In this manuscript, Dr. Zhang and colleagues conducted a genome-wide methylation analysis to skeletal muscle satellite cells from different development stages of the mouse (2W, 6W, 8W and 12W) with MeDIP-seq. Meanwhile, the authors applied RNA-seq to identify differential expressed genes, which might be caused by hyper/hypo-methylation. The study was performed rigorously and the findings are interesting. However, the manuscript was not well prepared, especially for the data analysis. The following comments hope to be helpful to improve the study.

**Major Compulsory Revisions**

1. The authors should explain why “higher coverage area had lower sequencing depth”
2. The author observed 52,809-123,317 peaks which covering 1.7%-1.79% mouse genome, the question is what’s the expected regions?
3. Figure 2C, different features have different distance unit, how to compare them within one figure? Same distance unit should be guaranteed.
4. The manuscript should be slimed and remove duplicated words, such as: The top 30 GO terms were showed in Figure 4A, including positive regulation of cell migration, positive regulation of smooth muscle cell proliferation, Wnt signaling pathway, calcium 172 modulating pathway, and 173 regulation of cell proliferation (Figure 4A). Figure 4A was repeat used twice. Please check the full manuscript.
5. The raw fastq files of MeDIP-Seq and RNA-seq should be uploaded to GEO and SRA database.
6. Please replace “non-CpG island” with outside of CpG island regions.
7. Satellite cell isolation should be briefly introduced rather than completely ignored and just mention the reference.
8. What’s the exactly sample size for MeDIP-seq and RNA-seq data, 8 or 12? Whether the MeDIP-seq data is paired with RNA-seq data?
9. Theoretically, I quite understand DEGs in Wnt, Tgfb are enriched in the development of skeletal muscle, However, I don’t understand why the overlap genes between DMR and DEG should be enriched in Wnt and Tgfb.
10. In the method section, RNA-seq and data analysis should be ahead of DMGs.
11. I am wondering why 4W and 10W were ignored in the study. Is there any preliminary data to support the time-window selection.
12. Figure 1 actually provided nothing to the study. It would be helpful to show some other statistics such as 1) the change of the peak numbers between difference stage 2) the change of the genomic coverage between difference phases. 3) the consistence between MeDIP data with previous published BS-Seq data if they are existed.
13. How to understand the difference between Figure 2A and 2B should be explained, specially the number peaks in intron regions from 6W is significantly higher compared with other stages while the unique peaks don’t have this features. Figure 2C have too many curves with different colors, curves from same phases can be merged so that it is easy to be recognized.
14. Figure 3B should have cluster information for samples, not only genes.