

Table S2. Differentially expressed genes screened out by transcriptome sequencing under acid stress.

Original geneID	New geneID	geneLength	K-Express	1-Express	Express	CK-FPKM	T1-FPKM	Ratio(T1/	P-value	FDR	GG Orthol	Component	Function	GO Process	Blast nr
Ldb1956	LDB_RS08505	330	1	26	0.69	17.66	4.677452	2.62E-07	4.32E-07	-	-	-	-	-	-
Ldb0606	LDB_RS02620	558	1610	23170	613.81	8682.24	3.8222032	0	0	-	-	-	-	-	-
Ldb1239	LDB_RS05285	2289	2557	35653	220.74	3029.95	3.778874	0	0	∫T_11322	-	-	-	-	per-exporting P-type ATPase A [Beauveria bassiana D1-5]
Ldb1595	LDB_RS06880	246	11	111	10.87	107.4	3.3045701	6.82E-22	1.55E-21	-	-	-	-	-	-
Ldb0095	LDB_RS03070	856	1243	10807	297.7	2545.92	3.096256	0	0	∫mgr:MG	-	-	-	-	lyoxal reductase [Lichtheimia corymbifera [JRC:FSU:9682]
Ldb1039	LDB_RS04545	519	197	1491	81.36	605.15	2.8949012	6.16E-242	5.09E-241	-	-	-	-	-	-
Ldb1915	LDB_RS08325	750	837	5825	231.44	1584.03	2.7748895	0	0	-	-	-	-	-	-
Ldb1914	LDB_RS08325	444	246	1579	120.98	762.76	2.6564606	7.95E-234	6.46E-233	-	-	-	-	-	-
Ldb0144	LDB_RS05885	381	58	341	33.96	196.03	2.5291661	3.55E-49	1.12E-48	-	-	-	-	-	-
Ldb1095	LDB_RS10060	1470	86.5	474	11.78	63.53	2.4310985	6.46E-65	2.33E-64	-	-	-	-	-	rate reductase flavoprotein subunit [Beauveria bassiana D1-5]
Ldb1112	LDB_RS10075	1470	86.5	474	11.78	63.53	2.4310985	6.46E-65	2.32E-64	-	-	-	-	-	rate reductase flavoprotein subunit [Beauveria bassiana D1-5]
Ldb0262	LDB_RS01085	366	2228	12038	1366.57	7247.83	2.4069898	0	0	-	-	-	-	-	-
Ldb2020	LDB_RS08785	474	94.28	495.84	43.08	222.59	2.3692986	1.28E-65	4.68E-65	-	-	-	-	-	4/Chemotaxis protein LafT [Beauveria bassiana D1-5]
malG	LDBND_0175	807	34	167	8.69	41.99	2.2726177	4.54E-22	1.03E-21	-	-	-	-	-	ansport system permease protein malG [Beauveria bassiana D1-5]
pmi	LDB_RS0230	963	522	2529	110.62	527.24	2.2528476	6.00E-308	5.60E-307	-	-	-	-	-	protein YPEUBRA_SCAF23g01578 [Pseudozyma brasiliensis CHG001]
Ldb1968	LDB_RS08560	990	77	371	15.85	75.12	2.2447142	1.77E-46	5.49E-46	-	-	-	-	-	-
Ldb0057	LDB_RS02225	357	51	220	32.2	136.33	2.0819705	7.63E-26	1.84E-25	-	-	-	-	-	-
Ldb0063	LDB_RS00250	603	47	199.72	16.46	68.75	2.0623954	3.71E-23	8.59E-23	-	-	-	-	-	-
Ldb0143	LDB_RS00580	336	65	270	44.05	179.56	2.0272521	2.28E-30	5.92E-30	-	-	-	-	-	-
usp1	LDBND_0649	462	1204	4987	566.19	2303.9	2.0247199	0	0	-	-	-	-	-	-
Ldb0289	LDB_RS01180	426	1677	6803	864.27	3443.44	1.9942965	0	0	∫CCIG_05	-	-	-	-	2/Hsp42p [Rhizophagus irregularis DAOM 197198w]
Ldb1597	LDB_RS06890	369	1530	5821	929.61	3471.83	1.9009988	0	0	-	-	-	-	-	-
Ldb1548	LDB_RS06685	366	33	125	20.24	75.26	1.894674	1.06E-13	2.07E-13	-	-	-	-	-	-
Ldb1598	LDB_RS06895	420	1306	4603	684	2367.61	1.7913632	0	0	-	-	-	-	-	8/Tmnm related protein [Saccharomyces cerevisiae]
ppx	LDB_RS02235	1512	412	1438	54.49	187.18	1.7803629	1.23E-129	7.26E-129	-	-	-	-	-	-
Ldb1790	LDB_RS07770	306	11	37	8.33	27.48	1.7219936	0.0001745	0.0002569	-	-	-	-	-	-
Ldb1651	LDB_RS07140	441	35	116	17.34	56.47	1.7033807	2.93E-11	5.46E-11	-	-	-	-	-	-
Ldb1902	LDB_RS08265	447	163	535	79.55	256.49	1.6889687	4.66E-46	1.42E-45	-	-	-	-	-	-
Ldb2158	LDB_RS09405	1815	11002	35145	1205.09	3789.19	1.6527486	0	0	27038g C	-	-	-	-	9826e-51/YALI02D7038p [Yarrowia lipolytica]
Ldb0782	LDB_RS10750	141	25	79	51.76	159.22	1.621112	1.04E-07	1.75E-07	-	-	-	-	-	-
Ldb1300	LDB_RS05555	855	121	370	29.09	87.49	1.5885948	9.70E-30	2.51E-29	-	-	-	-	-	protein BATDEDRAFT_93072 [Batrachytrium dendrobatidis JAM81]
Ldb1145	LDB_RS04910	1941	257	774	26.27	77.89	1.5680219	3.17E-59	1.12E-58	-	-	-	-	-	-
Ldb0123	LDB_RS00495	837	22	66	5.41	15.96	1.5607602	2.67E-06	4.24E-06	-	-	-	-	-	-
Ldb0526	LDB_RS02250	324	173	505	122.38	350.49	1.5180055	1.16E-37	3.26E-37	-	-	-	-	-	-
Ldb1355	LDB_RS05810	237	201	563	208.03	570.6	1.4556882	1.70E-39	4.87E-39	-	-	-	-	-	-
Ldb1640	LDB_RS07105	279	222	619	187.85	513.48	1.450727	5.58E-43	1.66E-42	-	-	-	-	-	-
Ldb1767	LDB_RS07675	183	40	111	57.83	156.77	1.4387595	7.52E-09	1.31E-08	-	-	-	-	-	-
Ldb1599	LDB_RS06900	852	2062	5295	497.55	1256.73	1.3367613	0	0	-	-	-	-	-	Potassium efflux system KefA [Beauveria bassiana D1-5]
glmS	LDB_RS02110	1812	6234	15850	684	1711.79	1.3234375	0	0	ne-fructos	-	-	-	-	ructose-6-phosphate aminotransferase [Nematocida parisii ERTm3]
Ldb1711	LDB_RS07405	852	722	1834	174.21	435.29	1.3211494	3.57E-107	1.82E-106	-	-	-	-	-	-
Ldb0324	LDB_RS01340	267	101	255	90.17	223.12	1.3071004	3.79E-16	7.88E-16	-	-	-	-	-	-
Ldb1963	LDB_RS08540	843	6181	15220	1508.4	3653.38	1.2762128	0	0	-	-	-	-	-	-
Ldb0641	LDB_RS02765	885	1160	2852	268.82	650.14	1.2741099	1.18E-156	7.92E-156	-	-	-	-	-	protein BATDEDRAFT_93175 [Batrachytrium dendrobatidis JAM81]
Ldb1886	LDB_RS01885	861	636	1554	151.76	364.74	1.2650768	2.63E-85	1.16E-84	-	-	-	-	-	-
pepD2	LDB_RS08995	1401	1169	2756	167.33	388.23	1.2142155	1.79E-140	1.11E-139	-	-	-	-	-	57e-10/peptidase U34 [Magnaporthe oryzae Y34]
Ldb0640	LDB_RS02760	570	661	1503	246.18	550.21	1.1602688	2.21E-72	8.60E-72	-	-	-	-	-	-
glnH2	LDBND_0464	846	2445	5414	594.42	1294.67	1.1230299	1.85E-242	1.54E-241	-	-	-	-	-	amine-binding periplasmic protein [Beauveria bassiana D1-5]
glnP	LDBND_0663	669	2546	5571	796.31	1713.24	1.1053252	2.25E-243	1.88E-242	-	-	-	-	-	rate transport system permease protein in glnK [Beauveria bassiana D1-5]
Ldb1885	LDB_RS01810	804	493	1077	126.54	271.9	1.1034827	2.13E-48	6.70E-48	-	-	-	-	-	1/hydrolase fold-3 domain protein [Aspergillus kawachii IFO 4308]
glnA	LDB_RS06340	1338	12612	27410	1893.67	4050.14	1.0967868	0	0	C_059871g	-	-	-	-	-62/Glutamine synthetase [Beauveria bassiana D1-5]
glnH1	LDB_RS02215	840	4164	8816	1020.04	2124.21	1.0583007	0	0	-	-	-	-	-	amine-binding periplasmic protein [Beauveria bassiana D1-5]
Ldb1710	LDB_RS07400	561	784	1658	297.14	617.64	1.0556234	1.12E-68	4.20E-68	-	-	-	-	-	-
glnM	LDBND_0462	642	2345	4884	766.95	1570.47	1.033992	6.31E-192	4.72E-191	-	-	-	-	-	0/D-cysteine desulfhydrase [Beauveria bassiana D1-5]
Ldb1263	LDB_RS05380	1185	2574	5301	438.65	888.91	1.0189671	7.24E-203	5.50E-202	∫T_127711	-	-	-	-	atative aminotransferase YfdZ [Beauveria bassiana D1-5]
pox1	LDB_RS09670	1851	2398	53848	257.41	568.58	4.4661822	0	0	∫lacetolac	-	-	-	-	5/Pyruvate dehydrogenase [Beauveria bassiana D1-5]
fumC	LDB_RS01000	1404	2473	14684	353.2	2063.93	2.5468368	0	0	∫776g fum24 intrace24 catalyt	-	-	-	-	[Putative Fumarase [Absidia idahoensis var. thermophila]
citT	LDB_RS09095	1419	3230	17105	456.25	2377.86	2.3817673	0	0	-	-	-	-	-	L-traitrate/succinate antiporter [Beauveria bassiana D1-5]
pyrE	LDB_RS06615	624	1041	2742	351.16	909.35	1.3727072	6.51E-169	4.54E-168	∫C orotat	-	-	-	-	sphoribosyl transferase [Trichosporon asahii var. asahii CBS 2479]
pyrF	LDB_RS06610	723	851	2030	244.77	574.18	1.2300763	3.14E-106	1.59E-105	-	-	-	-	-	Uncharacterized protein ycm [Beauveria bassiana D1-5]
Ldb1893	LDB_RS08220	246	0	14	0.001	13.55	13.726005	6.83E-05	0.0001024	-	-	-	-	-	-
Ldb1234	LDB_RS05270	180	3	32	4.43	46.19	3.3822019	2.85E-07	4.67E-07	-	-	-	-	-	-
groES	LDB_RS06995	285	627	4280	517.05	3460.43	2.7425756	0	0	∫137e-1317	-	-	-	-	rotein BOTBODRAFT_122058 [Botryobasidium botrysosum FD-172 SS1]
groEL	LDB_RS06990	1614	16666	112415	2060.34	13678.34	2.7309388	0	0	∫ngl:MGL_	005488 biur	-	-	-	proteinin BOTBODRAFT_122070, partial [Botryobasidium botrysosum FD-172 SS1]
mscL	LDB_RS01315	477	81	547	36.75	243.83	2.7300595	1.33E-84	5.80E-84	∫large cc	-	-	-	-	protein BATDEDRAFT_34461 [Batrachytrium dendrobatidis JAM81]
Ldb0482	LDB_RS02060	651	297	1881	95.68	595.79	2.6385146	5.99E-276	5.32E-275	-	-	-	-	-	9/Universal stress protein E [Beauveria bassiana D1-5]
Ldb0568	Ldb0568	249	3	19	2.92	18.11	2.6327463	0.0005555	0.0008006	-	-	-	-	-	-
Ldb0848	LDB_RS03720	705	199	1231	58.81	357.76	2.6048587	1.11E-178	7.91E-178	-	-	-	-	-	-
Ldb1266	LDB_RS05395	696	37	223	11.09	65.71	2.5668536	3.38E-33	9.08E-33	-	-	-	-	-	-
Ldb0659	LDB_RS02850	375	32	192	19.08	112.41	2.5586373	1.03E-28	2.63E-28	-	-	-	-	-	-
fruK	LDB_RS08890	915	3488	20283	780.24	4463.31	2.5161241	0	0	-	-	-	-	-	Uncharacterized protein yniA [Beauveria bassiana D1-5]
Ldb0759	LDB_RS03340	1350	9106	50858	1354.62	7445.46	2.4584728	0	0	∫idihydrol	-	-	-	-	al protein HMPREF1541_03883 [Cyphellophora europaea CBS 101466]
Ldb2143	LDB_RS09345	390	1882	10515	1072.77	5884.94	2.4556689								



Ldb1591	LDB_RS06860	1431	985	2139	137.93	294.77	1.0956534	3.52E-93	1.67E-92	AN5939.21	-	-	-	protein BATDEDRAFT_28917 [Batrachochytrium dendrobatidis JAM81]
rpoZ	LDB_RS06070	222	487	1055	547.46	1160.77	1.0842567	1.23E-46	3.81E-46	-	-	-	-	-
Ldb1589	LDB_RS06850	771	790	1697	212.07	448.03	1.0790548	1.23E-72	4.81E-72	g531914-ni	-	-	-	thetical protein RO3G_08703 [Rhizopus delemar RA 99-880]
Ldb1432	LDB_RS06160	357	703	1513	443.84	937.58	1.0789021	3.21E-65	1.17E-64	-	-	-	-	nyl-diaminopimelate desuccinylase [Beauveria bassiana D1-5]
Ldb0208	LDB_RS00875	1401	3200	6840	458.04	963.54	1.072871	7.94E-284	7.19E-283	-	-	-	-	-
Ldb1984	LDB_RS08625	888	295	629	68.12	142.87	1.0685527	1.42E-27	3.57E-27	-	-	-	-	-
Ldb1632	LDB_RS07065	237	393	841	406.74	852.35	1.0673391	1.37E-36	3.83E-36	-	-	-	-	-
Ldb2045	LDB_RS008910	1209	1217	2578	203.1	423.34	1.0596266	3.89E-106	1.97E-105	n:AFUA_6	-	-	-	24/putative protease yegQ [Beauveria bassiana D1-5]
Ldb0044	LDB_RS00175	2766	983	2080	69.95	145.71	1.0587039	8.61E-86	3.82E-85	tion enzym	-	-	-	AD box family helicase [Schizosaccharomyces japonicus yFS275]
Ldb2093	LDB_RS09135	813	136	288	34.5	71.85	1.0583918	2.85E-13	5.53E-13	-	-	-	-	M3e-19/KLTH0D13992p [Lachancea thermotolerans]
truB	LDB_RS05685	897	584	1235	133.42	277.54	1.0567208	1.32E-51	4.30E-51	81tRNA p	-	-	-	cal protein LRAMOSA00334 [Absidia idahoensis var. thermophila]
Ldb2188	LDB_RS09535	372	138	292	83.06	172.54	1.0547051	2.05E-13	3.99E-13	-	-	-	-	-
Ldb1797	LDB_RS07805	363	46	97	28.49	58.96	1.0492809	2.61E-05	4.01E-05	-	-	-	-	-
htrA	LDB_RS00570	1284	4309	9039	675.34	1394.09	1.0456378	0	0	-	-	-	-	protein BATDEDRAFT_24209 [Batrachochytrium dendrobatidis JAM81]
Ldb0677	LDB_RS02935	732	9340	19571	2650.95	5462.58	1.043073	0	0	-	-	-	-	52/Aspartate-tRNA ligase [Beauveria bassiana D1-5]
Ldb1691	LDB_RS07310	525	118	247	48.12	98.98	1.0405004	2.51E-11	4.68E-11	12381ADP-	-	-	-	9/MutT/nudix family protein [Cordyceps militaris CM01]
glpQ	LDB_RS08360	693	1303	2724	392.3	806.43	1.039592	7.92E-109	4.10E-108	rophosph	-	-	-	protein BATDEDRAFT_28907 [Batrachochytrium dendrobatidis JAM81]
Ldb1151	LDB_RS04940	309	38	79	28.44	57.99	1.0278827	0.000191	0.0002801	095g1aden	-	-	-	ferase and sulfurtransferase UBA4 [Ogataea parapolyomorpha DL-1]
Ldb0341	LDB_RS01420	2691	8452	17491	618.51	1260.14	1.0267152	0	0	3.6.3.2}K	-	-	-	24//catalyt
Ldb1732	LDB_RS07515	936	6187	12797	1351.14	2749.24	1.0248557	0	0	-	-	-	-	-transporting ATPase, P-type 1 [Beauveria bassiana D1-5]
Ldb1553	LDB_RS06700	1548	7908	16291	1020.75	2069.61	1.0197294	0	0	-	-	-	-	-
hisS	LDB_RS03900	1287	2463	5070	385.08	780.05	1.0184084	6.64E-194	5.00E-193	9601histid	-	-	-	82/Histidine-tRNA ligase [Beauveria bassiana D1-5]
Ldb0697	LDB_RS03025	1005	601	1237	121.75	246.54	1.0179	1.05E-48	3.31E-48	-	-	-	-	e-25/beta-lactamase [Moniliophthora roeri MCA 2997]
ilvE	LDB_RS05575	1026	2511	5168	497.73	1007.85	1.0178457	1.53E-197	1.16E-196	nched-cha	-	-	-	hain amino acid aminotransferase [Rhizopus delemar RA 99-880]
Ldb1684	LDB_RS07280	1026	158	325	31.32	63.38	1.0169434	6.13E-14	1.21E-13	-	-	-	-	-
Ldb1985	LDB_RS08630	3648	1549	3176	83.19	167.94	1.0134639	4.15E-121	2.36E-120	-	-	-	-	alar protein transport protein USO1 [Kluyveromyces marxianus]
Ldb2070	LDB_RS09300	1059	97	199	18.6	37.54	1.013126	4.92E-09	8.62E-09	-	-	-	-	-
Ldb0720	LDB_RS03140	1305	2072	4244	319.3	643.6	1.0112518	8.67E-161	5.91E-160	ECHADR/	-	-	-	tical protein S40288_00663 [Stachybotrys chartarum IBT 40288]
Ldb0331	LDB_RS01375	711	104	213	30.46	61.34	1.0099122	1.53E-09	2.71E-09	12171.61pt	-	-	-	protein BATDEDRAFT_10172 [Batrachochytrium dendrobatidis JAM81]
Ldb1301	LDB_RS05560	2259	1546	3155	135.28	271.77	1.0064376	5.09E-119	2.83E-118	137361H-t	-	-	-	tical protein MVEG_06061 [Mortierella verticillata NRRL 6337]
Ldb1357	LDB_RS05820	849	2926	5975	708.68	1423.45	1.0061856	6.12E-224	4.84E-223	-	-	-	-	cal protein CGLQ_13827 [Colletotrichum gloeosporioides Cg-14]
ppc	LDB_RS02135	2730	6118	12475	441.19	885.68	1.0053854	0	0	-	-	-	-	osphoenolpyruvate carboxylase [Beauveria bassiana D1-5]
Ldb1803	LDB_RS07835	1224	272.16	554.59	44.83	89.9	1.0038566	3.29E-22	7.53E-22	-	-	-	-	-
Ldb0364	LDB_RS01535	243	46	94	46.14	92.35	1.001094	6.54E-05	9.82E-05	-	-	-	-	-



rpsB	LDB_RS05760	762	26185	11767	7118.35	3145.94	-1.178052	0	0	B01254g s	-	-	-	stical protein NDA1_0A03840 [Naumovozyma dairenensis CBS 421]
Ldb0644	LDB_RS02780	486	2256	1030	1002.41	449.67	-1.156534	6.26E-108	3.21E-107	-	-	-	-	-
Ldb0539	LDB_RS02315	1293	1563	728	243.19	111.47	-1.125428	2.02E-72	7.87E-72	18971 ami	-	-	-	stical protein MVEG_06206 [Mortierella verticillata NRRL 6337]
typA	LDB_RS03360	1848	13267	6184	1426.49	654.49	-1.124027	0	0	6 2 2e-29	-	-	-	GTP-binding protein typA/BipA [Beauveria bassiana D1-5]
rimM	LDB_RS05880	504	470	220	200.54	92.24	-1.120426	9.90E-23	2.29E-22	-	-	-	-	(guanine-N(1))-methyltransferase [Beauveria bassiana D1-5]
Ldb0823	LDB_RS03615	1566	1446	680	184.43	85.36	-1.111441	7.66E-66	2.80E-65	AN5939.2	-	-	-	rotein BOTBODRAFT_99843 [Botryobasidium botryosum FD-172 551]
Ldb0162	LDB_RS00665	1146	505	238	89.13	41.33	-1.108722	5.53E-24	1.30E-23	-	-	-	-	Inner membrane protein YbiR [Beauveria bassiana D1-5]
purL	LDB_RS06200	2223	990	470	88.06	41.16	-1.097244	9.20E-45	2.79E-44	osphoribos	-	-	-	ribosylformylglycinamide synthase [Beauveria bassiana D1-5]
rpsP	LDB_RS05880	273	8114	3908	7050.07	3328.28	-1.082861	0	0	1064.1 sm	-	-	-	al protein RirG_055850 [Rhizophagus irregularis DAOM 197198w]
Ldb1368	LDB_RS05860	477	491	236	222.77	105.2	-1.08242	1.83E-22	4.21E-22	-	-	-	-	-
tsf	LDB_RS05755	1029	43792	21065	8653.73	4095.45	-1.0793	0	0	or:MPER_1	-	-	-	stical protein MVEG_08529 [Mortierella verticillata NRRL 6337]
purF	LDB_RS06195	1479	747	360	101.08	47.94	-1.076196	3.73E-33	1.00E-32	530 amidc	-	-	-	midophosphoribosyltransferase [Beauveria bassiana D1-5]
rplA	LDB_RS07190	696	32367	15660	9699.5	4614.58	-1.071711	0	0	_006380 z	-	-	-	uction Of The 80s-eif5b-met-itramet Eukaryotic Translation Initiation Complex
purN	LDB_RS06185	582	241	117	87.73	41.86	-1.067498	1.46E-11	2.74E-11	osphoribc	-	-	-	26/Polyphosphate kinase [Beauveria bassiana D1-5]
Ldb2162	LDB_RS09425	1095	310	151	57.38	27.5	-1.061116	2.32E-14	4.61E-14	-	-	-	-	stical protein MVEG_02649 [Mortierella verticillata NRRL 6337]
Ldb1686	LDB_RS07290	837	213	105	52.38	25.4	-1.044188	4.43E-10	7.98E-10	-	-	-	-	-
epsIM	LDB_RS08420	912	3859	1908	866.24	421.32	-1.03985	7.96E-155	5.28E-154	-	-	-	-	-
Ldb1336	LDB_RS05715	477	559	278	253.62	123.92	-1.033259	1.30E-23	3.05E-23	-	-	-	-	-
eno	LDB_RS05525	1278	82961	41551	13065.84	6439.74	-1.020726	0	0	:CC1G_00044464//cd	-	-	-	551e-99/CTP synthase [Beauveria bassiana D1-5]
Ldb0672	LDB_RS02910	1632	1233	620	150.69	74.58	-1.014723	7.41E-49	2.34E-48	05168 ami	-	-	-	sothetical protein PDE_00321 [Penicillium oxalicum 114-2]
gmk2	LDB_RS08800	543	168	85	66	32.82	-1.007891	7.75E-08	1.31E-07	C05956.1 f	-	-	-	17/guanylate kinase [Fusarium graminearum PH-1]
Ldb1587	LDB_RS06840	660	1172	593	371.98	185.05	-1.00731	7.12E-46	2.18E-45	-	-	-	-	A carboxylase carboxyl transferase subunit beta [Beauveria bassiana D1-5]
Ldb0442	LDB_RS01875	1056	589	298	113.26	56.38	-1.006383	7.01E-24	1.65E-23	-	-	-	-	-
phnE	LDB_RS00860	813	2083	1056	528.35	263.45	-1.003965	8.90E-80	3.71E-79	-	-	-	-	liketo-D-gluconic acid reductase A [Beauveria bassiana D1-5]