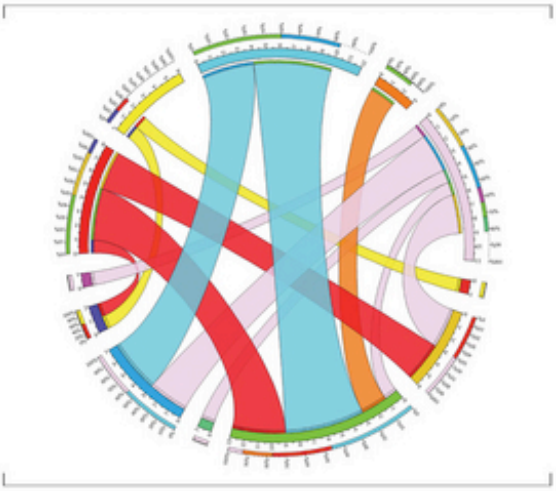
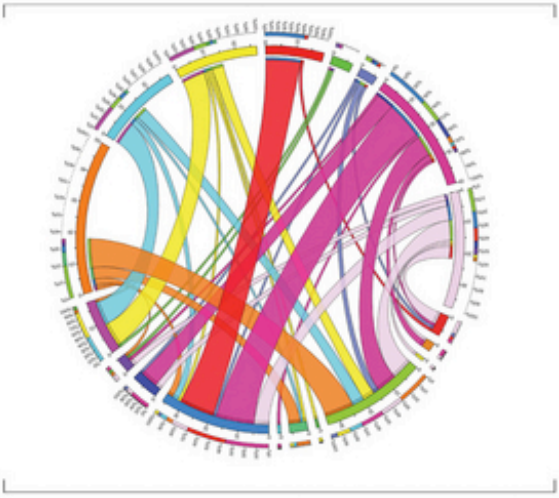
# THE GENETIC BASIS OF HAEMATOLOGICAL CANCERS

EDITED BY **Sabrina Tosi & Alistair G. Reid**





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EDITED BY

**Sabrina Tosi**
Division of Biosciences
Brunel University London
UK

**Alistair G. Reid**
Centre for Haematology
Imperial College London
UK

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The Atrium, Southern Gate, Chichester, West Sussex, PO19 8SQ, UK
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# Contents

# List of contributors

**Mary Alikian**
Centre for Haematology, Imperial College London, UK

**Anna Andersson**
Department of Pathology, St Jude's Children's Research Hospital, USA

**Philip A. Beer**
Terry Fox Laboratory, BC Cancer Agency, UK

**Csaba Bödör**
Barts Cancer Institute, Queen Mary, University of London, UK, and MTA-SE Lendulet Molecular Oncohematology Research Group, Budapest, Hungary

**Jasmijn D.E. de Rooij**
Department of Pediatric Oncology/Hematology, Erasmus MC-Sophia Children's Hospital, The Netherlands

**Valeria Di Battista**
Hematology Unit, CREO, University of Perugia, Italy

**Jude Fitzgibbon**
Barts Cancer Institute, Queen Mary, University of London, UK

**Christine J. Harrison**
Northern Institute for Cancer Research, Newcastle University, Sir James Spence Institute, UK

**Jamshid S. Khorashad**
Huntsman Cancer Institute, University of Utah, USA

**Philippa C. May**
Centre for Haematology, Imperial College London, UK

**Thomas McKerrell**
Wellcome Trust Sanger Institute, University of Cambridge, UK, and Department of Haematology, Cambridge University Hospitals NHS Trust, UK

**Cristina Mecucci**
Hematology Unit, CREO, University of Perugia, Italy

**Anthony V. Moorman**
Northern Institute for Cancer Research, Newcastle University, Sir James Spence Institute, UK

**Charles Mullighan**
Department of Pathology, St Jude's Children's Research Hospital, USA

**Valeria Nofrini**
Hematology Unit, CREO, University of Perugia, Italy

**Danilo Perrotti**
Greenebaum Cancer Center, University of Maryland, USA

**Alistair G. Reid**
Centre for Haematology, Imperial College London, UK

**Matthew J.J. Rose-Zerilli**
Cancer Genomics, Academic Unit of Cancer Sciences, University of Southampton, UK

**Matthew L. Smith**
Department of Haematology, St Bartholomew's Hospital, UK

**Jonathan C. Strefford**
Cancer Genomics, Academic Unit of Cancer Sciences, University of Southampton, UK

**Marry van den Heuvel-Eibrink**
Department of Pediatric Oncology/Hematology, Erasmus MC-Sophia Children's Hospital, The Netherlands

**Christian Michel Zwaan**
Department of Pediatric Oncology/Hematology, Erasmus MC-Sophia Children's Hospital, The Netherlands

# Preface

The haematological malignancies are a complex group of neoplastic diseases, linked by their origin in bone marrow-derived cells. Since the discovery of the Philadelphia chromosome, in the 1960s, as the pathognomonic marker of chronic myeloid leukaemia, the field of haematological malignancy has provided several important paradigms for the direct contribution of causal genetic lesions to the initiation of human cancer.

The subsequent leap in our understanding of leukaemia and lymphoma pathogenesis via a variety of molecular and cytogenetic abnormalities that disrupt normal cellular processes has challenged traditional approaches to disease classification and transformed both the diagnosis and management of patients. The characterization of tumour cells by genetic methods is now regarded as being as important as the traditional morphological approach to diagnosis. This trend is being accelerated by the introduction of monoclonal antibody therapy and by novel drugs designed to target specifically the molecular abnormalities responsible for the development of the tumour. Somatic genetic changes therefore increasingly define not just the diseases themselves, but the way in which an individual patient should best be treated and monitored.

With the following chapters, compiled by leading researchers in the field, we aim to provide a summary of current knowledge on the contribution of genetic and epigenetic lesions to the biology and management of haematological malignancies. A unifying factor of these biologically diverse diseases is the recent explosion of information on hitherto unrecognized molecular lesions arising from the application of novel next-generation sequencing technologies. In most diseases, these newly identified aberrations are already contributing to improved stratification and, in some cases, showing early promise as therapeutic targets. It is hoped that further functional analysis of recurrent lesions will permit the development of additional therapies targeted against critical oncogenic drivers. Although the majority of recurrent changes appear to have been identified, there remains scope for further refinement of this knowledge with studies of larger cohorts,