Genomic patterns associated with hypoplastic compared to hyperplastic myelodysplastic syndromes

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Supplementary Materials

Supplementary Table 1: Genes for targeted multi-amplicon sequencing panel and functionally associated categories.

Genes	Position	Functionally associated pathways
APC	5q22.2	N/A
ASXL1	20q11.21	N/A
BCOR	Xp11.4	BCOR family
BCORL1	Xq25.1	BCOR family
BTRC	10q24.32	N/A
CALR	19p13.2	N/A
CBL	11q23.3	N/A
CDH23	10q22.1	N/A
CEBPA	19q13.11	N/A
CFTR	7q31.2	N/A
CSF1R	5q32	Receptor tyrosine kinase (RTK) family
CSF3R	1p34.3	Receptor tyrosine kinase (RTK) family
CUX1	7q22.1	N/A
DDX41	5q35.3	DEAD(H)-box protein family
DDX54	12q24.13	DEAD(H)-box protein family
DHX29	5q11.2	DEAD(H)-box protein family
DNMT3A	2p23.3	N/A
EED	11q14.2	PRC2 family
ERBB4	2q34	N/A
ETV6	12p13.2	N/A
EZH2	7q36.1	PRC2 family
FLT3	13q12.2	Receptor tyrosine kinase (RTK) family
GATA2	3q21.3	N/A
GLI1	12q13.3	Hedgehog family
GLI2	2q14.2	Hedgehog family
GNB1	1p36.33	N/A
IDH1	2q34	IDH family
IDH2	15q26.1	IDH family
IRF4	6p25.3	N/A
JAK2	9p24.1	N/A
KDM6A	Xp11.3	N/A
KIT	4q12	Receptor tyrosine kinase (RTK) family
KRAS	12p12.1	RAS family
LUC7L2	7q34	N/A
MECOM	3q26.2	N/A
MED12	Xq13.1	N/A
MLL	11q23	N/A
NF1	17q11.2	RAS family
NPM1	5q35.1	N/A
NRAS	1p13.2	RAS family
PHF6	Xq26.2	N/A
PRPF8	17p13.3	N/A
PTCH1	9q22.32	Hedgehog family

PTPN11	12q24.13	RAS family
RAD21	8q24.11	Cohesin family
RNF25	2q35	N/A
RUNX1	21q22.12	N/A
SETBP1	18q12.3	N/A
SF3B1	2q33.1	N/A
SIMC1	5q35.2	N/A
SMC3	10q25.2	Cohesin family
SRSF2	17q25.1	N/A
STAG2	Xq25	Cohesin family
STAT3	17q21.2	N/A
SUZ12	17q11.2	PRC2 family
TET2	4q24	N/A
TP53	17p13.1	N/A
U2AF1	21q22.3	U2AF family
U2AF2	19q13.42	U2AF family
WT1	11p13	N/A
ZRSR2	Xp22.1	N/A
N/A; not applicable		

Supplementary Table 2. Patient characteristics

	ALL No.	(%)/ [Range]	Hyper-MDS No.	(%)/ [Range]	Hypo-MDS No.	(%)/ [Range]	*P*
Total No.	237		205		32		
Median Age, years	68	[19-87]	68	[19-87]	68	[20-87]	.88
Gender							.53
Male	145	(61)	124	(60)	21	(66)	
Female	92	(39)	81	(40)	11	(34)	
Median WBC x10^9/L	3.3	[.69-30.2]	3.7	[.69-30.2]	2.4	[.85-10.6]	.002
Median ANC x10^9/L	1.5	[.02-170]	1.67	[.02-170]	1.07	[.14-170]	.01
Median hemoglobin, g/dl	9.6	[3.9-14.6]	9.5	[5.9-14.6]	10.4	[3.9-13.2]	.36
Median platelet x10^3/mL	89	[7-776]	90	[7-776]	85	[12-509]	.66
Median BM cellularity %	60	[5-100]	60	[30-100]	20	[5-25]	
IPSS							.08
Low	52	(22)	50	(24)	2	(6)	
Intermediate-1	116	(49)	97	(47)	19	(59)	
Intermediate-2	47	(20)	41	(20)	6	(19)	
High	22	(9)	17	(8)	5	(16)	
IPSS-R							.68
Very Low	32	(14)	29	(14)	3	(9)	
Low	86	(36)	75	(37)	11	(34)	
Intermediate	44	(19)	39	(19)	5	(16)	
High	45	(19)	36	(18)	9	(28)	
Very high	30	(13)	26	(13)	4	(13)	
Cytogenetics by IPSS-R							0.13
Very good	5	(2)	3	(1)	2	(6)	
Good	139	(59)	122	(60)	17	(53)	
Intermediate	42	(18)	33	(16)	9	(28)	
Poor	19	(8)	18	(9)	1	(3)	
Very Poor	32	(14)	29	(14)	3	(9)	

Abbreviations: WBC = white blood cell count, hb = hemoglobin, ANC = absolute neutrophil s count, BM = bone marrow, IPSS = International Prognostic Scoring System, IPSS-R = revised IPSS.

Supplementary Table 3: Mutations type in hypo-MDS

Gene	Mutation	RefSeq	AA change	Chromosome	Change
APC	Missense	NM_001127511	p.Y719H	chr5	c.T2155C
APC	Missense	NM_001127511	p.R1622Q	chr5	c.G4865A
APC	Missense	NM_001127511	p.P2351S	chr5	c.C7051T
ASXL1	Frameshift deletion	NM_015338	p.G643fs	chr20	c.1927delG
ASXL1	Nonsense	NM_015338	p.Y591X	chr20	c.C1773A
BCORL1	Nonsense	NM_021946	p.Q1523X	chrX	c.C4567T
C7orf55	Frameshift deletion	NM_016019	p.248_249del	chr7	c.744_745del
CBL	Missense	NM_005188	p.G415S	chr11	c.G1243A
CDH26	Missense	NM_177980	p.P304S	chr20	c.C910T
CEBPA	Missense	NM_004364	p.T337S	chr19	c.A1009T
DDX41	Missense	NM_016222	p.R525H	chr5	c.G1574A
DDX41	Missense	NM_016222	p.R525H	chr5	c.G1574A
DDX54	Missense	NM_001111322	p.K191N	chr12	c.G573C
DDX54	Missense	NM_001111322	p.M255I	chr12	c.G765A
DNMT3A	Missense	NM_153759	p.G539S	chr2	c.G1615A
EZH2	Missense	NM_001203249	p.D608E	chr7	c.T1824G
GATA2	Missense	NM_001145662	p.K376E	chr3	c.A1126G
GPR98	Nonsense	NM_032119	p.W433X	chr5	c.G1298A
IRF4	Missense	NM_001195286	p.C213F	chr6	c.G638T
JAK2	Missense	NM_004972	p.V617F	chr9	c.G1849T
KDM6A	Missense	NM_021140	p.G284V	chrX	c.G851T
KDM6B	Missense	NM_001080424	p.A879S	chr17	c.G2635T
KRAS	Missense	NM_004985	p.G77A	chr12	c.G230C
MECOM	Missense	NM_004991	p.E60A	chr3	c.A179C
NF1	Missense	NM_000267	p.S2121N	chr17	c.G6362A
NPM1	Missense	NM_199185	p.L258F	chr5	c.C772T
NPM1	Missense	NM_199185	p.L258F	chr5	c.C772T
NPM1	Frameshift insertion	NM_199185	p.L258fs	chr5	c.772_773insTCTG
PRPF8	Missense	NM_006445	p.N287S	chr17	c.A860G
RUNX1	Missense	NM_001001890	p.P68R	chr21	c.C203G
RUNX1	Missense	NM_001001890	p.R135K	chr21	c.G404A
SETBP1	Missense	NM_015559	p.D868N	chr18	c.G2602A
SF3B1	Missense	NM_012433	p.K666N	chr2	c.G1998C
STAG2	Nonsense	NM_006603	p.R604X	chrX	c.C1810T
STAG2	Frameshift insertion	NM_006603	p.V585fs	chrX	c.1753_1754insT
SUZ12	Missense	NM_015355	p.N389D	chr17	c.A1165G
TET2	Frameshift deletion	NM_001127208	p.T621fs	chr4	c.1861delA
TET2	Frameshift deletion	NM_001127208	p.K1004fs	chr4	c.3010delA

TET2	Nonsense	NM_001127208	p.G1407X	chr4	c.G4219T
TET2	Nonsense	NM_001127208	p.Q317X	chr4	c.C949T
TP53	Nonsense	NM_001126112	p.S94X	chr17	c.C281G
U2AF1	Missense	NM_001025203	p.S34F	chr21	c.C101T
U2AF1	Missense	NM_001025203	p.S34F	chr21	c.C101T

Supplementary Figure 1: Overall Survival for Hyper-MDS compared to Hypo-MDS