List of Changes and Updates to Make:

* Update numbers in table because the model has changed. In particular, the gene associated reaction % is definitely wrong, so I need to fix that
* Update the KO figure and the numbers, which are off by 1
* Include a more intricate description of the paper from the Whitman lab about gene function and explain that we get about 65% accuracy and 0.3-something MCC. These aren’t super, but keep in mind that this genome-wide study is 1) not necessarily completely accurate, it’s more of a proxy and 2) our model can’t account for polar effects.
  + I imagine it’ll go something like “first of all there’s this whole-genome study, which is great. We compared to that and here’s our numbers, which look terrible. However, remember that this is just a proxy via transposon mutagenesis, which can tell us a lot of interesting stuff but isn’t the same as doing an actual knockout. Also, our model can’t account for things like polar effects, which drive up actual essentiality and, here, are causing us to predict too many false positives. For actual KO data to compare to…”
* Can talk about how it compares with our other methanogen models in terms of gene and reaction essentiality. Then talk some about how this makes sense to have higher gene essentiality, because we’re a smaller organism so we’d expect our network to be less robust and, therefore, have a higher percentage of essential reactions/genes.
* Update numbers in the subsystems figure to make it look better
* Add hyperlink info for the ChEBI IDs:

Imanishi T and Nakaoka H (2009) Nucleic Acids Research 37: W17-W22

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* Add the fact that we added ChEBI IDs
* Add in the fact that SBML doesn’t include freeEnergy, so the code for it is separate and needs to be run to add the freeEnergy. Should include exactly which code to run to add the freeEnergy (check the createLatestModel code)