In this manuscript, Dr. Cheng and colleagues conducted an association study between two SNPs in PTPN12 and non-small cell lung cancer in a large Chinese population (1113 NSCLC vs 915 control). I only several tiny concerns:

**Major Compulsory Revisions**

1. The author mentioned the GWAS study, however, they didn’t mentioned whether significant SNPs were identified nearby PTPN12 regions? and what’s the LD between two candidate SNPs with these GWAS significant SNPs. Why the author select these two SNPs if the LD is not strong should be explained.
2. When the author select candidate SNPs, why allele count=2 and MAF>0.05 were applied? The authors want to identify functional variants or the associations variants should be declared in the background section.
3. The samples collected in the study were belong to South Chinese population or North Chinese population should be declared.