Comments to the Editor,

This manuscript studied the association between the LILRA3 deletion and SSc in large-scale Japanese population. In the present study, LILRA3 deletion polymorphisms were found significantly associated with risk of ATA+ SSc. In addition, LILRA3 deletion allele was found significantly increased in ATA+ACA- Ssc . The study was performed rigorously and the findings are interesting. In general, I'd recommend publication if the authors can address the following concerns.

1, Gene deletion is a specific form of copy number variation. The progress of associations between the copy number variations and SSC should be introduced carefully in the background section.

2, The relationship between LILRA3 deletion and ATA+ Ssc should be reported after the adjustment with the covariates of ACA, age, gender and ILD.

3, The primer design is interesting. What will happen suppose certain small fragment was deleted between exon 1 to exon 6?

4, Is there any median significant region which is located in or adjacent with LILRA3 from previous GWAS study?

5, Power estimation for recessive and dominant model also should be provided as supplementary.

6, All the possible comparison between the subtypes of the cases should be carried out in Table 4, although there are no significant association were found. There are still lots of information for the readers.

7, Is there any evidence showed the gene expression of LILRA3 was decreased in ATA+ SSC patients?

8, How to understand the complex directions of the association between LILRA3 and different autoimmune diseases?