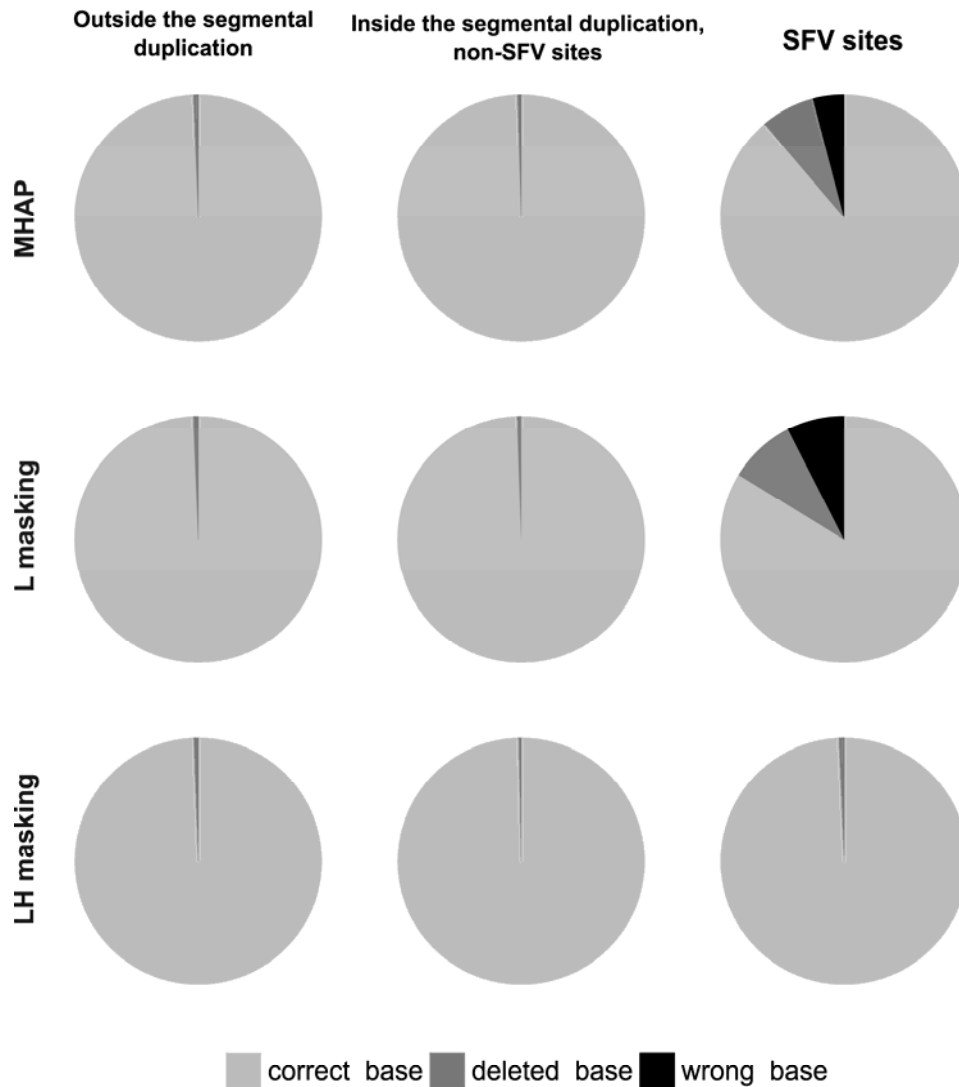Supplemental Figure S10. Read correction accuracy in the "model genome" (human 10q11 region), with the pbdagcon algorithm. Corrected reads were aligned with the original sequence, and each base of each read was scored as "correct", "wrong", or "deleted". Left column, sites outside the segmental duplication; middle column, sites within the segmental duplication and identical between the two copies; right column, "SFV sites " (for "sequence family variant"), which are located within the segmental duplication, at positions where two copies are different. Note that standard MHAP and MHAP with L-masking frequently fail at SFV sites, whereas LH-masking correctly handle them. Data from 450 sites of each type; reads were corrected with the pbdagcon algorithm (see Fig. 5 for the falconsense correction). The actual values at SFV sites (correct/deleted/wrong) are 89/7/4 (M), 84/9/8 (L-masking), and 99/1/0 (LH-masking); for the other sites it is always above 99% correct.