

1 Supplementary Figures

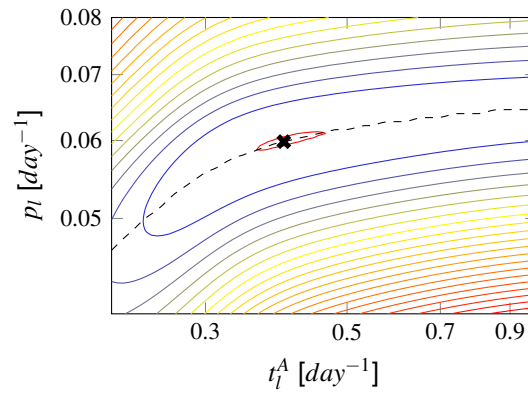


Figure S1: Identifiability analysis for leukemic proliferation rate p_l and leukemic activation rate t_l^A using the profile likelihood. \mathbf{x} indicates starting parameter combination. The red line close to the \mathbf{x} indicates the identifiability threshold.

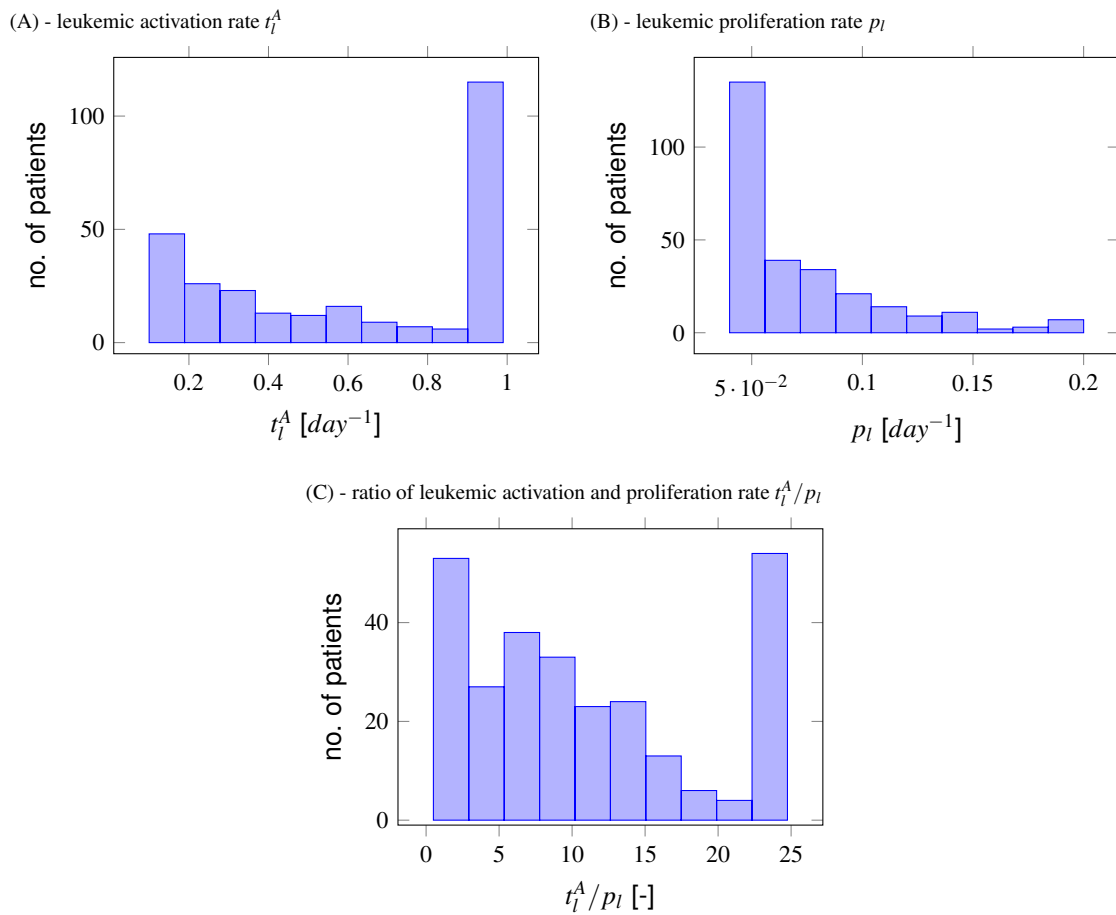


Figure S2: Distribution of leukemic activation rates, leukemic proliferation rates and ratio of leukemic activation and proliferation in the patient cohort.

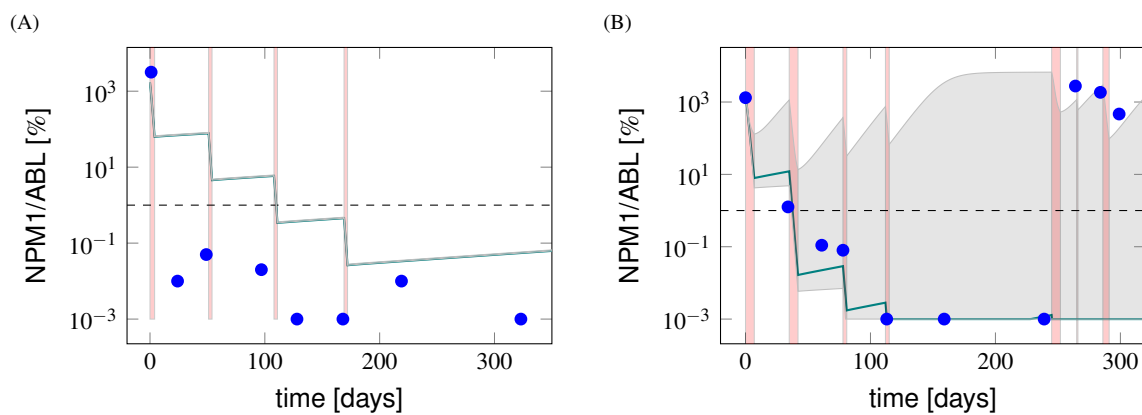


Figure S3: Example time courses with model fit of two patients that the model could not fit adequately.

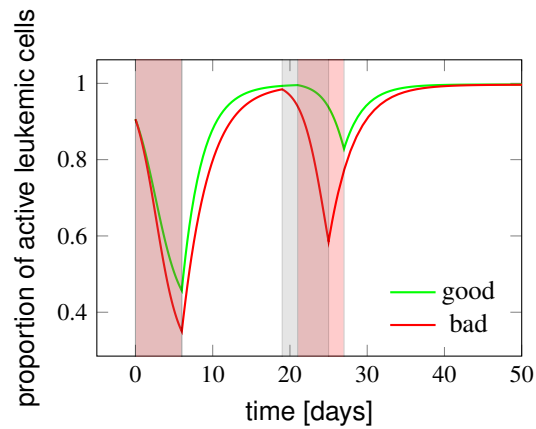


Figure S4: Proportion of active cells within the leukemic cell population for a good therapy responder example patient (PatientID = 3137, therapy marked red) and a bad therapy responder example patient (PatientID = 104, therapy times marked gray). Data and model fit can be found in Figure 2.

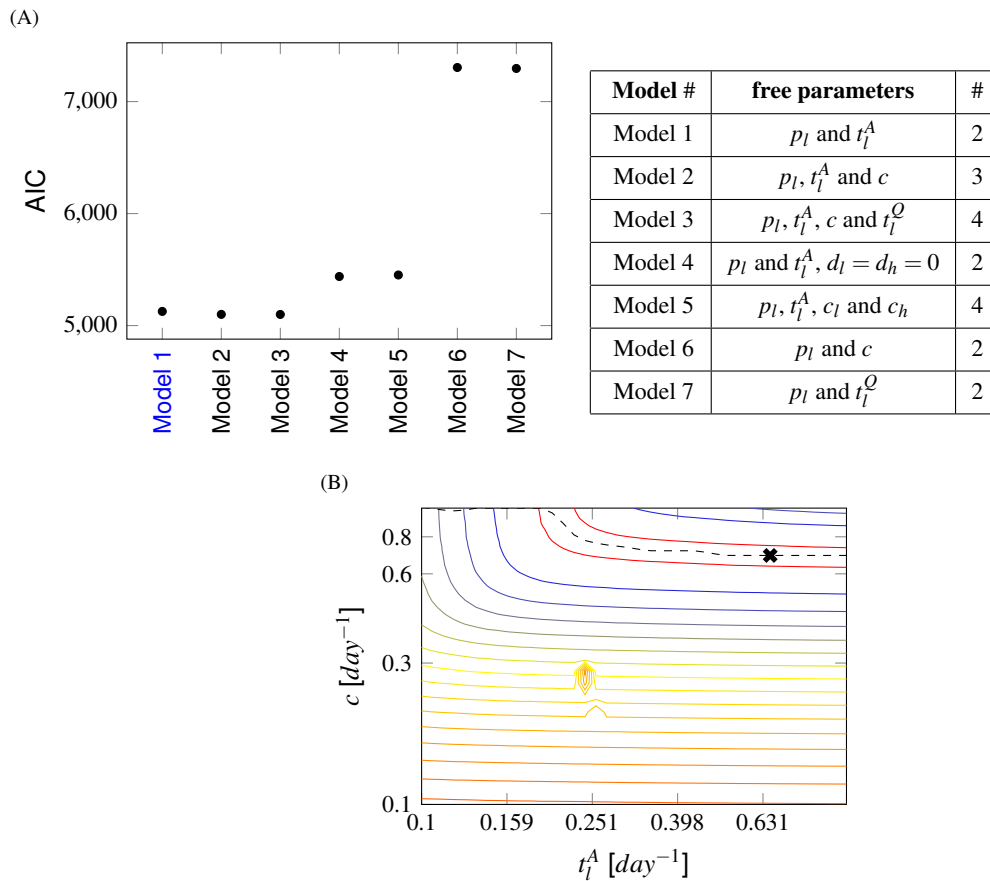


Figure S5: **A** Comparison of 7 different nested models using the Akaike information criterion (AIC), once computed for each individual patient and once for the entire population using the Monolix software (©Lixoft). Model 1: the model used throughout the paper, with 2 free parameters: p_l and t_l^A . Model 2: 3 free parameters: p_l, t_l^A and c . Model 3: 4 free parameters: p_l, t_l^A, c and t_l^Q . Model 4: as Model 1 (2 free parameters) with $d_l = d_h = 0$. Model 5: 4 free parameters: p_l, t_l^A, c_l and c_h . Model 6: 2 free parameters: p_l and c . Model 7: 2 free parameters: p_l and t_l^Q . For details see Supplementary Material. **B** Identifiability analysis for chemotherapeutic kill rate c and leukemic activation rate t_l^A , used as free parameters in model 2 and 3, using the profile likelihood. \mathbf{x} indicates starting parameter combination. The red line close to the \mathbf{x} indicates the identifiability threshold. As the area of this threshold is open to at least one side, the parameters are not identifiable.

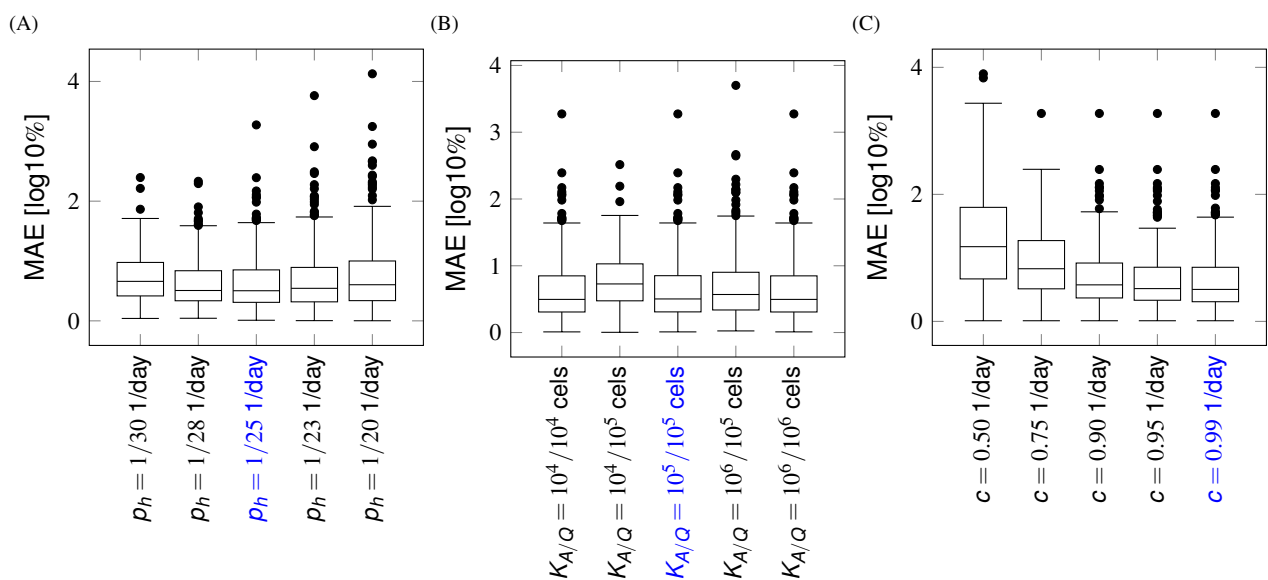


Figure S6: **A** Comparison of boxplots of the mean absolute error (MAE) in log10% for all patient fits for different values of the proliferation rate of healthy cells (p_h). Baseline value is marked blue. **B** Comparison of boxplots of the MAE in log10% for all patient fits for different values of the carrying capacities of the active (K_A) and the quiescent state (K_Q). Baseline value is marked blue. **C** Comparison of boxplots of the MAE in log10% for all patient fits for different values of the chemotherapeutic kill rate c . Baseline value is marked blue. For details see Supplementary Material.

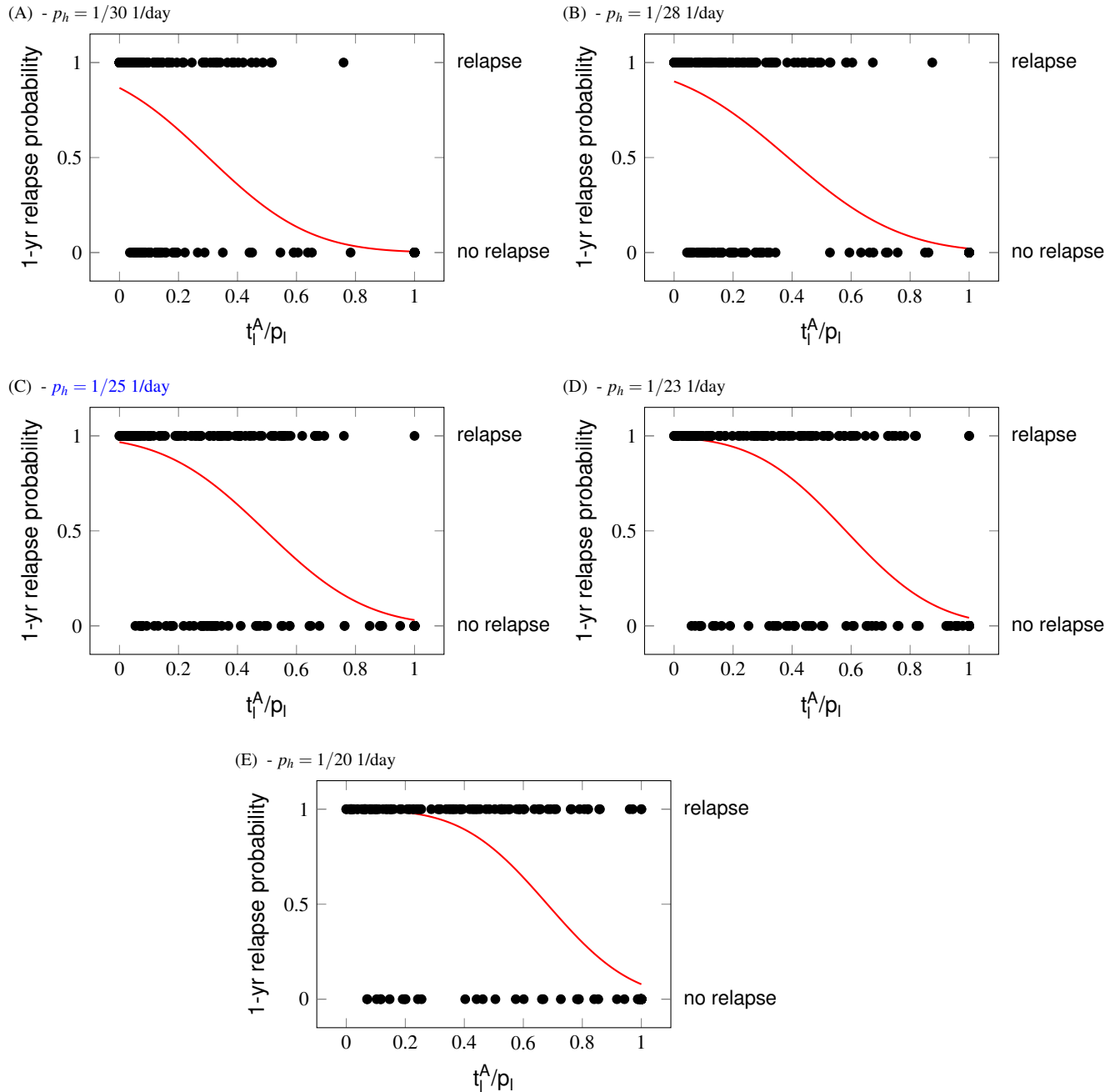


Figure S7: Comparison of 1-year relapse probability (sigmoid function) as estimated by a logistic regression for different values of the proliferation rate of healthy cells (p_h). Baseline value is marked blue. Corresponding patient data (\bullet) indicate the 1-year relapse status (relapse/no relapse) depending on the normalized ratio of the two fitted parameters (t_1^A/p_1).