

Supplementary materials for

# Unraveling the divergent gene expression profiles in bicuspid and tricuspid aortic valve patients with thoracic aortic aneurysm – the ASAP study

*The supplemental materials can be printed, but several pages contain high-resolution small text sizes meant only to be read using electronic zoom on the pdf-file.*

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## Detailed Supplementary Methods

### *Sample collection*

The Advanced Study of Aortic Pathology (ASAP) biobank was generated after written informed consent from all participants had been obtained according to the declaration of Helsinki and with approval by the ethics committee of the Karolinska Institute (application number 2006/784-31/1). The study included patients undergoing aortic valve surgery and / or surgery for aortic aneurysm at the Karolinska University Hospital, Stockholm, Sweden, starting from February 13<sup>th</sup> 2007. Patients with significant coronary artery disease according to angiography and patients with Marfan syndrome were excluded. Of the patients invited to participate, 68% accepted amongst a total of 413 patients. In the 300 patients who have completed one-year follow up, 30-day mortality was 1.67% and 1-year mortality was 2.33%.

Patients were classified as having either BAV or TAV and as having either dilated or non-dilated thoracic aorta. The criteria for the latter were >45 mm (dilated) and < 40 mm (non-dilated), respectively. Measurements of the end-diastolic diameter of the thoracic aorta were made during anesthesia at the point of the aorta showing maximal dilation using transesophageal echocardiography.

Biopsies were obtained at surgery from mammary artery and dilated and non-dilated ascending aorta. The intima-medial and adventitial layers of the vascular specimens were isolated by adventicectomy, incubated with RNAlater (Ambion, Austin, TX) and homogenized with a FastPrep using Lysing Matrix D tubes (MP Biomedicals, Germany). Aortic biopsies were taken from the anterior (convex) part of the aorta, i.e. the site of aortotomy a few cm above the aortic valve.

The transplant control samples of normal walls of the thoracic aorta were obtained from deceased subjects at the time of organ collection for heart/lung transplantation after authorization from the French National Biomedicine Agency. Frozen biopsies were shipped to Sweden and RNA was purified following the same protocol as for the patient samples.

### *Expression analysis*

Total RNA was isolated using Trizol (BRL-Life Technologies) and RNeasy Mini kit (Qiagen, Crawley, UK) including treatment with RNase-free DNase set (Qiagen) according to manufacturer's instructions. The quality of RNA was analyzed with an Agilent 2100 bioanalyzer (Agilent, Santa Clara, CA) (RNA integrity numbers (RIN) of  $7.1 \pm 0.6$ ) and quantity was measured by a NanoDrop (Thermo Scientific, Waltham, MA), excluding samples of low quality.

A total of 345 RNA samples were analyzed using expression microarrays: aortic intima-media from patients ( $n = 131$ ), aortic adventitia from patients ( $n = 113$ ), mammary artery intima-media from patients ( $n = 88$ ), transplant control aortic intima-media ( $n = 13$ ). There was a considerable overlap of individuals in the patient groups, but no overlap with the transplant control donors: Altogether, microarray data from 192 different individuals has been included in the study. All samples were hybridized and scanned at the Karolinska Institute gene expression core facility using Affymetrix GeneChip® Human Exon 1.0 ST arrays and protocols. All obtained *cel* files were pre-processed together using Robust Multichip Average (RMA) normalization<sup>1</sup> as implemented in the Affymetrix Power Tools 1.10.2 package apt-probeset-summarize. Image files of raw data were manually inspected for scratches. Plots of normalized signal intensities showed that no sample was noticeably deviating from the rest. The core set of meta probe sets were used in the analysis. All expression measurements were log<sub>2</sub> transformed as part of the RMA normalization. Expression of sex specific transcripts were checked for concordance with database-registered sex and found to

match for all samples. Sex specific transcripts were also used to estimate a lower boundary of detectable expression; by highlighting the expression of Y-chromosome genes in female samples in the overall distribution of gene expression we estimated a cutoff of 5.5 expression units, below which no gene is included in analysis (Supplementary S1).

Microarray results from aortic intima-media were confirmed using real-time PCR on a partially independent sample set of 171 samples (127 overlap with microarray cohort). TaqMan probes and primers were purchased as assay-on-demand and run on a 7900 HT fast real-time PCR system (Applied Biosystems). Data was analyzed according to the  $\Delta\Delta C_t$  method normalizing against the total RNA concentration as previously described<sup>2,3</sup>.

### ***Statistics***

All two-sample comparisons reported were performed using a two-sided Student's t-test, assuming unequal variance. Raw P-values are always reported. Multiple testing adjustment of significance thresholds were done using a false discovery rate (FDR) of 5%, as calculated using the *qvalue* Bioconductor package with default settings<sup>4</sup>. Summarized values are reported as mean  $\pm$  SD unless otherwise specified. Principal component analysis (PCA) was performed using the *made4* Bioconductor package with mean centering unit variance scaling, and no column weighting<sup>5</sup>. For gene set enrichment analysis the GAGE-algorithm was used<sup>6</sup>, based on all functional groupings of genes defined by the gene ontology (GO) consortium<sup>7</sup>. Default settings were used, except *same.dir* which was set to false and *compare* which was set to *as.group*. All calculations and plots were performed with R 2.11.0 and Bioconductor 2.6.<sup>8</sup>.

### ***Immunohistochemistry***

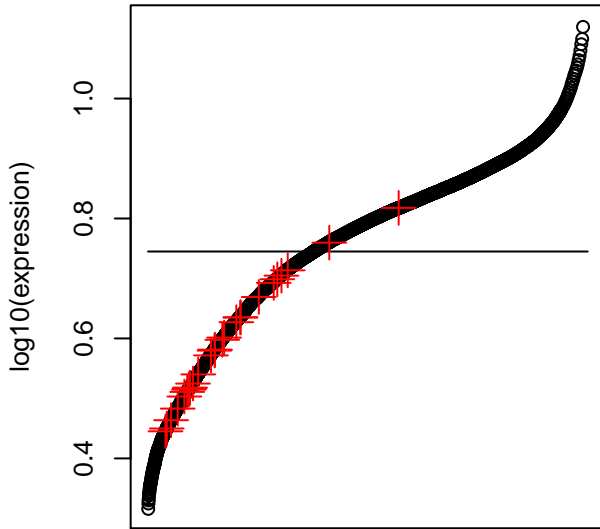
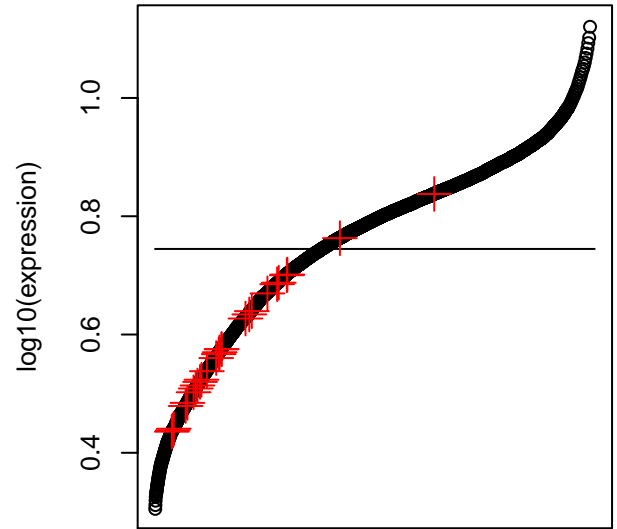
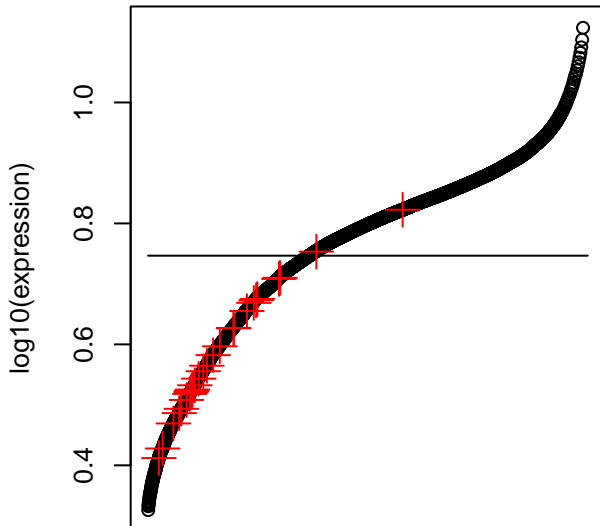
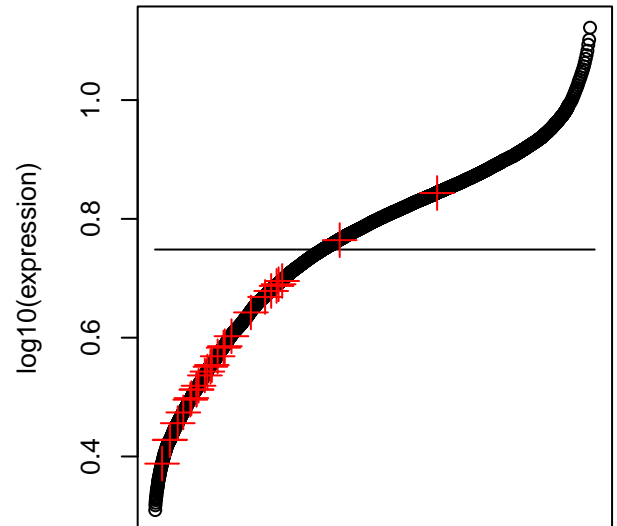
Serial sections (5  $\mu$ m) of paraffin embedded thoracic aortas were immunohistochemically stained using a standard protocol. Briefly, serial sections (5  $\mu$ m) were stained for CD4 (goat anti-human, R&D Systems, 1:100), CD68 (mouse anti-human, Leica Microsystems, Newcastle, UK, 1:100) and CD163 (mouse anti-human, Acris, Herford, Germany, 1:100) over night at +4°C. The sections were then incubated with biotinylated secondary goat anti-mouse antibody or horse anti-goat (Vector Laboratories, 1:1500) for 30 minutes, followed by avidin-biotin peroxidase complexes (ABC, Vector Laboratories) for 30 minutes and 3,3'-diaminobenzidine tetrahydrochloride (DAB, Vector Laboratories) for 2 minutes. Nucleus staining was performed with Hematoxylin QS (Vector Laboratories).

## Supplemental References

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**Distribution of all gene expression levels**

Horizontal line indicates a cutoff at 5.5 intensity, red marks indicate Y-chromosome genes in female arrays

**Aortic intima-media****Mammary artery intima-media****Aortic adventitia****Transplant control**

## Gene set enrichment comparisons of BAV vs. TAV patients

Gene ontology	BAV vs. TAV				Set size
	Aorta intima-media		Aorta adventitia		
	Dilated	Non-dilated	Dilated	Non-dilated	
Cell adhesion	**		.		180
Extracellular region	***	**	**		457
Extracellular space	***	.	.		198
Immune response	**	*			85
Inflammatory response	*				58
Integral to plasma membrane	**				315

## Gene set enrichment comparisons of non-dilated vs. dilated patients

Gene ontology	Non-dilated vs. dilated				Set size
	Aorta intima-media		Aorta adventitia		
	TAV	BAV	TAV	BAV	
Cell adhesion	*	**	*	*	180
Extracellular region	***	**	**	***	457
Extracellular space	*	*	*	**	198
Immune response				**	85
Integral to plasma membrane	.			*	315

All GO gene sets with significant association to dilation, stratified by aorta tissue type and cuspidity of patient. All GO gene sets with association  $P < 0.05$  in any of the four stratifications are included. The following P-values are marked: .  $< 0.1$ , \*  $< 0.05$ , \*\*  $< 0.005$ , \*\*\*  $< 0.0005$ . All P-values are calculated using the GAGE algorithm and Benjamini-Hochberg multiple testing corrected values are reported. For any pairwise comparison, the significance reflects the number of differentially expressed genes in a specific GO set relative to the total number of genes that are differentially expressed in this comparison. This is illustrated for the two gene sets *extracellular region* and *immune response* in figure 4.



## aorta intima-media, only dilated patients, comparing BAV and TAV, for all genes

meta probeset ID	genesymbol	genename	p-value	fold-change	log2(BAV)	log2(TAV)
2591421	TFPI	tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)	4.26E-08	-1.93	7.08±0.61	8.03±0.55
2608419	SETMAR	SET domain and mariner transposase fusion gene	7.35E-08	1.25	6.86±0.24	6.53±0.19
2881370	CD74	CD74 molecule, major histocompatibility complex, class II invariant chain	9.19E-08	-3.76	8.42±1.3	10.3±1.1
3101681	C8orf46	chromosome 8 open reading frame 46	9.41E-08	1.24	6.07±0.2	5.77±0.19
2903189	HLA-DRA	major histocompatibility complex, class II, DR alpha	1.13E-07	-4.35	8.47±1.5	10.6±1.3
2950329	HLA-DPA1	major histocompatibility complex, class II, DP alpha 1	1.15E-07	-4.07	8.66±1.4	10.7±1.2
3512874	LCP1	lymphocyte cytosolic protein 1 (L-plastin)	1.36E-07	-3.93	6.27±1.1	8.24±1.3
2777447	NAP1L5	nucleosome assembly protein 1-like 5	1.51E-07	1.43	7.28±0.28	6.77±0.33
3340449	SLCO2B1	solute carrier organic anion transporter family, member 2B1	1.91E-07	-2.72	6.07±0.66	7.51±0.95
2878437	CD14	CD14 molecule	2.66E-07	-3.53	7.12±0.92	8.94±1.2
2514969	GAD1	glutamate decarboxylase 1 (brain, 67kDa)	3.42E-07	1.68	6.04±0.37	5.29±0.5
2669979	CX3CR1	chemokine (C-X3-C motif) receptor 1	3.48E-07	-3.96	5.98±0.96	7.96±1.3
3256590	PAPSS2	3'-phosphoadenosine 5'-phosphosulfate synthase 2	3.62E-07	-1.73	6.42±0.44	7.2±0.53
3456840	PPP1R1A	protein phosphatase 1, regulatory (inhibitor) subunit 1A	3.73E-07	1.37	5.95±0.4	5.49±0.26
3973839	CYBB	cytochrome b-245, beta polypeptide	3.81E-07	-3.81	7.23±1.1	9.16±1.3
2578028	CXCR4	chemokine (C-X-C motif) receptor 4	3.96E-07	-3.76	5.31±0.79	7.22±1.3
3442941	C3AR1	complement component 3a receptor 1	4.01E-07	-3.51	5.99±0.95	7.81±1.2
2386943	ACTN2	actinin, alpha 2	4.42E-07	1.8	6.99±0.53	6.15±0.56
2440943	FCGR3A	Fc fragment of IgG, low affinity IIIa, receptor (CD16a)	5.01E-07	-3.61	6.28±0.93	8.13±1.3
3381241	ARAP1	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 1	5.02E-07	-1.2	7.26±0.18	7.52±0.17
2320188	ANGPTL7	angiopoietin-like 7	5.33E-07	2.26	6.59±0.75	5.42±0.79
2345239	LOC339524	hypothetical LOC339524	6.16E-07	1.22	5.88±0.18	5.59±0.19
2805232	PDZD2	PDZ domain containing 2	6.28E-07	1.47	5.62±0.35	5.06±0.38
3516228	PCDH20	protocadherin 20	7.37E-07	1.79	5.43±0.7	4.6±0.52
3416577	NCKAP1L	NCK-associated protein 1-like	7.47E-07	-2.87	5.09±0.64	6.62±1.1
2351572	CD53	CD53 molecule	7.58E-07	-3.86	6.47±1	8.41±1.4
2362991	CASQ1	calsequestrin 1 (fast-twitch, skeletal muscle)	8.08E-07	1.5	5.93±0.47	5.34±0.38
3672489	IRF8	interferon regulatory factor 8	8.12E-07	-2.46	5.9±0.51	7.2±0.93
2404158	LAPTM5	lysosomal multispinning membrane protein 5	8.55E-07	-4.16	7.57±1.2	9.63±1.4
2950277	HLA-DMA	major histocompatibility complex, class II, DM alpha	9.06E-07	-2.55	6.35±0.57	7.7±0.97
3904691	SAMHD1	SAM domain and HD domain 1	9.44E-07	-1.98	7.57±0.66	8.55±0.68
3969081	TLR7	toll-like receptor 7	9.78E-07	-2.48	5.18±0.54	6.5±0.95
2411799	BEND5	BEN domain containing 5	1.19E-06	1.4	6.53±0.27	6.04±0.35
2602770	DNER	delta/notch-like EGF repeat containing	1.24E-06	1.48	6.39±0.24	5.82±0.42
3860137	TYROBP	TYRO protein tyrosine kinase binding protein	1.39E-06	-3	7.51±0.71	9.09±1.2
3862188	FCGBP	Fc fragment of IgG binding protein	1.40E-06	-2.84	6.87±0.83	8.38±1.1
2324873	C1QC	complement component 1, q subcomponent, C chain	1.43E-06	-3.07	6.58±0.85	8.2±1.2
3866276	SLC1A5	solute carrier family 1 (neutral amino acid transporter), member 5	1.48E-06	-1.37	5.81±0.24	6.27±0.33
4011008	VSIG4	V-set and immunoglobulin domain containing 4	1.51E-06	-2.91	6.18±0.67	7.72±1.1
3555340	TEP1	telomerase-associated protein 1	1.52E-06	-1.16	7.02±0.14	7.23±0.15
3442706	CD163	CD163 molecule	1.56E-06	-3.57	5.55±0.89	7.38±1.4
2732844	ANXA3	annexin A3	1.57E-06	2.06	7.46±0.68	6.41±0.75
2950263	HLA-DMB	major histocompatibility complex, class II, DM beta	1.78E-06	-3.14	5.34±0.8	6.99±1.2
3385769	CTSC	cathepsin C	1.78E-06	-2.51	6.45±0.6	7.77±0.99
3659966	ADCY7	adenylate cyclase 7	1.87E-06	-1.51	6.37±0.25	6.96±0.44
3753500	SLFN11	schlafen family member 11	1.87E-06	-1.43	7.17±0.38	7.69±0.37
2354634	PHGDH	phosphoglycerate dehydrogenase	1.93E-06	1.51	7.98±0.35	7.38±0.44
2881187	CSF1R	colony stimulating factor 1 receptor	1.93E-06	-2.45	6.04±0.51	7.33±0.97
2363689	FCGR2A	Fc fragment of IgG, low affinity IIa, receptor (CD32)	2.01E-06	-3.6	7±1.2	8.85±1.4
2902427	LST1	leukocyte specific transcript 1	2.41E-06	-1.48	6.52±0.24	7.08±0.43
2903401	HLA-DPB1	major histocompatibility complex, class II, DP beta 1	2.43E-06	-3.23	7.8±0.87	9.49±1.3
3484060	ALOX5AP	arachidonate 5-lipoxygenase-activating protein	2.62E-06	-3.23	6.4±0.77	8.09±1.3
2736462	BMPR1B	bone morphogenetic protein receptor, type IB	2.74E-06	2.21	7.88±0.51	6.73±0.88
2940202	F13A1	coagulation factor XIII, A1 polypeptide	2.74E-06	-4.56	6.27±1.4	8.46±1.6
3870824	LAIR1	leukocyte-associated immunoglobulin-like receptor 1	2.75E-06	-2.59	6.07±0.5	7.45±1.1
3300749	RBP4	retinol binding protein 4, plasma	2.84E-06	1.97	7.11±0.57	6.13±0.74
3716950	ADAP2	ArfGAP with dual PH domains 2	2.98E-06	-1.99	6.07±0.43	7.06±0.77
3351166	IL10RA	interleukin 10 receptor, alpha	3.00E-06	-2.12	5.86±0.45	6.95±0.84
2357845	FCGR1B	Fc fragment of IgG, high affinity Ib, receptor (CD64)	3.18E-06	-3.25	5.02±0.58	6.72±1.3
2792166	MARCH1	membrane-associated ring finger (C3HC4) 1	3.28E-06	-3.19	4.98±0.83	6.65±1.3
3752258	EVI2B	ecotropic viral integration site 2B	3.39E-06	-3.5	4.44±0.72	6.24±1.4
3177880	DAPK1	death-associated protein kinase 1	3.40E-06	-1.69	6.7±0.5	7.45±0.57
2373842	PTPRC	protein tyrosine phosphatase, receptor type, C	3.57E-06	-3.36	4.62±0.71	6.37±1.4
2567167	LONRF2	LON peptidase N-terminal domain and ring finger 2	3.79E-06	1.93	7.2±0.35	6.25±0.75
3851545	MAN2B1	mannosidase, alpha, class 2B, member 1	3.81E-06	-1.47	7.25±0.25	7.81±0.44
3788097	MAPK4	mitogen-activated protein kinase 4	3.88E-06	1.28	5.73±0.3	5.38±0.25
3374934	MS4A6A	membrane-spanning 4-domains, subfamily A, member 6A	4.42E-06	-2.97	5.89±0.88	7.46±1.2
3712062	TRPV2	transient receptor potential cation channel, subfamily V, member 2	4.42E-06	-1.41	5.64±0.17	6.13±0.39
3944690	CYTH4	cytohesin 4	4.42E-06	-2.03	6.19±0.37	7.21±0.81
2922215	MARCKS	myristoylated alanine-rich protein kinase C substrate	4.52E-06	-1.84	8.61±0.47	9.5±0.69
3655986	CORO1A	coronin, actin binding protein, 1A	4.57E-06	-1.97	6.46±0.38	7.44±0.78
2496382	NPAS2	neuronal PAS domain protein 2	4.58E-06	1.33	6.45±0.32	6.04±0.3
3527662	RNASE6	ribonuclease, RNase A family, k6	4.65E-06	-2.5	4.95±0.52	6.28±1.1
2794006	SCRG1	scrapie responsive protein 1	4.66E-06	1.89	7.42±0.46	6.5±0.73
3339382	FOLR2	folate receptor 2 (fetal)	5.15E-06	-2.12	6.97±0.59	8.06±0.86
3127199	DOK2	docking protein 2, 56kDa	5.26E-06	-1.39	6±0.28	6.47±0.37
3454006	FMNL3	formin-like 3	5.49E-06	-1.55	7.04±0.54	7.67±0.46
3125571	MSR1	macrophage scavenger receptor 1	5.78E-06	-3.46	5.23±1	7.03±1.4
3222534	ASTN2	astrotactin 2	5.94E-06	1.21	5.94±0.27	5.66±0.19
2773545	BTC	betacellulin	6.53E-06	1.48	5.48±0.43	4.91±0.43
3178952	SYK	spleen tyrosine kinase	6.80E-06	-2.16	5.59±0.32	6.7±0.91
3861948	GMFG	glia maturation factor, gamma	6.96E-06	-2.58	6.06±0.52	7.42±1.1
3402786	CD4	CD4 molecule	7.11E-06	-2	6.4±0.43	7.41±0.82
3839920	FPR3	formyl peptide receptor 3	7.23E-06	-2.61	5.55±0.76	6.93±1.1
3923702	TRPM2	transient receptor potential cation channel, subfamily M, member 2	7.30E-06	-1.25	6.01±0.21	6.34±0.26
3458551	ARHGAP9	Rho GTPase activating protein 9	7.34E-06	-1.27	5.4±0.17	5.74±0.28
3301914	PIK3AP1	phosphoinositide-3-kinase adaptor protein 1	7.51E-06	-1.93	5.81±0.36	6.76±0.78
2883349	HAVCR2	hepatitis A virus cellular receptor 2	7.59E-06	-1.96	5.16±0.38	6.13±0.8
2817212	BHMT	betaine-homocysteine methyltransferase	7.62E-06	1.45	7.68±0.38	7.15±0.42
3722917	GRN	granulin	7.64E-06	-1.49	9.46±0.4	10±0.45
2324856	C1QA	complement component 1, q subcomponent, A chain	8.01E-06	-2.55	5.88±0.66	7.23±1.1
3934729	ITGB2	integrin, beta 2 (complement component 3 receptor 3 and 4 subunit)	8.22E-06	-2.07	6.82±0.52	7.87±0.87
3619326	PLCB2	phospholipase C, beta 2	8.33E-06	-1.56	5.32±0.2	5.96±0.53
3403092	PTPN6	protein tyrosine phosphatase, non-receptor type 6	8.53E-06	-1.63	5.97±0.24	6.67±0.59
2324884	C1QB	complement component 1, q subcomponent, B chain	8.54E-06	-2.3	6.84±0.51	8.04±1
2518272	CERKL	ceramide kinase-like	8.56E-06	-2.51	4.96±0.49	6.29±1.1
2966193	C6orf168	chromosome 6 open reading frame 168	8.59E-06	1.47	6.29±0.31	5.73±0.46
2925953	ENPP1	ectonucleotide pyrophosphatase/phosphodiesterase 1	8.62E-06	1.95	8.78±0.44	7.82±0.8
2570350	LOC151009	hypothetical LOC151009	8.63E-06	1.8	6.81±0.59	5.96±0.68
2417362	DIRAS3	DIRAS family, GTP-binding RAS-like 3	8.92E-06	1.47	6.36±0.36	5.8±0.45
3098977	LYN	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	8.99E-06	-1.92	5.88±0.38	6.82±0.78
3853453	RASAL3	RAS protein activator like 3	9.00E-06	-1.25	6.45±0.22	6.78±0.26
2886595	LCP2	lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte protein of 76kDa)	9.06E-06	-2.05	5.91±0.37	6.94±0.86

meta probeset ID	genesymbol	genename	p-value	fold-change	log2(BAV)	log2(TAV)
2961347	FILIP1	filamin A interacting protein 1	9.35E-06	1.48	8.51±0.46	7.94±0.44
3335465	SIPA1	signal-induced proliferation-associated 1	9.85E-06	-1.25	6.16±0.19	6.49±0.27
3286602	CXCL12	chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1)	9.96E-06	-1.78	8.57±0.8	9.4±0.59
3678186	C16orf5	chromosome 16 open reading frame 5	1.02E-05	1.23	6.94±0.25	6.64±0.23
2563785	IGKC	immunoglobulin kappa constant	1.04E-05	-7.5	5.72±0.91	8.63±2.5
2623922	STAB1	stabilin 1	1.10E-05	-1.78	6.6±0.37	7.43±0.7
2376849	RASSF5	Ras association (RalGDS/AF-6) domain family member 5	1.18E-05	-1.38	5.95±0.18	6.41±0.39
3742285	CXCL16	chemokine (C-X-C motif) ligand 16	1.19E-05	-2.09	6.34±0.52	7.4±0.9
3073267	PLXNA4	plexin A4	1.19E-05	1.36	6.05±0.38	5.6±0.34
2656837	ST6GAL1	ST6 beta-galactosamide alpha-2,6-sialyltransferase 1	1.21E-05	-1.43	7.77±0.47	8.29±0.39
3608787	SLCO3A1	solute carrier organic anion transporter family, member 3A1	1.21E-05	-1.24	7.47±0.23	7.79±0.26
2429556	CASQ2	calsequestrin 2 (cardiac muscle)	1.24E-05	2.37	8.81±0.97	7.56±0.99
2973694	ARHGAP18	Rho GTPase activating protein 18	1.30E-05	-1.77	6.55±0.59	7.37±0.67
3382698	LRRC32	leucine rich repeat containing 32	1.33E-05	-1.7	8.44±0.7	9.2±0.58
3654175	IL4R	interleukin 4 receptor	1.34E-05	-1.61	6.5±0.35	7.19±0.59
2834282	STK32A	serine/threonine kinase 32A	1.35E-05	1.75	7.19±0.37	6.38±0.69
2491661	VAMP8	vesicle-associated membrane protein 8 (endobrevin)	1.36E-05	-2.7	6.53±0.7	7.97±1.2
2855058	OXCT1	3-oxoacid CoA transferase 1	1.36E-05	1.43	8.23±0.38	7.72±0.42
2462160	NID1	nidogen 1	1.37E-05	-1.32	6.89±0.3	7.3±0.33
3843525	ZNF586	zinc finger protein 586	1.42E-05	-1.23	5.69±0.27	5.99±0.23
3421511	LYZ	lysozyme (renal amyloidosis)	1.43E-05	-5.3	5.12±1.3	7.53±2
2974935	SLC2A12	solute carrier family 2 (facilitated glucose transporter), member 12	1.43E-05	1.54	7.36±0.34	6.73±0.53
3525498	RAB20	RAB20, member RAS oncogene family	1.55E-05	-1.21	6.38±0.22	6.66±0.22
3153428	ASAP1	ArfGAP with SH3 domain, ankyrin repeat and PH domain 1	1.55E-05	-1.49	7.2±0.43	7.77±0.47
3321512	PDE3B	phosphodiesterase 3B, cGMP-inhibited	1.55E-05	1.51	6.48±0.44	5.88±0.49
3830993	HCST	hematopoietic cell signal transducer	1.58E-05	-2.14	5.65±0.42	6.74±0.95
2434575	CTSS	cathepsin S	1.59E-05	-3.13	5.56±0.85	7.21±1.4
2793401	MFAP3L	microfibrillar-associated protein 3-like	1.60E-05	1.37	5.86±0.39	5.41±0.36
3608427	FES	feline sarcoma oncogene	1.68E-05	-1.12	5.64±0.11	5.8±0.14
3142217	PAG1	phosphoprotein associated with glycosphingolipid microdomains 1	1.69E-05	-1.91	5.26±0.29	6.2±0.82
2772566	IGJ	immunoglobulin J polypeptide, linker protein for immunoglobulin alpha and mu polypeptides	1.71E-05	-8.19	4.22±1.2	7.25±2.7
3881651	HCK	hemopoietic cell kinase	1.72E-05	-1.73	6.0±0.2	6.79±0.69
2351854	C1orf162	chromosome 1 open reading frame 162	1.73E-05	-2.22	6.07±0.53	7.22±1
3707095	ARRB2	arrestin, beta 2	1.74E-05	-1.64	6.84±0.26	7.56±0.63
3458400	NDUFA4L2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4-like 2	1.77E-05	-2.19	6.79±0.69	7.92±0.97
3731826	PRKCA	protein kinase C, alpha	1.81E-05	-1.49	5.54±0.33	6.12±0.5
3573152	SPTLC2	serine palmitoyltransferase, long chain base subunit 2	1.85E-05	-1.33	7.0±0.25	7.4±0.35
3572209	PGF	placental growth factor	1.92E-05	-1.66	5.91±0.44	6.65±0.63
3031533	GIMAP4	GTPase, iMAP family member 4	1.94E-05	-2.21	4.71±0.42	5.86±1
2381177	MARK1	MAP/microtubule affinity-regulating kinase 1	1.98E-05	1.39	6.63±0.35	6.16±0.4
3268059	TACC2	transforming, acidic coiled-coil containing protein 2	2.01E-05	1.48	7.52±0.35	6.96±0.48
3439178	PXMP2	peroxisomal membrane protein 2, 22kDa	2.03E-05	1.3	8.03±0.28	7.66±0.31
3942838	LIMK2	LIM domain kinase 2	2.07E-05	-1.27	6.77±0.17	7.12±0.3
2696040	RAB6B	RAB6B, member RAS oncogene family	2.08E-05	1.2	5.68±0.2	5.42±0.22
3286776	C10orf10	chromosome 10 open reading frame 10	2.14E-05	-1.93	7.8±0.59	8.75±0.82
3354443	SLC37A2	solute carrier family 37 (glycerol-3-phosphate transporter), member 2	2.25E-05	-1.54	5.45±0.29	6.07±0.55
2716328	ADRA2C	adrenergic, alpha-2C, receptor	2.31E-05	1.39	7.97±0.38	7.49±0.39
3431892	SH2B3	SH2B adaptor protein 3	2.39E-05	-1.26	6.66±0.22	6.99±0.29
3131741	RAB11FIP1	RAB11 family interacting protein 1 (class I)	2.41E-05	-1.33	5.94±0.34	6.35±0.34
3244488	RASSF4	Ras association (RalGDS/AF-6) domain family member 4	2.42E-05	-1.75	5.67±0.29	6.47±0.72
2732655	FRAS1	Fraser syndrome 1	2.50E-05	1.71	6.44±0.65	5.66±0.64
3070873	GPR37	G protein-coupled receptor 37 (endothelin receptor type B-like)	2.51E-05	1.5	6.25±0.45	5.66±0.5
2694817	PLXND1	plexin D1	2.51E-05	-1.4	7.28±0.28	7.77±0.43
3849044	MYO1F	myosin IF	2.52E-05	-1.52	5.79±0.22	6.4±0.54
2363562	FCER1G	Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide	2.53E-05	-3.06	5.5±0.91	7.11±1.4
2903285	PSMB9	proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional peptidase 2)	2.55E-05	-1.89	7.08±0.4	8±0.82
2704441	EVI1	ecotropic viral integration site 1	2.58E-05	1.67	7.91±0.32	7.17±0.67
3824874	IFI30	interferon, gamma-inducible protein 30	2.58E-05	-2.82	6.69±0.78	8.18±1.3
2902444	AIF1	allograft inflammatory factor 1	2.64E-05	-2.12	5.39±0.51	6.47±0.97
3610110	NR2F2	nuclear receptor subfamily 2, group F, member 2	2.64E-05	-1.45	8.79±0.43	9.33±0.46
3015682	PCOLCE	procollagen C-endopeptidase enhancer	2.69E-05	-1.86	8.12±0.55	9.02±0.79
2647015	AGTR1	angiotensin II receptor, type 1	2.71E-05	1.35	5.97±0.43	5.54±0.33
3841621	LILRB4	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 4	2.77E-05	-1.8	5.82±0.35	6.66±0.76
3837257	CSAR1	complement component 5a receptor 1	2.85E-05	-1.61	6.06±0.32	6.75±0.62
3020192	TES	testis derived transcript (3 LIM domains)	2.89E-05	1.54	10.5±0.34	9.92±0.56
3647993	CIITA	class II, major histocompatibility complex, transactivator	2.97E-05	-1.56	5.88±0.24	6.53±0.59
2427791	DENND2D	DENN/MADD domain containing 2D	2.98E-05	-1.85	5.31±0.39	6.19±0.8
3409364	KLHDCC5	kelch domain containing 5	3.00E-05	1.49	8.72±0.31	8.15±0.51
2816459	F2R	coagulation factor II (thrombin) receptor	3.00E-05	-1.69	8.61±0.69	9.37±0.61
2532699	INPP5D	inositol polyphosphate-5-phosphatase, 145kDa	3.05E-05	-1.66	6.08±0.25	6.81±0.67
2486811	PLEK	pleckstrin	3.12E-05	-2.49	4.97±0.58	6.28±1.2
3708858	CD68	CD68 molecule	3.25E-05	-2.05	7.94±0.54	8.98±0.94
3638188	HAPLN3	hyaluronan and proteoglycan link protein 3	3.28E-05	-1.38	8.66±0.34	7.32±0.41
3723378	FMNL1	formin-like 1	3.41E-05	-1.39	6.22±0.18	6.69±0.44
2362892	ATP1A2	ATPase, Na <sup>+</sup> /K <sup>+</sup> transporting, alpha 2 (+) polypeptide	3.47E-05	1.81	7.41±0.64	6.56±0.75
3577443	ASB2	ankyrin repeat and SOCS box-containing 2	3.48E-05	1.28	6.07±0.34	5.71±0.29
2463567	PLD5	phospholipase D family, member 5	3.57E-05	2.46	7.64±0.57	6.34±1.2
2875348	IRF1	interferon regulatory factor 1	3.58E-05	-1.47	5.96±0.25	6.51±0.51
3334257	FERMT3	fermitin family homolog 3 (Drosophila)	3.59E-05	-1.62	6.54±0.27	7.24±0.65
2829947	TGFB1	transforming growth factor, beta-induced, 68kDa	3.73E-05	-2.02	7.87±0.75	8.88±0.89
3256164	SNCG	synuclein, gamma (breast cancer-specific protein 1)	3.91E-05	-1.48	6.38±0.26	6.95±0.53
3442854	SLC2A3	solute carrier family 2 (facilitated glucose transporter), member 3	3.94E-05	-1.69	7.18±0.34	7.93±0.7
2403446	PTAFR	platelet-activating factor receptor	3.96E-05	-2.02	5.24±0.43	6.25±0.94
3244622	ALOX5	arachidonate 5-lipoxygenase	4.08E-05	-2.06	5.52±0.32	6.56±0.98
2806643	SLC1A3	solute carrier family 1 (glial high affinity glutamate transporter), member 3	4.09E-05	-2.05	5.05±0.46	6.08±0.96
2893392	LY86	lymphocyte antigen 86	4.14E-05	-2.11	5.31±0.31	6.39±1
3662444	NLRCS	NLR family, CARD domain containing 5	4.18E-05	-1.29	5.97±0.14	6.34±0.34
3027204	TBXAS1	thromboxane A synthase 1 (platelet)	4.18E-05	-1.66	5.76±0.24	6.49±0.69
2777639	GPRIN3	GPRIN family member 3	4.20E-05	-1.71	5.88±0.31	6.65±0.72
3315675	IFITM1	interferon induced transmembrane protein 1 (9-27)	4.21E-05	-2.41	6.3±0.55	7.57±1.2
3441849	TNFRSF1A	tumor necrosis factor receptor superfamily, member 1A	4.29E-05	-1.28	7.86±0.21	8.22±0.33
2939034	SERPINB9	serpin peptidase inhibitor, clade B (ovalbumin), member 9	4.29E-05	-1.5	6.16±0.43	6.74±0.53
3577612	SERPINA1	serpin peptidase inhibitor, clade A (alpha-1 antiprotease, antitrypsin), member 1	4.50E-05	-1.92	5.89±0.38	6.83±0.88
2793441	AADAT	aminoadipate aminotransferase	4.58E-05	1.25	5.94±0.29	5.61±0.28
2440549	ARHGAP30	Rho GTPase activating protein 30	4.59E-05	-1.51	5.73±0.21	6.32±0.56
3737338	RNF213	ring finger protein 213	4.69E-05	-1.32	7.9±0.35	8.3±0.35
2735027	SPP1	secreted phosphoprotein 1	4.71E-05	-6.06	6.51±1.3	9.11±2.4
3775038	C17orf62	chromosome 17 open reading frame 62	4.74E-05	-1.17	7.41±0.16	7.64±0.21
2373336	CFH	complement factor H	4.90E-05	-1.91	8.58±0.97	9.52±0.74
7385547	CCL2	chemokine (C-C motif) ligand 2	4.94E-05	-2.3	7.12±0.66	8.32±1.1
3019793	FOXP2	forkhead box P2	4.95E-05	1.39	5.64±0.37	5.16±0.43
3944243	APOL6	apolipoprotein L, 6	5.02E-05	-1.5	5.98±0.32	6.57±0.55
3179551	FGD3	FYVE, RhoGEF and PH domain containing 3	5.03E-05	-1.16	5.54±0.16	5.76±0.2
3545130	VASH1	vasohibin 1	5.05E-05	-1.22	6.87±0.16	7.15±0.26

meta probeset ID	genesymbol	genename	p-value	fold-change	log2(BAV)	log2(TAV)
3553531	TNFAIP2	tumor necrosis factor, alpha-induced protein 2	5.14E-05	-1.48	5.97±0.23	6.53±0.54
2327283	C1orf38	chromosome 1 open reading frame 38	5.15E-05	-1.51	5.49±0.24	6.09±0.56
3955185	GGT5	gamma-glutamyltransferase 5	5.32E-05	-1.4	7.15±0.26	7.63±0.46
2652801	NLGN1	neuroligin 1	5.34E-05	1.7	6.46±0.46	5.7±0.72
3290875	ANK3	ankyrin 3, node of Ranvier (ankyrin G)	5.36E-05	-1.67	6.26±0.64	7±0.65
3447694	BCAT1	branched chain aminotransferase 1, cytosolic	5.49E-05	-2.52	6.01±0.53	7.35±1.3
3336801	ADRBK1	adrenergic, beta, receptor kinase 1	5.63E-05	-1.21	7.02±0.17	7.29±0.25
3859946	HSPB6	heat shock protein, alpha-crystallin-related, B6	5.63E-05	1.4	8.22±0.51	7.73±0.4
3226097	ENG	endoglin	5.69E-05	-1.62	8.55±0.65	9.25±0.6
2639225	PDIA5	protein disulfide isomerase family A, member 5	6.02E-05	-1.25	6.73±0.27	7.05±0.28
3848039	C3	complement component 3	6.12E-05	-3.79	5.9±0.65	7.82±1.9
3418007	SHMT2	serine hydroxymethyltransferase 2 (mitochondrial)	6.13E-05	-1.33	7.32±0.26	7.73±0.39
3037344	DAGLB	diacylglycerol lipase, beta	6.27E-05	-1.24	6.12±0.15	6.43±0.3
2900974	HLA-F	major histocompatibility complex, class I, F	6.30E-05	-1.38	6.14±0.3	6.6±0.44
2597347	ACADL	acyl-Coenzyme A dehydrogenase, long chain	6.31E-05	2.02	7.81±0.45	6.8±0.98
3581221	AHNAK2	AHNAK nucleoprotein 2	6.33E-05	-1.72	7.47±0.69	8.25±0.69
2903258	HLA-DQA1	major histocompatibility complex, class II, DQ alpha 1	6.38E-05	-1.93	6.19±0.42	7.14±0.91
2356115	TXNIP	thioredoxin interacting protein	6.59E-05	-1.51	10.6±0.49	11.2±0.54
3759778	ARHGAP27	Rho GTPase activating protein 27	6.62E-05	-1.13	5.9±0.14	6.08±0.17
3023318	TSPAN33	tetraspanin 33	6.63E-05	-1.42	5.88±0.27	6.39±0.49
3446910	KCNJ8	potassium inwardly-rectifying channel, subfamily J, member 8	6.68E-05	1.36	6.92±0.31	6.48±0.41
2331857	SMAP2	small ArfGAP2	6.71E-05	-1.74	6.72±0.26	7.51±0.78
3470523	SELPLG	selectin P ligand	6.72E-05	-1.69	5.2±0.28	5.95±0.74
3008164	LAT2	linker for activation of T cells family, member 2	6.73E-05	-1.23	5.79±0.15	6.09±0.28
3737274	KIAA1618	KIAA1618	6.92E-05	-1.25	7.64±0.3	7.96±0.29
3349293	NCAM1	neural cell adhesion molecule 1	6.95E-05	2.04	7.61±0.49	6.58±1
3542145	KIAA0247	KIAA0247	7.01E-05	-1.32	7.26±0.3	7.66±0.37
2439842	TAGLN2	transgelin 2	7.01E-05	-1.28	10.7±0.27	11.1±0.33
3288518	C10orf72	chromosome 10 open reading frame 72	7.15E-05	1.39	7.61±0.37	7.13±0.44
3203990	KIAA1161	KIAA1161	7.18E-05	1.3	5.81±0.38	5.44±0.31
2511153	KCNJ3	potassium inwardly-rectifying channel, subfamily J, member 3	7.25E-05	1.73	7.34±0.5	6.55±0.75
2326561	RP56KA1	ribosomal protein S6 kinase, 90kDa, polypeptide 1	7.31E-05	-1.36	5.73±0.17	6.17±0.44
3555675	RNASE1	ribonuclease, RNase A family, 1 (pancreatic)	7.46E-05	-2.54	8.44±0.68	9.79±1.3
3797032	EPB41L3	erythrocyte membrane protein band 4.1-like 3	7.70E-05	-1.82	5.29±0.29	6.15±0.85
2950199	PSMB8	proteasome (prosome, macropain) subunit, beta type, 8 (large multifunctional peptidase 7)	7.80E-05	-1.54	6.27±0.33	6.89±0.6
3966000	TYMP	thymidine phosphorylase	7.83E-05	-1.27	7.16±0.21	7.51±0.33
4024420	LDOC1	leucine zipper, down-regulated in cancer 1	7.83E-05	1.6	9.94±0.43	9.26±0.65
3772279	SOC3	suppressor of cytokine signaling 3	7.88E-05	-1.52	5.91±0.21	6.52±0.6
3224087	TTL11	tubulin tyrosine ligase-like family, member 11	8.01E-05	1.24	7.73±0.22	7.42±0.3
2643901	PPP2R3A	protein phosphatase 2 (formerly 2A), regulatory subunit B", alpha	8.01E-05	1.31	6.59±0.3	6.2±0.37
2704504	MDS1	myelodysplasia syndrome 1	8.04E-05	1.35	6.71±0.3	6.29±0.41
2766788	RBM47	RNA binding motif protein 47	8.12E-05	-1.56	6.06±0.31	6.71±0.63
3395464	ASAM	adipocyte-specific adhesion molecule	8.19E-05	1.58	9.61±0.32	8.95±0.65
2828520	SLC22A5	solute carrier family 22 (organic cation/carnitine transporter), member 5	8.24E-05	1.22	6.5±0.23	6.22±0.27
3262535	GSTO2	glutathione S-transferase omega 2	8.24E-05	1.14	5.99±0.21	5.8±0.16
2903219	HLA-DQA1	major histocompatibility complex, class II, DQ alpha 1	8.40E-05	-5.18	5.6±1.8	7.97±2.2
3869030	SIGLEC10	sialic acid binding Ig-like lectin 10	8.47E-05	-1.31	5.49±0.19	5.88±0.38
2348992	VCAM1	vascular cell adhesion molecule 1	8.49E-05	-1.89	7.96±0.94	8.87±0.78
2788366	ZNF827	zinc finger protein 827	8.56E-05	1.28	7.62±0.26	7.27±0.34
3367673	MPPED2	metallophosphoesterase domain containing 2	8.59E-05	2	8.95±0.42	7.95±0.99
4012511	NAP1L2	nucleosome assembly protein 1-like 2	8.67E-05	1.66	7.03±0.38	6.3±0.72
2859601	ADAMTS6	ADAM metalloproteinase with thrombospondin type 1 motif, 6	8.71E-05	1.81	6.73±0.54	5.87±0.83
3335029	POLA2	polymerase (DNA directed), alpha 2 (70kD subunit)	8.86E-05	-1.13	5.77±0.15	5.95±0.17
3040967	RAPGEF5	Rap guanine nucleotide exchange factor (GEF) 5	8.96E-05	-1.57	6.91±0.46	7.56±0.63
3598165	PLEKHO2	pleckstrin homology domain containing, family O member 2	9.15E-05	-1.35	7.34±0.22	7.78±0.43
2683763	ROBO1	roundabout, axon guidance receptor, homolog 1 (Drosophila)	9.28E-05	1.36	8.14±0.32	7.7±0.42
3830189	FXYD1	FXYD domain containing ion transport regulator 1	9.31E-05	1.36	9.16±0.35	8.71±0.42
3684486	IGSF6	immunoglobulin superfamily, member 6	9.32E-05	-2.02	5.87±0.57	6.88±0.99
3043648	CPVL	carboxypeptidase, vitellogenic-like	9.35E-05	-2.38	4.88±0.53	6.13±1.2
3426502	PLXNC1	plexin C1	9.41E-05	-1.93	5.68±0.3	6.62±0.95
2904329	ANKS1A	ankyrin repeat and sterile alpha motif domain containing 1A	9.61E-05	1.18	8.05±0.25	7.81±0.21
3866958	CARD8	caspase recruitment domain family, member 8	9.78E-05	-1.38	6.39±0.18	6.86±0.47
2449391	KCNT2	potassium channel, subfamily T, member 2	9.98E-05	-1.8	5.97±0.87	6.82±0.74
3854627	JAK3	Janus kinase 3	1.00E-04	-1.3	5.57±0.2	5.95±0.37
3886294	TOX2	TOX high mobility group box family member 2	0.000101	1.17	6.15±0.21	5.92±0.21
2931763	ESR1	estrogen receptor 1	0.000102	1.2	6.33±0.25	6.07±0.23
2440354	CD48	CD48 molecule	0.000102	-2.03	5.16±0.43	6.18±1
3389976	SLC35F2	solute carrier family 35, member F2	0.000102	1.66	8.06±0.5	7.32±0.71
3405587	GPRC5A	G protein-coupled receptor, family C, group 5, member A	0.000105	1.58	7.58±0.46	6.92±0.64
3571904	NPC2	Niemann-Pick disease, type C2	0.000106	-1.62	9.18±0.53	9.87±0.66
3869237	FPR1	formyl peptide receptor 1	0.000106	-1.58	5.25±0.23	5.91±0.67
3535628	GNG2	guanine nucleotide binding protein (G protein), gamma 2	0.000106	-1.88	4.79±0.37	5.7±0.92
3375091	SLC15A3	solute carrier family 15, member 3	0.000106	-1.48	6.83±0.26	7.4±0.57
3656990	ITGAM	integrin, alpha M (complement component 3 receptor 3 subunit)	0.000107	-1.75	5.21±0.22	6.01±0.82
3154263	SLA	Src-like-adaptor	0.000107	-1.76	5.08±0.31	5.9±0.82
3960061	RAC2	ras-related C3 botulinum toxin substrate 2 (rho family, small GTP binding protein Rac2)	0.000107	-1.62	6.57±0.32	7.26±0.7
3411721	CNTN1	contactin 1	0.000108	3.51	9.41±0.55	7.6±1.8
2602653	PID1	phosphotyrosine interaction domain containing 1	0.00011	1.47	8.11±0.29	7.55±0.55
3854954	LRRC25	leucine rich repeat containing 25	0.00011	-1.21	6.5±0.18	6.77±0.27
3719980	LASP1	LIM and SH3 protein 1	0.000111	-1.27	8.68±0.32	9.03±0.32
3315658	IFITM2	interferon induced transmembrane protein 2 (1-8D)	0.000112	-1.21	6.93±0.24	7.2±0.26
3588658	C15orf41	chromosome 15 open reading frame 41	0.000112	1.24	7.07±0.27	6.76±0.3
4001850	SH3KBP1	SH3-domain kinase binding protein 1	0.000112	-1.44	7.07±0.4	7.6±0.51
3360006	RHOG	ras homolog gene family, member G (rho G)	0.000112	-1.3	7.5±0.28	7.88±0.37
2807621	PTGER4	prostaglandin E receptor 4 (subtype EP4)	0.000113	-1.56	6.16±0.35	6.8±0.64
3381817	UCP2	uncoupling protein 2 (mitochondrial, proton carrier)	0.000113	-1.61	6.28±0.3	6.97±0.7
3127610	PEBP4	phosphatidylethanolamine-binding protein 4	0.000114	1.35	6.68±0.4	6.24±0.4
3396107	ESAM	endothelial cell adhesion molecule	0.000115	-1.48	6.34±0.39	6.91±0.56
3770606	HN1	hematological and neurological expressed 1	0.000115	-1.29	6.09±0.17	6.46±0.38
3772525	CYTH1	cytohesin 1	0.000116	-1.43	6.66±0.24	7.17±0.52
2993206	MPP6	membrane protein, palmitoylated 6 (MAGUK p55 subfamily member 6)	0.000116	1.79	7.72±0.47	6.89±0.84
3278401	FRMD4A	FERM domain containing 4A	0.000116	-1.36	6.65±0.39	7.1±0.42
3945585	APOBEC3D	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3D	0.000118	-1.19	6.08±0.16	6.33±0.24
3059667	SEMA3D	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3D	0.000118	2.61	7.19±0.99	5.8±1.4
3950405	ZBED4	zinc finger, BED-type containing 4	0.000118	-1.1	6±0.17	6.14±0.11
2617188	ITGA9	integrin, alpha 9	0.000122	1.4	8.6±0.36	8.11±0.47
3355733	FLJ1	Friend leukemia virus integration 1	0.000123	-1.69	6.29±0.33	7.04±0.77
2880051	PPP2R2B	protein phosphatase 2 (formerly 2A), regulatory subunit B, beta isoform	0.000123	1.42	7.24±0.26	6.73±0.51
3907524	PLTP	phospholipid transfer protein	0.000127	-2.32	7.17±0.6	8.38±1.2
3824471	GLT25D1	glycosyltransferase 25 domain containing 1	0.000127	-1.28	8.27±0.24	8.63±0.35
3250373	TSPAN15	tetraspanin 15	0.000128	-1.79	5.32±0.23	6.16±0.87
2447414	NCF2	neutrophil cytosolic factor 2	0.000129	-2.21	5.18±0.45	6.32±1.2
3361041	TPP1	tripeptidyl peptidase I	0.000132	-1.33	7.91±0.29	8.32±0.41
2948926	HLA-B	major histocompatibility complex, class I, B	0.000132	-1.83	10.6±0.51	11.5±0.88

meta probeset ID	genesymbol	genename	p-value	fold-change	log2(BAV)	log2(TAV)
3237396	CACNB2	calcium channel, voltage-dependent, beta 2 subunit	0.000136	1.33	6.3±0.4	5.89±0.38
3613725	NDN	neccdin homolog (mouse)	0.000136	1.29	6.19±0.36	5.83±0.33
3838385	CD37	CD37 molecule	0.000137	-2.01	6.11±0.38	7.12±1
4026842	ARHGAP4	Rho GTPase activating protein 4	0.000139	-1.25	6.32±0.19	6.65±0.33
2680046	ADAMT59	ADAM metalloproteinase with thrombospondin type 1 motif, 9	0.000139	1.62	8.01±0.52	7.32±0.68
3939125	GNAZ	guanine nucleotide binding protein (G protein), alpha z polypeptide	0.000145	1.16	6.49±0.19	6.28±0.2
3558745	NOVA1	neuro-oncological ventral antigen 1	0.000146	1.25	5.86±0.28	5.54±0.31
2777333	PPM1K	protein phosphatase 1K (PP2C domain containing)	0.000148	1.38	7.71±0.4	7.25±0.45
3807595	MYO5B	myosin VB	0.000148	1.92	7.15±0.62	6.21±0.95
3448152	ITPR2	inositol 1,4,5-triphosphate receptor, type 2	0.000152	-1.47	6.88±0.4	7.43±0.55
3966891	XG	Xg blood group	0.000156	1.4	9.21±0.42	8.73±0.47
2888800	DBN1	drebrin 1	0.000159	1.23	8.05±0.25	7.75±0.29
3922037	MX2	myxovirus (influenza virus) resistance 2 (mouse)	0.000161	-1.66	5.52±0.32	6.25±0.77
2948630	IER3	immediate early response 3	0.000162	-1.36	6.86±0.34	7.3±0.44
3708462	ACAP1	ArfGAP with coiled-coil, ankyrin repeat and PH domains 1	0.000162	-1.21	5.78±0.17	6.05±0.28
2766219	TLR1	toll-like receptor 1	0.000163	-1.77	5.39±0.41	6.22±0.86
2369463	FAM20B	family with sequence similarity 20, member B	0.000164	1.22	8.38±0.27	8.09±0.27
3850278	TYK2	tyrosine kinase 2	0.00017	-1.14	7.11±0.17	7.29±0.18
3480508	IL17D	interleukin 17D	0.000173	1.17	7.64±0.2	7.41±0.22
3250863	SGPL1	sphingosine-1-phosphate lyase 1	0.000174	-1.21	7.5±0.18	7.78±0.29
3013565	DYNC111	dynein, cytoplasmic 1, intermediate chain 1	0.000174	1.46	7.68±0.32	7.13±0.56
3472312	SLC24A6	solute carrier family 24 (sodium/potassium/calcium exchanger), member 6	0.000174	-1.15	7.11±0.17	7.31±0.2
3151970	MTSS1	metastasis suppressor 1	0.000175	-1.68	5.67±0.23	6.42±0.79
3339880	RELT	RELT tumor necrosis factor receptor	0.000175	-1.15	5.46±0.19	5.67±0.2
3153328	FAM49B	family with sequence similarity 49, member B	0.000176	-1.73	5.83±0.33	6.62±0.83
3046197	ELMO1	engulfment and cell motility 1	0.000176	-1.53	6.03±0.4	6.64±0.63
3094334	GPR124	G protein-coupled receptor 124	0.000178	-1.29	6.73±0.24	7.09±0.37
3031624	TMEM176A	transmembrane protein 176A	0.000178	-2.03	5.54±0.41	6.57±1.1
2777113	SPARCL1	SPARC-like 1 (hevin)	0.000181	1.55	12.3±0.25	11.7±0.67
3815493	HMHA1	histocompatibility (minor) HA-1	0.000181	-1.17	6.3±0.2	6.52±0.22
2887048	STK10	serine/threonine kinase 10	0.000182	-1.45	6.12±0.19	6.66±0.57
3633148	SCAMP2	secretory carrier membrane protein 2	0.000183	-1.18	8.39±0.23	8.62±0.22
3270270	PTPRE	protein tyrosine phosphatase, receptor type, E	0.000184	-1.3	5.59±0.2	5.96±0.39
3210497	PRUNE2	prune homolog 2 (Drosophila)	0.000185	1.6	10.1±0.37	9.38±0.71
3641560	LYSMD4	LysM, putative peptidoglycan-binding, domain containing 4	0.000185	1.13	6.14±0.16	5.96±0.18
2341083	GADD45A	growth arrest and DNA-damage-inducible, alpha	0.000188	1.34	9.36±0.31	8.94±0.43
2352609	MAG3	membrane associated guanylate kinase, WW and PDZ domain containing 3	0.000188	1.12	6.63±0.21	6.47±0.14
3819016	STXBP2	syntaxin binding protein 2	0.000189	-1.4	5.85±0.24	6.33±0.51
3923257	PDXK	pyridoxal (pyridoxine, vitamin B6) kinase	0.000191	-1.19	7.69±0.17	7.94±0.26
3605268	TM6SF1	transmembrane 6 superfamily member 1	0.000196	-1.79	5.82±0.48	6.66±0.88
3044072	NOD1	nucleotide-binding oligomerization domain containing 1	0.000197	-1.19	5.74±0.2	5.99±0.25
3566495	C14orf37	chromosome 14 open reading frame 37	0.000198	1.58	6.56±0.42	5.9±0.69
3457752	STAT2	signal transducer and activator of transcription 2, 113kDa	0.000198	-1.25	7.91±0.38	8.23±0.28
3910260	ZNF217	zinc finger protein 217	2.00E-04	-1.32	6.43±0.31	6.83±0.41
3311269	FAM53B	family with sequence similarity 53, member B	0.000201	-1.2	5.87±0.15	6.14±0.28
3983549	PCDH11X	protocadherin 11 X-linked	0.000202	2.28	6.76±0.73	5.57±1.2
3294159	P4HA1	prolyl 4-hydroxylase, alpha polypeptide I	0.000202	-1.39	8.16±0.47	8.64±0.45
3664843	CMTM3	CKLF-like MARVEL transmembrane domain containing 3	0.000202	-1.25	7.36±0.28	7.68±0.33
3960110	MFNG	MFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase	0.000203	-1.48	5.28±0.23	5.84±0.6
3337390	TCIRG1	T-cell, immune regulator 1, ATPase, H+ transporting, lysosomal V0 subunit A3	0.000203	-1.17	7.6±0.15	7.83±0.24
3678083	CORO7	coronin 7	0.000205	-1.14	6.5±0.14	6.69±0.19
3903778	EDEM2	ER degradation enhancer, mannosidase alpha-like 2	0.000205	-1.22	6.55±0.19	6.83±0.29
2604390	ARL4C	ADP-ribosylation factor-like 4C	0.000215	-1.7	6.51±0.41	7.28±0.81
2639054	PARP14	poly (ADP-ribose) polymerase family, member 14	0.000215	-1.41	7.52±0.35	8.01±0.51
3708764	TNFSF13	tumor necrosis factor (ligand) superfamily, member 13	0.000215	-1.24	7.01±0.18	7.33±0.33
3864551	PLAUR	plasminogen activator, urokinase receptor	0.000216	-1.61	6.08±0.24	6.77±0.74
3814701	PQLC1	PQ loop repeat containing 1	0.000216	-1.1	6.95±0.14	7.09±0.14
2693409	ALDH1L1	aldehyde dehydrogenase 1 family, member 11	0.000217	1.28	6.63±0.28	6.27±0.37
3303165	DNMBP	dynamitin binding protein	0.000218	-1.23	5.94±0.22	6.24±0.31
3604287	IL16	interleukin 16 (lymphocyte chemoattractant factor)	0.000222	-1.33	5.42±0.15	5.83±0.45
2363784	HSPA6	heat shock 70kDa protein 6 (HSP70B)	0.000224	-1.32	6.09±0.18	6.49±0.43
2478269	TMEM178	transmembrane protein 178	0.000224	1.44	7.85±0.56	7.33±0.49
3329983	PTPRJ	protein tyrosine phosphatase, receptor type, J	0.000226	-1.45	6.61±0.28	7.14±0.57
2951916	STK38	serine/threonine kinase 38	0.000227	-1.32	7.52±0.35	7.92±0.4
3796428	MYOM1	myomesin 1, 185kDa	0.000227	1.43	7.62±0.39	7.14±0.53
3688311	PYCARD	PYD and CARD domain containing	0.000229	-1.32	6.19±0.23	6.59±0.42
3738629	SLC16A3	solute carrier family 16, member 3 (monocarboxylic acid transporter 4)	0.000229	-1.7	6.91±0.58	7.68±0.79
3132782	SFRP1	secreted frizzled-related protein 1	0.000231	2.65	10.3±0.6	8.88±1.5
2902348	MICB	MHC class I polypeptide-related sequence B	0.000233	-1.17	6.25±0.24	6.48±0.21
3333899	RARRES3	retinoic acid receptor responder (tazarotene induced) 3	0.000233	-1.57	5.55±0.32	6.19±0.7
3372174	SP1	spleen focus forming virus (SFFV) proviral integration oncogene spi1	0.000236	-1.44	6.38±0.32	6.91±0.55
3734379	CD300A	CD300a molecule	0.000236	-1.58	5.79±0.26	6.45±0.71
3661718	LPCAT2	lysophosphatidylcholine acyltransferase 2	0.000239	-1.38	7.9±0.54	8.37±0.42
2934521	SLC22A3	solute carrier family 22 (extraneuronal monoamine transporter), member 3	0.000242	2.01	10.1±0.42	9.06±1.1
2424524	DPYD	dihydropyrimidine dehydrogenase	0.000244	-1.45	8±0.36	8.54±0.57
3985008	TCEAL4	transcription elongation factor A (SII)-like 4	0.000244	2.11	7.87±0.61	6.79±1.2
3057955	FGL2	fibrinogen-like 2	0.000246	1.38	11.7±0.31	11.2±0.49
3301218	PDLIM1	PDZ and LIM domain 1	0.000248	1.24	9.38±0.29	9.07±0.3
2833924	APOOL	apolipoprotein O-like	0.00025	1.28	6.26±0.26	5.9±0.37
3709838	NTN1	netrin 1	0.000252	1.26	7.26±0.31	6.93±0.33
2363808	FCGR2B	Fc fragment of IgG, low affinity IIb, receptor (CD32)	0.000253	-2.04	5.83±0.36	6.86±1.1
3463821	PPFIA2	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), i	0.000253	1.38	6.57±0.39	6.11±0.48
3704376	FAM38A	family with sequence similarity 38, member A	0.000254	-1.16	6.95±0.2	7.17±0.21
2691668	HCLS1	hematopoietic cell-specific Lyn substrate 1	0.000255	-1.6	6.94±0.31	7.61±0.73
3252036	PLAU	plasminogen activator, urokinase	0.000258	-1.58	6.57±0.27	7.22±0.72
3838624	FCGRT	Fc fragment of IgG, receptor, transporter, alpha	0.000262	-1.35	7.71±0.25	8.14±0.46
3042610	SKAP2	src kinase associated phosphoprotein 2	0.000265	-1.82	5.08±0.45	5.94±0.94
3513514	P2RY5	purinergic receptor P2Y, G-protein coupled, 5	0.000268	-1.87	6.06±0.49	6.96±0.98
3821893	JUNB	jun B proto-oncogene	0.000272	-1.5	8.6±0.52	9.18±0.59
2381309	MOSCC1	MOSCC sulphurase C-terminal domain containing 1	0.000273	1.22	6.54±0.24	6.25±0.3
3901055	CD93	CD93 molecule	0.000273	-1.51	7.8±0.48	8.4±0.62
2470165	TRIB2	tribbles homolog 2 (Drosophila)	0.000274	-1.23	7.44±0.26	7.74±0.31
2562932	CD8A	CD8a molecule	0.000274	-1.18	5.86±0.16	6.11±0.26
2339786	PGM1	phosphoglucomutase 1	0.000276	1.3	9.34±0.32	8.97±0.39
3063685	MCM7	minichromosome maintenance complex component 7	0.000283	1.13	7.46±0.21	7.28±0.16
3577078	LGMM	legumain	0.000284	-1.53	8.98±0.46	9.59±0.65
3579546	WARS	tryptophanyl-tRNA synthetase	0.000285	-1.27	7.1±0.29	7.45±0.36
3185498	SLC31A2	solute carrier family 31 (copper transporters), member 2	0.000286	-1.42	6.22±0.25	6.72±0.55
3701000	MAF	v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)	0.000286	-1.32	6.31±0.23	6.72±0.44
2338487	FGGY	FGGY carbohydrate kinase domain containing	0.000287	1.17	6.53±0.27	6.3±0.21
3601229	CD276	CD276 molecule	0.000287	-1.16	7.31±0.22	7.52±0.21
3539070	HIF1A	hypoxia inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)	0.000288	-1.53	8.15±0.35	8.77±0.67
3293724	C10orf54	chromosome 10 open reading frame 54	0.00029	-1.27	6.48±0.17	6.82±0.38
3382216	ARRB1	arrestin, beta 1	0.000294	-1.73	5.77±0.28	6.55±0.87

meta probeset ID	genesymbol	genename	p-value	fold-change	log2(BAV)	log2(TAV)
3543355	WDR21A	WD repeat domain 21A	0.000297	1.26	6.54±0.33	6.2±0.34
2417095	SLC35D1	solute carrier family 35 (UDP-glucuronic acid/UDP-N-acetylgalactosamine dual transporter), me	0.000297	1.31	7.79±0.38	7.4±0.39
3008108	LIMK1	LIM domain kinase 1	0.000298	-1.16	6.8±0.17	7.01±0.22
2688813	CCDC80	coiled-coil domain containing 80	0.000299	-2.13	8.11±0.67	9.2±1.2
3529701	IRF9	interferon regulatory factor 9	3.00E-04	-1.18	7.72±0.23	7.95±0.24
2716810	CRMP1	collapsin response mediator protein 1	3.00E-04	1.17	8.54±0.22	8.31±0.23
3387259	SESN3	sestrin 3	0.000302	-1.47	8.79±0.54	9.35±0.56
2550339	HAAO	3-hydroxyanthranilate 3,4-dioxygenase	0.000305	1.23	8.58±0.18	8.28±0.33
3575103	GALC	galactosylceramidase	0.000308	-1.36	6.44±0.27	6.89±0.48
2842157	HRH2	histamine receptor H2	0.000312	-1.22	5.46±0.28	5.75±0.29
3895891	ADRA1D	adrenergic, alpha-1D-, receptor	0.000312	1.2	6.02±0.27	5.75±0.26
3442475	C1R	complement component 1, r subcomponent	0.000313	-1.5	9.69±0.56	10.3±0.59
3127334	REEP4	receptor accessory protein 4	0.000313	-1.2	5.7±0.18	5.97±0.29
3337329	ALDH3B1	aldehyde dehydrogenase 3 family, member B1	0.000314	-1.18	6.87±0.2	7.11±0.25
3452323	SLC38A2	solute carrier family 38, member 2	0.000323	-1.27	10.5±0.33	10.8±0.35
3527514	NP	nucleoside phosphorylase	0.000327	-1.54	6.58±0.45	7.2±0.67
2592268	STAT1	signal transducer and activator of transcription 1, 91kDa	0.000329	-1.33	8.7±0.37	9.11±0.43
3175119	OSTF1	osteoclast stimulating factor 1	0.000329	-1.4	7.44±0.32	7.92±0.53
2850071	MYO10	myosin X	0.00033	-1.47	5.97±0.5	6.53±0.57
3767480	AXIN2	axin 2	0.00033	1.28	6.9±0.33	6.55±0.36
2950307	HLA-DOA	major histocompatibility complex, class II, DO alpha	0.000331	-1.39	6.2±0.27	6.67±0.52
2353717	PTGFRN	prostaglandin F2 receptor negative regulator	0.000334	1.23	8.24±0.3	7.94±0.3
3933923	CBS	cystathionine-beta-synthase	0.000337	1.24	6.69±0.29	6.38±0.32
2585701	STK39	serine threonine kinase 39 (STE20/SPS1 homolog, yeast)	0.000338	1.23	8.42±0.29	8.12±0.31
2605321	COL6A3	collagen, type VI, alpha 3	0.000339	-1.45	8.42±0.39	8.96±0.58
4019160	KLHL13	kelch-like 13 (Drosophila)	0.00034	1.45	6.45±0.29	5.92±0.59
3722355	RND2	Rho family GTPase 2	0.000341	1.29	6.22±0.29	5.85±0.39
2609347	LMCD1	LIM and cysteine-rich domains 1	0.000345	1.34	10.1±0.23	9.7±0.47
3159483	KANK1	KN motif and ankyrin repeat domains 1	0.00035	1.47	9.29±0.28	8.74±0.62
3379269	UNC93B1	unc-93 homolog B1 (C. elegans)	0.000353	-1.24	6.46±0.27	6.77±0.33
2534509	RAMP1	receptor (G protein-coupled) activity modifying protein 1	0.000353	1.33	8.49±0.33	8.08±0.45
2405284	TMEM54	transmembrane protein 54	0.000354	-1.19	6.62±0.27	6.88±0.25
3556816	SLC7A7	solute carrier family 7 (cationic amino acid transporter, y+ system), member 7	0.000355	-1.49	5.69±0.34	6.27±0.64
2320727	TNFRSF1B	tumor necrosis factor receptor superfamily, member 1B	0.000358	-1.36	6.06±0.19	6.51±0.5
4019486	SEPT6	septin 6	0.000358	-1.37	5.87±0.25	6.32±0.5
2638962	DTX3L	deltex 3-like (Drosophila)	0.000364	-1.45	6.7±0.42	7.24±0.58
3254521	TSPAN14	tetraspanin 14	0.000364	-1.38	6.95±0.21	7.42±0.52
2717593	SH3TC1	SH3 domain and tetratricopeptide repeats 1	0.000371	-1.14	5.99±0.18	6.18±0.19
2735221	PKD2	polycystic kidney disease 2 (autosomal dominant)	0.000376	1.43	11±0.28	10.5±0.57
2645387	ACPL2	acid phosphatase-like 2	0.000376	1.4	7.16±0.4	6.67±0.53
3872053	PEG3	paternally expressed 3	0.000378	1.3	6.97±0.21	6.6±0.42
3634458	TBC1D2B	TBC1 domain family, member 2B	0.000381	-1.23	7.87±0.4	8.17±0.25
2392584	TNFRSF14	tumor necrosis factor receptor superfamily, member 14 (herpesvirus entry mediator)	0.000382	-1.23	6.9±0.18	7.19±0.33
3320169	AMPD3	adenosine monophosphate deaminase (isoform E)	0.000385	-1.43	5.68±0.23	6.2±0.59
3624607	MYO5A	myosin VA (heavy chain 12, myosin)	0.000386	-1.42	6.39±0.35	6.9±0.56
2674762	UBA7	ubiquitin-like modifier activating enzyme 7	0.000386	-1.18	7.43±0.21	7.67±0.26
2911372	BAG2	BCL2-associated athanogene 2	0.000389	1.48	8.23±0.56	7.66±0.59
3568667	MAX	MYC associated factor X	0.000392	-1.14	6.72±0.16	6.91±0.2
3774906	SECTM1	secreted and transmembrane 1	0.000394	-1.36	5.81±0.23	6.26±0.5
2763278	GPR125	G protein-coupled receptor 125	0.000398	1.23	6.4±0.28	6.1±0.3
2930418	UST	urolyn-2-sulfotransferase	0.000398	1.28	7.34±0.41	6.98±0.35
3960902	NPTXR	neuronal pentraxin receptor	0.000398	1.18	6.84±0.23	6.6±0.25
3962219	NAGA	N-acetylgalactosaminidase, alpha-	0.000399	-1.25	7.75±0.25	8.06±0.34
3210616	PRUNE2	prune homolog 2 (Drosophila)	4.00E-04	1.83	9.9±0.49	9.03±0.98
3990512	SASH3	SAM and SH3 domain containing 3	0.000401	-1.32	5.38±0.23	5.78±0.45
4014759	NAP1L3	nucleosome assembly protein 1-like 3	0.000405	1.37	8.03±0.36	7.57±0.49
2385797	KIAA1804	mixed lineage kinase 4	0.000407	1.1	5.9±0.14	5.76±0.13
2598099	BAR1	BRCA1 associated RING domain 1	0.000407	1.35	7.33±0.45	6.89±0.44
3632298	ADPGK	ADP-dependent glucokinase	0.00041	-1.24	6.34±0.23	6.65±0.34
2520533	OBFC2A	oligonucleotide/oligosaccharide-binding fold containing 2A	0.000411	-1.52	6.73±0.32	7.34±0.69
2636695	ZDHHC23	zinc finger, DHHC-type containing 23	0.000411	1.15	6.04±0.19	5.84±0.21
3893086	SLC17A9	solute carrier family 17, member 9	0.000418	-1.14	6.68±0.18	6.88±0.2
2428425	PPM1J	protein phosphatase 1J (PP2C domain containing)	0.000418	1.12	5.67±0.14	5.5±0.17
3645477	PAQR4	progesterin and adipoQ receptor family member IV	0.000421	-1.14	6.13±0.24	6.32±0.17
2816681	PDE8B	phosphodiesterase 8B	0.000422	1.9	8.01±0.68	7.09±1
2807359	OSMR	oncostatin M receptor	0.000424	-1.4	7.94±0.41	8.42±0.52
2908179	VEGFA	vascular endothelial growth factor A	0.000424	-1.84	6.27±0.58	7.14±0.98
2519577	COL3A1	collagen, type III, alpha 1	0.000428	-1.41	10.7±0.45	11.2±0.53
3339774	P2RY6	pyrimidinergic receptor P2Y, G-protein coupled, 6	0.000429	-1.25	5.5±0.26	5.81±0.34
3217123	TRIM14	tripartite motif-containing 14	0.00043	-1.26	6.1±0.32	6.44±0.35
2902326	HCP5	HLA complex P5	0.000437	-1.58	5.21±0.23	5.87±0.76
3949229	TBC1D22A	TBC1 domain family, member 22A	0.000441	-1.13	7.69±0.17	7.87±0.19
3846238	C19orf28	chromosome 19 open reading frame 28	0.000442	-1.2	6.79±0.14	7.05±0.3
2790368	SFRP2	secreted frizzled-related protein 2	0.000445	-3.1	4.89±0.74	6.52±1.9
3225952	FAM129B	family with sequence similarity 129, member B	0.000448	-1.24	8.17±0.34	8.48±0.31
3222170	TNC	tenascin C	0.00045	-1.94	5.84±0.56	6.79±1.1
3091403	EPHX2	epoxide hydrolase 2, cytoplasmic	0.000451	1.22	6.01±0.26	5.73±0.31
3923436	TRAPPCC10	trafficking protein particle complex 10	0.000452	-1.17	6.78±0.24	7.01±0.23
2765865	C4orf19	chromosome 4 open reading frame 19	0.000453	-1.25	7.63±0.18	7.95±0.37
2738378	NPNT	nephronectin	0.000454	1.76	10.2±0.27	9.39±0.95
3722338	IFI35	interferon-induced protein 35	0.000455	-1.29	6.67±0.26	7.04±0.41
3228523	GBGT1	globoside alpha-1,3-N-acetylgalactosaminyltransferase 1	0.000456	-1.26	5.89±0.23	6.23±0.37
2715580	SH3BP2	SH3-domain binding protein 2	0.000457	-1.23	5.78±0.17	6.08±0.34
3744680	PIK3R5	phosphoinositide-3-kinase, regulatory subunit 5	0.000457	-1.24	5.72±0.19	6.03±0.35
3983537	PABPC5	poly(A) binding protein, cytoplasmic 5	0.000458	1.26	5.81±0.31	5.49±0.35
3388365	PGR	progesterone receptor	0.000459	1.55	8.08±0.39	7.45±0.71
3823842	TMEM38A	transmembrane protein 38A	0.000463	1.16	6.52±0.2	6.31±0.23
3432090	ALDH2	aldehyde dehydrogenase 2 family (mitochondrial)	0.000464	1.24	9.26±0.26	8.96±0.33
2950214	TAP1	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	0.000467	-1.3	6.85±0.18	7.23±0.44
3623031	FBN1	fibrillin 1	0.00047	-1.3	9.76±0.37	10.1±0.4
3638760	IDH2	isocitrate dehydrogenase 2 (NADP+), mitochondrial	0.000477	-1.26	7.19±0.22	7.53±0.37
3951927	BID	BH3 interacting domain death agonist	0.000477	-1.16	5.79±0.18	6.01±0.24
3468345	IGF1	insulin-like growth factor 1 (somatomedin C)	0.000481	-1.86	6.36±0.49	7.25±1
3188697	NEK6	NIMA (never in mitosis gene a)-related kinase 6	0.000481	-1.26	7.68±0.31	8.01±0.36
3415576	KRT18	keratin 18	0.000489	-2.41	5.92±0.88	7.19±1.4
2562271	CAPG	capping protein (actin filament), gelsolin-like	0.00049	-1.59	6.87±0.37	7.53±0.76
3997946	PRKX	protein kinase, X-linked	0.000496	-1.42	5.85±0.31	6.35±0.58
2859565	ADAMTS6	ADAM metalloproteinase with thrombospondin type 1 motif, 6	0.000498	1.43	6.04±0.38	5.52±0.58
3394192	DPAGT1	dolichyl-phosphate (UDP-N-acetylglucosamine) N-acetylglucosaminylphosphotransferase 1 (Glc)	0.000499	-1.16	6.53±0.23	6.74±0.22
3177111	NTRK2	neurotrophic tyrosine kinase, receptor, type 2	0.000504	-1.51	5.7±0.36	6.3±0.68
3751625	SSH2	slingshot homolog 2 (Drosophila)	0.000507	-1.41	5.69±0.3	6.19±0.57
3895614	SIGLEC1	sialic acid binding Ig-like lectin 1, sialoadhesin	0.000508	-1.23	6.09±0.2	6.39±0.33
3331926	FAM111A	family with sequence similarity 111, member A	0.000513	-1.21	7.12±0.22	7.39±0.3
3485292	NBEA	neurobeachin	0.000515	1.31	6.42±0.3	6.02±0.44

meta probeset ID	genesymbol	genename	p-value	fold-change	log2(BAV)	log2(TAV)
2601648	DOCK10	dedicator of cytokinesis 10	0.000515	-1.68	7.51±0.73	8.25±0.79
3979912	AR	androgen receptor	0.000519	1.59	7.9±0.38	7.24±0.77
2975014	SGK1	serum/glucocorticoid regulated kinase 1	0.000519	-1.71	7.11±0.54	7.88±0.87
3538893	PRKCH	protein kinase C, eta	0.00052	-1.61	5.13±0.27	5.81±0.8
3557614	AP1G2	adaptor-related protein complex 1, gamma 2 subunit	0.000522	-1.19	5.81±0.17	6.07±0.29
3163982	ADAMTSL1	ADAMTS-like 1	0.000523	1.39	7.3±0.3	6.82±0.55
3968512	CLCN4	chloride channel 4	0.000528	1.2	6.09±0.2	5.83±0.29
3949722	FAM19A5	family with sequence similarity 19 (chemokine (C-C motif)-like), member A5	0.000528	1.31	7.7±0.31	7.31±0.44
2622696	SEMA3B	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3B	0.000529	1.17	7.22±0.17	6.99±0.26
3781531	CABLES1	Cdk5 and Abl enzyme substrate 1	0.000529	1.57	7.49±0.36	6.84±0.76
2567242	CHST10	carbohydrate sulfotransferase 10	0.000536	1.17	6.59±0.21	6.37±0.24
3961068	PDGFB	platelet-derived growth factor beta polypeptide (simian sarcoma viral (v-sis) oncogene homolog	0.000536	-1.18	5.44±0.22	5.67±0.25
2699145	ST13	suppression of tumorigenicity 13 (colon carcinoma) (Hsp70 interacting protein)	0.000541	-1.53	5.88±0.36	6.49±0.71
2615060	RBMS3	RNA binding motif, single stranded interacting protein	0.000546	1.26	9.54±0.28	9.2±0.37
3442641	CD163L1	CD163 molecule-like 1	0.000548	-1.65	5.24±0.5	5.96±0.82
3228884	VAV2	vav 2 guanine nucleotide exchange factor	0.000549	-1.13	5.86±0.18	6.03±0.18
2458629	LEFTY2	left-right determination factor 2	0.000552	1.96	9.57±0.87	8.59±1.1
2327482	RCC1	regulator of chromosome condensation 1	0.000554	-1.2	5.55±0.17	5.82±0.31
3445820	RERG	RAS-like, estrogen-regulated, growth inhibitor	0.000555	1.55	8.4±0.61	7.77±0.68
3866302	AP2S1	adaptor-related protein complex 2, sigma 1 subunit	0.000556	-1.28	7.87±0.2	8.23±0.42
2902804	C2	complement component 2	0.000556	-1.72	5.26±0.36	6.04±0.92
2323172	IGSF21	immunoglobulin superfamily, member 21	0.00056	-1.23	5.72±0.18	6.01±0.34
2611848	SLC6A6	solute carrier family 6 (neurotransmitter transporter, taurine), member 6	0.000561	-1.42	7.27±0.43	7.78±0.56
2807686	CARD6	caspase recruitment domain family, member 6	0.000568	-1.35	5.65±0.37	6.08±0.48
2358360	ECM1	extracellular matrix protein 1	0.000572	-1.45	6.31±0.37	6.85±0.61
2607923	CNTN4	contactin 4	0.000578	2.03	7.81±0.56	6.79±1.2
3113280	DEPDC6	DEP domain containing 6	0.000581	-2.01	5.57±0.45	6.58±1.2
2488038	NAGK	N-acetylglucosamine kinase	0.000591	-1.15	8.74±0.2	8.94±0.22
2663130	TIMP4	TIMP metalloproteinase inhibitor 4	6.00E-04	1.44	7.09±0.57	6.57±0.55
2548776	ATL2	atlastin GTPase 2	0.000603	1.25	8±0.38	7.68±0.32
3918535	IL10RB	interleukin 10 receptor, beta	0.000605	-1.29	7.62±0.33	7.99±0.41
3820443	ICAM1	intercellular adhesion molecule 1	0.00061	-1.65	5.38±0.4	6.1±0.85
2385343	DISC1	disrupted in schizophrenia 1	0.000613	-1.26	5.53±0.17	5.86±0.39
3645626	IL32	interleukin 32	0.000617	-1.53	6.39±0.34	7±0.72
3161113	PDCD1LG2	programmed cell death 1 ligand 2	0.000618	-1.47	5.53±0.39	6.08±0.64
3497881	FARP1	FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived)	0.000624	-1.42	6.98±0.54	7.49±0.54
3102372	SULF1	sulfatase 1	0.00063	-1.42	9.74±0.55	10.2±0.53
3695631	TPPP3	tubulin polymerization-promoting protein family member 3	0.000633	-1.55	5.89±0.46	6.52±0.72
3655723	MVP	major vault protein	0.00064	-1.16	7.56±0.21	7.78±0.24
2331822	ZMPSTE24	zinc metalloproteinase (STE24 homolog, S. cerevisiae)	0.000642	1.3	9.4±0.35	9.02±0.42
2518729	DUSP19	dual specificity phosphatase 19	0.000644	1.31	6.37±0.35	5.98±0.44
2362394	IFI16	interferon, gamma-inducible protein 16	0.000646	-1.65	6.75±0.42	7.48±0.85
3956781	AP1B1	adaptor-related protein complex 1, beta 1 subunit	0.000648	-1.26	7.37±0.3	7.7±0.38
2725061	LIMCH1	LIM and calponin homology domains 1	0.00065	1.35	9.21±0.31	8.77±0.5
3736636	C1QTNF1	C1q and tumor necrosis factor related protein 1	0.000656	-1.3	7.55±0.31	7.93±0.42
3670918	PLCG2	phospholipase C, gamma 2 (phosphatidylinositol-specific)	0.000656	-1.49	5.06±0.19	5.64±0.69
2556302	PELL1	pellino homolog 1 (Drosophila)	0.000664	-1.43	6.61±0.35	7.12±0.6
3576749	FBLN5	fibulin 5	0.000672	1.44	11.8±0.33	11.2±0.62
3356328	ADAMTS15	ADAM metalloproteinase with thrombospondin type 1 motif, 15	0.000672	-1.2	5.47±0.22	5.73±0.29
3031517	GIMAP7	GTPase, IMAP family member 7	0.000673	-1.95	5.67±0.33	6.64±1.2
3301263	SORBS1	sorbin and SH3 domain containing 1	0.000676	1.51	10±0.4	9.45±0.69
2457842	TP53BP2	tumor protein p53 binding protein, 2	0.000676	1.26	8.27±0.28	7.93±0.38
3494706	SLAIN1	SLAIN motif family, member 1	0.000676	1.49	6.09±0.43	5.52±0.67
3995392	ZNF185	zinc finger protein 185 (LIM domain)	0.000676	1.3	6.49±0.46	6.12±0.38
3124537	CTSB	cathepsin B	0.000676	-1.45	9.66±0.34	10.2±0.62
3985511	TCEAL7	transcription elongation factor A (SII)-like 7	0.000679	1.36	7.03±0.34	6.58±0.52
2620448	CLEC3B	C-type lectin domain family 3, member B	0.000679	-1.35	6.23±0.32	6.66±0.5
2408499	SCMH1	sex comb on midleg homolog 1 (Drosophila)	0.000687	1.2	8.39±0.29	8.13±0.28
3734966	MYO15B	myosin XVb pseudogene	0.000687	-1.15	5.99±0.16	6.19±0.23
2375144	LGR6	leucine-rich repeat-containing G protein-coupled receptor 6	0.00069	1.93	8±0.42	7.06±1.1
3657041	ITGAX	integrin, alpha X (complement component 3 receptor 4 subunit)	0.00069	-1.5	5.51±0.3	6.09±0.69
2387126	RYR2	ryanodine receptor 2 (cardiac)	0.000693	1.65	7.02±0.74	6.3±0.78
2732942	BMP2K	BMP2 inducible kinase	0.000696	-1.5	7.02±0.25	7.6±0.7
3664785	CKLF	chemokine-like factor	0.000697	-1.54	6.55±0.43	7.17±0.72
3028858	EPHB6	EPH receptor B6	0.000705	1.17	6.46±0.19	6.23±0.25
2919669	PRDM1	PR domain containing 1, with ZNF domain	0.000707	-1.68	5.16±0.24	5.9±0.9
3597125	TLN2	talin 2	0.000708	1.41	7.48±0.32	6.99±0.59
3446919	ABCC9	ATP-binding cassette, sub-family C (CFTR/MRP), member 9	0.000717	1.68	7.3±0.62	6.56±0.86
2369110	RASAL2	RAS protein activator like 2	0.000726	-1.26	7.56±0.33	7.89±0.38
3632037	PARP6	poly (ADP-ribose) polymerase family, member 6	0.000729	-1.13	7.39±0.21	7.57±0.18
3167553	IL11RA	interleukin 11 receptor, alpha	0.00073	1.2	7.61±0.24	7.35±0.29
2800711	ADCY2	adenylate cyclase 2 (brain)	0.000733	1.35	6.6±0.23	6.17±0.51
3887117	CTSA	cathepsin A	0.000735	-1.26	9.19±0.41	9.52±0.33
2854445	DAB2	disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila)	0.000736	-1.53	8.3±0.45	8.91±0.72
3717870	TMEM98	transmembrane protein 98	0.000736	1.31	8.22±0.38	7.83±0.44
3838067	BAX	BCL2-associated X protein	0.000737	-1.19	6.58±0.25	6.83±0.27
3673091	BANP	BTG3 associated nuclear protein	0.00074	-1.08	6.58±0.16	6.69±0.086
3762198	COL1A1	collagen, type I, alpha 1	0.00074	-1.67	9.97±0.6	10.7±0.86
3766621	ICAM2	intercellular adhesion molecule 2	0.000742	-1.34	5.31±0.25	5.74±0.51
3220977	ROD1	ROD1 regulator of differentiation 1 (S. pombe)	0.000742	-1.29	8.56±0.3	8.93±0.43
3164086	ADAMTSL1	ADAMTS-like 1	0.000747	1.36	7.65±0.33	7.21±0.52
3154317	NDRG1	N-myc downstream regulated 1	0.000767	-1.27	9.03±0.4	9.38±0.37

#### aorta intima-media, only undilated patients, comparing BAV and TAV, for all genes

meta probeset ID	genesymbol	genename	p-value	fold-change	log2(BAV)	log2(TAV)
2458629	LEFTY2	left-right determination factor 2	4.57E-05	1.83	9.47±0.44	8.6±0.64
2376168	NFASC	neurofascin homolog (chicken)	0.000411	-1.2	5.84±0.25	6.1±0.18
2794792	VEGFC	vascular endothelial growth factor C	0.000628	-1.23	5.62±0.23	5.92±0.26
2732655	FRAS1	Fraser syndrome 1	0.000668	1.51	6.36±0.57	5.77±0.45
3623270	SHC4	SHC (Src homology 2 domain containing) family, member 4	0.000691	1.56	7.82±0.56	7.18±0.54
3846507	DAPK3	death-associated protein kinase 3	0.000724	1.21	7.81±0.23	7.53±0.24
3317071	LSP1	lymphocyte-specific protein 1	0.000731	-1.4	7.92±0.38	8.4±0.43

#### aorta adventitia, only dilated patients, comparing BAV and TAV, for all genes

meta probeset ID	genesymbol	genename	p-value	fold-change	log2(BAV)	log2(TAV)
2407224	RSPO1	R-spondin homolog (Xenopus laevis)	3.45E-08	1.27	6.05±0.27	5.7±0.16
3417574	SPRYD4	SPRY domain containing 4	1.59E-06	1.26	6.43±0.27	6.1±0.2
3647421	ABAT	4-aminobutyrate aminotransferase	2.24E-06	1.4	7.63±0.34	7.15±0.32
2478748	EML4	echinoderm microtubule associated protein like 4	1.46E-05	-1.33	7.91±0.29	8.32±0.31
2565902	ANKRD36	ankyrin repeat domain 36	1.78E-05	-1.73	7.79±0.55	8.58±0.62
2602770	DNER	delta/notch-like EGF repeat containing	1.96E-05	1.32	6.02±0.29	5.63±0.31
3028858	EPHB6	EPH receptor B6	2.27E-05	1.18	6.38±0.14	6.15±0.19
3757108	KRT19	keratin 19	2.69E-05	1.38	7.47±0.51	7±0.29
2603844	ECEL1	endothelin converting enzyme-like 1	2.79E-05	1.15	5.88±0.19	5.67±0.15

meta probeset ID	genesymbol	genename	p-value	fold-change	log2(BAV)	log2(TAV)
2409770	TMEM53	transmembrane protein 53	3.05E-05	1.18	5.92±0.23	5.69±0.17
2693409	ALDH1L1	aldehyde dehydrogenase 1 family, member L1	4.43E-05	1.26	6.41±0.23	6.08±0.28
2519577	COL3A1	collagen, type III, alpha 1	7.04E-05	-1.58	10.7±0.45	11.3±0.58
3542275	SMOC1	SPARC related modular calcium binding 1	9.22E-05	1.24	6.59±0.33	6.28±0.24
3416921	RDH5	retinol dehydrogenase 5 (11-cis/9-cis)	0.000102	1.25	6.72±0.37	6.39±0.24
3153428	ASAP1	ArfGAP with SH3 domain, ankyrin repeat and PH domain 1	0.000104	-1.33	7.39±0.43	7.8±0.32
2842194	CPLX2	complexin 2	0.000108	1.28	6.73±0.35	6.38±0.29
3762198	COL1A1	collagen, type I, alpha 1	0.000136	-1.85	9.74±0.6	10.6±0.83
3886576	WISP2	WNT1 inducible signaling pathway protein 2	0.000139	1.43	8.9±0.36	8.39±0.48
2651989	SKIL	SKI-like oncogene	0.00014	-1.35	7.98±0.35	8.4±0.39
2584134	FAP	fibroblast activation protein, alpha	0.000174	-1.98	6.81±0.75	7.8±0.92
3788097	MAPK4	mitogen-activated protein kinase 4	0.000178	1.21	5.64±0.27	5.37±0.24
3543673	ACOT2	acyl-CoA thioesterase 2	0.000179	1.27	7.52±0.33	7.17±0.31
2961177	COL12A1	collagen, type XII, alpha 1	0.000179	-1.61	7.86±0.45	8.55±0.66
3854132	CPAMD8	C3 and PZP-like, alpha-2-macroglobulin domain containing 8	0.000184	1.2	6.21±0.31	5.95±0.19
3761806	PHB	prohibitin	0.000193	1.21	7.61±0.26	7.33±0.25
3540091	ZBTB1	zinc finger and BTB domain containing 1	0.000209	-1.24	7.71±0.27	8.02±0.29
3997825	MXRA5	matrix-remodelling associated 5	0.000212	-1.93	6.69±0.71	7.63±0.91
2922972	DCBLD1	discoidin, CUB and LCCI domain containing 1	0.000218	-1.3	6.64±0.29	7.02±0.36
3678462	PPL	perioplakin	0.000222	1.26	6.4±0.24	6.07±0.32
3089401	PPP3CC	protein phosphatase 3 (formerly 2B), catalytic subunit, gamma isoform	0.000223	-1.24	7.12±0.27	7.43±0.29
2785282	SCLT1	sodium channel and clathrin linker 1	0.000246	-1.33	6.01±0.41	6.42±0.37
3178679	GADD45G	growth arrest and DNA-damage-inducible, gamma	0.000267	1.27	6.31±0.31	5.97±0.32
3844094	ZNF584	zinc finger protein 584	0.000279	1.14	6.78±0.13	6.59±0.19
2446047	ABL2	v-abl Abelson murine leukemia viral oncogene homolog 2 (arg, Abelson-related gene)	0.000283	-1.26	6.73±0.25	7.06±0.33
3103187	TERF1	telomeric repeat binding factor (NIMA-interacting) 1	0.000291	1.16	7.85±0.2	7.63±0.21
3690034	C16orf87	chromosome 16 open reading frame 87	0.000296	-1.22	5.67±0.3	5.96±0.26
2962767	PGM3	phosphoglucomutase 3	0.000302	-1.37	7.11±0.36	7.56±0.45
2417362	DIRAS3	DIRAS family, GTP-binding RAS-like 3	0.000341	1.33	6.16±0.38	5.75±0.39
2492898	C2orf51	chromosome 2 open reading frame 51	0.00035	1.2	6±0.33	5.73±0.21
3320123	ADM	adrenomedullin	0.000358	1.36	7.44±0.58	6.99±0.34
2413115	SLC1A7	solute carrier family 1 (glutamate transporter), member 7	0.000362	1.18	6.37±0.23	6.13±0.22
3843662	ZNF587	zinc finger protein 587	0.000364	-1.49	7.04±0.66	7.62±0.5
2756630	CPLX1	complexin 1	0.000453	1.18	6.95±0.23	6.71±0.24
3819474	ANGPTL4	angiopoietin-like 4	0.000512	1.18	6.06±0.22	5.82±0.24
2514969	GAD1	glutamate decarboxylase 1 (brain, 67kDa)	0.000515	1.33	5.5±0.49	5.09±0.36
2622359	RBM6	RNA binding motif protein 6	0.000527	-1.27	7.23±0.29	7.58±0.36
3181642	COL15A1	collagen, type XV, alpha 1	0.000564	-1.31	7.62±0.5	8.01±0.32
2622153	BSN	bassoon (presynaptic cytomatrix protein)	0.000574	1.12	5.74±0.14	5.58±0.16
3015786	ZAN	zonadhesin	0.000633	1.09	5.63±0.14	5.5±0.13
3174224	SMC5	structural maintenance of chromosomes 5	0.000667	-1.21	7.66±0.27	7.93±0.28
2539821	ADAM17	ADAM metalloproteinase domain 17	0.000672	-1.27	6.97±0.3	7.31±0.36
2392267	MORN1	MORN repeat containing 1	0.000683	1.09	5.78±0.13	5.66±0.12
2769539	CHIC2	cysteine-rich hydrophobic domain 2	0.000722	-1.26	7.49±0.25	7.82±0.36
3278401	FRMD4A	FERM domain containing 4A	0.000734	-1.18	6.77±0.26	7.01±0.24
4028716	PCDH11X	protocadherin 11 X-linked	0.000735	2.78	6.2±1.6	4.73±1.5
3896594	LRRN4	leucine rich repeat neuronal 4	0.000758	1.25	6.11±0.43	5.79±0.27
3632037	PARP6	poly (ADP-ribose) polymerase family, member 6	0.00076	-1.17	7.23±0.24	7.46±0.23

**aorta adventitia, only undiluted patients, comparing BAV and TAV, for all genes**

meta probeset ID	genesymbol	genename	p-value	fold-change	log2(BAV)	log2(TAV)
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**aorta intima-media, only BAV patients, comparing dilated and undilated, for all genes**

meta probeset ID	genesymbol	genename	p-value	fold-change	log2(dilated)	log2(undilated)
3360401	HBB	hemoglobin, beta	2.02E-06	-2.91	5.95±0.99	7.49±1.2
2322103	SPEN	spen homolog, transcriptional regulator (Drosophila)	1.55E-05	1.36	8.38±0.35	7.93±0.37
3982293	MAGEE1	melanoma antigen family E, 1	2.59E-05	1.19	6.73±0.26	6.48±0.18
3268059	TACC2	transforming, acidic coiled-coil containing protein 2	3.26E-05	1.25	7.52±0.35	7.21±0.24
3591459	MAP1A	microtubule-associated protein 1A	4.00E-05	1.38	6.93±0.38	6.47±0.41
2400793	HSPG2	heparan sulfate proteoglycan 2	4.96E-05	1.32	9.68±0.37	9.27±0.36
3633578	CSPG4	chondroitin sulfate proteoglycan 4	6.05E-05	1.35	8.01±0.41	7.58±0.37
3351385	MLL	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila)	8.17E-05	1.35	8.9±0.32	8.47±0.42
3903525	NCOA6	nuclear receptor coactivator 6	8.89E-05	1.26	7.29±0.29	6.96±0.31
3677795	CREBBP	CREB binding protein	1.00E-04	1.27	8.69±0.35	8.34±0.31
3164086	ADAMTSL1	ADAMTS-like 1	0.000108	1.31	7.65±0.33	7.26±0.37
3645253	SRRM2	serine/arginine repetitive matrix 2	0.000109	1.29	8.87±0.38	8.5±0.32
3978453	GNL3L	guanine nucleotide binding protein-like 3 (nucleolar)-like	0.00011	1.17	7.21±0.22	6.98±0.22
3465274	DCN	decorin	0.000118	-1.82	8.17±1	9.03±0.7
3981027	TAF1	TAF1 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 250kDa	0.000122	1.23	7.42±0.26	7.13±0.28
3465248	LUM	lumican	0.000137	-1.85	6.95±1.1	7.84±0.71
2599500	ZNF142	zinc finger protein 142	0.000137	1.21	6.59±0.24	6.32±0.26
3264621	TCF7L2	transcription factor 7-like 2 (T-cell specific, HMG-box)	0.000147	1.3	8.09±0.42	7.71±0.34
3946615	EP300	E1A binding protein p300	0.000156	1.31	8.12±0.36	7.73±0.38
3708704	POLR2A	polymerase (RNA) II (DNA directed) polypeptide A, 220kDa	0.000157	1.24	8.1±0.31	7.78±0.3
2326640	ARID1A	AT rich interactive domain 1A (SWI-like)	0.000159	1.21	7.38±0.25	7.09±0.28
2316953	PRDM16	PR domain containing 16	0.000167	1.21	7.98±0.3	7.71±0.25
3377669	LTBP3	latent transforming growth factor beta binding protein 3	0.000179	1.31	9.78±0.42	9.38±0.37
2899243	HIST1H4F	histone cluster 1, H4f	0.000186	-1.29	6.57±0.34	6.94±0.36
3168210	C9orf127	chromosome 9 open reading frame 127	0.00019	1.18	7.64±0.21	7.41±0.23
3192117	BAT2L	HLA-B associated transcript 2-like	0.000202	1.33	8.61±0.4	8.2±0.4
3858285	TSHZ3	teashirt zinc finger homeobox 3	0.000204	1.4	6±0.51	5.51±0.46
2435989	S100A8	S100 calcium binding protein A8	0.000236	-1.39	4.37±0.51	4.85±0.46
2902574	LY6G5B	lymphocyte antigen 6 complex, locus G5B	0.000238	1.27	6.9±0.36	6.55±0.34
2359817	INTS3	integrator complex subunit 3	0.000244	1.22	8.43±0.32	8.13±0.28
3740479	PRPF8	PRPF8 pre-mRNA processing factor 8 homolog (S. cerevisiae)	0.000244	1.24	9.41±0.27	9.1±0.33
4009315	HUWE1	HECT, UBA and WWE domain containing 1	0.000256	1.29	8.76±0.35	8.39±0.37
2363679	GenBank	Homo sapiens cDNA FLJ38759 fis, clone KIDNE2013263.	0.000264	1.28	6.22±0.31	5.87±0.37
2949380	VARS	valyl-tRNA synthetase	0.000305	1.08	6.63±0.13	6.52±0.11
2392985	FLJ42875	hypothetical LOC440556	0.000324	1.22	7.5±0.3	7.21±0.28
2895159	HIVEP1	human immunodeficiency virus type I enhancer binding protein 1	0.000334	1.32	7.62±0.3	7.22±0.44
3698256	ZFX3	zinc finger homeobox 3	0.00034	1.26	8.08±0.34	7.75±0.34
3816645	ZNF554	zinc finger protein 554	0.000347	-1.11	6.48±0.15	6.63±0.15
2761321	BOD1L	bioorientation of chromosomes in cell division 1-like	0.00035	1.31	7.74±0.4	7.35±0.41
3833620	LTBP4	latent transforming growth factor beta binding protein 4	0.000353	1.32	10.3±0.4	9.94±0.41
3191338	GPR107	G protein-coupled receptor 107	0.000362	1.22	7.76±0.34	7.47±0.28
3922921	NDUFV3	NADH dehydrogenase (ubiquinone) flavoprotein 3, 10kDa	0.00038	1.14	6.97±0.2	6.78±0.2
3417842	LRP1	low density lipoprotein-related protein 1 (alpha-2-macroglobulin receptor)	0.000395	1.29	10.3±0.39	9.95±0.38
3104013	ZFX4	zinc finger homeobox 4	0.000398	1.28	6.36±0.4	6±0.36
2902463	BAT2	HLA-B associated transcript 2	0.000402	1.27	7.93±0.37	7.59±0.34
3853108	NOTCH3	Notch homolog 3 (Drosophila)	0.000417	1.36	8.95±0.41	8.5±0.49
3553141	TECPR2	tectonin beta-propeller repeat containing 2	0.000422	1.13	7.19±0.18	7.01±0.19
2374746	NAV1	neuron navigator 1	0.000431	1.3	8.23±0.46	7.85±0.37
2696309	AMOTL2	angiomotin like 2	0.000435	1.24	7.73±0.33	7.42±0.33

meta probeset ID	genesymbol	genename	p-value	fold-change	log2(dilated)	log2(undilated)
3980758	MED12	mediator complex subunit 12	0.000436	1.2	7.47±0.25	7.21±0.28
3610982	SYNM	synemin, intermediate filament protein	0.000442	1.19	9.25±0.23	9.01±0.27
2491676	VAMP5	vesicle-associated membrane protein 5 (myobrevin)	0.000463	-1.17	7.63±0.27	7.86±0.23
3947123	SREBF2	sterol regulatory element binding transcription factor 2	0.000474	1.3	7.84±0.39	7.45±0.41
3453592	MLL2	myeloid/lymphoid or mixed-lineage leukemia 2	0.000478	1.2	6.97±0.31	6.71±0.26
2367154	BAT2D1	BAT2 domain containing 1	0.000481	1.31	8.7±0.35	8.31±0.43
3825650	KIAA0892	KIAA0892	0.000496	1.16	6.96±0.24	6.74±0.22
3665550	FAM65A	family with sequence similarity 65, member A	0.000498	1.22	7.31±0.31	7.03±0.3
4026956	HCFC1	host cell factor C1 (VP16-accessory protein)	0.000504	1.21	7.71±0.3	7.43±0.29
2390976	ZNF596	zinc finger protein 596	0.000508	-1.16	6.96±0.24	7.18±0.22
3380901	NUMA1	nuclear mitotic apparatus protein 1	0.000508	1.19	8.96±0.29	8.7±0.26
2536071	SNED1	sushi, nidogen and EGF-like domains 1	0.000508	1.16	6.95±0.24	6.74±0.22
2886174	SLIT3	slit homolog 3 (Drosophila)	0.000513	1.4	8.17±0.47	7.69±0.53
2395890	CLSTN1	calsyntenin 1	0.000514	1.25	8.38±0.33	8.06±0.34
3822657	CD97	CD97 molecule	0.000517	1.3	9.13±0.32	8.76±0.42
3339812	ARHGEF17	Rho guanine nucleotide exchange factor (GEF) 17	0.00052	1.25	8.52±0.4	8.2±0.32
3438617	EP400	E1A binding protein p400	0.000524	1.19	7.36±0.26	7.11±0.26
3580498	CDC42BPB	CDC42 binding protein kinase beta (DMPK-like)	0.000528	1.22	8.35±0.33	8.06±0.3
3734797	KIAA0195	KIAA0195	0.000569	1.15	7.12±0.18	6.92±0.23
2640579	PLXNA1	plexin A1	0.00057	1.19	8.04±0.33	7.79±0.24
3748026	TOM1L2	target of myb1-like 2 (chicken)	0.000573	1.24	8.37±0.33	8.05±0.34
2715476	C4orf8	chromosome 4 open reading frame 8	0.000578	1.22	6.31±0.29	6.03±0.31
2709606	RPL39L	ribosomal protein L39-like	0.000602	-1.29	6.01±0.35	6.38±0.42
3204744	TLN1	talin 1	0.00062	1.25	10.8±0.32	10.5±0.36
3373675	TNKS1BP1	tankyrase 1 binding protein 1, 182kDa	0.000627	1.16	7.5±0.21	7.29±0.23
3837431	EHD2	EH-domain containing 2	0.000642	1.26	8.45±0.35	8.11±0.37
2599153	TNS1	tensin 1	0.000649	1.28	11.3±0.41	11±0.37
3959451	MYH9	myosin, heavy chain 9, non-muscle	0.000651	1.26	11.5±0.37	11.2±0.36
3502570	LAMP1	lysosomal-associated membrane protein 1	0.000665	1.24	9.34±0.32	9.03±0.34
3924573	PCNT	pericentrin	0.000683	1.13	6.51±0.21	6.33±0.18
3704717	ANKRD11	ankyrin repeat domain 11	0.000697	1.23	7.56±0.34	7.27±0.31
3071630	GenBank	Homo sapiens cDNA FU10522 fis, clone NT2RP2000845.	0.000704	1.3	6.32±0.31	5.94±0.44
3874498	MAVS	mitochondrial antiviral signaling protein	0.000705	1.17	7.71±0.23	7.49±0.25
3014411	TRRAP	transformation/transcription domain-associated protein	0.000706	1.17	7.42±0.23	7.19±0.26
2906824	FOXP4	forkhead box P4	0.00071	1.25	7.17±0.39	6.85±0.33
3821200	PRKCSH	protein kinase C substrate 80K-H	0.000711	1.17	8.77±0.24	8.54±0.25
3928070	CCT8	chaperonin containing TCP1, subunit 8 (theta)	0.000715	-1.15	6.91±0.25	7.11±0.21
2413907	DHCR24	24-dehydrocholesterol reductase	0.000717	1.37	7.07±0.56	6.62±0.47
3715703	SUPT6H	suppressor of Ty 6 homolog (S. cerevisiae)	0.000721	1.22	8.84±0.33	8.56±0.3
2609608	SETD5	SET domain containing 5	0.000726	1.24	8.57±0.32	8.25±0.35
3976163	USP11	ubiquitin specific peptidase 11	0.000735	1.19	9.1±0.29	8.85±0.26
2800477	SRD5A1	steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5 alpha-steroid delta 4-dehydrogenase al	0.000757	-1.12	6.78±0.2	6.95±0.18

#### aorta intima-media, only TAV patients, comparing dilated and undilated, for all genes

meta probeset ID	genesymbol	genename	p-value	fold-change	log2(dilated)	log2(undilated)
3772719	LGALS3BP	lectin, galactoside-binding, soluble, 3 binding protein	1.17E-07	1.75	9.33±0.43	8.52±0.35
2428425	PPM1J	protein phosphatase 1J (PP2C domain containing)	1.12E-06	-1.27	5.5±0.17	5.85±0.19
3101681	C8orf46	chromosome 8 open reading frame 46	1.54E-06	-1.27	5.77±0.19	6.11±0.19
3131741	RAB11FIP1	RAB11 family interacting protein 1 (class I)	1.54E-06	1.42	6.35±0.34	5.84±0.21
3382698	LRRRC32	leucine rich repeat containing 32	1.62E-06	1.88	9.2±0.58	8.29±0.44
3256590	PAPS2	3'-phosphoadenosine 5'-phosphosulfate synthase 2	2.23E-06	1.85	7.2±0.53	6.32±0.47
3167553	IL11RA	interleukin 11 receptor, alpha	4.88E-06	-1.32	7.35±0.29	7.75±0.17
3722917	GRN	granulin	5.10E-06	1.62	10.0±0.45	9.34±0.37
3626826	MYO1E	myosin IE	5.12E-06	1.47	8.33±0.32	7.77±0.33
2886174	SLIT3	slit homolog 3 (Drosophila)	6.37E-06	1.92	8.5±0.5	7.56±0.58
3853108	NOTCH3	Notch homolog 3 (Drosophila)	6.40E-06	1.74	9.25±0.56	8.46±0.4
394192	DPAQT1	dolichyl-phosphate (UDP-N-acetylglucosamine) N-acetylglucosaminophosphotransferase 1 (Glc	7.55E-06	1.28	6.74±0.22	6.39±0.21
2736462	BMPRI1B	bone morphogenetic protein receptor, type IB	8.58E-06	-2.25	6.73±0.88	7.9±0.55
3996381	ATP6AP1	ATPase, H+ transporting, lysosomal accessory protein 1	1.02E-05	1.25	9.08±0.22	8.75±0.19
3762198	COL1A1	collagen, type I, alpha 1	1.04E-05	2.12	10.7±0.86	9.63±0.47
3294231	NUDT13	nudix (nucleoside diphosphate linked moiety X)-type motif 13	1.13E-05	1.32	6.12±0.24	5.72±0.24
3843566	ZNF587	zinc finger protein 587	1.21E-05	1.69	6.16±0.29	5.4±0.51
2443120	DPT	dermatopontin	1.24E-05	-2.17	8.37±0.75	9.48±0.65
3278401	FRMD4A	FERM domain containing 4A	1.28E-05	1.42	7.1±0.42	6.59±0.2
3632037	PARP6	poly (ADP-ribose) polymerase family, member 6	1.31E-05	1.29	7.57±0.18	7.21±0.24
3623031	FBN1	fibrillin 1	1.46E-05	1.64	10.1±0.4	9.43±0.46
2956217	C6orf138	chromosome 6 open reading frame 138	1.54E-05	-1.27	5.94±0.21	6.28±0.22
2702610	SHOX2	short stature homeobox 2	1.55E-05	-1.32	6.05±0.22	6.44±0.26
3293762	PSAP	prosaposin	1.70E-05	1.27	11.4±0.22	11.1±0.21
3891006	STX16	syntaxin 16	1.97E-05	1.32	7.93±0.22	7.53±0.26
2437152	THBS3	thrombospondin 3	2.02E-05	1.31	7.62±0.25	7.23±0.25
2794006	SCRG1	scrapie responsive protein 1	2.07E-05	-1.84	6.5±0.73	7.37±0.39
3417842	LRP1	low density lipoprotein-related protein 1 (alpha-2-macroglobulin receptor)	2.21E-05	1.39	10.5±0.36	10±0.27
2345239	LOC339524	hypothetical LOC339524	2.24E-05	-1.23	5.59±0.19	5.89±0.19
2602770	DNER	delta/notch-like EGF repeat containing	2.24E-05	-1.43	5.82±0.42	6.34±0.25
3555340	TEP1	telomerase-associated protein 1	2.32E-05	1.21	7.23±0.15	6.95±0.19
3608787	SLCO3A1	solute carrier organic anion transporter family, member 3A1	2.52E-05	1.33	7.79±0.26	7.38±0.27
3722820	TMUB2	transmembrane and ubiquitin-like domain containing 2	2.68E-05	1.14	7.11±0.11	6.91±0.13
2648305	P2RY1	purinergic receptor P2Y, G-protein coupled, 1	2.68E-05	-1.37	6.17±0.35	6.62±0.25
3516228	PCDH20	protocadherin 20	2.86E-05	-1.6	4.6±0.52	5.27±0.38
3631397	UACA	uveal autoantigen with coiled-coil domains and ankyrin repeats	3.17E-05	1.55	9.88±0.42	9.25±0.41
3750740	PIGS	phosphatidylinositol glycan anchor biosynthesis, class 5	3.20E-05	1.21	7.48±0.15	7.21±0.19
3639070	VPS33B	vacuolar protein sorting 33 homolog B (yeast)	3.21E-05	1.15	5.98±0.13	5.77±0.14
3829638	KIAA0355	KIAA0355	3.28E-05	1.4	7.58±0.33	7.09±0.31
3886294	TOX2	TOX high mobility group box family member 2	3.29E-05	-1.22	5.92±0.21	6.2±0.17
2716328	ADRA2C	adrenergic, alpha-2C-, receptor	3.38E-05	-1.48	7.49±0.39	8.06±0.36
3568485	SPTB	spectrin, beta, erythrocytic	3.60E-05	1.36	6.44±0.31	5.99±0.29
3290875	ANK3	ankyrin 3, node of Ranvier (ankyrin G)	3.74E-05	1.74	7±0.65	6.21±0.42
3557898	TM9SF1	transmembrane 9 superfamily member 1	3.99E-05	1.26	7.74±0.24	7.41±0.2
2617796	EXOG	endo/exonuclease (5'-3'), endonuclease G-like	4.15E-05	1.34	6.98±0.29	6.56±0.28
3294476	ZMYND17	zinc finger, MYND-type containing 17	4.29E-05	1.27	5.77±0.2	5.43±0.24
2726396	ZAR1	zygote arrest 1	4.38E-05	-1.21	6.86±0.16	7.14±0.2
3480508	IL17D	interleukin 17D	4.47E-05	-1.28	7.41±0.22	7.76±0.24
3190035	CDK9	cyclin-dependent kinase 9	5.55E-05	1.17	8.72±0.18	8.5±0.13
3031181	ATP6VOE2	ATPase, H+ transporting V0 subunit e2	5.72E-05	-1.18	6.98±0.2	7.22±0.14
3300749	RBP4	retinol binding protein 4, plasma	5.73E-05	-1.82	6.13±0.74	6.99±0.45
3823842	TMEM38A	transmembrane protein 38A	5.82E-05	-1.28	6.31±0.23	6.66±0.25
2805078	CDH6	cadherin 6, type 2, K-cadherin (fetal kidney)	5.90E-05	1.4	5.84±0.43	5.36±0.22
3820612	SLC44A2	solute carrier family 44, member 2	5.95E-05	1.39	9.53±0.32	9.05±0.32
3026969	C7orf55	chromosome 7 open reading frame 55	6.03E-05	-1.22	6.72±0.21	7.01±0.18
3970214	REPS2	RALBP1 associated Eps domain containing 2	6.03E-05	-1.43	6.47±0.44	6.99±0.28
3497881	FRP1	FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived)	6.28E-05	1.61	7.49±0.54	6.8±0.42
3340589	SERPINH1	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein	6.55E-05	1.33	8.88±0.28	8.46±0.29
3064541	PLOD3	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3	6.91E-05	1.2	7.25±0.21	6.99±0.17

meta probeset ID	genesymbol	genename	p-value	fold-change	log2(dilated)	log2(undilated)
3962219	NAGA	N-acetylgalactosaminidase, alpha-	7.34E-05	1.33	8.06±0.34	7.65±0.25
2462160	NID1	nidogen 1	8.26E-05	1.49	7.3±0.33	6.72±0.43
3881686	TM9SF4	transmembrane 9 superfamily protein member 4	8.30E-05	1.2	7.9±0.17	7.64±0.19
3540398	FNTB	farnesyltransferase, CAAX box, beta	8.61E-05	1.2	6.77±0.19	6.5±0.18
2362991	CASQ1	calsequestrin 1 (fast-twitch, skeletal muscle)	8.62E-05	-1.44	5.34±0.38	5.87±0.37
3266934	NANOS1	nanos homolog 1 (Drosophila)	8.85E-05	-1.29	6.67±0.28	7.04±0.25
3227159	FNBP1	formin binding protein 1	8.92E-05	1.41	8.34±0.24	7.85±0.39
3385175	PICALM	phosphatidylinositol binding clathrin assembly protein	8.97E-05	1.52	9.24±0.38	8.63±0.45
3610110	NR2F2	nuclear receptor subfamily 2, group F, member 2	9.05E-05	1.46	9.33±0.46	8.79±0.33
3901055	CD93	CD93 molecule	9.23E-05	1.72	8.4±0.62	7.62±0.51
3851545	MAN2B1	mannosidase, alpha, class 2B, member 1	9.51E-05	1.39	7.81±0.44	7.33±0.24
3445820	RERG	RAS-like, estrogen-regulated, growth inhibitor	9.71E-05	-1.72	7.77±0.68	8.55±0.45
3942838	LIMK2	LIM domain kinase 2	1.00E-04	1.28	7.12±0.3	6.76±0.21
3950405	ZBED4	zinc finger, BED-type containing 4	0.000102	1.14	6.14±0.11	5.96±0.14
2899171	HIST1H1E	histone cluster 1, H1e	0.000102	-1.43	9.92±0.39	10.44±0.36
3078435	PDIA4	protein disulfide isomerase family A, member 4	0.000105	1.25	7.4±0.19	7.08±0.25
3815165	PTBP1	polypyrimidine tract binding protein 1	0.000109	1.23	8.81±0.21	8.52±0.21
3288707	ERCC6	excision repair cross-complementing rodent repair deficiency, complementation group 6	0.000109	1.53	7.91±0.45	7.3±0.43
3454006	FMNL3	formin-like 3	0.00011	1.51	7.67±0.46	7.07±0.41
3788097	MAPK4	mitogen-activated protein kinase 4	0.000112	-1.39	5.38±0.25	5.85±0.37
3512294	TSC22D1	TSC22 domain family, member 1	0.000113	1.37	9.08±0.34	8.62±0.31
3887117	CTSA	cathepsin A	0.000118	1.39	9.52±0.33	9.04±0.35
2773545	BTC	betacellulin	0.000119	-1.4	4.91±0.43	5.39±0.28
3638188	HAPLN3	hyaluronan and proteoglycan link protein 3	0.00012	1.43	7.32±0.41	6.8±0.36
3335894	CST6	cystatin E/M	0.000121	-1.44	6.46±0.33	6.99±0.41
3711986	PIGL	phosphatidylinositol glycan anchor biosynthesis, class L	0.000121	1.29	6.4±0.28	6.03±0.26
3719980	LASP1	LIM and SH3 protein 1	0.000122	1.42	9.03±0.32	8.52±0.39
2829947	TGFBI	transforming growth factor, beta-induced, 68kDa	0.000124	2.35	8.88±0.89	7.65±0.89
3686339	XPO6	exportin 6	0.000125	1.31	8.46±0.21	8.07±0.31
3617574	GOLGA8A	golgi autoantigen, golgin subfamily a, 8A	0.000126	1.91	8.83±0.6	7.89±0.71
2946383	HIST1H4H	histone cluster 1, H4h	0.000127	-1.32	7.13±0.3	7.53±0.28
3063035	TMEM130	transmembrane protein 130	0.000128	1.53	8.64±0.52	8.03±0.39
3607332	ACAN	aggrecan	0.000128	1.79	7.04±0.83	6.2±0.33
3403077	C12orf57	chromosome 12 open reading frame 57	0.000128	-1.4	9.56±0.31	10.1±0.38
2663130	TIMP4	TIMP metalloproteinase inhibitor 4	0.000129	-1.82	6.57±0.55	7.43±0.67
3679533	CARHSP1	calcium regulated heat stable protein 1, 24kDa	0.00013	1.38	8.05±0.36	7.59±0.32
4001850	SH3KBP1	SH3-domain kinase binding protein 1	0.000132	1.5	7.6±0.51	7.02±0.36
2669979	CX3CR1	chemokine (C-X3-C motif) receptor 1	0.000136	3.03	7.96±1.3	6.36±1
2524301	NRP2	neuropilin 2	0.000145	1.38	7.17±0.34	6.7±0.34
3372352	C1QTNF4	C1q and tumor necrosis factor related protein 4	0.000145	-1.32	6.88±0.26	7.28±0.31
3502570	LAMP1	lysosomal-associated membrane protein 1	0.000151	1.31	9.3±0.21	8.91±0.32
2593464	ANKRD44	ankyrin repeat domain 44	0.000154	1.42	7.83±0.28	7.32±0.41
3396144	C11orf61	chromosome 11 open reading frame 61	0.000155	1.35	6.93±0.25	6.5±0.35
3281621	ARHGAP21	Rho GTPase activating protein 21	0.000165	1.4	9.56±0.29	9.08±0.38
3525313	COL4A1	collagen, type IV, alpha 1	0.000167	1.56	9.35±0.6	8.71±0.37
3227696	RAPGEF1	Rap guanine nucleotide exchange factor (GEF) 1	0.00017	1.21	7.83±0.18	7.56±0.21
3548538	C14orf159	chromosome 14 open reading frame 159	0.000171	1.19	6.52±0.23	6.27±0.14
3303165	DNMBP	dynamitin binding protein	0.000173	1.29	6.24±0.31	5.88±0.25
3235516	CAMK1D	calcium/calmodulin-dependent protein kinase ID	0.000173	1.32	7.74±0.2	7.34±0.33
3737338	RNF213	ring finger protein 213	0.000175	1.54	8.3±0.35	7.68±0.5
3057499	#GenBank	Homo sapiens clone DNA108759 PIKR2786 (UNQ2786) mRNA, complete cds.	0.000187	1.79	8.28±0.66	7.45±0.61
3361041	TPP1	tripeptidyl peptidase 1	0.000189	1.46	8.32±0.41	7.78±0.4
2767710	KCTD8	potassium channel tetramerisation domain containing 8	0.000192	-1.23	6.04±0.24	6.34±0.22
3581221	AHNAK2	AHNAK nucleoprotein 2	0.000194	1.71	8.25±0.69	7.48±0.49
2612508	IMPDH1	IMP (inosine monophosphate) dehydrogenase 1	0.000195	-2.11	6.55±0.92	7.63±0.73
2619120	TRAK1	trafficking protein, kinesin binding 1	2.00E-04	1.25	6.75±0.27	6.42±0.23
3396107	ESAM	endothelial cell adhesion molecule	0.000201	1.48	6.91±0.56	6.34±0.28
3405032	ETV6	ets variant 6	0.000203	1.41	8.3±0.26	7.81±0.41
3472312	SLC24A6	solute carrier family 24 (sodium/potassium/calcium exchanger), member 6	0.000203	1.2	7.31±0.2	7.05±0.19
3484497	FRY	furry homolog (Drosophila)	0.000204	1.54	7.81±0.51	7.19±0.44
2383915	GJC2	gap junction protein, gamma 2, 47kDa	0.000205	-1.17	7.51±0.14	7.74±0.18
2834282	STK32A	serine/threonine kinase 32A	0.000208	-1.69	6.38±0.69	7.14±0.47
3770632	SUMO2	SMT3 suppressor of mif two 3 homolog 2 (S. cerevisiae)	0.000208	1.78	6.7±0.34	5.87±0.71
3676113	NME3	non-metastatic cells 3, protein expressed in	0.000209	-1.24	7.33±0.22	7.64±0.24
2716655	MSX1	msh homeobox 1	0.000216	-1.2	7.14±0.21	7.41±0.2
3528864	MMP14	matrix metalloproteinase 14 (membrane-inserted)	0.000217	1.39	8.49±0.43	8.01±0.31
3153428	ASAP1	ArfGAP with SH3 domain, ankyrin repeat and PH domain 1	0.000218	1.51	7.77±0.47	7.17±0.44
3229741	LHX3	LIM homeobox 3	0.00022	-1.19	6.48±0.11	6.74±0.22
3861243	DPF1	D4, zinc and double PHD fingers family 1	0.000227	-1.22	5.45±0.24	5.74±0.21
3903525	NCOA6	nuclear receptor coactivator 6	0.000228	1.36	7.32±0.19	6.88±0.38
3638760	IDH2	isocitrate dehydrogenase 2 (NADP+), mitochondrial	0.000229	1.31	7.53±0.37	7.14±0.23
3704376	FAM38A	family with sequence similarity 38, member A	0.000233	1.19	7.17±0.21	6.92±0.18
3944404	APOL1	apolipoprotein L, 1	0.000238	1.58	6.97±0.62	6.3±0.41
3573994	C14orf145	chromosome 14 open reading frame 145	0.000245	1.35	6.32±0.39	5.89±0.28
3847959	TUBB4	tubulin, beta 4	0.00025	-1.25	5.73±0.23	6.05±0.25
3300597	MYOF	myoferlin	0.000252	1.45	9.61±0.36	9.08±0.43
2788287	GenBank	Homo sapiens cDNA clone IMAGE:5724430.	0.00026	-1.25	8.17±0.21	8.5±0.26
3874008	C20orf141	chromosome 20 open reading frame 141	0.00026	-1.2	6.38±0.22	6.65±0.19
3448744	PTH LH	parathyroid hormone-like hormone	0.00026	-1.31	6±0.29	6.4±0.31
2966193	C6orf168	chromosome 6 open reading frame 168	0.00026	-1.39	5.73±0.46	6.21±0.29
2621949	NDUFAF3	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 3	0.000261	-1.15	7.28±0.14	7.48±0.16
3895224	AVP	arginine vasopressin	0.000262	-1.22	5.71±0.17	6±0.25
2993206	MPP6	membrane protein, palmitoylated 6 (MAGUK p55 subfamily member 6)	0.00027	-1.78	6.89±0.84	7.72±0.45
3902560	DUSP15	dual specificity phosphatase 15	0.000272	-1.21	6.3±0.14	6.57±0.24
4019160	KLHL13	kelch-like 13 (Drosophila)	0.000274	-1.58	5.92±0.59	6.57±0.45
3888721	PTPN1	protein tyrosine phosphatase, non-receptor type 1	0.000275	1.18	7.86±0.2	7.62±0.18
3666146	SLC7A6	solute carrier family 7 (cationic amino acid transporter, y+ system), member 6	0.00028	1.44	6.82±0.36	6.3±0.43
3081205	SHH	sonic hedgehog homolog (Drosophila)	0.000282	-1.17	6.67±0.17	6.9±0.18
3742783	NLRP1	NLR family, pyrin domain containing 1	0.000286	1.22	7.28±0.25	6.99±0.21
3824471	GLT25D1	glycosyltransferase 25 domain containing 1	0.000287	1.29	8.63±0.35	8.26±0.24
3047581	INHBA	inhibin, beta A	0.000294	1.82	8.6±0.84	7.74±0.51
3757329	JUP	junction plakoglobin	0.000297	1.24	7.35±0.27	7.04±0.22
3401119	ITFG2	integrin alpha FG-GAP repeat containing 2	0.000298	1.15	7.29±0.16	7.08±0.16
4027345	LAGE3	L antigen family, member 3	0.000299	-1.25	5.33±0.28	5.85±0.23
2417362	DIRAS3	DIRAS family, GTP-binding RAS-like 3	0.000314	-1.39	5.8±0.45	6.28±0.31
2779527	DDIT4L	DNA-damage-inducible transcript 4-like	0.000315	-1.53	6.51±0.5	7.13±0.46
3590853	CAPN3	calpain 3, (p94)	0.00032	1.24	6.34±0.2	6.03±0.26
3908831	ZNF1	zinc finger, NFX1-type containing 1	0.00032	1.33	8.36±0.29	7.94±0.34
2899223	HIST1H2AE	histone cluster 1, H2ae	0.00032	-1.5	6.07±0.47	6.66±0.46
3130161	GSR	glutathione reductase	0.000321	1.46	8±0.45	7.45±0.41
3699044	RFWD3	ring finger and WD repeat domain 3	0.000322	1.27	6.09±0.23	5.74±0.29
3469319	APPL2	adaptor protein, phosphotyrosine interaction, PH domain and leucine zipper containing 2	0.000325	1.26	7.89±0.2	7.56±0.29
3235414	SEC61A2	Sec61 alpha 2 subunit (S. cerevisiae)	0.000326	1.25	5.89±0.2	5.56±0.28
3835467	ZNF234	zinc finger protein 234	0.000333	1.36	7.04±0.24	6.6±0.38

meta probeset ID	genesymbol	genename	p-value	fold-change	log2(dilated)	log2(undilated)
3708422	EIF5A	eukaryotic translation initiation factor 5A	0.000335	-1.33	6.36±0.3	6.77±0.33
3970338	NHS	Nance-Horan syndrome (congenital cataracts and dental anomalies)	0.000337	1.43	7.87±0.45	7.36±0.37
2933175	ZDHHC14	zinc finger, DHHC-type containing 14	0.000338	1.29	6.89±0.26	6.52±0.31
3188656	LHX2	LIM homeobox 2	0.000339	-1.24	5.76±0.23	6.06±0.24
3744324	C17orf68	chromosome 17 open reading frame 68	0.000341	1.17	7.28±0.16	7.05±0.19
2902574	LY6G5B	lymphocyte antigen 6 complex, locus G5B	0.000342	1.41	7.01±0.46	6.51±0.33
3553872	KLC1	kinesin light chain 1	0.000348	1.26	8.99±0.26	8.66±0.27
3056226	STX1A	syntaxin 1A (brain)	0.000351	-1.18	6.03±0.16	6.27±0.2
3966225	RABL2B	RAB, member of RAS oncogene family-like 2B	0.000358	1.41	7.4±0.42	6.91±0.37
3695631	TPPP3	tubulin polymerization-promoting protein family member 3	0.000365	1.6	6.52±0.72	5.84±0.32
3969081	TLR7	toll-like receptor 7	0.000369	1.97	6.5±0.95	5.52±0.63
3837431	EHD2	EH-domain containing 2	0.000372	1.36	8.55±0.33	8.12±0.36
3494706	SLAIN1	SLAIN motif family, member 1	0.000389	-1.57	5.52±0.67	6.16±0.37
3634458	TBC1D2B	TBC1 domain family, member 2B	0.000392	1.35	8.17±0.25	7.73±0.38
2484841	B3GNT2	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 2	0.000399	1.47	7.77±0.51	7.21±0.39
3722355	RND2	Rho family GTPase 2	4.00E-04	-1.38	5.85±0.39	6.32±0.36
3605268	TM6SF1	transmembrane 6 superfamily member 1	4.00E-04	1.92	6.66±0.88	5.72±0.65
3748957	ALDH3A1	aldehyde dehydrogenase 3 family, member A1	0.000404	-1.19	5.86±0.17	6.11±0.22
3457614	CS	citrate synthase	0.000408	1.35	8.99±0.24	8.56±0.39
3568534	SPTB	spectrin, beta, erythrocytic	0.00041	1.33	5.97±0.42	5.55±0.25
3571347	NUMB	numb homolog (Drosophila)	0.000421	1.27	7.96±0.21	7.61±0.31
2413032	ECHDC2	enoyl Coenzyme A hydratase domain containing 2	0.000424	1.27	7.64±0.34	7.3±0.22
2369110	RASAL2	RAS protein activator like 2	0.000427	1.43	7.89±0.38	7.38±0.43
3189932	STXBP1	syntaxin binding protein 1	0.000433	1.22	7.29±0.22	7.01±0.23
3561703	FOXA1	forkhead box A1	0.000451	-1.27	6.35±0.26	6.69±0.28
3410384	C12orf35	chromosome 12 open reading frame 35	0.000451	1.68	8.4±0.6	7.66±0.6
3157901	PLEC1	plectin 1, intermediate filament binding protein 500kDa	0.000453	1.26	8.77±0.31	8.43±0.25
3685610	ARHGAP17	Rho GTPase activating protein 17	0.000458	1.26	6.98±0.24	6.65±0.28
3158697	CYHR1	cysteine/histidine-rich 1	0.000465	-1.2	6.85±0.17	7.12±0.23
3645253	SRRM2	serine/arginine repetitive matrix 2	0.000466	1.39	8.95±0.36	8.48±0.39
3395464	ASAM	adipocyte-specific adhesion molecule	0.000477	-1.5	8.95±0.65	9.53±0.27
3886598	KCNK15	potassium channel, subfamily K, member 15	0.000478	-1.3	7.19±0.3	7.56±0.31
2954771	GTPBP2	GTP binding protein 2	0.000481	1.16	7.69±0.19	7.47±0.17
3935300	MCM3AP	minichromosome maintenance complex component 3 associated protein	0.000487	1.17	7.13±0.14	6.9±0.21
3335952	PACS1	phosphofurin acidic cluster sorting protein 1	0.000489	1.3	7.64±0.34	7.27±0.28
3886576	WISP2	WNT1 inducible signaling pathway protein 2	0.00049	-1.47	8.33±0.44	8.88±0.45
3261544	GBF1	golgi-specific brefeldin A resistant guanine nucleotide exchange factor 1	0.000491	1.29	8.18±0.2	7.81±0.34
3389647	GUCY1A2	guanylate cyclase 1, soluble, alpha 2	0.000503	1.65	6.41±0.79	5.68±0.36
3457696	PAN2	PAN2 poly(A) specific ribonuclease subunit homolog (S. cerevisiae)	0.000504	1.19	6.48±0.22	6.24±0.19
3619595	FAM82A2	family with sequence similarity 82, member A2	0.000513	1.14	7.25±0.18	7.06±0.13
3569441	ZFYVE26	zinc finger, FYVE domain containing 26	0.000513	1.19	6.68±0.16	6.42±0.23
2469627	KCNF1	potassium voltage-gated channel, subfamily F, member 1	0.000513	-1.24	6.38±0.19	6.69±0.27
3638337	POLG	polymerase (DNA directed), gamma	0.000514	1.12	7.04±0.13	6.88±0.14
3453592	MLL2	myeloid/lymphoid or mixed-lineage leukemia 2	0.00052	1.26	7.02±0.32	6.68±0.24
2315951	ATAD3B	ATPase family, AAA domain containing 3B	0.000522	-1.24	7.56±0.21	7.87±0.27
3956781	AP1B1	adaptor-related protein complex 1, beta 1 subunit	0.000528	1.33	7.7±0.38	7.29±0.31
2674762	UBA7	ubiquitin-like modifier activating enzyme 7	0.000533	1.23	7.67±0.26	7.37±0.24
3718791	TAF15	TAF15 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 68kDa	0.000537	1.23	9.15±0.21	8.85±0.26
3873874	NOP56	NOP56 ribonucleoprotein homolog (yeast)	0.000537	-1.32	8.21±0.26	8.62±0.36
3601511	ISLR	immunoglobulin superfamily containing leucine-rich repeat	0.000539	1.45	10.1±0.46	9.51±0.43
3468103	GNPTAB	N-acetylglucosamine-1-phosphate transferase, alpha and beta subunits	0.000539	1.45	7.54±0.44	7±0.44
3874498	MAVS	mitochondrial antiviral signaling protein	0.00054	1.17	7.75±0.18	7.51±0.19
2566504	C2orf55	chromosome 2 open reading frame 55	0.00054	-1.18	6.84±0.18	7.08±0.2
2593733	HSPD1	heat shock 60kDa protein 1 (chaperonin)	0.000556	-1.3	7.25±0.34	7.62±0.29
3605832	ZNF592	zinc finger protein 592	0.000559	1.2	7.6±0.22	7.34±0.21
3070873	GPR37	G protein-coupled receptor 37 (endothelin receptor type B-like)	0.000561	-1.5	5.66±0.5	6.25±0.47
3501661	ARHGEF7	Rho guanine nucleotide exchange factor (GEF) 7	0.000566	1.27	8.01±0.22	7.67±0.31
2763278	GPR125	G protein-coupled receptor 125	0.000568	-1.29	6.1±0.3	6.47±0.3
2320581	PLOD1	procollagen-lysine 1, 2-oxoglutarate 5-dioxygenase 1	0.00057	1.34	8.53±0.4	8.11±0.32
3329724	MADD	MAP-kinase activating death domain	0.000589	1.24	7.25±0.22	6.94±0.28
3902489	BCL2L1	BCL2-like 1	0.000591	1.25	9.4±0.24	9.07±0.29
3178679	GADD45G	growth arrest and DNA-damage-inducible, gamma	0.000602	-1.34	6.01±0.37	6.43±0.33
3858285	TSHZ3	teashirt zinc finger homeobox 3	0.000606	1.51	6.21±0.41	5.61±0.54
3261971	CNNM2	cyclin M2	0.000606	1.42	8.13±0.52	7.63±0.33
2411799	BEND5	BEN domain containing 5	0.000611	-1.28	6.04±0.35	6.4±0.26
3671695	WFDC1	WAP four-disulfide core domain 1	0.000626	1.83	7.58±0.99	6.7±0.41
2534509	RAMP1	receptor (G protein-coupled) activity modifying protein 1	0.000626	-1.38	8.08±0.45	8.54±0.34
2899216	HIST1H4E	histone cluster 1, H4e	0.000627	-1.45	8.98±0.37	9.52±0.48
2345128	SH3GLB1	SH3-domain GRB2-like endophilin B1	0.000631	-1.3	8.05±0.35	8.43±0.3
3601387	PML	promyelocytic leukemia	0.000634	1.22	7.39±0.25	7.1±0.22
3329983	PTPRJ	protein tyrosine phosphatase, receptor type, J	0.000638	1.52	7.14±0.57	6.54±0.46
3724989	CDK5RAP3	CDK5 regulatory subunit associated protein 3	0.00064	1.28	7.63±0.34	7.27±0.27
3927226	APP	amyloid beta (A4) precursor protein	0.000649	1.27	11.2±0.23	10.8±0.32
3601229	CD276	CD276 molecule	0.000656	1.24	7.52±0.21	7.21±0.28
2781914	PITX2	paired-like homeodomain 2	0.000662	-1.17	5.99±0.14	6.21±0.21
3743119	KIAA0753	KIAA0753	0.000663	1.32	6.08±0.2	5.68±0.38
3923982	C21orf70	chromosome 21 open reading frame 70	0.000667	-1.29	6.44±0.14	6.81±0.36
3632298	ADPGK	ADP-dependent glucokinase	0.000669	1.27	6.65±0.34	6.31±0.24
3742727	DHX3	DEAH (Asp-Glu-Ala-His) box polypeptide 33	0.00067	1.16	6.48±0.13	6.27±0.2
3913335	C20orf166	chromosome 20 open reading frame 166	0.000673	-1.23	6.56±0.2	6.86±0.28
3336402	RBM14	RNA binding motif protein 14	0.000683	1.38	7.07±0.42	6.61±0.37
3251848	SEC24C	SEC24 family, member C (S. cerevisiae)	0.000685	1.22	7.89±0.16	7.61±0.27
3542145	KIAA0247	KIAA0247	0.000695	1.3	7.66±0.37	7.28±0.28
3510362	C13orf23	chromosome 13 open reading frame 23	0.000702	1.39	6.19±0.26	5.72±0.45
3260829	FAM178A	family with sequence similarity 178, member A	0.000716	1.31	6.67±0.29	6.28±0.34
2381249	C1orf115	chromosome 1 open reading frame 115	0.000725	-1.32	6.57±0.41	6.97±0.28
2948188	RNF39	ring finger protein 39	0.000727	-1.13	5.67±0.12	5.85±0.16
3542847	SIPA1L1	signal-induced proliferation-associated 1 like 1	0.00073	1.31	8.02±0.32	7.62±0.34
3157147	LYNX1	Ly6/neurotoxin 1	0.000736	-1.2	7.95±0.26	8.22±0.2
3978943	KLF8	Kruppel-like factor 8	0.000747	1.21	6.22±0.22	5.96±0.23
3937587	MED15	mediator complex subunit 15	0.000758	1.2	7.94±0.23	7.67±0.22

**aorta adventitia, only BAV patients, comparing dilated and undilated, for all genes**

meta probeset ID	genesymbol	genename	p-value	fold-change	log2(dilated)	log2(undilated)
2324919	EPHB2	EPH receptor B2	2.27E-05	1.12	6.11±0.18	5.94±0.099
2893895	BMP6	bone morphogenetic protein 6	2.49E-05	1.32	6.32±0.39	5.92±0.27
2842707	TSPAN17	tetraspanin 17	4.12E-05	1.16	7.03±0.2	6.82±0.16
3762198	COL1A1	collagen, type I, alpha 1	4.52E-05	1.49	9.74±0.6	9.17±0.4
3049292	IGFBP3	insulin-like growth factor binding protein 3	4.85E-05	1.4	8.55±0.44	8.06±0.37
2987632	TTYH3	tweety homolog 3 (Drosophila)	6.58E-05	1.19	7.44±0.26	7.2±0.17
3456732	ITGA5	integrin, alpha 5 (fibronectin receptor, alpha polypeptide)	9.00E-05	1.38	8.15±0.34	7.68±0.4
2403027	MAP3K6	mitogen-activated protein kinase kinase kinase 6	9.24E-05	1.16	7.12±0.17	6.9±0.19
3560673	CFL2	cofilin 2 (muscle)	0.000195	-1.31	8.35±0.47	8.74±0.28
3601511	ISLR	immunoglobulin superfamily containing leucine-rich repeat	0.000205	1.65	9.61±0.48	8.89±0.68

meta probeset ID	genesymbol	genename	p-value	fold-change	log2(dilated)	log2(undilated)
3119945	GRINA	glutamate receptor, ionotropic, N-methyl D-aspartate-associated protein 1 (glutamate binding)	0.000223	1.28	8.57±0.3	8.22±0.32
3226097	ENG	endoglin	0.000229	1.44	8.77±0.5	8.25±0.46
2878368	APBB3	amyloid beta (A4) precursor protein-binding, family B, member 3	0.000244	1.16	6.98±0.21	6.76±0.19
2404158	LAPTM5	lysosomal multispinning membrane protein 5	0.000246	1.82	10.1±0.66	9.27±0.81
2622912	MAPKAPK3	mitogen-activated protein kinase-activated protein kinase 3	0.000262	1.22	6.85±0.32	6.56±0.24
2436526	TPM3	tropomyosin 3	0.000263	1.2	5.86±0.23	5.6±0.24
3988638	LONRF3	LON peptidase N-terminal domain and ring finger 3	0.000269	-1.2	5.83±0.25	6.09±0.24
2816459	F2R	coagulation factor II (thrombin) receptor	0.000308	1.27	8.02±0.35	7.67±0.3
3324447	FIBIN	fin bud initiation factor homolog (zebrafish)	0.000317	-1.56	9.71±0.84	10.4±0.46
3015865	SLC12A9	solute carrier family 12 (potassium/chloride transporters), member 9	0.000328	1.11	6.78±0.13	6.62±0.14
2360887	RUSC1	RUN and SH3 domain containing 1	0.000335	1.14	7.03±0.16	6.84±0.18
2886174	SLIT3	slit homolog 3 (Drosophila)	0.000347	1.43	8.51±0.45	7.99±0.49
2352169	WNT2B	wingless-type MMTV integration site family, member 2B	0.000356	1.22	6.18±0.26	5.9±0.26
2351063	CSF1	colony stimulating factor 1 (macrophage)	0.000361	1.31	7.27±0.42	6.88±0.34
3252036	PLAU	plasminogen activator, urokinase	0.000369	1.31	7.35±0.42	6.95±0.35
2598099	BARD1	BRCA1 associated RING domain 1	0.000372	-1.34	6.96±0.47	7.38±0.36
2363689	FCGR2A	Fc fragment of IgG, low affinity IIa, receptor (CD32)	0.000385	1.66	9.5±0.56	8.77±0.72
2881370	CD74	CD74 molecule, major histocompatibility complex, class II invariant chain	0.000396	1.62	10.7±0.55	9.99±0.68
3214845	ASPN	asporin	4.00E-04	-1.47	9.74±0.64	10.3±0.47
3693788	SLC38A7	solute carrier family 38, member 7	0.00042	1.1	6.07±0.15	5.94±0.12
2878437	CD14	CD14 molecule	0.000424	1.6	9.57±0.69	8.89±0.63
2358360	ECM1	extracellular matrix protein 1	0.000424	1.33	6.62±0.45	6.22±0.36
3282601	MPP7	membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7)	0.000445	-1.37	8.22±0.55	8.68±0.38
3008164	LAT2	linker for activation of T cells family, member 2	0.000445	1.15	6.23±0.18	6.03±0.19
4021433	ELF4	E74-like factor 4 (ets domain transcription factor)	0.000455	1.24	5.81±0.35	5.5±0.27
2708407	ALG3	asparagine-linked glycosylation 3, alpha-1,3- mannosyltransferase homolog (S. cerevisiae)	0.000456	1.18	8.18±0.2	7.94±0.24
2623441	ACY1	aminoacylase 1	0.00049	1.12	6.55±0.17	6.38±0.16
3846238	C19orf28	chromosome 19 open reading frame 28	0.000499	1.14	6.91±0.21	6.72±0.17
2845973	LPCAT1	lysophosphatidylcholine acyltransferase 1	0.000524	1.14	7.01±0.17	6.82±0.19
3417842	LRP1	low density lipoprotein-related protein 1 (alpha-2-macroglobulin receptor)	0.000526	1.31	10.2±0.35	9.81±0.38
2899216	HIST1H4E	histone cluster 1, H4e	0.000548	-1.28	8.84±0.39	9.2±0.33
2757347	TMEM129	transmembrane protein 129	0.000579	1.15	7.05±0.18	6.85±0.21
3382698	LRR32	leucine rich repeat containing 32	0.000582	1.43	8.21±0.39	7.69±0.53
2398736	ATP13A2	ATPase type 13A2	0.000603	1.12	6.73±0.15	6.56±0.16
3056264	ABHD11	abhydrolase domain containing 11	0.000604	1.1	6.18±0.13	6.04±0.13
2436283	DENND4B	DENN/MADD domain containing 4B	0.000627	1.12	6.89±0.19	6.73±0.14
2623922	STAB1	stabilin 1	0.000627	1.41	8.1±0.62	7.6±0.43
3600621	SEN8	SUMO/sentrin specific peptidase family member 8	0.000656	-1.2	5.69±0.24	5.95±0.27
2889916	ADAMTS2	ADAM metalloproteinase with thrombospondin type 1 motif, 2	0.000664	1.13	7.1±0.25	6.91±0.14
3362795	RNF141	ring finger protein 141	0.000668	-1.29	8.45±0.44	8.82±0.32
3664843	CMTM3	CKLF-like MARVEL transmembrane domain containing 3	0.000688	1.2	7.65±0.33	7.38±0.24
2749222	GRIA2	glutamate receptor, ionotropic, AMPA 2	0.000694	-2.04	7.24±1.3	8.27±0.87
3009198	RHBDD2	rhomoid domain containing 2	0.000727	1.25	8.28±0.31	7.97±0.32
2949885	GPSM3	G-protein signaling modulator 3 (AGS3-like, C. elegans)	0.000745	1.15	6.06±0.2	5.86±0.21

#### aorta adventitia, only TAV patients, comparing dilated and undilated, for all genes

meta probeset ID	genesymbol	genename	p-value	fold-change	log2(dilated)	log2(undilated)
3153428	ASAP1	ArfGAP with SH3 domain, ankyrin repeat and PH domain 1	8.63E-07	1.56	7.8±0.32	7.16±0.26
2619120	TRAK1	trafficking protein, kinesin binding 1	1.20E-06	1.28	6.71±0.21	6.35±0.13
3762198	COL1A1	collagen, type I, alpha 1	1.01E-05	2.6	10.6±0.83	9.26±0.63
2611848	SLC6A6	solute carrier family 6 (neurotransmitter transporter, taurine), member 6	1.37E-05	1.63	8.02±0.51	7.31±0.28
3939125	GNAZ	guanine nucleotide binding protein (G protein), alpha z polypeptide	1.86E-05	-1.28	6.33±0.26	6.68±0.15
2951916	STK38	serine/threonine kinase 38	2.02E-05	1.52	8.11±0.44	7.5±0.26
2733287	PRDM8	PR domain containing 8	3.83E-05	-1.16	5.68±0.14	5.89±0.11
2398894	RCC2	regulator of chromosome condensation 2	4.15E-05	1.27	7.7±0.25	7.36±0.17
2354634	PHGDH	phosphoglycerate dehydrogenase	5.79E-05	-1.59	7.44±0.57	8.11±0.25
2434129	HIST2H2AB	histone cluster 2, H2ab	6.88E-05	-1.77	9.02±0.57	9.84±0.44
2587841	WIPF1	WAS/WASL interacting protein family, member 1	6.97E-05	1.42	9.02±0.31	8.51±0.28
2441043	OLFML2B	olfactomedin-like 2B	7.17E-05	1.63	7.38±0.57	6.68±0.31
3766893	DDX5	DEAD (Asp-Glu-Ala-Asp) box polypeptide 5	7.60E-05	1.34	10.5±0.33	10.1±0.2
3923857	KRTAP10-9	keratin associated protein 10-9	8.21E-05	-1.34	7.02±0.34	7.44±0.21
2461473	TARBP1	TAR (HIV-1) RNA binding protein 1	9.69E-05	1.47	6.95±0.49	6.39±0.21
3824666	CKNN1	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 1	9.70E-05	-1.22	5.58±0.17	5.87±0.17
2680571	GenBank	Homo sapiens clone DNA71234 HHSL751 (UNQ751) mRNA, complete cds.	0.000101	2.06	6.23±0.71	5.19±0.58
3078435	PDIA4	protein disulfide isomerase family A, member 4	0.000111	1.4	7.48±0.31	7±0.28
2587961	CHN1	chimerin (chimaerin) 1	0.000114	1.5	6.87±0.48	6.28±0.29
3929775	DONSON	downstream neighbor of SON	0.000127	1.28	6.03±0.29	5.67±0.17
3923436	TRAPPC10	trafficking protein particle complex 10	0.000129	1.31	6.97±0.27	6.58±0.22
2460368	TTC13	tetratricopeptide repeat domain 13	0.000135	1.31	6.89±0.35	6.5±0.15
2446047	ABL2	v-abl Abelson murine leukemia viral oncogene homolog 2 (arg, Abelson-related gene)	0.000136	1.33	7.06±0.33	6.65±0.21
3497881	FARP1	FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived)	0.000138	1.4	6.89±0.41	6.41±0.22
2403557	SNHG12	small nucleolar RNA host gene 12 (non-protein coding)	0.000139	1.62	6.92±0.5	6.22±0.39
2568687	FHL2	four and a half LIM domains 2	0.00014	1.39	8.12±0.4	7.65±0.23
3046444	SFRP4	secreted frizzled-related protein 4	0.000158	2.24	10.1±0.87	8.95±0.65
2605321	COL6A3	collagen, type VI, alpha 3	0.000164	1.7	9.29±0.56	8.52±0.44
2500919	SLC20A1	solute carrier family 20 (phosphate transporter), member 1	0.000184	1.57	7.75±0.49	7.09±0.38
2850071	MYO10	myosin X	0.000202	1.34	6.3±0.32	5.88±0.25
2603051	SP110	SP110 nuclear body protein	0.000218	1.43	7.2±0.43	6.68±0.28
3089401	PPP3CC	protein phosphatase 3 (formerly 2B), catalytic subunit, gamma isoform	0.000229	1.31	7.43±0.29	7.04±0.23
2862696	ENC1	ectodermal-neural cortex (with BTB-like domain)	0.000229	1.7	6.64±0.66	5.87±0.39
2436526	TPM3	tropomyosin 3	0.000229	1.33	5.96±0.28	5.54±0.26
2617796	EXO	endo/exonuclease (5'-3'), endonuclease G-like	0.000246	1.32	6.87±0.25	6.47±0.26
3902560	DUSP15	dual specificity phosphatase 15	0.00026	-1.18	6.23±0.24	6.48±0.096
2578028	CXCR4	chemokine (C-X-C motif) receptor 4	0.000266	3.09	8.86±1.4	7.23±0.9
3209384	TMEM2	transmembrane protein 2	0.000278	1.69	7.66±0.69	6.9±0.38
3701297	CDYL2	chromodomain protein, Y-like 2	0.00028	1.21	6.36±0.2	6.09±0.17
2961177	COL12A1	collagen, type XII, alpha 1	0.000283	1.9	8.55±0.66	7.62±0.58
3028858	EPHB6	EPH receptor B6	0.000284	-1.18	6.15±0.19	6.38±0.14
2896177	JARID2	jumonji, AT rich interactive domain 2	0.000298	1.29	6.56±0.32	6.2±0.2
2361612	HAPLN2	hyaluronan and proteoglycan link protein 2	0.000303	-1.2	5.88±0.17	6.14±0.17
3685610	ARHGAP17	Rho GTPase activating protein 17	0.000305	1.24	6.91±0.21	6.59±0.2
3944404	APOL1	apolipoprotein L, 1	0.000308	1.38	7.18±0.32	6.71±0.3
2399988	RNF186	ring finger protein 186	0.000311	-1.27	5.83±0.29	6.18±0.2
2883440	ADAM19	ADAM metalloproteinase domain 19 (meltrin beta)	0.00032	1.28	6.55±0.35	6.2±0.14
2437645	GON4L	gon-4-like (C. elegans)	0.000322	1.27	6.8±0.32	6.45±0.18
3227696	RAPGEF1	Rap guanine nucleotide exchange factor (GEF) 1	0.000327	1.23	7.74±0.22	7.44±0.18
3997825	MXRA5	matrix-remodelling associated 5	0.000333	2.18	7.63±0.91	6.51±0.67
3329724	MADD	MAP-kinase activating death domain	0.000343	1.26	7.27±0.22	6.94±0.22
3095815	AGPAT6	1-acylglycerol-3-phosphate O-acyltransferase 6 (lysophosphatidic acid acyltransferase, zeta)	0.000352	1.23	8.08±0.22	7.78±0.19
2519577	COL3A1	collagen, type III, alpha 1	0.000366	1.81	11.3±0.58	10.5±0.56
2835848	SLC36A1	solute carrier family 36 (proton/amino acid symporter), member 1	0.000379	1.24	6.66±0.26	6.35±0.18
2601414	SERPINE2	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2	0.000387	3.19	8.57±1.6	6.9±0.85
2434776	CDC42SE1	CDC42 small effector 1	0.000388	1.37	8±0.41	7.54±0.25
2852591	ADAMTS12	ADAM metalloproteinase with thrombospondin type 1 motif, 12	0.000388	1.26	5.88±0.28	5.55±0.19

meta probeset ID	genesymbol	genename	p-value	fold-change	log2(dilated)	log2(undilated)
3221822	KIF12	kinesin family member 12	0.000395	-1.19	6.2±0.21	6.45±0.15
2693409	ALDH1L1	aldehyde dehydrogenase 1 family, member L1	0.000397	-1.37	6.08±0.28	6.53±0.31
3688362	COX6A2	cytochrome c oxidase subunit VIa polypeptide 2	0.00041	-1.31	6.85±0.32	7.24±0.23
2473991	CENPA	centromere protein A	0.000417	-1.19	5.72±0.19	5.98±0.16
3894601	FKBP1A	FK506 binding protein 1A, 12kDa	0.000436	1.65	6.8±0.61	6.08±0.43
3597421	LACTB	lactamase, beta	0.000436	1.34	6.56±0.34	6.14±0.27
3654175	IL4R	interleukin 4 receptor	0.00044	1.32	7.28±0.34	6.88±0.24
3056163	MLXIPL	MLX interacting protein-like	0.000453	-1.29	5.89±0.21	6.26±0.26
3638760	IDH2	isocitrate dehydrogenase 2 (NADP+), mitochondrial	0.00046	1.26	7.59±0.22	7.26±0.23
2448073	IVNS1ABP	influenza virus NS1A binding protein	0.000483	1.58	8.91±0.49	8.25±0.43
3707175	TM4SF5	transmembrane 4 L six family member 5	0.000493	-1.3	5.5±0.28	5.88±0.25
2829947	TGFBI	transforming growth factor, beta-induced, 68kDa	0.000499	1.63	9.09±0.56	8.39±0.45
3605268	TM6SF1	transmembrane 6 superfamily member 1	0.00051	1.74	6.84±0.59	6.04±0.53
2565902	ANKRD36	ankyrin repeat domain 36	0.000529	1.67	8.58±0.62	7.85±0.46
3662387	HERPUD1	homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member	0.000529	1.46	9.78±0.56	9.24±0.22
2369110	RASAL2	RAS protein activator like 2	0.000541	1.37	7.77±0.39	7.31±0.28
3061456	SAMD9L	sterile alpha motif domain containing 9-like	0.000543	1.43	7.02±0.41	6.5±0.33
2878662	DIAPH1	diaphanous homolog 1 (Drosophila)	0.000552	1.29	7.33±0.28	6.97±0.24
2769539	CHIC2	cysteine-rich hydrophobic domain 2	0.000556	1.31	7.82±0.36	7.43±0.23
2484358	REL	v-rel reticuloendotheliosis viral oncogene homolog (avian)	0.000556	1.7	6.79±0.63	6.03±0.49
3377322	GPHA2	glycoprotein hormone alpha 2	0.000571	-1.44	5.71±0.29	6.24±0.38
3858285	TSHZ3	teashirt zinc finger homeobox 3	0.000579	1.42	6.26±0.46	5.75±0.3
2410283	CCDC17	coiled-coil domain containing 17	0.000583	-1.1	5.77±0.14	5.91±0.074
2540007	CYS1	cystin 1	0.000584	-1.29	8.55±0.36	8.91±0.19
3788097	MAPK4	mitogen-activated protein kinase 4	0.000588	-1.2	5.37±0.24	5.63±0.16
2759582	AFAP1	actin filament associated protein 1	0.000599	1.25	7.26±0.25	6.94±0.21
2556302	PELL1	pellino homolog 1 (Drosophila)	0.000616	1.61	7.63±0.58	6.94±0.44
2622359	RBM6	RNA binding motif protein 6	0.000617	1.42	7.58±0.36	7.08±0.35
2327630	YTHDF2	YTH domain family, member 2	0.000655	1.38	6.65±0.34	6.18±0.32
2551189	SIX2	SIX homeobox 2	0.00067	-1.27	7.88±0.25	8.22±0.24
2407224	RSP01	R-spondin homolog (Xenopus laevis)	0.000681	-1.2	5.7±0.16	5.96±0.19
3740304	PITPNA	phosphatidylinositol transfer protein, alpha	0.000684	1.24	8.45±0.24	8.15±0.21
2604390	ARL4C	ADP-ribosylation factor-like 4C	0.000685	1.51	7.59±0.6	6.99±0.31
3548152	TDP1	tyrosyl-DNA phosphodiesterase 1	0.000686	1.28	6.6±0.31	6.25±0.22
3374402	LPXN	leupaxin	0.000695	1.47	7.32±0.46	6.77±0.36
2975014	SGK1	serum/glucocorticoid regulated kinase 1	0.000705	1.89	9.05±0.83	8.14±0.56
3768474	WIP1	WD repeat domain, phosphoinositide interacting 1	0.000708	1.23	7.58±0.23	7.29±0.2
2612508	IMPDH1	IMP (inosine monophosphate) dehydrogenase 1	0.000716	-1.58	7.01±0.72	7.67±0.25
3119792	MAPK15	mitogen-activated protein kinase 15	0.000732	-1.21	6.68±0.16	6.95±0.2
3336486	C11orf80	chromosome 11 open reading frame 80	0.000749	1.32	6.18±0.39	5.78±0.22
3624607	MYO5A	myosin VA (heavy chain 12, myosin)	0.000756	1.55	7.37±0.53	6.74±0.42
3820414	MRPL4	mitochondrial ribosomal protein L4	0.00076	-1.15	6.59±0.22	6.8±0.095
3329983	PTPRJ	protein tyrosine phosphatase, receptor type, J	0.000761	1.44	7.46±0.52	6.94±0.28

**aorta intima-media, only dilated patients, comparing BAV and TAV, for extracellular region genes**

meta probeset ID	genesymbol	genename	p-value	fold-change	log2(BAV)	log2(TAV)
2878437	CD14	CD14 molecule	2.66E-07	-3.53	7.12±0.92	8.94±1.2
2320188	ANGPTL7	angiopoietin-like 7	5.33E-07	2.26	6.59±0.75	5.42±0.79
2324873	C1QC	complement component 1, q subcomponent, C chain	1.43E-06	-3.07	6.58±0.85	8.2±1.2
3442706	CD163	CD163 molecule	1.56E-06	-3.57	5.55±0.89	7.38±1.4
3300749	RBP4	retinol binding protein 4, plasma	2.84E-06	1.97	7.11±0.57	6.13±0.74
3527662	RNASE6	ribonuclease, RNase A family, k6	4.65E-06	-2.5	4.95±0.52	6.28±1.1
2794006	SCRG1	scrapie responsive protein 1	4.66E-06	1.89	7.42±0.46	6.5±0.73
3339382	FOLR2	folate receptor 2 (fetal)	5.15E-06	-2.12	6.97±0.59	8.06±0.86
3722917	GRN	granulin	7.64E-06	-1.49	9.46±0.4	10±0.45
2324856	C1QA	complement component 1, q subcomponent, A chain	8.01E-06	-2.55	5.88±0.66	7.23±1.1
2324884	C1QB	complement component 1, q subcomponent, B chain	8.54E-06	-2.3	6.84±0.51	8.04±1
3742285	CXCL16	chemokine (C-X-C motif) ligand 16	1.19E-05	-2.09	6.34±0.52	7.4±0.9
2656837	ST6GAL1	ST6 beta-galactosamide alpha-2,6-sialyltransferase 1	1.21E-05	-1.43	7.77±0.47	8.29±0.39
3654175	IL4R	interleukin 4 receptor	1.34E-05	-1.61	6.5±0.35	7.19±0.59
2462160	NID1	nidogen 1	1.37E-05	-1.32	6.89±0.3	7.3±0.33
3421511	LYZ	lysozyme (renal amyloidosis)	1.43E-05	-5.3	5.12±1.3	7.53±2
2434575	CTSS	cathepsin S	1.59E-05	-3.13	5.56±0.85	7.21±1.4
2772566	IGJ	immunoglobulin J polypeptide, linker protein for immunoglobulin alpha and mu polypeptides	1.71E-05	-8.19	4.22±1.2	7.25±2.7
3572209	PGF	placental growth factor	1.92E-05	-1.66	5.91±0.44	6.65±0.63
3015682	PCOLCE	procollagen C-endopeptidase enhancer	2.69E-05	-1.86	8.12±0.55	9.02±0.79
2486811	PLEK	pleckstrin	3.12E-05	-2.49	4.97±0.58	6.28±1.2
2829947	TGFBI	transforming growth factor, beta-induced, 68kDa	3.73E-05	-2.02	7.87±0.75	8.88±0.89
2893392	LYR6	lymphocyte antigen R6	4.14E-05	-2.11	5.31±0.31	6.39±1
3441849	TNFRSF1A	tumor necrosis factor receptor superfamily, member 1A	4.29E-05	-1.28	7.86±0.21	8.22±0.33
3577612	SERPINA1	serpin peptidase inhibitor, clade A (alpha-1 antitrypsin, antitrypsin), member 1	4.50E-05	-1.92	5.89±0.38	6.83±0.88
7385547	CCL2	chemokine (C-C motif) ligand 2	4.94E-05	-2.3	7.12±0.66	8.32±1.1
3545130	VASH1	vasohibin 1	5.05E-05	-1.22	6.87±0.16	7.15±0.26
3848039	C3	complement component 3	6.12E-05	-3.79	5.9±0.65	7.82±1.9
3349293	NCAM1	neural cell adhesion molecule 1	6.95E-05	2.04	7.61±0.49	6.58±1
3555675	RNASE1	ribonuclease, RNase A family, 1 (pancreatic)	7.46E-05	-2.54	8.44±0.68	9.79±1.3
3907524	PLTP	phospholipid transfer protein	0.000127	-2.32	7.17±0.6	8.38±1.2
2680046	ADAMTS9	ADAM metalloproteinase with thrombospondin type 1 motif, 9	0.000139	1.62	8.01±0.52	7.32±0.68
3604287	IL16	interleukin 16 (lymphocyte chemoattractant factor)	0.000222	-1.33	5.42±0.15	5.83±0.45
3132782	SFRP1	secreted frizzled-related protein 1	0.000231	2.65	10.3±0.6	8.88±1.5
3709838	NTN1	netrin 1	0.000252	1.26	7.26±0.31	6.93±0.33
3252036	PLAU	plasminogen activator, urokinase	0.000258	-1.58	6.57±0.27	7.22±0.72
2562932	CD8A	CD8a molecule	0.000274	-1.18	5.86±0.16	6.11±0.26
3442475	C1R	complement component 1, r subcomponent	0.000313	-1.5	6.99±0.56	10.3±0.59
3632298	ADPGK	ADP-dependent glucokinase	0.00041	-1.24	6.34±0.23	6.65±0.34
2790368	SFRP2	secreted frizzled-related protein 2	0.000445	-3.1	4.89±0.74	6.52±1.9
3222170	TNC	tenascin C	0.00045	-1.94	5.84±0.56	6.79±1.1
2738378	NPNT	nephronectin	0.000454	1.76	10.2±0.27	9.39±0.95
3623031	FBN1	fibrillin 1	0.00047	-1.3	9.76±0.37	10.1±0.4
3468345	IGF1	insulin-like growth factor 1 (somatomedin C)	0.000481	-1.86	6.36±0.49	7.25±1
3163982	ADAMTSL1	ADAMTS-like 1	0.000523	1.39	7.3±0.3	6.82±0.55
3949722	FAM19A5	family with sequence similarity 19 (chemokine (C-C motif)-like), member A5	0.000528	1.31	7.7±0.31	7.31±0.44
2622696	SEMA3B	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3B	0.000529	1.17	7.22±0.17	6.99±0.26
3961068	PDGFB	platelet-derived growth factor beta polypeptide (simian sarcoma viral (v-sis) oncogene homolog	0.000536	-1.18	5.44±0.22	5.67±0.25
3442641	CD163L1	CD163 molecule-like 1	0.000548	-1.65	5.24±0.5	5.96±0.82
2458629	LEFTY2	left-right determination factor 2	0.000552	1.96	9.57±0.87	8.59±1.1
2902804	C2	complement component 2	0.000556	-1.72	5.26±0.36	6.04±0.92
2323172	IGSF21	immunoglobulin superfamily, member 21	0.00056	-1.23	5.72±0.18	6.01±0.34
2607923	CNTN4	contactin 4	0.000578	2.03	7.81±0.56	6.79±1.2
3645626	IL32	interleukin 32	0.000617	-1.53	6.39±0.34	7±0.72
3161113	PDCD1LG2	programmed cell death 1 ligand 2	0.000618	-1.47	5.53±0.39	6.08±0.64
3664785	CKLF	chemokine-like factor	0.000697	-1.54	6.55±0.43	7.17±0.72

meta probeset ID	genesymbol	genename	p-value	fold-change	log2(BAV)	log2(TAV)
3762198	COL1A1	collagen, type I, alpha 1	0.00074	-1.67	9.97±0.6	10.7±0.86
3164086	ADAMTSL1	ADAMTS-like 1	0.000779	1.36	7.65±0.33	7.21±0.52
3465248	LUM	lumican	0.000779	-2.41	6.95±1.1	8.22±1.5
2437152	THBS3	thrombospondin 3	0.000848	-1.19	7.36±0.33	7.62±0.25
3959388	APOL4	apolipoprotein L, 4	0.000878	-1.34	5.23±0.22	5.65±0.51
3600283	THSD4	thrombospondin, type I, domain containing 4	0.000899	1.29	7.46±0.36	7.1±0.42
3442514	C1RL	complement component 1, r subcomponent-like	9.00E-04	-1.22	7.13±0.27	7.42±0.33
2884623	C1QTNF2	C1q and tumor necrosis factor related protein 2	0.000974	1.27	6.76±0.33	6.41±0.41
3997825	MXRA5	matrix-remodelling associated 5	0.00103	-1.63	6.52±0.63	7.22±0.83
3886576	WISP2	WNT1 inducible signaling pathway protein 2	0.00104	1.33	8.74±0.48	8.33±0.44
3581637	IGHG1	immunoglobulin heavy constant gamma 1 (G1m marker)	0.00113	-1.66	5.57±0.2	6.3±0.93
2530425	COL4A3	collagen, type IV, alpha 3 (Goodpasture antigen)	0.00116	1.39	6.45±0.27	5.97±0.59
3671695	WFDC1	WAP four-disulfide core domain 1	0.00118	-1.75	6.77±0.62	7.58±0.99
3293435	PRF1	perforin 1 (pore forming protein)	0.00126	-1.21	5.48±0.24	5.76±0.34
3129065	CLU	clusterin	0.00134	1.48	12±0.44	11.4±0.7
3319352	TUB	tubby homolog (mouse)	0.00142	1.16	6.19±0.22	5.98±0.26
2437118	MUC1	mucin 1, cell surface associated	0.00145	-1.21	6.5±0.22	6.78±0.35
2855285	SEPP1	selenoprotein P, plasma, 1	0.00155	-1.94	6.49±0.78	7.44±1.2
4053085	PRELP	proline/arginine-rich end leucine-rich repeat protein	0.00163	1.41	11.6±0.49	11.1±0.61
3959350	APOL3	apolipoprotein L, 3	0.0017	-1.31	5.63±0.33	6.03±0.5
3103745	CRISPLD1	cysteine-rich secretory protein LCCL domain containing 1	0.00177	1.47	10.1±0.5	9.5±0.69
2443120	DPT	dermatopontin	0.00187	1.53	8.98±0.66	8.37±0.75
2865327	HAPLN1	hyaluronan and proteoglycan link protein 1	0.00188	1.61	8.33±0.62	7.64±0.87
2685304	PROS1	protein S (alpha)	0.00188	1.37	11±0.43	10.5±0.58
2794792	VEGFC	vascular endothelial growth factor C	0.00206	-1.28	5.66±0.24	6.01±0.47
2719440	C1QTNF7	C1q and tumor necrosis factor related protein 7	0.00233	1.41	8.52±0.41	8.02±0.65
3445544	PLBD1	phospholipase B domain containing 1	0.00246	-1.63	5.7±0.31	6.4±0.98
2433371	ACP6	acid phosphatase 6, lysophosphatidic	0.00253	1.15	6.56±0.27	6.36±0.24
2705706	TNFSF10	tumor necrosis factor (ligand) superfamily, member 10	0.00259	-1.77	5.35±0.47	6.17±1.1
3939470	MMP11	matrix metalloproteinase 11 (stromelysin 3)	0.00296	-1.16	6.17±0.23	6.38±0.28
2985781	THBS2	thrombospondin 2	0.00315	-1.51	10.6±0.62	11.1±0.78
3725714	NXPH3	neurexophilin 3	0.00324	1.28	8.81±0.26	8.46±0.49
3839464	CLEC11A	C-type lectin domain family 11, member A	0.00334	-1.14	6.67±0.28	6.86±0.22
3607332	ACAN	aggrecan	0.00338	-1.54	6.42±0.62	7.04±0.83
3339261	IL18BP	interleukin 18 binding protein	0.00364	-1.13	5.81±0.18	5.99±0.24
2902844	CFB	complement factor B	0.00392	-1.29	6.64±0.37	7.01±0.51
3496637	GPC6	glypican 6	0.00395	-1.69	7.65±0.99	8.41±0.97
2441043	OLFM2L2B	olfactomedin-like 2B	0.00406	-1.25	6.84±0.36	7.16±0.44
3310041	FGFR2	fibroblast growth factor receptor 2	0.00414	1.22	5.75±0.3	5.46±0.4
3592023	B2M	beta-2-microglobulin	0.00426	-1.34	10.6±0.37	11.1±0.6
2435989	S100A8	S100 calcium binding protein A8	0.00496	-1.82	4.37±0.51	5.24±1.3

**aorta intima-media, only undilated patients, comparing BAV and TAV, for extracellular region genes**

meta probeset ID	genesymbol	genename	p-value	fold-change	log2(BAV)	log2(TAV)
2458629	LEFTY2	left-right determination factor 2	4.57E-05	1.83	9.47±0.44	8.6±0.64
2794792	VEGFC	vascular endothelial growth factor C	0.000628	-1.23	5.62±0.23	5.92±0.26

**aorta adventitia, only dilated patients, comparing BAV and TAV, for extracellular region genes**

meta probeset ID	genesymbol	genename	p-value	fold-change	log2(BAV)	log2(TAV)
3762198	COL1A1	collagen, type I, alpha 1	0.000136	-1.85	9.74±0.6	10.6±0.83
3886576	WISP2	WNT1 inducible signaling pathway protein 2	0.000139	1.43	8.9±0.36	8.39±0.48
3997825	MXRA5	matrix-remodelling associated 5	0.000212	-1.93	6.69±0.71	7.63±0.91
3320123	ADM	adrenomedullin	0.000358	1.36	7.44±0.58	6.99±0.34
3819474	ANGPTL4	angiopoietin-like 4	0.000512	1.18	6.06±0.22	5.82±0.24
3181642	COL15A1	collagen, type XV, alpha 1	0.000564	-1.31	7.62±0.5	8.01±0.32
3631397	UACA	uveal autoantigen with coiled-coil domains and ankyrin repeats	0.000775	-1.31	9.28±0.29	9.67±0.43
3818047	HSD11B1L	hydroxysteroid (11-beta) dehydrogenase 1-like	0.00117	1.13	5.84±0.19	5.66±0.19
2656837	ST6GAL1	ST6 beta-galactosamide alpha-2,6-sialyltransferase 1	0.00126	-1.36	7.86±0.32	8.31±0.52
3046444	FRP4	secreted frizzled-related protein 4	0.00127	-1.7	9.35±0.68	10.1±0.87
3875423	BMP2	bone morphogenetic protein 2	0.00168	1.2	5.76±0.28	5.5±0.28
3300749	RBP4	retinol binding protein 4, plasma	0.00186	1.55	7.05±0.83	6.41±0.64
3132782	FRP1	secreted frizzled-related protein 1	0.00203	1.77	9.32±0.65	8.5±1
2441043	OLFM2L2B	olfactomedin-like 2B	0.00246	-1.38	6.91±0.45	7.38±0.57
2835715	GPX3	glutathione peroxidase 3 (plasma)	0.00267	1.36	8.96±0.62	8.52±0.46
3013054	COL1A2	collagen, type I, alpha 2	0.00276	-1.26	11.7±0.37	12.1±0.39
2890741	SCGB3A1	secretoglobin, family 3A, member 1	0.00292	1.18	6.45±0.27	6.21±0.28
2678468	FAM3D	family with sequence similarity 3, member D	0.00327	1.1	5.78±0.19	5.64±0.15
3226027	TOR2A	torsin family 2, member A	0.00354	1.12	5.78±0.23	5.61±0.19
2566414	MGAT4A	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme A	0.00368	-1.45	6.18±0.57	6.71±0.67
2544625	POMC	proopiomelanocortin	0.00392	1.12	7.52±0.2	7.35±0.2
3193482	COL5A1	collagen, type V, alpha 1	0.00417	-1.18	7.26±0.26	7.5±0.3
3510066	POSTN	periostin, osteoblast specific factor	0.00419	-1.96	7.97±0.87	8.95±1.3
3623031	FBN1	fibrillin 1	0.00425	-1.3	9.88±0.41	10.3±0.48
3380126	FGF19	fibroblast growth factor 19	0.00455	1.15	6.21±0.27	6.01±0.24
3089090	FGF17	fibroblast growth factor 17	0.00505	1.16	5.79±0.23	5.57±0.29

**aorta adventitia, only undilated patients, comparing BAV and TAV, for extracellular region genes**

meta probeset ID	genesymbol	genename	p-value	fold-change	log2(BAV)	log2(TAV)
-	-	-	-	-	-	-

**aorta intima-media, only BAV patients, comparing dilated and undilated, for extracellular region genes**

meta probeset ID	genesymbol	genename	p-value	fold-change	log2(dilated)	log2(undilated)
3164086	ADAMTSL1	ADAMTS-like 1	0.000108	1.31	7.65±0.33	7.26±0.37
3465274	DCN	decorin	0.000118	-1.82	8.17±1	9.03±0.7
3465248	LUM	lumican	0.000137	-1.85	6.95±1.1	7.84±0.71
2435989	S100A8	S100 calcium binding protein A8	0.000236	-1.39	4.37±0.51	4.85±0.46
3833620	LTBP4	latent transforming growth factor beta binding protein 4	0.000353	1.32	10.3±0.4	9.94±0.41
2536071	SNED1	sushi, nidogen and EGF-like domains 1	0.000508	1.16	6.95±0.24	6.74±0.22
2886174	SLIT3	slit homolog 3 (Drosophila)	0.000513	1.4	8.17±0.47	7.69±0.53
2395890	CLSTN1	calystenin 1	0.000514	1.25	8.38±0.33	8.06±0.34
3822657	CD97	CD97 molecule	0.000517	1.3	9.13±0.32	8.76±0.42
3751164	DHRS13	dehydrogenase/reductase (SDR family) member 13	0.000801	-1.11	6.61±0.16	6.75±0.16
3002640	EGFR	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, av	0.000916	1.25	7.6±0.35	7.44±0.37
2543163	APOB	apolipoprotein B (including Ag(x) antigen)	0.00127	1.23	6.79±0.34	6.48±0.36
2361612	HAPLN2	hyaluronan and proteoglycan link protein 2	0.00177	-1.11	5.9±0.16	6.05±0.19
3163982	ADAMTSL1	ADAMTS-like 1	0.00188	1.2	7.3±0.3	7.04±0.31
4027176	FLNA	filamin A, alpha (actin binding protein 280)	0.0024	1.19	12.4±0.27	12.1±0.32
2904485	SCUBE3	signal peptide, CUB domain, EGF-like 3	0.0024	1.38	8.79±0.49	8.32±0.6
2622121	DAG1	dystroglycan 1 (dystrophin-associated glycoprotein 1)	0.0025	1.21	8±0.23	7.72±0.38
2674047	LAMB2	laminin, beta 2 (laminin S)	0.00267	1.23	9.54±0.31	9.24±0.39
3195034	PTGDS	prostaglandin D2 synthase 21kDa (brain)	0.00327	-1.27	7.55±0.47	7.9±0.43
3772661	TIMP2	TIMP metalloproteinase inhibitor 2	0.00341	1.25	11.6±0.47	11.3±0.38
3331355	SERPING1	serpin peptidase inhibitor, clade G (C1 inhibitor), member 1	0.00384	1.29	10.4±0.49	10±0.47

## aorta intima-media, only TAV patients, comparing dilated and undilated, for extracellular region genes

meta probeset ID	genesymbol	genename	p-value	fold-change	log2(dilated)	log2(undilated)
3722917	GRN	granulin	5.10E-06	1.62	10.0±0.45	9.34±0.37
2886174	SLIT3	slit homolog 3 (Drosophila)	6.37E-06	1.92	8.5±0.5	7.56±0.58
3762198	COL1A1	collagen, type I, alpha 1	1.04E-05	2.12	10.7±0.86	9.63±0.47
2443120	DPT	dermatopontin	1.24E-05	-2.17	8.37±0.75	9.48±0.65
3623031	FBN1	fibrillin 1	1.46E-05	1.64	10.1±0.4	9.43±0.46
3293762	PSAP	prosaposin	1.70E-05	1.27	11.4±0.22	11.1±0.21
2437152	THBS3	thrombospondin 3	2.02E-05	1.31	7.62±0.25	7.23±0.25
2794006	SCRG1	scrapie responsive protein 1	2.07E-05	-1.84	6.5±0.73	7.37±0.39
3631397	UACA	uveal autoantigen with coiled-coil domains and ankyrin repeats	3.17E-05	1.55	9.88±0.42	9.25±0.41
3300749	RBP4	retinol binding protein 4, plasma	5.73E-05	-1.82	6.13±0.74	6.99±0.45
2462160	NID1	nidogen 1	8.26E-05	1.49	7.3±0.33	6.72±0.43
3335894	CST6	cystatin E/M	0.000121	-1.44	4.66±0.33	6.99±0.41
2829947	TGFBI	transforming growth factor, beta-induced, 68kDa	0.000124	2.35	8.88±0.89	7.65±0.89
3607332	ACAN	aggrecan	0.000128	1.79	7.04±0.83	6.2±0.33
3525313	COL4A1	collagen, type IV, alpha 1	0.000167	1.56	9.35±0.6	8.71±0.37
3448744	PTHLLH	parathyroid hormone-like hormone	0.00026	-1.31	6±0.29	6.4±0.31
3895224	AVP	arginine vasopressin	0.000262	-1.22	5.71±0.17	6±0.25
3047581	INHBA	inhibin, beta A	0.000294	1.82	8.6±0.84	7.74±0.51
3056226	STX1A	syntaxin 1A (brain)	0.000351	-1.18	6.03±0.16	6.27±0.2
3886576	WISP2	WNT1 inducible signaling pathway protein 2	0.00049	-1.47	8.33±0.44	8.88±0.45
3671695	WFDC1	WAP four-disulfide core domain 1	0.000626	1.83	7.58±0.99	6.7±0.41
3927226	APP	amyloid beta (A4) precursor protein	0.000649	1.27	11.2±0.23	10.8±0.32
3632298	ADPGK	ADP-dependent glucokinase	0.000669	1.27	6.65±0.34	6.31±0.24
3013054	COL1A2	collagen, type I, alpha 2	0.000855	1.41	12.2±0.39	11.7±0.45
2865327	HAPLN1	hyaluronan and proteoglycan link protein 1	0.000898	-1.95	7.64±0.87	8.6±0.8
3358950	CTSD	cathepsin D	0.000928	1.29	11±0.33	10.6±0.31
3742285	CXCL16	chemokine (C-X-C motif) ligand 16	0.00104	1.75	7.4±0.9	6.59±0.53
2352804	OLFML3	olfactomedin-like 3	0.00105	-1.44	7.25±0.51	7.78±0.42
3654175	IL4R	interleukin 4 receptor	0.00109	1.42	7.19±0.59	6.69±0.29
3441849	TNFRSF1A	tumor necrosis factor receptor superfamily, member 1A	0.00119	1.26	8.22±0.33	7.88±0.28
3997825	MXRA5	matrix-remodelling associated 5	0.0012	1.67	7.22±0.83	6.48±0.49
3545130	VASH1	vasohibin 1	0.00144	1.18	7.15±0.26	6.92±0.17
2320188	ANGPTL7	angiopoietin-like 7	0.00145	-1.79	5.42±0.79	6.26±0.74
3129065	CLU	clusterin	0.00151	-1.48	11.4±0.7	12±0.31
2656837	ST6GAL1	ST6 beta-galactosamide alpha-2,6-sialyltransferase 1	0.00171	1.46	8.29±0.39	7.75±0.55
2323951	VWA5B1	von Willebrand factor A domain containing 5B1	0.00178	-1.18	5.59±0.2	5.83±0.23
2361612	HAPLN2	hyaluronan and proteoglycan link protein 2	0.00191	-1.13	5.9±0.16	6.07±0.16
2985781	THBS2	thrombospondin 2	0.00199	1.66	11.1±0.78	10.4±0.61
2674047	LAMB2	laminin, beta 2 (laminin 5)	0.00205	1.31	9.57±0.44	9.18±0.31
2622696	SEMA3B	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3B	0.00208	-1.17	6.99±0.26	7.22±0.18
3924144	COL18A1	collagen, type XVIII, alpha 1	0.00269	1.25	8.74±0.34	8.41±0.3
2401018	WNT4	wingless-type MMTV integration site family, member 4	0.00335	-1.15	5.98±0.23	6.18±0.17
2889916	ADAMTS2	ADAM metalloproteinase with thrombospondin type 1 motif, 2	0.00394	1.25	7.34±0.46	7.02±0.13
3252036	PLAU	plasminogen activator, urokinase	0.00406	1.47	7.22±0.72	6.67±0.42
2670725	CCK	cholecystokinin	0.00411	-1.17	5.94±0.19	6.17±0.25
2326126	SEPN1	selenoprotein N, 1	0.00416	-1.49	9.97±0.6	10.5±0.58
2893392	LY86	lymphocyte antigen 86	0.00432	1.71	6.39±1	5.61±0.59
3442514	C1RL	complement component 1, r subcomponent-like	0.00437	1.23	7.42±0.33	7.13±0.28
3380142	FGF4	fibroblast growth factor 4	0.00473	-1.2	6.37±0.22	6.63±0.29
3818047	HSD11B1L	hydroxysteroid (11-beta) dehydrogenase 1-like	0.00488	-1.18	5.8±0.14	6.04±0.29
3193482	COL5A1	collagen, type V, alpha 1	0.00509	1.26	7.8±0.44	7.47±0.27

## aorta adventitia, only BAV patients, comparing dilated and undilated, for extracellular region genes

meta probeset ID	genesymbol	genename	p-value	fold-change	log2(dilated)	log2(undilated)
2893895	BMP6	bone morphogenetic protein 6	2.49E-05	1.32	6.32±0.39	5.92±0.27
3762198	COL1A1	collagen, type I, alpha 1	4.52E-05	1.49	9.74±0.6	9.17±0.4
3049292	IGFBP3	insulin-like growth factor binding protein 3	4.85E-05	1.4	8.55±0.44	8.06±0.37
2886174	SLIT3	slit homolog 3 (Drosophila)	0.000347	1.43	8.51±0.45	7.99±0.49
2352169	WNT2B	wingless-type MMTV integration site family, member 2B	0.000356	1.22	6.18±0.26	5.9±0.26
3252036	PLAU	plasminogen activator, urokinase	0.000369	1.31	7.35±0.42	6.95±0.35
2878437	CD14	CD14 molecule	0.000424	1.6	9.57±0.69	8.89±0.63
2889916	ADAMTS2	ADAM metalloproteinase with thrombospondin type 1 motif, 2	0.000664	1.13	7.1±0.25	6.91±0.14
3214800	OGN	osteolectin	0.000804	-1.31	11±0.53	11.4±0.31
3722917	GRN	granulin	0.00107	1.43	9.92±0.44	9.4±0.56
2324873	C1QC	complement component 1, q subcomponent, C chain	0.00107	1.56	8.84±0.73	8.2±0.63
2865327	HAPLN1	hyaluronan and proteoglycan link protein 1	0.00108	-1.65	7.46±1.1	8.19±0.53
2441043	OLFML2B	olfactomedin-like 2B	0.00115	1.29	6.91±0.45	6.54±0.36
2719440	C1QTNF7	C1q and tumor necrosis factor related protein 7	0.00149	-1.39	7.87±0.66	8.34±0.43
2462160	NID1	nidogen 1	0.00179	1.31	7.16±0.43	6.77±0.42
2324884	C1QB	complement component 1, q subcomponent, B chain	0.0023	1.44	8.36±0.75	7.83±0.51
3742285	CXCL16	chemokine (C-X-C motif) ligand 16	0.00231	1.33	7.1±0.46	6.69±0.46
2601414	SERPINE2	serpin peptidase inhibitor, clade E (nexin), plasminogen activator inhibitor type 1), member 2	0.00298	1.83	7.82±1.1	6.95±0.95
2656837	ST6GAL1	ST6 beta-galactosamide alpha-2,6-sialyltransferase 1	0.00326	1.31	7.86±0.32	7.47±0.49
3359134	IGF2	insulin-like growth factor 2 (somatomedin A)	0.00368	1.16	6.94±0.37	6.72±0.19
3143660	MMP16	matrix metalloproteinase 16 (membrane-inserted)	0.00383	-1.37	7.02±0.64	7.47±0.49
2358393	ADAMTSL4	ADAMTS-like 4	0.0043	1.13	6.75±0.21	6.58±0.21
3015682	PCOLCE	procollagen C-endopeptidase enhancer	0.00434	1.42	9.24±0.64	8.73±0.59
2323172	IGSF21	immunoglobulin superfamily, member 21	0.00475	1.11	6.03±0.2	5.88±0.18
2893392	LY86	lymphocyte antigen 86	0.00504	1.32	6.43±0.67	6.03±0.4

## aorta adventitia, only TAV patients, comparing dilated and undilated, for extracellular region genes

meta probeset ID	genesymbol	genename	p-value	fold-change	log2(dilated)	log2(undilated)
3762198	COL1A1	collagen, type I, alpha 1	1.01E-05	2.6	10.6±0.83	9.26±0.63
2441043	OLFML2B	olfactomedin-like 2B	7.17E-05	1.63	7.38±0.57	6.68±0.31
3046444	SFRP4	secreted frizzled-related protein 4	0.000158	2.24	10.1±0.87	8.95±0.65
2361612	HAPLN2	hyaluronan and proteoglycan link protein 2	0.000303	-1.2	5.88±0.17	6.14±0.17
3997825	MXRA5	matrix-remodelling associated 5	0.000333	2.18	7.63±0.91	6.51±0.67
2601414	SERPINE2	serpin peptidase inhibitor, clade E (nexin), plasminogen activator inhibitor type 1), member 2	0.000387	3.19	8.57±1.6	6.9±0.85
3654175	IL4R	interleukin 4 receptor	0.00044	1.32	7.28±0.34	6.88±0.24
2829947	TGFBI	transforming growth factor, beta-induced, 68kDa	0.000499	1.63	9.09±0.56	8.39±0.45
3049292	IGFBP3	insulin-like growth factor binding protein 3	0.000867	1.68	8.75±0.83	8±0.3
3225855	ANGPTL2	angiopoietin-like 2	0.000914	1.35	7.82±0.35	7.39±0.3
3632298	ADPGK	ADP-dependent glucokinase	0.00118	1.35	6.91±0.44	6.48±0.26
2889916	ADAMTS2	ADAM metalloproteinase with thrombospondin type 1 motif, 2	0.0013	1.32	7.37±0.45	6.97±0.19
3193482	COL5A1	collagen, type V, alpha 1	0.00142	1.24	7.5±0.3	7.19±0.2
2566414	MGAT4A	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme A	0.00147	1.6	6.71±0.67	6.03±0.44
3623031	FBN1	fibrillin 1	0.00147	1.48	10.3±0.48	9.69±0.41
3181642	COL15A1	collagen, type XV, alpha 1	0.00165	1.63	8.01±0.32	7.3±0.59
2886174	SLIT3	slit homolog 3 (Drosophila)	0.00221	1.5	8.54±0.55	7.96±0.43
3333572	C1orf83	chromosome 11 open reading frame 83	0.00228	-1.3	6.23±0.31	6.61±0.3
3191805	LAMC3	laminin, gamma 3	0.0023	-1.12	6.44±0.18	6.61±0.11
3525313	COL4A1	collagen, type IV, alpha 1	0.00249	1.42	8.82±0.49	8.32±0.37
2878074	NRG2	neuregulin 2	0.00267	-1.13	6.62±0.17	6.8±0.14

meta probeset ID	genesymbol	genename	p-value	fold-change	log2(dilated)	log2(undilated)
3380181	FGF3	fibroblast growth factor 3 (murine mammary tumor virus integration site (v-int-2) oncogene hor	0.00285	-1.16	5.96±0.23	6.18±0.16
2656837	ST6GAL1	ST6 beta-galactosamide alpha-2,6-sialyltransferase 1	0.00303	1.5	8.31±0.52	7.72±0.48
3604287	IL16	interleukin 16 (lymphocyte chemoattractant factor)	0.00315	1.39	6.39±0.49	5.92±0.35
3252036	PLAU	plasminogen activator, urokinase	0.00348	1.39	7.58±0.54	7.11±0.31
3013054	COL1A2	collagen, type I, alpha 2	0.00356	1.55	12.1±0.39	11.4±0.57
2893392	LY86	lymphocyte antigen 86	0.00424	1.61	6.84±0.75	6.16±0.52
3365249	SAAL1	serum amyloid A-like 1	0.0045	1.23	6.27±0.28	5.98±0.25

**aorta intima-media, only dilated patients, comparing BAV and TAV, for immune response genes**

meta probeset ID	genesymbol	genename	p-value	fold-change	log2(BAV)	log2(TAV)
2903189	HLA-DRA	major histocompatibility complex, class II, DR alpha	1.13E-07	-4.35	8.47±1.5	10.6±1.3
3904691	SAMHD1	SAM domain and HD domain 1	9.44E-07	-1.98	7.57±0.66	8.55±0.68
2950263	HLA-DMB	major histocompatibility complex, class II, DM beta	1.78E-06	-3.14	5.34±0.8	6.99±1.2
2902427	LST1	leukocyte specific transcript 1	2.41E-06	-1.48	6.52±0.24	7.08±0.43
2357845	FCGR1B	Fc fragment of IgG, high affinity I <sub>b</sub> receptor (CD64)	3.18E-06	-3.25	5.02±0.58	6.72±1.3
3402786	CD4	CD4 molecule	7.11E-06	-2	6.4±0.43	7.41±0.82
2886595	LCP2	lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte protein of 76kDa)	9.06E-06	-2.05	5.91±0.37	6.94±0.86
3286602	CXCL12	chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1)	9.96E-06	-1.78	8.57±0.8	9.4±0.59
2772566	IGJ	immunoglobulin J polypeptide, linker protein for immunoglobulin alpha and mu polypeptides	1.71E-05	-8.19	4.22±1.2	7.25±2.7
3837257	CSAR1	complement component 5a receptor 1	2.85E-05	-1.61	6.06±0.32	6.75±0.62
3647993	CIITA	class II, major histocompatibility complex, transactivator	2.97E-05	-1.56	5.88±0.24	6.53±0.59
2939034	SERPINB9	serpin peptidase inhibitor, clade B (ovalbumin), member 9	4.29E-05	-1.5	6.16±0.43	6.74±0.53
3684486	IGSF6	immunoglobulin superfamily, member 6	9.32E-05	-2.02	5.87±0.57	6.88±0.99
3315658	IFITM2	interferon induced transmembrane protein 2 (1-8D)	0.000112	-1.21	6.93±0.24	7.2±0.26
2807621	PTGER4	prostaglandin E receptor 4 (subtype EP4)	0.000113	-1.56	6.16±0.35	6.8±0.64
2948926	HLA-B	major histocompatibility complex, class I, B	0.000132	-1.83	10.6±0.51	11.5±0.88
2766219	TLR1	toll-like receptor 1	0.000163	-1.77	5.39±0.41	6.22±0.86
3708764	TNFSF13	tumor necrosis factor (ligand) superfamily, member 13	0.000215	-1.24	7.01±0.18	7.33±0.33
2902348	MICB	MHC class I polypeptide-related sequence B	0.000233	-1.17	6.25±0.24	6.48±0.21
2363808	FCGR2B	Fc fragment of IgG, low affinity I <sub>b</sub> receptor (CD32)	0.000253	-2.04	5.83±0.36	6.86±1.1
3601229	CD276	CD276 molecule	0.000287	-1.16	7.31±0.22	7.52±0.21
2950307	HLA-DOA	major histocompatibility complex, class II, DO alpha	0.000331	-1.39	6.2±0.27	6.67±0.52
2392584	TNFRSF14	tumor necrosis factor receptor superfamily, member 14 (herpesvirus entry mediator)	0.000382	-1.23	6.9±0.18	7.19±0.33
3774906	SECTM1	secreted and transmembrane 1	0.000394	-1.36	5.81±0.23	6.26±0.5
2376799	IKBKE	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase epsilon	0.000791	-1.09	5.98±0.14	6.11±0.14
3432438	OAS1	2',5'-oligoadenylate synthetase 1, 40/46kDa	0.000897	-1.49	6.22±0.47	6.8±0.68
3581637	IGHG1	immunoglobulin heavy constant gamma 1 (G1m marker)	0.00113	-1.66	5.57±0.2	6.3±0.93
3318443	TRIM22	tripartite motif-containing 22	0.00125	-1.27	8.06±0.4	8.41±0.4
3830306	HAMP	hepcidin antimicrobial peptide	0.0015	-1.33	6.66±0.32	7.07±0.52
3241316	ZEB1	zinc finger E-box binding homeobox 1	0.00153	1.28	9.44±0.38	9.09±0.42
3397589	ETS1	v-ets erythroblastosis virus E26 oncogene homolog 1 (avian)	0.00156	-1.28	7.91±0.25	8.27±0.45
3432467	OAS3	2'-5'-oligoadenylate synthetase 3, 100kDa	0.00231	-1.3	6.21±0.36	6.58±0.48
2705706	TNFSF10	tumor necrosis factor (ligand) superfamily, member 10	0.00259	-1.77	5.35±0.47	6.17±1.1
2748346	TLR2	toll-like receptor 2	0.00274	-1.53	5.98±0.39	6.6±0.85
2950629	TAPBP	TAP binding protein (tapasin)	0.00302	-1.25	8.2±0.3	8.51±0.42
3589458	THBS1	thrombospondin 1	0.00345	-1.73	9.53±1.1	10.3±0.95
3888613	CEBPB	CCAAT/enhancer binding protein (C/EBP), beta	0.00419	-1.14	7.4±0.26	7.59±0.24
3870733	LILRB2	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 2	0.00566	-1.3	5.5±0.28	5.88±0.58
3822551	IL27RA	interleukin 27 receptor, alpha	0.00747	-1.13	5.47±0.2	5.65±0.27

**aorta intima-media, only undilated patients, comparing BAV and TAV, for immune response genes**

meta probeset ID	genesymbol	genename	p-value	fold-change	log2(BAV)	log2(TAV)
2376799	IKBKE	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase epsilon	0.0046	-1.08	5.96±0.11	6.07±0.12

**aorta adventitia, only dilated patients, comparing BAV and TAV, for immune response genes**

meta probeset ID	genesymbol	genename	p-value	fold-change	log2(BAV)	log2(TAV)
3589458	THBS1	thrombospondin 1	0.00182	-1.67	9.18±0.63	9.92±0.89
3397589	ETS1	v-ets erythroblastosis virus E26 oncogene homolog 1 (avian)	0.00742	-1.29	8.64±0.41	9±0.5

**aorta adventitia, only undilated patients, comparing BAV and TAV, for immune response genes**

meta probeset ID	genesymbol	genename	p-value	fold-change	log2(BAV)	log2(TAV)
-	-	-	-	-	-	-

**aorta intima-media, only BAV patients, comparing dilated and undilated, for immune response genes**

meta probeset ID	genesymbol	genename	p-value	fold-change	log2(dilated)	log2(undilated)
3945396	GTPBP1	GTP binding protein 1	0.00375	1.14	7.73±0.24	7.54±0.26
3598959	SMAD3	SMAD family member 3	0.00402	1.14	8.12±0.27	7.92±0.25

**aorta intima-media, only TAV patients, comparing dilated and undilated, for immune response genes**

meta probeset ID	genesymbol	genename	p-value	fold-change	log2(dilated)	log2(undilated)
3601229	CD276	CD276 molecule	0.000656	1.24	7.52±0.21	7.21±0.28
2950629	TAPBP	TAP binding protein (tapasin)	0.0018	1.34	8.51±0.42	8.09±0.36
3402786	CD4	CD4 molecule	0.00232	1.61	7.41±0.82	6.72±0.51
2357845	FCGR1B	Fc fragment of IgG, high affinity I <sub>b</sub> receptor (CD64)	0.00353	2.09	6.72±1.3	5.65±0.83
3844781	PRG2	plasticity-related gene 2	0.00611	-1.2	6.48±0.18	6.75±0.33
3904691	SAMHD1	SAM domain and HD domain 1	0.00714	1.56	8.55±0.68	7.91±0.72
3397589	ETS1	v-ets erythroblastosis virus E26 oncogene homolog 1 (avian)	0.00756	1.31	8.27±0.45	7.88±0.41
2902427	LST1	leukocyte specific transcript 1	0.00761	1.28	7.08±0.43	6.73±0.36

**aorta adventitia, only BAV patients, comparing dilated and undilated, for immune response genes**

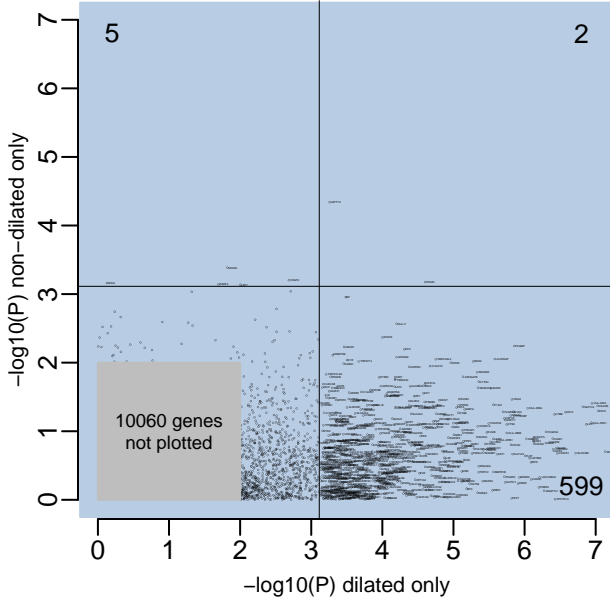
meta probeset ID	genesymbol	genename	p-value	fold-change	log2(dilated)	log2(undilated)
3837257	CSAR1	complement component 5a receptor 1	0.000836	1.41	6.94±0.46	6.45±0.51
3939875	SUSD2	sushi domain containing 2	0.000854	1.2	6.82±0.27	6.55±0.26
2950629	TAPBP	TAP binding protein (tapasin)	0.000855	1.33	8.47±0.36	8.06±0.43
3256074	BMPRI1A	bone morphogenetic protein receptor, type IA	9.00E-04	-1.28	8.17±0.44	8.53±0.33
2357845	FCGR1B	Fc fragment of IgG, high affinity I <sub>b</sub> receptor (CD64)	0.00132	1.5	6.45±0.81	5.86±0.53
2950307	HLA-DOA	major histocompatibility complex, class II, DO alpha	0.00135	1.23	7.01±0.36	6.71±0.3
2902427	LST1	leukocyte specific transcript 1	0.00295	1.21	7.34±0.38	7.07±0.29
2392584	TNFRSF14	tumor necrosis factor receptor superfamily, member 14 (herpesvirus entry mediator)	0.00405	1.13	7.26±0.23	7.09±0.2
3402786	CD4	CD4 molecule	0.00598	1.34	7.59±0.61	7.17±0.49
2886595	LCP2	lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte protein of 76kDa)	0.00683	1.34	7.31±0.59	6.88±0.52
3432467	OAS3	2'-5'-oligoadenylate synthetase 3, 100kDa	0.00718	1.17	6.64±0.38	6.41±0.25

**aorta adventitia, only TAV patients, comparing dilated and undilated, for immune response genes**

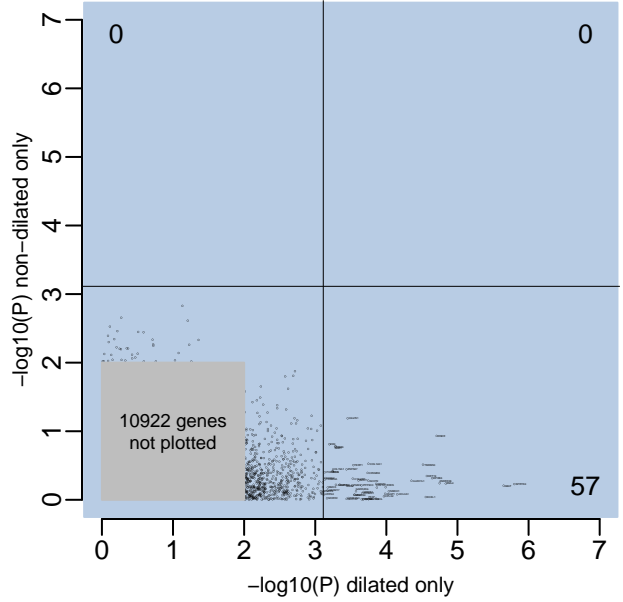
meta probeset ID	genesymbol	genename	p-value	fold-change	log2(dilated)	log2(undilated)
3397589	ETS1	v-ets erythroblastosis virus E26 oncogene homolog 1 (avian)	0.000903	1.48	9±0.5	8.44±0.36
3589458	THBS1	thrombospondin 1	0.00216	1.99	9.92±0.89	8.93±0.75
2939034	SERPINB9	serpin peptidase inhibitor, clade B (ovalbumin), member 9	0.00222	1.5	6.87±0.55	6.29±0.43
2886595	LCP2	lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte protein of 76kDa)	0.00261	1.51	7.63±0.63	7.04±0.4

## All genes

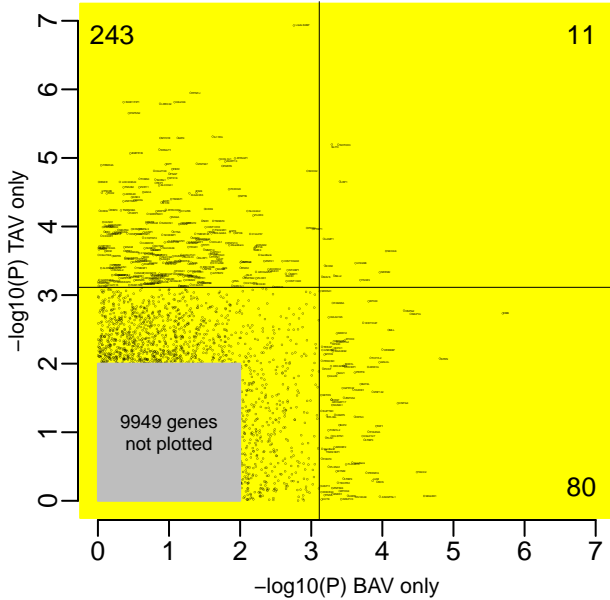
Tissue: aorta intima-media  
Comparison: TAV vs BAV



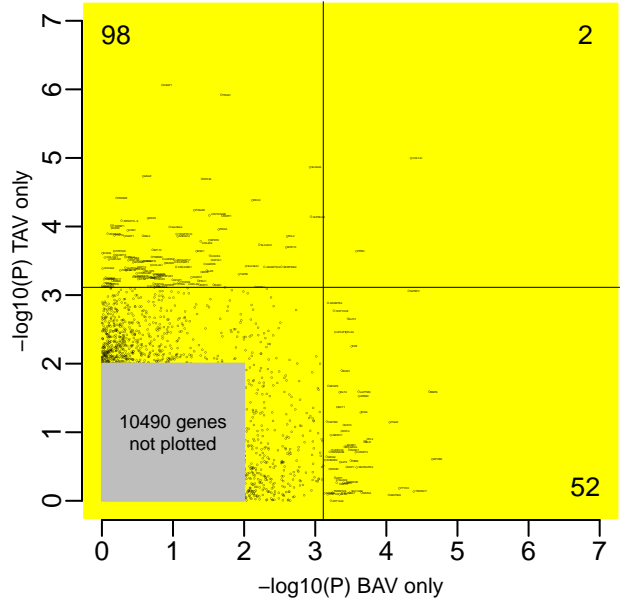
Tissue: aorta adventitia  
Comparison: TAV vs BAV



Tissue: aorta intima-media  
Comparison: dilated vs non-dilated

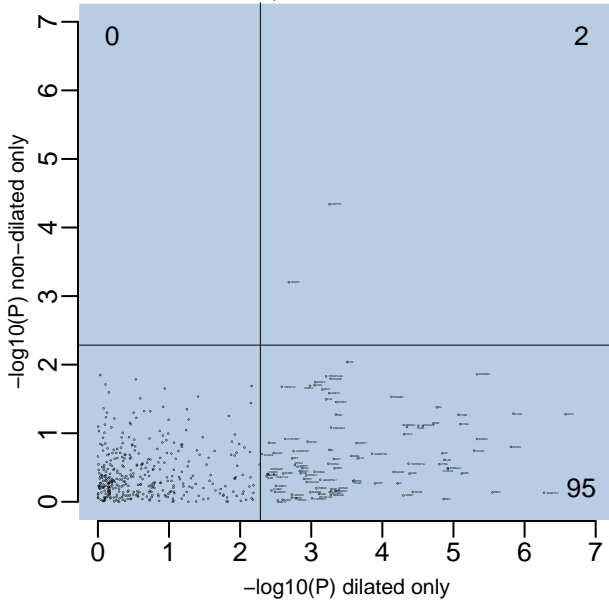


Tissue: aorta adventitia  
Comparison: dilated vs non-dilated

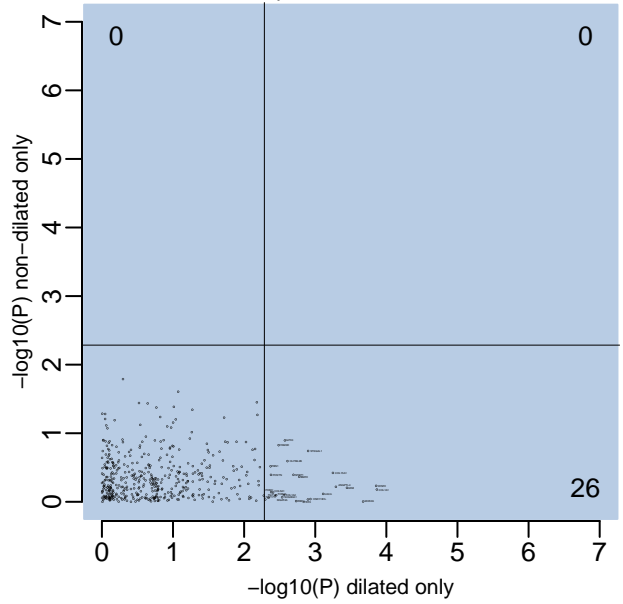


## Extracellular region genes

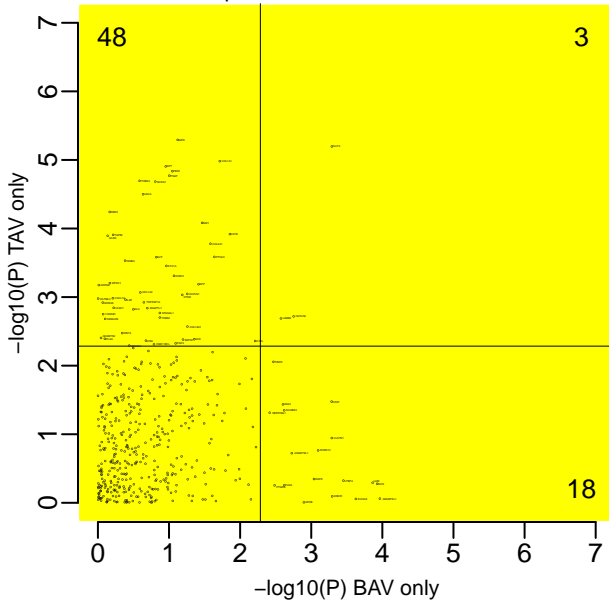
Tissue: aorta intima-media  
Comparison: TAV vs BAV



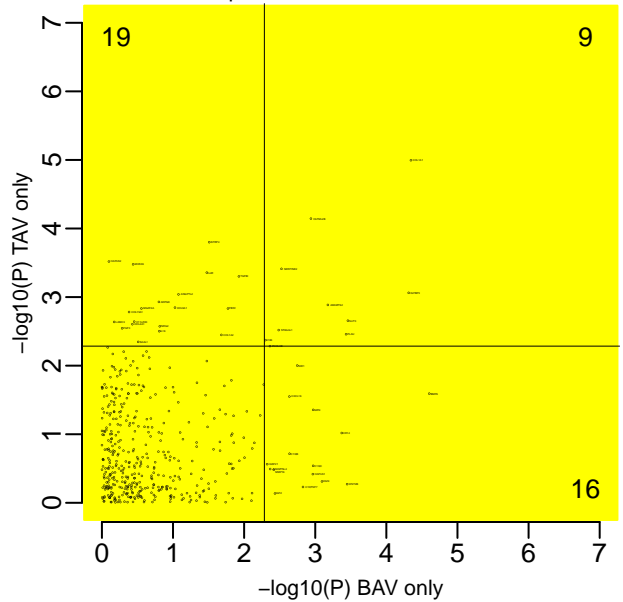
Tissue: aorta adventitia  
Comparison: TAV vs BAV



Tissue: aorta intima-media  
Comparison: dilated vs non-dilated

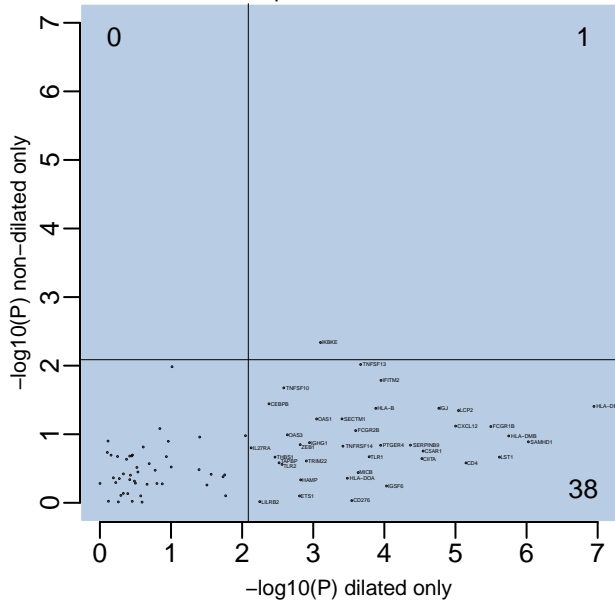


Tissue: aorta adventitia  
Comparison: dilated vs non-dilated

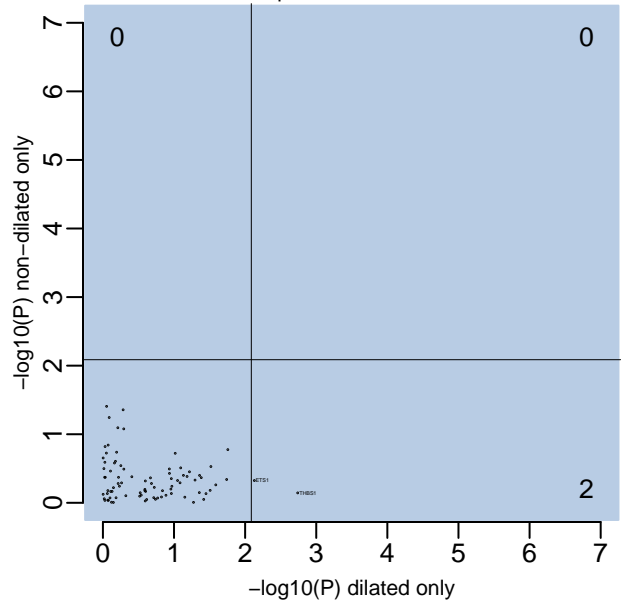


## Immune response genes

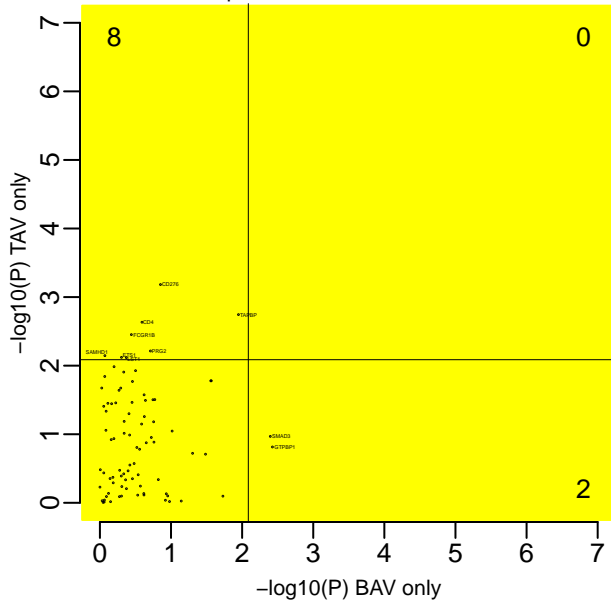
Tissue: aorta intima-media  
Comparison: TAV vs BAV



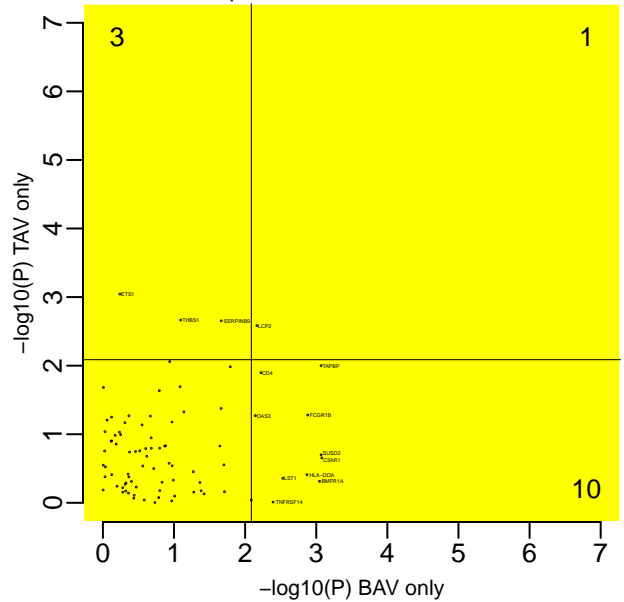
Tissue: aorta adventitia  
Comparison: TAV vs BAV



Tissue: aorta intima-media  
Comparison: dilated vs non-dilated

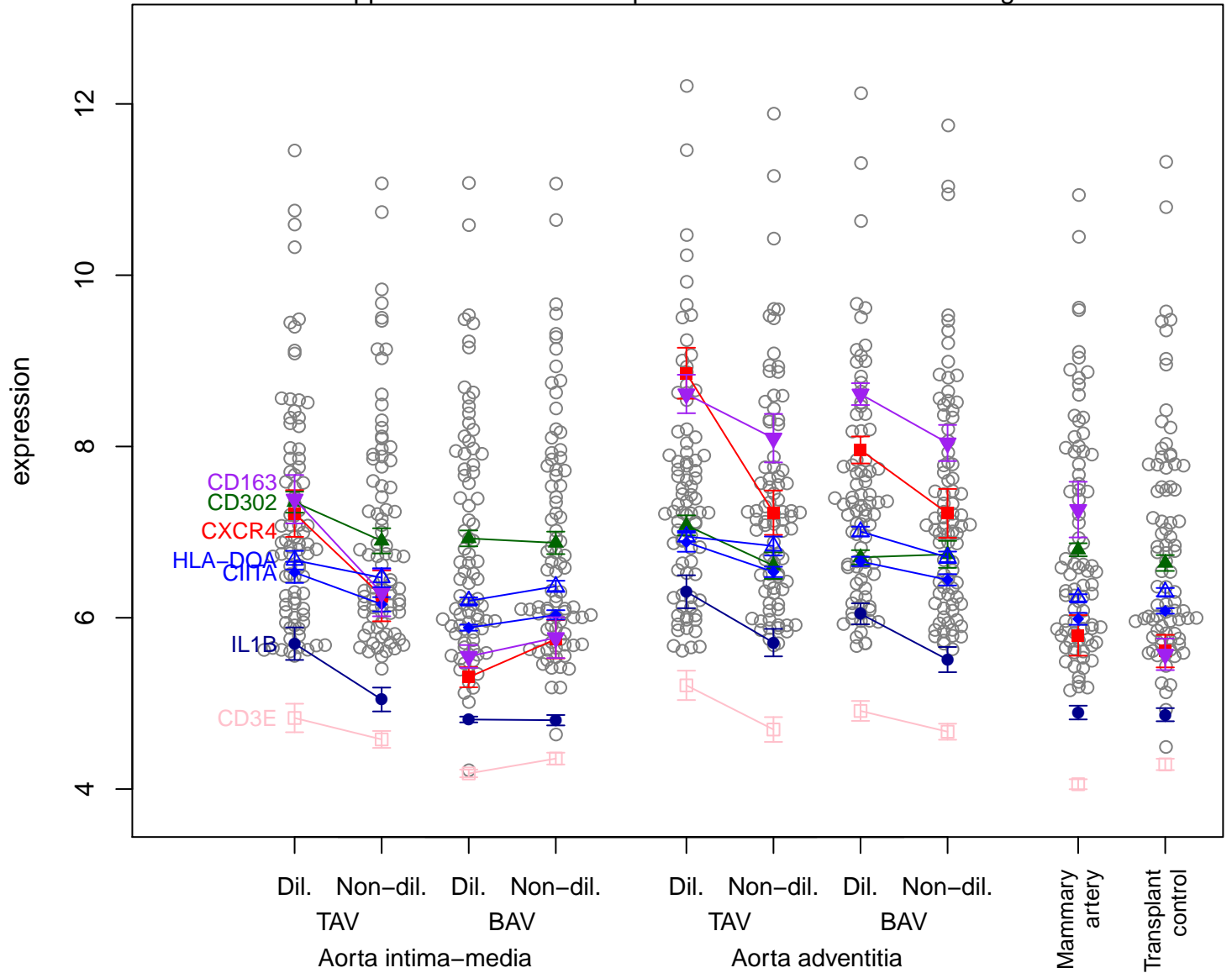


Tissue: aorta adventitia  
Comparison: dilated vs non-dilated



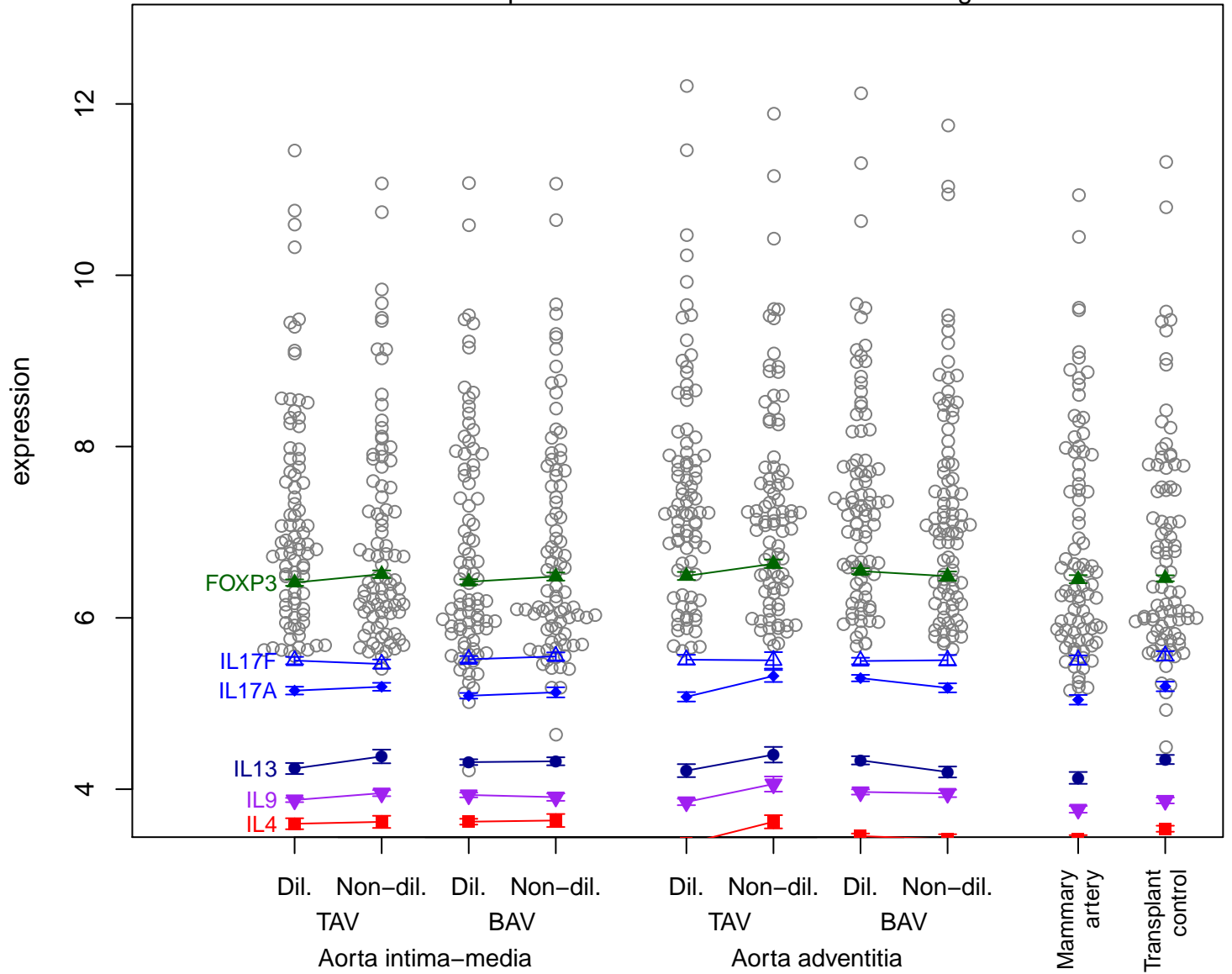
## immune response

supplemental immune response cell markers which change



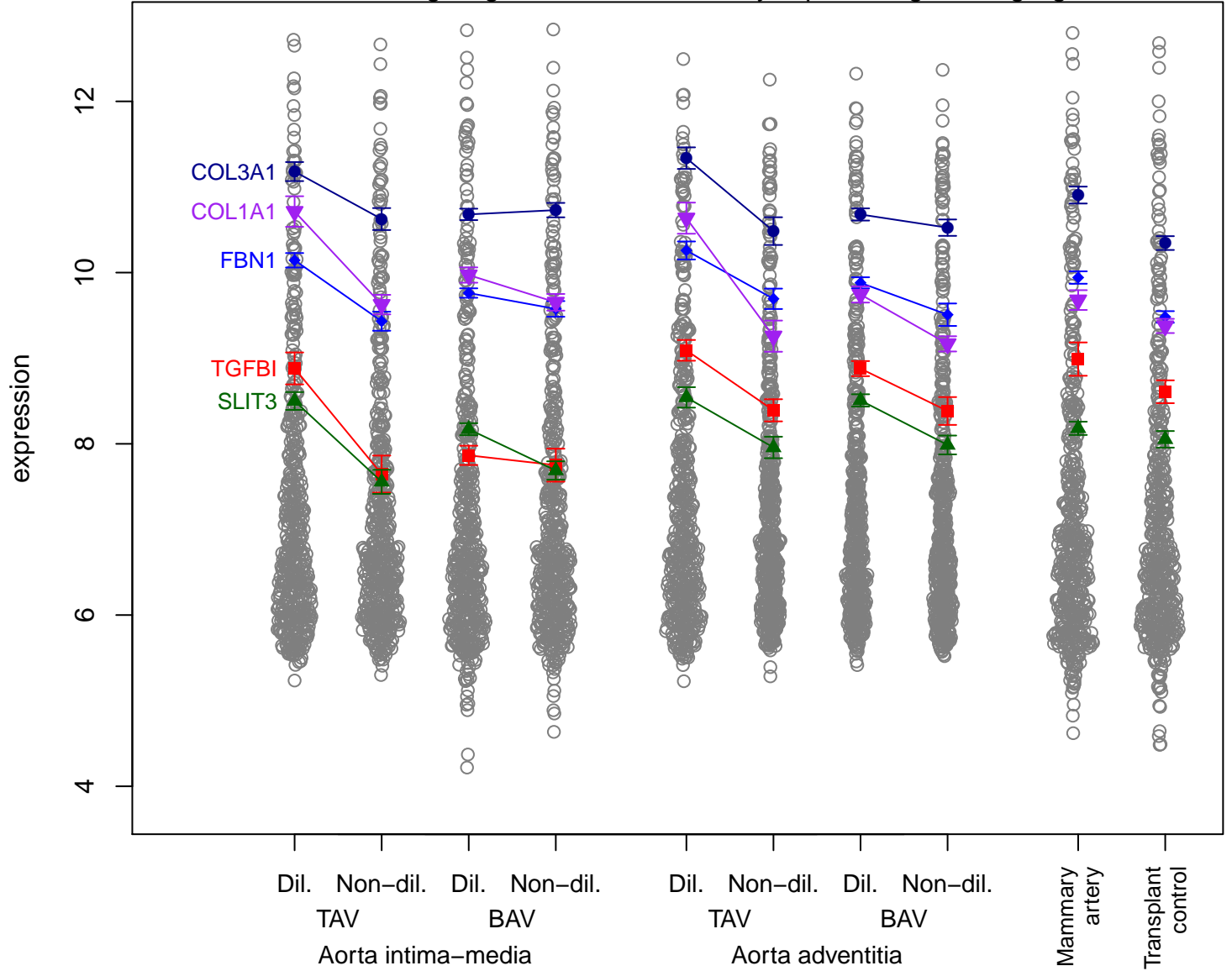
## immune response

immune response cell markers which do not change



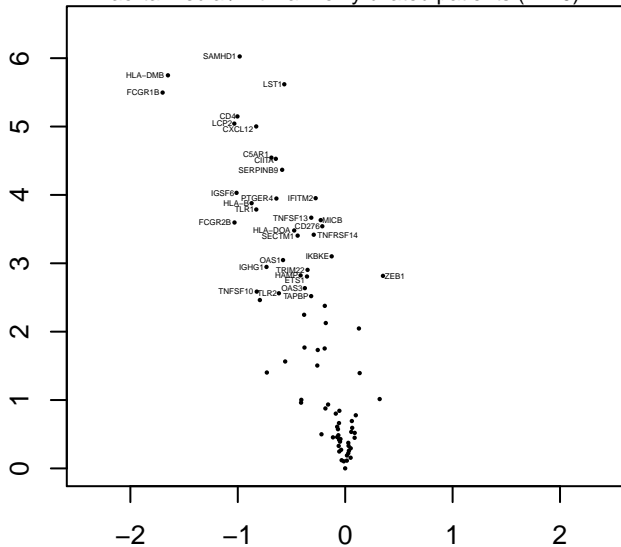
## extracellular region

extracellular region genes, with differentially expressed genes highlighted



Immune response genes  
 ← TAV overexpression    – BAV overexpression →

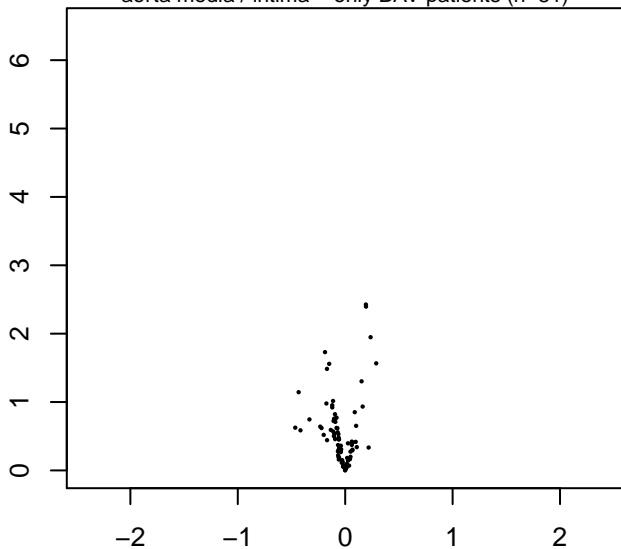
aorta media / intima – only dilated patients (n=70)



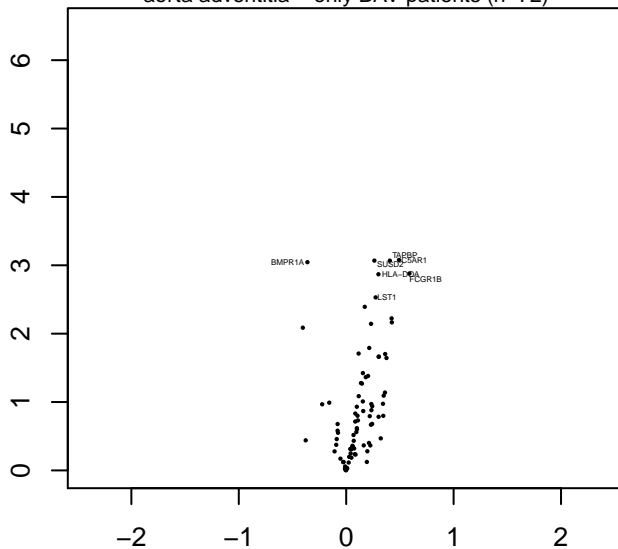
## Immune response genes

&lt;- Dilated overexpression - Non-dilated overexpression-&gt;

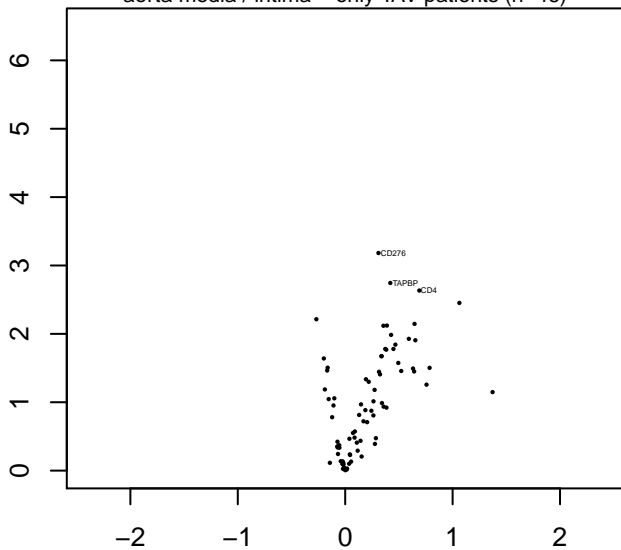
aorta media / intima - only BAV patients (n=81)



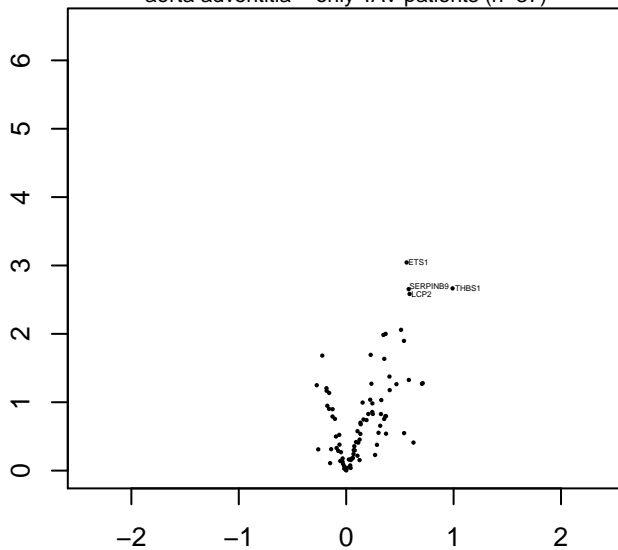
aorta adventitia - only BAV patients (n=72)



aorta media / intima - only TAV patients (n=46)

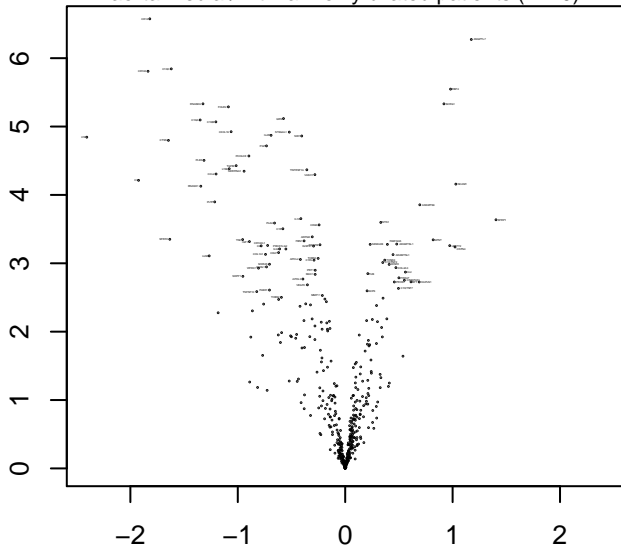


aorta adventitia - only TAV patients (n=37)

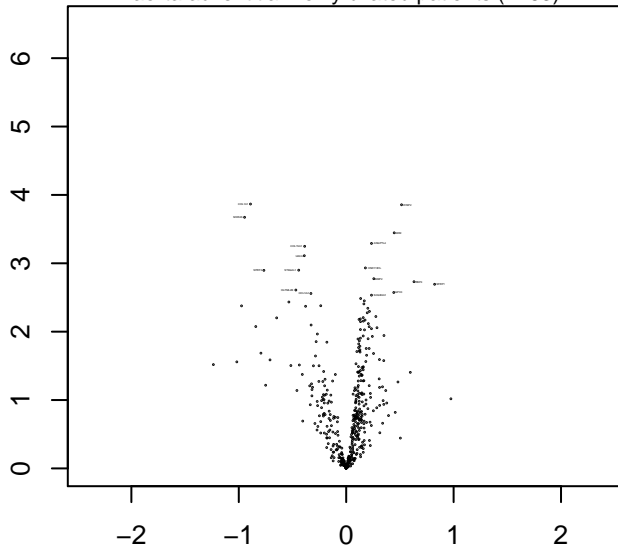


Extracellular region genes  
← TAV overexpression    -    BAV overexpression →

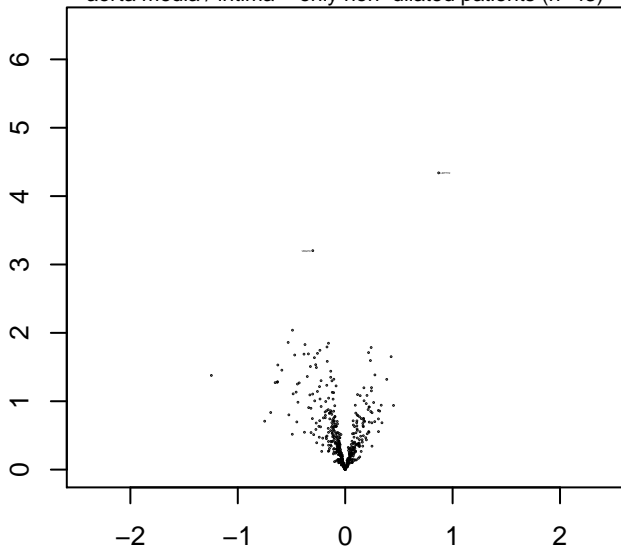
aorta media / intima – only dilated patients (n=70)



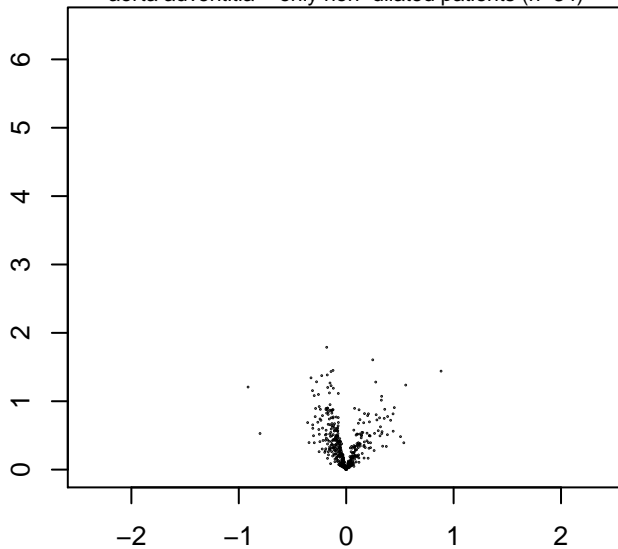
aorta adventitia – only dilated patients (n=63)



aorta media / intima – only non-dilated patients (n=43)



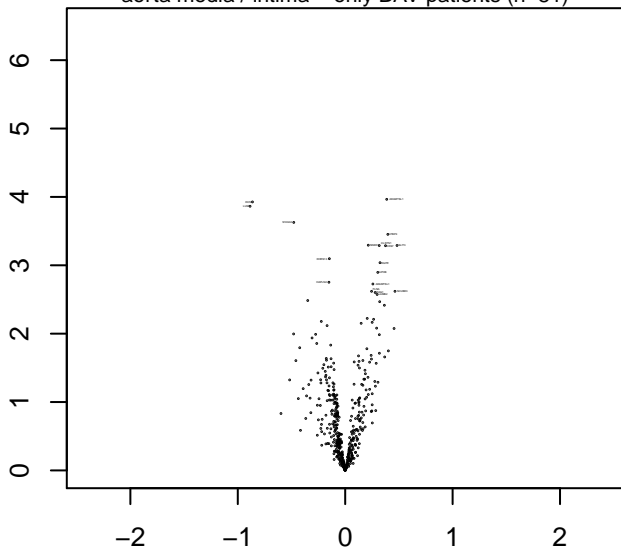
aorta adventitia – only non-dilated patients (n=34)



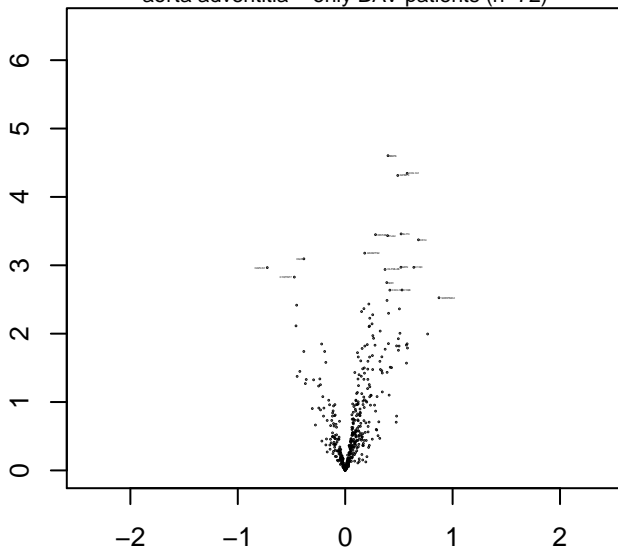
## Extracellular region genes

&lt;- Dilated overexpression - Non-dilated overexpression-&gt;

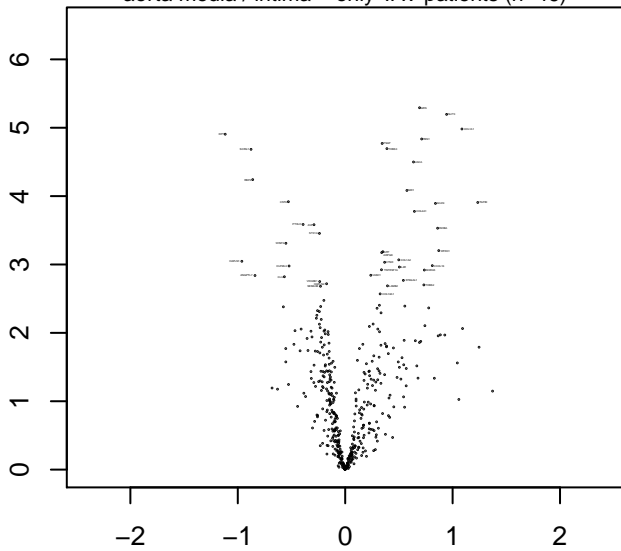
aorta media / intima - only BAV patients (n=81)



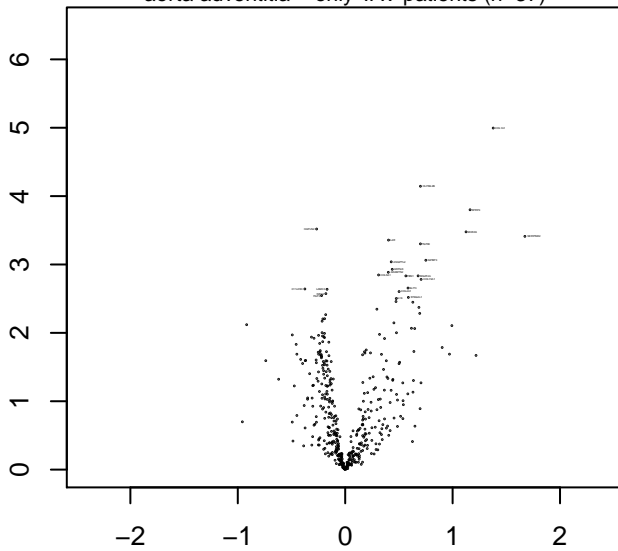
aorta adventitia - only BAV patients (n=72)



aorta media / intima - only TAV patients (n=46)



aorta adventitia - only TAV patients (n=37)



CD4

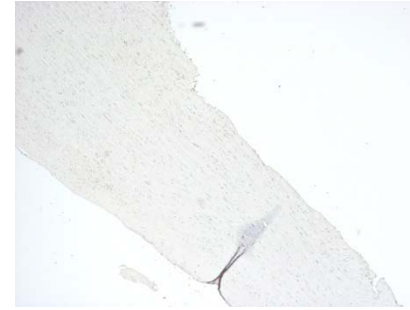
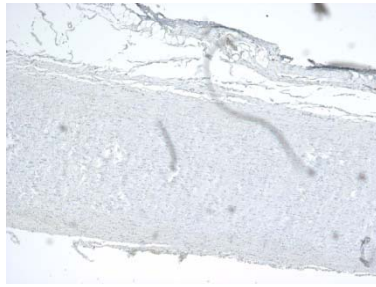
BAV non-dil

BAV dil

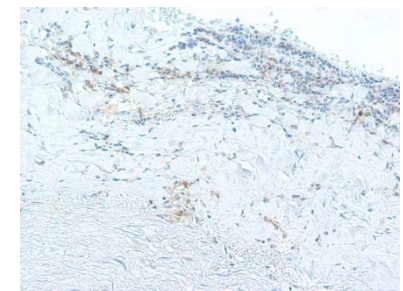
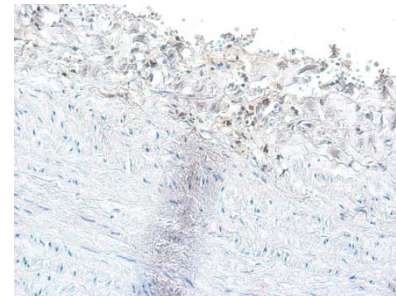
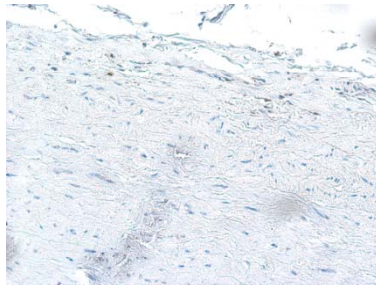
TAV non-dil

TAV dil

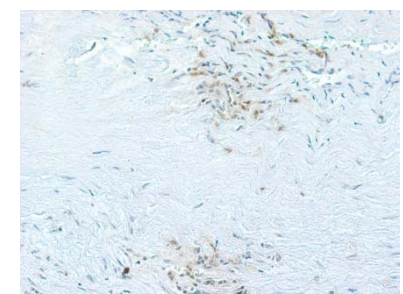
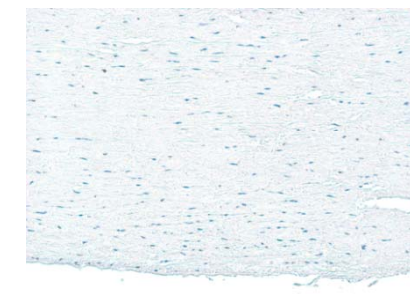
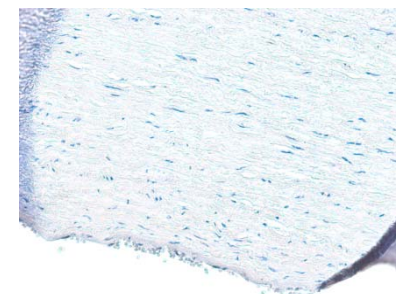
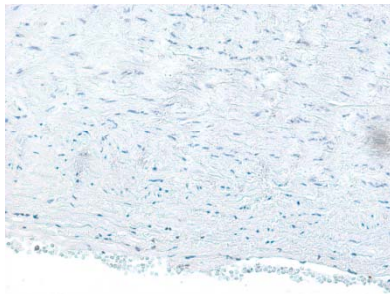
x5



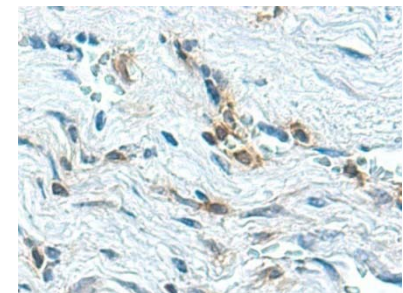
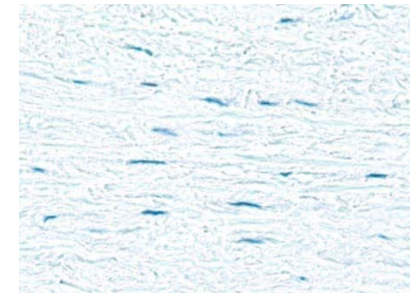
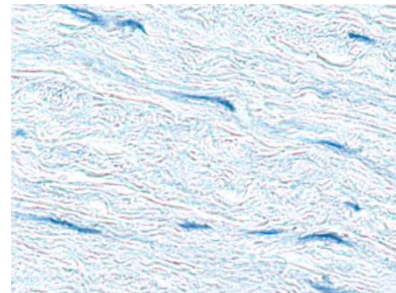
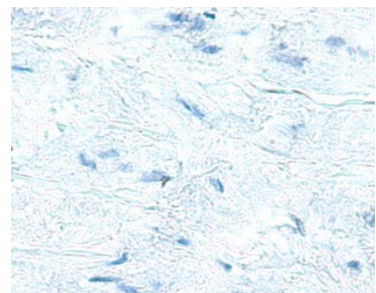
x20  
adventitia



x20  
intima-  
media



x40  
media



272

308

257

266

CD68

BAV non-dil

BAV dil

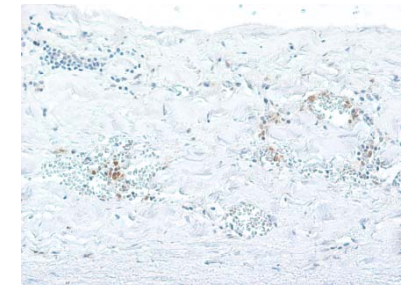
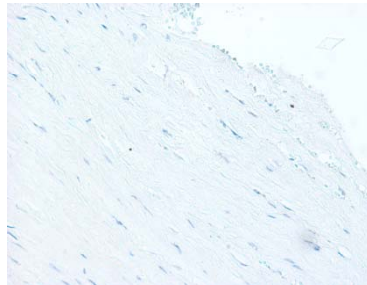
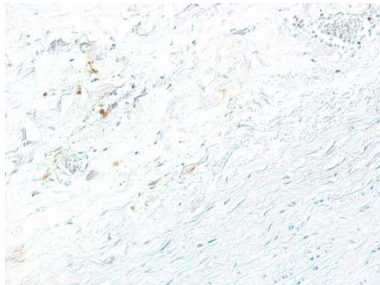
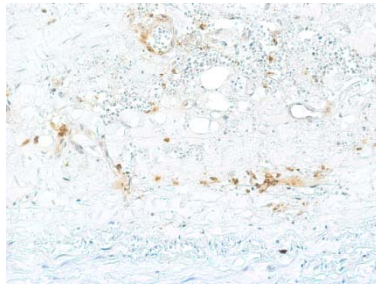
TAV non-dil

TAV dil

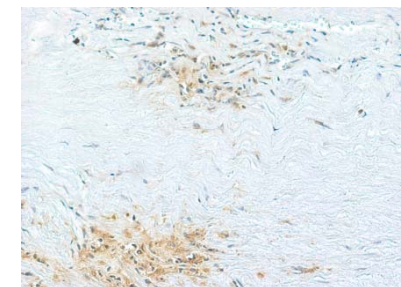
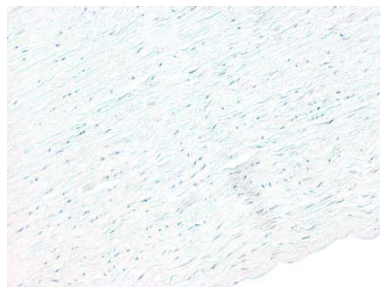
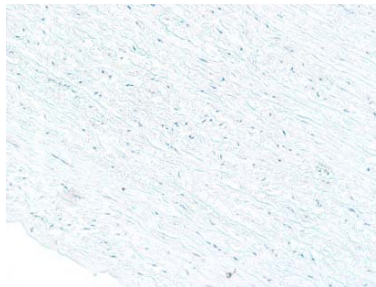
x5



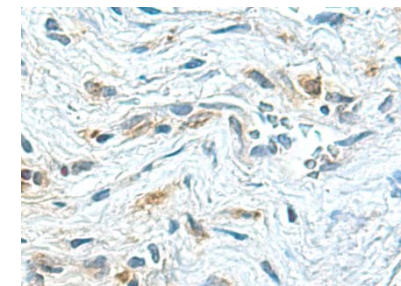
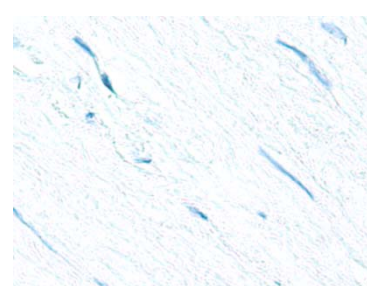
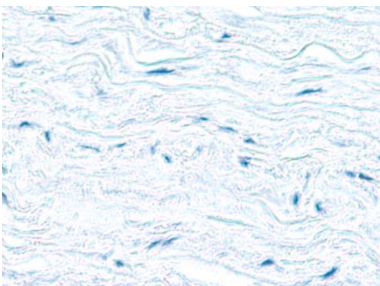
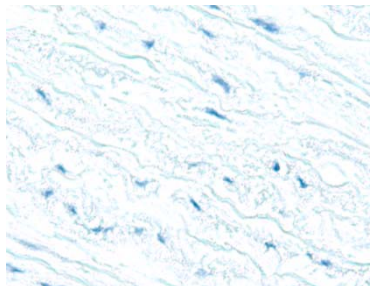
x20  
adventitia



x20  
intima-  
media



x40  
media



233

303

254

266

CD163

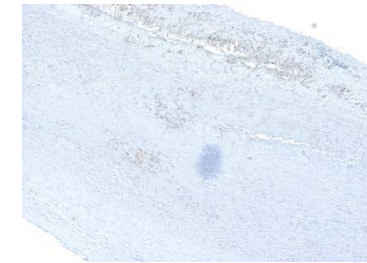
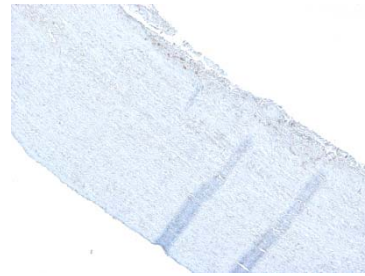
BAV non-dil

BAV dil

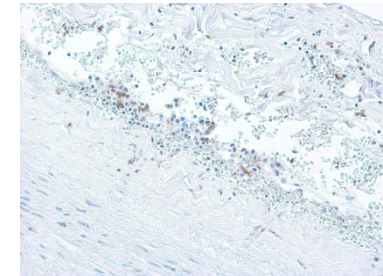
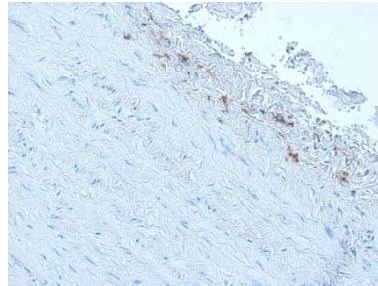
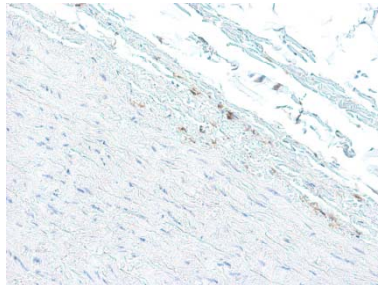
TAV non-dil

TAV dil

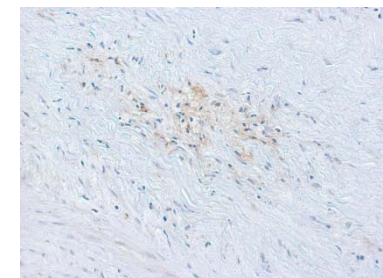
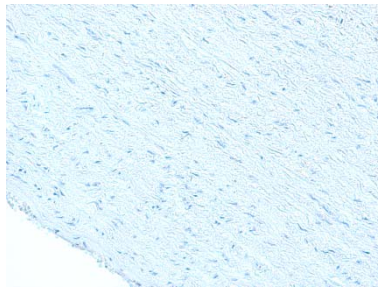
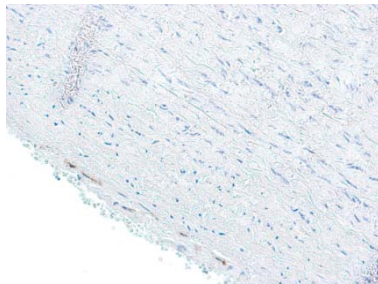
x5



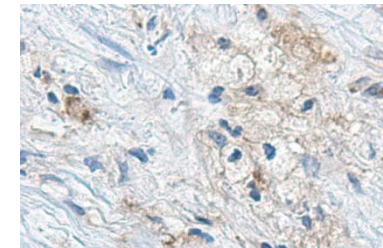
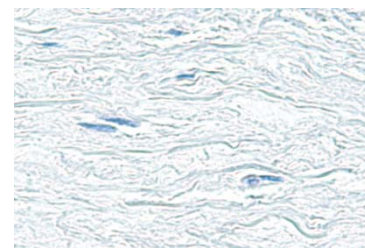
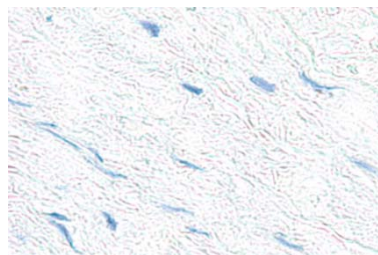
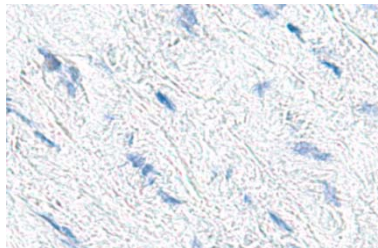
x20  
adventitia



x20  
intima-  
media



x40  
media



272

308

254

266