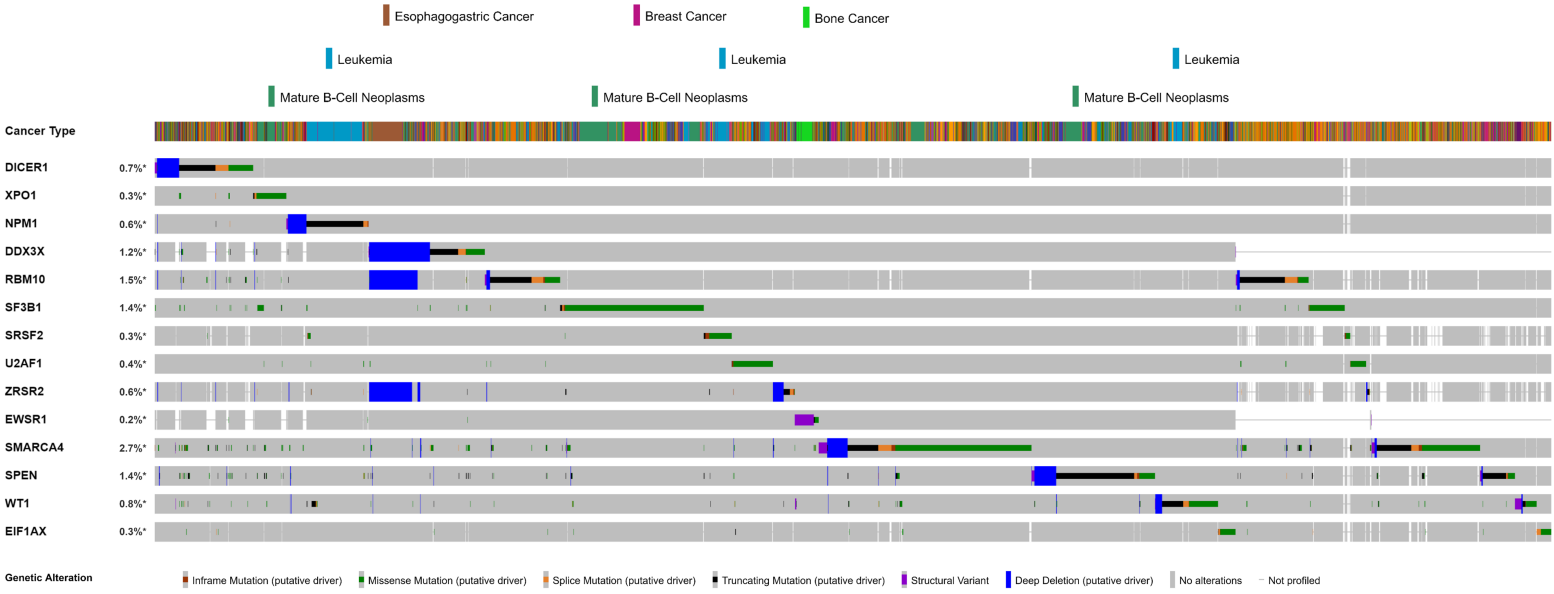
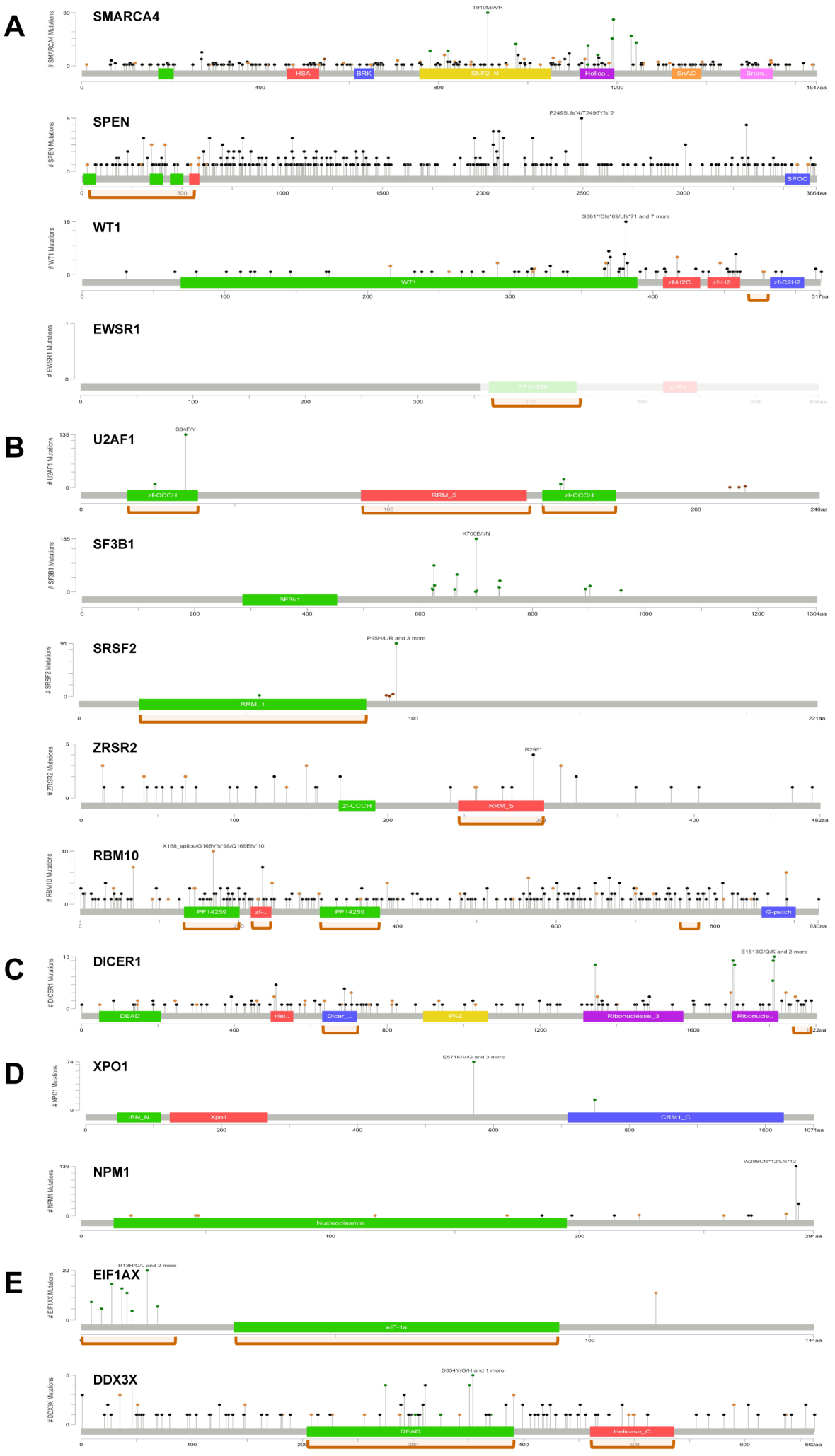


Supplemental Figure S1. Somatic mutations in genes encoding select RBPs. Included are 14 genes classified as drivers, per the cBio Portal for Cancer Genomics. Designation as driver mutations is based on annotations provided by Precision Oncology Knowledge Base as well as recurrent patterns of genetic alterations, including in-frame, missense, splice site, and truncating mutations, as well as gene fusions and deep deletions. Samples include the cBio Portal 'curated set of non-redundant studies' which include The Cancer Genome Atlas (TCGA) and non-TCGA samples [48081 specimens from 45604 patients as of April 21, 2021]. Various types of mutation are color-coded as per the legend below. Apparent clusters of tumors featuring similar mutations are shown at the top. Note that copy-number calls are not manually reviewed by cBioPortal, and due to differences in purity and ploidy between samples, there may be false positives and false negatives. For additional information about specific cancer types, visit https://www.cbioportal.org/results/oncoprint?plots_horz_selection=%7B%7D&plots_vert_selection=%7B%7D&plots_coloring_selection=%7B%7D&data_priority=0&tab_index=tab_visualize&Action=Submit&session_id=60760ec6e4b015b63e9e5d00.



Supplemental Figure S2. Driver mutations in RBP-encoding cancer drivers. Plots of driver mutations in RBPs generated using the cBio Portal. Black, green, orange and dark red "lollipops" represent truncating, missense, splice-site and in-frame mutations, respectively. In the case of EWSR1 the domains lost to chromosomal rearrangements are whited-out. Approximate locations of RBDs (if known) are indicated using brown brackets. A, B, C, D, and E refer to proteins known to be involved in transcription, mRNA splicing, microRNA biogenesis, nuclear export, and translation, respectively.