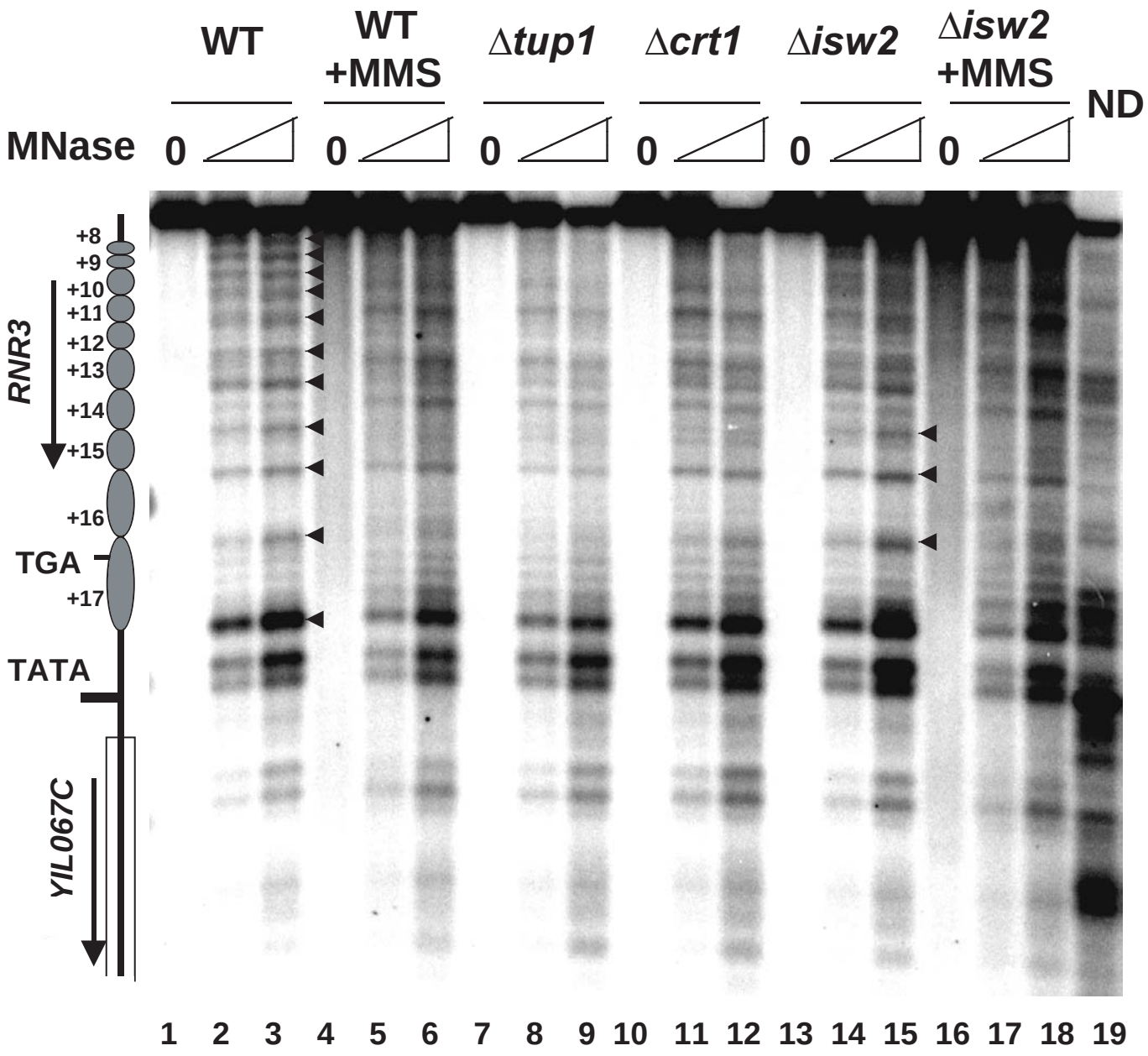
WT
WT +MMS
Δtup1
Δcrt1
Δisw2
Δisw2 +MMS
ND
MNase
0
0
0
0
0
0
+8
+9
+10
+11
+12
+13
+14
+15
+16
+17
TGA
TATA
RNR3
YIL067C
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19

Sup Fig. 1. Nucleosome positioning at the end of *RNR3*. MNase mapping of *RNR3* in wild type (WT), *Δtup1*, *Δcrt1* and *Δisw2* strains. Some strains were treated with MMS (0.03%, 2 hours) where indicated. The restriction enzyme Kpn I that cuts at +3459 (relative to ATG) was used to digest the DNA, and a probe corresponding to +4249-4567 was used in Southern blotting. The locations of the *RNR3* gene and the neighbor open reading frame YIL067C relative to the digestion pattern are indicated on the left. The filled triangles are putative internucleosomal hypersensitive sites that are relatively resistant to digestion in naked DNA. Notice that the chromatin structure from nucleosome +8 to +17 in derepressed cells (*Δtup1*, *Δcrt1* and MMS-treated strains) resembles that of the naked DNA, while the structure downstream of nucleosome +17 is unaffected. The chromatin changes caused by deleting *ISW2* appear to diminish downstream of nucleosome +14. Notice that hypersensitive sites are preserved in digestion pattern from the untreated *Δisw2* mutant (lanes 14 and 15), which are lost after MMS treatment (lanes 17 and 18).