

pTagBFP-H2B 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 red. The location given specifies the 3' end of the cut DNA (the base to the left of the cut site). TagBFP amino acids are shown in bold blue, H2B amino acids are shown in green, linker amino acids are shown in black.



```
                Aat2                                Eci1
                |                                  |
TAGCGGTTTGACTCACGGGGATTTC CAAGTCTCCACCCCAT TGACGTCAATGGGAGTTTGT TTTGGCACCAA AATCAACGGGACTTTCCAAAATGTCGTA
401 | | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * 500
ATCGCCAAACTGAGTGCCCTAAAGGTT CAGAGGTGGGGTA AACTGCAGTTACCCTCAAACAA AACCGTGGT TTTTAGTTGCCCTGAAAGGTTTTACAGCAT
```

```
                                Nhe1 Afe1
                                |   |
ACAACTCCGCCCCATTGACGCAAATGGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTGGT TTTAGTGAACCGTCAGATCCGCTAGCGCTA
501 | | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * 600
TGTTGAGGCGGGTA AACTGCGTTTACCCGCCATCCGCACATGCCACCCTCCAGATATATTCGTCTCGACCAAATCACTTGGCAGTCTAGGCGATCGCGAT
```

```
                    Hind3
          Xho1  Sac1 | EcoR1      Sall   Kpn1
    BpuE1 Bgl2 | Ecl2 | | BstB1 | Pst1 | Acc65 |
          |   |   | |   |   |   | |   |   |
CCGACTCAGATCTCGAGCTCAAGCTTCGAAT TCTGCAGTCGACGGTACCGCCACCATGCCAGAGCCAGCGAAGTCTGCTCCCGCCCCGAAAAGGGCTC
601 | | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * 700
GGCTGAGTCTAGAGCTCGAGTTTGAAGCTTAAGACGTCAGCTGCCATGGCGGTGGTACGGTCTCGGTTCGCTTCAGACGAGGGCGGGGCTTTTTCCCGAG
```

H2B > M P E P A K S A P A P K K G S

```
                                BspM1
                          BsrG1 BfuA1
                                |   |
CAAGAAGGCGGTGACTAAGGCGCAGAAGAAAGGCGGCAAGAAGCGCAAGCGCAGCCGCAAGGAGAGCTATTCCATCTATGTGTACAAGTTTCTGAAGCAG
701 | | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * 800
GTTCTTCCGCCACTGATTCCGCGTCTTCTTTCCGCGTTCCTTCGCGTTCGCGTCCGGCGTTCCTCTCGATAAGGTAGATACACATGTTCCAAGACTTTCGTC
```

H2B > K K A V T K A Q K K G G K K R K R S R K E S Y S I Y V Y K V L K Q

```
                                BspM1
                          BfuA1
                                |   |
                Eco57      BstX1      EcoR1          BtgZ1      Aar1      SpDon
                |          |   |   |   |   |   |   |
GTCCACCCCTGACACCGCATTTTCGTCCAAGGCCATGGGCATCATGAATTCGTTTGTGAACGACATTTTCGAGCGCATCGCAGGTGAGGCTTCCCGCCTGG
801 | | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * 900
CAGGTGGGACTGTGCCGTAAAGCAGGTTCCGGTACCCGTAGTACTTAAGCAAACACTTGCTGTAAAAGCTCGCGTAGCGTCCACTCCGAAGGGCGGACC
```

H2B > V H P D T G I S S K A M G I M N S F V N D I F E R I A G E A S R L A

		SpDon		BsmB1																															
			BseY1		Stu1																														
1401		TACAACGTC	AAGATCAGAG	GGGTGAACTTCACATCC	AACGGCCCTGTGATGCAG	AAGAAAAACTCGGCTGG	GAGGCCTTCACCCGAG	ACGCTGTACCCCG		1500																									
		*	*	*	*	*	*	*	*																										
		ATGTTGCAGTTCT	AGTCTCCCCACTTGA	AGTGTAGGTTGCCGGG	ACTACTACGTTCTTTT	GTGAGCCGACCCTCCG	GAAAGTGGCTCTGCG	ACATGGG																											
TagBFP	>	Y	N	V	K	I	R	G	V	N	F	T	S	N	G	P	V	M	Q	K	K	T	L	G	W	E	A	F	T	E	T	L	Y	P	A
			Bgl1		BssS1		Eco57		BpuE1																										
1501		CTGACGGCGGCCT	TGAAGGCAGAAACG	ACATGGCCCTGAAGCT	CGTGGGCGGGAGCCAT	CTGATCGCAAACATCA	AAGACCACATATAGAT	CCAAGAAAC																											
		*	*	*	*	*	*	*	*																										
		GACTGCCGCCGACCT	TCCGTCCTTGCTGT	ACCGGACTTCGAGCAC	CCCGCCCTCGGTAGAC	TAGCCTTTGTAGTTCT	GGTGTATATCTAGGTT	CCTTTGG																											
TagBFP	>	D	G	G	L	E	G	R	N	D	M	A	L	K	L	V	G	G	S	H	L	I	A	N	I	K	T	T	Y	R	S	K	K	P	
				SpAcc		Bsa1		PshA1		BssS1		Dra3																							
1601		CGCTAAGAACCTCA	AAGATGCCTGGCGT	CTACTATGTGGACTAC	AGACTGGAAAGAATCA	AGGAGGCCAACACGAG	ACCTACGTCGAGCAG	CACGAGGTG																											
		*	*	*	*	*	*	*	*	*																									
		GCGATCTTTGGAGT	TTCTACGACCGCAG	ATGATACACCTGATG	TCTGACCTTTCTTAGT	TCTCCTCCGTTGTTG	CTCTGGATGCAGCTC	CGTCGTGCTCCAC																											
TagBFP	>	A	K	N	L	K	M	P	G	V	Y	Y	V	D	Y	R	L	E	R	I	K	E	A	N	N	E	T	Y	V	E	Q	H	E	V	
			Bts1		Hind3		Not1		Eag1		Xba1		BsaB1																						
		Msc1	AlwN1		SpAcc		Bmr1		Pac1		Eag1		Xba1																						
1701		GCAGTGGCCAGATA	CTGCGACCTCCCTAG	CAAACCTGGGGCACAA	GCTTAATTAAGCGGCCG	GACTCTAGATCATAAT	CAGCCATACCACATTT	GTAGA																											
		*	*	*	*	*	*	*	*	*																									
		CGTCACCGGTCTAT	GACGCTGGAGGGAT	CGTTTACCCTGTTT	CGAATTAATTTCCGCGG	CGCTGAGATCTAGTAT	TAGTTCGGTATGGTGT	AAACATCT																											
TagBFP	>	A	V	A	R	Y	C	D	L	P	S	K	L	G	H	K	L	N	*																
			SpDon		Dra1		Bsm1		MfeI		Hpa1		polyA																						
				Pac1		Eag1		Xba1		BsaB1																									
1801		GGTTTTACTTTGCT	TTAAAAAACCTCCCA	CACCTCCCCCTGAAC	CTGAAACATAAAATGA	ATGCAATTGTTGTTG	TAACTTGTTTATTG	CAGCTTATAAT																											
		*	*	*	*	*	*	*	*	*																									
		CCAAAATGAACGAA	ATTTTTTGGAGGGT	GTTGGAGGGGACTTTG	GACTTTTGTATTTTTAC	TTACGTTAAACAACA	CAATTGAACAAATAAC	GCATATTA																											

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polyA              polyA              Bts1 Bsm1              Af12
|                  |                  |   |                   |
GGTTACAAATAAAGCAATAGCATCACAAATTTACAAATAAAGCATTTTTTTTCACTGCATTCTAGTTGTGGTTTTGTCCAAACTCATCAATGTATCTTAAG
1901 ||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||* 2000
CCAATGTTTATTTTCGTTATCGTAGTGTTTAAAGTGTATTTTCGTAAAAAAAGTGACGTAAGATCAACACCAAACAGGTTTGAGTAGTTACATAGAATTC

SpDon             Ssp1
|                 |
GCGTAAATTGTAAGCGTTAATATTTTGTAAAAATTCGCGTTAAATTTTTGTAAATCAGCTCATTTTTTAAACCAATAGGCCGAAATCGGCAAAATCCCTT
2001 ||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||* 2100
CGCATTTAACATTCGCAATTATAAAACAATTTAAAGCGCAATTTAAAAACAATTTAGTCGAGTAAAAAATTGGTTATCCGGCTTTAGCCGTTTLAGGGAA

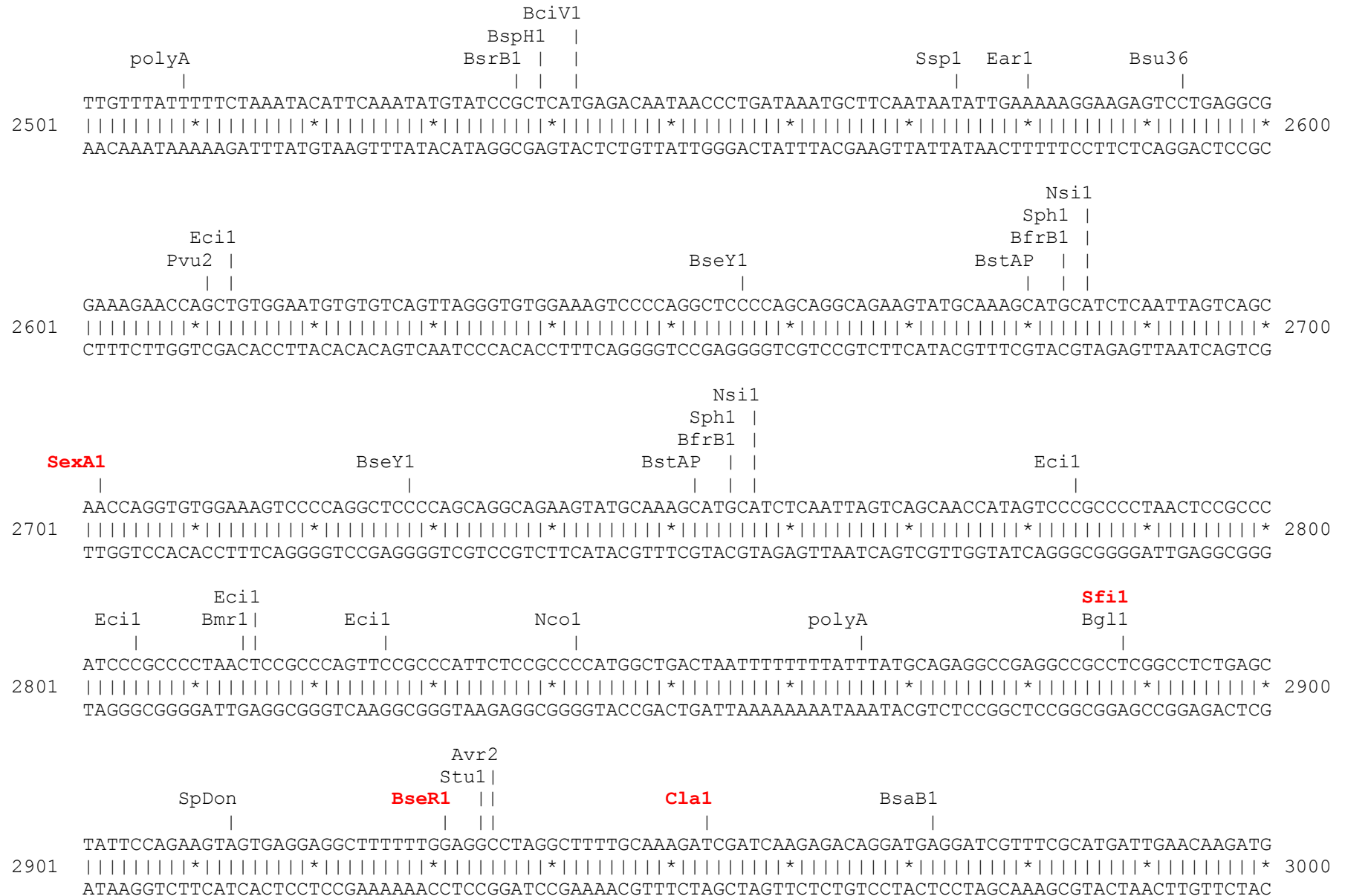
Psil              BsaXb              Drd1             BsaXa
|                  |                   |                 |
ATAAATCAAAAAGAAATAGACCGAGATAGGGTTGAGTGTGTTCAGTTTGGAAACAAGAGTCCACTATTAAAGAACGTGGACTCCAACGTCAAAGGGCGAAA
2101 ||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||* 2200
TATTTAGTTTTTCTTATCTGGCTCTATCCCAACTACAACAAGGTCAAACCTTGTTCTCAGGTGATAATTTCTTGACCTGAGGTTGCAGTTTCCCGCTTT

BtgZ1
Dra3 |
||
AACCGTCTATCAGGGCGATGGCCCACTACGTGAACCATCACCCATAATCAAGTTTTTTGGGGTTCGAGGTGCCGTAAAGCACTAAATCGGAACCCTAAAGGG
2201 ||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||* 2300
TTGGCAGATAGTCCCGCTACCGGGTGATGCACTTGGTAGTGGGATTAGTTCAAAAAACCCAGCTCCACGGCATTTCGTGATTTAGCCTTGGGATTTCCC

NaeI              NgoM4 |              BsrB1
|                 |   |                   |
AGCCCCGATTTAGAGCTTGACGGGGAAAGCCGGCGAACGTGGCGAGAAAGGAAGGGAAGAAAGCGAAAGGAGCGGGGCGCTAGGGGCGCTGGCAAGTGTAG
2301 ||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||* 2400
TCGGGGGCTAAATCTCGAACTGCCCTTTTCGGCCGCTTGCACCGCTCTTTCCTTCCCTTCTTTCGCTTTCTTTCGCCCCGCGATCCCGCGACCGTTCACATC

CGGTCACGCTGCGCGTAACCACCACACCCGCCGCGCTTAATGCGCCGCTACAGGGCGCGTCAGGTGGCACTTTTTCGGGGAAATGTGCGCGGAACCCCTAT
2401 ||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||* 2500
GCCAGTGCGACGCGCATTGGTGGTGTGGGCGGCGGAATTACGGGCGGATGTCCC GCGCAGTCCACCGTGAAAAGCCCCTTTACACGCGCCTTGGGGATA

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polyA polyA
| |
CGCGCTATGACGGCAATAAAAAAGACAGAATAAAAACGCACGGTGTGGGTCGTTTGTTCATAAACCGGGGTTCCGGTCCCAGGGCTGGCACTCTGTTCGATA
4001 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4100
GCGGATACTGCCGTTATTTTCTGTCTTATTTTTCGCGTCCACAACCCAGCAAACAAGTATTTGCGCCCCAAGCCAGGGTCCCAGCCGTGAGACAGCTAT

Bsa1
|
CCCCACCGAGACCCCATTTGGGGCCAATACGCCCAGTTTCTTCCTTTTCCCCACCCCAAGTTCCGGGTGAAGGCCAGGGCTCGCAGCCAACGT
4101 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4200
GGGGTGGCTCTGGGGTAACCCCGGTTATGCGGGCGCAAAGAAGGAAAAGGGGTGGGGTGGGGGTTCAAGCCCACTTCCGGGTCCCAGCGTTCGGTTGCA

BstAP AlwN1 Bsu36 Dra1 Dra1
| | | | |
CGGGGCGGCAGGCCCTGCCATAGCCCTCAGGTTACTCATATATACTTTAGATTGATTTAAACTTTCATTTTTAATTTAAAAGGATCTAGGTGAAGATCCTT
4201 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4300
GCCCCGCGTCCGGGACGGTATCGGAGTCCAATGAGTATATATGAAATCTAACTAAATTTTGAAGTAAAAATTAATTTTCTTAGATCCACTTCTAGGAA

BspH1
|
TTTGATAATCTCATGACCAAAAATCCCTTAACGTGAGTTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTT
4301 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4400
AAACTATTAGAGTACTGGTTTTAGGGAATTGCACTCAAAGCAAGGTGACTCGCAGTCTGGGGCATCTTTTCTAGTTTCTTAGAAGAACTCTAGGAAAAA

BpuE1 Eco57
| |
TTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTGGTTTGTGTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAAC
4401 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4500
AAGACGCGCATTAGACGACGAACGTTTGTTTTTTGGTGGCGATGGTTCGCCACCAAAACAAACGGCCTAGTTCTCGATGGTTGAGAAAAGGCTTCCATTG

SpAcc
|
TGGCTTCAGCAGAGCGCAGATAACAAATACTGTCTTCTAGTGTAGCCGTAGTTAGGCCACCCTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCT
4501 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4600
ACCGAAGTCGTCTCGCGTCTATGGTTTTATGACAGGAAGATCACATCGGCATCAATCCGGTGGTGAAGTTCTTGAGACATCGTGGCGGATGTATGGAGCGA

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                AlwN1                BpuE1
                |                      |
4601 CTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGG
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4700
   GACGATTAGACAATGGTCACCGACGACGGTCACCGCTATTCAGCACAGAATGGCCCAACCTGAGTTCTGCTATCAATGGCCTATTCGCGCTGCCAGCC

                ApaL1      BseY1                SpAcc
                |          |                      |
4701 GCTGAACGGGGGGTTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCC
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4800
   CGACTTGCCCCCAAGCACGTGTGTCGGGTCGAACCTCGCTTGCTGGATGTGGCTTGACTCTATGGATGTCGCACTCGATACTCTTTCGCGGTGCGAAGG

                BciV1
                Ecil  |          BssS1                SpAcc
                |    |          |                      |
4801 CGAAGGGAGAAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGAAACGCCTGGTATCTTTATAGT
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4900
   GCTTCCCTCTTTCCGCCTGTCCATAGGCCATTCGCCGTCCCAGCCTTGTCCTCTCGCGTGCTCCCTCGAAGGTCCCCCTTTGCGGACCATAGAAATATCA

                Drd1                BpuE1                SpAcc      Ecil
                |                      |          |          |
4901 CCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTTAC
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5000
   GGACAGCCCAAAGCGGTGGAGACTGAACTCGCAGCTAAAAAACTACGAGCAGTCCCCCGCCTCGGATACCTTTTTTTCGGTTCGTTGCGCCGAAAAATG

                SpDon
                BspLU|
                ||
5001 GGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCATGCAT
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5089
   CCAAGGACCGGAAAACGACCGGAAAACGAGTGTACAAGAAAGGACGCAATAGGGGACTAAGACACCTATTGGCATAATGGCGGTACGTA
```

Found:

Aar1	Aat2	Acc65	Afe1	Afl2	Age1	AlwN1	ApaL1	Ase1	Avr2	BamH1	Bbs1	BciV1	BfrB1
BfuA1	Bgl1	Bgl2	Bmr1	Bpm1	Bpu10	BpuE1	Bsa1	BsaB1	BsaXa	BsaXb	BseR1	BseY1	Bsm1
BsmB1	BspH1	BspLU	BspM1	BsrB1	BsrD1	BsrG1	BssS1	BstAP	BstB1	BstX1	Bsu36	BtgZ1	Bts1
Clal	Dra1	Dra3	Drd1	Eag1	Ear1	Eci1	Ecl2	Eco57	EcoR1	Fsp1	Hind3	Hpa1	Kas1
Kpn1	Mfe1	Msc1	Nae1	Nar1	Nco1	Nde1	NgoM4	Nhe1	Not1	Nsi1	Pac1	PflF1	polyA
PshA1	Psi1	Pst1	Pvu2	Rsr2	Sac1	Sall	Sap1	SexA1	Sfi1	SnaB1	SpAcc	SpDon	Sph1
Ssp1	Stu1	Xba1	Xho1										

Unique:

Aar1	Acc65	Afl2	Age1	Ase1	BamH1	Bbs1	Bgl2	Bpu10	BsaXa	BsaXb	BseR1	BsmB1	BspLU
BsrD1	BstX1	Clal	Ecl2	Fsp1	Hpa1	Kas1	Kpn1	Mfe1	Nar1	Nde1	Nhe1	Not1	Pac1
PflF1	PshA1	Pst1	Rsr2	Sac1	Sall	SexA1	Sfi1	SnaB1	Xba1	Xho1			

Not found:

Acc1	Ahd1	Ale1	Apa1	Asc1	AsiS1	Baela	Baelb	BbvC1	Bcg1a	Bcg1b	Bcl1	Blp1	BmgB1
Bsg1	BsiW1	BspE1	BssH2	BstE2	BstZ1	BxatB	BxatL	BxatR	BxatP	_Chi	EcoK	EcoN1	EcoRV
FCatB	FCatL	FCatR	FCatP	ScFRT	Fse1	FspA1	I_Ceu	loxP	Mlu1	Nru1	PflM1	Pme1	Pml1
PspOM	Pvu1	R4atB	R4atL	R4atP	R4atR	Sac2	SanD1	Sbf1	Sca1	Sgf1	SgrA1	Sma1	Spe1
Srf1	Swa1	T3RNA	T7RNA	T7Ter	PISce	Xcm1	Xmn1						

Excluded by site complexity:

Acc1	Acil	Afl3	Alu1	Alw1	Apo1	Ava1	Ava2	Ban1	Ban2	Bbv1	BceA1	Bfa1	Bme15
BsaA1	BsaH1	BsaJ1	BsaW1	BseM2	BsiE1	BsiH1	Bs11	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													