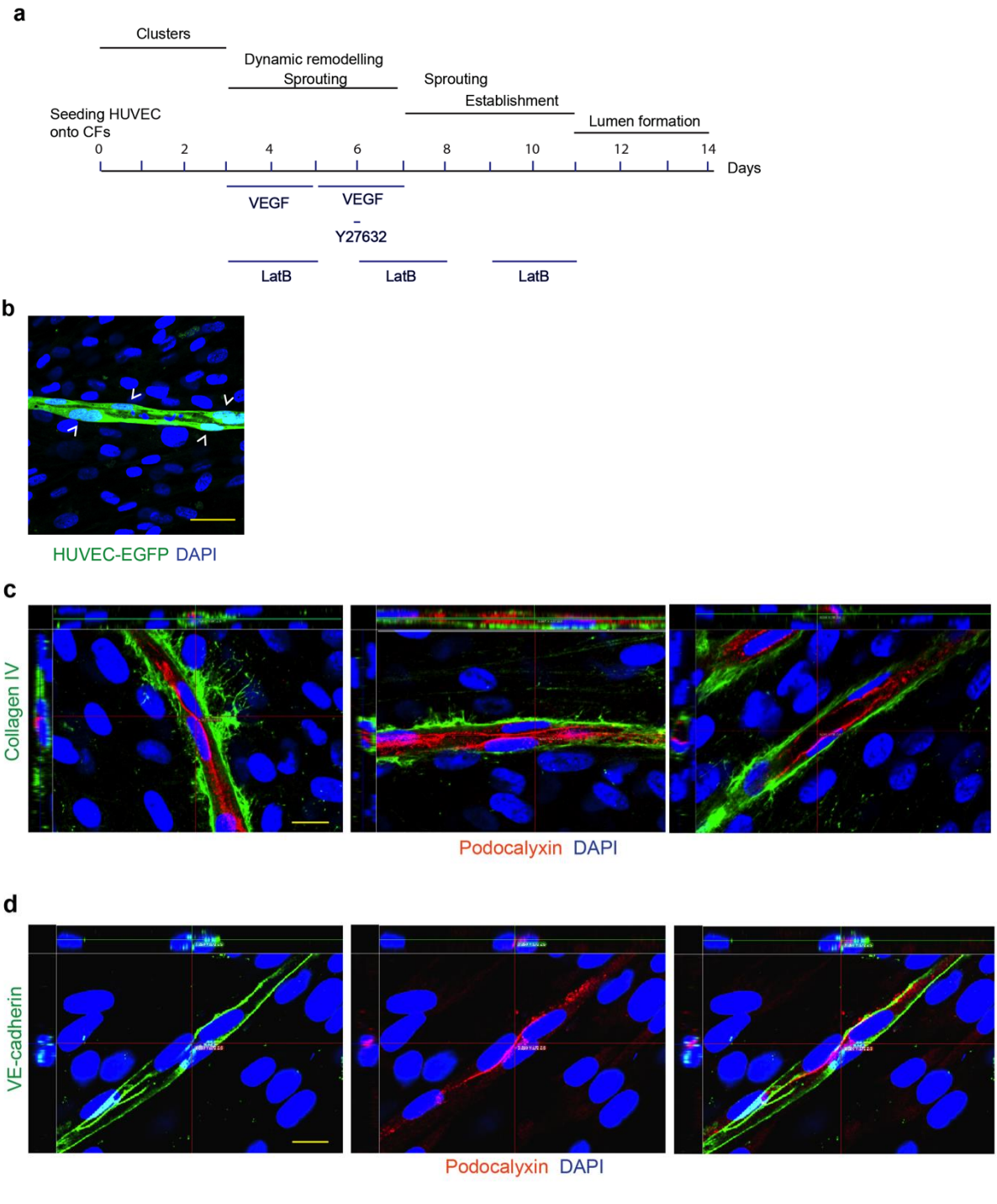
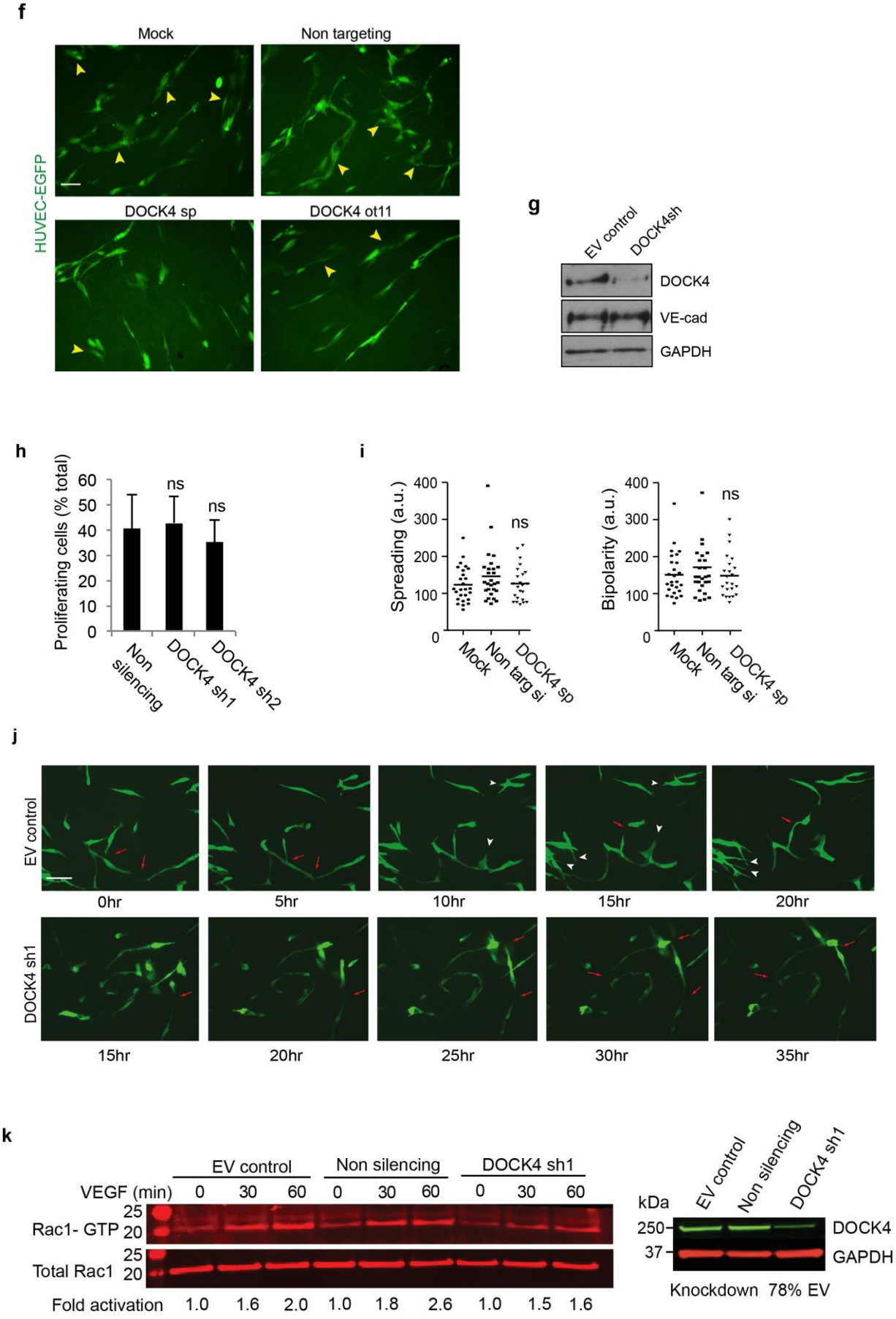
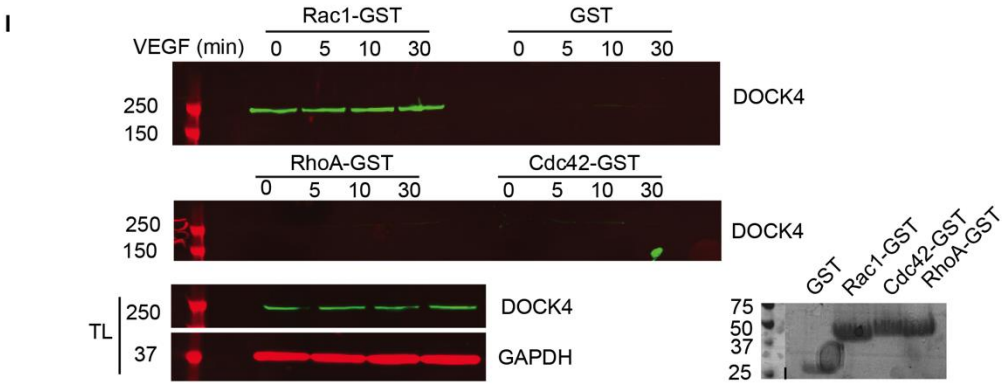
**Supplementary Figure 1**



**Supplementary Figure 1**

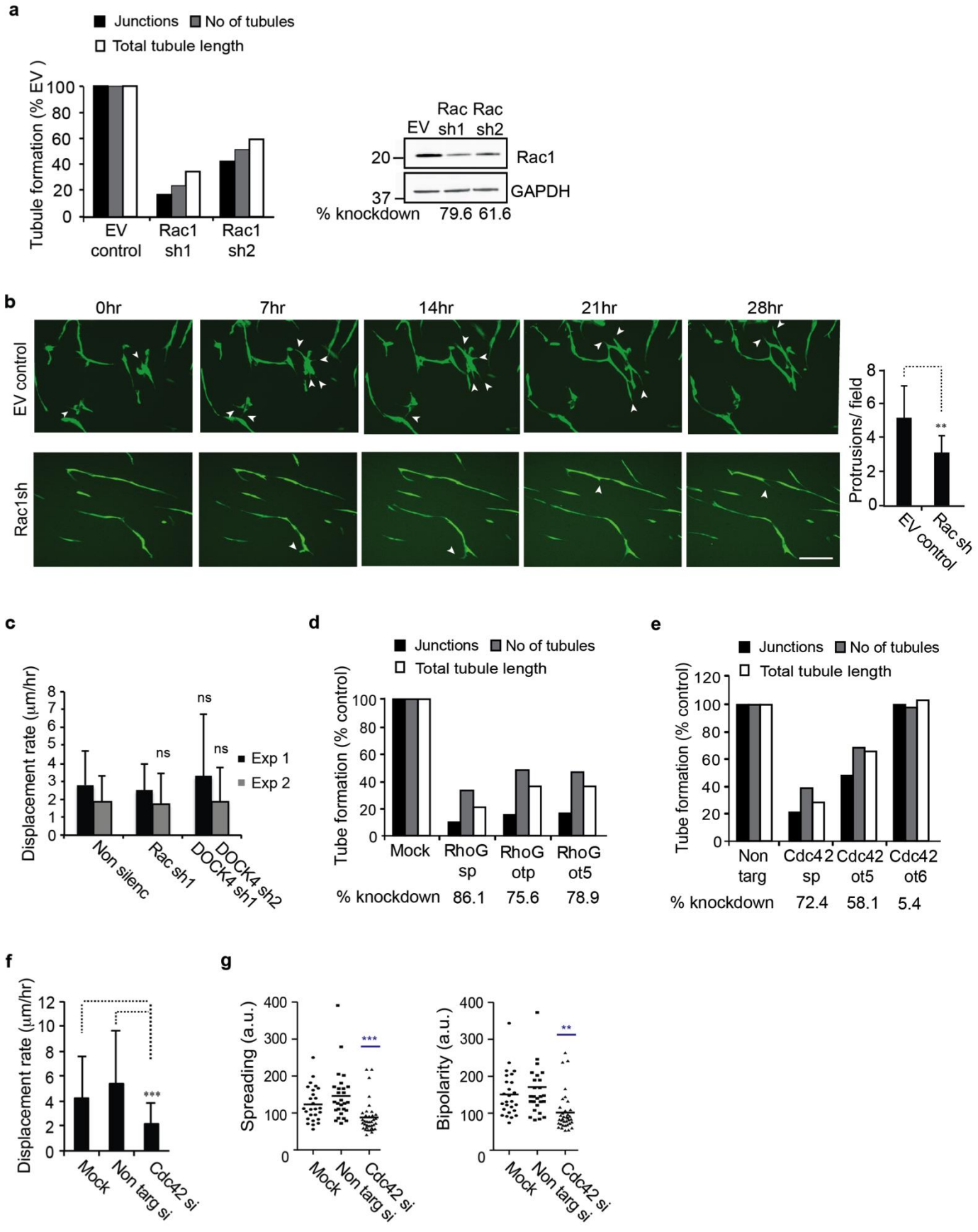


**Supplementary Figure 1**



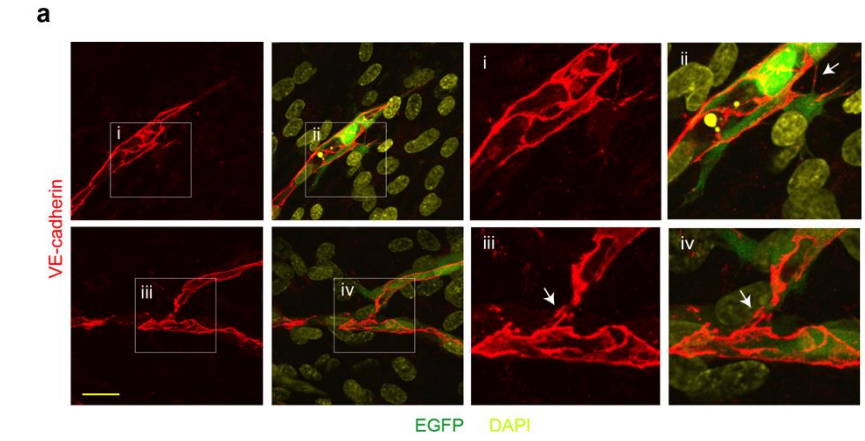

**Supplementary Figure 1. Rac GEF DOCK4 controls clusters and protrusive activity.** (**a**) Stages of tubule morphogenesis in the coculture system and treatment schedules. (**b**) Onset of lumen formation at 11d after seeding of HUVEC-EGFP onto CFs. Note the presence of apposing endothelial cells (white arrows) around the developing lumen. Scale bar 50µm. (**c**) Confocal images of developing tubes 14d after seeding HUVEC onto CFs show apical localization of podocalyxin; collagen IV marks basement membrane. Scale bar 15µm. (**d**) Lateral adhesions at onset of lumen formation visualized by VE-cadherin staining. Scale bar 15µm. (**e**) Histogram: total tubule length, tubules and branch points 5d after seeding HUVEC with DOCK4 depletion (sp, smartpool siRNA) onto CFS; *n*= 18 microscopic fields from three organotypic cocultures, representative experiment from two rounds of screens. (**f**) Endothelial cell clusters (yellow arrowheads) 2d after seeding HUVEC-EGFP with DOCK4 depletion (sp, smartpool siRNA; ot, on-target plus siRNA) onto CFs. Scale bar 100µm. (**g**) VE-cadherin immunoblot following DOCK4 depletion in HUVEC (sh, shRNA1). (**h**) Histogram: endothelial cell proliferation by Ki67 staining 2d after seeding HUVEC with DOCK4 depletion (sh, shRNA) onto CFs. Values represent Ki67 positive cells as percentage of total ± s.e.m.; *n*=12 microscopic fields (20x objective), representative experiment. Knockdown: 76.6% reduction compared to non silencing control. ns, non significant by two-tailed *t* test compared to non silencing control. (**i**) Scatter plot: spreading and bipolarity following DOCK4 depletion (sp, smartpool siRNA) of HUVEC-EGFP 3d after seeding onto CFs; n=24 cells from four organotypic cocultures; knockdown: 84.0% reduction compared to non targeting. ns, non significant by two-tailed *t* test compared to non targeting. (**j**) Still images from Supplemental movies S5 and S6 of tubule formation following DOCK4 depletion (shRNA, sh; EV, empty vector) 5d after seeding HUVEC onto CFs. White arrowheads: protrusions persisting over 5hrs; red arrows: anastomoses. Scale bar 50µm. (**k**) Left panel: immunoblot of Rac1 activation on VEGF stimulation (25ng/ml) in HUVEC following DOCK4 depletion (shRNA, sh; EV, empty vector); fold activation (Rac1-GTP/ total Rac1) compared to unstimulated controls. Right panel: DOCK4 knockdown by immunoblot. (**l**) Immunoblots of DOCK4 in GST-Rac1, RhoA and Cdc42 pulldowns in HUVEC. Bottom left panels: total lysate (TL); bottom right: GST proteins in pulldowns.

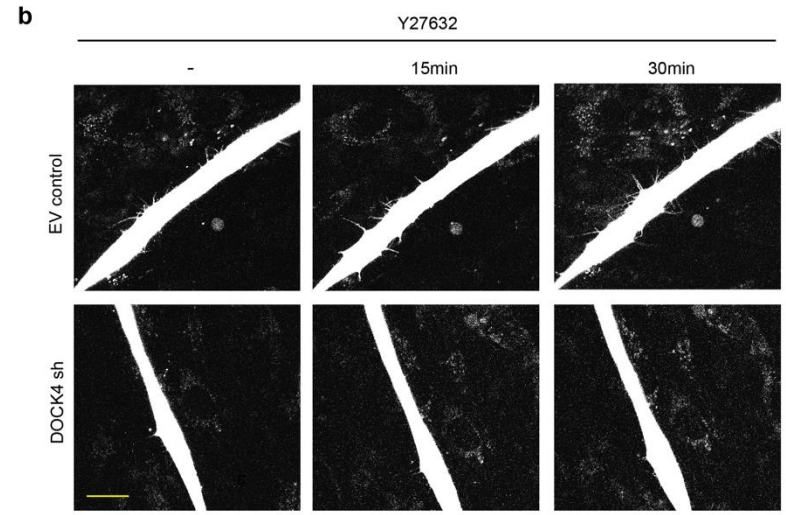
**Supplementary Figure 2**

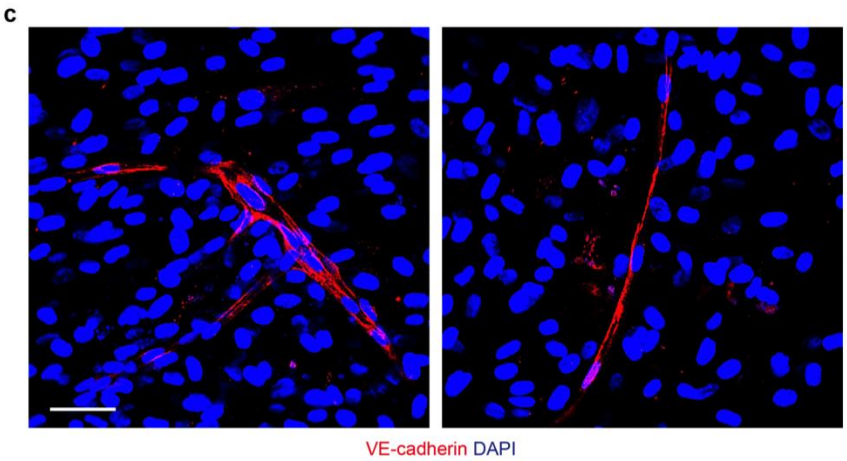


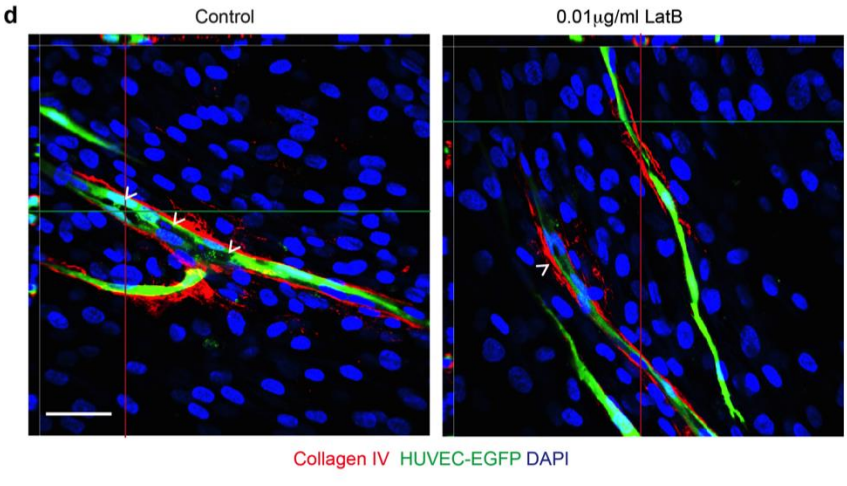
**Supplementary Figure 2. RhoGTPases required for angiogenesis.** (**a**) Quantification of tubule formation 7d after seeding HUVEC with Rac1 depletion (shRNA, sh) onto CFs (*n*=12 microscopic fields), representative experiment. (**b**) Still images from Supplemental movies S7 and S8 of HUVEC with Rac1 depletion in **a**. Arrowheads point to protrusions persisting for over 5hrs. Histogram: quantification over 48hrs of protrusions persisting for over 5 hrs. (**c**) Histogram: quantification of displacement rate (linear distance travelled) over 24hrs following Rac1 or DOCK4 depletion (shRNA, sh) starting at 3d after seeding onto CFs; error bars indicate s.d.; *n*= number of single cells tracked in two experiments (exp 1: non silencing, *n*=61; Rac sh1, *n*=45; DOCK4 sh1, *n*=54; exp 2: non silencing, *n*=32; Rac sh1, *n*=31; DOCK4 sh2, *n*=42) from timelapse movies (exp 1: non silencing, 8; Rac sh1, 8; DOCK4 sh1, 10; exp 2: non silencing, 5; Rac sh1, 6; DOCK4 sh2, 7). (**d, e**) Quantification of tubule formation after RhoG (**d**) or Cdc42 (**e**) depletion (sp, smartpool siRNAs; ot, on-target plus siRNAs) in HUVEC 5d after seeding onto CFs, (*n*= 12 microscopic fields), representative experiment. (**f**) Histogram: quantification of displacement rate as in **c** following Cdc42 depletion (sp, smartpool siRNA) starting at 2d after seeding onto CFs; error bars indicate s.d.; *n*= 24 single cells tracked from 4 movies. (**g**) Scatter plot: quantification of cell spreading and bipolarity following Cdc42 depletion (sp, smartpool siRNA; ot, on-target plus siRNA) of HUVEC-EGFP at 3d after seeding onto CFs; error bars indicate s.d.; *n*= 24 single cells from four cocultures. ** $P<0.01$, *** $P<0.001$ by two-tailed *t* test.

**Supplementary Figure 3**

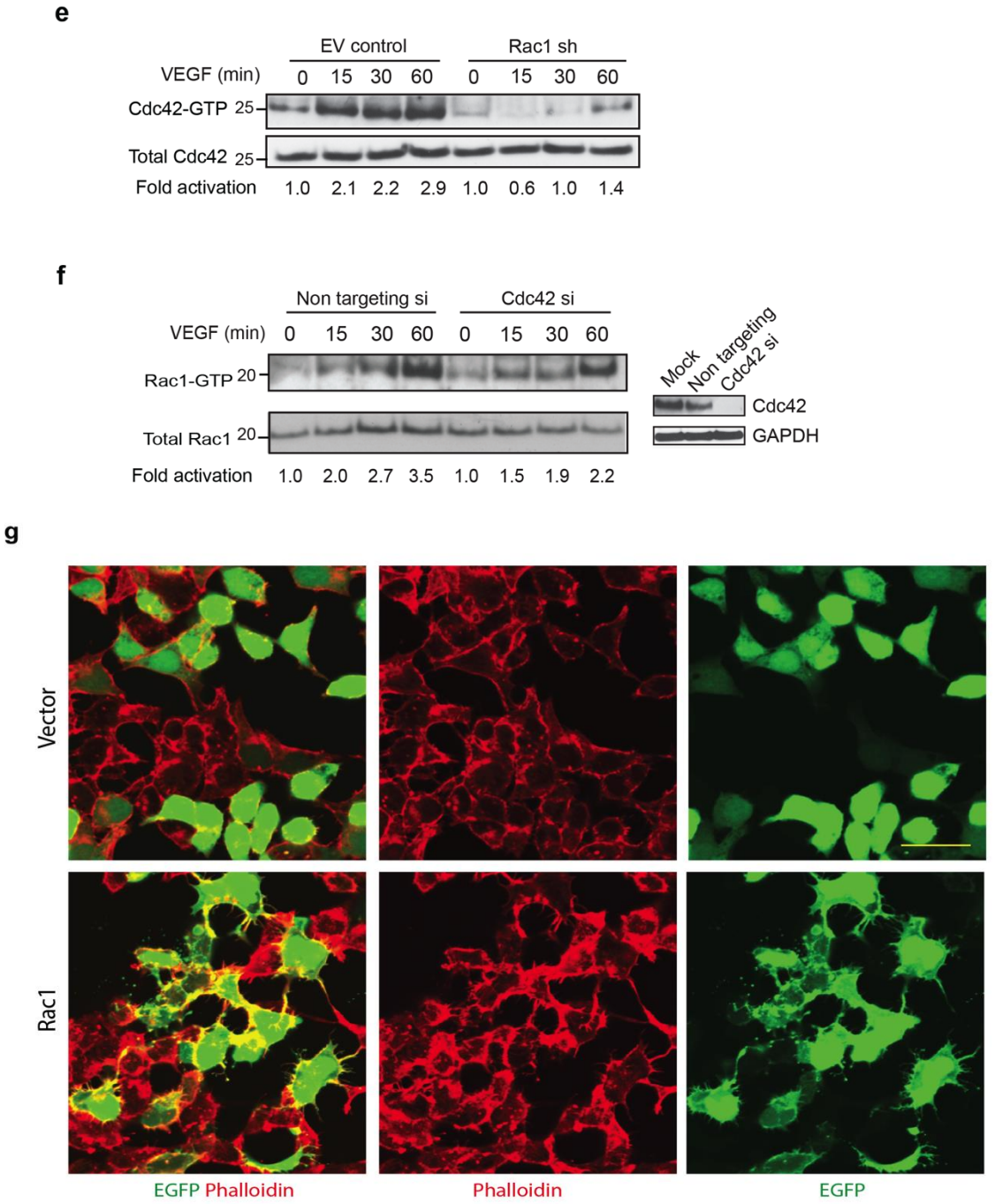


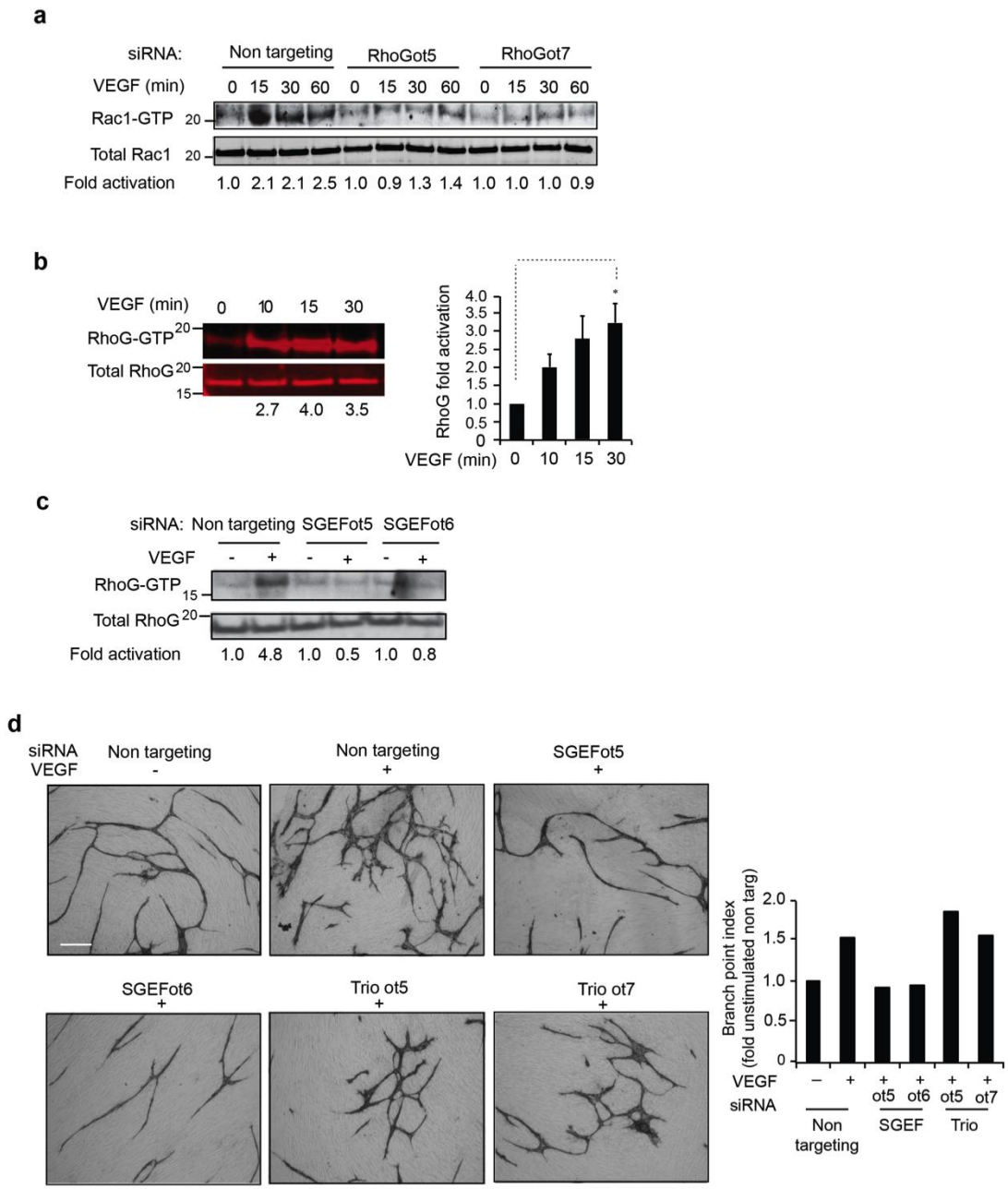
**Supplementary Figure 3**



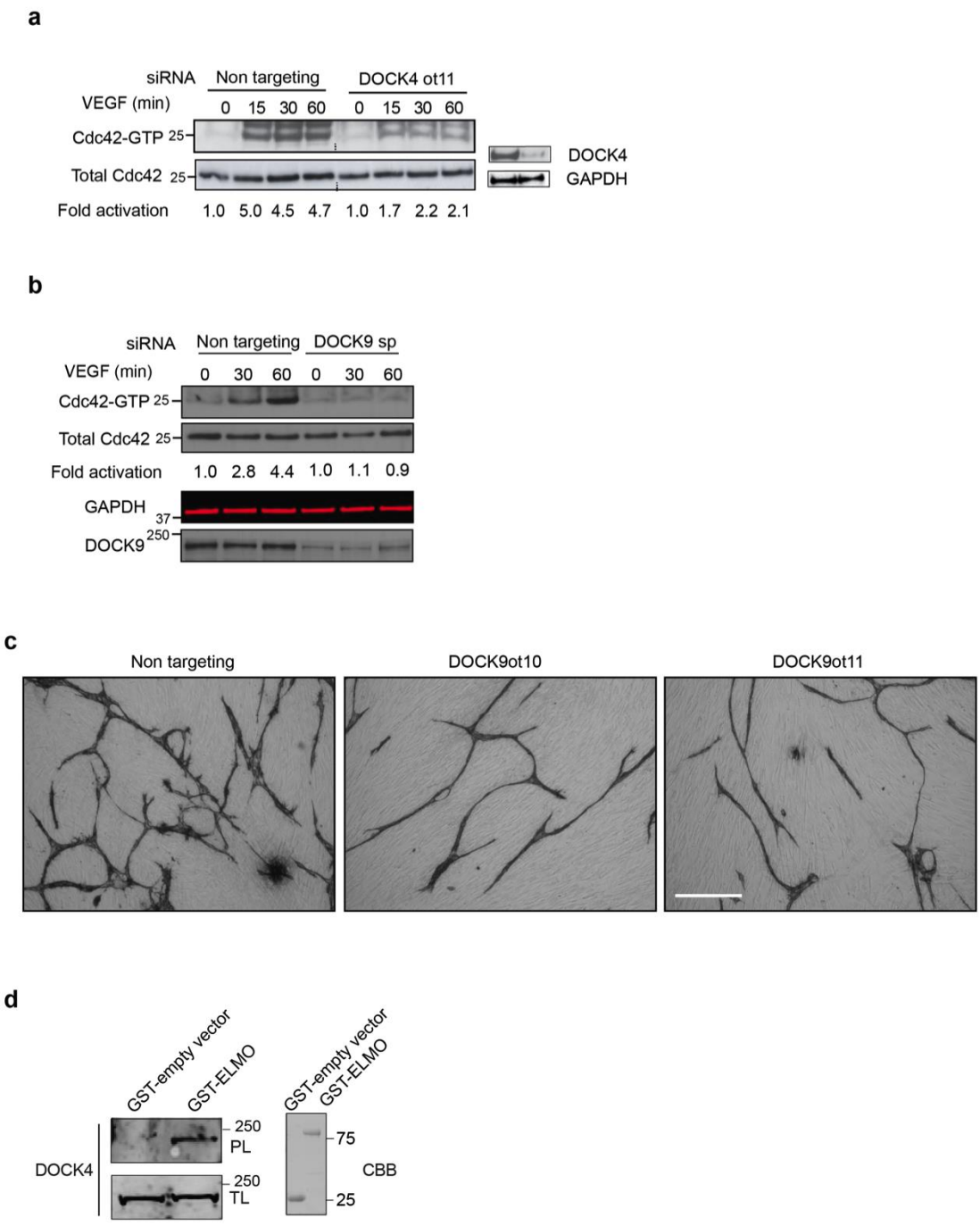

**Supplementary Figure 3. Rac1 controls Cdc42 activation and filopodia formation.** (**a**) VE-cadherin localization at filopodia (white arrows) in HUVEC-EGFP on 24 hr VEGF treatment (25ng/ml) 6d after seeding HUVEC onto CFs. White arrows point to VE-cadherin localization at filopodia at sites of cell-cell contact. (**b**) Filopodia blockade with DOCK4 depletion (shRNA1, sh; EV, empty vector) persists on Y27632 treatment. Tubules were treated with Y27632 at 6d after seeding onto CFs for the indicated timepoints. Scale bar 50μm. (**c-d**) Appearance of tubules and adherens junctions on treatment with 0.01μg/ml Latrunculin B (LatB). Cocultures were treated with 0.01μg/ml LatB for 48hrs at 3d, 6d and 9d after seeding HUVEC onto CFs (6 day total treatment), fixed and stained for VE-cadherin to mark adherens junctions and collagen IV to mark the basement membrane. Note the lack of sprouts and thinner appearance of treated tubules compared to controls in **c**; treatment allowed junction formation but resulted in fewer lateral cell-cell contacts. White arrowheads

in **d** point to sites of lumen formation. (**e**) Immunoblot of Cdc42 activation on VEGF stimulation (25ng/ml) in HUVEC following Rac1 depletion (shRNA, sh; EV, empty vector); fold Cdc42 activation (Cdc42-GTP/ total Cdc42) is compared to unstimulated controls. (**f**) Immunoblot of Rac1 activation on VEGF stimulation (25ng/ml) in HUVEC following Cdc42 depletion (siRNA, si); fold Rac1 activation (Rac1-GTP/ total Rac1) is compared to unstimulated controls. (**g**) Images of phalloidin stained 293T cells following overexpression of EGFP-Rac1 or Vector (EGFP) corresponding to Figure 3h. Scale bar, 50μm.

**Supplementary Figure 4**

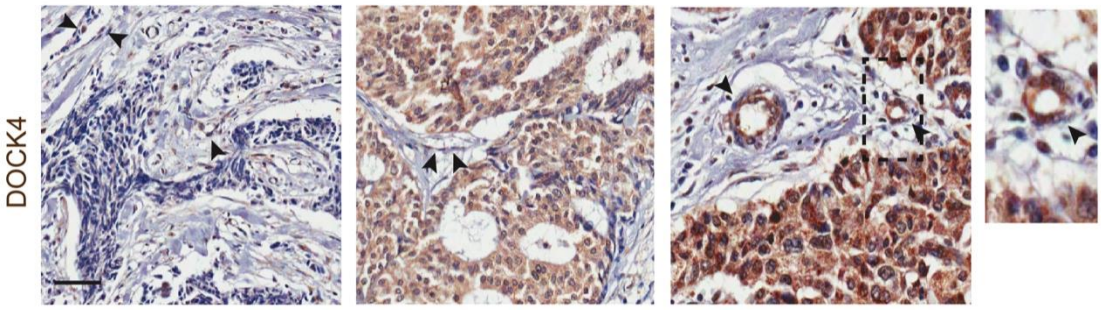



**Supplementary Figure 4. SGEF driven RhoG activation regulates Rac1 activation downstream of VEGF.** (**a**) Immunoblot of Rac1 activation (Rac-GTP/ total Rac) on VEGF stimulation (25ng/ml) in HUVEC following RhoG depletion (ot, on-target plus siRNAs). (**b**) Immunoblot of RhoG activation on VEGF stimulation (25ng/ml) in HUVEC. Histogram shows fold RhoG activation (GTP-bound RhoG/ total RhoG) compared to unstimulated control; error bars s.e.m. (*n*= 3 independent experiments). (**c**) Immunoblot of RhoG activation on 30min VEGF stimulation (25ng/ml) in HUVEC after SGEF depletion (ot, on-target plus siRNAs); fold RhoG activation (RhoG-GTP/ total RhoG) compared to unstimulated controls. (**d**) Images of organotypic cocultures (CD31 staining) treated with VEGF (25ng/ml) and following depletion of SGEF or Trio (ot, on-target plus siRNAs) in HUVEC 5d after seeding onto CFs. Scale bar, 200μm. Histogram: branch point index (*n*= 12 microscopic fields from three cocultures, representative experiment).

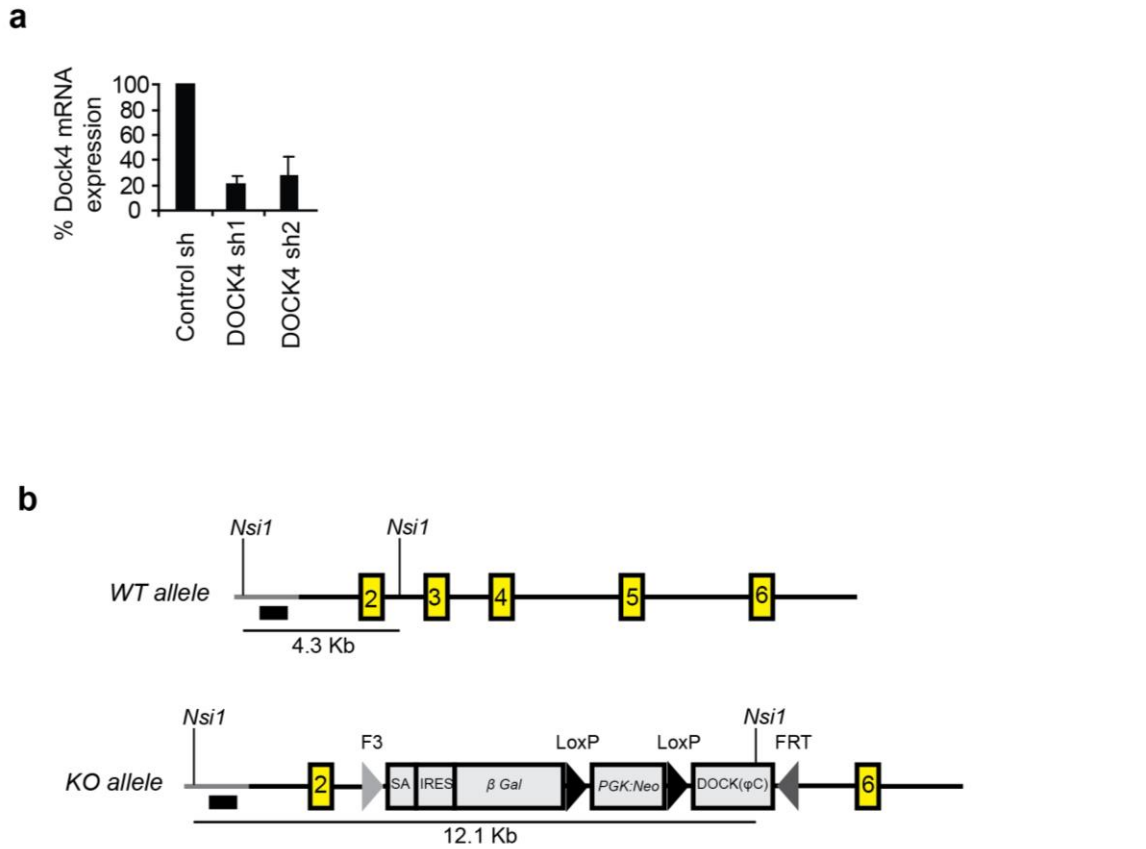



**Supplementary Figure 5. DOCK4 and DOCK9 control Cdc42 activation and interaction of DOCK4 with ELMO.** (**a**) Immunoblot of Cdc42 activation following DOCK4 depletion (ot, on-target plus siRNA); fold Cdc42 activation (Cdc42-GTP/ total Cdc42) compared to unstimulated controls. Knockdown: 80.6% reduction compared to the non targeting control. (**b**) Immunoblot of Cdc42 activation (Cdc42-GTP/total Cdc42) on VEGF stimulation (25ng/ml) in HUVEC following depletion of DOCK9 (smartpool siRNA, sp). (**c**) Images of organotypic cocultures (CD31 staining) treated with VEGF (25ng/ml) following depletion of DOCK9 (ot, on-target plus siRNAs) in HUVEC 5d after seeding onto CFs. Scale bar, 200μm. (**d**) Pulldown assay shows interaction of DOCK4 with RhoG effector ELMO in 293T cells.

**Supplementary Figure 6**



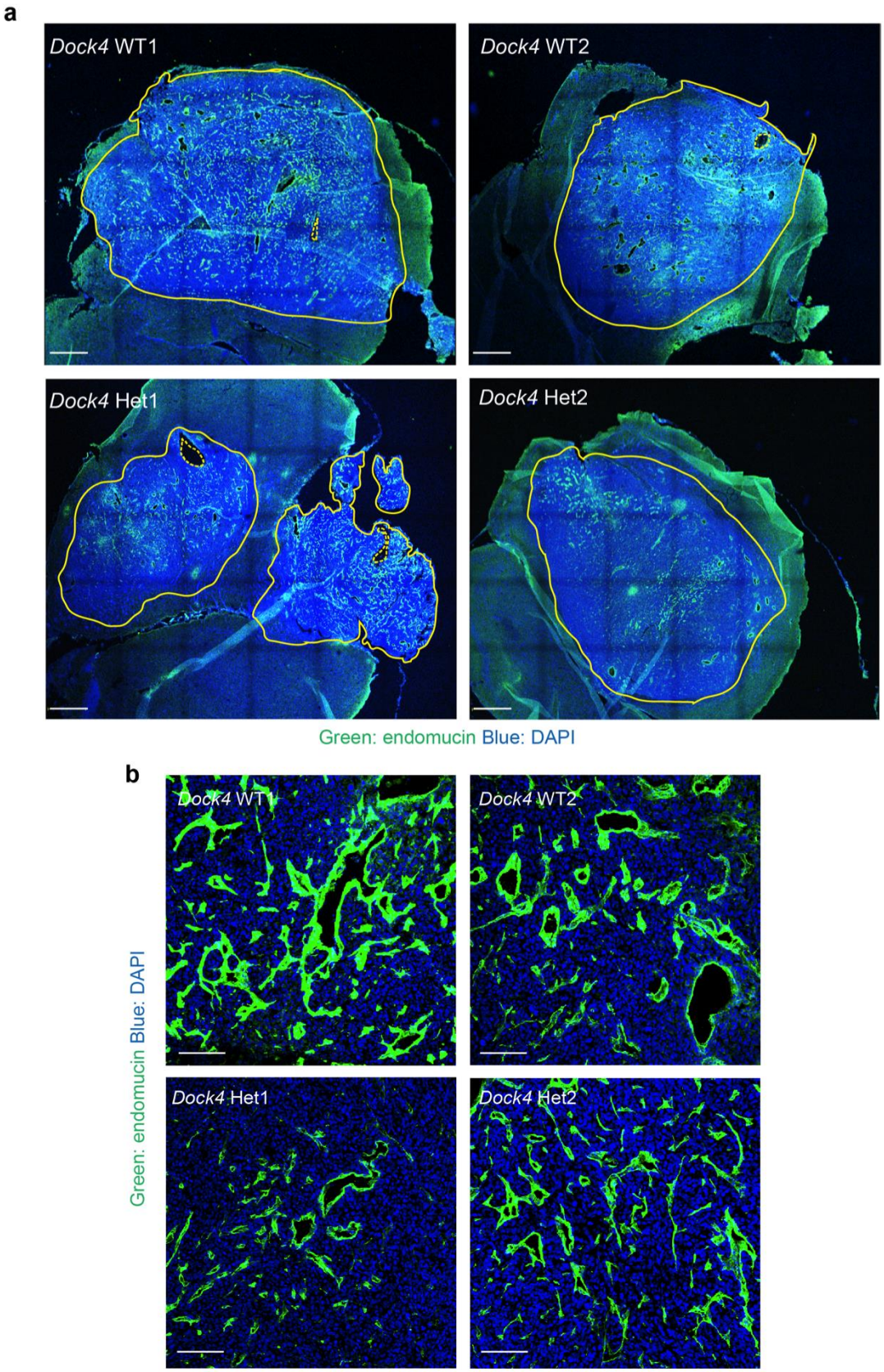

**Supplementary Figure 6. DOCK4 expression in patient tumours.** DOCK4 expression in blood vessels (black arrowheads) of ductal breast carcinoma specimens showing different levels of DOCK4 expression in the tumour cell compartment and blood vessels. Scale bar, 200μm.



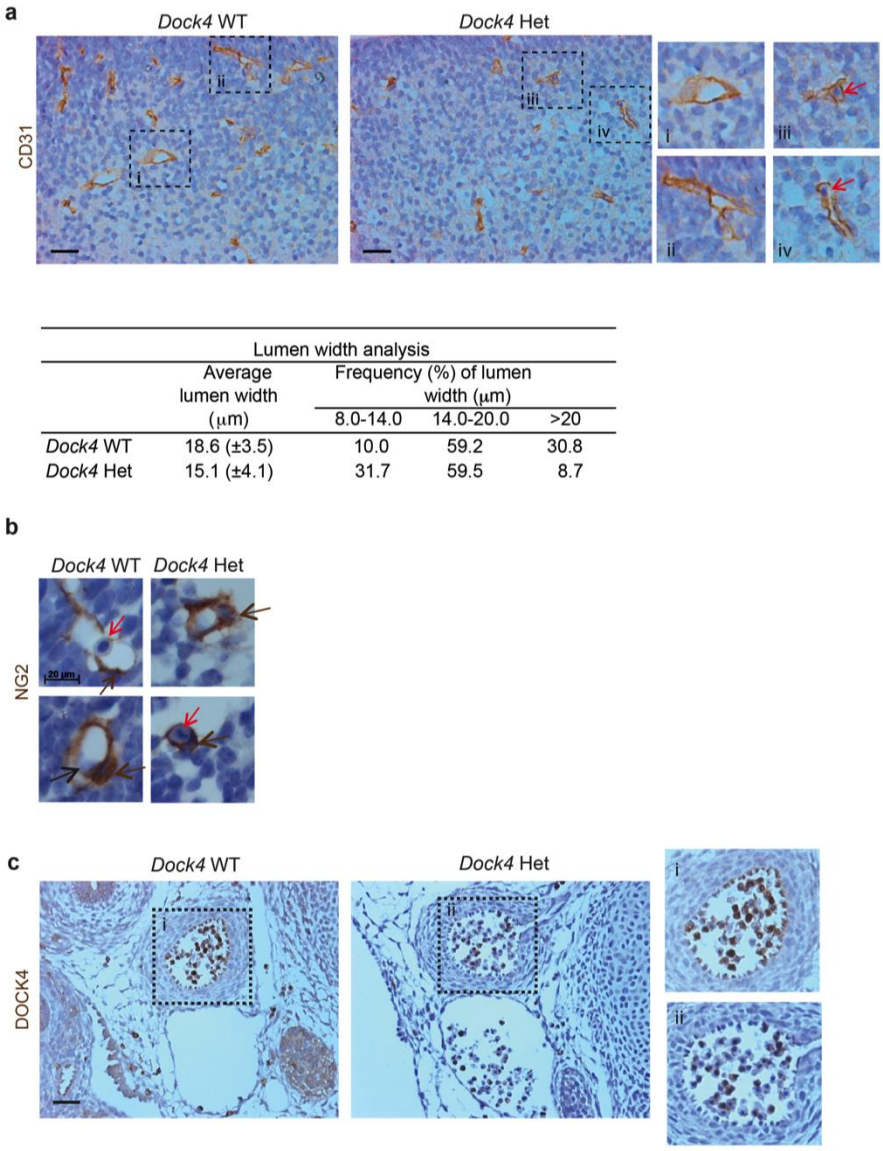

| | *Dock4* WT | *Dock4* Het | *Dock4* KO |
|---|---|---|---|
| **E11.5** | 6 | 9 | 0 |
| **E10.5** | 2 | 6 | 0 |
| **E9.5** | 0 | 6 | 0 |
| **E8.5** | 5 | 14 | 0 |
| **E7.5** | 2 | 13 | 0 |

**Supplementary Figure 7. Retroviruses used in the *in vivo* tumour co-injection model and generation of the *Dock4* null heterozygous mouse line.** (**a**) Ecotropic retroviruses harbouring DOCK4 shRNAs were tested in NIH3T3 fibroblasts. Histogram: shRNA-mediated DOCK4 knockdown determined by qPCR. (**b**) Schematic showing the wild type (WT) and the targeted knockout (KO) *Dock4* alleles. In the targeted allele, exons 3-5 were replaced by the targeting cassette for frameshift of the open reading frame. Yellow boxes show exons, main black lines show homology regions, grey lines show homology outside of the targeting vector. SA = Splice Acceptor, IRES = Internal Ribosomal Entry Site. Black boxes show position of the Southern probe that detects bands shown upon NsiI digestion. (**c**) Southern blot of tail DNA from an F1 litter of *Dock4* mice derived from a chimaera crossed to C57BL/6J females. + = WT allele, - = KO allele. (**d**) Table shows numbers of embryos analysed from *Dock4*+/- incrosses. Note the absence of *Dock4* null homozygous embryos.

**Supplementary Figure 8**




**Supplementary Figure 8. DOCK4 controls blood vessel lumen calibre in tumours.** (**a**) Examples of tiled images of intracranial tumours used for lumen analysis. (**b**) Confocal images obtained with a 20x objective representative of tumour areas with lumenized blood vessels.




| Lumen width analysis | | | | |
|---|---|---|---|---|
| | Average lumen width (µm) | Frequency (%) of lumen width (µm) | | |
| | | 8.0-14.0 | 14.0-20.0 | >20 |
| *Dock4* WT | 18.6 (±3.5) | 10.0 | 59.2 | 30.8 |
| *Dock4* Het | 15.1 (±4.1) | 31.7 | 59.5 | 8.7 |

**Supplementary Figure 9. DOCK4 controls blood vessel lumen calibre during embryonic development.** (**a**) Images of sections immunostained with CD31 to visualize blood vessel lumens in the brain of E13.5 *Dock4* wild type (WT) and *Dock4* heterozygous (Het) embryos. Scale bar, 50 µm. *i-iv*: magnifications of areas outlined in larger images. Red arrows point to blood cells in small calibre lumens. Table shows analysis of lumen size (three embryos for each condition) in microscopic fields across the whole hemisphere. 40 vessels with largest diameter lumens were analysed for each embryo. (**b**) Images show pericyte coverage of blood vessels with different lumen sizes in the brain of E13.5 *Dock4* wild type (WT) and *Dock4* heterozygous (Het) embryos as detected by NG2 staining. Brown arrows point to NG2 positive pericytes; black arrows point to endothelial cells; red arrows point to blood cells in lumens. (**c**) Images of aortas of E13.5 *Dock4* WT and Het embryos, immunostained for DOCK4. Scale bar, 50 µm. *i-ii*: magnifications of areas indicated with boxes in larger images.

**Supplementary Figure 10**

**a**

| siRNA | Target sequence or catalogue number |
|---|---|
| Rac1 SMARTpool | 1- CGGCACCACUGUCCCAACA<br>2- UAAAGACACGAUCGAGAAA<br>3- UAAGGAGAUUGGUGCUGUA<br>4- AGACGGAGCUGUAGGUAAA |
| RhoG SMARTpool | 1- CUACACAACUAACGCUUUC<br>2- CCAGUCCGCCGUCCUAUGA<br>3- GCAACAGGAUGGUGUCAAG<br>4- CGUCAUCUGUUUCUCCAUU |
| RhoG ON-TARGETplus | 5- CUACACAACUAACGCUUUC<br>7- GCUGUGCGCUACCUCGAAU |
| Cdc42 SMARTpool | 1- GGAGAACCAUAUACUCUUG<br>2- GAUUACGACCGCUGAGUUA<br>3- GAUGACCCCUCUACUAUUG<br>4- CGGAAUAUGUACCGACUGU |
| Cdc42 ON-TARGETplus | 5- ACAGTCGGTACATATTCCGTT<br>6- CAATCATAACTGTGACTGCTT<br>7- CAATAGTAGAGGGGTCATCTT |
| Dock4 SMARTpool | 1- CAAAGGGUCUGGAGCAUUA<br>2- UAAGAGAGCUGAUGCUUGA<br>3- GGAAAUAGAUGUGAUAGUG<br>4- CCUCUUAUAUGACGAGCUA |
| Dock4 ON-TARGETplus | 11- GGAGAAAAUUGCACGAUUA |
| SGEF SMARTpool | 1- GAGAUGAUGUACACAAUUA<br>2- GAAGGAAGUUAGCAAGUUG<br>3- CAAAUGGCCUUGCCGCUAA<br>4- GAAAGGACAAGGAACAUUU |
| SGEF ON-TARGETplus | 5- CAAAUGGCCUUGCCGCUAA<br>6- UUGGAGAUCUUGAUACGAA |
| Trio SMARTpool | Dharmacon: M-005047-00-0005 |
| FLJ10665 SMARTpool | Dharmacon: M-020318-01-0005 |
| Dock9 SMARTpool | 1- GUAAACGAACGUCUGAUUA<br>2- ACUCAGAAGUUUCGAGAUA<br>3- CAGCUUGACUACUCAUUAA<br>4- CGGCAUUGCUUCUCCAUAU |
| Dock9 ON-TARGETplus | 10- UCUGGAAAGCCGAGCGCUA<br>11- GCACAAUGGUUCACGGGAU |
| zyxin SMARTpool | 1- GACAAGAACUUCCACAUGA<br>2- GAAUGUGGCUGUCAACGAA<br>3- GACCAAGAAUGAUCCUUUC<br>4- GGUGAGCAGUAUUGAUUUG |
| Non targeting | Allstars (Qiagen; Catalogue number #1027281) |

**Lentiviral shRNAs:**

| | |
|---|---|
| Rac1 shRNA1 | CCCTACTGTCTTTGACAATTAT |
| Rac1 shRNA2 | ACAGCTGGACAAGAAGATT |
| Dock4 shRNA1 | CTCAGTATTTGCAGATATA |
| Dock4 shRNA2 | CGCAAGGTCTCTCAGTTAT |
| Non silencing pGIPZ | ATCTCGCTTGGGCGAGAGTAAG |

**Retroviral shRNAs:**

| | |
|---|---|
| Dock4 retro shRNA1 | CAGTTTCCCTCCAACTGTT |
| Dock4 retro shRNA2 | CGTGAGCTCTTCAACAGTA |
| Nonsilecing pSMC | ATCTCGCTTGGGCGAGAGTAAG |

**b**

Sequence of DOCK4 SH3 domain used for expression of GST-fusion protein

>DOCK4 SH3

ATGAGCACTTTTAAAGTTCTGCTATGTGGCGCGGTATTATCCCGTGTTGACG
CCGGGCAAGAGCAACTCGGTCGCCGCATACACTATTCTCAGAATGACTTGG
TTGAGTACTCACCAGTCACAGAAAAGCATCTTACGGATGGCATGACAGTAAG
AGAATTATGCAGTGCTGCCATAACCATGAGTGATAACACTGCGGCCAACTTA
CTTCTGACAACGATCGGAGGACCGAAGGAGCTAACCGCTTTTTTGCACAAC
ATGGGGGATCATGTAACTCGCCTTGATCGTTGGGAACCGGAGCTGAATGAA
GCCATACCAAACGACGAGCGTGACACCACGATGCCTGCAGCAATGGCAACA
ACGTTGCGCAAACTATTAACTGGCGAACTACTTACTCTAGCTTCCCGGCAAC
AATTAATAGACTGGATGGAGGCGGATAAAGTTGCAGGACCACTTCTGCGCT
CGGCCCTTCCGGCTGGCTGGTTTATTGCTGATAAATCTGGAGCCGGTGAGC
GTGGGTCTCGCGGTATCATTGCAGCACTGGGGCCAGATGGTAAGCCCTCC
CGTATCGTAGTTATCTACACGACGGGGAGTCAGGCAACTATGGATGAACGA
AATAGACAGATCGCTGAGATAGGTGCCTCACTGATTAAGCATTGGTAA

**Supplementary Figure 10. Sequences of oligonucleotide duplexes and constructs.** (**a**) Sequences siGENOME SMARTpool and individual ON-TARGETplus oligonucleotide duplexes used in the study (sense sequences shown). (**b**) Sequence of DOCK4 SH3 domain used for expression of GST-fusion protein.

**Supplementary Figure 11**

Figure 2a

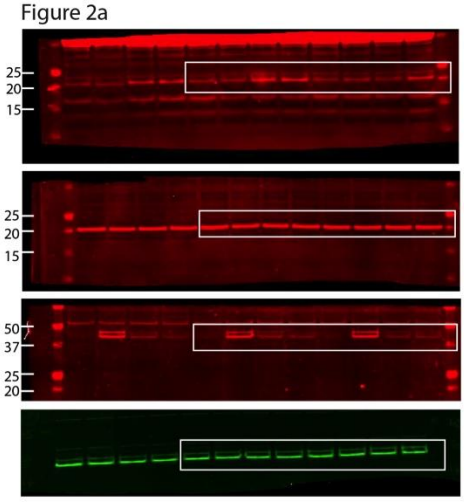



Figure 3g

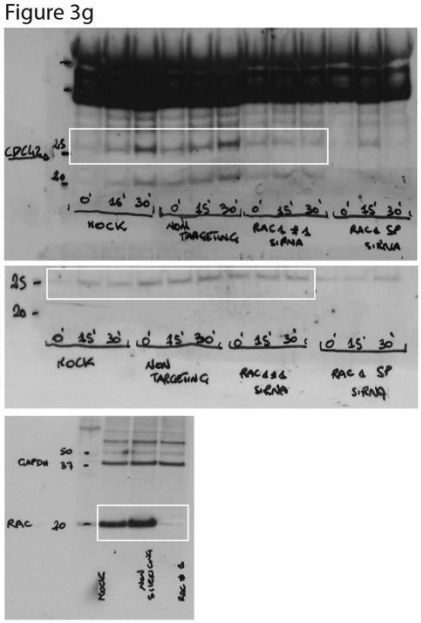



Figure 4a

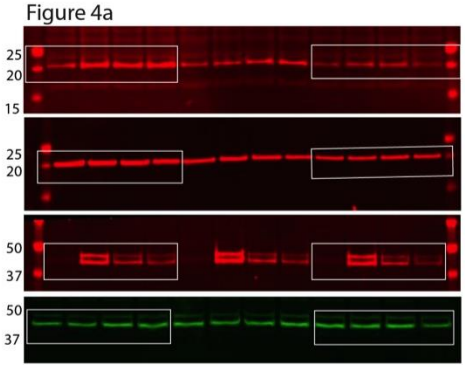



Figure 4b

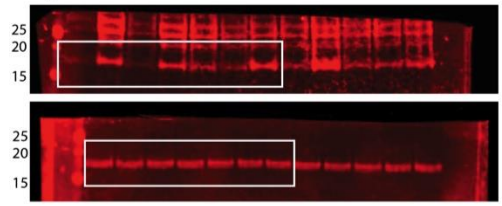



Figure 4d

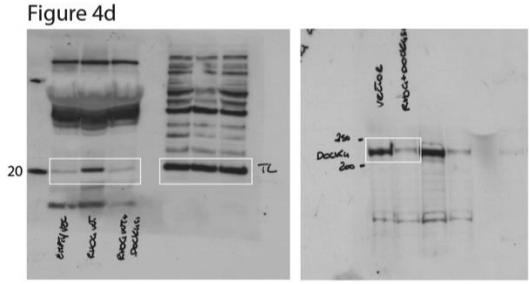



Figure 5a

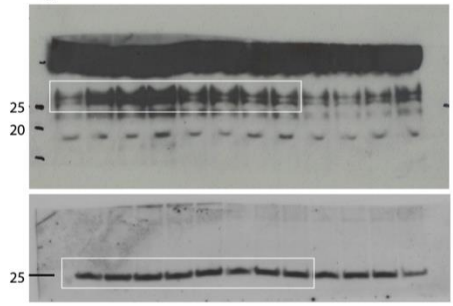



Figure 5b

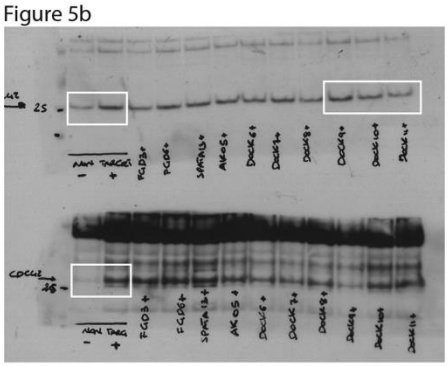



Figure 5d

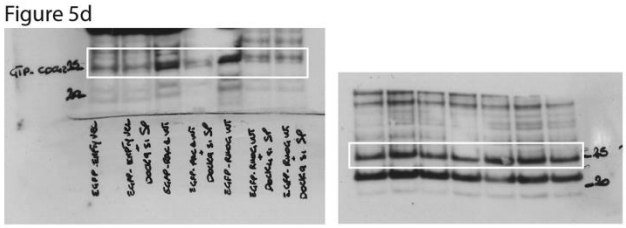
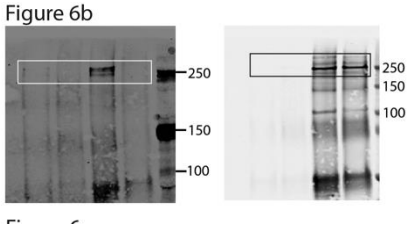
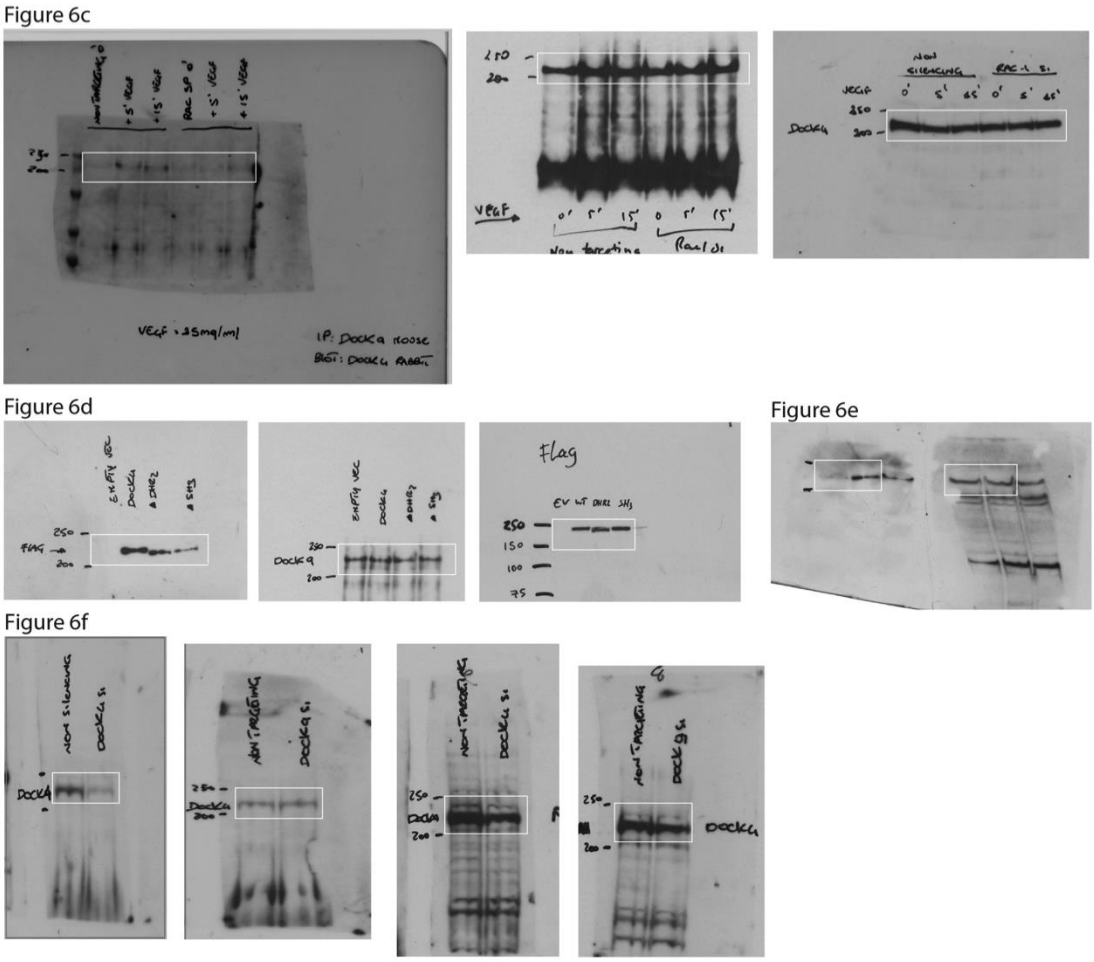



Figure 6b



**Supplementary Figure 11**




**Supplementary Figure 11. Uncropped scans of key western blots in main figures.** Boxes mark lanes depicted in figures.

**Supplementary Table 1**

| GEF | Tubule morphology |
|---|---|
| FGD3 | short & unbranched, rounded cells |
| ARHGEF18 | short & unbranched, rounded cells |
| SOS1 | short & unbranched |
| SOS2 | short & unbranched |
| Trio | less tubules |
| RGNEF | clusters |
| SPATA13 | clusters, rounded cells |
| SGEF | long & unbranched |
| FLJ10665 | less tubules |
| FARP2 | clusters |
| AKO57416 | less tubules |
| FLJ10357 | less tubules |
| Trad | less tubules, rounded cells |
| DOCK180 | less branches or less tubules |
| DOCK2 | less tubules |
| DOCK3 | less branches or less tubules |
| DOCK4 | less branches |
| DOCK5 | short & unbranched |
| DOCK6 | clusters |
| DOCK7 | short & unbranched |
| DOCK8 | short & unbranched |
| DOCK9 | less branches |

**Supplementary Table 1. Rho GEFs required for angiogenesis.** Tubule morphology in organotypic cocultures following knockdown of individual GEFs[22] in HUVEC at 5d after seeding onto CFs. Table shows GEFs with phenotypes observed over two or more independent experiments.

**Supplementary Table 2**

| | Total tubule length (% mock) | *P* | Tubules (% mock) | *P* | Junctions (% mock) | *P* | Knockdown (% mock) |
|---|---|---|---|---|---|---|---|
| Non targeting | 90.6 | | 86.9 | | 88.1 | | |
| Cdc42 | 26.7 | ** | 39.7 | ** | 16.1 | *** | 70.4 |
| RhoQ | 56.9 | * | 65.9 | ns | 49.0 | ns | 88.0 |
| RhoV | 52.3 | ns | 58.0 | ** | 31.7 | * | 36.8 |
| RhoU | 68.1 | ns | 68.7 | ns | 55.5 | ns | 28.1 |
| Rac1 | 53.2 | ** | 48.8 | ** | 19.9 | *** | 80.0 |
| Rac2 | 85.9 | ns | 78.5 | ns | 64.0 | ns | 82.0 |
| Rac3 | 58.1 | ns | 59.8 | ns | 34.9 | * | 88.0 |
| RhoG | 52.7 | * | 55.4 | * | 33.0 | ** | 85.0 |
| RhoA | 59.1 | * | 65.6 | ns | 46.2 | ** | 85.2 |
| RhoB | 74.0 | ns | 75.4 | ns | 56.2 | ns | 77.0 |
| RhoC | 60.5 | ** | 53.5 | ** | 37.9 | ** | 76.0 |
| RhoF | 73.3 | ns | 75.3 | ns | 63.7 | ns | 47.9 |
| RhoD | 60.5 | ns | 61.6 | ns | 44.2 | * | n.d. |
| | | | | | | | |

**Supplementary Table 2. Rho GTPases required for angiogenesis.** Tubule formation in organotypic cocultures following knockdown of Rho GTPases in HUVEC at 5d after seeding onto CFs. Values represent mean of multiple experiments: non targeting, RhoQ, RhoG, $n$=4; Cdc42, RhoV, RhoU, Rac1, Rac2, Rac3, RhoA, RhoB, RhoC, RhoF, RhoD, $n$=3; RhoV, $n$=2); 6 or more images were quantified for each coculture. *$P$<0.05; **$P$<0.01; ***$P$<0.001 by Student's $t$ test compared to mock transfected; ND, not determined. RhoG, Rac1 and Cdc42 were validated using additional oligonucleotide duplexes (see Supplemental Figure S2). Note that RhoJ regulates tubule formation[13]; ns, not significant.

**Supplementary Table 3**

| Gene ID | Gene Name | Protein ID | Total Peptide Number |
|---|---|---|---|
| 23348 | DOCK9 | 194239705 | 461 |
| 254225 | RNF169 | 148839382 | 33 |
| 31 | ACACA | 38679960 | 30 |
| 139818 | DOCK11 | 145699123 | 20 |
| 23269 | MGA | 256017159 | 19 |
| 440689 | HIST2H2BF | 66912162 | 12 |
| 3188 | HNRNPH2 | 9624998 | 11 |
| 7791 | ZYX | 4508047 | 11 |
| 6628 | SNRPB | 4507125 | 9 |
| 9732 | DOCK4 | 92091572 | 8 |
| 63916 | ELMO2 | 19718769 | 7 |
| 9406 | ZRANB2 | 42741682 | 7 |
| 1153 | CIRBP | 4502847 | 6 |
| 23524 | SRRM2 | 118572613 | 5 |
| 144455 | E2F7 | 145580626 | 5 |
| 136319 | MTPN | 21956645 | 5 |
| 552900 | BOLA2 | 73622130 | 5 |
| 494115 | RBMXL1 | 21361809 | 5 |
| 57662 | CAMSAP3 | 122937255 | 5 |
| 23396 | PIP5K1C | 31317309 | 5 |
| 983 | CDK1 | 4502709 | 5 |
| 23396 | PIP5K1C | 31317309 | 5 |
| 23112 | TNRC6B | 148491080 | 4 |
| 55183 | RIF1 | 56676335 | 4 |
| 57606 | SLAIN2 | 149588928 | 4 |
| 5209 | PFKFB3 | 4758900 | 4 |
| 57532 | NUFIP2 | 32698730 | 4 |
| 5202 | PFDN2 | 12408675 | 4 |
| 10625 | IVNS1ABP | 24475847 | 4 |
| 28971 | C11orf67 | 34147384 | 4 |
| 6625 | SNRNP70 | 29568103 | 3 |
| 84081 | NSRP1 | 14149807 | 3 |
| 51479 | ANKFY1 | 110815813 | 3 |
| 79596 | RNF219 | 88759348 | 3 |
| 10523 | CHERP | 119226260 | 3 |
| 57396 | CLK4 | 10190706 | 3 |
| 284695 | ZNF326 | 33946297 | 3 |
| 26292 | MYCBP | 57242777 | 3 |
| 58525 | WIZ | 151301215 | 3 |
| 4131 | MAP1B | 153945728 | 3 |
| 9589 | WTAP | 21361159 | 3 |
| 23155 | CLCC1 | 13194195 | 3 |

**Supplementary Table 3. DOCK9 interaction partners identified by mass spectrometry.** Number of peptide spectra are shown with Mascot score in parentheses. None of these proteins were identified in control IPs with 3xFLAG-mCherry.