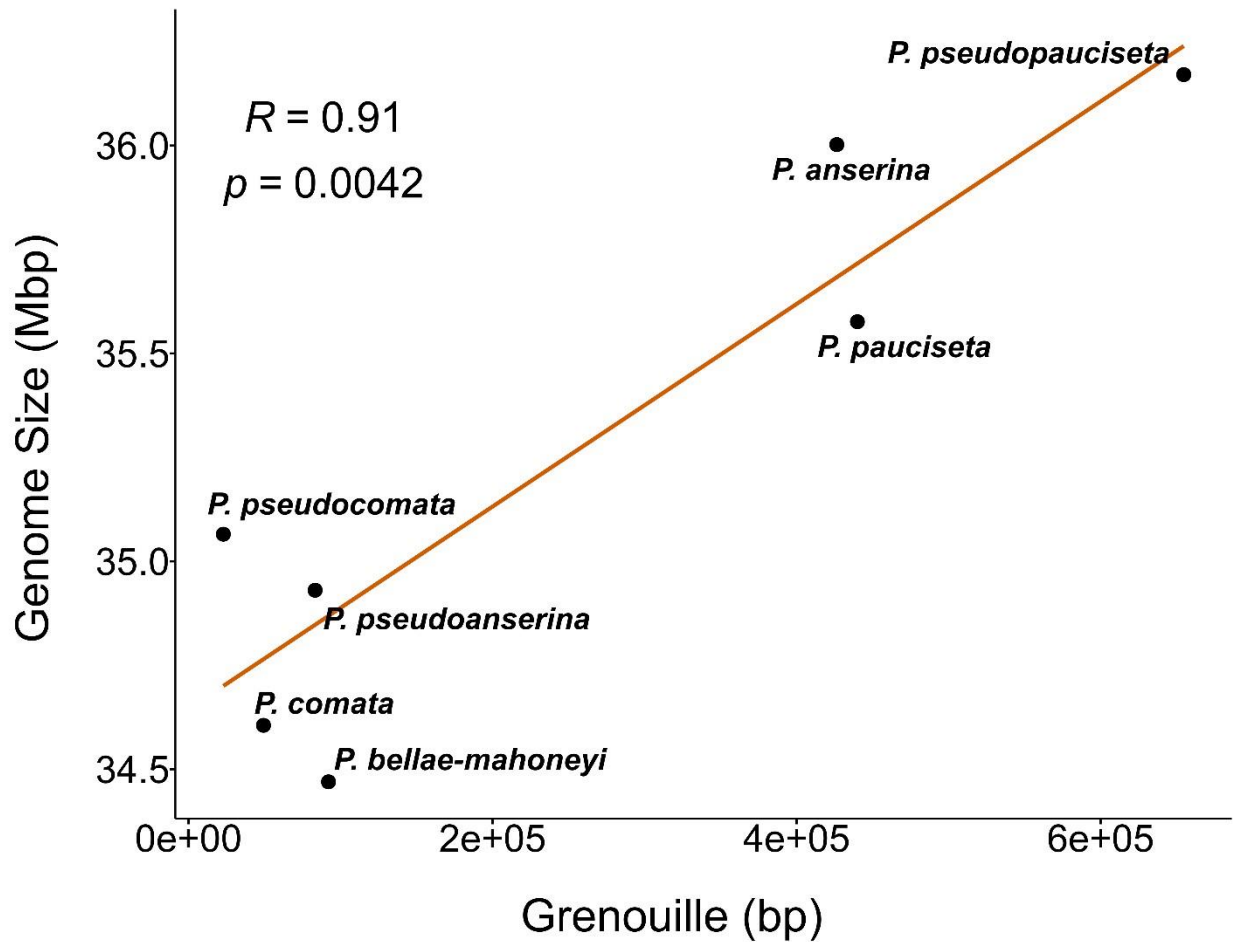
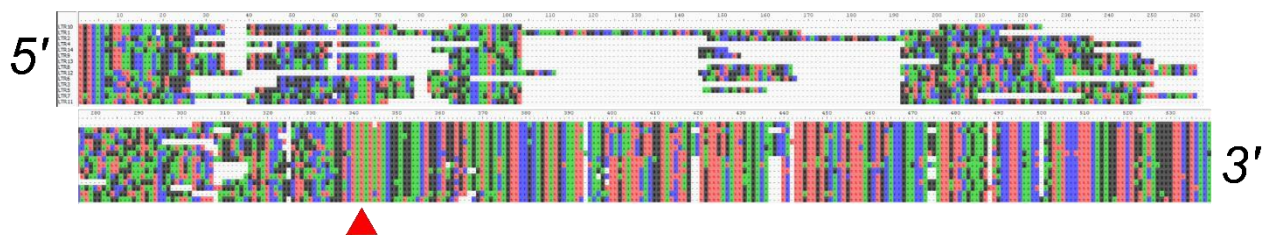
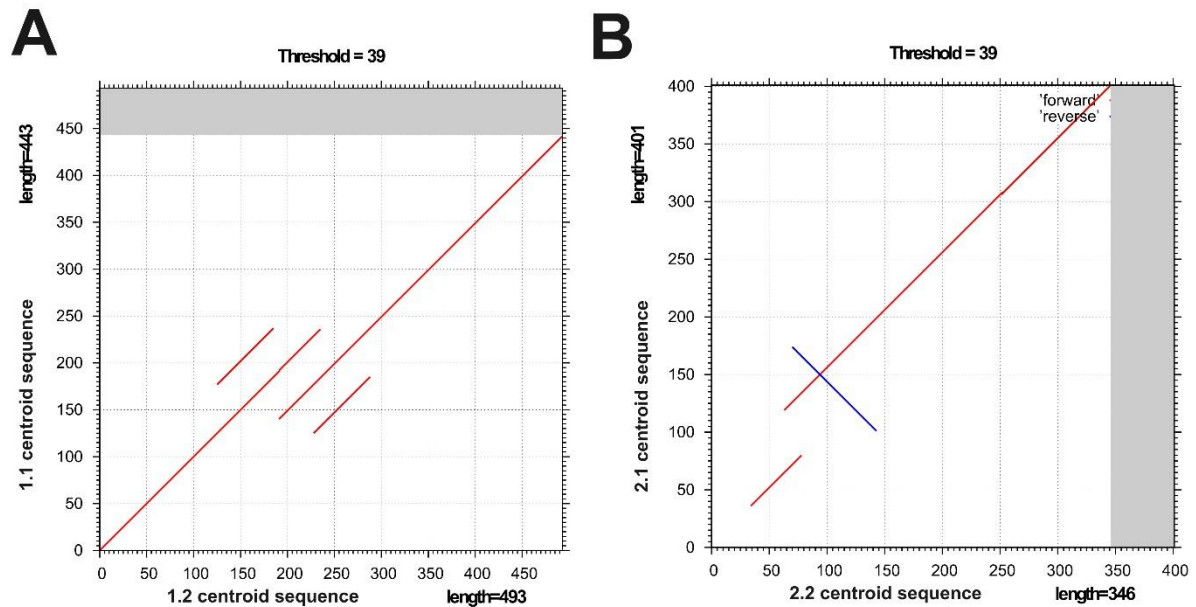




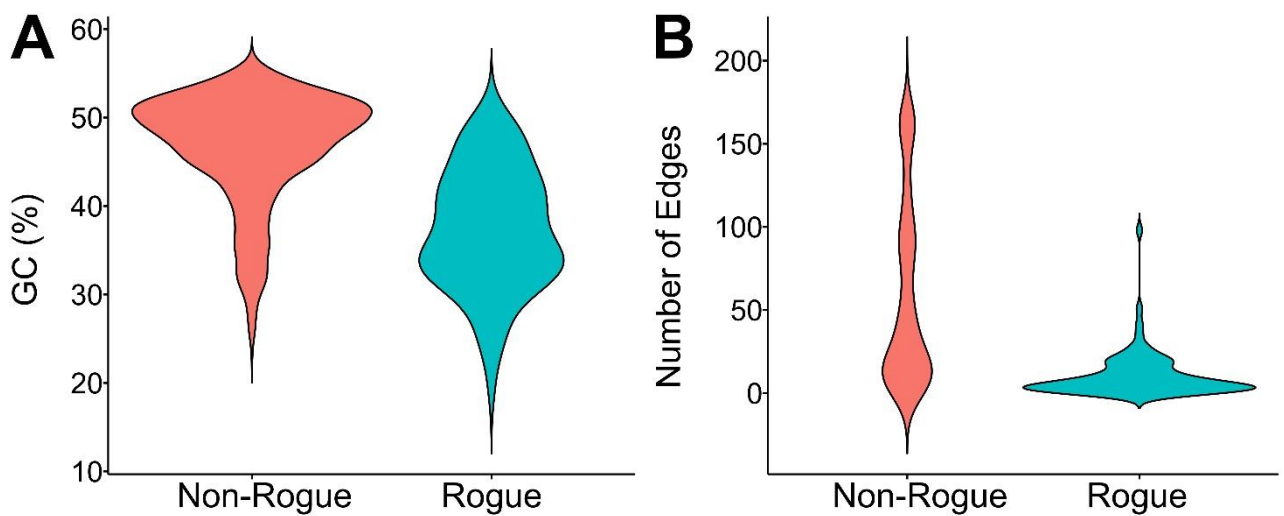
Supplementary figure 1: The LTR element grenouille abundance in base pairs is significantly associated with genome size in the species complex. Pearson's correlation, $p = 0.0042$, $R = 0.91$.



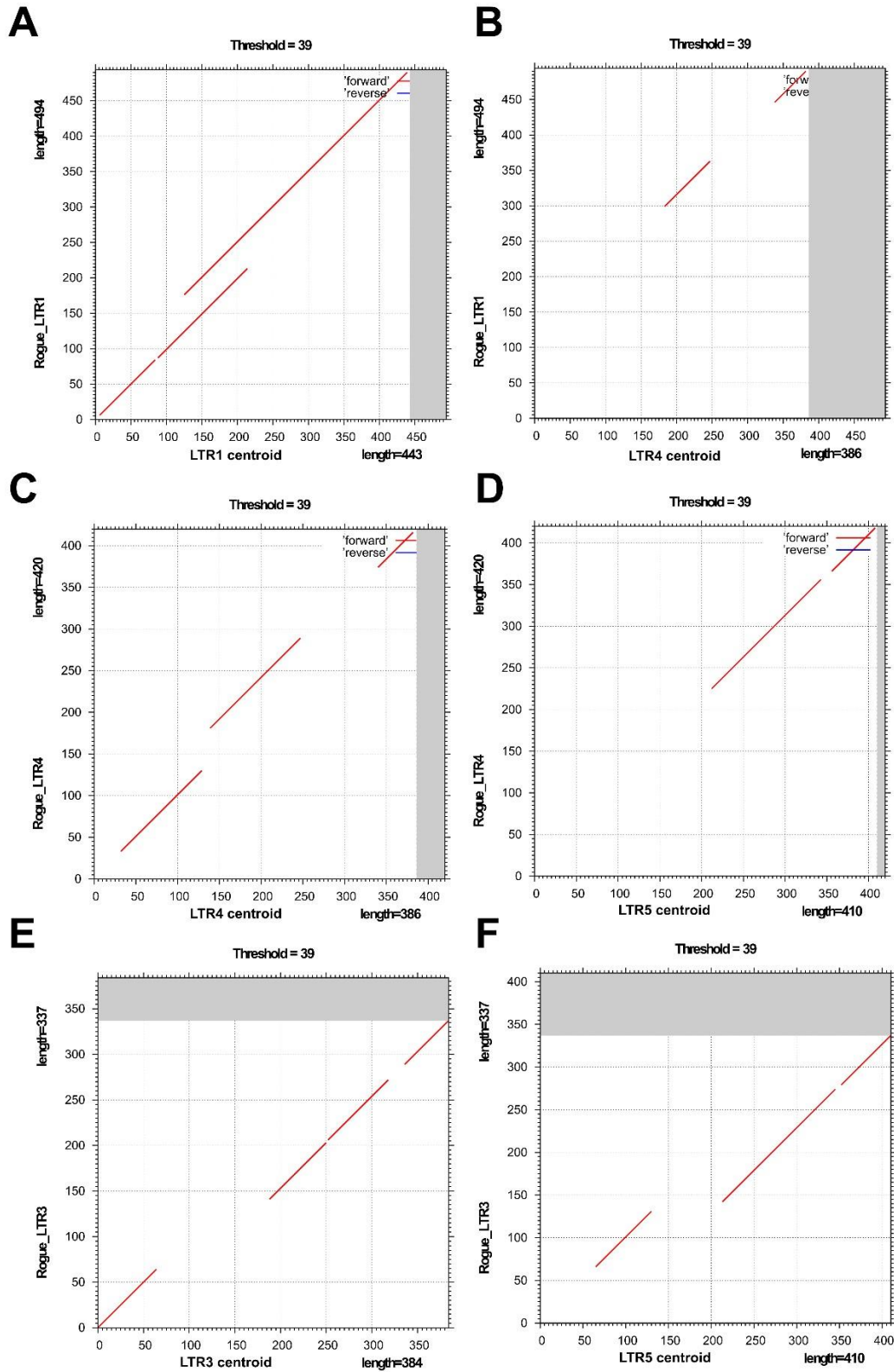
Supplementary figure 2: Alignment of Crapaud subfamily centroids. Top = 5'-half, bottom = 3'-Half. The different colors represent the nucleotides; C = blue, G = black, T = red, and A = green. The TATA-box is marked with a red arrow.



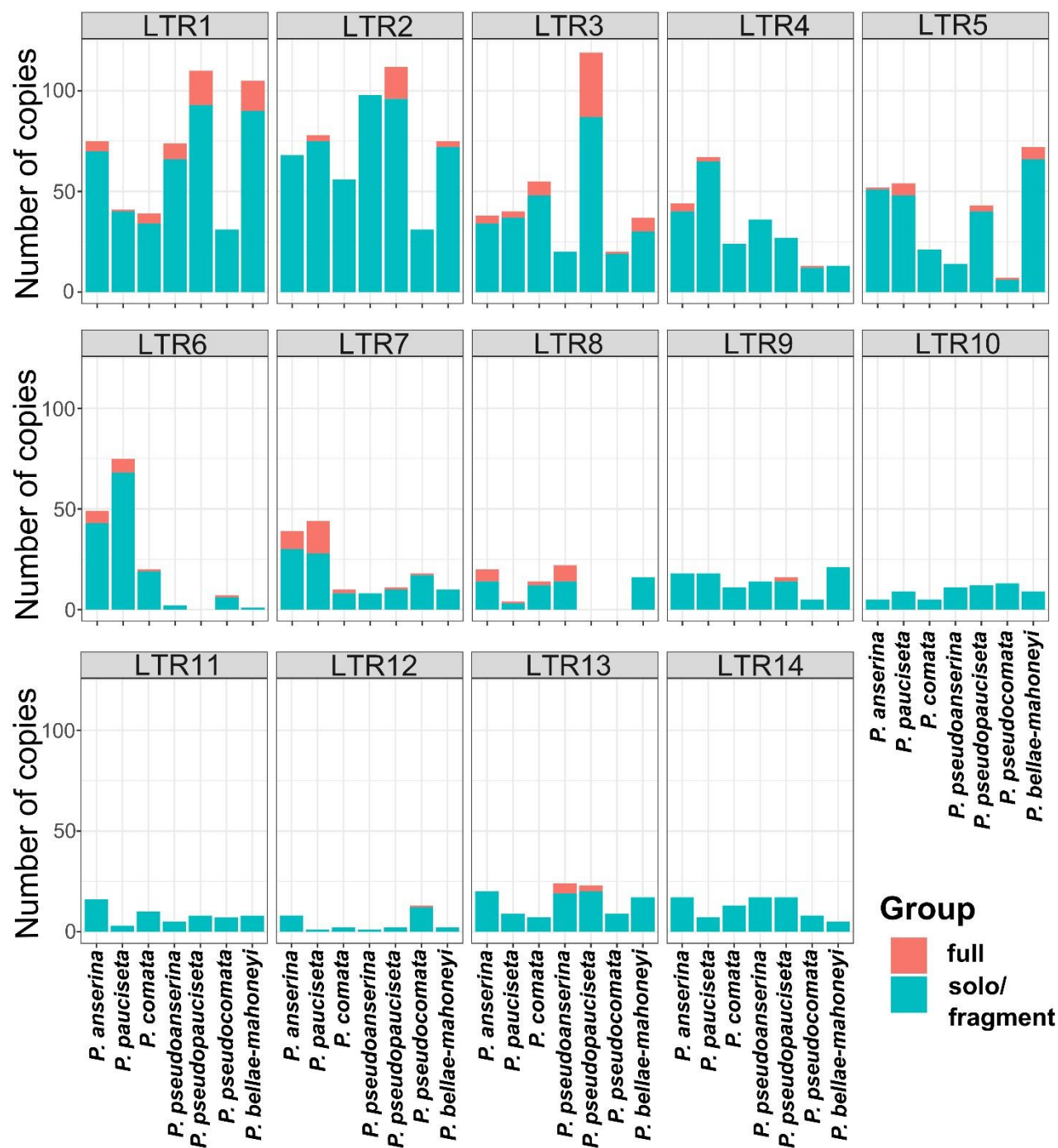
Supplementary figure 3: Dotplots between the nested cluster centroids. Red lines indicate alignments between the sequences in the forward strand. Blue lines indicate alignments in the reverse strand **A)** Community 1.1 and Community 1.2. **B)** Community 2.1 and Community 2.2.



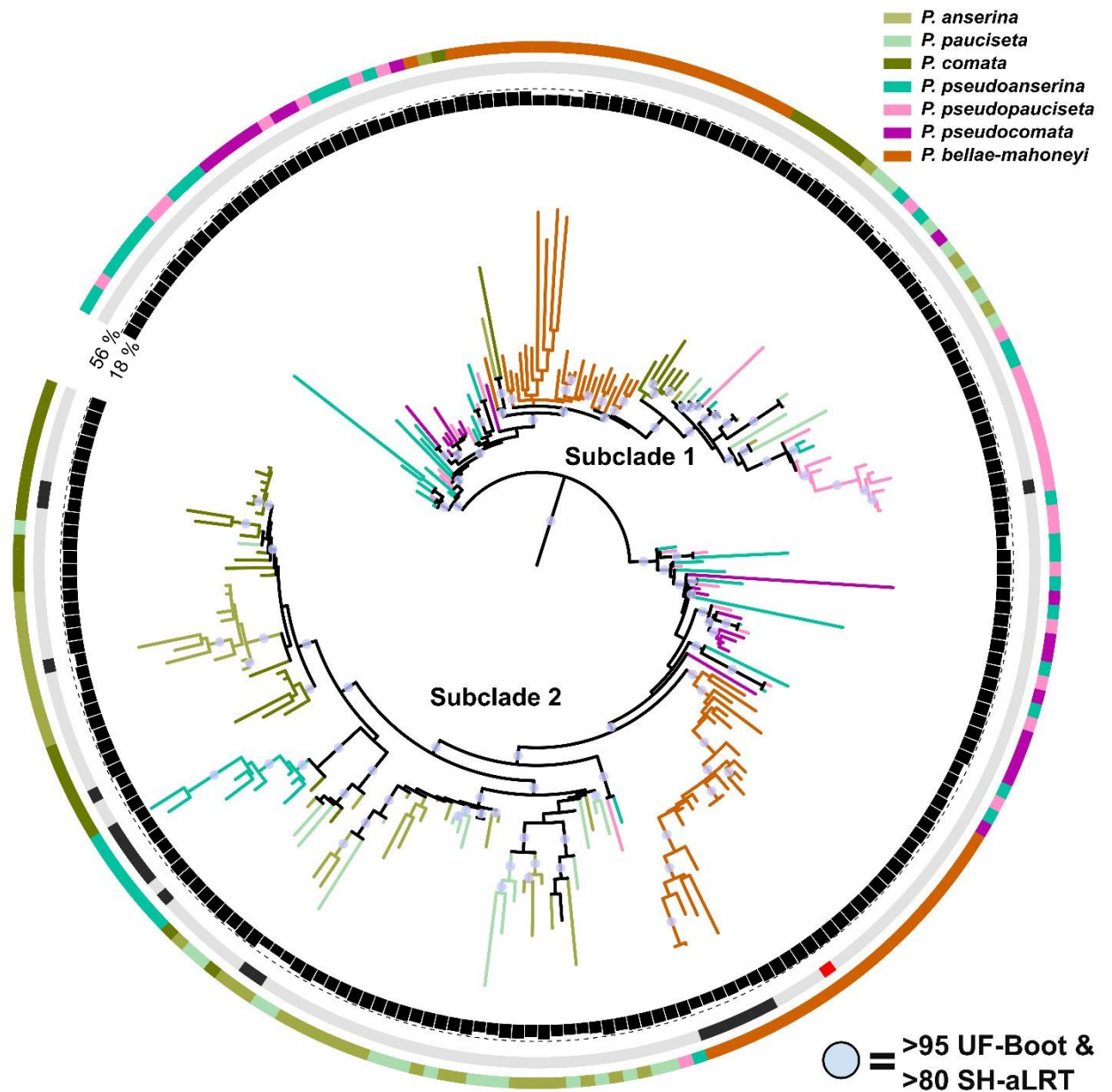
Supplementary figure 4: Comparison between classified copies inside and outside their subfamily's main clade in the ML phylogeny. **A)** GC content comparison, mean (Non-Rogue) = 48.4, mean (Rogue) = 37.4. **B)** Number of edges connected to the sequence in the SSN (Degrees), median (Non-Rogue) = 36, median (Rogue) = 6. $n(\text{Non-Rogue}) = 997$, $n(\text{Rogue}) = 82$.



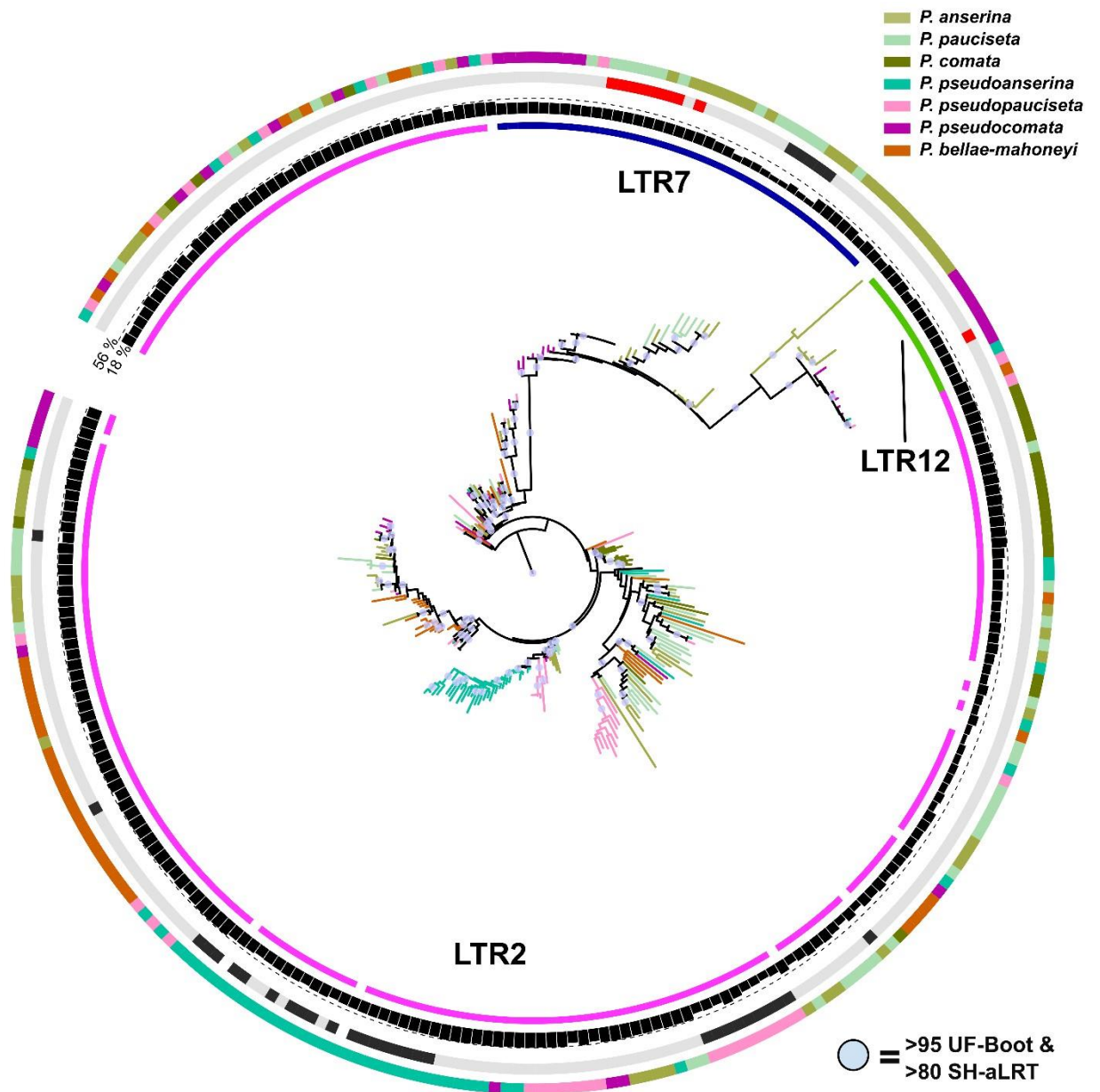
Supplementary figure 5: MAFFT alignment dotplots between representative rogue copies, the subfamily centroid, and the centroid of the clade it clusters with in the ML phylogeny. **A)** LTR1 rogue with LTR1 centroid. **B)** LTR1 rogue with LTR4 centroid. **C)** LTR4 rogue with LTR4 centroid. **D)** LTR4 rogue with LTR5 centroid. **E)** LTR3 rogue with LTR3 centroid. **F)** LTR3 rogue with LTR5 centroid



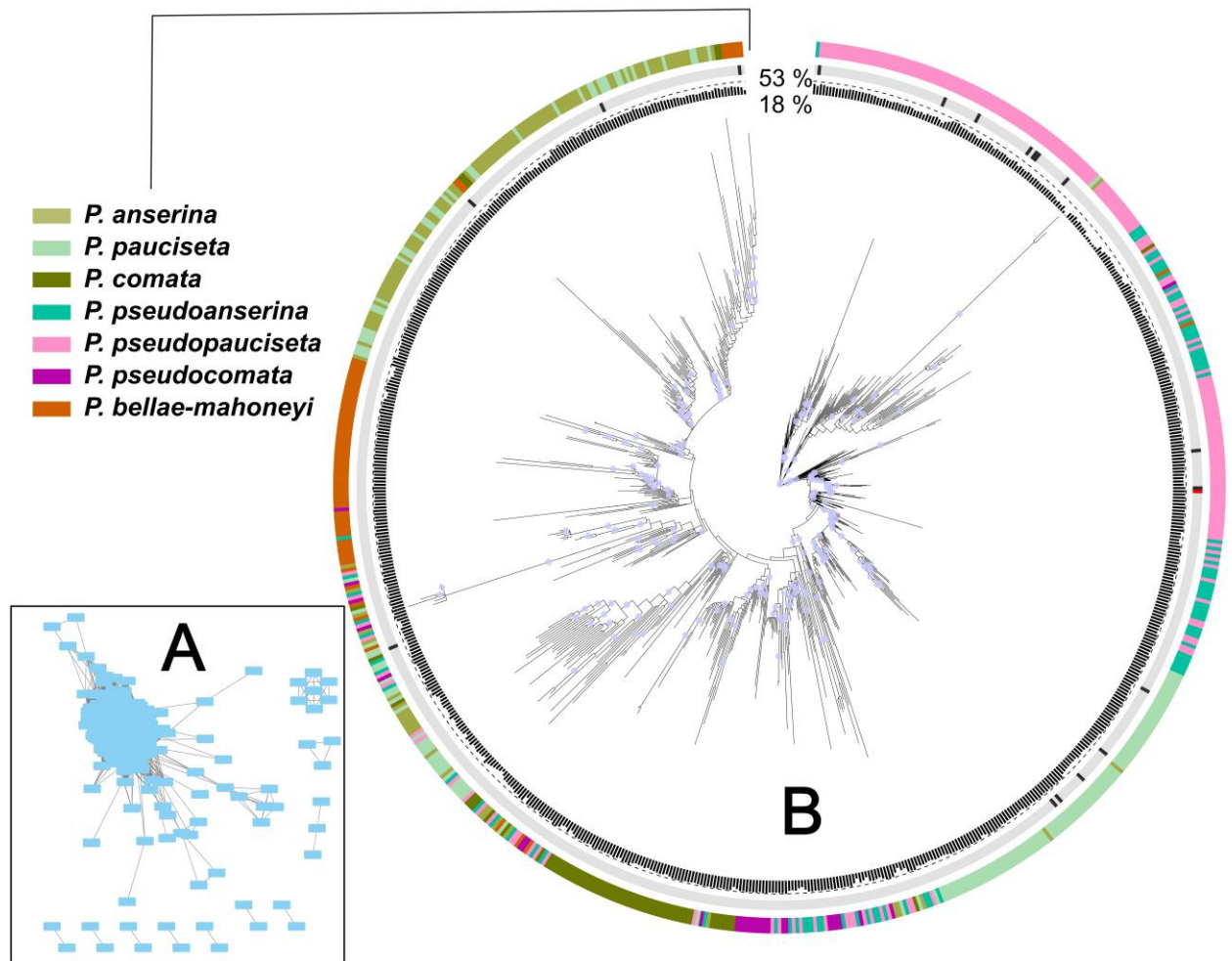
Supplementary figure 6: Number of Repeatmasker hits of LTR subfamilies in the *P. anserina* species-complex of both full copy LTRs and solo/fragment LTRs.



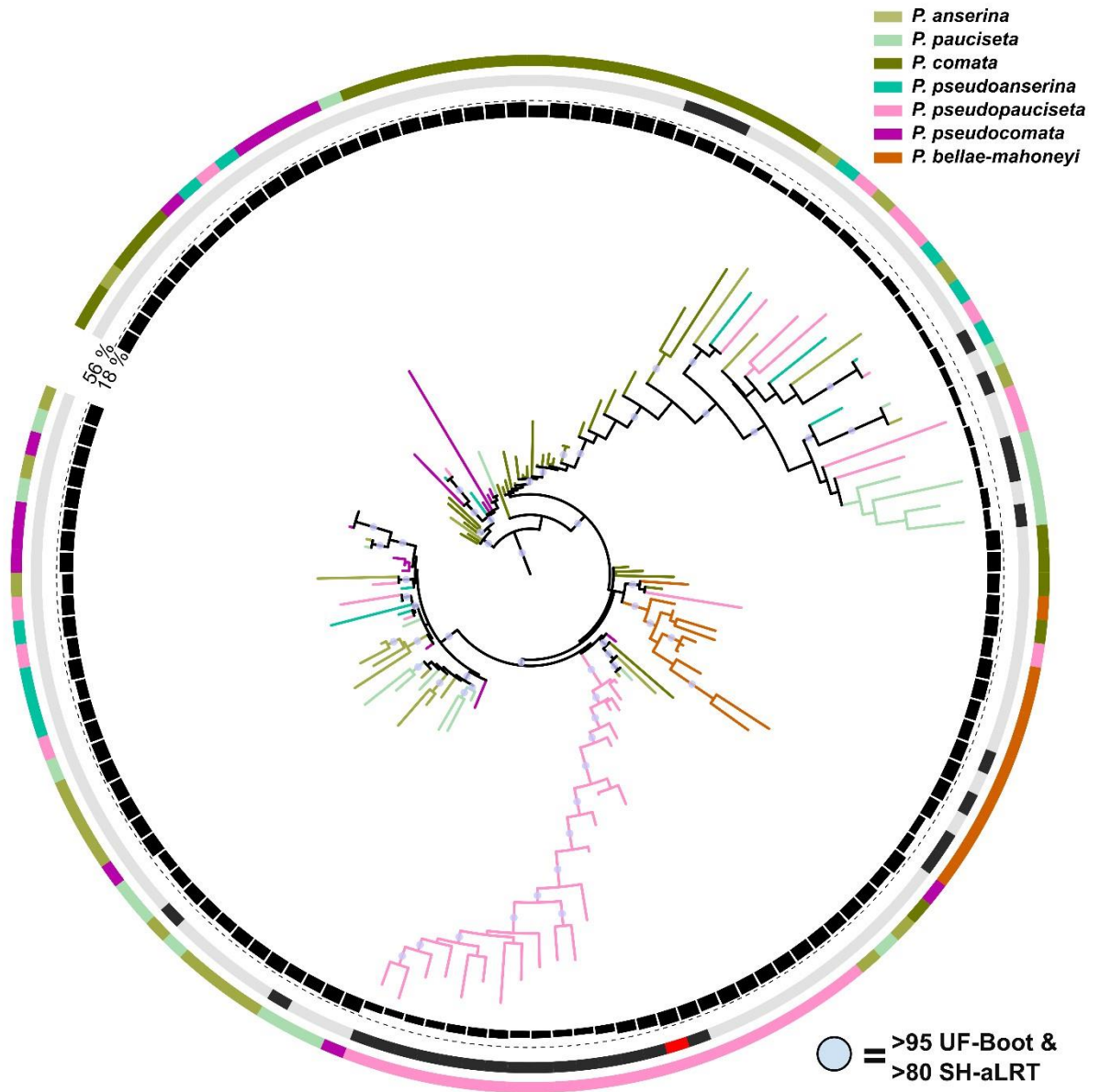
Supplementary figure 7: Pruned phylogeny of the LTR1 clade. Tracks from inner to outer: GC-content, Solo/fragment (grey) / Full (black) / Active (red), Species. Species are also indicated by colors of branches. The phylogeny was rooted based on the phylogeny including all LTR copies of the dataset.



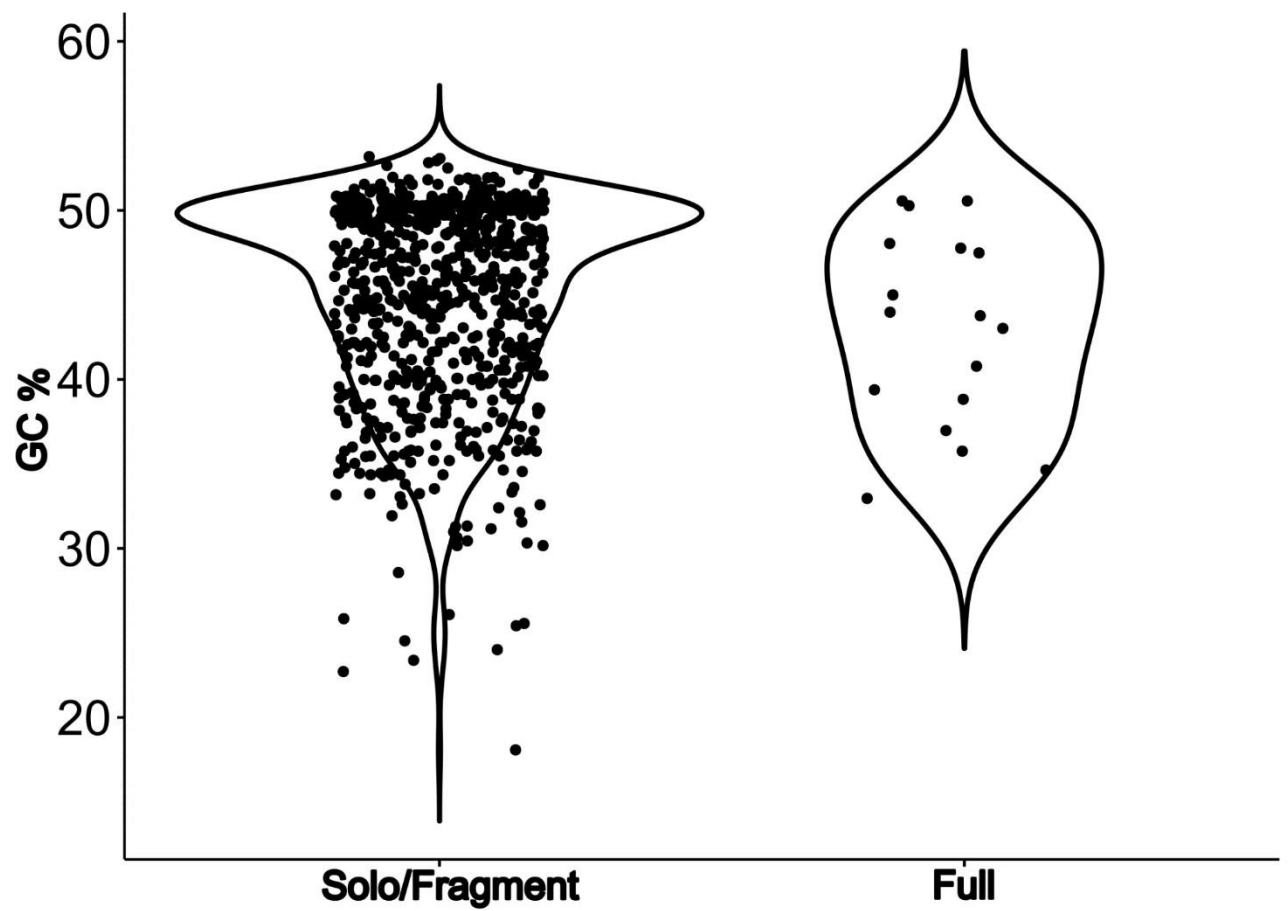
Supplementary figure 8: Pruned phylogeny of the LTR2, LTR7 and LTR12 clade. Tracks from inner to outer: GC-content, Solo/fragment (grey) / Full (black) / Active (red), Species. Species are also indicated by colors of branches. The phylogeny was rooted based on the phylogeny including all LTR copies of the dataset.



Supplementary figure 9: Analysis of the *grenouille* LTR element **A)** SSN of the *grenouille* terminal repeats using the thresholds >80% identity over >80% sequence coverage. 692 terminal repeat copies clustered in the largest network cluster. The second largest had seven copies. n= 753. **B)** ML phylogeny of the 753 terminal repeats of *grenouille*. Tracks from inner to outer: GC-content ranging between 18% to 53%; Full copies (black), putative active copies (red), and solo/fragment copies (grey); Species



Supplementary figure 10: Pruned phylogeny of the LTR3 clade. Tracks from inner to outer: GC-content, Solo/fragment (grey) / Full (black) / Active (red), Species. Species are also indicated by colors of branches. The phylogeny was rooted based on the phylogeny including all LTR copies of the dataset.



Supplementary figure 11: GC% content of the terminal repeat sequences of the *grenouille* element, divided into solo/fragment copies and full copies. $n(\text{solo/fragment}) = 736$, $n(\text{full}) = 17$.