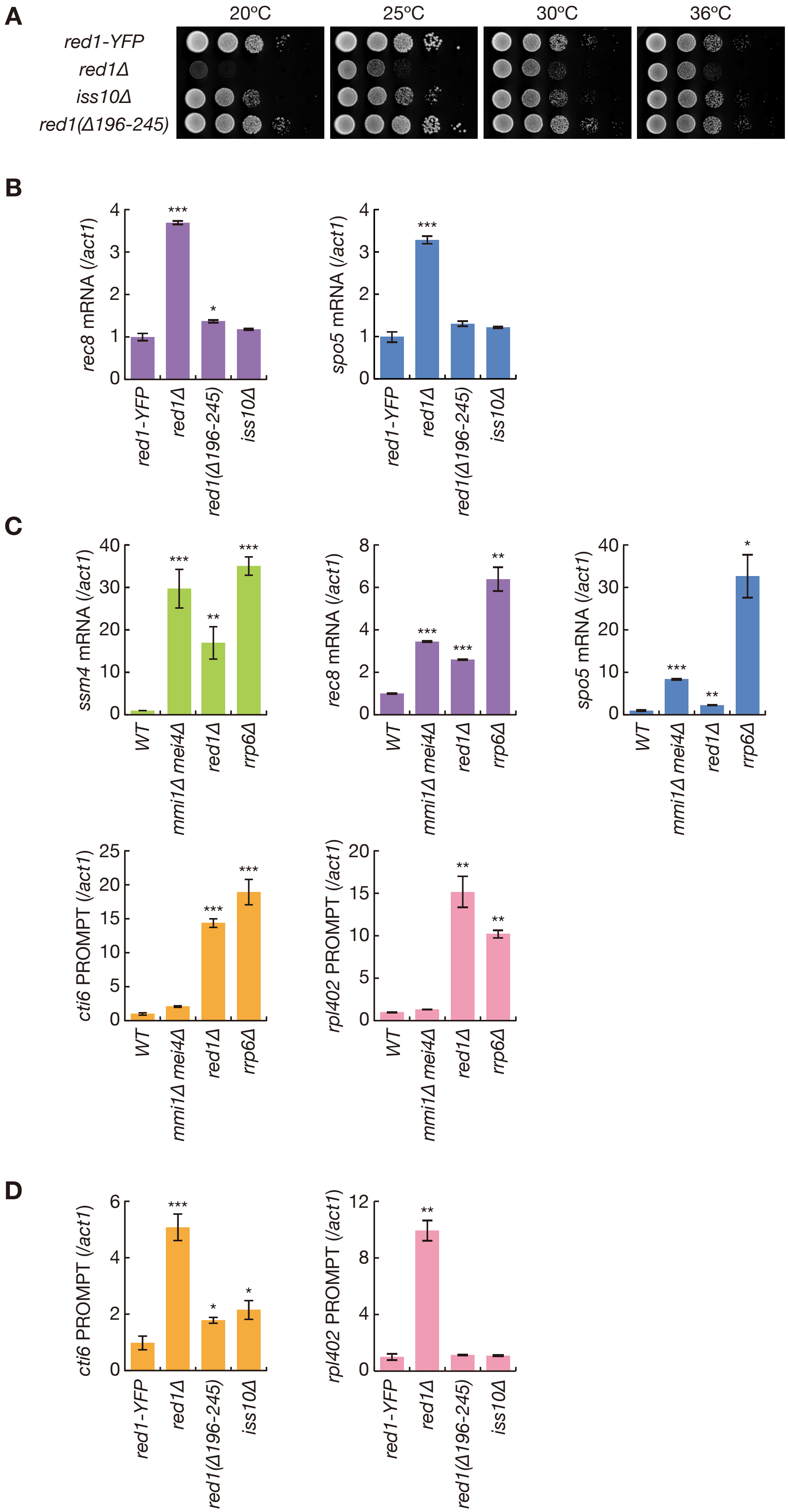
S3 Fig.


A
20°C
25°C
30°C
36°C
red1-YFP
red1Δ
iss10Δ
red1(Δ196-245)
B
rec8 mRNA (/act1)
spo5 mRNA (/act1)
0
1
2
3
4
***
*
***
red1-YFP
red1Δ
red1(Δ196-245)
iss10Δ
C
ssm4 mRNA (/act1)
0
10
20
30
40
***
**
***
rec8 mRNA (/act1)
0
2
4
6
8
***
***
**
spo5 mRNA (/act1)
0
10
20
30
40
***
**
*
WT
mmi1Δ mei4Δ
red1Δ
rrp6Δ
cti6 PROMPT (/act1)
0
5
10
15
20
25
***
***
rpl402 PROMPT (/act1)
0
5
10
15
20
**
**
D
cti6 PROMPT (/act1)
0
2
4
6
***
*
*
rpl402 PROMPT (/act1)
0
4
8
12
**
red1-YFP
red1Δ
red1(Δ196-245)
iss10Δ

S3 Fig. Red1(Δ196-245) is defective in meiotic transcript degradation.

(**A**) Growth profiles of wild-type (*red1-YFP*), *red1Δ*, *iss10Δ* and *red1(Δ196-245)* cells. Ten-fold serial dilutions of cells were spotted on YE medium and incubated at the indicated temperatures.

(**B**) Expression of *rec8* mRNA and *spo5* mRNA in wild-type (*red1-YFP*), *red1Δ*, *iss10Δ* and *red1(Δ196-245)* cells. Transcripts were quantified by RT-qPCR and normalized to *act1*. Error bars represent standard error of three independent samples. *$P < 0.05$; ***$P < 0.001$ compared with the wild-type *red1-YFP* strain (Student's *t*-test).

(**C**) Expression of *ssm4* mRNA, *rec8* mRNA, *spo5* mRNA, *cti6* PROMPT and *rpl402* PROMPT in wild-type, *mmi1Δ mei4Δ*, *red1Δ* and *rrp6Δ* cells. Transcripts were quantified by RT-qPCR and normalized to *act1*. Error bars represent standard error of three independent samples. *$P < 0.05$; **$P < 0.01$; ***$P < 0.001$ compared with the wild-type strain (Student's *t*-test).

(**D**) Expression of *cti6* PROMPT and *rpl402* PROMPT in wild-type (*red1-YFP*), *red1Δ*, *red1(Δ196-245)*, and *iss10Δ* cells. Transcripts were quantified by RT-qPCR and normalized to *act1*. Error bars represent standard error of three independent samples. *$P < 0.05$; **$P < 0.01$; ***$P < 0.001$ compared with the wild-type *red1-YFP* strain (Student's *t*-test).