Integrative genome and transcriptome sequencing analysis indicates genetic and epigenetic dysregulation in DS-AML

Xiaotu Ma1, Reis Rhonda2, Quang Tran1, Yanling Liu1, Pandurang Kolekar1, Ramzi Alsallaq1, Zhikai Liang1, Timothy I. Shaw3, Meghana Devineni1, Anne Deslattes Mays4, Ching Lau#4, Johann Hitzler#5, Soheil Meshinchi#2

1: Department of Computational Biology, St. Jude Children's Research Hospital, Memphis, TN. 2: Clinical Research Division, Fred Hutchinson Cancer Research Center, Seattle, WA 3: Department of Biostatistics and Bioinformatics, H. Lee Moffitt Cancer Center and Research Institute, Tampa, FL
4: The Jackson Laboratory for Genomic Medicine, Farmington, CT. 5: The Hospital for Sick Children, Toronto, Canada

Fig.1

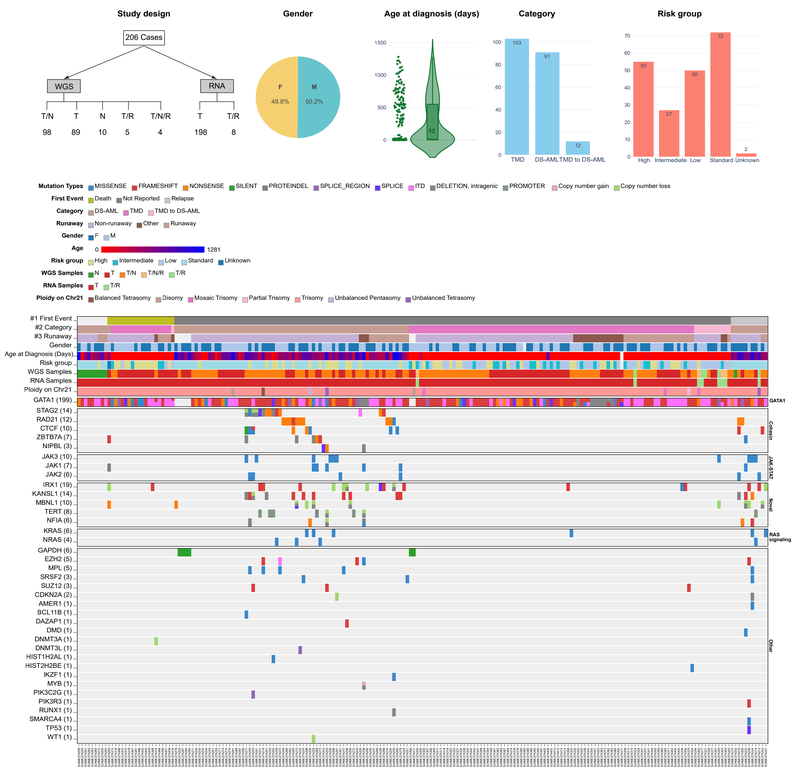


Fig. 2

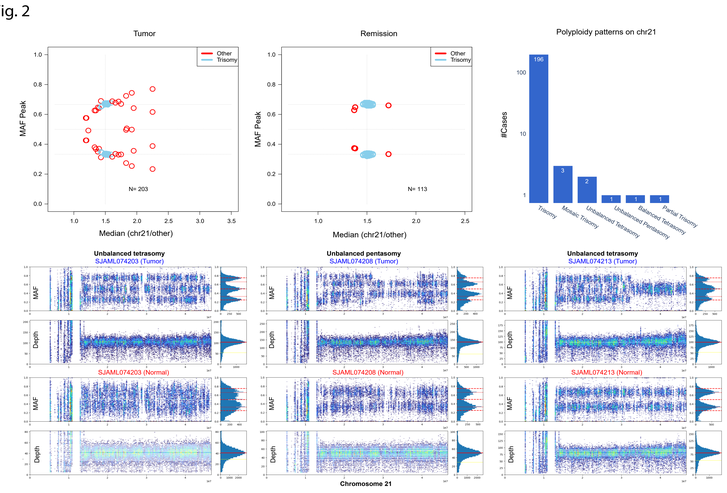


Fig. 3

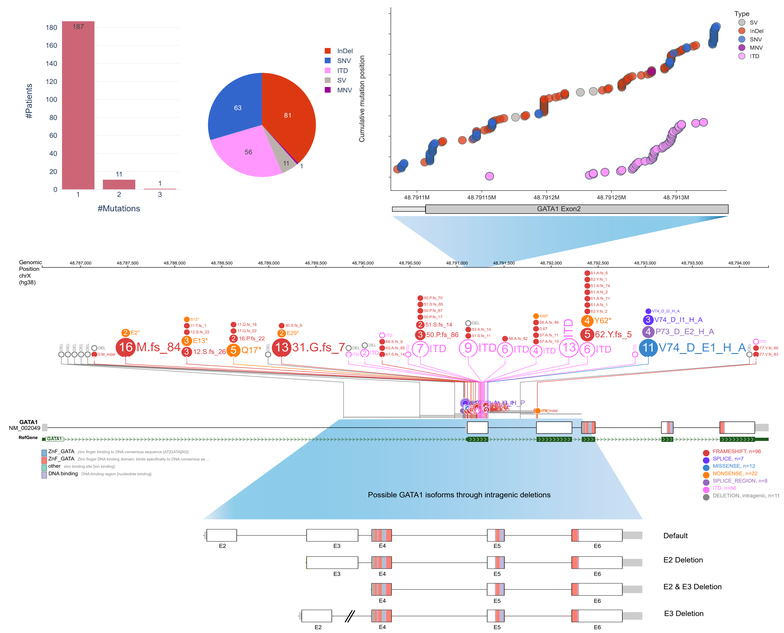


Fig. 5

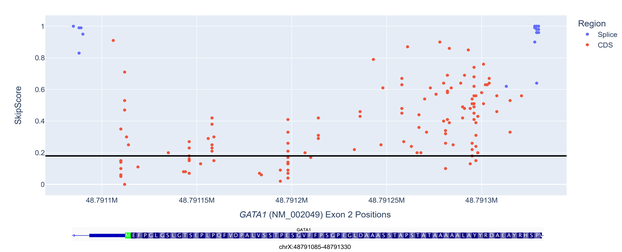


Fig. 6

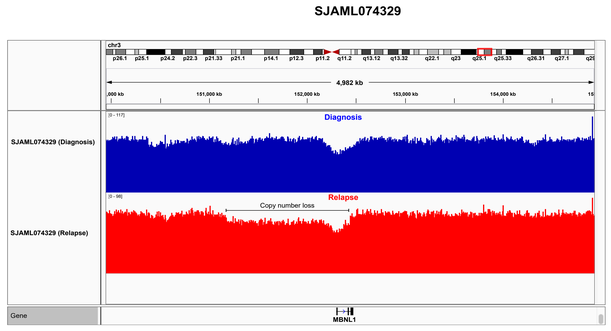
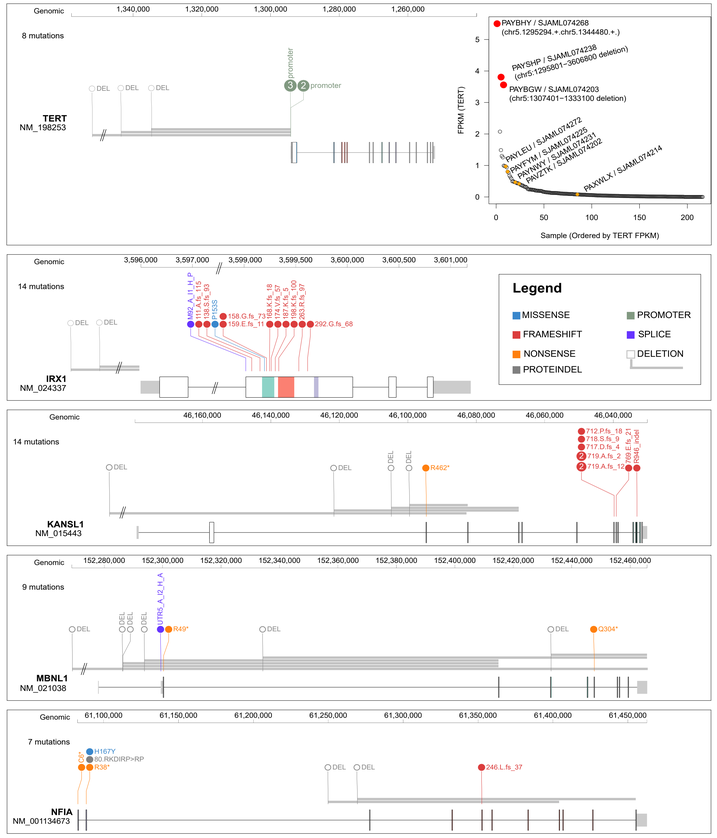
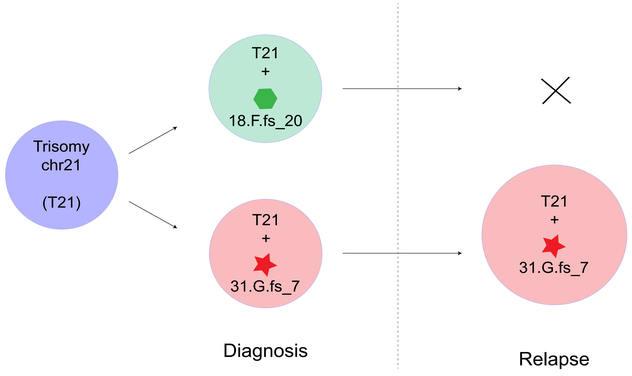


Fig. 4



SJAML074304 (RNA)
GATA1 (NM_002049)



Poster Session Online
American Society of Hematology
Helping hematologists conquer blood diseases worldwide
602. Myeloid Oncogenesis: Basic: Poster III
Xiaotu Ma
MON-4117
ASH2023