

## FUSIONPlex Pan Solid Tumor v2

### Description

The FUSIONPlex Pan Solid Tumor v2 panel is a balanced pool of gene-specific primer (GSP) oligonucleotides that is optimized for use with FUSIONPlex reagents and molecular barcode (MBC) adapters to produce targeted NGS libraries. This product insert should be used in conjunction with FUSIONPlex protocol for Illumina® (RA-DOC-047) or FUSIONPlex protocol for Ion Torrent<sup>™</sup> (RA-DOC-048).

FUSIONPlex Pan Solid Tumor v2 libraries contain **1086** GSPs targeting **137** genes commonly mutated in many solid tumor cancer types.

Description	Part number	Storage
FUSIONPlex Pan Solid Tumor v2 GSP1, 8 reactions	SA18091081	-20°C ± 10°C
FUSIONPlex Pan Solid Tumor v2 GSP2, 8 reactions	SA18091082	
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	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	
	3	60	10 sec	20†
	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

FUSIONPlex 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 (v7.0, or greater). The FUSIONPlex Pan Solid Tumor v2 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 FUSIONPlex Pan Solid Tumor v2 libraries requires a one-time upload of the Panel GTF. Files can be obtained by contacting [archer-tech@idtdna.com](mailto: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'

Gene	Accession	Exon	Variant Type	Description**
AKT2	NM_001626	11	Fusion	3'
AKT3	NM_005465	2, 3, 4, 9	Fusion	5'
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 AT1Y, 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'

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

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<i>CSF1</i>	NM_000757	5, 6, 7, 8*, mid-exon9*	Fusion	3'
<i>CSF1</i>	NM_172212	9*	Fusion	3'
<i>CSF1R</i>	NM_005211	11, 12, 13	Fusion	5'
<i>CTNNB1</i>	NM_001904	3	Mutation	p.D32-p.S37
<i>DNAJB1</i>	NM_006145	1, 2	Fusion	3'
<i>EGF</i>	NM_001963	16, 17, 18, 19	Fusion	5'
<i>EGFR</i>	NM_005228	7, 8, 9, 14, 15, 16, 17, 18, 19, 20	Fusion, Exon 2-7 Skipping (EGFRvIII), Kinase Domain Duplication	5'
<i>EGFR</i>	NM_005228	1, 24, 25, mid-exon25, 26	Fusion, Exon 2-7 Skipping (EGFRvIII), Kinase Domain Duplication	3'
<i>EGFR</i>	NM_005228	18, 19, 20, 21	Mutation	p.E709-p.G719,p.E746-p.L760,p.V774-p.G796,p.L858-p.L861
<i>EPC1</i>	NM_025209	9, 10, 11	Fusion	3'
<i>ERBB2</i>	NM_004448	4, 5, 13, 15, 17	Fusion, Exon 16 skipping (Δ16HER)	5'
<i>ERBB2</i>	NM_004448	15, 23, 24, 25, mid-exon26, 26	Fusion, Exon 16 skipping (Δ16HER)	3'
<i>ERBB2</i>	NM_004448	8, 20	Mutation	p.G309-p.S310,p.Y772-p.P780, p.C805
<i>ERBB4</i>	NM_005235	2, 3, 4, 14, 15, 16, 17, 18, 23	Fusion	5'
<i>ERG</i>	NM_004449	2*, 3*, 4, 5, 6, 7, 8, 9, 10, 11	Fusion	5'
<i>ESR1</i>	NM_000125	5, 6, 7, 8	Fusion	5'
<i>ESR1</i>	NM_000125	1, 2, 3, 4, 5, 6, 7	Fusion	3'
<i>ESRRA</i>	NM_004451	2, 3	Fusion	3'

Gene	Accession	Exon	Variant Type	Description**
<i>ETV1</i>	NM_004956	3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13	Fusion	5'
<i>ETV4</i>	NM_001986	2, 3, 4, 5, 6, 7, 8, 9, 10	Fusion	5'
<i>ETV5</i>	NM_004454	2*, 3, 7, 8, 9	Fusion	5'
<i>ETV6</i>	NM_001987	2, 3, 4, 5, 6, 7	Fusion	5'
<i>ETV6</i>	NM_001987	1, 2, 3, 4, 5, 6	Fusion	3'
<i>ETV6</i>	NM_001987	3	Mutation	p.Y104-p.R105
<i>EWSR1</i>	NM_005243	8	Fusion	5'
<i>EWSR1</i>	NM_005243	4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14	Fusion	3'
<i>FGF1</i>	NM_00800	mid-exon 2, 2	Fusion	5'
<i>FGFR1</i>	NM_015850	2*, 3, 4, 5, 6, 7, 8, 9, 10, 11, 17	Fusion, Kinase Domain Duplication	5'
<i>FGFR1</i>	NM_015850	12, 17	Fusion, Kinase Domain Duplication	3'
<i>FGFR1</i>	NM_023110	4, 13, 14	Mutation	p.T141,p.V561,p.K656
<i>FGFR2</i>	NM_000141	2*, 3, 5, 6, 7, 8, 9, 10	Fusion	5'
<i>FGFR2</i>	NM_000141	16, 17, 18	Fusion	3'
<i>FGFR2</i>	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
<i>FGFR3</i>	NM_000142	3, 5, 8, 9, 10, 11, 12, 13, 14	Fusion	5'
<i>FGFR3</i>	NM_000142	16, 17, intron17, mid-exon18	Fusion	3'
<i>FGFR3</i>	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

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<i>FGR</i>	NM_005248	2*, 3	Fusion	5'
<i>FOS</i>	NM_005252	mid-exon4	Fusion	3'
<i>FOSB</i>	NM_006732	1*, mid-exon1*, 1, 2	Fusion	5'
<i>FOXO1</i>	NM_002015	1*, 2, 3*	Fusion	5'
<i>FOXO1</i>	NM_002015	1*, 2*, 3*	Fusion	3'
<i>FOXO4</i>	NM_005938	2, mid-exon2, 3	Fusion	5'
<i>FOXR2</i>	-	cryptic upstream exon2,3 (chrX:55562068, chrX:55634636)	Fusion	5'
<i>FUS</i>	NM_004960	3, 4, 5, mid-exon6, 6, 7, 8, 9, 10, 11, 13, 14	Fusion	3'
<i>GLI1</i>	NM_005269	4, 5, 6, 7	Fusion	5'
<i>GLI1</i>	NM_005269	4, 5, mid-exon5, 6, 7	Fusion	3'
<i>GRB7</i>	NM_005310	10, 11, 12	Fusion	5'
<i>HMGA2</i>	NM_003483	1, 2, 3, 4, mid- exon5*, 5*	Fusion	3'
<i>HRAS</i>	NM_005343	2, 3, 4	Mutation	p.G12- p.G13,p.Q61,p.K117,p.A 146
<i>IDH1</i>	NM_005896	4	Mutation	p.R132
<i>IDH2</i>	NM_002168	4	Mutation	p.R140, p.R172
<i>IGF1R</i>	NM_000875	13, 14, 15	Fusion	5'
<i>INSR</i>	NM_000208	2, 12, 13, 14, 15, 16, 17, 18, 19	Fusion	5'
<i>INSR</i>	NM_000208	20, 21, 22	Fusion	3'

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<i>JAK2</i>	NM_004972	6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20	Fusion	5'
<i>JAK2</i>	NM_004972	9, 10, 11, 12, 22	Fusion	3'
<i>JAK2</i>	NM_004972	12, 14, 16, 19, 20	Mutation	p.F537-p.F547,p.V617-p.C618,p.L681-p.R683, p.L855, p.V863
<i>JAK3</i>	NM_000215	10, 11, 12, 17, 18, 19	Fusion	5'
<i>JAK3</i>	NM_000215	23	Fusion	3'
<i>JAK3</i>	NM_000215	11, 17	Mutation	p.M511,p.S789
<i>JAZF1</i>	NM_175061	2, 3, 4	Fusion	3'
<i>KIT</i>	NM_000222	8	Fusion	5'
<i>KIT</i>	NM_000222	1	Fusion	3'
<i>KRAS</i>	NM_004985	2, 3, 4	Mutation	p.G12-p.G13,p.Q61,p.K117,p.A146
<i>MAML2</i>	NM_032427	2, 3	Fusion	5'
<i>MAML2</i>	NM_032427	2	Fusion	3'
<i>MAP2K1</i>	NM_002755	2	Fusion	5'
<i>MAP2K1</i>	NM_002755	2	Mutation	p.F53-p.D67
<i>MAST1</i>	NM_014975	7, 8, 9, 18, 19, 20, 21	Fusion	5'
<i>MAST2</i>	NM_015112	2, 3, 5, 6	Fusion	5'
<i>MAST2</i>	NM_015112	15, 16, 17	Fusion	3'
<i>MBTD1</i>	NM_017643	3*	Fusion	5'
<i>MBTD1</i>	NM_017643	15, 16, 17	Fusion	3'



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<i>MDM2</i>	NM_002392	5, 9	Fusion, Expression	5'
<i>MDM2</i>	NM_002392	2, 4, 6, 8, 10	Fusion, Expression	3'
<i>MEAF6</i>	NM_001270875	4, 5	Fusion	3'
<i>MET</i>	NM_000245	2, 4, 5, 6, 13, 14, 15, 16, 17, 21	Fusion, Exon 14 Skipping (METΔex14)	5'
<i>MET</i>	NM_000245	2, 13	Fusion, Exon 14 Skipping (METΔex14)	3'
<i>MGEA5</i>	NM_012215	4, 5, 6, 7, 8, 9, 12, 13, 14, 15	Fusion, Expression	5'
<i>MKL2</i>	NM_014048	11, 12, 13	Fusion	5'
<i>MN1</i>	NM_002430	1, 2	Fusion	3'
<i>MSMB</i>	NM_002443	2, 3, 4	Fusion	3'
<i>MUSK</i>	NM_005592	7, 9, 10, 12, 13, 14, 15	Fusion	5'
<i>MYB</i>	NM_001130173	7, 8, 9, 11, 12, 13, 14, 15, 16	Fusion	3'
<i>MYBL1</i>	NM_001080416	8, 9, mid-exon10, 10, 11, 12, 13, 14, 15	Fusion	3'
<i>MYC</i>	NM_002467	1, 2	Expression	3'
<i>MYC</i>	NM_002467	1*, mid-exon1*, 2, 3	Fusion, Expression	5'
<i>MYOD1</i>	NM_002478	1	Mutation	p.L122, full CDS coverage for mutation detection
<i>NCOA1</i>	NM_147223	11, 12, 13, 14, 15	Fusion	5'
<i>NCOA2</i>	NM_006540	11, 12, 13, 14, intron14, 15, 16, 22	Fusion	5'
<i>NCOA2</i>	NM_006540	14	Fusion	3'
<i>NCOA3</i>	NM_006534	2*, 13, 14, 15, 16	Fusion	5'

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<i>NCOA3</i>	NM_006534	20	Fusion	3'
<i>NFATC2</i>	NM_012340	2, 3, 9, 10	Fusion	5'
<i>NFE2L2</i>	NM_006164	1, 2, 3, 4, 5	Exon skipping, Fusion	5'
<i>NFIB</i>	NM_001369458	10, 11	Fusion	5'
<i>NFIB</i>	NM_005596	9*, mid-exon 9	Fusion	5'
<i>NFIB</i>	NM_005596	2	Fusion	3'
<i>NOTCH1</i>	NM_017617	2, 4, 24, 29, 30, 31	Fusion	3'
<i>NOTCH1</i>	NM_017617	5, 24, 25, 26, 27, 28, 29	Fusion, Exon Skipping(NOTCH1Δ2 -27, NOTCH1Δ21- 27, NOTCH1Δ3- 27, NOTCH1Δ3-28)	5'
<i>NOTCH2</i>	NM_024408	24, 25, 26, 27, 28, 29	Fusion	5'
<i>NOTCH2</i>	NM_024408	5, 6, 7	Fusion	3'
<i>NR4A3</i>	NM_173200	2*, 3*, 4, 5, 7, 9	Fusion, Expression	5'
<i>NR4A3</i>	NM_173200	8	Fusion, Expression	3'
<i>NRAS</i>	NM_002524	2, 3, 4	Mutation	p.G12- p.G13,p.Q61,p.K117,p.A 146
<i>NRG1</i>	NM_001159996	1*, 3, 4, 5	Fusion	5'
<i>NRG1</i>	NM_004495	1, 2, 3, 4, 5, 6	Fusion	5'
<i>NRG1</i>	NM_013958	1*	Fusion	5'
<i>NRG1</i>	NM_013959	1*, 3	Fusion	5'
<i>NRG1</i>	NM_013962	1*	Fusion	5'

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<i>NRG1</i>	NM_013962	1	Fusion	3'
<i>NTRK1</i>	NM_001007792	1, 2	Fusion	5'
<i>NTRK1</i>	NM_002529	1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14	Fusion	5'
<i>NTRK1</i>	NM_002529	13, 14, 15, 16, 17	Mutation	Full Kinase Domain coverage for resistance mutations including p.G595
<i>NTRK2</i>	NM_006180	4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18	Fusion	5'
<i>NTRK2</i>	NM_006180	11, 14	Fusion	3'
<i>NTRK2</i>	NM_006180	16, 17, 18, 19, 20, 21	Mutation	Full Kinase Domain coverage for resistance mutations
<i>NTRK3</i>	NM_001007156	15	Fusion	5'
<i>NTRK3</i>	NM_002530	3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16	Fusion	5'
<i>NTRK3</i>	NM_002530	13, 14, 15, 17	Fusion	3'
<i>NTRK3</i>	NM_002530	15, 16, 17, 18, 19	Mutation	Full Kinase Domain coverage for resistance mutation detection including p.F617,p.G623,p.G696
<i>NUMBL</i>	NM_004756	2, 3	Fusion	5'
<i>NUTM1</i>	NM_175741	2*, 3, mid-exon3, 4, 5, mid-exon6, 6	Fusion	5'
<i>PAX3</i>	NM_181459	2, 4, 8	Fusion, Expression	5'
<i>PAX3</i>	NM_181459	3, 5, 6, 7, 8	Fusion, Expression	3'
<i>PAX8</i>	NM_003466	3	Fusion	5'
<i>PAX8</i>	NM_003466	1*, 2, 6, 7, 8, 9, 10	Fusion	3'

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<i>PDGFB</i>	NM_002608	2, 3	Fusion	5'
<i>PDGFD</i>	NM_025208	5, 6, 7	Fusion	5'
<i>PDGFRA</i>	NM_006206	10, 11, 12, mid-exon12, 13, 14, 15	Fusion,PDGFRAΔ8,9	5'
<i>PDGFRA</i>	NM_006206	7	Fusion,PDGFRAΔ8,9	3'
<i>PDGFRA</i>	NM_006206	15, 18	Mutation	p.T674,p.D842
<i>PDGFRB</i>	NM_002609	8, 9, 10, 11, 12, mid-exon12, 13, 14	Fusion	5'
<i>PHF1</i>	NM_024165	1*, 2	Fusion	5'
<i>PHF1</i>	NM_024165	10, 11, 12	Fusion	3'
<i>PHKB</i>	NM_000293	4	Fusion	3'
<i>PIK3CA</i>	NM_006218	2, 15	Fusion	5'
<i>PIK3CA</i>	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
<i>PKN1</i>	NM_002741	10, 11, 12, 13	Fusion	5'
<i>PLAG1</i>	NM_002655	1, 2, 3, 4	Fusion	5'
<i>PPARG</i>	NM_015869	1, 2, 3	Fusion	5'
<i>PRDM10</i>	NM_020228	13, 14	Fusion	5'
<i>PRKACA</i>	NM_002730	2	Fusion	5'
<i>PRKACB</i>	NM_182948	2, 3, 4	Fusion	5'

Gene	Accession	Exon	Variant Type	Description**
<i>PRKCA</i>	NM_002737	4, 5, 6, 9, 15	Fusion	5'
<i>PRKCB</i>	NM_002738	1, 3, 7, 8, 9	Fusion	5'
<i>PRKCD</i>	NM_006254	9, 10, 11, 12, 15	Fusion	5'
<i>PRKCD</i>	NM_006254	18	Fusion	3'
<i>PRKD1</i>	NM_002742	2, 10, 11, 12, 13	Fusion	5'
<i>PRKD2</i>	NM_016457	10, 11, 12, 13	Fusion	5'
<i>PRKD3</i>	NM_005813	10, 11, 12, 13	Fusion	5'
<i>RAD51B</i>	NM_133509	8	Fusion	5'
<i>RAD51B</i>	NM_133509	3, 4, 5, 6, 7, 8, 9	Fusion	3'
<i>RAF1</i>	NM_002880	2*, 4, 5, 6, 7, 8, 9, 10, 11, 12	Fusion	5'
<i>RAF1</i>	NM_002880	4, 5, 6, 7, 8, 9	Fusion	3'
<i>RELA</i>	NM_021975	1, 2, 3, 4, 11	Fusion	5'
<i>RET</i>	NM_020630	2, 4, 6, 8, 9, 10, 11, mid-exon11, 12, 13, 14	Fusion	5'
<i>RET</i>	NM_020630	15, 16	Mutation	p.A883,p.M918
<i>ROS1</i>	NM_002944	2, 4, 7, 31, 32, 33, 34, 35, 36, 37	Fusion	5'
<i>ROS1</i>	NM_002944	38	Mutation	p.G2032
<i>RSPO2</i>	NM_178565	1, 2*, 3*	Fusion	5'
<i>RSPO3</i>	NM_032784	2	Fusion	5'
<i>SS18</i>	NM_001007559	2, 3, 4, 5, 6, 10, 11	Fusion	5'

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<i>SS18</i>	NM_001007559	4, 5, 6, 8, 9, 10	Fusion	3'
<i>SS18L1</i>	NM_198935	1, 2, 3, 8, 9, 10	Fusion	3'
<i>STAT6</i>	NM_001178078	1*, 2*, 3, 4, 5, 6, 7, 15, 16, 17, 18, 19, 20	Fusion	5'
<i>TAF15</i>	NM_139215	6, 7	Fusion	5'
<i>TAF15</i>	NM_139215	5, 6, 7, 9	Fusion	3'
<i>TCF12</i>	NM_207036	4, 5, 6	Fusion	3'
<i>TERT</i>	NM_198253	2, 3, 5, 7, 10, 11, 12	Fusion,Expression	5'
<i>TERT</i>	NM_198253	3, 9, 15	Fusion,Expression	3'
<i>TFE3</i>	NM_006521	2, 3, 4, 5, 6, 7, 8	Fusion	5'
<i>TFE3</i>	NM_006521	2, 3, 4, 5, 6	Fusion	3'
<i>TFEB</i>	NM_007162	1*, 2*, 3, mid-exon3, 4, mid-exon4, mid- exon 5, 6	Fusion	5'
<i>TFEB</i>	NM_007162	9, mid-exon 10	Fusion	3'
<i>TFG</i>	NM_006070	6	Fusion	5'
<i>TFG</i>	NM_006070	3, 4, 5, 6, 7, mid- exon8	Fusion	3'
<i>THADA</i>	NM_022065	24, 25, 26, 27, 28, 29, 30, 31, 36, 37	Fusion	3'
<i>TMPRSS2</i>	NM_001135099	1	Fusion	3'
<i>TMPRSS2</i>	NM_005656	1*, 2, 3, 4, 5, 6	Fusion	3'
<i>USP6</i>	NM_004505	1*, mid-exon1*, 2*, 3	Fusion	5'
<i>VGLL2</i>	NM_182645	1, 2, 3, intron3, 4	Fusion	3'

Gene	Accession	Exon	Variant Type	Description**
WWTR1	NM_015472	3, 4	Fusion	5'
WWTR1	NM_015472	3, 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 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.

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

## Limitations of use

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

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## Revision History

Document Number	Date	Description of change
RA-DOC-021/REV01	June 2023	Initial release.
RA-DOC-021/REV02	November 2023	Updated First and Second PCR cycling conditions to include separate anneal and extended steps.  Updated branding.