**Ll.LtrB-EBS1/Mut-ΔLtrA+LtrA**

| Gene name | | 5′ flanking | additional nts | 3′ flanking |
|---|---|---|---|---|
| | | EBS2 EBS1 | EBS2 EBS1 | |
| | | **GUGUA** **CACAAC** | **GUGUA** **CACAAC** | |
| Threonine dehydrogenase | (2) | AAC**CA**GC**U**A**GUGUUG**/ACAUGGCAAAAUUAG | -132- | UUGA**U**A**A**A**G**G**UU**U**UG**/AUACUUUGAUUCAUC |
| Hydrolase | (1) | CAGG**AUAU**G**GUGUUG**/CUAUGGCGAAUGCUG | -18- | -ACC**A**A**CAU**GC**UGUUG**/CUCAUAUUAUUGAAA |
| Membrane protease | (1) | GCU**UGCAU**G**GUGUUG**/GGAUUGCCGAACAAC | -45- | -AAA**A**A**CU**U**G**G**UGU**G**G**/CACUUGAUGAAGAAC |
| **Ribosomal protein S12/S7** | (3) | AAGA**ACA**CA**GUGUUG**/UACUUCUUCGUGGUG | -161- | AAA**CGUG**A**A**G**UU**U**UG**/GCAGAUCCAAUGUAC |
| Elongation factor Tu | (2) | CUUAACAA**AGCA**GAC/C**UUG**UUGAUGAUGAA | -112- | AAC**CACA**A**U**G**G**G**UUG**/CUAAAGUUGAAGAAU |
| Phosphomannomutase | (5) | GAA**CA**G**A**CG**GUGUU**C/GCGGAGAAGCAAAUG | -189- | CGA**CAC**C**U**G**GUGUUG**/CGUAUUUGGUAAAAA |
| Signal recognition particle | (1) | AAAGAU**UAUGUGUUG**/AUUGAUACGGCAGGU | -178- | ACA**CACGU**G**GUG**G**UG**/CGGCUUUAUCAAUUC |
| Uracil Permease | (9) | CA**CACAU**GA**GUGUU**A/CAAAAUUUAAGGUUC | -241- | GUA**UAC**CGA**UGUUG**C/AAAUCUAAAAGGAUA |
| Ribose-P pyrophosphokinase | (1) | AUUA**ACAU**U**GU**C**UU**A/CCUUACUAUGGUUAU | -13- | -GUA**A**A**G**C**U**C**GUG**C**UC**/GUGAACCAAUCACAU |
| Relaxase (*ltrB*) | (1) | AA**CACAU**UAU**UGUU**C/AUAAAUUAAAACAUU | -422- | GAA**CACAU**C**GUG**CC**G**/CAUAUCAUUUUUAAU |
| Putative Fe-S oxidoreductase | (1) | UAC**CGGAU**GA**UGUUG**/UAGAAUAUUUAGCAG | -185- | AUGAUGU**UGGA**A**A**A**U/GU**GCGCCGUAUGGUU |
| Putative transport protein | (1) | GG**UACGG**UG**GUGUCG**/CACCAUUUGGUCAAG | -147- | ACU**UAUAU**CU**UUAUA/G**UGCGCCAGCAGUUG |

**Figure S4.** mRNA fragments identified at the splice junction of Ll.LtrB-EBS1/Mut-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. Sequence spanning two genes and including a short intergenic region is underlined. The gene in bold (*S12/S7*) was further studied for Ll.LtrB reverse splicing analyses and the detection of E1-mRNA chimeras (Figure 8).