FIGURE S7.—Predicting alleles from mate-pair sets. The process used to chain sets into predicted alleles entails tracking the affected genome region and jumping junctions when sets are encountered. Diagrams show the results of tracking beginning from the left side when applied to (A) a deletion set, (B) a duplication set, (C) overlapping deletion and duplication sets, and (D) overlapping inversion sets. Sets are drawn as in Figure S3. Solid lines denote the DNA segments incorporated into predicted alleles, with arrows to indicate the tracking direction, connected by dashed lines to indicate the jumped anomalous junctions. Predicted CNVs are indicated. In (C), tracking assumes the duplication and deletion are on the same allele, but they could be on separate alleles. In (D), the two inversion sets must be on the same allele to be consistent with chromosome continuity. In all, actual junction positions are unknown and so are estimated from the closest read position.