Summary of Supplementary Data

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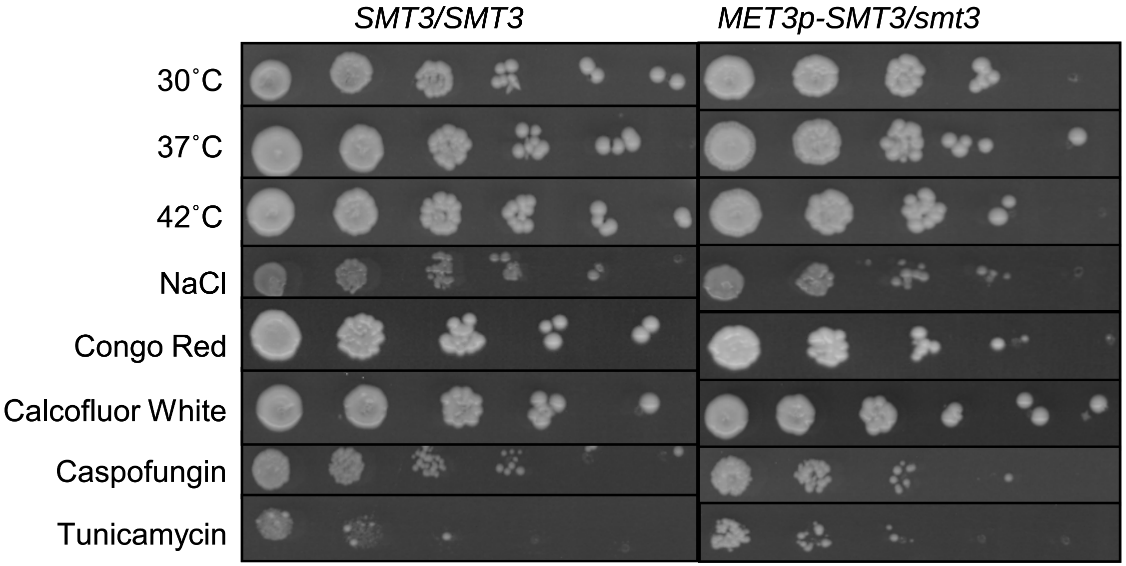
List of sumoylation targets in *C. albicans*

Sample Ref	Accession Number (CandidaDB)	Accession Number (CGD)	Protein Name	Mol. Wt. (Da)	pI	Mascot Score	Peptides Matched	Sequence Coverage	ELDP	Function	Sumoylated in *S. cerevisiae* ?	Predicted Sumoylation Site	Sumoylation detected in absence of stress?	Sumoylation upregulated in response to stress?	Sample gel used for spot cutting
Constitutively sumolylated															
1 (1)	CA5549	orf19.7312	ERG13	49952	5.67	1086	24	63%	14	Ergosterol Biosynthesis	Yes	TypeI: Ψ-K-X-E Position 311	Yes	No	NS
8 (10)	CA0585	orf19.5061	ADE5,7	86120	5.14	654	25	43%	15	Enzyme of adenine biosynthesis	No	TypeI: Ψ-K-X-E Position 107	Yes	No	O
9 (11)	CA4672	orf19.900	NSP1	74656	5.15	288	13	28%	11	Essential component of the nuclear pore complex	No	TypeII: Non-consensus position 421, 672, 715 (medium)	Yes	No	O
9 (11)	CA1911	orf19.2435	SSE1 (MSI3)	78818	5.2	48	5	11%	5	Protein of the HSP70 family	Yes	TypeI: Ψ-K-X-E Position 94, 393, 610, 630 and TypeII: Non-consensus position 681	Yes	No	O
30 (28)	CA3534	orf19.6367	SSB1	66580	5.25	561	15	35%	7	Putative HSP70 family heat shock protein	Yes	TypeI: Ψ-K-X-E Position 245	Yes	No	H
30 (28)	CA2480	orf19.3206	CCT7	61011	5.15	154	8	18%	8	cytosolic chaperonin Cct ring complex, required for the assembly of actin and tubulins	No	TypeI: Ψ-K-X-E Position 254 and 478	Yes	No	H
34 (8)	CA5920	orf19.6785	RPS12	15973	4.63	1140	10	62%	4	Putative ribosomal protein	No	TypeII: Non-consensus position 54	Yes	No	O
34 (8)	CA6058	orf19.7678	ATP16	17571	5.15	291	6	47%	2	subunit of the mitochondrial F1F0 ATP synthase	No	TypeII: Non-consensus position 115 (low)	Yes	No	O
34 (8)	CA2454	orf19.3504	RPL23A	13199	10.1	201	6	47%	6	Putative ribosomal protein	No	TypeI: Ψ-K-X-E Position 245	Yes	No	O
34 (8)	CA3045	orf19.2416.1	MLC1	15899	4.64	133	3	25%	3	Protein with microtubule-dependent localization to the Spitzenkorper	No	No sites predicted	Yes	No	O
Increased sumolylation in response to heat															
22 (3)	CA3730	orf19.4180	SEC72	23411	5.01	553	17	63%	9	Component of ER protein-translocation complex	ND (Not detected)	TypeI: Ψ-K-X-E Position 31 and 103	Yes	Heat	H
Increased sumolylation in response to H_2O_2															
6 (2)	CA0685	orf19.5591	ADO1	38345	5.04	294	13	58%	11	Adenosine kinase	No	TypeI: Ψ-K-X-E Position 19	No	H2O2	O
6 (2)	CA0622	orf19.3149	LSP1	35569	4.89	233	8	34%	8	Component of eisosomes, associated with endocytosis	No	TypeI: Ψ-K-X-E Position 63	No	H2O2	O
6 (2)	CA1024	orf19.3934	CAR1	34649	4.88	143	6	29%	4	Arginine degradation	No	TypeII: Non-consensus position 13, 56 and 178 (low)	No	H2O2	O
6 (2)	CA5773	orf19.5417	DOT5	29177	4.69	97	3	17%	3	Nuclear thiol peroxidase	No	TypeI: Ψ-K-X-E Position 208 and TypeII: Non-consensus position 204	No	H2O2	O
6 (2)	CA2582	orf19.4371	TAL1	35661	4.63	72	6	25%	6	Transaldolase	Yes	TypeI: Ψ-K-X-E Position 271	No	H2O2	O
7 (5)	CA0870	orf19.3590	IPP1	32336	5.15	1299	18	67%	10	Putative inorganic pyrophosphatase	Yes	TypeI: Ψ-K-X-E Position 58 and 233	No	H2O2	O
7 (5)	CA0784	orf19.3930	YUH2	33859	5.28	75	2	10%	2	Ubiquitin C-terminal hydrolase	No	TypeI: Ψ-K-X-E Position 261 and TypeII: Non-consensus position 311	No	H2O2	O
10 (12)	CA1239	orf19.717	HSP60	60374	5.22	2034	37	72%	21	Mitochondrial HS protein	Yes	TypeI: Ψ-K-X-E Position 324	No	H2O2	O
12 (14)	CA4139	orf19.4233	THR4	57723	5.18	1131	31	67%	17	Threonine synthase	No	TypeI: Ψ-K-X-E Position 505	No	H2O2	O
Increased sumolylation in response to heat and H_2O_2															

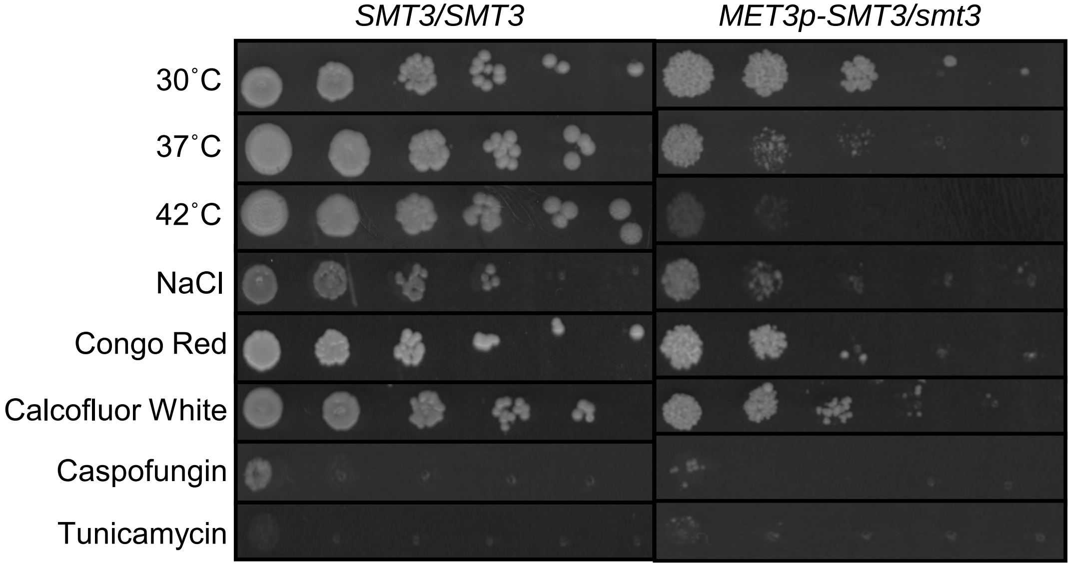
11 (13)	CA2474	orf19.2877	PDC11	62744	5.39	2129	32	71%	26	Pyruvate decarboxylase	Yes	TypeII: Non-consensus position 177, 271 and 275 (medium)	No	Heat and H2O2	O
11 (13)	CA4875	orf19.6561	LAT1	50145	5.73	267	7	20%	7	Component of pyruvate dehydrogenase complex	No	TypeI: Ψ-K-X-E Position 153 and TypeII: Non-consensus position 154	No	Heat and H2O2	O
33 (7)	CA4474	orf19.1896	SSC1	69876	5.48	2342	36	62%	16	Heat shock protein	Yes	TypeI: Ψ-K-X-E Position 269 and 294	No	Heat and H2O2	O
33 (7)	CA3534	orf19.6367	SSB1	66580	5.25	670	14	31%	10	Putative HSP70 family heat shock protein	Yes	TypeI: Ψ-K-X-E Position 245	No	Heat and H2O2	O
33 (7)	CA0838	orf19.1680	TFP1	63060	5.24	83	6	12%	4	Subunit of vacuolar H+-ATPase	No	TypeI: Ψ-K-X-E Position 117	No	Heat and H2O2	O
35 (9)	CA2239	orf19.3915	IPF10029	48029	5.05	484	14	44%	10	Putative Cys-Gly dipeptidase involved in GSH degradation	No	TypeI: Ψ-K-X-E Position 71 and 336	No	Heat and H2O2	O
35 (9)	CA4456	orf19.6854	ATP1	52881	8.49	200	11	27%	11	Protein similar to ATP synthase alpha subunit	No	TypeII: Non-consensus position 170, 419, 529 (medium)	No	Heat and H2O2	O
35 (9)	CA5546	orf19.7308	TUB1	50162	4.98	61	6	20%	6	Alpha-tubulin	Yes	TypeII: Non-consensus position 97, 305, 337, 340 (low)	No	Heat and H2O2	O
35 (9)	CA4331	orf19.4089	SGT1	47368	4.92	52	1	3%	1	Co-chaperone protein involved in kinetochore assembly	No	TypeI: Ψ-K-X-E Position 119 and 245	No	Heat and H2O2	O
23 (4)	CA5135	orf19.6389	HSP104	100171	5.42	929	41	50%	31	Functional homolog of *S. cerevisiae* Hsp104p	No	TypeI: Ψ-K-X-E Position 356	No	Heat and H2O2	H
23 (4)	CA0958	orf19.4732	SEC24	102683	5.26	554	21	29%	17	ER to Golgi transport	No	TypeI: Ψ-K-X-E Position 214	No	Heat and H2O2	H

Effects of stress upon *C. albicans MET3p-SMT3/smt3* in the absence of methionine and cysteine

NO Met/Cys control



PLUS Met/Cys (Figure 4B)



Oligonucleotides used in this study

Primer	Sequence (5’ to 3’)	Application
SMT3d-F	GCAAGATAGCATATTTGTTC	Diagnosis of *SMT3, ARG4* and *URA3* alleles
SMT3d2-F	GCACCAGGTTATCATAAGGA	Diagnosis of *SMT3* allele
SMT3d-R	CGCATAGTATCGGGAGATG	Diagnosis of *SMT3* and URA3-MET3-*SMT3* alleles
SMT3d2-R	GGCCGCAAATGAGATTTGGTAACA	Diagnosis of *SMT3, ARG4, URA3* and URA3-MET3-*SMT3* alleles
MET3p-F	ATTGCTGTGGATCACGTGC	Diagnosis of *URA3-MET3-SMT3* allele
LALd-R	GCCCATCTAATAGGTTGAGC	Diagnosis of *smt3::ARG4* allele
LULd-R	GTATGGGGTTGTTGCTCAGG	Diagnosis of *smt3::URA3* allele
MetUS-F	CGATTCTAATCAACAGAGGTTCCTGTTGTATCAGAAAGACATGAAAACAAGGTCGTGCAGCATACACAATTGTGGTGGTGGCGGCCGACTTGGCCAAGCCTAGATC	Amplification of *URA3-MET3-SMT3* cassette
MetUS-R	ATGTCCGACACTGAAAACACAGGAGGCTCACCACCAGCTGCTGAAGCAGGTCCAAAAGAAGAAAAAGGAACACATATAAATGTGGGGAGGGTATTTACTTTTAAATA	Amplification of *URA3-MET3-SMT3* cassette
LAL-F	GGTGGTGGTCTGAACCAACGCGACTGAAGAAACAAGAAATACGCCACCAGACAACAACAACAATTCTATTATTTTTTCCTGTTGTTCTTCATTACCCCAGGGTTTTCCCAGTCACG	Amplification of *smt3::ARG4* cassette
LAL-R	CCGTTCAACATTAAACAAAGACTACTATTCAACATAAACCAGCAATACCTTGCCTCTACAATCTTGAATTAAGAATACAATTACCTCCATTAAGTACACTAAAGGGAACAAAAGC	Amplification of *smt3::ARG4* cassette
LUL-F	GGTTATCATAAGGACATTTTATATTTCTAGCAAAGAATTACTTGAAACACTGTTGAAACATCAATGAAACGATCATTACTTTTCAGCCACTTAAACACATTCTACTACGCCAGGGTTTTCCCAGTCACG	Amplification of *smt3::URA3* cassette
LUL-R	GGTCCTATATAGACAACCTTTTTGGAGAGTATAGCATAATAGCATCGGTTTAGTGATTAATTTTGTAACCATTTGAATATTCTATGTAAATAATGTTACCAAATCTCACTAAAGGGAACAAAAGC	Amplification of *smt3::URA3* cassette
SMT3FL-F	AAGGTGGTTTAAGCTTAATGTCCGACACTGAAAACACAGGAGGCTCAC	Amplification of *SMT3 for* FLAG tagging
SMT3FL-R	AAATAGGGACGCTAGCTTATAAACAACCACCAATTTGTGCACGGTGAG	Amplification of *SMT3 for* FLAG tagging
SMT3S-F	CAGTCACAACTACATACTCG	Amplification of *SMT3* probe for Southern analysis
SMT3S-R	CGACTTTCGTGCTCAAGAG	Amplification of *SMT3* probe for Southern analysis
LALS-F	GGTAGATCAAGAAATGATC	Amplification of *ARG4* probe for Southern analysis
LALS-R	CAATCAGTAAAGTAGAAATC	Amplification of *ARG4* probe for Southern analysis
LULS-F	CCTATAGTGAGAGAGCAG	Amplification of *URA3* probe for Southern analysis
LULS-R	GGATCTCTTCCTTTACC	Amplification of *URA3* probe for Southern analysis

FLAG-F	AGCTACGGATCCACCATGGATTACAAAGATGATGATGATAAAGGTGGTGATTACAAAGATGATGATGATAAAGGTGGTGGTGATTACAAAGATGATGATGATAAAGGTGGTTTA	Cloning of FLAG tag
FLAG-R	AGCTTAAACCACCTTTATCATCATCATCTTTGTAATCACCACCACCTTTATCATCATCATCTTTGTAATCACCACCTTTATCATCATCATCTTTGTAATCCATGGTGGATCCGT	Cloning of FLAG tag
ACT1-F	ACCACCGGTATTGTTTTGGA	Real time RT-PCR of *ACT1* transcript levels
ACT1-R	AGCGTAAATTGGAACAACGTG	Real time RT-PCR of A*CT1* transcript levels
ACT1-P	ACCACCGGTATTGTTTTGGATTCTGGTGATGGTGTTACTCACGTTGTTCCAATTTACGCT	Probe for real time RT-PCR of *ACT1* transcript levels
SMT3q-F	CTCCCGATACTATGCGTTTCTT	Real time RT-PCR of *SMT3* transcript levels
SMT3q-R	CTGGTGTTTGATCAGCATGAA	Real time RT-PCR of *SMT3* transcript levels
SMT3q-P	CTCCCGATACTATGCGTTTCTTAGTTGATGGTGGAAGAGTTCATGCTGATCAAACACCAG	Probe for real time RT-PCR of SMT3 transcript levels
HSP104-F	CCCTTCCCTAAATCCTCAAGTC	Amplification of *HSP104*
HSP104-R	GGTTTATCCATTGAGCCAGAATC	Amplification of *HSP104*
HSP104-CTF	TATCGAATTCACGCGTCACTATTAGATCATGGAAGATTTTACAGATAACGCTATCAAG	Cloning of *HSP104*
HSP104-CTR	TCCAGGTACCGGATCCTTAGTCAAGTCCAGGTGAAGTGAATCTGGCTTCG	Cloning of *HSP104*
HSP104-LAL-F	CCACCCTTCCCTAAATCCTCAAGTCTTTTTCATTTCTCTTTTTTTCTTTTTTTTTTCAACTTCAATTCATTATTAATAACAATTATACACTATTAGATCCCAGGGTTTTCCCAGTCACG	Amplification of *hsp104::ARG4* cassette
HSP104-LAL-R	GCATCTAGTTCCTTTACGCTTTTTTCTAATTATTAACAGAATGATGGTTTATCCATTGAGCCAGAATCTTATATATACACAAAACAAGTTCC ACTAAAGGGAACAAAAGC	Amplification of *hsp104::ARG4* cassette
HSP104-WT-F	GTTCATTTCCAAAGATGGTGCATTTGAAAGAAGATTCCAAAAAATCGATGTTCCTGCCGCCACCGTGCAAGAAACTGTGCCATTTTTAAGAGGTATCCAGCCT**AAA**TATGAAATTCACCATGGGGTCCG	Amplification of CIp20-*HSP104* (HIS1)
HSP104-SDM-K356R-F	GTTCATTTCCAAAGATGGTGCATTTGAAAGAAGATTCCAAAAAATCGATGTTCCTGCCGCCACCGTGCAAGAAACTGTGCCATTTTTAAGAGGTATCCAGCCT**CGA**TATGAAATTCACCATGGGGTCCG	Amplification of CIp20-*HSP104* changing K356R (HIS1)
HSP104-SDM-R	GCCTAGCTAGCTCAATCGGCTTAGAGCGTGAGACTTTTAATCTCAAGGTTGCGGGTTCGAGTCCCGCGTTGGGCTTATATTTTTGCATCTAGTTCCTTTACGCACTAGTGATTGGTCTGGTGCTAGC	Amplification of CIp20-*HSP104* (HIS1)
HSP104d-F	GGAACCAACTAGAGTGACTC	Diagnosis of *HSP104* alleles
HSP104-WTd-F	CATTTTTAAGAGGTATCCAGCCTAA	Diagnosis of CIp20-HSP104 (HIS1) allele
HSP104-SDMd-F	CATTTTTAAGAGGTATCCAGCCTCG	Diagnosis of CIp20-HSP104 K356R (HIS1) allele
HSP104d-R	GTAGTTACACAAGACATATTCC	Diagnosis of CIp20-HSP104 [K356R] (HIS1) allele
HSP60-F	CACCAACACTTTAGTAGCATTAG	Amplification of *HSP60*

HSP60-R	CTTTAGTAAACTTCTCACAGTGG	Amplification of *HSP60*
HSP60-CTF	CGGTATCGATAAGCTTTAGCATTAGAATATCATGTTGAGAGTTAATTCTAAATCATC	Cloning of *HSP60*
HSP60-CTR	GTTCACCACCACGCGTGAACATACCTGGCATACCTCCCATACCTGG	Cloning of *HSP60*
HSP60-LAL-F	GGGTGGGTCTCTCTCACTGTTGTGTAATTCGTACCAACAATTCCGGAACCAAGTTTCTCTCACCAAATAAATACCCTCTTTTGTTCCTCCCTCCACCCAGGGTTTTCCCAGTCACG	Amplification of *hsp60::ARG4* cassette
HSP60-LAL-R	CACAAACAATAACACCAACACCAACACCAACGTATAAATACAGCAATGCTTTAGTAAACTTCTCACAGTGGAATTAGACTAGGCAACCTCAGC ACTAAAGGGAACAAAAGC	Amplification of *hsp60::ARG4* cassette
HSP60-WT-F	GTGCTGTTAAAGCTCCAGGTTTTGGTGACAATAGAAAAAACACTTTGGGTGATATTGCCATTTTAAGTGGTGGTACTGTATTCACTGAAGAATTGGATATT**AAA**CCAGAAAATGCCACTATTGAAC	Amplification of CIp20-*HSP60* (HIS1)
HSP60-SDM-K324R-F	GTGCTGTTAAAGCTCCAGGTTTTGGTGACAATAGAAAAAACACTTTGGGTGATATTGCCATTTTAAGTGGTGGTACTGTATTCACTGAAGAATTGGATATT**CGA**CCAGAAAATGCCACTATTGAAC	Amplification of CIp20-*HSP60* changing K324R (HIS1)
HSP60-SDM-R	CACAAACAATAACACCAACACCAACACCAACGTATAAATACAGCAATGCTTTAGTAAACTTCTCACAGTGGAATTAGACTAGGCAACCTCAGCACTAGTGATTGGTCTGGTGCTAGC	Amplification of CIp20-*HSP60* (HIS1)
HSP60d-F	CAAATATGTATGTGAGAGAGAGACGG	Diagnosis of *HSP60* alleles
HSP60-WTd-F	GTATTCACTGAAGAATTGGATATTAA	Diagnosis of CIp20-HSP60 (HIS1) allele
HSP60-SDMd-F	TCACTGAAGAATTGGATATTCG	Diagnosis of CIp20-HSP60 K324R (HIS1) allele
HSP60d-R	GTAGTTACACAAGACATATTCC	Diagnosis of CIp20-HSP60 [K324R] (HIS1) allele

Confirmation of genomic SDM of sumoylation sites by PCR