

Supplementary materials

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Exploring the effect of the *Cardinium* endosymbiont on

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spiders

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Population	Country	Year of collection	Map	n	Prevalence (n)	95% c.i.
Cap Breton	France	2010	A	16	0.00 (0)	(0.00-0.21)
Toulouse	France	2010	B	19	0.16 (3)	(0.03-0.40)
Barcelona	Spain	2010	C	7	0.00 (0)	(0.00-0.41)
Castelnaudary	France	2009	D	21	0.86 (18)	(0.64-0.97)
Castres	France	2010	E	10	0.30 (3)	(0.07-0.65)
Perpignan	France	2010	F	17	0.18 (3)	(0.04-0.43)
Faveyrolles	France	2010	G	34	0.50 (17)	(0.32-0.68)
Béziers	France	2010	H	10	0.60 (6)	(0.26-0.88)
Montpellier	France	2009-2010	I	159	0.79 (126)	(0.72-0.85)
Saint Gilles	France	2010	J	28	0.07 (2)	(0.01-0.24)
Château-Renard	France	2010	K	18	0.72 (13)	(0.47-0.90)
Valence	France	2009	L	15	0.73 (11)	(0.45-0.92)
Pierrelatte	France	2010	M	11	0.27 (3)	(0.06-0.61)
Lyon Saint Exupéry	France	2010	N	10	0.10 (1)	(0.00-0.45)
Univeristé Lyon 1	France	2010	O	23	0.17 (4)	(0.05-0.39)
La Varenne	France	2009	P	10	0.10 (1)	(0.00-0.45)
Saint Romain en Gier	France	2009	Q	12	0.33 (4)	(0.10-0.65)
Plan de la Tour	France	2010	R	3	0.00 (0)	(0.00-0.71)
Sari d'Orcino	France (Corsica)	2010	S	14	0.00 (0)	(0.00-0.23)
Heraklion	Crete	2010	T	10	0.00 (0)	(0.00-0.31)
Petra	Jordan	2011	U	6	0.00 (0)	(0.00-0.46)
Sede Boqer Campus	Israel	2010	V	11	0.09 (1)	(0.00-0.41)
Merced	California	2010	W	12	0.00 (0)	(0.00-0.26)
Madera	California	2010	X	16	0.00 (0)	(0.00-0.21)
Mariposa	California	2010	Y	2	0.00 (0)	(0.00-0.84)
Yosemite	California	2010	Z	16	0.00 (0)	(0.00-0.21)

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7 **Table S1.** Description of the *Holocnemus pluchei* samples: location, sample size and prevalence of
8 *Cardinium*. Map letters indicate references in Figure 1. Confidence intervals (c.i.) were calculated
9 from the binomial distribution.

Organism	Gene	Gene product	Primer (5' - 3')	Annealing temperature	Size	Positive control for infection screening	Reference (primers)
<i>Holocnemus pluchei</i>	<i>COI</i>	Cytochrome oxidase subunit I	Ron – GGAGCYCCWGATATAGCTTTCCC * Nancy – CCTGGTAAAAATTAAAAATATAAACTTC *	52°C	488bp	–	(Simon et al. 1994)
<i>Cardinium hertigi</i>	<i>16S rRNA</i>	Small ribosomal subunit	ChF – TACTGTAAGAATAAGCACCCGGC * ChR – GTGGATCACTTAAACGCTTTCG * CLOfI – GAACCTTACCTGGCTAGAAATGTAAT CLOrI – GCCACTGTCTTCAAGCTCTACCAAC	54°C 54°C 54°C	ChF/ChR: 394bp CLOfI/CLOrI: 466bp ChF/CLOrI: 954bp	<i>H. pluchei</i>	(Zchori-Fein & Perlman 2004) (Gotoh et al. 2007)
	<i>gyrB</i>	DNA gyrase subunit B	gyrF – CCTATYCTTGTAGARGGRGAAA * gyrR – GCTCATCAAHACATTTTTGCGTIGG *	52°C	483bp	<i>H. pluchei</i>	This study
<i>Wolbachia pipiensis</i>	<i>wsp</i>	Surface protein	81F – TGGTCCAATAAGTGTGAAGAAAC * 691R – AAAAAATTAAACGCTACTCCA *	50°C	602bp	<i>Culex pipiens</i> (Diptera: Culicidae)	(Zhou et al. 1998)
<i>Arsenophonus</i> spp.	<i>ftsK</i>	Cell division protein (DNA translocase)	ftsKf – GTTGTATGGTYGATGAAATTTGC * ftsKr – GCTCTTCATCACYATCAWAACC *	52°C	445bp	<i>Hippobosca equina</i> (Diptera: Hippoboscidae)	(Duron et al. 2010)
<i>Spiroplasma ixodetis</i>	<i>16S rRNA</i>	Small ribosomal subunit	Spixof – TTAGGGGCTCAACCCCTAACC * Spixor – TCTGGCATTGCCAACTCTC *	52°C	810bp	<i>Cicadella viridis</i> (Hemiptera: Cicadellidae)	(Duron et al. 2008a)
<i>Rickettsia</i> spp.	<i>gltA</i>	Citrate synthase	RICS741F – CATCCGGAGCTAATGGTTTTGC * RCT1197R – CATTTCTTTCCATTGTGCCAATC *	50°C	470bp	<i>Meta</i> sp. (Aranea: Tetragnathidae)	(Goodaere et al. 2006) (Davis et al. 1998)

12 **Table S2.** Genes and primer features. The sizes of PCR products provided are those of positive controls in base pairs (bp). * Primers used in initial screen of
13 the spider collection; the other primers were used to obtain additional sequences.

15 **References**

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26 **Figure legends**

27 **Figure S1.** Numbers of eggs regressed against mother's tibia-patella length. Black squares,
28 *Cardinium*-infected females (n = 50); with squares, uninfected females (n = 17).

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30 **Figure S2.** Variation of *Cardinium* frequencies in the south of France and Spain. The figure
31 encompasses 18 populations (from A to R on Figure 1). Left: distance measured from Castelnaudary
32 (population D); right: distance measured from Béziers (population H).

33 *Cardinium* frequency significantly decreases from reference locations (Castelnaudary: $t_{16} = -2.056$; P
34 = 0.05; Béziers: $t_{16} = -2.467$; $P = 0.02$). No *Cardinium*-infected specimen was found in populations
35 more than 400km from reference locations.

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37 **Figure S3.** *Cardinium* phylogeny constructed via maximum-likelihood using (a) *16S rRNA* and (b)
38 *gyrb* sequences. The symbionts of arthropods have the prefix S followed by the proper name of their
39 host, whereas other bacteria have proper binomial nomenclature. *Cardinium* hosts are encoded with
40 shape symbols, with Araneae designated by diamonds, Acari by squares, Hemiptera by circles,
41 Hymenoptera by black triangles and Diptera by white triangles. Associated GenBank accession
42 numbers are shown in parentheses. Sequences from *Holocnemus pluchei* are underlined. Effect of
43 infection is indicated in bold type if known (CI, cytoplasmic incompatibility; P, parthenogenesis; EF,
44 enhancing of fecundity). The three *Cardinium* groups (a-c) are indicated. The closest known relative
45 of *Cardinium*, the *Acanthamoeba* symbiont *Amoebophilus asiaticus*, was used as an outgroup.
46 Numbers on branches indicate percentage bootstrap support for major branches (1000 replicates; only
47 bootstrap values of 60% or more are shown). The scale bar is in units of substitutions/site.

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49 **Figure S4.** Distribution of mtDNA haplotypes among populations, partitioned by *Cardinium* infection
50 status. The sample letter above each box corresponds to the populations listed in Table S1. Within
51 each population, the colours within bars indicate the relative proportion of haplotypes within each
52 infection status (U = uninfected, I = infected). Numbers within bars indicate the number of specimens.

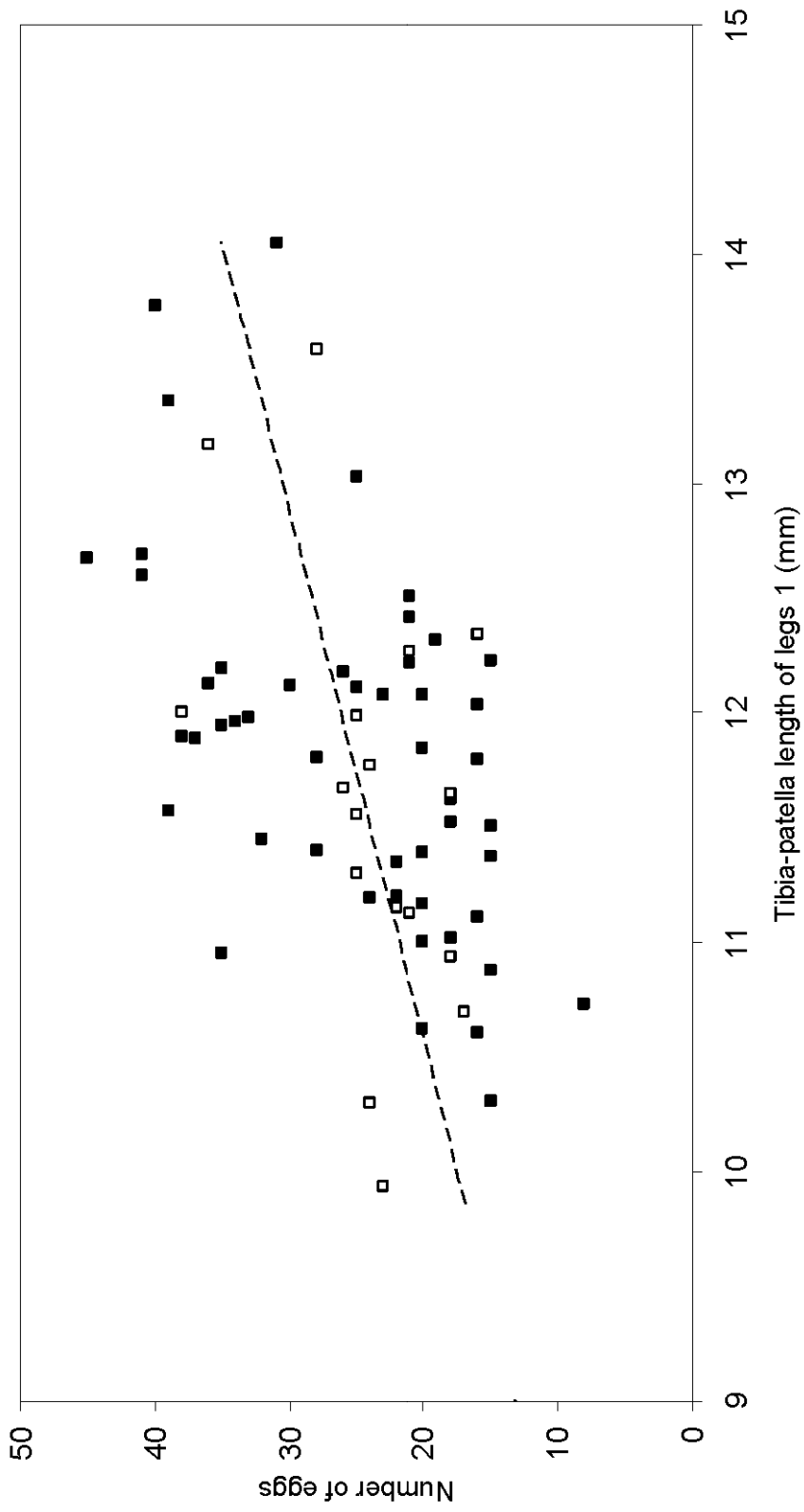


Figure S1

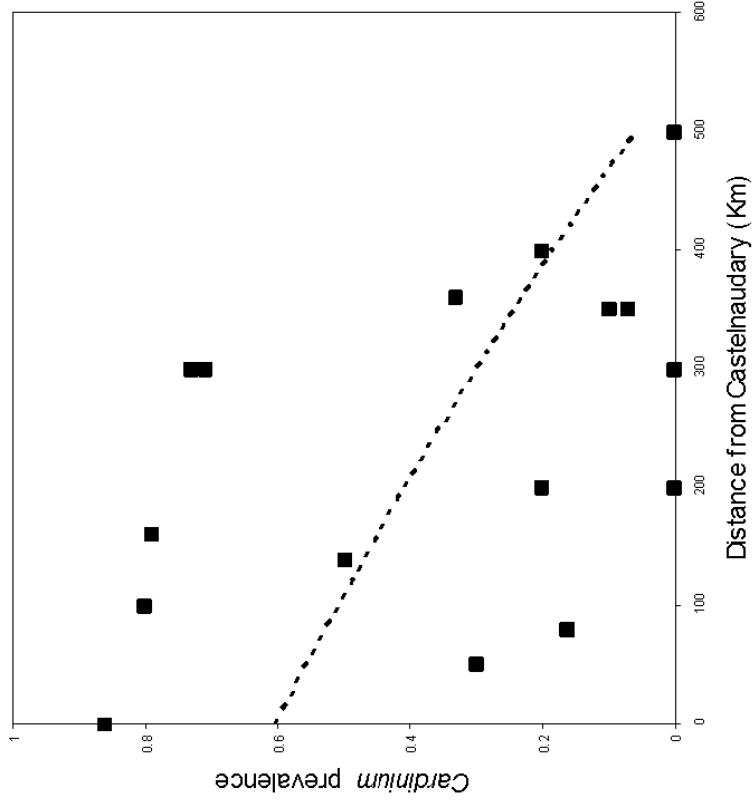
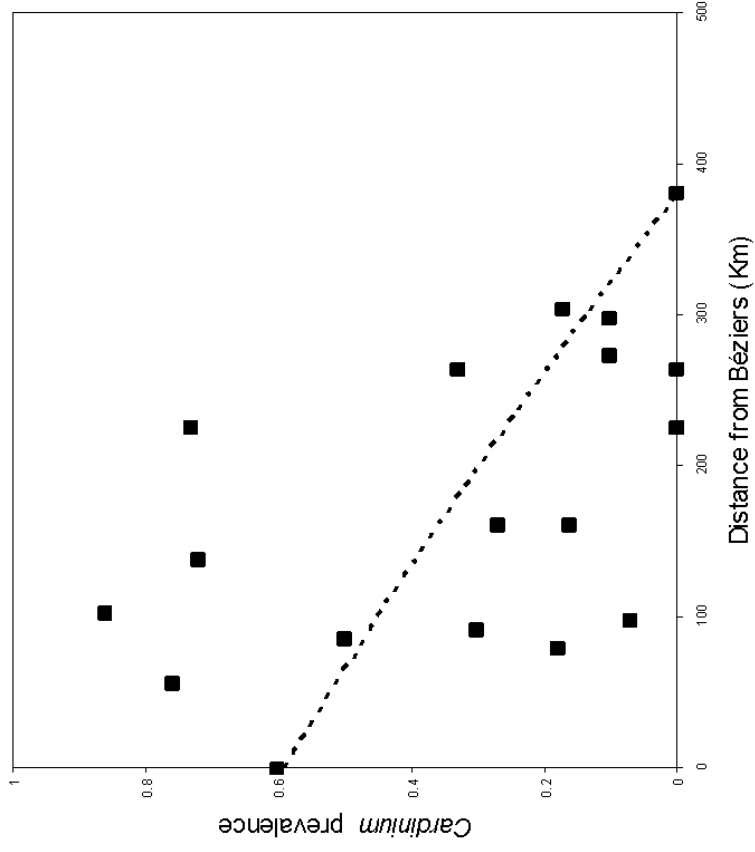
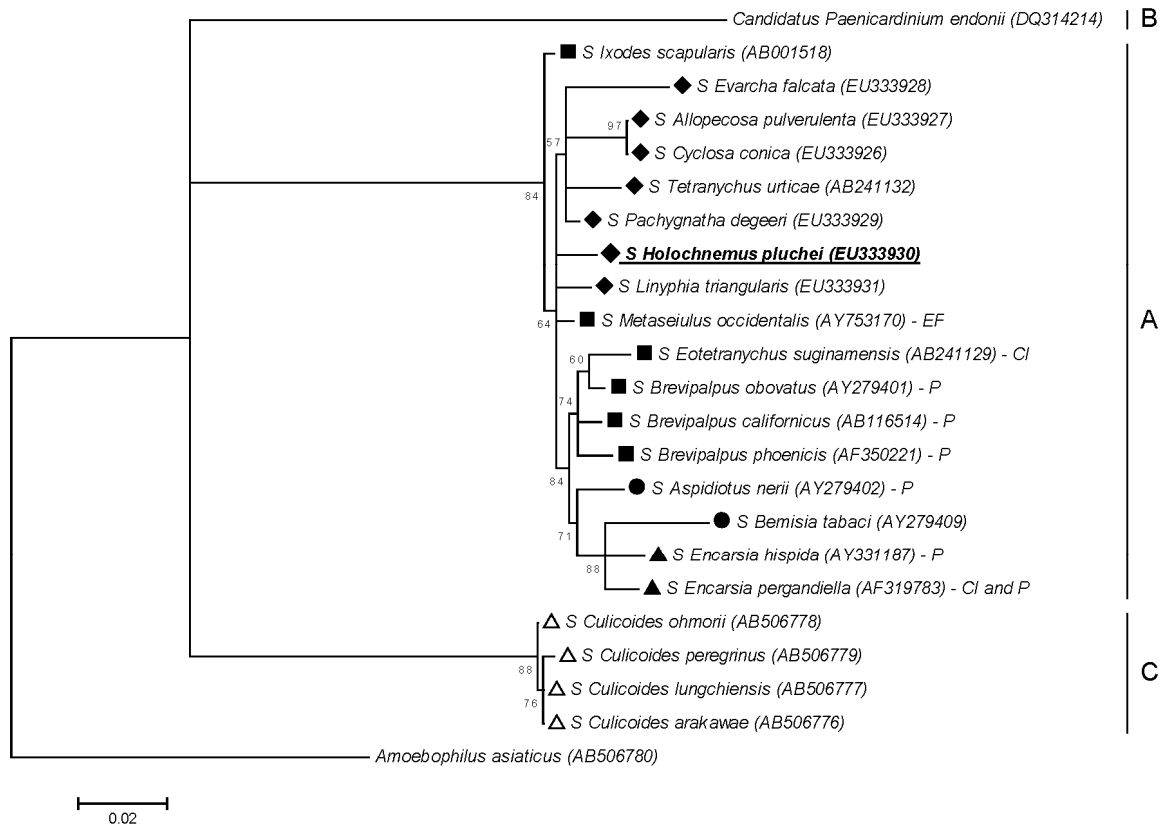


Figure S2

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Figure S3A

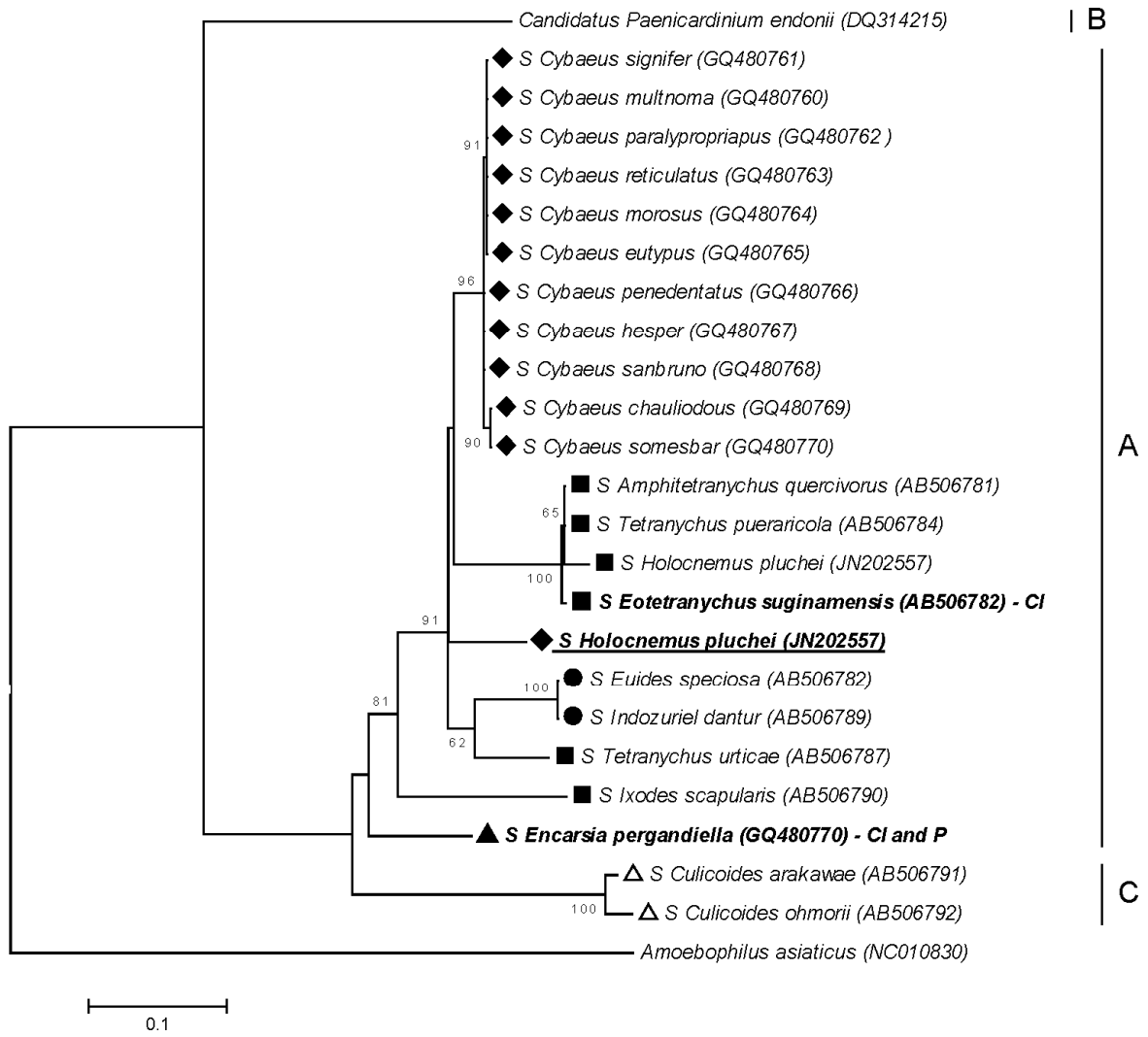
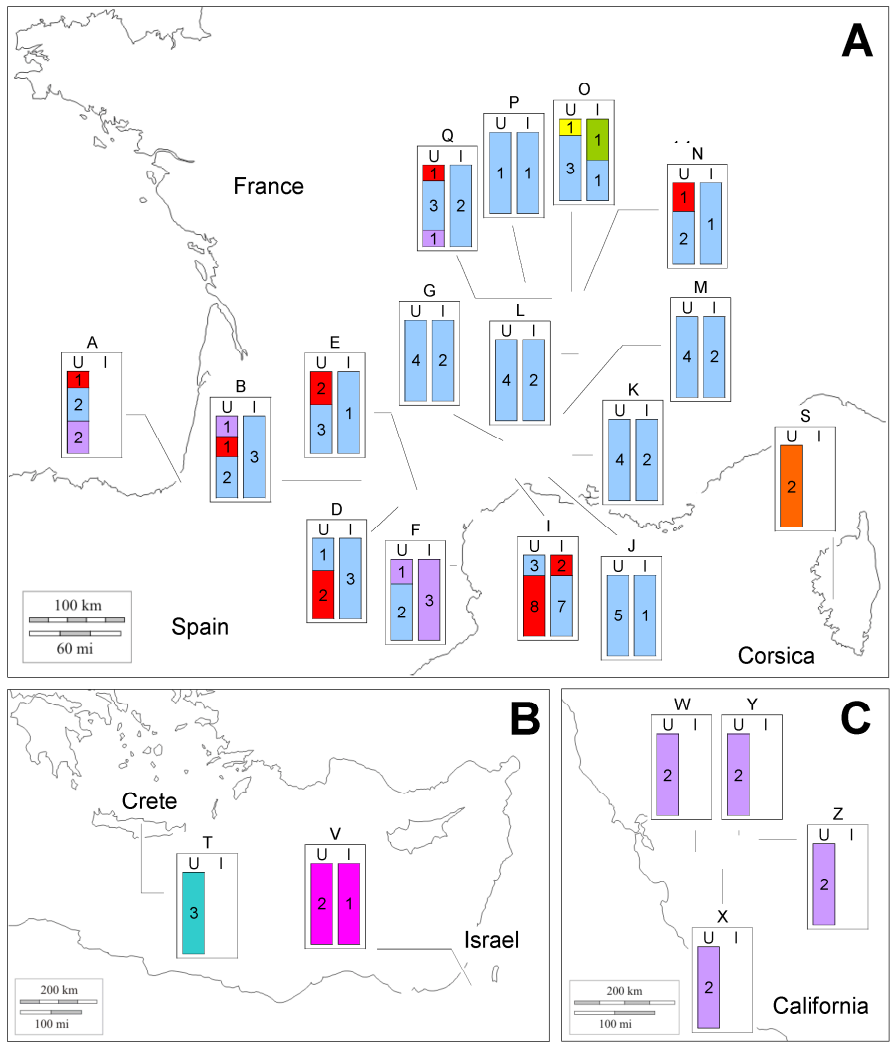


Figure S3B



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Figure S4