

Multi-Cancer RNA Fusion v2 Panel

The **oncoReveal™ Multi-Cancer RNA Fusion v2 Panel** is a robust NGS assay that interrogates multiple gene rearrangement regions of interest* across multiple solid tumor cancer types. The panel uses proprietary Stem-Loop Inhibition-Mediated amplification (SLIMamp®) technology, a tiled amplicon-based library prep chemistry for efficient single-tube target enrichment.

| Driver Genes | Fusion Partners |
|---------------------|---|
| ALK | EML4, CLTC, HIP1, KIF5B, KLC1, STRN, TFG, TPM3, TPR, MSN |
| BRAF | KIAA1549, MKRN1, FAM131B, AKAP9 |
| EGFR | SEPT14, PSPH, RAD51 |
| ERG | TMPRSS2 |
| FGFR2 | BICC1, CASP7 |
| FGFR3 | TACC3, BAIAP2L1 |
| MET | KIF5B |
| NRG1 | CD74, SLC3A2, VAMP2 |
| NTRK1 | TPM3, TFG, LMNA, SQSTM1, CHTOP, ARHGEF2, NFASC, IRF2BP2, PPL, BCAN, SCYL3, TP53, CD74, MPRIP, TPR |
| NTRK2 | AFAP1, NACC2, BCR, TRIM24, QKI, PAN3, SQSTM1, STRN |
| NTRK3 | ETV6, BTBD1, EML4, SQSTM1, TFG, RBPMS |
| PBX1 | TCF3 |
| PPARG | PAX8, CREB3L2 |
| PRKACA | DNAJB1 |
| RAF1 | ESRP1, SRGAP3 |
| RET | CCDC6, CUX1, KIF5B, NCOA4, TRIM33, PRKAR1A |
| ROS1 | CCDC6, CD74, CLTC, EZR, GOPC, LRIG3, MSN, SDC4, SLC34A2, TFG, TPM3 |
| TFE3 | SFPQ, ASPSCR1, CLTC, PRCC, NONO |
| | MET exon 14 skipping, EGFR variant III |

3'/5' Expression Imbalance Ration Assessed

ALK ROS1 RET NTRK1 NTRK2 NTRK3 FGFR3 NRG1 PBX1

Expression Control Genes

HMBS TBP

Simple NGS library prep workflow

Maintain control of samples and results with single-tube, tiled amplification that can be performed in-house by any NGS lab

Sensitive and robust chemistry

Achieve sensitive and robust fusion detection without UIDs[‡], even with limited RNA input or poor sample quality

Reduced fullyloaded lab costs

Improve lab efficiency and reduce "no calls", repeat testing, and difficult interpretation decisions

^{*} Content is based on data from ongoing clinical trials along with sources that include the College of American Pathologists (CAP), the Association for Molecular Pathology (AMP), the National Comprehensive Cancer Network (NNCN), and the Catalog of Somatic Mutations in Cancer (COSMIC) database. UID, unique ID; also known as unique molecular ID (UMI). For Research Use Only. Not for use in diagnostic procedures.

Simple, one-day workflow



Gene-specific PCR & cleanup

Indexing PCR & cleanup

Quantitation & normalization

Load sequencer

Panel specifications*

| Enrichment chemistry | Multiplex PCR using tiled amplicons |
|--|--|
| Number of pools | 1 pool |
| Number of genes/partners | 18 genes and >80 partners, plus MET exon 14 skipping |
| Variant types | Fusion RNA transcripts |
| Average amplicon size | 120bp |
| Recommended RNA input range | 20ng - 100ng RNA |
| Sample types | RNA from FFPE or tissue; cfRNA |
| Recommended reads per sample | ~50,000 paired-end reads |
| Total assay time (from RNA to sequencer) | <9 hours |

^{*} Mapping rate, percentage of on-target aligned reads, and coverage uniformity metrics are based on internal testing performed using reference standard materials

Ordering information

Select the panel AND one of the index kit options listed below.

| Panel | Part number |
|---|----------------|
| oncoReveal™ Multi-Cancer RNA Fusion v2 Panel (24 reactions) | HRA-HS-1002-24 |

| Pillar Index Kit options | Reactions | Part number |
|-----------------------------------|--------------------------------|-----------------|
| Pillar Custom Index Primers Kit A | 32 Combinations, 96 reactions | IDX-PI-1001-96 |
| Pillar Custom Index Primers Kit D | 96 Combinations, 192 reactions | IDX-PI-1004-192 |

TO ORDER OR LEARN MORE: pillarbiosci.com

For research use only. Not for use in diagnostic procedures.

© 2022 Pillar Biosciences. Pillar*, SLIMamp*, PiVAT* and oncoReveal™ are trademarks of Pillar Biosciences, Inc.
Current as of 12.17.2023 | MK-0022-4 v1.0



Pillar Biosciences, Inc. 9 Strathmore Rd Natick, MA 01760 (800) 514-9307 info@pillarbiosci.com