

SEQUENCE

QUEN	ICE								
1								AAGCGGGCAG TTCGCCCGTC	
101		 						TGTGAGCGGA ACACTCGCCT	
						BamHI	KpnI ~~~~~		
						Sma	aI		
						Xma			
			HindIII	PstI ~~~~~	~	Ava			
201								GCGCGCGCAGT	
301								TAAACTTTGG ATTTGAAACC	
401								ACTTTCGGCG TGAAAGCCGC	
501					-			GTTCTTCGTT CAAGAAGCAA	
601								AGAACCGGCG TCTTGGCCGC	
				HindII			indIII	Pac	
701								CCACTATTAA GGTGATAATT	
	EcoRI								
801								AAGTAATACA TTCATTATGT	
901								ATTAATTACC TAATTAATGG	
1001		 						GCCAATTTTT CGGTTAAAAA	
1101								CGGTGAAGAC GCCACTTCTG	

						SacI						
						Saci	~~~~~ II ~~~~	EcoRI				
1201									GGCCGTCGTT CCGGCAGCAA			
1301	GTGACTGGGA CACTGACCCT								GAGGCCCGCA CTCCGGGCGT			
1401									ACCGCATATA TGGCGTATAT			
1501	CTTGTTACCC GAACAATGGG						-		TAATATATAG ATTATATATC			
1601	TACGGAAGAC ATGCCTTCTG								CGGTTCATTT GCCAAGTAAA			
1701	CATCTTGCAC GTAGAACGTG								GCTAATTTTT CGATTAAAAA			
1801	ATCTGAGCTG TAGACTCGAC							-	TAAAACAAAA ATTTTGTTTT			
1901	AGAGCGCTAA TCTCGCGATT								ACAAAGAATC TGTTTCTTAG			
			AvaI									
2001	TTTTGTTCTA AAAACAAGAT		TCCCGAGAGC						CTCTATAATG GAGATATTAC			
2101									GACTCCACTT CTGAGGTGAA			
2201									CATACTTTGT GTATGAAACA			
2301									AATGTTTACA TTACAAATGT			
2401	GTTTTCGATT	CACTCTATGA	ATAGTTCTTA	CTACAATTTT	TTTGTCTAAA	GAGTAATACT	AGAGATAAAC	ATAAAAAATG		GTTTAGATGC		
2501	AAGTTCAAGG TTCAAGTTCC								CAATGTTTGT GTTACAAACA			
2601									TCAAAAGCGC AGTTTTCGCG			

2701	CTATACTTTC GATATGAAAG						ACGAGCGCTT TGCTCGCGAA			
2801	AGCTCACTGT TCGAGTGACA				-		AGAACGGCAT TCTTGCCGTA			
2901	TATGCGTCTA ATACGCAGAT						CCATGCGGGG GGTACGCCCC			
								ClaI ~~~~~	~	
3001	AGCTGTTCTA TCGACAAGAT						TCCTTTGATA AGGAAACTAT			
3101	ATGAGAATTA TACTCTTAAT						ATGAATTTCA TACTTAAAGT			
3201	AAAAGAGAAT TTTTCTCTTA						TCGGTGGTAC AGCCACCATG			
3301	TACCTGCATC ATGGACGTAG						TCAATGACAA AGTTACTGTT			
3401	GGCGATAGGG CCGCTATCCC						CAAACCAAAT GTTTGGTTTA			
3501	GACGCAGATG CTGCGTCTAC						TCACCAAACA AGTGGTTTGT		-	
3601	GGGTTGGGTT CCCAACCCAA						ATGTAGGAAA TACATCCTTT			
3701	TCTCCATAAT AGAGGTATTA						TGGCTCATGT ACCGAGTACA			
3801	ATTCTTTGCA TAAGAAACGT						TCTTCCTTTC AGAAGGAAAG			
3901	CTCTGACAAC GAGACTGTTG						AAAGAGAGTC TTTCTCTCAG			
4001	GTACAATTGA CATGTTAACT						ACCCCATTTA TGGGGTAAAT			
						ClaI				
4101	TCAACCTTCT AGTTGGAAGA						GCAGCACCAC CGTCGTGGTG			
4201	CATTGGAACG	AACATCAGAA	ATAGCTTTAA	GAACCTTAAT	GGCTTCGGCT	GTGATCTTGA	CCAACGTGGT	CACCTGGCAA	AACGACGATC	TTCTTAGGGG

	GTAACCTTGC	TTGTAGTCTT	TATCGAAATT	CTTGGAATTA	CCGAAGCCGA	CACTAGAACT	GGTTGCACCA	GTGGACCGTT	TTGCTGCTAG	AAGAATCCCC
4301	CAGACATAGG GTCTGTATCC		AGAATGTATA TCTTACATAT							
4401	CACCTATTGG GTGGATAACC		AGGTCCTTAA TCCAGGAATT	_						-
4501	AGCCGGTTCC TCGGCCAAGG		CTTTCCTTTT GAAAGGAAAA							
4601	TCGAATTTGT AGCTTAAACA		GCGCCCCTGT CGCGGGGACA							
4701	TGAGTATTCC ACTCATAAGG		TCTTGAAGAC AGAACTTCTG							
4801	TGGCACTTTT ACCGTGAAAA		TGCGCGGAAC ACGCGCCTTG				_			
4901	CTTCAATAAT GAAGTTATTA		GAAGAGTATG CTTCTCATAC							
					ApaLI					
5001	CAGAAACGCT GTCTTTGCGA		AAAGATGCTG TTTCTACGAC							
5101	TCGCCCCGAA AGCGGGGCTT		CAATGATGAG GTTACTACTC							
5201	CGCATACACT GCGTATGTGA		TGACTTGGTT ACTGAACCAA							
5301	TAACCATGAG ATTGGTACTC		GCGGCCAACT CGCCGGTTGA							
5401	TCGCCTTGAT AGCGGAACTA		CGGAGCTGAA GCCTCGACTT							
5501	TTAACTGGCG AATTGACCGC		TCTAGCTTCC AGATCGAAGG							
5601	CTGGCTGGTT GACCGACCAA		AAATCTGGAG TTTAGACCTC							
5701			AGGCAACTAT TCCGTTGATA							
5801	GTTTACTCAT	ATATACTTTA	GATTGATTTA	AAACTTCATT	TTTAATTTAA	AAGGATCTAG	GTGAAGATCC	TTTTTGATAA	TCTCATGACC	AAAATCCCTT

	CAAATGAGTA	TATATGAAAT	CTAACTAAAT	TTTGAAGTAA	AAATTAAATT	TTCCTAGATC	CACTTCTAGG	AAAAACTATT	AGAGTACTGG	TTTTAGGGAA
5901		TTCGTTCCAC AAGCAAGGTG								
6001		CCGCTACCAG GGCGATGGTC								
6101		TAGTGTAGCC ATCACATCGG								
									Apa	aLI
6201		TAAGTCGTGT ATTCAGCACA							GGGGGTTCGT	GCACACAGCC
6301		CGAACGACCT GCTTGCTGGA								
6401		GGGTCGGAAC CCCAGCCTTG								
6501		TTTGTGATGC AAACACTACG								
6601		TTTCCTGCGT AAAGGACGCA								
6701		TGAGCGAGGA ACTCGCTCCT								