

Supplementary Materials:

Supplementary Figures

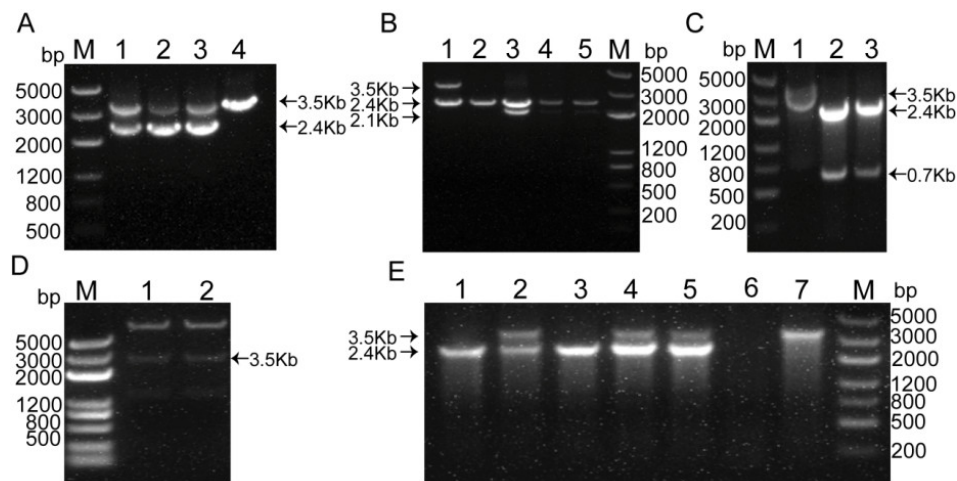


Figure S1. Construction and identification of *vam6Δ/VAM6* mutants. (A) Identification of *vam6Δ/VAM6*. Line 1-4, the amplified fragment. (B) Identification of *vam6Δ/Δ* (URA3). Line 1-5, the amplified fragment. (C) Identification of *vam6Δ/Δ* (-URA3). Line 1-3, the amplified fragment. (D) Enzyme digestion identification of pDDB78-VAM6. (E) PCR identification of VAM6 complemented stains.

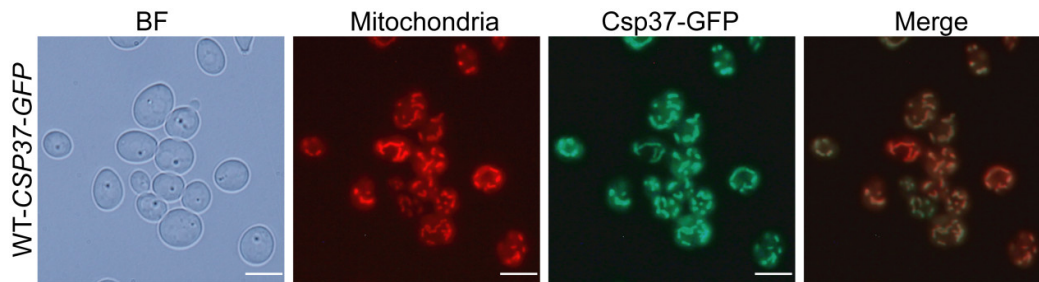


Figure S2. Localization of Csp37 was observed in WT-CSP37-GFP. Csp37-GFP: Csp37 localization, green fluorescence. Mito Tracker Red: Mitochondrial localization, red fluorescence. BF: Bright field.

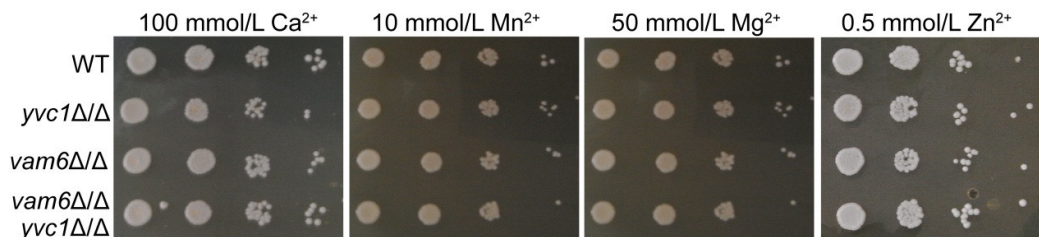


Figure S3. Ions sensitivity analysis of the *vam6Δ/Δ* mutant. (A) Cells were overnight cultured in liquid YPD, spotted on YPD plates containing 100 mM Ca²⁺, 10 mM Mn²⁺, 50 mM Mg²⁺, or 0.5 mM Zn²⁺. The plates were then cultured and photographed.

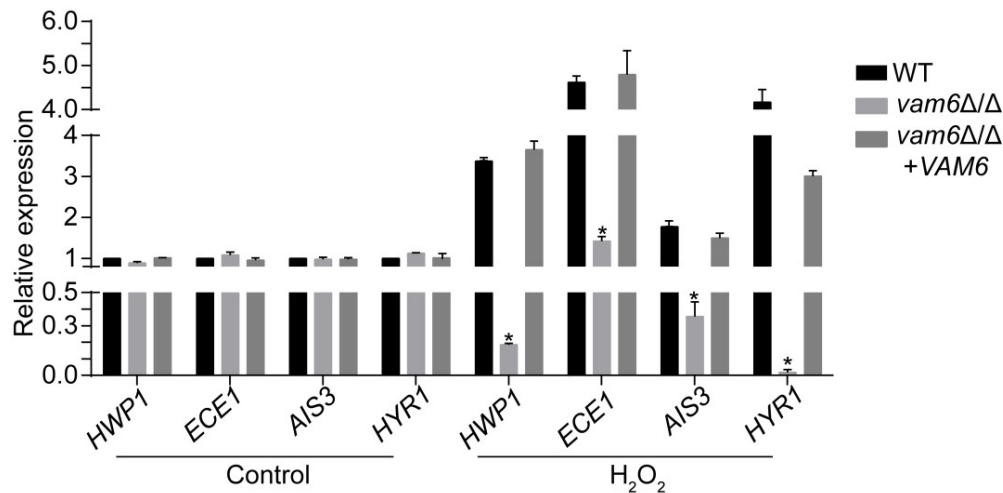


Figure S4. Effect of VAM6 deletion on expression of hypha related genes. Cells were collected after treated by 5 mM H₂O₂ in liquid RPMI-1640 medium for 1 h, and then RNA was extracted. The expression of *AIS3*, *ECE1*, *HYR1*, and *HWP1* were measured by RT-PCR using *ACT1* as the normalization gene. This value represents the mean ± SD with three replicates. * indicates a significant difference between the mutant and the control strains ($p < 0.05$).

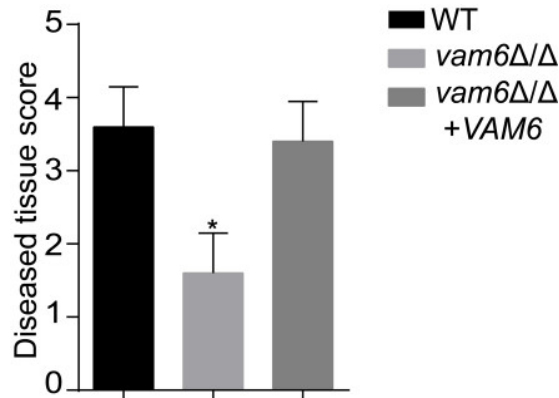


Figure S5. Quantify the tissue damage of kidneys. Take 5 fields for each histopathological images, calculate the ratio of the area of the lesion to the entire field in each field, 0 points for no disease, 1 point for <25%, 2 points for 25%-50%, 3 points for 50%-75 %, 4 points for >75%.* indicates a significant difference between the mutant and the control strains ($p < 0.05$).

Supplementary Tables:

Table 1. Strains and plasmids used in this study.

Strain/ Plasmid	Description	Source/Purpose
BWP17	<i>ura3Δ::limm434/ura3Δ::limm434 his1::hisG/his1::hisG arg4::hisG/arg4::hisG</i>	[51]
BWP17 ^a	<i>URA3/ura3Δ::limm434his1::hisG/his1::hisG arg4::hisG/arg4::hisG</i>	This study
<i>vam6Δ/Δ</i> (+URA3)	<i>ura3Δ::limm434/ura3Δ::limm434his1::hisG/his1::hisGarg4::hisG/arg4::hisG vam6::ARG4/vam6::dpl200-URA3</i>	This study
<i>yvc1Δ/Δ</i>	<i>ura3Δ::limm434/ura3Δ::limm434 his1::hisG/his1::hisG arg4::hisG/arg4::hisG yvc1::ARG4/yvc1::dpl200</i>	[1]
<i>vam6Δ/Δ</i>	<i>ura3Δ::limm434/ura3Δ::limm434 his1::hisG/his1::hisG arg4::hisG/arg4::hisG vam6::ARG4/vam6::dpl200</i>	This study
<i>vam6Δ/Δ</i> ^a	<i>URA3/ura3Δ::limm434his1::hisG/his1::hisGarg4::hisG/arg4::hisG vam6::ARG4/vam6::dpl200</i>	This study
<i>vam6Δ/Δyvc1Δ/Δ</i>	<i>ura3Δ::limm434/ura3Δ::limm434 his1::hisG/his1::hisG</i>	This study

	<i>arg4::hisG/arg4::hisG yvc1::ARG4/yvc1::dpl200, vam6::dpl200/vam6::dpl200</i>	
<i>vam6Δ/Δ+VAM6</i>	<i>ura3Δ::limm434/ura3Δ::limm434 his1::hisG/his1::hisG arg4::hisG/arg4::hisG vam6::ARG4/vam6::dpl200, pDDB78-VAM6</i>	This study
<i>vam6Δ/Δ+VAM6^a</i>	<i>URA3/ura3Δ::limm434his1::hisG/his1::hisGarg4::hisG/arg4::hisG vam6::ARG4/vam6::dpl200, pDDB78-VAM6</i>	This study
<i>vam6Δ/Δ-CSP37-GFP</i>	<i>ura3Δ::limm434/ura3Δ::limm434 his1::hisG/his1::hisG arg4::hisG/arg4::hisG vam6::ARG4/vam6::dpl200 CSP37/CSP37-GFP::URA3</i>	This study
WT-VAM6-GFP	<i>ura3Δ::limm434/ura3Δ::limm434 his1::hisG/his1::hisG arg4::hisG/arg4::hisG VAM6/VAM6-GFP::URA3</i>	This study
WT-VAM6	<i>ura3Δ::limm434/ura3Δ::limm434 his1::hisG/his1::hisG arg4::hisG/arg4::hisG VAM6/VAM6::URA3</i>	This study
WT-CSP37-GFP	<i>ura3Δ::limm434/ura3Δ::limm434 his1::hisG/his1::hisG arg4::hisG/arg4::hisG CSP37/CSP37-GFP::URA3</i>	This study
Plasmid		
pRS-ArgΔ <i>SpeI</i>	Amp ^r ARG4	[51]
pDDB57	Amp ^r URA3	[51]
pDDB78	Amp ^r TRP1 HIS1	[51]
pLUBP	Amp ^r IRO1-URA3	[52]
pDDB78-VAM6	Amp ^r VAM6 TRP1 HIS1	This study
pAu34M-GFP	Amp ^r P _{ACT1} -GFP URA3	This study
pAu34M-VAM6-GFP	Amp ^r P _{ACT1} -VAM6-GFP URA3	This study

^a Strain that URA3 was reintroduced at its common locus.

Table 2. Primers used in this study.

Primer	Sequence (5'→3')	Function
VAM6-5DR	AAATTAAGGGGAATT- AGGGTTAACAAAATTACACGTCC- TACAGATGCATTGTTTTGTTTATTTCCCAGTCAC- GACGTT	Gene knockout
VAM6-3DR	AATATGAGACTTTTTAAAAATTACTTGTATGA- TAAGATATATATTTAATTAACCTAACGTTGGAATT- GTGAGCGGATA	Gene knockout
VAM6-5det	AAATGGAAATCGTAGAAAGT	Genetic validation
VAM6-3det	CTTAGATGTGTTGTTGTTTT	Genetic validation
VAM6-5com	ATATAATCATTCAAAAATGGTAATGAATATAGATGT	Complement gene
VAM6-3com	ATATAATCATTCAAAAATGGTAATGAATATAGATGT	Complement gene
VAM6-5GFP	GGACTAGTATGGTTTCAAAAGGTGAAG	Transcriptional fusion
VAM6-3GFP	TTCCAGAATTCACCTCTTATTTATA- TAATTCATCCATA	Transcriptional fusion
COX2-5RT	TAGATGTACCTACACCTTGA	RT-PCR
COX2-3RT	CCTATAGAGTCAACAAAATC	RT-PCR
NAD2-5RT	ACATACATAGTTTATATCGC	RT-PCR
NAD2-3RT	GAGAGTAAGATTGTAATTCA	RT-PCR
NAD5-5RT	TACTTGAATTAGTCTAGGTG	RT-PCR
NAD5-3RT	CTACAAACTCTCAACCAATG	RT-PCR

<i>ATP6</i> -5RT	TTCACCTTTAGATCAATTCTG	RT-PCR
<i>ATP6</i> -3RT	AAACTAAATGATACAATAGC	RT-PCR
<i>SCR1</i> -5RT	CTGCTCGTGACCTGCTGTT	RT-PCR
<i>SCR1</i> -3RT	CTTCCCTCCAGTGGTTATGCT	RT-PCR
<i>URA3</i> -5inner	CGCGGGATTGGATGGTAT	URA test
<i>URA3</i> -3inner	TCTTGGCTCTTGTTGGTG	URA test
<i>GLR1</i> -5RT	GGAGATTTTCGATTGGGCTAA	RT-PCR
<i>GLR1</i> -3RT	GACTTCAACTTCACCTTCAG	RT-PCR
<i>TRR1</i> -5RT	TGGAGGATCTGAATTGATGG	RT-PCR
<i>TRR1</i> -3RT	CACCAGTAGCAATGATAACG	RT-PCR
<i>CAT1</i> -5RT	TCCAGAACCATTGCCACTCA	RT-PCR
<i>CAT1</i> -3RT	GGAACCTTTAGCGTGGACAAC	RT-PCR
<i>SOD1</i> -5RT	GCTGTTGTCAGAGGTGATTCA	RT-PCR
<i>SOD1</i> -3RT	TGAAATGAGGACCAGCAGA	RT-PCR
<i>HWP1</i> -5RT	TGTCTACACTACATTCTGTC	RT-PCR
<i>HWP1</i> -3RT	AGGAATAGATGGTTGTGAAC	RT-PCR
<i>ECE1</i> -5RT	CCAAGCACCTACTGTTCC	RT-PCR
<i>ECE1</i> -3RT	GATACCAGCAACAACAGAAT	RT-PCR
<i>ALS3</i> -5RT	CTCATTACACCAACCATAACA	RT-PCR
<i>ALS3</i> -3RT	GGATTCTGTGGTTGTAGTAT	RT-PCR
<i>HYR1</i> -5RT	CTCATTACACCAACCATAACA	RT-PCR
<i>HYR1</i> -3RT	TCCAGAACCAGAGCCATC	RT-PCR
<i>ACT1</i> -5RT	GGTAGACCAAGACATCAAGG	RT-PCR
<i>ACT1</i> -3RT	CCGTGTTCAATTGGGTATCT	RT-PCR
