

Table S1 Detection and characteristics of full-length LTR-RTs in Cucurbitaceae species

Species	Assembled genome size	Number of full-length LTR-RTs	Cumulative length	Number/Mb	Number of each type			Average length of each type (bp)		
					<i>Copia</i>	<i>Gypsy</i>	Unknown	<i>Copia</i>	<i>Gypsy</i>	Unknown
<i>Cucumis hystrix</i>	289	625	3,275,727	2.2	211	365	49	5520	5357	3175
<i>Cucumis sativus</i>	226.2	450	2,645,514	2.0	164	215	71	6104	6754	2625
<i>Cucumis melo</i>	417	269	1,494,679	0.6	108	148	13	6052	5436	2818
<i>Cucumis metuliferus</i>	316.8	522	3,810,409	1.6	261	233	28	5774	9225	5500
<i>Benincasa hispida</i>	913	914	6,101,374	1.0	514	319	81	5958	8289	4861
<i>Citrullus lanatus</i>	396.4	349	2,788,382	0.9	118	172	59	6272	9092	8211
<i>Lagenaria siceraria</i>	313.4	646	3,682,561	2.1	321	221	104	5749	6578	3689
<i>Cucurbita argyrosperma</i>	255.2	528	2,523,365	2.1	289	157	82	4631	5776	3393
<i>Cucurbita moschata</i>	269.9	605	2,786,293	2.2	358	116	131	4876	6167	2484
<i>Cucurbita pepo</i>	261.4	339	1,530,852	1.3	224	49	66	4928	5507	2380
<i>Cucurbita maxima</i>	271.4	472	2,300,796	1.7	333	49	90	5235	6498	2657
<i>Sechium edule</i>	606.4	3567	23,790,490	5.9	1069	1723	775	5531	7310	6800
<i>Trichosanthes anguina</i>	919.8	7833	63,807,282	8.5	3763	2877	1193	8579	8640	5590
<i>Momordica charantia</i>	285.6	242	1,230,197	0.8	136	74	32	4760	6117	4070
<i>Siraitia grosvenorii</i>	467.1	1836	10,585,418	3.9	976	654	206	5505	6745	3890
<i>Gynostemma pentaphyllum</i>	582.9	4739	34,541,089	8.1	1812	1908	1019	5597	9505	6141

Table S2 Detailed information of the genomes of 16 Cucurbitaceae species and 1 related Begoniaceae species

Species	Genus	Tribe	Family	Estimated genome size (Mb)	Assembled genome size (Mb)	Genome download linkage
<i>Cucumis hystrix</i>	<i>Cucumis</i>	Benincaseae	Cucurbitaceae	416.0	289.0	https://figshare.com/articles/dataset/Genome_assembly_of_Cucumis_hystrix/13377671
<i>Cucumis sativus</i>	<i>Cucumis</i>	Benincaseae	Cucurbitaceae	350.0	226.6	https://www.ncbi.nlm.nih.gov/genome/1639?genome_assembly_id=749658
<i>Cucumis melo</i>	<i>Cucumis</i>	Benincaseae	Cucurbitaceae	450.0	417.0	ftp://cucurbitgenomics.org/pub/cucurbit/genome/melon/v3.6.1/
<i>Cucumis metuliferus</i>	<i>Cucumis</i>	Benincaseae	Cucurbitaceae	368.0	316.8	https://ngdc.cncb.ac.cn/gwh/Assembly/10134/show
<i>Benincasa hispida</i>	<i>Benincasa</i>	Benincaseae	Cucurbitaceae	1030.0	913.0	https://www.ncbi.nlm.nih.gov/genome/18245?genome_assembly_id=747481
<i>Citrullus lanatus</i>	<i>Citrullus</i>	Benincaseae	Cucurbitaceae	419.2	396.4	ftp://cucurbitgenomics.org/pub/cucurbit/genome/watermelon/WCG/
<i>Lagenaria siceraria</i>	<i>Lagenaria</i>	Benincaseae	Cucurbitaceae	334.0	313.4	http://cucurbitgenomics.org/organism/13
<i>Cucurbita argyrosperma</i>	<i>Cucurbita</i>	Cucurbiteae	Cucurbitaceae	238.0	255.2	https://www.ncbi.nlm.nih.gov/genome/75408?genome_assembly_id=1634948
<i>Cucurbita moschata</i>	<i>Cucurbita</i>	Cucurbiteae	Cucurbitaceae	372.0	269.9	https://www.ncbi.nlm.nih.gov/genome/18321?genome_assembly_id=351850
<i>Cucurbita pepo</i>	<i>Cucurbita</i>	Cucurbiteae	Cucurbitaceae	283.0	261.4	https://www.ncbi.nlm.nih.gov/genome/12199?genome_assembly_id=380250

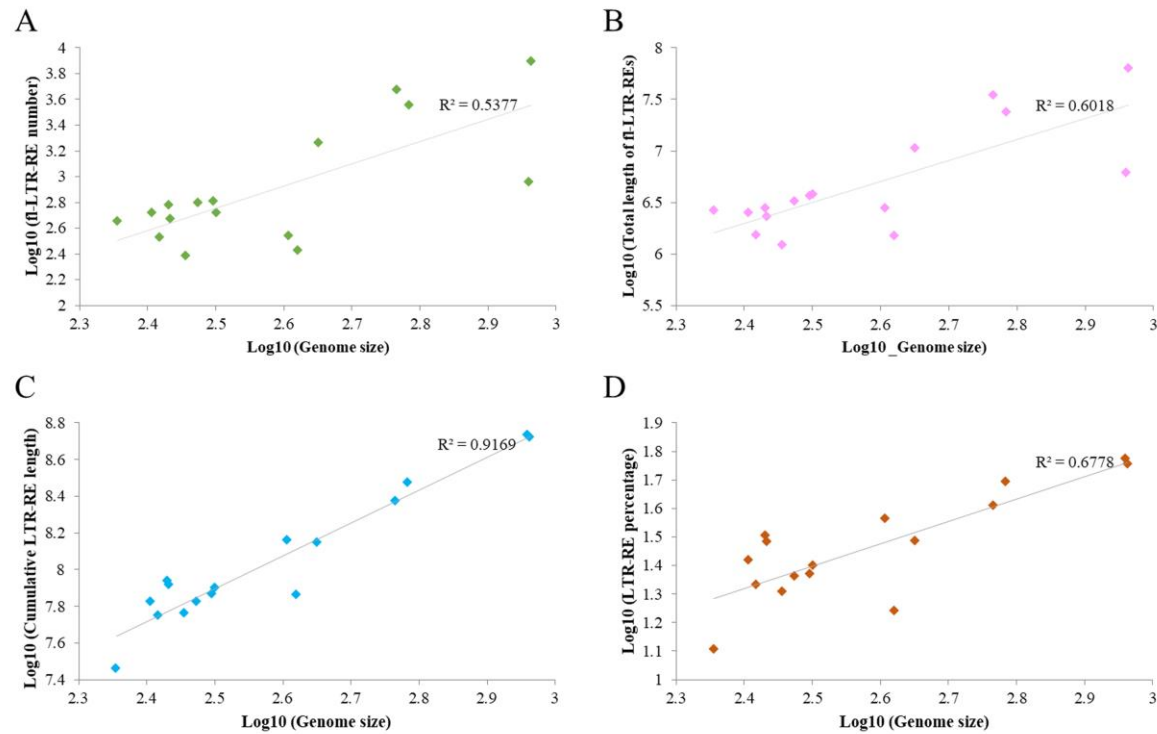


Figure S1. Correlation between genome size and full-length LTR-RT fraction or LTR-RT fractions in Cucurbitaceae species. (A) Genome size versus number of full-length LTR-RTs; (B) genome size versus cumulative length of full-length LTR-RTs; (C) genome size versus the total length of LTR-RTs including full-length and fractionated elements; (D) genome size versus the percentage of genomes occupied by LTR-RTs including full-length and fractionated elements.

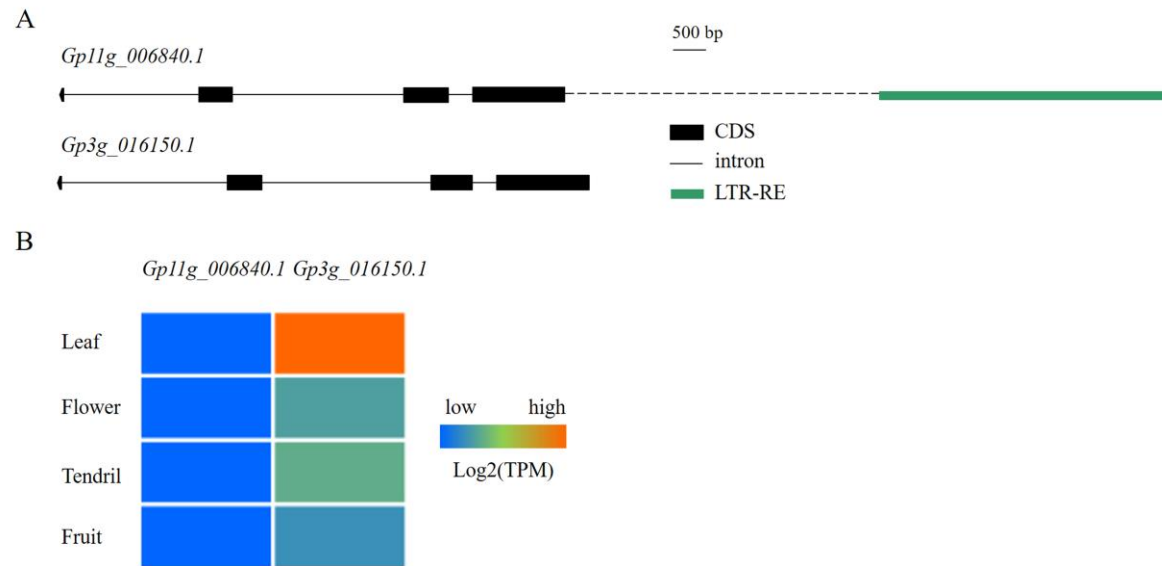


Figure S2. Example of gene with promoter LTR-RT insertion showed lower expression level than its paralog. **(A)** Gene structure of a paralogous gene pair with or without LTR-RT insertion; **(B)** Expression level of this paralogous gene pair.

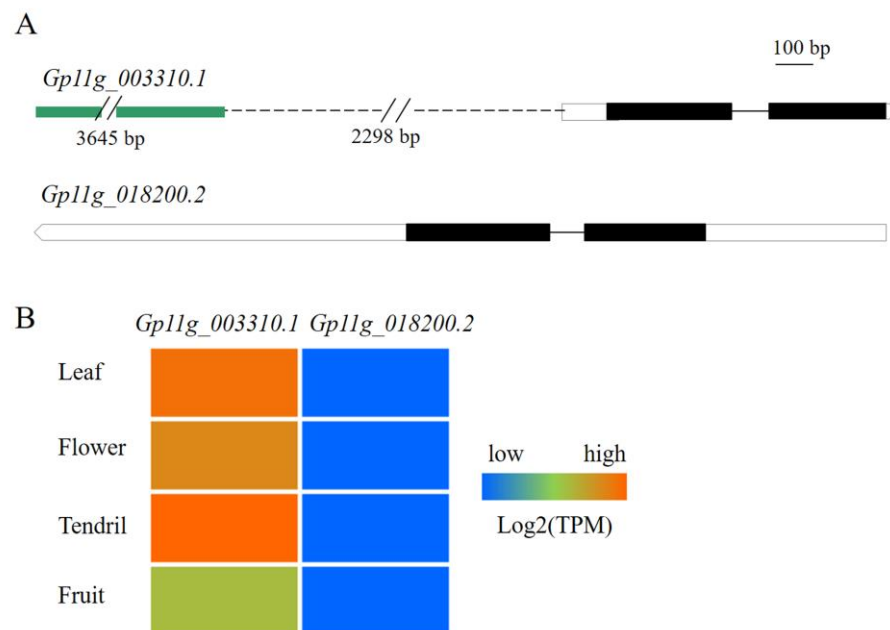


Figure S3. Example of gene with promoter LTR-RT insertion showed elevated expression level than its paralog. **(A)** Gene structure of a paralogous gene pair with or without LTR-RT insertion; **(B)** Expression level of this paralogous gene pair.