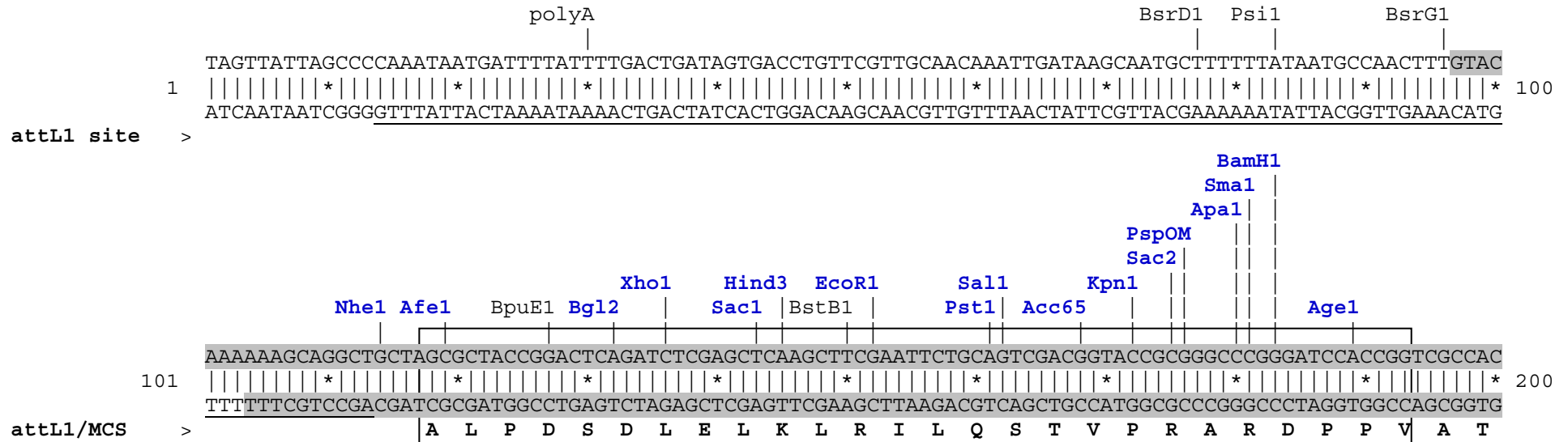
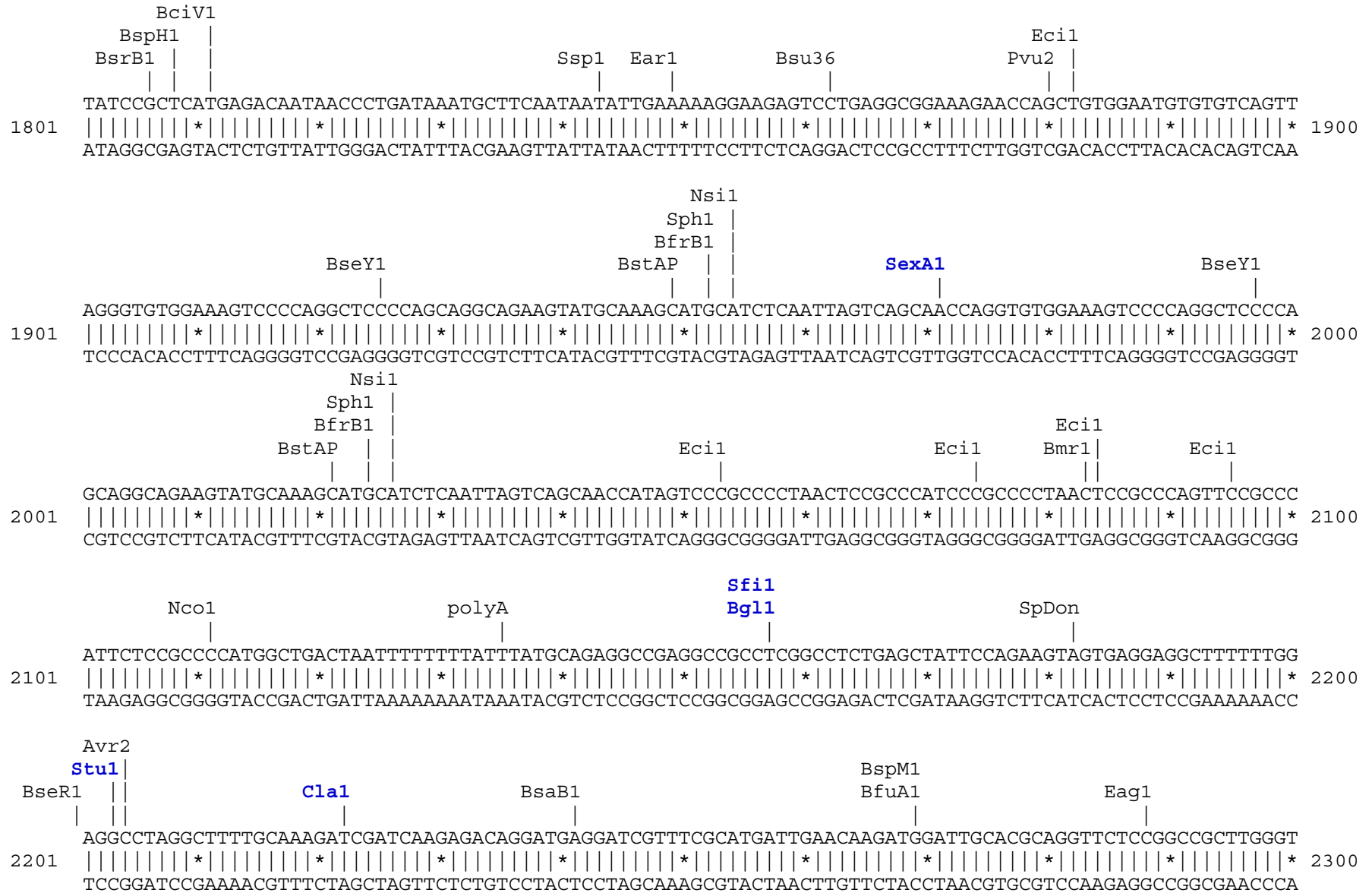


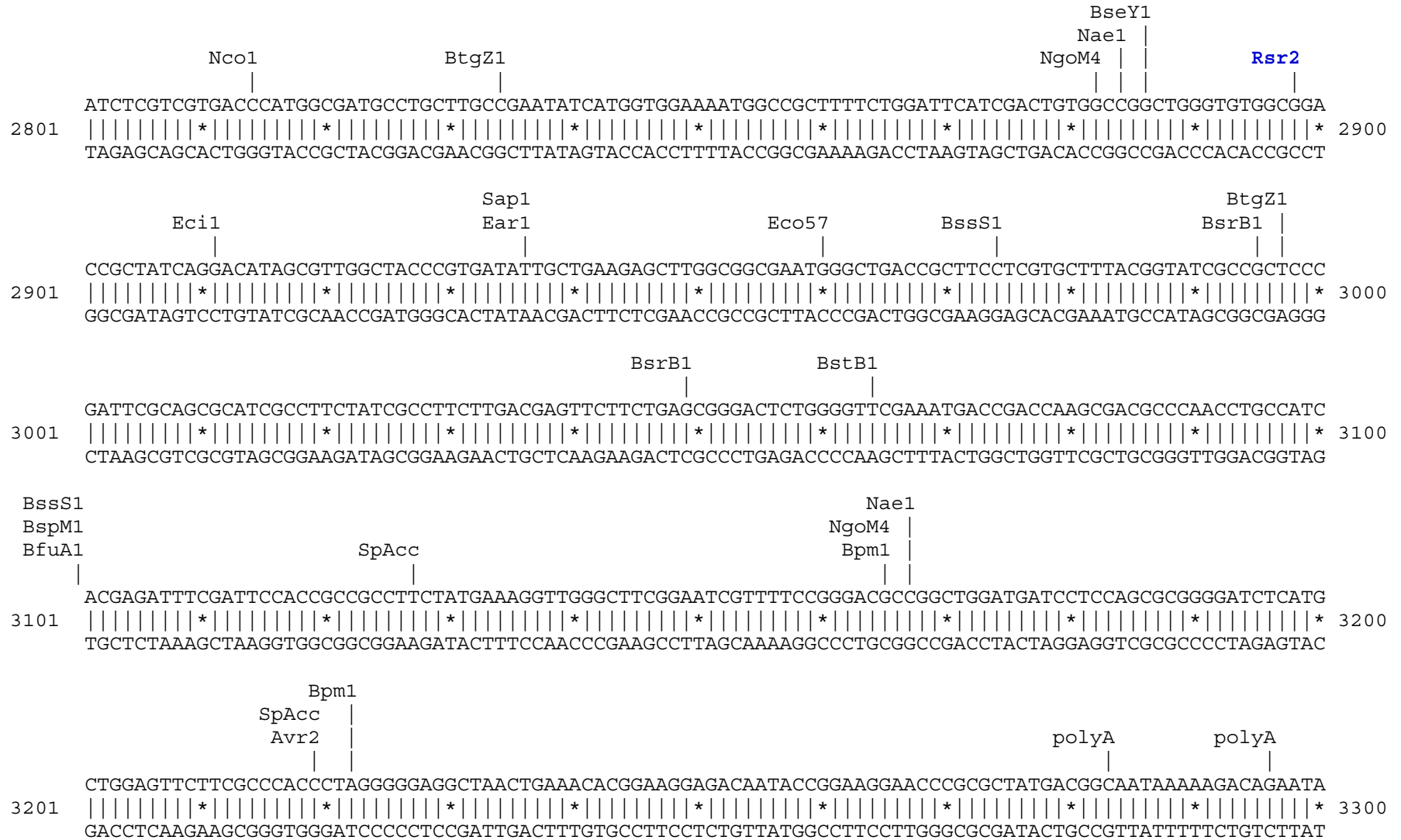
Gateway® Dendra2-At-N entry clone restriction map

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). MCS sequence is shown in frame, the attL sites are underlined. Shaded regions correspond to DNA sequences transferred from the entry clone into the destination vector following recombination. Non-Dendra2 amino acids coded by those DNA sequences are shown in black, Dendra2 amino acids are shown in red.







```

                                     Bsa1
                                     |
3301 AAACGCACGGTGTGGGTGCGTTTGTTCATAAACGCGGGGTTTCGGTCCCAGGGCTGGCACTCTGTGATACCCACCGAGACCCCATTGGGGCCAATACGC 3400
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      TTTGCGTGCCACAACCCAGCAAACAAGTATTTGCGCCCCAAGCCAGGGTCCCAGCCGTGAGACAGCTATGGGGTGGCTCTGGGGTAACCCCGTTATGCG

                                     BstAP
                                     AlwN1
                                     Bsu36
3401 CCGCGTTTCTTCCTTTTCCCCACCCCAAGTTCGGGTGAAGGCCAGGGCTCGCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCTCAGGT 3500
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      GGCGCAAAGAAGGAAAAGGGTGGGGTGGGGGTTCAAGCCACTTCCGGGTCCCAGCGTTCGGTTGCAGCCCCGCCGTCCGGGACGGTATCGGAGTCCA

                                     Dra1
                                     Dra1
                                     BspH1
3501 TACTCATATATACTTTAGATTGATTTAAAACCTTCATTTTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTTGATAATCTCATGACCAAAATCCCTTAAC 3600
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      ATGAGTATATATGAAATCTAACTAAATTTGAAGTAAAAATTAAATTTTCCTAGATCCACTTCTAGGAAAACTATTAGAGTACTGGTTTTAGGGAATTG

                                     BpuE1
3601 GTGAGTTTTCGTTCCTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAA 3700
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      CACTCAAAGCAAGGTGACTCGCAGTCTGGGCATCTTTTCTAGTTTCTAGAGAAGTCTAGGAAAAAAGACGCGCATTAGACGACGAACGTTTGT

                                     Eco57
3701 AAAACCACCGCTACCAGCGGTGGTTTGTGTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAAGTGGCTTCAGCAGAGCGCAGATACCAAATACT 3800
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      TTTTGGTGGCGATGGTTCGCCACCAAACAAACGGCCTAGTTCTCGATGGTTGAGAAAAAGGCTTCCATTGACCGAAGTCGTCTCGCGTCTATGGTTTTATGA

                                     SpAcc
                                     AlwN1
3801 GTCCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCA 3900
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      CAGGAAGATCACATCGGCATCAATCCGGTGGTGAAGTCTTGTAGACATCGTGGCGGATGTATGGAGCGAGACGATTAGGACAATGGTCACCGACGACGGT
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          BpuE1                                     ApaL1       BseY1
          |                                         |           |
GTGGCGATAAGTCTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCTGGGCTGAACGGGGGGTTTCGTGCACACAGCCCAG
3901 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 4000
CACCGCTATTCAGCACAGAATGGCCCAACCTGAGTTCTGCTATCAATGGCCTATTCCGCGTCGCCAGCCCAGACTTGCCCCCAAGCACGTGTGTCTGGGTC

          SpAcc                                     Eci1
          |                                         |
CTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAAGCGCCACGCTTCCCGAAGGGAGAAAAGGCGGACAGGTATCCGGTA
4001 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 4100
GAACCTCGCTTGCTGGATGTGGCTTGACTCTATGGATGTCGCACTCGATACTCTTTTCGCGGTGCGAAGGGCTTCCCTCTTTCCGCTGTCCATAGGCCAT

BciV1          BssS1          SpAcc          Drd1
|             |             |             |
AGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTCTGGGTTTTCGCCACCTCTGACTTGAGC
4101 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 4200
TCGCCGTCCCAGCCTTGTCTCTCGCGTGCTCCCTCGAAGGTCCCCCTTTGCGGACCATAGAAATATCAGGACAGCCCAAAGCGGTGGAGACTGAACTCG

          BpuE1          SpAcc          Eci1
          |             |             |
GTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACCGGGCCTTTTTACGGTTCTGGCCTTTTGTGGCCTTTTGTCTCA
4201 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 4300
CAGCTAAAAAACACTACGAGCAGTCCCCCGCTCGGATACCTTTTTTTCGGTTCGTTGCGCCGAAAAATGCCAAGGACCGGAAAAACGACCGGAAAAACGAGT

SpDon          NsiI
BspLU          |             |
||             |             |
CATGTTCTTTTCCTGCGTTATCCCTGATTCTGTGGATAACCGTATTACCGCCATGCAT
4301 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 4358
GTACAAGAAAAGGACGCAATAGGGGACTAAGACACCTATTGGCATAATGGCGGTACGTA

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Found:

Acc65	Acl1	Afe1	Afl2	Age1	Ale1	AlwN1	Apa1	ApaL1	Avr2	BamH1	BciV1	BfrB1	BfuA1
Bgl1	Bgl2	Bmr1	Bpm1	BpuE1	Bsa1	BsaB1	BsaXa	BsaXb	BseR1	BseY1	Bsm1	BspH1	BspLU
BspM1	BsrB1	BsrD1	BsrG1	BssS1	BstAP	BstB1	Bsu36	BtgZ1	Bts1	Cla1	Dra1	Dra3	Drd1
Eag1	Ear1	Eci1	Eco57	EcoR1	Fsp1	Hind3	Hpa1	Kas1	Kpn1	Mfe1	Msc1	Nae1	Nar1
Nco1	NgoM4	Nhe1	Not1	Nsi1	PflF1	polyA	Psi1	PspOM	Pst1	Pvu2	Rsr2	Sac1	Sac2
Sal1	Sap1	SexA1	Sfi1	Sma1	SpAcc	SpDon	Sph1	Ssp1	Stu1	T7Ter	Xcm1	Xho1	Xmn1

Unique:

Acc65	Acl1	Afe1	Afl2	Age1	Ale1	Apa1	ApaL1	BamH1	Bgl1	Bgl2	Bsa1	BsaXa	BsaXb
BspLU	Bts1	Cla1	EcoR1	Fsp1	Hind3	Hpa1	Kas1	Kpn1	Mfe1	Msc1	Nar1	Nhe1	Not1
PflF1	PspOM	Pst1	Rsr2	Sac1	Sac2	Sal1	SexA1	Sfi1	Sma1	Stu1	T7Ter	Xcm1	Xho1
Xmn1													

Not found:

Aar1	Aat2	Ahd1	Asc1	Ase1	AsiS1	Bae1a	Bae1b	Bbs1	BbvC1	Bcg1a	Bcg1b	Bcl1	Blp1
BmgB1	Bpu10	Bsg1	BsiW1	BsmB1	BspE1	BssH2	BstE2	BstX1	BstZ1	_Chi	EcoK	EcoN1	EcoRV
ScFRT	Fse1	FspA1	I_Ceu	loxP	Mlu1	Nde1	Nru1	Pac1	PflM1	Pme1	Pml1	PshA1	Pvu1
SanD1	Sbf1	Sca1	Sgf1	SgrA1	SnaB1	Spe1	Srf1	Swa1	T3RNA	T7RNA	PISce	Xba1	

Excluded by site complexity:

Acc1	Aci1	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													