

BCS 10-2010\_WO\_ST25.txt  
SEQUENCE LISTING

<110> Bayer BioScience N.V.  
D'Halluin, Kathleen

<120> Methods and means to modify a plant genome at a nucleotide  
sequence commonly used in plant genome engineering

<130> BCS 10-2010

<160> 18

<170> PatentIn version 3.5

<210> 1  
<211> 22  
<212> DNA  
<213> Artificial

<220>  
<223> Recognition site for BAY39/40

<400> 1  
gacgaggtcg tccgtccact cc 22

<210> 2  
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<212> DNA  
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<220>  
<223> Complement of the recognition site for BAY39/40

<400> 2  
ggagtggacg gacgacctcg tc 22

<210> 3  
<211> 552  
<212> DNA  
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<223> Coding region of the phosphinotricin actetyltransferase gene  
derived from S. hygrosopicus (bar)

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caggaaccgc aggagtggac ggacgacctc gtccgtctgc gggagcgcta tccctggctc 180  
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<223> Plasmid pCV177

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 <222> (2004)..(2522)

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tttcgcagat ctgtcgaacc acc atg gca ccg aag aag aag cgc aag gtg cat	2033
Met Ala Pro Lys Lys Lys Arg Lys Val His	
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atg aac acc aag tac aac aag aag ttc ctg ctc tac ctg gcg ggc ttc	2081
Met Asn Thr Lys Tyr Asn Lys Lys Phe Leu Leu Tyr Leu Ala Gly Phe	
15 20 25	
gtg gac ggg gac ggc tcc atc atc gcc tcc atc tcc ccg aac cag tcc	2129
Val Asp Gly Asp Gly Ser Ile Ile Ala Ser Ile Ser Pro Asn Gln Ser	
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cgc aag ttc aag cat cag ctg cgc ctc acc ttc acc gtc acc cag aag	2177
Arg Lys Phe Lys His Gln Leu Arg Leu Thr Phe Thr Val Thr Gln Lys	
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Thr Gln Arg Arg Trp Phe Leu Asp Lys Leu Val Asp Lys Ile Gly Val	
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Gly Lys Val Arg Asp Arg Gly Ser Val Ser Asp Tyr Arg Leu Ser Gln	
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Ile Lys Pro Leu His Asn Phe Leu Thr Gln Leu Gln Pro Phe Leu Lys	
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ctc aag cag aag cag gcc aac ctc gtg ctg aag atc atc gag cag ctg	2369
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Pro Ser Ala Lys Glu Ser Pro Asp Lys Phe Leu Glu Val Cys Thr Trp	
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Val Asp Gln Ile Ala Ala Leu Asn Asp Ser Lys Thr Arg Lys Thr Thr	
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Ser Glu Thr Val Arg Ala Val Leu Asp Ser Leu Ser Glu Lys Lys Lys	
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Met Ala Pro Lys	
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aag aag cgc aag gtg cat atg aac acc aag tac aac gag gag ttc ctg	4944
Lys Lys Arg Lys Val His Met Asn Thr Lys Tyr Asn Glu Glu Phe Leu	
180 185 190	
ctc tac ctg gcg ggc ttc gtg gac ggg gac ggc tcc atc atc gcc tcc	4992
Leu Tyr Leu Ala Gly Phe Val Asp Gly Asp Gly Ser Ile Ile Ala Ser	
195 200 205	
atc tcc ccg cgc cag tcc tac aag ttc aag cat gag ctg cgc ctc acc	5040
Ile Ser Pro Arg Gln Ser Tyr Lys Phe Lys His Glu Leu Arg Leu Thr	
210 215 220 225	
ttc cag gtc acg cag aag aca cag cgc cgt tgg ttc ctc gac gag ctg	5088
Phe Gln Val Thr Gln Lys Thr Gln Arg Arg Trp Phe Leu Asp Glu Leu	
230 235 240	
gtg gac gag atc ggg gtg ggc aag gtg cgc gac cgc ggc agc gtc tcc	5136
Val Asp Glu Ile Gly Val Gly Lys Val Arg Asp Arg Gly Ser Val Ser	
245 250 255	
gac tac cgc ctg tcc cag atc aag cct ctg cac aac ttc ctg acc cag	5184
Asp Tyr Arg Leu Ser Gln Ile Lys Pro Leu His Asn Phe Leu Thr Gln	
260 265 270	

## BCS 10-2010\_WO\_ST25.txt

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aag atc atc gag cag ctg ccc tcc gcc aag gaa tcc ccg gac aag ttc 5280  
 Lys Ile Ile Glu Gln Leu Pro Ser Ala Lys Glu Ser Pro Asp Lys Phe  
 290 295 300 305

ctg gag gtg tgc acc tgg gtg gac cag atc gcc gct ctg aac gac tcc 5328  
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aag acc cgc aag acc act tcc gag acc gtc cgc gcc gtt cta gac agt 5376  
 Lys Thr Arg Lys Thr Thr Ser Glu Thr Val Arg Ala Val Leu Asp Ser  
 325 330 335

ctc tcc gag aag aag aag tcg tcc ccc tagcatgccg ttcaaacatt 5423  
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<220>  
 <223> Synthetic Construct

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Ile Ile Ala Ser Ile Ser Pro Asn Gln Ser Arg Lys Phe Lys His Gln  
 35 40 45

Leu Arg Leu Thr Phe Thr Val Thr Gln Lys Thr Gln Arg Arg Trp Phe  
 50 55 60

Leu Asp Lys Leu Val Asp Lys Ile Gly Val Gly Lys Val Arg Asp Arg  
65 70 75 80

Gly Ser Val Ser Asp Tyr Arg Leu Ser Gln Ile Lys Pro Leu His Asn  
85 90 95

Phe Leu Thr Gln Leu Gln Pro Phe Leu Lys Leu Lys Gln Lys Gln Ala  
100 105 110

Asn Leu Val Leu Lys Ile Ile Glu Gln Leu Pro Ser Ala Lys Glu Ser  
115 120 125

Pro Asp Lys Phe Leu Glu Val Cys Thr Trp Val Asp Gln Ile Ala Ala  
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Leu Asn Asp Ser Lys Thr Arg Lys Thr Thr Ser Glu Thr Val Arg Ala  
145 150 155 160

Val Leu Asp Ser Leu Ser Glu Lys Lys Lys Ser Ser Pro  
165 170

<210> 6  
<211> 173  
<212> PRT  
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<220>  
<223> Synthetic Construct

<400> 6

Met Ala Pro Lys Lys Lys Arg Lys Val His Met Asn Thr Lys Tyr Asn  
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Glu Glu Phe Leu Leu Tyr Leu Ala Gly Phe Val Asp Gly Asp Gly Ser  
20 25 30

Ile Ile Ala Ser Ile Ser Pro Arg Gln Ser Tyr Lys Phe Lys His Glu  
35 40 45

Leu Arg Leu Thr Phe Gln Val Thr Gln Lys Thr Gln Arg Arg Trp Phe  
50 55 60

Leu Asp Glu Leu Val Asp Glu Ile Gly Val Gly Lys Val Arg Asp Arg  
65 70 75 80

Gly Ser Val Ser Asp Tyr Arg Leu Ser Gln Ile Lys Pro Leu His Asn  
85 90 95

Phe Leu Thr Gln Leu Gln Pro Phe Leu Glu Leu Lys Gln Lys Gln Ala  
100 105 110

Asn Leu Val Leu Lys Ile Ile Glu Gln Leu Pro Ser Ala Lys Glu Ser  
115 120 125

Pro Asp Lys Phe Leu Glu Val Cys Thr Trp Val Asp Gln Ile Ala Ala  
130 135 140

Leu Asn Asp Ser Lys Thr Arg Lys Thr Thr Ser Glu Thr Val Arg Ala  
145 150 155 160

Val Leu Asp Ser Leu Ser Glu Lys Lys Lys Ser Ser Pro  
 165 170

<210> 7  
 <211> 68  
 <212> DNA  
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 <223> PCR amplicon of bar coding region around the BAY 39/40  
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 tgcgggac 68

<210> 8  
 <211> 68  
 <212> DNA  
 <213> Artificial

<220>  
 <223> PCR amplicon of bar coding region around the BAY 39/40  
 recognition site (PPT tolerant plant line1)

<400> 8  
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 tgcgggac 68

<210> 9  
 <211> 67  
 <212> DNA  
 <213> Artificial

<220>  
 <223> PCR amplicon of bar coding region around the BAY 39/40  
 recognition site (PPT sensitive plant line1 1)

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 gcggggac 67

<210> 10  
 <211> 27  
 <212> DNA  
 <213> Artificial

<220>  
 <223> PCR amplicon of bar coding region around the BAY 39/40  
 recognition site (PPT sensitive plant line1 2)

<400> 10  
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<210> 11  
 <211> 61  
 <212> DNA  
 <213> Artificial

<220>  
 <223> PCR amplicon of bar coding region around the BAY 39/40  
 recognition site (PPT sensitive plant line1 3)

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c

61

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 <211> 49  
 <212> DNA  
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<220>  
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 recognition site (PPT sensitive plant line1 4)

<400> 12  
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49

<210> 13  
 <211> 48  
 <212> DNA  
 <213> Artificial

<220>  
 <223> PCR amplicon of bar coding region around the BAY 39/40  
 recognition site (PPT sensitive plant line1 5)

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48

<210> 14  
 <211> 56  
 <212> DNA  
 <213> Artificial

<220>  
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 recognition site (PPT sensitive plant line1 6)

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56

<210> 15  
 <211> 68  
 <212> DNA  
 <213> Artificial

<220>  
 <223> PCR amplicon of bar coding region around the BAY 39/40  
 recognition site (PPT sensitive plant line1 7)

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 tgcgggac

60

68

<210> 16  
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 <212> PRT  
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<220>  
 <223> I-CreI

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Val Asp Gly Asp Gly Ser Ile Ile Ala Gln Ile Lys Pro Asn Gln Ser  
 20 25 30

Tyr Lys Phe Lys His Gln Leu Ser Leu Thr Phe Gln Val Thr Glu Lys



35

40

45

Thr Gln Arg Arg Trp Phe Leu Asp Lys Leu Val Asp Glu Ile Gly Val  
 50 55 60

Gly Tyr Val Arg Asp Arg Gly Ser Val Ser Asp Tyr Ile Leu Ser Glu  
 65 70 75 80

Ile Lys Pro Leu His Asn Phe Leu Thr Gln Leu Gln Pro Phe Leu Lys  
 85 90 95

Leu Lys Gln Lys Gln Ala Asn Leu Val Leu Lys Ile Ile Glu Gln Leu  
 100 105 110

Pro Ser Ala Lys Glu Ser Pro Asp Lys Phe Leu Glu Val Cys Thr Trp  
 115 120 125

Val Asp Gln Ile Ala Ala Leu Asn Asp Ser Lys Thr Arg Lys Thr Thr  
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Ser Ser Pro

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 <222> (1267)..(1605)

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