Extended Materials and Methods - Modification of VCFtools to provide variance components of F_{ST}

VCFtools v0.1.14 source file variant_file_output.cpp available at https://github.com/vcftools/vcftools/blob/master/src/cpp/variant_file_output.cpp was modified so that the output of –weir-fst-pop command includes the numerator and denominator of Weir and Cockerham (1984) F_{ST} estimator, allowing to calculate average F_{ST} over multiple sites appropriately, as a ratio of averages, as suggested by (Reynolds *et al.* 1983) and described in the main text.

Line 3628 of variant_file_output.cpp was originally:

```
out « e->get_CHROM() « "\t" « e->get_POS() « "\t" « fst « endl;
```

We modified it to:

```
out « e->get_CHROM() « "\t" « e->get_POS() « "\t" « fst « "\t" « sum_a
« "\t" « sum_all « endl;
```

Following a suggestion by Travis Collier on the VCFtools mailing list (http://sourceforge.net/p/vcftools/mailman/message/33927517/).

Literature Cited

Reynolds, J., B. S. Weir, and C. C. Cockerham, 1983 Estimation of the coancestry coefficient: basis for a short-term genetic distance. Genetics **105**: 767–79.

Weir, B. S. and C. C. Cockerham, 1984 Estimating F-statistics for the analysis of population structure. Evolution **38**: 1358–1370.