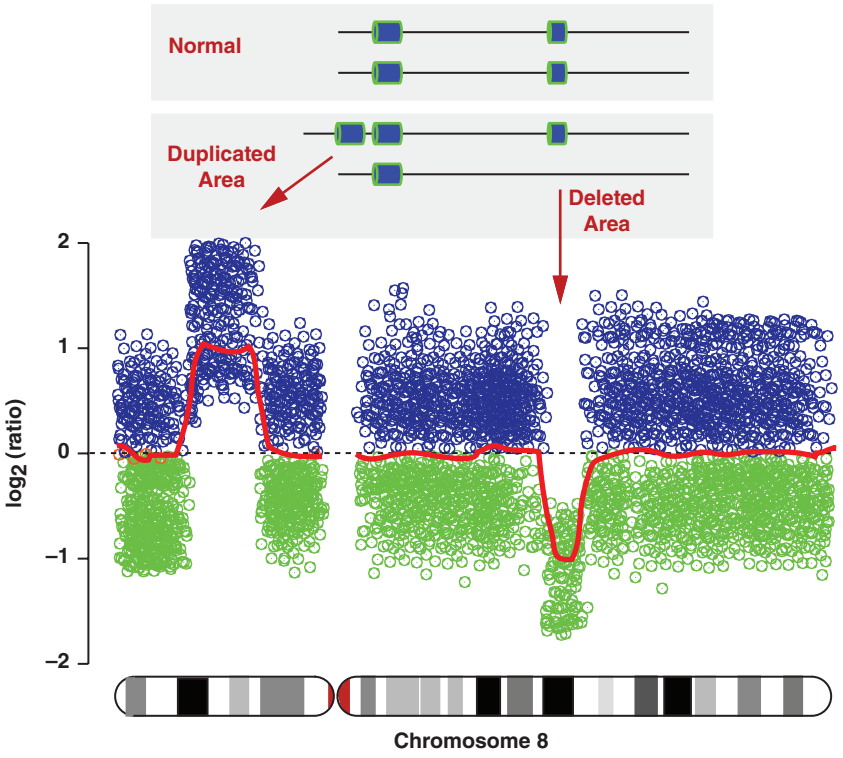

FIGURE 82-5 **Copy number variations (CNV)** encompass relatively large regions of the genome that have been duplicated or deleted. Chromosome 8 is shown with CNV detected by genomic hybridization. An increase in the signal strength indicates a duplication, a decrease reflects a deletion of the covered chromosomal regions.

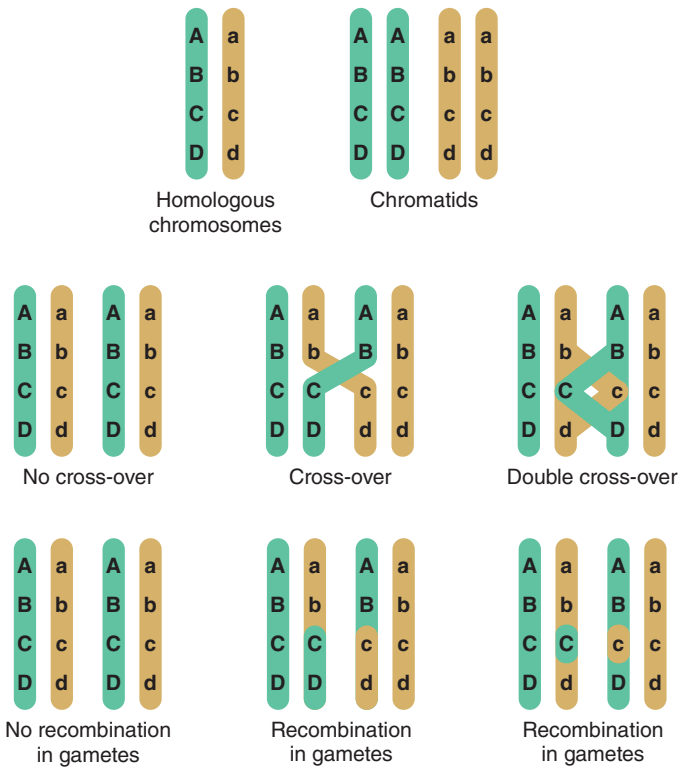

FIGURE 82-6 **Crossing-over and genetic recombination.** During chiasma formation, either of the two sister chromatids on one chromosome pairs with one of the chromatids of the homologous chromosome. Genetic recombination occurs through crossing-over and results in recombinant and nonrecombinant chromosome segments in the gametes. Together with the random segregation of the maternal and paternal chromosomes, recombination contributes to genetic diversity and forms the basis of the concept of linkage.

usually restricted to cytosines of CpG dinucleotides, which are abundant throughout the genome. Methylation of these dinucleotides is thought to represent a defense mechanism that minimizes the expression of sequences that have been incorporated into the genome such as retroviral sequences. CpG dinucleotides also exist in so-called *CpG islands*, stretches of DNA characterized by a high CG content, which are found in the majority of human gene promoters. CpG islands in promoter regions are typically unmethylated, and the lack of methylation facilitates transcription.

Histone methylation involves the addition of a methyl group to lysine residues in histone proteins (Fig. 82-7). Depending on the specific lysine residue being methylated, this alters chromatin configuration, either making it more open or tightly packed. Acetylation of histone proteins is another well-characterized mechanism that results in an open chromatin configuration, which favors active transcription. Acetylation is generally more dynamic than methylation, and many transcriptional activation complexes have histone acetylase activity, whereas repressor complexes often contain deacetylases and remove acetyl groups from histones. Other histone modifications, whose effects are incompletely characterized, include phosphorylation and sumoylation. Lastly, noncoding RNAs that bind to DNA can have a significant impact on transcriptional activity.

Physiologically, epigenetic mechanisms play an important role in several instances. For example, X-inactivation refers to the relative silencing of one of the two X chromosome copies present in females. The inactivation process is a form of dosage compensation such that females (XX) do not generally express twice as many X-chromosomal gene products as males (XY). In a given cell, the choice of which chromosome is inactivated occurs randomly in humans. But once the maternal or paternal X chromosome is inactivated, it will remain inactive, and this information is transmitted with each cell division. The *X-inactive specific transcript* (*Xist*) gene encodes a large noncoding RNA that mediates the silencing of the X chromosome from which it is transcribed by coating it with Xist RNA. The inactive X chromosome is highly methylated and has low levels of histone acetylation.

Epigenetic gene inactivation also occurs on selected chromosomal regions of autosomes, a phenomenon referred to as *genomic imprinting*. Through this mechanism, a small subset of genes is only expressed in a monoallelic fashion. Imprinting is heritable and leads to the preferential expression of one of the parental alleles, which deviates from the usual biallelic expression seen for the majority of genes. Remarkably, imprinting can be limited to a subset of tissues. Imprinting is mediated through DNA methylation of one of the alleles. The epigenetic marks on imprinted genes are maintained throughout life, but during zygote formation, they are activated or inactivated in a sex-specific manner (imprint reset) (Fig. 82-8), which allows a differential expression pattern in the fertilized egg and the subsequent mitotic divisions. Appropriate expression of imprinted genes is important for normal development and cellular functions. Imprinting defects and uniparental disomy, which is the inheritance of two chromosomes or chromosomal regions from the same parent, are the cause of several developmental disorders such as Beckwith-Wiedemann syndrome, Silver-Russell syndrome, Angelman's syndrome, and Prader-Willi syndrome (see below). Monoallelic loss-of-function mutations in the *GNAS1* gene lead to Albright's hereditary osteodystrophy (AHO). Paternal transmission of *GNAS1* mutations leads to an isolated AHO phenotype (pseudopseudohypoparathyroidism), whereas maternal transmission leads to AHO in combination with hormone resistance to parathyroid hormone, thyrotropin, and gonadotropins (pseudohypoparathyroidism type IA). These phenotypic differences are explained by tissue-specific imprinting of the *GNAS1* gene, which is expressed primarily from the maternal allele in the thyroid, gonadotropes, and the proximal renal tubule. In most other tissues, the *GNAS1* gene is expressed biallelically.