In this manuscript, Dr. Xia and colleagues conducted functional variant scanning for rheumatoid arthritis by the bioinformatics analysis to miRNA binding sites and eQTL database and the prediction result was validated by serials of biological experiments including allelic expression imbalance and dual-luciferase reporter gene assay. The author demonstrate that rs907091 in 3’UTR of IKZF3 contribute to the pathogenesis of RA through binding to miR-326 and miR-330-5p.The study was performed rigorously and the findings are interesting except the biological validation is limited. I only have several concerns:

**Major Compulsory Revisions**

1. The manuscript was disordered with large number reference in the result section, please re-order the manuscript and provide a clear background and result section. Parts of the contents should be placed in method section for example TargetScan, Miranda etc.
2. The author should give the clear method how the 11,186 RA-SNPs were selected and what’s the list for these 11,186 RA-SNP since as I known GWAS have never identified as much as 11,186 significant SNPs.
3. What’s the logic to do the Gene Ontology analysis to 28 overlapped genes? And what’s enrichment could demonstrate should be mentioned in the method section.

**Minor Essential Revisions and Discretionary Revisions**

1. In the page 6, line 209, the GSE ID for the dataset should be provided in the manuscript.
2. It will be helpful if the author should provide a Figure to show the biological hypothesis between miR-326 and miR-330-5p, rs907091 and IKZF3.
3. Only rs907091was validated by TargetScan, Miranda, PITA and miRTarBase validation in the study, actually, all the SNPs should be conducted similar analysis and show it in the supplementary Table 1.
4. Table 1 and Table 2 didn’t give any meaningful conclusion and can be moved to the supplementary Tables while Supplementary Figure 1 will be helpful for the main manuscript.
5. Table 3 should be give statistical significance.
6. Figure 1 should be change to dot plot to show the sample size.
7. Expression levels of miR-326 and miR-330-5p should be mentioned in RA and check whether it is consistent with the model provided by the authors.