***Faculty member 1:****The proposal is to extend/refine Network-based stratification (Hofree) with gene expression.*

Thanks for your time reviewing my proposal. Since the feedback pointed out my proposed method only providing methodological difference/improvement, I decided to improve the method to make biological significance. After this revision, I not only refine clustering technique but also extend model for novel and meaningful data integration.

*How is this distinct from Chang et al 2016?*

Chang's paper is merely a direct use case of NBS package and standard NMF package. Revised proposal distinct from that paper in both clustering method and integrated data sources.

*Iit is fine if the distinction is purely methodological, just describe more clearly.*

I rewrite most of the description and introduction to clarify my goal.

*Then include in your data analysis, a comparison between your method and the previously published ones.*

Yes, I will generate test and use real dataset to make comparison. Since there is no NMF based method integrating both mutation and expression data, I will compare with other methods integrating those data types, such as iCluster. I will also compare to standard NMF and NBS to test the non-smooth network-regularized NMF I proposed.

***Faculty member 2:****I see the scientific question and the big picture. However, after reading the abstract, I’m unclear about the difference of the proposed method with existing works. Also I don’t see how the proposed method can improve over existing methods.*

Thanks for incisive comments, I agree that my previous description is unclear about what is existed already and what is my novelty, so I re-wrote most of the introduction and updated methods. Also, I decided to improve my previous method by adding biological significance. So I revised my proposal to integrate both mutation and expression data for comprehensive stratification. Also mutation and expression clusters can be discovered together for stratified patients.

*Before using technical terms, the abstract should explain the limitations and drawbacks of existing works in layman terms first.*

Introduction is mostly re-written, strength and limitations are explicitly pointed out in existing works section.

*When using technical terms, the abstract should specifically point out which parts of the proposed method are novel and different from existing works.*

The novelty section is updated. The proposed model is distinct from existing models in terms of data integration and a more compact clustering ability.