Hi Orli,

Thanks for giving us the opportunity to send you a draft of the paper. We have attached a fairly late stage draft. But please realize this is not a final version and it's still rough. Fundamentally, this paper is about a resource specific for cancer research, which is supposed to sit next to the main encyclopedia resource. The main contribution of this paper is that we're able to collect many really novel assays, such as as STARR-seq, Hi-C, RAMPAGE, and eCLIP together with a broader spectrum of traditional assays, such as hundreds of ChIP-seq experiments, to deeply annotate the cancer genomes. With such data, for the first time we are able to,

1. Build up background mutation rate model with unprecedented accuracy and jointly evaluate the gene mutation burden in coding and noncoding regulatory regions
2. Analyze the rewiring events in matched tumor-to-normal networks to delineate regulatory changes in cancer and investigate how they are related to known events in tumorigenesis
3. Identify key regulators in generalized TF/RBP networks that driver tumor-to-normal differential expressions and understand how such TF interact with each other
4. Prioritize key regulators, functional elements, and functional variants in a stepwise manner, and validate our prioritizations by various small-scale functional assays

We are really keen to get some feedback from you. One concern is that resource paper is not a typical type of nature paper so we are really not sure how to connect the normal nature formatting with our paper. Please advise on this. We haven't included the supplement that this point but we plan to send you a draft soon to get you a sense of we’re thinking about for formatting the supplementary.

We've also sent a provisional list of referees which you might think about.

* Matthieu Lupien (University of Toronto)
* Han Liang (MD Anderson)
* Josh Stuart (UCSC)
* Ewan Birney (EBI)
* Gad Getz (the Broad Institute)

Many thanks.