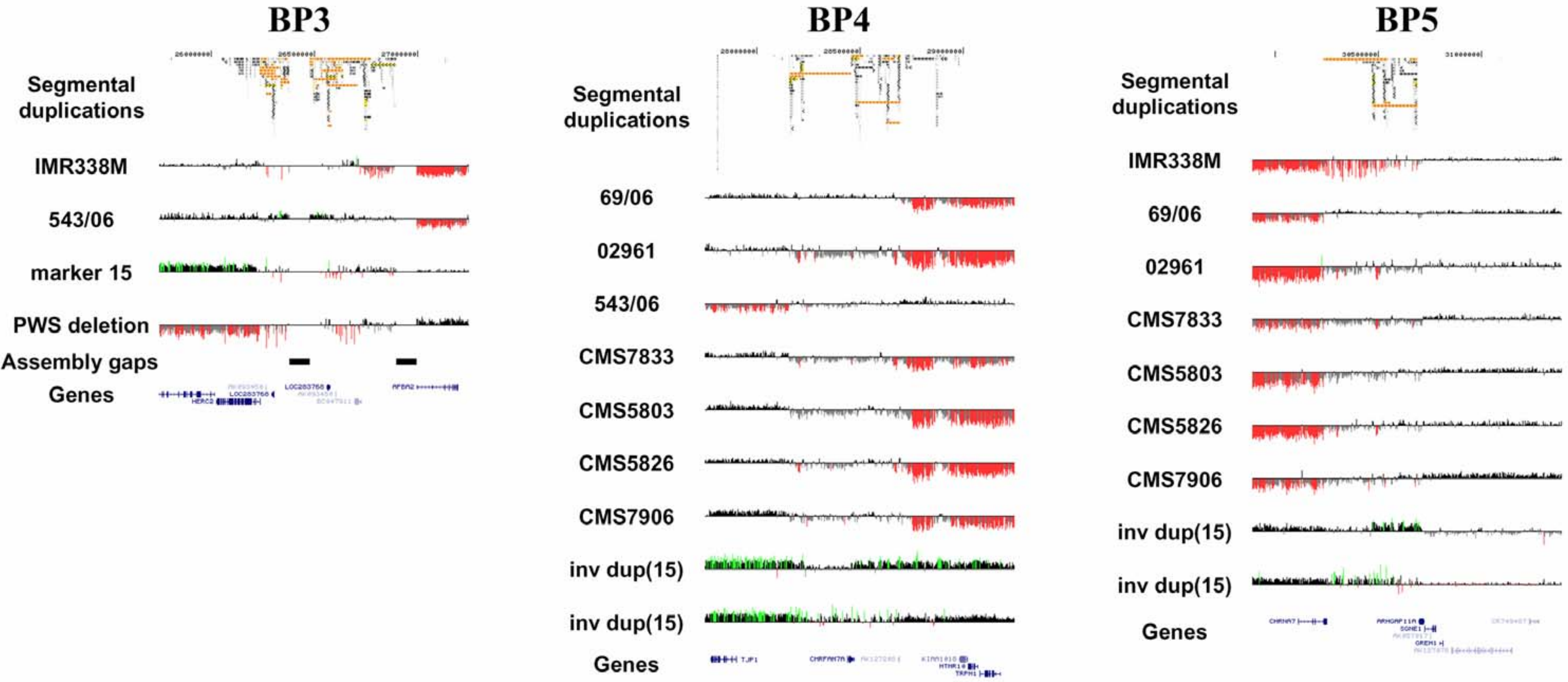

Supplementary Figure 3. High-resolution breakpoint mapping of 15q13 rearrangements. Each panel shows oligonucleotide array data for a 1.5 Mb region surrounding BP3, BP4, and BP5 (BP3, chr15:25,750,000-27,250,000; BP4, chr15:27,750,000-29,250,000; BP5, chr15:29,900,000-31,400,000). For each individual, deviations of probe log2 ratios from zero are depicted by grey/black bars, with those exceeding a threshold of 1.5 standard deviations from the mean probe ratio colored green and red to represent relative gains and losses, respectively. Tracks above each plot indicate segmental duplications (grey/yellow/orange bars representing duplications with 90-98%/98-99%/99-100% sequence identity, respectively).