

THE Lymphomas

SECOND EDITION

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THE LYMPHOMAS

Second Edition

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*To the memory of our
colleague, Dr. Stanley Korsmeyer.*

Preface

Research in the field of malignant lymphoma has moved faster than any other component of medical oncology. The second edition of *The Lymphomas* is an attempt to bring the changing basic science and clinical information up-to-date and to conform with the new understanding of the biological features and natural history of the various malignant lymphomas. Since the last edition, there has been a comprehensive review by the World Health Organization resulting in a classification scheme that embodied some of the principles of the REAL [revised European American lymphoma] classification as well as a consensus among pathologists and clinicians regarding the appropriateness of the various subdivisions of Hodgkin lymphoma and non-Hodgkin's lymphoma. New contributors who are active in their various fields of specialization have been brought into the second edition, bringing a new vitality to this edition. A molecular biologic basis of the cytogenetic translocations that characterize the various forms of lymphoma has been completely updated. The immunophenotypic as well as molecular genetic abnormalities are described, which may lend themselves to the targeted therapy. To that end, the section on biological therapy has been completely rewritten with a comprehensive consideration of all of the new information available on the biological therapy of lymphoma. The major subdivisions within the WHO classification have been separated and discussed individually. As in the previous edition, the therapeutic modalities—such as

chemotherapy, radiation therapy, and bone marrow transplantation—are updated in separate chapters.

The pace of biological discovery is very quick leading to a host of new agents targeted to cell surface markers as well as unique molecular abnormalities. Microarray technology has begun to define the various lymphomas according to molecular genetic signatures which correlate with natural history. In addition, this technique may define specific abnormalities against which targeted therapies could be developed. The basic scientific sections have a new editor in Dr. Bryan Young, who has been an active investigator in the field. This second edition is an attempt to offer the reader a comprehensive view of the basic and clinical science in the field with recommendations as to therapeutic approaches. It is assumed that this field will continue to change as new therapeutic tactics emerge.

The editors wish to thank all of the contributors, their administrative assistants and secretaries for their dedicated efforts with this Second Edition. The editors gratefully acknowledge the inspiration of their mentors in the field of lymphoma therapy, some of whom have passed on, including Professor G. Hamilton Fairley, Professor Timothy McElwain, Drs. Paul Carbone and John Ultmann.

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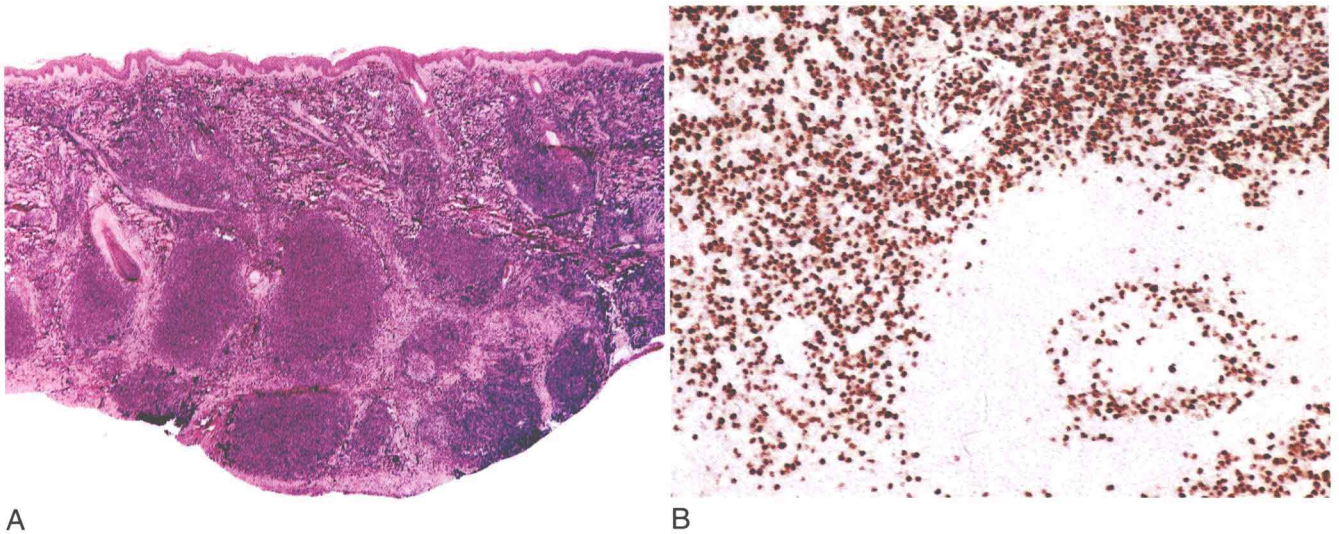


Figure 1-1. Precursor B-lymphoblastic leukemia/lymphoma. **A:** This scalp lesion was the initial presenting site of disease in this 10-year-old female. The tumor infiltrates the reticular dermis, but leaves a Grenz zone beneath the epidermis. **B:** Lymphoblasts demonstrate nuclear staining for terminal deoxynucleotidyl transferase (TdT). This example of lymph node involvement shows diffuse paracortical involvement with relative sparing of germinal centers (**lower right**).

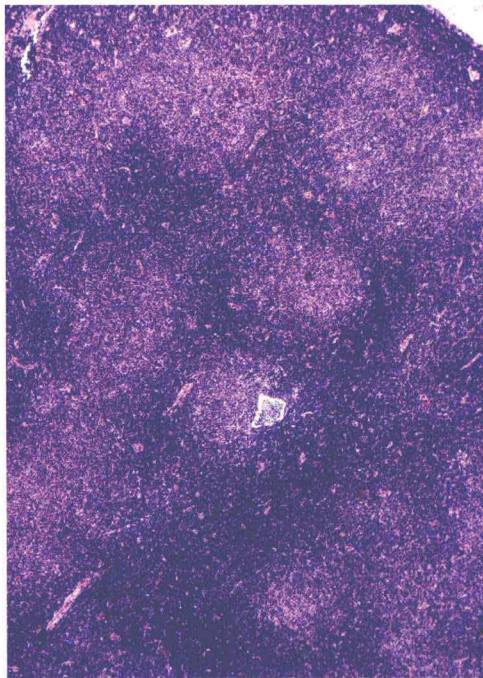


Figure 1-2. CLL/SLL, lymph node. **A:** The lymph node shows diffuse architectural effacement with a pseudofollicular pattern, seen as pale areas representing proliferation or growth centers.

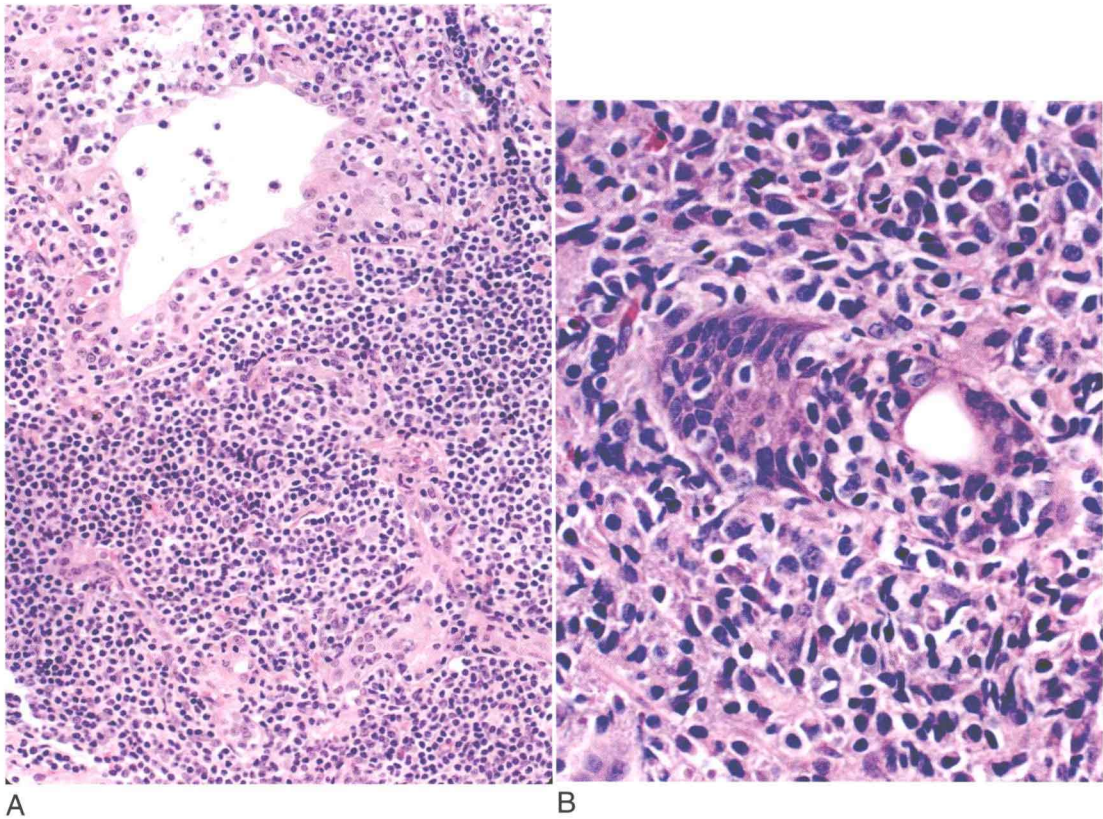


Figure 1-4. MALT lymphoma. **A:** In this lung lesion, monocytoid-appearing cells with pale cytoplasm infiltrate and surround the bronchial epithelium. **B:** Lymphoepithelial lesion in a case of gastric MALT lymphoma, showing lymphoma cells invading an epithelial gland.

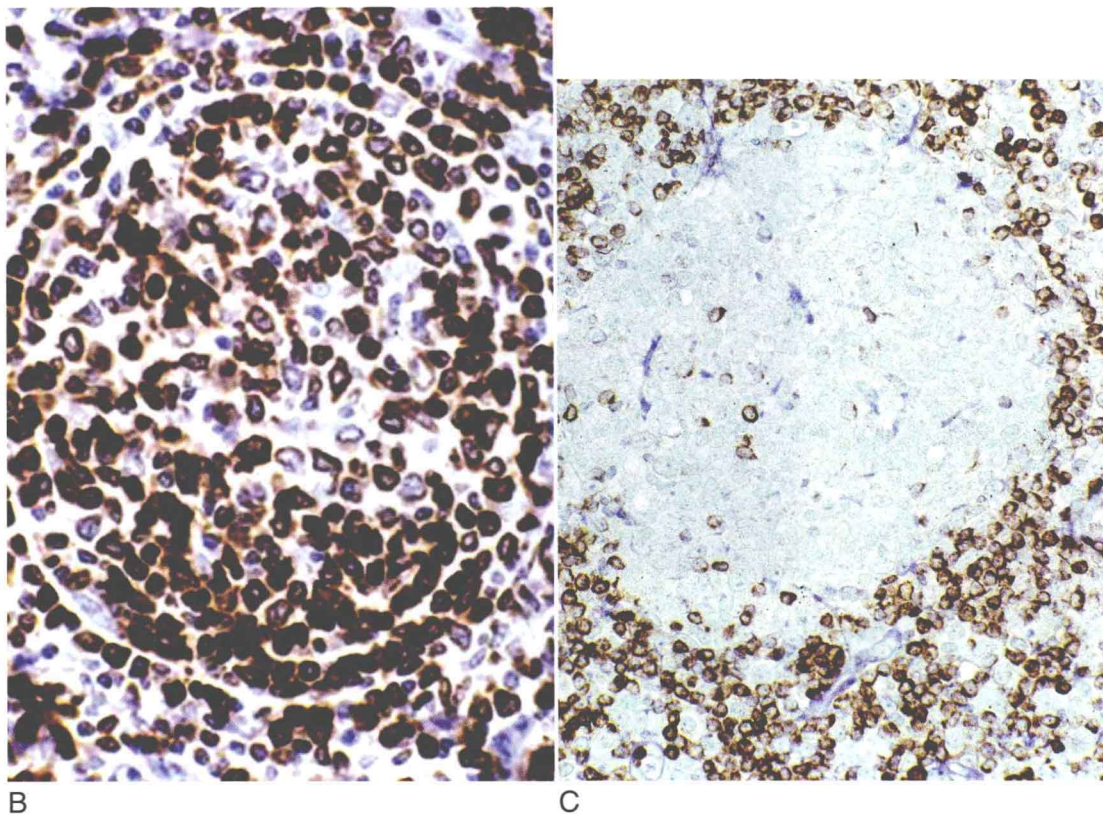


Figure 1-5. Follicular lymphoma, lymph node. **B:** The t(14;18) translocation leads to overexpression of Bcl-2 protein in the neoplastic follicles of follicular lymphoma (dark cytoplasmic staining). **C:** Bcl-2 protein is not expressed in reactive, non-neoplastic germinal center B cells. The positive cells seen represent reactive T cells.

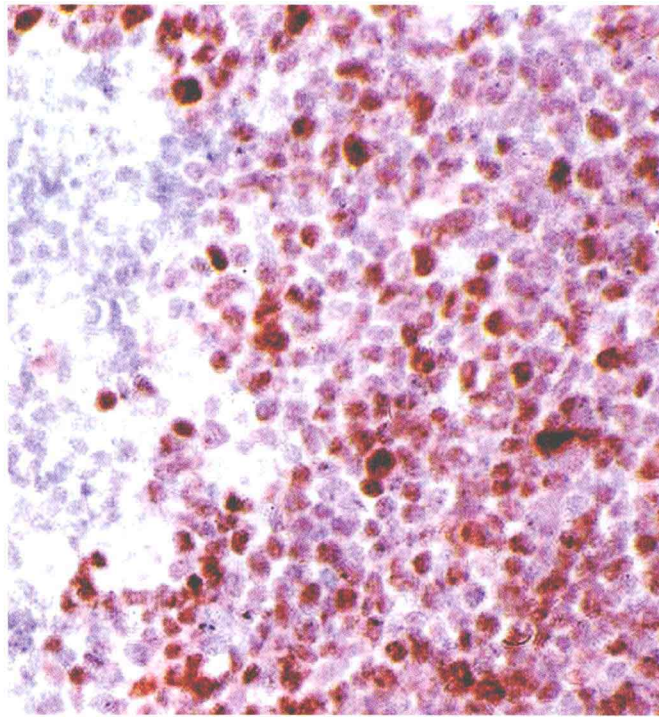


Figure 1-6. Mantle cell lymphoma, lymph node. A monotonous lymphoid infiltrate highlighted by nuclear staining for cyclin D1 maintains its mantle zone pattern, surrounding a non-neoplastic germinal center (negative staining, **left**).

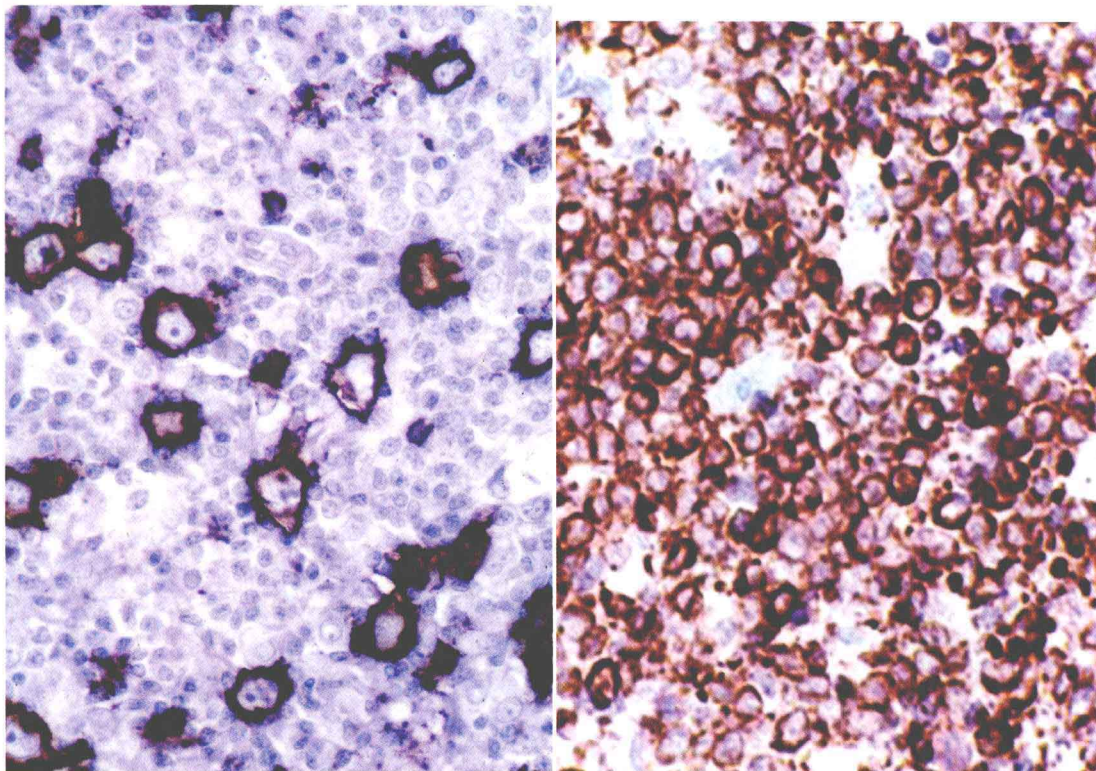


Figure 1-7. Diffuse large B-cell lymphoma. **B:** In the T-cell/histiocyte-rich variant of DLBCL, a background of small non-neoplastic T cells surrounds the large neoplastic B lymphocytes, which are highlighted by immunostaining for CD20. **C:** A case of DLBCL demonstrating Bcl-2 protein expression (dark cytoplasmic staining), a finding generally associated with adverse outcome.

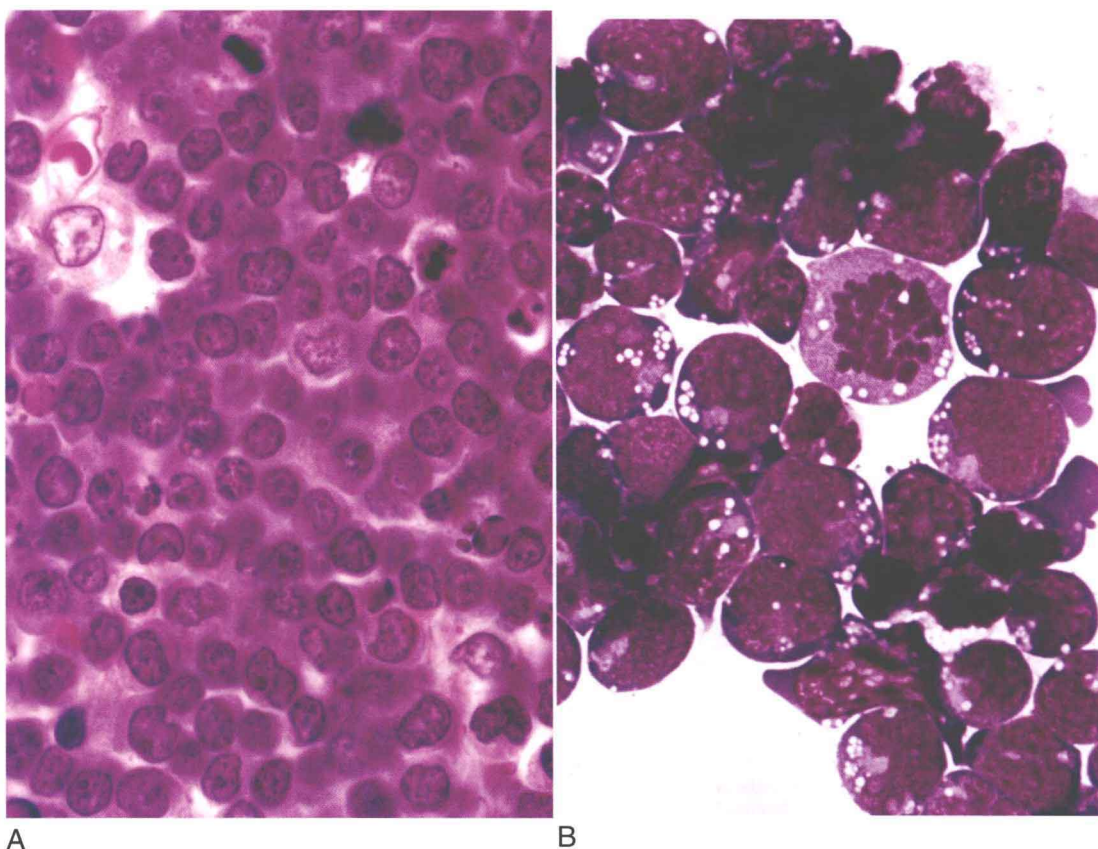


Figure 1-8. Burkitt's lymphoma. **A:** The cells are uniform, round to oval, with multiple small basophilic nucleoli. The nuclear size is similar to that of the "starry sky" histiocyte in the **upper left**. Mitotic activity is present. **B:** A touch preparation demonstrates lipid vacuoles in the deeply basophilic cytoplasm.

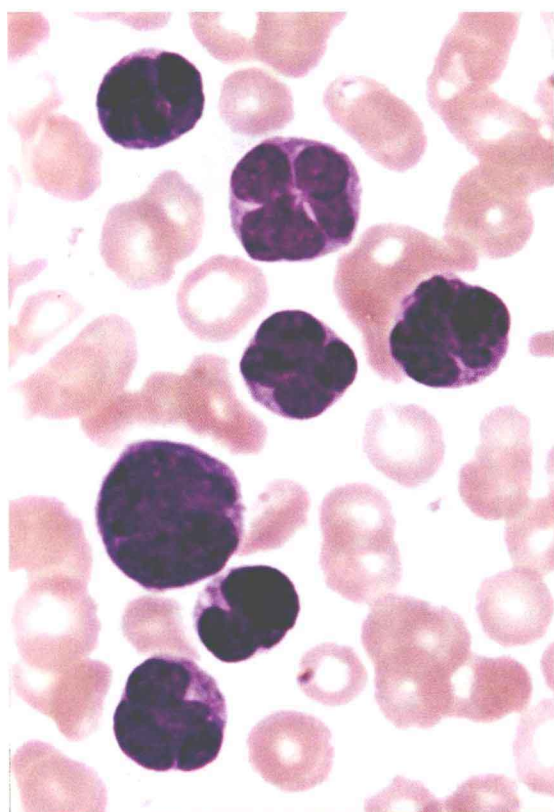


Figure 1-10. Adult T-cell leukemia/lymphoma. Markedly polylobated ("flower") cells circulate in the peripheral blood.

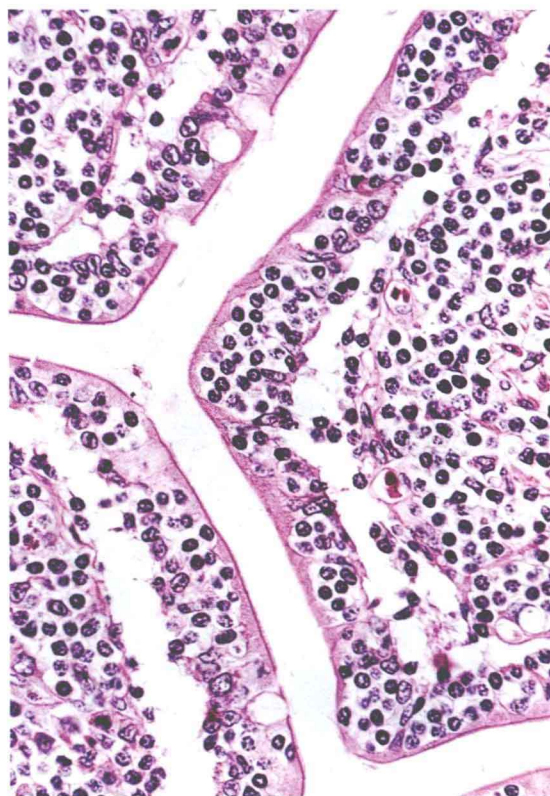


Figure 1-12. Enteropathy-type T-cell lymphoma. Atypical lymphocytes with pale cytoplasm infiltrate the epithelial mucosa and lamina propria of small intestinal villi.

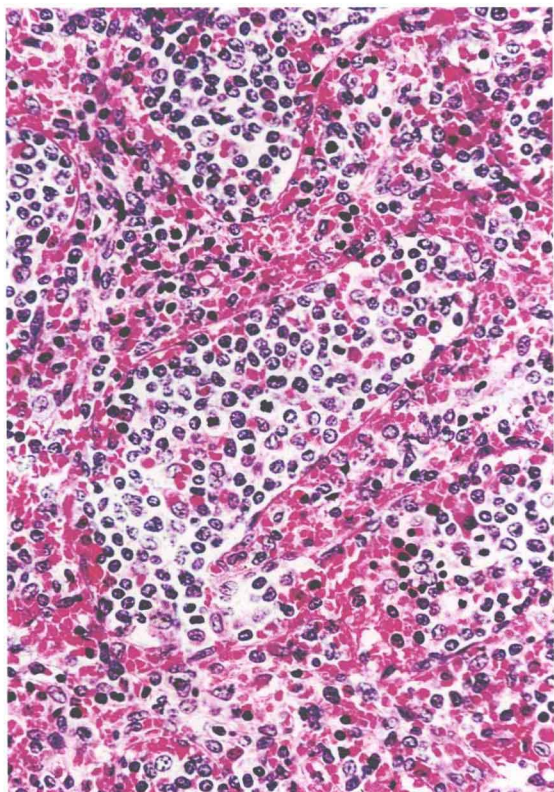


Figure 1-13. Hepatosplenic T-cell lymphoma. This liver biopsy shows a monotonous population of medium-sized cells with pale cytoplasm distending the hepatic sinusoids.

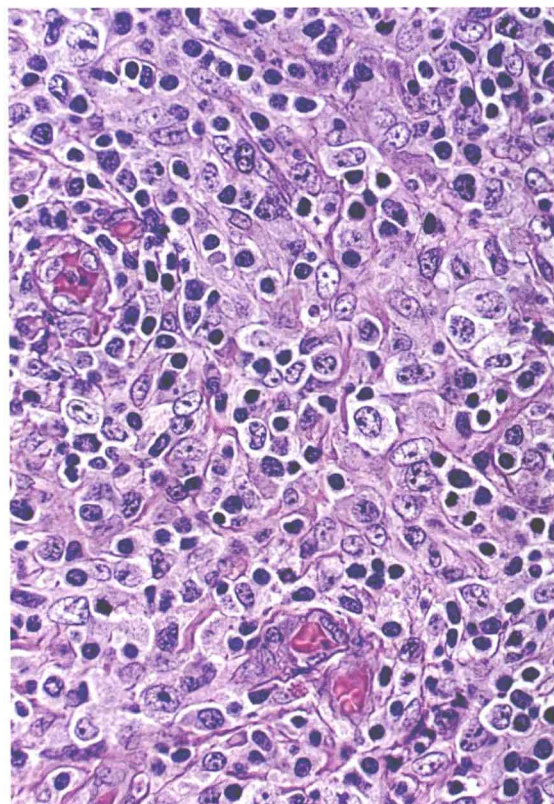


Figure 1-16. Angioimmunoblastic T-cell lymphoma. There is an infiltrate of atypical lymphoid cells with pale cytoplasm in a mixed inflammatory background, and prominent post-capillary venules with plump endothelial cells.

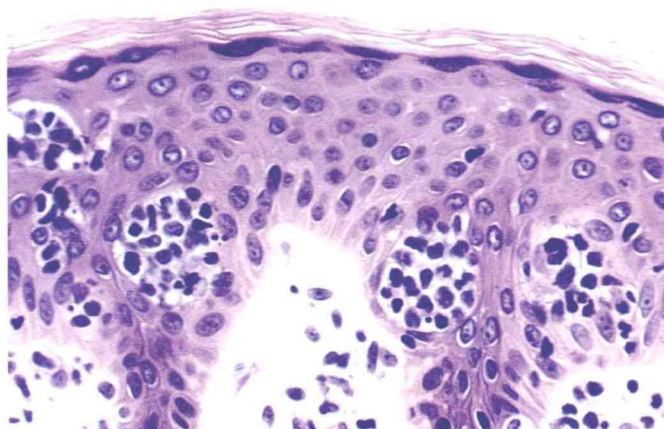
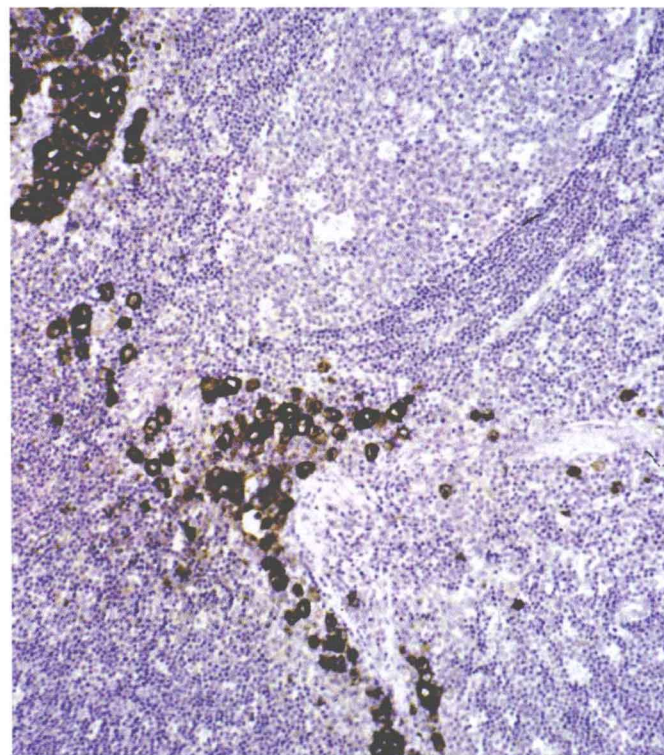


Figure 1-15. Mycosis fungoides. This skin biopsy shows neoplastic lymphocytes with convoluted nuclei forming Pautrier microabscesses within the epidermis.



B

Figure 1-18. Systemic anaplastic large cell lymphoma (ALCL). **B:** The malignant cells are strongly positive for CD30 by immunohistochemistry.

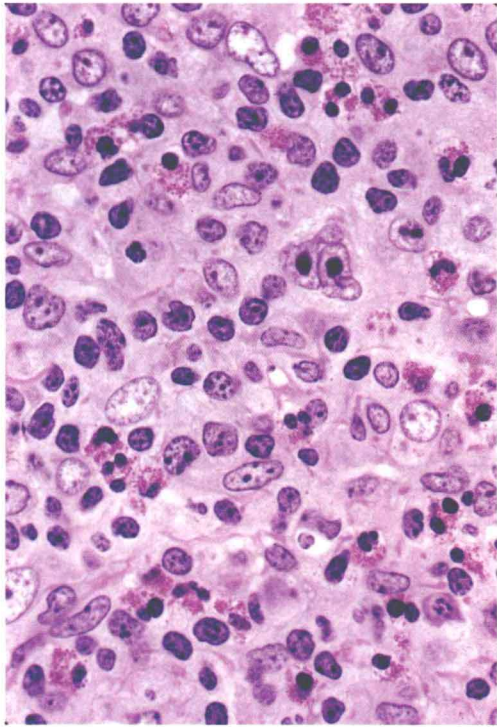


Figure 1–19. Hodgkin's lymphoma. **B:** Mixed-cellularity Hodgkin's lymphoma, showing classic Reed–Sternberg cells admixed with lymphocytes, plasma cells, and eosinophils.

B

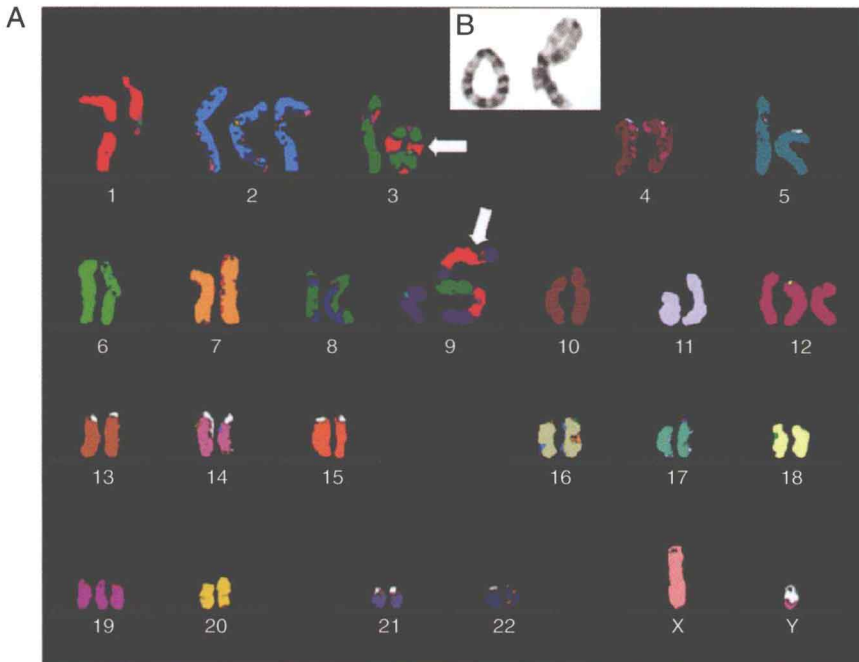


Figure 2–3. Multicolor karyotype (MFISH) of a representative case of diffuse, large B-cell lymphoma. **A:** The karyotype reveals a deletion of the q arm of chromosome 1, trisomy for chromosomes 2, 12, and 19, and two complex rearrangements (*white arrows*) representing a large-ring chromosome 3 composed of alternating segments of material from chromosome 1 and chromosome 3, and a large derivative chromosome 9 composed of alternating segments of material from chromosomes 1, 3, and 9. **B:** G-banded image of ring (3) and der (9). **C:** Multicolor banding pattern of the chromosome 1 segments of der (1), der (9), and ring (3). Normal chromosome 1 is shown on the left.

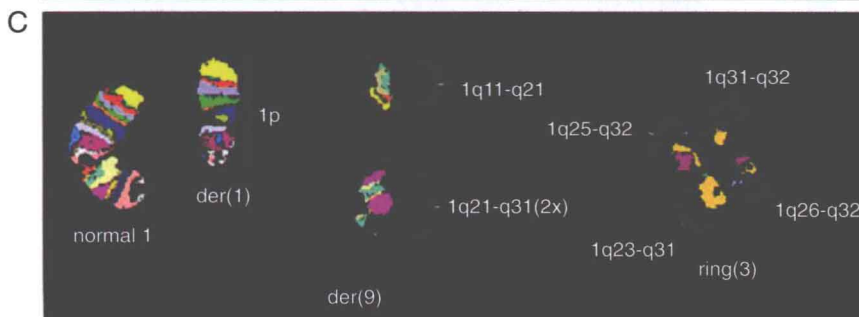


Figure 2–4. Locus-specific FISH images of a representative case of mantle cell lymphoma obtained with a commercial Vysis LSI IGH/BCL1 dual-color, dual-fusion translocation probe. The normal pattern of two BCL1 (red) and two IGH (green) signals are evident in **(A)**, an interphase nucleus, and **(B)**, a metaphase. An abnormal pattern of one BCL1 signal (red), one IGH signal (green), and two IGH-BCL1 fusion signals are evident in **(C)**, an interphase nucleus (fusion signals indicated by *white arrows*), and **(D)**, in a metaphase containing the t(11;14) of MCL (normal and derivative chromosomes indicated with *white lettering*).

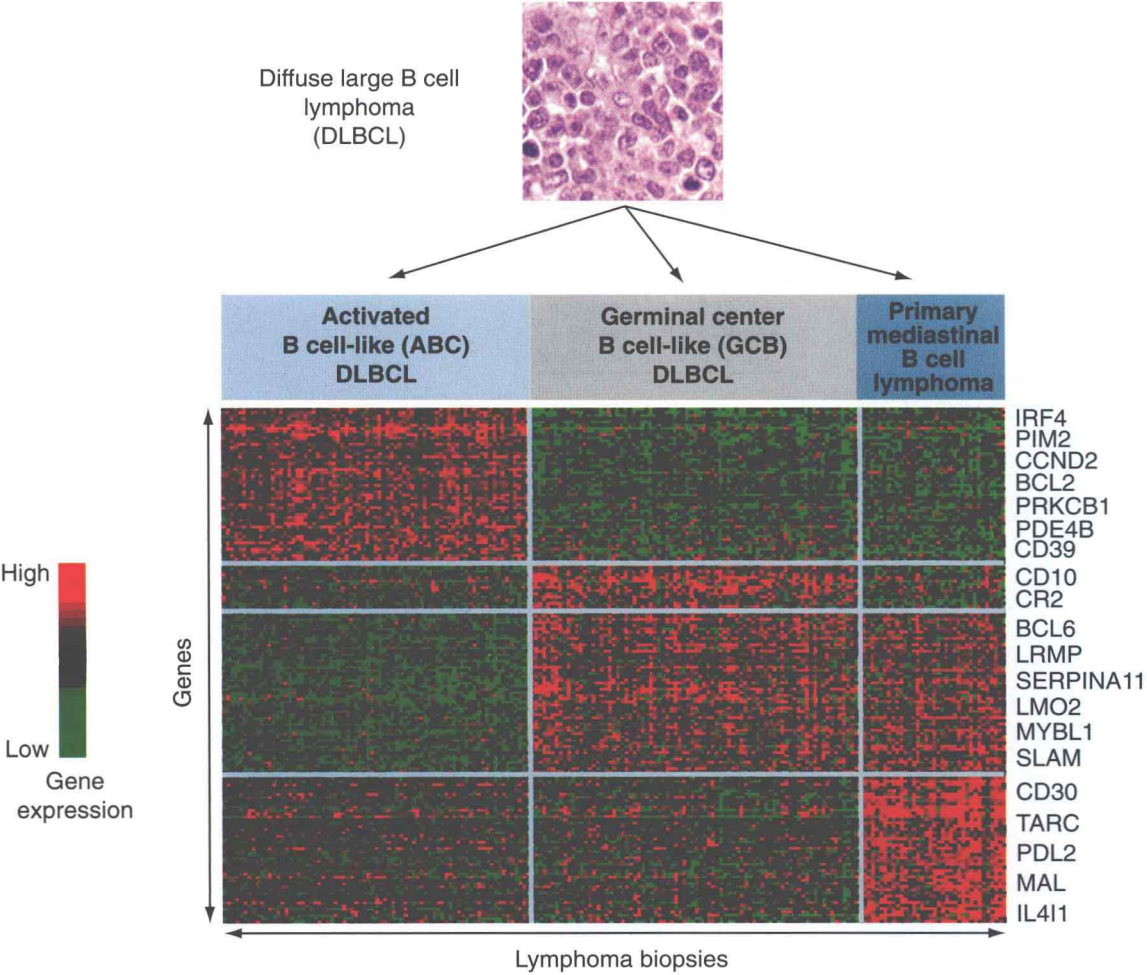
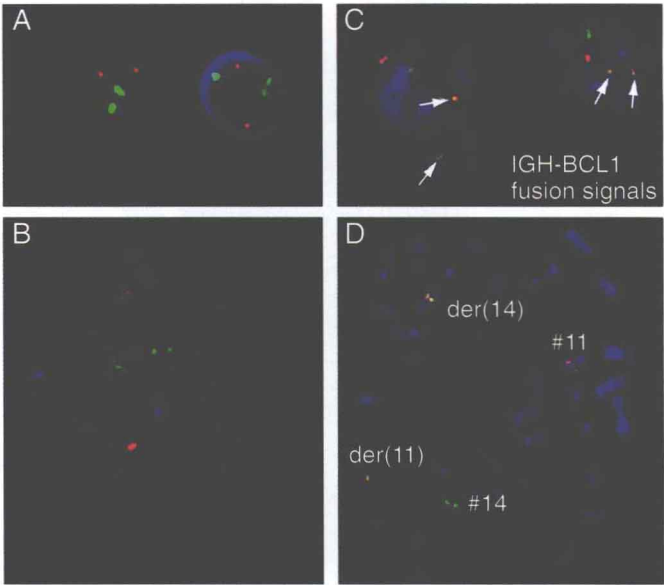


Figure 5–1. Definition of molecularly and clinically distinct subgroups of diffuse large B-cell lymphoma (DLBCL) by gene expression profiling. Gene expression differences between germinal center B-cell-like (GCB) DLBCL, activated B-cell-like DLBCL, and primary mediastinal B-cell lymphoma (PMBL). Each row represents gene expression data from an individual biopsy sample, and each column represents a single gene on the DNA microarray. Relative gene expression is indicated according to the color bar shown at the left. Representative genes that distinguish the DLBCL subgroups are indicated. Not shown are ~18% of DLBCLs that do not fit any of the three gene expression subgroups well.

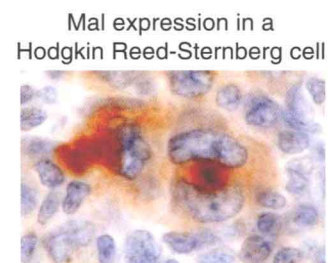
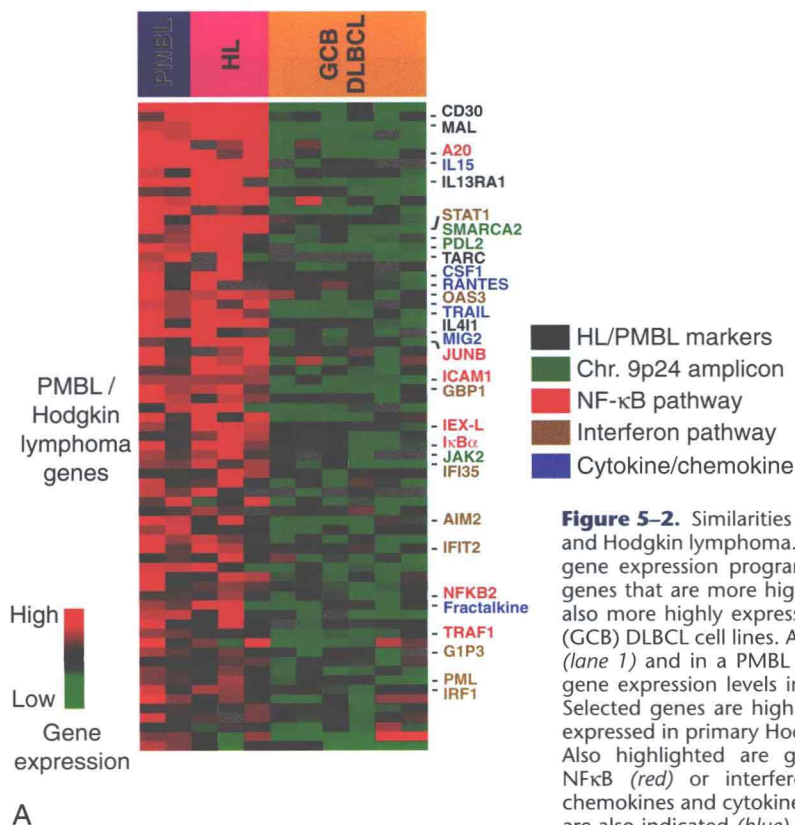


Figure 5-2. Similarities between primary mediastinal B-cell lymphoma (PMBL) and Hodgkin lymphoma. **A:** PMBL and Hodgkin's lymphoma (HL) share a broad gene expression program. The 69 genes depicted are all PMBL "signature" genes that are more highly expressed in PMBL than in other DLBCLs, and are also more highly expressed in HL cell lines than in germinal center B-cell-like (GCB) DLBCL cell lines. Average gene expression levels in primary PMBL tumors (lane 1) and in a PMBL cell line, K1106 (lane 2), are shown. Also shown are gene expression levels in three HL cell lines and in six GCB DLBCL cell lines. Selected genes are highlighted that have been shown to be characteristically expressed in primary Hodgkin's Reed-Sternberg cells and/or PMBL cells (black). Also highlighted are genes that are activated by signaling through the NFκB (red) or interferon (brown) pathways. Numerous genes encoding chemokines and cytokines, many of which are activated by the NF-κB pathway, are also indicated (blue). PMBL and HL tumors frequently harbor a gain/amplification of chromosome region 9p24, which contains several genes that are characteristically expressed in both lymphoma types (green). **B:** Detection of Mal protein expression in a primary Hodgkin's Reed-Sternberg cell by immunohistochemistry.

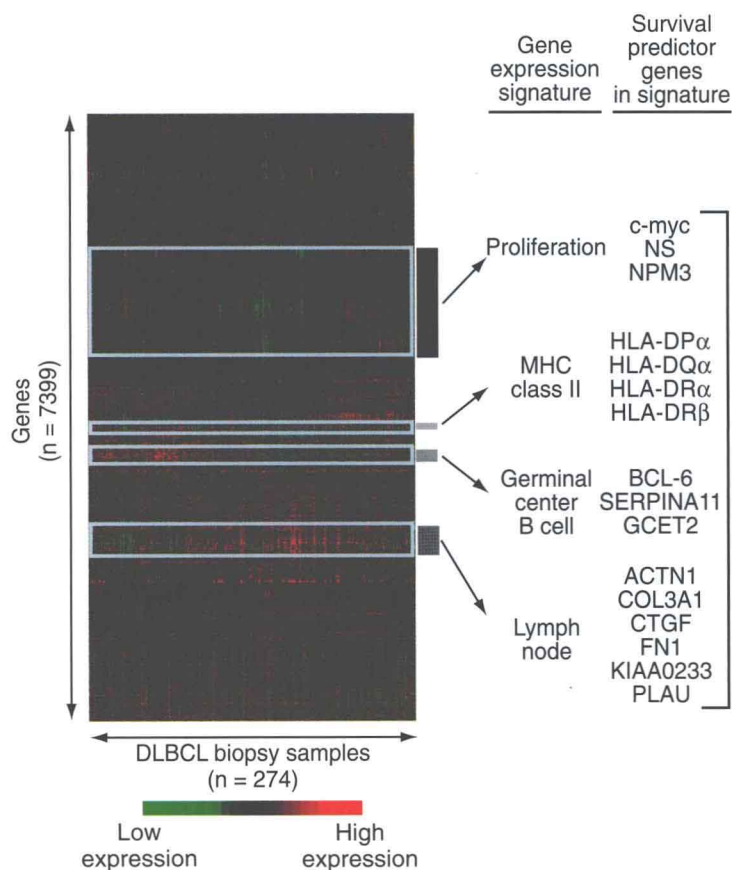


Figure 5-4. A gene expression-based predictor of survival following chemotherapy for DLBCL. Hierarchical clustering of the gene expression data reveals gene expression signatures containing survival predictor genes. A hierarchical clustering algorithm was used to organize genes based on their expression across 274 DLBCL biopsy samples. Four gene expression signatures are indicated, each of which is composed of coordinately expressed genes that reflect a specific biological aspect of the tumors (see text for details). A supervised method was used to discover genes whose expression patterns were correlated with the length of survival, and the majority of these "survival predictor genes" belonged to one of the four indicated gene expression signatures.¹⁰ Shown are 16 representative survival predictor genes from these four signatures that were used to create a multivariate model of survival.