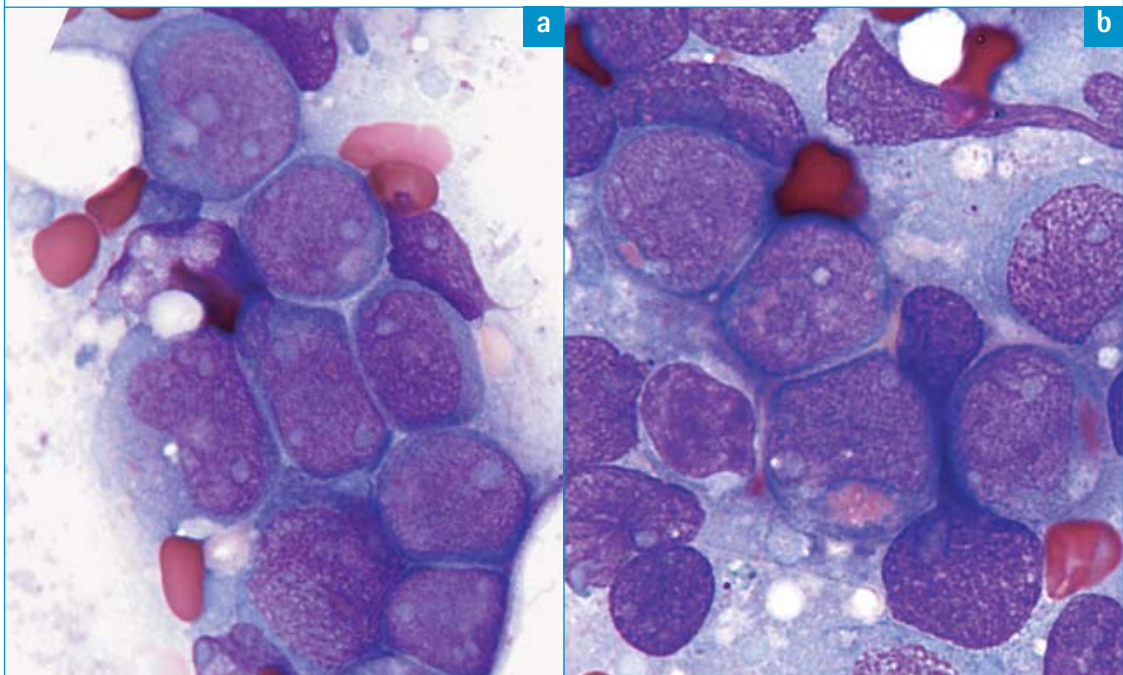


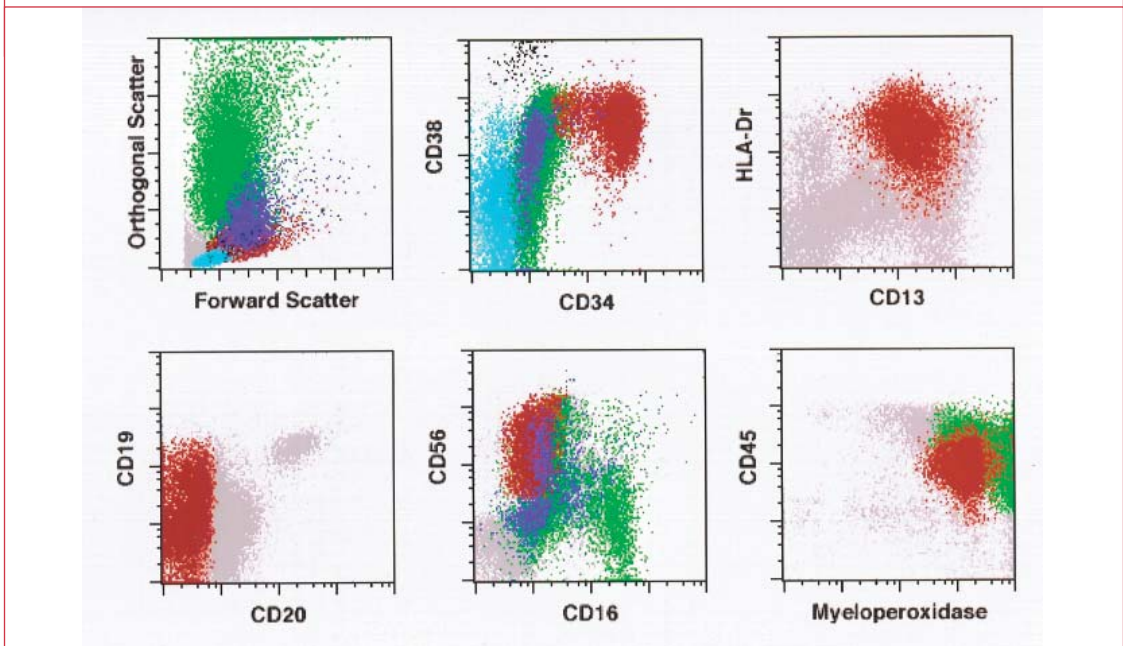
i46.5 AML with t(8;21)(q22;q22); (RUNX1-RUNX1T1)

Myeloblasts show **a** characteristic perinuclear hofs and **b** salmon colored cytoplasmic granules. These features are typically more prominent in the bone marrow and less apparent in the peripheral blood.



f46.1 Flow cytometry histograms of the bone marrow from a patient with AML with t(8;21)(q22;q22)

The leukemic blasts (red) express CD34, CD38, CD13, HLA-Dr, partial CD19, CD56, CD45 and myeloperoxidase, characteristic of AML with a t(8;21). The blasts lack expression of CD20 and CD16.



AML with *t(8;21)(q22;q22)* (*RUNX1-RUNX1T1*) and AML with *inv(16)*

(p13.1q22) or *t(16;16)(p13.1;q22)* (*CBFB-MYH11*) comprise the core binding factor leukemias, with disruption of the core binding factor α and β subunits, respectively. Core binding factor leukemias are associated with a favorable prognosis in children and adults, especially when treated with repetitive cycles of high-dose cytarabine (HiDAC) post-remission. Cases of *t(8;21)* AML with a WBC $>20 \times 10^3/\text{mm}^3$ ($>20 \times 10^9/\text{L}$) at presentation appear to behave more like intermediate risk disease and may benefit from allo-SCT in first remission. Mutations of *KIT* in core binding factor AML are common (20%-25%). In adults, *KIT* mutations in exons 8 and exon 17 appear to worsen prognosis. It is unclear if they have a similar prognostic effect in children, or whether *t(8;21)* AML with *KIT* mutation benefits from allo-SCT in first remission. Mutations in *FLT3* are very uncommon in core binding factor leukemia. Additional cytogenetic abnormalities are present in the majority of *t(8;21)* AML, most commonly including loss of a sex chromosome, or partial deletion of the long arm of chromosome 9 [del(9q)]. The presence of an unfavorable additional cytogenetic abnormality, such as monosomy 7, may adversely impact prognosis.

RT-PCR may detect *RUNX1-RUNX1T1* transcripts in the absence of any clinical disease. The mRNA can be detected in some stem cells, mature monocytes, and hematopoietic progenitors during remission. Quantitative PCR, measuring the kinetics of *RUNX1-RUNX1T1* transcripts, appears more useful for monitoring minimal residual disease.

46.1.2 AML With *inv(16)(p13;q22)* or *t(16;16)(p13;q22)*, (*CBFB-MYH11*)

AML with an *inv(16)(p13;q22)* or *t(16;16)(p13;q22)* comprises 10% of adult AML, and approximately 6% of childhood AML. The *inv(16)(p13;q22)* is a pericentric inversion of chromosome 16 [i46.6](#). The genes at the breakpoint junction are the β subunit of CBF factor

i46.6 Typical bone marrow karyotype of AML with *inv(16)(p13.1q22)*