

Table S2. Differentially expressed genes related to melanin biosynthesis and pathogenesis in $\Delta Monap1$ mutant using $|\log_2\text{FoldChange}|$ values >1.5 and $\text{P}_{\text{adj}} < 0.05$

Gene ID	Description	Log ₂ -fold Change	Name
Pathogenesis			
MGG_04404	pisatin demethylase	-13.53	<i>PDA</i>
MGG_07404	tripeptidyl-peptidase 1	-7.46	<i>TPP1</i>
MGG_15508	hypothetical protein	-4.07	<i>ZFP6</i>
MGG_16196	hypothetical protein	-3.40	<i>QDR3</i>
MGG_07626	cytochrome P450 monooxygenase	-3.09	<i>DIT2</i>
MGG_06872	hypothetical protein	-2.96	<i>YEP1</i>
MGG_08519	aflatoxin B1 aldehyde reductase member 3	-2.66	<i>ALR1</i>
MGG_00863	hypothetical protein	-2.49	<i>SCW4</i>
MGG_06772	hypothetical protein	-2.31	<i>PRY2</i>
MGG_12773	aminopeptidase Y	-1.73	<i>APE3</i>
MGG_01336	bacteriodes thetaiotaomicron symbiotic chitinase	-1.72	<i>CTS2</i>
MGG_13177	hypothetical protein	-1.55	<i>SOD1</i>
MGG_09246	protease	1.52	<i>PRB1</i>
MGG_09322	hypothetical protein	1.66	<i>PLP</i>
MGG_08850	cAMP-independent regulatory protein pac2	1.90	<i>MIT1</i>
MGG_04699	C2H2 finger domain-containing protein FlbC	2.05	<i>FLBC</i>
MGG_12442	aminopeptidase Y	2.31	<i>APE3</i>
MGG_07982	cytochrome P450 monooxygenase	2.32	<i>DIT2</i>
MGG_00681	hypothetical protein	2.44	<i>COQ5</i>
MGG_00416	MFS transporter	5.52	<i>TPO1</i>
MGG_10671	pentalenene synthase	6.95	<i>PSS</i>
Melanin biosynthesis			
MGG_07219	conidial yellow pigment biosynthesis polyketide synthase	-4.90	<i>ALB1</i>
MGG_13464	laccase	-4.75	<i>LAC</i>
MGG_07216	versicolorin reductase	-4.30	<i>STCU2</i>
MGG_02252	tetrahydroxynaphthalene reductase	-3.22	<i>BUF1</i>
MGG_05059	scytalone dehydratase	-2.90	<i>SDH1</i>
MGG_07215	transcription factor Cmr1	-2.72	<i>CMR1</i>