Supplemental Figures for "Transcription Factor-Centric Approach to Identify Non-Recurring Putative Regulatory Drivers in Cancer"

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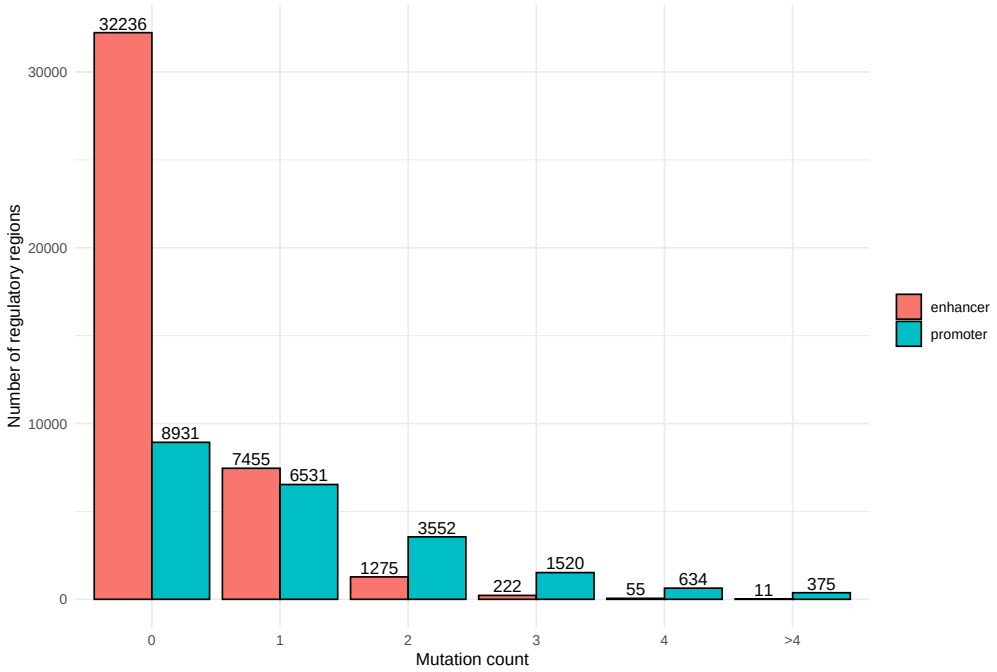

Fig. S1. Number of mutations in each regulatory region. The average mutation rate is $3.6x10^{-6}$ in enhancers and $2.1x10^{-6}$ in promoters.

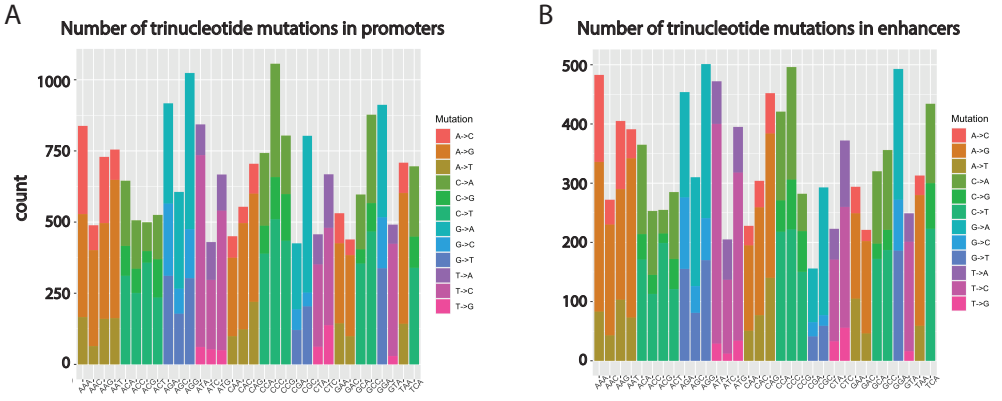

Fig. S2. The number of mutations in promoters (A) and enhancers (B), computed for each mutation type in each trinucleotide context .

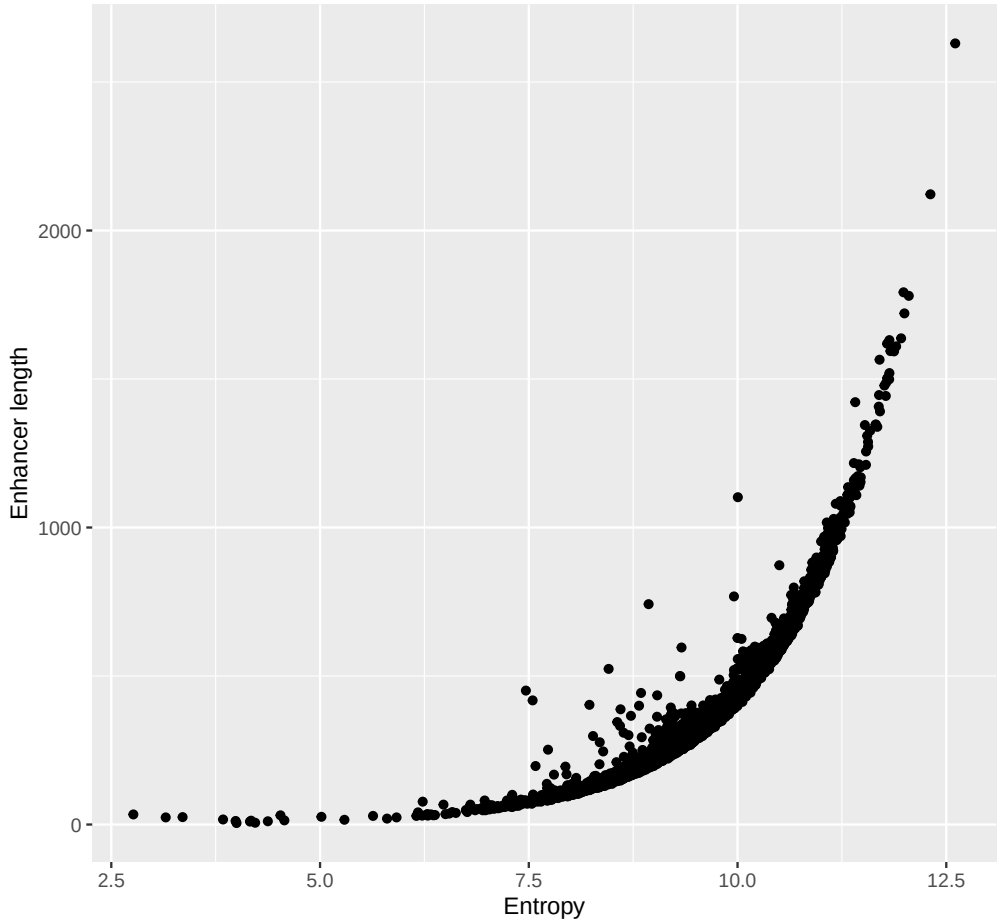

Fig. S3. Comparison between the entropy computed for each enhancer, based on the probabilities of all possible mutations, versus the enhancer's length.

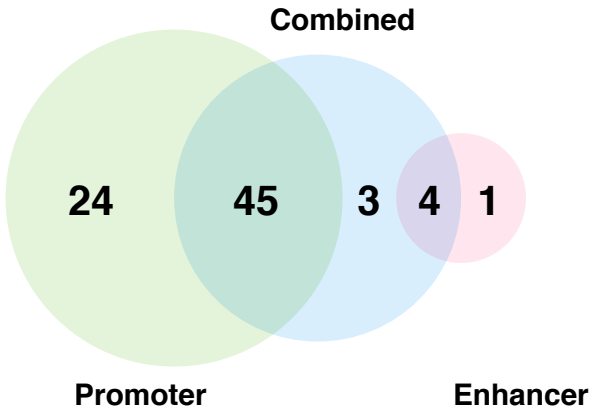

Fig. S4. Number of prioritized genes in the promoter-only (green), combined (blue), and enhancer-only (pink) analyses.

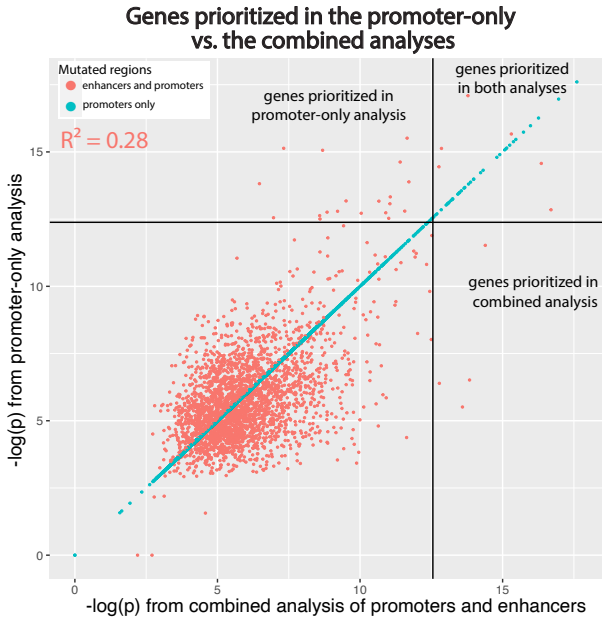

Fig. S5. Comparison between the genes' significance in the promoter-only versus the combined analysis, shown as negative logarithm of the p-value. The R^2 shows the correlation for genes with mutations in both promoters and enhancers (shown in orange).

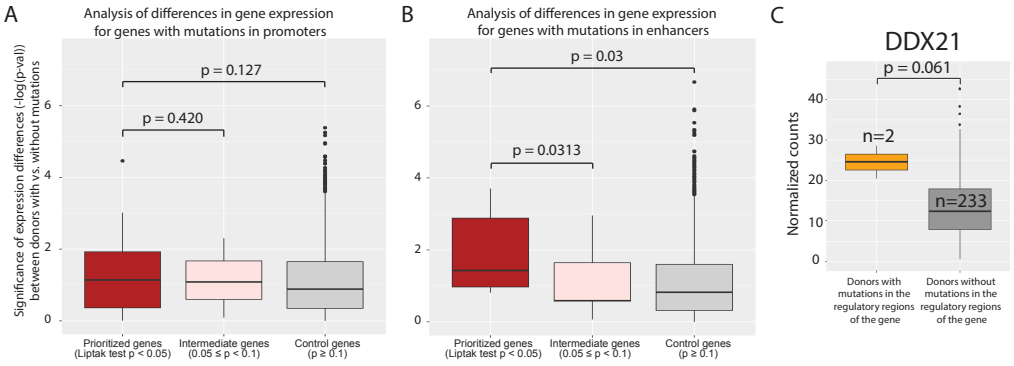

Fig. S6. (A) Significance of gene expression differences between donors with vs. without mutations in promoters, shown for prioritized genes (minimum adjusted Liptak's test $p < 0.05$), intermediate genes ($0.05 \leq p < 0.1$) and control genes ($p \geq 0.1$) genes. (B) Similar to panel A, but analyzing mutations only in enhancers. (C) Only one gene (DDX21) that was prioritized in the promoter-only analysis but not in the combined analysis, has a significant expression difference between donors with vs. without mutations.