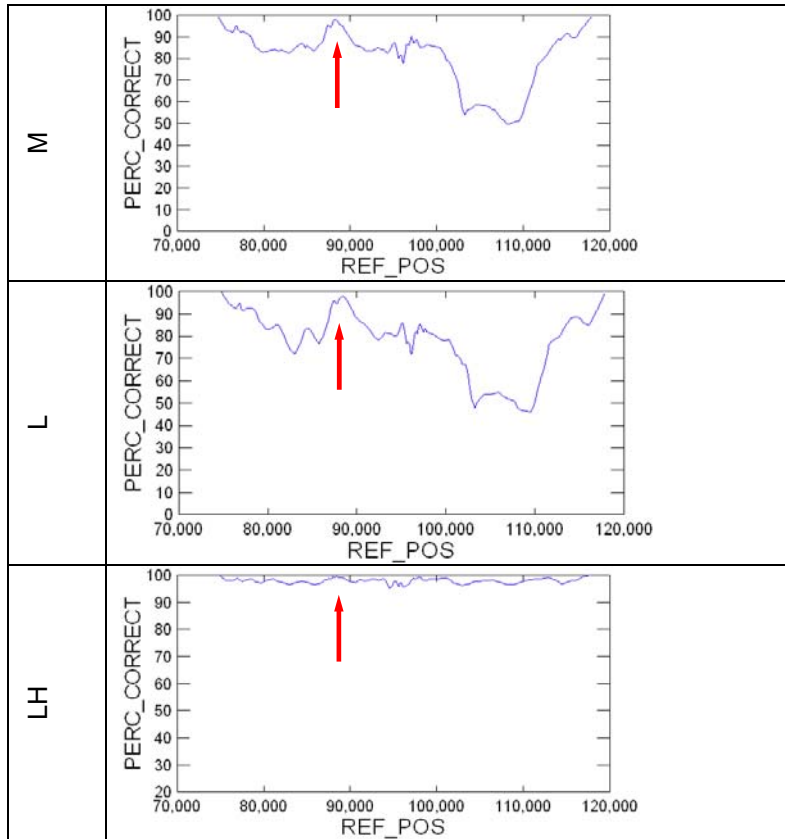


Supplemental Fig. S9



Supplemental Figure S9. Read correction accuracy along a segmental duplication (human 10q11 region, "right contig"). The figure only shows the "sequence family variant" sites (SFV; the other sites have constant, nearly 100% correction), and the right contig (the left contig has similar results). Corrected reads were aligned with the original sequence, and each base of each read was scored as "correct", "wrong", or "deleted". The X-axis is the coordinate of the "right contig"; the segmental duplication is located between positions 74741 and 117912. The red arrow point to the position of a large deletion between the two copies of the segmental duplication (1.5 kb; at position 88035). Note that standard MHAP ("M") and MHAP with L-masking ("L") fails at SFV sites, particularly at positions far from the edges of the segmental duplication and from the large internal deletion ; LH-masking ("LH") correctly handles the SFV throughout the whole segmental duplication. Data from 450 SFV sites; reads were corrected with the default falconsense algorithm.