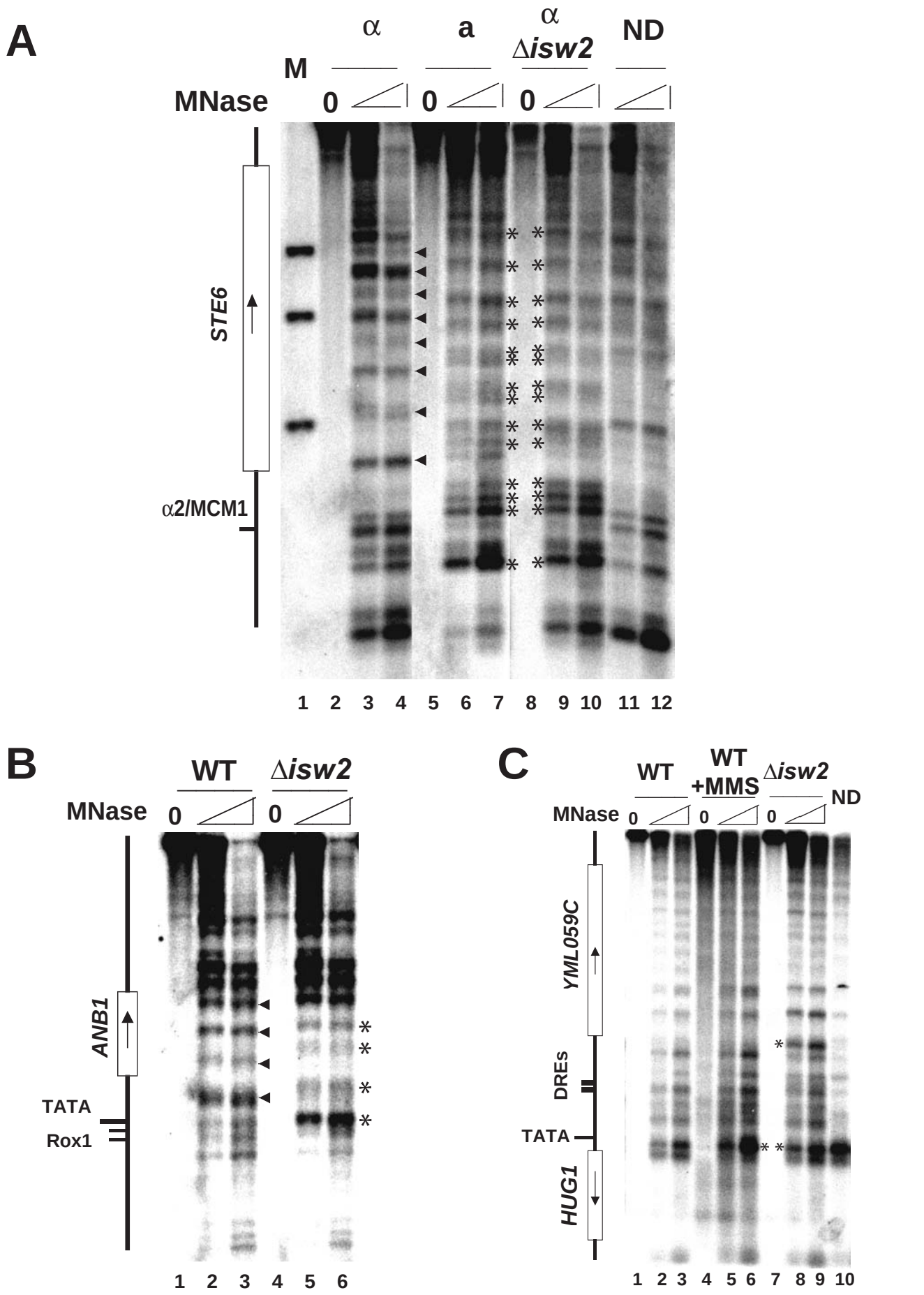
A
α
a
α
Δisw2
ND
M
MNase
0
0
0
STE6
α2/MCM1
1 2 3 4 5 6 7 8 9 10 11 12
B
WT
Δisw2
MNase
0
0
ANB1
TATA
Rox1
1 2 3 4 5 6
C
WT
WT
+MMS
Δisw2
ND
MNase
0
0
0
YML059C
DREs
TATA
HUG1
1 2 3 4 5 6 7 8 9 10

Sup. Fig 4. ISW2 dependent nucleosome positioning at other Ssn6-Tup1 regulated genes. The chromatin structure of *STE6*, *ANB1*, and *HUG1* loci was examined by MNase mapping. Black triangles point to the hypersensitive sites that are unique or enhanced under the repressed state, while the asterisks indicate the hypersensitive sites exposed in mutants or under the derepressed condition. (A) Chromatin structure at the *STE6* locus in repressed *Mat* α cells compared to that in derepressed *Mat a* cells and in *Mat α* cell containing the *Δisw2* mutation. Notice that deletion of *ISW2* in *Matα* cell results a digestion pattern similar to that of *Mat a* cell or naked DNA, and that ISW2-dependent nucleosome positioning extends far into the ORF. The open reading frame and the α2/MCM1-binding sites are indicated on the left. DNA was digested with Bgl II (at –678) and a probe corresponding to -685—444 was used for Southern Blotting. Our data agrees with reports published after the submission of this manuscript showing that deleting *ISW2* derepresses mating type specific genes and affects the chromatin structure over the promoter of *STE6* (Ruiz et al. 2003; McConnell et al., 2004). However, the mapping of the coding sequence of *STE6* or comparison to the derepressed state (*Mat a*) was not presented in the later publication (McConnell et al., 2004). (B) Deleting *ISW2* disrupts nucleosome positioning over *ANB1*. *ANB1* locus was mapped by indirect end-labeling after digestion with EcoR I (at –964) and using a probe specific for bp -975—643. The locations of the TATA-box and Rox1 binding sites are indicated on the left. (C) *Δ isw2* mutants have disrupted chromatin over *HUG1*. *HUG1* was mapped by indirect end-labeling after digestion with Sac II (at +398) and using a probe specific to bp +267-+394. The putative Crt1 binding sites (DREs) and TATA box of *HUG1* gene are indicated on the left. The ORF of *HUG1* is only 207 bp long, approximately 1 nuc, and the underlying DNA is relatively insensitive to MNase so assigning a nucleosome position is not possible. However, changes in the digestion pattern over the TATA box and promoter are observed and are highlighted by asterisks.