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Dear Dr. Cho,

Thank you for the opportunity to publish in Nature Communications. We have the following comments in response to the editorial requests.

1) We have reviewed and made the necessary changes to the manuscript, using ‘track changes’ to mark out all the amendments.

2) Regarding our results being deposited in publically hosted databases, we have reviewed the criteria for NCBI and EBI data submission and concluded that they will not be accommodated. Our datasets are already publicly available (e.g. ENCODE and gEUVADIS) and our allele-specific results are not experimentally verified from experiments such as microarrays. In any case, we have arranged to deposit the personal genomes of 382 individuals on the 1000 Genomes Project DCC at URL ftp://ftp.1000genomes.ebi.ac.uk/vol1/ftp/data\_collections/1000\_genomes\_project/working/, so that the resource can be accessed by more people. Furthermore, we will provide our results of SNVs associated with allele-specific binding and expression as Supplementary Data (tab-delimited files).

3) For reporting of our statistical results, we have described very clearly the tests we used in various analyses, the p values, FDR thresholds and the parameters. For describing Methods, we have provided detailed descriptions of all the datasets we used in this study and the tests and methodologies we implemented to obtain accessible and allele-specific SNVs. We have also made sure that the ‘methods’ and ‘legends’ sections comply with the checklist for authors.

4) We would like to amend the editor’s summary to the following:

Using variants from the 1000-Genomes Project, RNA-seq and ChIP-seq data from related projects, this study describes a resource and survey of allele-specific binding and gene expression. A catalog of allelic SNPs and annotation elements is available as an online resource at [alleledb.gersteinlab.org](http://www.alleledb.gersteinlab.org).

5) The referees did not have any comments in this round of submission, hence we are not providing a separate document for point-by-point response.

Yours sincerely,

Mark Gerstein

Albert L. Williams Professor of Biomedical Informatics,

 Co-chair of 1000 Genomes Project Consortium Functional Interpretation Group