Corrigendum

COHCAP: an integrative genomic pipeline for single-nucleotide resolution DNA methylation analysis

Charles D. Warden¹,²,* , Heehyoung Lee³, Joshua D. Tompkins⁴,⁵, Xiaojin Li⁶,⁷, Charles Wang⁶,⁷, Arthur D. Riggs⁴,⁵, Hua Yu³, Richard Jove² and Yate-Ching Yuan¹,²,*

¹Bioinformatics Core, City of Hope National Medical Center, Duarte, CA, 91010, USA, ²Department of Molecular Medicine, City of Hope National Medical Center, Duarte, CA, 91010, USA, ³Cancer Immunotherapeutics and Immunology, City of Hope National Medical Center, Duarte, CA, 91010, USA, ⁴Department of Biology, City of Hope National Medical Center, Duarte, CA, 91010, USA, ⁵Department of Diabetes and Metabolic Disease Research, City of Hope National Medical Center, Duarte, CA, 91010, USA and ⁶Functional Genomics Core, City of Hope National Medical Center, Duarte, CA, 91010, USA

Nucleic Acids Research, 2013, 41(11): e117, https://doi.org/10.1093/nar/gkt242

The Authors wish to make the following corrections to their article.

1. In the Discussion, the sentence ‘Interestingly, the region with the clearest differential methylation is located near the translation start site for ESR1 but not the Ref/Seq transcription start site’ should refer to the overall consensus transcription start site: there are other transcripts that start closer to the coding sequence.

2. The Linux operating system information in Table S4 and Table S12 is not correct: ‘CentOS Red Hat’ should be ‘CentOS’

3. Typos: extra ‘Supplemental’ in Figure reference on page #7 in Results (including partial sentence re-write):

CURRENT: Therefore, the estrogen receptor scatter plot (Supplementary Figure 3B) also does a good job of showing that the correlation between DNA methylation and gene expression not only is limited to population-level differences between two groups (such as shown in Supplementary Figure 3A) but also can detect covariance within groups (especially for large heterogeneous datasets like the TCGA dataset).

CORRECTED: Therefore, the estrogen receptor scatter plot (Figure 3B) also does a good job of showing the correlation between DNA methylation and gene expression in a large heterogeneous dataset like the TCGA dataset, in addition to the overall difference in methylation between primary and normal samples (Figure 3A).

4. Typo: Supplementary Figure S15 instead of S11 in a different sentence on page #7 of Results:

*To whom correspondence should be addressed. Charles D. Warden. Tel: +16 262 180375; Email: cwarden@coh.org
Correspondence may also be addressed to Yate-Ching Yuan. Tel: +16 262 183161; Email: yyuan@coh.org

Present addresses:
Charles D. Warden, Integrative Genomics Core, Department of Molecular & Cellular Biology, City of Hope National Medical Center, Duarte, CA, 91010, USA.
Heehyoung Lee, LumeBio, Inc., Seoul, Korea.
Joshua D. Tompkins, Diabetes and Metabolism Research Institute, City of Hope National Medical Center, Duarte, CA, 91010, USA.
Xiaojin Li, Guardant Health, Redwood City, CA 94063, USA.
Charles Wang, Center for Genomics, Loma Linda University, CA, 92350, USA, and Department of Basic Sciences, Loma Linda University, CA, 92350, USA.
Arthur D. Riggs, Diabetes and Metabolism Research Institute, City of Hope National Medical Center, Duarte, CA, 91010, USA.
Hua Yu, Department of Immuno-Oncology, City of Hope National Medical Center, Duarte, CA, 91010, USA.
Richard Jove, Cell Therapy Institute, Nova Southeastern University, Fort Lauderdale, FL 33314, USA.
Yate-Ching Yuan, Bioinformatics Core, City of Hope National Medical Center, Duarte, CA, 91010, USA and Division of Research Informatics, Center for Informatics, City of Hope National Medical Center, Duarte, CA, 91010, USA.

© The Author(s) 2019. Published by Oxford University Press on behalf of Nucleic Acids Research. This is an Open Access article distributed under the terms of the Creative Commons Attribution Non-Commercial License (http://creativecommons.org/licenses/by-nc/4.0/), which permits non-commercial re-use, distribution, and reproduction in any medium, provided the original work is properly cited. For commercial re-use, please contact journals.permissions@oup.com
CURRENT: As expected, ESR1 methylation levels are significantly negatively correlated with gene expression levels in tumours alone \( (r = 0.63, p = 4.1 \times 10^{-38}, \text{Supplementary Figure S11}) \).

CORRECTED: As expected, ESR1 methylation levels are significantly negatively correlated with gene expression levels in tumours alone \( (r = 0.63, p = 4.1 \times 10^{-38}, \text{Supplementary Figure S15}) \).

5. Typo: should be ‘>’ instead of ‘<’ on page #4 in Supplemental Methods:

CURRENT: Sample TCGA-BH-A0AW-01A was removed from the ER+ vs. ER- analysis because it showed a high proportion of probes with detection p-value < 0.05.

CORRECTED: Sample TCGA-BH-A0AW-01A was removed from the ER+ vs. ER- analysis because it showed a high proportion of probes with detection p-value > 0.05.