In the manuscript “Interferon-Gamma and Interleukin-10 Genetic Polymorphisms among Pulmonary Tuberculosis Caused by the Malaysia-Specific Mycobacterium tuberculosis Strain: SIT745/EAI1-MYS” by Nik Mohd Noor Nik Zuraina et al., the authors aim to investigate the role of IFN-γ (+874) A/T and IL-10 (-1082) A/G SNPs in tuberculosis (TB) disease susceptibility among patients infected with the M. tuberculosis SIT745/EAI1-MYS strain. While the study addresses an important question, there are several significant methodological issues that need to be addressed before it can be considered for publication in PeerJ.

Main concerns:

Sample Size: The sample sizes of the groups are insufficient (n = 9) to reliably detect significant differences. Statistical power analysis should have been conducted prior to the study to ensure that the sample size is adequate. Given that the TB-SIT745/EAI1-MYS lineage is common in Malaysia, it would be more appropriate to analyze larger sample groups to provide more meaningful and generalizable results.

Statistical Tests: The statistical tests used in the manuscript do not align with the study’s primary objective. To properly assess the role of genetic variants in TB susceptibility, the authors should have separately compared the genetic variants in the TB-SIT745/EAI1-MYS group to those in healthy controls and patients infected with non-SIT745/EAI1-MYS strains, ideally using much larger groups. This comparison would provide a more robust framework to interpret the genetic associations.

Clinical Group Matching: The authors state that subjects had no history of immune-related disorders. However,most of their patients have diabetes mellitus, which is known to suppress the immune system. This discrepancy raises concerns regarding the comparability of the groups. It is essential to match the groups by clinical parameters, including diabetes status, to minimize confounding effects.