

SUPPORTING INFORMATION

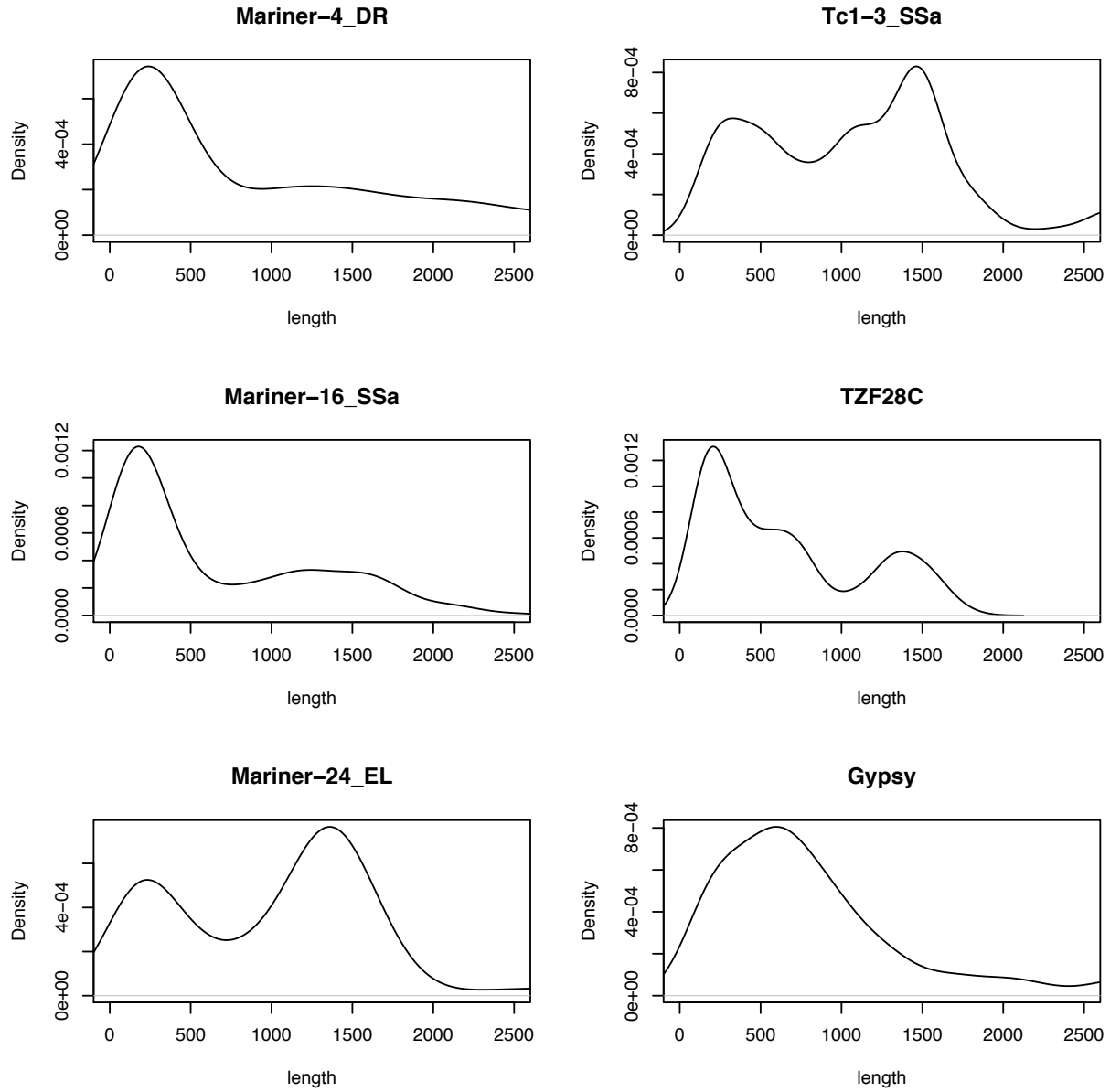


Figure S1 - . Length Distributions for Contigs assembled *Mariner*, *Tc1*, and *Gypsy* TE contigs. Some elements are assembled in fragments, contributing to non-normal length distributions.

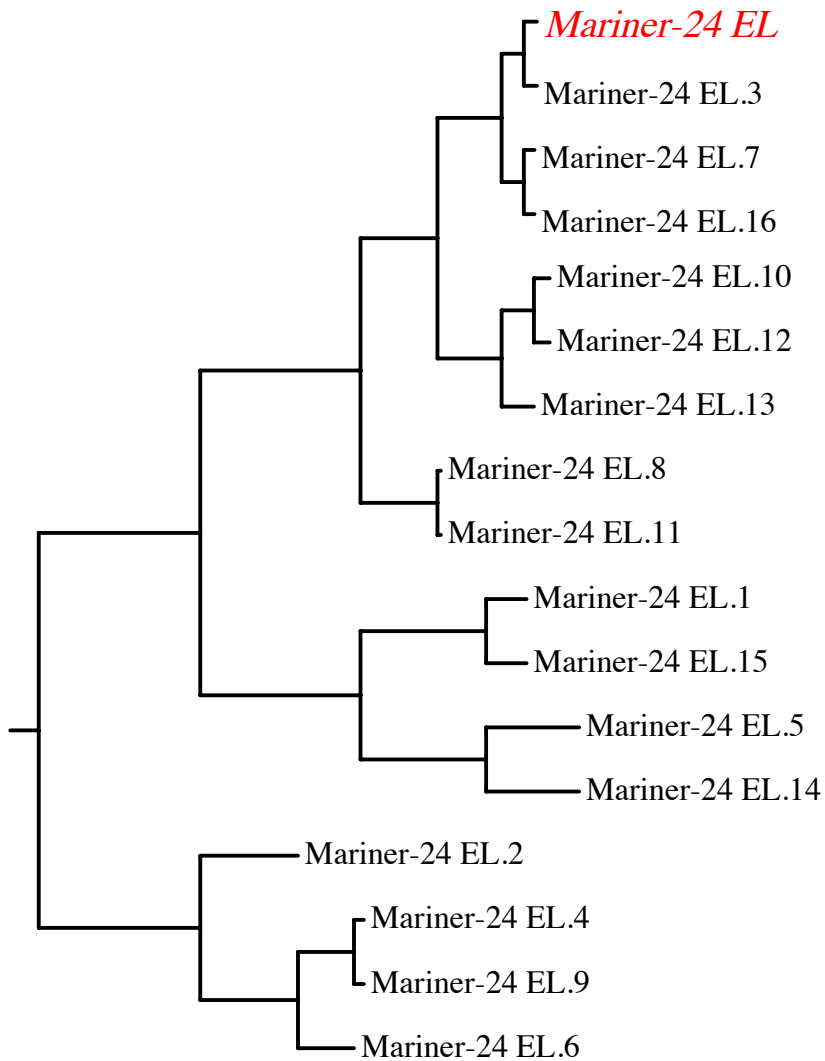


Fig S2 - Phylogenetic relationships between horizontally transmitted repetitive elements in *O. pumilio* (black) and annotated TE *Mariner-24_EL* (red), an *Esox lucius* TE in RepBase. Similar patterns are observed in other TE families. For each of the most diverse TEs that are candidates for horizontal transfer, the RepBase element lies within the diversity of TEs in *O. pumilio*. All of these diverse and rapidly proliferating horizontally transferred elements are a close match with a TE from freshwater fish.

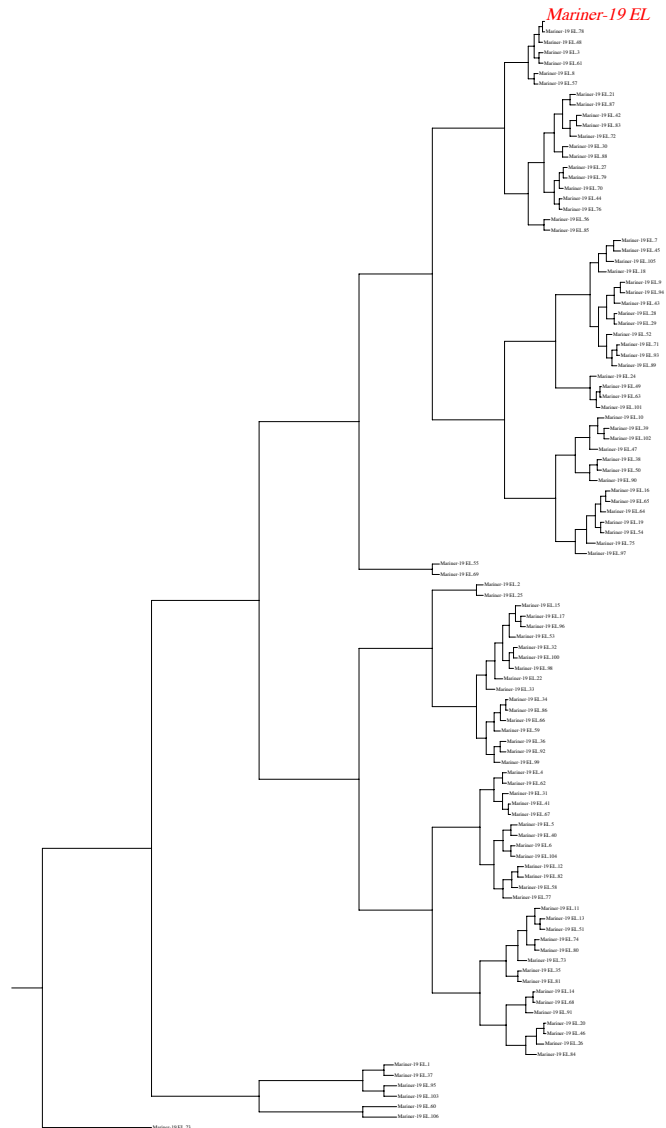


Figure S3- Phylogenetic relationships between horizontally transmitted repetitive elements in *O. pumilio* (black) and annotated TE *Mariner-19_EL* (red), an *Esox lucius* TE in RepBase. Similar patterns are observed in other TE families. For each of the most diverse TEs that are candidates for horizontal transfer, the RepBase element lies within the diversity of TEs in *O. pumilio*. All of these diverse and rapidly proliferating horizontally transferred elements are a close match with a TE from freshwater fish.

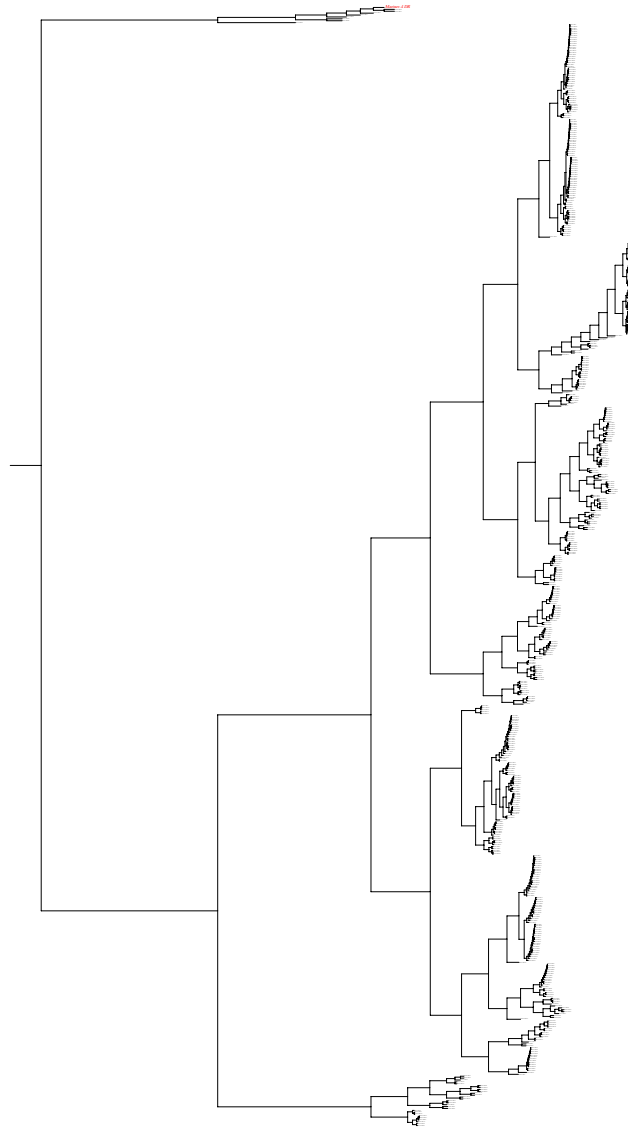


Figure S4- *Mariner-4_DR* phylogeny. For each of the most diverse TEs that are candidates for horizontal transfer, the RepBase element lies within the diversity of TEs in *O. pumilio*. All of these diverse and rapidly proliferating horizontally transferred elements are a close match with a TE from freshwater fish.

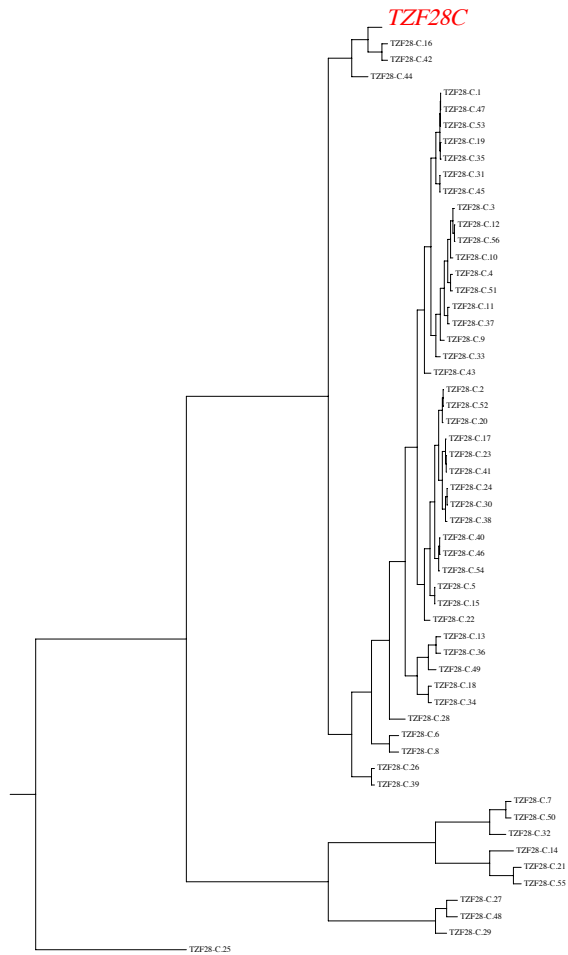


Figure S5 - TZF28C Phylogeny. For each of the most diverse TEs that are candidates for horizontal transfer, the RepBase element lies within the diversity of TEs in *O. pumilio*. All of these diverse and rapidly proliferating horizontally transferred elements are a close match with a TE from freshwater fish.

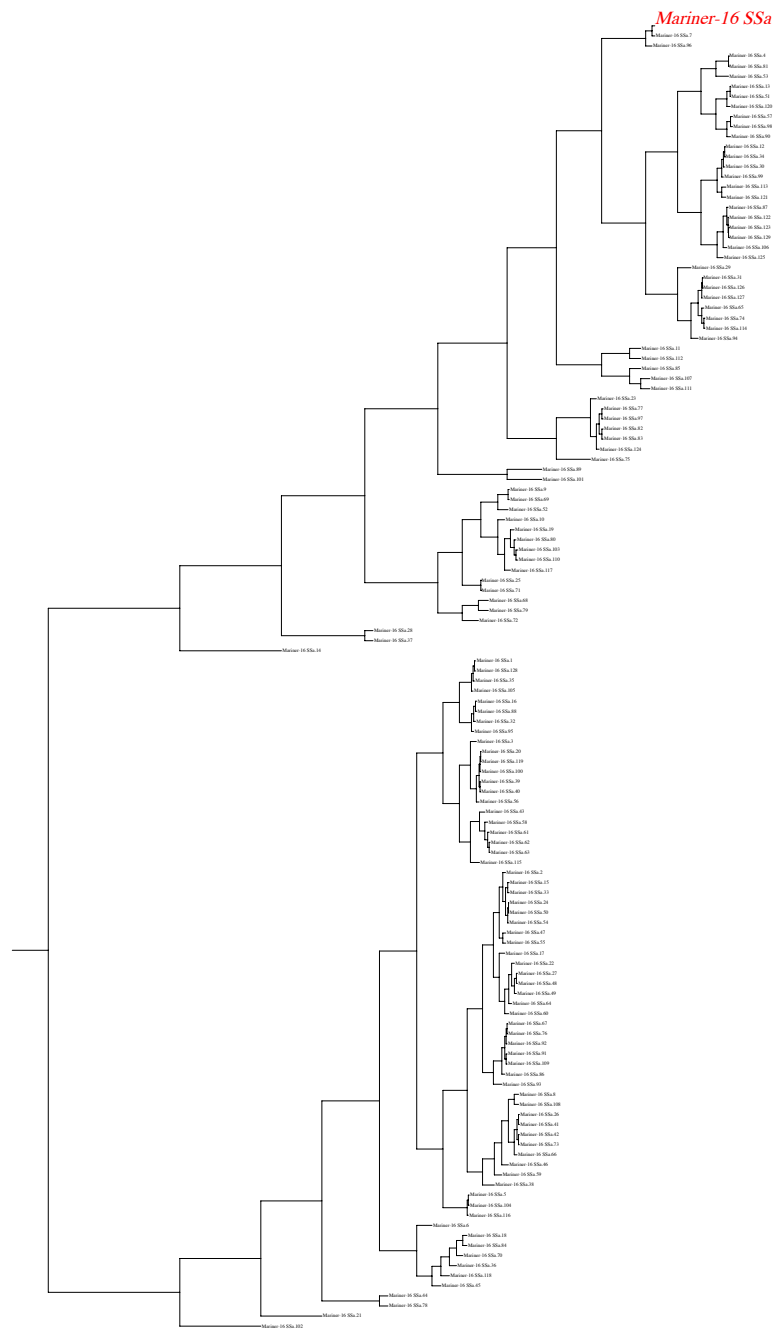


Figure S6 – Mariner 16_SSa phylogeny. For each of the most diverse TEs that are candidates for horizontal transfer, the RepBase element lies within the diversity of TEs in *O. pumilio*. All of these diverse and rapidly proliferating horizontally transferred elements are a close match with a TE from freshwater fish.

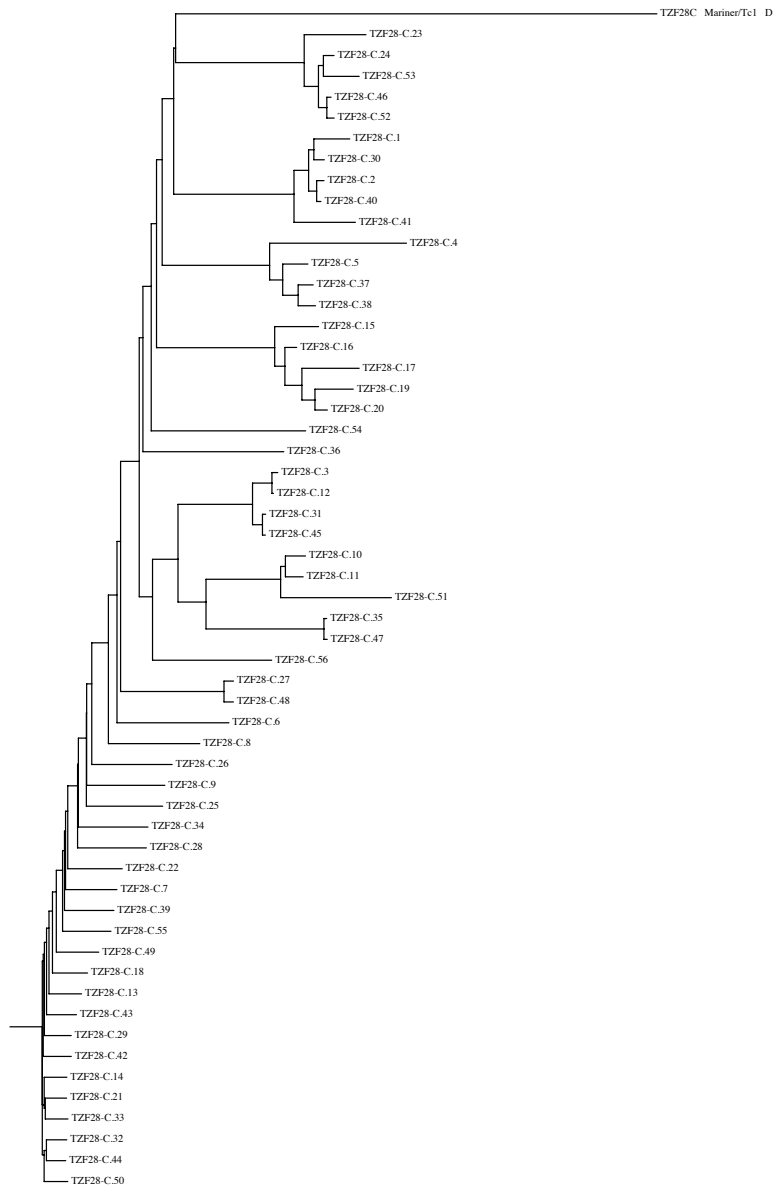


Figure S7 - Neighbor-joining relationships between horizontally transmitted repetitive elements in *O. pumilio* (black) and annotated *TZF28-C*, TE in RepBase.

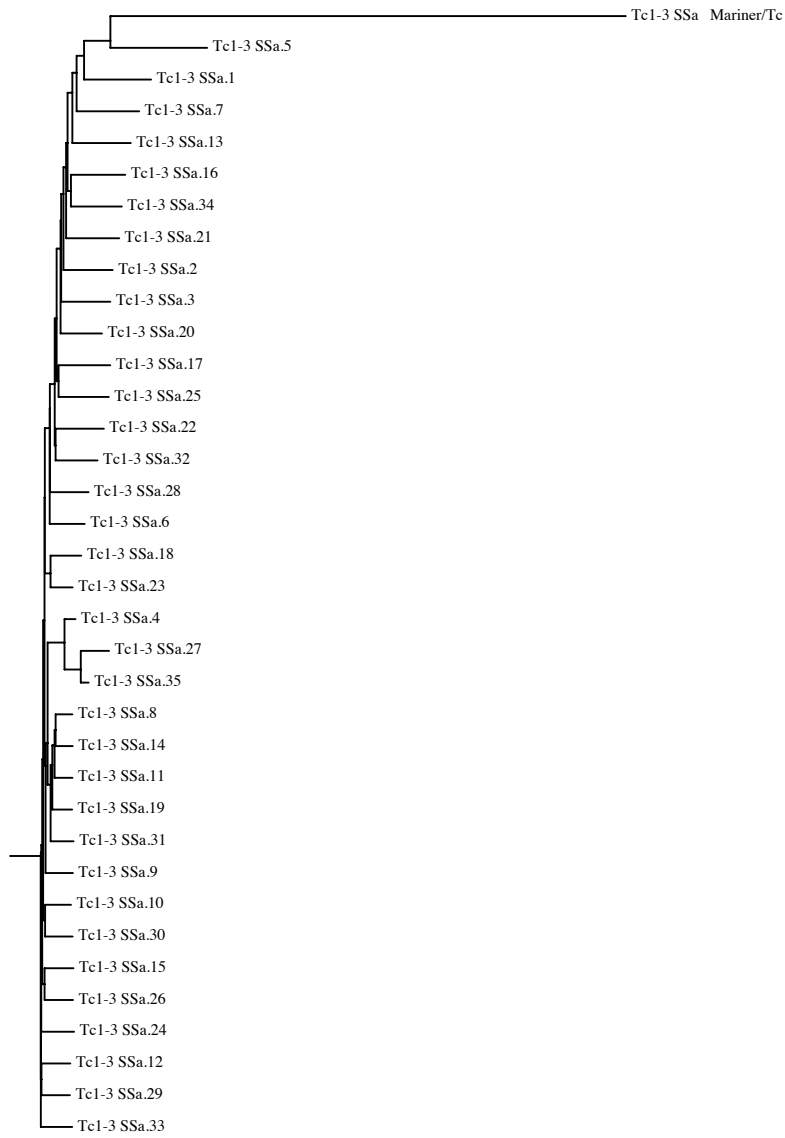


Fig S8 - Neighbor-joining relationships between horizontally transmitted repetitive elements in *O. pumilio* and annotated TE Tc1-3_SSa in RepBase.

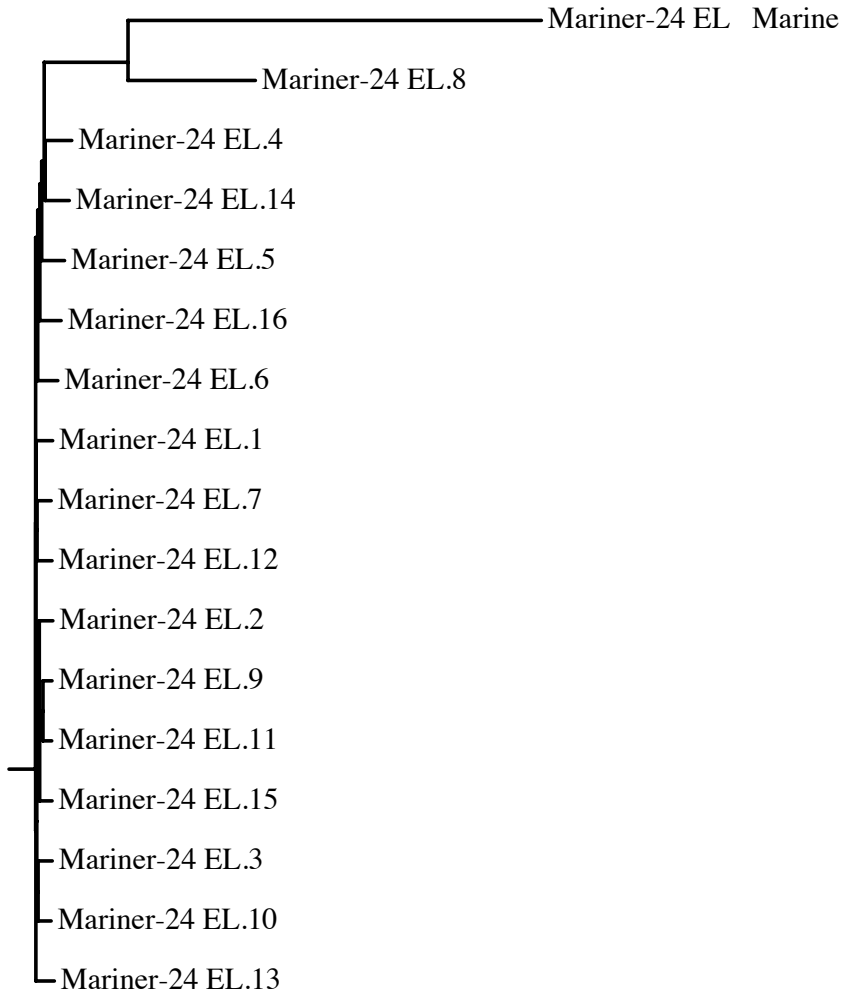


Figure S9 - Neighbor-joining relationships between horizontally transmitted repetitive elements in *O. pumilio* and annotated TE *Mariner-24_EL* in RepBase.

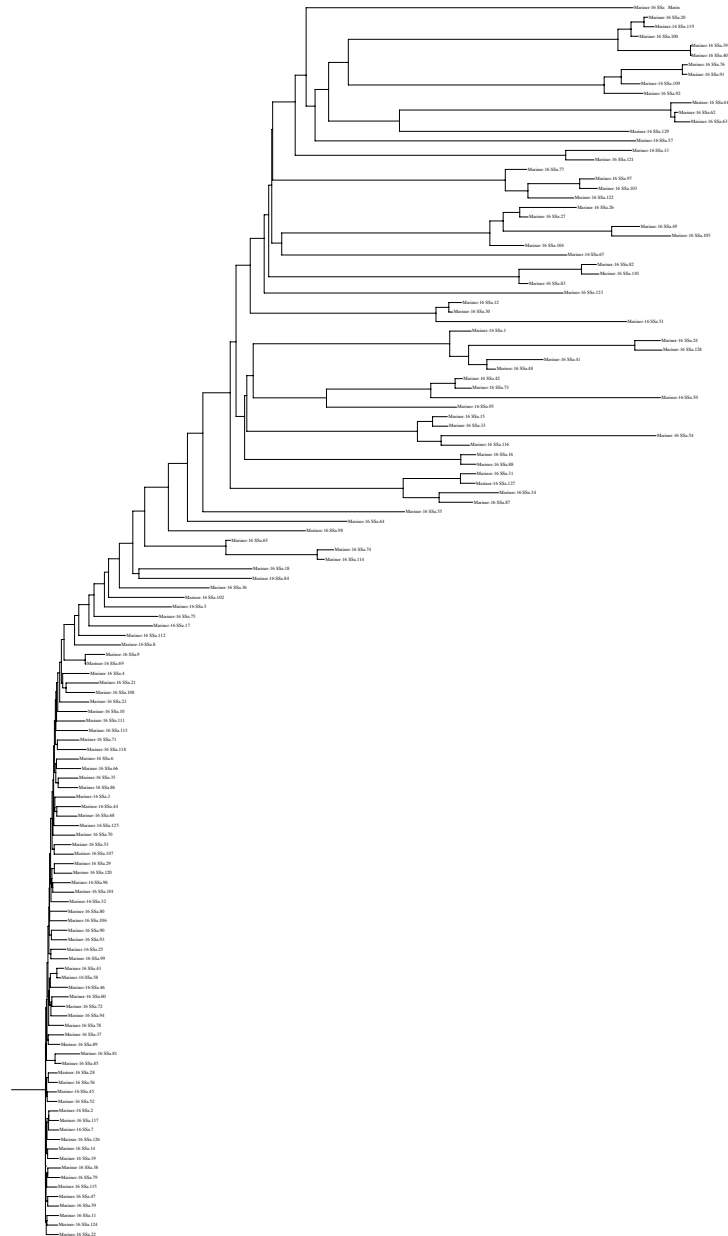


Fig S11 - Neighbor-joining relationships between horizontally transmitted repetitive elements in *O. pumilio* (black) and annotated TE *Mariner-16_SSa* TE in RepBase.

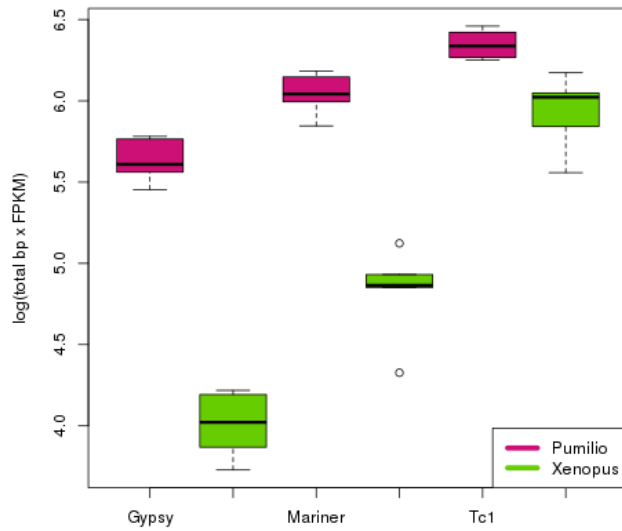


Figure S12 - Expression data considering only expression level, not sequence length for TEs in *O. pumilio* oocytes. Expression levels for TE classes in *O. pumilio* and *Xenopus laevis*. *Gypsy* and *Mariner* elements are expressed at significantly higher levels in *O. pumilio*, but *Tc1* elements are not.

Table S1. Transposable element content for TEs in the *O. pumilio* assembly

| TE Family | Total bp | TE Type |
|----------------|---------------|---------------------|
| <i>Gypsy</i> | 1,036,288,222 | LTR Retrotransposon |
| <i>Copia</i> | 297,874,058 | LTR Retrotransposon |
| hAT | 255,508,647 | DNA Transposon |
| <i>Mariner</i> | 197,322,803 | DNA Transposon |
| <i>Tcl</i> | 181,804,487 | DNA Transposon |

Table S2. Highest copy number repeats in the *O. pumilio* sequence data

| TE Family | Copy Number |
|-----------------------|--------------------|
| <i>Mariner-9_SSa</i> | 10640 |
| <i>Tc1-9_Xt</i> | 10853 |
| <i>U6</i> | 11134 |
| <i>Gypsy-60_GA-I</i> | 12184 |
| <i>Mariner-5_EL</i> | 12579 |
| <i>Mariner-16_SSa</i> | 14020 |
| <i>SINE2-1_XT</i> | 15251 |
| <i>Tc1-12_Xt</i> | 18727 |
| <i>Mariner-24_EL</i> | 22021 |
| <i>Tc1-15_Xt</i> | 25551 |
| <i>Tc1-2_Xt</i> | 26527 |
| <i>TZF28C</i> | 29893 |
| <i>Gypsy-15_Ano-I</i> | 58354 |
| <i>Mariner-4_DR</i> | 73395 |
| <i>Tc1-3_SSa</i> | 78037 |

Table S3. Most highly expressed TE transcripts in the *O. pumilio* genome.

| Transposon Type | Expression (FPKM) |
|------------------------|--------------------------|
| <i>Tc1-3_SSa</i> | 2001 |
| <i>Tc1-3_SSa</i> | 1228 |
| <i>Tc1-3_SSa</i> | 1032 |
| <i>Tc1-2_Xt</i> | 366 |
| <i>Gypsy-15_Ano-I</i> | 352 |
| <i>TZF28B</i> | 333 |
| <i>Tc1-3_SSa</i> | 277 |
| <i>TE-5_EL</i> | 266 |
| <i>Mariner-4_DR</i> | 253 |
| <i>Gypsy-60_GA-I</i> | 240 |
| <i>Tc1-2_Xt</i> | 223 |
| <i>Mariner-13_SSa</i> | 211 |
| <i>Tc1-3_SSa</i> | 204 |
| <i>TE-5_EL</i> | 203 |
| <i>Mariner-8_EL</i> | 199 |
| <i>Mariner-13_SSa</i> | 176 |
| <i>SINE2-1_XT</i> | 170 |
| <i>Tc1-1_OL</i> | 162 |
| <i>Tc1-2_Xt</i> | 152 |
| <i>Tc1-9_Xt</i> | 150 |
| <i>Mariner-19_SSa</i> | 135 |
| <i>Tc1-3_SSa</i> | 116 |
| <i>Mariner-2_SSa</i> | 114 |
| <i>Tc1-9_Xt</i> | 110 |
| <i>Mariner-9B_EL</i> | 107 |
| <i>MER34B_I</i> | 107 |