Supplementary tables

Table S1 | Number of loci across the genome using different filtering settings for 10 kb non-overlapping windows: minimum read depth (DP), minimum percentage of the window covered by data (PW), and missing data per site (MD).

Filtering setting	Number of total windows	Number of no intra-locus recombination windows	Number of no intra-locus and free inter-locus recombination windows
DP=1, PW=50%, MD=15%	29,730	10,051	6,791
DP=5, PW=50%, MD=15%	19,062	6,701	5,788
DP=1, PW=50%, MD=5%	26,030	9,600	6,476
DP=1, PW=80%, MD=10%	22,652	6,970	5,267

Table S2 | Selection of the best models among the maximum pseudo-likelihood networks in phyloNet 3.6.9.

| Complex	Gene trees	Inferred admixtures	Likelihood	BIC
O. picata	7,310	0	-33,633.58	67,278.88
		1	**-33,559.56**	**67,131.21**
		2	-33,569.10	67,150.56
		3	-33,617.49	67,247.56
		4	-33,979.37	67,971.48
		5	-33,982.37	67,977.62
O. hispanica	7,335	0	-33,326.92	66,665.57
		1	-33,180.89	66,373.86
		2	**-33,153.96**	**66,320.28**
		3	-33,265.29	66,543.14
		4	-33,276.89	66,566.51
		5	-33,637.19	67,287.26
O. lugens	,7323	0	-86,457.1	17,2926.3
		1	-85,643.3	17,1299.0
		2	**-85,014.9**	**17,0042.3**
		3	-86,498.8	17,3010.4
		4	-86,574.7	17,3162.3
		5	-86,095.2	17,2203.3

Supplementary Figures
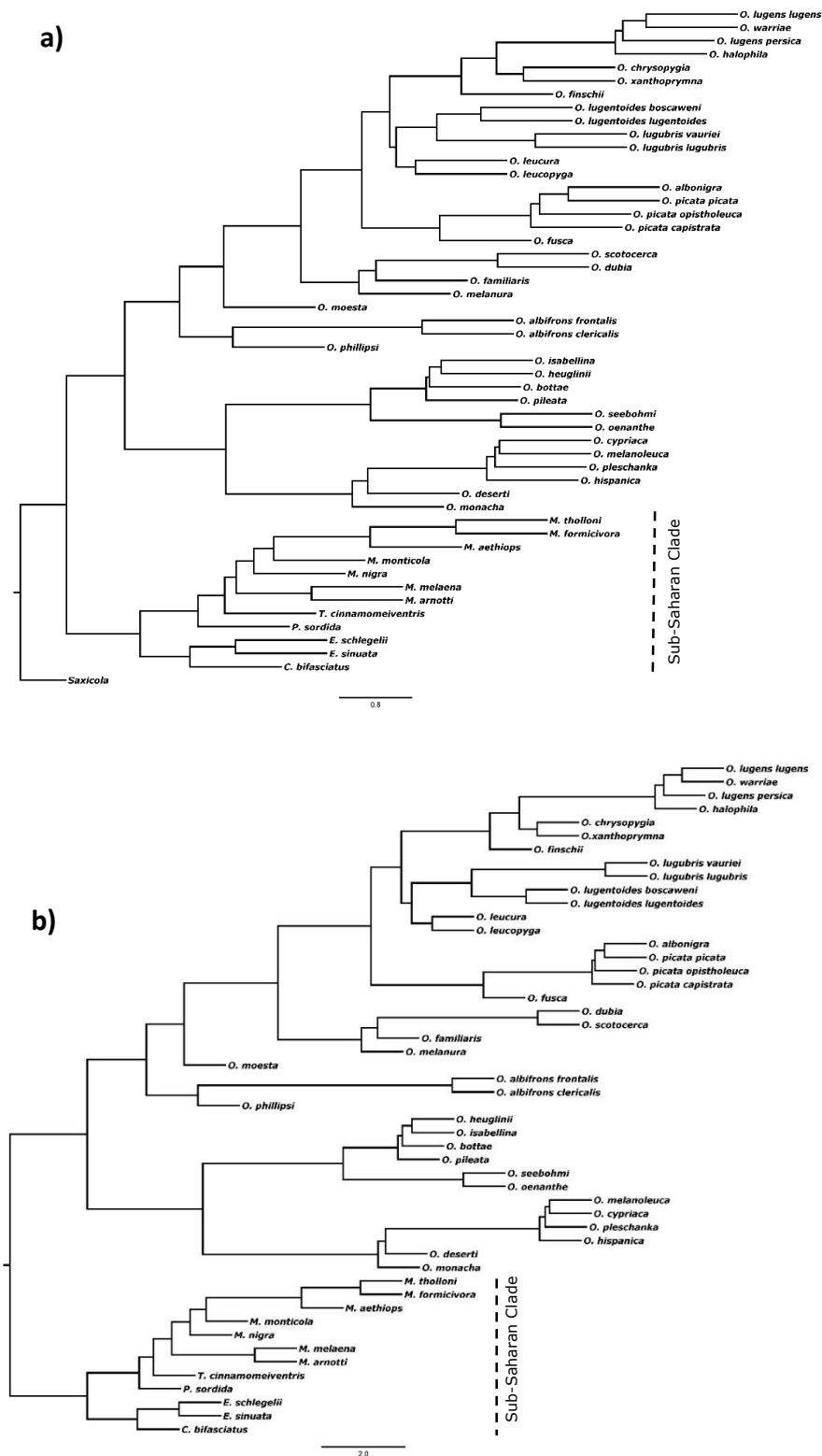
Figure S1 | Genome-wide multispecies coalescent species tree of open-habitat chats estimated in ASTRAL-III. All nodes have 1.0 local posterior probabilities. a) Species tree based on 2,091 BUSCOs, using *Saxicola* as an outgroup. b) Species tree based on 5,788 loci (non-overlapping 10 kb windows across the genome) using the sub-Saharan clade as an outgroup.
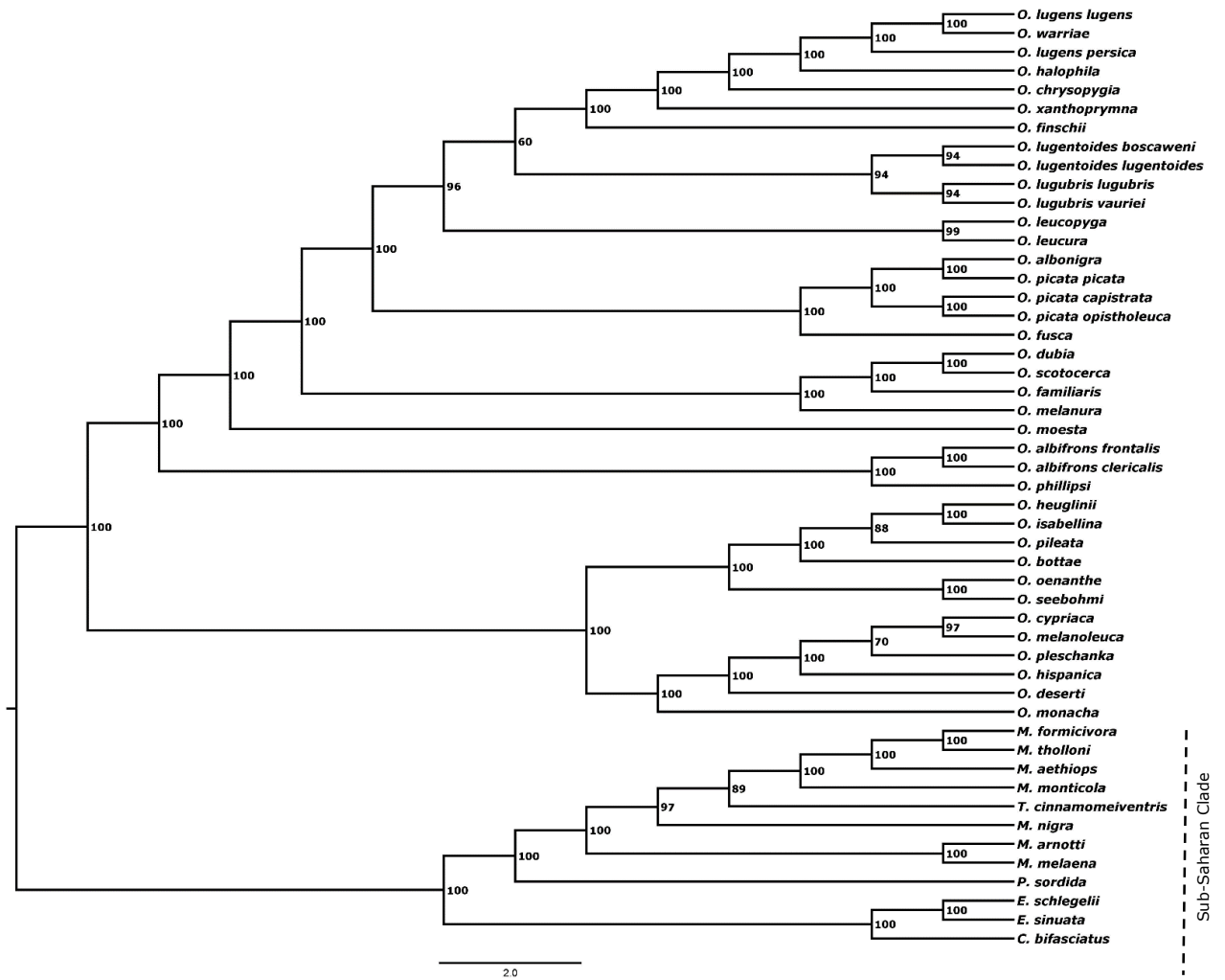
Figure S2 | SNP-based multispecies coalescent species tree of open-habitat chats inferred with SVDquartets in PAUP* 4. Maximum likelihood bootstrap support values are shown above branches.
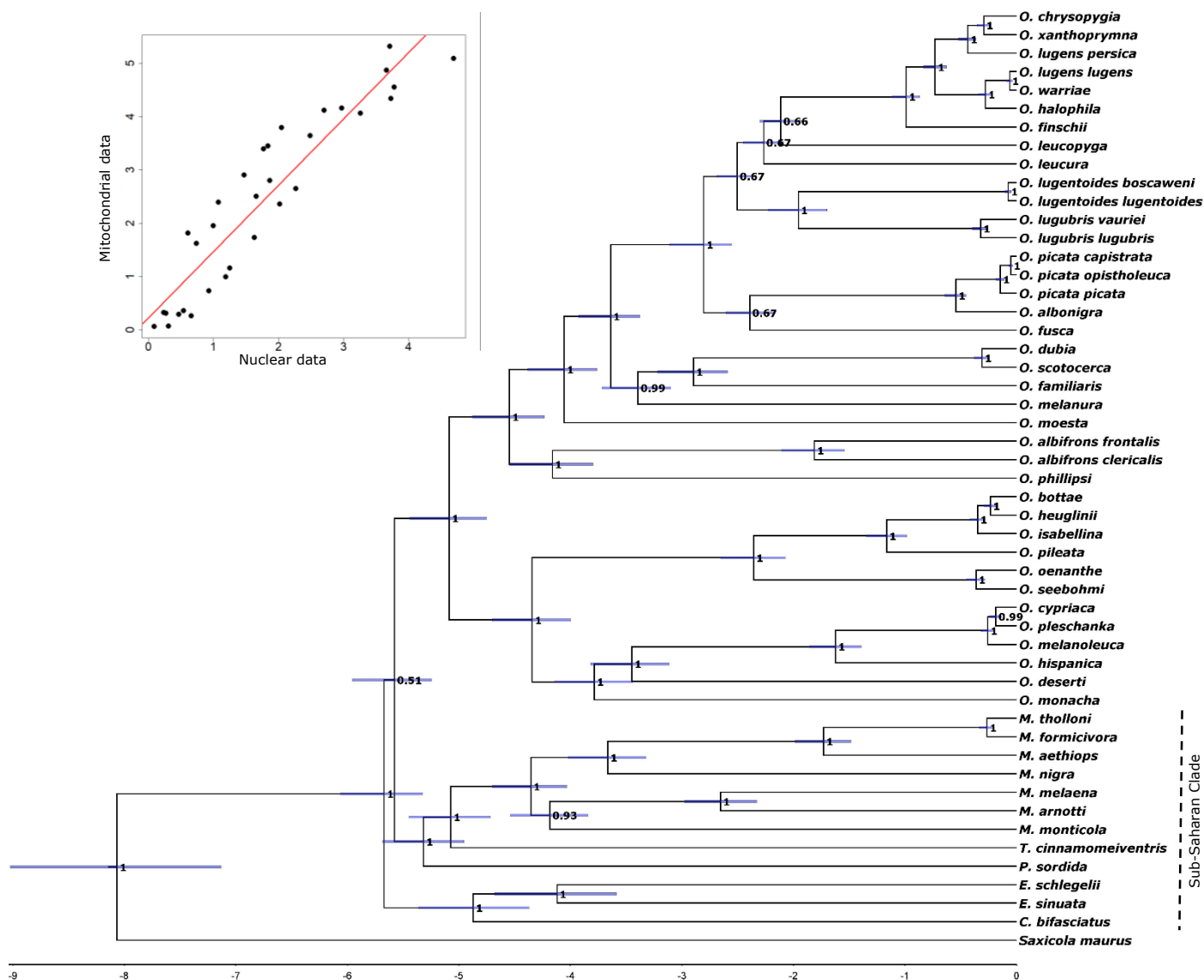
Figure S3 | Time-calibrated maximum clade credibility tree of the BEAST 2.6.6 analyses based on 13 protein-coding mitochondrial genes of open-habitat chats. Blue bars represent the 95% highest posterior density (HPD) distributions for the estimated divergence times. Posterior probabilities are indicated at nodes. The correlation between the dating based on the nuclear (BUSCOs) and mitochondrial data is shown at the top left (Pearson's r=0.93, p<0.001).
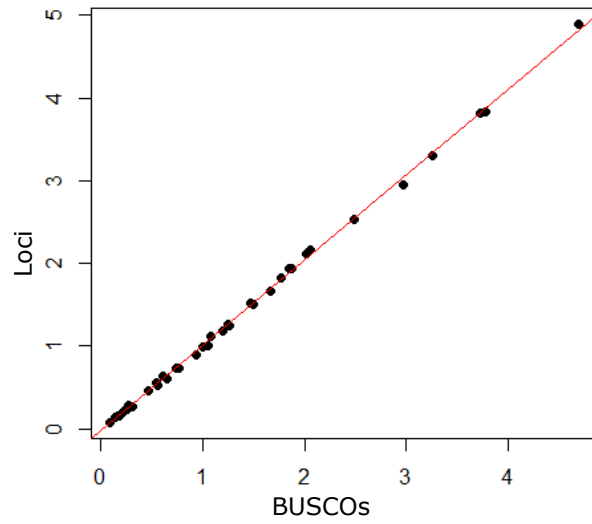
Figure S4 | Correlation between the time calibration based on 1.8 Mb high confidence BUSCOs and 3.8 Mb high confidence loci (10 kb non-overlapping windows across the genome) using RelTime-ML implemented in MEGA 11 (Pearson's r=0.99, p<2.2e-16).
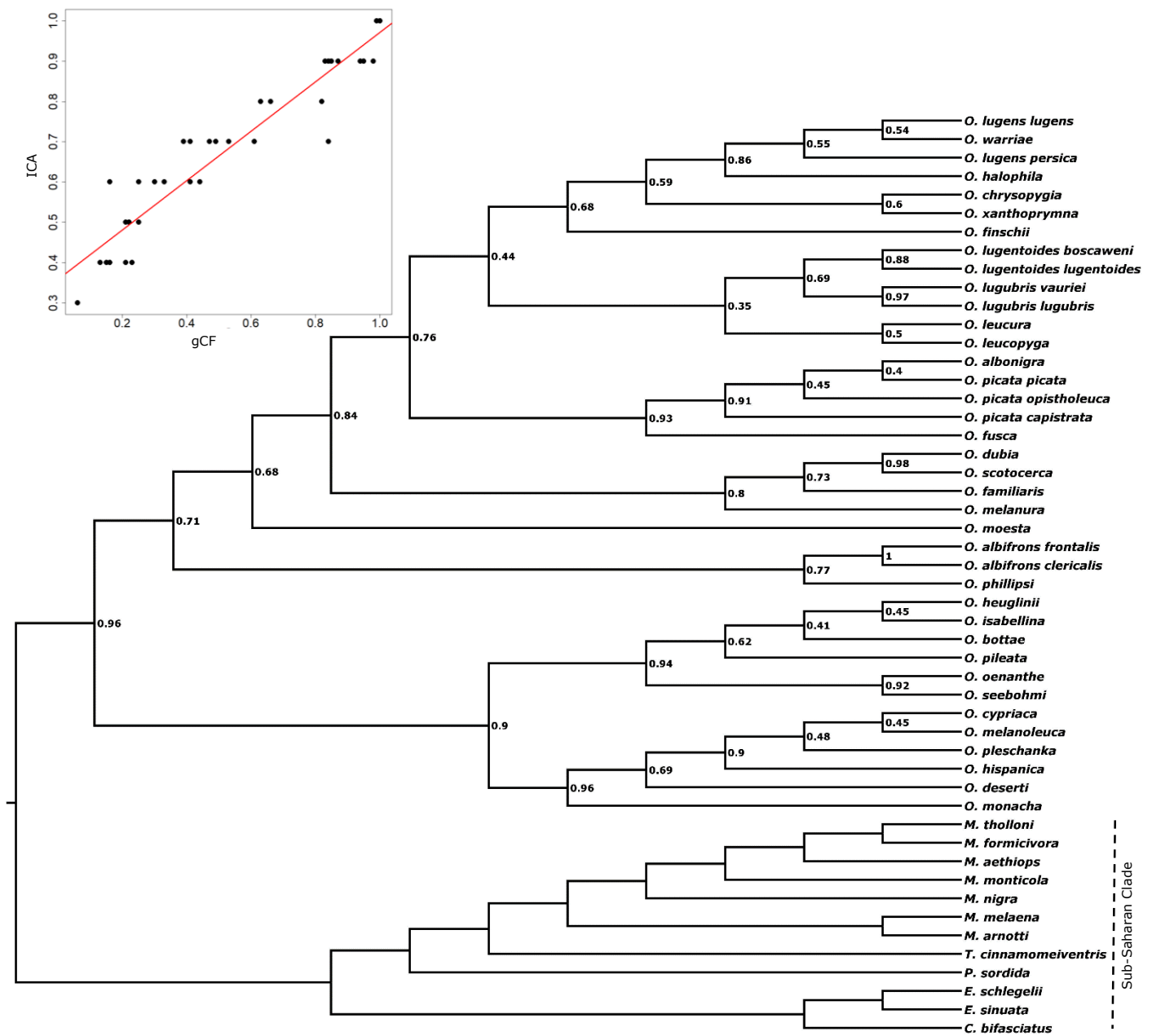
Figure S5 | Genome-wide multispecies coalescent species tree of open-habitat chats estimated in ASTRAL-III. ICA values for 29,730 maximum-likelihood gene trees are shown for each node. The high correlation between the gCF values calculated in IQ-TREE 2.1.2 and ICA values calculated in PhyParts 0.0.1 is shown at the top left (Pearson's r=0.94, p<0.001).