

L1.LtrB-ΔLtrA+LtrA

Gene name		5' flanking		additional nts	3' flanking	
		EBS2 GUGUA	EBS1 GUGUUG	EBS2 GUGUA	EBS1 GUGUUG	
Cam resistance (pLE-P ₂₃ ² -LtrA)	(2)	AAA CUCAAA UACAGC	/UUUUAGAACUGGU-----	UACAAU UAGCGAC GG	/AGAGUUAGGUUAUU	
Cam resistance (pLE-P ₂₃ ² -LtrA)	(2)	AAAC CUCAAA UACAGC	/UUUUAGAACUGGU-----	UACAAU UAGCGAC G	/GAGAGUUAGGUUAUU	
Cam resistance (pLE-P ₂₃ ² -LtrA)	(1)	UAUUC CAUG ACUUC	/AUUUACUGG-----	GUUUA CUUAAA	/UAUCAUUAUUUAUAG	
Cam resistance (pLE-P ₂₃ ² -LtrA)	(1)	GCC CACUU UACAAU	/UUUUAGAUGGUGUAUC-----	UAA ACAAU UCUCUGG	/UAUUUGGACUCCUGU	
Unknown (pLE-P ₂₃ ² -LtrA)	(8)	CAA GACACA CACACC	/AAAAAUCAAAAUUCC-17-CC ACGUA CCACAAG	/AACUAAUCCAAUCCA		
Unknown (pLE-P ₂₃ ² -LtrA)	(1)	CAAG GACACA CACACC	/AAAAUCA-----	AAAAU UCACUAC	/UUUUAGUUAAAAACC	
Unknown (pDL-P ₂₃ ² -L1.LtrB-ΔLtrA)	(2)	AUG CGCAA ACCAACC	/CUUGGCAGAACAUUAUC-16-UCC AGCAG CCGCACG	/CGGCGCAUCUCGGGC		
Unknown (pDL-P ₂₃ ² -L1.LtrB-ΔLtrA)	(1)	AUG CGCAA ACCAACC	/CUUGGCAGAACAUUAUC-12-CAUC CCAGC AGCCG	/C ACG CGGCGCAUCUC		
Unknown (pDL-P ₂₃ ² -L1.LtrB-ΔLtrA)	(1)	AUG CGCAA ACCAACC	/CUUGGCAGAA-----	CAUAU CCAUCGC	/GUCCGCCAUCUCCAG	
<i>ltrB</i> EI (pDL-P ₂₃ ² -L1.LtrB-ΔLtrA)	(1)	UAC ACAAA CACAAU	/AUUGUUCAUAAAUU-----	AAA ACAAU UAGCC AG	/GCAAAAGACUAUGUA	
Glucose-6 phosphate isomerase	(1)	AUA CACUU UACAAA	/UGUUAUGAAAAUGAU-13-CUG CACUU CGCAAU	/UCCUUUACCGUAAAAG		
Glucose-6 phosphate synthetase	(1)	AGC CACUU UACAAA	/GUUAAUUGGAGCUGGU-23-AAA AGCUA CACUGa	/UCAGAUUGCAACUUU		
Glucose-6 phosphate synthetase	(1)	AGC GACUU UACAAU	/GUUAAUUGGAGCUGGU-23-AAA AGCUA CACUGa	/UCAGAUUGCAACUUU		
Glucose-6 phosphate synthetase	(1)	AGC GACUU UACAAU	/GUUAAUUGGAGCUGGU-24-AA AGCUA ACUGGU	/CAGAUUGCAACUUUG		
Uncharacterized protein	(1)	AAG CACA AGCACAAG	/CACAAUUGA-----	UAGCU UGCAAU CA	/AAAGUUGCAGCUGUA	
Uncharacterized protein	(1)	AAG CACA AGCACAAG	/CACAAUUGA-----	UAGCU UGCAAU C	/AAAAGUUGCAGCUGU	
Beta-lactamase	(1)	CUC CAACA ACAGAU	/GUGGAUACAAAAAAU--21-AGCC AGUA AGUGCA	/AGUCCCUUUUAUGAU		
Permease/transporter (DMU)	(1)	UUA CACAU CAUUC	/UUGCCACUUUUAA-----	AG ACAAU UCUCCAC	/UAAAUGUCGUCGCUU	
Glutamine synthetase	(1)	UC UACUU UACAAU	/GCGGUUAAAGCCUUUGC--5-GA CACA UUGUAACG	/GAAGCACUGGGCGAA		
Glutamine synthetase	(1)	CAU CACA ACCCAAC	/AGUUAAUCU-----	UACAA GUUUG /GU	/UCCUGGCUAUGAA	
Cation transport ATPase	(1)	GUU CAAAU UACAAA	/AUUUUUUCAAACU-----	UGGUU UACAAACG	/AAUAAAUAUGUUUUG	
Ribosomal protein L4	(1)	ACU UGACUU UUGCAGC	/UCCAAAACUGCUGAA-16-C CGCAU UUCAAU CG	/AACGUAAAAGUACUUG		
Ribosomal protein L21	(1)	AAA ACACU UCACACC	/GUAAACAAGGUCACC---GUC ACCA UACACUAA	/AGUUGUUUAUCAAUUC		
Glyceraldehyde-3P dehydrogenase	(3)	AAAGUCA UACACUUC	/AAA CCUUGUUCGU -----	ACACU UGCAUACU	/UCGCUAAAAUUCGCUA	
Glycerol uptake facilitator	(5)	CA CACGU UGCACAAU	/ACAUAUUGCGCAAG-546-CAU CACUUG CAGCCG	/UGCAUUAUUUAAAA		
Glycerol uptake facilitator	(2)	CA CACGU UGCACAAU	/ACAUAUUGCGCAAG-546-CAU CACUUG CAGCCa	/UUGCAUUAUUUAAAA		
Uncharacterized protein	(1)	GG AAACUA UACAAAC	/UCAGGAUUUACAGA-475-CAA UACAU UUGCAACa	/AGGAUAUGUUUUAACA		
Alanyl-tRNA synthetase (<i>alaS</i>)	(2)	ACUCACU UACUUCAU	/GCU GCUUUGCAUAAU -274-GAA CACA UACGCAAA	/CAACUUCUGAAAUUG		
Ser/Thr protein kinase	(1)	AGG AAAAU CGCAAU	/ACAAUUCUCAAACUA-211-ACA ACAA AGCACAAC	/CGUUGCGAAGGUAA		
Ser/Thr protein kinase	(1)	A ACAA UACAUCAAC	/CAAAAUGCUCUCCUA-166-CUU CACUU UACUCAA	/CAAAUACAAUGUUUG		
Ser/Thr protein kinase/phos	(1)	AAA CACA AGCAGAG	/AGGUUAGUUGAUGAU-371-UGGC UACUU UACAUG	/GAUUUUUACCCGUG		
Ribosomal protein L19	(1)	UCA ACGCU CGCAAC	/UUCGCACUGAUUUC-173-CAGUU CACAG UCCAC	/GUGUUGAAAAAUUCG		
Ribosomal protein S3	(1)	AAA CAAGU GCACAU	/AACAUUGGUUAAAUC-242-AGA AGCA ACACAAC	/UUUUGGUAACUCGG		
Ribosomal protein L13/S9	(2)	ACU CACAU CACUUC	/ACCCAGGUGGAUUGA-202-ACA UUAUG UACAAG	/UACAAUAUGCCGGCA		
Ribosomal protein L13	(1)	ACC AAACAU CACACC	/ACAUGCUGAUACAGG-236-A CACAC UACAGCUC	/AAAACCUGAAGUCC		
2',3'-cyclic phosphodiesterase	(1)	ACA CACUU CACAAA	/AAAGAUCAGAUUAG-253-CUU CACAU UACUGG	/UGAGGAACUUCGGCA		
Enolase (<i>enoA</i>)	(1)	UUC CACUU UACAACU	/ACCUUGCGGAUUA-137-GAA AAUCU UCCAGCa	/CUUUAAGAAAAUUCUU		
DNA gyrase	(1)	UCU CUUCU CACAAAC	/ACGCAACGGAAUUGU-160-GCC AUUGU UCGGAU	/AUGGGCCGUGCUGCA		

Figure S2. mRNA fragments identified at the splice junction of L1.LtrB-ΔLtrA+LtrA circles. Additional nts are shown along with their flanking sequences (5' flanking) (3' flanking), their origin (Gene name) and frequency of identification between parentheses. The junctions between the additional nts and their flanking regions (/) as well as the IBS1- (yellow) and IBS2- (green) like sequences are denoted. Some IBS1/2-like sequences were adjusted to optimize their potential base pairing with the EBS1/2 sequences of the intron. The number of nts separating the IBS1/2-like sequences was fixed between 0-2 nts, and their maximum distance from the junction with the intron was fixed between -14, +4 nts. The bolded nts represent residues from the IBS1- and IBS2-like sequences that can potentially base pair with the intron's EBS1 and EBS2 sequences specified above. Sequences spanning two genes and including a short intergenic region are underlined. The genes in bold (*alaS* and *enoA*) were further studied for L1.LtrB reverse splicing analyses and the detection of E1-mRNA and mRNA-mRNA chimeras (Figure 7).