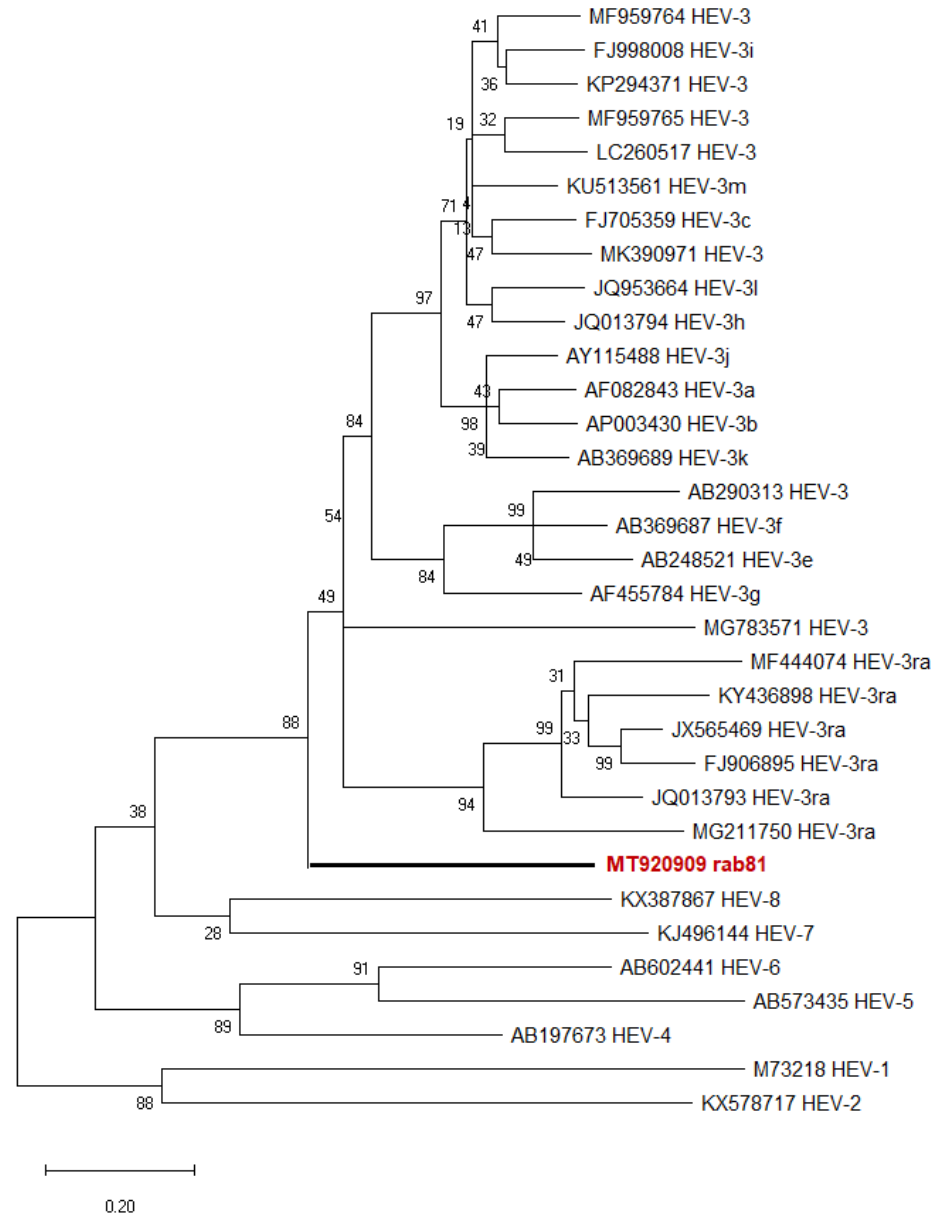


Table S1 : Primers used for HEV RNA quantification, genotyping, and genome sequencing

Name	Sequence	nucleotide position*	use	Reference
JVHEVR	AGGGGTTGGTTGGATGAA	5348 - 5331	qPCR	Jothikumar et al., 2006
JVHEVF	GGTGGTTTCTGGGGTGAC	5279 - 5926	qPCR	Jothikumar et al., 2006
JVHEV.P81	TGATTCTCAACCCCTTCGC	5302 - 5319	qPCR	this work
JVHEV.P	TGATTCTCAGCCCTTCGC	5302 - 5319	qPCR	Jothikumar et al., 2006
HEV.R	GCGAAGGGGTTGGTTGGATG	5325 - 5333	RT-PCR/Sequencing	Vina-Rodriguez et al., 2015
HEV.RdRp_F2b	GTGCTCTGTTTGGCCNTGGTTYMG	4280 - 4304	RT-PCR/Sequencing	Hammerschmidt et al., 2017
R5674	TGAGTGTGGTGCCGTCCTG	5685 - 5666	Sequencing	this work
R5625	CATACAAGACAAGATTAGTGCC	5636 - 5615	RT-PCR/Sequencing	this work
F5086	GGACCTTACAAATTCTATTATACAG	5094 - 5118	Sequencing	this work
F5048	GGCAAGGCTCACTTTACCGA	5056 - 5075	RT-PCR/Sequencing	this work
AAP mod	GGCCACGCGTCGACTAGTACGGGGGGGGGGGGGGGG	RACE adapter	Sequencing	ThermoFisher (adapted)
AP	GGCCACGCGTCGACTAGTACTTTTTTTTTTTTTTTT	RACE adapter	Sequencing	ThermoFisher
AUAP	GGCCACGCGTCGACTAGTAC	RACE adapter	Sequencing	ThermoFisher
R6591	GAAAATGGTCTGATCGTACTC	6622 - 6602	RT-PCR/Sequencing	this work
R6578	GAGAGCCACAACACATCATT	6588 - 6569	Sequencing	this work
R5926	CCTGGTTACGATAATGGAGG	5936 - 5917	Sequencing	this work
R2429	CACAATCCGACTCGAATAAGG	2449 - 2429	Sequencing	this work
K081.RACE5'700	GACAACCTACGCGACTTCCATC	684 - 664	Sequencing	this work
K081.RACE5'400	CGCGAGTTGGGGCAGAGTAC	400 - 381	Sequencing	this work
K081.RACE3'300	GGCCCTGTGTCCATTCTGC	6938 - 6957	Sequencing	this work
F5906	CCTCCATTATCGTAACCAGG	5917 - 5936	RT-PCR/Sequencing	this work
F1610	CTTGAGGCCCTTTATAGTGC	1609 - 1628	Sequencing	this work
R6506	GTCTGTTCATGTTGATTGTCTG	6517 - 6496	RT-PCR/Sequencing	this work
R3157	CAGCAAATGCGGTGGTAATGAC	3165 - 3144	Sequencing	this work
F6485	CGACAATCAACATGAACAGGAC	6496 - 6517	RT-PCR/Sequencing	this work
F5305	CCTTCGCCCTCCCCTATATTC	5313 - 5333	RT-PCR/Sequencing	this work
F960	CATTCCACGCAGTCCCAGTTC	959 - 979	Sequencing	this work
R1042	CGAGCAACAAAAGGCCTGATC	1041 - 1021	Sequencing	this work
R725	CATCATGGTTATACCCTGCACTAG	724 - 701	Sequencing	this work
F2991	CTATCCAGCAGGGGGATGTTG	2999 - 3019	RT-PCR/Sequencing	this work
F705	GTGCAGGGTATAACCATGATG	704 - 724	Sequencing	this work
F32	GAGGCCCATCAGTTTATTAAGG	31 - 52	RT-PCR/Sequencing	this work
terR	CTCCCGGTYTTRCCTACCYTC	7144 - 7123	RT-PCR/Sequencing	this work
4R	CACATAAAATGTTTTAGAAATGC	6781 - 6760	Sequencing	this work
3R	CATAAGACCATTGAATCATCTC	4718 - 4697	RT-PCR/Sequencing	this work
3F	GAGATGATTCAATGGTCTTATG	4697 - 4718	Sequencing	this work
2R	GCCGTAGCAATAATAGTAGTC	3518 - 3498	RT-PCR/Sequencing	this work
2F	GACTACTATTATTGCTACGGC	3498 -3518	Sequencing	this work

*numbering according to MT920909

a



b

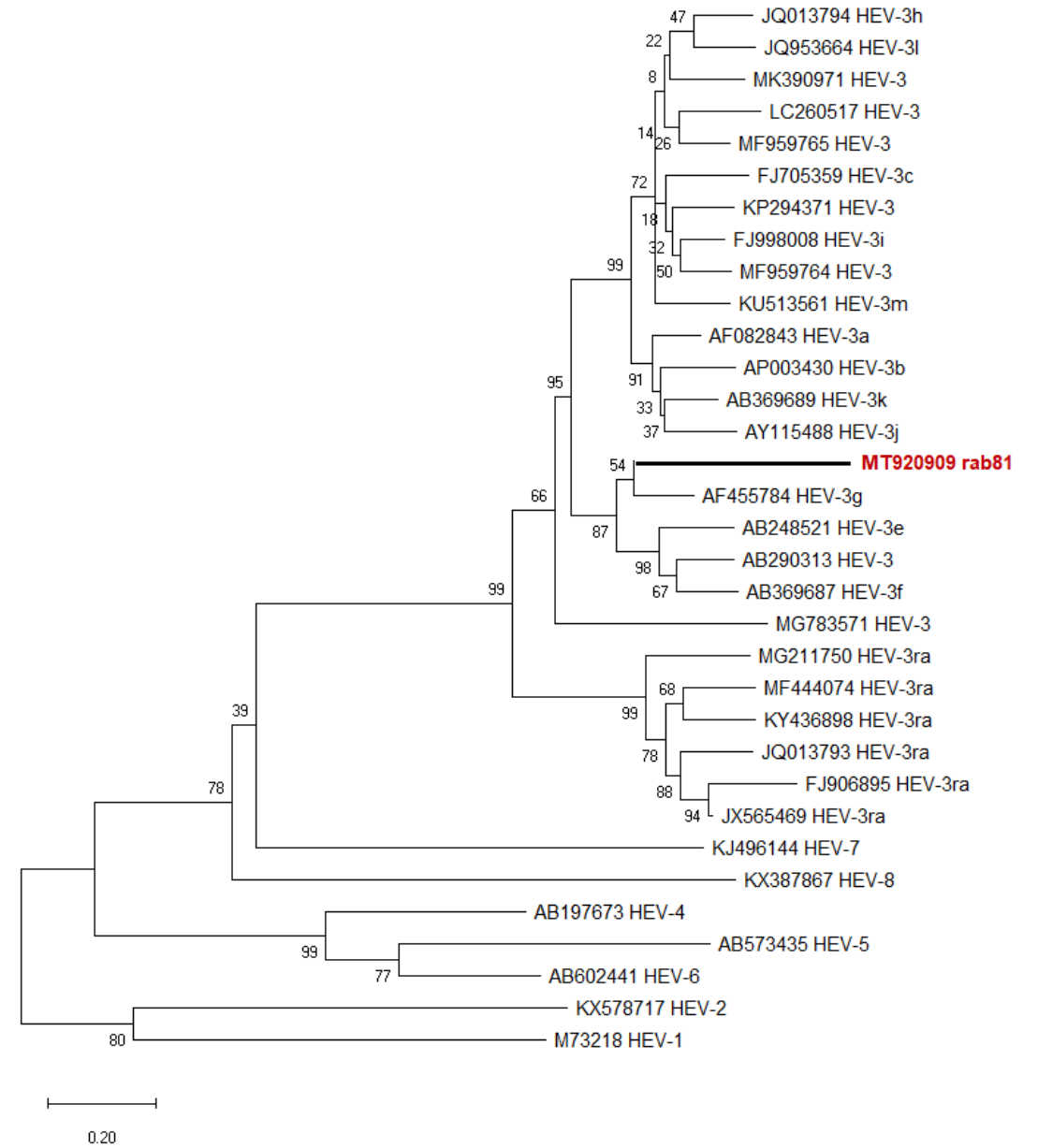
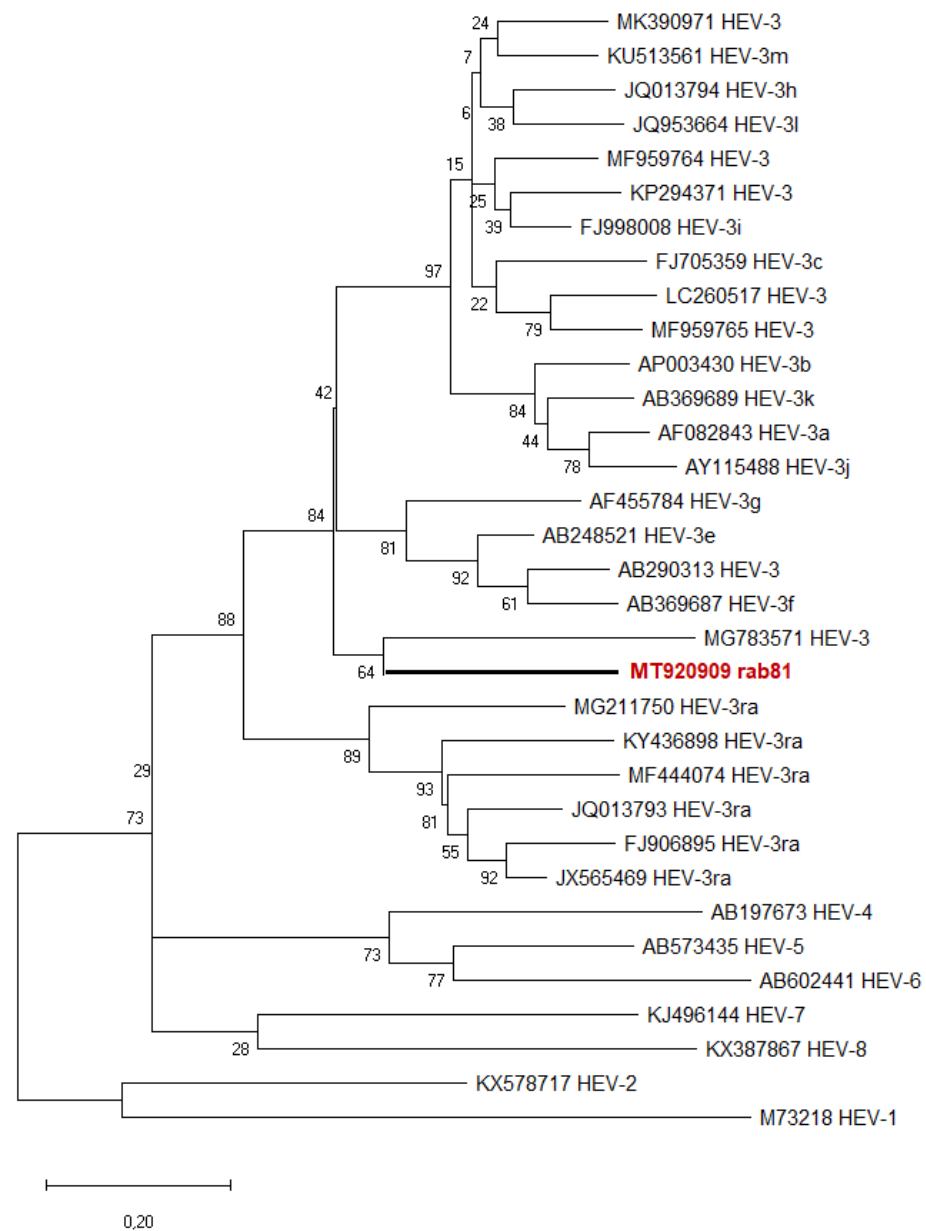
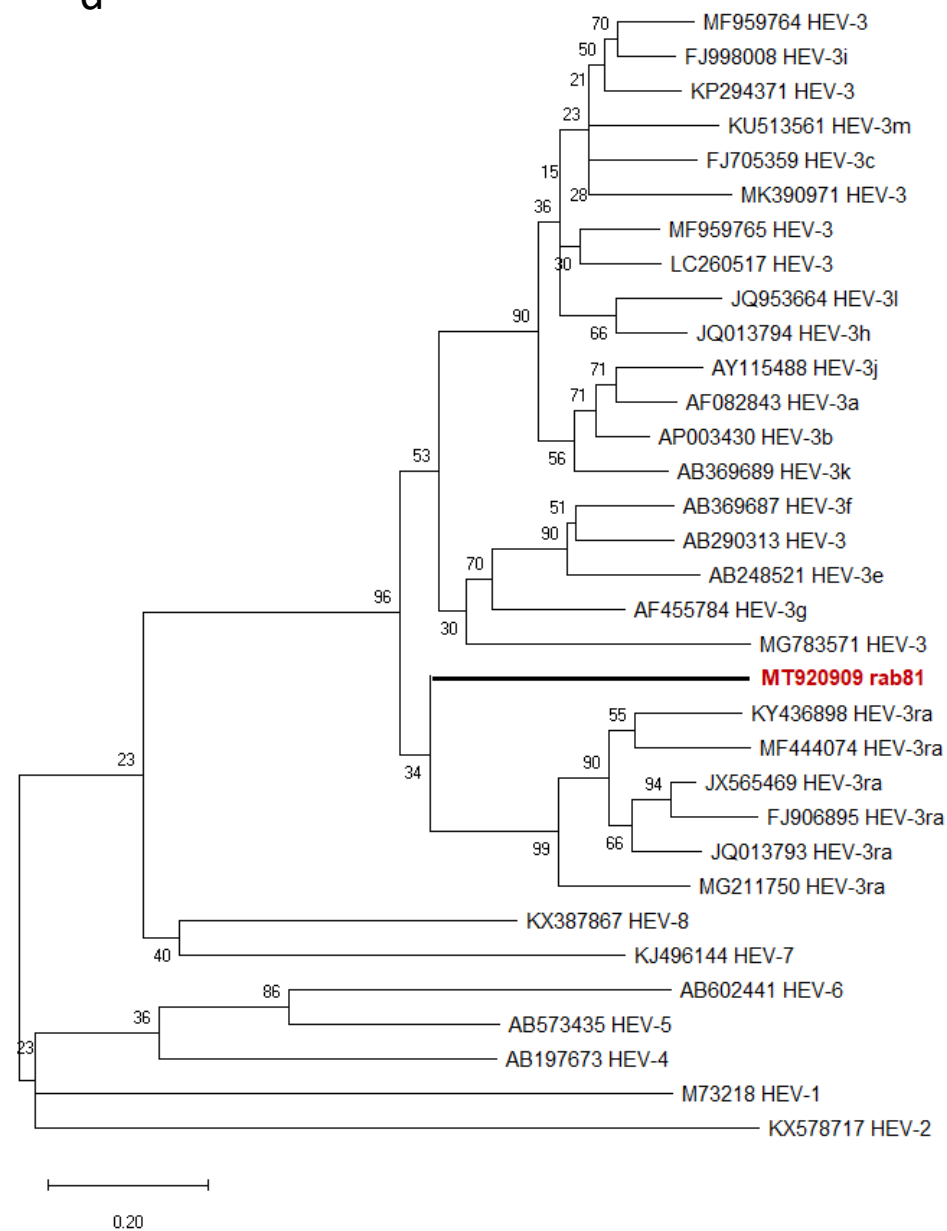


Figure S1: Molecular phylogenetic analysis of seven partial HEV sequences (a-g) as determined by SimPlot analysis

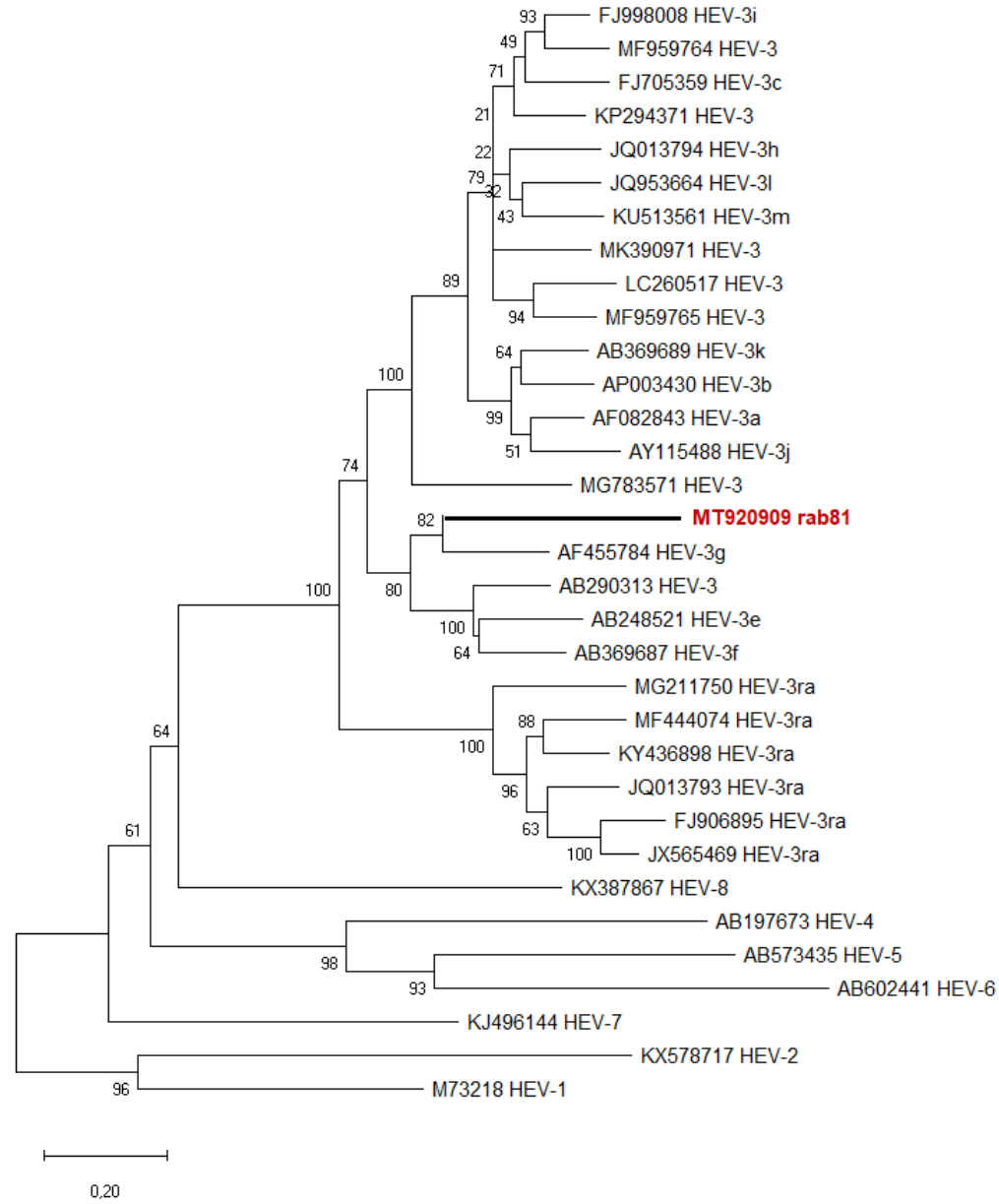
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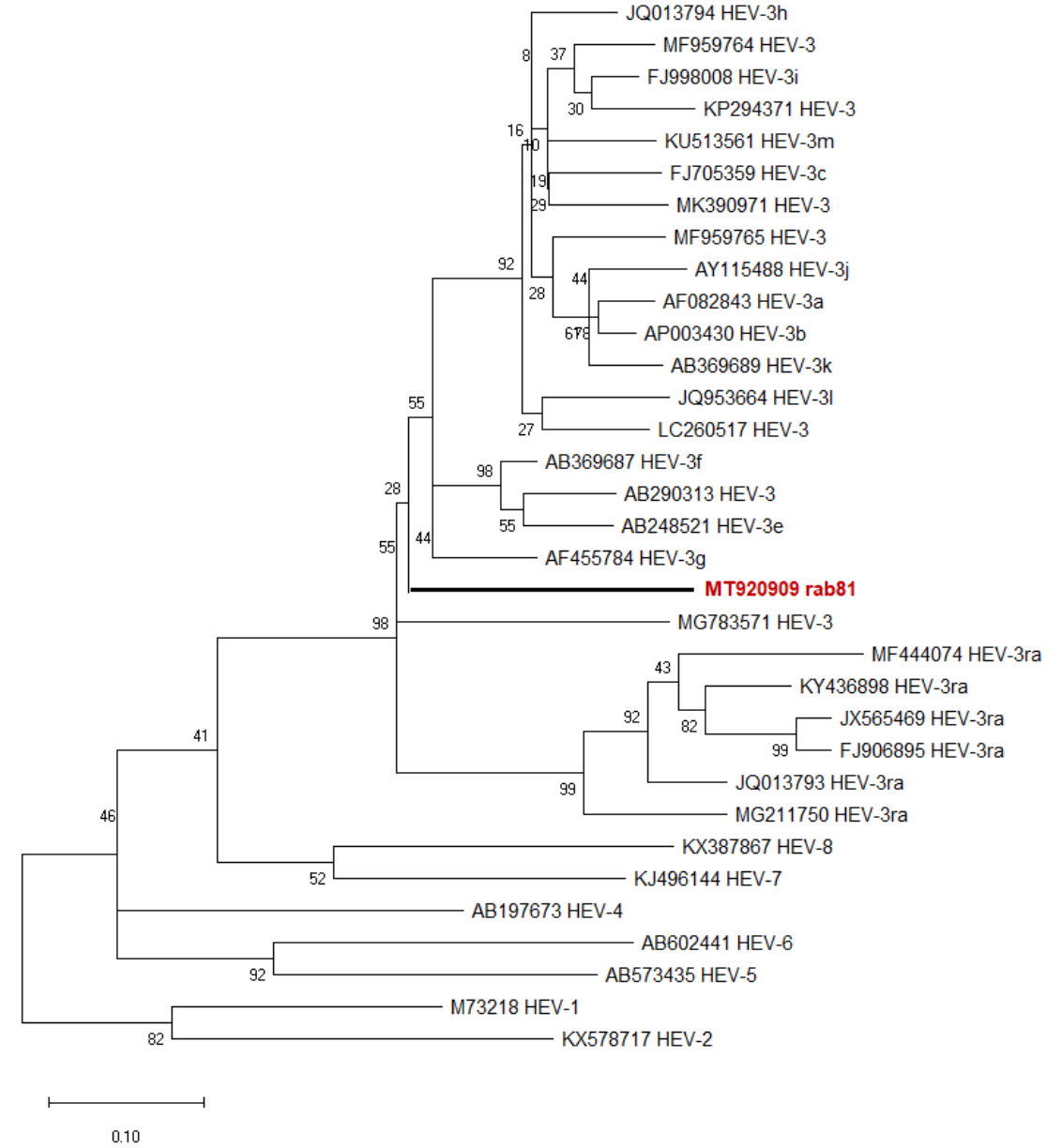
d

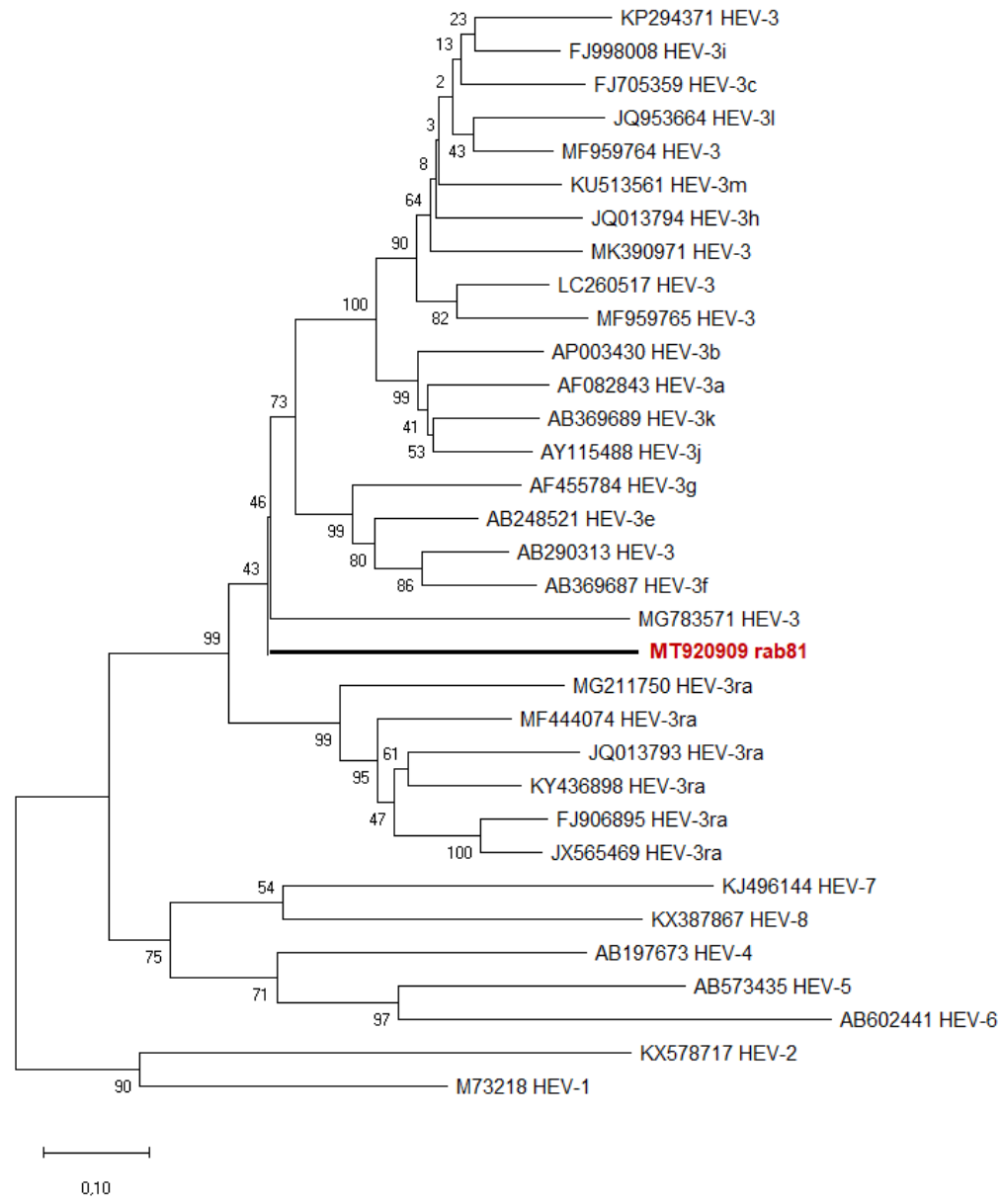


e

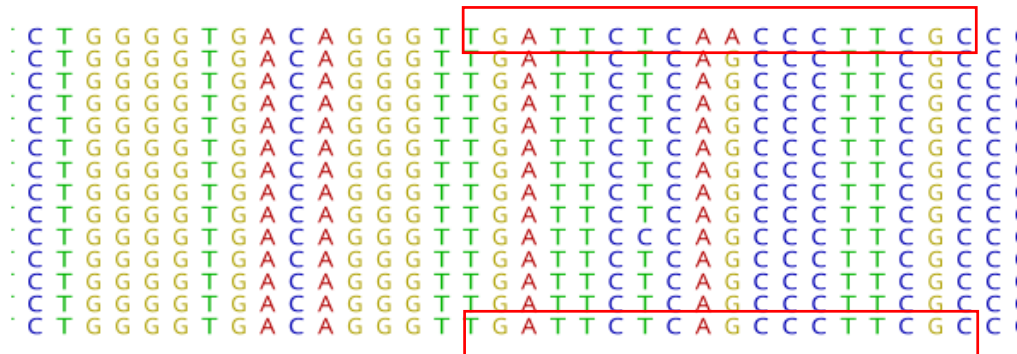


f





b



	ct value (average of three)	
dilution	adapted probe	original probe
10^{-3}	30.9	33.4
10^{-4}	26.3	29.2
10^{-5}	22.0	24.3

Figure S2: Nucleotide sequence alignment of quantitative real-time RT-PCR (qRT-PCR) probe target region (a), qRT-PCR runs (triplicate) at three dilution steps (b) and bean ct-values yielded by original probe or adapted probe (c)