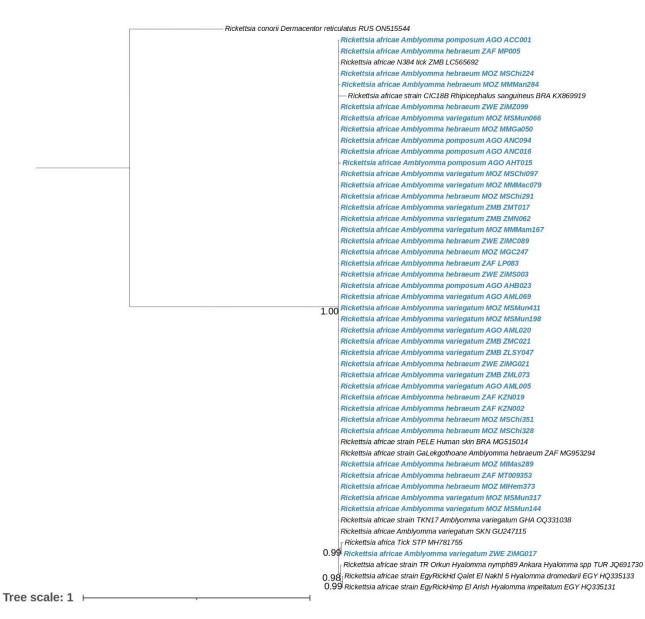
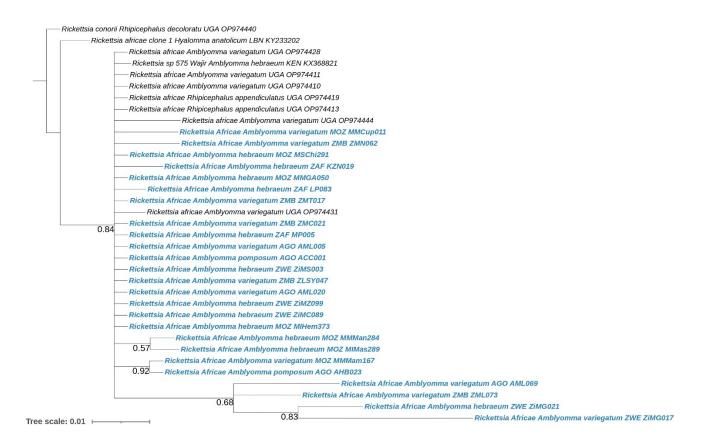
**Supplementary Figure S1-S4:** Individual figures of the Bayesian inference phylogenetic analyses of *R*. *afircae* for ompA, ompB, omp and gltA genes



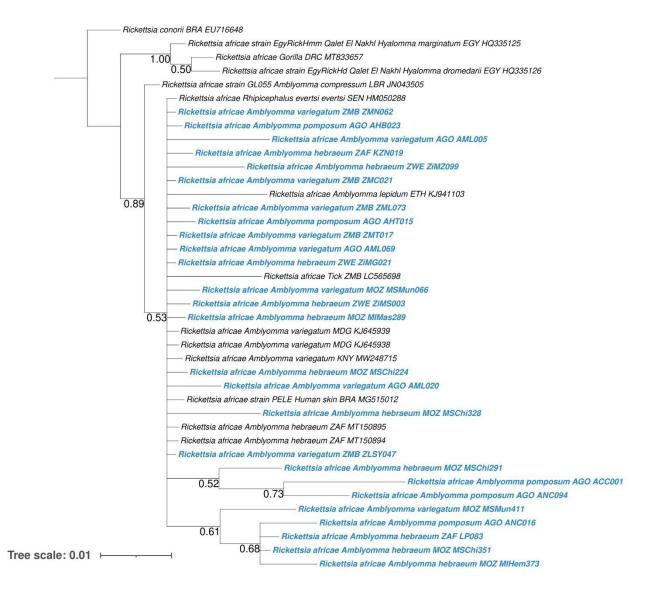
**Figure S1**: Bayesian inference analysis of the *ompA Rickettsia africae* gene. Analysis was done using the HKY model. Posterior probability is indicated at each branch node. Posterior probabilities < 0.85 have been removed. Sequences from this study are in blue. Country of origin is indicated in the sample ID as: AGO – Angola, BRA – Brazil, EGY - Egypt, GHA – Ghana, MOZ – Mozambique, RUS – Russia, SKN-Saint Kitts and Nevis, STP - Sao Tome and Principe, TUR – Turkey, ZAF – South Africa, ZMB – Zambia and ZWE – Zimbabwe.

Rickettsia conorii AF123721	
Rickettsia africae AF123706	
Rickettsia africae isolate 214 Amblyomma variegatum KEN KF660533 Rickettsia africae Amblyomma variegatum MOZ MMMac079	}
Rickettsia africae Amblyomma variegatum ZWE ZiMG017	
——Rickettsia africae Amblyomma hebraeum ZAF MP005	
Rickettsia sp isolate Av0810 Amblyomma variegatum STP MF667453	
— Rickettsia africae isolate 30966 Homo sapiens TZA KU721071	
— Rickettsia sp clone Av Dj492 Amblyomma variegatum DJI KT032136	
— Rickettsia sp clone Ra Dj349 Rhipicephalus annulatus DJI KT032137	
Rickettsia africae Amblyomma hebraeum ZWE ZIMC089	
- Rickettsia africae Amblyomma hebraeum MOZ MSChi291	
- Rickettsia africae Amblyomma hebraeum MOZ MSChi251	
— Rickettsia africae Amblyomma variegatum MOZ MSChi097	
— Rickettsia africae Amblyomma hebraeum ZWE ZiMG021	
Rickettsia africae Amblyomma hebraeum ZAF LP083	
- Rickettsia africae Amblyomma hebraeum ZAF KZN002	
- Rickettsia africae Amblyomma pomposum AGO ANC094	
— Rickettsia africae Amblyomma pomposum AGO ANCOS4	
— Rickettsia africae Amblyomma variegatum ZMB ZMC021	
- Rickettsia africae Amblyomma hebraeum ZWE ZiMS003	
— Rickettsia africae Amblyomma variegatum ZMB ZML073	
— Rickettsia africae Amblyomma variegatum ZMB ZMN062	
Rickettsia africae Amblyomma variegatum MOZ MMMam167	
0.86	
— Rickettsia africae Amblyomma variegatum AGO AML020 — Rickettsia africae Amblyomma variegatum AGO AML069	
— Rickettsia africae Amblyomma pomposum AGO ATH015 — Rickettsia africae Amblyomma hebraeum ZAF KZN019	
— Rickettsia africae Amblyomma hebraeum MOZ MSChi224	
— Rickettsia africae Amblyomma variegatum ZMB ZLSY047 Dickettsia africae Amblyomma nomnosum ACO ANC016	
— Rickettsia africae Amblyomma pomposum AGO ANC016 Pickettsia africae Amblyomma pomposum AGO ACC001	
- Rickettsia africae Amblyomma pomposum AGO ACC001	
— Rickettsia africae Amblyomma hebraeum ZAF GP041	
- Rickettsia africae Amblyomma variegatum AGO AML005	
— Rickettsia africae Amblyomma hebraeum MOZ MMMan284 Dislattais africae Amblyomma hebraeum MOZ MMChi222	
— Rickettsia africae Amblyomma hebraeum MOZ MSChi328	
— Rickettsia africae Amblyomma hebraeum MOZ MMGa050	
- Rickettsia africae Amblyomma hebraeum MOZ MIMas289	
— Rickettsia africae Amblyomma hebraeum ZWE ZiMZ099	
— Rickettsia africae Amblyomma hebraeum MOZ MIHem373	
— Rickettsia africae Amblyomma variegatum ZMB ZMT017	
- Rickettsia africae Amblyomma variegatum MOZ MSMun144	
— Rickettsia africae Amblyomma variegatum MOZ MSMun411	
- Rickettsia africae Amblyomma variegatum MOZ MSMun317	
— Rickettsia africae Amblyomma variegatum MOZ MSMun198	
0.98 Rickettsia africae Amblyomma eburneum MOZ MSMun1015	
Rickettsia africae Amblyomma variegatum AGO AML193	
- Rickettsia africae Amblyomma variegatum MOZ MSMun066	
— Rickettsia africae Amblyomma eburneum MOZ MSMun998	
Rickettsia africae Amblyomma variegatum MOZ MMCup011	

**Figure S2**: Bayesian inference analysis of the *ompB Rickettsia africae* gene. Analysis was done using the HKY model, with gamma rates. Posterior probability is indicated at each branch node. Posterior probabilities < 0.85 have been removed. Sequences from this study are in blue. Country of origin is indicated in the sample ID as: AGO – Angola, DJI - Djibouti, ETH – Ethiopia, KEN – Kenya, MOZ – Mozambique, STP - São Tomé and Príncipe, TZA – Tanzania, ZAF – South Africa, ZMB – Zambia and ZWE – Zimbabwe.



**Figure S3**: Bayesian inference analysis of the *omp Rickettsia africae* gene. Analysis was done using the HKY model. Posterior probability is indicated at each branch node. Posterior probabilities < 0.50 have been removed. Sequences from this study are in bold. Country of origin is indicated in the sample ID as: AGO – Angola, KEN – Kenya, KNY – Knysna, LBN - Lebanon, MOZ – Mozambique, ZAF – South Africa, UGA – Uganda, ZMB – Zambia and ZWE – Zimbabwe.



**Figure S4**: Bayesian inference analysis of the *gltA Rickettsia africae* gene. Analysis was done using the HKY model, with gamma rates. Posterior probability is indicated at each branch node. Posterior probabilities < 0.50 have been removed. Sequences from this study are in blue. Country of origin is indicated in the sample ID as: AGO – Angola, BRA – Brazil, DRC -Democratic Republic of the Congo, EGY - Egypt, ETH – Ethiopia, KEN – Kenya, KNY – Knysna, LBR - Liberia, MOZ – Mozambique, SEN – Senegal, ZAF – South Africa, ZMB – Zambia and ZWE – Zimbabwe