In this manuscript, Dr. Saw T. Wah and colleagues conducted a candidate based association study between 3 miR-SNPs (rs895819, rs57095329, rs2910164) and risk of Cerebral Malaria in 110 cerebral malaria and 207 uncomplicated malaria cases collected from Thai Population. The authors first enriched the potential cerebral Malaria associated miRNA with text-mining and bioinformatics method and then validated 3 interesting miR-SNPs in specific Thai population. This study has some specific interesting points, such as first miR-SNP research in cerebral Malaria patients, specific Thai population. It is quite good research strategy to identify cerebral Malaria associated functional miR-SNPs. However, there are several important concerns should be paid attention. I’d like to recommend the manuscript to be published if the authors could solve all the problems.

Major Compulsory Revisions

1, The text-mining and bioinformatics strategy significantly influence the study design and miRNA-SNPs enrollment. A full and clear diagram should be provided to show the details of the miRNA-SNP selection.

2, Power estimation should be provided to show the negative association is not caused by limited samples size or some other confounders.

3, Please check the Table 3 carefully, especially the P-values and OR. Such as OR=0.84(0.41-1.73) with P-value=0.045, it is a little confusing. Meanwhile, reference should be noted clearly in Table 3.

4, In the table 2, I don’t know why some other different models are ignored, such as additive model, multiplicative models.

5, Another independent validation must be conducted to make sure the association is consistent and stable, considering the sample size is quite limited in current study as well as the P-values are quite nearby the marginal statistical significance levels.

6, As a systemic study, all the miRNA-SNPs are recommended to be investigate in current study and then it will be an interesting, comprehensive and solid study design and will have high citation to this research field.

Minor Revisions

1, Genomic coordination of the miRNA could be provided and apply full official miRNA name is fully recommended.

2, In the Figure 2D, the SNPs locations are recommend to be noted.

3, Title of the Figure 2 can make little change since some miRNA target are validated such as [ATP10B](http://www.ensembl.org/Homo_sapiens/Gene/Summary?g=ENSG00000118322.8) and miR-27-3p while some miRNA are predicted and without experimental validation.

4, a full explanation model should be provided among polymorphism, miRNA-Gene-target interaction and gene expression in