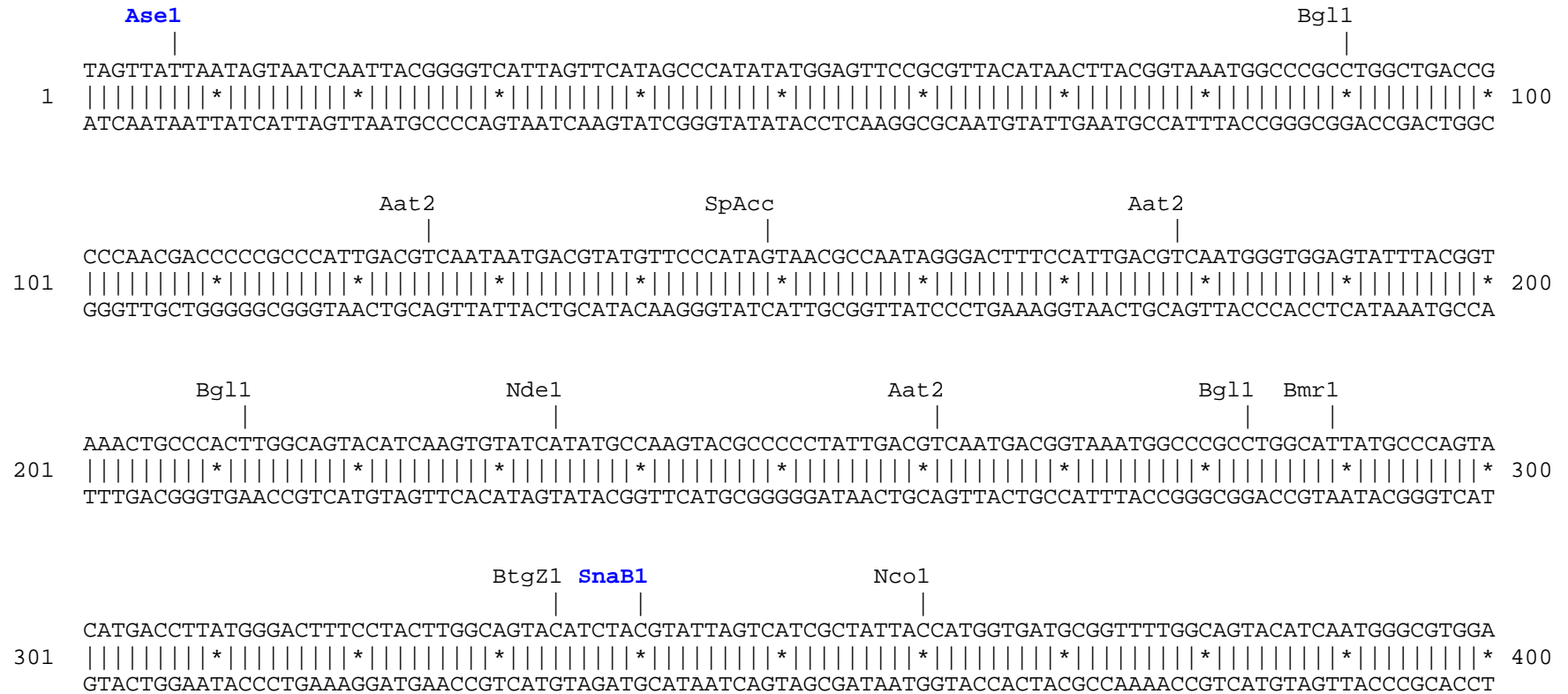


**pPA-TagRFP-tubulin vector restriction map**

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).

PA-TagRFP amino acids are shown in red, Tubulin amino acids are shown in green, linker amino acids are shown in black.



Aat2 Eci1

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TAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTTGACGTCAATGGGAGTTTGTGTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTA
401 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 500
ATCGCCAAACTGAGTGCCCTAAAGGTTTCAGAGGTGGGGTAACTGCAGTTACCCTCAAACAAAACCGTGGTTTTAGTTGCCCTGAAAGGTTTTACAGCAT

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Nhe1

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ACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTGGTTTTAGTGAACCGTCAGATCCGCTAGCGGTG
501 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 600
TGTTGAGGCGGGGTAAGTGCCTTTACCCGCCATCCGCACATGCCACCCTCCAGATATATTCGTCTCGACCAAATCACTTGGCAGTCTAGGCGATCGCCAC

```

Ale1 BsrG1 ApaL1

Nco1 | Sap1

Msc1 | Ear1

```

GCCACCATGGTGTCTAAGGGCGAAGAGCTGATTAAGGAGAACATGCACATGAAGCTGTACATGGAGGGCACCGTGAACAACCACCACTTCAAGTGCACAT
601 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 700
CGGTGGTACCACAGATTCCCCTTCTCGACTAATTCCTCTTGTACGTGTACTTTCGACATGTACCTCCCCTGGCACTTGTGGTGGTGAAGTTACAGTGT
PA-TagRFP > M V S K G E E L I K E N M H M K L Y M E G T V N N H H F K C T S

```

SpAcc

```

CCGAGGGCGAAGGCAAGCCCTACGAGGGCACCCAGACCATGAGAATCAAGGTGGTTCGAGGGCGGCCCTCTCCCCTTCGCCTTCGACATCCTGGCTACCAG
701 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 800
GGCTCCCGCTTCCGTTTCGGGATGCTCCCGTGGGTCTGGTACTCTTAGTTCCACCAGCTCCCGCCGGGAGAGGGGAAGCGGAAGCTGTAGGACCGATGGTC
PA-TagRFP > E G E G K P Y E G T Q T M R I K V V E G G P L P F A F D I L A T S

```

Bsu36 SpDon

```

CTTCATGTACGGCAGCAGCACCTTTCATCAACCACACCCAGGGCATCCCCGACTTCTGGAAGCAGTCCTTCCCTGAGGGCTTCACATGGGAGAGAGTACC
801 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 900
GAAGTACATGCCGTCGTCGTGGAAGTAGTTGGTGTGGGTCCCCTAGGGGCTGAAGACCTTCGTCAGGAAGGGACTCCCGAAGTGTACCCTCTCTCAGTGG
PA-TagRFP > F M Y G S S T F I N H T Q G I P D F W K Q S F P E G F T W E R V T

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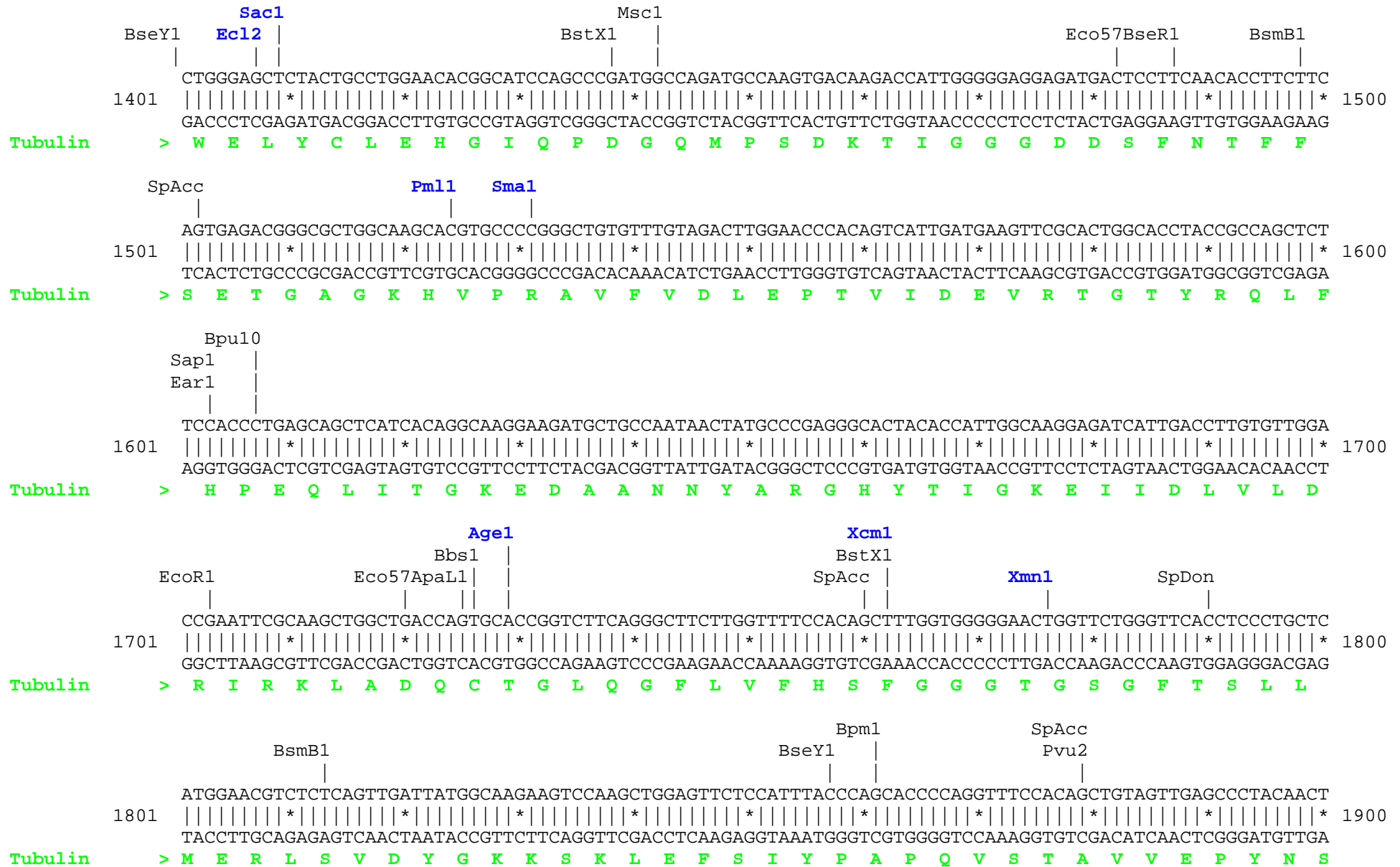
Bbs1 Bpm1  
ACATACGAAGACGGGGCGTGCTGACCGCTACCCAGGACACCAGCCTCCAGGACGGCTGCCTCATCTACAACGTCAAGATCAGAGGGGTGAACTTCCCAT  
901 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 1000  
TGTATGCTTCTGCCCCGCACGACTGGCGATGGGTCTGTGGTCGGAGGTCTGCCGACGGAGTAGATGTTGCAGTTCTAGTCTCCCCACTTGAAGGGTA  
PA-TagRFP > T Y E D G G V L T A T Q D T S L Q D G C L I Y N V K I R G V N F P S

BseY1 Bgl1 Sall  
CCAACGGCCCTGTGATGAAGAAGAAAACACTCGGCTGGGAACCGAGCACCGAGAAACTGAAACCCGCTGACGGCGGCCTGGAAGGCAGGGTTCGACATGGC  
1001 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 1100  
GGTTGCCGGGACACTACTTCTTCTTTGTGAGCCGACCCTTGCTCGTGGCTCTTTGACTTTGGGCGACTGCCGCCGACCTTCCGTCCCAGCTGTACCG  
PA-TagRFP > N G P V M K K K T L G W E P S T E K L K P A D G G L E G R V D M A

BssS1 Eco57 BpuE1  
CCTGAAGCTCGTGGGCGGGGGCCACCTGATCTGCAACTTCAAGACCACATACAGATCCAAGAAACCCGCTAAGAACCTCAAGATGCCCGGCGTCTACTAT  
1101 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 1200  
GGACTTCGAGCACCCGCCCCGGTGGACTAGACGTTGAAGTTCTGGTGTATGTCTAGGTTCTTTGGGCGATTCTTGAGTTCTACGGGCCGACAGATGATA  
PA-TagRFP > L K L V G G G H L I C N F K T T Y R S K K P A K N L K M P G V Y Y

Bsa1 BssS1 Bmr1 Dra3 Msc1 SpAcc  
GTGGACCGCAGACTGGAAATCATCAAGGAGGCCGACAAAGAGACCTACTGGGAGCAGCACGAGGTGGCTGTGGCCAGATACTCCGACCTCCCTAGCAAAC  
1201 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 1300  
CACCTGGCGTCTGACCTTTAGTAGTTCTCCGGCTGTTTCTCTGGATGACCCTCGTCTGTGCTCCACCGACACCGGTCTATGAGGCTGGAGGGATCGTTTG  
PA-TagRFP > V D R R L E I I K E A D K E T Y W E Q H E V A V A R Y S D L P S K L

Ale1 Bmr1 BspE1 BseR1 Bgl2 Xho1 Msc1 BsrD1 BstAP1  
TGGGGCACAGAGGTGGAGGAGGTTCCGGACTCAGATCTCGAGTGCCTGAGTGCATCTCCATCCACGTTGGCCAGGCTGGTGTCCAGATTGGCAATGCCTG  
1301 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 1400  
ACCCCGTGTCTCCACCTCCTCCAAGGCCTGAGTCTAGAGCTCACGCACTCACGTAGAGGTAGGTGCAACCGGTCCGACCACAGGTCTAACCGTTACGGAC  
PA-TagRFP/Tub.> G H R G G G G S G L R S R V R E C I S I H V G Q A G V Q I G N A C



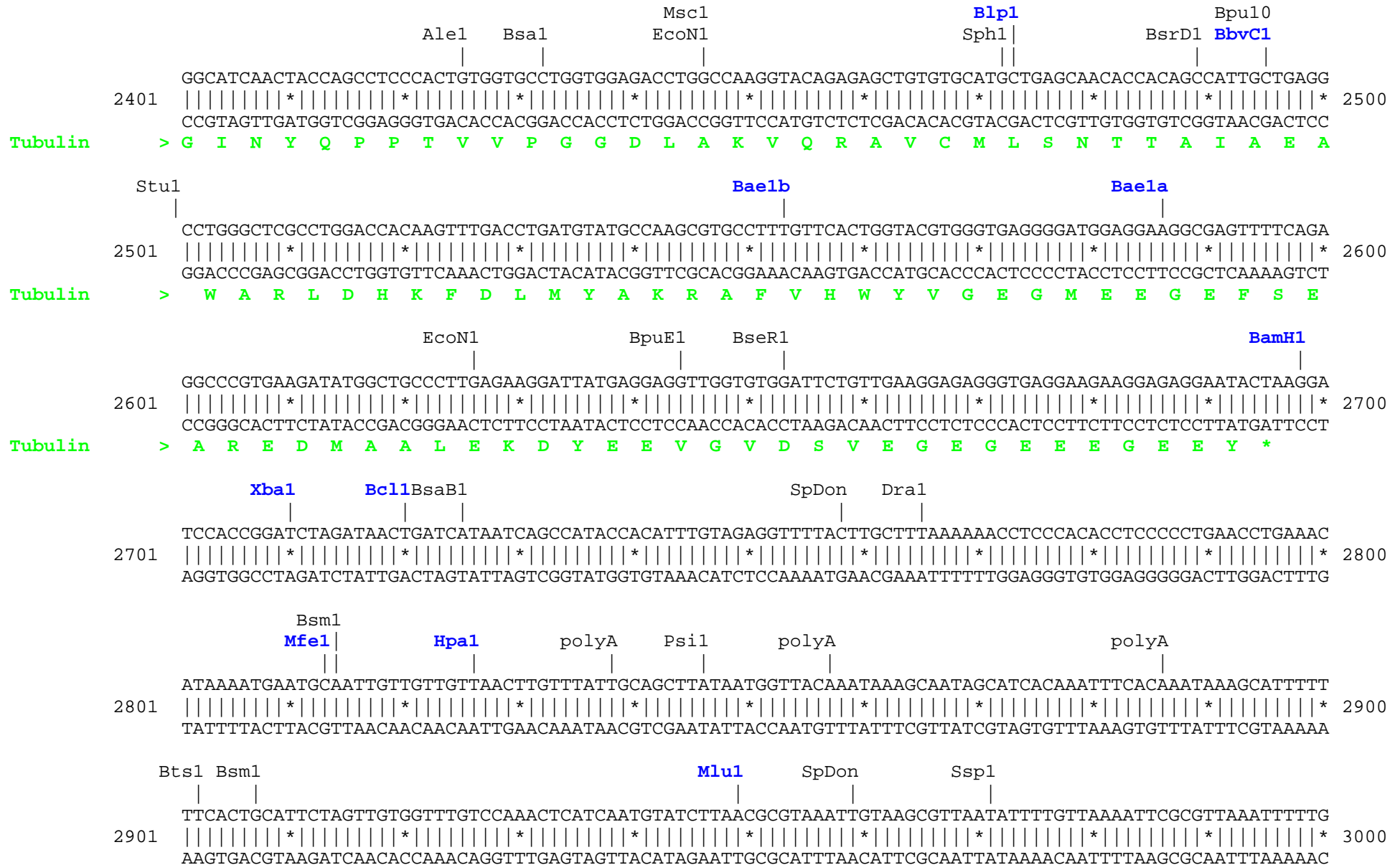
SpDon | Bpm1 | PshA1 | EcoRV  
 CCATCCTCACCACCCACACCACCTGGAGCACTCTGATTGTGCCTTCATGGTAGACAATGAGGCCATCTATGACATCTGTTCGTAGAAACCTCGATATCGA  
 1901 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 2000  
 GGTAGGAGTGGTGGGTGTGGTGGGACCTCGTGAGACTAACACGGAAGTACCATCTGTTACTCCGGTAGATACTGTAGACAGCATCTTTGGAGCTATAGCT  
**Tubulin** > I L T T H T T L E H S D C A F M V D N E A I Y D I C R R N L D I E

Bts1  
 GCGCCCAACCTTACACTAACCTTAACCGCCTTATTAGCCAGATTGTGTCTCCATCACTGCTTCCCTGAGATTTGATGGAGCCCTGAATGTTGACCTGACA  
 2001 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 2100  
 CGCGGGTTGGATGTGATTGGAATTGGCGGAATAATCGGTCTAACACAGGAGGTAGTGACGAAGGGACTCTAAACTACCTCGGGACTTACAACCTGGACTGT  
**Tubulin** > R P T Y T N L N R L I S Q I V S S I T A S L R F D G A L N V D L T

EcoR1 | SexA1 | Msc1 Nde1 | SpAcc  
 GAATTCAGACCAACCTGGTGCCTTACCCCGCATCCACTTCCCTCTGGCCACATATGCCCTGTCATCTCTGCTGAGAAAGCCTACCATGAACAGCTTT  
 2101 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 2200  
 CTTAAGGTCTGGTTGGACCACGGGATGGGGCGTAGGTGAAGGGAGACCGGTGTATACGGGGACAGTAGAGACGACTCTTTTCGGATGGTACTTGTTCGAAA  
**Tubulin** > E F Q T N L V P Y P R I H F P L A T Y A P V I S A E K A Y H E Q L S

SpAcc | SpDon | SpDon  
 SpAcc | BstX1 | Nco1 | SpDon  
 CTGTAGCAGAGATCACCAATGCTTGCTTTGAGCCAGCCAACCAGATGGTGAAATGTGACCCTCGCCATGGTAAATACATGGCTTGCTGCCTGTTGTACCG  
 2201 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 2300  
 GACATCGTCTCTAGTGGTTACGAACGAAACTCGGTTCGGTTGGTCTACCACTTTACACTGGGAGCGGTACCATTTATGTACCGAACGACGGACAACATGGC  
**Tubulin** > V A E I T N A C F E P A N Q M V K C D P R H G K Y M A C C L L Y R

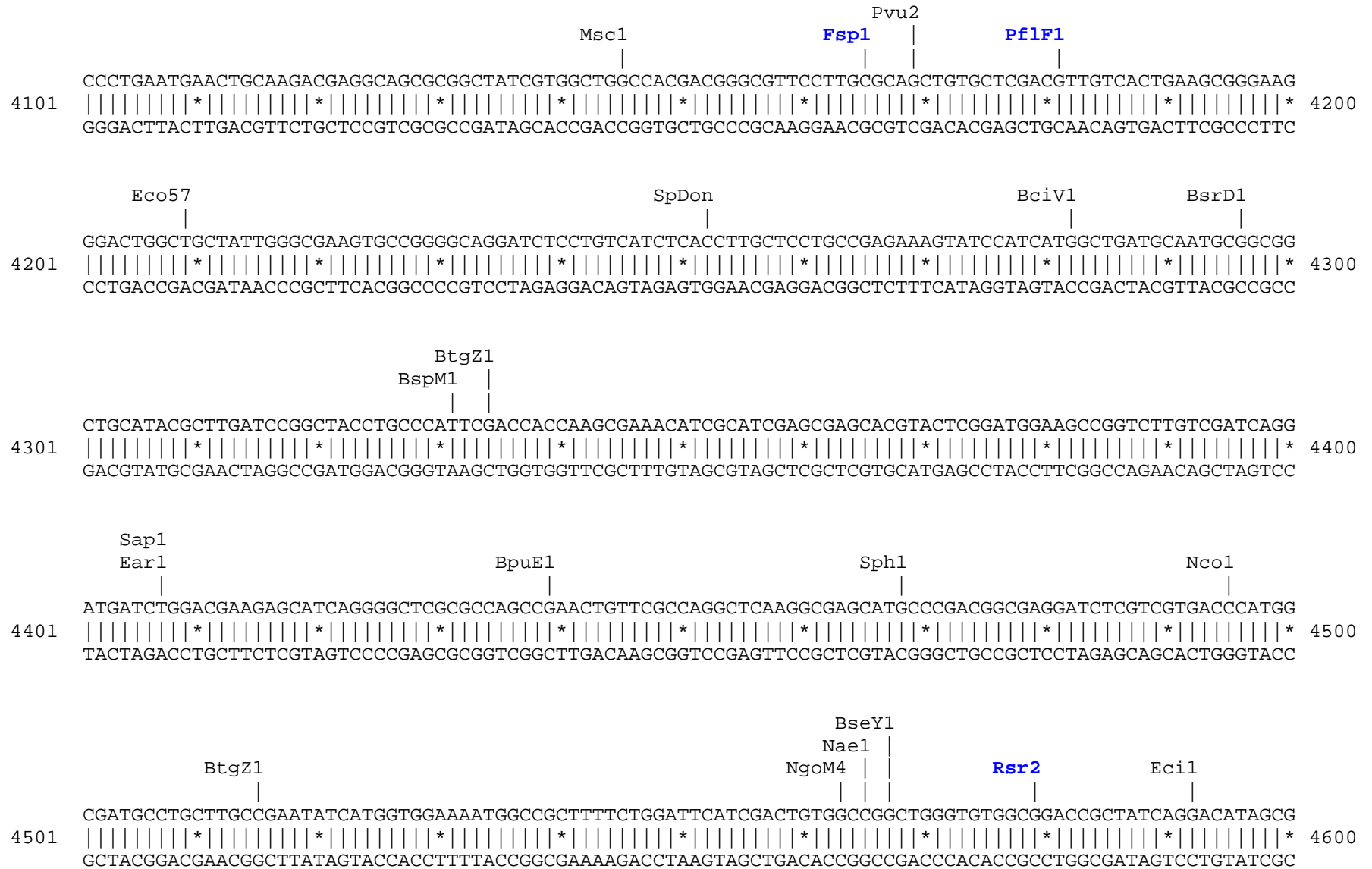
BmgB1 | BsrD1 | PflM1 | Bgl1  
 TGGTGACGTGGTTCCCAAAGATGTCAATGCTGCCATTGCCACCATCAAAACCAAGCGCAGCATCCAGTTTGTGGATTGGTGCCCCACTGGCTTCAAGGTT  
 2301 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 2400  
 ACCACTGCACCAAGGGTTTCTACAGTTACGACGGTAACGGTGGTAGTTTTGGTTTCGCGTCGTAGGTCAAACACCTAACCACGGGGTGACCGAAGTTCCAA  
**Tubulin** > G D V V P K D V N A A I A T I K T K R S I Q F V D W C P T G F K V













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                                     BstAP
                                     AlwN1       Bsu36
                                     |           |
5101 CCACCCACCCCAAGTTCGGGTGAAGGCCAGGGCTCGCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCTCAGGTTACTCATATATACTTTAGA 5200
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
    GGTGGGGTGGGGGGTTCAAGCCCACCTCCGGGTCCCAGCGTCGGTTGCAGCCCCGCCGTCGGGACGGTATCGGAGTCCAATGAGTATATATGAAATCT

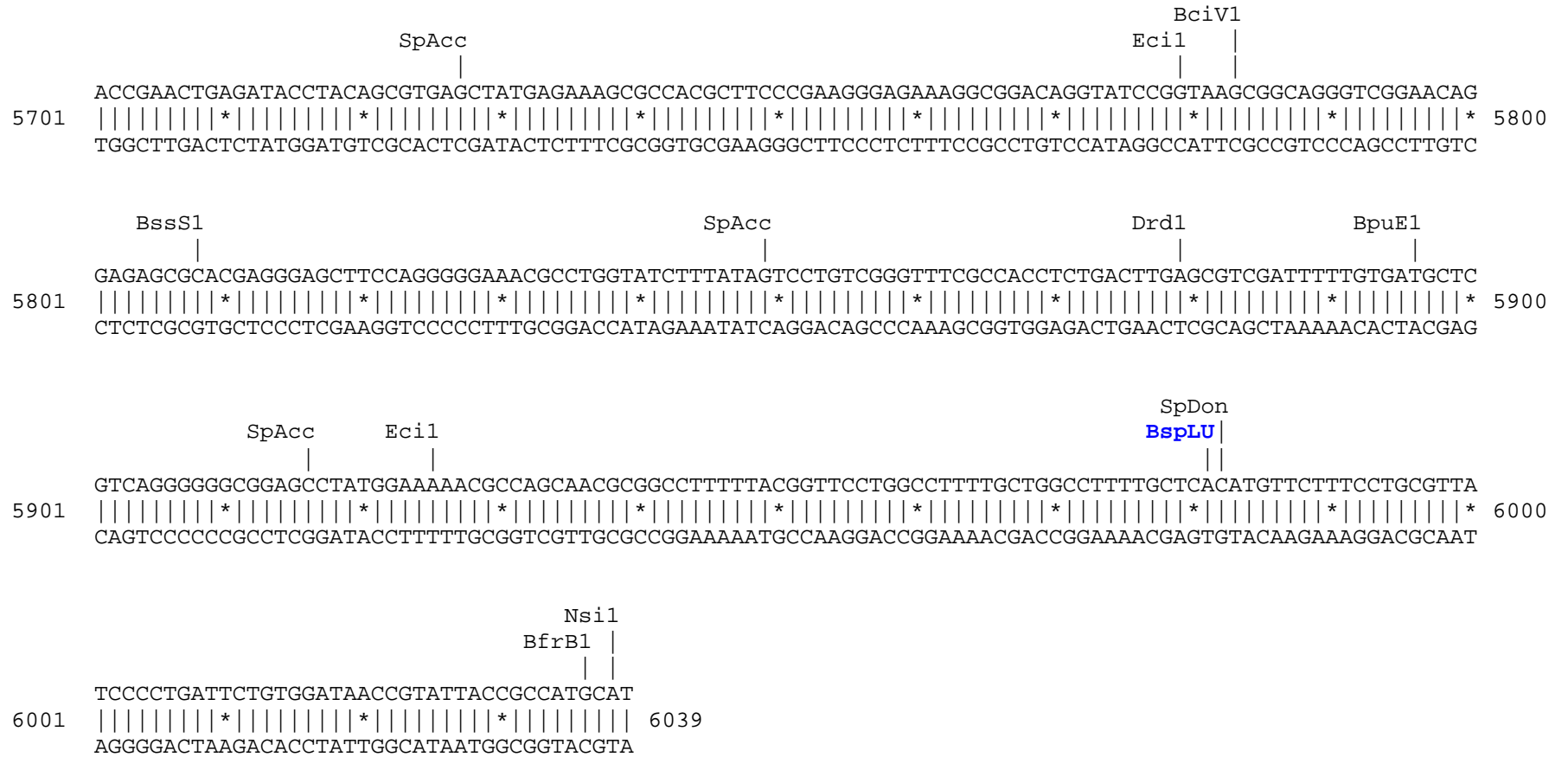
    Dra1           Dra1           BspH1
    |             |             |
5201 TTGATTTAAAACTTCATTTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTTCGTTCCACTG 5300
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
    AACTAAATTTTGAAGTAAAAATTAATTTTCTAGATCCACTTCTAGGAAAACTATTAGAGTACTGGTTTTAGGGAATTGCACTCAAAGCAAGGTGAC

                                     BpuE1
                                     |
5301 AGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTTGAGATCCTTTTTTTTCTGCGGTAATCTGCTGCTTGCAAACAAAAAACACCGCTACCAGCG 5400
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
    TCGCAGTCTGGGGCATCTTTTCTAGTTTCTTAGAAGAACTCTAGGAAAAAAGACGCGCATTAGACGACGAACGTTTGTTTTTTTGGTGGCGATGGTTCGC

                                     Eco57           SpAcc
                                     |             |
5401 GTGGTTTGTGGCCGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAAGTGGCTTCAGCAGAGCGCAGATACCAAATACTGTCCTTCTAGTGTAGCCGT 5500
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
    CACCAAACAAACGGCCTAGTTCTCGATGGTTGAGAAAAAGGCTTCCATTGACCGAAGTCGTCTCGCGTCTATGGTTTATGACAGGAAGATCACATCGGCA

                                     AlwN1           BpuE1
                                     |             |
5501 AGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCT 5600
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
    TCAATCCGGTGGTGAAGTTCTTGAGACATCGTGGCGGATGTATGGAGCGAGACGATTAGGACAATGGTCAACGACGACGGTCAACCGCTATTGAGCAGAGA

                                     ApaI1       BseY1
                                     |           |
5601 TACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTAC 5700
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
    ATGGCCCAACCTGAGTTCTGCTATCAATGGCCTATTCCGCGTCGCCAGCCGACTTGCCCCCAAGCACGTGTGTTCGGGTGGAACCTCGCTTGGTGGATG
```



Found:

Aat2	<b>Age1</b>	Ale1	AlwN1	ApaL1	<b>Ase1</b>	Avr2	<b>Baela</b>	<b>Baelb</b>	<b>BamH1</b>	Bbs1	<b>BbvC1</b>	BciV1	<b>Bcl1</b>
BfrB1	Bgl1	<b>Bgl2</b>	<b>Blp1</b>	<b>BmgB1</b>	Bmr1	Bpm1	Bpu10	BpuE1	Bsa1	BsaB1	<b>BsaXa</b>	<b>BsaXb</b>	BseR1
BseY1	Bsm1	BsmB1	<b>BspE1</b>	BsrD1	<b>BsrG1</b>	BssS1	BstAP	<b>BstB1</b>	BstX1	BspH1	<b>BspLU</b>	BspM1	BsrB1
Bsu36	BtgZ1	Bts1	<b>Clal</b>	Dra1	Dra3	Drd1	<b>Eag1</b>	Ear1	Ecil	<b>Ecl2</b>	Eco57	EcoN1	EcoR1
<b>EcoRV</b>	<b>Fsp1</b>	<b>Hpa1</b>	<b>Kas1</b>	<b>Mfe1</b>	<b>Mlu1</b>	Msc1	Nae1	<b>Nar1</b>	Nco1	Nde1	NgoM4	<b>Nhe1</b>	Nsi1
<b>PflF1</b>	<b>PflM1</b>	<b>Pml1</b>	polyA	<b>PshA1</b>	Psi1	Pvu2	<b>Rsr2</b>	<b>Sac1</b>	<b>Sall1</b>	Sap1	SexA1	<b>Sfi1</b>	<b>Sma1</b>
<b>SnaB1</b>	SpAcc	SpDon	Sph1	Ssp1	Stul	<b>Xba1</b>	<b>Xcm1</b>	<b>Xho1</b>	<b>Xmn1</b>				

Unique:

<b>Age1</b>	<b>Ase1</b>	<b>Baela</b>	<b>Baelb</b>	<b>BamH1</b>	<b>BbvC1</b>	<b>Bcl1</b>	<b>Bgl2</b>	<b>Blp1</b>	<b>BmgB1</b>	<b>BsaXa</b>	<b>BsaXb</b>	<b>BspE1</b>	<b>BsrG1</b>
<b>BstB1</b>	<b>BspLU</b>	<b>Clal</b>	<b>Eag1</b>	<b>Ecl2</b>	<b>EcoRV</b>	<b>Fsp1</b>	<b>Hpa1</b>	<b>Kas1</b>	<b>Mfe1</b>	<b>Mlu1</b>	<b>Nar1</b>	<b>Nhe1</b>	<b>PflF1</b>
<b>PflM1</b>	<b>Pml1</b>	<b>PshA1</b>	<b>Rsr2</b>	<b>Sac1</b>	<b>Sall1</b>	<b>Sfi1</b>	<b>Sma1</b>	<b>SnaB1</b>	<b>Xba1</b>	<b>Xcm1</b>	<b>Xho1</b>	<b>Xmn1</b>	

Not found:

Aar1	Acc65	Ac11	Afe1	Afl2	Ahd1	Apal	Asc1	AsiS1	BcglA	Bcglb	Bsg1	BsiW1	BssH2
BstE2	BstZ1	BxatB	BxatL	BxatR	BxatP	_Chi	EcoK	FCatB	FCatL	FCatR	FCatP	ScFRT	Fse1
FspA1	Hind3	I_Ceu	Kpn1	loxP	Not1	Nru1	Pac1	Pme1	PspOM	Pst1	Pvu1	R4atB	R4atL
R4atP	R4atR	Sac2	SanD1	Sbf1	Sca1	Sgf1	SgrA1	Spe1	Srf1	Swal	T3RNA	T7RNA	T7Ter
PISce													

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	BsrF1
BssK1	BstF5	BstN1	BstU1	BstY1	Bsr1	Btg1	Cac8	CviJ1	Dde1	Eae1	EcoO1	Faul	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													