Table S1. RNAi screen results

Gene / control	CG number	Functional Group	% internalized bacteria	p-value	normalized % internalization	p-value normalized
Untreated cells (no RNAi) + *R. parkeri*	-------	-------	54 ± 10	-------	1 ± 0.09	-------
Untreated cells + *Rp*, fixed at time=0	-------	*negative control*	19 ± 9	<0.0001	0.36 ± 0.18	<0.0001
Untreated cells + *Rp*, 4mM latrunculin A	-------	*negative control*	15 ± 5	<0.0001	0.33 ± 0.13	<0.0001
Untreated cells + 56C Heat-killed *R.parkeri*	-------	*negative control*	23 ± 8	<0.0001	0.48 ± 0.1	<0.0001
Untreated cells + *Listeria monocytogenes*	-------	*negative control*	24 ± 5	<0.0001	0.41 ± 0.05	<0.0001
Untreated cells + *E. coli* XL-10	-------	*negative control*	5 ± 6	<0.0001	0.09 ± 0.09	<0.0001
Abi	CG9749	WAVE complex subunit	17 ± 10	<0.0001	0.34 ± 0.18	<0.0001
Abl	CG4032	Kinase	42 ± 10	0.0431	0.86 ± 0.06	0.0068
ADF/cofilin	CG6873	Actin monomer dynamics	51 ± 13	0.5961	0.99 ± 0.16	0.7844
Aip1	CG10724	Actin monomer dynamics	47 ± 9	0.2366	1.06 ± 0.09	0.2799
α-actinin	CG4376	Actin filament bundling/organizing	34 ± 14	0.0004	0.71 ± 0.19	<0.0001
α-actinin 3	CG8953	Actin filament bundling/organizing	51 ± 7	0.5532	0.85 ± 0.12	0.0056
Anillin	CG2092	Actin filament binding / cytokinesis	57 ± 4	0.6946	0.98 ± 0.06	0.6766
Arp2/3 complex ARP3	CG7558	Actin filament nucleator	34 ± 9	0.0002	0.67 ± 0.07	<0.0001
Arp2/3 complex ARP2	CG9901	Actin filament nucleator	29 ± 9	<0.0001	0.59 ± 0.15	<0.0001
Arp2/3 complex ARPC1	CG8978	Actin filament nucleator	33 ± 16	0.0013	0.66 ± 0.25	<0.0001
Arp2/3 complex ARPC2	CG10954	Actin filament nucleator	30 ± 9	<0.0001	0.63 ± 0.21	<0.0001
Arp2/3 complex ARPC3	CG4560	Actin filament nucleator	51 ± 8	0.5061	1.05 ± 0.19	0.3124
Arp2/3 complex ARPC4	CG5972	Actin filament nucleator	36 ± 12	0.001	0.61 ± 0.22	<0.0001
Arp2/3 complex ARPC5	CG9881	Actin filament nucleator	25 ± 6	<0.0001	0.5 ± 0.04	<0.0001
Band 4.1 FERM-like	CG34347	Membrane-cytoskeleton linker	42 ± 9	0.019	0.95 ± 0.14	0.2692
Basket (c-Jun N-terminal kinase)	CG5680	Kinase	56 ± 7	0.7782	0.97 ± 0.17	0.6022
By blistery tensin	CG9379	Membrane-cytoskeleton linker / focal adhesions	49 ± 14	0.397	0.97 ± 0.15	0.5125
CAP1	CG5061	Actin monomer dynamics / filament binding	40 ± 4	0.0211	1.02 ± 0.3	0.708

Capping protein (beta)	CG17158	Actin monomer dynamics / filament binding	41 ± 12	0.0142	0.87 ± 0.18	0.0088
Cappucino	CG3399	Actin filament nucleator	51 ± 22	0.6488	0.93 ± 0.33	0.2241
Cdc42	CG12530	Rho family GTPases	48 ± 8	0.2047	1.02 ± 0.05	0.7433
Citron kinase	CG10522	Kinase	39 ± 12	0.0156	0.8 ± 0.11	0.0003
Cofilin (twinstar)	CG4254	Actin monomer dynamics	40 ± 12	0.0088	0.8 ± 0.09	<0.0001
Coracle	CG11949	Membrane-cytoskeleton linker	62 ± 5	0.2264	0.94 ± 0.06	0.2558
Coronin	CG9446	Arp2/3 complex regulator	53 ± 15	0.7956	1.03 ± 0.2	0.6399
Cortactin	CG3637	Arp2/3 complex regulator	43 ± 15	0.0669	0.87 ± 0.18	0.0144
Cyclin-dep kinase 5	CG8203	Kinase	59 ± 2	0.4054	1.05 ± 0.09	0.3399
Dab (disabled)	CG9695	Adapter / WASP regulator	66 ± 5	0.0506	1.09 ± 0.13	0.1033
Dah	CG6157	Membrane-cytoskeleton linker / cortical furrow	55 ± 12	0.858	1.17 ± 0.08	0.0003
Dcarmil	CG1399	Arp2/3 complex regulator	52 ± 17	0.7566	0.89 ± 0.12	0.0301
Diaphanous	CG1768	Actin filament nucleator	54 ± 14	0.9939	0.93 ± 0.06	0.1633
DLAR	CG10443	Tyrosine phosphatase	59 ± 9	0.4422	1.05 ± 0.29	0.3746
Drebrin-like	CG10083	Actin filament binding / endocytosis	62 ± 17	0.2443	1.05 ± 0.08	0.3076
Drk	CG6033	Adapter/ WAVE complex subunit	44 ± 9	0.0863	0.96 ± 0.04	0.4541
DROK	CG9774	Kinase	39 ± 3	0.0138	0.88 ± 0.14	0.0272
E-cadherin (shotgun)	CG3722	Membrane-cytoskeleton linker / cell-cell junctions	59 ± 9	0.4101	0.96 ± 0.11	0.3906
Enabled (Ena)	CG15112	Actin monomer dynamics / filament binding	57 ± 13	0.7007	0.98 ± 0.17	0.6929
Fascin	CG1536	Actin filament bundling/organizing	56 ± 16	0.7845	0.98 ± 0.24	0.7512
Filamin	CG3937	Actin filament bundling/organizing	57 ± 4	0.6544	0.93 ± 0.11	0.1922
Fimbrin	CG8649	Actin filament bundling/organizing	38 ± 6	0.0078	0.86 ± 0.05	0.0055
Forked	CG5424	Actin filament bundling/organizing	49 ± 7	0.3574	0.8 ± 0.12	0.0002
Formin/DIA-like	CG14622	Actin filament nucleator	59 ± 8	0.4736	0.95 ± 0.07	0.3161
Form 3	CG33556	Actin filament nucleator	45 ± 12	0.1229	0.92 ± 0.11	0.1347
Formin FRL group	CG32138	Actin filament nucleator	44 ± 21	0.1143	0.87 ± 0.31	0.037

Formin FHOD3 group	CG32030	Actin filament nucleator	46 ± 8	0.1612	0.96 ± 0.08	0.3847
Gelsolin	CG1106	Actin monomer dynamics	55 ± 9	0.8639	0.91 ± 0.15	0.0758
Genghis Kahn	CG4012	Cdc42 effector	54 ± 8	0.9626	0.94 ± 0.06	0.2302
Hemipterous	CG4353	Map kinase kinase	65 ± 10	0.0848	0.99 ± 0.13	0.8308
Hip1R	CG10971	endocytic / phagocytic adapter protein	35 ± 7	0.0005	0.74 ± 0.17	<0.0001
HSPC300	CG30173	WAVE complex subunit	58 ± 6	0.5415	1.01 ± 0.07	0.8098
Kelch	CG7210	Actin filament binding / ring canals	52 ± 11	0.7108	0.85 ± 0.14	0.006
Kette HEM-protein	CG5837	WAVE complex subunit	31 ± 9	<0.0001	0.57 ± 0.24	<0.0001
Ku70	CG5247	Mammalian receptor for *R. conori* entry	42 ± 16	0.0263	0.83 ± 0.16	0.0005
Lethal (2) giant larvae	CG2671	Membrane-cytoskeleton linker	56 ± 2	0.7352	1.01 ± 0.08	0.9133
Lim kinase	CG1848	Actin binding kinase	61 ± 12	0.3031	0.99 ± 0.15	0.882
Merlin	CG14228	Membrane-cytoskeleton linker	48 ± 15	0.2916	0.81 ± 0.11	0.0005
MIM homolog	CG33558	Membrane-cytoskeleton linker	33 ± 8	0.0001	0.69 ± 0.21	<0.0001
Moesin	CG10701	Membrane-cytoskeleton linker	40 ± 4	0.0183	0.83 ± 0.16	0.0015
Mtl (rac-like)	CG5588	Rho family GTPases	48 ± 4	0.3279	1.1 ± 0.15	0.0725
Mushroom bodies tiny	CG18582	Kinase	62 ± 8	0.1905	1.01 ± 0.05	0.8091
Myoblast city	CG10379	Membrane-cytoskeleton linker / focal adhesions	38 ± 4	0.0089	0.87 ± 0.11	0.011
Myosin IA	CG7438	Myosin / phagocytosis	28 ± 12	<0.0001	0.62 ± 0.37	<0.0001
Myosin IB	CG9155	Myosin	48 ± 9	0.306	0.85 ± 0.06	0.0032
Myosin II (zipper)	CG15792	Myosin / phagocytosis	33 ± 6	0.0002	0.72 ± 0.27	<0.0001
Myosin V	CG2146	Myosin	47 ± 9	0.216	1.01 ± 0.09	0.9136
Myosin VI	CG5695	Myosin	54 ± 16	0.9636	1.19 ± 0.18	0.0006
Myosin VII	CG7595	Myosin	51 ± 11	0.5934	0.82 ± 0.09	0.0006
Myosin VII (28B)	CG6976	Myosin	67 ± 3	0.0342	1.09 ± 0.12	0.0901
Myosin XV	CG2174	Myosin	66 ± 4	0.0567	1.08 ± 0.14	0.1529
Myosin XVIII (PDZ-myosin)	CG10218	Myosin	47 ± 10	0.2597	1.06 ± 0.17	0.2461

Myosin 29D XX	CG10595	Myosin	67 ± 10	0.0471	1.11 ± 0.09	0.0312
Nck	CG3727	Adapter/ WAVE complex subunit	54 ± 12	0.8843	0.89 ± 0.13	0.0178
Nullo	CG14426	Membrane-cytoskeleton linker / basal junctions	57 ± 5	0.64	0.93 ± 0.09	0.1032
Ovarian tumor	CG12743	Actin filament bundling/organizing	55 ± 10	0.8567	0.93 ± 0.16	0.12
Pak1 kinase	CG10295	Kinase	55 ± 8	0.8561	0.96 ± 0.19	0.4252
PKN	CG2049	Rho, Rac1 kinase	61 ± 8	0.2083	1.02 ± 0.17	0.6535
POD-1/coronin	CG4532	Arp2/3 complex regulator	46 ± 15	0.1467	0.88 ± 0.09	0.0083
Pp2A	CG17291	Phosphatase	52 ± 8	0.6327	0.87 ± 0.13	0.0055
Profilin	CG9553	Actin monomer dynamics	45 ± 5	0.0668	0.87 ± 0.1	0.0055
Pten	CG5671	Membrane-cytoskeleton linker / ring canals	52 ± 14	0.713	0.87 ± 0.18	0.0148
Quail	CG6433	Actin monomer dynamics	60 ± 7	0.2158	1.03 ± 0.06	0.4976
Rab5	CG3664	Rab family GTPase	53 ± 14	0.7785	0.91 ± 0.22	0.0734
Rac1	CG2248	Rho family GTPases	37 ± 17	0.0021	0.84 ± 0.5	0.0237
Rac2	CG8556	Rho family GTPases	37 ± 8	0.002	0.77 ± 0.09	<0.0001
RacGAP50C	CG13345	GAP for Rac GTPase	65 ± 14	0.0532	1.12 ± 0.06	0.0116
Rho1	CG8416	Rho family GTPases	43 ± 4	0.0277	0.89 ± 0.11	0.0142
RhoBTB	CG5701	Rho family GTPases	60 ± 2	0.2575	1.01 ± 0.02	0.8836
RhoL	CG9366	Rho family GTPases	44 ± 7	0.0612	0.76 ± 0.12	<0.0001
Rhophilin	CG8497	Rho GTPase effector	56 ± 6	0.7812	0.93 ± 0.12	0.1205
Slingshot	CG6238	Phosphatase of cofilin	44 ± 15	0.1039	0.96 ± 0.18	0.4078
Spire	CG10076	Actin filament nucleator	50 ± 9	0.4491	0.91 ± 0.13	0.0394
Sra-1	CG4931	WAVE complex subunit	35 ± 6	0.0027	0.55 ± 0.07	<0.0001
Taf110	CG5444	DNA binding, cytokinesis	39 ± 7	0.0124	0.81 ± 0.09	0.0005
Talin	CG6831	Membrane-cytoskeleton linker / cell-cell junctions	48 ± 15	0.2377	0.95 ± 0.17	0.2818
Trio (GEF)	CG18214	GEF for Rho GTPases	48 ± 9	0.2236	0.91 ± 0.17	0.0593
Tropomodulin	CG1539	Actin monomer dynamics / filament binding	57 ± 12	0.5516	0.98 ± 0.09	0.5323

Tropomyosin1	CG4898	Actin monomer dynamics	52 ± 9	0.6681	0.86 ± 0.09	0.0028
Tropomyosin2	CG4843	Actin monomer dynamics	43 ± 13	0.0451	0.72 ± 0.19	<0.0001
Twinfillin	CG3172	Actin monomer dynamics	53 ± 8	0.8331	0.89 ± 0.15	0.0325
Vav	CG7893	GEF for Rac1 GTPase	41 ± 6	0.0319	0.69 ± 0.16	<0.0001
Villin-like	CG33232	Actin monomer dynamics	60 ± 6	0.3213	1.01 ± 0.04	0.8604
Vinculin	CG3299	Membrane-cytoskeleton linker / focal adhesions	41 ± 17	0.0379	0.76 ± 0.17	<0.0001
WASP	CG1520	Arp2/3 Nucleation Promoting Factor	49 ± 16	0.3635	0.99 ± 0.16	0.8127
WAVE (SCAR)	CG4636	Arp2/3 Nucleation Promoting Factor	18 ± 6	<0.0001	0.38 ± 0.08	<0.0001
WIP veroprolin	CG13503	WASP binding, regulation	38 ± 16	0.005	0.78 ± 0.34	0.0003
Rac1 + Cdc42	CG2248 + CG12530	Rho family GTPases	34 ± 5	0.0003	0.68 ± 0.11	<0.0001
Rac1 + Rac2	CG2248 + CG8556	Rho family GTPases	39 ± 18	0.0031	0.84 ± 0.46	0.0162

Column A, common gene name. Column B, FlyBase gene annotation symbol. Column C, type of control or protein function. Column D, raw percentage of internalized *R. parkeri* expressed as mean ± standard deviation, *n*>3 biological replicates. Column E, p-value based on a pairwise comparison of the raw percentages of internalized bacteria for RNAi treated cells versus untreated control cells using the Student's t-test, with $p<0.05$ considered statistically significant. Column F, percentage of internalized R. parkeri normalized to the mean value for untreated control cells (n=2)in the same day's experiment, expressed as mean ± standard deviation. Column F, p-value based on a pairwise comparison of the normalized percentages of internalized bacteria for RNAi treated cells versus normalized untreated control cells using the Student's t-test, with $p<0.05$ considered statistically significant. Red signifies those targets for which values were significantly reduced compared with controls, while green signifies those targets for which values were significantly increased when compared with controls. Functional classification derived from: http://www.ihop-net.org ; http://flybase.org ; Siripala and Welch 2007, Cell 128:626 ; Siripala and Welch 2007 Cell 128:1014