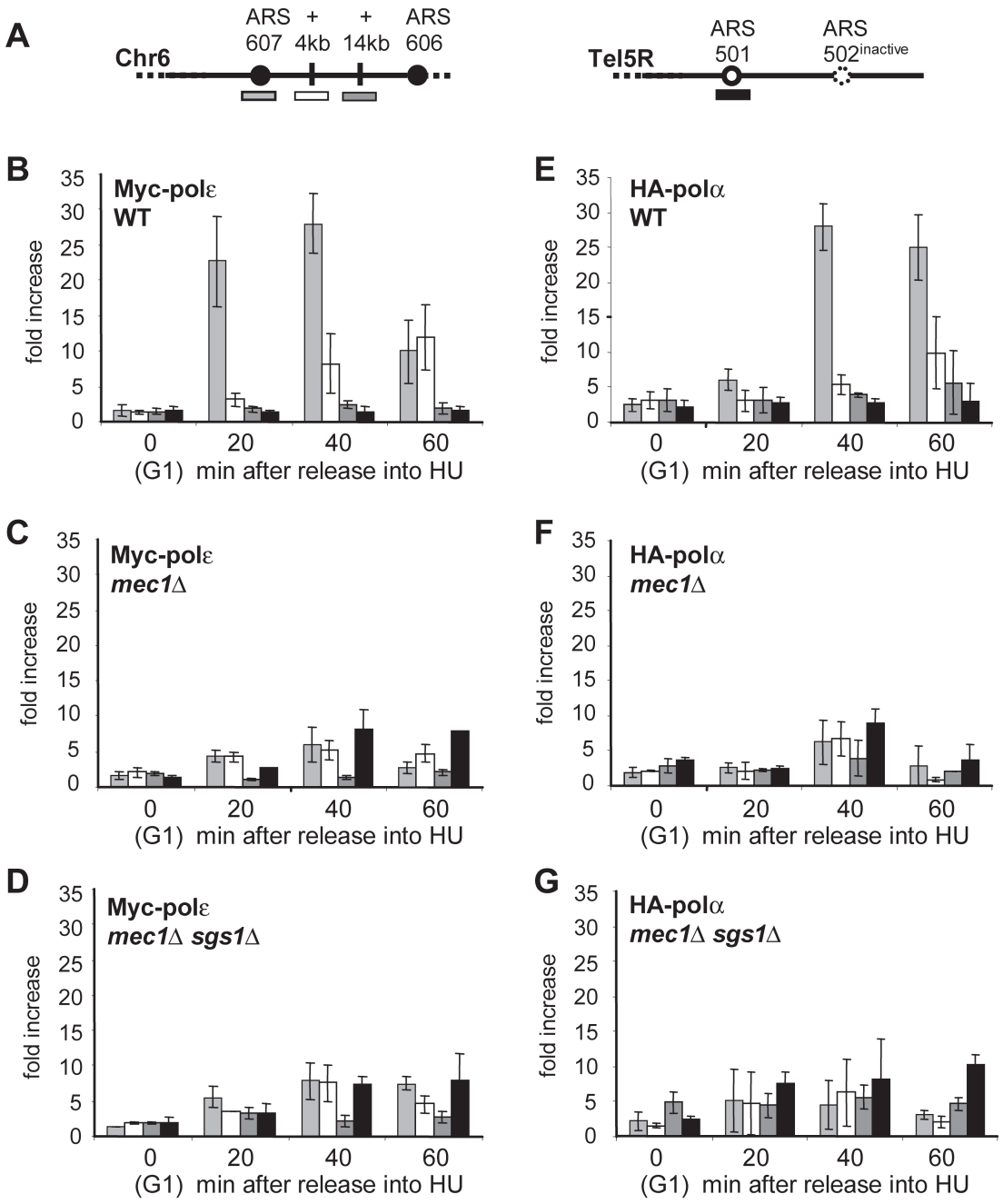

A. Primers were designed to amplify regions in the *S. cerevisiae* genome corresponding to the early firing origin ARS607 (stippled bars), and non-origin sites 4 kb (white) and 14 kb (gray) away on Chr 6, and the late firing origin ARS501 (black). The active and inactive origins (ARS) have been previous described (Raghuraman et al., 2001; Reynolds et al., 1989). ChIP was performed at 30ºC on either Myc-tagged DNA pol ε for isogenic **B.** wild-type (GA-2448), **C**. *mec1*Δ *sml1*Δ (GA-2588), and **D**. *mec1*Δ *sml1*Δ *sgs1*Δ (GA-2589) cells or HA-tagged DNA pol α for isogenic **E**. wild-type (GA-2238), **F**. *mec1*Δ *sml1*Δ (GA-2579), and **G**. *mec1*Δ *sml1*Δ *sgs1*Δ (GA-2580) cells. The height of the bars represents the real time PCR signal fold increase over the background signal.