Supplementary Information

Integration of transcriptomics and proteomics to elucidate inhibitory effect and mechanism of Antifungalmycin B from marine *Streptomyces hiroshimensis* in treating *Talaromyces marneffei*

Qiqi Li_ *et al*.

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Table S1. Differential genes related to oxidative phosphorylation pathway.

Sequence	Description	Gene ID	Gene_ FC
1	COX5B; cytochrome c oxidase subunit 5b	EYB26_008124	3.08224072
2	COX6A; cytochrome c oxidase subunit 6a	EYB26_008905	2.262598176
3	NDUFA9; NADH dehydrogenase (ubiquinone) 1 alpha subcomplex subunit 9	EYB26_003901	1.612019156
4	ATPeV1C; V-type H+-transporting ATPase subunit C	EYB26_005467	1.661657246
5	NDUFB3; NADH dehydrogenase (ubiquinone) 1 beta subcomplex subunit 3	EYB26_002228	1.308807591
6	NDUFA6; NADH dehydrogenase (ubiquinone) 1 alpha subcomplex subunit 6	EYB26_009701	1.287439753
7	ATPeV1B; V-type H+-transporting ATPase subunit B	EYB26_006240	1.150602238
8	ATPeV1E; V-type H+-transporting ATPase subunit E	EYB26_000329	1.807928397

9	SDHA; succinate dehydrogenase (ubiquinone) flavoprotein subunit	EYB26_004355	1.806831087
10	NDUFB8; NADH dehydrogenase (ubiquinone) 1 beta subcomplex subunit 8	EYB26_009588	3.116852792
11	ATPeV0C; V-type H+-transporting ATPase 16kDa proteolipid subunit	EYB26_009276	1.130928366
12	NDUFA5; NADH dehydrogenase (ubiquinone) 1 alpha subcomplex subunit 5	EYB26_003534	2.44977619
13	COX15; cytochrome c oxidase assembly protein subunit 15	EYB26_001685	2.589845593
14	QCR7; ubiquinol-cytochrome c reductase subunit 7	EYB26_001262	1.260015214
15	UQCRFS1; ubiquinol-cytochrome c reductase iron-sulfur subunit	EYB26_005972	1.172612672
16	NDUFV2; NADH dehydrogenase	EYB26_001365	2.055303602

	(ubiquinone) flavoprotein 2		
17	NDUFA8; NADH dehydrogenase (ubiquinone) 1 alpha subcomplex subunit 8	EYB26_006738	1.464788918
18	ATPeF1B; F-type H+-transporting ATPase subunit beta	EYB26_006715	1.200165774
19	COX4; cytochrome c oxidase subunit 4	EYB26_006716	2.367776909
20	COX17; cytochrome c oxidase assembly protein subunit 17	EYB26_004826	1.076732069
21	ATPeFG; F-type H+-transporting ATPase subunit g	EYB26_002806	1.383070652
22	ATPeV0E; V-type H+-transporting ATPase subunit e	EYB26_003590	1.657362986
23	ATPeV0C; V-type H+-transporting ATPase 16kDa proteolipid subunit	EYB26_004024	1.022543187
24	QCR8; ubiquinol-cytochrome c reductase subunit 8	EYB26_009990	1.42680194

25	COX7C; cytochrome c oxidase subunit 7c	EYB26_001172	2.053901709
26	ndh; NADH dehydrogenase	EYB26_002689	1.712287034
27	PMA1; H+-transporting ATPase	EYB26_007018	-3.333448711
28	ATPeF0C; F-type H+-transporting ATPase subunit c	EYB26_007962	1.437932956
29	NDUFS2; NADH dehydrogenase (ubiquinone) Fe-S protein 2	EYB26_001977	1.671584533
30	QCR6; ubiquinol-cytochrome c reductase subunit 6	EYB26_005358	2.609036977
31	ATPeV1A; V-type H+-transporting ATPase subunit A	EYB26_004172	1.297651401
32	NDUFV1; NADH dehydrogenase (ubiquinone) flavoprotein 1	EYB26_005326	2.394030718
33	SDHA; succinate dehydrogenase (ubiquinone) flavoprotein subunit	EYB26_009824	1.350863574

34	COX5A; cytochrome c oxidase subunit 5a	EYB26_004132	2.203499808
35	NDUFS7; NADH dehydrogenase (ubiquinone) Fe-S protein 7	EYB26_001293	1.771755492
36	ATPeV1H; V-type H+-transporting ATPase subunit H	EYB26_005452	1.469428354
37	NDUFB7; NADH dehydrogenase (ubiquinone) 1 beta subcomplex subunit 7	EYB26_000359	2.445641372
38	ATPeFH; F-type H+-transporting ATPase subunit h	EYB26_000168	1.251497321
39	ATPeV0B; V-type H+-transporting ATPase 21kDa proteolipid subunit	EYB26_002147	1.124455849
40	COX11; cytochrome c oxidase assembly protein subunit 11	EYB26_007312	1.83976441
41	COX6B; cytochrome c oxidase subunit 6b	EYB26_006277	2.487947703
42	ATPeF1D; F-type H+-transporting ATPase	EYB26_008572	1.280303553

	subunit delta		
43	TIM11; F-type H+-transporting ATP synthase subunit e	EYB26_007711	1.029740051
41	COX6B; cytochrome c oxidase subunit 6b	EYB26_006277	2.487947703
42	ATPeF1D; F-type H+-transporting ATPase subunit delta	EYB26_008572	1.280303553
43	TIM11; F-type H+-transporting ATP synthase subunit e	EYB26_007711	1.029740051
44	NDUFS6; NADH dehydrogenase (ubiquinone) Fe-S protein 6	EYB26_004190	1.577616073
45	SDHD; succinate dehydrogenase (ubiquinone) membrane anchor subunit	EYB26_002738	2.489689474
46	QCR9; ubiquinol-cytochrome c reductase subunit 9	EYB26_005945	1.138518628
47	SDHC; succinate dehydrogenase (ubiquinone) cytochrome b560 subunit	EYB26_003674	5.771029607

48	CYC1; ubiquinol-cytochrome c reductase cytochrome c1 subunit	EYB26_004932	1.621556471
49	ATPeV1F; V-type H+-transporting ATPase subunit F	EYB26_003583	1.331117006
50	PMA1; H+-transporting ATPase	EYB26_004307	-3.904182734
51	NDUFS5; NADH dehydrogenase (ubiquinone) Fe-S protein 5	EYB26_000896	2.597125079
52	NDUFS4; NADH dehydrogenase (ubiquinone) Fe-S protein 4	EYB26_005814	1.891075924
53	ATPeFF; F-type H+-transporting ATPase subunit f	EYB26_005813	1.342083867
54	ATPeV0D; V-type H+-transporting ATPase subunit d	EYB26_000424	1.282706174
55	NDUFA2; NADH dehydrogenase (ubiquinone) 1 alpha subcomplex subunit 2	EYB26_000193	1.327878474
56	ATPeFK; F-type H+-	EYB26_004574	1.144127406

	transporting ATPase subunit k		
57	ppa; inorganic pyrophosphatase	EYB26_009816	1.40484405
58	NDUFS3; NADH dehydrogenase (ubiquinone) Fe-S protein 3	EYB26_002632	1.574430102

Table S2. Differential genes related to fatty acid biosynthesis pathway.

Sequence	Description	Gene ID	Gene_ FC
1	fabG; 3-oxoacyl-[acyl-carrier protein] reductase	EYB26_007596	-1.214559979
2	FAS2; fatty acid synthase subunit alpha, fungi type	EYB26_007410	-1.48387266
3	FAS1; fatty acid synthase subunit beta, fungi type	EYB26_005505	-2.212732207
4	fabF; 3-oxoacyl-[acyl-carrier-protein] synthase II	EYB26_005784	-2.163709367
5	MECR; mitochondrial enoyl-[acyl-carrier protein] reductase / trans-2-enoyl-CoA reductase	EYB26_009154	1.878104867
6	FAS1; fatty acid synthase subunit beta, fungi type	EYB26_007408	-2.971329171
7	fabD; [acyl-carrier-protein] S-malonyltransferase	EYB26_001295	1.191037026
8	fabG; 3-oxoacyl-[acyl-carrier protein] reductase	EYB26_003029	3.334812692
9	ACSL; long-chain acyl-CoA synthetase	EYB26_007004	-1.306451119
10	fabG; 3-oxoacyl- [acyl-carrier protein] reductase	EYB26_004247	7.290608832

Table S3. Diferentially expressed genes and proteins associated with glycolysis.

Sequence	Description	Gene ID	Gene_ FC	Protein ID	Protein _ FC
1	Glucose-6-phosphate isomerase			B6QD47	3.1572
2	phosphoglycerate mutase (2,3-diphosphoglycerate -independent)			B6QQZ2	2.02026
3	Dihydrolipoyl dehydrogenase			B6QDG2	0.25669
4	Pyruvate kinase			B6QLL0	0.22326
5	Glyceraldehyde-3-phosphate dehydrogenase	EYB26_005170	1.846541054	B6QPY8	1.43226
6	Pyruvate decarboxylase	EYB26_000781、EYB26_002404	2.922035078、-2.068083368	B6Q5P1	0.06452
7	Alcohol dehydrogenase,	EYB26_008794、	-3.942344696	B6QUF8	0.29618

	putative	EYB26_009405	` 4.139296221
8	phosphoglucomutase PgmA	EYB26_000179	1.707177
9	aldose 1-epimerase, putative	EYB26_000408	1.134358
10	oxidoreductase, zinc-binding	EYB26_000845	-2.041727056
11	hexokinase Kxk, putative	EYB26_001345	3.365587156
12	phosphoenolpyruvate carboxykinase AcuF	EYB26_001690	-3.204783187
13	triosephosphate isomerase	EYB26_001873	1.078262079
14	hypothetical protein	EYB26_002600	-2.13552
15	glucokinase, putative	EYB26_002848	-3.24747
16	hypothetical protein	EYB26_003128	1.12695
17	hypothetical	EYB26_003829	-2.39076

	protein		
18	phosphoglucomutase, putative	EYB26_004807	1.069974
19	hypothetical protein	EYB26_004953	-1.76248
20	acetate--CoA ligase	EYB26_005323	1.663043
21	Aldehyde dehydrogenase	EYB26_006542	-3.6127
22	possible apospory-associated protein c	EYB26_008017	1.305996
23	aldehyde dehydrogenase, putative	EYB26_008367	-2.71348
24	aldehyde dehydrogenase, putative	EYB26_008793	-3.88531
25	aldose 1-epimerase, putative	EYB26_009058	2.67812
26	pyruvate dehydrogenase E1 beta subunit PdbA, putative	EYB26_009152	1.179216

Table S4. Tricarboxylic acid cycle related dffrentially expressed genes and proteins.

Sequence	Description	Gene ID	Gene_ FC	Protein ID	Protein_ FC
1	Citrate synthase	EYB26_007011	1.426640237	B6QHT1	1.687
2	Succinate--CoA ligase [ADP-forming] subunit beta, mitochondrial			B6QGK4	0.42886
3	Dihydrolipoyl dehydrogenase			B6QDG2	0.25669
4	oxoglutarate dehydrogenase (succinyl-transferring)			B6QQB9	0.42133
5	fumarate hydratase, putative	EYB26_000291	1.720929598		
6	phosphoenolpyruvate carboxykinase AcuF	EYB26_001690	-3.204783187		
7	hypothetical protein	EYB26_002041	1.220148119		
8	ATP citrate lyase subunit (Acl), putative	EYB26_002042	2.365916525		
9	hypothetical protein	EYB26_002600	-2.1355223		
10	succinate dehydrogenase	EYB26_002738	2.489689474		

	subunit CybS, putative isocitrate	
11	dehydrogenase, NAD-dependent NAD(+)-isocitrate	EYB26_002971 1.36606609
12	dehydrogenase subunit I	EYB26_0033662.284234975
13	hypothetical protein	EYB26_0036745.771029607
14	hypothetical protein	EYB26_0043551.806831087
15	hypothetical protein	EYB26_0054691.491683985
16	pyruvate carboxylase, putative	EYB26_0071202.777246306
17	pyruvate dehydrogenase E1 beta subunit PdbA, putative	EYB26_0091521.179215939
18	succinate dehydrogenase subunit Sdh1, putative	EYB26_0098241.350863574