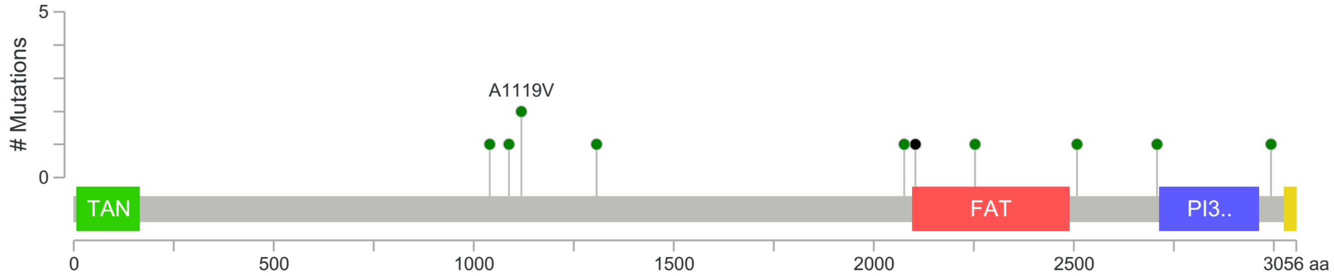
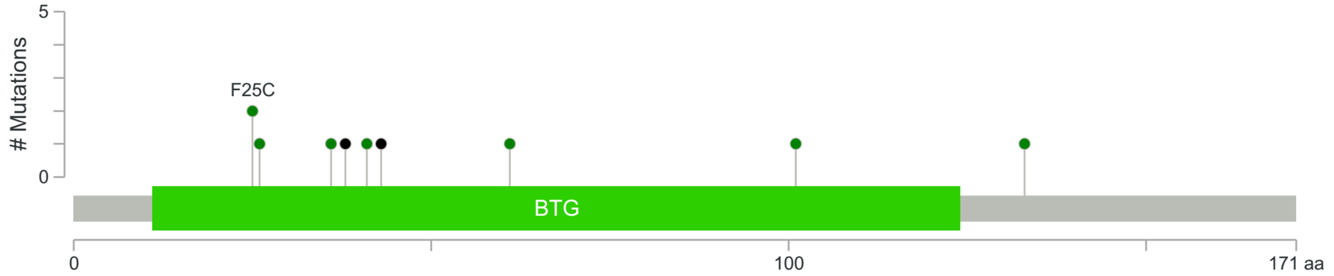
ATM

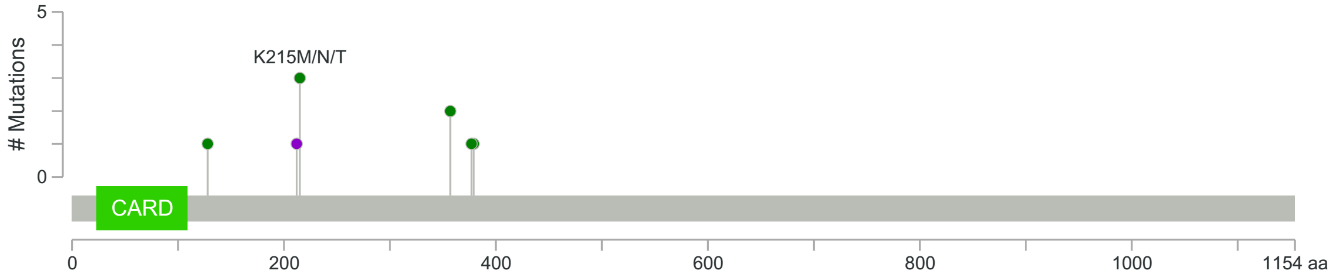


B2M

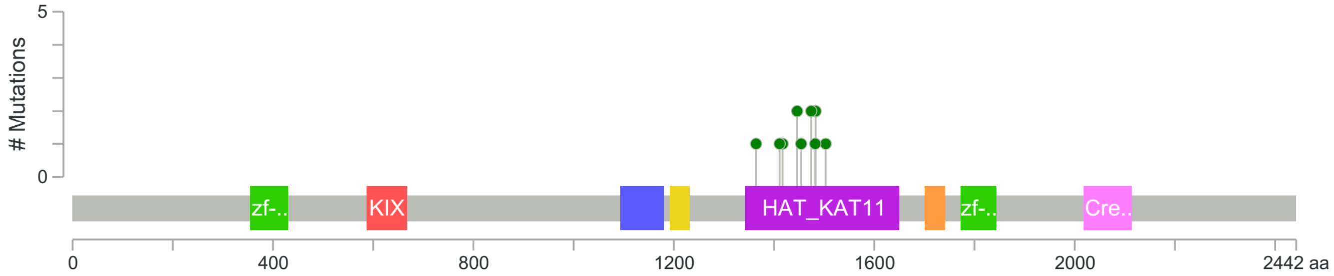
BTG1

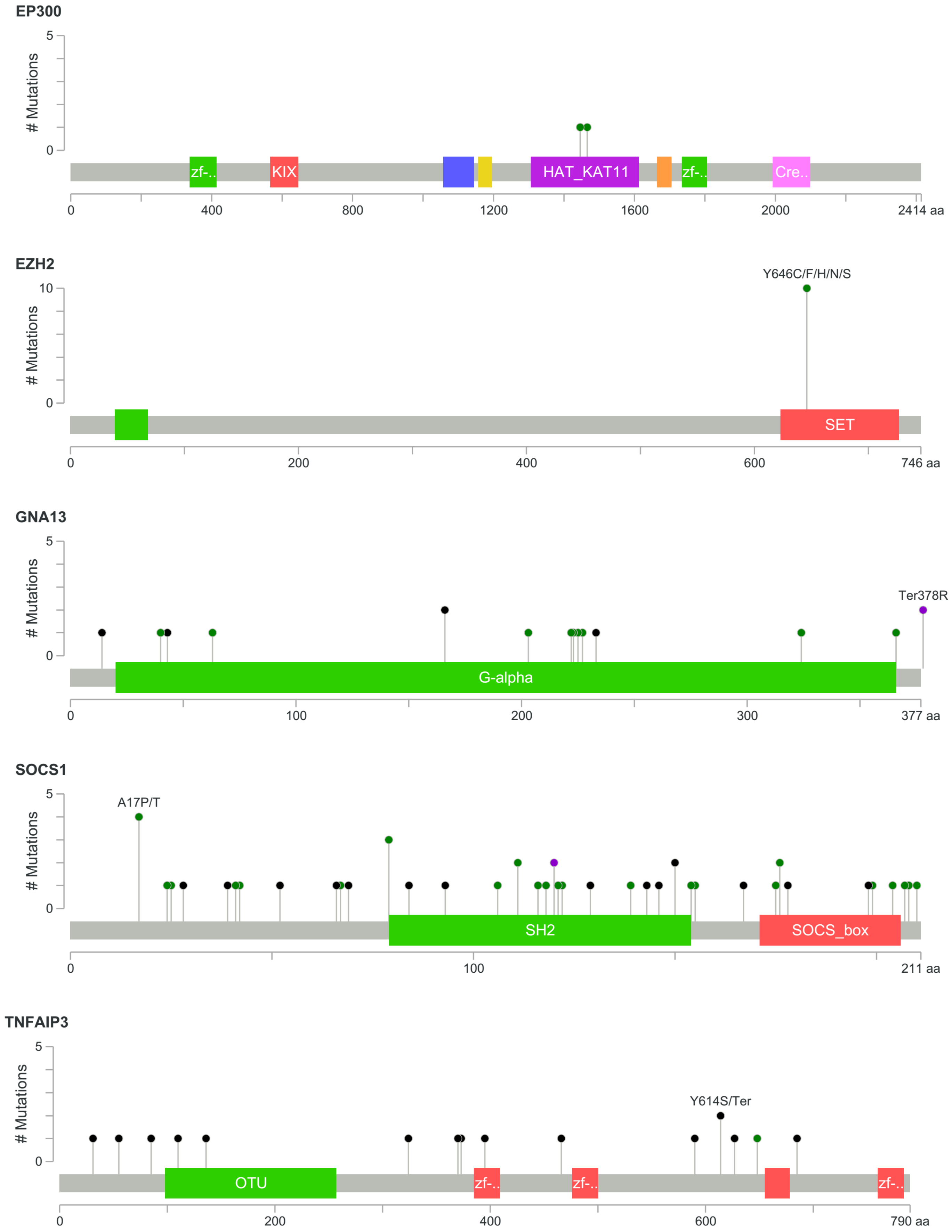


CARD11



CREBBP





Supplementary Figure 1. Mapping of the detected mutations to the protein sequences within respective domains in the 10 most frequently mutated and relevant genes is this study. Mutations in *CREBBP* and *EP300* always occurred within the HAT domain responsible for acetylation. In *SOCS1*, mutations were distributed evenly along the protein sequence. Y-axis represents number of mutations detected at a particular amino acid position. green – missense mutation; black – frameshift insertion/deletion; purple – nonsense mutation.