**Experience with the ENCODE- GTEx and ENTEx personalized functional genomics resource.**

ENTEx is a joint effort between ENCODE and GTEx consortia towards the goal of comparing the functional genomics data from a variety of assays between different sequenced individuals and tissues (14). The ENTEx working group has been comprehensively characterizing the personal genomes, chromatin, and transcriptome of 20-25 tissues from four individuals. Collectively, ENTEx has generated more than ~1,500 different functional genome experiments. Namely, we performed RNA-seq (long and short RNAs and RAMPAGE), chromatin characterization assays such as ATAC-seq, DNase, histone modification ChIP-Seq (H3K27ac, H3K27me3, H3K36me3, H3K4me1, H3K4me3, H3K9me3) and other marks (RNA POLII, EP300, CTCF). Tissues were also characterized in regard to their DNA methylation (WGBS and chip-array) and 3D structure (Hi-C). The data analysis committee (DAC) of which several of us were members carried out analyses of these individual data types individually and integrated fashion leading to a better understanding how these functional elements operate in and interdependent fashion.

**Experience with personal genomes and analyses of allele-specific expression and binding**

We have developed a computational tool, AlleleSeq, for the construction of personal genomes (14). The tool integrates an individual’s genomic variation data (SNVs, indels, and SVs) into the reference genome. Phase information of heterozygous variants is also incorporated, producing maternal and paternal haplotypes. Chain files generated by the program can be used to account for coordinate offsets between the individual’s parental haplotypes and the original reference genomic sequence. We have previously constructed the personal diploid genome, splice-junction libraries and personalized gene annotations for NA12878 (available as a resource at alleleseq.gersteinlab.org). Furthermore, we have implemented this on a larger scale in a recent publication (15) where we built 382 personal genomes using the variant call sets from the 1000 Genomes Project.

We have extensive experience with analyses of allele-specific expression and binding and developed a pipeline, AlleleSeq] (14), to measure and detect allele-specific events. We have spearheaded allele-specific analyses in several major consortia publications, including ENCODE and the 1000 Genomes Project (16-18). We have annotated variants associated with allele-specific expression and binding in a large pool of individuals from the 1000 Genomes Project. These results were made available as an online resource, AlleleDB (alleledb.gersteinlab.org) (15). Most recently, we constructed a high-resolution map of allelic imbalances in DNA methylation, histone marks, and transcription in 71 epigenomes from 36 distinct cell and tissue types from 13 donors (19).

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