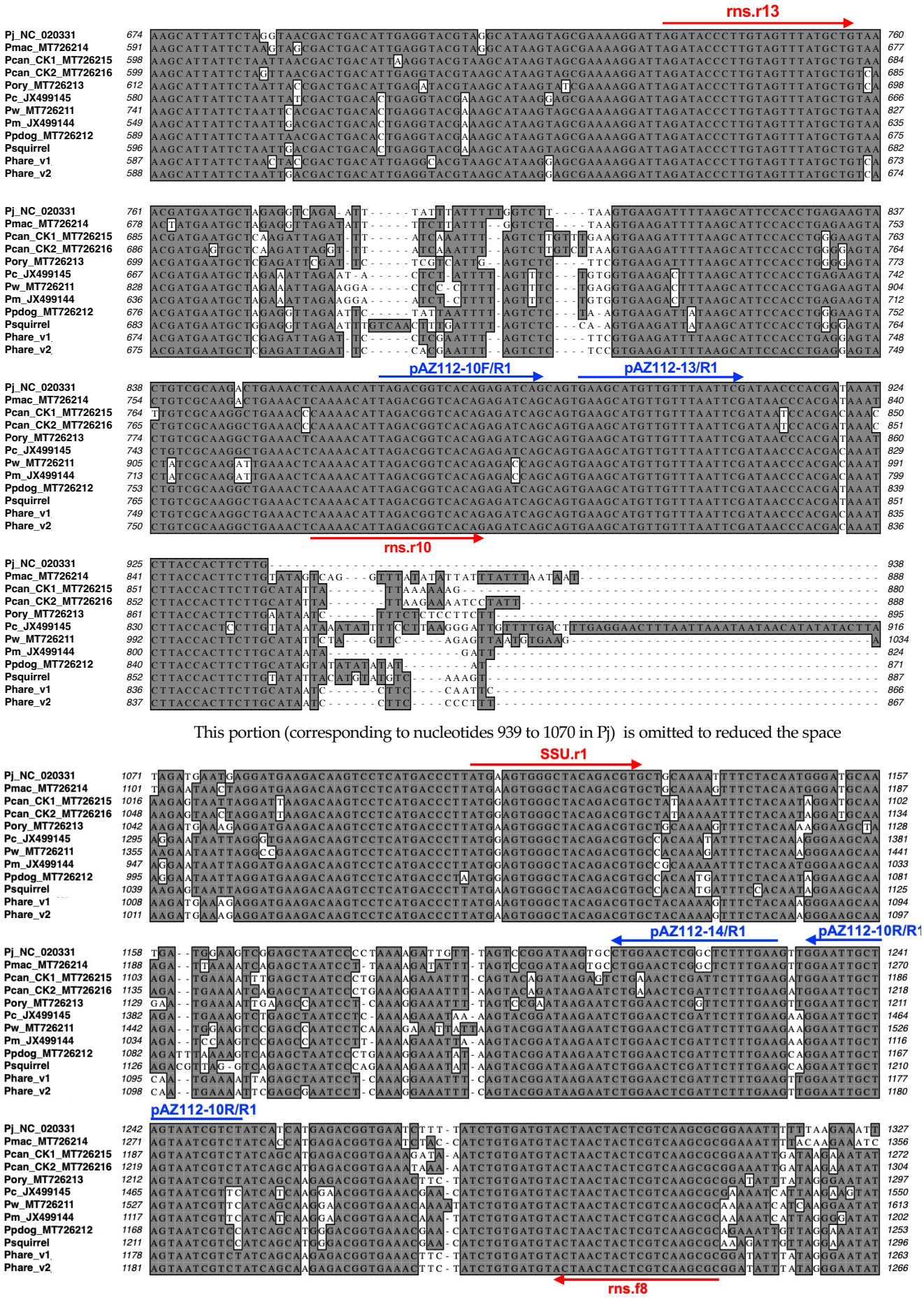
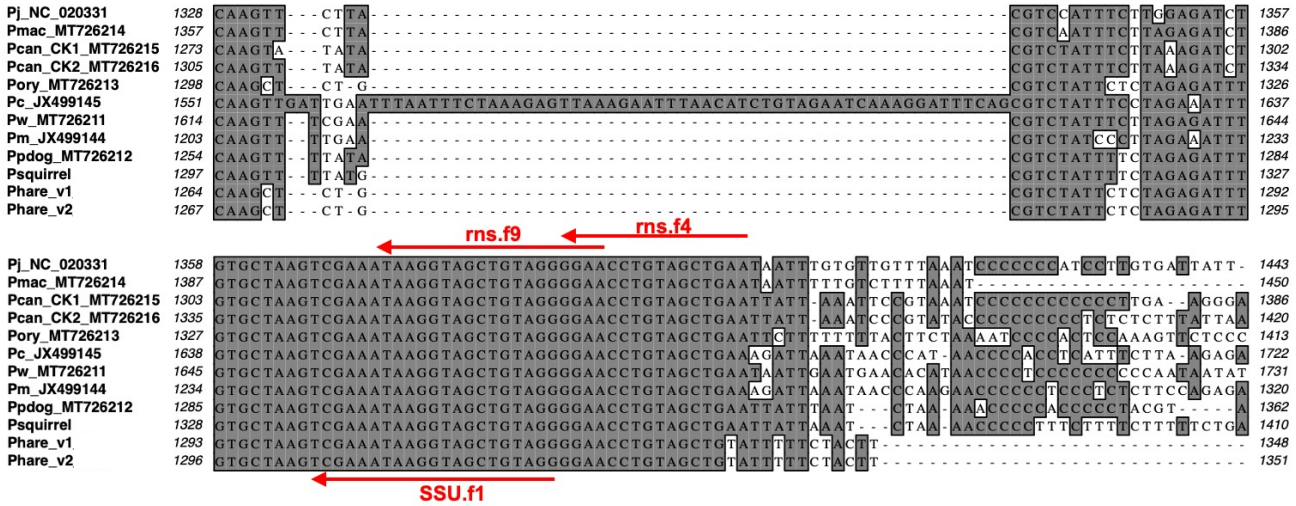


This portion (corresponding to nucleotides 939 to 1070 in Pj) is omitted to reduced the space



Supplemental Figure S2. Alignment of mitochondrial small-subunit (mtSSU) rRNA sequences of different *Pneumocystis* species and strains. Highly conserved sequences are highlighted in dark shadow. Dashes represents gaps introduced to optimize alignment. New primers designed in this study are indicated in red. The locations of the previously used universal *Pneumocystis* primers [38] were indicated in blue. The sequences of primers pAZ112-10F/R1 and pAZ112-13/R1 are identical to the respective regions in *P. jirovecii* (Pj), primer pAZ112-10R/R1 sequence is identical to the respective regions in *P. carinii* (Pc), and primer pAZ112-14/R1 contains a degenerate nucleotide (Y) at two positions (5'-TTCAAAGAAYCGAGTTYCAG-3'), which were omitted in the reference [37]. GenBank accession numbers are indicated after the names of *Pneumocystis* species/strains abbreviated as follows: Pj, *P. jirovecii;* Pmac, *P. macacae;* Pcan_CK1, *P. canis* strain CK1; Pcan_CK2, *P. canis* strain CK2; Pory, *P. oryctolagi;* Pc, *P. carinii;* Pw, *P. wakefieldiae;* Pm, *P. murina,* Ppdog, *Pneumocystis ludoviciani* from prairie dogs (Table S6); Psquirrel, *Pneumocystis* from squirrels; Phare_v1, *P.* sp. '*townsendii*' variant 1 from hares; Phare_v2, *P.* sp. '*townsendii*' variant 2 from hares. GenBank accession numbers for the last 3 sequences are PP484879, PP477339 and PP477340. Numbers on the two ends of each sequence correspond to the nucleotide positions of the full-length mtLSU gene in GenBank.