

## Supplemental Information

### **Mig6 Is a Sensor of EGF Receptor Inactivation that Directly Activates c-Abl to Induce Apoptosis during Epithelial Homeostasis**

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#### **Inventory of Supplemental Data**

##### **Figure S1**

Relating to Figure 1, showing **i)** histological characterization of the mammary ductal morphogenesis defects in the *Errfi1*<sup>-/-</sup> mice and **ii)** normal proliferation rate of *Errfi1*<sup>-/-</sup> pMECs cultured in vitro.

##### **Figure S2**

Relating to Figure 2, showing **i)** normal apoptotic response of *Errfi1*<sup>-/-</sup> pMECs upon cell detachment and DNA damage induced by Adriamycin, **ii)** that *Errfi1*<sup>-/-</sup> MECs express wild-type levels of markers for mammary epithelial differentiation and display normal cellular morphology and **iii)** that EGF-independent survival displayed by *Errfi1*<sup>-/-</sup> cells is not due to a gain in basal EGFR signalling or canonical mitogenic signalling and finally that **iv)** the binding of Mig6 and Abl is direct.

##### **Figure S3**

Relating to Figure 4. **i)** Maps the region of Abl that binds Mig6 and **ii)** models the structural similarity of the predicted Abl-Mig6 contact residues based on the analogy with the EGFR-Mig6 structure.

##### **Figure S4**

Relating to Figure 7, showing that RNAi-mediated knockdown of c-Abl in vivo, prevents mammary outgrowth.

## SUPPLEMENTAL FIGURES

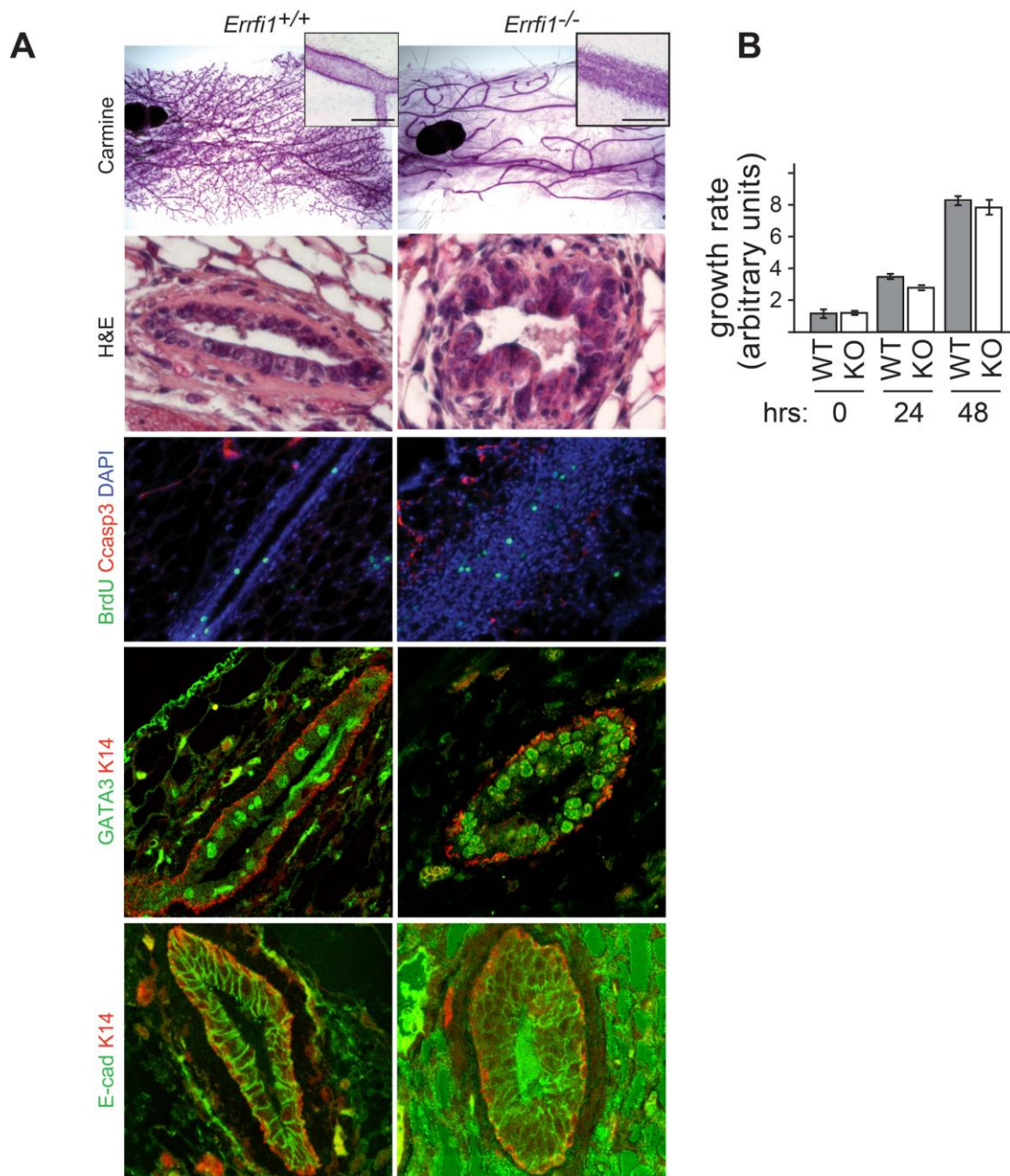


Figure S1 - Hopkins

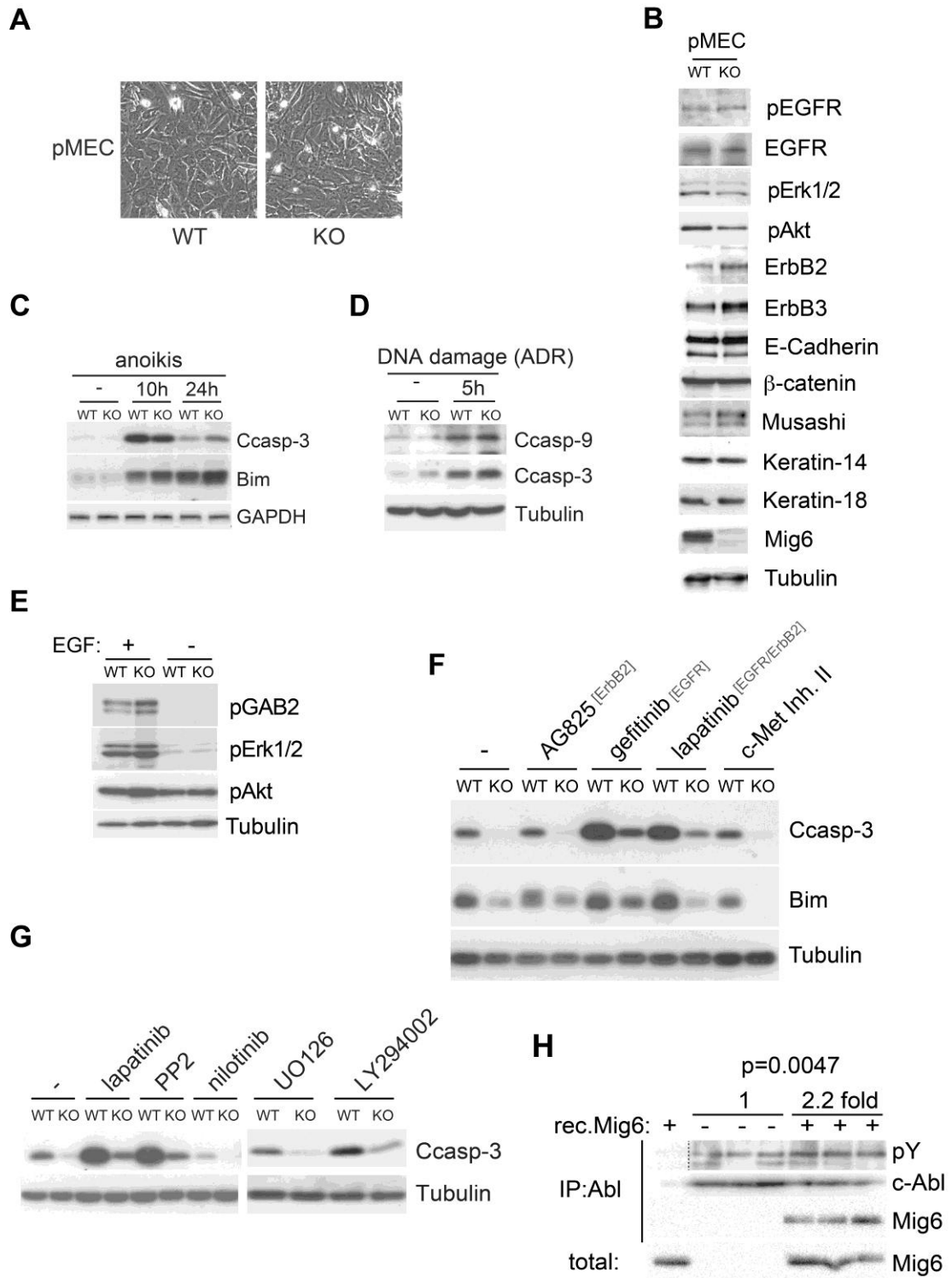


Figure S2 - Hopkins

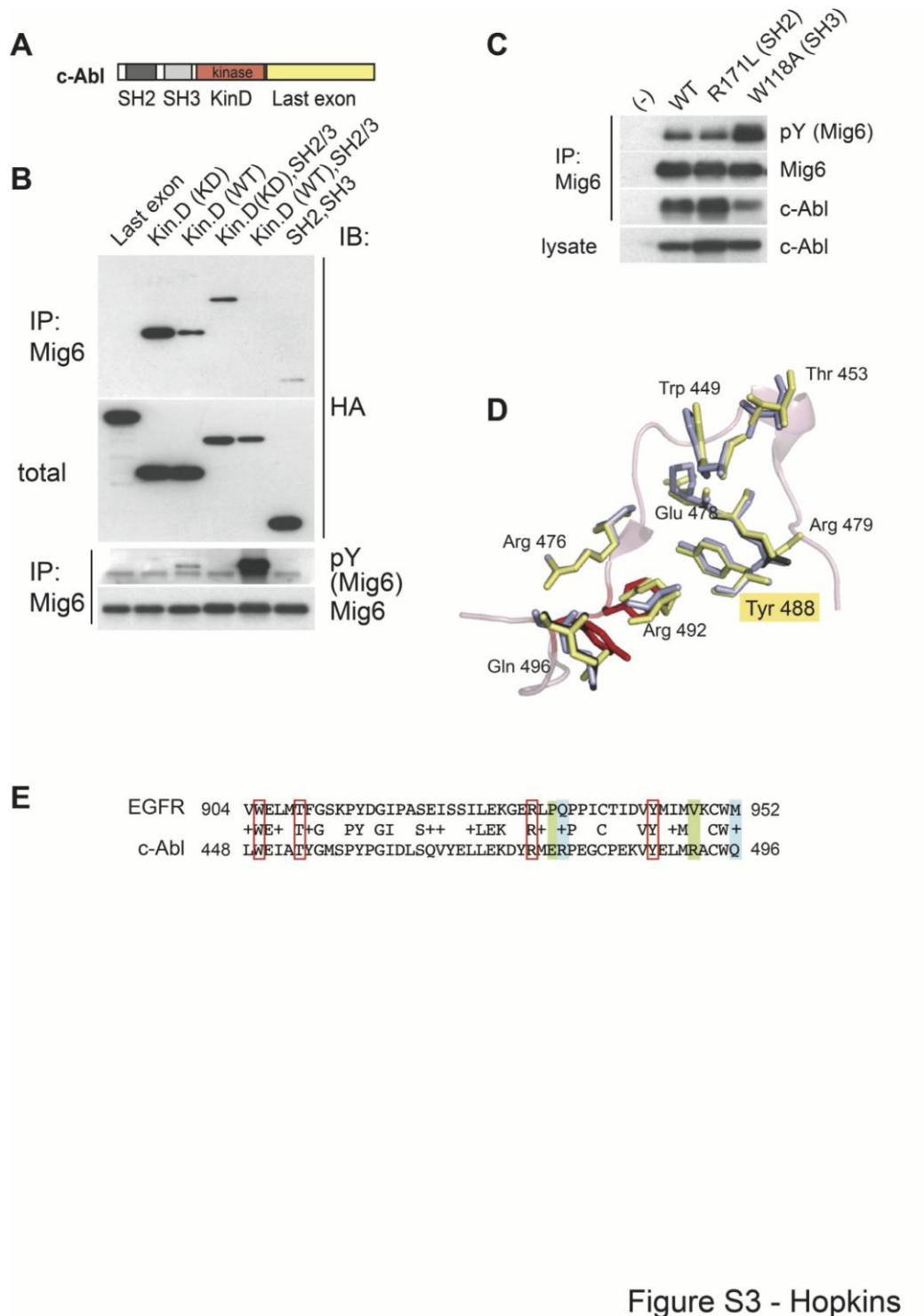


Figure S3 - Hopkins



normal morphology of KO pMECs. (B) Western analysis of cell lysates from confluent *Errfi1*<sup>-/-</sup> (KO) or littermate wild-type (WT) pMECs against indicated proteins cultured in the presence of EGF. (C,D) *Errfi1*<sup>-/-</sup> or wild-type pMECs isolated from 7-10 weeks old mice were either (A) cultured on cell repellent, poly-Hema-coated, tissue culture dishes (anoikis) or (B) treated with 1µg/ml adriamycin (ADR) for indicated times and cell lysates subjected to immunoblotting as indicated (n=2 independent experiments). (E) pMECs from WT or KO mice were either cultured in the presence or absence of EGF for 6 hours and analysed by western against indication proteins. (F) KO or littermate WT pMECs were deprived of EGF for 9 hours in the absence (-) or presence of 1µM AG825, 1µM Gefitinib, 1µM Lapatinib, 1µM c-Met inhibitor II, prior to western analysis for indicated proteins (representative of 2 independent experiments). (G) KO or littermate WT pMECs were deprived of EGF for 9 hours in the absence (-) or presence of 1µM Lapatinib, 0.8µM PP2, 2 µM nilotinib, 100nM UO126 or 1 µM LY294002, prior to western analysis for indicated proteins (representative of 2 independent experiments). (H) c-Abl was overexpressed in HEK293T cells, immunopurified, incubated with bacterially produced recombinant Mig6 (Abcam) and subjected to a kinase assay as described under Experimental Procedures. Samples were subjected to western analysis as shown. The indicated values denote fold change in pY signal intensity normalized against total c-Abl levels as determined by densitometry. The P-value were determined by two-tailed unpaired Student *t*-test (n=3).

**Figure S3 related to Figure 4. Mapping the Mig6 interaction site on c-Abl** (A) Outline of the domain structure of c-Abl (B) Co-immunopurification of Mig6 with HA-tagged fragments of c-Abl ectopically co-expressed in HEK293T cells, followed

by western analysis as indicated. The c-Abl fragments are the C-terminal last exon region, the wild-type catalytic domain alone (Kin.D), a point mutant catalytically inactive form of the kinase domain (Kin.D (KD)), the N-terminal SH2 and SH3 domains alone (SH2, SH3) or the wild-type and kinase inactive catalytic domain including the SH2 and SH3 domains. Note that Mig6 binds preferentially to the catalytically inactive kinase domain. (C) Co-immunopurification of Mig6 with wildtype or mutant forms of c-Abl that disrupt the SH2 (R171L) or SH3 domain (W118A) expressed in HEK293T cells. (D) High similarity between the Mig6 binding site of EGFR and c-Abl. Molecular modeling shows that the identified contact residues of EGFR (blue) involved in Mig6 (pink) binding and the corresponding residues of c-Abl (yellow, and denoted) are strikingly similar; 4 out of 8 contact residues are identical while 2 represent conservative changes (EGFR/Mig6: PDB 2RF9 and c-Abl: PDB 1OPK). The non-conserved changes are: V924 and P510 in EGFR are R492 and E478 in c-Abl respectively. (E) Alignment of human EGFR and c-Abl protein sequences highlighting the conserved contact residues (boxed).

**Figure S4, related to Figure 7. In vivo silencing of c-Abl leads to impaired mammary outgrowth.** (A,B) Cleared fat pad transplants of pMECs infected with lentivirus carrying c-Abl-targeting shRNA or non-targeting control shRNA. GFP marks infected cells. (A) Representative fluorescence image of whole GFP-positive outgrowths. (B) The maximum diameter of individual GFP-positive mammary outgrowths: Ctrl (n=12) or Abl knock-down (n=11). Individual glands are plotted and black bar indicates the mean while red bars represent s.e.m. The p-value was determined by two-tailed unpaired Student *t*-test. Scale bars=500 $\mu$ m.

## SUPPLEMENTAL EXPERIMENTAL PROCEDURES

**cdNA constructs.** Mammalian expression constructs with wild-type, point mutant and HA-tagged truncation mutant c-Abl1b were previously described (Hantschel et al., 2003). Mig6 was cloned into pcDNA4.1/TO and point mutants of Mig6: the F352A/Y358A, Y394/5F, deletion aa328-361, PP319/20AA as well as the c-Abl1b Y488E/F, W449T, L471A and R476A were generated by site-directed mutagenesis using the QuikChange XL Site-Directed Mutagenesis Kit (Agilent) and mutations confirmed by DNA sequencing. The HA-tagged Mig6 deletion mutants (AH1+2: aa314-403 and AH1: aa335-365) were cloned by PCR into pcDNA4.1/TO.

**shRNA and siRNA.** shRNA sequences used to target c-Abl were Abl#1: 5' AAAAGCAAGAACCTGTACACTTTCTTTTCGAGAAAGTGTACAGGTTCTTGC3' Abl#1 or 5' AAAAGCAACAAGTCCACTATCTACGTTTCGCGTAGATAGTGGGCTTGTTG C3' (Abl#2). Sequence of siRNA oligo targeting p73 was: GAATGAAAGTACCACCAAATT (Applied Biosystems).

**Antibodies.** The following antibodies were used for immunofluorescence: Cleaved Caspase-3, phopho-Y877-ErbB2 (Cell Signaling), Mig6 (Sigma), E-cadherin (BD Transduction Laboratories), Cytokeratin 14 (Covance), Cytokeratin 18 (Novocastra) GATA-3 (Santa Cruz) and anti-BrdU conjugated Alexa 488. Secondary antibodies used were Cy3, Cy5 (Molecular Probes) or Alexa 488 or Alexa 594 (Jackson ImmunoResearch)-conjugated antibodies. The following antibodies were used for western blotting: a phosphospecific c-Abl (Tyr488) antibody generated against



KVpYELMRA (Eurogentech), Mig6 (Sigma),  $\alpha$ -Tubulin, EGFR, Cleaved Caspase-3 (Asp175), Cleaved Caspase-9 (Asp353) and Phospho-c-Abl Tyr412 (Cell Signaling), Bim (Abcam, ab7888), c-Abl1 (Hantschel et al., 2003), c-Abl1 (8E9), Phospho-cAbl Tyr245 and Phospho-Tyr (4G10). Secondary HRP conjugated antibodies were from Jackson ImmunoResearch.

**SiRNA transfection of MEFs.** Immortalized primary *Errfi1*<sup>-/-</sup> MEFs were grown in DMEM containing 10%FBS to 50-60% confluence and transfected with a siRNA oligo targeting p73 using Jetprime (Polyplus).

**MTT cell proliferation assay.** Freshly isolated pMECs from *Errfi1*<sup>-/-</sup> or wild-type 8-week old mice were cultured were seeded at a density of 30000 cells/cm<sup>2</sup> in 24-well plates and cultured for indicated times. 3-(4-dimethylthiazol-2-yl) 2,5-diphenyl-tetrazolium bromide (MTT, Sigma) was added to the cells for 2 hours at 37C prior to harvest of cells and measurement of absorbance at 570nm.

**Flow cytometry.** pMECs were resuspended in mammary epithelial cell medium. Endothelial (CD31<sup>+</sup>) cells and leukocytes (CD45<sup>+</sup>) were labelled with rat anti-mouse CD31 antibody (MEC 13.3; BD Biosciences), anti-rat IgG microbeads and monoclonal anti-mouse CD45 conjugated microbeads (30f11.1; Miltenyi Biotec) and removed via magnetic cell separation using a MACS column and separator (Miltenyi Biotec). Separation of myoepithelial and luminal pMECs was obtained by incubation with anti-CD29 FITC (HM beta 1-1; AbD serotec) and biotin conjugated anti-CD61 (2C9.G2; BD Biosciences) in combination with APC-streptavidin (BD Biosciences) 4°C. Dead cells were excluded using 7-AAD.

**Co-Immunoprecipitation.** pMECs were lysed in 50mM Tris-HCL (pH7.5), 150mM NaCl, 1% v/v NP-40 and cleared by centrifugation at 9500g for 15 minutes. Soluble proteins were incubated with anti-c-Abl antibody (Hantschel et al., 2003) or anti-Mig6 antibody overnight at 4°C followed by a 2 hour incubation in protein G conjugated sepharose beads at 4°C. Immunocomplexes were washed twice with lysis buffer, twice with lysis buffer excluding NaCl and subjected to SDS-PAGE and western analysis of interacting proteins. Transfected HEK293T cells were lysed in RIPA lysis buffer (50 mM Tris-Cl pH 7.4, 150 mM NaCl, 1% NP-40, 0.5% sodium deoxycholate, 0.1% SDS) and insoluble material removed by centrifugation for 15 min at 9500g. Cleared lysates were incubated with anti-c-Abl (Hantschel et al., 2003), anti-Mig6 or anti-HA antibodies overnight at 4°C followed by a 1 hour incubation in protein G conjugated sepharose beads at 4°C. Immunocomplexes were washed four times with RIPA buffer and subjected to SDS-PAGE and western analysis for interacting proteins.

## **SUPPLEMENTAL REFERENCE**

Hantschel, O., Nagar, B., Guettler, S., Kretzschmar, J., Dorey, K., Kuriyan, J., and Superti-Furga, G. (2003). A myristoyl/phosphotyrosine switch regulates c-Abl. *Cell* 112, 845-857.