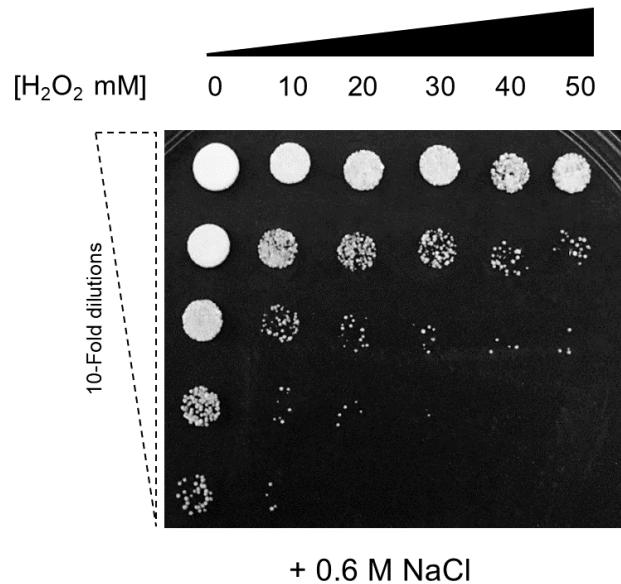
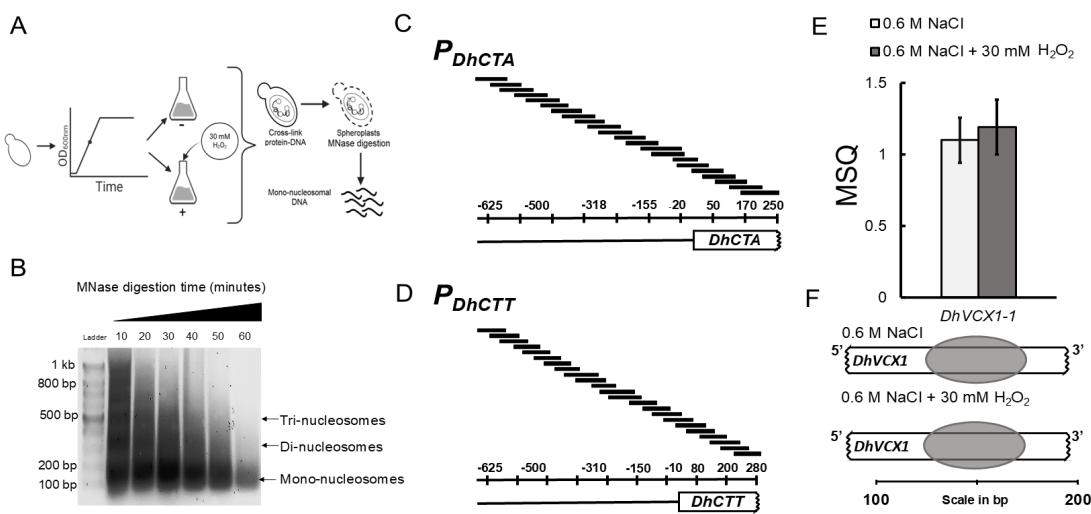


## Supplementary materials



**Figure S1.** Assessment of cell survival of *D. hansenii* following H<sub>2</sub>O<sub>2</sub> shock at different concentrations under NaCl condition. Wild-type cells were treated with 0, 10, 20, 30, 40, and 50 mM H<sub>2</sub>O<sub>2</sub> with shaking for 3 hours, followed by tenfold serial dilutions (10<sup>-1</sup>, 10<sup>-2</sup>, 10<sup>-3</sup>, 10<sup>-4</sup>, 10<sup>-5</sup>). A 10- $\mu$ L 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. hansenii*. (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 H<sub>2</sub>O<sub>2</sub> for 60 minutes. DNA-protein 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 H<sub>2</sub>O<sub>2</sub>, 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.

DhMSN2	--MSQEFQPF--LFETT-----	0	DhMSN2	--KRRNSIQQLVTFBSSYIN	290
CmMSN4	--PYNFS---CML---	20	CmMSN4	KTRNNHSSY33GVM4HSS3RGT3SRNSVCLL3MNGII3GNGNTWGGVJILTTATAATANGLT	523
ScMSN2	MIVTMHDNSEDILFPIIISMSNSIOYEVNDNPININNDIIPYFLDILONTFLWDALLDND---	56	ScMSN2	NGC-----MLP-----	515
ScMSN4	-MLVFGPN-----S3FVRHANKQEQD83S3MDEPENGIMDFVLSTLNTVBAT3N	46	ScMSN4	DPT-----NILK-----SSPAQDQFIRPSMMLSDNASA-----AAKLATSGUDNITP	481
DhMSN2	--MPVNA-----IMTGEFQG-----PA	16	DhMSN2	--OH-----NSFDD-----	298
CmMSN4	--SNIPMTNGNTAGNQNNTAATPLTGHNPNPWNNETIDL	59	CmMSN4	NSLHSGSPITLTAHMPENINEENDSINDSSIDTN-NP-----TGITTPKPIITSVDEGDD	576
ScMSN2	--IQNGETSISLNLFPLFLFDSLPLVTE-----T-IPSITSONL-HLKAD5-----	97	ScMSN2	LTPEEGEPMANJNTMIDL-----SITQ-MMMPLPSA33373IHNTHJHBYXNGG-----	567
ScMSN4	DNSAAMNIS1SSPEPYTFGKFSMDSLTNTDNTF-----ILTATHTNAMNLMKTDASLA	102	ScMSN4	PAFQR-----R8YDI-----SMON3-SFKILPTBSQA-----HHAQHMQO-----P	516
DhMSN2	SQPGNEMDNEFVFLRQNQEYL-IGSEV-----	42	DhMSN2	;	;
CmMSN4	SFPTSHSLDIEIFIINNRYQNRNLQGSDSTHN-----NAFLS-QQQFEEQQQFLYNNQSQ8LQ	112	CmMSN4	ARVQKKKRRRSYNNHYAKNST-KQDTPAAS-----ANNPEFVG-----TVH-NRPNFD	345
ScMSN2	--HNMURDART-----EX-----KSTHNA3BGS3TSPYKPMNDBHNSNPF-----	147	ScMSN2	--AKHRSKRKRS3SAIMGETIGPLSDS3TSITNSNTNUITMATSTVATRNKITE	632
ScMSN4	TNWAKRNSNNAQEVNNG-----ERQSHANGKRNQGOIIXSVATQPAQNLDEBLKNLEQLGK	158	ScMSN4	MANFSIGSSLR3E-AVFIMPFTVPL-----HQONN1335VNSTGNGA-G-----	612
DhMSN2	--MEGENNG/WF/FEELA3N3NRS3S-----	63	DhMSN2	TRQATVSFNTTRAKS3SSVLSPT1SHN-----N-----NNG-----	547
CmMSN4	PPPPPPDODGRINQINISATSAHSFONEI3N3N3N3N3LNTYVF3NPHASS3T3S3S3S3S3S3-----	172	CmMSN4	TIKE-----P-----SNDRS-F3NDEBECODEPFFPCPDCAROFRR	379
ScMSN2	SPBPSBSPUQPNTFNPNTA-----S3HNLSPQTS-WGNE-TLISFRAQONTSIR-----	198	ScMSN2	LMRKKS3H3K3SASTRNTTATNERK3ST-----AHMISPNNGNGNSQAF-PONECDKQFRR	690
ScMSN4	VTFPNE1INLCHNEN2-----ELSH-----QMAIS3-----IN	189	ScMSN4	VTKERF-----STRKSMF73-R4S5V1E73TRELEP-----HUCHICF3SFPRR	658
DhMSN2	LANMPVGCOT--TYST-----TTTPELSSP--PKSHF-----V---SRS2FSL	99	DhMSN2	KVFWQFRKRS3I1TIDFNNDMNP-FCKDCEKAFPR	554
CmMSN4	SS5FSAGST---NNINNNGGNNNNNGCATSKVTPQFQTHH-----G-----RQNTTII	218	CmMSN4	;	;
ScMSN2	F3L3LNGA3N3L3T3P3H3N3-----EFLRNOLNSD3T3S3H3S3H3S3H3S3H3S3H3-----	257	ScMSN2	SEHLKRHR1S3H3N3R3P3H3C3K3Y3-----	439
ScMSN4	LLEAP3P3T3S3H3L3D3P3H3N3-N3T3-GL-WDN3D3N-Y3D-----T3NN3NT3N	233	ScMSN4	SEHLKRHR1S3H3N3R3P3H3C3K3Y3-----SEHLKRHR1S3H3N3R3P3H3C3K3Y3-----	750
DhMSN2	Mod B		DhMSN2	SEHLKRHR1S3H3N3R3P3H3C3K3Y3-----SEHLKRHR1S3H3N3R3P3H3C3K3Y3-----	750
CmMSN2	PIDQI-----NLLS1K3MS3STQ-----SSK-----3SPSEPYNLYSIRE	133	DhMSN2	SEHLKRHR1S3H3N3R3P3H3C3K3Y3-----SEHLKRHR1S3H3N3R3P3H3C3K3Y3-----	704
ScMSN2	PIDQI-----TLL3L3R3T3G3T-----FVNQNLIPQNFQHN3QCPFD3S3P3Q	263	CmMSN4	SEHLKRHR1S3H3N3R3P3H3C3K3Y3-----SEHLKRHR1S3H3N3R3P3H3C3K3Y3-----	704
ScMSN4	N1H3L3H3D3V3S3-----L3N3C3D3N3-----3R3H3R3F3C3T3P3H3-----S3T3	317	ScMSN2	SEHLKRHR1S3H3N3R3P3H3C3K3Y3-----SEHLKRHR1S3H3N3R3P3H3C3K3Y3-----	630
DhMSN2	SM3S1L3D3F3V3S3E3R3P3H-----PD4GDRDARRYSEV3T3S3F3M3D3S3N3I3H3I3E3F3N3L3H3K	292	ScMSN4	SEHLKRHR1S3H3N3R3P3H3C3K3Y3-----SEHLKRHR1S3H3N3R3P3H3C3K3Y3-----	630
CmMSN4	;	;	DhMSN2	*****	*****
ScMSN2	;	;	CmMSN4	*****	*****
ScMSN4	;	;	ScMSN2	*****	*****
DhMSN2	--NP-----	135	ScMSN4	*****	*****
CmMSN4	PPSQQCCCCQCNQLSQ3GQFQPVSSSN3PALVNN3UDANTIAAAA-----AATAATEDITVGFV	320	DhMSN2	*****	*****
ScMSN2	PPW3Q3Q3Q3Q3Q3-----Q3W3A3W3A3W3A3-----W3A3W3A3W3A3-----W3A3W3A3-----	347	CmMSN4	*****	*****
ScMSN4	NNSSN3R3K3T3Q-----Q11PEF3G1AT-----ERRG3T3S3F3T-----INNN3N3F3K3L3H3D	337	ScMSN2	*****	*****
DhMSN2	EERKT1F3P3L3F3E3D3I3G3A3A3A3A3A3F3T3K3T3D3T3E3T3G3Y3L3P3S33S3P3L3T3F3	195	CmMSN4	*****	*****
CmMSN4	LE3G3T3F3L3P3H3N3L3G3T-----3R3P3S3L3T3F3-----	355	ScMSN2	*****	*****
ScMSN2	3L3T3G3P3F3P3H3-----T3G3N3-----S3A3A3-----S3A3A3-----S3A3A3-----S3A3A3-----	400	ScMSN4	*****	*****
ScMSN4	V3S3L3G3S3M3F3K3D3G3T-----S3T3R3A3S3L3-----	362	DhMSN2	*****	*****
DhMSN2	G7QGRAS-----Y-----P-----KAKH3S13MS3G3D3I	216	CmMSN4	*****	*****
CmMSN4	NNFA3C3Q3Q3Q3Q3-----Q3Q3L3P3F3Q3E3G3N3L3S3T3A3P3D3Q3S-----T3Q3L3A3M3Q3Q3Q3Q3V3F3N3H3K3R3	408	ScMSN2	*****	*****
ScMSN2	AN3M3T3N3F3Q3Q3Q3Q3N3-----S3R3Q3L3T3S3H3S3-----S3T3K3M3T3Y3S3D3L3Y3S3R3Q3R3A3P3I3D3G3-----	459	ScMSN4	*****	*****
ScMSN4	-----S3S3L3N3H3S3-----S3T3R3A3S3L3-----S3T3R3A3S3L3-----	389	DhMSN2	*****	*****
DhMSN2	TASKKFDF1MMNECNFAIS1YIN3T1LQN3VNS3R3N3D3E3L3G3A3E3I3M3V3F3G3I3K3N3Y-----	275	CmMSN4	*****	*****
CmMSN4	S3T3P3H3F3D3F3D3F3-----S3T3S3F3H3N3G3N3L3D3P3H3Q3Q-----I3D3E3N3N3L3F3P3H3N3H3T3H3N3I-----	463	ScMSN2	*****	*****
ScMSN2	-----T3G3D3P3H3-----T3G3D3P3H3-----T3G3D3P3H3-----T3G3D3P3H3-----	471	ScMSN4	*****	*****
ScMSN4	S3A3F3A3-----N3D3M3A3M3A3-----S3A3F3A3-----S3A3F3A3-----S3A3F3A3-----	437	DhMSN2	*****	*****

**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.

ScSKN7	TNNVQQP-AGNTNISSANAGAKAPANE <del>FVRKLF</del> FAILENNYEVDIVIWTENGKSFVVLDTG	119
DhSKN7	MRRIPKSEDSLMLPSTASSNQSGSNDFVKLFLQMLQEDTYKDVWWTSSGDSFVVINTT	62
CaSKN7	S--LQQPIPPNSTLATTASSNQSGSNDFV/KKLFLMLQEDSYKEVURWTVKGDSFVVINTN	60
ScSKN7	<b>KETTHILPNHFKHSEN</b> <b>FASFVRQLNKYDFHKVKIRSPEERQRCKYGEQSWEFQHPEFRVHYG</b>	179
DhSKN7	EFTKEILPRHFKHSEN <b>FASFVRQLNKYDFHKVKIPNEEKQSYEYGEDAWEFQHPEFRINDR</b>	122
CaSKN7	EFTKDILPKHFKHSEN <b>FASFVRQLNKYDFHKVKISNEAKASYPYGEDAWEFQHPEFRINDA</b>	120
ScSKN7	<b>EGLDNIKRKIPAPAQRKVLLDESQWALLHFNMSEGTPNNP3GSLLNESTTELLSNTVSKD</b>	239
DhSKN7	ESLENIKRKSSWKKSTQNYMPNVA-----NSG-----SVDSEFG	155
CaSKN7	EALENIKRKGPTAKKSASNVTIKT--EAMNGNTQPTCN-----HNY-----SQLVSA	165
ScSKN7	<b>FGNLRRREVEMLORELMSRME</b> SYATKVELQKLNISKYNTVIESLITPFTIMENLLNNFNTL	299
DhSKN7	YQNLKD-----EMDNLRBENKSLKQDISVLTHTKYKTLIVENIV3LKSFDEKYRYSM3VL	208
CaSKN7	TMHLKE-----QVESLKNMDKHSLYQEISVLERKYKTVVENVIAINTFMERRYRYSMNVL	218
ScSKN7	CSTLANNNGIEVPIFGDN-----GNRNP-----	321
DhSKN7	INCLVQAGIMMPEPLDFPNPNALYPQKPWNAAHQH-----SHHHHHSSSLPQ-----	254
CaSKN7	INSIVQNGMKLPPLDFFPPPVQLGPDSGIGSNSNLGPISSDTALPSI3HHLSSPLPHHQQLLN	278
ScSKN7	-----TGNTINPATT-----AIQ-----	334
DhSKN7	-LSPPLLLSPNGGT-----GQQGGIGVPLGSGLPAQRFDHNTISQANTLQHQTP	301
CaSKN7	RTIRPISSPIDGIPLVQLQQ3LGQNLLQAPIGTPSAV--PFSEEASSSIQA---ATPAP	322
ScSKN7	-----SNNNTTMN-----ASPATSTV-----SQLP-	354
DhSKN7	LQTIMSQPNQQSTKQTPPTNDNLNSKPKQSPHLMGE--STSGSPLVGNGLDAASTTAPV	359
CaSKN7	LAQPVAQPINQFPFFFFFATQQQPLFFPPPPATATQIPSAPPFTQQVGTSSSSVPT	392
ScSKN7	-----NLPDQNSL--TPNA-QNNVTILRKGFH/VLLVEDDAVSIQLCSKFLRKYG	400
DhSKN7	-MSRTSSISTNRVPQPANGASTDQPQVTTNLTNPKFHVLLVEDDNVC1QLCRKFLVKYG	418
CaSKN7	ISPKSQ----GIVV8NSASPTTSAQ13TTSVPMPKFHVLLVEDDNVC1QLCRKFLVKYG	447
ScSKN7	CTVQVVSQDGLSAISTLEKRYDLVLMQIVMPNLDGATATSVRSFDNETPIIAMI GTGNIMN	460
DhSKN7	CQVIIATDGLNAISTVEHTKDYDLVLMQIVMPNLDGATATSVRSFDTHTPIIAMI GTGNIED	478
CaSKN7	CSVTVVTDGLNAISTVEHTKDYDLVLMQIVMPNLDGATATSVRSFDTHTPIIAMI GTGNIED	507
ScSKN7	QDLITYLQHGMDILAKPFTRDDLHSILIRYIKDRIPLCQQLPPRNSSPQTHSNTNTAN	520
DhSKN7	NDLVTYLQNGMSDILAKPFTKDDLYSIL3KWHLLISTD8A3VTTD---EPSET---MSSL	531
CaSKN7	NDLVTYLQNGMSDILAKPFTKDDLYAILSKWHLDPKENKQDN---EPTVK---KQKL	558
ScSKN7	SNPNTINEQ8LAMLQPQDNPSTTFVTPGASIS3AQHVQQQQEQQQHQIFHAQQQQHHNA	560
DhSKN7	QGP---AQQTIVLPQEVQQQDSW---CEPMP-----	556
CaSKN7	S*-----	559
ScSKN7	IANARSQVAIPNLEHEINTVPHSSMG3TPQLPQSTLQENQLS*	622
DhSKN7	---EPHSKKPRLI-----	566
CaSKN7	-----	559

**Figure S4. Sequence conservation of Skn7 protein in *S. cerevisiae*, *D. hansenii*, and *C. albicans*.**  
The amino acid sequences of Skn7 from *S. cerevisiae* (ScSKN7, ID: KZV10951.1), *D. hansenii* (DhSKN7, ID: CAG85310.2), and *C. albicans* (CaSKN7, ID: AAAQ08008.1) were aligned using the EMBL-EBI Clustal Omega on 9 July 2024 [50]. In the *S. cerevisiae* sequence the following features are highlighted: Heat-shock factor type DNA binding domain (HSF-type DBD) (yellow), critical for ScSkn7 activity marked in red and helix-3 residues known to be involved in contacting DNA (S137, R140, N143, Y145 and K149) marked in blue; the ROCK1/Kinectin homology region (HR) motif involved in interaction with Rho1 and Mbp1 (pink) and the Response Regulator domain (RR) (gray) with phospho-accepting aspartate residue (D427) [91,92] important for the SLN1-YPD1-SKN7 regulation branch related to the HOG pathway is shaded in green, as well as tyrosine residue (T437) fundamental for interaction with Yap1 is shaded in blue [93,94]. Asterisks represent conserved residues (\*), and colons (:) indicate semi-conserved residues.

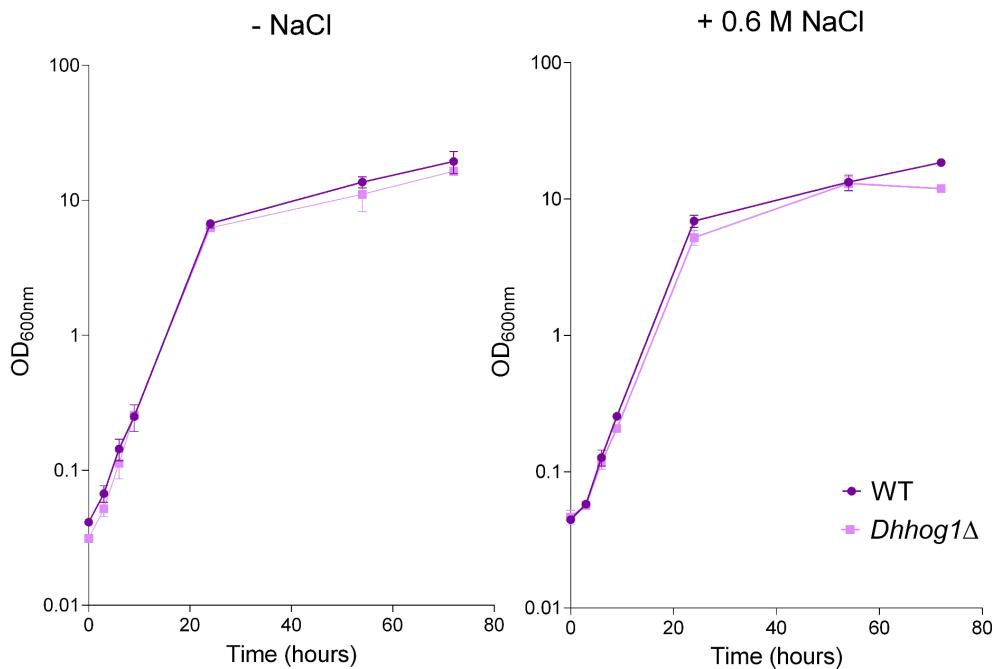
ScSKO1	MSSSEERSRQPSTVSTFDLEPNPFFEQSFASSKKALSLPGTISHPSLPKELSRNNNSTTITQ	60
DhSKO1	-----MSSD8KTSFDFLEPNPFERSFATKDGDREGGDGAEQR-----GKGK-----	41
CaSKO1	-----MSSDHKSFKDFLELNPFERSFATKESSSVSLSNELAAASNNDAISDVNSVAT-----	50
ScSKO1	HSQR8THSLNS1PEENGN3TVTDNSNHNDVKKDPSFLPGQQ <b>RPTIISFPILTPGGSKRL</b>	120
DhSKO1	----NGKSA--NVGEQKRNETNKHNLIHPN1STLDPN-I---N <b>RAPVGTSPSLTPGD-RKL</b>	90
CaSKO1	----SGSSI----NNGSSSNKHNLIHPN1SS8VNQQ-QGVNG <b>KLPGITTPLFPTCG-RRL</b>	99
ScSKO1	<b>PPLLLSP</b> SILYQANSTTNPSQN3H3V3VSN8NPAIGV88TSGS8LYPNSS-----	170
DhSKO1	<b>PPLGLSP</b> GGHLNLGG-----GTPGSN-LWN8L8SATNNPN8GTNAAT	131
CaSKO1	<b>PPIGLSP</b> GGTT8RQYSN8TN--SG8L---Q8NTD8LGSN-1WGGLPTNQ-----	142
ScSKO1	---SPSGTSLIRQP--RN8NVTTSNSGNG-----FPTND8QMPGFLLNLSKSG	213
DhSKO1	N8TS8NDGSNTVANGINAN8NYTTGQNS-GAP--NHEG8FHPSNQNNNTINQF18MLRKSG	188
CaSKO1	-----TFQPQPQPQPQPQQQQPQQQQQTQQPHNFNQFMSGMRKRTG	183
ScSKO1	LTPNES8NIR8LGLTPGILTQS8Y8VLP8INKNTITG8K8N8V8K8T8VNG8SIENH8PHV <b>WIMH</b>	273
DhSKO1	LTPNES8NLR8LGLTPG8GVNHH8GGN-MFAF-----NNQLPGL8TP-----	225
CaSKO1	LTPNES8NIR8LGLTPG8GLTNFGFG-----SNLV8PGL8TP-----	216
ScSKO1	<b>P1VNGT8L8P8L8Q8L8L8P8T8V8L8N8</b> --V8F8-----S8T8T8NT8D8T8V8N8S8	320
DhSKO1	GAFL8NS8P8T8P8L8S8N8L8G8M8P8Q8N8H8A8T8Q8T8N8-----I8P8P8N8S8A8N8H8D8Y8-N	275
CaSKO1	GALL8NG8P8T8P8L8S8L8L8G8T8Q8T8S8L8--P8T8S8F8Q8N8Q8H8L8I8Q8A8T8V8G8P8E-----	271
ScSKO1	<b>M8N8F8P8N8T8K8A8</b> -----	332
DhSKO1	M8N8F8D8M8G8H8Q8R8E8Q8Q8S8Q8H8--Q8T8Q8A8P8Q8S8P8Q8E8Q8H8Q8K8E8Q8Q8Q8Q8Q8Q8H8Q8Q	333
CaSKO1	STAL8GP8H8V8N8I8P8Q8A8Q8L8Q8D8Q8S8Q8A8L8V8G8L8P8S8Q8P8Q8P8Q8F8-----IA8Q8	316
ScSKO1	-----AVRMD8N8P8A8F8N8-1E8H8A8H8K8---E8N8E8N8T8Q8I-----	362
DhSKO1	Q8H8Q8Q8Q8Q8H8Q8Q8Q8H8Q8P8Q8H8Q8Q8Q8Q8H8Q8Q8H8Q8-----P-----Q8Q8P8Q8H8T8P8Q8Q8A8Q8H8Q8	385
CaSKO1	I8H8T8I8P8E8N8I8F8D8M8T8Q8A8V8A8-----A8A8H8L8P8E8K8P8D8L8E8T8A8N8Q8R8D8L8N8P8A8T8D8T8T8T8A8T8K8K8	373
ScSKO1	<b>E8N8D8F8N8K8--TR8K8R8M8S8T8S8T8S8-K8A8R8K8N8I-----S8K8N8S8V8T8A8P8Q8-----</b>	407
DhSKO1	L8Q8N8Q8L8P8Q8S8Y8A8T8K8I8N8K8E8D8E8K8G8K8R8K8S8R8N8S8E8S8-----K8K8Q8T8D8A8V8K8T8K8L8K8E8E-----	441
CaSKO1	R8K8N8D8T8A8G8T8G8K8K8A8V8K8G8K8R8K8P8K8S8-K8G8K8N8Q8E8D8Q8N8A8N8K8P8E8D8E8N8V8P8G8K8E8N8E8E-----	431
ScSKO1	-----K8D8V8-----N8N8I8N8V8I8L8D8E8E8Q8R8K8R8F8E-----	437
DhSKO1	-----P8K8D8V8L8D-----D8T8V8P8D8T8S8T8G8G8P8N8 <b>K8R8K8S8F8E</b>	473
CaSKO1	H8K8V8A8E8K8E8H8L8Q8N8G8N8E8T8T8T8K8S8K8K8N8N8V8E8D8D8 <b>K8R8N8F8E</b>	491
ScSKO1	<b>R8N8R8A8A8K8F8R8K8R8K8E8Y8I8K8I8E8N8D8Y8D8I8T8Q8V8I8G8R8I-----C8G8I8P8S8S8N8S8Q8F8N8V8S8T8</b>	497
DhSKO1	<b>R8N8R8A8A8K8C8R8Q8R8K8Q8L8I8Q8M8E8D8E8L8S8F8Y8T8G8Y8R8I-----L8A8Q8V8T8Q8V8L8R8D8Q8L8I-----</b>	530
CaSKO1	<b>R8N8R8A8A8K8C8R8Q8R8K8L8I8Q8M8E8L8Q8F8Y8S8N8G8Y8R8E-----L8A8E8V8N8E8L8R8A8I8L8K8E8K8H8N8I8Q8D-----</b>	547
ScSKO1	P8S8S8P8P8T8L8I8A8--L8E8S8I8R8D8Y8S8A8-----V8L8N8M8Q8L8I8C8I-----	538
DhSKO1	-----C8P8M8V8S8V8G8F8D8Q8N8I8Q8S8N8Y8V8T8Q8I-----A8G8S8Q8T8N8M8P8T8I-----	586
CaSKO1	-----E8I8D8G8-----L-----L8K8P8T8V8P8T8N8I8P8T8I-----	578

**Figure S5. Sequence conservation of Sko1 protein in *S. cerevisiae*, *D. hansenii*, and *C. albicans*.** The amino acid sequences of Sko1 from *S. cerevisiae* (*ScSKO1*, ID: NP\_014232.1), *D. hansenii* (*DhSKO1*, ID: XP\_458864.2), and *C. albicans* (*CaSKO1*, ID: XP\_019330633.1) were aligned using the EMBL-EBI Clustal Omega on 9 July 2024 [50]. The *S. cerevisiae* Hog1 phosphorylation site (yellow), with conserved/semi-conserved residues in underlying blue; the PKA phosphorylation site (pink) with conserved residues in boldface; and the DNA-binding domain (blue), with conserved leucine zipper residues in red [56]. Repression-mediated domains (green) show conserved hydrophobic amino acids in purple [95]. Asterisks represent conserved residues (\*), and colons (:) indicate semi-conserved residues.

**Figure S6. Sequence conservation of the Yap1 protein in *S. cerevisiae*, *D. hansenii*, and *C. albicans*.** The amino acid sequences of Yap1 from *S. cerevisiae* (*ScYAP1*, ID: KZV08838.1), *D. hansenii* (*DhYAP1*, ID:XP\_461648.2), and *C. albicans* (*CaCAP1*, ID: KAL1577880.1) were aligned using the EMBL-EBI Clustal Omega on 09/07/2024 [50]. In the *S. cerevisiae* sequence, the basic leucine zipper domain (bZIP) is highlighted in yellow. Within this domain, the basic region residues that directly interact with base pairs (N74, A77, Q78, F81 and R82) are marked in green, and Yap1-specific residues (Q73, Q78, A80, and F81) are underlined. In the leucine zipper region, the typically hydrophobic residues at positions of the coiled coil are shown in blue, and conserved leucine residues are marked in red [96–98]. The nuclear localization signal (NLS) and nuclear exportation signal (NES) are indicated with black and red boxes, respectively. The two cysteine-rich domains, nCRD and cCRD, are underlined in blue and gray, with conserved cysteine residues highlighted in purple (C303, C310 and C315; C598, C620 and C629, respectively) [99–103]. Asterisk (\*) indicate fully conserved residues; colons (:) indicate semi-conserved residues.

**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 ± 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>	TCAGACGGCCAGGCC	-625.5	-676	101
<i>DhCTA1Rv</i>	AGATCAGGAGAAAGTTTACAAGTA		-575	
<i>DhCTA2Fw</i>	CTAATTAAATGTCTACGAATATCAC	-582	-631	98
<i>DhCTA2Rv</i>	GCTTGAGAAAGAGGTTAGAATATA		-533	
<i>DhCTA3Fw</i>	TACTTGTAAAACCTCTCCTGATCT	-547.5	-599	103
<i>DhCTA3Rv</i>	GACCACCATCGGTACAGATT		-496	
<i>DhCTA4Fw</i>	TATATTCTAACCTCTTCTCAAGC	-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
<i>DhCTA6Rv</i>	GATGAGGCCATGTGAAGAAC	-387
<i>DhCTA7Fw</i>	CGCTCTGATAGATTGTGGAG	-391
<i>DhCTA7Rv</i>	CTTGAAAGTGTGGACTATCTAG	-344
<i>DhCTA8Fw</i>	GTTCTCACATGGCCTCATC	-355
<i>DhCTA8Rv</i>	TGAGCACCATCAATCAAGAAC	-303
<i>DhCTA9Fw</i>	CTAGATAGTCCACACTCAAAG	-318.5
<i>DhCTA9Rv</i>	TTTCTACATCCTACAGGTATGC	-271
<i>DhCTA10Fw</i>	ACTTCTTGATTGATGGTGCTCA	-273.5
<i>DhCTA10Rv</i>	GGGGTTTCAGAAAAGCAGAGT	-222
<i>DhCTA11Fw</i>	GCATACCTGTAGGATGTAGAAA	-239.5
<i>DhCTA11Rv</i>	TAAGTCGCACCCAAGCATC	-186
<i>DhCTA12Fw</i>	ACTCTGCTTTCTGAACCCC	-192.5
<i>DhCTA12Rv</i>	GCTTCTAAGTGGCCAGCG	-143
<i>DhCTA13Fw</i>	GATGCTTGGAGTGCAGCTTA	-154.5
<i>DhCTA13Rv</i>	ATTTTAGGTAAGCGGGGTGAA T	-103
<i>DhCTA14Fw</i>	CGCTGGCCACTTAGAAC	-96.5
<i>DhCTA14Rv</i>	TGATGAGATTGTATGATACTTTAA	-32
<i>DhCTA15Fw</i>	ATTCACCCCGCTTACCTAAAAT	-74.5
<i>DhCTA15Rv</i>	CCTGTAATTGATGAGATTGTATGA	-24
<i>DhCTA16Fw</i>	TTAAAAGGTATCATACAATCTCATCA	-18
<i>DhCTA16Rv</i>	AGTTAGTGTAAACAGGGAGCCAT	+22
<i>DhCTA17Fw</i>	TCATACAATCTCATCAATTACAGG	+2.5
<i>DhCTA17Rv</i>	GCAAATGGTTCTGGATTGG	+53
<i>DhCTA18Fw</i>	ATGGCTCCTGTTACACTAACT	+50.5
<i>DhCTA18Rv</i>	ATCTTGCAATAATAATGGACCAGT	+99
<i>DhCTA19Fw</i>	CCAATCCCAGAACCAATTG	+86
<i>DhCTA19Rv</i>	CTTTCTCTGTCGAAGTGTGC	+137
<i>DhCTA20Fw</i>	CATGGTCATTATTATTGCAAGAT	+123
<i>DhCTA20Rv</i>	AGATCCCTGGCGTGCAC	+171
<i>DhCTA21Fw</i>	GCACACTTCGACAGAGAAAG	+168.5
		+117
		103

<i>DhCTA21Rv</i>	TACAAACATCACTAATATCGTCAG	+220
<i>DhCTA22Fw</i>	GTGCACGCCAAGGGATCT	+153
<i>DhCTA22Rv</i>	GAATCTGGTAAAACCTTGGTC	+273

**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>	GATATGTACGTGTTGGTAATTGT	-625	-676	102
<i>DhCTT1Rv</i>	CTCACTATATGCATACCAACGA		-574	
<i>DhCTT2Fw</i>	TCACAACACTCCACTAACGTAT	-580	-632	105
<i>DhCTT2Rv</i>	CGGAACGAAGTCCGAATCAA		-527	
<i>DhCTT3Fw</i>	TCGTTGGTATGCATATAGTGAG	-546	-596	101
<i>DhCTT3Rv</i>	ACGATCATTCAATCATACGAAGTT		-495	
<i>DhCTT4Fw</i>	TTGATTGGACTTCGTTCCG	-500	-547	95
<i>DhCTT4Rv</i>	GCTTAACAGCAACTCAAATATTGT		-452	
<i>DhCTT5Fw</i>	AACTTCGTATGATTGAATGATCGT	-467	-519	104
<i>DhCTT5Rv</i>	AGTGGATGTGAATATAATGACG		-415	
<i>DhCTT6Fw</i>	ACAATATTGAGTTGCTGTTAACG	-429	-476	95
<i>DhCTT6Rv</i>	CTTAACTGGAAGCTTGTGTTGC		-381	
<i>DhCTT7Fw</i>	CGTCATTATATTACACATCCACT	-393	-439	93
<i>DhCTT7Rv</i>	CGTGAATTCAACGTCAAGATAC		-346	
<i>DhCTT8Fw</i>	GCAAACAAAGCTCCAGTTAAG	-360	-403	87
<i>DhCTT8Rv</i>	ATATTCAAGAGTGTGTTGGGTC		-316	
<i>DhCTT9Fw</i>	GTATCTGACGTTGAATTACG	-309	-368	119
<i>DhCTT9Rv</i>	CGACGAATTACTATACTTGAAC		-267	
<i>DhCTT10Fw</i>	ACACTCTGAATATGTTCATTTCC	-276	-330	109
<i>DhCTT10Rv</i>	TCGATTGTTGCTATTGGCTCAA		-221	
<i>DhCTT11Fw</i>	AGTTCAAAGTATAGTAATTCGTCG	-230	-273	87

<i>DhCTT11Rv</i>	AAATTTCTGAAGTTGAATAACATGATA	-186
<i>DhCTT12Fw</i>	TTGAGCCAATAGCAACAATCGA	-243
<i>DhCTT12Rv</i>	GAACATCGCCTATATTAGTCAG	-118
<i>DhCTT13Fw</i>	TATCATGTATTCAACTTCAGAAAAATT	-214
<i>DhCTT13Rv</i>	GCAAGCTATGTCTCACTTTCTA	-97
<i>DhCTT14Fw</i>	CTGACTAATATAGGCGATGTT	-141
<i>DhCTT14Rv</i>	AATGTGTGCTAGGCAGTCGT	-41
<i>DhCTT15Fw</i>	TTGAGTTAGTGCTATAATGAAGG	-93
<i>DhCTT15Rv</i>	AACCATTTCACAATAAGCAGTTAGA	+6
<i>DhCTT16Fw</i>	ACGACTGCCTAGCACACATT	-62
<i>DhCTT16Rv</i>	CACTGCTGGATCTTCTTCG	+44
<i>DhCTT17Fw</i>	TCTAACTGCTTATTGTAAAAATGGTT	-20
<i>DhCTT17Rv</i>	ATGGATGATTGGCATAAGGAAC	+85
<i>DhCTT18Fw</i>	CGAAGAAAGATCCAGCAGTG	+26
<i>DhCTT18Rv</i>	TTGCAATAATAGTGGCCCGC	+130
<i>DhCTT19Fw</i>	GTTCCTTATGCCAATCATCCAT	+63
<i>DhCTT19Rv</i>	CGAAGTGAGAAATGTCGTCC	+163
<i>DhCTT20Fw</i>	GCGGGCCACTATTATTGCAA	+109
<i>DhCTT20Rv</i>	ACCTTTGCGTGAACAACTCTT	+205
<i>DhCTT21Fw</i>	GGACGACATTCTCACTTCG	+143
<i>DhCTT21Rv</i>	GTAAATCAGACAATGAATCAGTC	+254
<i>DhCTT22Fw</i>	AAGAGTTGTTCACGCCAAAGGT	+181
<i>DhCTT22Rv</i>	TAGCCTGGGATTGTAATGG	+283
<i>DhCTT23Fw</i>	GACTGATTCAATTGTCTGATTAAAC	+279
<i>DhCTT23Rv</i>	TTCACCTCCAATGTAGAGAAT	+327