S1 Table. Repetitive content and length aligned to the existing Wormbase *C. remanei* genome

Assembly	% Genome estimated repetitive	Length aligned
PX356 (1/2 data)	20	108.62
PX356 (full dataset)	22	106.64
1/2 data, haploidify	22	109.41
full data, haploidify option	20	104.69
full data, k-mer filtered (k=15)	16	110.01
full data, haploidify, k=11	10	89.63
full data, haploidify, k=13	12	96.35
full data, haploidify, k=15	**15**	**119.72**
full data, haploidify, k=17	15	114
full data, haploidify, filtered mate pairs	15	98.66