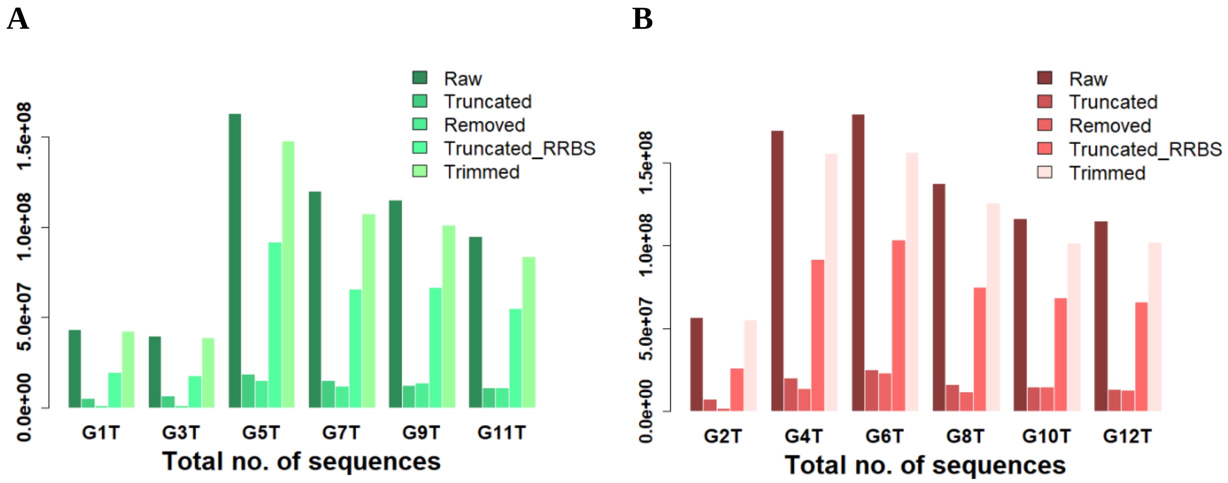
Supplementary Material

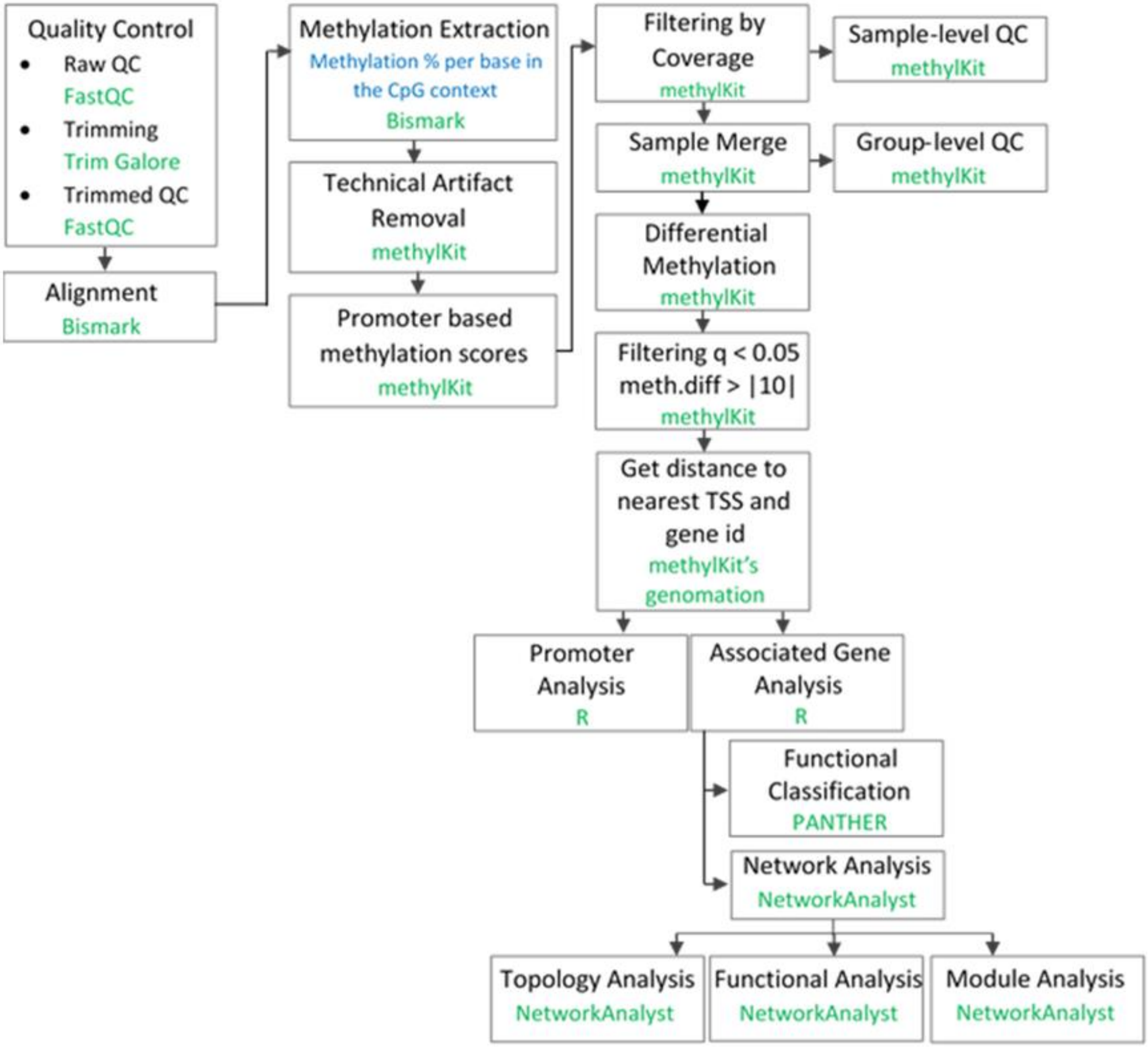
1 Supplementary Figures

1.1 Figure S1. Total no. of sequences for all samples before and after trimming



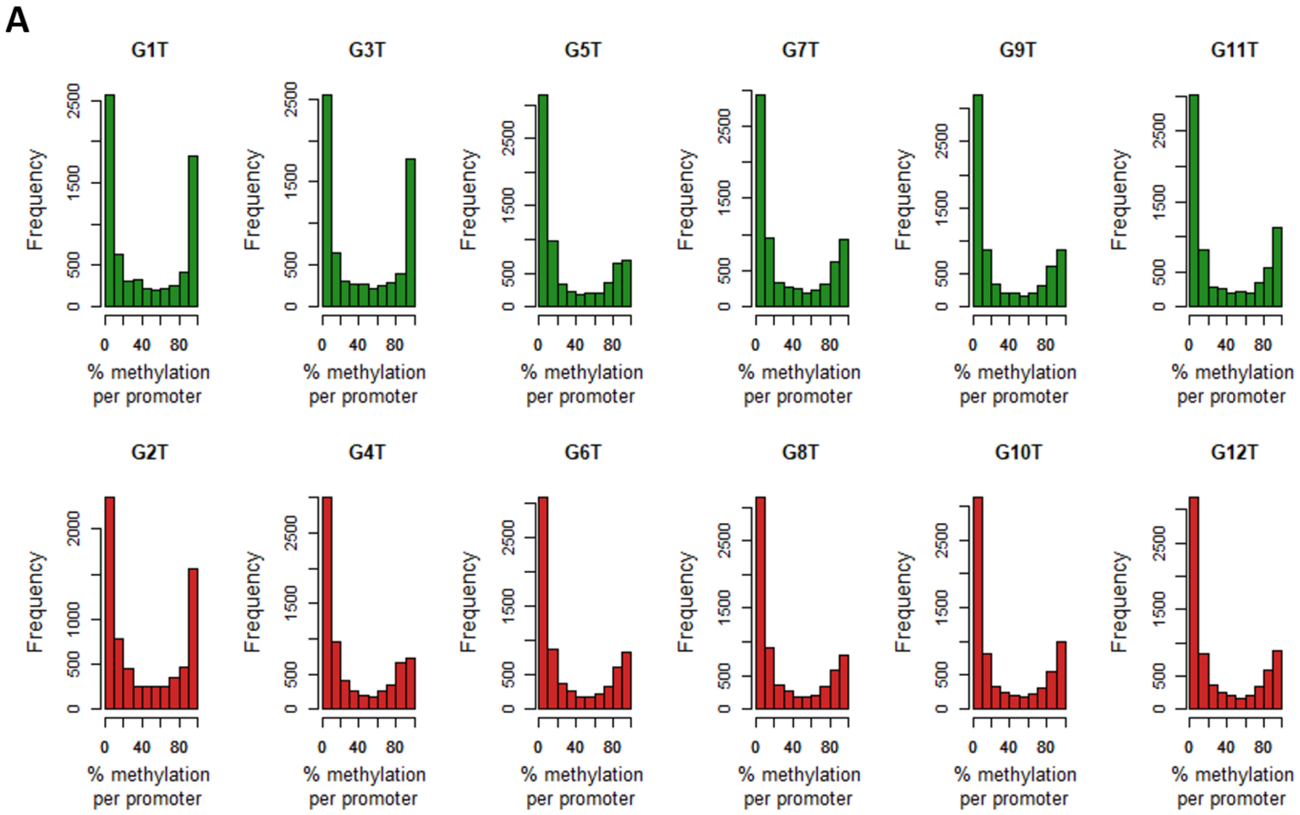
Supplementary Figure 1. Total no. of sequences for (**A**) aortic tissue (TA) samples G1T, G3T, G5T, G7T, G9T and G11T and (**B**) mitral tissue (TM) samples G2T, G4T, G6T, G8T, G10T and G12T. "Raw" refers to the total no. of sequences processed before trimming; "Truncated" denotes sequences that were truncated to a varying degree because of deteriorating qualities (Phred score < 20); "Removed" represents sequences that were removed as they became shorter than 20 bps after trimming; "Truncated_RRBS" represents sequences trimmed by an additional 2 bp characteristic of RRBS when adapter contamination was detected; "Trimmed" refers to the total no. of sequences processed after trimming. The total number of sequences processed for samples G1T, G3T and G2T before and after trimming were significantly less compared to the rest of the samples. The threshold set to remove technical artifacts (**see Methods**), automatically removed these samples from our analysis ensuring that no technical bias is introduced.

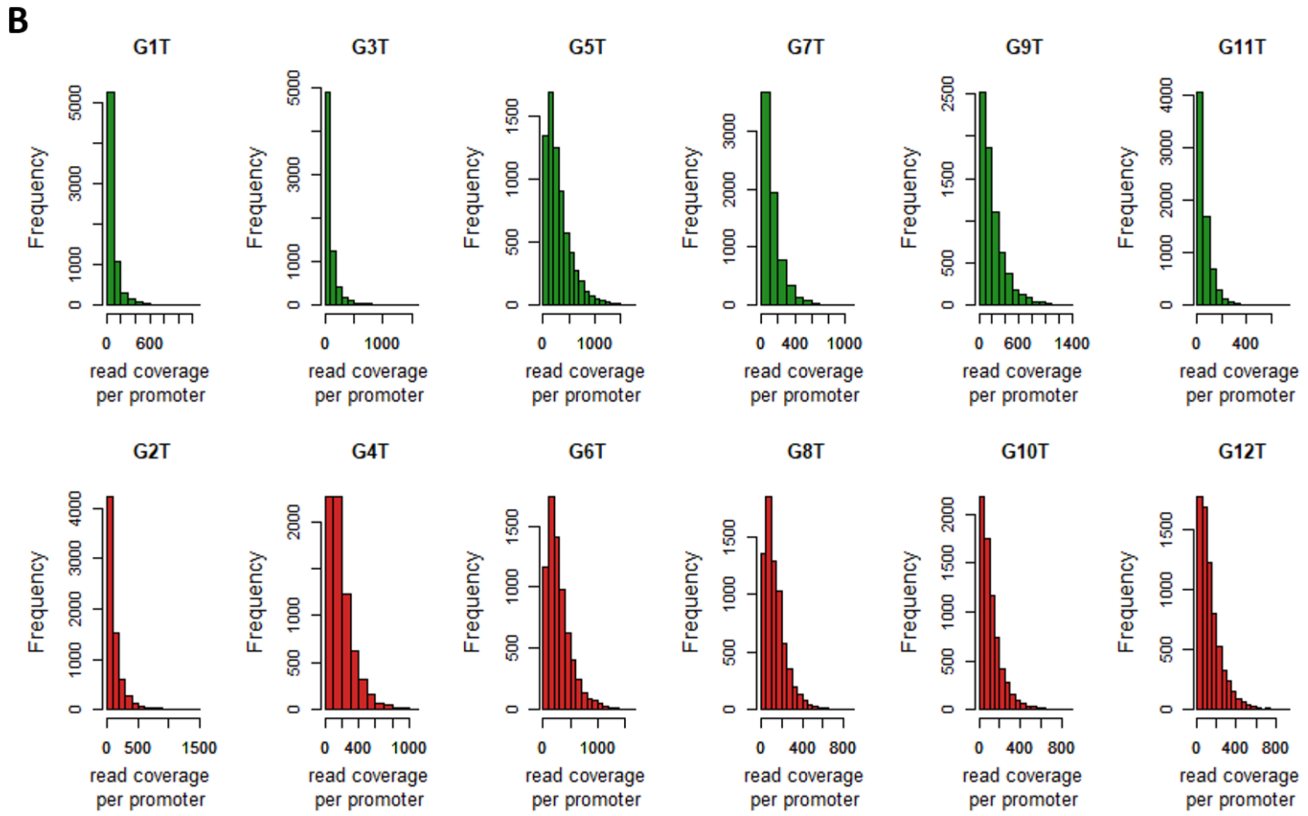
1.2 Figure S2. Detailed data analysis workflow.



Supplementary Figure 2. Analyses are indicated in black, software utilized in green and software specifications in blue.

1.3 Figure S3. Methylation percentage and read coverage distribution per promoter for aortic and mitral tissue samples

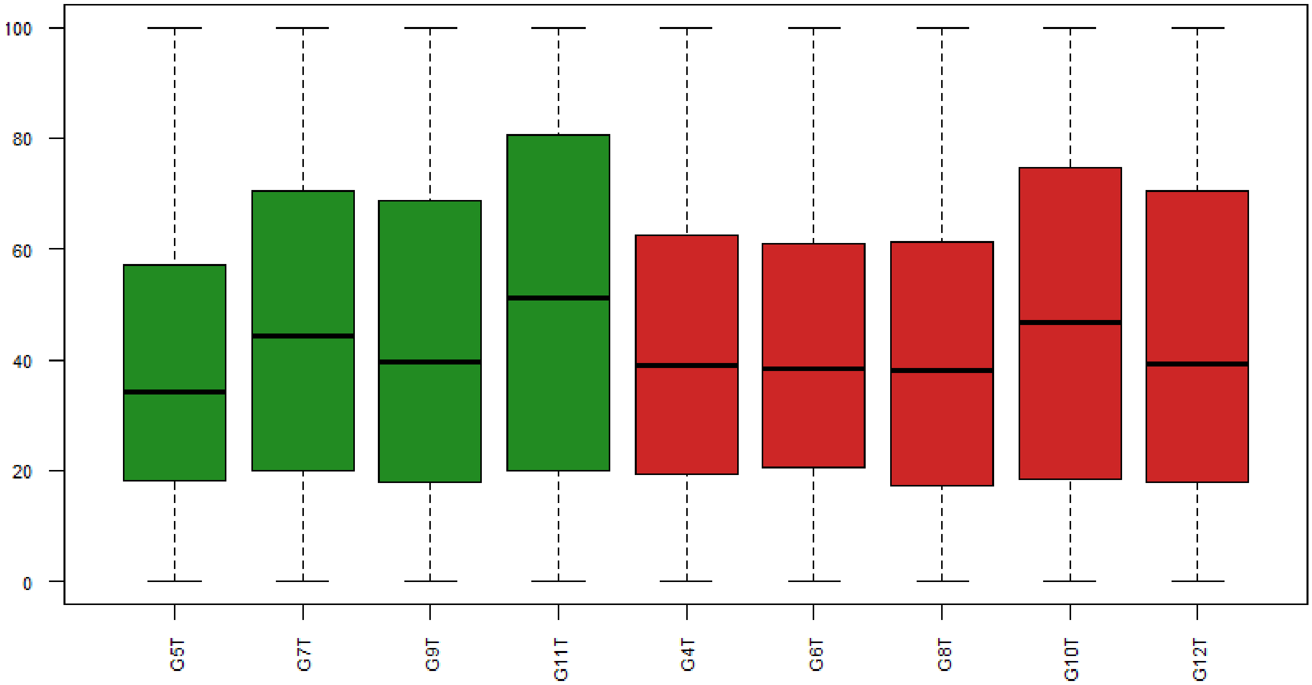




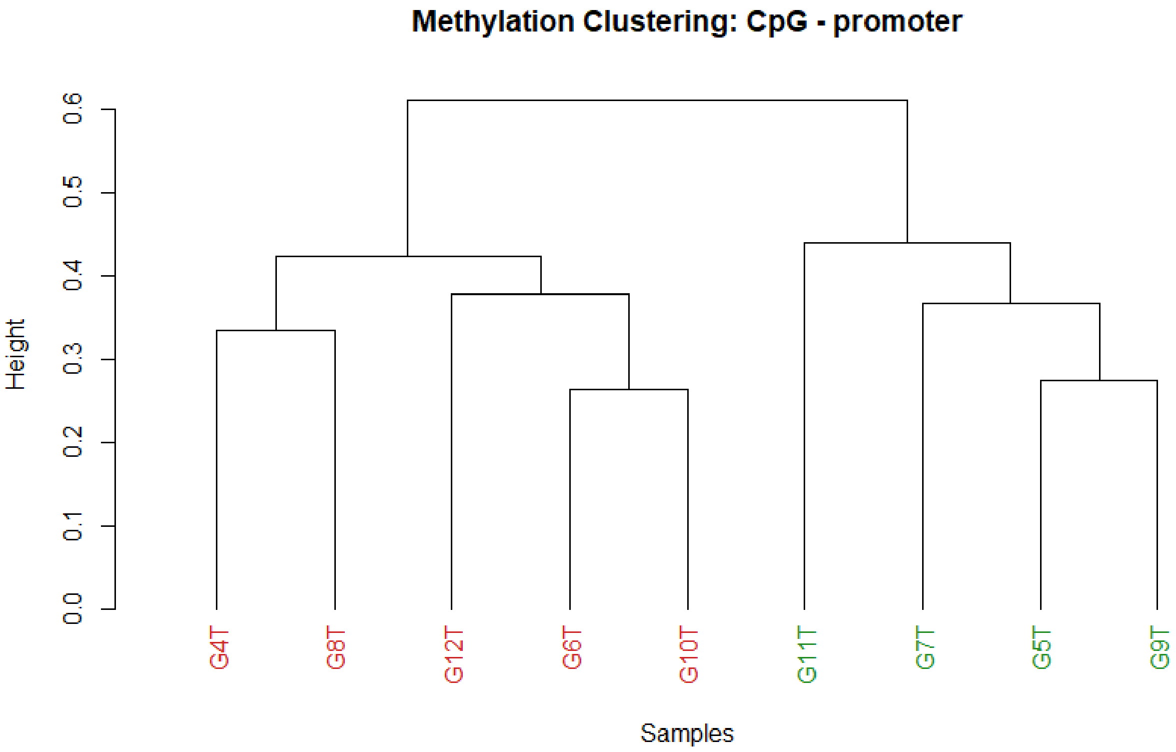
Supplementary Figure 3. (**A**) Methylation percentage- and (**B**) read coverage distribution per promoter for aortic (G1T, G3T, G5T, G7T, G9T, G11T) and mitral (G2T, G4T, G6T, G8T, G10T, G12T) tissue samples. The promoter percent methylation per sample exhibited a bimodal distribution, which is expected as reads of normal cells are either methylated (100%) or unmethylated (0%) (1). Promoter read coverage distribution did not show a secondary peak to the right, reflecting low PCR duplication levels (1). Both distributions reflect sufficient sample quality.

1.4 Figure S4. Boxplots of % methylation per sample, clustering, heatmap and PCA based on significant differential promoter methylation for aortic and mitral tissue samples

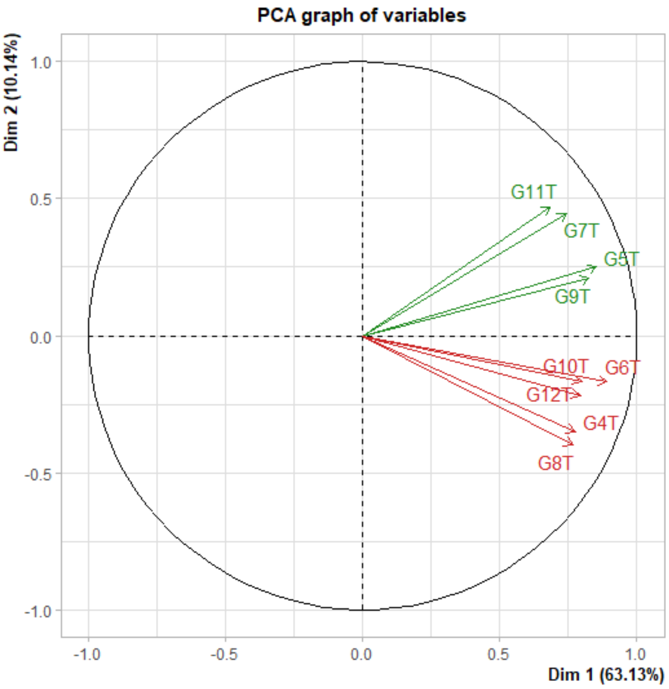
(A) Boxplots of promoter % methylation per sample



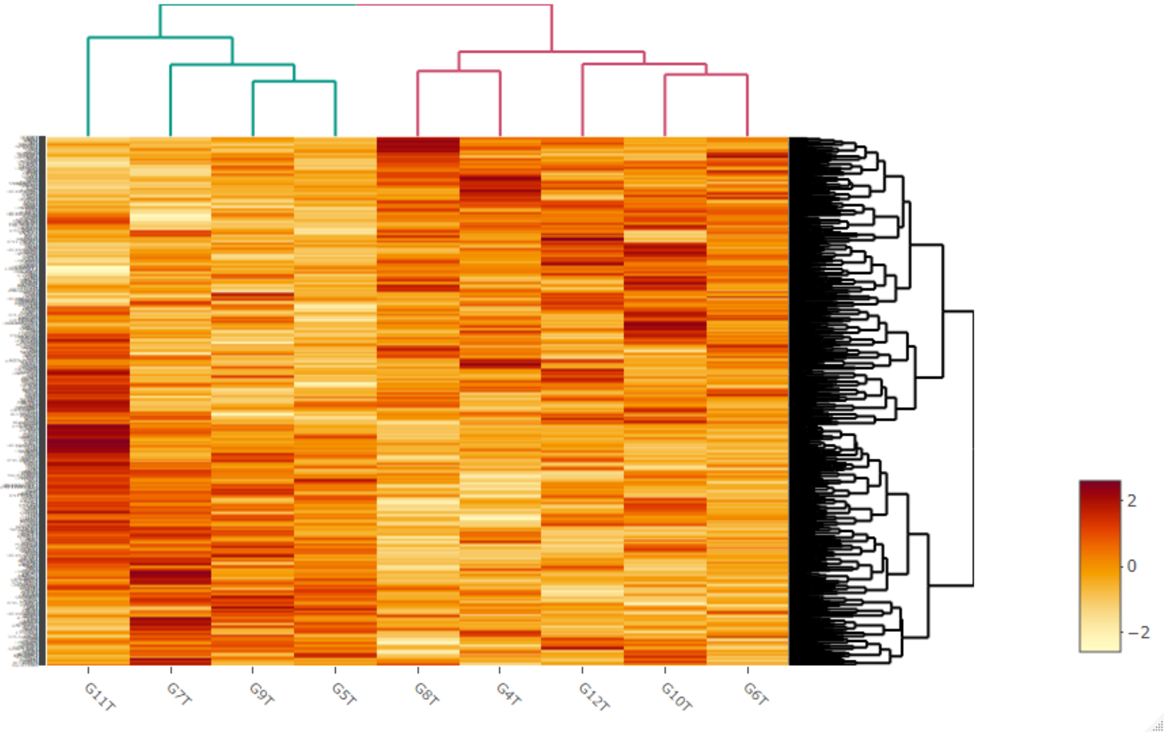
(B) Clustering



(C) PCA

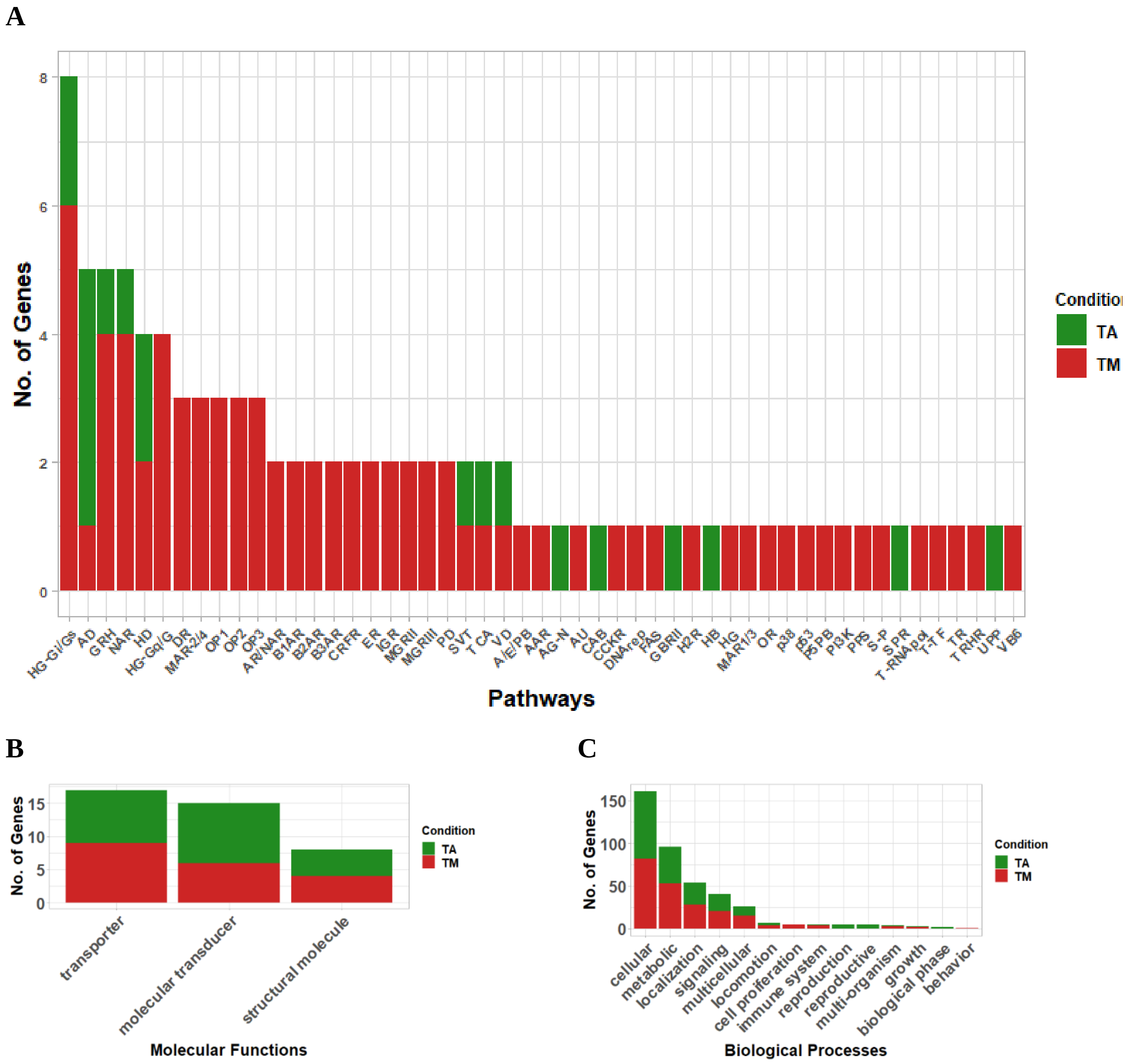


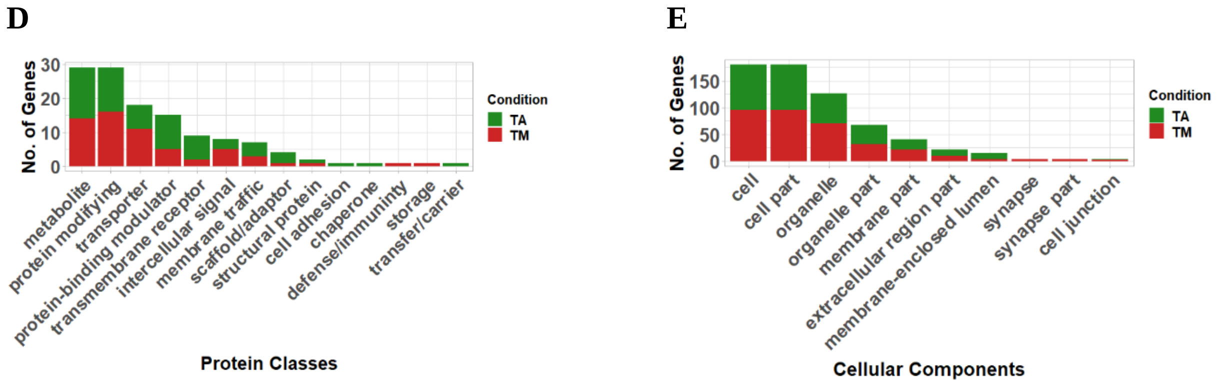
(D) Heatmap



Supplementary Figure 4. (**A**) Boxplots, (**B**) Clustering, (**C**) PCA and (**D**) Heatmap analysis reflect the grouping of aortic and mitral tissue samples based on promoter percent methylation. Each row and column in the heatmap represent a gene linked to a significantly differentially methylated promoter and sample. Samples and genes are clustered according to the correlation among the genes and among the samples, respectively. The percent methylation values of the promoters linked to the genes are color-coded and scaled for each gene (ie, by row). **Figures S3A-D** reflect meaningful sample grouping with aortic tissue samples (G5T, G7T, G9T and G11T) being clustered together and mitral tissue samples (G4T, G6T, G8T, G10T and G12T) being grouped together.

1.5 Figure S5. Additional functional categories that classify the genes associated with differentially methylated promoters in aortic vs. mitral tissue according to the PANTHER's Pathway, Molecular Function, Biological Process, Protein Class and Cellular Component annotation sets



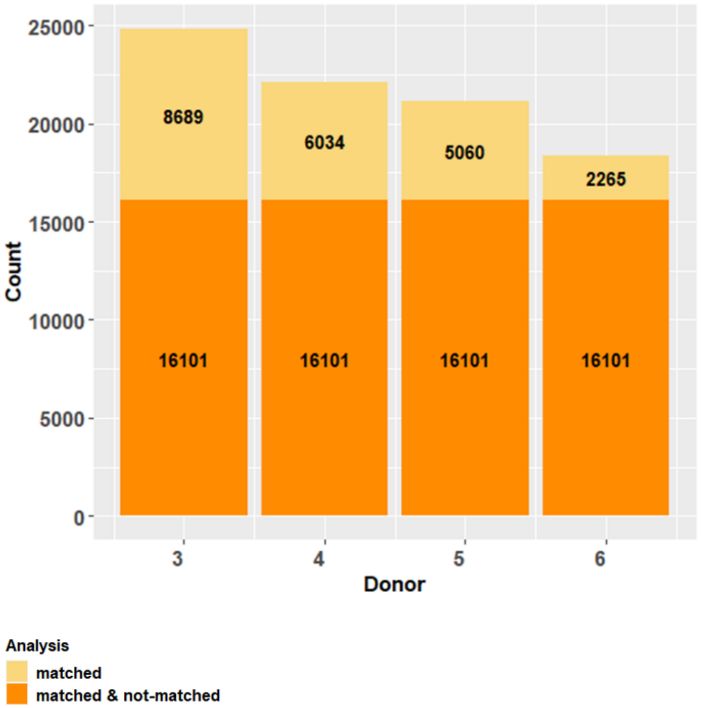


Supplementary Figure 5. Additional pathways/functions that result from the functional classification of genes that are associated with differentially methylated promoters (q-valuealue < 0.05 & meth.diff > |10|) between aortic and mitral tissue according to PANTHER (**A**) Pathways, (**B**) Molecular Functions, (**C**) Biological Processes, (**D**) Protein Classes and (**E**) Cellular Components. HG-Gi/Gs: "Heterotrimeric G-protein signaling pathway-Gi alpha and Gs alpha mediated pathway (P00026)"; AD: "Alzheimer disease-presenilin pathway (P00004)"; NAR: "Nicotinic acetylcholine receptor signaling pathway (P00044)"; GRH: "Gonadotropin-releasing hormone receptor pathway (P06664)"; HD: "Huntington disease (P00029)"; HG-Gq/G: "Heterotrimeric G-protein signaling pathway-Gq alpha and Go alpha mediated pathway (P00027)"; OP1: "Opioid proopiomelanocortin pathway (P05917)" ; OP2: "Opioid prodynorphin pathway (P05916)" ; OP3: "Opioid proenkephalin pathway (P05915)"; MAR-2/4: "Muscarinic acetylcholine receptor 2 and 4 signaling pathway (P00043)"; DR: "Dopamine receptor mediated signaling pathway (P05912)"; B3AR: "Beta3 adrenergic receptor signaling pathway (P04379)"; MGRIII: "Metabotropic glutamate receptor group III pathway (P00039)"; B2AR: "Beta2 adrenergic receptor signaling pathway (P04378)"; B1AR: "Beta1 adrenergic receptor signaling pathway (P04377)"; IGR: "Ionotropic glutamate receptor pathway (P00037)"; AR/NAR: "Adrenaline and noradrenaline biosynthesis (P00001)"; SVT: "Synaptic vesicle trafficking (P05734)"; VD: "Vitamin D metabolism and pathway (P04396)"; TCA: "T cell activation (P00053)"; PD: "Parkinson disease (P00049)"; ER: "Enkephalin release (P05913)"; CRFR: "Cortocotropin releasing factor receptor signaling pathway (P04380)"; MGRII: "Metabotropic glutamate receptor group II pathway (P00040)"; AG-N: "Axon guidance mediated by netrin (P00009)"; CAB: "Coenzyme A biosynthesis (P02736)"; AAR: "Alpha adrenergic receptor signaling pathway (P00002)"; UPP: "Ubiquitin proteasome pathway (P00060)"; GBRII: "GABA-B receptor II signaling (P05731)"; HG: "Heterotrimeric G-protein signaling pathway-rod outer segment phototransduction (P00028)"; P53: "p53 pathway feedback loops 2 (P04398)"; P5PB: "Pyridoxal-5-phosphate biosynthesis (P02759)"; A/E/PB: "Androgen/estrogene/progesterone biosynthesis (P02727)"; T-TF: "Transcription regulation by bZIP transcription factor (P00055)"; TRHR: "Thyrotropin-releasing hormone receptor signaling pathway (P04394)"; VB6: "Vitamin B6 metabolism (P02787)"; TR: "Toll receptor signaling pathway (P00054)"; T-RNApol: "General transcription by RNA polymerase I (P00022)"; AU: "Acetate utilization (P02722)"; OR: "Oxytocin receptor mediated signaling pathway (P04391)"; FAS: "FAS signaling pathway (P00020)"; p38: "p38 MAPK pathway (P05918)"; DNArep: "DNA replication (P00017)"; PI3K: "PI3 kinase pathway (P00048)"; H2R: "Histamine H2 receptor mediated signaling pathway (P04386)"; HB: "Heme biosynthesis (P02746)"; S-P: "Succinate to proprionate conversion (P02777)"; SPR: "Salvage pyrimidine ribonucleotides (P02775)"; MAR1/3: "Muscarinic acetylcholine receptor 1 and 3 signaling pathway (P00042)"; CCKR: "CCKR signaling map (P06959)"; PPS: "Pyridoxal phosphate salvage pathway (P02770)". In the stacked bar graphs, TA (green) labels genes with promoters that show increased methylation in the aortic compared to the mitral valves and TM (red) shows genes whose promoters exhibit increased methylation in the mitral compared to the aortic valves.

1.6 Figure S6. Promoters assessed in unmatched versus matched comparisons

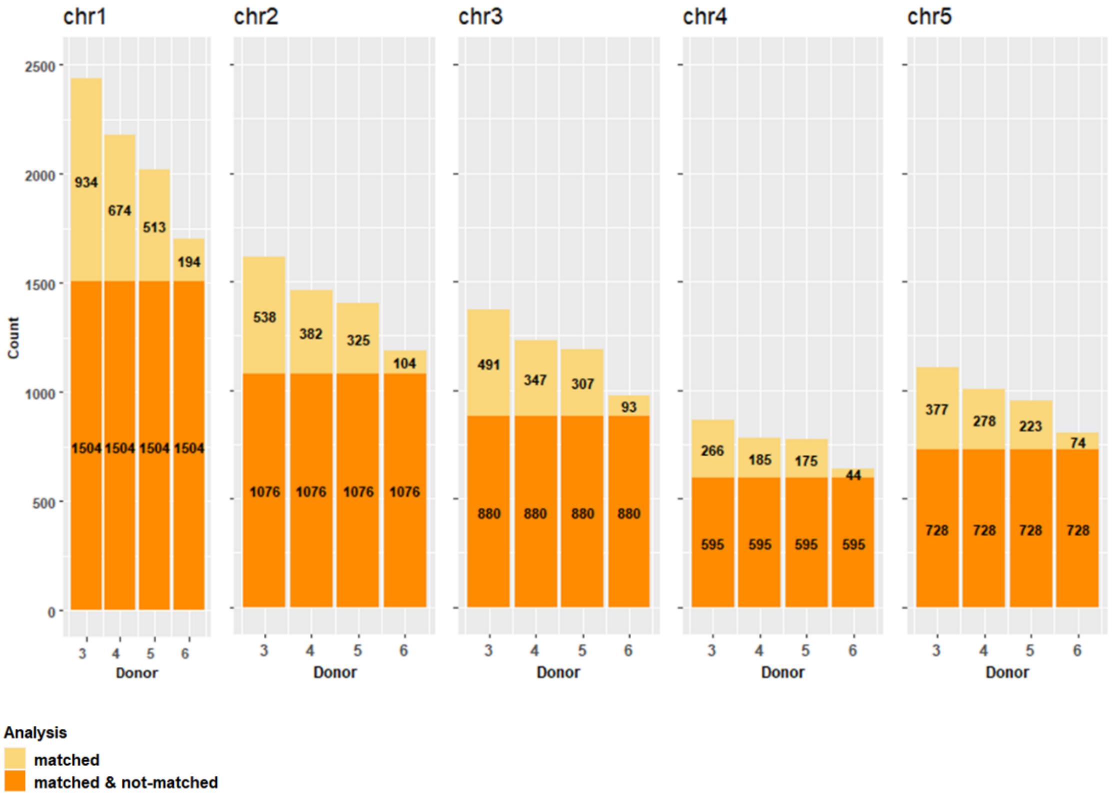
Total

A

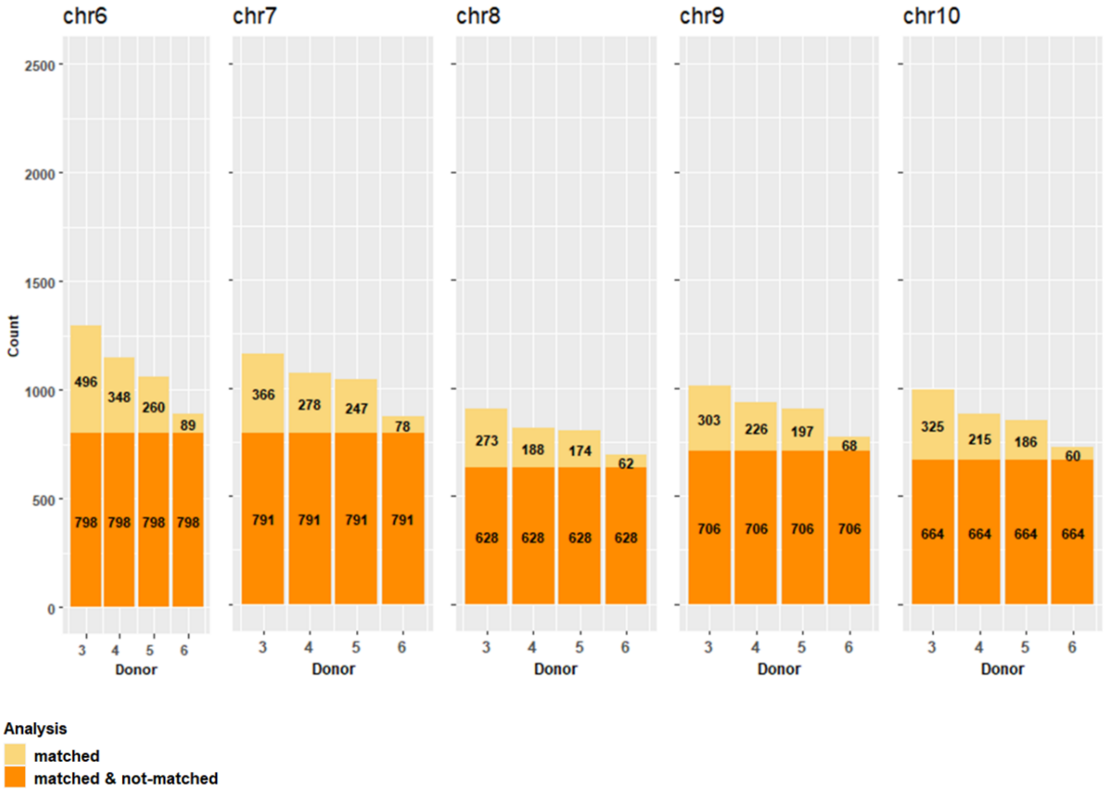


By Chromosome

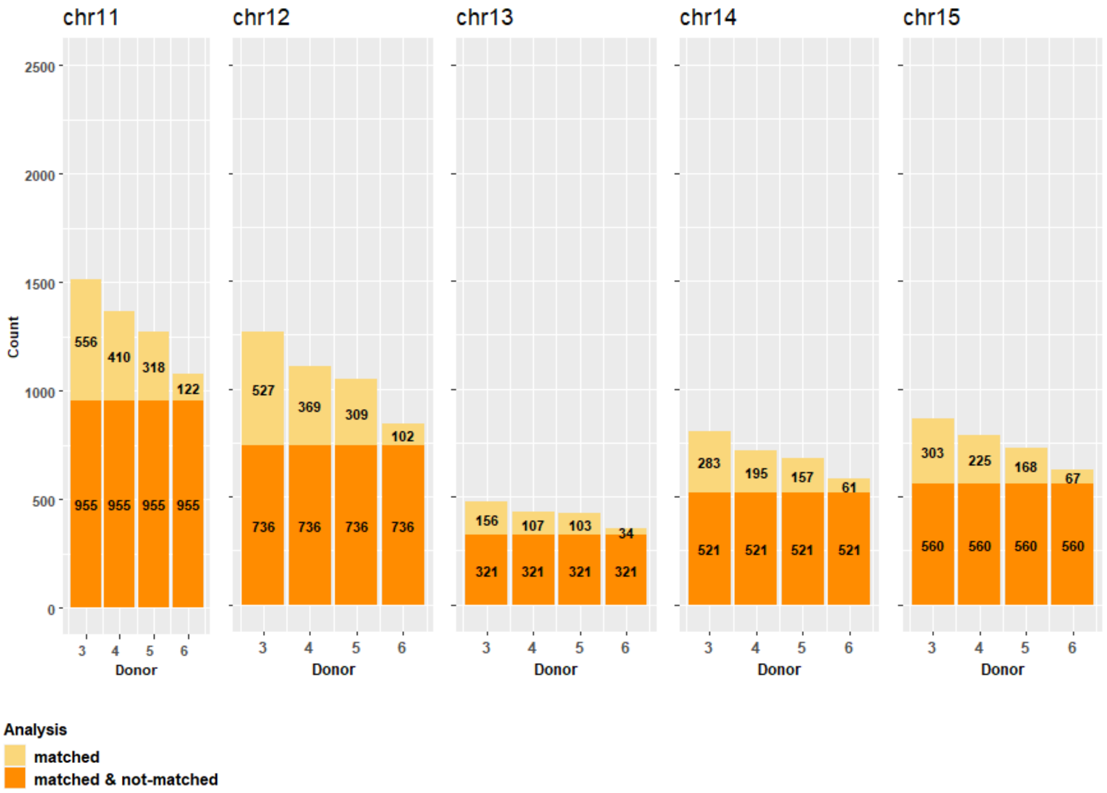
B



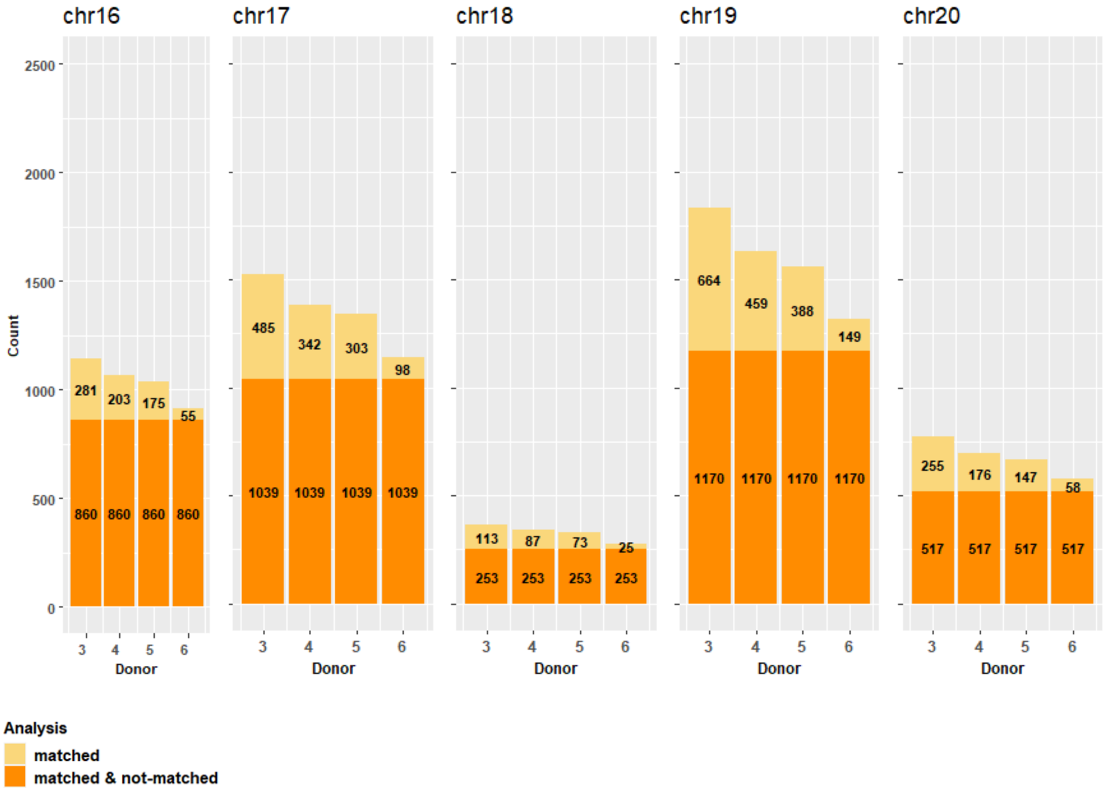
C

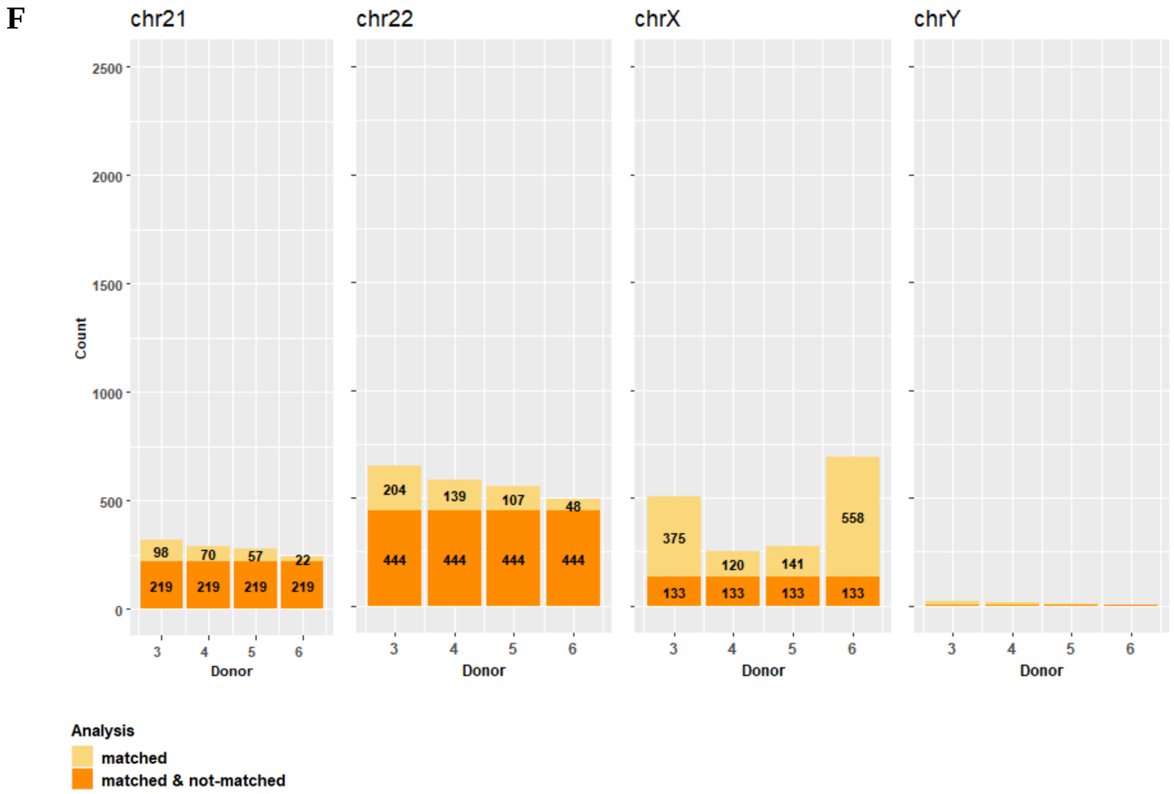


D


chr11
chr12
chr13
chr14
chr15
Count
2500
2000
1500
1000
500
0
556
410
318
122
955
955
955
955
527
369
309
102
736
736
736
736
156
107
103
34
321
321
321
321
283
195
157
61
521
521
521
521
303
225
168
67
560
560
560
560
3
4
5
6
Donor
Analysis
matched
matched & not-matched

E


chr16
chr17
chr18
chr19
chr20
Count
2500
2000
1500
1000
500
0
281
203
175
55
860
860
860
860
485
342
303
98
1039
1039
1039
1039
113
87
73
25
253
253
253
253
664
459
388
149
1170
1170
1170
1170
255
176
147
58
517
517
517
517
3
4
5
6
Donor
Analysis
matched
matched & not-matched



Supplementary Figure 6. Promoter count (A) total per donor and (B-F) total per chromosome per donor.

2 Supplementary Tables

2.1 Table S1. Differentially methylated promoters between aortic and mitral valve tissue (q value < 0.05 and a meth.diff > |10|) and their associated genes

No	prom. chr	prom. start	prom. end	meth.diff	qvalue	assoc.gene-Symbol	gene.descr	dir
1	chr15	93616216	93618216	28.14311	1.66E-24	RGMA	repulsive guidance molecule family member a	TM
2	chr6	121654646	121656646	-41.2808	2.36E-18	TBC1D32	TBC1 domain family, member 32	TA
3	chr19	45260913	45262913	-22.2115	6.74E-16	BCL3	B-cell CLL/lymphoma 3	TA
4	chr8	23081680	23083680	-23.3939	1.13E-15	RP11-1149O23.3	lncRNA RP11-1149O23.3	TA
5	chr8	23081733	23083733	-23.3939	1.13E-15	RP11-1149O23.3	lncRNA RP11-1149O23.3	TA
6	chr1	205818276	205820276	28.39292	2.66E-15	PM20D1	peptidase M20 domain containing 1	TM
7	chr4	135121903	135123903	51.02311	5.10E-14	PABPC4L	poly(A) binding protein, cytoplasmic 4-like	TM
8	chr4	1005251	1007251	16.31575	5.58E-14	FGFRL1	fibroblast growth factor receptor-like 1	TM
9	chr7	65234797	65236797	29.14172	9.29E-14	LOC441242	Uncharacterized lncRNA LOC441242	TM
10	chr5	28925976	28927976	22.90971	1.14E-12	LSP1P3	lymphocyte-specific protein 1 pseudogene 3	TM
11	chr14	75421467	75423467	17.0601	1.14E-12	PGF	placental growth factor	TM
12	chr2	106014575	106016575	20.47804	1.34E-12	FHL2	four and a half LIM domains 2	TM
13	chr19	3061964	3063964	15.34849	1.44E-12	AES	amino-terminal enhancer of split	TM
14	chr15	93615939	93617939	22.89901	1.64E-12	RGMA	repulsive guidance molecule family member a	TM
15	chr2	106014681	106016681	19.94949	5.65E-12	FHL2	four and a half LIM domains 2	TM
16	chr15	93615389	93617389	21.8204	8.55E-12	RGMA	repulsive guidance molecule family member a	TM
17	chr3	57529071	57531071	-54.9545	8.97E-12	DNAH12	dynein, axonemal, heavy chain 12	TA
18	chr4	89298890	89300890	-22.4831	8.97E-12	HERC6	HECT and RLD domain containing	TA

								E3 ubiquitin protein ligase family member 6	
19	chr17	62777117	62779117	-25.8995	1.11E-11	hsa-mir-6080	hsa-mir-6080	TA
20	chr12	113795370	113797370	-17.4555	2.42E-11	PLBD2	phospholipase B domain containing 2	TA
21	chr12	50355705	50357705	-17.1681	2.84E-11	LOC101927318	Novel Transcript, Antisense To AQP5	TA
22	chr12	50355707	50357707	-17.1681	2.84E-11	LOC101927318	Novel Transcript, Antisense To AQP5	TA
23	chr2	3621852	3623852	-31.7708	2.96E-11	RPS7	ribosomal protein S7	TA
24	chr17	37823233	37825233	16.11642	2.96E-11	PNMT	phenylethanolamine N-methyltransferase	TM
25	chr7	131593978	131595978	17.91091	5.00E-11	LOC101928782	Uncharacterized lncRNA LOC101928782	TM
26	chrX	19904744	19906744	-27.6015	6.95E-11	SH3KBP1	SH3-domain kinase binding protein 1	TA
27	chr15	40530291	40532291	-29.1746	7.01E-11	PAK6	p21 protein (Cdc42/Rac)-activated kinase 6	TA
28	chr7	99868855	99870855	17.23618	7.78E-11	GATS	CASTOR Family Member 3	TM
29	chr7	154861033	154863033	-15.1473	7.78E-11	HTR5A	5-hydroxytryptamine (serotonin) receptor 5A, G protein-coupled	TA
30	chr1	193074187	193076187	16.09079	1.15E-10	GLRX2	glutaredoxin 2	TM
31	chr1	193074244	193076244	16.09079	1.15E-10	GLRX2	glutaredoxin 2	TM
32	chr2	224701319	224703319	-10.957	1.84E-10	AP1S3	adaptor-related protein complex 1, sigma 3 subunit	TA
33	chr9	95708600	95710600	-27.3259	3.15E-10	FGD3	FYVE, RhoGEF and PH domain containing 3	TA
34	chr21	15351765	15353765	23.3534	4.53E-10	ANKRD20A11P	ankyrin repeat domain 20 family, member A11, pseudogene	TM
35	chr12	123463606	123465606	12.77897	4.94E-10	ARL6IP4	ADP-ribosylation-like factor 6 interacting protein 4	TM
36	chr12	111050911	111052911	25.19245	7.93E-10	TCTN1	tectonic family member 1	TM
37	chr20	45337278	45339278	-17.9246	9.04E-10	SLC2A10	solute carrier family 2 (facilitated glucose transporter), member 10	TA

38	chr19	58873214	58875214	-10.2772	1.30E-09	ZNF497	zinc finger protein 497	TA
39	chr7	1125442	1127442	-25.5795	4.25E-09	GPER1	G Protein-Coupled Estrogen Receptor 1	TA
40	chr7	23570660	23572660	23.11953	4.84E-09	TRA2A	transformer 2 alpha homolog (Drosophila)	TM
41	chr20	36792700	36794700	23.42375	4.84E-09	TGM2	transglutaminase 2	TM
42	chr16	1582657	1584657	16.97891	5.56E-09	TMEM204	transmembrane protein 204	TM
43	chr10	135339866	135341866	17.71944	5.67E-09	CYP2E1	cytochrome P450, family 2, subfamily E, polypeptide 1	TM
44	chr13	52732670	52734670	11.21173	5.67E-09	NEK3	NIMA-related kinase 3	TM
45	chr13	52732996	52734996	11.21173	5.67E-09	NEK3	NIMA-related kinase 3	TM
46	chr15	40530997	40532997	-21.4367	6.20E-09	PAK6	p21 protein (Cdc42/Rac)-activated kinase 6	TA
47	chr19	58192336	58194336	17.70154	6.20E-09	ZNF551	zinc finger protein 551	TM
48	chr3	13113617	13115617	-15.2565	9.83E-09	IQSEC1	IQ motif and Sec7 domain 1	TA
49	chr19	3800810	3802810	-27.0836	1.10E-08	MATK	megakaryocyte-associated tyrosine kinase	TA
50	chr12	111050831	111052831	23.61542	1.16E-08	TCTN1	tectonic family member 1	TM
51	chr9	117348993	117350993	-14.9785	1.35E-08	ATP6V1G1	ATPase, H+ transporting, lysosomal 13kDa, V1 subunit G1	TA
52	chr19	19051041	19053041	10.61533	1.44E-08	HOMER3	homer homolog 3 (Drosophila)	TM
53	chr17	37823705	37825705	13.8831	1.95E-08	PNMT	phenylethanolamine N-methyltransferase	TM
54	chr16	86611114	86613114	13.67516	2.52E-08	FOXL1	forkhead box L1	TM
55	chr16	2847485	2849485	12.20137	3.13E-08	PRSS41	protease, serine, 41	TM
56	chr4	1165999	1167999	-17.0739	3.74E-08	SPON2	spondin 2, extracellular matrix protein	TA
57	chr16	1145244	1147244	13.73378	4.24E-08	C1QTNF8	C1q and tumor necrosis factor related protein 8	TM
58	chr7	148717	150717	-14.877	4.81E-08	LOC100507642	Uncharacterized ncRNA LOC100507642	TA

59	chr16	1727277	1729277	15.51686	5.44E-08	HN1L	hematological and neurological expressed 1-like	TM
60	chr7	154862267	154864267	-11.8912	6.55E-08	HTR5A-AS1	HTR5A antisense RNA 1	TA
61	chr15	91497105	91499105	-19.0998	1.12E-07	RCCD1	RCC1 domain containing 1	TA
62	chr7	27160537	27162537	40.16618	1.19E-07	HOXA-AS2	HOXA cluster antisense RNA 2	TM
63	chr16	89265529	89267529	22.03084	1.67E-07	SLC22A31	solute carrier family 22, member 31	TM
64	chr17	80185281	80187281	13.40508	1.78E-07	SLC16A3	solute carrier family 16 (monocarboxylate transporter), member 3	TM
65	chr1	149286450	149288450	-15.861	2.23E-07	LOC388692	Uncharacterized LOC388692 (LOC388692), mRNA.	TA
66	chr5	178486606	178488606	-17.1657	2.47E-07	ZNF354C	zinc finger protein 354C	TA
67	chr11	63438446	63440446	-12.325	2.94E-07	ATL3	atlastin GTPase 3	TA
68	chr18	21976833	21978833	10.37672	3.14E-07	OSBPL1A	oxysterol binding protein-like 1A	TM
69	chr20	62611430	62613430	22.41379	3.36E-07	PRPF6	pre-mRNA processing factor 6	TM
70	chr11	62413198	62415198	-14.0199	4.16E-07	GANAB	glucosidase, alpha; neutral AB	TA
71	chr15	85196521	85198521	17.49581	5.71E-07	WDR73	WD repeat domain 73	TM
72	chr11	124608828	124610828	-19.3274	5.95E-07	NRGN	neurogranin (protein kinase C substrate, RC3)	TA
73	chr13	76209130	76211130	12.25364	7.02E-07	LMO7-AS1	LMO7 Antisense RNA 1	TM
74	chr17	7530194	7532194	27.33811	8.64E-07	SHBG	sex hormone-binding globulin	TM
75	chr19	707952	709952	11.65544	1.11E-06	PALM	paralemmin	TM
76	chrX	107068083	107070083	-15.7236	1.11E-06	MID2	midline 2	TA
77	chr15	91446419	91448419	23.64103	1.14E-06	MAN2A2	mannosidase, alpha, class 2A, member 2	TM
78	chr9	71735179	71737179	14.32164	1.15E-06	TJP2	tight junction protein 2	TM
79	chr5	1633120	1635120	-18.7866	1.28E-06	LOC728613	Programmed Cell Death 6 Pseudogene	TA
80	chr1	228352213	228354213	10.60424	1.46E-06	IBA57	IBA57, iron-sulfur cluster assembly	TM

							homolog (S. cerevisiae)	
81	chr11	115629918	115631918	17.28773	1.47E-06	LINC00900	long intergenic non-protein coding RNA 900	TM
82	chr17	79138306	79140306	-12.2283	1.50E-06	AATK-AS1	AATK antisense RNA 1	TA
83	chr2	85838225	85840225	-19.2001	1.51E-06	C2orf68	chromosome 2 open reading frame 68	TA
84	chr21	46828980	46830980	10.76715	1.75E-06	COL18A1-AS2	COL18A1 antisense RNA 2	TM
85	chr11	63438202	63440202	-10.8075	1.90E-06	ATL3	atlastin GTPase 3	TA
86	chr20	57581309	57583309	12.42827	1.93E-06	CTSZ	cathepsin Z	TM
87	chr17	44319929	44321929	17.53909	1.94E-06	AC139677.11	Homo sapiens chromosome 17, clone RP11-1070B7	TM
88	chr1	149286129	149288129	-14.6303	2.16E-06	LOC388692	Uncharacterized LOC388692 (LOC388692), mRNA.	TA
89	chr22	19703742	19705742	10.05661	2.46E-06	SEPT5-GP1BB	CDNA FLJ60582, Highly Similar To Septin-5	TM
90	chr22	46662860	46664860	14.57203	2.59E-06	TTC38	tetratricopeptide repeat domain 38	TM
91	chr3	126112641	126114641	23.22841	2.72E-06	RP11-71E19.5	Uncharacterized antisense RNA LOC100506907	TM
92	chr1	1368953	1370953	-12.51	3.21E-06	LINC01770	Long Intergenic Non-Protein Coding RNA 1770	TA
93	chr16	12009519	12011519	12.36027	3.36E-06	GSPT1	G1 to S phase transition 1	TM
94	chr19	4182350	4184350	-25.1634	3.36E-06	SIRT6	sirtuin 6	TA
95	chr4	1165657	1167657	-12.4642	3.39E-06	SPON2	spondin 2, extracellular matrix protein	TA
96	chr10	115437920	115439920	12.29278	3.44E-06	CASP7	caspase 7, apoptosis-related cysteine peptidase	TM
97	chr10	102789995	102791995	-20.2387	3.49E-06	PDZD7	PDZ domain containing 7	TA
98	chr7	150496853	150498853	-13.2631	3.68E-06	TMEM176B	transmembrane protein 176B	TA
99	chr4	122853268	122855268	-10.1457	3.91E-06	TRPC3	transient receptor potential cation channel, subfamily C, member 3	TA
100	chr10	52498687	52500687	15.99461	3.91E-06	ASAH2B	N-acylsphingosine amidohydrolase	TM

							(non-lysosomal ceramidase) 2B	
101	chr13	32888616	32890616	16.35677	3.91E-06	BRCA2	breast cancer 2, early onset	TM
102	chr1	24741244	24743244	-24.5803	3.93E-06	STPG1	sperm-tail PG-rich repeat containing 1	TA
103	chr7	99101272	99103272	-22.365	4.17E-06	ZKSCAN5	zinc finger with KRAB and SCAN domains 5	TA
104	chr5	170287895	170289895	10.46477	4.29E-06	RANBP17	RAN binding protein 17	TM
105	chr12	50355566	50357566	-12.3252	4.45E-06	LOC101927318	Novel Transcript, Antisense To AQP5	TA
106	chr8	144416061	144418061	15.78471	4.52E-06	TOP1MT	topoisomerase (DNA) I, mitochondrial	TM
107	chr1	12676737	12678737	11.88141	4.80E-06	DHRS3	dehydrogenase/reductase (SDR family) member 3	TM
108	chr9	95819969	95821969	13.07512	5.40E-06	SUSD3	sushi domain containing 3	TM
109	chr3	150420742	150422742	17.0898	5.44E-06	ERICH6-AS1	ERICH6 Antisense RNA 1	TM
110	chr3	150420761	150422761	17.0898	5.44E-06	ERICH6-AS1	ERICH6 Antisense RNA 1	TM
111	chr3	126112781	126114781	22.19131	5.55E-06	RP11-71E19.5	Uncharacterized antisense RNA LOC100506907	TM
112	chr17	7530286	7532286	25.47182	5.93E-06	SHBG	sex hormone-binding globulin	TM
113	chr4	111396228	111398228	15.28657	6.42E-06	ENPEP	glutamyl aminopeptidase (aminopeptidase A)	TM
114	chr11	46401333	46403333	18.33024	6.42E-06	MDK	midkine (neurite growth-promoting factor 2)	TM
115	chr11	18414935	18416935	14.12136	6.58E-06	LDHA	lactate dehydrogenase A	TM
116	chr7	143058840	143060840	-14.5264	6.80E-06	FAM131B	family with sequence similarity 131, member B	TA
117	chr22	45704784	45706784	-11.1274	6.85E-06	FAM118A	family with sequence similarity 118, member A	TA
118	chr2	133173146	133175146	18.21649	7.04E-06	GPR39	G protein-coupled receptor 39	TM
119	chr19	19728725	19730725	-18.8354	7.34E-06	PBX4	pre-B-cell leukemia homeobox 4	TA

120	chr5	70882114	70884114	10.53042	7.88E-06	MCCC2	methylcrotonoyl-CoA carboxylase 2 (beta)	TM
121	chr15	96875568	96877568	13.56675	7.88E-06	NR2F2	nuclear receptor subfamily 2, group F, member 2	TM
122	chr19	38754097	38756097	-12.5734	7.88E-06	SPINT2	serine peptidase inhibitor, Kunitz type, 2	TA
123	chr22	45704080	45706080	-12.1701	7.88E-06	FAM118A	family with sequence similarity 118, member A	TA
124	chrX	152989201	152991201	-12.6222	7.88E-06	ABCD1	ATP-binding cassette, sub-family D (ALD), member 1	TA
125	chr2	96675298	96677298	-27.0275	8.19E-06	FAHD2CP	fumarylacetoacetate hydrolase domain containing 2C, pseudogene	TA
126	chr9	130711993	130713993	-16.0597	8.34E-06	FAM102A	family with sequence similarity 102, member A	TA
127	chr16	4302790	4304790	-13.9405	8.42E-06	RP11-95P2.1	Uncharacterized lncRNA LOC100507501	TA
128	chr19	29217601	29219601	14.7972	8.42E-06	LOC100420587	SHC Binding And Spindle Associated 1 Pseudogene	TM
129	chr12	124154659	124156659	-19.7495	8.51E-06	TCTN2	tectonic family member 2	TA
130	chr20	35723403	35725403	22.97564	9.46E-06	RBL1	retinoblastoma-like 1 (p107)	TM
131	chr16	56671577	56673577	-15.9538	9.67E-06	MT1A	metallothionein 1A	TA
132	chr5	131592350	131594350	12.58185	1.19E-05	PDLIM4	PDZ and LIM domain 4	TM
133	chr4	128801015	128803015	19.96967	1.20E-05	PLK4	polo-like kinase 4	TM
134	chr9	140171279	140173279	-10.1032	1.23E-05	TOR4A	torsin family 4, member A	TA
135	chr16	85721588	85723588	-13.764	1.33E-05	GINS2	GINS complex subunit 2 (Psf2 homolog)	TA
136	chr22	42948867	42950867	-11.0445	1.39E-05	SERHL2	serine hydrolase-like 2	TA
137	chrX	41781287	41783287	16.94494	1.53E-05	CASK	calcium/calmodulin-dependent serine protein kinase (MAGUK family)	TM
138	chr15	96875489	96877489	11.04891	1.67E-05	NR2F2	nuclear receptor subfamily 2, group F, member 2	TM

139	chr13	114017463	114019463	-11.8419	1.93E-05	GRTP1	growth hormone regulated TBC protein 1	TA
140	chr1	244623672	244625672	-20.1678	1.95E-05	C1orf101	chromosome 1 open reading frame 101	TA
141	chr8	41385724	41387724	-20.5911	1.98E-05	GINS4	GINS complex subunit 4 (Sld5 homolog)	TA
142	chr2	85838179	85840179	-17.2037	2.19E-05	C2orf68	chromosome 2 open reading frame 68	TA
143	chr20	56285592	56287592	-31.0166	2.25E-05	PMEPA1	prostate transmembrane protein, androgen induced 1	TA
144	chr16	68876508	68878508	-24.1921	2.40E-05	TANGO6	transport and golgi organization 6 homolog (Drosophila)	TA
145	chr19	10120147	10122147	16.65573	2.40E-05	COL5A3	collagen, type V, alpha 3	TM
146	chr17	74098652	74100652	15.42378	2.42E-05	EXOC7	exocyst complex component 7	TM
147	chr14	75388145	75390145	-15.4658	2.53E-05	RPS6KL1	ribosomal protein S6 kinase-like 1	TA
148	chr6	88181642	88183642	12.37947	2.65E-05	SLC35A1	solute carrier family 35 (CMP-sialic acid transporter), member A1	TM
149	chr15	90357072	90359072	-17.3052	2.67E-05	ANPEP	alanyl (membrane) aminopeptidase	TA
150	chr11	124628029	124630029	12.65104	2.88E-05	LOC101929340	Uncharacterized lncRNA LOC101929340	TM
151	chr20	61582998	61584998	18.99397	2.88E-05	SLC17A9	solute carrier family 17 (vesicular nucleotide transporter), member 9	TM
152	chr17	26552588	26554588	-15.2789	3.27E-05	PYY2	peptide YY, 2 (pseudogene)	TA
153	chr15	89181038	89183038	26.67957	3.29E-05	ISG20	interferon stimulated exonuclease gene 20kDa	TM
154	chr3	73045118	73047118	14.40733	3.57E-05	PPP4R2	protein phosphatase 4, regulatory subunit 2	TM
155	chr22	18592452	18594452	10.36429	3.63E-05	TUBA8	tubulin, alpha 8	TM
156	chr18	13640756	13642756	-10.4618	3.72E-05	LDLRAD4	low density lipoprotein receptor	TA

							class A domain containing 4	
157	chr14	24657124	24659124	12.19301	3.78E-05	IPO4	importin 4	TM
158	chr5	76010867	76012867	-10.0456	3.95E-05	F2R	coagulation factor II (thrombin) receptor	TA
159	chr11	64862586	64864586	18.47006	3.98E-05	VPS51	vacuolar protein sorting 51 homolog (S. cerevisiae)	TM
160	chr20	47803904	47805904	13.74715	4.33E-05	STAU1	staufen double-stranded RNA binding protein 1	TM
161	chr14	23425351	23427351	17.86834	4.37E-05	MIR4707	microRNA 4707	TM
162	chr1	10092040	10094040	14.35139	4.79E-05	UBE4B	ubiquitination factor E4B	TM
163	chr3	139107522	139109522	18.85098	5.08E-05	LOC100507291	Uncharacterized lncRNA LOC100507291	TM
164	chr3	139107644	139109644	18.85098	5.08E-05	LOC100507291	Uncharacterized lncRNA LOC100507291	TM
165	chr17	40713091	40715091	-19.2769	5.22E-05	COASY	CoA synthase	TA
166	chr10	73610082	73612082	-20.4424	5.42E-05	PSAP	prosaposin	TA
167	chr10	134777793	134779793	-12.021	5.47E-05	LINC01166	long intergenic non-protein coding RNA 1166	TA
168	chr16	14396823	14398823	-20.0739	5.54E-05	MIR193B	microRNA 193b	TA
169	chr19	40323873	40325873	15.87205	5.56E-05	DYRK1B	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1B	TM
170	chr17	38170613	38172613	-30.7312	5.71E-05	CSF3	colony stimulating factor 3 (granulocyte)	TA
171	chr2	201449730	201451730	-17.8466	6.10E-05	AOX1	aldehyde oxidase 1	TA
172	chr19	49519347	49521347	-15.5705	6.10E-05	LHB	luteinizing hormone beta polypeptide	TA
173	chr17	46017770	46019770	16.87888	6.43E-05	PNPO	pyridoxamine 5'-phosphate oxidase	TM
174	chr17	46017888	46019888	16.87888	6.43E-05	PNPO	pyridoxamine 5'-phosphate oxidase	TM
175	chr9	132082294	132084294	-19.5545	6.82E-05	C9orf106	chromosome 9 open reading frame 106	TA
176	chr12	8379214	8381214	19.62302	6.87E-05	FAM90A1	family with sequence similarity 90, member A1	TM
177	chr22	45808500	45810500	-13.5464	7.61E-05	RIBC2	RIB43A domain with coiled-coils 2	TA
178	chr8	22959326	22961326	16.4231	8.36E-05	TNFRSF10C	tumor necrosis factor receptor	TM

							superfamily, member 10c, decoy without an intracellular domain	
179	chr16	68032421	68034421	-19.6122	9.29E-05	DPEP2	dipeptidase 2	TA
180	chr19	10542110	10544110	-18.6557	9.33E-05	PDE4A	phosphodiesterase 4A, cAMP-specific	TA
181	chr1	20125410	20127410	13.29795	9.47E-05	TMCO4	transmembrane and coiled-coil domains 4	TM
182	chr2	71679752	71681752	-12.6866	9.47E-05	DYSF	dysferlin	TA
183	chr12	6579065	6581065	12.39162	9.92E-05	VAMP1	vesicle-associated membrane protein 1 (synaptobrevin 1)	TM
184	chr6	31238913	31240913	14.75902	0.000105	HLA-C	major histocompatibility complex, class I, C	TM
185	chr22	18957010	18959010	-11.4021	0.000111	DGCR5	DiGeorge syndrome critical region gene 5 (non-protein coding)	TA
186	chr1	12078298	12080298	23.4642	0.000113	MIIP	migration and invasion inhibitory protein	TM
187	chr10	102026437	102028437	-17.8845	0.000117	CWF19L1	CWF19-like 1, cell cycle control (S. pombe)	TA
188	chr19	55677090	55679090	-14.7451	0.000118	DNAAF3	dynein, axonemal, assembly factor 3	TA
189	chr19	47633079	47635079	-19.1342	0.00012	SAE1	SUMO1 activating enzyme subunit 1	TA
190	chr19	47633114	47635114	-19.1342	0.00012	SAE1	SUMO1 activating enzyme subunit 1	TA
191	chr17	42091345	42093345	-19.3123	0.000122	TMEM101	transmembrane protein 101	TA
192	chr2	98329030	98331030	12.89195	0.000123	ZAP70	zeta-chain (TCR) associated protein kinase 70kDa	TM
193	chrX	152952751	152954751	11.05677	0.000127	SLC6A8	solute carrier family 6 (neurotransmitter transporter), member 8	TM
194	chrX	153714009	153716009	13.04122	0.00013	UBL4A	ubiquitin-like 4A	TM
195	chr16	85169755	85171755	-16.6253	0.000138	LINC02139	Long Intergenic Non-Protein Coding RNA 2139	TA
196	chr16	121629	123629	10.29471	0.000141	RHBDF1	rhomboid 5 homolog 1 (Drosophila)	TM

197	chr12	50343523	50345523	-21.134	0.000142	AQP2	aquaporin 2 (collecting duct)	TA
198	chr19	11545603	11547603	-23.8105	0.000142	PRKCSH	protein kinase C substrate 80K-H	TA
199	chr1	18956499	18958499	-11.7985	0.000148	PAX7	paired box 7	TA
200	chr18	43305917	43307917	-19.1652	0.000149	SLC14A1	solute carrier family 14 (urea transporter), member 1 (Kidd blood group)	TA
201	chr19	52226245	52228245	-22.1536	0.00015	HAS1	hyaluronan synthase 1	TA
202	chr4	2365604	2367604	11.95305	0.00016	ZFYVE28	zinc finger, FYVE domain containing 28	TM
203	chr2	197503355	197505355	14.84426	0.000161	CCDC150	coiled-coil domain containing 150	TM
204	chr8	21910080	21912080	-20.3027	0.000161	DMTN	dematin actin binding protein	TA
205	chr17	77680074	77682074	11.94744	0.000166	CTD-2116F7.1	Long Intergenic Non-Protein Coding RNA 2078	TM
206	chr22	45808571	45810571	-12.9984	0.000178	RIBC2	RIB43A domain with coiled-coils 2	TA
207	chr17	39596596	39598596	18.20972	0.000184	KRT38	keratin 38	TM
208	chrX	152989322	152991322	-10.2904	0.000192	ABCD1	ATP-binding cassette, sub-family D (ALD), member 1	TA
209	chr15	44068293	44070293	10.78098	0.000216	SERF2	small EDRK-rich factor 2	TM
210	chr3	170587045	170589045	-18.7738	0.000232	RPL22L1	ribosomal protein L22-like 1	TA
211	chr16	34403762	34405762	14.08228	0.000235	UBE2MP1	ubiquitin-conjugating enzyme E2M pseudogene 1	TM
212	chr19	55590759	55592759	-10.982	0.000245	EPS8L1	EPS8-like 1	TA
213	chr2	238767186	238769186	-11.374	0.000249	RAMP1	receptor (G protein-coupled) activity modifying protein 1	TA
214	chr19	52955828	52957828	32.07625	0.000249	ZNF578	zinc finger protein 578	TM
215	chr14	101520023	101522023	19.92582	0.000258	MIR485	microRNA 485	TM
216	chr1	161067150	161069150	-10.4153	0.000265	KLHDC9	kelch domain containing 9	TA
217	chr1	161067180	161069180	-10.4153	0.000265	KLHDC9	kelch domain containing 9	TA
218	chr1	24512765	24514765	-13.2818	0.000267	IFNLR1	interferon, lambda receptor 1	TA

219	chr17	77680058	77682058	11.37794	0.00027	CTD-2116F7.1	Long Intergenic Non-Protein Coding RNA 2078	TM
220	chr6	143832020	143834020	11.09653	0.000275	FUCA2	fucosidase, alpha-L-2, plasma	TM
221	chr7	135346220	135348220	14.94687	0.000276	C7orf73	chromosome 7 open reading frame 73	TM
222	chr7	100463949	100465949	-13.5053	0.000283	TRIP6	thyroid hormone receptor interactor 6	TA
223	chr14	101519642	101521642	19.66746	0.000307	MIR668	MicroRNA 668	TM
224	chr19	49989810	49991810	-12.3628	0.000308	RPL13A	ribosomal protein L13a	TA
225	chrX	153638876	153640876	-15.9405	0.000311	DNASE1L1	deoxyribonuclease I-like 1	TA
226	chrX	153639427	153641427	-15.9405	0.000311	DNASE1L1	deoxyribonuclease I-like 1	TA
227	chr10	70479900	70481900	-10.1892	0.000313	CCAR1	cell division cycle and apoptosis regulator 1	TA
228	chr11	67209983	67211983	-16.6003	0.000313	CORO1B	coronin, actin binding protein, 1B	TA
229	chr17	63132455	63134455	14.68599	0.000331	RGS9	regulator of G-protein signaling 9	TM
230	chr19	2014702	2016702	14.78213	0.000335	BTBD2	BTB (POZ) domain containing 2	TM
231	chr19	55314066	55316066	13.07365	0.000342	KIR2DL4	killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 4	TM
232	chr12	114844999	114846999	17.03896	0.000346	TBX5-AS1	TBX5 antisense RNA 1	TM
233	chr14	23651869	23653869	-40.7436	0.000353	SLC7A8	solute carrier family 7 (amino acid transporter light chain, L system), member 8	TA
234	chr1	6549640	6551640	10.6383	0.000355	PLEKHG5	pleckstrin homology domain containing, family G (with RhoGef domain) member 5	TM
235	chr1	6549654	6551654	10.6383	0.000355	PLEKHG5	pleckstrin homology domain containing, family G (with RhoGef domain) member 5	TM
236	chr14	23425238	23427238	15.50245	0.000357	MIR4707	microRNA 4707	TM
237	chr5	169723822	169725822	-24.2105	0.000359	LCP2	lymphocyte cytosolic protein 2	TA

							(SH2 domain containing leukocyte protein of 76kDa)	
238	chr17	1181956	1183956	12.28963	0.000361	TUSC5	tumor suppressor candidate 5	TM
239	chr14	103654365	103656365	-15.0979	0.000417	LINC00605	long intergenic non-protein coding RNA 605	TA
240	chr19	1131273	1133273	11.57252	0.000423	SBNO2	strawberry notch homolog 2 (Drosophila)	TM
241	chr3	50272588	50274588	16.0433	0.000442	GNAI2	Guanine Nucleotide Binding Protein (G Protein), Alpha Inhibiting Activity	TM
242	chr1	220219000	220221000	-11.5031	0.000444	EPRS	glutamyl-prolyl-tRNA synthetase	TA
243	chr19	56047435	56049435	-14.1007	0.000445	SBK2	SH3 domain binding kinase family, member 2	TA
244	chr15	52262998	52264998	14.16123	0.000474	LEO1	Leo1, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	TM
245	chr6	30850860	30852860	24.4129	0.00051	DDR1	discoidin domain receptor tyrosine kinase 1	TM
246	chr7	155325539	155327539	10.92188	0.000519	CNPY1	canopy FGF signaling regulator 1	TM
247	chr11	67170383	67172383	22.5974	0.000521	TBC1D10C	TBC1 domain family, member 10C	TM
248	chr17	73779688	73781688	-15.3648	0.000554	UNK	unkempt family zinc finger	TA
249	chr17	16119508	16121508	-19.4778	0.000595	PIGL	phosphatidylinositol glycan anchor biosynthesis, class L	TA
250	chr3	195942382	195944382	14.35947	0.000608	SLC51A	solute carrier family 51, alpha subunit	TM
251	chr13	113776112	113778112	-13.1739	0.000612	F10	coagulation factor X	TA
252	chr17	56768933	56770933	-13.9093	0.000687	RAD51C	RAD51 paralog C	TA
253	chr19	49338934	49340934	12.72056	0.000697	HSD17B14	hydroxysteroid (17-beta) dehydrogenase 14	TM
254	chr20	44538633	44540633	-21.9858	0.000732	PLTP	phospholipid transfer protein	TA
255	chr3	46734194	46736194	10.70251	0.000734	ALS2CL	ALS2 C-terminal like	TM

256	chrX	54521599	54523599	13.42415	0.000739	FGD1	FYVE, RhoGEF and PH domain containing 1	TM
257	chr4	154124565	154126565	-22.5228	0.000747	TRIM2	tripartite motif containing 2	TA
258	chr11	63257680	63259680	-15.3228	0.000749	HRASLS5	HRAS-like suppressor family, member 5	TA
259	chr17	75446325	75448325	11.70022	0.000772	9-Sep	septin 9	TM
260	chr6	6003277	6005277	10.22646	0.000801	NRN1	neuritin 1	TM
261	chr1	28695092	28697092	14.90113	0.000818	PHACTR4	phosphatase and actin regulator 4	TM
262	chr7	65337256	65339256	12.57696	0.000818	VKORC1L1	vitamin K epoxide reductase complex, subunit 1-like 1	TM
263	chr1	27960727	27962727	10.67886	0.000831	FGR	feline Gardner-Rasheed sarcoma viral oncogene homolog	TM
264	chr20	3139556	3141556	-17.923	0.000845	UBOX5	U-box domain containing 5	TA
265	chr17	73779919	73781919	-14.9291	0.000869	UNK	unkempt family zinc finger	TA
266	chr3	150420350	150422350	16.12591	0.000878	ERICH6-AS1	ERICH6 Antisense RNA 1	TM
267	chr16	2891752	2893752	10.85568	0.000927	PRSS30P	protease, serine, 30, pseudogene	TM
268	chr20	3761102	3763102	24.88764	0.00094	SPEF1	sperm flagellar 1	TM
269	chr1	36548675	36550675	17.63048	0.000971	TEKT2	tektin 2 (testicular)	TM
270	chr4	466998	468998	19.93379	0.000972	ABCA11P	ATP-binding cassette, sub-family A (ABC1), member 11, pseudogene	TM
271	chr19	11545560	11547560	-21.2864	0.000972	PRKCSH	protein kinase C substrate 80K-H	TA
272	chr17	74098868	74100868	12.58592	0.000973	EXOC7	exocyst complex component 7	TM
273	chr2	27885337	27887337	-11.8543	0.000974	SUPT7L	suppressor of Ty 7 (S. cerevisiae)-like	TA
274	chr3	127293174	127295174	13.06528	0.001045	MIR6825	MicroRNA 6825	TM
275	chr19	35772409	35774409	28.14539	0.001053	HAMP	hepcidin antimicrobial peptide	TM
276	chr22	17488112	17490112	12.51904	0.00113	GAB4	GRB2-associated binding protein family, member 4	TM
277	chr11	76570916	76572916	12.32268	0.001131	ACER3	alkaline ceramidase 3	TM

278	chr22	39794758	39796758	17.0131	0.001141	TAB1	TGF-beta activated kinase 1/MAP3K7 binding protein 1	TM
279	chr17	73936119	73938119	12.48031	0.001185	FBF1	Fas (TNFRSF6) binding factor 1	TM
280	chr19	12404714	12406714	21.20105	0.001205	ZNF44	zinc finger protein 44	TM
281	chr15	90727151	90729151	14.38911	0.001207	SEMA4B	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4B	TM
282	chr19	49954115	49956115	-20.1308	0.001207	PIH1D1	PIH1 domain containing 1	TA
283	chr20	61146659	61148659	10.48776	0.001213	MIR1-1HG	MIR1-1 Host Gene	TM
284	chr19	49989864	49991864	-11.2688	0.001228	RPL13A	ribosomal protein L13a	TA
285	chr17	33813758	33815758	-17.454	0.001229	SLFN12L	schlafen family member 12-like	TA
286	chr20	42142075	42144075	-10.3181	0.001229	L3MBTL1	l(3)mbt-like 1 (Drosophila)	TA
287	chr1	27560006	27562006	13.39718	0.001235	WDTC1	WD and tetratricopeptide repeats 1	TM
288	chr11	63996752	63998752	-18.4865	0.001259	DNAJC4	DnaJ (Hsp40) homolog, subfamily C, member 4	TA
289	chr1	40203516	40205516	13.61707	0.001307	PPIE	peptidylprolyl isomerase E (cyclophilin E)	TM
290	chr5	176783843	176785843	11.14789	0.001307	RGS14	regulator of G-protein signaling 14	TM
291	chr10	103602677	103604677	-12.926	0.001307	KCNIP2	Kv channel interacting protein 2	TA
292	chr1	27708823	27710823	-11.6899	0.001338	CD164L2	CD164 sialomucin-like 2	TA
293	chr17	7337761	7339761	13.90491	0.001373	TMEM102	transmembrane protein 102	TM
294	chr19	36000391	36002391	-14.0408	0.001373	DMKN	dermokine	TA
295	chr1	231154670	231156670	14.40972	0.00138	MIR1182	microRNA 1182	TM
296	chr6	28863306	28865306	14.25183	0.001475	HCG14	HLA complex group 14 (non-protein coding)	TM
297	chr6	43483728	43485728	10.54313	0.001475	POLR1C	polymerase (RNA) I polypeptide C, 30kDa	TM
298	chr17	42274529	42276529	13.65551	0.001485	ATXN7L3	ataxin 7-like 3	TM

299	chr19	36000412	36002412	-14.0217	0.001511	DMKN	dermokine	TA
300	chr6	41702997	41704997	10.38316	0.001522	TFEB	transcription factor EB	TM
301	chr1	1355824	1357824	-11.8637	0.001553	ANKRD65	ankyrin repeat domain 65	TA
302	chr12	53342650	53344650	11.90578	0.001624	KRT8	keratin 8	TM
303	chr11	70934842	70936842	16.65019	0.001657	SHANK2	SH3 and multiple ankyrin repeat domains 2	TM
304	chr19	51225604	51227604	-24.7239	0.001686	CLEC11A	C-type lectin domain family 11, member A	TA
305	chr6	134209258	134211258	-14.2044	0.0018	TCF21	transcription factor 21	TA
306	chr6	134209259	134211259	-14.2044	0.0018	TCF21	transcription factor 21	TA
307	chr20	3139532	3141532	-16.682	0.001809	UBOX5	U-box domain containing 5	TA
308	chr19	10696991	10698991	17.4369	0.001825	AP1M2	adaptor-related protein complex 1, mu 2 subunit	TM
309	chr4	698572	700572	12.46448	0.001856	PCGF3	polycomb group ring finger 3	TM
310	chr15	67457492	67459492	10.24798	0.00186	SMAD3	SMAD family member 3	TM
311	chr19	7693439	7695439	-18.5554	0.001925	XAB2	XPA binding protein 2	TA
312	chr12	54426733	54428733	11.95233	0.002017	MIR615	microRNA 615	TM
313	chr17	39295739	39297739	11.09814	0.002071	KRTAP4-6	keratin associated protein 4-6	TM
314	chr5	60239905	60241905	-12.4476	0.002117	ERCC8	excision repair cross-complementing rodent repair deficiency, complementation group 8	TA
315	chr6	43970387	43972387	-11.4486	0.002163	LOC101929705	Uncharacterized lncRNA LOC101929705	TA
316	chr5	175664369	175666369	-12.6952	0.002201	SIMC1	SUMO-interacting motifs containing 1	TA
317	chr1	53703281	53705281	-11.7801	0.002305	MAGOH	mago-nashi homolog, proliferation-associated (Drosophila)	TA
318	chr1	53703282	53705282	-11.7801	0.002305	MAGOH	mago-nashi homolog,	TA

							proliferation-associated (Drosophila)	
319	chr1	202136178	202138178	-26.7227	0.00233	PTPRVP	protein tyrosine phosphatase, receptor type, V, pseudogene	TA
320	chr2	3641421	3643421	14.12858	0.002333	COLEC11	collectin sub-family member 11	TM
321	chr7	73497106	73499106	19.58291	0.002365	LIMK1	LIM domain kinase 1	TM
322	chr17	75445612	75447612	12.63949	0.002365	9-Sep	septin 9	TM
323	chr2	175189754	175191754	18.15453	0.002394	AC018470.4	long intergenic non-protein coding RNA 1305	TM
324	chr6	134209144	134211144	-14.5438	0.002412	TCF21	transcription factor 21	TA
325	chr12	114845247	114847247	12.61802	0.002412	TBX5-AS1	TBX5 antisense RNA 1	TM
326	chr11	63992341	63994341	-11.9831	0.002422	NUDT22	nudix (nucleoside diphosphate linked moiety X)-type motif 22	TA
327	chr5	60239955	60241955	-12.1293	0.002461	ERCC8	excision repair cross-complementing rodent repair deficiency, complementation group 8	TA
328	chr20	62583736	62585736	12.93398	0.002577	UCKL1-AS1	Uridine-Cytidine Kinase 1-Like 1 Opposite Strand	TM
329	chr17	56768416	56770416	-12.132	0.002578	RAD51C	RAD51 paralog C	TA
330	chr6	82956471	82958471	-10.8012	0.002601	IBTK	inhibitor of Bruton agammaglobulinemia tyrosine kinase	TA
331	chr7	128501856	128503856	11.53754	0.002601	ATP6V1F	ATPase, H+ transporting, lysosomal 14kDa, V1 subunit F	TM
332	chr12	6755580	6757580	10.31926	0.002688	ACRBP	acrosin binding protein	TM
333	chr1	11917992	11919992	15.58047	0.002737	NPPB	natriuretic peptide B	TM
334	chr17	3818960	3820960	-11.2617	0.002753	P2RX1	purinergic receptor P2X, ligand-gated ion channel, 1	TA
335	chr21	41238346	41240346	25.13228	0.002767	PCP4	Purkinje cell protein 4	TM
336	chr11	75110434	75112434	13.1239	0.002795	RPS3	ribosomal protein S3	TM

337	chr19	8407146	8409146	14.46009	0.002798	KANK3	KN motif and ankyrin repeat domains 3	TM
338	chr19	49557997	49559997	11.25661	0.002827	CGB7	chorionic gonadotropin, beta polypeptide 7	TM
339	chr3	10804877	10806877	14.70725	0.002857	LINC00606	long intergenic non-protein coding RNA 606	TM
340	chr10	114134955	114136955	-16.8043	0.002871	ACSL5	acyl-CoA synthetase long-chain family member 5	TA
341	chr1	35543963	35545963	14.52109	0.002895	ZMYM1	zinc finger, MYM-type 1	TM
342	chr13	97635426	97637426	-24.506	0.002947	LINC00359	long intergenic non-protein coding RNA 359	TA
343	chr17	47571654	47573654	-10.6905	0.002967	NGFR	nerve growth factor receptor	TA
344	chr14	73392039	73394039	-11.4017	0.003029	DCAF4	DDB1 and CUL4 associated factor 4	TA
345	chr4	1302578	1304578	11.85714	0.003061	MAEA	macrophage erythroblast attacher	TM
346	chr13	110052042	110054042	-30.4521	0.003084	LINC00399	long intergenic non-protein coding RNA 399	TA
347	chr7	154001296	154003296	-13.3974	0.003137	DPP6	dipeptidyl-peptidase 6	TA
348	chr16	30995518	30997518	14.91577	0.003164	HSD3B7	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 7	TM
349	chr10	71903484	71905484	11.10034	0.003167	TYSND1	trypsin domain containing 1	TM
350	chr15	40632168	40634168	35.86635	0.003262	C15orf52	chromosome 15 open reading frame 52	TM
351	chr13	100150560	100152560	14.52733	0.003291	LINC01232	Long Intergenic Non-Protein Coding RNA 1232	TM
352	chr17	62776622	62778622	-10.3273	0.003292	hsa-mir-6080	hsa-mir-6080	TA
353	chr9	97020547	97022547	14.47194	0.003389	ZNF169	zinc finger protein 169	TM
354	chr15	25469349	25471349	17.44365	0.003454	SNORD115-30	small nucleolar RNA, C/D box 115-30	TM
355	chr19	36427021	36429021	12.27521	0.003539	LRFN3	leucine rich repeat and fibronectin type	TM

							III domain containing 3	
356	chr20	62581527	62583527	-11.8067	0.003539	UCKL1	uridine-cytidine kinase 1-like 1	TA
357	chr7	56018610	56020610	-15.8956	0.003656	MRPS17	28S ribosomal protein S17, mitochondrial; HCG1984214, isoform CRA_a	TA
358	chr7	143598172	143600172	19.41143	0.003656	FAM115A	family with sequence similarity 115, member A	TM
359	chr7	143598278	143600278	19.41143	0.003656	FAM115A	family with sequence similarity 115, member A	TM
360	chr16	8961869	8963869	11.42266	0.003735	CARHSP1	calcium regulated heat stable protein 1, 24kDa	TM
361	chr14	24562339	24564339	18.05556	0.003814	PCK2	phosphoenolpyruvate carboxykinase 2 (mitochondrial)	TM
362	chr12	52714182	52716182	-17.007	0.003843	KRT83	keratin 83	TA
363	chr10	134778037	134780037	-11.3927	0.003864	LINC01166	long intergenic non-protein coding RNA 1166	TA
364	chr20	60173816	60175816	10.00651	0.003886	CDH4	cadherin 4, type 1, R-cadherin (retinal)	TM
365	chr12	185541	187541	-11.706	0.004034	IQSEC3	IQ motif and Sec7 domain 3	TA
366	chr16	56690854	56692854	17.07041	0.004035	MT1F	metallothionein 1F	TM
367	chr17	18758611	18760611	-21.9978	0.004163	PRPSAP2	phosphoribosyl pyrophosphate synthetase-associated protein 2	TA
368	chr17	75282972	75284972	-13.5262	0.004204	9-Sep	septin 9	TA
369	chr9	130692076	130694076	13.75349	0.004287	PIP5KL1	phosphatidylinositol-4-phosphate 5-kinase-like 1	TM
370	chr11	113257512	113259512	10.87553	0.004338	ANKK1	ankyrin repeat and kinase domain containing 1	TM
371	chr11	3646689	3648689	-10.9217	0.004353	TRPC2	transient receptor potential cation channel, subfamily C, member 2, pseudogene	TA
372	chr2	120435742	120437742	10.78137	0.004354	TMEM177	transmembrane protein 177	TM
373	chr12	56861300	56863300	15.09637	0.004368	SPRYD4	SPRY domain containing 4	TM

374	chr8	22088851	22090851	-18.6134	0.004371	PHYHIP	phytanoyl-CoA 2-hydroxylase interacting protein	TA
375	chr11	35158579	35160579	-23.9574	0.004372	CD44	CD44 molecule (Indian blood group)	TA
376	chr20	25387322	25389322	-16.2449	0.004473	GINS1	GINS complex subunit 1 (Psf1 homolog)	TA
377	chr6	43275530	43277530	20.88509	0.004549	CRIP3	cysteine-rich protein 3	TM
378	chr15	34628045	34630045	-19.505	0.004601	SLC12A6	solute carrier family 12 (potassium/chloride transporter), member 6	TA
379	chr20	23585610	23587610	-21.9986	0.004623	CST9	cystatin 9 (testatin)	TA
380	chr19	49928687	49930687	-26.1588	0.004698	GFY	golgi-associated, olfactory signaling regulator	TA
381	chr9	116839752	116841752	-20.2306	0.004791	AMBP	alpha-1-microglobulin/bikunin precursor	TA
382	chr20	48908256	48910256	12.71843	0.004817	RP11-290F20.1	Uncharacterized LOC284751	TM
383	chr16	30621096	30623096	10.64867	0.004901	ZNF689	zinc finger protein 689	TM
384	chr8	67089846	67091846	10.87427	0.00493	CRH	corticotropin releasing hormone	TM
385	chr8	133686863	133688863	-16.1293	0.004994	LRRC6	leucine rich repeat containing 6	TA
386	chr1	2283100	2285100	-12.1487	0.005083	RP4-740C4.6	DNA sequence from clone RP4-740C4.67 on chromosome 1	TA
387	chr1	43734664	43736664	-20.3902	0.005188	TMEM125	transmembrane protein 125	TA
388	chr16	30022669	30024669	10.76773	0.005286	DOC2A	double C2-like domains, alpha	TM
389	chr19	2281181	2283181	14.59343	0.005531	C19orf35	chromosome 19 open reading frame 35	TM
390	chr11	67382135	67384135	-14.3312	0.005535	DOC2GP	double C2-like domains, gamma, pseudogene	TA
391	chr12	53011343	53013343	15.59735	0.005647	KRT73	keratin 73	TM
392	chrX	47478256	47480256	-11.5391	0.005647	SYN1	synapsin I	TA
393	chr7	73255855	73257855	14.87455	0.00567	WBSCR27	Williams Beuren syndrome	TM

							chromosome region 27	
394	chr9	35859270	35861270	20.63095	0.005701	LINC00950	Long Intergenic Non-Protein Coding RNA 950	TM
395	chr16	77755388	77757388	-13.0214	0.005825	NUDT7	nudix (nucleoside diphosphate linked moiety X)-type motif 7	TA
396	chr10	121136483	121138483	-12.6676	0.006033	MIR4681	microRNA 4681	TA
397	chr12	32831133	32833133	11.23387	0.006154	DNM1L	dynamin 1-like	TM
398	chr4	142252771	142254771	-15.7284	0.006221	LINC02432	Long Intergenic Non-Protein Coding RNA 2432	TA
399	chr11	67170446	67172446	18.43995	0.006221	TBC1D10C	TBC1 domain family, member 10C	TM
400	chr20	32307136	32309136	-10.516	0.006576	PXMP4	peroxisomal membrane protein 4, 24kDa	TA
401	chr1	155289639	155291639	-18.9879	0.006821	RUSC1	RUN and SH3 domain containing 1	TA
402	chr17	38443145	38445145	10.73009	0.006821	CDC6	cell division cycle 6	TM
403	chr1	20616411	20618411	-22.6006	0.006889	VWA5B1	von Willebrand factor A domain containing 5B1	TA
404	chr9	116326233	116328233	14.64135	0.006898	RGS3	regulator of G-protein signaling 3	TM
405	chr16	15743082	15745082	-10.8377	0.006969	NDE1	nudE neurodevelopment protein 1	TA
406	chr17	4462891	4464891	-12.062	0.007095	GGT6	gamma-glutamyltransferase 6	TA
407	chr19	49140295	49142295	-18.8843	0.007095	DBP	D site of albumin promoter (albumin D-box) binding protein	TA
408	chr11	118900616	118902616	10.36137	0.00719	SLC37A4	solute carrier family 37 (glucose-6-phosphate transporter), member 4	TM
409	chr4	123357	125357	-10.2693	0.007205	ZNF718	zinc finger protein 718	TA
410	chr6	159184785	159186785	-10.1498	0.007248	MIR3918	microRNA 3918	TA
411	chr1	227750219	227752219	15.74628	0.007251	ZNF678	zinc finger protein 678	TM
412	chr1	161574848	161576848	-11.4265	0.007315	HSPA7	heat shock 70kDa protein 7 (HSP70B)	TA

413	chr6	34481648	34483648	13.28454	0.007407	PACSIN1	protein kinase C and casein kinase substrate in neurons 1	TM
414	chr20	25012342	25014342	16.32035	0.007477	ACSS1	acyl-CoA synthetase short-chain family member 1	TM
415	chr9	135229372	135231372	-11.8024	0.007588	SETX	senataxin	TA
416	chr2	96990934	96992934	-12.7256	0.007602	ITPRIPL1	inositol 1,4,5-trisphosphate receptor interacting protein-like 1	TA
417	chr2	96990944	96992944	-12.7256	0.007602	ITPRIPL1	inositol 1,4,5-trisphosphate receptor interacting protein-like 1	TA
418	chr17	38217445	38219445	13.74375	0.007664	THRA	thyroid hormone receptor, alpha	TM
419	chr1	213187851	213189851	-10.2297	0.007685	ANGEL2	angel homolog 2 (Drosophila)	TA
420	chr1	213188217	213190217	-10.2297	0.007685	ANGEL2	angel homolog 2 (Drosophila)	TA
421	chr1	2487450	2489450	14.52923	0.00779	RP3-395M20.8	Uncharacterized lncRNA LOC100996583	TM
422	chr6	29941891	29943891	16.00103	0.007828	HCG9	HLA complex group 9 (non-protein coding)	TM
423	chr17	42991920	42993920	-11.3621	0.007858	GFAP	glial fibrillary acidic protein	TA
424	chr19	11545465	11547465	-17.9402	0.007933	PRKCSH	protein kinase C substrate 80K-H	TA
425	chr22	20136431	20138431	10.77494	0.008253	CCDC188	Coiled-Coil Domain Containing 188	TM
426	chr20	44485048	44487048	10.13341	0.008282	ZSWIM3	zinc finger, SWIM-type containing 3	TM
427	chr6	31773761	31775761	-11.7983	0.008304	LSM2	LSM2 homolog, U6 small nuclear RNA associated (S. cerevisiae)	TA
428	chr7	142959521	142961521	-15.2584	0.00831	GSTK1	glutathione S-transferase kappa 1	TA
429	chr4	15963859	15965859	-17.3064	0.008392	FGFBP2	fibroblast growth factor binding protein 2	TA
430	chr4	141418531	141420531	15.3645	0.008433	RP11-542P2.1	Glycosyltransferase 54 domain-containing protein	TM

431	chr1	202935404	202937404	-10.7196	0.008616	CYB5R1	cytochrome b5 reductase 1	TA
432	chr11	116657739	116659739	-20.501	0.008825	ZNF259	zinc finger protein 259	TA
433	chr17	34078897	34080897	17.50334	0.009176	GAS2L2	growth arrest-specific 2 like 2	TM
434	chr11	298526	300526	11.40773	0.009271	IFITM5	interferon induced transmembrane protein 5	TM
435	chr14	101520594	101522594	17.4333	0.009417	MIR323B	microRNA 323b	TM
436	chr5	138724605	138726605	14.0925	0.009581	MZB1	marginal zone B and B1 cell-specific protein	TM
437	chr7	150651917	150653917	11.70187	0.009683	KCNH2	potassium voltage-gated channel, subfamily H (eag-related), member 2	TM
438	chrX	153045455	153047455	13.3666	0.010347	SRPK3	SRSF protein kinase 3	TM
439	chr22	29976085	29978085	-12.7895	0.010357	NIPSNAP1	nipsnap homolog 1 (C. elegans)	TA
440	chr22	29976326	29978326	-12.7895	0.010357	NIPSNAP1	nipsnap homolog 1 (C. elegans)	TA
441	chr1	228351549	228353549	12.55147	0.010725	IBA57	IBA57, iron-sulfur cluster assembly homolog (S. cerevisiae)	TM
442	chr4	103939896	103941896	10.60606	0.010725	SLC9B1	solute carrier family 9, subfamily B (NHA1, cation proton antiporter 1), member 1	TM
443	chr13	111521655	111523655	-14.3305	0.010729	LINC00346	long intergenic non-protein coding RNA 346	TA
444	chr14	91709852	91711852	-20.6573	0.010949	GPR68	G protein-coupled receptor 68	TA
445	chr3	149955486	149957486	-13.9535	0.011095	RP11-167H9.6	lncRNA RP11-167H9.6	TA
446	chr2	241563661	241565661	-10.2644	0.011169	GPR35	G protein-coupled receptor 35	TA
447	chr3	9943295	9945295	22.87611	0.01117	IL17RE	interleukin 17 receptor E	TM
448	chr2	239139318	239141318	-11.3793	0.011262	LOC643387	TAR DNA Binding Protein Pseudogene	TA
449	chr2	239139326	239141326	-11.3793	0.011262	LOC643387	TAR DNA Binding Protein Pseudogene	TA
450	chr15	21939739	21941739	-21.4194	0.011262	RP11-32B5.1	LincRNA RP11-32B5.1	TA

451	chr19	7693670	7695670	-15.8337	0.011546	XAB2	XPA binding protein 2	TA
452	chr5	10307168	10309168	10.29807	0.011637	CMBL	carboxymethylenebutenolidase homolog (Pseudomonas)	TM
453	chr5	270639	272639	13.54642	0.011904	PDCD6	programmed cell death 6	TM
454	chr12	50296760	50298760	15.4851	0.011908	FAIM2	Fas apoptotic inhibitory molecule 2	TM
455	chr11	17564963	17566963	-15.0957	0.011965	USH1C	Usher syndrome 1C (autosomal recessive, severe)	TA
456	chr8	10382055	10384055	18.13581	0.012218	PRSS55	protease, serine, 55	TM
457	chr3	183992798	183994798	-10.8052	0.01231	ECE2	endothelin converting enzyme 2	TA
458	chr10	103985034	103987034	-13.1778	0.01296	ELOVL3	ELOVL fatty acid elongase 3	TA
459	chr12	111357404	111359404	11.13942	0.013008	MYL2	myosin, light chain 2, regulatory, cardiac, slow	TM
460	chr2	26623783	26625783	10.48454	0.013216	DRC1	dynein regulatory complex subunit 1 homolog (Chlamydomonas)	TM
461	chr11	124542739	124544739	14.31302	0.013288	SPA17	sperm autoantigenic protein 17	TM
462	chr11	124542777	124544777	14.31302	0.013288	SPA17	sperm autoantigenic protein 17	TM
463	chr20	61667380	61669380	14.29952	0.0134	LINC00029	long intergenic non-protein coding RNA 29	TM
464	chr17	27223715	27225715	-10.1928	0.013499	FLOT2	flotillin 2	TA
465	chr13	103718196	103720196	19.11392	0.013537	SLC10A2	solute carrier family 10 (sodium/bile acid cotransporter), member 2	TM
466	chr17	43509282	43511282	-13.7495	0.013788	ARHGAP27	Rho GTPase activating protein 27	TA
467	chr2	242822513	242824513	18.09524	0.013988	AC131097.3	Lnc-RTP5-10	TM
468	chr17	4872066	4874066	-12.2891	0.014215	MIR6864	MicroRNA 6864	TA
469	chr16	70322412	70324412	-10.4788	0.014544	DDX19B	DEAD (Asp-Glu-Ala-Asp) box polypeptide 19B	TA
470	chr5	159625047	159627047	14.57521	0.015176	FABP6	fatty acid binding protein 6, ileal	TM

471	chr19	47735023	47737023	-18.2591	0.015511	BBC3	BCL2 binding component 3	TA
472	chr19	52429687	52431687	12.80945	0.015873	ZNF613	zinc finger protein 613	TM
473	chr5	140200360	140202360	-18.6032	0.015932	PCDHA5	protocadherin alpha 5	TA
474	chr2	152145430	152147430	11.6639	0.015936	NMI	N-myc (and STAT) interactor	TM
475	chr16	30750511	30752511	-10.8739	0.016061	TMEM265	Transmembrane Protein 265	TA
476	chr16	19534178	19536178	13.90348	0.016605	CCP110	centriolar coiled coil protein 110kDa	TM
477	chr17	7831753	7833753	10.49175	0.016605	KCNAB3	potassium voltage-gated channel, shaker-related subfamily, beta member 3	TM
478	chr19	58280019	58282019	14.64212	0.016742	ZNF586	zinc finger protein 586	TM
479	chr2	106681112	106683112	10.67008	0.016743	C2orf40	chromosome 2 open reading frame 40	TM
480	chr10	116443414	116445414	-26.2642	0.016743	ABLIM1	actin binding LIM protein 1	TA
481	chr2	237415178	237417178	-15.9873	0.016766	IQCA1	IQ motif containing with AAA domain 1	TA
482	chrX	139172825	139174825	-12.4628	0.017057	LOC389895	Uncharacterized Protein LOC389895	TA
483	chr7	99062824	99064824	13.03034	0.01707	ATP5J2	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit F2	TM
484	chr3	9943511	9945511	22.55102	0.017102	IL17RE	interleukin 17 receptor E	TM
485	chr8	144765621	144767621	-10.5052	0.017776	ZNF707	zinc finger protein 707	TA
486	chr8	55046780	55048780	11.08811	0.017999	MRPL15	mitochondrial ribosomal protein L15	TM
487	chr8	143822829	143824829	-10.3043	0.017999	SLURP1	secreted LY6/PLAUR domain containing 1	TA
488	chr1	24740587	24742587	-13.0601	0.018235	STPG1	sperm-tail PG-rich repeat containing 1	TA
489	chr10	98861512	98863512	24.11235	0.018293	RP11-453E2.2	Uncharacterized antisense RNA LOC100505540	TM
490	chr17	38519945	38521945	10.64665	0.018354	GJD3	gap junction protein, delta 3, 31.9kDa	TM

491	chr9	137297427	137299427	12.61173	0.019303	RXRA	retinoid X receptor, alpha	TM
492	chr22	37607416	37609416	13.69205	0.019303	SSTR3	somatostatin receptor 3	TM
493	chr7	73274488	73276488	14.13858	0.019728	WBSCR28	Williams-Beuren syndrome chromosome region 28	TM
494	chr10	106033886	106035886	10.83864	0.019774	GSTO2	glutathione S-transferase omega 2	TM
495	chr10	71175674	71177674	-13.018	0.019903	TACR2	tachykinin receptor 2	TA
496	chr8	145700718	145702718	-10.9324	0.020524	FOXH1	forkhead box H1	TA
497	chr9	130880013	130882013	-14.4271	0.020663	RP11-395P17.3	Uncharacterized LOC100289019	TA
498	chr21	43482067	43484067	-13.5714	0.020903	UMODL1	uromodulin-like 1	TA
499	chr13	100057554	100059554	15.8803	0.020905	MIR548AN	microRNA 548an	TM
500	chr2	128292377	128294377	-12.8972	0.021389	MYO7B	myosin VIIB	TA
501	chr14	31027328	31029328	12.0582	0.021407	G2E3	G2/M-phase specific E3 ubiquitin protein ligase	TM
502	chr16	2835708	2837708	-11.2196	0.021509	PRSS33	protease, serine, 33	TA
503	chr16	70206351	70208351	13.25758	0.022178	LOC400541	Uncharacterized LOC400541	TM
504	chr16	70206927	70208927	13.25758	0.022178	LOC400541	Uncharacterized LOC400541	TM
505	chr6	42017250	42019250	10.96999	0.02252	TAF8	TAF8 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 43kDa	TM
506	chr1	24017268	24019268	-18.8214	0.022786	RPL11	ribosomal protein L11	TA
507	chr6	26224382	26226382	12.35772	0.023018	HIST1H3E	histone cluster 1, H3e	TM
508	chr3	10435246	10437246	-11.9396	0.023923	MIR885	microRNA 885	TA
509	chr20	30134184	30136184	11.81962	0.023923	RP3-324O17.4	DNA sequence from clone RP3-324O17 on chromosome 20	TM
510	chr12	110210292	110212292	-22.5954	0.024117	FAM222A-AS1	FAM222A antisense RNA 1	TA
511	chr1	160231277	160233277	12.2113	0.024882	DCAF8	DDB1 and CUL4 associated factor 8	TM
512	chr1	160231318	160233318	12.2113	0.024882	DCAF8	DDB1- and CUL4-associated factor 8	TM

513	chr1	160231350	160233350	12.2113	0.024882	DCAF8	DDB1- and CUL4-associated factor 8	TM
514	chr12	58002962	58004962	-18.985	0.025015	ARHGEF25	Rho guanine nucleotide exchange factor (GEF) 25	TA
515	chr19	4516716	4518716	-10.4404	0.025577	PLIN4	perilipin 4	TA
516	chr18	47016717	47018717	16.76172	0.025621	SNORD58A	small nucleolar RNA, C/D box 58A	TM
517	chr19	4769681	4771681	26.02496	0.025822	MIR7-3	microRNA 7-3	TM
518	chr1	115396423	115398423	14.5074	0.02598	SYCP1	synaptonemal complex protein 1	TM
519	chr3	124302505	124304505	-11.4357	0.026425	KALRN	kalirin, RhoGEF kinase	TA
520	chr17	18011019	18013019	11.24752	0.026434	MYO15A	myosin XVA	TM
521	chr19	22789817	22791817	19.42623	0.026587	LOC100996349	Testis Expressed 264, ER-Phagy Receptor	TM
522	chr19	35835415	35837415	10.56165	0.026728	MIR5196	microRNA 5196	TM
523	chr1	154126592	154128592	-14.658	0.027089	NUP210L	nucleoporin 210kDa-like	TA
524	chr14	101520755	101522755	13.63332	0.027196	MIR323B	microRNA 323b	TM
525	chr2	162271619	162273619	-13.0461	0.027208	TBR1	T-box, brain, 1	TA
526	chr14	23351431	23353431	-25.0196	0.027323	REM2	RAS (RAD and GEM)-like GTP binding 2	TA
527	chr2	97172846	97174846	-10.1111	0.027418	NEURL3	neuralized E3 ubiquitin protein ligase 3	TA
528	chr16	3492490	3494490	10.88286	0.028267	ZNF597	zinc finger protein 597	TM
529	chr16	3492667	3494667	10.88286	0.028267	ZNF597	zinc finger protein 597	TM
530	chr1	112398527	112400527	-16.3276	0.028417	KCND3-IT1	KCND3 intronic transcript 1 (non-protein coding)	TA
531	chr7	99690266	99692266	14.05375	0.028417	MIR93	microRNA 93	TM
532	chr13	47470211	47472211	-10.2348	0.028528	HTR2A	5-hydroxytryptamine (serotonin) receptor 2A, G protein-coupled	TA
533	chr11	133901166	133903166	-16.9268	0.029654	RP11-713P17.3	Uncharacterized lncRNA LOC100128239	TA
534	chr12	52280792	52282792	13.27711	0.029654	ANKRD33	ankyrin repeat domain 33	TM
535	chr1	26550810	26552810	-10.2673	0.030125	LOC101928303	Uncharacterized LOC101928303 pseudogene	TA

536	chr15	25455838	25457838	-15.2301	0.030353	PWAR4	Prader Willi/Angelman Region Gene 4	TA
537	chr15	25455942	25457942	-15.2301	0.030353	PWAR4	Prader Willi/Angelman Region Gene 4	TA
538	chr1	120438147	120440147	-12.6512	0.031161	ADAM30	ADAM metallopeptidase domain 30	TA
539	chr14	93672459	93674459	-10.9617	0.031261	UBR7	ubiquitin protein ligase E3 component n-recognin 7 (putative)	TA
540	chr16	56650372	56652372	-13.2511	0.031329	MT1L	metallothionein 1L (gene/pseudogene)	TA
541	chr16	69759533	69761533	15.32276	0.031329	NQO1	NAD(P)H dehydrogenase, quinone 1	TM
542	chr16	69759571	69761571	15.32276	0.031329	NQO1	NAD(P)H dehydrogenase, quinone 1	TM
543	chr7	23220445	23222445	11.45322	0.031601	NUPL2	nucleoporin like 2	TM
544	chr4	25313395	25315395	-12.7752	0.032105	ZCCHC4	zinc finger, CCHC domain containing 4	TA
545	chr1	151687792	151689792	22.17164	0.032201	CELF3	CUGBP, Elav-like family member 3	TM
546	chr5	111495222	111497222	10.8883	0.033526	SNORA13	small nucleolar RNA, H/ACA box 13	TM
547	chr22	39708916	39710916	-11.23	0.034184	SNORD83B	small nucleolar RNA, C/D box 83B	TA
548	chr17	56405152	56407152	-10.898	0.034647	BZRAP1-AS1	BZRAP1 antisense RNA 1	TA
549	chr17	10706416	10708416	11.47239	0.034795	LINC00675	long intergenic non-protein coding RNA 675	TM
550	chr14	93672400	93674400	-11.2695	0.034889	UBR7	ubiquitin protein ligase E3 component n-recognin 7 (putative)	TA
551	chr17	56405298	56407298	-11.7383	0.035356	BZRAP1-AS1	BZRAP1 antisense RNA 1	TA
552	chr11	117694459	117696459	-15.1296	0.03544	FXYD2	FXYD domain containing ion transport regulator 2	TA
553	chr12	123751801	123753801	-11.0233	0.035552	CDK2AP1	cyclin-dependent kinase 2 associated protein 1	TA

554	chr1	248683947	248685947	11.90989	0.03584	OR2G6	olfactory receptor, family 2, subfamily G, member 6	TM
555	chr11	116662136	116664136	15.30117	0.036755	APOA5	apolipoprotein A-V	TM
556	chr10	51564107	51566107	-11.3203	0.03676	NCOA4	nuclear receptor coactivator 4	TA
557	chr12	54777514	54779514	-15.1393	0.036863	ZNF385A	zinc finger protein 385A	TA
558	chr6	10886063	10888063	-15.2941	0.036952	SYCP2L	synaptonemal complex protein 2-like	TA
559	chr8	143850246	143852246	11.30636	0.038311	LYNX1	Ly6/neurotoxin 1	TM
560	chr1	32280652	32282652	-12.6043	0.038458	SPOCD1	SPOC domain containing 1	TA
561	chr16	16461732	16463732	14.40033	0.038661	MIR6511A2	MicroRNA 6511a-2	TM
562	chr10	42969938	42971938	12.50518	0.039583	LINC00839	long intergenic non-protein coding RNA 839	TM
563	chr12	1737411	1739411	-14.1133	0.039778	WNT5B	wingless-type MMTV integration site family, member 5B	TA
564	chr3	157260132	157262132	-10.5148	0.039853	C3orf55	chromosome 3 open reading frame 55	TA
565	chr17	41475352	41477352	-12.2316	0.039853	ARL4D	ADP-ribosylation factor-like 4D	TA
566	chr17	8150413	8152413	-17.328	0.039888	CTC1	CTS telomere maintenance complex component 1	TA
567	chr3	75678913	75680913	16.8673	0.040121	MIR1324	microRNA 1324	TM
568	chr12	117746215	117748215	17.85714	0.040211	NOS1	nitric oxide synthase 1 (neuronal)	TM
569	chr18	595997	597997	-16.463	0.040992	CLUL1	clusterin-like 1 (retinal)	TA
570	chr16	85338931	85340931	14.25516	0.041762	MIR5093	microRNA 5093	TM
571	chr19	55586220	55588220	-16.5421	0.04221	EPS8L1	EPS8-like 1	TA
572	chr16	50299450	50301450	22.55754	0.043474	ADCY7	adenylate cyclase 7	TM
573	chr5	150137657	150139657	17.75736	0.043494	DCTN4	dynactin 4 (p62)	TM
574	chr14	72053287	72055287	-15.6464	0.045006	SIPA1L1	signal-induced proliferation-associated 1 like 1	TA
575	chr7	99690470	99692470	13.28321	0.045123	MIR93	microRNA 93	TM
576	chr12	116865123	116867123	-13.5337	0.046002	MIR4472-2	microRNA 4472-2	TA
577	chr17	46650810	46652810	-14.3978	0.046726	HOXB3	homeobox B3	TA
578	chr2	11271302	11273302	-10.1419	0.04747	C2orf50	chromosome 2 open reading frame 50	TA

579	chr11	18746777	18748777	11.53846	0.047866	IGSF22	immunoglobulin superfamily, member 22	TM
580	chr14	23856875	23858875	10.10697	0.048608	MIR208A	microRNA 208a	TM
581	chr15	35086927	35088927	11.23474	0.04905	ACTC1	actin, alpha, cardiac muscle 1	TM
582	chr16	67225067	67227067	-10.9158	0.049669	E2F4	E2F transcription factor 4, p107/p130-binding	TA
583	chr20	39968492	39970492	14.14352	0.049669	LPIN3	lipin 3	TM
584	chr7	143078778	143080778	-17.5471	0.049833	MIR6892	MicroRNA 6892	TA

Supplementary Table 1. Differentially methylated promoters between aortic and mitral valve tissue (q value < 0.05 and a meth.diff > |10|) and their associated genes ordered by significance (q-value). There is a total of 584 promoters that are differentially methylated between aortic and mitral valve tissue. prom.chr, prom.start and prom.end identify the location of each promoter. meth.diff represents the difference between the weighted average of the percent methylation values of aortic (TA) and mitral (TM) samples (**see Methods**). qvalue denotes the corrected statistical significance of this difference (**see Methods**). assoc.gene-Symbol represents the gene associated with the corresponding differentially methylated promoter. Finally, dir identifies the tissue (aortic (TA)/ mitral (TM) tissue) in which the particular promoter exhibits increased methylation.

2.2 Table S2. Functional Classification based on PANTHER Pathways for the genes associated with differentially methylated promoters between the non-diseased aortic and mitral valve tissue – full list

No.	PANTHER Pathway	No. of genes	genes (Symbol)
1	Heterotrimeric G-protein signaling pathway-Gi alpha and Gs alpha mediated pathway (P00026)	8	RGS3, RGS9, HTR5A, HTR2A, ADCY7, SSTR3, RGS14, GNAI2
2	**Inflammation mediated by chemokine and cytokine signaling pathway (P00031)**	6	PAK6, ACTC1, CASK, BCL3, RGS14, GNAI2
3	Alzheimer disease-presenilin pathway (P00004)	5	TRIM2, ACTC1, WNT5B, CD44, TRPC3
4	**Wnt signaling pathway (P00057)**	5	AES, ACTC1, PCDHA5, WNT5B, CDH4
5	Nicotinic acetylcholine receptor signaling pathway (P00044)	5	ACTC1, VAMP1, MYO15A, SLC6A8, MYO7B
6	Gonadotropin-releasing hormone receptor pathway (P06664)	5	LHB, SMAD3, PCP4, NOS1, GNAI2
7	Huntington disease (P00029)	4	PACSIN1, ARL4D,

			ACTC1, KALRN
8	Heterotrimeric G-protein signaling pathway-Gq alpha and Go alpha mediated pathway (P00027)	4	RGS3, RGS9, SSTR3, RGS14
9	**Cadherin signaling pathway (P00012)**	4	ACTC1, PCDHA5, WNT5B, CDH4
10	**5HT1 type receptor mediated signaling pathway (P04373)**	3	VAMP1, ADCY7, GNAI2
11	**TGF-beta signaling pathway (P00052)**	3	SMAD3, FOXH1, TAB1
12	Opioid proopiomelanocortin pathway (P05917)	3	VAMP1, ADCY7, GNAI2
13	**Cytoskeletal regulation by Rho GTPase (P00016)**	3	PAK6, ACTC1, LIMK1
14	Opioid prodynorphin pathway (P05916)	3	VAMP1, ADCY7, GNAI2
15	Opioid proenkephalin pathway (P05915)	3	VAMP1, ADCY7, GNAI2
16	Muscarinic acetylcholine receptor 2 and 4 signaling pathway (P00043)	3	VAMP1, SLC6A8, GNAI2
17	Dopamine receptor mediated signaling pathway (P05912)	3	VAMP1, ADCY7, GNAI2
18	Beta3 adrenergic receptor signaling pathway (P04379)	2	VAMP1, ADCY7
19	Metabotropic glutamate receptor group III pathway (P00039)	2	VAMP1, GNAI2
20	Beta2 adrenergic receptor signaling pathway (P04378)	2	VAMP1, ADCY7

21	Beta1 adrenergic receptor signaling pathway (P04377)	2	VAMP1, ADCY7
22	**Apoptosis signaling pathway (P00006)**	2	CASP7, TNFRSF10C
23	Ionotropic glutamate receptor pathway (P00037)	2	VAMP1, SHANK2
24	**5HT4 type receptor mediated signaling pathway (P04376)**	2	VAMP1, ADCY7
25	**Angiogenesis (P00005)**	2	F2R, WNT5B
26	**5HT2 type receptor mediated signaling pathway (P04374)**	2	VAMP1, HTR2A
27	**Integrin signalling pathway (P00034)**	2	ACTC1, COL5A3
28	Adrenaline and noradrenaline biosynthesis (P00001)	2	VAMP1, PNMT
29	Synaptic vesicle trafficking (P05734)	2	VAMP1, SYN1
30	Vitamin D metabolism and pathway (P04396)	2	DBP, RXRA
31	T cell activation (P00053)	2	ZAP70, LCP2
32	**Endothelin signaling pathway (P00019)**	2	ADCY7, ECE2
33	Parkinson disease (P00049)	2	CASK, FGR
34	**PDGF signaling pathway (P00047)**	2	ARHGAP27, RPS6KL1
35	Enkephalin release (P05913)	2	ADCY7, GNAI2
36	**Blood coagulation (P00011)**	2	F2R, F10
37	Cortocotropin releasing factor receptor signaling pathway (P04380)	2	CRH, VAMP1
38	Metabotropic glutamate receptor group II pathway (P00040)	2	VAMP1, GNAI2
39	Axon guidance mediated by netrin (P00009)	1	ABLIM1
40	**5HT3 type receptor mediated signaling pathway (P04375)**	1	VAMP1
41	Coenzyme A biosynthesis (P02736)	1	COASY
42	Alpha adrenergic receptor signaling pathway (P00002)	1	VAMP1

43	Ubiquitin proteasome pathway (P00060)	1	SAE1
44	GABA-B receptor II signaling (P05731)	1	ADCY7
45	Heterotrimeric G-protein signaling pathway-rod outer segment phototransduction (P00028)	1	RGS9
46	p53 pathway feedback loops 2 (P04398)	1	RBL1
47	Pyridoxal-5-phosphate biosynthesis (P02759)	1	PNPO
48	Androgen/estrogene/progesterone biosynthesis (P02727)	1	HSD3B7
49	**Transcription regulation by bZIP transcription factor (P00055)**	1	TAF8
50	Thyrotropin-releasing hormone receptor signaling pathway (P04394)	1	VAMP1
51	**General transcription regulation (P00023)**	1	TAF8
52	Vitamin B6 metabolism (P02787)	1	PNPO
53	Toll receptor signaling pathway (P00054)	1	TAB1
54	**Methylmalonyl pathway (P02755)**	1	MCCC2
55	**General transcription by RNA polymerase I (P00022)**	1	TAF8
56	Acetate utilization (P02722)	1	ACSS1
57	Oxytocin receptor mediated signaling pathway (P04391)	1	VAMP1
58	FAS signaling pathway (P00020)	1	CASP7
59	p38 MAPK pathway (P05918)	1	TAB1
60	DNA replication (P00017)	1	TOP1MT
61	PI3 kinase pathway (P00048)	1	GNAI2
62	Histamine H2 receptor mediated signaling pathway (P04386)	1	ADCY7
63	**Notch signaling pathway (P00045)**	1	AC018470
64	Heme biosynthesis (P02746)	1	EPRS
65	Succinate to proprionate conversion (P02777)	1	MCCC2
66	Salvage pyrimidine ribonucleotides (P02775)	1	UCKL1
67	Muscarinic acetylcholine receptor 1 and 3 signaling pathway (P00042)	1	VAMP1
68	CCKR signaling map (P06959)	1	NOS1
69	Pyridoxal phosphate salvage pathway (P02770)	1	PNPO

Supplementary Table 2. PANTHER Pathways classifying the genes associated with differentially methylated promoters between the non-diseased aortic and mitral valve tissue. Pathways of interest are indicated in bold. The methylation direction of the pathways' constituent genes can be found in **Supplementary Table 1**.

2.3 Table S3. Functional Classification based on PANTHER Molecular Functions for the genes associated with differentially methylated promoters between the non-diseased aortic and mitral valve tissue – full list

No.	PANTHER Molecular Function	No. of genes	genes (Symbol)
1	**binding (GO:0005488)**	103	NDE1, PACSIN1, HOXB3, AES, GSPT1, AC131097, HLA-C, TOP1MT, RAD51C, HN1L, NR2F2, DNM1L, SEMA4B, ARL4D, RPL22L1, HTR5A, DMTN, ACTC1, EPS8L1, DBP, RBL1, GRTP1, LEO1, TBC1D10C, SETX, ZNF597, ABLIM1, IL17RE, RPL13A, LHB, VAMP1, APOA5, SPA17, REM2, UNK, RXRA, TBR1, THRA, DBP, MT1L, RPL11, LYNX1, CTC1, SEPT9, HTR2A, PPP4R2, UBOX5, ANGEL2, CLUL1, OSBPL1A, PPIE, RPS3, PCK2, DYSF, WNT5B, NGFR, FAM115A, TACR2, ATL3, PDLIM4, MT1A, ZNF497, PABPC4L, CYP2E1, AOX1, IPO4, TUBA8, CELF3, SPEF1, CD44, SHBG, IFNLR1, NOS1, FGR, ZAP70, ANPEP, FGFBP2, PLTP, AMBP, ZNF169, COLEC11, SSTR3, NPPB, CORO1B, CARHSP1, E2F4, HSPA7, PGF, TRPC3, MDK, LSM2, SBNO2, CDC6, CYB5R1, ZNF259, ENPEP, HOMER3, GNAI2, DDR1, SHANK2, PCGF3, MT1F, CGB7

2	**catalytic activity (GO:0003824)**	77	PAK6, ATP6V1F, VKORC1L1, EPRS, PRPSAP2, GSPT1, TYSND1, TRIM2, TOP1MT, PDE4A, RAD51C, GINS2, CTSZ, HAS1, CASP7, DNM1L, LPIN3, NEURL3, ELOVL3, DYRK1B, DHRS3, GRTP1, TBC1D10C, GSTO2, GINS4, APOA5, PRSS33, SEPT9, PPP4R2, UBOX5, ANGEL2, TGM2, UBE4B, PPIE, RPS3, PCK2, SRPK3, CWF19L1, SBK2, PNMT, NUDT7, ACER3, ATL3, ADCY7, CYP2E1, UCKL1, AOX1, LIMK1, NQO1, NUDT22, TAB1, ISG20, SAE1, NOS1, FGR, ZAP70, ANPEP, MCCC2, ERCC8, SUPT7L, SIRT6, AMBP, FUCA2, NEURL3, HSPA7, POLR1C, COASY, ATP6V1G1, PLK4, C19orf35, MAN2A2, ENPEP, GNAI2, DDR1, MAEA, HSD3B7, TOR4A
3	transcription regulator activity (GO:0140110)	21	HOXB3, AES, CCAR1, NR2F2, LPIN3, DYRK1B, AC018470.4, ZNF597, RXRA, TBR1, ATXN7L3, THRA, ZNF497, FOXL1, SUPT7L, SIRT6, ZNF169, E2F4, FHL2, ZMYM1, PCGF3
4	**molecular function regulator (GO:0098772)**	17	PRSS41, FXYD2, SEMA4B, EPS8L1, GRTP1, TBC1D10C, LHB, APOA5, REM2, LYNX1, PPP4R2, CWF19L1, AMBP, NPPB, PGF, MDK, CGB7
5	transporter activity (GO:0005215)	17	ATP6V1F, PRSS41, SLC12A6, RANBP17, FXYD2, SLC7A8, REM2, SLC16A3, OSBPL1A, P2RX1, IPO4, SLC35A1, KCNH2, PLTP, SLC10A2, TRPC3, ATP6V1G1

6	molecular transducer activity (GO:0060089)	15	HTR5A, IL17RE, THRA, LYNX1, F2R, HTR2A, NGFR, TACR2, CD44, IFNLR1, RGMA, RAMP1, GPR35, SSTR3, DDR1
7	structural molecule activity (GO:0005198)	8	MRPS17, RPL22L1, RPL13A, RPL11, RPS3, MRPL15, TUBA8, MRPL15
8	translation regulator activity (GO:0045182)	1	GSPT1

Supplementary Table 3. PANTHER Molecular Functions classifying the genes associated with differentially methylated promoters between the non-diseased aortic and mitral valve tissue. Molecular functions of interest are indicated in bold. The methylation direction of the molecular functions' constituent genes can be found in **Supplementary Table 1.**

2.4 Table S4. Functional Classification based on PANTHER Biological Processes for the genes associated with differentially methylated promoters between the non-diseased aortic and mitral valve tissue – full list

No.	PANTHER Biological Process	No. of genes	genes (Symbol)
1	cellular process (GO:0009987)	161	NDE1, PAK6, PACSIN1, IBA57, HOXB3, VKORC1L1, EPRS, AES, PRPSAP2, GSPT1, AC131097.3, SLC12A6, SYCP2L, CCAR1, TRIM2, TOP1MT, RAD51C, MRPS17, GINS2, CTSZ, RPS7, HAS1, CASP7, NR2F2, DNM1L, IQSEC1, C2orf40, SEMA4B, TCTN2, GPR68, LPIN3, ELOVL3, RPL22L1, HTR5A, EXOC7, DMTN, DYRK1B, DHRS3, ACTC1, EPS8L1, RBL1, LEO1, AC018470.4, ZNF597, ABLIM1, GINS4, RPL13A, LHB, VAMP1, APOA5, TCTN1, UNK, RXRA, TBR1, ATXN7L3, THRA, TBC1D32, MT1L, DNASE1L1, TRIP6, RPL11, F2R, DMKN, CTC1, SEPT9, TMEM101, HTR2A, PPP4R2, UBOX5, ANGEL2, TGM2, UBE4B, PPIE, RPS3, PCK2, SRPK3, LRFN3, DYSF, WNT5B, CWF19L1, IQSEC3, SBK2, NUDT7, NGFR, XAB2, TACR2, ATL3, PDLIM4, MT1A, WDTC1, ZNF497, VPS51, ADCY7, CYP2E1, HTR5A, BTBD2, PRPF6, MAGOH, AOX1, TUBA8, LIMK1, FBF1, CELF3, FOXL1, TRA2A, SPEF1, DRC1, TAB1, IFNLR1, ISG20, SAE1, NOS1, FGR, ZAP70, ANPEP, RGMA, FGFBP2, RAMP1, TEKT2, MCCC2, ERCC8, PLTP, SUPT7L, GPR35, SIRT6, SSTR3, NPPB, CORO1B, CARHSP1, TANGO6, NEURL3, E2F4, MZB1, GINS1, PSAP, HSPA7, PGF, ZMYM1, KANK3, RHBDF1, BRCA2, TRPC3, COASY, LSM2, PLK4, SBNO2, CDC6, C19orf35, ZNF259, MAN2A2, ENPEP, TNFRSF10C, SYN1, HOMER3, GNAI2, LCP2, SHANK2, MAEA, PCGF3, MT1F, CGB7
2	**biological regulation (GO:0065007)**	98	PAK6, PACSIN1, HOXB3, AES, SLC12A6, CCAR1, HLA-C, CASK, FXYD2, NR2F2, DNM1L, C2orf40, SEMA4B, TCTN2, LPIN3, HTR5A, DYRK1B, DHRS3, ARHGAP27, EPS8L1, RBL1, GRTP1, LEO1, TBC1D10C, AC018470.4, ZNF597, RPL13A, LHB, APOA5, RXRA, TBR1, ATXN7L3, THRA, MT1L, TRIP6, F2R, CTC1, TMEM101, HTR2A, ANGEL2, RPS3, PCK2, SRPK3, LRFN3, DYSF, WNT5B, SBK2, NGFR, FAM115A, TACR2, MT1A, WDTC1, ZNF497, ADCY7, LIMK1, CELF3, FOXL1, TRA2A, SPEF1, DRC1, TAB1, IFNLR1, ISG20, KCNH2, NOS1, FGR, ZAP70, RGMA, RAMP1, ERCC8, PLTP, GPR35, SIRT6, SSTR3, NPPB, CARHSP1, E2F4, MZB1, PSAP, PGF, ZMYM1, KANK3,

			RHBDF1, BRCA2, TRPC3, PLK4, SBNO2, CDC6, ZNF259, TNFRSF10C, SYN1, HOMER3, GNAI2, LCP2, SHANK2, PCGF3, MT1F, CGB7
3	metabolic process (GO:0008152)	96	PAK6, DDX19B, IBA57, HOXB3, VKORC1L1, EPRS, PRPSAP2, GSPT1, TYSND1, CCAR1, TRIM2, TOP1MT, RAD51C, MRPS17, GINS2, CTSZ, RPS7, HAS1, NR2F2, DNM1L, C2orf40, LPIN3, ELOVL3, RPL22L1, DYRK1B, DHRS3, LEO1, AC018470.4, ZNF597, GSTO2, GINS4, RPL13A, APOA5, PRSS33, RXRA, TBR1, ATXN7L3, THRA, DNASE1L1, TRIP6, CTC1, TMEM101, PPP4R2, UBOX5, ANGEL2, TGM2, UBE4B, RPS3, PCK2, SRPK3, CWF19L1, SBK2, NUDT7, XAB2, WDTC1, ZNF497, CYP2E1, PRPF6, MAGOH, AOX1, CELF3, FOXL1, TRA2A, TAB1, ISG20, SAE1, NOS1, FGR, ZAP70, ANPEP, RGMA, RAMP1, MCCC2, ERCC8, SUPT7L, SIRT6, PM20D1, NPPB, CARHSP1, FUCA2, E2F4, MZB1, GINS1, PSAP, PGF, ZMYM1, BRCA2, COASY, LSM2, SBNO2, C19orf35, ZNF259, MAN2A2, ENPEP, MAEA, PCGF3
4	**cellular component organization or biogenesis (GO:0071840)**	64	NDE1, PAK6, PACSIN1, IBA57, GSPT1, AC131097.3, SLC12A6, SYCP2L, TOP1MT, RAD51C, RPS7, HAS1, DNM1L, IQSEC1, SEMA4B, TCTN2, EXOC7, DMTN, ACTC1, EPS8L1, RBL1, ABLIM1, VAMP1, APOA5, TCTN1, UNK, TBR1, ATXN7L3, TBC1D32, RPL11, DMKN, CTC1, SEPT9, SRPK3, LRFN3, DYSF, IQSEC3, XAB2, ATL3, PDLIM4, VPS51, HTR5A, PRPF6, TUBA8, LIMK1, FBF1, CELF3, SPEF1, DRC1, RAMP1, TEKT2, PLTP, SUPT7L, SIRT6, CORO1B, NEURL3, GINS1, ZMYM1, KANK3, PLK4, CDC6, ZNF259, SHANK2, PCGF3
5	**response to stimulus (GO:0050896**)	58	PAK6, AES, AC131097.3, HLA-C, RAD51C, GINS2, CASK, C2orf40, SEMA4B, TCTN2, GPR68, LPIN3, HTR5A, DHRS3, EPS8L1, GINS4, LHB, RXRA, THRA, MT1L, TRIP6, F2R, TMEM101, HTR2A, UBE4B, RPS3, PCK2, SRPK3, DYSF, WNT5B, SBK2, NGFR, MT1A, ADCY7, CYP2E1, IFNLR1, ISG20, NOS1, FGR, ZAP70, RGMA, RAMP1, ERCC8, GPR35, SSTR3, NPPB, PSAP, HSPA7, PGF, RHBDF1, BRCA2, TNFRSF10C, HOMER3, GNAI2, LCP2, SHANK2, MT1F, CGB7
6	localization (GO:0051179)	54	NDE1, DDX19B, PACSIN1, AC131097.3, SLC12A6, SLC9B1, CASK, RANBP17, FXYD2, DNM1L, SLC14A1, SEMA4B, TCTN2, ARL4D, EXOC7, ACTC1, DBP, GRTP1, TBC1D10C, VAMP1, APOA5, TCTN1, SLC7A8, SLC6A8, TBC1D32, SLC16A3, SEPT9, HTR2A, DYSF, FAM115A, TACR2, VPS51, HTR5A, IPO4, FBF1, DRC1,

			KCNH2, RAMP1, TEKT2, PLTP, AP1S3, SLC10A2, CORO1B, TANGO6, NEURL3, HSPA7, PGF, RHBDF1, TRPC3, ZNF259, SLC51A, SYN1, HOMER3, SHANK2
7	signaling (GO:0023052)	41	PAK6, AES, SLC12A6, SEMA4B, TCTN2, HTR5A, DHRS3, EPS8L1, LHB, RXRA, THRA, TRIP6, F2R, TMEM101, HTR2A, RPS3, SRPK3, WNT5B, SBK2, NGFR, ADCY7, IFNLR1, NOS1, FGR, ZAP70, RGMA, FGFBP2, RAMP1, GPR35, SSTR3, NPPB, PSAP, PGF, RHBDF1, TNFRSF10C, SYN1, HOMER3, GNAI2, LCP2, SHANK2, CGB7
8	**developmental process (GO:0032502)**	26	PACSIN1, HOXB3, CASK, NR2F2, C2orf40, SEMA4B, RBL1, UNK, RXRA, TBR1, THRA, PCK2, LRFN3, DYSF, WNT5B, PDLIM4, BTBD2, FOXL1, FGR, ZAP70, RAMP1, PSAP, PGF, ZMYM1, ZNF259, SHANK2
9	multicellular organismal process (GO:0032501)	26	PACSIN1, HOXB3, AC131097.3, CASK, C2orf40, SEMA4B, APOA5, UNK, TBR1, THRA, PCK2, LRFN3, WNT5B, PDLIM4, BTBD2, CLEC11A, NOS1, RAMP1, PLTP, NPPB, PSAP, USH1C, PGF, PDZD7, ZNF259, SHANK2
10	locomotion (GO:0040011)	7	NDE1, SEMA4B, TACR2, DRC1, TEKT2, CORO1B, PGF
11	reproduction (GO:0000003)	5	SYCP2L, RAD51C, TACR2, PSAP, TRPC3
12	cell population proliferation (GO:0008283)	5	C2orf40, FGR, ZAP70, MZB1, PGF
13	reproductive process (GO:0022414)	5	SYCP2L, RAD51C, TACR2, PSAP, TRPC3
14	immune system process (GO:0002376)	5	HLA-C, DYSF, ISG20, MZB1, PGF
15	multi-organism process (GO:0051704)	4	ISG20, NOS1, TRPC3, SHANK2
16	**biological adhesion (GO:0022610)**	3	LRFN3, PCDHA5, SPON2
17	growth (GO:0040007)	3	SEMA4B, PSAP, SHANK2

18	biological phase (GO:0044848)	2	SYCP2L, RAD51C
19	behavior (GO:0007610)	1	SHANK2

Supplementary Table 4. PANTHER Biological Processes classifying the genes associated with differentially methylated promoters between the non-diseased aortic and mitral valve tissue. Biological processes of interest are indicated in bold. The methylation direction of the biological processes' constituent genes can be found in **Supplementary Table 1.**

2.5 Table S5. Functional Classification based on PANTHER Protein Classes for the genes associated with differentially methylated promoters between the non-diseased aortic and mitral valve tissue – full list

No.	PANTHER Protein Class	No. of genes	genes (Symbol)
1	metabolite interconversion enzyme (PC00262)	29	VKORC1L1, EPRS, PRPSAP2, PNPO, HAS1, PIP5KL1, ELOVL3, ACSL5, SERHL2, GSTK1, ACSS1, TGM2, PCK2, PNMT, NUDT7, PIGL, CASK, UCKL1, HSD17B14, SERHL2, AOX1, NOS1, PLBD2, MCCC2, FUCA2, COASY, GANAB, LDHA, HSD3B7
2	protein modifying enzyme (PC00260)	29	PRSS41, TYSND1, TRIM2, CTSZ, CASP7, MID2, NEURL3, DYRK1B, RPS6KL1, PRSS33, DCAF8, PRSS55, UBE4B, DPP6, SRPK3, F10, ADAM30, SPRYD4, WDTC1, BTBD2, ATL3, TAB1, SAE1, ANPEP, NEURL3, RHBDF1, C19orf35, ECE2, ENPEP
3	**gene-specific transcriptional regulator (PC00264)**	21	AES, NR2F2, AC018470.4, ZNF597, SMAD3, RXRA, TBR1, THRA, DBP, ZNF44, PBX4, ZNF497, TCF21, NMI, ZNF613, FOXL1, ZNF169, FHL2, ZMYM1, ZNF707, NCOA4
4	**cytoskeletal protein (PC00085)**	20	PACSIN1, DMTN, ACTC1, ABLIM1, RIBC2, MYO15A, TRIP6, SEPT9, MYL2, PDLIM4, TUBA8, TEKT2, CRIP3, CORO1B, DCTN4, USH1C, KANK3, PDZD7, PDCD6, MYO7B
5	**nucleic acid binding protein (PC00171)**	20	NOS1, TOP1MT, GINS2, HN1L, ZCCHC4, LEO1, SETX, SPOCD1, ANGEL2, XAB2, PRPF6, ISG20, CARHSP1, E2F4, GINS1, BRCA2, POLR1C, G2E3, LSM2, CDC6
6	transporter (PC00227)	18	ATP6V1F, RANBP17, FXYD2, NUP210L, ABCD1, SLC6A8, SLC16A3, SLC17A9, AQP2, P2RX1, ATP5J2, IPO4, SLC35A1, SLC10A2, TRPC3, ATP6V1G1, SLC51A, SLC37A4
7	protein-binding activity modulator (PC00095)	15	ARL4D, ARHGAP27, GRTP1, TBC1D10C, PRKCSH, FGD3, KALRN, FGD1, SIPA1L1, ATL3, PHACTR4, CDK2AP1, ARHGEF25, AC018470.4, GNAI2
8	**translational protein (PC00263)**	9	GSPT1, MRPS17, RPS7, RPL22L1, RPL13A, RPL11, RPS3, MRPL15, MRPL15
9	transmembrane signal receptor (PC00197)	9	GPR68, HTR5A, HTR2A, CD44, IFNLR1, RAMP1, SSTR3, FGFRL1, GPER1

10	intercellular signal molecule (PC00207)	8	SEMA4B, LHB, CRH, WNT5B, CLEC11A, PGF, MDK, CGB7
11	membrane traffic protein (PC00150)	7	DNM1L, EXOC7, AP1M2, DYSF, BCL3, AP1S3, SYN1
12	**chromatin/chromatin-binding, or -regulatory protein (PC00077)**	5	SYCP2L, CCAR1, RBL1, L3MBTL1, PCGF3
13	scaffold/adaptor protein (PC00226)	4	GAB4, EPS8L1, PSAP, LCP2
14	**cell junction protein (PC00070)**	2	GJD3, TJP2
15	structural protein (PC00211)	2	STPG1, COLEC11
16	**extracellular matrix protein (PC00102)**	1	COL5A3
17	cell adhesion molecule (PC00069)	1	SPON2
18	**calcium-binding protein (PC00060)**	1	DRC1
19	defense/immunity protein (PC00090)	1	KIR2DL4
20	transfer/carrier protein (PC00219)	1	DBP
21	chaperone (PC00072)	1	TOR4A
22	storage protein (PC00210)	1	CASK

Supplementary Table 5. PANTHER Protein Classes classifying the genes associated with differentially methylated promoters between the non-diseased aortic and mitral valve tissue. Protein classes of interest are indicated in bold. The methylation direction of the protein classes' constituent genes can be found in **Supplementary Table 1.**

2.6 Table S6. Functional Classification based on PANTHER Cellular Components for the genes associated with differentially methylated promoters between the non-diseased aortic and mitral valve tissue – full list

No.	PANTHER Cellular Component	No. of genes	genes (Symbol)
1	cell (GO:0005623)	180	NDE1, PAK6, DDX19B, PACSIN1, HOXB3, EPRS, AES, PRPSAP2, GSPT1, SYCP2L, TYSND1, CCAR1, TOP1MT, PDE4A, RAD51C, MRPS17, GINS2, RANBP17, CTSZ, RPS7, HAS1, CASP7, HN1L, NR2F2, DNM1L, SEMA4B, TCTN2, ARL4D, LPIN3, ELOVL3, HTR5A, EXOC7, DMTN, DYRK1B, DHRS3, ARHGAP27, ACTC1, EPS8L1, NUP210L, DBP, RBL1, LEO1, AC018470.4, ABLIM1, GINS4, ACRBP, RPL13A, LHB, VAMP1, TCTN1, REM2, SLC6A8, RXRA, TBR1, ATXN7L3, THRA, DBP, CD164L2, MT1L, DNASE1L1, TRIP6, DCAF8, RPL11, LYNX1, F2R, SLC16A3, CTC1, SEPT9, PLIN4, HTR2A, PPP4R2, UBOX5, TGM2, CLUL1, OSBPL1A, AQP2, UBE4B, RPS3, PCK2, SRPK3, LRFN3, PCDHA5, DYSF, CWF19L1, PNMT, NGFR, XAB2, FAM115A, TACR2, ACER3, PDLIM4, MT1A, WDTC1, ZNF497, VPS51, PABPC4L, ADCY7, CYP2E1, PIH1D1, HTR5A, NMI, BTBD2, P2RX1, PRPF6, MAGOH, AOX1, IPO4, TUBA8, LIMK1, NQO1, FBF1, CELF3, FOXL1, TRA2A, SPEF1, SLC35A1, CD44, DRC1, IFNLR1, NIPSNAP1, ISG20, KCNH2, SAE1, NOS1, FGR, ZAP70, ANPEP, UBR7, RGMA, RAMP1, TEKT2, ERCC8, SUPT7L, GPR35, SIRT6, AP1S3, AMBP, ZFYVE28, ZNF169, SLC10A2, SSTR3, NPPB, CARHSP1, FUCA2, DCTN4, RUSC1, NEURL3, E2F4, FHL2, MZB1, GINS1, HSPA7, USH1C, ZMYM1, KANK3, RHBDF1, POLR1C, TRPC3, ATP6V1G1, PDZD7, LSM2, PLK4, SBNO2, CYB5R1, C19orf35, ZNF259, MAN2A2, ENPEP, TNFRSF10C, SLC51A, SYN1, HOMER3, GNAI2, SHANK2, MAEA, PCGF3, TOR4A, MT1F, PXMP4, CGB7
2	cell part (GO:0044464)	180	NDE1, PAK6, DDX19B, PACSIN1, HOXB3, EPRS, AES, PRPSAP2, GSPT1, SYCP2L, TYSND1, CCAR1, TOP1MT, PDE4A, RAD51C, MRPS17, GINS2, RANBP17, CTSZ, RPS7, HAS1, CASP7, HN1L, NR2F2, DNM1L, SEMA4B, TCTN2, ARL4D, LPIN3, ELOVL3, HTR5A, EXOC7, DMTN, DYRK1B, DHRS3, ARHGAP27, ACTC1, EPS8L1, NUP210L, DBP, RBL1, LEO1, AC018470.4, ABLIM1, GINS4, ACRBP, RPL13A, LHB, VAMP1, TCTN1, REM2, SLC6A8, RXRA, TBR1, ATXN7L3, THRA, DBP, CD164L2, MT1L, DNASE1L1,

			TRIP6, DCAF8, RPL11, LYNX1, F2R, SLC16A3, CTC1, SEPT9, PLIN4, HTR2A, PPP4R2, UBOX5, TGM2, CLUL1, OSBPL1A, AQP2, UBE4B, RPS3, PCK2, SRPK3, LRFN3, PCDHA5, DYSF, CWF19L1, PNMT, NGFR, XAB2, FAM115A, TACR2, ACER3, PDLIM4, MT1A, WDTC1, ZNF497, VPS51, PABPC4L, ADCY7, CYP2E1, PIH1D1, HTR5A, NMI, BTBD2, P2RX1, PRPF6, MAGOH, AOX1, IPO4, TUBA8, LIMK1, NQO1, FBF1, CELF3, FOXL1, TRA2A, SPEF1, SLC35A1, CD44, DRC1, IFNLR1, NIPSNAP1, ISG20, KCNH2, SAE1, NOS1, FGR, ZAP70, ANPEP, UBR7, RGMA, RAMP1, TEKT2, ERCC8, SUPT7L, GPR35, SIRT6, AP1S3, AMBP, ZFYVE28, ZNF169, SLC10A2, SSTR3, NPPB, CARHSP1, FUCA2, DCTN4, RUSC1, NEURL3, E2F4, FHL2, MZB1, GINS1, HSPA7, USH1C, ZMYM1, KANK3, RHBDF1, POLR1C, TRPC3, ATP6V1G1, PDZD7, LSM2, PLK4, SBNO2, CYB5R1, C19orf35, ZNF259, MAN2A2, ENPEP, TNFRSF10C, SLC51A, SYN1, HOMER3, GNAI2, SHANK2, MAEA, PCGF3, TOR4A, MT1F, PXMP4, CGB7
3	organelle (GO:0043226)	127	NDE1, DDX19B, PACSIN1, HOXB3, AES, SYCP2L, TYSND1, CCAR1, TOP1MT, RAD51C, MRPS17, GINS2, RANBP17, CTSZ, RPS7, HN1L, NR2F2, DNM1L, TCTN2, LPIN3, ELOVL3, DMTN, DYRK1B, DHRS3, ACTC1, EPS8L1, NUP210L, RBL1, LEO1, AC018470.4, ABLIM1, GINS4, ACRBP, RPL13A, TCTN1, RXRA, TBR1, ATXN7L3, THRA, DBP, CD164L2, MT1L, DNASE1L1, TRIP6, RPL11, CTC1, SEPT9, PPP4R2, UBOX5, TGM2, CLUL1, OSBPL1A, UBE4B, RPS3, PCK2, SRPK3, LRFN3, DYSF, CWF19L1, XAB2, TACR2, ACER3, PDLIM4, MT1A, ZNF497, VPS51, PABPC4L, CYP2E1, HTR5A, BTBD2, P2RX1, PRPF6, MAGOH, IPO4, TUBA8, LIMK1, FBF1, CELF3, FOXL1, TRA2A, SPEF1, SLC35A1, DRC1, NIPSNAP1, ISG20, SAE1, NOS1, TEKT2, ERCC8, SUPT7L, SIRT6, AP1S3, ZFYVE28, ZNF169, NPPB, FUCA2, DCTN4, RUSC1, NEURL3, E2F4, FHL2, MZB1, GINS1, HSPA7, USH1C, ZMYM1, KANK3, RHBDF1, POLR1C, ATP6V1G1, PDZD7, LSM2, PLK4, SBNO2, CYB5R1, C19orf35, ZNF259, MAN2A2, SLC51A, SYN1, HOMER3, SHANK2, MAEA, PCGF3, TOR4A, MT1F, PXMP4
4	membrane (GO:0016020)	69	PACSIN1, RANBP17, HAS1, DNM1L, SEMA4B, TCTN2, ARL4D, ELOVL3, HTR5A, EPS8L1, NUP210L, ACRBP, VAMP1, TCTN1, REM2, SLC6A8, LYNX1, F2R, SLC16A3, PLIN4, HTR2A, AQP2, LRFN3,

			PCDHA5, DYSF, NGFR, FAM115A, TACR2, ACER3, VPS51, ADCY7, HTR5A, P2RX1, FBF1, SPEF1, SLC35A1, CD44, DRC1, IFNLR1, KCNH2, NOS1, FGR, ZAP70, ANPEP, RGMA, GPR35, AMBP, ZFYVE28, SLC10A2, SSTR3, NEURL3, MZB1, HSPA7, USH1C, RHBDF1, TRPC3, ATP6V1G1, PDZD7, ZNF259, MAN2A2, ENPEP, TNFRSF10C, SLC51A, SYN1, HOMER3, GNAI2, SHANK2, TOR4A, PXMP4
5	organelle part (GO:0044422)	68	NDE1, SYCP2L, TOP1MT, RAD51C, MRPS17, GINS2, RANBP17, RPS7, DNM1L, TCTN2, ELOVL3, ACTC1, NUP210L, RBL1, GINS4, RPL13A, TCTN1, RXRA, ATXN7L3, THRA, TRIP6, RPL11, CTC1, SEPT9, RPS3, LRFN3, CWF19L1, XAB2, TACR2, ACER3, PDLIM4, ZNF497, VPS51, P2RX1, PRPF6, MAGOH, TUBA8, FBF1, TRA2A, SPEF1, SLC35A1, DRC1, SAE1, NOS1, ERCC8, SUPT7L, SIRT6, ZFYVE28, DCTN4, E2F4, FHL2, MZB1, GINS1, HSPA7, USH1C, RHBDF1, POLR1C, ATP6V1G1, PDZD7, LSM2, PLK4, ZNF259, MAN2A2, SLC51A, SYN1, PCGF3, TOR4A, PXMP4
6	protein-containing complex (GO:0032991)	66	NDE1, DDX19B, EPRS, AES, PRPSAP2, GSPT1, TOP1MT, RAD51C, MRPS17, GINS2, RANBP17, RPS7, TCTN2, EXOC7, ACTC1, NUP210L, RBL1, GINS4, RPL13A, VAMP1, APOA5, TCTN1, RXRA, ATXN7L3, THRA, DCAF8, RPL11, CTC1, SEPT9, PPP4R2, RPS3, CWF19L1, XAB2, TACR2, PDLIM4, WDTC1, VPS51, PABPC4L, BTBD2, PRPF6, MAGOH, FBF1, CELF3, TRA2A, SPEF1, DRC1, SAE1, RAMP1, MCCC2, ERCC8, SUPT7L, DCTN4, E2F4, MZB1, GINS1, HSPA7, USH1C, POLR1C, TRPC3, ATP6V1G1, PDZD7, LSM2, GNAI2, SHANK2, MAEA, PCGF3
7	membrane part (GO:0044425)	41	HAS1, SEMA4B, TCTN2, ELOVL3, HTR5A, EPS8L1, VAMP1, TCTN1, LYNX1, F2R, SLC16A3, HTR2A, AQP2, LRFN3, PCDHA5, DYSF, TACR2, ACER3, ADCY7, P2RX1, FBF1, SPEF1, SLC35A1, DRC1, IFNLR1, KCNH2, FGR, ZAP70, GPR35, SLC10A2, SSTR3, USH1C, RHBDF1, TRPC3, ATP6V1G1, PDZD7, ZNF259, SLC51A, HOMER3, GNAI2, SHANK2
8	extracellular region part (GO:0044421)	22	CASK, CTSZ, C2orf40, SEMA4B, DBP, LHB, APOA5, PRSS33, DMKN, TGM2, CLUL1, F10, WNT5B, CLEC11A, PLTP, COLEC11, NPPB, PSAP, HSPA7, PGF, SPON2, CGB7
9	**extracellular region (GO:0005576)**	22	CASK, CTSZ, C2orf40, SEMA4B, DBP, LHB, APOA5, PRSS33, DMKN, TGM2, CLUL1, F10, WNT5B, CLEC11A, PLTP, COLEC11, NPPB, PSAP, HSPA7, PGF, SPON2, CGB7

10	membrane-enclosed lumen (GO:0031974)	15	SYCP2L, TOP1MT, MRPS17, GINS2, RPS7, GINS4, ATXN7L3, CTC1, ZNF497, SUPT7L, SIRT6, GINS1, POLR1C, ZNF259, TOR4A
11	supramolecular complex (GO:0099080)	9	TRIP6, TACR2, PDLIM4, TUBA8, SPEF1, DRC1, FHL2, USH1C, PDZD7
12	synapse part (GO:0044456)	4	LRFN3, SYN1, HOMER3, SHANK2
13	synapse (GO:0045202)	4	LRFN3, SYN1, HOMER3, SHANK2
14	cell junction (GO:0030054)	3	TRIP6, PDLIM4, C19orf35

Supplementary Table 6. PANTHER Cellular Components classifying the genes associated with differentially methylated promoters between the non-diseased aortic and mitral valve tissue. Cellular components of interest are indicated in bold. The methylation direction of the cellular components' constituent genes can be found in **Supplementary Table 1.**

2.7 Table S7. Node characteristics of the network with the minimum interactions constructed for genes associated with differentially methylated promoters between non-diseased aortic and mitral valve tissue

Node No.	Gene Name	Degree	Betweenness Centrality	Meth.diff
1	UBC	200	129377.98	0
2	SMAD3	75	27152.04	10.24797714
3	UBL4A	50	13019.92	13.04122333
4	RPS3	50	9508.1	13.123899
5	RXRA	47	12661.72	12.61173363
6	SH3KBP1	44	13005.65	-27.60149769
7	APP	42	12097.08	0
8	HNF4A	40	10699.51	0
9	MAGOH	39	7183.66	-11.78014905
10	RPL11	36	3977.57	-18.82135283
11	RBL1	30	7986.23	22.97564187
12	RPS7	30	4608.25	-31.77081637
13	SUMO2	28	5688.95	0
14	TRIP6	27	7374.14	-13.50530214
15	STAU1	27	6396.77	13.74715119
16	TGM2	27	5622.28	23.42375367
17	TAB1	26	5178.21	17.01310089
18	LDHA	25	5515.63	14.12136251
19	FHL2	24	4672.28	20.21376557
20	KRT8	23	5003.67	11.90578465
21	TRA2A	23	4523	23.11952934
22	ELAVL1	23	3646.08	0
23	E2F4	22	4251.37	-10.91575092
24	UBE4B	22	3845.25	14.3513937

25	LCP2	22	2710.17	-24.21052632
26	PRPF6	21	2211.77	22.4137931
27	GSTK1	20	4185.53	-15.25840084
28	ZAP70	20	3991.93	12.89194545
29	CD44	20	2575.69	-23.95740905
30	SHBG	20	2503.5	26.40496882
31	HSP90AA1	20	2310.66	0
32	BCL3	20	2209.78	-22.21153846
33	CASP7	19	2658.38	12.29277823
34	UNK	19	1253.48	-15.14692026
35	BRCA2	18	5519.91	16.35676628
36	ESR1	18	1911.01	0
37	FN1	18	1677.57	0
38	EGR1	17	3430.25	0
39	NMI	17	3321.82	11.66389975
40	GRB2	17	3228.05	0
41	GSPT1	17	2911.37	12.36027239
42	THRA	17	2613.06	13.74375284
43	TP53	17	2571.84	0
44	HSP90AB1	17	1488.24	0
45	IPO4	16	3055.36	12.19300654
46	GANAB	16	2848.85	-14.01992187
47	GFAP	16	2705.77	-11.3620941
48	PDCD6	16	2563.05	13.54642314
49	ACTC1	16	2450.25	11.2347351
50	MYC	16	1993.41	0
51	LEO1	15	3282.64	14.16123089
52	BTBD2	15	2126.7	14.78212999

53	CUL3	15	1028.75	0
54	GNAI2	14	3677.97	16.04330204
55	LSM2	14	3531.09	-11.79832117
56	ATP6V1F	14	2229.8	11.53754185
57	NGFR	14	2192.03	-10.69046155
58	PAK6	14	1982.42	-25.30567215
59	TRIM2	14	1483.96	-22.52276867
60	SUMO1	14	1142.11	0
61	CAND1	14	991.97	0
62	YWHAZ	14	893.51	0
63	COPS5	14	860.52	0
64	TJP2	13	3141.78	14.3216432
65	FGR	13	3049.4	10.6788552
66	RGS14	13	2147.7	11.14789411
67	FBF1	13	1936.35	12.48030734
68	SP1	13	1690.29	0
69	YWHAQ	13	1649.32	0
70	POLR1C	13	1534.29	10.54313099
71	DYRK1B	13	1401.02	15.87205316
72	CDK2	13	1302.1	0
73	SHANK2	13	1106.01	16.65018901
74	RPL13A	13	1010.94	-11.81580267
75	EP300	13	954.41	0
76	XAB2	13	897.97	-17.19454457
77	FLOT2	12	2935.56	-10.19283747
78	CDC6	12	2482.34	10.7300885
79	DNM1L	12	2287.39	11.23387061
80	DCAF8	12	2209.18	12.21130221

81	KALRN	12	2184.4	-11.43568841
82	CCP110	12	1951.26	13.90348395
83	SRC	12	1451.86	0
84	SUPT7L	12	1368.89	-11.85426244
85	HSPA4	12	1217.56	0
86	SRPK3	12	1065.38	13.3665988
87	PACSIN1	12	683.47	13.28454478
88	TRAF6	12	597.06	0
89	PHYHIP	12	511.72	-18.61342387
90	CASK	11	2525.78	16.94493884
91	PSAP	11	1765.43	-20.44239631
92	UBOX5	11	1709.49	-17.30249467
93	ABLIM1	11	1655.14	-26.26418989
94	CUL1	11	1408.23	0
95	CORO1B	11	1264.69	-16.60028824
96	DDX19B	11	1243.98	-10.47878223
97	LIMK1	11	1241.28	19.58291321
98	RELA	11	904.57	0
99	ERCC8	11	694.93	-12.28840789
100	SYN1	11	559.06	-11.53911922
101	IKBKG	11	384.9	0
102	TERF1	10	1628.49	0
103	MID2	10	1534.37	-15.72362855
104	L3MBTL1	10	1511.63	-10.3180913

105	CRK	10	1436.3	0
106	NOS1	10	1409.8	17.85714286
107	SAE1	10	1222.72	-19.13422885
108	HNF1A	10	1184.5	0
109	AMBP	10	1042.72	-20.23057429
110	CCAR1	10	1029.58	-10.18921065
111	EGFR	10	748.01	0
112	HDAC1	10	665.78	0
113	TAF8	10	408.11	10.96999406
114	COPS6	10	320.69	0
115	DDR1	9	1422.88	24.41290323
116	POT1	9	1169.22	0
117	SIRT6	9	1026.3	-25.16339869
118	GINS4	9	1015.21	-20.5911083
119	PPIE	9	935.05	13.61707009
120	NCOA4	9	905.8	-11.32027902
121	KCNH2	9	808.38	11.70187061
122	SMAD2	9	596.67	0
123	ILF3	9	589.33	0
124	CDK2AP1	9	493.8	-11.02325581
125	UBD	9	448.23	0
126	F10	8	3153.89	-13.17388003
127	MATK	8	1516.76	-27.08355414
128	PIH1D1	8	1361.59	-20.13082734
129	IBTK	8	1359.57	-10.80118972
130	HOMER3	8	1335.1	10.61532606

131	MRPL15	8	1332.61	11.08810785
132	VIM	8	1025.24	0
133	PIK3R1	8	553.07	0
134	SRRM2	8	380.99	0
135	UBE2D1	8	333.14	0
136	AR	8	278.68	0
137	MDK	8	224.34	18.33024119
138	HNRNPM	8	223.57	0
139	CUL4B	8	216.39	0
140	MDM2	8	215.1	0
141	NR2F2	7	1130.92	12.30783391
142	CBL	7	1068.57	0
143	RGS3	7	873.05	14.64135021
144	F2R	7	857.33	-10.04558482
145	PHACTR4	7	803.49	14.90112994
146	DYSF	7	786.99	-12.68664758
147	GINS2	7	754.36	-13.763999
148	ATXN7L3	7	732.5	13.65551171
149	YWHAG	7	694.84	0
150	TRAF2	7	615.02	0
151	SUMO3	7	589.3	0
152	PRKCSH	7	581.72	-21.01236017
153	ACTB	7	544.31	0
154	CTNNB1	7	530.79	0
155	FOS	7	517.91	0
156	SRPK2	7	487.24	0
157	UBQLN4	7	424	0
158	HSPA8	7	421.13	0
159	EEF1A1	7	386.96	0

160	FOXH1	7	375.26	-10.93239444
161	VCP	7	341.28	0
162	AKT1	7	339.31	0
163	STAT3	7	310.52	0
164	RPL3	7	276.53	0
165	PDCD6IP	7	250.59	0
166	CSNK2B	7	227.98	0
167	TMEM177	7	161.12	10.7813703
168	IGBP1	7	150.13	0
169	EIF4A3	7	41.66	0
170	EXOC7	6	1478.4	14.00485374
171	SSTR3	6	1124.27	13.69205298
172	PPP4R2	6	953.08	14.40733332
173	PAK2	6	898.28	0
174	AP1M2	6	874.97	17.43690472
175	CALM3	6	771.71	0
176	TNFRSF10C	6	681.73	16.42309636
177	ARL4D	6	637.28	-12.23162088
178	NR3C1	6	570.79	0
179	CDC42	6	494.77	0
180	ARL6IP4	6	469.72	12.77897455
181	CDK1	6	430.89	0
182	HNRNPU	6	423.97	0
183	CDKN1A	6	398.58	0
184	NCL	6	357.5	0
185	SNRPD2	6	344.53	0
186	PCGF3	6	334.9	12.46448229
187	GSK3B	6	320.48	0
188	HSPA1A	6	302.53	0
189	SRPK1	6	294.44	0
190	LCK	6	282.32	0

191	SIMC1	6	261.89	-12.69516375
192	VHL	6	251.74	0
193	NQO1	6	246.16	15.32276203
194	SQSTM1	6	175.25	0
195	ZNF689	6	161.7	10.64866543
196	XRCC6	6	154.24	0
197	DNAJA1	6	153.49	0
198	CDKN2A	6	147.86	0
199	VPS26A	6	144.31	0
200	UBE2C	6	116.54	0
201	HIST1H3H	6	111.91	0
202	SAP18	6	111.37	0
203	RB1	6	95.44	0
204	NEDD8	6	82.63	0
205	LNX1	5	1319.28	0
206	ATP6V1G1	5	1274.25	-14.97846937
207	WDR73	5	1268.08	17.49580981
208	PAX7	5	875.36	-11.79847495
209	PPP1CA	5	867.36	0
210	DBP	5	853.36	-18.88432179
211	SIPA1L1	5	851.03	-15.64637198
212	ATXN1	5	806.13	0
213	VAV2	5	739.58	0
214	PLK4	5	727.84	19.9696697
215	SETX	5	716.24	-11.80237604
216	VPS51	5	635.08	18.47006129
217	MYL2	5	606.7	11.13942483
218	KAT2A	5	596.52	0

219	MCCC2	5	563.68	10.53041743
220	UBR7	5	523.68	-11.11563381
221	SERF2	5	494.32	10.78098472
222	CEBPB	5	474.99	0
223	CMBL	5	384.49	10.2980713
224	PABPC1	5	378.31	0
225	PRPSAP2	5	345.91	-21.99777613
226	SIRT1	5	328.8	0
227	CDC5L	5	305.07	0
228	SNRNP70	5	285.82	0
229	KPNA2	5	267.04	0
230	EPB49	5	265.22	-20.3026714
231	EPS8L1	5	258.04	-13.76208018
232	PPP1CC	5	257.96	0
233	NFKB1	5	250.06	0
234	EIF6	5	243.42	0
235	AOX1	5	220.72	-17.84657214
236	DCAF4	5	218.38	-11.40170693
237	APOA1	5	214.64	0
238	MAPK1	5	198.3	0
239	RUSC1	5	195.3	-18.98785425
240	NCOA6	5	187.89	0
241	SF3A1	5	178.37	0
242	ETS1	5	155.66	0
243	NDRG1	5	145.49	0
244	MAPK6	5	144.79	0
245	UBE2D3	5	144.45	0
246	POLR2A	5	141.49	0

247	HAS1	5	133.29	-22.15357458
248	RPL18A	5	131.04	0
249	PCK2	5	124.7	18.05555556
250	UBE2D2	5	110.68	0
251	PLCG1	5	110.03	0
252	SFN	5	109.1	0
253	CUL2	5	103.49	0
254	MCM7	5	102.38	0
255	UPF1	5	98.98	0
256	NPPB	5	84.04	15.58047344
257	SHC1	5	83.64	0
258	CD2BP2	5	78.99	0
259	YWHAE	5	77.94	0
260	PRPF19	5	77.68	0
261	APOA5	5	70.59	15.3011658
262	CELF3	5	69.72	22.17164279
263	RPL5	5	54.06	0
264	MDFI	4	1244.06	0
265	ABCD1	4	1185.35	-11.45628411
266	TINF2	4	851.11	0
267	CREBBP	4	777.6	0
268	TJP1	4	754.95	0
269	SH3GL2	4	750.43	0
270	USHBP1	4	606.42	0
271	ARHGAP27	4	546.59	-13.74946375
272	CHD3	4	467.89	0
273	TRIM63	4	439.79	0
274	RAD51C	4	416.17	-13.02061055

275	COASY	4	408.87	-19.27691347
276	SERTAD1	4	397.25	0
277	KRT73	4	393.93	15.59735114
278	RAC1	4	386.86	0
279	PCP4	4	377.3	25.13227513
280	ISG20	4	361.3	26.67956769
281	SPTBN1	4	335.27	0
282	IRAK1	4	334.02	0
283	USH1C	4	333.41	-15.09568525
284	PNPO	4	324.26	16.87888199
285	KIR2DL4	4	318	13.07364836
286	KPNB1	4	306.7	0
287	HDAC4	4	288.64	0
288	DCTN4	4	288.61	17.75735843
289	FAS	4	281.11	0
290	CARHSP1	4	275.38	11.42265952
291	HNRNPF	4	233.89	0
292	UCHL3	4	232.26	0
293	ATP5A1	4	228.57	0
294	MAN2A2	4	218.82	23.64103121
295	RAP1A	4	210.46	0
296	CEBPA	4	204.33	0
297	DYRK1A	4	196.04	0
298	CTTN	4	187.42	0
299	TUBA8	4	178.75	10.36429324
300	PDE4A	4	170.26	-18.65566534
301	DYNLL1	4	165.69	0
302	DLG4	4	163.57	0
303	WAS	4	161.37	0
304	TUBA1A	4	160.61	0

305	USP9X	4	160.23	0
306	ANXA7	4	156.59	0
307	TBP	4	156.27	0
308	CYP2E1	4	146.81	17.71943624
309	HIST3H3	4	141.66	0
310	PMEPA1	4	137.81	-31.01662309
311	C14orf1	4	136.62	0
312	PRMT5	4	132.46	0
313	EPS15	4	132.22	0
314	DSTN	4	132.22	0
315	TUBB	4	121.22	0
316	TRADD	4	118.93	0
317	NEDD4L	4	118.54	0
318	BIRC3	4	114.71	0
319	A2M	4	110.68	0
320	ALB	4	107.86	0
321	CSF3	4	105.46	-30.7312253
322	PTPN6	4	102.62	0
323	KAT5	4	100.34	0
324	PTN	4	96.22	0
325	TERF2IP	4	94.03	0
326	ANPEP	4	92.81	-17.30523014
327	VDR	4	86.67	0
328	UBE2E1	4	83.66	0
329	TSR1	4	81.94	0
330	UBE2E2	4	81.87	0
331	PAICS	4	78.19	0
332	BARD1	4	69.17	0
333	LYN	4	68.93	0
334	PA2G4	4	67.26	0

335	PARK2	4	54.47	0
336	SNRPB	4	51.21	0
337	GAPDH	4	46.32	0
338	NCK1	4	41.55	0
339	HDAC11	4	33.84	0
340	SNRPA1	4	31.73	0
341	CAV1	4	25.56	0
342	PHB	3	2155.43	0
343	PDLIM4	3	934.03	12.58184713
344	VKORC1L1	3	879.41	12.57696127
345	CEBPD	3	734.72	0
346	CDK5RAP3	3	726.39	0
347	CCNA1	3	723.84	0
348	PITX3	3	721.55	0
349	PSMA1	3	664.09	0
350	NFYC	3	562.25	0
351	ACTG1	3	378.63	0
352	KRT83	3	307.1	-17.00700701
353	MT1A	3	285.52	-15.95382168
354	FASLG	3	279.88	0
355	MAEA	3	260.22	11.85714286
356	CTSZ	3	256.47	12.42827198
357	PCBP1	3	244.35	0
358	HIF1A	3	233.68	0
359	PEX5	3	232.76	0
360	FGD1	3	224.66	13.42414861
361	PPARA	3	182.11	0
362	IKBKB	3	175.61	0
363	KCNAB3	3	174.83	10.49174661
364	GFI1B	3	167.23	0
365	JUN	3	157.82	0

366	USF1	3	155.97	0
367	NIPSNAP1	3	148.79	-12.78946721
368	ACD	3	148.07	0
369	ONECUT1	3	140.97	0
370	HTR2A	3	139.58	-10.23484608
371	APOE	3	138.36	0
372	NR1H4	3	132.46	0
373	ADCY7	3	129.99	22.55754476
374	UBA52	3	129.76	0
375	ZKSCAN5	3	127.15	-22.36495829
376	DNM2	3	114.32	0
377	TUBGCP4	3	106.81	0
378	WDTC1	3	105.47	13.3971831
379	PLAT	3	100.03	0
380	ATL3	3	96.94	-11.56622611
381	WASL	3	96.62	0
382	TUBA3D	3	92.18	0
383	ZBTB16	3	92.04	0
384	DTNBP1	3	90.34	0
385	TCF21	3	87.78	-14.31752365
386	UBE2E3	3	87.61	0
387	CREB1	3	87.39	0
388	MYD88	3	86.41	0
389	HDAC6	3	85.9	0
390	TAF1	3	83.11	0
391	POM121	3	81.98	0
392	TCF12	3	76.27	0
393	SCRIB	3	72.9	0

394	TLE1	3	71.55	0
395	DDX1	3	71.13	0
396	STAM2	3	70.75	0
397	RPL22L1	3	70.52	-18.77380205
398	TAF7	3	66.36	0
399	XPO1	3	65.95	0
400	ESR2	3	65.79	0
401	MIIP	3	63.54	23.46419997
402	APEH	3	62.42	0
403	TNFRSF1A	3	62.32	0
404	MAP3K3	3	58.88	0
405	G2E3	3	56.48	12.05819958
406	HERC6	3	56.48	-22.48307525
407	THOC5	3	56.2	0
408	SPOCD1	3	55.08	-12.60432378
409	EWSR1	3	54.37	0
410	NFKBIB	3	54.27	0
411	SRF	3	54.22	0
412	TSC22D4	3	52.47	0
413	ACTA2	3	52.12	0
414	ZFYVE19	3	51.42	0
415	SRSF3	3	50.36	0
416	MLH1	3	49.03	0
417	FLOT1	3	48.54	0
418	UBE2K	3	48.17	0
419	UBE2B	3	46.78	0
420	TAF9	3	46.17	0
421	GPR39	3	45.05	18.21648984
422	UBE2H	3	44.09	0
423	HOXA9	3	43.82	0

424	BIRC2	3	43.4	0
425	TAF10	3	42.59	0
426	DHX30	3	39.93	0
427	USP7	3	39.76	0
428	UBXN1	3	39.61	0
429	SNAPIN	3	39.41	0
430	ZNF408	3	39.17	0
431	TTR	3	38.99	0
432	MYO15A	3	38.95	11.24751826
433	SNCA	3	36.99	0
434	MED1	3	36.52	0
435	TYSND1	3	34.79	11.1003409
436	XIAP	3	31.47	0
437	CIAO1	3	31.1	0
438	XPO7	3	30.88	0
439	ATP6V1B2	3	29.95	0
440	GNA11	3	27.82	0
441	GOLGA2	3	27.62	0
442	MYL12A	3	27.55	0
443	TRPC3	3	27.35	-10.14567874
444	HAMP	3	27.01	28.14538677
445	CRH	3	26.79	10.87427493
446	MLL	3	24.54	0
447	CRMP1	3	24	0
448	COL5A3	3	22.61	16.65572874
449	UBA2	3	21.82	0
450	PSEN1	3	21.51	0
451	IQGAP1	3	21.28	0
452	NFKBIA	3	21.03	0
453	IQSEC1	3	20.55	-15.25651229

454	CDH1	3	19.53	0
455	TSC22D1	3	19.01	0
456	ERBB2	3	18.55	0
457	ARF6	3	18.52	0
458	GNB2L1	3	16.91	0
459	FAM131B	3	16.38	-14.52636895
460	NFKB2	3	14.78	0
461	COPS2	3	14.56	0
462	GNAI1	3	11.56	0
463	PLTP	3	4.85	-21.9858156
464	RNPS1	3	3.09	0
465	GINS1	3	0	-16.24493927
466	DPP6	2	1424	-13.39739856
467	PPP1R16A	2	715.25	0
468	NAA38	2	713	0
469	KCND2	2	713	0
470	SPP1	2	713	0
471	RPA2	2	713	0
472	VEGFA	2	713	0
473	CKAP4	2	434.88	0
474	VAMP2	2	376.73	0
475	USP13	2	360.76	0
476	SCP2	2	306.92	0
477	MT1F	2	302.81	17.07041344
478	SOS1	2	292.99	0
479	IRF7	2	281.26	0
480	WDR61	2	270.77	0
481	ITPR3	2	267.8	0
482	ACOX1	2	256.05	0
483	SLC10A2	2	223.77	19.11392405

484	TMCO7	2	216.34	-24.19205701
485	RND3	2	212.37	0
486	MRPS17	2	184.23	-15.89559927
487	GATA4	2	173.97	0
488	UBA1	2	170.92	0
489	CD3E	2	167.88	0
490	PNMT	2	167.2	14.99975986
491	FGD3	2	151.81	-27.32594937
492	EPS8	2	147.19	0
493	RBPMS	2	131.62	0
494	PALM	2	126.8	11.65543558
495	VKORC1	2	126.15	0
496	RHOXF2	2	123.47	0
497	HSD3B7	2	120.05	14.91576912
498	RANBP17	2	120.05	10.46476762
499	ABI1	2	115.87	0
500	PSMC5	2	103.8	0
501	USF2	2	103.13	0
502	IQCB1	2	101.25	0
503	PAX6	2	97.08	0
504	GIT1	2	96.89	0
505	TRPC4	2	90.85	0
506	MZB1	2	88.99	14.09249831
507	TRIM28	2	83.34	0
508	FAIM2	2	81.99	15.48509588
509	NFYB	2	81.42	0
510	TAF6	2	81.25	0
511	TMEM102	2	80.16	13.90491422
512	NMNAT1	2	80.03	0
513	DDIT3	2	76.92	0

514	SPINT2	2	72.78	-12.57339571
515	11-Sep	2	72.47	0
516	VAMP1	2	72.09	12.39162089
517	TTC38	2	72.09	14.57203134
518	ZNF586	2	72.09	14.64212077
519	CWF19L1	2	72.09	-17.88451309
520	TPM4	2	69.4	0
521	RGMA	2	67.92	24.28750772
522	GNB1	2	64.61	0
523	NFATC3	2	60.46	0
524	SLC25A3	2	59.18	0
525	DHRS3	2	56.7	11.88140956
526	TCTN2	2	56.7	-19.74948079
527	ANGEL2	2	56.7	-10.22966507
528	ATXN7	2	55	0
529	ZNF44	2	53.98	21.20105498
530	GJB5	2	53.89	0
531	YBX1	2	53.63	0
532	STAM	2	52.77	0
533	ITPRIPL1	2	52.72	-12.72555503
534	CYB5R1	2	52.72	-10.71956022
535	GK	2	48.49	0
536	ASAP1	2	47.46	0
537	ERBB2IP	2	44.68	0
538	CTSB	2	44.06	0
539	ZNF385A	2	41.81	-15.13931889
540	RARA	2	40.84	0
541	SMAD7	2	40.24	0

542	S100A9	2	39.8	0
543	TUBB2B	2	39.49	0
544	ENO3	2	38.24	0
545	PACSIN2	2	37.25	0
546	SORD	2	36.92	0
547	FAM90A1	2	33.53	19.62301587
548	NUDT7	2	33.21	-13.02141011
549	CBX5	2	33.19	0
550	UBB	2	31.94	0
551	ZFYVE28	2	31.94	11.95305224
552	PRKD2	2	31.89	0
553	ACER3	2	31.81	12.32267585
554	KAT7	2	31.68	0
555	SMARCAD1	2	31.2	0
556	TMEM101	2	31.09	-19.31227782
557	UBE2O	2	30.76	0
558	APEX1	2	30.69	0
559	RGS9	2	30.33	14.68599225
560	ABCA1	2	30.23	0
561	TNNT1	2	30.21	0
562	CRKL	2	27.95	0
563	CACNA1A	2	27.26	0
564	PLA2G4A	2	27.01	0
565	DMKN	2	26.83	-14.03125067
566	CARS	2	26.73	0
567	HSD17B14	2	26.07	12.72055505
568	ZMYM1	2	25.96	14.52109141
569	LRSAM1	2	25.89	0
570	STAT5A	2	25.73	0
571	SH3GL1	2	24.28	0

572	DYNLL2	2	24.16	0
573	NLK	2	23.68	0
574	NFE2	2	23.21	0
575	LSM4	2	23.2	0
576	MED8	2	22.46	0
577	CD320	2	22.43	0
578	PLEKHG5	2	21.25	10.63829787
579	FUCA2	2	21.23	11.09652771
580	TRIM29	2	21.2	0
581	TOLLIP	2	20.98	0
582	RCHY1	2	20.77	0
583	CPSF3	2	20.31	0
584	USP6	2	19.77	0
585	CEBPE	2	19.41	0
586	PYGL	2	19.11	0
587	PSPC1	2	19.11	0
588	CTSD	2	18.95	0
589	SIRT3	2	18.53	0
590	SUPT5H	2	18.13	0
591	QKI	2	17.42	0
592	BCL2L11	2	17.2	0
593	NEK3	2	16.37	11.21173141
594	SNX2	2	16.14	0
595	ARHGEF7	2	16.05	0
596	TRIP11	2	15.79	0
597	PTBP1	2	15.76	0
598	GRAP2	2	15.6	0
599	NCK2	2	15.17	0
600	MPDZ	2	15.1	0
601	FANCD2	2	14.59	0
602	BTK	2	14.53	0
603	MYCN	2	14.5	0

604	CDK2AP2	2	13.24	0
605	BRF2	2	13.2	0
606	ITK	2	13.1	0
607	ZNF143	2	12.72	0
608	CBLB	2	12.53	0
609	ATXN2	2	11.98	0
610	PTPN11	2	11.79	0
611	PROCR	2	10.81	0
612	KRT38	2	10.72	18.20971867
613	PLAUR	2	10.61	0
614	TFEB	2	10.57	10.3831553
615	DNAJC4	2	10.52	-18.48648649
616	AKR1B1	2	10.36	0
617	CCDC85B	2	10.16	0
618	RAF1	2	10	0
619	BEGAIN	2	9.8	0
620	POLA1	2	9.33	0
621	POLR1D	2	8.66	0
622	TCF3	2	7.61	0
623	PINX1	2	7.48	0
624	MCM4	2	7.2	0
625	ATP6V1E1	2	7.05	0
626	CEP76	2	6.81	0
627	CHEK2	2	6.56	0
628	UBE2L3	2	6.17	0
629	NDE1	2	5.91	-10.83774474
630	RAD51	2	5.5	0
631	PUF60	2	4.99	0
632	ETF1	2	4.65	0
633	TRIM55	2	4.63	0

634	AHSA1	2	4.45	0
635	PTP4A3	2	3.96	0
636	FKBP8	2	3.03	0
637	ARHGEF25	2	2.5	-18.98496241
638	AP2B1	2	2.24	0
639	UBE2I	2	2.19	0
640	SLFN12L	2	1.96	-17.45401338
641	RPS6KL1	2	0.3	-15.46579445
642	TBR1	2	0	-13.0460917
643	FABP6	2	0	14.57521178
644	SLC12A6	2	0	-19.50497788
645	ZNF707	1	0	-10.50522846
646	WNT5B	1	0	-14.11333659
647	PGF	1	0	17.06009966
648	SPRYD4	1	0	15.09637188
649	P2RX1	1	0	-11.26171279
650	SEMA4B	1	0	14.38911013
651	UCKL1	1	0	-11.80669064
652	PBX4	1	0	-18.83535088
653	IGSF22	1	0	11.53846154
654	SLC7A8	1	0	-40.74363992
655	AQP2	1	0	-21.13402062
656	RCCD1	1	0	-19.09976674
657	TOP1MT	1	0	15.78471484

658	NRGN	1	0	-19.32741357
659	IBA57	1	0	11.57785584
660	OSBPL1A	1	0	10.37672439
661	LRRC6	1	0	-16.12932196
662	TMEM176B	1	0	-13.26311973
663	ENPEP	1	0	15.28656529
664	SLC17A9	1	0	18.99396593
665	PLIN4	1	0	-10.44036895
666	SUSD3	1	0	13.07512479
667	KCNIP2	1	0	-12.92603632
668	FGFBP2	1	0	-17.30638201
669	SYCP2L	1	0	-15.29411765
670	TBC1D10C	1	0	20.51867862
671	PRSS33	1	0	-11.21960356
672	PLBD2	1	0	-17.45553827
673	IL28RA	1	0	-13.28182049
674	SLC51A	1	0	14.35946769
675	SPA17	1	0	14.3130227
676	PCDHA5	1	0	-18.60317124
677	GJD3	1	0	10.64665127
678	C6orf170	1	0	-41.28076063
679	CDH4	1	0	10.00650699
680	KLHDC9	1	0	-10.41534165

681	ALS2CL	1	0	10.70251436
682	SLC16A3	1	0	13.40507788
683	TOR4A	1	0	-10.1031555
684	SLC6A8	1	0	11.05676882
685	HOXB3	1	0	-14.3977591
686	SYCP1	1	0	14.50739668
687	SLC35A1	1	0	12.37947316
688	FAM102A	1	0	-16.0597161
689	ZSWIM3	1	0	10.1334111
690	AP1S3	1	0	-10.95702069
691	COLEC11	1	0	14.12857674
692	REM2	1	0	-25.01960784
693	GAS2L2	1	0	17.50334033
694	ACSL5	1	0	-16.80434783
695	PXMP4	1	0	-10.51601631
696	ZNF551	1	0	17.70154374
697	NUDT22	1	0	-11.98311417
698	CLEC11A	1	0	-24.72385967
699	GRTP1	1	0	-11.84194818
700	SLC2A10	1	0	-17.92462066
701	ZNF597	1	0	10.88286327
702	NUP210L	1	0	-14.65801887
703	ZNF354C	1	0	-17.16573796
704	MYO7B	1	0	-12.89716112

705	LDLRAD4	1	0	-10.46176976
706	GSTO2	1	0	10.83863537
707	ASAH2B	1	0	15.99460916
708	CTC1	1	0	-17.32804233
709	SERHL2	1	0	-11.04450096
710	C2orf50	1	0	-10.14194139
711	C2orf68	1	0	-18.20188872
712	IQCA1	1	0	-15.98734108
713	DNAAF3	1	0	-14.74512147
714	RHBDF1	1	0	10.29470688
715	ACRBP	1	0	10.31926174

Supplementary Table 7. Node characteristics of the minimum PPI network (**Figure 4A**) constructed based on the genes associated with differentially methylated promoters between non-diseased aortic and mitral valve tissue. Each node represents a gene. Degree refers to the number of connections/edges/PPIs that a node has to other nodes and betweenness centrality reflects the number of shortest paths passing through a node (2).

2.8 Table S8. List of enriched pathways in the network constructed upon the genes associated with the differentially methylated hyo- and hypermethylated promoters between the non-diseased aortic and mitral valve tissue based on the Reactome pathway database (selected results)

Reactome Pathway	**Total**	**Expected**	**Hits**	**P.Value**	**FDR**	**Seed genes**	**Other genes**
Immune System	1140	67.8	125	2.73E-13	3.82E-10	CD44, AP1M2, ZAP70, TAB1, LIMK1, LCP2, SH3KBP1, ISG20, FGR, DCTN4, OSBPL1A, AP1S3, KIR2DL4, ADCY7, UBOX5, PRKCSH	ZBTB16, TRAF6, YWHAZ, DYNLL1, POM121, AP2B1, GRAP2, PSMA1, NFKBIB, IKBKG, MAP3K3, NFKB2, CDH1, MDM2, CREBBP, RELA, NFKBIA, EIF4A3, ACTB, STAT5A, STAT3, WAS, CBLB, RAF1, CRK, CTSB, ERBB2, EGFR, HSP90AA1, SQSTM1, MYD88, TOLLIP, PIK3R1, CDK1, FOS, NFKB1, AKT1, GRB2, NCK1, SRC, MAPK1, CDKN1A, APP, UBE2H, UBE2E2, UBE2K, UBE2L3, UBE2E1, UBE2E3, UBE2B, EP300, PTPN6, PARK2, ABI1, IKBKB, EGR1, CBL, SH3GL2, SOS1, RAC1, CDC42, CUL1, SUMO1, TUBA1A, GSK3B, UBE2D3, UBE2D2, WASL, CRKL, RCHY1, CUL3, CUL2, NEDD4L, SHC1, UBE2C, UBA1, PAK2, UBE2D1, UBA52, LCK, HSP90AB1,

							LRSAM1, TRAF2, TUBB2B, VAV2, RAP1A, LYN, ITPR3, TRIM63, JUN, CREB1, CD3E, PLCG1, ACTG1, PSMC5, KPNB1, KPNA2, VHL, BIRC2, ITK, BTK, PTPN11, IRAK1, BIRC3, IRF7, DNM2, CTSD, DYNLL2, UBE2O
Signaling by Interleukins	116	6.91	29	1.68E-11	7.86E-09	TAB1	TRAF6, YWHAZ, IKBKG, MAP3K3, STAT5A, STAT3, RAF1, CRK, SQSTM1, MYD88, TOLLIP, PIK3R1, CDK1, NFKB1, GRB2, MAPK1, PTPN6, IKBKB, CBL, SOS1, CUL1, CRKL, SHC1, UBA52, LCK, LYN, PTPN11, IRAK1
Developmental Biology	417	24.9	55	1.05E-08	1.05E-06	RXRA, ABLIM1, SMAD3, LIMK1, TRPC3, FOXH1, COL5A3, CDH4, RGMA	CRMP1, AP2B1, CREBBP, ACTB, SMAD2, RAF1, ERBB2, EGFR, HSP90AA1, MED1, CTNNB1, CDK1, TCF12, AKT1, GRB2, NCK1, SRC, MAPK1, HNF4A, EP300, SPTBN1, DLG4, SH3GL2, TRPC4, SOS1, RAC1, CDC42, TUBA1A, GSK3B, WASL, ONECUT1, PAK2, HSP90AB1, MED8, TUBB2B, CSNK2B, VAV2, CEBPB, TCF3, CREB1, PLCG1,

							CEBPD, ACTG1, NCK2, PTPN11, DNM2
Apoptosis	158	9.42	28	1.42E-07	8.66E-06	TJP2, DNM1L, CASP7	VIM, YWHAQ, YWHAZ, YWHAG, DYNLL1, PSMA1, TNFRSF1A, TRADD, CDH1, CTNNB1, AKT1, YWHAE, TJP1, BCL2L11, PAK2, UBA52, TRAF2, SFN, FASLG, FAS, PSMC5, KPNB1, BIRC2, XIAP, DYNLL2
Signaling by TGF-beta Receptor Complex	70	4.17	17	4.55E-07	2.06E-05	RBL1, SMAD3, PMEPA1, E2F4	MYC, SMAD2, PPP1CA, SMAD7, SP1, UBE2D3, XPO1, NEDD4L, HDAC1, PPP1CC, UBE2D1, UBA52, USP9X
Signaling by constitutively active EGFR	19	1.13	9	4.70E-07	2.06E-05	NA	EGFR, HSP90AA1, PIK3R1, GRB2, CBL, SOS1, SHC1, UBA52, PLCG1
Transcriptional activity of SMAD2/SMAD3:SMAD4 heterotrimer	43	2.56	13	6.99E-07	2.72E-05	RBL1, SMAD3, E2F4	MYC, SMAD2, SMAD7, SP1, UBE2D3, NEDD4L, HDAC1, UBE2D1, UBA52, USP9X

Cellular responses to stress	27	1.61	10	1.71E-06	5.09E-05	NA	CREBBP, HIF1A, EP300, UBE2D3, UBE2D2, CUL2, UBE2D1, UBA52, VHL, VEGFA
Cellular response to hypoxia	27	1.61	10	1.71E-06	5.09E-05	NA	CREBBP, HIF1A, EP300, UBE2D3, UBE2D2, CUL2, UBE2D1, UBA52, VHL, VEGFA
Regulation of Hypoxia-inducible Factor (HIF) by Oxygen	27	1.61	10	1.71E-06	5.09E-05	NA	CR+A7:H14EBBP, HIF1A, EP300, UBE2D3, UBE2D2, CUL2, UBE2D1, UBA52, VHL, VEGFA
Interleukin-3, 5 and GM-CSF signaling	51	3.04	13	5.87E-06	0.000151	NA	YWHAZ, STAT5A, CRK, PIK3R1, GRB2, PTPN6, CBL, SOS1, CRKL, SHC1, UBA52, LYN, PTPN11
Signaling by PDGF	189	11.3	28	5.93E-06	0.000151	COL5A3, ADCY7	MDM2, STAT5A, STAT3, RAF1, CRK, ERBB2, EGFR, PIK3R1, CDK1, AKT1, GRB2, NCK1, SRC, MAPK1, CDKN1A, PLAT, SOS1, GSK3B, CRKL, SPP1, LCK, ITPR3, CREB1, PLCG1, NCK2, PTPN11
Interleukin-1 signaling	45	2.68	12	8.12E-06	0.000187	TAB1	TRAF6, IKBKG, MAP3K3, SQSTM1, MYD88, TOLLIP, NFKB1, IKBKB, CUL1, UBA52, IRAK1

mRNA Splicing	115	6.85	20	1.21E-05	0.000249	LSM2, MAGOH, PRPF6, CCAR1	CD2BP2, RNPS1, SNRPB, SNRPA1, CPSF3, HNRNPM, SNRPD2, PCBP1, SF3A1, POLR2A, HNRNPF, HNRNPU, PTBP1, SRSF3, YBX1, SNRNP70
Downregulation of TGF-beta receptor signaling	27	1.61	9	1.55E-05	0.000316	SMAD3, PMEPA1	SMAD2, PPP1CA, SMAD7, XPO1, NEDD4L, PPP1CC, UBA52
NOTCH1 Intracellular Domain Regulates Transcription	50	2.98	12	2.61E-05	0.000515	NA	TLE1, CREBBP, MYC, HIF1A, EP300, HDAC4, KAT2A, CUL1, HDAC6, HDAC1, UBA52, HDAC11
Downregulation of SMAD2/3:SMAD4 transcriptional activity	23	1.37	8	3.29E-05	0.000624	SMAD3	SMAD2, UBE2D3, NEDD4L, HDAC1, UBE2D1, UBA52, USP9X
TGF-beta receptor signaling activates SMADs	30	1.79	9	4.04E-05	0.000736	SMAD3, PMEPA1	SMAD2, PPP1CA, SMAD7, XPO1, NEDD4L, PPP1CC, UBA52
mRNA Processing	140	8.35	21	7.32E-05	0.00125	LSM2, MAGOH, PRPF6, CCAR1	CD2BP2, RNPS1, SNRPB, SNRPA1, CPSF3, HNRNPM, SNRPD2, PCBP1, SF3A1, POLR2A, HNRNPF, HNRNPU, PTBP1, SRSF3, YBX1, SUPT5H, SNRNP70
Signaling by FGFR	162	9.66	22	0.000222	0.00311	ADCY7	MDM2, RAF1, ERBB2, EGFR, PIK3R1, CDK1, AKT1, GRB2, SRC, MAPK1, CDKN1A, CBL, SOS1, GSK3B, SHC1, UBA52, LCK, ITPR3, CREB1, PLCG1, PTPN11

Interleukin-2 signaling	42	2.5	10	0.000133	0.002	NA	STAT5A, RAF1, PIK3R1, CDK1, GRB2, MAPK1, PTPN6, SOS1, SHC1, LCK
SMAD2/SMAD3:SMAD4 heterotrimer regulates transcription	28	1.67	8	0.00016	0.00232	RBL1, SMAD3, E2F4	MYC, SMAD2, SMAD7, SP1, UBA52
Regulation of Lipid Metabolism by Peroxisome proliferator-activated receptor alpha (PPARalpha)	76	4.53	13	0.000482	0.00582	RXRA, APOA5, FHL2	CREBBP, NCOA6, MED1, PPARA, APOA1, SP1, ACOX1, NFYB, NFYC, ABCA1

Supplementary Table 8. List of enriched pathways in the network (**Figure 4A**) constructed upon the genes associated with the differentially methylated hyo- and hypermethylated promoters between the non-diseased aortic and mitral valve tissue based on the Reactome pathway database (selected results). "Total" refers to the total number of genes that belong to the particular Reactome pathway as per the chosen reference list of genes, which is hg19 in our case, "Expected" denotes the number of genes to be expected in our gene list for the particular Reactome pathway, "Hits" describes the number of genes in our list that map to the particular Reactome pathway, "P.Value" is equivalent to the enrichment p-value computed using the hypergeometric test (**see Methods**), FDR stands for false discovery rate, which is the method used to correct the corresponding p-value for multiple testing, "Seed genes" represent genes associated with significantly differentially hyper- and hypomethylated promoters and "Other genes" denote genes that are part of the minimum non-seed genes that are necessarily required to connect the seed genes to construct the network. The methylation direction of the seed genes can be found in **Supplementary Table 1**.

2.9 Table S9. List of enriched biological processes in the network constructed upon the genes associated with the differentially methylated hyo- and hypermethylated promoters between the non-diseased aortic and mitral valve tissue based on the Gene Ontology (GO) Biological Processes database (selected results)

GO_BP	Total	Expected	Hits	P.Value	FDR	Seed genes	Other genes
Epidermal growth factor receptor signaling pathway	167	7.56	38	6.90E-17	9.54E-15	SH3KBP1, ZFYVE28, RHBDF1, ADCY7	AP2B1, MDM2, UBB, RAF1, ERBB2, EGFR, PIK3R1, CDK1, AKT1, GRB2, SRC, MAPK1, APP, UBC, EPS15, CBL, SH3GL2, SOS1, CDC42, GSK3B, SHC1, UBA52, STAM, STAM2, ITPR3, CREB1, FASLG, PLCG1, EPS8, ARHGEF7, NCK2, PTPN11, ERBB2IP, PSEN1
Positive regulation of transcription, DNA_dependent	1260	57	123	6.98E-17	9.54E-15	RXRA, PRPF6, RBL1, TBR1, ABLIM1, SMAD3, DYRK1B, BRCA2, ATXN7L3, MDK, LEO1, THRA, TCF21, NR2F2, FHL2, E2F4, BCL3, NCOA4, CSF3, F2R, FOXH1, PBX4, TAF8,	PAX6, KAT5, ZBTB16, TRAF6, CDK2, DDIT3, MLL, TNFRSF1A, CDH1, ATXN1, CREBBP, CHEK2, AR, RELA, NFKBIA, MYCN, UBB, EIF4A3, STAT5A, STAT3, NCOA6, TP53, SERTAD1, MYC, ILF3, SMAD2, XRCC6, ERBB2, MED1, SMAD7, SQSTM1, PIK3R1, CTNNB1, FOS, NFKB1, HIF1A,

						CASK, TFEB	TCF12, PPARA, RB1, CDKN2A, AKT1, NCK1, MAPK1, SP1, NR1H4, HNF4A, HNF1A, APP, NFATC3, GATA4, USF2, EP300, UBC, IKBKB, EGR1, DLG4, COPS5, HDAC4, IGBP1, CDK5RAP3, TAF1, GSK3B, TAF7, ONECUT1, DBP, PITX3, CAND1, HDAC1, SMARCAD1, CEBPA, SIRT1, ESR1, UBA52, TRIM28, NFE2, ETS1, TCF3, TBP, JUN, NFYB, NFYC, CREB1, USF1, WDR61, PSMC5, VHL, PRKD2, RARA, NCK2, IRAK1, PHB, VDR, IRF7, DNM2, ATXN7, SUPT5H, VEGFA, SRF

Positive regulation of transcription from RNA polymerase II promoter	800	36.2	91	1.64E-16	1.92E-14	RXRA, PRPF6, RBL1, TBR1, ABLIM1, SMAD3, LEO1, THRA, TCF21, E2F4, BCL3, CSF3, FOXH1, DBP, CASK, TFEB	PAX6, KAT5, TRAF6, DDIT3, MLL, TNFRSF1A, ATXN1, AR, RELA, NFKBIA, MYCN, UBB, EIF4A3, STAT5A, STAT3, NCOA6, TP53, MYC, SMAD2, XRCC6, MED1, SMAD7, SQSTM1, PIK3R1, CTNNB1, FOS, NFKB1, HIF1A, PPARA, RB1, CDKN2A, AKT1, NCK1, SP1, NR1H4, HNF4A, HNF1A, APP, NFATC3, GATA4, USF2, EP300, UBC, EGR1, DLG4, COPS5, HDAC4, IGBP1, CDK5RAP3, TAF1, GSK3B, TAF7, ONECUT1, CAND1, HDAC1, CEBPA, SIRT1, ESR1, UBA52, ETS1, TCF3, JUN, CREB1, USF1, WDR61, PRKD2, RARA, NCK2, IRAK1, VDR, IRF7, ATXN7, SUPT5H, VEGFA, SRF

Transcription initiation from RNA polymerase II promoter	219	9.92	40	2.96E-14	1.87E-12	RXRA, RBL1, SMAD3, THRA, E2F4	CREBBP, AR, UBB, NCOA6, MYC, SMAD2, MED1, SMAD7, PPARA, SP1, NR1H4, HNF4A, HNF1A, POLR2A, UBC, TAF10, NR3C1, TAF6, TAF1, UBE2D3, TAF7, CAND1, NEDD4L, HDAC1, ESR1, UBE2D1, UBA52, TRIM28, USP9X, MED8, TBP, RARA, VDR, ESR2, SRF
DNA_dependent transcription, initiation	257	11.6	42	3.47E-13	1.67E-11	RXRA, RBL1, POLR1C, SMAD3, THRA, E2F4	CREBBP, AR, UBB, NCOA6, MYC, SMAD2, MED1, SMAD7, PPARA, SP1, NR1H4, HNF4A, HNF1A, BRF2, POLR2A, UBC, TAF10, NR3C1, TAF6, TAF1, UBE2D3, TAF7, CAND1, NEDD4L, HDAC1, ESR1, UBE2D1, UBA52, TRIM28, USP9X, MED8, TBP, RARA, VDR, ESR2, SRF

Protein modification by small protein conjugation	713	32.3	73	3.76E-11	1.34E-09	ERCC8, SAE1, LIMK1, LEO1, MID2, HERC6, UBOX5, DCAF4, UBE4B, DCAF8, RUSC1, G2E3	PAX6, ZBTB16, TRAF6, UBE2I, SUMO3, UBA2, CDK2, PSMA1, MDM2, UBB, VCP, SMAD7, TOLLIP, CDK1, BARD1, NEDD8, CDKN2A, UBXN1, AKT1, UBE2H, UBE2E2, UBE2K, UBE2L3, UBE2E1, UBE2E3, UBE2B, PARK2, UBC, CUL4B, EGR1, CBL, HDAC4, CUL1, HDAC6, SUMO1, UBE2D3, UBE2D2, RCHY1, CUL3, CAND1, CUL2, LNX1, NEDD4L, UBD, SUMO2, SIRT1, UBE2C, UBA1, UBE2D1, UBA52, TRIM28, LRSAM1, MED8, TRAF2, PSMC5, VHL, PRPF19, BIRC2, CAV1, IRAK1, PSEN1

Blood coagulation	564	25.5	60	5.39E-10	1.13E-08	F10, GNAI2, RAD51C, LCP2, TRPC3, F2R, NOS1, P2RX1, FGR, SLC7A8, PSAP, SLC16A3	YWHAZ, CDK2, ACTB, TP53, WAS, RAF1, CRK, PIK3R1, GNA11, PLAUR, AKT1, GRB2, SRC, MAPK1, APOA1, ALB, HNF4A, APP, GATA4, PLAT, PTPN6, CBX5, GNAI1, A2M, SOS1, RAC1, CDC42, FN1, SHC1, HDAC1, LCK, NFE2, PROCR, VAV2, RAP1A, LYN, ITPR3, USF1, PLCG1, ACTG1, CAV1, PTPN11, APOE, DTNBP1, GNB1, PLA2G4A, VEGFA, SRF
Apoptotic process	2130	96.4	150	7.53E-09	1.12E-07	TNFRSF10C, ACTC1, CD44, TJP2, SMAD3, RPS3, CCAR1, BRCA2, TRIM2, THRA, SH3KBP1, TGM2, FHL2, BCL3, NGFR, F2R, PAX7, CRH, P2RX1, DNM1L, FGD1, SSTR3, UBE4B, FAIM2, AQP2,	VIM, GAPDH, ZBTB16, TLE1, GNB2L1, TSC22D1, TRAF6, YWHAZ, ARF6, DYNLL1, PDCD6IP, DDIT3, PSMA1, MLH1, MLL, TNFRSF1A, TRADD, IKBKG, CDH1, MDM2, CHEK2, AR, RELA, NFKBIA, UBB, STAT5A, TP53, MYC, SCRIB, VCP, RAF1, CTSB, EGFR, MED1, SMAD7, SQSTM1, PIK3R1,

						FGD3, TMEM102, MZB1, PLEKHG5, ACSL5, CASP7, G2E3, KALRN, NQO1, PDCD6, MAEA	CTNNB1, CDK1, BARD1, NFKB1, FKBP8, HIF1A, RB1, CDKN2A, PUF60, AKT1, SRC, MAPK1, ALB, CDKN1A, APP, UBE2B, EP300, YWHAE, PTPN6, PARK2, UBC, TERF1, TJP1, NR3C1, EGR1, CBL, SOS1, IGBP1, RAC1, CDC42, KAT2A, CUL1, HDAC6, GSK3B, UBE2D3, BCL2L11, CUL3, CUL2, UBD, SNCA, HDAC1, SIRT1, ESR1, S100A9, PAK2, UBA52, LCK, HSP90AB1, SRPK2, TRAF2, SFN, VAV2, CEBPB, LYN, ETS1, JUN, FASLG, CD3E, FAS, PSMC5, KPNB1, VHL, BIRC2, CAV1, XIAP, ARHGEF7, BTK, PHB, BIRC3, PSEN1, APOE, ESR2, IRF7, DNM2, DYNLL2, GNB1, VEGFA
Positive regulation of I_kappaB kinase/NF_kappaB cascade	150	6.79	23	2.69E-07	2.34E-06	TGM2, F2R, TMEM101, PLEKHG5	TRAF6, TNFRSF1A, TRADD, IKBKG, MAP3K3, RELA, UBB, MYD88, CTNNB1, PARK2, UBC,

							IKBKB, TERF2IP, UBD, UBA52, FASLG, BIRC2, IRAK1, BIRC3
Regulation of cellular component organization	1520	69	110	3.84E-07	3.23E-06	MYL2, TBR1, PLK4, GFAP, PACSIN1, SMAD3, LIMK1, THRA, L3MBTL1, CDC6, SIPA1L1, SH3KBP1, CSF3, NGFR, APOA5, DNM1L, FGR, FGD1, NPPB, FGD3, PALM, CDH4, GAS2L2, DDR1, PRKCSH, RPL13A	VIM, EPB49, GNB2L1, PRMT5, ARF6, CD320, CEP76, UPF1, ATXN2, MYL12A, AR, TP53, MYC, SMAD2, VCP, RAF1, CRK, ERBB2, SMAD7, PIK3R1, CTNNB1, ETF1, RB1, CDKN2A, AKT1, GRB2, NCK1, SRC, MAPK1, APOA1, CDKN1A, HNF4A, HNF1A, UBE2E1, UBE2B, PARK2, TERF1, SPTBN1, DLG4, CBL, SH3GL2, RAC1, CDC42, POT1, HDAC6, TAF1, SUMO1, GSK3B, TAF7, FN1, WASL, XPO1, BCL2L11, TERF2IP, CAND1, TINF2, NEDD4L, UBD, SNCA, SPP1, SIRT1, PEX5, S100A9, UBE2C, UBE2D1, LRSAM1, SFN, LYN, ETS1, WDR61, FAS, CCDC85B, PRKD2, NCK2,

							PHB, PSEN1, APOE, ESR2, ANXA7, ACD, DSTN, PACSIN2, VEGFA, SRF

Supplementary Table 9. List of enriched biological processes in the network (**Figure 4A**) constructed upon the genes associated with the differentially methylated hyo- and hypermethylated promoters between the non-diseased aortic and mitral valve tissue based on the Gene Ontology (GO) Biological Processes (BPs) database (selected results). “Total” refers to the total number of genes that belong to the particular GO BP as per the chosen reference list of genes, which is hg19 our case, “Expected” denotes the number of genes to be expected in our gene list for the particular GO BP, “Hits” describes the number of genes in our list that map to the particular GO BP, “ P.value” is equivalent to the enrichment p-value computed using the hypergeometric test (**see Methods**), FDR stands for false discovery rate, which is the method used to correct the corresponding p-value for multiple testing. “Seed genes” represent genes associated with significantly differentially hyper- and hypomethylated promoters and “Other genes” denote genes that are part of the minimum non-seed genes that are necessarily required to connect the seed genes to construct the network. The methylation direction of the seed genes can be found in **Supplementary Table 1**.

2.10 Table S10. List of enriched molecular functions in the network constructed upon the genes associated with the differentially methylated hyo- and hypermethylated promoters between the non-diseased aortic and mitral valve tissue based on the Gene Ontology (GO) Molecular Functions database (selected results)

GO MF	**Total**	**Expected**	**Hits**	**P.Value**	**FDR**	**Seed genes**	**Other genes**
Transcription factor binding	509	22.5	75	1.39E-20	2.70E-18	RXRA, RBL1, TRIP6, SMAD3, RPS3, THRA, E2F4, BCL3, FOXH1, TCF21, FHL2	PAX6, KAT5, TLE1, YWHAZ, UBE2I, UBA2, MDFI, DDIT3, CREBBP, AR, RELA, NFKBIA, ACTB, STAT3, NCOA6, TP53, MYC, SMAD2, MED1, CTNNB1, FOS, HIF1A, PPARA, RB1, CDKN2A, MAPK1, SP1, NR1H4, HNF4A, HNF1A, GATA4, USF2, EP300, USP7, APEX1, CBX5, EGR1, HDAC4, TAF1, SUMO1, GSK3B, TAF7, CAND1, HDAC1, CEBPA, SIRT1, ESR1, HDAC11, CSNK2B, CEBPB, ETS1, TCF3, TBP, JUN, NFYB, CREB1, USF1, PSMC5, VHL, RARA, VDR, NLK, GFI1B, SRF

Positive regulation of transcription, DNA_dependent	1260	55.7	123	1.16E-17	1.50E-15	RXRA, PRPF6, RBL1, TBR1, ABLIM1, SMAD3, DYRK1B, BRCA2, ATXN7L3, MDK, LEO1, THRA, E2F4, BCL3, NCOA4, CSF3, F2R, FOXH1, PBX4, TAF8, DBP, CASK, TFEB, TCF21, FHL2, NR2F2	PAX6, KAT5, ZBTB16, TRAF6, CDK2, DDIT3, MLL, TNFRSF1A, CDH1, ATXN1, CREBBP, CHEK2, AR, RELA, NFKBIA, MYCN, UBB, EIF4A3, STAT5A, STAT3, NCOA6, TP53, SERTAD1, MYC, ILF3, SMAD2, XRCC6, ERBB2, MED1, SMAD7, SQSTM1, PIK3R1, CTNNB1, FOS, NFKB1, HIF1A, TCF12, PPARA, RB1, CDKN2A, AKT1, NCK1, MAPK1, SP1, NR1H4, HNF4A, HNF1A, APP, NFATC3, GATA4, USF2, EP300, UBC, IKBKB, EGR1, DLG4, COPS5, HDAC4, IGBP1, CDK5RAP3, TAF1, GSK3B, TAF7, ONECUT1, PITX3, CAND1, HDAC1, SMARCAD1, CEBPA, SIRT1, ESR1, UBA52, TRIM28, NFE2, ETS1, TCF3, TBP, JUN, NFYB, NFYC, CREB1, USF1, WDR61, PSMC5, VHL, PRKD2, RARA, NCK2, IRAK1, PHB, VDR, IRF7, DNM2, ATXN7,

							SUPT5H, VEGFA, SRF
Transcription from RNA polymerase II promoter	1930	85.4	151	4.25E-13	2.75E-11	RXRA, MAGOH, PRPF6, RBL1, TBR1, ABLIM1, NMI, SMAD3, LEO1, THRA, CDC6, WDTC1, E2F4, BCL3, CSF3, FOXH1, PBX4, DBP, SETX, HOXB3, CASK, TFEB, TCF21, FHL2, NR2F2	PAX6, KAT5, CHD3, PRMT5, TSC22D1, TRAF6, RNPS1, SNRPB, UBE2I, SAP18, CPSF3, TRIP11, CIAO1, MDFI, DDIT3, MLL, TNFRSF1A, ATXN1, MDM2, CREBBP, AR, RELA, NFKBIA, MYCN, UBB, EIF4A3, STAT5A, STAT3, NCOA6, TP53, MYC, SMAD2, XRCC6, CRK, MED1, SMAD7, SQSTM1, PIK3R1, CTNNB1, CDK1, FOS, NFKB1, HIF1A, COPS2, TCF12, NEDD8, PPARA,

							RB1, CDKN2A, AKT1, NCK1, SP1, NR1H4, HNF4A, ZNF143, HNF1A, APP, NFATC3, GATA4, USF2, EP300, POLR2A, UBC, TAF10, NR3C1, EGR1, DLG4, TAF6, TRIM29, COPS5, CCNA1, HDAC4, IGBP1, CDK5RAP3, KAT2A, POLA1, TAF1, GSK3B, UBE2D3, UBE2D2, TAF7, ONECUT1, XPO1, CAND1, CUL2, NEDD4L, HDAC1, CEBPA, SIRT1, ESR1, UBE2D1, UBA52, TRIM28, SRSF3, USP9X, YBX1, NFE2, MED8, CEBPB, ETS1, TCF3, TBP, JUN, NFYC, CREB1, USF1, FASLG, WDR61, CEBPD, PSMC5, VHL, CAV1, PRKD2, RARA, NCK2, IRAK1, PHB, VDR, PSEN1, ESR2, IRF7, ATXN7, SUPT5H, GFI1B, VEGFA, SRF

Structure_specific DNA binding	242	10.7	32	2.91E-08	7.06E-07	RXRA, SMAD3, BRCA2, THRA, FOXH1, CTC1	PAX6, MCM4, MCM7, MLH1, RAD51, SMAD2, XRCC6, PCBP1, EGFR, CTNNB1, FOS, NFKB1, SP1, HNF1A, USF2, EP300, TERF1, APEX1, EGR1, POT1, YBX1, RPA2, JUN, USF1, RARA, SRF
Transcription coactivator activity	312	13.8	35	4.10E-07	8.84E-06	SUPT7L, RXRA, PRPF6, DYRK1B, CCAR1, ATXN7L3, NCOA4, FHL2	KAT5, TRIP11, RBPMS, NFKBIB, NFKB2, CREBBP, NCOA6, MED1, CTNNB1, RB1, NR1H4, UBE2L3, EP300, APEX1, TAF10, COPS5, KAT2A, TAF1, TAF7, TRIM28, NFE2, TCF3, JUN, NFYC, BIRC2, RARA, ESR2
Histone deacetylase binding	65	2.88	14	7.24E-07	1.32E-05	WDTC1, TCF21	TRAF6, HIF1A, SP1, YWHAE, CBX5, HDAC4, KAT2A, HDAC6, HDAC1, USF1, KPNA2, PHB
Chromatin binding	338	15	32	4.33E-05	0.00041	RXRA, SMAD3, THRA, L3MBTL1, CDC6	TLE1, PRMT5, UPF1, CREBBP, AR, RELA, NCOA6, TP53, SMAD2, DHX30, MED1, CTNNB1, NFATC3, GATA4, EP300, TERF1, APEX1, CBX5, KAT2A, POLA1, ESR1, TCF3, RARA, ATXN7, DDX1, CDC5L, SRF

Histone acetyltransferase activity	52	2.3	9	0.000411	0.00319	SUPT7L, BRCA2	KAT5, KAT7, CREBBP, EP300, TAF10, KAT2A, TAF1
RNA binding	976	43.2	65	0.00059	0.00432	CARHSP1, LSM2, GSPT1, MAGOH, PRPF6, TRA2A, RPS3, RPS7, THRA, STAU1, ISG20, DDX19B, PPIE, RPL11, CELF3, MRPS17, PRKCSH, NUDT7	RPL18A, RNPS1, SNRPB, PINX1, SNRPA1, CPSF3, HNRNPM, RBPMS, PSMA1, EWSR1, NAA38, UPF1, LSM4, ATXN1, ATXN2, EIF4A3, PA2G4, ILF3, PCBP1, SF3A1, DHX30, BARD1, ETF1, PUF60, PABPC1, SRRM2, RPL5, CARS, APEX1, COPS5, XPO1, HNRNPF, ELAVL1, THOC5, NCL, HNRNPU, PTBP1, SRSF3, EEF1A1, YBX1, QKI, RPL3, PSPC1, DDX1, CDC5L, EIF6, SNRNP70
NF_kappaB binding	25	1.11	6	0.000632	0.00446	RPS3	RELA, NFKBIA, CDKN2A, APEX1, GSK3B
SMAD binding	68	3.01	10	0.000768	0.00523	SMAD3, FOXH1	PAX6, SMAD2, SMAD7, CTNNB1, FOS, GATA4, USP9X, JUN

Supplementary Table 10. List of enriched molecular functions in the network (**Figure 4A**) constructed upon the genes associated with the differentially methylated hyo- and hypermethylated promoters between the non-diseased aortic and mitral valve tissue based on the Gene Ontology (GO) Molecular Functions (MFs) database (selected results). “Total” refers to the total number of genes that belong to the particular GO MF as per the chosen reference list of genes, which is hg19 in our case, “Expected” denotes the number of genes to be expected in our gene list for the particular GO MF, “Hits” describes the number of genes in our list that map to the particular GO MF, “P.value” is equivalent to the enrichment p-value computed using the hypergeometric test (**see Methods**), FDR stands for false discovery rate, which is the method used to correct the corresponding p-value for multiple testing, “Seed genes” represent genes associated with significantly differentially hyper- and hypomethylated promoters and “Other genes” denote genes that are part of the minimum non-seed genes that are necessarily required to connect the seed genes to construct the network. The methylation direction of the seed genes can be found in **Supplementary Table 1**.

2.11 Table S11. List of enriched cellular components in the network constructed upon the genes associated with the differentially methylated hyo- and hypermethylated promoters between the non-diseased aortic and mitral valve tissue based on the Gene Ontology (GO) Cellular Components database (selected results)

GO CC	Total	Expected	Hits	P.Value	FDR	Seed genes	Other genes
Transcription factor complex	303	12.2	40	3.36E-11	7.57E-10	RBL1, SMAD3, E2F4, FOXH1, TAF8, TFEB	KAT5, TLE1, CDK2, HOXA9, CREBBP, RELA, NCOA6, TP53, SMAD2, XRCC6, SMAD7, CTNNB1, FOS, HIF1A, TCF12, RB1, HNF1A, EP300, APEX1, TAF10, TAF6, KAT2A, TAF1, TAF7, CEBPA, ETS1, TCF3, TBP, JUN, NFYB, NFYC, CREB1, USF1, GFI1B
Spliceosomal complex	161	6.47	21	1.99E-06	1.82E-05	LSM2, MAGOH, PRPF6, PPIE, XAB2	SNRPB, SNRPA1, HNRNPM, UPF1, SNRPD2, EIF4A3, SF3A1, PABPC1, SRRM2, HSPA8, HNRNPF, HNRNPU, YBX1, PRPF19, CDC5L, SNRNP70
Cytoskeleton	2200	88.3	128	6.94E-06	5.38E-05	MYO15A, ACTC1, MYL2, GNAI2, TRIP6, KRT8, PLK4, HOMER3, ABLIM1, GFAP, RGS14, CORO1B, TUBA8, NDE1, BRCA2, USH1C, RPS7, CDC6, SIPA1L1, STAU1, SH3KBP1, MID2, FBF1, CCP110, NOS1, DNM1L, FGR,	VIM, CRMP1, GAPDH, CHD3, EPB49, NDRG1, GNB2L1, YWHAZ, PINX1, DYNLL1, PDCD6IP, TRIP11, CIAO1, CDK2, MTUS2, PSMA1, TUBGCP4, CEP76, TRADD, CDH1, MYL12A, ACTB, MYC, WAS, CTNNB1, CDK1, TRIM55, RB1, AKT1, SRC, MAPK1, APP, TUBB, IQGAP1, YWHAE, TERF1, APEX1, TPM4, SPTBN1, GNAI1, ABI1, DLG4, TRPC4, CCNA1, HDAC4, CDC42, KAT2A, HDAC6, TUBA1A, GSK3B, WASL, BCL2L11, CUL3, SNCA, THOC5, S100A9, IQCB1, LCK, 11-Sep, NFE2, PROCR, TUBB2B, MPDZ, LYN,

						FGD1, DCTN4, KRT73, FGD3, RUSC1, KRT38, HSD17B14, SLC16A3, GAS2L2, KRT83, CLEC11A, MYO7B, TCTN2, EXOC7, CASK, KALRN, ZNF44, SHANK2, PPP4R2, MAEA, FHL2	TRIM63, ACTG1, TNNT1, CKAP4, EPS8, CCDC85B, PRPF19, PSEN1, DNM2, CTTN, ATXN7, DYNLL2, DTNBP1, ACTA2, DSTN, FLOT1, EIF6
Transcription factor TFIID complex	21	0.844	7	1.17E-05	8.74E-05	TAF8	TP53, TAF10, TAF6, TAF1, TAF7, TBP
Nuclear chromatin	159	6.39	19	2.16E-05	0.000155	RXRA, SIRT6	PAX6, CREBBP, AR, TP53, NR1H4, UBE2B, CBX5, HDAC1, SIRT1, TRIM28, CEBPB, TCF3, TBP, JUN, CREB1, RARA, SRF
Chromatin	326	13.1	30	2.21E-05	0.000155	RXRA, L3MBTL1, SIRT6	PAX6, KAT5, MCM7, UPF1, CREBBP, AR, MYCN, TP53, RB1, CDKN2A, NR1H4, UBE2B, CBX5, POLA1, HDAC1, SMARCAD1, SIRT1, HIST3H3, TRIM28, CEBPB, TCF3, TBP, JUN, CREB1, WDR61, RARA, SRF
Actin cytoskeleton	430	17.3	30	0.00247	0.0096	MYO15A, ACTC1, MYL2, ABLIM1, CORO1B, FGR,	EPB49, CDH1, MYL12A, WAS, IQGAP1, TPM4, SPTBN1, HDAC4, WASL, SNCA, 11-Sep, NFE2, ACTG1, TNNT1, DYNLL2, ACTA2

						SLC16A3, GAS2L2, MYO7B, CASK, KALRN, MAEA, FHL2	
Histone deacetylase complex	53	2.13	7	0.00507	0.0175	NA	CHD3, SAP18, CBX5, HDAC4, HDAC6, HDAC1, HDAC11

Supplementary Table 11. List of enriched cellular components in the network (**Figure 4A**) constructed upon the genes associated with the differentially methylated hyo- and hypermethylated promoters between the non-diseased aortic and mitral valve tissue based on the Gene Ontology (GO) Cellular Components (CCs) database (selected results). “Total” refers to the total number of genes that belong to the particular GO CC as per the chosen reference list of genes, which is hg19 in our case, “Expected” denotes the number of genes to be expected in our gene list for the particular GO CC, “Hits” describes the number of genes in our list that map to the particular GO CC, “P.value” is equivalent to the enrichment p-value computed using the hypergeometric test (**see Methods**), FDR stands for false discovery rate, which is the method used to correct the corresponding p-value for multiple testing, “Seed genes” represent genes associated with significantly differentially hyper- and hypomethylated promoters and “Other genes” denote genes that are part of the minimum non-seed genes that are necessarily required to connect the seed genes to construct the network. The methylation direction of the seed genes can be found in **Supplementary Table 1**.

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2.12 Table S12. Node characteristics of subnetwork 1/module 1 of the NW (pvalue 3.04 e-13)

Node No.	Gene name	Degree	Betweenness Centrality	Meth.diff
1	UBC	43	939	0
2	UBQLN4	4	3	0
3	PMEPA1	2	10	-31.0166
4	ITPRIPL1	2	10	-12.7256
5	UBR7	2	10	-11.1156
6	CYB5R1	2	10	-10.7196
7	WNT5B	1	0	-14.1133
8	SEMA4B	1	0	14.38911
9	UCKL1	1	0	-11.8067
10	SLC7A8	1	0	-40.7436
11	AQP2	1	0	-21.134
12	RCCD1	1	0	-19.0998
13	TOP1MT	1	0	15.78471
14	IBA57	1	0	11.57786
15	OSBPL1A	1	0	10.37672
16	PLIN4	1	0	-10.4404
17	PLBD2	1	0	-17.4555
18	SPA17	1	0	14.31302
19	C6orf170	1	0	-41.2808
20	ALS2CL	1	0	10.70251
21	SLC16A3	1	0	13.40508
22	TOR4A	1	0	-10.1032
23	SLC6A8	1	0	11.05677
24	SYCP1	1	0	14.5074
25	AP1S3	1	0	-10.957
26	FUCA2	1	0	11.09653
27	ACSL5	1	0	-16.8043
28	PXMP4	1	0	-10.516
29	ZNF551	1	0	17.70154

30	NUDT22	1	0	-11.9831
31	CLEC11A	1	0	-24.7239
32	GRTP1	1	0	-11.8419
33	SLC2A10	1	0	-17.9246
34	ZNF597	1	0	10.88286
35	NUP210L	1	0	-14.658
36	ZNF354C	1	0	-17.1657
37	MYO7B	1	0	-12.8972
38	LDLRAD4	1	0	-10.4618
39	GSTO2	1	0	10.83864
40	ASAH2B	1	0	15.99461
41	CTC1	1	0	-17.328
42	SERHL2	1	0	-11.0445
43	IQCA1	1	0	-15.9873
44	DNAAF3	1	0	-14.7451
45	RHBDF1	1	0	10.29471

Supplementary Table 12. Node characteristics of subnetwork 1/module 1 of the network in **Figure 4B** (pvalue 3.04 e-13). Each node represents a gene. Degree refers to the number of connections/edges/PPI-interactions that a node has to other nodes and betweenness centrality reflects the number of shortest paths passing through a node (2).

2.13 Table S13. List of enriched pathways, biological processes, molecular functions and cellular components in subnetwork 1/module 1 (pvalue 3.04 e-13) of the network constructed upon the genes associated with the differentially methylated hyo- and hypermethylated promoters between the non-diseased aortic and mitral valve tissue based on KEGG/Reactome, Gene Ontology (GO) Biological Processes database, Gene Ontology (GO) Molecular Functions database and Gene Ontology (GO) Cellular Components database (full list)

KEGG					
Pathway	**Total**	**Expected**	**Hits**	**P.Value**	**FDR**
PPAR signaling pathway	74	0.172	2	0.0125	1
Drug metabolism - other enzymes	79	0.184	2	0.0142	1
Peroxisome	83	0.193	2	0.0156	1
Fatty acid biosynthesis	18	0.0419	1	0.0411	1
Other glycan degradation	18	0.0419	1	0.0411	1
Axon guidance	181	0.421	2	0.0652	1
Ferroptosis	40	0.0931	1	0.0892	1
Fatty acid degradation	44	0.102	1	0.0977	1
Vasopressin-regulated water reabsorption	44	0.102	1	0.0977	1
Herpes simplex infection	492	1.14	3	0.102	1
Reactome					
Pathway	**Total**	**Expected**	**Hits**	**P.Value**	**FDR**
Basigin interactions	32	0.0671	2	0.00195	1
Proton-coupled monocarboxylate transport	4	0.00839	1	0.00836	1
SLC-mediated transmembrane transport	251	0.526	3	0.014	1
Transport of glucose and other sugars, bile salts and organic acids, metal ions and amine compounds	95	0.199	2	0.0163	1
Vitamin C (ascorbate) metabolism	8	0.0168	1	0.0167	1
Transmembrane transport of small molecules	504	1.06	4	0.0175	1
Cell surface interactions at the vascular wall	99	0.208	2	0.0176	1
Creatine metabolism	9	0.0189	1	0.0187	1

MHC class II antigen presentation	118	0.247	2	0.0245	1
Bile salt and organic anion SLC transporters	12	0.0252	1	0.0249	1
Facilitative Na+-independent glucose transporters	12	0.0252	1	0.0249	1
Passive Transport by Aquaporins	12	0.0252	1	0.0249	1
Nef mediated downregulation of MHC class I complex cell surface expression	13	0.0273	1	0.0269	1
Synthesis of very long-chain fatty acyl-CoAs	14	0.0294	1	0.029	1
Fatty Acyl-CoA Biosynthesis	18	0.0377	1	0.0371	1
Pyruvate metabolism	21	0.044	1	0.0432	1
Nef-mediates down modulation of cell surface receptors by recruiting them to clathrin adapters	24	0.0503	1	0.0492	1
GO BP					
Biological Process	**Total**	**Expected**	**Hits**	**P.Value**	**FDR**
Organic acid transport	246	0.551	3	0.0173	1
Carboxylic acid transport	246	0.551	3	0.0173	1
Meiosis I	91	0.204	2	0.0176	1
Regulation of transforming growth factor beta receptor signaling pathway	107	0.24	2	0.0238	1
Amino acid transport	143	0.32	2	0.0406	1
Carbohydrate transport	147	0.329	2	0.0426	1
Neutral amino acid transport	23	0.0515	1	0.0503	1
Anion transport	374	0.838	3	0.0504	1
Epidermal growth factor receptor signaling pathway	167	0.374	2	0.0536	1
Carboxylic acid metabolic process	1270	2.85	6	0.0605	1
GO MF					
Molecular Function	**Total**	**Expected**	**Hits**	**P.Value**	**FDR**
Carbohydrate transmembrane transporter activity	33	0.0775	2	0.0027	0.365
Carboxylic acid transmembrane transporter activity	127	0.298	3	0.00323	0.365

Organic acid transmembrane transporter activity	130	0.305	3	0.00345	0.365
Symporter activity	134	0.315	3	0.00376	0.365
Organic anion transmembrane transporter activity	147	0.345	3	0.00487	0.378
Secondary active transmembrane transporter activity	212	0.498	3	0.0133	0.857
Amino acid transmembrane transporter activity	84	0.197	2	0.0165	0.917
GTPase activator activity	267	0.627	3	0.0243	1
Ras GTPase activator activity	117	0.275	2	0.0307	1
Anion transmembrane transporter activity	304	0.714	3	0.0339	1
Small GTPase regulator activity	319	0.749	3	0.0383	1
Cofactor transporter activity	20	0.047	1	0.046	1
Active transmembrane transporter activity	347	0.815	3	0.0472	1
GO CC					
Cellular Component	**Total**	**Expected**	**Hits**	**P.Value**	**FDR**
Lytic vacuole	401	0.938	4	0.014	1
Lysosome	401	0.938	4	0.014	1
Vacuole	486	1.14	4	0.0262	1
Vacuolar part	279	0.653	3	0.0272	1
Trans_Golgi network	120	0.281	2	0.032	1
Lysosomal membrane	153	0.358	2	0.0497	1
Basolateral plasma membrane	162	0.379	2	0.055	1
Peroxisome	181	0.423	2	0.0669	1
Microbody	181	0.423	2	0.0669	1
Cytoplasmic vesicle membrane	403	0.943	3	0.0676	1

Supplementary Table 13. List of enriched pathways, biological processes, molecular functions and cellular components in subnetwork 1/module 1 (pvalue 3.04 e-13, **Figure 4B**) of the network constructed upon the genes associated with the differentially methylated hyo- and hypermethylated promoters between the non-diseased aortic and mitral valve tissue based on KEGG/Reactome, Gene Ontology (GO) Biological Processes database, Gene Ontology (GO) Molecular Functions database and Gene Ontology (GO) Cellular Components database (full list). “Total” refers to the total number of genes that belong to a particular category as per the chosen reference list of genes, which is hg19 in our case, "Expected" denotes the number of genes to be expected in our gene list for a particular category, "Hits" describes the number of genes in our list that map to a particular category, "P.value" is equivalent to the enrichment p-value computed using the hypergeometric test (**see Methods**) and FDR stands for false discovery rate, which is the method used to correct the corresponding p-value for multiple testing.

2.14 Table S14. Node characteristics of subnetwork 2/module 2 of the NW (pvalue 0.047)

Node No.	**Gene name**	**Degree**	**Betweenness Centrality**	**Meth.diff**
1	BRCA2	5	33.5	16.35677
2	APOA5	4	32.5	15.30117
3	USF2	2	12.5	0
4	USF1	2	12.5	0
5	PPARA	2	10	0
6	NR1H4	2	10	0
7	RPA2	2	10	0
8	FANCD2	1	0	0
9	BARD1	1	0	0
10	FABP6	1	0	14.57521
11	SLC10A2	1	0	19.11392
12	SLC17A9	1	0	18.99397

Supplementary Table 14. Node characteristics of subnetwork 2/module 2 of the network in **Figure 4C** (pvalue 0.047). Each node represents a gene. Degree refers to the number of connections/edges/PPI-interactions that a node has to other nodes and betweenness centrality reflects the number of shortest paths passing through a node (2).

2.15 Table S15. List of enriched pathways, biological processes, molecular functions and cellular components in subnetwork 2/module 2 (pvalue 0.047) of the network constructed upon the genes associated with the differentially methylated hyo- and hypermethylated promoters between the non-diseased aortic and mitral valve tissue based on KEGG/Reactome, Gene Ontology (GO) Biological Processes database, Gene Ontology (GO) Molecular Functions database and Gene Ontology (GO) Cellular Components database (full list)

KEGG					
Pathway	**Total**	**Expected**	**Hits**	**P.Value**	**FDR**
Homologous recombination	41	0.0477	3	1.14E-05	0.00361
Fanconi anemia pathway	54	0.0628	3	2.62E-05	0.00417
PPAR signaling pathway	74	0.0861	3	6.77E-05	0.00718
Bile secretion	72	0.0838	2	0.00295	0.234
Mismatch repair	23	0.0268	1	0.0265	1
DNA replication	36	0.0419	1	0.0411	1
Nucleotide excision repair	47	0.0547	1	0.0534	1
Adipocytokine signaling pathway	69	0.0803	1	0.0775	1
Pancreatic cancer	75	0.0872	1	0.084	1
Glucagon signaling pathway	103	0.12	1	0.114	1
Reactome					
Pathway	**Total**	**Expected**	**Hits**	**P.Value**	**FDR**
Homologous DNA pairing and strand exchange	6	0.00719	2	1.88E-05	0.0132
Presynaptic phase of homologous DNA pairing and strand exchange	6	0.00719	2	1.88E-05	0.0132
Recycling of bile acids and salts	11	0.0132	2	6.87E-05	0.0321
Homologous recombination repair of replication-independent double-strand breaks	16	0.0192	2	0.000149	0.0419
Homologous Recombination Repair	16	0.0192	2	0.000149	0.0419
DNA Repair	117	0.14	3	0.000275	0.0644
Double-Strand Break Repair	24	0.0288	2	0.000342	0.0685
Bile acid and bile salt metabolism	28	0.0335	2	0.000468	0.0728
Fanconi Anemia pathway	28	0.0335	2	0.000468	0.0728
Nuclear Receptor transcription pathway	53	0.0635	2	0.00168	0.229

Metabolism of lipids and lipoproteins	507	0.607	4	0.0018	0.229
PPARA Activates Gene Expression	59	0.0707	2	0.00208	0.243
Regulation of Lipid Metabolism by Peroxisome proliferator-activated receptor alpha (PPARalpha)	76	0.0911	2	0.00342	0.36
Processing of DNA double-strand break ends	3	0.00359	1	0.00359	0.36
Meiotic Recombination	84	0.101	2	0.00417	0.39
Assembly of the RAD51-ssDNA nucleoprotein complex	5	0.00599	1	0.00598	0.524
Meiosis	117	0.14	2	0.00796	0.656
Fatty acid, triacylglycerol, and ketone body metabolism	139	0.167	2	0.0111	0.864
Removal of the Flap Intermediate from the C-strand	10	0.012	1	0.0119	0.88
Processive synthesis on the C-strand of the telomere	11	0.0132	1	0.0131	0.919
Regulation of the Fanconi anemia pathway	13	0.0156	1	0.0155	0.952
Removal of the Flap Intermediate	14	0.0168	1	0.0167	0.952
BMAL1:CLOCK/NPAS2 Activates Circadian Expression	14	0.0168	1	0.0167	0.952
Processive synthesis on the lagging strand	15	0.018	1	0.0178	0.952
Repair synthesis of patch ~27-30 bases long by DNA polymerase	15	0.018	1	0.0178	0.952
Repair synthesis for gap-filling by DNA polymerase in TC-NER	15	0.018	1	0.0178	0.952
Gap-filling DNA repair synthesis and ligation in GG-NER	16	0.0192	1	0.019	0.952
Gap-filling DNA repair synthesis and ligation in TC-NER	16	0.0192	1	0.019	0.952
Lagging Strand Synthesis	20	0.024	1	0.0237	1
Telomere C-strand (Lagging Strand) Synthesis	22	0.0264	1	0.0261	1
Dual incision reaction in GG-NER	23	0.0276	1	0.0272	1

Formation of incision complex in GG-NER	23	0.0276	1	0.0272	1
Extension of Telomeres	24	0.0288	1	0.0284	1
DNA strand elongation	31	0.0371	1	0.0366	1
Activation of the pre-replicative complex	32	0.0383	1	0.0377	1
Circadian Clock	35	0.0419	1	0.0412	1
Global Genomic NER (GG-NER)	36	0.0431	1	0.0423	1
Activation of ATR in response to replication stress	41	0.0491	1	0.0481	1
GO BP					
Biological Process	**Total**	**Expected**	**Hits**	**P.Value**	**FDR**
Bile acid metabolic process	59	0.0496	3	1.43E-05	0.0118
Monocarboxylic acid metabolic process	567	0.476	5	6.07E-05	0.0127
Monocarboxylic acid transport	103	0.0865	3	7.63E-05	0.0127
Lipid homeostasis	103	0.0865	3	7.63E-05	0.0127
Response to nutrient levels	295	0.248	4	7.73E-05	0.0127
Response to extracellular stimulus	320	0.269	4	0.000106	0.0145
Cellular response to nutrient levels	126	0.106	3	0.000139	0.0163
Response to nutrient	147	0.123	3	0.000219	0.0208
Cellular response to extracellular stimulus	149	0.125	3	0.000228	0.0208
DNA repair	538	0.452	4	0.000773	0.0624
Organic acid transport	246	0.207	3	0.000989	0.0624
Regulation of lipid metabolic process	246	0.207	3	0.000989	0.0624
Carboxylic acid transport	246	0.207	3	0.000989	0.0624
Positive regulation of transcription, DNA_dependent	1260	1.06	5	0.00245	0.115
Positive regulation of transcription, DNA_dependent	1260	1.06	5	0.00245	0.115
Meiosis I	91	0.0764	2	0.00254	0.115
Carboxylic acid metabolic process	1270	1.07	5	0.0026	0.115
Response to radiation	345	0.29	3	0.00261	0.115

Positive regulation of metabolic process	2690	2.26	7	0.00272	0.115
Steroid metabolic process	361	0.303	3	0.00297	0.115
Positive regulation of RNA metabolic process	1330	1.12	5	0.00317	0.115
Anion transport	374	0.314	3	0.00328	0.115
Nucleotide_excision repair	104	0.0873	2	0.0033	0.115
Positive regulation of transcription from RNA polymerase II promoter	800	0.672	4	0.00336	0.115
Response to UV	112	0.0941	2	0.00382	0.12
Response to ionizing radiation	112	0.0941	2	0.00382	0.12
Organic acid metabolic process	1430	1.2	5	0.0043	0.124
Response to DNA damage stimulus	862	0.724	4	0.00441	0.124
DNA_dependent DNA replication	121	0.102	2	0.00444	0.124
Lipoprotein metabolic process	124	0.104	2	0.00466	0.124
Response to abiotic stimulus	876	0.736	4	0.00467	0.124
Positive regulation of nucleobase_containing compound metabolic process	1490	1.25	5	0.00518	0.133
Homeostatic process	1510	1.26	5	0.00542	0.135
Double_strand break repair	139	0.117	2	0.00582	0.14
S phase of mitotic cell cycle	144	0.121	2	0.00623	0.146
S phase	153	0.128	2	0.00701	0.16
Lipid metabolic process	1730	1.45	5	0.00981	0.214
Meiotic cell cycle	183	0.154	2	0.0099	0.214
Cellular lipid catabolic process	188	0.158	2	0.0104	0.218
Positive regulation of cellular metabolic process	2530	2.12	6	0.0106	0.218
Negative regulation of nucleobase_containing compound metabolic process	1130	0.95	4	0.0115	0.231
Regulation of catabolic process	595	0.5	3	0.0119	0.233
Transcription initiation from RNA polymerase II promoter	219	0.184	2	0.014	0.266
Response to light stimulus	229	0.192	2	0.0152	0.283

Regulation of DNA metabolic process	235	0.197	2	0.0159	0.286
DNA metabolic process	1240	1.05	4	0.0161	0.286
Viral infectious cycle	241	0.202	2	0.0167	0.292
Response to hypoxia	245	0.206	2	0.0173	0.293
DNA recombination	247	0.207	2	0.0175	0.293
Wound healing	700	0.588	3	0.0185	0.303
DNA_dependent transcription, initiation	257	0.216	2	0.0189	0.304
Lipid transport	268	0.225	2	0.0204	0.321
Intracellular receptor mediated signaling pathway	270	0.227	2	0.0207	0.321
Response to endogenous stimulus	1360	1.15	4	0.0219	0.332
Response to hormone stimulus	751	0.631	3	0.0223	0.332
Glucose metabolic process	290	0.244	2	0.0237	0.341
Developmental growth	290	0.244	2	0.0237	0.341
Cell cycle process	1420	1.19	4	0.0248	0.35
Gland development	303	0.254	2	0.0257	0.356
Lipid catabolic process	305	0.256	2	0.026	0.356
Negative regulation of DNA binding	37	0.0311	1	0.0306	0.406
Response to external stimulus	1510	1.27	4	0.0307	0.406
Response to stress	4150	3.49	7	0.0325	0.421
DNA replication	346	0.291	2	0.0329	0.421
Chromosome organization	878	0.737	3	0.0335	0.423
Regulation of cell cycle	886	0.744	3	0.0343	0.425
Negative regulation of DNA replication	42	0.0353	1	0.0347	0.425
Regulation of transcription from RNA polymerase II promoter	1610	1.35	4	0.0377	0.455
Centrosome cycle	47	0.0395	1	0.0388	0.457
Cellular response to stress	1620	1.36	4	0.039	0.457
Protein export from nucleus	48	0.0403	1	0.0396	0.457
Intrinsic apoptotic signaling pathway in response to DNA damage	51	0.0428	1	0.042	0.469
Negative regulation of cellular metabolic process	1660	1.4	4	0.0421	0.469

Fatty acid metabolic process	397	0.333	2	0.0423	0.469
Regulation of biological quality	3400	2.85	6	0.0435	0.476
Cell cycle arrest	428	0.359	2	0.0484	0.512
Reproductive process	1740	1.46	4	0.0489	0.512
Negative regulation of RNA metabolic process	1020	0.86	3	0.0496	0.512
Interphase of mitotic cell cycle	435	0.365	2	0.0499	0.512
GO MF					
Molecular Function	**Total**	**Expected**	**Hits**	**P.Value**	**FDR**
Structure_specific DNA binding	242	0.184	4	2.29E-05	0.00888
RNA polymerase II distal enhancer sequence_specific DNA binding transcription factor activity	110	0.0836	3	6.73E-05	0.0131
Enzyme binding	1200	0.911	6	0.000102	0.0132
Transcription factor binding	509	0.387	4	0.000409	0.0397
Steroid hormone receptor activity	56	0.0425	2	0.00079	0.0529
Ligand_activated sequence_specific DNA binding RNA polymerase II transcription factor activity	57	0.0433	2	0.000818	0.0529
Single_stranded DNA binding	65	0.0494	2	0.00106	0.0589
Positive regulation of transcription, DNA_dependent	1260	0.956	5	0.00145	0.0692
Sequence_specific DNA binding	732	0.556	4	0.00161	0.0692
Lipid binding	788	0.599	4	0.00211	0.0819
Protein heterodimerization activity	374	0.284	3	0.00242	0.0852
Phosphatase binding	116	0.0881	2	0.00334	0.108
Double_stranded DNA binding	149	0.113	2	0.00544	0.162
Protein homodimerization activity	573	0.435	3	0.00802	0.222
DNA binding	2760	2.1	6	0.00909	0.235
Monocarboxylic acid transmembrane transporter activity	36	0.0273	1	0.027	0.637
Identical protein binding	910	0.691	3	0.0279	0.637
Protein dimerization activity	996	0.757	3	0.0353	0.71
Kinase binding	418	0.318	2	0.0385	0.71

Histone acetyltransferase activity	52	0.0395	1	0.0388	0.71
Transport	4830	3.67	7	0.0389	0.71
Solute:sodium symporter activity	54	0.041	1	0.0403	0.71
Transcription from RNA polymerase II promoter	1930	1.47	4	0.0478	0.781
Histone deacetylase binding	65	0.0494	1	0.0483	0.781
GO CC					
Cellular Component	**Total**	**Expected**	**Hits**	**P.Value**	**FDR**
Nucleoplasm	1820	1.31	6	0.000876	0.197
Nuclear part	3330	2.4	7	0.00388	0.436
Nuclear lumen	2690	1.94	6	0.00673	0.463
Nucleus	7600	5.47	10	0.00885	0.463
Nuclear chromosome part	273	0.197	2	0.0158	0.463
Chromosome	784	0.564	3	0.0166	0.463
Nuclear ubiquitin ligase complex	26	0.0187	1	0.0186	0.463
Nuclear replication fork	28	0.0202	1	0.02	0.463
Organelle lumen	3380	2.44	6	0.0208	0.463
Nuclear chromosome	320	0.23	2	0.0214	0.463
Membrane_enclosed lumen	3440	2.48	6	0.0226	0.463
Replication fork	50	0.036	1	0.0354	0.664

Supplementary Table 15. List of enriched pathways, biological processes, molecular functions and cellular components in subnetwork 2/module 2 (pvalue 0.047, **Figure 4C**) of the network constructed upon the genes associated with the differentially methylated hyo- and hypermethylated promoters between the non-diseased aortic and mitral valve tissue based on KEGG/Reactome, Gene Ontology (GO) Biological Processes database, Gene Ontology (GO) Molecular Functions database and Gene Ontology (GO) Cellular Components database (full list). “Total” refers to the total number of genes that belong to a particular category as per the chosen reference list of genes, which is hg19 in our case, “Expected” denotes the number of genes to be expected in our gene list for a particular category, “Hits” describes the number of genes in our list that map to a particular category, “P.value” is equivalent to the enrichment p-value computed using the hypergeometric test (**see Methods**) and FDR stands for false discovery rate, which is the method used to correct the corresponding p-value for multiple testing.

3 References

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