

FUSION*Plex*™-HT Heme v2 panel

FUSIONPlex-HT Heme v2

Description

The FUSION *Plex*-HT Heme v2 panel is a balanced pool of gene-specific primer (GSP) oligonucleotides that is optimized for use with FUSION *Plex*-HT reagents and molecular barcode (MBC) adapters to produce targeted NGS libraries. This product insert should be used in conjunction with FUSION *Plex*-HT protocol for Illumina® (RA-DOC-049).

FUSION*Plex*-HT Heme v2 contains **607** GSPs targeting **87** genes commonly mutated in hematological malignancies.

| Description | Part number | Storage | |
|--|------------------------------|--------------|--|
| FUSION <i>Plex</i> -HT Heme v2 GSP1, 24 reactions or FUSION <i>Plex</i> -HT Heme v2 GSP1, 96 reactions | SA0073241 or SA0073961 | | |
| FUSION <i>Plex</i> -HT Heme v2 GSP2, 24 reactions or FUSION <i>Plex</i> -HT Heme v2 GSP2, 96 reactions | SA0073242 or SA0073962 | −20°C ± 10°C | |
| 10X VCP Primer Mix, 24 reactions or 10X VCP Primer Mix, 96 reactions | SA0840 or SA0841 | | |

Recommended PCR cycling

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

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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

FUSION*Plex*-HT Heme v2 libraries should be sequenced to a minimum of **1.5M** 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, or greater). The FUSION Plex-HT Heme v2 panel requires selection of the **Fusion** pipeline and (optional) **SNV/Indel** pipeline, found under the **RNA** Input Type. See the Archer Analysis User Guide for more details on setting up your analysis.

Processing of FUSION *Plex*-HT Heme v2 libraries requires a one-time upload of the Custom Panel GTF. Files can be obtained by contacting <u>archer-tech@idtdna.com</u>.

Assay targets

| Gene | Accession | Exon | Variant Type | Description* |
|------|-----------|---------------------|-------------------------|---|
| ABL1 | NM_005157 | N/A | Mutation | Y253-E255, V299, T315- F317, M351-F359 |
| ABL1 | NM_005157 | 1, 2, 3, 4, 5 | Fusion | 5' |
| ABL1 | NM_005157 | N/A | Expression Imbalance | N/A |
| ABL2 | NM_005158 | 2, 3, 4, 5, 6, 7, 8 | Fusion | 5' |
| ALK | NM_004304 | N/A | Mutation | T1151-C1156, F1174, L1196-S1206, G1269 |

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| Gene | Accession | Exon | Variant Type | Description* |
|--------|-----------|--|--------------|--------------|
| ALK | NM_004304 | 2, 4, 6, 10,1 6, 17, 18, 19, 20, 21, 22, 23 | Fusion | 5' |
| BCL11B | NM_138576 | 3, 4 | Fusion | 5' |
| BCL11B | NM_138576 | 2, 3 | Fusion | 3' |
| BCL2 | NM_000633 | N/A | Mutation | F104 |
| BCL2 | NM_000633 | N/A | Expression | N/A |
| BCL2 | NM_000633 | 3 | Fusion | 3' |
| BCL2 | NM_000633 | 2 | Fusion | 5' |
| BCL3 | NM_005178 | N/A | Expression | N/A |
| BCL6 | NM_001706 | 2,3 | Fusion | 5' |
| BCL6 | NM_001706 | N/A | Expression | N/A |
| BCR | NM_004327 | 1, 2, 3, 8, 12, 13, 14, 15, 16 | Fusion | 3' |
| BIRC3 | NM_001165 | N/A | Mutation | Q547 |
| BIRC3 | NM_001165 | 4, 5, 6, 7 | Fusion | 3' |
| CBFB | NM_022845 | 4, 5 | Fusion | 3' |
| CCND1 | NM_053056 | N/A | Expression | N/A |
| CCND1 | NM_053056 | 5 | Fusion | 3' |
| CCND1 | NM_053056 | N/A | Mutation | E36, V42-C47 |
| CCND2 | NM_001759 | N/A | Expression | N/A |
| CCND3 | NM_001760 | 2 | Fusion | 5' |

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| Gene | Accession | Exon | Variant Type | Description* |
|--------|-----------|-----------------------|--------------|-------------------------------------|
| CCND3 | NM_001760 | N/A | Expression | N/A |
| CD274 | NM_014143 | N/A | Expression | N/A |
| CDK6 | NM_001259 | 1, 2, 3, 4 | Fusion | 3' |
| CDKN2A | NM_000077 | N/A | Expression | N/A |
| CEBPA | NM_004364 | N/A | Mutation | P23-H24, Q83, K304- L317 |
| CEBPA | NM_004364 | N/A | Expression | N/A |
| CEBPD | NM_005195 | N/A | Expression | N/A |
| CEBPE | NM_001805 | N/A | Expression | N/A |
| CEBPG | NM_001806 | N/A | Expression | N/A |
| CHD1 | NM_001270 | 1, 2 | Fusion | 5' |
| CHIC2 | NM_012110 | 1, 2, 3 | Fusion | 3' |
| CIITA | NM_000246 | 1, 2 | Fusion | 3' |
| CREBBP | NM_004380 | N/A | Mutation | P1053, C1240, R1446, S1680-L1681 |
| CREBBP | NM_004380 | 2, 3, 4, 5, 6 | Fusion | 5' |
| CRLF2 | NM_022148 | N/A | Mutation | F232 |
| CRLF2 | NM_022148 | 1 | Fusion | 5' |
| CRLF2 | NM_022148 | N/A | Expression | N/A |
| CSF1R | NM_005211 | 9, 10, 11, 12, 13, 14 | Fusion | 5' |
| CTLA4 | NM_005214 | N/A | Expression | N/A |
| | | | | |

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| Gene | Accession | Exon | Variant Type | Description* |
|--------|-----------|---------------------------------------|---------------|--------------|
| DEK | NM_003472 | 2, 3 | Fusion | 3' |
| DUSP22 | NM_020185 | 1, 2 | Fusion | 3' |
| EBF1 | NM_024007 | 10, 11, 12, 13, 14, 15 | Fusion | 3' |
| EIF4A1 | NM_001416 | 2, 3 | Fusion | 5' |
| EPOR | NM_000121 | 7, 8 | Fusion | 3' |
| ERG | NM_004449 | 7, 8, 9, 10, 11 | Fusion | 5' |
| ETV6 | NM_001987 | N/A | Mutation | Y104-R105 |
| ETV6 | NM_001987 | 1, 2, 3, 4, 5, 6 | Fusion | 3' |
| ETV6 | NM_001987 | 2, 3, 4, 5, 6 | Fusion | 5' |
| FGFR1 | NM_023110 | 12, 17 | Fusion | 3' |
| FGFR1 | NM_023110 | 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 17 | Fusion | 5' |
| FOXP1 | NM_032682 | N/A | Expression | N/A |
| GLIS2 | NM_032575 | 2, 3 | Fusion | 5' |
| ID4 | NM_001546 | N/A | Expression | N/A |
| IKZF1 | NM_006060 | 1, 2, 3 | Exon Skipping | 3' |
| IKZF1 | NM_006060 | 7, 8 | Exon Skipping | 5' |
| IKZF2 | NM_016260 | 3, 4 | Fusion | 3' |
| IKZF3 | NM_012481 | 2, 3, 4, 5, 6, 7 | Fusion | 3' |
| IKZF3 | NM_012481 | N/A | Mutation | L162 |
| | | | | |

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|--------|--------------|--|--------------|--|
| IRF4 | NM_002460 | N/A | Expression | N/A |
| IRF8 | NM_002163 | N/A | Expression | N/A |
| JAK2 | NM_004972 | N/A | Mutation | F537-F547, V617-C618, L681-R683, L855, V863, A880, V911, M929- R938, I960, R980-E985, D994 |
| JAK2 | NM_004972 | 6, 7, 8, 9, 10, 11, 12, 13, 15, 16, 17, 18, 19, 20 | Fusion | 5' |
| JAK2 | NM_004972 | 9, 10, 11, 12 | Fusion | 3' |
| KAT6A | NM_006766 | 13, 14, 15, 16 | Fusion | 3' |
| KLF2 | NM_016270 | 2, 3 | Fusion | 5' |
| KMT2A | NM_005933 | 2, 3 | Fusion | 5' |
| KMT2A | NM_005933 | 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 | Fusion | 3' |
| MALT1 | NM_006785 | 9 | Fusion | 3' |
| MECOM | NM_004991 | N/A | Expression | N/A |
| MECOM | NM_004991 | 1, 2, 3, 4 | Fusion | 5' |
| MKL1 | NM_020831 | 4, 5, 6 | Fusion | 5' |
| MLF1 | NM_022443 | 2, 3, 4 | Fusion | 5' |
| MLLT10 | NM_004641 | 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18 | Fusion | 5' |
| MLLT10 | NM_004641 | 7, 8, 9, 10 | Fusion | 3' |
| MLLT4 | NM_001040000 | 2 | Fusion | 5' |

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|--------|--------------|---|-------------------------|--|
| MUC1 | NM_002456 | N/A | Expression | N/A |
| MYC | NM_002467 | N/A | Expression | N/A |
| MYC | NM_002467 | 1, 2 | Fusion | 5' |
| MYH11 | NM_002474 | N/A | Expression Imbalance | N/A |
| MYH11 | NM_002474 | 7, 8, 9, 10, 11, 14, 15, 16 | Fusion | 5' |
| NF1 | NM_000267 | 14 | Fusion | 3' |
| NF1 | NM_000267 | 36 | Fusion | 5' |
| NFKB2 | NM_002502 | 14, 15, 16, 17, 18, 19, 20, 21 | Fusion | 3' |
| NOTCH1 | NM_017617 | N/A | Mutation | L1574, V1578, L1585, F1592-L1593, R1598- L1600, L1678-I1680, P2514-E2515, P2525 |
| NOTCH1 | NM_017617 | 24, 25, 26, 27, 28, 29 | Fusion | 5' |
| NOTCH1 | NM_017617 | 24 | Fusion | 3' |
| NOTCH1 | NM_017617 | 34 | Exon Skipping | N/A |
| NTRK3 | NM_002530 | N/A | Expression Imbalance | N/A |
| NTRK3 | NM_002530 | 13, 14, 15 | Fusion | 5' |
| NTRK3 | NM_001007156 | 15 | Fusion | 5' |
| NUP214 | NM_005085 | 17, 18, 19 | Fusion | 5' |
| NUP98 | NM_016320 | 8, 9, 10, 11, 12, 13, 14, 15, 16, 17 | Fusion | 3' |
| NUP98 | NM_016320 | 12, 13 | Fusion | 5' |
| P2RY8 | NM_178129 | 1 | Fusion | 3' |
| | | | | |

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|----------|-----------|-----------------------------|-------------------------|---|
| PAG1 | NM_018440 | 2 | Fusion | 5' |
| PAX5 | NM_016734 | N/A | Mutation | P80 |
| PAX5 | NM_016734 | 1, 4, 5, 6, 7, 8 | Fusion | 3' |
| PAX5 | NM_016734 | 6, 7, 8 | Fusion | 5' |
| PDCD1 | NM_005018 | N/A | Expression | N/A |
| PDCD1LG2 | NM_025239 | N/A | Expression | N/A |
| PDCD1LG2 | NM_025239 | 1, 2, 3 | Fusion | 5' |
| PDCD1LG2 | NM_025239 | 5, 6 | Fusion | 3' |
| PDGFRA | NM_006206 | N/A | Mutation | T674 |
| PDGFRA | NM_006206 | 9, 10, 11, 12, 13, 14 | Fusion | 5' |
| PDGFRB | NM_002609 | 8, 9, 10, 11, 12, 13, 14 | Fusion | 5' |
| PICALM | NM_007166 | 16, 17, 18, 19 | Fusion | 3' |
| PML | NM_002675 | N/A | Mutation | C212-S220 |
| PML | NM_002675 | 2 | Fusion | 5' |
| PML | NM_002675 | 2, 3, 4, 5, 6, 7 | Fusion | 3' |
| PRDM16 | NM_022114 | 1, 2, 3, 4 | Fusion | 5' |
| PTK2B | NM_173176 | 2, 3, 4, 5, 6, 7, 8 | Fusion | 5' |
| RARA | NM_000964 | N/A | Mutation | E197, R272, T283- M284, L290-M297, R394, Q411 |
| RARA | NM_000964 | N/A | Expression Imbalance | N/A |

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| Description* 5' |
|------------------|
| |
| 3' |
| |
| N/A |
| 5' |
| 5' |
| 3' |
| N/A |
| N/A |
| 5' |
| 3' |
| 3' |
| 3' |
| N/A |
| 5' |
| 5' |
| 3' |
| 3' |
| 5' |
| 5' |
| |

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| Gene | Accession | Exon | Variant Type | Description* |
|--------|-----------|---------|--------------|--------------|
| TYK2 | NM_003331 | N/A | Mutation | W327 |
| ZCCHC7 | NM_032226 | 1, 2 | Fusion | 3' |
| ZCCHC7 | NM_032226 | 2, 3, 4 | Fusion | 5' |

^{*}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.

Note: Fusions involving BCR and TCR loci, including IGH, IGL and IGK, are targeted for expression and may not be explicitly called as a fusion because these often do not result in chimeric transcripts. For the "Expression" assay type, unique molecules originating from probes across these genes can be counted and normalized to target control genes to enable relative expression level detection. Results are visualized in Archer Analysis.

SNPs and sites targeted for sample tracking

| | | - | | |
|------------|-----------|------------|------------|---------------|
| rs560681 | rs430046 | rs987640 | rs10776839 | rs12393891 |
| rs740598 | rs8078417 | rs6444724 | rs6530357 | chrX 4429309 |
| rs1498553 | rs9951171 | rs6811238 | rs5971553 | chrX 11314433 |
| rs10773760 | rs576261 | rs13182883 | rs5953060 | chrY 6738552 |
| rs1058083 | rs1109037 | rs214955 | rs6524626 | chrY 19490214 |
| rs4530059 | rs1523537 | rs321198 | rs5940270 | |
| rs1821380 | rs221956 | rs4606077 | rs722847 | |

SNPs may be used in combination to uniquely tag and track samples over time. Contact archer-tech@idtdna.com for further details.

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Product Insert FUSION*Plex*™-HT Heme v2 panel

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-449/REV01 | October 2023 | Initial release. |
| RA-DOC-449/REV02 | November 2023 | Updated First and Second PCR cycling conditions to include separate anneal and extended steps. |
| | | Updated branding. |

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