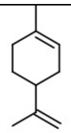
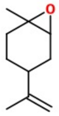
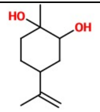
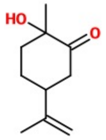
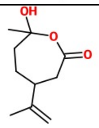
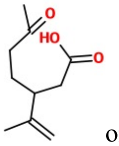
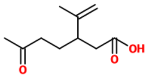
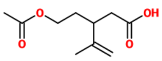
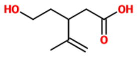
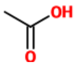
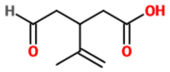
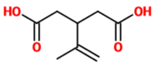
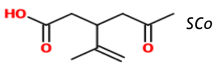
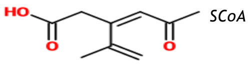
Table S1. mRNA abundance of *Gs* beta-oxidation genes when the fungus is grown on oleic acid (YNB+OC) or monoterpene mixture (YNB+MT) as single carbon. * indicates genes that are significantly up-regulated (P<0.05)

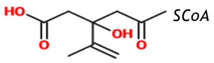
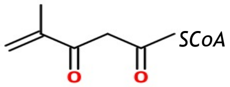
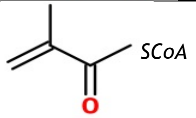
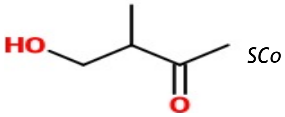
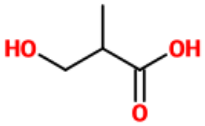
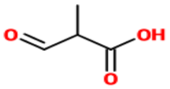
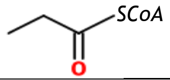
Gene ID	Gene description	YNB+OC	YNB+MT
CMQ_5823	3-hydroxyacyl-CoA dehydrogenase	1.23	2.14 *
CMQ_3893	enoyl-coA hydratase	15.75*	1.89*
CMQ_1252	3-ketoacyl-CoA thiolase peroxisomal a precursor	17.28*	-1.02
CMQ_5429	acyl-dehydrogenase domain containing protein	24.18*	1.08
CMQ_3456	acyl-CoA dehydrogenase	3.08*	3.45*
CMQ_3669	short chain dehydrogenase reductase	12.79*	1.01
CMQ_2282	3-ketoacyl-ketothiolase	12.26*	-1.47
CMQ_5806	enoyl-hydratase isomerase family protein	34.47*	4.71*
CMQ_8299	acyl-dehydrogenase domain containing protein	13.27*	1,482.13*
CMQ_2938	acetyl-CoA c-acyltransferase	4.4*	1.37*
CMQ_2559	acyl-dehydrogenase domain containing protein	15.83*	2.76*
CMQ_2556	acyl-dehydrogenase domain containing protein	18.07*	1.08
CMQ_7074	3-ketoacyl-thiolase	2.22*	2.84

Table S2. Protein IDs of the 24 fatty acid metabolic proteins used in the manuscript

Species	ID	Description
Magnaporthe grisea	MGG_01551	long-chain-fatty-acid-CoA ligase 1
Magnaporthe grisea	MGG_08661	acyl-CoA dehydrogenase
Magnaporthe grisea	MGG_12868	enoyl-CoA hydratase
Magnaporthe grisea	MGG_09512	3-ketoacyl-CoA thiolase
Magnaporthe grisea	MGG_01755	acetyl-CoA acetyltransferase
Laccaria bicolor	189447	Acylcarnitine transferase
Laccaria bicolor	191220	Acyl-CoA dehydrogenase
Laccaria bicolor	301012	Carnitine/acylcarnitine translocase
Laccaria bicolor	234621	Enoyl-CoA hydratase
Laccaria bicolor	319094	Long-chain FA-CoA ligase
Laccaria bicolor	185981	3-ketoacyl-CoA thiolase
Laccaria bicolor	187873	3-hydroxyacyl-CoA dehyogenase
Laccaria bicolor	188234	Acetylcarnitine transferase
Laccaria bicolor	319093	Acyl-CoA oxidase
Laccaria bicolor	234865	peroxisomal multifunctional protein
Laccaria bicolor	242594	peroxisomal ABC transporter 1
Laccaria bicolor	141760	peroxisomal ABC transporter 2
Laccaria bicolor	301021	3-ketoacyl-CoA thiolase
Laccaria bicolor	317084	dependent isocitrate dehydrogenase
Yarrowia lipolytica	YALI0F23749	glutaryl-CoA dehydrogenase
Yarrowia lipolytica	YALI0F04095p	isocitrate dehydrogenase
Yarrowia lipolytica	YALI0E34672p	mitochondrial citrate transporter)
Yarrowia lipolytica	YALI0E09405	peroxin-14
Yarrowia lipolytica	YALI0C16885	socitrate lyase

Table S3. Proposed (+)-limonene degradation intermediates and the potential enzymes involved in the conversion

Reaction step	Compound name	Compound structure	Enzymes	Fold changes	Remarks
1	Limonene		FAD-binding monooxygenase (CMQ_6740) or P450	7099	Jeffery is the natural mutant
2	Limonene 1,2-expoxide		Epoxide hydrolase (CMQ_7009) or α-β hydrolase(s)	28.31	Found in Metabolite Mutant gives the phenotype (partially)
3	Limonene –1,2-diol		DCPIP type dehydrogenase (CMQ_238)	39.48	Found in Metabolite
4	(1S,4R)-1-Hydroxy-2-oxolimonene		Baeyer-Villager monooxygenase (CMQ_6956)	356	Found in metabolite. Mutant gives the phenotype
5	7-hydroxy-4-isopropenyl-7-menthyl-2-oxo-oxepanone		Spontaneous reaction		Found in metabolite (derivatised sample)
6	(3R)-3-Isopropenyl-6-oxoheptanoate	 or 	Baeyer-Villager monooxygenase (CMQ_7007)	2571	Found in metabolite (derivatised sample). Mutant gives the phenotype
7	3-(2-acetoxyethyl)-4-methylpent-4-enoic acid		Lipase esterase (CMQ_6642)	429	Break C10 to C8
8	3-(2-hydroxyethyl)-4-methylpent-4-enoic acid	 and 	Alcohol dehydrogenase (CMQ_8234)	2956	
9	4-methyl-3-(2-oxoethyl)pent-4-enoic acid		Aldehyde dehydrogenase (CMQ_6937)	279	
10	3-(prop-1-en-2yl) pentanedioic acid		Ligase (CMQ_4361)	2.08	
11	3-isopropenyl-glutaryl-coA		Acyl CoA-dehydrogenase (CMQ_8299)	1482	
12	3-isopropenyl-glutaconyl-coA		enoyl-coA hydratase (CMQ_4626)	3.29	Beta-oxidation gene

13	3-hydroxy-3-isopropenyl-glutaconyl-coA		Hydroxymethylglutaryl-CoA lyase (CMQ_8094)	18483	Breaking C8 to C6
14	4-methyl-4-penenoyl-coA		3-ketoacyl-thiolase (CMQ_7074)	2.84	Bata-oxidation gene
15	Mecharylyl-CoA		Crotonase (CMQ_613)	6.39	Intermediate of valine catabolism pathway
16	Beta-hydroxyisobutyryl-CoA		3-hydroxyisobutyryl-CoA hydrolase (CMQ_4626)	3.29	Valine catabolism pathway
17	Beta-hydroxyisobutyric acid		3-hydroxyisobutyrate dehydrogenase (CMQ_4029)	23.08	Valine catabolism pathway
18	Methylmalonic acid		Methylmalonate-semialdehyde dehydrogenase (CMQ_3621)	22.39	Valine catabolism pathway
19	Propionyl -CoA				Precursor of TCA cycle