

Table S2. The list of proteins detected from phagosomes in control and CPBF6gs strains.

Identified proteins		Averaged coverage from phagosomes		standard deviation %coverage from phagosomes (percentage point) ¹		(Coverage of CPBF6gs strain) - (Coverage of control strain) (percentage point)	p-value ²	Significance ³	Detected in the previous study ⁴
		Control strain	CPBF6gs strain	Control strain	CPBF6gs strain				
EAL41855	CPBF6	33	33	0	0	-35	0.00142	x	x
EAL4320	RabX31	71%	42%	15	19	-22	0.22206	x	x
EAL4348	Rab9B	44%	16%	21	10	-28	0.4287851	x	x
EAL50253	alpha-amylase family protein	28%	2%	5	2	-27	0.0001017	o	o
XP_653922	40S ribosomal protein S15a	37%	11%	22	13	-26	0.5862859	x	x
EAL49999	hypothetical protein	50%	26%	23	20	-24	0.758455	x	x
EAL51966	sgp86	35%	11%	14	9	-24	0.188365	x	x
EAL47201	hypothetical protein	36%	15%	20	14	-21	0.1552867	x	x
BAB40674	Rab7A	59%	38%	20	23	-21	0.8051289	x	o
EAL48855	calreticulin	36%	15%	9	9	-20	0.096301	x	x
EDS89284	hypothetical protein	31%	11%	10	13	-20	0.121229	x	x
EAL45256	cysteine proteinase 2	46%	28%	7	5	-20	0.0121078	o	o
EAL44037	hypothetical protein	38%	20%	13	10	-18	0.4602297	x	o
EAL43471	hypothetical protein	37%	19%	9	10	-18	0.2663781	x	x
EDS89207	granin	29%	11%	11	13	-18	0.3675491	x	x
BAB40673	Rab5	39%	21%	14	13	-17	0.6293862	x	o
EAL52074	Gal/GalNAc lectin light subunit	49%	32%	15	10	-17	0.8151219	x	o
EAL45367	hypothetical protein	28%	11%	11	8	-17	0.2350205	x	o
EAL48172	hypothetical protein	33%	16%	19	18	-17	0.9691599	x	x
EAL49320	ADP-ribosylation factor	27%	10%	14	9	-17	0.3520286	x	x
EAL50412	hypothetical protein	12%	12%	10	3	-16	0.0701953	x	o
EAL48966	RabC3	39%	23%	12	9	-16	0.4387284	x	x
EAL48129	Vacuolar ATP synthase subunit d	31%	15%	15	9	-16	0.8997717	x	o
CAA62835	cysteine proteinase	49%	34%	11	10	-15	0.3936681	x	o
XP_001738779	Ras family GTPase	42%	27%	8	2	-15	0.0623889	x	o
BAD34971	EnRab7p	39%	13%	8	6	-15	0.0587336	x	o
EAL50759	calactose-inhibitable lectin 95 kDa subunit precursor	49%	25%	18	9	-15	0.9586117	x	o
EAL44451	N-acetylneuraminidase	35%	30%	14	12	-14	0.7150852	x	x
EAL45317	Ras family GTPase	28%	14%	15	6	-14	0.7067372	x	x
EAL43030	dipeptidyl peptidase	33%	19%	13	8	-14	0.4733478	x	x
XP_656206	RabX30	23%	9%	14	8	-14	0.7710198	x	x
EDS89335	hypothetical protein	13%	13%	7	6	-13	0.3945992	x	o
BAB40669	Rab1A	37%	24%	11	12	-13	0.8841427	x	o
EH_059670	RabD1	21%	8%	12	9	-13	0.5263419	x	x
EAL48551	Receptor mediated endocytosis protein	32%	19%	9	5	-13	0.3441457	x	o
EAL47808	lysozyme	50%	37%	16	8	-13	0.8376193	x	o
AAF43042	malic enzyme	15%	2%	11	2	-12	0.3558418	x	x
EDS89288	hypothetical protein	15%	9%	9	3	-12	0.3581265	x	o
EAL48914	alcohol dehydrogenase	18%	5%	9	5	-12	0.3344019	x	x
EAL48719	vacuolar sorting protein VPS4	21%	9%	14	14	-12	0.9230076	x	x
EAL48166	hypothetical protein	36%	23%	6	4	-12	0.0929954	x	o
EAL45006	protein phosphatase family protein	22%	9%	11	8	-12	0.8122316	x	x
XP_648717	elongation factor 1-alpha 1	30%	18%	9	4	-12	0.1544165	x	x
EAL45816	thrombospondin	30%	16%	14	12	-12	0.9748036	x	x
EAL48580	hypothetical protein	20%	8%	5	2	-12	0.0379193	o	x
EAL51170	hypothetical protein	24%	12%	7	5	-12	0.0686164	x	x
BAB40670	RabC1	24%	12%	9	9	-12	0.4348907	x	o
EAL4582	beta-keto acyl reductase	14%	2%	7	4	-11	0.2123294	x	x
EAL51539	hypothetical protein	11%	0%	8	0	-11	0.1880645	x	x
EAL48788	alcohol dehydrogenase	19%	5%	7	5	-11	0.2235791	x	x
PS1555	pectate	34%	23%	11	3	-11	0.74315	x	x
EAL44887	beta-N-acetylhexosaminidase	37%	26%	10	7	-11	0.6187389	x	o
EAL42646	URE3-BP sequence specific DNA binding protein	17%	5%	9	6	-11	0.5264412	x	x
EAL52013	ganglioside gm2 activator protein	23%	12%	6	5	-11	0.1912871	x	x
EAL47855	ARP2/3 complex 21 kDa subunit	22%	11%	10	7	-11	0.351598	x	x
EAL48995	alpha-amylase	15%	12%	9	2	-11	0.0031794	o	x
AALF2264	dipeptidyl peptidase	15%	8%	6	5	-11	0.1902823	x	x
EAL50936	EnRabX11	28%	16%	14	7	-10	0.9130904	x	x
XP_001739563	triosphosphate isomerase	17%	7%	12	4	-10	0.549929	x	x
EAL48866	EnRabM2	13%	3%	4	3	-10	0.0597297	x	o
EAL49001	hypothetical protein	15%	4%	3	6	-10	0.0425177	o	x
EAL47513	CPBF6	33%	23%	5	4	-10	0.0891385	x	x
EAL45671	hypothetical protein	18%	6%	8	2	-10	0.2873805	x	x
EAL44332	acid phosphatase	25%	14%	7	9	-10	0.4498522	x	o
AAA29114	RacName_Full/Rac-like GTP-binding protein RHO1	21%	11%	8	7	-10	0.4892885	x	x
EAL51529	hypothetical protein	22%	11%	8	3	-10	0.2471148	x	o
EAL47892	actin	15%	5%	9	6	-10	0.3839564	x	x
AP_208300	actinin-like protein	15%	3%	7	2	-10	0.1588995	x	x
AAA28996	RacName_Full/Cytosine proteinase 1; Flag; Precursor	30%	20%	5	4	-10	0.1113264	x	o
EAL50768	Ras GTPase activating protein	13%	3%	5	3	-10	0.1028811	x	x
EAL49122	immuno-dominant variable surface antigen	22%	12%	7	2	-10	0.5102768	x	o
XP_001913357	type A flavoprotein	11%	2%	8	2	-10	0.3448895	x	x
EAL45068	heat shock protein 70	13%	3%	7	4	-10	0.4310124	x	x
XP_651737	guanine nucleotide-binding protein alpha-16 subunit [Entamoeba dispar SAW780]	32%	22%	8	12	-10	0.5685201	x	x
EDS89884	hypothetical protein	29%	19%	26	2	-10	0.1721973	x	o
EAL49871	lecithin:cholesterol acyltransferase domain-containing protein	17%	10%	10	7	-10	0.849327	x	o
EDS89370	adenylylase-associated protein	11%	2%	7	4	-9	0.1128876	x	o
EAL51216	cysteine proteinase	19%	10%	6	8	-9	0.3904464	x	o
EAL46868	hypothetical protein	11%	2%	7	3	-9	0.388442	x	x
EAL46302	actophorin	18%	9%	10	8	-9	0.5341147	x	x
AAF14855	dyrannin 2	39%	26%	7	6	-9	0.3407242	x	x
EAL45484	hypothetical protein	35%	27%	6	3	-9	0.108724	x	o
EAL47035	cortactin II	13%	4%	7	5	-9	0.452502	x	x
EAL42895	peptidyl prolyl cis-trans isomerase	14%	5%	4	4	-9	0.1018191	x	x
EDS89285	hypothetical protein	10%	2%	4	3	-9	0.0518414	x	x
EAL45540	actin-binding protein	17%	8%	12	7	-9	0.4893811	x	x
XP_648628	actin	15%	4%	8	6	-9	0.411812	x	x
EAL51636	peroxylate:ferredoxin oxidoreductase	11%	2%	5	2	-9	0.1558585	x	x
EAL48243	lysine and glutamic acid-rich protein 1 (KERP1)	10%	2%	6	4	-8	0.1887512	x	x
EAL47961	guanine nucleotide-binding protein subunit beta	18%	9%	10	8	-8	0.9317493	x	x
EAL50295	EH-domain containing protein	22%	14%	9	5	-8	0.9205897	x	x
EDS89126	hypothetical protein	13%	5%	4	3	-8	0.1051217	x	x
EAL49351	70 kDa heat shock protein	13%	5%	9	4	-8	0.3982859	x	x
EAL48178	vacuolar protein ATPase subunit	19%	11%	7	3	-8	0.8649652	x	x
EAL50171	hypothetical protein	9%	1%	2	2	-8	0.2687719	x	x
EAL42894	synactin binding protein	11%	2%	4	4	-8	0.1807404	x	x
EAL51221	hypothetical protein	56%	48%	8	7	-8	0.523942	x	o
EAL51030	hypothetical protein	22%	14%	7	2	-8	0.7321633	x	o
EAL48544	hypothetical protein	9%	1%	6	9	-8	0.2520789	x	x
EAL40351	hypothetical protein	8%	0%	4	4	-8	0.0371463	x	x
EAL51294	small GTPase ArfB1	9%	1%	6	3	-8	0.3722437	x	x
AAA21446	Ras family GTPase	19%	11%	6	10	-8	0.4196214	x	x
EAL47848	hypothetical protein	18%	10%	5	9	-8	0.5020275	x	x
XP_654359	glyoxaldehyde-3-phosphate dehydrogenase	26%	18%	11	7	-8	0.8939638	x	x
EDS89796	hypothetical protein	11%	3%	4	4	-7	0.1526539	x	x
EAL45323	actinin	17%	10%	6	4	-7	0.3655051	x	o
EAL43716	enhancer binding protein-2	9%	2%	5	3	-7	0.4047164	x	x
EAL48809	hypothetical protein	53%	46%	14	18	-7	0.8848529	x	o
EAL46860	hypothetical protein	7%	0%	4	0	-7	0.1339746	x	x
EAL49773	RhoGAP domain containing protein	11%	4%	5	4	-7	0.3208719	x	x
EAL50624	SNF7 family protein	12%	6%	7	5	-7	0.607072	x	x
EAL50026	cell surface protease ggd3	12%	13%	6	2	-7	0.4944105	x	o
BAD34978	Rab1A	15%	11%	6	4	-7	0.5050709	x	x
EAL44987	fructose-1,6-bisphosphate aldolase	14%	7%	8	4	-7	0.6467654	x	x
EAL52137	Ran family GTPase	7%	0%	7	0	-7	0.3559177	x	x
EAL49200	hypothetical protein	7%	0%	7	0	-7	0.3559177	x	x
EAL47854	granin	9%	2%	6	3	-7	0.5586875	x	x
EAL48913	hypothetical protein	10%	3%	5	4	-7	0.3820978	x	x
EAL51212	Pr-alycoactosin B	8%	2%	4	1	-7	0.1821446	x	x
EAL44481	hypothetical protein	8%	2%	4	3	-6	0.2157169	x	x
EAL47477	F-actin capping protein beta subunit	9%	3%	5	3	-6	0.2995989	x	x
EAL45315	hypothetical protein	18%	12%	7	6	-6	0.3858792	x	x
AAA18944	pyruvate phosphate dikinase	11%	5%	5	4	-6	0.3913954	x	x
EAL48703	serine carboxypeptidase (S28) family protein	16%	16%	5	4	-6	0.3739866	x	o
EAL44223	Rab1C	23%	24%	8	30%	-6	0.8958958	x	o
EAL47899	high-affinity potassium uptake transporter	6%	1%	3	1	-5	0.0677708	x	x

EAL43400	C2 domain containing protein	8%	3%	8	4	-5	0.8278065	x	x
EAL43348	enhancer binding protein 2 (EBP2)	9%	5%	6	6	-5	1	x	x
EAL50906	hypothetical protein	6%	1%	4	1	-5	0.3827383	x	x
EAL43285	phosphoglucomutase/phosphomannomutase family protein	0%	0%	4	2	-5	0.4568276	x	x
EAL43378	nucleic dehydrogenase	3%	1%	3	1	-3	0.2880739	x	x
AKK92361	hypothetical protein	38%	34%	4	5	-4	0.6014174	x	○
XP_001912541	nicotinamide nucleotide transhydrogenase	34%	29%	4	4	-4	0.6654176	x	x
EDS89309	hypothetical protein	20%	16%	11	8	-4	0.9003405	x	x
EAL43804	lecithin:cholesterol acyltransferase domain-containing protein	9%	4%	4	4	-4	0.6208942	x	x
EAL45537	WD domain containing protein	5%	1%	2	1	-4	0.50179153	○	x
EAL50665	hypothetical protein	7%	3%	3	3	-4	0.437064	x	x
EAL48132	hypothetical protein	4%	0%	3	0	-4	0.1651984	x	x
EAL49821	Rab22	11%	7%	6	10	-4	0.8388525	x	x
EAL46589	hypothetical protein	13%	8%	3	2	-4	0.2878632	x	x
EAL43613	hypothetical protein	5%	1%	3	1	-4	0.3242437	x	x
EAL47110	hypothetical protein	9%	5%	3	5	-4	0.4858355	x	x
EAL48139	Plasma membrane calcium-transporting ATPase	11%	7%	3	4	-4	0.6059578	x	○
EHL164800	CPBF1	29%	22%	4	2	-4	0.576327	x	○
EAL51399	hypothetical protein	6%	2%	3	2	-4	0.2715069	x	x
EAL46316	multidrug resistance protein	9%	5%	3	4	-4	0.718506	x	○
EAL45296	vacuolar ATP synthase subunit C	5%	1%	5	1	-4	0.5355706	x	x
EAL48457	hypothetical protein	11%	7%	0	9	-4	0.4290407	x	x
EAL45923	elongation factor 2	4%	1%	2	1	-4	0.2664176	x	x
EAL51407	Vesicle-fusing ATPase	8%	5%	4	4	-4	0.8752567	x	x
EAL47525	competence protein ComEC	5%	2%	3	2	-4	0.6875632	x	x
XP_001913620	hypothetical protein [Entamoeba dispar SAW760]	4%	0%	3	1	-4	0.1343558	x	x
EAL49497	protein kinase	4%	1%	7	4	-4	0.3902585	x	x
BAE94769	hypothetical protein	7%	4%	9	10	-4	0.420407	x	x
BAO34999	Rab70	10%	14%	4	0	-4	0.7116294	x	○
EAL51523	endo-1,4-beta-xylanase	4%	1%	4	2	-4	0.8110968	x	x
EAL48354	RabM3	13%	9%	6	0	-3	0.5201788	x	x
EAL51401	EhRab2C	8%	4%	4	3	-3	0.6991563	x	x
EAL51906	MIT domain protein	10%	6%	2	3	-3	0.2102842	x	x
AAU43735	SecE1 alpha subunit	3%	0%	2	0	-3	0.0536363	x	x
EAL5178	hypothetical protein	7%	10%	5	5	-3	0.1	x	x
EAL41460	hypothetical protein	21%	18%	2	2	-3	0.1825325	x	x
EAL52042	hypothetical protein	7%	4%	3	4	-3	0.8364233	x	x
EAL50904	acetyl-CoA synthetase	5%	2%	3	2	-3	0.4124198	x	x
EAL45346	hypothetical protein	4%	1%	2	1	-3	0.36455	x	x
QAA57862	hexokinase	3%	0%	3	0	-3	0.3559177	x	x
EAL48247	glucosylase II alpha subunit	3%	0%	2	0	-3	0.1030374	x	x
EAL43167	hypothetical protein	7%	3%	3	3	-3	0.5732616	x	x
EAL51014	hypothetical protein	3%	0%	2	1	-3	0.3221905	x	x
EAL50124	hypothetical protein	21%	18%	7	8	-3	0.597782	x	○
P19476	peroxiredoxin	10%	7%	6	5	-3	0.8021161	x	x
AAO03565	cysteine proteinase	11%	9%	8	7	-3	0.1812244	x	x
EAL48623	hypothetical protein	7%	4%	4	3	-3	0.1	x	x
EAL50314	alpha-amylase family protein	4%	2%	3	2	-3	0.8243163	x	x
XP_654747	ARP2/3 complex 34 kDa subunit	10%	8%	4	6	-3	0.838506	x	x
EAL48861	hypothetical protein	4%	1%	2	1	-3	0.5125481	x	x
EAL52155	hypothetical protein	5%	2%	2	5	-3	0.2080637	x	x
EAL51316	hypothetical protein	14%	11%	5	7	-3	0.8152192	x	x
EAL48413	Rho family GTPase	27%	25%	4	8	-3	0.8161755	x	○
EAL44421	hypothetical protein	3%	2%	2	3	-3	0.6572938	x	x
AAP73788	longin-type vesicle-associated membrane protein	8%	6%	2	4	-3	0.4986401	x	x
EAL48907	hypothetical protein	2%	0%	7	0	-2	0.2022024	x	x
EAL4888	nucleoside transporter	11%	9%	3	4	-2	0.8817855	x	○
EAL48832	short chain dehydrogenase family protein	4%	2%	2	4	-2	0.5769605	x	x
EAL47897	calpain homology domain protein	0%	0%	2	0	-2	0.1740074	x	x
EAL46028	hypothetical protein	4%	1%	4	4	-2	0.8317281	x	x
EAL46577	hypothetical protein	22%	19%	4	7	-2	0.8526541	x	○
EAL43464	hypothetical protein	29%	26%	5	11	-2	0.9345754	x	x
EAL49096	hypothetical protein	8%	5%	2	1	-2	0.5763186	x	○
EAL45033	alcohol dehydrogenase	5%	3%	3	4	-2	0.8030049	x	x
EDS89778	hypothetical protein	6%	3%	2	3	-2	0.2893919	x	x
EAL51958	hypothetical protein	4%	1%	2	3	-2	0.4993066	x	x
EAL47106	protein kinase	2%	0%	2	0	-2	0.3558177	x	x
EAL44584	80 kDa heat shock protein	5%	3%	3	2	-2	0.7646229	x	x
EAL43748	hypothetical protein	3%	1%	2	1	-2	0.5582922	x	x
EDS89560	hypothetical protein	3%	1%	1	1	-2	0.1404828	x	x
EAL49998	thioredoxin	4%	2%	5	4	-2	0.5393633	x	x
EAL48997	hypothetical protein	1%	2%	2	1	-2	0.5116266	x	x
XP_650865	ARPP23 complex 30 kDa subunit	10%	9%	8	9	-2	0.8547122	x	x
EAL45284	protein disulfide isomerase	13%	11%	1	4	-2	0.3117823	x	x
EAL46705	hypothetical protein	9%	7%	3	3	-2	0.7789914	x	x
AACA1577	NAD(P) transhydrogenase subunit alpha	7%	5%	1	2	-2	0.3498486	x	x
EAL45200	hypothetical protein	13%	11%	6	5	-2	0.8420136	x	x
EAL48896	hypothetical protein	23%	21%	3	4	-2	0.7694228	x	○
EAL48698	hypothetical protein	3%	2%	2	1	-2	0.8550456	x	x
EAL51029	EF-hand calcium-binding domain containing protein	2%	0%	2	0	-2	0.3559177	x	x
EAL48332	hypothetical protein	4%	2%	3	2	-2	0.6680099	x	x
EAL49058	Rho guanine nucleotide exchange factor	3%	1%	2	1	-2	0.7480238	x	x
EAL50856	WD repeat	4%	2%	4	2	-2	0.8561016	x	x
EAL43129	hypothetical protein	2%	1%	2	1	-2	0.3818972	x	x
EAL48728	protein kinase domain containing protein	2%	0%	2	2	-2	0.2133936	x	x
EAL43605	receptor protein kinase	2%	1%	1	2	-2	0.5387758	x	x
EAL50138	hypothetical protein	6%	5%	2	2	-2	0.1	x	○
EAL45091	hypothetical protein	3%	1%	2	1	-2	0.2619664	x	x
EAL43848	hypothetical protein	2%	0%	3	0	-2	0.051238	x	x
AAP04256	adhesin 112 (EPAH112)	7%	6%	5	4	-1	0.930023	x	x
EAL50467	protein tyrosine phosphatase	4%	2%	2	3	-1	0.7623386	x	x
EAL47310	Rho family GTPase	15%	13%	2	3	-1	0.32032	x	○
EAL51888	filamin 2	3%	1%	1	1	-1	0.6460143	x	x
EAL51082	WD domain containing protein	3%	1%	3	1	-1	0.1	x	x
EAL50740	hypothetical protein	11%	10%	2	2	-1	0.8510184	x	x
EAL48899	lecithin:cholesterol acyltransferase	9%	8%	5	7	-1	0.8225372	x	x
EAL48426	Rho family GTPase	3%	2%	5	3	-1	0.1874716	x	x
EAL48747	HEAT repeat domain containing protein	1%	0%	1	0	-1	0.3558177	x	x
EAL48973	hypothetical protein	3%	2%	3	2	-1	0.8848146	x	x
EAL49915	hypothetical protein	3%	2%	0	3	-1	0.8222747	x	x
EAL50093	hypothetical protein	7%	6%	1	4	-1	0.9907392	x	x
EAL49577	hypothetical protein	2%	1%	1	1	-1	0.5881407	x	x
EAL45274	hypothetical protein	2%	1%	2	1	-1	0.9160952	x	x
EAL51626	hypothetical protein	2%	1%	3	1	-1	0.2443872	x	x
EAL50029	galactose-specific adhesin 170ND subunit	3%	2%	1	1	-1	0.8788986	x	x
EAL50633	SH3 domain protein	5%	4%	3	2	-1	0.8957651	x	x
EAL44614	thioredoxin	2%	1%	4	2	-1	0.41044	x	x
EAL43134	synaptin	4%	3%	5	2	-1	0.1801959	x	x
EAL45601	putative plasma membrane calcium ion-transporting ATPase	2%	1%	1	1	-1	0.3001676	x	x
EAL48102	hypothetical protein	2%	2%	2	3	-1	0.7180105	x	x
EAL50641	hypothetical protein	8%	8%	2	3	-1	0.783977	x	○
EAL50824	beta-N-acetylhexosaminidase	5%	5%	3	5	-1	0.5959384	x	x
BAB40678	Rab11B	31%	30%	4	4	-1	0.6364064	x	○
EAL45971	endoribonuclease L-PSP	9%	9%	7	7	0	0.1	x	x
EAL51098	tyrosine kinase	1%	1%	1	0	0	0.7994908	x	x
EAL42112	Rab family GTPase	3%	2%	3	3	0	0.7402265	x	x
EAL50843	serine-threonine-isoleucine rich protein	7%	6%	2	2	0	0.6879153	x	x
AF338235	diaphanous protein	2%	1%	0	0	0	0.5995778	x	x
BAB40676	Rab11D	14%	14%	6	13	0	0.8861246	x	x
EAL50553	hypothetical protein	2%	2%	2	2	0	0.8236374	x	x
EAL51845	myosin heavy chain	0%	0%	1	0	0	0.3517628	x	x
XP_001735596	14-3-3 protein 3	3%	3%	3	3	0	0.8603095	x	x
JEAL50648	diaphanous protein	1%	1%	1	1	0	0.5236647	x	x
EAL48972	leucine rich repeat / protein phosphatase 2C domain containing protein	2%	2%	2	1	0	0.3506307	x	x
EAL51834	thioredoxin	1%	1%	1	2	0	0.8722103	x	x
EAL44647	protein kinase domain containing protein	0%	0%	1	0	0	0.658228	x	x
EAL92563	tyrosine kinase	0%	0%	1	0	0	0.1522893	x	x
EAL47395	hypothetical protein	0%	0%	0	4	0	0.1588543	x	x
EAL47383	hypothetical protein	0%	0%	3	0	0	0.3559177	x	x
EAL45499	hypothetical protein	16%	16%	0	0	0	0.1	x	x
XP_650527	ubiquitin	32%	32%	0	0	0	0.1	x	x
EAL50587	hypothetical protein	0%	0%	0	0	0	0.8573017	x	x
EAL47239	V-type ATPase	11%	11%	4	3	0	0.8852377	x	x
EAL48414	hypothetical protein	11%	11%	1	3	0	0.5952081	x	x
EAL50872	Rho family GTPase	3%	3%	3	6	0	0.8820553	x	x
EAL48917	flotillin	1%	1%	1	2	0	0.6387391	x	○
EAL48310	SNF7 family protein	6%	6%	3	8	0	0.8107381	x	x
EAL45958	hypothetical protein	1%	1%	1	2	0	0.6338474	x	x
EAL47864	hypothetical protein	9%	9%	6	3	0	0.250709	x	x
EAL45215	hypothetical protein	1%	1%	3	3	0	0.360227	x	x
EAL50297	Gal/GalNAc lectin heavy subunit	35%	35%	4	6	0	0.5052776	x	○
EAL43139	hypothetical protein	0%	0%	0	0	0	0.3559177	x	x
EAL48882	hypothetical protein	15%	15%	5	7	0	0.5279088	x	○
EDS89128	hypothetical protein	3%	3%	1	1	0	0.4141496	x	x
EAL50616	hypothetical protein	6%	6%	1	2	0	0.5553567	x	○

GAB45102	phospholipid-transporting P-type ATPase	1%	1%	1	1	0	0.6282226	x	x
EAL50268	hypothetical protein	0%	0%	0	1	0	0.559998	x	x
EAL52048	hypothetical protein	0%	0%	0	1	0	0.1989923	x	x
EAL52049	hypothetical protein	0%	1%	0	1	1	0.3559177	x	x
EDS8939	galactose-specific adhesin 170kD subunit	2%	2%	1	0	1	0.2559177	x	x
EAL49391	Filopodin	0%	1%	0	1	1	0.1694083	x	x
EAL43982	serine-threonine-isoleucine rich protein	0%	1%	0	1	1	0.2285892	x	x
EAL51553	lysosyme	13%	14%	3	6	1	0.542783	x	O
EAL48725	Fibrillin	3%	3%	3	7	1	0.8619001	x	x
EAL47684	hypothetical protein	11%	12%	1	7	1	0.5264018	x	O
EAL47890	CPB2	0%	1%	0	2	1	0.2559177	x	x
EAL49854	adenylyl cyclase-associated protein	2%	3%	2	4	1	0.6390215	x	x
EAL49416	hypothetical protein	0%	1%	0	2	1	0.3559177	x	x
EAL48775	hypothetical protein	0%	1%	0	2	1	0.3559177	x	x
EAL48984	Grainin 1	15%	15%	4	6	1	0.2670211	x	x
EAL47171	fatty acid elongase	3%	4%	1	5	1	0.7616924	x	x
EAL48810	hypothetical protein	20%	23%	7	6	1	0.2543235	x	x
EAL50915	Rho family GTPase	11%	12%	8	5	1	0.5130248	x	x
EAL49058	hypothetical protein	6%	7%	3	2	1	0.1265489	x	x
EAL44222	hypothetical protein	5%	6%	4	8	1	0.916027	x	x
EAL48248	dynamitin-like protein	1%	2%	2	2	1	0.916237	x	x
EAL48877	hypothetical protein	2%	3%	2	3	1	0.3489958	x	x
EDS8955	hypothetical protein	3%	5%	6	3	1	0.3631634	x	x
EAL4866	Alpha-adaptin gamma subunit isoform 1	0%	1%	0	3	1	0.3559177	x	x
EAL48792	ribonuclease	4%	5%	4	6	1	0.5524987	x	x
EAL50374	hypothetical protein	7%	8%	3	2	1	1	x	x
EDS8969	Alpha adaptin beta subunit isoform b	1%	2%	1	4	1	0.3472205	x	x
EAL52203	actin-like protein	7%	8%	4	8	1	0.325694	x	x
EAL45064	alpha-actinin NSF attachment protein	2%	4%	3	5	2	0.6050176	x	x
AAM21054	postdyr-prolyl cis-trans isomerase	40%	41%	12	7	2	0.1838986	x	O
EAL49631	actin binding protein	0%	2%	2	3	2	0.7714981	x	x
EAL47130	hypothetical protein	0%	2%	0	3	2	0.3559177	x	x
EAL48658	hypothetical protein	2%	4%	2	5	2	0.3631364	x	x
EAL51874	actin-related protein 2/3 complex subunit 1A	8%	9%	5	6	2	0.4277913	x	x
EAL48708	20 kDa antigen	7%	8%	3	8	2	0.987181	x	x
EDS89215	hypothetical protein	2%	4%	0	2	2	0.1165017	x	x
EDS89625	serine-threonine-isoleucine rich protein	1%	3%	1	2	2	0.0503183	x	x
EAL43802	serine carboxypeptidase (S28) family protein	13%	14%	2	4	2	0.4652331	x	x
EAL48741	papain family cysteine protease domain containing protein	1%	3%	1	2	2	0.1869188	x	O
EAL45887	hypothetical protein	0%	2%	0	4	2	0.3559177	x	x
XP_854460	80S ribosomal protein L5	0%	2%	2	4	2	0.6630463	x	x
EAL51357	glucose-inducible protein	0%	2%	0	5	2	0.3559177	x	x
EAL48261	hypothetical protein	29%	32%	12	28	3	0.467753	x	O
EAL49954	RabK family protein	0%	3%	0	6	3	0.3559177	x	x
EAL44220	hypothetical protein	5%	8%	2	3	3	0.4062022	x	x
AAK62471	Rab8	18%	21%	5	3	3	0.2843749	x	O
EAL4863	hypothetical protein	8%	12%	5	9	4	0.1688846	x	x
EAL49303	hypothetical protein	3%	5%	3	5	4	0.6631792	x	x
EAL49302	hypothetical protein	8%	10%	7	9	4	0.5060782	x	x
EAL42484	Actin-related protein 3	6%	9%	6	9	4	0.4886645	x	x
EAL51814	calmodulin	5%	4%	0	8	4	0.3559177	x	x
EAL48046	hypothetical protein	0%	4%	0	5	4	0.157218	x	x
EAL47078	80S ribosomal protein L9	0%	4%	0	5	4	0.1666612	x	x
EAL48510	beta-amylase	1%	5%	5	2	4	0.495323	x	x
EAL43538	Rax family GTPase	2%	7%	2	11	5	0.4351973	x	x
EAL45280	hypothetical protein	2%	7%	5	8	5	0.7864362	x	x
EAL45400	hypothetical protein	0%	5%	0	4	5	0.0393948	O	x
EAL45446	thioredoxin	5%	11%	5	3	6	0.2114486	x	x
EDS89794	galactose-specific adhesin light subunit	8%	16%	4	2	7	0.0258209	O	x
EAL47570	hypothetical protein	2%	10%	3	10	8	0.1290994	x	x
Q24814	Rho family GTPase	14%	23%	2	2	9	0.0042961	O	O
EAL45900	80S ribosomal protein L38	0%	11%	0	9	11	0.0540175	x	x

- 1: standard deviation was calculated using quadruplicate value from each strain
- 2: p-value was calculated using quadruplicate data sets of control strain and CPBFigs.
- 3: "O" indicates p-value equal to or less than 0.05, while "X" indicates p-value higher than 0.05.
- 4: "O" indicates that the protein was previously identified in [32].