Leids Universitair Medisch Centrum

FusionPLex ® Sarcoma

This panel is no longer in use. This panel was replaced by ASARv3

Panel description

The Archer FusionPlex Sarcoma (ASARv1, # AB0003) panel targets 26 genes commonly mutated in sarcoma. The Anchored Multiplex PCR technology (RNA-NGS) identifies both known and novel fusion partners.

Gene	*RefSeq accession number*	*Target Exons*	*Direction*	*Assay Type*
ALK	NM_004304	19, 20, 21, 22	5'	Fusion
CAMTA1	NM_015215	8, 9, 10	5'	Fusion
CCNB3	NM_033031	2, 3, 4, 5, 6	5'	Fusion
CIC	NM_015125	19, 20	3'	Fusion
EPC1	NM_025209	9, 10, 11	3'	Fusion
EWSR1	NM_005243	4,5,6,7,8,9,10,11,12,13	3'	Fusion
FOXO1	NM_002015	2,3	3'	Fusion
FOXO1	NM_002015	1,2	5'	Fusion
FOXO1	NM_002015	3	5'	Fusion
FOXO1	NM_002015	1	3'	Fusion
FUS	NM_004960	4, 5, 6, 7, 8, 9, 10, 11, 14	3'	Fusion
GLI1	NM_005269	4,5,6,7	5'	Fusion
GLI1	NM_005269	4,5,6,7	3'	Fusion
HMGA2	NM_003483	1,2,3,4,5	3'	Fusion
JAZF1	NM_175061	2,3,4	3'	Fusion
MEAF6	NM_001270875	4,5	3'	Fusion
MKL2	NM_014048	11,12,13	5'	Fusion
NCOA2	NM_006540	11, 12, 13, 14	5'	Fusion
NTRK3	NM_002530	13, 14, 15	3'	Fusion
NTRK3	NM_002530	13, 14, 15, 16	5'	Fusion
PDGFB	NM_002608	2,3	5'	Fusion
PLAG1	NM_002655	1,2,3,4	5'	Fusion
ROS1	NM_002944	31,32,33,34,35,36,37	5'	Fusion
SS18	NM_001007559	10, 11	5'	Fusion
SS18	NM_001007559	4,5,6,8,9,10	3'	Fusion
STAT6	NM_001178078	1,2,3,4,5,6,7,16,17,18,19	5'	Fusion
TAF15	NM_139215	6,7	5'	Fusion
TAF15	NM_139215	5,6,7	3'	Fusion

TCF12	NM_207036	4,5,6	3'	Fusion
TFE3	NM_006521	3,4,5,6	5'	Fusion
TFG	NM_006070	4,5,6,7	3'	Fusion
TFG	NM_006070	6	5'	Fusion
USP6	NM_004505	1,2,3,	5'	Fusion
YWHAE	NM_006761	5	3'	Fusion

Panel characteristics

General: Data analysis is performed in Archer Analysis software. The used "pipeline" version can be obtained on request. Unless otherwise stated only " strong evidence" fusions are reported.

Detection of fusion, variants and exon skipping events can be detected depending on the variant type, sequence context, sample DNA quality and quantity.

For reliable analysis the following requirements have to be met:

(1) QC score (Cq) should be < 30. If Cq 30-31, the fusionplex is less reliable, if Cq >31, quality is unsuitable.

(2) The number of reads per sample should be > 1.5M

(3) The percentage of RNA reads should be > 40%