Associations between dysplastic findings and somatic mutations in de novo acute myeloid leukemia (AML)

Patients with de novo AML without WHO-defined cytogenetic abnormalities
- 81% (n=137) normal karyotype
- 18% (n=31) abnormal karyotype

Targeted sequencing on bone marrow aspirates for recurrent mutations associated with myeloid malignancies:
- DNA methylation
- Epigenetic regulators
- Transcription factors
- Cohesin complex
- RAS pathway
- Splicesome pathway

Degree of displasia according to mutational pathways

- **Cohesin pathway mutations**
  - STAG2 mutations
    - a higher degree of megakaryocytic dysplasia (q=0.046)
    - marginally with greater overall megakaryocytic dysplasia (q=0.064)
    - and marginally with greater overall myeloid lineage dysplasia (q=0.052)

- **RAS pathway mutations**
  - RIT1 mutations
    - marginally with greater degree of megakaryocytic dysplasia
    - marginally with greater overall myeloid lineage dysplasia (q=0.056)

Dysplastic features in de novo AML

- Megakaryocytes with separated nuclear lobes
- Small size megakaryocytes
- Megakaryocytes with hypogranular cytoplasm and abnormal nuclear lobulation
- Dysplastic erythroid cells with irregular nuclear contours

*Weinberg et al., Haematologica, 2018*