Fig. S1. Flow cytometric analysis of RAET1γ surface expression in wild-type and β3-null endothelial cells. RAET1γ was not detectable on the surface of mouse endothelial cells. Mouse IgG1 was used as negative control, and antibody against β3-integrin was used to confirm β3-integrin deficiency in β3-null endothelial cells.

Fig. S2. Cell proliferation assay of wild-type, Rpl29-heterozygous and Rpl29-null endothelial cells. Two thousand cells were seeded into each well of a 96-well plate (Coultar) pre-coated with a mixture of PureCol (Nutacon, Netherlands), human plasma fibronectin (Millipore) and 0.1% gelatine. Cell viability was measured using cell proliferation reagent WST1 (Roche) following manufacturer’s protocol at different time points. No reduction in viability was observed in Rpl29-heterozygous and Rpl29-null endothelial cells in comparison to wild-type endothelial cells (n=3, mean ± s.e.m.).
Fig. S3. Flow cytometric analysis of FLK1 and β3-integrin in Rpl29-wild-type, Rpl29-heterozygous and Rpl29-null primary endothelial cells. Mouse IgG1 was used as negative control. No changes in surface expression of either (A) FLK1 or (B) β3 integrin were observed in Rpl29-heterozygous or Rpl29-null endothelial cells when compared with wild-type controls.
**Fig. S4. VEGF-stimulated ERK-phosphorylation.** Western blot analysis of pERK1/2 levels to total ERK1/2 in endothelial cells treated with SCM and Rpl29-siRNA show that pERK1/2 protein levels were not decreased following Rpl29 knockdown with siRNA in comparison to SCM-siRNA when cells were exposed to VEGF. Bar charts represent densitometry readings of RPL29 levels were compared to loading control HSC70 and pERK1/2 protein levels relative to total ERK1/2.
Fig. S5. Metastatic analysis of LLC grown in wild-type and Rpl29-heterozygous mice. Lewis Lung Carcinoma tumour cells (0.5 x 10^6 cells) were injected subcutaneously into the flank of 8-week-old WT and Rpl29-heterozygous mice and tumours were allowed to grow for 14 days. Size-matched tumours were resected and tumours allowed to metastasise to the lungs. The mice were then killed 6 weeks later at which point they showed no adverse effects. Lungs were removed from the mice and examined for surface metastases. No significant difference in lung metastasis was observed between wild-type and Rpl29-null mice. Metastasis was measured by counting LLC metastasis on the surface of lungs/mouse (n=4-5, mean ± s.e.m.).

Fig. S6. Tumour proliferation and apoptosis analysis. No gross difference was observed in cell proliferation and apoptosis in LLC tumours from wild-type and Rpl29-heterozygous mice. Representative images of Ki67, Active-Caspase-3 and PECAM staining in size matched age matched LLC tumours grown in wild-type and Rpl29-heterozygous mice. Sections were counter stained with DAPI to reveal nuclei.
Fig. S7. Blood vessels density in the skin from wild-type and Rpl29-heterozygous mice. No significant difference was observed in blood vessel density in the skin between wild-type and Rpl29-heterozygous mice. Bar chart represents mean number blood vessels/mm² of dermal section (mean ± s.e.m.; n=7 mice per genotype; nsd, not significant).
Fig. S8. Aortic ring assay following Rpl29-siRNA treatment. Depletion of Rpl29 with siRNA inhibits microvessel sprouting in β3-null aortic rings. (A) Quantitation of VEGF stimulated microvessel sprouting following treatment with SCM, Rpl29 or Flk1 siRNA in β3-null aortic rings on day 8. VEGF stimulated the number of microvessel sprouts emerging for aortic rings in Cont and SCM-siRNA treated samples. Rpl29-depletion reduced VEGF-stimulated microvessel sprouting to level similar to Flk1-depletion (mean ± s.e.m., *P<0.05, **P<0.01, n=12-20 aortic rings per treatment). (B) Real-time PCR to validate knockdown of Rpl29 in aortic rings following treatment with either 100nM SCM or Rpl29 siRNA (mean ± s.e.m., **P <0.01, n=3 per group).
Fig. S9. Cell proliferation assay of PMT-endothelial cells treated with Rpl29 siRNA. No significant difference was observed in endothelial cell proliferation following Rpl29 siRNA treatment in comparison to SCM siRNA and control sample using WST-1 assay (n=3, mean ± s.e.m.).
**Fig. S10. Cell migration assay.** Six-well plates were coated with a mixture of PureCol (Nutacon), human plasma fibronectin (Millipore), and 0.1% gelatine and seeded with 300,000 endothelial cells per well. Cells were allowed to proliferate until confluent, washed with Opti-MEM and incubated for 2 hours in Opti-MEM 2.5% FCS. Cells in each well were scratched in a straight line with a P200 tip, and media was exchanged with a fresh Opti-MEM 2.5% FCS media with or without 30 ng/ml VEGFA. An inverted time-lapse microscope was used to follow wound healing due to cell migration for up to 24 hours, and data was analysed using ImageJ. No significant difference was observed in serum-stimulated endothelial cell migration between 8 and 24 hours between samples treated with Rpl29 and SCM siRNA. Values are given as representations of wound closure in pixels.
Fig. S11. Protein synthesis assay. Ten thousand cells were plated in each well of a 96-well plate pre-coated with PureCol (Nutacon), human plasma fibronectin (Millipore) and 0.1% gelatine. Protein synthesis was measured using Click-iT AHA Alexa Fluor 488 Protein Synthesis HCS Assay (Invitrogen) following the manufacturers protocol with methionine-free RPMI (Invitrogen). No significant difference was observed in protein synthesis between samples treated with Rpl29 and SCM siRNA. Puromycin (1 μM) was used as a positive control for protein synthesis inhibition. (n=3; nsd, not significant; **P<0.01).
Table S1. List of genes whose expression was upregulated in β3-null endothelial cells compared with wild-type ($P<0.01$).

| Symbol   | Accession   | $P$-value | Definition                                                      |
|----------|-------------|-----------|----------------------------------------------------------------|
| NeoR     | NG_008567.1 | 4.4E-13   | Neomycin resistant gene                                        |
| Mcm6     | NG_009082.2 | 4.7E-12   | Minichromosome maintenance deficient 6                        |
| Rpl29    | NG_026218.1 | 1.1E-11   | Ribosomal protein L29                                          |
| Fgfr1op2 | NG_122498.1 | 4.9E-11   | FGFR1 oncogene partner 2                                       |
| Tm7sf1   | NG_009018   | 1.2E-09   | Retinoic acid early transcript gamma                            |
| Psmd8    | NG_026545.1 | 2.1E-07   | Proteasome (prosome macropain) 26S subunit non-ATPase 8        |
| Cuedc1   | NG_198013.1 | 2.2E-07   | CUE domain-containing protein 1                                |
| Mgst1    | NG_019946.3 | 3.7E-07   | Microsomal glutathione S-transferase 1                        |
| Gdi3     | NG_008112.2 | 6.2E-07   | Guanosine diphosphate (GDP) dissociation inhibitor 3           |
| 9430077D24Rik | XM_135109   | 1.2E-06  | RIKEN cDNA 9430077D24 gene                                     |
| Rai3     | NG_181444   | 1.3E-06   | Retinoic acid induced 3                                        |
| 9630038C08Rik | AK036131   | 9.6E-05  |                                                            |
| Cald1    | AF439859.1  | 1.1E-04   | h-caldesmon                                                   |
| 9830123K24Rik | AK036507   | 1.4E-04  |                                                            |
| Scarb2   | NG_007644.2 | 3.0E-04   | Scavenger receptor class B member 2                             |
| Cops8    | NG_133805.2 | 3.8E-04   | Constitutive photomorphogenic homolog subunit 8                |
| 5730409G07Rik | XM_126359.2 | 5.7E-04   | RIKEN cDNA 5730409G07 gene                                     |
| Atp2c1   | NG_175025.2 | 6.8E-04   | ATPase Ca**-sequestering                                       |
| Deadc1   | NG_025748.2 | 8.7E-04   | Deaminase domain containing 1                                  |
| Ipo9     | XM_129442.3 | 9.5E-04   | Importin 9                                                    |
| Abhd1    | NG_021304.2 | 1.3E-03   | Abhydrolase domain containing 1                                |
| 2010323F13Rik | NG_177157.2 | 1.9E-03   | RIKEN cDNA 2010323F13 gene                                     |
| 2810417H13Rik | NG_026515.1 | 2.0E-03   | RIKEN cDNA 2810417H13 gene                                     |
| Thap4    | NG_025920   | 2.3E-03   | THAP domain containing 4                                      |
| Pi16     | NG_023734.2 | 2.5E-03   | Peptidase inhibitor 16 precursor                                |
| Psmc4    | XM_355872.1 | 2.5E-03   | Prosome macropain 26S subunit ATPase 4                         |
| 6430544H17Rik | NG_183140.1 | 2.6E-03   |                                                            |
| Abhd1    | NG_021304.2 | 2.7E-03   | Abhydrolase domain containing 1                                |
| C4300014G13Rik | AK049453   | 3.1E-03   | Hypothetical protein                                           |
| Tm7sf3   | XM_132970.3 | 3.2E-03   | Transmembrane 7 superfamily member 3                           |
| Acbd4    | NG_025988.1 | 4.1E-03   | Acyl-coenzyme A binding domain containing 4                    |
| Stk4     | NG_021420.2 | 4.5E-03   | Serine/threonine kinase 4                                      |
| Insiq2   | NG_133748.1 | 5.5E-03   | Insulin induced gene 2                                         |
| Glis1    | NG_147221.1 | 6.1E-03   | GLIS family zinc finger 1                                      |
| Mrpl3    | AK054185    | 6.8E-03   | Mitochondrial ribosomal protein L3                             |
| Nt5c3    | NG_026004.1 | 6.8E-03   | 5-nucleotidase cytosolic III                                   |
| Ugt1a9   | NG_201410   | 7.0E-03   | UDP glucuronosyltransferase 1 family, polypeptide A9            |
| 2610018I03Rik | XM_135023.2 | 7.1E-03   | RIKEN cDNA 2610018I03 gene                                     |
| B230312I18Rik | NG_172740.1 | 7.9E-03   | RIKEN cDNA B230312I18 gene                                     |
| Elmo1    | NG_080288.1 | 8.5E-03   | Engulfment and cell motility 1 ced-12 homolog                  |
| D730035F11Rik | NG_019505   | 9.1E-03   |                                                            |
| Dgke     | NG_026230.2 | 9.9E-03   | RIKEN cDNA E03003016 gene                                      |
| E03003016Rik | XM_286230.2 | 9.9E-03   | RIKEN cDNA E03003016 gene                                      |
| Pnrc2    | NG_026383.1 | 8.2E-03   | Proline-rich nuclear receptor coactivator 2                    |
| Kira18   | NG_053153.1 | 8.1E-03   | Killer cell lectin-like receptor subfamily A member 18         |
Table S2. List of genes whose expression was downregulated in β3-null endothelial cells compared with wild-type (P<0.01).

| Symbol | Accession | P-value | Definition |
|--------|-----------|---------|------------|
| Rgs17  | NM_019958 | 7.6E-03 | Regulator of G-protein signaling 17 |
| Agtrap | NM_009642.3 | 7.6E-03 | Angiotensin II type I receptor-associated protein |
| Nr1d2  | NM_011584.2 | 6.7E-03 | Nuclear receptor subfamily 1 group D member 2 |
| Mtap7  | NM_008635 | 6.4E-03 | Microtubule-associated protein 7 |
| Kira22 | NM_053152.1 | 6.2E-03 | Killer cell lectin-like receptor subfamily A member 22 |
| 1810057P16Rik | XM_126676.3 | 6.0E-03 | RIKEN cDNA 1810057P16 gene |
| E030030106Rik | XM_286230.2 | 5.3E-03 | RIKEN cDNA E030030106 gene |
| 1810041M07Rik | AK007746 | 4.7E-03 | |
| D630046D15Rik | AK052765 | 4.6E-03 | Hypothetical BTB/POZ domain/Speract receptor (Scavenger receptor) containing protein |
| Nt5    | AK047143 | 4.1E-03 | 5’ nucleotidase |
| AI838661 | NM_133864.1 | 3.9E-03 | Expressed sequence AI838661 |
| 2610203C22Rik | | 3.6E-03 | |
| Bcat1  | NM_007532.1 | 3.5E-03 | Branched chain aminotransferase 1 cytosolic |
| 1810064L21Rik | AK007954 | 2.9E-03 | |
| MGC67181 | NM_198619.1 | 2.8E-03 | Unknown (protein for MGC:67181) |
| 3110001A05Rik | AK013931 | 2.6E-03 | |
| 2810408F11Rik | AK021409.1 | 2.5E-03 | 0 day neonate eyeball cDNA RIKEN full-length enriched library clone:E130302J09 product:hypothetical protein full insert sequence. |
| LOC232532 | XM_132963.2 | 1.2E-03 | Similar to IgE-binding protein |
| Ehd3   | NM_020578.1 | 1.2E-03 | EH-domain containing 3 |
| Hebp2  | NM_019487.2 | 1.1E-03 | Heme binding protein 2 |
| 2610305D13Rik | NM_145078 | 1.0E-03 | RIKEN cDNA 2610305D13 gene |
| MGC67181 | NM_198619.1 | 9.3E-04 | |
| Raet1e | NM_198193.1 | 9.2E-04 | Retinoic acid early transcript 1E |
| LOC381142 | XM_355058.1 | 7.3E-04 | Similar to hypothetical protein FLJ38968 |
| C530044C16Rik | | 2.4E-04 | |
| Cdkl2  | NM_177270.3 | 1.2E-04 | Cyclin-dependent kinase-like 2 (CDC2-related kinase) |
| Bcat1  | NM_007532.1 | 1.1E-04 | Branched chain aminotransferase 1 cytosolic |
| Fxr2h  | NM_011814 | 8.1E-05 | Fragile X mental retardation gene 2 autosomal homolog |
| Ybx3   | AK029441 | 8.0E-05 | Y box protein 3 |
| Ppfbp1 | AK044496 | 7.9E-05 | PTPRF interacting protein binding protein 1 |
| E030030106Rik | XM_286230.2 | 5.9E-05 | RIKEN cDNA E030030106 gene |
| 4933427D14Rik | NM_028963.1 | 5.4E-05 | RIKEN cDNA 4933427D14 gene |
| 1110005F07Rik | NM_025383 | 1.7E-05 | RIKEN cDNA 1110005F07 gene |
| Abca5  | NM_147219.1 | 8.7E-06 | ATP-binding cassette sub-family A (ABC1) member 5 |
| Hebp1  | NM_013546.1 | 8.2E-06 | Heme binding protein 1 |
| Kira20 | NM_053150.1 | 4.8E-06 | Killer cell lectin-like receptor subfamily A member 20 |
| Gp38   | NM_010329.1 | 1.8E-06 | Glycoprotein 38 |
| LOC229810 | XM_124173.2 | 1.2E-06 | Similar to Alpha enolase (2-phospho-D-glyceraldehyde glycerate hydro-lyase) (Non-neural enolase) (NNE) (Enolase 1) |
| Itgb3  | NM_016780.1 | 6.9E-07 | Integrin beta 3 |
| Raet1a | NM_009016.1 | 4.2E-07 | Retinoic acid early transcript 1 alpha |
Table S3. List of genes and primer sequences for real-time PCR.

| Gene   | Forward             | Reverse             |
|--------|---------------------|---------------------|
| Actin  | AAGGCCAACCGTGAAAAGAT | GTGGTACGACCAGAGGCATAC |
| β3-itgn| TCCAACATCTGTACCACACGA | GGGTGAGCCCTGAGACAA |
| Flk1   | CAGTGGTACTGCGAGCTAGAG | CAGTGGTACTGCGAGCTAGAG |
| Rpl29  | TCCGATGACATCCGCTGACTA | CCATTTCGTGCCATTTGC |
| Raet1γ | ATACACACACGGGCTGGAT  | CTTCGCTTCATACCAGAGG |
| Mgst1  | ACTGACGAGAAGGTGGAACG | GAAATGCATGAGGGCTTGAGA |
| Mcm6   | ACCTGTACCACATCTCTGCAC | CACCACGTTTACTTCAAG |
| Cuedc1 | GGGACAAGTTGAAACATGG | CTTCGCTTTTGGCTTCTCAG |
| Fgfr1op2 | CCTGAAGCACCTCAGCAG  | TCTCGGTGATTTGCTCAACA |
| Gdl3   | TGGAGGGAGAAAGTGCCTTATAA | CTGGCGGTTGTCCCTGGA |
| Psmd8  | ATCCCCGGGAGAAGTTTACAC | TACGGCCTTCTCAATGGCATCC |
| Tm7sf1 | AGTCAGAAATCCACGAGAGG | CGGGGTTGCAAGAAAGAAGTA |