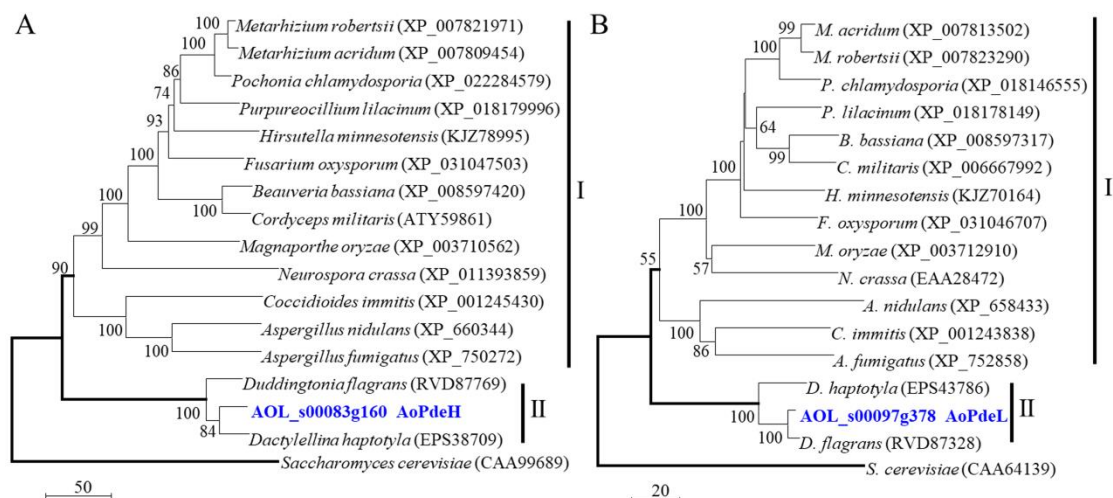
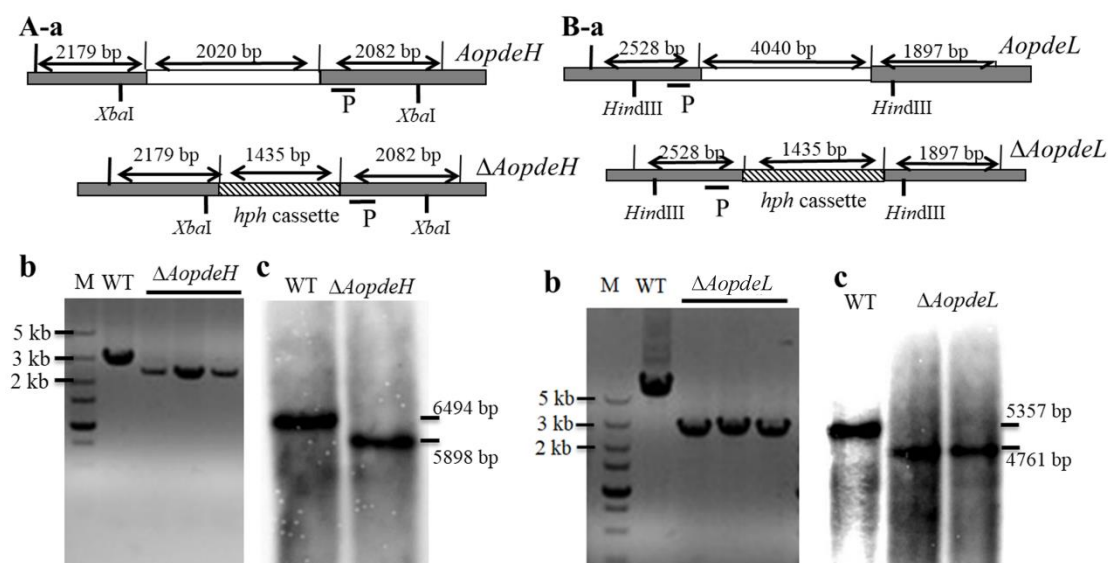


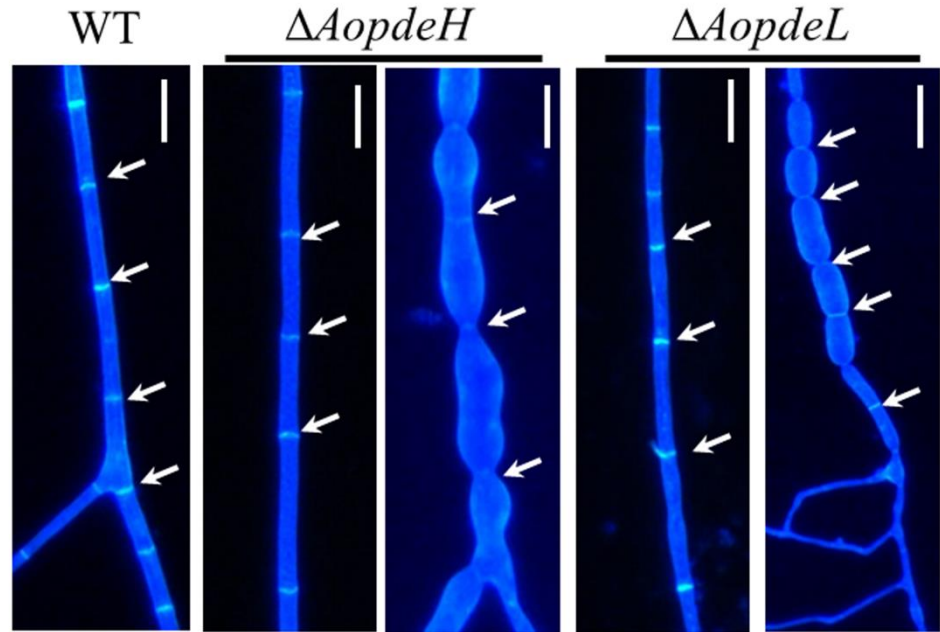
## Supporting Information



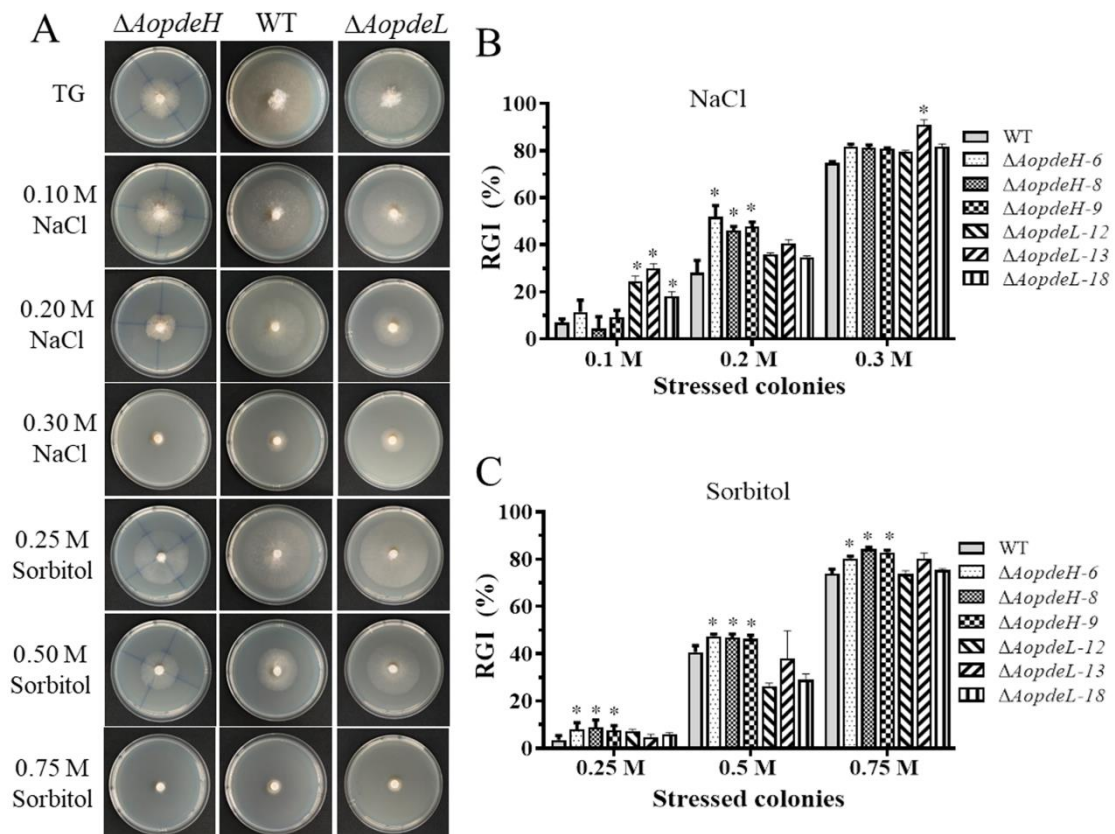
**Figure S1.** Phylogenetic tree analysis based on the amino acid sequences of PdeH and PdeL homologous proteins from different fungi. (A) Phylogenetic tree of PdeH orthologs from various fungi. (B) Phylogenetic tree of PdeL orthologs from various fungi. GenBank accession numbers are provided in brackets. The amino acid sequences of PdeH and PdeL proteins were aligned with ClustalX version 1.83, and MEGA 7 was used to construct a neighbor-joining tree, including bootstrap analysis with 1,000 replicates.



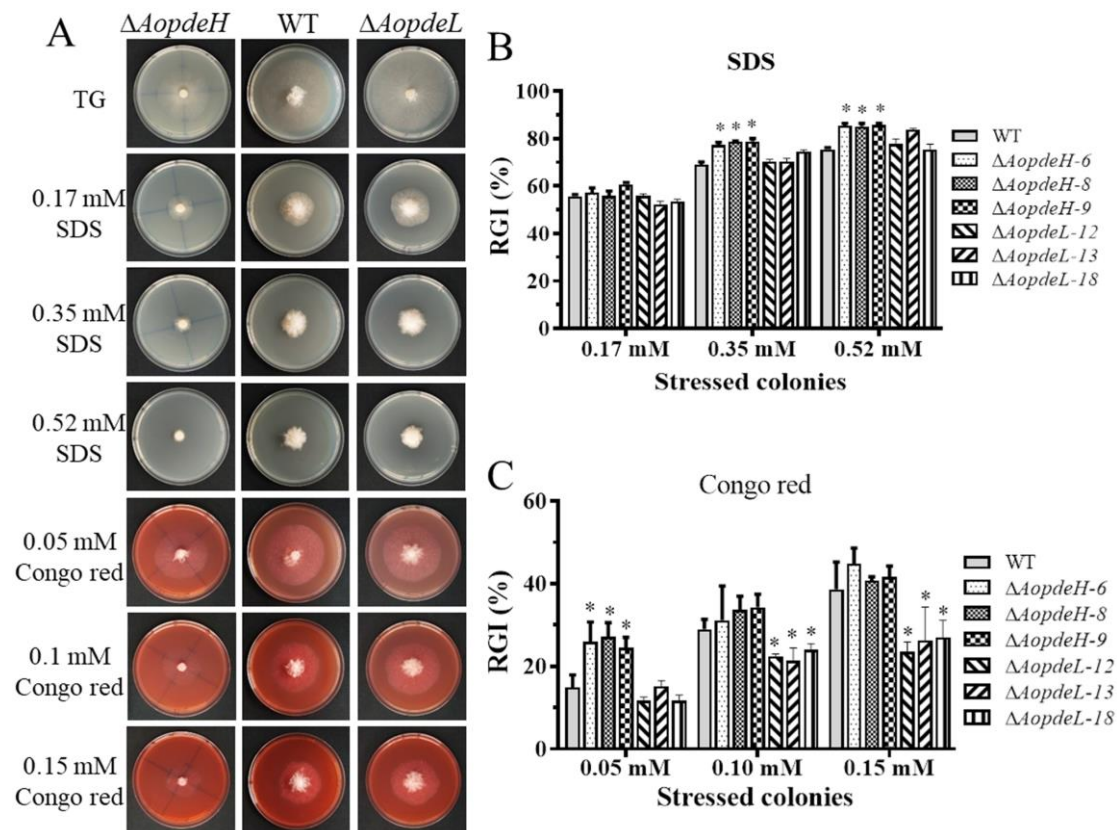
**Figure S2.** Deletion of *AopdeH* and *AopdeL* in *A. oligospora*. (A) Deletion of *AopdeH* and verification of transformants. (A-a) The diagrammatic sketch of homologous recombination of *AopdeH* and the homologous flanks of the target gene. (A-b) *AopdeH*-deleted transformants were confirmed by PCR amplification. M, DNA marker; WT, Wild-type strain;  $\Delta AopdeH$ , transformants. (A-c) Southern blotting analysis of wild-type (WT) and transformant ( $\Delta AopdeH$ ). (B) Deletion of *AopdeL* and verification of transformants. (B-a) The diagrammatic sketch of homologous recombination of *AopdeL* and the homologous flanks of the target gene. (B-b) *AopdeL*-deleted transformants were confirmed by PCR amplification. M, DNA marker; WT, Wild-type strain;  $\Delta AopdeL$ , transformants. (B-c) Southern blotting analysis of wild-type (WT) and transformants ( $\Delta AopdeL$ ).



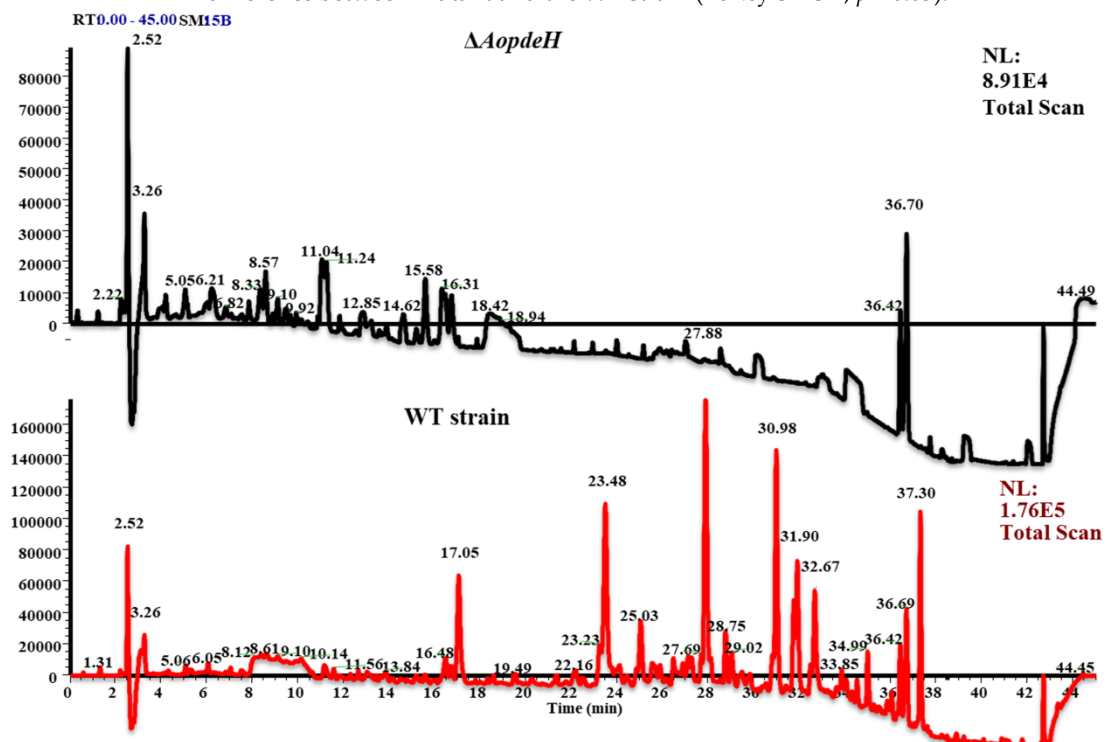
**Figure S3.** Comparison of the hyphal septum between WT and mutants. The hyphal septa of the WT and mutants were stained with 20  $\mu\text{g/mL}$  calcofluor white (CFW). Arrow, hyphal septum. Bar = 10  $\mu\text{m}$ .



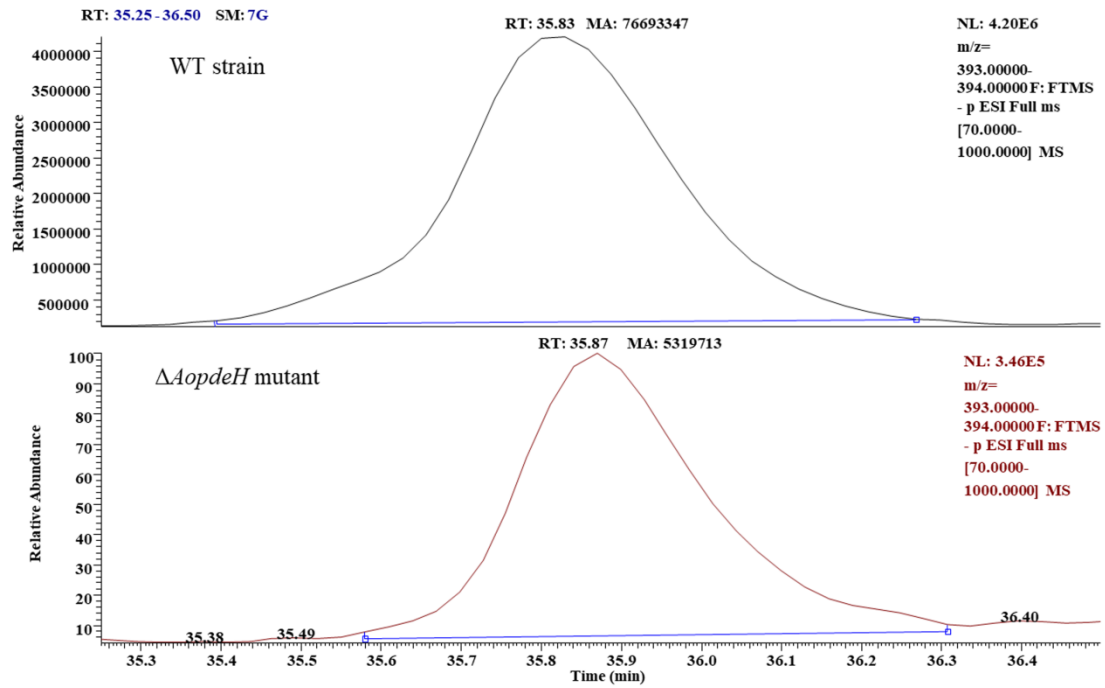
**Figure S4.** Comparison of osmotic stress responses between WT and mutants. (A) Colonial morphology of fungal strains under osmotic stress. (B) and (C) Relative growth inhibition (RGI) of fungal colonies after being grown for five days at 28  $^{\circ}\text{C}$  on TG plates supplemented with different concentrations of NaCl and sorbitol, respectively. An asterisk indicates a significant difference between mutant and the WT strain (Tukey's HSD,  $p < 0.05$ ).



**Figure S5.** Comparison of cell wall stress agent responses between WT and mutants. (A) Colonial morphology of fungal strains under cell wall stress agents. (B) and (C) Relative growth inhibition (RGI) of fungal colonies after being grown for five days at 28 °C on TG plates supplemented with different concentrations of SDS and Congo red, respectively. An asterisk indicates a significant difference between mutant and the WT strain (Tukey's HSD,  $p < 0.05$ ).



**Figure S6.** Comparison of high-performance liquid chromatography profiles of the WT and  $\Delta AopdeH$  mutant strains.



**Figure S7.** Comparison of the relative peak area of arthrobotrisins between WT and  $\Delta AopdeH$  mutant strains.

**Table S1.** The sequence similarity between AoPdeH/AoPdeL and orthologs from different fungi. The sequence similarity of orthologous PdeH/PdeL was analyzed using DNAMAN software.

Species	Simialrity to AoPdeH (%)	Simialrity to AoPdeL (%)	Group
<i>Arthrobotrys oligospora</i>	100	100	NT fungi
<i>Duddingtonia flagrans</i>	89.9	93.3	
<i>Dactylellina haptotyla</i>	89.8	72.7	
<i>Neurospora crassa</i>	31.7	34.3	Other filamentous fungi
<i>Aspergillus nidulans</i>	31.5	30.9	
<i>Aspergillus fumigatus</i>	32.8	38.4	
<i>Purpureocillium lilacinum</i>	34.8	41.5	
<i>Hirsutella minnesotensis</i>	34.4	43.1	
<i>Pochonia chlamydosporia</i>	34.8	42.1	
<i>Metarhizium robertsii</i>	33.5	43.2	
<i>Metarhizium acridum</i>	32.9	42.7	
<i>Beauveria bassiana</i>	33.9	41.7	
<i>Cordyceps militaris</i>	32.9	39.5	
<i>Fusarium oxysporum</i>	34.6	42.9	
<i>Magnaporthe oryzae</i>	34.8	40.6	
<i>Coccidioides immitis</i>	32.2	39.4	
<i>Saccharomyces cerevisiae</i>	19.0	28.5	yeast

**Table S2.** Comparison of the differential compounds-metabolic pathways between the WT and  $\Delta AopdeH$  mutant strains.

Compounds-metabolic pathways	upregulated	downregulated
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Superpathway of aromatic compound degradation via 2-oxopent-4-enoate	4	39
Anaerobic aromatic compound degradation ( <i>Thauera aromatica</i> )	4	27
Superpathway of aerobic toluene degradation	2	28
Superpathway of aromatic compound degradation via 3-oxoadipate	4	21
Superpathway of chorismate metabolism	4	15
Toluene degradation IV (aerobic) (via catechol)	2	23
Naphthalene degradation to acetyl-CoA	2	23
Mandelate degradation to acetyl-CoA	2	14
Toluene degradation III (aerobic) (via p-cresol)	2	20
Superpathway of aromatic amino acid biosynthesis	4	10
Superpathway of 4-hydroxybenzoate biosynthesis (yeast)	2	13
L-tyrosine degradation IV (to 4-methylphenol)	2	14
Superpathway of scopolin and esculin biosynthesis	2	10
Benzoate biosynthesis I (CoA-dependent, ss-oxidative)	2	14
Superpathway of rosmarinic acid biosynthesis	2	10
Meta cleavage pathway of aromatic compounds	2	8
Superpathway of L-lysine degradation	2	1
Novobiocin biosynthesis	2	9
Toluene degradation I (aerobic) (via o-cresol)	0	12
Other	13	114
Not set	84	1715

**Table S3.** List of primers used for gene disruption in this study.

Primers	Sequence (5'-3')	Description
83g160-5F	GTAACGCCAGGGTTTTCCCAGTCACGACGG AAATGGCTCCCGTGACTT-3	Amplify the <i>AopdeH</i> gene 5' flank
83g160-5R	ATCCACTTAACGTTACTGAAATCTCCAACCTC AGGCTCAACAACACCGT-3	
83g160-3F	CTCCTTCAATATCATCTTCTGTCTCCGACAG TATCGCCTCTTCGTTGTCC-3	Amplify the <i>AopdeH</i> gene 3' flank
83g160-3R	GCGGATAACAATTTACACAGGAAACAGC CCTATTACTGGACCCGCATT-3	
97g378-5F	GTAACGCCAGGGTTTTCCCAGTCACGACGT TCCCATCCTTATCGGTCTC-3	Amplify the <i>AopdeL</i> gene 5' flank
97g378-5R	ATCCACTTAACGTTACTGAAATCTCCAACA TCCGTCGTTGTCCCCTTA-3	
97g378-3F	CTCCTTCAATATCATCTTCTGTCTCCGACGG GAGAAAAGGCGGGATTA-3	Amplify the <i>AopdeL</i> gene 3' flank
97g378-3R	GCGGATAACAATTTACACAGGAAACAGC GGATAGCCGAGACTGACCCA-3	
hphF	GTCGGAGACAGAAGATGATATTGAAGGAG C	Amplify the <i>hph</i> cassette

hphR	GTTGGAGATTTTCAGTAACGTTAAGTGGAT	
83g160-YZF	GTCAGGGCAACGGAGTGTAAG	Verify the
83g160-YZR	GGAATAGCATCATCGGTAGGA	transformants for
		<i>AopdeH</i> gene
97g378-YZF	GCTTGCTGATAATCTTTCCTCG	Verify the
97g378-YZR	GAACCAACAACCTCCGCATAACT	transformants for
		<i>AopdeL</i> gene
83g160-TZF	GTCAGGGCAACGGAGTGTAAG	Make Southern blotting
83g160-TZR	GACGCACAGTAACGACAACCATA	probe for <i>AopdeH</i> gene
97g378-TZF	GAGTTATGCGGAGTTGTTGGT	Make Southern blotting
97g378-TZR	ACTGGAGGGTTGCTAGAAAGA	probe for <i>AopdeL</i> gene

**Table S4.** List of RT-PCR primers used in this study.

Sporulation-related genes	Sequence (5'-3')
AOL_s00007g157 ( <i>flbC</i> )	157-5F-CTCTCCGGCAAAGACAATCG 157-3R-GTCGACTGAGGATAGTAGCT
AOL_s00043g361 ( <i>fluG</i> )	361-5F-GATTCCAGTCCCGTGAATTC 361-3R-GCTAAGGAGAGGATGGGCAT
AOL_s00054g700 ( <i>vosA</i> )	700-5F- CAAACCACCCACCACCAAAT 700-3R-GGATGGACAGGAGAAGGACC
AOL_s00054g811 ( <i>velB</i> )	811-5F- ATTCCGCAACTTCTCCCTCA 811-3R- GGCATGTTTGGATTCTGGGG
AOL_s00080g63 ( <i>abaA</i> )	63-5F-AACTTTATGCGCCTTGTCGT 63-3R-TTGGCTAGGTGGTCTGTACG
AOL_s00083g487 ( <i>lreA</i> )	487-5F-CCCTCCATACAGTCAGTGCTA 487-3R-CCCTACCCACCAAGATGATAC
AOL_s00080g93 ( <i>lreB</i> )	93-5F-CGAAGAGCAAGAAGAACAAGC 93-3R-AGATGGGTATGGGATAGAGGG
AOL_s00215g893 ( <i>aspB</i> )	893-5F-ATACCGCCAACACCCTCTAC 893-3R-AACCATCTTCATCTCGGCCT
$\beta$ -tubulin gene	tub-5F-CCACCTTCGTCGGTAACTC
AOL_s00076g640 ( <i>tub</i> )	tub-3R-TCGTCCATACCCTCACCAG