

## FusionPlex® Sarcoma v2

### Description

The FusionPlex Sarcoma v2 panel is an optimized, balanced pool of gene-specific primer (GSP) oligonucleotides that is used in conjunction with FusionPlex Reagents and Molecular Barcode (MBC) Adapters to produce targeted NGS libraries.

FusionPlex Sarcoma v2 contains **659** GSPs targeting **63** genes commonly mutated in sarcomas.

### Contents

Description	Part Number	Storage Conditions
FusionPlex Sarcoma v2 GSP1 - 8 reactions	SA19191081	-20°C ± 10°C
FusionPlex 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	63	5 min (100% ramp rate)	
	4	72	3 min	1
	5	4	Hold	1
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 200nM.

### Recommended Reads and Multiplexing

FusionPlex Sarcoma v2 libraries should be sequenced to a minimum of **2M reads**. Based on end-user experience, fewer reads may be sufficient for libraries prepared using limited input masses.

### Archer Analysis Settings

Sequencing data should be processed using **Archer Analysis** (v6.0 or greater). The FusionPlex Sarcoma v2 panel requires selection of the **RNA Fusion and** (optional) **RNA SNP/Indel** pipeline(s), found under the RNA Analysis Type (see the software user manual for further details on setting up analyses).

## Assay Targets

Gene	Accession	Exon	Assay 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 ATL7, 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
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'

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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'
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'

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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'
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'
NTRK2	NM_006180	16, 17, 18, 19, 20, 21	Mutation	Full Kinase Domain coverage for resistance mutations

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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'
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'
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 are targeted by the assay design. Version 6.3 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). RNA SNV/InDel mutation detection is not supported on the Ion Torrent Sequencing Platform

†ALK-AT1 currently requires review outside of Archer Analysis.

## Limitations of Use

**For Research Use Only.** Not for use in diagnostic procedures. Not intended to be used in treatment of animal or human diseases.

Safety data sheets pertaining to this product are available upon request.

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