

## Hkera, a human transcriptome partitioner

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**Abstract.** Developing a reliable housekeeping (HK) and tissue-specific (TS) gene classifier is of importance because it can provide an initial clue to a gene's cellular role and function. We describe here a novel HK/TS gene classifier, called HKera, developed based on a novel property of HK genes that we have previously uncovered (Shaw et al., PLoS ONE e29314 (2011)), namely that the ranking order of their expression levels, as opposed to the expression levels themselves, tends to be preserved from one tissue to another. Evaluated against multiple benchmark sets of human HK genes, including one recently derived from next generation sequencing, HKera was shown to perform significantly better than five other classifiers that use different methodologies. An enrichment analysis of pathway and gene ontology annotations showed that HKera-predicted HK and TS genes have distinct functional roles and, together, cover most of the ontology categories. These results show that HKera is a good human transcriptome partitioner that can be used to search for, and obtain useful expression and functional information for, novel HK (TS) genes.

**Keywords:** House-keeping genes; Tissue-specific genes; Transcriptome; Support vector machines