

Supporting table 2

Table 2. Genes identified from three independent RNAi screens with three strains of *L. monocytogenes*.

A. Fewer infected cells						
CG n°	Gene name	Function	Probability	H gene	E value	Human homologue
1379	CG1379	Transcription Factor	*	AML1/AMP19	2.00E-56	Transcriptional Factor
1994	CG1994	N-acetyltransferase	***	FLJ10774	0	N-acetyltransferase
3403		(phoecin)	**	PREI3	1.00E-104	preimplantation protein 3
3605	CG3605	Pre-mRNA splicing Factor	*	SF3B2	1.00E-151	splicing factor 3b, subunit 2, 145kDa
3848	Trr	Trithorax-related (Transcription Factor)	***	MLL3	1.00E-167	myeloid/lymphoid or mixed-lineage leukemia 3
3911	CG3911	(TRAPP)	***	BET3L	7.00E-41	BAT3 like (<i>S. cerevisiae</i>) (TRAPP complex)
3992	Srp	Serpent (Transcriptional Activator)	***	GATA4	6.00E-19	GATA binding protein 4
4185	NC2beta	General transcriptional activity repressor	**	DR1	8.00E-35	down-regulator of transcription 1, TBP-binding (negative cofactor 2)
4214	Syx5	syntaxin 5A, t-SNARE activity	*	STX5A	5.00E-73	syntaxin 5A
4268	PitsIre	Serine Threonine Kinase	***	CDC2L1	1.00E-149	cell division cycle 2-like 1
32743	Smg1	Phosphatidyl 3 and 4 Kinase	**	SMG-1	1.00E-141	PI-3-kinase-related kinase SMG-1
4921	Rab4	Small GTPase	**	RAB4A	1.00E-92	RAB4A, member RAS oncogene family
4943	lack	Ubiquitin-protein ligase activity	**	SMURF1	1.00E-171	SMAD specific E3 ubiquitin protein ligase 1
4950	CG4950	Receptor activity	*	LRRTM4	7.00E-17	leucine rich repeat transmembrane neuronal 4
5036	CG5036	Regulator of G-protein signaling activity	**	RGS20	1.00E-49	regulator of G-protein signalling 20
5161	CG5161	(TRAPP)	***	TRAPPC2	4.00E-42	trafficking protein particle complex 2
5837	Hem	Receptor binding (Kette)	**	NCKAP1	0	NCK-associated protein 1
33106	Mask	Multiple ankyrin repeats single KH domain	***	ANKRD17	0	ankyrin repeat domain 17
6292	CycT		**	CCNT2	8.00E-22	Cyclin T2
6510	RpL18a	Structural constituent of ribosome	**	RPL18A	5.00E-62	ribosomal protein L18a
6523	CG6523	Thiol-disulfide exchange intermediate activity	**	TXNL2	3.00E-46	thioredoxin-like 2
6742	CenB1A	Arf GTPase activator	***	CENTB5	1.00E-130	centaurin, beta 5
6759	cdc16	ubiquitin-protein ligase activity	*	CDC16	7.00E-88	CDC16 cell division cycle 16 homolog (<i>S. cerevisiae</i>)
6905	CG6905	pre-mRNA splicing factor	*	CDC5L	0	CDC5 cell division cycle 5-like (<i>S. pombe</i>)
7380	CG7380	DNA binding	*	BANF1	1.00E-29	barrier to autointegration factor 1
7392	Cka	Connector of kinase to AP-1 (JNK cascade)	****	STRN3	0	striatin, calmodulin binding protein 3
7456	CG7456		*	COG4	1.00E-147	component of oligomeric golgi complex 4
8487	garz	guanyl-nucleotide exchange factor activity ER-Golgi transport	*	GBF1	0	golgi-specific brefeldin A resistance factor 1
8610	cdc27		**	CDC27 (APC3)	1.00E-113	cell division cycle 27
8651	Trx	Trithorax (Transcription Factor)	**	MLL4	2.00E-86	myeloid/lymphoid or mixed-lineage leukemia 4
31756	CG31756 (or ?)		**	KIAA1040	0	
9298	CG9298	(TRAPP)	***	TRAPPC4	6.00E-74	trafficking protein particle complex 4 (TRAPP complex)
9712	TSG101	Tumor suppressor protein 101, ubiquitin-protein ligase activity	*	TSG101	2.00E-92	tumor susceptibility gene 101
10153	CG10153	(TRAPP)	***	TRAPPC5	6.00E-67	trafficking protein particle complex 5 (TRAPP complex)
11098	CG11098	"similar to C219 reactive peptide"	*	CTAGE5	5.00E-07	CTAGE family, member 5
11526	CG11526	?	***	FAM40A	0	
15483	CG15483	N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase	*	B3GNT6	4.00E-19	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 6
16941	CG16941	pre-mRNA splicing factor activity	*	SF3A1	1.00E-130	splicing factor 3a, subunit 1, 120kDa
17839	CG17839	DB, immunoglobulin subtype and fibronectin type III domains	*	TTN	3.00E-05	titin

B. Fewer infected cells, less vacuolar escape						
1088	Vha26	Vacuolar H+ ATPase 26 Kda E subunit V1 domain	***	ATP6V1E1	9.00E-52	ATPase, H+ transporting, lysosomal 31kDa, V1 subunit E isoform 1
1404	ran	Small GTPase	**	RAN	1.00E-112	RAN, member RAS oncogene family
1422	p115	Protein transport activity	***	VDP	0	vesicle docking protein p115
1515	I(1)G0155	v-SNARE YKT6	***	YKT6	7.00E-60	SNARE protein Ykt6 (v-SNARE)
1528	gammaCOP	COPI vesicle coat component	***	COPG2	0	coatomer protein complex, subunit gamma 2
3161	Vha16	Vacuolar H+ ATPase 16 Kda V0 domain	****	ATP6V0C	8.00E-44	ATPase, H+ transporting, lysosomal 16kDa, V0 subunit c
3320	Rab1	Small GTPase	*	RAB1B	8.00E-92	RAB1B, member RAS oncogene family
3664	Rab5	Small GTPase	***	RAB5C	1.00E-82	RAB5C, member RAS oncogene family
3948	zetaCOP	COPI vesicle coat component	***	COPZ1	7.00E-57	coatomer protein complex, subunit zeta 1
5650	Pp1-87B	Protein phosphatase 1 at 87B	****	PPP1CC	1.00E-173	protein phosphatase 1, catalytic subunit, gamma isoform
5884	Par-6	Structural molecule activity	*	PAR6B	3.00E-69	par-6 partitioning defective 6 homolog beta (<i>C. elegans</i>)
6213	Vha13	Vacuolar H+ ATPase 13 Kda G subunit V1 domain	****	LOC473030	6.00E-06	ATPase, H+ transporting, lysosomal 13kD, V1 subunit G
6223	betaCOP	COPI vesicle coat component	***	COPB	0	coatomer protein complex, subunit beta

7961	alphaCOP	COPI vesicle coat component	***	COPA	0	coatomer protein complex, subunit alpha
8048	Vha44	Vacuolar H+ ATPase 44 Kda C	**	ATP6V1C1	1.00E-140	ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C, isoform 1
9115	Myotubularin	PI-3P and PI-3,5-biP Phosphatase	***	MTMR2	0	myotubularin related protein 2
12403	Vha68-1	ATPase A subunit V1 domain	**	ATP6V1A	0	ATPase, H+ transporting, lysosomal 70kDa, V1 subunit A
17332	Vha SFD	Vacuolar H+ SFD subunit V1 domain	***	ATP6V1H	5.00E-163	ATPase, H+ transporting, lysosomal 50/57kDa, V1 subunit H
17369	Vha55	Vacuolar H+ ATPase 55KDa B subunit V1 domain	**	ATP6V1B2	0	ATPase, H+ transporting, lysosomal 56/58kDa, V1 subunit B, isoform 2
18627	betaggtII	Beta subunit of type II geranylgeranyl transferase	**	RABGGTB	1.00E-119	Rab geranylgeranyltransferase, beta subunit

C. Fewer infected cells, less vacuolar escape, fewer bacteria per cell

3573	EG:86E4.5	Inositol-1,4,5-triphosphatase	****	INPP5B	1.00E-107	Inositol polyphosphate-5-phosphatase
4422	Gdi	GDP dissociation inhibitor	****	GDI1 (or RAB)	1.00E-177	GDP dissociation inhibitor 1
6842	CG6842	ATPase activity (VPS4)	***	VPS4A (SKD1)	1.00E-174	vacuolar protein sorting 4A (yeast)
6939	Sbf	Diacylglycerol binding; Y/S/T phosphatase activity	***	SBF1	0	SET binding factor 1
8055	CG8055	SNF7 homologue, intracellular transport	***	SNF7-2	8.00E-34	Snf7 homologue associated with Alix1
8280	Efalpa48D	Elongation factor 1alpha48D	*	EEF1A1	0	eukaryotic translation elongation factor 1 alpha 1
9575	Rab35	Small GTPase	***	RAB35 (or Ra)	3.00E-73	RAB35, member RAS oncogene family

D. Fewer infected cells, fewer bacteria per cell

4173	septin 2	Cell division/GTP binding	***	SEPT	1.00E-161	Septin 11
5164	Gst1	Glutathione S-transferase	*	GSTT2	5.00E-16	glutathione S-transferase theta 2
6509	CG6509	Structural molecule activity	***	DLG5	6.00E-69	discs, large homolog 5 (Drosophila)
7436	Nmt	N-myristoyl transferase	*	NMT2	1.00E-156	N-myristoyltransferase 2
7581	Bub3	RNA binding	**	BUB3	1.00E-115	BUB3 budding uninhibited by benzimidazoles 3 homolog (yeast)
8705	peanut	Septin ring	**	SEPT7 (CDC1)	1.00E-133	septin 7
9012	Chc	Clathrin heavy chain	**	CLTCL1	0	clathrin, heavy polypeptide-like 1
9697	CG9697		***	PGLYRP4	8.00E-29	peptidoglycan recognition protein 4

E. Less vacuolar escape, fewer bacteria per cell

4303	Bap60	Brahma associated protein 60 kD	**	SMARCD1	1.00E-163	SWI/SNF related, matrix associated, actin dependent regulator of chromatin
6375	Pitchoune	RNA helicase	**	DDX18	0	DEAD (Asp-Glu-Ala-Asp) box polypeptide 18
17737	CG17737	Translation initiation factor	*	LOC441916	2.00E-35	similar to Eukaryotic translation initiation factor 1 (eIF1)

F. Less vacuolar escape

4153	eIF-2&bgr	eukaryotic initiation factor 2 & bgr (GTP binding, tRNA binding)	*	EIF2S2	8.00E-77	eukaryotic translation initiation factor 2, subunit 2 beta, 38kDa
4651	RpL13	structural constituent of ribosome	*	RPL13	3.00E-48	ribosomal protein L13
31064	CG31064	Intracellular transport	*	RIPX	1.00E-96	rap2 interacting protein x

G. Fewer bacteria per cell

4494	Smt3	ubiquitin-like protein	*	LOC441512	7.00E-32	similar to SMT3 suppressor of mif two 3 homolog 2
18028	lt	Light, ubiquitin-protein ligase	*	VPS41	1.00E-153	vacuolar protein sorting 41 (yeast)

H. More bacteria per cell

1395	stg	String, protein tyrosine /serine /threonine phosphatase	***	CDC25C	6.00E-45	cell division cycle 25C
4903	MESR4		***	ZNF585A	5.00E-14	Zinc finger protein 585A
5451	CG5451	WD40 repeats	***	SMU1	0	smu-1 suppressor of mec-8 and unc-52 homolog (C. elegans)
5505	CG5505	Ubiquitin specific protease activity	***	USP36	1.00E-61	ubiquitin specific protease 36

I. Less infected cells or fewer bacteria per cell with LLO_{S44A} producing strain specifically

CG n°	Gene name	Function	Probability	H gene	E value	Human homologue
3329	Prosbeta2	Proteasome beta subunit 2	***	PSMB7	3.00E-93	proteasome (prosome, macropain) subunit, beta type, 7
3416	Mov34	Proteasome subunit	***	PSMD7	1.00E-132	proteasome (prosome, macropain) 26S subunit non-ATPase, 7
3998	zf30C	Zinc finger protein 30C, transcription factor activity	***	FLJ14345	3.00E-34	hypothetical protein FLJ14345
4016	Spt-I	Serine palmitoyltransferase subunit I	***	SPTLC1	1.00E-127	serine palmitoyltransferase, long chain base subunit 1
4162	Lace	Serine palmitoyltransferase subunit II	***	SPTLC2	1.00E-155	serine palmitoyltransferase, long chain base subunit 2

5802	CG5802	UDP-Galactose transporter	**	SLC35B1	3.00E-72	solute carrier family 35, member B1,UDP-galactose transporter related
5873	CG5873	Peroxidase activity	*	D2S448	1.00E-89	Melanoma associated gene
11139	p47		**	NSFL1C	4.00E-56	NSFL1 (p97) cofactor (p47)

J. Escape of LLO strain

CG n°	Gene name	Function	Probability	H gene	E value	Human homologue
2048	dco	casein kinase 1; serine/threonine protein kinase	*	CSNK1E	1.00E-156	casein kinase 1 epsilon
2939	slp2	Transcription	*	FOXG1B	3.00E-38	forkhead transcription factor slp2
3093	dor	Ubiquitin-protein ligase activity, protein binding, Pep3/Vps18/deep orange	****	VPS18	1.00E-149	vacuolar protein sorting protein 18
3269	Rab2	Small GTP binding protein, intracellular transport (ER to Golgi)	****	RAB2	1.00E-105	small GTP binding protein RAB2A
3299	vinculin	actin binding; structural constituent of cytoskeleton	**	VCL	2.00E-94	vinculin/alpha catenin
3473	CG3473	Ubiquitin-conjugating enzyme E2 N	**	Ube2n	2.00E-66	Ubiquitin-conjugating enzyme E2 N
4173	septin 2	Cell division/GTP binding	*	SEPT	1.00E-161	Septin 11
32743	Smg1	phosphatidyl 3 and 4 kinase	*	SMG1	1.00E-141	PI-3-kinase-related kinase SMG-1
4943	lack	E3 ubiquitiny ligase SMURF,Rsp5p	**	SMURF1	1.00E-171	SMAD specific E3 ubiquitin protein ligase 1
5923		alpha DNA polymerase activity	*	POLA2	5.00E-51	polymerase (DNA directed), alpha 2 (70kD subunit)
31064		endocytosis, intracellular transport	*/?	RIPX	1.00E-96	rap2 interacting protein x
6842	CG6842	ATP binding, intracellular protein transport	****	VPS4	1.00E-171	Vps4 (homologue vacuolar sorting)
6946		similarly to hnRNA	****	HNRPF	4.00E-22	heterogeneous nuclear ribonucleoprotein F
7146	CG7146	intracellular protein transport- VAM6	**	VPS 39	1.00E-135	Vps39/VAM6
7169	S1P	Serine type endopeptidase; subtilisin activity involved in sterol regulatory elen	****	MBTSP1	0	membrane-bound transcription factor site-1 protease isoform 1
7555	Nedd4	ubiquitin-protein ligase activity, protein ubiquination	*	NEDD4	0	Ubiquitin ligase Nedd4h
7776	E(Pc)	establishment and/or maintenance of chromatin architecture	**	EPC1	4.00E-92	enhancer of polycomb homolog 1
8055	CG8055	SNF7 homologue, intracellular transport	****	SNF7-2	8.00E-34	Snf7 homologue associated with Alix1
8454	CG8454	intracellular protein transport; lysosomal transport, Vps16	****	VPS16	1.00E-148	vacuolar protein sorting protein 16, isoform 1
8705	peanut	Septin ring	*	SEPT7 (CDC1	1.00E-133	septin 7
8882	Trip1	Translation initiation factor activity	*	EIF3S2	1.00E-116	eukaryotic translation initiation factor 3, subunit 2 beta
8952	CG8952	serine type endopeptidase; proteolysis and peptidolysis	*	TMPRSS3	7.00E-28	transmembrane protease, serine 3
9012	chc	clathrin heavy chain, intracellular transport, clathrin coat of coated pit	*	CLTCL1	0	clathrin, heavy polypeptide-like 1
9177	elF5	translation initiation factor activity, eukaryotic translation initiation factor 5'	**	EIF5	1.00E-113	eukaryotic translation initiation factor 5
9086	CG9086	ubiquitin protein ligase activity	**	UBR1	0	ubiquitin protein ligase E3 component n-recognin 1
9311	CG9311	protein tyrosine phosphatase activity; BRO1 protein/Vps 31; G-protein coupled	****	PTPN23	1.00E-134	protein tyrosine phosphatase, non-receptor type 23
9712	TSG101	tumor suppressor gene 101	*	TSG101	1.00E-97	tumor susceptibility gene 101
12230	car	SNARE binding; Vps33; sec1 like domain	****	VPS33A	1.00E-116	vacuolar protein sorting 33A
18028	lt	Light, ubiquitin-protein ligase	**	VPS41	1.00E-153	vacuolar protein sorting 41 (yeast)

Genes were organized according to phenotypes as observed by immunofluorescence microscopy.

The "probability" of the phenotype was scored as strength of the manifested phenotype in the corresponding category with four stars (****) indicating a very strong mutant phenotype and one star (*) indicating a mild phenotype. Gene function was as described in Flybase or by gene homologies. The genes were compared with the *Homo sapiens* gene database by BLAST analysis to determine E values and human gene homology. Phenotype groups A to H were observed in at least the wild type and LLO_{S44A} producing mutant screens. Phenotype group I was more prominent in the LLO_{S44A} producing mutant screen. Phenotype group J was specific for the LLO-minus screen.