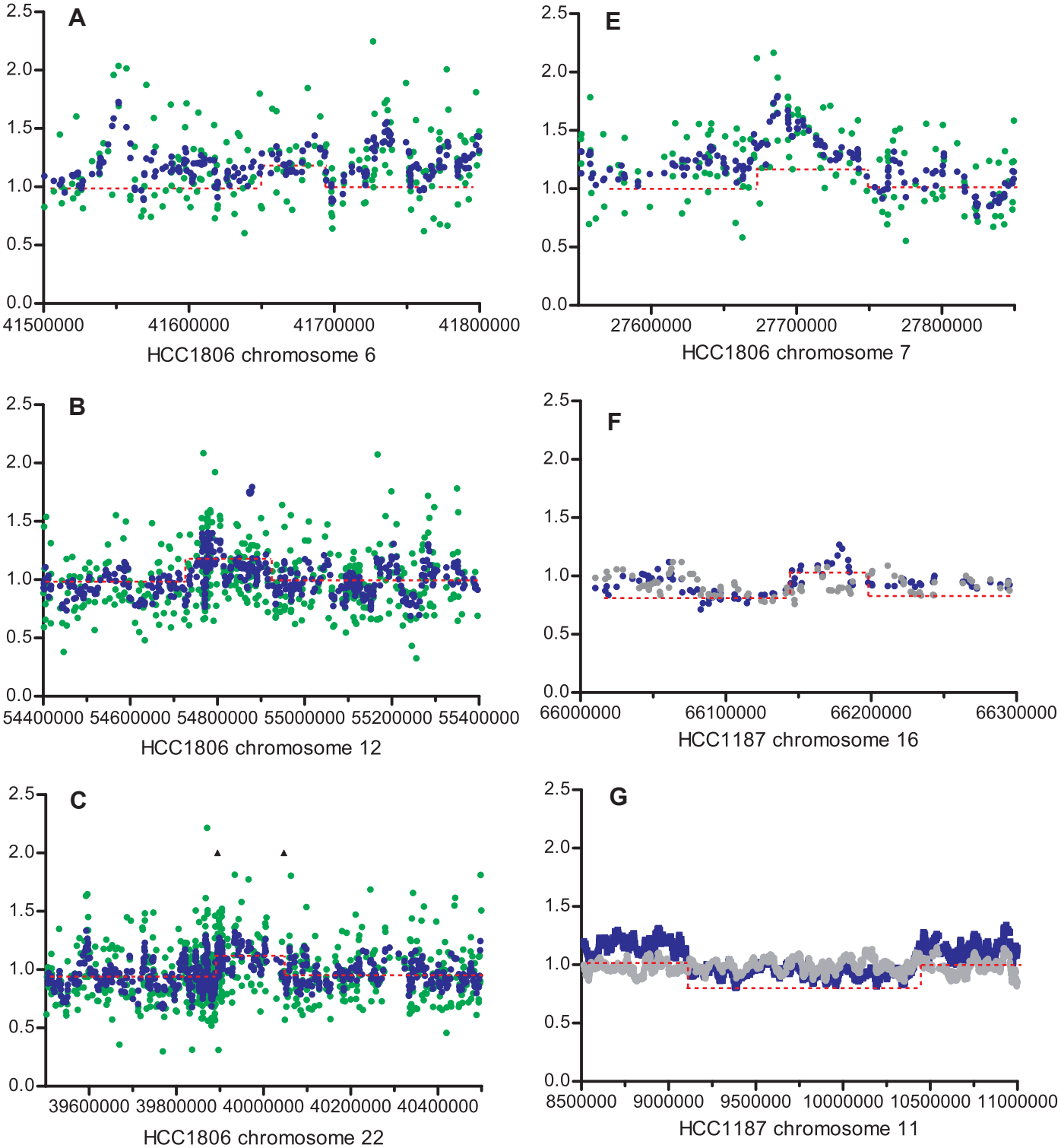
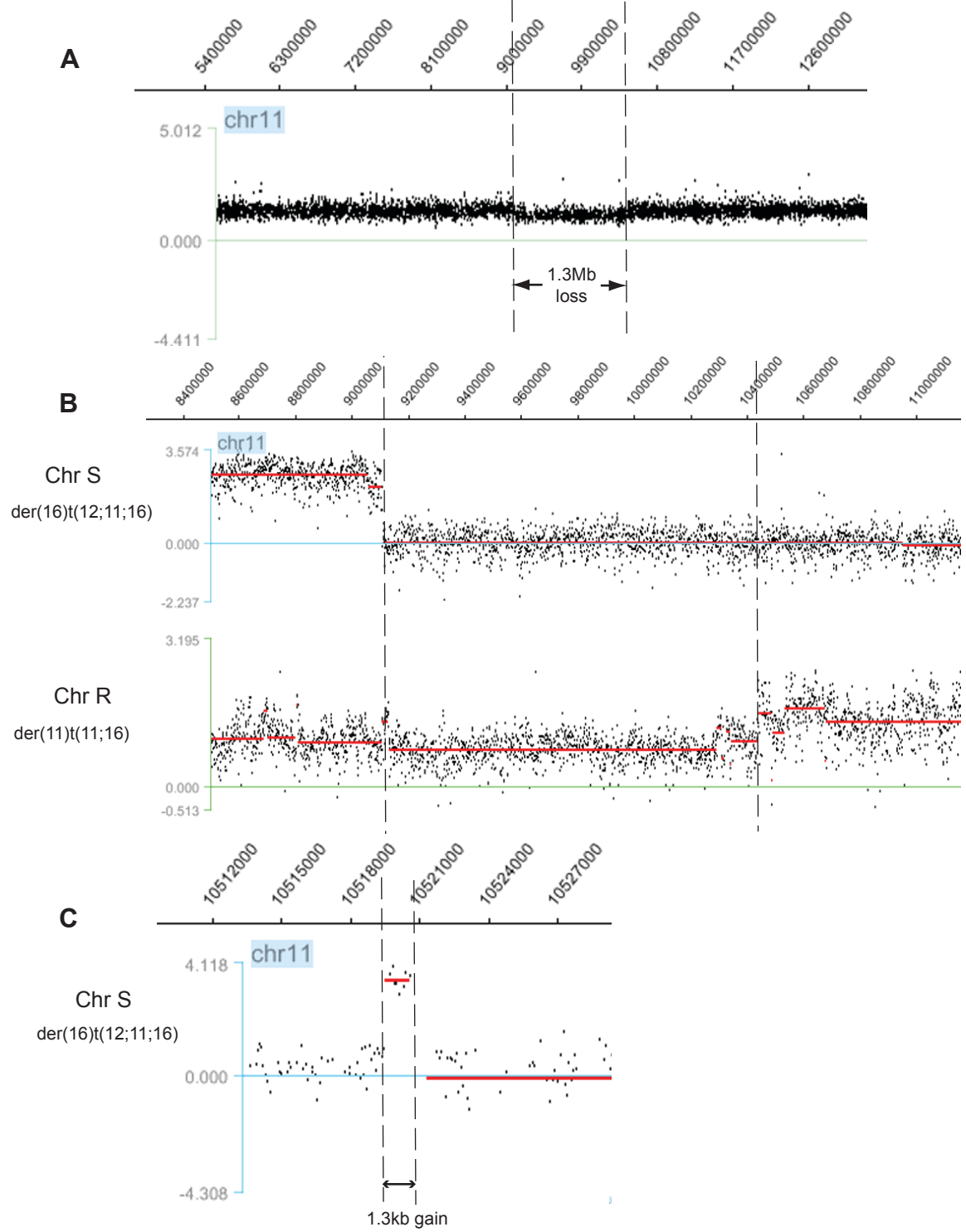
Suppplemental Figure 1. Regions of overlap of translocation products by array-CGH



SNP6 array CGH profiles (Bignell et al. 2010) for regions with an apparently balanced translocation on chromosome 6 (A), chromosome 12 (B), chromosome 22 (C), chromosome 3 (D), chromosome 7 (E), chromosome 16 (F) and chromosome 11 (G). Copy number intensity measurement from the PICNIC algorithm (Greenman et al. 2010) is shown on the vertical axis and genomic position is shown on the horizontal axis. The interval shown is 0.3, 1 or 2.5 Mb. Red dashed lines indicate the expected region of copy number gain due to overlap and approximate expected step intensity, based on median values for flanking regions at the expected copy number. The data shown is: raw probe data (green spots); running averages of 5 points (blue spots); running average of 21 points (blue square, G only); matched normal cell line (grey spots, F and G only).

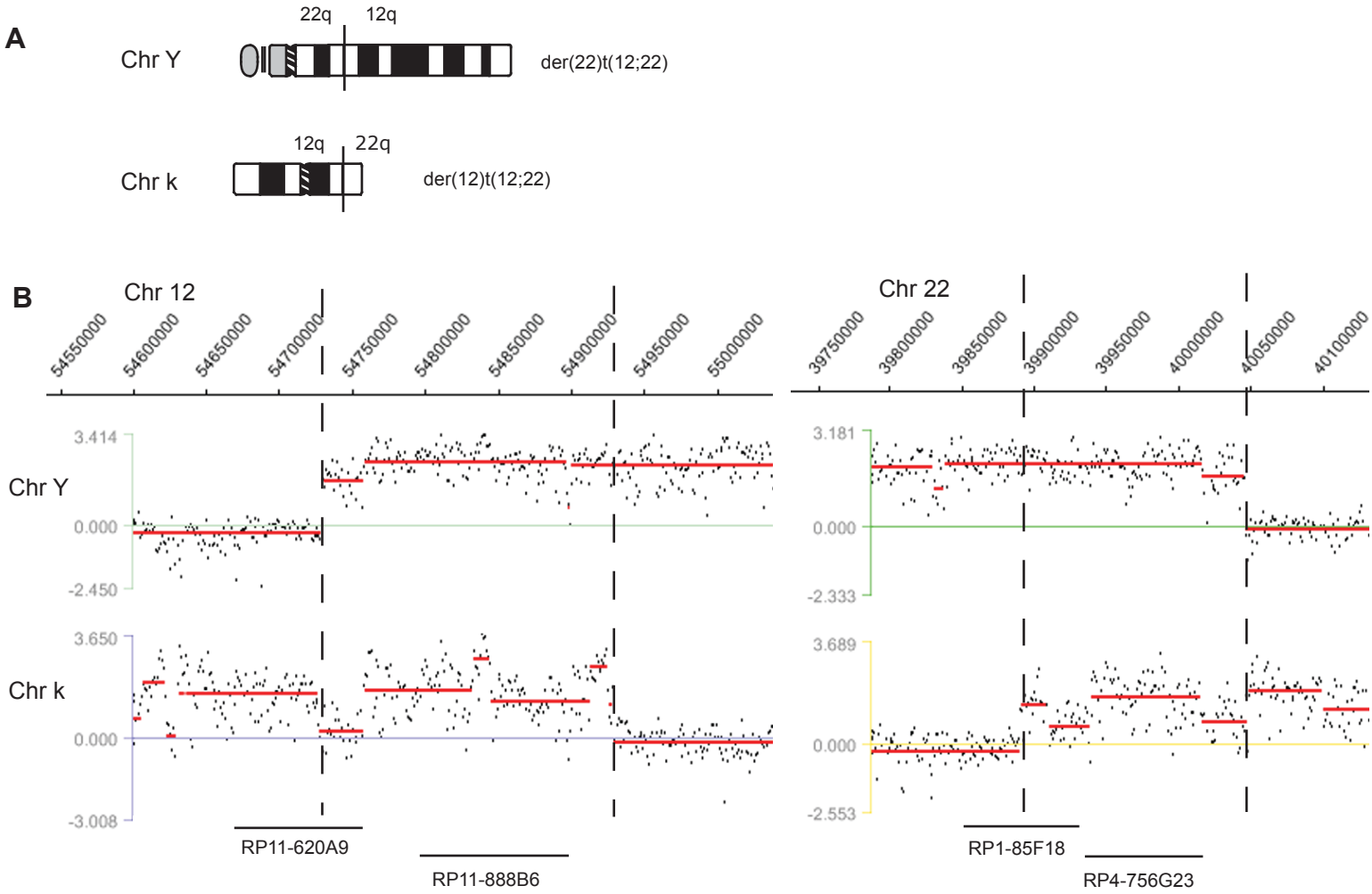


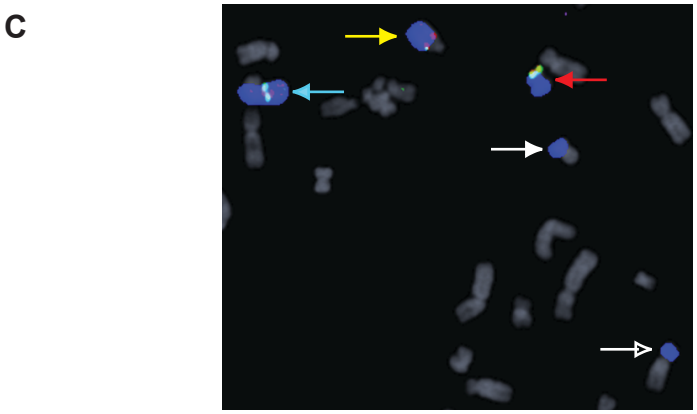
Supplemental Figure 2 Loss of 1.3Mb on chromosome 11 at the reciprocal t(11;16) translocation in HCC1187

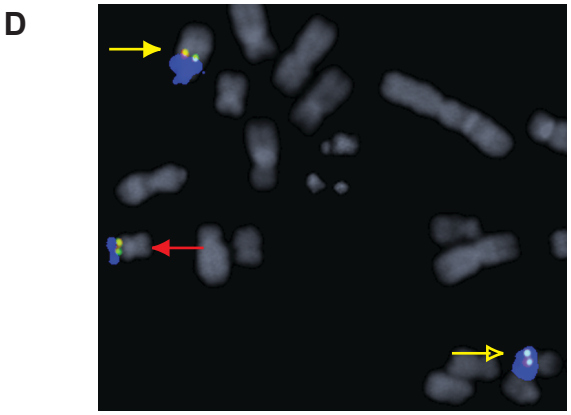
A. SNP6 array CGH profile for a region of chromosome 11 in HCC1187 (Bignell et al., 2010). A region of loss is shown between broken lines.

B. Hybridization of Chr S and Chr R to a custom Nimblegen oligonucleotide array covering a specified region on chromosome 11. Breakpoints are indicated with a broken line.

C. Hybridization of Chr S to a custom Nimblegen oligonucleotide array covering a specified region on chromosome 11. A small 1.3kb gain is shown, which is seen at the cloned breakpo junction.







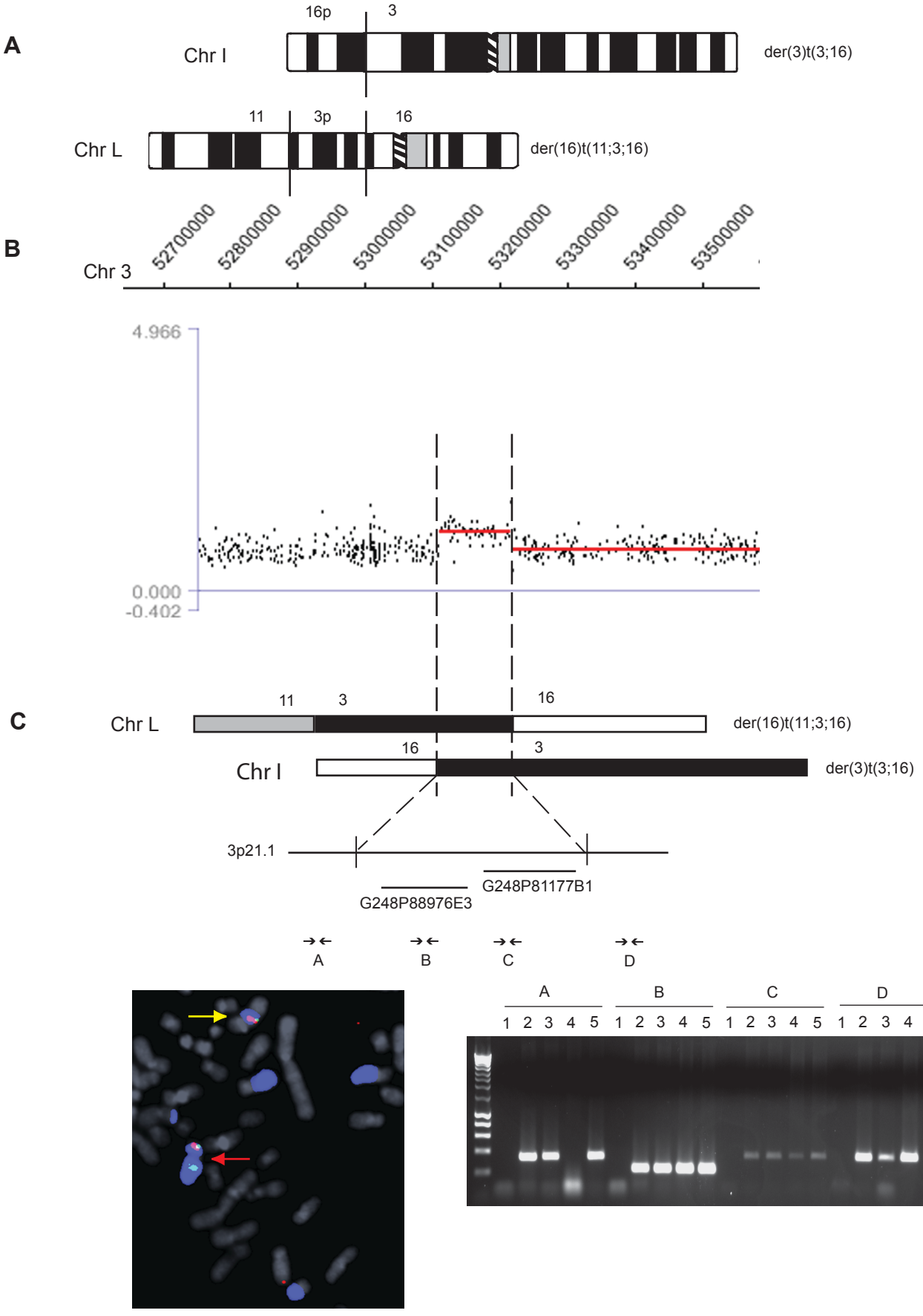
Supplemental Figure 3 HCC1806 t(12;22) 'overlapping breakpoint' duplication

A. Schematic representation of the products of the reciprocal translocation between chromosomes 12 and 22 in HCC1806 (Chr Y and Chr k).

B. Hybridization of Chr Y and Chr k to a custom Nimblegen oligonucleotide array covering specified regions on chromosome 12 (left) and chromosome 22 (right). Breakpoints are indicated with a broken line. The approximate location of BAC clones used in FISH mapping is shown.

C. Breakpoint mapping by FISH using chromosome 12 BACs, RP11-888B6 (shown in red) and RP11-620A9 (shown in green). Chromosome 12 is shown in blue. The der(22)t(12;22) (Chr Y) is indicated with a yellow arrow, the der(12)t(12;22) (Chr k) with a red arrow, the der(12)t(12;13) with a blue arrow, the der(12)t(2;12) with a white arrow and the der(9)t(9;12) with an open white arrow.

D. FISH mapping with chromosome 22 PACs. Chromosome 22 is shown in blue and PACs RP4-756G23 and RP1-85F18 are shown in red and green respectively. The der(22)t(12;22) (Chr Y) is indicated with a yellow arrow, the der(12)t(12;22) (Chr k) with a red arrow and the der(21)t(21;22) with an open yellow arrow.

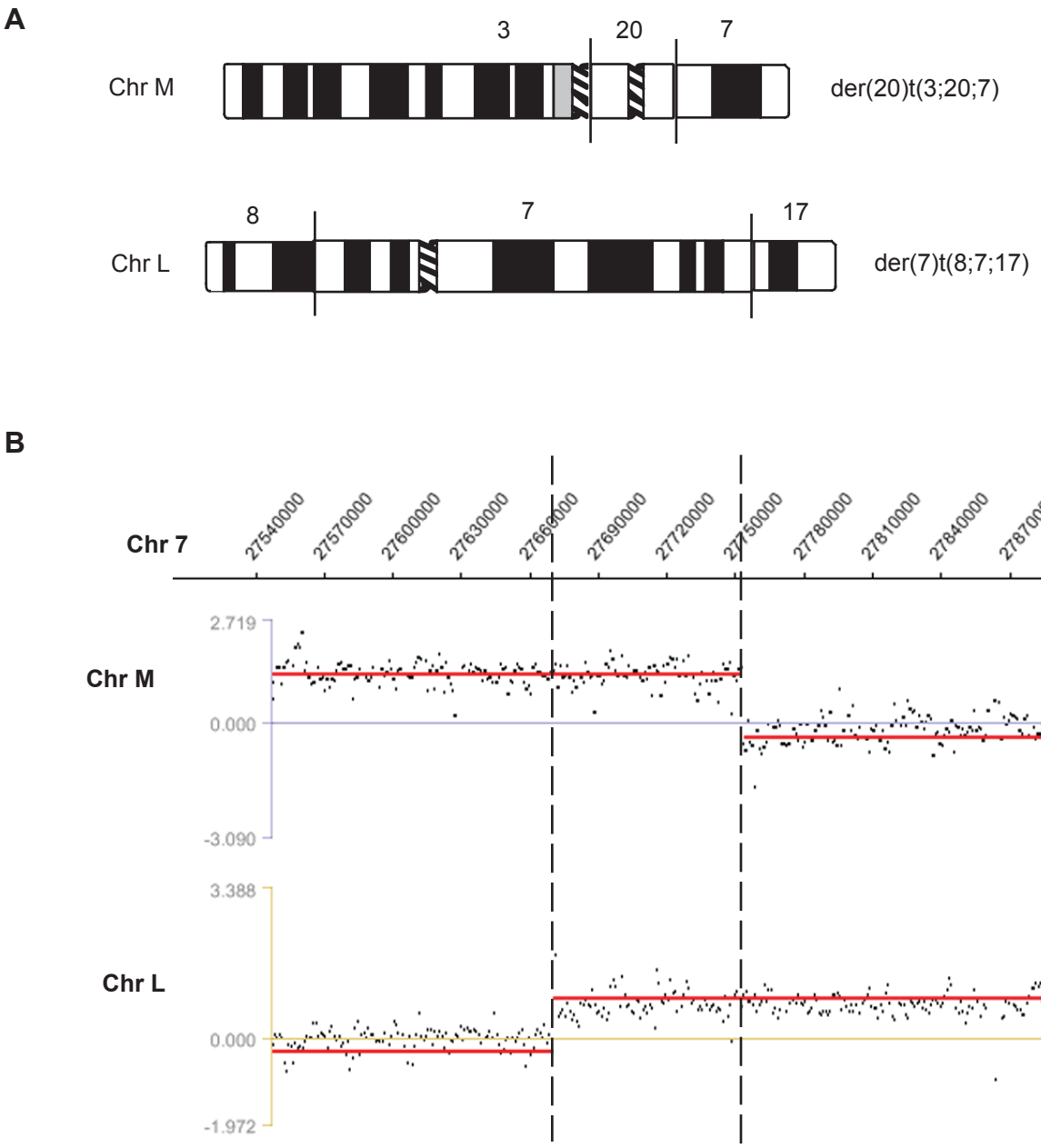


Supplemental Figure 4 HCC1806 t(3;16) 'overlapping breakpoint' duplication

A. Schematic representation of the products of the reciprocal translocation between chromosomes 3 and 16 in HCC1806. Breakpoint junctions are indicated with a black line.

B. SNP6 array CGH profile for a region of chromosome 3p in HCC1806. A region of duplication is shown between broken lines.

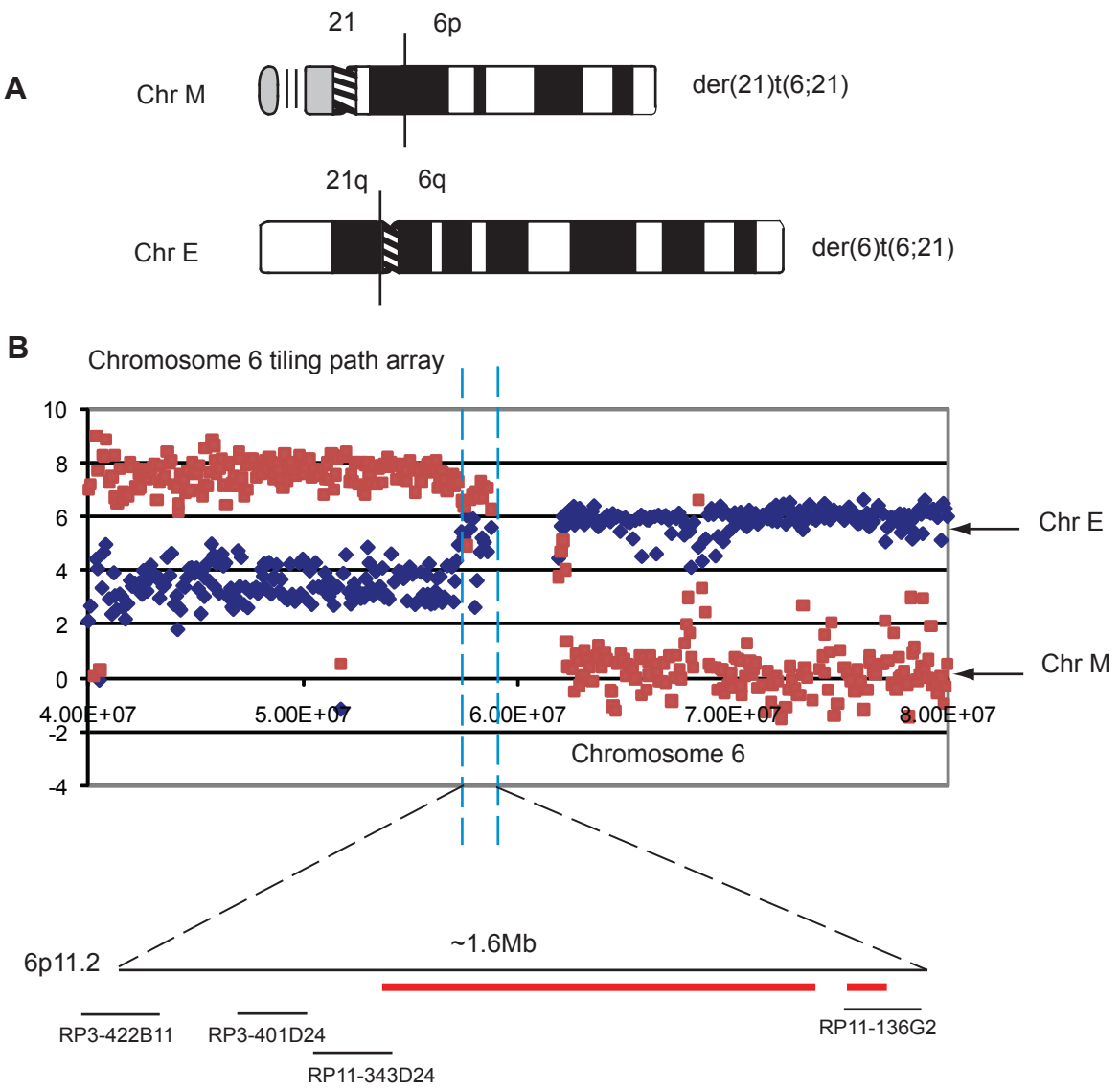
C. Breakpoint mapping using FISH and PCR on flow-sorted chromosomes. The approximate location of fosmids G248P88976E3 and G248P81177B1 and chromosome 3 primer pairs A, B, C and D are shown. FISH with fosmids G248P88976E3 (red) and G248P81177B1 (green) is shown. Chromosome 3 is shown in blue. Chr I is indicated with a yellow arrow and Chr L is indicated with a red arrow. PCR results with primers A, B, C and D are shown. Lanes are labelled 1 (negative water control), 2 (normal female genomic DNA), 3 (HCC1806 genomic DNA), 4 (HCC1806 Chr I) and 5 (HCC1806 Chr L).



Supplemental Figure 5 HCC1806 Balanced chromosome 7 'overlapping breakpoint' duplication

A. Schematic representation of the products of the balanced chromosome 7 breakpoint in HCC1806. Breakpoint junctions are indicated with a black line.

B. Hybridization of Chr M and Chr L to a custom Nimblegen oligonucleotide array covering a specified region on chromosome 7. Breakpoints are indicated with a broken line.



Supplemental Figure 6 DU4475 t(6;21) 'overlapping breakpoint' duplication

A. Schematic representation of the products of the reciprocal translocation between chromosomes 6 and 21 in DU4475. Breakpoint junctions are indicated with a black line.

B. Hybridization of flow-sorted chromosomes der(21)t(6;21) (Chr M; red squares) and der(6)t(6;21) (Chr E; blue diamonds) to a chromosome 6 tiling path BAC array. Fluorescence log2ratios for chromosome 6 are shown. A change in the log2ratio represents the translocation breakpoint, indicated with a broken line. The duplicated region of chromosome 6 is shown between the broken lines. The approximate location of BACs and PACs used in FISH mapping is shown. Approximate regions of segmental duplication are indicated with red bars (based on the UCSC browser track, duplications of >1000 bp).

C. Breakpoint mapping by FISH using PAC RP3-422B11 (shown in red) and BAC RP11-136G2 (shown in green). Chromosome 6 is shown in blue. Normal chromosome 6 is indicated with a red arrow, the der(6) (Chr E) with a white arrow and the der(21) (Chr M) with an open white arrow.

D. Breakpoint mapping by FISH using PAC RP3-401D24 (shown in red) and BAC RP11-343D24 (shown in green). Chromosome 6 is shown in blue. Translocation products are indicated as in C.

Supplemental Figure 7 Replication bubbles can give tandem duplications and interstitial deletions. **A**, tandem duplication: a replication bubble is shown as in Figure 5, with points on the sequence a,b,c etc. To generate a tandem duplication from a replication bubble without inversion, a newly synthesised strand has to be joined to an old strand (as in sister chromatid exchange). One way this could perhaps happen is shown: a single-strand break causes fork stalling at the right-hand end of the replication bubble, and is ligated to the lagging strand on the other replication complex, where normally the next Okazaki fragment would be ligated. **B**, the resulting product with duplication, showing 5' to 3' strand only. **C**, deletion, the mirror-image of **A**: either the other broken end in **A** could be concatenated to new Okazhaki fragments, or, as shown, a break in the other parent strand could initiate synthesis of a new leading strand on the other end of the bubble. **D**, resulting deleted product, 3' to 5' strand only.