

Primers used for whole genome sequencing

Primer	Sequence (5' – 3')	Binding position (on 14-16753 genome)
‡ 5'-RACE_s	AAGCAGTGGTATCAACGCAGAGTACGCGGG	on 5' (dCTP) _n tail
† 1_s	GCAGACCACGTATGTGGTCGA	2 – 22
S_s	CGGCCAATTCTGCCCTGG	94 – 111
Sn_s	CGAATGCTGTGGTGGTTCGG	112 – 131
§ 5'-GS5n_as	TCTCAGTTTGTACACGGGACA	139 – 159
§ 5'-GS5_as	GCTGTCGGGGTTGCATCAGGTTAATA	164 – 189
§ 5'-GS4n_as	GAAATACGAGCTGCCGGGGTTGC	176 – 198
289_as	TCTAGACAACGACCAGCCCCG	270 – 289
§ 5'-GS4_as	CACCGGTGCAAGACATTAGGGTTATCAT	316 – 343
§ 5'-GS2n_as	GGGTCGGGGCAGAATACCAACGCTGT	371 – 396
393_as	TAGGAGCAGAGTACCAGCGC	374 – 393
409_s	CTAACTGCCGCCGTTCTG	409 – 426
440_as	GAGGCCACGCAAAGCAGAAC	421 – 440
427_s	CACTGCGTGGTTTGCCCC	427 – 444
† 2_s	GATCGTACCTAYTGYTTTGATGG	450 – 472
§ 5'-GS1n_as	CCCCAGTTTCTGCGGCAAATGAGC	484 – 507
§ 5'-GS1_as	CCGGCCAGAGGTCATGCAGAGAATAAAG	513 – 540
† 1_as	GGGCCATAGCCTCBGCAACATC	543 – 564
560g_s	GGCCCGYCA YGGGATGAC	560 – 577
Sn_as	CAAGCGTGTCATCCCGTGC	566 – 584
A_s	CGGTGATCGTGCTGTTGTGAC	665 – 685
S_as	GGTCACAACAGCACGATCACC	666 – 686
An1_s	CATACTTCGTGCATGGATCCGC	728 – 749
874_as	CGAGGGTACGGAACATAAGGCA	853 – 874
897_as	ACCTAACATACACCTCCGTGA	876 – 897
902g_s	ATTYGGCCCTGGYGGGTC	902 – 919
F1_s	TCATGCTGTTCCGGTCCACA	962 – 981
† 3_s	CATATTTGGGACCGGCTYATGCT	978 – 1000
† 2_as_m1	TAGGTCATAAGYCGTGARCAGCA	1032 – 1054
F2_s	TCCGCGGGATCAGTTATAAGGT	1057 – 1078
Fn1_s	GGTTGGAACGCATCAGAGGA	1107 – 1126
Fn2_s	TGATTACCGCGGCGTATTTAACT	1141 – 1163
An1_as	GTCGGCGCATACCCTTGAT	1199 – 1218
Fun2_s	CAGTGCCGCCGCTGGCT	1323 – 1339
† 4_s	GGGTAAGTTCTGCTGYTTTATG	1427 – 1448
† 3_as_m1	TCYAAAAAGCAGGTRCACTCCTG	1461 – 1483
† 1500_s_m1	CTGCTTTTTRGAACCAGCAGAGG	1472 – 1494
1542g_s	GARGTGACCCYGGCTGAG	1542 – 1559
An2_s	TGACTGCCACCGTCGAACTC	1669 – 1688
† 1800_as_m1	KGACTGGCGAGAGGCRTCAAC	1805 – 1826

1825g_as	GCCTGGCGRGARTCATCAAA	1806 – 1825
Fun2_as	CAGGGGTGAGCTCATATG	1852 – 1869
H1_s	AGACTGTACTGCTGTTTTCCCC	1904 – 1925
† 5_s_m1	GCAGCCTTTTGCAGTGCYCTTTA	1962 – 1984
2001g_s	ACCCAGCGYCATTGCTG	2001 – 2018
H1n_s	GGTGGGCTGTGGTTGCAC	2022 – 2039
† 4_as_m1	GGGAARATACCCAACARCCCCTC	2043 – 2065
Fn1_as	GTGTGCCCCGGGAGAAAAGG	2066 – 2084
Fn2_as	TTTGCGGACTCCCAGGTGT	2083 – 2101
An2_as	CATGTCCGGGTGTACAAAGTTCC	2118 – 2140
F1_as	CCAGGTCCGGGTGTAAAGTGT	2121 – 2141
A_as	CAGGAGGTGTAGAGTGGCGT	2216 – 2235
† ins_s_m1	CCTGTTAGTGACRTTTGGGTGT	2232 – 2253
F2_as	GCACCCAAGCGTCACTAACA	2234 – 2253
G1_s	TAGTGACGCTTGGGTGCTTC	2237 – 2256
G2/Gn1_s	TCTGAGGGGTGCGTGGCTA	2265 – 2283
Gn2_s	TAGTAAGCCCACTAGCCCGC	2306 – 2325
H1n_as	TGGTGGCTTACGAACAGGGG	2347 – 2366
† 2600_s	ACCTATCCGGATGGGGCAAAGG	2403 – 2424
† ins_as	ACACCTTTGCCCCATCCGGATA	2406 – 2427
2418g_s	GCYAAGGTGTAYGCAGGCTC	2418 – 2437
H1_as	AGGGTTGGACGCATTGACC	2465 – 2483
2539g_as	GACTCCGGRAAVCGCTGG	2522 – 2539
Gun2_s	CCGATCATTGCTGTGG	2601 – 2619
Gun3_s	GCGTACCGTGAGACCTG	2664 – 2680
Gun2_as	AGTGGGTAAGCGGCTGTG	2693 – 2710
B_s	CTACCCACTCCTCGGCTC	2702 – 2719
Bn1_s	ACCAAGTTCCCGTTAGCCTCAG	2728 – 2749
2757g_s	GCCTGGGARCGTAACCAYCGC	2757 – 2777
† 3150_s_m1	TATCAGTTYACTGCTGGGGTCC	2964 – 2985
2986g_as	GGGACCCCGGCRGTRAAC	2969 – 2986
† 3200_as_m1	TGCTGTATAGARCGCGACTTCC	2995 – 3016
3034g_as	ACAACRTCAACATCSCCCTG	3015 – 3034
Bn1_as	TGGTTTGGGTCGCCGAGAAG	3207 – 3226
I1_s	TTCAGACTACTAGCCGCGTT	3364 – 3383
C/Bn2_s	TCTGGAATGAGCCTGCCATTGG	3397 – 3418
I1n_s	CGCAATCACCGTCCATGAGG	3464 – 3483
3553g_s	CYCGYGACATGCCATCG	3553 – 3570
Gun3_as	ACACATTTCTCTGTGTGGC	3583 – 3601
† 8_s	CCCCCGCTTGTTWCGTGAGGT	3613 – 3634
3800_as_m1	ACCRACCTCACGTAACAAGCCG	3617 – 3638
3700g_as	GGGCGRTGRTGGCCCACT	3683 – 3700
Bn2_as	ACCGTGAGCTCCTGAGGCAT	3873 – 3892
Cn1_s	AGCTCACGGTGTCTGATAGC	3883 – 3902

Gun4_as	TGTCCGTGAGCTCAAAAACC	3908	–	3927
Gn1_as	CTGACTAGGGGCCGCCATTC	3940	–	3959
G1_as	CCTCATACAACCTTCGTCCGGC	4000	–	4020
Gn2_as	ACATGTGGTGGCCTGGACC	4076	–	4094
† 9_s_m1	CYACYACGTGTGAGTTRTATGAG	4083	–	4106
† 8_as	CCATCCTGACCTTTCTCCACCAT	4119	–	4141
G2_as	CGTCCTGGCCTTTCTCAACC	4121	–	4140
4143g_as	AGCCRTCCTGRCCCTTCTCCAC	4122	–	4143
4276g_as	CTCCARGCCGARATGCCC	4259	–	4276
Iln_as	GGGCACAGAAGGTCTTACTCCA	4272	–	4293
I1_as	AGGTGGGAGTAGGGCTAAGA	4330	–	4349
B/Cn1_as	CCGTAGAAAATATTAGGCGGGAG	4341	–	4363
Cn2_s	CTGTCTCAGGGGCAGGTTCA	4396	–	4415
J1_s	AGCCGGCTCTAGTATGGTCT	4406	–	4425
J1n_s	GCGTTATCATGGAAGAGTGTGGC	4486	–	4508
† 10_s_m1	CTYAAGGGATTTTGAAGAARCA	4581	–	4603
† 9_as_m1	GCCATRTTCCARACAGTRTTCCA	4629	–	4651
J1n_as	TCCCCTTTGAACGCTGCTACT	4688	–	4708
J1_as	CCACAACCAGCAATCAAGGC	4758	–	4777
Cn2_as	TTCTCAGACAGCCGGCCG	4874	–	4891
D_s	AGAAGAACTGGGGCCCTGGG	4888	–	4907
C_as	CACATACCTGCGCAACATTCGT	4962	–	4983
Dn1_s	ACGAATGTTGCGCAGGTATGT	4962	–	4982
† 11_s-neu	CGGCAGTGGTTTCTGGRGTGAC	5283	–	5304
† 10_as	GCGAAGGGCTGAGAATCAACCC	5306	–	5327
Dn1_as	TCAACATCAGGTACAGGGGCT	5529	–	5549
K1_s	TCTATATGCCGCCCCGCTC	5634	–	5652
E/Dn2_s	AAACCCTCTGCTGCCCCTTC	5652	–	5671
K1n_s	GGCAACTGAGGCGTCTAATT	5697	–	5716
† 12_s	CTAATTATGCCCAGTAYCGGGTTG	5711	–	5734
† 11_as	GTAATAGAGTTCATRTCAACAGA	5833	–	5855
K1n_as	ACCCTGATTGCGGTAATGGA	5924	–	5943
K1_as	AGGGGAGCCATGAATACAAAGC	6003	–	6024
En1_s	GGGCGCTTGGA CTCTTGAT	6056	–	6075
6062_s	TGGGGCTTCTCGATTTTGCAC	6062	–	6082
Dn2_as	TGCTTGTATACCGGGACACACG	6127	–	6148
6196_s	ACA ACTACTGCAGCCACACGT	6196	–	6216
† 13_s	CTCACACTCTTTAATCTTGCTGA	6280	–	6302
† 12_as_m1	AACTGTCCCCRGCCGACGAAAT	6334	–	6356
§ 3'-GS2_s	TCCCGCCCAGTTGTCTCAGCCAATGG	6364	–	6389
6387_as	ATTGGCTGAGACGACTGGGC	6368	–	6387
6525_as	CCGATCCTGTT CATGCTGGTTG	6504	–	6525
§ 3'-GS1_s	ACCCCTTCGCCTGCCCTTCTCG	6529	–	6551
D/En1_as	CGAGAAGGGGCAGGCGAAG	6533	–	6551

§ 3'-GSn2_s	TTGTGGCTCTCTCTCACTGCTGCCGA	6583 – 6608
En2_s	GCCGCCGAGTATGACCAGAC	6601 – 6620
§ 3'-GS4_s	TGTTAATGTGGCGACGGGTGCTCAGG	6672 – 6697
§ 3'-GS1n_s	GCTGTCGCCCCGTTCCCTTGACTGGTC	6697 – 6722
§ 3'-GSn4_s	GACGGTCGGCCTCTCACTAC	6736 – 6755
† 14_s_m1	GGAAGTTATCYTTTTGGGAGGC	6800 – 6821
§ 3'-GS3_s	TTTTGGGAGGCTGGCACTACTAAGGC	6811 – 6836
† 13_as_m1	AGTTGTGTTTAAATTATASGGGTA	6841 – 6864
§ 3'-GSn3_s	CCCTGAGTGCCGTAATCTTGCCCTAC	7053 – 7078
En2_as	CACACCCCTGCAAACCGAGA	7068 – 7087
E_as	TCAGCAATAGTAGACTGGAAGGC	7087 – 7109
† 14_as_m1	TTTTTTTTTTTTCCWGGGAGCGCG	7213 – 7236
‡ 3'-RACE_as	AAGCAGTGGTATCAACGCAGAGTAC(T) ₃₀ VN	on 3' poly(A) tail
‡ LUP	CTAATACGACTCACTATAGGGCAAGCAGTGGTATCAACGCAGAGT	on 5'-RACEs or 3'-RACEas
‡ SUP	CTAATACGACTCACTATAGGGC	on LUP
‡ NUP	AAGCAGTGGTATCAACGCAGAGT	on LUP

Table S4. Positions and nucleotide sequences of primers used for whole genome sequencing.

† Primers based on Johne et al. ¹; m1, modified; s, sense; as, antisense; ‡ primers based on BD SMART™ RACE cDNA Amplification Kit User Manual; § primers designed according to recommendations of BD SMART™ RACE cDNA Amplification Kit User Manual.

Supplementary Reference

1. Johne R, Reetz J, Ulrich RG, et al. An ORF1-rearranged hepatitis E virus derived from a chronically infected patient efficiently replicates in cell culture. *Journal of Viral Hepatitis*. 2014;21(6):447-456. doi:10.1111/jvh.12157.