

pDendra2-C 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). MCS sequence is shown in frame, additional amino acids and those encoded by MCS are shown in black.



Aat2 |
Eci1 |

401 TAGCGGTTTACTCACGGGATTTCCAAGTCTCCACCCATTGACGTCAATGGGAGTTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTTCGTA
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*||| 500
 ATCGCCAAACTGAGTGCCCTAAAGGTTTCAGAGGTGGGGTAACTGCAGTTACCCCTCAAACAAAACCCTGGTTTTAGTTGCCCTGAAAGGTTTTACAGCAT

NheI | Afel |

501 ACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGACGGTGGGAGGTCTATATAAGCAGAGCTGGTTTTAGTGAACCGTCAGATCCGCTAGCGCTA
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*||| 600
 TGTTGAGGCGGGTAACTGCGTTTTACCCGCCATCCGCACATGCCACCCTCCAGATATATTCGTCTCGACCAAATCACTTGGCAGTCTAGGCGATCGCGAT

EcoN1 |

AgeI | SmaI | BclI | ApaI1 |

601 CCGGTCGCCACCATGAACACCCCGGAATTAACCTGATCAAGGAGGACATGCGCGTGAAGGTGCACATGGAGGGCAACGTGAACGGCCACGCCTTCGTGA
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*||| 700
 GGCCAGCGGTGGTACTTGTGGGGCCCTTAATTGGACTAGTTTCTTCTGTACGCGCACTTCCACGTGTACTTCCCCTTGCACCTTGCCGGTGCGGAAGCACT

Dendra2 > M N T P G I N L I K E D M R V K V H M E G N V N G H A F V I

NarI | KasI | Eco57 |

SpAcc |

701 TCGAGGGCGAGGGCAAGGGCAAGCCCTACGAGGGCACCCAGACCGCCAACCTGACCGTGAAGGAGGGCGCCCCCTGCCCTTCAGCTACGACATCCTGAC
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*||| 800
 AGCTCCCCTCCGTTCCCGTTCGGGATGCTCCCGTGGGTCTGGCGTTGGACTGGCACTTCTCCCGCGGGGGACGGGAAGTCGATGCTGTAGGACTG

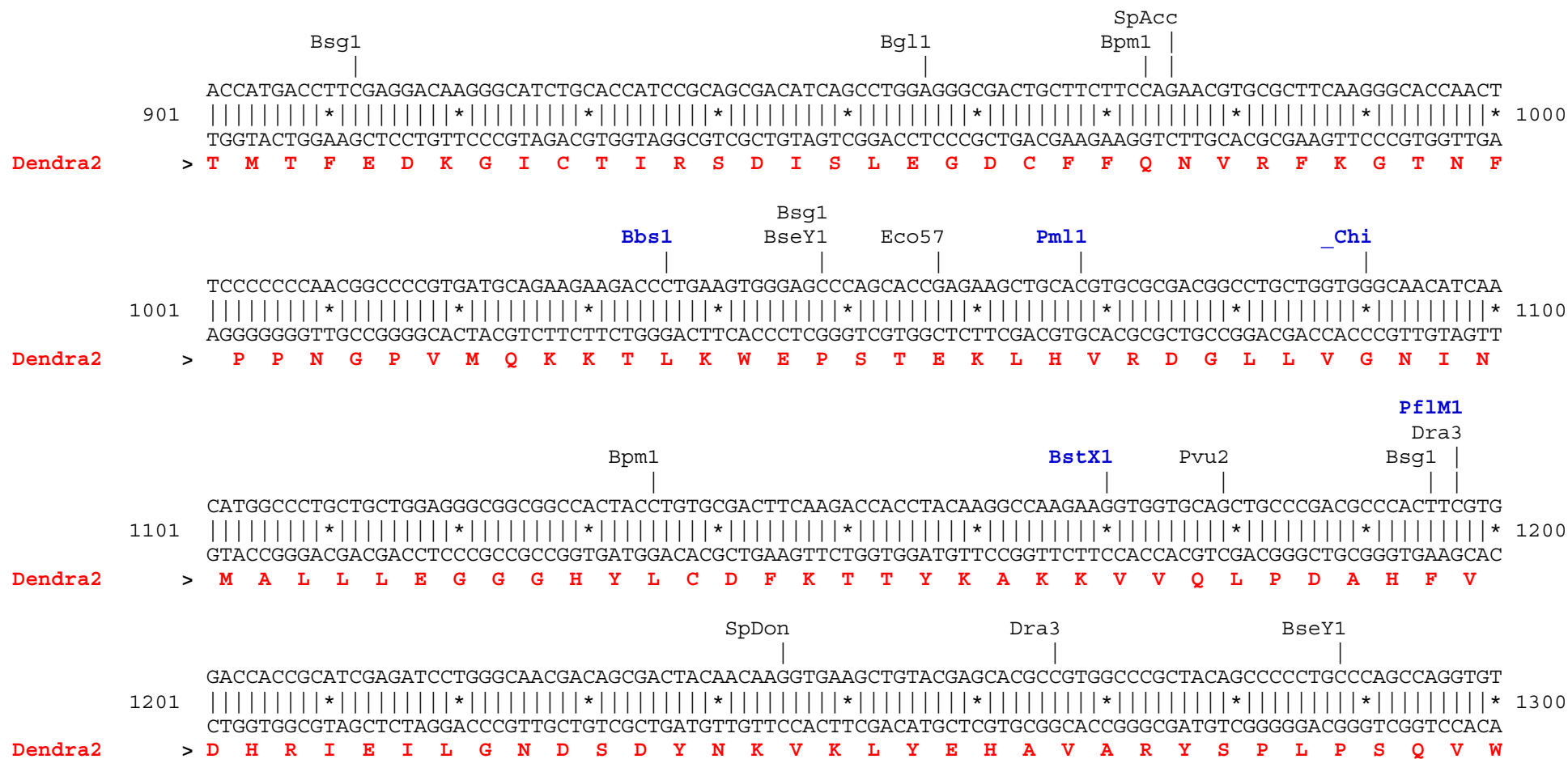
Dendra2 > E G E G K G K P Y E G T Q T A N L T V K E G A P L P F S Y D I L T

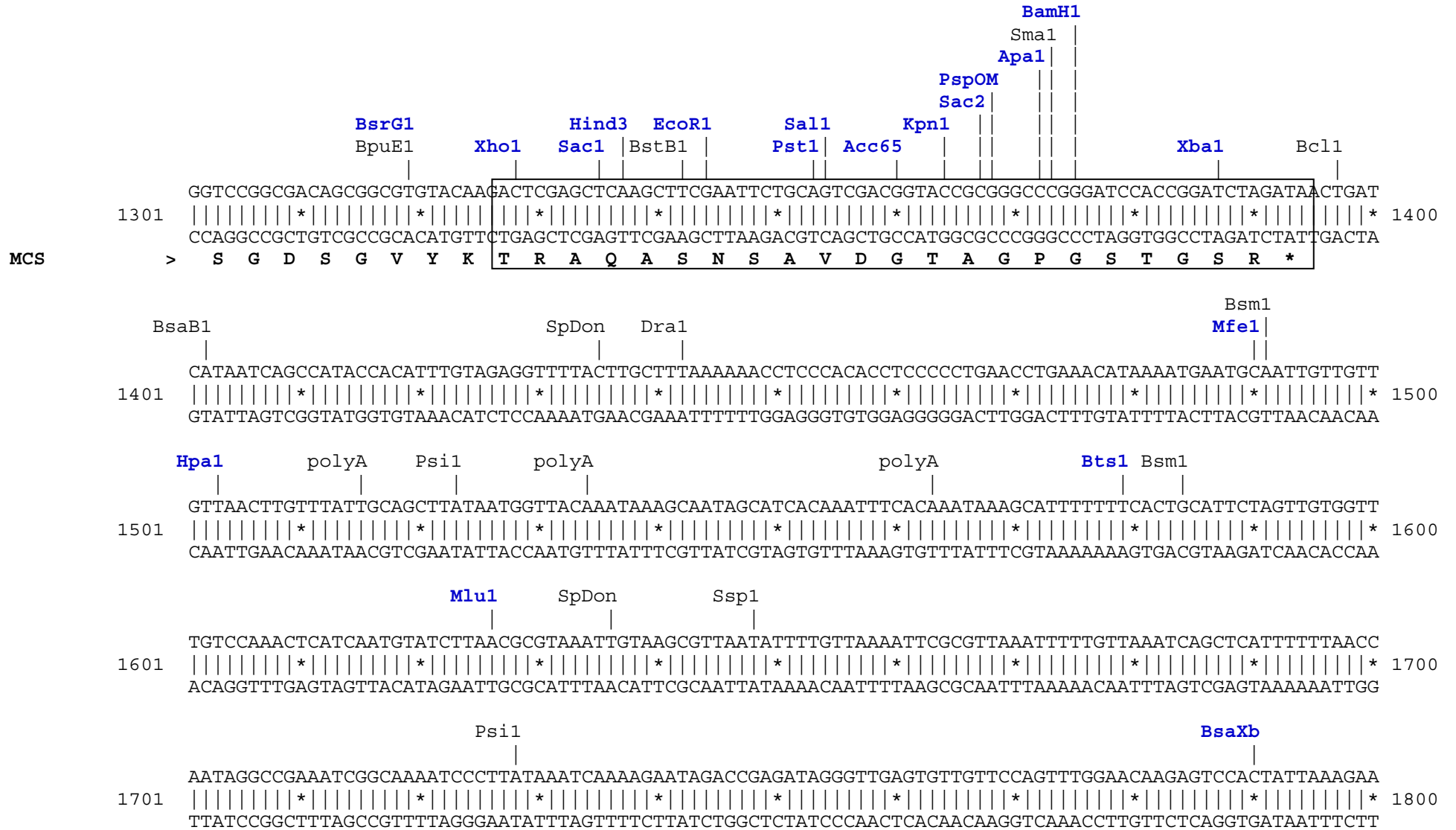
AleI | Pvu2 | BseY1 |

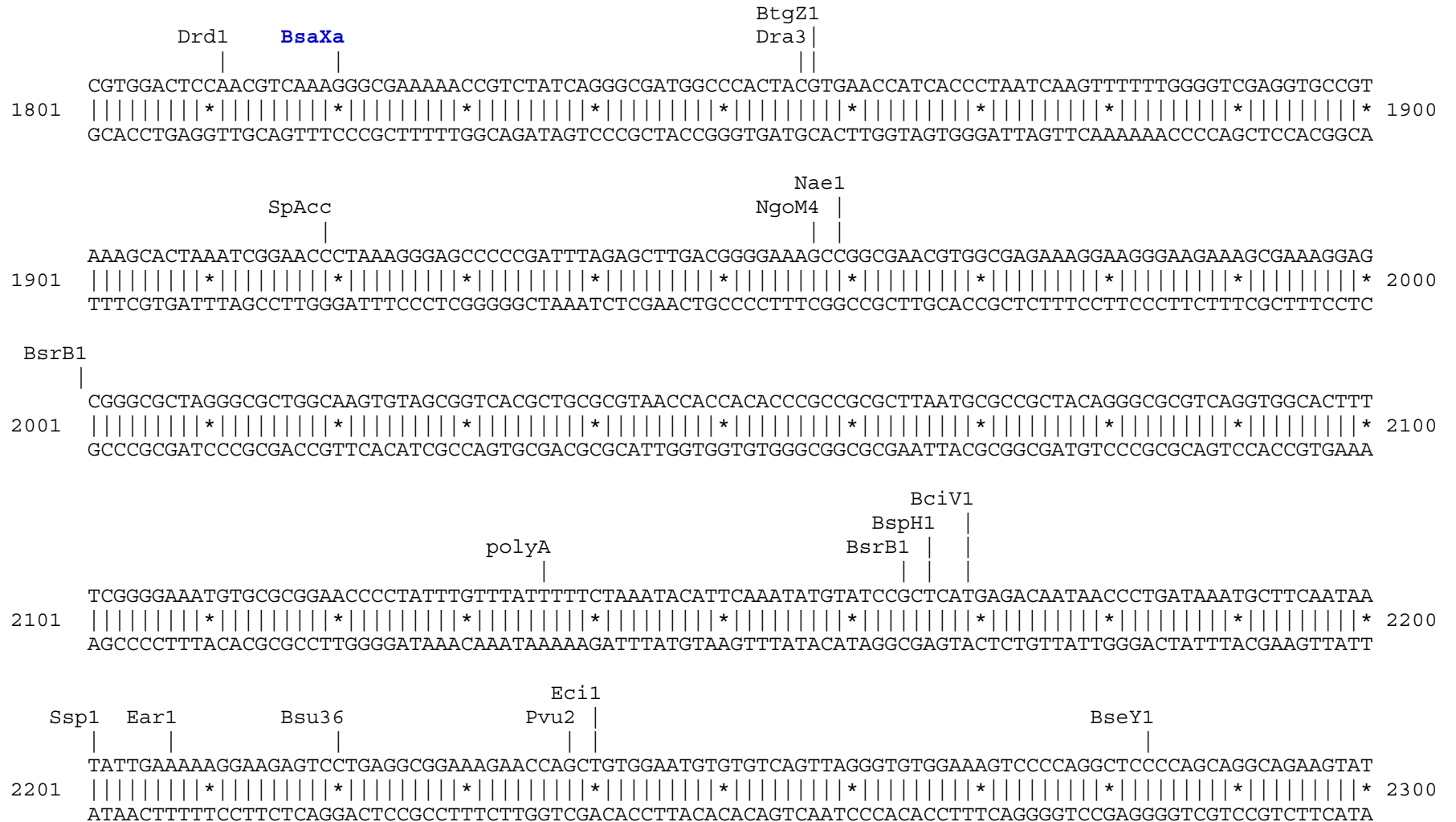
ApaL1 |

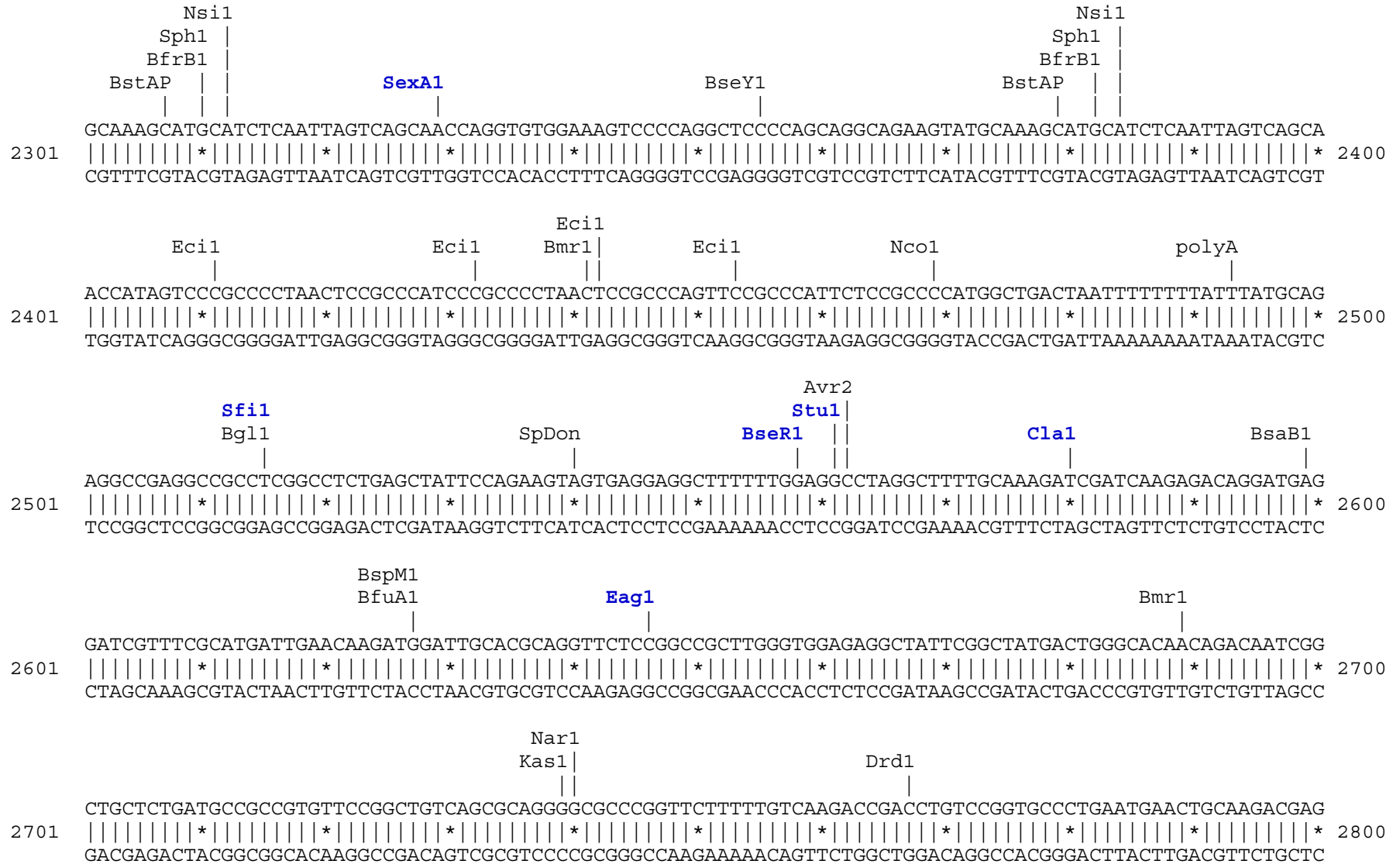
801 CACCGCCGTGCACTACGGCAACCGGGTGTTCACCAAGTACCCGAGGACATCCCCGACTACTTCAAGCAGAGCTTCCCCGAGGGCTACAGCTGGGAGCGC
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*||| 900
 GTGGCGGCACGTGATGCCGTTGGCCACAAGTGGTTTCATGGGGCTCCTGTAGGGGCTGATGAAGTTTCGTCTCGAAGGGCTCCCCTGTCGACCCCTCGCG

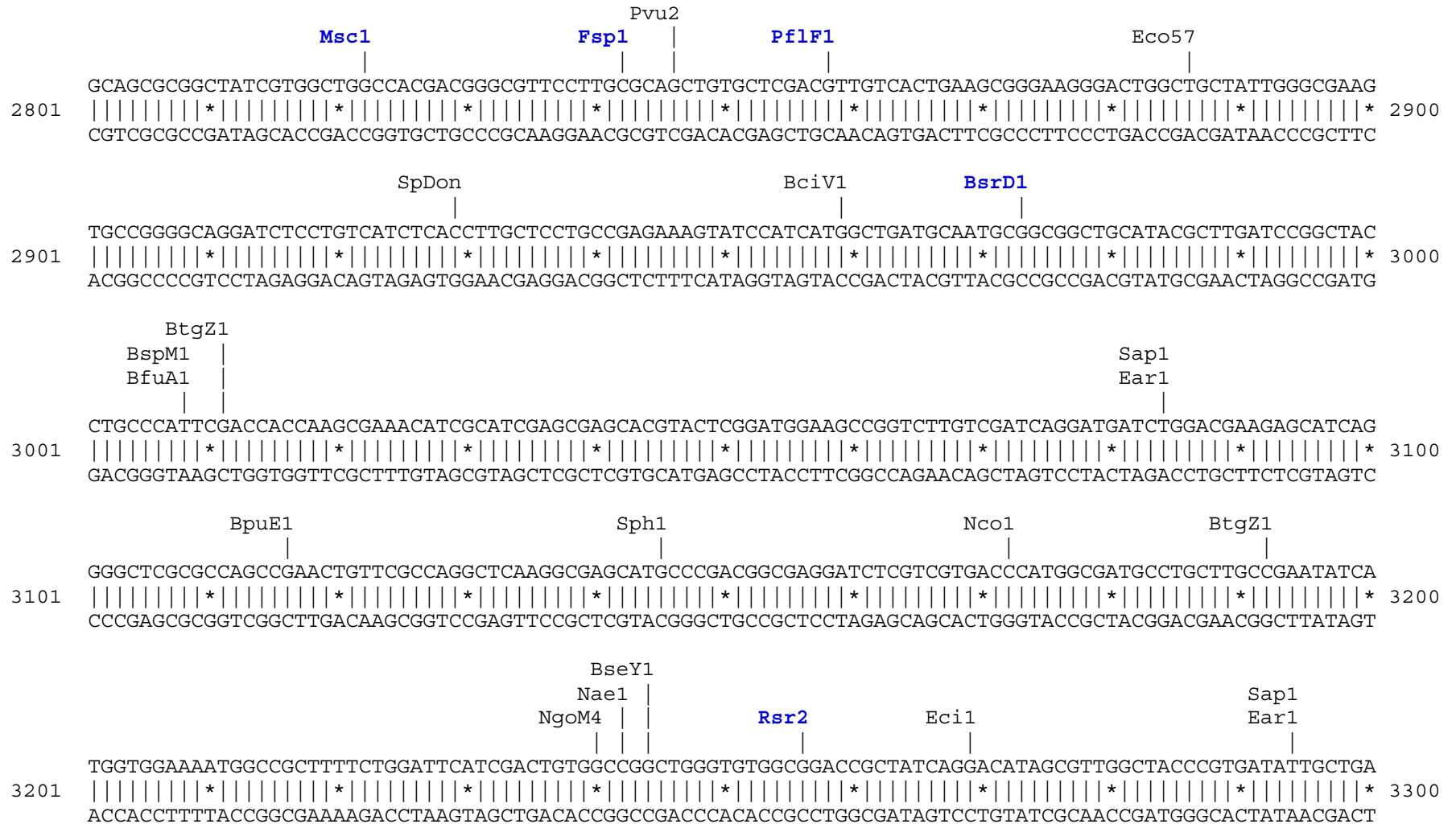
Dendra2 > T A V H Y G N R V F T K Y P E D I P D Y F K Q S F P E G Y S W E R












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                                     BstAP
                                     AlwN1      Bsu36
                                     |           |
TGAAGGCCAGGGCTCGCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCTCAGGTTACTCATATATACTTTAGATTGATTTAAAACTTCATTTTTTAA
3801 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 3900
ACTTCCGGGTCCCGAGCGTCGGTTGCAGCCCCGCCGTCCGGGACGGTATCGGAGTCCAATGAGTATATATGAAATCTAACTAAATTTTGAAGTAAAAATT

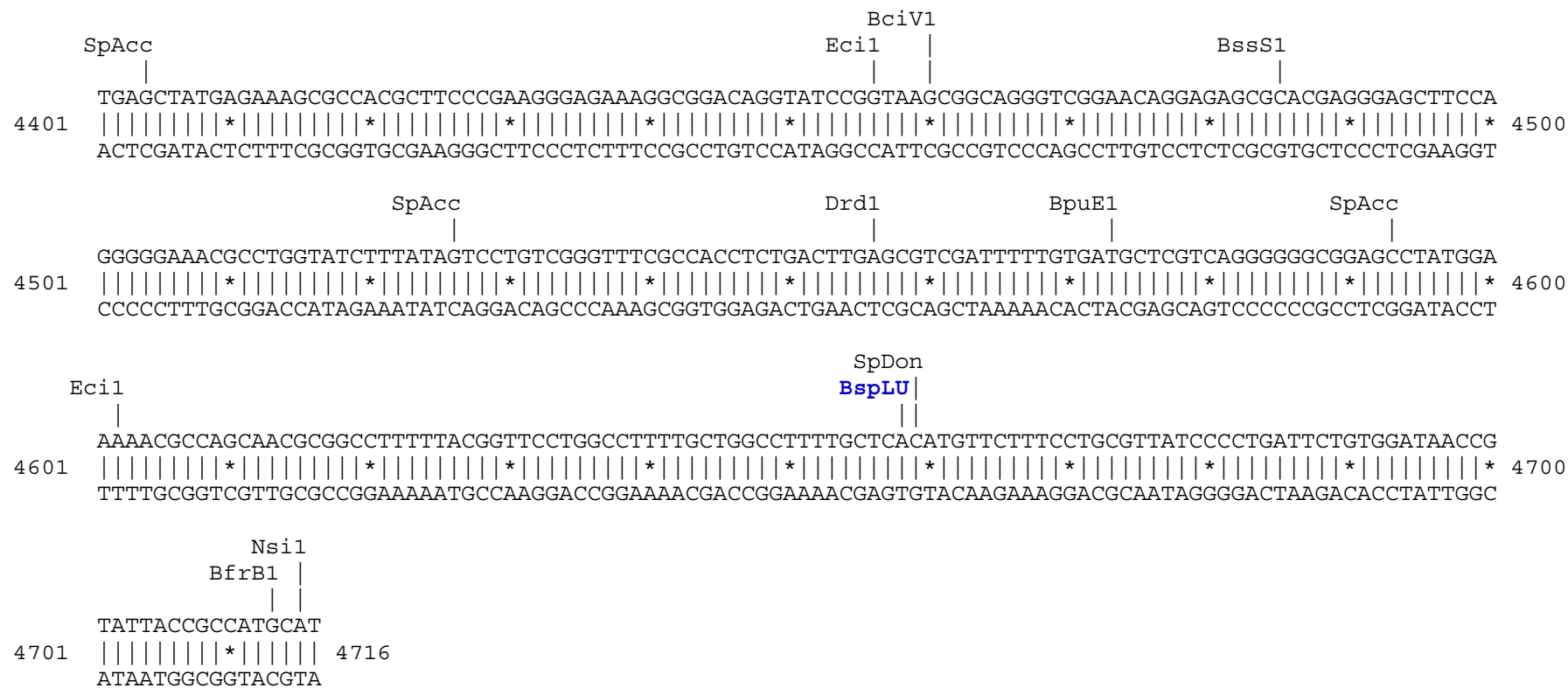
Dra1                                     BspH1
|                                       |
TTTAAAAGGATCTAGGTGAAGATCCTTTTTTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGA
3901 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 4000
AAATTTTCTAGATCCACTTCTAGGAAAAACTATTAGAGTACTGGTTTTAGGGAATTGCACTCAAAGCAAGGTGACTCGCAGTCTGGGGCATCTTTTCT

                                     BpuE1
                                     |
TCAAAGGATCTTCTTGAGATCCTTTTTTCTGCGGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTGGTTTTGTTTGCCGGATCAAGA
4001 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 4100
AGTTTCTTAGAAGAACTCTAGGAAAAAAGACGCGCATTAGACGACGAACGTTTGTTTTTTTGGTGGCGATGGTCGCCACCAAACAAACGGCCTAGTTCT

Eco57                                     SpAcc
|                                       |
GCTACCAACTCTTTTTCCGAAGGTAAGTGGCTTCAGCAGAGCGCAGATACCAAATACTGTCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAAC
4101 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 4200
CGATGGTTGAGAAAAAGGCTTCCATTGACCGAAGTCGTCTCGCGTCTATGGTTTTATGACAGGAAGATCACATCGGCATCAATCCGGTGGTGAAGTTCTTG

                                     AlwN1      BpuE1
                                     |           |
TCTGTAGCACCGCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGAT
4201 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 4300
AGACATCGTGGCGGATGTATGGAGCGAGACGATTAGGACAATGGTCACCGACGACGGTCACCGCTATTTCAGCACAGAATGGCCCAACCTGAGTTCTGCTA

                                     ApaL1      BseY1
                                     |           |
AGTTACCGGATAAGGCGCAGCGGTCCGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCG
4301 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 4400
TCAATGGCCTATTCCGCGTCGCCAGCCGACTTGCCCCCAAGCACGTGTGTCCGGTTCGAACCTCGCTTGCTGGATGTGGCTTGACTCTATGGATGTCCG
```



Found:

Aat2	Acc65	Afe1	Age1	Ale1	AlwN1	Apa1	ApaL1	Ase1	Avr2	BamH1	Bbs1	BciV1	Bcl1
BfrB1	BfuA1	Bgl1	Bmr1	Bpm1	BpuE1	Bsa1	BsaB1	BsaXa	BsaXb	BseR1	BseY1	Bsg1	Bsm1
BspH1	BspLU	BspM1	BsrB1	BsrD1	BsrG1	BssS1	BstAP	BstB1	BstX1	Bsu36	BtgZ1	Bts1	_Chi
Clal	Dra1	Dra3	Drd1	Eag1	Ear1	Eci1	Eco57	EcoN1	EcoR1	Fsp1	Hind3	Hpa1	Kas1
Kpn1	Mfe1	Mlu1	Msc1	Nae1	Nar1	Nco1	Nde1	Ngom4	Nhe1	Nsi1	PflF1	PflM1	Pml1
polyA	Psi1	PspOM	Pst1	Pvu2	Rsr2	Sac1	Sac2	Sal1	Sap1	SexA1	Sfi1	Sma1	SnaB1
SpAcc	SpDon	Sph1	Ssp1	Stu1	Xba1	Xho1							

Unique:

Acc65	Afe1	Age1	Ale1	Apa1	Ase1	BamH1	Bbs1	Bsa1	BsaXa	BsaXb	BseR1	BspLU	BsrD1
BsrG1	BstX1	Bts1	_Chi	Clal	Eag1	EcoN1	EcoR1	Fsp1	Hind3	Hpa1	Kpn1	Mfe1	Mlu1
Msc1	Nde1	Nhe1	PflF1	PflM1	Pml1	PspOM	Pst1	Rsr2	Sac1	Sac2	Sal1	SexA1	Sfi1
SnaB1	Stu1	Xba1	Xho1										

Not found:

Aar1	Acl1	Afl2	Ahd1	Asc1	AsiS1	Baela	Baelb	BbvC1	Bcg1a	Bcg1b	Bgl2	Blp1	BmgB1
Bpu10	BsiW1	BsmB1	BspE1	BssH2	BstE2	BstZ1	EcoK	EcoRV	ScFRT	Fse1	FspA1	I_Ceu	loxP
Not1	Nru1	Pac1	Pme1	PshA1	Pvu1	SanD1	Sbf1	Sca1	Sgf1	SgrA1	Spe1	Srf1	Swal
T3RNA	T7RNA	T7Ter	PISce	Xcm1	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	Tfi1	Tse1	Tsp45	Tsp50
TspR1													