

Circovirus Hepatitis Infection in Heart-Lung Transplant Patient, France

Appendix

Appendix Table 1. Control characteristics for assessment of human circovirus type 1 (HCirV-1) presence in 36 blood and 20 stool samples performed with specific HCirV-1 qPCR*

Controls	Hepatitis†(n=16)	Immunocompetent, no hepatitis (n=12)	Immunocompromised, no hepatitis (n=28)	Total (n = 56)
Age, mean (range), y	17 (3–53)	30 (0.2–67)	44 (1–84)	33 (0.2–84)
Adults >15 years old, n (%)	5 (31)	7 (58)	22 (78)	35 (63)
Sex, female, n (%)	4 (25)	7 (58)	11 (39)	22 (39)
Samples tested, n (%)				
Blood	10 (62)	8 (66)	18 (64)	36 (64)
Stool	6 (38)	NA	NA	NA
Known hepatitis etiology‡	8 (50)	NA	NA	NA
Immunological status, n (%)				
Immunocompetent	5 (31)	12 (100)	0	17 (30)
HIV seropositive	0	0	2 (7)	2 (4)
Solid organ transplant	1 (6)	0	12 (43)	13 (23)
Primary immune deficiency	10 (63)	0	9 (32)	19 (34)
HSCT or immunosuppressive therapy	0	0	5 (18)	5 (9)

*HSCT, hematopoietic stem cell transplant; NA, not applicable

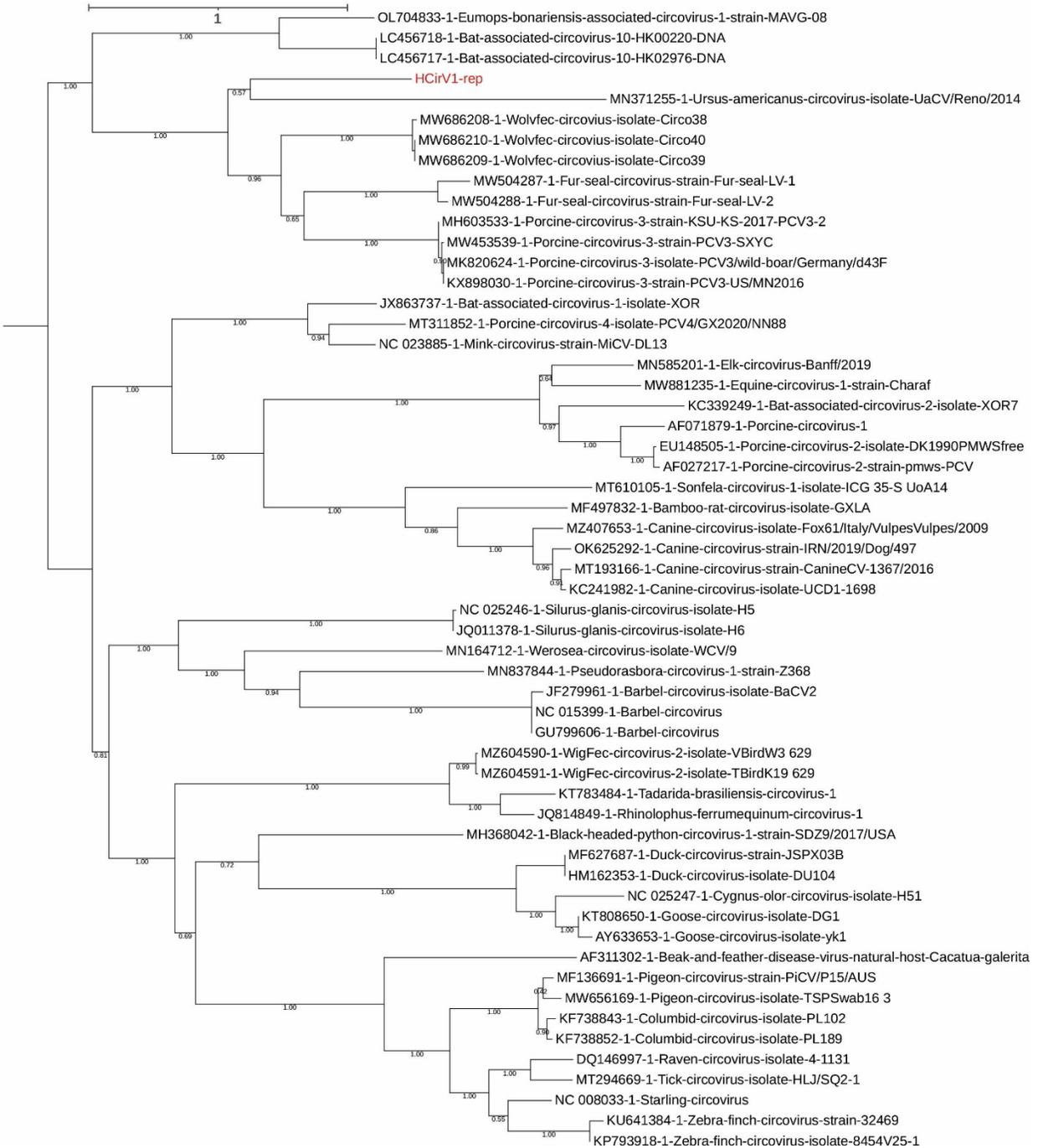
†hepatomegaly or liver cytolysis

‡Infectious (4 viral, 1 bacterial), dysimmune (1), metabolic (1) and toxic (1) etiologies

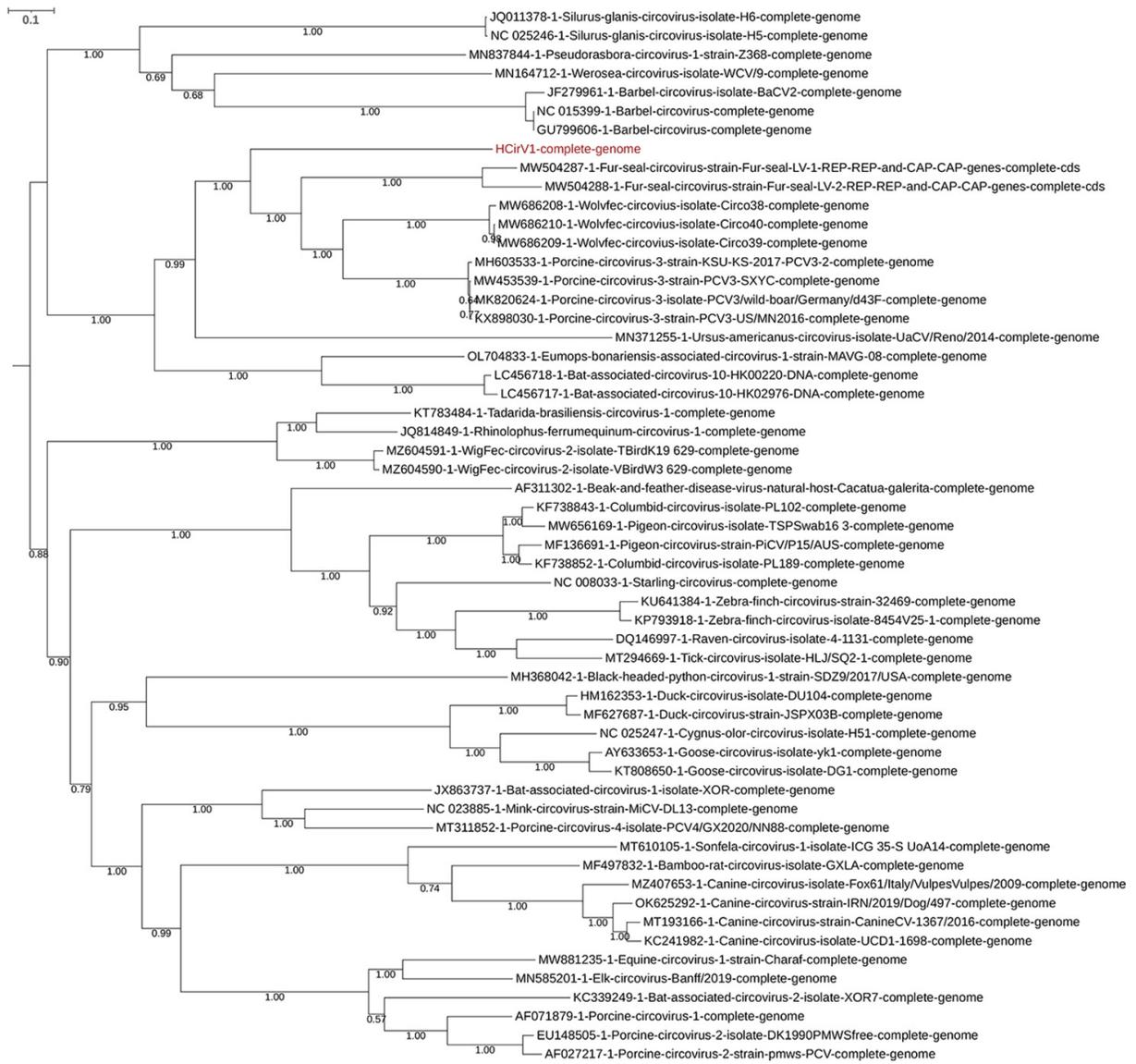
Appendix Table 2. Control characteristics for assessment of human circovirus type 1 (HCirV-1) presence in 57 liver biopsies samples screened with metagenomic next generation sequencing

Controls	Total (n=57)
Age, y, mean (range)	13 (0.3–68)
Adults >15 y, n (%)	10 (18)
Sex, female, n (%)	20 (35)
Immunological status, n (%)	
Immunocompetent	5 (9)
HIV seropositive	2 (4)
Solid organ transplant	5 (9)
Primary immune deficiency	25 (44)
HSCT or immunosuppressive therapy	20 (35)

*HSCT, hematopoietic stem cell transplant



Appendix Figure 1. Phylogenetic analysis of human circovirus type 1 (HCoV-1). Phylogenetic analysis of replicase (Rep) protein sequences of HCoV-1 and representative of circovirus strains. Sequences were aligned with MAFFT under the L-INS-I parameter, and maximum-likelihood phylogenetic reconstruction was performed with PhyML implemented through the NGPhylogeny portal. HCoV-1 protein sequence is depicted in red. The tree scale indicates the number of amino acid substitutions per site.



Appendix Figure 2. Phylogenetic analysis of human circovirus type 1 (HCoV-1). Phylogenetic analysis of complete nucleotide sequences of HCoV-1 and representative of circovirus strains. Sequences were aligned with MAFFT under the L-INS-I parameter, and maximum-likelihood phylogenetic reconstruction was performed with PhyML implemented through the NGPhylogeny portal. HCoV-1 complete genome is depicted in red. The tree scale indicates the number of amino acid substitutions per site.