Comments to the Authors,

This manuscript conducted a meta-analysis to quantitatively evaluate the association between VDP and chronic obstructive pulmonary disease (COPD). The authors found the significant association between the polymorphism of a triallelic SNP in GC genes and COPD. In addition, GC1F allele was demonstrated to be a risk factor while the GC1S and GC2 allele were indicated to be protective factors. What’s more interesting, the authors found such association might be population specific event which existed in Asian population rather than in the Caucasians population. The study was performed rigorously and the findings are interesting. In general, I'd recommend publication if the authors can address the following concerns.

**Major Compulsory Revisions**

1, the meta-analysis between VDP and COPD should be conducted in co-dominant genetic model and the most appreciated genetic model (dominant, recessive or co-dominant model) should be selected to make the eventual meta-analysis. The following paper can be taken as the reference.

[Association between ABCG2 Q141K polymorphism and gout risk affected by ethnicity and gender: a systematic review and meta‐analysis](https://scholar.google.com/citations?view_op=view_citation&hl=en&user=4tIViCAAAAAJ&sortby=pubdate&citation_for_view=4tIViCAAAAAJ:QUX0mv85b1cC). Z Dong, S Guo, Y Yang, J Wu, M Guan, H Zou, L Jin, J Wang, 2014, International Journal of Rheumatic Diseases.

**Minor Essential Revisions**

1, as authors mentioned, VDP might be the one of the most important COPD associated genes, except Alpha 1-Antitrypsin gene, therefore, I want to know the diagnosis potential of the polymorphism of VDP to COPD. The diagnostic performance of polymorphism of VDP to COPD could be evaluated with its summary ROC. I guess the AUC of the SROC would not be very high, however, I still want to check the result of the SROC analysis. The following paper can be taken as the reference.

[Quantitative assessment of the diagnostic role of APC promoter methylation in non-small cell lung cancer](https://scholar.google.com/citations?view_op=view_citation&hl=en&user=4tIViCAAAAAJ&sortby=pubdate&citation_for_view=4tIViCAAAAAJ:-jrNzM816MMC), S Guo, L Tan, W Pu, J Wu, K Xu, J Wu, Q Li, Y Ma, J Xu, L Jin, J Wang. Clinical epigenetics 6 (1), 5.

2, Meta-regression analysis should be conducted to check the heterogeneity source which caused the great difference between the individual studies. The procedure of meta-regression can also be found in above reference.

3, I cannot find the location of reference 1-16 in the main body of the manuscript.

4, I think Gc-globulin (GC) gene should be assigned with the more popular gene symbol of “vitamin D binding protein (Gc)”. In the association, gene name rather than a protein name should be used in the association and meta-analysis.

5, rarer variants should be rare in page 5.

6, GC1F, GC1S and GC2 could be used only after the definition in the abstract.

7, The latest progress of the GWAS and twins-based heritability study to COPD should be introduced in the background section.

8, The Rs-number for the variation should be provided in the abstract.

9, The risk to be a COPD patient when the allele is GC1s compared to GC2 should be provided.

10, The figure of the sensitivity analysis should be provided even as the supplementary.

11, The sentence of “Future studies are needed to validate our conclusions” in the abstract, should be removed because it is not the conclusion.