The focus of this thesis is on the prognosis of patients with AML and the detection of leukemic cells that remain after treatment. The method that is used to detect these cells is immunophenotyping by FACS analysis. This technique allows to confirm lymphatic or myeloid origin of cells, as well as differentiation stage of cells, based on the expression of cell surface lineage markers. This is of importance not only at diagnosis, but also at relapse. Apart from that, aberrant expression of cell surface markers has been shown to be of importance in predicting prognosis of patients with AML, but also to discriminate normal from neoplastic cells. Since AML is a very heterogeneous disease with respect to the cell surface marker “make up” of the cells, every newly diagnosed AML needs to be analyzed for aberrantly expressed marker combinations, to assess a unique immunophenotypic fingerprint. This unique fingerprint can then be used to detect leukemic cells among normal blasts in the bone marrow of patients treated with high dose chemotherapy. Minimal residual disease (MRD) is the term for the bulk of leukemic cells that remain in the bone marrow from patients who are morphologically in remission. Since MRD is the resultant of many resistance mechanisms, present both at diagnosis and revealed during treatment, it is generally anticipated that MRD may become the strongest predictor of relapse. During the last two decades there has been increasing interest in the role of the leukemic stem cell (LSC). It has been hypothesized that a primitive cell, resembling the hematopoietic stem cell, is at the origin of AML and, by virtue of inherent therapy resistance, is also responsible for relapse after treatment. Following our previous research, we have focused on the immunophenotypically defined (CD34+CD38-) stem cell, to further fine-tune this LSC compartment by using other flowcytometric parameters. By using a gating strategy that included all parameters, we assessed whether this compartment too has clinical impact in AML.