Figure S8  Correlation between wild-type (WT) and rpd1 mutant uniquely mapping GRO-seq coverage at genes. Near-genic regions were divided into five sections: 1 kb upstream, the first 1 kb after the TSS, a variable internal region, the last 1 kb before the gene end, and 1 kb downstream. GRO-seq coverage is plotted for both sense and antisense directions (relative to the gene model) in reads per kb per million uniquely mapped. To include genes with zero read abundance on the logarithmic scale, they were forced to 1/10th the minimum non-zero abundance of both datasets for that plot. Data fit lines represent linear regression models of the log_{10} transformed WT and rpd1 mutant abundances. Rho (ρ) values represent the Spearman’s rank correlation coefficient for each region. Total number of genes in each plot is 31,794 except for the interior of the gene where the total gene length had to be greater than 2 kb; 23,050 genes in total.