



**FIGURE S7. Cells with ‘High G1’, ‘Low G1’ DNA content, or carrying deletions of genes in the gene ontology process GO:0000077 (DNA damage checkpoint) have cell size profiles with similar Anderson-Darling associated p-values for gamma distribution fits.** The deletion strains with ‘High’ or ‘Low’ G1 DNA content were those identified in (Hoose et al. 2012). The GO:0000077 group contained the cell size profiles of strains lacking any single non-essential gene belonging to this ontology group and analyzed by Jorgensen et al. The ‘All other’ group were all other mutants analyzed by (Jorgensen et al. 2002), which were not in the groups of mutants shown in the plot. The cell size distributions of the corresponding deletion mutants in each case were analyzed as in Figure 2A, fitted to a gamma distribution, with the p-values from the Anderson-Darling test (AD p-value) representing each data point. The groups were not statistically different from each other (Kruskal-Wallis rank sum test,  $p=0.4841$ ).