**Introduction**

A small fraction of mutations associated with cancer have been well characterized, particularly those in coding regions of key oncogenes and tumor suppressors. However, the overwhelming bulk of mutations in cancer genomes – particularly those discovered over the course of recent large-scale whole genome cancer genomics initiatives – lie within non-coding regions \cite{25261935}. Whether these mutations have substantial functional impact on cancer progression remains an open question \cite{26781813}.

Several recent studies have begun to address this question by incorporating limited functional genomics data for variant interpretation \{cite 25261935, 27064257, 27807102}. For example, *Hoadley et al.* integrated five genome-wide platforms and one proteomic platform to uniformly classify various tumor types \{cite 25109877}. *Torchia et al.* integrated various genomic and epigenetic signals to identify promising therapeutic targets in rhabdoid tumors \cite{27960086}. *Lawrence et al.* incorporated large-scale genomics profiles to identify cancer drivers \{cite 23770567}. However, there is no systematic integration of thousands of functional genomic data sets from a broad spectrum of advanced assays to interpret the cancer genome.

The rich functional assays and annotation resources developed by the ENCODE Consortium allows us to characterize these non-coding regions at a great depth across many cancer types. In the initial release of the ENCODE annotation years ago, this was predominantly accomplished by using RNA-seq and ChIP-seq assays on a limited number of cell types \cite{22955616}. The new release of ENCODE took two new directions. First, it considerably broadened the number of cell types with the main RNA-seq, ChIP-seq, and DNase-seq assays; the main ENCODE encyclopedia aims to utilize these to provide a general, unified annotation resource applicable across many cells. Secondly, ENCODE expanded the number of sophisticated assays such as STARR-seq, Hi-C, ChIA-PET, eCLIP and RAMPAGE on several top-tier cell lines, many of which are cancer-associated. This enables precise definitions of enhancers, direct identification of enhancer-target gene links, and the construction of RNA-binding protein (RBP) networks. Here, we focus on top-tier cell lines by performing large-scale integration of these various assays to construct an in-depth cancer related companion resource to the general encyclopedia. We complied these resources as the “companion *ENCODE* encyclopedia resource for *C*ancer” (or “EN-CODEC” for short) to interpret cancer-related genomic data, such as mutational and transcriptional profiles.

## **Comprehensive functional characterization by ENCODE data integration**

The ENCODE data is well-suited for cancer research as around eighty percent of the ENCODE cell lines are associated with cancerous tissue (Figure S1). Moreover, the ENCODE top-tier cell lines are enriched with a broad spectrum of novel assays suitable for accurate functional characterization. They can be modeled to understand various types of cancers including the blood (K562), breast (MCF-7), liver (HepG2), lung (A549), and cervical (HeLa-S3) cancers. In addition, another top-tier cell line H1-hESC is from a human stem cell. It has been thought for decades that at least a subpopulation of the tumor cells have the ability to self-renew, differentiate, and regenerate, similar to what is conceptualized in normal stem cells \cite{24333726}. Hence, H1-hESC can serve as a valuable comparison to cancer cells to check the degree to which their oncogenic transformation is in a more differentiated or undifferentiated direction \cite{24333726}. Here, we endeavor to collect the data catalog from these model cell lines for cancer to provide deep annotations of the cancer genomes.

## **Multi-level data integration improves variant recurrence analysis in cancer**

One of the most powerful ways of identifying key elements in cancer is with recurrence analysis to discover regions that mutate more than expected. Hence, in the EN-CODEC resource, we first attempted to construct an accurate background mutation rate (BMR) model in various cancer types. However, this is a challenging problem since the somatic mutational process can be influenced by numerous confounding factors (in the form of both external genomic factors and local sequence context factors), which can result in many false positives or negatives without appropriate correction \{cite 23770567}. Here, we tackled these problems by removing effects of confounding factors in a cancer-specific manner. Specifically, we separated the whole genome into bins (1Mb) and calculated mutation counts under each local context category. For each category, we used a negative binomial regression of the mutation counts against features like replication timing, chromatin accessibility, Hi-C signal, and expression profiles for BMR prediction. In contrast to methods that use unmatched data \{cite 23770567}, our approach automatically selects the most relevant features, thereby providing noticeable improvements in BMR estimation (Fig 2A). Notably the combination of many different genomic significantly improves the estimation accuracy in multiple cancer types (Fig 2 B). In addition, it is worth mentioning that due to the correlated nature of these genomic features, some cancers without features from seemingly matched cell types can still automatically learn from related cell types and achieve decent BMR precision. Hence, our analyses could be easily extended to other cancer types. [[JZ2MG: do we need to add another cancer type to show this in the sup? Not difficult just need a little bit extra effort on prostate cancer in supp]]

A second step to utilize the ENCODE annotation in the burden analysis in cancer is to focus on compact annotation set with high confidence. In fact, testing every nucleotide in the genome will subject to large multiple test correction, which could appreciably dilute the signal and significantly reduce the calculation power (see supplementary file). Therefore, we tried to provide the minimum number of high confident annotations to look for burdened regions. Specifically, we start from defining enhancers that supported by multiple evidence. We used genomic signal tracks from a battery of 5 to 10 histone modification marks in combination with DNase-seq. These were used as input into CASPER, a machine learning predictor that we developed to integrate the signal shapes of these various signals. We then assembled these predictions with peaks called from STARR-seq experiments, which directly read out candidate enhancers in the genome. Such an integrative approach gives accurate definitions of enhancers (see supplement). We also reconciled these enhancers with the main encyclopedia annotations by reporting the overlapped one and providing new IDs to the novel ones. In addition, it is also important to increase power by confining the burdening tests on core regions of the annotated elements with shorter length but larger functional impact (see supplement). Hence, we refined the above-mentioned enhancers through the CASPER algorithm by trimming down candidate regions to a smaller size at the center of histone marks. [[JZ2MG: we want to be clear otherwise experts like Shirley will keep on asking what did you do exactly? But potentially by only selecting the center of histone mark is dangerous. I have mixed feeling of the last sentence]]

A final aspect to increase the power is to link the refined, high confidence noncoding regulatory elements to the protein coding genes to form a whole test unit (the so-called extended gene region) to jointly pick up the mutational signals from distributed yet biologically relevant genomic regions. The extended gene concept also results in much more interpretable burdened regions as they are often associated with well-known oncogenic genes. Traditional methods have to solely rely on computational correlation due to the lack of data, resulting in problematic extended gene definition. Here we use direct experimental evidence and physical interaction from the Hi-C and ChIA-PET, combined with a machine learning algorithm that takes into account the wide variety of histone modification marks and expressions to achieve accurate enhancer target gene linkages. Finally, the conserved enhancer-target linkages, refined promoters, and RNA-binding sites from eCLIP experiments within genes constitute a so-called extended gene neighborhood (Fig1 C).

We demonstrate that our scheme can effectively remove false positives and discover meaningful regions with higher-than-expected mutation counts (Fig 2C). For example, in the context of chronic lymphocytic leukemia (CLL), our analysis identifies well-known highly mutated genes, such as TP53 and ATM, which has been reported from previous coding region analysis. It also discovered genes that are missed by the exclusive analysis of coding regions, such as BCL6. Note that BCL6 has strong prognostic value with respect to patient survival (Fig. 2D), indicating that the extended gene neighborhood could be used as an annotation set for recurrence analysis.

## **Integrating regulatory networks and tumor expression profiles identifies key regulators in cancer**

ENCODE annotation also provides detailed regulatory networks instantiated from experimental assays suitable for cancer research. Compared to imputed networks from motif analysis, ENCODE TF and RBP regulatory networks were built upon actual ChIP-seq and eCLIP expriments, which provide much more accurate regulatory interactions between functional elements. Specifically, for the TF network we first built distal and proximal TF regulatory networks by linking TF to genes, either directly by TF-promoter interactions or indirectly via TF-enhancer-gene interactions in each cell type (Fig1 B). We then pruned these networks to include only the strongest edges using another signal shape algorithm called TIP \{cite 22039215}. In addition, we merged our cell-type-specific networks to get a generalized network for pan-cancer analysis.

Such network is a valuable resource for interpreting the wealth of cancer gene expression from cancer tissue. Then using a machine learning method, we integrated 8,202 tumor expression profiles from TCGA to systematically search for the TFs and RBPs that most strongly drive tumor-specific expression patterns. For each patient, our method tests to the degree a regulators’ regulation potentials are sufficiently correlated with their targets’ tumor-to-normal expression changes. We then calculated the percentage of patients with these relationships in each cancer type and presented the overall trends for key TFs and RBPs in Fig. 4A.

We find that the target genes of MYC are significantly up-regulated in numerous cancers, which is consistent with its well-known role as an oncogenic TF and a transcription activator \cite{22464321}. We further validate MYC’s regulatory effect through knock down experiments (Fig 4). Consistent with our predictions, the expression of MYC targets is significantly reduced after MYC knockdown (Fig 4A). After confirming the importance of MYC, we use the regulatory network to understand how MYC works with other TFs. We first looked at all triplets involving MYC by requiring that a second TF both interacts and shares a common target with MYC. In all cancer types, we found that MYC’s expression levels are positively correlated with the expressions of most of its targets, while the second TF shows only a limited influence as determined from partial correlations. We then investigated the exact structure of such regulatory relationships. The most common triplet interaction type is a well-understood feed-forward loop (FFL) structure in which MYC regulates both the common target and the second TF. Most of these FFLs involve well-known MYC partners such as Max and Mxl1. However, we also discovered that many involve another factor called NRF1. Upon further study, we found that that the MYC-NRF1 FFL relationships were mostly coherent ("amplifying") FFLs. We further studied these FFLs by forming these triplets into a logical gate, in which the two TFs act as inputs and the target gene expression represents the output \{cite 25884877}. We can show that the predominant number of these gates follow either OR or MYC-always-dominant logic. Thus, the ENCODE regulatory network not only helps find key regulators, but also to really demonstrate how they work in combination with other regulators.

We also analyzed the RBP network derived from ENCODE eCLIP data and found key regulators associated with cancer. For example, the ENCODE eCLIP experiment has profiled many SUB1 peaks on the 3’UTR regions of genes, and we find that the predicted targets of the RBP SUB1 were significantly up-regulated in many cancer types (Fig. 4C). As a RBP, SUB1 has not been associated with cancer before. We thus validated this new association in liver cancer. After knocking down SUB1 in HepG2 cells, its predicted targets are also down-regulated relative to other genes (Fig. 4D). In addition, we found that the decay rate of SUB1 target genes are significantly shorter than non-targets (Fig. 4C). These results indicate that SUB1 may bind to 3’UTR regions to stabilize transcripts. Moreover, we found that the up-regulation of SUB1 target genes is correlated with a poorer patient survival in other cancer types such as lung cancer (Fig. 4).

We further present the overall regulatory network by systematically arranging it into a hierarchy. TFs are placed into different levels where TFs on the top tend to regulate the expression of other TFs and the ones at the bottom ones are in turn more regulated by others \{cite 25880651}. A final hierarchical network structure is shown in Fig1 D. We find that the top layer TFs are not only enriched in cancer associated genes but also more significantly drive tumor-to-normal gene differential expressions.

## **Extensive rewiring events in regulatory network**

For the top-tier cell types with numerous TF ChIP-seq experiments, we constructed cell-type-specific regulatory networks and compared it with networks built from their paired normal cell types. We proposed the concept of composite normal by reconciling multiple related normal cell types as shown in figure XX. We admit that these pairings, including relating cancerous cell lines to specific tumors and match them to normal cell types, are highly approximate in nature. However, many of such pairings have been widely used in literature before. Furthermore, with the enrichment of functional characterization assays in ENCODE, they provide us the first opportunity to directly understand the regulatory alterations in cancer by looking at specific TF to target changes that are rewired in the process of oncogenesis.

In paired "tumor-normal" cell lines, we measured the signed, fractional number of edges changing, the rewiring index, to study how the targets of each common TF changed (i.e., rewired) over the course of oncogenic transformation. We first ranked TFs according the “rewiring index” (Fig. 3 A). In leukemia, well-known oncogenes such as MYC and NRF1 were among the top edge gainers, while the well-known tumor suppressor IKZF1 is the most significant edge loser (Fig 3A). Mutations in this latter factor serve as a hallmark of various forms of high-risk leukemia \cite{26202931, 26713593, 26069293 }. Interestingly, IKZF1 loss has been found to be associated with well-known BCR-ABL fusion transcript, which is present in K562, and usually confers poor clinical outcome \cite{26069293}. In contrast, several ubiquitously distributed TFs retain their regulatory linkages (Fig 3A). We observed a similar trend in TFs using a distal, proximal, and combined network (see details in supplementary file). The trend was consistent across highly rewired TFs such as BHLHE40, JUND, and MYC in lung, liver, and breast cancers (Fig 3).

In addition to the simple direct TF to gene connection-based model, the rewiring index was also evaluated using more complex gene community model. The targets within the TF regulatory network were characterized by heterogeneous network modules (so called “gene communities”), which usually come from multiple biologically relevant genes. Instead of directly measuring the TF’s target changes for each gene, we determined the change in gene communities via a mixed-membership model. This enabled us to evaluate each TF’s overall association changes to these gene communities in tumor and normal cells. Similar rewiring patterns were observed using this model (Fig 3A).

We then tested whether the gain or loss events from the normal to tumor transition will result in a network that is more similar or different from those in stem cells like H1-hESC. Interestingly, we find that the gainer group tends to rewire away from the stem cell’s regulatory network while the loser groups are more likely to rewire toward the stem cell.

We also find that the majority of rewiring events were associated with noticeable gene expression and chromatin status changes, but not necessarily with variant-induced motif loss or gain events (Fig. 3A). This is consistent with previous discoveries that most non-coding risk variants are not well-explained by the current model \cite{25363779}. For example, JUND is a top gainer in CLL. The majority of its gained targets in tumor cell lines demonstrate higher gene expression, stronger active and weaker repressive histone modification mark signals. We found a similar trend for the rewiring events associated with JUND in liver cancer. Related to the mutational burdening of targets, we can formulate the cell-type-specific networks to cell-type-specific hierarchies, as shown in figure XXX. Specifically, in blood cancer that the more mutationally burdened TFs actually sit at the bottom of the hierarchy, whereas the TFs that are more associated with driving cancer gene expression tend to be at the top, providing further support that the mutational burdening does not play a driving role of cancer transformation. [[JZ2MG, I strongly suggest to remove the last sentence. It does not add much but will intrigue quite a lot of problems during revision]]

## **Step-wise prioritization schemes pinpoint deleterious SNVs in cancer**

Summarizing the analysis described above, EN-CODEC consists of numerous annotation resources summarized in figure XXX : (1) a BMR model with matching procedure and a list of regions with higher-than-expected mutations in various cancers, (2) accurate and refined enhancers, promotors and enhancer-target-gene linkages by integrating tens of different functional assays and their comparison with those in ENCODE encyclopedia; (3) extended gene neighborhoods, (4) tumor-normal differential expression and chromatin changes, (5) TF regulatory networks in various formats; (6) TFs’ position in the network hierarchy and their rewiring status; (7) an analogous but less annotated network for RBPs. Collectively, these resources allow us to prioritize key features as being associated with oncogenesis. The workflow in Fig. 5A describes this prioritization scheme in a systematic fashion. We first search for key regulators that are frequently rewired, located in network hubs or at top of the network hierarchy, or significantly driving expression changes in cancer. We then prioritize functional elements that are associated with top regulators, undergo large regulatory changes in terms of expression levels, TF binding, and chromatin status, or are highly mutated in tumors. Finally, on a nucleotide level, we can pinpoint impactful SNVs for small-scale functional characterization by their ability to disrupt or create specific binding sites, or which occur in positions under strong purifying selection.

Using this framework, as we described above, we subject a number of key regulators, such as MYC and SUB1, to knockdown experiments to validate their regulatory effects in particular cancer contexts (Fig 4D). Next here, we also identified several candidate enhancers in noncoding regions, associated with breast cancer, and validated their ability to influence transcription using luciferase assays in MCF7. We selected key SNVs, based on significantly recurrent mutations in breast cancer cohorts, within these enhancers that are important for controlling gene expression. Of the eight motif-disrupting SNVs that we tested, six showed consistent up- or down-regulation relative to the wild type in multiple biological replicates. One particularly interesting example, illustrating the unique value of ENCODE data integration, is in the intronic region of CDH26 in chromosome 20 (Fig. 5C). Both histone modification and chromatin accessibility (DNase-seq) signals indicated an active regulatory role in MCF7, which was further confirmed as an enhancer by both CASPER and ESCAPE (STARR-seq) (Fig. 5D). Hi-C and ChIA-PET data indicated that the region is within a topologically associated domain (TAD) and validated a regulatory linkage to the downstream breast-cancer-associated gene SYCP2 \cite{26334652, 24662924}. We observed massive binding events from TFs in this region in MCF-7. Motif analysis predicts that the particular mutations found in the cohorts can significantly disrupt the binding affinity of several TFs, such as FOSL2, in this region (Fig. 5D). Luciferase assays demonstrate that this mutation introduces a 3.6-fold reduction in expression relative to wild type expression levels, indicating a strong repressive effect on this enhancer’s functionality.

## Conclusion

This study highlights the value of our companion to the main ENCODE encyclopedia as a resource for cancer research. First, we show that, by integrating many different types of assays on a large scale, we can build a very accurate BMR model in various cancer types. We also demonstrated how to improve the statistical power for burden analysis and functional interpretation of the detected mutational hotspot by confining annotation quality and quantity and improving their linkage to genes. Second, we are able to build extensive regulatory networks from thousands of ChIP-seq and eCLIP experiments, which are much more accurate than those from imputed binding sites \cite{25409825}. These networks can be directly combined with the expression profiles of various cancer types to prioritize key regulators that are involved in cancer progression. Specifically, we also build cell type specific networks for the first time in the top-tier cell lines and relate them to corresponding normal one to direct study the regulatory alteration during the transformation to cancer. Then we demonstrate how such comparisons can illuminate potential regulatory changes in cancer (e.g. key rewiring TFs). We did notice that the representative tumor and normal cell types used here are very rough. However, cancer is such a heterogeneous disease that even the tumor cells from one patient usually shows distinct molecular, morphological, and genetic profiles \cite{24048065}. It is difficult to obtain a "perfect" match even from data of real tumor and normal tissues. Finally, we show how we can leverage the companion resource to provide a prioritization scheme to pinpoint key regulatory elements and SNVs for small-scale follow-up.

This study underscores the value of large-scale data integration, and we note that expanding this approach (either by integrating additional data types and/or using tumor mutation and expression data on a larger scale) is straightforward. We also anticipate that an additional step would be to carry out many of the ENCODE assays on specific tissues and tumor samples. Though volume of material needed for such analyses may present challenges, we show that such a framework is technically feasible and provides further opportunities for the future.