Supplementary Text

$$inormal <- function(x)$$

$$\{$$

$$qnorm((rank(x, na.last = "keep") - 0.5) / sum(!is.na(x)))$$

$$\}$$

Custom R function to perform the quantile normal transformation, designated as *inormal*. This function accepts a dataframe, x, containing the original data values that are presumed to be non-linearly distributed. The core operation of the function is to first rank the data values while handling any NA values by keeping their position (na.last = "keep"). Each data value's rank is then normalized by subtracting 0.5 and dividing by the total count of non-NA values in the dataset. Finally, the quantile function of the standard normal distribution, qnorm, is applied to these normalized ranks, resulting in inverse normal transformed values. The transformation aims to reshape the data into a more Gaussian-like distribution, facilitating analyses that rely on the assumption of normality.

Formula was derived from the Yang J., Loos,R., Powell,J. et al 2012 [1].

1. Yang J, Loos RJF, Powell JE, et al. FTO genotype is associated with phenotypic variability of body mass index. *Nature*. 2012;490(7419):267-272. doi:10.1038/nature11401