

**pPA-TagRFP-actin 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, beta-actin amino acids are shown in green, linker amino acids are shown in black.



	Aat2		Eci1
401			
	TACGCGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTTGACGTCAATGGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTA		
	*           *           *           *           *           *           *           *           *           *           *           *           *           *           *           *           *		500
	ATCGCCAAACTGAGTGCCCTAAAGGTTTTCAGAGGTGGGGTAACTGCAGTTACCCTCAAACAAAACCCTGGTGGTTTAGTTGCCCTGAAAGGTTTTACAGCAT		
			Nhe1
501	ACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTGGTTTAGTGAACCGTCAGATCCGCTAGCGGTG		
	*           *           *           *           *           *           *           *           *           *           *           *           *           *           *           *           *		600
	TGTTGAGGCGGGTAACTGCGTTTACCCGCCATCCGCACATGCCACCCTCCAGATATATTCTGTCTCGACCAAATCACTTGGCAGTCTAGGCGATCGCCAC		
	Ale1		
	Nco1	Sap1	
601	Msc1	Ear1	BsrG1
	GCCACCATGGTGTCTAAGGGCGAAGAGCTGATTAAGGAGAACATGCACATGAAGCTGTACATGGAGGGCACCCTGAACAACCACCACCTTCAAGTGCACAT		ApaL1
	*           *           *           *           *           *           *           *           *           *           *           *           *           *           *           *		700
	CGGTGGTACCACAGATTTCCCGCTTCTCGACTAATTCCTCCTTTGTACGTGTACTTTCGACATGTACCTCCCGTGCCACTTGTGGTGGTGAAGTTCACGTGTA		
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		
701	CCGAGGGCGAAGGCAAGCCCTACGAGGGCACCCAGACCATGAGAATCAAGGTGGTTCGAGGGCGGCCCTCTCCCTTCGCCTTCGACATCCTGGCTACCAG		
	*           *           *           *           *           *           *           *           *           *           *           *           *           *           *		800
	GGCTCCCGCTTCGGTTCGGGATGCTCCCGTGGGTCTGGTACTCTTAGTTCCACCAGCTCCCGCCGGGAGAGGGGAAGCGGAAGCTGTAGGACCGATGGTC		
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
801	CTTCATGTACGGCAGCAGCACCTTCATCAACCACACCCAGGGCATCCCCGACTTCTGGAAGCAGTCCTTCCCTGAGGGCTTCACATGGGAGAGAGTCACC		
	*           *           *           *           *           *           *           *           *           *           *           *           *           *           *		900
	GAAGTACATGCCGTCGTCGTTGGAAGTAGTTGGTGTGGGTCCCGTAGGGCTGAAGACCTTCGTCAGGAAGGGACTCCCGAAGTGTACCCTCTCTCAGTGG		
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		
	Bbs1	Bpm1	
901	ACATACGAAGACGGGGCGTGTGACCGCTACCCAGGACACCAGCCTCCAGGACGGCTGCCTCATCTACAACGTCAAGATCAGAGGGGTGAACCTTCCCAT		
	*           *           *           *           *           *           *           *           *           *           *           *           *           *		1000
	TGATATGCTTCTGCCCCGACGACTGGCGATGGGTCTGTGGTTCGGAGGTCCTGCCGACGGAGTAGATGTTGCAGTTCTAGTCTCCCACTTGAAGGGTA		
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		

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                                BseY1                                Bgl1    Sall
                                |                                |      |
1001 CCAACGGCCCTGTGATGAAGAAGAAAACACTCGGCTGGGAACCGAGCACCCGAGAAACTGAAACCCGCTGACGGCGGCCTGGAAGGCAGGGTTCGACATGGC 1100
      |||||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*
      GGTGCGGGACACTACTTCTTCTTTGTGAGCCGACCCCTTGGCTCGTGGCTCTTTGACTTTGGGCGACTGCCGCCGGACCTTCCGTCCCAGCTGTACCG
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
                                |          |                                |
1101 CCTGAAGCTCGTGGGCGGGGGCCACCTGATCTGCAACTTCAAGACCACATACAGATCCAAGAAACCCGCTAAGAACCTCAAGATGCCCGGGCTCTACTAT 1200
      |||||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*
      GGACTTCGAGCACCCGCCCCGGTGGACTAGACGTTGAAGTTCTGGTGTATGTCTAGGTTCTTTGGGCGATTCTTGGAGTTCTACGGGCCGCAGATGATA
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    Dra3    Msc1                                SpAcc
                                |                                ||    |    |                                |
1201 GTGGACCGCAGACTGGAAATCATCAAGGAGGCCGACAAAGAGACCTACTGGGAGCAGCACGAGGTGGCTGTGGCCAGATACTCCGACCTCCCTAGCAAAC 1300
      |||||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*
      CACCTGGCGTCTGACCTTTAGTAGTTCTCTCCGGCTGTTTCTCTGGATGACCCTCGTCTGTGCTCCACCGACACCCGGTCTATGAGGCTGGAGGGATCGTTTG
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

                                Hind3    Bmr1    BspE1    Bgl2    Xho1                                EcoRV    BsaXb    Sall                                BsaXa    NgoM4    Nae1
                                |    |    |    |    |                                |    |    |                                |    |    |
1301 TGGGGCACAAGCTTAATTCCGGACTCAGATCTCGAGCTATGGATGATGATATCGCCGCGCTCGTCTGTCGACAACGGCTCCGGCATGTGCAAGGCCGGCTT 1400
      |||||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*
      ACCCCGTGTTTCAATTAAGGCCTGAGTCTAGAGCTCGATACCTACTACTATAGCGGCGGAGCAGCAGCTGTTGCCGAGGCCGTACACGTTCCGGCCGAA
PA-TagRFP/β-Act. G H K L N S G L R S R A M D D D I A A L V V D N G S G M C K A G F

                                Sma1                                Nar1
                                |          |                                |
1401 CGCGGGCGACGATGCCCCCGGGCCGCTTCCCTCCATCGTGGGGCGCCCCAGGCACCCAGGGCGTGATGGTGGGCATGGGTCAGAAGGATTCCCTATGTG 1500
      |||||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*
      GCGCCCGCTGCTACGGGGGGCCCGCAGAAGGGGAGGTAGCACCCCGGGGTCCGTGGTCCCGCACTACCACCCGTACCCAGTCTTCCCTAAGGATACAC
β-Actin >  A G D D A P R A V F P S I V G R P R H Q G V M V G M G Q K D S Y V

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Eco57 Bmr1  
1501 GCGCAGAGGCCAGAGCAAGAGAGGCATCCTCACCTGAAGTACCCCATCGAGCACGGCATCGTCACCAACTGGGACGACATGGAGAAAATCTGGCACC 1600  
|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 1600  
CCGCTGCTCCGGGTCTCGTTCTCTCCGTAGGAGTGGGACTTCATGGGGTAGCTCGTGCCGTAGCAGTGGTTGACCCTGCTGTACCTCTTTTAGACCGTGG  
**β-Actin** > G D E A Q S K R G I L T L K Y P I E H G I V T N W D D M E K I W H H

BseR1  
Dra3  
BstAP  
1601 ACACCTTCTACAATGAGCTGCGTGTGGCTCCCGAGGAGCACCCCGTGCTGCTGACCGAGGCCCCCTGAACCCCAAGGCCAACCGCGAGAAGATGACCCA 1700  
|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 1700  
TGTGGAAGATGTTACTCGACGCACACCGAGGGCTCCTCGTGGGGCACGACGACTGGCTCCGGGGGACTTGGGGTTCCGGTTGGCGCTCTTCTACTGGGT  
**β-Actin** > T F Y N E L R V A P E E H P V L L T E A P L N P K A N R E K M T Q

Bsa1 BseY1  
1701 GATCATGTTTGGAGACCTTCAACACCCAGCCATGTACGTTGCTATCCAGGCTGTGCTATCCCTGTACGCCTCTGGCCGTACCACTGGCATCGTGATGGAC 1800  
|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 1800  
CTAGTACAAACTCTGGAAGTTGTGGGGTCCGGTACATGCAACGATAGGTCCGACACGATAGGGACATGCGGAGACCGGCATGGTGACCGTAGCACTACCTG  
**β-Actin** > I M F E T F N T P A M Y V A I Q A V L S L Y A S G R T T G I V M D

BstE2 Bcg1a  
PflF1 Dra3 SpAcc Bcg1b Xcm1  
1801 TCCGGTGACGGGGTCACCCACACTGTGCCCATCTACGAGGGGTATGCCCTCCCCCATGCCATCCTGCGTCTGGACCTGGCTGGCCGGGACCTGACTGACT 1900  
|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 1900  
AGGCCACTGCCCCAGTGGGTGTGACACGGGTAGATGCTCCCCATACGGGAGGGGGTACGGTAGGACGCAGACCTGGACCGACCGGCCCTGGACTGACTGA  
**β-Actin** > S G D G V T H T V P I Y E G Y A L P H A I L R L D L A G R D L T D Y

BspH1 SpDon Eag1 BsrB1 BsaXa BsaXb  
1901 ACCTCATGAAGATCCTCACCGAGCGGGCTACAGCTTACCACCACGGCCGAGCGGAAATCGTGCGTGACATTAAGGAGAAGCTGTGCTACGTCGCCCT 2000  
|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 2000  
TGGAGTACTTCTAGGAGTGGCTCGCGCCGATGTCGAAGTGGTGGTGCCGGCTCGCCCTTTAGCACGCACTGTAATTCCTCTTCGACACGATGCAGCGGGA  
**β-Actin** > L M K I L T E R G Y S F T T T A E R E I V R D I K E K L C Y V A L

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                                     SapI
                                     EarI
                             MscI  BseR1  XcmI  SpAcc  BpmI  DrdI  BsrB1  BsrD1
                                  |       |       |       |       |       |
2001  GGACTTCGAGCAAGAGATGGCCACGGCTGCTTCCAGCTCCTCCCCTGGAGAAGAGCTACGAGCTGCCTGACGGCCAGGTCAACCATTTGGCAATGAGCGG
    |||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||
CCTGAAGCTCGTTCTCTACCGGTGCCGACGAAGGTCGAGGAGGGACCTCTTCTCGATGCTCGACGGACTGCCGGTCCAGTAGTGGTAACCGTTACTCGCC
β-Actin  > D F E Q E M A T A A S S S S L E K S Y E L P D G Q V I T I G N E R

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                         SpAcc
                    Bsu36  EarI  BspH1  BmgB1
                              |       |
2101  TTCCGCTGCCCTGAGGCACTCTTCCAGCCTTCCCTTCCCTGGGCATGGAGTCCTGTGGCATCCACGAAACTACCTTCAACTCCATCATGAAGTGTGACGTGG
    |||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||
AAGGCGACGGGACTCCGTGAGAAGGTCGGAAGGAAGGACCCGTACCTCAGGACACCGTAGGTGCTTTGATGGAAGTTGAGGTAGTACTTCACACTGCACC
β-Actin  > F R C P E A L F Q P S F L G M E S C G I H E T T F N S I M K C D V D

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                                     BsrD1  BtsI
                                       |       |
2201  ACATCCGCAAAGACCTGTACGCCAACACAGTGCTGTCTGGCGGCACCACCATGTACCCTGGCATTGCCGACAGGATGCAGAAGGAGATCACTGCCCTGGC
    |||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||
TGTAGGCGTTTTCTGGACATGCGGTTGTGTACAGACAGACCGCCGTGGTGGTACATGGGACCGTAACGGCTGTCTTCTTCTCTAGTGACGGGACCG
β-Actin  > I R K D L Y A N T V L S G G T T M Y P G I A D R M Q K E I T A L A

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                                     BsrD1
                                 BseR1  Bpu10  ScaI
                                |       |       |
BseY1  BsaB1  |
          ||
2301  ACCCAGCACAATGAAGATCAAGATCATTGCTCCTCCTGAGCGCAAGTACTCCGTGTGGATCGGCGGCTCCATCCTGGCCTCGCTGTCCACCTTCCAGCAG
    |||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||
TGGGTCGTGTTACTTCTAGTTCAGTAACGAGGAGGACTCGCGTTCATGAGGCACACCTAGCCGCCGAGGTAGGACCGGAGCGACAGGTGGAAGGTCGTC
β-Actin  > P S T M K I K I I A P P E R K Y S V W I G G S I L A S L S T F Q Q

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BsaB1  BamH1  XbaI  Bcl1BsaB1
          |       |       |
2401  ATGTGGATCAGCAAGCAGGAGTATGACGAGTCCGGCCCCCTCCATCGTCCACCAGCAAATGCTTCTAGGGATCCACCGGATCTAGATAACTGATCATAATCA
    |||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||
TACACCTAGTCGTTTCGTCCTCATACTGCTCAGGCCGGGGAGGTAGCAGGTGGCGTTTACGAAGATCCCTAGGTGGCCTAGATCTATTGACTAGTATTAGT
β-Actin  > M W I S K Q E Y D E S G P S I V H R K C F *

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SpDon    Dra1    Bsm1  
           |     |                    Mfe1 |                    Hpa1  
 2501    GCCATACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTGAAACATAAAATGAATGCAATTGTTGTTGTTAACTT 2600  
 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 2600  
 CGGTATGGTGTAACATCTCCAAATGAACGAAATTTTTGGAGGGTGTGGAGGGGACTTGGACTTTGTATTTACTTACGTTAACAACAACAATTGAA

polyA    Psil    polyA    polyA    Bts1    Bsm1  
           |     |            |                    |            |  
 2601    GTTTATGTCAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATTTACAAATAAAGCATTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAAA 2700  
 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 2700  
 CAAATAACGTCGAATATTACCAATGTTTATTTTCGTTATCGTAGTGTTTAAAGTGTTTATTTTCGTAATAAAAGTGACGTAAGATCAACACCAAACAGGTTT

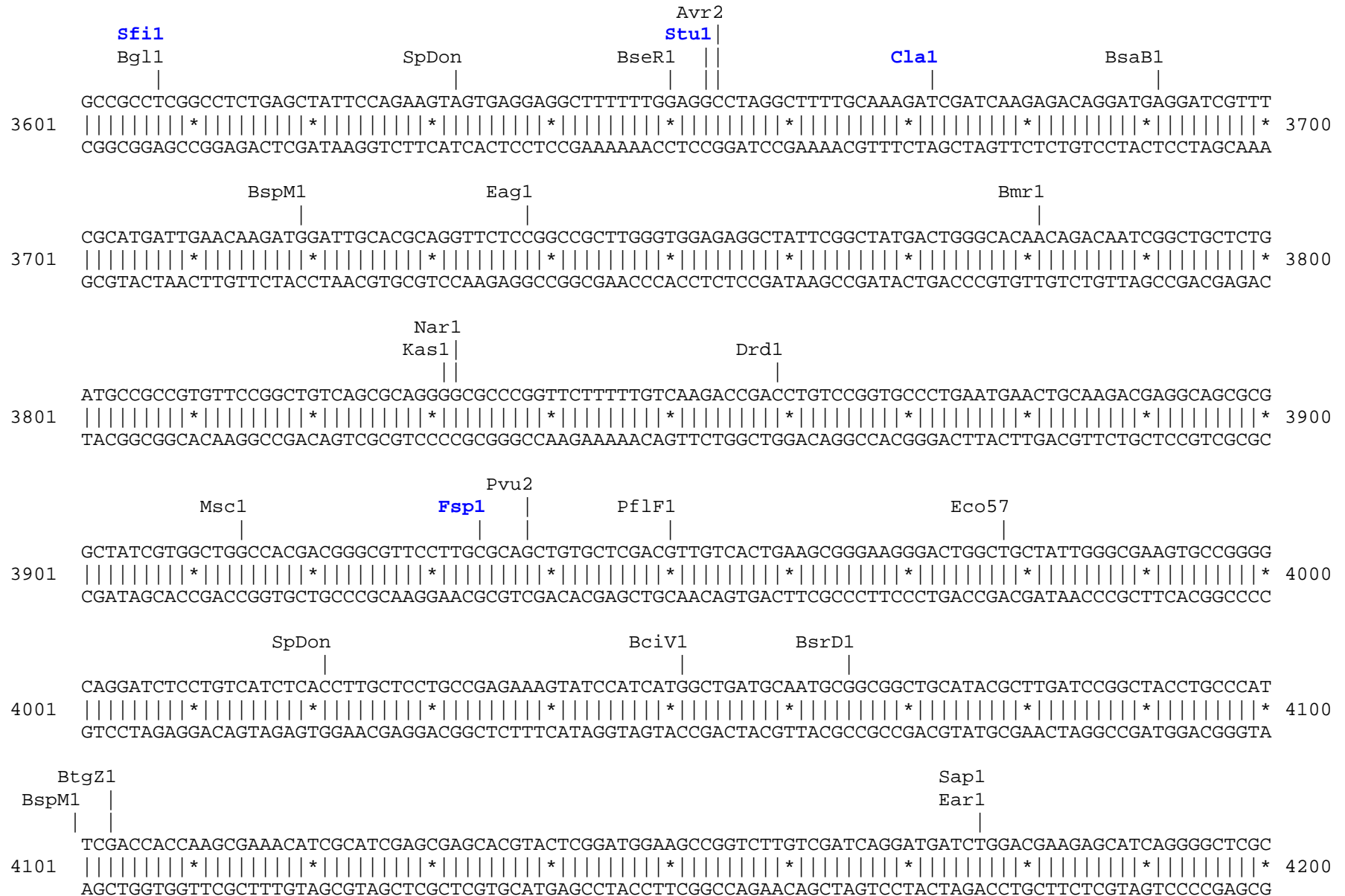
          Mlu1    SpDon    Ssp1  
 2701    CTCATCAATGTATCTTAACGCGTAAATTTGTAAGCGTAAATATTTTGTAAAATTCGCGTTAAATTTTTGTTAAATCAGCTCATTTTTAAACCAATAGGCC 2800  
 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 2800  
 GAGTAGTTACATAGAATTGCGCATTAAACATTCGCAATTATAAAACAATTTAAAGCGCAATTTAAAACAATTTAGTCGAGTAAAAAATTGGTTATCCGG

          Psil    BsaXb  
 2801    GAAATCGGCAAAATCCCTTATAAATCAAAGAATAGACCGAGATAGGGTTGAGTGTTGTTCCAGTTTGAACAAGAGTCCACTATTAAAGAACGTGGACT 2900  
 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 2900  
 CTTTAGCCGTTTTAGGAATATTTAGTTTTTCTTATCTGGCTCTATCCCACTCACAACAAGGTCAAACCTTGTTCTCAGGTGATAATTTCTTGCACCTGA

Drd1    BsaXa    BtgZ1    Dra3  
           |     |                    |            |  
 2901    CCAACGTCAAAAGGCGAAAAACCGTCTATCAGGGCGATGGCCCACTACGTGAACCATCACCTAATCAAGTTTTTTGGGGTTCGAGGTGCCGTAAAGCACT 3000  
 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 3000  
 GGTGTCAGTTTCCCGCTTTTTGGCAGATAGTCCCCTACCGGGTGATGCACTTGGTAGTGGGATTAGTTCAAAAACCCAGCTCCACGGCATTTCGTGA

          SpAcc    Nae1    NgoM4    BsrB1  
           |     |            |            |            |  
 3001    AAATCGGAACCCCTAAAGGGAGCCCCCGATTTAGAGCTTGACGGGGAAAGCCCGGCGAACGTGGCGAGAAAGGAAGGAAGAAAGCGAAAGGAGCGGGCGCT 3100  
 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 3100  
 TTTAGCCTTGGGATTTCCCTCGGGGGCTAAATCTCGAACTGCCCTTTTCGGCCGCTTGACACCGCTCTTTCCTTCCCTTCTTTTCGCTTCTTTCGCCC CGA







BpuE1 Sph1 Nco1 BtgZ1  
GCCAGCCGAAGTGTTCGCCAGGCTCAAGGCGAGCATGCCCCACGGCGAGGATCTCGTTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAA  
4201 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 4300  
CGGTCGGCTTGACAAGCGGTCCGAGTTCGCTCGTACGGGCTGCCGCTCCTAGAGCAGCACTGGGTACCGCTACGGACGAACGGCTTATAGTACCACCTT

BseY1 Nae1 Ssp1  
NcoM4 Rsr2 Eci1 Ear1  
AATGGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTG  
4301 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 4400  
TTACCGGCGAAAAGACCTAAGTAGCTGACACCGGCCGACCCACACCGCCTGGCGATAGTCCTGTATCGCAACCGATGGGCACTATAACGACTTCTCGAAC

Eco57 BssS1 BtgZ1 BsrB1 BsrB1  
GCGGCGAATGGGCTGACCGCTTCTCTCGTGTCTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTCTTCTGAGC  
4401 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 4500  
CGCCGCTTACCCGACTGGCGAAGGAGCACGAAATGCCATAGCGGCGAGGGCTAAGCGTCGCGTAGCGGAAGATAGCGGAAGAACTGCTCAAGAAGACTCG

BstB1 BspM1 BssS1 SpAcc  
GGGACTCTGGGGTTCGAAATGACCGACCAAGCGACGCCAACCTGCCATCACGAGATTTTCGATTCCACCGCCGCCTTCTATGAAAGGTTGGGCTTCGGAA  
4501 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 4600  
CCCTGAGACCCCAAGCTTTACTGGCTGGTTTCGCTGCGGGTTGGACGGTAGTGCTCTAAAGCTAAGGTGGCGGGCGGAAGATACTTTCCAACCCGAAGCCTT

Nae1 Bpm1 SpAcc Avr2  
NcoM4 Bpm1  
TCGTTTTCCGGGACCCGGCTGGATGATCCTCCAGCGGGGATCTCATGCTGGAGTTCTTCGCCCACCCTAGGGGGAGGCTAACTGAAACACGGAAGGA  
4601 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 4700  
AGCAAAAGGCCCTGCGGCCGACCTACTAGGAGGTCGCGCCCTAGAGTACGACCTCAAGAAGCGGGTGGGATCCCCCTCCGATTGACTTTGTGCCTTCTT

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                                polyA      polyA
                                |           |
4701 GACAATACCGGAAGGAACCCGCGCTATGACGGCAATAAAAAGACAGAATAAAACGCACGGTGTGGGTGCGTTTGTTCATAAACGCGGGGTTCCGGTCCCAG 4800
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
    CTGTTATGGCCTTCCTTGGGCGCGATACTGCCGTTATTTTTCTGTCTTATTTTGCCTGCCACAACCCAGCAAACAAGTATTTGCGCCCCAAGCCAGGGTC

                                Bsa1
                                |
4801 GGCTGGCACTCTGTTCGATAACCCACCGAGACCCCATTTGGGGCCAATACGCCCGCGTTTCTTCCCTTTTCCCCACCCCAAGTTCGGGTGAAGGCC 4900
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
    CCGACCGTGAGACAGCTATGGGGTGGCTCTGGGGTAACCCCGTTATGCGGGCGCAAAGAAGGAAAAGGGGTGGGGTGGGGGTTCAAGCCCACTTCCGG

                                BstAP      AlwN1      Bsu36      DraI      DraI
                                |           |           |           |           |
4901 CAGGGCTCGCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCCTCAGGTTACTCATATATACTTTAGATTGATTTAAACTTCATTTTAAATTTAAAG 5000
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
    GTCCCGAGCGTCGGTTGCAGCCCCGCCGTCCGGGACGGTATCGGAGTCCAATGAGTATATATGAAATCTAACTAAATTTTGAAGTAAAAATTAATTTTC

                                BspH1
                                |
5001 GATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGA 5100
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
    CTAGATCCACTTCTAGGAAAAACTATTAGAGTACTGGTTTTAGGGAATTGCACTCAAAGCAAGGTGACTCGCAGTCTGGGGCATCTTTTCTAGTTTCCT

                                BpuE1
                                |
5101 TCTTCTTGAGATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTGGTTTGTGGCCGGATCAAGAGCTACCAA 5200
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
    AGAAGAACTCTAGGAAAAAAGACGCGCATTAGACGACGAACGTTTTGTTTTTTGGTGGCGATGGTTCGCCACCAAACAAACGGCCTAGTTCTCGATGGTT

                                Eco57      SpAcc
                                |           |
5201 CTCTTTTCCGAAGGTAAGTGGCTTTCAGCAGAGCGCAGATAACCAATACTGTCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAAGTCTGTAGC 5300
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
    GAGAAAAAGGCTTCCATTGACCGAAGTCGTCTCGCGTCTATGGTTTATGACAGGAAGATCACATCGGCATCAATCCGGTGGTGAAGTTCTTGAGACATCG

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                                     AlwN1                               BpuE1
ACCGCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCG
5301 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5400
TGGCGGATGTATGGAGCGAGACGATTAGGACAATGGTCACCGACGACGGTCACCGCTATTTCAGCACAGAATGGCCCAACCTGAGTTCTGCTATCAATGGC

                                     ApaL1       BseY1                                               SpAcc
GATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTAT
5401 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5500
CTATTCCGCGTCGCCAGCCCAGACTTGCCCCCAAGCACGTGTGTCTGGGTCGAACCTCGCTTGCTGGATGTGGCTTGACTCTATGGATGTGCGACTCGATA

                                     BciV1
                                     Eci1                               BssS1
GAGAAAGCGCCACGCTTCCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAA
5501 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5600
CTCTTTCGCGGTGCGAAGGGCTTCCCTCTTTCCGCTGTCCATAGGCCATTGCGCGTCCCAGCCTTGTCCTCTCGCGTGCTCCCTCGAAGGTCCCCCTTT

                                     SpAcc       Drd1                               BpuE1       SpAcc       Eci1
CGCTGGTATCTTTATAGTCCTGTCTGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGCGGAGCCTATGGAAAAACGCC
5601 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5700
GCGGACCATAGAAATATCAGGACAGCCCAAAGCGGTGGAGACTGAACTCGCAGCTAAAAACACTACGAGCAGTCCCCCGCCTCGGATACCTTTTTGCGG

                                     SpDon
                                     BspLU
AGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCG
5701 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5800
TCGTTGCGCCGGAAAAATGCCAAGGACCGGAAAACGACCGGAAAACGAGTGTACAAGAAAGGACGCAATAGGGGACTAAGACACCTATTGGCATAATGGC

Nsil
BfrB1 |
      | |
CCATGCAT
5801 ||||| 5808
GGTACGTA
```

Found:

Aat2	<b>Ale1</b>	AlwN1	ApaL1	<b>Ase1</b>	Avr2	<b>BamH1</b>	Bbs1	<b>Bcg1a</b>	<b>Bcg1b</b>	BciV1	<b>Bcl1</b>	BfrB1	Bgl1
<b>Bgl2</b>	<b>BmgB1</b>	Bmr1	Bpm1	<b>Bpu10</b>	BpuE1	Bsa1	BsaB1	BsaXa	BsaXb	BseR1	BseY1	Bsm1	<b>BspE1</b>
BsrD1	<b>BsrG1</b>	BssS1	BstAP	<b>BstB1</b>	<b>BstE2</b>	BspH1	<b>BspLU</b>	BspM1	BsrB1	Bsu36	BtgZ1	Bts1	<b>Clal</b>
Dra1	Dra3	Drd1	Eag1	Ear1	Ecil	Eco57	<b>EcoRV</b>	<b>Fsp1</b>	<b>Hind3</b>	<b>Hpa1</b>	Kas1	<b>Mfe1</b>	<b>Mlu1</b>
Msc1	Nae1	Nar1	Nco1	<b>Nde1</b>	NgoM4	<b>Nhe1</b>	Nsi1	PflF1	polyA	Psi1	Pvu2	<b>Rsr2</b>	Sall
Sap1	<b>Sca1</b>	<b>SexA1</b>	<b>Sfi1</b>	<b>Sma1</b>	<b>SnaB1</b>	SpAcc	SpDon	Sph1	Ssp1	<b>Stu1</b>	<b>Xba1</b>	Xcm1	<b>Xho1</b>

Unique:

<b>Ale1</b>	<b>Ase1</b>	<b>BamH1</b>	<b>Bcg1a</b>	<b>Bcg1b</b>	<b>Bcl1</b>	<b>Bgl2</b>	<b>BmgB1</b>	<b>Bpu10</b>	<b>BspE1</b>	<b>BsrG1</b>	<b>BstB1</b>	<b>BstE2</b>	<b>BspLU</b>
<b>Clal</b>	<b>EcoRV</b>	<b>Fsp1</b>	<b>Hind3</b>	<b>Hpa1</b>	<b>Mfe1</b>	<b>Mlu1</b>	<b>Nde1</b>	<b>Nhe1</b>	<b>Rsr2</b>	<b>Sca1</b>	<b>SexA1</b>	<b>Sfi1</b>	<b>Sma1</b>
<b>SnaB1</b>	<b>Stu1</b>	<b>Xba1</b>	<b>Xho1</b>										

Not found:

Aar1	Acc65	Ac11	Afe1	Afl2	Age1	Ahd1	Apal	Asc1	AsiS1	Baela	Baelb	BbvC1	Blp1
Bsg1	BsiW1	BsmB1	BssH2	BstX1	BstZ1	BxatB	BxatL	BxatR	BxatP	_Chi	Ecl2	EcoK	EcoN1
EcoR1	FCatB	FCatL	FCatR	FCatP	ScFRT	Fse1	FspA1	I_Ceu	Kpn1	loxP	Not1	Nru1	Pac1
PflM1	Pme1	Pml1	PshA1	PspOM	Pst1	Pvu1	R4atB	R4atL	R4atP	R4atR	Sac1	Sac2	SanD1
Sbf1	Sgf1	SgrA1	Spe1	Srf1	Swal	T3RNA	T7RNA	T7Ter	PISce	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	BsrF1
BssK1	BstF5	BstN1	BstU1	BstY1	Bsr1	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													