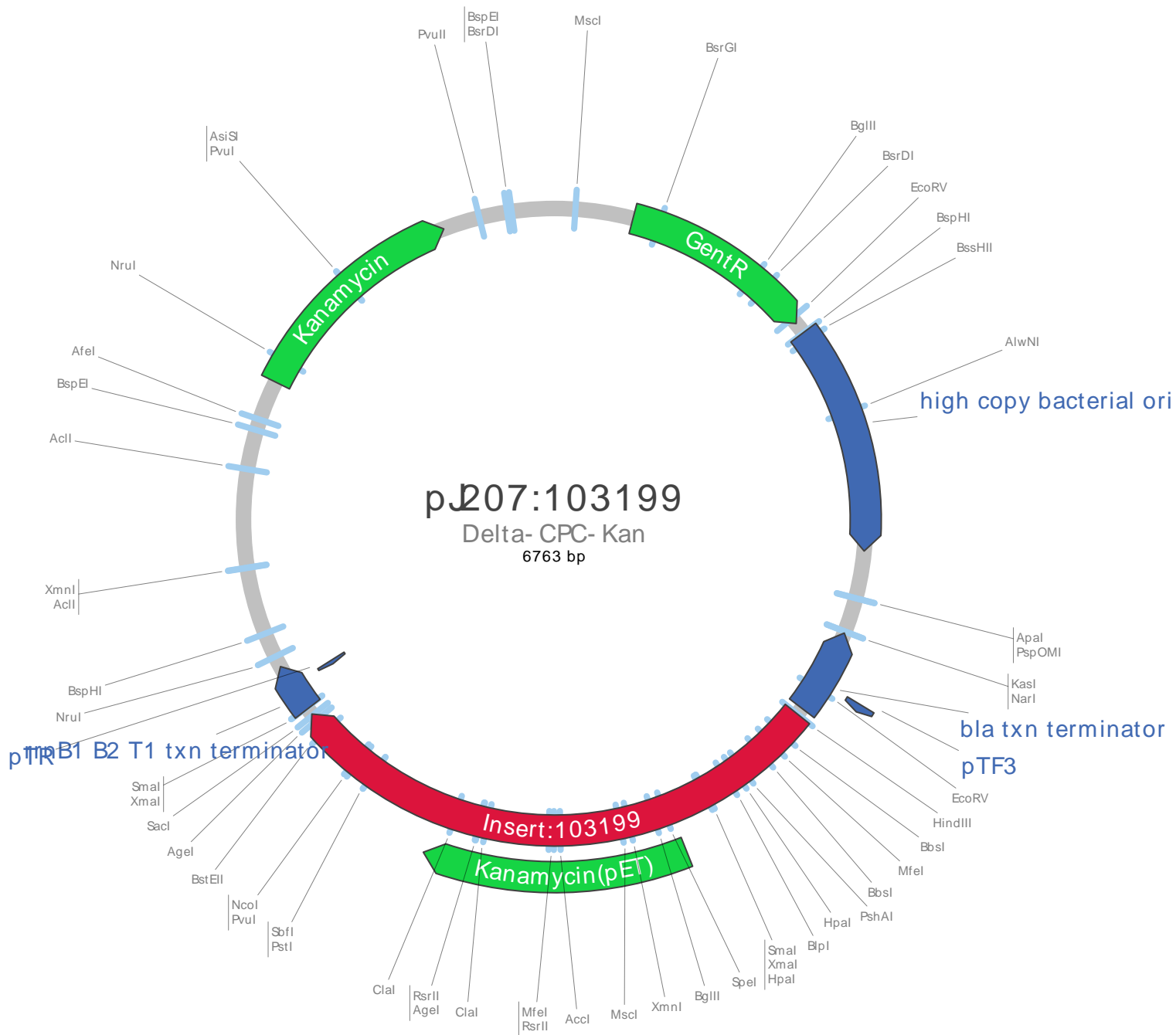


Plasmid Map

pJ207:103199

Only single cutters are shown in the map.



Original Author

DNA2.0, Inc.

1430 OBrien Drive, Suite E

Menlo Park, CA 94025-1438

1-877-DNA-TOGO (Toll free) 1-650-853-8351 (Fax).

info@dna20.com

www.dna20.com

Feature Map

Name	Start	End	
Insert: 103199	2418	4345	
GentR	274	957	
high copy bacterial ori	997	1800	
pTF3	2277	2302	
bla txn terminator	2393	2093	Complement
Kanamycin(pET)	2974	3786	
rrnB1 B2 T1 txn terminator	4368	4542	
pTR	4467	4451	Complement
Kanamycin	5565	6371	

Restriction Map

Name	Sequence	5' Cut Positions
AccI	GTMKAC	3363
AclI	AACGTT	4906, 5248
AfeI	AGCGCT	5426
AgeI	ACCGGT	3644, 4318
AlwNI	CAGNNNCTG	1317
ApaI	GGGCCC	1970
ApaLI	GTGCAC	1412, 4836, 5137, 6679
AseI	ATTAAT	2966, 5302, 6189
AsiSI	GCGATCGC	5990
AvaI	CYCGRG	380, 625, 1963, 2838, 4374
AvrII	CCTAGG	2487, 2745, 3678
BbsI	GAAGAC	2491(C), 2592(C)
BglI	GCCNNNNNGGC	1974, 4208, 5359
BglII	AGATCT	740, 3036
BlnI	GCTNAGC	2753
BspEI	TCCGGA	5386, 6598
BspHI	TCATGA	998, 4668
BsrBI	CCGCTC	1797, 4301, 4666
BsrDI	GCAATG	788(C), 6621
BsrGI	TGTACA	366
BssHII	GCGCGC	1028
BstEII	GGTNACC	4268
BtsI	GCAGTG	335, 890, 4016, 5089, 5109(C), 5851(C), 5938
ClaI	ATCGAT	3617, 3731
EcoRV	GATATC	936, 2310
HincII	GTYRAC	2328, 2717, 2848, 3197
HindIII	AAGCTT	2418
HpaI	GTTAAC	2717, 2848

Name	Sequence	5' Cut Positions
KasI	GGCGCC	2087
MfeI	CAATTG	2552, 3384
MscI	TGGCCA	74, 3157
NarI	GGCGCC	2088
NcoI	CCATGG	4113
NruI	TCGCGA	4583, 5647
NsiI	ATGCAT	2384, 3255, 3521, 5840, 6106
PciI	ACATGT	511, 1726, 2322
PshAI	GACNNNGTC	2691
PspOMI	GGGCC	1966
PstI	CTGCAG	4052
PvuI	CGATCG	4128, 5990
PvuII	CAGCTG	6502
RsrII	CGGWCCG	3402, 3642
SacI	GAGCTC	4344
SbfI	CCTGCAGG	4052
SmaI	CCCGGG	2840, 4376
SpeI	ACTAGT	2995
SspI	AATATT	119, 2079, 2240, 4703, 5915
XmaI	CCCGGG	2838, 4374
XmnI	GAANNNTTC	3128, 4908
Acc65I	GGTACC	no cuts
AscI	GGCGGCC	no cuts
BamHI	GGATCC	no cuts
BclI	TGATCA	no cuts
BsaI	GGTCTC	no cuts
BsiWI	CGTACG	no cuts
BsmBI	CGTCTC	no cuts
BstBI	TTCGAA	no cuts
BstXI	CCANNNNTGG	no cuts
EagI	CGGCCG	no cuts
EcoRI	GAATTC	no cuts
FseI	GGCCGGCC	no cuts
KpnI	GGTACC	no cuts
MluI	ACGCGT	no cuts
NdeI	CATATG	no cuts
NheI	GCTAGC	no cuts
NotI	GCGGCCGC	no cuts
Pacl	TTAATTAA	no cuts
PmeI	GTTTAAAC	no cuts
PmlI	CACGTG	no cuts
PpuMI	RGGWCCY	no cuts
PspXI	VCTCGAGB	no cuts
SacII	CCGCGG	no cuts
SalI	GTCGAC	no cuts
SanDI	GGGWCCC	no cuts
SapI	GCTCTC	no cuts
SfiI	GGCCNNNNGGCC	no cuts
SnaBI	TACGTA	no cuts
SphI	GCATGC	no cuts
Swal	ATTTAAAT	no cuts
XbaI	TCTAGA	no cuts
XhoI	CTCGAG	no cuts

Sequence

1 AGGGTTTATT GAGAATATGT TTTTCGTCAG CGCCAATCCC TGGGTGAGTT TCACCAGTTT
61 TGATTTAAAC GTGGCCAATA TGGACAACCTT CTTCGCCCCC GTTTTCACTA TGGGCAAATA
121 TTATACGCAA GGCACAAAGG TGCTGATGCC GCTGGCGATT CAGGTTTCATC ATGCCGTCTG
181 TGATGGCTTC CATGTCCGCA GAATGCTTAA TGAATTACAA CAGTACTGCG ATGAGTGGCA
241 GGGCGGGGCG TAAACGCCGA GGAGGAAAAA AAAATGCGCT CACGCAACTG GTCCAGAACC
301 TTGACCGAAC GCAGCGGTGG TAACGGCGCA GTGGCGGTTT TCATGGCTTG TTATGACTGT
361 TTTTTTGTAC AGTCTATGCC TCGGGCATCC AAGCAGCAAG CGCGTTACGC CGTGGGTCGA
421 TGTTTGATGT TATGGAGCAG CAACGATGTT ACGCAGCAGG GCAGTCGCC TAAAACAAAG
481 TTAGGTGGCT CAAGTATGGG CATCATTCCG ACATGTAGGC TCGGCCCTGA CCAAGTCAA
541 TCCATGCGGG CTGCTCTTGA TCTTTTCGGT CGTGAGTTCG GTGACGTAGC CACCTACTCC
601 CAACATCAGC CGGACTCCGA TTACCTCGGG AACTTGCTCC GTAGTAAGAC ATTCATCGCG
661 CTTGCTGCCT TCGACCAAGA AGCGGTTGTT GGCCTCTCG CGGCTTACGT TCTGCCAAG
721 TTTGAGCAGC CGCGTAGTGA GATCTATATC TATGATCTCG CAGTCTCCGG CGAGCACCGG
781 AGGCAGGGCA TTGCCACCGC GCTCATCAAT CTCTCAAGC ATGAGGCCAA CGCGCTTGGT
841 GCTTATGTGA TCTACGTGCA AGCAGATTAC GGTGACGATC CCGCAGTGGC TCTCTATACA
901 AAGTTGGGCA TACGGGAAGA AGTGATGCAC TTTGATATCG ACCCAAGTAC CGCCACCTAA
961 GCAGAGCATT ACCTGACTT GACGGGACGG CGCAAGCTCA TGACCAAAAT CCCTTAACGT
1021 GAGTTACGCG CGCGTCGTTT CACTGAGCGT CAGACCCCGT AGAAAAGATC AAAGGATCTT
1081 CTTGAGATCC TTTTTTCTG CGCGTAATCT GCTGCTTGCA AACAAAAAAA CCACCGCTAC
1141 CAGCGGTGGT TTGTTTGCCG GATCAAGAGC TACCAACTCT TTTTCCGAAG GTAACGGCT
1201 TCAGCAGAGC GCAGATACCA AATACTGTTT TTCTAGTGTA GCCGTAGTTA GCCCACCCT
1261 TCAAGAACTC TGTAGCACCG CCTACATACC TCGCTCTGCT AATCCTGTTA CCAGTGGCTG
1321 CTGCCAGTGG CGATAAGTCG TGTCTTACCG GGTGGACTC AAGACGATAG TTACCGGATA
1381 AGGCGCAGCG GTCGGGCTGA ACGGGGGGTT CGTGCACACA GCCCAGCTTG GAGCGAACGA
1441 CCTACACCGA ACTGAGATAC CTACAGCGTG AGCTATGAGA AAGCGCCACG CTTCCCGAAG
1501 GGAGAAAGGC GGACAGGTAT CCGTAAGCG GCAGGGTCGG AACAGGAGAG CGCACGAGGG
1561 AGCTTCCAGG GGGAAACGCC TGGTATCTTT ATAGTCCTGT CGGGTTTCGC CACCTCTGAC
1621 TTGAGCGTCG ATTTTTGTGA TGCTCGTCAG GGGGGCGGAG CCTATGAAA AACGCCAGCA
1681 ACGCGGCCCT TTTACGGTTC CTGGCCTTTT GCTGGCCTTT TGCTCACATG TTCTTTCCTG
1741 CGTTATCCCC TGATTCTGTG GATAACCGTA TTACCGCCTT TGAGTGAGCT GATACCGCTC
1801 GCCGACCGG AACGACCGAG CGCAGCGAGT CAGTGAGCGA GGAAGCGGAA GGCGAGAGTA
1861 GGAACTGCC AGGCATCAAA CTAAGCAGAA GGCCCTGAC GGATGGCCTT TTTGCGTTT
1921 TACAAACTCT TTCTGTGTTG TAAAACGACG GCCAGTCTTA AGCTCGGGCC CCCTGGGCGG
1981 TTCTGATAAC GAGTAATCGT TAATCCGCAA ATAACGTAAA AACCCGCTTC GCGGGGTTTT
2041 TTTATGGGGG GAGTTTAGGG AAAGAGCATT TGTCAGAATA TTTAAGGGCG CCTGTCACTT
2101 TGCTTGATAT ATGAGAATTA TTTAACCTTA TAAATGAGAA AAAAGCAACG CACTTTAAAT
2161 AAGATACGTT GCTTTTTCGA TTGATGAACA CCTATAATTA AACTATTCAT CTATTATTTA
2221 TGATTTTTTG TATATACAAT ATTTCTAGTT TGTTAAAGAG AATTAAGAAA ATAAATCTCG
2281 AAAATAATAA AGGGAATAAT AGTTTTTGAT ATCAAAATTA TACATGTCAA CGATAATACA
2341 AAATATAATA CAACTATAA GATGTTATCA GTATTTATTA TGCATTTAGA ATAAATTTTG
2401 TGTCGCCCTT CGCTGAAAAG CTTAAGAGTC CCTGAATATC AAAATGGTGG GATAAAAAGC
2461 TCAAAAAGGA AAGTAGGCTG TGGTTCCTA GGCAACAGTC TTCCCTACCC CACTGGAAC
2521 TAAAAAACG AGAAAAGTTC GCACCGAACA TCAATTGCAT AATTTTAGCC CTAAAACATA

2581 AGCTGAACGA AACTGGTTGT CTTCCCTTCC CAATCCAGGA CAATCTGAGA ATCCCCTGCA
2641 ACATTACTTA ACAAAAAAGC AGGAATAAAA TTAACAAGAT GTAACAGACA TAAGTCCCAT
2701 CACCGTTGTA TAAAGTTAAC TGTGGGATTG CAAAAGCATT CAAGCCTAGG CGCTGAGCTG
2761 TTTGAGCATC CCGTGGCCC TTGTCGCTGC CTCCTGTTTT CTCCCTGGAT TTATTTAGGT
2821 AATATCTCTC ATAAATCCCC GGGTAGTTAA CGAAAGTTAA TGGAGATCAG TAACAATAAC
2881 TCTAGGGTCA TTACTTTGGA CTCCTCAGT TTATCCGGGG GAATTGTGTT TAAGAAAATC
2941 CCAACTCATA AAGTCAAGTA GGAGATTAAT TCAATGAGTC ACATCCAGAG AGAAACTAGT
3001 TGTTCCTGAC CTCGTTTGAA TAGCAATATG GATGCAGATC TGTACGGATA TAAATGGGCG
3061 CGAGATAACG TAGGCCAATC TGGGGCCACT ATTTATCGGT TATATGGCAA ACCAGATGCT
3121 CCCGAACTGT TTCTCAAACA TGGCAAAGGG TCTGTGGCCA ATGATGTTAC CGATGAAATG
3181 GTGCGGTTGA ACTGGTTGAC AGAATTTATG CCCCTCCCGA CCATCAAACA TTTTATCAGG
3241 ACTCCAGACG ATGCATGGCT ATTAACACG GCCATTCTTG GGAAACTGC CTTTCAGGTG
3301 TTGGAAGAAT ATCCCGATTC TGGTGAGAAT ATCGTCGATG CGTTAGCGGT TTTTCTAAGA
3361 CGTCTACATA GCATTCCTG TTGCAATTGT CCCTTTAATT CGGACCGGGT GTTCCGCTTG
3421 GCGCAGGCTC AGTCCCGGAT GAATAACGGT TTGGTAGATG CCTCGGACTT TGATGATGAA
3481 CGGAACGGCT GGCCGTTGA ACAGTTTGG AAAGAGATGC ATAAGCTGCT GCCCTTCTCC
3541 CCCGACAGCG TTGTTACTCA TGGAGATTTT TCTCTCGATA ATCTGATTTT CGACGAAGGC
3601 AAGCTAATTG GCTGTATCGA TGTGGGACGG GTAGGGATTG CGGACCGGTA TCAAGACCTA
3661 GCAATTTTGT GGAAGTGCCT AGGTGAATTT TCCCCAGCC TACAAAAACG GCTGTTTCAA
3721 AAATACGGAA TCGATAATCC CGACATGAAC AAATTACAAT TTCATCTGAT GCTAGATGAG
3781 TTCTTTTAGG CTATTTTGTT AATTACTATT TGAGCTGAGT GTAAAATACC TTACTTACTC
3841 AAAAGCATTG ACTAACCATA ACAATGACTA ATCTCTTTTT TTGATTGAAC TCCAACTAG
3901 AATAGCCATC GAGTCAGTCC ATTTAGTTCA TTATTAGTGA AAGTTTGTG GCGGTGGGT
3961 ATCCGTTGAT AAACCACCGT TTTTGTGTTG GCAAAGTAAC GATTTGATGC AGTGATGGGT
4021 TTAAAGATAA TCCCGTTTGA GGAAATCTG CAGGACGACG GGAACTTTAA CCTGACCGCT
4081 GCTGGGTTG TAATAATTTT CTAAAATTGC CGCCATGGTG CGCCGATCG CCAAACCGGA
4141 ACCGTTGAGA GTGTGAACAA ATTGGGTGCC TTTTTGCCC TTTTCTTGT AGCGAATGTT
4201 GGCCGACGG GCTTGAAAT CGTGGAAGTT AGAACAACG GAAATTTCCC GGTAGGTGTT
4261 AGCCGATGGT AACCAAATT CCAAGTCGTA GCATTTAGCC GCTCCAAAAC CTAAATCACC
4321 GGTACATAAT TCCACCACTG AGCTCCGTCA AAAGGGCGAC ACCCCTCAAT TAGCCCGGGC
4381 GAAAGGCCA GTCTTTCGAC TGAGCCTTTC GTTTTATTTG ATGCCTGGCA GTTCCCTACT
4441 CTCGCATGGG GAGTCCCCAC ACTACCATCG GCGCTACGGC GTTTCACTTC TGAGTTCGGC
4501 ATGGGGTCAG GTGGGACCAC CGCGCTACTG CCGCCAGGCA AACAAAGGGT GTTATGAGCC
4561 ATATTCAGGT ATAAATGGGC TCGCGATAAT GTTCAGAATT GGTAAATTGG TTGTAACACT
4621 GACCCTATT GTTTATTTT TCTAAATACA TTCAAATATG TATCCGCTCA TGAGACAATA
4681 ACCCTGATAA ATGCTTCAAT AATATTGAAA AAGGAAGAAT ATGAGTATTC AACATTTCCG
4741 TGTCGCCCTT ATTCCTTTT TTGCGGCATT TTGCCTTCCT GTTTTTGCTC ACCCAGAAAC
4801 GCTGGTGAAG GTAAAAGATG CTGAAGATCA GTTGGGTGCA CGAGTGGGT ACATCGAACT
4861 GGATCTCAAC AGCGGTAAGA TCCTTGAGAG TTTTCGCCCC GAAGAACGTT TTCCAATGAT
4921 GAGCACTTTT AAAGTTCTGC TATGTGGCGC GGTATTATCC CGTATTGACG CCGGGCAAGA
4981 GCAACTCGGT CGCCGCATAC ACTATTCTCA GAATGACTTG GTTGAGTACT CACCAGTCAC
5041 AGAAAAGCAT CTTACGGATG GCATGACAGT AAGAGAATTA TGCAGTGCTG CCATAACCAT
5101 GAGTGATAAC ACTGCGGCCA ACTTACTTCT GACAACGTGC ACAACATGGG GGATCATGTA
5161 ACTCGCCTTG ATCGTTGGGA ACCGGAGCTG AATGAAGCCA TACCAAACGA CGAGCGTGAC

5221 ACCACGATGC CTGTAGCGAT GGCAACAACG TTGCGCAAAC TATTAAGTGG CGAACTACTT
5281 ACTCTAGCTT CCCGGCAACA ATTAATAGAC TGGATGGAGG CGGATAAAGT TGCAGGACCA
5341 CTTCTGCGCT CGGCCCTTCC GGCTGGCTGG TTTATTGCTG ATAAATCCGG AGCCGGTGAG
5401 CGTGGTTTCTC GCGGTATCAT CGCAGCGCTG GGGCCAGATG GTAAGCCCTC CCGTATCGTA
5461 GTTATCTACA CGACGGGGAG TCAGGCAACT ATGGATGAAC GAAATAGACA GATCGCTGAG
5521 ATAGGTGCCT CACTGATTAA GCATTGGTAA AGGAGGAAAA AAAAAATGAGC CATATTCAAC
5581 GGGAAACGTC GAGGCCGCGA TTAAATTCCA ACATGGATGC TGATTTATAT GGGTATAAAT
5641 GGGCTCGCGA TAATGTCGGG CAATCAGGTG CGACAATCTA TCGCTTGTAT GGAAGCCCCG
5701 ATGCGCCAGA GTTGTCTCTG AACATGGCA AAGGTAGCGT TGCCAATGAT GTTACAGATG
5761 AGATGGTCAG ACTAAACTGG CTGACGGAAT TTATGCCACT TCCGACCATC AAGCATTTTA
5821 TCCGTACTCC TGATGATGCA TGTTACTCA CCACTGCGAT CCCCAGAAAA ACAGCGTTCC
5881 AGGTATTAGA AGAATATCCT GATTCAGGTG AAAATATTGT TGATGCGCTG GCAGTGTTC
5941 TCGCCCGGTT GCACTCGATT CCTGTTTGTA ATTGTCCTTT TAACAGCGAT CGCGTATTT
6001 GCCTCGCTCA GCGCAATCA CGAATGAATA ACGGTTTGGT TGATGCGAGT GATTTTGATG
6061 ACGAGCGTAA TGGCTGGCCT GTTGAACAAG TCTGGAAAGA AATGCATAAA CTTTTGCCAT
6121 TCTCACCGGA TTCAGTCGTC ACTCATGGTG ATTTCTCACT TGATAACCTT ATTTTTGACG
6181 AGGGGAAATT AATAGGTTGT ATTGATGTTG GACGAGTCGG AATCGCAGAC CGATACCAGG
6241 ATCTTGCCAT CCTATGGAAC TGCCTCGGTG AGTTTTCTCC TTCATTACAG AAACGGCTTT
6301 TTCAAAAATA TGGTATTGAT AATCCTGATA TGAATAAATT GCAGTTTCAT TTGATGCTCG
6361 ATGAGTTTTT CTAAAGGAGG AAAAAAAAT GGAGAAAAA ATCACTGGAT ATACCACCGT
6421 TGATATATCC CAATGGCATC GTAAAGAACA TTTTGAGGCA TTTCAGTCAG TTGCTCAATG
6481 TACCTATAAC CAGACCGTTC AGCTGGATAT TACGGCCTTT TTAAAGACCG TAAAGAAAA
6541 TAAGCACAAG TTTTATCCGG CCTTTATTCA CATTCTTGCC CGCCTGATGA ATGCTCATCC
6601 GGAGTTCCGT ATGGCAATGA AAGACGGTGA GCTGGTGATA TGGGATAGTG TTCACCCTG
6661 TTACACCGTT TTCCATGAGT GCACACGACG ATTTCCGGCA GTTTCTACAC ATATATTCGC
6721 AAGATGTGGC GTGTACGGT GAAAACCTGG CCTATTTCCC TAA

Only the synthesized DNA fragment (in red) has been sequence verified. We do not guarantee the vector sequence.