

Supplementary Material

Table S1. Distributions of TE superfamilies in the genomes of *Rhodnius* species.

Class	Order	Superfamily	<i>R. prolixus</i> ¹			<i>R. prolixus</i> ²			<i>R. montenegrensis</i>			<i>R. marabaensis</i>		
			bp	TE (%)	G (%)	bp	TE (%)	G (%)	bp	TE (%)	G (%)	bp	TE (%)	G (%)
Class I	LTR	<i>Bel-Pao</i>	201,352	0.59	0.111	220,151	0.55	0.13	300,928	0.7	0.165	175,680	0.45	0.096
		<i>Copia</i>	98,637	0.29	0.054	173,466	0.43	0.10	150,535	0.35	0.083	86,906	0.22	0.048
		<i>Gypsy</i>	1,045,433	3.06	0.576	1,028,327	2.56	0.59	1,570,001	3.66	0.862	1,220,975	3.12	0.671
		<i>LTR</i>	4,111	0.01	0.002	4,423	0.01	0.003	4,344	0.01	0.002	5,740	0.01	0.003
		<i>Ngaro</i>	2,125	0.01	0.001	1,261	0.003	0.001	1,619	0.004	0.001	2,217	0.01	0.001
		<i>EVR</i>	11,241	0.03	0.006	40,801	0.10	0.02	21,791	0.05	0.012	11,463	0.03	0.006
		<i>Other</i>	4,587	0.01	0.003	10,339	0.03	0.01	12,562	0.03	0.007	3,866	0.01	0.002
	DIRS	<i>DIRS</i>	1,428	0.004	0.001	983	0.002	0.001	2,197	0.01	0.001	1,451	0.004	0.001
	LTR		1,368,914	4.01	0.755	1,479,751	3.69	0.85	2,063,977	4.81	1.133	1,508,298	3.85	0.828
	PLE	<i>Penelope</i>	32,756	0.1	0.018	132,732	0.33	0.08	59,125	0.14	0.032	35,225	0.09	0.019
		<i>Dong</i>	15,534	0.05	0.009	9,394	0.02	0.01	8,918	0.02	0.005	13,833	0.04	0.008
		<i>I</i>	1,676,573	4.91	0.924	1,642,933	4.09	0.94	1,662,201	3.88	0.913	1,294,364	3.31	0.711
	LINEs	<i>Jockey</i>	4,061,974	11.89	2.24	4,317,911	10.76	2.48	5,349,244	12.48	2.938	3,823,545	9.77	2.1
		<i>L1</i>	33,382	0.1	0.018	35,597	0.09	0.02	43,402	0.1	0.024	148,498	0.38	0.082
		<i>L2</i>	440,876	1.29	0.243	494,172	1.23	0.28	568,084	1.32	0.312	1,583	0.004	0.001
		<i>LOA</i>	1,358,805	3.98	0.749	1,564,284	3.90	0.90	1,440,781	3.36	0.791	1,402,359	3.58	0.77
		<i>R1</i>	159,236	0.47	0.088	168,718	0.42	0.10	135,272	0.32	0.074	160,032	0.41	0.088
		<i>R2</i>	5,078	0.01	0.003	15,324	0.04	0.01	5,428	0.01	0.003	12,974	0.03	0.007
		<i>RTE</i>	1,195,745	3.5	0.659	1,606,425	4.00	0.92	1,261,756	2.94	0.693	1,627,588	4.16	0.894
		<i>CR1</i>	28,858	0.08	0.016	27,705	0.07	0.02	40,172	0.09	0.022	12,194	0.03	0.007
		<i>Tad</i>	0	0	0	11,770	0.03	0.01	26,768	0.06	0.015	0	0	0
		<i>CRE</i>	1,070	0.003	0.001	980	0.002	0.001	1,414	0.003	0.001	1,018	0.003	0.001
	Other	3,444	0.01	0.002	61,831	0.15	0.04	41,491	0.1	0.023	1,682	0.004	0.001	
non-LTR		9,013,331	26.38	4.97	10,089,776	25.15	5.79	10,644,056	24.83	5.84	8,534,895	21.8	4.69	
SINEs	<i>tRNA</i>	2,803,303	8.21	1.546	3,186,236	7.94	1.83	3,115,727	7.27	1.711	3,141,039	8.02	1.725	
	Other	1,316	0.004	0.001	6,146	0.02	0.004	18,637	0.04	0.01	397	0.001	0.0002	
SINEs		2,804,619	8.21	1.55	3,192,382	7.96	1.83	3,134,364	7.31	1.72	3,141,436	8.02	1.73	

Table S1. Cont.

<i>Class II</i>	TIR	<i>Tc1/Mariner</i>	9,533,907	27.91	5.257	12,200,944	30.41	7.00	11,769,349	27.45	6.463	9,679,802	24.73	5.316	
		<i>hAT</i>	4,586,181	13.42	2.529	4,576,551	11.41	2.63	5,930,663	13.83	3.257	6,866,612	17.54	3.771	
		<i>P</i>	7,644	0.02	0.004	7,337	0.02	0.004	9,288	0.02	0.005	7,257	0.02	0.004	
		<i>PiggyBac</i>	517,632	1.52	0.285	659,990	1.64	0.38	852,261	1.99	0.468	223,120	0.57	0.123	
		<i>Academ</i>	18,926	0.06	0.01	22,960	0.06	0.01	20,877	0.05	0.011	25,048	0.06	0.014	
		<i>DNA</i>	1,874,250	5.49	1.033	2,385,238	5.94	1.37	2,253,378	5.26	1.237	1,940,122	4.96	1.065	
		<i>CMC</i>	74,028	0.22	0.041	145,583	0.36	0.08	99,206	0.23	0.054	96,095	0.25	0.053	
		<i>Ginger</i>	20,225	0.06	0.011	35,089	0.09	0.02	16,173	0.04	0.009	31,626	0.08	0.017	
		<i>Kolobok</i>	42,928	0.13	0.024	58,732	0.15	0.03	63,921	0.15	0.035	49,243	0.13	0.027	
		<i>Merlin</i>	115,636	0.34	0.064	88,769	0.22	0.05	92,058	0.21	0.051	77,697	0.2	0.043	
		<i>MULE</i>	38,069	0.11	0.021	111,843	0.28	0.06	36,997	0.09	0.02	46,164	0.12	0.025	
		<i>PIF</i>	549,999	1.61	0.303	551,677	1.37	0.32	594,789	1.39	0.327	198,132	0.51	0.109	
		<i>Sola</i>	150,560	0.44	0.083	176,058	0.44	0.10	173,582	0.4	0.095	211,840	0.54	0.116	
		<i>Zator</i>	7,337	0.02	0.004	10,734	0.03	0.01	12,289	0.03	0.007	1,868	0.005	0.001	
		<i>Zisupton</i>	0	0	0	2,344	0.01	0.001	0	0	0	1,712	0.004	0.001	
		<i>Other</i>	3,972	0.01	0.002	152,821	0.38	0.09	121,702	0.28	0.067	2,685	0.01	0.001	
		Crypton	<i>Crypton</i>	251,886	0.74	0.139	430,830	1.07	0.25	379,108	0.88	0.208	338,279	0.86	0.186
		Helitron	<i>Helitron</i>	2,565,502	7.51	1.415	3,492,481	8.70	2.00	4,118,237	9.61	2.262	5,521,963	14.11	3.032
		Maverick	<i>Maverick</i>	616,445	1.8	0.34	254,247	0.63	0.15	489,341	1.14	0.269	644,424	1.65	0.354
		DNA transposons		20,975,127	61.4	11.56	25,364,228	63.21	14.55	27,033,219	63.05	14.84	25,963,689	66.32	14.26
Total TEs			34,161,991	100	19	40,126,137	100	23.02	42,875,616	100	23.5	39,148,318	100	21.5	
Other (non TEs)			147,200,430		81	134,211,513		76.98	139,222,998		76.5	142,945,507		78.5	
Total in genome			18,136,241		100	174,337,650		100	182,098,614		100	182,093,825		100	

bp = aligned base pairs (BLASTN 2); TE = TE percentage in relation to the total TE annotated ; G = genome percentage

Table S2. Number of base pairs (bp) and proportion (%) of repetitive sequences annotated using dnaPipeTE in the genomes of *Rhodnius* species.

	<i>R. prolixus</i> ¹		<i>R. prolixus</i> ²		<i>R. montenegrensis</i>		<i>R. marabaensis</i>	
	bp	%	bp	%	bp	%	bp	%
LTR	1,369,283	0.8	1,479,751	0.8	2,063,977	1.1	1,513,639	0.8
LINE	9,036,881	5.0	10,089,740	5.8	10,644,012	5.8	9,067,148	5.0
SINE	2,804,457	1.5	3,192,382	1.8	3,133,083	1.7	3,145,279	1.7
DNA	1,848,1976	10.2	21,871,447	12.5	22,913,643	12.6	21,255,599	11.7
Helitron	2,688,281	1.5	3,492,481	2.0	4,118,237	2.3	3,704,583	2.0
rRNA	54,665	0.0	42,102	0.0	56,709	0.0	99,074	0.1
Low complexity DNA	5668	0.0	207,322	0.1	8,794	0.0	17,928	0.0
Satellite DNA	7,416,288	4.1	3,448,113	2.0	4,984,264	2.7	7,529,581	4.1
Simple repeat	62,168	0.0	559,259	0.3	93,037	0.1	41,712	0.0
Other repeats	1,131,288	0.6	561,684	0.3	555,406	0.3	565,611	0.3
Unknown	11,565,271	6.4	8,768,638	5.0	40,061,977	22.0	14,704,919	8.1
Not repeated	126,746,195	69.9	120,624,731	69.2	93,465,475	51.3	120,448,752	66.1
Total	181,362,421	100	174,337,650	100	182,098,614	100	182,093,825	100

Table S3. Most abundant TE families identified (> 0.10%) in the genomes of *Rhodnius* species.

<i>R. prolixus</i>					<i>R. robustus II</i>					<i>R. robustus III</i>				
G (%)	TE (%)	N	Superfamily RM	Family RM	G (%)	TE (%)	N	Superfamily RM	Family RM	G (%)	TE (%)	N	Superfamily RM	Family RM
0.38	2.01	7108	RC/Helitron	Helitron-2N1	0.54	2.31	123675	DNA/Tc1-Mariner	Mariner-1*	1.18	5.92	14002	DNA/Tc1-Mariner	Mariner-1*
0.3	1.58	5626	DNA/Tc1-Mariner	Mariner-1*	0.44	1.91	44262	RC/Helitron	Helitron-2N1	0.45	2.27	5464	RC/Helitron	Helitron-2N1
0.3	1.55	5637	SINE/tRNA	SINE2-2	0.36	1.56	273628	DNA/Tc1-Mariner	Mariner-1*	0.28	1.4	3484	DNA/Tc1-Mariner	Mariner-1*
0.28	1.47	5275	LINE/I	I-5	0.34	1.46	174427	DNA/Tc1-Mariner	Mariner-1*	0.21	1.08	2723	LINE/I	I-5
0.28	1.45	5613	DNA/Tc1-Mariner	Mariner-1*	0.29	1.24	288162	DNA/Tc1-Mariner	Mariner-1*	0.2	1.04	2459	RC/Helitron	Helitron-2N1
0.25	1.29	4715	SINE/tRNA	SINE2-2	0.28	1.23	250592	DNA/Tc1-Mariner	Mariner-1*	0.19	0.99	2425	SINE/tRNA	SINE2-2
0.23	1.22	4555	DNA/Tc1-Mariner	Mariner-N9B*	0.26	1.14	72624	LINE/I	I-5	0.17	0.89	2108	DNA/Tc1-Mariner	Mariner-N9B*
0.23	1.21	4267	DNA/Tc1-Mariner	Mariner-1*	0.26	1.14	85525	SINE/tRNA	SINE2-1	0.16	0.84	2011	SINE/tRNA	SINE2-2
0.2	1.08	3953	DNA/Tc1-Mariner	Mariner-1*	0.22	0.96	279671	DNA/Tc1-Mariner	Mariner-1*	0.16	0.82	2254	SINE/tRNA	SINE2-1
0.2	1.07	3990	DNA/Tc1-Mariner	Mariner-1*	0.22	0.96	132097	DNA	DNA4-1	0.16	0.82	2063	RC/Helitron	Helitron-2N3
0.2	1.04	4168	DNA/DNA4-1	-	0.2	0.89	182993	RC/Helitron	Helitron-2N3	0.15	0.75	1788	DNA/hAT-Tip100	hAT-N27
0.17	0.91	3208	DNA/Tc1-Mariner	Mariner-1*	0.2	0.86	63156	DNA/TcMar-Tc1	Mariner-N17	0.15	0.74	1866	LINE/R1-LOA	Loa-2
0.16	0.86	3659	DNA/Tc1-Mariner	Mariner-1*	0.19	0.84	112036	DNA/Tc1-Mariner	Mariner-N9B*	0.14	0.73	1859	DNA/Tc1-Mariner	Mariner-N9*
0.16	0.83	3213	DNA/DNA4-1	-	0.18	0.78	77323	LINE/R1-LOA	Loa-2	0.14	0.72	2156	DNA4-1	-
0.16	0.82	3117	SINE/tRNA	SINE2-2	0.16	0.72	159441	SINE/tRNA	SINE2-1	0.13	0.67	1555	RC/Helitron	Helitron-2
0.15	0.78	2941	LINE/I-Jockey	Jockey-2	0.16	0.68	194765	DNA/Tc1-Mariner	Mariner-N9B*	0.13	0.67	1614	DNA/Tc1-Mariner	SMAR26
0.15	0.77	2810	SINE/tRNA	SINE2-2	0.15	0.68	167441	SINE/tRNA	SINE2-1	0.13	0.66	1667	DNA/Tc1-Mariner	Mariner-N11
0.14	0.73	2633	DNA/Tc1-Mariner	Mariner-1*	0.15	0.66	113816	DNA/Tc1-Mariner	Mariner-N9*	0.13	0.64	1487	DNA/Maverick	Polinton-3
0.13	0.69	2819	DNA/Tc1-Mariner	Mariner-1*	0.14	0.61	141776	RC/Helitron	Helitron-2N1	0.12	0.63	1540	DNA/Tc1-Mariner	SMAR26
0.13	0.67	2410	DNA/PIF-ISL2EU	ISL2EU-N1	0.14	0.6	200329	DNA	DNA4-1	0.12	0.62	1586	SINE/tRNA	SINE2-2
0.12	0.65	2525	SINE/tRNA	SINE2-1	0.13	0.58	47096	LINE/I-Jockey	Jockey-6	0.11	0.56	1322	DNA/TcMar-Tc1	Mariner-N39
0.12	0.65	2347	RC/Helitron	Helitron-2N3	0.13	0.57	30909	LINE/I-Jockey	Jockey-2	0.11	0.56	1347	DNA/TcMar-Tc1	DNA-2
0.12	0.62	2438	RC/Helitron	Helitron-2N1	0.13	0.56	69149	DNA/PIF-ISL2EU?	ISL2EU-N1	0.1	0.53	1266	DNA/Tc1-Mariner	Mariner-1*
0.12	0.62	2525	SINE/tRNA	SINE2-1	0.13	0.56	184500	RC/Helitron	Helitron-2N1	0.1	0.53	1331	RC/Helitron	Helitron-2N1
0.12	0.61	2428	SINE/tRNA	SINE2-1	0.12	0.53	153363	DNA/TcMar-Tc1	DNA-2	0.1	0.53	1289	RC/Helitron	Helitron-2N3
0.11	0.57	2105	RC/Helitron	Helitron-2N3	0.12	0.53	223695	DNA/Tc1-Mariner	Mariner-1*	0.1	0.51	1227	DNA/TcMar-Tc1	Mariner-N17
0.11	0.56	2083	RC/Helitron	Helitron-2N1	0.12	0.52	1480	LINE/I	I-5	0.1	0.48	1274	DNA/TcMar-Tc1	DNA-4
					0.11	0.5	125086	LINE/I-Jockey	Jockey-2					
					0.11	0.48	163160	LINE/I-Jockey	Jockey-1					

G = genome percentage; TE= TE percentage in relation to the total TE annotated; N=estimated copy number; Superfamily RM and Family RM=superfamily and family according to RepeatMasker; *most representative clades of *Mariner*

Table S4. Pairwise comparisons of specific TE families with the highest variation between the genomes of *Rhodnius* species.

Class	Family	R.	R.	R.
		<i>prolixus</i> ¹ G (%)	<i>montenegrensis</i> G (%)	<i>marabaensis</i> G (%)
Class I	<i>Jockey-2</i>	0.12	0.0005	---
	<i>Gypsy-N1</i>	0.0004	0.013	---
Class II	<i>Helitron-2</i>	0.01	0.0001	---
	<i>Helitron-2N2</i>	0.0006	0.04	---
Class I	<i>Gypsy-11</i>	0.01	---	0.0001
	<i>RTE-10</i>	0.0003	---	0.01
Class II	<i>SMAR26</i>	0.66	---	0.001
	<i>hAT-N30</i>	0.0001	---	0.02
Class I	<i>Jockey-1</i>	---	0.060	0.0004
	<i>Loa-2</i>	---	0.0007	0.054
Class II	<i>Helitron-2N2</i>	---	0.018	0.0002
	<i>Helitron-2N3</i>	---	0.05	1.03

G=genome percentage

Table S5. Shared and not shared TE families identified in the genomes of *Rhodnius* species.

Genome Comparisons	N	Families	<i>R. prolixus</i>		<i>R. montenegrensis</i>		<i>R. marabaensis</i>	
			G (%)	TE (%)	G (%)	TE (%)	G (%)	TE (%)
<i>R. prolixus</i> <i>R. montenegrensis</i> <i>R. marabaensis</i>	321	<i>Mariner-12_Sln</i> <i>Ginger2-N2_RPr</i> <i>CryptonI-1N3_RPro</i> <i>Jockey-1_Dro</i> <i>RTEX-1_DRh</i> <i>RTE-3_DR</i> <i>hAT-N27_RPr</i> <i>Mariner-23_RPr</i> <i>I-6_RPr</i> <i>RTEX-11_RPr</i> <i>hAT-N36_RPr</i> <i>Jockey-4_RPr</i> <i>piggyBac-N4_RPr</i> <i>RTE-56_LMi</i> <i>hAT-N23B_RPr</i> <i>Gypsy-1_RP-LTR</i> <i>Sola1-1_RPr</i> <i>RTE-2B_PPo</i> <i>BEL-1_RP-I</i> <i>Mariner-N3_RPr</i> <i>Mariner-N9B_RPr</i> <i>Mariner-5_RPr</i> <i>Gypsy-N1B_RPr-LTR</i> <i>RTEX-21_CGi</i> <i>Myotis_hAT1</i> <i>Gypsy-9_RP-I</i> <i>Mariner-32_RPr</i> <i>Mariner-N12_RPr</i> <i>Helitron-2_RPr</i> <i>BEL-1_RP-LTR</i> <i>Merlin-N2_RPr</i> <i>hAT-N20_RPr</i> <i>Mariner-21_RPr</i> <i>Mariner-29_RPr</i> <i>hAT-N18_RPr</i> <i>Jockey-2_RPr</i> <i>Gypsy-1_RP-I</i> <i>RTE-6_Hmel</i> <i>RTE-4562_AMi</i> <i>hAT-1_RPr</i> <i>Gypsy-5_RP-LTR</i> <i>MuDR-1_RPr</i> <i>Mariner-N4_RPr</i> <i>Mariner-21_LMi</i> <i>Mariner-15_RPr</i> <i>Gypsy-5_RP-I</i> <i>R1-2_DYa</i> <i>hATx-22_SM</i> <i>Jockey-8_RPr</i> <i>hAT-N3_RPr</i> <i>SART-1_MOc</i> <i>Polinton-2_RPr</i> <i>RTE-2_DBp</i> <i>Gypsy-14_LH-I</i> <i>Nimb-2_RPr</i> <i>hAT-N9_RPr</i> <i>Helitron-1_RPr</i> <i>Gypsy-16_RP-I</i> <i>Gypsy-9_RP-LTR</i> <i>Copia-14_SI-I</i> <i>Gypsy-41_LMi-I</i> <i>hAT-16_HRo</i> <i>Mariner-20_RPr</i> <i>Merlin-N3_RPr</i> <i>hAT-N19B_RPr</i> <i>hAT-3_RPr</i> <i>Gypsy-7_RP-I</i> <i>I-7_RPr</i> <i>OposCharlie1</i> <i>Mariner-N9_RPr</i> <i>Mariner-30_RPr</i> <i>hAT-N19_RPr</i> <i>hAT-N26_RPr</i> <i>Mariner-4_RPr</i> <i>RTEX-1_RPr</i> <i>R1-5_DK</i> <i>Mariner-37_SM</i> <i>Dong</i> <i>Ginger2-N1_RPr</i> <i>RTE_Ele5</i> <i>Mariner-98_HSal</i> <i>RTEX-13_RPr</i> <i>Mariner-N11_RPr</i> <i>CryptonI-1_RPro</i> <i>Polinton-4_RPr</i> <i>Gypsy-18_RP-I</i> <i>Gypsy-6_RP-I</i> <i>Mariner-N6_RPr</i> <i>hAT-N31_RPr</i> <i>Mariner-N10_RPr</i> <i>DNA-2_RPr</i> <i>DNA-2C_RPr</i> <i>hAT-N14_RPr</i> <i>hAT-N23_RPr</i> <i>Mariner-61_LMi</i> <i>Gypsy-21_RPr-I</i> <i>Mariner-N12B_RPr</i>	18.7	98.7	22.9	97.7	21	97.6

		<p>Mariner-99_HSal Gypsy-12_RP-LTR piggyBac-2_RPr RTE-4_LCh hAT-N10_RPr Mariner-N5_RPr Polinton-1_RPr Gypsy-4_RP-I Copia-1_MMa-I Gypsy-21_RPr-LTR hAT-N12_RPr DNA-1_RPr DNA3-2_RPr DNA-6_RPr hAT-N6_RPr Sola2-1_RPr Helitron-2N1_RPr LINER1-3_NVi Gypsy-4_RP-LTR Mariner-47_HSal Helitron-2_PM Mariner-N8_RPr Mariner-N23_RPr hAT-N34_RPr Gypsy-12_RP-I Gypsy-23_RPr-LTR EnSpm-3N1_RPr Gypsy-3_RP-I Gypsy-14_RP-I Daphne-39_LMi Kolobok-N1_RPr RTE-9_RPr Gypsy-20_RP-I RTE-18_HMM Helitron-2N2_RPr Mariner-3_RPr RTE-19_PPo Mariner-N31_RPr Gypsy-23_RPr-I Mariner-N36_RPr Mariner-25_RPr Mariner-14_RPr Mariner-13_RPr hAT-N38_RPr RTE-11_LMi piggyBac-14_SM Mariner-17_RPr hAT-N39C_RPr RTE-29_LMi hAT-N35_RPr Gypsy-N1_RPr-LTR I-2_RPr DNA-4_RPr I-5_RPr hAT-N1_RPr Mariner-N1_RPr hAT-N32_RPr Mariner-2_RPr I-1_RPr Gypsy-2_TCa-I Ingi-1_Rpro Mariner-N2_RPr Penelope-3_CQ MARIAM1 hAT-N30_RPr RTE-12_RPr Mariner-13_LHu hAT-N13_RPr hAT-N17_RPr Mariner-18_RPr hAT-2_MMa RTE-6_RPr RTE-2_PPo DNA4-1_RPr Helitron-2N3_RPr BEL-11_LH-I Mariner-N13_RPr RTE-3_RPr Gypsy-11_RP-I Nimb-3_RPr Harbinger-N1_RPr Gypsy-8_RP-I DNA8-1D_RPr LINER1-2_NVi Mariner-N18_RPr Gypsy-25_LH-I Gypsy-17_RP-I Copia-1_RP-LTR Mariner-12_RPr Mariner-N21_RPr Helitron-3_RPr RTE-12_HMM Mariner-24_RPr piggyBac-N2_RPr Copia-2_RP-I EnSpm-N2_RPr RTE-34_LMi CryptonI-1N1_RPro Nimb-4_RPr RTE-46_LMi Nimb-4B_RPr hAT-2N1_RPr Mariner-1_RPr piggyBac-N1_RPr Gypsy-8_RP-LTR Mariner-69_LMi ISL2EU-N1_RPr Gypsy-15_RP-I Gypsy-22_RPr-I hAT-N1_PPo Gypsy-4_LH-I RTE-5_RPr hAT-N2_RPr RTE-8_RPr I-3_RPr Mar1a_Tarsi Gypsy-2_RP-I BEL-9_LH-I Gypsy-217_DR-I EnSpm-1_RPr Helitron-N1_RPr Mariner-N38_RPr R1-3_DF Gypsy-13_RP-I hAT-N39B_RPr RTE-2_DAn Mariner-N39_RPr piggyBac-N3_RPr R2-1_RPr Loa-1_LMi Mariner-N20_RPr hAT-N33_RPr Mariner-N14_RPr Mariner-7_RPr Mariner-10_RPr hAT-N5_RPr nMariner-10_EF hAT-N28_RPr Mariner-N27_RPr RTE-2_RPr Jockey-6_RPr SINE2-2_RPr hAT-N21_RPr Mariner-6_RPr Loa-3_RPr Mariner-N35_RPr RTE-12_Hmel Polinton-3_RPr RTE-4_PXu Mariner-N41_RPr hAT-N11_RPr piggyBac-N5_RPr DNA8-1_RPr Mariner-11_RPr Jockey-5_RPr Mariner-27_RPr RTE-4_RPr piggyBac-1_RPr piggyBac-3_RPr MarsTigger4 L2-1_SIn Mariner-42_HSal Jockey-1_RPr RTE-63_LMi Nimb-1_RPr I-4_RPr Gypsy-7_RP-LTR Polinton-1_HM hAT-N16_RPr Mariner-2N1_RPr RTE-1_DBi hAT-N24_RPr Gypsy-10_RP-I hAT-N22_RPr Polinton-3_NVi Helitron2_AG Mariner-11N1_RPr Helitron-N5_RPr Mariner-N34_RPr Gypsy-N1_RP-I RTE-1_AG Mariner-N30_RPr Mariner-9_RPr RTE-1_DT Loa-1_RPr hAT-N15_RPr SINE2-1_RPr RTE-4_DF RTE-10_RPr Helitron-N6_RPr Loa-2_RPr hAT-3N1_RPr Copia-1_RP-I RTE-25_LMi Ingi-2_RPr Mariner-8_RPr RTE-2_DR LTR-1_RPr-LTR Mariner-N24_RPr Mariner-N7_RPr Mariner-25_SIn RTE-7_RPr Academ-N1_RPr Gypsy-19_CPB-I Gypsy-11_RP-LTR Mariner-N17_RPr Jockey-7_RPr Mariner-N15_RPr hAT-N37_RPr R1-1_NVi Gypsy-22_RPr-LTR R1-1_LMi Mariner-N26_RPr DNA2-1_RPr Merlin-N1_RPr Mariner-66_HSal hAT-N8_RPr Mariner-N38_LSal L2-1_RPr Mariner-N32_RPr Jockey-3_RPr SPIN_Ml Mariner-N29_RPr Mariner-39_SM</p>						
<i>R. prolixus</i> <i>R. montenegrensis</i>	28	<p>BEL-44_CQ-I Gypsy-45-I_NV RTE-26_LMi RTE-1_MMa nMar-10_Hmel Zator-N1_RPr L2-1_NVi Gypsy-10_PBa-I RTE-2_DT R1-2_DF Jockey-11_AAe EnSpm-3_RPr L2-2_SIn Gypsy-196_AA-I L2-2_NVi BEL-5_CQ-I Copia-3_RPr-I Mariner-18_SIn Ag-Jock-12 Gypsy-106_AA-I Loa-2_DTa Gypsy58-I_DR hAT-N4_RPr CR1-19_HM RTE-12_SP Helitron-1_DF Gypsy-13_RP-LTR Copia-4_RPr-LTR</p>	0.05	0.26	0.06	0.23	-----	-----

Table S5. Cont.

<i>R. prolixus</i> <i>R. marabaensis</i>	47	Gypsy-24_DBp-1 RTE-10_LMi BEL-7_SI-I Gypsy14-I_SP R1-5B_DK Gypsy13-NVi_I-int RTE-66_LMi Copia16-NVi_I-int DNA-6-3_NV Gypsy-3_Ami-I Mariner-31_RPr Gypsy-32_DYa-I Daphne-29_LMi RTE-13_Hmel RTE-6_HMM R4_Hmel RTE-70_LMi Dong-2_Lch RTE-17_LMi RTE-5_PXu RTE-17_CPB ENSPM1_VV Gypsy-39_Ami-I DNA4-2_RPr SMAR26 Jockey-2_DK hAT-20_HM Gypsy4-I_AP nhAT-2a_Nhu OSVALDO_I-int hAT-26_LMi RTE-2_MMa RTE-13_Lch Gypsy-4_SI-I hAT-2_RPr RTEX-11_SK hAT-N10_XT Mariner-N16_RPr R1-3_DYa Harbinger-1_DW Mariner-26_SM Polinton-1_AcE R1-4_DAn LYDIA_I-int R1-3_DBp Kiri-3_CQ R1-1_AEc	0.06	0.32	-----	-----	0.3	1.5
<i>R. montenegrensis</i> <i>R. marabaensis</i>	56	Daphne-75_LMi RTE-1_DT SMAR16_R1_DYa Mariner-N33_RPr Gypsy24-I_AG DNA8-4B_LMi Mariner-N19_RPr Mariner-32N1_RPr Academ-3_CS DNA-2B_RPr Copia-4_RPr-I RTE-16_PPo Copia1-I_XT Gypsy-25_SP-I RTE-1_NVi Gypsy8-I_AP Jockey-13_DBp Sola1-6_AP Mariner-36_LMi Sola2-6_LSal hAT-N7_RPr piggyBac-17_SM Jockey-13_AAe hAT-1_DAn Mariner-13_DF Gypsy-11_XT-I hAT-N29_RPr Mariner-2N1_PM Mariner-29_SM R1-11_DWi Mariner-19_RPr Mariner-26_RPr hAT-4_CPB Ag-Jock-1 hAT-3_SM Gypsy-7-I_HM RTE_Ele4 hAT-4_RPr Gypsy-93_CQ-I Mariner-6_Sln LIN4b_SM Crypton1-IN2_RPro Jockey-1_Hmel Mariner-16_RPr Penelope-5_HRo RTE-2_CQ RTE-8_Hmel Gyps1_I-int Gypsy15-I_SP Mariner-9_PBa Mariner-16_DRh hAT-6_SM Jockey-14_AAe hAT-47_SM Gypsy-5_Ami-I	-----	-----	0.06	0.22	0.08	0.4
<i>R. prolixus</i>	125	BEL-13_DEI-I Copia-46_ALY-I R1_DPs EXPANDER1_DR I-50_AAe Daphne-12_HRo hAT-N28_LMi Mariner-13_AcE Nimb-5_LMi MARINER2_GT hAT-6_Crp BEL-3_DBp-I BEL-73_AA-I RTE-1_DBp Kiri-1_DPer hAT-4_PBa BEL-618_AA-I BEL-21_DTa-I RTEX-16_CGi Gypsy-3_RP-LTR RTEX-2_SK Gypsy-25_AA-I LOA_Ele7 Kiri-5_LMi Gypsy-15_RP-LTR RTEX-2_CGi RTEX-20_CGi Gypsy-7_LCh-I Gypsy12-I_SP Gypsy-8_CFI-I Jockey-1_CQ TRAS3_SC Zator-3_HM Baggins-3_NVi Jockey-6_DVi DNA-like-1_Hmel piggyBac-3_SM Jockey_Ele8 BEL-123_AA-I RTE-32_LMi Polinton-4_PBa Gypsy-5_DEI-I Gypsy-26_CSa-I SARTBm3 Copia-2_RP-LTR Gypsy-14_LVa-I RINS-1_CQ Nimb-33_LMi BEL-16_DWi-I Copia-1_SPDB-I Crack-14_AAe Polinton-2_TC piggyBac-14_LMi Loa-2_MMa Gypsy-71_PTr-LTR Loa-2_DF Polinton-7_NVi Gypsy5-I_AP hAT-31_LMi R1-3_DTa R1-4_DWi BEL-145_AA-I SART-6_APi Nimb-42_LMi RTE-1_SK R1-1C_DK LOA_Ele2B_AAe Polinton-1_NVi BEL-13_DP-I MARINA Gypsy-167_AA-I Copia-130_AA-I RTEX-22_SK Copia-41_ST-I MAX_I-int RTE-2_AG Gypsy-3_SI-I BEL-1_PBa-I Gypsy142-I_DR BEL-3_DGri-I Mariner-N2_Crp nMar-8_Hmel Gypsy6-I_Dmoj Gypsy-7_DRh-I ACCORD2_I-int JAM1B_AAe BARE1A_HV-int Sadhu7-1_SART-5_MOc hAT-2_AP Gypsy-33_CT-I Mariner-28_RPr Mariner-2_Sln BEL-210_AA-I Gypsy-44_DEI-I Gypsy-49_SSa-I Loa-1_DK Polinton-2_DK BEL-21_DAn-I Gypsy-1_CGi-I Gypsy2-NVi_I-int Gypsy-16_CFI-I Tigger17c LOA-1_DGri Chapaev3-1_PM R1-4_DK Mariner-N28_RPr RTEX-3_SK MonGyp1 DOC6_DM CR1-5_Hmel R1-3_DK RTEX-19_SK hAT-15_SM R1_Ele8 Jockey-4_DEu BS Polinton-4_LMi BEL-43_AA-I Jockey-6_DEI BEL-4_SSa-I R1-5_DPer R1-2_DK Helitron-2_AAe	0.13	0.71	-----	-----	-----	-----
<i>R. montenegrensis</i>	198	Mariner-3_AF Copia-91_VV-I I-6_AO Gypsy-31_BG-I Gypsy-8_CH_I-int Copia-84_PT-I Gypsy-8_CCO-I RTE-11_SP Gypsy-32_ADe-I RETROSAT4_I-int Mariner-1_AN Copia-5_MN-I Gypsy-71_PAb-I BEL-3-I_NVi BEL-12_Adi-I RTEX-5_ACar Copia27-PTR_I-int Gypsy-2_Cop-I Copia-32_Sit-I Mariner-2_LMi Gypsy-20_SI-I Mariner-7_AF Gypsy-1-I_AN Tad1-4_BG Gypsy-93_MLP-I Gypsy-22_CSa-I Mariner-2_TMe Copia-8_LH-I hAT-2_HRo BEL29-I_DR copia-2-I_AF Mariner-1N1_RPr SINE3-1_AO Copia-7_TMe-I Helitron1_DM Tc1-5_DR RTE-16_Hmel Gypsy-1-LTR_AF Gypsy-57_CQ-I Mariner-N24_LMi Mariner-4_AN Gypsy-58_BG-I SARTTc3 BEL-625_AA-I Daphne-17_LMi Gypsy-51_BG-I Gypsy5_I-int Gypsy-2_Adi-I Gypsy-151_AA-I Gypsy-3_CH EnSpm-1_HV BEL-5_LH-I Gypsy-5_ADe-I AFLAV_LTR Gypsy4-LTR_AO Gypsy-17_Alp-I Gypsy-23_PSo-I Gypsy-2_SSa-I RTE-27_LMi Copia-52_BD-I Gypsy-11_SCH-I BEL-40_AA-I EnSpm-1_AEc Copia-61_VV-I MarinerL-1_AO Gypsy-7_Ano-I L1PA4 Gypsy-3_CT-I Gypsy-17-I_NVi Gypsy-12_SSa-I Gypsy-1_Trm-I Jockey-7_DAn Gypsy-59_CQ-I Mariner-5_AF Gypsy-98_MLP-I EnSpm-5_HM RTE-4_BM Copia-1-I_AN RTE-8_PPo Gypsy-44-I_NV Gypsy-7_CH MARY1_TM R1_Ele4 Gypsy-1-I_AF PENEL1_NVi Gypsy-1_ADJ-I Mariner-7_AN Jockey-2_DAn Gypsy-6_AA-I Sola1-1_Smoe hAT-1_DP Gypsy-11_PPa-I Gypsy4-I_AO Gypsy56-I_AG I-1_AO Mariner5_AO Gypsy-3-I_XT RTE-57_LMi Gypsy-41_LSal-I RTAg4 Mariner-5_LMi TCN1-I EnSpm-15_HM piggyBac-1_Sln BEL-196_AA-I Gypsy-5_DVir-I Copia-3-I_AN Gypsy-9_BG-I I-4_AO Gypsy-31-LTR_DR Gypsy-7_BG-I AgaP8 Copia-4_PGr-I Copia-10_DPu-I Gypsy-5_DSe-I Gypsy-4_PPC-I Polinton-5_PBa RTE-2_LVa Gypsy-29_BG-I AFUT1-I NHT2_I-int Gypsy-135_SBi-I EnSpm-17_OS Mariner-15_SM CryptonF-1_ACap Gypsy-13_SI-I Baggins-1_NVi R2A_NVi_I_Ele19 TART_DV Copia-76_AA-I Gypsy-8_LG-I RTE-50_LMi Gypsy-6_ATr-I Gypsy58-ZM_I-int Gypsy-3_ST-I R1-7_DPer Jockey-1_DF RTE_Ele2C_AAe BEL-3_AEc-I Copia-14_BG-I Gypsy-20_PIT-I RTE_Ele2_Sola1-1_LMi Gypsy-2_MGI-I Copia-18_BD-I I-5_AO RTE1_Sar Juan-A_AA Gypsy-1_AC-I Gypsy-21_DWi-I Gypsy-2_MMa-I hAT-N23_LMi Gypsy-4_TMe-I Gypsy-1_GDe-I Cheshire_Mars_Copia-1_ATe-I Copia-19_CCri-I Mariner-2_DEu Gypsy-4_Trm-I Mariner-5_AN Gypsy-3-I_AF Ag-Jock-13 hAT-45_SM AFLAV_I-int piggyBac-10_SM R1-3_DAn Gypsy-27_BG-I Gypsy-2-I_AF Howilli1 Jockey-6_DAn BEL-104_AA-I Gypsy-30_SI-I Gypsy-19_RP-I Transib-1_Sln Gypsy-58_AA-I Mariner2N1_AO Gypsy-41_BG-I Mariner-37_Sln Mariner-1_AF Gypsy-6_SCH-I copia-1-I_AF BEL-10_SSa-I Gypsy-4_BG-I RTEX-9_CGi Copia-10_SB-I RTE-6_BF Gypsy-56_BG-I Gypsy-1_BFB-I MuDR-5_Mad RTE-10_PXu Mariner-6_AN Gypsy3-I_SP BEL-256_AA-I Daphne-53_LMi Copia-2-I_AN hAT-N4_ALy CR1-18_HRo	-----	-----	0.44	0.86	-----	-----

Table S5. Cont.

<p><i>R. marabaensis</i></p>	<p>160</p>	<p>RTE-15_Hmel MamRTE1 Mariner-9_AEc WaldoAg2 Mariner-1_PBa Helitron-1_AC R2-2_RPr RTE-60_LMi Charlie8 Jockey-9_DY Mariner-59_LMi Waldo-4_AAe Gypsy-6_CFI-I Copia-30_TC-I EnSpm-4N1_HM Gypsy-58-I_NV hAT-23_LMi Gypsy-175_DR-I piggyBac-1_BM Copia-6_LH-I BEL3-I_AP BEL-8_DEI-I Mariner-4_ACar Tx1-51_DR Mariner-25_LMi Copia-26_MN-I RTE-20_HMM Gypsy-49_LMi-I RTEX-7_SK Gypsy93-I_DR Mariner-7_LMi Mariner-20_DK Mariner-7_DBi BEL-2_DGri-I DIRS-8_DR SPIN_Og Pokey_Cis Gypsy-50_AA-I Mariner-2_TCa piggyBac-1_AAe Mariner-N6_LSal Nimb-1_GA Kiri-37_AAe Gypsy-26_LH-I RTE-14_SP LTR1B_OG RTE-21_PPo Sola1-3_AP ISL2EU-5_CFI EnSpm-1_JC Penelope-13_HM R1-1_DbP EnSpm-2_RPr Harbinger-1_DF HARB-3_Mad RTE-2_BM Mariner-N25_RPr Transib-12_HM Gypsy-31_SI-I Gypsy-3_DGri-I Gypsy-9_Ami-I G3_DM Nimb-2_LVa hAT-10_CPB Gypsy-17_Sit-I hAT-39_SM Gypsy-5_CSa-1 Sola2-N1_LMi piggyBac-1_DBi RTE-20_PPo DNA11_AFC Polinton-5_LMi RTE-13_CPB Mariner-N20_LSal RTE-4_CPB Gypsy-7_ST-I Mariner-N22_RPr Copia-14_Cia-I Gypsy-15_LH-I Gypsy-135_GM-I OposCharlie1a TIRANT_I-int Gypsy-20_GA-I R1 Gypsy-10_RP-LTR RTE-65_LMi Copia2-VV_I-int hAT-11_CPB Mariner-10_HSal RTE-22_PPo Mariner-N15_SIn SARTTc1 Gypsy-45_AA-I Gypsy-11-I_NV Mariner-26_SSa Mariner-N37_RPr SMARN3 Gypsy-1_ACe-I Tx1-3_PM Baggins1_Cis Mariner-22_AEc Polinton-2_ACe RTE-3B_SP Gypsy-75_AA-I nhAT-5a_Nhu R5-1_SM hAT-14_HRo L2-46_DR Gypsy-32_SSa-I RTE-11_Hmel BovB_Pb Harbinger-N15_BF CR1-6F_Ami CR1-2_TCa Gypsy-2_RP-LTR Mariner-14_LHu hATN-1_SM Waldo-6_AAe Gypsy57-I_DR BEL-2_DVir-I Ginger2-1_AP Nimb-12_DR Mariner-15_HSal Mariner-15_LMi Copia-1-I_DY Gypsy66-I_AG Jockey-11_DAn Mariner-25_HSal Gypsy-8_CGi-I RTEX-11_BF Jockey-6_LMi Gypsy-71_AA-I Copia-41_ATr-I SARTTc2 hAT-5_RPr Polinton-1_LMi Copia-3_MMa-I Helitron-3_HMM hAT-17_SM Gypsy45-I_AG Mariner-51_LMi Lian-Aa1 Gypsy160-I_DR DNA6-1_CGi Gypsy-18_CSa-I RTE-7_Hmel Gypsy-92_AA-I BEL-47_AA-I R1-4_DPer Gypsy-37_CQ-I Copia-70_Mad-I Mariner-22_RPr Gypsy-7_TCa-I Gypsy-274_AA-I SMAR15 Expander hAT-3_PM Copia-21_SI-I Gypsy-24_AA-I Jockey-1_DSi</p>	<p>-----</p>	<p>-----</p>	<p>0.10 0.46</p>
<p>Total TEs</p>			<p>----- 100</p>	<p>----- 100</p>	<p>----- 100</p>
<p>Total in genome</p>			<p>19 -----</p>	<p>23.5 -----</p>	<p>21.5 -----</p>

G =genome percentage; TE= TE percentage in relation to the total TE annotated

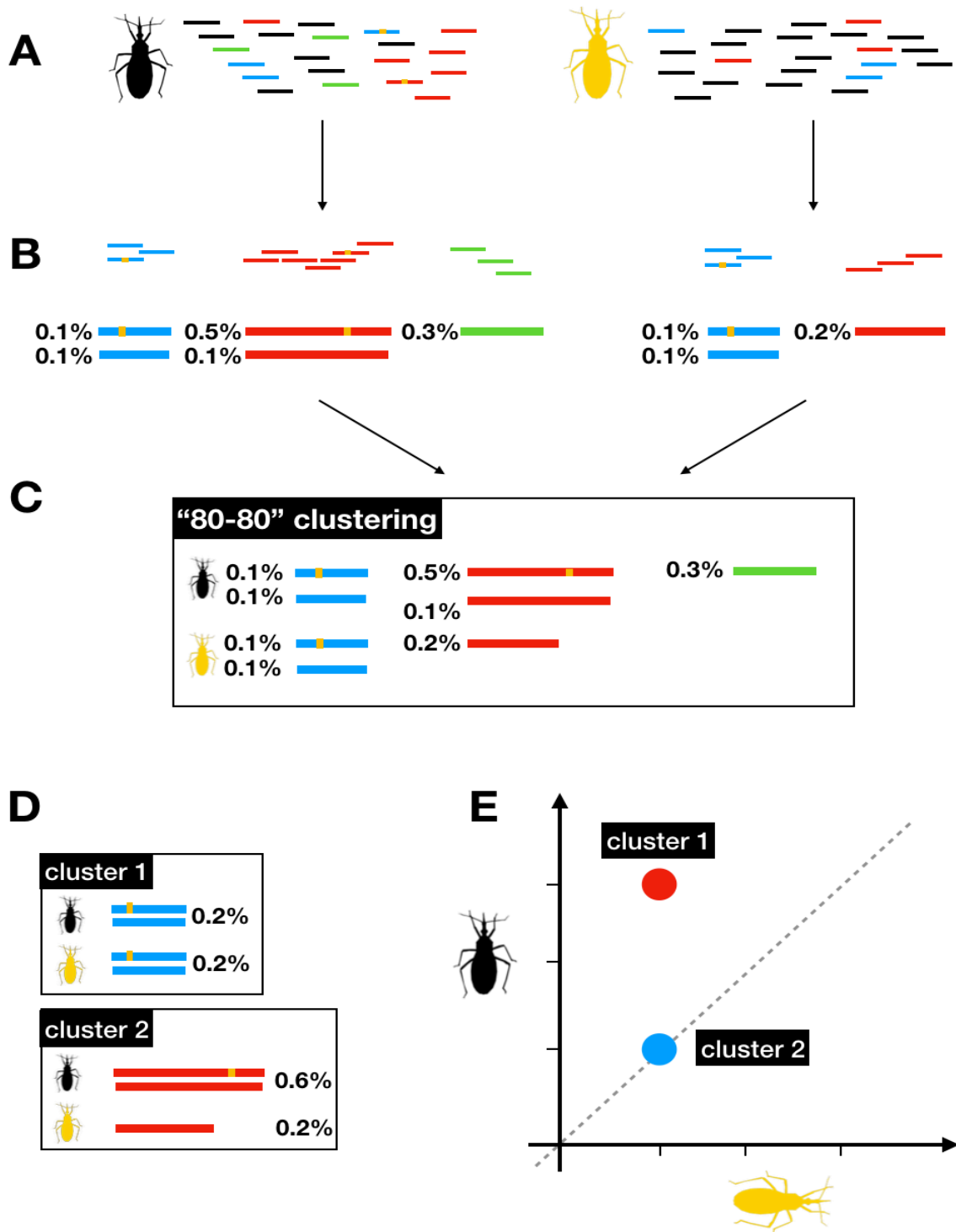


Figure S1. dnaPipeTE analysis and comparison of shared TE family content. **A:** sequencing reads are generated for each species. Colored reads represent repeats, yellow strokes structural variants or point mutations **B:** Repeats are assembled with dnaPipeTE and TE are quantified. Thick lines represent dnaPipeTE contigs. **C:** Repeat contigs of each species are labelled, grouped by pair of species and clustered to identify shared TE families following the "80-80" rule (Wicker et al, 2007 and see also Methods). **D:** Shared clusters, representing shared TE families are kept and the proportion of each family is calculated for each species. **E:** linear regression is performed to analyze the relative TE content of the species pair.

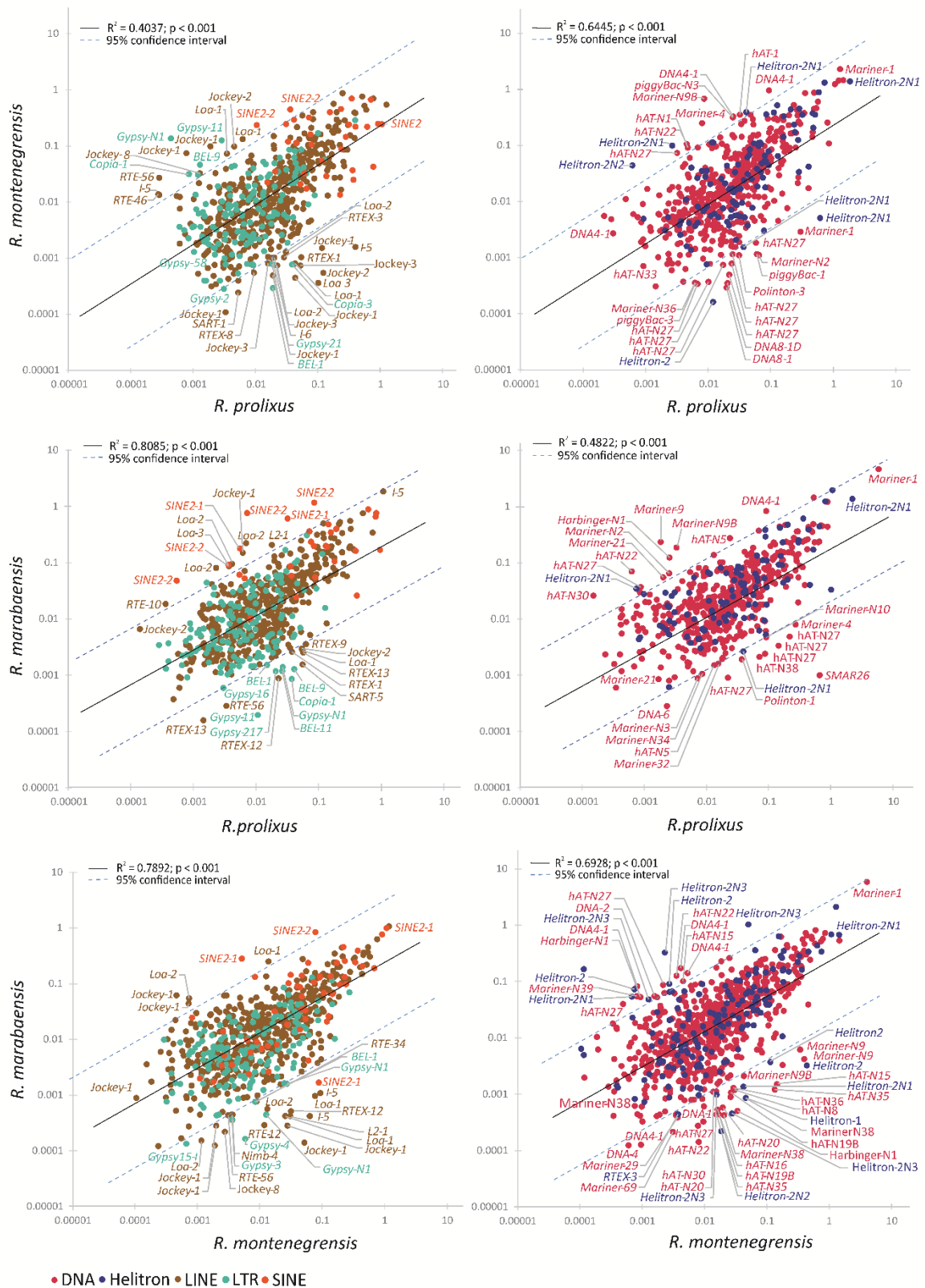


Figure S2. Scatter plot and analysis of linear regression of the relative genome proportions of shared TE families between the *Rhodnius* genomes in terms of genome percentage (log₁₀ scale). Each dot represents a shared TE family, defined by the highest BLAST hit between the TE family reference contig of each species. On the left: Class I elements; on the right: Class II elements.