A use case study

Through a recent study

1. identify the putative GATA2 direct downstream genes by comparing the gene list between GATA2 DEG (GATA2-High-2461.xlsx) and GATA2 ChIP-seq peaks (0620BCM\_GATA2\_Intervals.xlsx) with the following criteria –
2. GATA2 DEGs that have GATA2 binding at immediate promoter regions (+/-2kb of TSS);
3. GATA2 DEGs that have GATA2 binding at extended promoter regions (-7.5kb/+2kb of TSS);
4. GATA2 DEGs that have GATA2 binding at distal regions (+/-20kb of TSS);
5. Annotate the “high” and “low” categories in these gene lists in compliance with the SEMIP app format.

I agree that Rong’s comment should be addressed before submitting to the journal.

Here are options I could think of –

1. Include an extension of analyses on the existing dataset as proposed yesterday.
2. Add a description in the current case study section using the proposal of option 1 as a “future direction” without actually conducting the assay.

I guess if option 1 unearths biology that may be too much or not possible to definitively digest in a succinct way without opening up a possible contest from reviewers about biological plausibility, then we can switch to option 2 and be done with it.  If the journal reviewers aren’t satisfied, or challenge the biological interpretation, then we can address it from there.

Step 1: getting the T-score for three cases

Step 2: combining the data to \_sampleDAT.txt by adding three columns, and rename it to sampleDAT.txt and run the SEM model

Step 3: testing the bootstrapping simulation