaagaaccccctcagtgagaagctcggcagggagga 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: 1702 tccaatgactcggccttctcgtccgagccatact 1733
|| |||||
Sbjct: 7601 tctaatactcggccttctcgtccgagccatact 7632

Score = 73.8 bits (37), Expect = 3e-09
Identities = 136/169 (80%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgcgccaggtaggggtgtgtccttgatctgagctagctcaatg 109
|||
Sbjct: 5981 aaacaccgacaactagcgcgccaggtaggggtgtgtcactgatccaagctagcttaatg 6040

Query: 110 accattacctccaaatgcaagatcgcccttcgccccgggactatgttttgctttggaacc 169
|||
Sbjct: 6041 gccgtcactttctagcacaagatcgctctcegcctggatccgtgttctgcttcagaacc 6100

Query: 170 atctcatccatagcagatgaagaggaactctgcaccgcatagcagatc 218
|||
Sbjct: 6101 atctcatccatggcagacgaagaaggaactctacatctcatagcggatc 6149

Score = 61.9 bits (31), Expect = 1e-05
Identities = 136/171 (79%)
Strand = Plus / Plus

Query: 913 gatagctgacggcctcccgcgaaccctagacacggaaggctaccggcggctgcttactcg 972
|||
Sbjct: 6811 gatagccgatggcctccccggactccagacgccgaggctatcggcggctgctcactcg 6870

Query: 973 agcagttaatcaccttctaccatcactaatctccaagcagctacgccatgccatcaa 1032
|||
Sbjct: 6871 ggcagctaaccatattctgcctctcgtcctcctccgagcgatctacgacagccattaa 6930

Query: 1033 cagccggcgagacacgggagctccatcaacgcttcgcgcgaccgatgaca 1083
|||
Sbjct: 6931 tagtcgacgggacgcacggagctccatcaatgcttcgctcgaacgatgaca 6981

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

Query: 504 ctcctttctaccccgacgtcctctttcatcagggggagattgga 546
||||| ||||||||||||||||||||| ||| ||||||| |||||
Sbjct: 6414 ctccgttctaccccgacgtcctctttatcgaggggagagtgga 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 gcgacggaggacgtgatgacagtgtattttccattgtcctagggcaagacgcaatgcag 1470
||||| ||||||||| ||||| | ||| || || ||||||||||| ||||||||| |||||
Sbjct: 54735 gcgaccgaggacgtaatgaccgcgtacttaccattgtcctcgggcaagacgtgctgcaa 54676

Query: 1471 tggctccgacatctacccaacattgcatagacaattggagcgacttcagttggtgcttc 1530
||||| ||||||||||| | ||| ||||| ||| | ||||||||||||||| |||||||||
Sbjct: 54675 tggctgcgacatctacctcgacactgcatcgacgactggagcgacttcagtcggtgcttc 54616

Query: 1531 atcgccaacttccagtcaccttggacaagccggcgagccatgggacctaaaatccat 1589
| ||||||||||| ||||||||||| ||||| ||||||| ||||||| ||||||| |||||||
Sbjct: 54615 accgccaactttcagtcacctctctgacaaaaccggcgcaacctgggacctcaaatccat 54557

Score = 103 bits (52), Expect = 4e-18
Identities = 148/180 (82%)
Strand = Plus / Minus

Query: 31 ggggtgtgcggacggactctaaacaccgacagctggcgcgccaggtagggggtgtgtcttt 90
||||| ||||| ||||| | ||||||| ||||||||||||||||||||||||||||| |||
Sbjct: 56090 ggggtgcgcggtcggaccctaaacactgacagctggcgcgccaggtagggggtgtgtcatc 56031

Query: 91 gatctgagctagctcaatgaccattacctccaaatgcaagatcgcccttcgccccgggac 150
||||| ||||||||||||||||| | ||||| | ||||||||| | ||||| ||| |
Sbjct: 56030 gatccaagctagctcaatgaccgtcaccttctcgcacaagatcgcccttcgccccgggac 55971

Query: 151 tatgttttgctttggaaccatctcatccatagcagatgaagaggggaactctgcaccgcat 210
 | || ||||| ||||||||||||| |||| || | ||||||||||||| |||||
Sbjct: 55970 cacattatgcttcggaaccatctcatctgtagcggataaaggaggggaactctgcatcgcat 55911

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

Query: 848 aacctgtaccccgacttcgctcgtgcaatgaacacgccgagtggaagtcggaggggtactg 907
 ||||| ||||||||||||| || || ||||||||||||| ||||||||||||| |||
Sbjct: 55299 aacctgaaccccgacttcgcccagccatgaacacgccgagtggaagtcggaggggtgctg 55240

Query: 908 gcccagatagctgacggcctcccgcgaaccctagacacggaaggctaccggcggtgctt 967
 || | ||||||||| || ||||| || || || || || || || || || ||
Sbjct: 55239 gctcggatagctgatgggtccctcggactcacgacgccgagggtatcgacggctgttc 55180

Query: 968 actcgagcagttaatcaccttctacccatcactaatcctccaagcgacctacgccatgcc 1027
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Sbjct: 55179 actcagcgaccaatcaccttctacctctcgtcaccgccgaacaatctacgacacacc 55120

Query: 1028 atcaacagccggcgagacacgccgagctccatcaacgcttcgcgcgaccgatgacacga 1086
 ||||||| || || || ||||||||||||| || ||||| || || |||||||
Sbjct: 55119 atcaacagtcgctgggacgcgagctccatcaatgcctcgcgtgaacgacgacacga 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 aaacaccgacagctggcgccaggtagggg 80

Query: 848 aacctgtaccccgacttcgctcgtgcaatgaacacgccgagtgaagtcggaggggtactg 907
||||| ||||||||||||| || || ||||| || | ||| || ||||| || || ||
Sbjct: 3464 aacctgaaccccgacttcgcccagccatgaaaacactgagcgaggtcggtggagtgtg 3523

Query: 908 gccagatagctgacggcctcccgcgaaccctagacacggaaggctaccggcggtgctt 967
||| ||||| || ||||||| || || | |||| | || ||||| ||| ||||| ||
Sbjct: 3524 ccccgatagccgatggcctccccggactccagacgccgagggctatcggtggctactc 3583

Query: 968 actcgagcagttaatcaccttctacccatcactaatcctccaagcgacctacgcatgcc 1027
||||| |||| ||| || ||||| || | || ||||||| ||||| ||||| ||||| ||
Sbjct: 3584 actcgggcagctaaccatcttctgcctcttgcctcatcctccgagcgatctacgcatgcc 3643

Query: 1028 atcaacagccggcgagacacgccggagctccatcaacgcttcgcgc 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 ctccattctaccctgacgtcctcttcatcagggggagattgga 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 ggtgtgctggcagcactctaaacaccgacagctggcgcgccaggtaggggtgtgtcttt 90
||||||||| ||||| | |||||||||||||||||||||||||
Sbjct: 1380 ggtgtgctgg-cggacccaaaacaccgacagctggcgcgccaggtaggggtgtgtcgc 1438

Query: 91 gatctgagctagctcaatgaccattacctccaaatgcaagatcgcccttcgccccggac 150
||||| ||||||||||||| || | |||| | | ||||||| ||||| ||||| ||
Sbjct: 1439 gatctaagctagctcaatggccgtcaccttccaccgcaagatcacctccgccccgatc 1498

Query: 151 tatgttttgctttggaacctctcatccatagcagatgaagaggggaactctgcaccgcat 210
| ||||| ||||||||||| ||||||||||| ||||||||||| ||||||||| || |||||
Sbjct: 1499 tgtgttctgctttggaactatctcatccgtagcagatgaagaaggaactctacatcgcat 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 aacctgaaccccgacttcgcccgagccatgaacacgccgagtgaagtcggaggggtacta 2228

Query: 908 gccagatagctgacggcctcccgcaaccctagacacggaaggctaccggcggctgctt 967
|| | ||||||||| || ||||| || | | ||| | || ||||| || || ||| |
Sbjct: 2229 gctcggatagctgatggactccctcggaatcccgacgccgagggtatcgacgactgttc 2288

Query: 968 actcgcagcagttaatcaccttctaccatcactaatcctccaagcgacctacgccatgcc 1027
|| | ||||| || || ||||||||| || || || || || ||||||||| || |||||
Sbjct: 2289 acccaagcagccaaccatcttctacctatcgtcaccgccgaacgacctacgacacgcc 2348

Query: 1028 atcaacagccggcgagacacgcggagctccatcaacgcttcgcg 1071
||||||||||| || ||||| | ||||||||| || |||||||||
Sbjct: 2349 atcaacagccgctcgggacacgtgaagctccataaatgcttcgcg 2392

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

Query: 509 ttetaccccgacgtcctcttcatc 532
|||||||||||||||||||
Sbjct: 1845 ttetaccccgacgtcctcttcatc 1868

Strand = Plus / Minus

Query: 503 gtcctttctaccccgacgtcctcttcatcagggg 537
||||| ||||||||||||||||||||||||||| |||||
Sbjct: 80108 gtcctattctaccccgacgtcctcttcatcagggg 80074

Score = 52.0 bits (26), Expect = 0.012
Identities = 47/54 (87%)
Strand = Plus / Minus

Query: 643 gcgacatcacgaggctggggaacgggatccggcgcaaccgatatccgggacga 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 aaacccgacagttggcgcgccaggtagggg 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 cgacatgaagacagctgcgagctcttcgacttactccgtgtctccgggccatccagtgg 1312
||||| || |||| | ||||||||| | ||||| ||||| || ||| ||||||| || |||
Sbjct: 55410 cgacaggaggacatgtgcgagtatcggcactcactccatgcctcagggccattcaatgg 55469

Query: 1313 cccc-taacttcaaggtctccaacgtcagcaagtatgagcgcaagcaggacctgggtggc 1371
|||| | ||||||||||||||||||||| ||||| || | ||||||||| || || |||
Sbjct: 55470 ccccctaacttcaaggtctccaacgtcgataagtacgaacctaaagcaggatccggaaggc 55529

Query: 1372 tggttagccatctacacgattgtcacatgggccgagcgacggaggacgtgatgaca 1431

Sbjct: 55530 tggctggccatctacaccactgctgcccagcagcaggggcaaccgaggacgtgatgacc 55589

Query: 1432 gtgtattttccattgtcctagggcaagacgcaatgcagtggtccgacatctacccaa 1491

Sbjct: 55590 gcgacttgccctattgtcctcgggcaagacgcgctgcaatggctgtgacacctacccga 55649

Query: 1492 cattgcatagacaattggagcgcacttcagttggtgcttcatcgccaacttccagtcctc 1551

Sbjct: 55650 cactgcatcgacgactggagcgatttcagtcggcgcttcaccgccaacttccagtcctc 55709

Query: 1552 ttgacaagccggcgcagccatgggacctaaaatccattgggcatcagggcgatgaaacg 1611

Sbjct: 55710 tccgacaaaccggcgaaccatgggacctcaatccatcaagcggcgaggggacgaaact 55769

Query: 1612 ctccggttgacctcaagaggttttagacatgaggaaccacacccccgaagtgcggag 1671

Sbjct: 55770 cttcggtcatacctaaaaagattccagacctgagagattgtatccccgaggtcgggaa 55829

Query: 1672 gcgggggtgattgaagacttctaccaggatccaatgactcggctttcgtccgagccata 1731

Sbjct: 55830 gcagcaatgatcgaggacttctatagggatccaatgactcggcattcgttcgagccata 55889

Query: 1732 ctccagaaaagcgtcggccacctccgaacacttggtccgggaggcagacctctacatcac 1791

Sbjct: 55890 ttacag-aaggcgtcgactacctccgagcaactattccgggaggccgacctctatatcac 55948

Query: 1792 cacggattaacgggcccaggacctcatcgagg 1824

Sbjct: 55949 cgcgacgaacgagctcaggacctcatcgagg 55981

Score = 79.8 bits (40), Expect = 5e-11
Identities = 184/232 (79%)
Strand = Plus / Plus

Query: 855 accccgacttcgctcgtgcaatgaacacgccagtggaagtcggaggggtactggccaga 914

Sbjct: 55013 accccgatttcgcccagccatgaacacgccagtggaagtcggtggagtattggctcga 55072

Sbjct: 25162 aacctgaacccccgacttcgccccgagccatgaagacgccgagtggaagtcggaggagtattg 25103

Query: 908 gccagatagctgacggcctcccgcgaaccctagacacggaaggctaccggcggctgctt 967
|| | ||||| ||||| ||||| || | | || | || ||||| ||||| ||

Sbjct: 25102 gctcggatagctgatggcctccccggactcccgacgctgagggtatcggcggctattc 25043

Query: 968 actcgagcagttaatcaccttctaccatcactaatcctccaagcgacctacgccatgcc 1027
|||| |||| | |||| | ||||| || | | | | | | || | ||||| || ||

Sbjct: 25042 actcaagcagccaatcatcttctaccctcgctcaccgccgaacgatctacgacacacc 24983

Query: 1028 atcaacagccggcgagacacgaggctccatcaacgcttcgcgca 1074
||||||| ||||| ||| | | ||||| ||||| ||||| |||||

Sbjct: 24982 atcaacagtcggcgggacgcacagagctccatcaacgcttcgtgca 24936

Score = 93.7 bits (47), Expect = 4e-15
Identities = 80/91 (87%)
Strand = Plus / Minus

Query: 19 agggtagccctgggtgtgcgacggactctaaacaccgacagctggcgcgccaggtagg 78
||||||| ||| ||||| |||| | ||||| | ||||| ||||| ||||| |||||

Sbjct: 25954 aggggtaacccccgggtgcgcggtcggaccnaaacaccgacagctggcgcgccaggtagc 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 cggcgacatcacgaggctggggaacgggatccggcgcaaccctatcccgggacga 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 aaacaccgacagctggcgcgccaggtagggg 80
||||| ||||||| ||||||||||||||||
Sbjct: 106752 aaacgccgacagtggcgcgccaggtagggg 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 gtgatgacagtgtattttccattgtcctagggcaagacgcaatgcagtggctccgacat 1482
||||||| | ||||| ||||| ||||| ||||| ||||| || || || ||||| |||||
Sbjct: 4118 gtgatgactgcgtatttgccatcatccttggcgaagatgcgctacaatggctacgacac 4177

Query: 1483 ctaccccaacattgcatagacaattggagcgaacttcagttggtgcttcatcgccaacttc 1542
|| ||||| ||| ||||| ||| ||||||||| ||||| || | || ||||| |||||
Sbjct: 4178 ctgccccgacactgcatcgacgattggagcgaatttcagtcggcgttttatcgccaacatc 4237

Query: 1543 cagtccctctttgacaagccggcgcagccatgggacctaaaatccattgggcatcagggc 1602
|| ||||| || ||||||||| ||||||||| ||||||||| ||||| ||| |||
Sbjct: 4238 caatccctctccgacaagccggcgcacccatgggacctcaaatccatcaggcgcgaggg 4297

Query: 1603 gatgaaacgctccggtgtacctcaagaggttttagaccatgaggaaccacacccccgaa 1662
||||||| ||||| || ||||||||| ||||||||| ||||| || | || |||
Sbjct: 4298 gatgaaacttccgatcatacctcaaaagatttttagaccatgagaaatcgtatccttgag 4357

Query: 1663 gtcgccgaggcgggggtgattgaagacttctaccgaggatccaatgactcggctttcgtc 1722
|| | || || | ||||| || ||||||||| ||||| ||||||||| |||||
Sbjct: 4358 gttgtggaagcagcgggtgatcaggacttctaccgggatctaatactcggccttcgtc 4417

Query: 908 gccagatagctgacggcctcccgcgaaccctagacacggaaggctaccggcggtgctt 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 gtgatgacagtgtatTTTTCCATTGCTCCTAGGCAAGACGCAATGCAGTGGCTCCGACAT 1482
||||||| | ||||| ||||| ||||| ||||| || | || | ||||| |||||
Sbjct: 11447 gtgatgactgcgtatTTGCCATCATCCTTGGCAAGATGCCTACAATGGCTACGACAC 11506

Query: 1483 ctacccaacattgcatagacaattggagcgacttcagttggtgcttcacgccaacttc 1542
|| ||||| ||| ||||| ||| ||||| ||||| ||||| || | || | ||||| |||
Sbjct: 11507 ctgccccgacactgcatcgacgattggagcgatttcagtcggcgttttatcgccaacatc 11566

Query: 1543 cagtccctctttgacaagccggcgagccatgggacctaaaatccattgggcatcagggc 1602
|| ||||| ||||| ||||| ||||| ||||| ||||| ||| | |||
Sbjct: 11567 caatccctctccgacaagccggcgcaacctgggacctaaaatccatcaggcgccgaggg 11626

Query: 1603 gatgaaacgctccggttgacctcaagaggttttagaccatgaggaaccacacccccgaa 1662
||||||| |||| | ||||||| || ||||||||||||||| || | || ||
Sbjct: 11627 gatgaaactttccgatcatacctcaaaagatttttagaccatgagaaatcgtatccttgag 11686

Query: 1663 gtcgccgaggcgggggtgattgaagacttctaccgaggatccaatgactcggctttcgtc 1722
|| | || || | |||||| | ||||||||||||||| ||||| ||||||||||| |||||
Sbjct: 11687 gttgtggaagcagcggtgatcgaggacttctaccgggatctaatactcggccttcgtc 11746

Query: 1723 cgagccatactccagaaaagcgtcggccacctccgaacacttgttccgggagcagacct 1782
||||||||||| || ||| || || | ||||||||| || | ||| |||| | |||||
Sbjct: 11747 cgagccatactgca-aaaggcacccgactacctccgagcagctattcaggaagtggacct 11805

Query: 1783 ctacatcaccacggattaacgggccaggacctcatcggaggcacgaa 1830
||||||||||| | || ||||||| ||||||||||| ||||| |||||
Sbjct: 11806 ctacatcacccgctgacgaacgggctcaggacctcattggaggaacgaa 11853

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

Query: 7 aaaagcacgcaaggggtagccctgggtgtgcggacggactctaaacaccgacagctggc 66
||||||| | ||||| | || ||||| ||||| ||||| | ||||| |||||||||
Sbjct: 10080 aaaagcacctcgaggggcaacccgggtgctcggtcggacccaaacactgacagctggc 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 ctccctttctaccccagctcctctttcatcaggggagattgga 546
||| ||||||||||||||||||| ||| ||||||| |||||
Sbjct: 10540 ctccgtttctaccccagctcctctttatcgggggagattgga 10582

Score = 50.1 bits (25), Expect = 0.048
Identities = 145/185 (78%)
Strand = Plus / Plus

Query: 848 aacctgtaccccgaacttcgctcgtgcaatgaacacgccgagtggaagtcggaggggtactg 907
||||| ||||||||| || | ||||||| ||||| || ||||| || ||
Sbjct: 10872 aacctgaaccccgaacttcgtccgatccatgaacacaccgagcgaggtcggagggtgtg 10931

Query: 908 gccagatagctgacggcctcccgcaaccctagacacggaaggctaccggcggtgctt 967
|| | ||||| | ||||||| || || | |||| | || ||||| |||||||||
Sbjct: 10932 gctcggatagccaatggcctcccccggactccagacgccgagggtatcggcggtgctc 10991

Query: 968 actcgagcagttaatcaccttctaccatcactaatcctccaagcgacctacgccatgcc 1027
||||| |||| ||| || ||||| || || || ||||||||| |||| | || |||
Sbjct: 10992 actcgggcagctaaccatcttctgcctctcgtcatcctccaagcgatctatgacacgcc 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 acccgaaaaactccgctgtccacttcgccacaaaggagtgacacggatta 392
||||||| ||| ||| ||||||| || ||||||| |||||||||
Sbjct: 10398 acccgagaaccccgttgtccacctatccacaaaagagtgacacggatta 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 gtctccgggccatccagtggeccc-taacttcaaggtctccaacgtcagcaagtatgagc 1351
||||| ||||||| || ||||||| ||||||||| ||||||||| ||||| || |
Sbjct: 3074 gtctcagggccattcattggccccctaacttcaaggtctccaacgtcagcaagtacgaac 3133

Query: 110 accattacctccaaatgcaagatcgcccttcgccccgggactatgttttgctttggaacc 169
||||| ||| | | ||||||||| || | ||| | | |||| | |||| | |||||
Sbjct: 1924 gacatcactttccagcacaagatcgctctcctcctggatccgtgttctgcttcggaacc 1983

Query: 170 atctcatccatagcagatgaagagggaaactctgcaccgcatagcagatc 218
||||||| | ||||| ||||| ||||||| || ||||||| ||||
Sbjct: 1984 atctcatccgtggcagacgaagaaggaactctacatcgcgatagcggatc 2032

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

Query: 848 aacctgtaccccgacttcgctcgtgcaatgaacacgccgagtgaagtcgg 897
|||||| | ||||||||| || || ||||||| ||||| || |||||
Sbjct: 2629 aacctgaaccccgacttcgcccggagccatgaacacaccgagcgaggtcgg 2678

Score = 44.1 bits (22), Expect = 3.0
Identities = 31/34 (91%)
Strand = Plus / Plus

Query: 1050 ggagctccatcaacgcttcgcgcgaccgatgaca 1083
||||||||||| ||||||||| ||| ||||
Sbjct: 2831 ggagctccatcaatgcttcgcggaacgacgaca 2864

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

Score = 129 bits (65), Expect = 7e-26
Identities = 421/537 (78%), Gaps = 2/537 (0%)
Strand = Plus / Plus

Query: 1283 cttactccgtgtctccgggccatccagtggcccc-taacttcaaggtctccaacgtcagc 1341
||||||| |||| | ||||| ||||||||| ||||||||| ||||| || |
Sbjct: 4027 cttactccaagtcctcagggccattcagtggccccctaacttcaaggtctccaacatcgac 4086

Query: 1342 aagtatgagcgaagcaggacctgggtggctggttagccatctacacgattgtcacatgg 1401
||||||||| ||||| | ||||||| ||||||||| | |||| | | || | |

Query: 915 tagctgacggcctcccgcgaaccctagacacggaaggctaccggcggtgcttactcgag 974
|||| | | ||||| | | | ||||| | | | ||||| ||||| ||||| |
Sbjct: 3659 tagccgatggcctcccctggactctagacgccgagggtatcggcggtgctcactcggg 3718

Query: 975 cagttaatcaccttctacccatcactaatcctccaagcgacctacgccatgccatcaaca 1034
||| ||| | | ||||| | | | | ||||| | ||||| ||||| | | ||||| |
Sbjct: 3719 cagtaaccatcttctgcctctcgtctatccttcgagcgatctacgacacgccatcaata 3778

Query: 1035 gccggcgagacacgggagctccatcaacgcttcgcgacccgatgaca 1083
| | | | | | | | | | ||||| ||||| ||||| ||||| | | | | | |
Sbjct: 3779 gtcgacgggacgcacggagctccatcaatgcttcgcggaacgacgaca 3827

Score = 67.9 bits (34), Expect = 2e-07
Identities = 82/98 (83%)
Strand = Plus / Plus

Query: 7 aaaagcaccgcaagggtagccctgggtgtgcgacggactctaacaccgacagctggc 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 gtgatgacagtgtattttccattgtcctagggcaagacgcaatgcagtggctccgacat 1482
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 8545 gtgatgactgtgtatttgccatcgtccttgggcaagatgcgctccaatggctacgacac 8486

Query: 1483 ctacccaacattgcatagacaattggagcgacttcagttggtgcttcacgccaacttc 1542
|| |||| | | | | | ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 8485 ctgccccgacactacatcgatgattggagcgatttcagtcggtgttttatcacaacttc 8426

Score = 56.0 bits (28), Expect = 8e-04
Identities = 184/236 (77%)
Strand = Plus / Minus

Query: 848 aacctgtaccccgacttcgctcgtgcaatgaacacgccgagtgaagtcggaggggtactg 907
||||| ||||||||| | || ||||||| ||||| || ||||| || || ||
Sbjct: 9121 aacctgaaccccgacttcgctcgtgagccatgaacacaccgagcgaggtcggtggagtgtg 9062

Query: 908 gccagatagctgacggcctcccgcgaaccctagacacggaaggtaccggcggtgctt 967
|| | |||||| | ||||||| | || | |||| | || ||||| |||||||||
Sbjct: 9061 gctcggatagccgatggcctcccctgactccagacgctgaggctatcggcggtgctc 9002

Query: 968 actcggcagttaatcaccttctacccatcactaatcctccaagcgacctacgccatgcc 1027
||||| |||| ||| | |||||| | || || ||||||| ||||| ||| | || ||
Sbjct: 9001 actcgggcagctaacaatcttctgcctctcgtcctcctccgagcgatctatgacacacc 8942

Query: 1028 atcaacagccggcgagacacgcggagctccatcaacgcttcgcgcgaccgatgaca 1083
||||| || || || ||| | | ||||||||| ||||||||| ||| ||||
Sbjct: 8941 atcaatagtcgacgggacgcacagagctccatcaatgcttcgcgcgaaacgacgaca 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 aagtatgagcgcaagcaggacctgggtggctggtagccatctacacgattgtcacatgg 1401
|| || |||| ||||| |||| ||| ||||||| | | |||| |||| | |||| |
Sbjct: 410 aaatagcagcctaagcaagacccgggaggtggttggtcgtctatacgaccgccacacag 351

Query: 1402 gccgccgagcgacggaggacgtgatgacagtgatatttccattgtcctagggcaagac 1461
||||| || || | || ||||||||| || || ||||| ||||| |||||||

Sbjct: 350 gccgctggggcaatcgaagacgtgatgacagcatagttgcccatcgtccttaggcaagat 291

Query: 1462 gcaatgcagtggtccgacatctacccaacattgcatagacaattggagcgacttcagt 1521
||| | ||||| ||||| ||||| || || ||||| || ||||| ||||| |||||

Sbjct: 290 gcattacagtggtcgcacatctgccgtggcactgcatcgatgattggagcgacttcagt 231

Query: 1522 tggtgcttcatcgccaacttccagtcctctttgacaagccggcgagccatgggaccta 1581
|| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 230 cggcatttcattgccaacttctagtccctctccgacaagccagcgcacatccatgggacctc 171

Query: 1582 aaatccattgggcatcagggcgatgaaacgctccggtgtacctcaagaggttttagacc 1641
||| ||||| ||| | ||||| || ||||| || ||||| ||||| |||||

Sbjct: 170 aaaccataagggcgcgagggcgatgaaagccttcggtcatatctcaagaggtttcagacc 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 gtgatgactgcgtatttgccatcgtccttgggcaagatgcgctgcaatggctacgacac 8476

Query: 1483 ctacccaacattgcatagacaattggagcgacttcagttggtgcttcatcgccaacttc 1542
|| ||||| ||| ||||| ||| ||||| ||||| ||||| | | || ||||| |||||

Sbjct: 8477 ctgccccgacactgcattgacgattggagcgatttcagtcgcccgttttgtcgccaacttc 8536

Query: 1543 cagtcctctttgacaagccggcgagccatgggacctaaaatccattgggcatcagggc 1602
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 8537 caatccctctccgacaagccggcgcaacatgggacctcaatccataagggcgcgaggg 8596

Query: 1603 gatgaaacgctccggtgtacctcaagaggttttagaccatgag 1646
||||||| ||||| | ||||| || ||||| ||||| |||||

Sbjct: 8597 gatgaaactctccgatcatacctcaaaagatttcagaccatgag 8640

Strand = Plus / Minus

Query: 7 aaaagcaccgcaaggggtagccctgggtgtgcggacggactctaaacaccgacagctggc 66
 ||||| | | | | | | | | | | | | | |
Sbjct: 109028 aaaagcaccgtgaggggcaacccgggtgtgcggtcggacccaaaacaccgacagctggc 108969

Query: 67 gcgccaggtaggggtgtgtctttgatctgagctagctcaatg 109
 ||||| | | | | | | | | | | | | |
Sbjct: 108968 gcgccaggtaggggtgtgtcgcgacgatccaagctagctcaatg 108926

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

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
 |||| | | | | | | | | | | | | | |
Sbjct: 30117 aaacgccgacagttggcgcgccaggtagggg 30087

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

Query: 510 tctaccccgacgtcctcttcatc 532
 ||||| | | | | | | | | | | | | |
Sbjct: 108558 tctaccccgacgtcctcttcatc 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 aaaagcacctcgaggggcaacccgggtgtgcggtcggacccaaaacaccgacagctggc 475

Query: 67 gcgccaggtaggggtgtgtctttgatctgagctagctcaatg 109

|||||
Sbjct: 476 ggccaggtagggggtgtgtcactgatccaagctagctcaatg 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 aaaagcacctcgaggggcaaccccggtgtgcggtcggacccaaacaccgacagctggt 478

Query: 67 ggccaggtagggggtgtgtctttgatctgagctagctcaatg 109
|||||

Sbjct: 479 ggccaggtagggggtgtgtcactgatccaagctagctcaatg 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 gtcactactttccagcacaagattgctctccgcttgatccgtgttctgcttcggaacc 2039

Query: 170 atctcatccatagcagatgaagaggaactctgcaccgcatagcagatc 218
|||||

Sbjct: 2040 atctcatccgtggcagacgaagaaggaactctacatcgcacatagcagatc 2088

Score = 58.0 bits (29), Expect = 2e-04
Identities = 47/53 (88%)
Strand = Plus / Plus

Strand = Plus / Plus

Query: 5 ccaaaagcaccgcaaggggtagccctgggtgtgctggacggactctaaacaccgacagctg 64
||||||| ||| ||||||| | ||| ||||||| | ||| ||||||| | ||||||| | ||||||| | ||||||| |
Sbjct: 284 ccaaaaacacctcaaggggcaaccccgggtgctggtcggacccaaaacaccgacagctg 343

Query: 65 gcgcccaggtagggggtgtgtctttgatctgagctagctcaatgaccattac 117
||||||| ||||||| ||||||| || || || ||||||| ||||||| |||||||
Sbjct: 344 gcgcccaggtagggggtgtgtcactggtccaagctagctcaatggcattac 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 ccaaaagcaccgcaaggggtagccctgggtgtgctggacggactctaaacaccgacagctg 64
||||||| ||| ||||||| | ||| ||||||| | ||| ||||||| | ||||||| | ||||||| | ||||||| |
Sbjct: 284 ccaaaaacacctcaaggggcaaccccgggtgctggtcggacccaaaacaccgacagctg 343

Query: 65 gcgcccaggtagggggtgtgtctttgatctgagctagctcaatgaccattac 117
||||||| ||||||| ||||||| || || || ||||||| ||||||| |||||||
Sbjct: 344 gcgcccaggtagggggtgtgtcactggtccaagctagctcaatggcattac 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 aaaagcaccgcaaggggtagccctgggtgtgctggacggactctaaacaccgacagctggc 66
||||||| | ||||| | ||| ||||| ||||| ||||| | ||||||| ||||||| |||||||
Sbjct: 416 aaaagcacctctaggggcaaccccgggtgctggtcggacccaaaacaccgacagctggc 475

Query: 67 gcgccaggtagggggtgtgtctttgatctgagctagctcaatg 109
||||||| ||||||| ||||||| ||||| ||||||| |||||||
Sbjct: 476 gcgccaggaagggggtgtgttactgatccaagctagctcaatg 518

Score = 67.9 bits (34), Expect = 2e-07
Identities = 68/78 (87%), Gaps = 1/78 (1%)
Strand = Plus / Plus

Query: 37 gcggacggactctaaacaccgacagctggcgccaggtaggggtgtgtctttgatctg 96
||||| ||||| | ||||||||||||||||||||||||||||||||||| |||||
Sbjct: 446 gcggtcggacccaaaacaccgacagctggcgccaggta-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 tacccaaaagcactgcgagggtaaccccggtgtgcggtcgggtccaaacaccgacag 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%)

>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 aacaccgacagctggcgccaggtagggg 80
 ||||| |
Sbjct: 29283 aacaccgacagtggcgccaggtagggg 29253

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

Query: 55 ccgacagctggcgccaggtagggg 80
 ||||| |
Sbjct: 165564 ccgacagtggcgccaggtagggg 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 aacaccgacagctggcgccaggtagggg 80
 ||||| |
Sbjct: 48261 aacaccgacagtggcgccaggtagggg 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 aacaccgacagctggcgccaggtagggg 80
 ||||| |
Sbjct: 49821 aacaccgacagtggcgccaggtagggg 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 aacaccgacagctggcgcgccaggtagggg 80
 ||||| |||||||||||||||||||||||||
Sbjct: 91452 aacatcgacagctggcgcgccaggtagggg 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 aacaccgacagctggcgcgccaggtagggg 80
 ||||||||||| |||||||||||||||||||
Sbjct: 168287 aacaccgacagttggcgcgccaggtagggg 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 ccgacagctggcgcgccaggtaggggg 81
 |||||||||||||||||||||||||||
Sbjct: 53099 ccgacagctggcgcgccaggtaggggg 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 tggcgcgccaggtaggggtgtg 85
|||||
Sbjct: 27029 tggcgcgccaggtaggggtgtg 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 tggcgcgccaggtaggggtgtg 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: 44219 cgcacagctggcgcgccaggtagggg 44194

>gb|AC213133.1| Oryza glaberrima clone OG_BB042C22, complete sequence
Length = 112632

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

Query: 56 cgcacagctggcgcgccaggtagggg 81
|||||
Sbjct: 79649 cgcacagctggcgcgccaggtagggg 79624

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

Query: 56 cgcacagctggcgcgccaggtagggg 81
|||||
Sbjct: 67240 cgcacagctggcgcgccaggtagggg 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 aaacaccgacagctggcgcgccaggtagggggtg 83
|||||
Sbjct: 73626 aaacaccgacagctggcgcgccaggtagggggtg 73593

>gb|EF659467.1| Zea mays clone BAC m.pk066.114 AP2 domain transcription factor (Rap2.7)
gene, partial cds
Length = 133964

Score = 52.0 bits (26), Expect = 0.012
Identities = 32/34 (94%)
Strand = Plus / Minus

Query: 50 aacaccgacagctggcgccaggtaggggtg 83
 |||||
Sbjct: 61954 aacaccgacagctggcgccaggtaggggtg 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 cgacagctggcgccaggtagggg 81
 |||||
Sbjct: 141993 cgacagctggcgccaggtagggg 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 cgacagctggcgccaggtagggg 81
 |||||
Sbjct: 105195 cgacagctggcgccaggtagggg 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 cgacagctggcgccaggtagggg 81
 |||||
Sbjct: 56260 cgacagctggcgccaggtagggg 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 cgacagctggcgcgccaggtaggggg 81
|||||
Sbjct: 55487 cgacagctggcgcgccaggtaggggg 55462

>gb|AC130598.2| Oryza sativa Japonica Group chromosome 5 clone OSJNBa0056I11,
complete sequence
Length = 145796

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

Query: 56 cgacagctggcgcgccaggtaggggg 81
|||||
Sbjct: 4119 cgacagctggcgcgccaggtaggggg 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 cgacagctggcgcgccaggtaggggg 81
|||||
Sbjct: 588003 cgacagctggcgcgccaggtaggggg 587978

Score = 46.1 bits (23), Expect = 0.76
Identities = 26/27 (96%)
Strand = Plus / Plus

Query: 55 cgcacagctggcgcgccaggtaggggg 81
|||||

Sbjct: 1793581 cgcacatctggcgcgccaggtagggg 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 cgacagctggcgcgccaggtagggg 81
||||||||||||||||||||||||||||||
Sbjct: 86800 cgacagctggcgcgccaggtagggg 86775

>gb|AC068654.2| Genomic Sequence For Oryza sativa (japonica cultivar-group) cultivar
Nipponbare Clone OSJNBa0015022 From Chromosome 10,
complete sequence
Length = 189349

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

Query: 56 cgacagctggcgcgccaggtagggg 81
||||||||||||||||||||||||||||||
Sbjct: 55611 cgacagctggcgcgccaggtagggg 55586

>dbj|AP006233.3| Oryza sativa Japonica Group genomic DNA, chromosome 1, BAC
clone:B1249E06
Length = 126534

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

Query: 56 cgacagctggcgcgccaggtagggg 81
||||||||||||||||||||||||||||||
Sbjct: 59441 cgacagctggcgcgccaggtagggg 59416

>dbj|AP005460.3| Oryza sativa Japonica Group genomic DNA, chromosome 6, PAC
clone:P0610D01
Length = 146418

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

Query: 56 cgacagctggcgcgccaggtagggg 81
|||||
Sbjct: 73246 cgacagctggcgcgccaggtagggg 73271

>dbj|AP004729.3| Oryza sativa Japonica Group genomic DNA, chromosome 6, BAC
clone:OSJNBa0006A22
Length = 190690

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

Query: 56 cgacagctggcgcgccaggtagggg 81
|||||
Sbjct: 37650 cgacagctggcgcgccaggtagggg 37675

>dbj|AP003458.4| Oryza sativa Japonica Group genomic DNA, chromosome 6, PAC clone:P0701E03
Length = 183245

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

Query: 56 cgacagctggcgcgccaggtagggg 81
|||||
Sbjct: 153905 cgacagctggcgcgccaggtagggg 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 cgacagctggcgcgccaggtagggg 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 cgacagctggcgcgccaggtagggg 81
|||||
Sbjct: 125370 cgacagctggcgcgccaggtagggg 125345

>dbj|AP004821.4| Oryza sativa Japonica Group genomic DNA, chromosome 1, PAC clone:P0676G08
Length = 153154

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

Query: 56 cgacagctggcgcgccaggtagggg 81
|||||
Sbjct: 115721 cgacagctggcgcgccaggtagggg 115746

>emb|AL606634.2| Oryza sativa genomic DNA, chromosome 4, BAC clone: OSJNBb0072N21,
complete sequence
Length = 130433

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

Query: 56 cgacagctggcgcgccaggtagggg 81
|||||
Sbjct: 127992 cgacagctggcgcgccaggtagggg 127967

>dbj|AP003760.4| Oryza sativa Japonica Group genomic DNA, chromosome 1, BAC
clone:OSJNBb0063G05
Length = 182681

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

Strand = Plus / Plus

Query: 56 cgacagctggcgcgccaggtagggg 81
|||||
Sbjct: 167523 cgacagctggcgcgccaggtagggg 167548

>dbj|AP004194.3| Oryza sativa Japonica Group genomic DNA, chromosome 1, PAC
clone:P0014E08
Length = 144219

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

Query: 56 cgacagctggcgcgccaggtagggg 81
|||||
Sbjct: 69901 cgacagctggcgcgccaggtagggg 69926

>dbj|AP002482.1| Oryza sativa Japonica Group genomic DNA, chromosome 1, clone:P0706B05
Length = 187835

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

Query: 56 cgacagctggcgcgccaggtagggg 81
|||||
Sbjct: 40167 cgacagctggcgcgccaggtagggg 40142

>emb|AL713941.3| Oryza sativa chromosome 12, . BAC OSJNBa0006M08 of library OSJNBa from
chromosome 12 of cultivar Nipponbare of ssp. japonica of
Oryza sativa (rice), complete sequence
Length = 136254

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

Query: 56 cgacagctggcgcgccaggtagggg 81
|||||
Sbjct: 62956 cgacagctggcgcgccaggtagggg 62931

>emb|AL731592.2| Oryza sativa genomic DNA, chromosome 4, BAC clone: OSJNBa0036B17,
complete sequence
Length = 99093

Score = 52.0 bits (26), Expect = 0.012
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

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 aaacaccgacagctggcgcgccaggtaggggt 82
|||| ||||| |||||
Sbjct: 111324 aaacccgacagttggcgcgccaggtaggggt 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 ctaaaccgacagctggcgccaggtaggggtg 83
||||| ||||||||| ||||| |||||||||
Sbjct: 83102 ctaaaccgacagctggcgccaggtaggggtg 83067

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

Query: 50 aaacaccgacagctggcgccaggtagggg 80
||||| ||||||| ||||||||| |||||||||
Sbjct: 177040 aaacaccgacagctggcgccaggtagggg 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 ccgacagctggcgccaggtagg 78
||||||||| ||||||||| |||||||||
Sbjct: 28434 ccgacagctggcgccaggtagg 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 cgacagctggcgccaggtagg 79
||||||||| ||||||||| |||||||||
Sbjct: 32770 cgacagctggcgccaggtagg 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 cgacagctggcgcgccaggtaggggggtg 83
|||||
Sbjct: 121233 cgacagttggcgcgccaggtaggggggtg 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 acagctggcgcgccaggtaggggg 81
|||||
Sbjct: 12190 acagctggcgcgccaggtaggggg 12167

>gb|AC078839.4| Oryza sativa Japonica Group chromosome X clone OSJNBa0094J09, complete
sequence
Length = 168192

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

Query: 56 cgacagctggcgcgccaggtaggggggtgtgtc 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 cgacagctggcgcgccaggtagggggtg 83
|||||

Sbjct: 65303 cgacagttggcgcgccaggtagggggtg 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 cgacagctggcgcgccaggtagggggtg 83
|||||

Sbjct: 6508 cgacagttggcgcgccaggtagggggtg 6481

>dbj|AP005456.3| Oryza sativa Japonica Group genomic DNA, chromosome 6, PAC
clone:P0513E02
Length = 141477

Score = 48.1 bits (24), Expect = 0.19
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 cgacagctggagcgcgccaggtaggggg 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 cgcacagctggcgcgccaggtaggggtgtgt 86
||||| ||||||||||||||||||| |||||
Sbjct: 121878 cgcacatctggcgcgccaggtaggtgtgtgt 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 cgacagctggcgcgccaggtaggggtg 83
||||| ||||||||||||||||||| |||||
Sbjct: 54023 cgacagttggcgcgccaggtaggggtg 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 cgacagctggcgcgccaggtaggggtgtgtc 87
||||| ||||||||||||||||||| |||||
Sbjct: 146215 cgacagttggcgcgccaggtaggggtgtgtc 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 acagctggcgcgccaggtagggg 81
||||| ||||||||||||||||||| |||||
Sbjct: 66981 acagctggcgcgccaggtagggg 67004

>dbj|AP004030.2| Oryza sativa Japonica Group genomic DNA, chromosome 2, BAC
clone:OJ1145_E05
Length = 101333

Score = 48.1 bits (24), Expect = 0.19
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 cgacagctggcgcgccaggtaggggtgtgtc 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 cgacagctggcgcgccaggtaggggtgtgtc 83
||||| ||||||||||||||||||| |||||
Sbjct: 144424 cgacagttggcgcgccaggtaggggtgtgtc 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 cgacagctggcgcgccaggtaggggtgtgtc 83
||||| ||||||||||||||||||| |||||
Sbjct: 24812 cgacagttggcgcgccaggtaggggtgtgtc 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 cgacagctggcgcgccaggtaggggtgtgtc 83
||||| ||||||||||||||||||| |||||
Sbjct: 35648 cgacagttggcgcgccaggtaggggtgtgtc 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 cgcacagctggcgcgccaggtagggg 80
 ||||| | ||||| ||||| ||||| |||||
Sbjct: 45119 cgcacagttggcgcgccaggtagggg 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 aacaccgacagctggcgcgccaggtagggg 80
 |||| | ||||| | ||||| ||||| ||||| |||||
Sbjct: 112762 aacgccgacagttggcgcgccaggtagggg 112792

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

Query: 50 aacaccgacagctggcgcgccaggtagggg 80
 |||| | ||||| | ||||| ||||| ||||| |||||
Sbjct: 158316 aacgccgacagttggcgcgccaggtagggg 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 aacaccgacagctggcgcgccaggtagggg 80
 |||| | ||||| | ||||| ||||| ||||| |||||
Sbjct: 57140 aacgccgacagttggcgcgccaggtagggg 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 aaacgccgacagttggcgcgccaggtagggg 77603

>gb|AC226721.2| Zea mays BAC clone CH201-150M20 from chromosome 10, complete sequence
Length = 207605

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

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
||||| ||||||| |||||||||||||||||||
Sbjct: 148376 aaacgccgacagttggcgcgccaggtagggg 148346

>gb|AC213983.4| Zea mays BAC clone CH201-326E16 from chromosome 5, complete sequence
Length = 180103

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

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
||||| ||||||| |||||||||||||||||||
Sbjct: 6768 aaacgccgacagttggcgcgccaggtagggg 6738

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

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
||||| ||||||| |||||||||||||||||||
Sbjct: 126670 aaacgccgacagttggcgcgccaggtagggg 126640

>gb|AC225944.3| Zea mays BAC clone CH201-127G5 from chromosome 10, complete sequence
Length = 216347

Score = 46.1 bits (23), Expect = 0.76
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

Query: 50 aacaccgacagctggcgcgccaggtagggg 80
 |||| | | | | |
Sbjct: 95001 aacgccgacagttggcgcgccaggtagggg 95031

>gb|AC203071.4| Zea mays BAC clone CH201-184N10 from chromosome 5, complete sequence
 Length = 194840

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

Query: 50 aacaccgacagctggcgcgccaggtagggg 80
 |||| | | | | |
Sbjct: 21578 aacgccgacagttggcgcgccaggtagggg 21608

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

Query: 50 aacaccgacagctggcgcgccaggtagggg 80
 |||| | | | | |
Sbjct: 45262 aacgccgacagttggcgcgccaggtagggg 45232

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

Query: 50 aacaccgacagctggcgcgccaggtagggg 80
 |||| | | | | |
Sbjct: 79745 aacgccgacagttggcgcgccaggtagggg 79715

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

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

Query: 50 aacaccgacagctggcgcgccaggtagggg 80

Query: 50 aacaccgacagctggcgcgccaggtagggg 80
 |||| | ||||| | ||||| ||||| |||||
Sbjct: 28715 aacgccgacagtggcgcgccaggtagggg 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 aacaccgacagctggcgcgccaggtagggg 80
 |||| | ||||| | ||||| ||||| |||||
Sbjct: 156086 aacgccgacagtggcgcgccaggtagggg 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 aacaccgacagctggcgcgccaggtagggg 80
 |||| | ||||| | ||||| ||||| |||||
Sbjct: 13212 aaacatcgacagtggcgcgccaggtagggg 13242

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

Query: 50 aacaccgacagctggcgcgccaggtagggg 80
 |||| | ||||| | ||||| ||||| |||||
Sbjct: 19723 aaacatcgacagtggcgcgccaggtagggg 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 aacaccgacagctggcgcgccaggtagggg 80
 ||||| ||||||| |||||||||||||||||||
Sbjct: 39396 aacatcgacagttggcgcgccaggtagggg 39426

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

Query: 50 aacaccgacagctggcgcgccaggtagggg 80
 ||||| ||||||| |||||||||||||||||||
Sbjct: 97242 aacatcgacagttggcgcgccaggtagggg 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 aacaccgacagctggcgcgccaggtagggg 80
 ||||| ||||||| |||||||||||||||||||
Sbjct: 115132 aacatcgacagttggcgcgccaggtagggg 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 aacaccgacagctggcgcgccaggtagggg 80
 ||||| ||||||| |||||||||||||||||||
Sbjct: 51769 aaacgccgacagttggcgcgccaggtagggg 51799

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

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
|||||
Sbjct: 131072 aaacaccgacagttggcagccaggtagggg 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 tggcgcgccaggtaggggtgtg 85
|||||
Sbjct: 353 tggcgcgccaggtaggggtgtg 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 tggcgcgccaggtaggggtgtg 85
|||||
Sbjct: 26 tggcgcgccaggtaggggtgtg 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_BBa0031E23, 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 aaacaccgacagctggcgccaggtagggg 80
||||| ||||||| ||||||||||||||||
Sbjct: 144830 aaacgccgacagttggcgccaggtagggg 144800

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

Query: 50 aaacaccgacagctggcgccaggtagggg 80
||||| ||||||| ||||||||||||||||
Sbjct: 161365 aaacgccgacagttggcgccaggtagggg 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 aaacaccgacagctggcgccaggtagggg 80
||||| ||||||| ||||||||||||||||
Sbjct: 52583 aaacgccgacagttggcgccaggtagggg 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 aaacaccgacagctggcgccaggtagggg 80
||||| ||||||| ||||||||||||||||
Sbjct: 43923 aaacgccgacagttggcgccaggtagggg 43953

>gb|AC231617.2| Zea mays BAC clone CH201-190G15 from chromosome 8, complete sequence
Length = 166972

>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: 26152 aaacaccgatagttggcgcgccaggtagggg 26182

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 aaacgccgacagttggcgccaggtagggg 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

Query: 50 aaacaccgacagctggcgccaggtagggg 80
||||| ||||| ||||| ||||| |||||
Sbjct: 3582 aaacaccgacagttggcgccagatagggg 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

Query: 50 aaacaccgacagctggcgccaggtagggg 80
|||| | ||||| | ||||| ||||| |||||
Sbjct: 16033 aaacgccgacagttggcgccaggtagggg 16003

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

Query: 50 aaacaccgacagctggcgccaggtagggg 80
||||| |||| | ||||| ||||| |||||
Sbjct: 72192 aaacaccaacagttggcgccaggtagggg 72222

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

Query: 50 aaacaccgacagctggcgccaggtagggg 80
|||| | ||||| | ||||| ||||| |||||

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 cgcacagctggcgcgccaggtagggg 81
||||| |||||||||||||||||||
Sbjct: 109246 cgcacatctggcgcgccaggtagggg 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 cgcacagctggcgcgccaggtagggg 81
||||| |||||||||||||||||||
Sbjct: 134285 cgcacatctggcgcgccaggtagggg 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 cgcacagctggcgcgccaggtagggg 81
||||| ||||||||||||||||||||
Sbjct: 31648 cgcacatctggcgcgccaggtagggg 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 aaacaccgacagctggcgcgccaggtagggg 80
||||| ||||||| ||||||||||||||||
Sbjct: 45031 aaacgccgacagtggcgcgccaggtagggg 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 ccgacagctggcgcgccaggtaggggg 81
||||| ||||||||||||||||
Sbjct: 91750 ccgacatctggcgcgccaggtaggggg 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 tggcgcgccaggtagggggtgtg 85
||||||||||||||
Sbjct: 80721 tggcgcgccaggtagggggtgtg 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 aaacgccgacagtggcgcgccaggtagggg 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 cgcacagctggcgcgccaggtagggg 81
 ||||| |||||||||
Sbjct: 150371 cgcacatctggcgcgccaggtagggg 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 aaacgccgacagttggcgcgccaggtagggg 54677

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

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
 |||| | ||||||| |||||||||
Sbjct: 86382 aaacgccgacagttggcgcgccaggtagggg 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 cgcacagctggcgcgccaggtagggg 81
||||| |||||||||||||||||||
Sbjct: 12034 cgcacatctggcgcgccaggtagggg 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 cgcacagctggcgcgccaggtagggg 81
||||| |||||||||||||||||||
Sbjct: 45155 cgcacatctggcgcgccaggtagggg 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

>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 aaacaccgacagctggcgccaggtagggg 80
||||| ||||||| ||||||||||||||||
Sbjct: 149217 aaacgccgacagttggcgccaggtagggg 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 ccgacagctggcgccaggtaggggg 81
||||| ||||||| ||||||||||||||||
Sbjct: 42085 ccgacatctggcgccaggtaggggg 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 ccgacagctggcgccaggtaggggg 81
||||| ||||||| ||||||||||||||||
Sbjct: 109345 ccgacatctggcgccaggtaggggg 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 acagctggcgccaggtagggg 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)