

TG199	MAT $\alpha$ <i>rpt1::rpt1-R173C(TRP1)</i>	S4
TG203	MAT $\alpha$ <i>rpt2::rpt2-E111C(HYG)</i>	S4
TG211	MAT $\alpha$ <i>rpt4::rpt4-R145C(NAT)</i>	S4
TG215	MAT $\alpha$ <i>rpt5::rpt5-E84C(KAN)</i>	S4
TG223	MAT $\alpha$ <i>rpt1::rpt1-R173C(TRP1) rpt2::rpt2-E111C(HYG)</i>	S4
TG247	MAT $\alpha$ <i>rpt4::rpt4-R145C(NAT) rpt5::rpt5-E84C(KAN)</i>	S4
Part B: Strains used for spotting assay and native PAGE of total cell lysate**		
Sub61	MAT $\alpha$	S2,S4
TG577	MAT $\alpha$ <i>scl1::scl1-I87C-6HA (HYG)</i>	S2
TG579	MAT $\alpha$ <i>pre8::pre8-G79C-6HA (HYG)</i>	S2
TG581	MAT $\alpha$ <i>pre9::pre9-T81C-6HA (HYG)</i>	S2
TG646	MAT $\alpha$ <i>pre6::pre6-C32A C46A N79C-6HA (HYG)</i>	S2
TG585	MAT $\alpha$ <i>pup2::pup2-T82C-6HA (HYG)</i>	S2
TG587	MAT $\alpha$ <i>pre5::pre5-A78C-6HA (HYG)</i>	S2
TG589	MAT $\alpha$ <i>pre10::pre10-I82C-6HA (HYG)</i>	S2
SP47	MAT $\alpha$ <i>rpt1::rpt1-N467C (KAN)</i>	S2
TG641	MAT $\alpha$ <i>rpt2::rpt2-L437C (KAN)</i>	S2
TG643	MAT $\alpha$ <i>rpt3::rpt3-K428C (KAN)</i>	S2
SP304	MAT $\alpha$ <i>rpt4::rpt4-L437C (NAT)</i>	S2
SP309	MAT $\alpha$ <i>rpt5::rpt5-A434C (NAT)</i>	S2
SP311	MAT $\alpha$ <i>rpt6::rpt6-K405C (NAT)</i>	S2
TG530	MAT $\alpha$ <i>rpt1::rpt1-N467C (KAN) pup2::pup2-T82C-6HA (HYG)</i>	S2
TG681	MAT $\alpha$ <i>rpt2::rpt2-L437C (KAN) pre6::pre6- C32A C46A N79C-6HA (HYG)</i>	S2
TG629	MAT $\alpha$ <i>rpt3::rpt3-K428C (KAN) pre8::pre8-G79C-6HA (HYG)</i>	S2
TG536	MAT $\alpha$ <i>rpt4::rpt4-L437C (NAT) scl1::scl1-I87C-6HA (HYG)</i>	S2
TG562	MAT $\alpha$ <i>rpt5::rpt5-A434C (NAT) pre10::pre10-I82C-6HA (HYG)</i>	S2
TG568	MAT $\alpha$ <i>rpt6::rpt6-K405C (NAT) pre9::pre9-T81C-6HA (HYG)</i>	S2

\*All strains listed in part A have a background genotype of sDL66 (ref. 8): *lys2-801 leu2-3, 2-112 ura3-52 his3- $\Delta$ 200 trp1-1 rpn11::RPN11-TEVProA(HIS3)*. All Rpt salt-bridge and  $\alpha$  subunit mutants were initially constructed in strain sDL66. Rpt C-terminal Cys mutants were made by transformation of strain DF5 (ref. 9) and subsequent dissection of the diploids. Double mutants were constructed by mating and tetrad analysis. Note  $\alpha$ 1 is encoded by *SCL1*,  $\alpha$ 2 by *PRE8*,  $\alpha$ 3 by *PRE9*,  $\alpha$ 4 by *PRE6*,  $\alpha$ 5 by *PUP2*,  $\alpha$ 6 by *PRE5*, and  $\alpha$ 7 by *PRE10*.

\*\*All strains listed in part B have a background genotype of SUB61 (ref. 9): *lys2-801 leu2-3, 2-112 ura3-52 his3- $\Delta$ 200 trp1-1*.