

Table S1 Strains used in this study

Strain	Genotype	Source
BWP17	<i>ura3::imm434/ura3::imm434 IRO1/iro1::imm434 his1::hisG/ his1::hisG arg4::hisG/arg4::hisG</i>	Wilson <i>et al.</i> , 1993
SN152	<i>URA3/ura3::imm434 IRO1/iro1::imm434 his1Δ/his1Δ leu2Δ/leu2Δ arg4Δ/arg4Δ</i>	Noble and Johnson, 2005
<i>chs8Δ/Δ</i>	<i>ura3Δ/ura3Δ IRO1/iro1::imm434 his1Δ/his1Δ arg4Δ/arg4Δ chs8::C.d.HIS1/chs8::C.d.ARG4</i>	Beckwith <i>et al.</i> , 2022
<i>alg11Δ/Δ</i>	<i>URA3/ura3::imm434 IRO1/iro1::imm434 his1Δ/his1Δ leu2Δ/leu2Δ arg4Δ/arg4Δ alg11::C.d.HIS1/alg11::C.m.LEU2</i>	Mitchell <i>et al.</i> , 2015
<i>alg11Δ/Δ</i> , +	<i>URA3/ura3::imm434 IRO1/iro1::imm434 his1Δ/his1Δ leu2::ALG11-C.d. ARG4/leu2Δ arg4Δ/arg4Δ alg11::C.d.HIS1/alg11::C.m.LEU2</i>	Mitchell <i>et al.</i> , 2015
<i>fks1Δ/FKS1</i>	<i>ura3::imm434/ura3::imm434 IRO1/iro1::imm434 his1Δ/his1Δ arg4Δ/arg4Δ fks1::C.d.HIS1/FKS1</i>	This study
<i>kre5Δ/Δ</i>	<i>ura3::imm434/ura3::imm434 IRO1/iro1::imm434 his1Δ/his1Δ arg4Δ/arg4Δ kre5::C.d.HIS1/kre5::C.d.ARG4</i>	Mitchell <i>et al.</i> , 2015
<i>mnn9Δ/Δ</i>	<i>ura3::imm434/ura3::imm434 his1::hisG/ his1::hisG arg4::hisG/arg4::hisG mnn9::ARG4/mnn9::URA3</i>	Rauceo <i>et al.</i> , 2008
<i>mnn22Δ/Δ</i>	<i>URA3/ura3::imm434 IRO1/iro1::imm434 his1Δ/his1Δ leu2Δ/leu2Δ arg4Δ/arg4Δ mnn22::C.d.HIS1/mnn22::C.m.LEU2</i>	Noble <i>et al.</i> , 2010
<i>phr1Δ/Δ</i>	<i>ura3::imm434/ura3::imm434 IRO1/iro1::imm434 his1Δ/his1Δ arg4Δ/arg4Δ phr1::C.d.HIS1/phr1::C.d.ARG4</i>	Mitchell <i>et al.</i> , 2015
<i>pmr1Δ/Δ</i>	<i>ura3::imm434/ura3::imm434 IRO1/iro1::imm434 his1Δ/his1Δ arg4Δ/arg4Δ pmr1::C.d.HIS1/pmr1::C.d.ARG4</i>	This study
<i>pmr1Δ/Δ</i> , +	<i>ura3::imm434/ura3::imm434 IRO1/iro1::imm434 his1Δ/his1Δ arg4Δ/arg4Δ pmr1::C.d.HIS1/pmr1::C.d.ARG4, PMR1-SAT1</i>	This study

van1Δ/Δ *URA3/ura3::imm434 IRO1/iro1::imm434 his1Δ/his1Δ* Noble *et al.*, 2010
leu2Δ/leu2Δ arg4Δ/arg4Δ van1::C.d.HIS1/van1::C.m.LEU2

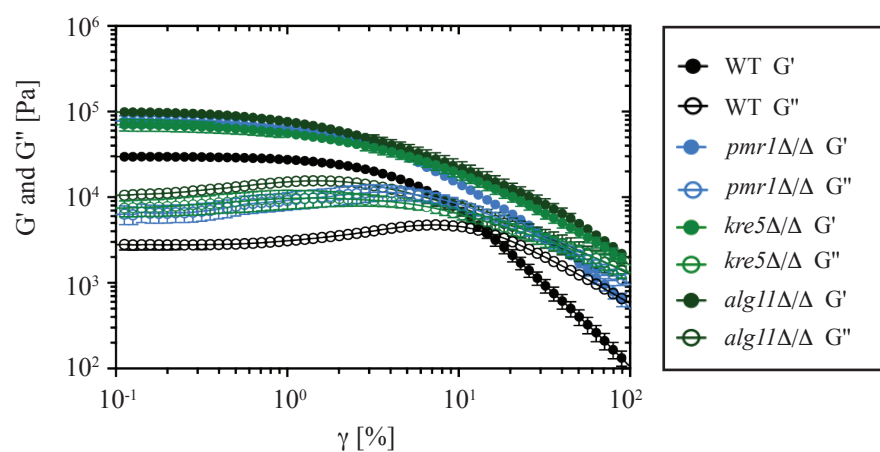


Figure S1. Strain amplitude sweeps of biofilms for the indicated strains at $\omega = 1$ rad/s. The graph legend is shown to the right. Error bars indicate standard error of the mean.

A <i>alg11Δ/Δ</i> Gene sets with altered RNA transcript levels relative to WT:			
GO Biological Process Term (ID):	<i>p</i> -Value:	Genes:	
Cellular amino acid metabolic process (1901605)	1.70 x 10 ⁻²	↓ : <i>ALA1, GLN1, HIS3, HIS4, HOM2, ILS1, ILV5, LEU4, MET13, NAM2, tG(UCC)3mt, C2_10460C_A, C6_00390W_A, CR03110W_A</i>	↑ : <i>FRS2, GLN1</i>
[α-amino acid metabolic process (1901605)]	1.70 x 10 ⁻²		
[Cellular amino acid biosynthetic process (0008652)]	2.77 x 10 ⁻²		
Metal ion transport (0030001)	2.14 x 10 ⁻²	↓ : <i>ATM1, CCS1, HGT12, HNM3, MDL2, MDR1, NAG3, NHX1, TNA1, TOM40, C1_09220W_A, C3_07850W_A, C6_01520W_A, C6_01870C_A, C6_03540W_A</i>	↑ : <i>AGP2, ALR1, CRP1, CTR2, DAL7, FLU1, GAP5, GIT3, GIT4, HAK1, HGT9, HGT19, HNM4, HXT5, ITR1, MID1, NGT1, OPT4, OPT5, PHO87, PSD1, SSU1, TPO4, ZRT3, C5_03080C_A, CR_09390C_A</i>
[Transmembrane transport (0055085)]	3.49 x 10 ⁻²		
Lipid catabolic process (0016042)	2.77 x 10 ⁻²	↓ : <i>LIP4, PLB2</i>	↑ : <i>LIP2, LIP3, PLB1, PLB4.5</i>
B			
KEGG Term (ID):	<i>p</i> -Value:	Genes:	
Ubiquinone and other terpenoid-quinone biosynthesis (cal00130)	8.34 x 10 ⁻⁴	↓ : <i>COQ3, COQ5</i>	↑ : <i>PST1, PST2, PST3, YCP4</i>
Proteasome (cal03050)	1.04 x 10 ⁻³	↓ : <i>BLM3, PR26, RPN1, RPN2, RPN6, RPN7, RPN9, RPN10, RPN11, RPT6, SEM1</i>	
Porphyrin metabolism (cal00860)	6.97 x 10 ⁻³	↓ : <i>COX15, CYT2, HEM15, C2_10860C, CR_03110W_A</i>	↑ : <i>HEM3</i>
Valine, leucine, and isoleucine biosynthesis (cal00290)	9.17 x 10 ⁻³	↓ : <i>ILV2, ILV5, ILV6, LEU4</i>	↑ : <i>CHAI</i>
Longevity-regulating pathway biosynthesis (cal04213)	1.52 x 10 ⁻²	↓ : <i>SNF4</i>	↑ : <i>GPR1, HSP70, HSP104, MSN4, SOD1, SSA2, TPK2</i>

Fig. S2 GO and KEGG term enrichment in the set of genes differentially expressed in *alg11Δ/Δ* relative to wild type. a) GO Biological Process terms enriched in the gene set are indicated along with respective GO IDs in parentheses. Unadjusted *p*-values are shown; adjusted and unadjusted values are presented in Files S6 and S7. Genes within the set of transcripts differentially abundant in *alg11Δ/Δ* belonging to the respective GO Biological Process terms are listed, with up and down arrows indicating whether transcript abundance is increased or decreased in *alg11Δ/Δ* relative to wild type. Highly related GO terms are bracketed. b) Enriched KEGG terms are shown as above, with KEGG IDs indicated in parentheses.

Figure S2

A kre5Δ/Δ Gene sets with altered RNA transcript levels relative to WT:			
GO Biological Process Term (ID):	p-Value:	Genes:	
Proteolysis (0006508)	5.47 x 10 ⁻⁴	↓ : <i>AFG3, CYM1, DAP2, DOA4, GPI8, OCT1, PIM1, PRE2, PRE3, PRE5, PRE6, PRE8, PRE9, PRE10, PUP3, RAD23, SCL1, UBP6, C1_06390W_A, C2_02020W_A, C2_00700W_A, C6_00170C_A, C6_02300C_A, CR_05980W_A,</i>	↑ : <i>LAP3, LAP4, OMA1, PRC2, PRC3, RIM13, C1_10820C_A, CR_00660W_A,</i>
Protein catabolic process (0030163)	1.95 x 10 ⁻²	↓ : <i>PRE2, PRE3, PRE5, PRE6, PRE8, PRE9, PRE10, PUP3, RAD23, SCL1, C1_06390W_A, C6_02300C_A,</i>	
Organonitrogen compound catabolic process (1901565)	2.43 x 10 ⁻²		
Amino acid activation (0043038)	2.53 x 10 ⁻²	↓ : <i>ALA1, CDC60, FRS1, GUS1, ILS1, KRS1, MES1, MSM1, MST1, NAM2, THS1, C1_01530C_A, CR_03110W_A, CR_03400W_A,</i>	
tRNA aminoacylation (0043039)	2.53 x 10 ⁻²		
Organelle localization (0051640)	1.88 x 10 ⁻²		↑ : <i>RCY1, SEC1, SEC10, SEC15, C1_02960C_A, C4_06810C_A</i>
Exocytosis (0006887)	3.27 x 10 ⁻²		↑ : <i>RCY1, SEC1, SEC3, SEC10, SEC15, C4_06810C_A</i>
Secretion by cell (0032940)	3.27 x 10 ⁻²		
Secretion (0046903)	3.27 x 10 ⁻²		
Membrane lipid metabolic process (0006643)	3.27 x 10 ⁻²	↓ : <i>C6_01370W_A</i>	↑ : <i>GPI14, GWT1, SPT14, YDC1, C4_03130W_A, C4_10820C_A, CR_00660W_A,</i>
B			
KEGG Term (ID):	p-Value:	Genes:	
Butanoate metabolism (cal00650)	4.89 x 10 ⁻³	↓ : <i>ERG13, IFE2, UGA1, C3_00640W_A, C3_03470W_A,</i>	↑ : <i>IFE1, UGA11, C2_07240C_A,</i>
Purine metabolism (cal00230)	1.32 x 10 ⁻²	↓ : <i>AAH1, ADE2, ADE4, ADE5, ADE6, ADE13, ADK1, ADO1, APA2, APT1, GUA1, RNR1, RNR21, YNK1</i>	↑ : <i>CYR1, DAL1, C4_01820C_A, C4_04270W_A, C4_06230C_A</i>
Val, Leu, and Ile degradation (cal00280)	1.37 x 10 ⁻²	↓ : <i>ERG13, LPD1, UGA1</i>	↑ : <i>ALD6, HPT1, UGA11, C1_00410C_A, C7_02010C_A, CR_08920W_A</i>
Glyoxylate and dicarboxylate metabolism (cal00630)	2.40 x 10 ⁻²	↓ : <i>GCV2, LPD1, SHM2</i>	↑ : <i>CAT1, FDH1, GOR1, MDH1-1, C2_10070W_A, C3_02060W_A, C5_03770C_A, CR_09500C_A</i>
Inositol phosphate metabolism (cal00562)	3.89 x 10 ⁻²	↓ : <i>INO1, TPI1, C1_05980W_A</i>	↑ : <i>ALD6, FAB1, FGR22, INP51, STT4, VPS34</i>

Fig. S3 GO and KEGG term enrichment in the set of genes differentially expressed in *kre5Δ/Δ* relative to wild type. a) Enriched GO Biological Process terms and b) KEGG terms are shown with respective IDs in parantheses. The *p*-values indicating the significance of enrichment for each term are listed, along with the mapped genes. Highly related GO terms are bracketed, and the set of genes for the grouped GO Biological Process terms is shown. Full datasets are provided in Files S8 and S9.