NEW TOOL TO FIND SUITABLE REFERENCEGENES

RefGenes

SUMMARY
The choice of appropriate reference genes is crucial for qRT-PCR experiments. In many cases, classical reference genes fail to provide accurate normalization because their expression varies significantly within the tested conditions. RefGenes is a user-friendly online tool that helps to find those genes that are most stable within a chosen set of tissues or conditions. This is achieved by meta-analysis of thousands of microarray experiments. Several validation experiments carried out on animal and plant species have shown that the candidates proposed by RefGenes performed significantly better as normalizers than previously used classical housekeeping genes.

BACKGROUND AND HYPOTHESIS
Reference genes are often used as internal controls for transcript quantification assays. For practical reasons, many labs tend to use “general purpose housekeeping genes” such as ACTB for any type of experiment. It has been previously shown, however, that these genes do not always perform well as normalizers. Hypothesis: for each condition there is a subset of genes that is most suitable to normalize data from this type of condition.

METHODS AND RESULTS
• The analysis was performed using 3051 mouse Affymetrix arrays
• Several tissue types were selected and the most stable genes within each of these datasets were identified.
• We compared the variance of expression of 20 classical reference genes and of the new candidate genes a) across all tissues, and b) within each tissue type

Conclusion: genes that were selected to be stable within a set of conditions had a standard deviation of 2 to 5 times lower than classical reference genes in these conditions, and 2 to 3 times lower than RefGenes candidates selected for their stability over all conditions.

TOOL DESCRIPTION
• RefGenes is a new tool from Genevestigator. It allows you to choose an organism and a set of conditions, and it will return a list of genes stable within these conditions.
• You can define the range of expression so that you can find reference genes with low, medium, or high transcript abundance.
• It also allows you to display other genes for comparison, for example your traditional reference genes, or the target genes that you are amplifying by qRT-PCR.

ACCESS
RefGenes is accessible at www.genevestigator.com.

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