

pTagGFP2-mito 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 shown in bold blue. The location given specifies the 3' end of the cut DNA (the base to the left of the cut site). Mitochondrial targeting sequence (MTS) shown in bold black.



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                                Aat2
                                |
TAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCATTGACGTCAATGGGAGTTTGTGTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTA
401  |||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||* 500
ATCGCCAAACTGAGTGCCCTAAAGGTTTCAGAGGTGGGGTAACTGCAGTTACCCTCAAACAAAACCGTGGTTTTAGTTGCCCTGAAAGTTTTACAGCAT

                                Eci1
                                |
ACA ACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTGGTTTAGTGAACCGTCAGATCCGCTAGCATGT
501  |||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||* 600
TGTGAGGGCGGGTAACTGCGTTTACCCGCCATCCGCACATGCCACCCTCCAGATATATTCGTCTCGACCAAATCACTTGGCAGTCTAGGCGATCGTACA
MTS > M S

                                Bmr1
                                |
                                BssH2
                                |
                                PflM1
                                |
                                BamH1
                                |
                                AgeI
                                |
CCGTCC TGACGCCGCTGCTGCTGCGGGGCTTGACAGGCTCGGCCCGGGCTCCCAGTGCCGCGCCAAGATCCATTCGTTGGGGGATCCACCGGTCCG
601  |||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||* 700
GGCAGGACTGCGGCGACGACGACGCCCCGAAGTGTCCGAGCCGGGCCCGCCGAGGGTTCACGGCGCGCGGTTCTAGGTAAGCAACCCCCCTAGGTGGCCAGCG
MTS > V L T P L L L R G L T G S A R R L P V P R A K I H S L G D P P V A

                                BseR1
                                |
                                NaeI
                                |
                                ApaL1
                                |
                                BmgB1
                                |
                                BsrB1
                                |
                                NgoM4
                                ||
                                ||
CACCATGAGCGGGGCGAGGAGCTGTTCGCCGGCATCGTGCCCGTGCTGATCGAGCTGGACGGCGACGTGCACGGCCACAAGTTCAGCGTGCCGGCGGAG
701  |||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||* 800
GTGGTACTCGCCCCGCTCCTCGACAAGCGGCCGTAGCACGGGCACGACTAGCTCGACCTGCCGCTGCACGTGCCGGTGTTC AAGTCGCACGCGCCGCTC
TagGFP2 > T M S G G E E L F A G I V P V L I E L D G D V H G H K F S V R G E

                                BsaXb
                                |
                                BsaXa
                                |
                                Bsp1
                                |
                                Bpm1
                                |
                                |
                                BstE2
                                |
                                Ale1
                                |
                                |
GGCGAGGGCGACCCGACTACGGCAAGCTGGAGATCAAGTTCATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCCACCCTGGTGACCACCTCTGCT
801  |||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||* 900
CCGCTCCCCTGCGGCTGATGCCGTTTCGACCTCTAGTTC AAGTAGACGTGGTGGCCGTTTCGACGGGCACGGGACCGGTTGGGACCACTGGTGGGAGACGA
TagGFP2 > G E G D A D Y G K L E I K F I C T T G K L P V P W P T L V T T L C Y

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          BstAP                               Xmn1                               EcoK
          |                                   |                                   |
ACGGCATCCAGTGCTTCGCCCGCTACCCCGAGCACATGAAGATGAACGACTTCTTCAAGAGCGCCATGCCCGAGGGCTACATCCAGGAGCGCACCATCCA
901  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1000
TGCCGTAGGTCACGAAGCGGGCGATGGGGCTCGTGTACTTCTACTTGTCTGAAGAAGTTCTCGCGGTACGGGCTCCCGATGTAGGTCCTCGCGTGGTAGGT
TagGFP2 > G I Q C F A R Y P E H M K M N D F F K S A M P E G Y I Q E R T I Q

          Sac2 SpDon                               SpDon                               Ale1 |                               Eco57
          |   |                                   |   |                                   |   |                                   |
GTTCCAGGACGACGGCAAGTACAAGACCCGCGGCGAGGTGAAGTTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCAAGGACTTCAAGGAG
1001  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1100
CAAGGTCTTGCTGCCGTTTCTGTTCTGGGCGCCGCTCCACTTCAAGCTCCCGCTGTGGGACCACTTGGCGTAGCTCGACTTCCCCTTCCCTGAAGTTCCTC
TagGFP2 > F Q D D G K Y K T R G E V K F E G D T L V N R I E L K G K D F K E

          BsrG1
          Dra3 |
          Eci1 | |
          PflM1                               Bpm1 | | |                               Xcm1
          |   |   |   |                                   |
GACGGCAACATCCTGGGCCACAAGCTGGAGTACAGCTTCAACAGCCACAACGTGTACATCCGCCCCGACAAGGCCAACAACGGCCTGGAGGCTAACTTCA
1101  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1200
CTGCCGTTGTAGGACCCGGTGTTCGACCTCATGTCTGAAGTTGTTCGGTGTTCACATGTAGGCGGGGCTGTTCCGGTTGTTGCCGGACCTCCGATTGAAGT
TagGFP2 > D G N I L G H K L E Y S F N S H N V Y I R P D K A N N G L E A N F K

          Bpm1                               Pvu2                               Bsp1                               Xcm1                               BsaB1
          |   |   |   |                                   |   |   |   |                                   |   |   |   |
AGACCCGCCACAACATCGAGGGCGGCGGCGTGCAGCTGGCCGACCACTACCAGACCAACGTGCCCTGGGCGACGGCCCCGTGCTGATCCCCATCAACCA
1201  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1300
TCTGGGCGGTGTTGTAGCTCCCGCCGCGCACGTCGACCGGCTGGTGTGATGGTCTGGTTGCACGGGGACCCGCTGCCGGGGCACGACTAGGGGTAGTTGGT
TagGFP2 > T R H N I E G G G V Q L A D H Y Q T N V P L G D G P V L I P I N H

          Bpu10                               Eco57                               Dra3                               AlwN1 Bpm1
          |   |   |   |                                   |   |   |   |                                   |   |   |   |
CTACCTGAGCACTCAGACCAAGATCAGCAAGGACCGCAACGAGGCCCGCGACCACATGGTGTCTCCTGGAGTCCTTCAGCGCCTGCTGCCACACCCACGGC
1301  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1400
GATGGACTCGTGAGTCTGGTCTTAGTTCCTGGCGTTGCTCCGGGCGCTGGTGTACCACGAGGACCTCAGGAAGTCGCGGACGACGGTGTGGGTGCCG
TagGFP2 > Y L S T Q T K I S K D R N E A R D H M V L L E S F S A C C H T H G

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                                BsrB1
                                |
2001 CGAACGTGGCGAGAAAAGGAAGGGAAGAAAGCGAAAGGAGCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGTACGCTGCGCGTAACCACCACACCCGCCGC
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2100
    GCTTGCACCGCTCTTTCCTTCCCTTCTTTCGCTTTCCTCGCCCGCGATCCCGCGACCGTTCACATCGCCAGTGCACGCGCATTGGTGGTGTGGGCGGCG

                                polyA
                                |
2101 GCTTAATGCGCCGCTACAGGGCGCGTCAGGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTAT
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2200
    CGAATTACGCGGCGATGTCCCGCGCAGTCCACCGTGAAAAGCCCCTTACACGCGCCTTGGGGATAAACAAATAAAAAGATTTATGTAAGTTTATACATA

    BciV1
    BspH1 |
    BsrB1 | |
    | | |
                                Ssp1  Ear1
                                |    |
                                Bsu36
                                |
                                Ecil
                                Pvu2 |
                                | |
2201 CCGCTCATGAGACAATAACCCTGATAAATGCTTCAATAATATTGAAAAAGGAAGAGTCCTGAGGCGGAAAGAACCAGCTGTGGAATGTGTGTCAGTTAGG
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2300
    GGCGAGTACTCTGTTATTGGGACTATTTACGAAGTTATTATAACTTTTTCTTCTCAGGACTCCGCCTTCTTGGTCGACACCTTACACACAGTCAATCC

                                Nsi1
                                Sph1 |
                                BfrB1 |
                                BseY1
                                |
                                BstAP | |
                                | | |
                                SexA1
                                |
                                BseY1
                                |
2301 GTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCAGGTGTGGAAAGTCCCCAGGCTCCCCAGCA
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2400
    CACACCTTTCAGGGGTCCGAGGGGTTCGTCCGTCTTCATACGTTTTTCGTACGTAGAGTTAATCAGTCGTTGGTCCACACCTTTCAGGGGTCCGAGGGGTTCGT

                                Nsi1
                                Sph1 |
                                BfrB1 |
                                BstAP | |
                                | | |
                                Ecil
                                |
                                Ecil
                                |
                                Ecil
                                Bmr1|
                                | |
                                Ecil
                                |
2401 GGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCATAGTCCCGCCCTAACTCCGCCCATCCCGCCCTAACTCCGCCAGTTCCGCCATT
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2500
    CCGTCTTCATACGTTTTTCGTACGTAGAGTTAATCAGTCGTTGGTATCAGGGCGGGGATTGAGGCGGGTAGGGCGGGGATTGAGGCGGGTCAAGGCGGGTAA
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2501 NcoI polyA SfiI BglI SpDon BseR1
| | | | | | | |
CTCCGCCCCATGGCTGACTAATTTTTTTTATTTATGCAGAGGCCGAGGCCGCCTCGGCCTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTGGAGG
| | | | | | | | | * | | | | | | | | | * | | | | | | | | | * | | | | | | | | | * | | | | | | | | | * | | | | | | | | | * | | | | | | | | | * | | | | | | | | | * | | | | | | | | | * | | | | | | | | | * | | | | | | | | | * | 2600
GAGGCGGGTACCGACTGATTAAAAAAAATAAATACGTCTCCGGCTCCGGCGGAGCCGGAGACTCGATAAGGTCTTCATCACTCCTCCGAAAAAACCTCC

Avr2 ClaI BsaB1 BspM1 BfuA1 EagI
StuI | | | | | | |
|| | | | | | | |
CCTAGGCTTTTGC AAAAGATCGATCAAGAGACAGGATGAGGATCGTTTCGCATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGA
| | | | | | | | | * | | | | | | | | | * | | | | | | | | | * | | | | | | | | | * | | | | | | | | | * | | | | | | | | | * | | | | | | | | | * | | | | | | | | | * | | | | | | | | | * | | | | | | | | | * | 2700
GGATCCGAAAACGTTTCTAGCTAGTTCTCTGTCTACTCCTAGCAAAGCGTACTA AACTTGTTCTACCTAACGTGCGTCCAAGAGGCCGGCGAACCCACCT

Bmr1 NarI KasI
| | ||
GAGGCTATTTCGGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCCGGTGTTCCGGCTGTCCAGCGCAGGGGCGCCCGGTTCTTTTTGTCAAG
| | | | | | | | | * | | | | | | | | | * | | | | | | | | | * | | | | | | | | | * | | | | | | | | | * | | | | | | | | | * | | | | | | | | | * | | | | | | | | | * | | | | | | | | | * | 2800
CTCCGATAAGCCGATACTGACCCGTGTTGTCTGTTAGCCGACGAGACTACGGCGGCACAAGGCCGACAGTTCGCGTCCCCGCGGGCCAAGAAAAACAGTTC

Drd1 MscI Pvu2 FspI PflF1
| | | | | | |
ACCGACCTGTCCGGTGCCCTGAATGAACTGCAAGACGAGGCAGCGCGGCTATCGTGCTGGCCACGACGGGCGTTTCCCTTGCGCAGCTGTGCTCGACGTTG
| | | | | | | | | * | | | | | | | | | * | | | | | | | | | * | | | | | | | | | * | | | | | | | | | * | | | | | | | | | * | | | | | | | | | * | | | | | | | | | * | | | | | | | | | * | 2900
TGGCTGGACAGGCCACGGGACTTACTTACGTTTCTGCTCCGTCGCGCCGATAGCACCAGCCGGTGCTGCCCCGAAGGAACCGCTCGACACGAGCTGCAAC

Eco57 SpDon BciV1
| | |
TCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAGGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGC
| | | | | | | | | * | | | | | | | | | * | | | | | | | | | * | | | | | | | | | * | | | | | | | | | * | | | | | | | | | * | | | | | | | | | * | | | | | | | | | * | | | | | | | | | * | | | | | | | | | * | 3000
AGTGACTTCGCCCTTCCCTGACCGACGATAACCCGCTTCACGGCCCCGTCTAGAGGACAGTAGAGTGGAACGAGGACGGCTCTTTCATAGGTAGTACCG

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              BtgZ1
            BspM1 |
            BfuA1 |
    BsrD1      |
    |          |
3001 TGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTACTCGGATGGAAGCC
  | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * 3100
  ACTACGTTACGCCGCCGACGTATGCGAACTAGGCCGATGGACGGGTAAGCTGGTGGTTTCGCTTTGTAGCGTAGCTCGCTCGTGCATGAGCCTACCTTCGG

              Sap1
            Ear1 |
              BpuE1
              Sph1
3101 GGTCTTGTTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCCGCCAGGCTCAAGGCGAGCATGCCCGACGGCGAGGATC
  | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * 3200
  CCAGAACAGCTAGTCTACTAGACCTGCTTCTCGTAGTCCCGAGCGCGGTCGGCTTGACAAGCGGTCCGAGTTCCGCTCGTACGGGCTGCCGCTCCTAG

              BseY1
            Nae1 |
            NgoM4 | |
              Rsr2
    Nco1      |      BtgZ1
    |          |
3201 TCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAATGGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCG
  | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * 3300
  AGCAGCACTGGGTACCCTACGGACGAACGGCTTATAGTACCACCTTTTACC GGCGAAAAGACCTAAGTAGCTGACACCGGCCGACCCACACCGCCTGGC

              EcoI
              Sap1
            Ear1 |      Eco57
            BssS1
              BtgZ1
            BsrB1 |
3301 CTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCTCGTGCTTTACGGTATCGCCGCTCCCGAT
  | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * 3400
  GATAGTCTCTGTATCGCAACCGATGGGCACTATAACGACTTCTCGAACCGCCGCTTACCCGACTGGCGAAGGAGCACGAAATGCCATAGCGGCGAGGGCTA

              BsrB1
              BstB1
              BssS1
            BspM1
            BfuA1
3401 TCGCAGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTCTTCTGAGCGGGACTCTGGGGTTTCGAAATGACCGACCAAGCGACGCCCAACCTGCCATCACG
  | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * 3500
  AGCGTCGCGTAGCGGAAGATAGCGGAAGAACTGCTCAAGAAGACTCGCCCTGAGACCCCAAGCTTTACTGGCTGGTTTCGCTGCGGGTTGGACGGTAGTGC

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                SpAcc                Nae1
                |                    NgoM4 |
                |                    Bpm1 |
                |                    |
3501  AGATTTTCGATTCCACCGCCGCTTCTATGAAAGGTTGGGCTTCGGAATCGTTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATGCTG
      |||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||* 3600
      TCTAAAGCTAAGGTGGCGCGGAAGATACTTTCCAACCCGAAGCCTTAGCAAAGGCCCTGCGGCCGACCTACTAGGAGGTTCGCGCCCCTAGAGTACGAC

                Bpm1
                SpAcc |
                Avr2  |
                |    |
3601  GAGTTCTTCGCCCACCTAGGGGGAGGCTAACTGAAACACGGAAGGAGACAATACCGGAAGGAACCCGCGCTATGACGGCAATAAAAAGACAGAATAAAA
      |||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||* 3700
      CTCAAGAAGCGGGTGGGATCCCCCTCCGATTGACTTTGTGCCTTCTCTGTTATGGCCTTCCTTGGGCGCGATACTGCCGTTATTTTTCTGTCTTATTTT

                                                BsaI
                                                |
3701  CGCACGGTGTGGGTGCTTTGTTTCATAAACCGGGGTTCGGTCCCAGGGCTGGCACTCTGTGCATACCCACCGAGACCCCATTTGGGGCCAATACGCCCG
      |||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||* 3800
      GCGTGCCACAACCCAGCAAACAAGTATTTGCGCCCAAGCCAGGGTCCCAGCGTGAGACAGCTATGGGGTGGCTCTGGGGTAACCCCGGTTATGCGGGC

                                                                    BstAP
                                                                    AlwN1       Bsu36
                                                                    |           |
3801  CGTTTCTTCCTTTTCCCCACCCCAACCAAGTTCGGGTGAAGGCCAGGGCTCGCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCTCAGGTTAC
      |||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||* 3900
      GCAAAGAAGGAAAAGGGGTGGGGTGGGGGTTCAAGCCACTTCCGGGTCCCAGCGTCGGTTGCAGCCCCCGCGTCCGGGACGGTATCGGAGTCCAATG

                DraI           DraI           BspH1
                |             |             |
3901  TCATATATACTTTAGATTGATTTAAAAC TTCATTTTAAATTTAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAATCCCTTAACGTG
      |||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||* 4000
      AGTATATATGAAATCTAACTAAATTTGAAGTAAAATTTAATTTTCTAGATCCACTTCTAGGAAAACTATTAGAGTACTGGTTTTAGGGAATTGCAC
```


		BpuE1 	
4001	AGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAA		4100
	* *		
	TCAAAAGCAAGGTGACTCGCAGTCTGGGCGCATCTTTCTAGTTTCTTAGAAGAACTCTAGGAAAAAAGACGCGCATTAGACGACGAACGTTTGTTTTT		
		Eco57 	
4101	ACCACCGCTACCAGCGGTGGTTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAAGTGGCTTCAGCAGAGCGCAGATACCAAATACTGTC		4200
	* *		
	TGGTGGCGATGGTCGCCACCAAACAAACGGCCTAGTTCTCGATGGTTGAGAAAAAGGCTTCCATTGACCGAAGTCGTCTCGCGTCTATGGTTTATGACAG		
	SpAcc 		AlwN1
4201	CTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCCGCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTG		4300
	* *		
	GAAGATCACATCGGCATCAATCCGGTGGTGAAGTTCTTGAGACATCGTGGCGGATGTATGGAGCGAGACGATTAGGACAATGGTCACCGACGACGGTCAC		
	BpuE1 	ApaL1 	BseY1
4301	GCGATAAGTCGTGCTTACCGGGTTGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCTGGGCTGAACGGGGGGTTCGTGCACACAGCCAGCTT		4400
	* *		
	CGCTATTCAGCACAGAATGGCCCAACCTGAGTTCTGCTATCAATGGCCTATTCCGCGTCGCCAGCCCGACTTGCCCCCAAGCACGTGTGTCGGGTCTGAA		
	SpAcc 	BciV1 	Eci1
4401	GGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGC		4500
	* *		
	CCTCGCTTGTGGATGTGGCTTACTCTATGGATGTGCACTCGATACTCTTTCGCGGTGCGAAGGGCTTCCCTCTTCCGCCTGTCCATAGGCCATTTCG		

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                                     BssS1                               SpAcc                               Drd1
                                     |                               |                               |
GGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCTGTCTGGGTTTCGCCACCTCTGACTTGAGCGTC
4501 |||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||* 4600
CCGTCCCAGCCTTGTCTCTCGCGTGCTCCCTCGAAGGTCCCCCTTTGCGGACCATAGAAAATATCAGGACAGCCCAAAGCGGTGGAGACTGAACTCGCAG

                                         BpuE1                   SpAcc          Eci1                                       SpDon
                                         |                   |                   |                   BspLU|
GATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACCGGCCTTTTTACGGTTCTGGCCTTTTGCTGGCCTTTTGCTCACAT
4601 |||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||* 4700
CTAAAAACACTACGAGCAGTCCCCCGCCTCGGATACCTTTTTGCGGTGCTTGCGCCGAAAAATGCCAAGGACCGGAAAACGACCGGAAAACGAGTGTA

                                                                 NsiI
                                                                 BfrB1 |
                                                                 | |
GTTCTTTCTGCGTTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCATGCAT
4701 |||||||*||||||||*||||||||*||||||||*||||||||*|||| 4755
CAAGAAAGGACGCAATAGGGGACTAAGACACCTATTGGCATAATGGCGGTACGTA
```

Found:

Aat2	Afl2	Age1	Ale1	AlwN1	ApaL1	Ase1	Avr2	BamH1	BciV1	BfrB1	BfuA1	Bgl1	BmgB1
Bmr1	Bpm1	Bpu10	BpuE1	Bsa1	BsaB1	BsaXa	BsaXb	BseR1	BseY1	Bsg1	Bsm1	BspH1	BspLU
BspM1	BsrB1	BsrD1	BsrG1	BssH2	BssS1	BstAP	BstB1	BstE2	Bsu36	BtgZ1	Bts1	Clal	Dra1
Dra3	Drd1	Eag1	Ear1	Eci1	Eco57	EcoK	Fsp1	Hpa1	Kas1	Mfe1	Msc1	Nae1	Nar1
Nco1	Nde1	NgoM4	Nhe1	Not1	Nsi1	PflF1	PflM1	polyA	Psi1	Pvu2	Rsr2	Sac2	Sap1
SexA1	Sfi1	SnaB1	SpAcc	SpDon	Sph1	Ssp1	Stu1	Xba1	Xcm1	Xmn1			

Unique:

Afl2	Age1	Ase1	BamH1	BmgB1	Bpu10	Bsa1	BspLU	BsrD1	BssH2	BstB1	BstE2	Bts1	Clal
EcoK	Fsp1	Hpa1	Kas1	Mfe1	Msc1	Nar1	Nde1	Nhe1	Not1	PflF1	Rsr2	Sac2	SexA1
Sfi1	SnaB1	Stu1	Xba1	Xmn1									

Not found:

Aar1	Acc65	Ac11	Afe1	Ahd1	Apa1	Asc1	AsiS1	Baela	Baelb	Bbs1	BbvC1	Bcg1a	Bcg1b
Bcl1	Bgl2	Blp1	BsiW1	BsmB1	BspE1	BstX1	BstZ1	BxatB	BxatL	BxatR	BxatP	_Chi	Ecl2
EcoN1	EcoR1	EcoRV	FCatB	FCatL	FCatR	FCatP	ScFRT	Fse1	FspA1	Hind3	I_Ceu	Kpn1	loxP
Mlu1	Nru1	Pac1	Pme1	Pml1	PshA1	PspOM	Pst1	Pvu1	R4atB	R4atL	R4atP	R4atR	Sac1
Sall	SanD1	Sbf1	Sca1	Sgf1	SgrA1	Sma1	Spe1	Srf1	Swa1	T3RNA	T7RNA	T7Ter	PISce
Xho1													

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	Tfi1	Tse1	Tsp45	Tsp50
TspR1													