A

Repeat #1

```
S288c   TCCAGTTCAAATTCGAATTCGAACTCCAATTCTAATTCGAACTCCAACTCCAAC
w303    TCCAGTTCAAATTCGAATTCGAACTCCAATTCTAATTCGAACTCCAACTCCAAC
SK1     TCCAGTTCAAATTCGAATTCGAACTCCAATTCTAATTCGAACTCCAACTCCAAC
NCYC110 TCCAGTTCAAATTCGAATTCGAACTCCAATTCTAATTCGAACTCCAACTCCAAC
YJM789  TCCAGTTCAAATTCGAATTCGAACTCCAATTCTAATTCGAACTCCAACTCCAAC
RM11    TCCAGTTCTAATTCTAATTCGAACTCCAACTCCAAC------------------
y55     TCCAGTTCTAATTCTAATTCGAACTCCAACTCCAAC------------------
Sigma   TCCAGTTCTAATTCTAATTCGAACTCCAACTCCAAC------------------
         S  S  S  N  S  N  S  N  S  N  S  N  S  N  S  N  S  N
```

B

Repeat #2

```
S288c   AACAAGAATGGTACTAATGATAATATTAATAACCATTATTATAATAATTGTAACAATAACAATAATAATATTAA----------------------------------------------CAATAGTAACAATAGCAACAATAATAATAGCAATAATATTAATAGGAATAGTAATCATAGTACTAAT
w303    AACAAGAATGGTACTAATGATAATATTAATAACCATTATTATAATAATTGTAACAATAACAATAATAATATTAA----------------------------------------------CAATAGTAACAATAGCAACAATAATAATAGCAATAATATTAATAGGAATAGTAATCATAGTACTAAT
SK1     AACAAGAATGGTACTAATGATAATATTAATAACCATTATTATAATAATAGTAACAATAACAATAATAATATTAA----------------------------------------------CAATAGTAACAATAGCAACAATAATAATAGCAATAATATTAATAGGAATAGTAATCATAGTACTAAT
NCYC110 AACAAGAATGGTACTAATGATAATATTAATAACCATTATTATAATAATAGTAACAATAACAATAATAATATTAA----------------------------------------------CAATAGTAACAATAGCAACAATAATAATAGCAATAATATTAATAGGAATAGTAATCATAGTACTAAT
YJM789  AACAAGAATGGTACTAATGATAATATTAATAACCATTATTATAATAATAGTAACAATAACAATAATAATATTAA---CAATAGTAACAATAATAA----------------------------TAATAGTAACAATAGCAACAATAATAATAGCAATAATATTAATAGGAATAGTAATCATAGTACTAAT
RM11    AACAAGAATGGTACTAATGATAATATTAATAACCATTATTATAATAATAGTAACAATAACAATAATAATAATAATAATTAACAATAGTAA----------------------------------CAATAATAATAATAGTAACAATAATAATAGCAATAATATTAATAGGAATAGTAATCATAGTACTAAT
y55     AACAAGAATGGTACTAATGATAATATTAATAACCATTATTATAATAATAGTAACAATAACAATAATAATAATAATAATTAACAATAGTAACAATAATAATAATAGTAA----------------CAATAATAATAATAGTAACAATAATAATAGCAATAATATTAATAGGAATAGTAATCATAGTACTAAT
Sigma   AACAAGAATGGTACTAATGATAATATTAATAACCATTATTATAATAATAGTAACAATAACAATAATAATAATAATAATTAACAATAGTAACAATAATAATAATAGTAACAATAATAATAATAGTAACAATAATAATAGCAATAATATTAATAGGAATAGTAATCATAGTACTAAT
          N  K  N  G  T  N  D  N  I  N  N  H  Y  Y  N  N  S  N  N  N  N  N  N  N  N  N  S  N  N  N  N  N  S  N  N  N  N  N  S  N  N  N  N  N  S  N  N  N  N  N  S  N  N  I  N  R  N  S  N  H  S  T  N
```

Figure S6 Comparison of *RPI1* repeat regions between different *S. cerevisiae* strains. The sequences for the repeat regions from *RPI1* were aligned using ClustalW. (A) 5' repeat region and (B) central repeat region. For repeat #1 the translation for the S288c sequence is shown, and for repeat #2 the translation for the Sigma sequence is shown. Strain names in blue are wild isolates and nucleotides in red represent nucleotide polymorphisms. In S288c, the repeats account for 16% of the coding sequence (195/1224 bases). The 5' repeat region consists of a hexanucleotide repeat. In S288c there are nine repeated units while in Sigma there are only six repeated units. The central repeat region consists of a trinucleotide repeat. In S288c there are 46 repeated units but in Sigma they have expanded to 63 repeated units. Both repeats encode primarily for serines and asparagines.