

Erratum to: Evidence of statistical epistasis between DISC1, CIT and NDEL1 impacting risk for schizophrenia: biological validation with functional neuroimaging

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Authors regret that Figs. 2 and 3 labeling in the online published article, color indication for graph bars “Non-risk” and “Risk” were inadvertently swapped. The corrected figures are given below.

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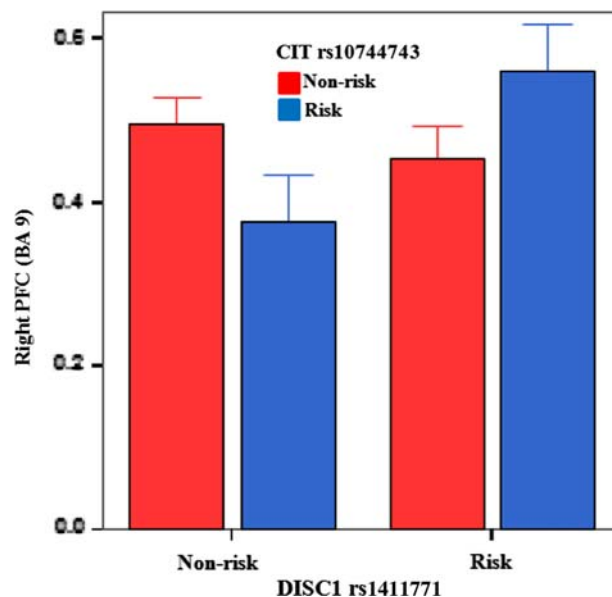
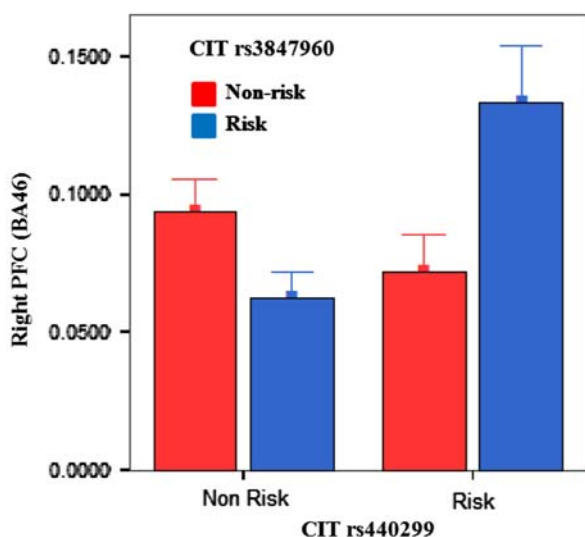
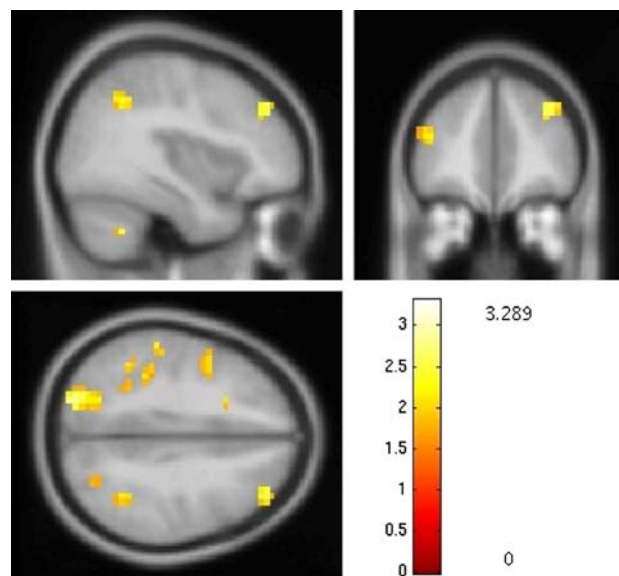
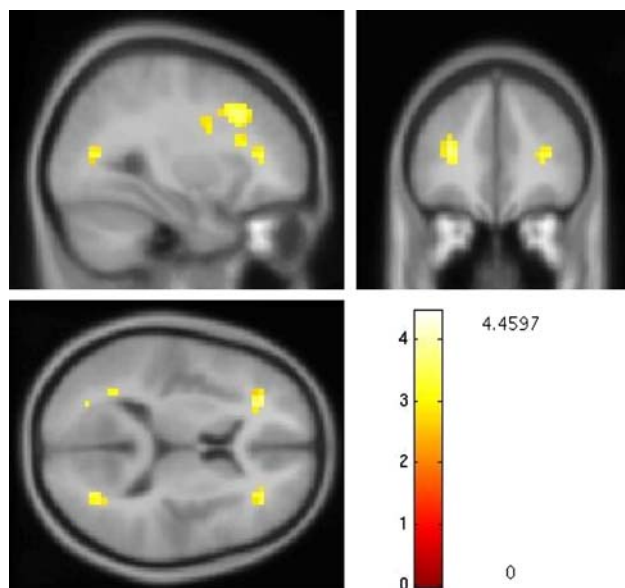


Fig. 2 CIT intragenic neuroimaging epistasis. CIT rs3847960 by CIT rs440299 interaction in normal subjects studied with BOLD fMRI during the N back working memory task. Figure at the *top* shows loci (in *yellow*) within brain in which significant interaction is found ($p < 0.05$ corrected) for all voxels within prefrontal cortical region of interest. Image at *bottom* shows relative degree of activation of DLPFC region showing imaging interaction based on genotypes at these two SNPs [fMRI signal extracted from maximum voxel and run as ANOVA in SPSS yielded $F(1,256) = 9.960$, $p = 0.002$]. The combination of both risk associated genotypes is disproportionately inefficient, i.e., have greatest activation without any difference in performance. *Error bars* represent 1 standard error of the mean. Frontal lobe (sub-gyral) mean activation extracted from 10 mm sphere at (30 37 8) Talairach

Fig. 3 DISC1 by CIT neuroimaging epistasis. DISC1 rs1411771 by CIT rs10744743 interaction in 217 normal subjects studied with BOLD fMRI during the N-back working memory task. The cross-sectional brain images at top figure show loci (in *yellow*) within brain showing a significant inefficiency effect associated with DISC1 risk \times CIT risk SNPs ($p < 0.05$ small volume correction SVC). The graph at bottom compares a measure of fMRI activation during this task for each genotype combination extracted from right PFC yielding a significant epistatic interaction [fMRI signal extracted from maximum voxel and run as ANOVA in SPSS yielded $F(1,213) = 5.3$ $p < 0.05$]