Figure S6  Alternative TSS definition has little effect on coverage profiles. TSS sites were defined by the 5' end of full-length cDNAs (flcDNAs) from a library of predominantly 7 day-old seedling tissue (Soderlund et al. 2009). Metagene analysis was performed across all flcDNA defined TSSs in 10 nt non-overlapping windows with the total coverage in reads per million uniquely mapped (RPMUM) displayed. Pair-wise Welch's t-tests evaluated the difference between WT and rpd1 mutant read abundance at each window, and a Holm-Bonferoni correction ($\alpha = 0.05$) was applied to identify the windows that were significantly different (red horizontal bar and pink shading).