

Supplementary Online Material Wendegatz et al.:

Table S1: Plasmids constructed and used in this work:

Plasmid	Genotype
p423-MET25	2 μ m <i>HIS3</i> (Mumberg et al. 1994)
p424-MET25	2 μ m <i>TRP1</i> (Mumberg et al. 1994)
p426-MET25HA	2 μ m <i>URA3 MET25_{Pr}</i> -HA ₃ (Mumberg et al. 1994)
pECW31	2 μ m <i>URA3 MET25_{Pr}</i> -HA ₃ - <i>STH1</i> ₁₋₃₀₀ (Wendegatz et al. 2024)
pECW38	2 μ m <i>URA3 MET25_{Pr}</i> -HA ₃ - <i>INO80</i> ₁₋₆₇₀ (Wendegatz et al. 2024)
pECW39	2 μ m <i>URA3 MET25_{Pr}</i> -HA ₃ - <i>SWI1</i> ₃₂₉₋₆₅₇ (Wendegatz et al. 2024)
pECW40	2 μ m <i>URA3 MET25_{Pr}</i> -HA ₃ - <i>SNF5</i> ₁₋₃₃₄ (Wendegatz et al. 2024)
pECW41	2 μ m <i>URA3 MET25_{Pr}</i> -HA ₃ - <i>SWI2</i> ₁₋₃₀₀ (Wendegatz et al. 2024)
pEW1	2 μ m <i>URA3 MET25_{Pr}</i> -HA ₃ - <i>TAF6</i> (full length; Hintze et al. 2017)
pGBD-C1	2 μ m <i>TRP1 ADH1_{Prom}</i> - <i>GAL4_{DBD}</i> (James et al. 1996)
pGEX-2TK	<i>tac_{Pr/Op}</i> - <i>GST</i>
pJS470	2 μ m <i>TRP1 MET25_{Pr}</i> - <i>INO2</i>
pJS471	2 μ m <i>HIS3 MET25_{Pr}</i> - <i>INO4</i>
pKB1	2 μ m <i>URA3 MET25_{Pr}</i> -HA ₃ - <i>SNF6</i> ₁₋₃₃₂ (Wendegatz et al. 2024)
pKH15	2 μ m <i>URA3 MET25_{Pr}</i> -HA ₃ - <i>MAX</i>
pKH16	2 μ m <i>HIS3 MET25_{Pr}</i> - <i>MAX</i>
pKH19	2 μ m <i>URA3 MET25_{Pr}</i> -HA ₃ - <i>MYC</i>
pKH21	2 μ m <i>TRP1 MET25_{Pr}</i> - <i>MYC</i>
pLvD1	2 μ m <i>LEU2 MET25_{Pr}</i> -HA ₃ - <i>TAF1</i> ₁₋₂₅₀ (Hintze et al. 2017)
pMD2	2 μ m <i>URA3 MET25_{Pr}</i> -HA ₃ - <i>INO2</i>
pMD5	2 μ m <i>URA3 MET25_{Pr}</i> -HA ₃ - <i>INO4</i>
pME562	Coding region of <i>MAX</i> (Prof. Dr. M. Eilers, Würzburg)
pME920	Coding region of <i>MYC</i> (Prof. Dr. M. Eilers, Würzburg)
pMS1	2 μ m <i>URA3 MET25_{Pr}</i> -HA ₃ - <i>TAF4</i> (full length; Hintze et al. 2017)
pMS3	2 μ m <i>URA3 MET25_{Pr}</i> -HA ₃ - <i>TAF10</i> (full length; Hintze et al. 2017)
pMS4	2 μ m <i>URA3 MET25_{Pr}</i> -HA ₃ - <i>TAF12</i> (full length; Hintze et al. 2017)
pSG14	2 μ m <i>TRP1 ADH1_{Prom}</i> - <i>GAL4_{DBD}</i> - <i>INO2</i> ₁₋₃₅ (<i>TAD1</i>)
pSH117	<i>tac_{Pr/Op}</i> - <i>GST-INO2</i> ₁₋₃₅ (<i>TAD1</i>) (Hintze et al. 2017)
pSH153	2 μ m <i>URA3 MET25_{Pr}</i> -HA ₃ - <i>TOA1</i> (full length; Engelhardt et al. 2023)
pWW1	2 μ m <i>TRP1 ADH1_{Prom}</i> - <i>GAL4_{DBD}</i> - <i>MYC</i> ₁₋₁₅₆
pWW2	2 μ m <i>TRP1 ADH1_{Prom}</i> - <i>GAL4_{DBD}</i> - <i>MYC</i> ₁₋₃₁₃
pWW3	2 μ m <i>TRP1 ADH1_{Prom}</i> - <i>GAL4_{DBD}</i> - <i>MYC</i> ₁₋₄₁
pWW4	2 μ m <i>TRP1 ADH1_{Prom}</i> - <i>GAL4_{DBD}</i> - <i>MYC</i> ₄₁₋₁₅₆

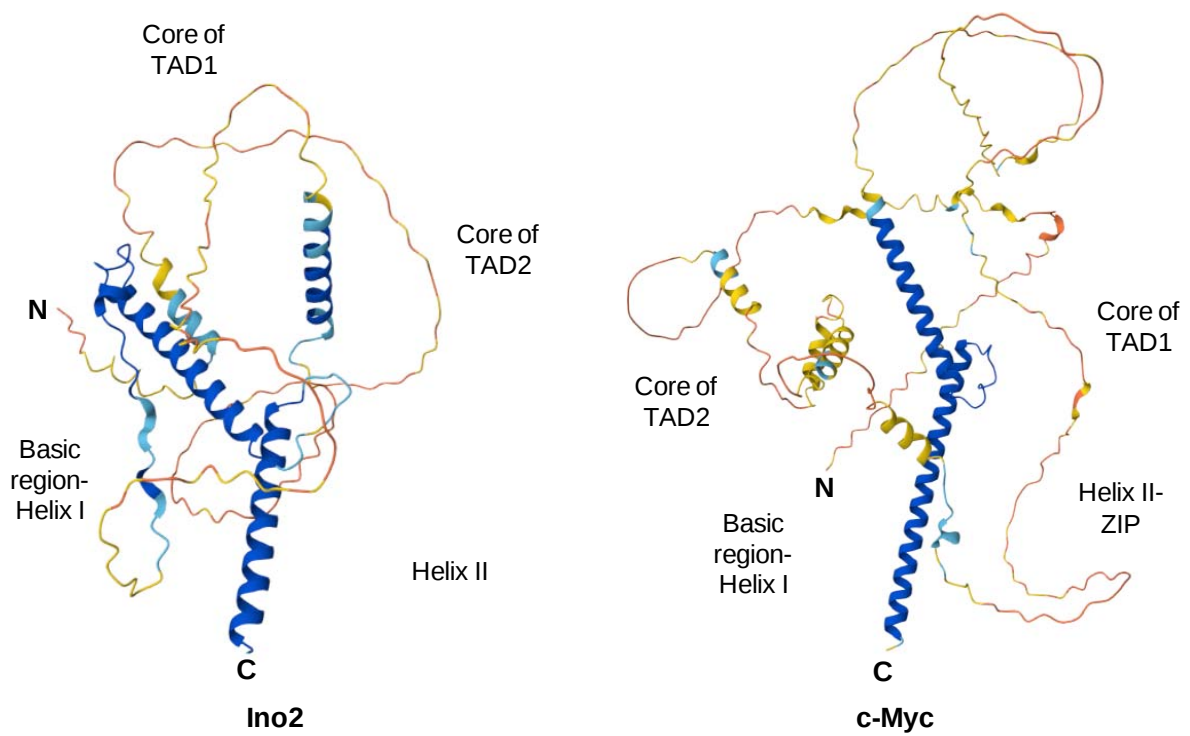
pWW5	2 μ m <i>TRP1 ADH1_{Prom}-GAL4_{DBD}-MYC₁₅₄₋₃₁₃</i>
pWW6	2 μ m <i>TRP1 ADH1_{Prom}-GAL4_{DBD}-MYC₉₁₋₁₄₀</i>
pWW8	taC _{Pr/Op} - <i>GST-MYC₉₁₋₁₄₀</i> (TAD2)
pWW9	taC _{Pr/Op} - <i>GST-MYC₁₋₄₁</i> (TAD1)
pWW10	2 μ m <i>TRP1 ADH1_{Prom}-GAL4_{DBD}-MYC₁₁₋₄₁</i>
pWW12	2 μ m <i>TRP1 ADH1_{Prom}-GAL4_{DBD}-MYC₉₆₋₁₄₀</i>

Pr, promoter; Op, operator; all positions refer to the protein encoded by the gene given.

Table S2: Oligonucleotides used (PCR primers for amplification of *MAX* and *MYC*, construction of length variants for *MYC*):

Name	Gene	Position	Sequence 5'-3'
Max-Bam	<i>MAX</i>	-3/+20	gact ggatcc ATAATGAGCGATAACGATGACAT
Max-Hind	<i>MAX</i>	+483/+461	gact aagctt TTAGCTGGCCTCCATCCGGAGCT
cMyc-Bam	<i>MYC</i>	-3/+20	gact ggatcc ATAATGCCCCTCAACGTTAGCTT
cMyc-Hind	<i>MYC</i>	+1320/+1301	gact aagctt TTACGCACAAGAGTTCCGTA
cMyc-Bam_1	<i>MYC</i>	+1/+20	gact ggatcc ATGCCCCTCAACGTTAGCTT
cMyc-Bam_11F	<i>MYC</i>	+31/+50	gact ggatcc AACTATGACCTCGACTACGA
cMyc-Bam_41F	<i>MYC</i>	+121/+140	gact ggatcc CAGCCCCCGGCGCCCAGCGA
cMyc-Bam_91F	<i>MYC</i>	+271/+290	gact ggatcc GGGAGCTTCTCCACGGCCGA
cMyc-Bam_96F	<i>MYC</i>	+286/+305	gact ggatcc GCCGACCAGCTGGAGATGGT
cMyc-Bam_154F	<i>MYC</i>	+460/+479	gact ggatcc GCTGCGCGCAAAGACAGCGG
cMyc-Hind_41R	<i>MYC</i>	+123/+104	gact aagctt <u>CTA</u> CTGCAGCTCGCTCTGCTGCT
cMyc-Sal_140R	<i>MYC</i>	+420/+401	gact gtcgac <u>CTA</u> GGCCGAGAAGCCGCTCCACA
cMyc-SalA_156	<i>MYC</i>	+468/+449	gact gtcgac <u>CTA</u> GCGCGCAGCCTGGTAGGAGG
cMyc-SalB_313	<i>MYC</i>	+939/+920	gact gtcgac <u>CTA</u> GGGAGGCGCTGCGTAGTTGT

Artificially inserted cleavage sequences for restriction enzymes are shown in **bold**; capital letters represent genuine gene-specific sequences; artificial stop codons are underlined.



Supplementary Fig. S1: Comparison of AlphaFold-generated structural predictions for Ino2 and c-Myc. DNA-binding domains (basic-helix-loop-helix or basic-helix-loop-helix-leucine zipper) and core sequences of transcriptional activation domains are indicated by black arrows.