

Sequence Range: 1 to 9846

>SacII
|
| 10 20 30 40 50 60 70
CCCCGCGGCAGGCCCTCCGAGCGTGGTGGAGCCGTTCTGTGAGACAGCCGGGTACGAGTCGTGACGCTGGAAGGG
GGGGCGCCGTCCGGGAGGCTCGCACACCTCGCAAGACACTCTGTCCGCCCATGCTCAGCACTGCGACCTTCCC
----- ROSA 26 5' FRAGMENT -----

>RsrII
|
80 90 100 | 110 120 130 140 150
GCAAGCGGGTGGTGGGCAGGAATGCGGTCCGCCCTGCAGCAACCGGAGGGGGAGGGAGAAGGGAGCGGAAAAGTC
CGTTCGCCCACCACCCGTCCTTACGCCAGGCGGGACGTCGTTGGCCTCCCCCTCCCTCTTCCCTCGCCTTTTCAG
----- ROSA 26 5' FRAGMENT -----

>AfeI >AatII
| |
160 170 180 190 200 210 | 220
TCCACCGGACGCGGCCATGGCTCGGGGGGGGGGGGGCAGCGGAGGASCCTTCCGGCCGACGTCTCGTCGCTGAT
AGGTGGCCTGCGCCGTACCGAGCCCCCCCCCCCCCGTCGCTCCTSGCGAAGGCCGGCTGCAGAGCAGCGACTA
----- ROSA 26 5' FRAGMENT -----

>HpaI
|
230 240 250 260 270 280 290 300
TGGCTTYTTTTCTCCCGCCGTGTGTGAAAACACAAATGGCGTGTTTTTGGTTGGCGTAAGGCGCCTGTCAATTAA
ACCGAARAAAAGGAGGGCGGCACACACTTTTGTGTTTACCGCACAAAACCAACCGCATTCCGCGGACAGTCAATT
----- ROSA 26 5' FRAGMENT -----

310 320 330 340 350 360 370
CGGCAGCCGGAGTGCAGCCCGCCGCGCAGCCTCGCTCTGCCACTGGGTGGGGCGGGAGGTAGGTGGGGTGAGGC
GCCGTCGGCCTCACGCGTCGGCGGCCGTCGGAGCGAGACGGGTGACCCACCCCGCCCTCCATCCACCCCACTCCG
----- ROSA 26 5' FRAGMENT -----

>Pml I
|
380 | 390 400 410 420 430 440 450
GAGCTGNACGTGCGGGCGCGGTCCGCCCTCTGGCGGGGCGGGGAGGGGAGGGGTCAGCGAAAGTAGCTCGCG
CTCGACNTGCACGCCCGCCAGCCGGAGACCGCCCCGCCCTCCCTCCCTCCAGTCGCTTTCATCGAGCGC
----- ROSA 26 5' FRAGMENT -----

>NotI
|
| 460 470 480 490 500 510 520
CGCGAGCGGCCGCCACCCTCCCCTTCCCTCTGGGGGAGTCGTTTTACCCGCCCGCCGGCCGGCCCTCGTCGTCTGA
GCGCTCGCCGGCGGGTGGGAGGGGAAGGAGACCCCTCAGCAAAATGGGCGGCGGCCGGCCCGGAGCAGCAGACT
----- ROSA 26 5' FRAGMENT -----

530 540 550 560 570 580 590 600
TTGGCTCTCGGGGCCAGAAAAGTGGCCCTTGCCATTGGCTCGTGTTCGTGCAAGTTGAGTCCATCCGCCGGCCA
AACCGAGAGCCCCGGGTCTTTTACCAGGGAACGGTAACCGAGCACAAGCACGTTCAACTCAGGTAGGCGGCCGGT
----- ROSA 26 5' FRAGMENT -----

610 620 630 640 650 660 670
GCGGGGGCGGCGAGGAGGCGCTCCAGGTTCCGGCCCTCCCCTCGGCCCGCGCCGAGAGTCTGGCCGCGCGCC
CGCCCCCGCCCTCCTCCGCGAGGGTCCAAGGCCGGGAGGGGAGCCGGGGCGCGGCTCTCAGACCGGCGCGCGG

----- ROSA 26 5' FRAGMENT -----

680 690 700 710 720 730 740 750
CCTGCGCAACGTGGCAGGAAGCGCGCGCTGGGGGCGGGGACGGGCAGTAGGGCTGAGCGGCTGCGGGGCGGGTGC
GGACGCGTTGCACCGTCCTTCGCGCGCGACCCCGCCCCTGCCCGTCATCCCGACTCGCCGACGCCCCGCCACG

----- ROSA 26 5' FRAGMENT -----

760 770 780 790 800 810 820
AAGCACGTTTTCCGACTTGAGTTGCCTCAAGAGGGGCGTGCTGAGCCAGACCTCCATCGCGCACTCCGGGGAGTGG
TTCGTGCAAAGGCTGAACTCAACGGAGTTCTCCCCGACGACTCGGTCTGGAGGTAGCGCGTGAGGCCCTCACC

----- ROSA 26 5' FRAGMENT -----

830 840 850 860 870 880 890 900
AGGGAAGGAGCGAGGGCTCAGTTGGGCTGTTTTGGAGGCAGGAAGCACTTGCTCTCCCAAAGTCGCTCTGAGTTG
TCCCTTCTCGCTCCCGAGTCAACCCGACAAAACCTCCGTCCTTCGTGAACGAGAGGGTTTCAGCGAGACTCAAC

----- ROSA 26 5' FRAGMENT -----

910 920 930 940 950 960 970
TTATCAGTAAGGGAGCTGCAGTGGAGTAGGCGGGGAGAAGGCCGACCCTTCTCCGGAGGGGGGAGGGGAGTGT
AATAGTCATTCCCTCGACGTCACCTCATCCGCCCTCTTCCGGCGTGGGAAGAGGCCTCCCCCTCCCCTCACA

----- ROSA 26 5' FRAGMENT -----

980 990 1000 1010 1020 1030 1040 1050
GCAATACCTTTCTGGGAGTTCTCTGCTGCCTCCTGGCTTCTGAGGACCGCCCTGGGCTGGGAGAATCCCTTGCC
CGTTATGGAAGACCCTCAAGAGACGACGGAGGACCGAAGACTCCTGGCGGGACCCGGACCCTCTTAGGGAACGG

----- ROSA 26 5' FRAGMENT -----

>XbaI

1060 1070 1080 | 1090 1100 1110 1120
CCCTCTTCCCCTCGTGATCTGCAACTCCAGTCTTTCTAGAAGATGGGCGGGAGTCTTCTGGGCAGGCTTAAAGGC
GGGAGAAGGGGAGCACTAGACGTTGAGGTCAGAAAGATCTTCTACCCGCCCTCAGAAGACCCGTCCGAATTTCCG

----- ROSA 26 5' FRAGMENT ----->

-----> ROSA 26 3' FRAGMENT -----

1130 1140 1150 1160 1170 1180 1190 1200
TAACCTGGTGTGTGGGCGTTGTCCTGCAGGGGAATTGAACAGGTGTAATAATTGGAGGGACAAGACTTCCCACAGA
ATTGGACCACACACCCGCAACAGGACGTCCCCTTAACTTGTCCACATTTTAACTCCCTGTTCTGAAGGGTGTCT

----- ROSA 26 3' FRAGMENT -----

1210 1220 1230 1240 1250 1260 1270
TTTTCGGTTTTGTGCGGAAGTTTTTTAATAGGGGCAAATAGGAAAATGGAGGATAGGAGTCATCTGGGGTTTTATG
AAAAGCCAAAACAGCCCTTCAAAAAATTATCCCCGTTTATCCTTTTACCTCCTATCCTCAGTAGACCCCAAATAC

----- ROSA 26 3' FRAGMENT -----

1280 1290 1300 1310 1320 1330 1340 1350
CAGCAAACTACAGGTATATTGCTTGTATCCGCCTCGGAGATTTCCATGAGGAGATAAAGACATGTCAACCCGAGT
GTCGTTTTGATGTCCATATAACGAACATAGGCGGAGCCTCTAAAGGTA CTCTATTTCTGTACAGTGGGCTCA

----- ROSA 26 3' FRAGMENT -----

>NruI

1360 1370 1380 1390 1400 1410 1420
TTATACTCTCCTGCTTAGATCCTACTACAGTATGAAATACAGTGTGCGGAGGTAGACTATGTAAGCAGATTTAAT
AATATGAGAGGACGAATCTAGGATGATGTCATACTTTATGTACARCGCTCCATCTGATACATTCGTCTAAATTA

----- ROSA 26 3' FRAGMENT -----

1430 1440 1450 1460 1470 1480 1490 1500
CATTTTAAAGAGCCCGACTTTCATATCCATTTCTCCCGCTCCTTCTGCAGCCTTATCAAAAGGTATTTAGAACA
GTAAAATTTCTCGGGTCATGAAGTATAGGTAAGAGGGGCGAGGAAGACGTCGGAATAGTTTTCCATAAATCTTGT
ROSA 26 3' FRAGMENT

1510 1520 1530 1540 1550 1560 1570
CTCATTTTAGCCCCATTTTCATTTATTATACTGGCTTATCCAACCCCTAGACAGAGCATTGGCATTTCCTTTTC
GAGTAAAATCGGGGTAAAAGTAAATAATATGACCGAATAGGTTGGGGATCTGTCTCGTAACCGTAAAAGGGAAAG
ROSA 26 3' FRAGMENT

1580 1590 1600 1610 1620 1630 1640 1650
CTGATCTTAGAAGTCTGATGACTCATGAAACCAGACAGATTAGTTACATACACCACAAATCGAGGCTGTAGCTGG
GACTAGAATCTTCAGACTACTGAGTACTTTGGTCTGTCTAATCAATGTATGTGGTGTTTAGCTCCGACATCGACC
ROSA 26 3' FRAGMENT

1660 1670 1680 1690 1700 1710 1720
GGCCTCAACACTGCAGTTCTTTTATAACTCCTTAGTACACTTTTTGTTGATCCTTTGCCTTGATCCTTAATTTTC
CCGGAGTTGTGACGTCAAGAAAATATTGAGGAATCATGTGAAAAACAACACTAGGAAACGGAACCTAGGAATTAAG
ROSA 26 3' FRAGMENT

1730 1740 1750 1760 1770 1780 1790 1800
AGTGTCTATCACCTCTCCCGTCAGGTGGTGTTCACATTTGGGCCTATTCTCAGTCCAGGGAGTTTTACAACAAT
TCACAGATAGTGGAGAGGGCAGTCCACCACAAGGTGTAACCCGGATAAGAGTCAGGTCCCTCAAATGTTGTTA
ROSA 26 3' FRAGMENT

1810 1820 1830 1840 1850 1860 1870
AGATGTATTGAGAATCCAACCTAAAGCTTAACTTTCCACTCCCATGAATGCCTCTCTCCTTTTTCTCCATTATAA
TCTACATAACTCTTAGGTTGGATTTTGAATTGAAAGGTGAGGGTACTTACGGAGAGAGGAAAAAGAGGTAATATT
ROSA 26 3' FRAGMENT

1880 1890 1900 1910 1920 1930 1940 1950
CTGAGCTATWACCATTAATGGTTTTAGGTGGATGTCTCCTCCCCAATATACTGATGTATCTACATATTGCCAG
GACTCGATAWTGGTAATTACCAAAGTCCACCTACAGAGGAGGGGTTATATGGACTACATAGATGTATAACGGTC
ROSA 26 3' FRAGMENT

1960 1970 1980 1990 2000 2010 2020
GCTGATATTTTAAGACATWAAAGGTATATTTTCATTATTGAGCCACATGGTATTGACTACTAAAATTTTG
CGACTATAAAATTTCTGTAWTTTCCATATAAAGTAATAACTCGGTGTACCATAACTAATGACGATGATTTTAAAC
ROSA 26 3' FRAGMENT

>BsrGI

|
2030 2040 2050 2060 2070 2080 2090 2100
TCATTGTACACATCTGTAAGGTGGTTCTTTTTGGAATGCAAAGTTTCAGGTGTTTGTGTCTTTCTGACCTAA
AGTAACATGTGTAGACATTTTCCACCAAGGAAAACCTTACGTTTCAAGTCCACAAACAACAGAAAGGACTGGATT
ROSA 26 3' FRAGMENT

2110 2120 2130 2140 2150 2160 2170
GGTCTTGTGAGCTTGTATTTTTCTATTTAAGCAGTGCTTTCTCTTGGACTGGCTTGACTCATGGCATTCTACAC
CCAGAACACTCGAACATAAAAAAGATAAATTCGTCACGAAAGAGAACCTGACCGAAGTACCGTAAGATGTG
ROSA 26 3' FRAGMENT

2180 2190 2200 2210 2220 2230 2240 2250
GTTATTGCTGGTCTAAATGTGATTTTGGCAAGCTTCTTCAGGACCTATAATTTTGTGCTTGTAGCCAAACAC
CAATAACGACCAGATTTACTATAAACGGTTTGAAGAAGTCTGGATATTAACGAACTGAACATCGGTTTGTG
ROSA 26 3' FRAGMENT

2260 2270 2280 2290 2300 2310 2320
AAGTAAAATGATTAAGCAACAAATGATTTTGTGAAGCTTGGTTTTTAGGTTGTTGTGTGTGTGCTTGTGCTC
TTCATTTTACTAATTCGTTGTTTACATAAACACTTTCGAACCAAAAATCCAACAACACAACACACACGAACACGAG
ROSA 26 3' FRAGMENT

>BstAPI
|
2330 2340 2350 2360 2370 2380 2390 2400
TATAATAATACTATCCAGGGGCTGGAGAGGTGGCTCGGAGTTCAAGAGCACAGACTGCTCTTCCAGAAGTCTCTGA
ATATTATTATGATAGGTCCCCGACCTCTCCACCGAGCCTCAAGTTCTCGTGTCTGACGAGAAGGTCTTCAGGACT
ROSA 26 3' FRAGMENT

2410 2420 2430 2440 2450 2460 2470
GTTCAATTTCCAGCAACCACATGGTGGCTCACAACCATCTGTAATGGGATCTGATGCCCTCTTCTGGTGTGTCTG
CAAGTTAAGGGTCGTTGGTGTACCACCGAGTGTGGTAGACATTACCCTAGACTACGGGAGAAGACCACACAGAC
ROSA 26 3' FRAGMENT

2480 2490 2500 2510 2520 2530 2540 2550
AAGACCACAAGTGTATTCACATTAATAATAATCCTCCTTCTTCTTTTTTTTTTTTTTAAAGAGAATWCTGT
TTCTGGTGTTCACATAAGTGTAAATTTATTTATTAGGAGGAAGAAGAAGAAAAAAAAAAAAAAAAATTTCTCTTAWGACA
ROSA 26 3' FRAGMENT

2560 2570 2580 2590 2600 2610 2620
CTCCAGTAGAATTACTGAAGTAATGAAATACTTTGTGTTTTGTTCCAATATGGWAGCCAATAATCAAATACTCTTW
GAGGTCATCTTAATGACTTCATTACTTTATGAAACACAAACAAGGTTATACCWTGCGTTATTAGTTTATGAGAAW
ROSA 26 3' FRAGMENT

2630 2640 2650 2660 2670 2680 2690 2700
AGCACTGGAAATGTACCAAGGAACTATTTTTATTTAAGTGWACTGTGGACAGAGGAGCCATAACTGCAGACTTGTG
TCGTGACCTTTACATGGTTCCTTGATAAAATAAATTCACWTGACACCTGTCTCCTCGGTATTGACGTCTGAACAC
ROSA 26 3' FRAGMENT

2710 2720 2730 2740 2750 2760 2770
GGATACAGAAGACCAATGCAGACTTAATGTCTTTTCTCTTACTACTAAGCAATAAAGAAATAAAAAATTGAACTTCT
CCTATGTCTTCTGGTTACGTCTGAATTACAGAAAAGAGAATGTGATTGTTATTTCTTTATTTTTAACTTGAAGA
ROSA 26 3' FRAGMENT

>NheI
|
2780 2790 2800 2810 2820 2830 2840 2850
AGTATCCTATTTGTTAAACTGCTAGCTTTACTAACTTTTGTGCTTCATCTATACAAAGCTGAAAGCTAAGTCTGC
TCATAGGATAAACAATTTGACGATCGAAATGATTGAAAACACGAAGTAGATATGTTTTCGACTTTTCGATTACAGCG
ROSA 26 3' FRAGMENT

2860 2870 2880 2890 2900 2910 2920
AGCCATTACTAAACATGAAAGCAAGTAATGATAATTTTGGATTTCAAAAATGTAGGGCCAGAGTTTAGCCAGCCA
TCGGTAATGATTTGTACTTTTCGTTTCACTACTATTAACCTAAAGTTTTTACATCCCGGTCTCAAATCGGTTCGGT
ROSA 26 3' FRAGMENT

>Bgl II
|
2930 2940 2950 2960 2970 2980 2990 3000
GTGGTGGTGCCTTTATGCCTTAATCCCAGCACTCTGGAGGCAGAGACAGGCAGATCTCTGAGTTTGTAGCCC
CACCACCACGAACGAAATACGGAATTAGGGTCGTGAGACCTCCGTCTCTGTCCGTCTAGAGACTCAAACCTCGGG
ROSA 26 3' FRAGMENT

3010 3020 3030 3040 3050 3060 3070
AGCCTGGTCTACACATCAAGTTCTATCTAGGATAGCCAGGAATACACACAGAAACCCTGTTGGGGAGGGGGGCTC
TCGGACCAGATGTGTAGTTCAAGATAGATCCTATCGGTCCTTATGTGTGTCTTTGGGACAACCCCTCCCCCGAG
ROSA 26 3' FRAGMENT

3080 3090 3100 3110 3120 3130 3140 3150
TGAGATTTTCATAAAATTATAATTGAAGCATTCCCTAATGAGCCACTATGGATGTGGCTAAATCCGTCTACCTTTC
ACTCTAAAGTATTTTAATATTAACCTTCGTAAGGGATTACTCGGTGATACCTACACCGATTTAGGCAGATGGAAAG
ROSA 26 3' FRAGMENT

3160 3170 3180 3190 3200 3210 3220
TGATGAGATTTGGGTATTATTTTTCTGTCTCTGCTGTTGGTTGGGTCTTTTTGACACTGTGGGCTTTCTTAAAGC
ACTACTCTAAACCCATAATAAAAAAGACAGAGACGACAACCAACCCAGAAAACCTGTGACACCCGAAAGAATTTTCG
ROSA 26 3' FRAGMENT

3230 3240 3250 3260 3270 3280 3290 3300
CTCCTTCCCTGCCATGTGGTCTCTTGTGTTGCTACTAACTTCCCATGGCTTAAATGGCATGGCTTTTTGCCTTCTA
GAGGAAGGGACGGTACACCAGAGAACAACGATGATTGAAGGGTACCGAATTTACCGTACCGAAAAACGGAAGAT
ROSA 26 3' FRAGMENT

3310 3320 3330 3340 3350 3360 3370
AGGGCAGCTGCTGAGWTTTGCAGCCTGATTTCCAGGGTGGGGTTGGGAAATCTTTCAAACACTAAAATTGTCCTT
TCCCGTCGACGACTCWAACGTCGGACTAAAGGTCCCACCCCAACCCTTTAGAAAAGTTTGTGATTTTAAACAGGAA
ROSA 26 3' FRAGMENT

3380 3390 3400 3410 3420 3430 3440 3450
TAATTTTTTTTTTAAAAAATGGGTTATATAATAAACCTCATAAAATAGTTATGAGGAGTGAGGTGGACTAATATTA
ATTAATAAAAAAATTTTTTACCCAATATATTATTTGGAGTATTTTATCAATACTCCTCACTCCACCTGATTATAAT
ROSA 26 3' FRAGMENT

3460 3470 3480 3490 3500 3510 3520
ATGAGTCCCTCCCCTATAAAAGAGCTATTAAGGCTTTTTGTCTTATACTAACTTTTTTTTTTAAATGTGGTATCTT
TACTCAGGGAGGGGATATTTTCTCGATAATTCCGAAAAACAGAATATGATTGAAAAAAAATTTACACCATAGAA
ROSA 26 3' FRAGMENT

3530 3540 3550 3560 3570 3580 3590 3600
TAGAACCAAGGGTCTTAGAGTTTTAGTATACAGAAACTGTTGCATCGCTTAATCAGATTTTCTAGTTTCAAATCC
ATCTTGGTTCCAGAAATCTCAAAATCATATGTCTTTGACAACGTAGCGAATTAGTCTAAAAGATCAAAGTTTAGG
ROSA 26 3' FRAGMENT

3610 3620 3630 3640 3650 3660 3670
AGAGAATCCAAATTCTTACAGCCAAAGTCAAATTAAGAATTTCTGACTTTAATGTTATTTGCTACTGTGAATAT
TCTCTTAGGTTTAAAGAAGTGTGGTTTTAGTTTAAATTCTTAAAGACTGAAATTACAATAAACGATGACACTTATA
ROSA 26 3' FRAGMENT

3680 3690 3700 3710 3720 3730 3740 3750
AAAATGATAGCTTTTCTGAGGCAGGGTCTCACTATGTATCTCTGCCTGATCTGCAACAAGATATGTAGACTAAA
TTTTACTATCGAAAAGGACTCCGTCCAGAGTGATACATAGAGACGGACTAGACGTTGTTCTATACATCTGATTT
ROSA 26 3' FRAGMENT

3760 3770 3780 3790 3800 3810 3820
GTTCTGCCTGCTTTTTGTCTCCTGAATACTAAGGTTAAAATGTAGTAATACTTTTTGGAACCTGCAGGTCAGATTCT
CAAGACGGACGAAAACAGAGGACTTATGATTCCAATTTTACATCATTATGAAAACCTTGAACGTCCAGTCTAAGA
ROSA 26 3' FRAGMENT

3830 3840 3850 3860 3870 3880 3890 3900
TTTTATAGGGGACACACTAAGGGAGCTTGGGTGATAGTTGGTAAATGTGTTTAAAGTGATGAAAACCTTGAATTATTA

----- ROSA 26 3' FRAGMENT -----

4660 4670 4680 4690 4700 4710 4720
AGTGTATACTAGTTATATGTTGGAGGACATGTTTATCCAGAAGATATTCAGGACTATTTTTGACTGGGCTAAGGA
TCACATATGATCAATATACAACCTCCTGTACAAATAGGTCTTCTATAAGTCTGATAAAAACTGACCCGATTCTCT

----- ROSA 26 3' FRAGMENT -----

4730 4740 4750 4760 4770 4780 4790 4800
ATTGATTCTGATTAGCACTGTTAGTGAGCATTGAGTGGCCTTTAGGCTTGAATTGGAGTCACTTGTATATCTCAA
TAACTAAGACTAATCGTGACAATCACTCGTAACTCACCGGAAATCCGAACTTAACCTCAGTGAACATATAGAGTT

----- ROSA 26 3' FRAGMENT -----

4810 4820 4830 4840 4850 4860 4870
ATAATGCTGGCCTTTTTTWWAAAAGCCCTTGTTCTTTATCACCTGTTTTCTACATAATTTTTGTTCAAAGAAATA
TATTACGACCGGAAAAAAWTTTTTCGGGAACAAGAAATAGTGGGACAAAAGATGTATTA AAAACAAGTTTCTTTAT

----- ROSA 26 3' FRAGMENT -----

4880 4890 4900 4910 4920 4930 4940 4950
CTTGTGGGATCTCCTTTTGACAACAATAGCATGTTTTCAAGCCATATTTTTTTTTCTTTTTTTTTTTTTTTTTTG
GAACAAACCTAGAGGAAAACCTGTTGTTATCGTACAAAAGTTCCGTATAAAAAAAGGAAAAAAAAAAAAAAAAAAC

----- ROSA 26 3' FRAGMENT -----

4960 4970 4980 4990 5000 5010 5020
GTTTTTCGAGACAGGGTTTCTCTGTATAGCCCTGGCTGTCCTGGAACCTCACTTTGTAGACCAGGCTGGCCTCGAA
CAAAAAGCTCTGTCCCAAAGAGACATATCGGGACCGACAGGACCTTGAGTGAAACATCTGGTCCGACCGGAGCTT

----- ROSA 26 3' FRAGMENT -----

5030 5040 5050 5060 5070 5080 5090 5100
CTCAGAAATCCGCCTGCCTCTGCCTCCTGAGTGCCGGGATTAAGGCGTGCACCACCACGCCTGGCTAAGTTGGA
GAGTCTTTAGGCGGACGGAGACGGAGGACTCACGGCCCTAATTTCCGCACGTGGTGGTGGGACCGATTCAACCT

----- ROSA 26 3' FRAGMENT -----

5110 5120 5130 5140 5150 5160 5170
TATTTTGTATATAACTATAACCAATACTAACTCCACTGGGTGGATTTTTAATTCAGTCAGTAGTCTTAAGTGGTC
ATAAAACATATATTGATATTGGTTATGATTGAGGTGACCCACCTAAAAATTAAGTCAGTCATCAGAATTCACCAG

----- ROSA 26 3' FRAGMENT -----

5180 5190 5200 5210 5220 5230 5240 5250
TTTATTGGCCCTTATTAATAATCTACTGTTCACTCTAACAGAGGCTGTTGGACTAGTGGSACTAAGCAACTTCCTA
AAATAACCGGGAATAATTTTAGATGACAAGTGAGATTGTCTCCGACAACCTGATCACCCSTGATTGTTGAAGGAT

----- ROSA 26 3' FRAGMENT -----

5260 5270 5280 5290 5300 5310 5320
CGGATATACTAGCAGATAAGGGTCAGGGATAGAACTAGTCTAGCGTTTTGTATACCTACCAGCTTATACTACCT
GCCTATATGATCGTCTATTCCCAGTCCCTATCTTTGATCAGATCGCAAAACATATGGATGGTCGAATATGATGGA

----- ROSA 26 3' FRAGMENT -----

5330 5340 5350 5360 5370 5380 5390 5400
TGTTCTGATAGAAATATTTAGGACATCTAGCTTATCGATCCGTCGACGGTATCGATAAGCTTGATATCGAATTCT
ACAAGACTATCTTTATAAATCCTGTAGATCGAATAGCTAGGCAGCTGCCATAGCTATTGAACTATAGCTTAAGA

----- ROSA 26 3' FRAGMENT -----

>Sal I | >EcoRV |
----->

----- PGK DTA BPA -----

5410 5420 5430 5440 5450 5460 5470
ACCGGGTAGGGGAGGCGCTTTTCCAAGGCAGTCTGAGCATGCGCTTAGCAGCCCCGCTGGCACTTGGCGCTACAC

TGGCCCATCCCCTCCGCGAAAAGGTTCCGTCAGACTCGTACGCGAATCGTCGGGGCGACCGTGAACCGCGATGTG

PGK DTA BPA

>AgeI
|
5480 5490 5500 5510 5520 5530 5540 5550
AAGTGGCCTYTGGCCTCGCACACATTCCACATCCACCGGTAGGCGCCAACCGGCTCCGTTCTTTGGTGGCCCCTT
TTCACCGGARACCGGAGCGTGTGTAAGGTGTAGGTGGCCATCCGCGGTTGGCCGAGGCAAGAAACCACCGGGGAA

PGK DTA BPA

5560 5570 5580 5590 5600 5610 5620
CGCGCCACCTTCTWCTCCTCCCCTAGTCAGGAAGTTCCCCCGCCCCGAGCTCGCGTCGTSAGGACGTGACAA
GCGCGGTGGAAGAWGAGGAGGGGATCAGTCCTTCAAGGGGGGGCGGGGCGTCGAGCGCAGCASTCCTGCACTGTT

PGK DTA BPA

5630 5640 5650 5660 5670 5680 5690 5700
ATGGAAGTAGCACGTCTCACTAGTCTCGTCAGATGGACAGCACCGCTGAGCAATGGAAGCGGGTAGGCCTTTGGG
TACCTTCATCGTGCAGAGTGATCAGAGCAGTCTACCTGTCGTGGCGACTCGTTACCTTCGCCCATCCGAAACCC

PGK DTA BPA

5710 5720 5730 5740 5750 5760 5770
GCAGCGCCAATAGCAGCTTTGCTCCTTCGCTTTCTGGGCTCAGAGGCTGGGAAGGGGTGGGTCCGGGGGCGGGC
CGTCGCCGTTATCGTCGAAACGAGGAAGCGAAAGACCCGAGTCTCCGACCCTTCCCCACCCAGGCCCCCGCCCG

PGK DTA BPA

5780 5790 5800 5810 5820 5830 5840 5850
TCAGGGGCGGGCTCAGGGGCGGGGCGGGCGCCGAAGGTCCTCCGGAGGCCCGGCATTCTGCACGCTTCAAAAGC
AGTCCCCGCCGAGTCCCCGCCCGCCCGGGGCTTCCAGGAGGCTCCGGGCGGTAAGACGTGCGAAGTTTTTCG

PGK DTA BPA

5860 5870 5880 5890 5900 5910 5920
GCACGTCTGCCGCGCTGTTCTCCTCTTCCTCATCTCCGGGCTTTTCGACCTGCAGGTCCTCGCCATGGATCCTGA
CGTGCAGACGGCGGACAAGAGGAGAAGGAGTAGAGGCCCGAAAGCTGGACGTCCAGGAGCGGTACCTAGGACT

PGK DTA BPA

5930 5940 5950 5960 5970 5980 5990 6000
TGATGTTGTTATTCTTCTAATCTTTTTGTATGGA AAACTTTTCTTCGTACCACGGGACTAAACCTGGTTATGTAGA
ACTACAACAATAAGAAGATTAGAAAACATACCTTTTTGAAAAGAAGCATGGTGCCTGATTTGGACCAATACATCT

PGK DTA BPA

6010 6020 6030 6040 6050 6060 6070
TTCCATTCAAAAAGGTATACAAAAGCCAAAATCTGGTACACAAGGAAATTATGACGATGATTGGAAGGGTTTTTA
AAGGTAAGTTTTTCCATATGTTTTCGGTTTTAGACCATGTGTTCTTTAATACTGCTACTAACCTTTCCAAAAT

PGK DTA BPA

6080 6090 6100 6110 6120 6130 6140 6150
TAGTACCGACAATAAATACGACGCTGCGGGATACTCTGTAGATAATGAAAACCGCTCTCTGGAAAAGCTGGAGG
ATCATGGCTGTTATTTATGCTGCGACGCCCTATGAGACATCTATTACTTTTGGGCGAGAGACCTTTTCGACCTCC

PGK DTA BPA

6160 6170 6180 6190 6200 6210 6220
CGTGGTCAAAGTGACGTATCCAGGACTGACGAAGGTTCTCGCACTAAAAGTGGATAATGCCGAAACTATTAAGAA
GCACCAGTTTTCACTGCATAGGTCCTGACTGCTTCCAAGAGCGTGATTTTACCTATTACGGCTTTGATAATTCTT

PGK DTA BPA

6230 6240 6250 6260 6270 6280 6290 6300
AGAGTTAGGTTTTAAGTCTCACTGAACCGTTGATGGAGCAAGTCGGAACGGAAGAGTTTTATCAAAAAGGTTTCGGTGA

TCTCAATCCAAATTCAGAGTGACTTGGCAACTACCTCGTTTCAGCCTTGCCTTCTCAAATAGTTTTCCAAGCCACT

PGK DTA BPA

>BbvCI

6310 6320 6330 | 6340 6350 6360 6370
TGGTGCTTCGCGTGTAGTGCTCAGCCTTCCCTTCGCTGAGGGGAGTTCTAGCGTTGAATATATTAATAACTGGGA
ACCACGAAGCGCACATCACGAGTCGGAAGGGAAGCGACTCCCCTCAAGATCGCAACTTATATAATTATTGACCCT

PGK DTA BPA

>MscI

6380 6390 6400 6410 6420 6430 | 6440 6450
ACAGGCGAAAGCGTTAAGCGTAGAACTTGAGATTAATTTTTGAAACCCGTGGAAAACGTGGCCAAGATGCGATGTA
TGTCCGCTTTTCGCAATTCGCATCTTGAACCTCTAATTAATAAACTTTGGGCACCTTTTGCACCGGTTCTACGCTACAT

PGK DTA BPA

6460 6470 6480 6490 6500 6510 6520
TGAGTATATGGCTCAAGCCTGTGCAGGAAATCGTGTGCAGGCGATCTCTTTGTGAAGGAACCTTACTTCTGTGGTG
ACTCATATAACCGAGTTCGGACACGTCCTTTAGCACAGTCCGCTAGAGAAACACTTTCCTTGAATGAAGACACCAC

PGK DTA BPA

6530 6540 6550 6560 6570 6580 6590 6600
TGACATAATTGGACAAACTACCTACAGAGATTTAAAGCTCTAAGGTAAATATAAAATTTTTAAGTGTATAATGTG
ACTGTATTAACCTGTTTGATGGATGTCTCTAAATTTTCGAGATTCCATTTATATTTTTAAAAATTCACATATTACAC

PGK DTA BPA

6610 6620 6630 6640 6650 6660 6670
TTAAACTACTGATTCTAATTGTTTGTGTATTTTGTAGATTCCAACCTATGGAAGTGAATGGGAGCAGTGGTGGGA
AATTTGATGACTAAGATTAACAAACACATAAAATCTAAGGTTGGATACCTTGACTACTTACCCTCGTCACCACCT

PGK DTA BPA

6680 6690 6700 6710 6720 6730 6740 6750
ATGCAGATCCTAGAGCTCGCTGATCAGCCTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGGCCCTCCC
TACGTCTAGGATCTCGAGCGACTAGTCGGAGCTGACACGGAAGATCAACGGTTCGGTAGACAACAAACGGGGAGGG

PGK DTA BPA

6760 6770 6780 6790 6800 6810 6820
CCGTGCCTTCCCTTGACCCTGGAAGGTGCCACTCCCCTGTCCTTTTCTAATAAAAATGAGGAAATTGCATCGCATT
GGCACGGAAGGAACTGGGACCTTCCACGGTGAGGGTGACAGGAAAGGATTATTTTACTCCTTTAACGTAGCGTAA

PGK DTA BPA

6830 6840 6850 6860 6870 6880 6890 6900
GTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAATA
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|

>XhoI

|

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