Materials and Methods

Bacterial and eukaryotic cell growth conditions. *Listeria monocytogenes* strains were grown in brain heart infusion medium (BHI; Difco, Detroit, MI) for 15-18 hrs at 30ºC without agitation prior to infection of SL2 cells. SL2 cells were cultured in Schneider's *Drosophila* medium (SDM; Invitrogen, Carlsbad, CA) supplemented with 10% fetal bovine serum (FBS; Mediatech, Herndon, VA), SDM-10. SL2 cell cultures were maintained in a humidified chamber at 25°C to 29°C.

***L. monocytogenes* infection of SL2 cells.** For high-resolution microscopy studies, sterile 18 mm square glass coverslips were placed in each well of a 6-well plate. Two hundred microliters of 0.5 mg/ml ConA (Sigma, St. Louis, MO) in dH_2O were added to each coverslip. Following 1 hr of incubation at room temperature (RT; 18°C to 25°C), coverslips were washed with PBS and 1.0×10^6 SL2 cells in 2 ml of SDM-10 were added to each well. SL2 cultures were subsequently incubated at 27°C for 15-18 hrs. The following day, cultures of *L. monocytogenes* (DH-L1039 or DH-L1137) (*S1*) were washed with PBS and diluted in SDM-10. Five million bacteria in 2 ml of medium were added to PBS washed SL2 cells (MOI=5) and infected cultures were subsequently incubated at 27°C. One hour post-addition of bacteria, SL2 cells were washed with PBS and SDM-10 containing 50 μg/ml gentamicin was added to kill extracellular bacteria. At 8 hrs post-infection, SL2 cells were washed with PBS and coverslips fixed for 15 hrs in 3.2% paraformaldehyde in PBS at 4°C. Fixed coverslips were washed with TBS supplemented with 0.1% Triton X-100 (TBS-TX) and stained for 30 min with 33 nM Texas-Red phalloidin (Molecular Probes, Eugene, OR) in TBS-TX supplemented with

1% BSA. Following an additional wash, samples were stained with Hoechst 33342 (Molecular Probes, Eugene, OR) in TBS-TX for 10 min. Coverslips were washed with TBS-TX and mounted with Vectashield (Vector Laboratories, Burlingame, CA).

For analysis of intracellular *L. monocytogenes* growth rates, 5.0 x 10^6 SL2 cells (either untreated or treated with dsRNA for 3 days) were seeded onto 12 mm ConA-treated glass coverslips placed in a 60 mm diameter dish and incubated 15-18 hrs in SDM-10 at 27°C. Two milliliter aliquots of BHI medium were inoculated with a single colony of *L. monocytogenes* (DH-L1039 or DH-L1137) (*S1*) and grown 15-18 hrs at 30°C without agitation. SL2 cells were infected with 2.5 x 10^7 bacteria (MOI=5) in 6 ml of SDM-10. Infected SL2 cells were incubated at 27°C. At 1 hr post-infection, SL2 cells were washed and SDM-10 containing 50 μg/ml gentamicin was added. At varying time points post-infection, coverslips were removed and placed in 5 ml of sterile dH_2O in 15 ml conical tubes and SL2 cells were lysed by vortexing. Dilutions of lysates were plated on LB-agar plates and incubated 24 hours at 37°C to determine numbers of intracellular bacteria (cfu per coverslip).

Generation of dsRNAs. The dsRNA library used for the primary RNAi screen was made available by the *Drosophila* RNAi Screening Center (DRSC) at Harvard Medical School (http://flyrnai.org/). Briefly, the synthesis of dsRNAs in a high-throughput format was performed in a two-step PCR amplification procedure. In the first step, gene-specific primers were used with attached adaptors to amplify target sequences from *Drosophila* genomic DNA. In the second step, the PCR products were re-amplified using combinations of primers specific for the common adaptor sequences. This procedure

resulted in the addition of T7 RNA polymerase promoter sequences on both ends of all PCR products. The PCR products served as templates for the generation of dsRNAs. The PCR products representing the candidate dsRNAs used in the secondary screening assays were re-amplified by using T7 promoter specific primers and the second round PCR products as templates in 50 μl PCR reactions performed in a 96-well plate format. The candidate dsRNAs targeting ribosome and proteasome components were not re-amplified. Additionally, with the exception of dsRNAs targeting Actin, we did not re-amplify dsRNAs with predicted overlaps of > 21 base pairs with more than five mRNAs in addition to their intended target. In both the initial dsRNA synthesis and the synthesis of dsRNAs specific for secondary screening candidates, 10 μl of the PCR reaction products were used to perform *in vitro* transcription reactions using the T7 MEGAscript kit (Ambion, Austin, TX) and the manufacture's recommended specifications. dsRNA concentrations were determined and aliquots of *in vitro* transcription reactions were subjected to quality control by gel electrophoresis analysis. For screening purposes, approximately 0.3 μg of dsRNA was aliquoted into each well of black, clear-bottom 384-well plates (Corning, Acton, MA).

***Listeria monocytogenes* infections for RNAi screens.** *L. monocytogenes* infections of SL2 cells for the primary and secondary RNAi screens were performed in 384-well plates. SL2 cells were resuspended in serum-free SDM and 1.8 x 10^4 SL2 cells in 10 μl were added to each well of the 384-well plates containing dsRNAs using a Multidrop384 liquid dispenser (Thermo Labsystems, Franklin, MA). Following incubation for 1 hr at RT, 30 μl of SDM-10 were added to each well. Cells were then incubated at 25°C for 4

days to allow for knockdown of target transcripts and protein degradation. SL2 cells were then infected by adding 10 μl of a suspension of GFP-expressing *L. monocytogenes* (DH-L1039) (*S1*) (2.5 x 10^5 bacteria per well) in SDM-10 using an automated multi-channel pipettor. SL2 cells were incubated at 29°C for 2 hrs followed by addition of 10 μl of gentamicin in SDM-10 to achieve a final concentration of 50 μg/ml gentamicin. Cells were then incubated at 25°C. Twenty-four hours post-infection, the 384-well plates were centrifuged, medium was removed using a multi-channel vacuum apparatus and samples were fixed by adding 10 μl of 3.2% paraformaldehyde in PBS per well and incubating for 10 min at RT. Wells were washed with 30 μl of PBS and SL2 cells were stained with Hoechst dye in PBS supplemented with 0.1 % Triton X-100 for 10 min at RT. Samples were then washed with 30 μl of PBS per well and 30 μl of PBS supplemented with 0.1% sodium azide was added to each well. Plates were maintained at 4°C until automated fluorescence microscopy analysis was performed.

Automated fluorescence microscopy. Fluorescence images of infected SL2 cells in 384-well plates were acquired using an automated Nikon TE300 microscope equipped with: a 20X lens objective (Nikon, Corporation, Melville, NY); motorized stage and controller, filter wheel and shutter (Ludl Electronic Products, Hawthorne, NY); an automated Pifoc focusing motor (Piezo Systems Inc., Cambridge, MA); a cooled-coupled device camera (Hamamatsu Corporation, Bridgewater, NJ) and MetaMorph image acquisition software (Universal Imaging Corporation, Downingtown, PA). Automated focusing was performed on Hoechst-stained nuclei. Images from the stained nuclei and GFP-

expressing bacteria were collected at two sites within each well. All images were visually analyzed and categorized independently by two individuals.

Electron microscopy. One million SL2 cells in 1 ml of serum-free SDM were added to 25 μg of *in vitro* synthesized dsRNA in each well of a 6-well tissue-culture treated plate. Cells were incubated for 1 hr at RT followed by addition of 3 ml of SDM-10. Treated SL2 cells were then incubated at 27°C. After 4 days, 4.0 x 10^6 dsRNA treated SL2 cells were seeded in 60 mm tissue-culture treated dishes in 3 ml of SDM-10. Cultures of 10403S *L. monocytogenes* were washed with PBS and 2.0 x 10^7 bacteria in 1 ml of SDM-10 were added to SL2 cells (MOI=5) and infected cultures were subsequently incubated at 27°C. One hour post-addition of bacteria, 1 ml of SDM-10 containing 250 μg/ml gentamicin was added to kill extracellular bacteria (final concentration of 50 μg/ml gentamicin). At 16 hrs post-infection, SL2 cells were washed with 0.1M sodium cacodylate buffer and fixed in 2.5% gluteraldehyde in 0.1 M sodium cacodylate buffer at 4°C for 1 hr (Electron Microscopy Sciences, Hatfield, PA). Samples were then treated with 1% osmium tetraoxide/1.5% potassium ferrocyanide for 1 hr followed by 1% uranyl acetate for 30 min. Prior to sectioning, the samples were dehydrated in ethanol and embedded in Epon/Araldite resin with propylene oxide. Samples were viewed with a JEOL 1200EX 60kV transmission electron microscope.

Comparison of *L. monocytogenes* and *M. fortuitum* screens. For comparative analysis, dsRNAs identified from both the *L. monocytogenes* and *M. fortuitum* primary screens were tested for effects on infection by each pathogen. *L. monocytogenes* infections were

performed as described above. Infections with *M. fortuitum* were performed using strain EJR154 containing a *map24::gfp* fusion essentially as described in the accompanying report (*S2*) with the exception that cells were incubated with dsRNAs for four days prior to infection. For both pathogens, visual inspection was used as the primary method of analysis, and data was not stratified based upon the number of *Drosophila* nuclei as it was in the primary *M. fortuitum* screen (*S2*). These technical differences are likely to account for the disparities between host factors identified in the *M. fortuitum* screen (*S2*) as compared to this analysis. Infections were performed at least six times for each pathogen. dsRNAs causing inconsistent phenotypes in these six infections were repeated six additional times. Of those tested twelve times, only those candidates that produced reproducible phenotypes at least nine times were included in Table S3.

Supporting Text

The RNAi screens for host factors affecting intracellular infection by *Listeria monocytogenes* and *Mycobacterium fortuitum* reaffirmed roles for previously implicated host cell components and identified numerous host factors with prior unrecognized roles during multiple stages of infection. Previous work has shown that increased levels of LLO in the host cell cytosol, due to deletion of a PEST-like sequence within LLO, can cause permeablization of the host cell during *L. monocytogenes* infection (*S3*). Additionally, degradation of LLO has been shown to be blocked by addition of the proteasome inhibitor LLnL (*S4*). The results of the RNAi screen further confirmed the importance of proteasome-mediated protein degradation during *L. monocytogenes* infection as knockdown of any of 25 proteasomal subunits decreased intracellular infection by *L. monocytogenes*. The RNAi screen results were further validated by the observation that dsRNAs targeting four different vacuolar ATPase subunits inhibited infection by both pathogens. The activity of LLO is pH-dependent, such that cytosolic access requires host acidification of the vacuole to allow LLO-dependent lysis (*S5*), therefore, knockdown of vacuolar ATPase subunits likely altered the efficiency or kinetics of vacuole escape by *L. monocytogenes*. Knockdown of vacuolar ATPase subunits also inhibited infection by *M. fortuitum*. Although the mycobacterial phagosome does not fully acidify, some degree of vATPase-mediated vacuolar acidification may be required for *M. fortuitum* infection as several mycobacterial promoters are regulated in a pH-dependent manner (*S6*).

When targeted in the RNAi screen, several Rab small GTPase proteins with diverse roles in vesicular trafficking altered intracellular infection by *L. monocytogenes*

and *M. fortuitum*. Knockdown of some Rab proteins, such as Rab11, caused very strong phagocytosis defects that could explain the observed effect on infection. The result with Rab11 is consistent with data showing that in mammalian macrophages, Rab11 is found associated with nascent phagosomes and regulates endosome recycling, which has been proposed to be an important source of membrane during phagocytosis (*S7*). Knockdown of other Rab proteins, such as Rab5 and Rab2, had a small effect on phagocytosis for *E. coli* relative to the decreased intracellular infection observed for both pathogens (*S2*). For *L. monocytogenes*, knockdown of Rab5 appeared to affect both entry as well as intracellular growth. Rab5 has been shown to be important for recycling and cell surface localization of transferrin receptor (*S8*). The pathogen-specific entry defect in cells treated with Rab5 dsRNA may be the result of altered recycling of receptors required for *L. monocytogenes* uptake such as CG7228 (Pes). When the infection was examined with high-resolution microscopy, the number of infected SL2 cells was reduced to ~10% when treated with Rab5 dsRNA compared to approximately 40% in untreated cells. Furthermore, antibiotic (gentamicin) protection assays demonstrated a decrease of approximately 75% in the number of intracellular bacteria at two hours post-infection in Rab5 dsRNA-treated cells (S*9*). In addition to the decreased number of SL2 cells infected, the number of *L. monocytogenes* per infected SL2 cell was also reduced indicating a possible defect in intracellular growth (fig. S4). This observation is in contrast to previous data showing an increase in intracellular growth of *L. monocytogenes* upon knockdown of Rab5a with antisense oligonucleotides in murine macrophages (*S10*). The results observed in *Drosophila* SL2 cells may imply different or additional functions of Rab5 in *Drosophila* cells.

When targeted in the RNAi screen, several Rab proteins that are not known to be involved in vacuolar maturation were identified as causing decreased infection. For *L. monocytogenes*, Rab2 and Rab10 knockdown caused phenotypes consistent with decreased numbers of bacteria per cell, indicating that the roles of these proteins during intracellular infection extend beyond bacterial uptake. Rab2 is involved in ER-to-Golgi transport and localizes to vesicular–tubular clusters that are pre-Golgi intermediates (*S11*). Rab2 is important for recruitment of the atypical protein kinase C iota/lambda and soluble components, including COPI coatamer subunits required for proper protein sorting (*S12*). Proteomic approaches identified Rab2 as a component of phagosomes surrounding latex-beads, suggesting that Rab2 or Rab2-associated vesicles may also interact with phagocytic vacuoles containing *L. monocytogenes* (*S13*). Less is known about the role of Rab10 in cells, but GFP-tagged versions of Rab10 localize to the Golgi apparatus. Rab10 was also shown to co-localize with *Chlamydia pneumoniae* inclusion bodies (*S14*). Neither Rab2 nor Rab10 have reported roles in infection by either *L. monocytogenes* or *M. fortuitum*. Therefore, these observations reveal a previously unrecognized role for certain vesicular trafficking components during infection by both a cytosolic and vacuolar bacterial pathogen.

In addition to the vesicular trafficking proteins affecting both *L. monocytogenes* and *M. fortuitum*, we also identified several dsRNA targets that caused the Spots phenotype when knocked down by RNAi. These host factors appear to be specifically important for *L. monocytogenes* escape from the vacuole and span a range of functions, likely reflecting the fact that vacuole maturation is a complex and multi-step process. Interestingly, wild-type *L. monocytogenes* appeared to replicate within Spot-phenotype

vacuoles to a greater extent than LLO-negative *L. monocytogenes* in untreated SL2 cells. Further analysis of intracellular replication demonstrated that LLO-negative bacteria replicated to a 2-fold greater extent in SL2 cells treated with CG11814 dsRNA compared to untreated SL2 cells (fig. S3). CG11814 is homologous to the human gene responsible for the Chediak-Higashi syndrome (CHS) and to the mouse CHS homologue, *beige*. Cells from CHS patients or from *beige* mice contain abnormally large lysosomes, suggesting a role for Beige in lysosomal trafficking (*S15*). It is possible that CG11814 dsRNA treatment leads to a defect in lysosome-mediated vacuole acidification and maturation. This may explain the failure in vacuole escape, due to a lack of pH-dependent LLO activation, and the observed increased replication within the vacuole, as the vacuolar environment may be more permissive.

CG11814 dsRNA treatment also led to an increase in multilamellar structures surrounding intracellular *L. monocytogenes* (Fig. 3E). Similar structures were recently observed surrounding mutants of another cytosolic bacterial pathogen, *Shigella flexneri*. These multilamellar structures were shown to be the result of an attempt of the host cell to control intracellular infection by a process related to autophagy (*S16*). *L. monocytogenes* has been shown to interact with host cell autophagic pathways during intracellular infection (*S17*). The negative regulator of autophagy, Tor (target of rapamycin) (*S18*), was also found in our RNAi screen as a candidate leading to decreased numbers of *L. monocytogenes* per host cell at 24 hours post-infection (Fig. 1D). Additional fluorescence microscopy experiments indicated that Spots-like structures were present at 8 hours post-infection in cells treated with Tor dsRNA (*S9*). It is unknown whether the disappearance of the Spots-like structures by 24 hours post-infection

indicates degradation of *L. monocytogenes* within autophagic compartments or eventual escape of *L. monocytogenes* into the cytosol. Altogether, these observations reveal a possible role for autophagy as a defense mechanism limiting *L. monocytogenes* infection. If autophagic pathways are indeed involved in the multilamellar structures observed surrounding bacteria containing compartments, the Spots phenotype could be the result of an inability of bacteria to escape multi-membrane structures, while the autophagic vesicle fusion process could be providing nutrients for bacterial replication. Since lysosomes are also involved in the degradation of autophagic vesicle compartments (*S19*), it is possible that in CG11814-treated cells and in cells treated with other dsRNAs causing the Spots phenotype, the end of the autophagic pathway is blocked allowing compartments with single or multiple bacteria to accumulate.

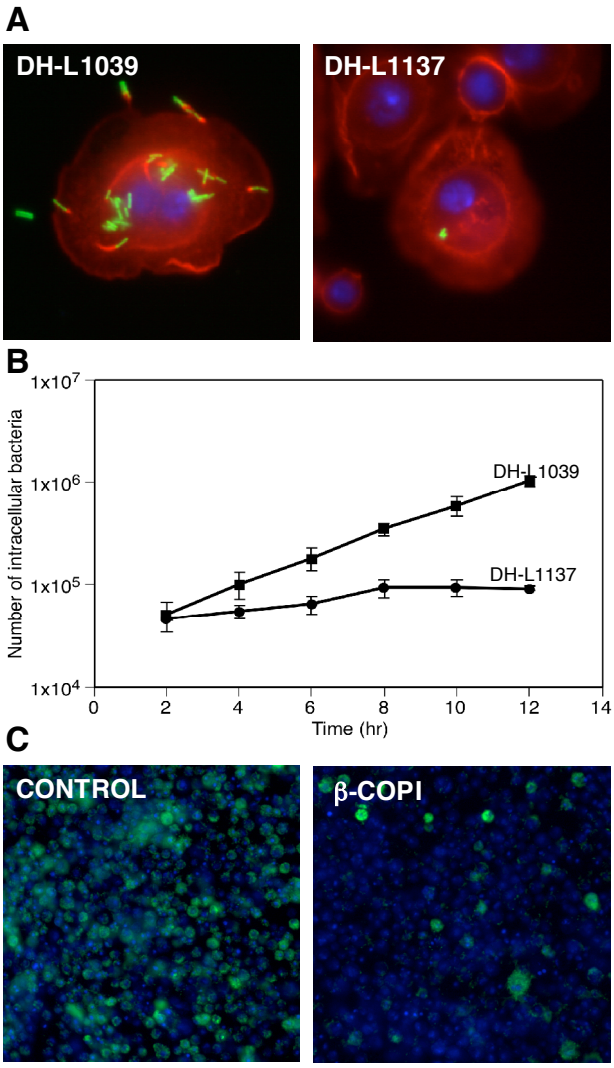

Figure S1. *L. monocytogenes* infection of *Drosophila* SL2 cells.
(A) *Drosophila* SL2 cells were infected with wild-type or LLO-negative, GFP-expressing *L. monocytogenes* (DH-L1039 or DH-L1137, respectively) (green). At 8 hours post-infection, SL2 cells were fixed and stained with phalloidin to detect host F-actin (red) and Hoechst dye to detect SL2 cell nuclei (blue). Images were taken at 100X magnification. (B) SL2 cells were infected and numbers of intracellular bacteria, DH-L1039 (squares) or DH-L1137 (circles), were determined at the indicated time periods post-infection. (C) SL2 cells were left untreated (control) or treated with β-COPI dsRNA. SL2 cells were infected with DH-L1039 (green) for 24 hrs followed by fixation and nuclei staining with Hoechst (blue). Approximately 57% of untreated cells were infected, while only 6% of β-COPI dsRNA-treated cells had associated bacteria. Images were taken at 20X magnification.

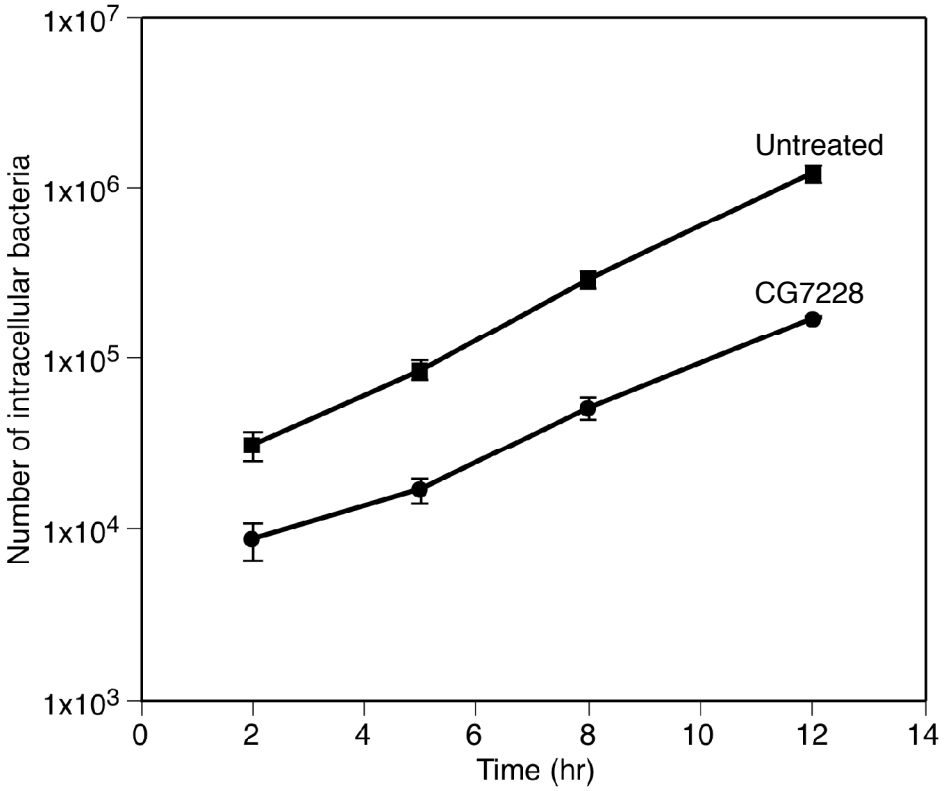

Figure S2. Knockdown of CG7228 (Pes) inhibits uptake, but not intracellular growth of *L. monocytogenes*. SL2 cells were left untreated (squares) or treated with CG7228 dsRNA (circles). After 3 days of incubation, 5 x 10^6 SL2 cells were seeded on ConA-coated coverslips. The following day (4 days after addition of dsRNA), the SL2 cells were infected with DH-L1039 at an MOI=5 and numbers of intracellular bacteria were determined at the indicated time periods post-infection. Data presented represents the means and standard deviations of one of three independent experiments performed in triplicate with similar results.

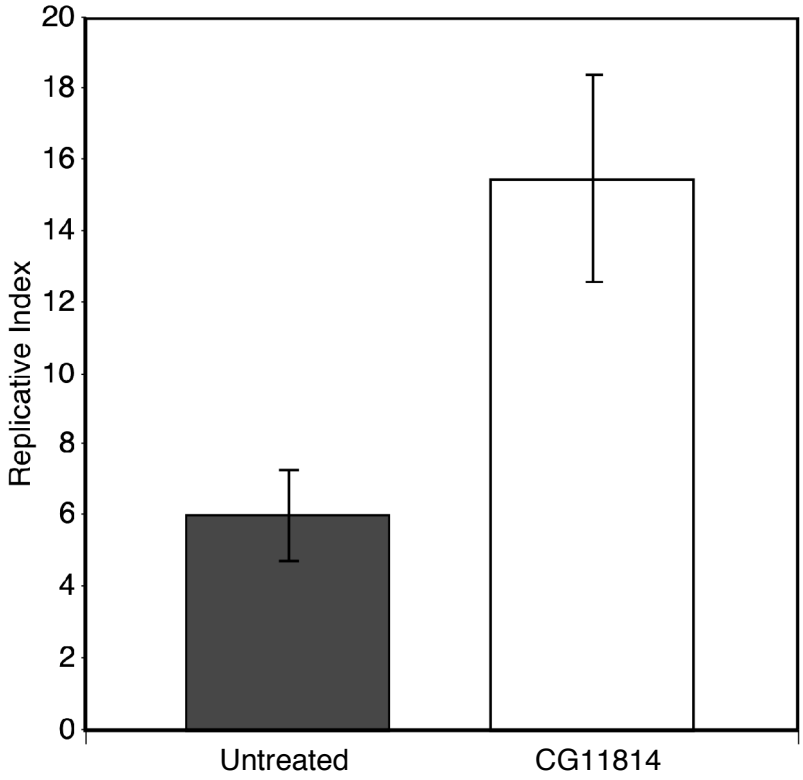

Figure S3. LLO-negative *L. monocytogenes* replicate to a greater extent in SL2 cells treated with CG11814 dsRNA. SL2 cells were left untreated (gray bar) or treated with CG11814 dsRNA (white bar). After 3 days of incubation, 5 x 10^6 SL2 cells were seeded on ConA-coated coverslips. The following day (4 days after addition of dsRNA), the SL2 cells were infected with DH-L1137 at an MOI=5 and numbers of intracellular bacteria were determined at 2 hours and 24 hours post-infection. Numbers of intracellular bacteria at 2 hours post-infection were the same in both untreated and CG11814 dsRNA-treated cells. The replicative index was determined by dividing the number of intracellular bacteria at 24 hours post-infection by the number of intracellular bacteria at 2 hours post-infection. Data presented are the means and standard deviations of 4 independent experiments.

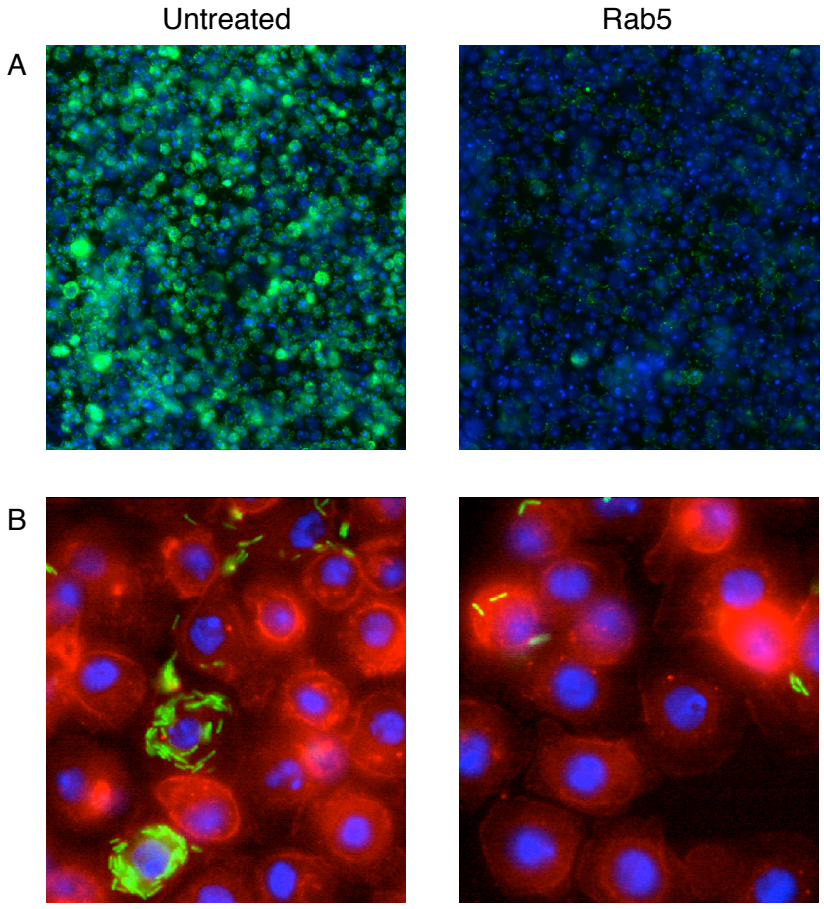

Figure S4. Knockdown of Rab5 inhibits *L. monocytogenes* intracellular infection in SL2 cells. (A) SL2 cells were left untreated (left) or treated with Rab5 dsRNA (right). SL2 cells were infected with DH-L1039 (green) for 24 hrs followed by fixation and nuclei staining with Hoechst (blue). Images were taken at 20X magnification. (B) SL2 cells were left untreated (left) or treated with Rab5 dsRNA (right). SL2 cells were infected with DH-L1039 (green). At 8 hours post-infection, SL2 cells were fixed and stained with phalloidin to detect host F-actin (red) and Hoechst dye to detect SL2 cell nuclei (blue). Images were taken at 100X magnification.

Supporting Table Legends

Table S1. Host factors targeted by dsRNAs that altered *L. monocytogenes* infection of SL2 cells. dsRNAs identified from the *L. monocytogenes* primary screen and from a comparison with a screen performed with *Mycobacterium fortuitum* were tested at least six times and the resulting infection phenotypes and phenotypic strength designations assigned. Examples of phenotypes are shown in Figure 1. In the viability column, Y indicates dsRNAs identified in an RNAi screen for cellular factors important for *Drosophila* cell viability (*S20*). The functional categories were assigned based on gene ontology (GO) biological function terms and the annotation is based on GO molecular function, cellular component, or protein domains as indicated in FlyBase (http://flybase.org). Mammalian homologues were determined with protein-protein BLAST searching of the non-redundant protein database at NCBI (http://www.ncbi.nlm.nih.gov/BLAST/). The homolog with the lowest e-score for each species is given in the table. None, indicates no homologues with an e-score below $1e^{-10}$. DRSC numbers correspond to amplicons targeting putative ORFs that are not annotated with a CG number in FlyBase (see http://flyrnai.org).

Table S2. Proteasome and ribosomal subunits identified in the primary RNAi screen as host factors affecting *L. monocytogenes* infection. Each dsRNA-targeted gene was assigned a resulting phenotype and phenotypic strength designation. Examples of phenotypes are shown in Figure 1. The functional categories were assigned based on gene ontology (GO) biological function terms and the annotation is based on GO molecular function, cellular component, or protein domains as indicted in FlyBase.

Table S3. Comparative analysis of *L. monocytogenes* and *M. fortuitum* RNAi screens. There were differences in the duration of RNAi treatment and methods of analysis in the primary screens performed to identified host factors required for *L. monocytogenes* and *M. fortuitum* infection (*S2*). Therefore, for the comparative analysis, the combined set of potential candidates from both screens was tested in parallel in a manner similar to the primary *L. monocytogenes* screen, in particular using four days of RNAi treatment followed by visual analysis. (A) Functional categories and annotations of dsRNA targets that decreased infection by both *L. monocytogenes* and *M. fortuitum*. (B) Functional categories and annotations of dsRNA targets that only decreased infection by *L. monocytogenes*. * indicates dsRNAs identified as causing an Up phenotype for *M. fortuitum*. (C) Functional categories and annotations of dsRNA targets that only decreased infection by *M. fortuitum*. * indicates dsRNAs identified as causing an Up phenotype for *L. monocytogenes.* The functional categories were assigned based on gene ontology (GO) biological function terms and the annotation is based on GO molecular function, cellular component, or protein domains as indicted in FlyBase.

Table S4. Amplicon information. DRSC amplicon numbers, primers used to amplify the dsRNAs, expected sizes of dsRNAs and potential secondary dsRNA targets are given. For additional information about the amplicons used in the RNAi screen, see http://flyrnai.org.

Table S1

Gene	CG#	Phenotype	Strength	Viability	Functional Category	Annotation	Mouse homolog	Human homolog
Cdc27	CG8610	down	strong	Y	Cell Cycle	mitosis	Cdc27	CDC27
cdc2rk	CG1362	down	moderate		Cell Cycle	cyclin-dependent kinase	Cdk10	PISSLRE
CG12343	CG12343	down	moderate		Cell cycle	cyclin regulator	Gcipip	P29
CG7597	CG7597	down	moderate		Cell Cycle	protein kinase activity	Cdc2l5	CDC2L5
CycT	CG6292	down	moderate	Y	Cell Cycle	cyclin T	Ccnt2	CCNT2
Mi-2	CG8103	down	strong		Cell Cycle	chromodomain, DNA binding	Chd4	Mi-2
mts	CG7109	down	moderate		Cell Cycle	protein phosphatase type 2A	Ppp2cb	PPP2CA
mus209	CG9193	down	moderate		Cell Cycle	nucleic acid binding	Pcna	PCNA
pim	CG5052	down	moderate		Cell Cycle	sister chromatid separation	None	None
Pp4-19C	CG18339	down	weak		Cell Cycle	serine-threonine phosphatase	PPX	ACP2
thr	CG5785	down	moderate		Cell Cycle	mitosis	None	None
raw	CG9321	down	moderate	Y	Cell Death	programmed cell death	None	None
smt3	CG4494	down	strong	Y	Cell Death	antiapoptosis	Sumo3	SUMO2
th	CG12284	down	strong	Y	Cell Death	negative regulator of apoptosis	MIHA	BIRC2
Act57B	CG30294	down	moderate		Cytoskeleton	actin filament	Actg2	ACTB
Act5C	CG4027	down	moderate		Cytoskeleton	actin filament	Actg2	ACTG1
alphaTub84B	CG1913	down	moderate	Y	Cytoskeleton	alpha tubulin, microtubules	Tuba3	TUBA2
alphaTub84D	CG2512	down	moderate	Y	Cytoskeleton	alpha tubulin, microtubules	Tuba3	TUBA2
alphaTub85E	CG9476	down	strong	Y	Cytoskeleton	alpha tubulin, microtubules	Tuba1	K-ALPHA-1
Arc-p20	CG5972	down	strong		Cytoskeleton	actin binding	Arpc4	ARPC4
Arc-p34	CG10954	down	moderate		Cytoskeleton	Arp2/3 protein complex	Arpc2	ARC34
Arp14D	CG9901	down	moderate		Cytoskeleton	actin binding, Arp2/3 complex	Actr2	ACTR2
Arp66B	CG7558	down	moderate		Cytoskeleton	actin binding, Arp2/3 complex	Actr3	ARP3BETA
betaTub56D	CG9277	down	weak		Cytoskeleton	beta tubulin, microtubules	4930542G03Rik	TUBB2
Ced-12	CG5336	down	weak		Cytoskeleton	Plekstrin-like	Elmo1	ELMO1
CG1017	CG1017	down	moderate		Cytoskeleton	microfibril	Mfap1	MFAP1
CG10540	CG10540	down	moderate		Cytoskeleton	F actin cappping	Capza1	CAPZA3
chic	CG9553	down	moderate		Cytoskeleton	actin binding	None	None
Lam	CG6944	down	moderate	Y	Cytoskeleton	lamin filament	Lmnb1	LMNB1
p16-ARC	CG9881	down	strong		Cytoskeleton	actin binding, Arp2/3 complex	Arpc5	ARPC5L
Sop2	CG8978	down	moderate		Cytoskeleton	actin-binding, Arp2/3 complex	Arpc1a	ARPC1A
tsr	CG4254	down	strong		Cytoskeleton	actin binding	Dstn	CFL2
CG8029	CG8029	down	moderate		Ion Transporter	hydrogen/potassium ATPase	Atp6ap1	None
CG8743	CG8743	down	moderate		Ion Transporter	calcium channel	Mcoln3	MCOLN3
Vha26	CG1088	down	moderate		Ion Transporter	hydrogen-export channel	Atp6e2	ATP6V1E1
Vha55	CG17369	down	strong		Ion Transporter	hydrogen-export channel	Atp6v1b1	ATP6V1B2
Vha68-2	CG3762	down	moderate		Ion Transporter	hydrogen-export channel	Atp6v1a1	ATP6V1A
VhaSFD	CG17332	down	strong		Ion Transporter	hydrogen-export channel	Atp6v1h	ATP6V1H
CG10960	CG10960	down	moderate		Metabolism	glucose transporter	Slc2a8	SLC2A8
CG11198	CG11198	down	strong	Y	Metabolism	acetyl-CoA carboxylase	Acac	ACACA
CG11451	CG11451	down	moderate	Y	Metabolism	sugar transporter	None	None
CG3523	CG3523	down	strong		Metabolism	fatty acid biosynthesis	Fasn	FASN
CG8199	CG8199	down	weak		Metabolism	acyl-CoA biosynthesis	Bckdha	BCHEL1
Fad2	CG7923	down	moderate		Metabolism	stearoyl-CoA 9-desaturase	Scd3	SCD
HLH106	CG8522	down	strong	Y	Metabolism	transcription factor	Srebf1	SREBF1
Hmgcr	CG10367	down	moderate		Metabolism	HMG-CoA reductase	Hmgcr	HMGCR
CG7228	CG7228	down	moderate		Miscellaneous	scavenger receptor/CD36 family	mSR-BI	SCARB1

Table S1

CkIalpha	CG2028	down	moderate		Miscellaneous	casein serine-threonine kinase	Csnk1a1	CSNK1A1
DDB1	CG7769	down	weak		Miscellaneous	damaged DNA binding	Ddb1	DDB1
Nxt1	CG12752	down	moderate		Miscellaneous	nuclear transport	Nxt1	NXT2
Sec61beta	CG10130	down	strong		Miscellaneous	protein transporter	Sec61b	SEC61B
CG10107	CG10107	down	moderate		Proteolysis	cysteine-type peptidase	Senp6	SENP6
CG11700	CG11700	down	strong	Y	Proteolysis	polyubiquitin-like	Ubc	UBC
CG3775	CG3775	down	moderate		Proteolysis	neprilysin-like	DINE	ECE2
CSN4	CG8725	down	moderate		Proteolysis	signalosome, protease	COPS4	COPS4
Ubi-p63E	CG11624	down	strong	Y	Proteolysis	Ub-dependent protein catabolism	Ubc	UBC
vihar	CG10682	down	moderate	Y	Proteolysis	Ubiquitin conjugating enzyme activity	Ube2c	UBE2C
Cbp80	CG7035	down	weak		RNA processing	Cap binding protein	LOC433702	NCBP1
CG1542	CG1542	down	weak		RNA processing	rRNA processing	Ebna1bp2	EBNA1BP2
CG16941	CG16941	down	moderate	Y	RNA processing	mRNA splicing	Sf3a1	SF3A1
CG18591	CG18591	down	moderate		RNA processing	mRNA splicing	None	LOC158352
CG2807	CG2807	down	moderate	Y	RNA processing	mRNA splicing	Sf3b1	SF3B1
CG3058	CG3058	down	moderate		RNA processing	mRNA splicing	LOC435611	TXNL4
CG5931	CG5931	down	moderate		RNA processing	RNA helicase	mKIAA0788	ASCC3L1
CG6015	CG6015	down	strong		RNA processing	mRNA splicing	Cdc40	CDC40
CG6905	CG6905	down	strong		RNA processing	mRNA splicing	Cdc5l	PCDC5RP
CG8241	CG8241	down	moderate		RNA processing	mRNA splicing	Dhx8	DHX8
CG8877	CG8877	down	strong		RNA processing	mRNA splicing	Prpf8	PRPF8
crn	CG18842	down	strong		RNA processing	mRNA splicing	Crnkl1	MST021
fne	CG4396	down	moderate		RNA processing	RNA binding	Elavl4	ELAVL2
Hel25E	CG7269	down	moderate		RNA processing	RNA helicase	Ddx39	DDX39
Hrb27C	CG10377	down	moderate		RNA processing	mRNA splicing	Dazap1	DAZAP1
lark	CG8597	down	moderate		RNA processing	RNA binding	4921506I22Rik	RBM30
snf	CG4528	down	moderate		RNA processing	mRNA splicing	Snrpb2	SNRPB2
14-3-3epsilon	CG31196	down	moderate		Signal Transduction	protein kinase C inhibitor	Ywhae	LOC440917
Abi	CG9749	down	moderate		Signal Transduction	signal transducer	Abi2	SSH3BP
Cdc42	CG12530	down	strong		Signal Transduction	GTPase	Cdc42	CDC42
CG17493	CG17493	down	weak		Signal Transduction	calcium ion binding	Cetn1	CETN2
CG1796	CG1796	down	moderate		Signal Transduction	Trp-Asp repeat	Plrg1	PLRG1
CG31302	CG31302	down	moderate		Signal Transduction	Fibronectin/SH3	RIMBP2	KIAA0318
CG3573	CG3573	down	strong		Signal Transduction	IP3 phosphatase activity	Inpp5b	INPP5B
CG6124	CG6124	down	moderate		Signal Transduction	receptor binding	Fbn2	FBN1
CG9753	CG9753	down	moderate		Signal Transduction	adenosine receptor activity	Adora2a	A2
mXr	CG30361	down	moderate		Signal Transduction	GABA-B like receptor	Grm8	GRM8
nej	CG15319	down	moderate	Y	Signal Transduction	cAMP response	Crebbp	CREBBP
puc	CG7850	down	weak		Signal Transduction	MAP phosphatase, JUN phosphatase	Dusp10	DUSP10
RacGAP50C	CG13345	down	moderate		Signal Transduction	GTPase activating	Racgap1	RACGAP1
ran	CG1404	down	moderate		Signal Transduction	small monomeric GTPase activity	1700009N14Rik	RAN
RhoGAP92B	CG4755	down	moderate		Signal Transduction	GTPase activating	AU040829	KIAA0672
shn	CG7734	down	moderate		Signal Transduction	transcription factor, zinc finger	Hivep2	HIVEP2
Sra-1	CG4931	down	moderate		Signal Transduction	Rho interactor, signal transduction	Cyfip2	PIR121
Tor	CG5092	down	moderate		Signal Transduction	protein kinase, PI3, PI4	Frap1	FRAP1
ush	CG2762	down	moderate		Signal Transduction	transcription factor, zinc finger	Zfpm1	ZFPM1
Bx42	CG8264	down	moderate	Y	Transcription	transcription factor	Skiip	SNW1
CG31258	CG31258	down	moderate		Transcription	cell cycle	None	None

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CG5591	CG5591	down	moderate		Transcription	transcription regulation	LOC433859	KIAA1506
CG8092	CG8092	down	moderate	Y	Transcription	zinc finger containing protein	POGZ	POGZ
RpII140	CG3180	down	weak		Transcription	RNA polymerase	Polr2b	POLR2B
RpII215	CG1554	down	moderate		Transcription	RNA polymerase	Polr2a	POLR2A
Spt5	CG7626	down	weak		Transcription	transcriptional elongation regulator	Supt5h	SUPT5H
Spt6	CG12225	down	strong		Transcription	transcription factor, elongation	Supt6h	SUPT6H
Taf4	CG5444	down	strong		Transcription	general transcription factor	Taf4a	TAF4
Taf6	CG32211	down	moderate		Transcription	general transcription factor	Taf6	TAF6
TfIIB	CG5193	down	moderate		Transcription	general transcription factor	LOC435886	GTF2B
Trap95	CG5465	down	moderate		Transcription	transcription factor	Thrap5	THRAP5
Trf2	CG18009	down	moderate		Transcription	TATA-box binding	Tbpl1	TBPL1
zfh1	CG1322	down	moderate		Transcription	zinc finger containing protein	Zfhx1a	TCF8
CG14712	CG14712	down	weak	Y	Translation	Aminoacyl-tRNA synthetase	Pom121	POM121
CG13258	CG13258	down	weak		Unknown	Unknown	None	None
CG15321	CG15321	down	moderate		Unknown	Unknown	None	None
CG15415	CG15415	down	moderate	Y	Unknown	Unknown	None	None
CG18561	CG18561	down	moderate		Unknown	Unknown	None	None
CG32280	CG32280	down	weak		Unknown	Unknown	5730403B10Rik	C16orf5
CG32737	CG32737	down	strong		Unknown	dicistronic cassette	None	None
CG33456	CG33456	down	moderate		Unknown	Unknown	None	None
CG3911	CG3911	down	strong		Unknown	Unknown	None	dJ493F7.1
CG8435	CG8435	down	moderate		Unknown	Unknown	LOC210562	FLJ10374
CG9324	CG9324	down	moderate	Y	Unknown	Unknown	2510048O06	HSPC014
CG9616	CG9616	down	weak		Unknown	Unknown	None	None
DRSC01346	sanger	down	moderate		Unknown	Existence Uncertain	NA	NA
DRSC05057	sanger	down	moderate		Unknown	Existence Uncertain	NA	NA
CG11990	CG11990	down	moderate		Unknown (PD)	Cdc73 family	None	HRPT2
CG30349	CG30349	down	moderate		Unknown (PD)	Trp-Asp repeat	2610318G08Rik	KIAA0007
CG6018	CG6018	down	moderate		Unknown (PD)	carboxylesterase	BC026374	ACHE
alphaCop	CG7961	down	strong		Vesicular Trafficking	COP vesicle coat	Copa	COPA
Arf102F	CG11027	down	moderate		Vesicular Trafficking	ADP-ribosylation, GTPase	Arf5	ARF4
Arf79F	CG8385	down	moderate		Vesicular Trafficking	ADP-ribosylation factor	Arf2	ARF4
betaCop	CG6223	down	strong		Vesicular Trafficking	COP vesicle coat	Copb1	COPB
beta'Cop	CG6699	down	strong		Vesicular Trafficking	COP vesicle coat	Copb2	COPB2
CG3885	CG3885	down	strong		Vesicular Trafficking	synaptic vesicle	2810407P21Rik	SEC3L1
CG8055	CG8055	down	strong	Y	Vesicular Trafficking	vacuolar protein sorting	2010012F05Rik	C20ORF178
CG9298	CG9298	down	weak		Vesicular Trafficking	vesicle mediated protein transport	synbindin	CGI-104
comt	CG1618	down	weak		Vesicular Trafficking	ATPase activity, protein transport	Nsf	NSF
deltaCop	CG14813	down	strong		Vesicular Trafficking	COPI vesicle coat	Arcn1	ARCN1
gammaCop	CG1528	down	moderate		Vesicular Trafficking	COPI vesicle coat	Copg	COPG2
garz	CG8487	down	strong		Vesicular Trafficking	GEF activity, intra-Golgi transport	Gbf1	GBF1
l(1)G0155	CG1515	down	strong		Vesicular Trafficking	SNAP receptor activity	Ykt6	YKT6
Rab1	CG3320	down	moderate		Vesicular Trafficking	GTPase, endocytosis, exocytosis	mKIAA3012	RAB1B
Rab10	CG17060	down	moderate		Vesicular Trafficking	GTPase, endocytosis, exocytosis	Rab8a	RAB10
Rab11	CG5771	down	moderate		Vesicular Trafficking	GTPase, receptor-mediated endocytosis	Rab11a	RAB11A
Rab2	CG3269	down	moderate		Vesicular Trafficking	vesicle transport	Rab2	RAB2
Rab21	CG17515	down	strong		Vesicular Trafficking	exoytosis, GTPase activity	Rab21	RAB21
Rab35	CG9575	down	moderate		Vesicular Trafficking	GTPase, endocytosis, exocytosis	mKIAA3012	RAB1B

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Rab5	CG3664	down	strong		Vesicular Trafficking	GTPase, endosome	Rab5c	RAB5A
Rab7	CG5915	down	strong		Vesicular Trafficking	GTPase, lysosome transport	Rab7	RAB7
Rab8	CG8287	down	strong		Vesicular Trafficking	GTPase, exocytosis	Rab8a	RAB8A
Rop	CG15811	down	strong		Vesicular Trafficking	SNARE binding, exocytosis	Stxbp1	STXBP1
sar1	CG7073	down	strong		Vesicular Trafficking	RAS small monomeric GTPase activity	Sara2	SARA2
sec23	CG1250	down	moderate		Vesicular Trafficking	GTPase activator activity	Sec23b	SEC23A
sec5	CG8843	down	moderate		Vesicular Trafficking	vesicle-mediated transport	Sec5l1	SEC5L1
sec6	CG5341	down	strong		Vesicular Trafficking	vesicle-mediated transport	Sec6l1	SEC6L1
Slh	CG3539	down	moderate		Vesicular Trafficking	SNARE binding, exocytosis	Scfd1	SCFD1
Snap	CG6625	down	moderate		Vesicular Trafficking	soluble NSF attachment protein	Napa	NAPA
Syb	CG12210	down	strong		Vesicular Trafficking	synaptobrevin, v-SNARE	Vamp2	VAMP2
Syx1A	CG31136	down	moderate		Vesicular Trafficking	t-SNARE activity ; SNAP receptor activity	Stx1a	STX1A
Syx5	CG4214	down	strong		Vesicular Trafficking	t-SNARE	Stx5a	STX5A
Syx7	CG5081	down	moderate		Vesicular Trafficking	t-SNARE activity ; SNAP receptor activity	Stx12	STX12
TER94	CG2331	down	moderate		Vesicular Trafficking	ATPase, microtubules, exocytosis	Vcp	VCP
Vps28	CG12770	down	strong		Vesicular Trafficking	vacuolar protein sorting	Ciia	VPS28
zetaCOP	CG3948	down	strong		Vesicular Trafficking	COPI vesicle coat	Copz1	COPZ2
Hsp70Ab, Hsp70Aa	CG18743	spots	weak		Heat Shock Protein	heat shock protein	Hspa1a	HSPA1B
Hsp70Ba, Hsp70Bc	CG31359	spots	weak		Heat Shock Protein	heat shock protein	Hspa1a	HSPA1B
NPC1	CG5722	spots	moderate		Metabolism	cholesterol transporter	Npc1	NPC1
Acp29AB	CG17797	spots	moderate		Miscellaneous	galactose binding	None	None
CG14210, CG33066	CG14210	spots	weak		Miscellaneous	dicistronic (protein translocase)	None	None
CkIIbeta	CG15224	spots	moderate		Miscellaneous	casein serine-threonine kinase	None	CSNK2B
klg	CG6669	spots	moderate		Signal Transduction	signal transduction	Hnt-pending	HNT
CG10660	CG10660	spots	moderate		Unknown (PD)	calcium-lipid binding domain	None	None
dpr6	CG14162	spots	weak		Unknown (PD)	Immunoglobulin domain	None	None
CG11814	CG11814	spots	strong		Vesicular Trafficking	lysosomal transport	Lyst	CHS1
CG5691	CG5691	spots	strong		Vesicular Trafficking	lysosomal organization	None	None
Bub1	CG7838	up	moderate		Cell Cycle	serine-threonine kinase	Bub1	BUB1
cdc2	CG5363	up	moderate		Cell Cycle	cyclin-dependent kinase	Cdc2a	CDK3
CycA	CG5940	up	moderate		Cell Cycle	cyclin A	McycA2	CCNA1
CycE	CG3938	up	strong	Y	Cell Cycle	cyclin E	Ccne1	CCNE1
Dp	CG4654	up	moderate		Cell Cycle	transcription factor	A330080J22Rik	DP-2
E2f	CG6376	up	weak	Y	Cell Cycle	transcription factor	E2f3	E2F3
fzy	CG4274	up	moderate	Y	Cell Cycle	cyclin catabolism	Cdc20	CDC20
geminin	CG3183	up	strong		Cell Cycle	regulator of DNA replication	None	None
His2A:CG31618	CG31618	up	moderate		Cell Cycle	Histone 2A	H2a(B)-613	HIST2H2AB
His2B:CG17949	CG17949	up	moderate		Cell Cycle	Histone 2B	Hist1h2bp	HIST2H2BE
His3:CG31613	CG31613	up	moderate		Cell Cycle	Histone 3	Hist2h3c1	LOC441906
His4:CG31611	CG31611	up	moderate		Cell Cycle	Histone 4	Hist1h4i	HIST1H4F
His4r	CG3379	up	moderate	Y	Cell Cycle	Histone 4 replacement	Hist1h4i	HIST1H4F
His-Psi:CR31616		up	moderate		Cell Cycle	histone pseudogene	NA	NA
Klp61F	CG9191	up	strong		Cell Cycle	microtubule motor activity	Kif11	KIF11
mad2	CG17498	up	moderate		Cell Cycle	mitotic spindle	Mad2l1	MAD2L1
Rca1	CG10800	up	strong		Cell Cycle	regulator of cyclin A	None	None
RnrS	CG8975	up	moderate		Cell Cycle	ribonucleoside reductase	Rrm2	RRM2
Su(var)3-9	CG6476	up	moderate		Cell Cycle	chromatin assembly	Eif2s3x	EIF2S3
dlg1	CG1725	up	moderate		Cytoskeleton	structural constituent	Dlgh1	DLG1

Table S1

pav	CG1258	up	moderate		Cytoskeleton	microtubule motor activity	Kif23	KIF23
Hsc70-3	CG4147	up	moderate		Heat Shock Protein	heat shock protein	Hspa5	HSPA5
CG32000	CG32000	up	weak		Ion Transporter	cation transporter	Atp13a3	AFURS1
sphinx, CG4692	CG4692	up	strong		Ion Transporter	hydrogen-exporting ATPase	None	None
Ald	CG6058	up	moderate		Metabolism	fructose bisphosphate aldolase activity	Aldoa	ALDOA
CG17119	CG17119	up	moderate		Metabolism	L-cystine transporter	Ctns	CTNS
CG2249	CG2249	up	moderate		Metabolism	cytochrome-c oxidase	None	None
CG3731	CG3731	up	moderate		Metabolism	mitochondrial peptidase	Pmpcb	PMPCB
CG5844	CG5844	up	moderate	Y	Metabolism	fatty acid beta-oxidation	Echs1	FLJ10948
cactin	CG1676	up	weak		Miscellaneous	defense response	LOC226972	C19orf29
CG11779	CG11779	up	moderate		Miscellaneous	protein translocase	Timm44	TIMM44
CG8057	CG8057	up	weak		Miscellaneous	serine/threonine kinase	Prkab1	PRKAB1
dmt	CG8374	up	moderate		Miscellaneous		None	None
Nup153	CG4453	up	moderate		Miscellaneous	nuclear pore/protein transport	Nup153	NUP358
Nup98	CG10198	up	moderate		Miscellaneous	nuclear pore/protein transport	AI849286	NUP98
CG9772	CG9772	up	moderate		Proteolysis	Ub-dependent protein catabolism	Skp2	SKP2
granny-smith	CG7340	up	moderate		Proteolysis	amino peptidase	Npepl1	NPEPL1
CG1420	CG1420	up	moderate		RNA processing	mRNA splicing	D11Ertd730e	SLU7
CG3605	CG3605	up	moderate		RNA processing	mRNA splicing	Sf3b2	SF3B2
DebB	CG16792	up	moderate		RNA processing	mRNA splicing	LOC384091	SNRPF
sbr	CG17335	up	moderate	Y	RNA processing	mRNA nuclear transporter	Nxf1	NXF1
SmD3	CG8427	up	moderate		RNA processing	ribonucleoprotein	Snrpd3	SNPD3
Spx	CG3780	up	moderate		RNA processing	mRNA binding	Sf3b4	SF3B4
pbl	CG8114	up	moderate		Signal Transduction	Rho GEF activity	Ect2	ECT2
Rho1	CG8416	up	moderate		Signal Transduction	GTPase activity	ArhA	RHOA
CG6197	CG6197	up	strong		Transcription	transcription, nucleic acid metabolism	Xab2	HCNP
CG4699	CG4699	up	moderate		Unknown	Unknown	1700081L11Rik	LOC284058
CG6694	CG6694	up	moderate	Y	Unknown (PD)	zinc finger containing protein	Zc3hdc3	ZC3HDC3

Table S2

Gene	CG Number	Phenotype	Strength	Functional Category	Annotation
CG12000	CG12000	down	Strong	Proteolysis	proteasomal subunit
CG17331	CG17331	down	Moderate	Proteolysis	proteasomal subunit
CG8877	CG8877	down	Strong	Proteolysis	proteasomal subunit
Dox-A2	CG10484	down	Moderate	Proteolysis	proteasome regulatory protein
l(2)05070	CG8392	down	Strong	Proteolysis	proteasomal subunit
Mov34	CG3416	down	Strong	Proteolysis	proteasomal subunit
Pros25	CG5266	down	Strong	Proteolysis	proteasomal subunit
Pros26	CG4097	down	Strong	Proteolysis	proteasomal subunit
Pros26.4	CG5289	down	Strong	Proteolysis	proteasomal subunit
Pros35	CG4904	down	Strong	Proteolysis	proteasomal subunit
Pros54	CG7619	down	Moderate	Proteolysis	proteasomal subunit
Prosalpha6	CG18495	down	Strong	Proteolysis	proteasomal subunit
Prosalpha7	CG1519	down	Moderate	Proteolysis	proteasomal subunit
Prosbeta2	CG3329	down	Moderate	Proteolysis	proteasomal subunit
Prosbeta3	CG11981	down	Strong	Proteolysis	proteasomal subunit
Prosbeta5	CG12323	down	Strong	Proteolysis	proteasomal subunit
ProsMA5	CG10938	down	Strong	Proteolysis	proteasomal subunit
Rpn1	CG7762	down	Strong	Proteolysis	proteasomal subunit
Rpn11	CG18174	down	Moderate	Proteolysis	proteasome regulatory protein
Rpn6	CG10149	down	Strong	Proteolysis	proteasomal subunit
Rpn7	CG5378	down	Strong	Proteolysis	proteasomal subunit
Rpt1	CG1341	down	Strong	Proteolysis	proteasomal subunit
Rpt3	CG16916	down	Strong	Proteolysis	proteasome regulatory protein
Rpt4	CG3455	down	Strong	Proteolysis	proteasome regulatory protein
Tbp-1	CG10370	down	Strong	Proteolysis	proteasomal subunit
CG11583	CG11583	up	Weak	Translation	ribosomal subunit biogenesis
CG1161	CG1161	up	Moderate	Translation	ribosomal protein
CG3203	CG3203	up	Moderate	Translation	ribosomal protein
hoip	CG3949	up	Moderate	Translation	ribosomal protein
oho23B	CG2986	up	Moderate	Translation	ribosomal protein
Qm	CG17521	up	Moderate	Translation	ribosomal protein
RpL10Ab	CG7283	up	Moderate	Translation	ribosomal protein
RpL12	CG3195	up	Moderate	Translation	ribosomal protein
RpL13	CG4651	up	Moderate	Translation	ribosomal protein
RpL13A	CG1475	up	Moderate	Translation	ribosomal protein

Table S2

RpL14	CG6253	up	Moderate	Translation	ribosomal protein
RpL15	CG17420	up	Moderate	Translation	ribosomal protein
RpL18	CG8615	up	Moderate	Translation	ribosomal protein
RpL18A	CG6510	up	Moderate	Translation	ribosomal protein
RpL19	CG2746	up	Moderate	Translation	ribosomal protein
RpL21	CG12775	up	Strong	Translation	ribosomal protein
RpL23	CG3661	up	Weak	Translation	ribosomal protein
RpL24	CG9282	up	Moderate	Translation	ribosomal protein
RpL26	CG6846	up	Moderate	Translation	ribosomal protein
RpL27	CG4759	up	Moderate	Translation	ribosomal protein
RpL27A	CG15442	up	Moderate	Translation	ribosomal protein
RpL28	CG12740	up	Moderate	Translation	ribosomal protein
RpL30	CG10652	up	Strong	Translation	ribosomal protein
RpL32	CG7939	up	Strong	Translation	ribosomal protein
RpL35	CG4111	up	Strong	Translation	ribosomal protein
RpL35A	CG2099	up	Moderate	Translation	ribosomal protein
RpL36A	CG7424	up	Moderate	Translation	ribosomal protein
RpL37	CG9091	up	Moderate	Translation	ribosomal protein
RpL37A	CG5827	up	Moderate	Translation	ribosomal protein
RpL38	CG18001	up	Strong	Translation	ribosomal protein
RpL39	CG3997	up	Moderate	Translation	ribosomal protein
RpL40	CG2960	up	Moderate	Translation	ribosomal protein
RpL5	CG17489	up	Strong	Translation	ribosomal protein
RpL7	CG4897	up	Moderate	Translation	ribosomal protein
RpL7A	CG3314	up	Strong	Translation	ribosomal protein
RpL8	CG1263	up	Strong	Translation	ribosomal protein
RpL9	CG6141	up	Moderate	Translation	ribosomal protein
RpLP0	CG7490	up	Moderate	Translation	ribosomal protein
RpLP1	CG4087	up	Weak	Translation	ribosomal protein
RpLP2	CG4918	up	Weak	Translation	ribosomal protein
RpS10b	CG14206	up	Moderate	Translation	ribosomal protein
RpS11	CG8857	up	Strong	Translation	ribosomal protein
RpS14a	CG1524	up	Weak	Translation	ribosomal protein
RpS14b	CG1527	up	Weak	Translation	ribosomal protein
RpS15	CG8332	up	Moderate	Translation	ribosomal protein
RpS15Ab, RpS15Aa	CG12324, CG2033	up	Moderate	Translation	ribosomal protein

Table S2

RpS16	CG4046	up	Moderate	Translation	ribosomal protein
RpS17	CG3922	up	Moderate	Translation	ribosomal protein
RpS18	CG8900	up	Moderate	Translation	ribosomal protein
RpS19a	CG4464	up	Moderate	Translation	ribosomal protein
RpS24	CG3751	up	Weak	Translation	ribosomal protein
RpS26	CG10305	up	Weak	Translation	ribosomal protein
RpS27A	CG5271	up	Moderate	Translation	ribosomal protein
RpS28b	CG2998	up	Moderate	Translation	ribosomal protein
RpS29	CG8495	up	Weak	Translation	ribosomal protein
RpS3	CG6779	up	Moderate	Translation	ribosomal protein
RpS30	CG15697	up	Weak	Translation	ribosomal protein
RpS4	CG11276	up	Moderate	Translation	ribosomal protein
RpS5a	CG8922	up	Moderate	Translation	ribosomal protein
RpS6	CG10944	up	Moderate	Translation	ribosomal protein
RpS9	CG3395	up	Moderate	Translation	ribosomal protein

Table S3

A dsRNA targets that decreased infection by both *L. monocytogenes* and *M. fortuitum*

Gene	CG Number	Functional Category	Annotation
Cdc27	CG8610	Cell Cycle	mitosis
CG7597	CG7597	Cell Cycle	protein kinase activity
CycT	CG6292	Cell Cycle	cyclin T
mts	CG7109	Cell Cycle	protein phosphatase type 2A
smt3	CG4494	Cell Death	antiapoptosis
th	CG12284	Cell Death	negative regulator of apoptosis
Act57B	CG30294	Cytoskeleton	actin filament
Act5C	CG4027	Cytoskeleton	actin filament
alphaTub84B	CG1913	Cytoskeleton	alpha tubulin, microtubules
alphaTub84D	CG2512	Cytoskeleton	alpha tubulin, microtubules
alphaTub85E	CG9476	Cytoskeleton	alpha tubulin, microtubules
Arc-p20	CG5972	Cytoskeleton	actin binding
Arc-p34	CG10954	Cytoskeleton	Arp2/3 protein complex
Arp14D	CG9901	Cytoskeleton	actin binding, Arp2/3 complex
Arp66B	CG7558	Cytoskeleton	actin binding, Arp2/3 complex
betaTub56D	CG9277	Cytoskeleton	beta tubulin, microtubules
Ced-12	CG5336	Cytoskeleton	Plekstrin-like
CG10540	CG10540	Cytoskeleton	F actin cappping
chic	CG9553	Cytoskeleton	actin binding
p16-ARC	CG9881	Cytoskeleton	actin binding, Arp2/3 complex
Sop2	CG8978	Cytoskeleton	actin-binding, Arp2/3 complex
tsr	CG4254	Cytoskeleton	actin binding
CG8029	CG8029	Ion Transporter	hydrogen/potassium ATPase
CG8743	CG8743	Ion Transporter	calcium channel
Vha26	CG1088	Ion Transporter	hydrogen-export channel
Vha55	CG17369	Ion Transporter	hydrogen-export channel
Vha68-2	CG3762	Ion Transporter	hydrogen-export channel
VhaSFD	CG17332	Ion Transporter	hydrogen-export channel
CG11198	CG11198	Metabolism	acetyl-CoA carboxylase
CG11451	CG11451	Metabolism	sugar transporter
CG3523	CG3523	Metabolism	fatty acid biosynthesis
Fad2	CG7923	Metabolism	stearoyl-CoA 9-desaturase
HLH106	CG8522	Metabolism	transcription factor
Hmgcr	CG10367	Metabolism	HMG-CoA reductase
CG7228	CG7228	Miscellaneous	scavenger receptor/CD36 family
DDB1	CG7769	Miscellaneous	damaged DNA binding
CG10107	CG10107	Proteolysis	cysteine-type peptidase
CG11700	CG11700	Proteolysis	polyubiquitin-like
Ubi-p63	CG11624	Proteolysis	Ub-dependent protein catabolism
vihar	CG10682	Proteolysis	Ubiquitin conjugating enzyme activity
CG2807	CG2807	RNA processing	mRNA splicing
CG5931	CG5931	RNA processing	RNA helicase
CG6015	CG6015	RNA processing	mRNA splicing
CG8241	CG8241	RNA processing	mRNA splicing
crn	CG18842	RNA processing	mRNA splicing
Hel25E	CG7269	RNA processing	RNA helicase
Abi	CG9749	Signal Transduction	signal transducer
Cdc42	CG12530	Signal Transduction	GTPase
nej	CG15319	Signal Transduction	cAMP response
RhoGAP92B	CG4755	Signal Transduction	GTPase activating
Sra-1	CG4931	Signal Transduction	Rho interactor, signal transduction
ush	CG2762	Signal Transduction	transcription factor, zinc finger
Bx42	CG8264	Transcription	transcription factor
CG14712	CG14712	Translation	Aminoacyl-tRNA synthetase
CG15415	CG15415	Unknown	Unknown
CG3911	CG3911	Unknown	Unknown
CG11990	CG11990	Unknown (PD)	Cdc73 family
alphaCop	CG7961	Vesicular Trafficking	COP vesicle coat
Arf102F	CG11027	Vesicular Trafficking	ADP-ribosylation, GTPase
Arf79F	CG8385	Vesicular Trafficking	ADP-ribosylation factor
betaCop	CG6223	Vesicular Trafficking	COP vesicle coat
beta'Cop	CG6699	Vesicular Trafficking	COP vesicle coat
CG3885	CG3885	Vesicular Trafficking	synaptic vesicle
CG8055	CG8055	Vesicular Trafficking	vacuolar protein sorting
deltaCop	CG14813	Vesicular Trafficking	COPI vesicle coat
gammaCop	CG1528	Vesicular Trafficking	COPI vesicle coat
garz	CG8487	Vesicular Trafficking	GEF activity, intra-Golgi transport

Table S3

l(1)G0155	CG1515	Vesicular Trafficking	SNAP receptor activity
Rab1	CG3320	Vesicular Trafficking	GTPase, endocytosis, exocytosis
Rab10	CG17060	Vesicular Trafficking	GTPase, endocytosis, exocytosis
Rab11	CG5771	Vesicular Trafficking	GTPase, receptor mediated endocytosis
Rab2	CG3269	Vesicular Trafficking	vesicle transport
Rab21	CG17515	Vesicular Trafficking	exoytosis, GTPase activity
Rab35	CG9575	Vesicular Trafficking	GTPase, endocytosis, exocytosis
Rab5	CG3664	Vesicular Trafficking	GTPase, endosome
Rab7	CG5915	Vesicular Trafficking	GTPase, lysosome transport
Rab8	CG8287	Vesicular Trafficking	GTPase, exocytosis
Rop	CG15811	Vesicular Trafficking	SNARE binding, exocytosis
sar1	CG7073	Vesicular Trafficking	RAS small monomeric GTPase activity
sec23	CG1250	Vesicular Trafficking	GTPase activator activity
sec5	CG8843	Vesicular Trafficking	vesicle-mediated transport
sec6	CG5341	Vesicular Trafficking	vesicle-mediated transport
Slh	CG3539	Vesicular Trafficking	SNARE binding, exocytosis
Snap	CG6625	Vesicular Trafficking	soluble NSF attachment protein
Syb	CG12210	Vesicular Trafficking	synaptobrevin, v-SNARE
Syx1A	CG31136	Vesicular Trafficking	t-SNARE activity ; SNAP receptor activity
Syx5	CG4214	Vesicular Trafficking	t-SNARE
Syx7	CG5081	Vesicular Trafficking	t-SNARE activity ; SNAP receptor activity
TER94	CG2331	Vesicular Trafficking	ATPase, microtubules, exocytosis
Vps28	CG12770	Vesicular Trafficking	vacuolar protein sorting
zetaCOP	CG3948	Vesicular Trafficking	COPI vesicle coat

B dsRNA targets that only decreased infection by *L. monocytogenes*

Gene	CG Number	Functional Category	Annotation
cdc2rk	CG1362	Cell Cycle	cyclin-dependent kinase
CG12343	CG12343	Cell cycle	cyclin regulator
Mi-2	CG8103	Cell Cycle	chromodomain, DNA binding
mus209*	CG9193	Cell Cycle	nucleic acid binding
pim*	CG5052	Cell Cycle	sister chromatid separation
Pp4-19C	CG18339	Cell Cycle	serine-threonine phosphatase
thr*	CG5785	Cell Cycle	mitosis
raw*	CG9321	Cell Death	programmed cell death
CG1017	CG1017	Cytoskeleton	microfibril
Lam	CG6944	Cytoskeleton	lamin filament
CG10960	CG10960	Metabolism	glucose transporter
CG8199	CG8199	Metabolism	acyl-CoA biosynthesis
CkIalpha	CG2028	Miscellaneous	casein serine-threonine kinase
Nxt1	CG12752	Miscellaneous	nuclear transport
Sec61beta	CG10130	Miscellaneous	protein transporter
CG3775	CG3775	Proteolysis	neprilysin-like
CSN4*	CG8725	Proteolysis	signalosome, protease
Cbp80	CG7035	RNA processing	Cap binding protein
CG1542	CG1542	RNA processing	rRNA processing
CG16941	CG16941	RNA processing	mRNA splicing
CG18591	CG18591	RNA processing	mRNA splicing
CG3058	CG3058	RNA processing	mRNA splicing
CG6905	CG6905	RNA processing	mRNA splicing
CG8877	CG8877	RNA processing	mRNA splicing
fne	CG4396	RNA processing	RNA binding
Hrb27C	CG10377	RNA processing	mRNA splicing
lark	CG8597	RNA processing	RNA binding
14-3-3epsilon	CG31196	Signal Transduction	protein kinase C inhibitor
CG17493	CG17493	Signal Transduction	calcium ion binding
CG1796	CG1796	Signal Transduction	Trp-Asp repeat
mXr	CG30361	Signal Transduction	GABA-B like receptor
CG31302	CG31302	Signal Transduction	Fibronectin/SH3
CG3573	CG3573	Signal Transduction	IP3 phosphatase activity
CG6124	CG6124	Signal Transduction	receptor binding
CG9753	CG9753	Signal Transduction	adenosine receptor activity
puc*	CG7850	Signal Transduction	MAP phosphatase, JUN phosphatase
RacGAP50C*	CG13345	Signal Transduction	GTPase activating,
ran	CG1404	Signal Transduction	GTPase activating
shn	CG7734	Signal Transduction	transcription factor, zinc finger
Tor*	CG5092	Signal Transduction	protein kinase, PI3, PI4
CG31258	CG31258	Transcription	cell cycle
CG5591	CG5591	Transcription	transcription regulation

Table S3

CG8092	CG8092	Transcription	zinc finger containing protein
RpII140	CG3180	Transcription	RNA polymerase
RpII215	CG1554	Transcription	RNA polymerase
snf	CG4528	Transcription	RNA polymerase
Spt5	CG7626	Transcription	transcriptional elongation regulator
Spt6	CG12225	Transcription	transcription factor, elongation
Taf4	CG5444	Transcription	general transcription factor
Taf6	CG32211	Transcription	general transcription factor
TfIIB*	CG5193	Transcription	general transcription factor
Trap95	CG5465	Transcription	transcription factor
Trf2	CG18009	Transcription	TATA-box binding
zfh1	CG1322	Transcription	zinc finger containing protein
CG13258	CG13258	Unknown	Unknown
CG15321	CG15321	Unknown	Unknown
CG18561	CG18561	Unknown	Unknown
CG32280	CG32280	Unknown	Unknown
CG32737	CG32737	Unknown	dicistronic cassette
CG33456	CG33456	Unknown	Unknown
CG8435*	CG8435	Unknown	Unknown
CG9324	CG9324	Unknown	Unknown
CG9616	CG9616	Unknown	Unknown
DRSC01346	sanger	Unknown	Existence Uncertain
DRSC05057	sanger	Unknown	Existence Uncertain
CG30349	CG30349	Unknown (PD)	Trp-Asp repeat
CG6018	CG6018	Unknown (PD)	carboxylesterase
CG9298	CG9298	Vesicular Trafficking	vesicle mediated protein transport
comt	CG1618	Vesicular Trafficking	ATPase activity, protein transport

C dsRNA targets that only decreased infection by *M. fortuitum*

Gene	CG Number	Functional Category	Annotation
fzy*	CG4274	Cell Cycle	cyclin catabolism
Act42A	CG12051	Cytoskeleton	actin
CG14782	CG14782	Cytoskeleton	Plekstrin-like
cpb	CG17158	Cytoskeleton	F-actin capping protein complex
CG6121	CG6121	Establishment or Maintenace of Chromatin	histone acetyltransferase activity
CG7752	CG7752	Establishment or Maintenace of Chromatin	DNA binding
Chro	CG10712	Establishment or Maintenace of Chromatin	Chromo domain
dom	CG9696	Establishment or Maintenace of Chromatin	DEAD/DEAH box helicase, N-terminal
E(Pc)	CG7776	Establishment or Maintenace of Chromatin	enhancer of polycomb
Hsc70-3*	CG4147	Heat Shock Protein	heat shock protein
CG9467	CG9467	Ion Transport	Potassium ion transport
Ald*	CG6058	Metabolism	Fructose bisphosphate aldolase activity
Ufd1-like	CG6233	Proteolysis	Ubiquitin fusion degradation protein
CG1420*	CG1420	RNA processing	mRNA splicing
sbr*	CG17335	RNA processing	mRNA nuclear transporter
Gbeta76C	CG8770	Signal Transduction	Heterotrimeric G-protein complex
kay	CG1550	Signal Transduction	Fos transforming protein
Rac2	CG8556	Signal Transduction	Ras small GTPase, Rho type
CG13038	CG13038	Unknown	Unknown
CG14542	CG14542	Unknown	Unknown
CG14657	CG14657	Unknown	Unknown
CG4699*	CG4699	Unknown	Unknown
Ras85D	CG9375	Vesicular Trafficking	Ras small GTPase, Ras type

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Gene	CG Number	DRSC Amplicon	'S' Primer	'R' Primer	Amp. Length	FBGN	Num Potential 2ary Targets	Max 2ary Targ Overlap
CG3523	CG3523	DRSC00268	GCCTGTCTTGGTGTAAGTG	AGCGTCGTCCTGGCAC	503	FBgn0027571	0	0
CG15415	CG15415	DRSC00430	GGAGCTTCCAACTCCTTTTT	CGCTTTGAGTCCCTAAAATC	506	FBgn0031549	0	0
CG2807	CG2807	DRSC00535	TGGCCAAGGCTGTAATTGT	GTCATTTATTAGTGAAGGTAATTGA	480	FBgn0031266	0	0
CG3058	CG3058	DRSC00563	GTATCTGTACTTGGTAGAGTAGT	AATACGTTTCGGTCACGATT	346	FBgn0031601	0	0
CG3605	CG3605	DRSC00619	CAGAGCAATGCGCAACT	GCGGAAACTTAAGAAACTGAC	499	FBgn0031493	0	0
sec5	CG8843	DRSC00714	GGCAGATCCAGGCTGATG	TCCCATTGGCGATAAACTG	504	FBgn0031537	0	0
p16-ARC	CG9881	DRSC00730	GACAGCACGCGGACAAT	GCCAAAAACACGTCCAGC	496	FBgn0031437	0	0
Rab5	CG3664	DRSC00777	TCCTGGCCAGCCGTGT	GGCAACCACTCCACGCA	264	FBgn0014010	1	23
Slh	CG3539	DRSC00789	GCCTGCAGCGCCTCC	AAAACCCAAGGCCTGTGAC	507	FBgn0015816	0	0
ush	CG2762	DRSC00843	TCGGATTGGGCGTAACTC	GCCAAGGAGCTGACCCT	481	FBgn0003963	0	0
	sanger	DRSC01346	GTAAACGGGCTCGAGGTTA	GAAGCAGCGACCAGGAC	210		4	25
Acp29AB	CG17797	DRSC01857	TTTTTTTTGTATCCTGATTACTCTT	CACAAACGCCGCAAAATAC	507	FBgn0015583	0	0
Arc-p34	CG10954	DRSC02113	AATGTGACATAGCCAATGTTGT	CCAAGCCTGATCGTGTCA	208	FBgn0032859	0	0
CG13258	CG13258	DRSC02244	GGATGCGCAACATCGTTT	TCGCCCAGGATTGGGTG	498	FBgn0032582	0	0
CG18561	CG18561	DRSC02675	AATCTTCGCCAGACGGAC	CCCAAGAAGATGAATCAACATT	274	FBgn0032301	5	22
CG18591	CG18591	DRSC02680	GGGACTGACGTTCTGTATGA	TCAAAGGAAATCCCAAGGTG	266	FBgn0031962	0	0
Vha68-2	CG3762	DRSC02721	GGTCACCTCCGGTGATGT	CCCTGAAGGACATTAACGAG	138	FBgn0020367	0	0
Tor	CG5092	DRSC02811	TACCTTGTGAGCAGACCTTC	ACCACAAACGAACTACGAAC	515	FBgn0021796	0	0
Ced-12	CG5336	DRSC02840	GCGGCGTCTCAATGAAAT	GGAGAACATTGTTATGTGCAG	515	FBgn0032409	1	21
Arc-p20	CG5972	DRSC02917	GAACCGTTTGAGGAACTCC	ACATTGAAGCCCTACCTGAC	495	FBgn0031781	0	0
CG7228	CG7228	DRSC03033	ACTTTCCTCCGACGCAATA	GGCGTTAACATTGCCAATAAA	508	FBgn0031969	0	0
CG9298	CG9298	DRSC03190	GGCATCTCCAGGGAGTAGA	CACGCATTGAGCACGAG	562	FBgn0032060	0	0
CG9324	CG9324	DRSC03201	GCAGGCGGCCCACCT	ATCAGCCATCACTGAAAGTC	249	FBgn0032884	0	0
CycE	CG3938	DRSC03295	GGGTAGATAAAGGCATCGTC	GTTTGGCGCCTGATGTGT	512	FBgn0010382	0	0
Hel25E	CG7269	DRSC03342	TATGTAGAGAGATCGATTTCCT	GGTCATCTTTGTGAAGTCTGT	399	FBgn0014189	0	0
Hrb27C	CG10377	DRSC03347	CGCGAGTACATGTCAGTG	GGCCGAGCCTCGTGAT	504	FBgn0004838	0	0
Lam	CG6944	DRSC03359	CCATAAGGTCCTGGTACTCC	GGAGAACACCATTCAGAGTC	512	FBgn0002525	0	0
NPC1	CG5722	DRSC03378	CCGAGTATTCGACCAACTT	GCGATCATTCTGACATTCCT	518	FBgn0024320	0	0
Rca1	CG10800	DRSC03407	GCCTCGCTTATGAAAACCC	TTTCAATCGCCACACAGTAG	515	FBgn0017551	0	0
Syx5	CG4214	DRSC03432	CTCAACGATGGTAGATTCTATAT	AAAAAGAAGAGCTTATTTGATGA	507	FBgn0011708	0	0
Sop2	CG8978	DRSC03438	GCAGTGGCACACAGCTAT	GCGTCAAGTGGTCGCC	516	FBgn0001961	0	0
TfIIB	CG5193	DRSC03454	CAGAAGCGGCACATGAAG	GCACAGGATCCGCATCC	452	FBgn0004915	0	0
VhaSFD	CG17332	DRSC03471	GAAGCAGGCGACGGAAA	ATACCAGTTGATCTTTTGCCT	517	FBgn0027779	0	0
beta'Cop	CG6699	DRSC03492	CTCTTTAACCAGAGACATGTTG	TTTCGGAGTGCGTCAAAAC	506	FBgn0025724	0	0
cdc2	CG5363	DRSC03504	AGTCGGGTAGCGAAGTAAC	GTCTGTTTGGAGGATGTTTTG	577	FBgn0004106	0	0
chic	CG9553	DRSC03507	TGTGTTGTCTTCATGCAGTG	CAAAAGAGGAGCTCTCCAAA	166	FBgn0000308	0	0
fzy	CG4274	DRSC03534	CTTGATGGTCGTTGAATTTGT	GATTGGAGTGCCGACAATAT	499	FBgn0001086	0	0
mts	CG7109	DRSC03574	CACGAGGCGAGATTCCC	AAATGCCCGGTGACAGTG	499	FBgn0004177	0	0
pim	CG5052	DRSC03591	AATTTAATAAGTATTCAGGCTCTG	CCAGCGAATCCCATTAAAAAT	574	FBgn0003087	0	0
raw	CG9321	DRSC03599	CGCCGGTGTATGGAAACT	CCCGATGTGGACATTTACTAC	513	FBgn0003209	0	0
smt3	CG4494	DRSC03611	ATGGAGCGCCACCAGTC	GTCTGACGAAAAGAAGGGAG	269	FBgn0026170	0	0
His2B:CG17949	CG17949	DRSC03757	TTATTTAGAGCTGGTGTACTTG	GAACAGCTTTGTAAATGATATTTTC	193	FBgn0061209	0	0
His-Psi:CR31615	pseudogene	DRSC03760	TTGTGCAATTGTGACGCC	AGGTTCTCAAGTTGGCTGG	131, 688, 913	FBgn0051615	2	114
His-Psi:CR31616	pseudogene	DRSC03760	TTGTGCAATTGTGACGCC	AGGTTCTCAAGTTGGCTGG	131, 688, 913	FBgn0051616	2	114
CG17493	CG17493	DRSC03798	AGTCTTCTTCATGATTCGCA	GGCTGGCAACGCCAAC	517	FBgn0040010	0	0
Act57B	CG30294	DRSC04042	AGGATTCCATTCCCAGGAAG	CCGTCCTGCTGACTGAG	510	FBgn0000044	5	62
CG10540	CG10540	DRSC04080	ACCTCCTTGGCCACCTG	GTCGCTTCTACGACCCG	494	FBgn0034577	0	0
CG5591	CG5591	DRSC04291	AATCCTCCGCTGGAAACC	CCGTTGCTGTACGAGACT	179	FBgn0034926	0	0
Trap95	CG5465	DRSC04506	GCCAAAAAATTAGCATAATAAAAG	GGAGGAGGTGCCAACAAC	515	FBgn0034707	0	0
CG6018	CG6018	DRSC04521	AGCATGTAAAGCGGATCATC	CGTTGGGTCAAGGAGAACA	518	FBgn0034736	0	0
Nxt1	CG12752	DRSC04630	ACCTCCTGCATTCGGTAG	TGGACGCCTCTATTTGGAC	297	FBgn0028411	0	0
tsr	CG4254	DRSC04718	CATTTCTGGATATCTTCTAGAAAC	TGGTGTAACTGTGTCTGATGT	168	FBgn0011726	0	0
Bub1	CG7838	DRSC04838	TTGTGGGAGTGTTTCAGTTTT	CTCCGTCACGTCAATTTGG	479	FBgn0025458	0	0
geminin	CG3183	DRSC04984	TGTCGTCCTCCTCCACCT	ACAGAGGCCGAGCAGAA	508	FBgn0033081	0	0
Rab2	CG3269	DRSC05017	GACACCTTCCTGGATCTTCT	CTATCACACGCTCTTATTACC	317	FBgn0014009	0	0
	sanger	DRSC05057	AATCATAGTAAGTGGAACATAGC	CAATACGATGGCTCCACAAA	291		2	23

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mXr	CG30361	DRSC05106	TTGGCTCCCGTTGTTTCC	GCTAAAGACGAAGAAATTGTG	493	FBgn0050361	4	21
CG12343	CG12343	DRSC06135	CCTCTCGTTGATGAAGTCC	GCGTACGGACAACCACC	508	FBgn0033556	0	0
Vps28	CG12770	DRSC06168	AGGAACTGGCGGACCTG	GCCGATCTATACGCAATCA	497	FBgn0021814	0	0
CG30349	CG30349	DRSC06421	TCCATGGATACGTCAGAGTC	GACAATCATCTCAACGATAACA	268	FBgn0050349	0	0
CG33456	CG33456	DRSC06562	CTTGCTGGATTCCTCCAATT	CGCACACGTCGCAATTT	504	FBgn0053455	0	0
CG2249	CG2249	DRSC06831	GAGCAGTTGGTGCCTGAC	GCGGACATGGTGGAGTTC	242	FBgn0040773	0	0
sec6	CG5341	DRSC06932	ACGATGGTGATGATGTAGTGA	GGCTTGGAGGGCAATGAA	488	FBgn0034367	0	0
CG6197	CG6197	DRSC06967	CGAGGAACATTCCGTAATTG	TGGCACAAGCGGGTGAC	508	FBgn0033859	0	0
CG8029	CG8029	DRSC07058	GGAGTCGCCGAAGGGAA	CGCCATAGCTGCTATCAG	514	FBgn0033393	0	0
CG8055	CG8055	DRSC07061	TGGTTGTCGCCTTTTTCTTT	GCACGACATGATGGATGAC	248	FBgn0033385	0	0
CG8057	CG8057	DRSC07062	GCTTGGGATCGTGCTTCC	GCTGCGGGGGGTGGA	475	FBgn0033383	1	21
CG8092	CG8092	DRSC07077	TGATACAGACGCTGAGTGA	TCCCTAGGAACCACATCCC	512	FBgn0033998	0	0
CG8241	CG8241	DRSC07120	GTGAGCCTCATCCAACATAA	GCCAACATGCGAGGAATG	498	FBgn0033898	0	0
CG8435	CG8435	DRSC07179	TCTTCGCGCTCCTCCC	GCAGTACACCGTGAGATTG	492	FBgn0034084	0	0
garz	CG8487	DRSC07193	TTGCACAAACTTTGATTCCTG	CATATCGGCGCACTATAATC	508	FBgn0033714	0	0
CG11198	CG11198	DRSC07249	CTGCCTCTACGGCTTCC	CACCAGCCGGCTTATGA	514	FBgn0033246	0	0
CG8877	CG8877	DRSC07293	TTAACATCGTGCTTCATTAAAC	ATTTGAAAAGCTGTACGAGAAA	504	FBgn0033688	0	0
CSN4	CG8725	DRSC07350	CCGAGATCTGGTCGATGT	AAGTCTGTTATGCTCGTGTC	507	FBgn0027054	0	0
DebB	CG16792	DRSC07397	CGCATTTCGCCCTCCT	CCCAAGCCCTTCCTGAAC	236	FBgn0000426	1	21
Dp	CG4654	DRSC07402	AATTTGCGGGCAGTCCTAT	ACTCGTTGCACTCCATGTC	309	FBgn0011763	0	0
Rho1	CG8416	DRSC07530	CAAAAGGCATCTGGTCTTCT	AAGCAGGAGCCGGTGAA	171	FBgn0014020	0	0
RnrS	CG8975	DRSC07533	ACATCAGCACGGCAAAGT	GATTTGTCCAAGGACCTTACT	508	FBgn0011704	1	21
Sec61beta	CG10130	DRSC07548	CGAGTCGTCCGTGTAGAA	TCCAGCCAGTTCAACGTC	193	FBgn0010638	0	0
SmD3	CG8427	DRSC07553	TGTGCGCGCAGAATGG	TATCGGAGTGCCCATTAAAG	312	FBgn0023167	0	0
Spt5	CG7626	DRSC07556	CCGGCAGCGGTATAACT	CGTTCCGGCGAGATCAA	515	FBgn0040273	0	0
Syb	CG12210	DRSC07559	GAGCAGCACAACGGCTAT	ACAATGCAGCCCAGAAGAA	248	FBgn0003660	0	0
TER94	CG2331	DRSC07560	ATCGCGGAGTTCTGATTTT	GTGGTTCGGCGAGTCTG	513	FBgn0024923	0	0
RacGAP50C	CG13345	DRSC07575	TGACACTGAACGCAATTGTC	CGATGTGCGCACATCAAA	510	FBgn0033881	0	0
betaTub56D	CG9277	DRSC07583	GGCGGCCATCATGTTCTT	ACTGGCTCCGGTATGGG	480	FBgn0003887	2	41
cdc2rk	CG1362	DRSC07590	AGCCAGGCCAAATGGACT	TCCGCTTGCGTGAGGT	554	FBgn0013435	0	0
mus209	CG9193	DRSC07653	GCCTTTGTGAAGGCGTTC	CGATGGCTTCGACAAGTTT	492	FBgn0005655	0	0
shn	CG7734	DRSC07681	AGAAGTCCACTGCCACTG	ACCTGCCCCCCAGATTG	513	FBgn0003396	0	0
thr	CG5785	DRSC07706	GATAGGTAAAACGATCTTCCAG	TTGCCGAACGAGTGACTAT	512	FBgn0003701	0	0
CG32280	CG32280	DRSC08024	GACGGTATCGCCCCAAATA	TGCTCCTCCGCAGTTCA	440	FBgn0052280	0	0
CG1017	CG1017	DRSC08154	CATTCGCTTGAGTTCACG	GGAGCACAGGGAGCGAT	519	FBgn0035294	0	0
CG11814	CG11814	DRSC08208	TGCAGATACAGACGTAAGAG	CAGTCATCATTGCCGAATAG	500	FBgn0035296	0	0
CG5691	CG5691	DRSC08570	ATACTCAGGCATTCGTGTAG	CTGCAGGAGCATAGCGT	500	FBgn0035297	0	0
CG6905	CG6905	DRSC08577	GGGAGACTACGCTGAATAAC	GCACGAGTCAGACTTCTC	504	FBgn0035136	0	0
Klp61F	CG9191	DRSC08671	CTATTTTTGGACCGCAAGTT	CCAACGCCTTGCACTAAAT	498	FBgn0004378	2	21
Rop	CG15811	DRSC08693	CCCATGGCCAGATCCTGT	GAAGCTGGACGCCTACAA	498	FBgn0004574	0	0
Ubi-p63E	CG11624	DRSC08703	GGGGGATTCCCTCCTTATCT	AGCAGCTTGAGGATGGAC	426	FBgn0003943	3	44
alphaCop	CG7961	DRSC08706	AGGAAGCTAAGCTTGTCAAA	GGACGAGTCTGGAGTGTTT	513	FBgn0025725	0	0
pav	CG1258	DRSC08730	ATTCTCATCATAGTCCTCAATTC	ATGCCAATCGACACATGTTC	518	FBgn0011692	1	23
dpr6	CG14162	DRSC09005	CATCACAATCACGACGAGG	ACTGCCGCCCATGTTGA	333	FBgn0040823	2	21
CycA	CG5940	DRSC09132	ATTTCACGTCATGGTTCTCTT	GCCAAGAAATCGAATGTGGT	139	FBgn0000404	0	0
Arp66B	CG7558	DRSC09669	GATCCGGAGACGTGTGTC	CGAGGGCTATGTGATCGG	505	FBgn0011744	0	0
CG10107	CG10107	DRSC09698	GGATTAAAGGTTGCTTTACGG	GGTGCAAAAGTGGACCAAG	500	FBgn0035713	0	0
CG10660	CG10660	DRSC09769	CAGTTTCTTGCCCATCTTCT	TTAACTCCACCAAGGGTGTG	512	FBgn0036288	0	0
CG10960	CG10960	DRSC09807	AAGTAGGTGGGCGATTCC	GCCGCCGGTACCGTC	515	FBgn0036316	0	0
mad2	CG17498	DRSC10274	GTCCCATTTGGCCGGTAAT	CCCAGCCGAAGACTTTAAC	464	FBgn0035640	0	0
CG3885	CG3885	DRSC10384	GACTAATAACGTCCATCTGAAAA	CCACGGTCAGTCGGTTTA	579	FBgn0036718	0	0
CG3911	CG3911	DRSC10388	GCTGAGTATGGCACTGTAG	CAAGCAGCTGGAGCGAA	271	FBgn0035992	0	0
CG5931	CG5931	DRSC10559	TGTGGCTCTAGATCGTAAAG	GCCTCTCACTATTACCTAACC	515	FBgn0036548	0	0
CG6694	CG6694	DRSC10696	TTGGGCTGCGCTTCATT	ATCCATATCAATCCGCACTTT	500	FBgn0035900	0	0
CG8743	CG8743	DRSC11032	CCAGTCGGCCGTCAAAG	TCCTACATTTTCGATCCACATA	493	FBgn0036904	0	0
Cdc27	CG8610	DRSC11112	CCATCGGCCGATTGTTTC	GATGATGGGCAAAAAGCTAAA	519	FBgn0012058	1	21
CycT	CG6292	DRSC11124	ATGGGCTCCTTTTTAATGTCT	TGGGCATGCCACCTCAC	478	FBgn0025455	4	21

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Fad2	CG7923	DRSC11165	CACACGGAAAAATATGAGGAA	GGGCTCATCGCACATTCA	512	FBgn0029172	2	23
HLH106	CG8522	DRSC11182	GCGGTGTCAGTAGATTGTG	AGTTCCTGGATATGGCTATTG	493	FBgn0015234	0	0
Mi-2	CG8103	DRSC11222	ACCCATTCGCAATGCCAG	CGGAGGGCGAAGATGG	514	FBgn0013591	1	24
Rab8	CG8287	DRSC11261	CGGTCAATTCGCACTTGTT	CACTGCCGGCCAGGAG	191	FBgn0015796	0	0
Snap	CG6625	DRSC11285	TGATGAGCTTGAACTCCCT	CCAAGTCTATTCAGCACTATG	318	FBgn0011712	0	0
Taf4	CG5444	DRSC11297	GGCGTCGCGTTTCTTTT	ATTGTGCAAATACGTGGACC	501	FBgn0010280	0	0
Taf6	CG32211	DRSC11299	CAGAAACAGCGAAGGATTATC	GAAATCACATCCACCAACTCT	510	FBgn0010417	0	0
lark	CG8597	DRSC11362	GCCATCCATGATGCGGTC	ATACGCTGAACGAGTTCG	509	FBgn0011640	1	22
pbl	CG8114	DRSC11381	CCATGCGCGATTCGGT	TTTTAAAAACAAGTTGGAAGAGTT	518	FBgn0003041	0	0
th	CG12284	DRSC11404	GCCACCGTATCGATATAGAG	CCAACGACTCGACGCT	502	FBgn0003691	0	0
zetaCOP	CG3948	DRSC11412	CCGTCGCAGATCTCGTC	GCATCCTGGCCAAGTACTA	322	FBgn0040512	0	0
Arf79F	CG8385	DRSC11606	TAGCGATTAGCGTTCTTCA	CTGCCAAATGCAATGAACG	161	FBgn0010348	0	0
CG11451	CG11451	DRSC11663	ATCAGTAATTGAAAATAGGGCAT	CGTAGGGTGCAAACTAACA	519	FBgn0037025	0	0
Syx7	CG5081	DRSC11763	TTGAGCTCCGGAGAATCTT	GGACTTACAGCATATGGAGAAT	247	FBgn0033583	0	0
CG7597	CG7597	DRSC11836	CGACACTGTCCGGAACAT	GGTTCGCATCACTATCATCA	517	FBgn0037093	1	21
CG9772	CG9772	DRSC12329	TGGGCCAGACGTATTACAA	GAGAAGCTGCAGATTCTGG	509	FBgn0037236	0	0
Vha26	CG1088	DRSC12371	GGCCAGCAGCTCAACAC	GCGCGAGGACCATGTG	298	FBgn0015324	1	21
sec23	CG1250	DRSC12387	GGAATGGGGGCTGCATG	ACGACGAGCTGAAGCAC	508	FBgn0037357	0	0
alphaTub84B	CG1913	DRSC12622	CGGGGATCGCACTTGAC	CTCGTTCGGTGGAGGTAC	507	FBgn0003884	2	94
alphaTub84D	CG2512	DRSC12623	GTGACGGGGATCCACCTT	TTCGGTGGAGGTACCGG	507	FBgn0003885	2	90
Su(var)3-9	CG6476	DRSC13081	CAACGGCGCCTAGCAC	AGAGCCAGGCGAAAGAG	495	FBgn0003600	0	0
Abi	CG9749	DRSC14099	TGCTGCTGCGATCGTC	ATCGACTACTCGATGTTGG	517	FBgn0020510	0	0
Ald	CG6058	DRSC14109	AACGGCGGCGGGAAC	AGATCCTGAAGAAGAAGGGA	506	FBgn0000064	1	22
granny-smith	CG7340	DRSC14165	CCACCGAGTTTTTCATATCAG	GTTGCAACAGGCAAATATCAT	172	FBgn0040493	0	0
Nup98	CG10198	DRSC14209	AATGCCTGTTGGATGTGATTC	GCCCCAATCTCGACCCAA	502	FBgn0039120	0	0
CG31258	CG31258	DRSC14371	GGTACCAGTTCGTTCTCCA	TGGTAAACTATTTGGGTCTCTC	514	FBgn0051258	0	0
CG11779	CG11779	DRSC14384	GTCCCGCACGCACATAA	ATGGAGCTGCACAAGGAC	513	FBgn0038683	0	0
CG11990	CG11990	DRSC14462	GCTCCCGCTATTACACCC	CCATCAAGGCAAAGCGTC	496	FBgn0037657	0	0
CG1420	CG1420	DRSC14729	GCTTCTCTGCTTTAAGTTGTC	AAGTCCCGTGAGGACTGG	508	FBgn0039626	1	21
CG14712	CG14712	DRSC14935	GTAGTCGGAGCAACTGTAG	ACTAAGTAACCAGGTTATAAAGC	510	FBgn0037924	0	0
CG1542	CG1542	DRSC15035	TGCTTGGACTCAAGCGC	TGGACATGATCAACACACTAG	508	FBgn0039828	0	0
CG16941	CG16941	DRSC15166	TATCCGTACGACGCTCAG	AGTCGGACGACGAGGG	507	FBgn0038464	0	0
CG17119	CG17119	DRSC15175	TGATAGAAAAAGCACTGAAGG	GAAGGATGTGTTCGTACGC	357	FBgn0039045	0	0
Syx1A	CG31136	DRSC15359	TCTCGCCCTGCGACTC	ACTCGGCCATCCTGTCC	513	FBgn0013343	0	0
CG3731	CG3731	DRSC15508	AGGTTGGAGGCGTTGTTG	GGCAAGGCCGATCTGAC	341	FBgn0038271	0	0
CG4699	CG4699	DRSC15625	TAGCGAGAGCTGCTGGT	GTCCGAGCTCAACCTTCT	512	FBgn0038364	0	0
RhoGAP92B	CG4755	DRSC15637	GACTTCGCCGATGAAAAAG	GGGTCTGCTGCGAGTG	508	FBgn0038747	0	0
Sra-1	CG4931	DRSC15679	CATTGAGGGCTCCTTCGT	TGTCGGTGCGAGAGACA	515	FBgn0038320	0	0
CG31302	CG31302	DRSC15724	CAGGCCCCGTCGAGG	TAACCCAGAACCGACAGAC	486	FBgn0051302	0	0
CG5844	CG5844	DRSC15890	ATTCTGCACCGCCTGGT	CTTTTGCTCCGGCTTCG	514	FBgn0038049	0	0
CG6015	CG6015	DRSC15948	AGCGTCGACTTCTCCTC	CCACGCTCAAGGAGGTAA	499	FBgn0038927	0	0
CG6124	CG6124	DRSC15969	TGTCCATTTCATATCCATCATTG	CTCCTGTTTGCAAGGATGG	480, 84	FBgn0039484	0	0
14-3-3epsilon	CG31196	DRSC16370	TTCAATGCCAAGCCCAAAC	AATGGTGGAGGCCATGAAG	462	FBgn0020238	0	0
CG8199	CG8199	DRSC16395	GGACTGGAGATGGTGACAAA	CAGCTGCGCGGGACT	511	FBgn0037709	0	0
CG9616	CG9616	DRSC16518	AGAGTAGTTGATCGTTGAGATA	CTTGTTTGCGTTATTGGTTCT	411	FBgn0038214	0	0
CG9753	CG9753	DRSC16556	TTGCCCATTGGCCTGGA	GCAGGAGGCCCTGAAGA	489	FBgn0039747	0	0
DDB1	CG7769	DRSC16639	AGAGGCACTATTGCGAAGT	AATAATTCCCCGCTCCATTC	514	FBgn0027049	0	0
E2f	CG6376	DRSC16655	GCGCCTTGATCACGATAAC	CGCTGTCGACGCCCC	492	FBgn0011766	0	0
His4r	CG3379	DRSC16703	AACCGCCAAATCCGTAAAG	CGTGGAAAGGGAGGCAAA	365	FBgn0013981	0	0
Hmgcr	CG10367	DRSC16704	GGTAGTCAAAGTGTTCATAAGG	TCATCGCCTTGGTAGTTAAAT	519	FBgn0001205	0	0
Rab1	CG3320	DRSC16808	TGGTGTGGTCGACTACTTTC	CACCATCACGTCTTCATATTAT	191	FBgn0016700	0	0
Rab11	CG5771	DRSC16809	TGTGAGTATGTTCTGGAATGC	AAAACAATTAAAGCGCAAATCT	339	FBgn0015790	2	23
Rab7	CG5915	DRSC16810	CTCCAACTCTAACGCATTCT	GACACTGCTGGTCAGGAAC	345	FBgn0015795	0	0
RpII140	CG3180	DRSC16831	TGACCGTTTCCTCCTCAAG	CAATACTCTTTGGGGTATGTTG	515	FBgn0003276	0	0
Vha55	CG17369	DRSC16896	ATGGGGATCTGGGTGATGG	GCCCGTGGCCAGAAGAT	512	FBgn0005671	0	0
alphaTub85E	CG9476	DRSC16899	CCCGTGGGACACCAGTC	CTGTGGTCGAGCCATACAA	511	FBgn0003886	3	35
dmt	CG8374	DRSC16932	AAGTTCTCCGCATTCTCTTC	TAATTTGGCCCGATCCGTA	516	FBgn0016792	0	0

Table S4

gammaCop	CG1528	DRSC16955	GTCCATCTGGCAACGACC	TCGGTAGAGCGTCTGATG	492	FBgn0028968	0	0
klg	CG6669	DRSC16978	AACACATCCAGTCGCATATC	AAGTCAACGGCCAGGATC	137	FBgn0017590	0	0
puc	CG7850	DRSC17034	GCTGCCGCCGAAGTG	GATGCACGGAAAACGGGT	506	FBgn0004210	0	0
sar1	CG7073	DRSC17049	GGTTGTTAGCTGATACAGTCC	GACGCGTCTGGAAGGAC	227	FBgn0038947	0	0
zfh1	CG1322	DRSC17098	GCCTGCCGCCTGATTG	TCGCAAGCAATCAAACAAG	516	FBgn0004606	0	0
CG32000	CG32000	DRSC17103	CAGATTCGGTTTCAGCCATA	GTACTCTTACGGAAGATGGAC	318	FBgn0052000	0	0
sphinx	CG11091	DRSC17191	CAAAACACAAAAGCCAAATAGA	GGGACGCCGCAACAAG	301, 306	FBgn0039931	0	0
CG4692	CG4692	DRSC17191	CAAAACACAAAAGCCAAATAGA	GGGACGCCGCAACAAG	301, 306	FBgn0035032	0	0
Arf102F	CG11027	DRSC17195	GTTCTCTTTCAGCTTCAGTTAT	GGCTTGGATGCTGCTGG	250	FBgn0013749	0	0
Act5C	CG4027	DRSC17723	CCGCAAGCCTCCATTCC	GAGGCCCCGCTGAACC	500	FBgn0000042	5	77
Bx42	CG8264	DRSC17743	TTTGGCGTTCTTCCAGTTC	TGGACGACAAGGGAAAGG	506	FBgn0004856	0	0
CG11700	CG11700	DRSC17794	ACCAAGTGAAGGGTCGATT	CCTGCGTCTGCGGGG	456	FBgn0029856	3	61
l(1)G0155	CG1515	DRSC17970	GCTCTGCAGCGACAATTT	CGAGGCGCGTCTCCT	591	FBgn0026664	0	0
CG15321	CG15321	DRSC18006	GCTGCTCCGCTTTTTATTG	AAAACAAATTGCAGCTAAAAAAG	478	FBgn0030150	2	21
CG3367	CG3367	DRSC18305	TTGCTGCTGCACAGTGG	GTCTGGGCGTCGGATTG	473	FBgn0029871	2	24
CG32737	CG32737	DRSC18370	CCGGACGATCCGGAAAC	CGCATCCAAGTTCTATCAGT	477	FBgn0052737	0	0
Cbp80	CG7035	DRSC18450	TAGGCACTTCTGCAACACC	CCGCATGTTCGACTACAC	505	FBgn0022942	0	0
CG3573	CG3573	DRSC18576	TGCTCGGCTCGTTAAATC	CGATTTGAATTACCGCATCC	491	FBgn0023508	0	0
Spx	CG3780	DRSC18720	TAGCATGCCCATATTGTTATTC	GTCGGCGCATCAGAAGA	508	FBgn0015818	1	23
Trf2	CG18009	DRSC18727	GTAACGTGGACGCTTATTCT	CTAGCGTAAACCACGTTGA	515	FBgn0026758	0	0
crn	CG18842	DRSC18755	GCTCAGATGCAATAGCTGTA	TAGCCCTAGGCGAAACAG	495	FBgn0000377	0	0
deltaCOP	CG14813	DRSC18760	CCGCCTTGGATTTGGTGT	TCCCGAGTACAGCCACT	407	FBgn0028969	0	0
nej	CG15319	DRSC18801	CTTTTTCTTGTCACCTGCATT	GAGACAACGACGATGAGAC	506	FBgn0015624	0	0
snf	CG4528	DRSC18835	CTTCTCATCGGTACCCGG	TACCCAACCAAACGATTTACAT	341	FBgn0003449	0	0
Spt6	CG12225	DRSC18836	CGGACCCAAGCCACAGA	TGGCCGACCTTCGAAAG	494	FBgn0028982	0	0
Arp14D	CG9901	DRSC19332	CGTATCGTTCTTGAGTACCC	GTGGCTACGCTTTCAATCA	404	FBgn0011742	0	0
CG14210	CG14210	DRSC19566	CTGACGTCCCGCTTCTC	GAATCCGCACCGGAAACT	461	FBgn0031040	0	0
CG33066	CG33066	DRSC19566	CTGACGTCCCGCTTCTC	GAATCCGCACCGGAAACT	461	FBgn0053066	0	0
CG1796	CG1796	DRSC19786	TCCCACAGACGCACCG	CACGCACCCTGGAAACT	503	FBgn0030365	1	23
CG3775	CG3775	DRSC19877	GCATCGCCCTCAGTTTATC	CTGCGAAAGCCCCAGAG	499	FBgn0030425	0	0
Nup153	CG4453	DRSC19904	CGCGTGAAGGAAATATCAAA	ATCGATTCAAGAAATCGACG	499	FBgn0061200	0	0
Cdc42	CG12530	DRSC20228	CCTCGTCGAATACATTTTTCA	ACGGAGCCGTGGGTAAG	544	FBgn0010341	1	21
CkIIbeta	CG15224	DRSC20230	GGCTGACTTTCACAGTAGAC	AGCTCGAGGACAATCCAC	172	FBgn0000259	0	0
CkIalpha	CG2028	DRSC20231	AGCCCTTGCAGAGGACC	GGCAAGGAAAAGAACTTCAAC	517	FBgn0015024	3	36
Hsc70-3	CG4147	DRSC20253	GGACAATAGCATCGGTATCTT	GGCCACCAACGGTGATAC	512	FBgn0001218	2	35
RpII215	CG1554	DRSC20280	TCGTTGGCCTGCTTTGAA	CTATGGAGTCGGTGATGGTT	505	FBgn0003277	0	0
betaCop	CG6223	DRSC20312	ACTCTGGGTGGCATAGGTT	GGACACTGGCAAGTACAGG	502	FBgn0008635	0	0
comt	CG1618	DRSC20319	CCCAATCGATCCGTAGTCC	CCGTGCCGCCCAGTC	511	FBgn0000346	1	29
dlg1	CG1725	DRSC20324	ATCACTGAATCCACCGACTT	CACCACCCGACCCAAGC	282	FBgn0001624	0	0
fne	CG4396	DRSC20332	GTGGTTTTGGTCTTGTTAGTCT	TGGCTGGCGATCTATTGG	310	FBgn0040222	2	28
ran	CG1404	DRSC20364	CTGCGCCTGCCAATCC	TCAAGCGGCACATGACC	587	FBgn0020255	0	0
sbr	CG17335	DRSC20368	TTGTTATCCCCCAAATAGAGAA	AACGCCCAGATATACGAAAA	515	FBgn0003321	0	0
Rab10	CG17060	DRSC20572	TCTATATTCCGTAACCATTTGAC	CATCGATTTCAAAATCAAAACAG	195	FBgn0015789	2	28
cactin	CG1676	DRSC20576	CAGCGACAGCTTCTCG	CGAGATGGACGTGCCAA	513	FBgn0031114	0	0
Rab35	CG9575	DRSC20691	TTTTAACCACATCGCAGTTATT	CAAGTCGTCGCTGCTCA	284	FBgn0031090	0	0
Rab21	CG17515	DRSC20968	ATCCGTATCCGGATTCTGG	TGGTGCTGCGCTACATG	506	FBgn0039966	0	0
Hsp70Ab	CG18743	DRSC21246	CGGTCTCAATTCCCAATGAA	TGGCGGACGAGTTCAAG	495	FBgn0013276	4	109
Hsp70Aa	CG31366	DRSC21246	CGGTCTCAATTCCCAATGAA	TGGCGGACGAGTTCAAG	495	FBgn0013275	4	109
Hsp70Bb	CG31359	DRSC21247	CGGTCTCAATTCCCAATGAA	GGCGGAGGAGTTCAAGC	494	FBgn0013278	2	109
Hsp70Ba	CG31449	DRSC21247	CGGTCTCAATTCCCAATGAA	GGCGGAGGAGTTCAAGC	494	FBgn0013277	2	109
Hsp70Bbb	CG5834	DRSC21247	CGGTCTCAATTCCCAATGAA	GGCGGAGGAGTTCAAGC	494	FBgn0051354	2	109
Hsp70Bc	CG6489	DRSC21247	CGGTCTCAATTCCCAATGAA	GGCGGAGGAGTTCAAGC	494	FBgn0013279	2	109
Pp4-19C	CG18339	DRSC21251	GGTGTGCACGGCAAATCA	GGTTGGCGGCGATGTG	515	FBgn0023177	1	22
His2A:CG31618	CG31618	DRSC21264	CTCAGCGGCCAGATATTC	TCTGGACGTGGAAAAGGTG	180	FBgn0051618	2	107
His3:CG31613	CG31613	DRSC21267	ACGCTCGCCGCGAAT	GGCTCGTACCAAGCAAAC	403	FBgn0051613	1	296
His4:CG31611	CG31611	DRSC21268	AGAGGGTGCGGCCTTG	GTGGCGTTCTGAAGGTTTT	129	FBgn0051611	0	0
vihar	CG10682	DRSC23625	GTTGGCAGTAGGTCTTCGGA	AACATCTTCAAGTGGGTGGG	460	FBgn0027936	0	0

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