Supplementary Materials.

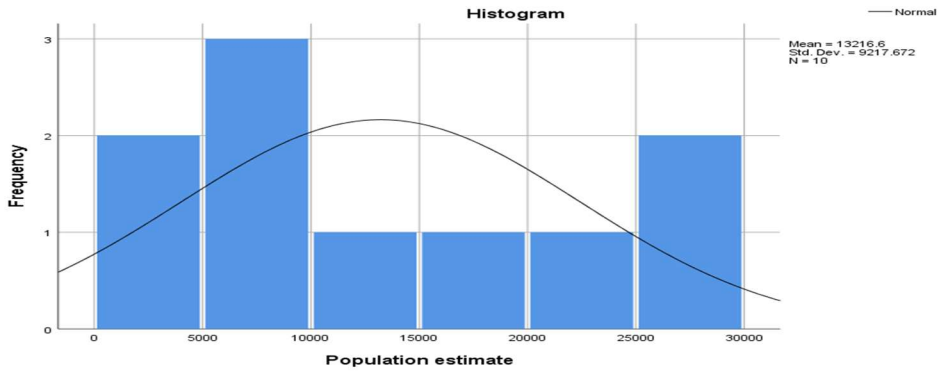


Figure S1. Histogram showing the frequency of the population estimates that serve the different plants. The chart was generated in the test for normality using IBM SPSS Statistics 27 version.

Table S1. Descriptive statistics for the normality test of population estimates.

			Statistic	Std. Error
Population estimate	**Mean**		13216.60	2914.884
	95% Confidence Interval for Mean	Lower Bound	6622.67	
		Upper Bound	19810.53	
	5% Trimmed Mean		13140.22	
	Median		10480.00	
	Variance		84965482.044	
	Std. Deviation		9217.672	
	Minimum		2140	
	Maximum		25668	
	Range		23528	
	Interquartile Range		18785	
	Skewness		.416	.687
	Kurtosis		-1.438	1.334

Table S2. Tests of Normality for population estimates.

	Kolmogorov-Smirnov[a]			**Shapiro-Wilk**		
	Statistic	**df**	**Sig.**	**Statistic**	**df**	**Sig.**
Population estimate	.193	10	.200*	.874	10	.110

*. This is a lower bound of the true significance.
a. Lilliefors Significance Correction

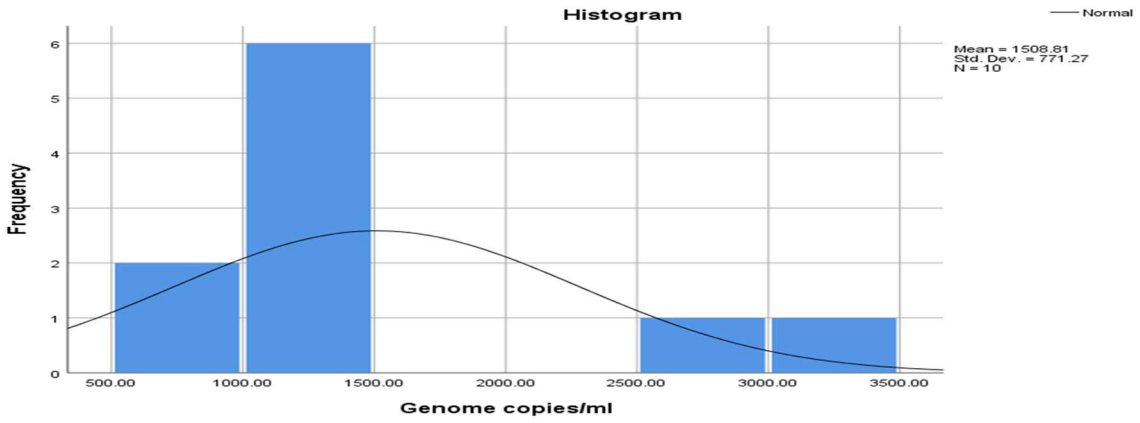


Figure S2. Histogram shows the frequency of the genome copies for the different plants. The chart was generated in the test for normality using SPSS.

Table S3. Tests of Normality for GC/ml

	Kolmogorov-Smirnov[a]			Shapiro-Wilk		
	Statistic	**df**	**Sig.**	Statistic	df	Sig.
Genome copies/ml	.323	10	.004	.746	10	.003

a. Lilliefors Significance Correction

Table S4. Descriptive statistics for the normality test of GC/ml

			Statistic	Std. Error
Genome copies/ml	Mean		1508.8123	243.89698
	95% Confidence Interval for Mean	Lower Bound	957.0790	
		Upper Bound	2060.5456	
	5% Trimmed Mean		1455.8156	
	Median		1238.1477	
	Variance		594857.376	
	Std. Deviation		771.26998	
	Minimum		852.22	
	Maximum		3119.34	
	Range		2267.12	
	Interquartile Range		776.43	
	Skewness		1.589	.687
	Kurtosis		1.368	1.334

Table S5. Pearson correlation showing possible link between clinical cases and genome copies.

Bayes Factor Inference on Pairwise Correlations[a]

		Average GC/ml	COVID clinical cases ECP
Average GC/ml	Pearson Correlation	1	.134
	Bayes Factor		5.898
	N	50	50
COVID clinical cases ECP	Pearson Correlation	.134	1
	Bayes Factor	5.898	
	N	50	50

a. Bayes factor: Null versus alternative hypothesis.

Posterior Distribution Characterization for Pairwise Correlations[a]

			Average GC/ml	COVID clinical cases ECP
Average GC/ml	Posterior	Mode		.132
		Mean		.124
		Variance		.018
	95% Credible Interval	Lower Bound		-.146
		Upper Bound		.379
	N		50	50
COVID clinical cases ECP	Posterior	Mode	.132	
		Mean	.124	
		Variance	.018	
	95% Credible Interval	Lower Bound	-.146	
		Upper Bound	.379	
	N		50	50

a. The analyses assume reference priors (c = 0).

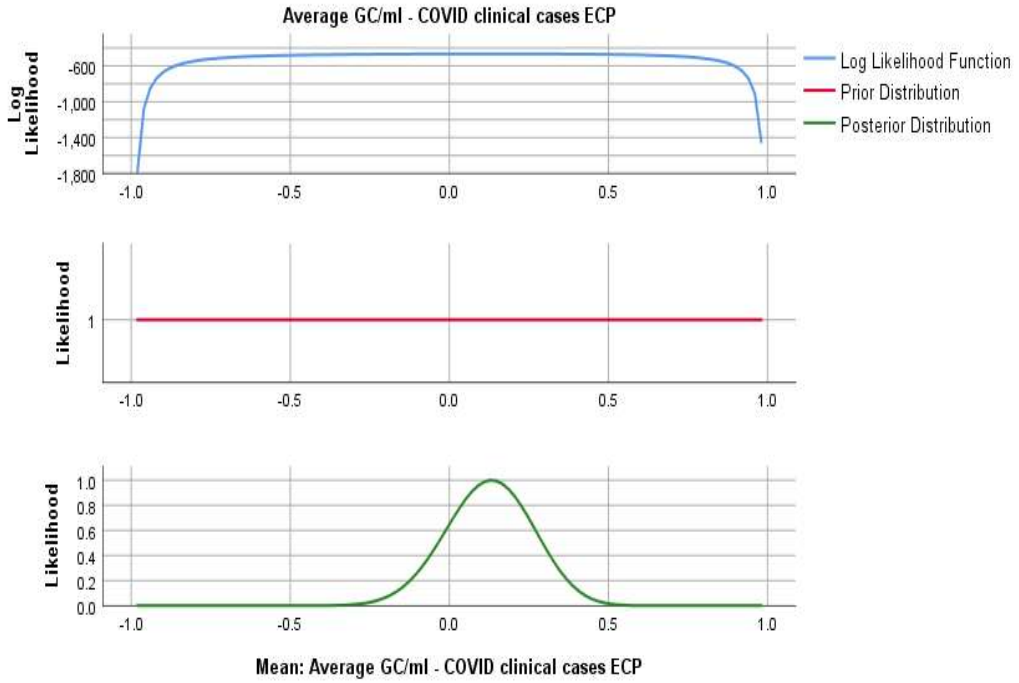


Figure S3. Pictorial representation of the Pearson correlation of the genome copies/ml of the different plants in relation to the COVID clinical cases in ECP. The chart was generated in the test for normality using IBM SPSS Statistics 27 version.