Thanks for reviewing my WQE work. I have revised my paper according to reviewers’ comments. Below are my responses to faculty comments:

*1. The methods section is difficult to understand, and many technical details necessary to understand the methods are lacking.*

I addressed this general concern regarding Methods section in following ways:

First, for the methods cited and used, like mutation matrix smoothing, I re-wrote the entire paragraph to elaborate the details, which includes how it works, the rationale using it, and the parameters I used. Following the same frame, I updated other used methods like consensus clustering, etc.

Second, for the evaluation metrics used in the paper, like Rand Index/Adjusted Rand Index, Cophenetic correlation coefficient, etc. now are described thoroughly by the not only the definition but also how it was calculated and what does it means.

Last, I fixed definition of mathematic notations and typos in the text.

*2. Every mathematical notation used should be clearly defined before the use.*

Fixed now. Sorry about missing some of definitions of mathematical notations. Now I have revised the two sections in Methods describing the proposed methods, to make sure the definitions of notations are adequately provided.

*3. For every method cited and used, please clearly explain their use and how they work. For example, the mutation matrix smoothing is unclear. Why is it good? How does it work? What is the output like?*

Thanks reviewers for bringing up this issue and providing guidance. For mutation matrix smoothing, I was hesitated to spend too much space on it since it was not the focus of this work and I just merely cited and used it. But I do agree it is necessary to provide a well-rounded description if the method was used in my work.

Now I have completely revised this section and several other sections under Methods if there is a method or measurement I cited and used. The cited techniques or pipelines are elaborated clearly with the explanation why this is used, how it works and the parameters (if applicable) used.

*4. Jargons should be avoided as much as possible. The paper should be understandable to a large group of audience who work on genomic data.*

I was trying to avoid jargons in this manuscript but as reviewer pointed out, there are still some left causing difficulties for large group of audience to understand this work. So in the revised version the changes have been made throughout the paper, including terms in Materials and Methods section, Results section and even in figure legends. Words like ‘H’ or ‘W’ matrix, ‘binary matrix’, ‘inputs’ were replaced by more concrete terms like ‘gene-patient matrix’; measurements ‘ARI’ or ‘Cophenentic coefficient’ were replaced by their actual meaning, like ‘accuracy’ or ‘stability’.

*5. Please define the evaluation metrics clearly before using them in figures.*

I’ve now provided clear and direct sentences in the main text linking evaluation metrics to their definition, so that readers can understand figures more easily. I also revised figure legends, instead of using ‘ARI’ or ‘Cophenetic coefficient’, I use accuracy (ARI) or ‘stability (Cophenetic coefficient)’ to make it easier to understand for a large group of audience.