MAYO CLINIC LABORATORIES

Targeted Gene Regions Interrogated by Lung Panel

Next-generation sequencing (NGS) is performed to test for the presence of a single nucleotide and/or copy number variants in these genes. When appropriate, reported alterations detected by NGS are confirmed by an independent reference method, such as multiplex ligation-dependent probe amplification (MLPA), polymerase chain reaction (PCR), and/or Sanger sequencing.

Genomic Build: GRCh37 (hg19)

Gene	RefSeq Transcript[1]	Targeted Regions[2]
ALK	NM_004304	29445213 – 29445334
ALK	NM_004304	29443589 – 29443707
ALK	NM_004304	29432646 – 29432776
BRAF	NM_004333	140453118 – 140453196
EGFR	NM_005228	55211043 – 55211132
EGFR	NM_005228	55221785 – 55221871
EGFR	NM_005228	55232966 – 55233071
EGFR	NM_005228	55241601 – 55241733
EGFR	NM_005228	55242417 – 55242514
EGFR	NM_005228	55248961 – 55249084
EGFR	NM_005228	55249133 – 55249229
EGFR	NM_005228	55259506 – 55259609
ERBB2	NM_004448	37880161 – 37880289
ERBB2	NM_004448	37880964 – 37881057
ERBB2	NM_004448	37881334 – 37881460
HRAS	NM_005343	534238 – 534313
HRAS	NM_005343	533808 – 533918
HRAS	NM_005343	533463 – 533565
KRAS	NM_004985	25398257 – 25398312
KRAS	NM_004985	25380233 – 25380304
KRAS	NM_004985	25378559 – 25378660
MET	NM_001127500	116411837 – 116411962
MET	NM_001127500	116412026 – 116412089
NRAS	NM_002524	115258729 – 115258774
NRAS	NM_002524	115256521 – 115256585
NRAS	NM_002524	115252194 – 115252297

[1] Reference transcript numbers may have been updated due to database re-versioning. Always refer to the final patient report for gene transcript information referenced at the time of testing.

[2] Default reportable range offset is +/- 2 base pairs around each targeted exon region. Exception: *MET* intron 13 and 14 expanded coverage.

To verify if a specific region/exon/variant is covered by this assay, contact a laboratory genetic counselor at 800-533-1710.