Supplemental Figures for Roth et al. 2018, Genetics, “A High Resolution Map of Meiotic Recombination in Cryptococcus deneoformans Demonstrates Decreased Recombination in Unisexual Reproduction”
Figure S1: Distribution of inter-marker interval size across progeny from the XL280a × 431α and XL280αSS × 431α crosses. The total number of inter-marker intervals is 86,753. There are 86,278 inter-marker intervals with size < 2 kb. Only 0.548% of the inter-marker intervals have a size greater than 2 kb (data not shown). The median inter-marker interval size is 87 bases.
Figure S2: Distributions of crossovers per chromosome. The means of each distribution are displayed as red and black vertical lines for the segregants from the unisexual and bisexual crosses, respectively. Numbers in the upper right corners indicate chromosomes and "*" indicates chromosomes that show significant difference in the mean number of crossovers per segregant between progeny from the α-α unisexual (red) and a-α bisexual (black) crosses.
Figure S3: Changes in detected crossover along chromosome 4 are due to increased marker density. A) Distributions of crossovers along chromosome 4 for segregants from the a–a bisexual bisexual crosses. Recapitulated crossover counts from Sun et al. 2014 are shown in blue and current counts in red. The overlap (purple) depict crossover counts that are unchanged for segregants between Sun et al. 2014 and this study. B) Marker locations, SNP density, and inferred haplotypes across chromosome 4. Locations of SNPs used to recapitulate results from Sun et al. 2014 are shown as vertical, black lines and the SNP density every 10 kb is shown in green. For segregants with detected differences in crossover counts between the current study and Sun et al. 2014(y-axis), the haplotype inferred from SNPs (vertical, black lines) near marker locations used in Sun et al. 2014(above grey horizontal lines) and haplotypes from SNP data generated in this study (below grey horizontal lines) are shown. Blue and orange regions represent genetic material inherited from the XL280a or 431a parental strains, respectively. The approximate locations of the centromere and MAT locus are shown as black and green bars, respectively.
Figure S4: Distributions of GC content for inter-marker interval sequences associated with recombination hot (red) and cold (blue) spots. Vertical lines show mean GC content for sequences associated with recombination hot (red) and cold (blue) spots.
Figure S5: Poly(G) motif associated with crossover hot spots. This motif was found in all of the randomly chosen 100 inter-marker interval sequences associated with crossover hot spots submitted to MEME.
Figure S6: Allele bias in segregants from bisexual crosses. The genome-wide frequencies of the 431α parental allele in the 39 progeny from the a-α bisexual crosses. Triangles denote five regions along chromosomes 1, 2, 4, 6, and 12 with lengths of ~364, 260, 303, 41, and 60 kb, respectively, biased towards the XL280a parental allele. Solid and dashed lines indicate an expected allele frequency of 0.5 and the median, genome-wide allele frequency of 0.46, respectively.
Figure S7: Size of regions deviating from the expected 2:2 parental allele ratio. A) The log$_{10}$ of region size (bp) with distorted allele frequencies per chromosome. Statistical outliers are displayed as black diamonds. B) The percentage of regions with distorted allele frequencies possessing the XL280a parental allele per chromosome.
Figure S8: Genome-wide analysis of regions with distorted allele frequencies. The log of the average number of regions within a basidium with allele frequencies deviating from the expected 2:2 parental ratio as a function of chromosome length is shown. The red line represents a log-linear model, shaded regions represent the 95% confidence interval for regression estimates. Numbers dictate chromosomes.
Figure S9: Effect of bin size on detection of crossover hot and cold spots. The number of detected hot (red) and cold (blue) crossover spots (y-axis) was investigated as a function of bin size (x-axis), from 0.5 to 100 kb. A bin size of 41.5 kb (black dashed vertical line) was chosen because it minimized the difference in the number of detected hot and cold spots.