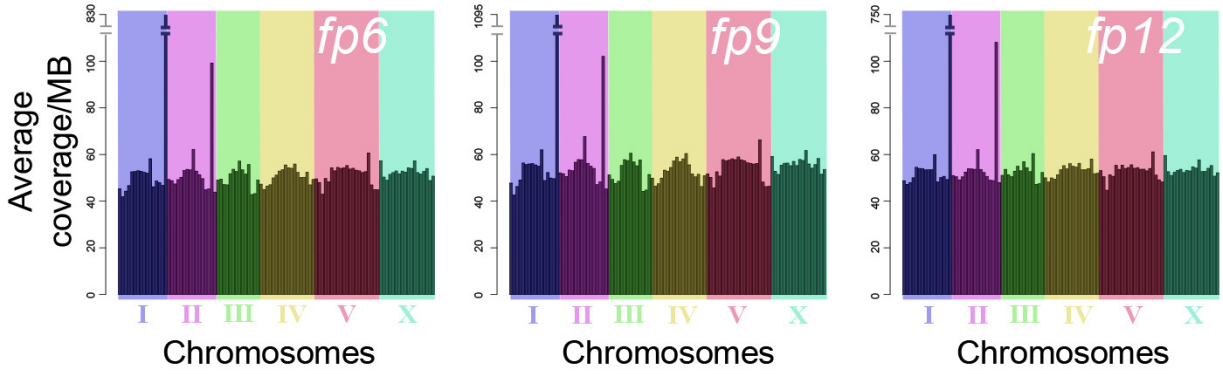

FIGURE S1.—Distribution of deep sequencing coverage. For each mutant (*fp6*, *fp9*, and *fp12*), average coverage of each nucleotide per MB is shown across all chromosomes for combined 2-lanes paired-end data. The large peak at the very end of chromosome I may represent a highly repetitive element aligned to only a single location (within 1MB). The large peak on chromosome II maps to the location of the *cog-1* gene. This most likely corresponds to sequencing of the *cog-1*::*gfp* transgene integrated into the background strain PS3662. Subsequent alignment to the native *cog-1* sequence would thus over-represent coverage in this region.