FUSION*Plex*-HT Heme v3

Description

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

Description	Part number	Storage
FUSION*Plex*-HT Heme v3 GSP1, 24 reactions or FUSION*Plex*-HT Heme v3 GSP1, 96 reactions	10034117 or 10034093	–20°C ± 10°C
FUSION*Plex*-HT Heme v3 GSP2, 24 reactions or FUSION*Plex*-HT Heme v3 GSP2, 96 reactions	10034118 or 10034094	
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 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*-HT 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*-HT Heme v3 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 v3 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
ABL2	NM_005158	2, 3, 4, 5, 6, 7, 8	Fusion	5'

Gene	Accession	Exon	Assay Type	Description**
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
BTK	NM_000061	11, 15, 16	Mutation	p.C481, p.T474, p.L528, p.T316, p.V537

Gene	Accession	Exon	Assay Type	Description**
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	–
CRLF2	NM_022148	1*	Fusion	5'

Gene	Accession	Exon	Assay Type	Description**
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-651/REV01	March 2026	Initial release