

HT Atlas v1.0 database: redefining human and mouse housekeeping genes by mining massive RNA-seq datasets

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Abstract

Housekeeping (HK) genes are constitutively expressed genes that are required for the maintenance of basic cellular functions. Despite their importance in the calibration of gene expression, as well as the understanding of many genomic and evolutionary features, important discrepancies have been observed in studies that previously identified these genes. Here, we present Housekeeping Transcript Atlas (HT Atlas v1.0, www.housekeeping.unicamp.br) a web-based database which addresses some of the previously observed limitations in the identification of these genes, and offers a more accurate database of human and mouse HK genes and transcripts. The database was generated by mining massive human and mouse RNA-seq data sets from GTEx portal and ARCHS4 database. In total, 12, 482 and 507 high-quality RNA-seq data sets from 82 human non-disease tissues/cells and 15 healthy tissues/cells of C57BL/6 wild type mouse, were respectively included in our workflow. 2, 158 human transcripts from 2, 176 genes fulfilled our criteria and were referred as HK transcripts and HK genes. In the mouse database, 3, 024 HK transcripts from 3, 277 HK genes were identified. From the web interface, user can visualize the expression of those transcripts across tissues and download full lists of HK genes and transcripts. HT Atlas v1.0 also offers the most stable and suitable tissue selective reference transcripts for normalization of qPCR experiments. Some reference transcript-specific primers and predicted modifiers of gene expression for some of these HK transcripts are also proposed. All of these resources can be accessed and downloaded from any computer or small device web browsers. The database is a dockerized ShinyApp that can also be pulled from docker hub ([bidosessi/ht_atlas_v1.0](https://hub.docker.com/r/bidosessi/ht_atlas_v1.0)) in order to be locally deployed by the user.

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