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author contribution form

Title	<i>Next-generation-sequencing-spectratyping reveals public T-cell receptor repertoires in pediatric very severe aplastic anemia and identifies a beta chain CDR3 sequence associated with hepatitis-induced pathogenesis</i>
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Specific contributions of each author are listed on page 2 of this document.

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Please describe the contributions of each author, indicating who was responsible for each part of the study and the preparation of the manuscript (collection of data, experiments, data analysis, generation of figures, collection of images, interpretation of data, preparation of the text, etc.)

Authors who participated in the conception of the study: Arndt Borkhardt, Jens Stoye, Pina F. I. Krell.

Authors who participated in the collection of data and patient samples: Friedhelm R. Schuster, Roland Meisel, Polina Stepensky, Brigitte Strahm, Ute Fischer, Susanne Reuther

Authors who designed research: Susanne Reuther, Friedhelm R. Schuster, Michael Gombert, Corinna Asang, Ute Fischer

The following authors performed experiments or developed tools:

- Susanne Reuther isolated RNA of CD8+ T cells from bone marrow of SAA and transplanted patients as well as from peripheral blood of healthy individuals. She performed cDNA synthesis, PCR and next generation sequencing as well as TCR spectratyping.*
- Michael Gombert performed next generation sequencing.*
- Ute Fischer isolated CD8+ T-cells from bone marrow of healthy children and isolated RNA*
- Corinna Asang performed cDNA synthesis, PCR and next generation sequencing.*
- Pina F. I. Krell and Jens Stoye developed the TCR profiler software tool.*
- Thomas Keller and Stephan Weber developed mathematical scores to determine TCR diversity in clinical samples.*

Authors who analyzed data: Pina F. I. Krell, Ute Fischer, Thomas Keller, Stephan Weber, Jens Stoye, Roland Meisel, Brigitte Strahm, Polina Stepensky, Friedhelm R. Schuster

Authors who generated figures and tables: Ute Fischer, Pina F. I. Krell, Thomas Keller, Stephan Weber

Authors who interpreted the data:

Pina F. I. Krell was responsible for the bioinformatic interpretation of the data. Ute Fischer and Arndt Borkhardt interpreted clinical aspects.

Writing the manuscript

Ute Fischer was responsible for outlining, writing, proof-reading and revising the manuscript. Arndt Borkhardt was responsible for the outline and content of the manuscript, revision and proof-reading.

Pina F. I. Krell was responsible for outlining and writing the bioinformatics parts of the manuscript, proof-reading and revising the manuscript.

Thomas Keller was responsible for writing the mathematical parts of the manuscript, proof-reading and revising the manuscript.

Jens Stoye, Roland Meisel, Polina Stepensky, Brigitte Strahm, Stephan Weber, Susanne Reuther, Michael Gombert, Corinna Asang, Friedhelm R. Schuster were responsible for revising and proof-reading the manuscript.