FUSION*Plex*-HT Core Solid Tumor

Description

The FUSION*Plex*-HT Core Solid Tumor 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 Core Solid Tumor contains **797** GSPs targeting **57** genes commonly mutated in solid tumors.

Description	Part number	Storage
FUSION*Plex*-HT Core Solid Tumor GSP1, 24 reactions or FUSION*Plex*-HT Core Solid Tumor GSP1, 96 reactions	SA22408241 or SA22408961	–20°C ± 10°C
FUSION*Plex*-HT Core Solid Tumor GSP2, 24 reactions or FUSION*Plex*-HT Core Solid Tumor GSP2, 96 reactions	SA22408242 or SA22408962	
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	63	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 Core Solid Tumor libraries should be sequenced to a minimum of **3M** 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 Core Solid Tumor 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 Core Solid Tumor 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**
AKT1	NM_005163	3	Mutation	Hotspot coverage including p.E17
AKT1	NM_005163	2, 3, 4, 5, mid-exon5	Fusion, Expression	5'
ALK	NM_004304	1, 2	Internal deletion (ALKΔ2-17, ALKΔ2-3)	3'

Gene	Accession	Exon	Variant type	Description**
ALK	NM_004304	2, 4, 6, 8, 10, 12, 14, 16, 17, 18, 19, intron19, 20, mid-exon20, 21, 22, 23, 26	Fusion, ALK ATIˠ, Internal deletion (ALKΔ2-17, ALKΔ2-3), Expression	5'
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
AXL	NM_021913	18, 19, mid-exon20, 20	Fusion	3'
AXL	NM_021913	11	Fusion	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'
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
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'
CTNNB1	NM_001904	3	Mutation	Full exon coverage
CTNNB1	NM_001904	8	Mutation	Hotspot coverage including p.W383-p.N387
CYSLTR2	NM_020377	5	Mutation	Hotspot p.L129
DDR2	NM_006182	17	Mutation	Full exon coverage
DNAJB1	NM_006145	1, 2	Fusion	3'
EGFR	NM_005228	1, 24, 25, mid-exon25, 26	Fusion, Exon 2-7 Skipping (EGFRvIII), Kinase Domain Duplication	3'

Gene	Accession	Exon	Variant type	Description**
EGFR	NM_005228	7, 8, 9, 14, 15, 16, 17, 18, 19, 20	Fusion, Exon 2-7 Skipping (EGFRvIII), Kinase Domain Duplication, Expression	5'
EGFR	NM_005228	18, 19, 20, 21	Mutation	Full exon coverage including p.E709-p.G719,p.E746-p.L760,p.V774-p.G796,p.L858-p.L861
ERBB2	NM_004448	15, 23, 24, 25, mid-exon26, 26	Fusion, Exon 16 skipping (Δ16HER)	3'
ERBB2	NM_004448	4, 5, 13, 15, 17	Fusion, Exon 16 skipping (Δ16HER), Expression	5'
ERBB2	NM_004448	17, 18, 19, 20, 21	Mutation	Full exon coverage including p.Y772-p.P780, p.C805
ERBB2	NM_004448	6, 7, 8, 12, 16	Mutation	Hotspot coverage including p.G222, p.E265, p.D277, p.G309, p.S310, p.C311, p.E321, p.C334, p.A440, p.R487, p.A644, p.E645, p.S649
ERBB4	NM_005235	2, 3, 4, 14, 15, 16, 17, 18, 23	Fusion	5'
ERBB4	NM_005235	7, 8, 12, 14, 15, 18, 20, 21, 23, 25, 27, 28	Mutation	Hotspot coverage including p.Y285, p.S303, p.R306, p.E317, p.E452, p.E542, p.R544, p.E563, p.D595, p.Q707, p.S774, p.L798, p.E836, p.D843, p.E872, p.D931, p.K935, p.K1002, p.F1102, p.K1223, p.R1275, p.S1289
ERG	NM_004449	2*, 3*, 4, 5, 6, 7, 8, 9, 10, 11	Fusion	5'
ESR1	NM_000125	1, 2, 3, 4, 5, 6, 7	Fusion	3'
ESR1	NM_000125	5, 6, 7, 8	Fusion	5'
ESR1	NM_000125	5, 6, 7, 8	Mutation	Hotspot coverage including p.E380, p.V422, p.S463, p.L469, p.L536, p.Y537, p.D538

Gene	Accession	Exon	Variant type	Description**
FGFR1	NM_015850	12, 17	Fusion, Kinase Domain Duplication	3'
FGFR1	NM_015850	2*, 3, 4, 5, 6, 7, 8, 9, 10, 11, 17	Fusion, Kinase Domain Duplication, Expression	5'
FGFR1	NM_023110	4, 13, 14	Mutation	Hotspot coverage including p.T141, p.V561, p.N546, p.K656
FGFR2	NM_000141	16, 17, 18	Fusion	3'
FGFR2	NM_000141	2*, 3, 5, 6, 7, 8, 9, 10	Fusion	5'
FGFR2	NM_000141	7, 8, 9, 12, 13, 14	Mutation	Hotspot coverage including p.S252, p.P253, p.G305, p.A314, p.Y375, p.C382, p.M391, p.V395 , p.M537, p.I547, p.N549, p.V564, p.E565 , p.K641, p.A648, p.K659
FGFR3	NM_000142	16, 17, intron17, mid-exon18	Fusion	3'
FGFR3	NM_000142	3, 5, 8, 9, 10, 11, 12, 13, 14	Fusion	5'
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
GNA11	NM_002067	4, 5	Mutation	Hotspot coverage including p.R183, p.Q209
GNAQ	NM_002072	4, 5	Mutation	Hotspot coverage including p.R183, p.Q209
GNAS	NM_000516	8, 9	Mutation	Hotspot coverage including p.R201, p.Q227
H3F3A	NM_002107	2	Mutation	Hotspot coverage including p.K28
HIST1H3B	NM_003537	1	Mutation	Full exon coverage including p.K28
HRAS	NM_005343	2, 3, 4	Mutation	Full exon coverage including p.G12, p.G13, p.Q61, p.K117, p.A146

Gene	Accession	Exon	Variant type	Description**
IDH1	NM_005896	4, 5	Mutation	Hotspot coverage including p.G97, p.R100, p.R132, p.Y139
IDH2	NM_002168	4	Mutation	Hotspot coverage including p.R140, p.R172
KEAP1	NM_203500	2, 3, 4, 5, 6	Mutation	Full exon coverage
KIT	NM_000222	1	Fusion	3'
KIT	NM_000222	8	Fusion	5'
KIT	NM_000222	9, 10, 11, 13, 14, 17, 18	Mutation	Full exon coverage
KRAS	NM_004985	2, 3, 4	Mutation	Full exon coverage including p.G12, p.G13, p.Q61, p.K117, p.A146
KRAS	NM_004985	5	Mutation	Hotspot coverage including p.D153, p.F156
LTK	NM_002344	2, 3, 4, 5, 8, 9, 10, 11, 12, 13	Fusion	5'
LTK	NM_001135685	10	Fusion	5'
MAP2K1	NM_002755	2	Fusion	5'
MAP2K1	NM_002755	2, 3, 5, 6	Mutation	Full exon coverage including p.F53, p.D67
MAP3K3	NM_002401	8	Fusion	5'
MAP3K8	NM_005204	8	Fusion	3'
MET	NM_000245	2, 13	Fusion, Exon 14 Skipping (METΔex14)	3'
MET	NM_000245	2, 4, 5, 6, 13, 14, 15, 16, 17, 21	Fusion, Exon 14 Skipping (METΔex14)	5'
MET	NM_000245	14, 15, 16, 17, 18, 19, 20	Mutation	Full exon coverage
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'
NRAS	NM_002524	2, 3, 4	Mutation	Full exon coverage including p.G12, p.G13, p.Q61, p.K117, p.A146
NRG1	NM_001159996	1*, 3, 4, 5	Fusion	5'

Gene	Accession	Exon	Variant type	Description**
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	3'
NRG1	NM_013962	1*	Fusion	5'
NTRK1	NM_001007792	1, 2	Fusion	5'
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	11, 14	Fusion	3'
NTRK2	NM_006180	11, 14	Fusion	5'
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	13, 14, 15, 17	Fusion	3'
NTRK3	NM_002530	3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16	Fusion	5'
NTRK3	NM_002530	15, 16, 17, 18, 19	Mutation	Full Kinase Domain coverage for resistance mutation detection including p.F617,p.G623,p.G696
NUTM1	NM_175741	2*, 3, mid-exon3, 4, 5, mid-exon6, 6	Fusion	5'
PAX8	NM_003466	1*, 2, 6, 7, 8, 9, 10	Fusion	3'
PAX8	NM_003466	3	Fusion	5'
PDGFRA	NM_006206	6, 7	Fusion,PDGFRAΔ8,9	3'
PDGFRA	NM_006206	10, 11, 12, mid-exon12, 13, 14, 15	Fusion,PDGFRAΔ8,9	5'
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
PIK3CA	NM_006218	2, 15	Fusion	5'

Gene	Accession	Exon	Variant type	Description**
PIK3CA	NM_006218	2, 3, 4, 5, 6, 8, 9, 10, 11, 12, 13, 14, 19, 20, 21	Mutation	Hotspot coverage including p.E81K-p.G118,p.L339-p.D350,p.G364,p.E418-p.C420,p.E453-p.K468,p.P539-p.Q546,p.E726,p.Y1021-p.T1052
POLD1	NM_002691	8, 9, 10, 11, 12	Mutation	Full exon coverage
POLE	NM_006231	9, 10, 11, 12, 13, 14	Mutation	Full exon coverage
PPARG	NM_015869	1, 2, 3	Fusion	5'
PRKCA	NM_002737	4, 5, 6, 9, 15	Fusion	5'
PRKCB	NM_002738	1, 3, 7, 8, 9	Fusion	5'
RAF1	NM_002880	4, 5, 6, 7, 8, 9	Fusion	3'
RAF1	NM_002880	2*, 4, 5, 6, 7, 8, 9, 10, 11, 12	Fusion	5'
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	2, 4, 7, 31, 32, 33, 34, 35, 36, 37	Fusion	5'
ROS1	NM_002944	38	Mutation	Hotspot coverage including p.G2032
STK11	NM_000455	1, 2, 3, 4, 5, 6, 7, 8, 9	Mutation	Full exon coverage
TMPRSS2	NM_001135099	1	Fusion	3'
TMPRSS2	NM_005656	1*, 2, 3, 4, 5, 6	Fusion	3'
TP53	NM_000546	2, 3, 4, 5, 6, 7, 8, 9, 10, 11	Mutation	Full exon coverage
TRIM11	NM_145214	2, 3	Fusion	5'

*Indicates exons that are entirely untranslated region (UTR), or for which the UTR is targeted.

**Contact archer-tech@idtdna.com for the panel target file to view complete list of targeted regions. De Novo RNA SNV/Indel detection is not supported on the Ion Torrent sequencing platform.

ɣALK-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.

Revision History

Document Number	Date	Description of change
RA-DOC-448/REV01	October 2023	Initial release.
RA-DOC-448/REV02	November 2023	Updated First and Second PCR cycling conditions to include separate anneal and extended steps. Updated branding.