

Abnormal Hedgehog pathway in myelodysplastic syndrome and its impact on patients' outcome

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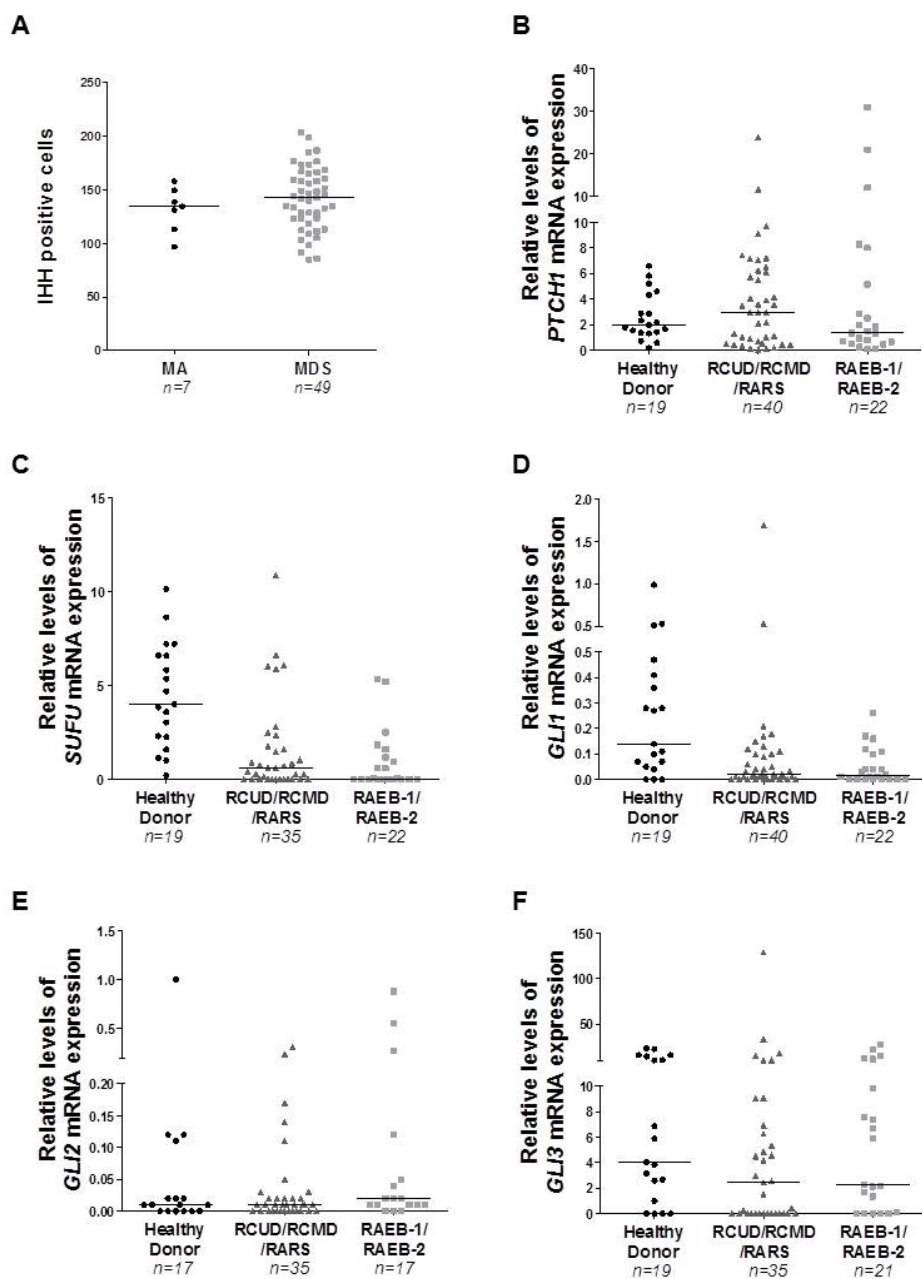
SUPPLEMENTAL DATA MANUSCRIPT 2015/124040

Supplemental Table 1. Multivariate analyses of survival outcomes.

<i>Factor</i>	<i>Event-free survival</i>		<i>Overall survival</i>		<i>AML evolution</i>	
	<i>Hazard Ratio*</i> <i>(95% CI)</i>	<i>P</i>	<i>Hazard Ratio*</i> <i>(95% CI)</i>	<i>P</i>	<i>Hazard Ratio*</i> <i>(95% CI)</i>	<i>P</i>
WHO 2008 classification						
RAEB-1/RAEB-2 vs RCUD/RCMD/RARS	3.08 (1.27-7.48)	0.01	3.38 (1.34-8.55)	0.01	7.75 (2.33-25.75)	0.001
IPSS risk group						
Int-2 / High vs Int-1 /Low	2.85 (1.10-7.40)	0.03	3.11 (1.18-8.13)	0.02	-	-

Abbreviations: MDS: myelodysplastic syndromes; AML: acute myeloid leukemia; WHO: World Health Organization; RCUD: Refractory Cytopenia with Unilineage Dysplasia; RCMD: Refractory Cytopenia with Multilineage Dysplasia; RARS: Refractory Anemia with Ringed sideroblasts; RAEB-1: Refractory Cytopenia with Excess Blasts – 1; RAEB-2: Refractory Cytopenia with Excess Blasts – 2 IPSS: International Prognostic Scoring System; Int: intermediate.

* Hazard ratio >1 indicates that the first feature has the poorest outcome.



Supplemental Figure 1. Hedgehog pathway element expressions in MDS bone marrow. (A) Immunohistochemical quantification of IHH in bone marrow biopsies from MDS, and from megaloblastic anemia (MA) patients. Graph shows quantitative analysis of IHQ, where random four high-powered fields from stained slides were captured at 20x objective magnification and visualized

for manual scoring for positive cells, using ImageJ (<http://imagej.nih.gov/ij/>). Horizontal lines indicate medians of positive cells for IHH. Quantitative PCR analysis of (B) *PTCH1*, (C) *SUFU*, (D) *GLI1*, (E) *GLI2* and (F) *GLI3* mRNA expression in total bone marrow cells from healthy donors and from patients with MDS stratified according to the WHO 2008 classification. Expression of *HPRT* transcripts was used as an endogenous control. The relative gene expression was calculated using the equation $2^{-\Delta\Delta CT}$ ¹⁷. Horizontal lines indicate medians. The numbers of individuals are indicated in the graph. ANCOVA followed by post-hoc Tukey. After adjustment for age, *P* values were >0.05 for all gene expressions shown.