One Workflow. Clear Heme Insights.

Reliable fusion identification for hematologic malignancy questions that matter most.

Archer FUSION*Plex* Heme Solutions

Confidently identify known and novel gene fusions in hematologic malignancy research even when fusions are structurally complex, heterogeneous, and difficult to identify. FUSION*Plex* next generation sequencing (NGS) solutions meet this challenge using Anchored Multiplex PCR (AMP™) chemistry and purpose-built Archer Analysis to deliver partner-agnostic gene fusion identification.

Why FUSION*Plex*?

Designed for fusion discovery

AMP chemistry uses anchored gene-specific primers designed to identify known and novel fusions. By targeting RNA to capture expressed fusion transcripts, FUSION*Plex* **avoids the economic and technical challenges** that arise from sequencing large, repeat-rich intronic regions in DNA-based assays. Paired with de novo read assembly in Archer Analysis FUSION*Plex* delivers **analytically sensitive** and biologically meaningful fusion identification.

Designed to evolve with heme research

FUSION*Plex* panels are curated to cover established biomarkers and **built to grow** as new targets emerge. Designed for flexibility, panels scale effortlessly from small exploratory studies to fast-paced, time sensitive projects, providing **long-term confidence** and continuity to advance heme malignancy research.

Designed for practical, end-to-end use

FUSION*Plex* combines easy-to-use library preparation chemistry for manual or **automated workflows** with purpose-built NGS analytics, making results straightforward to generate. The intuitive, user-friendly fusion visualizations on Archer Analysis and the curated Quiver fusion database support **efficient data exploration and interpretation**.

A foundation for confident fusion research

FUSION*Plex* delivers the reliability and flexibility you need to understand fusion biology across heme malignancies.

> “One of the most significant recent advances in blood cancer research has been improved access to accurate, reliable, and rapid genomic profiling tools. Using the Archer FUSIONPlex Pan Heme panel has enabled identification of rare fusion genes and other RNA variants of interest. Insights generated can inform downstream assay development, including the design of custom real time PCR and digital PCR assays. The flexibility and sensitivity of these approaches support studies into residual disease biology and related research questions.”
>
> **Robert Baker, BSc, MSc**
>
> Molecular Haematology Operations Manager, Health Service Laboratories

Watch the webinar by Robert Baker

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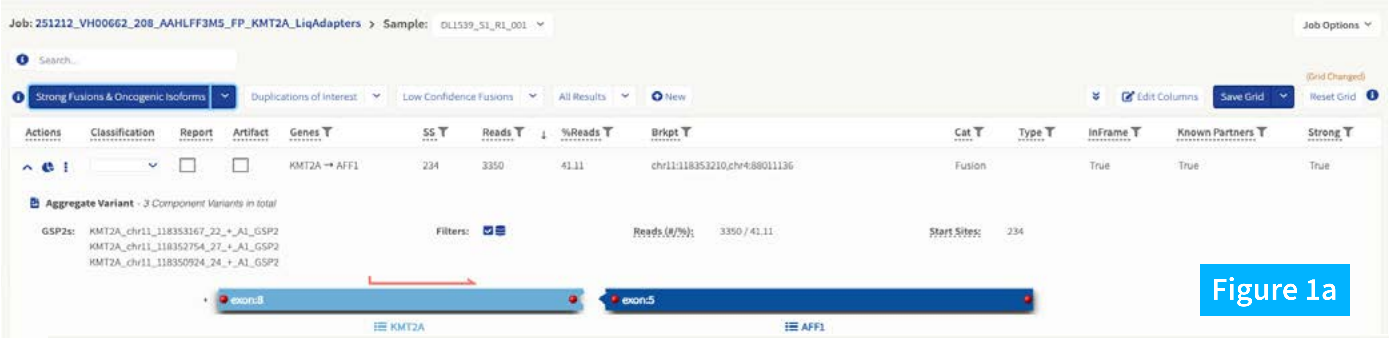
INTEGRATED DNA TECHNOLOGIES

Proven performance on a challenging fusion gene: KMT2A

KMT2A rearrangements are among the most relevant yet most complex fusion events in heme malignancies. The gene's size, breakpoint diversity, and numerous fusion partners make KMT2A a strong test of any fusion identification assay.

FUSION*Plex* is designed to address complexity

Bring FUSIONPlex into your lab to confidently call difficult fusions, such as KMT2A, and accelerate discovery of novel fusion partners with strong read support and consistent on-target performance. Powered by AMP chemistry, it reliably handles complex fusion biology that is often difficult or inefficient with traditional PCR-based approaches, FISH, opposing-primer RNA-based NGS, or hybrid-capture DNA-based NGS. FUSION*Plex* delivers high-confidence KMT2A fusion calls in two canonical KMT2A cell line models (MV411 and THP1).



Job: 251212_VH00662_208_AAHLFF3M5_FP_KMT2A_LiqAdapters > Sample: DL1539_S1_R1_001

Actions	Classification	Report	Artifact	Genes	SS	Reads	%Reads	Brkpt	Cat	Type	InFrame	Known Partners	Strong
		☐	☐	KMT2A → AFF1	234	3350	41.11	chr11:118353210,chr4:88011136	Fusion		True	True	True

Aggregate Variant - *3 Component Variants in total*

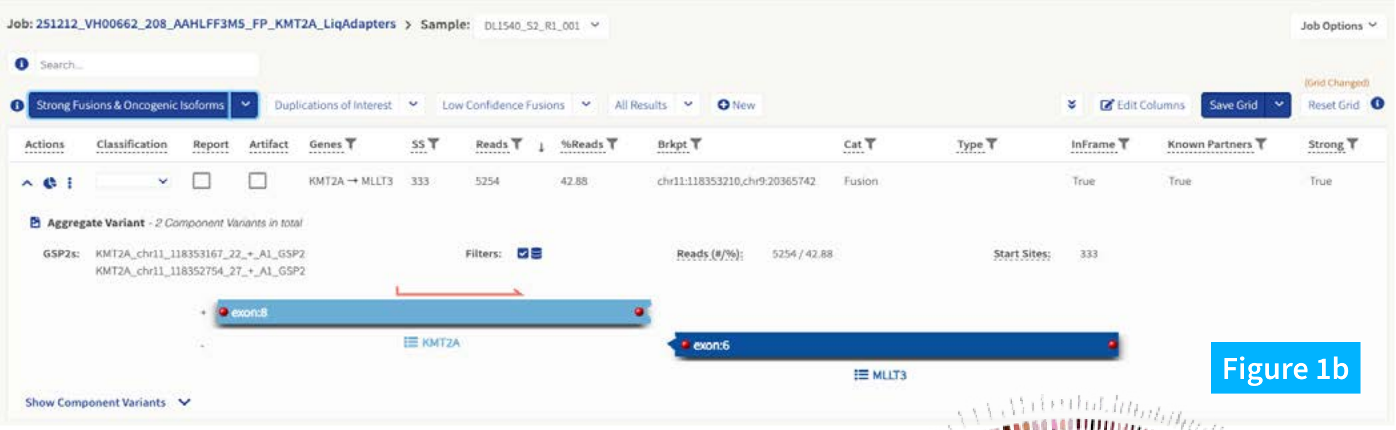
GSP2s: KMT2A_chr11_118353167_22_+_A1_GSP2
KMT2A_chr11_118352754_27_+_A1_GSP2
KMT2A_chr11_118350924_24_+_A1_GSP2

Filters: ☑

Reads (#/%): 3350 / 41.11

Start Sites: 234

Figure 1a



Job: 251212_VH00662_208_AAHLFF3M5_FP_KMT2A_LiqAdapters > Sample: DL1540_S2_R1_001

Actions	Classification	Report	Artifact	Genes	SS	Reads	%Reads	Brkpt	Cat	Type	InFrame	Known Partners	Strong
		☐	☐	KMT2A → MLLT3	333	5254	42.88	chr11:118353210,chr9:20365742	Fusion		True	True	True

Aggregate Variant - *2 Component Variants in total*

GSP2s: KMT2A_chr11_118353167_22_+_A1_GSP2
KMT2A_chr11_118352754_27_+_A1_GSP2

Filters: ☑

Reads (#/%): 5254 / 42.88

Start Sites: 333

Figure 1b

Figure 1a and 1b. Archer Analysis shows strong, in frame KMT2A fusion calls with high read support and Quiver annotation across two independent KMT2A-positive cell lines MV4 11 (KMT2A:AFF1) and THP 1 (KMT2A:MLLT3).

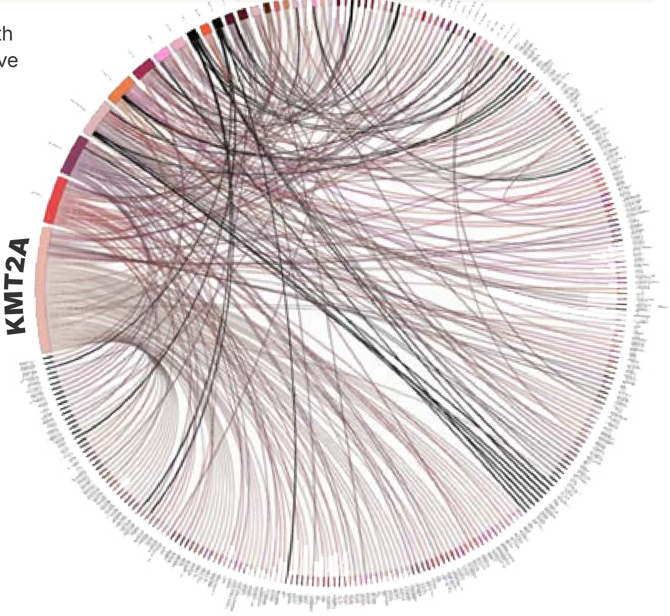


Figure 2. Circos plot shows the broad landscape of gene fusions in hematological neoplasms.

Because FUSIONPlex confidently identifies **KMT2A** rearrangements, you can trust its performance across the broader spectrum of heme malignancy fusions.

To discover our comprehensive heme solutions, visit **idtdna.com/blood-cancer-research**