Sem mutação:

tctgcgtcgaaatgtcaaggaaagttgcaagtctgtgattttgtgtttggttttttgcatgttgcttctatggaaaaa
caaaacaacaacagcagacctccctgcccaaagtgttaaaatgcctccttcataacctgagacttactttcattttc
tagGTGCTGGAGAATCTGGTAAAAGCACCATTGTGAAGCA**GAT**GAGGATCCTGCATGT
TAATGGGTTTAATGGAGAgtaagtgtcaaatctgtgcaggggggcaccaagtaagaggaacagacttt
atactaacctttaggaagtataggtgggctttgggggctgggcagccagttttcacttaattttcctgatttacata
ttagaaaatcctgggaagggctctttagggtccctcacc

Name	Sequence	Site Length	Overhang	Frequency	Cut Positions
BsaBI	GATNNNNATC	6	blunt	1	200
OliI	CACNNNNGTG	6	blunt	1	185
AvaII	GGWCC	5	five_prime	1	388
BamHI	GGATCC	6	five_prime	1	201
BbvI	GCAGC	5	five_prime	1	335
BseYI	CCCAGC	6	five_prime	1	318
BsmAI	GTCTC	5	five_prime	1	131
DraII	RGGNCCY	6	five_prime	1	388
EcoP15I	CAGCAG	6	five_prime	1	120
EcoRII	CCWGG	5	five_prime	1	368
PpuMI	RGGWCCY	7	five_prime	1	388
SanDI	GGGWCCC	7	five_prime	1	388
TfiI	GAWTC	5	five_prime	1	167
TseI	GCWGC	5	five_prime	1	323
XhoII	RGATCY	6	five_prime	1	201
BseMII	CTCAG	5	three_prime	1	126
BseSI	GKGCMC	6	three_prime	1	259
BsgI	GTGCAG	6	three_prime	1	268
BsrI	ACTGG	5	three_prime	1	327
Eco57MI	CTGRAG	6	three_prime	1	183
GsuI	CTGGAG	6	three_prime	1	183

Name	Sequence	Site Length	Overhang	Frequency	Cut Positions
HphI	GGTGA	5	three_prime	1	386
Hpy99I	CGWCG	5	three_prime	1	9
MslI	CAYNNNNRTG	6	blunt	2	185, 213
BsaXI	ACNNNNNCTCC	6	three_prime	2	219, 249
Hin4I	GAYNNNNNVTC	6	three_prime	2	221, 253
NspI	RCATGY	6	three_prime	2	61, 212
SduI	GDGCHC	6	three_prime	2	259, 381
TspDTI	ATGAA	5	three_prime	2	117, 137
TstI	CACNNNNNNTCC	6	three_prime	2	219, 251

Com mutação:

tctgcgtcgaaatgtcaaggaaagttgcaagtctgtgattttgtgtttggttttttgcatgttgcttctatggaaaaa
caaaacaacaacagcagacctccctgcccaaagtgttaaaatgcctccttcataacctgagacttactttcattttc
tagGTGCTGGAGAATCTGGTAAAAGCACCATTGTGAAGCAGGTGAGGATCCTGCATGT
TAATGGGTTTAATGGAGAgtaagtgtcaaatctgtgcaggggggcaccaagtaagaggaacagacttt
atactaacctttaggaagtataggtgggctttgggggctgggcagccagttttcacttaattttttcctgatttacata
ttagaaaatcctgggaagggctctttagggtccctcacc

Name	Sequence	Site Length	Overhang	Frequency	Cut Positions
OliI	CACNNNNGTG	6	blunt	1	185
AarI	CACCTGC	7	five_prime	1	184
AvaII	GGWCC	5	five_prime	1	388
BamHI	GGATCC	6	five_prime	1	201
BbvI	GCAGC	5	five_prime	1	335
BseYI	CCCAGC	6	five_prime	1	318
BsmAI	GTCTC	5	five_prime	1	131
BspMI	ACCTGC	6	five_prime	1	184
DraII	RGGNCCY	6	five_prime	1	388

Name	Sequence	Site Length	Overhang	Frequency	Cut Positions
EcoP15I	CAGCAG	6	five_prime	1	120
EcoRII	CCWGG	5	five_prime	1	368
PpuMI	RGGWCCY	7	five_prime	1	388
SanDI	GGGWCCC	7	five_prime	1	388
TfiI	GAWTC	5	five_prime	1	167
TseI	GCWGC	5	five_prime	1	323
XhoII	RGATCY	6	five_prime	1	201
BseMII	CTCAG	5	three_prime	1	126
BseSI	GKGCMC	6	three_prime	1	259
BsgI	GTGCAG	6	three_prime	1	268
BsrI	ACTGG	5	three_prime	1	327
Eco57MI	CTGRAG	6	three_prime	1	183
GsuI	CTGGAG	6	three_prime	1	183
Hpy99I	CGWCG	5	three_prime	1	9
MslI	CAYNNNNRTG	6	blunt	2	185, 213
BsaXI	ACNNNNNCTCC	6	three_prime	2	219, 249
Hin4I	GAYNNNNNVTC	6	three_prime	2	221, 253
HphI	GGTGA	5	three_prime	2	208, 386
NspI	RCATGY	6	three_prime	2	61, 212
SduI	GDGCHC	6	three_prime	2	259, 381
TspDTI	ATGAA	5	three_prime	2	117, 137
TstI	CACNNNNNNTCC	6	three_prime	2	219, 251