Transcription Factor-Centric Approach to Identify Non-Recurring Regulatory Driver Mutations in Cancer

1. SUPPLEMENTAL FIGURES

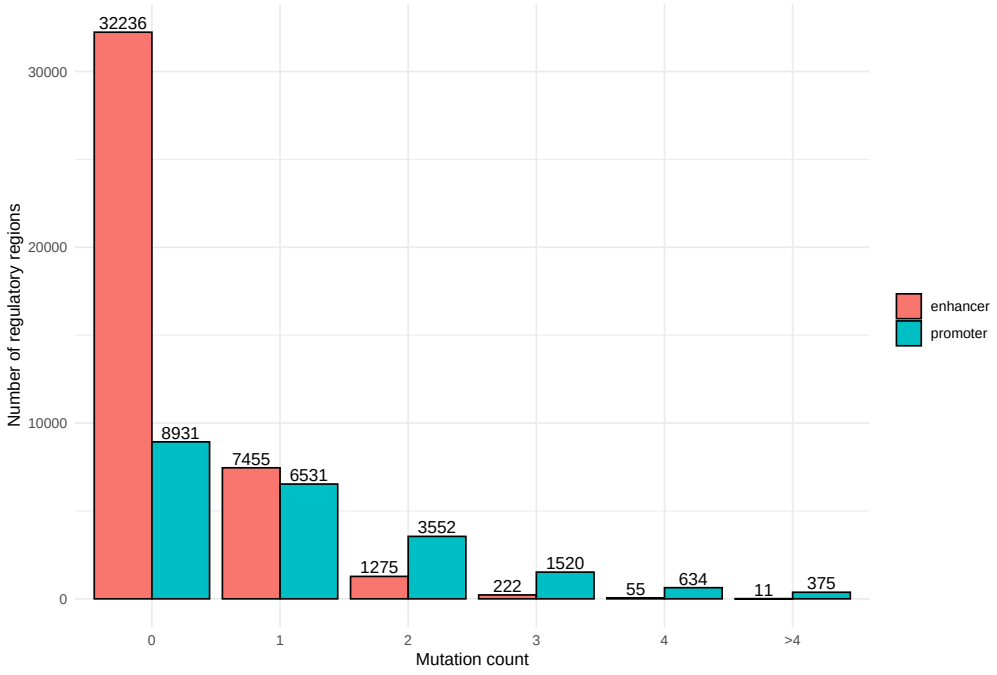

Fig. S1. Number of mutations in each regulatory region. The average mutation rate is $3.6x10^{-6}$ in enhancers and $2.1x10^{-6}$ in promoters.

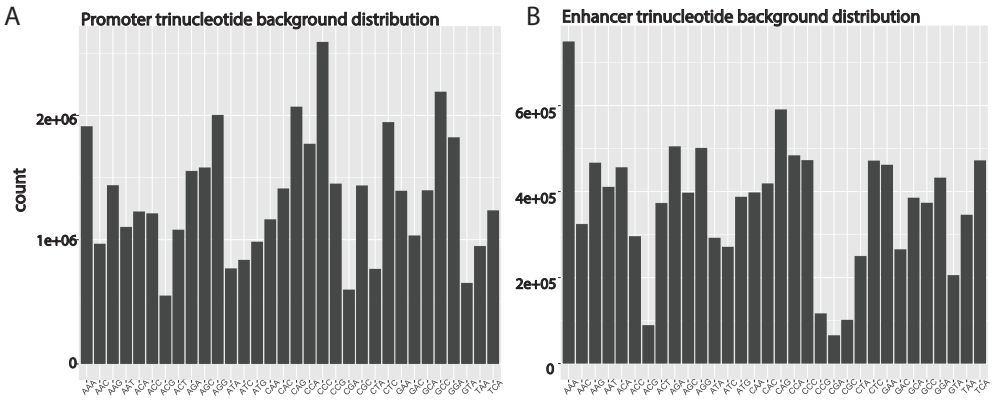

Fig. S2. The number of trinucleotide mutations in promoters (A) and enhancers (B).

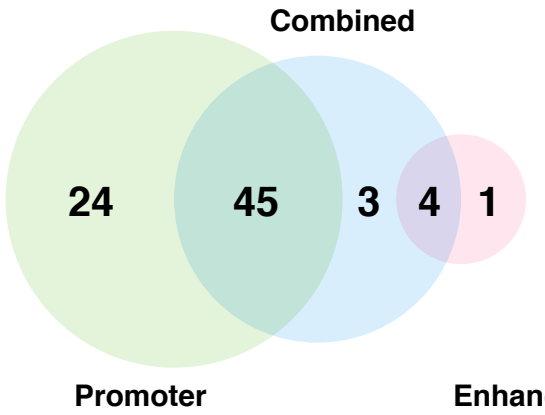

Fig. S3. Number of prioritized genes in the promoter (green), combined (blue), and enhancer (pink) analyses.

Fig. S4. Negative log p-values between genes in the promoter (y-axis) versus combined (x-axis) analyses. Only genes exist in the two analyses are used. The R^2 shows correlation for genes with mutations in both promoters and enhancers.

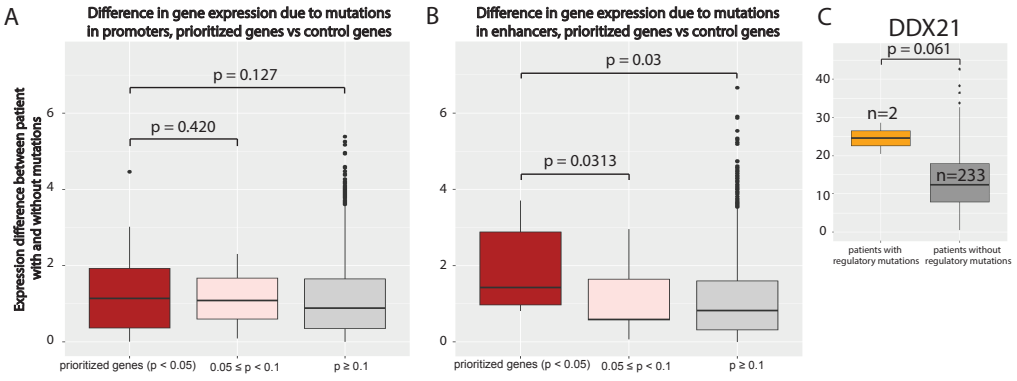

Fig. S5. Gene expression differences between patients with and without the gene regulatory mutations between prioritized genes ($p \leq 0.05$) compared to intermediate ($0.05 \leq p \leq 0.1$) and control ($p \geq 0.1$) genes. (A) Promoter-only analysis (B) Enhancer-only analysis. (C) Only one gene (DDX21) that is in the promoter-only analysis but not included in the combined analysis, has significant expression difference.