

AUTHOR CORRECTION

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Correction to: Novel risk genes and mechanisms implicated by exome sequencing of 2572 individuals with pulmonary arterial hypertension

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Correction to: *Genome Med* 11, 69 (2019)
<https://doi.org/10.1186/s13073-019-0685-z>

Following publication of the original article [1], two errors were identified in the Results section.

1. The sentence currently reads:

“For IPAH, we observed significant associations for BMPR2 ($p = 1.0E - 7$, FDR = $9.0E - 04$), KLK1 ($p = 1.0E - 7$, FDR = $9.0E - 04$), and GGCX ($p = 5.0E - 07$, FDR = 0.002) (see Fig. 4).

The sentence should read

“For IPAH, we observed significant associations for BMPR2 ($p = 1.0E - 7$, FDR = $9.0E - 04$), KLK1 ($p = 1.0E - 7$, FDR = $9.0E - 04$), and GGCX ($p = 1.9E - 06$, FDR = 0.013).

Further down in the text:

2. The sentence currently reads:

“Likewise, while the association signal for GDF2 fell below the cutoff ($p = 3.0E - 07$, FDR = 0.002), we clearly provide confirmation of this new PAH risk gene”.

The sentence should read:

“Likewise, while the association signal for GDF2 fell below the cutoff ($p = 3.2E - 06$, FDR = 0.016), we clearly provide confirmation of this new PAH risk gene”.

The original article [1] has been corrected.

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The original article can be found online at <https://doi.org/10.1186/s13073-019-0685-z>.

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