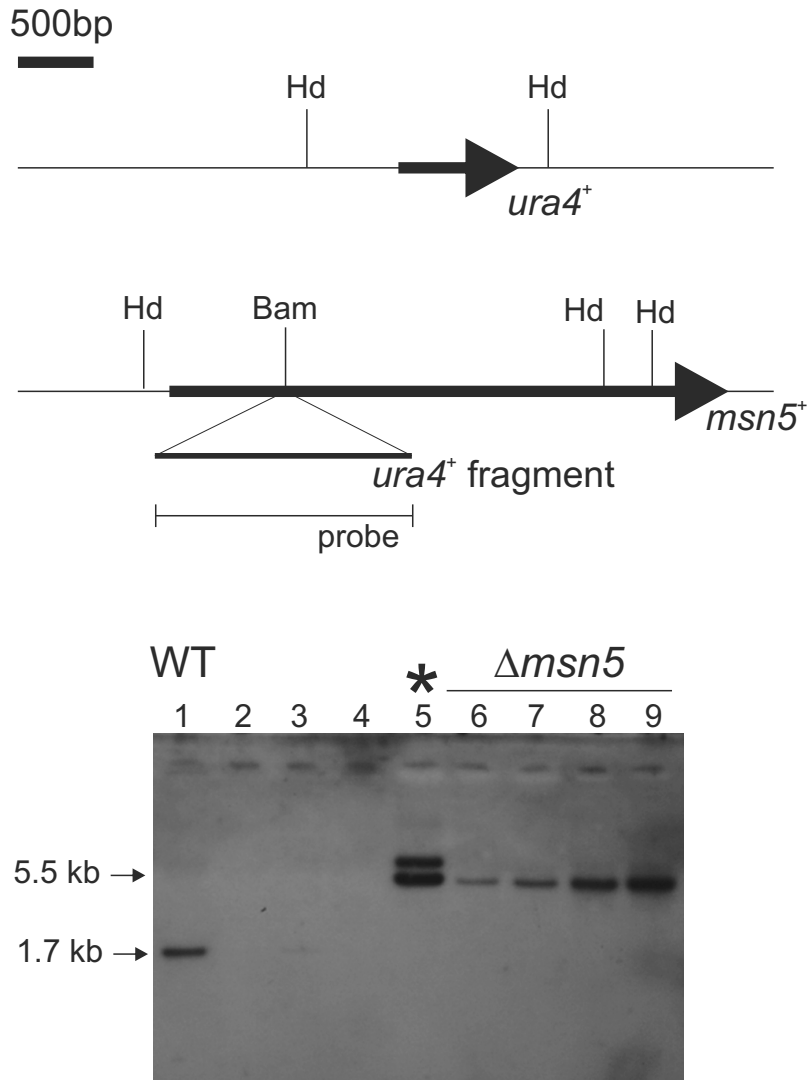


# Supplemental Figure S1



**Supplemental Figure S1.** Southern blot analysis of the *msn5* gene deletions. Top, restriction map of the *ura4<sup>+</sup>* and *msn5<sup>+</sup>* region, and disruption of *msn5<sup>+</sup>*. The arrow indicates the extent and direction of the *ura4<sup>+</sup>* or *msn5<sup>+</sup>* open reading frame (ORF). A disruption construct used to replace the chromosomal *msn5<sup>+</sup>* gene is shown schematically below the arrow. Restriction site: *Hd*, *Hind*III; *Bam*, *Bam*HI. Bottom, genomic DNA from wild-type cells or *msn5* deletion mutants were digested with *Bam*HI and resolved on a 0.8% agarose gel. The DNAs were blotted onto Hybond-N<sup>+</sup> (Amersham) and hybridized with a *ura4* probe. Lane 1, HM123 (wild-type), Lanes 6-9, KP2795 (*Δmsn5*; *h<sup>-</sup> leu1 ura4-D msn5::ura4<sup>+</sup>*). The relevant size of DNA fragments are shown in kilobases (kb) on the left. The asterisk (lane 5) is an unrelated data.