



## Author Correction: Exome sequencing identifies breast cancer susceptibility genes and defines the contribution of coding variants to breast cancer risk

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In the version of the article initially published, in the sentence in the Abstract now reading “Associations were also observed for *LZTR1*, *ATRIP* and *BARD1* with  $P < 1 \times 10^{-4}$ ”, “*ATRIP*” appeared incorrectly as “*ATR*”. This has now been corrected in the PDF and HTML versions of the article.

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