SUPPLEMENTAL MATERIAL

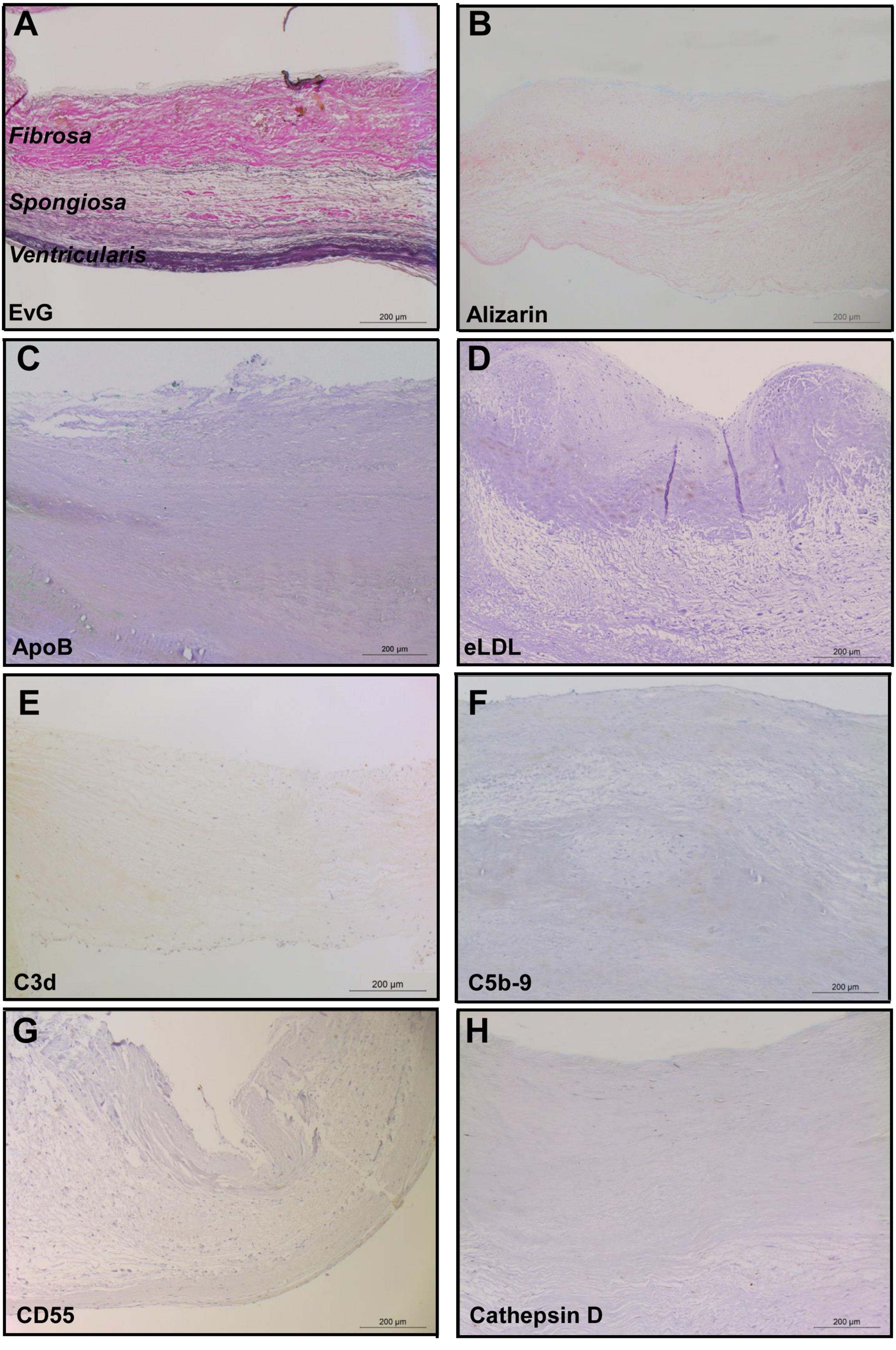
A
Fibrosa
Spongiosa
Ventricularis
EvG
200 µm
B
Alizarin
200 µm
C
ApoB
200 µm
D
eLDL
200 µm
E
C3d
200 µm
F
C5b-9
200 µm
G
CD55
200 µm
H
Cathepsin D
200 µm

Figure S1

Figure S1. Internal control tissues for both histochemistry and immunohistochemistry comprising unaffected areas of eight different aortic valves. In **A,** note the aortic valve leaflet composed of three anatomic layers: the fibrosa, a collagen-rich layer on the aortic side of the valve (top layer); the spongiosa, a layer of variable thickness lying between the fibrosa and ventricularis, with a less dense matrix and often containing adipose cells and the ventricularis, a layer with prominent elastin fibers located on the ventricular side of the valve (bottom layer). In **B** to **F**, note the lack of calcified areas (**B**) as well as any of the antigens detected from Grade 1 upward (**C** to **F**, compare with figures 1, 2, 3 and 5).

		Table S1	Affymetrix Human Gene 1.0 ST		Affymetrix Human Genome U133 Plus 2.0 (Bossé et al.)		Affymetrix Human Gene 1.0 ST vs Affymetrix Human Genome U133 Plus 2.0 (Bossé et al.)				
Gene Symbol	**Heatmap ID**	**Gene Description**	**Probe Set Name**	**Mean log2 Signal**	**Probe Set Name**	**Mean log2 Signal**	**Fold Change**	**unadjusted limma p-Value**	**Holm-adjusted p-Value**	**Percent Identity**	**SIF Percent Identity**
C1QA		complement component 1, q subcomponent, A chain	7898793	6,66	218232_at	9,14	0,18	7,22E-06	3,01E-05	98,14	100
C1RL	[I]	complement component 1, r subcomponent-like	7960757	6,74	233645_s_at	8,58	0,28	2,07E-07	1,90E-06	95,53	99,36
	[II]	complement component 1, r subcomponent-like	7960757	6,74	218983_at	5,49	2,38	2,11E-05	7,30E-05	99,88	100
C1S	[I]	complement component 1, s subcomponent	7953603	9,78	208747_s_at	10,88	0,46	6,58E-04	0,0014	99,81	100
	[II]	complement component 1, s subcomponent	7953603	9,78	1555229_a_at	9,09	1,61	0,0135	0,021	55,8	99,22
C2	[I]	complement component 2	8118324	6,39	1554533_at	4,33	4,2	4,07E-06	1,88E-05	94,3	100
	[II]	complement component 2	8118324	6,39	203052_at	6,9	0,7	0,0684	0,0913	99,96	100
C3		complement component 3	8033257	10,2	217767_at	9,21	2	0,0035	0,00618	99,92	99,82
C4A	[I]	complement component 4A (Rodgers blood group)	8118409	6,92	214428_x_at	7,88	0,51	9,31E-04	0,00191	96,04	55,9
	[II]	complement component 4A (Rodgers blood group)	8118409	6,92	208451_s_at	7,44	0,7	0,0497	0,0685	99,94	100
C4BPA		complement component 4 binding protein, alpha	7909318	4,19	205654_at	6,44	0,21	4,10E-07	3,18E-06	99,91	100
C4BPB		complement component 4 binding protein, beta	7909306	4,44	208209_s_at	5,86	0,37	1,26E-05	4,77E-05	0	100
C5		complement component 5	8163839	5,26	205500_at	4,8	1,38	0,0141	0,0219	99,87	100
C6		complement component 6	8111864	5,58	210168_at	8,21	0,16	3,58E-06	1,69E-05	99,97	100
C7		complement component 7	8105084	10,7	202992_at	11,82	0,46	4,99E-04	0,0011	99,77	100
C8A		complement component 8, alpha polypeptide	7901732	4,33	206305_s_at	5,01	0,62	0,00194	0,00364	99,79	100
C8B		complement component 8, beta polypeptide	7916526	4,75	206979_at	5,69	0,52	8,04E-04	0,00167	99,95	99,8
C8G		complement component 8, gamma polypeptide	8159491	5,93	210324_at	5,01	1,91	1,40E-04	3,64E-04	99,12	99,8
CD46	[I]	CD46 molecule, complement regulatory protein	7909400	7,82	207549_x_at	5,34	5,55	3,10E-07	2,57E-06	99,52	100
	[II]	CD46 molecule, complement regulatory protein	7909400	7,82	211574_s_at	6,16	3,15	2,05E-05	7,11E-05	100	100
	[III]	CD46 molecule, complement regulatory protein	7909400	7,82	208783_s_at	7,88	0,95	0,788	0,819	98,4	100
CD55	[I]	CD55 molecule, decay accelerating factor for complement (Cromer blood group)	7909332	8,96	1555950_a_at	5,79	8,97	3,75E-08	5,47E-07	95,94	100
	[II]	CD55 molecule, decay accelerating factor for complement (Cromer blood group)	7909332	8,96	201925_s_at	6,88	4,21	3,50E-05	1,12E-04	54,57	100
CFB	[I]	complement factor B	8118345	7,01	211920_at	5,04	3,89	3,54E-06	1,67E-05	99,89	100
	[II]	complement factor B	8118345	7,01	202357_s_at	5,64	2,57	1,90E-04	4,73E-04	99,92	100
CFD		complement factor D (adipsin)	8024062	7,54	205382_s_at	8,54	0,5	3,65E-04	8,37E-04	99,44	100
CFH		complement factor H	7908459	10,44	213800_at	9,89	1,46	0,0149	0,023	94,6	100
CFHR1		complement factor H-related 1	7908488	6,03	215388_s_at	9,67	0,08	6,30E-11	1,00E-08	99,08	98,46
CLU	[I]	clusterin	8149927	11,44	208791_at	12,42	0,5	0,00117	0,00234	99,88	99,75
	[II]	clusterin	8149927	11,44	208792_s_at	10,57	1,82	0,00401	0,00699	99,88	100
	[III]	clusterin	8149927	11,44	222043_at	12,29	0,56	0,0044	0,00761	95,36	100
CR1	[I]	complement component (3b/4b) receptor 1 (Knops blood group)	7909371	5,79	244313_at	4,76	2,05	0,0164	0,025	98,62	99,04
	[II]	complement component (3b/4b) receptor 1 (Knops blood group)	7909371	5,79	239205_s_at	6,69	0,54	0,0362	0,0514	52,56	95,96
	[III]	complement component (3b/4b) receptor 1 (Knops blood group)	7909371	5,79	206244_at	5,39	1,32	0,299	0,348	99,86	99,81
	[IV]	complement component (3b/4b) receptor 1 (Knops blood group)	7909371	5,79	208488_s_at	5,71	1,06	0,836	0,861	99,87	99,81
CR2		complement component (3d/Epstein Barr virus) receptor 2	7909350	4,11	205544_s_at	5,57	0,36	1,90E-05	6,67E-05	99,9	99,8
CRP	[I]	C-reactive protein, pentraxin-related	7921449	4,38	205753_at	5,34	0,51	7,77E-04	0,00162	99,45	99,77
	[II]	*C-reactive protein, pentraxin-related*	*7921449*	*4,38*	*37020_at*	*4,68*	*0,81*	*0,178*	*0,217*	*94,59*	*90,62*
CTSC	[I]	cathepsin C	7950906	8,8	225647_s_at	5,14	12,71	1,58E-06	8,89E-06	94,63	100
	[II]	cathepsin C	7950906	8,8	225646_at	5,75	8,29	1,04E-05	4,04E-05	94,63	100
	[III]	cathepsin C	7950906	8,8	201487_at	8,47	1,26	0,44	0,49	99,95	100
CTSD		cathepsin D	7945666	9,66	200766_at	7,2	5,53	1,76E-06	9,68E-06	99,95	100
CTSZ		cathepsin Z	8067279	8,37	210042_s_at	7,33	2,06	0,00231	0,00426	99,16	99,24
FCN2		ficolin (collagen/fibrinogen domain containing lectin) 2 (hucolin)	8159211	5,89	207804_s_at	4,48	2,66	1,56E-05	5,66E-05	99,62	99,7
FCN3		ficolin (collagen/fibrinogen domain containing) 3 (Hakata antigen)	7914075	6,13	205866_at	4,44	3,23	8,24E-07	5,36E-06	66,09	99,76
IL6R	[I]	interleukin 6 receptor	7905789	5,83	205945_at	4,92	1,89	5,09E-05	1,53E-04	99,64	99,57
	[II]	interleukin 6 receptor	7905789	5,83	226333_at	5,51	1,24	0,0532	0,0728	98,25	100
IL6ST	[I]	interleukin 6 signal transducer (gp130, oncostatin M receptor)	8112139	9,27	211000_s_at	5,23	16,47	1,89E-09	7,41E-08	99,95	100
	[II]	interleukin 6 signal transducer (gp130, oncostatin M receptor)	8112139	9,27	204864_s_at	5,88	10,56	2,37E-08	3,98E-07	99,97	100
	[III]	interleukin 6 signal transducer (gp130, oncostatin M receptor)	8112139	9,27	204863_s_at	7,21	4,2	2,15E-06	1,13E-05	99,26	100
	[IV]	interleukin 6 signal transducer (gp130, oncostatin M receptor)	8112139	9,27	212195_at	10,81	0,35	3,04E-05	9,91E-05	98,85	100
	[V]	interleukin 6 signal transducer (gp130, oncostatin M receptor)	8112139	9,27	212196_at	8,22	2,08	7,70E-04	0,00161	98,85	100
KRT1		keratin 1	7963491	4,52	205900_at	5,83	0,4	9,50E-05	2,60E-04	99,28	98,32
MASP1	[I]	mannan-binding lectin serine peptidase 1 (C4/C2 activating component of Ra-reactive factor)	8092661	6,43	232224_at	7,52	0,47	5,43E-04	0,00119	96,96	99,22
	[II]	mannan-binding lectin serine peptidase 1 (C4/C2 activating component of Ra-reactive factor)	8092661	6,43	210680_s_at	5,56	1,83	0,00179	0,0034	90,42	99,64
	[III]	mannan-binding lectin serine peptidase 1 (C4/C2 activating component of Ra-reactive factor)	8092661	6,43	206449_s_at	6,13	1,23	0,195	0,237	98,39	99,56
MASP2	[I]	mannan-binding lectin serine peptidase 2	7912361	4,86	207041_at	7,53	0,16	1,53E-09	6,42E-08	99,23	100
	[II]	mannan-binding lectin serine peptidase 2	7912361	4,86	210798_x_at	6,14	0,41	3,34E-06	1,60E-05	100	100
MMP12		matrix metallopeptidase 12 (macrophage elastase)	7951297	4,49	204580_at	5,78	0,41	9,36E-04	0,00191	99,61	99,61
MMP13		matrix metallopeptidase 13 (collagenase 3)	7951309	4,39	205959_at	5,46	0,48	0,0023	0,00424	99,71	99,75
MMP14	[I]	matrix metallopeptidase 14 (membrane-inserted)	7973336	6,92	217279_x_at	7,61	0,62	0,00855	0,0139	94,21	83,58
	[II]	matrix metallopeptidase 14 (membrane-inserted)	7973336	6,92	202827_s_at	6,44	1,39	0,0631	0,085	99,35	100
	[III]	matrix metallopeptidase 14 (membrane-inserted)	7973336	6,92	202828_s_at	6,45	1,38	0,0642	0,0863	99,97	100
MMP16	[I]	matrix metallopeptidase 16 (membrane-inserted)	8151686	5,55	207013_s_at	6,89	0,39	2,62E-06	1,33E-05	99,86	99,81
	[II]	matrix metallopeptidase 16 (membrane-inserted)	8151686	5,55	207012_at	4,8	1,68	1,96E-04	4,85E-04	99,64	99,58
	[III]	matrix metallopeptidase 16 (membrane-inserted)	8151686	5,55	208166_at	4,82	1,66	6,90E-04	0,00146	98,54	99,25
	[IV]	matrix metallopeptidase 16 (membrane-inserted)	8151686	5,55	208167_s_at	5,02	1,45	0,00291	0,00524	98,54	100
	[V]	matrix metallopeptidase 16 (membrane-inserted)	8151684	5,94	223614_at	5,09	1,8	0,00398	0,00695	99,75	0
MMP17		matrix metallopeptidase 17 (membrane-inserted)	7959946	5,18	206234_s_at	5,56	0,77	0,0335	0,0479	99,42	99,49
MMP19	[I]	matrix metallopeptidase 19	7956038	7,04	227106_at	8,38	0,4	4,44E-05	1,36E-04	91,52	100
	[II]	matrix metallopeptidase 19	7963946	6,87	204574_s_at	7,76	0,54	0,00301	0,0054	99,72	100
	[III]	matrix metallopeptidase 19	7963946	6,87	204575_s_at	7,77	0,54	0,00369	0,00648	98,79	99,81
MMP23B		matrix metallopeptidase 23B	7897006	7,17	207118_s_at	4,96	4,64	5,49E-09	1,49E-07	98,46	100
MMP25	[I]	matrix metallopeptidase 25	7992811	5,51	207289_at	7,42	0,27	1,27E-06	7,47E-06	99,84	0
	[II]	matrix metallopeptidase 25	7992811	5,51	207890_s_at	4,79	1,65	0,00119	0,00237	65,79	100
MMP28	[I]	matrix metallopeptidase 28	8014282	6,1	224207_x_at	9,09	0,13	1,87E-10	1,73E-08	96,62	99,25
	[II]	matrix metallopeptidase 28	8014282	6,1	222937_s_at	8,59	0,18	1,45E-09	6,19E-08	99,83	100
	[III]	matrix metallopeptidase 28	8014282	6,1	239273_s_at	4,55	2,93	5,43E-07	3,92E-06	95,64	100
	[IV]	matrix metallopeptidase 28	8014282	6,1	219909_at	4,9	2,29	5,97E-06	2,57E-05	98,43	100
PLAT		plasminogen activator, tissue	8150509	9,04	201860_s_at	7,38	3,18	9,33E-04	0,00191	99,96	100
PLAU	[I]	plasminogen activator, urokinase	7928429	6,81	211668_s_at	6,29	1,43	0,0231	0,0341	99,86	99,77
	[II]	plasminogen activator, urokinase	7928429	6,81	205479_s_at	7,01	0,87	0,361	0,411	99,13	99,2
PLG	[I]	plasminogen	8123259	5,31	209978_s_at	4,63	1,59	0,00176	0,00335	18,26	99,75
	[II]	plasminogen	8123259	5,31	209977_at	4,96	1,27	0,0663	0,0888	18,26	99,74
SERPING1		serpin peptidase inhibitor, clade G (C1 inhibitor), member 1	7940028	10,32	200986_at	7,65	6,38	4,46E-08	6,22E-07	100	100
TPSD1		tryptase delta 1	7992191	6,58	214568_at	5,44	2,2	2,33E-05	7,94E-05	100	100

Table S1. Results of comparison between cases (n = 4) and controls (n = 4) for selected genes by microarray analysis.