

Figure S1. Proportionality between chosen f_4 -statistic and FRO ancestry, related to Figure 4. FRO ancestry proportions inferred from *qpAdm* for groups from Remote Oceania are shown as a function of the statistic $f_4(X, \text{New Guinea Highlanders; Kankanaey, Australian})$, which serves as the x-axis for our allele-sharing regression tests. The regression line was computed using all populations. Bars show two standard errors in each direction. Polyn., Polynesian.

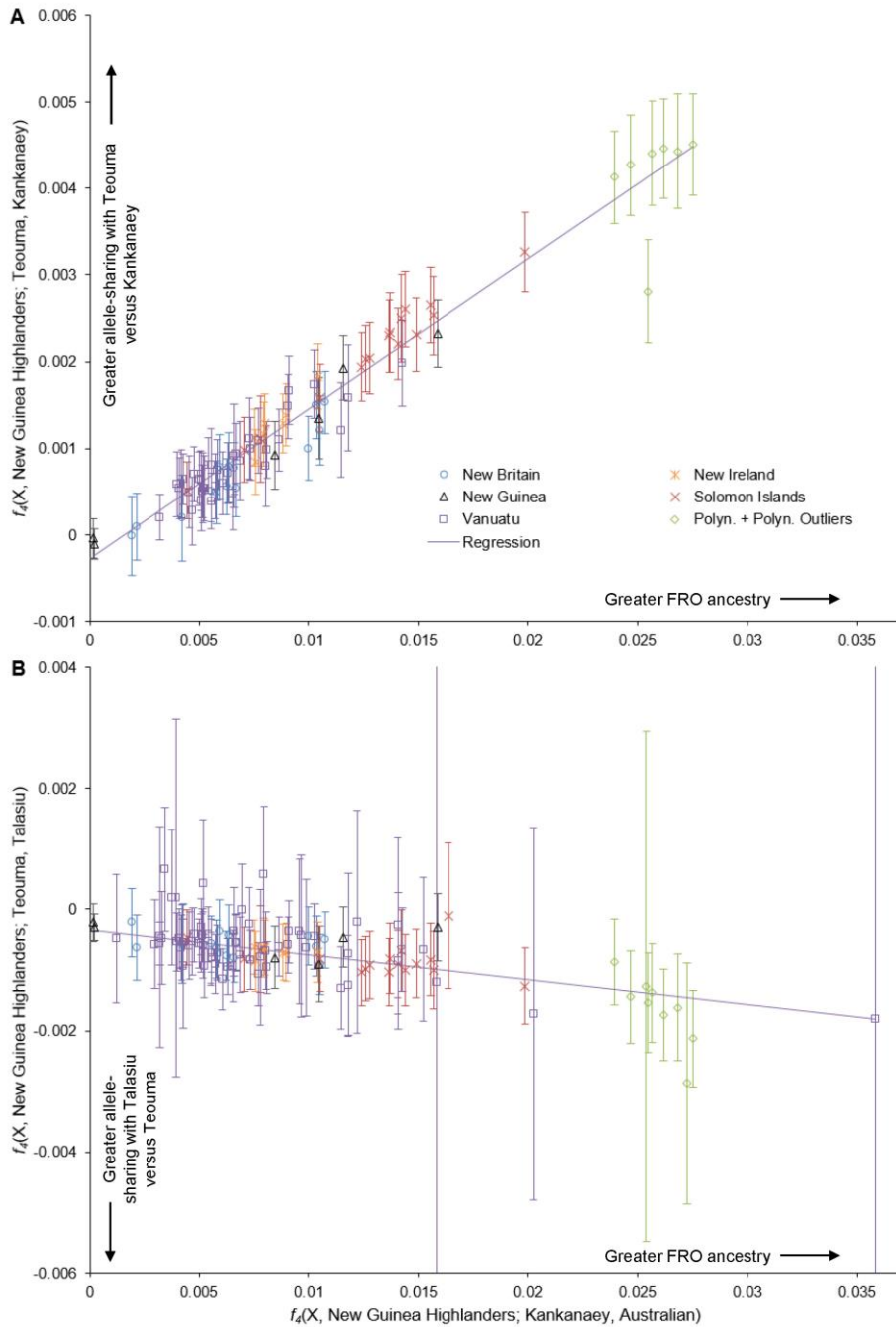


Figure S2. Test for differential FRO ancestry sources, related to Figure 4. (A) The statistic $f_4(X, \text{New Guinea Highlanders; Teouma, Kankanaey})$ (y-axis; higher values indicate greater allele-sharing with Teouma) is plotted against $f_4(X, \text{New Guinea Highlanders; Kankanaey, Australian})$ (x-axis; higher values indicate more FRO ancestry). We restricted to present-day populations X to avoid artificial signals of allele sharing between ancient groups. (B) The statistic $f_4(X, \text{New Guinea Highlanders; Teouma, Talasiu})$ (y-axis; higher values indicate greater allele-sharing with Teouma) is plotted against $f_4(X, \text{New Guinea Highlanders; Kankanaey, Australian})$ (x-axis; higher values indicate more FRO ancestry). In both panels, the regression lines were computed using all populations. Bars show two standard errors in each direction. Polyn., Polynesian.

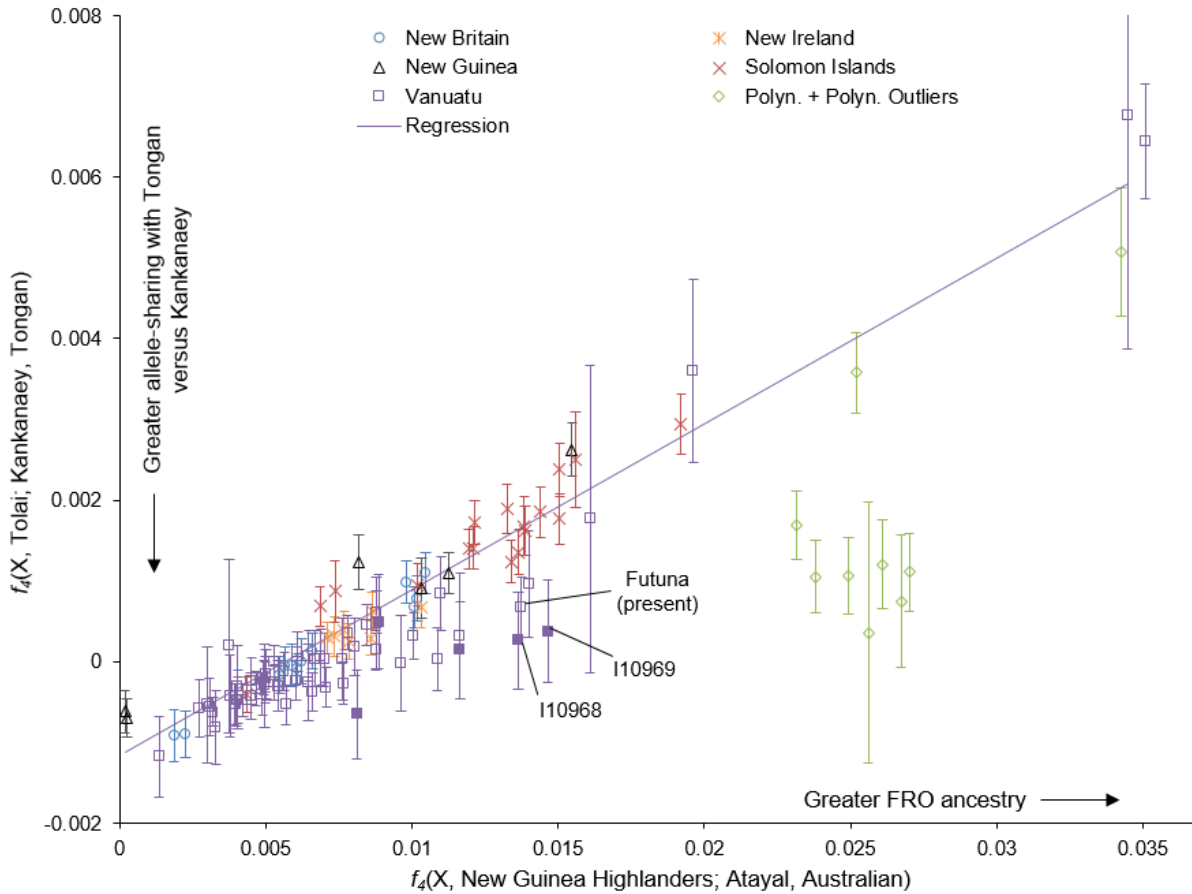


Figure S3. Alternative test for Polynesian influence, related to Figure 4. The statistic $f_4(X, \text{Tolai}; \text{Kankanaey}, \text{Tongan})$ (y-axis; higher values indicate relatively lower allele-sharing with present-day Tongans) is plotted against $f_4(X, \text{New Guinea Highlanders}; \text{Atayal}, \text{Australian})$. The regression line was computed on Near Oceanian populations. Filled points represent the five individuals from Eretok and Mangaas. Compared to **Figure 4B**, we use Atayal rather than Kankanaey in the x-axis statistic to confirm that specific relatedness to Kankanaey does not drive the deviations from the regression line. Polyn., Polynesian.

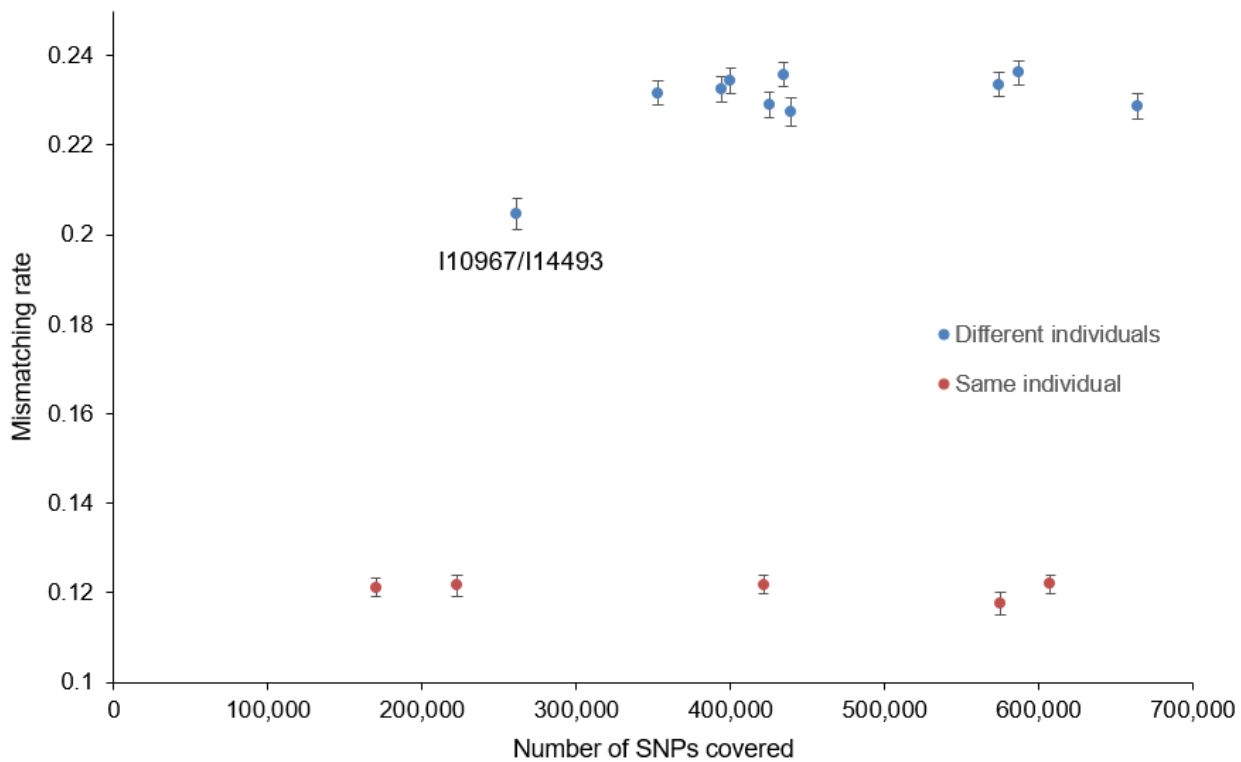


Figure S4. Kinship analysis, related to Figure 4. Intra-individual allelic mismatch rates (red points) are approximately one-half those of inter-individual comparisons (blue points), as expected for unrelated individuals, except for the I10967/I14493 comparison (labeled), which is roughly seven-eighths as high as the other blue points, indicating a second-degree familial relationship (grandparent-grandchild, aunt/uncle-nephew/niece, half siblings, or double cousins). Bars show two standard errors in each direction.

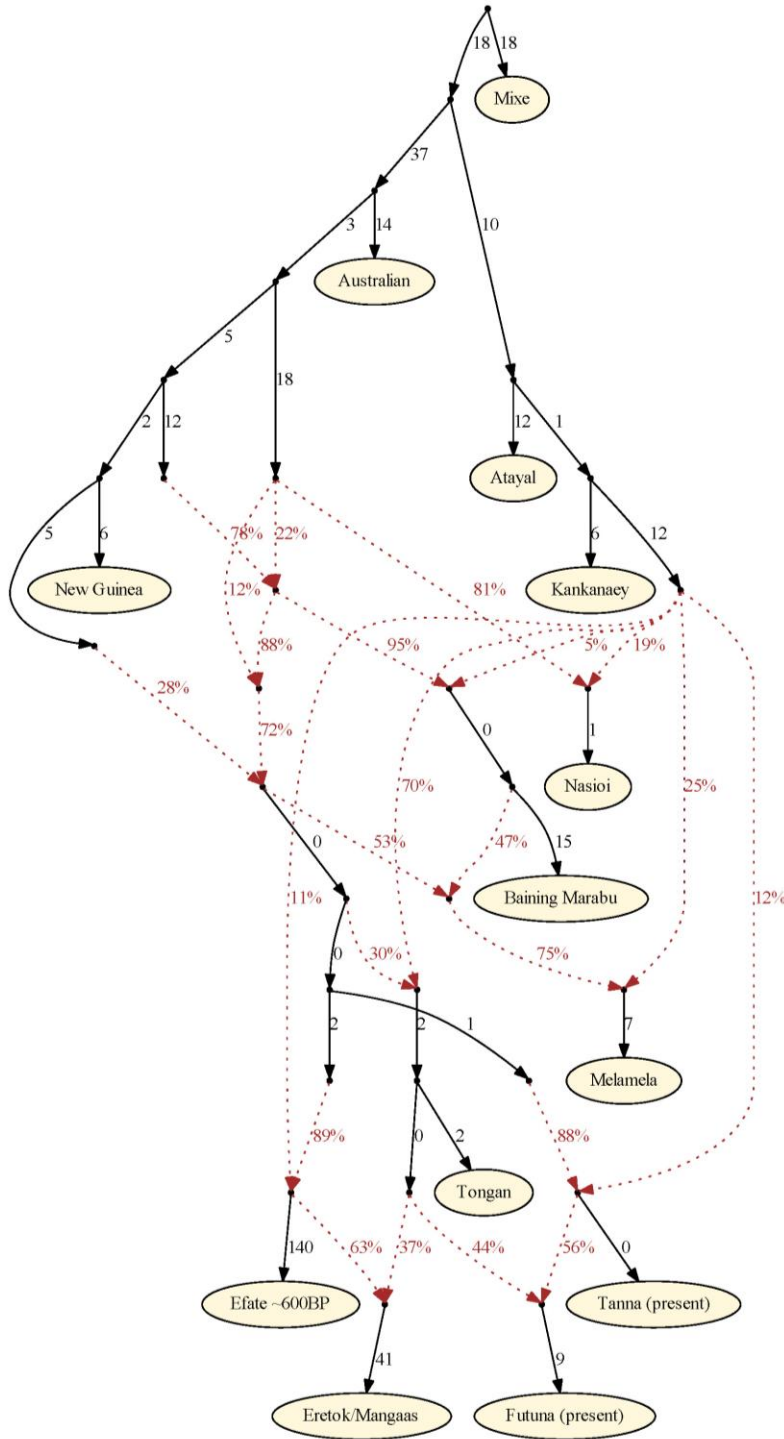


Figure S5. Full admixture graph results, related to Figure 5. Branch lengths are shown in units of average squared allele frequency divergence (multiplied by 1000, rounded to the nearest integer). Since we lack sufficient constraint to determine the precise FRO and Papuan topologies simultaneously, we simplified the model by specifying all FRO ancestry as being derived from exactly the same source; we then also did not resolve apparent trifurcations within the clade of New Britain-related ancestry.