## CORRECTION



## Correction to: Sequencing and comparative genome analysis of three Indians

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## Correction to: Mammalian Genome https://doi.org/10.1007/s00335-021-09882-4

The original version of this article unfortunately contained a mistake. Reference citations has been introduced in wrong places under the Introduction section in the first and fourth paragraph, instead the citations should be replaced with numerical bullet points.

Please find below the corrected paragraphs:

First paragraph.

Since 2003 when the first human genome was sequenced and analyzed (Lander et al. 2001), the sequencing technology has become affordable. Many more individual genomes sequenced since then have enriched the database of human genomic variants. The genome sequence analysis from more individuals offers several advantages. [1] The human genome variant database is still not representative of the 'human' population as several populations are either not represented at all or underrepresented. [2] Our understanding of genomic variants and their relationship with health and disease has improved over the period. Hence, individual's genomic variant analysis has now a better predictive value for the health and disease profile for an individual. [3] Haplogroups of Y-chromosome and mitochondrial chromosome have also enriched our understanding of how humans have spread out of Africa to other continents, which has substantiated our understanding of human development and history, earlier based on anthropology, linguistics, archeology, and other traditional methodology.

The original article can be found online at https://doi.org/10.1007/ s00335-021-09882-4.

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The present study was undertaken to enhance the understanding of the genomic background of the Indian population. With this objective, we initiated [1] complete sequencing and analysis of genomes of three Indians from different regions to develop their health and disease profile, [2] to look for and identify novel variants present in the Indian population, and [3] to analyze mitochondrial and Y-chromosome haplogroups to understand the routes and the time frame of the arrival of their maternal and paternal ancestors on the subcontinent.

The original article has been corrected.

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