

IQ-TREE multicore version 2.1.3 COVID-edition for Mac OS X 64-bit built Oct 4 2021
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Host: shuqis-MacBook-Pro.local (AVX2, FMA3, 8 GB RAM)
Command: /Users/shuqi/documents/Virus-project/iqtree-2.1.3-MacOSX/bin/iqtree2 -s
BHV1_plus.txt
Seed: 496314 (Using SPRNG - Scalable Parallel Random Number Generator)
Time: Sat Jan 29 14:46:43 2022
Kernel: AVX+FMA - 1 threads (4 CPU cores detected)

HINT: Use -nt option to specify number of threads because your CPU has 4 cores!
HINT: -nt AUTO will automatically determine the best number of threads to use.

Reading alignment file BHV1_plus.txt ... Fasta format detected
Alignment most likely contains DNA/RNA sequences
Alignment has 50 sequences with 144551 columns, 2745 distinct patterns
2080 parsimony-informative, 15894 singleton sites, 126577 constant sites

		Gap/Ambiguity	Composition	p-value
1	BHV5	4.66%	failed	0.00%
2	MN1	6.68%	passed	96.57%
3	MN2	6.64%	passed	74.63%
4	MN3	6.68%	passed	96.28%
5	MN4	6.68%	passed	96.29%
6	MN5	6.69%	passed	97.23%
7	MN6	6.69%	passed	97.86%
8	MN7	6.69%	passed	97.63%
9	MN8	6.69%	passed	97.59%
10	MN9	6.67%	passed	95.72%
11	MN10	6.68%	passed	96.11%
12	MN11	6.68%	passed	96.25%
13	MN12	6.69%	passed	97.29%
14	MN13	6.68%	passed	96.85%
15	MN14	6.69%	passed	96.66%
16	MN15	6.68%	passed	96.45%
17	PA1	6.69%	passed	97.31%
18	PA2	6.69%	passed	97.06%
19	PA3	6.68%	passed	97.02%
20	C14_CSU_034_10640	7.00%	passed	82.15%
21	C18	7.06%	passed	81.15%
22	C26	6.92%	passed	86.52%
23	C28_55771	6.47%	passed	84.66%
24	C29	6.94%	passed	87.40%
25	C33	6.96%	passed	86.98%
26	C35_1839_9847	7.16%	passed	89.72%
27	C36_876_459	7.14%	passed	90.49%
28	C42	6.80%	passed	89.10%
29	C43	6.78%	passed	84.71%
30	C44	7.60%	passed	98.57%
31	C45	7.59%	passed	98.58%
32	C46	7.61%	passed	98.31%
33	C47	7.69%	passed	96.09%
34	Nasalgen_IP_MLV_vaccine	7.50%	passed	98.67%
35	TSV-2_Nasal_MLV_vaccine	6.68%	passed	94.67%
36	Bovishield_Gold_FP5_MLV_vaccine	6.86%	passed	90.95%
37	BovSh_IBR_MLV_vaccine	6.78%	passed	91.78%
38	Vista_IBR_MLV_vaccine	6.66%	passed	90.63%
39	Pyramid_IBR_MLV_vaccine	6.78%	passed	91.71%
40	Express1_IBR_MLV_vaccine	6.73%	passed	90.82%

41	Titanium_IBR_MLV_vaccine	6.85%	passed	88.68%
42	Arsenal_IBR_MLV_vaccine	7.48%	passed	99.65%
43	VR188_Los_Angeles	6.77%	passed	81.35%
44	NVSL_challenge_97_11	6.68%	passed	96.27%
45	216_II	6.42%	passed	99.85%
46	SP1777	6.66%	passed	80.59%
47	SM023	6.66%	passed	57.32%
48	K22	6.44%	passed	65.94%
49	B589	6.64%	passed	79.38%
50	Cooper	7.30%	passed	99.71%
****	TOTAL	6.81%	1 sequences failed composition	chi2

test (p-value<5%; df=3)
NOTE: minimal branch length is reduced to 0.000000691797 for long alignment

Create initial parsimony tree by phylogenetic likelihood library (PLL)... 0.060 seconds

Perform fast likelihood tree search using GTR+I+G model...

Estimate model parameters (epsilon = 5.000)

Perform nearest neighbor interchange...

Estimate model parameters (epsilon = 1.000)

1. Initial log-likelihood: -276619.211

Optimal log-likelihood: -276618.055

Rate parameters: A-C: 1.03734 A-G: 7.88071 A-T: 0.80702 C-G: 0.88969 C-T: 7.75275 G-T: 1.00000

Base frequencies: A: 0.135 C: 0.359 G: 0.366 T: 0.140

Proportion of invariable sites: 0.433

Gamma shape alpha: 0.402

Parameters optimization took 1 rounds (0.151 sec)

Time for fast ML tree search: 3.170 seconds

NOTE: ModelFinder requires 44 MB RAM!

ModelFinder will test up to 286 DNA models (sample size: 144551) ...

No.	Model	-LnL	df	AIC	AICc	BIC
1	GTR+F	278431.900	105	557073.799	557073.954	558111.345
2	GTR+F+I	276816.146	106	553844.293	553844.450	554891.720
3	GTR+F+G4	276770.176	106	553752.353	553752.510	554799.780
4	GTR+F+I+G4	276600.018	107	553414.036	553414.196	554471.345
5	GTR+F+R2	275935.442	107	552084.885	552085.045	553142.193
6	GTR+F+R3	275912.701	109	552043.403	552043.569	553120.474
7	GTR+F+R4	275887.685	111	551997.370	551997.542	553094.204
8	GTR+F+R5	275861.418	113	551948.836	551949.015	553065.433
9	GTR+F+R6	275839.611	115	551909.222	551909.407	553045.582
10	GTR+F+R7	275823.788	117	551881.576	551881.767	553037.698
11	GTR+F+R8	275812.444	119	551862.888	551863.086	553038.773
22	SYM+R6	294443.853	112	589111.706	589111.882	590218.422
23	SYM+R7	294436.677	114	589101.354	589101.536	590227.832
35	TVM+F+R6	275805.869	114	551839.738	551839.920	552966.216
36	TVM+F+R7	275801.675	116	551835.350	551835.537	552981.590
48	TVMe+R6	294439.386	111	589100.773	589100.945	590197.607
49	TVMe+R7	294437.753	113	589101.506	589101.684	590218.103
61	TIM3+F+R6	275805.746	113	551837.493	551837.671	552954.090
62	TIM3+F+R7	275803.698	115	551837.397	551837.582	552973.757
74	TIM3e+R6	294673.303	110	589566.606	589566.775	590653.559
75	TIM3e+R7	294672.600	112	589569.200	589569.375	590675.916
87	TIM2+F+R6	275760.548	113	551747.097	551747.275	552863.693
WARNING: Log-likelihood -275878 of TIM2+F+R7 worse than TIM2+F+R6 -275761						
88	TIM2+F+R7	275877.575	115	551985.150	551985.335	553121.510
100	TIM2e+R6	294666.062	110	589552.124	589552.293	590639.076

WARNING: Log-likelihood -294834 of TIM2e+R7 worse than TIM2e+R6 -294666

101	TIM2e+R7	294833.578	112	589891.157	589891.332	590997.872
113	TIM+F+R6	275749.572	113	551725.144	551725.322	552841.741

WARNING: Log-likelihood -275879 of TIM+F+R7 worse than TIM+F+R6 -275750

114	TIM+F+R7	275878.820	115	551987.640	551987.825	553124.000
126	TIME+R6	294732.116	110	589684.231	589684.400	590771.184

WARNING: Log-likelihood -294900 of TIME+R7 worse than TIME+R6 -294732

127	TIME+R7	294899.616	112	590023.232	590023.407	591129.948
139	TPM3u+F+R6	275746.894	112	551717.788	551717.964	552824.504

WARNING: Log-likelihood -275885 of TPM3u+F+R7 worse than TPM3u+F+R6 -275747

140	TPM3u+F+R7	275884.678	114	551997.356	551997.538	553123.834
152	TPM3+F+R6	275745.283	112	551714.566	551714.741	552821.281

WARNING: Log-likelihood -275880 of TPM3+F+R7 worse than TPM3+F+R6 -275745

153	TPM3+F+R7	275879.977	114	551987.953	551988.135	553114.431
165	TPM2u+F+R6	275744.230	112	551712.460	551712.635	552819.175

WARNING: Log-likelihood -275880 of TPM2u+F+R7 worse than TPM2u+F+R6 -275744

166	TPM2u+F+R7	275880.101	114	551988.203	551988.384	553114.681
178	TPM2+F+R6	275744.182	112	551712.364	551712.539	552819.079

WARNING: Log-likelihood -275884 of TPM2+F+R7 worse than TPM2+F+R6 -275744

179	TPM2+F+R7	275884.079	114	551996.158	551996.340	553122.636
191	K3Pu+F+R6	275743.097	112	551710.194	551710.369	552816.909

WARNING: Log-likelihood -275875 of K3Pu+F+R7 worse than K3Pu+F+R6 -275743

192	K3Pu+F+R7	275874.774	114	551977.548	551977.729	553104.026
204	K3P+R6	294730.760	109	589679.521	589679.687	590756.592

WARNING: Log-likelihood -294900 of K3P+R7 worse than K3P+R6 -294731

205	K3P+R7	294900.335	111	590022.670	590022.842	591119.504
217	TN+F+R6	275744.249	112	551712.498	551712.673	552819.213

WARNING: Log-likelihood -275883 of TN+F+R7 worse than TN+F+R6 -275744

218	TN+F+R7	275883.229	114	551994.457	551994.639	553120.935
230	TNe+R6	294866.812	109	589951.624	589951.790	591028.695

WARNING: Log-likelihood -295040 of TNe+R7 worse than TNe+R6 -294867

231	TNe+R7	295039.704	111	590301.408	590301.580	591398.242
243	HKY+F+R6	275744.268	111	551710.537	551710.709	552807.371

WARNING: Log-likelihood -275883 of HKY+F+R7 worse than HKY+F+R6 -275744

244	HKY+F+R7	275882.954	113	551991.908	551992.087	553108.505
256	K2P+R6	294867.848	108	589951.697	589951.860	591018.887

WARNING: Log-likelihood -295036 of K2P+R7 worse than K2P+R6 -294868

257	K2P+R7	295036.248	110	590292.495	590292.664	591379.448
269	F81+F+R6	281321.986	110	562863.972	562864.141	563950.925

WARNING: Log-likelihood -281435 of F81+F+R7 worse than F81+F+R6 -281322

270	F81+F+R7	281435.009	112	563094.018	563094.193	564200.733
282	JC+R6	298828.809	107	597871.618	597871.778	598928.926

WARNING: Log-likelihood -298978 of JC+R7 worse than JC+R6 -298829

283	JC+R7	298978.479	109	598174.958	598175.124	599252.029
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Akaike Information Criterion: K3Pu+F+R6
Corrected Akaike Information Criterion: K3Pu+F+R6
Bayesian Information Criterion: HKY+F+R6
Best-fit model: HKY+F+R6 chosen according to BIC

All model information printed to BHV1_plus.txt.model.gz
CPU time for ModelFinder: 2099.657 seconds (0h:34m:59s)
Wall-clock time for ModelFinder: 2141.563 seconds (0h:35m:41s)

NOTE: 26 MB RAM (0 GB) is required!
Estimate model parameters (epsilon = 0.100)
1. Initial log-likelihood: -275744.268
Optimal log-likelihood: -275744.201
Rate parameters: A-C: 1.00000 A-G: 5.94832 A-T: 1.00000 C-G: 1.00000 C-T:
5.94832 G-T: 1.00000

Base frequencies: A: 0.135 C: 0.359 G: 0.366 T: 0.140
Site proportion and rates: (0.354,0.314) (0.173,0.317) (0.194,0.317) (0.203,0.317)
(0.062,2.913) (0.013,41.084)
Parameters optimization took 1 rounds (0.461 sec)
Computing ML distances based on estimated model parameters...
Computing ML distances took 0.090991 sec (of wall-clock time) 0.089927 sec(of CPU
time)
Computing RapidNJ tree took 0.000206 sec (of wall-clock time) 0.000202 sec (of CPU
time)
Log-likelihood of RapidNJ tree: -275992.886

INITIALIZING CANDIDATE TREE SET

Generating 98 parsimony trees... 6.211 second
Computing log-likelihood of 98 initial trees ... 3.554 seconds
Current best score: -275744.201

Do NNI search on 20 best initial trees
Estimate model parameters (epsilon = 0.100)
BETTER TREE FOUND at iteration 1: -275743.975
Estimate model parameters (epsilon = 0.100)
BETTER TREE FOUND at iteration 2: -275695.937
Iteration 10 / LogL: -275707.665 / Time: 0h:0m:16s
Iteration 20 / LogL: -275707.727 / Time: 0h:0m:20s
Finish initializing candidate tree set (7)
Current best tree score: -275695.937 / CPU time: 20.136
Number of iterations: 20

OPTIMIZING CANDIDATE TREE SET

Iteration 30 / LogL: -275721.143 / Time: 0h:0m:27s (0h:1m:8s left)
Iteration 40 / LogL: -275730.556 / Time: 0h:0m:34s (0h:0m:55s left)
Iteration 50 / LogL: -275707.019 / Time: 0h:0m:41s (0h:0m:43s left)
Estimate model parameters (epsilon = 0.100)
BETTER TREE FOUND at iteration 52: -275692.999
Estimate model parameters (epsilon = 0.100)
BETTER TREE FOUND at iteration 59: -275690.163
Iteration 60 / LogL: -275730.592 / Time: 0h:0m:50s (0h:1m:24s left)
Estimate model parameters (epsilon = 0.100)
BETTER TREE FOUND at iteration 69: -275688.120
Iteration 70 / LogL: -275701.972 / Time: 0h:0m:58s (0h:1m:23s left)
Estimate model parameters (epsilon = 0.100)
BETTER TREE FOUND at iteration 74: -275682.327
Iteration 80 / LogL: -275692.742 / Time: 0h:1m:7s (0h:1m:20s left)
Estimate model parameters (epsilon = 0.100)
UPDATE BEST LOG-LIKELIHOOD: -275682.005
Iteration 90 / LogL: -275684.513 / Time: 0h:1m:16s (0h:1m:12s left)
Estimate model parameters (epsilon = 0.100)
UPDATE BEST LOG-LIKELIHOOD: -275681.644
Iteration 100 / LogL: -275700.647 / Time: 0h:1m:26s (0h:1m:4s left)
Iteration 110 / LogL: -275701.895 / Time: 0h:1m:33s (0h:0m:54s left)
Iteration 120 / LogL: -275686.200 / Time: 0h:1m:41s (0h:0m:46s left)
Iteration 130 / LogL: -275685.663 / Time: 0h:1m:50s (0h:0m:37s left)
Iteration 140 / LogL: -275684.252 / Time: 0h:1m:57s (0h:0m:28s left)
UPDATE BEST LOG-LIKELIHOOD: -275681.642
Iteration 150 / LogL: -275681.642 / Time: 0h:2m:4s (0h:0m:20s left)
Estimate model parameters (epsilon = 0.100)
UPDATE BEST LOG-LIKELIHOOD: -275681.448
Iteration 160 / LogL: -275684.089 / Time: 0h:2m:11s (0h:0m:11s left)

Iteration 170 / LogL: -275684.399 / Time: 0h:2m:19s (0h:0m:3s left)
TREE SEARCH COMPLETED AFTER 175 ITERATIONS / Time: 0h:2m:23s

FINALIZING TREE SEARCH

Performs final model parameters optimization

Estimate model parameters (epsilon = 0.010)

1. Initial log-likelihood: -275681.448

2. Current log-likelihood: -275681.092

3. Current log-likelihood: -275681.056

4. Current log-likelihood: -275681.045

Optimal log-likelihood: -275681.035

Rate parameters: A-C: 1.00000 A-G: 5.99417 A-T: 1.00000 C-G: 1.00000 C-T:
5.99417 G-T: 1.00000

Base frequencies: A: 0.135 C: 0.359 G: 0.366 T: 0.140

Site proportion and rates: (0.204,0.317) (0.195,0.317) (0.174,0.317) (0.356,0.317)
(0.060,3.143) (0.012,42.583)

Parameters optimization took 4 rounds (1.837 sec)

BEST SCORE FOUND : -275681.035

Total tree length: 0.356

Total number of iterations: 175

CPU time used for tree search: 138.770 sec (0h:2m:18s)

Wall-clock time used for tree search: 142.236 sec (0h:2m:22s)

Total CPU time used: 141.520 sec (0h:2m:21s)

Total wall-clock time used: 144.915 sec (0h:2m:24s)

Analysis results written to:

IQ-TREE report:	BHV1_plus.txt.iqtree
Maximum-likelihood tree:	BHV1_plus.txt.treefile
Likelihood distances:	BHV1_plus.txt.mldist
Screen log file:	BHV1_plus.txt.log

Date and Time: Sat Jan 29 15:24:50 2022