

Supplementary materials

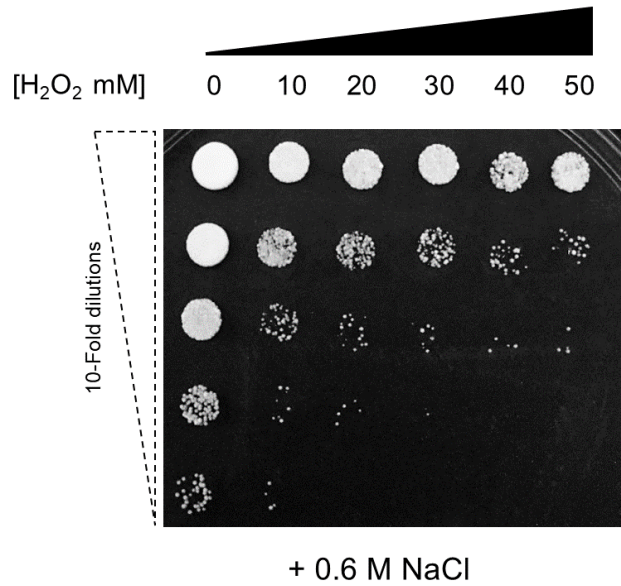


Figure S1. Assessment of cell survival of *D. hanseni* following H₂O₂ shock at different concentrations under NaCl condition. Wild-type cells were treated with 0, 10, 20, 30, 40, and 50 mM H₂O₂ with shaking for 3 hours, followed by tenfold serial dilutions (10⁻¹, 10⁻², 10⁻³, 10⁻⁴, 10⁻⁵). A 10-μL aliquot of each dilution was spotted onto YPD agar plates and incubated for 3 days at 28 °C. Representative image of three independent experiments.

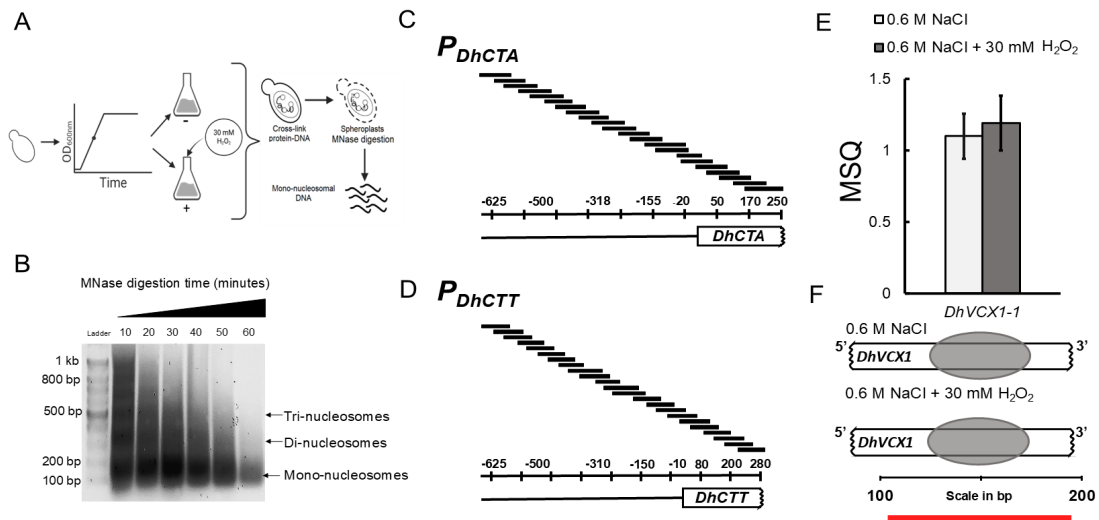


Figure S2. Nucleosome scanning assays in *D. hanseni*. (A) Cells were grown in YPD medium with 0.6 M NaCl (0 minutes) to the mid-log growth phase and treated with 30 mM H₂O₂ for 60 minutes. DNA-proteins cross-linking was performed, and spheroplasts were obtained by zymolyase digestion, followed by MNase digestion at different times, as described in the Materials and Methods section. (B) Gel electrophoresis was used to isolate mono-nucleosomal DNA (140–160 bp), as described in Materials and Methods. (C–D) qPCR analysis was performed to amplify the region of each gene from -625 bp to +250 bp (*DhCTA*) or +280 bp (*DhCTT*) relative to the start of the coding region. The tiled black bars above the scale indicate the DNA fragments amplified by qPCR to examine nucleosome occupancy. (E–F) A well-positioned nucleosome within the *DhVCX1* coding region (gray oval) was observed in NaCl or NaCl plus 30 mM H₂O₂, as the mean starting quantity (MSQ).

The relative protection of *DhCTA* or *DhCTT* region (**C-D**) was determined respectively using the peak of the *DhVCX1* region. The red horizontal line represents the amplicon used to normalize.

[illegible]

Figure S3. Sequence conservation of Msn2 or Msn4 proteins in *S. cerevisiae*, *D. hansenii*, and *C. albicans*. The amino acid sequences of Msn2/4 from *S. cerevisiae* (ScMSN2, ID: NP_013751.1/ScMSN4, ID: NP_012861.1), *D. hansenii* (DhMSN2, ID: CAG84649.2), and *C. albicans* (CaMSN4, ID: XP_723438.2) were aligned using the EMBL-EBI Clustal Omega on 9 July 2024 [50]. In the *S. cerevisiae* sequence, functional features are highlighted, Transcriptional Activation Domain (TAD) (blue) with Motive B (black, underlined), Nuclear Export Signal (NES) (green) and Nuclear Localization Signal (NLS) (yellow). The DNA-binding domain (DBD) (gray) contains the C2H2 Zinc finger structure with conserved cysteine and histidine residues in red and folding-related sites in blue [90]. Asterisks (*) indicate fully conserved residues; colons (:) indicate semi-conserved residues.

[illegible]

Table S1. Total percentage identity of each *D. hansenii* protein to their homologues in *S. cerevisiae* and *C. albicans*.

Protein in <i>D. hansenii</i>	Total % identity			
	<i>S. cerevisiae</i>		<i>C. albicans</i>	
<i>DhMsn2/4</i>	<i>ScMsn2</i>	23	<i>CaMsn2</i>	26
	<i>ScMsn4</i>	27		
<i>DhSkn7</i>	<i>ScSkn7</i>	35	<i>CaSkn7</i>	54
<i>DhSko1</i>	<i>ScSko1</i>	22	<i>CaSko1</i>	35
<i>DhYap1</i>	<i>ScYap1</i>	28	<i>CaCap1</i>	53

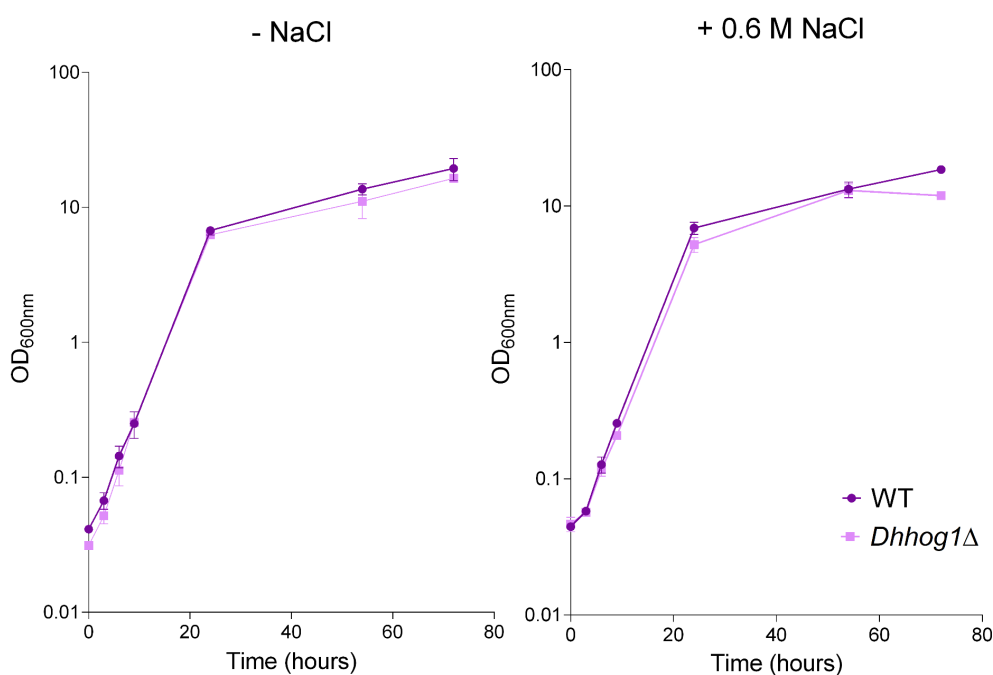


Figure S7. Growth curves of *D. hansenii* WT and *Dhhog1Δ* mutant without and with NaCl. Cells of WT and *Dhhog1Δ* mutant were cultured in rich medium YPD without NaCl (- NaCl) or YPD with NaCl (+ 0.6 M NaCl). Growth curves were followed for 72 hours. n = 3, and data are the mean \pm standard deviation (SD).

Table S2. Deoxyoligonucleotides used for nucleosome scanning assays in *DhCTA* locus.

Primer	Sequence (5' – 3')	Middle of amplicon (Promoter coordinate)	5'/3' end	Size (bp)
<i>DhCTA1Fw</i>	TCAGACGGCCAGCCC	-625.5	-676	101
<i>DhCTA1Rv</i>	AGATCAGGAGAAGTTTTACAAGTA		-575	
<i>DhCTA2Fw</i>	CTAATTTAAATGTCTACGAATATCAC	-582	-631	98
<i>DhCTA2Rv</i>	GCTTGAGAAAGAGGTTAGAATATA		-533	
<i>DhCTA3Fw</i>	TACTTGTAAAACTTCTCCTGATCT	-547.5	-599	103
<i>DhCTA3Rv</i>	GACCACCATCGGTACAGATT		-496	
<i>DhCTA4Fw</i>	TATATTCTAACCTCTTTCTCAAGC	-503.5	-557	107
<i>DhCTA4Rv</i>	TTGTGTCAACCCGATATGGC		-450	
<i>DhCTA5Fw</i>	AATCTGTACCGATGGTGGTC	-467.5	-516	97

<i>DhCTA5.Rv</i>	CTCCACAATCTATCAGAGCG		-419	
<i>DhCTA6Fw</i>	GCCATATCGGGTTGACACAA	-428.5	-470	83
<i>DhCTA6Rv</i>	GATGAGGCCATGTGAAGAAC		-387	
<i>DhCTA7Fw</i>	CGCTCTGATAGATTGTGGAG	-391	-439	96
<i>DhCTA7Rv</i>	CTTTGAAGTGTGGACTATCTAG		-344	
<i>DhCTA8Fw</i>	GTTCTTCACATGGCCTCATC	-355	-407	104
<i>DhCTA8Rv</i>	TGAGCACCATCAATCAAGAAGT		-303	
<i>DhCTA9Fw</i>	CTAGATAGTCCACACTTCAAAG	-318.5	-366	95
<i>DhCTA9Rv</i>	TTTCTACATCCTACAGGTATGC		-271	
<i>DhCTA10Fw</i>	ACTTCTTGATTGATGGTGCTCA	-273.5	-325	103
<i>DhCTA10Rv</i>	GGGGTTCAGAAAAGCAGAGT		-222	
<i>DhCTA11Fw</i>	GCATACCTGTAGGATGTAGAAA	-239.5	-293	107
<i>DhCTA11Rv</i>	TAAGTCGCACTCCAAGCATC		-186	
<i>DhCTA12Fw</i>	ACTCTGCTTTTCTGAACCCC	-192.5	-242	99
<i>DhCTA12Rv</i>	GCTTCTAAGTGGCCAGCG		-143	
<i>DhCTA13Fw</i>	GATGCTTGGAGTGCGACTTA	-154.5	-206	103
<i>DhCTA13Rv</i>	ATTTTAGGTAAGCGGGGTGAA T		-103	
<i>DhCTA14Fw</i>	CGCTGGCCACTTAGAAGC	-96.5	-161	129
<i>DhCTA14Rv</i>	TGATGAGATTGTATGATACCTTTTAA		-32	
<i>DhCTA15Fw</i>	ATTCACCCCGCTTACCTAAAAT	-74.5	-125	101
<i>DhCTA15Rv</i>	CCTGTAATTGATGAGATTGTATGA		-24	
<i>DhCTA16Fw</i>	TTAAAAGGTATCATACAATCTCATCA	-18	-58	80
<i>DhCTA16Rv</i>	AGTTAGTGTAACAGGAGCCAT		+22	
<i>DhCTA17Fw</i>	TCATACAATCTCATCAATTACAGG	+2.5	-48	101
<i>DhCTA17Rv</i>	GCAAATGGTTCTGGGATTGG		+53	
<i>DhCTA18Fw</i>	ATGGCTCCTGTTTACACTAACT	+50.5	+1	99
<i>DhCTA18Rv</i>	ATCTTGCAATAATAATGGACCATG		+99	
<i>DhCTA19Fw</i>	CCAATCCCAGAACCATTGTC	+86	+34	104
<i>DhCTA19Rv</i>	CTTTCTCTGTCTGAAGTGTGC		+137	
<i>DhCTA20Fw</i>	CATGGTCCATTATTATTGCAAGAT	+123	+75	96
<i>DhCTA20Rv</i>	AGATCCCTTGGCGTGCAC		+171	
<i>DhCTA21Fw</i>	GCACACTTCGACAGAGAAAG	+168.5	+117	103

<i>DhCTA21Rv</i>	TACAAACATCACTAATATCGTCAG		+220	
<i>DhCTA22Fw</i>	GTGCACGCCAAGGGATCT		+153	
<i>DhCTA22Rv</i>	GAATCTGGTTAAACCTTGGTC	+213	+273	120

Table S3. Deoxyoligonucleotides used for nucleosome scanning assays in *DhCTT* locus.

Primer	Sequence (5' – 3')	Middle of amplicon (Promoter coordinate)	5'/3' end	Size (bp)
<i>DhCTT1Fw</i>	GATATGTACGTGTTGGTTAATTGT		-676	
<i>DhCTT1Rv</i>	CTCACTATATGCATACCAACGA	-625	-574	102
<i>DhCTT2Fw</i>	TCACAACACTCCACTAACGTAT		-632	
<i>DhCTT2Rv</i>	CGGAACGAAGTCCGAATCAA	-580	-527	105
<i>DhCTT3Fw</i>	TCGTTGGTATGCATATAGTGAG		-596	
<i>DhCTT3Rv</i>	ACGATCATTCAATCATACGAAGTT	-546	-495	101
<i>DhCTT4Fw</i>	TTGATTCGGACTTCGTTCCG		-547	
<i>DhCTT4Rv</i>	GCTTAACAGCAACTCAAATATTGT	-500	-452	95
<i>DhCTT5Fw</i>	AACCTTCGTATGATTGAATGATCGT		-519	
<i>DhCTT5Rv</i>	AGTGGATGTGTAATATAAATGACG	-467	-415	104
<i>DhCTT6Fw</i>	ACAATATTTGAGTTGCTGTAAAGC		-476	
<i>DhCTT6Rv</i>	CTTAACTGGAAGCTTTGTTTGC	-429	-381	95
<i>DhCTT7Fw</i>	CGTCATTATATTACACATCCACT		-439	
<i>DhCTT7Rv</i>	CGTGAATTCAACGTCAAGATAC	-393	-346	93
<i>DhCTT8Fw</i>	GCAAACAAAGCTTCCAGTTAAG		-403	
<i>DhCTT8Rv</i>	ATATTCAAGAGTGTGTGGGTC	-360	-316	87
<i>DhCTT9Fw</i>	GTATCTTGACGTTGAATTCACG		-368	
<i>DhCTT9Rv</i>	CGACGAATTACTATACTTTGAACT	-309	-267	119
<i>DhCTT10Fw</i>	ACACTCTTGAATATGTTTCATTTC		-330	
<i>DhCTT10Rv</i>	TCGATTGTTGCTATTGGCTCAA	-276	-221	109
<i>DhCTT11Fw</i>	AGTTCAAAGTATAGTAATTCGTCG	-230	-273	87

<i>DhCTT11Rv</i>	AAATTTTCTGAAGTTGAATACATGATA		-186	
<i>DhCTT12Fw</i>	TTGAGCCAATAGCAACAATCGA		-243	
<i>DhCTT12Rv</i>	GAACATCGCCTATATTAGTCAG	-181	-118	125
<i>DhCTT13Fw</i>	TATCATGTATTCAACTTCAGAAAAATTT		-214	
<i>DhCTT13Rv</i>	GCAAGCTATGTCTCACTTTCTA	-156	-97	117
<i>DhCTT14Fw</i>	CTGACTAATATAGGCGATGTTC		-141	
<i>DhCTT14Rv</i>	AATGTGTGCTAGGCAGTCGT	-91	-41	100
<i>DhCTT15Fw</i>	TTGAGTTAGTTGCTATAATGAAGG		-93	
<i>DhCTT15Rv</i>	AACCATTTTACAATAAGCAGTTAGA	-44	+6	99
<i>DhCTT16Fw</i>	ACGACTGCCTAGCACACATT		-62	
<i>DhCTT16Rv</i>	CACTGCTGGATCTTTCTTCG	-9	+44	106
<i>DhCTT17Fw</i>	TCTAACTGCTTATTGTAAAAATGGTT		-20	
<i>DhCTT17Rv</i>	ATGGATGATTGGCATAAGGAAC	+32	+85	105
<i>DhCTT18Fw</i>	CGAAGAAAGATCCAGCAGTG		+26	
<i>DhCTT18Rv</i>	TTGCAATAATAGTGGCCCGC	+78	+130	104
<i>DhCTT19Fw</i>	GTTCCCTATGCCAATCATCCAT		+63	
<i>DhCTT19Rv</i>	CGAAGTGAGAAATGTCGTCC	+113	+163	100
<i>DhCTT20Fw</i>	GCGGGCCACTATTATTGCAA		+109	
<i>DhCTT20Rv</i>	ACCTTTTGCGTGAACAACCTCTT	+157	+205	96
<i>DhCTT21Fw</i>	GGACGACATTTCTCACTTCG		+143	
<i>DhCTT21Rv</i>	GTAAATCAGACAATGAATCAGTC	+198	+254	111
<i>DhCTT22Fw</i>	AAGAGTTGTTACGCAAAAGGT		+181	
<i>DhCTT22Rv</i>	TAGCCTGGGGATTGTAATGG	+232	+283	102
<i>DhCTT23Fw</i>	GACTGATTCATTGTCTGATTTAAC		+230	
<i>DhCTT23Rv</i>	TTCACCTCCAACGTAGAGAAT	+279	+327	97