Additional file 5. Pairwise divergence matrix between amino acid lineages. Fifteen complete sequences have been aligned using Aliview. The alignment was then transferred in GENEDOC software [64] to obtain the identity percentage.

Sequences name: Apismar: elements from Acyrthosiphon pisum, Dnomar: elements from Diuraphis noxia and Mpmar: elements from Myzus persicae.

| | Macrosiphinimar | | | | | Batmar-like element | | | | Dnomar-like element | Rosa | | | LTIR-like element | |
|------------|-----------------|-----------|-----------|-----------|-----------|---------------------|------------|-----------|-----------|---------------------|------------|------------|------------|-------------------|------------|
| | Apismarl.1 | Apismar12 | Dnomarl.1 | Dnomarl 2 | Mpmar 1.1 | Apismar2.1 | Apismar2.2 | Dnomar2.1 | Dnomar2.2 | Dnomar3.1 | Apismar4.1 | Apismar4.2 | Apismar4.3 | Apismar5.1 | Apismar5.2 |
| Apismarl.l | | 66% | 88% | 62% | 95% | 54% | 49% | 47% | 52% | 58% | 32% | 31% | 30% | 29% | 33% |
| Apismarl 2 | | | 62% | 79% | 67% | 50% | 48% | 43% | 48% | 54% | 34% | 32% | 31% | 32% | 34% |
| Dnomarl.1 | | | | 59% | 89% | 53% | 48% | 46% | 52% | 55% | 32% | 32% | 29% | 28% | 33% |
| Dnomarl.2 | | | | | 63% | 49% | 45% | 42% | 43% | 52% | 32% | 33% | 30% | 31% | 34% |
| Mpmarl.1 | | | | | | 55% | 51% | 47% | 52% | 59% | 33% | 33% | 31% | 30% | 33% |
| Apismar2.1 | | | | | | | 66% | 78% | 64% | 53% | 36% | 37% | 36% | 34% | 34% |
| Apismar2.2 | | | | | | | | 56% | 66% | 50% | 35% | 35% | 37% | 31% | 32% |
| Dnomar2.1 | | | | | | | | | 53% | 44% | 32% | 34% | 33% | 34% | 31% |
| Dnomar2.2 | | | | | | | | | | 52% | 35% | 34% | 35% | 32% | 32% |
| Dnomar3.1 | | | | | | | | | | | 36% | 32% | 38% | 35% | 33% |
| Apismar4.1 | | | | | | | | | | | | 68% | 60% | 44% | 42% |
| Apismar4.2 | | | | | | | | | | | | | 56% | 46% | 44% |
| Apismar4.3 | | | | | | | | | | | | | | 43% | 41% |
| Apismar5.1 | | | | | | | | | | | | | | | 52% |
| Apismar5.2 | | | | | | | | | | | | | | | |