# FUSION*Plex* Heme v3

## Description

The FUSION*Plex* Heme v3 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 FUSIONPlex protocol for Illumina® (RA-DOC-047), FUSIONPlex-LAC protocol for Illumina® (RA-DOC-471), or FUSIONPlex protocol for Ion Torrent™ (RA-DOC-048).

FUSION*Plex* Heme v3 contains **1205** GSPs targeting **121** genes commonly mutated in hematological malignancies.

| Description | Part number | Storage |
|---|---|---|
| FUSION*Plex* Heme v3 GSP1, 8 reactions | 10034041 | –20°C ± 10°C |
| FUSION*Plex* Heme v3 GSP2, 8 reactions | 10034045 | |
| 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 | 15 |
| | **3** | 60 | 10 sec | |
| | **4** | 62 | 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 | 20† |
| | **3** | 60 | 10 sec | |
| | **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* Heme v3 libraries should be sequenced to a minimum of **3.5M 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 (v7.5, or greater). The FUSION*Plex* Heme v3 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 FUSION*Plex* Heme v3 panel 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 | Assay Type | Description** |
|---|---|---|---|---|
| *ABL1* | NM_005157 | – | Expression Imbalance | – |
| *ABL1* | NM_005157 | 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11 | Fusion | 5' |
| *ABL1* | NM_005157 | 4, 5, 6 | Mutation | Full exon coverage including, p.Y253–p.E255, p.V299, p.T315–p.F317, p.M351–p.F359 |

| Gene | Accession | Exon | Assay Type | Description** |
|---|---|---|---|---|
| *ABL2* | NM_005158 | 2, 3, 4, 5, 6, 7, 8 | Fusion | 5' |
| *ALK* | NM_004304 | 2, 4, 6, 8, 10, 12, 13, 14, 16, 17, 18, 19, intron19, 20, mid–exon20, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29 | Fusion, ALK ATI$^{V}$, Internal deletion (ALKΔ2–17, ALKΔ2–3), Expression | 5' |
| *ALK* | NM_004304 | 1, 2 | Internal deletion (ALKΔ2–17, ALKΔ2–3) | 3' |
| *ALK* | NM_004304 | 21, 22, 23, 24, 25 | Mutation | Full exon coverage including p.P1153–p.C1156, p.F1174, p.L1196–p.S1206, p.G1269 |
| *ALK* | NM_004304 | 9, 12, 16, 20 | Mutation | Hotspot coverage including p.V597, p.H694, p.G881, p.K1062 |
| *BCL11B* | NM_138576 | 1, 2, 3, 4 | Fusion, Expression | 5' |
| *BCL11B* | NM_138576 | 2, 3 | Fusion, Expression | 3' |
| *BCL2* | NM_000633 | *1, 2, 3 | Fusion, Expression | 3' |
| *BCL2* | NM_000633 | 1*, 2, 3*, mid exon 3 | Fusion, Expression | 5' |
| *BCL2* | NM_000633 | 2 | Mutation | p.F104 |
| *BCL3* | NM_005178 | – | Expression | – |
| *BCL6* | NM_001706 | 2, 3, 4, 5, 8, 9 | Fusion, Expression | 5' |
| *BCR* | NM_004327 | 1, 2, 3, 4, 8, 12, 13, 14, 15, 16 | Fusion | 3' |
| *BIRC3* | NM_182962 | 4, 5, 6, 7, 8 | Fusion, Expression | 3' |
| *BIRC3* | NM_182962 | 9 | Mutation | p.Q547 |
| *BRAF* | 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, Expression | 3' |
| *BRAF* | 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, Expression | 5' |
| *BRAF* | NM_004333 | 11, 15 | Mutation | Full exon coverage including p.V600 |

| Gene | Accession | Exon | Assay Type | Description** |
|---|---|---|---|---|
| *BTK* | NM_000061 | 11, 15, 16 | Mutation | p.C481, p.T474, p.L528, p.T316, p.V537 |
| *CARD11* | NM_032415 | 5, 6 | Mutation | p.D230 p.K215T |
| *CBFB* | NM_022845 | 4, 5 | Fusion | 3' |
| *CCND1* | NM_053056 | 2, 3, 4, 5 | Fusion, Expression | 5' |
| *CCND1* | NM_053056 | 1, 2, 3, 4, mid–exon5* | Fusion, Expression | 3' |
| *CCND1* | NM_053056 | 1 | Mutation | p.E36, p.V42–p.C47 |
| *CCND2* | NM_001759 | – | Expression | – |
| *CCND3* | NM_001760 | 2, 3, 4, 5 | Fusion, Expression | 5' |
| *CCND3* | NM_001760 | 2, 4 | Fusion, Expression | 3' |
| *CD274* | NM_014143 | – | Expression | – |
| *CD28* | NM_006139 | 2, 4 | Fusion | 5' |
| *CDK6* | NM_001259 | 1, 2, 3, 4 | Fusion, Expression | 3' |
| *CDKN2A* | NM_000077 | – | Expression | – |
| *CEBPA* | NM_004364 | 1 | Mutation | Full exon coverage |
| *CEBPD* | NM_005195 | – | Expression | – |
| *CEBPE* | NM_001805 | – | Expression | – |
| *CEBPG* | NM_001806 | – | Expression | – |
| *CHD1* | NM_001270 | 2*, 3 | Fusion | 5' |
| *CHIC2* | NM_012110 | 1, 2, 3 | Fusion | 3' |
| *CIITA* | NM_000246 | 1, 2 | Fusion | 3' |
| *CREBBP* | NM_004380 | – | Expression | – |
| *CREBBP* | NM_004380 | 16, 20, 26, 30 | Mutation | p.P1053, p.C1240, p.R1446, p.S1680–p.L1681 |
| *CRLF2* | NM_022148 | – | Expression | – |

| Gene | Accession | Exon | Assay Type | Description** |
|---|---|---|---|---|
| *CRLF2* | NM_022148 | 1* | Fusion | 5' |
| *CRLF2* | NM_022148 | 6 | Mutation | p.F232 |
| *CSF1R* | NM_005211 | 9, 10, 11, 12, 13, 14 | Fusion | 5' |
| *CTLA4* | NM_005214 | – | Expression | – |
| *DDX41* | NM_016222 | 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17 | Fusion, Expression | 3' |
| *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 | 6, 7, 8 | Fusion | 3' |
| *ERG* | NM_004449 | 2*, 3*, 4, 5, 6, 7, 8, 9, 10, 11 | Fusion | 5' |
| *ETV6* | NM_001987 | 2, 3, 4, 5, 6, 7 | Fusion | 5' |
| *ETV6* | NM_001987 | 1, 2, 3, 4, 5, 6 | Fusion | 3' |
| *ETV6* | NM_001987 | 3 | Mutation | p.Y104–p.R105 |
| *FGFR1* | NM_023110 | 2*, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18 | Fusion | 5' |
| *FGFR1* | NM_023110 | 12, 17 | Fusion | 3' |
| *FGFR1* | NM_023110 | 4, 12, 13, 14 | Mutation | Hotspot coverage including p.T141, p.V561, p.N546, p.K656 |
| *FGFR2* | NM_000141 | 2*, 3, 5, 6, 7, 8, 9, 10 | Fusion | 5' |
| *FGFR2* | NM_000141 | 11, 16, 17, 18 | Fusion | 3' |
| *FGFR2* | NM_000141 | 2, 7, 9, 12, 13, 14 | Mutation | p.R6, p.S252–p.P253, p.G305, p.Y375–V395, p.I547–p.N549, p.V564, p.A648–p.K659 |
| *FGFR3* | NM_000142 | 3, 5, 8, 10, 11, 12, 13, 14 | Fusion | 5' |
| *FGFR3* | NM_000142 | 16, 17, intron17, mid–exon18 | Fusion | 3' |

| Gene | Accession | Exon | Assay Type | Description** |
|---|---|---|---|---|
| *FGFR3* | NM_000142 | 7, 9, 13, 14, 16 | Mutation | Hotspot coverage including p.R248, p.S249, p.G370, p.S371, p.Y373, p.G380, p.R399, p.V555, p.D641, p.K650, p.G697, p.K715 |
| *FLT3* | NM_004119 | 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24 | Fusion, Internal Tandem Duplication, Expression | 5' |
| *FLT3* | NM_004119 | 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 19, 20, 21 | Mutation | Full exon coverage including p.F590–p.N609, p.D835–p.S838 |
| *FOXP1* | NM_032682 | – | Expression | – |
| *GLIS2* | NM_032575 | 2, 3 | Fusion | 5' |
| *ID4* | NM_001546 | – | Expression | – |
| *IDH1* | NM_005896 | 3, 4 | Mutation | Full exon coverage including p.R132 |
| *IDH2* | NM_002168 | 4, 6 | Mutation | Full exon coverage including p.R140 and p.R172 |
| *IKZF1* | NM_006060 | 1*, 2*, 3, 4, 5, 6, 7, 8 | Fusion, Exon Skipping | 5' |
| *IKZF1* | NM_006060 | 1*, 2, 3, 5 | Fusion, Exon Skipping | 3' |
| *IKZF2* | NM_016260 | 3, 4, 6 | Fusion | 3' |
| *IKZF3* | NM_012481 | 2, 3, 4, 5, 6, 7 | Fusion | 3' |
| *IKZF3* | NM_012481 | 5 | Mutation | p.L162 |
| *IL2RB* | NM_000878 | 2 | Fusion | 5' |
| *IRF4* | NM_002460 | – | Expression | – |
| *IRF8* | NM_002163 | – | Expression | – |
| *JAK1* | NM_002227 | 5, 14, 15, 16, 17 | Mutation | Full exon coverage including, p.V658, p.S703, p.R724, p.A634D, p.V658, p.R724 |
| *JAK1* | NM_002227 | 13 | Mutation | p.R629_D630del |
| *JAK2* | NM_004972 | 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22 | Fusion | 5' |
| *JAK2* | NM_004972 | 9, 10, 11, 12, 18, 19, 20, 22 | Fusion | 3' |

| Gene | Accession | Exon | Assay Type | Description** |
|---|---|---|---|---|
| *JAK2* | NM_004972 | 12, 13, 14, 15, 16, 19, 20, 21, 22 | Mutation | Full exon coverage including p.F537–F547, p.V617–C618, p.L681–R683, p.L855, p.V863, p.A880, p.V911, p.M929–R938, p.I960, p.R980–E985, p.D994 |
| *JAK3* | NM_000215 | 22, 23 | Fusion | 3' |
| *JAK3* | NM_000215 | 10, 11, 12, 17, 18, 19 | Fusion | 5' |
| *JAK3* | NM_000215 | 4, 13, 15, 16, 18 | Mutation | Full exon coverage including p.A572–A573, p.R657, p.S789 |
| *JAK3* | NM_000215 | 11 | Mutation | p.M511 |
| *KAT6A* | NM_006766 | 13, 14, 15, 16, 17* | Fusion | 3' |
| *KIT* | NM_000222 | 2, 8, 9, 10, 11, 12, 13, 14, 15, 17, 18 | Mutation | Full exon coverage including p.T417–p.D419, p.T670, p.R796, p.D816, p.N822–p.V825 |
| *KLF2* | NM_016270 | 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' |
| *KMT2A* | NM_005933 | 2, 3 | Fusion | 5' |
| *LYN* | NM_001111097 | 2*, 3, 4, 5, 6, 7, 8 | Fusion | 5' |
| *MALT1* | NM_006785 | 9 | Fusion | 3' |
| *MECOM* | NM_004991 | 1*, 2, 3, 4, 5, 8 | Fusion, Expression | 5' |
| *MEF2C* | NM_002397 | 5 | Fusion | 3' |
| *MEF2D* | NM_005920 | 3, 4, 5, 6, 7, 9 | Fusion | 3' |
| *MEN1* | NM_130799 | 2, 3, 4, 5, 6, 7, 8, 9, 10 | Mutation | Full exon coverage |
| *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' |

| Gene | Accession | Exon | Assay Type | Description** |
|---|---|---|---|---|
| *MLLT10* | NM_004641 | 7, 8, 9, 10 | Fusion | 3' |
| *MLLT4* | NM_001040000 | 2 | Fusion | 5' |
| *MUC1* | NM_002456 | – | Expression | – |
| *MYC* | NM_002467 | 1, 2 | Fusion, Expression | 3' |
| *MYC* | NM_002467 | 1, 2, 3 | Fusion, Expression | 5' |
| *MYH11* | NM_002474 | – | Expression Imbalance | – |
| *MYH11* | NM_002474 | 5, 6, 7, 8, 9, 10, 11, 14, 15, 16, 18, 19, 20, 33 | 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 | 34 | Exon Skipping | – |
| *NOTCH1* | NM_017617 | 2, 4, 24, 29, 30, 31 | Fusion | 3' |
| *NOTCH1* | NM_017617 | 5, 24, 25, 26, 27, 28, 29 | Fusion | 5' |
| *NOTCH1* | NM_017617 | 26, 27, 34 | Mutation | p.L1574, p.V1578, p.L1585, p.F1592–p.L1593, p.R1598–p.L1600, p.L1678–p.I1680, p.P2514–p.E2515, p.P2525 |
| *NPM1* | NM_002520 | 11 | Mutation | p.W22–W290 |
| *NTRK1* | NM_001007792 | 1, 2 | Fusion | 5' |
| *NTRK1* | NM_002529 | 15, 16, 17 | Fusion | 3' |
| *NTRK1* | NM_002529 | 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14 | Fusion | 5' |
| *NTRK1* | NM_002529 | 13, 14, 15, 16, 17 | Mutation | Full kinase domain coverage for resistance mutations including p.G595 |
| *NTRK2* | NM_006180 | 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18 | Fusion | 5' |
| *NTRK2* | NM_006180 | 11, 14 | Fusion | 3' |

| Gene | Accession | Exon | Assay Type | Description** |
|---|---|---|---|---|
| *NTRK2* | NM_006180 | 16, 17, 18, 19, 20, 21 | Mutation | Full kinase domain coverage for resistance mutations |
| *NTRK3* | NM_001007156 | 15 | Fusion | 5' |
| *NTRK3* | NM_002530 | 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16 | Fusion | 5' |
| *NTRK3* | NM_002530 | 13, 14, 15, 17 | Fusion | 3' |
| *NTRK3* | NM_002530 | 15, 16, 17, 18, 19 | Mutation | Full kinase domain coverage for resistance mutations detection including p.F617, p.G623, p.G696 |
| *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' |
| *NUTM1* | NM_175741 | 2*, 3, mid–exon3, 4, 5, mid–exon6, 6 | Fusion | 5' |
| *P2RY8* | NM_178129 | 1 | Fusion | 3' |
| *PAG1* | NM_018440 | 2 | Fusion | 5' |
| *PAX5* | NM_016734 | 6, 7, 8 | Fusion | 5' |
| *PAX5* | NM_016734 | 1, 4, 5, 6, 7, 8 | Fusion | 3' |
| *PAX5* | NM_016734 | 3 | Mutation | p.P80 |
| *PDCD1* | NM_005018 | – | Expression | – |
| *PDCD1LG2* | NM_025239 | 3, 5, 6 | Fusion | 3' |
| *PDCD1LG2* | NM_025239 | 1*, 2, 3 | Fusion | 5' |
| *PDGFRA* | NM_006206 | 9, 10, 11, 12, mid–exon12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23 | Fusion,PDGFRAΔî8,9 | 5' |
| *PDGFRA* | NM_006206 | 7 | Fusion,PDGFRAΔî8,9 | 3' |
| *PDGFRA* | NM_006206 | 12, 14, 18 | Mutation | Full exon coverage including p.D842 |
| *PDGFRA* | NM_006206 | 6, 15 | Mutation | Hotspot coverage including p.Y288, p.T674 |

| Gene | Accession | Exon | Assay Type | Description** |
|---|---|---|---|---|
| *PDGFRB* | NM_002609 | 8, 9, 10, 11, 12, mid–exon 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23 | Fusion | 5' |
| *PICALM* | NM_007166 | 16, 17, 18, 19 | Fusion | 3' |
| *PLCG2* | NM_002661 | 19, 20, 24 | Mutation | p.R665, p.L845, p.S707 |
| *PML* | NM_002675 | 2, 3, 4, 5, 6, 7* | Fusion | 3' |
| *PML* | NM_002675 | 2 | Fusion | 5' |
| *PML* | NM_002675 | 3 | Mutation | p.C212–p.S220 |
| *PRDM16* | NM_022114 | 1*, 2, 3, 4 | Fusion | 5' |
| *PTK2B* | NM_173176 | 2*, 3, 4, 5, 6, 7, 8 | Fusion | 5' |
| *RARA* | NM_000964 | – | Expression Imbalance | – |
| *RARA* | NM_000964 | 1*, 2*, 3, 4, 5, 6, 8, 9 | Fusion | 5' |
| *RARA* | NM_000964 | 5, 7, 9 | Mutation | p.E197, p.R272, p.T283–p.M284, p.L290–p.M297, p.R394, p.Q411 |
| *RBM15* | NM_022768 | 1 | Fusion | 3' |
| *RET* | NM_020630 | 2, 4, 6, 8, 9, 10, 11, mid–exon11, 12, 13, 14 | Fusion | 5' |
| *RET* | NM_020630 | 8, 10, 11, 13, 14, 15, 16 | Mutation | Hotspot coverage including p.A883, p.M918 |
| *ROS1* | NM_002944 | – | Expression Imbalance | – |
| *ROS1* | NM_002944 | 2, 4, 7, 31, 32, 33, 34, 35, 36, 37 | Fusion | 5' |
| *ROS1* | NM_002944 | 38, 39, 40 | Mutation | Hotspot coverage including p.G2032, p.C2060, p.V2098, p.G2101 |
| *RUNX1* | NM_001122607 | 1, 5 | Mutation | Full exon coverage |
| *RUNX1* | NM_001754 | – | Expression Imbalance | – |
| *RUNX1* | NM_001754 | 2, 3, 4, 5, 6, 7, 8 | Fusion | 3' |
| *RUNX1* | NM_001754 | 2, 3, 4, 5, 6, 7, 8, 9 | Fusion | 5' |

| Gene | Accession | Exon | Assay Type | Description** |
|---|---|---|---|---|
| *RUNX1* | NM_001754 | 2, 3, 4, 5, 6, 7, 8, 9 | Mutation | Full exon coverage |
| *RUNX1T1* | NM_001198679 | – | Expression Imbalance | – |
| *RUNX1T1* | NM_001198679 | 2, 3 | Fusion | 5' |
| *SEMA6A* | NM_020796 | 1*, 2 | Fusion | 3' |
| *SETBP1* | NM_015559 | 2*, 3 | Fusion | 5' |
| *SETBP1* | NM_015559 | 4 | Mutation | p.D868–p.I871 |
| *SETD2* | NM_014159 | 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12 | Fusion | 3' |
| *SF3B1* | NM_012433 | 14, 15, 16 | Mutation | p.E622–p.N626, p.H662–p.K666, p.K700, p.I704, pG740, p.G742 |
| *SH2B3* | NM_005475 | 2, 3, 6, 7 | Mutation | p.E208, p.M211fs, p.D231–p.D234, p.M268, p.R392, p.E400, p.L438 |
| *STAT3* | NM_003150 | 21, 23 | Fusion | 3' |
| *STAT3* | NM_003150 | 21 | Mutation | p.Y640–p.N647, p.D661 |
| *STIL* | NM_003035 | 1*, 2 | Fusion | 3' |
| *TAL1* | NM_001290404 | 2, 3 | Fusion | 5' |
| *TAL1* | NM_003189 | – | Expression | – |
| *TAL1* | NM_003189 | 2, 4 | Fusion | 5' |
| *TCF3* | NM_003200 | 11, 12, 13, 14, 15, 16, 17, 18 | Fusion | 3' |
| *TFG* | NM_006070 | 2, 3, 4, 5, 6, 7, 8 | Fusion | 3' |
| *TFG* | NM_006070 | 6 | Fusion | 5' |
| *TP53* | NM_000546 | 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11 | Mutation | Full exon coverage |
| *TP53* | NM_001276695 | 10 | Mutation | Full exon coverage |
| *TP53* | NM_001276696 | 10 | Mutation | Full exon coverage |
| *TP63* | NM_003722 | 3, 4, 5 | Fusion | 5' |
| *TSLP* | NM_033035 | 1, 3 | Fusion | 3' |

| Gene | Accession | Exon | Assay Type | Description** |
|---|---|---|---|---|
| *TSLP* | NM_033035 | 1, 2, 4 | Fusion | 5' |
| *TYK2* | NM_003331 | 16, 18, 19 | Fusion | 5' |
| *TYK2* | NM_003331 | 7 | Mutation | p.W327 |
| *UBA1* | NM_003334 | 3 | Mutation | p.M41 |
| *UBTF* | NM_014233 | 14, 15, 16, 17, 18, 19, 20 | Fusion, Internal Tandem Duplication, Expression | 3' |
| *UBTF* | NM_014233 | 14 | Fusion, Internal Tandem Duplication, Expression | 5' |
| *UBTF* | NM_014233 | 9, 13 | Mutation | Full exon coverage |
| *XPO1* | NM_003400 | 15 | Mutation | p.E571 |
| *ZCCHC7* | NM_032226 | 2*, 3, 4 | Fusion | 5' |
| *ZCCHC7* | NM_032226 | 1*, 2, 3 | Fusion | 3' |
| *ZNF384* | NM_001039920 | 5 | Fusion | 5' |
| *ZNF384* | NM_001135734 | 8 | Fusion | 5' |
| *ZNF384* | NM_133476 | 2*, 3, 4, 5, 6, 7, 8 | Fusion | 5' |

*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. *De Novo* RNA SNV/Indel and Internal Tandem Duplication mutation detection are not supported on the Ion Torrent Sequencing System.

ᵞALK-ATI currently requires review outside of Archer Analysis.

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.

## 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.



## Revision History

| Document Number | Date | Description of change |
|---|---|---|
| *RA-DOC-650/REV01* | March 2026 | Initial release |