

Original Article

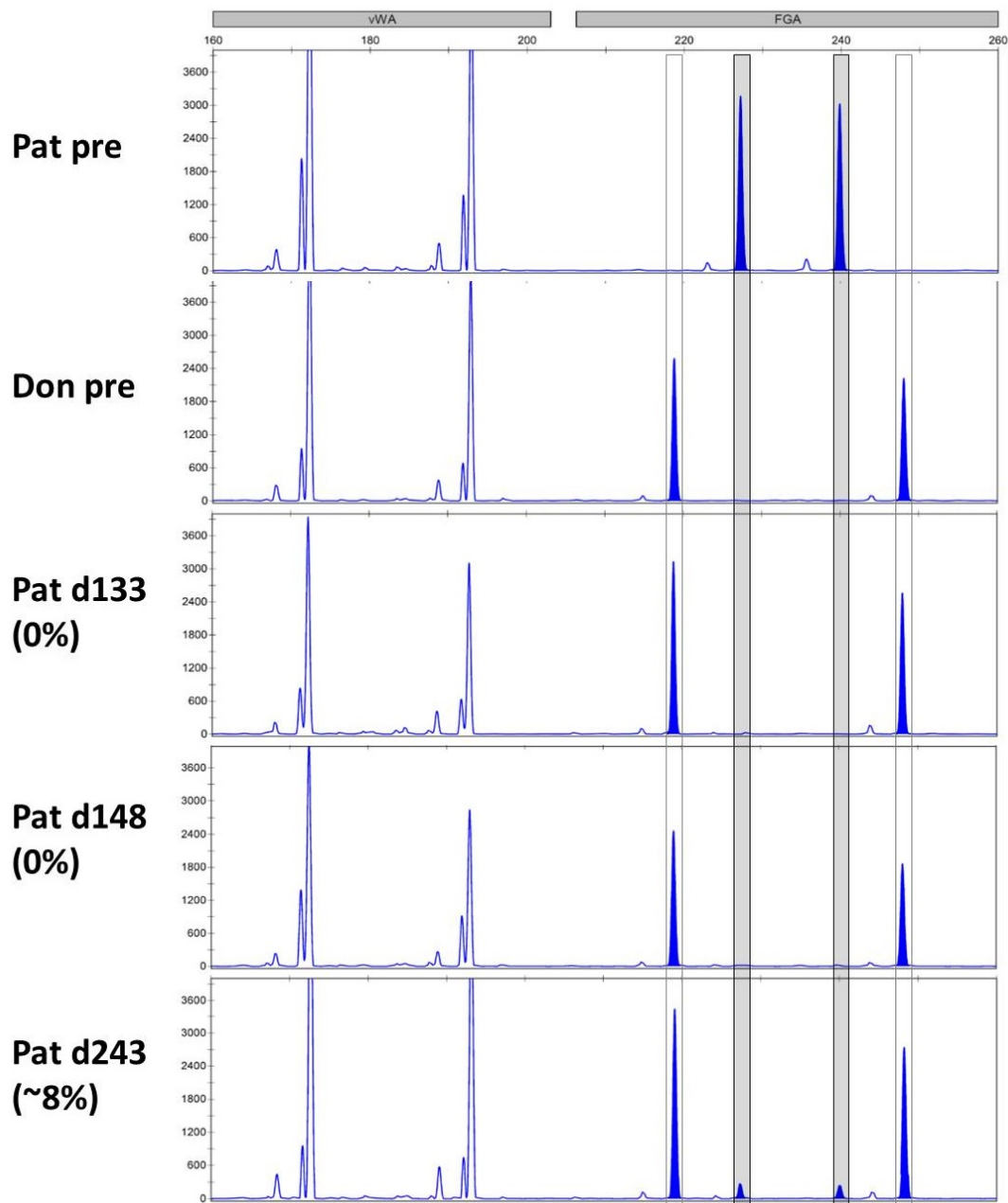
Monitoring of Hematopoietic Chimerism by Real-Time Quantitative PCR of Micro Insertions/Deletions in Samples with Low DNA Quantities

Christian Bach^a Elmira Tomova^a Katja Goldmann^a Volker Weisbach^b
Wolf Roesler^a Andreas Mackensen^a Julia Winkler^a Bernd
M. Spriewald^a

^aDepartment of Internal Medicine 5, Hematology/Oncology, University Hospital Erlangen, Erlangen, Germany; ^bDepartment of Transfusion Medicine and Hemostaseology, University Hospital Erlangen, Erlangen, Germany

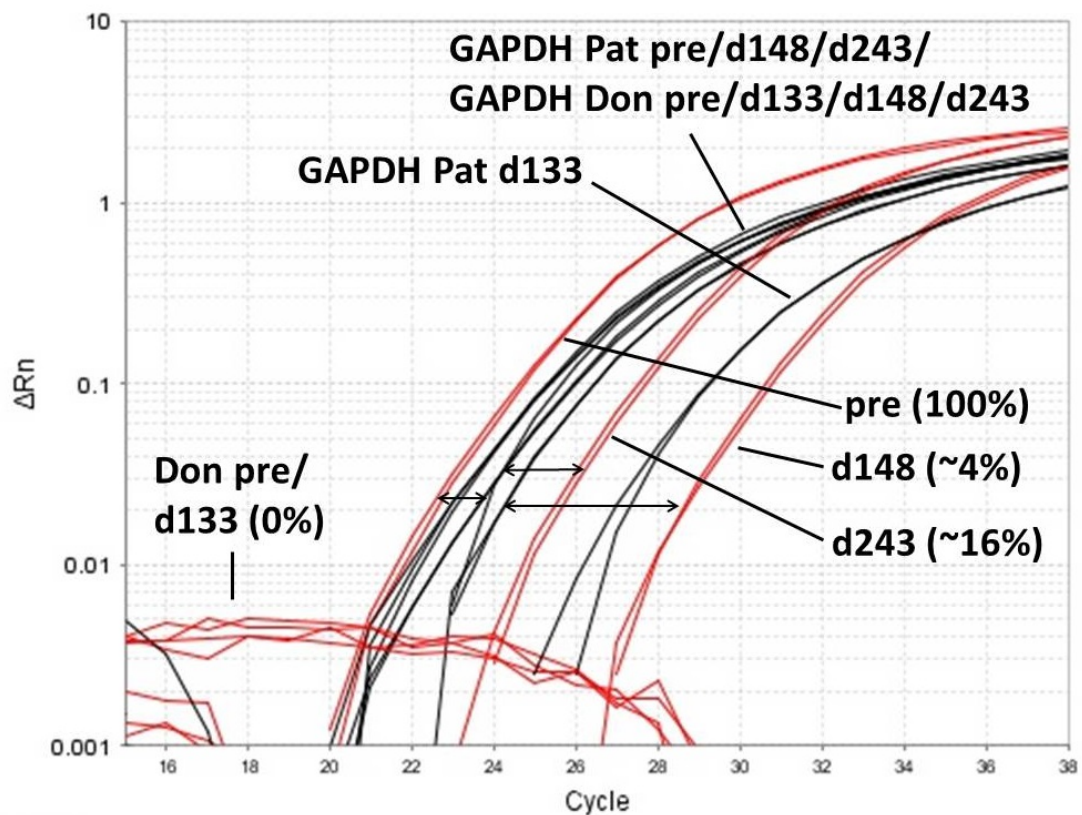
Supplemental Material

Christian Bach, PhD
Department of Internal Medicine 5, Hematology/Oncology
Laboratory for Immunogenetics, University Hospital Erlangen
Glücksstraße 4a, 91054 Erlangen, Germany
christian.bach@uk-erlangen.de



Supplemental fig. 1. Graphical example of STR-PCR analysis.

A visual example of STR-PCR peak analysis of patient 13 (compare to supplemental fig. 2). Fluorescence peaks of donor alleles in the FGA locus are boxed, patient alleles are boxed and shaded. Re-emerging recipient chimerism is revealed by re-appearance of patient allele peaks in the sample from day 243. Note that only one of the 3 alleles used for analysis is shown as an example.



Supplemental fig. 2. Graphical example of indel-qPCR analysis.

A visual example of indel-qPCR analysis of patient 13 (compare to supplemental fig. 1). ΔR_n (change of normalized fluorescence) on a logarithmic scale is plotted against the PCR cycle (= amplification plot). Curves for GAPDH and the marker 8a at different time points are colored black and red respectively. Double headed arrows roughly indicate the delta ct for quantification. Re-emerging recipient chimerism is evident by a decrease in delta ct in samples from day 148 and 243, whereas no recipient allele could be detected in the sample from day 133. Note that only one of the 2 alleles used for analysis is shown as an example.