## Figure 1 – source data 3. FIS by sub-population

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| Population analysed | n isolates | FIS median | FIS average | FIS std error | Proportion of loci with FIS = -1 | Proportion of loci with low FIS |
| Bonon | 14 | -1 | -0.971 | 0.004 | 95.9% | 84.8% |
| Boffa | 18 | -1 | -0.981 | 0.004 | 97.6% | 98.2% |
| Dubreka | 19 | -1 | -0.984 | 0.003 | 97.4% | 98.4% |

FIS was calculated across the *T.b. gambiense* Group 1 genome utilising the set of ‘ancient’ SNP loci (Figure 1 – figure supplement 7). A median figure of -1 was calculated for the entire set of *T.b. gambiense* Group 1 isolates (All Tbg1) and for each of the Bonon, Boffa and Dubreka sub-populations. The proportion of SNP loci exhibiting a statistically significant lower than expected FIS (P<0.001) was calculated using a randomisation method (n iterations = 30,000)38.