Mehlitz et al., http://www.jcb.org/cgi/content/full/jcb.200909095/DC1

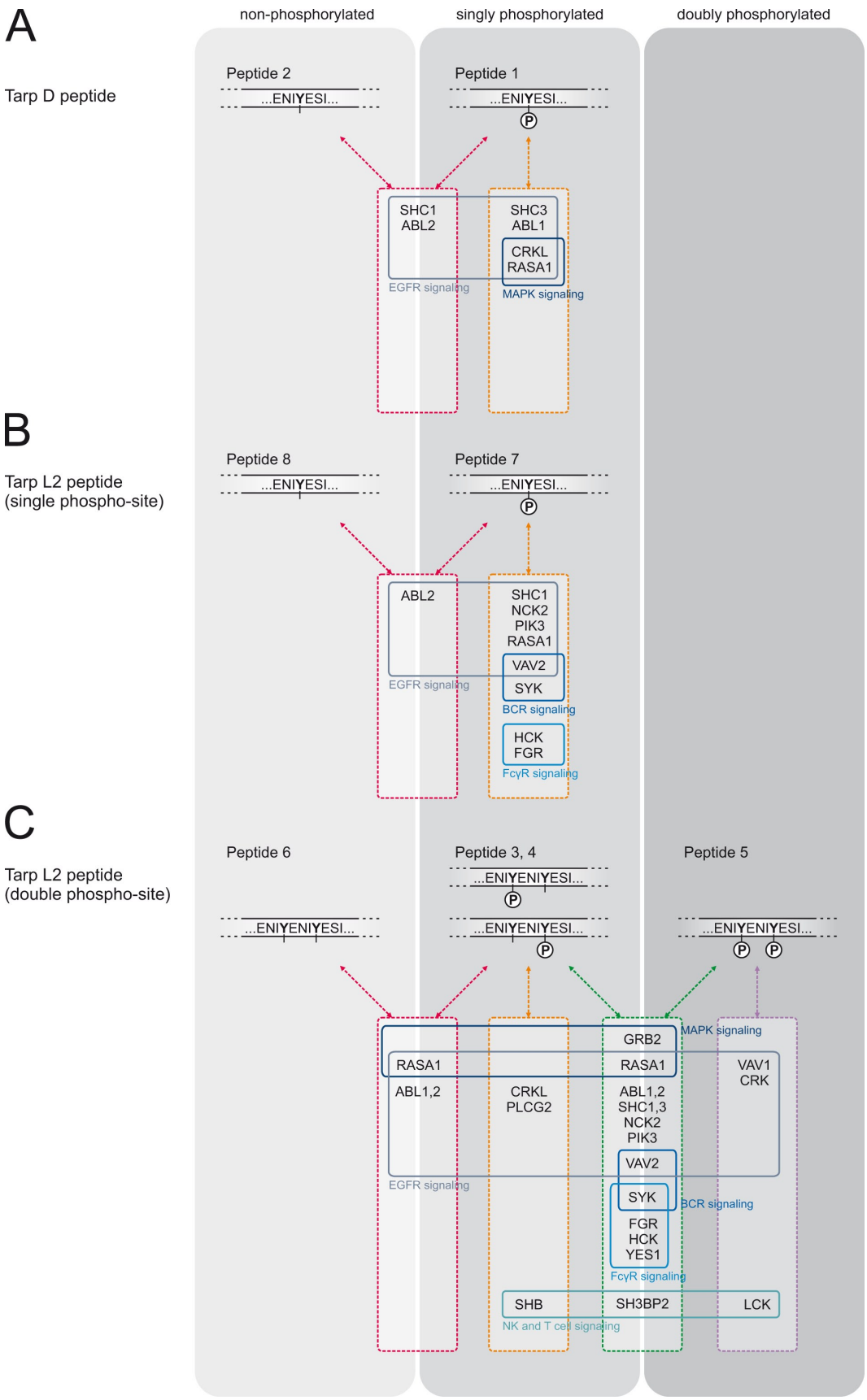

Figure S1. **Summary of Tarp interactions and putative signaling.** Model showing interaction partners and possible downstream signaling pathways of a single-phosphorylation site of Tarp D (A), a single-phosphorylation site of Tarp L2 (B), or a double-phosphorylation site of Tarp L2 (C). Interacting proteins are listed in columns corresponding to the different phosphorylation states of the respective site (highlighted by dashed colored lines). Interaction partners were analyzed for their participation in signaling pathways (marked by continuous colored lines) using IPA software and the KEGG. Only signaling pathways with the involvement of at least two Tarp interaction partners identified on our protein microarrays were included in the model.

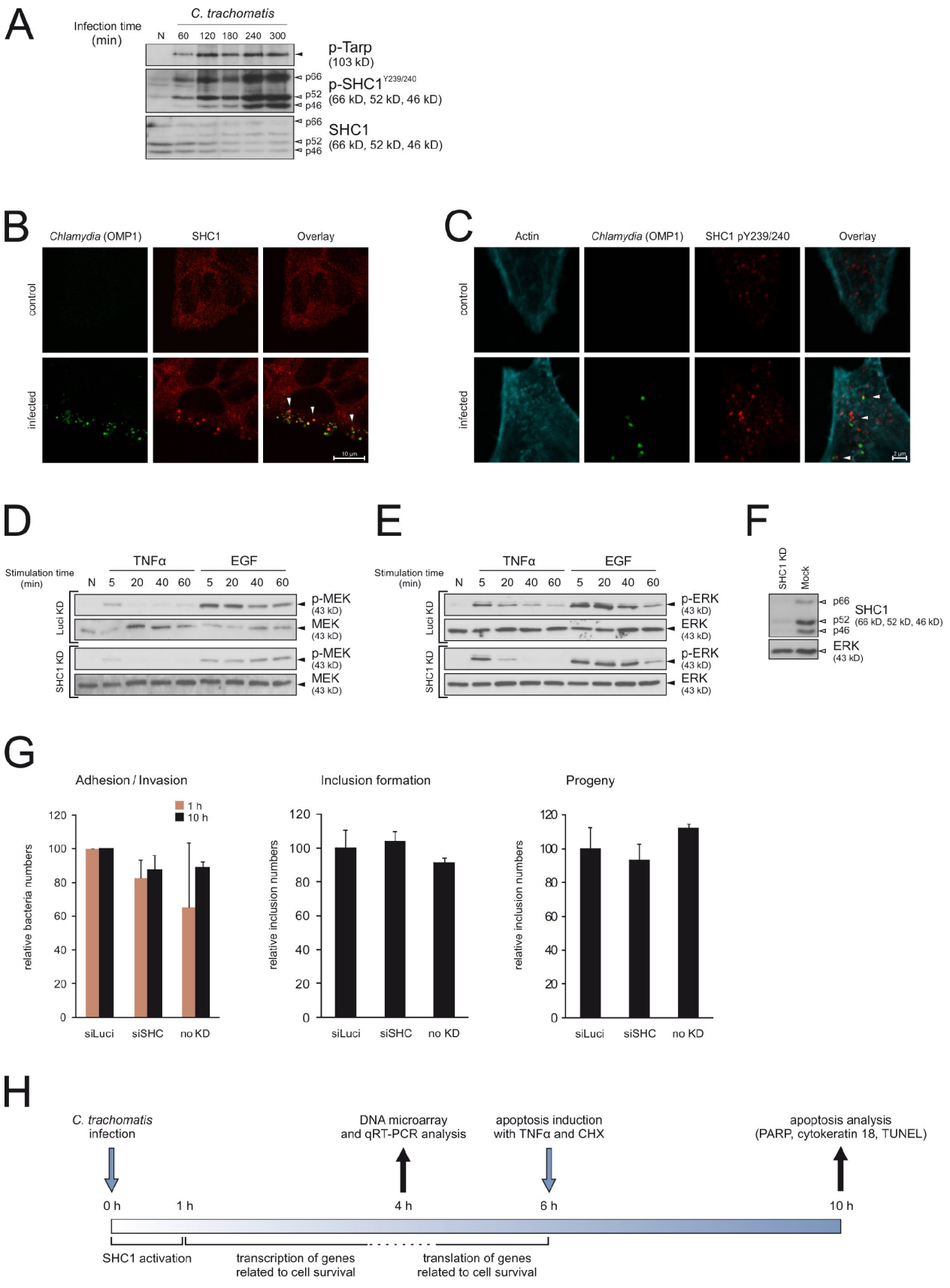

Figure S2. **SHC1 phosphorylation and subcellular localization upon infection; and MEK/ERK signaling, chlamydial invasion, inclusion formation, and progeny after SHC1 knockdown, plus experimental time scale.** (A) Western blots showing SHC1 pY239/240 phosphorylation (white arrowheads) during a time course infection of HeLa cells with *C. trachomatis* (6 h). Tarp phosphorylation is shown through phosphotyrosine-specific antibodies (black arrowhead). Immunofluorescence staining of SHC1 (B; red, white arrowheads) and p-SHC1 (C; red, white arrowheads) after infection of HeLa cells for 60 min

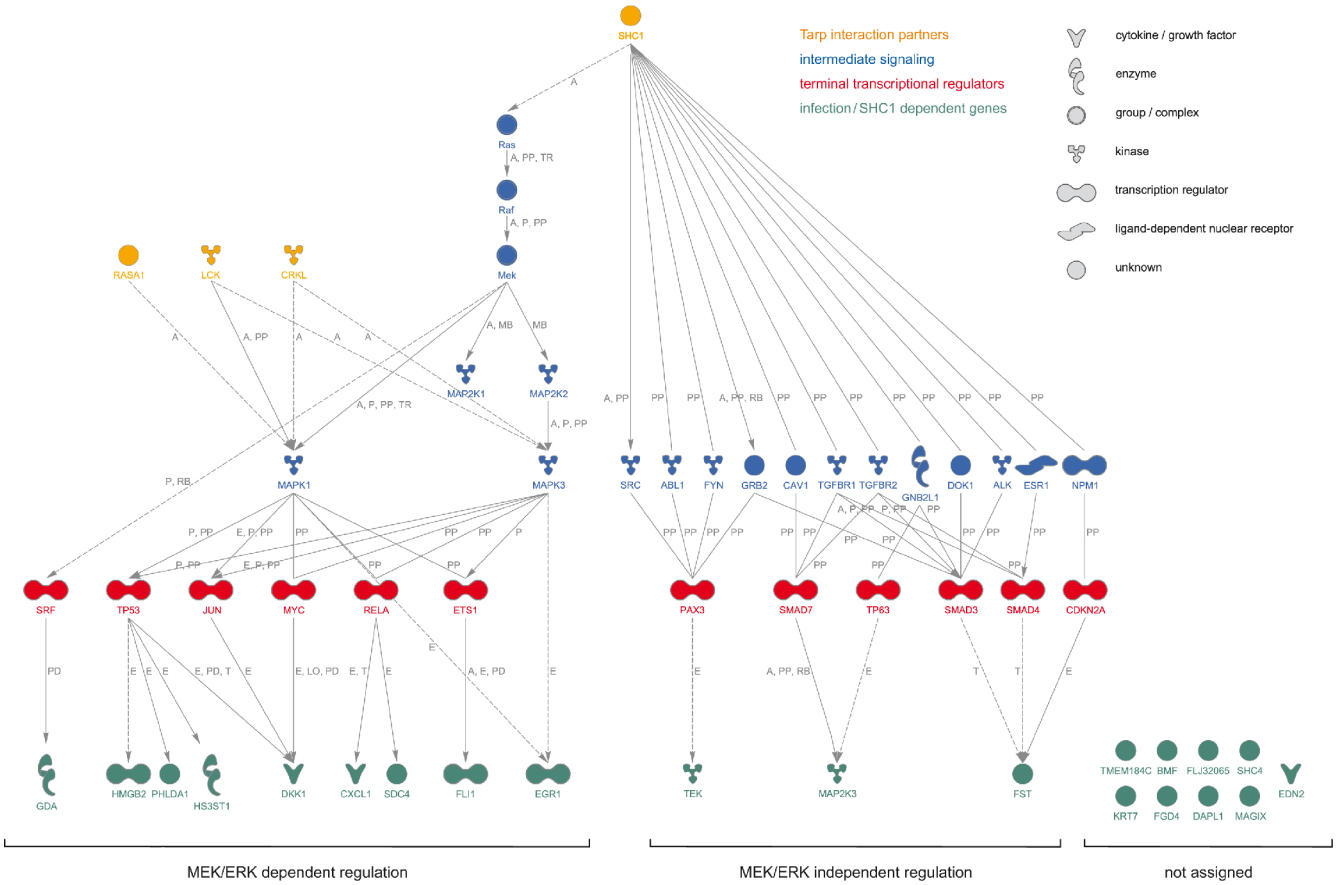

Figure S3. **Signaling interactions between SHC1 and its downstream genes related to apoptosis and cell growth.** Model showing different pathways of SHC1 signaling in connection with the 21 SHC1-dependently regulated apoptosis and cell growth genes. Genes are grouped into the three categories "MEK/ERK dependent regulation," "MEK/ERK independent regulation," and "not assigned." Among the 21 genes (depicted in green), only nine genes were MEK/ERK-dependently regulated, whereas 12 genes are controlled by other pathways. Relationships were analyzed using IPA software (straight line, direct relationship; dashed line, indirect relationship; A, activation; E, expression; LO, localization; MB, group/complex membership; P, phosphorylation/dephosphorylation; PD, protein–DNA binding; PP, protein–protein binding; RB, regulation of binding; T, transcription; TR, translocation). Color coding is as follows. Yellow, potential Tarp interactions; blue, intermediate signaling molecules; red, terminal transcriptional regulators; and green, 21 infection and SHC1 dependently regulated genes.

(*C. trachomatis* L2, green, MOI 200). Vesicular structures of SHC1 and p-SHC1 were located in close proximity to *C. trachomatis* EBs. These structures were not observed in control cells. (D and E) Western blots showing MEK phosphorylation (D; black arrowheads) and ERK phosphorylation (E; black arrowheads) during a time course after stimulation of cells with 25 ng/ml TNF or 50 ng/ml EGF. HeLa cells were either treated with siRNA against Luciferase (control) or SHC1. (F) Western blot showing nearly complete knockdown of all three SHC1 isoforms after siRNA-mediated gene silencing. (G) Bar diagrams showing adhesion/invasion efficiency, inclusion formation, and progeny formation after knockdown with Luciferase (siLuci), SHC1 (siSHC) siRNA, or transfection reagent only (no knockdown). Adhesion/invasion efficiency was determined by automated microscopy detecting particle numbers associated with host cells at 1 or 10 h (n = 2, ~8,000 cells per experiment and condition). Inclusion formation was determined by manually counting the number of inclusions per 40× field (n = 2, 10 fields per experiment and condition). Progeny formation was determined manually by counting the number of inclusions per 40× field after transfer of end cycle bacteria to fresh HeLa monolayers (n = 2, 10 fields per experiment and condition). SHC1 knockdown did not result in significant regulation of *C. trachomatis* invasion, inclusion formation, and progeny (error bars indicate SE). (H) Workflow scheme of DNA microarray, qRT-PCR, and apoptosis experiments in this study. Blue bar shows time course of infection up to 10 h. Arrows indicate treatment of cells (blue) and sample collection (black).

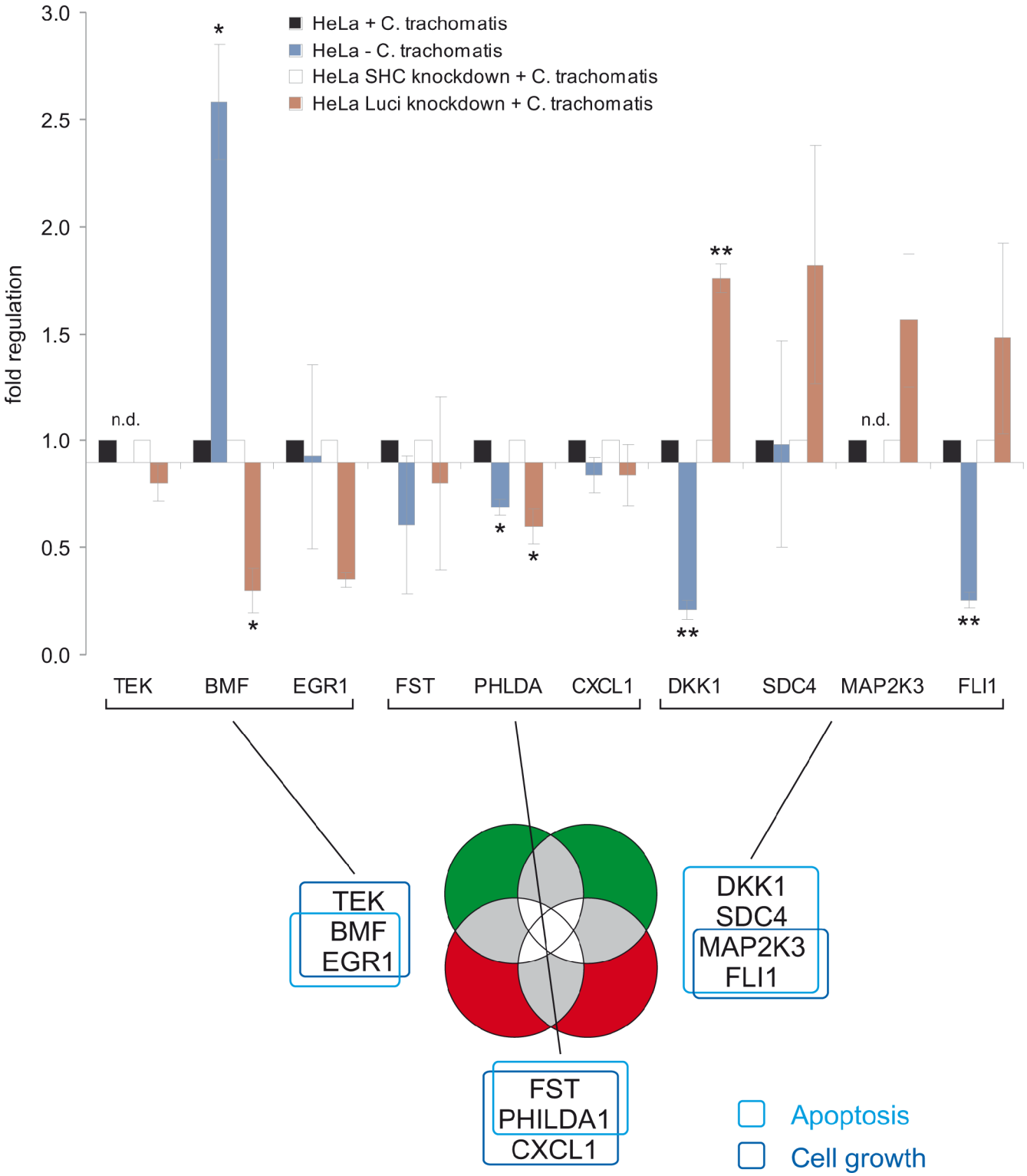

Figure S4. **qRT-PCR confirmation of SHC1-dependent regulation of apoptosis and cell growth genes.** HeLa cells were infected for 4 h (*C. trachomatis* L2, MOI 20) before RNA isolation and qRT-PCR. Bar diagrams shows gene expression of infected versus noninfected cells (black vs. blue bars) and infected SHC1 knockdown versus infected Luciferase knockdown cells (white vs. red bars; $n = 2$, bars indicate SE; *, $P < 0.05$; **, $P < 0.01$). 10 genes identified in the array experiments and classified into apoptosis or growth regulation were selected for experimental verification by qRT-PCR. (bottom) Comparison of the qRT-PCR results to the Venn diagram; Table S2 confirms regulatory tendency of all the genes tested.

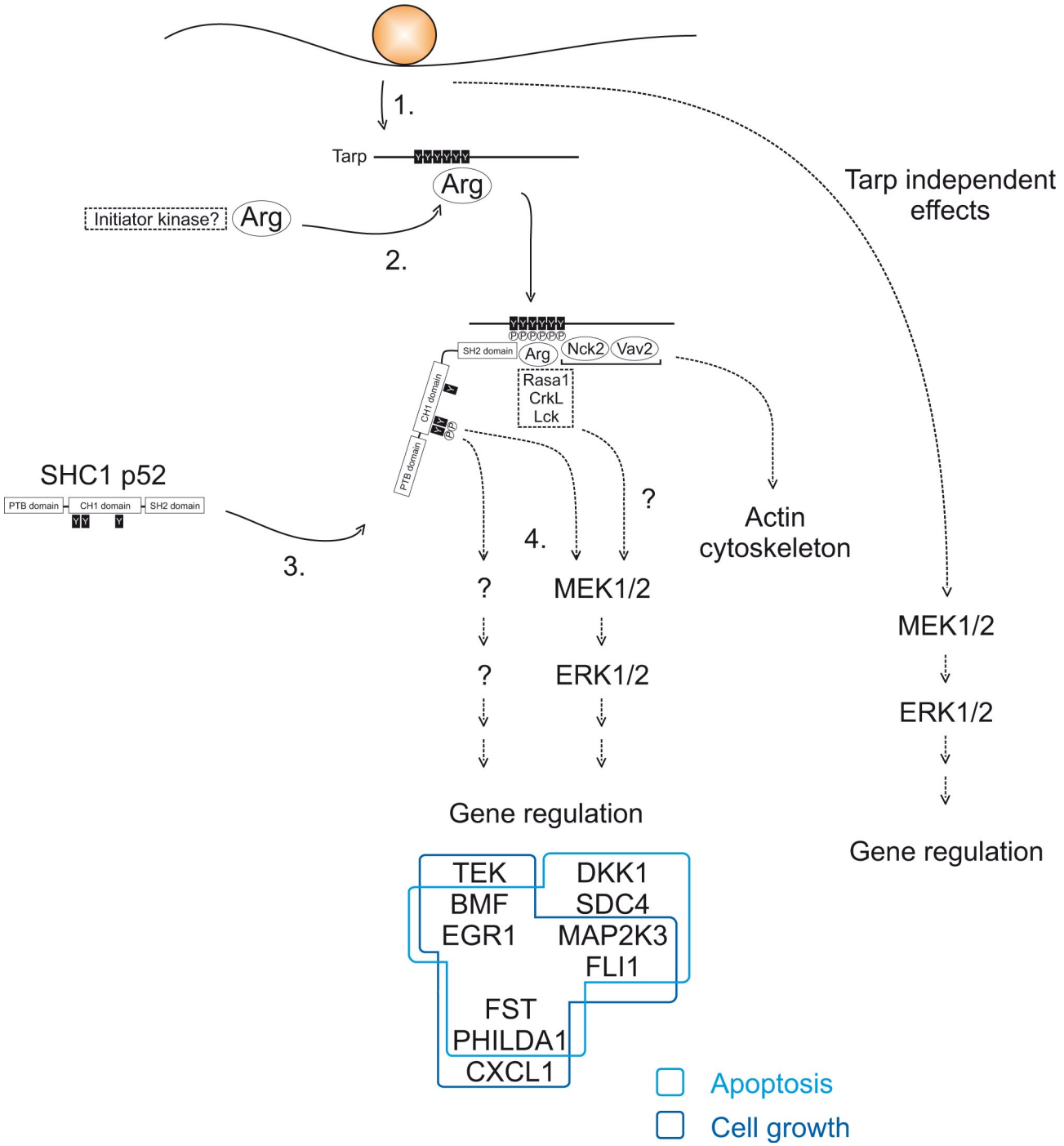

Figure S5. **Model of the role of Tarp in host cell signaling.** (1) *C. trachomatis* injects Tarp via its type III secretion system into the host cell. (2) Tarp becomes phosphorylated by an initiator kinase, probably through interaction of the kinase to nonphosphorylated Tarp. This might be through ABL/ARG kinases, as we detected strong binding to nonphosphorylated Tarp peptides. Subsequently, phosphorylated Tarp is able to bind to a plethora of host SH2 domain–containing proteins, which indicates that it functions as a signaling hub. We experimentally validated SHC1 as a serovariant D and L2 common interaction partner. (3) SHC1 binds Tarp through its C-terminal SH2 domain and becomes tyrosine phosphorylated on residues Y239/240. Other effectors are likely able to bind Tarp either in a timely or spatially regulated manner. We experimentally confirmed NCK2 as a serovariant L2–specific interaction partner, and protein arrays indicate further interaction partners like VAV2 (which has previously been shown to interact with Tarp via immunoprecipitation; Lane et al., 2008), RASA1, CRKL, and LCK. (4) SHC1 was found to be an important regulator of anti-apoptotic and growth-related genes, and knockdown of SHC1 sensitized host cells for apoptosis induction via TNF. Activation of MEK/ERK was not solely dependent on SHC1. The exact role of the MEK/ERK regulators RASA1 and CRKL on gene regulation and *C. trachomatis* growth and the redundancy with SHC1 in MEK/ERK activation needs further investigation. Additionally, Tarp-independent effects such as TLR signaling might influence the activation state of MEK/ERK.

Table S2. **List of the 21 regulated genes and their function**

Group[a]	Gene identifier	Gene name	Full name	Function	Reference	Regulation array 1[b]	P-value array 1[b]	Regulation array 2[c]	P-value array 2[c]	Apoptosis[d]	Cell growth[d]	MEK/ERK dependent[d]
						Fold change		*Fold change*				
1	NM_000459	TEK	Tyrosine kinase, endothelial	Receptor signaling, angiogenesis	Jones and Dumont, 2000	−1.90	3×10^{-5}	1.87	9.24×10^{-7}	–	+	–
1	BU729607	HMGB2	High mobility group box 2	DNA binding, formation of nucleoprotein complexes, V(D)J recombination, transcription initiation, DNA repair	Thomas and Travers, 2001	−1.73	1.64×10^{-3}	2.21	5.58×10^{-8}	–	–	+
1	NM_001964	EGR1	Early growth response 1	Transcription factor, suppression of transformation, upregulation of proapoptotic genes	Arora et al., 2008	−1.89	1.79×10^{-7}	2.32	7.84×10^{-42}	+	+	+
1	NM_153032	FLJ32065	Hypothetical protein			−1.97	2.13×10^{-7}	2.41	2.94×10^{-16}	–	–	–
1	NM_033503	BMF	Bcl2 modifying factor	BH3-only protein, inhibits prosurvival proteins	Willis and Adams, 2005	−2.44	2.01×10^{-9}	3.15	6.73×10^{-14}	+	+	–
2	AF086541	DAPL1	Death associated protein-like 1	Apoptosis and cell differentiation	Ashburner et al., 2000	−1.61	9.43×10^{-3}	−1.72	5.50×10^{-4}	–	–	–
2	NM_024859	MAGIX	MAGI family member, X-linked	Tight junction PDZ protein, caspase substrate	Gregorc et al., 2007	−1.87	7.03×10^{-3}	−1.61	2.55×10^{-3}	–	–	–
2	NM_139241	FGD4	F+VE, RhoGEF and PH domain containing 4	Guanine nucleotide exchange factor specific for Cdc42	Chen et al., 2004	−2.00	1.59×10^{-8}	−1.82	5.34×10^{-10}	–	–	–
2	NM_001956	EDN2	Endothelin 2	21 aa peptide, activates endothelin receptors, raises blood pressure, induces vascular and myocardial hypertrophy	Goraca, 2002	−2.94	0.00	−2.05	1.76×10^{-2}	–	–	–
2	AL833897	AL833897	cDNA clone			−1.65	8.03×10^{-7}	−1.68	9.47×10^{-3}	–	–	–
3	NM_012242	DKK1	dickkopf homolog 1	Wnt inhibitor	Zhao et al., 2009	3.53	0.00	−1.99	4.67×10^{-11}	+	-	+
3	NM_002017	FLI1	Friend leukemia virus integration 1	ETS transcription factor, proto-oncogene	Juban et al., 2009	1.81	7.00×10^{-5}	−1.95	1.57×10^{-9}	+	+	+
3	BC033310	GDA	Guanine deaminase	Converts guanine to xanthine		1.65	2.82×10^{-11}	−1.70	2.73×10^{-3}	–	–	+
3	NM_005556	KRT7	Cytokeratin 7	Cytoskeletal component		1.62	2.66×10^{-8}	−2.13	0.00	–	–	–
3	NM_145110	MAP2K3	Mitogen-activated protein kinase kinase 3	Stress signaling, activates p38MAPK, proapoptotic	Dhanasekaran and Premkumar Reddy, 1998	1.72	1.26×10^{-12}	−1.96	4.00×10^{-10}	+	+	–
3	NM_002999	SDC4	Syndecan 4	Transmembrane heparan sulfate proteoglycan, regulation of cytoskeleton, proliferation	Oh and Couchman, 2004	1.64	1.57×10^{-14}	−1.66	2.64×10^{-10}	+	–	+
4	NM_001511	CXCL1	Chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity, alpha)	Neutrophil attraction, cytoskeletal control	Reutershan and Ley, 2004	1.67	5.88×10^{-24}	1.75	1.18×10^{-9}	–	+	+
4	NM_013409	FST	Follistatin	Activin binding protein, proliferation, differentiation, and apoptosis	McDowall et al., 2008	2.32	1.38×10^{-33}	1.98	1.04×10^{-9}	+	+	–
4	NM_005114	HS3ST1	Heparan sulfate (glucosamine) 3-O-sulfotransferase 1	Heparin sulfate biogenesis, sulfotransferase	Muñoz et al., 2006	2.29	2.75×10^{-19}	1.75	1.77×10^{-28}	–	–	+

Table S2. **List of the 21 regulated genes and their function** *(Continued)*

Group[a]	Gene identifier	Gene name	Full name	Function	Reference	Regulation array 1[b]	P-value array 1[b]	Regulation array 2[c]	P-value array 2[c]	Apoptosis[d]	Cell growth[d]	MEK/ERK dependent[d]
4	BC037430	PHLDA1	Pleckstrin homology–like domain, family A, member 1	Expression increases basal apoptosis, regulation of cell growth, and apoptosis	Neef et al., 2002	2.23	6.38×10^{-10}	1.67	6.92×10^{-14}	+	+	+
4	NM_203349	SHC4	SHC (Src homology 2 domain containing) family, member 4	Cell migration and growth regulation	Fagiani et al., 2007	1.65	4.50×10^{-2}	1.91	1.22×10^{-17}	–	–	–

List of 21 genes regulated in an infection- and SHC1-dependent manner. Genes are grouped according to regulation pattern and functional sorting by IPA software. Full gene names and a short functional description including references are additionally provided.

[a]Groups according to Fig. 5 D.

[b]Array 1 (Inf. vs. NI).

[c]Array 2 (SHC1 KD + Inf. vs. Luci KD + Inf.).

[d]Functional sorting according to IPA.

Table S3. **qRT-PCR results table**

Sample name	Gene	RQ 1	RQ 2	RQ 1 Min	RQ 1 Max	RQ 2 Min	RQ 2 Max	Mean RQ	SE	P value[a]
HeLa + *C. trachomatis*	TEK	1.000	1.000	0.588	1.702	0.542	1.844	1.000	0.000	ND
HeLa + *C. trachomatis*	BMF	1.000	1.000	0.506	1.975	0.654	1.530	1.000	0.000	0.028
HeLa + *C. trachomatis*	EGR1	1.000	1.000	0.581	1.721	0.528	1.895	1.000	0.000	0.877
HeLa + *C. trachomatis*	FST	1.000	1.000	0.620	1.613	0.697	1.435	1.000	0.000	0.346
HeLa + *C. trachomatis*	PHLDA	1.000	1.000	0.422	2.371	0.534	1.873	1.000	0.000	0.015
HeLa + *C. trachomatis*	CXCL1	1.000	1.000	0.562	1.781	0.632	1.583	1.000	0.000	0.183
HeLa + *C. trachomatis*	DKK1	1.000	1.000	0.725	1.379	0.771	1.297	1.000	0.000	0.003
HeLa + *C. trachomatis*	SDC4	1.000	1.000	0.813	1.231	0.759	1.318	1.000	0.000	0.976
HeLa + *C. trachomatis*	MAP2K3	ND	1.000	ND	ND	0.615	1.627	ND	ND	ND
HeLa + *C. trachomatis*	FLI1	1.000	1.000	1.000	1.000	0.506	1.976	1.000	0.000	0.003
HeLa − *C. trachomatis*	TEK	0.329	ND	0.220	0.493	ND	ND	ND	ND	ND
HeLa − *C. trachomatis*	BMF	2.853	2.308	2.084	3.906	0.994	5.361	2.581	0.273	0.028
HeLa − *C. trachomatis*	EGR1	0.496	1.354	0.365	0.674	0.412	4.453	0.925	0.429	0.877
HeLa − *C. trachomatis*	FST	0.288	0.928	0.216	0.384	0.390	2.207	0.608	0.320	0.346
HeLa − *C. trachomatis*	PHLDA	0.729	0.651	0.534	0.994	0.229	1.848	0.690	0.039	0.015
HeLa − *C. trachomatis*	CXCL1	0.753	0.917	0.510	1.113	0.567	1.486	0.835	0.082	0.183
HeLa − *C. trachomatis*	DKK1	0.168	0.252	0.109	0.257	0.116	0.548	0.210	0.042	0.003
HeLa − *C. trachomatis*	SDC4	1.465	0.502	1.262	1.702	0.298	0.844	0.984	0.482	0.976
HeLa − *C. trachomatis*	MAP2K3	ND	ND	ND	ND	ND	ND	ND	ND	ND
HeLa − *C. trachomatis*	FLI1	0.293	0.214	0.213	0.402	0.122	0.376	0.253	0.039	0.003
HeLa SHC KD + *C. trachomatis*	TEK	1.000	1.000	0.550	1.819	0.201	0.664	1.000	0.000	0.152
HeLa SHC KD + *C. trachomatis*	BMF	1.000	1.000	0.545	1.834	0.787	2.647	1.000	0.000	0.021
HeLa SHC KD + *C. trachomatis*	EGR1	1.000	1.000	0.542	1.844	2.299	7.815	1.000	0.000	0.003
HeLa SHC KD + *C. trachomatis*	FST	1.000	1.000	0.545	1.834	0.773	2.600	1.000	0.000	0.674
HeLa SHC KD + *C. trachomatis*	PHLDA	1.000	1.000	0.530	1.887	1.319	4.697	1.000	0.000	0.038
HeLa SHC KD + *C. trachomatis*	CXCL1	1.000	1.000	0.388	2.577	0.650	4.319	1.000	0.000	0.372
HeLa SHC KD + *C. trachomatis*	DKK1	1.000	1.000	0.831	1.203	0.788	1.141	1.000	0.000	0.008
HeLa SHC KD + *C. trachomatis*	SDC4	1.000	1.000	0.869	1.151	0.588	0.779	1.000	0.000	0.277
HeLa SHC KD + *C. trachomatis*	MAP2K3	1.000	1.000	0.583	1.715	0.717	2.108	1.000	0.000	0.213
HeLa SHC KD + *C. trachomatis*	FLI1	1.000	1.000	0.612	1.634	0.246	0.656	1.000	0.000	0.398
HeLa Luci KD + *C. trachomatis*	TEK	0.890	0.715	0.404	1.265	0.147	0.462	0.802	0.087	0.152
HeLa Luci KD + *C. trachomatis*	BMF	0.402	0.195	0.099	0.384	0.143	0.555	0.298	0.103	0.021
HeLa Luci KD + *C. trachomatis*	EGR1	0.383	0.314	0.215	0.457	0.912	1.938	0.348	0.035	0.003
HeLa Luci KD + *C. trachomatis*	FST	0.397	1.208	0.670	2.177	0.951	3.086	0.802	0.406	0.674
HeLa Luci KD + *C. trachomatis*	PHLDA	0.519	0.680	0.495	0.934	1.232	2.326	0.599	0.080	0.038
HeLa Luci KD + *C. trachomatis*	CXCL1	0.694	0.980	0.551	1.741	0.924	2.917	0.837	0.143	0.372
HeLa Luci KD + *C. trachomatis*	DKK1	1.823	1.688	1.195	2.384	1.133	2.260	1.756	0.068	0.008
HeLa Luci KD + *C. trachomatis*	SDC4	2.377	1.266	0.818	1.959	0.554	1.326	1.822	0.556	0.277
HeLa Luci KD + *C. trachomatis*	MAP2K3	1.872	1.250	0.618	2.527	0.760	3.107	1.561	0.311	0.213
HeLa Luci KD + *C. trachomatis*	FLI1	1.926	1.029	0.658	1.610	0.264	0.646	1.478	0.448	0.398

List showing the real-time quantitative (RQ) values and analysis of the 10 genes selected for further experimental verification and significance analysis. Values are graphically represented in Fig. S4. RQ, real-time quantitative value.

[a]P-value according to Student's *t* test.

Table S4. **qRT-PCR primers**

Primer	Sequence	Length	Start	Stop	T_m	GC	Product length
		bp	*bp*	*bp*	*°C*	*%*	*bp*
TEK forward	5′-GTGCTGTTCCTTCTTGCCTC-3′	20	300	319	60.00	55.00%	117
TEK reverse	5′-TCCACAAATGTGCATGAGGT-3′	20	416	397	59.97	45.00%	117
BMF forward	5′-AGTCAAACTTTGTGACCGGC-3′	20	58	77	60.16	50.00%	148
BMF reverse	5′-AGTAGGCTCTGGGCAAACAG-3′	20	205	186	59.50	55.00%	148
EGR1 forward	5′-GACCGCAGAGTCTTTTCCTG-3′	20	570	589	59.99	55.00%	110
EGR1 reverse	5′-AGCGGCCAGTATAGGTGATG-3′	20	679	660	60.12	55.00%	110
FST forward	5′-ATCTTGCAACTCCATTTCGG-3′	20	969	988	60.07	45.00%	115
FST reverse	5′-CACTGAACACTTATAGAGAGTTTACCA-3′	27	1083	1057	57.41	37.04%	115
PHLDA1 forward	5′-GGCAAGACAAGGTTTTGAGG-3′	20	176	195	59.71	50.00%	139
PHLDA1 reverse	5′-CGCCAAGTTGTTCAGTAGGG-3′	20	314	295	60.68	55.00%	139
CXCL1 forward	5′-GAAAGCTTGCCTCAATCCTG-3′	20	325	344	59.96	50.00%	107
CXCL1 reverse	5′-CACCAGTGAGCTTCCTCCTC-3′	20	431	412	59.99	60.00%	107
DKK1 forward	5′-ATCATAGCACCTTGGATGGG-3′	20	636	655	59.77	50.00%	112
DKK1 reverse	5′-CCTGAGGCACAGTCTGATGA-3′	20	747	728	59.98	55.00%	112
SDC4 forward	5′-GTCTGGCTCTGGAGATCTGG-3′	20	220	239	59.94	60.00%	139
SDC4 reverse	5′-TAGTTTCTTGGGTTCGGTGG-3′	20	358	339	59.96	50.00%	139
MAP2K3 forward	5′-ATTAGTCAGGCAGGGCAGTG-3′	20	81	100	60.28	55.00%	105
MAP2K3 reverse	5′-GGACTCCAGGGCCTTATCTC-3′	20	185	166	60.04	60.00%	105
FLI1 forward	5′-CGAGAGGAGAGTCATCGTCC-3′	20	701	720	59.94	60.00%	107
FLI1 reverse	5′-TGTCGATCTCCATCAAGCTG-3′	20	807	788	59.94	50.00%	107

List shows the PCR primers used in this study for amplification in qRT-PCR. Primers were chosen as described in Materials and methods. GC, guanine-cytosine content; T_m, melting temperature.

An Excel file of Table S1 gives an overview of Tarp peptides and their dissociation constants.

References

Ashburner, M., C.A. Ball, J.A. Blake, D. Botstein, H. Butler, J.M. Cherry, A.P. Davis, K. Dolinski, S.S. Dwight, J.T. Eppig, et al. 2000. Gene ontology: tool for the unification of biology. *Nat. Genet.* 25:25–29. doi:10.1038/75556

Arora, S., Y. Wang, Z. Jia, S. Vardar-Sengul, A. Munawar, K.S. Doctor, M. Birrer, M. McClelland, E. Adamson, and D. Mercola. 2008. Egr1 regulates the coordinated expression of numerous EGF receptor target genes as identified by ChIP-on-chip. *Genome Biol.* 9:R166. doi:10.1186/gb-2008-9-11-r166

Chen, X.M., P.L. Splinter, P.S. Tietz, B.Q. Huang, D.D. Billadeau, and N.F. LaRusso. 2004. Phosphatidylinositol 3-kinase and frabin mediate *Cryptosporidium parvum* cellular invasion via activation of Cdc42. *J. Biol. Chem.* 279:31671–31678. doi:10.1074/jbc.M401592200

Dhanasekaran, N., and E. Premkumar Reddy. 1998. Signaling by dual specificity kinases. *Oncogene.* 17(11 Reviews):1447–1455. doi:10.1038/sj.onc.1202251

Fagiani, E., G. Giardina, L. Luzi, M. Cesaroni, M. Quarto, M. Capra, G. Germano, M. Bono, M. Capillo, P. Pelicci, and L. Lanfrancone. 2007. RaLP, a new member of the Src homology and collagen family, regulates cell migration and tumor growth of metastatic melanomas. *Cancer Res.* 67:3064–3073. doi:10.1158/0008-5472.CAN-06-2301

Goraca, A. 2002. New views on the role of endothelin (minireview). *Endocr. Regul.* 36:161–167.

Gregorc, U., S. Ivanova, M. Thomas, E. Guccione, B. Glaunsinger, R. Javier, V. Turk, L. Banks, and B. Turk. 2007. Cleavage of MAGI-1, a tight junction PDZ protein, by caspases is an important step for cell-cell detachment in apoptosis. *Apoptosis.* 12:343–354. doi:10.1007/s10495-006-0579-6

Jones, N., and D.J. Dumont. 2000. Tek/Tie2 signaling: new and old partners. *Cancer Metastasis Rev.* 19:13–17. doi:10.1023/A:1026555121511

Lane, B.J., C. Mutchler, S. Al Khodor, S.S. Grieshaber, and R.A. Carabeo. 2008. *Chlamydial* entry involves TARP binding of guanine nucleotide exchange factors. *PLoS Pathog.* 4:e1000014. doi:10.1371/journal.ppat.1000014

McDowall, M., N.M. Edwards, C.A. Jahoda, and P.I. Hynd. 2008. The role of activins and follistatins in skin and hair follicle development and function. *Cytokine Growth Factor Rev.* 19:415–426. doi:10.1016/j.cytogfr.2008.08.005

Muñoz, E., D. Xu, M. Kemp, F. Zhang, J. Liu, and R.J. Linhardt. 2006. Affinity, kinetic, and structural study of the interaction of 3-O-sulfotransferase isoform 1 with heparan sulfate. *Biochemistry.* 45:5122–5128. doi:10.1021/bi052403n

Neef, R., M.A. Kuske, E. Pröls, and J.P. Johnson. 2002. Identification of the human PHLDA1/TDAG51 gene: down-regulation in metastatic melanoma contributes to apoptosis resistance and growth deregulation. *Cancer Res.* 62:5920–5929.

Oh, E.S., and J.R. Couchman. 2004. Syndecans-2 and -4; close cousins, but not identical twins. *Mol. Cells.* 17:181–187.

Reutershan, J., and K. Ley. 2004. Bench-to-bedside review: acute respiratory distress syndrome - how neutrophils migrate into the lung. *Crit. Care.* 8:453–461. doi:10.1186/cc2881

Thomas, J.O., and A.A. Travers. 2001. HMG1 and 2, and related 'architectural' DNA-binding proteins. *Trends Biochem. Sci.* 26:167–174. doi:10.1016/S0968-0004(01)01801-1

Willis, S.N., and J.M. Adams. 2005. Life in the balance: how BH3-only proteins induce apoptosis. *Curr. Opin. Cell Biol.* 17:617–625. doi:10.1016/j.ceb.2005.10.001

Zhao, J., K.A. Kim, and A. Abo. 2009. Tipping the balance: modulating the Wnt pathway for tissue repair. *Trends Biotechnol.* 27:131–136. doi:10.1016/j.tibtech.2008.11.007