Supplemental Table S6. Assembly in the presence of coverage bias of Illumina reads. Note that the tested coverage gap (zero coverage over 2kb) is harmless for LH *k*-mer validation assembly.

Method*	Contig JSAF02032866		
	% sequence lost	% sequence duplicated	Number of contigs
M	3.3	10.0	7
LH	2.4	0	1
LH bias	2.4	0	1

<sup>\* &</sup>quot;M", standard MHAP; "LH", MHAP with low and high frequency k-mer masking, without bias in Illumina coverage bias; "LH bias", MHAP with low and high frequency k-mer masking, with full Illumina bias (zero coverage) across 2 kb.