Supplemental Table S7. Assembly of the "model genome" (human 10q11 segmental duplication) with the three methods.

| Method* | Both contigs | | | Left contig (401 kb) | | | Right contig (201 kb) | | |
|---|---|---|---|---|---|---|---|---|---|
| | % sequence lost | % duplicated | Number of contigs | % sequence lost | % duplicated | Number of contigs | % sequence lost | % duplicated | Number of contigs |
| M | 6.3 | 19.2 | 11 | 4.2 | 15.0 | 6 | 10.6 | 27.7 | 5 |
| L | 3.3† | 1.0 | 3 | 2.5 | 0 | 1 | 4.9 | 3.0 | 2 |
| LH | 3.7† | 0 | 2 | 2.4 | 0 | 1 | 6.3 | 0 | 1 |

* "M", standard MHAP; "L", MHAP with low-frequency *k*-mer masking; "LH", MHAP with low and high frequency *k*-mer masking.

† Sequence lost is in the edges due to low coverage of the reads (this is an artifact caused by read simulation).