Prdm16 and Notch functionally and physically interact during artery development

Short title: Prdm16 and Notch co-determine arterial development

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SUBJECT TERMS: Developmental Biology; Aortic Coarctation; Cardiovascular Disease; Arteriovenous Malformation; Gene expression/Regulation

ABSTRACT

Rationale: Proper functionality of the circulatory system requires correct arteriovenous (AV) endothelial cell (EC) differentiation. While Notch signaling and its downstream effector Hes-Related Family bHLH Transcription Factor with YRPW Motif (Hey)2 favor arterial specification, transcription factor (TF) chicken ovalbumin upstream transcription factor 2 (Coup-TFII) inhibits canonical Notch activity to induce venous identity. However, transcriptional programs that compete with Coup-TFII to orchestrate arterial specification upstream of Notch remain largely unknown. We identified positive regulatory domain-containing protein (Prdm)16 as an arterial EC-specific TF, but its role during arterial EC specification and development remains unexplored.

Objective: To unravel the role of Prdm16 during arterial endothelial lineage specification and artery formation.

Methods and Results: Transcriptomic data of freshly isolated arterial and venous ECs from humans and mice revealed that Prdm16 is exclusively expressed by arterial ECs throughout development. This expression pattern was independent of hemodynamic factors and conserved in zebrafish. Accordingly, loss of *prdm16* in zebrafish perturbed AV endothelial specification and caused AV malformations in an EC-autonomous manner. This coincided with reduced canonical Notch activity in arterial ECs and was amplified when *prdm16* and *notch* pathway members were concomitantly knocked down. *In vitro* studies further indicated that Prdm16 not only amplified Notch signaling, but also physically and functionally interacted with Hey2 to drive proper arterial specification.

Conclusion: We showed that Prdm16 plays a pivotal role during arterial development through its physical and functional interaction with canonical Notch. As both Hey2 and Prdm16 have been

associated with diverse vascular disorders including migraine and atherosclerosis, Prdm16 represents an attractive new target to treat these vascular disorders.

Keywords: Prdm16, arterial endothelial specification, artery formation, canonical Notch signaling, arterial disease

Non-standard Abbreviations and Acronyms

AV	arteriovenous
bHLH	basic helix-loop-helix
BOECs	blood outgrowth endothelial cells
coA	co-activators
co-IP	co-immunoprecipitation
coR	co-repressors
Coup-tfII	Chicken ovalbumin upstream transcription factor 2
DA	dorsal aorta
DAPT	N-[N(3,5-difluorophenacetyl)-L-alanyl]-S-phenylglycine t-butyl ester
DBZ	dibenzazepine
DFF	dorsal fin fold
DIG	digoxygenin
Dkk2	Dickkopf WNT signaling pathway inhibitor 2
Dll4	Delta-like ligand 4
DMSO	dimethyl sulfoxide
dpf	days post-fertilization
DT	double transgenic
E	embryonic day

EC	endothelial cell
(e)GFP	(enhanced) green fluorescent protein
Emcn	Endomucin
FACS	fluorescence-activated cell sorting
Flrt2	Fibronectin Leucine Rich Transmembrane protein 2
FoxC	Forkhead box C
Gja5	Gap junction protein alpha 5
GO	Gene Ontology
GSEA	Gene Set Enrichment Analysis
GWAS	Genome-Wide Association Studies
HEK	human embryonic kidney
Hey	Hes-Related Family bHLH Transcription Factor with YRPW Motif
hpf	hours post-fertilization
HUAECs	human umbilical artery endothelial cells
HUVECs	human umbilical vein endothelial cells
IHC	immunohistochemistry
ISV	intersomitic vessel
KO	knockout
Mo	morpholino
NICD	Notch receptor intracellular domain
NFR	nuclear fast red
PCV	posterior cardinal vein
Prdm	Positive regulatory domain-containing protein

qRT-PCR	quantitative real-time PCR
r	recombinant
RBPJ-κ	Recombination Signal Binding Protein for Immunoglobulin Kappa J
SEM	standard error of the mean
Sox	SRY-Box Transcription Factor
TF	transcription factor
WISH	whole-mount *in situ* hybridization

INTRODUCTION

Normal circulatory function of higher organisms requires finely tuned specification of endothelial cells (ECs) into arterial and venous lineages with discrete functions. Notch is a prerequisite for arterial endothelial specification in zebrafish,[1-6] mice[7-9] and human cells,[10, 11] while the transcription factor (TF) chicken ovalbumin upstream transcription factor 2 (COUP-TFII) instructs ECs to adopt a venous identity by inhibiting canonical Notch signaling.[12-14] Aberrant Notch activity results in severe vascular defects, including the occurrence of arteriovenous (AV) malformations or shunts that can be life-threatening.[15-17] Despite its clinical relevance, our understanding of the molecular events governing arterial endothelial specification upstream of or parallel to canonical Notch activity remains incomplete. Gaining insight into these mechanisms will result in more profound knowledge on vascular development and disease and on overarching principles of Notch-mediated lineage specification outside the cardiovascular system.

Positive regulatory domain-containing (Prdm)16 belongs to a TF family involved in binary cell fate decisions. In adipose tissue, Prdm16 is exclusively expressed by and regulates the transcriptional program of brown/beige adipocytes, while concomitantly suppressing white adipose-specific gene expression.[18, 19] In contrast, COUP-TFII drives white adipogenesis and *Coup-TFII* deletion results in marked upregulation of brown adipose-selective genes in white fat deposits.[20] It remains unknown if Prdm16 and Coup-TFII also act as opposing forces in fate decisions made by vascular (precursor) cells, although this notion is supported by the arterial-specific expression pattern in human umbilical cord ECs reported by us[21] and others.[22]

We previously demonstrated that ~70% of genes regulated by the Notch downstream effector Hes-Related Family bHLH Transcription Factor with YRPW Motif (HEY)2 in human umbilical vein ECs (HUVECs) were equally controlled by Prdm16,[21] indicating that Prdm16 may

play a key role during arterial specification through modulation of Notch or Hey2 activity. This idea is reinforced by the intricate interplay between Prdm family members and Notch[23-25] and the direct binding of Prdm proteins to basic helix-loop-helix (bHLH) TFs – a TF family to which HEY2 belongs – in various cell types.[26, 27]

Despite these observations and genome-wide association studies (GWAS) linking *PRDM16* to various vascular disorders,[28, 29] the functional role of Prdm16 within the developing vasculature remains elusive. Recently, we reported that deletion of *Prdm16* in postnatal endothelium leads to ischemia-induced endothelial dysfunction in mice,[30] while Matrone and colleagues used zebrafish to demonstrate that Prdm16 positively regulates developmental angiogenesis.[31] Whether Prdm16 also orchestrates arteriovenous endothelial specification, arterial morphology and arterial Notch activity during development is not known.

Here, by using a combination of genetic and pharmacological approaches in zebrafish embryos and primary human EC (progenitor)s, we demonstrate that endothelial Prdm16 is indispensable for arterial endothelial differentiation and vascular development, by activating and potentiating the canonical Notch pathway.

METHODS

Extended methods and a Major Resources Table (**Online TableI**) are provided online.

Data availability

The majority of supporting data are presented within this article and online. Data not directly presented are available from the corresponding author upon request. Microarray data will be made accessible at the Gene Expression Omnibus website.

EC isolation, profiling and drug treatment

Human ECs were isolated from umbilical cords (HUVECs) and peripheral blood (blood outgrowth ECs or BOECs) as described online. To study Prdm16 overexpression effects, BOECs were transduced with pRRL2-empty-PGK-Cherry or pRRL2-Prdm16-PGK-Cherry lentiviral particles and RNA was collected 6 days later. RNA from 3 experiments was used for microarray (Affymetrix HG-U133 Plus2.0 GeneChip). Data processing and functional annotation analyses were performed as described online. Inhibition or activation of Notch signaling was established by adding N-[N(3,5-difluorophenacetyl)-L-alanyl]-S-phenylglycine t-butyl ester (DAPT) or by culture on recombinant delta-like4 (rDLL4)-containing gelatin, respectively. The use of human cells was approved by the Ethics Committee of University Hospitals Leuven. Mouse ECs were isolated by fluorescence-activated cell sorting (FACS) from the thoracic aorta and vena cava from *Tie2-GFP* mice.[32] RNA from 5 selected isolations per tissue was used for microarray (Affymetrics Mo Gene1.0 ST array) and a species-conserved AV signature was defined by conducting a meta-analysis on this and our previous human AV signature,[21] as described online. Mouse studies were approved by the Ethical Committee of the animal facilities at KU Leuven. Zebrafish ECs were isolated by FACS from *Tg(kdr:eGFP)*^{s843} embryos.[32]

Lentiviral production and transduction

Lentiviral particles were produced in human embryonic kidney (HEK)293 cells after co-transfection with helper plasmids (psPax2 and PMD2G) and pRRL2-empty-PGK-Cherry or pRRL2-mPrdm16-PGK-Cherry. For transduction, cells were plated in 24-wells 24 hours prior to lentivirus exposure and RNA lysates were collected 6 days later using TRIzol® (Invitrogen). For Western blotting, cells were collected in Laemmli buffer supplemented with proteinase/phosphatase inhibitors.

Luciferase Assays

Cells were transduced with pRRL2-mPrdm16-PGK-Cherry lentiviral particles, combined with a Recombination Signal Binding Protein for Immunoglobulin Kappa J (RBPJκ)-luciferase reporter virus and a lentiviral Renilla control to normalize for transduction efficiency. Six days later, cells were collected in lysis buffer and Firefly/Renilla luciferase activity were measured according to the manufacturers' protocol using the Dual-Luciferase® Reporter Assay System (E1910; Promega) on a Microplate Luminometer LB 96V (EG&G Berthold). To measure *HEY1* and *HEY2* promoter activity, cells were co-transfected with pRRL2-mPrdm16-PGK-Cherry (or pRRL2-empty-PGK-Cherry control), pTK-renilla and pGL3-HEY1:luc or pGL3-HEY2:luc (gifts from Dr. Manfred Gessler) and Firefly/Renilla luciferase activity was measured 24 hours later.

Expression analysis

Embryonic day (E)9.5 or E10.5 embryos of *Prdm16*^{Gt683Lex} mice[33] (Mouse Mutant Resource Repository Center) were stained whole-mount for β-galactosidase activity, as described online. For Prdm16 immunohistochemistry (IHC) staining, E14.5 or E17.5 FvB mouse embryos were dissected and snap-frozen in liquid nitrogen. Unfixed cryopreserved embryos were sectioned and stained with sheep-anti-Prdm16 antibody (AF6295, R&D Systems) and FITC-conjugated anti-

αSMA (F3777, Sigma). A similar procedure was followed to stain human umbilical cords for PRDM16. For whole mount *in situ* hybridization (WISH), AB/TU zebrafish embryos were collected and fixed with 4% PFA. Digoxygenin (DIG)-labeled probes were used and probe binding was revealed with anti-DIG-AP antibody followed by chromogenic detection based on alkaline phosphatase activity, as described online. Whole mount pictures were taken using a Zeiss Axio Imager Z1 microscope. Alternatively, embryos were paraffin-embedded, sectioned and counterstained with nuclear fast red (NFR).

RNA/cDNA preparation, qRT-PCR, co-immunoprecipitation (co-IP) and Western blotting

Total RNA was extracted from cultured ECs, cDNA was prepared using the Superscript III First Strand Kit and for qRT-PCR, SYBR green dye was used during amplification on a Step One Plus (Applied Biosystems). A primer list is added in **Online TableII**. For co-IP, HEK293 cells were plated and transfected with different combinations of pRRL2-Myc-Prdm16-PGK-Cherry; pRRL2-Myc-empty-PGK-Cherry; pReceiverM04-GST-HEY2 and pReceiverM04-GST-GFP plasmids (GeneCopoeia) 24 hours later. IP lysates were incubated with anti-Myc antibody-conjugated dynabeads, as described online and bound proteins were isolated by boiling the dynabeads once resuspended in Laemmli buffer and magnetic removal of the dynabeads. Western blotting was performed as described online, pictures were recorded with a Chemidoc XRS+ imager (Bio-Rad laboratories) and band density analysis was performed using NIH Image software.

***In vivo* zebrafish experiments**

Zebrafish husbandry and procedures were approved by the Harvard Medical Area Standing Committee on Animals, the local Institutional Animal Care and Use Committee. Zebrafish embryos were incubated at 28.5°C in standard E3 medium. Confocal images were taken on a Fluoview FV1000 (Olympus) to visualize the vasculature or analyzed with ImageJ software to

assess canonical Notch activity in the dorsal aorta (DA) or whole embryo where indicated. Cardiac performance was measured as previously described.[34] Angiograms were generated by video microscopy of laterally positioned embryos using an Axioplan (Zeiss) upright microscope equipped with a FastCam PCI high-speed digital camera (Photron) and subsequent digital image subtraction in ImageJ. For morpholino (Mo)-mediated knockdown, antisense Mo oligomers (GeneTools LLC) targeting *prdm16*, *dll4*, *rbpj*, *hey2* (**Online TableII**) were injected at the one-cell stage. Embryos were exposed to DAPT (25 μM), dibenzazepine (DBZ; 250 nM) or vehicle (dimethyl sulfoxide; DMSO) from 6 hours post-fertilization (hpf) onwards until imaging.

Statistical Analyses

Quantitative data are presented as mean ± standard error of the mean (SEM). Detailed information on statistical analysis is provided online.

RESULTS

Prdm16's expression is compatible with a role in AV specification during development

Whole-genome transcriptional profiling of freshly isolated arterial and venous ECs of mouse origin confirmed that, like in humans,[21] *Prdm16* is enriched in arterial ECs. Using *Hey2* and *Coup-TFII* as markers of arterial and venous endothelial identity respectively, we confirmed by qRT-PCR that *Prdm16* was highly enriched in arterial ECs from human umbilical cords (**Online Fig.Ia**) and mouse thoracic aorta (**Online Fig.IIb**). A meta-analysis of the mouse and our previous human[21] transcriptomic dataset revealed that *Prdm16* belonged to a limited set of TFs with an arterial-specific or venous-restricted expression pattern conserved across species (**Online Fig.Ic**; **Online TableIII**) suggesting its involvement in AV specification. Notably, many genes in this species-conserved AV signature had previously documented arterial or venous-specific endothelial expression patterns, confirming that our approach could lead to the identification of novel arterial/venous-specific markers (**Online TableIII**). Gene Ontology (GO) analysis revealed enrichment for key biological processes like 'circulatory and cardiovascular system development', 'aorta development', 'blood vessel morphogenesis' and 'artery development' (**Online TableIV**). β-galactosidase activity staining on embryonic day (E)9.5 and E10.5 embryos of the *Prdm16*^{Gt683Lex} reporter mouse strain revealed that arterial-specific Prdm16 expression was established early during development in the intra- and extraembryonic vasculature (**Fig.1a-f**) and maintained throughout development and across different AV pairs as evidenced by immunohistochemistry stainings in E14.5 and E17.5 embryos (**Fig.1g-l'**). Accordingly, we detected PRDM16 protein in ECs lining the human umbilical artery but not umbilical vein (**Fig.1m,n**). Consistent with these findings, Genotype-Tissue Expression (GTex) database

analysis revealed high *PRDM16* mRNA levels in aortic, coronary and tibial artery tissues (**Online Fig.Id**).

We then analyzed whether *prdm16* was also enriched in arterial ECs of developing zebrafish. Expression analysis of sorted eGFP+ ECs from *Tg(kdrl:eGFP)*^{s843} zebrafish embryos[32] throughout development demonstrated endothelial enrichment of *prdm16* at 24 hpf, consistent with its potential role during AV endothelial specification (**Online Fig.Ie**). WISH revealed that *prdm16* is exclusively expressed by ECs of the DA, but not the posterior cardinal vein (PCV) prior to the onset of flow and as early as 18 hpf (**Fig.1o**). As in mice, arterial *prdm16* expression persisted throughout development as evidenced by WISH at 20, 22, 24 and 30 hpf (**Fig.1p; Online Fig.II**) and confocal imaging of the *tud28Gt* prdm16 reporter line[35] at 48 hpf and 6 days post-fertilization (dpf; **Fig.1q-r'**).

Prdm16 ***controls arterial development in an EC-autonomous manner***

To test if prdm16 plays a role during AV differentiation, we performed Mo-mediated *prdm16* knockdown studies in *Tg(kdrl:eGFP)*^{s843} zebrafish embryos. This caused dose-dependent vascular defects, hallmarked by abnormal arterial intersomitic vessel (ISV) development, consistent with a previous report,[31] and aortic hypoplasia at 24 hpf (**Fig.2a-d**). At 48 hpf, unlike controls, *prdm16* morphants frequently displayed impaired ISV growth, reduced aortic diameters (**Fig.2e-h')** and, occasionally, aortic coarctation and/or AV shunting between axial vessels (**Fig.2h,h'**; **Online MoviesI,II**). This phenotype was replicated by a splice-site Mo ('Mo2'; not shown).

In line with its described role during cardiac development,[34, 36] we observed severe cardiac defects in *prdm16* morphants, precluding the visualization and reliable quantification of aortic

anomalies. We therefore generated *Tg(cmlc2:PRDM16)* zebrafish which overexpress human full-length PRDM16 in their cardiomyocytes. As expected, *Tg(cmlc2:PRDM16)* zebrafish were partially protected from *prdm16* Mo-induced cardiac defects and more often carried flow through their vessels compared to control *Tg(cmlc2:GFP)* embryos. In embryos with flow, AV shunts were more frequently observed in *prdm16* Mo-injected *Tg(cmlc2:PRDM16)* compared to *Tg(cmlc2:GFP)* embryos (33% *vs.* 5%; **Fig.2i,j**; **Online MoviesIII,IV**), suggesting that non-cardiomyocyte cell-types mediate the vascular defects observed in *prdm16* morphants.

We next created *Tg(fli1a:mPrdm16;Tg(kdrl:dsRed)* zebrafish overexpressing mouse (m)Prdm16 in dsRed$^+$ ECs. *Tg(fli1a:mPrdm16; kdrl:dsRed)* larvae did not display vascular defects under baseline conditions compared to *Tg(kdrl:dsRed)* controls (**Fig.2k,l**) but were protected against *prdm16* Mo-induced DA hypoplasia (**Fig.2m-n'; Online MovieV**). Moreover, angiographies revealed that *Tg(fli1a:mPrdm16;kdrl:dsRed)* larvae displayed less AV shunts upon *prdm16* Mo knockdown (**Fig.2o-r'**) compared to control embryos (20% *vs*. >40%; **Fig.2s**), highlighting the EC-autonomous role of prdm16 during arterial development.

***Prdm16 activates Notch signaling and regulates AV endothelial expression* in vitro**

We then overexpressed mPrdm16 or Cherry control in human endothelial progenitor cells (BOECs) and transcriptionally profiled these cells. GO analysis revealed that Prdm16 influenced genes involved in aorta/artery development and morphogenesis, in line with the arterial defects observed in *prdm16*-deficient zebrafish embryos (**Online TableV**). Notably, gene set enrichment analysis (GSEA) for canonical pathways indicated that Prdm16 regulated many genes involved in the Notch and HES-HEY pathway (**Fig.3a**), both instrumental for arterial endothelial specification and artery development. Further analysis emphasized that the inductive effect of Prdm16 on the Notch pathway was most profound on Notch components with a reported arterial-restricted

expression profile (**Fig.3b**; red bars). Accordingly, mRNA levels of the Notch pathway members *DLL4, HEY1, HEY2* and *EphrinB2* (*EFNB2*) were significantly increased in HUVECs overexpressing mPrdm16 compared to control cells, while expression of the venous-restricted marker *Neuropilin-2* (*NRP2*) was downregulated (**Fig.3c**). The enhanced expression of *HEY1/2* corresponded with increased promoter activity (**Online Fig.IIIa,b**) and with considerably higher levels of canonical Notch activity in HUVECs and BOECs (**Fig.3d,e**). Moreover, Prdm16's effect on Notch was markedly attenuated in the presence of canonical Notch inhibitor DAPT in both HUVECs and BOECs (**Fig.3f,g**; **Online Fig.IIIc)**. Prdm16 also induced the expression of previously published (*e.g.*, Gap junction protein alpha 5; *GJA5)*)[37, 38] and *de novo* identified (*e.g.*, Dickkopf WNT signaling pathway inhibitor 2; *DKK2*) arterial-specific markers in a canonical Notch-dependent manner in both HUVECs and BOECs (**Online Fig.IIId,e**). Conversely, Prdm16 failed to suppress *NRP2* mRNA levels in the presence of DAPT (**Online Fig.IIId**) indicating that Prdm16 defines the arterial endothelial program through canonical Notch.

***Prdm16 drives Notch signaling to orchestrate arteriovenous EC identity* in vivo**

Dose-dependent knockdown of *prdm16* in the canonical Notch reporter line *Tg(Tp1:eGFP)*^{um14},[39] demonstrated that prdm16 also determines Notch signaling *in vivo* (**Fig.4a-d**), evidenced by the loss of eGFP signal in the DA (**Fig.4a'-d',e**) and consistent with the largely overlapping expression profiles of prdm16 and notch in zebrafish larvae. Loss of arterial Notch activity coincided with ectopic expression of venous markers *flt4*, *dab2* and *nrp2a* in the DA of 30 hpf *prdm16* morphants (**Fig.4f-k**) and AV shunting between axial vessels of *prdm16* morphant but not control embryos at 48 hpf (**Fig.4l**; **Fig.2o,q**).

Crossing *Tg(fli1a:mPrdm16)* with *Tg(Tp1:eGFP)*^{um14} zebrafish revealed that mPrdm16 overexpression failed to induce ectopic Notch signaling in the PCV under baseline conditions. As

expected, knockdown *of prdm16* resulted in substantial loss of Notch activity in non-ECs (exemplified by the dorsal fin fold (DFF; **Fig.4m'-p'**)), in both *Tg(Tp1:eGFP)^{um14}* and *Tg(fli1a:mPrdm16);Tg(Tp1:eGFP)^{um14}* embryos (**Fig.4m-p**). However, we observed more residual Notch activity in the DA of *Tg(fli1a:mPrdm16);Tg(Tp1:eGFP)^{um14}* compared to *Tg(Tp1:eGFP)^{um14}* embryos upon *prdm16* knockdown (**Fig.4m"-p"**). This endothelial-specific retention of canonical Notch in *prdm16*-deficient ECs in *Tg(fli1a:mPrdm16);Tg(Tp1:eGFP)^{um14}* embryos (**Fig.4q**) supports an EC-autonomous role for prdm16 during AV cell-fate specification. Furthermore, DAPT-treatment repressed arterial Notch activity to a lesser extent in the DA of *Tg(fli1a:mPrdm16);Tg(Tp1:eGFP)^{um14}* compared to *Tg(Tp1:eGFP)^{um14}* embryos (**Fig.4r-v**; **Fig.4r"-u"**), but not in non-ECs (*e.g.*, the DFF; **Fig.4r'-u'**), reinforcing that prdm16 coordinates arterial Notch activity in an EC-autonomous fashion.

Prdm16 and Notch interact in ECs during early vascular development

Notch-deficiency in zebrafish leads to vascular defects strikingly similar to those observed upon *prdm16* knockdown.[1, 2, 4, 6] Given the exquisite dose-dependency of Notch signaling and to avoid early lethality, we used Mo-mediated strategies rather than CRISPR-based knockout strategies to explore a potential epistatic interaction between prdm16 and Notch in ECs. We therefore injected *Tg(kdrl:eGFP)^{s843}* embryos with a subthreshold dose of the *prdm16* Mo and partially blocked distinct members of the canonical Notch signaling cascade. The latter starts with binding of Notch ligand DLL4 to its cognate receptors Notch1/4 and results in active transcription of the Notch downstream effectors *Hey1* and *Hey2* (**Fig.5a**). As expected, partial loss of *prdm16* did not perturb vascular morphology nor did it result in AV shunting when Notch signaling is not perturbed (**Fig.5a-d**).

Concomitant knockdown of the ligands *dlc* and *dll4* results in vascular defects characterized by AV shunts in zebrafish[2] as arterial ECs fail to activate the Notch pathway (**Fig.5e**). Incomplete *dll4* knockdown did not result in overt vascular defects, but compound *prdm16*/*dll4* morphants displayed aortic coarctation of the DA and AV shunts in more than 40% of *prdm16/dll4* double morphants (**Fig.5f-i**; **Online MoviesVI-IX**).

The vascular deficits of *Dll4*$^{-/-}$ mice[40-42] are mirrored in mice lacking one allele of both *Notch1* and *Notch4*.[9] We therefore treated control or *prdm16* morphant *Tg(kdrl:eGFP)*^{s843} embryos with γ-secretase inhibitor DAPT – which prevents cleavage of all Notch receptors (**Fig.5j**). Subthreshold DAPT-treatment did not affect vascular development in control embryos but robustly induced aortic coarctation and AV shunting in ~50% of embryos injected with a suboptimal dose of *prdm16* Mo, reminiscent of the phenotype observed in *prdm16*/*dll4* double morphants (**Fig.5k-n**; **Online MoviesX,XI**). Similar results were obtained with a second *prdm16* Mo ('Mo2') (**Online Fig.IVa-f**), in the presence of another γ-secretase inhibitor (DBZ; **Online Fig.IVg-l**). In line with these findings, we observed that partial knockdown of *prdm16* or subthreshold dosing with DAPT only partially inhibited canonical Notch activity in the DA, while DAPT-treated *prdm16* morphants displayed no residual Notch activity at 24 and 48 hpf (**Online Fig.IVm-t')**. Similar results were observed with DBZ (not shown). To validate our morpholino-based results, we adopted an acute CRISPR knockout (KO) system demonstrated to generate complete null phenotypes in F0 zebrafish.[43] Acute KO of prdm16 did not result in overt vascular phenotypes but was associated with DAPT-induced vascular malformations at 48 hpf (**Online Fig.Va-e**) reminiscent of those observed in our morpholino studies. Hence, both antisense Mo- and CRISPR-mediated knockdown of prdm16 sensitize to arteriovenous shunt formation when canonical Notch is inhibited.

In the absence of RBPJκ, ECs fail to undergo correct arterial differentiation and *Hey1/2* promoter activity remains low (**Fig.5o**), coinciding with AV shunting both during zebrafish embryogenesis[1] and in adult mice.[44] AV shunts were not observed upon partial knockdown of *rbpj* using a previously validated *rbpja/b* Mo (ref.[45]) in zebrafish embryos (**Fig.5p,s**; **Online MovieXII**), but partial knockdown of both *prdm16* and *rbpj* phenocopied the vascular deformations observed in *prdm16*/*dll4* double-morphants and *prdm16* morphants treated with γ-secretase inhibitors (**Fig.5q-s**). Occasionally, *prdm16*/*rbpj* morphants exhibited partial loss of the DA, with blood flow bypassing the missing arterial segment through sequential ISVs ('aortic skipping'; **Fig.5r,s**; **Online MovieXIII**).

Endothelial overexpression of the dominant-negative PRDM16^{K702Q} variant sensitizes to DAPT-induced AV shunting

To better understand the EC-autonomous effect of the Prdm16-Notch interaction on vascular development, we leveraged the dominant-negative effect of the pathogenic PRDM16^{K702Q} variant[34] and created zebrafish overexpressing PRDM16^{K702Q} in ECs using the UAS-Gal4 driver system. *Tg(kdrl:Gal4;UAS:PRDM16^{K702Q})* double transgenic (DT) embryos did not display overt vascular anomalies under baseline conditions (**Fig.6a,b**; **Online MovieXIV**), most likely due to the presence of endogenous zebrafish prdm16. However, unlike *Tg(kdrl:Gal4)* or *Tg(UAS:PRDM16^{K702Q})* controls, >50% of *Tg(kdrl:Gal4;UAS:PRDM16^{K702Q})* embryos displayed AV shunts when treated with DAPT (**Fig.6c-e**; **Online MovieXV**). Notably, cardiac performance (heart rate, stroke volume and cardiac output) did not differ between *Tg(kdrl:Gal4;UAS:PRDM16^{K702Q})* and control embryos in the presence or absence of DAPT (**Fig.6f-h**). Thus, PRDM16^{K702Q} acts as a dominant-negative variant in ECs like previously

described in cardiomyocytes[34] and increases the risk for AV shunting induced by canonical Notch inhibition.

Prdm16 amplifies the endothelial response downstream of a given NICD input signal

The aggravated vascular phenotypes observed with concomitant knockdown of *prdm16* and Notch raised the question whether Prdm16 – like Sox17 (ref.[46]) – augments canonical Notch signaling by increasing NICD levels. Western blot analysis for the cleaved, activated form of the NOTCH1 receptor, revealed similar N1ICD protein levels in mPrdm16 ('mPrdm16') *versus* Cherry-overexpressing ('Cherry') HUVECs (**Fig.7a**), despite elevated mRNA levels for *DLL4*, *HEY1* and *HEY2*. We then examined whether excess Prdm16 could amplify the endothelial response downstream a Dll4-mediated Notch input and cultured mPrdm16 and Cherry HUVECs on BSA- or rDll4-containing gelatin. Both ectopic mPrdm16 and rDll4 treatment augmented mRNA levels of *DLL4*, *HEY1* and *HEY2* compared to Cherry- or BSA-treated cells respectively. However, rDll4-treated mPrdm16 cells featured much higher levels of Notch pathway components compared to either single treatment (**Fig.7b**). In contrast, mRNA levels of the venous markers *COUP-TFII*, *NRP2*, *Endomucin* (*EMCN*) and *Fibronectin Leucine Rich Transmembrane Protein 2* (*FLRT2)* were trended downwards in rDll4+mPrdm16 HUVECs (**Online Fig.VIa**). Likewise, DLL4 protein levels were higher and FLRT2 protein levels lower in rDll4+mPrdm16 HUVECs despite similar levels of mPrdm16-overexpression in BSA-mPrdm16 and rDll4+mPrdm16 cells (**Online Fig.VIb,c**). A similar synergistic effect was observed in BOECs for the classical Dll4-HEY1/2 cascade and for the arterial-specific markers *GJA5* and *DKK*2 (**Online Fig.VId,e**). As in HUVECs, rDll4+mPrdm16 BOECs displayed lower *NRP2* and *EPHB4* mRNA levels (**Online Fig.VIf**) compared to BSA-mPrdm16 or rDll4+Cherry BOECs. These results demonstrate that

Prdm16 strengthened canonical Notch signaling through amplification of a NICD input signal without increasing NICD levels directly.

Prdm16 orchestrates arterial development by its physical and functional interaction with Hey2

Prdm family members physically interact with bHLH TFs,[26, 27] a family of TFs to which HEY2 belongs. Co-IP studies in HEK293 cells confirmed that PRDM16 and HEY2 reside in the same protein complex (**Fig.7c**). To test the impact of this physical interaction on arterial development, we partially knocked-down *prdm16* or *hey2* alone or in combination in zebrafish larvae. Compound *prdm16*/*hey2* morphants exhibited AV shunts and aortic coarctation defects while virtually all *hey2* or *prdm16* single morphants developed normally (**Fig.7d-f**). We next took advantage of the hey2 hypomorph mutant, gridlock ($grl^{m145/m145}$),[6] which lacks circulation to the tail due to aortic coarctation and crossed phenotypically normal $grl^{m145/+}$ fish with $Tg(kdrl{:}eGFP)^{s843}$ zebrafish. Partial *prdm16* knockdown did not evoke vascular defects in wild-type embryos, but triggered aortic coarctation and AV shunting in $Tg(kdrl{:}eGFP)^{s843}{;}grl^{m145/+}$ embryos (**Fig.7g,h**; **Online MoviesXVI,XVII**) validating the link between HEY2 and PRDM16.

Altogether, our data indicate that Prdm16 shapes the vasculature during development by finely coordinating AV endothelial specification by amplifying canonical Notch activity and more downstream by binding to the main arterial Notch effector, Hey2.

DISCUSSION

Correct arteriovenous endothelial differentiation is a prerequisite for proper functioning of our cardiovascular circuitry in health and disease but the exact molecular mechanisms orchestrating this event remain incompletely understood, partly due to the phenotypic drift of ECs upon culture. Here, we obtained *ex vivo* transcriptomic profiles of arterial and venous ECs from mice and, in combination with our previous human dataset,[21] identified a unique list of 52 arterial/venous-specific genes in mammalian ECs to which Prdm16 belonged. While we[23] and others[24,46,47] have reported arterial enrichment for Prdm16 and demonstrated that Prdm16 controls vascular maintenance postnatally,[30] the role of this metabolic factor during arterial differentiation and development is unclear. By detailed analysis of Prdm16's expression pattern across species, we provide evidence that Prdm16 co-defines arteriovenous identity of ECs in mammals and zebrafish across the vascular system, irrespective of developmental stage, anatomical location and hemodynamic factors. Studies in zebrafish embryos further revealed that the cardiovascular role of prdm16 extends beyond the heart muscle,[34, 36] as *prdm16* deficiency resulted in cell-autonomous arterial defects.

Canonical Notch signaling coordinates arterial endothelial differentiation in zebrafish,[1-6] mice[7, 41, 42, 44, 48] and human ECs,[10, 11, 49, 50] while Coup-TFII is instrumental for establishing a venous identity.[12-14] Although several other TFs – most notably Sox family members[3, 46] and FoxC1/2 (refs.[49, 50]) – have been implicated in Notch-mediated AV specification, our knowledge on the upstream mechanisms that tightly coordinate Notch is incomplete. We show that Prdm16 regulates canonical Notch activity to coordinate AV specification in ECs, simultaneously suppressing the venous EC program, in analogy with its role in adipogenesis.[18, 19] We further defined an epistatic interaction between prdm16 and canonical Notch in zebrafish embryos, where

combined, but partial, inhibition of prdm16 and Notch components invariably resulted in vascular defects resembling those observed in zebrafish[1, 2, 4-6, 51] or mouse[52-56] Notch mutants.

A positive link between Prdm proteins and the Notch pathway was previously reported in mice[24] and zebrafish.[25, 57] However, hamlet – the drosophila Prdm16 homologue – negatively impacts Notch during drosophila neurogenesis,[23] while in adipose tissue canonical Notch suppresses Prdm16 to drive white adipogenesis.[58] Altogether, these data indicate that Prdm proteins and the Notch pathway regulate various binary cell fate decisions by modulating each other's activity in a context-dependent manner, the definition of which is unknown.

Acute KO of prdm16 did not result in obvious vascular defects under baseline conditions, suggesting that other prdm family members might compensate for complete loss of prdm16, in concordance with the redundant role of Prdm3 and Prdm16 in various tissues. [59, 60, 61] However, both prdm16 morphant and prdm16 crispant zebrafish embryos were predisposed to DAPT-induced AV shunts, indicating that prdm16 signaling controls unique aspects of vascular development that are not shared with other prdm proteins.

Recent evidence suggests that a Sox17-mediated increase of N1ICD levels arterializes ECs.[46] However, our data indicated that Prdm16 does not alter N1ICD levels, but rather complements Sox17 and amplifies the NICD signaling output. In support of these findings, we did not observe ectopic Notch in the PCV of *Tg(fli1a:mPrdm16);Tg(Tp1:eGFP)*^{um14} embryos, although the latter displayed significantly higher residual arterial Notch activity compared to *Tg(Tp1:eGFP)*^{um14} control embryos when challenged with DAPT. The effect of Prdm16 on canonical Notch activity is thus reliant on NICD availability, without a direct effect of Prdm16 on NICD levels *per se*. Additionally, Prdm16 influenced arterial specification and development by

physically and functionally interacting with Hey2, in line with previous studies describing interactions between Prdm and bHLH TFs.[26, 27, 62] As Prdm16 also boosted HEY2 promoter activity, Prdm16 may activate canonical Notch signaling and drive arterial endothelial specification by potentiating NICD first, to complex with Hey2 to maintain endothelial arterial identity later on. Future studies interrogating the dynamic interplay between Prdm16 and Hey2 would provide key insights into the binary cell fate decisions made by (endothelial) precursors.

Finally, recent GWAS have implicated both PRDM16 and NOTCH in vascular disorders, including migraine[28] and coronary artery disease[29], while a recent report suggested a potential role for Prdm16 during coronary artery development. Hence, our findings documenting the role of Prdm16 as a rheostat for arterial endothelial Notch activity may have important clinical implications for vascular disease during development and throughout adulthood. Studies to determine whether Prdm16 is involved in arterial pathologies could therefore provide additional information on its role during these pathophysiological processes and the potential use of therapeutics targeting the Prdm16-Notch axis.

ACKNOWLEDGMENTS

The authors thank P. Vandervoort, B. Hoekman and T. Vervoort for technical assistance. We also thank P. Carmeliet for the zebrafish WISH probes and the VIB Nucleomics Core for their help with the whole-genome transcriptomic data analysis.

FUNDING SOURCES

Research was supported by the European Research Council Starting Grant FP7-StG-IMAGINED203291 (A.L.), internal funding from KU Leuven (a Program Financing Grant (PF/10/014; A.L.) and a C1 grant (C14/19/095 to A.L. and M.D.)), a pre-doctoral research fellowship from the 'Agentschap voor Innovatie door Wetenschap en Technologie' (IWT; SB/0881071; M.B.), research grants from the 'Fonds voor Wetenschappelijk Onderzoek Vlaanderen' (FWO; G0B0913N and G0A2214N; A.L.), an FWO Strategic Basic Research pre-doctoral fellowship (1S25817N; J.V.W.), the NIH (5R24OD017870-06; C.M.) and One Brave Idea (414110-68953; C.M.).

DISCLOSURES

None.

SUPPLEMENTAL MATERIALS

Expanded materials and methods

Online FiguresI-V

Online TablesI-V

Online MoviesI-XVII

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FIGURES AND LEGENDS

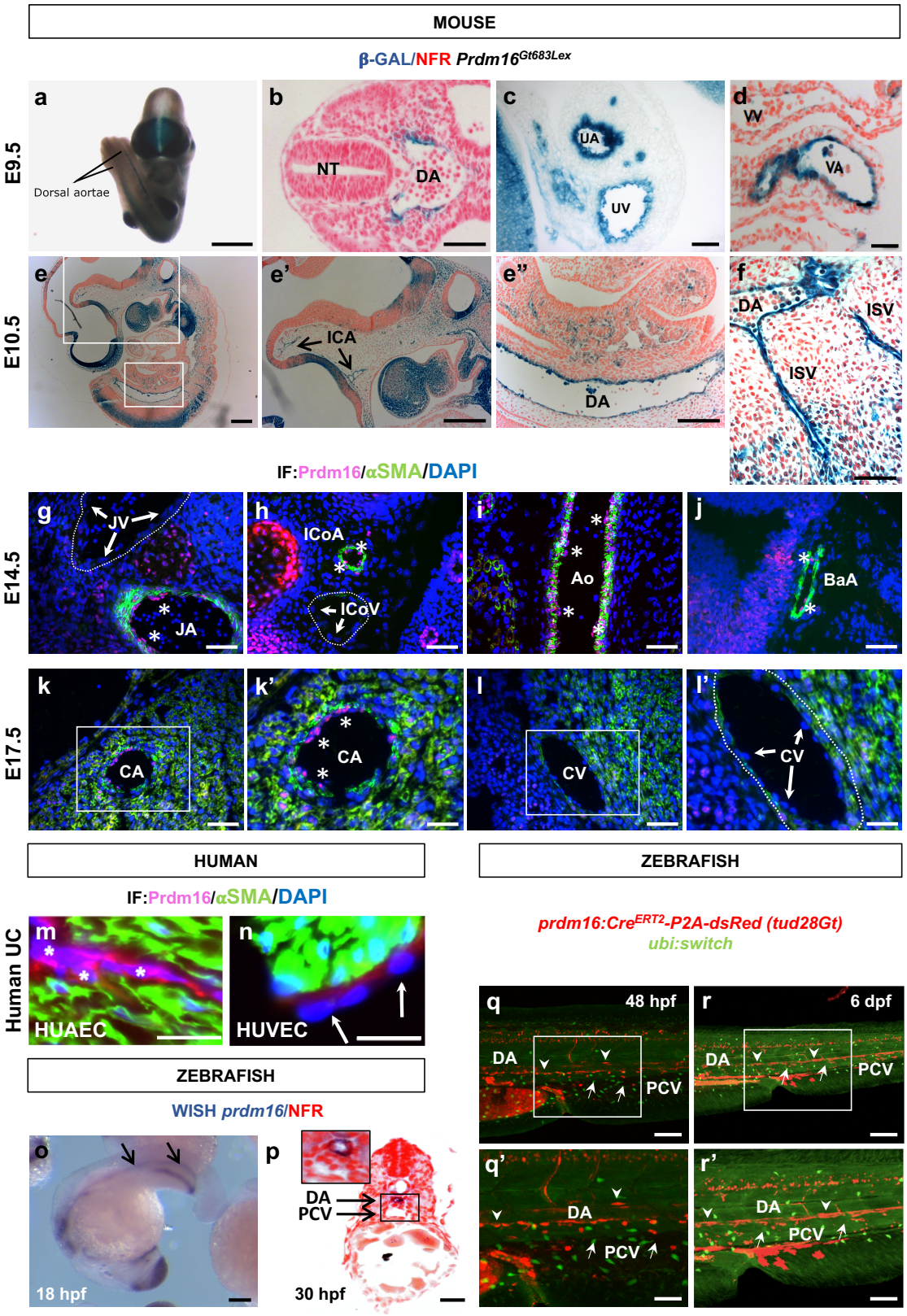
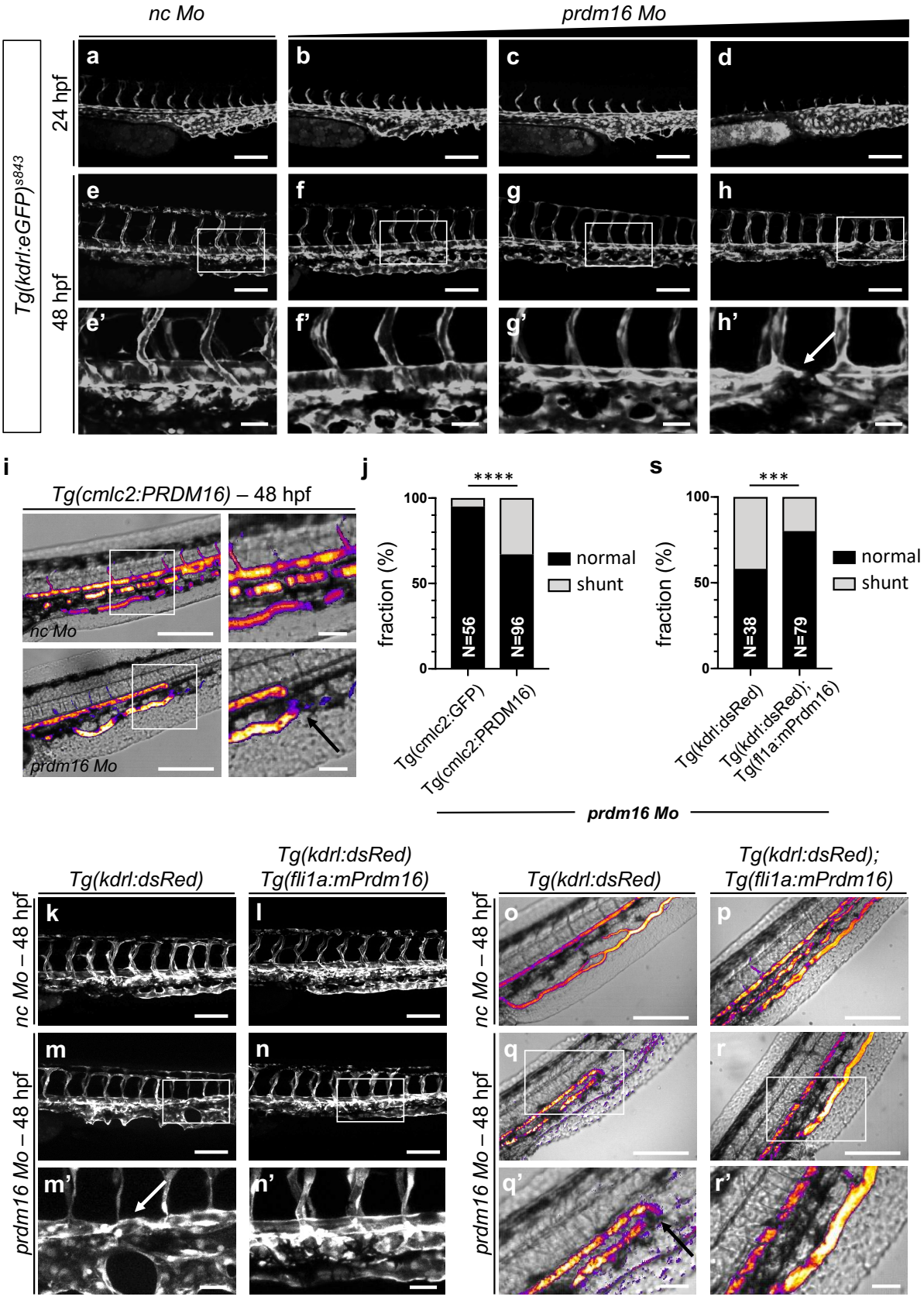


Figure 1. Prdm16 displays an arterial-specific expression profile in mammals and zebrafish. **(a-h)** Whole embryo view (*a*), cross-sections (*b-d*) or sagittal sections (*e-h*) of β-galactosidase (β-GAL) activity staining on embryonic day (E)9.5 (*a-d*) or E10.5 (*e-f*) embryos of the Prdm16 reporter mouse strain (*Prdm16*^{Gt683Lex}). NFR counterstaining was used in *b*,*d-f*. NT: neural tube; DA: dorsal aorta; UA: umbilical artery; UV: umbilical vein; VA: vitelline artery; VV: vitelline vein; ICA: intracranial artery; ISV: intersomitic vessel. (**g-n**) Immunofluorescence (IF) staining for Prdm16 (magenta), α-smooth muscle actin (αSMA; green) and cell nuclei (DAPI; blue) on cross-sections of E14.5 (*g-j*) or E17.5 (*k-l'*) FvB mouse embryos or human umbilical cord (*m,n*). Asterisks indicate Prdm16-expressing arterial ECs, white arrows Prdm16-negative venous ECs. Veins are lined with white dotted lines in *g*,*h*,*l'*. JA: jugular artery; JV: jugular vein; ICoA: intercostal artery; ICoV: intercostal vein; Ao: aorta; BaA: basilar artery; CA: coronary artery; CV: coronary vein; HUAEC: human umbilical artery endothelial cell; HUVEC: human umbilical vein endothelial cell. (**o**) WISH for *prdm16* in an 18 hpf zebrafish embryo. Black arrows indicate *prdm16* expression in the DA. (**p**) Cross-section of a 30 hpf zebrafish embryo after WISH for *prdm16* counter-stained with NFR. PCV: posterior cardinal vein. (**q-r'**) Confocal images of *tud28Gt* zebrafish embryos, reporting prdm16 activity (red) crossed with ubi:switch (green) embryos for better contrast. The DA (white arrowheads), but not the PCV (white arrows) expresses prdm16 at 48 hpf (*q,q'*) and 6 dpf (*r,r'*). Panels labeled with *'* represent insets. Scale bars: 1mm in *a*; 200μm in *o*; 100μm in *b*, *e-f*, *o,p*; 50μm in *g-l*, *q*, *q'*, *r*, *r'*; 25μm in *k'*, *l'*, *p*.


nc Mo
prdm16 Mo
Tg(kdrl:eGFP)s843
24 hpf
48 hpf
a
b
c
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e
f
g
h
e'
f'
g'
h'
i
Tg(cmlc2:PRDM16) – 48 hpf
nc Mo
prdm16 Mo
j
****
100
50
0
fraction (%)
N=56
N=96
normal
shunt
Tg(cmlc2:GFP)
Tg(cmlc2:PRDM16)
s
***
N=38
N=79
Tg(kdrl:dsRed)
Tg(kdrl:dsRed);
Tg(fli1a:mPrdm16)
prdm16 Mo
Tg(kdrl:dsRed)
Tg(kdrl:dsRed)
Tg(fli1a:mPrdm16)
Tg(kdrl:dsRed);
Tg(fli1a:mPrdm16)
nc Mo – 48 hpf
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q'
r'

Figure 2. *prdm16* deficiency leads to vascular defects in an EC-autonomous manner. (a-h') Confocal images of *Tg(kdrl:eGFP)*^{s843} embryos injected with negative control (*nc*) or increasing amounts of *prdm16* Mo, evaluated at 24 (*a-d*) or 48 hpf (*e-h'*). **(i)** Angiograms of 48 hpf *Tg(cmlc2:PRDM16)* zebrafish larvae injected with *nc* Mo (*upper* panels) or a high-dose of *prdm16* Mo (*lower* panels). *Tg(cmlc2:PRDM16) prdm16* morphants frequently displayed AV shunts (black arrow in *lower right*). **(j)** Quantification of AV shunting in *Tg(cmlc2:GFP)* and *Tg(cmlc2:PRDM16)* zebrafish embryos injected with high-dose *prdm16* Mo. **(k-r')** Confocal images (*k-n'*) and angiograms (*o-r'*) of 48 hpf *Tg(kdrl:dsRed)* (*left* panels) and *Tg(kdrl:dsRed;fli1a:mPrdm16)* (*right* panels) embryos injected with *nc* Mo (*upper* panels) or high-dose *prdm16* Mo (*middle+lower* panels). *prdm16* deficiency in *Tg(kdrl:dsRed)* resulted in vascular abnormalities with apparent coarctation of the DA (white arrow in *m'*) and AV shunts (black arrow in *q'*). (**s**) Quantification of AV shunting in *prdm16* morphant *Tg(kdrl:dsRed)* and *Tg(kdrl:dsRed; fli1a:mPrdm16)* zebrafish embryos at 48 hpf. Panels labeled with *'* represent insets. ***P<0.001; ****P<0.0001 by Chi square test. Scale bars: 100μm in *a-i, k-n, o-r'*; 25μm in *e'-h'*, *m'*,*n'*.

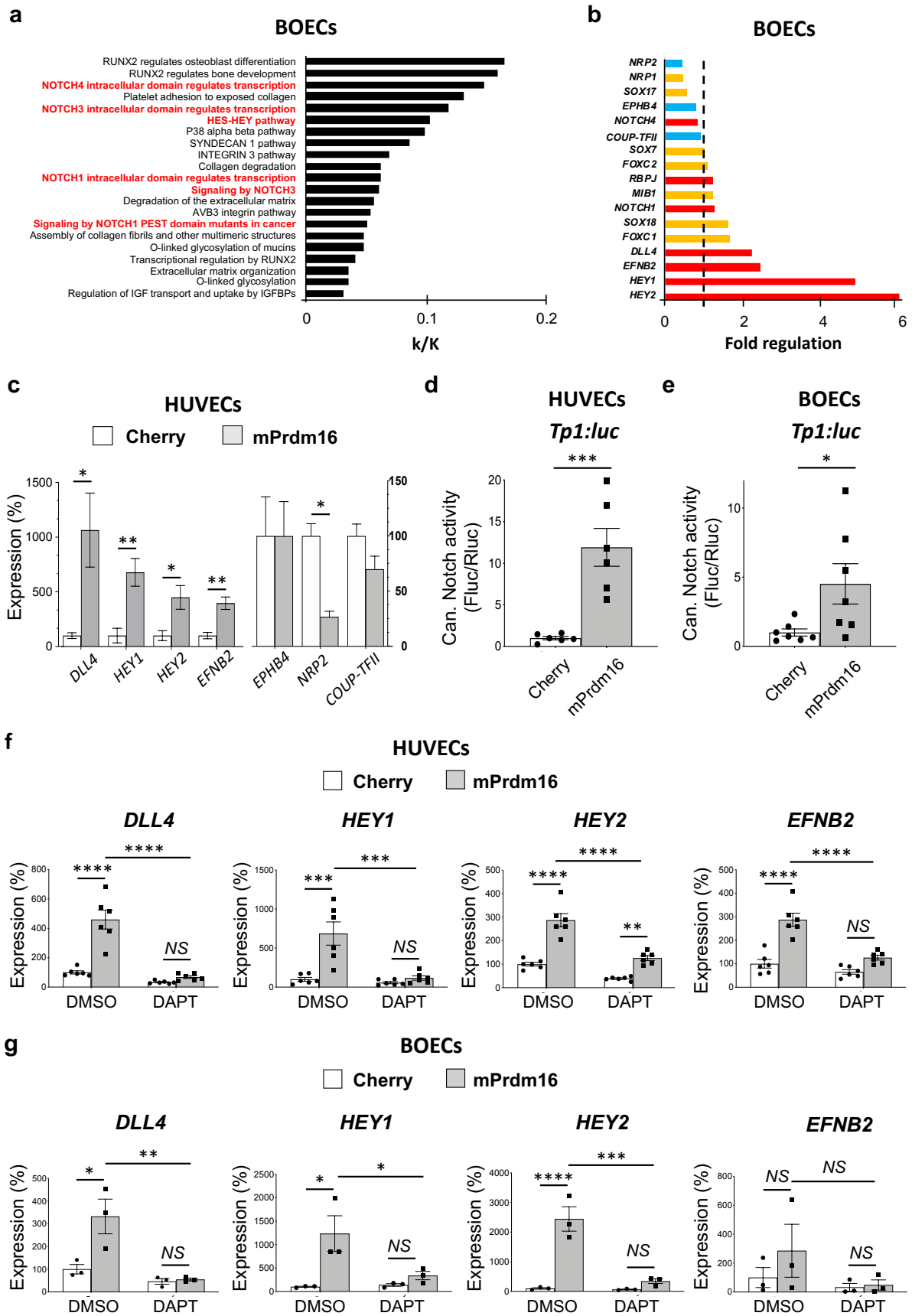
a
BOECs
RUNX2 regulates osteoblast differentiation
RUNX2 regulates bone development
NOTCH4 intracellular domain regulates transcription
Platelet adhesion to exposed collagen
NOTCH3 intracellular domain regulates transcription
HES-HEY pathway
P38 alpha beta pathway
SYNDECAN 1 pathway
INTEGRIN 3 pathway
Collagen degradation
NOTCH1 intracellular domain regulates transcription
Signaling by NOTCH3
Degradation of the extracellular matrix
AVB3 integrin pathway
Signaling by NOTCH1 PEST domain mutants in cancer
Assembly of collagen fibrils and other multimeric structures
O-linked glycosylation of mucins
Transcriptional regulation by RUNX2
Extracellular matrix organization
O-linked glycosylation
Regulation of IGF transport and uptake by IGFBPs
0
0.1
0.2
k/K
b
BOECs
NRP2
NRP1
SOX17
EPHB4
NOTCH4
COUP-TFII
SOX7
FOXC2
RBPJ
MIB1
NOTCH1
SOX18
FOXC1
DLL4
EFNB2
HEY1
HEY2
0
2
4
6
Fold regulation
c
HUVECs
Cherry
mPrdm16
Expression (%)
DLL4
HEY1
HEY2
EFNB2
EPHB4
NRP2
COUP-TFII
d
HUVECs
Tp1:luc
Can. Notch activity (Fluc/Rluc)
Cherry
mPrdm16
e
BOECs
Tp1:luc
Can. Notch activity (Fluc/Rluc)
Cherry
mPrdm16
f
HUVECs
Cherry
mPrdm16
DLL4
HEY1
HEY2
EFNB2
Expression (%)
DMSO
DAPT
NS
g
BOECs
Cherry
mPrdm16
DLL4
HEY1
HEY2
EFNB2
Expression (%)
DMSO
DAPT
NS

Figure 3. Prdm16 regulates canonical NOTCH activity in human ECs. (a) GSEA for canonical pathways enriched in genes differentially expressed between Prdm16 overexpressing ('mPrdm16') and control ('Cherry') blood outgrowth endothelial cells (BOECs; N=3). NOTCH-related biological pathways are highlighted in red. **(b)** Diagram showing the fold regulation as determined by microarray analysis in mPrdm16 *vs.* Cherry BOECs (N=3) of select NOTCH pathway members known to be important for arterial development and of venous markers. Red and orange mark classical canonical Notch pathway members or Notch modifiers, respectively, while blue marks venous-specific genes. **(c)** qRT-PCR mRNA analysis (N=5) for *DLL4*, *HEY1*, *HEY2* and *EFNB2* and the venous markers *EPHB4*, *NRP2* and *COUP-TFII* in Cherry (white bars) *vs.* mPrdm16 (gray bars) human umbilical venous ECs (HUVECs). **(d,e)** Ratiometric Firefly/Renilla-based assay for canonical (can.) NOTCH activity in Cherry+ (white bars) *vs.* mPrdm16 (gray bars) HUVECs (*d,* N=6) and BOECs (*e,* N=7). **(f,g)** qRT-PCR mRNA analysis for *DLL4*, *HEY1, HEY2* and *EFNB2* in Cherry (white bars) or mPrdm16 (gray bars) HUVECs (*f,* N=6) and BOECs (*g,* N=3) treated with DMSO or the canonical NOTCH inhibitor DAPT. **P*<0.05; ***P*<0.01; ****P*<0.001; *****P*<0.0001; NS: not significant by paired Student's *t*-test (*c*-*e*) or 2-way ANOVA (*f*,*g*).

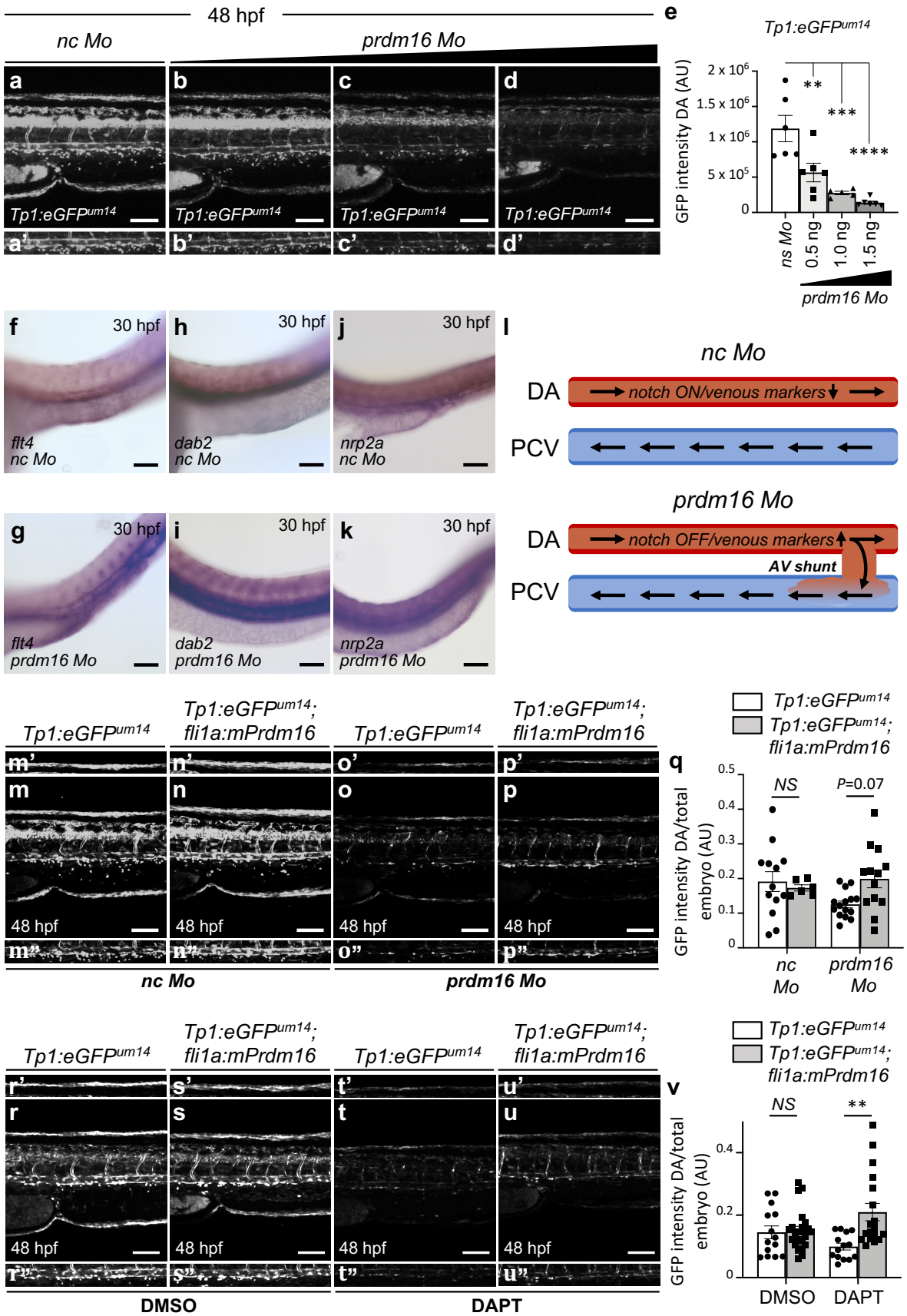
48 hpf
nc Mo
prdm16 Mo
a
b
c
d
Tp1:eGFPum14
a'
b'
c'
d'
e
Tp1:eGFPum14
GFP intensity DA (AU)
2 x 10^6
1.5 x 10^6
1 x 10^6
5 x 10^5
0
**
***
****
ns Mo
0.5 ng
1.0 ng
1.5 ng
prdm16 Mo
f
30 hpf
flt4
nc Mo
h
dab2
nc Mo
j
nrp2a
nc Mo
g
flt4
prdm16 Mo
i
dab2
prdm16 Mo
k
nrp2a
prdm16 Mo
l
nc Mo
DA
notch ON/venous markers
PCV
prdm16 Mo
notch OFF/venous markers
AV shunt
Tp1:eGFPum14
Tp1:eGFPum14; fli1a:mPrdm16
m'
n'
o'
p'
m
n
o
p
m"
n"
o"
p"
nc Mo
prdm16 Mo
q
GFP intensity DA/total embryo (AU)
NS
P=0.07
nc Mo
prdm16 Mo
r'
s'
t'
u'
r
s
t
u
r"
s"
t"
u"
DMSO
DAPT
v
GFP intensity DA/total embryo (AU)
NS
**
DMSO
DAPT

Figure 4. prdm16 drives proper AV endothelial specification during zebrafish embryogenesis. (a-e) Confocal images of 48 hpf *Tg(Tp1:eGFP)*^{um14} zebrafish embryos treated with control morpholino (*nc* Mo; *a*) or increasing doses of *prdm16* Mo (*b-d*) and corresponding quantification (*e*) of canonical notch activity (GFP intensity, N=5-6) in the dorsal aorta (DA; shown separately in *a'-d'*) of control (black bar) and *prdm16* Mo-injected *Tg(Tp1:eGFP)*^{um14} embryos (gray bars). **(f-k)** WISH for the venous markers *flt4* (*f,g*), *dab2* (*h,i*) and *nrp2a* (*j,k*) in control (*f,h,j*) and *prdm16* morphant (*g,i,k*) embryos at 30 hpf. **(l)** Schematic overview of the perturbed arteriovenous endothelial specification and AV shunting in *prdm16* morphants *vs.* control embryos. **(m-q)** Confocal images of 48 hpf *Tg(Tp1:eGFP)*^{um14} (*m,o*) and *Tg((Tp1:eGFP)*^{um14}*;fli1a:mPrdm16)* (*n,p*) embryos injected with subthreshold dose of *nc* (*m,n*) or *prdm16* Mo (*o,p*) and corresponding ratiometric quantification (*q*) of canonical notch activity (GFP intensity, N=6-13) in the DA (shown separately in *m"-p"*) relative to the total embryo of *Tg(Tp1:eGFP)*^{um14} (white bars) and *Tg((Tp1:eGFP)*^{um14}*;fli1a:mPrdm16)* (black bars) embryos injected with *nc* or *prdm16* Mo. Note that *prdm16* Mo knockdown caused a similar reduction of GFP signal in non-endothelial tissue (including the dorsal fin fold shown separately in *m'-p'*). **(r-v)** Confocal images of 48 hpf *Tg(Tp1:eGFP)*^{um14} (*r,t*) and *Tg((Tp1:eGFP)*^{um14}*;fli1a:mPrdm16)* (*s,u*) embryos treated with DMSO (*r,s*) or DAPT (*t,u*) and corresponding ratiometric quantification (*v*) of canonical notch activity (GFP intensity, N=14-23) in the DA (shown separately in *r"-u"*) relative to the total embryo of *Tg(Tp1:eGFP)*^{um14} (white bars) and *Tg((Tp1:eGFP)*^{um14}*;fli1a:mPrdm16)* (black bars) embryos treated with DMSO or DAPT. Note that DAPT caused a similar reduction of GFP signal in non-endothelial tissue (including the dorsal fin fold shown separately in *r'-u'*). ***P*<0.01; ****P*<0.001; *****P*<0.0001; NS: not significant by one-way (*e*) or 2-way ANOVA (*q,v*). Scale bars: 100µm.

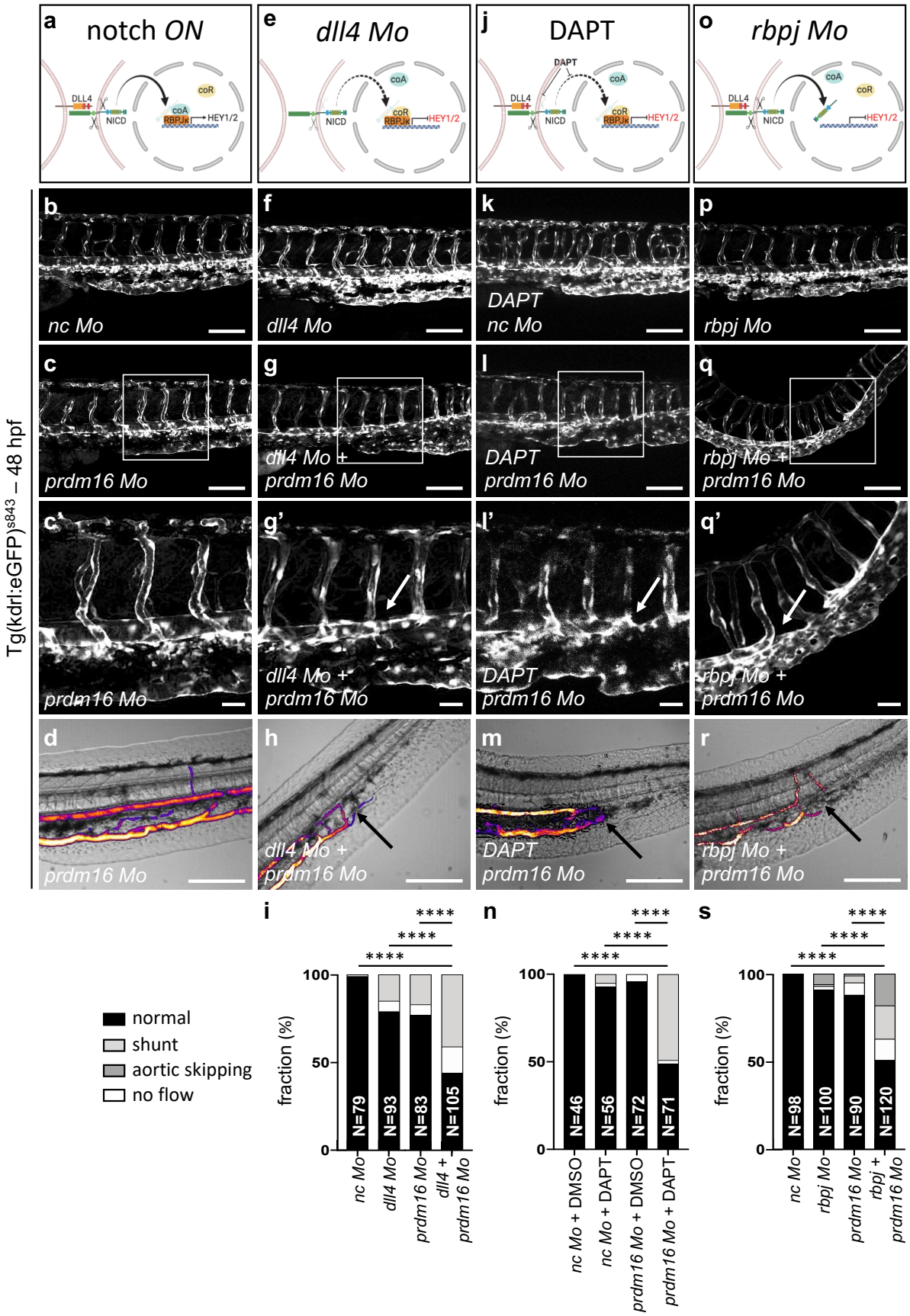
a
notch ON
DLL4
NICD
coR
coA
RBPJκ
HEY1/2
e
dll4 Mo
j
DAPT
o
rbpj Mo
Tg(kdrl:eGFP)s843 – 48 hpf
b
nc Mo
f
dll4 Mo
k
DAPT
nc Mo
p
rbpj Mo
c
prdm16 Mo
g
dll4 Mo +
prdm16 Mo
l
DAPT
prdm16 Mo
q
rbpj Mo +
prdm16 Mo
c'
g'
l'
q'
d
h
m
r
normal
shunt
aortic skipping
no flow
i
n
s
fraction (%)
100
50
0
****
N=79
N=93
N=83
N=105
nc Mo
dll4 Mo
prdm16 Mo
dll4 + prdm16 Mo
N=46
N=56
N=72
N=71
nc Mo + DMSO
nc Mo + DAPT
prdm16 Mo + DMSO
prdm16 Mo + DAPT
N=98
N=100
N=90
N=120
rbpj Mo
rbpj + prdm16 Mo

Figure 5. Genetic interaction between prdm16 and the notch signaling pathway during zebrafish vascular development. (a) Schematic overview of normal canonical NOTCH signaling. **(b-c')** Confocal images of 48 hpf *Tg(kdrl:eGFP)*^{s843} embryos injected with subthreshold dose of negative control (*nc*; *b*) or *prdm16* Mo (*c,c'*) when notch is ON. **(d)** Angiogram of a 48 hpf *Tg(kdrl:eGFP)*^{s843} embryo injected with a suboptimal *prdm16* Mo dose. **(e)** Schematic overview of canonical NOTCH signaling in the absence of the notch ligand DLL4. **(f-g')** Confocal images of 48 hpf *Tg(kdrl:eGFP)*^{s843} embryos injected with a subthreshold dose of *dll4* Mo alone (*f*) or both *dll4* and *prdm16* Mo's (*g,g'*), demonstrating aortic coarctation defects in compound *dll4*/*prdm16* (white arrow in *g'*), but not single *dll4* or *prdm16* morphants. **(h)** Angiogram of *dll4*/*prdm16* double morphants indicating AV shunting (black arrow). **(i)** Quantification of the vascular defects in *dll4*/*prdm16* and control embryos. (**j**) Schematic overview of canonical Notch signaling in the presence of DAPT. **(k-l')** Confocal images of 48 hpf *Tg(kdrl:eGFP)*^{s843} *nc* (*k*) or *prdm16* morphant (*l,l'*) embryos treated with DAPT, indicating aortic coarctation defects (white arrow in *l'*) in *prdm16* Mo-injected embryos in the presence of DAPT. **(m)** Angiogram of DAPT-treated *prdm16* morphants highlighting AV shunting (black arrow). **(n)** Quantification of the vascular defects in DAPT or DMSO-treated *prdm16* morphant or control embryos. **(o)** Schematic overview of canonical Notch signaling in the absence of RBPJ*κ*. **(p-q')** Confocal images of *Tg(kdrl:eGFP)*^{s843} embryos injected with suboptimal dose of *rbpj* Mo (*p*) or subthreshold doses of both *rbpj* and *prdm16* Mo (*q,q'*), the latter resulting in 'aortic skipping' and aortic coarctation (white arrow in *q'*). **(r)** Angiogram of *rbpj*/*prdm16* double morphants illustrating the presence of an AV shunt (black arrow). **(s)** Quantification of the vascular defects in *rbpj*/*prdm16* double morphant *vs.* control embryos. Panels labeled with *'* represent insets. ****$P<0.0001$ by Chi square test. Scale bars: 100μm in *b-d*,*f-h*,*k-m*,*p-r*; 25μm in *c'*,*g'*,*l'*,*q'*.

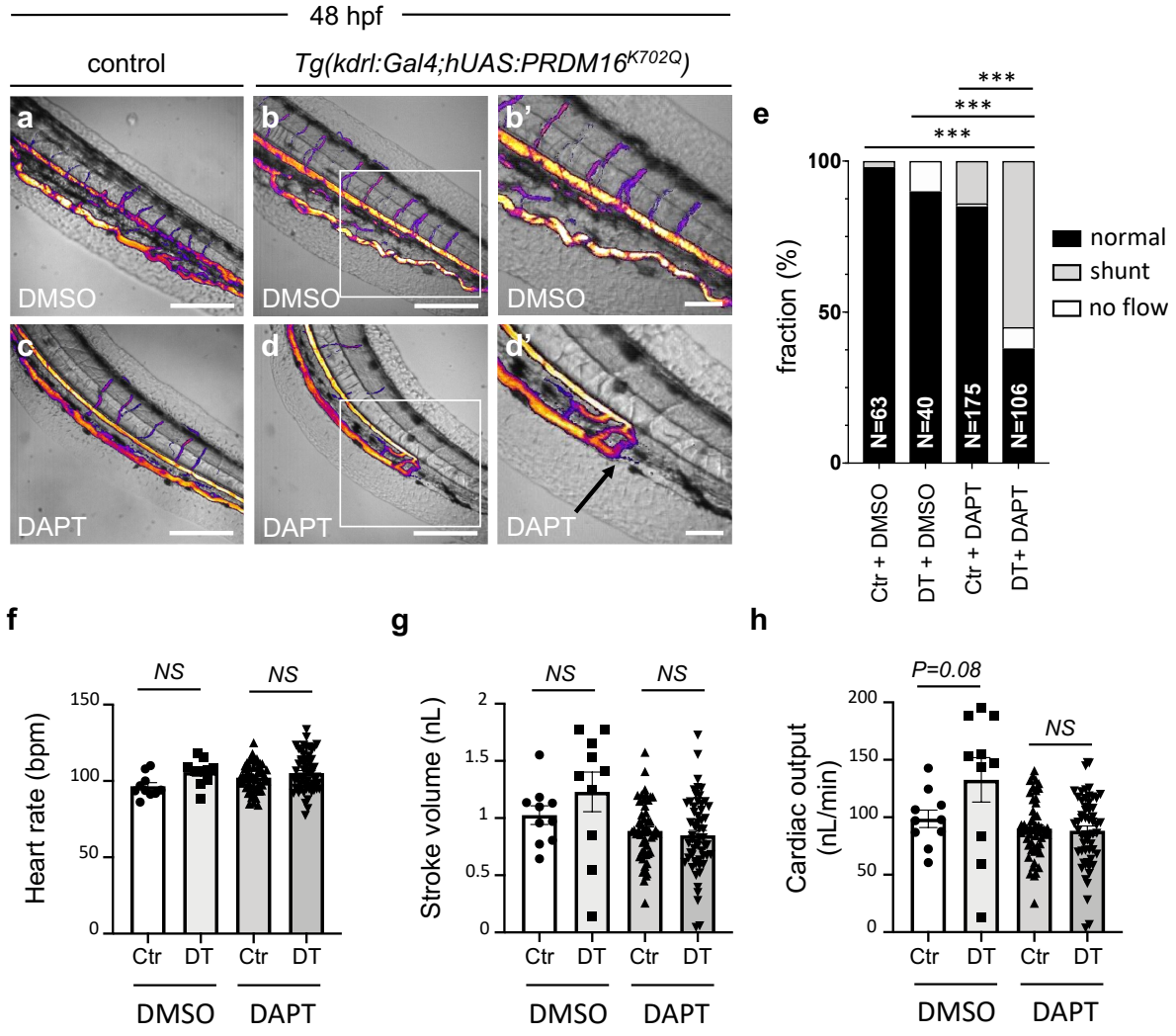

Figure 6. EC-specific overexpression of the dominant-negative PRDM16^{K702Q} variant results in AV shunting in the presence of DAPT. (a-e) Angiograms of 48 hpf control (*a,c*) and double-transgenic (DT) *Tg(kdrl:Gal4;UAS:PRDM16^{K702Q})* (*b,b',d,d'*) zebrafish larvae treated with DMSO (*a-b'*) or DAPT (*c-d'*), indicating shunt formation in DAPT-treated *Tg(kdrl:Gal4;UAS:PRDM16^{K702Q})* embryos (black arrow in *d'*). **(*e*)** Quantification of cardiovascular phenotypes in DMSO and DAPT-treated control and

Tg(kdrl:Gal4;UAS:PRDM16^{K702Q}) embryos. **(f-h)** Quantification of heart rate (*f*), stroke volume (*g*) and cardiac output (*h*) of control and DT embryos treated with DMSO or DAPT. ***P<0.001; NS: not significant by Chi square (*e*) or 2-way ANOVA (*f*-*h*). Panels labeled with *'* represent insets. Scale bars: 100µm.

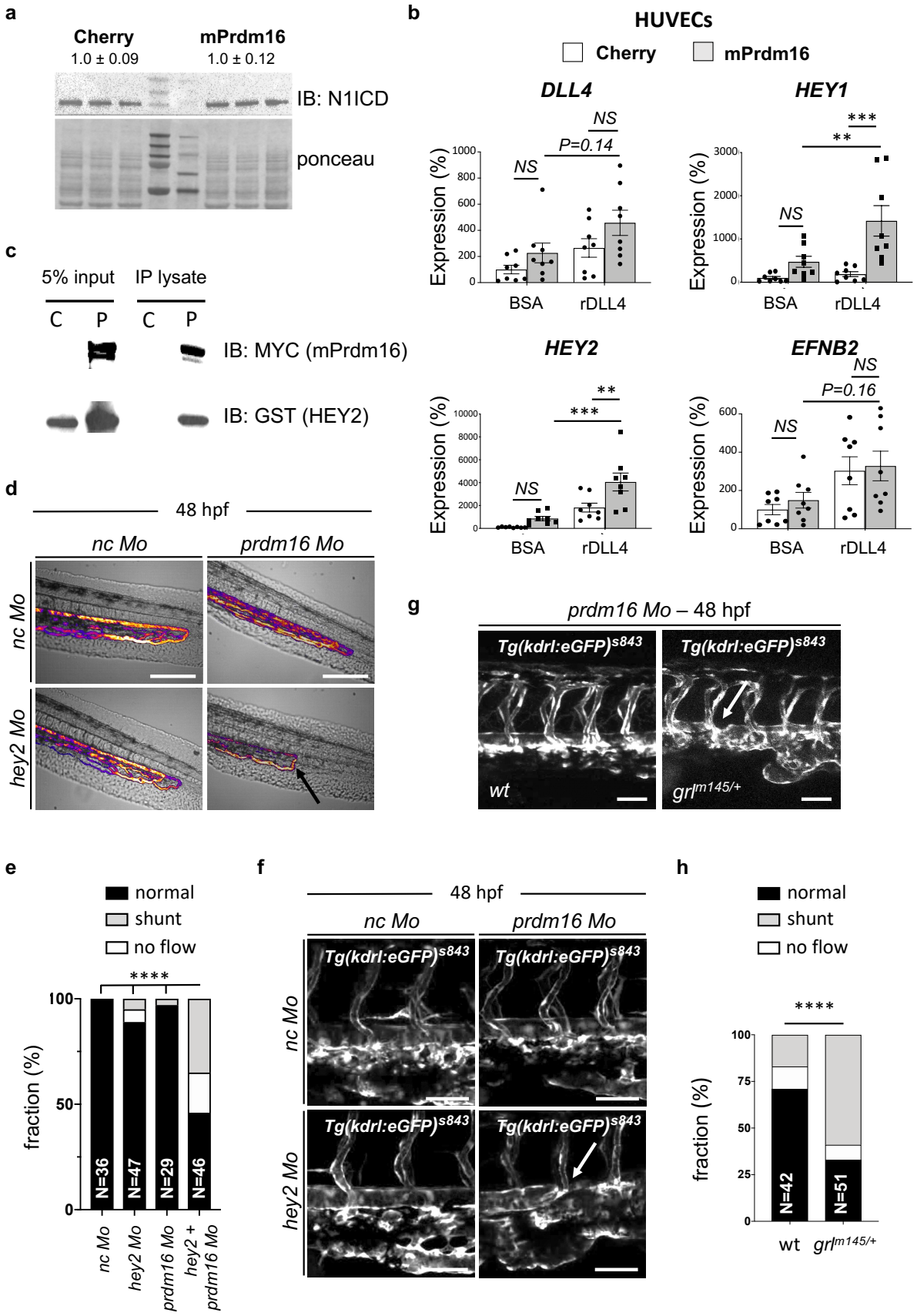
a
Cherry
1.0 ± 0.09
mPrdm16
1.0 ± 0.12
IB: N1ICD
ponceau
b
HUVECs
Cherry
mPrdm16
DLL4
HEY1
HEY2
EFNB2
Expression (%)
NS
P=0.14
P=0.16
**
***
BSA
rDLL4
c
5% input
IP lysate
C
P
IB: MYC (mPrdm16)
IB: GST (HEY2)
d
48 hpf
nc Mo
prdm16 Mo
hey2 Mo
g
prdm16 Mo – 48 hpf
Tg(kdrl:eGFP)s843
wt
grlm145/+
e
normal
shunt
no flow
****
fraction (%)
N=36
N=47
N=29
N=46
nc Mo
hey2 Mo
prdm16 Mo
hey2 + prdm16 Mo
f
48 hpf
nc Mo
prdm16 Mo
hey2 Mo
h
normal
shunt
no flow
****
fraction (%)
N=42
N=51
wt
grlm145/+

Figure 7. PRDM16 interacts with HEY2 to establish proper arterial development. (a) Western blot for cleaved Notch1ICD (N1ICD) in HUVECs transduced with Cherry or mPrdm16-lentiviral particles. Ponceau red was used to normalize for protein loading. **(b)** qRT-PCR mRNA analysis for *DLL4*, *HEY1*, *HEY2* and *EFNB2* in Cherry (white bars) or mPrdm16 (gray bars) overexpressing HUVECs grown on BSA or rDLL4-containing gelatin. **(c)** Co-immunoprecipitation of Myc-mPrdm16 and GST-HEY2 in Cherry ('C')) or mPrdm16-overexpressing ('P') HEK293 cells indicating that PRDM16 and HEY2 reside in the same protein complex. **(d)** Angiograms of embryos injected with subthreshold doses of *nc*, *hey2* or *prdm16* Mo and zebrafish larvae co-injected with *hey2* and *prdm16* Mo's, demonstrating AV shunting (black arrow) between the DA and PCV in *hey2*/*prdm16* double morphants. **(e)** Quantification of the vascular defects in *hey2*/*prdm16* double morphant *vs.* control embryos. **(f)** Confocal imaging of control (*nc*), *prdm16* or *hey2* single morphant and *hey2*/*prdm16* double morphant zebrafish embryos at 48 hpf, indicating aortic coarctation (white arrow) in *hey2*/*prdm16* double morphants. **(g)** Confocal imaging of wild-type (*wt*) and $grl^{m145/+}$ heterozygous embryos on the $Tg(kdrl{:}eGFP)^{s843}$ background injected with a suboptimal dose of *prdm16* Mo. Incomplete knockdown of *prdm16* resulted in aortic coarctation (white arrow) in $grl^{m145/+}$, but not *wt* embryos. **(h)** Quantification of AV shunting in *wt* and $grl^{m145/+}$ embryos. $^{**}P<0.01$; $^{***}P<0.001$; $^{****}P<0.0001$; NS: not significant by 2-way ANOVA (*b*) or Chi square test (*e*,*h*). Scale bars: 100μm in *d*; 50μm in *f*,*g*.