leukemia (CML), which is characterized by only one chromosomal abnormality (the Philadelphia chromosome), while at the other end of the spectrum is MDS, which has hundreds of different chromosomal abnormalities.

V. CHROMOSOMAL ABNORMALITIES IN SOLID TUMORS

Use of chromosomal abnormalities and cytogenetics is sometimes used in clinical trials on solid tumors, but at a frequency much less than that for hematological cancers. The following reveals this type of analysis for solid tumors. In a study of colorectal cancer, Bardi et al. (217) found that structural changes in chromosome 8, structural changes in chromosome 16, and loss of chromosome 18 are correlated with shorter survival. In a manner somewhat reminiscent to the distinction of the various leukemias using cytogenetic analysis, the Bardi study also found that colon cancer and rectal cancer were distinguished by different patterns of abnormal cytogenetics. To provide another example, studies of breast cancer from Larson et al. (218) and Heaphy et al. (219) identified certain chromosomal abnormalities that are correlated with poor prognosis for breast cancer patients. These abnormalities were allelic imbalances. Allelic imbalances are defined as a deviation from the normal 1:1 ratio of maternal and paternal alleles. Regarding chromosomal deletions, Ellsworth et al. (220) provide a diagram of all of the chromosomes, illustrating the most commonly deleted regions in breast cancers.

VI. CLINICAL ENDPOINTS AND EXAMPLES FROM CLINICAL TRIALS

Examples of a number of clinical endpoints, as well as data from several clinical trials, are shown below. Clinical endpoints used in clinical trials on hematological cancers include event-free survival (EFS), progression-free survival (PFS), and overall survival. Earlier chapters in this textbook detailed the oncology endpoint of PFS, as well as other surrogate endpoints, and the gold standard endpoint of overall survival. The following material further develops the concept of surrogate endpoints, with a narrative on minimal residual disease (MRD).

[217] Bardi G, Fenger C, Johansson B, Mitelman F, Heim S. Tumor karyotype predicts clinical outcome in colorectal cancer patients. *J Clin Oncol*. 2004;22:2623–2634.

[218] Larson PS, Schlechter BL, de las Morenas A, Garber JE, Cupples LA, Rosenberg CL. Allele imbalance, or loss of heterozygosity, in normal breast epithelium of sporadic breast cancer cases and BRCA1 gene mutation carriers is increased compared with reduction mammoplasty tissues. *J Clin Oncol*. 2005;23:8613–8619.

[219] Heaphy CM, Bisoffi M, Joste NE, Baumgartner KB, Baumgartner RN, Griffith JK. Genomic instability demonstrates similarity between DCIS and invasive carcinomas. *Breast Cancer Res Treat*. 2009;117:17–24.

[220] Ellsworth RE, Ellsworth DL, Lubert SM, Hooke J, Somiari RI, Shriver CD. High-throughput loss of heterozygosity mapping in 26 commonly deleted regions in breast cancer. *Cancer Epidemiol Biomarkers Prev*. 2003;12:915–919.