Hi Orli,

Thank you for giving us the opportunity to send you a rough draft of our paper. This work is intended to serve as a resource for cancer research, in complement to the main ENCODE encyclopedia resource. The main contribution of this paper is deep annotation of cancer genomes using advanced and novel assays like STARR-seq, Hi-C, RAMPAGE, and eCLIP, together with a broad spectrum of traditional assays including hundreds of ChIP-seq experiments. We were able to use these data to:

1. Build a background mutation rate model with unprecedented accuracy and jointly evaluate gene mutation burden in coding and noncoding regulatory regions.
2. Analyze rewiring events in matched tumor-normal gene regulatory networks to delineate network changes in cancer.
3. Identify key regulators in generalized TF/RBP networks that drive differential tumor-normal gene expression and understand interactions between TFs in cancer.
4. Prioritize key regulators, functional elements, and functional variants, and validate these prioritizations using small-scale functional assays.

We very much value your feedback. In particular, we’re concerned that *Nature* generally does not serve as an outlet for resource papers. As such, we are unsure about how to synchronize the formatting of our paper with formatting typically used by *Nature*. Related to manuscript formatting, we’re working towards sending you a draft of the supplement soon, to give you a sense of how we’re thinking of structuring this information in relation to the main text.

We're also sending along a provisional list of referees for consideration:

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

Many thanks,