YPLAL Put1 L P T G F L L V P K L S A E T E L Put5 L P A G L L L I P V L S A D S D P P G D G S S S L R I A S T F Q L L R T W L V Y S L I S F P G V V D Y S P K I L S I L N N S P L R L P T E W F V R A I P V P T S L T A S T T P E L L R T W F V Y A I I S M P G V V D Y S P T I L N F F I N S P L R G P T E W F V R SAEVDE SQLQGDN THGKEARREREREHR SAEVDE SOLTETGPS-KDERDKREREKK Put1 F V P G E T V E D C I P S L K A Put5 F V A G E T V E G C M P T L K A G D P R E L F A L K G K W Puti A T G F A L K V T G I V D P N V L E R A S Y T L L R L R S L A Q S S S I S I S A P N A P L F V P Y P G T P E S L D C Q V L A R T --Put5 V T G F A L K I I T G L I D A N V L E R A S Y T L L R L R P L A K S N S P T A P N T P L F V P Y P G T P E T L D Q Q V V A R T P E D L E V L S D L W Y K L R K I G E K A K E N D V A L I I D A E Y T W Y Q P A L N L E L B Q L W Y K L Q K I G Q K A K E N N I I L Y V D A E H T W Y Q P A L Put1 DDMGVLENDPGL Put5 DDMGVLEKDPGL S E K W N G P L E E I W T G P L Put1 IYGTYQSYLCRQPTHI Put5 IYGTYQSYLCRQPTHI G L K L V R G A Y Y L Q E R K K W G V K L V R G A Y F E O E R K K W TTL DEGRLG Put1 SDQLKSSHPERA Put5 ASQLKSAHPERA NAARFVND MASKFVND 640

Figure S2 ClustalW multiple sequence alignment of *C. neoformans* Put1 and Put5. Identical amino acid residues are shaded dark grey while similar residues are shaded light grey.