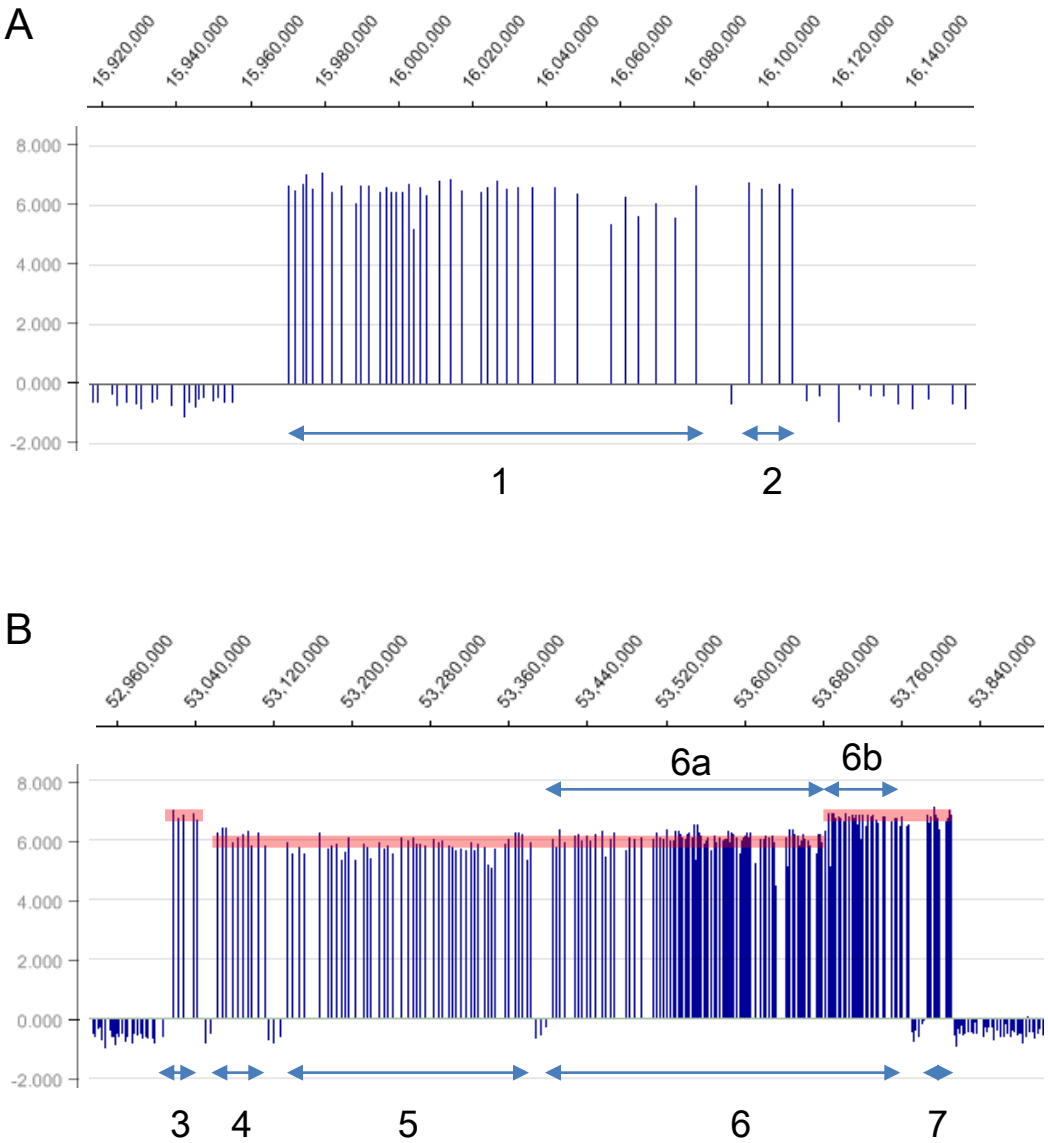
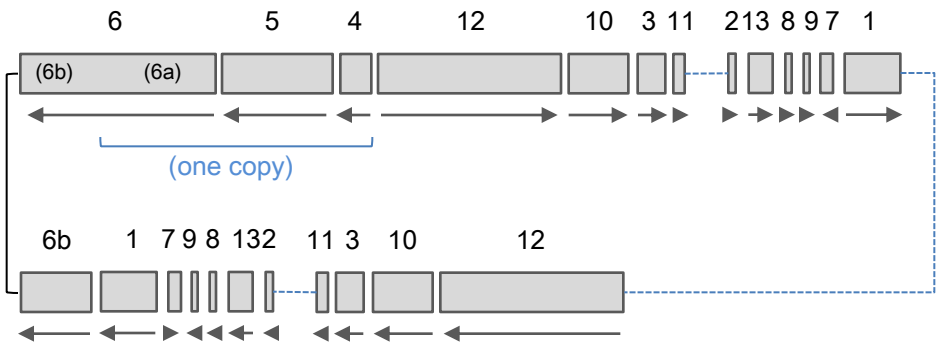
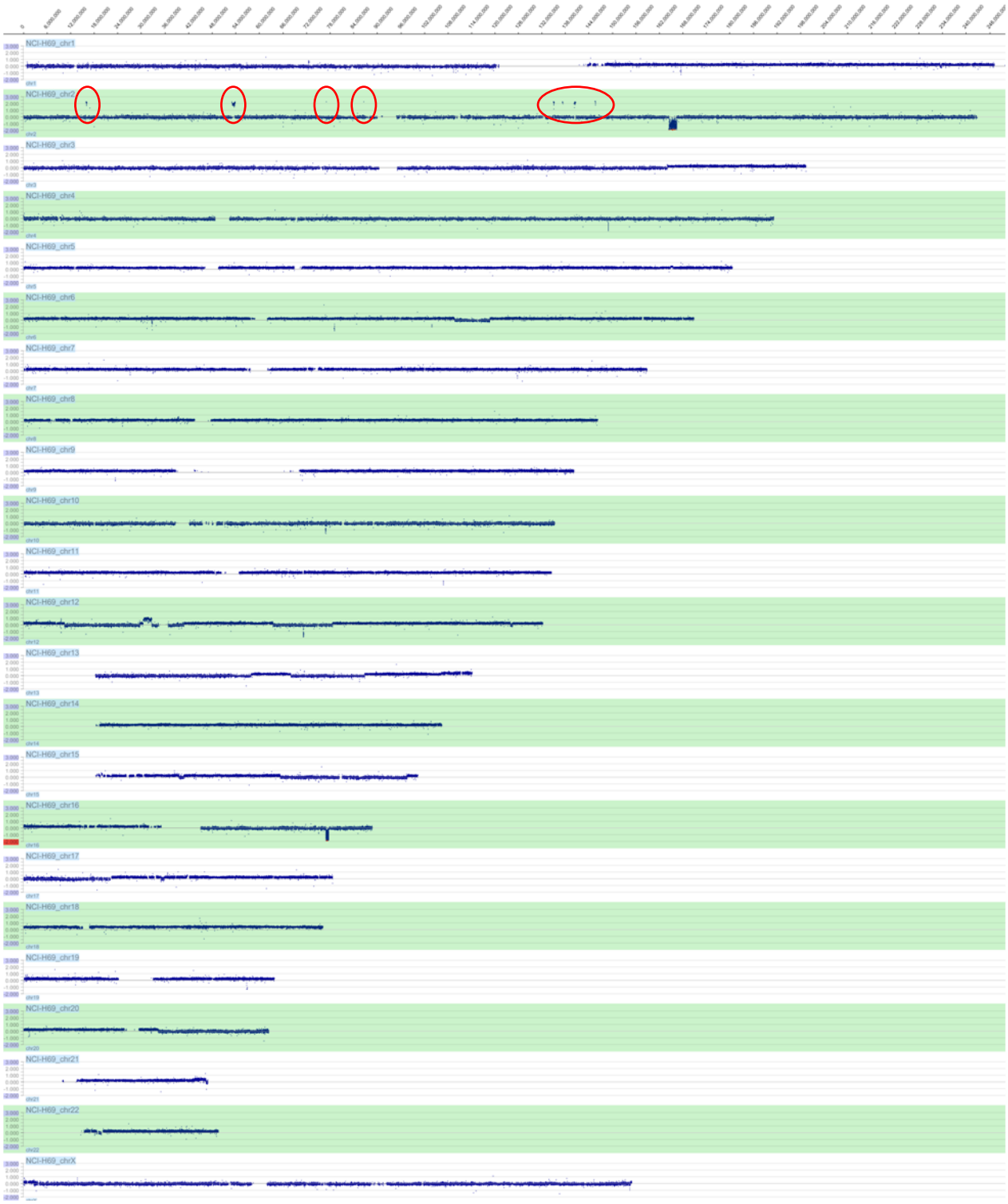


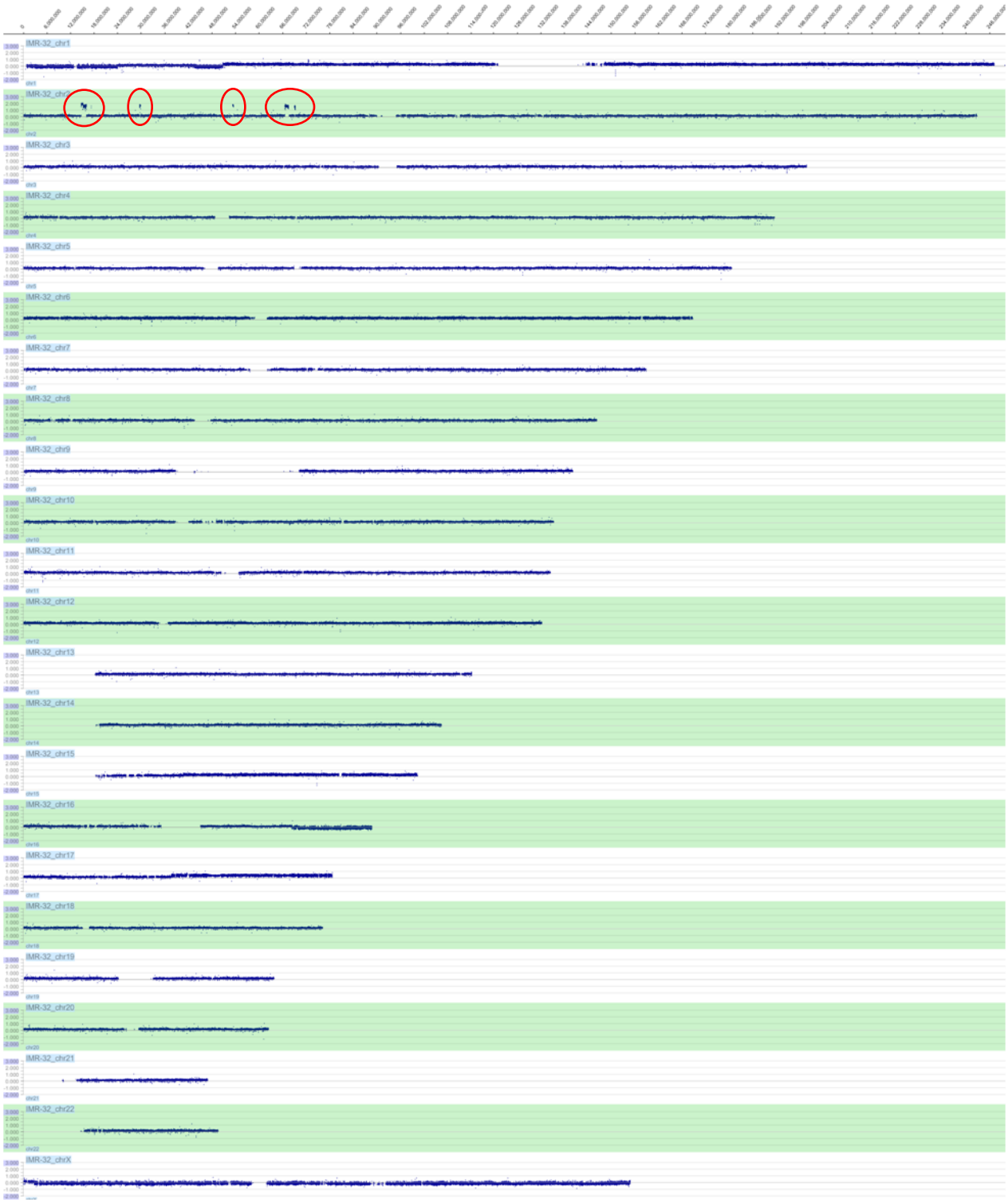
Supplementary Figure 1. Copy number profiles of chromosome 2 in NCI-H69 analyzed by a high-density array-CGH. Enlarged profiles of amplified regions including segments 1 and 2 (**A**) and segments 3 to 7 (**B**) are shown. Fold copy number changes relative to normal genomic DNA were plotted in $\log_2$ scale against the genome sequence coordinate. Each segment is indicated by a number with a blue line plus arrows. Segment 6 is divided into sub-segments 6a and 6b by their fold change values (5.8±0.3 and 6.8±0.4 in log2 scale, respectively), which are marked with red lines in **B**. Segments 4 and 5 exhibit the same fold change values as sub-segment 6a.



Supplementary Figure 2. Structural model of an incomplete dimeric amplicon represented by connectivity of the segments. Each segment is shown as a rectangular block with a segment number. Arrows below the blocks indicate sequence orientations against the human genome sequence. Note: Segments 4, 5 and 6a are in one copy, while the remaining segments are in two copies. Junction site sequences between segments 2 and 11 and between 1 and 12 have not been identified.



Supplementary Figure 3. Copy number profiles of the NCI-H69 genomic DNA analyzed by a high-density array-CGH. Fold copy number changes relative to normal genomic DNA are plotted in $\log_{10}$ scale against the genome sequence coordinate. Highly amplified regions are indicated by red circles.



Supplementary Figure 4. Copy number profiles of the IMR-32 genomic DNA analyzed by a high-density array-CGH. Fold copy number changes relative to normal genomic DNA are plotted in $\log_{10}$ scale against the genome sequence coordinate. Highly amplified regions are indicated by red circles.