GBR+GBR
GBR+CHS
GBR+YRI
CHS+GBR
CHS+CHS
CHS+YRI
YRI+GBR
YRI+CHS
YRI+YRI
1.2
1.0
0.8
0.6
Estimated/Intended Contamination
0.01
0.02
0.05
0.1
0.2
Intended Contamination
Method
Unequal_Ancestry_NumPC=4
Unequal_Ancestry_NumPC=2

Supplemental Figure S1. Impact of the number of principal components (PCs) on estimated DNA sample contamination using *verifyBamID2*. Horizontal (x) axis shows intended contamination rate, vertical (y) axis shows the ratio of estimated to intended contamination rates. Each color represents different number of PCs (PC=2 or PC=4) used to estimate contamination rates. We used Unequal_Ancestry mode as in Figure 4, which performed the best among the options considered. With Unequal_Ancestry, *verifyBamID2* ran allowing different genetic ancestry between intended and contaminating sample. Each panel represents different combinations of intended (row) and contaminating (column) populations, consistent with Figure 4.