Supplementary Information

Supplementary Figure S1. ADMIXTURE estimates for the best fitting model (K=4) for the Canary Islanders and the reference populations. EUR, Europeans (from left to right: FIN, GBR, CEU, TSI, and IBS); NAF, North Africans; SSA, sub-Saharan Africans. Colors represent genomic components (dark blue, North Europe; light blue, South Europe; pink, North Africa; green, sub-Saharan Africa).

Supplementary Table S1. Pearson’s product-moment correlation (R) between ancestry estimates from the experiment that did not include Toscani (TSI) or Iberian populations (IBS) vs. the experiment including them. EUR, Europeans; NAF, North Africans; SSA, sub-Saharan Africans. CI, confidence interval.

|               | p-value      | 95% CI       | R  |
|---------------|--------------|--------------|----|
| North-EUR     | < 2.2 x 10^{-16} | 0.985 - 0.989 | 0.987 |
| South-EUR     | < 2.2 x 10^{-16} | 0.816 - 0.861 | 0.840 |
| NAF           | < 2.2 x 10^{-16} | 0.843 - 0.881 | 0.863 |
| SSA           | < 2.2 x 10^{-16} | 0.976 - 0.982 | 0.979 |

Supplementary Table S2. Mean ancestry proportions obtained with ADMIXTURE per island population and overall, when the experiments included Toscani (TSI) and Iberian populations (IBS) as part of the European reference population dataset.

|              | EUR          | NAF          | SSA          |
|--------------|--------------|--------------|--------------|
| Canary Islands | 74.8 ± 4.0  | 21.9 ± 3.7   | 3.3 ± 1.5    |
| El Hierro    | 72.5 ± 2.6   | 25.4 ± 2.1   | 2.1 ± 0.6    |
| La Palma     | 78.9 ± 2.5   | 19.0 ± 2.0   | 2.1 ± 0.8    |
| La Gomera     | 70.2 ± 2.7   | 25.0 ± 2.5   | 4.8 ± 1.3    |
| Tenerife     | 77.9 ± 2.4   | 19.9 ± 2.1   | 2.2 ± 0.9    |
| Gran Canaria | 76.8 ± 2.5   | 19.2 ± 2.2   | 4.0 ± 1.5    |
| Fuerteventura | 71.4 ± 2.8  | 25.2 ± 2.1   | 3.4 ± 1.1    |
| Lanzarote   | 71.0 ± 2.5   | 25.4 ± 2.4   | 3.6 ± 1.0    |

EUR, European; NAF, North African; SSA, sub-Saharan African. Numbers refer to average ± standard deviation (in percentage).