FusionPlex-HT Pan Solid Tumor v2

Description

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

FusionPlex-HT Pan Solid Tumor v2 contains **1086** GSPs targeting **137** genes commonly mutated in solid tumors.

Description	Part number	Storage
FusionPlex-HT Pan Solid Tumor v2 GSP1, 24 reactions or FusionPlex-HT Pan Solid Tumor v2 GSP1, 96 reactions	SA18091241 or SA18091961	–20°C ± 10°C
FusionPlex-HT Pan Solid Tumor v2 GSP2, 24 reactions or FusionPlex-HT Pan Solid Tumor v2 GSP2, 96 reactions	SA18091242 or SA18091962	
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	62	5 min (100% ramp rate)	
	4	72	3 min	1
	5	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	65	5 min (100% ramp rate)	
	4	72	3 min	1
	5	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

FusionPlex-HT Pan Solid Tumor v2 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, or greater). The FusionPlex-HT Pan Solid Tumor 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 FusionPlex-HT Pan Solid Tumor v2 libraries requires a one-time upload of the Custom Panel GTF. Files can be obtained by contacting archer-tech@idtdna.com.

Assay targets

Gene	Accession	Exon	Variant Type	Description**
ACVR2A	NM_001616	1, 2, 3	Fusion	5'
AKT1	NM_005163	2, 3, 4, 5, mid-exon5	Fusion	5'
AKT2	NM_001626	2*, 5	Fusion	5'
AKT2	NM_001626	11	Fusion	3'
AKT3	NM_005465	2, 3, 4, 9	Fusion	5'

Gene	Accession	Exon	Variant Type	Description**
AKT3	NM_005465	6, 7, 8	Fusion	3'
ALK	NM_004304	2, 4, 6, 8, 10, 12, 14, 16, 17, 18, 19, intron19, 20, mid-exon20, 21, 22, 23, 26	Fusion, ALK ATIV, Internal deletion (ALKΔ2-17, ALKΔ2-3)	5'
ALK	NM_004304	1, 2	Internal deletion (ALKΔ2-17, ALKΔ2-3)	3'
ALK	NM_004304	22, 23, 25	Mutation	p.P1153-p.C1156,p.F1174,p.L1196-p.S1206,p.G1269
AR	NM_001011645	1	Fusion	3'
AR	NM_000044	1, 2, 3, 4, 5, 6, 7, 8*	Fusion, ARv7	3'
ARHGAP26	NM_015071	2, 10, 11, 12	Fusion	5'
ARHGAP6	NM_006125	2	Fusion	5'
AXL	NM_021913	11	Fusion	5'
AXL	NM_021913	18, 19, mid-exon20, 20	Fusion	3'
BCOR	NM_017745	8	Fusion	5'
BCOR	NM_001123385	mid-exon2, 3, 4, mid-exon4, 5, 6, 7, 8, 9, 11, 15	Fusion, Internal Tandem Duplication	5'
BCOR	NM_001123385	2, 4, mid-exon4, 6, 7, mid-exon7, 10, 12, 14, 15	Fusion, Internal Tandem Duplication	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	5'
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	3'

Gene	Accession	Exon	Variant Type	Description**
BRAF	NM_004333	15	Mutation	p.V600
BRD3	NM_007371	9, 10, 11, 12	Fusion	3'
BRD4	NM_058243	2*	Fusion	5'
BRD4	NM_058243	10, 11, 12, 13, 14	Fusion	3'
CAMTA1	NM_015215	8, 9, mid-exon9, 10	Fusion	5'
CAMTA1	NM_015215	3	Fusion	3'
CCNB3	NM_033031	2*, 3, 4, 5, 6, mid-exon 6, 7	Fusion	5'
CCND1	NM_053056	1*, 2, 3, 4, 5	Fusion	5'
CCND1	NM_053056	1, 2, 3, 4, mid-exon5*	Fusion	3'
CCND1	NM_053056	5*	Fusion	3'
CCND1	NM_053056	1	Mutation	p.E36-p.C47
CD274	NM_014143	7	Expression	5'
CD274	NM_014143	2, 3, 4, 5	Expression	3'
CIC	NM_015125	12	Fusion	5'
CIC	NM_015125	14, 15, 16, 17, 18, mid-exon19, 19, mid-exon20, 20*	Fusion	3'
CRTC1	NM_015321	1, 2, 3, 4	Fusion	3'
CSF1	NM_000757	2, 3, 4, 5, 6	Fusion	5'
CSF1	NM_000757	5, 6, 7, 8*, mid-exon9*	Fusion	3'
CSF1	NM_172212	9*	Fusion	3'

Gene	Accession	Exon	Variant Type	Description**
CSF1R	NM_005211	11, 12, 13	Fusion	5'
CTNNB1	NM_001904	3	Mutation	p.D32-p.S37
DNAJB1	NM_006145	1, 2	Fusion	3'
EGF	NM_001963	16, 17, 18, 19	Fusion	5'
EGFR	NM_005228	7, 8, 9, 14, 15, 16, 17, 18, 19, 20	Fusion, Exon 2-7 Skipping (EGFRvIII), Kinase Domain Duplication	5'
EGFR	NM_005228	1, 24, 25, mid-exon25, 26	Fusion, Exon 2-7 Skipping (EGFRvIII), Kinase Domain Duplication	3'
EGFR	NM_005228	18, 19, 20, 21	Mutation	p.E709-p.G719,p.E746-p.L760,p.V774-p.G796,p.L858-p.L861
EPC1	NM_025209	9, 10, 11	Fusion	3'
ERBB2	NM_004448	4, 5, 13, 15, 17	Fusion, Exon 16 skipping (Δ16HER)	5'
ERBB2	NM_004448	15, 23, 24, 25, mid-exon26, 26	Fusion, Exon 16 skipping (Δ16HER)	3'
ERBB2	NM_004448	8, 20	Mutation	p.G309-p.S310,p.Y772-p.P780, p.C805
ERBB4	NM_005235	2, 3, 4, 14, 15, 16, 17, 18, 23	Fusion	5'
ERG	NM_004449	2*, 3*, 4, 5, 6, 7, 8, 9, 10, 11	Fusion	5'
ESR1	NM_000125	5, 6, 7, 8	Fusion	5'
ESR1	NM_000125	1, 2, 3, 4, 5, 6, 7	Fusion	3'
ESRRA	NM_004451	2, 3	Fusion	3'
ETV1	NM_004956	3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13	Fusion	5'
ETV4	NM_001986	2, 3, 4, 5, 6, 7, 8, 9, 10	Fusion	5'

Gene	Accession	Exon	Variant Type	Description**
ETV5	NM_004454	2*, 3, 7, 8, 9	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
EWSR1	NM_005243	8	Fusion	5'
EWSR1	NM_005243	4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14	Fusion	3'
FGF1	NM_00800	mid-exon 2, 2	Fusion	5'
FGFR1	NM_015850	2*, 3, 4, 5, 6, 7, 8, 9, 10, 11, 17	Fusion, Kinase Domain Duplication	5'
FGFR1	NM_015850	12, 17	Fusion, Kinase Domain Duplication	3'
FGFR1	NM_023110	4, 13, 14	Mutation	p.T141,p.V561,p.K656
FGFR2	NM_000141	2*, 3, 5, 6, 7, 8, 9, 10	Fusion	5'
FGFR2	NM_000141	16, 17, 18	Fusion	3'
FGFR2	NM_000141	7, 9, 12, 13, 14	Mutation	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, 9, 10, 11, 12, 13, 14	Fusion	5'
FGFR3	NM_000142	16, 17, intron17, mid-exon18	Fusion	3'
FGFR3	NM_000142	7, 9, 13, 14, 16	Mutation	p.R248-p.S249,p.G370-p.R399,p.V555,p.D641-p.K650,p.G697-p.K715
FGR	NM_005248	2*, 3	Fusion	5'
FOS	NM_005252	mid-exon4	Fusion	3'

Gene	Accession	Exon	Variant Type	Description**
FOSB	NM_006732	1*, mid-exon1*, 1, 2	Fusion	5'
FOXO1	NM_002015	1*, 2, 3*	Fusion	5'
FOXO1	NM_002015	1*, 2*, 3*	Fusion	3'
FOXO4	NM_005938	2, mid-exon2, 3	Fusion	5'
FOXR2	-	cryptic upstream exon2,3 (chrX:55562068, chrX:55634636)	Fusion	5'
FUS	NM_004960	3, 4, 5, mid-exon6, 6, 7, 8, 9, 10, 11, 13, 14	Fusion	3'
GLI1	NM_005269	4, 5, 6, 7	Fusion	5'
GLI1	NM_005269	4, 5, mid-exon5, 6, 7	Fusion	3'
GRB7	NM_005310	10, 11, 12	Fusion	5'
HMGA2	NM_003483	1, 2, 3, 4, mid-exon5*, 5*	Fusion	3'
HRAS	NM_005343	2, 3, 4	Mutation	p.G12-p.G13,p.Q61,p.K117,p.A146
IDH1	NM_005896	4	Mutation	p.R132
IDH2	NM_002168	4	Mutation	p.R140, p.R172
IGF1R	NM_000875	13, 14, 15	Fusion	5'
INSR	NM_000208	2, 12, 13, 14, 15, 16, 17, 18, 19	Fusion	5'
INSR	NM_000208	20, 21, 22	Fusion	3'
JAK2	NM_004972	6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20	Fusion	5'
JAK2	NM_004972	9, 10, 11, 12, 22	Fusion	3'

Gene	Accession	Exon	Variant Type	Description**
JAK2	NM_004972	12, 14, 16, 19, 20	Mutation	p.F537-p.F547,p.V617-p.C618,p.L681-p.R683, p.L855, p.V863
JAK3	NM_000215	10, 11, 12, 17, 18, 19	Fusion	5'
JAK3	NM_000215	23	Fusion	3'
JAK3	NM_000215	11, 17	Mutation	p.M511,p.S789
JAZF1	NM_175061	2, 3, 4	Fusion	3'
KIT	NM_000222	8	Fusion	5'
KIT	NM_000222	1	Fusion	3'
KRAS	NM_004985	2, 3, 4	Mutation	p.G12-p.G13,p.Q61,p.K117,p.A146
MAML2	NM_032427	2, 3	Fusion	5'
MAML2	NM_032427	2	Fusion	3'
MAP2K1	NM_002755	2	Fusion	5'
MAP2K1	NM_002755	2	Mutation	p.F53-p.D67
MAST1	NM_014975	7, 8, 9, 18, 19, 20, 21	Fusion	5'
MAST2	NM_015112	2, 3, 5, 6	Fusion	5'
MAST2	NM_015112	15, 16, 17	Fusion	3'
MBTD1	NM_017643	3*	Fusion	5'
MBTD1	NM_017643	15, 16, 17	Fusion	3'
MDM2	NM_002392	5, 9	Fusion, Expression	5'
MDM2	NM_002392	2, 4, 6, 8, 10	Fusion, Expression	3'

Gene	Accession	Exon	Variant Type	Description**
MEAF6	NM_001270875	4, 5	Fusion	3'
MET	NM_000245	2, 4, 5, 6, 13, 14, 15, 16, 17, 21	Fusion, Exon 14 Skipping (METΔex14)	5'
MET	NM_000245	2, 13	Fusion, Exon 14 Skipping (METΔex14)	3'
MGEA5	NM_012215	4, 5, 6, 7, 8, 9, 12, 13, 14, 15	Fusion, Expression	5'
MKL2	NM_014048	11, 12, 13	Fusion	5'
MN1	NM_002430	1, 2	Fusion	3'
MSMB	NM_002443	2, 3, 4	Fusion	3'
MUSK	NM_005592	7, 9, 10, 12, 13, 14, 15	Fusion	5'
MYB	NM_001130173	7, 8, 9, 11, 12, 13, 14, 15, 16	Fusion	3'
MYBL1	NM_001080416	8, 9, mid-exon10, 10, 11, 12, 13, 14, 15	Fusion	3'
MYC	NM_002467	1, 2	Expression	3'
MYC	NM_002467	1*, mid-exon1*, 2, 3	Fusion, Expression	5'
MYOD1	NM_002478	1	Mutation	p.L122, full CDS coverage for mutation detection
NCOA1	NM_147223	11, 12, 13, 14, 15	Fusion	5'
NCOA2	NM_006540	11, 12, 13, 14, intron14, 15, 16, 22	Fusion	5'
NCOA2	NM_006540	14	Fusion	3'
NCOA3	NM_006534	2*, 13, 14, 15, 16	Fusion	5'
NCOA3	NM_006534	20	Fusion	3'
NFATC2	NM_012340	2, 3, 9, 10	Fusion	5'

Gene	Accession	Exon	Variant Type	Description**
NFE2L2	NM_006164	1, 2, 3, 4, 5	Exon skipping, Fusion	5'
NFIB	NM_001369458	10, 11	Fusion	5'
NFIB	NM_005596	9*, mid-exon 9	Fusion	5'
NFIB	NM_005596	2	Fusion	3'
NOTCH1	NM_017617	2, 4, 24, 29, 30, 31	Fusion	3'
NOTCH1	NM_017617	5, 24, 25, 26, 27, 28, 29	Fusion,Exon Skipping(NOTCH1Δ2-27,NOTCH1Δ21-27,NOTCH1Δ3-27,NOTCH1Δ3-28)	5'
NOTCH2	NM_024408	24, 25, 26, 27, 28, 29	Fusion	5'
NOTCH2	NM_024408	5, 6, 7	Fusion	3'
NR4A3	NM_173200	2*, 3*, 4, 5, 7, 9	Fusion, Expression	5'
NR4A3	NM_173200	8	Fusion, Expression	3'
NRAS	NM_002524	2, 3, 4	Mutation	p.G12-p.G13,p.Q61,p.K117,p.A146
NRG1	NM_001159996	1*, 3, 4, 5	Fusion	5'
NRG1	NM_004495	1, 2, 3, 4, 5, 6	Fusion	5'
NRG1	NM_013958	1*	Fusion	5'
NRG1	NM_013959	1*, 3	Fusion	5'
NRG1	NM_013962	1*	Fusion	5'
NRG1	NM_013962	1	Fusion	3'
NTRK1	NM_001007792	1, 2	Fusion	5'

Gene	Accession	Exon	Variant Type	Description**
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'
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 mutation detection including p.F617,p.G623,p.G696
NUMBL	NM_004756	2, 3	Fusion	5'
NUTM1	NM_175741	2*, 3, mid-exon3, 4, 5, mid-exon6, 6	Fusion	5'
PAX3	NM_181459	2, 4, 8	Fusion, Expression	5'
PAX3	NM_181459	3, 5, 6, 7, 8	Fusion, Expression	3'
PAX8	NM_003466	3	Fusion	5'
PAX8	NM_003466	1*, 2, 6, 7, 8, 9, 10	Fusion	3'
PDGFB	NM_002608	2, 3	Fusion	5'
PDGFD	NM_025208	5, 6, 7	Fusion	5'

Gene	Accession	Exon	Variant Type	Description**
PDGFRA	NM_006206	10, 11, 12, mid-exon12, 13, 14, 15	Fusion,PDGFRAΔ8,9	5'
PDGFRA	NM_006206	7	Fusion,PDGFRAΔ8,9	3'
PDGFRA	NM_006206	15, 18	Mutation	p.T674,p.D842
PDGFRB	NM_002609	8, 9, 10, 11, 12, mid-exon12, 13, 14	Fusion	5'
PHF1	NM_024165	1*, 2	Fusion	5'
PHF1	NM_024165	10, 11, 12	Fusion	3'
PHKB	NM_000293	4	Fusion	3'
PIK3CA	NM_006218	2, 15	Fusion	5'
PIK3CA	NM_006218	2, 3, 5, 6, 8, 10, 14, 21	Mutation	p.E81K-p.G118D,p.L339-p.D350,p.G364R,p.E418-p.C420,p.E453-p.K468,p.P539-p.Q546,p.E726,p.Y1021-p.T1052
PKN1	NM_002741	10, 11, 12, 13	Fusion	5'
PLAG1	NM_002655	1, 2, 3, 4	Fusion	5'
PPARG	NM_015869	1, 2, 3	Fusion	5'
PRDM10	NM_020228	13, 14	Fusion	5'
PRKACA	NM_002730	2	Fusion	5'
PRKACB	NM_182948	2, 3, 4	Fusion	5'
PRKCA	NM_002737	4, 5, 6, 9, 15	Fusion	5'
PRKCB	NM_002738	1, 3, 7, 8, 9	Fusion	5'

Gene	Accession	Exon	Variant Type	Description**
PRKCD	NM_006254	9, 10, 11, 12, 15	Fusion	5'
PRKCD	NM_006254	18	Fusion	3'
PRKD1	NM_002742	2, 10, 11, 12, 13	Fusion	5'
PRKD2	NM_016457	10, 11, 12, 13	Fusion	5'
PRKD3	NM_005813	10, 11, 12, 13	Fusion	5'
RAD51B	NM_133509	8	Fusion	5'
RAD51B	NM_133509	3, 4, 5, 6, 7, 8, 9	Fusion	3'
RAF1	NM_002880	2*, 4, 5, 6, 7, 8, 9, 10, 11, 12	Fusion	5'
RAF1	NM_002880	4, 5, 6, 7, 8, 9	Fusion	3'
RELA	NM_021975	1, 2, 3, 4, 11	Fusion	5'
RET	NM_020630	2, 4, 6, 8, 9, 10, 11, mid-exon11, 12, 13, 14	Fusion	5'
RET	NM_020630	15, 16	Mutation	p.A883,p.M918
ROS1	NM_002944	2, 4, 7, 31, 32, 33, 34, 35, 36, 37	Fusion	5'
ROS1	NM_002944	38	Mutation	p.G2032
RSPO2	NM_178565	1, 2*, 3*	Fusion	5'
RSPO3	NM_032784	2	Fusion	5'
SS18	NM_001007559	2, 3, 4, 5, 6, 10, 11	Fusion	5'
SS18	NM_001007559	4, 5, 6, 8, 9, 10	Fusion	3'
SS18L1	NM_198935	1, 2, 3, 8, 9, 10	Fusion	3'

Gene	Accession	Exon	Variant Type	Description**
STAT6	NM_001178078	1*, 2*, 3, 4, 5, 6, 7, 15, 16, 17, 18, 19, 20	Fusion	5'
TAF15	NM_139215	6, 7	Fusion	5'
TAF15	NM_139215	5, 6, 7, 9	Fusion	3'
TCF12	NM_207036	4, 5, 6	Fusion	3'
TERT	NM_198253	2, 3, 5, 7, 10, 11, 12	Fusion,Expression	5'
TERT	NM_198253	3, 9, 15	Fusion,Expression	3'
TFE3	NM_006521	2, 3, 4, 5, 6, 7, 8	Fusion	5'
TFE3	NM_006521	2, 3, 4, 5, 6	Fusion	3'
TFEB	NM_007162	1*, 2*, 3, mid-exon3, 4, mid-exon4, mid-exon 5, 6	Fusion	5'
TFEB	NM_007162	9, mid-exon 10	Fusion	3'
TFG	NM_006070	6	Fusion	5'
TFG	NM_006070	3, 4, 5, 6, 7, mid-exon8	Fusion	3'
THADA	NM_022065	24, 25, 26, 27, 28, 29, 30, 31, 36, 37	Fusion	3'
TMPRSS2	NM_001135099	1	Fusion	3'
TMPRSS2	NM_005656	1*, 2, 3, 4, 5, 6	Fusion	3'
USP6	NM_004505	1*, mid-exon1*, 2*, 3	Fusion	5'
VGLL2	NM_182645	1, 2, 3, intron3, 4	Fusion	3'
WWTR1	NM_015472	3, 4	Fusion	5'
WWTR1	NM_015472	3, 4	Fusion	3'

Gene	Accession	Exon	Variant Type	Description**
YAP1	NM_001130145	1, mid-exon1, 2, 3, 4, 8, 9	Fusion	5'
YAP1	NM_001130145	1, 2, 3, 4, 5, 6, 7	Fusion	3'
YWHAE	NM_006761	5	Fusion	3'

*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. 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.

ᵞALK-ATI currently requires review outside of Archer Analysis.

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.