

SUPPLEMENTARY MATERIAL

Aphids and ants, mutualistic species, share a *mariner* element with an unusual location on aphid chromosomes

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Supplementary Table 1. Oligonucleotides used for *mariner* PCR amplifications.

mariner family	Oligonucleotide	Sequence (5' - 3')
<i>Myrmar</i>	Mrug-MAR	CCAGGTCTGTAAATATGAAACCGGAAT
<i>Mboumar</i>	ITR-MAR	CCAGGTGTGTCGGTAATTCCTTTCCGG
<i>Sinvmar</i>	Sinv-mar-1	TTAGGTGTTAAACTTAATTCCTGCCGCT
	Sinv-mar-2	AATTGAAGGTAACTTAATTCCTGCCGTT
<i>Azteca</i>	Azteca-1	CGAGGTTTGTTAAAAAAAAGGTGA
	Azteca-2	CGAGGTGTGATCAAAAAGTAAGGTGA
	Azteca-3	CGAGGTTTGTTAAAAAAAAGGTGA
	Azteca-4	CGAGGTGTGTTCAAAAAGGTGA

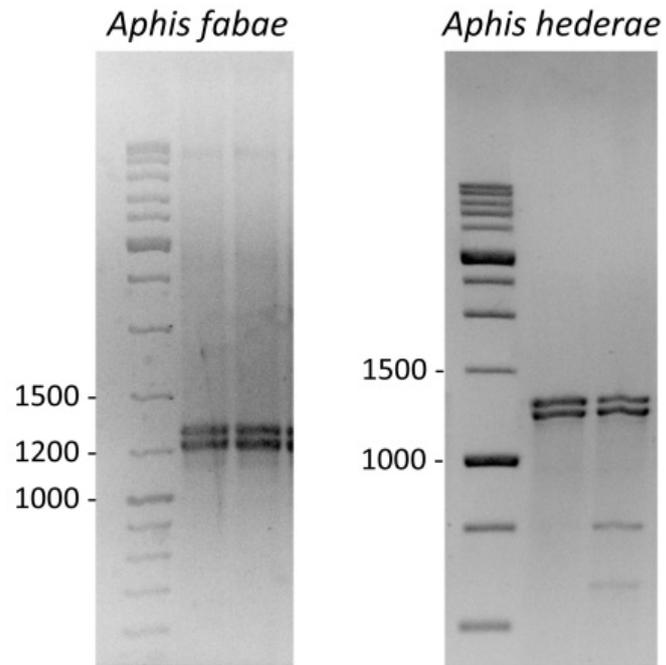


Figure S1. Agarose gel showing the PCR amplification of genomic DNA from *A. fabae* and *A. hederae* using primers based in the ITRs from *Myrmar* elements. The numbers indicate the size of DNA fragments in bp.

	410	420	430	440	450	460	470	480	490	500
AfabmarMr-50	CTGCAAGCCTTGTGGACGAAGACGACGCTCGAACACAACAAC	TGGCCGGATCAGTTAAAGGTGACCCGGGAAGCCATCTCCCTTCGGTTGAAAGCCA								
AfabmarMr-54		A	G							
AfabmarMr-57		A								
AfabmarMr-13		A								
AfabmarMr-25		A								
AfabmarMr-51		A								
AfabmarMr-55		A						C		
AfabmarMr-58		A								
AfabmarMr-26		A								
AfabmarMr-27		A								
AfabmarMr-65		A		AAC		G			C	
AfabmarMr-76		AG		AAC		G				
AfabmarMr-10		A		AAC		G		C		
AfabmarMr-96		A		AAC						
AfabmarMr-59		A		AAC						
AfabmarMr-94		A		AAC						
AfabmarMr-12		A		AAC					C	
AfabmarMr-63		A		AAC						
AfabmarMr-144		A		AAC						
AhedmarMr-700		A								
AhedmarMr-707		A								T
AhedmarMr-712		A								
AhedmarMr-713		A								
AhedmarMr-9		A		AAC						
AhedmarMr-33		A		AAC						
AhedmarMr-51		A		AAC						
AhedmarMr-61		A		AAC						
AhedmarMr-74		A		AAC						
AhedmarMr-77		A		AAC						
AhedmarMr-293		A		AAC		G				
AhedmarMr-301		A		AAC						
AhedmarMr-544		A		AAC						
AhedmarMr-808		A		AAC						
AhedmarMr-815		A		AAC						

	510	520	530	540	550	560	570	580	590	600
AfabmarMr-50	TGGGAAAGATACAAAAGGCGGGAAATGGGTTCCACATGAAC	TCAACGAAAGACAGCAGGAAAACCGCAAAACATCATGCGAAATGCTGCTCGCCAGGTT								
AfabmarMr-54										
AfabmarMr-57										
AfabmarMr-13							G			
AfabmarMr-25										
AfabmarMr-51										
AfabmarMr-55										
AfabmarMr-58										
AfabmarMr-26										
AfabmarMr-27										C
AfabmarMr-65										
AfabmarMr-76										
AfabmarMr-10										
AfabmarMr-96										C
AfabmarMr-59										
AfabmarMr-94										
AfabmarMr-12										
AfabmarMr-63										
AfabmarMr-144										
AhedmarMr-700						G		C		
AhedmarMr-707										
AhedmarMr-712										
AhedmarMr-713										
AhedmarMr-9										
AhedmarMr-33										
AhedmarMr-51										
AhedmarMr-61										T
AhedmarMr-74										
AhedmarMr-77						G				
AhedmarMr-293										
AhedmarMr-301										
AhedmarMr-544										
AhedmarMr-808										
AhedmarMr-815					T		G			

	610	620	630	640	650	660	670	680	690	700																																																																																						
AfabmarMr-50	C	A	A	A	G	A	A	A	G	T	C	A	T	T	T	C	T	C	C	A	T	C	G	A	A	T	T	G	T	G	A	C	T	G	G	C	G	A	T	G	G	A	A	A	A	G	T	G	G	A	T	A	T	A	T	T	T	C	G	A	G	A	A	T	C	C	T	A	A	G	C	C	A	A	A	A	G	T	C	A	T	G	G	G	T	T	A	C	T	C	C	G	G	T	G	A
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AhedmarMr-808																																																																																															
AhedmarMr-815																																																																																															

	710	720	730	740	750	760	770	780	790	800																																																																									
AfabmarMr-50	C	C	A	T	C	A	A	C	A	T	C	G	A	C	G	G	C	A	A	G	A	C	C	A	A	C	C	G	T	T	A	C	G	G	A	A	G	A	C	A	A	T	G	C	T	G	T	G	T	T	T	G	G	T	C	A	G	A	G	G	C	G	T	A	A	T	C	T	A	C	T	A	C	G	A	G	T	G	T	G	A	A	C
AfabmarMr-54																																																																																		
AfabmarMr-57																																																																																		
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AhedmarMr-544																																																																																		
AhedmarMr-808																																																																																		
AhedmarMr-815																																																																																		

	810	820	830	840	850	860	870	880	890	900
AfabmarMr-50	CTGGGAAACTGTGAATACTCAACGCTATCGACAA	CAATGACCGATT	TGGATCGAGTTT	TGCGTGAAAAACGACC	GAAATACCAACAAAGACAAC	CAA				
AfabmarMr-54
AfabmarMr-57
AfabmarMr-13
AfabmarMr-25G.....
AfabmarMr-51
AfabmarMr-55
AfabmarMr-58
AfabmarMr-26
AfabmarMr-27
AfabmarMr-65G.....
AfabmarMr-76G.....
AfabmarMr-10G.....
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AfabmarMr-59
AfabmarMr-94
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AfabmarMr-63
AfabmarMr-144
AhedmarMr-700
AhedmarMr-707
AhedmarMr-712G.....
AhedmarMr-713G.....
AhedmarMr-9
AhedmarMr-33
AhedmarMr-51G.....
AhedmarMr-61
AhedmarMr-74
AhedmarMr-77
AhedmarMr-293
AhedmarMr-301
AhedmarMr-544
AhedmarMr-808
AhedmarMr-815

	910	920	930	940	950	960	970	980	990	1000
AfabmarMr-50	GGTGATTTTGCTGCATGACAA	TGCACCAGCACCAAAGCAA	AACTGGTCCAGGAAACGATAGAGTCGTTCCGTTGGAAGATTCTTCAGCAGCGGGCTTAC							
AfabmarMr-54
AfabmarMr-57
AfabmarMr-13
AfabmarMr-25G.....
AfabmarMr-51
AfabmarMr-55T.....TT.....
AfabmarMr-58T.....TT.....
AfabmarMr-26T.....TT.....
AfabmarMr-27T.....TT.....
AfabmarMr-65G.....
AfabmarMr-76G.....
AfabmarMr-10G.....
AfabmarMr-96G.....
AfabmarMr-59G.....
AfabmarMr-94G.....
AfabmarMr-12G.....
AfabmarMr-63A.....
AfabmarMr-144C.....G.....
AhedmarMr-700T.....G.....TT.....
AhedmarMr-707T.....G.....TT.C.....
AhedmarMr-712T.....G.....TT.....
AhedmarMr-713T.....G.....TT.....
AhedmarMr-9G.....
AhedmarMr-33G.....
AhedmarMr-51G.....
AhedmarMr-61G.....
AhedmarMr-74G.....
AhedmarMr-77G.....
AhedmarMr-293G.....
AhedmarMr-301G.....
AhedmarMr-544G.....
AhedmarMr-808G.....
AhedmarMr-815G.....



Figure S2. Sequence alignment of all *Afabmar-Mr* and *Ahedmar-Mr* *rmariner* sequences. Full-length copies of *mariners* in both species are marked with blue shading.

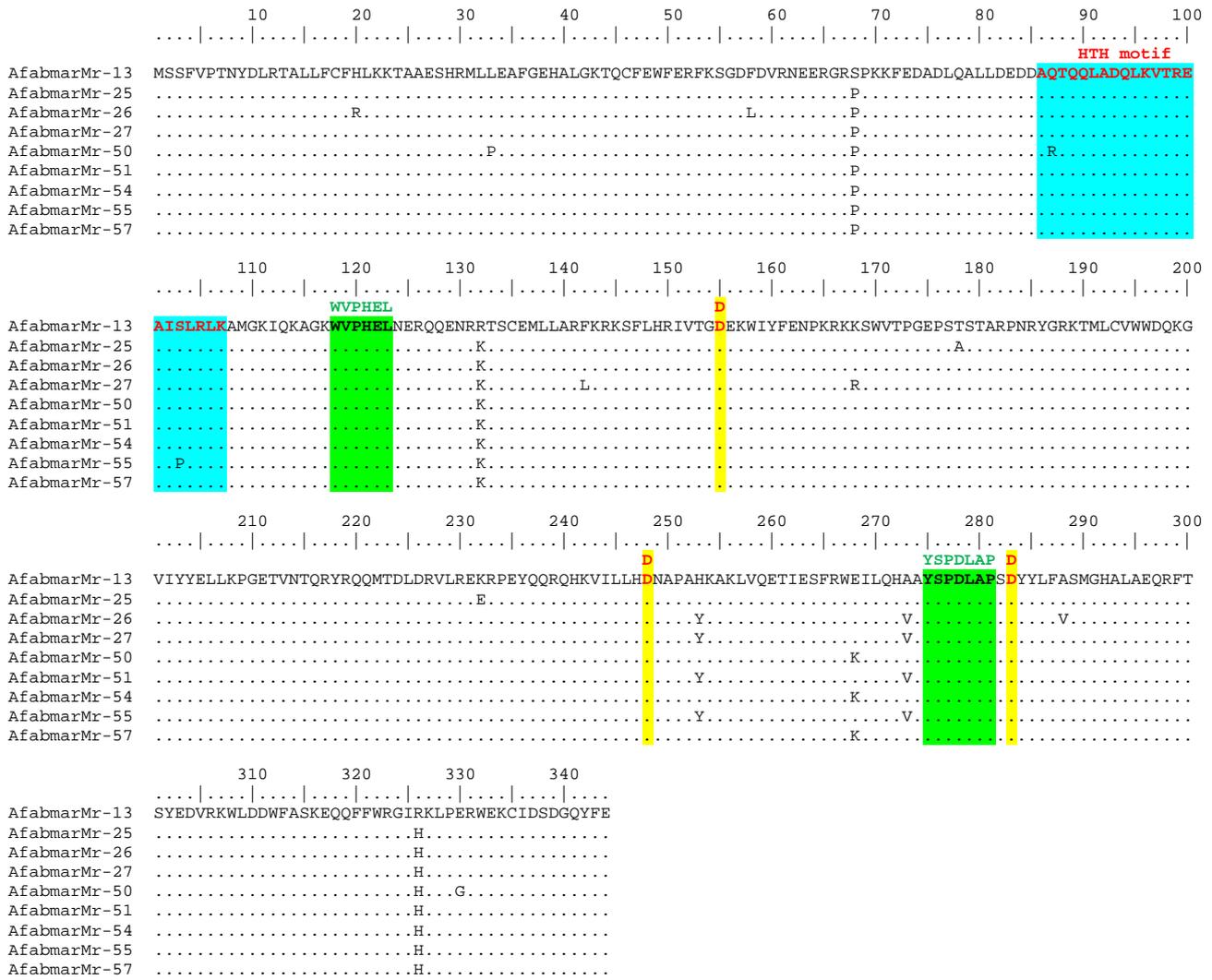


Figure S3. Sequence alignment of all putative *Afabmar-Mr* transposases. The conserved D,D(34)D motif, the also conserved *mariner* transposase WVPHEL and YSPDL motifs and the HTH motif are shown in different colors (yellow, green and blue respectively).

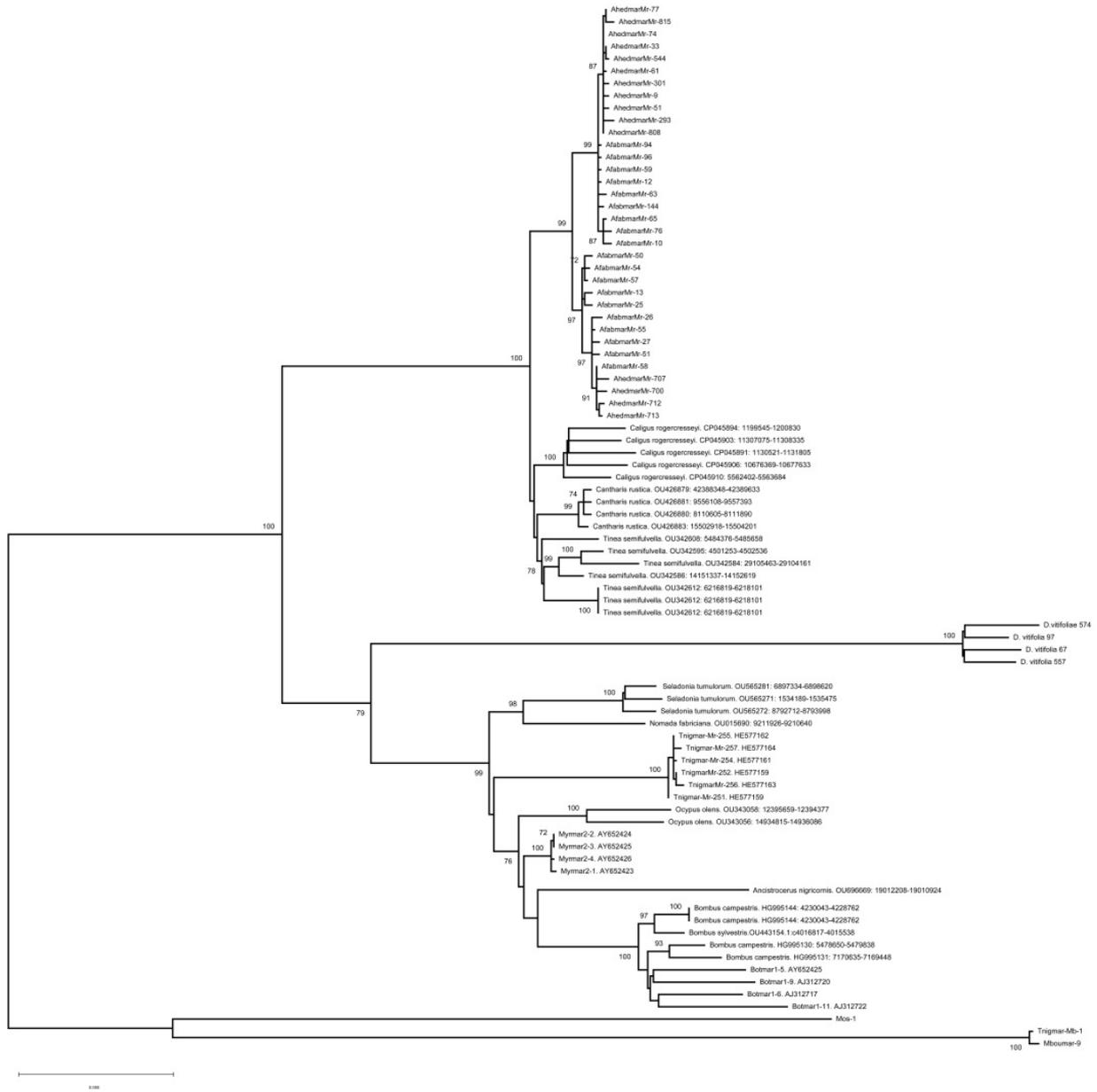


Figure S4. Maximum-likelihood analysis of the nucleotide *Myrmar* like *mariner* sequences. The accession numbers and nucleotide position of each *mariner* element are indicated. The data corresponding to the sequences of *Daktulosphaira vitifoliae* are shown in Figure S5. Numbers indicate the bootstrap values over 1000 replications. Only bootstrap support values greater than 70% are showed.

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>scaffold67 Apollo scaffold67:195087..196370 (+ strand) length=1284
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TTGCGTCAAAAAGAGCAACAATCTTCTGGCGTGGAAATCCATAAATGCCCCGAAAGATGGGAAAAATGTATAAGTAGCGAAGGGCAATACTTTGAATAGGAT
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>scaffold557 Apollo scaffold557:100292..101408 (+ strand) length=1117
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CGACCACCGAAAAAGTTTGAAGACACACCGGTAAAAGTGGTCAAGGAATTAATCGAGGCTTTGGTGGGAGACTTATCGCATGCCGCTTATTCGCCAGACTT
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>scaffold97 Apollo scaffold97:110013..111289 (- strand) class=match length=1277
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GCGAGGCAAAATCGCTTTGGAAAGAAAACAATGCTCTGTGTTTGGTGAATCAGAAAGGTTTATCTATATGAGCTTCTTAAACCTGGCGAAAATGTCAA
CACTGAACGTTACCTACAACAATTTGTTCAAGCTTTGGGAGACAAACGACCGGAACTTCAACGACGACAAACACCAGGTGATTTTGGCTTCAATG
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AAAAGAGCAACAATCTTCTGGCGTGGAAATCCATAAATGCCCCGAAAGATGGGAAAAATGTATAAGTAGCGAAGGGCAATACTTCGAATAGGATGTATAGT
ATCAGTTTTGTACAATAAACTAGTATTTTATGTCAAATAAATCCGGTTTCATATTTACACACCTGG

>scaffold574 Apollo scaffold574:127835..128944 (+ strand) class=match length=1270
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TGGAAGCTTACGGTGAGCATGCTCTGGGAGAGTCAAGTATTTTGGTGGTGAAGAAAATTTAAAAGTGGCGATTTCGATGTGAGGGATACAAAACGTGGT
CGACCACCGAAAAAGTTTGAAGACACAGGTTGCAAGCGTTGTTGGATGAGGATGCAACGCAACCCAAAAACAACCTGCGATCAATTTGAATGTGACCCG
GGAAGCCGTATCCATTCGTTTGAAGCCATGGGAAAGATCCAAAAGTGGGAAAAATGGGTTCCACATCAACTGACGGAAGGCAATGGGAAAAACCGACAAA
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TATGGCATGCCGCTTATTCGCCAGACTTGGCTCCTCAGACTACCATTTATTTGCATCTTTGGGACACGCAATCGCTGAGCAGCGCTTCTCTTCTACGAA
GATGTGCAAAAATGGCTCGAAAATTTGGTTTGGCTCAAAAAGAGCAAGAATCTTCTGGCGTGGAAATCCATAAATGCCCCGAAAGATGGGAAAAATGTATAAG
TAGCGAAGGGCAATACTTCGAATGGGATGTATAGTATCAGTTTTGTACAATAAACTAGTATTTTATGTCAAATAAATCCGGTTTCATATTTACATACCTGG

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Figure S5. Sequences found in the *Daktulosphaira vitifoliae* genome with similarity with the *Myrmar* elements. These sequences were obtained from the AphidBase web server (<https://bipaa.genouest.org/is/aphidbase/>).