

Supplementary material;

First identification of mammalian orthoreovirus type 3 by gut virome analysis in diarrheic child in Brazil

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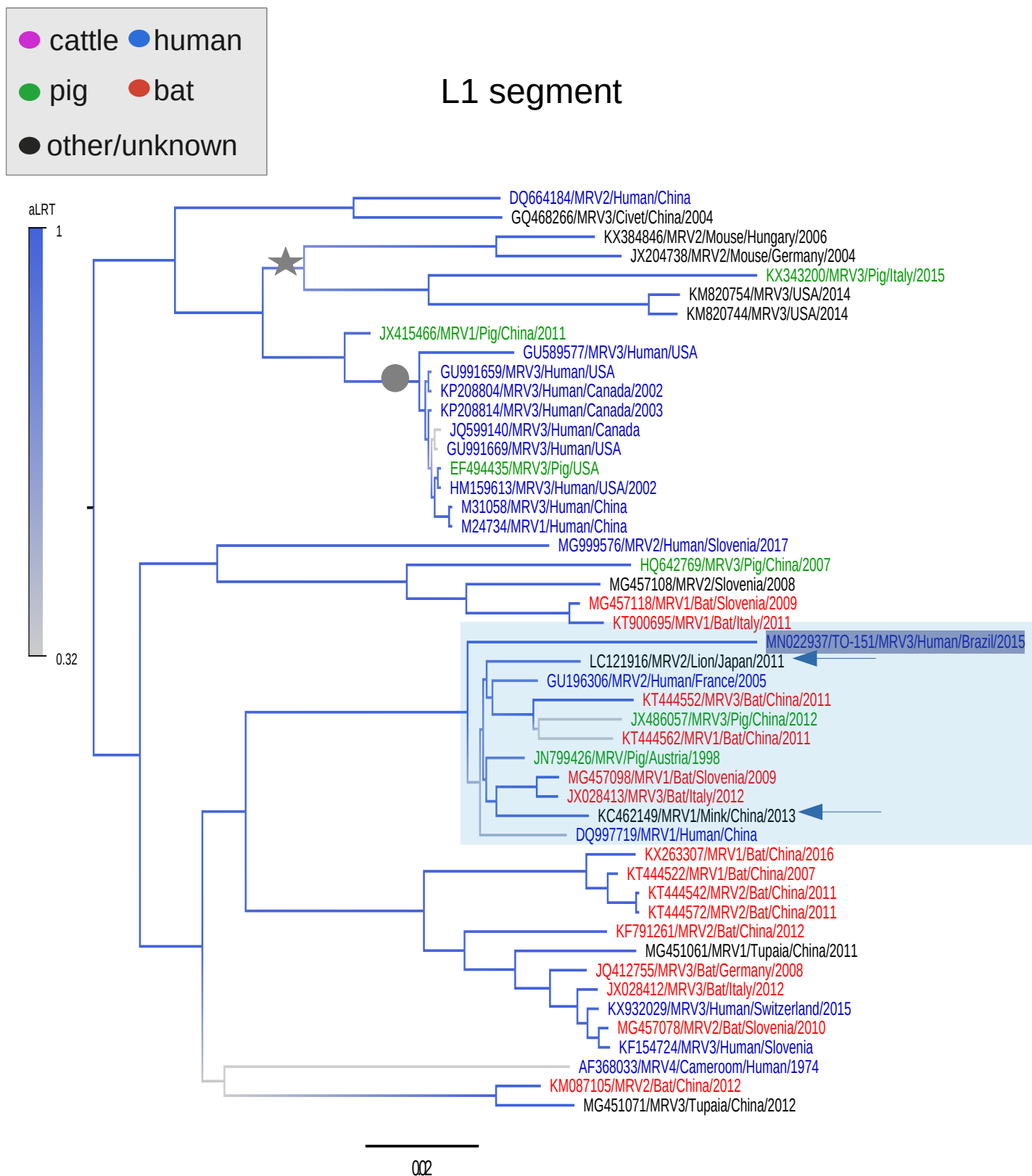


Figure S1. Phylogenetic tree inferred using the L1 segment of MRV3. Phylogenetic tree of the complete L1 segment (3639 bp) of the Brazilian TO-151/BR MRV3 strain (highlighted in the tree). The tree was performed using the maximum likelihood method GTR-G model within the jModeltest software with a bootstrap of 1000 replicates. Accession number, species, isolate, country and year are indicated for each strain. Different hosts are highlighted in different colors.

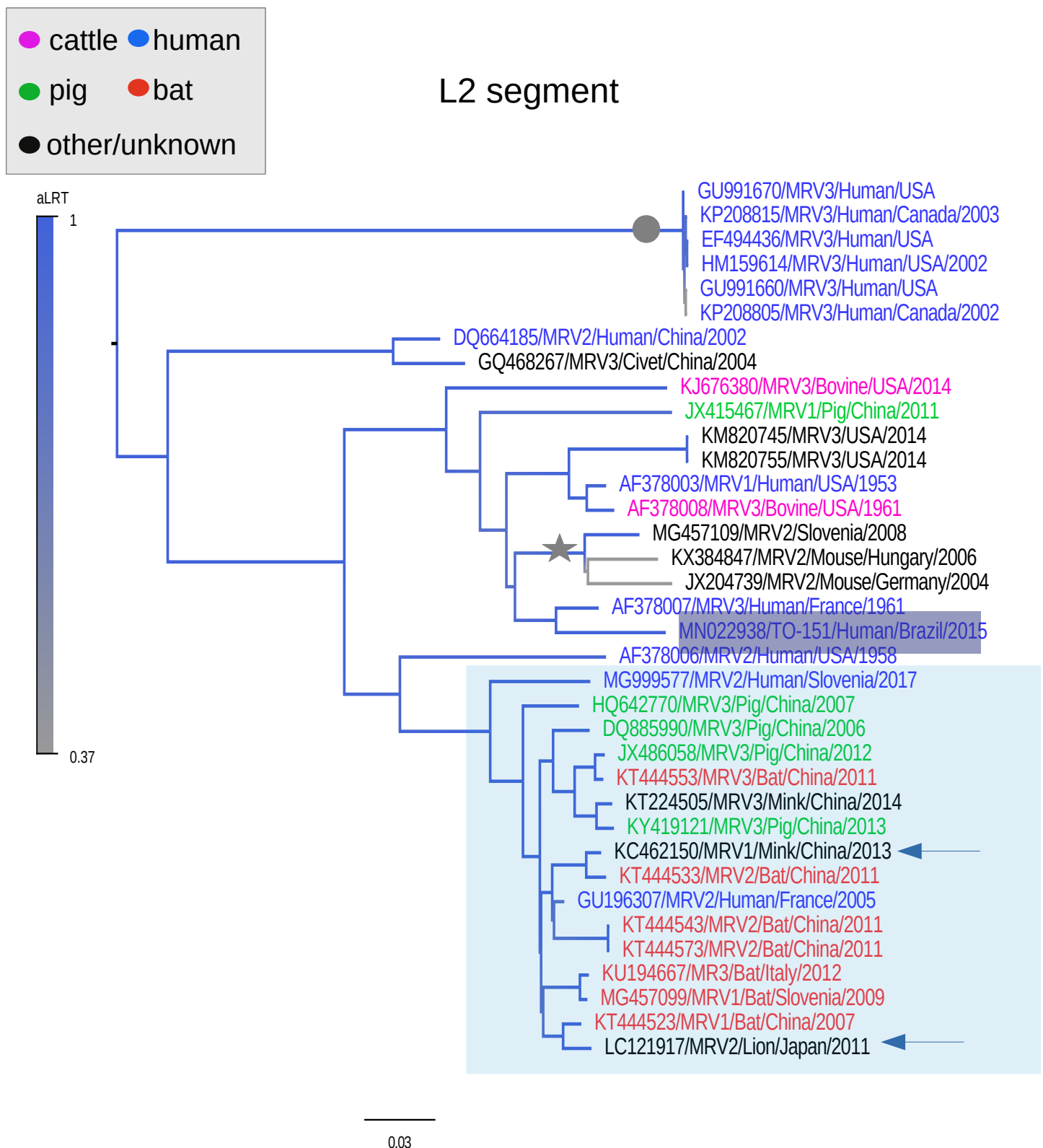
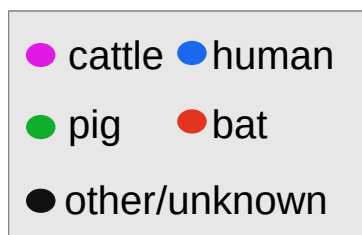


Figure S2. Phylogenetic tree inferred using the L2 segment of MRV3.

Phylogenetic tree of the complete L2 segment (3207 bp) of the Brazilian TO-151/BR MRV3 strain (highlighted in the tree). The tree was performed using the maximum likelihood method GTR-G model within the jModeltest software with a bootstrap of 1000 replicates. Accession number, species, isolate, country and year are indicated for each strain. Different hosts are highlighted in different colors.



L3 segment

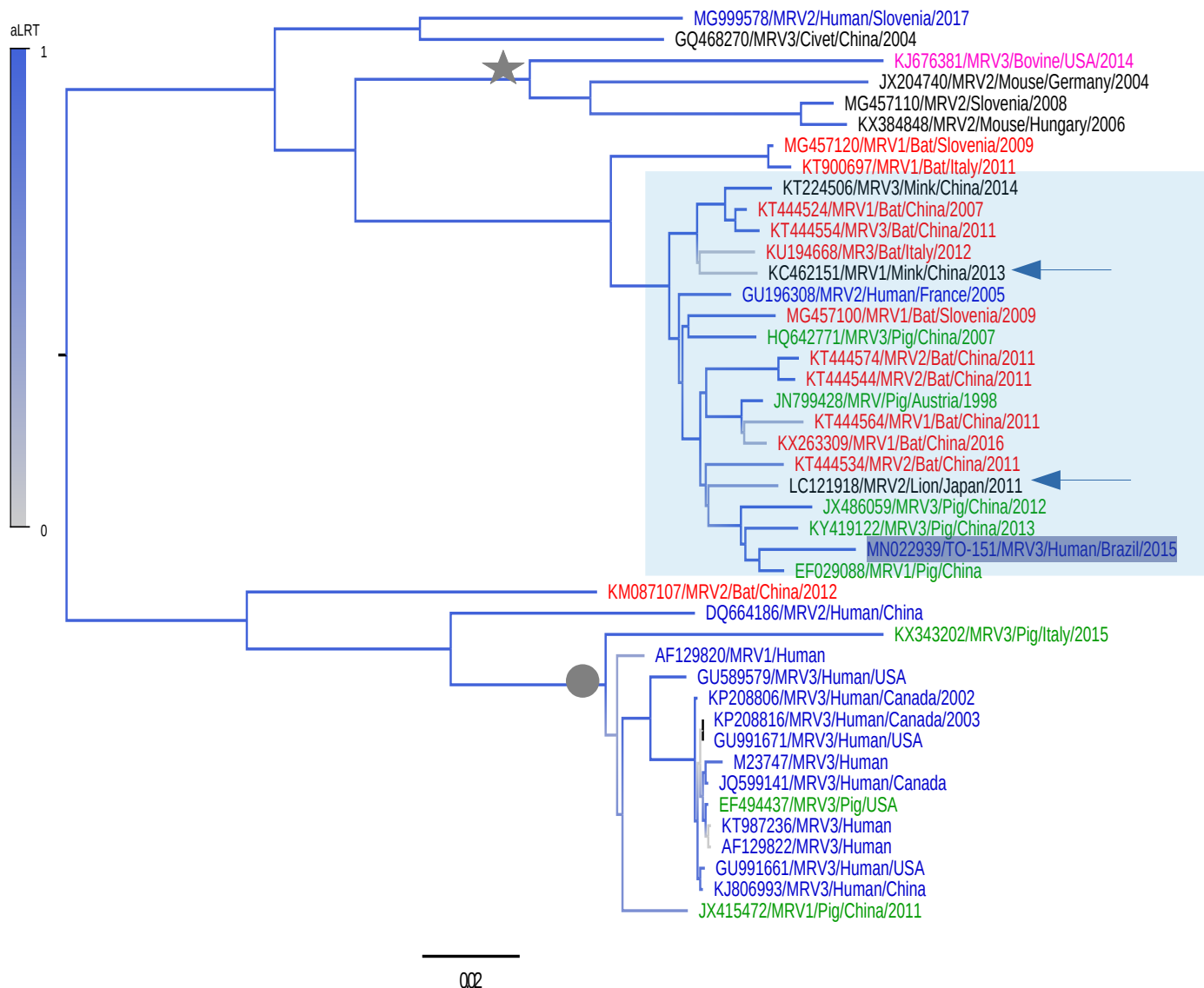


Figure S3. Phylogenetic tree inferred using the L3 segment of MRV3.

Phylogenetic tree of the complete L3 segment (3184 bp) of the Brazilian TO-151/BR MRV3 strain (highlighted in the tree). The tree was performed using the maximum likelihood method GTR-G model within the jModeltest software with a bootstrap of 1000 replicates. Accession number, species, isolate, country and year are indicated for each strain. Different hosts are highlighted in different colors.

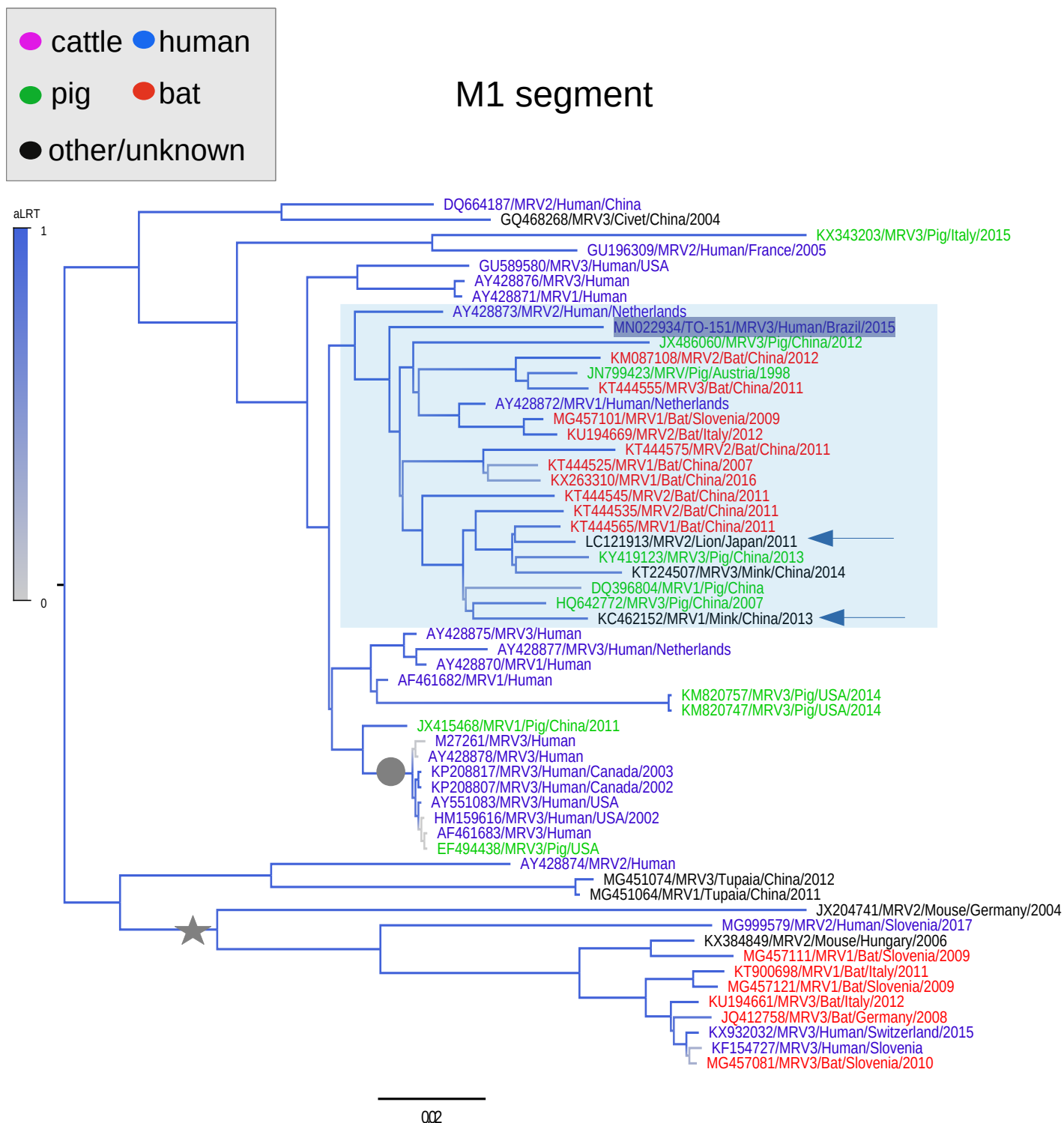


Figure S4. Phylogenetic tree inferred using the M1 segment of MRV3.

Phylogenetic tree of the complete M1 segment (2253 bp) of the Brazilian TO-151/BR MRV3 strain (highlighted in the tree). The tree was performed using the maximum likelihood method GTR-G model within the jModeltest software with a bootstrap of 1000 replicates. Accession number, species, isolate, country and year are indicated for each strain. Different hosts are highlighted in different colors.

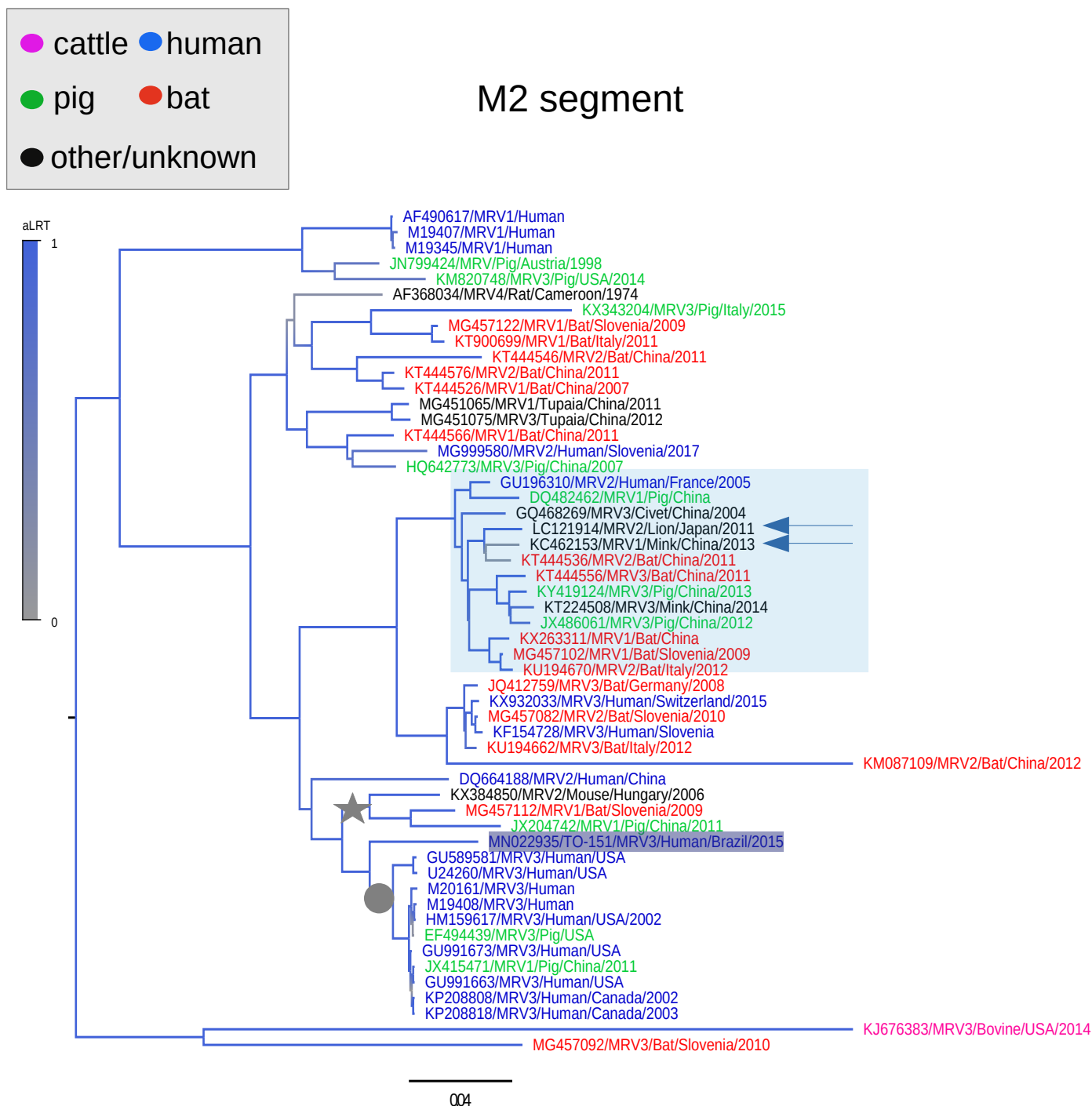
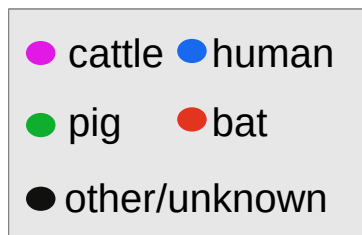


Figure S5. Phylogenetic tree inferred using the M2 segment of MRV3.

Phylogenetic tree of the complete M2 segment (2154 bp) of the Brazilian TO-151/BR MRV3 strain (highlighted in the tree). The tree was performed using the maximum likelihood method GTR-G model within the jModeltest software with a bootstrap of 1000 replicates. Accession number, species, isolate, country and year are indicated for each strain. Different hosts are highlighted in different colors.



M3 segment

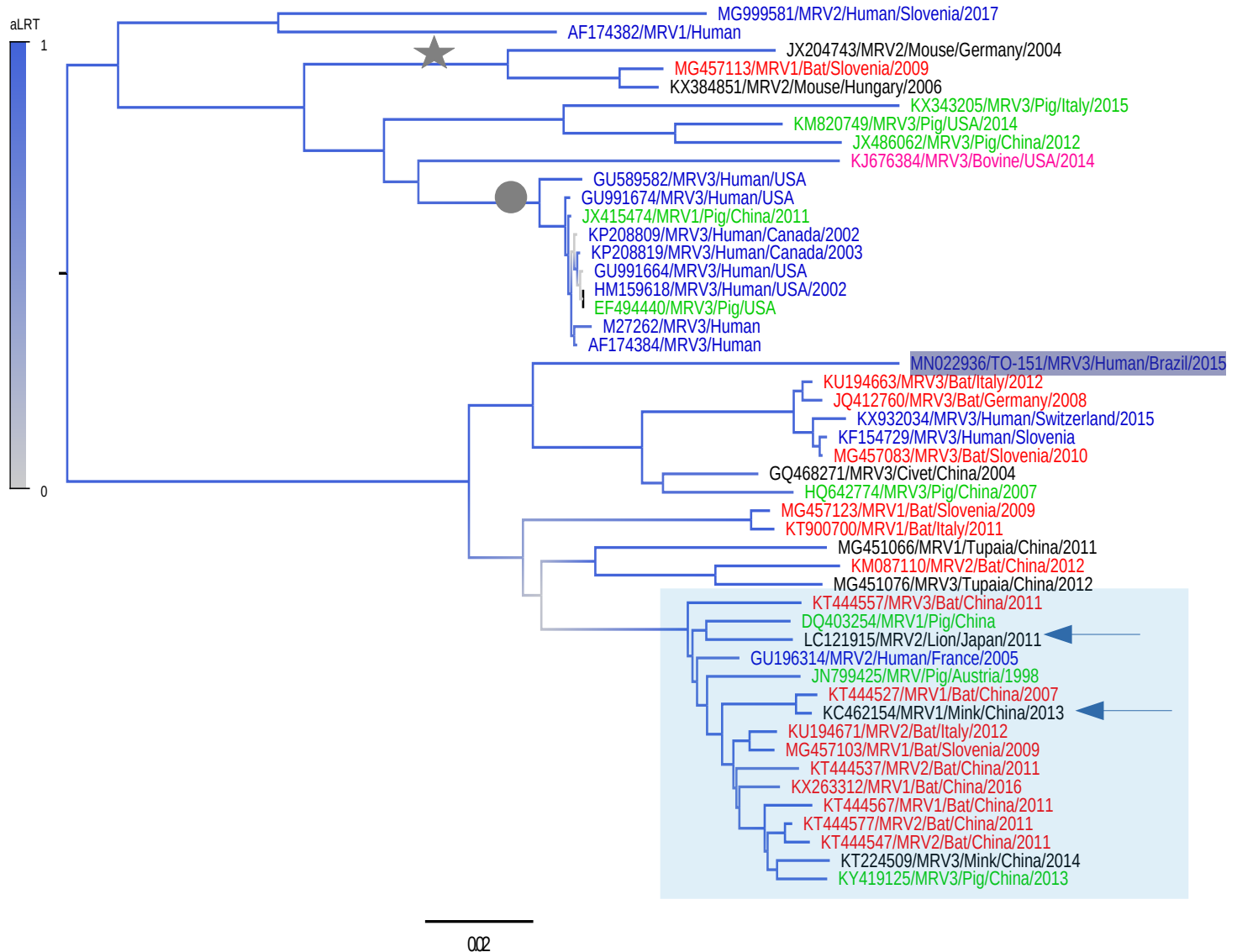
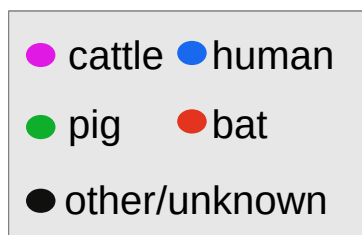


Figure S6. Phylogenetic tree inferred using the M3 segment of MRV3.

Phylogenetic tree of the complete M3 segment (2336 bp) of the Brazilian TO-151/BR MRV3 strain (highlighted in the tree). The tree was performed using the maximum likelihood method GTR-G model within the jModeltest software with a bootstrap of 1000 replicates. Accession number, species, isolate, country and year are indicated for each strain. Different hosts are highlighted in different colors.



S2 segment

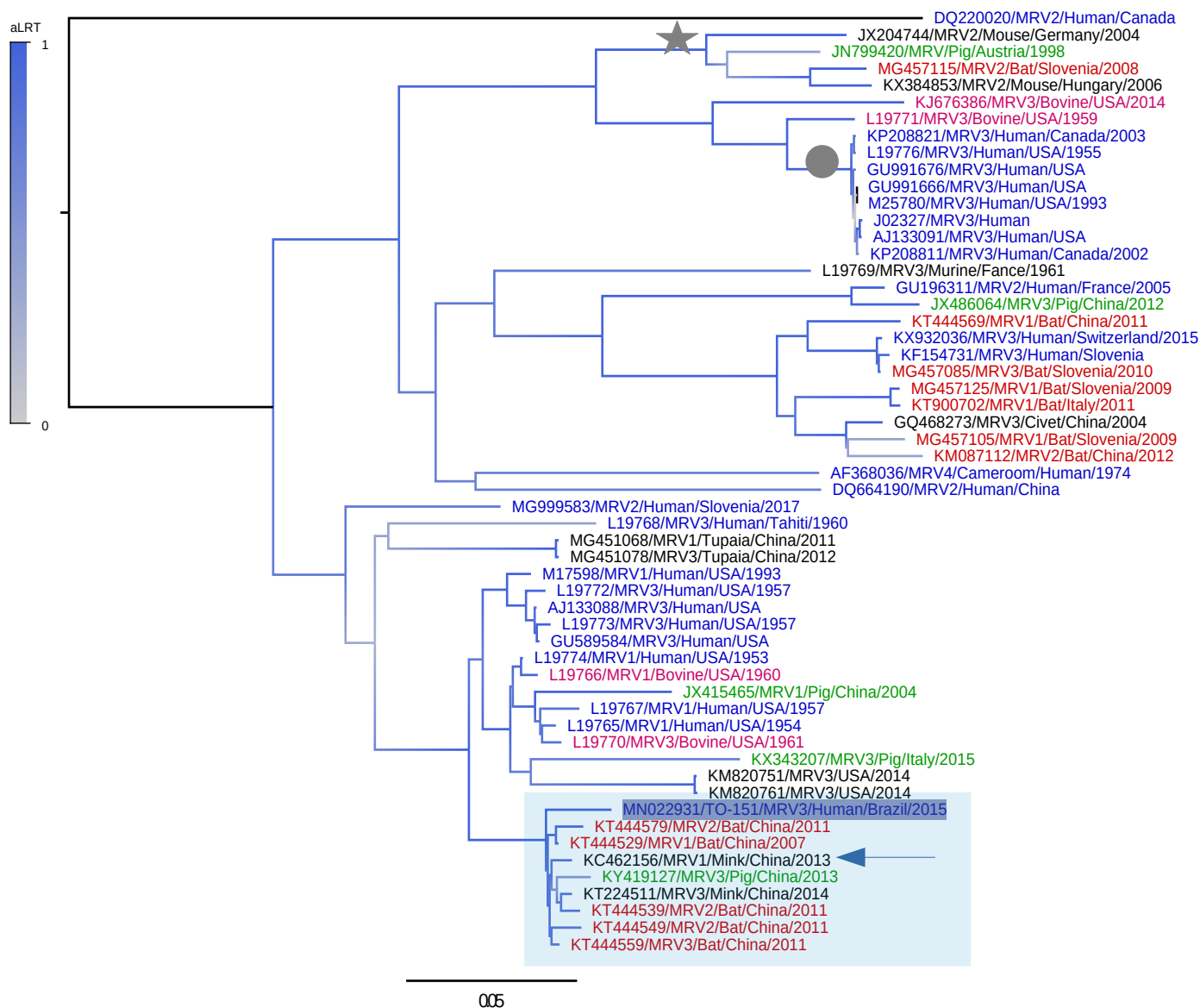
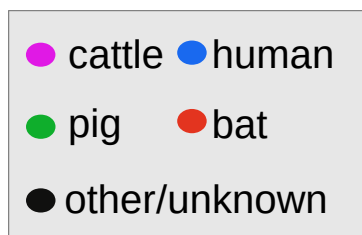


Figure S7. Phylogenetic tree inferred using the S2 segment of MRV3.

Phylogenetic tree of the complete S2 segment (1320 bp) of the Brazilian TO-151/BR MRV3 strain (highlighted in the tree). The tree was performed using the maximum likelihood method GTR-G model within the jModeltest software with a bootstrap of 1000 replicates. Accession number, species, isolate, country and year are indicated for each strain. Different hosts are highlighted in different colors.



S3 segment

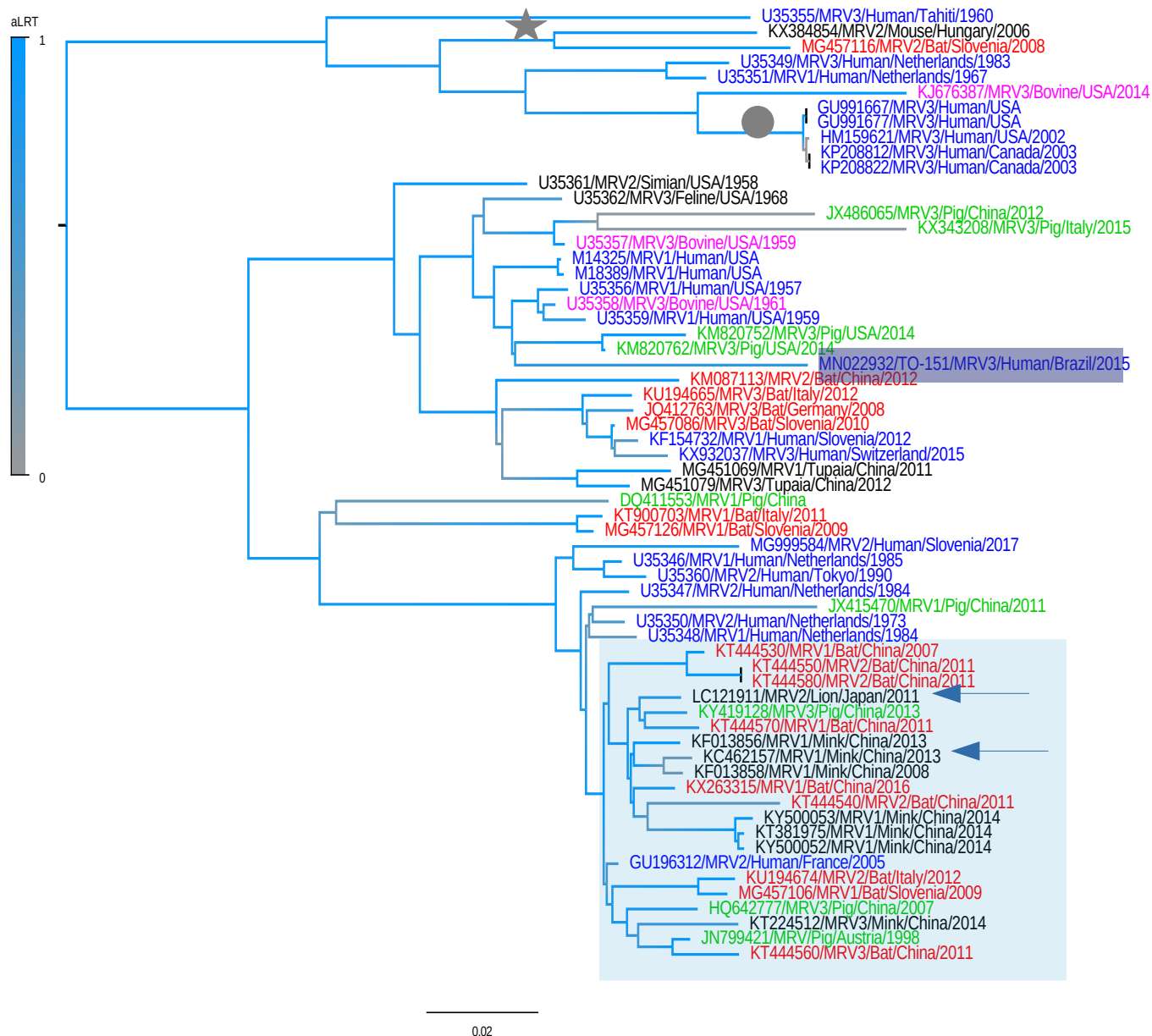
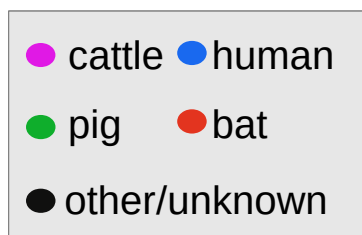


Figure S8. Phylogenetic tree inferred using the S3 segment of MRV3.

Phylogenetic tree of the complete S3 segment (925 bp) of the Brazilian TO-151/BR MRV3 strain (highlighted in the tree). The tree was performed using the maximum likelihood method GTR-G model within the jModeltest software with a bootstrap of 1000 replicates. Accession number, species, isolate, country and year are indicated for each strain. Different hosts are highlighted in different colors.



S4 segment

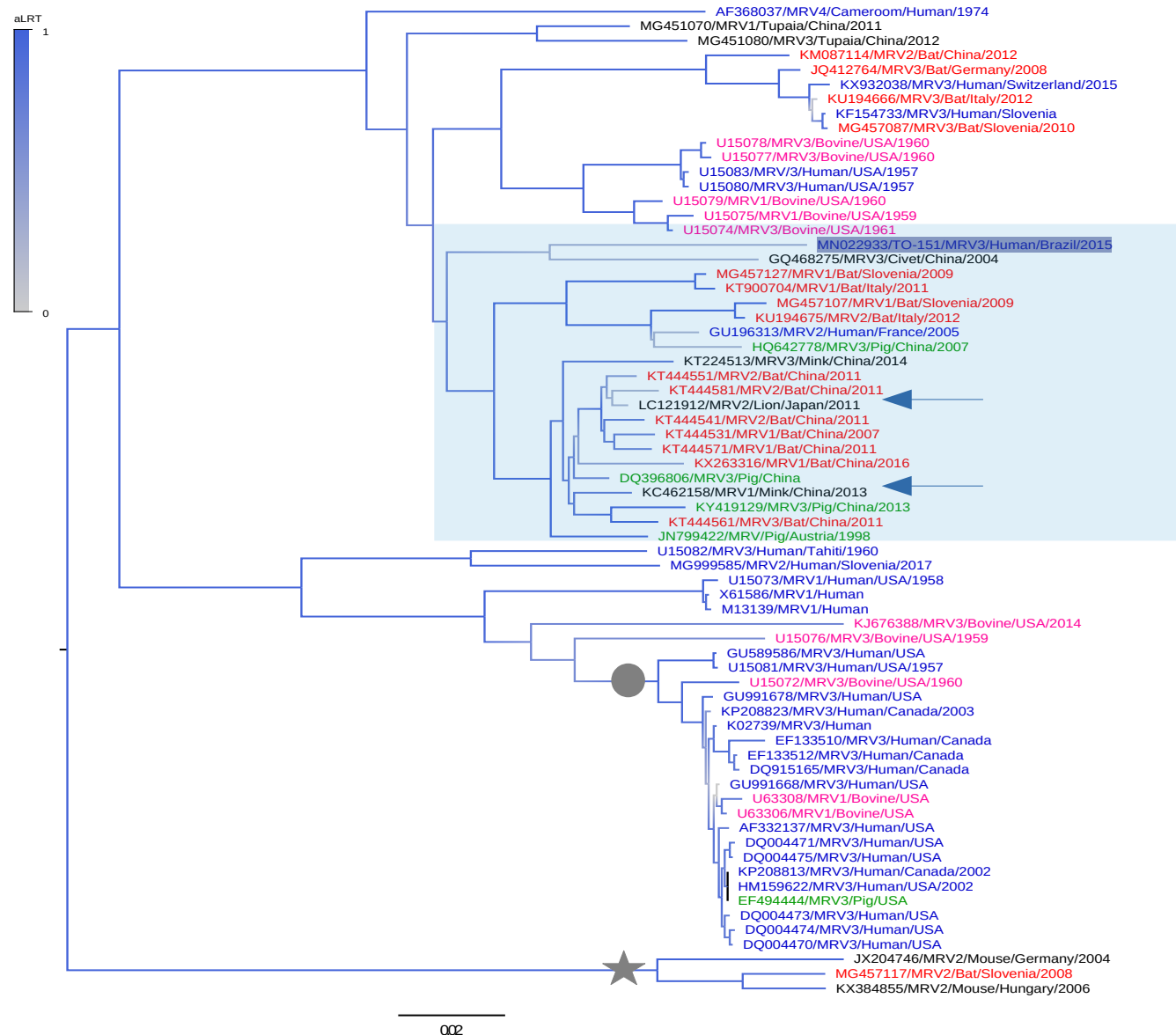


Figure S9. Phylogenetic tree inferred using the S4 segment of MRV3.

Phylogenetic tree of the complete S4 segment (1104 bp) of the Brazilian TO-151/BR MRV3 strain (highlighted in the tree). The tree was performed using the maximum likelihood method GTR-G model within the jModeltest software with a bootstrap of 1000 replicates. Accession number, species, isolate, country and year are indicated for each strain. Different hosts are highlighted in different colors.

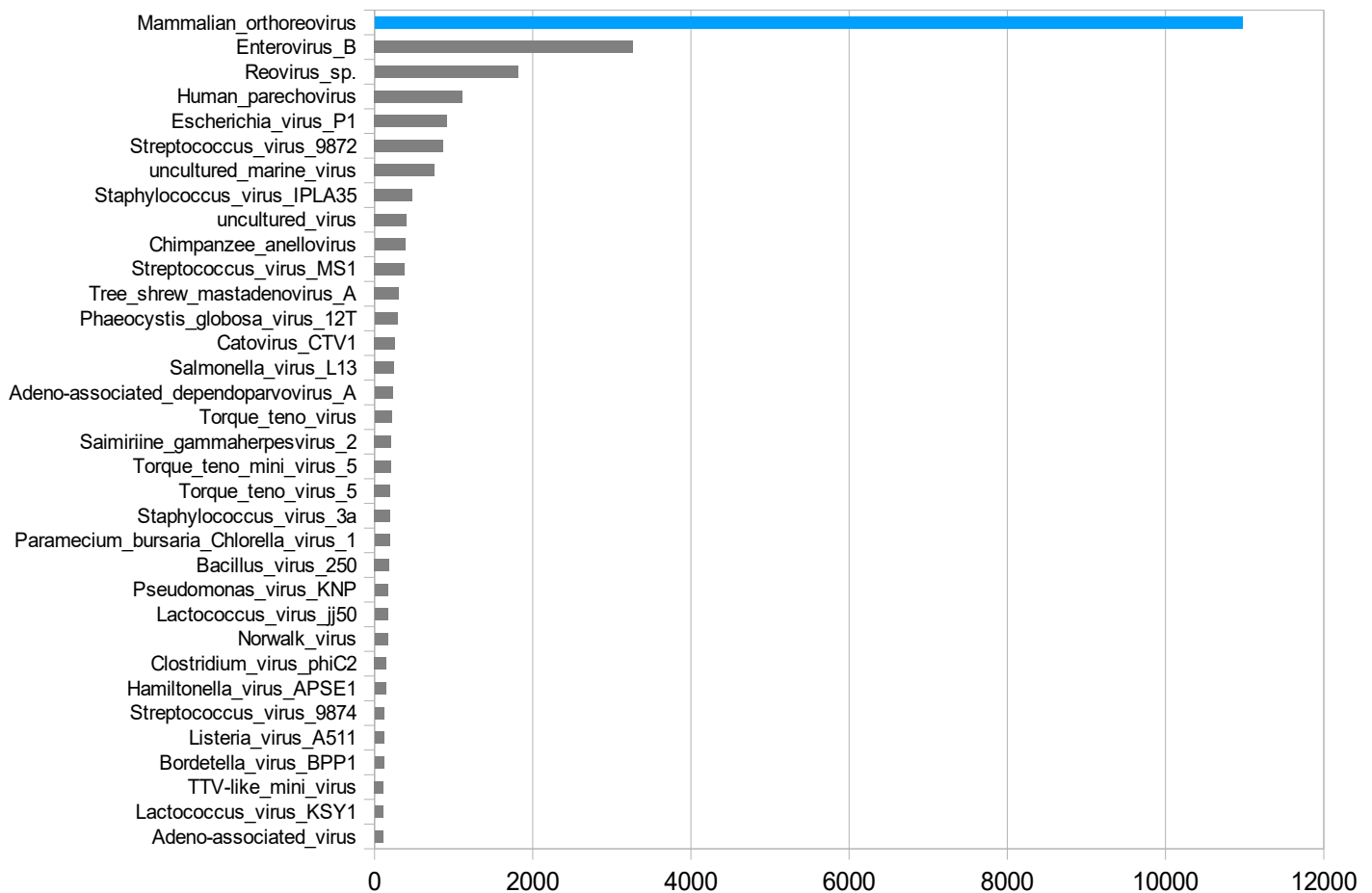


Figure S10. Virome of patient TO-151/BR. In the y-axis horizontal bars indicate all viruses detected in the patient TO-151/BR. In the x-axis the number of contigs of each virus found in the library is shown. The blue bar indicate the number of contigs of the MRV-3 detected in this library. Data were generated by the next generation sequencing of fecal sample (see the main text for details).

Accession number/Isolate Name/Host/Country/Isolation Year:

AY302467/T3/Human/Colorado/1996
AF368035/Ndelle/Murine/Cameroon/1974
JQ412761/T3/Bat/Germany/2008
KX343206/Pig/Italy/2015
JQ979272/Bat/Italy/2012
KX932035/Human/Switzerland
MG457084/Bat/Slovenia
KF154730/Human/Slovenia
JQ979276/Bat/Italy/2011
JQ979275/Bat/Italy/2011
L37676/France
JQ979271/T3/Bat/Italy/2011
JQ979273/Bat/Italy/2012
JQ979277/Bat/Italy/2011
JQ979283/Bat/Italy/2011
L37683/Human
L37684/Human
KKM820760/Pig/USA/2014
KM820750/Pig/USA/2014
L37679/MRV-3/Tahiti
AY860061/Canada
U53413/Cattle
X01161/MRV3
M10262/MRV3
JQ599138/Canada
EF133509/Canada
EF133511/Human/Canada
U53410/Cattle
U53409/Cattle
EF494441/MRV3
U53412/Cattle
U53411/Cattle
KP208810/Canada
GU991675/Human
KJ806994/Human
GU991665/MRV3
L37678/USA
U74291/Cattle
L37675/USA
GU589583/Human
L37680/Human
L37682/Human
U74293/Cattle
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U74292/Cattle
KY419126/Pig/China/2013
MN022930/TO-151/Human/Brazil/2015
DQ911244/Pig/China
JF829221/Pig/SouthKorea/2005
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JX486063/Pig/China/2003
KT444558/Bat/China/2011
GQ468272/Civet/China/2004
HQ642775/Pig/China/2007
MG451077/MRV-3/Treeshrew/China/2012
KP185124/Tupaia/China/2013