Acute myeloid leukaemia (AML) is a heterogeneous disease. Performance status, geriatric assessment, secondary leukaemia following myelodysplastic syndrome or cytotoxic treatment, common laboratory parameters, leukaemic stem cell frequency, bone marrow microenvironment, gene expression levels, epigenetic changes, micro-RNA's as well as kinetics and depth of response to treatment influence prognosis of AML patients. For patients with cytogenetically normal AML, prognosis can be specified by mutational status of the genes NPM1, FLT3 and CEBPA.