Additional file 2 - Characterization of IS elements of *Leifsonia xyli* subsp. *cynodontis*.

**IS1237**

(CGCGGCGGAACCGCATTTA)

**Sequence 1. IS1237 (899 bp version).** (a) In between parenthesis: adjacent sequences of one copy (4° occurrence – additional file 3); (b) letters highlighted in gray: DR; (c) letters highlighted in green and non complementary nucleotides highlighted in yellow: IR; (d) letters in red: transposase start and end; (e) letters beneath nucleotide sequence separated in triads: transposase coding sequence; (f) letters highlighted in brown: purine rich region possible associated with -1 frameshifting; (g) letters in boldface: missing sequence of IS1237d1 (798 bp); (h) letters in pink: premature stop codon; (i) letters within rectangles: DDE motif and conserved amino acids of IS5 family.
Sequence 2. IS\textsubscript{Lxc1} (2,631 bp) and the IS\textsubscript{1237} insertion represented in white letters highlighted in black. (a) In between parenthesis: adjacent sequences of one copy (11\textsuperscript{o} occurrence – additional file 3); (b) letters highlighted in gray: DR; (c) letters highlighted in green and non complementary nucleotides highlighted in yellow: IR; (d) letters in pink: premature stop codon of the disrupted \textit{istA}; (e) letters in red: \textit{istB} start and end; (f) letters beneath nucleotide sequence separated in triads: \textit{IstB} coding sequence; (g) letters highlighted in brown: purine rich region.
Sequence 3. ISLxc2 (1,105 bp). (a) In between parenthesis: adjacent sequences of one copy (5° occurrence – additional file 3); (b) letters highlighted in grey: DR; (c) letters highlighted in green and non complementary nucleotides highlighted in yellow: IR; (d) letters in orange: site of insertion of IS1237 (occurrences 17, 28 and 49); (e) letters in red: transposase start and end; (f) letters in pink: premature stop codon; (g) letters beneath nucleotide sequence separated in triads: transposase coding sequence; (h) letters within rectangles: DDE motif and other conserved amino acids of IS481 family.
Sequence 4. ISLxc3 (1,511 bp). (a) In between parenthesis: adjacent sequences of one copy (23° occurrence – additional file 3); (b) letters highlighted in green and non complementary nucleotides highlighted in yellow: IR; (c) letters in red: transposase start and end; (d) letters beneath nucleotide sequence separated in triads: transposase coding sequence; (e) letters within rectangles: DDE motif and other conserved amino acids of IS30 family.
ISLxc

(CAGCCGAGCCCCCTTGACA)

Sequence 5. ISLxc4 (1,311 bp version). (a) In between parenthesis: adjacent sequences of one copy (2ⁿ occurrence – additional file 3); (b) letters highlighted in green: IR; (c) letters in red: transposase start and end; (d) letters beneath nucleotide sequence separated in triplets: transposase coding sequence; (e) letters highlighted in brown: purine rich region possible associated with +1 frameshifting; (f) letters in boldface: missing sequences of ISLxc4 smaller version (ISLxc4d1 - 896 bp long); (g) letters within rectangles: DDE motif and conserved amino acids of IS30 family.