

pTagFP635-clathrin vector restriction map

The data has not been verified by restriction digestion with each enzyme listed and does not take into account possible methylation sites. Enzymes that recognize unambiguous sequences less than 6 basepairs long are not included – for the more complete enzyme list please refer to the Table of restriction sites.

Unique sites are shown in bold blue. The location given specifies the 3' end of the cut DNA (the base to the left of the cut site). TagFP635 amino acids are shown in red, Clathrin light chain LCB amino acids are shown in green, linker amino acids are shown in black.




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              BseY1      StuI                      Bgl1
              |         |                           |
1001 TCCCATCCAACGGCCCTGTGATGCAGAAGAAAACACTCGGCTGGGAGGCCTCCACCGAGATGCTGTACCCCGCTGACGGCGGCCTGGAAGGCAGAAGCGA 1100
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1100
TagFP635 > P S N G P V M Q K K T L G W E A S T E M L Y P A D G G L E G R S D

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          BssS1      Eco57                      Bbs1      BpuE1
          |         |                           |         |
1101 CATGGCCCTGAAGCTCGTGGGCGGGGGCCACCTGATCTGCAACTTGAAGACCACATACAGATCCAAGAAACCCGCTAAGAACCTCAAGATGCCCGGCGTC 1200
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1200
TagFP635 > M A L K L V G G G H L I C N L K T T Y R S K K P A K N L K M P G V

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              Bbs1
              |
          SpAcc |
              |         |         |         |         |         |         |         |         |         |
1201 TACTATGTGGACAGAAGACTGGAAAAGAATCAAGGAGGCCGACAAAGAGACCTACGTCGAGCAGCACGAGGTGGCTGTGGCCAGATACTGCGACCTCCCTA 1300
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1300
TagFP635 > Y Y V D R R L E R I K E A D K E T Y V E Q H E V A V A R Y C D L P S

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          SpAcc      Bmr1      BpuE1      Xho1      Hind3      EcoR1      Sal1
          |         |         |         |         |         |         |         |
1301 GCAAACCTGGGGCACAAACTTAATTCCGGACTCAGATCTCGAGCTCAAGCTTCGAATTCTGCAGTCGACATGGCTGATGACTTTGGCTTCTTCTCGTCGTC 1400
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1400
FP635/Clathrin > K L G H K L N S G L R S R A Q A S N S A V D M A D D F G F F S S S

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              BseR1
              |
          Not1 |
          Eag1 |
          Bgl1 |         |         |         |         |         |         |         |         |
          |         |         |         |         |         |         |         |         |         |
1401 GGAGAGTGGTCCCCGGAGGCGGCGGAGGAGGACCCGGCCCGCTTCTTGGCCCAGCAGGAGAGCGAGATTGCAGGCATAGAGAACGACGAGGGCTTC 1500
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1500
Clathrin > E S G A P E A A E E D P A A A F L A Q Q E S E I A G I E N D E G F

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BspM1
 BfuA1
 AarI
 NaeI
 NgoM4
 PspOM
 BssS1
 ApaI
 PshA1

1501 GGGGCACCTGCCGGCAGCCATGCGGCCCGCCCGCACAGCCGGGCCCCACGAGTGGGGCTGGTTCTGAGGACATGGGGACCACAGTCAATGGAGATGTGTTTC 1600
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1600
 CCCCCTGGACGGCCGTCGGTACGCCGGGGCGTGTTCGGCCCGGGGTGCTCACCCCGACCAAGACTCCTGTACCCCTGGTGTTCAGTTACCTCTACACAAAG
Clathrin > G A P A G S H A A P A Q P G P T S G A G S E D M G T T V N G D V F Q

BstAP
 BsrD1

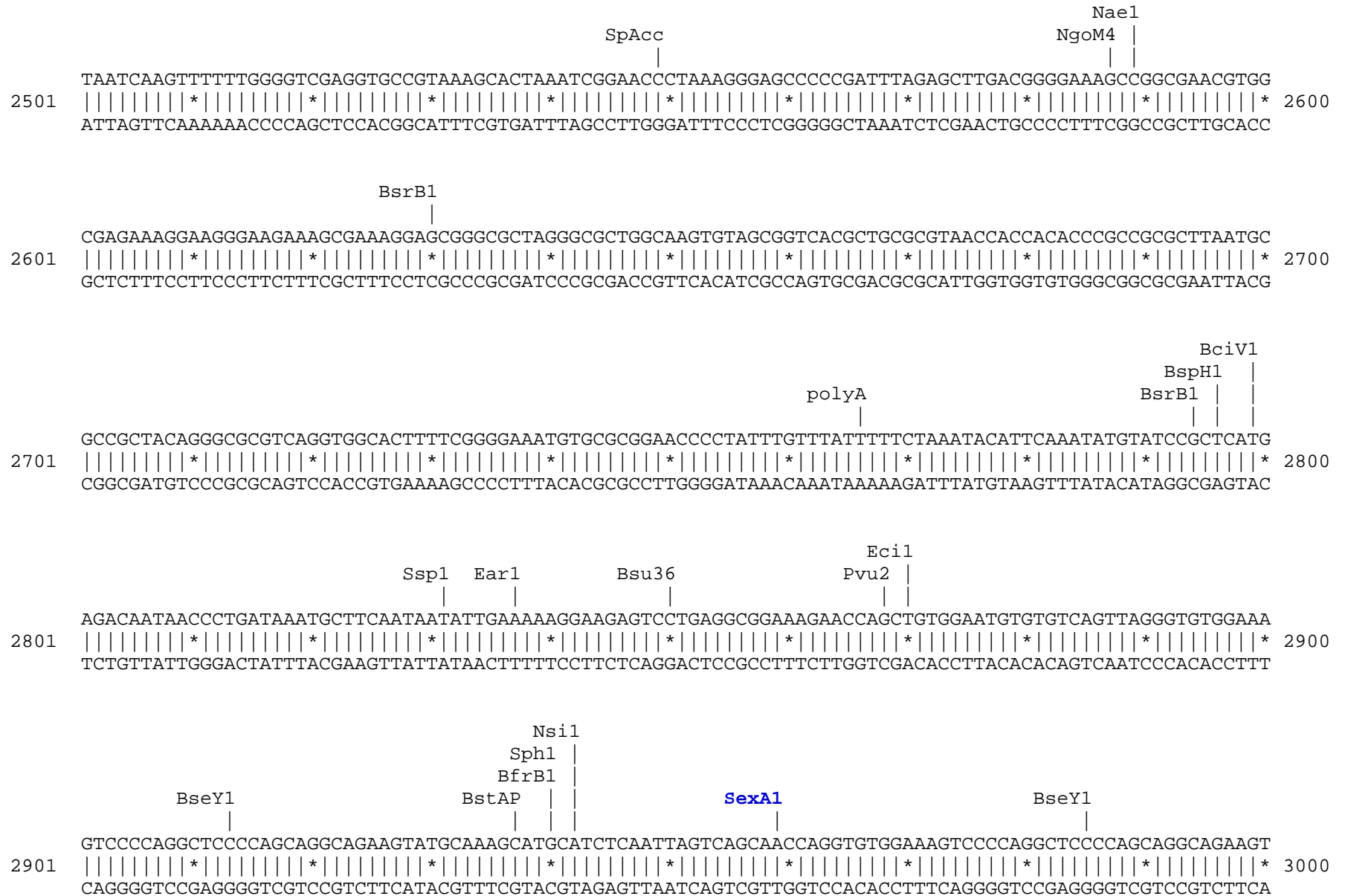
1601 AGGAGGCCAACGGTCCCTGCTGATGGCTACGCAGCCATTGCCAGGCTGACAGGCTGACCCAGGAGCCTGAGAGCATCCGCAAGTGGCGAGAGGAGCAGAG 1700
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1700
 TCCTCCGGTTGCCAGGACGACTACCGATGCGTTCGGTAACGGGTCCGACTGTCCGACTGGGTCTCGACTCTCGTAGGCGTTACCCGCTCTCCTCGTCTC
Clathrin > E A N G P A D G Y A A I A Q A D R L T Q E P E S I R K W R E E Q R

SpAcc
 BseR1
 Xcm1
 SpAcc
 Bpm1
 BseR1

1701 GAAACGGCTGCAAGAGCTGGATGCTGCATCTAAGGTCACGGAACAGGAATGGCGGGAGAAGGCCAAGAAGGACCTGGAGGAGTGAACAGCGCCAGAGT 1800
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1800
 CTTTGCCGACGTTCTCGACCTACGACGTAGATTCCAGTGCCTTGTCTTACCGCCCTCTTCCGGTCTTCTCCTGGACCTCCTCACCTTGGTTCGCGGTCTCA
Clathrin > K R L Q E L D A A S K V T E Q E W R E K A K K D L E E W N Q R Q S

Dra3
 Xcm1
 BseR1
 Bsa1
 BseR1

1801 GAACAAGTAGAGAAGAACAAGATCAACAACCGGGCATCCGAGGAGGCTTTTCGTGAAGGAATCCAAGGAGGAGACCCAGGCACAGAGTGGGAGAAGGTGG 1900
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1900
 CTTGTTTATCTCTTCTTGTCTAGTTGTTGGCCCGTAGGCTCCTCCGAAAGCACTTCTTAGGTTCTCCTCTGGGGTCCGTTGTCTCACCTCTTCCACC
Clathrin > E Q V E K N K I N N R A S E E A F V K E S K E E T P G T E W E K V A



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          NsiI
          SphI
          BfrB1
          BstAP
          Ecil
          Ecil
          Bmr1
          Ecil
          NcoI
3001 ATGCAAAGCATGCATCTCAATTAGTCAGCAACCATAGTCCCGCCCTAACTCCGCCCATCCCGCCCTAACTCCGCCCAGTTCCGCCCATTTCTCCGCCCC
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3100
      TACGTTTCGTACGTAGAGTTAATCAGTCGTTGGTATCAGGGCGGGGATTGAGGCGGGTAGGGCGGGATTGAGGCGGGTCAAGGCGGGTAAGAGGCGGGG

          polyA
          SfiI
          BglI
          SpDon
          Avr2
          StuI
          BseR1
3101 ATGGCTGACTAATTTTTTTTATTTATGCAGAGGCCGAGGCCGCCTCGGCCTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTGGAGGCCTAGGCTT
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3200
      TACCGACTGATTAAAAAATAAATACGTCTCCGGCTCCGGCGGAGCCGGAGACTCGATAAGGTCTTCATCACTCCTCCGAAAAAACCTCCGGATCCGAA

          ClaI
          BsaB1
          BspM1
          BfuA1
          EagI
3201 TTGCAAAGATCGATCAAGAGACAGGATGAGGATCGTTTTCGCATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATT
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3300
      AACGTTTCTAGCTAGTTCTCTGTCTACTCCTAGCAAAGCGTACTAACTTGTCTACCTAACGTGCGTCCAAGAGGCCGGCGAACCCACCTCTCCGATAA

          Bmr1
          NarI
          KasI
          Drd1
3301 CGGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCAGCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTG
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3400
      GCCGATACTGACCCGTGTTGTCTGTTAGCCGACGAGACTACGGCGGCACAAGGCCGACAGTCGCGTCCCCGCGGGCCAAGAAAAACAGTTCTGGCTGGAC

          MscI
          Pvu2
          FspI
          PflF1
3401 TCCGGTGCCCTGAATGAACTGCAAGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCCTTGCGCAGCTGTGCTCGACGTTGTCACTGAAG
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3500
      AGGCCACGGGACTTACTTGACGTTCTGCTCCGTCGCGCCGATAGCACCGACCGGTGCTGCCCGCAAGGAACGCGTCGACACGAGCTGCAACAGTGACTTC

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Eco57 SpDon BciV1
CGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAGGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAAT
3501 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3600
GCCCTTCCCTGACCGACGATAACCCGCTTCACGGCCCCGTCTAGAGGACAGTAGAGTGGAACGAGGACGGCTCTTTCATAGGTAGTACCGACTACGTTA

BsrD1 BtgZ1 BspM1 BfuA1
GCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTC
3601 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3700
CGCCCGGACGTATGCGAACTAGGCCGATGGACGGGTAAGCTGGTGGTTTCGCTTTGTAGCGTAGCTCGCTCGTGCATGAGCCTACCTTCGGCCAGAACAG

Sap1 Ear1 BpuE1 Sph1
GATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCCAGCCGAACTGTTTCGCCAGGCTCAAGGCGAGCATGCCCCGACGGCGAGGATCTCGTTCGTGA
3701 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3800
CTAGTCCTACTAGACCTGCTTCTCGTAGTCCCCGAGCGGGTTCGGCTTGACAAGCGGTCCGAGTTCGCTCGTACGGGCTGCCGCTCCTAGAGCAGCACT

Nco1 BtgZ1 BseY1 NaeI NgoM4 Rsr2 Eci1
CCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAATGGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGA
3801 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3900
GGGTACCGCTACGGACGAACGGCTTATAGTACCACCTTTTACCGGCGAAAAGACCTAAGTAGCTGACACCGGCCGACCCACACCGCCTGGCGATAGTCCT

Sap1 Ear1 Eco57 BssS1 BtgZ1 BsrB1
CATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCCTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGCAGCGC
3901 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4000
GTATCGCAACCGATGGGCACTATAACGACTTCTCGAACCGCCGCTTACCCGACTGGCGAAGGAGCACGAAATGCCATAGCGGCGAGGGCTAAGCGTCGCG


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                DraI          DraI          BspH1
                |            |            |
4501 CTTTAGATTGATTTAAAACCTTCATTTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTTGATAATCTCATGACCAAATCCCTTAACGTGAGTTTTTCGT
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4600
   GAAATCTAACTAAATTTTGAAGTAAAAATTAAATTTTCCTAGATCCACTTCTAGGAAAAACTATTAGAGTACTGGTTTTAGGGAATTGCACTCAAAGCA

                                BpuE1
                                |
4601 TCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAACCCCGCT
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4700
   AGGTGACTCGCAGTCTGGGGCATCTTTTCTAGTTTCTAGAAAGAACTCTAGGAAAAAAGACGCGCATTAGACGACGAACGTTTGTTTTTTTGGTGCGCA

                                Eco57
                                |
4701 ACCAGCGGTGGTTTGTGTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAAGTGGCTTCAGCAGAGCGCAGATACCAAATACTGTCTTCTAGTG
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4800
   TGGTCGCCACCAAACAAACGGCCTAGTTCTCGATGGTTGAGAAAAAGGCTTCCATTGACCGAAGTCGTCTCGCGTCTATGGTTTATGACAGGAAGATCAC

                                AlwN1
                                |
4801 TAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGT
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4900
   ATCGGCATCAATCCGGTGGTGAAGTTCTTGAGACATCGTGGCGGATGTATGGAGCGAGACGATTAGGACAATGGTCACCGACGACGGTCACCGCTATTCA

BpuE1          ApaL1          BseY1
|              |              |
4901 CGTGTCCTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCTGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAAC
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5000
   GCACAGAATGGCCCAACCTGAGTTCTGCTATCAATGGCCTATTCCGCGTCGCCAGCCCAGCTTGCCCCCAAGCACGTGTGTGCGGGTCGAACCTCGCTTG

                                SpAcc
                                |
                                BciV1
                                |
                                Ecil
                                |
5001 GACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCAGAGGGAGAAAGCGGACAGGTATCCGGTAAGCGGCAGGGTC
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5100
   CTGGATGTGGCTTGACTCTATGGATGTCGCACTCGATACTCTTTCGCGGTGCGAAGGGCTTCCCTCTTTCCGCTGTCCATAGGCCATTGCGCGTCCCAG
```

BssS1 SpAcc Drd1
5101 GGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTCTGGGTTTTCGCCACCTCTGACTTGAGCGTTCGATTTTTGT 5200
|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5200
CCTTGTCTCTCGCGTGTCCCTCGAAGGTCCCCCTTTGCGGACCATAGAAATATCAGGACAGCCCAAAGCGGTGGAGACTGAACTCGCAGCTAAAAACA

BpuE1 SpAcc Eci1 SpDon
5201 GATGCTCGTCAGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCC 5300
|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5300
CTACGAGCAGTCCCCCGCCTCGGATACCTTTTTGCGGTCTGTGCGCCGAAAAATGCCAAGGACCGGAAAACGACCGGAAAACGAGTGTACAAGAAAGG

Nsi1
BfrB1
5301 TGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCATGCAT 5346
|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5346
ACGCAATAGGGGACTAAGACACCTATTGGCATAATGGCGGTACGTA

Found:

Aar1	Aat2	Afe1	Age1	Ale1	AlwN1	Apal	ApaL1	Ase1	Avr2	BamH1	Bbs1	BciV1	Bcl1
BfrB1	BfuA1	Bgl1	Bgl2	Bmr1	Bpml	BpuE1	Bsa1	BsaB1	BsaXa	BsaXb	BseR1	BseY1	Bsm1
BspE1	BspH1	BspLU	BspM1	BsrB1	BsrD1	BsrG1	BssS1	BstAP	BstB1	Bsu36	BtgZ1	Bts1	Clal
Dra1	Dra3	Drd1	Eag1	Ear1	Ecil	Eco57	EcoR1	Fsp1	Hind3	Hpa1	Kas1	Mfe1	Mlu1
Msc1	Nae1	Nar1	Nco1	Nde1	NgoM4	Nhe1	Not1	Nsil	PflF1	polyA	PshA1	Psi1	PspOM
Pst1	Pvu2	Rsr2	Sac1	Sall	Sap1	SexA1	Sfil	SnaB1	SpAcc	SpDon	Sph1	Ssp1	Stu1
Xba1	Xcm1	Xho1											

Unique:

Aar1	Afe1	Age1	Ale1	Apal	Ase1	BamH1	Bcl1	Bgl2	BsaXa	BsaXb	BspE1	BspLU	BsrG1
Clal	EcoR1	Fsp1	Hind3	Hpa1	Kas1	Mfe1	Mlu1	Nar1	Nde1	Nhe1	Not1	PflF1	PspOM
Pst1	Rsr2	Sac1	Sall	SexA1	Sfil	SnaB1	Xba1	Xho1					

Not found:

Acc65	Ac11	Afl2	Ahd1	Asc1	AsiS1	Baela	Baelb	BbvC1	Bcg1a	Bcg1b	Blp1	BmgB1	Bpu10
Bsg1	BsiW1	BsmB1	BssH2	BstE2	BstX1	BstZ1	_Chi	EcoK	EcoN1	EcoRV	FCatB	FCatL	FCatR
FCatP	ScFRT	Fse1	FspA1	I_Ceu	Kpn1	loxP	Nru1	Pac1	PflM1	Pme1	Pml1	Pvu1	R4atB
R4atL	R4atP	R4atR	Sac2	SanD1	Sbf1	Scal	Sgf1	SgrA1	Sma1	Spe1	Srf1	Swal	T3RNA
T7RNA	T7Ter	PISce	Xmn1										

Excluded by site complexity:

Acc1	Ac11	Afl3	Alu1	Alw1	Apo1	Ava1	Ava2	Ban1	Ban2	Bbv1	BceA1	Bfa1	Bme15
BsaA1	BsaH1	BsaJ1	BsaW1	BseM2	BsiE1	BsiH1	Bsl1	BsmA1	BsmF1	Bsp12	BspCa	BspCb	Bsr1
BsrF1	BssK1	BstF5	BstN1	BstU1	BstY1	Btg1	Cac8	CviJ1	Dde1	Eae1	EcoO1	Fau1	Fnu4H
Fok1	Hae2	Hae3	Hga1	Hha1	Hinc2	Hinf1	HinP1	Hpa2	Hph1	Hpy99	Hpy1	Hpy3	HpyC3
HpyC4	HpyC5	Mae3	Mbo2	Mnl1	Mse1	Msl1	MspA1	Mwo1	Nci1	Nla3	Nla4	Nsp1	Ple1
PpuM1	Rsa1	Sau3A	Sau96	SfaN1	Sfc1	Sml1	Sty1	Taq1	Tat1	Tfil	Tse1	Tsp45	Tsp50
TspR1													