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.