

**Table S1. Primers used in this study.** Introduced overhangs required for yeast recombinational cloning are underlined.

Gene/ Construct	Primer	Sequence 5' → 3'
<b><i>F. verticillioides</i> deletion mutants</b>		
<b>FUM17</b>	fum17_5F	<u>GTAATACGACTCACTATAGGGAATATTGAGT</u> GCAATGCTTGCAGTACC
	fum17_5R	TAGTGCCACGTTCTAAATTC <u>AA</u> CCAAGGGGACGGAAGTTCAGTCAGTG
	fum17_3F	AGCACTCGTCCGAGGGCAAAGGAATAGGTAAGTGGCGATGGAATCTTTG
	fum17_3R	GACATAACTAATTACATGATGCGGCCCGTTGATTTGGGCTAAATCGCC
	fum17_5diag	CGGGTGCTCGTTCCTGAAGT
	fum17_3diag	CACACAAGACATGGGCATTGGC
	fum17_F	CAGACCCGGCCAAGGAAACAG
	fum17_R	GCTCGAAAGGACCAACGGTACG
<b>FUM18</b>	fum18_5F	<u>GTAATACGACTCACTATAGGGAATATT</u> CAGACTGTACTCCACTGG
	fum18_5R	TAGTGCCACGTTCTAAATTC <u>AA</u> CCAAGAAAGATTAATAAACGTCAAG
	fum18_3F	AGCACTCGTCCGAGGGCAAAGGAATAGGATAGTGAGATATTAGAAAAC
	fum18_3R	GACATAACTAATTACATGATGCGGCCCGAAGAGGCTTCTGCGGCCTC
	fum17/18_3F	AGCACTCGTCCGAGGGCAAAGGAATAGAAAGATTAATAAACGTCAAG
	fum17/18_3R	GACATAACTAATTACATGATGCGGCCCGACTGTACTCCACTGG
	fum18_5diag	CTATATCCGAGGCGGAGCAGGC
	fum18_3diag	CGCCAATGCTCTATTTCTCGCC
	fum18_F	GGCTTCACGTTACTGGCTGGTG
	fum18_R	GATCCATGGCTCAATCAAGTGCC
<b>FUM19</b>	fum19_5F	<u>GTAATACGACTCACTATAGGGAATATT</u> CTTGATTAACCCATCAATGTC
	fum19_5R	TAGTGCCACGTTCTAAATTC <u>AA</u> CCAAGGGCTTTAGAGTCTGTATTATAA
	fum19_3F	AGCACTCGTCCGAGGGCAAAGGAATAGATAATATGTAGGATCGATCC
	fum19_3R	GACATAACTAATTACATGATGCGGCCCTAGAAATGCCCTTCGGCAC
	fum19_5diag	CGGCGAGCCTCAATGTTGACTG
	fum19_3diag	CCTGTGCTGTCTCGCGAGCC
	fum19_F	GGCGATCTTGCGCTTACCG
	fum19_R	GTCGACTGACCGCACCCATTG
<b>FUM21</b>	fum21_5F	<u>GTAATACGACTCACTATAGGGAATATT</u> GTTTCATATCGGGACATCCAG
	fum21_5R	AGTGCTCCTTCAATATCATCTTCTGTCCGAAAAGTTGATGATGAAA
	fum21_3F	CTCTACATGAGCATGCCCTGCCCTGAATAATAAACATATCTATCC
	fum21_3R	GACATAACTAATTACATGATGCGGCCCGTAGGCCACTTCCAAGAGC
	fum21_5diag	GGTACACGTGGAAGCTGCGC
	fum21_3diag	CCACGCCAGTTCGTTTGGC
	fum21_F	GACGGAGATACAGAGCGTGGACC
	fum21_R	CTCCAAGACTAGGGCTGTCCCG
<b>hphR</b>	hph_F	CTTGGTTGAATTTAGAACGTGG
	hph_R	CTATTCCTTTGCCCTCGGACGAG
	hph_5diag	CCACGTTCTAAATTC <u>AA</u> CCAAG
	hph_3diag	GCACTCGTCCGAGGGCAAAG
<b>natR</b>	nat1_F	GACAGAAGATGATATTGAAGGAGC
	nat1_R	TCAGGGGCAGGGCATGCTCA
	nat1_5diag	CTGGTGCGGTACCGTAAGCC
	nat1_3diag	CGGACGGCGAGCGGCAGGCGC
<b><i>F. verticillioides</i> complementation, point-mutation and overexpression strains</b>		
<b>FUM18<sup>c</sup></b>	fum18_compl_R	<u>CACTTGT</u> TTAGAGGGCTCGTCGAAATCTACTCTTCATTGCAATGGATG
	fum18_compl_3F	AGTGCTCCTTCAATATCATCTTCTGTCCGATAGTGAGATATTAGAAAAC
	fum18_Seq1	CCAAATGCCTGAGATATCTGGGC
	fum18_Seq2	CATGAGAATCCAGCCCTGTTCCG

**Table S1 (continued)**

<b>FUM19<sup>C/mut</sup></b>	fum19_compl_R	<u>CACTTGTTTAGAGGGCTCGTCGAAATCTTAGACTCTTGACGCCTCC</u>
	fum19_compl_3F	<u>AGTGCTCCTTCAATATCATCTTCTGTCATAATATGTAGGATCGATCC</u>
	fum19_K631V_F	GTTGGATCAGGAGTGTGACGTTGTGC
	fum19_K631V_R	GCACAACGTCGACACTCTGATCCAAC
	fum19_K1260V_F	TATTCTAGTGGGGTATCTTCCATCATA
	fum19_K1260V_R	TATGATGGAAGATACCCCACTAGAATA
	fum19_D743K_F	CTCCTGATATTGAAAGATATTCTGAGT
	fum19_D743K_R	ACTCAGAATATCTTTCAATATCAGGAG
	fum19_D1397K_F	CTTCTCCTACTCAAAGAGCCTAGTTCT
	fum19_D1397K_R	AGAACTAGGCTCTTTGAGTAGGAGAAG
	fum19_Seq1	CTACCTTGCTCGATCATCTCGCC
	fum19_Seq2	CTCACGCCCTAACAGCAGCC
<b>OE::FUM19</b>	OE_fum19_F	<u>AACTCCATCACATACAATCGATCCAAATGATGAACTTTGAAGGCTG</u>
	OE_fum19_R	<u>CCTAATCATACTTATCTACATACGCGTCTTATGGAATATTGCGC</u>
	OE_fum19_diag	<u>CGATGCTGATCTGGCGTTGC</u>
<b>OE::FUM17::GFP</b>	OE_fum17_F	<u>TATCCCCGATCACAACCACATTACAATGTTCAAAGCCACGACCTC</u>
	fum17_GFP_R	<u>ATTACTTACCTCACCTTGGAAACCATGTCCCCATGCTCGATTCTG</u>
<b>OE::FUM18::DsRed</b>	OE_fum18_F	<u>AACTCCATCACATACAATCGATCCAAATGGCCACTACAGTTCAAAC</u>
	fum18_DsRed_R	<u>TTGATGACGTCCTCGGAGGAGGCCATCTTTCATTGCAATGGATGTTG</u>
<b>OE::CER1::BFP</b>	OE_cer1_F	<u>CTACCCCGCTTGAGCAGACATACAATGTCAGGCTCAGAACCCTTTC</u>
	cer1_BFP_R	<u>ACAGCTCCTCGCCCTTGCTCACCATGTTCTTTGCATCTTCAGGGATC</u>
	BFP_F	ATGGTGAGCAAGGGCGAGGAGCTG
	BFP_Tgluc_R	TAATCATACTTATCTACATACGCTACTTGTACAGCTCGTCCATGC
	BFP_Ttub_R	GCAAAGTAGGAATGACATCAGATATCTACTTGTACAGCTCGTCCATGC
<b>OE::DsRed::FUM8</b>	fum8_DsRed_F	<u>CGCCACCACCTGTTCTGGCGGCCGCTATGTCCACCCAGGAAATCAC</u>
	fum8_Ttub_R	<u>AAGCAAAGTAGGAATGACATCAGATATTCAACATGTCCCTCGCGATAA</u>
	fum8_Seq_F	GAGGAACTGGCCACATACTTGGG
	fum8_Seq_R	GGTTGGCGCATGCACTGAGC
<b>OE::FUM3::GFP</b>	OE_fum3_F	<u>AACTCCATCACATACAATCGATCCAAATGAACAAGGAAAAGTTCCC</u>
	fum3_GFP_R	<u>ATTACTTACCTCACCTTGGAAACCATATCATCTAACCCAAGATGTAAAG</u>
<b>natR</b>	nat1_TtrpC_R	GATTCGACGAGCCCTCTAAAC
<b>PoliC</b>	PoliC_Seq_F2	GGGAGACGTATTTAGGTGCTAGGG
<b>PglN1</b>	PglN1_Seq_F	ATGTCGAAGTATCTTCCCTGTGC
<b>PgpdA</b>	PgpdA_F	<u>GCCCAAAAAATGCTCCTTCAATATCCTTGGTTGAATTTAGAACGTGG</u>
	PgpdA_R	TGTGATGTCTGCTCAAGCGGGG
	PgpdA_Seq_F	CCCATCCAAGAACCTTTATTTCCC
<b>Tgluc</b>	Tgluc_Seq_R2	CCGCCCTCTTTGTCTTCCGC
<b>Ttub</b>	Ttub_Seq_R2	GGGTATCGACGATGTGTAGTCG
<b>GFP</b>	GFP_Seq_R	CGTCTCCCTCACCTCTCCGC
<b>Ceramide synthase yeast complementation assay</b>		
<b>TET::LAG1</b>	his3_Prom_TET_F	<u>TTTCCGGTTTCATACACCGGGCAAAGAAACACAGTCCTTTCCCGCAA</u>
	his3_Term_R	AATATGAAATGCTTTTCTTG
	TET_F	TCTTTGCCCGGTGTATGAAACC
	TET_R	TGTGATGTGATGGAGTTGAGATGGA
	lag1_5F	<u>GTAATACGACTCACTATAGGGAATATCCTGTTGTTCTAGCCTCTTC</u>
	lag1_5R	<u>AGAACAACAAGAAAAGCATTTTCATATTGTTGTCGTTATTTCTTCAGTT</u>
	lag1_3F	<u>CTCAACTCCATCACATACAATGACATCAGCTACGGACAA</u>
	lag1_3R	<u>GACATAACTAATTACATGATGCGGCCCGATAGTTAATGTCTTAGAC</u>
	lag1_5diag	TCCTGTCTTAAGCGGGAACCAC
	lag1_diag_R	CCCACGGAAGAGTTTCGTCTTC
	lag1_3diag	ACGAACAAGCCGAACACAAAGG
<b>Ptef1::ScLAG1</b>	lag1_Tef1_F	<u>CAATCTAATCTAAGTTTTAATTACAAAATGACATCAGCTACGGACAA</u>
	lag1_Cyc1T_R	<u>GTGACATAACTAATTACATGATGTTTAAACTTATTCACACTTTCTTAG</u>

**Table S1 (continued)**

<i>Ptef1::ScLAC1</i>	lac1_Tef1_F	<u>CAATCTAATCTAAGTTTTAATTACAAAATGTCGACAATAAAGCCAAG</u>
	lac1_Cyc1T_R	<u>GTGACATAACTAATTACATGATGTTTAAACTCAAATATCCTTTTTCGTTG</u>
<i>Ptef1::FvCER1</i>	cer1_Tef1_F	<u>CAATCTAATCTAAGTTTTAATTACAAAATGTCAGGCTCAGAACCCTTTC</u>
	cer1_Cyc1T_R	<u>GTGACATAACTAATTACATGATGTTTAAACCTAGTCTTTGCATCTTCAG</u>
<i>Ptef1::FvCER2</i>	cer2_Tef1_F	<u>CAATCTAATCTAAGTTTTAATTACAAAATGGCAGCAAAACTACGCTC</u>
	cer2_Cyc1T_R	<u>GTGACATAACTAATTACATGATGTTTAAACTTATCGTGATATCCTCTGTT</u>
<i>Ptef1::FvCER3</i>	cer3_Tef1_F	<u>CAATCTAATCTAAGTTTTAATTACAAAATGAGCGACCATCCAGTCATG</u>
	cer3_Cyc1T_R	<u>GTGACATAACTAATTACATGATGTTTAAACCTAGTCGACCTGCTTCTCGC</u>
<i>Ptef1::FUM17</i>	fum17_Tef1_F	<u>CAATCTAATCTAAGTTTTAATTACAAAATGTTCAAAGCCACGACCTC</u>
	fum17_Cyc1T_R	<u>GTGACATAACTAATTACATGATGTTTAAACTTAGTCCCATGCTCGATT</u>
<i>Ptef1::FUM18</i>	fum18_Tef1_F	<u>CAATCTAATCTAAGTTTTAATTACAAAATGGCCACTACAGTTCAAAC</u>
	fum18_Cyc1T_R	<u>GTGACATAACTAATTACATGATGTTTAAACTCACTCTTCATTGCAATGGA</u>
<i>Ptef1::FUM17::FUM18/FvCER3</i>	fum17_2A_R	<u>GAAGTTGGTGGCGCCAGAGCCGTCCCATGCTCGATTCTG</u>
	fum18_2A_F	<u>GACGTTGAAGAAAACCTGGCCCTATGGCCACTACAGTTCAAAC</u>
	cer3_2A_F	<u>GACGTTGAAGAAAACCTGGCCCTATGAGCGACCATCCAGTCATG</u>
<i>Ptef1::HsCERS2</i>	HsCERS2_Tef1_F	<u>CAATCTAATCTAAGTTTTAATTACAAAATGCTCCAGACCTTGTATGA</u>
	HsCERS2_Cyc1T_R	<u>TAAGCGTGACATAACTAATTACATGATTCAGTCATTCTTACGATGGT</u>
<i>Ptef1::HsCERS4</i>	HsCERS4_Tef1_F	<u>CAATCTAATCTAAGTTTTAATTACAAAATGCTGTCCAGTTTCAACGA</u>
	HsCERS4_Cyc1T_R	<u>TAAGCGTGACATAACTAATTACATGATCTATGTGGCTGTTGTGTGCC</u>
<i>Ptef1::HsCERS5</i>	HsCERS5_Tef1_F	<u>CAATCTAATCTAAGTTTTAATTACAAAATGGCGACAGCAGCGCAGGG</u>
	HsCERS5_Cyc1T_R	<u>TAAGCGTGACATAACTAATTACATGATTTACTCTTCAGCCCAGTAGC</u>
<i>Ptef1::HsCERS6</i>	HsCERS6_Tef1_F	<u>CAATCTAATCTAAGTTTTAATTACAAAATGGCAGGGATCTTAGCCTG</u>
	HsCERS6_Cyc1T_R	<u>TAAGCGTGACATAACTAATTACATGATTTAATCATCCATGGAGCAGG</u>
<b>2A sequence</b>	2A_F	GGCTCTGGCGCCACCAACTTCTCTCTCCTCAAACAGGCTGGCGACGTTGA AGAAAACCTGGCCCT
	2A_R	AGGGCCAGGGTTTTCTTCAACGTCGCCAGCCTGTTTGAGGAGAGAGAAG TTGGTGGCGCCAGAGCC
<i>Ptef1</i>	Ptef1_diag	GCTACAGGGCGCGTGGGGATGATCCACTAGTCAAATGTTTCTACTCCTT
<i>Cyc1T</i>	pYes2_Rev	CTTCAGGTTGTCTAACTCCTTCC
<b>qRT-PCR</b>		
<i>GMT (FVEG_09003)</i>	GMT_qRT_F	CCTGGTGCATCCGAGTCACCTC
	GMT_qRT_R	CAACGGTAACGGGAGCAGCG
<i>ACT (FVEG_02524)</i>	act_qRT_F	CGCCGCGCTCACACTCTCC
	act_qRT_R	GGGCTGCAGCAAGACCTCGG
<i>UBI (FVEG_11477)</i>	ubi_qRT_F	CCAGTGGAGTCCTGCGTTGACC
	ubi_qRT_R	GGCAATCTCGGGCACAAGAGG
<i>FUM8</i>	fum8_qRT_F	GCGCTTGAGAGACGACTGGCC
	fum8_qRT_R	GGTTGGCGCATGCACTGAGC
<i>FUM17</i>	fum17_qRT_F	CCTTAGCCACCGCCTCCAGAC
	fum17_qRT_R	GCTCGAAAGGACCAACGGTACG
<i>FUM18</i>	fum18_qRT_F	CGCCATTGGTGTCTTGGATGG
	fum18_qRT_R	GAGATTGCTGCCAGCCAGAACC
<i>FUM19</i>	fum19_qRT_F	CACAGCGTAGGGCAGGTTAGCG
	fum19_qRT_R	TCCAGAAGCTGAGCTGGATGGC
<i>FUM21</i>	fum21_qRT_F	CGGCGTCAACGTGTGCAGAG
	fum21_qRT_R	CTCAATCGGACACCTGCACC