

## Supplementary materials

### Identification of a novel flow-mediated gene expression signature in patients with bicuspid aortic valve

Shohreh Maleki<sup>1\*</sup>, Hanna M Björck<sup>2,3\*</sup>, Lasse Folkersen<sup>1</sup>, Roland Nilsson<sup>4</sup>, Johan Renner<sup>3,5</sup>, Kenneth Caidahl<sup>6</sup>, Anders Franco-Cereceda<sup>7</sup>, Toste Länne<sup>2,3</sup>, Per Eriksson<sup>1</sup>

\* Equal contribution

<sup>1</sup>Atherosclerosis Research Unit, Center for Molecular Medicine, Department of Medicine, Karolinska Institute, Stockholm, Sweden, <sup>2</sup>Division of Cardiovascular Medicine, Department of Medical and Health Sciences, Faculty of Health Sciences, Linköping University, Sweden, <sup>3</sup>Center for Medical Image Science and Visualization (CMIV), Linköping University, Sweden, <sup>4</sup>Computational Medicine, Karolinska Institute, <sup>5</sup>Division of Applied Thermodynamics and Fluid Mechanics, Department of Management and Engineering, Linköping University, Sweden, <sup>6</sup>Clinical Physiology, <sup>7</sup>Cardiothoracic Surgery Unit, Department of Molecular Medicine and Surgery, Karolinska Institute, Stockholm, Sweden.

## **MATERIALS AND METHODS**

### ***Human Material – the ASAP study***

The collection of biopsy samples from the Advanced Study of Aortic Pathology (ASAP) database has been described in detail previously (1). Briefly, biopsy samples were taken from ascending aortas of patients undergoing aortic valve surgery which were classified as having either BAV or TAV and dilated or non-dilated aorta. Demographic data have been presented in detail previously (2).

### ***Animals***

Male Wistar rats (Taconic, Lille Skensved, Denmark) weighing 400-450 g were used. The experimental protocol was approved by the Regional Ethics Committee for Animal Experiments, and followed institutional guidelines for care and treatment of experimental animals. Animals were maintained at the Animal Facility, Faculty of Health Sciences, Linköping University under constant environmental temperature (21°C), and a 12h:12h light/dark cycle, and had free access to standard rodent chow and water.

### ***Expression screening***

The expression screening algorithm has been previously described (3,4). Briefly, we used this algorithm to search a repository of 1,512 mouse and human Affymetrix microarray data sets for "informative" data sets where the query genes are co-expressed. Next, a weighted meta-analysis was performed to discover additional genes correlating with the query genes, where the most "informative" data sets are given largest weights. The outcome of the analysis is a posterior probability of true co-expression. We selected genes with a posterior probability greater than 0.5.

### ***Determination of flow regions in rat***

A total of nine rats were used for determination of flow regions. A detailed description of the examination procedure and methods employed can be found elsewhere (Björck et al. submitted manuscript). In brief, geometry and flow information from the rat aorta were obtained using a 1.5 T whole body magnetic resonance imaging (MRI) scanner and an eight channel wrist coil (Philips Achieva, Philips Medical Systems, Best, the Netherlands). Segmentation of the MRI image data material into a 3D geometry of the aortic arch was performed using a semi-automatic level-set approach, followed by subject specific estimation of time resolved wall shear stress (WSS) magnitude and WSS vector direction by the use of computational fluid dynamics (CFD). The flow was assumed to be laminar and the aortic wall was considered to be rigid with a no slip boundary condition.

### ***Isolation of RNA***

A second set of totally 70 rats was used for analysis of gene expression. A detailed description of the experimental procedure is provided elsewhere (Björck et al. manuscript). In brief, two regions within the same aorta, exposed to a disturbed and uniform flow pattern, respectively were cut out and directly put in pre-chilled Lysing Matrix D tubes (MP Biomedicals, Illkirch, France) containing Trizol (Invitrogen, Paisley, Scotland, UK). Tissue from the specific regions from five animals was pooled in order to yield significant amounts of RNA. Samples were homogenized with FastPrep. Total RNA was isolated using RNeasy Mini kit (Qiagen, Maryland, USA) as a cleanup, including DNase treatment for elimination of potential DNA contamination. RNA integrity was analyzed by the use of an Agilent 2100 Bioanalyzer (Agilent Technologies Inc., Palo Alto, CA, USA) and quantified using NanoDrop (NanoDrop products, Wilmington, DE, USA).

### ***Gene arrays***

The RNA samples were hybridized and scanned at the Karolinska Institute microarray core facility. Affymetrix GeneChip Human Exon 1.0 ST arrays, Affymetrix Rat 1.1 ST Titan arrays and protocols were used (Affymetrix, Santa Clara, CA). In both studies the raw cel files were

preprocessed and log<sub>2</sub> transformed using Robust Multichip Average normalization as implemented in the Affymetrix Power Tools 1.10.2 package apt-probeset-summarize (5). This normalization includes a step in which the distribution of gene expression levels on individual arrays are standardized, normalizing the expression levels to the overall mRNA levels.

Details for transcriptional profiling in the ASAP study has been described previously (1). Gene annotation for this study was downloaded from the Affymetrix web page as version HuEx-1\_0-st-v2.na29.hg18. All investigations were done on the core sets of meta probes provided by Affymetrix. The data from mammary artery intima-media and from ascending thoracic aorta intima-media are used.

Transcriptional profiling of rat aorta was performed on 28 samples (14 pairs of disturbed and uniform flow pattern samples) (Björck HM, et al. manuscript). Gene annotation was downloaded from the Affymetrix web page as version RaGene-1\_1-st-v1.na31.rn4.

### **Quantitative real-time polymerase chain reaction**

A total of 200 ng RNA from each sample was reversed transcribed with random primers and Superscript II (Invitrogen, Carlsbad, CA, USA). Amplification of cDNA was performed in 20 $\mu$ l reactions using 1xTaqMan Universal PCR Mastermix (Applied Biosystems, Foster City, CA, USA) on an ABI 7700 Sequence Detector. Each sample was analyzed in triplicates and standard curve method was used for quantification of specific gene targets (for reference see e.g. Cikos, S. et al. *BMC Mol Biol.* 2007;8:113). The following Assay on Demand kits (Applied Biosystems, Foster City, CA, USA) were used: *GPR116*, Rn00594813; *PKD2*, Rn01449962; *TNF- $\alpha$* , Rn00562055; *VCAM1*, Rn00563627; *ZFP36*, Rn01763978. TATA-binding protein (*TBP*, Rn01455646) served as an RNA loading control. Reactions without template were included as negative controls. The thermal protocol were as follows: 50°C for 2 min, 95°C for 10 min, followed by 45 repeats of 95°C for 15 sec, 60°C for 1 min.

### **Immunohistochemistry**

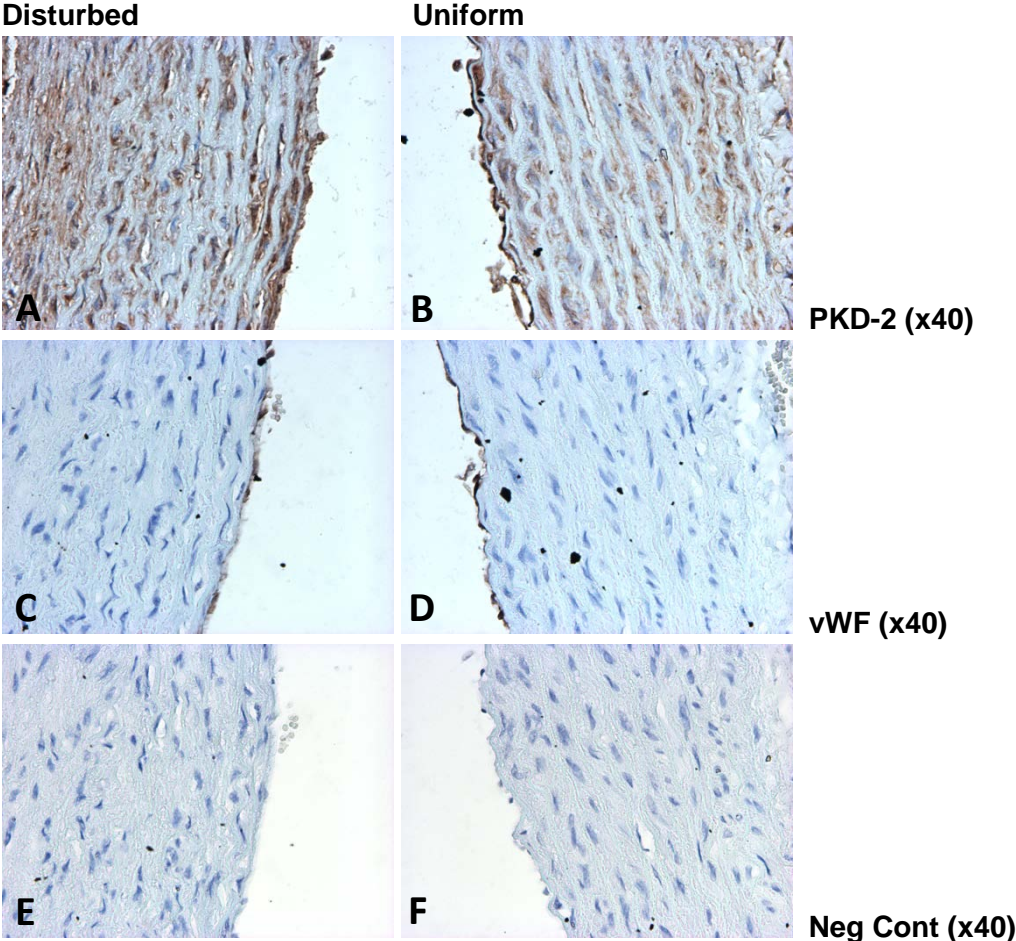
Immunostaining for PKD-2, ZFP36, GPR116 and vWF was performed on deparaffinised tissue sections treated with DIVA solution (Biocare Medical, Concord, CA) using rabbit-anti-human/mouse/rat PKD-2 polyclonal antibody (ab78622, Abcam, Cambridge, UK), rabbit-anti-human/mouse/rat ZFP36 polyclonal antibody (sc-14030, Santa Cruz, CA), goat-anti-human/mouse/rat GPR116 polyclonal antibody (sc-68978), and rabbit-anti-human vWF polyclonal antibody (A0082, DakoCytomation, Glostrup, Denmark), respectively. Endogenous peroxidase activity was quenched with 3% hydrogen peroxide for 5 min, and nonspecific binding sites were blocked with 20% goat or horse serum. Biotinylated anti-rabbit and anti-goat IgG (Vector, Peterborough, UK) was used as secondary antibody. Normal rabbit IgG (sc-2027, Santa Cruz, CA), normal goat IgG (sc-2028, Santa Cruz, CA) and PBS was included as controls. Avidin-biotin peroxidase complex (Vectastain ABC kit, Vector Laboratories, Burlingame, CA) was added for 30 min in room temperature, followed by visualization using 3,3'-diaminobenzidine tetrahydrochloride (Dako, Glostrup, Denmark). All sections were counterstained with Mayer's hematoxylin (Histolab Products, Göteborg, Sweden).

### **Statistical analysis**

Multivariate analysis models refer to the use of the linear model `lm` function as implemented in R 2.13.0. When P-values are reported (supplementary table II), they are from the association between gene expression and cuspidity, with dilation status, stenosis and regurgitation included in the model. Differential expression of rat RNA microarray data was investigated using a paired Student's T-test assuming unequal variance. Correction for multiple testing of gene expression between clinical phenotypes, and between flow regions in rat was done using Benjamini-Hochsberg False Discovery Rate correction (FDR) as implemented in the *multtest* R-package. Comparisons between the expression of different genes were performed using a Pearson product-moment correlation, with a cutoff of  $R > 0.40$ .

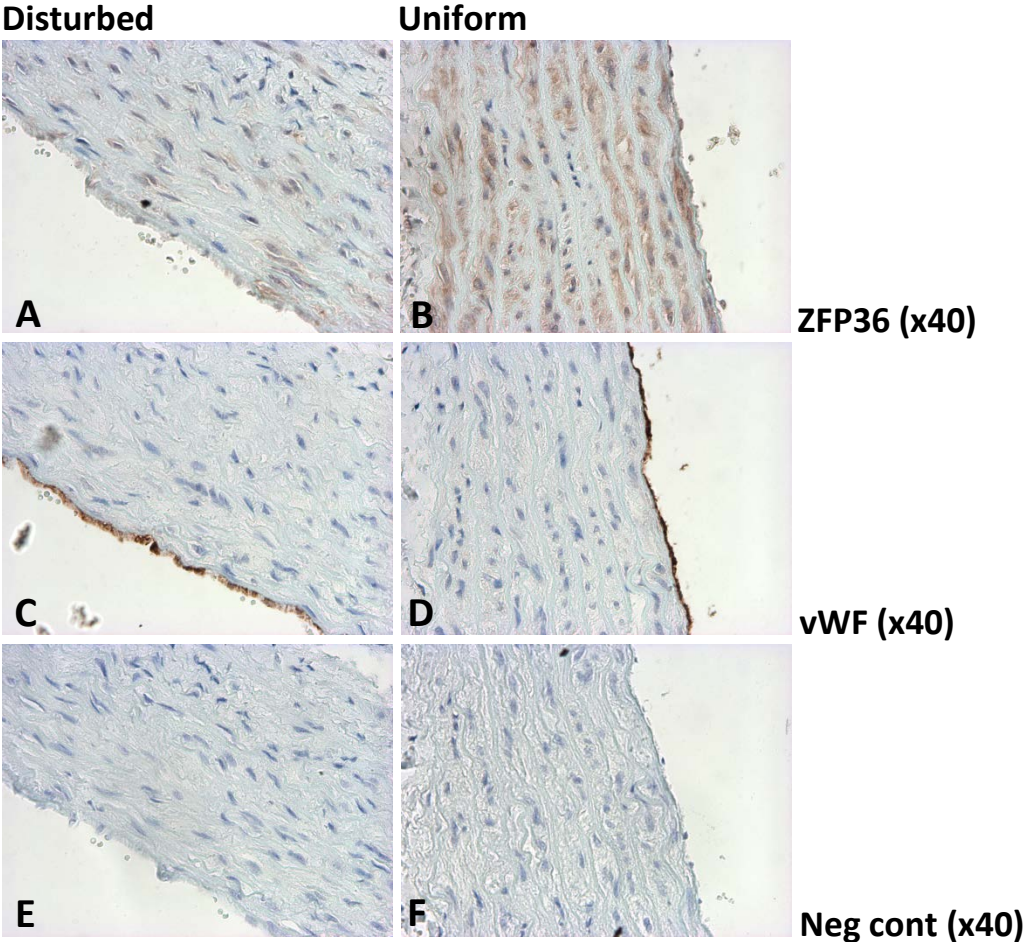
**Supplementary Fig 1**

Immunostaining of PDK2 in disturbed (A) and uniform (B) flow pattern regions of rat aorta. C and D, vWF staining in disturbed and uniform flow pattern regions, respectively; E and F, negative control.



**Supplementary Fig 2**

Immunostaining of ZFP36 in disturbed (A) and uniform (B) flow pattern regions of rat aorta. C and D, vWF staining in disturbed and uniform flow pattern regions, respectively; E and F, negative control.



**Supplementary Table 1A:** List of genes selected using expression screening (for detailed description of selection see materials and methods and result section). Arbitrary cut off of >0.50 was chosen for expression probability in Human dataset. **(RED\*)** Query genes.

Gene Symbol	Expression Probability	Name
<b>KLF2*</b>	0.87	Kruppel-like factor 2 (lung)
<b>DUSP1</b>	0.84	Dual specificity phosphatase 5
<b>LATS2</b>	0.84	Large tumor suppressor, homolog 2 (Drosophila)
<b>THBD*</b>	0.83	Thrombomodulin
<b>ZFP36</b>	0.83	Zinc finger protein 36
<b>CD93</b>	0.81	CD93 molecule
<b>MCL1</b>	0.79	Myeloid cell leukemia sequence 1 (BCL2-related)
<b>EMP1</b>	0.78	Epithelial membrane protein 1
<b>MYADM</b>	0.76	Myeloid-associated differentiation marker
<b>JUNB</b>	0.76	Jun B proto-oncogene
<b>SERTAD1</b>	0.75	SERTA domain containing 1
<b>GADD45B</b>	0.74	Growth arrest and DNA-damage-inducible, beta
<b>FOS</b>	0.73	C-FOS/AP-1 FBJ murine osteosarcoma viral oncogene homolog
<b>EPAS1</b>	0.73	Endothelial PAS domain protein 1
<b>KLF4*</b>	0.72	Kruppel-like factor 4 (gut)
<b>CRISPLD2</b>	0.72	Cysteine-rich secretory protein LCCL domain containing 2
<b>TGFBR2</b>	0.71	Transforming growth factor, beta receptor II (70/80kDa)
<b>ENG</b>	0.70	Endoglin
<b>CDKN1A</b>	0.70	Cyclin-dependent kinase inhibitor 1A /p21
<b>CYR61</b>	0.69	Cysteine-rich, angiogenic inducer, 61
<b>MAFF</b>	0.69	V-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian)
<b>HEG1</b>	0.68	HEG homolog 1 (zebrafish)
<b>PECAM1</b>	0.68	Platelet/endothelial cell adhesion molecule
<b>SOCS3</b>	0.68	Suppressor of cytokine signaling 3
<b>IL1R1</b>	0.68	Interleukin 1 receptor, type I
<b>ADAMTS1</b>	0.68	ADAM metalloproteinase with thrombospondin type 1 motif, 1
<b>HBEGF</b>	0.68	Heparin-binding EGF-like growth factor
<b>SH2B3</b>	0.68	SH2B adaptor protein 3
<b>SLC2A3</b>	0.67	Solute carrier family 2
<b>LOC387763</b>	0.67	Chromosome 11 open reading frame 96
<b>CEBPD</b>	0.66	CCAAT/enhancer binding protein (C/EBP), delta
<b>IGFBP7</b>	0.66	Insulin-like growth factor binding protein 7
<b>THBS1</b>	0.66	Thrombospondin 1
<b>PTPRE</b>	0.66	Protein tyrosine phosphatase, receptor type, E
<b>STOM</b>	0.66	Stomatin
<b>DSE</b>	0.65	Dermatan sulfate epimerase
<b>TIMP1</b>	0.65	TIMP metalloproteinase inhibitor 1
<b>RHOB</b>	0.64	Ras homolog gene family, member B
<b>SGK1</b>	0.64	Serum- and Glucocorticoid-Inducible Kinase 1
<b>ATF3</b>	0.64	Activating transcription factor 3



<b>EGR1</b>	0.64	Early growth response 1
<b>NID1</b>	0.63	Nidogen 1
<b>LAMC1</b>	0.63	Laminin, gamma 1
<b>KLF10</b>	0.63	Kruppel-like factor 10
<b>TAGLN</b>	0.63	Transgelin
<b>ITGA5</b>	0.63	Integrin, alpha 5
<b>KIAA1754</b>	0.63	Inositol 1,4,5-trisphosphate receptor interacting protein
<b>KIAA0247</b>	0.63	KIAA0247
<b>CHSY1</b>	0.62	Chondroitin sulfate synthase 1
<b>PICALM</b>	0.62	Phosphatidylinositol binding clathrin assembly protein
<b>CAV1</b>	0.62	CAV1 caveolin 1
<b>CSGALNACT2</b>	0.62	Chondroitin sulfate N-acetylgalactosaminyltransferase 2
<b>KIAA1949</b>	0.62	KIAA1949
<b>METRNL</b>	0.62	Meteorin
<b>ELTD1</b>	0.61	EGF, latrophilin and seven transmembrane domain containing 1
<b>TIMP3</b>	0.61	TIMP metalloproteinase inhibitor 3
<b>KLF6</b>	0.61	Kruppel-like factor 6
<b>BTG2</b>	0.61	BTG family, member 2
<b>SWAP70</b>	0.61	Switching B-cell complex 70kDa subunit
<b>IER2</b>	0.61	Immediate early response 2
<b>CDH5</b>	0.60	Cadherin 5, type 2
<b>PTRF</b>	0.60	Polymerase I and transcript release factor
<b>CTGF</b>	0.60	Connective tissue growth factor
<b>DAB2</b>	0.60	Disabled homolog 2, mitogen-responsive phosphoprotein
<b>SNF1LK</b>	0.60	SNF1-like kinase
<b>TIE1*</b>	0.59	Tyrosine kinase with immunoglobulin-like and EGF-like domains 1
<b>ZCCHC24</b>	0.59	Zinc finger, CCHC domain containing 24
<b>PMP22</b>	0.59	Peripheral myelin protein 22
<b>KCTD12</b>	0.59	Potassium channel tetramerisation domain containing 12
<b>GNG11</b>	0.59	Guanine nucleotide binding protein (G protein), gamma 11
<b>ZFP36L1</b>	0.59	Zinc finger protein 36, C3H type-like 1
<b>TRAM2</b>	0.59	Translocation associated membrane protein 2
<b>TUBB6</b>	0.58	Tubulin, beta 6
<b>PPP1R15A</b>	0.58	Protein phosphatase 1, regulatory (inhibitor) subunit 15A
<b>PLEKHO2</b>	0.58	Pleckstrin homology domain containing, family O member 2
<b>HLX</b>	0.57	H2.0-like homeobox
<b>CEBPB</b>	0.57	CCAAT/enhancer binding protein (C/EBP), beta
<b>FOSB</b>	0.57	FBJ murine osteosarcoma viral oncogene homolog B
<b>SNRK</b>	0.56	SNF related kinase
<b>DUSP5</b>	0.56	Dual specificity phosphatase 5
<b>RGS2</b>	0.56	Regulator of G-protein signaling 2, 24kDa
<b>ERG</b>	0.56	V-ets erythroblastosis virus E26 oncogene
<b>PKD2*</b>	0.55	Polycystic kidney disease 2
<b>PPAP2B</b>	0.55	Phosphatidic acid phosphatase type 2B
<b>EHD2</b>	0.55	EH-domain containing 2

<b>CRTC3</b>	0.55	CREB regulated transcription coactivator 3
<b>COL6A3</b>	0.55	Collagen, type VI, alpha 3
<b>FERMT2</b>	0.55	Fermitin family member 2
<b>FILIP1L</b>	0.54	Filamin A interacting protein 1-like
<b>LHFP</b>	0.54	Lipoma HMGIC fusion partner
<b>NRP1</b>	0.54	Neuropilin 1
<b>LAMA4</b>	0.54	Laminin, alpha 4 [
<b>FLI1</b>	0.54	Friend leukemia virus integration 1
<b>PEA15</b>	0.54	Phosphoprotein enriched in astrocytes 15
<b>TGFB111</b>	0.54	Transforming growth factor beta 1 induced transcript 1
<b>ZEB2</b>	0.54	Zinc finger E-box binding homeobox 2
<b>NR4A2</b>	0.54	Nuclear receptor subfamily 4, group A,
<b>GRK5</b>	0.53	G protein-coupled receptor kinase 5
<b>VWF</b>	0.53	Von Willebrand factor
<b>MSN</b>	0.53	Moesin
<b>ARRDC3</b>	0.53	Arrestin domain containing 3
<b>ANXA5</b>	0.53	Annexin A5
<b>RAB31</b>	0.53	Member RAS oncogene family
<b>GEM</b>	0.53	GTP binding protein
<b>NFIL3</b>	0.53	Nuclear factor, interleukin 3 regulated
<b>FAM26B</b>	0.52	Family with sequence similarity 26
<b>ETS2</b>	0.52	V-ets erythroblastosis virus E26 oncogene homolog 2 (avian)
<b>CXCR7</b>	0.52	Chemokine (C-X-C motif) receptor 7
<b>IL4R</b>	0.52	Interleukin 4 receptor
<b>MAP3K8</b>	0.52	Mitogen-activated protein kinase kinase kinase 8
<b>PTGER4</b>	0.52	Prostaglandin E receptor 4
<b>NR4A1</b>	0.52	Nuclear receptor subfamily 4, group A, member 1
<b>ESAM</b>	0.51	Endothelial cell adhesion molecule
<b>GPR116</b>	0.51	G protein-coupled receptor 116
<b>RAB6IP1</b>	0.51	DENN/MADD domain containing 5A
<b>COL4A1</b>	0.51	Collagen, type IV, alpha 1
<b>KLF9</b>	0.51	Kruppel-like factor 9
<b>CALD1</b>	0.51	Caldesmon 1
<b>ANXA1</b>	0.51	Annexin A1
<b>PHLDB2</b>	0.51	Pleckstrin homology-like domain, family B, member 2
<b>CCL2</b>	0.51	Chemokine (C-C motif) ligand 2
<b>SNX9</b>	0.51	Sorting nexin 9



**Supplementary Table 1B:** Expression screening using 5 and 9 query genes, respectively (see the Result section). Yellow marks the position of extra genes appearing in the selection with 5 query genes. #; query genes.

9 queries	5 Queries	9 queries	5 Queries	9 queries	5 Queries
<i>KLF2</i> <sup>#</sup>	<b><i>KLF2</i><sup>#</sup></b>	<i>NID1</i>	<i>NID1</i>	<b><i>PKD2</i><sup>#</sup></b>	<b><i>PKD2</i><sup>#</sup></b>
<i>DUSP1</i>	<i>DUSP1</i>	<i>LAMC1</i>	<i>LAMC1</i>	<i>PPAP2B</i>	<i>PPAP2B</i>
<i>LATS2</i>	<i>LATS2</i>	<i>KLF10</i>	<i>KLF10</i>	<i>EHD2</i>	<i>EHD2</i>
<b><i>THBD</i><sup>#</sup></b>	<b><i>THBD</i><sup>#</sup></b>	<i>TAGLN</i>	<i>TAGLN</i>	<i>CRTC3</i>	<i>CRTC3</i>
<i>ZFP36</i>	<i>ZFP36</i>	<i>ITGA5</i>	<i>ITGA5</i>	<i>COL6A3</i>	<i>COL6A3</i>
<i>CD93</i>	<i>CD93</i>	---	<b><i>KIAA1754</i></b>	<i>FERMT2</i>	<i>FERMT2</i>
<i>MCL1</i>	<i>MCL1</i>	<i>KIAA0247</i>	<i>KIAA0247</i>	<i>FILIP1L</i>	<i>FILIP1L</i>
<i>EMP1</i>	<i>EMP1</i>	<i>CHSY1</i>	<i>CHSY1</i>	<i>LHFP</i>	<i>LHFP</i>
<i>MYADM</i>	<i>MYADM</i>	<i>PICALM</i>	<i>PICALM</i>	<i>NRP1</i>	<i>NRP1</i>
<i>JUNB</i>	<i>JUNB</i>	<i>CAV1</i>	<i>CAV1</i>	<i>LAMA4</i>	<i>LAMA4</i>
<i>SERTAD1</i>	<i>SERTAD1</i>	<i>CSGALNACT2</i>	<i>CSGALNACT2</i>	<i>FLI1</i>	<i>FLI1</i>
<i>GADD45B</i>	<i>GADD45B</i>	<i>KIAA1949</i>	<i>KIAA1949</i>	<i>PEA15</i>	<i>PEA15</i>
<i>FOS</i>	<i>FOS</i>	<i>METRNL</i>	<i>METRNL</i>	<i>TGFB111</i>	<i>TGFB111</i>
<i>EPAS1</i>	<i>EPAS1</i>	<i>ELTD1</i>	<i>ELTD1</i>	<i>ZEB2</i>	<i>ZEB2</i>
<b><i>KLF4</i><sup>#</sup></b>	<b><i>KLF4</i><sup>#</sup></b>	<i>TIMP3</i>	<i>TIMP3</i>	<i>NR4A2</i>	<i>NR4A2</i>
<i>CRISPLD2</i>	<i>CRISPLD2</i>	<i>KLF6</i>	<i>KLF6</i>	<i>GRK5</i>	<i>GRK5</i>
<i>TGFBR2</i>	<i>TGFBR2</i>	<i>BTG2</i>	<i>BTG2</i>	<i>VWF</i>	<i>VWF</i>
<i>ENG</i>	<i>ENG</i>	<i>SWAP70</i>	<i>SWAP70</i>	<i>MSN</i>	<i>MSN</i>
<i>CDKN1A</i>	<i>CDKN1A</i>	<i>IER2</i>	<i>IER2</i>	<i>ARRDC3</i>	<i>ARRDC3</i>
<i>CYR61</i>	<i>CYR61</i>	<i>CDH5</i>	<i>CDH5</i>	<i>ANXA5</i>	<i>ANXA5</i>
<i>MAFF</i>	<i>MAFF</i>	<i>PTRF</i>	<i>PTRF</i>	<i>RAB31</i>	<i>RAB31</i>
<i>HEG1</i>	<i>HEG1</i>	<i>CTGF</i>	<i>CTGF</i>	<i>GEM</i>	<i>GEM</i>
<i>PECAM1</i>	<i>PECAM1</i>	<i>DAB2</i>	<i>DAB2</i>	<i>NFIL3</i>	<i>NFIL3</i>
<i>SOCS3</i>	<i>SOCS3</i>	---	<b><i>SNF1LK</i></b>	---	<b><i>FAM26B</i></b>
<i>IL1R1</i>	<i>IL1R1</i>	<b><i>TIE1</i><sup>#</sup></b>	<b><i>TIE1</i><sup>#</sup></b>	<i>ETS2</i>	<i>ETS2</i>
<i>ADAMTS1</i>	<i>ADAMTS1</i>	<i>ZCCHC24</i>	<i>ZCCHC24</i>	<i>CXCR7</i>	<i>CXCR7</i>
<i>HBEGF</i>	<i>HBEGF</i>	<i>PMP22</i>	<i>PMP22</i>	<i>IL4R</i>	<i>IL4R</i>
<i>SH2B3</i>	<i>SH2B3</i>	<i>KCTD12</i>	<i>KCTD12</i>	<i>MAP3K8</i>	<i>MAP3K8</i>
<i>SLC2A3</i>	<i>SLC2A3</i>	<i>GNG11</i>	<i>GNG11</i>	<i>PTGER4</i>	<i>PTGER4</i>
---	<b><i>LOC387763</i></b>	<i>ZFP36L1</i>	<i>ZFP36L1</i>	<i>NR4A1</i>	<i>NR4A1</i>
<i>CEBPD</i>	<i>CEBPD</i>	<i>TRAM2</i>	<i>TRAM2</i>	<i>ESAM</i>	<i>ESAM</i>
<i>IGFBP7</i>	<i>IGFBP7</i>	<i>TUBB6</i>	<i>TUBB6</i>	<i>GPR116</i>	<i>GPR116</i>
<i>THBS1</i>	<i>THBS1</i>	<i>PPP1R15A</i>	<i>PPP1R15A</i>	---	<b><i>RAB6IP1</i></b>
<i>PTPRE</i>	<i>PTPRE</i>	<i>PLEKHO2</i>	<i>PLEKHO2</i>	<i>COL4A1</i>	<i>COL4A1</i>
<i>STOM</i>	<i>STOM</i>	<i>HLX</i>	<i>HLX</i>	<i>KLF9</i>	<i>KLF9</i>
<i>DSE</i>	<i>DSE</i>	<i>CEBPB</i>	<i>CEBPB</i>	<i>CALD1</i>	<i>CALD1</i>
<i>TIMP1</i>	<i>TIMP1</i>	<i>FOSB</i>	<i>FOSB</i>	<i>ANXA1</i>	<i>ANXA1</i>
<i>RHOB</i>	<i>RHOB</i>	<i>SNRK</i>	<i>SNRK</i>	<i>PHLDB2</i>	<i>PHLDB2</i>
<i>SGK1</i>	<i>SGK1</i>	<i>DUSP5</i>	<i>DUSP5</i>	<i>CCL2</i>	<i>CCL2</i>
<i>ATF3</i>	<i>ATF3</i>	<i>RGS2</i>	<i>RGS2</i>	<i>SNX9</i>	<i>SNX9</i>
<i>EGR1</i>	<i>EGR1</i>	<i>ERG</i>	<i>ERG</i>		

**Supplementary Table 2:** Analysis steps 2 and 3 using data from the ASAP database on genes selected using expression screening. ASAP microarray data set was analyzed using multivariate analysis (for detailed description of selection see materials and methods and result section). **(a)** Thoracic aorta, **(b)** Mammary artery. #, Query genes; **red** indicates significant correlation with one or more query gene ( $R>0.40$ ) as well as differential expression following FDR 5%; **NA** Probe-set for gene missing. **Correlation coefficients:** Pink boxes indicate significant inverse correlations; blue boxes indicate significant positive correlations.

### (a) Thoracic Aorta

Gene Symbol	KLF2	KLF4	PKD2	THBD	TIE1	Cuspidity
<b>KLF2</b> #	1	0.6	-0.31	0.31	0.26	0.0105
<b>DUSP1</b>	0.12	0.42	0.26	0.18	-0.06	0.623
<b>LATS2</b>	0.33	0.15	0.36	0.37	-0.36	0.595
<b>THBD</b> #	0.31	0.44	-0.05	1	-0.01	0.246
<b>ZFP36</b>	0.38	0.69	-0.46	0.51	0.3	2.22E-05
<b>CD93</b>	0.2	0.41	-0.31	0.68	0.17	0.000794
<b>MCL1</b>	-0.14	0.22	0.34	0.25	-0.12	0.451
<b>EMP1</b>	0.13	0.39	-0.28	0.32	0.38	0.00106
<b>MYADM</b>	-0.05	0.14	0.2	0.53	-0.19	0.501
<b>JUNB</b>	0.47	0.66	-0.32	0.46	0.13	2.60E-05
<b>SERTAD1</b>	0.16	0.33	0.03	0.24	-0.09	0.358
<b>GADD45B</b>	0.14	0.39	-0.21	0.25	0.11	0.0327
<b>FOS</b>	0.43	0.75	-0.31	0.26	0.27	6.31E-05
<b>EPAS1</b>	-0.08	0.1	0.24	0.2	-0.19	0.395
<b>KLF4</b> #	0.6	1	-0.36	0.44	0.35	8.29E-05
<b>CRISPLD2</b>	0.26	0.52	-0.48	0.06	0.62	0.014
<b>TGFBR2</b>	0.02	0.04	0.33	0.41	-0.17	0.321
<b>ENG</b>	0.34	0.32	-0.32	0.48	0.15	0.000117
<b>CDKN1A</b>	0.27	0.5	-0.27	0.23	0.04	0.002
<b>CYR61</b>	0.14	0.1	0.26	0.16	-0.06	0.314
<b>MAFF</b>	0.48	0.3	0.09	0.34	-0.05	0.947
<b>HEG1</b>	-0.22	0.12	0.15	0.39	-0.01	0.853
<b>PECAM1</b>	0.26	0.51	-0.4	0.17	0.5	0.000899
<b>SOCS3</b>	0.49	0.7	-0.6	0.24	0.5	2.84E-07
<b>IL1R1</b>	0.2	0.34	-0.11	0.42	0.02	0.0104
<b>ADAMTS1</b>	0.2	0.22	0.3	0.43	-0.06	0.75
<b>HBEGF</b>	0.1	0.34	-0.08	-0.09	0.35	0.0399
<b>SH2B3</b>	0.6	0.5	-0.57	0.26	0.42	8.03E-07
<b>SLC2A3</b>	0.37	0.66	-0.49	0.39	0.42	6.51E-08
<b>LOC387763</b>						NA
<b>CEBPD</b>	0.58	0.63	-0.44	0.22	0.26	0.000296
<b>IGFBP7</b>	-0.08	-0.1	0.38	0.28	-0.4	0.0438
<b>THBS1</b>	0.21	0.16	-0.14	0.48	0.01	0.00201
<b>PTPRE</b>	0.29	0.5	-0.53	0.29	0.25	4.96E-07

<b>STOM</b>	0.19	0.33	0.07	0.29	0.08	0.153
<b>DSE</b>	-0.05	0.22	-0.1	0.1	0.12	0.00489
<b>TIMP1</b>	0.42	0.27	-0.3	0.36	0.08	0.00329
<b>RHOB</b>	0.04	0.27	0.27	0.14	0.03	0.315
<b>SGK1</b>	0.16	0.47	-0.31	0.29	0.2	0.000461
<b>ATF3</b>	0.21	0.45	-0.04	-0.04	0.18	0.0618
<b>EGR1</b>	0.25	0.57	-0.19	0.5	0.1	0.000777
<b>NID1</b>	-0.01	0.28	-0.16	0.47	0.13	0.00197
<b>LAMC1</b>	-0.33	-0	0.5	0.24	-0.28	0.0354
<b>KLF10</b>	-0.02	0.23	0.09	0.31	-0.21	0.597
<b>TAGLN</b>	0.06	-0.1	0.47	0.05	-0.57	0.0593
<b>ITGA5</b>	0.27	0.37	-0.28	0.47	0.12	9.00E-04
<b>KIAA1754</b>						NA
<b>KIAA0247</b>	0.32	0.39	-0.28	0.51	0.09	5.25E-05
<b>CHSY1</b>	0.4	0.3	-0.16	0.24	0.09	0.124
<b>PICALM</b>	-0.09	0.01	0.23	0.31	-0.09	0.991
<b>CAV1</b>	-0.03	0	0.4	0.03	-0.25	0.0491
<b>CSGALNACT2</b>	-0.06	0.06	0.35	0.02	-0.26	0.859
<b>KIAA1949</b>	0.39	0.47	-0.18	0.36	-0.04	0.107
<b>METRNL</b>	0.15	0.11	-0.22	-0.11	0.08	0.383
<b>ELTD1</b>	0.27	0.52	-0.51	0.16	0.68	3.03E-05
<b>TIMP3</b>	-0.08	0.18	0.03	-0.08	0.1	0.22
<b>KLF6</b>	0.07	0.13	0.26	0.19	-0.11	0.494
<b>BTG2</b>	0.33	0.77	-0.35	0.22	0.35	1.35E-05
<b>SWAP70</b>	0.03	0.15	0.37	0.31	-0.35	0.125
<b>IER2</b>	0.31	0.63	-0.23	0.48	0.26	0.000429
<b>CDH5</b>	0.42	0.47	-0.54	0.22	0.7	2.52E-05
<b>PTRF</b>	0.28	0.2	0.23	0.39	-0.41	0.594
<b>CTGF</b>	-0.02	-0.2	0.49	0.33	-0.25	0.0154
<b>DAB2</b>	0.08	0.42	-0.21	0.44	0.15	0.000298
<b>SNF1LK</b>						NA
<b>TIE1<sup>#</sup></b>	0.26	0.35	-0.51	-0.01	1	0.0333
<b>ZCCHC24</b>	0.37	0.34	-0.16	0.2	0.03	0.0879
<b>PMP22</b>	-0.09	0.2	-0.09	0.27	0.23	0.101
<b>KCTD12</b>	0.16	0.25	-0.13	0.05	0.19	0.193
<b>GNG11</b>	0.15	0.28	-0.01	-0.08	0.06	0.993
<b>ZFP36L1</b>	0.28	0.48	-0.25	0.47	0.11	0.0101
<b>TRAM2</b>	-0.09	0.17	0.21	0.4	-0.24	0.65
<b>TUBB6</b>	0.24	0.19	0.2	0.11	-0.25	0.324
<b>PPP1R15A</b>	0.45	0.49	0.11	0.37	-0.2	0.676
<b>PLEKHO2</b>	0.31	0.55	-0.58	0.37	0.41	6.75E-08
<b>HLX</b>	0.56	0.28	-0.52	-0.01	0.57	0.024
<b>CEBPB</b>	0.39	0.43	-0.36	0.15	0.05	0.000551
<b>FOSB</b>	0.51	0.74	-0.39	0.15	0.35	1.23E-05
<b>SNRK</b>	0.24	0.49	-0.02	0.27	0.26	0.0247
<b>DUSP5</b>	0.64	0.52	-0.49	0.05	0.52	8.17E-05

<b>RGS2</b>	0.23	0.17	-0.01	0.24	-0.06	0.11
<b>ERG</b>	0.2	0	0.51	0.35	-0.45	0.00718
<b>PKD2<sup>#</sup></b>	-0.31	-0.4	1	-0.05	-0.51	7.03E-07
<b>PPAP2B</b>	-0.11	0.07	0.21	0.12	-0.06	0.946
<b>EHD2</b>	0.21	0.29	-0.03	0.54	-0.16	0.502
<b>CRTC3</b>	0.08	0.18	0.22	0.29	-0.28	0.287
<b>COL6A3</b>	0.02	0.36	-0.32	0.44	0.14	9.00E-05
<b>FERMT2</b>	-0.18	-0.2	0.77	-0.05	-0.47	0.000179
<b>FILIP1L</b>	0.1	0	0.25	-0.11	-0.18	0.146
<b>LHFP</b>	0.03	0.07	0.24	0.18	-0.19	0.16
<b>NRP1</b>	0.14	0.37	-0.37	0.33	0.25	0.000259
<b>LAMA4</b>	0.06	0.35	-0.24	0.17	0.27	0.0324
<b>FLI1</b>	0.25	0.46	-0.5	0.22	0.4	3.66E-06
<b>PEA15</b>	-0.05	0.09	0.36	0.02	-0.17	0.132
<b>TGFB111</b>	0.1	0.03	0.41	0.42	-0.38	0.0725
<b>ZEB2</b>	-0.03	0.29	-0.01	0.25	0.01	0.0274
<b>NR4A2</b>	0.31	0.74	-0.17	0.32	0.26	0.057
<b>GRK5</b>	-0.2	-0.2	0.71	0.04	-0.49	8.30E-05
<b>VWF</b>	0.12	0.3	-0.19	0.23	0.54	0.739
<b>MSN</b>	0.2	0.27	0.2	0.63	-0.22	0.985
<b>ARRDC3</b>	-0.04	0.26	-0.07	0.02	0.07	0.0465
<b>ANXA5</b>	-0.28	0	0.46	0.07	-0.29	0.184
<b>RAB31</b>	0.09	0.12	0.04	0.16	-0.09	0.0848
<b>GEM</b>	-0.22	-0.3	0.74	-0.07	-0.51	0.000193
<b>NFIL3</b>	0.13	0.35	0.1	0.01	0.11	0.869
<b>FAM26B</b>						NA
<b>ETS2</b>	0.25	0.17	0.34	0.53	-0.29	0.366
<b>CXCR7</b>	-0.31	0.04	0.21	-0.11	0.16	0.068
<b>IL4R</b>	0.29	0.46	-0.43	0.29	0.23	1.23E-06
<b>MAP3K8</b>	0.25	0.41	-0.12	0.25	0.07	0.0152
<b>PTGER4</b>	0.31	0.42	-0.53	0.21	0.45	1.92E-06
<b>NR4A1</b>	0.42	0.77	-0.22	0.36	0.23	0.0188
<b>ESAM</b>	0.06	0.21	-0.37	0.17	0.24	0.00209
<b>GPR116</b>	0.27	0.48	-0.55	0.26	0.55	1.99E-08
<b>RAB6IP1</b>						NA
<b>COL4A1</b>	-0.07	0.02	0.09	0.3	-0.16	0.976
<b>KLF9</b>	0.05	0.16	0.05	0.15	-0.05	0.259
<b>CALD1</b>	-0.09	0	0.6	0.31	-0.45	0.00108
<b>ANXA1</b>	0.28	0.11	0.21	0.21	-0.25	0.579
<b>PHLDB2</b>	-0.27	0.08	0.49	0.27	-0.39	0.764
<b>CCL2</b>	0.3	0.48	-0.5	0.28	0.23	1.32E-06
<b>SNX9</b>	0	0.17	0.45	0.42	-0.39	0.36

**(b) Mammary Artery**

Gene Symbol	KLF2	KLF4	PKD2	THBD	TIE1	Cuspidity
<i>KLF2</i> <sup>#</sup>	1	0.51	-0.53	0.22	0.29	0.622
<i>DUSP1</i>	0.27	0.43	0.22	0.14	0.02	0.843
<i>LATS2</i>	0.21	0.36	0.22	0.4	0.06	0.261
<i>THBD</i> <sup>#</sup>	0.22	0.32	-0.02	1	0.14	0.006
<i>ZFP36</i>	0.67	0.52	-0.4	0.32	0.36	0.915
<i>CD93</i>	0.03	0.22	0.08	0.73	0.05	0.102
<i>MCL1</i>	-0.37	0.11	0.63	0.04	-0.38	0.11
<i>EMP1</i>	0.07	0.45	-0.13	0.25	0.38	0.992
<i>MYADM</i>	0.29	0.32	0.08	0.58	0.22	0.821
<i>JUNB</i>	0.48	0.49	-0.09	0.13	0.09	0.109
<i>SERTAD1</i>	0.24	0.34	0.04	0.22	0.22	0.982
<i>GADD45B</i>	0.14	0.18	-0.1	0.03	0.28	0.742
<i>FOS</i>	0.5	0.58	-0.16	0.27	0.15	0.57
<i>EPAS1</i>	-0.14	0.05	0.11	0.46	0.18	0.306
<i>KLF4</i> <sup>#</sup>	0.51	1	-0.07	0.32	0.19	0.15
<i>CRISPLD2</i>	0.27	0.36	-0.41	0.12	0.45	0.0923
<i>TGFBR2</i>	-0.21	0.07	0.32	0.22	-0.17	0.677
<i>ENG</i>	0.4	0.25	0.01	0.42	0.01	0.31
<i>CDKN1A</i>	0.38	0.31	-0.05	0.31	0.07	0.623
<i>CYR61</i>	0.26	0.47	0.22	0.31	0.06	0.354
<i>MAFF</i>	0.43	0.3	0.06	0.22	0.06	0.32
<i>HEG1</i>	-0.29	0.16	0.34	0.47	0.11	0.939
<i>PECAM1</i>	-0.11	0.19	-0.04	0.1	0.53	0.497
<i>SOCS3</i>	0.58	0.27	-0.52	0.2	0.25	0.336
<i>IL1R1</i>	-0.18	0.32	0.4	0.27	-0.16	0.947
<i>ADAMTS1</i>	0.09	0.24	0.37	0.28	-0.22	0.196
<i>HBEGF</i>	0.17	0.32	0.02	0.09	0.33	0.71
<i>SH2B3</i>	0.68	0.27	-0.57	0.31	0.28	0.494
<i>SLC2A3</i>	0.18	0.41	0.02	0.22	0.01	0.438
<i>LOC387763</i>	NA			NA		NA
<i>CEBPD</i>	0.41	0.28	-0.56	0.02	0.38	0.217
<i>IGFBP7</i>	0.13	0.16	0.21	0.46	0	0.655
<i>THBS1</i>	-0.05	0.27	0.24	0.39	-0.02	0.00701
<i>PTPRE</i>	0.23	0.35	-0.15	0.5	0.22	0.204
<i>STOM</i>	-0.21	0.24	0.47	0.28	0.17	0.747
<i>DSE</i>	-0.32	0.23	0.52	0.14	-0.18	0.953
<i>TIMP1</i>	0.34	0.27	-0.01	0.48	-0.02	0.0178
<i>RHOB</i>	0.27	0.5	0.17	0.4	0.27	0.914
<i>SGK1</i>	0.03	0.23	0.32	0.09	-0.08	0.523
<i>ATF3</i>	0.16	0.35	0.2	0.15	0.01	0.549
<i>EGR1</i>	0.33	0.54	0.07	0.45	0.01	0.324

<b>NID1</b>	-0.11	0.07	-0.05	0.35	0.36	0.971
<b>LAMC1</b>	-0.31	0.1	0.51	0.42	-0.04	0.595
<b>KLF10</b>	-0.22	0.1	0.18	0.25	0.13	0.923
<b>TAGLN</b>	0.17	0.19	0.06	0.25	0.21	0.792
<b>ITGA5</b>	0.13	0.34	0.06	0.39	0.17	0.00164
<b>KIAA1754</b>	NA			NA		NA
<b>KIAA0247</b>	0.07	0.3	0.22	0.52	-0.03	0.0342
<b>CHSY1</b>	0.38	0.3	-0.09	0.12	0.16	0.375
<b>PICALM</b>	-0.44	-0.06	0.62	0.23	-0.26	0.701
<b>CAV1</b>	-0.35	-0.06	0.31	0.12	0.06	0.302
<b>CSGALNACT2</b>	-0.53	-0.03	0.63	-0.1	-0.37	0.968
<b>KIAA1949</b>	0.01	0.33	0.19	0.19	0	0.425
<b>METRNL</b>	0.53	0.37	-0.32	0.26	0.36	0.949
<b>ELTD1</b>	0.07	0.31	-0.13	0.02	0.17	0.624
<b>TIMP3</b>	0.04	0.25	-0.1	0.29	0.4	0.00325
<b>KLF6</b>	0.19	0.44	0.29	0.36	-0.03	0.303
<b>BTG2</b>	0.18	0.43	-0.03	0.07	0.26	0.158
<b>SWAP70</b>	-0.44	0	0.36	0.27	-0.15	0.633
<b>IER2</b>	0.59	0.54	-0.29	0.27	0.32	0.689
<b>CDH5</b>	0.32	0.32	-0.4	0.22	0.75	0.861
<b>PTRF</b>	0.23	0.28	0.01	0.55	0.18	0.478
<b>CTGF</b>	0.21	0.37	0.2	0.43	0	0.0766
<b>DAB2</b>	-0.09	0.31	0.25	0.3	-0.11	0.346
<b>SNF1LK</b>	NA		NA			NA
<b>TIE1*</b>	0.29	0.19	-0.4	0.14	1	0.338
<b>ZCCHC24</b>	0.3	0.46	-0.2	0.35	0.34	0.273
<b>PMP22</b>	0.06	0.35	-0.07	0.3	0.33	0.242
<b>KCTD12</b>	0.24	0.47	0.06	0.21	0.13	0.364
<b>GNG11</b>	-0.13	0.13	0.15	-0.02	-0.03	0.0833
<b>ZFP36L1</b>	-0.12	0.12	0.07	0.35	0.06	0.0636
<b>TRAM2</b>	-0.27	0.12	0.44	0.29	-0.01	0.688
<b>TUBB6</b>	0.33	0.34	-0.01	0.37	0.24	0.824
<b>PPP1R15A</b>	0.28	0.41	0.17	0.3	0.02	0.478
<b>PLEKHO2</b>	0.41	0.46	-0.31	0.4	0.35	0.985
<b>HLX</b>	0.56	0.16	-0.66	-0.03	0.54	0.0377
<b>CEBPB</b>	0.48	0.28	-0.45	0.16	0.42	0.353
<b>FOSB</b>	0.56	0.48	-0.32	0.03	0.23	0.664
<b>SNRK</b>	-0.43	0.1	0.39	0.05	0.06	0.203
<b>DUSP5</b>	0.69	0.17	-0.59	-0.01	0.41	0.111
<b>RGS2</b>	-0.3	-0.23	0.18	-0.1	-0.4	0.909
<b>ERG</b>	-0.18	0.02	0.5	0.1	-0.47	0.0332
<b>PKD2<sup>#</sup></b>	-0.53	-0.07	1	-0.02	-0.4	0.113
<b>PPAP2B</b>	-0.04	0.22	0.05	0.33	0.29	0.104
<b>EHD2</b>	0.38	0.3	-0.16	0.6	0.28	0.873
<b>CRTC3</b>	0.03	0.17	0.13	0.48	0.13	0.597
<b>COL6A3</b>	0.04	0.38	0.09	0.26	0.06	0.243

<b>FERMT2</b>	-0.56	-0.08	0.66	0.03	-0.23	0.595
<b>FILIP1L</b>	0.01	0.01	0.03	0.01	-0.04	0.0821
<b>LHFP</b>	0.03	0.32	0.18	0.3	0.09	0.277
<b>NRP1</b>	-0.07	0.26	0.14	0.44	0.11	0.592
<b>LAMA4</b>	-0.28	0.17	0.21	0.26	-0.01	0.57
<b>FLI1</b>	0.23	0.48	-0.05	0.28	0.16	0.399
<b>PEA15</b>	-0.09	0.17	0.41	0.13	-0.13	0.574
<b>TGFB11</b>	0.37	0.3	-0.09	0.55	0.3	0.699
<b>ZEB2</b>	-0.46	-0.06	0.31	0.22	-0.07	0.537
<b>NR4A2</b>	0.39	0.33	-0.23	-0.14	0.23	0.23
<b>GRK5</b>	-0.33	0.04	0.53	0.29	-0.13	0.469
<b>VWF</b>	0.18	0.27	-0.18	0.4	0.61	0.0811
<b>MSN</b>	-0.01	0.37	0.37	0.46	-0.04	0.191
<b>ARRDC3</b>	-0.52	-0.11	0.22	-0.18	-0.21	0.178
<b>ANXA5</b>	-0.3	0.17	0.63	0.17	-0.21	0.973
<b>RAB31</b>	-0.28	0.11	0.55	0.28	-0.32	0.469
<b>GEM</b>	-0.19	0.13	0.65	0.11	-0.17	0.475
<b>NFIL3</b>	-0.36	0.03	0.38	-0.03	-0.05	0.0618
<b>FAM26B</b>	NA		NA			NA
<b>ETS2</b>	0.09	0.2	0.32	0.31	-0.11	0.775
<b>CXCR7</b>	0.03	0.34	0.2	0.15	0.05	0.612
<b>IL4R</b>	-0.03	0.23	0.13	0.59	0.12	0.226
<b>MAP3K8</b>	-0.03	0.37	0.39	0.17	-0.2	0.104
<b>PTGER4</b>	0.33	0.23	-0.15	0.37	0.25	0.271
<b>NR4A1</b>	0.6	0.55	-0.25	0.16	0.31	0.813
<b>ESAM</b>	0.06	0.11	0	0.5	0.06	0.244
<b>GPR116</b>	0.01	0.1	-0.25	0.17	0.04	0.722
<b>RAB6IP1</b>	NA		NA			NA
<b>COL4A1</b>	-0.03	0.16	0.25	0.5	0.13	0.256
<b>KLF9</b>	0.42	0.36	-0.18	0.32	0.28	0.59
<b>CALD1</b>	-0.54	-0.12	0.64	0.28	-0.38	0.478
<b>ANXA1</b>	-0.31	0.03	0.45	0.11	-0.4	0.223
<b>PHLDB2</b>	-0.62	-0.19	0.56	0.14	-0.36	0.326
<b>CCL2</b>	0.07	0.25	-0.05	0.33	-0.12	0.436
<b>SNX9</b>	-0.37	0.11	0.64	0.35	-0.27	0.707



**Supplementary table 3:** Genes differentially expressed between BAV and TAV (same as table 1 but with references)

Gene	Flow	Function(s) and properties
<b>ZFP36L1</b>	X* <sup>4</sup> (6)	Zinc finger protein, modulation and destabilization VEGF mRNA (7), <b>wound healing</b> (8)
<b>ZFP36</b>	X* <sup>4</sup> (6)	Modulation and destabilisation VEGF mRNA (9), <b>wound healing</b> (10)
<b>FLI1</b>	X (11)	<b>Angiogenesis</b> , maturation and stabilization of vessels (12), <b>wound healing</b> (13)
<b>EGR1</b>	X (14)	Regulates angiopoietin-1 induced EC migration and proliferation (15), <b>wound healing</b> (10)
<b>IER2</b>	X* <sup>4</sup> (6)	Mediates EGF-dependent left-right asymmetry patterning in zebrafish (16)
<b>SLC2A3</b>	X* <sup>4</sup> (6)	Involved in tumor <b>angiogenesis</b> (17)
<b>FOSB</b>	X (18)	Induced by mechanical stress and cardiac ischemia (19) and VEGF (20), <b>wound healing</b> (21)
<b>TIMP1</b>	X (22)	<b>Anti-angiogenesis</b> (23), <b>wound healing</b> (24)
<b>GRK5</b>	X (25)	Regulation of vasoconstriction in VSMC (26), histone deacetylase (HDAC) kinase in cardiomyocytes (27)
<b>CCL2</b>	X (28)	Involved in neovascularization and <b>angiogenesis</b> (29), <b>wound healing</b> (30)
<b>NID1</b>	X (31)	Ingredient of vascular basement membranes (32), <b>wound healing</b> (33)
<b>ITGA5</b>	X (34)	Fibronectin receptor (35)
<b>SOCS3</b>	X (36)	Negative regulator of cytokines (37), <b>wound healing</b> (38)
<b>FOS</b>	X (14)	Regulation of VEGF, <b>angiogenesis</b> (39), <b>wound healing</b> (21)
<b>KLF2<sup>#</sup></b>	X (40)	Regulates VEGFA, <b>angiogenesis</b> (41)
<b>BTG2</b>	X (36)	Anti-proliferative transcription factor (42), involved in modulation of VEGF regulated <b>wound repair</b> (43)
<b>SGK1</b>	X (44)	Involved in vascular remodelling during <b>angiogenesis</b> (45), <b>wound healing</b> (46)
<b>PLEKHO2</b>	?	No functional studies performed according to PubMed
<b>PTGER4</b>	X (36)	Mediates Prostaglandin E2 stimulated <b>VEGF</b> expression, <b>angiogenesis</b> (47), <b>wound healing</b> (48)
<b>COL6A3</b>	X* <sup>2</sup> (49)	ECM component, regulated by TGFβ (50)
<b>FERMT2</b>	?	<b>Wound healing</b> (51), regulated by TGF-β1 (52), <b>angiogenesis</b> (53)
<b>IL1R1</b>	X (44)	<b>Wound healing</b> (54)
<b>PKD2<sup>#</sup></b>	X (55)	Ca <sup>2+</sup> - permeable channel of cilia (55), embryonic left-right asymmetry (56), <b>wound healing</b> (57)

<b>GEM</b>	X (58)	Regulation of voltage-gated Ca <sup>2+</sup> - channel (59)
<b>DAB2</b>	X* <sup>2</sup> (49)	Embryonic <b>angiogenesis</b> via VEGF induction (60), TGFβ stimulated fibronectin synthesis in <b>wound healing</b> (61)
<b>GPR116</b>	X* <sup>2</sup> (49)	Specifically expressed in the microvasculature (62)
<b>DUSP5</b>	X (63)	strongly induced by VEGF in EC (64), EC specific in vessels development (65)
<b>CEBPB</b>	?	It interacts directly with subunits of NFκB to augment gene expression by FOS multimeric transcription factors (66)
<b>KLF4<sup>#</sup></b>	X (6)	Modulates phenotype of VSMCs (67), <b>angiogenesis</b> (68), <b>wound healing</b> (69)
<b>SH2B3</b>	?	Stabilization of thrombi within vessels (70), regulates EPC kinetics in vascular regeneration (71)
<b>JUNB</b>	X (36)	Regulates VEGF expression in an NFκB dependent manner (72), <b>angiogenesis</b> , <b>wound healing</b> (21)
<b>CDH5</b>	X (73)	Ingredient of shear stress sensor complex, <b>angiogenesis</b> (74), EC specific in vessels development (65)
<b>CD93</b>	X* <sup>2</sup> (49)	Vascular remodelling and <b>angiogenesis</b> (75)
<b>CDKN1A</b>	X (34)	Involved in regulation of EC senescence and permeability (76), <b>wound healing</b> (77)
<b>PTPRE</b>	X (25)	Negative regulation of EC proliferation, possible role in <b>angiogenesis</b> (78)
<b>CALD1</b>	X* <sup>2</sup> (49)	Cytoskeletal protein <b>anti-angiogenesis</b> (79), implicated in the migration of EPC (80)
<b>ERG</b>	X* <sup>2</sup> (81)	<b>Angiogenesis</b> (12), <b>wound healing</b> through regulation of ECM (82)
<b>ELTD1</b>	X* <sup>4</sup> (6)	Specifically expressed in the microvasculature (62)
<b>ENG</b>	X (83)	Vascular TGFβ co-receptor, <b>angiogenesis</b> (84), <b>wound healing</b> (85)
<b>PECAM1</b>	X (73)	Ingredient of shear stress sensor complex, <b>Angiogenesis</b> (86), <b>wound healing</b> (87)
<b>CEBPD</b>	X* <sup>4</sup> (6)	It interacts directly with subunits of NFκB to augment gene expression by FOS multimeric transcription factors (66)
<b>THBS1</b>	X (34)	<b>Anti-angiogenesis</b> (88), <b>wound healing</b> (89)
<b>KIAA0247</b>	?	Regulator of cell cycle (90)
<b>IL4R</b>	X (36)	IL4 receptor, IL4 has been indicated in both promoting (91) and blocking (92) <b>angiogenesis</b>

(X) Induced by shear stress according to the literature; (X\*<sup>2</sup>) by KLF2 or (X\*<sup>4</sup>) KLF4 over-expression (extracted from literature search); (?) Not cited in the literature. #; query genes.

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