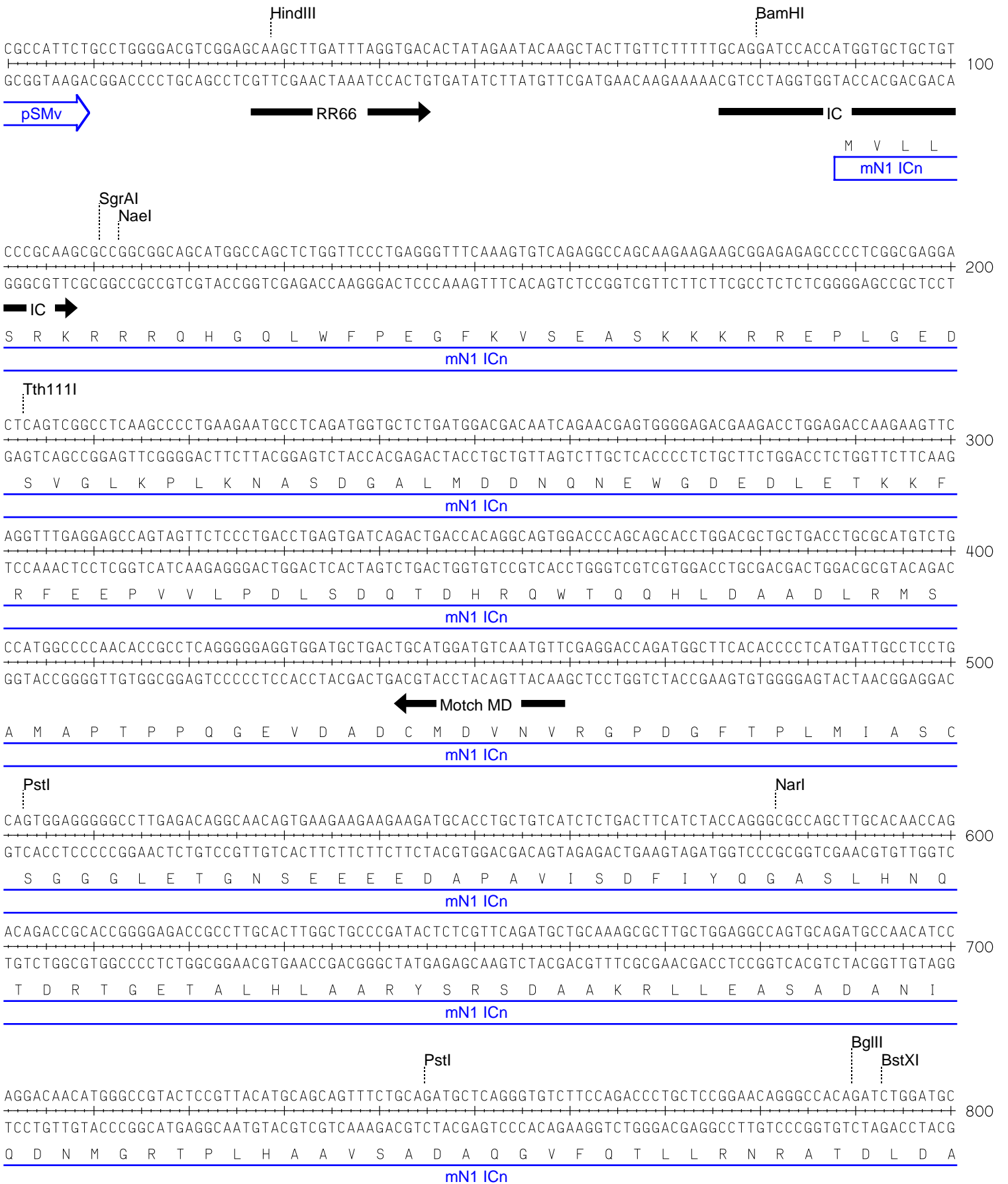
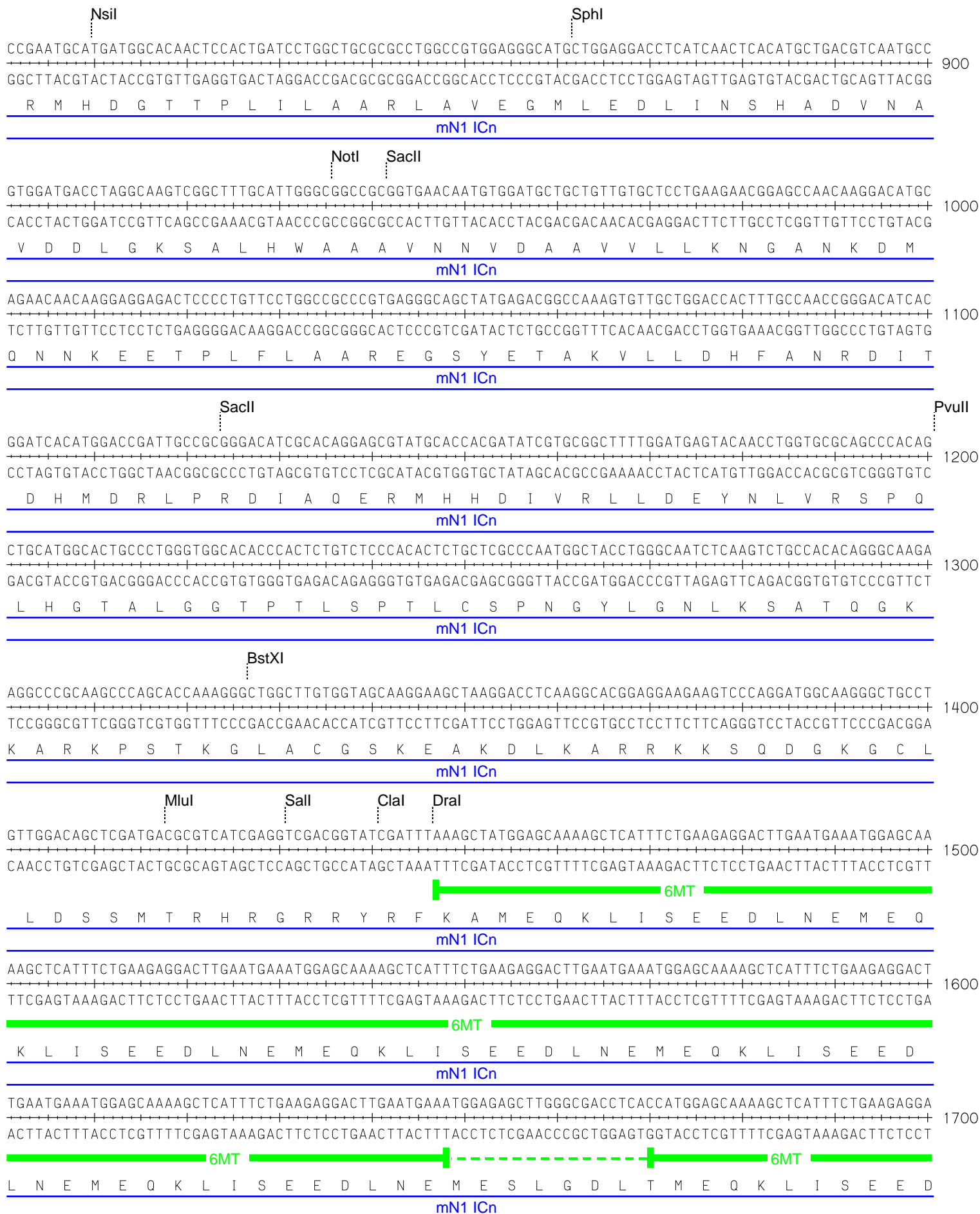


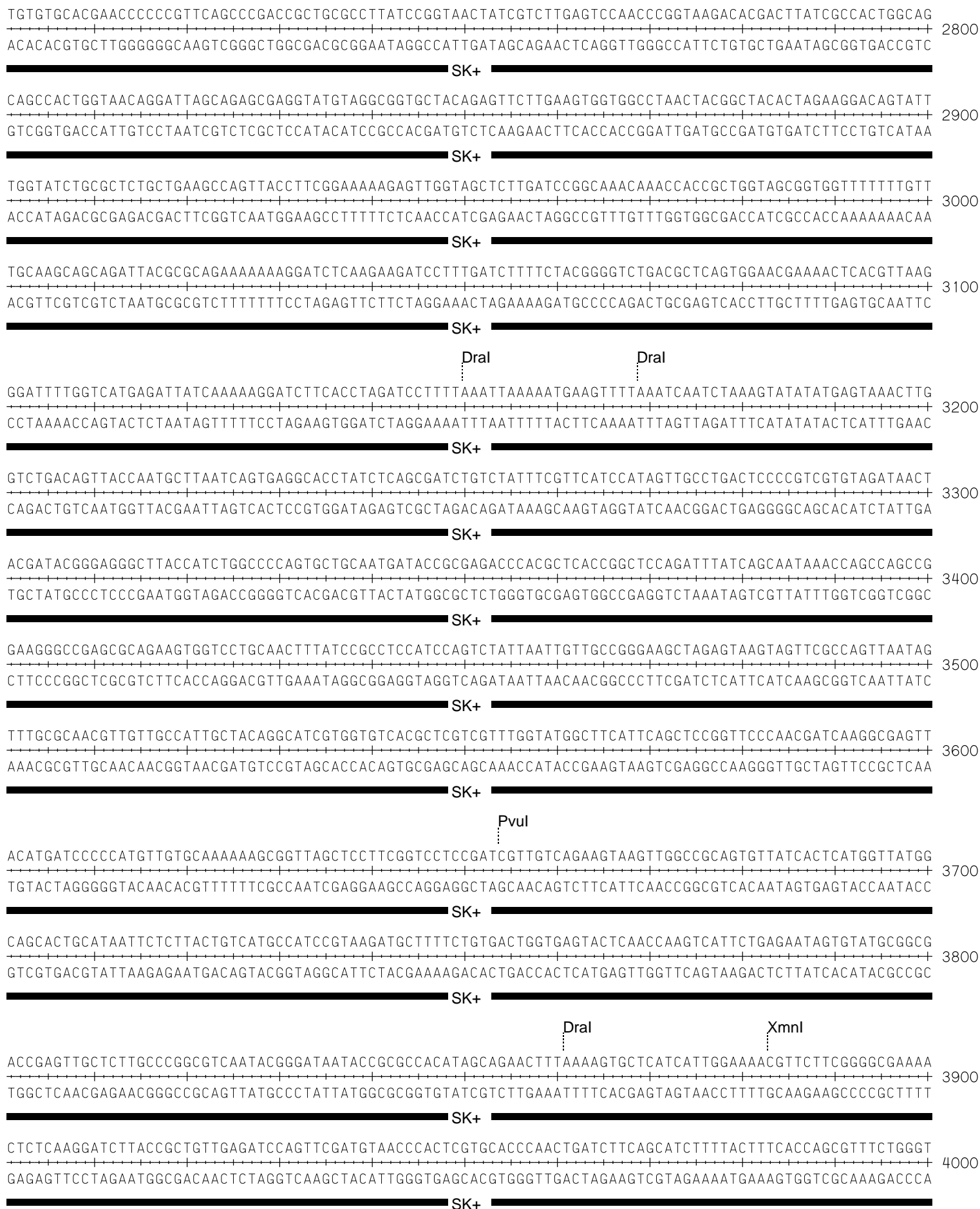
pCS2+ICV Map (1 > 5716) Site and Sequence

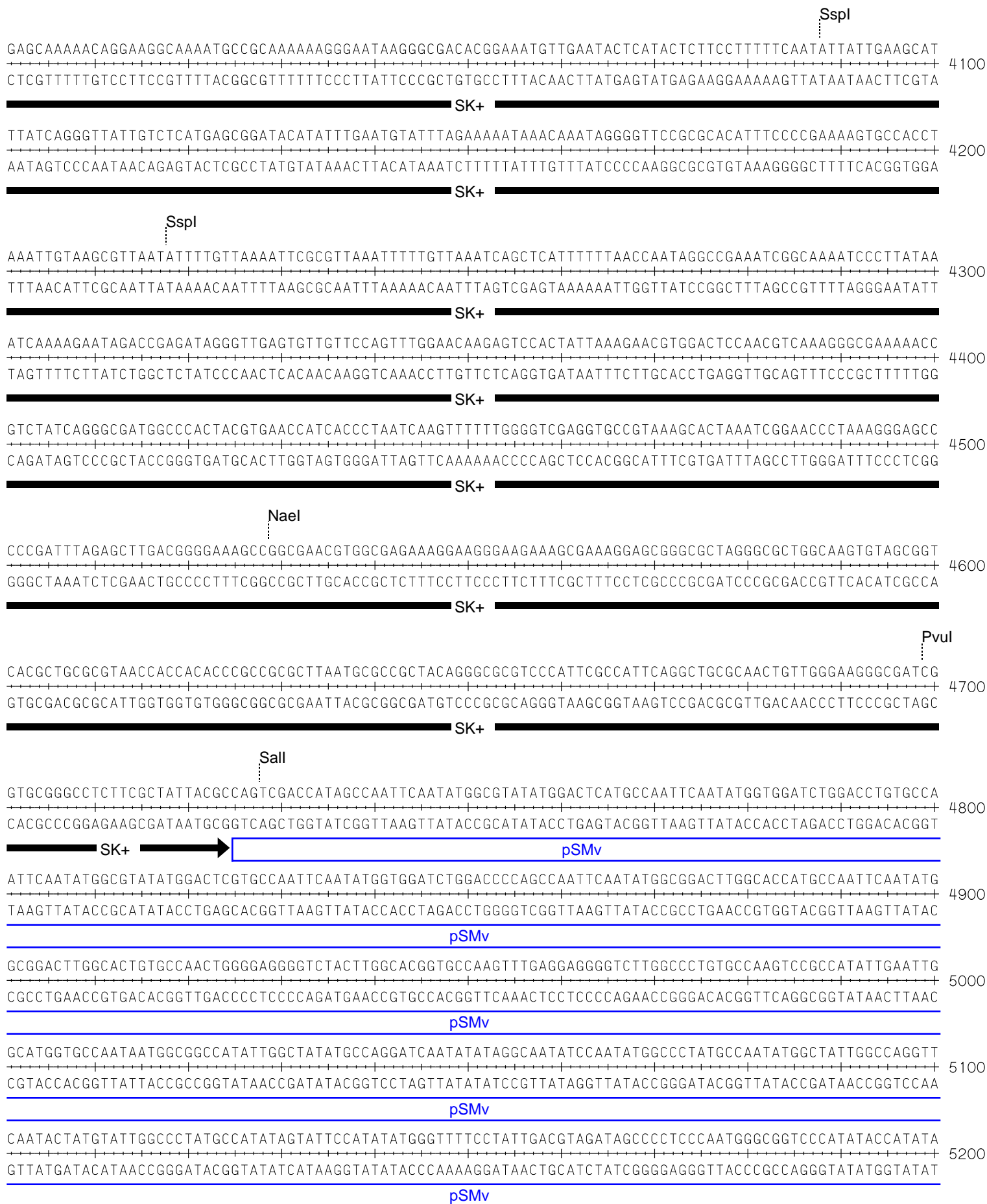
Enzymes : 39 of 212 enzymes (Filtered)

Settings : Circular, Subrange Context, Certain Sites Only, Standard Genetic Code









pCS2+ICV Map (1 > 5716) 221 Cut Sites Site Summary by Enzyme

Enzymes : 125 of 212 enzymes (Filtered), 94 Enzymes Cut

Settings : Circular, Subrange Context, Certain Sites Only, Standard Genetic Code

Enzyme	Freq	Position(s)
AatII <pre> ↓ G ACGT C C TGCA G ↑ </pre>	10	21 893 5243 5278 5325 5368 5393 5447 5563 5614
Acc65I <pre> ↓ G GTAC C C CATG G ↑ </pre>	1	1992
AcII <pre> ↓ AA CG TT TT GC AA ↑ </pre>	2	3509 3882
AfeI <pre> ↓ AGC GCT TCG CGA ↑ </pre>	1	667
AhdI <pre> ↓ GACNN N NNGTC CTGNN N NNCAG ↑ </pre>	1	3283
AlwNI <pre> ↓ CAG NNN CTG GTC NNN GAC ↑ </pre>	5	372 658 739 768 2806
ApaI <pre> ↓ G GGCC C C CCGG G ↑ </pre>	1	1990
ApaLI <pre> ↓ G TGCA C C ACGT G ↑ </pre>	2	2704 3950
AseI <pre> ↓ AT TA AT TA AT TA ↑ </pre>	4	2161 2220 3455 5490
AvrII <pre> ↓ C CTAG G G GATC C ↑ </pre>	1	909
BaeI <pre> ↓ NNNNN NNNNNNNNNNACN NNNNN NNNNNNNNNNTGN ↑ </pre>	1	666
BaeI <pre> ACNNNGTAYCNNNNNNN N TGNNNNCATRGNNNNNNN N ↑ </pre>	1	633

Site Summary by Enzyme

Enzyme	Freq	Position(s)
BamHI ↓ G GATC C C CTAG G ↑	2	79 1722
BbeI ↓ G GCGC C C CGCG G ↑	3	584 1976 5310
BbsI ↓ GAAGACNN NNNN CTTCTGNN NNNN ↑	2	284 750
BcgI ↓ NN NNNNNNNNNCGANNN NN NNNNNNNNNNGCTNNN ↑	1	3788
BcgI` CGANNNNNNNTGCNNNNNNNN GCTNNNNNNNACGNNNNNNNN ↑	1	3822
BciVI ↓ GTATCCNNNNN N CATAGGNNNNN N ↑	2	2593 4120
BclI ↓ T GATC A A CTAG T ↑	1	336
BglI ↓ GCCN NNN NGGC CGGN NNN NCCG ↑	6	3403 4670 5027 5083 5347 5469
BglII ↓ A GATC T T CTAG A ↑	1	789
BmrI ↓ ACTGGGNNNN N TGACCCNNNN N ↑	2	3323 4931
BpI ↓ NNNNN NNNNNNNNGAGNN NNNNN NNNNNNNNCTCNN ↑	2	173 205
BpI` GAGNNNNNCTCNNNNNNNN CTCNNNNNGAGNNNNNNNN ↑	2	173 205
BpmI CTGGAGNNNNNNNNNNNNNN GACCTCNNNNNNNNNNNNNN ↑	4	304 694 883 3353

Site Summary by Enzyme

Enzyme	Freq	Position(s)
Bpu10I ↓ CC TNA GC GG ANT CG ↑	2	749 1349
BsaI ↓ GGTCTCN NNNN CCAGAGN NNNN ↑	4	280 610 3344 5254
BsaXI ↓ NNN NNNNNNNNNACNNNN NNN NNNNNNNNNTGNNNN ↑	3	1221 2265 4359
BsaXI ACNNNNNCTCCNNNNNNN N TGNNNNNGAGGNNNNNNN N ↑	3	1251 2235 4389
BseRI ↓ GAGGAGNNNNNNNN NN CTCCTCNNNNNNNN NN ↑	3	322 1027 4972
BsgI GTGCAGNNNNNNNNNNNNNN CACGTCNNNNNNNNNNNNNN	1	704
BsmBI ↓ CGTCTCN NNNN GCAGAGN NNNN ↑	2	266 1048
BsmI ↓ GAATG CN CTTAC GN ↑	4	231 809 1818 1911
BspEI ↓ T CCGG A A GGCC T ↑	1	773
BspHI ↓ T CATG A A GTAC T ↑	3	485 3110 4118
BspMI ↓ ACCTGCNNNN NNNN TGGACGNNNN NNNN ↑	2	395 558
BsrBI ↓ CCG CTC GGC GAG ↑	4	2082 2323 4124 4569
BsrDI ↓ GCAATG NN CGTTAC NN ↑	5	3344 3518 5406 5634 5704

Site Summary by Enzyme

Enzyme	Freq	Position(s)
BssHII ↓ G CGCG C C GCGC G ↑	2	: 838 2029
BssSI ↓ C ACGA G G TGCT C ↑	3	: 2563 3947 4822
BstAPI ↓ GCAN NNN NTGC CGTN NNN NACG ↑	2	: 739 1394
BstXI ↓ CCAN NNNN NTGG GGTN NNNN NACC ↑	3	: 792 1326 1983
Bsu36I ↓ CC TNA GG GG ANT CC ↑	2	: 140 419
BtsI ↓ GCAGTG NN CGTCAC NN ↑	7	: 361 507 1208 1823 2176 3683 3703
ClaI ↓ AT CG AT TA GC TA ↑	1	: 1440
DraI ↓ TTT AAA AAA TTT ↑	4	: 1446 3149 3168 3860
DraIII ↓ CAC NNN GTG GTG NNN CAC ↑	1	: 4425
DrdI ↓ GACNN NN NNGTC CTGNN NN NNCAG ↑	2	: 2498 4380
EagI ↓ C GGCC G G CCGG C ↑	2	: 935 1965
EarI ↓ CTCTTCN NNN GAGAAGN NNN ↑	9	: 1469 1508 1547 1586 1625 1688 2274 4078 4715
EciI ↓ GGCGGANNNNNNNNN NN CCGCCTNNNNNNNNN NN ↑	6	: 2452 2598 3426 4886 4916 4974

Site Summary by Enzyme

Enzyme	Freq	Position(s)
Eco57I	10	241 994 1493 1532 1571 1610 1649 1712 2938 3950
CTGAAGNNNNNNNNNNNNNNN	:	:
GACTTCNNNNNNNNNNNNNNN	:	:
EcoNI	1	193
↓	:	:
CCTNN N NNAGG	:	:
GGANN N NNTCC	:	:
↑	:	:
EcoRI	1	1704
↓	:	:
G AATT C	:	:
C TTAA G	:	:
↑	:	:
EcoRV	1	1155
↓	:	:
GAT ATC	:	:
CTA TAG	:	:
↑	:	:
FspI	4	391 1189 3505 4677
↓	:	:
TGC GCA	:	:
ACG CGT	:	:
↑	:	:
HindIII	1	28
↓	:	:
A AGCT T	:	:
T TCGA A	:	:
↑	:	:
HpaI	1	1897
↓	:	:
GTT AAC	:	:
CAA TTG	:	:
↑	:	:
KasI	3	580 1972 5306
↓	:	:
G GCGC C	:	:
C CGCG G	:	:
↑	:	:
KpnI	1	1996
↓	:	:
G GTAC C	:	:
C CATG G	:	:
↑	:	:
MfeI	1	1906
↓	:	:
C AATT G	:	:
G TTAA C	:	:
↑	:	:
MluI	1	1417
↓	:	:
A CGCG T	:	:
T GCGC A	:	:
↑	:	:
MscI	2	125 5093
↓	:	:
TGG CCA	:	:
ACC GGT	:	:
↑	:	:
NaeI	2	112 4528
↓	:	:
GCC GGC	:	:
CGG CCG	:	:
↑	:	:

Site Summary by Enzyme

Enzyme	Freq	Position(s)
Nar I ↓ GG CG CC CC GC GG ↑	3	581 1973 5307
Nco I ↓ C CATG G G GTAC C ↑	3	86 401 1670
Nde I ↓ CA TA TG GT AT AC ↑	1	5280
NgoM I V ↓ G CCGG C C GGCC G ↑	2	110 4526
Not I ↓ GC GGCC GC CG CCGG CG ↑	2	935 1965
Nsi I ↓ A TGCA T T ACGT A ↑	2	809 1983
Pci I ↓ A CATG T T GTAC A ↑	1	2390
Ppu10 I ↓ A TGCA T T ACGT A ↑	2	805 1979
Psi I ↓ TTA TAA AAT ATT ↑	2	1877 4297
PspO M I ↓ G GGCC C C CCGG G ↑	1	1986
Pst I ↓ C TGCA G G ACGT C ↑	3	502 744 1714
Pvu I ↓ CG AT CG GC TA GC ↑	2	3653 4698
Pvu II ↓ CAG CTG GTC GAC ↑	2	1200 2214

Site Summary by Enzyme

Enzyme	Freq	Position(s)
SacII ↓ CC GC GG GG CG CC ↑	3	: 941 1123 1971
SalI ↓ G TCGA C C AGCT G ↑	2	: 1430 4727
SapI ↓ GCTCTTCN NNN CGAGAAGN NNN ↑	1	: 2274
ScaI ↓ AGT ACT TCA TGA ↑	2	: 3763 5549
SexAI ↓ A CCWGG T T GGWCC A ↑	1	: 1181
SfoI ↓ GGC GCC CCG CGG ↑	3	: 582 1974 5308
SgrAI ↓ CR CCGG YG GY GGCC RC ↑	1	: 110
SmaI ↓ CCC GGG GGG CCC ↑	1	: 1718
SnaBI ↓ TAC GTA ATG CAT ↑	1	: 1759
SpeI ↓ A CTAG T T GATC A ↑	1	: 1728
SphI ↓ G CATG C C GTAC G ↑	1	: 861
SspI ↓ AAT ATT TTA TAA ↑	2	: 4087 4217
Tth111I ↓ GACN N NGTC CTGN N NCAG ↑	1	: 202

Site Summary by Enzyme

Enzyme	Freq	Position(s)
XbaI ↓ T CTAG A A GATC T ↑	1	: 1734
XcmI ↓ CCANNNN N NNNNTGG GGTNNNN N NNNNACC ↑	3	: 1068 1263 5538
XmaI ↓ C CCGG G G GGCC C ↑	1	: 1716
XmnI ↓ GAANN NNTTC CTTNN NNAAG ↑	1	: 3882


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FEATURES                               Location/Qualifiers
  CDS                                   join(1447..1648,1670..1704)
                                         /note="6 myc tag"
  misc_feature                          27..45
                                         /note="rr66"
  CDS                                   88..1746
                                         /note="ICn ORF"
  misc_feature                          88..1746
                                         /note="mN1 ICn"
  misc_feature                          76..108
                                         /note="IC Oligos"
  misc_feature                          complement(442..459)
                                         /note="Motch MD"
  misc_feature                          1994..4724
                                         /note="SK+"
  misc_feature                          2120..2666
                                         /note="ORI"
BASE COUNT      1454 a    1423 c    1485 g    1354 t

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  1 CGCCATTCTG CCTGGGGACG TCGGAGCAAG CTTGATTTAG GTGACACTAT AGAATACAAG
 61 CTACTTGTTT TTTTTCAGG ATCCACCATG GTGCTGCTGT CCCGCAAGCG CCGGCGGCAG
121 CATGGCCAGC TCTGGTTCCC TGAGGGTTTC AAAGTGTTCAG AGGCCAGCAA GAAGAAGCGG
181 AGAGAGCCCC TCGGCGAGGA CTCAGTCGGC CTCAAGCCCC TGAAGAATGC CTCAGATGGT
241 GCTCTGATGG ACGACAATCA GAACGAGTGG GGAGACGAAG ACCTGGAGAC CAAGAAGTTC
301 AGGTTTGAGG AGCCAGTAGT TCTCCCTGAC CTGAGTGATC AGACTGACCA CAGGCAGTGG
361 ACCCAGCAGC ACCTGGACGC TGCTGACCTG CGCATGTCTG CCATGGCCCC AACACCGCCT
421 CAGGGGGAGG TGGATGCTGA CTGCATGGAT GTCAATGTTT GAGGACCAGA TGGCTTCACA
481 CCCCTCATGA TTGCCTCCTG CAGTGGAGGG GGCCTTGAGA CAGGCAACAG TGAAGAAGAA
541 GAAGATGCAC CTGCTGTCAT CTCTGACTTC ATCTACCAGG GCGCCAGCTT GCACAACCAG
601 ACAGACCGCA CCGGGGAGAC CGCCTTGAC TGGCTGCCC GATACTCTCG TTCAGATGCT
661 GCAAAGCGCT TGCTGGAGGC CAGTGCAGAT GCCAACATCC AGGACAACAT GGGCCGTAAT
721 CCGTTACATG CAGCAGTTTC TGCAGATGCT CAGGGTGTCT TCCAGACCCT GCTCCGGAAC
781 AGGGCCACAG ATCTGGATGC CCGAATGCAT GATGGCACAA CTCCACTGAT CCTGGCTGCG
841 CGCCTGGCCG TGGAGGGCAT GCTGGAGGAC CTCATCAACT CACATGCTGA CGTCAATGCC
901 GTGGATGACC TAGGCAAGTC GGCTTTGCAT TGGGCGGCCG CGGTGAACAA TGTGGATGCT
961 GCTGTTGTGC TCCTGAAGAA CGGAGCCAAC AAGGACATGC AGAACAACAA GGAGGAGACT
1021 CCCCTGTTCC TGGCCGCCC GAGGGCAGC TATGAGACGG CCAAAGTGTT GCTGGACCAC
1081 TTTGCCAACC GGGACATCAC GGATCACATG GACCGATTGC CGCGGGACAT CGCACAGGAG
1141 CGTATGCACC ACGATATCGT GCGGCTTTTG GATGAGTACA ACCTGGTTCG CAGCCCACAG
1201 CTGCATGGCA CTGCCCTGGG TGGCACACCC ACTCTGTCTC CCACACTCTG CTCGCCAAT
1261 GGCTACCTGG GCAATCTCAA GTCTGCCACA CAGGGCAAGA AGGCCCGCAA GCCCAGCACC
1321 AAAGGGCTGG CTTGTGGTAG CAAGGAAGCT AAGGACCTCA AGGCACGGAG GAAGAAGTCC
1381 CAGGATGGCA AGGGCTGCCT GTTGGACAGC TCGATGACGC GTCATCGAGG TCGACGGTAT
1441 CGATTTAAAG CTATGGAGCA AAAGCTCATT TCTGAAGAGG ACTTGAATGA AATGGAGCAA
1501 AAGCTCATT CTGAAGAGGA CTTGAATGAA ATGGAGCAAA AGCTCATTTT TGAAGAGGAC
1561 TTGAATGAAA TGGAGCAAAA GCTCATTTCT GAAGAGGACT TGAATGAAAT GGAGCAAAAAG
1621 CTCATTTCTG AAGAGGACTT GAATGAAATG GAGAGCTTGG GCGACCTCAC CATGGAGCAA
1681 AAGCTCATT CTGAAGAGGA CTTGAATTCC TGCAGCCCGG GGGATCCACT AGTTCTAGAA
1741 CTATAGTGAG TCGTATTACG TAGATCCAGA CATGATAAGA TACATTGATG AGTTTGGACA
1801 AACCACAAC AGAATGCAGT GAAAAAATG CTTTATTTGT GAAATTTGTG ATGCTATTGC
1861 TTTATTTGTA ACCATTATAA GCTGCAATAA ACAAGTTAAC AACAACAATT GCATTCAATTT
1921 TATGTTTCAG GTTCAGGGGG AGGTGTGGGA GGTTTTTTAA TTCGCGGCCG CGGCGCCAAT
1981 GCATTGGGCC CGGTACCCAG CTTTTGTTCC CTTTAGTGAG GGTTAATTGC GCGCTTGGCG
2041 TAATCATGGT CATAGCTGTT TCCTGTGTGA AATTGTTATC CGCTCACAAT TCCACACAAC
2101 ATACGAGCCG GAAGCATAAA GTGTAAAGCC TGGGGTGCCT AATGAGTGAG CTAACTCACA
2161 TTAATTGCGT TGCGCTCACT GCCCGCTTTC CAGTCGGGAA ACCTGTCTGT CCAGCTGCAT
2221 TAATGAATCG GCCAACGCGC GGGGAGAGGC GTTTTGCGTA TTGGGCGCTC TTCCGCTTCC

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2281	TCGCTCACTG	ACTCGCTGCG	CTCGGTCGTT	CGGCTGCGGC	GAGCGGTATC	AGCTCACTCA
2341	AAGGCGGTAA	TACGGTTATC	CACAGAATCA	GGGGATAACG	CAGGAAAGAA	CATGTGAGCA
2401	AAAGGCCAGC	AAAAGGCCAG	GAACCGTAAA	AAGGCCGCGT	TGCTGGCGTT	TTTCCATAGG
2461	CTCCGCCCCC	CTGACGAGCA	TCACAAAAAT	CGACGCTCAA	GTCAGAGGTG	GCGAAACCCG
2521	ACAGGACTAT	AAAGATACCA	GGCGTTTCCC	CCTGGAAGCT	CCCTCGTGCG	CTCTCCTGTT
2581	CCGACCCTGC	CGCTTACCGG	ATACCTGTCC	GCCTTTCTCC	CTTCGGGAAG	CGTGGCGCTT
2641	TCTCATAGCT	CACGCTGTAG	GTATCTCAGT	TCGGTGTAGG	TCGTTTCGCTC	CAAGCTGGGC
2701	TGTGTGCACG	AACCCCCCGT	TCAGCCCGAC	CGCTGCGCCT	TATCCGGTAA	CTATCGTCTT
2761	GAGTCCAACC	CGGTAAGACA	CGACTTATCG	CCACTGGCAG	CAGCCACTGG	TAACAGGATT
2821	AGCAGAGCGA	GGTATGTAGG	CGGTGCTACA	GAGTTCTTGA	AGTGGTGGCC	TAACTACGGC
2881	TACACTAGAA	GGACAGTATT	TGGTATCTGC	GCTCTGCTGA	AGCCAGTTAC	CTTCGGAAAA
2941	AGAGTTGGTA	GCTCTTGATC	CGGCAAACAA	ACCACCGCTG	GTAGCGGTGG	TTTTTTTTGTT
3001	TGCAAGCAGC	AGATTACGCG	CAGAAAAAAA	GGATCTCAAG	AAGATCCTTT	GATCTTTTCT
3061	ACGGGGTCTG	ACGCTCAGTG	GAACGAAAAC	TCACGTTAAG	GGATTTTGGT	CATGAGATTA
3121	TCAAAAAGGA	TCTTCACCTA	GATCCTTTTA	AATTA AAAAT	GAAGTTTTAA	ATCAATCTAA
3181	AGTATATATG	AGTAAACTTG	GTCTGACAGT	TACCAATGCT	TAATCAGTGA	GGCACCTATC
3241	TCAGCGATCT	GTCTATTTTCG	TTCATCCATA	GTTGCCTGAC	TCCCCGTCGT	GTAGATAACT
3301	ACGATACGGG	AGGGCTTACC	ATCTGGCCCC	AGTGCTGCAA	TGATAACCGG	AGACCCACGC
3361	TCACCGGCTC	CAGATTTATC	AGCAATAAAC	CAGCCAGCCG	GAAGGGCCGA	GCGCAGAAGT
3421	GGTCCTGCAA	CTTTATCCGC	CTCCATCCAG	TCTATTAATT	GTTGCCGGGA	AGCTAGAGTA
3481	AGTAGTTCGC	CAGTTAATAG	TTTGCGCAAC	GTTGTTGCCA	TTGCTACAGG	CATCGTGGTG
3541	TCACGCTCGT	CGTTTGGTAT	GGCTTCATTC	AGCTCCGGTT	CCCAACGATC	AAGGCGAGTT
3601	ACATGATCCC	CCATGTTGTG	CAAAAAAGCG	GTTAGCTCCT	TCGGTCTCTC	GATCGTTGTC
3661	AGAAGTAAGT	TGGCCGCAGT	GTTATCACTC	ATGGTTATGG	CAGCACTGCA	TAATTCTCTT
3721	ACTGTCATGC	CATCCGTAAG	ATGCTTTTCT	GTGACTGGTG	AGTACTCAAC	CAAGTCATTC
3781	TGAGAATAGT	GTATGCGGCG	ACCGAGTTGC	TCTTGCCCGG	CGTCAATACG	GGATAATACC
3841	GCGCCACATA	GCAGAACTTT	AAAAGTGCTC	ATCATTGGAA	AACGTTCTTC	GGGGCGAAAA
3901	CTCTCAAGGA	TCTTACCGCT	GTTGAGATCC	AGTTCGATGT	AACCCACTCG	TGCACCCAAC
3961	TGATCTTCAG	CATCTTTTAC	TTTTACCAGC	GTTTCTGGGT	GAGCAAAAAC	AGGAAGGCAA
4021	AATGCCGCAA	AAAAGGGAAT	AAGGGCGACA	CGGAAATGTT	GAATACTCAT	ACTCTTCCTT
4081	TTTCAATATT	ATTGAAGCAT	TTATCAGGGT	TATTGTCTCA	TGAGCGGATA	CATATTTGAA
4141	TGTATTTAGA	AAAATAAACA	AATAGGGGTT	CCGCGCACAT	TTCCCCGAAA	AGTGCCACCT
4201	AAATTGTAAG	CGTTAATATT	TTGTTAAAAT	TCGCGTTAAA	TTTTTTGTTAA	ATCAGCTCAT
4261	TTTTTAACCA	ATAGGCCGAA	ATCGGCAAAA	TCCCTTATAA	ATCAAAAGAA	TAGACCGAGA
4321	TAGGGTTGAG	TGTTGTTCCA	GTTTGAACA	AGAGTCCACT	ATTAAGA AAC	GTGGACTCCA
4381	ACGTCAAAGG	GCGAAAAACC	GTCTATCAGG	GCGATGGCCC	ACTACGTGAA	CCATCACCTT
4441	AATCAAGTTT	TTTGGGGTTCG	AGGTGCCGTA	AAGCACTAAA	TCGGAACCTT	AAAGGGAGCC
4501	CCCGATTTAG	AGCTTGACGG	GGAAAGCCGG	CGAACGTGGC	GAGAAAGGAA	GGGAAGAAAG
4561	CGAAAGGAGC	GGGCGCTAGG	GCGCTGGCAA	GTGTAGCGGT	CACGCTGCGC	GTAACCACCA
4621	CACCCGCCGC	GCTTAATGCG	CCGCTACAGG	GCGCGTCCCA	TTCGCCATTC	AGGCTGCGCA
4681	ACTGTTGGGA	AGGGCGATCG	GTGCGGGCCT	CTTCGCTATT	ACGCCAGTCG	ACCATAGCCA
4741	ATTCAATATG	GCGTATATGG	ACTCATGCCA	ATTCAATATG	GTGGATCTGG	ACCTGTGCCA
4801	ATTCAATATG	GCGTATATGG	ACTCGTGCCA	ATTCAATATG	GTGGATCTGG	ACCCAGCCA
4861	ATTCAATATG	GCGGACTTGG	CACCATGCCA	ATTCAATATG	GCGGACTTGG	CACTGTGCCA
4921	ACTGGGGAGG	GGTCTACTTG	GCACGGTGCC	AAGTTTGAGG	AGGGGTCTTG	GCCCTGTGCC
4981	AAGTCCGCCA	TATTGAATTG	GCATGGTGCC	AATAATGGCG	GCCATATTGG	CTATATGCCA
5041	GGATCAATAT	ATAGGCAATA	TCCAATATGG	CCCTATGCCA	ATATGGCTAT	TGGCCAGGTT
5101	CAATACTATG	TATTGGCCCT	ATGCCATATA	GTATTCCATA	TATGGGTTTT	CCTATTGACG
5161	TAGATAGCCC	CTCCAATGG	GCGGTCCCAT	ATACCATATA	TGGGGCTTCC	TAATAACCGC
5221	CATAGCCACT	CCCCCATTGA	CGTCAATGGT	CTCTATATAT	GGTCTTTTCT	ATTGACGTCA
5281	TATGGGCGGT	CCTATTGACG	TATATGGCGC	CTCCCCATT	GACGTCAATT	ACGGTAAATG
5341	GCCCGCCTGG	CTCAATGCC	ATTGACGTCA	ATAGGACCAC	CCACCATTGA	CGTCAATGGG
5401	ATGGCTCATT	GCCCATT CAT	ATCCGTTCTC	ACGCCCCCTA	TTGACGTCAA	TGACGGTAAA
5461	TGGCCCACTT	GGCAGTACAT	CAATATCTAT	TAATAGTAAC	TTGGCAAGTA	CATTACTATT
5521	GGCAAGTACG	CCAAGGGTAC	ATTGGCAGTA	CTCCCATTGA	CGTCAATGGC	GGTAAATGGC
5581	CCGCGATGGC	TGCCAAGTAC	ATCCCCATTG	ACGTCAATGG	GGAGGGGCAA	TGACGCAAAT
5641	GGGCGTTCCA	TTGACGTAAA	TGGGCGGTAG	GCGTGCCTAA	TGGGAGGTCT	ATATAAGCAA

// 5701 TGCTCGTTTA GGGAAC