Supplemental Table S9. Assembly of human chromosomes 15 and 17 (sorted reads). Note that *k*-mer validation (L and specially LH) decreases the assembly errors (last three columns). The improvement in contiguity (NG50, largest contig) is more clearly seen in Supplemental Fig. S11.

Assembly*	Contig number	Largest contig	Total length	NG50	Misassemblies > 1kb †	Mismatches/100kb	Indels/100kb
human_chr15_M	343	7309895	83890337	1602477	78	86.32	95.86
human_chr15_L	330	8894105	83396444	2152643	73	83.96	94.97
human_chr15_LH	322	9276182	83558937	1897981	77	82.60	90.37
human_chr17_M	414	5412440	83732343	2081827	182	73.84	103.51
human_chr17_L	388	6783205	82743477	1606756	190	72.78	104.28
human_chr17_LH	361	8323604	82720089	2081188	152	67.11	96.96

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

† As reported by Quast (Gurevich et al. 2013): misassemblies > 1kb, or joining different chromosomes..