

## SUPPLEMENTARY DATA

FIG. S1. Detailed annotation of the fosmid clones (c1086 – c1093) as a modified Sequin graphic display, where repetitive elements (REs) used for quantification are coloured according to Fig. 5 in the main text and the other REs are in grey scale. If not indicated otherwise, contigs are numbered in the correct order. Gaps between contigs are marked by █. For details see GenBank accession numbers: GU188675 – GU188682.

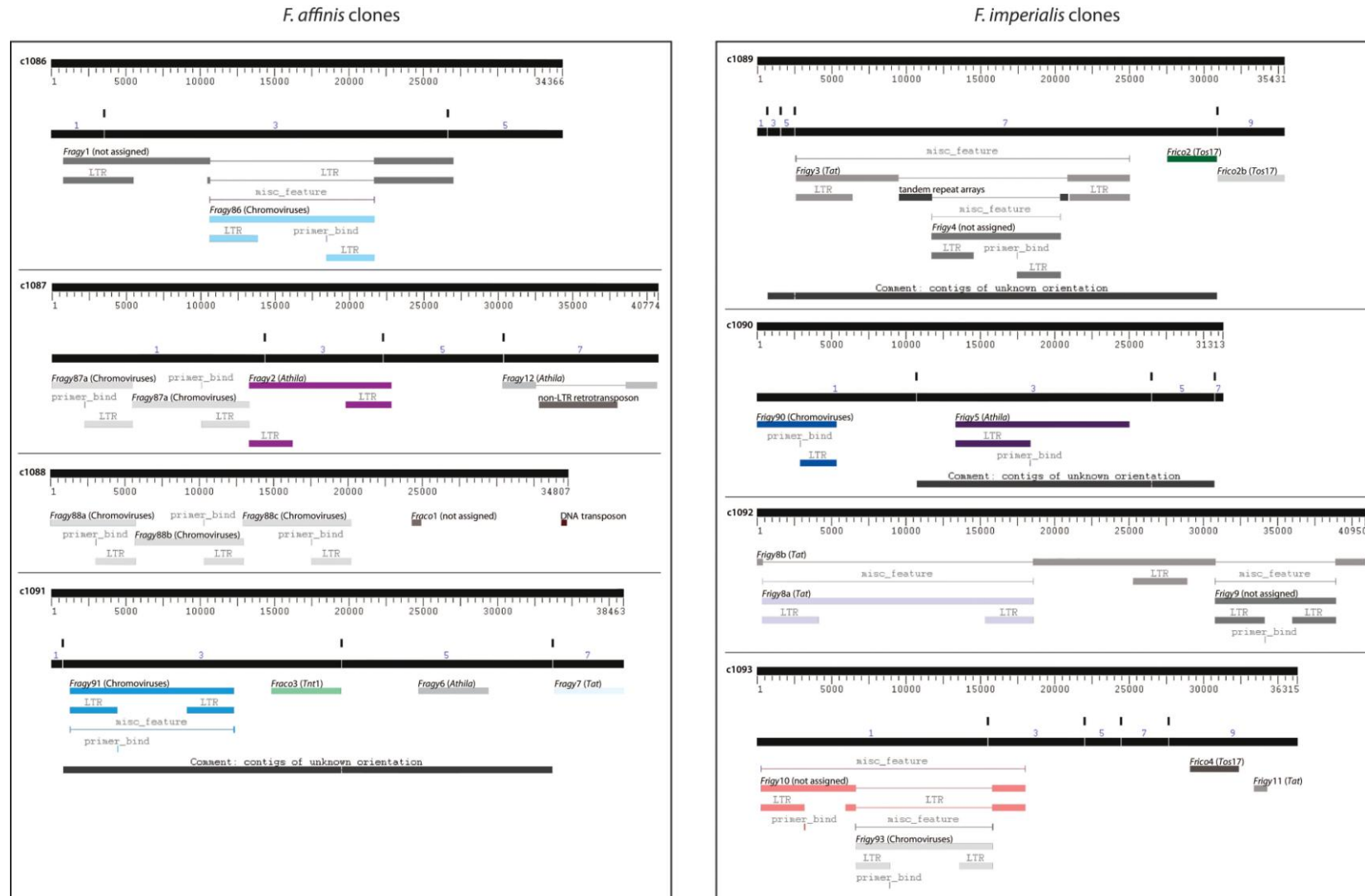


FIG. S2. A phylogenetic tree of RT-domains isolated from selected Ty1/*copia* type retrotransposons. The elements identified in *F. affinis* and *F. imperialis* are highlighted.

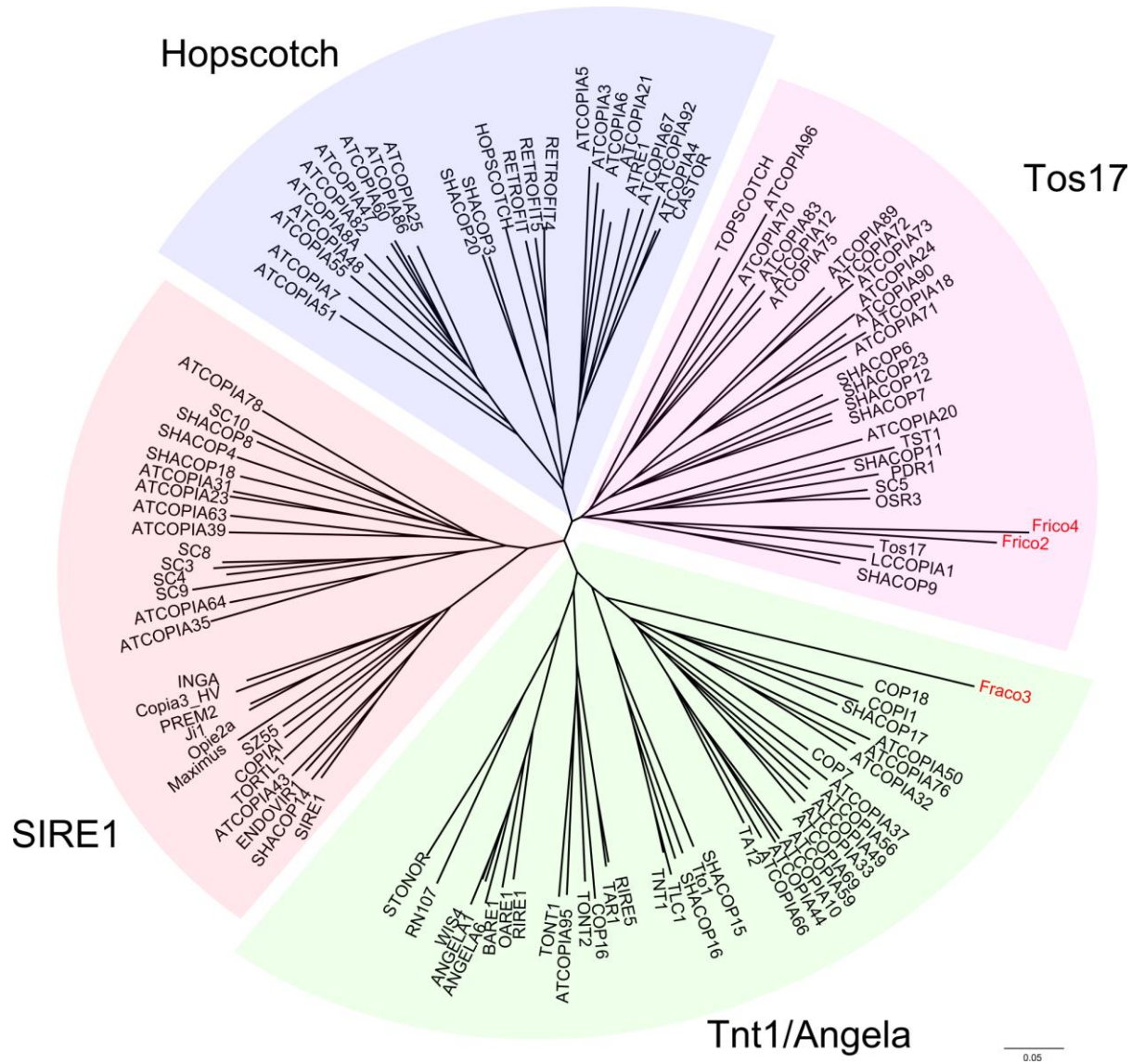




TABLE. S1A. Results of dot-blot quantification of selected Ty3/*gypsy* and Ty1/*copio* class LTR retrotransposons, and a DNA transposon performed under 85 % stringency in 11 *Fritillaria* species and *Lilium martagon*. The estimated amounts of individual repeat elements are given as copy number  $\times 1000 C_x^{-1}$  (upper number) and as genome proportion (in brackets). Genome proportion of all identified dispersed elements and FriSAT1 are also given.

	Tat lineage		Chromoviruses				Athila lineage		Tnt1-like	Tos17-like	DNA transposon	All dispersed repeats (%)	FriSAT1 (%)
	Frigy 8a	Fragy 7	Fragy 86	Frigy9 0	Fragy 91	Frigy1 0	Fragy 2	Frigy5	Fraco3	Frico2			
<i>F. ruthenica</i>	<0.1 (<0.1)	0.5 (<0.1)	<0.1 (<0.1)	0.8 (<0.1)	<0.1 (<0.1)	0.4 (<0.1)	<0.1 (<0.1)	1.4 (<0.1)	1.2 (<0.1)	0.3 (<0.1)	0.3 (<0.1)	<b>0.1</b>	<0.1
<i>F. gibbosa</i>	<0.1 (<0.1)	1.2 (<0.1)	0.5 (<0.1)	1.0 (<0.1)	<0.1 (<0.1)	0.1 (<0.1)	<0.1 (<0.1)	1.9 (0.1)	0.9 (<0.1)	0.6 (<0.1)	<0.1 (<0.1)	<b>0.2</b>	<0.1
<i>F. japonica</i>	<0.1 (<0.1)	1.1 (<0.1)	5.9 (0.1)	3.0 (<0.1)	2.2 (<0.1)	0.5 (<0.1)	0.1 (<0.1)	8.2 (0.1)	1.1 (<0.1)	0.6 (<0.1)	0.5 (<0.1)	<b>0.3</b>	<0.1
<b><i>F. imperialis</i></b>	<b>57.9</b> <b>(2.3)</b>	<b>&lt;0.1</b> <b>(&lt;0.1)</b>	<b>16.6</b> <b>(0.4)</b>	<b>40.9</b> <b>(0.9)</b>	<b>0.5</b> <b>(&lt;0.1)</b>	<b>8.4</b> <b>(0.2)</b>	<b>0.7</b> <b>(&lt;0.1)</b>	<b>43.9</b> <b>(0.9)</b>	<b>1.0</b> <b>(&lt;0.1)</b>	<b>1.0</b> <b>(&lt;0.1)</b>	<b>0.3</b> <b>(&lt;0.1)</b>	<b>4.7</b>	<b>&lt;0.1</b>
<i>F. sewerzowii</i>	<0.1 (<0.1)	0.3 (<0.1)	0.1 (<0.1)	9.6 (0.2)	<0.1 (<0.1)	1.7 (0.1)	0.2 (<0.1)	13.0 (0.3)	0.6 (<0.1)	1.2 (<0.1)	0.2 (<0.1)	<b>0.6</b>	<0.1
<i>F. persica</i>	<0.1 (<0.1)	0.8 (<0.1)	4.9 (0.1)	2.9 (0.1)	<0.1 (<0.1)	1.5 (<0.1)	0.2 (<0.1)	2.3 (0.2)	0.8 (<0.1)	1.0 (<0.1)	<0.1 (<0.1)	<b>0.4</b>	<0.1
<i>F. davidii</i>	<0.1 (<0.1)	1.6 (<0.1)	4.7 (0.2)	1.3 (<0.1)	0.2 (<0.1)	0.1 (<0.1)	0.3 (<0.1)	1.3 (<0.1)	1.1 (<0.1)	0.8 (<0.1)	0.3 (<0.1)	<b>0.4</b>	<0.1
<i>F. glauca</i>	<0.1 (<0.1)	<0.1 (<0.1)	2.0 (<0.1)	2.0 (<0.1)	0.3 (<0.1)	0.7 (<0.1)	0.4 (<0.1)	2.9 (0.1)	0.7 (<0.1)	1.0 (<0.1)	0.3 (<0.1)	<b>0.2</b>	6.0
<b><i>F. affinis</i></b>	<b>5.6</b> <b>(0.2)</b>	<b>10.4</b> <b>(0.2)</b>	<b>155.4</b> <b>(3.9)</b>	<b>2.23</b> <b>(&lt;0.1)</b>	<b>85.6</b> <b>(2.1)</b>	<b>0.1</b> <b>(&lt;0.1)</b>	<b>2.5</b> <b>(0.1)</b>	<b>4.9</b> <b>(0.1)</b>	<b>1.2</b> <b>(&lt;0.1)</b>	<b>1.0</b> <b>(&lt;0.1)</b>	<b>0.9</b> <b>(&lt;0.1)</b>	<b>6.7</b>	<b>25.8</b>
<i>F. falcata</i>	–	–	–	–	–	–	–	–	–	–	–	–	35.8
<i>F. pudica</i>	<0.1 (<0.1)	0.5 (<0.1)	22.8 (0.7)	1.7 (<0.1)	4.3 (0.1)	0.1 (<0.1)	0.7 (<0.1)	1.9 (<0.1)	0.8 (<0.1)	0.8 (<0.1)	<0.1 (<0.1)	<b>0.9</b>	1.1
<i>F. camschatcensis</i>	<0.1 (<0.1)	3.0 (0.1)	4.1 (0.1)	1.2 (<0.1)	0.7 (<0.1)	0.1 (<0.1)	2.1 (0.1)	6.9 (0.2)	1.2 (<0.1)	1.0 (<0.1)	1.0 (<0.1)	<b>0.5</b>	0.6
<i>Lilium martagon</i>	<0.1 (<0.1)	0.3 (<0.1)	3.2 (0.1)	0.6 (<0.1)	0.5 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	0.2 (<0.1)	0.5 (<0.1)	0.9 (<0.1)	0.2 (<0.1)	<b>0.1</b>	<0.1

TABLE. S1B. Quantification of selected repeats estimated using fosmid libraries hybridization performed under 85 % stringency in two model *Fritillaria* species. The estimated amount of individual repeat elements is given as copy number  $\times 1000 C_x^{-1}$  (upper number) and as genome proportion (in brackets).

	Tat lineage		Chromoviruses				Athila lineage		Tnt1-like	Tos17-like	DNA transposon	All dispersed repeats (%)	FriSAT1 (%)
	Frigy 8a	Fragy 7	Fragy 86	Frigy9 0	Fragy 91	Frigy1 0	Fragy 2	Frigy5	Frac03	Fric02			
<i>F. imperialis</i>	44.0 (1.7)	0.1 (<0.1)	25.0 (0.6)	30.9 (0.7)	0.4 (<0.1)	24.9 (0.5)	<0.1 (<0.1)	45.6 (0.9)	0.1 (<0.1)	3.1 (0.1)	<0.1 (<0.1)	<b>4.5</b>	<0.1
<i>F. affinis</i>	16.1 (0.7)	28.4 (0.6)	59.4 (1.4)	0.6 (<0.1)	44.7 (1.1)	0.1 (<0.1)	<0.1 (<0.1)	2.3 (0.1)	0.1 (<0.1)	1.6 (<0.1)	0.2 (<0.1)	<b>3.9</b>	<0.1