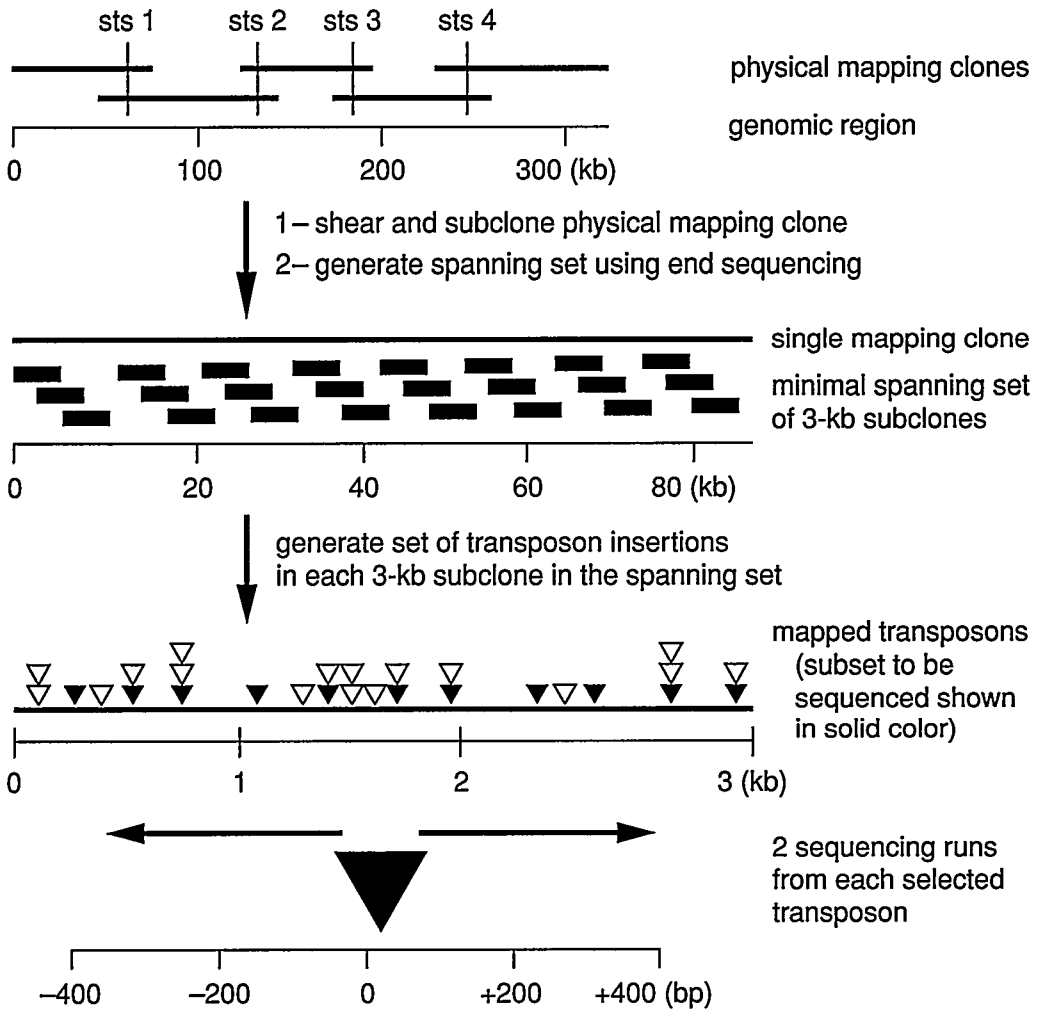

Sequencing Strategy. *The directed sequencing strategy used at LBNL involves four steps: (1) generate a P1-based physical map (using STS-content mapping) to provide a set of minimally overlapping clones, (2) shear and subclone each P1 clone into 3-kilobase fragments and identify a minimally overlapping subclone set, (3) generate and map transposon inserts in each subclone, and (4) sequence using commercial primer-binding sites engineered into the transposon. Subclone sequences are then assembled and edited, and the gaps are identified. P1 clones are reconstructed, and the resulting composite data is analyzed, annotated, and finally submitted to the databases. The production sequencing effort has generated 12 megabases of finished, double-stranded genomic DNA sequence from both* Drosophila *and human templates.* *[Source: Adapted from figure provided by LBNL]*

various methods of fingerprinting, hybridization, and identification of overlapping STSs. However, these techniques do not readily yield information about sequence orientation, the extent of overlap of these elements, or the size of gaps in the map. Ulli Weier of the Resource developed the QDFM method of physical map assembly that enables the mapping of cloned DNA directly onto linear, fully extended DNA molecules. QDFM allows unambiguous assembly of critical elements leading to high-resolution physical maps. This task now can be accomplished in less than 2 days, as compared with weeks by conventional methods. QDFM also enables detection and characterization of gaps in existing physical maps—a crucial step toward completing a definitive human genome map.