ERRATUM

Copy-number variation in control population cohorts
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*Human Molecular Genetics* 2007 16;R2, R168-R173; doi:10.1093/hmg/ddm241

The publisher would like to apologise for an error in the printing of the above article. On page R171 only Figure 3 was printed and the legend and article text was omitted. The complete page R171 including the omitted text is printed on the following page. This error only affected the print issue, the online version of the article is correct.
theory (33) of modern human origin, higher levels of genetic variation should exist in the more ancient African populations and less diversity in the younger, non-African populations, which is supported by SNP diversity studies (34). Accordingly, a higher number of distinct CNVs/ CNVRs within samples of African ancestry would also be expected. It is currently unclear whether the absence of such difference is due to the limited sample size or related to the distribution of CNVRs among populations. These observations further underscore the need to genotype large samples to determine CNV and CNVR frequencies and distribution across different populations.

**FUTURE CONSIDERATIONS**

**Next-Generation Platforms**

The next generation of SNP arrays (e.g. the commercial Affymetrix 5.0 and 6.0, and Illumina 1 M) has been designed to offer the potential to simultaneously interrogate SNPs and