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NET 4.0, 4GB RAM.All microarray images were background corrected, quantile-normalized and quality filtered with the LIMMA package ([@B9]) in the R statistical language (). Statistical analysis was performed using the MAS5.0 algorithm available in the robust multi-array average (RMA) package ([@B10]) in the Bioconductor project ([@B11]). All values of the signals were transformed to the logarithmic scale. 10.1136/gne-3-318-g001.Supplementary Data ========== Supplementary data are available at *Genome Biology and Evolution* online. 10.1128/gbe.00924-16.1 Signal intensity (intensity and spot signal) distribution of the microarray hybridization of each of the 12,504 genes. (A) Signal intensity distribution of all the genes analyzed by the microarrays; (B) Signal intensity distribution of genes with at least one assigned annotation; (C) Signal intensity distribution of genes with a functional annotation according to the GO and the Kegg database. The x axis represents the natural logarithm of the signal

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