Authors reporting human genetic association analyses are encouraged to review the journal standard's for the publication of such studies. Studies that do not meet these standards may be rejected by the Editors.

1. Studies need to be sufficiently large to have enough power to detect an effect. This is particularly important where minor allele frequencies are low.

2. Negative studies should always include effect sizes and a power analysis indicating that the study was sufficiently powered to detect an effect. Negative studies should be based on an attempt to replicate previous studies.

3. Where multiple markers and phenotypes are examined, P values must be corrected for multiple comparisons.

4. Studies are strengthened by reporting replication of findings in an independent sample, or replicating the findings in a directly comparable study(ies).

5. Non-replicated studies may be strengthened by convergent, corroborating evidence from other lines of evidence, for example by demonstrating the effect of the studied gene variant on molecular and/or neural functions, or showing relevant phenotypic alterations in genetically-engineered animals.

6. A clear rationale should be provided for candidate gene studies and for the selection of genetic polymorphisms. Tag SNPs should be selected to permit a comprehensive analysis of variation across the gene. The pattern of linkage disequilibrium across the gene should be demonstrated and haplotype analyses should be performed where appropriate. Studies that focus on the analysis of one polymorphism will only be considered for cases with compelling grounds of functionality from supporting evidence provided or from prior studies.

7. Information about subject ethnicity, and how it was determined, should be provided. Studies are strengthened by controlling for potential population stratification, for example by the use of family based association studies or ancestry informative markers.

8. For genome-wide association studies, the threshold for significance is a P value less than $5x10^{-8}$. This threshold should be adjusted for the total number of phenotypes investigated.