

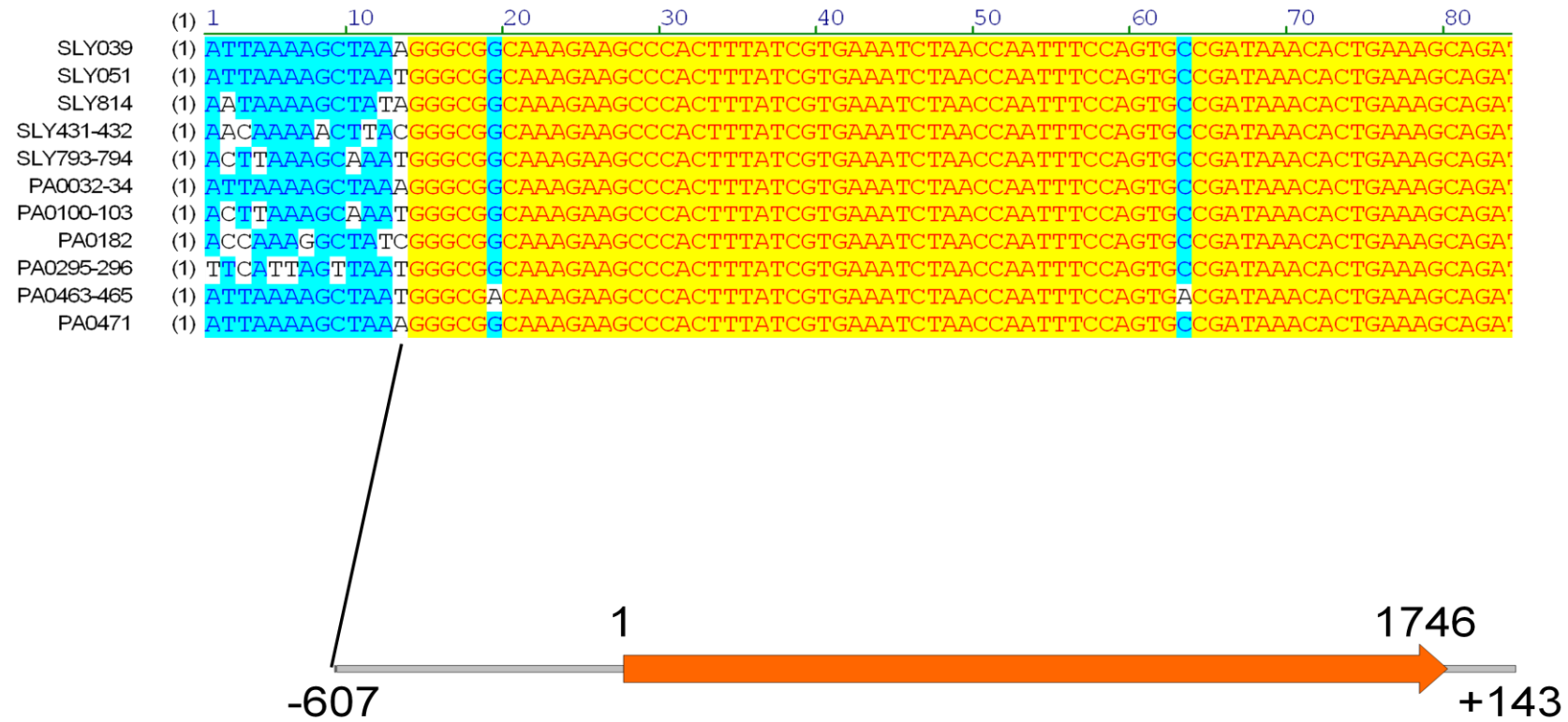
Additional file 9

Figure S3. Conserved sequences associated with *ltrA* in '*Ca. Phytoplasma australiense*'. Yellow colouring indicates exact nucleotide match and blue colouring is greatest consensus match. (A) Graphical representation of the 5' Untranslated Region (UTR) (607 bp), Open Reading Frame (1746 bp) and 3' UTR (143 bp) of SLY; (B) line-up of the approximately the 5' most 90 bp of the 5' UTR showing the boundary of the conserved sequence; (C) alignment of c. 150 bp of the 3' UTR. Lowest sequence of the alignment represents the 3' end of the *ltrA* ORF.

A



B



C

	(1764)	1764	1770	1780	1790	1800	1810	1820	1830	1840	1850	1860	1870	1880	1890	1900	1910	1920
SLY039(1749)	ACACAGTTAA	CCGCAAGGT	TAATCCCGT	TAAAAAGGGT	TAAATGAT	TGGAAAGCCGT	TGCTTGGAACT	TGCTGTAACGGT	TTGGAGGGGGG	CTGTTTGTAA	TAGAAAGT	TAGAAAAACAAAT	CCTACAAT	TGAAACGCAAA	TAACTAT	CCCTATAA	TATAT	CAATAT
SLY051(1737)	ACACAGTTAA	CCGCAAGGT	TAATCCCGT	TAAAAAGGGT	TAAATGAT	TGGAAAGCCGT	TGCTTGGAACT	TGCTGTAACGGT	TTGGAGGGGGG	CTGTTTGTAA	TAGAAAGT	TAGAAAAACAAAT	CCTACAAT	TGAAACGCAAA	TAACTAT	CCCTATAA	TATAT	CAATAT
SLY814(1737)	ACACAGTTAA	CCGCAAGGT	TAATCCCGT	TAAAAAGGGT	TAAATGAT	TGGAAAGCCGT	TGCTTGGAACT	TGCTGTAACGGT	TTGGAGGGGGG	CTGTTTGTAA	TAGAAAGT	TAGAAAAACAAAT	CCTACAAT	TGAAACGCAAA	TAACTAT	CCCTATAA	TATAT	CAATAT
PA0032(1668)	ACACAGTTAA	CCGCAAGGT	TAATCCCGT	TAAAAAGGGT	TAAATGAT	TGGAAAGCCGT	TGCTTGGAACT	TGCTGTAACGGT	TTGGAGGGGGG	CTGTTTGTAA	TAGAAAGT	TAGAAAAACAAAT	CCTACAAT	TGAAACGCAAA	TAACTAT	CCCTATAA	TATAT	CAATAT
SLY432(1737)	ACACAGTTAA	CCGCAAGGT	TAATCCCGT	TAAAAAGGGT	TAAATGAT	TGGAAAGCCGT	TGCTTGGAACT	TGCTGTAACGGT	TTGGAGGGGGG	CTGTTTGTAA	TAGAAAGT	TAGAAAAACAAAT	CCTACAAT	TGAAACGCAAA	TAACTAT	CCCTATAA	TATAT	CAATAT
PA0295(1738)	ACACAGTTAA	CCGCAAGGT	TAATCCCGT	TAAAAAGGGT	TAAATGAT	TGGAAAGCCGT	TGCTTGGAACT	TGCTGTAACGGT	TTGGAGGGGGG	CTGTTTGTAA	TAGAAAGT	TAGAAAAACAAAT	CCTACAAT	TGAAACGCAAA	TAACTAT	CCCTATAA	TATAT	CAATAT
PA0622(720)	ACACAGTTAA	CCGCAAGGT	TAATCCCGT	TAAAAAGGGT	TAAATGAT	TGGAAAGCCGT	TGCTTGGAACT	TGCTGTAACGGT	TTGGAGGGGGG	CTGTTTGTAA	TAGAAAGT	TAGAAAAACAAAT	CCTACAAT	TGAAACGCAAA	TAACTAT	CCCTATAA	TATAT	CAATAT
PA0463(1578)	ACACAGTTAA	CCGCAAGGT	TAATCCCGT	TAAAAAGGGT	TAAATGAT	TGGAAAGCCGT	TGCTTGGAACT	TGCTGTAACGGT	TTGGAGGGGGG	CTGTTTGTAA	TAGAAAGT	TAGAAAAACAAAT	CCTACAAT	TGAAACGCAAA	TAACTAT	CCCTATAA	TATAT	CAATAT
PA0212(1612)	ACACAGTTAA	CCGCAAGGT	TAATCCCGT	TAAAAAGGGT	TAAATGAT	TGGAAAGCCGT	TGCTTGGAACT	TGCTGTAACGGT	TTGGAGGGGGG	CTGTTTGTAA	TAGAAAGT	TAGAAAAACAAAT	CCTACAAT	TGAAACGCAAA	TAACTAT	CCCTATAA	TATAT	CAATAT
SLY746(1647)	ACACAGTTAA	CCGCAAGGT	TAATCCCGT	TAAAAAGGGT	TAAATGAT	TGGAAAGCCGT	TGCTTGGAACT	TGCTGTAACGGT	TTGGAGGGGGG	CTGTTTGTAA	TAGAAAGT	TAGAAAAACAAAT	CCTACAAT	TGAAACGCAAA	TAACTAT	CCCTATAA	TATAT	CAATAT
PA0259(279)	ACACAGTTAA	CCGCAAGGT	TAATCCCGT	TAAAAAGGGT	TAAATGAT	TGGAAAGCCGT	TGCTTGGAACT	TGCTGTAACGGT	TTGGAGGGGGG	CTGTTTGTAA	TAGAAAGT	TAGAAAAACAAAT	CCTACAAT	TGAAACGCAAA	TAACTAT	CCCTATAA	TATAT	CAATAT
PA0100(1747)	ACACAGTTAA	CCGCAAGGT	TAATCCCGT	TAAAAAGGGT	TAAATGAT	TGGAAAGCCGT	TGCTTGGAACT	TGCTGTAACGGT	TTGGAGGGGGG	CTGTTTGTAA	TAGAAAGT	TAGAAAAACAAAT	CCTACAAT	TGAAACGCAAA	TAACTAT	CCCTATAA	TATAT	CAATAT
SLY793(1738)	ACACAGTTAA	CCGCAAGGT	TAATCCCGT	TAAAAAGGGT	TAAATGAT	TGGAAAGCCGT	TGCTTGGAACT	TGCTGTAACGGT	TTGGAGGGGGG	CTGTTTGTAA	TAGAAAGT	TAGAAAAACAAAT	CCTACAAT	TGAAACGCAAA	TAACTAT	CCCTATAA	TATAT	CAATAT
SLY_039(1749)	ACACAGTTAA	CCGCAAGGT	TAATCCCGT	TAAAAAGGGT	TAAATGAT	TGGAAAGCCGT	TGCTTGGAACT	TGCTGTAACGGT	TTGGAGGGGGG	CTGTTTGTAA	TAGAAAGT	TAGAAAAACAAAT	CCTACAAT	TGAAACGCAAA	TAACTAT	CCCTATAA	TATAT	CAATAT

