

# XCeloSeq® Solid Cancer Fusion Kit

SEQ012

## Product Description

The XCeloSeq Solid Cancer Fusion Kit contains a pool of targeted RNA enrichment primers located in conserved fusion partners for identification of both known and unknown fusions from RNA. These primers are designed for use only with XCeloSeq Targeted RNA Core Reagents (GF031). Together they allow for the generation of high quality, high-complexity next-generation sequencing libraries that are suitable for use with Illumina® next-generation sequencing instruments.

## Kit Contents

| Component                            | Tube Colour | Cap Colour | Storage | Part Code |
|--------------------------------------|-------------|------------|---------|-----------|
| Solid Cancer Fusion Kit – Outer Pool | Transparent | Orange     | -20°C   | PC0053    |
| Solid Cancer Fusion Kit – Inner Pool | Transparent | Black      | -20°C   | PC0054    |

## Kit Specifications and Recommendations

|   |   |
|---|---|
| Gene Targets                              | 53  |
| Targeting Primers <sup>%</sup>            | 351                                       |
| Recommended Input Quantity <sup>*</sup>   | 5-200 ng FFPE derived total RNA           |
|   | 5-100 ng high quality total RNA           |
| Recommended Reads Per Sample <sup>#</sup> | 3,000,000 (Dual index, 150 bp paired-end) |
| Hands on Time                             | 2.0 hours                                 |
| Total Protocol Time                       | 7.25 hours                                |

<sup>%</sup>An additional 8 QC primers are included

<sup>\*</sup>Higher quantities within this range will improve maximum sensitivity. The product supports capture with down to 1.0 ng of RNA, however this is not recommended as it will lead to reduced sensitivity. Cell-free RNA and total cell-free nucleic acids may be used as alternative starting materials, however fusion detection sensitivity will be lower due to cell-free RNA concentrations typically being very low, when using this material maximising starting input quantity will help ensure the best possible results.

<sup>#</sup>When using cfrRNA up to 10 times as much sequencing may be needed to ensure that enough RNA derived reads are in the final sequencing library. Users are recommended to assess this on the sample-by-sample basis.

## Assay Targets

| Gene            | Accession      | Exon(s)  | Fusion Direction |
|-----------------|----------------|--|------------------|
| <b>AKT3</b>     | NM_005465.7    | 1, 2, 3  | 5'               |
| <b>ALK</b>      | NM_004304.5    | 2, 4, 6, 10, 16 17, 18, 19 (and intron 19), 20, 21, 22, 23, 26 | 5'               |
| <b>ARHGAP26</b> | NM_015071.6    | 2, 10, 11, 12  | 5'               |
| <b>AXL</b>      | NM_021913.5    | 19, 20   | 3'               |
| <b>BRAF</b>     | NM_004333.6    | 2, 7, 8, 9, 10, 11, 12, 15, 16                                 | 5'               |
|                 |                | 1, 3, 7, 8, 10, 13   | 3'               |
| <b>BRD3</b>     | NM_007371.4    | 9, 10, 11, 12  | 3'               |
| <b>BRD4</b>     | NM_058243.2    | 10, 11   | 3'               |
| <b>EGFR</b>     | NM_005228.5    | 7, 8 (Exon 2-7 Skipping), 9, 16, 19, 20                        | 5'               |
|                 |                | 1 (Exon 2-7 Skipping), 24, 25                                  | 3'               |
| <b>ERG</b>      | NM_004449.4    | 2, 3, 4, 5, 6, 7, 8, 9, 10, 11                                 | 5'               |
| <b>ESR1</b>     | NM_001122742.1 | 1, 2, 3, 4, 5, 6   | 3'               |
| <b>ETV1</b>     | NM_004956.5    | 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13                            | 5'               |
| <b>ETV4</b>     | NM_001986.4    | 2, 4, 5, 6, 7, 8, 9, 10  | 5'               |
| <b>ETV5</b>     | NM_004454.3    | 2, 3, 7, 8, 9  | 5'               |
| <b>ETV6</b>     | NM_001987.5    | 2, 3, 4, 5, 6, 7   | 5'               |
|                 |                | 1, 2, 3, 4, 5, 6   | 3'               |
| <b>EWSR1</b>    | NM_005243.4    | 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14                           | 3'               |
| <b>FGFR1</b>    | NM_015850.4    | 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 17                             | 5'               |
|                 |                | 12, 17   | 3'               |
| <b>FGFR2</b>    | NM_000141.4    | 2, 5, 7, 8, 9, 10  | 5'               |
|                 |                | 16, 17   | 3'               |
| <b>FGFR3</b>    | NM_000142.4    | 3, 5, 8, 9, 10   | 5'               |
|                 |                | 16, 17 (and intron 17)   | 3'               |
| <b>FGR</b>      | NM_005248.3    | 2  | 5'               |
| <b>INSR</b>     | NM_000208.4    | 12, 13, 14, 15, 16, 17, 18, 19                                 | 5'               |
|                 |                | 20, 21, 22   | 3'               |
| <b>MAML2</b>    | NM_032427.4    | 2, 3   | 5'               |
| <b>MAST1</b>    | NM_014975.3    | 7, 8, 9, 18, 19, 20, 21  | 5'               |
| <b>MAST2</b>    | NM_015112.3    | 2, 3, 5, 6   | 5'               |
| <b>MET</b>      | NM_000245.4    | 2, 4, 5, 6, 13, 14, 15 (exon 14 skipping event), 16, 17, 21    | 5'               |
|                 |                | 2, 13 (exon 14 skipping event)                                 | 3'               |
| <b>MSMB</b>     | NM_002443.4    | 2, 3, 4  | 3'               |
| <b>MUSK</b>     | NM_005592.4    | 7, 8, 9, 11, 12, 13, 14  | 5'               |
| <b>MYB</b>      | NM_001130173.2 | 7, 8, 9, 11, 12, 13, 14, 15, 16                                | 3'               |

| Gene           | Accession      | Exon(s)                             | Fusion Direction |
|----------------|----------------|-------------------------------------|------------------|
| <b>NOTCH1</b>  | NM_017617.25   | 26, 27, 29                          | 5'               |
|                |                | 2, 4, 29, 30, 31                    | 3'               |
| <b>NOTCH2</b>  | NM_024408.4    | 26, 27, 28                          | 5'               |
|                |                | 5, 6, 7                             | 3'               |
| <b>NRG1</b>    | NM_004495.4    | 1, 2, 3, 4, 6                       | 5'               |
|                | NM_013957.5    | 1, 8                                | 5'               |
|                | NM_013962.2    | 1                                   | 3'               |
| <b>NTRK1</b>   | NM_002529.3    | 2, 4, 6, 8, 10, 11, 12, 13          | 5'               |
| <b>NTRK2</b>   | NM_006180.4    | 5, 7, 9, 11, 12, 13, 14, 15, 16, 17 | 5'               |
| <b>NTRK3</b>   | NM_002530.4    | 4, 7, 10, 12, 13, 14, 15, 16        | 5'               |
|                |                | 13, 14, 15                          | 3'               |
|                | NM_001007156.2 | 15                                  | 5'               |
| <b>NUMBL</b>   | NM_004756.5    | 3                                   | 5'               |
| <b>NUTM1</b>   | NM_175741.2    | 3                                   | 5'               |
| <b>PDGFRA</b>  | NM_006206.6    | 10, 11, 12, 13, 14                  | 5'               |
|                |                | 7 (exon 8 deletion)                 | 3'               |
| <b>PDGFRB</b>  | NM_002609.4    | 8, 9, 10, 11, 12, 13, 14            | 5'               |
| <b>PIK3CA</b>  | NM_006218.4    | 2                                   | 5'               |
| <b>PKN1</b>    | NM_002741.5    | 10, 11, 12, 13                      | 5'               |
| <b>PPARG</b>   | NM_015869.4    | 1, 2, 3, 4                          | 5'               |
| <b>PRKCA</b>   | NM_002737.3    | 4, 5, 6                             | 5'               |
| <b>PRKCB</b>   | NM_002738.7    | 3                                   | 5'               |
| <b>RAF1</b>    | NM_002880.3    | 4, 5, 6, 7, 9, 10, 11, 12           | 5'               |
|                |                | 4, 5, 6, 7, 9                       | 3'               |
| <b>RELA</b>    | NM_021975.4    | 3, 4                                | 5'               |
| <b>RET</b>     | NM_020975.6    | 2, 4, 6, 8, 9, 10, 11, 12, 13, 14   | 5'               |
| <b>ROS1</b>    | NM_002944.2    | 2, 4, 7, 31, 32, 33, 34, 35, 36, 37 | 5'               |
| <b>RSPO2</b>   | NM_178565.5    | 1, 2                                | 5'               |
| <b>RSPO3</b>   | NM_032784.5    | 2                                   | 5'               |
| <b>TERT</b>    | NM_198253.3    | 2                                   | 5'               |
| <b>TFE3</b>    | NM_006521.6    | 2, 3, 4, 5, 6, 7, 8                 | 5'               |
|                |                | 2, 3, 4, 5, 6                       | 3'               |
| <b>TFEB</b>    | NM_007162.2    | 1, 2                                | 5'               |
| <b>THADA</b>   | NM_022065.4    | 24, 25, 26, 27, 28, 29, 30          | 3'               |
| <b>TMPRSS2</b> | NM_005656.4    | 1                                   | 3'               |
|                | NM_001135099.1 | 1, 2, 3, 4, 5, 6                    | 3'               |

## Additional Information

Please refer to “XCeloSeq Targeted RNA Enrichment Protocol with UDIs” for instructions for use.

## Limitations of Use

### For Research Use Only (RUO)

This product is not intended to be used for therapeutic or diagnostic purposes in humans or animals. SDS sheets relevant to this product are available upon request.