Supplemental Table 1: Sequences of synthetic histone tail peptides used in binding experiments

Name	Sequence
H2A	SGGKGGKAGSAAKASQSRSAK-GGK-biotin
H2AZ	SGKAHGGKGKSGAKDSGSLRS-GGK-biotin
H2B	PEPSKSAPAPKKGSKKAITKA-GGK-biotin
H3	ARTKQTARKSTGGKAPRKQLA-GGK-biotin
Ac-(K9,14)-H3	ART[$_{AC}$K]QTAR[$_{AC}$K]STGGKAPRKQLA-GGK-biotin
Me-(K4)-H3	ART[$_{me}$K]QTARKSTGGKAPRKQLA-GGK-biotin
Me_3-(K4)-H3	ART[$_{me3}$K]QTARKSTGGKAPRKQLA-GGK-biotin
H4	SGRGKGGKGLGKGGAKRHRKV-GGK-biotin
Ac-(K5,8,12,16)-H4	SGRG[$_{AC}$K]GG[$_{AC}$K]GLG[$_{AC}$K]GGA[$_{AC}$K]RH-GSGSK-biotin
Ac-(K5,12)-H4	SGRG[$_{AC}$K]GGKGLG[$_{AC}$K]GGAKRH-GSGSK-biotin
Ac-(K8,16)-H4	SGRGKGG[$_{AC}$K]GLGKGGA[$_{AC}$K]RH-GSGSK-biotin
Ac-(K8)-H4	SGRGKGG[$_{AC}$K]GLGKGGAKRHRC-GSGSK-biotin
Ac-(K12)-H4	SGRGKGGKGLG[$_{AC}$K]GGAKRHRC-GSGSK-biotin
Ac-(K16)-H4	SGRGKGGKGLGKGGA[$_{AC}$K]RHRC-GSGSK-biotin

Supplementary Information 2 – Amino Acid Sequence of ts mutants aligned to wild type sequence. Locations where a base pair change led to a change in the coding sequence are highlighted in red.

Med8

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med8-39          MSQSTASRVPEGNQGSLQKDVSFDFNGVPGQALDAVRMRLAQLTHSLRRIRDEVSKAGLP 60
WT MED8          MSQSTASLVPEGNQGSLQEDVSFDFNGVPGQALDAVRMRLAQLTHSLRRIRDEMSKAELP 60

med8-39          QWYTLQSQLNVTLSQLVSVTSTLQHFQETLDSTVVYPLPKFPTTSHESLVATLLRKKSIP 120
WT MED8          QWYTLQSQLNVTLSQLVSVTSTLQHFQETLDSTVVYPLPKFPTTSHESLVTTLLRKKNIP 120

med8-39          EVDEWMKYVGGTSGVTTALLKDEEIEMLLQQDREITNWARTTYRNEYGERDFKNEESLCE 180
WT MED8          EVDEWMKYVRETSGVTTALLKDEEIEKLLQQDREITNWARTTFRNEYGKHDFKNEESLSE 180

med8-39          EHASLLVRDSKPSKPFNVDDVLKSTFTWEKPIITGSTPTSSSN 223
WT MED8          EHASLLVRDSKPSKPFNVDDVLKFTFTGEKPIITGSTSTSSSN 223
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Med4

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med4-6           MSVQDTKAVEFSMGHIRSSSVSLVAEATSNTNSEDKLSKVQLYEELWRYEDTLSKLVESV 60
WT MED4          MSVQDTKAVEFSMGHIRSSSVSLVAEATSNTNSEDKLSKVQLYEDLCRYEDTLSKLVESV 60

mutant           DRFKPNLDIAKDLIRADEALFENVKLLAEYDNIYRNLQEIDKDSEELDSKTRKILEDPNE 120
WT MED4          DRFKPNLDIAKDLIRTDEALFENVKLLAEYDNIYRNLQKIDKDSEELDSKTRKILEILNE 120

mutant           CHDGLKALPTLEQVEFEKNAILQQRSKVNSTELLDYATKLSKFAKIPPTFGKGAVGPNNF 180
WT MED4          CHDELKALPMLEQVEFEKNTILQQRSKINSTELLDYATKLSKFTKIPPTFDKGAVGPNNF 180

mutant           IWPAEDALRGGMLAMASLHSKELTRIPGEEVEETEVPTVPPSQSEEQKGQMAKKEGTPKT 240
WT MED4          IWPAEDALRRGMLAMASLHSKELTRIPGEEVEETEVPTVPPSQSEEQKGQMAKKEGTPKT 240

mutant           DSFIFDGTAKEVGDEADDTKDEEKEENNDDALDLDLDLFGPDDF 284
WT MED4          DSFIFDGTAKEVGDEADNTKDKEKEENNDDALDLDLDLFDPDDF 284
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Med7

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med7-163         MSNDPGNEVSSLYPPPPPYVKFFTQSNLEKLPKYKEKKAASAKQTAPNNSNGGSEEEITC 60
WT MED7          MSNDPGNEVSSLYPPPPPYVKFFTQSNLEKLPKYKEKKAASAKQTAPNNSNGGSEEEITC 60

med7-163         ALDYLTPPPMPRNQQYRAFGSIRQVKDQLPDLESMGLTQLYKKSTENESTNYQCKIQELR 12
WT MED7          ALDYLIPPPMPKNQQYRAFGSIWQVKDQLPDLESMGLTQLYKKSTENESTNYQYKIQELR 120

med7-163         KLLKSLLLNYLEPIGVSSTNPDMYERKVENIRTILVDIHHLLNEYRPHQSRESLIVLLEE 1
WT MED7          KLLKSLLLNYLELIGVLSINPDMYERKVENIRTILVNIHHLLNEYRPHQSRESLIMLLEE 180

med7-163         QLEYKRGEIREIEQVCERVHGKLTSIQDTLRTGSQSPPSSSQ 222
WT MED7          QLEYKRGEIREIEQVCKQVHDKLTSIQDTLRTGSQSPPSSSQ 222
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