



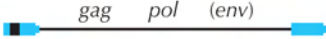



			Length	Copy number	Fraction of genome
LINEs	Autonomous		6–8 kb	850,000	21%
	Nonautonomous		100–300 kb		
Retrovirus-like elements	Autonomous		6–11 kb	450,000	8%
	Nonautonomous		1.5–3 kb		
DNA transposons	Autonomous		2–3 kb	300,000	3%
	Nonautonomous		80–3000 bp		

FIGURE 8.19. Examples of the more abundant repetitive sequences (all of which are some form of transposon) found in the human genome. These can be classified by the type of element and whether they are autonomous (encode the means of transposition) or nonautonomous (depend on exogenous factors for transposition). Shown are four types of elements, their general structure, length, copy number, and fraction of the genome they represent. The first three listed, LINEs, SINEs, and retrovirus-like elements, are forms of retroelements that transpose through an RNA intermediate. LINEs and SINEs are related forms of retrotransposons; LINEs are autonomous (encoding a pol protein) and SINEs are nonautonomous. Retrovirus-like elements, which include retrotransposons, have long terminal repeats at each end (shown in *blue*) with autonomous elements encoding a pol protein. DNA transposons are frequently flanked by inverted repeats (*small triangles*) with autonomous elements encoding a transposase protein.

8.19, redrawn from International Human Genome Sequencing Consortium, *Nature* **409**: 860–921, © 2001 Macmillan, www.nature.com