Supplementary Figure 1. Gene Prediction in region 15 kb upstream of ZmPEPC1

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fgenesh  Fri Jun 25 14:52:18 BST 2010
 FGENESH 1.1 Prediction of potential genes in Monocot genomic DNA
 Time    :   Fri Jun 25 14:52:18 2010
 Seq name: 9 dna:chromosome chromosome:AGPv1:9:59729275:59750163:1
 Length of sequence: 20889
 Number of predicted genes 3 in +chain 2 in -chain 1
 Number of predicted exons 14 in +chain 12 in -chain 2
 Positions of predicted genes and exons:
   G Str    Feature     Start      End      Score        ORF         Length
     1+      1CDSf       46-       867      49.36       46-867        822
     1+      2CDSl       942-      1688     35.11      942-1688       747
     1+      PolA        1736               -1.56

     2-      PolA        1848
     2-      1CDSl       2603-     3086     15.1      2603-3085       483
     2-      2CDSf       3445-     6557     156.73    3447-6557       3111
     2-      TSS         6933               -3.78

     3+      TSS        14107               -4.48
     3+      1CDSf      15359-     15538    15.95    15359-15538      180
     3+      2CDSi      15646-     16040    54.86    15646-16038      393
     3+      3CDSi      16156-     16240    20.09    16157-16240      84
     3+      4CDSi      17131-     17353    22.14    17131-17352      222
     3+      5CDSi      17802-     17905    9.54     17804-17905      102
     3+      6CDSi      18032-     18122    6.66     18032-18121      90
     3+      7CDSi      18260-     18414    10.63    18262-18414      153
     3+      8CDSi      18511-     19509    124.51   18511-19509      999
     3+      9CDSi      19607-     19993    49.73    19607-19993      387
     3+      10CDSl     20102-     20395    39.05    20102-20395      294
     3+      PolA       20592               0.64
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Supplementary Figure 2

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Predicted protein(s):
> FGENESH:   1   2 exon (s)     46  -   1688   522 aa, chain +
MTEALNEDEKEPSKKKIPKKRKASSPKQKISDEEETPASPSAPDVEEILKVMNESLPAKL
SPLGPQLTKFFQKEKEPEKTKKTAKAKRQRIITVTEVIDKTPPRASAQKTPVAEEKTSIE
ITPSEVAAAEAASVEDLNLESTIEDIDKILLDMATEEAATAAEEAMAAVPGKEKEIVDEA
SEDEAFMFQNLVGEKLSKPEIEELKEYAKSCGYKPGALLFGGIDDEKLDCIQDQTGAKVI
GTLSKSIGFPKLETDISRYRRQHIVGSLFYSNFKTMLLSKALKMQQDFEDKKHEVIIENL
ESKIKEQSAAIEKKNFELQATEGLLAEAEAKITELNTKLLCQSEQFEQEKQELKAKLETE
AQQNSDLKKLLAGLQEKCLEFSNKCIQRLRKIFHSVGASSEKFTPSAEDLPKTFEHIEGE
IDELDEVIAGHGDFCAWVASRGTAAAFLKAGCDHGKIVNRPNFTLSPSILDDIPDLARSI
SNRFVKMIWTKGGREKAGDEARSHLEPVRNHTFCLPLPSSSI
> FGENESH:   2   2 exon (s)   2603  -   6557  1198 aa, chain -
MASFNDQAGAASDPKLVLPITGGSCSEPANKKQKKEAQRRVQHVGVQGPFIKSRWSHIPI
TFSQEDLQLKDYTHNDAMVISCVIKGFLVHNVLVDTGSAADIIFAKAFRQMQEPEDKIHD
ATHPLCGFGGRQIVALGKITMSVTFGFINNTRTEQVVFDIVDMEYPYNAIIGRGTLNAFE
AILHPAYLCMKIPSDQGPIAIHGSQEAARRAKGNWTDSKAIHNIDGAEACEQYKFRREKA
ASADQPKPMLLCEDIAEQKVLLGSQLSEEQEKTLIRFLFNNKDVFAWSANDLCGVNRDVI
EHSLNVDPSFRPRKQRLRKMSDDKAEGARNEVKRLLSAGVIREVKYPEWLANTVMVKKAN
GEWRMCIDFTDLNKACPKDEFPLPRIDSLVDAAASSELMSLLDCYSGYHQIWMKKEDEPK
TSFITPSGTYCYLRMPEGLKNAGGSFSRMTAKVLQSQIGRNVLTYVDEIIVKSTKQENHI
ADLQETFASFRQAGLKLNPEKCVFGVKKGKFLGCLVSTKGIEANPSKIEAILRMEPPTTK
KGAQRLTGRLASLNRFISRSAERNLPFFEVLKSAEVFQWGPSQQKAFEELKQYLIDLTTL
TPPTPGAPLLLYVAASHSAVSAALVQEKLDGQVKKQVPVYFVSEVLSISKKNYTELEKVL
YAVLMASRKLRHYFQAYNIVVPSSQPLKDIMRNREATGRIGKWAAELNEFCIDYVHRSSI
QSQALADFIADWTPGAQDEEINKDAEVWTVFWDGSWGTFGAGAAAVLVSPSKVKTCYAAR
LDFSCTNNITEYEALLLGLRKLKAMGIRRAILKTDSQVVSGHIDKSCKAKDPKLEKYLDM
VRRVEASFEGFSVKNIPRGQNEHADLLAKSAAQGLPLPSDVFFETIKAPSVELLERAVLN
ISPVYSEDWRTEIISYLQGKFLSDDETYNRRIEARARPYVMIEGELYKHGVCAPLLKCLS
RTEGIELMKEIHAGLCESHIGSRPLLGKVFRQGFYWPKAASDAAELVQKCEGCQKCARDQ
KQPSSLTQLIQPIWPLQRGKWPDQLTKVVWSHNTTTSRSTGFTPFKLLFGDEAITPEEAK
TGSIRVVASSESGSEDAYSMEKDALEGIRLQAVENINKYQAETIKWRDRKVRLKNIEPGH
LVLRRVANPDTVGKLQLKWEGPFLVASSSRPGSYRLKDMDGNDIPRSWNADELRRYYV
> FGENESH:   3  10 exon (s)  15359  -  20395   970 aa, chain +
MASTKAPGPGEKHHSIDAQLRQLVPGKVSEDDKLIEYDALLVDRFLNILQDLHGPSLREF
VQECYEVSADYEGKGDTTKLGELGAKLTGLAPADAILVASSILHMLNLANLAEEVQIAHR
RRNSKLKKGGFADEGSATTESDIEETLKRLVSEVGKSPEEVFEALKNQTVDLVFTAHPTQ
SARRSLLQKNARIRNCLTQLNAKDITDDDKQELDEALQREIQAAFRTDEIRRAQPTPQDE
MRYGMSYIHETVWKGVPKFLRRVDTALKNIGINERLPYNVSLIRFSSWMGGDRDGNPRVT
PEVTRDVCLLARMMAANLYIDQIEELMFELSMWRCNDELRVRAEELHSSSGSKVTKYYIE
FWKQIPPNEPYRVILGHVRDKLYNTRERARHLLASGVSEISAESSFTSIEEFLEPLELCY
KSLCDCGDKAIADGSLLDLLRQVFTFGLSLVKLDIRQESERHTDVIDAITTHLGIGSYRE
WPEDKRQEWLLSELRGKRPLLPPDLPQTDEIADVIGAFHVLAELPPDSFGPYIISMATAP
SDVLAVELLQRECGVRQPLPVVPLFERLADLQSAPASVERLFSVDWYMDRIKGKQQVMVG
YSDSGKDAGRLSAAWQLYRAQEEMAQVAKRYGVKLTLFHGRGGTVGRGGGPTHLAILSQP
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PDTINGSIRVTVQGEVIEFCFGEEHLCFQTLQRFTAATLEHGMHPPVSPKPEWRKLMDEM
AVVATEEYRSVVVKEARFVEYFRSATPETEYGRMNIGSRPAKRRPGGGITTLRAIPWIFS
WTQTRFHLPVWLGVGAAFKFAIDKDVRNFQVLKEMYNEWPFFRVTLDLLEMVFAKGDPGI
AGLYDELLVAEELKPFGKQLRDKYVETQQLLLQIAGHKDILEGDPFLKQGLVLRNPYITT
LNVFQAYTLKRIRDPNFKVTPQPPLSKEFADENKPAGLVKLNPASEYPPGLEDTLILTMK
GIAAGMQNTG

Supplementary Figure 3. Gene Prediction in region 50 kb upstream of ZmPEPC1

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fgenesh  Fri Jun 25 14:54:29 BST 2010
 FGENESH 1.1 Prediction of potential genes in Monocot genomic DNA
 Time    :   Fri Jun 25 14:54:30 2010
 Seq name: 9 dna:chromosome chromosome:AGPv1:9:59694275:59750163:1
 Length of sequence: 55889
 Number of predicted genes 8 in +chain 7 in -chain 1
 Number of predicted exons 35 in +chain 33 in -chain 2
 Positions of predicted genes and exons:
   G Str      Feature    Start     End      Score          ORF           Length

     1+         TSS       3327               -1.68
     1+        1CDSf      5120     5296      4.31       5120-5296         177
     1+        2CDSi      5310     5372      1.38       5310-5372          63
     1+        3CDSi      5487     5768     20.58       5487-5768         282
     1+        4CDSl      7372     7461      3.39       7372-7461          90
     1+         PolA      7484                0.64

     2+         TSS       8734               -1.68
     2+        1CDSf      9384    11747    130.81      9384-11747        2364
     2+        2CDSi     11782    11938     10.52     11782-11937         156
     2+        3CDSi     12065    13041     43.04     12067-13041         975
     2+        4CDSl     13164    14795     79.04     13164-14795        1632
     2+         PolA     15421                0.64

     3+         TSS      16511               -1.68
     3+        1CDSf     17146    17171      0.81     17146-17169          24
     3+        2CDSi     17747    17877       7.4     17748-17876         129
     3+        3CDSi     17936    18057      1.68     17938-18057         120
     3+        4CDSi     18609    18794      4.63     18609-18794         186
     3+        5CDSi     18867    18936     12.59     18867-18935          69
     3+        6CDSi     19415    19539      4.98     19417-19539         123
     3+        7CDSl     19544    19675     -3.45     19544-19675         132
     3+         PolA     19983                0.64

     4+         TSS      21769               -2.48
     4+        1CDSf     22615    22924      9.87     22615-22923         309
     4+        2CDSl     22979    23067      -2.5     22981-23067          87
     4+         PolA     23456                0.64

     5+         TSS      28343               -6.58
     5+        1CDSf     29814    30291     26.59     29814-30290         477
     5+        2CDSl     30432    30577      1.77     30434-30577         144
     5+         PolA     32993                0.64

     6+         TSS      33642               -0.98
     6+        1CDSf     33835    34119     21.07     33835-34119         285
     6+        2CDSi     34272    34788     10.93     34272-34787         516
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6+	3CDSi	34912	35867	51.95	34914-35867	954
6+	4CDSl	35942	36688	35.11	35942-36688	747
6+	PolA	36736		-1.56		
7-	PolA	36848		-1.56		
7-	1CDSl	37603	38086	15.1	37603-38085	483
7-	2CDSf	38445	41557	156.73	38447-41557	3111
7-	TSS	41933		-3.78		
8+	TSS	49107		-4.48		
8+	1CDSf	50359	50538	15.95	50359-50538	180
8+	2CDSi	50646	51040	54.86	50646-51038	393
8+	3CDSi	51156	51240	20.09	51157-51240	84
8+	4CDSi	52131	52353	22.14	52131-52352	222
8+	5CDSi	52802	52905	9.54	52804-52905	102
8+	6CDSi	53032	53122	6.66	53032-53121	90
8+	7CDSi	53260	53414	10.63	53262-53414	153
8+	8CDSi	53511	54509	124.51	53511-54509	999
8+	9CDSi	54607	54993	49.73	54607-54993	387
8+	10CDSl	55102	55395	39.05	55102-55395	294
8+	PolA	55592		0.64		

Supplementary Figure 4

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Predicted protein(s):
> FGENESH:   1   4 exon (s)   5120  -   7461   203 aa, chain +
MLQQQQQASKSLASAWRGGVLEQRSVRDLMSGGADEETRRSWSCARLWLLVVCALTSLSS
PSPPGSPTTPTEDSRPYMLEGAFTHQDFAGHKGTIRTGDVQWMTAGRGIVHSEMPAGDDV
HKGLQLWINLSSKYKMIEPQYQELERKDISRGESENGGVEALGVATPVYTHPHHEAMLRR
LSDATMEQSNNSDSSIDERSIQP
> FGENESH:   2   4 exon (s)   9384  -  14795  1709 aa, chain +
MDPKGKGIVINDKEKESFVNEPKDDKPTDSGSGQRRKEGKKKKTRRIKEIVYYDSDESTS
SQKDEDHNDYERRKPVNSNFSFDYSRIPQSSHSHLLSIPLGKPPHFDGEDYGFWSHKMRS
HLFSLHPSIWEIVESGMHFDSSDSPMFINEQIHKNAQATTVLLASLCRNEYHKVSGLDNA
KQIWDTLKISHEGNDVTLLTKMELVEGELGRFAMIRGEEPTQTYNRLKTLINKIRSYGST
RWTDHDVVRLMLRSFTVLDPHLVNNIRENPRYTKMSPEEVLGKFVSGRMMIKEARYVDDA
LNGPINEPQPLALKATRSKEALPSKVAQIEAAGLNDEEMALIIKRFKTALNGRKGQPSKT
KTKGKRSCFKCGKLGHFIANCPDNESDQEKGNKREKKKQYKKAKGEAHLGKEWDSDCSSS
DSDNEGLAATAFNKSALFPNERLTCLMAREKKVSTQDSTYASSSDSESSDDDIDYSCLFK
GLDRSKIDKINELIDALNEKDRLLEKQEDLLYDEHDKFVEAQKSYALEVKRNEMLSYELS
TCHETISTLQGVNNDLNAKLEVANKSNSCVEHVKICTRCKDFDVDACSEHLVLISKLNKE
VASLNAQLKTSKNEVDKIKFARDAYTVGRHPSIKDGLGFKREAKNLTSHKAPIFVKEKGK
APMASNAKKNHAFMYYDRRNARNAYNDIDSHVYDSHAMFASSSSYKHDRDMPRRNIAHVP
RKNVIHAPRKVENEPSIIYCALNTSFAICRKDRKIVARKLGAKCKGDRTCIWVPKDICAN
LAGPNMSWVYASGGSSWIIDSGCTNHMTGEKKMFTSYVKNKDSQDSIIFGDGNQGKVKGL
DVSVFRRSDGSLAFKGVLDGKLYLVDFAKEEAGLDACLMAKTCMGWLWHRRLAHVGMKNL
HKLLKGEHVIGLTNVQFEKDRPCAACQAGKQVGGAHHSKNVMTTSRPLELLHMDLFGPVA
YLSIGGSKYGLVIVDDFSRFTWVFFLQDKSETQGTLKRFLRRAQNEFELKVKKIRSDNGS
EFKNLQVEEFLEEEGIKHEFSAPYTPQQNGVVERKNRTLIDMARTMLGEFKTPECFWTEA
VNTACHAINRVYLHRLLKKTSYELLTGNKPNVSYFRVFGSKCYILVKKGRNSKFAPKAVE
GFLLGFMTSNTQGRLRKSSNKSIGVLAGYNENIGDMEKVAAPGTQVGQDHPSSSIMVNPP
TQDDEQVHHKEACDQGGAQDDQVIEEEAHPAPPTQVRAMIQRDHPVDQILGDISKGVTTR
SRLVNFCEHYSFVSSIEPFRVEEALLDPDWVLAMQEELNNFKRNEVWTLVPRPKQNVVGT
KWVFRNKQDEHGVVTRNKARLVAKGYAQVAGLDFEETFAPVARLESIRILLAYAAHHSFR
LFQMDVKSAFLNGPIKEEVYVEQPPGFEDERYPDHVCKLSKALYGLKQAPRAWYECLRDF
LIANAFKVGKADPTLFTKTCNGDLFVCQIYVDDIIFGSTNQKSCEEFSRVMTQKFEMSMM
GELNYFLGFQVKQLKDGTFISQTKYTQDLLKRFGMKDAKPAKTPMGTDGHTDLNKGGKSV
DQKAYRSMIGSLLYLCASRPDIMLSVCMCARFQSDPKECHLVAVKRILRYLVATPCFGLW
YPKGSTFDLVGYSDSDYAGCKVDRKSTSGTCQFLGRSLVSWNSKKQTSVALSTAEARVCC
RRTVLRATTLDEANPQGLWLQSEQSPTPM
> FGENESH:   3   7 exon (s)  17146  -  19675   263 aa, chain +
MGANCSTGFEVQMLIPICLTLTLNPAENIQDANMEEQQSSLVDGLKTPTTVAGKLFLLKI
KNPQPWSACPTLHPIIIVTCGSVVMEITNLLSVTHNVTKELIKYHSQTLGYVIGGTNMRS
DTNHLTEGINILIATLDRLLDHLQNTGSFKYKELKSTKKVMPDDKLAEFALLDPKPPRGV
LKDVAGCDNAKQEIREFVHLFKNPKKYEDFGAKIPKGALLVILGHGSLCLPKLQQESGVP
FFVYFQFKFYGNVGLCWTIQATT
> FGENESH:   4   2 exon (s)  22615  -  23067   132 aa, chain +
MENKRLELGEIKRKATNQGQARSSTRPRYATPQGTPAHGSPRQQSQQVQSTPQASISVGL
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VAPNASTNGSCFKCGQVGHYTNYCPNKAPYTTPASMKQGQVSGEAEPEGPKYLEEVPREA
EEASEEGNEQQN
> FGENESH:   5   2 exon (s)  29814  -  30577   207 aa, chain +
MALFIKLRRFQYISFASGSSGLGIDKRHHGCRSHVLPGVEEVLRTVVALSDLIKNLPRSR
PFIFKASLLNVVVNPVEPLNKCIKVLLLLLEGSLVSENARLALALVFFFLDGVPQVPPSL
LPRGGVSTKQALSGTTSESKPSSIEELLKSSSRRSRMDIGGTPGPRDYGIGLILANGAEF
AGLLGEEVEGAKSDLAAWNESLTPGGR
> FGENESH:   6   4 exon (s)  33835  -  36688   834 aa, chain +
MARVRSTARVEREGDEADGSETVPISEAMQRSGLVTSEKIPSEDAEQAEQAMAEAEEEDI
EETDPEDDYRIAMPSKPSHLDFGKSTVSKADLSKMVLKRFGIYFHQLTPNAIVRLNVYIW
ALRSQAVEPFADSFCRVHELHYQTKARKDGLHDNFGCYNFAYRKTTKFPVISYRSKWAAG
WKSEWFYVKVDDDKEKLVQSPLELIFGETRPRCNMTPEGPTQQALNEFRIIAEHISTRDL
VQEFLAFKVFPSLKEWEMPKLKGEKKEEDQLMTAAFGTRPKRRLNRVLDALGFEYPDYEN
LNKGVGGQKRKRMTEALNEDEKEPSKKKIPKKRKASSPKQKISDEEETPASPSAPDVEEI
LKVMNESLPAKLSPLGPQLTKFFQKEKEPEKTKKTAKAKRQRIITVTEVIDKTPPRASAQ
KTPVAEEKTSIEITPSEVAAAEAASVEDLNLESTIEDIDKILLDMATEEAATAAEEAMAA
VPGKEKEIVDEASEDEAFMFQNLVGEKLSKPEIEELKEYAKSCGYKPGALLFGGIDDEKL
DCIQDQTGAKVIGTLSKSIGFPKLETDISRYRRQHIVGSLFYSNFKTMLLSKALKMQQDF
EDKKHEVIIENLESKIKEQSAAIEKKNFELQATEGLLAEAEAKITELNTKLLCQSEQFEQ
EKQELKAKLETEAQQNSDLKKLLAGLQEKCLEFSNKCIQRLRKIFHSVGASSEKFTPSAE
DLPKTFEHIEGEIDELDEVIAGHGDFCAWVASRGTAAAFLKAGCDHGKIVNRPNFTLSPS
ILDDIPDLARSISNRFVKMIWTKGGREKAGDEARSHLEPVRNHTFCLPLPSSSI
> FGENESH:   7   2 exon (s)  37603  -  41557  1198 aa, chain -
MASFNDQAGAASDPKLVLPITGGSCSEPANKKQKKEAQRRVQHVGVQGPFIKSRWSHIPI
TFSQEDLQLKDYTHNDAMVISCVIKGFLVHNVLVDTGSAADIIFAKAFRQMQEPEDKIHD
ATHPLCGFGGRQIVALGKITMSVTFGFINNTRTEQVVFDIVDMEYPYNAIIGRGTLNAFE
AILHPAYLCMKIPSDQGPIAIHGSQEAARRAKGNWTDSKAIHNIDGAEACEQYKFRREKA
ASADQPKPMLLCEDIAEQKVLLGSQLSEEQEKTLIRFLFNNKDVFAWSANDLCGVNRDVI
EHSLNVDPSFRPRKQRLRKMSDDKAEGARNEVKRLLSAGVIREVKYPEWLANTVMVKKAN
GEWRMCIDFTDLNKACPKDEFPLPRIDSLVDAAASSELMSLLDCYSGYHQIWMKKEDEPK
TSFITPSGTYCYLRMPEGLKNAGGSFSRMTAKVLQSQIGRNVLTYVDEIIVKSTKQENHI
ADLQETFASFRQAGLKLNPEKCVFGVKKGKFLGCLVSTKGIEANPSKIEAILRMEPPTTK
KGAQRLTGRLASLNRFISRSAERNLPFFEVLKSAEVFQWGPSQQKAFEELKQYLIDLTTL
TPPTPGAPLLLYVAASHSAVSAALVQEKLDGQVKKQVPVYFVSEVLSISKKNYTELEKVL
YAVLMASRKLRHYFQAYNIVVPSSQPLKDIMRNREATGRIGKWAAELNEFCIDYVHRSSI
QSQALADFIADWTPGAQDEEINKDAEVWTVFWDGSWGTFGAGAAAVLVSPSKVKTCYAAR
LDFSCTNNITEYEALLLGLRKLKAMGIRRAILKTDSQVVSGHIDKSCKAKDPKLEKYLDM
VRRVEASFEGFSVKNIPRGQNEHADLLAKSAAQGLPLPSDVFFETIKAPSVELLERAVLN
ISPVYSEDWRTEIISYLQGKFLSDDETYNRRIEARARPYVMIEGELYKHGVCAPLLKCLS
RTEGIELMKEIHAGLCESHIGSRPLLGKVFRQGFYWPKAASDAAELVQKCEGCQKCARDQ
KQPSSLTQLIQPIWPLQRGKWPDQLTKVVWSHNTTTSRSTGFTPFKLLFGDEAITPEEAK
TGSIRVVASSESGSEDAYSMEKDALEGIRLQAVENINKYQAETIKWRDRKVRLKNIEPGH
LVLRRVANPDTVGKLQLKWEGPFLVASSSRPGSYRLKDMDGNDIPRSWNADELRRYYV
> FGENESH:   8  10 exon (s)  50359  -  55395   970 aa, chain +
MASTKAPGPGEKHHSIDAQLRQLVPGKVSEDDKLIEYDALLVDRFLNILQDLHGPSLREF
VQECYEVSADYEGKGDTTKLGELGAKLTGLAPADAILVASSILHMLNLANLAEEVQIAHR
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RRNSKLKKGGFADEGSATTESDIEETLKRLVSEVGKSPEEVFEALKNQTVDLVFTAHPTQ
SARRSLLQKNARIRNCLTQLNAKDITDDDKQELDEALQREIQAAFRTDEIRRAQPTPQDE
MRYGMSYIHETVWKGVPKFLRRVDTALKNIGINERLPYNVSLIRFSSWMGGDRDGNPRVT
PEVTRDVCLLARMMAANLYIDQIEELMFELSMWRCNDELRVRAEELHSSSGSKVTKYYIE
FWKQIPPNEPYRVILGHVRDKLYNTRERARHLLASGVSEISAESSFTSIEEFLEPLELCY
KSLCDCGDKAIADGSLLDLLRQVFTFGLSLVKLDIRQESERHTDVIDAITTHLGIGSYRE
WPEDKRQEWLLSELRGKRPLLPPDLPQTDEIADVIGAFHVLAELPPDSFGPYIISMATAP
SDVLAVELLQRECGVRQPLPVVPLFERLADLQSAPASVERLFSVDWYMDRIKGKQQVMVG
YSDSGKDAGRLSAAWQLYRAQEEMAQVAKRYGVKLTLFHGRGGTVGRGGGPTHLAILSQP
PDTINGSIRVTVQGEVIEFCFGEEHLCFQTLQRFTAATLEHGMHPPVSPKPEWRKLMDEM
AVVATEEYRSVVVKEARFVEYFRSATPETEYGRMNIGSRPAKRRPGGGITTLRAIPWIFS
WTQTRFHLPVWLGVGAAFKFAIDKDVRNFQVLKEMYNEWPFFRVTLDLLEMVFAKGDPGI
AGLYDELLVAEELKPFGKQLRDKYVETQQLLLQIAGHKDILEGDPFLKQGLVLRNPYITT
LNVFQAYTLKRIRDPNFKVTPQPPLSKEFADENKPAGLVKLNPASEYPPGLEDTLILTMK
GIAAGMQNTG

Supplementary Table 1. Primers used for bisulphite sequencing

Primer	Gene	Orientation/Strand	Primer Sequence (5'-3')	Region Amplified	Region Interrogated	Code
PvuII control F	*PEPC1*	Sense Top	GATTATTTACCCTAGAGCAATG	-3197 to -2906	-3197 to -2906	A
PvuII control R	*PEPC1*	Sense Bottom	CATGCCACAACATGTGTATGT			
ZmPEPC ST	*PEPC1*	Sense Top	GATTATTTA**TTT**TAGAG**T**AATG**T**AGG**T**TATGTG**T**ATGA**TTT**	-3319 to -2973	-3178 to -2908	A
ZmPEPC SB	*PEPC1*	Sense Bottom	ACTCCAC**R**ACAT**A**CAT**A**CCACAACAT**A**T**A**TAT**A**T**AA**			
ZmPEPC ST CE	*PEPC1*	Sense Top	TTTG**T**ATTG**T**TA**T**TGTTTG**T**ATATGGGAAAATTGAGAATTGTAT**T**ATG**TT**	-1320 to -852	-1270 to -888	B
ZmPEPC SB CE	*PEPC1*	Sense Bottom	**A**ATAA**AA**AT**A**TT**A**TTCTACCAA**AAA**CACC**R**TACA**AA**			
ZmPEPC ST LRB	*PEPC1*	Sense Top	TAT**T**TTTGTTGG**T**TTGTG**T**A**Y**GGT**Y**GG**Y**G**TT**	-932 to -501	-902 to -551	C
ZmPEPC SB PAU	*PEPC1*	Sense Bottom	ATCT**AA**A**AAA**AT**A**T**AA**C**R**A**AAA**T**A**TCT**A**TTT**A**CA**AA**AT**A**T**AA**TT**A**A**AAA**			
ZmPEPC ST LRA	*PEPC1*	Sense Top	TTGAA**T**A**T**TTATTTGGAA**T**AATAAAATG**TT**GAGTT**TT**TAA**TT**	-817 to -373	-855 to -334	D
ZmPEPC SB LRA	*PEPC1*	Sense Bottom	CTCACCT**A**CCTTCTT**A**T**A**TTATTCC**R**TT**AA**CTAATT**AAA**			
ZmPEPC ST PEP-I	*PEPC1*	Sense Top	G**TY**G**TT**T**T**A**T**TG**T**A**TTT**T**T**AA**TT**A**T**AT**TT**TG**T**AAA**T**AGA**T**A**TTT**	-565 to -144	-521 to -176	E
ZmPEPC SB PEP-I	*PEPC1*	Sense Bottom	CC**RA**CT**A**C**RA**CT**A**A**AA**CTCCTTTTT**AA**CTT**AA**			
ZmPEPC ST ATG	*PEPC1*	Sense Top	**TY**G**T**TAA**T**AG**T**AG**T**AAG**TT**AAG**TT**AAAAAGGAG**TT**	-193 to +188	-158 to +155	F
ZmPEPC SB ATG	*PEPC1*	Sense Bottom	AT**A**A**A**CTT**A**TC**R**TCCTC**RA**A**A**ACCTT**A**CCT**AAA**			

*Cytosines converted to thymines are indicated in blue. Degenerate bases in red.