

## Supplemental Material (Supplemental Figures S1 – S3)

### Core genome multilocus sequence typing scheme for improved characterization and epidemiological surveillance of pathogenic *Brucella*

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### Supplemental Figures S1 – S3

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**Supplemental Figure S1:** A maximum-likelihood (ML) phylogenetic tree computed with RAxML based on 159,572 SNP positions identified in the 612 *Brucella* genomes using the NASP pipeline. Branch coloration highlights bootstrap values as indicated in the legend

0.005

### Geography

- Africa
- Asia
- Europe
- Middle East
- North America
- Oceania
- South America

### Brucella species

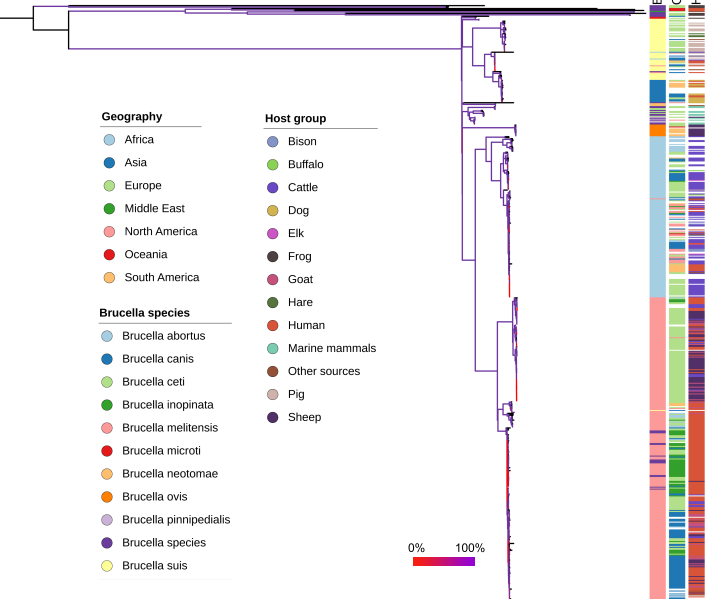
- Brucella abortus*
- Brucella canis*
- Brucella ceti*
- Brucella inopinata*
- Brucella melitensis*
- Brucella microti*
- Brucella neotomae*
- Brucella ovis*
- Brucella pinnipedialis*
- Brucella species*
- Brucella suis*

### Host group

- Bison
- Buffalo
- Cattle
- Dog
- Elk
- Frog
- Goat
- Hare
- Human
- Marine mammals
- Other sources
- Pig
- Sheep

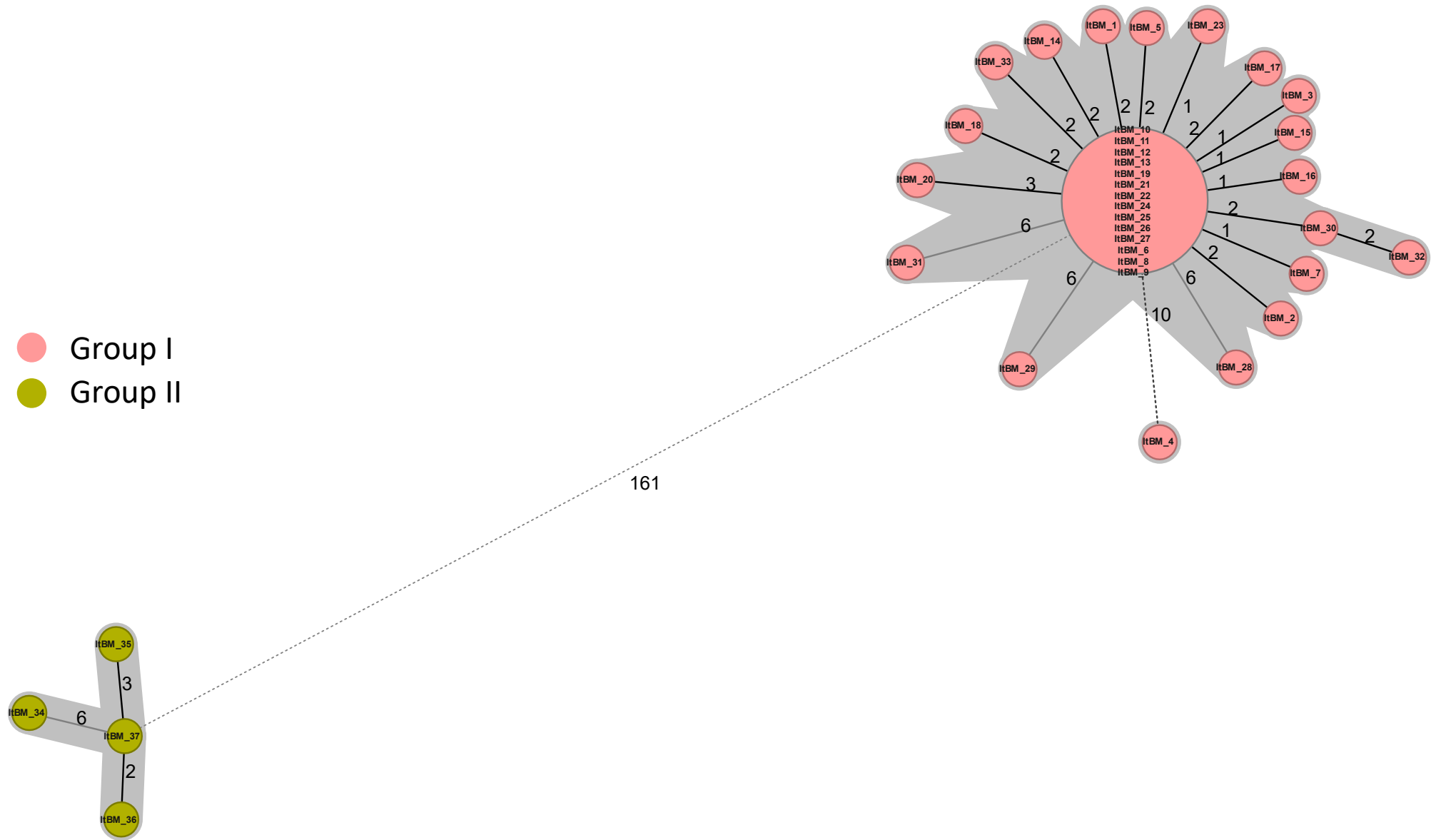
0% 100%

Brucella species  
Geography  
Host group



**Supplemental Figure S2:** Minimum spanning tree (MST) calculated for 37 *B. melitensis* genomes with known epidemiological relation using the *B. melitensis*-specific core genome MLST targets (n=2,704). The MST was generated using Ridom SeqSphere v07 with missing values being ignored in pairwise comparisons. Unique cgMLST profiles are represented with circles. The colors of the circles represent the genetic group of strains, while the circle size is related to the number of genomes assigned in each cgMLST genotype. The number of different alleles between cgMLST profiles is indicated on the connecting lines between the circles. The solid and dashed connecting lines represent allele differences below and above 10, respectively. Clusters were identified based on fewer than three allele mismatches and highlighted with grey shaded areas.

- Group I
- Group II



**Supplemental Figure S3:** A maximum-likelihood (ML) phylogenetic tree computed with RAxML for the 1,322 *Brucella* genomes. Branch coloration highlights bootstrap values as in Fig S1.

Tree scale: 0.01

### Brucella species

- Brucella abortus
- Brucella canis
- Brucella ceti
- Brucella inopinata
- Brucella melitensis
- Brucella microti
- Brucella neotomae
- Brucella ovis
- Brucella pinnipedialis
- Brucella species
- Brucella suis

### Geography

- Africa
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### Host group

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