

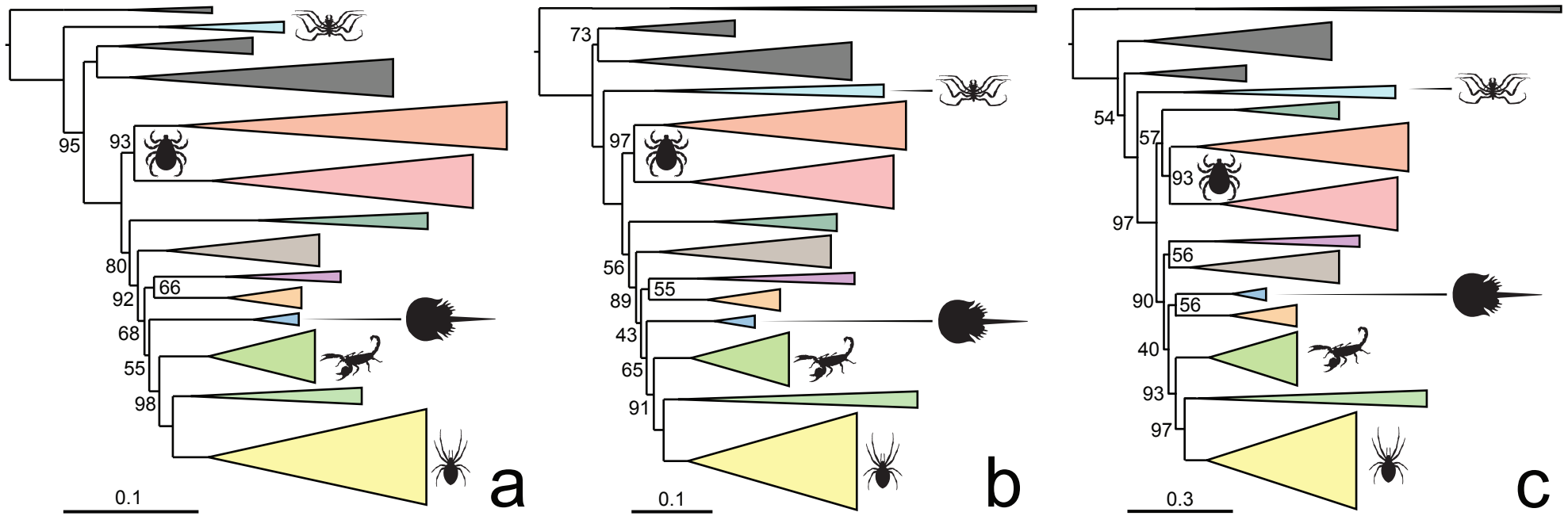
Supplementary Information

Increasing species sampling in chelicerate genomic-scale datasets provides support for monophyly of Acari and Arachnida

Lozano-Fernandez *et al.*

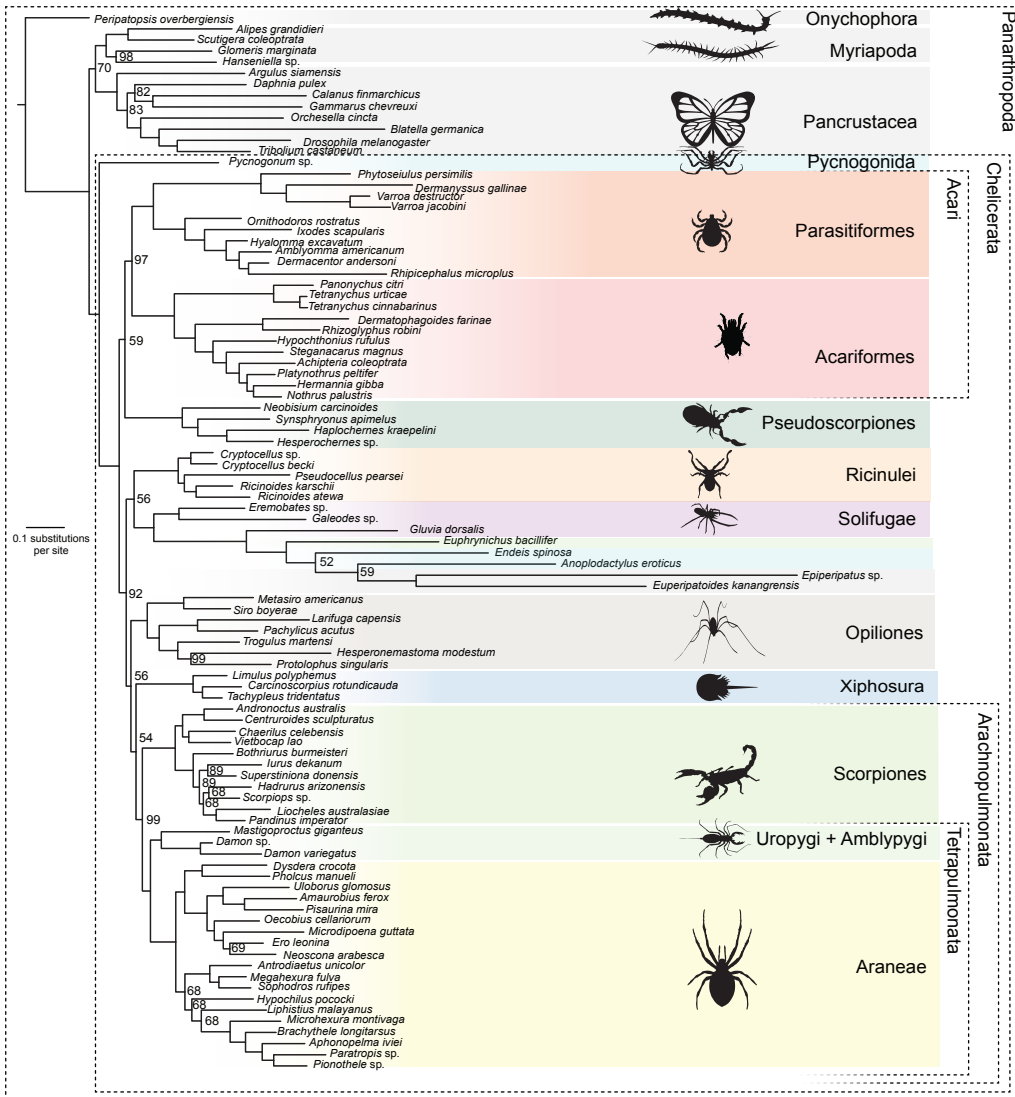
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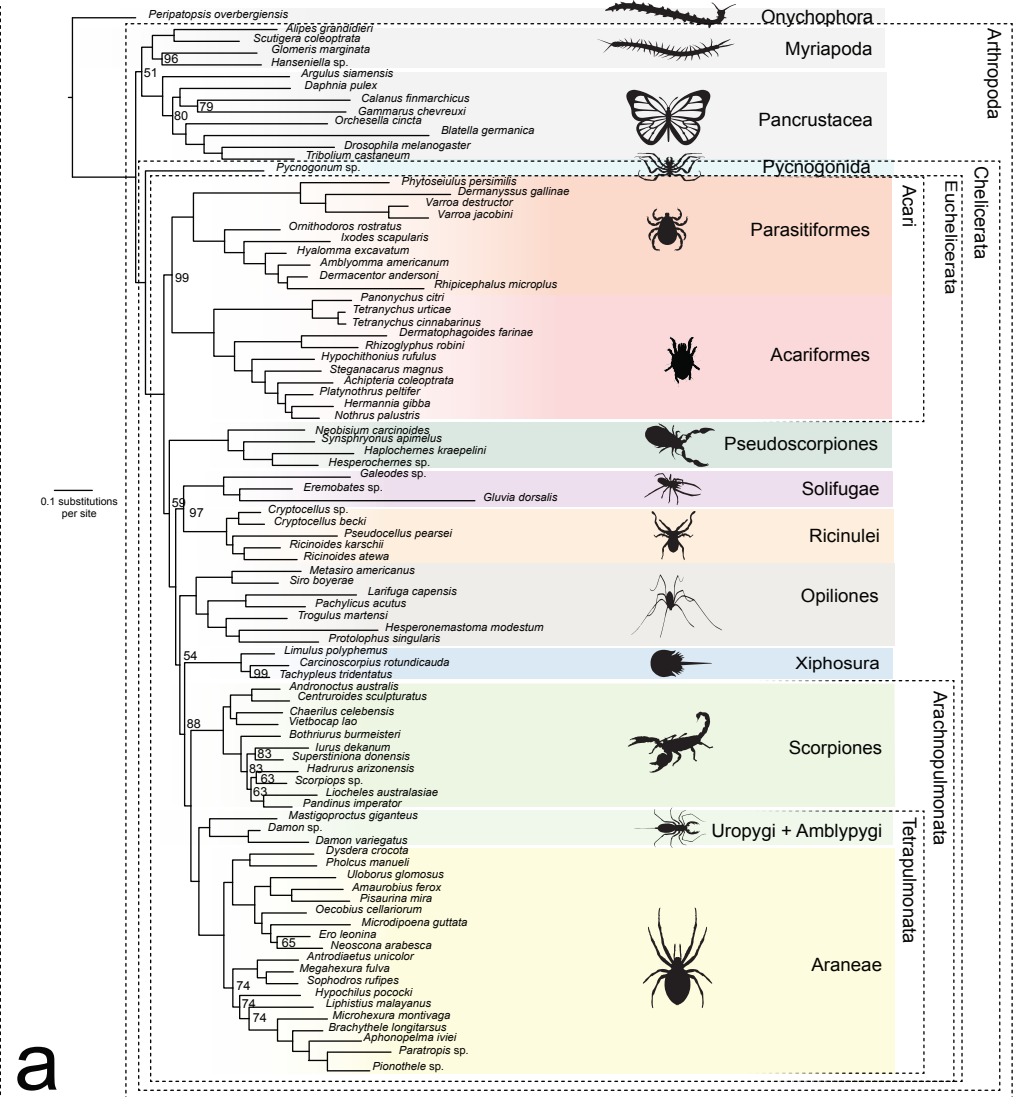


Supplementary Figure 1. Schematic representation of ML results. **(A)** Schematic representation of the relationships inferred from Matrix A using ML under the LG+I+G4 model. **(B)** Schematic representation of the relationships inferred from Matrix B using ML under the LG+I+G4 model. **(C)** Schematic representation of the relationships inferred from Matrix C using ML under the LG+F+I+G4 model. Support values represent bootstrap values, with lack of a number indicating maximum support. Silhouettes have been designed by ART.

OMA-based matrix, 3,982 genes using soft trimming
 trimal -gt 0.9 [keep columns with < 10% gaps]
 127,114 amino acids
 95 taxa



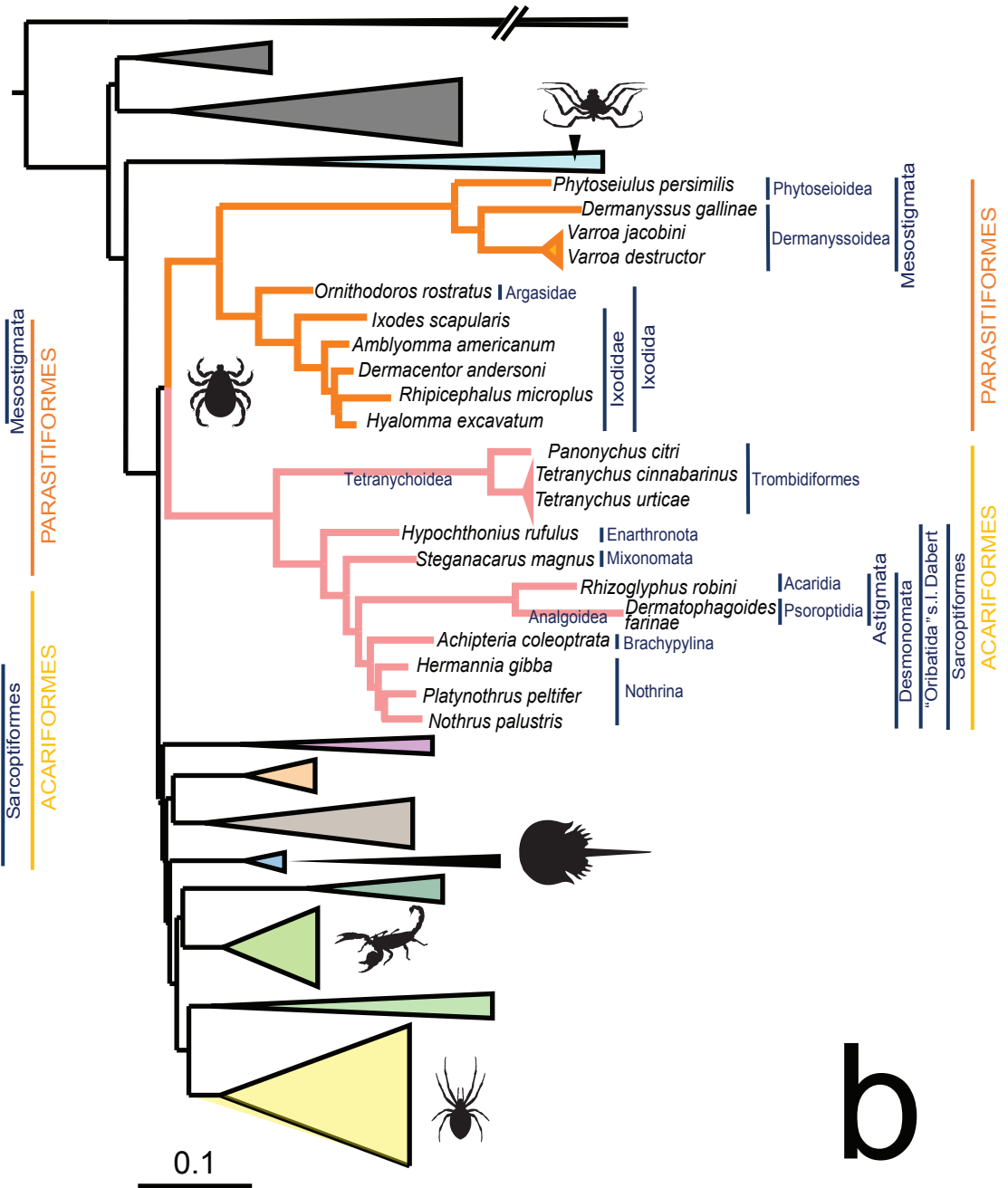
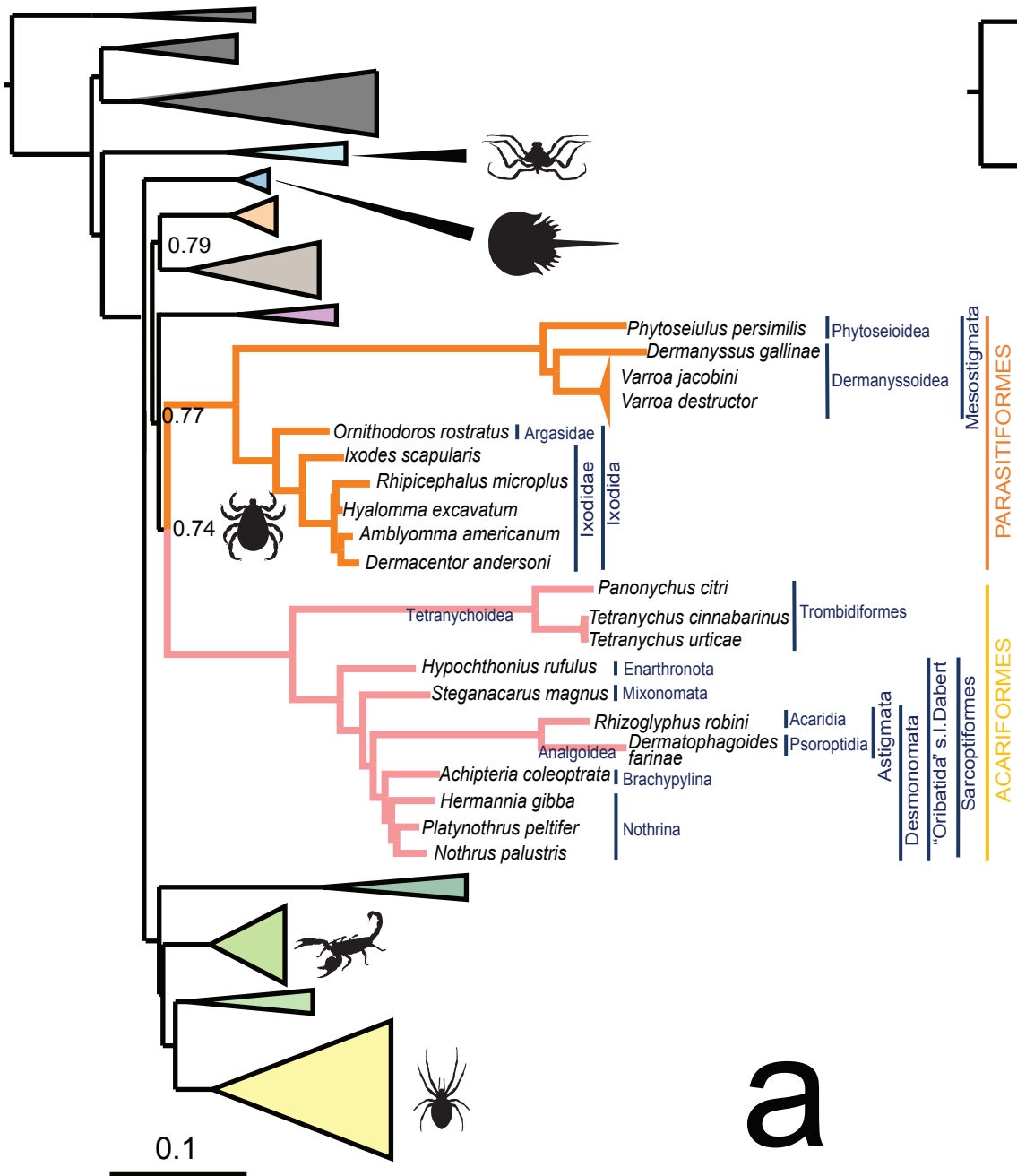
OMA-based matrix, 3,982 genes using soft trimming
 trimal -gt 0.9 [keep columns with < 10% gaps]
 127,114 amino acids
 90 taxa, removal of 5 low-quality transcriptomes

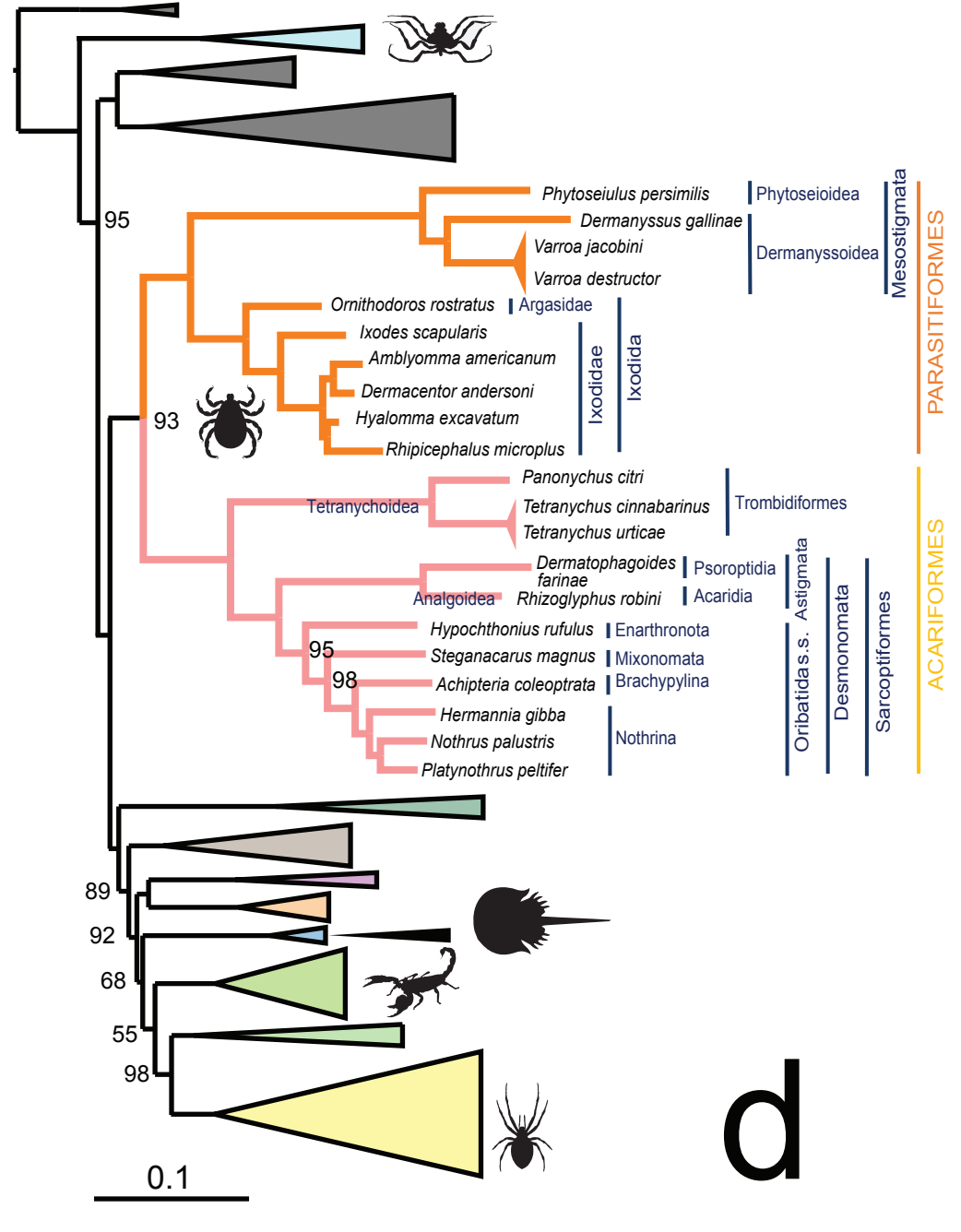
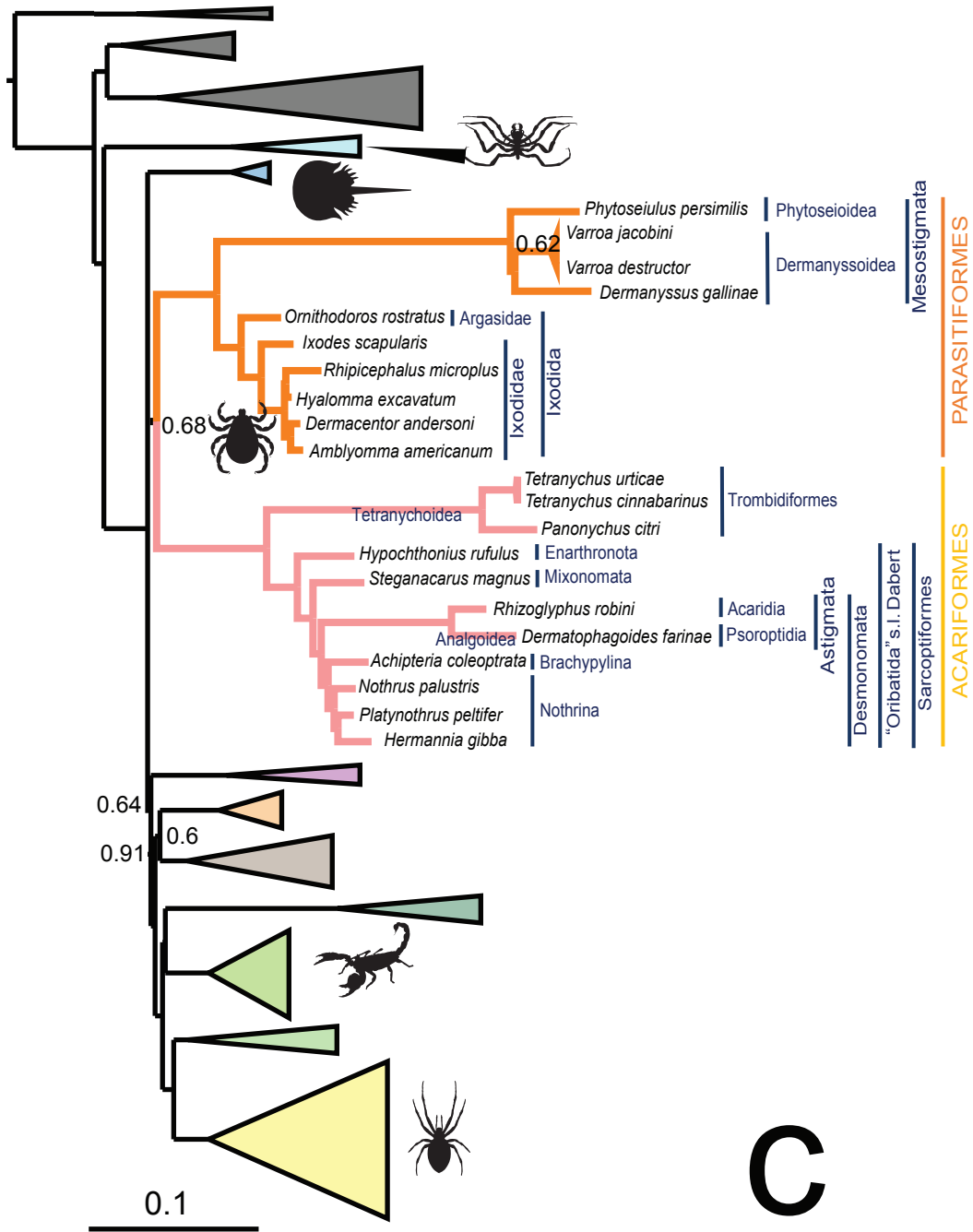


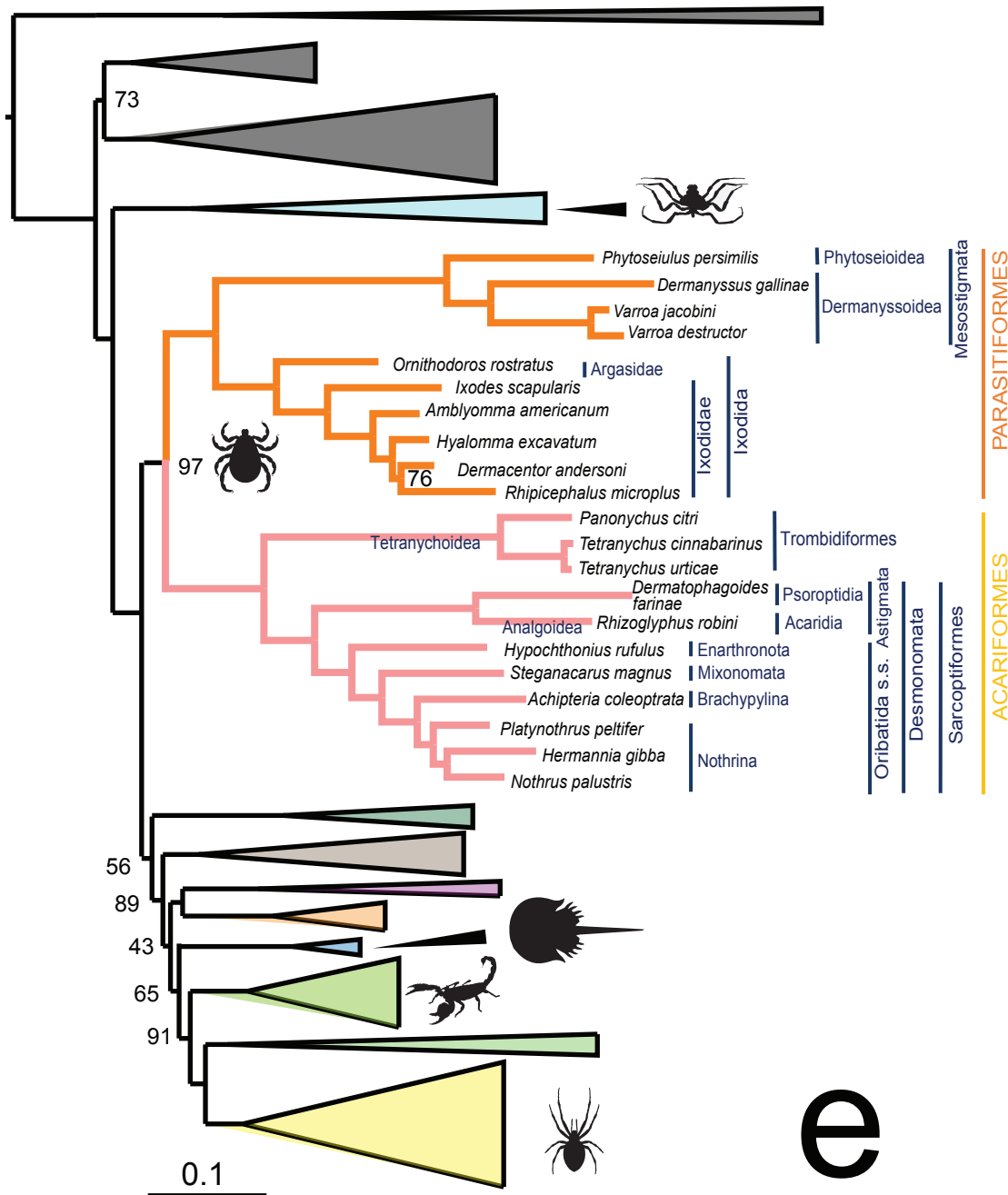
a

b

Supplementary Figure 2. Phylogenetic trees derived from the ML analysis of Matrix D. **(A)** Phylogeny recovered from the ML analysis of Matrix D. The tree obtained from this analysis is in excellent agreement with those obtained from our other ML analyses except that the five species with the worst quality transcriptomes (*Endeis spinosa*, *Anoplodactylus eroticus*, *Epiperipatus* sp., *Euperipatoides kanangrensis* and *Euphrynichus bacillifer*) formed a clearly artificial group nested inside Solifugae. **(B)** A reanalysis of this dataset that excluded the five species with the worst transcriptomes (*Endeis spinosa*, *Anoplodactylus eroticus*, *Epiperipatus* sp., *Euperipatoides kanangrensis* and *Euphrynichus bacillifer*) recovered a topology in excellent agreement with that from the analysis of Matrix B. In particular monophyletic Acari is recovered irrespective of whether the five species with poor quality transcriptomes are included or excluded. We conclude that neither the size of the matrix nor the trimming strategy impacts significantly on the retrieved topology.







Supplementary Figure 3. Schematic representation of the Bayesian and ML phylogenies at the order level with focus on the internal clades of Acari. **(A)** Schematic representation of the results of the CAT-GTR+G analysis of Matrix A. **(B)** Schematic representation of the results of the CAT-GTR+G analysis of Matrix B. **(C)** Schematic representation of the results of the CAT-GTR+G analysis of Matrix A, after Dayhoff-6 recoding **(D)** Schematic representation of the relationships inferred from Matrix A using ML under the LG+I+G4 model. **(E)** Schematic representation of the relationships inferred from Matrix B using ML under the LG+I+G4 model. Support values represent posterior probabilities in A, B and C, and bootstrap values in D and E, with lack of a number indicating maximum support. Convergence statistics for (A) Burnin = 3,000, Total Cycles = 10,000, subsampling frequency = 20, Maxdif = 0.87, Minimal effective size = 23, (B) Burnin = 3,000, Total Cycles = 10,000, subsampling frequency = 20, Maxdif = 0.07, Minimal effective size = 32 and (C) Burnin = 3,000, Total Cycles = 12,000, subsampling frequency = 20, Maxdif = 0.08; Minimal effective size = 72. Silhouettes have been designed by ART.

Supplementary Table 1. List of all species included in the study with NCBI accession numbers.

Order/Clade	Species	Source	Peptides prediction	Accession
Pycnogonida	<i>Endeis spinosa</i>	454	2930	LIBEST_025662
	<i>Pycnogonum sp.</i>	Illumina	26668	SRR8745912
	<i>Anoplodactylus eroticus</i>	454	2595	Sharma <i>et al.</i> 2014 (generated on Dunn <i>et al.</i> 2008)
Xiphosura	<i>Limulus polyphemus</i>	Illumina	17824	SRR1145732
	<i>Tachypleus tridentatus</i>	Illumina	47095	SRR946952
	<i>Carcinoscorpius rotundicauda</i>	Illumina	82789	SRR1511637
Acariformes	<i>Tetranychus urticae</i>	Illumina	26106	PRJEB6152
	<i>Dermatophagoides farinae</i>	Illumina	36507	SRR1016494
	<i>Panonychus citri</i>	Illumina	24400	SRR341928
	<i>Rhizoglyphus robini</i>	Illumina	72646	PRJNA213807
	<i>Steganacarus magnus</i>	Illumina	60104	SRR4039729
	<i>Hypochothonius rufulus</i>	Illumina	29268	SRR4039020
	<i>Platynothrus peltifer</i>	Illumina	42123	SRR4039728
	<i>Achipteria coleoprata</i>	Illumina	54612	SRR4039018
	<i>Hermannia gibba</i>	Illumina	64632	SRR4039019
	<i>Nothrus palustris</i>	Illumina	57025	SRR4039021
	<i>Tetranychus cinnabarinus</i>	Illumina	23425	SRR519097
Parasitiformes	<i>Amblyomma americanum</i>	Illumina	32598	PRJNA238773
	<i>Dermacentor andersoni</i>	Illumina	30501	PRJNA238802
	<i>Ixodes scapularis</i>	Illumina	56503	SRR1189647
	<i>Rhipicephalus microplus</i>	Illumina	13004	SRR1186998
	<i>Hyalomma excavatum</i>	Illumina	54671	PRJNA311286
	<i>Ornithodoros rostratus</i>	Illumina	37109	PRJNA270484
	<i>Dermanyssus gallinae</i>	454	39197	SRR658515
	<i>Varroa destructor</i>	Illumina	16085	SRR3927486
	<i>Varroa jacobini</i>	Illumina	12342	SRR3634772
	<i>Phytoseiulus persimilis</i>	454	21218	DRR001717
Ricinulei	<i>Pseudocellus sp. (pearsei)</i>	Illumina GAI	5922	SRR1146686
	<i>Ricinoides atewa</i>	Illumina GAI	14324	SRR1145743
	<i>Cryptocellus sp. n. RF-2015</i>	Illumina	49645	SRR1982218
	<i>Ricinoides karschii</i>	Illumina	87143	SRR1972991
	<i>Cryptocellus becki</i>	Illumina	128981	SRR1979416
Solifugae	<i>Eremobates sp.</i>	Illumina GAI	11,765	SRR1146672
	<i>Gluvia dorsalis</i>	454	5404	SRR1141096
	<i>Galeodes sp.</i>	Illumina	422228	SRR8745910
Pseudoscorpiones	<i>Synsphyronus apimelus</i>	Illumina	17820	SRR1145733
	<i>Haplochernes kraepelini</i>	Illumina	16376	SRR1767661
	<i>Hesperochernes sp.</i>	Illumina	30903	SRR1514877
	<i>Neobisium carcinoides</i>	Illumina	24142	SRR7293662
Scorpiones	<i>Bothriurus burmeisteri</i>	Illumina	20574	SRR1721670
	<i>Chaerilus celebensis</i>	Illumina	24310	SRR1721804
	<i>Centruroides sculpturatus</i>	Illumina	16440	SRR1515193
	<i>Hadrurus arizonensis</i>	Illumina	19266	SRR1721733
	<i>Iurus dekanum</i>	Illumina	17619	SRR1721734
	<i>Liocheles australasiae</i>	Illumina	22581	SRR1721664
	<i>Superstitionia donensis</i>	Illumina	23916	SRR1721951
	<i>Vietbocap lao</i>	Illumina	20007	SRR1721740

	<i>Androctonus australis</i>	Illumina	19170	SRR1724216
	<i>Pandinus imperator</i>	Illumina	20279	SRR1721600
	<i>Scorpiops sp.</i>	Illumina	24941	SRR1721951
Uropygi	<i>Mastigoproctus giganteus</i>	Illumina GAI	17674	SRR1145698
Amblypygi	<i>Damon variegatus</i>	Illumina GAI	11823	SRR1145694
	<i>Euphrynichus bacillifer</i>	454	3895	SRR1141095
	<i>Damon sp.</i>	Illumina	24564	SRR8745909
Opiliones	<i>Larifuga capensis</i>	Illumina	10506	SRR1145742
	<i>Metasiro americanus</i>	Illumina GAI	16556	SRR618563
	<i>Pachylicus acutus</i>	Illumina	14202	SRR1146670
	<i>Protolophus singularis</i>	Illumina	13987	SRR1145700
	<i>Trogulus martensi</i>	Illumina	12765	SRR1145730
	<i>Hesperonemastoma modestum</i>	Illumina	8845	SRR1145728
	<i>Siro boyerae</i>	Illumina	11387	SRR1145699
Araneae	<i>Liphistius malayanus</i>	Illumina	11221	SRR1145736
	<i>Neoscona arabesca</i>	Illumina	16594	SRR1145741
	<i>Dysdera crocota</i>	Illumina	30336	SRR1328258
	<i>Pholcus manuli</i>	Illumina	27519	SRR1365208
	<i>Oecobius cellariorum</i>	Illumina	30394	SRR1365089
	<i>Uloborus glomosus</i>	Illumina	15941	SRR1328334
	<i>Amaurobius ferox</i>	Illumina	19707	SRR1329250
	<i>Pisaurina mira</i>	Illumina	15940	SRR1365651
	<i>Microdipoena guttata</i>	Illumina	17704	SRR1333842
	<i>Sphodros rufipes</i>	Illumina	23297	SRR1514908
	<i>Antrodiaetus unicolor</i>	Illumina	20709	SRR1514897
	<i>Megahexura fulva</i>	Illumina	30559	SRR1514891
	<i>Microhexura montivaga</i>	Illumina	17718	SRR1514890
	<i>Brachythele longitarsus</i>	Illumina	19334	SRR1514875
	<i>Pionothele n. sp.</i>	Illumina	10538	SRR1514906
	<i>Paratropis sp.</i>	Illumina	9961	SRR1514893
	<i>Aphonopelma iviei</i>	Illumina	11968	SRR1514871
	<i>Hypochilus pococki</i>	Illumina	29268	SRR1514889
	<i>Ero leonina</i>	Illumina	33289	SRR1514886
Onychophora	<i>Peripatopsis overbergiensis</i>	Illumina	12846	SRX451023
Onychophora	<i>Euperipatoides kanangrensis</i>	EST	3267	Dunn et al. 2008
Onychophora	<i>Epiperipatus sp. TB-2001</i>	EST	514	Roeding, F., et al. 2007
Crustacea	<i>Argulus siamensis</i>	Illumina	48641	SRR514120
Crustacea	<i>Gammarus chevreuxi</i>	Illumina	28997	GFCV00000000.1
Crustacea	<i>Calanus finmarchicus</i>	Illumina	126873	SRR1153469
Crustacea	<i>Daphnia pulex</i>	WGS Sanger	30611	PRJNA12756
Hexapoda	<i>Orchesella cincta</i>	WGS	20257	PRJNA294050
Hexapoda	<i>Drosophila melanogaster</i>	WGS	30443	PRJNA13812
Hexapoda	<i>Blattella germanica</i>	454	7302	PRJNA248247
Hexapoda	<i>Tribolium castaneum</i>	WGS	18534	PRJNA12540
Myriapoda	<i>Alipes grandidieri</i>	Illumina	18814	SRR619311
Myriapoda	<i>Scutigera coleoptrata</i>	Illumina	31758	SRR1158078
Myriapoda	<i>Hanseniella sp.</i>	Illumina	50853	SRR3458647
Myriapoda	<i>Glomeris marginata</i>	Illumina	66936	SRR3458641

In black species used initially during the OMA orthology-assignment

Supplementary Table 2. List of orthologs shared between Matrix A and B.

BLAST genes	OMA equivalent OrthoGroup
<i>ar21</i>	OG12060
<i>arp23</i>	OG3395
<i>atpsynthalphamt</i>	OG1215
<i>cctA</i>	OG1188
<i>cctB</i>	OG1606
<i>cctD</i>	OG1685
<i>cctE</i>	OG1258
<i>cctG</i>	OG1666
<i>cctN</i>	OG1544
<i>cctZ</i>	OG1591
<i>cpn60mt</i>	OG1263
<i>crfg</i>	OG1895
<i>ef1EF1</i>	OG1279
<i>ef1RF3</i>	OG1393
<i>ef2EF2</i>	OG277
<i>EIF5a</i>	OG12223
<i>fibri</i>	OG5753
<i>fpps</i>	OG13935
<i>g122</i>	OG24237
<i>g127</i>	OG30226
<i>g46</i>	OG4754
<i>g70</i>	OG26595
<i>g78</i>	OG6693
<i>g7</i>	OG29912
<i>grc5</i>	OG7044
<i>hsp70E</i>	OG791
<i>hsp70mt</i>	OG827
<i>hsp90C</i>	OG518
<i>hsp90E</i>	OG577
<i>if1a</i>	OG13352
<i>if2b</i>	OG5408
<i>if2g</i>	OG1506
<i>if4aa</i>	OG2006
<i>if4ab</i>	OG1753
<i>if6</i>	OG7623
<i>l12eA</i>	OG16557
<i>l12eC</i>	OG19114
<i>l12eD</i>	OG5608

BLAST genes	OMA equivalent OrthoGroup
<i>mcmD</i>	OG1048
<i>nsf1C</i>	OG2299
<i>nsf1G</i>	OG1789
<i>nsf1J</i>	OG2110
<i>nsf1K</i>	OG1788
<i>nsf1L</i>	OG1954
<i>nsf1M</i>	OG1423
<i>nsf2A</i>	OG307
<i>orf2</i>	OG12179
<i>ornamtransa</i>	OG3188
<i>psmaA</i>	OG7137
<i>psmaB</i>	OG6270
<i>psmaC</i>	OG6195
<i>psmaD</i>	OG6991
<i>psmaE</i>	OG6938
<i>psmaF</i>	OG7384
<i>psmaG</i>	OG7144
<i>psmbH</i>	OG13150
<i>psmbI</i>	OG10010
<i>psmbJ</i>	OG11178
<i>psmbK</i>	OG8076
<i>psmbL</i>	OG11980
<i>psmbM</i>	OG7815
<i>psmbN</i>	OG12279
<i>pyrdehydroe1bmt</i>	OG4622
<i>rad23</i>	OG7719
<i>rf1</i>	OG1348
<i>rla2A</i>	OG30868
<i>rla2B</i>	OG28197
<i>rpl11b</i>	OG9660
<i>rpl12b</i>	OG13588
<i>rpl13</i>	OG8643
<i>rpl14a</i>	OG17699
<i>rpl15a</i>	OG8245
<i>rpl16b</i>	OG9413
<i>rpl17</i>	OG9435
<i>rpl18</i>	OG10858
<i>rpl19a</i>	OG8244

BLAST genes	OMA equivalent OrthoGroup
<i>rpl1</i>	OG7857
<i>rpl20</i>	OG10345
<i>rpl21</i>	OG12888
<i>rpl22</i>	OG18472
<i>rpl23a</i>	OG14123
<i>rpl24A</i>	OG14344
<i>rpl24B</i>	OG19045
<i>rpl25</i>	OG14181
<i>rpl26</i>	OG13968
<i>rpl27</i>	OG15207
<i>rpl2</i>	OG5237
<i>rpl30</i>	OG20031
<i>rpl31</i>	OG18135
<i>rpl32</i>	OG15164
<i>rpl33a</i>	OG17810
<i>rpl35</i>	OG20637
<i>rpl36</i>	OG21070
<i>rpl37a</i>	OG22673
<i>rpl3</i>	OG1953
<i>rpl42</i>	OG19715
<i>rpl43b</i>	OG24650
<i>rpl4B</i>	OG2935
<i>rpl6</i>	OG8371
<i>rpl7A</i>	OG7413
<i>rpl9</i>	OG10508
<i>rpp0</i>	OG4543
<i>rps10</i>	OG16379
<i>rps11</i>	OG12202
<i>rps13a</i>	OG12931
<i>rps14</i>	OG12579
<i>rps15</i>	OG13130
<i>rps16</i>	OG14312
<i>rps17</i>	OG16498
<i>rps18</i>	OG12247
<i>rps19</i>	OG14901
<i>rps1</i>	OG5421
<i>rps20</i>	OG20114
<i>rps22a</i>	OG15319
<i>rps23</i>	OG12881

BLAST genes	OMA equivalent OrthoGroup
<i>rps24</i>	OG17433
<i>rps25</i>	OG20215
<i>rps26</i>	OG18162
<i>rps27a</i>	OG15504
<i>rps2</i>	OG5265
<i>rps3</i>	OG6317
<i>rps4</i>	OG4960
<i>rps5</i>	OG7696
<i>rps6</i>	OG5777
<i>rps7</i>	OG9651
<i>rps8</i>	OG7796
<i>rps9</i>	OG9104
<i>sadhchydrolaseE1</i>	OG2304
<i>sap40</i>	OG6543
<i>srp54</i>	OG1177
<i>srs</i>	OG2547
<i>stbproptase2ab</i>	OG3204
<i>stcproptase2ac</i>	OG3672
<i>suca</i>	OG5310
<i>tif2a</i>	OG5313
<i>tribe1009</i>	OG6949
<i>tribe1015</i>	OG6355
<i>tribe1026</i>	OG7993
<i>tribe1047</i>	OG12765
<i>tribe1050</i>	OG29425
<i>tribe1054</i>	OG13294
<i>tribe1081</i>	OG7978
<i>tribe1099</i>	OG22457
<i>tribe1118</i>	OG6174
<i>tribe1132</i>	OG22480
<i>tribe1136</i>	OG27806
<i>tribe1169</i>	OG12849
<i>tribe1170</i>	OG28247
<i>tribe1181</i>	OG12369
<i>tribe1190</i>	OG23564
<i>tribe1200</i>	OG28566
<i>tribe1204</i>	OG24213
<i>tribe1244</i>	OG9939
<i>tribe1245</i>	OG15596

BLAST genes	OMA equivalent OrthoGroup
<i>tribe1294</i>	OG13896
<i>tribe1335</i>	OG12455
<i>tribe1378</i>	OG11886
<i>tribe1381A</i>	OG5055
<i>tribe1409</i>	OG26511
<i>tribe281</i>	OG23080
<i>tribe333</i>	OG22471
<i>tribe495</i>	OG7782
<i>tribe532</i>	OG16260
<i>tribe542</i>	OG19046
<i>tribe550</i>	OG18450
<i>tribe572</i>	OG12562
<i>tribe585A</i>	OG12661
<i>tribe586</i>	OG12786
<i>tribe613</i>	OG37992
<i>tribe622</i>	OG5261
<i>tribe629A</i>	OG18880
<i>tribe646</i>	OG31788
<i>tribe647</i>	OG14630
<i>tribe683</i>	OG29404
<i>tribe700</i>	OG17191
<i>tribe716</i>	OG16597
<i>tribe717</i>	OG29212
<i>tribe739</i>	OG36538
<i>tribe740</i>	OG27048
<i>tribe756</i>	OG6415
<i>tribe764</i>	OG20345
<i>tribe768</i>	OG19978
<i>tribe801mt</i>	OG10726
<i>tribe831</i>	OG8814
<i>tribe832</i>	OG5662
<i>tribe850</i>	OG12417
<i>tribe852</i>	OG21157
<i>tribe893</i>	OG17091
<i>tribe895</i>	OG12638
<i>tribe896</i>	OG10414
<i>tribe905</i>	OG34217
<i>tribe906</i>	OG17038
<i>tribe927</i>	OG32840

BLAST genes	OMA equivalent OrthoGroup
<i>tribe930</i>	OG18359
<i>tribe942</i>	OG10200
<i>u2snrnp</i>	OG7268
<i>vacaatpasepl21a</i>	OG12244
<i>vata</i>	OG845
<i>vatb</i>	OG1247
<i>vatc</i>	OG3579
<i>vate</i>	OG11672
<i>vatpased</i>	OG10153
<i>vdac2</i>	OG7309
<i>w09c</i>	OG6215

Supplementary Table 3: Comparison between OMA and the BLAST-based approach orthology assignments. Green represents exact match between both methods, orange represents ortholog presence in one method but not in the other, turquoise represents absence of orthologs in both methods, and magenta represents disagreement between methods.

High-occupancy genes

Species	BLAST ef1EF1	OMA OG1279	BLAST ef1EF3	OMA OG1393	BLAST ef2EF2	OMA OG277	BLAST if4aa	OMA OG2006	BLAST nsf1G.fas	OMA OG1789	BLAST nsf1J	OMA OG2110	BLAST nsf1K	OMA OG1788	BLAST nsf1L	OMA OG1954	BLAST nsf1M	OMA OG1423	BLAST nsf2A	OMA OG307
<i>Damon variegatus</i>	=	=	/	/	X		X		=	=	X		X		X		=	=	=	=
<i>Daphnia pulex</i>	=	=	=	=	=	X		=	=	=	=	=	=	=	=	=	=	=	=	=
<i>Dermatophagoides farinae</i>	=	=	=	=	=	=	X		=	=	X		=	=	=	=	=	=	=	=
<i>Dysdera crocata</i>	=	=	=	=	X			X	X		=	=	=	=	=	=	=	=	=	=
<i>Eremobates</i> sp.	=	=	=	=	X								X						X	
<i>Hypochthonius rufulus</i>	=	=	X		=	=	=	=	=	=	=	=	=	=	=	=	=	=	=	=
<i>Limulus polyphemus</i>	=	=	=	=	=	=	=	=	=	=	=	=	=	=	=	=	=	=	=	=
<i>Liocheles australasiae</i>	=	=	X		=	=	X		=	=	=	=	X		=	=	=	=	X	
<i>Liphistius malayanus</i>	=	=	=	=	=	=	=	=	=	=	=	=	=	=	=	=	=	=	=	=
<i>Mastigoproctus giganteus</i>	=	=	=	=	=	=	=	=	=	=	=	=	=	=	=	=	X		=	=
<i>Ornithodoros rostratus</i>	=	=	=	=	=	=	=	=	=	=	=	=	=	=	=	=	=	=	=	=
<i>Peripatopsis overbergiensis</i>	=	=	=	X	=	=	=	=	X		X		=	=	X		=	=	X	
<i>Pycnogonum</i> sp.	X	X	=	=	=	X		=	=	=	=	=	=	=	=	=	=	=	=	=
<i>Ricinoides atewa</i>	=	=	X		X		X		=	=	=	=	X		X		=	=	=	=
<i>Scutigera coleoptrata</i>	=	=	=	=	=	=	=	=	=	=	=	=	X		=	=	=	=	=	=
<i>Siro boyerae</i>	=	=	=	=	=	=	=	=	=	=	=	=	=	=	=	=	=	=	=	=
<i>Sphodros rufipes</i>	=	=	=	=	=	=	=	=	=	=	=	=	=	=	=	=	=	=	=	=
<i>Synsphyronus apimelus</i>	X	X	=	=	X									X						
<i>Tetranychus urticae</i>	=	=	=	=	=	=	=	=	=	=	=	=	=	=	X		=	=	X	
<i>Tribolium castaneum</i>	=	=	=	=	=	=	=	=	=	=	=	=	=	=	=	=	=	=	=	=
<i>Trogulus martensi</i>	=	=	=	=	=	=	=	=	=	=	=	=	=	=	=	=	=	=	=	=
<i>Varroa destructor</i>	=	=	X		=	=	X		=	=	=	=	=	=	=	=	=	=	=	=
<i>Vietbocap lao</i>	=	=	=	=	=	=	=	=	=	=	=	=	=	=	X		=	=	=	=

Single absence	39
Both absence (/)	2
Single presence (X)	39
Both presence (=)	376
Both presence different gen	4
Total	460

82% shared presence out of total possibilities
82% shared presence/absence
17% of genes are present in one matrix and not in the other
0.8% (2 cases out of 230) pair of orthologs were different

Low-occupancy genes

Species	BLAST rpl43b	OMA OG24650	BLAST tribe646	OMA OG18880	BLAST tribe740	OMA OG27048	BLAST fpps	OMA OG13935	BLAST rpl37a	OMA OG22673	BLAST tribe739	OMA OG36538	BLAST tribe683	OMA OG29404	BLAST rps10	OMA OG16379	BLAST tribe852	OMA OG21157	BLAST tribe1378	OMA OG11886
<i>Damon variegatus</i>	/	/	=	=	/	/	X		/	/	X			X	=	=	=	=	X	
<i>Daphnia pulex</i>	=	=	/	/	=	=	=	=	=	=	=	=	=	=	/	/	=	X	X	
<i>Dermatophagoidea farinae</i>	/	/	X		=	=	=	=	=	=	=	X		X			=	=	X	
<i>Dysdera crocata</i>	/	/	X		=	=	X		=	=	=	=	/	/	=	=	X		X	
<i>Eremobates</i> sp.	/	/	/	/	/	/	X		/	/	X		X		=	=	=	=	/	/
<i>Hypochthonius rufulus</i>		X	X		=	=	=	=	/	/	X			X	X		X		=	=
<i>Limulus polyphemus</i>	/	/	=	=	/	/	=	=	=	=	X			X	=	=	X		/	/
<i>Liocheles australasiae</i>	/	/	=	=	/	/	X		=	=	X		/	/	=	=	=	=	=	=
<i>Liphistius malayanus</i>	/	/	=	=	/	/	=	=	=	=	=	=	=	=	=	=	=	=	=	=
<i>Mastigoproctus giganteus</i>	/	/	=	=	/	/	X		=	=	X			X	=	=	=	=	X	
<i>Ornithodoros rostratus</i>	X		X		=	=	=	=	=	=	=	=	/	/	=	=	=	=	=	=
<i>Peripatopsis overbergensis</i>		X	X		/	/	X		X		=	=	=	=	X		=	=	=	=
<i>Pycnogonum</i> sp.	/	/	X		/	/		=	=	=	=		X	X			X		=	=
<i>Rictonoides atewa</i>	/	/	=	=	/	/	X		/	/	X			X	=	=	=	=	/	/
<i>Scutigera coleoptrata</i>	X		X		=	=	/	/	=	=	=	=	=	=	=	=	=	=	=	=
<i>Siro boyerae</i>	X			=	/	/	/	/	/	/		X	/	/	=	=	=	=	=	=
<i>Sphodros rufipes</i>	=	=	X		=	=	=	=	=	=	=	=	/	/	X		X		=	=
<i>Synsphyronus apimeilus</i>	/	/	=	=	/	/	=	=	/	/	=	=		X	X		X		=	=
<i>Tetranychus urticae</i>	/	/	X		=	=	=	=	/	/	X		/	/	X		=	/	=	=
<i>Tribolium castaneum</i>	/	/	=	=	=	=	X		=	=	=	=	=	=	=	=	=	=	=	=
<i>Trogulus martensi</i>	=	=	X		/	/		=	=	=	X		/	/	=	=	/	/	=	=
<i>Varroa destructor</i>		X	=	=	=	=	X		/	/	=	=		X	=	=	X		X	
<i>Vietbacap lao</i>	/	/	=	=	=	=	X		/	/	=	=	/	/	=	=	=	=	=	=

Single absence	68
Both absence (/)	106
Single presence (X)	68
Both presence (=)	218
Total	460

47% shared presence out of total possibilities
70.4% shared presence/absence
30% of genes are present in one matrix and not in the other