





pT2/Onc2.0

1	CCATTCGCCA	TTCAGGCTGC	GCAACTGTTG	GGAAGGGCGA	TCGGTGCGGG	CCTCTTCGCT	ATTACGCCAG	CTGGCGAAAAG	GGGGATGTGC	TGCAAGGCGA	
	GGTAAGCGGT	AAGTCCGACG	CGTTGACAAC	CCTTCCCGCT	AGCCACGCCC	GGAGAAGCGA	TAATGCGGTC	GACCGCTTTC	CCCCTACACG	ACGTTCCGCT	
								T7		BamHI	
101	TTAAGTTGGG	TAACGCCAGG	GTTTTCCCAG	TCACGACGTT	GTA AACGAC	GGCCAGTGAG	CGCGCGTAAT	ACGACTCACT	ATAGGGCGAA	TTGGAGCTCG	
	AATTCAACCC	ATTGCGGTCC	CAAAAGGGTC	AGTGCTGCAA	CATTTTGCTG	CCGGTCACTC	GCGCGCATT	TGCTGAGTGA	TATCCCGCTT	AACCTCGAGC	
			T2/Onc2 genotype 1 primer								
201	GATCCCTATA	CAGTTGAAGT	CGGAAGTTTA	CATACACTTA	AGTTGGAGTC	ATTAAAACTC	GTTTTTCAAC	TACTCCACAA	ATTTCTTGTT	AACAAACAAT	
	CTAGGGATAT	GTCAACTTCA	GCCTTCAAAT	GTATGTGAAT	TCAACCTCAG	TAATTTTGAG	CAAAAAGTTG	ATGAGGTGTT	TAAAGAACAA	TTGTTTGTTA	
											IR/DR(L) Lmut44
301	AGTTTTGGCA	AGTCAGTTAG	GACATCTACT	TTGTGCATGA	CACAAGTCAT	TTTTCCAACA	ATTGTTTACA	GACAGATTAT	TTCACTTATA	ATTTCACTGTA	
	TCAAAACCGT	TCAGTCAATC	CTGTAGATGA	AACACGTA	CTGTTCAGTA	AAAAGGTTGT	TAACAAATGT	CTGTCTAATA	AAGTGAATAT	TAAGTGACAT	
											IR/DR(L) Lmut44
											T2/Onc2 genotype 2 prim
401	TCACAATTCC	AGTGGGTCAG	AAGTTTACAT	ACACTAAGTT	GACTGTGCCT	TTAAACAGCT	TGGA AAAATTC	CAGAAAATGA	TGTCATGGCT	TTAGAAGCTT	
	AGTGTTAAGG	TCACCCAGTC	TTCAAATGTA	TGTGATTCAA	CTGACACGGA	AATTTGTCGA	ACCTTTTAAG	GTCTTTTACT	ACAGTACCGA	AATCTTCGAA	
											IR/DR(L) Lmut44
											splice acceptor
501	GATGGCCGCT	CTAGAACTAG	GATTGCAGCA	CGAAACAGGA	AGCTGACTCC	ACATGGTCAC	ATGCTCACTG	AAGTGTGAC	TTCCCTGACA	GCTGTGCACT	
	CTACCGGCGA	GATCTTGATC	CTAACGTCGT	GCTTTGTCCT	TCGACTGAGG	TGTACCAGTG	TACGAGTGAC	TTCACAACTG	AAGGGACTGT	CGACACGTGA	
											splice acceptor
601	TTCTAAACCG	GTTTTCTCAT	TCATTTACAG	TTCAGCCGAT	GATGAAATTG	CCGCACTGGT	TGTTAGCAAC	GTAGCCGGTA	TGTGAAAGAT	GGATTGCGGG	
	AAGATTTGGC	CAAAAGAGTA	AGTAAATGTC	AAGTCGGCTA	CTACTTTAAC	GGCGTGACCA	ACAATCGTTG	CATCGGCCAT	ACACTTTCTA	CCTAAGCGCC	
											exon
701	GAATTTAGTG	GATCCCCCGG	GCTGCAGGAA	TTGATCTGTA	AGCCTATAGA	GTACGAGCCA	TAGATAAAAT	AAAAGATTTT	ATTTAGTCTC	CAGAAAAAGG	
	CTTAAATCAC	CTAGGGGGCC	CGACGTCCTT	AAGCTAGACT	TCGGATATCT	CATGCTCGGT	ATCTATTTTA	TTTTCTAAAA	TAAATCAGAG	GTCTTTTTC	
											MSCV 5'LTR
801	GGGGAATGAA	AGACCCAC	TGTAGGTTTG	GCAAGCTAGC	TTAAGTAACG	CCATTTTGCA	AGGCATGGAA	AATACATAAC	TGAGAATAGA	GAAGTTCAGA	
	CCCCTTACTT	TCTGGGGTGG	ACATCCAAAC	CGTTCGATCG	AATTCATTGC	GGTAAAACGT	TCCGTACCTT	TTATGTATTG	ACTCTTATCT	CTTCAAGTCT	

MSCV 5'LTR										
901	TCAAGGTTAG	GAACAGAGAG	ACAGCAGAAAT	ATGGGCCCCAA	CAGGATATCT	GTGGTAAGCA	GTTCTTGCCC	CGGCTCAGGG	CCAAGAACAG	ATGGTCCCCA
	AGTTCCAATC	CTTGTCCTC	TGTCGTCTTA	TACCCGGTTT	GTCTATATAGA	CACCATTCGT	CAAGGACGGG	GCCGAGTCCC	GGTTCTTGTC	TACCAGGGGT
MSCV 5'LTR										
			Bfal							
1001	GATGCGGTCC	CGCCCTCAGC	AGTTTCTAGA	GAACCATCAG	ATGTTTCCAG	GGTGCCCCAA	GGACCTGAAA	ATGACCCTGT	GCCTTATTTG	AACTAACCAA
	CTACGCCAGG	GCGGGAGTCG	TCAAAGATCT	CTTGGTAGTC	TACAAAGGTC	CCACGGGGTT	CCTGGACTTT	TACTGGGACA	CGGAATAAAC	TTGATTGGTT
MSCV 5'LTR										
1101	TCAGTTCGCT	TCTCGCTTCT	GTTTCGCGCG	TTCTGCTCCC	CGAGCTCAAT	AAAAGAGCCC	ACAACCCCTC	ACTCGGCGCG	CCAGTCCTCC	GATAGACTGC
	AGTCAAGCGA	AGAGCGAAGA	CAAGCGCGCG	AAGACGAGGG	GCTCGAGTTA	TTTTCTCGGG	TGTTGGGGAG	TGAGCCGCGC	GGTCAGGAGG	CTATCTGACG
MSCV 5'LTR		HindIII	Bfal	splice site		Lun SD				
1201	GTCGCCCATC	AAGCTTGCTA	CTAGCACCAG	AACGCCCGCG	AGGATCTCTC	AGGTAATAAA	GAGCGCCAAG	GCTGGCTGCA	AGCGGAGCCT	CTGAGAGCCT
	CAGCGGGTAG	TTCGAACGAT	GATCGTGGTC	TTGCGGGCGC	TCCTAGAGAG	TCCATTATTT	CTCGCGGTTC	CGACCGACGT	TCGCCTCGGA	GACTCTCGGA
Lun SD										
					Bfal					
1301	CTGAGGGCCA	GGGCTACTGC	ACCCTTGGTC	CTCAACGCTG	GGGTCTTCAG	AACTAGAATG	CTGGGGGTGG	GGTGGGGATT	CGGTTCCCTA	TTCCATCGCG
	GACTCCCGGT	CCCGATGACG	TGGGAACCAG	GAGTTGCGAC	CCCAGAAGTC	TTGATCTTAC	GACCCCCACC	CCACCCCTAA	GCCAAGGGAT	AAGGTAGCGC
			Bfal							
1401	CGTTAAGATA	CATTGATGAG	TTTGACAAA	CCACAACCTAG	AATGCAGTGA	AAAAAATGCT	TTATTTGTGA	AATTTGTGAT	GCTATTGCTT	TATTTGTAAC
	GCAATTCTAT	GTAACCTACTC	AAACCTGTTT	GGTGTTGATC	TTACGTCAC	TTTTTTACGA	AATAAACACT	TTAAACACTA	CGATAACGAA	ATAAACATTG
SV40 polyA										
1501	CATTATAAGC	TGCAATAAAC	AAGTTGGCCG	CTCCTGTGCC	AGACTCTGGC	GCCGCTGCTC	TGTCAGGTAC	CTGTTGGTCT	GAAACTCAGC	CTTGAGCCTC
	GTAATATTCG	ACGTTATTTG	TTCAACCGGC	GAGGACACGG	TCTGAGACCG	CGGCGACGAG	ACAGTCCATG	GACAACCAGA	CTTTGAGTCG	GAAGTCGGAG
SV40 polyA				exon						
										NlaIII
1601	TGGAGCTGCT	CAGCAGTGAA	GGCTGTGCGA	GGCCGCTTGT	CCTCTTTGTT	AGGGTTCTTC	TTCTTTGGTT	TTCGGGACCT	GGGACCTGGT	TGTCATGGAG
	ACCTCGACGA	GTCGTCACTT	CCGACACGCT	CCGGCGAACA	GGAGAAACAA	TCCCAAGAAG	AAGAAACCAA	AAGCCCTGGA	CCCTGGACCA	ACAGTACCTC
exon										En-2 SA
			Bfal				HindIII			
1701	GAGAAAGGGC	AGAGGTTACT	GGTTGCTGGA	GTCTAGCTAC	TTATCCACAA	CCCACGCACC	CAAGCTTGAG	GTTGCAGATA	CTGGGGGTGG	GGGGGGGGGG
	CTCTTTCCCG	TCTCCAATGA	CCAACGACCT	CAGATCGATG	AATAGGTGTT	GGGTGCGTGG	GTTCGAACTC	CAACGTCTAT	GACCCCCACC	CCCCCCCCCC
En-2 SA										

1801	ATGACCCGCC CAAGGCCATA CAAGTGTGG GCATTGGGGG TGGTGATATA AACTTGAGGC TGGGCATGTG CCCACTGACC AGAAGGAAAAG TGGTGTGTGT TACTGGGCGG GTTCCGGTAT GTTCACAACC CGTAACCCCC ACCACTATAT TTGAACCTCC ACCCGTACAC GGGTGACTGG TCTTCCTTC ACCACACACA	NlaIII ~~~~~
En-2 SA		
1901	GTGTGAAAAT GAGATGGATT GGCAGATGTA GCTAAAAGGC CTATCACAAA CTAGGGGATC TAGCTTGTGG AAGGCTACTC GAAATGTTTG ACCCAAGTTA CACACTTTTA CTCTACCTAA CCGTCTACAT CGATTTTCCG GATAGTGTTT GATCCCCTAG ATCGAACACC TTCCGATGAG CTTTACAAAC TGGGTTC AAT	BfaI ~~~~~ BfaI ~~~~~
En-2 SA		
2001	AACAATTTAA AGGCAATGCT ACCAAATACT AATTGAGTGT ATGTAAACTT CTGACCCACT GGAATGTGA TGAAAGAAAT AAAAGCTGAA ATGAATCATT TTGTTAAATT TCCGTTACGA TGGTTTATGA TTAAC TCACA TACATTTGAA GACTGGGTGA CCCTTACACT ACTTCTTTA TTTTCGACTT TACTTAGTAA	IR/DR(R) Rmut13,Æ130,143,150
-3	Gln Thr Tyr Thr Phe Lys Gln Gly Val Pro Phe Thr Ile Phe Ser Ile Phe Ala Ser Ile Phe *** Glu	
2101	CTCTCTACTA TTATTCTGAT ATTTACACATT CTAAAAATAA AGTGGTGATC CTAAC TGACC TAAGACAGGG AATTTTACT AGGATTAAAT GTCAGGAATT GAGAGATGAT AATAAGACTA TAAAGTGTA GAATTTTATT TCACCACTAG GATTGACTGG ATTCTGTCCC TTAAAAATGA TCCTAATTTA CAGTCCTTAA	BfaI ~~~~~
-3	Glu Arg *** *** *** Glu Ser Ile Glu Cys Glu *** Phe Leu Thr Thr Ile Arg Val Ser Arg Leu Cys Pro Ile Lys Val Leu Ile Leu His *** Ser Asn	
2201	GTGAAAAAGT GAGTTTAAAT GTATTTGGCT AAGGTGTATG TAAACTTCCG ACTTCAACTG TATAGGGATC CTCTAGCTAG AGTCGACCTC GAGGGGGGGC CACTTTTTC A CTCAAATTTA CATAAACCGA TTCCACATAC ATTTGAAGGC TGAAGTTGAC ATATCCCTAG GAGATCGATC TCAGCTGGAG CTCCCCCCCCG	TATA ~~~~~ BamHI ~~~~~ BfaI ~~~~~ BfaI ~~~~~
-3	His Phe Leu Ser Asn Leu His Ile Gln Ser Leu His Ile Tyr Val Glu Ser Lys Leu Gln	
2301	CCGGTACCCA GCTTTTGTTC CCTTTAGTGA GGGTTAATTT CGAGCTTGGC GTAATCATGG TCATAGCTGT TTCCTGTGTG AAATTGTTAT CCGCTCACAA GGCCATGGGT CGAAAAAAG GGAAATCACT CCAATTAAA GCTCGAACCG CATTAGTACC AGTATCGACA AAGGACACAC TTTAACAATA GGCGAGTGTT	NlaIII ~~~~~
T3		
2401	TTCCACACAA CATAAGAGCC GGAAGCATAA AGTGTAAGC CTGGGGTGCC TAATGAGTGA GCTAACTCAC ATTAATTGCG TTGCGCTCAC TGCCCGCTTT AAGGTGTGTT GTATGCTCGG CCTTCGTATT TCACATTTTCG GACCCACGG ATTACTCACT CGATTGAGTG TAATTAACGC AACGCGAGTG ACGGGCGAAA	LacZ promoter
LacZ promoter		
2501	CCAGTCGGGA AACCTGTTCGT GCCAGCTGCA TTAATGAATC GGCCAACGCG CGGGGAGAGG CGGTTTGCGT ATTGGGCGCT CTTCCGCTTC CTCGCTCACT GGTCAGCCCT TTGGACAGCA CGGTCGACGT AATTACTTAG CCGGTTGCGC GCCCTCTCC GCCAAACGCA TAACCCGCGA GAAGGCGAAG GAGCGAGTGA	ColE Ori
ColE Ori		
2601	GACTCGCTGC GCTCGGTCGT TCGGCTGCGG CGAGCGGTAT CAGCTCACTC AAAGGCGGTA ATACGGTTAT CCACAGAATC AGGGGATAAC GCAGGAAAGA CTGAGCGACG CGAGCCAGCA AGCCGACGCC GCTCGCCATA GTCGAGTGAG TTTCCGCCAT TATGCCAATA GGTGTCTTAG TCCCTATTG CGTCCTTTCT	

ColE Ori											
	NlaIII										
2701	ACATGTGAGC	AAAAGGCCAG	AAAAAGGCCA	GGAACCGTAA	AAAGGCCGCG	TTGCTGGCGT	TTTTCCATAG	GCTCCGCCCC	CCTGACGAGC	ATCACAAAAA	
	TGTACACTCG	TTTTCCGGTC	GTTTTCCGGT	CCTTGGCATT	TTTCCGGCGC	AACGACCGCA	AAAAGGTATC	CGAGGCGGGG	GGACTGCTCG	TAGTGTTTTT	
ColE Ori											
2801	TCGACGCTCA	AGTCAGAGGT	GGCGAAACCC	GACAGGACTA	TAAAGATACC	AGGCGTTTCC	CCCTGGAAGC	TCCCTCGTGC	GCTCTCCTGT	TCCGACCCTG	
	AGCTGCGAGT	TCAGTCTCCA	CCGCTTTGGG	CTGTCCTGAT	ATTTCTATGG	TCCGCAAAGG	GGGACCTTCG	AGGGAGCACG	CGAGAGGACA	AGGCTGGGAC	
ColE Ori											
2901	CCGCTTACCG	GATACCTGTC	CGCCTTTCTC	CCTTCGGGAA	GCGTGGCGCT	TTCTCATAGC	TCACGCTGTA	GGTATCTCAG	TTCGGTGTAG	GTCGTTCGCT	
	GGCGAATGGC	CTATGGACAG	GCGGAAAGAG	GGAAGCCCTT	CGCACC CGA	AAGAGTATCG	AGTGCGACAT	CCATAGAGTC	AAGCCACATC	CAGCAAGCGA	
ColE Ori											
	ApaI										
3001	CCAAGCTGGG	CTGTGTGCAC	GAACCCCCCG	TTCAGCCCGA	CCGCTGCGCC	TTATCCGGTA	ACTATCGTCT	TGAGTCCAAC	CCGGTAAGAC	ACGACTTATC	
	GGTTCGACCC	GACACACGTG	CTTGGGGGGC	AAGTCGGGCT	GGCGACGCGG	AATAGGCCAT	TGATAGCAGA	ACTCAGGTTG	GGCCATTCTG	TGCTGAATAG	
ColE Ori											
	BfaI										
3101	GCCACTGGCA	GCAGCCACTG	GTAACAGGAT	TAGCAGAGCG	AGGTATGTAG	GCGGTGCTAC	AGAGTTCTTG	AAGTGGTGGC	CTAACTACGG	CTACACTAGA	
	CGGTGACCGT	CGTCGGTGAC	CATTGTCCTA	ATCGTCTCGC	TCCATACATC	CGCCACGATG	TCTCAAGAAC	TTCACCACCG	GATTGATGCC	GATGTGATCT	
ColE Ori											
3201	AGGACAGTAT	TTGGTATCTG	CGCTCTGCTG	AAGCCAGTTA	CCTTCGGAAA	AAGAGTTGGT	AGCTCTTGAT	CCGGCAAACA	AACCACCGCT	GGTAGCGGTG	
	TCCTGTCATA	AACCATAGAC	GCGAGACGAC	TTCGGTCAAT	GGAAGCCTTT	TTCTCAACCA	TCGAGAACTA	GGCCGTTTGT	TTGGTGGCGA	CCATCGCCAC	
ColE Ori											
3301	GTTTTTTTTGT	TTGCAAGCAG	CAGATTACGC	GCAGAAAAAA	AGGATCTCAA	GAAGATCCTT	TGATCTTTTC	TACGGGGTCT	GACGCTCAGT	GGAACGAAAA	
	CAAAAAACA	AACGTTCGTC	GTCTAATGCG	CGTCTTTTTT	TCCTAGAGTT	CTTCTAGGAA	ACTAGAAAAA	ATGCCCCAGA	CTGCGAGTCA	CCTTGCTTTT	
ColE Ori											
	NlaIII										
3401	CTCACGTTAA	GGGATTTTGG	TCATGAGATT	ATCAAAAAGG	ATCTTCACCT	AGATCCTTTT	AAATTAAAAA	TGAAGTTTTA	AATCAATCTA	AAGTATATAT	
	GAGTGCAATT	CCCTAAAACC	AGTACTCTAA	TAGTTTTTCC	TAGAAGTGGA	TCTAGGAAAA	TTTAATTTTT	ACTTCAAAAT	TTAGTTAGAT	TTCATATATA	
	BfaI										
3501	GAGTAACTT	GGTCTGACAG	TTACCAATGC	TTAATCAGTG	AGGCACCTAT	CTCAGCGATC	TGTCTATTTT	GTTTCATCCAT	AGTTGCCTGA	CTCCCCGTCG	
	CTCATTTGAA	CCAGACTGTC	AATGGTTACG	AATTAGTCAC	TCCGTGGATA	GAGTCGCTAG	ACAGATAAAG	CAAGTAGGTA	TCAACGGA	GAGGGGCAGC	
Amp											
3601	TGTAGATAAC	TACGATACGG	GAGGGCTTAC	CATCTGGCCC	CAGTGCTGCA	ATGATACCGC	GAGACCCACG	CTCACC GGCT	CCAGATTTAT	CAGCAATAAA	
	ACATCTATTG	ATGCTATGCC	CTCCGAATG	GTAGACCGGG	GTCACGACGT	TACTATGGCG	CTCTGGGTGC	GAGTGGCCGA	GGTCTAAATA	GTCGTTATTT	
Amp											

3701	CCAGCCAGCC	GGAAGGGCCG	AGCGCAGAA	TGGTCCTGCA	ACTTTATCCG	CCTCCATCCA	GTCTATTAAT	TGTTGCCGGG	^{Bfal} AAGCTAGAGT	AAGTAGTTCG
	GGTCGGTCGG	CCTTCCCGGC	TCGCGTCTTC	ACCAGGACGT	TGAAATAGGC	GGAGGTAGGT	CAGATAATTA	ACAACGGCCC	TTCGATCTCA	TTCATCAAGC
	Amp									
3801	CCAGTTAATA	GTTTGCACAA	CGTTGTTGCC	ATTGCTACAG	GCATCGTGGT	GTCACGCTCG	TCGTTTGGA	TGGCTTCATT	CAGCTCCGGT	TCCCAACGAT
	GGTCAATTAT	CAAACGCGTT	GCAACAACGG	TAACGATGTC	CGTAGCACCA	CAGTGCGAGC	AGCAAACCAT	ACCGAAGTAA	GTCGAGGCCA	AGGGTTGCTA
	Amp									
3901	CAAGGCGAGT	^{NlaIII} TACATGATCC	^{NlaIII} CCCATGTTGT	GCAAAAAAGC	GGTTAGCTCC	TTCGGTCCTC	CGATCGTTGT	CAGAAGTAAG	TTGGCCGCAG	TGTTATCACT
	GTTCCGCTCA	ATGTACTAGG	GGGTACAACA	CGTTTTTTCG	CCAATCGAGG	AAGCCAGGAG	GCTAGCAACA	GTCTTCATT	AACCGGCGTC	ACAATAGTGA
	Amp									
4001	^{NlaIII} CATGGTTATG	GCAGCACTGC	ATAATTCTCT	^{NlaIII} TACTGTCATG	CCATCCGTAA	GATGCTTTTC	TGTGACTGGT	GAGTACTCAA	CCAAGTCATT	CTGAGAATAG
	GTACCAATAC	CGTCGTGACG	TATTAAGAGA	ATGACAGTAC	GGTAGGCATT	CTACGAAAAG	ACACTGACCA	CTCATGAGTT	GGTTCAGTAA	GACTCTTATC
	Amp									
4101	TGTATGCGGC	GACCGAGTTG	CTCTTGCCCG	GCGTCAATAC	GGGATAATAC	CGCGCCACAT	AGCAGAACTT	TAAAAGTGCT	CATCATTGGA	AAACGTTCTT
	ACATACGCCG	CTGGCTCAAC	GAGAACGGGC	CGCAGTTATG	CCCTATTATG	GCGCGGTGTA	TCGTCTTGAA	ATTTTCACGA	GTAGTAACCT	TTTGCAAGAA
	Amp									
4201	CGGGGCGAAA	ACTCTCAAGG	ATCTTACCGC	TGTTGAGATC	CAGTTCGATG	TAACCCACTC	^{ApaI} GTGCACCCAA	CTGATCTTCA	GCATCTTTTA	CTTTCACCAG
	GCCCCGCTTT	TGAGAGTTCC	TAGAATGGCG	ACAACCTCTAG	GTCAGCTAC	ATTGGGTGAG	CACGTGGGTT	GACTAGAAGT	CGTAGAAAAAT	GAAAGTGGTC
	Amp									
4301	CGTTTCTGGG	TGAGCAAAAA	CAGGAAGGCA	AAATGCCGCA	AAAAAGGGAA	TAAGGGCGAC	ACGGAAATGT	TGAATACTCA	TACTCTTCCT	TTTTCAATAT
	GCAAAGACCC	ACTCGTTTTT	GTCCTTCCGT	TTTACGGCGT	TTTTTCCCTT	ATTCCCGCTG	TGCCTTTACA	ACTTATGAGT	ATGAGAAGGA	AAAAGTTATA
	Amp									
4401	TATTGAAGCA	TTTATCAGGG	^{NlaIII} TTATTGTCTC	ATGAGCGGAT	ACATATTTGA	ATGTATTTAG	AAAAATAAAC	AAATAGGGGT	TCCGCGCACA	TTTCCCCGAA
	ATAACTTCGT	AAATAGTCCC	AATAACAGAG	TACTCGCCTA	TGTATAAACT	TACATAAAATC	TTTTTATTTG	TTTATCCCCA	AGGCGCGTGT	AAAGGGGCTT
	F1 Ori									
4501	AAGTGCCACC	TGACGCGCCC	TGTAGCGGCG	CATTAAGCGC	GGCGGGTGTG	GTGGTTACGC	GCAGCGTGAC	CGCTACACTT	^{Bfal} GCCAGCGCCC	TAGCGCCCGC
	TTCACGGTGG	ACTGCGCGGG	ACATCGCCGC	GTAATTTCGCG	CCGCCCCACAC	CACCAATGCG	CGTCGCACTG	GCGATGTGAA	CGGTGCGGGG	ATCGCGGGCG
	F1 Ori									
4601	TCCTTTCGCT	TTCTTCCCTT	CCTTCTCGC	CACGTTGCGC	GGCTTTCCCC	GTCAAGCTCT	AAATCGGGGG	CTCCCTTTAG	GGTTCCGATT	TAGTGCTTTA
	AGGAAAGCGA	AAGAAGGGAA	GGAAAGAGCG	GTGCAAGCGG	CCGAAAGGGG	CAGTTCGAGA	TTAGCCCCC	GAGGGAAATC	CCAAGGCTAA	ATCACGAAAT

F1 Ori

4701 CGGCACCTCG ACCCCAAAAA ACTTGATTAG GGTGATGGTT CACGTAGTGG GCCATCGCCC TGATAGACGG TTTTTCGCCC TTTGACGTTG GAGTCCACGT
GCCGTGGAGC TGGGGTTTTT TGAAC TAATC CCACTACCAA GTGCATCACC CGGTAGCGGG ACTATCTGCC AAAAAGCGGG AAAGTCAAC CTCAGGTGCA

F1 Ori

4801 TCTTTAATAG TGGACTCTTG TTCCAAACTG GAACAACACT CAACCCTATC TCGGTCTATT CTTTGTATT ATAAGGGATT TTGCCGATTT CGGCCTATTG
AGAAATTATC ACCTGAGAAC AAGGTTTGAC CTTGTTGTGA GTTGGGATAG AGCCAGATAA GAAAGTAAA TATTCCTAA AACGGCTAAA GCCGGATAAC

F1 Ori

4901 GTTAAAAAAT GAGCTGATTT AACAAAAATT TAACGCGAAT TTTAACAAAA TATTAACGCT TACAATTT
CAATTTTTTA CTCGACTAAA TTGTTTTTAA ATTGCGCTTA AAATTGTTTT ATAATTGCGA ATGTTAAA
