

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

gb BE598886.1	PI1_83_C01.b1_A002 Pathogen induced 1 (PI1) Sorgh...	46	0.70
gb AW066079.1	687005G08.y1 687 - Early embryo from Delaware Zea...	46	0.70
gb FL163212.1	5748905 CERES-CB5 Zea mays cDNA clone 1154703 5',...	44	2.8
emb CU909173.1	CU909173 Mycelium grown for 48h Podospora anseri...	44	2.8
gb EG169589.1	MSAM269985_1792_2076 LCM-dissected maize inbred l...	44	2.8
gb DW939742.1	MSAM211340_3186_3768 LCM-dissected maize shoot ap...	44	2.8
gb EC102699.1	ACE00018328 1:1 combination of non-normalized and...	44	2.8
gb CA070197.1	SCSGAD1007H06.b AD1 Saccharum hybrid cultivar SP7...	44	2.8

>gb|FL470578.1| 25237854 CERES-CB5 Zea mays cDNA clone 1155571 3', mRNA sequence
Length = 610

Score = 418 bits (211), Expect = e-113
Identities = 506/603 (83%), Gaps = 1/603 (0%)
Strand = Plus / Minus

Query: 979 taatcaccttctacccatcactaatcctccaagcgacctacgccatgccatcaacagccg 1038
||||| ||||| || |||| || ||| ||||| ||| ||||| |||||
Sbjct: 606 taatcaccttctgcccategetcatccccgagcaacctacaccagccatcaacagccg 547

Query: 1039 gcgagacacgcggagctccatcaacgcttcgcgcgaccgatgacacgaaagtgagatagg 1098
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 546 acgagacgcgcggagctccatcaatgcttcgcgcgaccgacggcacgaaagcgagataag 487

Query: 1099 gaaccgagaggagtatgtccgagatcatgccatcctggcatgaagtcatgccacccgagc 1158
| ||| ||||| ||||| || ||||| ||| || ||||| ||||| |||||
Sbjct: 486 gcgccgggaggagtatgaccgggatcatggtgtcccagcttgaagttgcgccacccgagt 427

Query: 1159 tgagtcggttgcgccctcgaccagtgtcccgttcagggacgatcaagatgacacacaac 1218
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 426 tgagtcggttgcgccctcgaccagtggccccgaccgggacggtcgagacgacacaccac 367

Query: 1219 tggtccctccttgggaccgacctcacgaacgccgacatgaagacacgtgcggagtctt 1278
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 366 cagctccctccccgggaccgacctcacgaacgccgacaggaagacacatgcgggtctc 307

Query: 1279 cgcacttactccgtgtctccgggccatccagtgg-cccctaacttcaaggtctccaacgt 1337
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 306 tgcgcttactccgctctccgggccatccagtggcccccaacttcaaagttctcaaacgt 247

Query: 1338 cagcaagtatgagcgcaagcaggacctgggtggctgggttagccatctacacgattgtcac 1397
| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 246 cgacaagtacgagcccaagcagcaccaggggctagttggcgtctacacgaccgccg 187

Query: 1398 atgggcccggagcgacggaggacgtgatgacagtgtattttccattgtcctaggga 1457

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

Sbjct: 186 tcgggtcgtggtggcgacggaagacgtaatgacagcgtatttgcccatcgtcctaggga 127

Query: 1458 agacgcaatgcagtggctccgacatctaccccaacattgcatagacaattggagcgactt 1517

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

Sbjct: 126 tgacgcactgcagtggcttcgacatctgccacgacactgcacggttggggcgactt 67

Query: 1518 cagttggtgcttcacgccaacttcagtcctctttgacaagccggcgagccatggga 1577

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

Sbjct: 66 tagtcggcgtttcatcgccaacttcagtcctctctgacaagccgccgagccatggta 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 acctacgcatgccatcaacagccggcgagacacgaggagctccatcaacgcttcgcgcg 1073

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

Sbjct: 612 acctacaccacgcatcaacagccgacgagacgcgcggagctccatcaatgcttcgcgcg 553

Query: 1074 accgatgacacgaaagtgagatagggaaaccgagaggagtatgtccgagatcatgcatcc 1133

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

Sbjct: 552 accgacggcacgaaagcgagataaggcgccgggaggagtatgaccgggatcatggtgtcc 493

Query: 1134 tggcatgaagtcatgccacccgagctgagtcggttgcggcctcgaccagtgtcccgttcc 1193

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

Sbjct: 492 cagcttgaagttgcgccacccgagttgagtcggttgcggcctcgaccagtggcccgacc 433

Query: 1194 agggacgatcaagatgacacacaactggctcccctccttgggaccgacctcacgaacgcc 1253

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

Sbjct: 432 ggggacggtcgagacgacacaccaccagctcccctccccgggaccgacctcacgaacgcc 373

Query: 1254 gacatgaagacacgtgcgagtccttcgcacttactccgtgtctccgggccatccagtgg- 1312
||||| ||||||| ||||| ||||| || ||||||| ||||||| ||||||| |||||
Sbjct: 372 gacaggaagacacatgcggggtctctgcgcttactccgcgtctccgggccatccagtggc 313

Query: 1313 cccctaacttcaaggtctccaacgtcagcaagtatgagcgcaagcaggacctgggtggct 1372
||||| ||||||| ||||| ||||||| ||||||| ||||| ||||||| ||||| |||||
Sbjct: 312 cccccaacttcaaagtctcaaacgtcgacaagtacgagcccaagcagacccagggggct 253

Query: 1373 ggtagccatctacacgattgtcacatgggccgccggagcgacggaggacgtgatgacag 1432
||| ||| ||||||| ||| ||| ||| ||| ||||||| ||||||| |||||||
Sbjct: 252 agttggccgtctacacgaccgccgctcgggtcgtctggggcgacggaagacgtaatgacag 193

Query: 1433 tgtattttccattgtcctagggcaagacgcaatgcagtgggtccgacatctacccaac 1492
||||| ||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||| |||
Sbjct: 192 cgtatttgcccatgctcctagggcaagacgcaatgcagtgggttcgacatctgccacgac 133

Query: 1493 attgcatagacaattggagcgacttcagttggtgcttcacgccaacttccagtcctct 1552
| ||||| ||| ||||| ||||||| ||| ||| ||| ||| ||||||| ||||||| |||||||
Sbjct: 132 actgcatcgacggttggggcgacttttagtcggcgctttcatcgccaacttccagtcctct 73

Query: 1553 ttgacaagccggcgag-ccatgggacctaaaatccattgggcatcaggcgcatgaaac 1610
||||||| ||||| ||||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 72 ctgacaagccgccgagcccatggtacctcaaatccatcaggcgccaggcgcatgaaac 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 tcgagcagttaatcaccttctacccatcactaatcctccaagcgacctacgcatgccat 1029
||||| ||| ||||||| ||||||| ||||| ||| ||| ||| ||| ||||| |||||
Sbjct: 387 tcgagtagctaatcaccttctgcccatcgtcatccccgagcaacctacaccacgccat 328

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

Query: 1090 tgagataggaaccgagaggagtatgtccgagatcatgccatcctggcatgaagtcacgc 1149
||||| || ||| |||||||| ||| |||||| | ||| || |||||| | ||
Sbjct: 267 cgagataaggcgccgggaggagtatgaccgggatcatggtgtcccagcttgaagttgcgc 208

Query: 1150 cacccgagctgagtcggttgccgacctgaccagtgtcccggtccaggacgatcaagatg 1209
||||||| ||||||| ||||||||||||||||| |||| | |||||| | || ||| |
Sbjct: 207 cacccgagttgagtcggttgccgacctgaccagtggcccgaccggggacggtcgagacg 148

Query: 1210 acacacaactggctccctccttgggaccgacctcacgaacgccgacatgaagacacgtg 1269
|||||| | ||||||||| ||||||||||||||||||||| |||||||| | ||
Sbjct: 147 acacaccaccagctccctccccgggaccgacctcacgaacgccgacaggaagacacatg 88

Query: 1270 cggagtcttcgcacttactccgtgtctccgggccatccagtgg-cccctaacttcaaggt 1328
||| |||| | ||||||||| ||||||||||||||||||||| |||| |||||||| ||
Sbjct: 87 cggggtctctgcgttactccgcgtctccgggccatccagtggcccccaacttcaaagt 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 gacgtgatgacagtgtattttccattgtcctagggcaagacgcaatgcagtggctccga 1479
||||||||||| | |||||| | ||||||||| |||||||| | ||| ||||| |||
Sbjct: 525 gacgtgatgaccgcgtatttaccattgtccttgggcaagatgcgttgcaatggctgcga 466

Query: 1480 catctaccccaacattgcatagacaattggagcgacttcagttggtgcttcatcgccaac 1539
||||||||| |||||||| | || | ||| ||||||||| | |||||| | |||||
Sbjct: 465 catctaccccgacattgcatcgacgactggggcgacttcagtcgacgcttcaccgccaat 406

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

Query: 1600 ggcgatgaaacgctccggttgtaacctcaagaggttttagaccatgaggaaccacaccccc 1659
|| || |||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 345 ggggacaaaactctccggtcatacctcaaaaggttccagaccatgagaaatcgatatcccc 286

Query: 1660 gaagtcgccgaggcgggggtgattgaagacttctaccgaggatccaatgactcggctttc 1719
|| ||| | ||||| ||||| || ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 285 gaggtcacggaggcggccgtgatcgaggacttctacagaggatccaacgactcggctttc 226

Query: 1720 gtccgagccatactccagaaaagcgctcgccacctccgaacacttggtccgggaggcaga 1779
||||||| ||||| || |||| ||||| || ||||| || ||||| ||||| |||||
Sbjct: 225 gtccgagccatattaca-aaaggcgccgactacctccgaggagctgttccgggaagccga 167

Query: 1780 cctctacatcaccacggattaacgggcccaggacctcatcggagg 1824
||||||| ||||| || ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 166 cctctacatcacggcgacgagcgggcccaggacctcatcggagg 122

>gb|FL470559.1| 16105884 CERES-CB6 Zea mays cDNA clone 1165529 3', mRNA sequence
Length = 702

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

Query: 1420 gacgtgatgacagtgtattttccattgtcctagggcaagacgcaatgcagtggctccga 1479
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 686 gacgtgatgaccgcgtatttaccattgtccttgggcaagatgcgttgcaatggctcga 627

Query: 1480 catctaccccaacattgcatagacaattggagcgacttcagttggtgcttcacgccaac 1539
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 626 catctaccccgacattgcatcgacgactggggcgacttcagtcgacgcttcaccgccaat 567

Query: 1540 ttccagtccctctttgacaagccggcgagccatgggacctaaaatccattgggcatcag 1599
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 566 ttctagtccctctccgacaaaccggcacaacatgggacctcaaatccatcaagcgccgg 507

Query: 1600 ggcgatgaaacgctccggttgtaacctcaagaggttttagaccatgaggaaccacaccccc 1659
|| || |||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 506 ggggacaaaactctccggtcatacctcaaaaggttccagaccatgagaaatcgatatcccc 447

Query: 1660 gaagtcgccgaggcgggggtgattgaagacttctaccgaggatccaatgactcggctttc 1719

Sbjct: 446 gaggtcacggaggcgccgtgatcaggacttctacagaggatccaacgactcggtttc 387

Query: 1720 gtccgagccataactccagaaaagcgtcggccacctccgaacacttggttcgggaggcaga 1779

Sbjct: 386 gtccgagccatattaca-aaaggcgccgactacctccgaggagctgttccgggaagccga 328

Query: 1780 cctctacatcaccacggattaacgggcccaggacctcatcgagg 1824

Subjet: 327 cctctacatcaccgccgacgagcgggcccaggacctcatcggagg 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 gacgtgatgacagtgtattttccattgtcctagggcaagacgcaatgcagtggctccga 1479

Sbjct: 540 gacgtgatgaccgcgtattttaccattgtccttgggcaagatgcgttgcaatggctgcga 481

Query: 1480 catctaccccaacattgcatagacaattggagcgcacttcagttggtgcttcacgcgaac 1539

Sbjct: 480 catctaccccgacattgcatcgacgactggggcgacttcagtcgacgcttcaccgccaat 421

Query: 1540 ttccagtcctctttgacaagccggcgccagccatgggacctaaaatccattgggcatcag 1599

Sbjct: 420 ttctagtccctctccgacaaaccggcacaaccatgggacctcaaatccatcaagcgccgg 361

Query: 1600 ggcgatgaaacgctccggttgtaacctcaagaggttttagaccatgaggaaccacaccccc 1659

Objet: 360 ggggacaaaactctccggtcatacctcaaaagggttcagaccatgagaaatcgtatcccc 301

Query: 1660 gaagtcgccgaggcgggggtgattgaagacttctaccgaggatccaatgactcggttttc 1719

Sbjct: 300 gaggtcacggaggcggccgtgatcgaggacttctacagaggatccaacgactcggctttc 241

Query: 1720 gtccgagccatactccagaaaagcgtcggccacctccgaacacttgttccgggaggcaga 1779

Sbjct: 240 gtccgagccatattaca-aaaggcgccgactacctccgaggagctgttccgggaagccga 182

Query: 1780 cctctacatcaccacggattaacgggcccaggacctcatcggagg 1824

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

Sbjct: 181 cctctacatcaccgccgacgagcgggcccaggacctcatcggagg 137

>gb|CF273107.1| EST2669 Zea mays sperm cell cDNA library Zea mays cDNA clone Zmsp7195
5', mRNA sequence

Length = 627

Score = 165 bits (83), Expect = 1e-36

Identities = 304/375 (81%), Gaps = 2/375 (0%)

Strand = Plus / Plus

Query: 1447 gtcctagggcaagacgcaatgcagtggtccgacatctaccccaacattgcatagacaat 1506

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

Sbjct: 187 gtcctcgggcaaggtgcactgcagtggtacaacacttaccccgactgcatcgacgat 246

Query: 1507 tggagcgacttcagttggtgcttcatcgccaacttccagtcctctttgacaagccggcg 1566

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

Sbjct: 247 tggagcgacttcagtcggtgctttatcgccaacttccaatccctctccgacaagccggcg 306

Query: 1567 cagccatgggacctaataatccattgggcatcagggcgatgaaacgctccggttgacctc 1626

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

Sbjct: 307 tagccatgggacctcaaatccatcagcgccgagaggatgagactcttcggtcatacctc 366

Query: 1627 aagaggttttagaccatgaggaaccacacccccgaagtcgccgaggcgggggtgattgaa 1686

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

Sbjct: 367 aagaggtttcagaccatgagaaatcatattccggaggtcgctgaagcagcagtgatcgag 426

Query: 1687 gacttctaccgaggatccaatgactcggttttcgtccgagccatactccagaaaagcgtc 1746

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

Sbjct: 427 gacttctaccggggatctaataatgactcggccttcgtccagccatactaca-aaaggcgcc 485

Query: 1747 ggccacctccgaacacttggtccgggaggcagacctctacatcaccacggattaacgggc 1806

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

Sbjct: 486 gaccacttccgagcagctgtttaaggaggcggacctctacatcaccaccgacgaatgggc 545

Query: 1807 ccagg-acctcatcg 1820

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

Sbjct: 546 ccaggnacctcatcg 560

>gb|CF273097.1| EST2659 Zea mays sperm cell cDNA library Zea mays cDNA clone Zmsp7172
5', mRNA sequence
Length = 689

Score = 123 bits (62), Expect = 4e-24
Identities = 179/218 (82%)
Strand = Plus / Minus

Query: 857 cccgacttcgctcgtgcaatgaacacgccgagtgaagtcggaggggtactggcccagata 916
|||||
Sbjct: 555 cccgacttcgctcgagccatggacacaccgagtgaggtcgggtgggtattggctcggata 496

Query: 917 gctgacggcctcccgcaaccctagacacggaaggctaccggcggtgcttactcgagca 976
|||
Sbjct: 495 gccgatggcctccctggattccggacgctgagggtatcgggcggtgctcacccgagca 436

Query: 977 gttaatcaccttctacccatcactaatcctccaagcgacctacgccatgccatcaacagc 1036
|||
Sbjct: 435 gctaatcatcttctacctctcgctcatcctccgagtgatctacgacatgccatcaacagt 376

Query: 1037 cggcgagacacgcggagctccatcaacgcttcgcgcga 1074
|||
Sbjct: 375 cggcgggacgcatggagctccatcaacgcttcgcgcga 338

Score = 56.0 bits (28), Expect = 7e-04
Identities = 64/76 (84%)
Strand = Plus / Minus

Query: 1313 cccctaacttcaaggtctccaacgtcgacgaagtatgagcgcaagcaggacctgggtggct 1372
|||||
Sbjct: 98 cccctaacttcaaagttctccaacgtcgacaggtatgaacctaaagcaggatccgggaggct 39

Query: 1373 ggtagccatctacac 1388
|||
Sbjct: 38 ggttgccgtctacac 23

>gb|FL455073.1| 16632359 CERES-CB5 Zea mays cDNA clone 1146214 3', mRNA sequence

Length = 337

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

Identities = 195/242 (80%)

Strand = Plus / Minus

```
Query: 886  gagtgaagtcggaggggtactggcccagatagctgacggcctcccgcggaaccctagacac 945
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 334  gagtgaagttggaggagtactggcgcagatagccgacggcctcccgcggaacccagacgc 275
```

```
Query: 946  ggaaggctaccggcggtgcttactcgagcagttaatcaccttctacccatcactaatcc 1005
          ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 274  agaaggttatcggcggctgcttacacaggtggccaatcatcttctacccctcgctcatcc 215
```

```
Query: 1006 tccaagcgacctacgcatgccatcaacagccggcgagacacgcggagctccatcaacgc 1065
          ||| ||||| || ||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 214  tgcgaacgacctgcgtcacacaatcaatagctgacgagacgcacaaagcaccatcatcgc 155
```

```
Query: 1066 ttcgcgcgaccgatgacacgaaagtgagataggaaccgagaggagtatgtccgagatca 1125
          ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 154  ttcacgcgaccgatgaaatgaaatgagataaggcgccgggaggagtacgaccgagatca 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 acctacgcatgccatcaacagccggcgagacacgcggagctccatcaacgcttcgcgcg 1073
          ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 107  acctacaccacgcatcaacagccgacgagacgcgcggagctccatcaatgcttcgcgcg 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

```
Query: 158 tgctttggaaccatctcatccatagcagatgaagagggaactctgcaccgcatagcagat 217
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 77  tgctttggaacgatctcatccatagcagatgaagagggaactctacaccgcattgcagat 18
```

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

Query: 848 aacctgtaccccgacttcgctcgtgcaatgaacacgccgagtgagtcgagggggtactg 907
 ||||| |||||||||||| || || ||||||||||||||||||||||||||||
 Sbjct: 238 aacctgaaccccgacttcgcccgagccatgaacacgccgagtgagtcgagggggtacta 297

```
Query: 968  actcgagcagttaatcaccttctacccatcactaatcctccaagcgacctagccatgcc 1027
           ||| ||||| ||| ||||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 358  acccaagcagcaaccatcttctacctatcgctcaccgcgcgaacgacctagcacgcc 417
```

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

Zmsp4711 5', mRNA sequence
Length = 347

Score = 93.7 bits (47), Expect = 3e-15
Identities = 71/79 (89%)
Strand = Plus / Plus

Query: 31 ggggtgtcggacggactctaaacaccgacagctggcgcgccaggtagggggtgtgtcttt 90
||||||| ||||| | ||||||||||||||||||||||||||||
Sbjct: 74 ggggtgtcggtcggacccaaaacaccgacagctggcgcgccaggtagggggtgtgtcgac 133

Query: 91 gatctgagctagctcaatg 109
|||| ||||||||||||
Sbjct: 134 gatccaagctagctcaatg 152

>gb|EG136737.1| MSAM243415_0331_1740 LCM-dissected maize inbred line Mo17 shoot
apical meristem cDNA Zea mays cDNA, mRNA sequence
Length = 117

Score = 85.7 bits (43), Expect = 8e-13
Identities = 73/83 (87%)
Strand = Plus / Minus

Query: 5 ccaaaagcaccgcaaggggtagccctgggtgtgcggacggactctaaacaccgacagctg 64
||||||| ||||||| || ||||| ||| ||| | |||||||||||||
Sbjct: 117 ccaaaagcaccacaaggggtaaccccggtgcgcggtcgggtcccaaaccgacagctg 58

Query: 65 gcgcgccaggtagggggtgtgtc 87
|| ||||||||||||||||
Sbjct: 57 gcacgccaggtagggggtgtgtc 35

>gb|EG125154.1| MSAM218621_1422_0209 LCM-dissected maize inbred line Mo17 shoot
apical meristem cDNA Zea mays cDNA, mRNA sequence
Length = 106

Score = 85.7 bits (43), Expect = 8e-13
Identities = 61/67 (91%)
Strand = Plus / Plus

Query: 135 cccttcgccccgggactatgttttgctttggaaccatctcatccatagcagatgaagagg 194
|||| ||||||| ||||||||||||||||| ||||||| |||||||||
Sbjct: 34 ccctcgcgcccgatctatgttttgctttggaacaatctcatccgtagcagatgaagaag 93

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 aaacaccgacagctggcgcgccaggtagggggtgtgtctttgatctgagctagctcaatg 109
 |||||
Sbjct: 99 aaacaccgacagctggcgcaccaggtagggggtgtgtcgacgatccaagctagctcaatg 158

Query: 110 accattacctccaaatgaagatcgcccttcgccccgggactatgttttgctttggaacc 169
 |||
Sbjct: 159 gccgtcaccttccacagccagatcacctgtcgtcccggatctgtattctgcttcgggaca 218

Query: 170 atctcatccatagcagatgaagagggaactctgcaccgcatagcagatct 219
 |||||
Sbjct: 219 atctcatctatagcggatgaagagggaattctacaccgcctcgcagatct 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 taccctaaagcaccgcaaggggtagccctgggtgtgcggacggactctaaacaccgacag 61
 |||||
Sbjct: 103 taccctaaagcaccctcgaggggtaacctcgggtgtgcggtcgggtcccaaacaccgacag 44

Query: 62 ctggcgcgccaggtagggggtgtgtc 87
 |||
Sbjct: 43 ctagcgcgccaggtagggggtgtgtc 18

Sbjct: 83 gctttggaacaatctcatccatagcagatgaagatggaattctacaccgcattgcagatc 24

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 atctcatccatagcagatgaagagggaactctgcaccgcatagcagatc 218

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

Sbjct: 27 atctcattcgtagcagatgaagagggaactctacaccgcattgcagatc 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 atctcatccatagcagatgaagagggaactctgcaccgcat 210

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

Sbjct: 112 atctcgtccatagcagatgaagagggaactctacaccgcat 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 tgtccacttcgcccacaaaggagtgacacggattac 393

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

Sbjct: 46 tgtccacttcgtccacaaaggagtgacacggattac 10

>gb|FL476102.1| 2002854 CERES-227 Zea mays cDNA clone 400160 3', mRNA sequence
Length = 555

Score = 63.9 bits (32), Expect = 3e-06
Identities = 53/60 (88%)
Strand = Plus / Minus

Query: 2 tacccaaaagcaccgcaaggggtagccctgggtgtgcggacggactctaaacaccgacag 61
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 238 tacccaaaagcactgcgaggggtaaccccgggtgtgcggtcgggctccaaacaccgacag 179

>gb|FL307895.1| 2966196 CERES-227 Zea mays cDNA clone 507820 5', mRNA sequence
Length = 463

Score = 63.9 bits (32), Expect = 3e-06
Identities = 53/60 (88%)
Strand = Plus / Minus

Query: 2 tacccaaaagcaccgcaaggggtagccctgggtgtgcggacggactctaaacaccgacag 61
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 389 tacccaaaagcactgcgaggggtaaccccgggtgtgcggtcgggctccaaacaccgacag 330

>gb|EG176217.1| MSAM007276_3034_2445 LCM-dissected maize inbred line Mo17 shoot
apical meristem cDNA Zea mays cDNA, mRNA sequence
Length = 96

Score = 61.9 bits (31), Expect = 1e-05
Identities = 43/47 (91%)
Strand = Plus / Minus

Query: 164 ggaaccatctcatccatagcagatgaagagggaactctgcaccgcat 210
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 95 ggaacaatctcatcggtagcagatgaagagggaactctacaccgcat 49

>gb|DW870027.1| MSAM045979_3454_2175 LCM-dissected maize shoot apical meristem cDNA
Zea mays cDNA, mRNA sequence
Length = 127

Score = 61.9 bits (31), Expect = 1e-05
Identities = 37/39 (94%)
Strand = Plus / Minus

Query: 180 tagcagatgaagagggaactctgcaccgcatagcagatc 218
|||||||
Sbjct: 123 tagcagatgaagagggaactctacaccgattgcagatc 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 ctaaaccacgacagctggcgccaggtagggg 80
|||||||
Sbjct: 297 ctaaaccacgacagctggcggtccaggtagggg 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 aacacgccgagcgaagtcggaggggtactagctccgatatagctga 82

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

Strand = Plus / Plus

```
Query: 1012 cgacctacgccatgccatcaacagccggcgagacacgcggagctccatcaacgcttcgcg 1071
          ||||| ||||| || |||||||||||||||| || ||||||| | ||||||||| |||||||||
Sbjct: 173 cgacatacgacacgccatcaacagccgtcgggacacgtgaagctccataaacgcttcgcg 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 accgacagctggcgccaggtaggggtgtgtctttgatctgagctagctc 105
          ||||||||||||| ||||||||||||| ||||| ||||| |||||||||
Sbjct: 423 accgacagctggcacgccaggtaggggtgtgtcactgatccaagctagctc 372
```

>gb|EG131418.1| MSAM183153_0247_2918 LCM-dissected maize inbred line Mo17 shoot
apical meristem cDNA Zea mays cDNA, mRNA sequence
Length = 109

Score = 54.0 bits (27), Expect = 0.003
Identities = 56/63 (88%), Gaps = 2/63 (3%)
Strand = Plus / Minus

Query: 158 tgctttggaaccatctc-atccatagcagatgaagagggaactctgc-accgcatagcag 215
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 83 tgcttcggaacaatctctatccgtagcagatgaagagggaactctactaccgattgcag 24

Query: 216 atc 218
|||
Sbjct: 23 atc 21

>gb|EG278067.1| MSAM237051_2164_0313 LCM-dissected maize inbred line Mo17 shoot
apical meristem cDNA Zea mays cDNA, mRNA sequence
Length = 113

Score = 54.0 bits (27), Expect = 0.003
Identities = 30/31 (96%)
Strand = Plus / Minus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 61 aaacgccgacagctggcgcgccaggtagggg 31

>gb|DW974630.1| MSAM293083_3262_0305 LCM-dissected maize shoot apical meristem
cDNA Zea mays cDNA, mRNA sequence
Length = 137

Score = 54.0 bits (27), Expect = 0.003
Identities = 52/59 (88%), Gaps = 1/59 (1%)
Strand = Plus / Minus

Query: 2 tacccaaaagcaccgcaagggtagccctgggtgtgcggacggactctaaacaccgaca 60
||||||| ||||| || || ||||| ||||| || || ||||| ||||| ||||| |||||
Sbjct: 92 tacccaaaacaccgcaaagg-taacctgggtgtgcagtcgggctctaaacaccgaca 35

>gb|DW884389.1| MSAM085099_3297_2244 LCM-dissected maize shoot apical meristem cDNA

Zea mays cDNA, mRNA sequence
Length = 106

Score = 54.0 bits (27), Expect = 0.003
Identities = 36/39 (92%)
Strand = Plus / Minus

Query: 180 tagcagatgaagaggggaactctgcaccgcatagcagatc 218
||||||| ||||| ||||| |||||
Sbjct: 102 tagcagatgaagaggggactctacaccgcattgcagatc 64

>gb|CA129139.1| SCRFLR2034H10.g LR2 Saccharum hybrid cultivar SP80-3280 cDNA clone
SCRFLR2034H10 5', mRNA sequence
Length = 611

Score = 54.0 bits (27), Expect = 0.003
Identities = 30/31 (96%)
Strand = Plus / Plus

Query: 50 aaacaccgacagctggcgcgccaggtagggg 80
||||| ||||||| ||||||| |||||||
Sbjct: 440 aaacatcgacagctggcgcgccaggtagggg 470

>gb|DW945646.1| MSAM224719_2697_2993 LCM-dissected maize shoot apical meristem cDNA
Zea mays cDNA, mRNA sequence
Length = 101

Score = 52.0 bits (26), Expect = 0.011
Identities = 60/70 (85%), Gaps = 1/70 (1%)
Strand = Plus / Plus

Query: 103 ctcaatgaccattacctccaaatgcaagatcgccctt-cgccccgggactatgttttget 161
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 19 ctcaatggccatcaccttcaagtgaagatcgcccttttcgccccgaaactatgttctgct 78

Query: 162 ttggaaccat 171
|||||||
Sbjct: 79 ttggaaccat 88

>gb|CA179013.1| SCSGST1069C02.b ST1 Saccharum hybrid cultivar SP80-3280 cDNA clone
SCSGST1069C02 3', mRNA sequence
Length = 726

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 taccctaaagcaccgcaagggtag-ccctgggtgtgcggacggactctaaacaccgaca 60
|||||||

Sbjct: 390 tacccaaaagcactgcgaggggtaaaccgccggtgtgcggtcgggtccaaacaccgaca 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 gacttctaccgaggatccaatgactcggcttttcgtccgagc 1727
||||||| ||||||||| | |||||||||
Sbjct: 213 gacttctaccatggatccaatgactcagggttttcgtccgagc 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 caccgacagctggcgccaggtagggg 80
||||||| |||||||||
Sbjct: 1 caccgacagttggcgccaggtagggg 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 ctggcgcgccaggtaggggtgtg 85
|||||
Sbjct: 347 ctggcgcgccaggtaggggtgtg 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 aaacgccgacagttggcgcgccaggtagggg 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 aaacgccgacagttggcgcgccaggtagggg 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 aaagccgacagttggcgcgccaggtagggg 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 aaagccgacagttggcgcgccaggtagggg 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 aaagccgacagttggcgcgccaggtagggg 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 aaagccgacagttggcgcgccaggtagggg 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 aaagccgacagttggcgcgccaggtagggg 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 aaagccgacagttggcgcgccaggtagggg 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 aaagccgacagttggcgcgccaggtagggg 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 aaagccgacagttggcgcgccaggtagggg 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 aaaagcaccgcaaggggtagccctgggtgtgcggacggactctaaacaccgacag 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 aaaagcaccgcaaggggtagccctgggtgtgcggacggactctaaacaccgacag 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 cttcagttggtgcttcacgccaactt 1541
 |||||
Sbjct: 233 cttcagttggtgcttgatcgccaactt 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 cttcagttggtgcttcacgccaactt 1541
 |||||
Sbjct: 222 cttcagttggtgcttgatcgccaactt 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 agaccatgaggaaccacacccccgaagtcgccgaggcggggtgattgaagacttctacc 1696

Sbjct: 143 agacaatgaggaactgcattccccgacgtcacagaggcagtcgtgatcgaggatttctacc 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 atgacagtgtatccccattgtcctagggcaagacgcaatgcagtggctccgacatct 1484

Sbjct: 354 atgacagcgtaacttgccatcgctcctagggtgaagatgcgcgtgcagtggctccgacatct 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

||||| ||||||| ||||||||||||||||
Sbjct: 479 aaacgccgacagttggcgcgccaggtagggg 509

>gb|FL163212.1| 5748905 CERES-CB5 Zea mays cDNA clone 1154703 5', mRNA sequence
Length = 317

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

Query: 55 ccgacagctggcgcgccaggtagggg 80
||||||| ||||||||||||||||
Sbjct: 32 ccgacagttggcgcgccaggtagggg 7

>emb|CU909173.1| CU909173 Mycelium grown for 48h Podospora anserina cDNA clone
HH0AC19CB02., mRNA sequence
Length = 1279

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

Query: 695 gaagctttagaagtaggaaaaa 716
||||||||| ||||||||||||
Sbjct: 36 gaagctttagaagtaggaaaaa 15

>gb|EG169589.1| MSAM269985_1792_2076 LCM-dissected maize inbred line Mo17 shoot
apical meristem cDNA Zea mays cDNA, mRNA sequence
Length = 117

Score = 44.1 bits (22), Expect = 2.8
Identities = 46/54 (85%)
Strand = Plus / Plus

Query: 7 aaaagcaccgcaagggtagccctgggtgtgcggacggactctaacaccgaca 60
||||||| | ||||| | ||||||| ||| ||||| | |||||||||
Sbjct: 5 aaaagcacctcgaggggcaaccctgggtgcgcggtcggacccaaaacaccgaca 58

>gb|DW939742.1| MSAM211340_3186_3768 LCM-dissected maize shoot apical meristem cDNA
Zea mays cDNA, mRNA sequence
Length = 94

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 ccgacagtggcgcgccaggtagggg 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)