Project: Functional SNPs for Prostate Cancer

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Abstract:

Numerous GWASs have found more than 150 SNPs associated with prostate cancer (PCa). The majority of these SNPs are located in non-coding regions of the genome. A hypothesis is that at least some of the causal SNPs are on enhancers. On the other hand, genomic distribution of androgen receptor (AR) binding has been profiled. Efforts have been devoted to profiling the known SNPs in big databases (e.g. 1000 genomes variants) with biological active chromatin features. Particularly, Mathieu Lupien et al. scanned the known SNPs linked to those reported to be associated with breast cancer (BCa) in the GWAS catalog, proved that one BCa-associated SNP modulates the affinity of chromatin for FOXA1 and alters gene expression by integrating the FOXA1/ESR1 binding. However, those binding sites and chromatin features are generally not really accurately defined, and more importantly, starting from reported associations misses many other functional (e.g. binding-affecting) SNPs. To that end, we start from the precisely defined androgen responsive elements (AREs), build the linkage disequilibrium (LD) structure around the ARE-embraced SNPs, and check the associations between the ARE regions and PCa using several dbGaP GWAS datasets. Our aim is to provide a comprehensive profile of functional SNPs for prostate cancer.