

Identification and characterization of novel sequence variations in the cytochrome *P4502D6* (*CYP2D6*) gene in African Americans

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Correction:

The authors would like to clarify that the Human Genome Sequence Build used for the bioinformatic model mentioned on page 181 was 33 (and not 331) as described by Nalla and Rogan (Nalla VK, Rogan PK. Automated splicing mutation analysis by information theory. *Hum Mutat* 2005; **25**: 334-342). Furthermore, the *R_i* values given for maximum and average splice sites on the same page specifically refer to the splice donor site model.

The authors would like to apologise for any confusion caused.