

CORRECTION

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Genome-wide analysis of the mouse lung transcriptome reveals novel molecular gene interaction networks and cell-specific expression signatures

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Text

After publication of our article [1], we became aware of a typographical error in the Methods section, which concerned the statement about the p-value of an LRS of 18 or higher in our QTL analysis. Below is the first part of the corresponding chapter with the corrected p-value (marked in bold). We apologize for any inconvenience.

QTL Mapping and expression analyses

All probe sets were mapped using standard interval mapping methods at 1 cM intervals (~2 Mb) along all autosomes and the X chromosome. This procedure generates estimates of linkage between variation in transcript expression levels and chromosomal location. The entire set of values can be used to construct a set of QTL maps for all chromosomes (except Chr Y and the mitochondrial genome) in which position is plotted on the x-axis and the strength of linkage—the likelihood ratio statistic (LRS) or log of the odds ratio (LOD)—is plotted on the y-axis. An LRS of 18 or higher is significant at a genome-wide **p-value of < 0.05**.

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Reference

1. Alberts R, Lu L, Williams RW, Schughart K: Genome-wide analysis of the mouse lung transcriptome reveals novel molecular gene interaction networks and cell-specific expression signatures. *Respir Res* 2011, **12**:61.

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