ARCHER™ FUSIONPlex™

Archer™ FusionPlex™ Oncology Research Panel

The Archer FusionPlex Oncology Research Panel is a targeted next generation sequencing (NGS) assay to simultaneously detect and identify fusions and other mutations associated with 74 genes linked to various cancers. This panel is purpose built to advance fusion discovery and extend the reach of precision medicine, including research efforts in the area of Philadelphia chromosome-like acute lymphoblastic leukemia (Ph-like ALL).

FusionPlex RNA sequencing assays are powered by Anchored Multiplex PCR (AMP™) enrichment chemistry. By ligating molecular barcode adapters at random cDNA ends and using gene-specific primers, AMP delivers known and novel gene fusion detection.

This comprehensive fusion panel is designed for oncology research and includes these targets:

- Fusion genes associated with solid tumors, sarcomas and hematological cancers
- Well-characterized Ph-like ALL biomarkers
- Proto-oncogene targets to drive novel fusion discovery

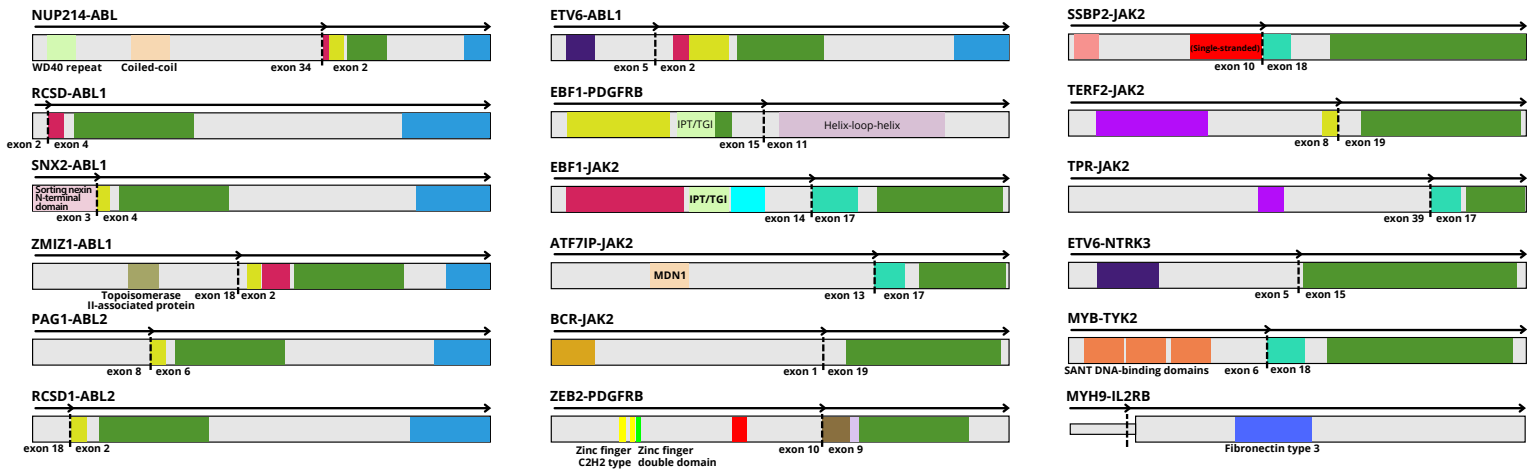For Research Use Only. Not for use in diagnostic procedures.

Assay Targets

This panel includes specific breakpoints in genes, known to form fusions in solid tumors, sarcomas and Ph-like ALL.

ABL1	ERBB2	INSR	NRG1	RARA
ABL2	ERBB4	JAK1	NTRK1	RELA
AKT1	ERG	JAK2	NTRK2	RET
AKT2	ESPR1	JAK3	NTRK3	ROS1
AKT3	ESRRA	KIT	NUMBL	RSPO2
ALK	ETV1	MAML2	NUT	RSPO3
ARHGAP26	ETV4	MAST1	PDGFRA	SYK
AXL	ETV5	MAST2	PDGFRB	TERT
BRAF	ETV6	MET	PIK3CA	TFE3
BRD3	EWSR1	MSMB	PKN1	TFEB
BRD4	FGFR1	MUSK	PPARG	THADA
CRLF2	FGFR2	MYB	PRKCA	TMPRSS2
CSF1R	FGFR3	MYC	PRKCB	TSLP
EGFR	IL2RB	NOTCH	RAF1	TYK2
EPOR	FGR	NOTCH1	PTK2B	

Learn more about the Oncology Research Panel at
archerdx.com/oncology-research

Includes solid tumor, sarcoma and Ph-like ALL targets

Philadelphia chromosome-like acute lymphoblastic leukemia is characterized by modifications in lymphoid transcription factor genes, poor outcomes and a gene-expression profile similar to that of BRC-ABL1 ALL. Ph-like ALL-specific fusions are indicated below[1].

Legend:
- Coiled-coil
- DNA binding domain
- F actin binding
- Helix-loop helix
- LisH domain
- Pointed domain
- Pseudokinase domain
- SH2 domain
- SH3 domain
- TPR/MLP1/MLP2-like protein
- Tyrosine kinase domain

NUP214-ABL — WD40 repeat, Coiled-coil, exon 34 / exon 2
RCSD-ABL1 — exon 2 / exon 4
SNX2-ABL1 — Sorting nexin N-terminal domain, exon 3 / exon 4
ZMIZ1-ABL1 — Topoisomerase II-associated protein, exon 18 / exon 2
PAG1-ABL2 — exon 8 / exon 6
RCSD1-ABL2 — exon 18 / exon 2

ETV6-ABL1 — exon 5 / exon 2
EBF1-PDGFRB — IPT/TGI, Helix-loop-helix, exon 15 / exon 11
EBF1-JAK2 — IPT/TGI, exon 14 / exon 17
ATF7IP-JAK2 — MDN1, exon 13 / exon 17
BCR-JAK2 — exon 1 / exon 19
ZEB2-PDGFRB — Zinc finger C2H2 type, Zinc finger double domain, exon 10 / exon 9

SSBP2-CSF1R — Single-stranded DNA binding protein, exon16 / exon 12
ETV6-JAK2 — exon 4 / exon 17
SSBP2-JAK2 — Single-stranded, exon 10 / exon 18
TERF2-JAK2 — exon 8 / exon 19
TPR-JAK2 — exon 39 / exon 17
ETV6-NTRK3 — exon 5 / exon 15
MYB-TYK2 — SANT DNA-binding domains, exon 6 / exon 18
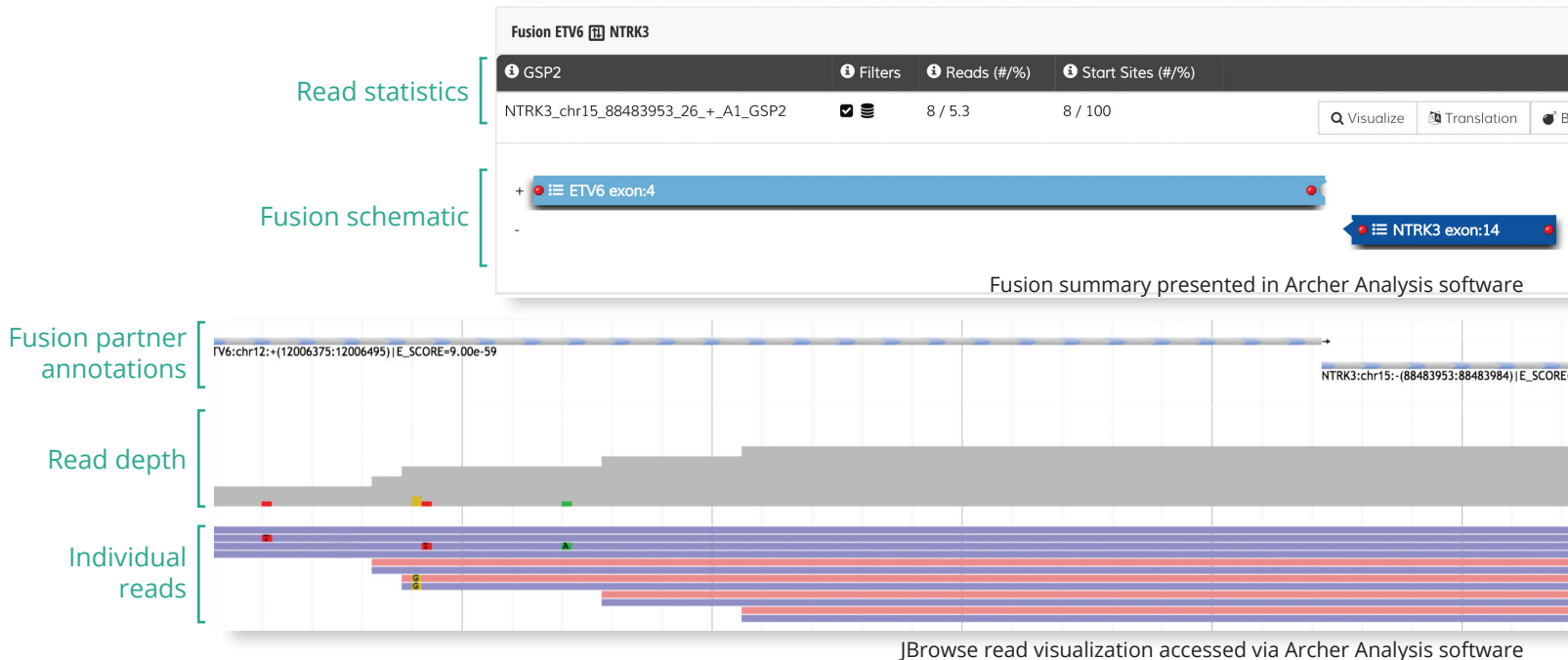MYH9-IL2RB — Fibronectin type 3

(1) Figure derived from Roberts, et al., NEJM 371, 1005-1015 (2014).

Fusion detection at single-nucleotide resolution

The FusionPlex Oncology Research Panel works in conjunction with Archer Analysis software to detect both known and novel fusions. By measuring unique reads and start sites, Archer Analysis delivers accurate and quantitative digital results. Archer Analysis uses a standard cutoff of 5 unique molecules to call a fusion.

In the figures below, RNA extracted from fusion-positive cells was mixed with normal lung RNA in a 1:100 ratio. Unique fusion molecules were detected in 100ng RNA containing 1% (1ng) fusion-positive material.

Fusion ETV6 NTRK3

Read statistics				
GSP2	Filters	Reads (#/%)	Start Sites (#/%)	
NTRK3_chr15_88483953_26_+_A1_GSP2	☑	8 / 5.3	8 / 100	Visualize / Translation / B

Fusion schematic: + ETV6 exon:4 — NTRK3 exon:14

Fusion summary presented in Archer Analysis software

Fusion partner annotations: ETV6:chr12:+(12006375:12006495)|E_SCORE=9.00e-59 ; NTRK3:chr15:-(88483953:88483984)|E_SCORE

Read depth

Individual reads

JBrowse read visualization accessed via Archer Analysis software

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