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Transcriptomic Analysis Revealed the Differences in Lipid Accumulation between Spores and Mycelia of *Mucor circinelloides* WJ11 under Solid–State Fermentation

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Table S1. Differential expression of lipid synthesis related genes in Mucor circinelloides WJ11 under solid-state fermentation conditions.

gene abbreviation	Full name of the gene	Genetic code	gene_id	Enhancement(mycelia/spores)	Enhancement(%)	log2(mycelia/spores)
GPAT	glycerol-3-phosphate acyltransferase	EC:2.3.1.15	HMPREF1544_01736	1.731001841	173.1001841	0.518114503
GPAT	glycerol-3-phosphate acyltransferase	EC:2.3.1.15	HMPREF1544_02089	9.335246843	933.5246843	2.430168112
GPAT	glycerol-3-phosphate acyltransferase	EC:2.3.1.15	HMPREF1544_02164	36.47806005	3647.806005	4.291461462
GPAT	glycerol-3-phosphate acyltransferase	EC:2.3.1.15	HMPREF1544_03730	4.7 in mycelia；0 in spores	4.7 in mycelia；0 in spores	8.401263384
GPAT	glycerol-3-phosphate acyltransferase	EC:2.3.1.15	HMPREF1544_09145	0.620504288	62.05042877	-0.233162835
GPAT	glycerol-3-phosphate acyltransferase	EC:2.3.1.15	HMPREF1544_09719	-0.611592272	-61.15922718	-2.287351582
GPAT	glycerol-3-phosphate acyltransferase	EC:2.3.1.15	HMPREF1544_09996	-0.565069185	-56.50691848	-2.115126744
GPAT	glycerol-3-phosphate acyltransferase	EC:2.3.1.15	HMPREF1544_11692	-0.68194225	-68.19422497	-2.565089567
GPAT	glycerol-3-phosphate acyltransferase	EC:2.3.1.15	HMPREF1544_12223	13.78070175	1378.070175	2.936423123
LPAT	lysophospholipid acyltransferase	EC:2.3.1.51	HMPREF1544_00403	0.024558365	2.455836508	-0.883405593
LPAT	lysophospholipid acyltransferase	EC:2.3.1.51	HMPREF1544_00466	-0.397363465	-39.73634652	-1.629121709
LPAT	lysophospholipid acyltransferase	EC:2.3.1.51	HMPREF1544_00966	137.9458333	13794.58333	6.151165982
LPAT	lysophospholipid acyltransferase	EC:2.3.1.51	HMPREF1544_01123	-0.243621519	-24.36215192	-1.323669914
LPAT	lysophospholipid acyltransferase	EC:2.3.1.51	HMPREF1544_01374	0.487555333	48.75553328	-0.4599863
LPAT	lysophospholipid acyltransferase	EC:2.3.1.51	HMPREF1544_02505	6.139689579	613.9689579	1.87302733
LPAT	lysophospholipid acyltransferase	EC:2.3.1.51	HMPREF1544_05477	13.45109135	1345.109135	2.901771808
LPAT	lysophospholipid acyltransferase	EC:2.3.1.51	HMPREF1544_05974	0.014930808	1.493080845	-0.904024085
LPAT	lysophospholipid acyltransferase	EC:2.3.1.51	HMPREF1544_06186	7.171903882	717.1903882	2.085608998
LPAT	lysophospholipid acyltransferase	EC:2.3.1.51	HMPREF1544_08415	0.707052841	70.7052841	0.30075397
LPAT	lysophospholipid acyltransferase	EC:2.3.1.51	HMPREF1544_12268	-0.764839872	-76.48398722	-2.971967053
PAP	phosphatidic acid phosphatase	EC:3.1.3.4	HMPREF1544_00222	55.64285714	5564.285714	4.757564056
PAP	phosphatidic acid phosphatase	EC:3.1.3.4	HMPREF1544_05372	-0.567687707	-56.76877071	-2.131164802
PAP	phosphatidic acid phosphatase	EC:3.1.3.4	HMPREF1544_07197	-0.451335878	-45.13358779	-1.572256722
PAP	phosphatidic acid phosphatase	EC:3.1.3.4	HMPREF1544_09371	0.040977927	4.097792735	-0.842860515
PAP	phosphatidic acid phosphatase	EC:3.1.3.4	HMPREF1544_09902	3.746219592	374.6219592	1.307846661
PAP	phosphatidic acid phosphatase	EC:3.1.3.4	HMPREF1544_11532	0.154088546	15.40885458	-0.50155988
PGAT	phospholipid: diacylglycerol acyltransferase	EC:2.3.1.158	HMPREF1544_10719	-0.362026103	-36.20261032	-1.575613026
PGAT	phospholipid: diacylglycerol acyltransferase	EC:2.3.1.158	HMPREF1544_10950	4.442072377	444.2072377	1.513640046
DGAT1	diacylglycerol acyltransferase 1	EC:2.3.1.20	HMPREF1544_03985	2.88999159	288.999159	1.027811149
DGAT2	diacylglycerol acyltransferase 2	EC:2.3.1.22	HMPREF1544_01075	0.449211402	44.92114021	-0.399881953
DGAT2	diacylglycerol acyltransferase 2	EC:2.3.1.22	HMPREF1544_06754	11.65493497	1165.493497	2.7187595
TLP	triglyceride lipase	EC:3.1.1.3	HMPREF1544_01123	-0.243621519	-24.36215192	-1.323669914

TLP	triglyceride lipase	EC:3.1.1.3	HMPREF1544_04725	2.935590969	293.5590969	1.09245856
TLP	triglyceride lipase	EC:3.1.1.3	HMPREF1544_06186	7.171903882	717.1903882	2.085608998
TLP	triglyceride lipase	EC:3.1.1.3	HMPREF1544_07763	3.278333333	327.8333333	1.170373638
ME	malic enzyme	EC:1.1.1.40	HMPREF1544_00580	-0.756623374	-75.66233739	-2.939867449
ME	malic enzyme	EC:1.1.1.40	HMPREF1544_01783	-0.15173527	-15.17352704	-1.155090604
ME	malic enzyme	EC:1.1.1.40	HMPREF1544_02119	-0.136693256	-13.6693256	-1.104899236
ME	malic enzyme	EC:1.1.1.40	HMPREF1544_06796	9.516831683	951.6831683	2.454332711
G6PDH	glucose-6-phosphate dehydrogenase	EC:1.1.1.49	HMPREF1544_01135	-0.772490608	-77.24906083	-3.058886681
G6PDH	glucose-6-phosphate dehydrogenase	EC:1.1.1.49	HMPREF1544_01557	5.153335346	515.3335346	1.667101273
G6PDH	glucose-6-phosphate dehydrogenase	EC:1.1.1.49	HMPREF1544_04771	22.93455099	2293.455099	3.640419023
PGLS	6-phosphogluconolactonase	EC:3.1.1.31	HMPREF1544_07909	1.300807601	130.0807601	0.270022802
6PGDH	6-phosphogluconate dehydrogenase	EC:1.1.1.44	HMPREF1544_00889	-0.575906835	-57.59068354	-2.156421782
6PGDH	6-phosphogluconate dehydrogenase	EC:1.1.1.44	HMPREF1544_06940	1.849060412	184.9060412	0.580735314
PC	pyruvate carboxylase	EC:6.4.1.1	HMPREF1544_00419	2.231390135	223.1390135	0.757170583
PC	pyruvate carboxylase	EC:6.4.1.1	HMPREF1544_11582	4.010869565	401.0869565	1.37151725
CS	citrate synthase	EC:2.3.3.1	HMPREF1544_06610	-0.600543689	-60.05436893	-2.224410383
CS	citrate synthase	EC:2.3.3.1	HMPREF1544_11917	5.610119048	561.0119048	1.800730846
ACL	ATP: citrate lyase	EC:2.3.3.8	HMPREF1544_02605	-0.454507496	-45.45074959	-1.791977901
ACL	ATP: citrate lyase	EC:2.3.3.8	HMPREF1544_03574	2.901621223	290.1621223	1.044070491
ACS	acetyl-CoA synthetase	EC:6.2.1.1	HMPREF1544_06364	-0.866402116	-86.64021164	-3.816375614
ACS	acetyl-CoA synthetase	EC:6.2.1.1	HMPREF1544_07558	9.39009139	939.009139	2.45723628
ACS	acetyl-CoA synthetase	EC:6.2.1.1	HMPREF1544_10323	1.566258718	156.6258718	1.484645997
ALD	aldehyde dehydrogenase (NAD^+)	EC:1.2.1.3	HMPREF1544_01661	11.60277509	1160.277509	2.72146225
ALD	aldehyde dehydrogenase (NAD^+)	EC:1.2.1.3	HMPREF1544_02814	14.05481481	1405.481481	2.966601892
ALD	aldehyde dehydrogenase (NAD^+)	EC:1.2.1.3	HMPREF1544_06169	2.601762115	260.1762115	0.919024039
ALD	aldehyde dehydrogenase (NAD^+)	EC:1.2.1.3	HMPREF1544_06275	-0.611796413	-61.17964134	-2.277090498
ALD	aldehyde dehydrogenase (NAD^+)	EC:1.2.1.3	HMPREF1544_08128	7.009675019	700.9675019	2.066961255
ALD	aldehyde dehydrogenase (NAD^+)	EC:1.2.1.3	HMPREF1544_08790	3.397260274	339.7260274	1.197628824
ALD	aldehyde dehydrogenase (NAD^+)	EC:1.2.1.3	HMPREF1544_09418	1.571127332	157.1127332	0.275430955
ALD	aldehyde dehydrogenase (NAD^+)	EC:1.2.1.3	HMPREF1544_09978	5.483766234	548.3766234	1.757525209
ALD	aldehyde dehydrogenase (NAD^+)	EC:1.2.1.3	HMPREF1544_10688	16.65004191	1665.004191	3.194504128
PDC	pyruvate decarboxylase	EC:4.1.1.1	HMPREF1544_01842	-0.224433103	-22.44331029	-1.285392436
PDC	pyruvate decarboxylase	EC:4.1.1.1	HMPREF1544_03889	-0.835847828	-83.5847828	-3.507447171
PDC	pyruvate decarboxylase	EC:4.1.1.1	HMPREF1544_09268	19.5	1950	3.257780231
PDC	pyruvate decarboxylase	EC:4.1.1.1	HMPREF1544_11961	-0.722595639	-72.25956387	-2.740283565
PDC	pyruvate decarboxylase	EC:4.1.1.1	HMPREF1544_12198	-0.08836811	-8.836811032	-1.064316986
PDH	pyruvate dehydrogenase	EC:1.2.4.1	HMPREF1544_01270	-0.299761282	-29.97612823	-1.392648477
PDH	pyruvate dehydrogenase	EC:1.2.4.1	HMPREF1544_02638	0.265952726	26.59527261	-0.572743
PDH	pyruvate dehydrogenase	EC:1.2.4.1	HMPREF1544_06537	0.626384673	62.63846726	-0.223050313
DLAT	dihydrolipoamide acetyltransferase	EC:2.3.2.12	HMPREF1544_02101	0.402107995	40.2107995	-0.43526002

DLAT	dihydrolipoamide acetyltransferase	EC:2.3.2.12	HMPREF1544_07382	4.834089436	483.4089436	1.614331641
DLAT	dihydrolipoamide acetyltransferase	EC:2.3.2.12	HMPREF1544_09204	-0.107013793	-10.7013793	-0.598272194
ILVH	acetolactate synthase I/III	EC:2.2.1.6	HMPREF1544_01100	2.311046512	231.1046512	0.794032787
ILVH	acetolactate synthase I/III	EC:2.2.1.6	HMPREF1544_07395	-0.815300593	-81.53005928	-3.393269248
ILVH	acetolactate synthase I/III	EC:2.2.1.6	HMPREF1544_09428	-0.352291193	-35.22911927	-1.553830264
LEUB	3-isopropyl malate dehydrogenase	EC:1.1.1.85	HMPREF1544_09430	39.98271605	3998.271605	4.420365557
ILVA	threonine dehydratase	EC:4.3.1.19	HMPREF1544_00593	-0.91202046	-91.20204604	-4.116526636
ILVA	threonine dehydratase	EC:4.3.1.19	HMPREF1544_00594	-0.44680673	-44.68067297	-1.786577173
ILVA	threonine dehydratase	EC:4.3.1.19	HMPREF1544_07646	-0.673615132	-67.36151322	-2.523538213
ILVA	threonine dehydratase	EC:4.3.1.19	HMPREF1544_08526	3.628802679	362.8802679	1.290118589
ILVA	threonine dehydratase	EC:4.3.1.19	HMPREF1544_10678	11.5787234	1157.87234	2.690683401
ILVC	ketol-acid reductoisomerase	EC:1.1.1.86	HMPREF1544_05426	0.39094624	39.09462401	-0.437327215
ILVC	ketol-acid reductoisomerase	EC:1.1.1.86	HMPREF1544_09429	-0.374954552	-37.49545515	-1.5951981
ILVE	branched-chain amino acid aminotransferase	EC:2.6.1.42	HMPREF1544_06739	-0.792885602	-79.2885602	-3.173147604
ILVE	branched-chain amino acid aminotransferase	EC:2.6.1.42	HMPREF1544_06855	4.844420601	484.4420601	1.512611422
BCK	2-oxoisovalerate dehydrogenase E1	EC:1.2.4.4	HMPREF1544_00636	2.994673295	299.4673295	0.782406934
BCK	2-oxoisovalerate dehydrogenase E1	EC:1.2.4.4	HMPREF1544_08340	14.72836538	1472.836538	3.027775708
BCK	2-oxoisovalerate dehydrogenase E1	EC:1.2.4.4	HMPREF1544_08341	1.652814308	165.2814308	0.471599735
BCK	2-oxoisovalerate dehydrogenase E1	EC:1.2.4.4	HMPREF1544_12114	-0.507579369	-50.75793689	-1.999363439
DBT	2-oxoisovalerate dehydrogenase E2	EC:2.3.1.168	HMPREF1544_03161	9.276923077	927.6923077	2.414393374
DBT	2-oxoisovalerate dehydrogenase E2	EC:2.3.1.168	HMPREF1544_11251	7.057296329	705.7296329	2.074150599
ACD	acyl-CoA dehydrogenase	EC:1.3.8.7	HMPREF1544_02538	12.1622248	1216.22248	2.775576987
ACD	acyl-CoA dehydrogenase	EC:1.3.8.7	HMPREF1544_03079	-0.002669903	-0.266990291	-1.123464425
ACD	acyl-CoA dehydrogenase	EC:1.3.8.7	HMPREF1544_07125	12.09901639	1209.901639	2.748241687
ACD	acyl-CoA dehydrogenase	EC:1.3.8.7	HMPREF1544_12381	7.400098851	740.0098851	2.127173913
ECH	enoyl-CoA hydratase	EC:4.2.1.17	HMPREF1544_01125	13.6 in mycelia;0 in spores	#VALUE!	5.274292358
ECH	enoyl-CoA hydratase	EC:4.2.1.17	HMPREF1544_02405	5.915964473	591.5964473	1.857165727
ECH	enoyl-CoA hydratase	EC:4.2.1.17	HMPREF1544_11003	3.23539823	323.539823	1.147809181
HCD	3-hydroxyacyl-CoA dehydrogenase	EC:1.1.1.35	HMPREF1544_04229	3.358844399	335.8844399	1.179100058
HCD	3-hydroxyacyl-CoA dehydrogenase	EC:1.1.1.35	HMPREF1544_06760	23.55581761	2355.581761	3.673359481
ACA	acetyl-CoA acyltransferase	EC:2.3.1.16	HMPREF1544_02136	4.093661022	409.3661022	1.41851716
ACA	acetyl-CoA acyltransferase	EC:2.3.1.16	HMPREF1544_02346	-0.849067399	-84.9067399	-3.646994549
ACA	acetyl-CoA acyltransferase	EC:2.3.1.16	HMPREF1544_03442	-0.641282565	-64.12825651	-2.417596292
ACA	acetyl-CoA acyltransferase	EC:2.3.1.16	HMPREF1544_06137	7.627230602	762.7230602	2.166434623
ACA	acetyl-CoA acyltransferase	EC:2.3.1.16	HMPREF1544_06878	0.496009122	49.6009122	-0.304754015
HMGCL	hydroxymethylglutaryl-CoA lyase	EC:4.1.3.4	HMPREF1544_03756	34.1 in mycelia;0 in spores	1021.8	9.608756647

AUH	methylglutaconyl-CoA hydratase	EC:4.2.1.18	HMPREF1544_01125	71.83928571	7183.928571	5.274292358
AUH	methylglutaconyl-CoA hydratase	EC:4.2.1.18	HMPREF1544_03261	4.475990774	447.5990774	1.522229364
AUH	methylglutaconyl-CoA hydratase	EC:4.2.1.18	HMPREF1544_11003	3.23539823	323.539823	1.147809181
MCL	3-methylcrotonyl-CoA carboxylase	EC:6.4.1.4	HMPREF1544_00936	3.233868695	323.3868695	0.930749443
MCL	3-methylcrotonyl-CoA carboxylase	EC:6.4.1.4	HMPREF1544_01036	1.530332681	153.0332681	0.404170279
MCL	3-methylcrotonyl-CoA carboxylase	EC:6.4.1.4	HMPREF1544_05511	3.76519337	376.519337	1.316571725
MCL	3-methylcrotonyl-CoA carboxylase	EC:6.4.1.4	HMPREF1544_05527	17	1700	3.212844849
MCL	3-methylcrotonyl-CoA carboxylase	EC:6.4.1.4	HMPREF1544_08287	1.64889336	164.889336	0.46012037
MCL	3-methylcrotonyl-CoA carboxylase	EC:6.4.1.4	HMPREF1544_09819	29.48214286	2948.214286	4.118545486
IVD	isovaleryl-CoA dehydrogenase	EC:1.3.8.4	HMPREF1544_02538	12.1622248	1216.22248	2.775576987
IVD	isovaleryl-CoA dehydrogenase	EC:1.3.8.4	HMPREF1544_03419	6.196384552	619.6384552	1.831440858
IVD	isovaleryl-CoA dehydrogenase	EC:1.3.8.4	HMPREF1544_10237	6.534774298	653.4774298	1.956213283
IVD	isovaleryl-CoA dehydrogenase	EC:1.3.8.4	HMPREF1544_10947	1.822338831	182.2338831	0.505215991
LEU1	3-isopropyl malate dehydratase	EC:4.2.1.33	HMPREF1544_05400	4.182835821	418.2835821 0	1.444604209
PKA	protein kinase A	EC:2.7.11.11	HMPREF1544_00317	-0.502800417	-50.28004172	-1.95283579
PKA	protein kinase A	EC:2.7.11.11	HMPREF1544_01201	-0.686880865	-68.68808645	-2.565352151
PKA	protein kinase A	EC:2.7.11.11	HMPREF1544_02342	-0.327034369	-32.70343687	-1.478453918
PKA	protein kinase A	EC:2.7.11.11	HMPREF1544_03325	16.30639731	1630.639731	3.165804504
PKA	protein kinase A	EC:2.7.11.11	HMPREF1544_04698	-0.731829893	-73.18298928	-2.811132122
PKA	protein kinase A	EC:2.7.11.11	HMPREF1544_04825	-0.530509159	-53.05091595	-2.660088126
PKA	protein kinase A	EC:2.7.11.11	HMPREF1544_04849	-0.475082018	-47.50820184	-1.848410951
PKA	protein kinase A	EC:2.7.11.11	HMPREF1544_06128	2.928104575	292.8104575	1.039783711
PKA	protein kinase A	EC:2.7.11.11	HMPREF1544_07170	9.649541284	964.9541284	2.496664164
PKA	protein kinase A	EC:2.7.11.11	HMPREF1544_10628	3.544871795	354.4871795	1.100136059
PKA	protein kinase A	EC:2.7.11.11	HMPREF1544_11107	4.282662765	428.2662765	1.433068903
PKA	protein kinase A	EC:2.7.11.11	HMPREF1544_11661	1.450331126	145.0331126	0.351463809
ATG1	protein kinase autophagy-related 1	EC:2.7.11.1	HMPREF1544_03591	0.092860244	9.28602444	-0.80322301
ATG1	protein kinase autophagy-related 1	EC:2.7.11.1	HMPREF1544_08653	11.01006036	1101.006036	2.65766523
ATG1	protein kinase autophagy-related 1	EC:2.7.11.1	HMPREF1544_11378	0.327483242	32.74832419	-0.256279196
ATG13	protein kinase autophagy-related 13		HMPREF1544_04164	1.551307847	155.1307847	0.419380751
ATG13	protein kinase autophagy-related 13		HMPREF1544_04405	6.5056926	650.56926	1.773981801
ATG13	protein kinase autophagy-related 13		HMPREF1544_04406	2.252525253	225.2525253	0.739776993
ATG13	protein kinase autophagy-related 13		HMPREF1544_06371	15.2 in mycelia; 0 in spores	#VALUE!	7.500548018
SNF1	carbon catabolite-derepressing protein kinase	EC:2.7.11.1	HMPREF1544_01004	200.7090909	20070.90909	6.634167356
SNF1	carbon catabolite-derepressing protein kinase	EC:2.7.11.1	HMPREF1544_01116	8.414826498	841.4826498	2.305396582

SNF1	carbon catabolite-derepressing protein kinase	EC:2.7.11.1	HMPREF1544_01487	7.016304348	701.6304348	2.083439116
SNF1	carbon catabolite-derepressing protein kinase	EC:2.7.11.1	HMPREF1544_01647	0.369296837	36.92968369	-0.463770973
SNF1	carbon catabolite-derepressing protein kinase	EC:2.7.11.1	HMPREF1544_02155	191.6923077	19169.23077	6.57237894
SNF1	carbon catabolite-derepressing protein kinase	EC:2.7.11.1	HMPREF1544_02297	-0.830630184	-83.06301845	-3.480086626
SNF1	carbon catabolite-derepressing protein kinase	EC:2.7.11.1	HMPREF1544_04133	108.0869565	10808.69565	5.795777801
SNF1	carbon catabolite-derepressing protein kinase	EC:2.7.11.1	HMPREF1544_04244	122.6111111	12261.11111	5.811940166
SNF1	carbon catabolite-derepressing protein kinase	EC:2.7.11.1	HMPREF1544_04361	3.072073841	307.2073841	1.088690867
SNF1	carbon catabolite-derepressing protein kinase	EC:2.7.11.1	HMPREF1544_04576	20.18616145	2018.616145	3.469854015
SNF1	carbon catabolite-derepressing protein kinase	EC:2.7.11.1	HMPREF1544_04691	16.48529412	1648.529412	3.189134491
SNF1	carbon catabolite-derepressing protein kinase	EC:2.7.11.1	HMPREF1544_06278	18.97777778	1897.777778	3.34651742
SNF1	carbon catabolite-derepressing protein kinase	EC:2.7.11.1	HMPREF1544_06667	26.26356589	2626.356589	3.781689423
SNF1	carbon catabolite-derepressing protein kinase	EC:2.7.11.1	HMPREF1544_08086	26.07104796	2607.104796	3.815114697
SNF1	carbon catabolite-derepressing protein kinase	EC:2.7.11.1	HMPREF1544_09019	-0.6100584	-61.00583996	-2.28940669
SNF1	carbon catabolite-derepressing protein kinase	EC:2.7.11.1	HMPREF1544_09491	-0.41762482	-41.76248197	-1.697645235
SNF1	carbon catabolite-derepressing protein kinase	EC:2.7.11.1	HMPREF1544_10763	0.273638968	27.36389685	-0.555928184
SCH9	serine/threonine protein kinase SCH9	EC:2.7.11.1	HMPREF1544_00573	-0.815412304	-81.54123041	-3.311050161
SCH9	serine/threonine protein kinase SCH9	EC:2.7.11.1	HMPREF1544_07572	47.13333333	4713.333333	4.637095819
SCH9	serine/threonine protein kinase SCH9	EC:2.7.11.1	HMPREF1544_10158	40.45762712	4045.762712	4.376417246
SCH9	serine/threonine protein kinase SCH9	EC:2.7.11.1	HMPREF1544_10452	2.139215686	213.9215686	0.732460059
LSB1/2	serine palmitoyltransferase	EC:2.3.1.50	HMPREF1544_05570	-0.156516636	-15.65166358	-1.161490973
LSB1/2	serine palmitoyltransferase	EC:2.3.1.50	HMPREF1544_07031	-0.651667403	-65.16674028	-2.437836327
LSB1/2	serine palmitoyltransferase	EC:2.3.1.50	HMPREF1544_11034	-0.565883669	-56.58836689	-2.12619394
LSB1/2	serine palmitoyltransferase	EC:2.3.1.50	HMPREF1544_12202	1.752292243	175.2292243	0.542511011
LST8	the target of rapamycin complex subunit LST8		HMPREF1544_09127	1.502566127	150.2566127	0.387499507

TOR	serine/threonine-protein kinase mTOR	EC:2.7.11.1	HMPREF1544_01651	-0.31959498	-31.959498	-1.485070764
TOR	serine/threonine-protein kinase mTOR	EC:2.7.11.1	HMPREF1544_03490	-0.435008666	-43.50086655	-1.761143934
TOR	serine/threonine-protein kinase mTOR	EC:2.7.11.1	HMPREF1544_05621	-0.015519568	-1.551956815	-0.961576429
TOR	serine/threonine-protein kinase mTOR	EC:2.7.11.1	HMPREF1544_11471	0.548174048	54.81740482	-0.305911619
RIM15	serine/threonine-protein kinase RIM15	EC:2.7.11.1	HMPREF1544_00624	-0.103983597	-10.3983597	-1.089465738
RIM15	serine/threonine-protein kinase RIM15	EC:2.7.11.1	HMPREF1544_08964	1.805471125	180.5471125	0.538825448
MSN2/4	zinc finger protein MSN2/4		HMPREF1544_06612	41.515625	4151.5625	4.491957414
MSN2/4	zinc finger protein MSN2/4		HMPREF1544_09737	9.397959184	939.7959184	2.391041927
MSN2/4	zinc finger protein MSN2/4		HMPREF1544_10654	-0.060135161	-6.013516093	-0.986069949
UME6	transcriptional regulatory protein UME6		HMPREF1544_07834	16.0790378	1607.90378	3.144066949
UME6	transcriptional regulatory protein UME6		HMPREF1544_10618	0.398226864	39.82268642	-0.440698776
ATG8	protein kinase autophagy-related 8		HMPREF1544_01982	-0.362217267	-36.22172666	-1.570582057
ATG8	protein kinase autophagy-related 8		HMPREF1544_11186	3.73565528	373.565528	1.310390039

Figure S1. Establishment of *Mucor circinelloides* WJ11 under solid-state fermentation condition.

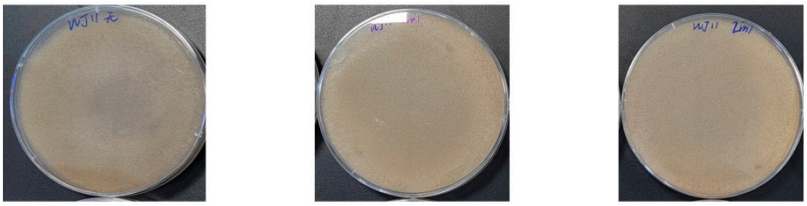


Figure S2. Wayne plot of DEGs between spores and mycelia under solid-state fermentation.

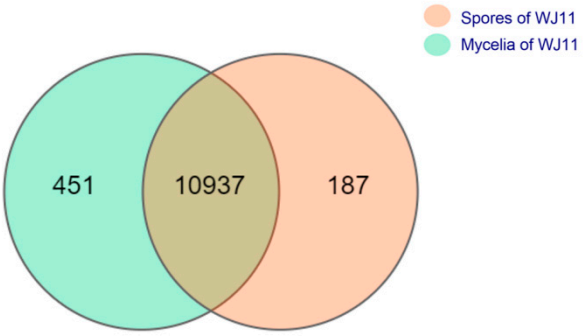


Figure S3. Differential gene GO enrichment histogram between spores and mycelia of *Mucor circinelloides* WJ11 under solid-state fermentation.

