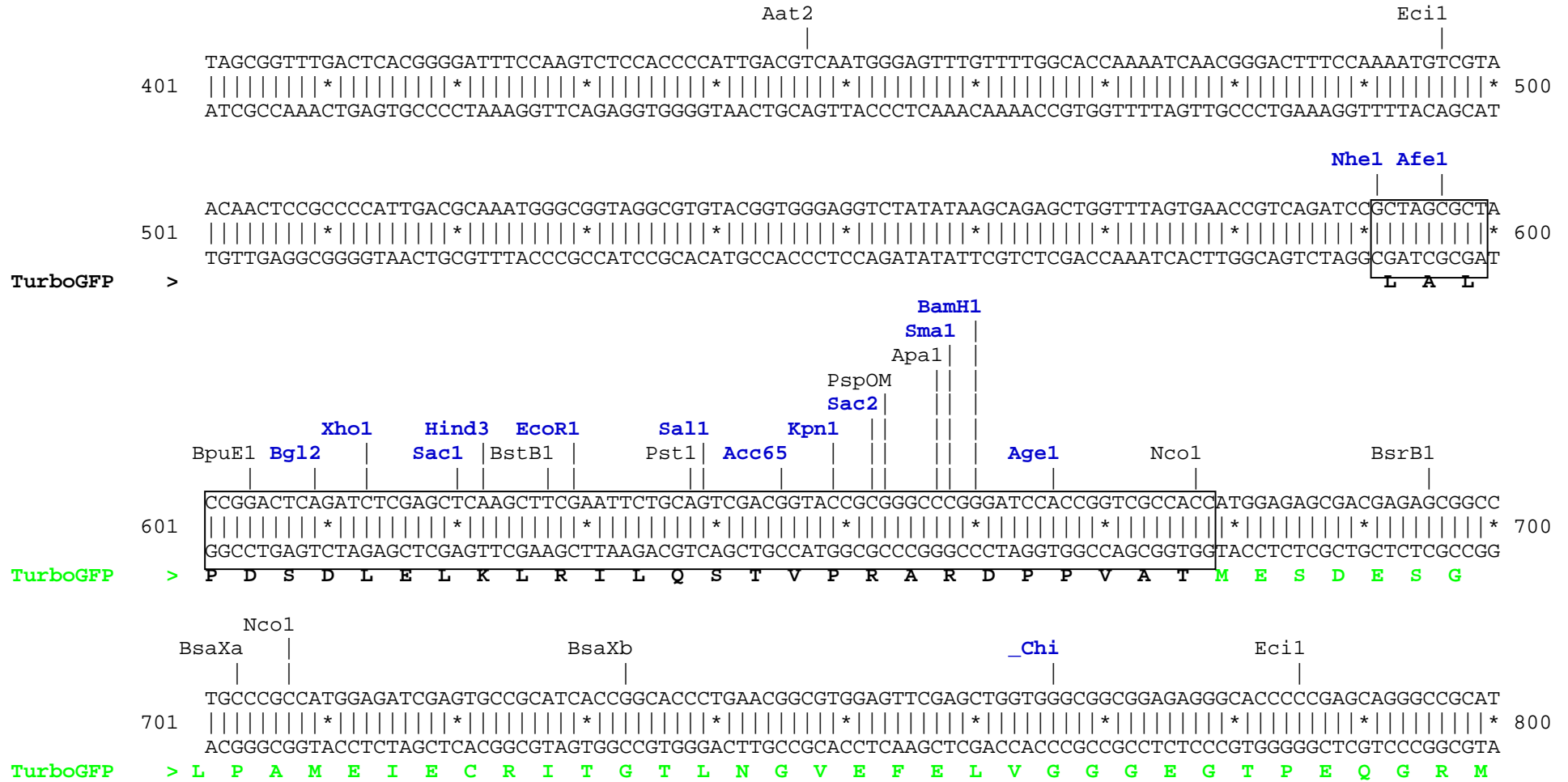


pTurboGFP-N vector restriction map

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). MCS sequence shown in frame, amino acids coded by MCS shown in black.

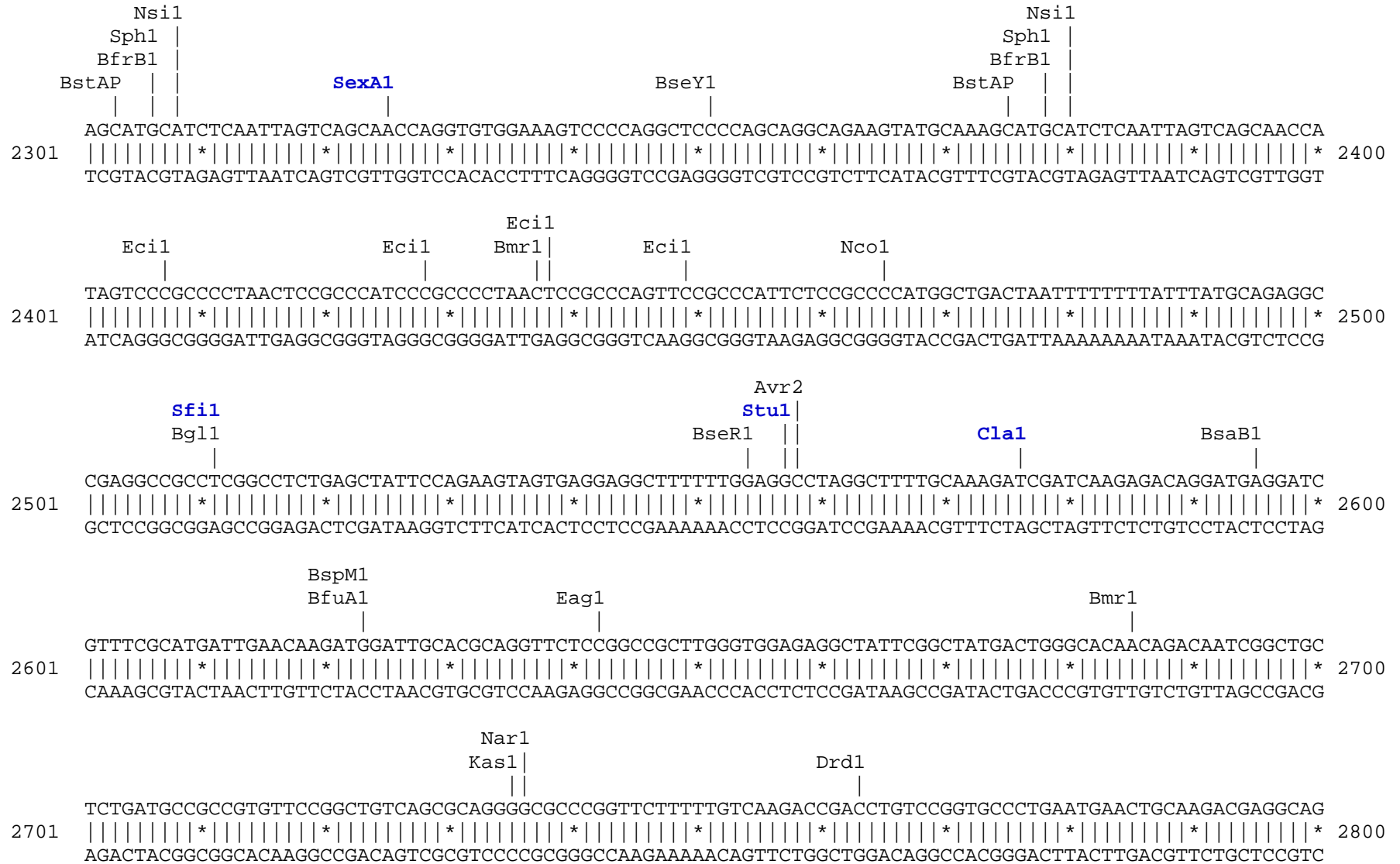


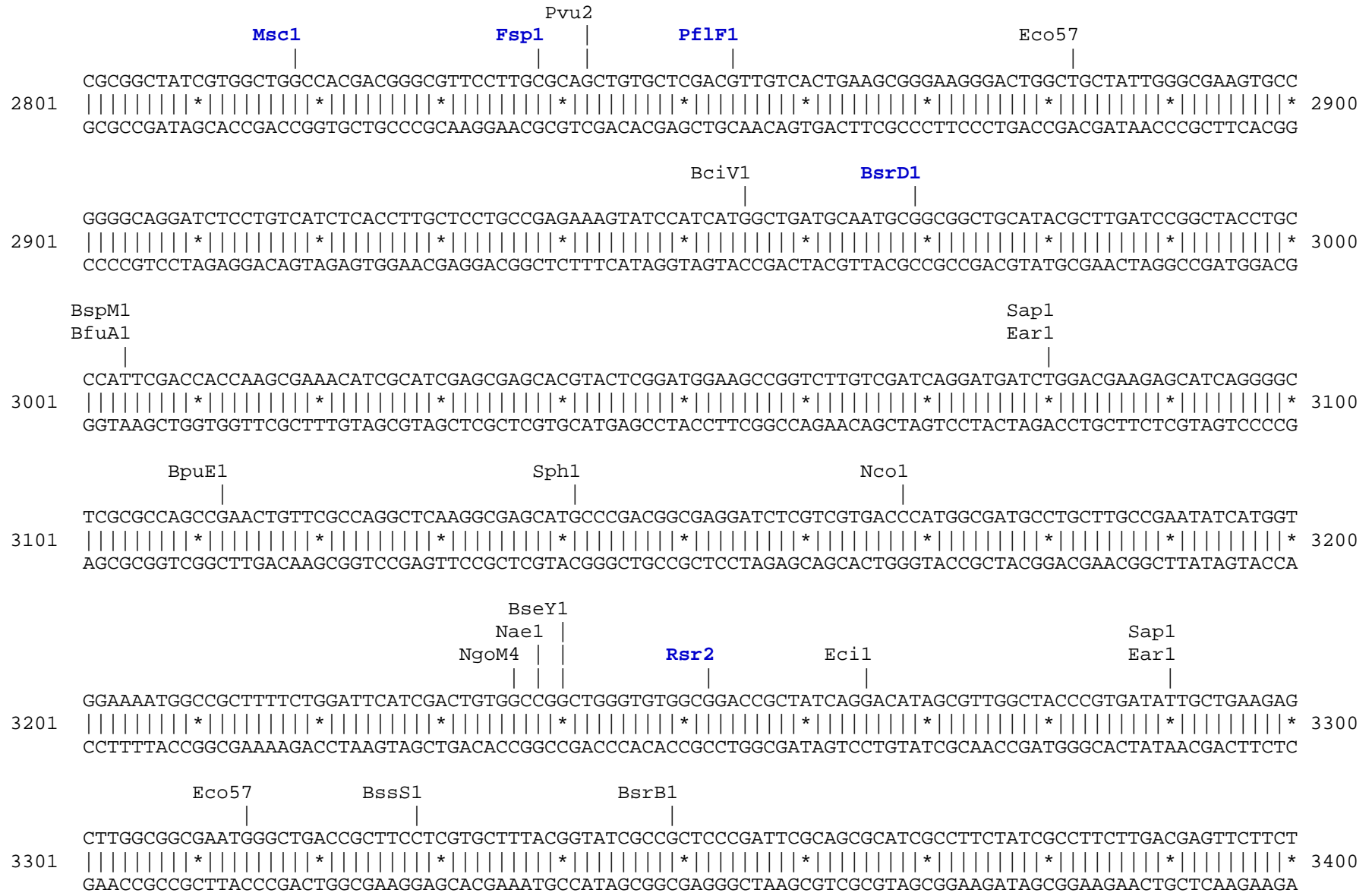



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                                     BsaXa
                                     |
TCCGTGGTGGACAGCCACATGCACTTCAAGAGCGCCATCCACCCAGCATCCTGCAGAACGGGGGCCCCATGTTTCGCCTTCCGCCGCGTGGAGGAGGATC
1201 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1300
AGGCACCACCTGTCGGTGTACGTGAAGTTCTCGCGGTAGGTGGGGTTCGTAGGACGTCTTGCCCCGGGGTACAAGCGGAAGGCGGCGCACCTCCTCCTAG
TurboGFP > S V V D S H M H F K S A I H P S I L Q N G G P M F A F R R V E E D
                                     BseY1
                                     |
ACAGCAACACCGAGCTGGGCATCGTGGAGTACCAGCACGCCTTCAAGACCCCGGATGCAGATGCCGGTGAAGAATAAAGCGGCCGCGACTCTAGATCATA
1301 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1400
TGTCGTTGTGGCTCGACCCGTAGCACCTCATGGTTCGTGCGGAAGTTCTGGGGCCTACGTCTACGGCCACTTCTTATTTTCGCCGGCGCTGAGATCTAGTAT
TurboGFP > H S N T E L G I V E Y Q H A F K T P D A D A G E E *
                                     Not1
                                     |
                                     Eag1
                                     |
                                     Xba1
                                     |
                                     BsaB1
                                     |
ATCAGCCATACCACATTTGTAGAGGTTTTACTTGGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTGAAACATAAAAATGAATGCAATTGTTGTTGTTA
1401 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1500
TAGTCGGTATGGTGTAAACATCTCAAAATGAACGAAATTTTTTGGAGGGTGTGGAGGGGACTTGGACTTTGTATTTTACTTACGTTAACAACAACAAT
                                     Dral
                                     |
                                     Bsm1
                                     |
                                     Mfe1
                                     |
                                     Hpa1
                                     |
ATCAGCCATACCACATTTGTAGAGGTTTTACTTGGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTGAAACATAAAAATGAATGCAATTGTTGTTGTTA
1401 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1500
TAGTCGGTATGGTGTAAACATCTCAAAATGAACGAAATTTTTTGGAGGGTGTGGAGGGGACTTGGACTTTGTATTTTACTTACGTTAACAACAACAAT
                                     Psil
                                     |
ACTTGTATTATTCAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATTTACAAATAAAGCATTTTTTTTCACTGCATTCTAGTTGTGGTTTGTC
1501 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1600
TGAACAAATAACGTCGAATATTACCAATGTTTATTTTCGTTATCGTAGTGTAAAGTGTAAATTTTCGTAATAAAGTACGTAAGATCAACACCAAAACAG
                                     Af12
                                     |
                                     Ssp1
                                     |
CAAACCTCATCAATGTATCTTAAGGCGTAAATTTGTAAGCGTTAATATTTTGTAAATTCGCGTTAAATTTTTGTTAAATCAGCTCATTTTTTAACCAATA
1601 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1700
GTTTGAGTAGTTACATAGAATTCCGCATTTAACATTCGCAATTATAAAACAATTTTAAAGCGCAATTTAAAAACAATTTAGTCGAGTAAAAAATTGGTTAT

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                                     BpuE1
                                     |
4001 AGGATCTTCTTGAGATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAACCACCGCTACCAGCGGTGGTTTGTGTTGCCGGATCAAGAGCTA
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4100
    TCCTAGAAGAACTCTAGGAAAAAAGACGCGCATTAGACGACGAACGTTTGTGTTTTTTGGTGGCGATGGTCGCCACCAAACAAACGGCCTAGTTCTCGAT

                                     Eco57
                                     |
4101 CCAACTCTTTTTCCGAAGGTAAGTGGCTTCAGCAGAGCGCAGATAACAAATACTGTCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTG
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4200
    GGTTGAGAAAAAGGCTTCCATTGACCGAAGTCGTCTCGCGTCTATGGTTTATGACAGGAAGATCACATCGGCATCAATCCGGTGGTGAAGTTCTTGAGAC

                                     AlwN1                                     BpuE1
                                     |                                     |
4201 TAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTT
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4300
    ATCGTGGCGGATGTATGGAGCGAGACGATTAGGACAATGGTCACCGACGACGGTCACCGCTATTCAGCACAGAATGGCCCAACCTGAGTTCTGCTATCAA

                                     ApaI1                                     BseY1
                                     |                                     |
4301 ACCGGATAAGGCGCAGCGGTGCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAG
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4400
    TGGCCTATTCCGCGTCGCCAGCCGACTTGCCCCCAAGCACGTGTGTCGGGTGCAACCTCGCTTGCTGGATGTGGCTTGAAGTCTATGGATGTGCGACTC

                                     BciV1                                     BssS1
                                     |                                     |
4401 CTATGAGAAAAGCGCCACGCTTCCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGG
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4500
    GATACTCTTTCGCGGTGCGAAGGGCTTCCCTCTTTCCGCTGTCCATAGGCCATTGCGCGTCCCAGCCTTGTCCTCTCGCGTGCTCCCTCGAAGGTCCCC

                                     Drd1                                     BpuE1                                     Eci1
                                     |                                     |                                     |
4501 GAAACGCCTGGTATCTTTATAGTCTGTGCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGCGGAGCCTATGGAAAA
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4600
    CTTTGGCGACCATAGAAATATCAGGACAGCCCAAAGCGGTGGAGACTGAACTCGCAGCTAAAAACACTACGAGCAGTCCCCCGCCTCGGATACCTTTTT

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Unique:

Aar1	Acc65	Afe1	Afl2	Age1	ApaL1	Ase1	BamH1	Bgl2	Blp1	Bsa1	BspLU	BsrD1	Bts1
_Chi	Clal	Dra3	EcoR1	Fse1	Fsp1	Hind3	Hpa1	Kpn1	Mfe1	Msc1	Nde1	Nhe1	Not1
PflF1	PflM1	Rsr2	Sac1	Sac2	Sal1	SexA1	Sfi1	Sma1	SnaB1	Stu1	Xba1	Xho1	Xmn1

Not found:

Acc1	Ahd1	Ale1	Asc1	AsiS1	Baela	Baelb	Bbs1	BbvC1	Bcgl1a	Bcgl1b	Bcl1	BmgB1	Bpu10
BsiW1	BsmB1	BspE1	BsrG1	BssH2	BstE2	BstX1	BstZ1	EcoK	EcoN1	EcoRV	ScFRT	FspA1	I_Ceu
loxP	Mlu1	Nru1	Pac1	Pme1	PshA1	Pvu1	SanD1	Sbf1	Sca1	Sgf1	SgrA1	Spe1	Srf1
Swal	PISce	Xcm1											

Excluded by site complexity:

Acc1	Ac1	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													