

Supplementary Materials

The mir-200 family regulates key pathogenic events in ascending aortas of individuals with bicuspid aortic valves

Short title: Mir-200 family in patients with BAV

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Supplementary Table S1. Patient characteristics

Patient characteristics						
	BAV-ND	TAV-ND	P	BAV-D	TAV-D	P
N	45	45		21	18	
Age, years	60 (13)	68 (12)	<0.01	58 (13)	68 (5)	<0.01
Male gender	33	26	0.12	16	11	0.49
BSA, m ²	1.98 (0.18)	1.95 (0.21)	0.36	2.06 (0.24)	2.04 (0.25)	0.80
Triglycerides, mmol/L	1.23 (0.60)	1.11 (0.37)	0.25	1.69 (1.13)	1.02 (0.37)	0.03
Cholesterol, mmol/L	4.45 (1.01)	4.84 (1.20)	0.10	5.25 (0.97)	5.14 (0.91)	0.74
hsCRP, mg/L	2.34 (3.23)	2.87 (3.83)	0.48	2.45 (3.30)	3.22 (4.11)	0.53
Systolic BP, mmHg	131 (15)	138 (22)	0.10	132 (18)	145 (18)	0.03
Diastolic BP, mmHg	78 (11)	77 (15)	0.91	82 (10)	74 (11)	0.03
Diabetes	5	4	0.74	1	0	1.00
Aortic aneurysm and valve disease						
Ascending aortic aneurysm, mm	32.9 (4.9)	31.2 (4.1)	0.08	49.6 (5.1)	53.6 (4.6)	0.04
Aortic valve stenosis	39	28	<0.05	12	0	<0.001
Aortic valve regurgitation	5	8	0.55	7	13	<0.05

Non-dilated (ND) ascending aorta <40mm; Dilated (D) ascending aorta >45mm. BSA, body surface area; hsCRP, high-sensitive C-reactive protein; BP, blood pressure. Diabetes was recorded via questionnaire of medical history. Continuous variables are presented as mean (SD) and ordinal variables are presented as n. P indicates significance for differences between groups using Student's t-test for continuous variables and a Fisher's exact test for nominal variables.

Supplementary Table S2. Primer sequences, MiR200c promoter region and control region.

Oligo Name	Sequence (written 5' - 3')	Length
Forward (200c promoter)	CTTAAAGCCCCTTCGTCTCC	20
Reverse (200c promoter)	GATTTACCCACCCTCATCCC	20
Forward (200c ctrl)	GCTCAGTGCTTCTCCAAGGT	20
Reverse (200c ctrl)	TAAGGACAGGGCCAGGGATT	20

Supplementary Table S3. MicroRNA spanning scores, BAV vs. TAV non-dilated and dilated aorta, respectively.

See separate pdf-file

Supplementary Table S4A. Top 10 microRNAs according to spanning score, selected by *in silico* method. BAV vs. TAV non-dilated aorta.

miRNA	Score	Genes targeted	Clusters targeted	P-value	References
miR-200bc/429/548a	2,875	44	7	0,0001	<i>See manuscript text</i>
miR-27abc/27a-3p	2,471213	41	7	0,0022	[1, 2]
miR-135ab/135a-5p	2,264296	29	7	0,0012	[3, 4]
miR-495/1192	2,256448	31	8	0,0062	[5, 6]
miR-204/204b/211	2,251015	28	7	0,0011	[7-11]
miR-133abc	2,210151	27	7	0,0013	[12]
miR-300/381/539-3p	2,171962	31	8	0,0135	[13-17]
miR-128/128ab	2,170606	34	7	0,0081	[18-20]
miR-124/124ab/506	2,167087	42	8	0,1412	[12, 21-24] [25, 26]
miR-29abcd	2,099049	33	7	0,0127	[27-29]

Supplementary Table S4B. Top 10 microRNAs according to spanning score, selected by *in silico* method. BAV vs. TAV dilated aorta.

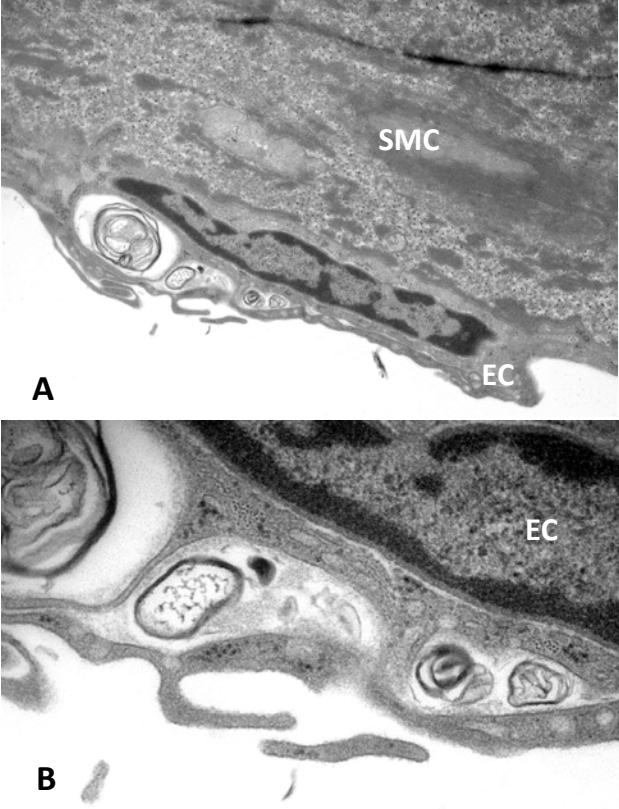
miRNA	Score	Genes targeted	Clusters targeted	P-value	References
miR-124/124ab/506	2,924743	152	8	0,0002	[30, 31]
miR-23abc/23b-3p	2,75	114	8	<0.0001	[32]
miR-200bc/429/548a	2,480263	111	6	<0.0001	<i>See manuscript text</i>
miR-1ab/206/613	2,434211	85	7	<0.0001	[33-38]
miR-181abcd/4262	2,275457	117	5	0,0003	[39, 40]
miR-144	2,236842	93	5	<0.0001	[41, 42]
miR-203	2,20234	81	8	0,0021	[43-46]
miR-15abc/16/16abc/ 195/322/424/497/1907	2,166147	115	6	0,0023	[47-52]
miR-145	2,144737	79	5	0,0001	[53-55]
miR-96/507/1271	2,12781	97	6	0,0011	[56-59]

Supplementary Table S5. Co-expression of miR-200b, miR-200c and miR-429 in BAV and TAV endothelial cells (Pearson correlation, R-values).

	miR-200b	miR-429	miR-200c
miR-200b	1	0,499	0,433
miR-429	0,499	1	0,569
miR-200c	0,433	0,569	1

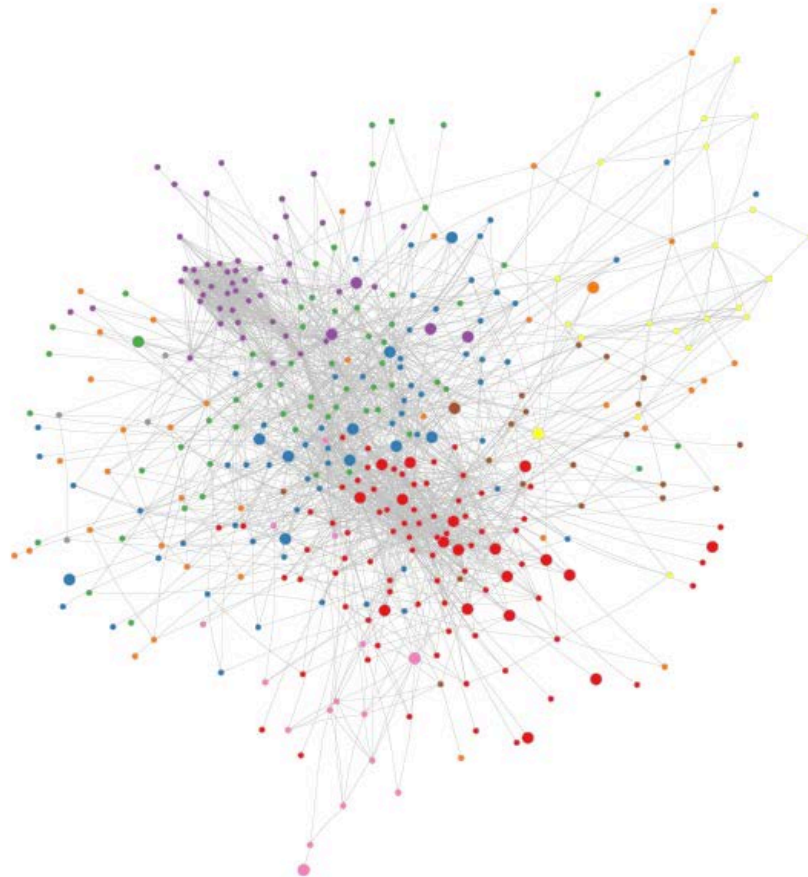
Supplementary Figure S1

Electron microscopy view of autophogosome-like structure. BAV endothelial cell membrane, non-dilated aorta. EC: Endothelial cells; SMC: Smooth muscle cells, (B) is the higher magnification of (A).



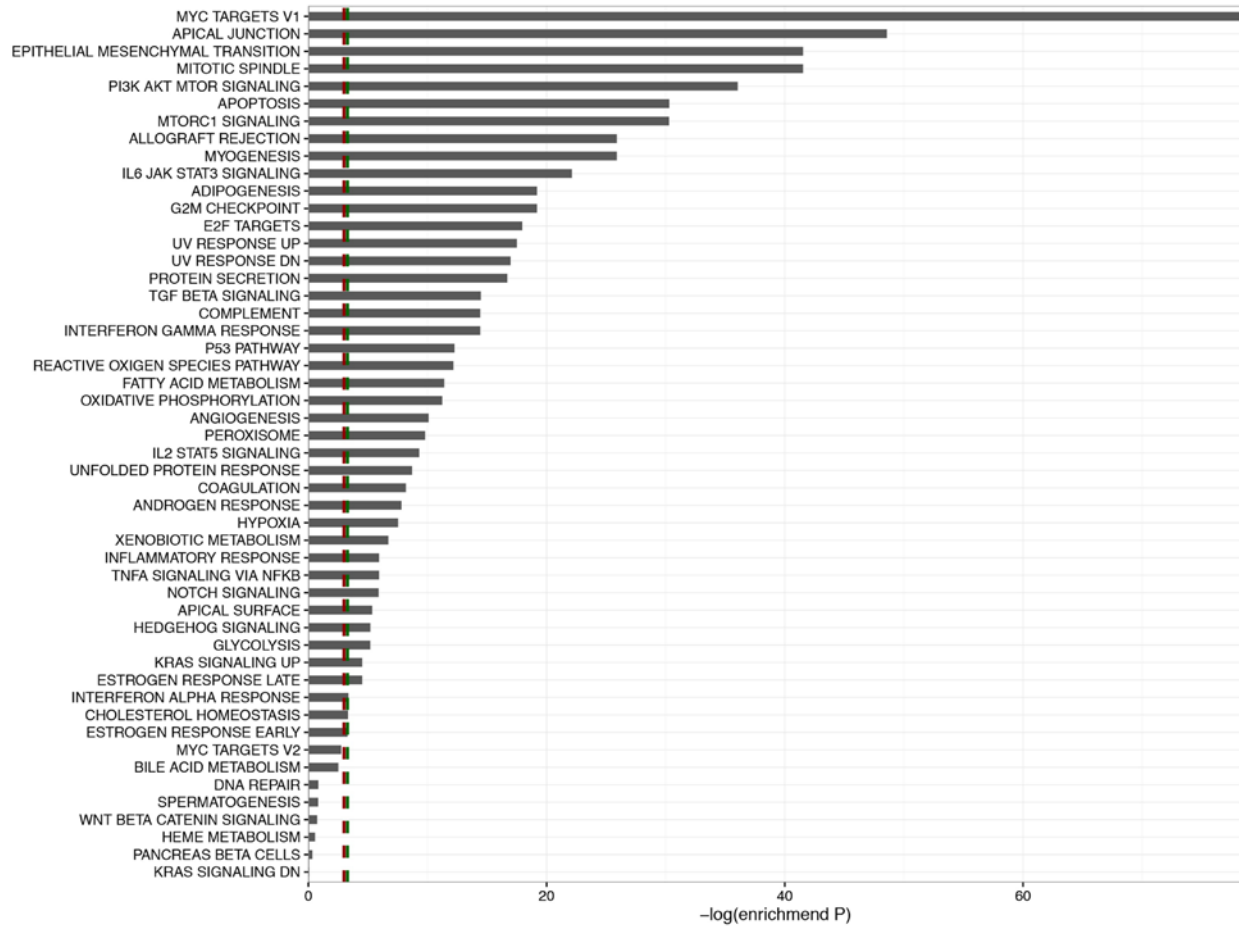
Supplementary Figure S2

Computational network analysis of dilated BAV and TAV aorta. Cluster modules of highly interacting groups of genes in the dilated (D) network. Different colors in the network represent different cluster modules (non-labeled). The network was clustered using a spectral partition-based algorithm, as implemented in the ReactomeFI tool for Cytoscape. miRNA targets were cross-referenced to the network and regulatory miRNAs were identified and ranked according to calculated spanning scores (see materials and methods for details). Node size represents spanning scores of each gene. Module assignments/labels and spanning scores are provided in supplementary Table S2B and S3.



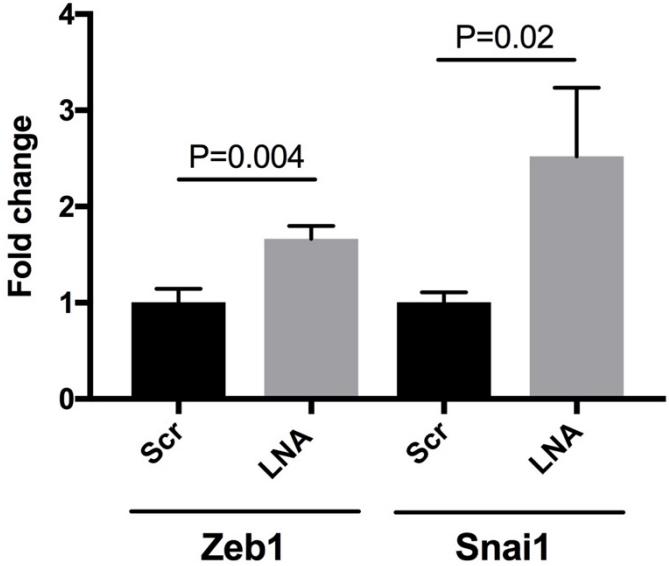
Supplementary Figure S3

Hallmark analysis of dilated network genes, BAV vs. TAV. $-\log P$ indicates the enrichment p-value (hypergeometric test). Red dashed line indicates p-value 0.05; green dashed line indicates FDR-adjusted p-value 0.05. Hallmark gene sets are curated by the Molecular Signatures Database (MSigDB).



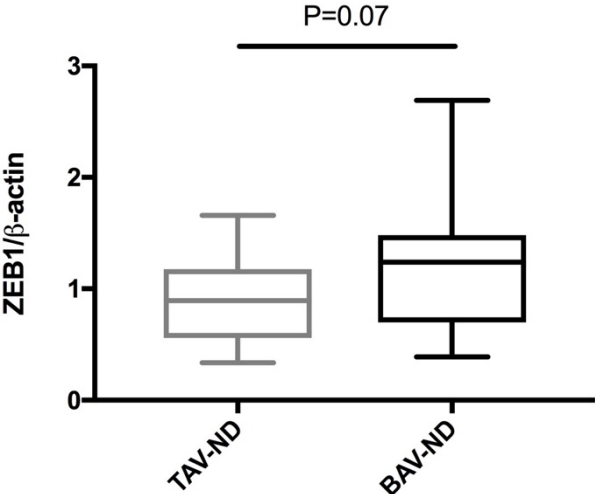
Supplementary Figure S4

ZEB1 and Snai1 expression in cultured endothelial cells (EA.hy926) after miR-200 family inhibition. Locked nucleic acid (LNA) were used for miR200 family down-regulation. Data are presented as fold change of control \pm SEM (Student's t-test).



Supplementary Figure S5

ZEB1 expression in BAV and TAV non-dilated aortas. Western blot analysis of 20 µg protein extract using anti-ZEB1 antibody. Data are shown as mean ZEB1/Actinβ ratio ± SEM. N=15 BAV and N=16 TAV (Student's t-test).



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