



S1 Fig. The mutational landscape of epidermal growth factor receptor (*EGFR*)–mutated non–small cell lung cancer patients. The x-axis represents each case sample, and the y-axis represents mutated genes. The bar graph at the top of the diagram provides the tumor mutational burden (TMB) value for each sample, and the bar graph on the right provides the mutation number for each mutated gene. Green indicates single nucleotide variant/insertion-deletion mutations, red indicates gene amplifications, blue indicates gene homozygous deletions, yellow indicates fusions/rearrangements, and purple indicates truncations.