

Figure S1 Pearson's correlation between density of reads and nuclear genome size for *gypsy* and *copia* elements.

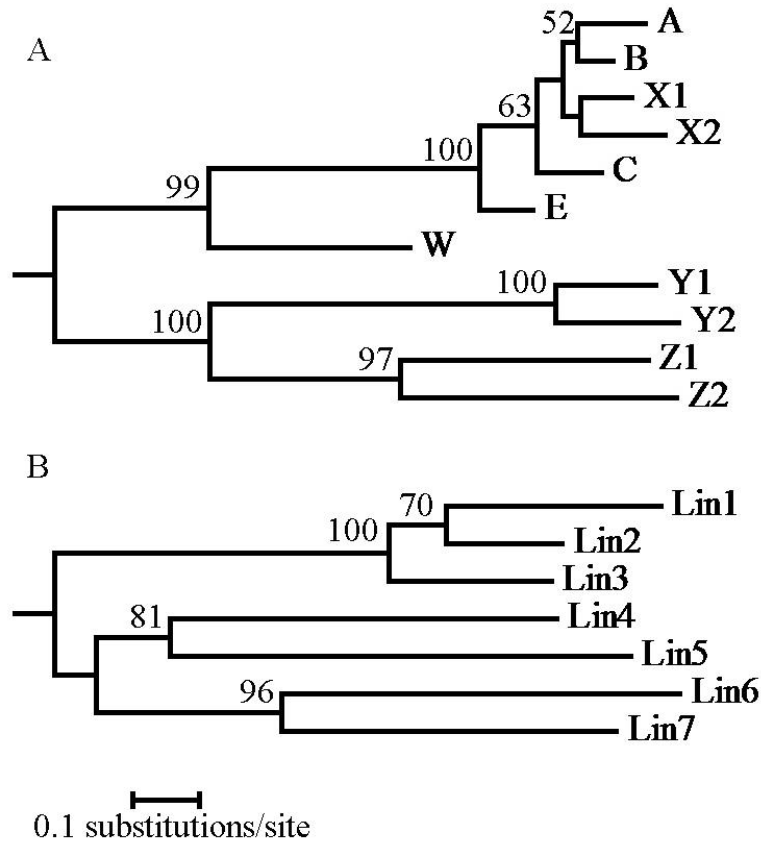


Figure S2 Phylogenetic relationship among different sublineages of (A) *gypsy* and (B) *copia* based on amino acid sequences of the reverse transcriptase domain (*gypsy*, 173 a.a.; *copia*, 250 a.a.) using maximum likelihood. Bootstrap scores are presented for internal branches with >50 % support.

Table S1 Summary statistics of DNA-seq and RNA-seq data

Sequencing type	Species	Replicates	Number of raw reads	Number of reads after trimming	Mean length of trimmed reads (bp)
DNA-seq	<i>H. agrestis</i>	AGR1	38,554,268	28,610,193	99.6
		AGR2	38,282,728	28,640,114	99.6
		AGR3	40,376,468	29,519,333	99.6
	<i>H. carnosus</i>	CAR1	34,000,952	24,639,844	99.6
		CAR2	36,392,088	26,776,432	99.6
		CAR3	38,609,046	28,317,411	99.6
	<i>H. porteri</i>	POR1	59,893,198	44,461,335	99.6
		POR2	63,510,716	48,040,581	99.7
		POR3	42,380,084	31,137,587	99.6
RNA-seq	<i>H. agrestis</i>	AGR1	39,956,738	36,263,031	93.7
		AGR2	43,991,344	39,901,894	93.8
		AGR3	41,116,568	37,346,480	93.9
	<i>H. carnosus</i>	CAR1	56,917,536	51,694,853	93.8
		CAR2	48,492,050	44,007,765	93.8
		CAR3	52,736,736	47,940,872	93.8
	<i>H. porteri</i>	POR1	44,362,868	40,207,966	93.8
		POR2	49,721,984	45,154,958	93.8
		POR3	35,754,786	32,591,321	93.8