

FUSION*Plex* Lung v2

Description

The FUSION*Plex* Lung v2 panel is a balanced pool of gene-specific primer (GSP) oligonucleotides that is optimized for use with FUSION*Plex* reagents and molecular barcode (MBC) adapters to produce targeted NGS libraries. This product insert should be used in conjunction with FUSION*Plex* protocol for Illumina® (RA-DOC-047), FUSION*Plex*-LAC protocol for Illumina® (RA-DOC-471), or FUSION*Plex* protocol for Ion Torrent™ (RA-DOC-048).

FUSION*Plex* Lung v2 contains **323** GSPs targeting **17** genes commonly mutated in non-small cell lung cancer (NSCLC).

Description	Part number	Storage
FUSION <i>Plex</i> Lung v2 GSP1, 8 reactions	SA18090081	
FUSION <i>Plex</i> Lung v2 GSP2, 8 reactions	SA18090082	-20°C ± 10°C
10X VCP Primer Mix	SA0126	

Recommended PCR cycling

	Step	Temperature (°C)	Time	Cycles
First PCR reaction	1	95	3 min	1
	2	95	30 sec	
	3	60	10 sec	15
	4	65	5 min (100% ramp rate)	
	5	72	3 min	1
	6	4	Hold	1

Recommended PCR cycling (cont.)

	Step	Temperature (°C)	Time	Cycles
Second PCR reaction	1	95	3 min	1
	2	95	30 sec	
	3	60	10 sec	20†
	4	65	5 min (100% ramp rate)	
	5	72	3 min	1
	6	4	Hold	1

†The number of PCR2 cycles may be decreased if you regularly experience library yields greater than 200 nM.

Recommended reads and multiplexing

FUSIONPlex Lung v2 libraries should be sequenced to a minimum of **1M reads**. Starting read depth recommendations for standard profiling may be adjusted based on user needs.

Archer™ Analysis settings

Sequencing data should be processed using Archer Analysis (v7.0, or greater). The FUSIONPlex Lung v2 panel requires selection of the **Fusion** and (optional) **SNV/Indel** pipeline(s), found under the **RNA** Input Type (see the Archer Analysis User Guide for more details on setting up your analysis).

Processing of FUSIONPlex Lung v2 libraries requires a one-time upload of the Panel GTF. Files can be obtained by contacting archer-tech@idtdna.com.

Assay targets

Gene	Accession	Exon	Variant Type	Description**
ALK	NM_004304	2, 4, 6, 8, 10, 12, 14, 16, 17, 18, 19, intron19, 20, mid-exon20, 21, 22, 23, 26	Fusion, ALK ATIV, Internal deletion (ALKΔ2-17, ALKΔ2-3)	5'
ALK	NM_004304	1, 2	Internal deletion (ALKΔ2-17, ALKΔ2-3)	3'

Gene	Accession	Exon	Variant Type	Description**
<i>ALK</i>	NM_004304	22, 23, 25	Mutation	p.P1153-p.C1156, p.F1174, p.L1196-p.S1206, p.G1269
<i>BRAF</i>	NM_004333	2, 3, 4, 5, 7, 8, 9, 10, 11, 12, 15, 16	Fusion, Kinase Domain Duplication, BRAFΔ2-10, BRAFΔ4-10, BRAFΔ2-8, BRAFΔ3-8, BRAFΔ4-8	5'
<i>BRAF</i>	NM_004333	1, 2, 3, 7, 8, 10, 13, 14, 18	Fusion, Kinase Domain Duplication, BRAFΔ2-10, BRAFΔ4-10, BRAFΔ2-8, BRAFΔ3-8, BRAFΔ4-8	3'
<i>BRAF</i>	NM_004333	15	Mutation	p.V600
<i>EGFR</i>	NM_005228	7, 8, 9, 14, 15, 16, 17, 18, 19, 20	Fusion, Exon 2-7 Skipping (EGFRvIII), Kinase Domain Duplication	5'
<i>EGFR</i>	NM_005228	1, 24, 25, mid-exon25, 26	Fusion, Exon 2-7 Skipping (EGFRvIII), Kinase Domain Duplication	3'
<i>EGFR</i>	NM_005228	18, 19, 20, 21	Mutation	p.E709-p.G719, p.E746-p.L760, p.V774-p.G796, p.L858-p.L861
<i>ERBB2</i>	NM_004448	4, 5, 13, 15, 17	Fusion, Exon 16 skipping (Δ16HER)	5'
<i>ERBB2</i>	NM_004448	15, 23, 24, 25, mid-exon26, 26	Fusion, Exon 16 skipping (Δ16HER)	3'
<i>ERBB2</i>	NM_004448	8, 20	Mutation	p.G309-p.S310, p.Y772-p.P780, p.C805
<i>FGFR1</i>	NM_015850	2*, 3, 4, 5, 6, 7, 8, 9, 10, 11, 17	Fusion, Kinase Domain Duplication	5'
<i>FGFR1</i>	NM_015850	12, 17	Fusion, Kinase Domain Duplication	3'
<i>FGFR1</i>	NM_023110	4, 13, 14	Mutation	p.T141, p.V561, p.K656
<i>FGFR2</i>	NM_000141	2*, 3, 5, 6, 7, 8, 9, 10	Fusion	5'
<i>FGFR2</i>	NM_000141	16, 17, 18	Fusion	3'

Gene	Accession	Exon	Variant Type	Description**
<i>FGFR2</i>	NM_000141	7, 9, 12, 13, 14	Mutation	p.S252-p.P253, p.G305, p.Y375-V395, p.I547-p.N549, p.V564, p.A648-p.K659
<i>FGFR3</i>	NM_000142	3, 5, 8, 9, 10, 11, 12, 13, 14	Fusion	5'
<i>FGFR3</i>	NM_000142	16, 17, intron17, mid-exon18	Fusion	3'
<i>FGFR3</i>	NM_000142	7, 9, 13, 14, 16	Mutation	p.R248-p.S249, p.G370-p.R399, p.V555, p.D641-p.K650, p.G697-p.K715
<i>KRAS</i>	NM_004985	2, 3, 4	Mutation	p.G12-p.G13, p.Q61, p.K117, p.A146
<i>MET</i>	NM_000245	2, 4, 5, 6, 13, 14, 15, 16, 17, 21	Fusion, Exon 14 Skipping (METΔex14)	5'
<i>MET</i>	NM_000245	2, 13	Fusion, Exon 14 Skipping (METΔex14)	3'
<i>NRG1</i>	NM_001159996	1*, 3, 4, 5	Fusion	5'
<i>NRG1</i>	NM_004495	1, 2, 3, 4, 5, 6	Fusion	5'
<i>NRG1</i>	NM_013958	1*	Fusion	5'
<i>NRG1</i>	NM_013959	1*, 3	Fusion	5'
<i>NRG1</i>	NM_013962	1*	Fusion	5'
<i>NRG1</i>	NM_013962	1	Fusion	3'
<i>NTRK1</i>	NM_001007792	1, 2	Fusion	5'
<i>NTRK1</i>	NM_002529	1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14	Fusion	5'
<i>NTRK1</i>	NM_002529	13, 14, 15, 16, 17	Mutation	Full kinase domain coverage for resistance mutations including p.G595
<i>NTRK2</i>	NM_006180	4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18	Fusion	5'
<i>NTRK2</i>	NM_006180	11, 14	Fusion	3'

Gene	Accession	Exon	Variant Type	Description**
<i>NTRK2</i>	NM_006180	16, 17, 18, 19, 20, 21	Mutation	Full kinase domain coverage for resistance mutations
<i>NTRK3</i>	NM_001007156	15	Fusion	5'
<i>NTRK3</i>	NM_002530	3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16	Fusion	5'
<i>NTRK3</i>	NM_002530	13, 14, 15, 17	Fusion	3'
<i>NTRK3</i>	NM_002530	15, 16, 17, 18, 19	Mutation	Full kinase domain coverage for resistance mutation detection including p.F617, p.G623, p.G696
<i>NUTM1</i>	NM_175741	2*, 3, mid-exon3, 4, 5, mid-exon6, 6	Fusion	5'
<i>PIK3CA</i>	NM_006218	2, 15	Fusion	5'
<i>PIK3CA</i>	NM_006218	2, 3, 5, 6, 8, 10, 14, 21	Mutation	p.E81K-p.G118D, p.L339-p.D350, p.G364R, p.E418-p.C420, p.E453-p.K468, p.P539-p.Q546, p.E726, p.Y1021-p.T1052
<i>RET</i>	NM_020630	2, 4, 6, 8, 9, 10, 11, mid-exon11, 12, 13, 14	Fusion	5'
<i>RET</i>	NM_020630	15, 16	Mutation	p.A883, p.M918
<i>ROS1</i>	NM_002944	2, 4, 7, 31, 32, 33, 34, 35, 36, 37	Fusion	5'
<i>ROS1</i>	NM_002944	38	Mutation	p.G2032

*Indicates exons that are entirely untranslated region (UTR), or for which the UTR is targeted.

**The mutations listed under the Description column are targeted by the assay design. Version 6.2 and earlier of Archer Analysis may not support RNA SNV/Indel variant calling at exon junctions depending on the sequence context (SNVs ≤5bp, indels ≤30bp). *De Novo* RNA SNV/Indel and Internal Tandem Duplication mutation detection are not supported on the Ion Torrent Sequencing System.

∇ALK-AT1 currently requires review outside of Archer Analysis.

Limitations of use

For research use only. Not for use in diagnostic procedures. Unless otherwise agreed to in writing, IDT does not intend these products to be used in clinical applications and does not warrant their fitness or suitability for any clinical diagnostic use. Purchaser is solely responsible for all decisions regarding the use of these products and any associated regulatory or legal obligations.

Safety data sheets pertaining to this product are available upon request.

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Revision History

Document Number	Date	Description of change
RA-DOC-019/REV01	June 2023	Initial release.
RA-DOC-019/REV02	November 2023	Updated First and Second PCR cycling conditions to include separate anneal and extended steps. Updated document number typo in footer. Updated branding.
RA-DOC-019/REV03	October 2024	Added FUSIONPlex-LAC protocol for Illumina® (RA-DOC-471) to Description section.