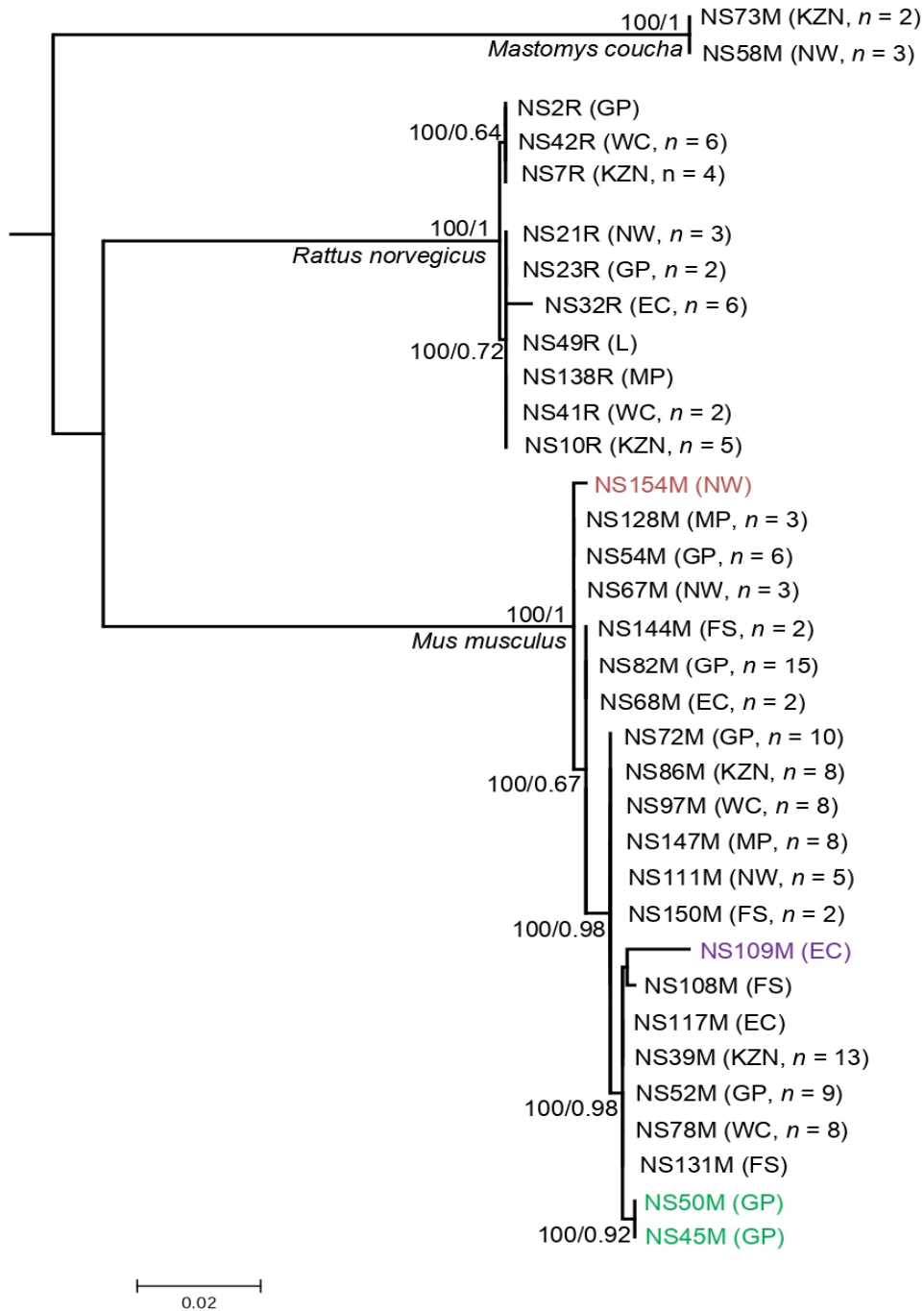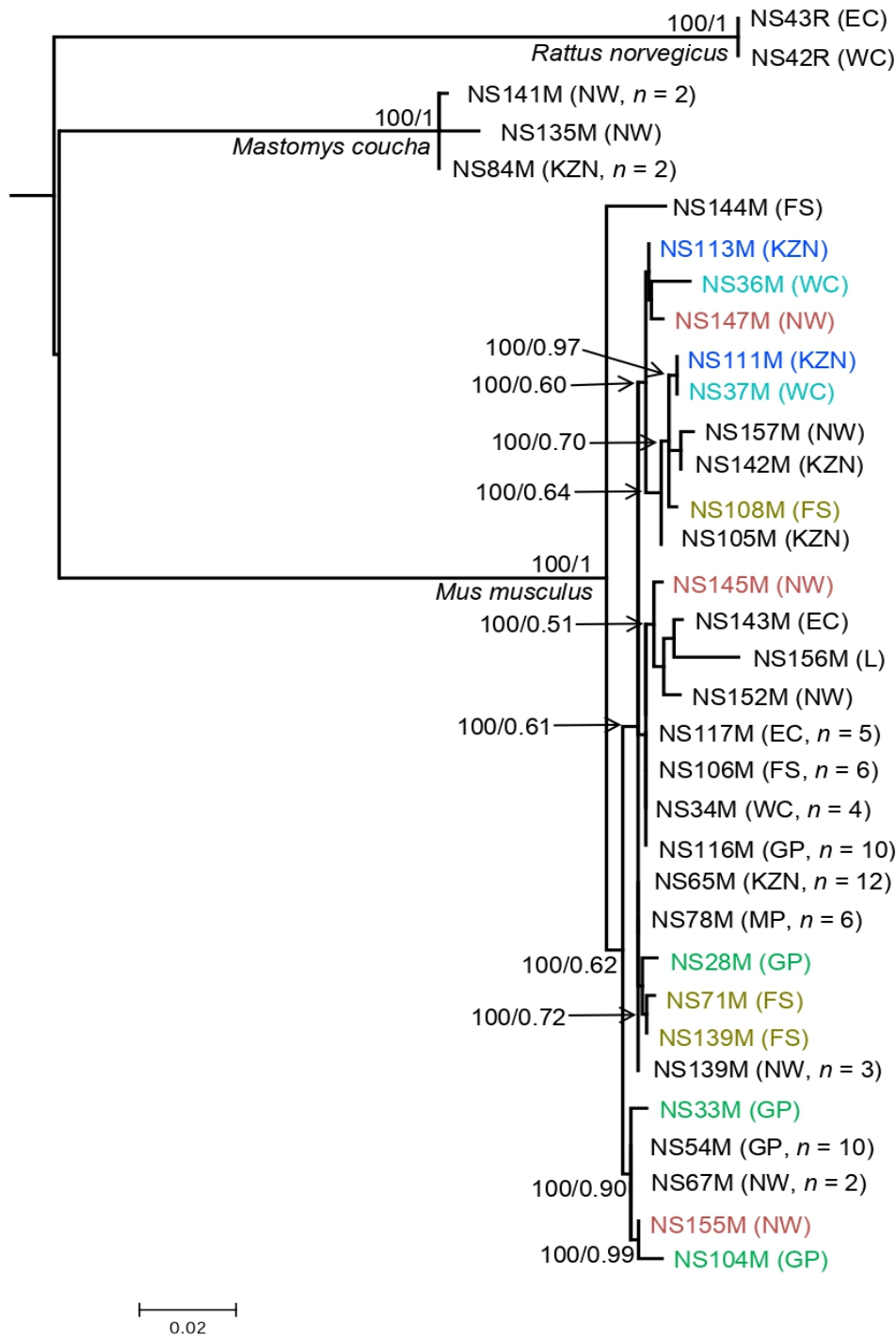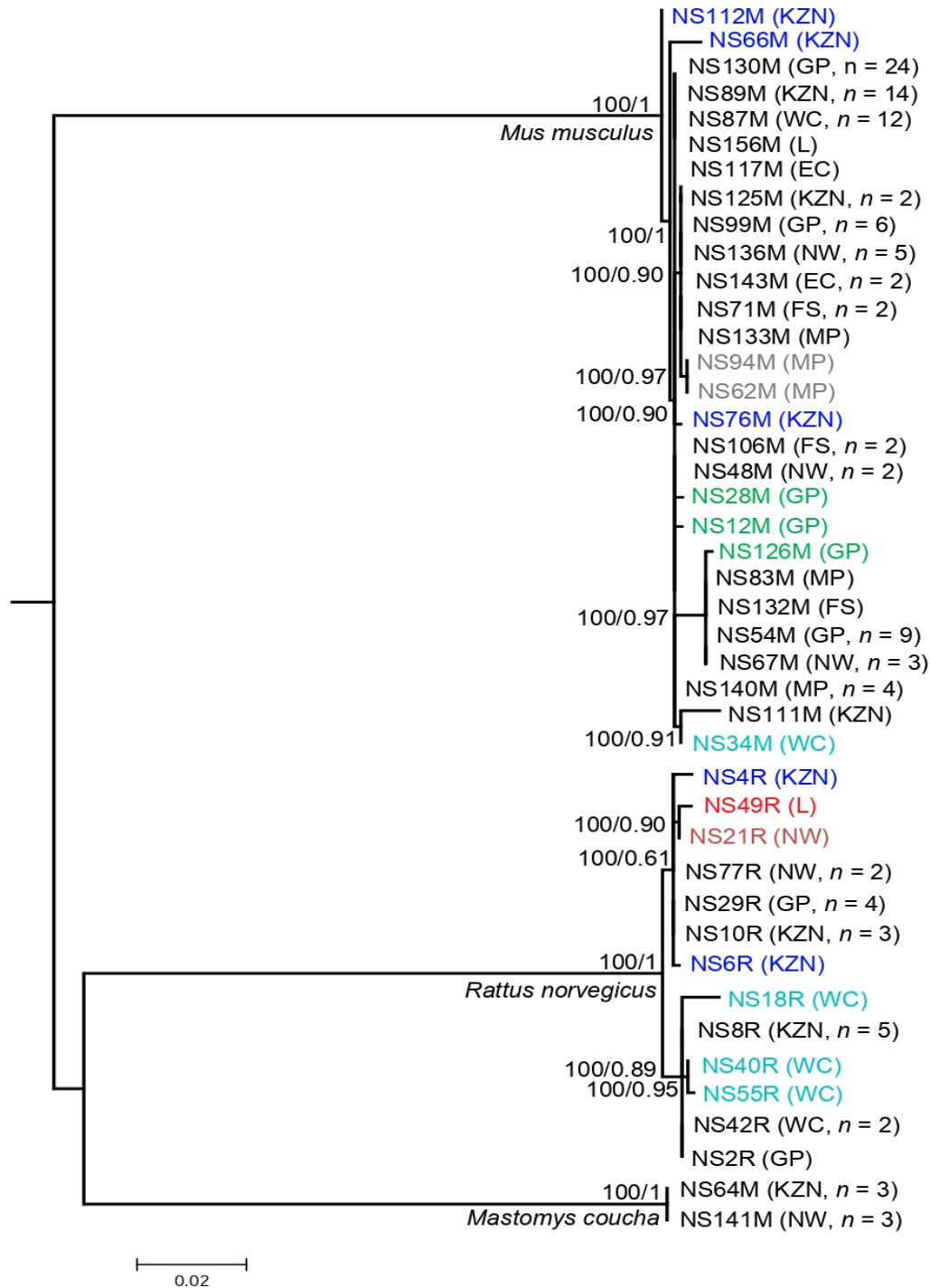**Supplementary material**

Supplementary Figure S1. Most likelihood tree based on the analysis of 16S ribosomal RNA (16S rRNA) including *Mus musculus*, *Rattus norvegicus*, and *Mastomys coucha* collected from South African pet shops. Nodal support values represent maximum likelihood bootstrap (>50%) and Bayesian posterior probability (>0.6) support. The number of identical sequences is shown in parentheses, and the colour coded taxa show unique individuals. The provinces where samples were collected are abbreviated as follows: EC-Eastern Cape, FS-Free State, GP-Gauteng Province, KZN-KwaZulu-Natal, L-Limpopo, MP-Mpumalanga, NW-North West, and WC-Western Cape.
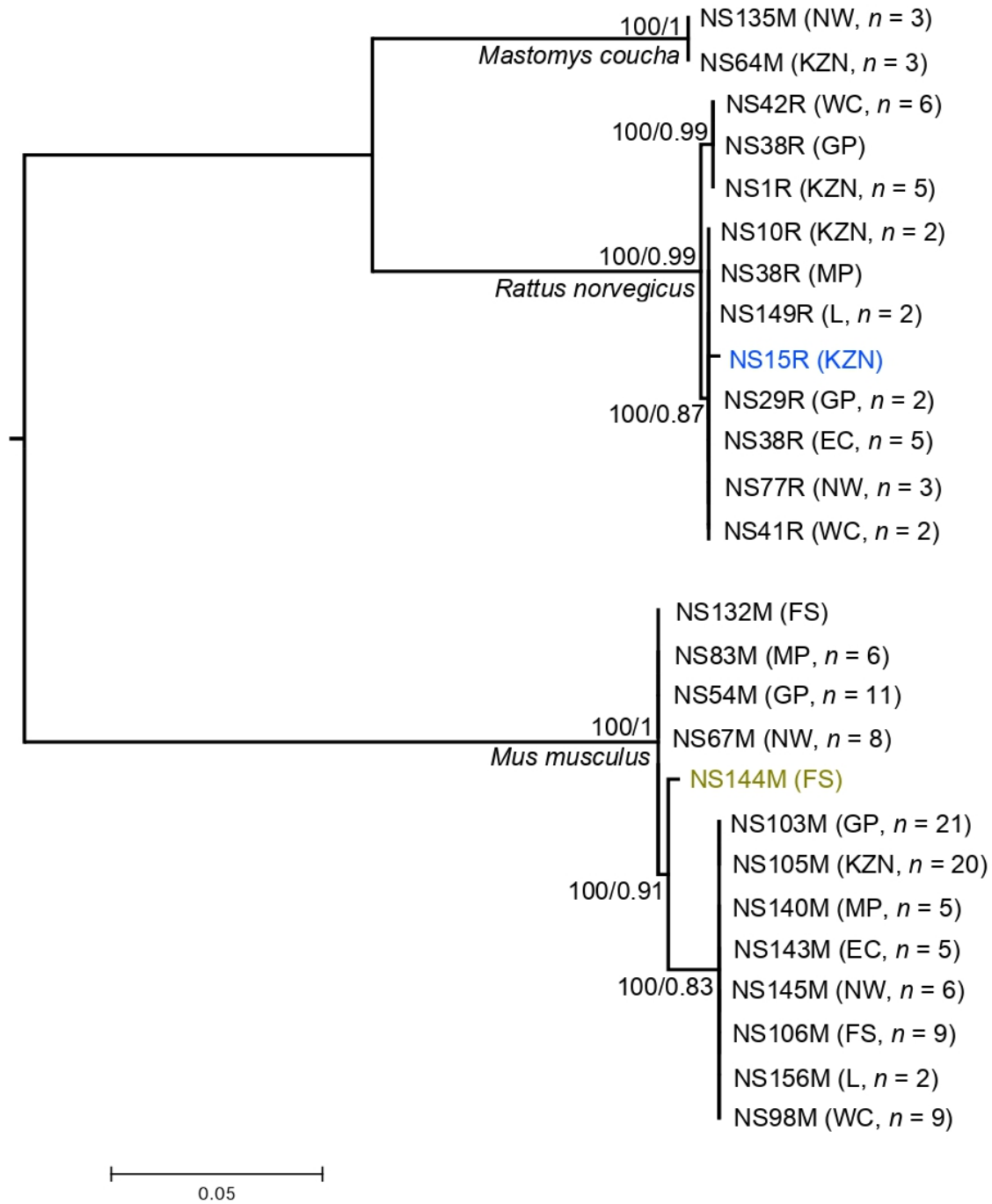
Supplementary Figure S2. Most likelihood tree based on the analysis of *Mus musculus*, *Rattus norvegicus*, and *Mastomys coucha* based on mtDNA cytochrome oxidase subunit 1 (CO1) gene region. The individuals were collected from South African pet shops. Nodal support values represent maximum likelihood bootstrap (>50%) and Bayesian posterior probability (>0.6) support. The number of identical sequences is shown in parentheses, and the colour coded taxa

show unique individuals. The provinces where samples were collected are abbreviated as follows: EC-Eastern Cape, FS-Free State, GP-Gauteng Province, KZN-KwaZulu-Natal, L-Limpopo, MP-Mpumalanga, NW-North West, and WC-Western Cape.

Supplementary Figure S3. Most likelihood tree based on the analysis of *Mus musculus, Rattus norvegicus,* and *Mastomys coucha* based on mtDNA cytochrome b (Cyt b) gene region. The individuals were collected from South African pet shops. Nodal support values represent maximum likelihood bootstrap (>50%) and Bayesian posterior probability (>0.6) support. The number of identical sequences is shown in parentheses, and the colour coded taxa show unique individuals. The provinces where samples were collected are abbreviated as follows: EC-Eastern Cape, FS-Free State, GP-Gauteng Province, KZN-KwaZulu-Natal, L-Limpopo, MP-Mpumalanga, NW-North West, and WC-Western Cape.

Supplementary Figure S4. Most likelihood tree based on the analysis of *Mus musculus*, *Rattus norvegicus*, and *Mastomys coucha* based on mtDNA hypervariable control region (CR) gene region. The individuals were collected from South African pet shops. Nodal support values represent maximum likelihood bootstrap (>50%) and Bayesian posterior probability (>0.6) support. The number of identical sequences is shown in parentheses, and the colour coded taxa show unique haplotypes. The provinces where samples were collected are abbreviated as follows: EC-Eastern Cape, FS-Free State, GP-Gauteng Province, KZN-KwaZulu-Natal, L-Limpopo, MP-Mpumalanga, NW-North West, and WC-Western Cape.
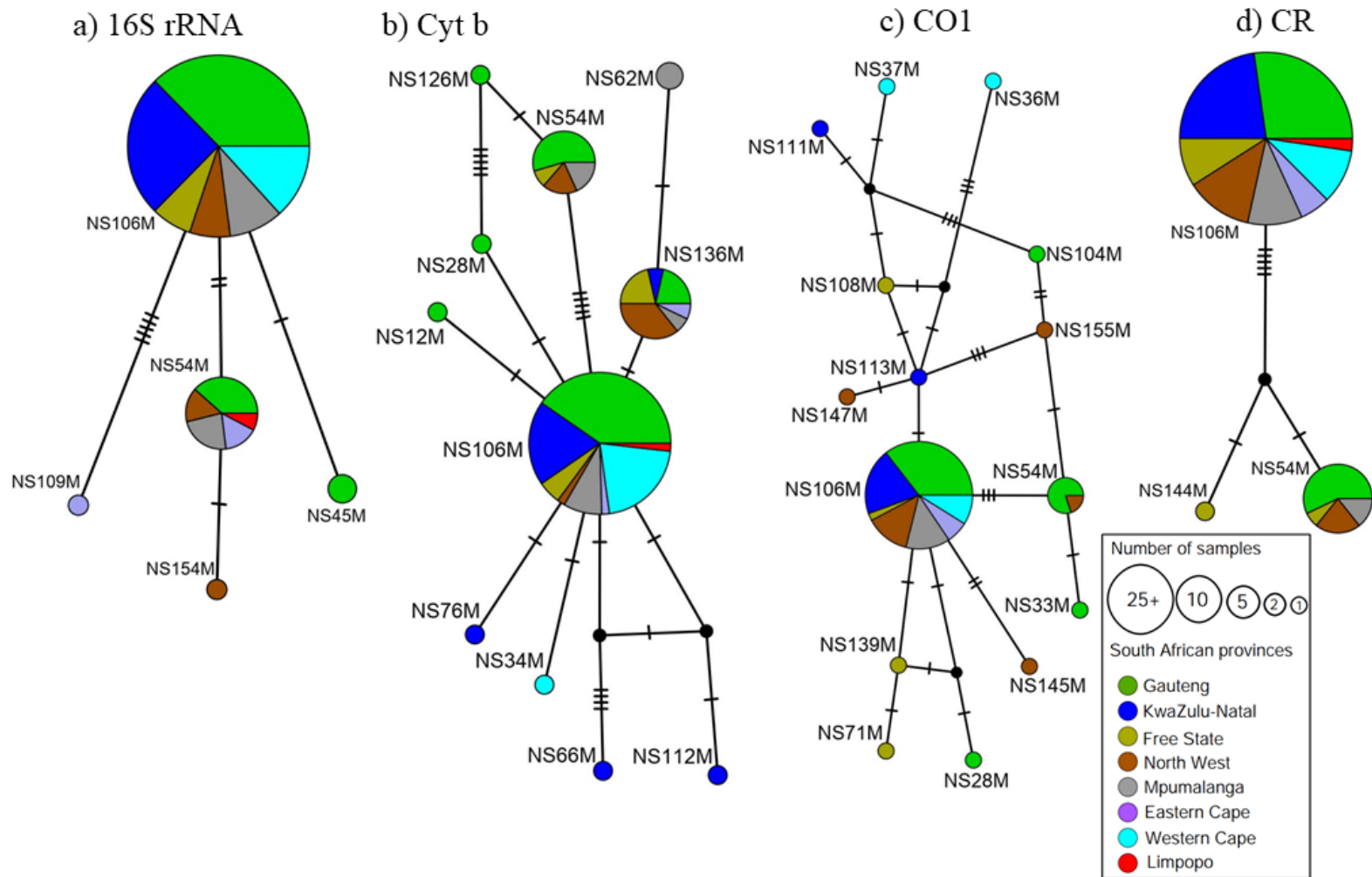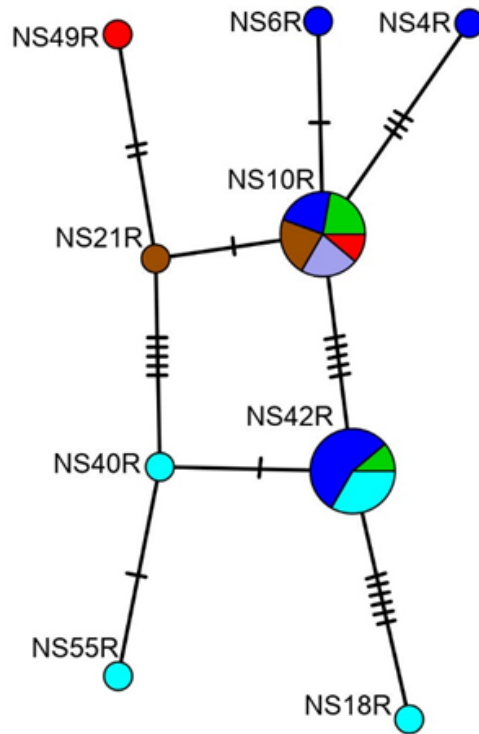
Supplementary Figure S5. Median-joining haplotype network constructed using data from four mtDNA gene regions (16S rRNA, Cyt b, CO1 and CR) based on sequences of *Mus musculus* sold in South African pet shops.
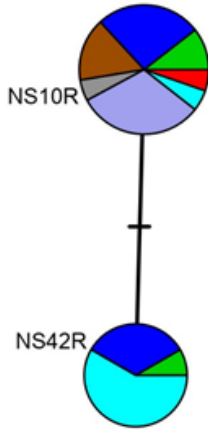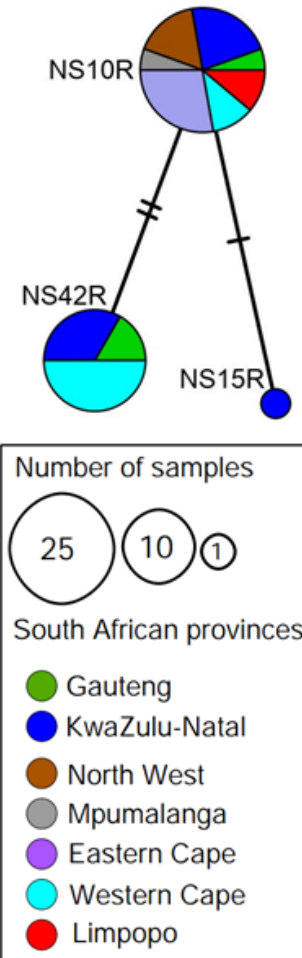
Supplementary Figure S6. Median-joining haplotype network constructed using data from four mtDNA gene regions (16S rRNA, Cyt b and CR) based on sequences of *Rattus norvegicus* sold in South African pet shops.