

CORRECTION

Open Access



Correction to: the impact of pharmacokinetic gene profiles across human cancers

Michael T. Zimmermann^{1,2}, Terry M. Therneau¹ and Jean-Pierre A. Kocher^{1*}

Correction to: BMC Cancer (2018) 18:577 DOI <https://doi.org/10.1186/s12885-018-4345-2>

It has been highlighted that in the original manuscript [1] Fig. 1 was omitted and Fig. 2 appeared twice. This Correction article shows the correct Fig. 1. The original article has been updated.

Author details

¹Division of Biomedical Statistics and Informatics, Department of Health Sciences Research, College of Medicine, Mayo Clinic, 200 First Street SW, Rochester, MN 55905, USA. ²Present Address: Genomic Science and Precision Medicine Center, Clinical and Translational Sciences Institute, Medical College of Wisconsin, Milwaukee, WI 53226, USA.

Received: 15 June 2018 Accepted: 15 June 2018

Published online: 18 July 2018

Reference

1. Zimmermann MT, et al. The impact of pharmacokinetic gene profiles across human cancers. *BMC Cancer*. 2018) May;18:577.

* Correspondence: kocher.jeanpierre@mayo.edu

¹Division of Biomedical Statistics and Informatics, Department of Health Sciences Research, College of Medicine, Mayo Clinic, 200 First Street SW, Rochester, MN 55905, USA



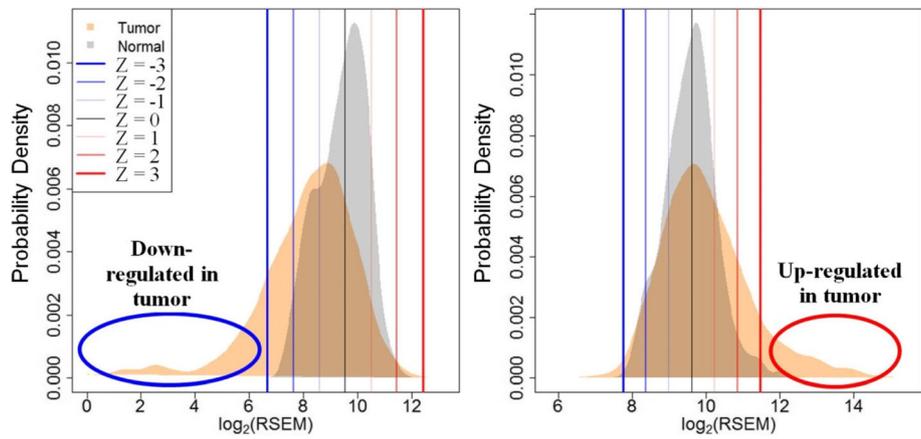


Fig. 1 Human tumors may up- or down-regulate PK genes. Each gene was scored relative to a composite-normal reference to generate conservative, Q6 f1:2 estimates of aberrant somatic gene expression. RSEM normalized gene expression data were used. The expression score of each gene in each tumor. f1:3 sample is the signed Z-score relative to normal tissue samples. Example probability density distributions of gene expression for two genes are shown: f1:4 (Left) drug importer SLC16A2 and (Right) drug exporter ABCC5