Supplemental information for: "**Transmission of the human relapsing fever spirochete *Borrelia persica* by the argasid tick *Ornithodoros tholozani* involves blood meals from wildlife animal reservoirs and mainly transstadial transfer"** by Gabriela Kleinerman, Tom Eshed, Yaarit Nachum-Biala, Roni King, Gad Baneth

Figure S1: A maximum likelihood phylogram comparing 236-bp DNA sequences of the *glpQ* gene from *B. persica* detected in *O. tholozani* included in the study, to sequences from other *B. persica* GenBank accessions and from other *Borrelia* spp. The Tamura-Nei model was used with a pairwise deletion procedure. Numbers at nodes correspond to a percentage confidence level higher than 70% in a bootstrap test performed on 1000 replicates. New sequences derived from this study are marked with black diamond squares with three sequences deposited in GenBank (MH923346, MH923347 and MH923348). The scale bar corresponds to a distance of 0.02.

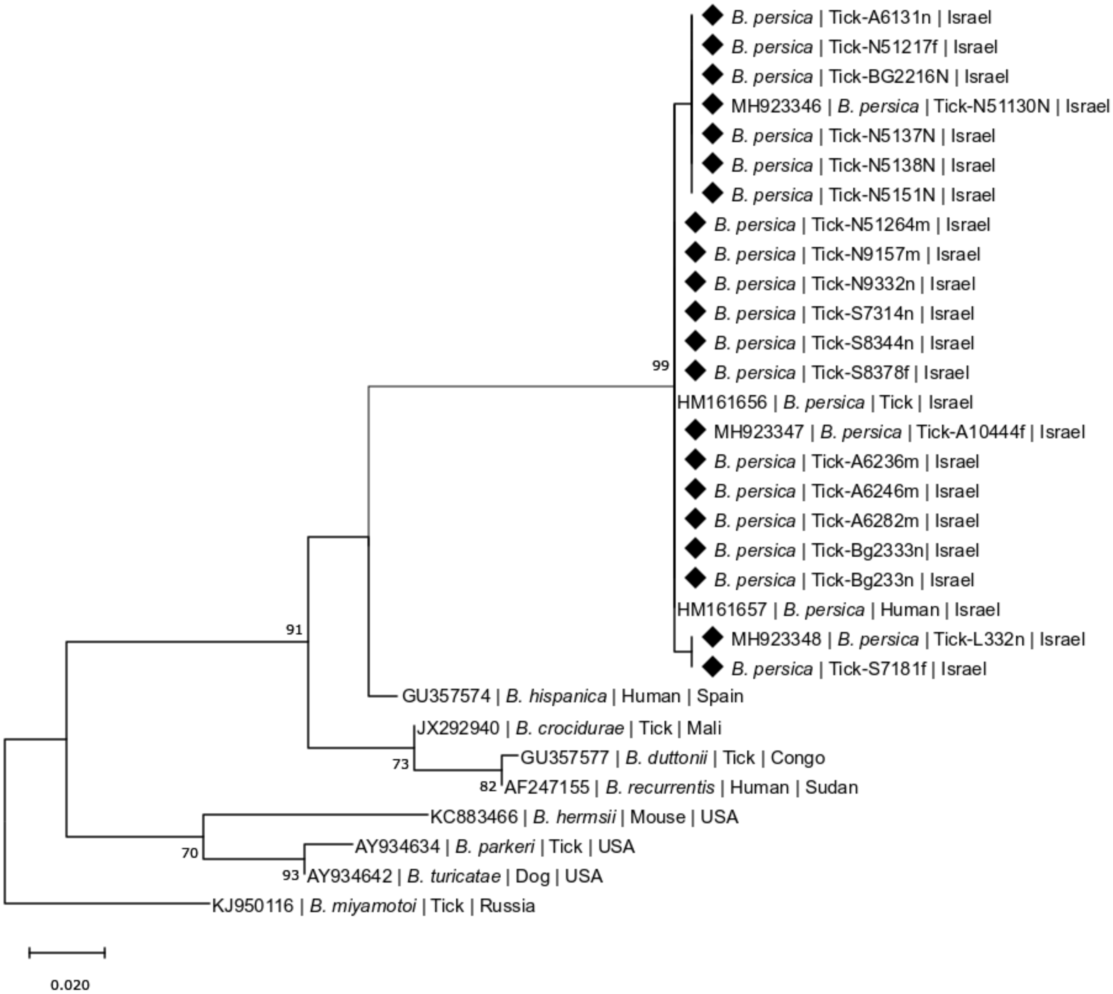

Figure S2: A maximum likelihood phylogram comparing 408 bp DNA sequences of the*16S rRNA* gene from *O. tholozani* ticks included in the study, to a sequence from *Ornithodoros moubata* GenBank accession (gi|28263048), used as outgroup. Two sequences from each site of collection were used for the analysis. The Hasegawa-Kishino-Yano model was chosen with a pairwise deletion procedure. Numbers at nodes correspond to a percentage confidence level higher than 70 % in a bootstrap test performed on 1000 replicates. New sequences derived from this study are marked with black diamond squares with several sequences deposited in GenBank. The scale bar corresponds to a distance of 0.02.

Figure S3: A maximum likelihood phylogram comparing 267–294-bp DNA sequences of the *flaB* gene from *B. persica* detected in wild animals in the study, to sequences from other *B. persica* GenBank accessions and from other *Borrelia* spp. The Tamura-3-Parameter model was used with a pairwise deletion procedure. Numbers at nodes correspond to a percentage confidence level higher than 70% in a bootstrap test performed on 1000 replicates. New sequences derived from this study are marked with black diamond squares with two sequences deposited in GenBank (MK138356 and MK138357). The scale bar corresponds to a distance of 0.05.

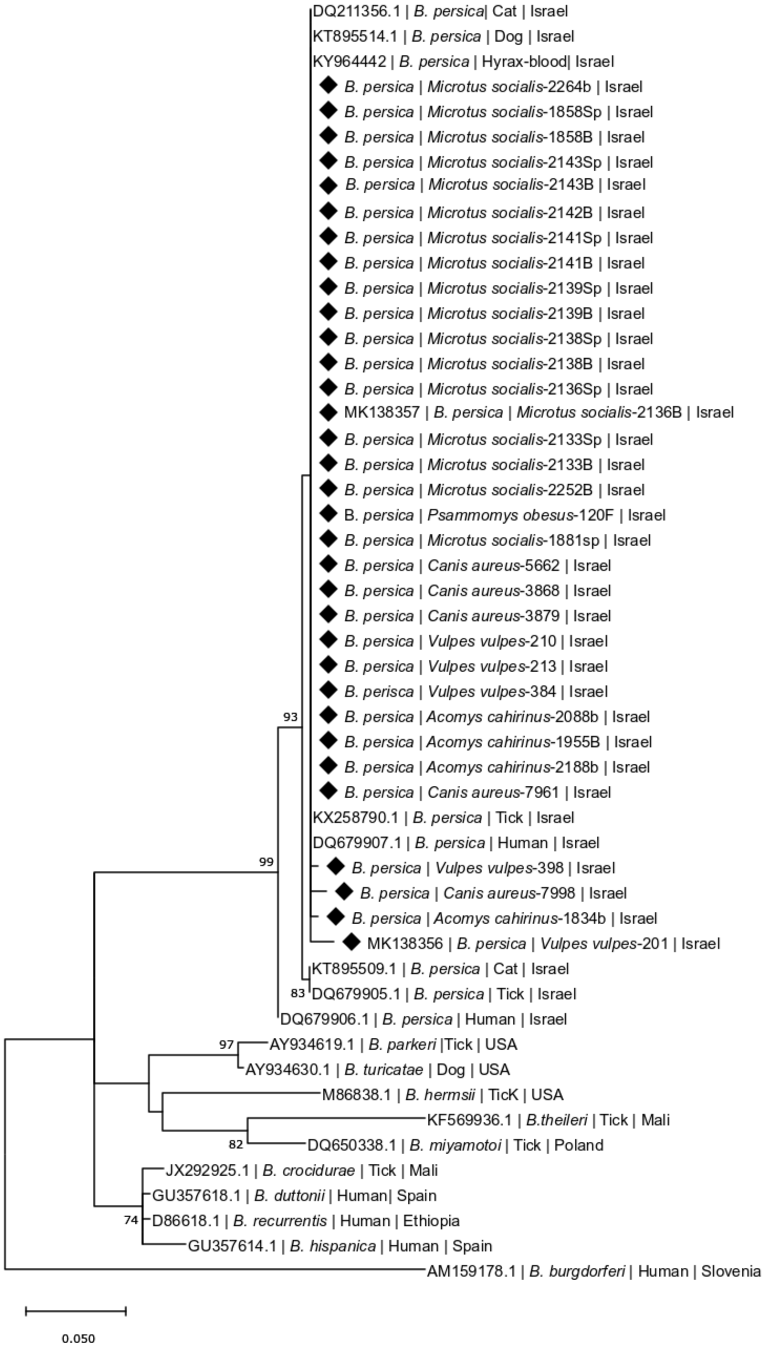

Figure S4: Map showing division of Israel into study zones. Reprinted with permission from Rose et al., Genetic characterization of spotted fever group rickettsiae in questing ixodid ticks collected in Israel and environmental risk factors for their infection. Parasitology. 2017. 144(8):1088-1101.

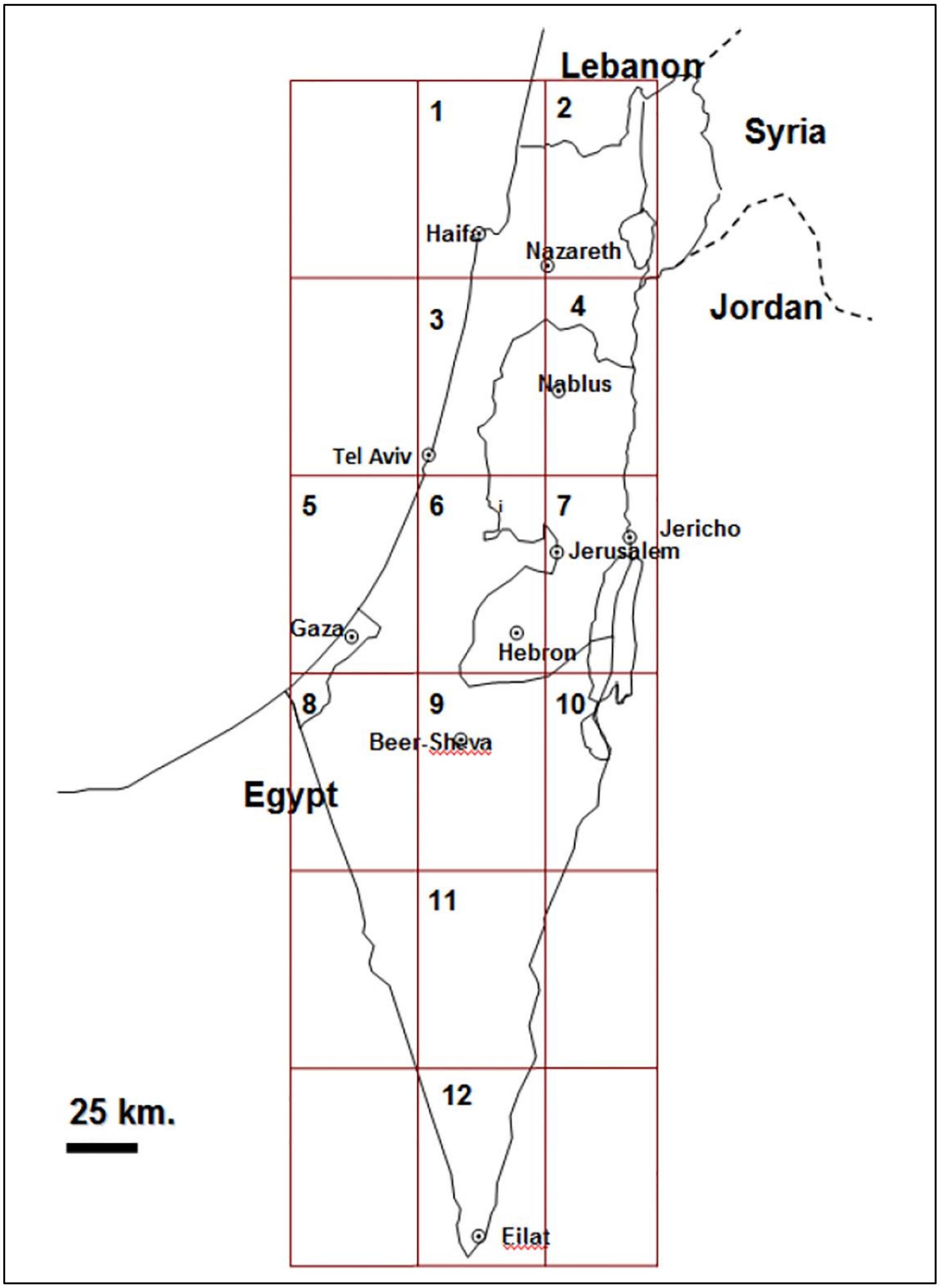

Figure S5: Flow chart of PCR to detect the host sources of blood meals