Single consolidated NGS workflow for DNA + RNA

With QIAseq[®] Lung Multimodal you no longer have to split your precious samples





Challenges of lung cancer profiling

Lung cancers are characterized by a wide range of genomic and transcriptomic changes including SNVs, InDels, fusions and exon-skipping events. Recent advances in NGS chemistries, platforms and bioinformatics pipelines have empowered users to efficiently interrogate DNA and RNA alterations in biological samples. Current approaches, however, require the use of 2 separate workflows to prepare libraries from separate DNA and RNA isolates. Limitations of such approaches include:

- Precious samples must be split to extract DNA and RNA in separate sample prep protocols
- Large amounts of sample material are required to generate sufficient amounts of input DNA and RNA for multiple workflows
- Workflow has added complexity of deriving integrated insights from results of different technical approaches, each with its own innate bias
- Separate workflows result in inefficient use of resources and long turnaround times

Streamlined, consolidated one-day workflow

To overcome the limitations associated with current approaches, the QIAseq Lung Multimodal panel starts with total nucleic acids (or DNA + RNA) and prepares targeted DNA and RNA libraries containing Unique Molecular Indices for use on Illumina® platforms using a one-day, consolidated workflow (see Figure 1).

The QIAseq Lung Multimodal panel delivers:

- The ONLY single consolidated workflow for DNA + RNA library prep using total nucleic acids as input
- Operational efficiency with a 50% reduction in user interventions
- Confident detection of low-frequency variants with Unique Molecular Indices (UMIs)
- Reduced index hopping with Unique Dual Indices (UDIs)
- Comprehensive coverage of known and novel fusions as well as all relevant alterations
- 70 DNA gene targets and 54 RNA gene targets (Table 1 and 2)

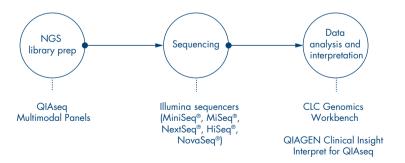


Figure 1. Extract more information, while reducing sample, time and cost with a simple, one-day workflow. This flexible solution enables the construction of libraries compatible with Illumina platforms from as little as 10 ng total nucleic acid isolated from a wide range of samples. The data analysis pipelines in CLC Genomics Workbench translate raw sequence data in FASTQ format to DNA and RNA variant files (VCFs), which can be further interpreted for biological significance through QCI® Interpret for QIAseq.

Confidently interpret NGS variants

Our software workflow makes it easy to extract, identify the variants of interest and deliver a comprehensive variant interpretation from your raw NGS data. The industry leading genomic analysis and interpretation software solutions, CLC Genomic Workbench and QCI Interpret for QIAseq, provide you with a comprehensive report to support your workflow, including variant classification, details on variant function, literature references, drug labels, drug interactions and relevant clinical trials. Accelerate your clinical research and go from raw NGS data to detailed and trusted insights in minutes – not hours.

Key differentiators

- The ONLY single consolidated workflow for DNA + RNA library prep using total nucleic acids as input
- Cuts user interventions by 50%
- Confident detection of low-frequency variants
- Detection of both known and novel fusions
- Increased target coverage of all relevant alterations

Table 1. 70 DNA gene targets

AKT1	EGFR	KIT	NTRK1	RET
ALK	EPHA5	KMT2D	NTRK2	RITI
AMER1	ERBB2	KRAS	NTRK3	ROS1
APC	ERBB4	LRP1B	PDGFRA	RUNXITI
ARID1A	FBXO7	MAP2K1	PIK3CA	SETD2
ATM	FBXW7	MDM2	PIK3CG	SMAD4
BAI3	FGFR1	MET	PIK3R1	SMARCA4
BAP1	FGFR2	MGA	PIK3R2	SOX2
BRAF	FGFR3	MLH1	PKHD1	STK11
CDKN2A	FHIT	MUC16	PTEN	TNFAIP3
CDKN2B	GRM8	МҮС	PTPRD	
CREBBP	HRAS	NF1	RARB	
CSMD3	JAK2	NFE2L2	RASSF1	
CTNNB1	KDR	NOTCHI	RB1	
DDR2	KEAP1	NRAS	RBM10	

Table 2. 54 RNA gene targets

BAG4-FGFR1	GOPC-ROS1	SLC3A2-NRG1
BCL11A-ALK	HIP1-ALK	SND1-BRAF
BRD4-C15orf55	IRF2BP2-NTRK1	SQSTM1-NTRK1
CCDC6-RET	KANSLI-ARLI7A	SQSTM1-NTRK3
CD74-NRG1	KIAA1217-RET	STARD3NL-MET
CD74-NTRK1	KIF5B-ALK	STRN-ALK
CD74-ROS1	KIF5B-MET	TCF3-PBX1
CLIP4-VSNL1	KIF5B-RET	TFG-ALK
CRTC1-MAML2	KLC1-ALK	TPM3-ROS1
CUX1-RET	LRIG3-ROS1	TPR-ALK
EGFR-EGFR	MAML2-CRTC1	TPR-NTRK1
EGFR-RAD51	MAN2A1-FER	TRA2B-DNAH5
EML4-ALK	MET-MET	TRIM24-NTRK2
ETV6-NTRK3	MPRIP-NTRK1	TRIM33-RET
EZR-ROS1	NCOA4-RET	
FGFR2-CCAR2	NSD3-NUTM1	
FGFR2-CIT	PTPRK-RSPO3	
FGFR3-BAIAP2L1	RUNX1-GLRX5	
FGFR3-TACC3	SDC4-ROS1	
GCC2-ALK	SLC34A2-ROS1	

Product	Contents	Number of samples	Panel variant number	Cat. no.
QIAseq Lung Multimodal	Kit containing ALL reagents (except indices) for multimodal (DNA and RNA) sequencing	12	UHS-005Z-12	333932
Panel		96	UHS-005Z-96	333935
QIAseq Multimodal Index I (12)	Box containing oligos, enough to process a total of 12 samples, for indexing up to a total of 12 samples for Multimodal panel sequencing on Illumina platforms			333962
QIAseq Multimodal Index I Set A (96)	Box containing oligos, enough to process a total of 48 samples, for indexing up to a total of 48 samples for Multimodal panel sequencing on Illumina platforms; one of two sets required for multiplexing 96 samples			333965
QIAseq Multimodal Index I Set B (96)	Box containing oligos, enough to process a total of 48 samples, for indexing up to a total of 48 samples for Multimodal panel sequencing on Illumina platforms; Two of two sets required for multiplexing 96 samples			333975

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Visit www.qiagen.com/QIAseqLungMM and discover how you can double your NGS insights and free up half of your resources.

Visit the QIAseq Knowledge Hub at **www.qiagen.com/clp/qiaseq-knowledge-hub/** – your one-stop shop for QIAseq Multimodal (RNA + DNA) and Targeted DNA webinars.

The QIAseq Lung Multimodal Panel is intended for molecular biology applications. This product is not intended for the diagnosis, prevention, or treatment of a disease.

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