Comments to the Authors,

In this manuscript, Dr. Rivandi provided a comprehensive summary and for the future Post-GWAS solution and strategy to elucidate the underlying functional mechanisms of breast cancer susceptibility.

**Major Compulsory Revisions**

1, It would be helpful to provide the evidence supporting 'these causal SNPs usually display a stronger association with breast cancer risk than the original GWAS-identified SNPs'

2, the most exciting gene edit technique CRSP was not mentioned in the manuscript and it should be mentioned in post-GWAS study.

3, More recent susceptibility studies on breast cancer based on TWAS and EWAS could be provided, especially, whether they could validated the GWAS discovery.

4. [PheWAS](https://phewascatalog.org/) in breast cancer is another field to be mentioned in the manuscript.