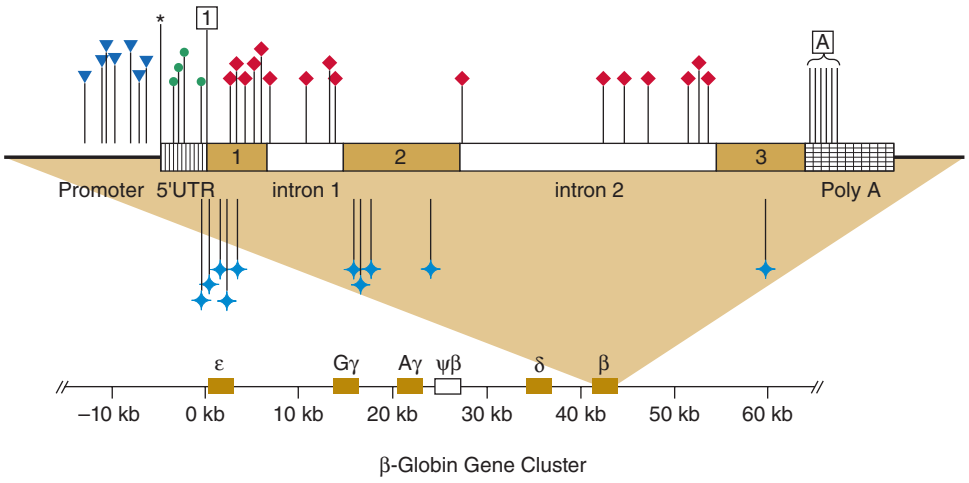

FIGURE 82-9 Point mutations causing β thalassemia as example of allelic heterogeneity. The β-globin gene is located in the globin gene cluster. Point mutations can be located in the promoter, the CAP site, the 5′-untranslated region, the initiation codon, each of the three exons, the introns, or the polyadenylation signal. Many mutations introduce missense or nonsense mutations, whereas others cause defective RNA splicing. Not shown here are deletion mutations of the β-globin gene or larger deletions of the globin locus that can also result in thalassemia. ▼, promoter mutations; *, CAP site; •, 5′UTR; 1, initiation codon; ♦, defective RNA processing; ✦, missense and nonsense mutations; A, Poly A signal.

an enhanced rate of deamination to uracil, which is then replaced with thymine. This C → T transition (or G → A on the opposite strand) accounts for at least one-third of point mutations associated with polymorphisms and mutations. In addition to the fact that certain types of mutations (C → T or G → A) are relatively common, the nature of the genetic code also results in overrepresentation of certain amino acid substitutions.

Polymorphisms are sequence variations that have a frequency of at least 1%. Usually, they do not result in a perceptible phenotype. Often they consist of single base-pair substitutions that do not alter the protein coding sequence because of the degenerate nature of the genetic code (synonymous polymorphism), although it is possible that some might alter mRNA stability, translation, or the amino acid sequence (nonsynonymous polymorphism) (Fig. 82-10). The detection of sequence variants poses a practical problem because it is often unclear whether it creates a mutation with functional consequences or a benign polymorphism. In this situation, the sequence alteration is described as *variant of unknown significance (VUS)*.

MUTATION RATES Mutations represent an important cause of genetic diversity as well as disease. Mutation rates are difficult to determine in humans because many mutations are silent and because testing is often not adequate to detect the phenotypic consequences. Mutation rates vary in different genes but are estimated to occur at a rate of ~10^{-10}/bp per cell division. Germline mutation rates (as opposed to somatic mutations) are relevant in the transmission of genetic disease. Because the population of oocytes is established very early in development, only ~20 cell divisions are required for completed oogenesis, whereas spermatogenesis involves ~30 divisions by the time of puberty and 20 cell divisions each year thereafter. Consequently, the probability of acquiring new point mutations is much greater in the male germline than the female germline, in which rates of aneuploidy are increased (Chap. 83e). Thus, the incidence of new point mutations in spermatogonia increases with paternal age (e.g., achondrodysplasia, Marfan's syndrome, neurofibromatosis). It is estimated that about 1 in 10 sperm carries a new deleterious mutation. The rates for new mutations are calculated most readily for autosomal dominant and X-linked disorders and are ~10^{-5}–10^{-6}/locus per generation. Because most monogenic diseases are relatively rare, new mutations account for a significant fraction of cases. This is important in the context of genetic counseling, because a new mutation can be transmitted to the affected individual but does not necessarily imply that the parents are at risk to transmit the disease to other children. An exception to this is when the new mutation occurs early in germline development, leading to *gonadal mosaicism*.

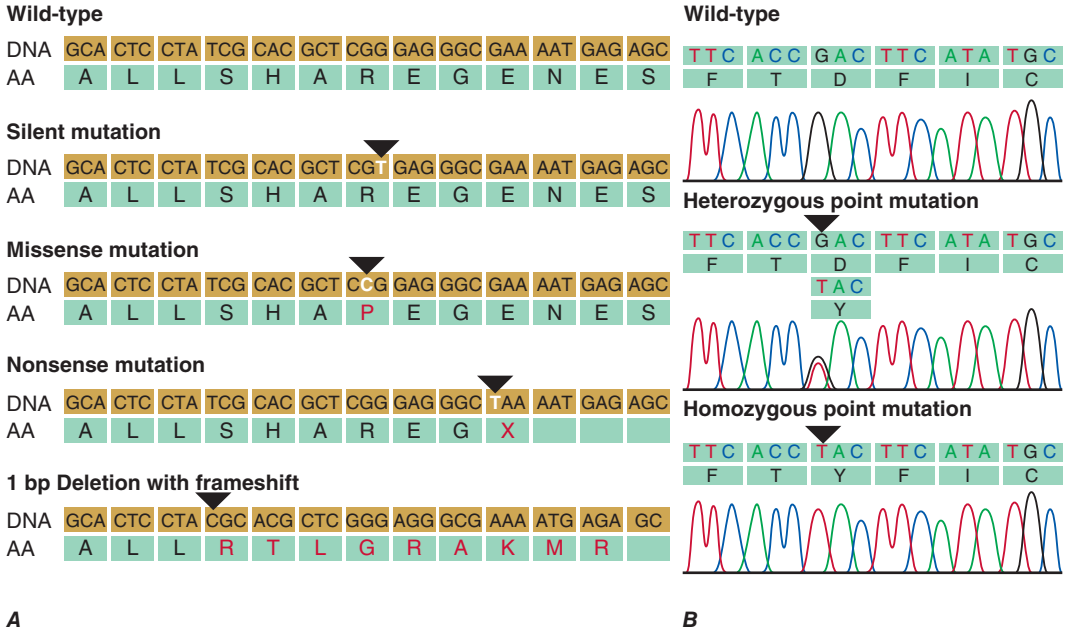

FIGURE 82-10 ***A.*** Examples of mutations. The coding strand is shown with the encoded amino acid sequence. ***B.*** Chromatograms of sequence analyses after amplification of genomic DNA by polymerase chain reaction.