Author's response to reviews

Title: Variants in KCNQ1 increase type II diabetes susceptibility in South Asians
A study of 3,310 subjects from India and the US

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Author's response to reviews: see over
Point-by-point response:
There is probably a typo on page 16 "0.94; 95% CI [0.72-1.21], p=0.003) for ACA" as it is not possible to get a p-value of 0.003 when the confidence interval is [0.72 - 1.21].

We rechecked these values and noticed that it was not a typo. After reanalyzing the data carefully and observed that the p-values in our haplotype analysis were correct but the 95% CIs were incorrect.

Logistic haplotype analysis in PLINK does not provide 95% CI. Therefore, we used conditional haplotype analysis in PLINK to calculate the p-values from the adjusted analysis with 95%CI – accounting for the covariates. The effect of the adjustments is typically that the unexplained variance is reduced, which leads to smaller standard deviations, that further leads to tighter/narrower 95% CIs. In conditional haplotype analysis, we noticed that while adjusting for the covariates we get the 95% CI, but it was comparing all results to one haplotype rather than comparing each haplotype to all other haplotypes. This was the reason for getting strange CI. Now we have corrected this option and obtained correct estimates of OR and CI. We further validated these findings in logistic haplotype analysis by calculating 95% CI manually. Accordingly, we have revised Table 4 and text on Page 16.

We thank you for pointing out this very critical error and we apologize for this discrepancy.

We also added our statistician Dr. Chris Aston as co-author as he reanalyzed the data and helped correcting this error.

The corrections in the manuscript on page 16 and Table 4 are presented in track-changes.

We hope to hear a positive response this time.

Sincere regards,

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