Supplementary tables and figures

Table S1. Summary of model comparisons.

	df	AIC	BIC	Log likelihood	Log likelihood ratio	p-value
Model 1: Only intercept is allowed to vary for each replicate nested within population	11	90026.92	90118.09	-45002.43		
Model 1 vs. Model 2: Model 1+Slope is also allowed to vary	27	88015.95	88239.72	-43980.97	2042.973	<0.0001
Model 2 vs. Model 3: Model 2+ variance as an exponential function of time	24	82791.00	82989.91	-41371.50	5218.948	<0.0001

Figure S1. Variance in size and the natural logarithm of this variance against time. Each point is the variance between 735 individuals in each replicate lineage. Shapes indicate the ancestral population and color denotes treatment (warm-UV and cool-No UV). Ln(variance) and time were linearly correlated (r=-0.507, df=230, p<0.00001).

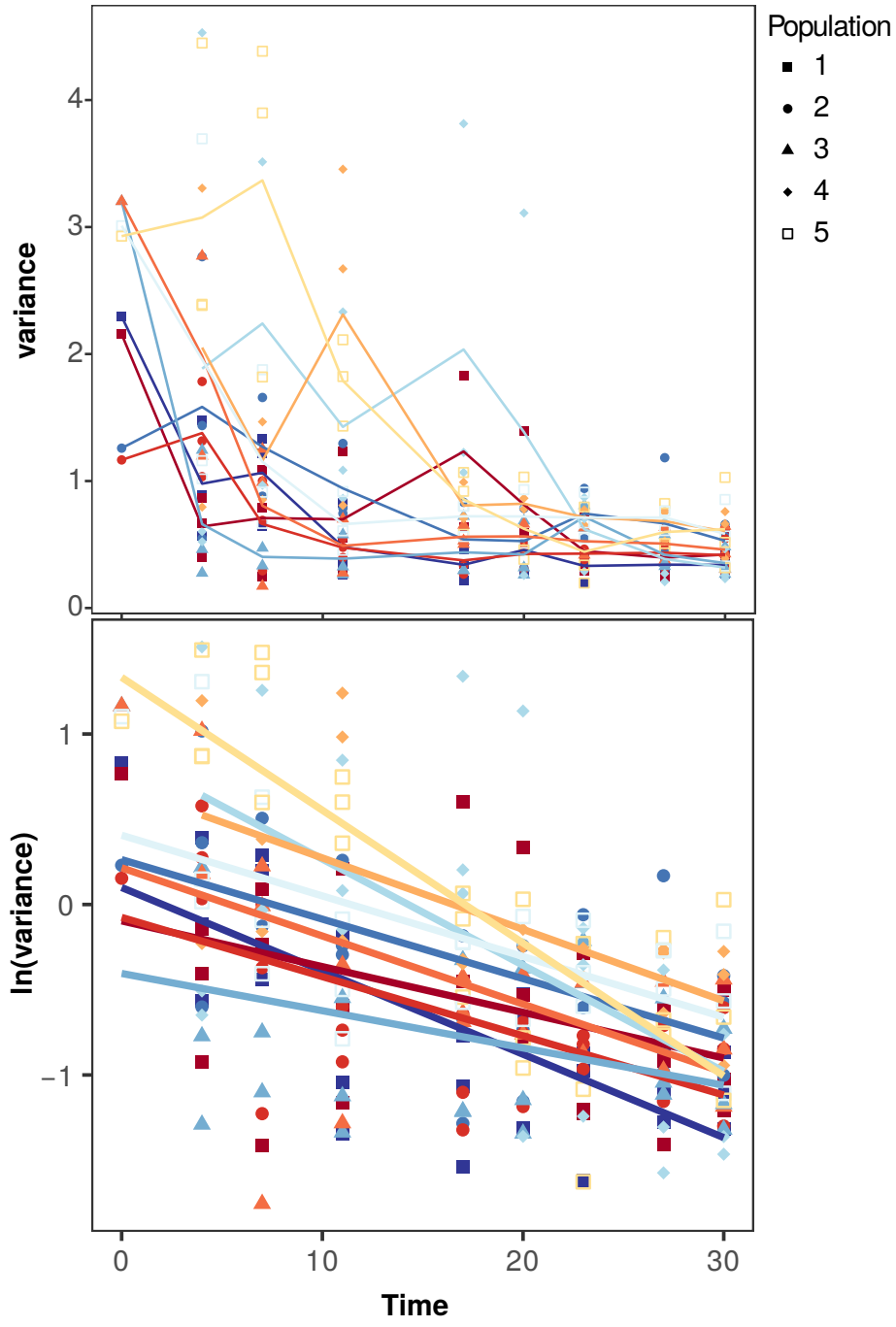

Figure S2. Plots testing normality (q-q plot) and heteroscedasticity (fitted values vs. residuals) for the ANCOVA and the generalized linear least squares model (GLS) with variance weights modeled as an exponential function of time.

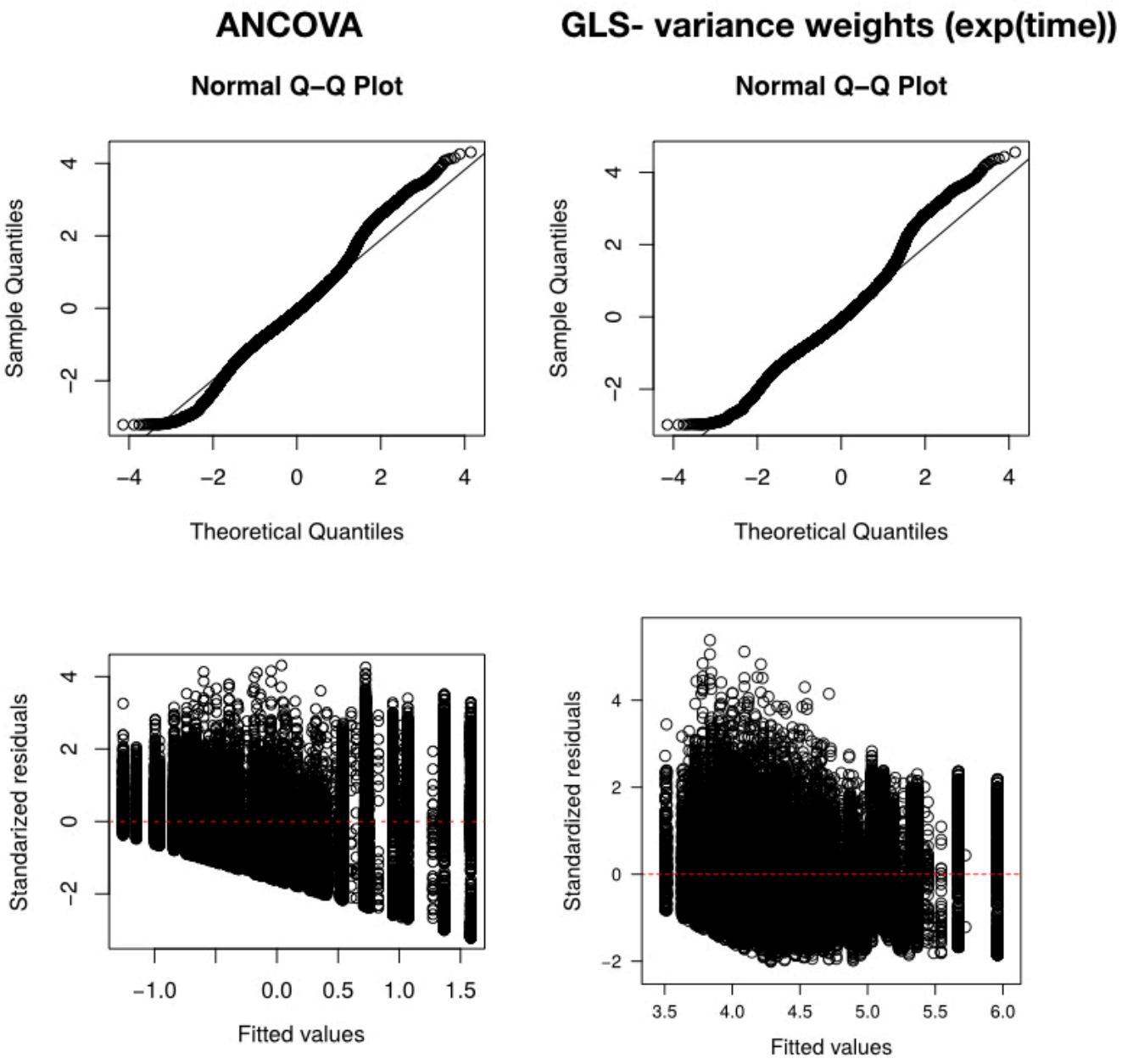

Figure S3. Distribution of sizes over time of each of the replicate lines (different shades of gray) of all of the populations in the control (upper panels) or UV (lower panels).

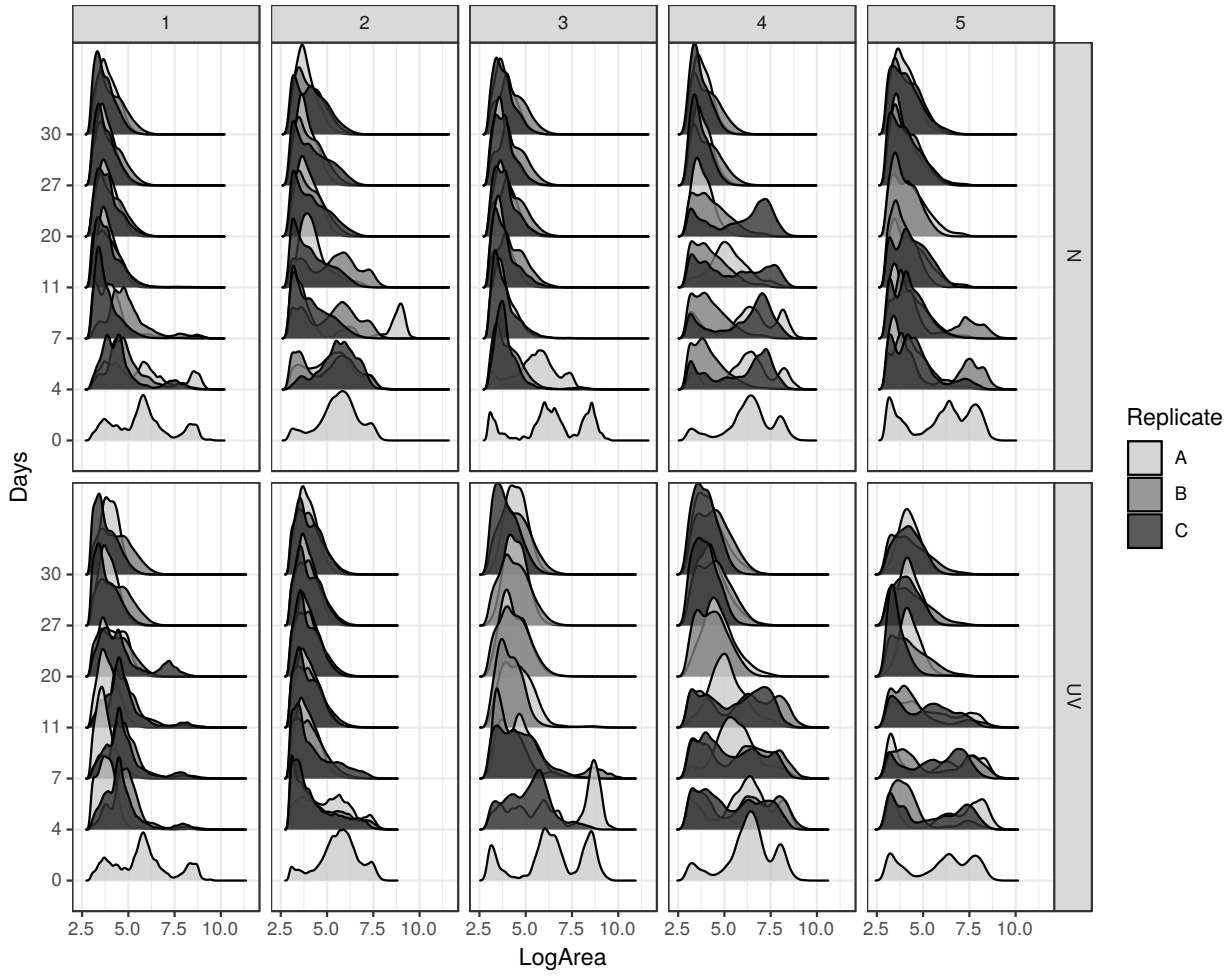
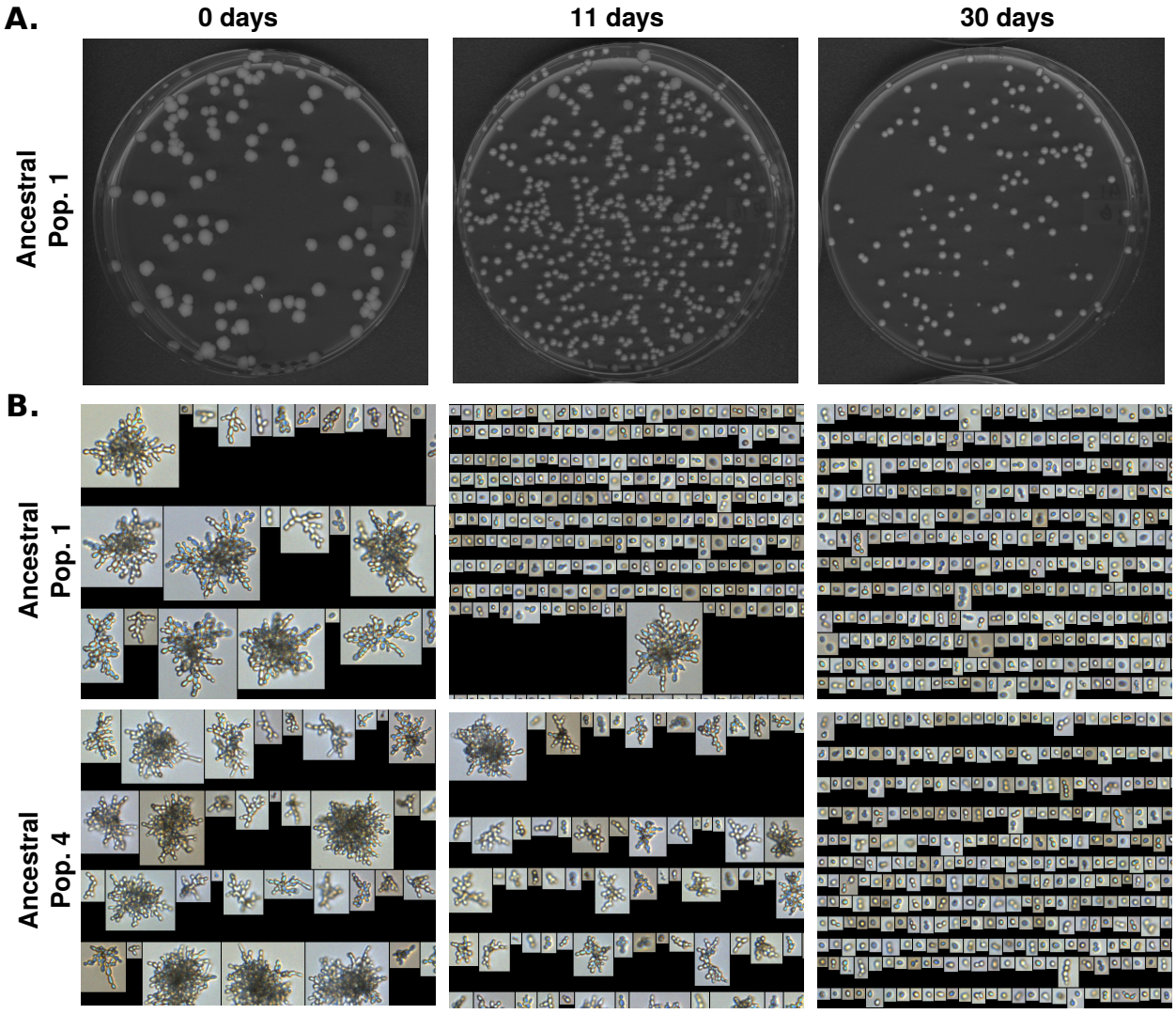
Figure S4. Changes in multicellular phenotypes over time. A. Pictures of plates at 0, 11 and 30 days of evolution of one of the replicate lines from population 1. Smooth colonies are either very small multicellular isolates or unicellular ones. B. Pictures at the bottom show individual clusters (or cells) of two lines from different ancestral populations (1 and 4).