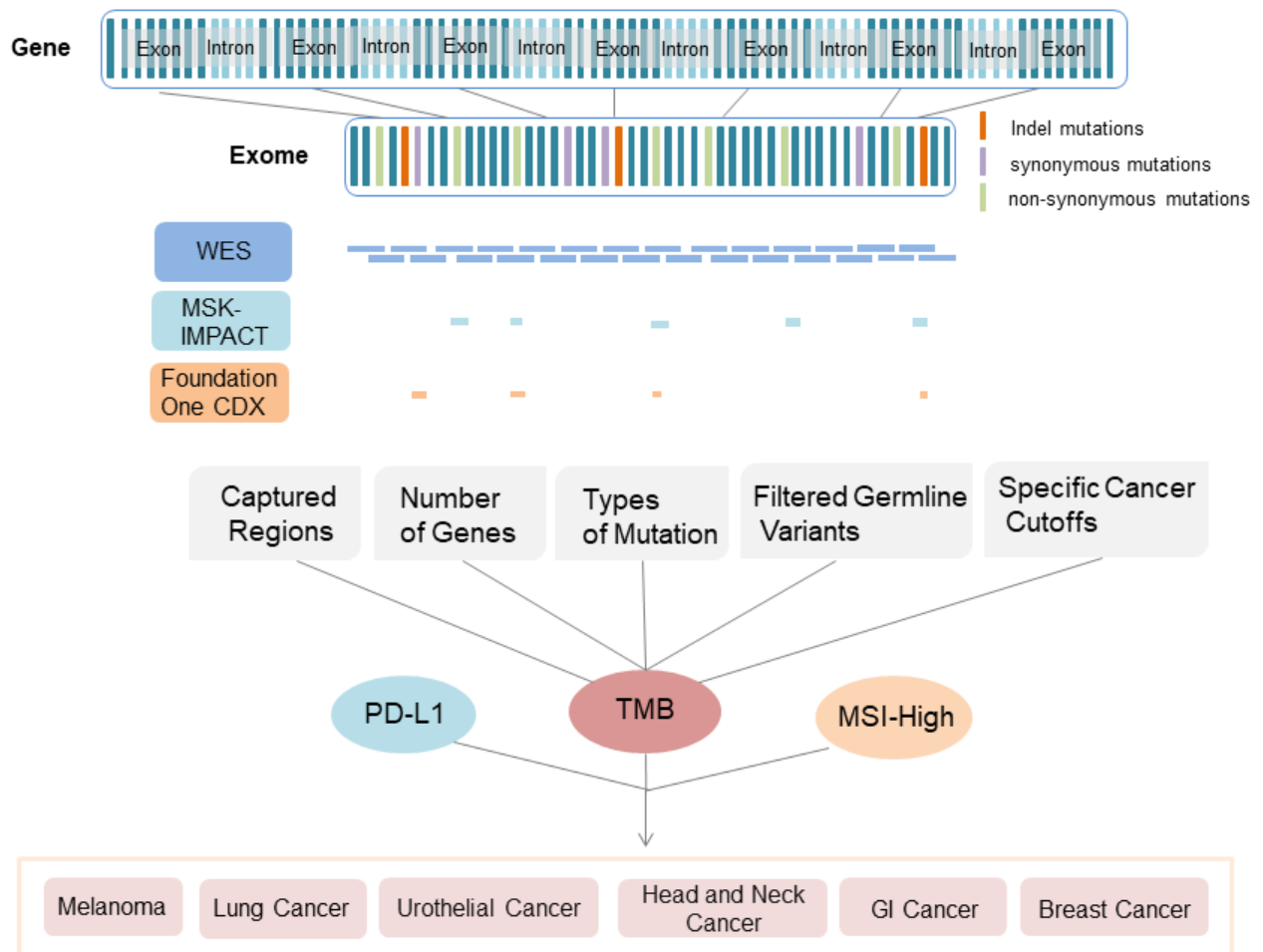**Supplementary Data**

Supplementary Fig. 1

Supplementary Figure Legend

TMB detection in solid tumors. Comparison between whole exome sequencing (WES) and two targeted gene panels (MSK-IMPACT and FoundationOne CDx®). WES detects mutations in the entire exome. Both panels detect somatic coding (non-synonymous) mutations per megabase of tumor genome examined inclusive of frameshift, point mutations, and small insertions and deletions (indels). FoundationOne CDx® also detects synonymous mutations. Multiple parameters, such as captured region, number of genes, types of mutation, filtered germline variants and specific cancer cutoffs, will influence TMB measurement. The complementary utilization of TMB, PD-L1 and MSI-high may predict ICIs responsiveness better than each alone (46,113).