Tessa’s Peer Review

I apologize in advance that the level of insight I can provide is limited based on my very limited exposure to network theory and complexity science.

Would you consider instead of writing out the description of the network in the second paragraph of the model description you instead simply display the casual graph of the network (like you have it) and state that green means activation and red means inhibition. You can then include only vital information about the proteins that you feel necessary to include. I only suggest this as a way to get the same information across.

Great decision quality to use the measurements you did (TE, Active Information, knocking out RB and CycD, etc...). For example the conclusion that TE could be thought of as a warning signal towards carcinogenesis (not sure if this is a result attained by your study or if it has been reached before) shows that choosing the measurements you did created meaningful results. More importantly it gives evidence to your preposition that analyzing GRN's by studying their network dynamics can be useful for developing treatments and other real world applications.

Another suggestion I would have is including either the current limitations of modeling GRN's this way or the areas of opportunity created by or that lay within your study.

Otherwise I think very highly of your paper, analysis, and model simulation and description. Other than the suggestions I made you did an incredible job writing your paper so that it is easy to follow the logic of your conclusions.