# Review of: "Statistical and functional convergence of common and rare variant risk for autism spectrum disorders at chromosome 16p"

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The authors demonstrated the feasibility of 33Mb genomic region in the p arm of chromosome 16 for the possible biological insight with regards to ASD. They have used common polygenic risk score, statistical framework, and chromatin contact patterns to provide insight into ASD liability.

The followings are the observations:

1. The strong statistical analysis being used to quantify the genomic variations in chromosome 16 p arm.
2. pTDT is more appropriate to establish the linkage with the variants.
3. Deletion analysis in the cell line is also an appropriate approach.
4. Hi-C analysis could have been explained better for the chromatin compaction.
5. Overall genome scan to link 16p arm for ASD is lacking.
6. The utilization of whole genome and exome data could have been used for the better interpretation.
7. It could have been supported by the pathway analysis to understand the function of the risk genes.