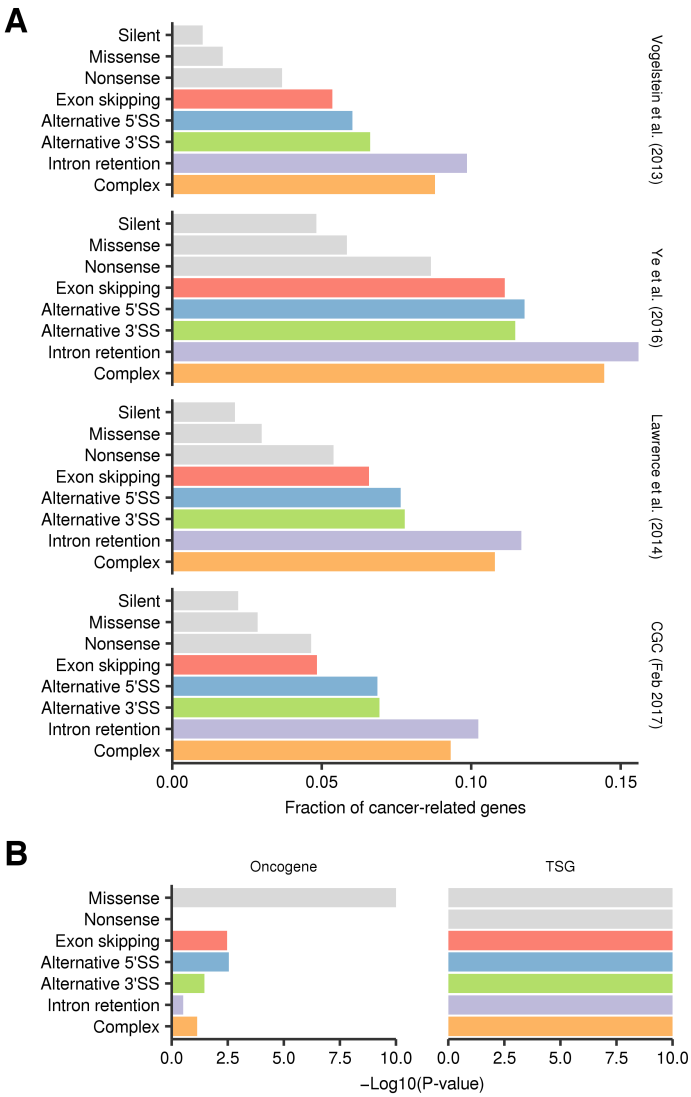

Supplementary Figure 6: Enrichment of SAVs in cancer-related genes.

(A) The fraction of SAVs affecting cancer-related genes relative to total SAVs according to splicing outcomes were compared with other types of somatic variants (silent, missense, and nonsense). These cancer-related gene sets are derived from three publications (Vogelstein et al. 2013; Lawrence et al. 2014; Ye et al. 2016) and the Cancer Gene Census database (CGC, as of Feb. 2017, http://cancer.sanger.ac.uk/census). **(B)** The fraction of somatic variants affecting oncogenes or TSGs (Vogelstein et al. 2013) for each type of abnormal splicing was compared with that of silent variants. The bar plot shows the logarithm of P-values calculated using a binomial test.