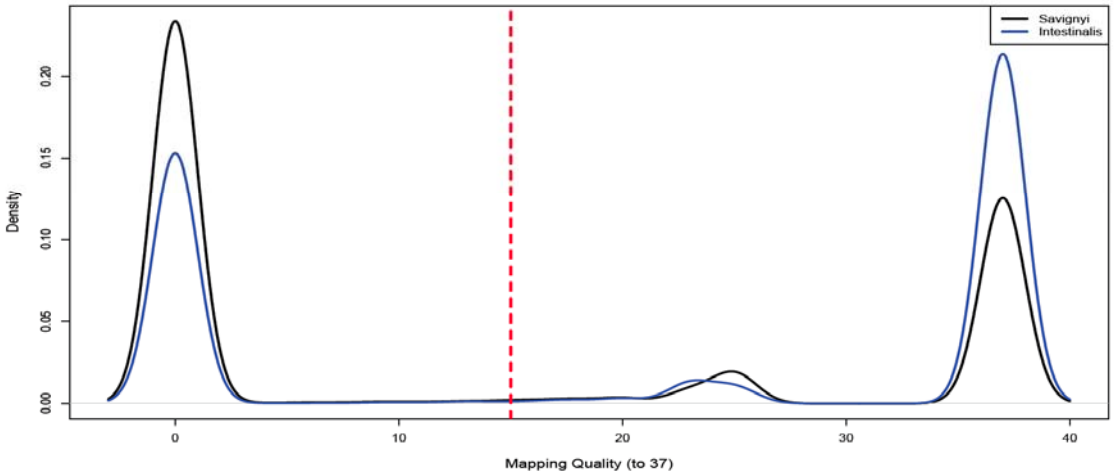
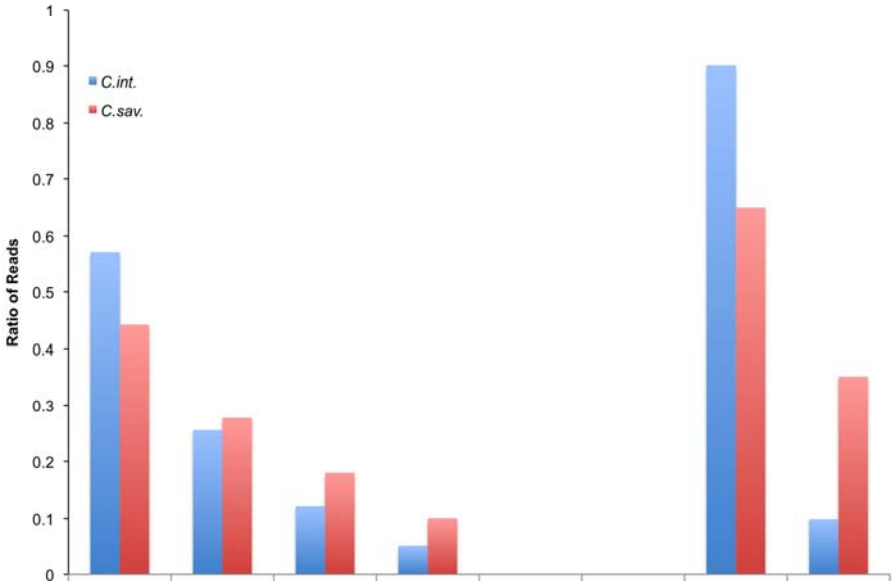


Figure S1 A probability density graph of distribution of read alignment mapping qualities in a *C. intestinalis (*blue line) and *C. savignyi* (black line) dataset is shown at bottom. Mapping qualities range from 0 to 37, with higher numbers meaning better quality alignment (Li *et al.* 2009). Red dashed line indicates the MapQ value of 15, which was used as the cutoff for mapping analysis.



	ED 0	ED 1	ED 2	ED 3	ED 4	ED 5	Unique	Repeat
C.int.	0.57164	0.25562	0.12199	0.05066	0.00009	0	0.90104	0.09896
C.sav.	0.44208	0.27714	0.18003	0.10058	0.00014	0.00003	0.64915	0.35085

Figure S2 Comparison of Edit Distance (ED), and Unique versus Repeat character, of sequence reads between *C. intestinalis* (C.int.) and *C. savignyi* (C.sav.). The analysis was performed on a sample of 5 million randomly-picked reads. The values given for the two species represent the fraction of aligned reads with either the indicated ED assignment (0-5), or the Unique versus Repeat characteristic. Overall greater ED was observed in the *C. savignyi* sequence alignments in comparison to those from *C. intestinalis*. In addition, a greater fraction of *C. savignyi* reads were characterized as Repeats post-alignment. Both these factors, as well as others, contribute to the differential mapping quality of the two species (Li *et al.* 2009).

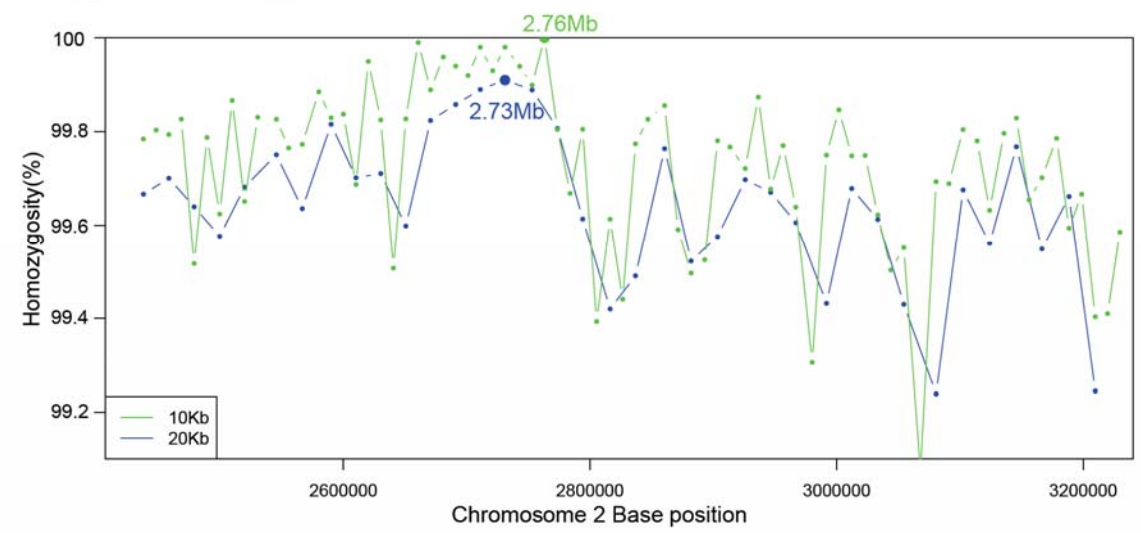


Figure S3 Window size differences for *C. intestinalis chongmague* genome-wide mapping. A zoomed in area of chromosome 2, near the peak calls for both a 10 Kb (green) and 20 Kb (blue) window analysis of homozygosity. Peaks of each analysis are shown as larger solid filled circles with positional values indicated next to each point.

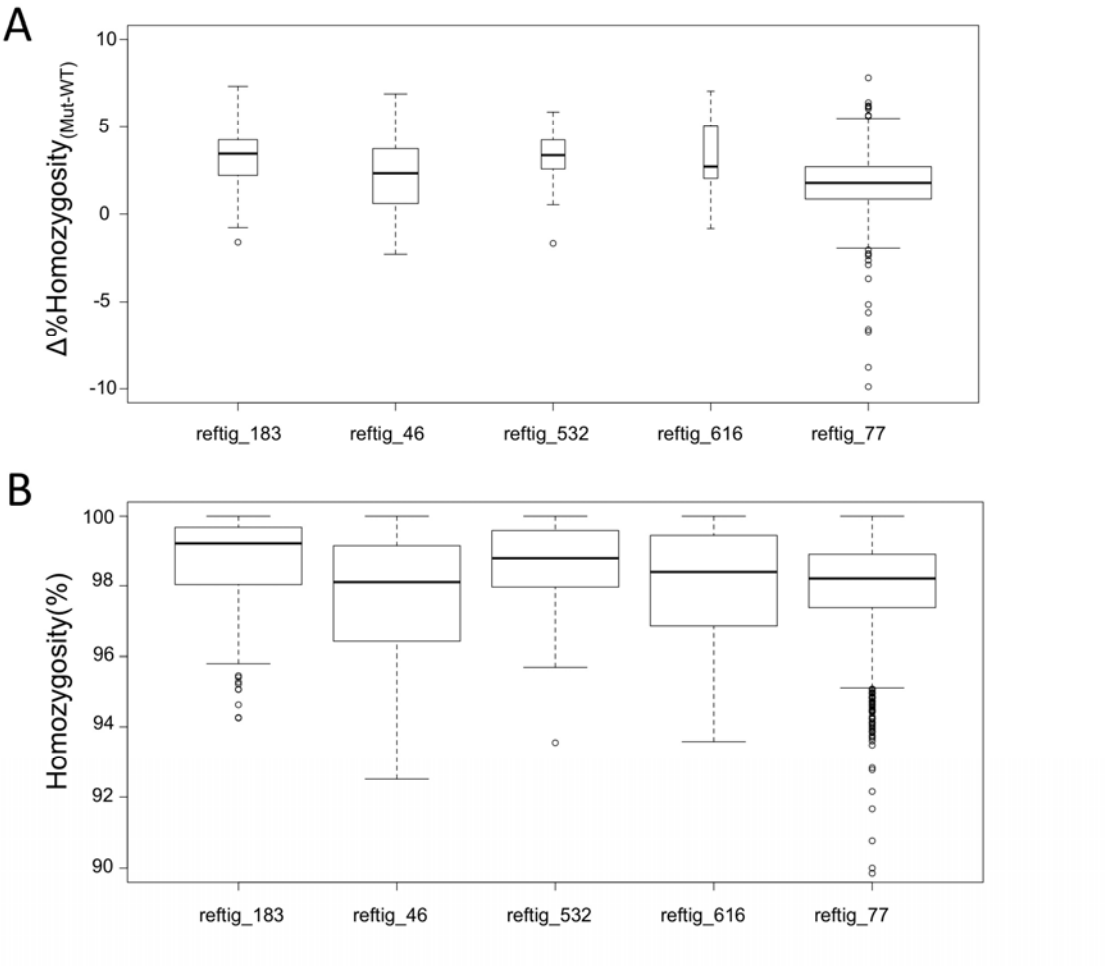


Figure S4 Homozygosity mapping analysis for *bugeye.* **A)** Box-whisker plot of Δhomozygosity values for each candidate high value reftig from Figure 2B. Δhomozygosity values were calculated for 1 Kb windows across each reftig. Width of boxplots depicts amount of data points for each reftig. Solid lines indicate median values, and whiskers indicate extreme values of reftig. Reftig 183 had the highest median Δhomozygosity value (3.46%)**. B)** Box-whisker plot of homozygosity values for the candidate reftigs (mutant sample only). Plots were done as above for panel A.

Table S1 Difference in coverage between coding and non-coding areas. Coding sequence regions were collected from Ensemble database (release 74) of each species' genome. A 5 Mb genomic region on Chromosome 1 of *C. intestinalis* and reftig 1 of *C. savignyi* were used for sampling differences in coverage in each sample.

Species	CDS		non-CDS		Average
	Coverage	Fraction of Average	Coverage	Fraction of Average	Coverage
C. savignyi	34.15	1.42	22.34	0.93	24.06
C. intestinalis	52.23	1.06	48.68	0.99	49.29

Table S2 Primers for qRT-PCR

Gene	Forward Primer	Reverse Primer
ci-Actin	CCAGCAGATTCCATACCAAG	CGTTTTCCCATCCATCGTAG
ci-alpha Laminin PP#1	CGGTGACGAAAATGAGGAAC	AGACACCACCACCCTCGTAG
ci-alpha Laminin PP#2	TCAAGTTGGTTCCGCATGTA	GTTCCACATTCCACCAATCC
cs-CAV3 PP#1	GCGCATTTTGGTCATGCTAC	GGCTTGCCCACTTGATAATG
cs CAV3 PP#2	ACCATTTTGTTTTCGCCTTTT	ATTGAAGA**T**ATTGGGGTCCA
cs RPS27A	CCACCTGATCAGCAGAGGTT	TTATTCGCCCTCTGGTTTGA
cs Rab21	TTCGTGGTGGGAAATAAAGC	GTTTTCCGTTTTCACGCAAT
cs FLRT2	GTACACTGCTGCGAGGAACA	CCGTCTGATTGGTGGAAAGT
cs M.R.	CCGATGCTACGCCTATGACT	AGCCTCTACGTCGCCATCTA