Strategies for identifying *NUP98* rearrangements in adult myeloid neoplasms

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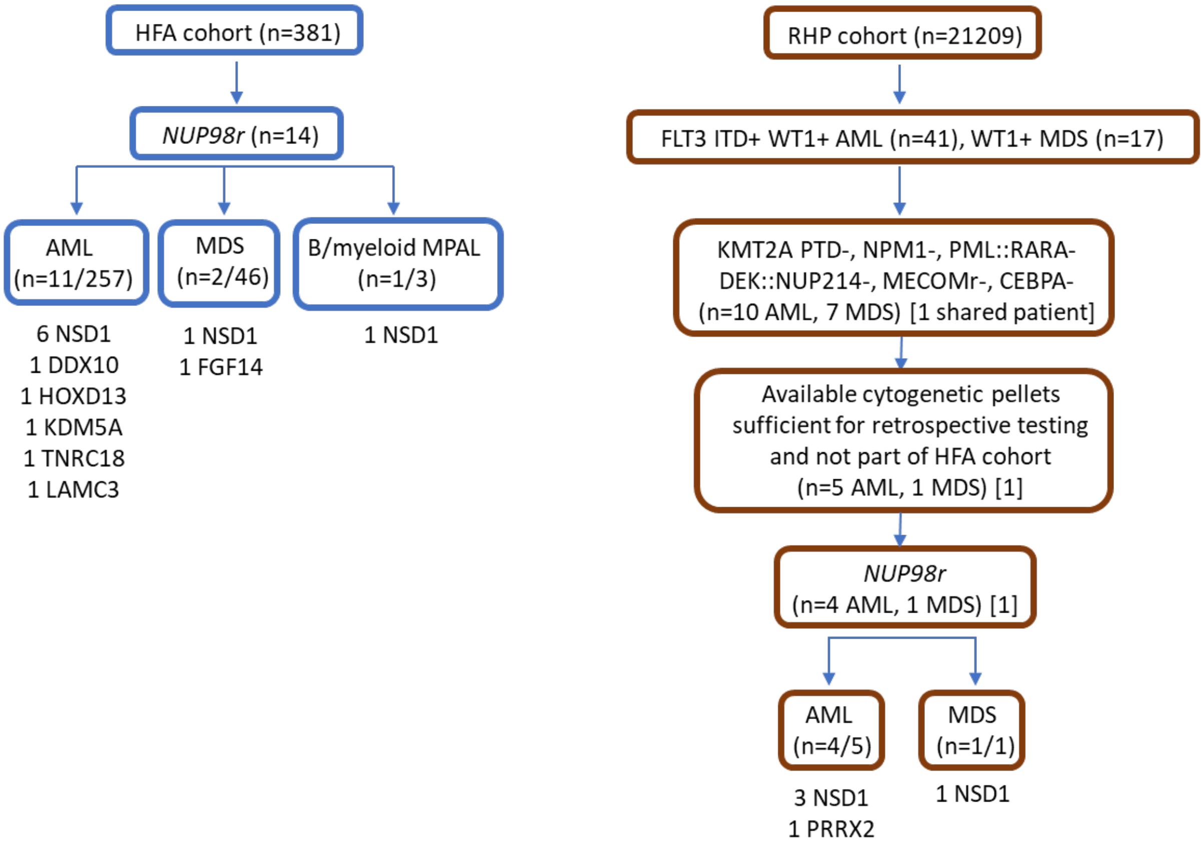
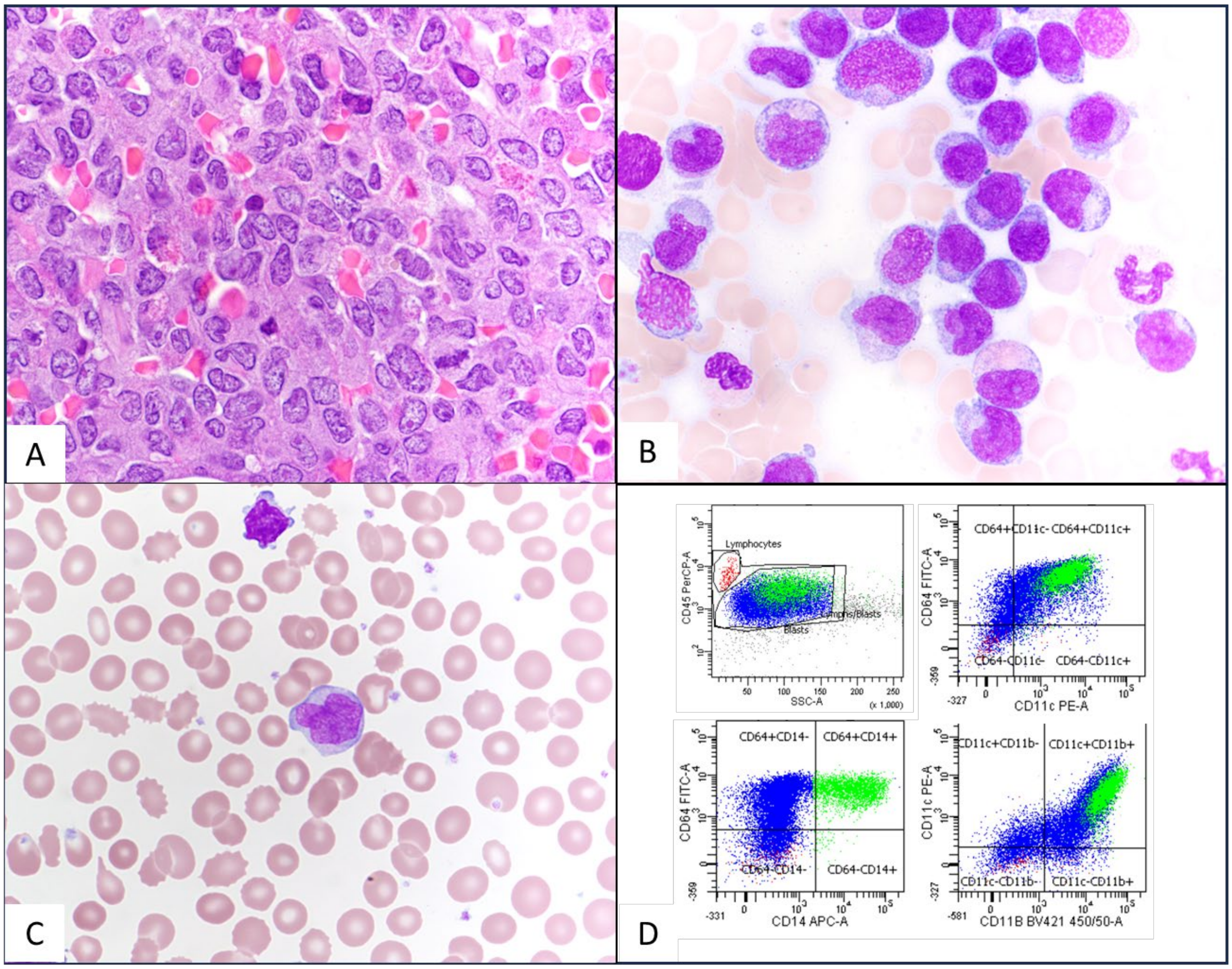
Supplemental Fig 1: HFA and RHP cohorts and *NUP98r* results



Supplemental Fig 2: *NUP98*r AML with monocytic differentiation



Supplemental Figure Legends

Supplemental Fig 1: Schematic of the Heme Fusion Assay (HFA) and Rapid Heme Panel (RHP) cohorts and *NUP98*r results.

Supplemental Fig 2. *NUP98*r AML with monocytic differentiation. Representative images of monocytic differentiation by morphology of A) bone marrow core biopsy (Hematoxylin and Eosin stain, 1000x), B) bone marrow aspirate smear (Wright-Giemsa stain, 1000x), and C) peripheral blood smear (Wright stain, 1000x), as well as flow cytometric analysis in D) showing monocytic blasts (blue population) expressing CD64 (largely), CD11C (dim) and CD11b (largely) and negative for CD14; mature monocytes are shown as the green population.

Supplemental Table Legends **See Excel File**

Supplemental Table 1: International Prognostic Scoring System-Molecular (IPSS-M) scores of MDS cases in the Heme Fusion Assay (HFA) clinical cohort

Supplemental Table 2: All mutations detected in cases from the HFA and Rapid Heme Panel (RHP) cohorts at the initial bone marrow biopsy, including transcript ID and variant allele fraction

Supplemental Table 3: Breakpoints of *NUP98* and the partner genes, including transcript, exon, and coordinates

Supplemental Table 4: *NUP98* fusions detected in public MDS RNA-sequencing data

Supplemental Table 5: *WT1* loss of function mutations expressed in public MDS RNA-sequencing data

Supplemental Table 6: Leucegene AML samples with *WT1* mutations +/- *FLT3*-ITD