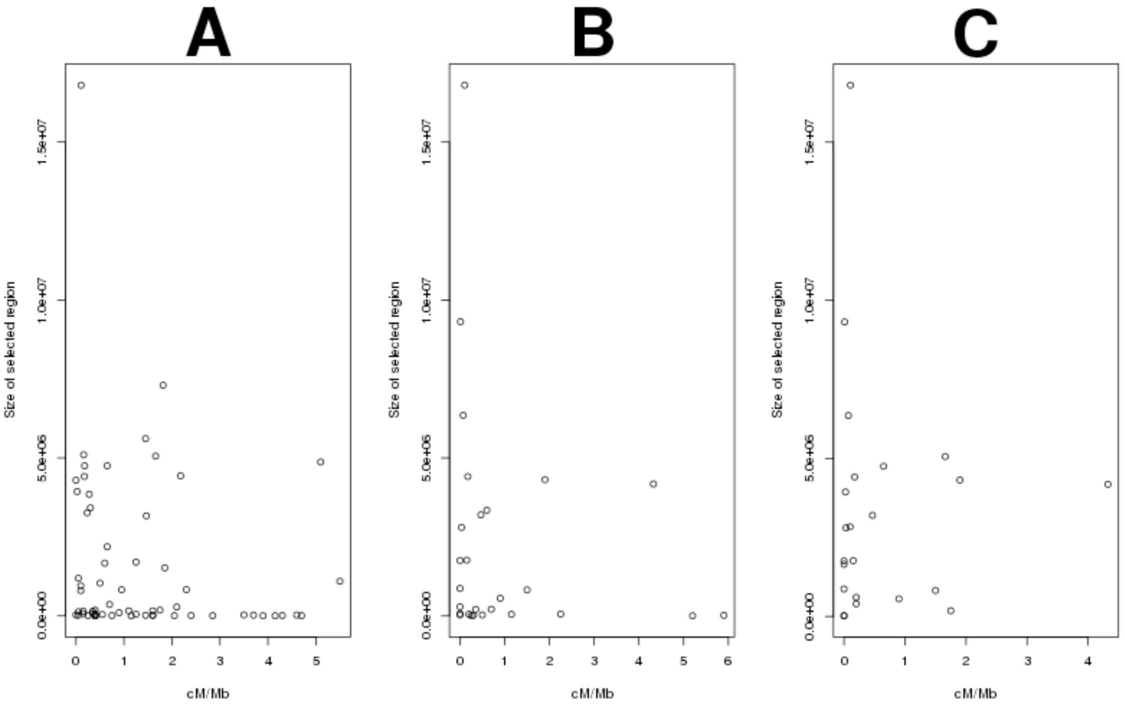

Figure S3 Region size versus relative recombination rate for each region identified as putatively under selection in the Krug long-term selection populations at the 99.9% outlier threshold. A) Regions identified by comparing Krug Yellow Dent to KLS_30, B) Regions identified by comparing Krug Yellow Dent to KSS_30, C) Regions identified by comparing KLS_30 and KSS_30. For all, relative levels of recombination across the genome were approximated based on recombination frequencies in the intermated B73 x Mo17 population. No significant correlations were observed.