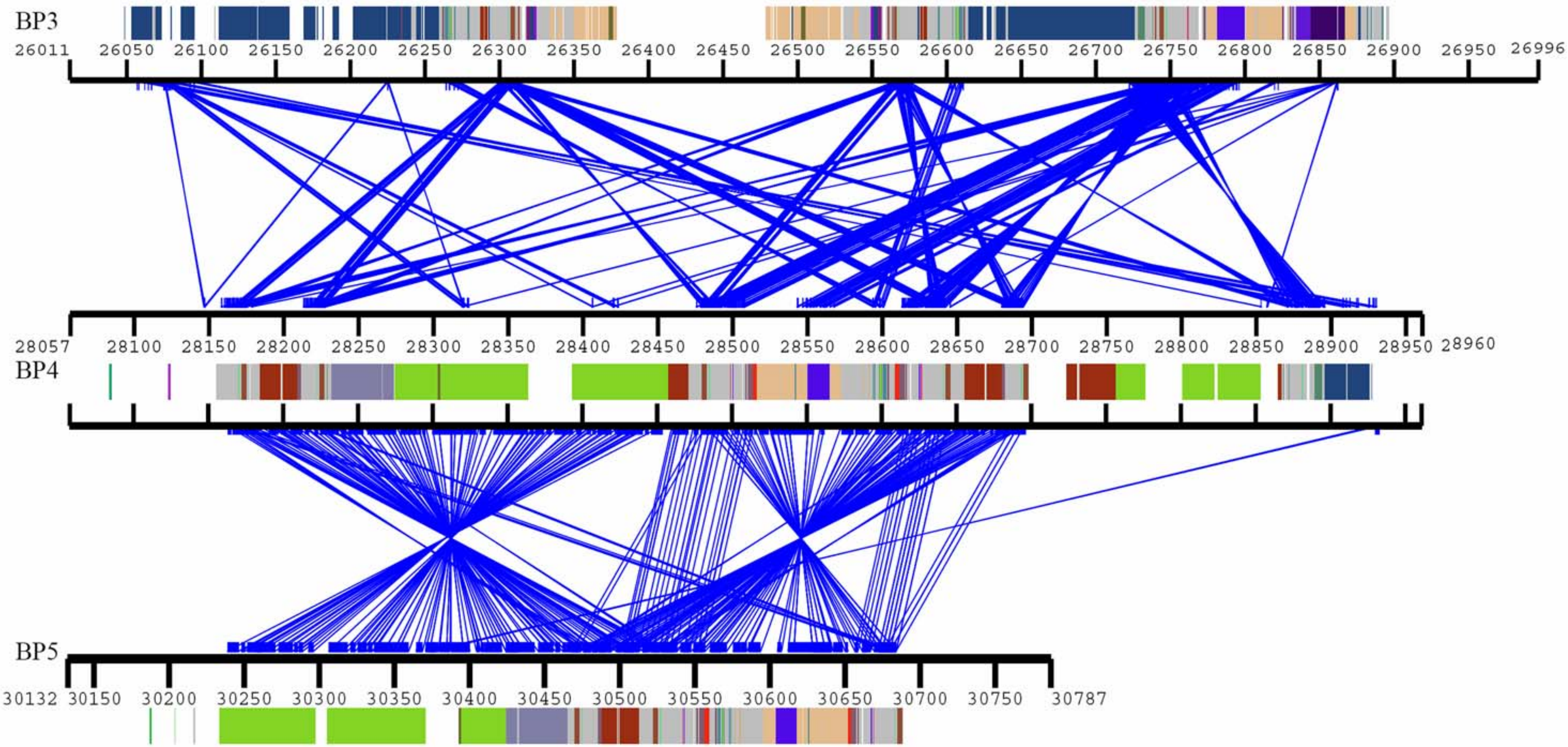

Supplementary Figure 2. Analysis of the duplication architecture of 15q13 breakpoint regions. For clarity, we used two different sensitivity thresholds, with homology between BP3, BP4, and BP5, as judged by pairwise WGAC alignments of identity ≥95% and ≥10kb in size (Bailey *et al*., 2001) represented by blue lines joining regions of 500 bp (BP3-BP4) or 2000 bp (BP4-BP5) of perfect identity. At each breakpoint, the underlying duplicon structure and orientation is shown by coloured arrows, with blocks of identical colour representing duplicons that share the same evolutionary origin (Jiang *et al*., 2007). The large, highly-identical duplicons which lie in an inverted orientation at BP4 relative to BP5 are clearly visible. In contrast, homology between BP3 and BP4/BP5 is much lower, consistent with the high frequency of BP4-BP5 rearrangements, relative to other 15q13 deletions.