

Supplementary Methods

Evaluation of immunotherapy efficacy and adverse events

The treatment response was assessed by computed tomography (CT) scans. The development of adverse events was assessed by electrocardiography and blood indicators.

Evaluation of the influence of mutations on gene functions

The protein structure was predicted by SWISS-MODEL (<https://swissmodel.expasy.org>) and Phyre2 (<http://www.sbg.bio.ic.ac.uk/phyre2/>) based on the amino acid sequence derived from UniProt (<https://www.uniprot.org>). These inferred structures along with mutation information were further subjected to a functional prediction by the MAESTRO (https://pbwww.services.came.sbg.ac.at/?page_id=416) algorithm.

Public Data collection

The gene expression profile consisting of 74 cases whose T cells were either extracted before or after ICI treatment were available from the Gene Expression Omnibus (GEO, <https://www.ncbi.nlm.nih.gov/geo>, GSE141479).