

S1 Table. The sequencing coverage and quality statistics for each sample

Sample ID	Total No. of sequenced reads	Total No. of uniquely mapped non-duplicate reads	Total No. of covered bases	Median coverage (and range) per base	Percentage of targeted bases with coverage \geq 10	Percentage of targeted bases with coverage > 200	Percentage of targeted bases with coverage > 300	Percentage of targeted bases with coverage > 400	Percentage of targeted bases with coverage > 500
Gate-Lung-0146 ^{a)}	53,234,408	42,100,586	2,867,542	1,112 (0-3,522)	99.9	98.2	96.5	93.9	90.5
LC180302 ^{b)}	98,627,672	60,313,855	2,867,542	1,609 (0-4,485)	99.9	98.8	98	96.9	95.4

^{a)}Gate-Lung-0146: pre-erlotinib formalin-fixed paraffin-embedded DNA sample, ^{b)}LC180302: post-erlotinib pleural effusion sample (acquired resistance). Reference genome – GRCh37 (hg19), targeted bases – LCP custom panel.