Corrigendum

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

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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 RefSeq 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:

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CURRENT: As expected, ESR1 methylation levels are significantly negatively correlated with gene expression levels in tumors alone (r = 0.63, p = 4.1 × 10∧38, Supplementary Figure **S11**).

CORRECTED: As expected, ESR1 methylation levels are significantly negatively correlated with gene expression levels in tumors alone (r = 0.63, p = 4.1 × 10∧38, 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.