Table S1 Sequence of primers used in quantitative RT-PCR.

ID	Primer	Nucleotide sequence	ID	Primer	Nucleotide sequence
116027	F	GCTGAGGAAGTGAGCGGTA	119940	F	TGAAACCTACTTGCCTGACG
	R	TTGTAGGGCACAGTAGGGATG		R	AGCACCTCTCACCAGAACG
114978	F	ACCGAAGGACAGGCTTATTG	154931	F	GCCTGCTCAAGGATTTCAAG
	R	CATTGTAGGCAGCAGTGAGATTA		R	CTGTGCTGTGGATGGTGGT
184845	F	TTCGCTCGTAAACTGATGGA	166875	F	GAAAGCAATCAAAGCGAAGG
	R	CCAAGGCAAACAAAGTCTCA		R	GAGGACAAATGGTGGTGGTC
34010	F	GGGACTGAAACACCCATTGA	35076	F	ACCCAAGGCTGACGATGTAG
	R	AGAGGCGGACTGATGATACG		R	CCAGAGGTTGAGAGGGACAA
115264	F	CACAATCACACCCAGAATGC	155817	F	ATTTGTTCCTGATGGCAAGC
	R	ACGCTACAAAGAATGGACAGC		R	GTGATGGCACTTCTGATGGA
81713	F	ATTGCTTATGGCTGGTGTGT	170034	F	TAACAATGCCCACAAAGACG
	R	GCATTCACTTGCTCGTTGAT		R	TTACGAGCAGGAACAACACG
113168	F	ATTTGCTGCGTTCTGTGCT	111734	F	CACAGCAAACAGCAAACAGG
	R	GCCTGCTGACCTACCAAGAG		R	GGCTCGTAGTGGACATAGGC
161426	F	GCTCAAACCACTGACATCCA	155202	F	CACCAAGAACACGGAATGG
	R	GACATCCATTCTGCCTCCAG		R	ATAAGCGGGAAGAGGAGGAG
104484	F	TGTCATTGCGGGAGATAGTG	111320	F	AGTTGATTACGCCAGCCAAG
	R	AAGATGGAGGGTAGCGAGTG		R	TCTGTGCTTTCATCGTCAGG
184709	F	AGCACAAGCAGAGGGCATTA	114445	F	TGTGTGAATACCGACCTTGG
	R	ACGGACCACCAAGAGATTTG		R	TTTGCGTTTGTTCGCTGATA
39585	F	CAGGAAAGGTGTGTGTGTGG	110553	F	TTTATCGCCAGAGACAGGAAA
	R	TCTGGCAATGGAAACTTGTCT		R	TCCAAGGCTCGTATTCACAA
130354	F	ACCTGAACAACACGGAATGG	167246	F	GCAATGAAGTCGTGGTCAAG
	R	TGCCCTTGATACTGACCACA		R	CGGGCGGAACAATAGAACT
115761	F	GCATCTTGTTTCGCATCCTC	143450	F	AAGCAGCACCCTCCATCA
	R	ATCACCACCTTCCAGTCCAC		R	TGCCATCCAAACAAGAAATG
107413	F	AGCAACAGAAGCAACCGAAT	167388	F	CGACAACCACCACCACATTA
	R	ATGATACGCACAATGCCAAA		R	TAGCAGGAGCAGCAGGAAAG
106404	F	AAGCAGCAGATGGCAACATT	185587	F	TGCGACCCAACAAGGTGTA
	R	ATTCTTCGTTTCATAGGGTCCA		R	AGAGCCCAGTGAATGAAGCA

Table S2 Sequence of primers used in gene over-expression of Lip6 (161426), Lip10 (115761), Lip19 (143450) and Lip24 (107413).

ID	Primer	Nucleotide sequence
161426	F	CTTTTATATACAAAATAACTAAATCTCGAGATGTCTGACATTGCATCC
	R	GTACTACTAGTCGCAATTGCCGCGGCTCGAGTTAGACAATCGTCGTGGCCT
115761	F	CTTTTATATACAAAATAACTAAATCTCGAGATGGCAAAAGGTAGAAA
	R	GTACTACTAGTCGCAATTGCCGCGGCTCGAGTCAATCATGAACATCTAC
143450	F	CTTTTATATACAAAATAACTAAATCTCGAGATGGTCTTGATCTCCTCTCT
	R	GTACTACTAGTCGCAATTGCCGCGGCTCGAGTTAGAGGCAGAGACCTTCATT
107413	F	CTTTTATATACAAAATAACTAAATCTCGAGATGTCTTCCAAGGGTAA
	R	GTACTACTAGTCGCAATTGCCGCGGCTCGAGTTACTTGTTTTTGCAGTC

Table S3 The sub-cellular location, and the presence and location of signal peptide of lipases from *M. circinelloides* CBS 277.49.

Protein ID	**Location**	**RC**	**Signal peptides**
130354	-	2	NO
34010	-	1	NO
116027	S	1	YES
114978	-	4	NO
81713	-	2	NO
104484	-	4	NO
106404	S	1	YES
113168	-	5	NO
111320	-	5	NO
107413	S	1	NO
115264	-	4	NO
161426	-	3	NO
154931	-	3	NO
166875	-	2	NO
39585	M	5	NO
111734	M	4	NO
110553	-	4	NO
119940	-	3	NO
115761	S	2	NO
167246	-	1	NO
170034	S	1	YES
184709	-	2	NO
35076	S	2	YES
155817	S	3	YES
155202	S	2	NO
114445	-	3	NO
143450	-	2	NO
167388	-	3	NO
72954	-	4	NO
185587	S	2	YES

Note: S: Secretory pathway, i.e. the sequence contains a signal peptide; M: Mitochondrion, i.e. the sequence contains a mitochnondrial targeting peptide; -: Any other location. RC：Reliability class, from 1 to 5, which is a measure of the size the difference between the highest and the second highest output scores. 1: diff>0.8, 2: 0.8>diff>0.6, 3: 0.6>diff>0.4, 4: 0.4>diff>0.2, 5: 0.2>diff.