

BLASTn Search Outputs of the 3' End Border Sequences against GenBank No-human and No-mouse ESTs (est_others)

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= Region4
(1868 letters)

Database: /usr/local/blast/db/blastlibs/est_others
52,386,385 sequences; 29,661,423,624 total letters

Searching..... done

Sequences producing significant alignments:						Score	E
						(bits)	Value
gb	FL470578.1	25237854	CERES-CB5	Zea mays cDNA clone 1155571 3'...	418	e-113	
gb	FL451864.1	10982021	CERES-CB5	Zea mays cDNA clone 1218827 3'...	410	e-110	
gb	FL432925.1	25247980	CERES-CB5	Zea mays cDNA clone 1220987 3'...	283	2e-72	
gb	FL470560.1	21702559	CERES-CB6	Zea mays cDNA clone 1165529 3'...	216	3e-52	
gb	FL470559.1	16105884	CERES-CB6	Zea mays cDNA clone 1165529 3'...	216	3e-52	
gb	FL470558.1	10396343	CERES-CB6	Zea mays cDNA clone 1165529 3'...	216	3e-52	
gb	CF273107.1	EST2669	Zea mays sperm cell cDNA library Zea mays...	165	1e-36		
gb	CF273097.1	EST2659	Zea mays sperm cell cDNA library Zea mays...	123	4e-24		
gb	FL455073.1	16632359	CERES-CB5	Zea mays cDNA clone 1146214 3'...	107	2e-19	
gb	FL451865.1	13100827	CERES-CB5	Zea mays cDNA clone 1218827 3'...	107	2e-19	
gb	EG211835.1	MSAM058196_3231_0905	LCM-dissected maize inbred l...	98	2e-16		
gb	FL470481.1	10606265	CERES-CB6	Zea mays cDNA clone 1168199 3'...	96	8e-16	
gb	CD526323.1	EST1750	Zea mays sperm cell cDNA library Zea mays...	94	3e-15		
gb	EG136737.1	MSAM243415_0331_1740	LCM-dissected maize inbred l...	86	8e-13		
gb	EG125154.1	MSAM218621_1422_0209	LCM-dissected maize inbred l...	86	8e-13		
gb	FF141400.1	OFAA-aaa62g06.b1	O. flexuosa_EST_pSMART Onchocerca...	84	3e-12		
gb	EG290874.1	MSAM213298_2794_1558	LCM-dissected maize inbred l...	84	3e-12		
gb	EG104957.1	MSAM177786_0974_2612	LCM-dissected maize inbred l...	84	3e-12		
gb	EG137547.1	MSAM244923_1299_3204	LCM-dissected maize inbred l...	84	3e-12		
gb	EG194598.1	MSAM001557_2247_1458	LCM-dissected maize inbred l...	80	5e-11		
gb	DW893845.1	MSAM113099_3559_0648	LCM-dissected maize shoot ap...	78	2e-10		
gb	DW830995.1	MSAM264173_0180_3518	LCM-dissected maize shoot ap...	72	1e-08		
gb	DW945813.1	MSAM225070_2378_1645	LCM-dissected maize shoot ap...	68	2e-07		
gb	EG243928.1	MSAM131731_3893_1136	LCM-dissected maize inbred l...	66	8e-07		
gb	EG261924.1	MSAM202212_2841_1387	LCM-dissected maize inbred l...	66	8e-07		
gb	DW972233.1	MSAM287451_3885_0583	LCM-dissected maize shoot ap...	66	8e-07		

gb	FL476102.1	2002854 CERES-227 Zea mays cDNA clone 400160 3', ...	64	3e-06
gb	FL307895.1	2966196 CERES-227 Zea mays cDNA clone 507820 5', ...	64	3e-06
gb	EG176217.1	MSAM007276_3034_2445 LCM-dissected maize inbred l...	62	1e-05
gb	DW870027.1	MSAM045979_3454_2175 LCM-dissected maize shoot ap...	62	1e-05
gb	FL967575.1	CCHY8225.b1 CCHY Panicum virgatum callus (N) Pani...	58	2e-04
gb	EG094627.1	MSAM117657_0944_3029 LCM-dissected maize inbred l...	58	2e-04
gb	FL470601.1	10391335 CERES-CB6 Zea mays cDNA clone 1166816 3'...	56	7e-04
gb	EG122367.1	MSAM213543_0399_2532 LCM-dissected maize inbred l...	56	7e-04
gb	EG064913.1	MSAM099669_0578_1949 LCM-dissected maize inbred l...	56	7e-04
gb	DT464774.1	GH_CHX16E04.r GH_CHX Gossypium hirsutum cDNA clon...	56	7e-04
gb	EG131418.1	MSAM183153_0247_2918 LCM-dissected maize inbred l...	54	0.003
gb	EG278067.1	MSAM237051_2164_0313 LCM-dissected maize inbred l...	54	0.003
gb	DW974630.1	MSAM293083_3262_0305 LCM-dissected maize shoot ap...	54	0.003
gb	DW884389.1	MSAM085099_3297_2244 LCM-dissected maize shoot ap...	54	0.003
gb	CA129139.1	SCRFLR2034H10.g LR2 Saccharum hybrid cultivar SP8...	54	0.003
gb	DW945646.1	MSAM224719_2697_2993 LCM-dissected maize shoot ap...	52	0.011
gb	CA179013.1	SCSGST1069C02.b ST1 Saccharum hybrid cultivar SP8...	52	0.011
gb	CA090649.1	SCSGAM2105C02.b AM2 Saccharum hybrid cultivar SP8...	52	0.011
gb	CA090562.1	SCSGAM2105C02.g AM2 Saccharum hybrid cultivar SP8...	52	0.011
gb	FL347392.1	1747881 CERES-227 Zea mays cDNA clone 400160 5',...	50	0.045
gb	EG171544.1	MSAM273353_0529_3957 LCM-dissected maize inbred l...	50	0.045
gb	CK701010.1	EST5112 Zea mays sperm cell cDNA library Zea mays...	50	0.045
gb	DW853896.1	MSAM318246_1248_2588 LCM-dissected maize shoot ap...	48	0.18
gb	BM322403.1	PIC1_4_D07.b1_A002 Pathogen-infected compatible l...	48	0.18
gb	FL163223.1	6653349 CERES-CB5 Zea mays cDNA clone 1217524 5',...	46	0.70
gb	FL163221.1	6659451 CERES-CB5 Zea mays cDNA clone 1223626 5',...	46	0.70
gb	FL163220.1	6669993 CERES-CB6 Zea mays cDNA clone 1234168 5',...	46	0.70
gb	FL163218.1	6662101 CERES-CB6 Zea mays cDNA clone 1226276 5',...	46	0.70
gb	FL163217.1	6654616 CERES-CB5 Zea mays cDNA clone 1218791 5',...	46	0.70
gb	FL163215.1	5738996 CERES-CB5 Zea mays cDNA clone 1146287 5',...	46	0.70
gb	FL163214.1	6646819 CERES-CB5 Zea mays cDNA clone 1210994 5',...	46	0.70
gb	FL163213.1	6659882 CERES-CB5 Zea mays cDNA clone 1224057 5',...	46	0.70
gb	FL061059.1	6665270 CERES-CB6 Zea mays cDNA clone 1229445 5',...	46	0.70
gb	FK991356.1	5740242 CERES-CB6 Zea mays cDNA clone 1147533 5',...	46	0.70
gb	FK991355.1	6665245 CERES-CB6 Zea mays cDNA clone 1229420 5',...	46	0.70
gb	FK991354.1	6660973 CERES-CB6 Zea mays cDNA clone 1225148 5',...	46	0.70
gb	FK991353.1	6664156 CERES-CB6 Zea mays cDNA clone 1228331 5',...	46	0.70
gb	EG126585.1	MSAM221137_0158_0475 LCM-dissected maize inbred l...	46	0.70
gb	DW984436.1	MSAM361482_2399_0555 LCM-dissected maize shoot ap...	46	0.70
gb	DW898353.1	MSAM118718_2397_0553 LCM-dissected maize shoot ap...	46	0.70
gb	DT464708.1	GH_CHX16C10.r GH_CHX Gossypium hirsutum cDNA clon...	46	0.70
dbj	BW497656.1	BW497656 Nori Satoh unpublished cDNA library, ma...	46	0.70
dbj	BW477003.1	BW477003 Nori Satoh unpublished cDNA library, ma...	46	0.70
gb	CK701021.1	EST5123 Zea mays sperm cell cDNA library Zea mays...	46	0.70
gb	CF919842.1	EST4142 Zea mays sperm cell cDNA library Zea mays...	46	0.70
gb	CA236929.1	SCSBFL5015D04.g Saccharum officinarum FL5 Sacchar...	46	0.70
gb	CA236928.1	SCSBFL5015D03.g Saccharum officinarum FL5 Sacchar...	46	0.70
gb	CD439487.1	EL01N0525E01.b Endosperm_5 Zea mays cDNA, mRNA se...	46	0.70
gb	CD437461.1	EL01N0501C03.b Endosperm_5 Zea mays cDNA, mRNA se...	46	0.70

Sbjct: 246 cgacaagtagcagcccaagcagcaccaggggctagttggccgtctacacgaccgccc 187

Query: 1398 atgggccgcccggagcgcgaggacgtgatgacagtgtatgttccattgtcctaggga 1457

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Sbjct: 186 tcgggtcgtggggcgcggaagacgtaatgacagcgtatgtgccatcgtcctaggga 127

Query: 1458 agacgcaatgcagtggtccgacatctacccaacattgcatagacaattggagcgactt 1517

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Sbjct: 126 tgacgactgcagtggttcgacatctgccacgacactgcatcgacggttggggcgactt 67

Query: 1518 cagttggtgcttcacgccaacttcagtcctctttgacaagccggcgcagccatggga 1577

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Sbjct: 66 tagtcggcgtttcagccaacttcagtcctctctgacaagccgcccagccatggta 7

Query: 1578 cct 1580

|||

Sbjct: 6 cct 4

>gb|FL451864.1| 10982021 CERES-CB5 Zea mays cDNA clone 1218827 3', mRNA sequence

Length = 613

Score = 410 bits (207), Expect = e-110
Identities = 503/599 (83%), Gaps = 2/599 (0%)
Strand = Plus / Minus

Query: 1014 acctacgccatgccatcaacagccggcgcgagacacgcggagctccatcaacgcttcgcgcg 1073

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Sbjct: 612 acctacaccacgccatcaacagccgacgagacgcgcggagctccatcaatgcttcgcgcg 553

Query: 1074 accgatgacacgaaagtgagatagggaaaccgagaggagtatgtccgagatcatgccatcc 1133

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Sbjct: 552 accgacggcagaaagcgagataaggcgcgggaggagtatgaccgggatcatggtgtcc 493

Query: 1134 tggcatgaagtcacgccaccgagctgagtcggttgccgctcgaccagtgctccgttcc 1193

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Sbjct: 492 cagcttgaagttgcccaccgagttgagtcggttgccgctcgaccagtgcccgacc 433

Query: 1194 agggacgatcaagatgacacacaactggctcccctccttgggaccgacctcacgaacgcc 1253

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Sbjct: 432 ggggacggtcgagacgacacaccaccagctcccctccccgggaccgacctcacgaacgcc 373

Query: 1254 gacatgaagacacgtgcgagctcttcgcacttactccgtgtctccgggcatccagtgg- 1312
||||| ||||||| ||||||| ||| || ||||||| ||||||| ||||||| |||||||
Sbjct: 372 gacaggaagacacatgccccgtctctgcgcttactccgctctccgggcatccagtggc 313

Query: 1313 cccctaacttcaaggtctccaacgtcagcaagtatgagcgcgaagcaggacctgggtggct 1372
||||| ||||||| ||||||| ||||||| ||||||| ||||| ||||||| ||| || |||||
Sbjct: 312 cccccaacttcaaagtctcaaacgtcgacaagtacgagccaagcagcaccagggggct 253

Query: 1373 ggttagccatctacacgattgtcacatgggccgccggagcgcaggaggacgtgatgacag 1432
||| ||| ||||||| | | | ||| ||| || ||||||| ||||||| |||||||
Sbjct: 252 agttggccgtctacacgaccgccgctcgggtcgtcggggcgacggaagacgtaatgacag 193

Query: 1433 tgtatthttccattgtcctagggcaagacgcaatgcagtggtccgacatctacccaac 1492
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||| |||
Sbjct: 192 cgtatthgcccacgtccttagggcaagacgcaatgcagtggtccgacatctgcccacgac 133

Query: 1493 attgcatagacaattggagcgcacttcagttggtgcttcatcgccaacttccagtcctct 1552
| ||||||| ||| ||||| ||||||| ||| ||| || ||||||| ||||||| |||||||
Sbjct: 132 actgcatcgacggttggggcgacttttagtcggcgcttcatcgccaacttccagtcctct 73

Query: 1553 ttgacaagccggcgag-ccatgggacctaaaatccattgggcatcaggcgatgaaac 1610
||||||||| ||||||| ||||||| ||||||| ||||||| ||| ||||||| |||||||
Sbjct: 72 ctgacaagccggcgagcccatggtacctcaaatccatcaggcgccaggcgatgaaac 14

>gb|FL432925.1| 25247980 CERES-CB5 Zea mays cDNA clone 1220987 3', mRNA sequence
Length = 387

Score = 283 bits (143), Expect = 2e-72
Identities = 324/383 (84%), Gaps = 1/383 (0%)
Strand = Plus / Minus

Query: 970 tcgagcagttaatcaccttctacccatcactaatcctccaagcgcactacgcatgcat 1029
||||| ||| ||||||| ||||||| ||||||| || ||| || ||||||| |||||||
Sbjct: 387 tcgagtagctaataccttctgccatcgctcatccccgagcaacctacaccacgcat 328

Query: 1030 caacagccggcgagacacgcggagctccatcaacgcttcgcgcgaccgatgacacgaaag 1089
||||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||| |||||||
Sbjct: 327 caacagccgacgagacgcggagctccatcaatgcttcgcgcgaccgacggcacgaaag 268

Query: 1090 tgagataggaaccgagaggagtatgtccgagatcatgccatcctggcatgaagtcatgc 1149
||||| || ||| ||||||||| ||| ||||||| ||| || ||||||| ||
Sbjct: 267 cgagataaggcgccgggaggagtatgaccgggatcatggtgtcccagcttgaagttgcg 208

Query: 1150 caccgagctgagtcggttgccgctcgaccagtgtcccgttccaggacgatcaagatg 1209
||||||| ||||||||| ||||||||| ||||| || ||||||| || ||| |
Sbjct: 207 caccgagttgagtcggttgccgctcgaccagtggcccgaccggggacggtcgagacg 148

Query: 1210 acacacaactggctcccctccttgggaccgacctcacgaacgccgacatgaagacacgtg 1269
||||||| || ||||||||| ||||||||| ||||||||| ||||||||| ||
Sbjct: 147 acacaccaccagctcccctccccgggaccgacctcacgaacgccgacaggaagacacatg 88

Query: 1270 cggagtcttcgcacttactccgtgtctccggccatccagtgg-cccctaacttcaaggt 1328
||| |||| || ||||||||| ||||||||| ||||||||| ||||| ||||||||| ||
Sbjct: 87 cggggtctctgcgcttactccgcgtctccggccatccagtggcccccaacttcaaagt 28

Query: 1329 ctccaacgtcagcaagtatgagc 1351
||| ||||||| ||||||| |||||
Sbjct: 27 ctcaaacgtcgacaagtacgagc 5

>gb|FL470560.1| 21702559 CERES-CB6 Zea mays cDNA clone 1165529 3', mRNA sequence
Length = 541

Score = 216 bits (109), Expect = 3e-52
Identities = 332/405 (81%), Gaps = 1/405 (0%)
Strand = Plus / Minus

Query: 1420 gacgtgatgacagtgatattttccattgtcctagggaagacgcaatgcagtggtccga 1479
||||||||||| | ||||||| ||||||||| ||||||||| || ||||| ||||| |||
Sbjct: 525 gacgtgatgaccgctatattaccattgtccttgggaagatgcgttgcaatggctgcca 466

Query: 1480 catctacccaacattgcatagacaattggagcgacttcagttggtgcttcatcgccaac 1539
||||||||||| ||||||||| ||| | ||| ||||||||| | ||||||| |||||
Sbjct: 465 catctaccccacattgcatcgacgactggggcgacttcagtcgacgcttcaccgccaat 406

Query: 1540 ttccagtcctctttgacaagccggcgagccatgggacctaaaatccattgggcatcag 1599
||| ||||||||| ||||| ||||| || ||||||||| ||||||||| || ||| |
Sbjct: 405 ttctagtcctctccgacaaaccggcacaaccatgggacctcaatccatcaagcgcgg 346

Sbjct: 446 gaggtcacggaggcggccgtgatcgaggacttctacagaggatccaacgactcggctttc 387

Query: 1720 gtccgagccataactccagaaaagcgtcggccacctccgaacacttgttccgggaggcaga 1779
|||||

Sbjct: 386 gtccgagccatattaca-aaaggcggcggactacctccgaggagctggtccgggaagccga 328

Query: 1780 cctctacatcaccacggattaacgggcccaggacctcatcggagg 1824
|||||

Sbjct: 327 cctctacatcaccgcccagcagcgggcccaggacctcatcggagg 283

>gb|FL470558.1| 10396343 CERES-CB6 Zea mays cDNA clone 1165529 3', mRNA sequence
Length = 556

Score = 216 bits (109), Expect = 3e-52
Identities = 332/405 (81%), Gaps = 1/405 (0%)
Strand = Plus / Minus

Query: 1420 gacgtgatgacagtgatattttccattgtcctagggcaagacgcaatgcagtggctccga 1479
|||||

Sbjct: 540 gacgtgatgaccgcgtattttaccattgtccttgggcaagatgcgttgcaatggctcgca 481

Query: 1480 catctacccaacattgcatagacaattggagcgacttcagttggtgcttcatcgccaac 1539
|||||

Sbjct: 480 catctaccccacattgcatcgacgactggggcgacttcagtcgacgcttcaccgccaat 421

Query: 1540 ttccagtcctctttgacaagccggcgcagccatgggacctaaaatccattgggcatcag 1599
|||

Sbjct: 420 ttctagtcctctccgacaaaaccggcacaaccatgggacctcaaatccatcaagcggcgg 361

Query: 1600 ggcgatgaaacgctccggttgctacctcaagaggttttagacctgaggaaccacaccccc 1659
|||

Sbjct: 360 ggggacaaaactctccggtcatacctcaaaaggtccagacctgagaaatcgatcccc 301

Query: 1660 gaagtcgccgaggcgggggtgattgaagacttctaccgaggatccaatgactcggctttc 1719
|||

Sbjct: 300 gaggtcacggaggcggccgtgatcgaggacttctacagaggatccaacgactcggctttc 241

Query: 1720 gtccgagccataactccagaaaagcgtcggccacctccgaacacttgttccgggaggcaga 1779
|||||

Length = 337

Score = 107 bits (54), Expect = 2e-19

Identities = 195/242 (80%)

Strand = Plus / Minus

Query: 886 gagtgaagtcggaggggtactggcccagatagctgacggcctcccgcgaaccctagacac 945
||||||| ||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||| |
Sbjct: 334 gagtgaagtggaggagtactggcgcagatagccgacggcctcccgcgaaccccagacgc 275

Query: 946 ggaaggctaccggcggtgcttactcgagcagttaatcaccttctacccatcactaatcc 1005
||||| || ||||||| ||||| | | | ||||| ||||||| || || |||||
Sbjct: 274 agaaggttatcggcggtgcttacacaggtggccaatcatcttctaccctcgctcatcc 215

Query: 1006 tccaagcgacctacgcatgccatcaacagccggcgagacacgcgagctccatcaacgc 1065
| | | ||||||| || || | ||||||| || | ||||||| | | ||| ||||||| |||
Sbjct: 214 tgcgaacgacctgcgtcacacaatcaatagctgacgagacgcacaaagcaccatcatcg 155

Query: 1066 ttcgcgacccgatgacacgaaagtgagataggaaccgagaggagtatgtccgagatca 1125
||| ||||||| ||||| | ||||| ||||| || ||| ||||||| | |||||||
Sbjct: 154 ttcacgacccgatgaaatgaaatgagataaggcgccgggaggagtacgaccgagatca 95

Query: 1126 tg 1127
||
Sbjct: 94 tg 93

>gb|FL451865.1| 13100827 CERES-CB5 Zea mays cDNA clone 1218827 3', mRNA sequence
Length = 108

Score = 107 bits (54), Expect = 2e-19

Identities = 90/102 (88%)

Strand = Plus / Minus

Query: 1014 acctacgccatgccatcaacagccggcgagacacgcgagctccatcaacgcttcgcgcg 1073
||||||| ||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||
Sbjct: 107 acctacaccagccatcaacagccgacgagacgcgagctccatcaatgcttcgcgcg 48

Query: 1074 accgatgacacgaaagtgagataggaaccgagaggagtatg 1115
||||| | ||||||| ||||||| || ||| |||||||
Sbjct: 47 accgacggcacgaaagcgagataaggcgccgggaggagtatg 6

>gb|EG211835.1| MSAM058196_3231_0905 LCM-dissected maize inbred line Mo17 shoot
apical meristem cDNA Zea mays cDNA, mRNA sequence
Length = 94

Score = 97.6 bits (49), Expect = 2e-16
Identities = 58/61 (95%)
Strand = Plus / Minus

Query: 158 tgctttggaaccatctcatccatagcagatgaagaggggaactctgcaccgcatagcagat 217
|||||
Sbjct: 77 tgctttggaacgatctcatccatagcagatgaagaggggaactctacaccgcatgagat 18

Query: 218 c 218
|
Sbjct: 17 c 17

>gb|FL470481.1| 10606265 CERES-CB6 Zea mays cDNA clone 1168199 3', mRNA sequence
Length = 778

Score = 95.6 bits (48), Expect = 8e-16
Identities = 180/224 (80%)
Strand = Plus / Plus

Query: 848 aacctgtacccccgacttcgctcgtgcaatgaacacgccgagtgaagtcggaggggtactg 907
|||||
Sbjct: 238 aacctgaacccccgacttcgccccgagccatgaacacgccgagtgaagtcggaggggtacta 297

Query: 908 gccagatagctgacggcctcccgcgaaccctagacacggaaggctaccggcggctgctt 967
|||
Sbjct: 298 gtcggatagctgatggactcctcggaatcccgcgagggctatcgacgactgttc 357

Query: 968 actcgagcagttaatcaccttctacccatcactaatcctccaagcgacctaagccatgcc 1027
|||
Sbjct: 358 acccaagcagccaaccatcttctacctatcgctcaccgcccgaacgacctaagcagcgc 417

Query: 1028 atcaacagccggcgagacacgcggagctccatcaacgcttcgcg 1071
|||||
Sbjct: 418 atcaacagccgctcgggacacgtgaagctccataaatgcttcgcg 461

>gb|CD526323.1| EST1750 Zea mays sperm cell cDNA library Zea mays cDNA clone

Query: 195 gaactct 201
 |||||
Sbjct: 94 gaactct 100

>gb|FF141400.1| OFAA-aaa62g06.b1 0.flexuosa_EST_pSMART Onchocerca flexuosa cDNA,
 mRNA sequence
 Length = 587

Score = 83.8 bits (42), Expect = 3e-12
Identities = 138/170 (81%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgcgccaggtaggggtgtgtctttgatctgagctagctcaatg 109
 |||||
Sbjct: 99 aaacaccgacagctggcgcaccaggtaggggtgtgtcgcacgatccaagctagctcaatg 158

Query: 110 accattacctccaaatgcaagatcgcccttcgccccgggactatgttttgctttggaacc 169
 || | ||| | | || |||| | | | |||| | | | || ||| || ||
Sbjct: 159 gccgtcacctccacagccagatcacctgctgctccggatctgtattctgcttcgggaca 218

Query: 170 atctcatccatagcagatgaagaggaactctgcaccgcatagcagatct 219
 ||||| |||| | ||||| ||| |||| | | |||||
Sbjct: 219 atctcatctatagcggatgaagaggaattctacaccgcctcgcagatct 268

>gb|EG290874.1| MSAM213298_2794_1558 LCM-dissected maize inbred line Mo17 shoot
 apical meristem cDNA Zea mays cDNA, mRNA sequence
 Length = 119

Score = 83.8 bits (42), Expect = 3e-12
Identities = 75/86 (87%)
Strand = Plus / Minus

Query: 2 taccctaaagcaccgcaaggggtagccctgggtgtgcggacggactctaacaccgacag 61
 |||||
Sbjct: 103 taccctaaagcaccctcgaggggtaacctcgggtgtgcggtcgggtcccaaacaccgacag 44

Query: 62 ctggcgcgccaggtaggggtgtgtc 87
 || |||||
Sbjct: 43 ctagcgcgccaggtaggggtgtgtc 18

>gb|EG104957.1| MSAM177786_0974_2612 LCM-dissected maize inbred line Mo17 shoot
apical meristem cDNA Zea mays cDNA, mRNA sequence
Length = 122

Score = 83.8 bits (42), Expect = 3e-12
Identities = 75/86 (87%)
Strand = Plus / Minus

Query: 2 taccctaaagcaccgcaagggtagccctgggtgtgctgacggactctaaacaccgacag 61
|||||
Sbjct: 106 taccctaaagcaccctcgaggggtaacctcggtgtgctgctgggtcccaaacaccgacag 47

Query: 62 ctggcgcgccaggtaggggtgtgtc 87
||
Sbjct: 46 ctaggcgcgccaggtaggggtgtgtc 21

>gb|EG137547.1| MSAM244923_1299_3204 LCM-dissected maize inbred line Mo17 shoot
apical meristem cDNA Zea mays cDNA, mRNA sequence
Length = 119

Score = 83.8 bits (42), Expect = 3e-12
Identities = 75/86 (87%)
Strand = Plus / Minus

Query: 2 taccctaaagcaccgcaagggtagccctgggtgtgctgacggactctaaacaccgacag 61
|||||
Sbjct: 103 taccctaaagcaccctcgaggggtaacctcggtgtgctgctgggtcccaaacaccgacag 44

Query: 62 ctggcgcgccaggtaggggtgtgtc 87
||
Sbjct: 43 ctaggcgcgccaggtaggggtgtgtc 18

>gb|EG194598.1| MSAM001557_2247_1458 LCM-dissected maize inbred line Mo17 shoot
apical meristem cDNA Zea mays cDNA, mRNA sequence
Length = 84

Score = 79.8 bits (40), Expect = 5e-11
Identities = 55/60 (91%)
Strand = Plus / Minus

Query: 159 gctttggaaccatctcatccatagcagatgaagagggaactctgcaccgcatagcagatc 218

Query: 113 at 114
||
Sbjct: 69 at 70

>gb|EG243928.1| MSAM131731_3893_1136 LCM-dissected maize inbred line Mo17 shoot
apical meristem cDNA Zea mays cDNA, mRNA sequence
Length = 98

Score = 65.9 bits (33), Expect = 8e-07
Identities = 45/49 (91%)
Strand = Plus / Plus

Query: 170 atctcatccatagcagatgaagaggggaactctgcaccgcatagcagatc 218
||||||| | ||||||||||||||||||||||||||||| ||||||| |||||||
Sbjct: 27 atctcattcgtagcagatgaagaggggaactctacaccgattgcagatc 75

>gb|EG261924.1| MSAM202212_2841_1387 LCM-dissected maize inbred line Mo17 shoot
apical meristem cDNA Zea mays cDNA, mRNA sequence
Length = 114

Score = 65.9 bits (33), Expect = 8e-07
Identities = 39/41 (95%)
Strand = Plus / Minus

Query: 170 atctcatccatagcagatgaagaggggaactctgcaccgcat 210
||||| ||||||||||||||||||||||||||||| |||||||
Sbjct: 112 atctcgtccatagcagatgaagaggggaactctacaccgcat 72

>gb|DW972233.1| MSAM287451_3885_0583 LCM-dissected maize shoot apical meristem cDNA
Zea mays cDNA, mRNA sequence
Length = 126

Score = 65.9 bits (33), Expect = 8e-07
Identities = 36/37 (97%)
Strand = Plus / Minus

Query: 357 tgtccacttcgccacaaaggagtggacacggattac 393
||||||||| |||||||||||||||||||||||||||||
Sbjct: 46 tgtccacttcgtccacaaaggagtggacacggattac 10

Query: 180 tagcagatgaagaggggaactctgcaccgcatagcagatc 218
|||||
Sbjct: 123 tagcagatgaagaggggaactctacaccgattgcagatc 85

>gb|FL967575.1| CCHY8225.b1 CCHY Panicum virgatum callus (N) Panicum virgatum cDNA
clone CCHY8225 5', mRNA sequence
Length = 738

Score = 58.0 bits (29), Expect = 2e-04
Identities = 32/33 (96%)
Strand = Plus / Minus

Query: 48 ctaaaccgacagctggcgccaggtagggg 80
|||||
Sbjct: 297 ctaaaccgacagctggcgtgccaggtagggg 265

>gb|EG094627.1| MSAM117657_0944_3029 LCM-dissected maize inbred line Mo17 shoot
apical meristem cDNA Zea mays cDNA, mRNA sequence
Length = 88

Score = 58.0 bits (29), Expect = 2e-04
Identities = 35/37 (94%)
Strand = Plus / Minus

Query: 158 tgctttggaaccatctcatccatagcagatgaagagg 194
|||||
Sbjct: 38 tgctttggaacgatctcgtccatagcagatgaagagg 2

>gb|FL470601.1| 10391335 CERES-CB6 Zea mays cDNA clone 1166816 3', mRNA sequence
Length = 558

Score = 56.0 bits (28), Expect = 7e-04
Identities = 40/44 (90%)
Strand = Plus / Plus

Query: 878 aacacgccgagtggaagtcggaggggtactggcccagatagctga 921
|||||
Sbjct: 39 aacacgccgagcgaagtcggaggggtactagctccgatagctga 82

Score = 56.0 bits (28), Expect = 7e-04
Identities = 52/60 (86%)

Strand = Plus / Plus

Query: 1012 cgacctacgccatgccatcaacagccggcgagacacggagctccatcaacgcttcgcg 1071
||||| ||||| || |||||||||||||||| || ||||||| | ||||||| |||||||||
Sbjct: 173 cgacatacgcacgccatcaacagccgtcgggacacgtgaagctccataaacgcttcgcg 232

>gb|EG122367.1| MSAM213543_0399_2532 LCM-dissected maize inbred line Mo17 shoot
apical meristem cDNA Zea mays cDNA, mRNA sequence
Length = 95

Score = 56.0 bits (28), Expect = 7e-04
Identities = 43/48 (89%)
Strand = Plus / Minus

Query: 947 gaaggctaccggcggtgcttactcgagcagttaatcaccttctaccc 994
||||||| || |||||||||||||||| |||| ||||||| |||||||||
Sbjct: 60 gaaggctatcgacgggtgcttactcgggcaggtaatcatcttctaccc 13

>gb|EG064913.1| MSAM099669_0578_1949 LCM-dissected maize inbred line Mo17 shoot
apical meristem cDNA Zea mays cDNA, mRNA sequence
Length = 98

Score = 56.0 bits (28), Expect = 7e-04
Identities = 37/40 (92%)
Strand = Plus / Minus

Query: 158 tgctttggaaccatctcatccatagcagatgaagaggaa 197
||||| ||||| ||||||||| |||||||||||||||||
Sbjct: 48 tgcttcggaacaatctcatccgtagcagatgaagaggaa 9

>gb|DT464774.1| GH_CHX16E04.r GH_CHX Gossypium hirsutum cDNA clone GH_CHX16E04 3',
mRNA sequence
Length = 875

Score = 56.0 bits (28), Expect = 7e-04
Identities = 46/52 (88%)
Strand = Plus / Minus

Query: 54 accgacagctggcgcgccaggtaggggtgtgtctttgatctgagctagctc 105
||||||||||||||| |||||||||||||||| ||||||| ||||| |||||||||
Sbjct: 423 accgacagctggcacgccaggtaggggtgtgtcactgatccaagctagctc 372

Score = 52.0 bits (26), Expect = 0.011
Identities = 29/30 (96%)
Strand = Plus / Plus

Query: 51 aacaccgacagctggcgcgccaggtagggg 80
 ||||| ||||| |||||
Sbjct: 207 aacaccgacagttggcgcgccaggtagggg 236

>gb|CA090649.1| SCSGAM2105C02.b AM2 Saccharum hybrid cultivar SP80-3280 cDNA clone
 SCSGAM2105C02 3', mRNA sequence
 Length = 568

Score = 52.0 bits (26), Expect = 0.011
Identities = 29/30 (96%)
Strand = Plus / Plus

Query: 51 aacaccgacagctggcgcgccaggtagggg 80
 ||||| ||||| |||||
Sbjct: 207 aacaccgacagttggcgcgccaggtagggg 236

>gb|CA090562.1| SCSGAM2105C02.g AM2 Saccharum hybrid cultivar SP80-3280 cDNA clone
 SCSGAM2105C02 5', mRNA sequence
 Length = 674

Score = 52.0 bits (26), Expect = 0.011
Identities = 29/30 (96%)
Strand = Plus / Minus

Query: 51 aacaccgacagctggcgcgccaggtagggg 80
 ||||| ||||| |||||
Sbjct: 493 aacaccgacagttggcgcgccaggtagggg 464

>gb|FL347392.1| 1747881 CERES-227 Zea mays cDNA clone 400160 5', mRNA sequence
 Length = 422

Score = 50.1 bits (25), Expect = 0.045
Identities = 53/61 (86%), Gaps = 1/61 (1%)
Strand = Plus / Minus

Query: 2 taccctaaagcaccgcaaggggtag-cctgggtgtgacggactctaacaccgaca 60
 ||||| || ||| ||||| ||| ||| |||||

Sbjct: 390 tacccaaaagcactgcgaggggtaaaccgccgggtgtgcggtcgggetccaaacaccgaca 331

Query: 61 g 61

Sbjct: 330 g 330

>gb|EG171544.1| MSAM273353_0529_3957 LCM-dissected maize inbred line Mo17 shoot
apical meristem cDNA Zea mays cDNA, mRNA sequence
Length = 109

Score = 50.1 bits (25), Expect = 0.045
Identities = 37/41 (90%)
Strand = Plus / Minus

Query: 170 atctcatccatagcagatgaagagggaactctgcaccgcat 210

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

Sbjct: 81 atctcatctatagcagatgaaaagggaattctacaccgcat 41

>gb|CK701010.1| EST5112 Zea mays sperm cell cDNA library Zea mays cDNA clone
Zmspl2668 5', mRNA sequence
Length = 425

Score = 50.1 bits (25), Expect = 0.045
Identities = 37/41 (90%)
Strand = Plus / Minus

Query: 1687 gacttctaccgaggatccaatgactcggctttcgtccgagc 1727

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

Sbjct: 213 gacttctaccatggatccaatgactcaggctttcgtccgagc 173

>gb|DW853896.1| MSAM318246_1248_2588 LCM-dissected maize shoot apical meristem
cDNA Zea mays cDNA, mRNA sequence
Length = 109

Score = 48.1 bits (24), Expect = 0.18
Identities = 27/28 (96%)
Strand = Plus / Plus

Query: 53 caccgacagctggcgcgccaggtagggg 80

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

Sbjct: 1 caccgacagttggcgcgccaggtagggg 28

>gb|BM322403.1| PIC1_4_D07.b1_A002 Pathogen-infected compatible 1 (PIC1) Sorghum
bicolor cDNA, mRNA sequence
Length = 512

Score = 48.1 bits (24), Expect = 0.18
Identities = 24/24 (100%)
Strand = Plus / Minus

Query: 62 ctggcgcgccaggtagggggtgtg 85
|||||
Sbjct: 347 ctggcgcgccaggtagggggtgtg 324

>gb|FL163223.1| 6653349 CERES-CB5 Zea mays cDNA clone 1217524 5', mRNA sequence
Length = 451

Score = 46.1 bits (23), Expect = 0.70
Identities = 29/31 (93%)
Strand = Plus / Minus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
|||| |
Sbjct: 37 aaacccgacagttggcgcgccaggtagggg 7

>gb|FL163221.1| 6659451 CERES-CB5 Zea mays cDNA clone 1223626 5', mRNA sequence
Length = 465

Score = 46.1 bits (23), Expect = 0.70
Identities = 29/31 (93%)
Strand = Plus / Minus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
|||| |
Sbjct: 306 aaacccgacagttggcgcgccaggtagggg 276

>gb|FL163220.1| 6669993 CERES-CB6 Zea mays cDNA clone 1234168 5', mRNA sequence
Length = 492

Score = 46.1 bits (23), Expect = 0.70
Identities = 29/31 (93%)
Strand = Plus / Minus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
||||| ||||||| |||||||||||||||||||
Sbjct: 306 aaacgccgacagttggcgcgccaggtagggg 276

>gb|FL163218.1| 6662101 CERES-CB6 Zea mays cDNA clone 1226276 5', mRNA sequence
Length = 319

Score = 46.1 bits (23), Expect = 0.70
Identities = 29/31 (93%)
Strand = Plus / Minus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
||||| ||||||| |||||||||||||||||||
Sbjct: 37 aaacgccgacagttggcgcgccaggtagggg 7

>gb|FL163217.1| 6654616 CERES-CB5 Zea mays cDNA clone 1218791 5', mRNA sequence
Length = 365

Score = 46.1 bits (23), Expect = 0.70
Identities = 29/31 (93%)
Strand = Plus / Minus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
||||| ||||||| |||||||||||||||||||
Sbjct: 306 aaacgccgacagttggcgcgccaggtagggg 276

>gb|FL163215.1| 5738996 CERES-CB5 Zea mays cDNA clone 1146287 5', mRNA sequence
Length = 475

Score = 46.1 bits (23), Expect = 0.70
Identities = 29/31 (93%)
Strand = Plus / Minus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
||||| ||||||| |||||||||||||||||||
Sbjct: 37 aaacgccgacagttggcgcgccaggtagggg 7

>gb|FL163214.1| 6646819 CERES-CB5 Zea mays cDNA clone 1210994 5', mRNA sequence
Length = 76

Score = 46.1 bits (23), Expect = 0.70
Identities = 29/31 (93%)

Strand = Plus / Minus

```
Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
      |||| | ||||| | ||||| ||||| |||||
Sbjct: 37 aaagccgacagttggcgcgccaggtagggg 7
```

>gb|FL163213.1| 6659882 CERES-CB5 Zea mays cDNA clone 1224057 5', mRNA sequence
Length = 429

Score = 46.1 bits (23), Expect = 0.70
Identities = 29/31 (93%)
Strand = Plus / Minus

```
Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
      |||| | ||||| | ||||| ||||| |||||
Sbjct: 37 aaagccgacagttggcgcgccaggtagggg 7
```

>gb|FL061059.1| 6665270 CERES-CB6 Zea mays cDNA clone 1229445 5', mRNA sequence
Length = 463

Score = 46.1 bits (23), Expect = 0.70
Identities = 29/31 (93%)
Strand = Plus / Minus

```
Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
      |||| | ||||| | ||||| ||||| |||||
Sbjct: 387 aaagccgacagttggcgcgccaggtagggg 357
```

>gb|FK991356.1| 5740242 CERES-CB6 Zea mays cDNA clone 1147533 5', mRNA sequence
Length = 445

Score = 46.1 bits (23), Expect = 0.70
Identities = 29/31 (93%)
Strand = Plus / Plus

```
Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
      |||| | ||||| | ||||| ||||| |||||
Sbjct: 258 aaagccgacagttggcgcgccaggtagggg 288
```

>gb|FK991355.1| 6665245 CERES-CB6 Zea mays cDNA clone 1229420 5', mRNA sequence
Length = 433

Score = 46.1 bits (23), Expect = 0.70
Identities = 29/31 (93%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
||||| ||||||| ||||||||||||||||
Sbjct: 258 aaacgccgacagttggcgcgccaggtagggg 288

>gb|FK991354.1| 6660973 CERES-CB6 Zea mays cDNA clone 1225148 5', mRNA sequence
Length = 443

Score = 46.1 bits (23), Expect = 0.70
Identities = 29/31 (93%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
||||| ||||||| ||||||||||||||||
Sbjct: 258 aaacgccgacagttggcgcgccaggtagggg 288

>gb|FK991353.1| 6664156 CERES-CB6 Zea mays cDNA clone 1228331 5', mRNA sequence
Length = 342

Score = 46.1 bits (23), Expect = 0.70
Identities = 29/31 (93%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
||||| ||||||| ||||||||||||||||
Sbjct: 258 aaacgccgacagttggcgcgccaggtagggg 288

>gb|EG126585.1| MSAM221137_0158_0475 LCM-dissected maize inbred line Mo17 shoot
apical meristem cDNA Zea mays cDNA, mRNA sequence
Length = 77

Score = 46.1 bits (23), Expect = 0.70
Identities = 29/31 (93%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
||||| ||||||| ||||||||||||||||
Sbjct: 23 aaacgccgacagttggcgcgccaggtagggg 53

>gb|DW984436.1| MSAM361482_2399_0555 LCM-dissected maize shoot apical meristem cDNA
Zea mays cDNA, mRNA sequence
Length = 145

Score = 46.1 bits (23), Expect = 0.70
Identities = 47/55 (85%)
Strand = Plus / Minus

Query: 7 aaaagcaccgcaagggtagccctgggtgtgcgacggactctaaacaccgacag 61
||||||| | ||||| | ||||| ||| ||||| | ||||| |||||
Sbjct: 124 aaaagcacctcgaggggcaaccctgggtgcgcggtcggacccaaaacaccgacag 70

>gb|DW898353.1| MSAM118718_2397_0553 LCM-dissected maize shoot apical meristem cDNA
Zea mays cDNA, mRNA sequence
Length = 146

Score = 46.1 bits (23), Expect = 0.70
Identities = 47/55 (85%)
Strand = Plus / Minus

Query: 7 aaaagcaccgcaagggtagccctgggtgtgcgacggactctaaacaccgacag 61
||||||| | ||||| | ||||| ||| ||||| | ||||| |||||
Sbjct: 125 aaaagcacctcgaggggcaaccctgggtgcgcggtcggacccaaaacaccgacag 71

>gb|DT464708.1| GH_CHX16C10.r GH_CHX Gossypium hirsutum cDNA clone GH_CHX16C10 3',
mRNA sequence
Length = 740

Score = 46.1 bits (23), Expect = 0.70
Identities = 29/31 (93%)
Strand = Plus / Minus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
|||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 494 aaacgccgacagttggcgcgccaggtagggg 464

>dbj|BW497656.1| BW497656 Nori Satoh unpublished cDNA library, mature adult whole
animal Ciona intestinalis cDNA clone cima007g15 3', mRNA
sequence
Length = 468

Score = 46.1 bits (23), Expect = 0.70
Identities = 26/27 (96%)
Strand = Plus / Plus

Query: 1515 cttcagttggtgcttcatcgccaactt 1541
 |||||
Sbjct: 233 cttcagttggtgcttcatcgccaactt 259

>dbj|BW477003.1| BW477003 Nori Satoh unpublished cDNA library, mature adult whole
 animal *Ciona intestinalis* cDNA clone cima007g15 5', mRNA
 sequence
 Length = 496

Score = 46.1 bits (23), Expect = 0.70
Identities = 26/27 (96%)
Strand = Plus / Minus

Query: 1515 cttcagttggtgcttcatcgccaactt 1541
 |||||
Sbjct: 222 cttcagttggtgcttcatcgccaactt 196

>gb|CK701021.1| EST5123 *Zea mays* sperm cell cDNA library *Zea mays* cDNA clone
 Zmsp12688 5', mRNA sequence
 Length = 294

Score = 46.1 bits (23), Expect = 0.70
Identities = 29/31 (93%)
Strand = Plus / Minus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
 |||| |
Sbjct: 81 aaacgccgacagttggcgcgccaggtagggg 51

>gb|CF919842.1| EST4142 *Zea mays* sperm cell cDNA library *Zea mays* cDNA clone Zmsp9991
 5', mRNA sequence
 Length = 690

Score = 46.1 bits (23), Expect = 0.70
Identities = 71/87 (81%)
Strand = Plus / Minus

Query: 1637 agaccatgaggaaccacacccccgaagtcgccaggcgggggtgattgaagacttctacc 1696

||||| ||||||||| || ||||||| ||| | |||||| | ||||| || || |||||||
Sbjct: 143 agacaatgaggaactgcatccccgacgtcacagaggcagtcgtgatcgaggatttctacc 84

Query: 1697 gaggatccaatgactcggctttcgtcc 1723

| || ||||||||||||||| |||||||
Sbjct: 83 gtgggtccaatgactcggccttcgtcc 57

Score = 46.1 bits (23), Expect = 0.70
Identities = 50/59 (84%)
Strand = Plus / Minus

Query: 1426 atgacagtgatattttccattgtcctagggaagacgcaatgcagtggtccgacatct 1484

||||||| ||| || || || ||||||||||| |||| || |||||||||||||||||||
Sbjct: 354 atgacagctacttgctatcgtcctagggtaagatgcgctgcagtggtccgacatct 296

>gb|CA236929.1| SCSBFL5015D04.g Saccharum officinarum FL5 Saccharum hybrid cultivar
(mixed) cDNA clone SCSBFL5015D04 5', mRNA sequence
Length = 923

Score = 46.1 bits (23), Expect = 0.70
Identities = 26/27 (96%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgcgccaggta 76

||||| |||||||||||||||||||
Sbjct: 383 aaacatcgacagctggcgcgccaggta 409

>gb|CA236928.1| SCSBFL5015D03.g Saccharum officinarum FL5 Saccharum hybrid cultivar
(mixed) cDNA clone SCSBFL5015D03 5', mRNA sequence
Length = 730

Score = 46.1 bits (23), Expect = 0.70
Identities = 26/27 (96%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgcgccaggta 76

||||| |||||||||||||||||||
Sbjct: 383 aaacatcgacagctggcgcgccaggta 409

>gb|CD439487.1| EL01N0525E01.b Endosperm_5 Zea mays cDNA, mRNA sequence

Length = 829

Score = 46.1 bits (23), Expect = 0.70
Identities = 29/31 (93%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
||||| ||||||| |||||||||||||||||||
Sbjct: 374 aaacgccgacagttggcgcgccaggtagggg 404

>gb|CD437461.1| EL01N0501C03.b Endosperm_5 Zea mays cDNA, mRNA sequence
Length = 727

Score = 46.1 bits (23), Expect = 0.70
Identities = 29/31 (93%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
||||| ||||||| |||||||||||||||||||
Sbjct: 371 aaacgccgacagttggcgcgccaggtagggg 401

>gb|BE598886.1| PI1_83_C01.b1_A002 Pathogen induced 1 (PI1) Sorghum bicolor cDNA,
mRNA sequence
Length = 465

Score = 46.1 bits (23), Expect = 0.70
Identities = 23/23 (100%)
Strand = Plus / Plus

Query: 63 tggcgcgccaggtagggggtgtg 85
|||||||||||||||||||||
Sbjct: 112 tggcgcgccaggtagggggtgtg 134

>gb|AW066079.1| 687005G08.y1 687 - Early embryo from Delaware Zea mays cDNA, mRNA
sequence
Length = 579

Score = 46.1 bits (23), Expect = 0.70
Identities = 29/31 (93%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80

Score = 44.1 bits (22), Expect = 2.8
Identities = 25/26 (96%)
Strand = Plus / Plus

Query: 153 tgttttgctttggaaccatctcatcc 178
||||| ||||||||||||||||||||
Sbjct: 65 tgttctgctttggaaccatctcatcc 90

>gb|EC102699.1| ACE00018328 1:1 combination of non-normalized and normalized-small
libraries Acanthamoeba castellanii cDNA, mRNA sequence
Length = 503

Score = 44.1 bits (22), Expect = 2.8
Identities = 22/22 (100%)
Strand = Plus / Plus

Query: 780 aggaccgagaacgagagcaagc 801
||||||||||||||||||||||
Sbjct: 417 aggaccgagaacgagagcaagc 438

>gb|CA070197.1| SCSGAD1007H06.b AD1 Saccharum hybrid cultivar SP70-1143 cDNA clone
SCSGAD1007H06 3', mRNA sequence
Length = 552

Score = 44.1 bits (22), Expect = 2.8
Identities = 25/26 (96%)
Strand = Plus / Plus

Query: 55 ccgacagctggcgcgccaggtagggg 80
||||||| ||||||||||||||||||||
Sbjct: 211 ccgacagttggcgcgccaggtagggg 236

Database: /usr/local/blast/db/blastlibs/est_others
Posted date: May 6, 2010 12:23 AM
Number of letters in database: 29,661,423,624
Number of sequences in database: 52,386,385

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: 52386385
Number of Hits to DB: 433,010,743
Number of extensions: 21306668
Number of successful extensions: 5566098
Number of sequences better than 10.0: 84
Number of HSP's gapped: 5566094
Number of HSP's successfully gapped: 106
Length of query: 1868
Length of database: 29,661,423,624
Length adjustment: 23
Effective length of query: 1845
Effective length of database: 28,456,536,769
Effective search space: 52502310338805
Effective search space used: 52502310338805
X1: 11 (21.8 bits)
X2: 15 (29.7 bits)
X3: 50 (99.1 bits)
S1: 12 (24.3 bits)
S2: 22 (44.1 bits)