

Molecular features of early onset adult myelodysplastic syndrome

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Supplementary Table 1. Panel of 64 genes for somatic targeted deep NGS sequencing

Gene Name			
APC	DHX29	JAK3	RNF25
ASXL1	DNMT3A	KDM6A	RUNX1
BCOR	EED	KIT	SETBP1
BCORL1	ERBB4	KRAS	SF3B1
BTRC	ETV6	MECOM	SIMC1
C7ORF55	EZH2	MED12	SMC3
CALR	FLT3	MLL	SRSF2
CBL	GATA2	NF1	STAG2
CCDC42B	GLI1	NPM1	STAT3
CDH23	GLI2	NRAS	SUZ12
CEBPA	GNB1	OGT	TET2
CFTR	GPR98	PHF6	TP53
CSF1R	IDH1	PRPF8	U2AF1
CUX1	IDH2	PTCH1	U2AF2
DDX41	IRF4	PTPN11	WT1
DDX54	JAK2	RAD21	ZRSR2

Supplementary Table 2. Panel of 66 genes for congenital targeted deep NGS sequencing

Gene Name					
APC	CDKN2A	FANCG	MRE11A	PRF1	SBDS
ATM	CFR	FANCI	MSH2	PRSS1	STK11
ATR	CHEK2	FANCL	MSH6	RAD50	TERT
BARD1	DKC1	FANCM	MUTYH	RAD51	TINF2
BRCA1	ELANE	FH	NBN	RAD51C	TP53
BRCA2	FANCA	G6PC3	NF1	RAD51D	VHL
BRIP1	FANCB	GAR1	NHP2	RPL5	WAS
BUB1B	FANCC	GFI1	NOP10	RPS10	WRAP53
CDAN1	FANCD2	HOXB13	PALB2	RPS19	WT1
CDH1	FANCE	KIF1	PMS2	RTEL1	XRCC2
CDK4	FANCF	MLH1	POT1	RUNX1	XRCC3

Supplementary Table 3. Characteristics of Patients with Myelodysplastic Syndrome (MDS). (MPN- myeloproliferative neoplasm, SAML- Secondary Acute Leukemia)

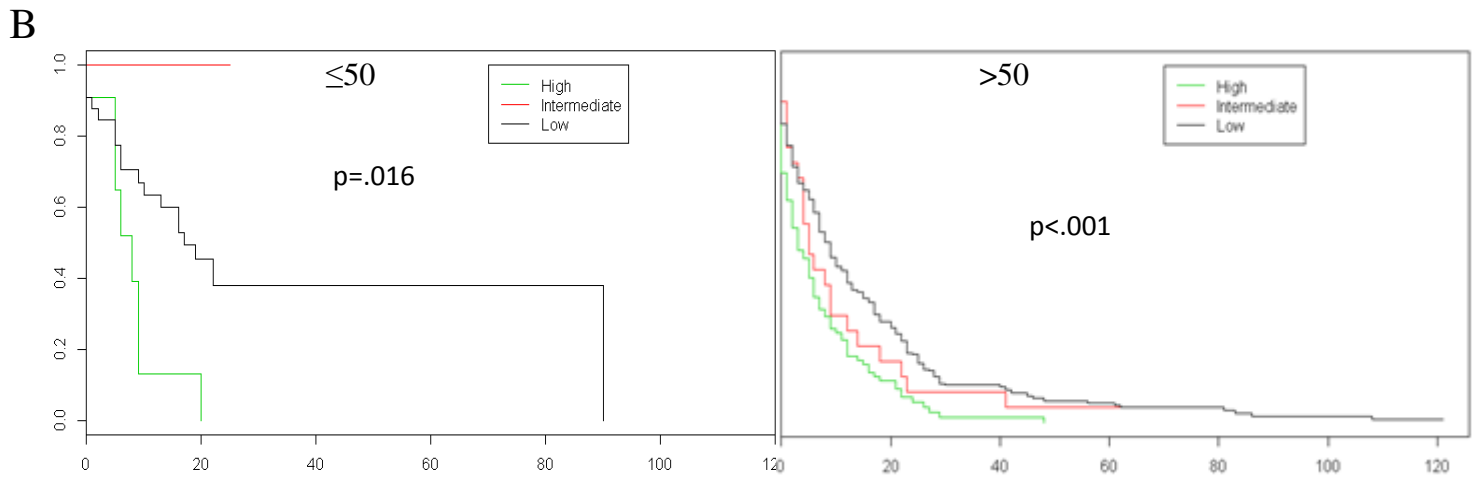
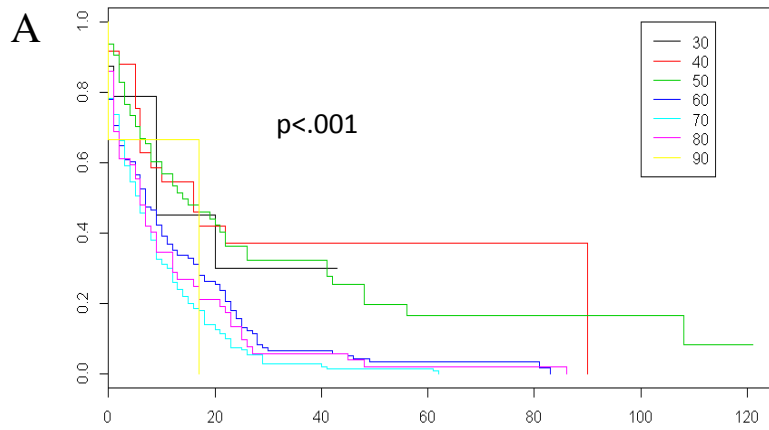
n	Median Age	Gender Male/Female	Low Risk MDS	High Risk MDS	MDS/MPN	sAML
634	68	411/225	249	157	133	95

Supplementary Table 4. Characteristics of Patients with Myelodysplastic Syndrome (MDS) ≤ 50 and >50 years of age.

	≤ 50	>50	p-value
n	65	569	
Age Range	20-50	51-94	
Median Age	44	70	
Gender	M= 26 F= 39	M=385 F= 184	$p < .0001^*$
Low Risk MDS	18	231	$p = .045^*$
High Risk MDS	23	134	$p = .048^*$
MDS/MPN	11	122	$p = .520$
sAML	13	82	$p = .269$
Strong Family History**	33	306	$p = .421$

**Strong family history defined as a patient having a parent or sibling with a history of cancer.

Supplemental Figure 1. A. Comparison of survival between age groups of MDS patients. B. Survival curves of patients ≤ 50 and >50 grouped by molecular risk, as determined by cytogenetics.



Supplemental Figure 2. A) Comparison of the mutational signatures between patients ≤ 50 and >50 . B) Comparison of the mutational signatures between patients with TET2 mutations and those that are wild-type for TET2. C) Number of mutations in patients with and without coexisting TET2 mutations. D) Number of mutations in young and old patients without TET2 mutations.

