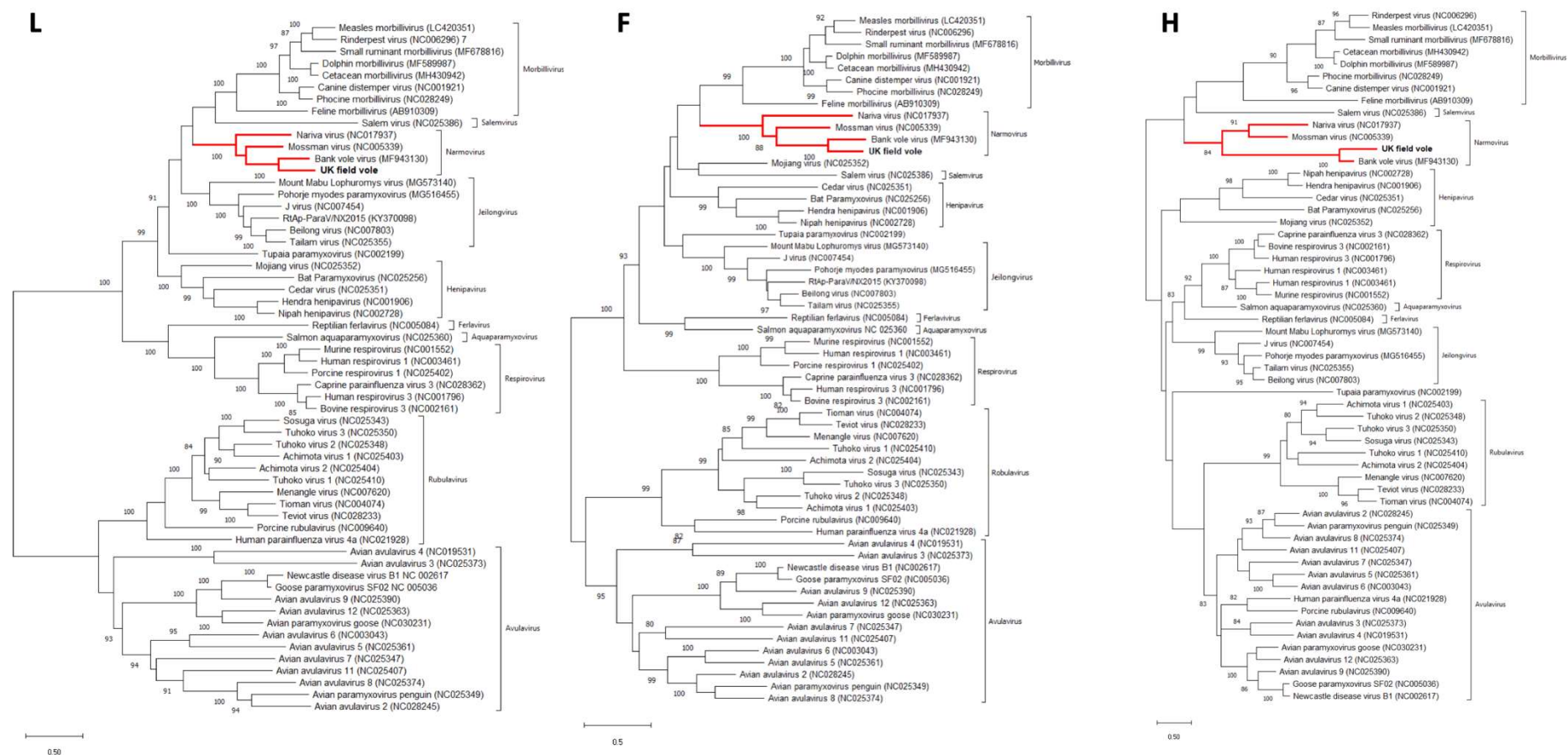
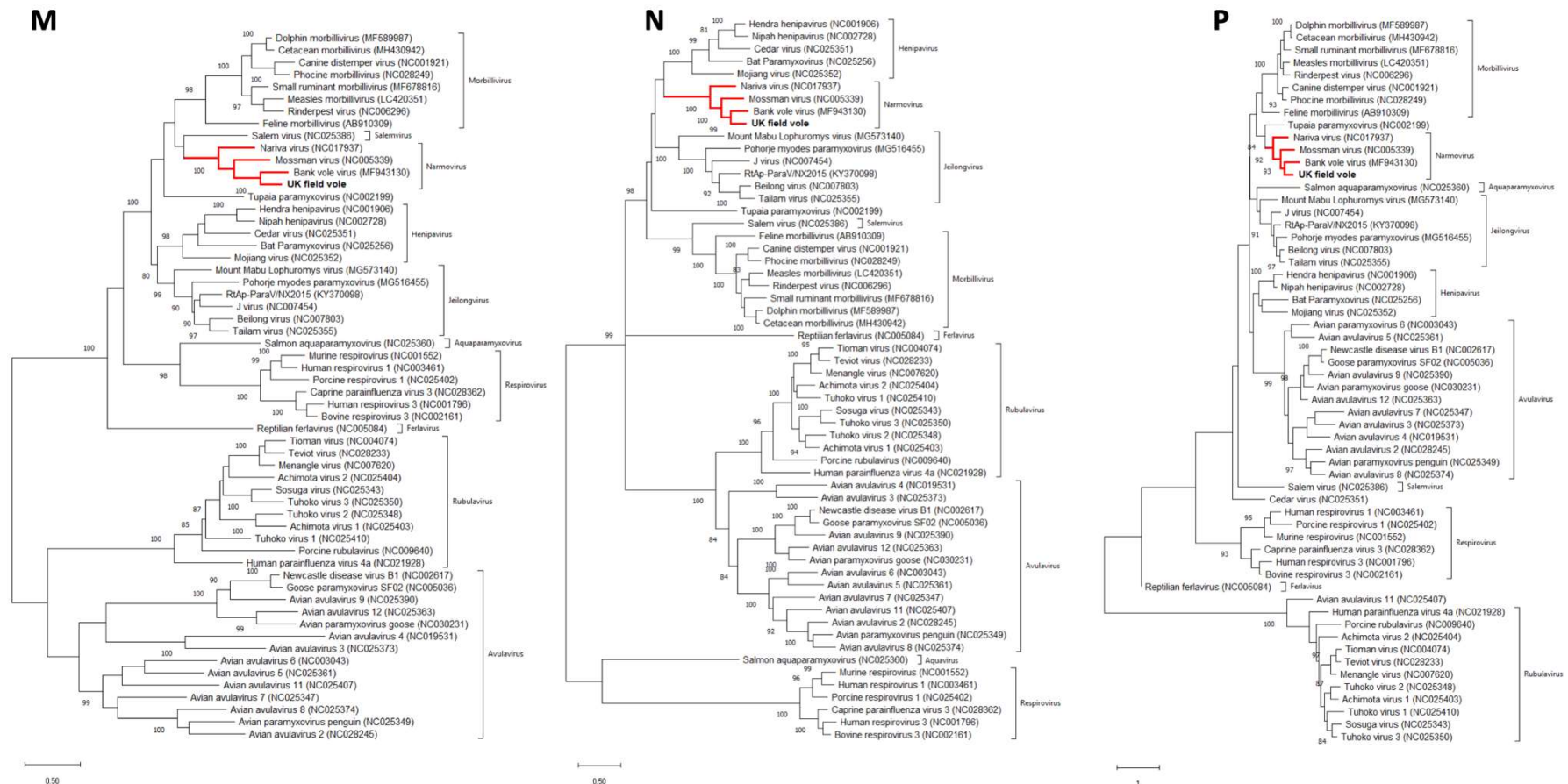
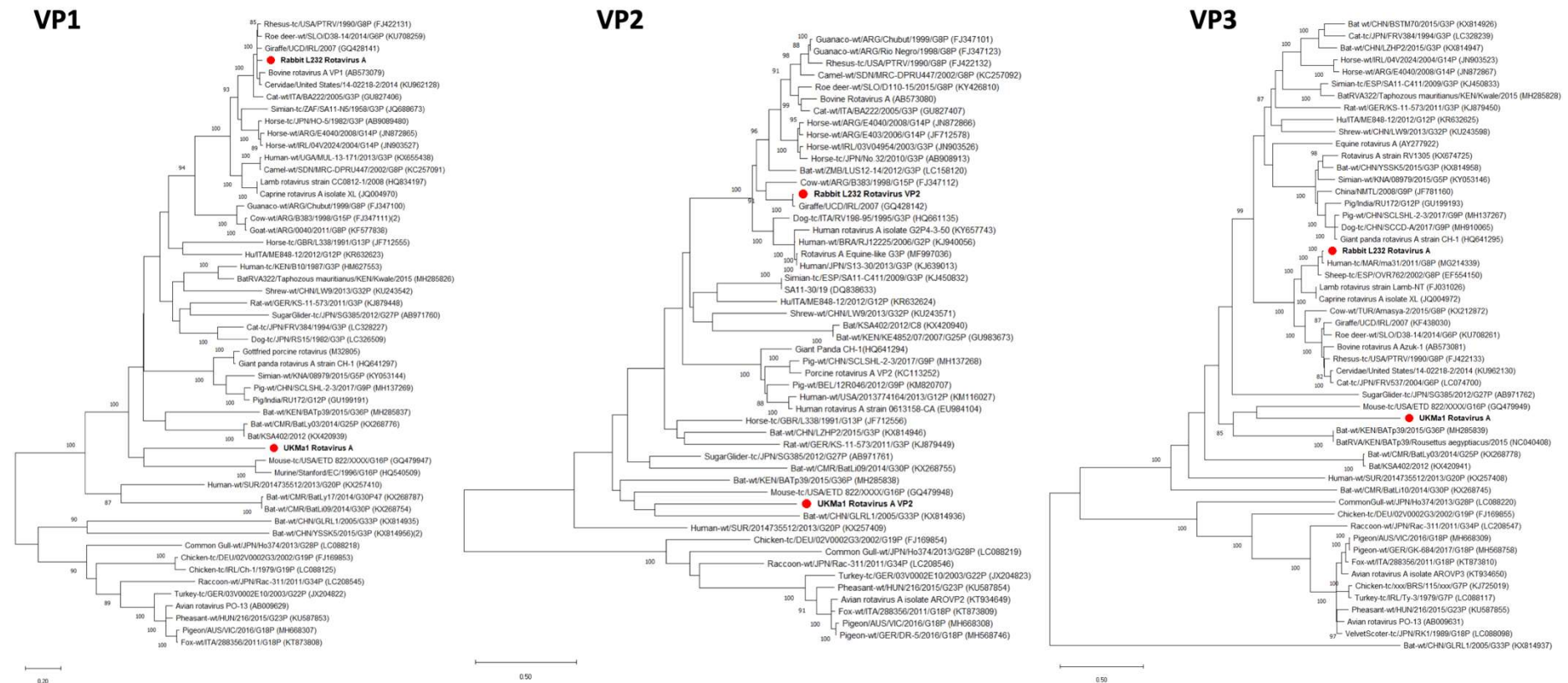




Supplementary Figure 1. Phylogenetic relationships of the field vole paramyxovirus based on the *L*, *F* and *H* genes. Maximum likelihood phylogenetic analysis of paramyxovirus partial *L* (2,730 nt), *F* (726 nt) and *H* (615 nt) gene sequences, revealing that the rodent narmoviruses formed a single clade within the *Paramyxoviridae*. The novel sequence obtained from the UK field vole UKMa K4D was analyzed alongside reference sequences representing diverse paramyxoviruses. Reference sequences are indicated by their GenBank accession numbers. Branch lengths are drawn to a scale of nucleotide substitutions per site. Numbers above individual branches indicate bootstrap support (100 replicates); only values >80% are shown. Narmoviruses are highlighted in red.

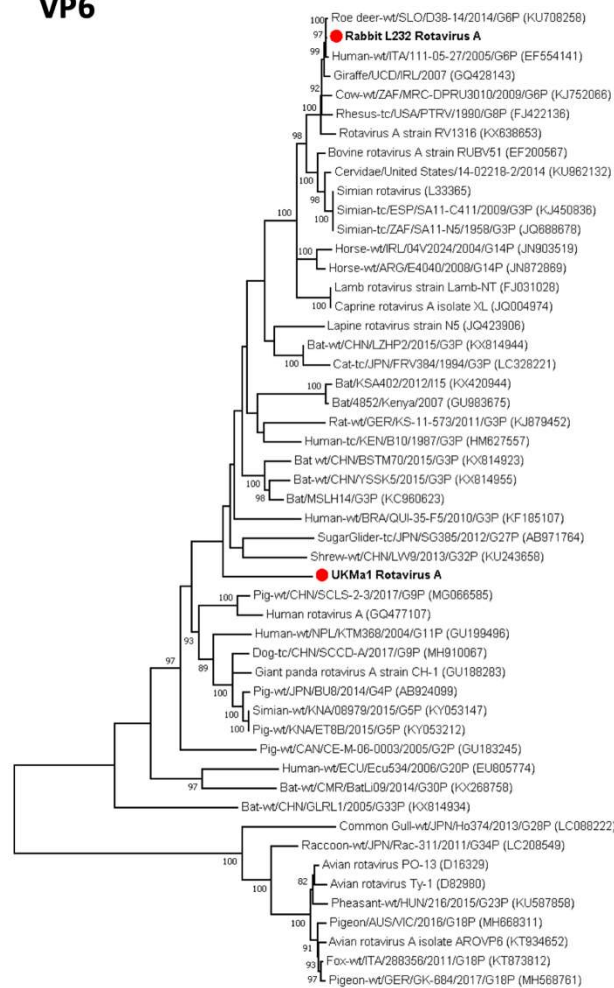


Supplementary Figure 2. Phylogenetic relationships of the field vole paramyxovirus based on the M, N and P genes. Maximum likelihood phylogenetic analysis of paramyxovirus partial M (760 nt), N (1,046 nt) and P (856 nt) gene sequences, revealing that the rodent narmoviruses formed a single clade within the *Paramyxoviridae*. The novel sequence obtained from the UK field vole UKMa K4D was analyzed alongside reference sequences representing all diverse paramyxoviruses. Reference sequences are indicated by their GenBank accession numbers. Branch lengths are drawn to a scale of nucleotide substitutions per site. Numbers above individual branches indicate bootstrap support (100 replicates); only values >80% are shown. Narmoviruses are highlighted in red.

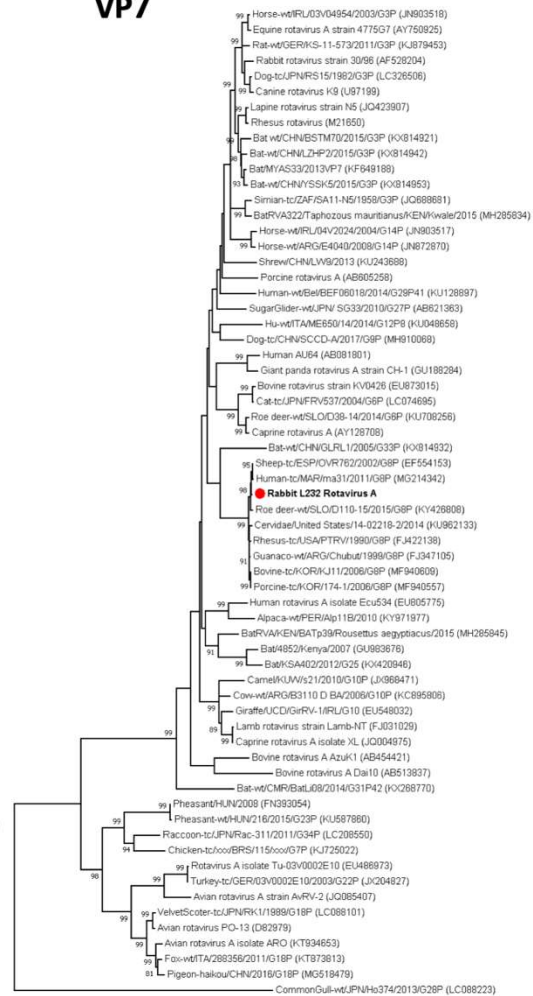


Supplementary Figure 3. Phylogenetic relationships of the field vole and the rabbit rotavirus A based on the VP1, VP2 and VP3 segments. Maximum likelihood phylogenetic analysis of rotavirus partial VP1 (1,944 nt), VP2 (987 nt) and VP3 (2,373 nt) segment sequences, revealing that the rabbit L232 rotavirus A clustered close to other species whereas the UKMa1 rotavirus A formed a distinct lineage. The novel sequences obtained from the UK field vole UKMa1 and the French rabbit L232 were analyzed alongside reference sequences representing rotaviruses A from different species. Reference sequences are indicated by their GenBank accession numbers. Branch lengths are drawn to a scale of nucleotide substitutions per site. Numbers above individual branches indicate bootstrap support (100 replicates); only values >80% are shown. The novel rotaviruses A are marked with a red dot.

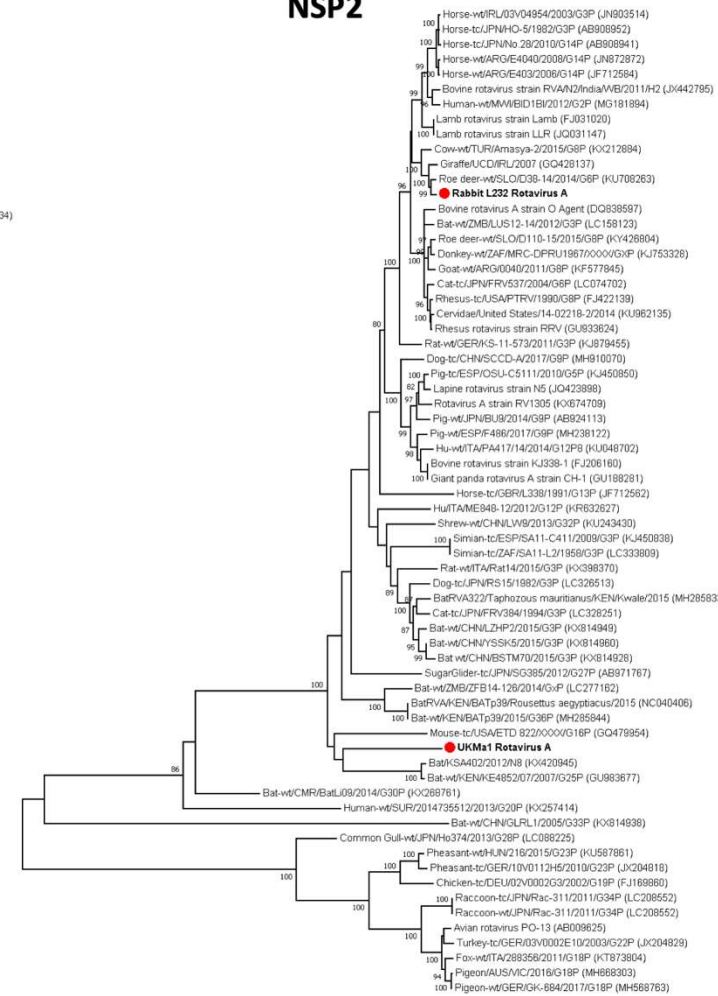
VP6



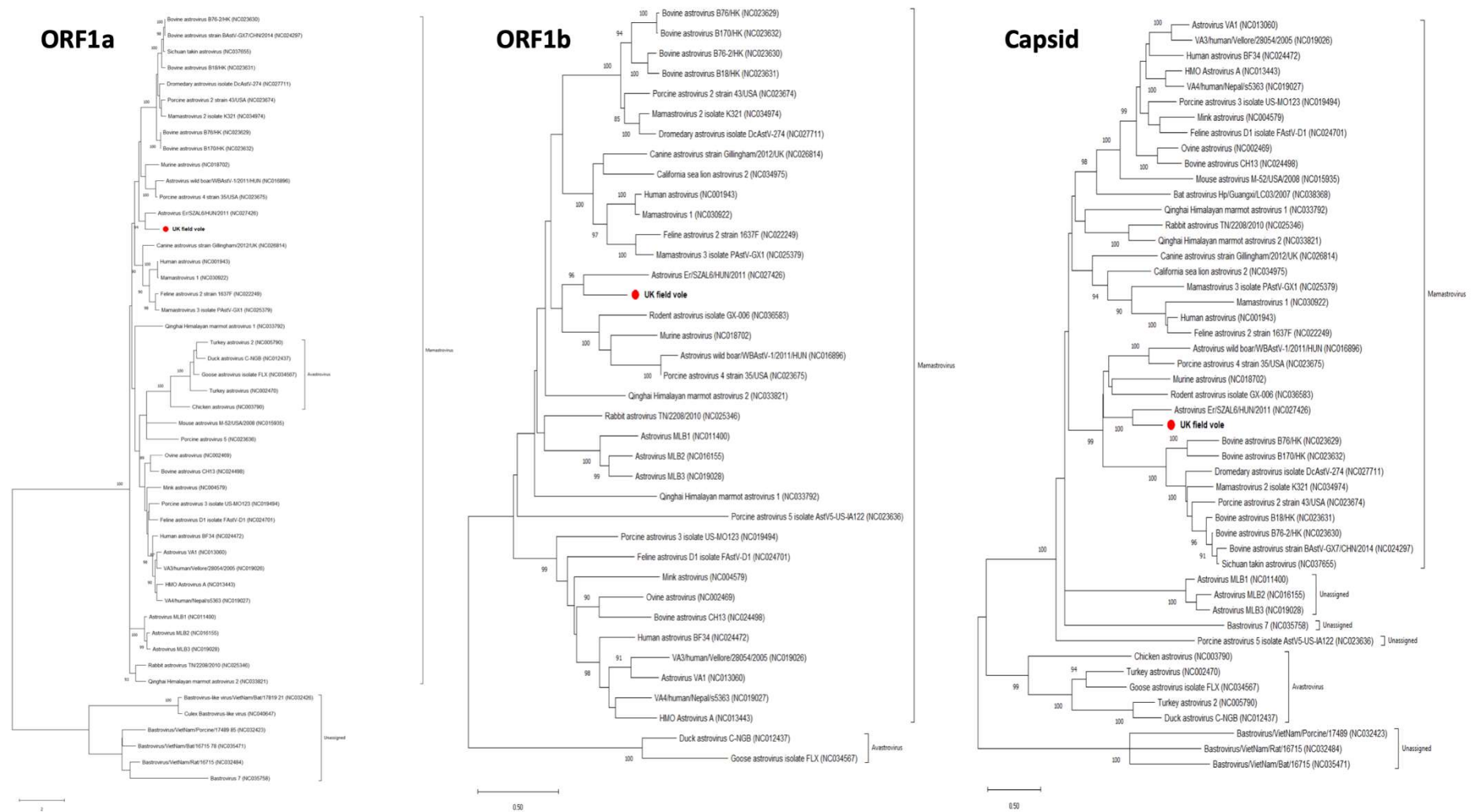
VP7



NSP2



Supplementary Figure 4. Phylogenetic relationships of the field vole and the rabbit rotavirus A based on the VP6, VP7 and NSP2 segments. Maximum likelihood phylogenetic analysis of paramyxovirus partial VP6 (882 nt), VP7 (98 7nt) and NSP2 (864 nt) segment sequences, revealing that the rabbit L232 rotavirus A was clustered close to other species whereas the UKMa1 rotavirus A formed a distinct lineage. The novel sequences obtained from the UK field vole UKMa1 and the French rabbit L232 were analyzed alongside reference sequences representing rotaviruses A from different species. Reference sequences are indicated by their GenBank accession numbers. Branch lengths are drawn to a scale of nucleotide substitutions per site. Numbers above individual branches indicate bootstrap support (100 replicates); only values >80% are shown. The novel rotaviruses A are marked with a red dot.



Supplementary Figure 5. Phylogenetic relationships of the novel field vole astrovirus based on the ORF1a, ORF1b and capsid genes. Maximum likelihood phylogenetic analysis of astrovirus partial *ORF1a* (1,525 nt), *ORF1b* (894 nt) and *capsid* (1,050 nt) gene sequences, revealing that the rodent astrovirus clustered with Er/SZAL6/HUN/2011 and formed a single clade within the genus *Mamastrovirus*. The novel sequence obtained from the UK field vole UKMa1 was analyzed alongside reference sequences representing different astrovirus genera. Reference sequences are indicated by their GenBank accession numbers. Branch lengths are drawn to a scale of nucleotide substitutions per site. Numbers above individual branches indicate bootstrap support (100 replicates); only values >80% are shown. The novel UKMa1 astrovirus is marked with a red dot.