

Supplementary information for:

Runs of homozygosity reveal contrasting histories of inbreeding across global lineages of the edible porcini mushroom, *Boletus edulis*

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Table S1: Descriptive summary of the difference in quality between the two genotyping approaches. From left to right, the lineage specific mean depth of coverage averaged across all sites, the lineage specific mean number of missing sites, and the lineage specific mean frequency of missing sites, for genotyping performed using the common reference and the lineage-specific references.

Table S2: Beta regressions of F_{ROH} with elevation as a predictor. Models are in the order: model with all individuals, model with all individuals and lineage as random effect and models for each individual lineage separately.

Table S3: Beta regressions of F_{ROH} with latitude as a predictor. Models are in the order: model with all individuals, model with all individuals and lineage as random effect and models for each individual lineage separately.

Table S4: Beta regressions of F_{ROH} with LGM habitat suitability as a predictor. Models are in the order: model with all individuals, model with all individuals and lineage as random effect and models for each individual lineage separately.

Figure S1: Flowchart of the two genotyping pipelines used in this study.

Figure S2: Comparison of individual inbreeding coefficients F_{ROH} and F_{IS} .

Figure S3: Maps of the LGM habitat suitability predicted by maxent models for each lineage (except GU for which maxent models failed due to low sample size). Areas of darker green indicate regions of higher climatic suitability.

Figure S4: Correlation coefficients of each quantitative variable of the PCA from Figure 2 with the two first principal components.

Figure S5: ROH length distributions for each lineage. Three minimum ROH length thresholds were used: (a) 1kb; (b) 10kb; and (c) 20kb.

Figure S6: Lineage-specific cumulative scaffold length plots. The red lines and their corresponding additional right axes represent the cumulative percentage of the total genome

length. The blue dashed lines (when visible) locate the first scaffold 50kb long or shorter. The points where the blue and red lines intersect therefore represent the percentage of the genome in scaffolds 50kb or larger.

Table S1: Descriptive summary of the two genotyping approaches

	Common reference			Lineage-specific references		
Lineage	Depth	Missing Frequency	N Missing	Depth	Missing Frequency	N Missing
AK	33.869	0.259	11493597.290	37.326	0.191	8625886.345
BC	35.545	0.240	10664540.520	41.225	0.159	6484541.435
CO	32.631	0.250	11116343.790	35.160	0.185	8001266.375
EC	30.011	0.253	11254154.320	33.192	0.172	7313777.839
EU	23.116	0.288	12819557.670	26.474	0.166	7041925.082
GU	30.583	0.246	10930946.0	37.094	0.108	4203717.545
WC	35.388	0.197	8775339.732	35.075	0.204	9106850.048

Table S2: Elevation

No random effect					
n = 201	Coefficients	Estimate	Std. Error	z value	Pr (> z)
	Intercept	-3.223e+00	9.181e-02	-35.106	<2e-16 ***
	elevation	1.273e-04	4.719e-05	2.697	0.00699 **
Lineage as random effect					
n = 201	Coefficients	Estimate	Std. Error	z value	Pr (> z)
	Intercept	-3.318e+00	3.059e-01	-10.849	<2e-16 ***
	elevation	2.166e-05	8.165e-05	0.265	0.791
groups = 7 (lineage)		lineage variance		lineage std. dev.	
		0.5718		0.7562	
Per lineage					

n = 29	AK				
	Coefficients	Estimate	Std. Error	z value	Pr (> z)
	Intercept	-1.9623509	0.1440755	-13.620	<2e-16 ***
n = 20	elevation	0.0001400	0.0002921	0.479	0.632
	BC				
	Coefficients	Estimate	Std. Error	z value	Pr (> z)
n = 24	Intercept	-3.491e+00	1.241e-01	-28.116	<2e-16 ***
	elevation	-3.551e-05	2.171e-04	-0.164	0.87
	CO				
n = 24	Coefficients	Estimate	Std. Error	z value	Pr (> z)
	Intercept	-4.6882985	1.3938481.4 710070	-3.187	0.00144 **
	elevation	0.0003426	0.0005113	0.670	0.50285
n = 49	EU				
	Coefficients	Estimate	Std. Error	z value	Pr (> z)
	Intercept	-5.1206668	0.1299042	-39.419	< 2e-16 ***
n = 31	elevation	0.0007333	0.0002464	2.975	0.00293 **
	EC				
	Coefficients	Estimate	Std. Error	z value	Pr (> z)
n = 11	Intercept	-3.5836582	0.1734366	-20.663	<2e-16 ***
	elevation	-0.0002599	0.0006107	-0.426	0.67
	GU				
n = 11	Coefficients	Estimate	Std. Error	z value	Pr (> z)
	Intercept	-9.9076231	1.7222878	-5.753	8.79e-09 ***
	elevation	0.0025805	0.0006519	3.959	7.54e-05 ***

WC				
Coefficients	Estimate	Std. Error	z value	Pr (> z)
Intercept	-2.704e+00	1.254e-01	-21.565	<2e-16 ***
elevation	-2.120e-06	5.460e-05	-0.039	0.969

n = 37

Table S3: Latitude

No random effect					
	Coefficients	Estimate	Std. Error	z value	Pr (> z)
n = 204	Intercept	-2.696484	0.240656	-11.205	<2e-16 ***
	Latitude	-0.008364	0.004832	-1.731	0.0834 .
Lineage as random effect					
	Coefficients	Estimate	Std. Error	z value	Pr (> z)
n = 204	Intercept	-2.468982	0.519263	-4.755	1.99e-06 ***
	Latitude	-0.018665	0.009392	-1.987	0.0469 *
groups = 7 (lineage)		lineage variance		lineage std. dev.	
		0.6578		0.811	
Per lineage					
AK					
	Coefficients	Estimate	Std. Error	z value	Pr (> z)
n = 29	Intercept	1.52217	1.07592	1.415	0.15714
	Latitude	-0.05684	0.01786	-3.182	0.00146 **
BC					
	Coefficients	Estimate	Std. Error	z value	Pr (> z)
n = 23	Intercept	-4.89648	1.17966	-4.151	3.31e-05 ***
	Latitude	0.02494	0.02145	1.163	0.245
CO					
	Coefficients	Estimate	Std. Error	z value	Pr (> z)
	Intercept	-1.92454	2.51172	-0.766	0.444
	Latitude	-0.04641	0.06521	-0.712	0.477

n = 24					
n = 49	EU				
	Coefficients	Estimate	Std. Error	z value	Pr (> z)
	Intercept	-5.086864	0.886180	-5.740	9.46e-09 ***
	Latitude	0.002124	0.015494	0.137	0.891
n = 31	EC				
	Coefficients	Estimate	Std. Error	z value	Pr (> z)
	Intercept	-5.61899	1.59438	-3.524	0.000425 ***
	Latitude	0.04279	0.03407	1.256	0.209093
n = 11	GU				
	Coefficients	Estimate	Std. Error	z value	Pr (> z)
	Intercept	63.629	16.856	3.775	0.00016 ***
	Latitude	-4.425	1.118	-3.959	7.54e-05 ***
n = 37	WC				
	Coefficients	Estimate	Std. Error	z value	Pr (> z)
	Intercept	-2.6865920	0.8976087	-2.993	0.00276 **
	Latitude	-0.0004972	0.0210792	-0.024	0.98118

Table S4: LGM Habitat suitability

No random effect					
	Coefficients	Estimate	Std. Error	z value	Pr (> z)
n = 192	Intercept	-3.1287	0.2583	-12.112	<2e-16 ***
	LGM HS	0.0405	0.2974	0.136	0.892
Lineage as random effect					
	Coefficients	Estimate	Std. Error	z value	Pr (> z)
n = 192	Intercept	-3.4532	0.3778	-9.141	<2e-16 ***
	LGM HS	0.1461	0.2092	0.698	0.485
groups = 6 (lineage without GU)		lineage variance		lineage std. dev.	
		0.6595		0.8121	
Per lineage					
AK					
	Coefficients	Estimate	Std. Error	z value	Pr (> z)
n = 28	Intercept	-2.0474	0.3103	-6.564	5.25e-11 ***
	LGM HS	0.1704	0.4050	0.421	0.674
BC					
	Coefficients	Estimate	Std. Error	z value	Pr (> z)
n = 23	Intercept	-3.44812	0.64230	-5.368	7.94e-08 ***
	LGM HS	-0.09835	0.72744	-0.135	0.892
CO					
	Coefficients	Estimate	Std. Error	z value	Pr (> z)
	Intercept	-5.5941	0.9194	-6.084	1.17e-09 ***
	LGM HS	2.1071	0.9966	2.114	0.0345 *

n =24					
EU					
	Coefficients	Estimate	Std. Error	z value	Pr (> z)
	Intercept	-5.2797	0.3764	-14.027	<2e-16 ***
	LGM HS	0.3873	0.4368	0.887	0.375
n = 49					
EC					
	Coefficients	Estimate	Std. Error	z value	Pr (> z)
	Intercept	-3.3796	0.5524	-6.118	9.5e-10 ***
	LGM HS	-0.3012	0.6422	-0.469	0.639
n = 31					
WC					
	Coefficients	Estimate	Std. Error	z value	Pr (> z)
	Intercept	-2.4649	0.3418	-7.212	5.51e-13 ***
	LGM HS	-0.2813	0.3875	-0.726	0.468
n = 37					

Figure S1

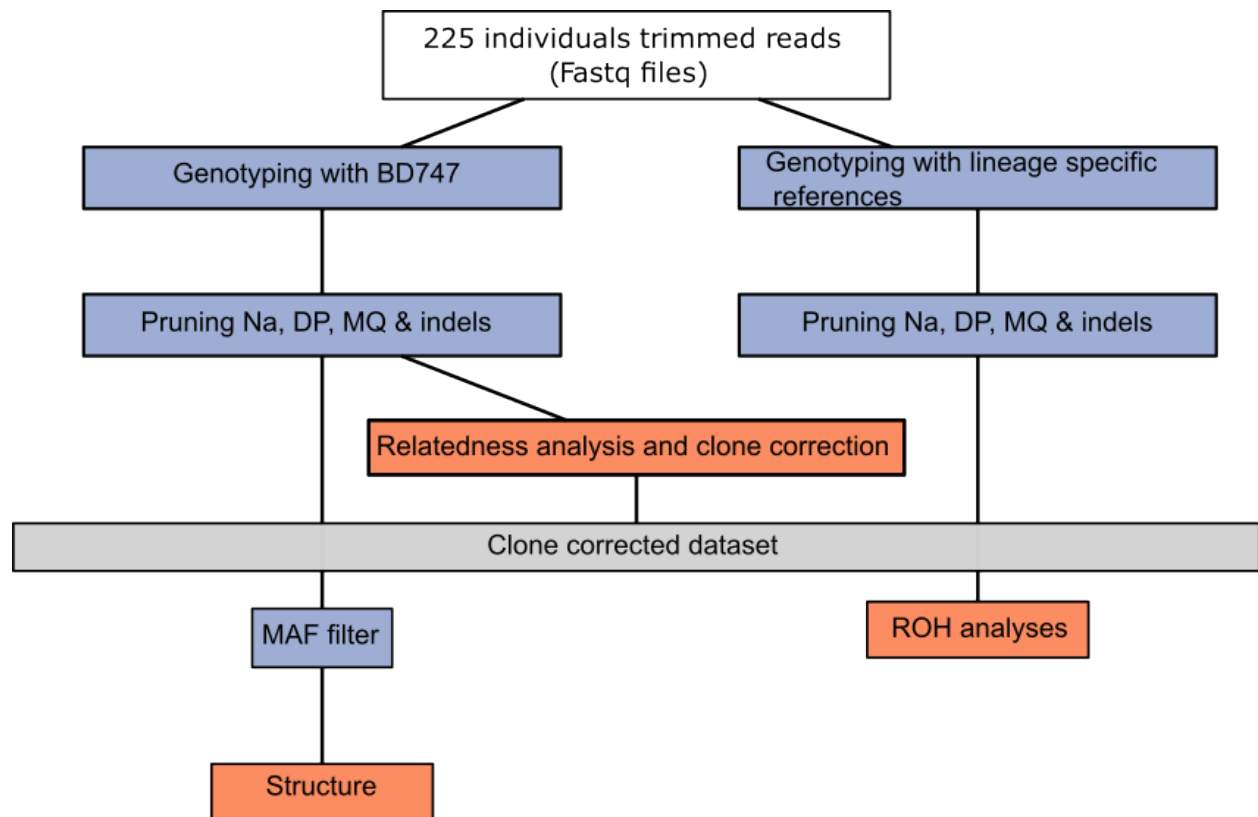


Figure S2

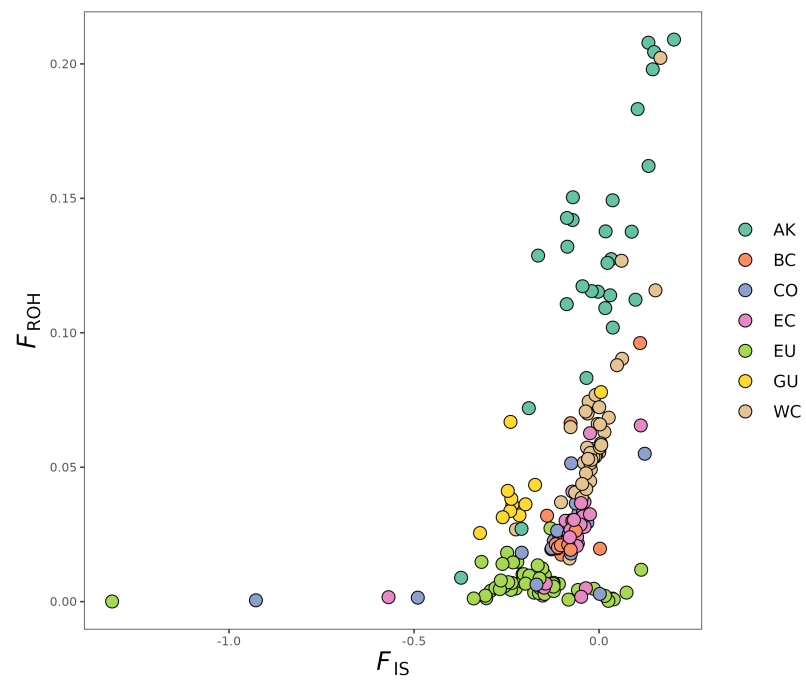
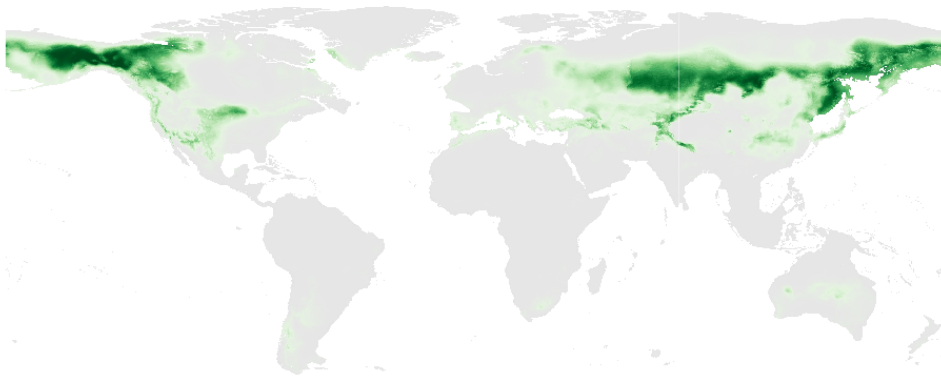


Figure S3

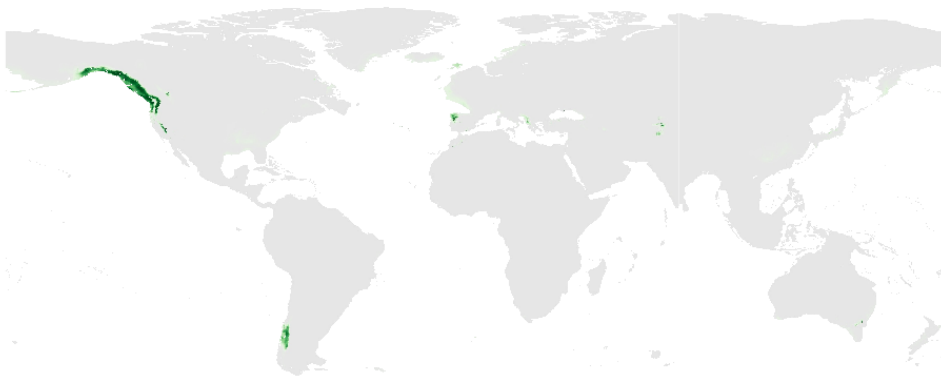
A) AK

0 10000 km



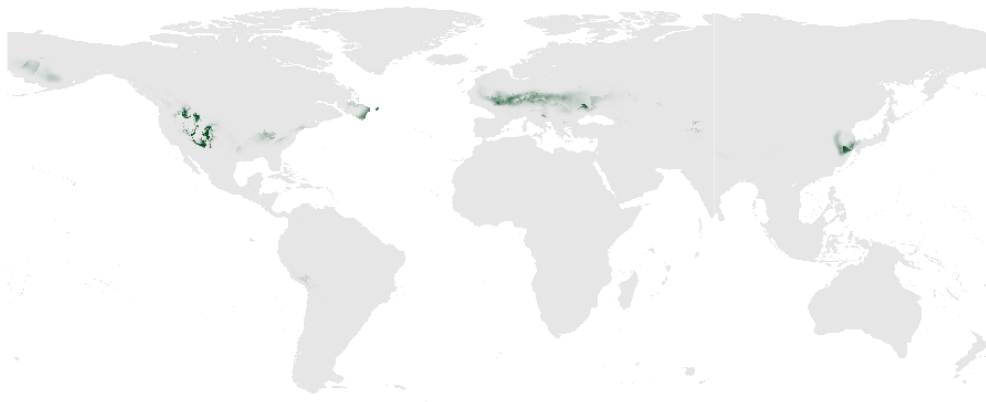
B) BC

0 10000 km



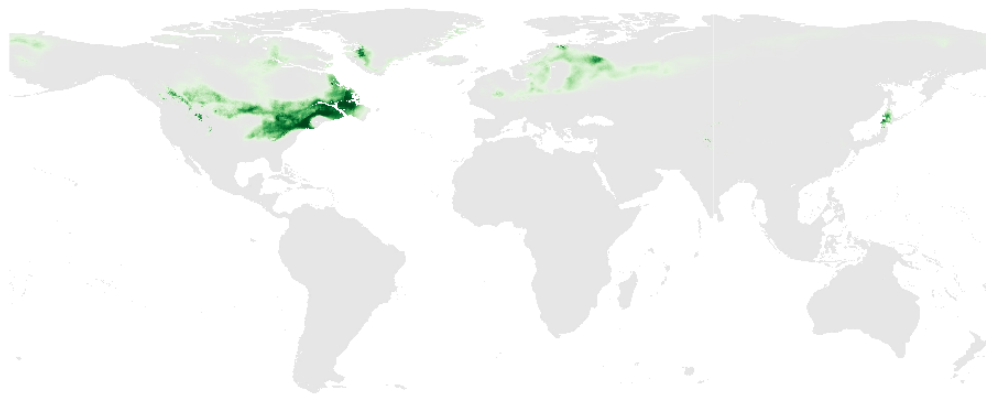
C) CO

0 10000 km



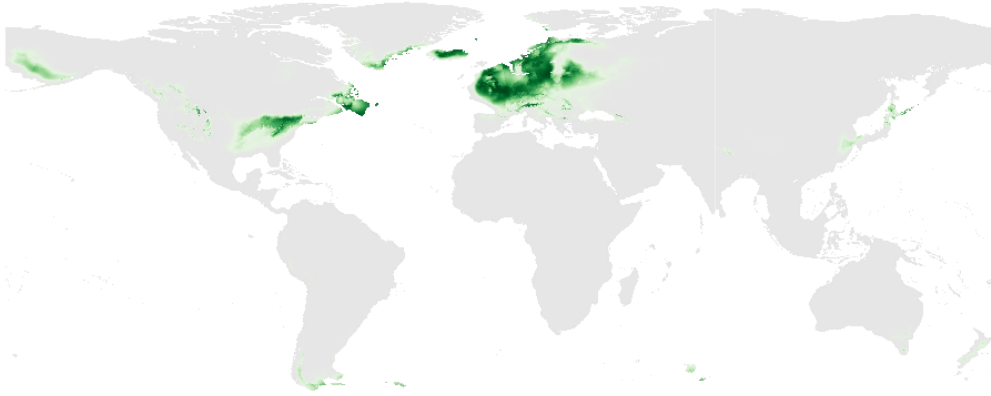
D) EC

0 10000 km



D) EU

0 10000 km



E) WC

0 10000 km

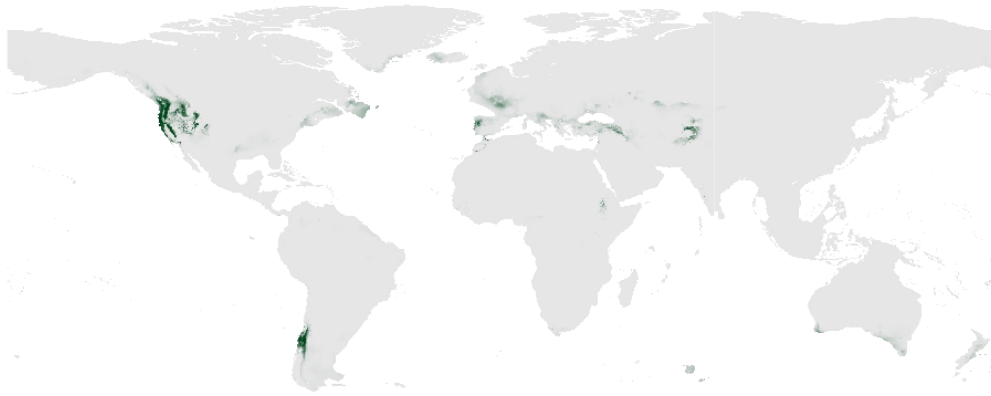


Figure S4

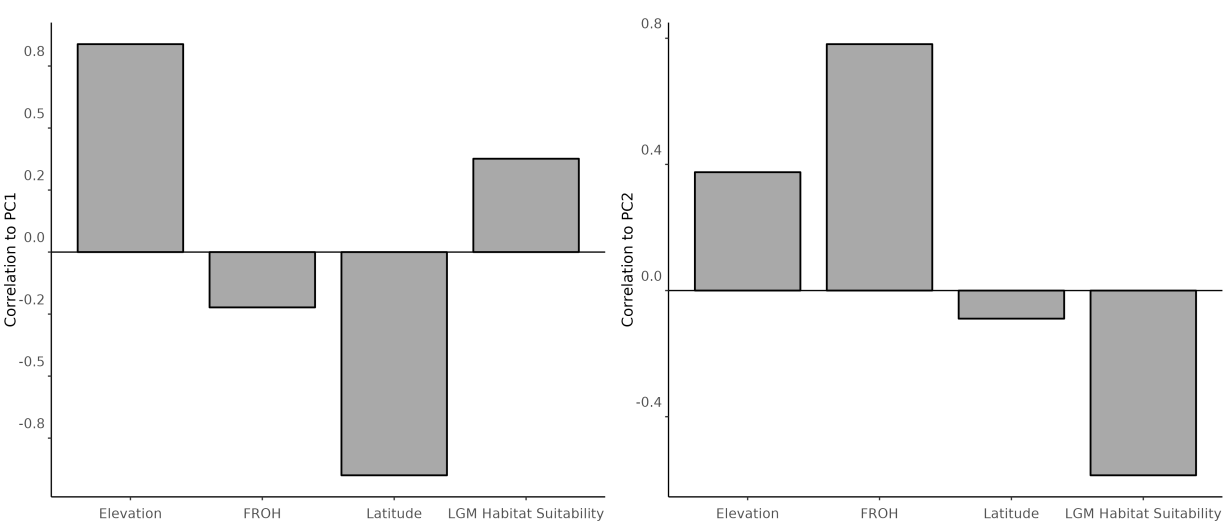


Figure S5

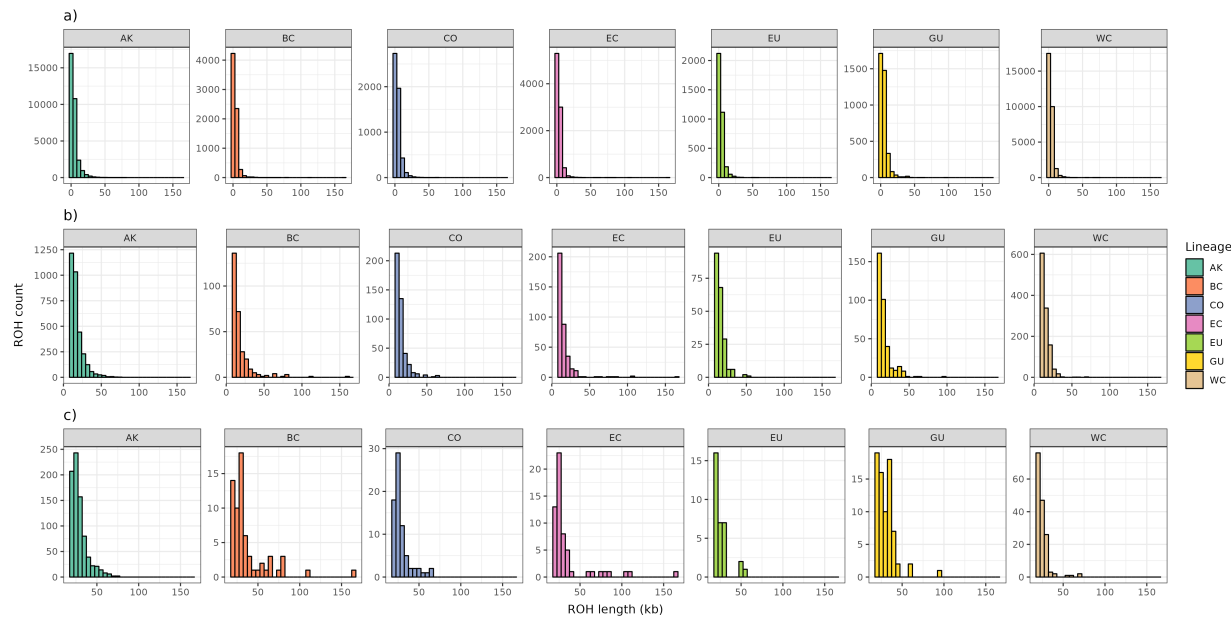


Figure S6

