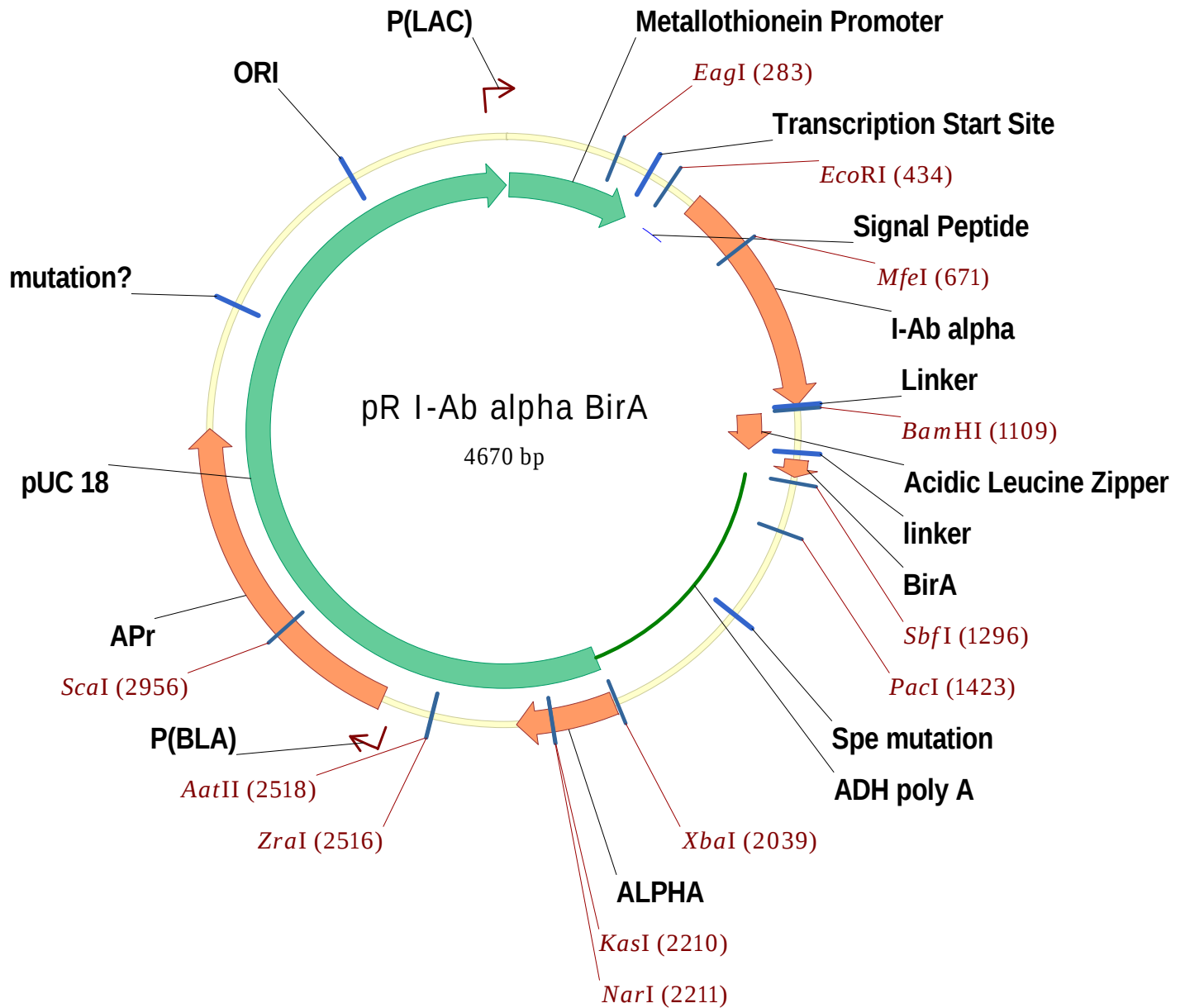


pR I-Ab alpha BirA



Metallothionein Promoter										
1	ATGATTACCG	TTGCAGGACA	GGATGTGGTG	CCCAGTGTGA	CTAGCTCTTT	GCTGCAAGCC	GTCCTATCCT	CTGGTTCCGA	TAAGAGACCC	AGAACTCCGG
	TACTAATGGC	AACGTCCTGT	CCTACACCAC	GGGCTACACT	GATCGAGAAA	CGAGCTCCGG	CAGGATAGGA	GACCAAGGCT	ATTCTCTGGG	TCTTGAGGCC
Metallothionein Promoter										
101	CCCCCACC	CCCACGCCA	CCCCATACA	TATGTGGTAC	GCAAGTAAGA	GTGCCTGCGC	ATGCCCCATG	TGCCCCACCA	AGAGCTTTGC	ATCCCATACA
	GGGGGGTGGC	GGGTGGCGGT	GGGGGTATGT	ATACACCATG	CGTTTATTCT	CACGGACGCG	TACGGGGTAC	ACGGGGTGGT	TCTCGAAACG	TAGGGTATGT
Metallothionein Promoter										
201	AGTCCCCAAA	GTGGAGAACC	GAACCAATTC	TTGCGGGGGA	GAACAAAAGC	TTTGCACAC	GTCCTCCACTC	GAATTTGGAG	EagI CCGCCCGCGC	TGTGCAAAAAG
	TCAGGGGTTT	CACCTCTTGG	CTTGGTAAAG	AAGCGCCCGT	CTTGTTTTCG	AAGACGTGTG	CAGAGGTGAG	CTTAAACCTC	GGCCGGCCGC	ACACGTTTTTC
Transcription Start Site										
Metallothionein Promoter										
301	AGGTGAATCG	AACGAAAGAC	CCGTGTGTAA	AGCCGCGTTT	CCAAAATGTA	TAAACCGCAG	AGCATCTGGC	CAATGTGCAT	CAGTTGTGGT	CAGCAGCAAA
	TCCACTTAGC	TTGCTTTCTG	GGCACACATT	TCGGCGCAAA	GGTTTTACAT	ATTTTGGCTC	TCGTAGACCG	GTTACACGTA	GTCAACACCA	GTCGTCGTTT
Signal Peptide										
+1	M P C S R A L I L G V L A L T T M L S L									
401	ATCAAGTGAA	TCATCTCAGT	GCAACTAAAG	GGGAATTCAG	GATGCCGTGC	AGCAGAGCTC	TGATTCTGGG	GGTCTCTGCC	CTGACCACCA	TGCTCAGCCT
	TAGTTCACCT	AGTAGAGTCA	CGTTGATTTC	CCCTTAAAGT	CTACGGCAGC	TCGCTCTCGAG	ACTAAGACCC	CCAGGAGCGG	GACTGTTGGT	ACGAGTCGGA
Signal Peptide										
I-Ab alpha										
+1	L C G G E D D I E A D H V G T Y G I S V Y Q S P G D I G Q Y T F E F									
501	CTGTGGAGGT	GAAGACGACA	TTGAGGCCGA	CCACGTAGCG	ACCTATGGTA	TAAGTGTATA	TCAGTCTCCT	GGAGACATTG	GCCAGTACAC	ATTTGAATTT
	GACACCTCCA	CTTCTGCTGT	AACTCCGGCT	GGTGATCCCG	TGGATACCAT	ATTCACATAT	AGTCAGAGGA	CCTCTGTAAC	CGGTCTATGT	TAAACTTAA
I-Ab alpha										
+1	D G D E L F Y V D L D K K E T V W M L P E F G Q L A S F D P Q G G L									
601	GATGGTGATG	AGTTGTTCTA	TGTGGACTTG	GATAAGAAGG	AGACTGTCTG	GATGCTTCCT	GAGTTTGCC	AATTGGCAAG	CTTTGACCCC	CAAGGTGGAC
	CTACCACTAC	TCAACAAGAT	ACACCTGAAC	CTATTCTTCC	TCTGACAGAC	CTACGAAGGA	CTCAAACCGG	TTAACCGTTC	GAAACTGGGG	GTTCCACCTG
I-Ab alpha										
+1	L Q N I A V V K H N L G V L T K R S N S T P A T N E A P Q A T V F P									
701	TGCAAAACAT	AGCTGTAGTA	AAACACAAC	TGGGAGTCTT	GACTAAGAGG	TCAAATTC	CCCCAGCTAC	CAATGAGGCT	CCTCAAGCGA	CTGTGTTCCC
	ACGTTTGTGA	TCGACATCAT	TTTGTGTTGA	ACCCTCAGAA	CTGATTCTCC	AGTTTAAGGT	GGGTCGATG	GTTACTCCGA	GGAGTTCGCT	GACACAAGGG
I-Ab alpha										
+1	P K S P V L L G Q P N T L I C F V D N I F P P V I N I T W L R N S K									
801	CAAGTCCCCT	GTGCTGCTGG	GTCAGCCCAA	CACCCTCATC	TGCTTTGTGG	ACAACATCTT	CCCTCCTGTG	ATCAACATCA	CATGGCTCAG	AAATAGCAAG
	GTTCAGGGGA	CACGACGACC	CAGTCGGGTT	GTGGGAGTAG	ACGAAACACC	TGTTGTAGAA	GGGAGGACAC	TAGTTGTAGT	GTACCGAGTC	TTTATCGTTC
I-Ab alpha										
+1	S V A D G V Y E T S F F V N R D Y S F H K L S Y L T F I P S D D D I									
901	TCAGTCGACG	ACGGTGTTTA	TGAGACGACG	TTCTTCGCTA	ACCGTGACTA	TTCTTCCAC	AAGCTGTCTT	ATCTCACCTT	CATCCCTTCT	GACGATGACA
	AGTCAGCGTC	TGCCACAAT	ACTCTGGTCG	AAGAAGCAGT	TGGCACTGAT	AAGGAAGGTG	TTCGACAGAA	TAGAGTGGA	GTAGGGAAGA	CTGCTACTGT
Linker										
I-Ab alpha										
+1	I Y D C K V E H W G L E E P V L K H W E P E I P A P M S E L T E T G									
1001	TTTATGACTG	CAAGGTGGAA	CACTGGGGCC	TGGAGGAGCC	GGTTCTGAAA	CACTGGGGAAC	CTGAGATTCC	AGCCCCCATG	TCAGAGCTGA	CAGAGACTGG
	AAATACTGAC	GTTCCACCTT	GTGACCCCGG	ACCTCCTCGG	CCAAGACTTT	GTGACCCTTG	GACTCTAAGG	TCGGGGGTAC	AGTCTCGACT	GTCTCTGACC
Acidic Leucine Zipper										
Linker										
+1	G G G G S T T A P S A Q L E K E L Q A L E K E N A Q L E W E L Q A L									
1101	AGGTGGAGGA	TCCACTACAG	CTCCATCAGC	TCAGCTCGAA	AAAGAGCTCC	AGGCCCTGGA	GAAGGAAAAT	GCACAGCTGG	AATGGGAGTT	GCAAGCACTG
	TCCACCTCCT	AGGTGATGTC	GAGGTAGTCG	AGTCGAGCTT	TTTCTCGAGG	TCCGGGACCT	CTTCTTTTAA	CGTGTCGACC	TTACCTCTAA	CGTTCTGTAC
linker										
Acidic Leucine Zipper										
+1	E K E L A Q G G S G G S G L N D I F E A Q K I E W H E *									
1201	GAAAAGGAAC	TGGCTCAGGG	CGGCAGCGGC	GGCAGCGGCC	TGAACGATAT	TTTTGAAGCG	CAGAAAATTG	AATGGCATGA	ATGACTCGAC	CTGCAGGCAT
	CTTTCTCTTG	ACCGAGTCCC	GCCGTCGCCG	CCGTGCGCCG	ACTTGCTATA	AAAACCTTCG	GTCTTTTAA	TTACCGTACT	TACTGAGCTG	GACGTCGCTA
SbfI ADH poly A										

	ADH poly A										
1301	GCAAGCTATT CGTTTCGATAA	CGATGCACAC GCTACGTGTG	TCACATTCTT AGTGTAAAGAA	CTCCTAATAC GAGGATTATG	GATAATAAAA CTATTATTTT	CTTTCCATGA GAAAGGTACT	AAAATATGGA TTTTATACCT	AAAATATATG TTTTATATAC	AAAATTGAGA TTTTAACTCT	AATCCAAAAA TTAGGTTTTT	
	ADH poly A										
	Pacl										
1401	ACTGATAAAC TGACTATTTG	GCTCTACTTA CGAGATGAAT	ATTAAAAATAG TAATTTTATC	ATAAATGGGA TATTTACCCT	GCGGCAGGAA CGCCGTCCTT	TGGCGGAGCA ACCGCCTCGT	TGGCCAAGTT ACCGGTTCAA	CCTCCGCCAA GGAGGCGGTT	TCAGTCGTAA AGTCAGCATT	AACAGAAGTC TTGTCTTCAG	
	ADH poly A										
1501	GTGGAAAGCG CACCTTTCGC	GATAGAAAGA CTATCTTTCT	ATGTTTCGATT TACAAGCTAA	TGACGGGCAA ACTGCCCGTT	GCATGTCTGC CGTACAGACG	TATGTGGCGG ATACACCGCC	ATTGCGGAGG TAACGCCTCC	AATTGCAC TG TTAACGTGAC	GAGACCAGCA CTCTGGTCGT	AGGTTCTCAT TCCAAGAGTA	
	Spe mutatioir										
	ADH poly A										
1601	GACCAAGAAT CTGGTTCTTA	ATAGCGGTGA TATCGCCACT	GTGAGCGGGA CACTCGCCCT	AGCTCGGTTT TCGAGCCAAA	CTGTCCAGAT GACAGGTCTA	CGAACTCAAA GCTTGAGTTT	ACTTGTCGAG TGAACAGGTC	CCAGTCGCTG GGTCAGCGAC	TCGAAACTAA AGCTTTGATT	TTAAGTTAAT AATTC AATTA	
	ADH poly A										
1701	GAGTTTTTCA CTCAAAAAGT	TGTTAGTTTC ACAATCAAAAG	GCGCTGAGCA CGCGACTCGT	ACAATTAAGT TGTTAATTCA	TTATGTTTCA AATACAAAGT	GTTTCGGCTTA CAAGCCGAAT	GATTTTCGCTG CTAAAGCGAC	AAGGACTTGC TTCCTGAACG	CAC TTTCAAT GTGAAAAGTTA	CAATACTTTA GTTATGAAAT	
	ADH poly A										
1801	GAACAAAATC CTTGTTTTAG	AAAAC TCA TT TTTTGAGTAA	CTAATAGCTT GATTATCGAA	GGTGTTTCATC CCACAAGTAG	TTTTTTTTTA AAAAAAAAT	ATGATAAGCA TACTATTCTG	TTTTGTGCTT AAAACAGCAA	TATACTTTTT ATATGAAAAA	ATATTTTCGAT TATAAAGCTA	ATTAAACCAC TAATTTGGTG	
	ADH poly A										
1901	CTATGAAGTC GATACTTCAG	TATTTTAATC ATAAAATTAG	GCCAGATAAG CGGTCTATT C	CAATATATTG GTTATATAAC	TGTAAATATT ACATTTATAA	TGTATTCCTT ACATAAGAAA	ATCAGGAAAT TAGTCCTTTA	TCAGGGAGAC AGTCCCTCTG	GGGGAAGTTA CCCCTTCAAT	CTATCTACTA GATAGATGAT	
	ADH poly A					ALPHA					
	ADH poly A					pUC 18					
	Xbal										
2001	AAAGCCAAAC TTTCGTTTTG	AATTTCTTAC TTAAGAATG	AGTTTTACTC TCAAAATGAG	TCTCTACTCT AGAGATGAGA	AGAGTAGCTT TCTCATCGAA	GGCACTGGCC CCGTGACCCG	GTCGTTTTAC CAGCAAAATG	AACGTCGTGA TTGCAGCACT	CTGGGAAAA C GACCTTTTTG	CCTGGCGTTA GGACCGCAAT	
	ALPHA					pUC 18					
	pUC 18										
2101	CCCAACTTAA GGGTGAATT	TCGCCTTGCA AGCGGAACGT	GCACATCCCC CGTG TAGGGG	CTTTCGCCAG GAAAGCGGTC	CTGGCGTAAT GACCGCATTA	AGCGAAGAGG TCGCTTCTCC	CCCGCACCGA GGGCGTGGCT	TCGCCCTTCC AGCGGGAAGG	CAACAGTTGC GTTGTCAACG	GCAGCCTGAA CGTCGGACTT	
	ALPHA					pUC 18					
	pUC 18										
	NarI KasI										
2201	TGGCGAATGG ACCGCTTACC	CGCCTGATGC GCGGACTACG	GGTATTTTCT CCATAAAAGA	CCTTACGCAT GGAATGCGTA	CTGTGCGGTA GACACGCCAT	TTTCACACCG AAAGTGTGGC	CATATGGTGC GTATACCACG	ACTCTCAGTA TGAGAGTCAT	CAATCTGCTC GTTAGACGAG	TGATGCCGCA ACTACGGCGT	
	pUC 18										
2301	TAGTTAAGCC ATCAATTCGG	AGCCCCGACA TCGGGGCTGT	CCCGCCAACA GGCGGTTGT	CCCGCTGACG GGGCGACTGC	CGCCCTGACG GCGGGACTGC	GGCTTGTCTG CCGAACAGAC	CTCCCGGCAT GAGGGCCGTA	CCGCTTACAG GGCGAATGTC	ACAAGCTGTG TGTTTCGACAC	ACCGTCTCCG TGGCAGAGGC	
	pUC 18										
2401	GGAGCTGCAT CCTCGACGTA	GTGTCAGAGG CACAGTCTCC	TTTTCAACGT AAAAGTGCCA	CATCACCAGAA GTAAGTGCTT	ACGCGCAGAGA TGCGCCTCT	CGAAAGGGCC GCTTTCGCCG	TCGTGATACG AGCACTATGC	CCTATTTTTA GGATAAAAA T	TAGGTTAATG ATCCAATTAC	TCATGATAAT AGTACTATTA	
	pUC 18										
	Zral AatII										
2501	AATGGTTTCT TTACCAAGA	TAGACGTCAG ATCTGCAGTC	GTGGCACTTT CACCGTGAAA	TCGGGGAAAT AGCCCCCTTA	GTGCGCGGAA CACGCGCTT	CCCTATTTTG GGGGATAAAC	TTTATTTTTT AAATAAAAA G	TAAATACATT ATTTATGTAA	CAAATATGTA GTTTATACAT	TCCGCTCATG AGGCAGTAGC	
	pUC 18										
	P(BLA)					APr					
2601	AGACAATAAC TCTGTTATTG	CCTGATAAAT GGACTATTTA	GCTTCAATAA CGAAGTTATT	TATTGAAAAA ATAACTTTTT	GGAAGAGTAT CCTTCTCATA	GAGTATTCAA CTCATAAGTT	CATTTCCGTG GTAAAGGCAC	TCGCCCTTAT AGCGGGAATA	TCCCTTTTTT AGGGAAAAAA	GCGGCATTTT CGCCGTAAAA	

pUC 18											
APr											
2701	GCCTTCCTGT	TTTTGCTCAC	CCAGAAACGC	TGGTGAAAGT	AAAAGATGCT	GAAGATCAGT	TGGGTGCACG	AGTGGGTTAC	ATCGAACTGG	ATCTCAACAG	
	CGGAAGGACA	AAAACGAGTG	GGTCTTTGCG	ACCACTTTCA	TTTTCTACGA	CTTCTAGTCA	ACCCACGTGC	TCACCCAATG	TAGCTTGACC	TAGAGTTGTC	
pUC 18											
APr											
2801	CGGTAAGATC	CTTGAGAGTT	TTGCCCCGA	AGAACGTTTT	CCAATGATGA	GCACTTTTAA	AGTTCTGCTA	TGTGGCGCGG	TATTATCCCG	TATTGACGCC	
	GCCATTCTAG	GAACCTCTCA	AAGCGGGGCT	TCTTGCAAAA	GTTTACTACT	CGTGAAAATT	TCAAGACGAT	ACACCGCGCC	ATAATAGGGC	ATAACTGCGG	
pUC 18											
APr											
2901	GGGCAAGAGC	AACTCGGTCG	CCGCATACAC	TATTCTCAGA	ATGACTTGTT	Scal TGAGTACTCA	CCAGTCACAG	AAAAGCATCT	TACGGATGGC	ATGACAGTAA	
	CCC GTTCTCG	TTGAGCCAGC	GGCGTATGTG	ATAAGAGTCT	TACTGAACCA	ACTCATGAGT	GGTCAGTGTC	TTTTCGTAGA	ATGCCTACCG	TACTGTCATT	
pUC 18											
APr											
3001	GAGAATTATG	CAGTGCTGCC	ATAACCATGA	GTGATAACAC	TGCGGCCAAC	TTACTTCTGA	CAACGATCGG	AGGACCGAAG	GAGCTAACCG	CTTTTTTGCA	
	CTCTTAATAC	GTCACGACGG	TATTGGTACT	CACTATTGTG	ACGCCGGTTG	AATGAAGACT	GTTGCTAGCC	TCCTGGCTTC	CTCGATTGGC	GAAAAACGT	
pUC 18											
APr											
3101	CAACATGGGG	GATCATGTAA	CTCGCCTTGA	TCGTTGGGAA	CCGAGCTGA	ATGAAGCCAT	ACCAAACGAC	GAGCGTGACA	CCACGATGCC	TGTAGCAATG	
	GTTGTACCCC	CTAGTACATT	GAGCGGAACT	AGCAACCCCT	GGCTCGACT	TACTTCGGTA	TGGTTTGCTG	CTCGCACTGT	GGTGCTACGG	ACATCGTTAC	
pUC 18											
APr											
3201	GCAACAACGT	TGCGCAAAC	ATTAACGTGC	GAACACTTTA	CTCTAGCTTC	CCGGCAACAA	TTAATAGACT	GGATGGAGGC	GGATAAAGTT	CGAGGACCAC	
	CGTTGTTGCA	ACGCGTTTGA	TAATTGACCG	CTTGATGAAT	GAGATCGAAG	GGCCGTTGTT	AATTATCTGA	CCTACCTCCG	CCTATTTCAA	CGTCTG6TG	
pUC 18											
APr											
3301	TTCTGCGCTC	GGCCCTTCCG	GCTGGCTGGT	TTATTGCTGA	TAAATCTGGA	GCCGGTGAGC	GTGGGTCTCG	CGGTATCATT	GCAGCACTGG	GGCCAGATGG	
	AAGACGCGAG	CCGGGAAGGC	CGACCGACCA	AATAACGACT	ATTTAGACCT	CGGCCACTCG	CACCCAGAGC	GCCATAGTAA	CGTCGTGACC	CCGGTCTACC	
pUC 18											
APr											
3401	TAGCCCTCC	CGTATCGTAG	TTATCTACAC	GACGGGGAGT	CAGGCAACTA	TGGATGAACG	AAATAGACAG	ATCGCTGAGA	TAGGTGCCCTC	ACTGATTAAG	
	ATTCGGGAGG	GCATAGCATC	AATAGATGTG	CTGCCCTCTA	GTCCGTGTAT	ACCTACTTGC	TTTATCTGTC	TAGCGACTCT	ATCCACGGAG	TGACTAATTC	
pUC 18											
APr											
3501	CATTGGTAAC	TGTCAGACCA	AGTTTACTCA	TATATACTTT	AGATTGATT	AAAACCTCAT	TTTTAATTTA	AAAGGATCTA	GGTGAAGATC	CTTTTTGATA	
	GTAACCATTG	ACAGTCTGGT	TCAAATGAGT	ATATATGAAA	TCTAACTAAA	TTTTGAAGTA	AAAATTAAAT	TTTCCTAGAT	CCACTTCTAG	GAAAACTAT	
pUC 18											
3601	ATCTCATGAC	CAAAATCCCT	TAACGTGAGT	TTTCGTTCCTA	CTGAGCGTCA	GACCCCGTAG	AAAAGATCAA	AGGATCTTCT	TGAGATCCTT	TTTTTCTGCG	
	TAGAGTACTG	GTTT TAGGGA	ATTGCACTCA	AAAGCAAGGT	GACTCGCAGT	CTGGGGCATC	TTTCTAGTT	TCCTAGAAGA	ACTCTAGGAA	AAAAAGACGC	
pUC 18											
3701	CGTAATCTGC	TGCTTGCAAA	CAAAAAAACC	ACCGCTACCA	GCGGTGGTTT	GTTTGCCGGA	TCAAGAGCTA	CCAACCTTTT	TTCCGAAGGT	AACTGGCTTC	
	GCATTAGACG	ACGAACGTTT	GTTTTTTTGG	TGGCGATGGT	CGCCACCAAA	CAAACGGCCT	AGTTCTCGAT	GGTTGAGAAA	AAGGCTTCCA	TTGACCGAAG	
mutation?											
pUC 18											
3801	AGCAGAGCGC	AGATACCAAA	TACTGTTCTT	CTAGTGTAGC	CGTAGTTAGG	CCACCACTTC	AAGAACTCTG	TAGCACCGCC	TACATACCTC	GCTCTGCTAA	
	TCGTCTCGCG	TCTATGTTT	ATGACAAGAA	GATCACATCG	GCATCAATCG	GGTGGTGAAG	TTCTTGAGAC	ATCGTGCGGG	ATGTATGGAG	CGAGACGATT	
pUC 18											
3901	TCCTGTTACC	AGTGGCTGCT	GCCAGTGCGG	ATAAGTCGTG	TCTTACCGGG	TTGGACTCAA	GACGATAGTT	ACCGGATAAG	GCGCAGCGGT	CGGGCTGAAC	
	AGGACAATGG	TCACCGACGA	CGGTCAACCG	TATTGAGCAC	AGAATGGCCC	AACCTGAGTT	CTGCTATCAA	TGGCCTATTG	CGCGTCGCCA	GCCCACATTG	
pUC 18											
4001	GGGGGGTTTG	TGCACACAGC	CCAGCTTGGA	GCGAACGACC	TACACCGAAC	TGAGATACCT	ACAGCGTGAG	CTATGAGAAA	GCGCCACGCT	TCCCGAAGGG	
	CCCCCAAGC	ACGTGTGTGC	GGTCGAACCT	CGTTGTGCTG	ATGTGGCTTG	ACTCTATGGA	TGTCGCACTC	GATACTCTTT	CGCGGTGCGA	AGGGCTTCCC	
pUC 18											
4101	AGAAAGGCGG	ACAGGTATCC	GGTAAGCGGC	AGGGTCGGAA	CAGGAGAGCG	CACGAGGGAG	CTTCCAGGGG	GAAACGCCTG	GTATCTTTAT	AGTCCTGTGC	
	TCITTCGCC	TGTCCATAGG	CCATTGCGCG	TCCAGGCCCT	GTCTCTCGC	GTGCTCCCTC	GAAGGTCCCC	CTTTCGCGAC	CATAGAAAAA	TCAGGACAGC	

pUC 18

ORI
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4201 GGTTTCGCCA CCTCTGACTT GAGCGTCGAT TTTTGTGATG CTCGTACAGG GGGCGGAGCC TATGGAAAA CGCCAGCAAC GCGGCCTTTT TACGGTTCCT
CCAAAGCGGT GGAGACTGAA CTCGCAGCTA AAAACACTAC GAGCAGTCCC CCCGCCTCGG ATACCTTTTT GCGGTCGTTG CGCCGGAAAA ATGCCAAGGA

pUC 18

4301 GGCCTTTTGC TGGCCTTTTG CTCACATGTT CTTTCCTGCG TTATCCCCTG ATTCTGTGGA TAACCGTATT ACCGCCTTTG AGTGAGCTGA TACCGCTCGC
CCGGAAAAAC ACCGGAAAAAC GAGGTACAA GAAAGGACGC AATAGGGGAC TAAGACACCT ATTGGCATAA TGGCGGAAAC TCACTCGACT ATGGCGAGCG

pUC 18

4401 CGCAGCCGAA CGACCGAGCG CAGCGAGTCA GTGAGCGAGG AAGCGGAAGA GCGCCCAATA CGCAAACCGC CTCTCCCCGC GCGTTGGCCG ATTCATTAAT
GCGTCGGCTT GCTGGCTCGC GTCGCTCAGT CACTCGCTCC TTCGCCCTCT CGCGGGTTAT GCGTTTGGCG GAGAGGGGCG CGCAACCGGC TAAGTAATTA

pUC 18

4501 GCAGCTGGCA CGACAGGTTT CCCGACTGGA AAGCGGGCAG TGAGCGCAAC GCAATTAATG TGAGTTAGCT CACTCATTAG GCACCCAGG CTTTACACTT
CGTCGACCGT GCTGTCCAAA GGGCTGACCT TTCGCCCGTC ACTCGCGTTG CGTTAATTAC ACTCAATCGA GTGAGTAATC CGTGGGGTCC GAAATGTGAA

pUC 18

P(LAC)
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4601 TATGCTTCG GCTCGTATGT TGTGTGGAAT TGTGAGCGGA TAACAATTC ACACAGGAAA CAGCTATGAC
ATACGAAGGC CGAGCATACA ACACACCTTA AACTCGCCT ATTGTTAAAG TGTGTCCTTT GTCGATACTG