

L13218.1	1	GGAAGGAGUGCCAGGCCAUUACCUUCCGCCCCUGCCUAAACAAAACUGGCUCGCCAGAGGCGGGGGGCGUGGUAGACGGUAUGUCUAGGUCCAGAGAAAGCGGCCGUGUUAGGCUGCUA
AF525216.1	1C.....UA.....U.....A..C..G
DQ238861.1	1C.....UA.....U.....A..C..G
CAT	1A.....A.....A.....A.....
HP	1A.....UA.....C.....A.....G
P2MER	1A.....G.....UA.....C.....A.....G
J1710_A	1A.....UA.....A.....G
L13218.1	121	GACUUCGCCACGCUUACACCAUUGAGAACACAUAGGUGGUGUAAUUAUUGUGUUUGGCUGCGUGUGUCACGAGCACGAUCUAUGGGGGAAUCUAACCCAGGUGGUGUUGUGUAUGAUGA
AF525216.1	121C.....A.....C.C...A.....A.
DQ238861.1	121C.....A.....C.C...A.....A.
CAT	121C.....
HP	121C.....A.....C.....A.
P2MER	121C.....A.....C.....A.
J1710_A	121C.....A.....C.....A.
L13218.1	241	GGUACAAGCCCGUCAACACCACAGGUGGAGAGGACAGGAGUCUAAUUCCCCUCCAAAAACAGCAGUGGUCGCCCCUCAUGCCCUAUGAAACAUUAGGGGGCCGACACUAGUGGGCA
AF525216.1	241C.....U.G.....G.....
DQ238861.1	241C.....U.G.....G.....
CAT	241C.....CUUU.....G.....
HP	241C.....U.G.....G.....
P2MER	241C.....U.G.....G.....
JA1710_A	241C.....U.G.....G.....
L13218.1	361	AGCCCCAUGGUGUGGGGGACUGGAUAUGGGAACCCAGUCCGUUAAACCCGUACGGCUUCGCCAGCCUACACCGGGGGGGCUUAAUCCCCUUAUU
AF525216.1	361A.....UUGGCACCUGAAAAUUAUACU
DQ238861.1	361A.....UUU.....C.....
CAT	361C.....
HP	361A.....UGA.....
P2MER	361A.....UGA.....
J1710_A	361A.....UGA.....Y.....
L13218.1	478	UUUGACACUUUAAACACACACAAUGAUCACGAGGAGACCCAUGGAGAGUCUCCAGAGGUUCCUAAGGCCUCGAUCGCGCCUGCCGGGAGGCAGAAUGUCCCGGUUCUCCAACAAAUAUCAA
AF525216.1	478G.....G.....C.....U.C.....A..
DQ238861.1	481G.....G.....C.....U.C.....A..
CAT	478	C.....U.....G.....C.....CU.....C.....
HP	479G.....G.....C.....U.C.....
P2MER	479G.....G.....C.....U.C.....
J1710_A	479	...C.....G.....G.....C.....U.C.....
L13218.1	598	GAAAACGAAGAUAAUACACGCGCUGGGCGGUAGCGAGGACGCCAAAGAUGAGCGCGAAAUACGAUUCUCAGCCAUA AAAACUCUCUACAAUUAUUAUCUACAGAGGGUCCUUCGACCCCAAUU
AF525216.1	598C.....C.....AG..U...U.....A.....U.....
DQ238861.1	601C.....C.....AG..U...U..U.....A.....U.....
CAT	598A.....C.....G.....
HP	599Y.....C.....C.....AG.CU...U.....A.....
P2MER	599G.....C.....C.....AG..U...U.....C.....A.....
J1710_A	599U.....Y.....C.....C.....AG.CU...U.....A.....

First cytosine insertion and premature CP ORF stop

L13218.1	718	AUGCCGCAUUUAGUUAACAGGUUACGUGGAUUAGAUGCCCUUGCCAAGAUAGACGCGACGCGUACCAAGGUGGAUAUGAACGCGGCCUACAUAUUCGCCUGAGACCGACUUUCCGUAU
AF525216.1	718A.....C.....A.....U..A.....G.....G.....C.....
DQ238861.1	721A.....C.....A.....U..A.....G.....G.....C.....
CAT	718C.....A.....U..A.....G.....G.....
HP	719A.....C.....A.....U..A.....G.....G..... R
P2MER	719A.....C.....A.....U..A..U..G.....G.....
J1710_A	719A.....C.....A.....U..A.....G.....G.....A.....
L13218.1	838	UCGUUAUGGUAUAAACAGCGCUUCAGUAACAGGAGAUUAACCACUAGUGCGCUUUGCUACGCAAGGACGGGCUAUCCCUCAUUUCUGACCGUCGACAAAACGUACACAUCUAACUCUCCA
AF525216.1	838A..U.....G.....A..C.....A.....G..C.....
DQ238861.1	841A..U...C.....G..G.....A..C.....A.....G..C.....
CAT	838G.....G.....C.....A.....C.....
HP	839A..U.....G.....A..C.....A.....G..C.....
P2MER	839A..U.....G.....A..C.....A.....G..C.....
J1710_A	839A..U.....G..... VA..C.....A.....G..C.....
L13218.1	958	UAAAAAGGGGGCUCUAGAGGGUGGCCCAUUUUAACGUGGAUGUUUCAUCACACGUGGCGGAGCCUCACAUGAGGACAUUGUCACCUAUCGGUCUUGAAGUAUUCAAUCUGGCUCACGUCU
AF525216.1	958U...A..A..G.....GC.....U...
DQ238861.1	961U...A..A..G.....GC.....U...
CAT	958A..G.....GC.....C.....G.....
HP	959 R ..A..G.....GC.....U...
P2MER	959	...G.....A..G.....GC.....U...
J1710_A	959 VT..A..G.....GC..... RU...
L13218.1	1078	CAAUUUUCGAAAACUCUAUUAACUGCAUCAUCGAAAGUCUUCACGCAAUCGCUCUACACUGCUGACAUACUAUCGAUCUUUGGUGAGGUGUUCUGCCACACGUGAUGCAACCGGUCUCA
AF525216.1	1078	..G.....G..A.....
DQ238861.1	1081	..G.....G..A.....
CAT	1078	..G.....G..A.....
HP	1079	..G.....A.....
P2MER	1079	..G.....A.....U.....T.....
J1710_A	1079	..G.....A.....
L13218.1	1198	AACUACACUCCAAUACUUGUGAGGGCACUAUUGGCCUUGAUCCACAUACUGGGGCCAGGAUCUGGUAUUGCUCACUUUCAUCGUCUAUCUUCGAGAGCUCAAUCCACAAUCCUACG
AF525216.1	1198G.....A.....U.....U.....U..A...
DQ238861.1	1201C.....G.....U.....U.....U..A...
CAT	1198G.....U.....U.....
HP	1199G VU.....U.....U..A...
P2MER	1199G.....U.....C.....U.....U..A...
J1710_A	1199GU.....U.....U.....U..A...
L13218.1	1318	GUAAGUCAUAGUACGAACAUGUCGAAUAGAACGAGGUACUGCUUACAUACGAGGUCUGCUUACAAGGAUAUGUUCAGGAACGGUAUCCCACCUCAGUCGACGUUGCCACCGACGCUCGCG
AF525216.1	1318	A....C.....A.....C.....AU.....A.....U.....
DQ238861.1	1321	A....C.....A.....C.....AU.....A..U.....C.....U.....
CAT	1318A.....C.....C..AU...C.....A..U.....
HP	1319	A....C.....A.....C.....AU.....A.....U.....
P2MER	1319	A....C.....A.....C.....AU.....A.....U.....
J1710_A	1319	A....C.....A.....C.....AU.....A.....U.....

L13218.1	1438	CCGGAGGGGUCCUCUGCUCGGGUUUUAAUCCAGAGGCCCUAGUGACCAGCCCUAUGUUUCCAUGGUUACUUUAGUCUCGAGCGGCCACAGUUCUUCUUGUAUUCAAAGGACGCU
AF525216.1	1438	..A.....A.C.....C.....G.A.....
DQ238861.1	1441	..A.....A.C.....C.....G.A.....
CAT	1438	..A.....C.....C...G.....U.....C.....GC.....
HP	1439	..A.....A.C.....C ^R ...G.....U.....C.....G.A.....
P2MER	1439	..A.....A.C.....C...G.....U.....C.....G.A.....
J1710_A	1439	..A..... ^M ...A.C.....CA...G.....U.....C.....U.A.....
L13218.1	1558	AGUAUUAAUACCGUAGACAUCGGUUCGAGGGGGAGGAUUACAUCACCAAUCCUGACGUCGCCAAGCUUGAUCUCCACAGACUCUGGAAUCUCUCCGUUUUGAUGGUUACCGCUACAC
AF525216.1	1558C.....U.....C.C.....U...
DQ238861.1	1561U.....C.C.....U...
CAT	1558G.....U.....C.....C.....
HP	1559C.C.....U...
P2MER	1559U.....U.....C.C.....U...
J1710_A	1559C.C.....U...
L13218.1	1678	GACGUGGUCAUAGUGGGCGCGGAUAGAGAUUACGUGUGGCCCUAUCAAAAUGGCGUGUAUGUACACGGCGGCAAGGGACCCAAUGGUACUGGCAACUACGGGAACGCUGACGUUCAUGAC
AF525216.1	1678UA.G.....U.....U.....A.....A.....A.....U.....C...
DQ238861.1	1681UA.G.....U.....U.....A.....A.....A.....U.....C...
CAT	1678U.U.....A.....U.....A.....
HP	1679U.....U.....U.....A.....A.....A.....U.....C...
P2MER	1679U.....U.....U.....A.....A.....U.....C...
J1710_A	1679U.....U.....U.....A.....AA.....A.....U.....C...
L13218.1	1798	GGAAUAGGGACGAUAAUUUCGUCUUUACAACAAGUUAACGUGCAAACGUGCCGACCUC AUGCUGGGCCUAUUGACCCUGUGGAACCACAUAAACGACUACGUACGCUACUGAGGAGGAG
AF525216.1	1798C..U..U.....C..A..U..C.....U.....G.....
DQ238861.1	1801C..U..U.....C..A..U..C.....U.....G.....
CAT	1798C..U..G.....U.....UU.....U.....
HP	1799C..U.....U.....A..U..C.....
P2MER	1799C..U..G.....U.....A..U..C.....
JA1710_A	1799C..U..... ^RU.....A..U..C.....
L13218.1	1918	GUCACCAUGGCGAUAAAGAUUGCAGCGGCUUUUGCCCUUGUCUACCCAGUACAGCCUUAUUGUCUACUCCGGUUGCCCCGAAAGCUUUUCAGAGACACACGUCUACUACCAGCCCUCAUCG
AF525216.1	1918	..U.....U..C..UU..GC.....U.AU.....U.U.....
DQ238861.1	1921	..U.....U..C..UU..GC.....U.AU.....U.U.....
CAT	1918C.....GG..C.....U.....U.....
HP	1919	..U.....U..C..U..GG..C..U.U.AU.....U.....
P2MER	1919	..U.....U..C.....GG..C..U.U.AU.....U.....
J1710_A	1919	..U.....U..C..U..GG..C..U.U.AU.....U.....
L13218.1	2038	GAGAACUGCUACGCAACCGACACGGCUGAAGUCAAGAGCGUGUGGGAUACGGUCGAGCUUAGCGUACAGGUUAAUAACGCUAUGGUACUAGGUUAGACACUACCGUUUGGCCAACCUACA
AF525216.1	2038A.....U.....G.....AC.....U.....CG.....
DQ238861.1	2041A.....U.....G.....AC.....U.....C.....CG.....
CAT	2038A.G.....U.....G.....AC.....U.....C.....
HP	2039A.....G.....AC.....U.....C.....
P2MER	2039A.....G.....AC.....U.....C.....A.....
J1710_A	2039A.....G.....AC.....U.....C.....

Second cytosine insertion and CP ORF frame shift

L13218.1	2878	AUAUGGGAUCCUACACAGGAAAGACACGC	ACAGGUUUCGUGUACACAUACUUUAGCCCCAAUUUCCUUUCGAGCUUUAAACGUGUCUGAGCCUAUAUUCAAUACGAGUAUCAACCUUACA
AF525216.1	2878G.....G.....C.....C.C.A.GCC.....
DQ238861.1	2881G.....G.....C.U.....C.C.A.GCC.....
CAT	2878G.....GU.....C.....C.....
HP	2879G.....G.....C.....C.A..CC.....
P2MER	2879G.....G.....C.....C.A..CC.....
J1710_A	2879G.....G.....C.....C.A..CC.....

CP ORF stop codon (Wang et al., 1993)

L13218.1	2997	CCACCUUAUGACGACACGAGCCAAGCUGAA	UUCAAAAUUUGUCCAUGCCACAGAUAGCUCAGCUUCGAUCCCUACUACGAGUCUACGUUCUAUGUGGUCUCCGCGGAUAACGAGUGGAUA
AF525216.1	2997C..U.....A.....
DQ238861.1	3000	...G...C..U.....A.....
CAT	2998C..C..U.....C.CA.....
HP	2999C..U.....A.....G..
P2MER	2999C..U.....A.....G..
J1710_A	2999C..U.....A.....G..

Uracil insertion

Alternative +1/-2 ribosomal frameshift

L13218.1	3117	CCGACUUCAGGGCCUGCUUGGAAGGUACCAUAUCUGGAAAACGUAGUUAAGCGGUCUGGCAGGCGCUUGCUGGCGGAGCUCAGGAUAGCAUCCAAUAACGGGUCUGGAGACCGUACCUU	-
AF525216.1	3117C.....	-
DQ238861.1	3120C.....	-
CAT	3118C.....C....G.....	CUUU
HP	3119C.....C.....	CUUU
P2MER	3119C.....C.....T.....C.....	CUUU
J1710_A	3119C.....C.....	CUUU

New CP ORF stop codon

L13218.1	3236	CUUGACGACGUGUAAGACAAGAAAGGGGAAGGCAUUUUACCUACUUCUCUGCUGCUUUGGGGGGCAAGAUCUGGAAUUCGUAUGCGCUCCACUGUCGAGUAUCAGUCUCCAGGGCGGGCA
AF525216.1	3236A.....A.G...U.....
DQ238861.1	3239A.....A.G...U.....
CAT	3238	CUUG.....UAA.....A.G...U.....A.....
HP	3239	CUUG.....UAA.....A.G...U.....E.....
P2MER	3239	CUUG.....UAA.....A.....C.A.G...U.....
J1710_A	3239	CUUG.....UAA.....A.....A.G...U.....A.....

L13218.1	3356	AACGAUCUACGCUCCGAUUCAGCUCCAAGACGUAUACCAAGUACGUAAGAGGAUCCAGUGCCAGGGAGCAUAUAUGCAGUCUUUAAGUUCUUCAGAACCAAGGCCUGGGAGGCACG
AF525216.1	3356C.....G...A.....C.....U.....U.....AU...
DQ238861.1	3359G...A.....C.....U.....U.....AU...
CAT	3358	..A.....C.....C...G.....C.....C...C..U.....G.....
HP	3359C.....G...A.....C.....U.....U.....A...
P2MER	3359C.....A.....A.....C.....U.....U.....
J1710_A	3359C.....G...A.....C.....U.....U.....U.....A...

L13218.1	3476	UGCGCUUAAGUCCUACAAAGUCAGGUUCCAAGAUCCCAAGCCACAUAGUGAUUAGUGAGUUGAAAGAGAGAGCGGGCAGAGAAGCUAUAUCGGGUCGAGGGGUUAUGUCGAUACAGGUUU
AF525216.1	3476	..A.....U.....C.A.....U.....
DQ238861.1	3479	..A.....U.....C.A.....U.....
CAT	3478	...UC.....A.....C.....
HP	3479	..A.....U.....C.A.....U.....
P2MER	3479U.....C.A.....U.....
J1710_A	3479	..A.....U.....C.A.....U.....

L13218.1	3596	UAAGGCUUUGGACAUUUAUUAAGAUAUUCUUUCCCAAUUGGAGCUGCCAAAGUACAUAACACGAGUUCUAAUUUUUACUCAGAGGCAAGGUGUGUGAAGUCUCGAGGUUGUACAAGAAGGA
AF525216.1	3596G.....U.....
DQ238861.1	3599G.....A..G.....U.....
CAT	3598U.....U.....AG.....U.....G.....
HP	3599G.....U.....
P2MER	3599G..C.....U.....
J1710_A	3599G.....U.....
L13218.1	3716	ACAGGUAAUUCGUAAAUUUACUAAACCGUAUUCUCUGAGCUCACAGCCAUAGUCCGCCAUAGAGGUAAACAAGUCCACGGGGUCGAUGGGGAGGAUGUGGACUUUGUUAUCAGACUUCGAGAC
AF525216.1	3716A.....C.....U.....
DQ238861.1	3719A.....C.....U.....U.....
CAT	3718U.....C.....C.....A.....
HP	3719C.....U.....
P2MER	3719C.....U.....
J1710_A	3719C.....U.....
L13218.1	3836	CUUGCUUGGGAAGGUGAGCUAUAAAGAACCCGAGUAUCAUUGAGGAGCAGGUUGUUCCUGGCUAACCUCAGACCCUAUACCACGUACCCCGACUUCUACUCUACAUAUUUCAAGACGGC
AF525216.1	3836	.C.....U.....U.....G.....U.....
DQ238861.1	3839	.C.....G.....U.....U.....G.....U.....
CAT	3838	.C.....A.....G.....
HP	3839	.C.....U.....U.....G.....
P2MER	3839	.C.....C.....U.....U.....G.....
J1710_A	3839	.C.....U.....U.....G.....
L13218.1	3956	UGUCCAGUUUAUGCACAGGACAUUCGUUCCCGUCACUCUCAGAAGUGCCCCUCCGUUAAACAUUUCACGAGUACUGUGGGAGGCCGAGCUCUGGGGAACCACGGGAUCCGGCUACAUCGG
AF525216.1	3956	G..U.....U.....U.....C.....U.....
DQ238861.1	3959	G..U.....C.....U.....U.....C.....U.....
CAT	3958	G.....U.....U.....CU.....U.....
HP	3959	G..U.....U.....C.....
P2MER	3959	G..U.....U.....C.....
J1710_A	3959	G..U.....U.....C.....
L13218.1	4076	CUAUGGCAAGCGUAGUUUUAACAAAUGGUCGAUCUACGGAGCUUAUCCUACCGAGGAGAUUUUACGGCUAGCACUCUAUGGAGAUAAUCCACCCCUCAAGCCGCUGGAAAAACCCGAACU
AF525216.1	4076C.....C.....C.....
DQ238861.1	4079C.....C.....C.....
CAT	4078C.....C.....CU..G.....U.....
HP	4079C.....C.....G.....CU..G.....U.....
P2MER	4079	..C.....C.....C.....G.....CU..G.....U.....
J1710_A	4079C.....C.....G.....CU..G.....U.....
L13218.1	4196	UACGAAGGUACGUGCUGUAAUCUCCGCCUCCCUCCAUCGUAUAUAUUGAUGUCUUACCUCGAGUACAUCAUGGCAGACACCAUAGUUGACAAAGCAUUCACUACAACUCUGAUGAACGA
AF525216.1	4196C.....C.....C.....U.....
DQ238861.1	4199UU.....C.....C.....U.....
CAT	4198UU.....C.....A.....A.....
HP	4199UU.....C.....C.....
P2MER	4199UU.....C.....C.....
J1710_A	4199UU.....C.....C.....

L13218.1	4316	CAGGCAGCUAGAGAACCUUGAGCGCCACAUGAUGACCAUGACCGGAGGAGUCAGGGUUCAGUGGACCAGUCCAUUUUUAUCGCCAGCCUGACUUGGUCCAAAUAGGCAUCUGGCAACA
AF525216.1	4316U.....U.....
DQ238861.1	4319UAU.....G.....U.....
CAT	4318
HP	4319U..... MC.....
P2MER	4319U.....C.....C.....
J1710_A	4319U.....U.....C.....
L13218.1	4436	GUUACUGUUUACACUGGCAUCUGCGUCAGCUCCGUACAGAGCCCGCGACAGUGUCUCAUUAGUCAUAUCACGUUUAGCUUACUACGACUUUCCCAAACCUAAAGGUACGGAUGUCGGA
AF525216.1	4436A.....A.....C.....G.....C.....C.....C.....G.....
DQ238861.1	4439A.....A.....C.....G.....C.....C.....C.....G.....
CAT	4438C.....A.....C.....C.....AG.....C.....U.....A.....C.....G.....A.....
HP	4439A.....C.....G.....C.....C.....C.....G.....
P2MER	4439A.....C.....G.....C.....C.....C.....G.....
J1710_A	4439A..... KC.....G.....C.....C.....G.....
L13218.1	4556	CGGUGACAAACGUGUGCUACACGGCCUCCCCUCGGGGUGGAAGUGGACCGCUCUGCUAGGGGCUCAUCAUCAAUGUGACACAAUUUAACCAUGGCGGAAUUGUCCAACACUCUGGCCUC
AF525216.1	4556U.....U.....G.....C.....
DQ238861.1	4559U.....G.....U.....G.....C.....
CAT	4558A.....U.....
HP	4559U.....C.....A.....
P2MER	4559U.....T.....C.....A.....
J1710_A	4559U.....C.....A.....
L13218.1	4676	GUUGAGGUCAACGGUGGUGCAGGGCGACGAUAUCGCUCUAAGUAUGACUGACCGGGAGCAGGCCACACAGUUAGUUGACACUUAUGCACGUCAGGGGUUCGAGGUCAACCCGAAGAAGUU
AF525216.1	4676A.....A.....
DQ238861.1	4679A.....A.....C.....G.....
CAT	4678G.....
HP	4679A.....G.....A.....
P2MER	4679A.....A.....G.....A.....
J1710_A	4679A.....G.....A.....
L13218.1	4796	CUGGAUAUCACCCGACCGGGACGAAUUCUUCGGAGGGUAGCAACCCCUUGGUUAUAGUCGCGGGGUACCCAGCUAGAAUGAUGAUUAAAUUGUUAUAUCAGCUGACGGAACCUGAAGAGCC
AF525216.1	4796C.....U.....
DQ238861.1	4799C.....U.....
CAT	4798C.....A.....A.....
HP	4799C.....
P2MER	4799C.....
J1710_A	4799C.....
L13218.1	4916	CUCACACUACAUCUCCAUGUUGCCAAAGUUAGCGAAGGUGCCUAACGUGGUCCAGGAGCAUGUAAAGCCCCGGUCUGAUGUGCCAUGGUCGGAGACCGUCGAAGAACUUGAUUGGCGCGCA
AF525216.1	4916C.....A.....G.....U.....GC.....
DQ238861.1	4919C.....A.....G.....U.....GC.....
CAT	4918	U.....C.....C.....G.....U.....GC.....
HP	4919C.....A.....G.....U.....GC.....
P2MER	4919C.....A.....G.....U.....GC.....
J1710_A	4919C.....A.....G.....U.....GC.....

L13218.1	5036	AGCUCUCGCUAUACUGAGGCAUAGGCCUGCCCGUACGUCAGAACUGGUGACUCAAUGGCUGCAACUGAUUGGUAGGUUUACAGCUGCUCAUCCAGAUAAAGCGAGCCUUAACUCUUCUCUA
AF525216.1	5036A.....U.....U..
DQ238861.1	5039A.....U.....U..
CAT	5038C.....C.....U..
HP	5039U..C.....U..
P2MER	5039U.....U.....U..
J1710_A	5039R.....U..C.....U..
L13218.1	5156	CCGUUGGUUCGUGAGAGAUUUGACACAUGCUACAAAAUAAAAAAAAAGAAUUCUUCUGGUCCUGUUACAGCAGCCGGGCUUCUGGGGGGUUAUUCCAGAGCCUGGUUGGCUGUUUAAAG
AF525216.1	5156	..A.....C.....G.....A.....
DQ238861.1	5159	..A.....C.....G.....A.....
CAT	5158A.....
HP	5159	..A.....A.....A.....
P2MER	5159	..A.....A.....A.....
J1710_A	5159	..A.....A.....A.....
L13218.1	5276	GACCACUCACCUCGCGAGAUUGAUAGUUAGCGAACUAGACAUAGGACUGCCAGGUCCUGGGCCACGUCUAGUCGCUUUGGGACAUCCCCUACCUCACUGGCCCCGCACUACCUCACUCU
AF525216.1	5276A.....U.....
DQ238861.1	5279A.....U.....
CAT	5278U..G.....
HP	5279G.....U.....
P2MER	5279G.....U.....
J1710_A	5279G.....U.....
L13218.1	5396	GAUAGUUCGAGUAGCGUGCAUGUGCAGUCGCAAAAGGAAUUGGAUUUGUGGGGGCUGUGCAGAUCCAGUAAAUAUGCUAAGCACUAUUAACAUAUUUCGAUACUACAAACUGACUCU
AF525216.1	5396C.....U.....
DQ238861.1	5399C.....U.....
CAT	5398C.....A.....C.....
HP	5399C.....U.....
P2MER	5399C.....C.....
J1710_A	5399C.....U.....
L13218.1	5516	UCCUACGUUGGUGCUUUGGGCCCAACGGCUAGGUGAUAAACACGUCACCGAUUUCAUUAAGAUUCUGUCACCCUGGGUUCAGAAAUACCAAAUAUGACCCGCAUGCGCGUCUAUUCACAAG
AF525216.1	5516A.....
DQ238861.1	5519A.....
CAT	5518	C.....C.....C.....A.....
HP	5519A.....
P2MER	5519A.....
J1710_A	5519R.....A.....
L13218.1	5636	UAACGGGGUGUCAGUAGGAAUGUUAUAAGGAUAAGAGUACGACAUUUUACCCACAGAGUGCUUCGAAGAGAGACACCUAAGUGUAUCCCCGUAAUCGUCGGGCUAUAUCGGGAGCAGAC
AF525216.1	5636C.....
DQ238861.1	5639C.....C.....
CAT	5638C.....
HP	5639C.....
P2MER	5639C.....
J1710_A	5639C.....

L13218.1	5756	ACUAUCCGUUCCGAGAGUGUUCGUCUAUCGGAACCGACAAAAUACUUAUUAAGCCUACAACGGGCGUCGGGUUACUCACUGAAUCUAGUUAAGAAGAUUUACAGAUACUAGGAAACC
AF525216.1	5756G.....C.....G.....
DQ238861.1	5759G.....C.....G.....
CAT	5758G.....C.....G.....G.....
HP	5759G.....C.....G.....
P2MER	5759G.....C.....G.....
J1710_A	5759G.....C.....G.....

L13218.1	5876	AGUGGACCAUCCGGUGGACGCGAGGUUCUCACAGGCAUCCCCAACAACUGGAGCGACUUGGCUAGAACGGCUGGCACCUUUUUGUUGACUGUACCGGCUUAGGAGGUUUCAGGAGACAA
AF525216.1	5876A.....
DQ238861.1	5879A.....A.....
CAT	5878U.....U.....
HP	5879A.....
P2MER	5879U.....A.....
J1710_A	5879A.....

L13218.1	5996	UGCUGACCUUGUGCCUGAGCGUUUGGGCUUCAACCAUAGCAGCUGGCCUUCACGCAAUUUUUAGGUCAAGGAAAUUUCUCCUUUGCGUAGUAGCAUAGCUGUUCAAAGAAAGAAAAAGAAA
AF525216.1	5996	...AG....CG.....C.....G.....C.....AG....
DQ238861.1	5999	...AG....CG.....C.....G.....C.....AG....
CAT	5997	...G....CG.....C.....C.....AG....
HP	5998	...G....CG.....C.....G.....C.....AG....
P2MER	5998	...G....CG.....C.....G.....C.....AG....
J1710_A	5998	...G....CG.....C.....G.....C.....AG....

GA (AA) deletion

L13218.1	6116	UACUGGUAAUUACCGCACACGAUCGGUGGGUCGACCAGCAUAGGGUGGUGUGCGGUUCGAGAACGGGGCUGGCCUUAGUACCGUCAUAACACCGUGACACGUGUAGAAACUGUCCCCCCU
AF525216.1	6112	...A.....U.....G.....C.....A.....U.....
DQ238861.1	6115	...A.....U.....G.....C.....C.....A.....G.....G.....G.....
CAT	6115	...A.....G.....U.....C.....
HP	6114	...A.....U.....G.....
P2MER	6114	...A.....U.....G.....U.....
J1710_A	6114	...A.....U.....G.....

L13218.1	6236	GUAGACUCCGUUGCCUGUAGGAGGCAGCGUACGAGGGGUCG
AF525216.1	6232G.....
DQ238861.1	6235
CAT	6235
HP	6234
P2MER	6234
J1710_A	6234