Proposal Review for NKOB

We thought the entire proposal was a great document. The significance of the project was clear and to the point; we thought your group did an excellent job in concisely communicating just the necessary information. The biological innovation for your project was also clear, but we thought the specific sentence regarding innovation could be revised to reduce ambiguity. The way it is currently stated can be interpreted two ways; either the technology itself is innovative or the technology is being used to answer an innovative application. While we assumed you meant the latter, that it could be misconstrued to suggest the software provides innovation detracts from the very fascinating biological innovation of your work. The software, as discussed thoroughly in the methods, is a great choice specifically because it is already well established.

For the division of labor, we thought the attempt to involve all group members in each step is a unique approach. A potential downside we saw here was that workflow may be slowed by having to wait for individual contributions. It was also noted by the review group that there was also an immense upside to this division of work, too, in the exposure of each member to the technical aspect of each program and an ability to expedite troubleshooting steps when everyone communicates. One detail that was missing: who will be in charge of the Ballgown script once the data sets need to be merged?

The approach was very well defined. We especially liked the detail and rationale given for each section of the pipeline, with clear expectations for what outputs you would generate and how you planned to conduct post-processing. The repetition of the pipeline steps in the expected outcomes could be removed in the future to improve efficiency, but certainly did not distract from the clarity of your approach. One thing we thought could strengthen the Expected Outcomes section would be to address more alternative outcomes. What if you receive less than 10 up and down regulated genes? If you receive dozens of results with equal values and significance, how will you sort them? Our review panel also discussed the chance that the treatment may show a general increased immune response rather than a different immune response- OR, the relevant differentially expressed genes may not experience the most fold change. Here, it may be more beneficial to use the Gene Ontology annotations first to inform other aspects of post processing rather than chose an arbitrary number of top results for table presentation.