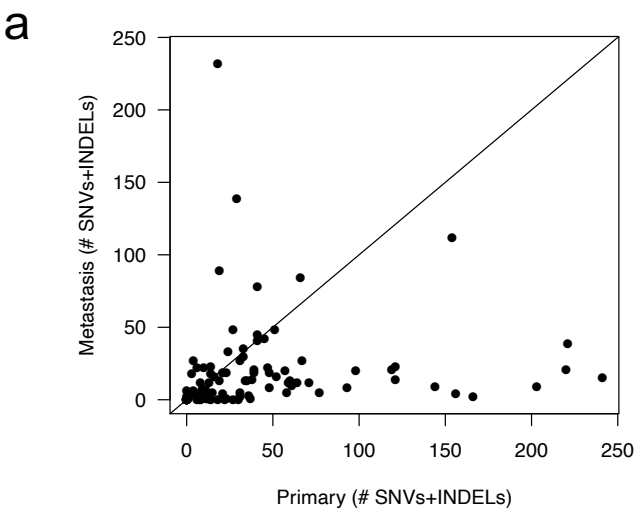
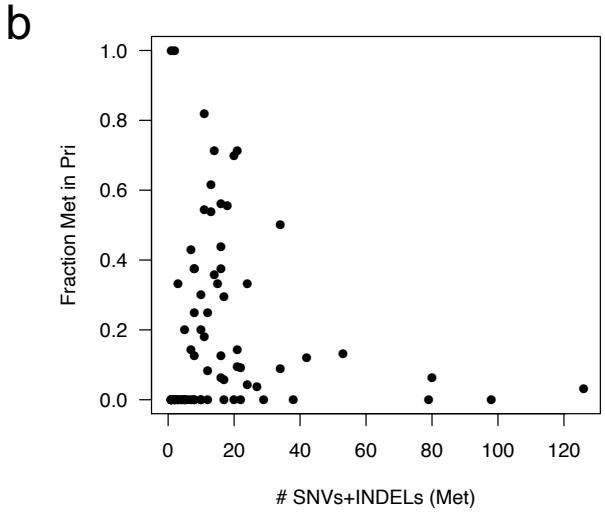
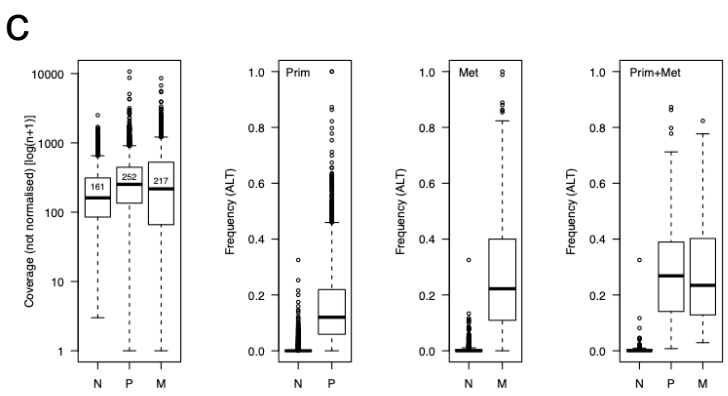
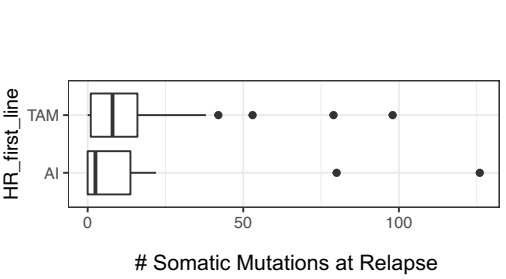
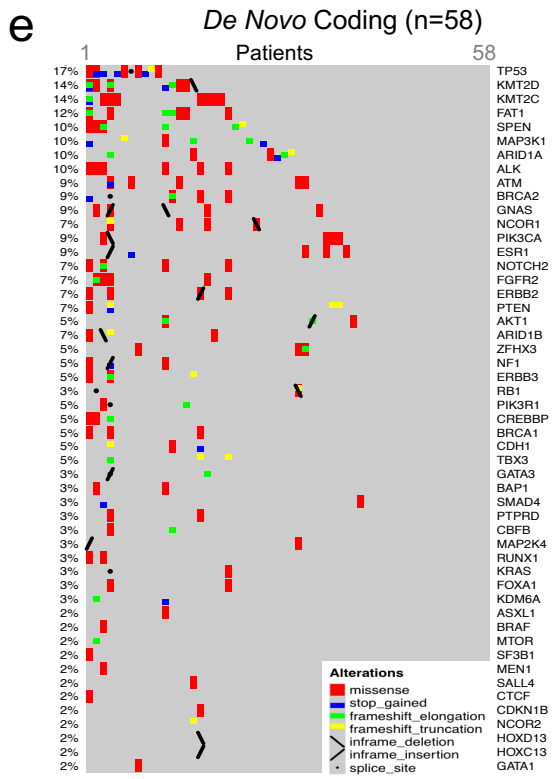
Supplementary Figure 19

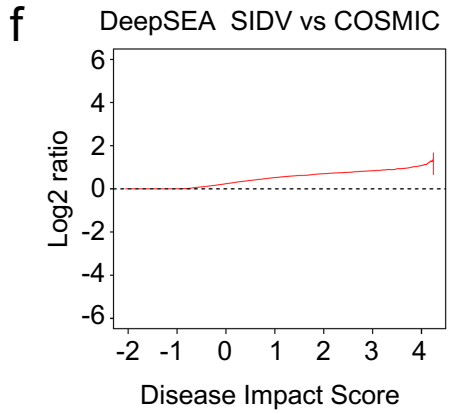


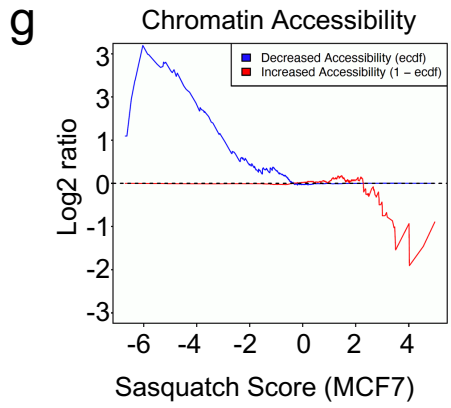












Supplementary Figure 19. SIDV functional analyses. (a) Scatterplot comparing the number of variants (SNVs plus INDELs) in matched primary and metastatic lesions. (b) Scatterplot showing the fraction (0-1) of mutations identified in the metastatic tumor that were also called in the corresponding matched primary. Each dot represent a pair of matched primary-met, with the x-axis indicating the total number of variants in the each metastatic sample. (c) (Left to right) Box plots showing the overall coverage of the regions showing variants, separately for matched normal (N), primary (P) and metastatic (M) samples. The other three box plots show the VAF (frequency of alternative alleles) in normal and tumour (either primary, metastatic, or both) specimens, for three sets of variants (left to right): those identifie only in primaries; those identified only in metastasis; those identified in both. (d) Box plot showing that lesions that were treated with TAM or AI did not show a different number of detected mutations at relapse (p-value = 0.21; Mann-Whitney Test). (e) Matched targeted coding profiling identified recurrently mutated (point mutations and indels) genes acquired in metastatic samples. The heat map is showing, for each patient and mutated genes, the type of lesions detected, and the fraction of lesions showing an alteration in each gene (left). (f-g) Functional characterization of SIDV calls as compared to the entire COSMIC catalogue.