

Supplementary material 4

The classification of the CACTA elements identified was verified using another phylogenetic analysis tool (iqTree <http://www.iqtree.org/>) using default parameters.

IQ-TREE 1.6.11 built Jun 6 2019

Input file name: 347.fa

Type of analysis: ModelFinder + tree reconstruction + ultrafast bootstrap (1000 replicates)

Random seed number: 627311

REFERENCES

To cite ModelFinder please use:

Subha Kalyaanamoorthy, Bui Quang Minh, Thomas KF Wong, Arndt von Haeseler, and Lars S Jermiin (2017) ModelFinder: Fast model selection for accurate phylogenetic estimates. *Nature Methods*, 14:587–589.
<https://doi.org/10.1038/nmeth.4285>

To cite IQ-TREE please use:

Lam-Tung Nguyen, Heiko A. Schmidt, Arndt von Haeseler, and Bui Quang Minh (2015) IQ-TREE: A fast and effective stochastic algorithm for estimating maximum likelihood phylogenies. *Mol Biol Evol*, 32:268-274.
<https://doi.org/10.1093/molbev/msu300>

Since you used ultrafast bootstrap (UFBoot) please also cite:

Diep Thi Hoang, Olga Chernomor, Arndt von Haeseler, Bui Quang Minh, and Le Sy Vinh (2017) UFBoot2: Improving the ultrafast bootstrap approximation. *Mol Biol Evol*, in press.
<https://doi.org/10.1093/molbev/msx281>

SEQUENCE ALIGNMENT

Input data: 347 sequences with 779 nucleotide sites

Number of constant sites: 217 (= 27.8562% of all sites)

Number of invariant (constant or ambiguous constant) sites: 217 (= 27.8562% of all sites)

Number of parsimony informative sites: 501

Number of distinct site patterns: 641

ModelFinder

Best-fit model according to BIC: TVM+F+I+G4

List of models sorted by BIC scores:

Model	LogL	AIC	w-AIC	AICc	w-AICc	BIC	w-BIC
TVM+F+I+G4		-24007.5878	49411.1756 + 0.7238	61608.7256 - 0.0000	52662.4673 + 0.9611		
GTR+F+I+G4		-24007.5511	49413.1021 + 0.2762	61800.4439 - 0.0000	52669.0518 - 0.0357		
K3Pu+F+I+G4		-24020.3164	49432.6328 - 0.0000	61264.6328 - 0.0000	52674.6085 - 0.0022		
TPM3+F+I+G4		-24021.9289	49435.8577 - 0.0000	61267.8577 - 0.0000	52677.8334 - 0.0004		
TPM3u+F+I+G4		-24021.9290	49435.8580 - 0.0000	61267.8580 - 0.0000	52677.8337 - 0.0004		
TIM+F+I+G4	-24020.2996	49434.5993 - 0.0000	61447.0931 - 0.0000	52681.2330 - 0.0001			
TIM3+F+I+G4	-24021.8559	49437.7119 - 0.0000	61450.2057 - 0.0000	52684.3456 - 0.0000			
TVM+F+G4	-24021.8742	49437.7483 - 0.0000	61450.2422 - 0.0000	52684.3820 - 0.0000			
GTR+F+G4	-24021.7131	49439.4262 - 0.0000	61636.9762 - 0.0000	52690.7179 - 0.0000			
TPM2u+F+I+G4		-24031.2879	49454.5757 - 0.0000	61286.5757 - 0.0000	52696.5514 - 0.0000		
TPM2+F+I+G4		-24031.2912	49454.5824 - 0.0000	61286.5824 - 0.0000	52696.5581 - 0.0000		
K3Pu+F+G4	-24035.0534	49460.1068 - 0.0000	61116.0105 - 0.0000	52697.4245 - 0.0000			
HKY+F+I+G4		-24035.5816	49461.1632 - 0.0000	61117.0668 - 0.0000	52698.4809 - 0.0000		
TPM3u+F+G4		-24036.1410	49462.2820 - 0.0000	61118.1857 - 0.0000	52699.5997 - 0.0000		
TPM3+F+G4		-24036.1411	49462.2821 - 0.0000	61118.1858 - 0.0000	52699.5998 - 0.0000		
TIM2+F+I+G4	-24031.2245	49456.4489 - 0.0000	61468.9428 - 0.0000	52703.0826 - 0.0000			
TIM+F+G4	-24034.9560	49461.9119 - 0.0000	61293.9119 - 0.0000	52703.8876 - 0.0000			
TN+F+I+G4	-24035.5681	49463.1362 - 0.0000	61295.1362 - 0.0000	52705.1119 - 0.0000			
TIM3+F+G4	-24035.9287	49463.8574 - 0.0000	61295.8574 - 0.0000	52705.8331 - 0.0000			
TPM2u+F+G4		-24046.2579	49482.5157 - 0.0000	61138.4193 - 0.0000	52719.8334 - 0.0000		
TPM2+F+G4		-24046.2589	49482.5177 - 0.0000	61138.4214 - 0.0000	52719.8354 - 0.0000		
HKY+F+G4	-24050.4414	49488.8829 - 0.0000	60972.9305 - 0.0000	52721.5425 - 0.0000			
TIM2+F+G4	-24046.1967	49484.3934 - 0.0000	61316.3934 - 0.0000	52726.3691 - 0.0000			

TN+F+G4	-24050.3544	49490.7087	- 0.0000	61146.6124	- 0.0000	52728.0264	- 0.0000
TVMe+I+G4	-24106.5828	49603.1657	- 0.0000	61259.0693	- 0.0000	52840.4834	- 0.0000
SYM+I+G4	-24105.5405	49603.0810	- 0.0000	61435.0810	- 0.0000	52845.0567	- 0.0000
TVMe+G4	-24119.8366	49627.6733	- 0.0000	61111.7209	- 0.0000	52860.3329	- 0.0000
SYM+G4	-24119.1282	49628.2563	- 0.0000	61284.1599	- 0.0000	52865.5740	- 0.0000
TIM3e+I+G4	-24148.9243	49685.8486	- 0.0000	61169.8962	- 0.0000	52918.5082	- 0.0000
TIM2e+I+G4	-24153.3377	49694.6755	- 0.0000	61178.7231	- 0.0000	52927.3351	- 0.0000
TIM3e+G4	-24162.4044	49710.8087	- 0.0000	61027.0911	- 0.0000	52938.8104	- 0.0000
TIM2e+G4	-24168.0232	49722.0463	- 0.0000	61038.3287	- 0.0000	52950.0480	- 0.0000
K3P+I+G4	-24168.2603	49722.5205	- 0.0000	61038.8029	- 0.0000	52950.5222	- 0.0000
TIMe+I+G4	-24166.9281	49721.8562	- 0.0000	61205.9038	- 0.0000	52954.5159	- 0.0000
K3P+G4	-24182.4352	49748.8705	- 0.0000	60901.3356	- 0.0000	52972.2141	- 0.0000
TIMe+G4	-24181.4779	49748.9559	- 0.0000	61065.2382	- 0.0000	52976.9575	- 0.0000
K2P+I+G4	-24187.6445	49759.2890	- 0.0000	60911.7542	- 0.0000	52982.6327	- 0.0000
TNe+I+G4	-24186.3016	49758.6032	- 0.0000	61074.8856	- 0.0000	52986.6049	- 0.0000
K2P+G4	-24201.8953	49785.7906	- 0.0000	60778.2504	+ 1.0000	53004.4762	- 0.0000
TNe+G4	-24200.9210	49785.8420	- 0.0000	60938.3071	- 0.0000	53009.1857	- 0.0000
F81+F+I+G4	-24453.2052	50294.4105	- 0.0000	61778.4581	- 0.0000	53527.0702	- 0.0000
F81+F+G4	-24467.7198	50321.4396	- 0.0000	61637.7220	- 0.0000	53549.4413	- 0.0000
JC+I+G4	-24592.9869	50567.9737	- 0.0000	61560.4335	- 0.0000	53786.6594	- 0.0000
JC+G4	-24607.6550	50595.3100	- 0.0000	61431.4463	- 0.0000	53809.3376	- 0.0000
K3Pu+F+I	-24645.1706	50680.3413	- 0.0000	62336.2449	- 0.0000	53917.6589	- 0.0000
TVM+F+I	-24639.1124	50672.2247	- 0.0000	62684.7186	- 0.0000	53918.8584	- 0.0000
TIM+F+I	-24645.1234	50682.2468	- 0.0000	62514.2468	- 0.0000	53924.2224	- 0.0000
GTR+F+I	-24639.0832	50674.1665	- 0.0000	62871.7165	- 0.0000	53925.4582	- 0.0000
TPM3u+F+I	-24649.2321	50688.4642	- 0.0000	62344.3678	- 0.0000	53925.7818	- 0.0000
TPM3+F+I	-24649.2321	50688.4642	- 0.0000	62344.3678	- 0.0000	53925.7819	- 0.0000
TIM3+F+I	-24649.1853	50690.3706	- 0.0000	62522.3706	- 0.0000	53932.3462	- 0.0000
HKY+F+I	-24658.4488	50704.8976	- 0.0000	62188.9452	- 0.0000	53937.5573	- 0.0000
TPM2u+F+I	-24657.7044	50705.4088	- 0.0000	62361.3124	- 0.0000	53942.7264	- 0.0000
TPM2+F+I	-24657.7054	50705.4107	- 0.0000	62361.3144	- 0.0000	53942.7284	- 0.0000
TN+F+I	-24658.3996	50706.7991	- 0.0000	62362.7028	- 0.0000	53944.1168	- 0.0000
TIM2+F+I	-24657.6563	50707.3126	- 0.0000	62539.3126	- 0.0000	53949.2883	- 0.0000
K3Pu+F	-24738.3373	50864.6746	- 0.0000	62348.7222	- 0.0000	54097.3343	- 0.0000
TVM+F	-24732.1141	50856.2281	- 0.0000	62688.2281	- 0.0000	54098.2038	- 0.0000
TIM+F	-24738.1381	50866.2762	- 0.0000	62522.1798	- 0.0000	54103.5939	- 0.0000
TPM3+F	-24741.6669	50871.3338	- 0.0000	62355.3815	- 0.0000	54103.9935	- 0.0000
TPM3u+F	-24741.6721	50871.3443	- 0.0000	62355.3919	- 0.0000	54104.0039	- 0.0000
GTR+F	-24731.9173	50857.8347	- 0.0000	62870.3285	- 0.0000	54104.4684	- 0.0000
TIM3+F	-24741.4750	50872.9501	- 0.0000	62528.8537	- 0.0000	54110.2677	- 0.0000
HKY+F	-24751.4078	50888.8155	- 0.0000	62205.0979	- 0.0000	54116.8172	- 0.0000
TPM2+F	-24751.2001	50890.4002	- 0.0000	62374.4478	- 0.0000	54123.0598	- 0.0000
TPM2u+F	-24751.2004	50890.4008	- 0.0000	62374.4484	- 0.0000	54123.0605	- 0.0000
TN+F	-24751.2047	50890.4094	- 0.0000	62374.4570	- 0.0000	54123.0690	- 0.0000

TIM2+F	-24750.9948	50891.9896	- 0.0000	62547.8933	- 0.0000	54129.3073	- 0.0000
TVMe+I	-24776.7938	50941.5877	- 0.0000	62425.6353	- 0.0000	54174.2473	- 0.0000
SYM+I	-24775.3854	50940.7709	- 0.0000	62596.6745	- 0.0000	54178.0886	- 0.0000
TIM3e+I	-24801.3170	50988.6339	- 0.0000	62304.9163	- 0.0000	54216.6356	- 0.0000
K3P+I	-24807.7410	50999.4821	- 0.0000	62151.9472	- 0.0000	54222.8257	- 0.0000
TIMe+I	-24806.3703	50998.7407	- 0.0000	62315.0230	- 0.0000	54226.7423	- 0.0000
TIM2e+I	-24809.8684	51005.7369	- 0.0000	62322.0192	- 0.0000	54233.7385	- 0.0000
K2P+I	-24826.3340	51034.6680	- 0.0000	62027.1277	- 0.0000	54253.3536	- 0.0000
TNe+I	-24824.9460	51033.8920	- 0.0000	62186.3572	- 0.0000	54257.2357	- 0.0000
TVMe	-24875.2561	51136.5122	- 0.0000	62452.7945	- 0.0000	54364.5138	- 0.0000
SYM	-24874.1798	51136.3595	- 0.0000	62620.4071	- 0.0000	54369.0192	- 0.0000
TIM3e	-24897.4236	51178.8471	- 0.0000	62331.3123	- 0.0000	54402.1908	- 0.0000
K3P	-24904.2001	51190.4002	- 0.0000	62182.8600	- 0.0000	54409.0858	- 0.0000
TIMe	-24903.1542	51190.3084	- 0.0000	62342.7735	- 0.0000	54413.6521	- 0.0000
TIM2e	-24909.4271	51202.8542	- 0.0000	62355.3194	- 0.0000	54426.1979	- 0.0000
K2P	-24922.8810	51225.7620	- 0.0000	62061.8984	- 0.0000	54439.7896	- 0.0000
TNe	-24921.7500	51225.5000	- 0.0000	62217.9598	- 0.0000	54444.1857	- 0.0000
F81+F+I	-25069.6446	51525.2892	- 0.0000	62841.5716	- 0.0000	54753.2909	- 0.0000
F81+F	-25162.9605	51709.9210	- 0.0000	62862.3861	- 0.0000	54933.2646	- 0.0000
JC+I	-25217.5610	51815.1220	- 0.0000	62651.2583	- 0.0000	55029.1496	- 0.0000
JC	-25312.9951	52003.9903	- 0.0000	62687.3611	- 0.0000	55213.3599	- 0.0000

AIC, w-AIC : Akaike information criterion scores and weights.

AICc, w-AICc : Corrected AIC scores and weights.

BIC, w-BIC : Bayesian information criterion scores and weights.

Plus signs denote the 95% confidence sets.

Minus signs denote significant exclusion.

SUBSTITUTION PROCESS

Model of substitution: TVM+F+I+G4

Rate parameter R:

A-C: 0.8730

A-G: 2.7783

A-T: 1.4067

C-G: 0.9892

C-T: 2.7783

G-T: 1.0000

State frequencies: (empirical counts from alignment)

pi(A) = 0.2826
pi(C) = 0.2297
pi(G) = 0.2022
pi(T) = 0.2856

Rate matrix Q:

A	-0.9466	0.1631	0.4568	0.3267
C	0.2006	-1.009	0.1626	0.6452
G	0.6385	0.1848	-1.056	0.2322
T	0.3233	0.519	0.1644	-1.007

Model of rate heterogeneity: Invar+Gamma with 4 categories
Proportion of invariable sites: 0.01821
Gamma shape alpha: 1.604

Category	Relative_rate	Proportion
0	0	0.01821
1	0.2454	0.2454
2	0.6162	0.2454
3	1.076	0.2454
4	2.137	0.2454

Relative rates are computed as MEAN of the portion of the Gamma distribution falling in the category.

MAXIMUM LIKELIHOOD TREE

Log-likelihood of the tree: -23855.2556 (s.e. 873.4117)
Unconstrained log-likelihood (without tree): -4878.1706
Number of free parameters (#branches + #model parameters): 698
Akaike information criterion (AIC) score: 49106.5113
Corrected Akaike information criterion (AICc) score: 61304.0613
Bayesian information criterion (BIC) score: 52357.8030

Total tree length (sum of branch lengths): 25.3625
Sum of internal branch lengths: 12.4962 (49.2702% of tree length)

WARNING: 58 near-zero internal branches (<0.0013) should be treated with caution
Such branches are denoted by '*' in the figure below

NOTE: Tree is UNROOTED although outgroup taxon 'HanXRQChr11_78963679_78964101' is drawn at root

Numbers in parentheses are SH-aLRT support (%) / ultrafast bootstrap support (%)

```

+--HanXRQChr11_78963679_78964101
|
|   +--HanXRQChr01_34887426_34894282
|   +**| (0/92)
|   | | +**HanXRQChr12_24613340_24614343
|   | +**| (0/95)
|   |   +**HanXRQChr08_22937900_22939039
|   +--| (87.6/98)
|   | +--HanXRQChr13_45702842_45703840
| +**| (0/98)
| | +--HanXRQChr17_205330461_205331450
+--| (76.7/100)
| +--HanXRQChr03_26205754_26213308
|
|   +--HanXRQChr04_67540092_67541320
|   +--| (89.9/100)
|   | | +--HanXRQChr06_27984911_27988051
|   | | +--| (90.5/100)
|   | | | +--HanXRQChr04_12175865_12181403
|   | | | +**| (0/55)
|   | | | | +--HanXRQChr17_211327788_211333859
|   | | | | +--| (90.6/100)
|   | | | | | +**HanXRQChr05_59284493_59290538
|   | | | | | +--| (98.4/100)
|   | | | | |   +**HanXRQChr05_106376295_106382341
|   | | | | | +**| (0/93)
|   | | | | | | +--HanXRQChr09_48889131_48889670
|   | | | | | | +--| (83.6/99)
|   | | | | | | | +--HanXRQChr15_55516101_55518531
|   | | | | | | +--| (98.8/99)
|   | | | | | | | +--HanXRQChr03_57480187_57481416
|   | | | | | | | +**| (0/80)
|   | | | | | | | | +--HanXRQChr05_166779247_166780763
|   | | | | | | | | +--| (79.5/100)
|   | | | | | | | |   +--HanXRQChr12_94875864_94876484
|   | | | | | | | | +--| (80.6/99)
|   | | | | | | | | | +--HanXRQChr04_92418435_92419412
|   | | | | | | | | | +--| (100/100)
|   | | | | | | | | | | +**HanXRQChr06_53262309_53263292
|   | | | | | | | | | | +--| (75.5/100)
|   | | | | | | | | | |   +--HanXRQChr05_9034545_9035531
|   | | | | | | | | | | +--| (95.9/99)

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[illegible]

[illegible]

[illegible]

												+-- (81.1/78)
												+--
HanXRQChr07_11945240_11945839												
												+-- (86.5/100)
												+--
HanXRQChr05_23977914_23979210												
												+-- (93.4/99)
												+--
HanXRQChr03_50693386_50694309												
												+-- (84/98)
												+--
HanXRQChr08_40474325_40480066												
												+-- (68.7/85)
												+--
HanXRQChr02_24653810_24657437												
												+-- (87.4/100)
												+--
HanXRQChr14_68289895_68297518												
												+-- (87/100)
												+--
HanXRQChr14_68273516_68281146												
												+-- (85.8/90)
+**HanXRQChr02_147295547_147297741												
												+-- (88.1/100)
+**HanXRQChr09_142942803_142944567												
												+-- (74.4/100)
												+--
HanXRQChr13_96620660_96621156												
												+-- (89.6/100)
												+--
HanXRQChr04_132271481_132272204												
												+-- (72.9/100)
												+--
HanXRQChr14_153324342_153328229												
												+-- (74.5/100)
												+--
HanXRQChr10_85192350_85197513												
												+-- (96.3/91)
												+--
HanXRQChr06_97006962_97010930												
												+-- (84.7/100)

[illegible]

															+	+	+		(96.1/100)
+**HanXRQChr13_179805528_179808054																			
															+	+	+		(0/56)
																		+	+
HanXRQChr05_64422906_64424659																			
																+	+	+	
																		+	+
HanXRQChr13_7315803_7323380																			
															+	+	+		(81.3/61)
																		+	+
HanXRQChr15_23213675_23214340																			
															+	+	+		(0/46)
																		+	+
HanXRQChr11_127530325_127537865																			
																+	+	+	
																		+	+
HanXRQChr12_23644236_23645297																			
															+	+	+		(92.4/92)
																		+	+
HanXRQChr14_116526279_116533821																			
																+	+	+	
																		+	+
HanXRQChr17_205323932_205330231																			
															+	+	+		(93.6/90)
																		+	+
+**HanXRQChr17_3057459_3059571																			
															+	+	+		(0/88)
																		+	+
HanXRQChr13_169241697_169244853																			
																+	+	+	
																		+	+
HanXRQChr01_90452614_90460077																			
															+	+	+		(79.3/100)
																		+	+
HanXRQChr13_45704069_45710378																			
															+	+	+		(71.6/100)
																		+	+
+**HanXRQChr08_22931465_22937801																			
															+	+	+		(89.5/100)
																		+	+
HanXRQChr13_196274607_196275703																			
															+	+	+		(90.5/94)

	+--
HanXRQChr13_48436772_48438877	
	+-- (85.6/89)
	+--
HanXRQChr15_129312466_129317224	
	+** (0/57)
	+--
HanXRQChr02_147809574_147817424	
	+-- (82/89)
	+--
HanXRQChr14_171031165_171032099	
	+-- (99.9/100)
	+--
HanXRQChr10_113962499_113970363	
	+** (0/81)
	+--
HanXRQChr11_23755532_23757425	
	+** (0/67)
	+--
HanXRQChr01_4643702_4650088	
	+-- (85.6/97)
	+--
HanXRQChr08_88222000_88228288	
	+-- (22.8/91)
	+--
HanXRQChr15_150283897_150291604	
	+-- (96.6/99)
	+--
HanXRQChr03_46527653_46534444	
	+-- (66.4/100)
	+--
HanXRQChr06_51391635_51395795	
	+-- (94.8/100)
	+--
HanXRQChr07_44435735_44436200	
	+-- (37.5/70)
	+--
HanXRQChr10_167884487_167885281	
	+-- (43.7/75)
	+--
HanXRQChr16_149753884_149754258	
	+-- (21.8/78)
	+--
HanXRQChr01_98528860_98530430	

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	+	--		(86.9/100)					
		+	--	HanXRQChr17_171676962_171677479					
	+	--		(75.8/100)					
		+	--	HanXRQChr04_11014761_11015279					
	+	--		(75.4/100)					
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	+	--	HanXRQChr10_36325499_36326037						
+	--		(71.1/69)						
	+	--	HanXRQChr09_16583017_16583476						
	+	--		(100/100)					
	+	--	HanXRQChr02_53194187_53194755						
+	--		(85.2/52)						
	+	--	HanXRQChr15_58262815_58263268						
+	--		(78.3/37)						
	+	--	HanXRQChr03_53881858_53882406						
	+	--		(73.9/100)					
	+	**	HanXRQChr15_50520164_50520709						
	+	--		(100/100)					
	+	--	HanXRQChr08_58106590_58107151						
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+--HanXRQChr09_6730323_6730857							
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(91.3/96)							
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(74.7/47)							
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+-- (70.4/96)							
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+** (0/61)							
+**HanXRQChr03_126121322_126121826							
+-- (96.2/100)							
+--HanXRQChr10_78375584_78376088							
+-- (95.5/100)							
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(71.7/55)							
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		+--
	HanXRQChr08_113839738_113840105	
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(74.1/96)		
		+--
	HanXRQChr04_28158629_28159233	
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(100/100)		
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(100/100)		
		+--
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(100/100)		

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

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+-- (93.4/100)			
		+--	
+** (0/92)			
		+--	
+-- (86.6/100)			
		+--	
+-- (89.6/100)			
	+--		
+-- (93.6/98)			
	+--		
+-- (74/98)			
	+--		
+-- (95.2/99)			
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+-- (72/100)			
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CONSENSUS TREE

Consensus tree is constructed from 1000bootstrap trees

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| | | | | +--HanXRQChr09_48889131_48889670
| | | | | +--| (99)
| | | | | +--HanXRQChr15_55516101_55518531
| | | | | +--| (99)
| | | | | +--HanXRQChr03_57480187_57481416
| | | | | +--| (80)
| | | | | | +--HanXRQChr05_166779247_166780763
| | | | | | +--| (100)
| | | | | | +--HanXRQChr12_94875864_94876484
| | | | | | +--| (99)
| | | | | | +--HanXRQChr04_92418435_92419412

```

[illegible]

[illegible]

[illegible]

[illegible]

		+--
HanXRQChr10_85192350_85197513		
		+-- (91)
		+--
HanXRQChr06_97006962_97010930		
		+-- (100)
		+--
HanXRQChr03_159793635_159795071		
		+-- (100)
		+--
HanXRQChr07_88885423_88893193		
		+-- (47)
		+--
HanXRQChr08_109696851_109697593		
		+-- (100)
		+--
HanXRQChr08_39439464_39440150		
		+-- (95)
		+--
HanXRQChr01_140346486_140347133		
		+-- (99)
		+--
HanXRQChr16_117883570_117885696		
		+-- (90)
		+--
HanXRQChr10_225800164_225801136		
		+-- (82)
		+--
HanXRQChr04_79257170_79260978		
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		+--
HanXRQChr09_141496442_141499885		
		+-- (85)
		+--
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		+--
HanXRQChr07_94262118_94263107		
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		+--
HanXRQChr17_170737481_170744938		
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		+--
HanXRQChr04_115339901_115344808		

[illegible]

[illegible]

[illegible]

	+--HanXRQChr09_90613212_90613775								
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	+--HanXRQChr14_164972043_164972420								
	+-- (100)								
	+--HanXRQChr17_171676962_171677479								
	+-- (100)								
	+--HanXRQChr04_11014761_11015279								
	+-- (100)								
	+--HanXRQChr04_11235868_11236386								
	+-- (100)								
	+--HanXRQChr10_36325499_36326037								
	+-- (69)								
	+--HanXRQChr09_16583017_16583476								
	+-- (100)								
	+--HanXRQChr02_53194187_53194755								
	+-- (52)								
	+--HanXRQChr15_58262815_58263268								
	+-- (37)								
	+--HanXRQChr03_53881858_53882406								
	+-- (100)								
	+--HanXRQChr15_50520164_50520709								
	+-- (100)								

				+	--	HanXRQChr08_58106590_58107151			
				+	--	(68)			
				+	--	HanXRQChr04_117734534_117735067			
				+	--	(58)			
				+	--	HanXRQChr07_39909716_39910258			
				+	--	(53)			
				+	--	HanXRQChr11_114599910_114600468			
				+	--	(34)			
				+	--	HanXRQChr08_102456485_102456998			
				+	--	(95)			
				+	--	HanXRQChr03_6367591_6368162			
				+	--	(95)			
				+	--	HanXRQChr08_32332017_32332576			
				+	--	(100)			
				+	--	HanXRQChr05_142623602_142624161			
				+	--	(60)			
				+	--	HanXRQChr10_160816414_160816781			
				+	--	(99)			
				+	--	HanXRQChr09_205724496_205724897			
				+	--	(57)			
				+	--	HanXRQChr05_5609714_5610098			
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[illegible]

	+--HanXRQChr07_12736562_12737068			
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	+--HanXRQChr05_164461706_164462192			
(55)				+--
	+--HanXRQChr13_134302109_134302509			
	+-- (100)			
	+--HanXRQChr10_95181243_95181772			
	+-- (100)			
	+--HanXRQChr17_160614824_160615353			
+-- (51)				
	+--HanXRQChr17_13361200_13361728			
	+-- (100)			
	+--HanXRQChr12_75917343_75917873			
	+-- (100)			
	+--HanXRQChr14_86341928_86342457			
	+-- (100)			
	+--HanXRQChr03_99988684_99989213			
	+-- (100)			
	+--HanXRQChr17_99228227_99228757			
+-- (92)				
	+--HanXRQChr16_15638745_15639274			
	+-- (100)			

	+--HanXRQChr05_144936503_144937032		
+-- (100)			
	+--HanXRQChr02_114840517_114841046		
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	+-- (73)		
	+--HanXRQChr01_29157382_29157877		
	+-- (98)		
	+--HanXRQChr13_104941607_104942137		
	+-- (66)		
	+--HanXRQChr08_25571094_25571648		
	+-- (100)		
	+--HanXRQChr05_44360152_44360708		
	+-- (53)		
	+--HanXRQChr10_187118315_187118736		
			+--
(42)			
	+--HanXRQChr09_8264746_8265314		
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(100)			
+--HanXRQChr16_71647538_71648109			
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(77)			
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	+--HanXRQChr17_31920748_31921235				
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(57)					
	+--HanXRQChr17_84099735_84100241				
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(99)					
	+--HanXRQChr10_11267406_11267923				
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(84)					
	+--HanXRQChr02_131243878_131244246				
	+-- (100)				
	+--HanXRQChr10_168209872_168210240				
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(90)					
	+--HanXRQChr08_113839738_113840105				
					+--
(96)					
	+--HanXRQChr04_28158629_28159233				
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(100)					
	+--HanXRQChr11_39830792_39831397				
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					+--
	HanXRQChr11_133792609_133792984				
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(100)					
					+--
	HanXRQChr11_133775764_133776143				
					+-- (100)
					+--
	HanXRQChr05_62558786_62559318				
					+-- (100)
					+--
	HanXRQChr09_124910897_124911250				

(100)				+--
				+--
HanXRQChr11_30817527_30817892				
				+-- (80)
				+--
HanXRQChr17_68193643_68194142				
				+-- (100)
				+--
HanXRQChr11_94539491_94539990				
				+-- (39)
+--HanXRQChr01_40849696_40850225				
				+--
(90)				
				+--
HanXRQChr11_135844467_135845030				
				+--
(100)				
				+--
HanXRQChr16_45835607_45836135				
				+--
(100)				
+--HanXRQChr04_141436125_141436654				
				+--
(79)				
				+--
HanXRQChr14_73178118_73178607				
				+-- (41)
				+--
HanXRQChr09_74883466_74883949				
				+--
(100)				
				+--
HanXRQChr05_179907532_179908035				
				+-- (25)
				+--
HanXRQChr10_170724767_170725228				
				+--
(95)				
				+--
HanXRQChr11_114441513_114442047				

[illegible]

[illegible]

	+--HanXRQChr07_94174100_94174724							
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	HanXRQChr17_139322691_139323166							
								+--
(100)								
	+--HanXRQChr10_145087013_145087418							
	+-- (100)							
	+--HanXRQChr10_175382210_175382618							
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(100)								
	+--HanXRQChr06_56355680_56356069							
								+--
(93)								
	+--HanXRQChr17_95938863_95939232							
	+-- (99)							
	+--HanXRQChr13_144225259_144225863							
								+--
(92)								
	+--HanXRQChr15_52286990_52287513							
	+-- (100)							
	+--HanXRQChr09_19029933_19030470							
	+-- (100)							
	+--HanXRQChr09_126494259_126494796							
	+-- (100)							
	+--HanXRQChr06_41524728_41525252							
								+--
(86)								

[illegible]

Chromosome	Start	End	Strand	Gene	Feature	Score
HanXRQChr09	59706805	59707181	+	HanXRQChr09_59706805_59707181		
(94)						
HanXRQChr04	65301484	65302016	+	HanXRQChr04_65301484_65302016		
(85)						
HanXRQChr07	35619467	35619941	+	HanXRQChr07_35619467_35619941		
HanXRQChr02	46053364	46053773	+	HanXRQChr02_46053364_46053773		
HanXRQChr10	100532038	100532438	+	HanXRQChr10_100532038_100532438		
HanXRQChr15	125481128	125481695	+	HanXRQChr15_125481128_125481695		
HanXRQChr10	140012131	140012699	+	HanXRQChr10_140012131_140012699		
HanXRQChr15	153093160	153093558	+	HanXRQChr15_153093160_153093558		
HanXRQChr11	77517539	77518062	+	HanXRQChr11_77517539_77518062		
HanXRQChr17	54907212	54907721	+	HanXRQChr17_54907212_54907721		
HanXRQChr09	50143993	50144471	+	HanXRQChr09_50143993_50144471		
HanXRQChr07	67769	68326	+	HanXRQChr07_67769_68326		
HanXRQChr10	170627841	170628410	+	HanXRQChr10_170627841_170628410		
HanXRQChr13	127794694	127795300	+	HanXRQChr13_127794694_127795300		

						+-- (95)
HanXRQChr16_150636591_150640613						
HanXRQChr17_47637609_47642782						
HanXRQChr09_42030904_42038738						
HanXRQChr08_88220498_88221890						
HanXRQChr15_74394306_74402182						
HanXRQChr05_177102059_177102727						
HanXRQChr05_199634091_199642069						
HanXRQChr04_4585394_4586317						
HanXRQChr10_201208107_201211833						

+--HanXRQChr12_94877770_94878735						
+--						
+-- (100)						
		+--				
+-- (92)						
		+--				
+-- (100)						
		+--				
+-- (100)						
	+--					
+-- (98)						
	+--					
+-- (98)						
	+--					
+-- (99)						
	+--HanXRQChr09_26818251_26820777					
+-- (70)						
	+--HanXRQChr03_34702985_34703845					
+-- (97)						
		+--HanXRQChr17_164543226_164545213				
		+-- (93)				
			+--HanXRQChr11_5059413_5062302			
			+-- (100)			
			+--HanXRQChr16_159464039_159466946			
	+-- (100)					
		+--				
		+-- (100)				
		+--HanXRQChr12_8060455_8064354				
	+-- (100)					
	+--HanXRQChr04_4414273_4418183					
+-- (100)						
		+--HanXRQChr16_154231921_154234094				
		+-- (100)				
			+--			

										+-- (100)
										+--
HanXRQChr06_1335657_1337253										
										+-- (95)
										+--HanXRQChr09_1135754_1136217
										+-- (100)
										+--HanXRQChr09_1132214_1133064
										+-- (99)
										+--
HanXRQChr14_171048254_171055488										
										+-- (100)
										+--HanXRQChr02_147305501_147307299
										+-- (96)
										+--HanXRQChr06_47763415_47764638
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										+--HanXRQChr05_52352508_52353847
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										+-- (100)
										+--HanXRQChr03_153476779_153477741
										+-- (99)
										+--HanXRQChr09_192317181_192318492
										+-- (86)
										+--HanXRQChr09_173686390_173688466
										+-- (79)
										+--HanXRQChr07_27412393_27412825
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										+--HanXRQChr07_27480885_27481317
										+-- (100)
										+--HanXRQChr10_167996501_167997306
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										+--HanXRQChr07_94263537_94264736
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										+--HanXRQChr10_200122501_200126511
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										+--HanXRQChr03_159773788_159776353
										+-- (100)
										+--HanXRQChr16_117885695_117887257
										+-- (85)
										+--HanXRQChr16_139387141_139394695
										+-- (100)
										+--HanXRQChr13_70292420_70293133

						+- (100)
						+-HanXRQChr12_74630615_74638291
						+- (100)
						+-HanXRQChr05_32799874_32806012
						+- (100)
						+-HanXRQChr05_66536036_66536958
						+- (99)
						+-HanXRQChr09_42108185_42108601
						+- (100)
						+-HanXRQChr14_70675600_70678361
						+- (99)
						+-HanXRQChr14_79208902_79211665
						+- (91)
						+-HanXRQChr14_77501682_77504443
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						+-HanXRQChr02_175774663_175777915
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						+-HanXRQChr08_40489307_40491198
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						+-HanXRQChr15_104285615_104286058
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						+-HanXRQChr05_209135841_209137273
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|   | +--| (99)
|   |     +--HanXRQChr11_69846093_69853687
|   +--| (98)
|   | | +--HanXRQChr06_20451348_20451704
|   | | +--| (97)
|   | |     +--HanXRQChr13_179591469_179595652
|   +--| (80)
|   | |     +--HanXRQChr12_45905678_45909951
|   | |     +--| (100)
|   | | | +--HanXRQChr15_74224040_74228313
|   | | | +--| (67)
|   | | | | +--HanXRQChr13_2986278_2987762
|   | | | +--| (67)
|   | |     +--HanXRQChr02_4724981_4726023
|   +--| (100)
| | +--HanXRQChr13_135223336_135224153
+--| (100)
    +--HanXRQChr13_196286900_196290049

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Consensus tree in newick format:

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03840:0.0086610080)98:0.0043188648,HanXRQChr17_205330461_205331450:0.0047369591
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anXRQChr04_67540092_67541320:0.0215906904,((HanXRQChr06_27984911_27988051:0.0
130523062,(HanXRQChr04_12175865_12181403:0.0223508270,((((HanXRQChr17_21132778
8_211333859:0.0130875744,(HanXRQChr05_59284493_59290538:0.0000022537,HanXRQC
hr05_106376295_106382341:0.0000022537)100:0.0270169043)100:0.0148907682,((HanXRQC
hr09_48889131_48889670:0.0525394261,HanXRQChr15_55516101_55518531:0.0430714462
)99:0.0253405579,((((((HanXRQChr03_57480187_57481416:0.0472729932,(HanXRQChr05_1
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:0.0113747932)80:0.0000022785,(HanXRQChr04_92418435_92419412:0.0044568713,(HanX
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TIME STAMP

Date and time: Wed Mar 11 09:47:29 2020

Total CPU time used: 1543.728984 seconds (0h:25m:43s)

Total wall-clock time used: 1550.515339 seconds (0h:25m:50s)