

**pArrestRed** 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 base pairs 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). ArrestRed amino acids are shown in dark red.



Aat2 | Ecil |  
TAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTTGACGTCAATGGGAGTTTGTGTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTA  
401 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 500  
ATCGCCAAACTGAGTGCCCTAAAGGTTTCAGAGGTGGGGTAACTGCAGTTACCCTCAAACAAAACCGTGGTTTTAGTTGCCCTGAAAGGTTTTACAGCAT

NheI | Acc65 |  
ACAACCTCCGCCCCATTGACGCAAATGGGCGGTAGGCGGTACGGTGGGAGGTCTATATAAGCAGAGCTGGTTTTAGTGAACCGTCAGATCCGCTAGCGGTA  
501 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 600  
TGTTGAGGCGGGTAACTGCGTTTACCCGCCATCCGCACATGCCACCCTCCAGATATATTCGTCTCGACCAAATCACTTGGCAGTCTAGGCGATCGCCAT

KpnI |  
CCGCCACCATGCCAGAGCCAGCGAAGTCTGCTCCCGCCCCGAAAAAGGGCTCCAAGAAGGCGGTGACTAAGGCGCAGAAGAAAGGCGGCAAGAAGCGCAA  
601 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 700  
GGCGGTGGTACGGTCTCGGTTCGCTTCAGACGAGGGCGGGGCTTTTTCCCGAGGTTCTTCCGCCACTGATTCCGCGTCTTCTTTCCGCCGTTCTTCGCGTT  
ArrestRed > M P E P A K S A P A P K K G S K K A V T K A Q K K G G K K R K

BsrGI | BspM1 | Eco57 | BstXI | EcoRI |  
NcoI | BspH1 |  
GCGCAGCCGCAAGGAGAGCTATTCCATCTATGTGTACAAGTTCTGAAGCAGGTCCACCCTGACACCGGCATTTTCGTCCAAGGCCATGGGCATCATGAAT  
701 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 800  
CGCGTCGGCGTTCTCTCGATAAGGTAGATACACATGTTCCAAGACTTTCGTCCAGGTGGGACTGTGGCCGTAAAGCAGGTTCCGGTACCCGTAGTACTTA  
ArrestRed > R S R K E S Y S I Y V Y K V L K Q V H P D T G I S S K A M G I M N

BtgZ1 | BspM1 | Aar1 | SpDon | Afel | Bpm1 | Eag1 |  
TCGTTTGTGAACGACATTTTCGAGCGCATCGCAGGTGAGGCTTCCCCTGGCGCATTACAACAAGCGCTCGACCATCACCTCCAGGGAGATCCAGACGG  
801 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 900  
AGCAAACACTTGCTGTAAAAGCTCGCGTAGCGTCCACTCCGAAGGGCGGACCGCGTAATGTTGTTTCGCGAGCTGGTAGTGGAGGTCCCTCTAGGTCTGCC  
ArrestRed > S F V N D I F E R I A G E A S R L A H Y N K R S T I T S R E I Q T A

BamH1  
Bpu10  
Msc1  
Dra3  
Afe1  
Age1

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901  CCGTGC GCCTGCTGCTGCCTG GGGAGTTGGCCAAGCACC GCCGTGTCCGAGGGTACTAAGGCCATCACCAAGTACACCAGCGCTAAGGATCCACCGGTGCGC
   |||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*
GGCACGCGGACGACGACGGACCCCTCAACCGGTTTCGTGCGGCACAGGCTCCCATGATTCCGGTAGTGGTTCATGTGGTTCGCGATTCTAGGTGGCCAGCG

ArrestRed  >  V R L L L P G E L A K H A V S E G T K A I T K Y T S A K D P P V A

Xho1  

Nco1  

SpDon
1001  CACCCTCGAGGCCACCATGGGTTT CAGAGGGCGGCCCGCCCTGTTCCAGAGCGACATGACCTTCAA AATCTTCATCGACGGCGAGGTGAACGGCCAGAAG
   |||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*
GTGGGAGCTCCGGTGGTACCCAAGTCTCCC GCCGGGCGGGACAAGGTCTCGCTGTACTGGAAGTTTTAGAAAGTAGCTGCCGCTCCACTTGCCGGTCTTTC

ArrestRed  >  T L E A T M G S E G G P A L F Q S D M T F K I F I D G E V N G Q K

Ale1  

SpDon  

ApaL1  

Dra3  

Bsa1  

PflM1
1101  TTCACCATCGTGCCGACGGCAGCAGCAAGTTCCCCCACC GGCGACTTCAACGTGCACGCCGTGTGCGAGACCGGCAAGCTGCCCATGAGCTGGAAGCCCA
   |||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*
AAGTGGTAGCACC GGCTGCCGTCGTCGTTCAAAGGGGGTGCCGCTGAAAGTTGCACGTGCGGCACACGCTCTGGCCGTTTCGACGGGTA CTGACCTTCCGGGT

ArrestRed  >  F T I V A D G S S K F P H G D F N V H A V C E T G K L P M S W K P I

Bpu10
1201  TCTGCCACCTGATCCAGTACGGCGAGCCCTTCTTTCGCCCGCTACCCCGACGGCATCAGCCATTTTCGCC CAGGAGTGCTTCCCCGAGGGCCTGAGCATCGA
   |||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*
AGACGGTGGACTAGGTCATGCCGCTCGGGAAGAAGCGGGCGATGGGGCTGCCGTAGTCGGTAAAGCGGGTCTCACGAAGGGGCTCCCGGACTCGTAGCT

ArrestRed  >  C H L I Q Y G E P F F A R Y P D G I S H F A Q E C F P E G L S I D

BspM1  

Aar1  

Ale1  

SpDon
1301  CCGCACCGTGCGCTTCGAGAACGACGGCACC ATGACCAGCCACCACACCTACGAGCTGGACGACACCTGCGTGGT GAGCCGCATCACCGTGAAC TGCGAC
   |||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*
GGCGTGGCAGCGAAGCTCTT GCTGCCGTGGTACTGGTTCGGTGGTGTGGATGCTCGACCTGCTGTGGACGCACC ACTCGGGCGTAGTGGCACCTTGACGCTG

ArrestRed  >  R T V R F E N D G T M T S H H T Y E L D D T C V V S R I T V N C D

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BsaXb
Drd1
BsaXa
BtgZ1
Dra3

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GTGTTGTTCCAGTTTGGAAACAAGAGTCCACTATTTAAAGAACGTGGACTCCAACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGCCCACTACGTGA
| | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | *
3001 CACAACAAGGTCAAACCTTGTTCTCAGGTGATAATTTCTTGCACCTGAGGTTGCAGTTTCCCGCTTTTTGGCAGATAGTCCCGCTACCGGGTGATGCACT

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SpAcc
NaeI
NgoM4

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ACCATCACCTAATCAAGTTTTTTGGGGTCGAGGTGCCGTAAAGCACTAAATCGGAACCCTAAAGGGAGCCCCGATTTAGAGCTTGACGGGGAAAGCCG
| | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | *
3101 TGGTAGTGGGATTAGTTCAAAAAACCCAGCTCCACGGCATTTTCGTGATTTAGCCTTGGGATTTCCCTCGGGGGCTAAATCTCGAACTGCCCCCTTTCGGC

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BsrB1

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GCGAACGTGGCGAGAAAAGGAAGGAAGAAAGCGAAAAGGAGCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGTACAGCTGCGCGTAACCACCACACCCGCCG
| | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | *
3201 CGCTTGACCCGCTCTTTCCTTCCCTTCTTTCGCTTTCCTCGCCCCGCGATCCC CGCACCGTTACATCGCCAGTGCGACGCGCATTGGTGGTGTGGGCGGC

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polyA

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CGCTTAATGCGCCGCTACAGGGCGCGTCAGGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTA
| | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | *
3301 GCGAATTACGCGGCATGTCCC CGCAGTCCACCGTGAAAAGCCCCTTTACACGCGCCTTGGGGATAAAACAAATAAAAAGATTTATGTAAGTTTATAACAT

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BspH1
BsrB1
BciV1
Ssp1
Ear1
Bsu36
Pvu2
Eci1

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TCCGCTCATGAGACAATAACCCTGATAAATGCTTCAATAATATTGAAAAAGGAAGAGTCCTGAGGCGGAAAGAACCAGCTGTGGAATGTGTGTCAGTTAG
| | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | *
3401 AGGCGAGTACTCTGTTATTGGGACTATTTACGAAGTTATTATAACTTTTTCTTCTCAGGACTCCGCTTTCTTGGTTCGACACCTTACACACAGTCAATC

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                    Nsil
                    Sph1
                    BfrB1
                BseY1      BstAP      SexA1      BseY1
                |         |         |         |
GGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCAGGTGTGGAAAGTCCCCAGGCTCCCCAGC
3401 |||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 3500
CCACACCTTTCAGGGGTCCGAGGGGTCGTCCGTCTTCATACGTTTCGTACGTAGAGTTAATCAGTCGTTGGTCCACACCTTTCAGGGGTCCGAGGGGTCG

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                    Nsil
                    Sph1
                    BfrB1
                BstAP      Ecil      Ecil      Bmr1      Ecil
                |         |         |         |         |
AGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCATAGTCCC GCCCTAACTCCGCCCATCCC GCCCCTAACTCCGCCCAGTTCCGCCCAT
3501 |||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 3600
TCCGTCTTCATACGTTTCGTACGTAGAGTTAATCAGTCGTTGGTATCAGGGCGGGGATTGAGGCGGGTAGGGCGGGGATTGAGGCGGGTCAAGGCGGGTA

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                    sfi1
                Nco1      polyA      Bgl1      SpDon      BseR1
                |         |         |         |         |
TCTCCGCCCATGGCTGACTAATTTTTTTTTATTTATGCAGAGGCCGAGGCCGCTCGGCCTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTTGGAG
3601 |||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 3700
AGAGGCGGGGTACCGACTGATTAATAAATAAATACGTCTCCGGCTCCGGCGGAGCCGGAGACTCGATAAGGTCTTCATCACTCCTCCGAAAAAACCTC

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Avr2
Stu1      Cla1      BsaB1      BspM1      Eag1
||         |         |         |         |
GCCTAGGCTTTTGC AAAAGATCGATCAAGAGACAGGATGAGGATCGTTTTCGCATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGG
3701 |||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 3800
CGGATCCGAAAACGTTTCTAGCTAGTTCTCTGTCTACTCCTAGCAAAGCGTACTAACTTGTTCTACCTAACGTGCGTCCAAGAGGCCGGCGAACCCACC

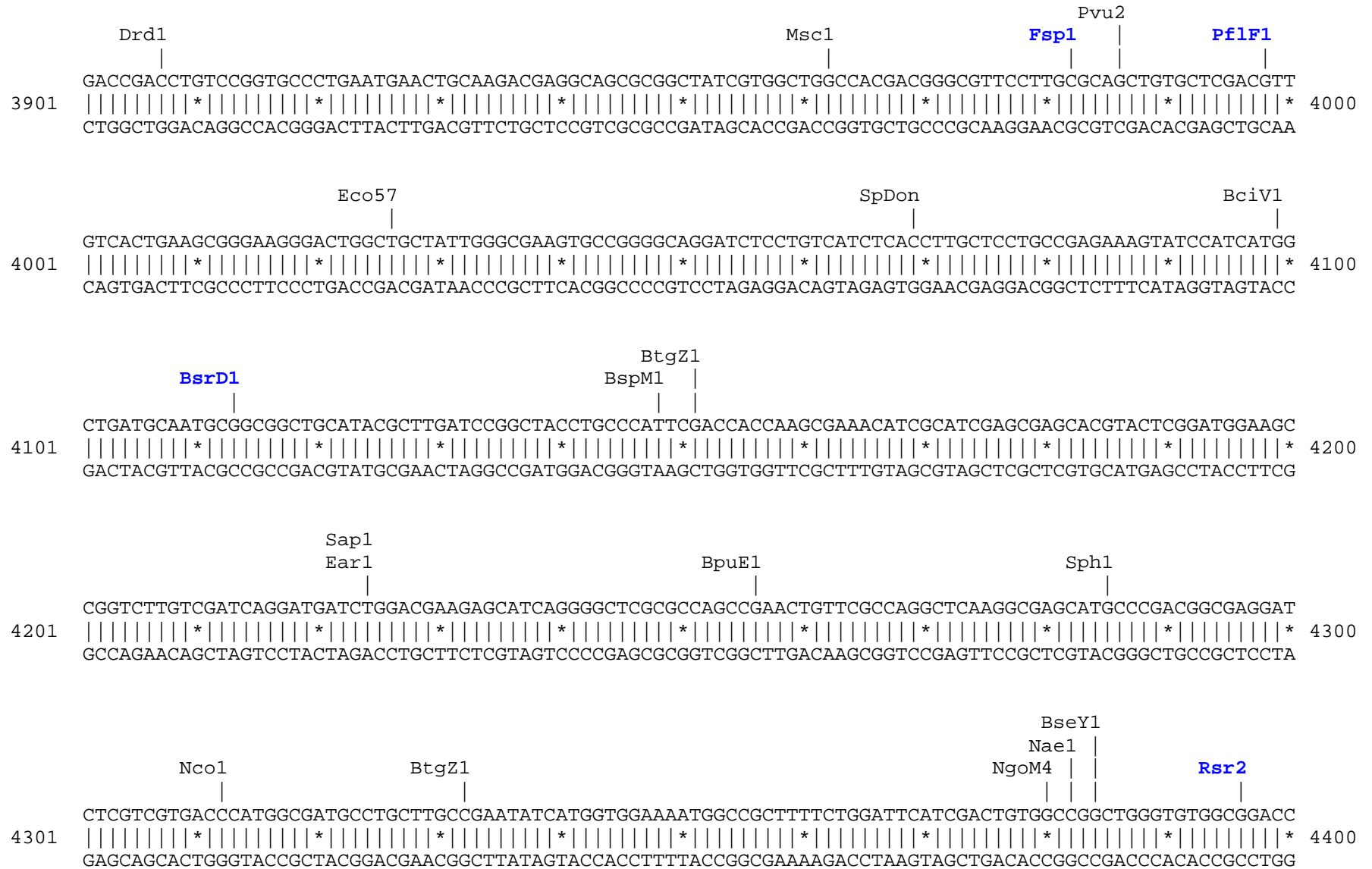
```

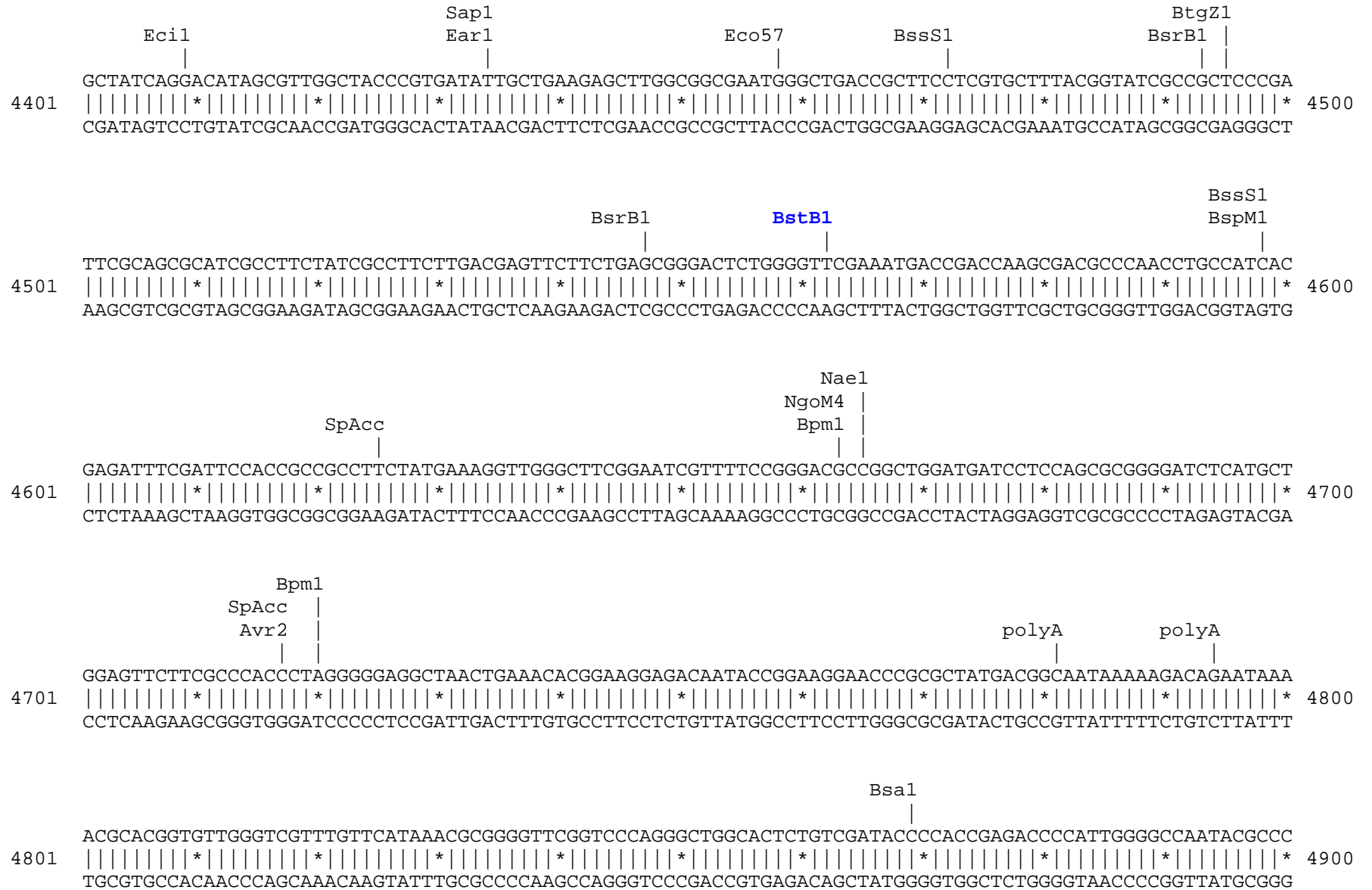
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                    Bmr1      Nar1      Kas1
                    |         |         |
AGAGGCTATTTCGGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCAGCGCAGGGGCGCCCGTTCTTTTTGTCAA
3801 |||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 3900
TCTCCGATAAGCCGATACTGACCCGTGTTGTCTGTTAGCCGACGAGACTACGGCGGCACAAGGCCGACAGTCGCGTCCCCGCGGGCCAAGAAAAACAGTT

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                                                                 BstAP
                                                                 AlwN1       Bsu36
                                                                 |           |
4901 GCGTTTCTTCCTTTTCCCCACCCCAAGTTCGGGTGAAGGCCAGGGCTCGCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCTCAGGTTA
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5000
    CGCAAAGAAGGAAAAGGGGTGGGGTGGGGGTTCAAGCCCACTTCCGGGTCCCGAGCGTCGGTTGCAGCCCCGCCGTCCGGGACGGTATCGGAGTCCAAT

                Dra1           Dra1           BspH1
                |             |             |
5001 CTCATATATACTTTAGATTGATTTAAAACCTTCATTTTAAATTTAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAATCCCTTAACGT
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5100
    GAGTATATATGAAATCTAACTAAATTTTGAAGTAAAAATTAATTTTCTAGATCCACTTCTAGGAAAACTATTAGAGTACTGGTTTTAGGGAATTGCA

                                                                 BpuE1
                                                                 |
5101 GAGTTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAA
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5200
    CTCAAAAGCAAGGTGACTCGCAGTCTGGGGCATCTTTTCTAGTTTCTAGAAAGAACTCTAGGAAAAAAGACGCGCATTAGACGACGAACGTTTGTTTTTT

                                                                 Eco57
                                                                 |
5201 AACCACCGCTACCAGCGGTGGTTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAAGTGGCTTCAGCAGAGCGCAGATACCAAATACTGT
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5300
    TTGGTGGCGATGGTCGCCACCAAACAAACGGCCTAGTTCTCGATGGTTGAGAAAAAGGCTTCCATTGACCGAAGTCGTCTCGCTCTATGGTTTTATGACA

                SpAcc           AlwN1
                |             |
5301 CCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAAGTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGT
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5400
    GGAAGATCACATCGGCATCAATCCGGTGGTGAAGTTCTTGAGACATCGTGGCGGATGTATGGAGCGAGACGATTAGGACAATGGTCACCGACGACGGTCA

                BpuE1           ApaL1       BseY1
                |             |           |
5401 GGCGATAAGTCGTGCTTACCAGGGTTGGACTCAAGACGATAGTTACCAGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCT
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5500
    CCGCTATTCAGCACAGAATGGCCCAACCTGAGTTCTGCTATCAATGGCCTATTCCGCGTCGCCAGCCCAGCTTGCCCCCAAGCACGTGTGTGCGGGTCA
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SpAcc | Ecil |  
TGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAG  
5501 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 5600  
ACCTCGCTTGCTGGATGTGGCTTGACTCTATGGATGTCGCACTCGATACTCTTTCGCGGTGCGAAGGGCTTCCCTCTTTCGCGCTGTCCATAGGCCATTC

BciV1 | BssS1 | SpAcc | Drd1 |  
CGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTGCGGGTTTCGCCACCTCTGACTTGAGCGT  
5601 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 5700  
GCCGTCCCAGCCTTGTCCTCTCGCGTGCTCCCTCGAAGGTCCCCCTTTCGCGGACCATAGAAATATCAGGACAGCCCAAAGCGGTGGAGACTGAACTCGCA

BpuE1 | SpAcc | Ecil | SpDon | BspLU |  
CGATTTTTGTGATGCTCGTCAGGGGGCGGAGCCTATGGAAAAACGCCAGCAACCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACA  
5701 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 5800  
GCTAAAAACACTACGAGCAGTCCCCCGCCTCGGATACCTTTTTGCGGTGCTTGCGCCGAAAAATGCCAAGGACCGGAAAACGACCGGAAAACGAGTGT

Nsil | BfrB1 |  
TGTTCTTTCCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCATGCAT  
5801 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 5856  
ACAAGAAAAGGACGCAATAGGGGACTAAGACACCTATTGGCATAATGGCGGTACGTA

Found:

Aar1	Aat2	Acc65	Afe1	<b>Afl2</b>	<b>Age1</b>	Ale1	AlwN1	ApaL1	<b>Ase1</b>	Avr2	<b>BamH1</b>	BciV1	BfrB1
Bgl1	Bmr1	Bpm1	Bpu10	BpuE1	Bsa1	BsaB1	<b>BsaXa</b>	<b>BsaXb</b>	BseR1	BseY1	Bsm1	BspH1	BspLU
BspM1	BsrB1	<b>BsrD1</b>	<b>BsrG1</b>	BssS1	BstAP	<b>BstB1</b>	<b>BstX1</b>	Bsu36	BtgZ1	<b>Bts1</b>	_Chi	<b>Clal</b>	Dra1
Dra3	Drd1	Eag1	Ear1	Ecil	Eco57	<b>EcoR1</b>	<b>Fsp1</b>	<b>Hpa1</b>	<b>Kas1</b>	Kpn1	<b>Mfe1</b>	Msc1	Nae1
<b>Nar1</b>	Nco1	<b>Nde1</b>	NgoM4	<b>Nhe1</b>	<b>Not1</b>	Nsi1	<b>PflF1</b>	PflM1	Pml1	polyA	Psi1	Pvu2	<b>Rsr2</b>
Sap1	<b>SexA1</b>	<b>Sfi1</b>	<b>SnaB1</b>	SpAcc	SpDon	Sph1	Ssp1	<b>Stu1</b>	<b>Xba1</b>	<b>Xho1</b>			

Unique:

<b>Afl2</b>	<b>Age1</b>	<b>Ase1</b>	<b>BamH1</b>	<b>BsaXa</b>	<b>BsaXb</b>	<b>BsrD1</b>	<b>BsrG1</b>	<b>BstB1</b>	<b>BstX1</b>	<b>Bts1</b>	<b>Clal</b>	<b>EcoR1</b>	<b>Fsp1</b>
<b>Hpa1</b>	<b>Kas1</b>	<b>Mfe1</b>	<b>Nar1</b>	<b>Nde1</b>	<b>Nhe1</b>	<b>Not1</b>	<b>PflF1</b>	<b>Rsr2</b>	<b>SexA1</b>	<b>Sfi1</b>	<b>SnaB1</b>	<b>Stu1</b>	<b>Xba1</b>
<b>Xho1</b>													

Not found:

Acl1	Ahd1	Apa1	Asc1	AsiS1	Baela	Baelb	Bbs1	BbvC1	Bcgl1a	Bcgl1b	Bcl1	Bgl2	Blp1
BmgB1	Bsg1	BsiW1	BsmB1	BspE1	BssH2	BstE2	BstZ1	BxatB	BxatL	BxatR	BxatP	Ecl2	EcoK
EcoN1	EcoRV	FCatB	FCatL	FCatR	FCatP	ScFRT	Fse1	FspA1	Hind3	I_Ceu	loxP	Mlu1	Nru1
Pac1	Pme1	PshA1	PspOM	Pst1	Pvu1	R4atB	R4atL	R4atP	R4atR	Sac1	Sac2	Sall1	SanD1
Sbf1	Sca1	Sgf1	SgrA1	Sma1	Spe1	Srf1	Swal	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	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													