Supplementary Online Figure: Disruption of adjacent reading frames by Tnt1 insertions

Sequences of the genomic regions flanking each Tnt1 insertion (names suffixed by "-nucl", lowercase letters), as well as their theoretical translation products (names suffixed by "-aas", uppercase letters), have been aligned with the closest aminoacid hit detected by blastx analysis (g41tr, gp91tr, gp93tr, gp95tr, s231f) or with the theoretical translation product (named suffixed by "-aas") of the closest hit detected by blastn (g72tr, t11d) or tblastx (g71tr) analysis. Aminoacid identities and similarities are indicated by white letters on a black background and black letters on a grey background, respectively. The beginning or end of each coding frame is indicated by a gap on the nucleotide sequence. Sequences are with respect to the orientation of the disrupted CDS (indicated by arrows), and the first 12 bp of each Tnt1 insertion are show (complementary strand for g41tr, g72tr, gp95tr and s231tr, for which Tnt1 is inserted in opposite orientation with respect to the flanking CDS).