Correction

Correction: A DNA microarray survey of gene expression in normal human tissues

Radha Shyamsundar*†, Young H Kim*, John P Higgins*, Kelli Montgomery*, Michelle Jorden*, Anand Sethuraman‡, Matt van de Rijn*†, David Botstein‡¶, Patrick O Brown†§ and Jonathan R Pollack*

Addresses: *Department of Pathology, Stanford University, Stanford, CA 94305, USA. †Department of Biochemistry, Stanford University, Stanford, CA 94305, USA. ‡Department of Genetics, Stanford University, Stanford, CA 94305, USA. § Howard Hughes Medical Institute, Stanford University, Stanford, CA 94305, USA. ¶Current address: Lewis-Sigler Institute for Integrative Genomics, Princeton University, Princeton, NJ 80544, USA.

Correspondence: Patrick O Brown. Email: pbrown@cmgm.stanford.edu. Jonathan R Pollack. Email: pollack1@stanford.edu

Published: 19 August 2005

Genome ***Biology*** 2005, **6:**404 (doi:10.1186/gb-2005-6-9-404)

The electronic version of this article is the complete one and can be found online at http://genomebiology.com/2005/6/9/404

Received: 22 July 2005
Accepted: 29 July 2005

We wish to report two corrections to our study [1], neither of which alters the interpretation of the data or the conclusions drawn. First, we have discovered that the data file from a microarray hybridization (prostate RNA versus normal genomic DNA) used to derive the plot in Figure 4a became corrupted during data processing. The corrected plot (Figure 4a) displays a stronger correlation between directly and indirectly estimated transcript levels, indicating even better performance of our method of estimating transcript abundance. The corrected data file has been deposited to the Stanford Microarray Database (SMD) and Gene Expression Omnibus (GEO) repositories. Second, we have identified a 'frame-shift' in the Additional data file 2 (Sheet 5) data set; the corrected data file has been deposited to the supplemental site.

Additional data files

Additional data file 2 contains a corrected list of the variably expressed genes.

References

1. Shyamsundar R, Kim YH, Higgins JP, Montgomery K, Jorden M, Sethuraman A, van de Rijn M, Botstein D, Brown PO, Pollack JR: **A DNA microarray survey of gene expression in normal human tissues**. *Genome Biol* 2005, **6:**R22.

(See the corrected figure on the next page)

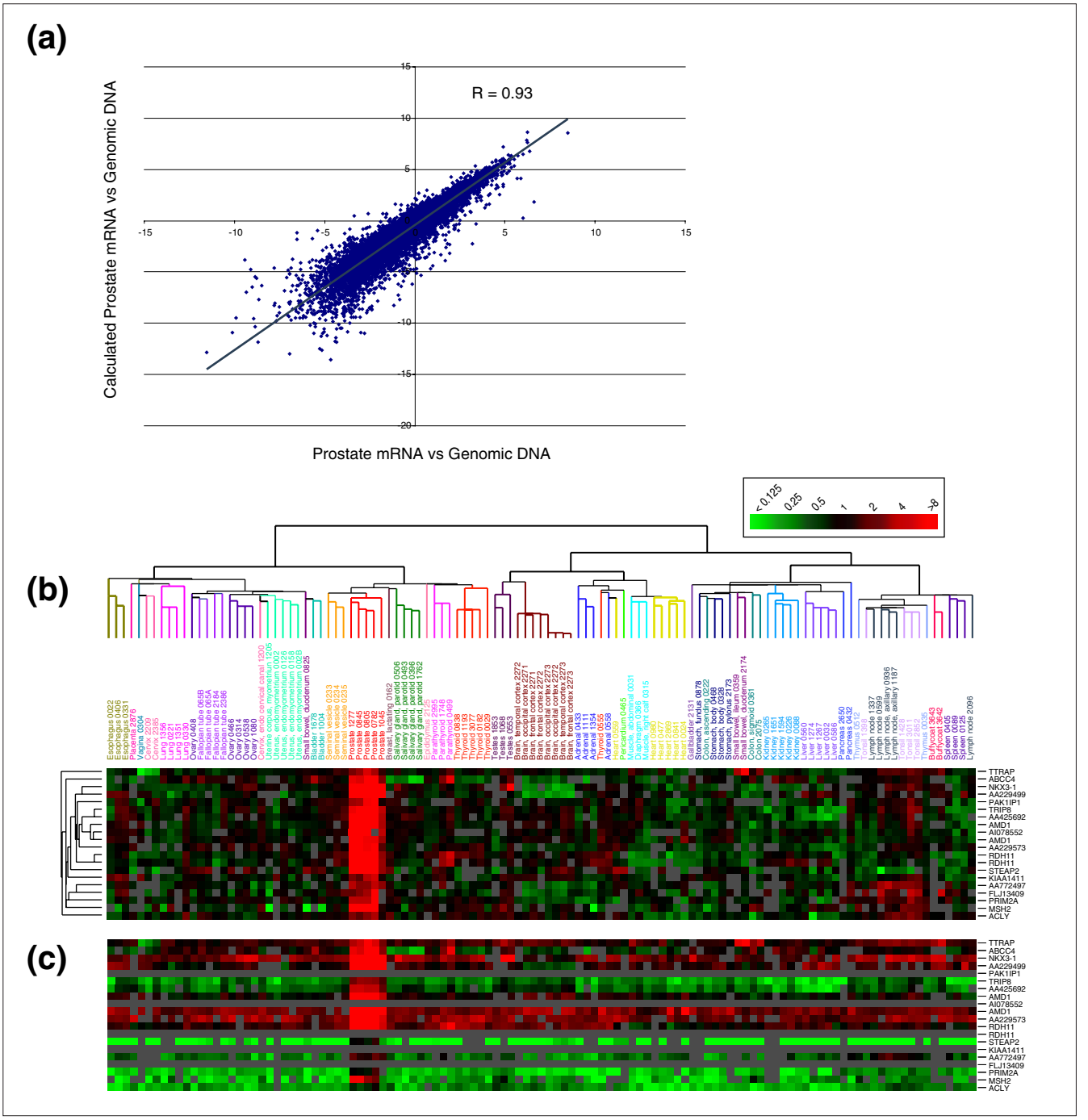

Figure 4
Estimating relative transcript abundance. **(a)** Comparison of transcript levels estimated either directly by hybridization of prostate sample mRNA versus normal female genomic DNA, or indirectly by multiplying the ratio of prostate sample mRNA versus common reference mRNA by the ratio of common reference mRNA versus normal female genomic DNA. The correlation value (R) is indicated. **(b)** Prostate-specific gene expression cluster, extracted from the hierarchical cluster shown in Figure 1a, displayed as mean-centered relative gene expression (ratio-fold change scale indicated). **(c)** The same gene expression feature as in (b), now displayed as transcript abundance (relative to the average transcript level for all expressed genes), calculated indirectly using the common reference mRNA versus normal female genomic DNA hybridization data.