

Table S4. *D. hansenii* proteins with major change in hydropathy value (Hydropathy values that varies ≥ 0.03 for Kyte & Doolittle and ≥ 0.3 for the two Eisenberg scales) tracked with AmiGO by Gene Ontology.

Protein	Variation value [32]	Variation value [33]	Variation value [34]	Associated gene	Homology (NCBI)	Function (AmiGO)
XP_456392.1	1	0.16	0.25	DEHA2A01232g	Similar to uniprot Q12287 <i>S. cerevisiae</i>	<ul style="list-style-type: none"> - Mitochondrial intermembrane space - Copper chaperone activity - Copper ion binding - Copper ion transport
XP_457499.1	0.4	0.07	0.11	DEHA2B12518g	Highly similar to uniprot P33331 <i>S. cerevisiae</i> YER009W NTF2 Nuclear envelope protein	<ul style="list-style-type: none"> - Intracellular anatomical structure - Transport
XP_458669.1	0.4	0.08	0.12	DEHA2D04664g	Similar to uniprot P40422 <i>S. cerevisiae</i>	<ul style="list-style-type: none"> - DNA-templated transcription - DNA binding - DNA-directed 5'-3' - RNA polymerase activity
XP_459366.1	0.4	0.06	0.11	DEHA2E00858g	Similar to gn1 GLV CAGL0K0 5841g <i>C. glabrata</i>	<ul style="list-style-type: none"> - DNA-binding transcription factor activity - RNA polymerase II-specific regulation of DNA-templated transcription - Nucleus - Zinc ion binding
XP_457269.1	0.5	0.09	0.14	DEHA2B07150g	Highly similar to CA2973 IPF14452.re peat1 <i>Candida</i>	<ul style="list-style-type: none"> - Proton-transporting ATPase activity, rotational mechanism - Proton-transporting ATP synthase activity, rotational mechanism - Proton motive force-driven ATP synthesis - Mitochondrial proton-transporting ATP synthase complex, catalytic sector F(1)
XP_459047.1	0.9	0.15	0.24	DEHA2D13178g	Similar to CA0138 CaINH1 <i>C. albicans</i> INH1	<ul style="list-style-type: none"> - Mitochondrion - Negative regulation of ATP-dependent activity - Negative regulation of nucleotide metabolic process - Enzyme inhibitor activity - ATPase inhibitor activity
XP_458059.2	0.3	0.05	0.07	DEHA2C08756g	Weakly similar to uniprot Q12223 <i>S. cerevisiae</i> YDL059C RAD59 Protein involved in the repair of double-	<ul style="list-style-type: none"> - Double-strand break repair via single-strand annealing - DNA repair - DNA recombination

					strand breaks in DNA during vegetative growth via recombination and single-strand annealing	
XP_458647.2	0.3	0.04	0.06	DEHA2D04136g	Similar to CA3804 CaRIM1 C. <i>albicans</i>	- Mitochondrial nucleoid - Single-stranded telomeric DNA binding - Single-stranded DNA binding - Mitochondrion - Single-stranded DNA binding
XP_456489.2	0.4	0.07	0.1	Putative mitochondrial 54S ribosomal protein RTC6	Similar to uniprot O14464 <i>S. cerevisiae</i>	No homology found
XP_457892.2	0.6	0.11	0.17	DEHA2C04730g	Weakly similar to CA2523 IPF4319 C. <i>albicans</i>	No homology found
XP_456721.1	0.3	0.05	0.08	DEHA2A08998g	Highly similar to uniprot Q02772 <i>S. cerevisiae</i> YJR034W PET191	No homology found
XP_457026.2	0.3	0.04	0.06	DEHA2B01364g	Similar to uniprot P42949 <i>S. cerevisiae</i> YJL104w PAM1	No homology found
XP_457333.2	0.3	0.04	0.07	DEHA2B08668g	Similar to CA4994 IPF2033 C. <i>albicans</i> IPF2033	No homology found
XP_458005.2	0.3	0.05	0.07	DEHA2C07436g	Some similarities with CA2824 IPF17888 C. <i>albicans</i>	No homology found
XP_458063.1	0.3	0.05	0.08	Mitochondrial 54S ribosomal protein IMG2	Weakly similar to uniprot P25642 <i>S. cerevisiae</i> YCR071C IMG2 Mitochondrial ribosomal protein of the small subunit	No homology found
XP_458072.1	0.3	0.06	0.1	DEHA2C09086g	Highly similar to uniprot Q6Q546 <i>S. cerevisiae</i> YNR032C-A HUB1 Ubiquitin-like protein modifier	No homology found

XP_458091.1	0.3	0.05	0.08	DEHA2C09438g	Similar to uniprot P53869 <i>S. cerevisiae</i> YNL211c	No homology found
XP_458277.2	0.3	0.04	0.05	DEHA2C13772g	Highly similar to uniprot O74700 <i>S. cerevisiae</i> YEL020W-A TIM9 Mitochondrial intermembrane space protein	No homology found
XP_458377.1	0.3	0.05	0.08	DEHA2C15884g	Similar to uniprot Q5KNV4 <i>Cryptococcus neoformans</i> var CNA05180 and gnl GLV YALI0C21789g <i>Yarrowia lipolytica</i>	No homology found
XP_458610.2	0.3	0.05	0.08	DEHA2D03278g	Weakly similar to uniprot Q08963 <i>S. cerevisiae</i> YPL213w LEA1 U2 A snRNP protein	No homology found
XP_459101.1	0.3	0.05	0.08	DEHA2D14322g	Similar to uniprot Q02771 <i>S. cerevisiae</i> YER058W PET117 Protein required for assembly of cytochrome c oxidase	No homology found
XP_459104.1	0.3	0.05	0.08	60S ribosomal protein L34	Highly similar to uniprot P40525 <i>S. cerevisiae</i> YIL052C RPL34B Protein component of the large (60S) ribosomal subunit nearly identical to Rpl34Ap and has similarity to rat L34 ribosomal protein	No homology found
XP_459358.1	0.5	0.08	0.12	DEHA2E00682g	No homology found	No homology found
XP_457675.2	0.4	0.07	0.1	DEHA2B16632g	No homology found	No homology found
XP_459093.2	0.6	0.11	0.17	DEHA2D14146g	No homology found	No homology found
XP_459116.2	0.6	0.11	0.17	DEHA2D14630g	No homology found	No homology found
XP_458415.1	0.4	0.07	0.11	DEHA2C16720g	No homology found	No homology found

XP_457158.1	0.7	0.12	0.19	DEHA2B04510g	No homology found	No homology found
XP_457278.1	0.7	0.12	0.18	DEHA2B07348g	No homology found	No homology found
XP_456695.1	0.3	0.04	0.07	DEHA2A08426g	No homology found	No homology found
XP_458496.1	0.4	0.07	0.12	DEHA2D00638g	No homology found	No homology found
XP_458602.1	0.4	0.08	0.12	DEHA2D03102g	No homology found	No homology found
XP_457547.1	1.0	0.18	0.28	DEHA2B13816g	No homology found	No homology found
XP_457581.2	0.3	0.04	0.07	DEHA2B14586g	No homology found	No homology found
XP_457070.2	0.4	0.06	0.1	DEHA2B02354g	No homology found	No homology found
XP_459460.1	0.4	0.07	0.1	DEHA2E03036g	No homology found	No homology found
XP_457089.1	0.5	0.09	0.14	DEHA2B02860g	No homology found	No homology found
XP_457615.2	0.4	0.06	0.1	DEHA2B15312g	No homology found	No homology found
XP_459330.1	0.5	0.07	0.12	DEHA2D19360g	No homology found	No homology found
XP_458622.1	0.3	0.05	0.08	DEHA2D03542g	No homology found	No homology found
XP_462639.2	0.3	0.04	0.06	DEHA2G25080g	No homology found	No homology found