Product Insert

FUSION*Plex*™ Sarcoma v2 Panel

FUSION*Plex* Sarcoma v2

Description

The FUSION*Plex* Sarcoma v2 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 FUSION*Plex* protocol for Illumina® (RA-DOC-047) or FUSION*Plex* protocol for Ion Torrent™ (RA-DOC-048).

FUSION*Plex* Sarcoma v2 libraries contain **659** GSPs targeting **63** genes commonly mutated in solid tumor cancer types.

Description	Part number	Storage
FUSION*Plex* Sarcoma v2 GSP1, 8 reactions	SA19191081	–20°C ± 10°C
FUSION*Plex* Sarcoma v2 GSP2, 8 reactions	SA19191082	
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	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* Sarcoma v2 libraries should be sequenced to a minimum of **2M 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 (v7.0, or greater). The FUSION*Plex* 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* Sarcoma v2 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	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 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

Gene	Accession	Exon	Variant Type	Description**
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'
BRAF	NM_004333	15	Mutation	p.V600
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'
CIC	NM_015125	12	Fusion	5'
CIC	NM_015125	14, 15, 16, 17, 18, mid-exon19, 19, mid-exon20, 20*	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'
CTNNB1	NM_001904	3	Mutation	p.D32-p.S37
EGFR	NM_005228	7, 8, 9, 14, 15, 16, 17, 18, 19, 20	Fusion, Exon 2-7 Skipping (EGFRvIII), Kinase Domain Duplication	5'

Gene	Accession	Exon	Variant Type	Description**
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'
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'
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'
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'
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'

Gene	Accession	Exon	Variant Type	Description**
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
FOS	NM_005252	mid-exon4	Fusion	3'
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'
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'
HMGA2	NM_003483	1, 2, 3, 4, mid-exon5*, 5*	Fusion	3'
JAZF1	NM_175061	2, 3, 4	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'
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'
NR4A3	NM_173200	2*, 3*, 4, 5, 7, 9	Fusion, Expression	5'
NR4A3	NM_173200	8	Fusion, Expression	3'
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	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	Variant 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 mutation detection including p.F617,p.G623,p.G696
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'
PDGFB	NM_002608	2, 3	Fusion	5'
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
PHF1	NM_024165	1*, 2	Fusion	5'
PHF1	NM_024165	10, 11, 12	Fusion	3'
PLAG1	NM_002655	1, 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'
PRKCD	NM_006254	9, 10, 11, 12, 15	Fusion	5'

Gene	Accession	Exon	Variant Type	Description**
PRKCD	NM_006254	18	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'
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
SS18	NM_001007559	2, 3, 4, 5, 6, 10, 11	Fusion	5'
SS18	NM_001007559	4, 5, 6, 8, 9, 10	Fusion	3'
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'
TFE3	NM_006521	2, 3, 4, 5, 6, 7, 8	Fusion	5'
TFE3	NM_006521	2, 3, 4, 5, 6	Fusion	3'
TFG	NM_006070	6	Fusion	5'
TFG	NM_006070	3, 4, 5, 6, 7, mid-exon8	Fusion	3'
USP6	NM_004505	1*, mid-exon1*, 2*, 3	Fusion	5'
VGLL2	NM_182645	1, 2, 3, intron3, 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.

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-020/REV01	June 2023	Initial release.
RA-DOC-020/REV02	November 2023	Updated First and Second PCR cycling conditions to include separate anneal and extended steps. Updated branding.