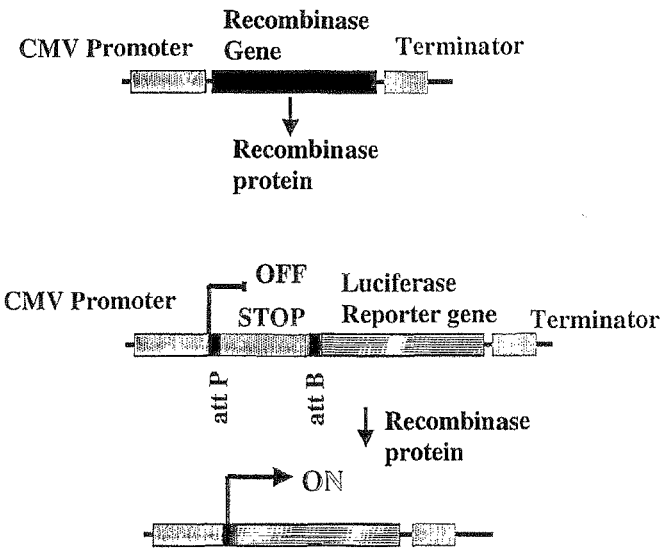

Recombinase
CMV Promoter
Gene
Terminator
Recombinase
protein
OFF
Luciferase
CMV Promoter
STOP
Reporter gene
Terminator
att P
att B
Recombinase
protein
ON

Figure 1

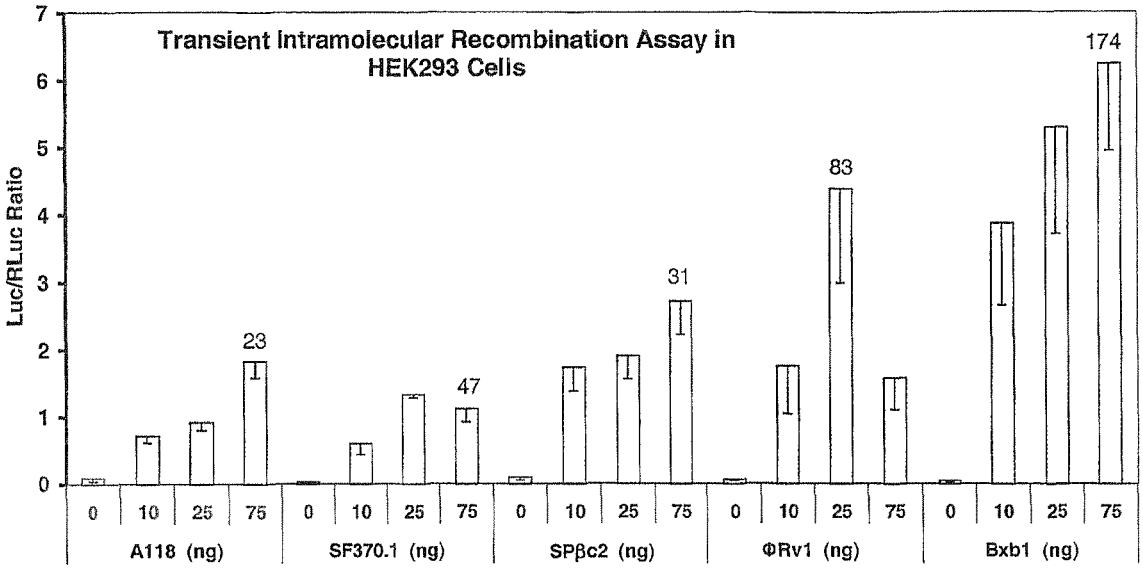

Transient Intramolecular Recombination Assay in HEK293 Cells
Luc/RLuc Ratio
0
1
2
3
4
5
6
7
23
47
31
83
174
0
10
25
75
A118 (ng)
SF370.1 (ng)
SPβc2 (ng)
ΦRv1 (ng)
Bxb1 (ng)

Figure 2

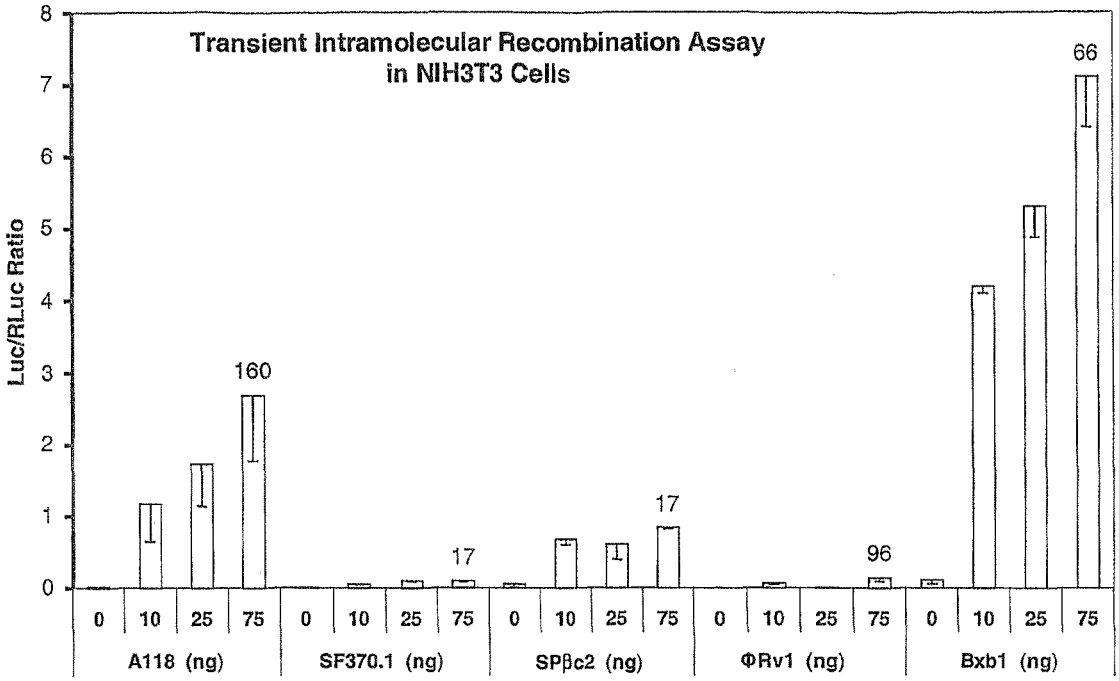

Transient Intramolecular Recombination Assay
in NIH3T3 Cells
Luc/RLuc Ratio
0
1
2
3
4
5
6
7
8
160
17
17
96
66
0
10
25
75
A118 (ng)
SF370.1 (ng)
SPβc2 (ng)
ΦRv1 (ng)
Bxb1 (ng)

Figure 3

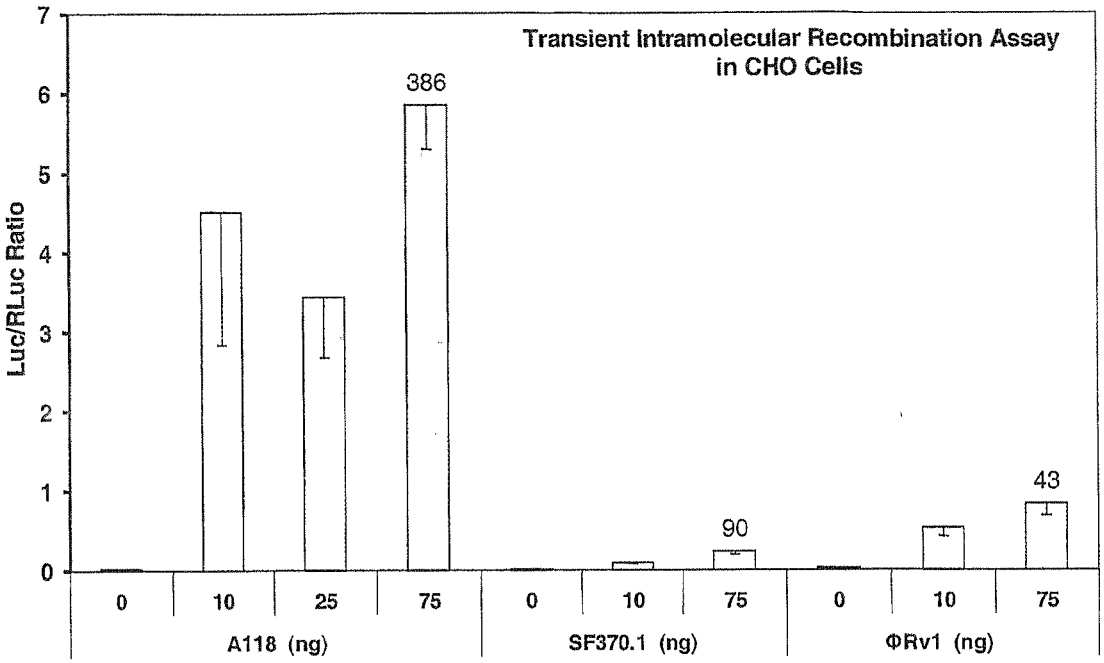

Transient Intramolecular Recombination Assay
in CHO Cells
Luc/RLuc Ratio
7
6
5
4
3
2
1
0
386
90
43
0
10
25
75
0
10
75
0
10
75
A118 (ng)
SF370.1 (ng)
ΦRv1 (ng)

Figure 4

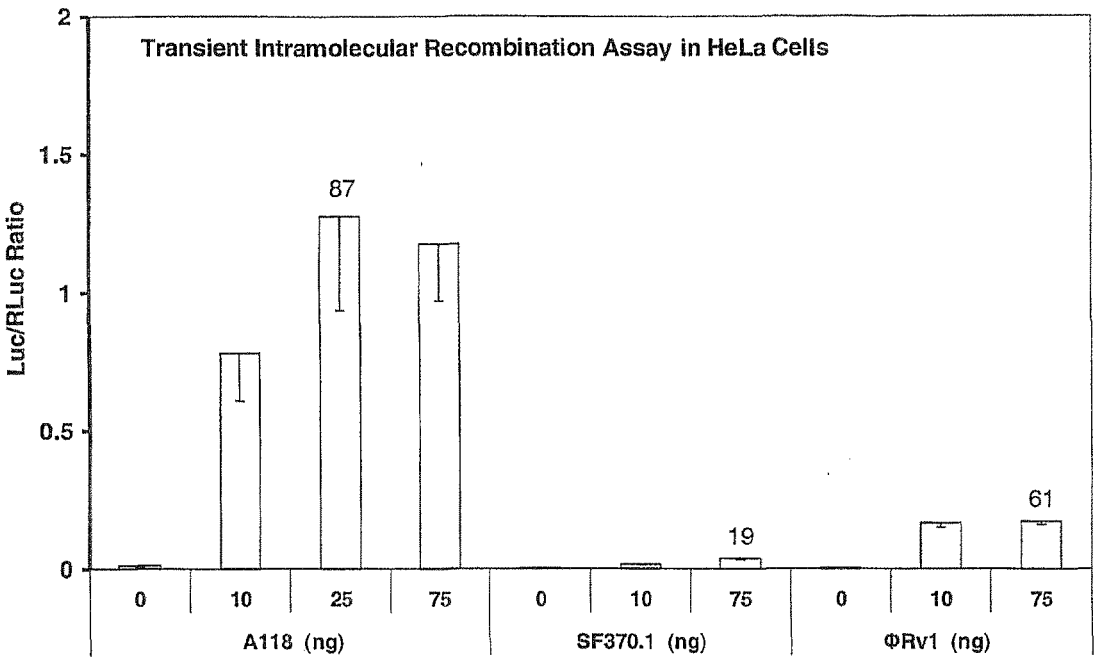

Transient Intramolecular Recombination Assay in HeLa Cells
Luc/RLuc Ratio
2
1.5
1
0.5
0
87
19
61
0
10
25
75
0
10
75
0
10
75
A118 (ng)
SF370.1 (ng)
ΦRv1 (ng)

Figure 5

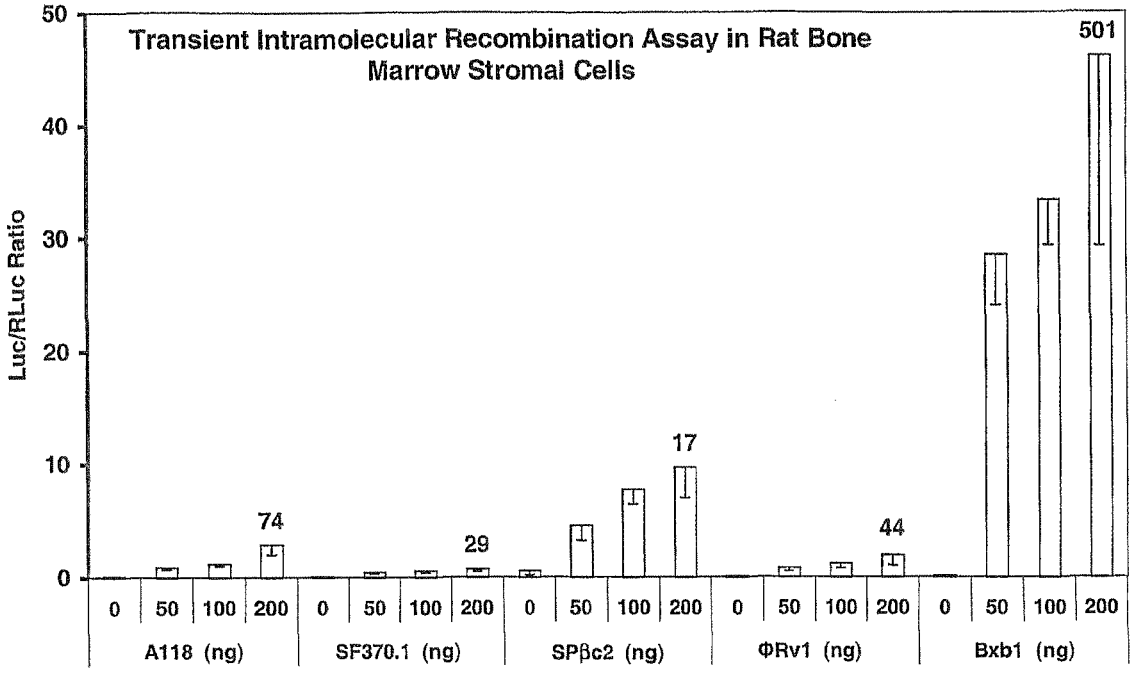

Transient Intramolecular Recombination Assay in Rat Bone Marrow Stromal Cells
Luc/RLuc Ratio
50
40
30
20
10
0
74
29
17
44
501
0 50 100 200 0 50 100 200 0 50 100 200 0 50 100 200 0 50 100 200
A118 (ng)
SF370.1 (ng)
SPβc2 (ng)
ΦRv1 (ng)
Bxb1 (ng)

Figure 6

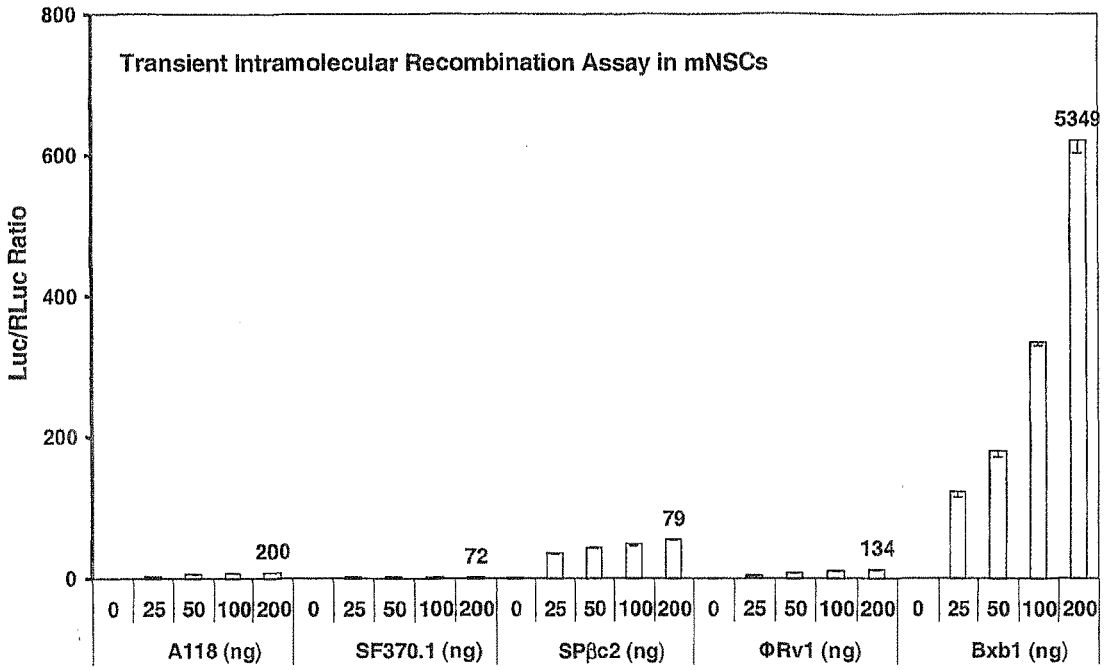

Transient Intramolecular Recombination Assay in mNSCs
Luc/RLuc Ratio
800
600
400
200
0
200
72
79
134
5349
0 25 50 100 200 0 25 50 100 200 0 25 50 100 200 0 25 50 100 200 0 25 50 100 200
A118 (ng)
SF370.1 (ng)
SPβc2 (ng)
ΦRv1 (ng)
Bxb1 (ng)

Figure 7

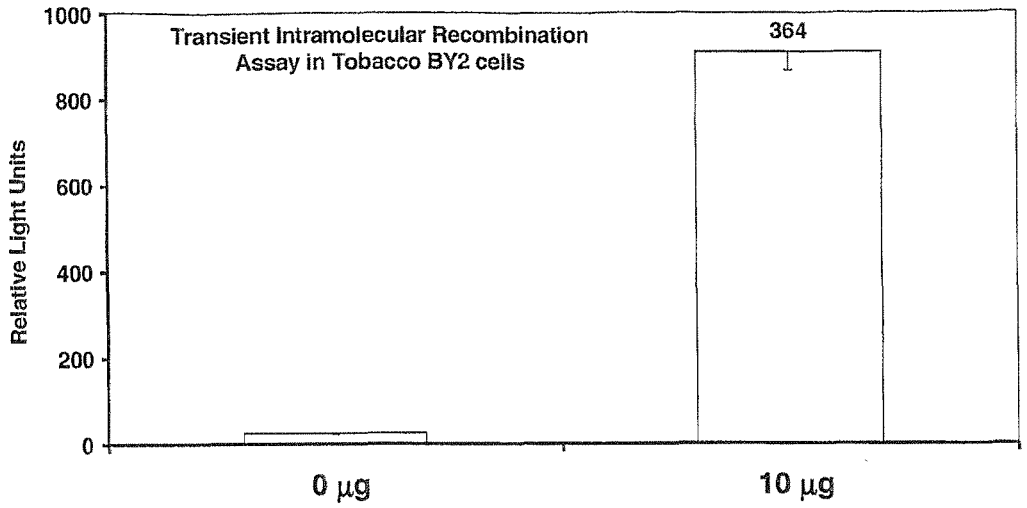

Transient Intramolecular Recombination
Assay in Tobacco BY2 cells
364
Relative Light Units
1000
800
600
400
200
0
0 µg
10 µg

Figure 8

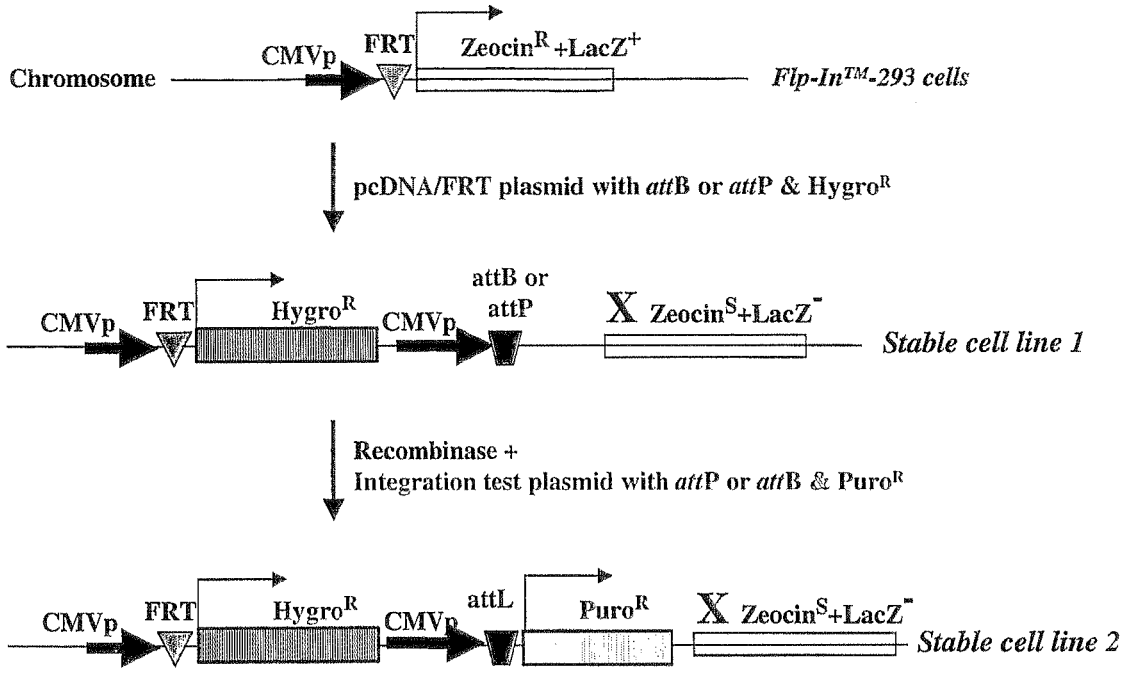

Chromosome
CMVp
FRT
Zeocin^R +LacZ$^+$
Flp-In™-293 cells
pcDNA/FRT plasmid with *att*B or *att*P & Hygro^R
CMVp
FRT
Hygro^R
CMVp
attB or attP
X Zeocin^S+LacZ$^-$
Stable cell line 1
Recombinase +
Integration test plasmid with *att*P or *att*B & Puro^R
CMVp
FRT
Hygro^R
CMVp
attL
Puro^R
X Zeocin^S+LacZ$^-$
Stable cell line 2

Figure 9

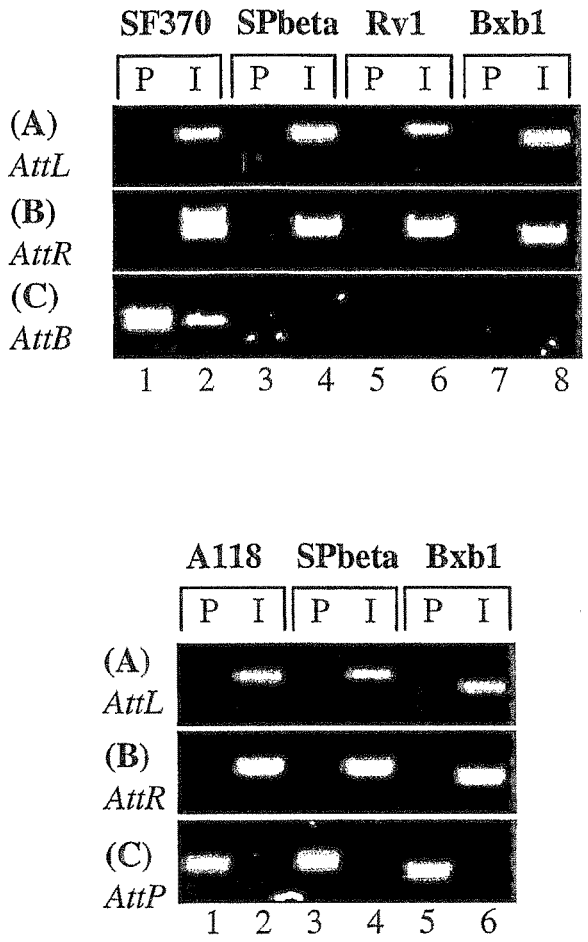

SF370 SPbeta Rv1 Bxb1
P I P I P I P I
(A)
AttL
(B)
AttR
(C)
AttB
1 2 3 4 5 6 7 8
A118 SPbeta Bxb1
P I P I P I
(A)
AttL
(B)
AttR
(C)
AttP
1 2 3 4 5 6

Figure 10

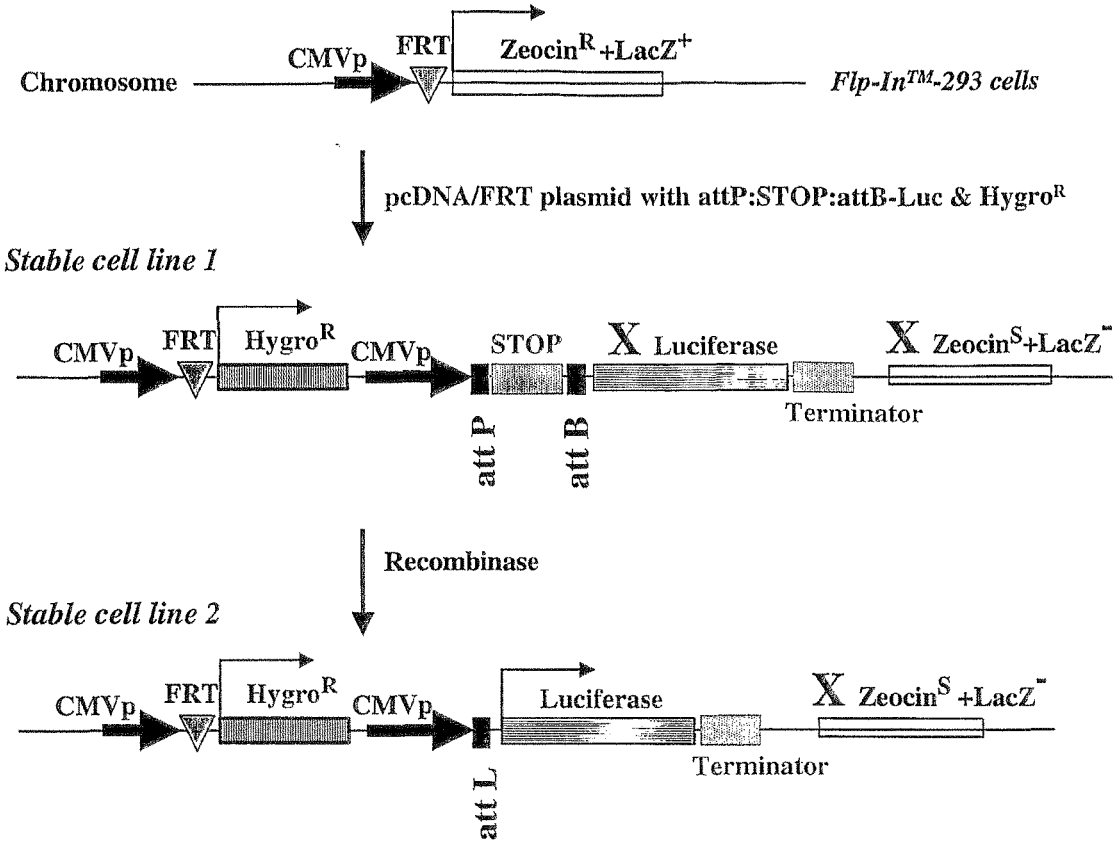

Chromosome
CMVp
FRT
Zeocin^R+LacZ$^+$
Flp-In™-293 cells
pcDNA/FRT plasmid with attP:STOP:attB-Luc & Hygro^R
Stable cell line 1
CMVp
FRT
Hygro^R
CMVp
STOP
X Luciferase
X Zeocin^S+LacZ$^-$
Terminator
att P
att B
Recombinase
Stable cell line 2
CMVp
FRT
Hygro^R
CMVp
Luciferase
X Zeocin^S +LacZ$^-$
Terminator
att L

Figure 11

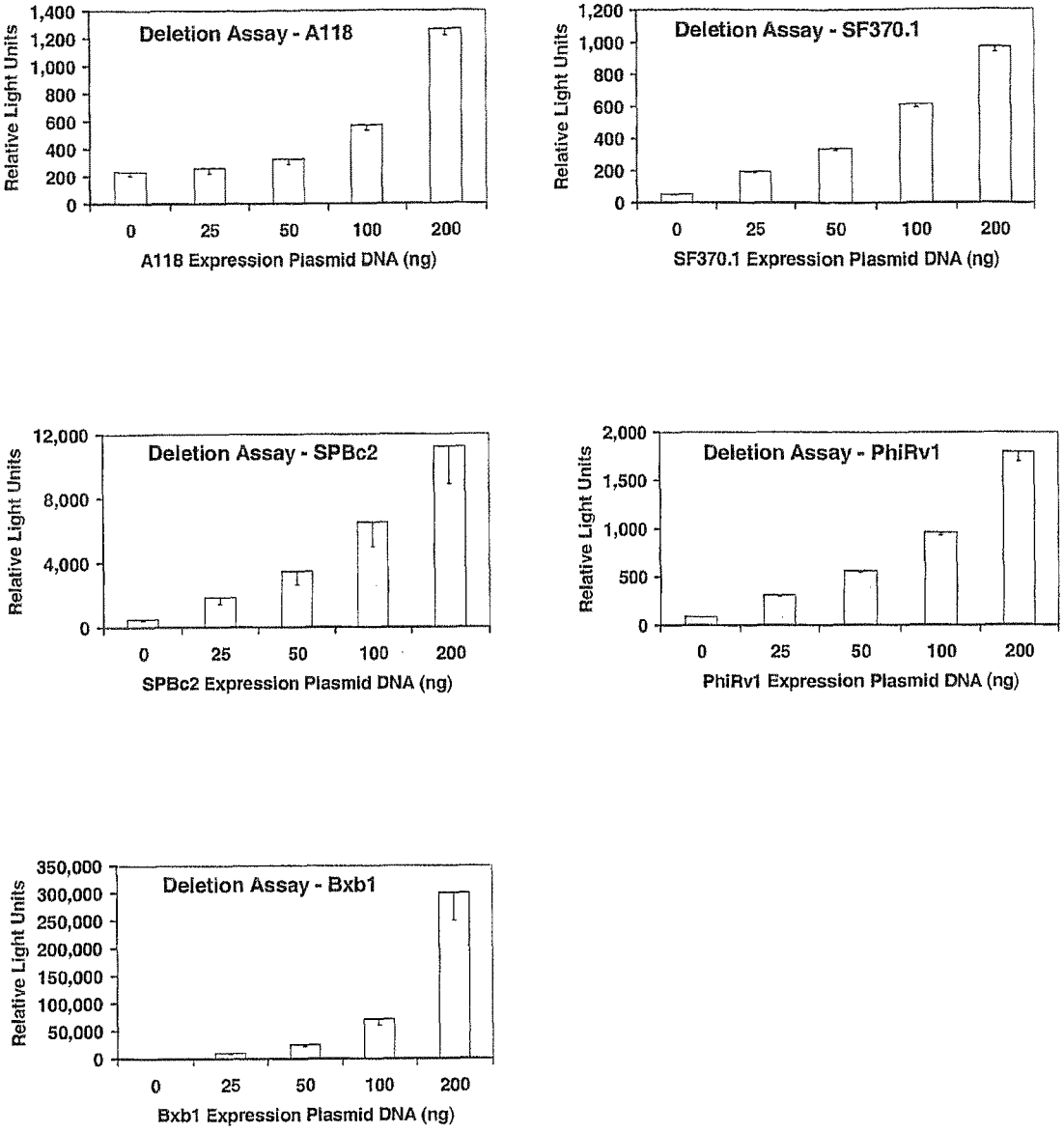

Deletion Assay - A118
Relative Light Units
1,400
1,200
1,000
800
600
400
200
0
0
25
50
100
200
A118 Expression Plasmid DNA (ng)
Deletion Assay - SF370.1
Relative Light Units
1,200
1,000
800
600
400
200
0
0
25
50
100
200
SF370.1 Expression Plasmid DNA (ng)
Deletion Assay - SPBc2
Relative Light Units
12,000
8,000
4,000
0
0
25
50
100
200
SPBc2 Expression Plasmid DNA (ng)
Deletion Assay - PhiRv1
Relative Light Units
2,000
1,500
1,000
500
0
0
25
50
100
200
PhiRv1 Expression Plasmid DNA (ng)
Deletion Assay - Bxb1
Relative Light Units
350,000
300,000
250,000
200,000
150,000
100,000
50,000
0
0
25
50
100
200
Bxb1 Expression Plasmid DNA (ng)

Figure 12

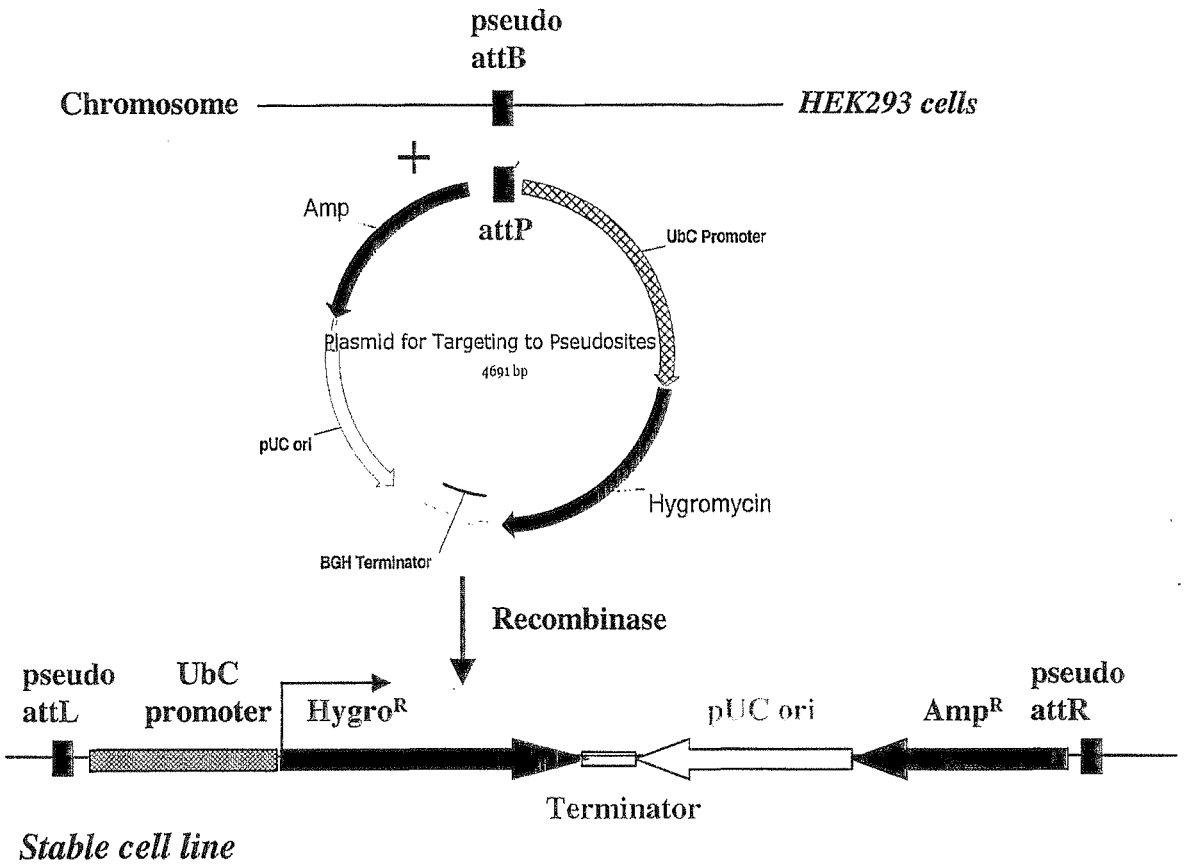

pseudo
attB
Chromosome
HEK293 cells
Amp
attP
UbC Promoter
Plasmid for Targeting to Pseudosites
4691 bp
pUC ori
Hygromycin
BGH Terminator
Recombinase
pseudo
attL
UbC
promoter
Hygro^R
pUC ori
Amp^R
pseudo
attR
Terminator
Stable cell line

Figure 13

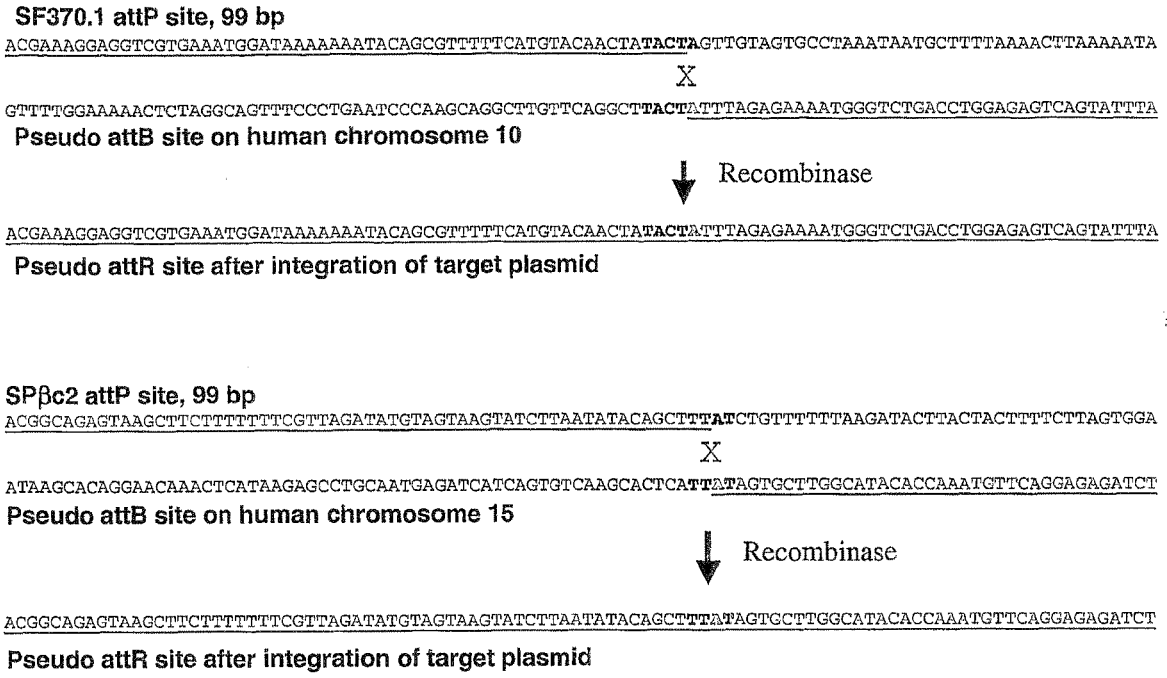

SF370.1 attP site, 99 bp
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X
GTTTTGGAAAAACTCTAGGCAGTTTCCCTGAATCCCAAGCAGGCTTGTTCAGGCTTACTATTTAGAGAAAATGGGTCTGACCTGGAGAGTCAGTATTTA
Pseudo attB site on human chromosome 10
Recombinase
ACGAAAGGAGGTCGTGAAATGGATAAAAAAATACAGCGTTTTTCATGTACAACTATACTATTTAGAGAAAATGGGTCTGACCTGGAGAGTCAGTATTTA
Pseudo attR site after integration of target plasmid
SPβc2 attP site, 99 bp
ACGGCAGAGTAAGCTTCTTTTTTTCGTTAGATATGTAGTAAGTATCTTAATATACAGCTTTATCTGTTTTTTAAGATACTTACTACTTTTCTTAGTGGA
X
ATAAGCACAGGAACAAACTCATAAGAGCCTGCAATGAGATCATCAGTGTCAAGCACTCATTATAGTGCTTGGCATACACCAAATGTTCAGGAGAGATCT
Pseudo attB site on human chromosome 15
Recombinase
ACGGCAGAGTAAGCTTCTTTTTTTCGTTAGATATGTAGTAAGTATCTTAATATACAGCTTTATAGTGCTTGGCATACACCAAATGTTCAGGAGAGATCT
Pseudo attR site after integration of target plasmid

Figure 14

SEQUENCE LISTING

<110> Intrexon Corporation

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<130> SP8830A

<140> Not yet assigned
<141> 2005-02-08

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aaggaactca tgaacaagat cctcaccgcc atcgagatcc cctacgagct gaagatggag 180

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tacagcgacg ccggccagat cgtgaacctg ctgcagagca agcggctcat catcatcacc 360

ccctacaagg tgtacgaccc cagaaacccc gtcgacatgc ggcagatccg gttcgagctg 420

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aaggacggca agcggaccat caggcctgag aaggagcaga tcgtggtgca ggacgcccac 840

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cccctgctgc ccaacaagga cgagttcgag ctgagcgagc tggccggagt gtgcacctgc 960

agcaagtgcg gcgagcctct gagcaagtac gagagcaagc gcatccggaa gaacaaggat 1020

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35 40 45

Thr Ala Ile Glu Ile Pro Tyr Glu Leu Lys Met Glu Ile Gly Ser Gly
50 55 60

Glu Ser Ile Asp Gly Arg Pro Val Phe Lys Glu Cys Leu Lys Asp Leu
65 70 75 80

Glu Glu Gly Lys Tyr Gln Ala Ile Ala Val Lys Glu Ile Thr Arg Leu
85 90 95

Ser Arg Gly Ser Tyr Ser Asp Ala Gly Gln Ile Val Asn Leu Leu Gln
100 105 110

Ser Lys Arg Leu Ile Ile Ile Thr Pro Tyr Lys Val Tyr Asp Pro Arg
115 120 125

Asn Pro Val Asp Met Arg Gln Ile Arg Phe Glu Leu Phe Met Ala Arg
130 135 140

Glu Glu Phe Glu Met Thr Arg Glu Arg Met Thr Gly Ala Lys Tyr Thr
145 150 155 160

Tyr Ala Ala Gln Gly Lys Trp Ile Ser Gly Leu Ala Pro Tyr Gly Tyr
165 170 175

Gln Leu Asn Lys Lys Thr Ser Lys Leu Asp Pro Val Glu Asp Glu Ala
180 185 190

Lys Val Val Gln Leu Ile Phe Asn Ile Phe Leu Asn Gly Leu Asn Gly

195 200 205

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Ile Pro Thr Pro Ser Gly Lys Lys Arg Trp Asn Gln Tyr Thr Ile Lys
225 230 235 240

Ala Ile Leu Gln Asn Glu Val Tyr Ile Gly Thr Val Lys Tyr Lys Val
245 250 255

Arg Glu Lys Thr Lys Asp Gly Lys Arg Thr Ile Arg Pro Glu Lys Glu
260 265 270

Gln Ile Val Val Gln Asp Ala His Ala Pro Ile Ile Asp Lys Glu Gln
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Phe Gln Gln Ser Gln Val Lys Ile Ala Asn Lys Val Pro Leu Leu Pro
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Asn Lys Asp Glu Phe Glu Leu Ser Glu Leu Ala Gly Val Cys Thr Cys
305 310 315 320

Ser Lys Cys Gly Glu Pro Leu Ser Lys Tyr Glu Ser Lys Arg Ile Arg
325 330 335

Lys Asn Lys Asp Gly Thr Glu Ser Val Tyr His Val Lys Ser Leu Thr
340 345 350

Cys Lys Lys Asn Lys Cys Thr Tyr Val Arg Tyr Asn Asp Val Glu Asn
355 360 365

Ala Ile Leu Asp Tyr Leu Ser Ser Leu Asn Asp Leu Asn Asp Ser Thr
370 375 380

Leu Thr Lys His Ile Asn Ser Met Leu Ser Lys Tyr Glu Asp Asp Asn
385 390 395 400

Ser Asn Met Lys Thr Lys Lys Gln Met Ser Glu His Leu Ser Gln Lys
405 410 415

Glu Lys Glu Leu Lys Asn Lys Glu Asn Phe Ile Phe Asp Lys Tyr Glu
420 425 430

Ser Gly Ile Tyr Ser Asp Glu Leu Phe Leu Lys Arg Lys Ala Ala Leu
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Asp Glu Glu Phe Lys Glu Leu Gln Asn Ala Lys Asn Glu Leu Asn Gly
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Leu Gln Asp Thr Gln Ser Glu Ile Asp Ser Asn Thr Val Arg Asn Asn
465 470 475 480

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Lys Asn Glu Leu Leu Arg Met Val Leu Lys Asp Val Ile Val Asn Met
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355 360 365

Thr Pro Leu Lys Lys Glu Ile Glu Ile Ile Asp Lys Lys Ile Asn Arg
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gtggtgatcg ccctgatggg cacagtggcc cagatggagc tggaggccat caaggagagg 420

aatcggtctg ccgcccactt caatatcagg gccggcaagt acagaggaag cctgcctcct 480

tggggctacc tgcccacaag agtggatggc gagtggagac tggtgcctga ccctgtgcag 540

agggagagaa tcctggaagt gtatcaccgc gtggtggaca atcacgagcc tctgcacctg 600

gtggcccacg acctgaatag gagaggcgtg ctgtccccca aggattactt cgcccagctc 660

cagggcagag agcctcaggg cagagagtgg tctgccaccg ccctgaaaag atctatgatc 720

agcgaggcca tgctgggcta cgccaccctg aatggcaaga ccgtgaggga tgatgatgga 780

gcccctctgg tgagagccga gcccatcctg acaagggaac agctggaggc tctgagagcc 840

gaactggtga aaaccagcag agccaagcct gccgtgagca cacctagcct gctgctgaga 900

gtgctgttct gtgccgtgtg tggcgagcct gcctacaagt ttgccggcgg aggcagaaag 960

caccccggt acagatgtag gagcatgggc ttccctaagc actgcggcaa tggcaccgtg 1020

gccatggccg aatgggacgc cttttgcgag gagcaagtgc tggatctgct gggagatgcc 1080

gagaggctgg agaaagtgtg ggtggccgga tccgattctg ccgtggaact ggccgaagtg 1140

aatgctgaac tggtggacct gaccagcctg atcggcagcc ctgcctatag agccggaagc 1200

cctcagagag aagccctgga cgccagaatt gccgccctgg ccgccagaca ggaggaactg 1260

gagggactgg aggccagacc ttctggctgg gagtggagag agaccggcca gagattcggc 1320

gattggtgga gggagcagga taccgccgcc aagaacacct ggctgcggag catgaacgtg 1380

aggctgacct tcgacgtgag aggcggcctg accagaacca tcgacttcgg cgacctccag 1440

gagtatgagc agcacctgag actgggaagc gtggtggaga gactgcacac aggcatgtcc 1500

tag 1503

<210> 6
<211> 500
<212> PRT
<213> Putative recombinase of mycobacteriophage Bxb1

<400> 6

Met Arg Ala Leu Val Val Ile Arg Leu Ser Arg Val Thr Asp Ala Thr
1 5 10 15

Thr Ser Pro Glu Arg Gln Leu Glu Ser Cys Gln Gln Leu Cys Ala Gln
20 25 30

Arg Gly Trp Asp Val Val Gly Val Ala Glu Asp Leu Asp Val Ser Gly
35 40 45

Ala Val Asp Pro Phe Asp Arg Lys Arg Arg Pro Asn Leu Ala Arg Trp
50 55 60

Leu Ala Phe Glu Glu Gln Pro Phe Asp Val Ile Val Ala Tyr Arg Val
65 70 75 80

Asp Arg Leu Thr Arg Ser Ile Arg His Leu Gln Gln Leu Val His Trp
85 90 95

Ala Glu Asp His Lys Lys Leu Val Val Ser Ala Thr Glu Ala His Phe
100 105 110

Asp Thr Thr Thr Pro Phe Ala Ala Val Val Ile Ala Leu Met Gly Thr
115 120 125

Val Ala Gln Met Glu Leu Glu Ala Ile Lys Glu Arg Asn Arg Ser Ala
130 135 140

Ala His Phe Asn Ile Arg Ala Gly Lys Tyr Arg Gly Ser Leu Pro Pro
145 150 155 160

Trp Gly Tyr Leu Pro Thr Arg Val Asp Gly Glu Trp Arg Leu Val Pro
165 170 175

Asp Pro Val Gln Arg Glu Arg Ile Leu Glu Val Tyr His Arg Val Val
180 185 190

Asp Asn His Glu Pro Leu His Leu Val Ala His Asp Leu Asn Arg Arg
195 200 205

Gly Val Leu Ser Pro Lys Asp Tyr Phe Ala Gln Leu Gln Gly Arg Glu
210 215 220

Pro Gln Gly Arg Glu Trp Ser Ala Thr Ala Leu Lys Arg Ser Met Ile
225 230 235 240

Ser Glu Ala Met Leu Gly Tyr Ala Thr Leu Asn Gly Lys Thr Val Arg
245 250 255

Asp Asp Asp Gly Ala Pro Leu Val Arg Ala Glu Pro Ile Leu Thr Arg
260 265 270

Glu Gln Leu Glu Ala Leu Arg Ala Glu Leu Val Lys Thr Ser Arg Ala
275 280 285

Lys Pro Ala Val Ser Thr Pro Ser Leu Leu Leu Arg Val Leu Phe Cys
290 295 300

Ala Val Cys Gly Glu Pro Ala Tyr Lys Phe Ala Gly Gly Gly Arg Lys
305 310 315 320

His Pro Arg Tyr Arg Cys Arg Ser Met Gly Phe Pro Lys His Cys Gly
325 330 335

Asn Gly Thr Val Ala Met Ala Glu Trp Asp Ala Phe Cys Glu Glu Gln
340 345 350

Val Leu Asp Leu Leu Gly Asp Ala Glu Arg Leu Glu Lys Val Trp Val
355 360 365

Ala Gly Ser Asp Ser Ala Val Glu Leu Ala Glu Val Asn Ala Glu Leu
370 375 380

Val Asp Leu Thr Ser Leu Ile Gly Ser Pro Ala Tyr Arg Ala Gly Ser
385 390 395 400

Pro Gln Arg Glu Ala Leu Asp Ala Arg Ile Ala Ala Leu Ala Ala Arg
405 410 415

Gln Glu Glu Leu Glu Gly Leu Glu Ala Arg Pro Ser Gly Trp Glu Trp
420 425 430

Arg Glu Thr Gly Gln Arg Phe Gly Asp Trp Trp Arg Glu Gln Asp Thr
435 440 445

Ala Ala Lys Asn Thr Trp Leu Arg Ser Met Asn Val Arg Leu Thr Phe
450 455 460

Asp Val Arg Gly Gly Leu Thr Arg Thr Ile Asp Phe Gly Asp Leu Gln
465 470 475 480

Glu Tyr Glu Gln His Leu Arg Leu Gly Ser Val Val Glu Arg Leu His
485 490 495

Thr Gly Met Ser
500

<210> 7
<211> 1359
<212> DNA
<213> Synthetic gene

<400> 7
atgaaggccg ccatctacat cagagtgagc acccaggagc aggtggagaa ctacagcatc 60

caggcccaga ccgagaagct caccgccctg tgcagaagca aggactggga cgtgtacgac 120

atcttcatcg acggcggcta cagcggcagc aacatgaaca gacccgccct gaacgagatg 180

ctgagcaagc tgcacgagat cgatgccgtg gtggtgtaca ggctggacag gctgagcaga 240

agccagaggg acaccatcac cctcatcgag gagtacttcc tgaagaacaa cgtggagttc 300

gtgagcctga gcgagaccct ggacaccagc agcccttcg gcagagccat gatcggcatc 360

ctgagcgtgt tcgcccagct cgagagagag accatccggg acaggatggt gatgggcaag 420

atcaagagga tcgaggccgg cctgcccctc accaccgcca agggcagaac cttcggctac 480

gacgtgatcg acaccaagct gtacatcaac gaggaggagg ccaagcagct gcagctcatc 540

tacgatatct tcgaggagga gcagagcatc accttcctgc agaagcggct gaagaagctg 600

ggcttcaagg tgcggaccta caaccggtac aacaactggc tcaccaacga cctgtactgc 660

ggctacgtga gctacaagga caaggtgcac gtgaagggga tccacgagcc catcatcagc 720

gaggagcagt tctaccgggt gcaggagatc ttcacccgca tgggcaagaa ccccaacatg 780

aaccgggaca gcgccagcct gctgaacaat ctggtggtgt gcagcaagtg cggcctgggc 840

ttcgtgcaca ggagaaagga caccatgagc cggggcaaga agtaccacta ccggtactac 900

agctgcaaga cctacaagca cacccacgag ctggagaagt gcggcaacaa gatctggagg 960

gccgacaagc tggaggagtt gatcatcaac cgggtgaaca actacagctt cgccagccgg 1020

aacgtggata aggaggacga gctggacagc ctgaatgaga agcttaagat cgagcacgcc 1080

aagaagaagc gcctgttcga cctgtacatt aacggcagct acgaggtgag cgagctggac 1140

tccatgatga acgacatcga cgcccagatc aactactacg agagccagat cgaggccaac 1200

gaggagctga agaagaacaa gaagatccag gagaacctgg ccgacctggc caccgtggat 1260

ttcgacagcc tggagttcag ggagaagcag ctgtacctga agtccctcat caataagatc 1320

tacatcgacg gggagcaggt gaccatcgag tggctgtag 1359

<210> 8
<211> 452
<212> PRT
<213> Putative recombinase of bacteriophage A118

<400> 8

Met Lys Ala Ala Ile Tyr Ile Arg Val Ser Thr Gln Glu Gln Val Glu
1 5 10 15

Asn Tyr Ser Ile Gln Ala Gln Thr Glu Lys Leu Thr Ala Leu Cys Arg
20 25 30

Ser Lys Asp Trp Asp Val Tyr Asp Ile Phe Ile Asp Gly Gly Tyr Ser
35 40 45

Gly Ser Asn Met Asn Arg Pro Ala Leu Asn Glu Met Leu Ser Lys Leu
50 55 60

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

Ser Gln Arg Asp Thr Ile Thr Leu Ile Glu Glu Tyr Phe Leu Lys Asn
85 90 95

Asn Val Glu Phe Val Ser Leu Ser Glu Thr Leu Asp Thr Ser Ser Pro
100 105 110

Phe Gly Arg Ala Met Ile Gly Ile Leu Ser Val Phe Ala Gln Leu Glu
115 120 125

Arg Glu Thr Ile Arg Asp Arg Met Val Met Gly Lys Ile Lys Arg Ile
130 135 140

Glu Ala Gly Leu Pro Leu Thr Thr Ala Lys Gly Arg Thr Phe Gly Tyr
145 150 155 160

Asp Val Ile Asp Thr Lys Leu Tyr Ile Asn Glu Glu Glu Ala Lys Gln
165 170 175

Leu Gln Leu Ile Tyr Asp Ile Phe Glu Glu Glu Gln Ser Ile Thr Phe
180 185 190

Leu Gln Lys Arg Leu Lys Lys Leu Gly Phe Lys Val Arg Thr Tyr Asn
195 200 205

Arg Tyr Asn Asn Trp Leu Thr Asn Asp Leu Tyr Cys Gly Tyr Val Ser
210 215 220

Tyr Lys Asp Lys Val His Val Lys Gly Ile His Glu Pro Ile Ile Ser
225 230 235 240

Glu Glu Gln Phe Tyr Arg Val Gln Glu Ile Phe Thr Arg Met Gly Lys
245 250 255

Asn Pro Asn Met Asn Arg Asp Ser Ala Ser Leu Leu Asn Asn Leu Val
260 265 270

Val Cys Ser Lys Cys Gly Leu Gly Phe Val His Arg Arg Lys Asp Thr
275 280 285

Met Ser Arg Gly Lys Lys Tyr His Tyr Arg Tyr Tyr Ser Cys Lys Thr
290 295 300

Tyr Lys His Thr His Glu Leu Glu Lys Cys Gly Asn Lys Ile Trp Arg
305 310 315 320

Ala Asp Lys Leu Glu Glu Leu Ile Ile Asn Arg Val Asn Asn Tyr Ser
325 330 335

Phe Ala Ser Arg Asn Val Asp Lys Glu Asp Glu Leu Asp Ser Leu Asn
340 345 350

Glu Lys Leu Lys Ile Glu His Ala Lys Lys Lys Arg Leu Phe Asp Leu
355 360 365

Tyr Ile Asn Gly Ser Tyr Glu Val Ser Glu Leu Asp Ser Met Met Asn
370 375 380

Asp Ile Asp Ala Gln Ile Asn Tyr Tyr Glu Ser Gln Ile Glu Ala Asn
385 390 395 400

Glu Glu Leu Lys Lys Asn Lys Lys Ile Gln Glu Asn Leu Ala Asp Leu
405 410 415

Ala Thr Val Asp Phe Asp Ser Leu Glu Phe Arg Glu Lys Gln Leu Tyr
420 425 430

Leu Lys Ser Leu Ile Asn Lys Ile Tyr Ile Asp Gly Glu Gln Val Thr
435 440 445

Ile Glu Trp Leu
450

<210> 9
<211> 1410
<212> DNA
<213> Synthetic gene

<400> 9
atgcggtaca ccacccccgt gagagccgcc gtgtacctga gaatcagcga ggacagaagc 60

ggcgagcagc tgggcgtggc cagacagaga gaggactgcc tgaagctgtg cggccagaga 120

aagtgggtgc ccgtggagta cctggacaac gatgtgagcg ccagcaccgg caagaggaga 180

cccgcctacg agcagatgct ggccgacatc accgccggca agatcgccgc cgtggtggcc 240

tgggacctgg ataggctgca caggagaccc atcgagctgg aggccttcat gagcctggcc 300

gatgagaaaa gactggccct ggccaccgtg gccggcgacg tggacctggc caccccccag 360

ggcagactgg tggccagact taagggcagc gtggccgccc acgagaccga gcacaagaag 420

gccagacagc ggagagccgc cagacagaag gccgagagag gccaccccaa ctggagcaag 480

gccttcggct acctgcctgg ccccaacggc cccgagcccg accctagaac cgcccctctg 540

gtgaagcagg cctacgccga catcctggcc ggagccagcc tgggcgacgt gtgcagacag 600

tggaatgacg ccggagcctt caccatcacc ggcagaccct ggaccaccac caccctgagc 660

aagttcctgc ggaagcccag aaacgccggc ctgagagcct acaagggcgc cagatacggc 720

cccgtcgaca gagatgccat cgtgggcaag gcccagtgga gccccctggt ggacgaggcc 780

accttctggg ccgctcaggc cgtgctggac gcccctggca gagccccagg cagaaagagc 840

gtgcggagac acctgctcac cggcctggcc ggctgcggca agtgcggcaa ccacctggcc 900

ggcagctaca gaaccgatgg gcaggtggtg tacgtgtgca aggcctgcca cggcgtggcc 960

attctggccg acaacatcga gcccatcctg taccacatcg tggccgagag actggccatg 1020

cccgacgccg tggatctgct gaggagggag atccacgacg ccgccgaggc cgagaccatc 1080

agactcgagc tggaaaccct gtacggcgag ctggacagac tggccgtgga gagagccgag 1140

ggcctgctca cagccagaca ggtgaagatc agcaccgaca tcgtgaacgc caagatcacc 1200

aagctgcagg ccaggcagca ggaccaggag aggctgagag tgttcgacgg catccccctg 1260

ggcacccctc aggtggccgg catgattgcc gagctgagcc ccgatagatt cagggctgtg 1320

ctggatgtgc tggccgaggt ggtggtgcag cccgtgggca agagcggcag aatcttcaac 1380

cccgagcggg tgcaggtgaa ctggagatag 1410

<210> 10
<211> 469
<212> PRT
<213> Putative recombinase of bacteriophage PhiRv1

<400> 10

Met Arg Tyr Thr Thr Pro Val Arg Ala Ala Val Tyr Leu Arg Ile Ser
1 5 10 15

Glu Asp Arg Ser Gly Glu Gln Leu Gly Val Ala Arg Gln Arg Glu Asp
20 25 30

Cys Leu Lys Leu Cys Gly Gln Arg Lys Trp Val Pro Val Glu Tyr Leu
35 40 45

Asp Asn Asp Val Ser Ala Ser Thr Gly Lys Arg Arg Pro Ala Tyr Glu
50 55 60

Gln Met Leu Ala Asp Ile Thr Ala Gly Lys Ile Ala Ala Val Val Ala
65 70 75 80

Trp Asp Leu Asp Arg Leu His Arg Arg Pro Ile Glu Leu Glu Ala Phe
85 90 95

Met Ser Leu Ala Asp Glu Lys Arg Leu Ala Leu Ala Thr Val Ala Gly
100 105 110

Asp Val Asp Leu Ala Thr Pro Gln Gly Arg Leu Val Ala Arg Leu Lys
115 120 125

Gly Ser Val Ala Ala His Glu Thr Glu His Lys Lys Ala Arg Gln Arg
130 135 140

Arg Ala Ala Arg Gln Lys Ala Glu Arg Gly His Pro Asn Trp Ser Lys
145 150 155 160

Ala Phe Gly Tyr Leu Pro Gly Pro Asn Gly Pro Glu Pro Asp Pro Arg
165 170 175

Thr Ala Pro Leu Val Lys Gln Ala Tyr Ala Asp Ile Leu Ala Gly Ala
180 185 190

Ser Leu Gly Asp Val Cys Arg Gln Trp Asn Asp Ala Gly Ala Phe Thr
195 200 205

Ile Thr Gly Arg Pro Trp Thr Thr Thr Leu Ser Lys Phe Leu Arg
210 215 220

Lys Pro Arg Asn Ala Gly Leu Arg Ala Tyr Lys Gly Ala Arg Tyr Gly
225 230 235 240

Pro Val Asp Arg Asp Ala Ile Val Gly Lys Ala Gln Trp Ser Pro Leu
245 250 255

Val Asp Glu Ala Thr Phe Trp Ala Ala Gln Ala Val Leu Asp Ala Pro
260 265 270

Gly Arg Ala Pro Gly Arg Lys Ser Val Arg Arg His Leu Leu Thr Gly
275 280 285

Leu Ala Gly Cys Gly Lys Cys Gly Asn His Leu Ala Gly Ser Tyr Arg
290 295 300

Thr Asp Gly Gln Val Val Tyr Val Cys Lys Ala Cys His Gly Val Ala
305 310 315 320

Ile Leu Ala Asp Asn Ile Glu Pro Ile Leu Tyr His Ile Val Ala Glu
325 330 335

Arg Leu Ala Met Pro Asp Ala Val Asp Leu Leu Arg Arg Glu Ile His
340 345 350

Asp Ala Ala Glu Ala Glu Thr Ile Arg Leu Glu Leu Glu Thr Leu Tyr
355 360 365

Gly Glu Leu Asp Arg Leu Ala Val Glu Arg Ala Glu Gly Leu Leu Thr
370 375 380

Ala Arg Gln Val Lys Ile Ser Thr Asp Ile Val Asn Ala Lys Ile Thr
385 390 395 400

Lys Leu Gln Ala Arg Gln Gln Asp Gln Glu Arg Leu Arg Val Phe Asp
405 410 415

Gly Ile Pro Leu Gly Thr Pro Gln Val Ala Gly Met Ile Ala Glu Leu
420 425 430

Ser Pro Asp Arg Phe Arg Ala Val Leu Asp Val Leu Ala Glu Val Val
435 440 445

Val Gln Pro Val Gly Lys Ser Gly Arg Ile Phe Asn Pro Glu Arg Val
450 455 460

Gln Val Asn Trp Arg
465

<210> 11
<211> 99
<212> DNA
<213> Artificial

<220>
<223> SPBc2 attP site

<400> 11
acggcagagt aagcttcttt ttttcgttag atatgtagta agtatcttaa tatacagctt 60

tatctgtttt ttaagatact tactactttt cttagtgga 99

<210> 12
<211> 1315
<212> DNA
<213> Artificial

<220>
<223> STOP sequence

<400> 12
aagcttactt accatgtcag atccagacat gataagatac attgatgagt ttggacaaac 60

cacaactaga atgcagtgaa aaaaatgctt tatttgtgaa atttgtgatg ctattgcttt 120

atttgtaacc attataagct gcaataaaca agttaacaac aacaattgca ttcattttat 180

gtttcaggtt caggggggagg tgtgggaggt tttttaaagc aagtaaaacc tctacaaatg 240

tggtatggct gattatgatc tctagtcaag gcactataca tcaaatattc cttattaacc 300

cctttacaaa ttaaaaagct aaaggtacac aatttttgag catagttatt aatagcagac 360

actctatgcc tgtgtggagt aagaaaaaac agtatgttat gattataact gttatgccta 420

cttataaagg ttacagaata tttttccata attttcttgt atagcagtgc agctttttcc 480

tttgtggtgt aaatagcaaa gcaagcaaga gttctattac taaacacagc atgactcaaa 540

aaacttagca attctgaagg aaagtccttg gggtcttcta cctttctctt ctttttttgga 600

ggagtagaat gttgagagtc agcagtagcc tcatcatcac tagatggcat ttcttctgag 660

caaaacaggt tttcctcatt aaaggcattc caccactgct cccattcatc agttccatag 720

gttggaatct aaaatacaca aacaattaga atcagtagtt taacacatta tacacttaaa 780

aattttatat ttaccttaga gctttaaatc tctgtaggta gtttgtccaa ttatgtcaca 840

ccacagaagt aaggttcctt cacaaagatc cctcgagaaa aaaaatataa aagagatgga 900

ggaacgggaa aaagttagtt gtggtgatag gtggcaagtg gtattccgta agaacaacaa 960

gaaaagcatt tcatattatg gctgaactga gcgaacaagt gcaaaattta agcatcaacg 1020

acaacaacga gaatggttat gttcctcctc acttaagagg aaaaccaaga agtgccagaa 1080

ataacatgag caactacaat aacaacaacg gcggctacaa cggtggccgt ggcggtggca 1140

gcttctttag caacaaccgt cgtggtggtt acggcaacgg tggtttcttc ggtggaaaca 1200

acggtggcag cagatctaac ggccgttctg gtggtagatg gatcgatggc aaacatgtcc 1260

cagctccaag aaacgaaaag gccgagatcg ccatatttgg tgtccccgag gatcc 1315

<210> 13

<211> 96
<212> DNA
<213> Artificial

<220>
<223> SPBc2 attB site

<400> 13
tcagataaca gcttggtggc acccattgtg ttcacaggag atacagcttt atctgtactg 60

atattaatga catgctgcac tcggtgtgaa agggca 96

<210> 14
<211> 99
<212> DNA
<213> Artificial

<220>
<223> SF370.1 attP site

<400> 14
acgaaaggag gtcgtgaaat ggataaaaaa atacagcgtt tttcatgtac aactatacta 60

gttgtagtgc ctaaataatg cttttaaaac ttaaaaata 99

<210> 15
<211> 96
<212> DNA
<213> Artificial

<220>
<223> SF370.1 attB site

<400> 15
taaaagggat aataacgttt gtaaaggaga ctgataatgg catgtacaac tatactcgtc 60

ggtaaaaagg catcttatga tggctcaacc atggtt 96

<210> 16
<211> 52
<212> DNA
<213> Artificial

<220>
<223> Bxb1 attP site

<400> 16
gtggtttgtc tggtcaacca ccgcggtctc agtggtgtac ggtacaaacc ca 52

<210> 17
<211> 46
<212> DNA
<213> Artificial

<220>
<223> Bxb1 attB site

<400> 17
ggccggcttg tcgacgacgg cggtctccgt cgtcaggatc atccgg 46

<210> 18
<211> 99
<212> DNA
<213> Artificial

<220>
<223> A118 attP site

<400> 18
acgctagtag cttgtttatt tagattgttt agttcctcgt tttctctcgt tggaagaaga 60

agaaacgaga aactaaaatt ataaataaaa agtaaccta 99

<210> 19
<211> 96
<212> DNA
<213> Artificial

<220>
<223> A118 attB site

<400> 19
ttgagctaat taaaaccagc tgtaactttt tcggatcaag ctatgaagga cgcaaagagg 60

gaactaaaca cttaattggt gttacccata agccac 96

<210> 20
<211> 99
<212> DNA
<213> Artificial

<220>
<223> PhiRv1 attP site

<400> 20
acgagacagc agcacgcaca ggtgtagtgt atctcacagg tccacggttg gccgtggact 60

gctgaagaac attccacgcc aggagatcaa ccatgacca 99

<210> 21
<211> 96
<212> DNA
<213> Artificial

<220>
<223> PhiRv1 attB site

<400> 21
tggcgtagca gcttctcgtg gtggtggaag gtgttggtgc ggggttggcc gtggtcgagg 60

tggggtggtg gtagccattc ggtgtggccg tgggtg 96