

```

Hs : -----MPVVRKIFRRR---RGDSESE--EDEQDSEEVRIKLEETREVQNLRRFPNGVSAVALLVGEKVQ-EETTLVDDFQMKTTGGMVDMKCLKERGGKDKIS
Mm : -----MRITGKTFRRR---RADSESE--EDEQSEEVRIKLEETREVQNLRRFPNGVSAVALLVGEKVQ-EETTLVDDFQMATGGMVDMKCLKERGGKDKVS
Xl : -----MFAG-RNFRRR---KASSSDEEVEDEGVTREVRMKLEEFKEVQSLRRFPNGVSAVALLVGEKLP-EEVNMADDFQKMQNGGMVDMKCLKDRGKDRIG
Lm : MS LAEETKAEATTKVLFKKA---GRKNLRQRKNSDEEEKKEEQTLDEIKERQRLRFPNGVSLVGLALGKKIAPETELAIKDFNVKTGGLVNMKQLKSGKMKEAD
At : -----MPPKRNFRKRSFEEE---EEDNDVNKAAISEEEEKRRIALEEVKFLQKLRPEKLGIEFLSSTAQSSIG-----KVKPVEKTETEG
Sp : ---MNSIHIKKKSNRSFRRRKVFGNEKEFDLEELDDNDIRLRQALPALK-RRKIRNSIIGINAEKILLNQETKKEKQINTANE-----HEANDQTSAQSSKLI

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```

Hs : EEDDHLGTSFSAETNRDEDADMMKYIETELKRRK-----IVEHEEQVKPKNAED-CLMELPENIRVSSAKKTEEMLSNQMISGIEVVDLGIITAKIKNIISTE
Mm : EEDDHLGTSFSAETNRDEDADMMKYIETELKRRK-----IVEQEEQKAKPKNAED-CLMELPENIRVSSAKKTEEMLSNQMISGIEVVDLGIITAKIKNIISTE
Xl : EEDDHLGTSFSAETNRDEDADMMKYIETELKRRK-----IVENEEKVKPKSAED-CLMELPENIRVSSAKKTEEMLSNQMISGIEVVDLGIITAKIKNIISTE
Lm : LAYDVGIGTQFSAETNRDEDEEMKYIETELKRRKGGTDLAAEDDGDVNKYLTPCALALALPDHLQSSSHRSEEMLSNQMISGIEVVDLGIITAKIRNIEATE
At : EKEDVVLQDTFAQETAFLIEDPNMVKYIETELAKRRK---RNIDLAAEVENELKRVEDELKIEDHLAVK--KRSSEESSTQWTTGIAEVQLFIEYKLNIEETE
Sp : EAQLPTVEDRFAKQTNVLIINHLNLFVEKKIKQERLIA---QNYSENGETNALNTKNESTVQNIKNSLHPN---EHSFIRLAAALGATREVDLGIIS--TDVDNLK

```

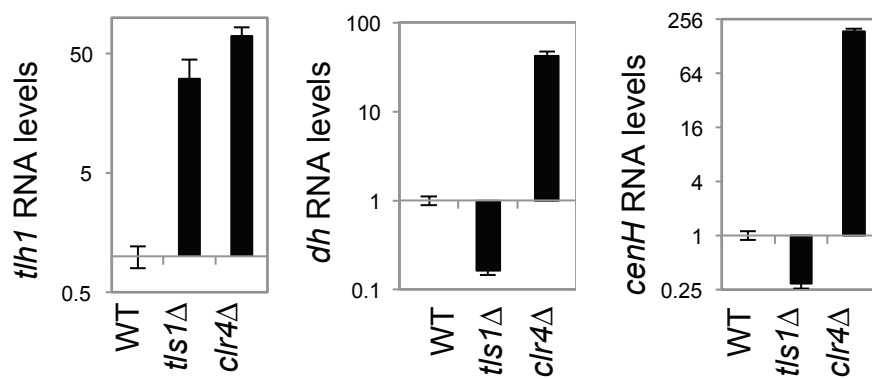
## HEP59

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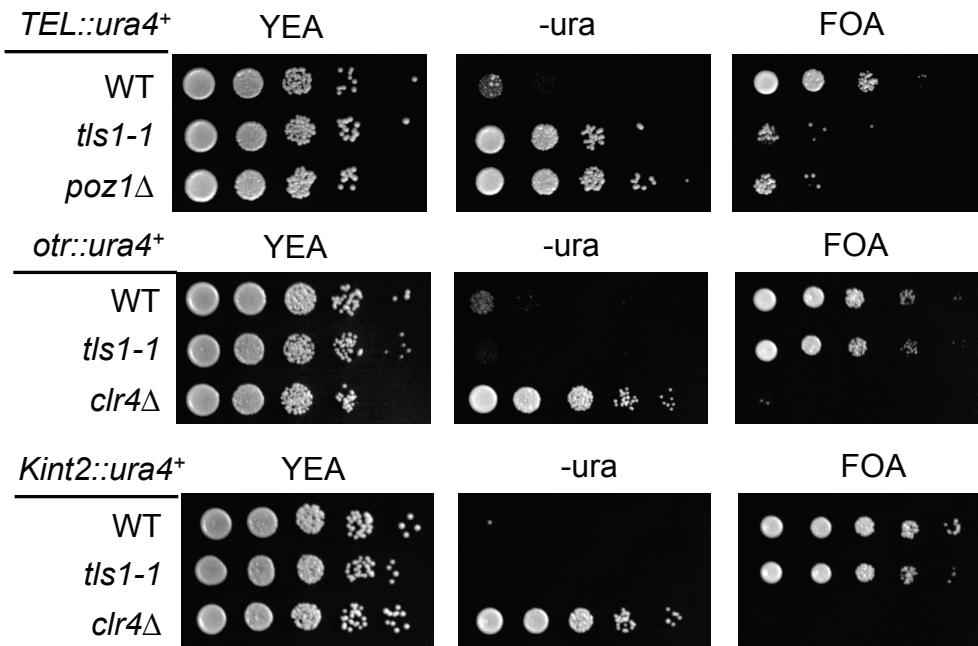
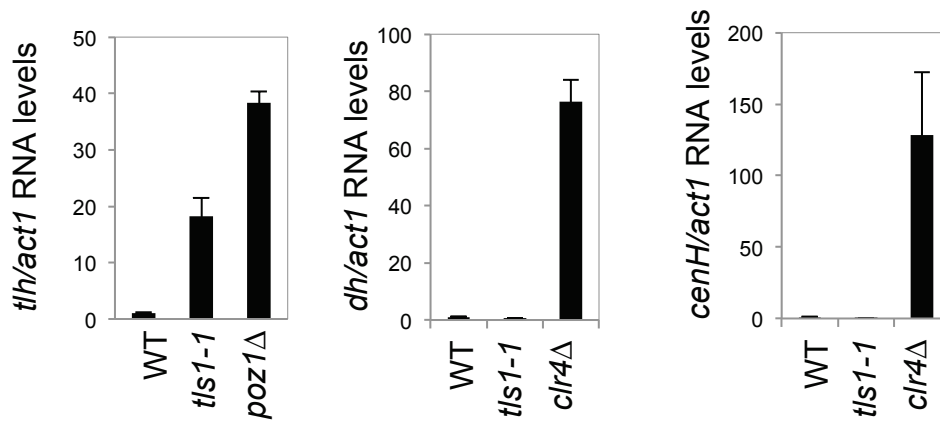
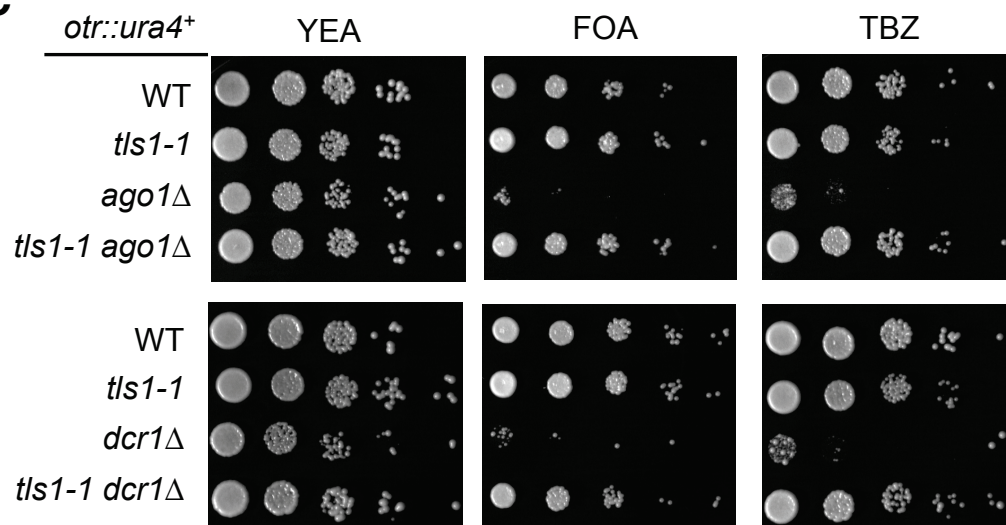
Hs : DAKARLLAEQQNKKKDSSETS FVPTNMAVNYVCHNRFYHEELNAPIRRNKLEPKARPLRVGDTEKPEPERSPPNRKRFANEK--ATDDYHYEKFKKMNRRY----
Mm : DAKARLLAEQQNKKKDSSETS FVPTNMAVNYVCHNRFYHEELNAPIRRNKLEPKARPLRVGDTEKPEPERSPPNRKRFANEK--ATDDYHYEKFKKMNRRY----
Xl : EAKARLLAEQQNKKKDKHTSFVPTNMAVNYVCHNRFYQEDQNTPMRRHKLEPKPRPLRVGDTEKPEPEKSPPNRKRPSNEK--ATDDYHYEKFKKMNRRY----
Lm : EAKQLLQLAKNKK-DGPSQFVPTNMAVNYVCHNRFNIEDNSDQRRRREE-----REGN--KSAHQITNPN----GVKR--ATDDYHYDKFRKQFRRY----
At : AAKK-LLQERRLMGRPKSEFSIPSSYSADYFQRGDAEKLRRHEPELYKD-RGGPQADGEAAKPSSTSSSTNNADSGKSRQAATDQIMLERFRFRERNRVMRR
Sp : NGRKRQKKRARMKEKLDKALRTSEDLAR-----DETEKMLKPISQDEFS-----KGIYR-----RFRVYKDGTDQD-----

```

**Figure S1:** Sequence alignment of Tls1 homologues.



**Figure S2:** qRT-PCR analyses of transcripts derived from repeat elements, normalized to *act1*. The data is the same as Fig. 2C, but plotted in log scale to show the down regulation of *dh* and *cenH* RNAs.

**A****B****C**

**Figure S3:** Characterization of *tls1-1*. (A and C) Serial dilution analyses to measure the expression of *ura4<sup>+</sup>* reporter genes and sensitivity to TBZ. (B) qRT-PCR analyses of transcripts derived from repeat elements, normalized to *act1*.