Editorial

I would like to welcome you to Volume 5, Issue 4 of *Human Genomics*. In this issue, following the *Research Highlights* by Scheinman, Baye describes a comprehensive strategy to analyse chromosome-based population structure and differentiation, demonstrating the usefulness of complementary statistical and functional network analysis in human genetic variation studies. Hamby *et al.* have then performed a meta-analysis of non-stop mutations in 87 different genes known to cause human-inherited disease. They have examined the sequence context of the mutated stop codons and the average distance to the next alternative in-frame stop codon downstream. Their studies lead to the speculation that recruitment of an alternative stop codon at a greater distance from the mutated stop codon may initiate mRNA decay, leading to decreased protein levels which, in turn, result in the clinical phenotype.

Ikediobi and colleagues have characterised the population frequencies of clinically relevant pharmacogenetic traits in two distinct South African population groups residing in the Western Cape (the Xhosa and Cape Mixed Ancestry). Their data indicate diverse allele frequencies of key pharmacogenetic genes within the African population. In the *Update on Gene Completions and Annotations* section, Jackson *et al.* provide an update on aldehyde dehydrogenase (*ALDH*) genes in several vertebrates and clarify the annotation found in the National Center for Biotechnology Information (NCBI) gene database. They also discuss gene-duplication and gene-loss events that may have occurred in the *ALDH* gene superfamily. In the *Software Review* section of the current issue, Lamy and colleagues discuss software for the genotyping of microarray single nucleotide polymorphisms, in particular software for Affymetrix and Illumina arrays. In *Genome Databases*, Jassal reviews the new version of the Reactome database and uses it to analyse the solute carrier (SLC) class of transporters. His study and the Reactome provide a basis for a number of analyses, which includes interactions, expression data, over-representation analysis and species comparison. Such analyses may provide the basis for further investigations using systems biology.

Finally, Dan Nebert reviews the book, *Designer Genes: A New Era in the Evolution of Man* by Stephen Potter (Random House; 2010).

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