Supplemental Information

A Combined Proteomic and Transcriptomic Approach Shows Diverging Molecular Mechanisms in Thoracic Aortic Aneurysm Development In Patients With Tricuspid- And Bicuspid Aortic Valve

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Supplemental Figure 1

PCA (A) and OPLS-DA (B) of protein spot expression data with TAV vs BAV contrast in OPLS-DA. The analyses were performed on 22 patients with TAV and BAV and non-dilated ascending aorta. The Hotelling's T2 (based on 95% confidence level) tolerance ellipsoid and ellipse are shown in the scores plots of PCA (A) and OPLS-DA (B), respectively. Three-dimensional scores plot showing the PC1-PC3 plane of TAV (blue) and BAV (green) samples with non-dilated aorta tissues. Three-dimensional score plots are rotated as to display the highest separation between the two groups of patients. Two-dimensional scores plot of OPLS-DA showing the first predictive component (tp1) and orthogal component (to1) plane of TAV(blue) and BAV (green) samples without dilatation. Bar plots of loadings and jack-knife confidence intervals contributing to the first PC for the 302 protein spots. Model parameters for both PCA and OPLS-DA are shown in Supplemental Table 1.

Supplemental Figure 2

PCA (A, D) and OPLS-DA (B-C, E-F) of LC-MS/MS protein expression data. The analyses were performed on 21 patients and 35 proteins found in the LC-MS/MS analysis that overlap with proteins identified by 2D gel analysis (Table 2). The Hotelling's T2 (based on 95% confidence level) tolerance ellipsoid and ellipse are shown in the scores plots of PCA (A, D)and OPLS-DA (B, E), respectively. Three-dimensional scores plot showing the PC1-PC3 plane of non-dilated (black) and dilated (red) thoracic aorta tissue samples with TAV (A) and BAV (D) patients separately. Three-dimensional score plots are rotated as to display the highest separation between the two groups of patients. Two-dimensional scores plot of OPLS-DA showing the first predictive component (tp1) and orthogal component (to1) plane of non-dilated (black) and dilated (red) thoracic aorta tissue samples with TAV (B) and BAV (E) separately. Bar plots of loadings and jack-knife confidence intervals contributing to the first PC for the chosen genes in TAV (C) and BAV (F). Model parameters for both PCA and OPLS-DA are shown in Supplemental Table 1.

Supplemental Figure 3

OPLS-DA of LC-MS/MS protein expression data. The analyses were performed on 21 patients and 286 proteins in A and 35 proteins found in the LC-MS/MS analysis that overlap with proteins identified by 2D gel analysis (Table 2) in B (corresponding PCA and loading plot for this particular analysis can be foundin Supplemental Figure 2). Combined model scatter plot where loadings from TAV model of dilated versus non-dilated aorta samples is plotted against loadings from BAV model of dilated versus non-dilated aorta samples, color coded according to significant proteins identified with 2D-DIGE where common proteins for TAV and BAV models are color coded as red dots, statistically significant only in TAV (blue dots), and BAV (green dots). Model parameters for OPLS-DA are shown in Supplemental Table 1.

Supplemental Figure 4

IHC staining of paraffin-embedded sections taken from aortic intima-media in non-dilated (ND) and dilated (D) aortas of TAV and BAV patients respectively. Pictures are aligned according to aortic phenotypes in perpendicular, and antibodies used in the vertical columns. Antibodies: anti-human, LDH, TGM2, TTR, VIM antibodies, top to bottom respectively.

Supplemental Figure 5

PCA (A, D) and OPLS-DA (B-C, E-F) of mRNA expression data. The analyses were performed on 81 patients (4) and 43 genes chosen based on the identfied protein spots in Figure 1, Table 1, Supplemental Table 3. The Hotelling's T2 (based on 95% confidence level) tolerance ellipsoid and ellipse are shown in the scores plots of PCA (A, D)and OPLS-DA (B, E), respectively. Three-dimensional scores plot showing the PC1-PC3 plane of non-dilated (black) and dilated (red) thoracic aorta tissue samples with TAV (A) and BAV (D) patients separately. Three-dimensional score plots are rotated as to display the highest separation between the two groups of patients. Two-dimensional scores plot of OPLS-DA showing the first predictive component (tp1) and orthogonal component (to1) plane of non-dilated (black) and dilated (red) thoracic aorta tissue samples with TAV (B) and BAV (E) separately. Bar plots of loadings and jack-knife confidence intervals contributing to the first PC for the chosen genes in TAV (C) and BAV (F). Model parameters for both PCA and OPLS-DA are shown in Supplemental Table 1.

Supplemental Figure 6

PCA (A, D) and OPLS-DA (B-C, E-F) of gene level normalized exon expression (splice index) data. The analyses were performed on 81 patients (4) and 393 exons chosen based on the identfied protein spots in Figure 1, Table 1, Supplemental Table 3. The Hotelling's T2 (based on 95% confidence level) tolerance ellipsoid and ellipse are shown in the scores plots of PCA (A, D)and OPLS-DA (B, E), respectively. Three-dimensional scores plot showing the PC1-PC3 plane of non-dilated (black) and dilated (red) thoracic aorta tissue samples with TAV (A) and BAV (D) patients separately. Three-dimensional score plots are rotated as to display the highest separation between the two groups of patients. Two-dimensional scores plot of OPLS-DA showing the first predictive component (tp1) and orthogal component (to1) plane of non-dilated (black) and dilated (red) thoracic aorta tissue samples with TAV (B) and BAV (E) separately. Bar plots of loadings and jack-knife confidence intervals contributing to the first PC for the chosen genes in TAV (C) and BAV (F). (G) Combined model scatter plot where loadings from TAV model of dilated versus non-dilated aorta samples is plotted against loadings from BAV model of dilated versus non-dilated aorta samples, color coded according to significant spots (derived from (C) and (F)) common for TAV and BAV models (red dots), statistically significant only in TAV (blue dots), and BAV (green dots). The black diagonal is aimed for the interpretation purposes. (H) Venn diagram based on ABS (loading) – ABS (jack-knife confidence interval) significant protein spots of dilated versus non-dilated samples in TAV and BAV patients separately, color coded according to (G). Model parameters for both PCA and OPLS-DA are shown in Supplemental Table 1.

Supplemental Table 1. Model quality parameters of PCA and OPLS-DA. No of PCs refers to the optimal number of PCs for a particular multivariate data model according to cross-validation. R_X^2 accounts for the explained variance while Q_Y^2 accounts for the cumulative fraction of the total variation of Y that can be predicted by the model. Q_X^2 accounts for the cumulative fraction of the total variation of X that can be predicted by the model. R_Y^2 accounts for the explained variance for the Y component.

PCA models

Model description	No of PCs	No of patients	No of protein spots/proteins/genes/exons	R_X^2	Q_X^2
Protein level 2D gel - TAV patients only - **Figure 2**	3	21	302	0.632	0.363
Protein level 2D gel - BAV patients only - **Figure 2**	3	23	302	0.526	0.254
Protein level 2D gel - Non-dilated patients only - **Supplemental Figure 1**	3	22	302	0.542	0.0746
Protein level LC-MS/MS - TAV patietnts only - **Supplemental Figure 2**	3	10	35	0.721	0.129
Protein level LC-MS/MS - BAV patietnts only - **Supplemental Figure 2**	3	11	35	0.706	0.142
Gene level - TAV patients only, genes from identified proteins - **Supplemental Figure 5**	4	29	43	0.64	0.22
Gene level - BAV patients only, genes from identified proteins - **Supplemental Figure 5**	4	52	43	0.55	0.25
Exon level - TAV patients only, exons from identified proteins - **Supplemental Figure 6**	4	29	393	0.45	0.15
Exon level - BAV patients only, exons from identified proteins - **Supplemental Figure 6**	4	52	393	0.37	0.16

OPLS-DA models

Model description	No of PCs	No of patients	No of protein spots/proteins/genes/exons	R_Y^2	Q_Y^2	R_X^2
Protein level - TAV patients only - **Figure 2, Figure 3**	1+4	21	302	0.992	0.783	0.699
Protein level - BAV patients only - **Figure 2, Figure 3**	1+4	23	302	0.988	0.464	0.581
Protein level - Non-dilated patients only, TAV vs BAV - **Supplemental Figure 1**	1+1	22	302	0.736	-0.419	0.263
Protein level LC-MS/MS only 2D gel identified proteins - TAV patietnts only - **Supplemental Figure 2, 3B**	1+1	10	35	0.937	0.725	0.602
Protein level LC-MS/MS only 2D gel identified proteins - BAV patietnts only - **Supplemental Figure 2, 3B**	1+1	11	35	0.924	0.435	0.527
Protein level LC-MS/MS all identified proteins - TAV patients only - **Supplemental Figure 3A**	1+1	10	286	0.976	0.773	0.448
Protein level LC-MS/MS all identified proteins - BAV patients only - **Supplemental Figure 3A**	1+1	11	286	0.954	0.416	0.423
Gene level - TAV patients only, genes from identified proteins - **Supplemental Figure 5**	1+1	29	43	0.784	0.537	0.41
Gene level - BAV patients only, genes from identified proteins - **Supplemental Figure 5**	1+1	52	43	0.6	0.3	0.35
Exon level - TAV patients only, exons from identified proteins - **Supplemental Figure 6**	1+1	29	393	0.91	0.48	0.18
Exon level - BAV patients only, exons from identified proteins - **Supplemental Figure 6**	1+2	52	393	0.89	0.34	0.25

Supplemental Table 2. Loadings and jack-knife (JK) confidence intervals for the 302 protein spots data set for both TAV and BAV OPLS-DA models, where dilated and non-dilated have been added as a Y variable.

TAV model					**BAV model**				
Protein spot number	**Loading value** [a]	**jack-knife (JK) confidence interval**[b]	**ABS(Loading value)-ABS(JK)**[c]	**Significant probe set = 1**[d]	Protein spot number	**Loading value** [a]	**jack-knife (JK) confidence interval**[b]	**ABS(Loading value)-ABS(JK)**[c]	**Significant probe set = 1**[d]
47	0.076	0.037	0.039	1	47	0.053	0.032	0.021	1
50	0.095	0.044	0.051	1	50	0.103	0.039	0.064	1
51	0.085	0.050	0.035	1	51	0.075	0.042	0.033	1
52	0.074	0.050	0.024	1	52	0.071	0.032	0.039	1
53	0.064	0.033	0.031	1	53	0.053	0.043	0.010	1
54	0.038	0.033	0.005	1	57	0.106	0.045	0.061	1
57	0.107	0.028	0.078	1	58	0.118	0.033	0.086	1
58	0.080	0.017	0.063	1	59	0.115	0.028	0.087	1
59	0.082	0.028	0.053	1	62	0.117	0.045	0.072	1
62	0.079	0.017	0.062	1	63	0.096	0.067	0.029	1
63	0.082	0.030	0.051	1	64	0.101	0.065	0.036	1
64	0.078	0.028	0.051	1	65	0.109	0.060	0.049	1
65	0.076	0.028	0.047	1	67	0.069	0.035	0.034	1
66	0.083	0.043	0.039	1	76	0.085	0.022	0.063	1
67	0.087	0.042	0.046	1	82	0.047	0.039	0.009	1
76	0.105	0.021	0.083	1	90	0.076	0.063	0.013	1
80	0.033	0.029	0.004	1	97	0.068	0.062	0.006	1
91	-0.042	0.022	0.019	1	112	0.065	0.054	0.011	1
94	-0.069	0.029	0.040	1	114	0.076	0.030	0.046	1
100	-0.057	0.038	0.020	1	122	0.060	0.039	0.021	1
101	-0.058	0.028	0.030	1	128	0.061	0.037	0.024	1
102	-0.065	0.029	0.035	1	130	0.048	0.036	0.012	1
106	-0.052	0.032	0.020	1	131	0.082	0.082	0.000	1
112	0.089	0.046	0.043	1	133	0.058	0.040	0.017	1
113	0.091	0.042	0.049	1	136	0.070	0.030	0.040	1
114	0.106	0.039	0.068	1	142	0.094	0.038	0.056	1
115	-0.051	0.022	0.029	1	149	0.073	0.042	0.031	1
116	-0.053	0.029	0.024	1	152	0.086	0.041	0.045	1
117	-0.045	0.033	0.012	1	153	0.068	0.052	0.017	1
119	-0.056	0.030	0.027	1	176	-0.067	0.067	0.000	1
120	-0.053	0.025	0.028	1	180	0.093	0.023	0.070	1
121	-0.055	0.034	0.021	1	182	0.083	0.032	0.050	1
123	-0.043	0.038	0.005	1	185	0.071	0.045	0.026	1
128	0.096	0.036	0.059	1	187	0.058	0.054	0.003	1
133	0.073	0.051	0.022	1	188	0.067	0.065	0.002	1
135	0.079	0.049	0.031	1	189	0.091	0.065	0.026	1
136	0.102	0.030	0.072	1	199	0.051	0.039	0.012	1
138	0.071	0.064	0.007	1	203	0.086	0.032	0.054	1
140	0.093	0.063	0.030	1	207	0.089	0.035	0.055	1
141	0.088	0.023	0.065	1	211	0.081	0.030	0.051	1
142	0.076	0.044	0.033	1	226	0.105	0.031	0.074	1
144	0.074	0.035	0.039	1	231	0.065	0.028	0.037	1
146	0.072	0.070	0.003	1	233	0.061	0.036	0.025	1
148	0.089	0.057	0.032	1	235	0.050	0.034	0.016	1
152	0.053	0.040	0.013	1	236	0.055	0.053	0.002	1
153	0.068	0.031	0.037	1	239	0.052	0.036	0.016	1
167	0.115	0.037	0.078	1	243	0.102	0.020	0.082	1
168	0.075	0.073	0.002	1	248	0.087	0.044	0.042	1
169	0.088	0.065	0.023	1	249	0.075	0.039	0.036	1
170	0.049	0.040	0.009	1	252	0.070	0.050	0.020	1
173	-0.038	0.036	0.002	1	262	0.064	0.049	0.015	1
175	0.049	0.035	0.014	1	265	0.071	0.045	0.026	1
179	-0.056	0.038	0.018	1	267	-0.083	0.056	0.027	1
180	0.046	0.040	0.006	1	269	-0.076	0.044	0.032	1
182	0.056	0.032	0.025	1	272	-0.059	0.051	0.008	1
185	0.061	0.033	0.028	1	284	-0.079	0.058	0.021	1
189	0.045	0.043	0.002	1	285	0.060	0.039	0.021	1
193	0.044	0.043	0.001	1	291	0.069	0.041	0.029	1
199	0.089	0.059	0.029	1	292	0.075	0.063	0.012	1
203	0.101	0.045	0.056	1	293	-0.086	0.047	0.038	1
207	0.091	0.047	0.044	1	296	0.043	0.024	0.018	1
211	0.053	0.033	0.020	1	305	0.059	0.053	0.006	1
222	0.086	0.037	0.049	1	316	0.079	0.035	0.044	1
223	0.077	0.025	0.052	1	317	0.072	0.055	0.017	1
231	0.053	0.027	0.027	1	318	0.095	0.061	0.034	1
233	0.045	0.024	0.021	1	328	0.077	0.036	0.040	1
235	0.030	0.030	0.001	1	330	0.084	0.039	0.045	1
239	0.040	0.016	0.024	1	331	0.070	0.035	0.035	1
241	-0.051	0.031	0.021	1	339	0.066	0.042	0.024	1
243	0.049	0.029	0.020	1	345	0.068	0.039	0.030	1
245	-0.050	0.035	0.015	1	346	0.064	0.027	0.037	1
252	0.059	0.054	0.005	1	347	-0.071	0.061	0.010	1
253	-0.049	0.039	0.010	1	350	0.074	0.041	0.033	1
260	-0.069	0.039	0.030	1	355	0.071	0.037	0.034	1
262	0.064	0.039	0.025	1	356	0.084	0.038	0.046	1
265	0.084	0.049	0.035	1	358	0.064	0.052	0.011	1
266	0.083	0.061	0.022	1	371	0.072	0.045	0.026	1
267	-0.073	0.027	0.046	1	375	0.059	0.058	0.001	1
268	0.083	0.053	0.030	1	378	0.061	0.060	0.001	1
269	-0.067	0.026	0.041	1	383	0.058	0.047	0.012	1
272	-0.052	0.019	0.032	1	387	0.088	0.018	0.070	1
276	0.072	0.062	0.009	1	392	0.091	0.039	0.051	1
280	0.076	0.037	0.039	1	393	0.096	0.040	0.056	1
282	0.088	0.038	0.050	1	401	0.056	0.034	0.022	1
283	0.044	0.036	0.009	1	412	0.066	0.017	0.049	1

285	0.061	0.056	0.005	1
287	0.094	0.028	0.065	1
293	-0.053	0.037	0.016	1
296	0.057	0.040	0.016	1
300	0.066	0.063	0.003	1
301	0.075	0.073	0.002	1
302	0.072	0.069	0.003	1
304	0.098	0.049	0.049	1
305	0.092	0.053	0.039	1
311	0.071	0.068	0.003	1
317	0.030	0.027	0.003	1
318	0.071	0.041	0.030	1
323	-0.051	0.047	0.004	1
330	0.064	0.043	0.021	1
333	0.086	0.065	0.021	1
346	0.067	0.037	0.030	1
347	-0.048	0.041	0.006	1
348	0.063	0.042	0.021	1
349	-0.053	0.017	0.036	1
350	0.045	0.024	0.021	1
358	0.078	0.030	0.049	1
360	0.093	0.051	0.042	1
374	0.072	0.036	0.037	1
378	0.076	0.046	0.030	1
386	0.067	0.065	0.002	1
387	0.097	0.044	0.053	1
388	0.086	0.059	0.027	1
389	0.081	0.051	0.030	1
392	0.112	0.025	0.086	1
393	0.094	0.047	0.047	1
394	0.074	0.052	0.022	1
401	0.070	0.049	0.020	1
412	0.072	0.051	0.021	1
421	0.051	0.049	0.002	1
422	0.078	0.052	0.026	1
423	0.069	0.043	0.026	1
429	0.032	0.023	0.009	1
434	-0.045	0.032	0.012	1
462	-0.076	0.024	0.052	1
464	-0.076	0.031	0.045	1
465	-0.076	0.027	0.049	1
468	-0.080	0.023	0.057	1
479	-0.030	0.029	0.000	1
480	-0.073	0.030	0.042	1
484	-0.072	0.026	0.046	1
488	-0.074	0.030	0.044	1
492	-0.077	0.024	0.053	1
544	0.089	0.050	0.039	1
548	0.103	0.024	0.080	1
747	-0.081	0.025	0.056	1
751	-0.078	0.024	0.054	1
753	0.098	0.038	0.059	1
754	0.084	0.029	0.055	1
755	0.085	0.031	0.053	1
761	0.101	0.029	0.072	1
762	0.071	0.022	0.049	1
764	0.095	0.042	0.053	1
765	0.093	0.047	0.046	1
769	0.095	0.045	0.049	1
771	0.062	0.031	0.031	1
776	0.092	0.038	0.054	1
778	0.082	0.032	0.050	1
781	0.109	0.041	0.069	1
783	0.068	0.026	0.042	1
785	0.070	0.026	0.044	1
787	0.078	0.065	0.014	1
791	0.106	0.030	0.076	1
792	0.060	0.036	0.024	1
793	0.052	0.031	0.021	1
796	0.060	0.050	0.009	1
799	0.088	0.043	0.045	1
803	0.060	0.053	0.007	1
812	0.040	0.038	0.002	1
825	-0.022	0.016	0.006	1
827	-0.019	0.014	0.005	1
835	-0.039	0.034	0.005	1
69	0.009	0.055	-0.045	0
70	0.017	0.051	-0.034	0
71	0.022	0.064	-0.041	0
72	-0.001	0.062	-0.062	0
73	-0.005	0.047	-0.042	0
74	0.036	0.071	-0.034	0
75	0.042	0.065	-0.023	0
82	0.045	0.054	-0.009	0
85	0.001	0.045	-0.044	0
87	-0.020	0.054	-0.034	0
90	-0.025	0.057	-0.032	0
95	-0.020	0.051	-0.030	0
96	0.073	0.073	-0.001	0
97	0.068	0.072	-0.004	0
98	0.010	0.065	-0.055	0
99	-0.030	0.059	-0.029	0

422	0.066	0.035	0.031	1
440	0.045	0.042	0.003	1
451	-0.062	0.057	0.005	1
462	-0.071	0.035	0.036	1
464	-0.074	0.027	0.047	1
465	-0.079	0.033	0.046	1
468	-0.079	0.036	0.043	1
480	-0.074	0.030	0.044	1
484	-0.086	0.026	0.060	1
488	-0.075	0.030	0.045	1
492	-0.091	0.029	0.062	1
544	0.070	0.035	0.035	1
592	-0.072	0.071	0.002	1
747	-0.082	0.038	0.044	1
751	-0.090	0.034	0.057	1
753	0.080	0.032	0.047	1
754	0.107	0.023	0.084	1
755	0.107	0.024	0.083	1
761	0.083	0.036	0.047	1
762	0.106	0.030	0.076	1
764	0.087	0.031	0.056	1
765	0.089	0.026	0.063	1
769	0.086	0.028	0.058	1
771	0.104	0.015	0.088	1
776	0.087	0.036	0.051	1
778	0.104	0.023	0.081	1
781	0.064	0.043	0.021	1
783	0.110	0.016	0.095	1
785	0.117	0.032	0.085	1
787	0.069	0.037	0.032	1
791	0.047	0.045	0.001	1
793	0.107	0.018	0.089	1
796	0.088	0.054	0.033	1
799	0.095	0.040	0.055	1
803	0.093	0.049	0.043	1
805	0.068	0.052	0.016	1
807	0.077	0.051	0.025	1
808	0.078	0.045	0.033	1
816	0.073	0.042	0.030	1
819	0.051	0.037	0.014	1
821	0.058	0.020	0.038	1
825	0.064	0.025	0.039	1
826	0.068	0.053	0.015	1
827	0.060	0.019	0.041	1
835	-0.043	0.031	0.012	1
54	0.035	0.045	-0.009	0
66	0.035	0.044	-0.009	0
69	0.061	0.082	-0.021	0
70	0.034	0.069	-0.036	0
71	0.014	0.048	-0.035	0
72	0.012	0.071	-0.059	0
73	0.029	0.083	-0.054	0
74	0.045	0.092	-0.047	0
75	0.027	0.058	-0.031	0
80	0.036	0.064	-0.027	0
85	0.053	0.065	-0.012	0
87	0.044	0.058	-0.014	0
91	0.005	0.037	-0.033	0
94	-0.036	0.055	-0.019	0
95	-0.003	0.062	-0.059	0
96	0.039	0.062	-0.023	0
98	0.021	0.069	-0.048	0
99	-0.009	0.063	-0.054	0
100	-0.015	0.062	-0.047	0
101	-0.028	0.061	-0.033	0
102	-0.031	0.056	-0.024	0
103	-0.014	0.057	-0.043	0
104	0.022	0.061	-0.040	0
105	0.057	0.066	-0.009	0
106	-0.032	0.057	-0.025	0
107	-0.031	0.056	-0.025	0
108	-0.011	0.074	-0.063	0
109	0.040	0.067	-0.027	0
113	0.042	0.047	-0.005	0
115	-0.031	0.071	-0.040	0
116	-0.020	0.085	-0.065	0
117	-0.012	0.049	-0.036	0
118	0.053	0.067	-0.014	0
119	-0.006	0.089	-0.083	0
120	0.004	0.089	-0.086	0
121	0.009	0.082	-0.073	0
123	0.010	0.073	-0.063	0
124	0.011	0.071	-0.061	0
125	0.017	0.056	-0.038	0
134	-0.018	0.070	-0.052	0
135	0.011	0.085	-0.074	0
137	-0.013	0.067	-0.054	0
138	-0.056	0.121	-0.065	0
139	-0.001	0.060	-0.059	0
140	0.026	0.072	-0.045	0
141	0.041	0.087	-0.046	0
144	0.058	0.065	-0.007	0

103	-0.031	0.046	-0.015	0
104	0.011	0.054	-0.043	0
105	0.040	0.063	-0.023	0
107	-0.042	0.042	0.000	0
108	-0.017	0.025	-0.008	0
109	0.014	0.057	-0.043	0
118	0.021	0.049	-0.028	0
122	0.006	0.055	-0.049	0
124	-0.030	0.040	-0.010	0
125	0.002	0.042	-0.040	0
130	0.020	0.055	-0.035	0
131	-0.011	0.051	-0.041	0
134	-0.036	0.057	-0.021	0
137	0.062	0.074	-0.012	0
139	0.045	0.061	-0.016	0
149	0.003	0.047	-0.044	0
155	0.043	0.064	-0.021	0
156	0.046	0.066	-0.020	0
157	0.042	0.063	-0.020	0
158	0.049	0.058	-0.009	0
159	0.045	0.064	-0.019	0
161	0.012	0.055	-0.043	0
162	0.046	0.062	-0.016	0
163	0.028	0.061	-0.033	0
164	0.010	0.038	-0.028	0
165	0.018	0.039	-0.021	0
166	-0.010	0.039	-0.029	0
171	0.036	0.047	-0.010	0
172	0.014	0.073	-0.059	0
174	-0.004	0.061	-0.056	0
176	-0.003	0.029	-0.026	0
177	0.034	0.053	-0.019	0
183	-0.021	0.051	-0.030	0
187	0.007	0.045	-0.037	0
188	0.008	0.036	-0.028	0
190	-0.008	0.042	-0.035	0
191	-0.024	0.031	-0.008	0
192	0.018	0.065	-0.047	0
194	-0.009	0.048	-0.040	0
198	0.056	0.073	-0.017	0
200	0.052	0.067	-0.016	0
218	0.059	0.061	-0.002	0
224	0.033	0.051	-0.018	0
226	0.001	0.026	-0.025	0
230	-0.002	0.033	-0.032	0
236	-0.011	0.048	-0.037	0
237	-0.031	0.036	-0.005	0
248	0.027	0.035	-0.008	0
249	0.028	0.067	-0.039	0
254	-0.019	0.045	-0.026	0
256	-0.035	0.043	-0.007	0
263	-0.028	0.049	-0.021	0
270	0.020	0.024	-0.004	0
273	-0.015	0.040	-0.025	0
277	-0.038	0.055	-0.017	0
278	0.002	0.061	-0.058	0
284	0.029	0.054	-0.026	0
291	-0.003	0.041	-0.037	0
292	0.065	0.085	-0.020	0
297	0.039	0.079	-0.041	0
299	0.038	0.071	-0.033	0
303	0.065	0.071	-0.006	0
306	0.052	0.065	-0.013	0
307	0.043	0.063	-0.020	0
309	0.065	0.082	-0.017	0
312	0.022	0.066	-0.044	0
314	-0.038	0.039	-0.002	0
316	0.019	0.053	-0.034	0
319	0.016	0.064	-0.047	0
320	-0.017	0.053	-0.036	0
321	-0.007	0.067	-0.060	0
322	-0.007	0.059	-0.052	0
326	0.048	0.060	-0.012	0
328	0.021	0.050	-0.029	0
331	0.030	0.034	-0.004	0
339	0.025	0.032	-0.007	0
345	0.026	0.035	-0.008	0
355	0.021	0.037	-0.016	0
356	0.033	0.041	-0.008	0
357	0.033	0.076	-0.043	0
362	-0.004	0.027	-0.023	0
363	-0.013	0.043	-0.030	0
371	0.028	0.048	-0.019	0
375	0.011	0.030	-0.019	0
382	-0.013	0.028	-0.014	0
383	0.044	0.044	-0.001	0
385	0.003	0.072	-0.069	0
395	-0.008	0.057	-0.049	0
398	-0.007	0.040	-0.033	0
411	-0.033	0.040	-0.007	0
414	0.052	0.058	-0.005	0
424	-0.034	0.036	-0.002	0

146	-0.031	0.058	-0.027	0
148	0.016	0.039	-0.023	0
155	0.008	0.059	-0.051	0
156	0.005	0.064	-0.059	0
157	0.002	0.069	-0.067	0
158	0.019	0.062	-0.043	0
159	0.020	0.065	-0.044	0
161	0.021	0.054	-0.033	0
162	0.035	0.058	-0.024	0
163	0.020	0.057	-0.037	0
164	0.028	0.091	-0.063	0
165	0.045	0.097	-0.052	0
166	0.017	0.101	-0.084	0
167	0.057	0.058	-0.001	0
168	-0.012	0.068	-0.056	0
169	0.005	0.071	-0.066	0
170	-0.028	0.100	-0.072	0
171	-0.039	0.080	-0.041	0
172	0.003	0.062	-0.059	0
173	-0.053	0.082	-0.030	0
174	0.019	0.092	-0.073	0
175	-0.024	0.090	-0.067	0
177	0.029	0.045	-0.015	0
179	0.000	0.126	-0.125	0
183	-0.038	0.049	-0.012	0
190	0.057	0.070	-0.013	0
191	0.037	0.093	-0.055	0
192	0.040	0.069	-0.029	0
193	0.046	0.064	-0.018	0
194	0.022	0.039	-0.016	0
198	0.053	0.059	-0.006	0
200	-0.027	0.083	-0.056	0
218	0.023	0.043	-0.020	0
222	0.051	0.065	-0.014	0
223	0.045	0.058	-0.014	0
224	0.048	0.075	-0.027	0
230	0.021	0.064	-0.043	0
237	-0.004	0.067	-0.063	0
241	-0.009	0.110	-0.101	0
245	0.006	0.115	-0.109	0
253	0.015	0.110	-0.095	0
254	0.023	0.050	-0.027	0
256	0.006	0.103	-0.097	0
260	-0.058	0.090	-0.032	0
263	0.003	0.092	-0.089	0
266	0.030	0.078	-0.049	0
268	0.015	0.073	-0.059	0
270	-0.001	0.042	-0.041	0
273	0.039	0.040	-0.001	0
276	0.045	0.053	-0.008	0
277	0.013	0.076	-0.063	0
278	0.043	0.062	-0.018	0
280	0.041	0.051	-0.010	0
282	0.035	0.072	-0.036	0
283	0.042	0.057	-0.015	0
287	0.048	0.062	-0.014	0
297	0.017	0.075	-0.058	0
299	0.042	0.050	-0.008	0
300	0.026	0.046	-0.020	0
301	0.049	0.060	-0.011	0
302	0.012	0.105	-0.093	0
303	0.021	0.060	-0.039	0
304	0.050	0.065	-0.014	0
306	0.024	0.046	-0.023	0
307	0.006	0.017	-0.011	0
309	0.021	0.049	-0.027	0
311	0.047	0.056	-0.010	0
312	0.033	0.053	-0.020	0
314	-0.001	0.048	-0.047	0
319	-0.009	0.056	-0.047	0
320	-0.046	0.093	-0.046	0
321	-0.011	0.101	-0.090	0
322	-0.020	0.098	-0.078	0
323	-0.035	0.103	-0.068	0
326	0.012	0.106	-0.094	0
333	0.049	0.075	-0.026	0
348	0.059	0.061	-0.002	0
349	-0.014	0.087	-0.073	0
357	0.065	0.068	-0.003	0
360	0.048	0.051	-0.004	0
362	0.023	0.053	-0.030	0
363	0.013	0.100	-0.088	0
374	0.027	0.080	-0.053	0
382	0.046	0.063	-0.017	0
385	0.019	0.078	-0.059	0
386	0.073	0.093	-0.020	0
388	0.056	0.085	-0.029	0
389	0.057	0.091	-0.035	0
394	0.071	0.087	-0.016	0
395	0.034	0.074	-0.040	0
398	0.042	0.067	-0.025	0
411	0.007	0.045	-0.038	0

426	0.059	0.072	-0.013	0	414	0.025	0.060	-0.035	0
430	0.014	0.093	-0.079	0	421	0.053	0.089	-0.036	0
431	-0.008	0.035	-0.027	0	423	0.018	0.059	-0.041	0
440	-0.013	0.042	-0.029	0	424	0.042	0.056	-0.014	0
443	-0.020	0.035	-0.016	0	426	-0.010	0.066	-0.056	0
451	-0.035	0.062	-0.027	0	429	-0.005	0.082	-0.076	0
483	0.023	0.035	-0.012	0	430	-0.024	0.056	-0.032	0
541	0.006	0.050	-0.044	0	431	0.053	0.060	-0.007	0
560	0.026	0.039	-0.013	0	434	-0.007	0.057	-0.050	0
563	0.036	0.060	-0.025	0	443	-0.021	0.056	-0.035	0
592	-0.034	0.045	-0.011	0	479	0.009	0.032	-0.023	0
593	-0.016	0.063	-0.047	0	483	0.025	0.102	-0.077	0
782	0.071	0.079	-0.008	0	541	-0.076	0.079	-0.002	0
795	-0.005	0.043	-0.038	0	548	0.023	0.055	-0.032	0
804	0.046	0.066	-0.020	0	560	0.055	0.063	-0.008	0
805	0.044	0.046	-0.002	0	563	0.004	0.106	-0.102	0
806	0.025	0.046	-0.021	0	593	-0.042	0.137	-0.095	0
807	0.027	0.040	-0.013	0	782	0.069	0.076	-0.008	0
808	0.037	0.044	-0.007	0	792	0.015	0.051	-0.036	0
809	0.025	0.054	-0.029	0	795	0.040	0.091	-0.050	0
810	0.037	0.065	-0.028	0	804	0.025	0.054	-0.029	0
811	0.047	0.069	-0.022	0	806	0.062	0.065	-0.003	0
813	0.048	0.063	-0.014	0	809	0.023	0.059	-0.037	0
814	0.037	0.066	-0.028	0	810	0.020	0.057	-0.037	0
816	0.042	0.044	-0.002	0	811	0.036	0.101	-0.065	0
819	-0.012	0.020	-0.008	0	812	0.031	0.069	-0.037	0
821	-0.007	0.022	-0.014	0	813	-0.001	0.050	-0.049	0
824	0.000	0.033	-0.032	0	814	0.021	0.072	-0.051	0
826	-0.013	0.027	-0.014	0	824	0.054	0.068	-0.014	0
829	0.021	0.059	-0.038	0	829	0.037	0.076	-0.038	0
831	0.022	0.056	-0.034	0	831	0.038	0.062	-0.023	0
833	-0.005	0.042	-0.037	0	833	0.010	0.040	-0.029	0
834	-0.037	0.039	-0.001	0	834	-0.018	0.042	-0.024	0

[a] Loading value from OPLS-DA model with controls vs dilated

[b] Jack-Knife confidence interval derived from cross-validation in OPLS-DA models

[c] Subtracting the jack-knife confidence intervals from the corresponding loading values, if positive indicates significance

[d] If the subtracting jack-knife cofidence interval from the corresponding loading is positive (significant), and indicated with 1, and if negative (non-singnificant), it is indicated with 0

Supplemental Table 3. Summary of identification measures for 109 protein spots from MALDI TOF/TOF m/z derived from Prfound (Prowl) search engine. In some cases several spots are included and considered as one due to limited possibilites to separate the two spots from the 2D gel. Both empiric and experimental pI and Mw are shown. Multivariate data analsyis statistics are alo shown. Green and blue color indicate higher expression in dilated and non-dilated respectively. All models are made on TAV and BAV patients separately comparing dilated (D) and non-dilated (C) thoracic aorta tissues. Multivarate data anaysis statistics are based on ABS (loading) – ABS (jack-knife confidence interval) values.

Spot number	Protein accession number	Gene name	Meta probe set ID	Protein name	No of protein spots identfied on gel	Experimental		In silica		Sequence Coverage (%)	No of peptides identified / No of possible peptides	Expectation value	TAV		BAV	
						pI	Mw	pI	MW				CvsD[a]	Fold (D-C)[b]	CvsD[c]	Fold (D-C)[b]
90	P02768	ALB	2731192	Serum albumin	11	5.77	62	6.1	71.37	7	5/10	6.1×10^{-4}		-1.05	0.013	1.15
94						5.55	59	6.1	71.37	13	8/32	2.1×10^{-4}	0.040	-1.23		-1.07
96						6.12	59	6.1	71.37	23	11/26	1.9×10^{-15}		1.57		1.13
97						6.03	59	6.1	71.37	15	7/16	6.3×10^{-8}		1.48	0.006	1.20
99						5.69	59	6.1	71.37	40	19/25	8.1×10^{-29}		-1.05		-1.01
100						5.62	59	6.1	71.37	17	12/33	1.6×10^{-10}	0.020	-1.12		-1.02
101						5.49	59	6.1	71.37	35	19/49	2.2×10^{-13}	0.030	-1.28		-1.06
105						5.95	59	6.1	71.37	23	9/46	5.5×10^{-7}		1.17		1.10
109						5.86	59	6.1	71.37	43	26/37	1.6×10^{-34}		1.06		1.05
112						6.84	55	6.1	71.37	21	8/27	1.7×10^{-6}	0.043	1.65	0.011	1.17
256						5.14	25	6.1	71.37	15	12/37	1.6×10^{-9}		-1.12		1.03
116_115	P07437	TUBB	2901913	Tubulin, beta	3	4.85	53	4.7	50.11	26	11/49	2.9×10^{-6}	0.024	-1.24		-1.15
152						4.86	42	4.7	50.11	40	25/42	3.4×10^{-15}	0.013	1.16	0.045	1.16
153						4.89	42	4.7	50.11	52	28/45	1.6×10^{-17}	0.037	1.23	0.017	1.11
198	P62736	ACTA2	3299504	actin, aortic smooth muscle	6	4.92	33	5.2	42.39	18	6/20	$1.1x10^{-4}$		1.22		1.20
203						4.97	33	5.2	42.39	29	12/63	$7.3x10^{-6}$	0.056	1.40	0.054	1.36
207						5.03	33	5.2	42.39	28	12/55	$2.8x10^{-8}$	0.044	1.43	0.055	1.38
762_761						5.28	32	5.2	42.39	21	6/21	9.0×10^{-5}	0.049	1.37	0.076	1.27
769_771						5.09	33	5.2	42.39	37	10/20	5.8×10^{-14}	0.049	1.72	0.058	1.54
778_776						5.33	32	5.2	42.39	31	10/22	6.5×10^{-12}	0.050	1.46	0.081	1.36
282	P27348	YWHAQ	2539869	tyrosine 3-monooxygenasea/tryptophan 5-monooxygenase activation protein (14-3-3 protein theta)	1	4.62	21	4.7	28.03	24	8/43	4.0×10^{-6}	0.050	1.80		1.23
287	P63104	YWHAZ	3146898	tyrosine 3-monooxygenasea/tryptophan 5-monooxygenase activation protein (14-3-3 protein zeta/delta)	2	4.66	21	4.7	27.90	24	8/24	3.3×10^{-11}	0.065	1.38		1.13
291						4.66	20	4.7	27.90	48	12/35	3.2×10^{-11}		-1.02	0.029	1.12
791	P31946	YWHAB	3886639	tyrosine 3-monooxygenasea/tryptophan 5-monooxygenase activation protein (14-3-3 protein beta/alpha)	2	4.69	20	4.8	28.18	27	11/30	7.9×10^{-5}	0.076	1.43	0.001	1.12
792						4.69	20	4.8	28.18	27	7/20	1.0×10^{-4}	0.024	1.25		1.02
224	P04083	ANXA1	3174816	annexin A1	2	6.6	28	6.6	38.92	44	13/33	1.7×10^{-10}		1.14		1.10
268						7.33	24	6.6	38.92	44	13/28	2.4×10^{-14}	0.030	1.42		1.04
270	P09525	ANXA4	2487412	annexin A4	1	5.57	24	5.8	36.30	46	17/31	2.6×10^{-12}		1.06		1.00
273	P08758	ANXA5	2784027	annexin A5	1	4.89	23	4.9	35.98	48	15/63	$1.8x10^{-8}$		-1.04		1.08
362	P24844	MYL9	3883921	myosin regulatory light polypeptide 9	2	4.69	15	5.6	13.85	27	4/14	1.3×10^{-3}		-1.07		1.06
371						4.74	15	5.6	13.85	42	5/13	1.7×10^{-4}		1.11	0.026	1.22
375	O14950	MYL12B	3776449	Myosin regulatory light chain 12B	2	4.63	15	4.7	19.83	19	5/10	3.3×10^{-4}		1.05	0.001	1.15
383						4.66	14	4.7	19.83	19	5/11	5.5×10^{-4}		1.14	0.012	1.14
422	P60660	MYL6	3417457	myosin light polypeptide 6	1	4.48	13	4.6	15.80	43	6/23	6.3×10^{-9}	0.026	1.47	0.031	1.28
58	O43707	ACTN4	3832643	alpha actinin 4	5	5.21	76	5.3	102.25	20	13/35	8.8×10^{-7}	0.063	1.44	0.086	1.35
59						5.19	76	5.3	102.25	27	22/50	5.7×10^{-13}	0.053	1.44	0.087	1.35
62						5.24	75	5.3	102.25	22	15/48	2.2×10^{-10}	0.062	1.42	0.072	1.35
755						5.16	76	5.2	105.29	18	13/50	4.3×10^{-6}	0.053	1.48	0.083	1.34
754						5.14	76	5.3	105.29	26	19/50	4.0×10^{-8}	0.055	1.46	0.084	1.32
64	P12814	ACTN1	3569814	alpha actinin 1	2	5.29	74	5.3	102.69	12	9/22	2.1×10^{-9}	0.051	1.44	0.036	1.32
65						5.26	74	5.3	102.69	33	23/50	1.7×10^{-13}	0.047	1.44	0.049	1.34
339	Q01995	TAGLN	3350830	transgelin	5	7.99	16	8.9	22.65	69	17/24	9.8×10^{-15}		1.19	0.024	1.29
345						7.84	16	8.9	22.65	62	17/35	1.2×10^{-13}		1.18	0.030	1.30
355						7.34	16	8.9	22.65	57	10/57	$4.8x10^{-6}$		1.15	0.034	1.27
389						6.38	14	8.9	22.65	58	17/42	1.1×10^{-11}	0.030	1.49		1.29
394						6.79	14	8.9	22.65	63	18/33	5.7×10^{-11}	0.022	1.41		1.34
363	P37802	TAGLN2	2439842	Transgelin 2	1	7.87	15	8.6	22.4	75	18/48	1.1×10^{-8}		-1.12		1.02
331	P02743	APCS	2362651	serum amyloid P-component precursor	1	5.51	17	6.1	25.48	26	6/14	2.0×10^{-9}		1.10	0.035	1.22
412	P09382	LGALS1	3944882	galectin-1	1	4.97	13	5.3	15.04	54	8/17	1.1×10^{-9}	0.021	1.38	0.049	1.27
346	Q99497	PARK7	2318736	protein DJ-1	1	6.18	16	6.3	20.04	35	6/23	5.1×10^{-3}	0.030	1.27	0.037	1.19
47	P06396	GSN	3187686	gelsolin	3	6.06	98	5.6	82.33	6	5/11	1.1×10^{-3}	0.039	1.55	0.021	1.23
52						5.98	98	5.6	82.33	8	6/18	3.9×10^{-4}	0.024	1.63	0.039	1.38
53						6.14	97	5.6	82.33	7	6/14	3.8×10^{-4}	0.031	1.48	0.010	1.26
70	P02787	TF	2643217	transferrin	4	6.18	66	7.1	76.94	6	4/13	2.9×10^{-3}		1.02		1.04
71						6.45	66	7.1	76.94	10	7/21	7.8×10^{-4}		1.04		1.01
72						6.35	66	7.1	76.94	11	11/31	1.7×10^{-4}		1.00		1.01
75						6.55	65	7.1	76.94	13	11/47	1.1×10^{-3}		1.07		1.02

155	P02675	FGB	2748542	fibrinogen beta chain, isoform CRA_d	1	7.26	42	8.7	52.77	18	7/17	$2.1x10^{-6}$		1.38		1.02
167	P02679	FGG	2790652	fibrinogen gamma	1	5.61	39	5.5	46.83	10	4/13	$4.9x10^{-3}$	0.078	1.79		1.14
80	P21980	TGM2	3905145	protein-glutamine gamma-glutamyltransferase 2 isoform a	1	5.06	64	5.1	78.47	19	12/41	3.2×10^{-6}	0.004	1.28		1.10
231_233	P04406	GAPDH	3402625	glyceraldehyde-3-phosphate dehydrogenase	2	7.85	27	8.4	36.21	24	7/14	8.9×10^{-4}	0.027	1.14	0.037	1.15
239						7.47	27	8.4	36.21	26	6/17	2.6×10^{-4}	0.024	1.14	0.016	1.11
266	P00338	LDHA	3322775	lactate dehydrogenase A variant	1	7.67	25	8.7	36.82	18	8/19	3.1×10^{-5}	0.022	1.39		1.08
180	P06733	ENO1	2395490	alpha-enolase isoform 1	3	6.72	36	7.0	47.49	43	16/30	$7.7x10^{-10}$	0.006	1.21	0.070	1.24
182						6.96	36	7.0	47.49	19	8/14	$3.1x10^{-8}$	0.025	1.30	0.050	1.25
185						6.48	36	7.0	47.49	27	10/19	$7.0x10^{-9}$	0.028	1.20	0.026	1.15
76	P08238	HSP90AB1	2908474	heat shock protein HSP 90-beta	1	4.93	65	5	83.59	21	13/30	3.1×10^{-9}	0.083	1.80	0.063	1.28
316	P04792	HSPB1	3009399	heat shock protein 27	2	6.01	18	8.1	22.42	40	8/14	1.4×10^{-6}		1.08	0.044	1.29
360						5.62	15	8.1	22.42	32	6/15	1.5×10^{-5}	0.042	1.64		1.19
243	P07951	TPM2	3204721	tropomyosin beta chain	3	4.61	26	4.6	32.97	12	7/14	1.6×10^{-6}	0.020	1.25	0.082	1.34
248						4.64	26	4.6	32.97	28	11/70	$6.4x10^{-13}$		1.12	0.042	1.25
280						4.61	22	4.6	32.97	9	5/46	9.5×10^{-6}	0.039	1.27		1.10
462	P68871	HBB	3360401	Hemoglobin subunit beta	7	6.75	10	6.8	15.94	69	9/18	2.4×10^{-12}	0.052	-2.48	0.036	-1.56
465_484						7.24	10	6.8	15.94	72	10/17	3.9×10^{-15}	0.049	-1.99	0.046	-1.51
468						6.9	10	6.8	15.94	69	10/39	$2.7x10^{-9}$	0.057	-2.62	0.043	-1.65
484						7.26	9	6.8	15.94	69	10/52	$5.4x10^{-7}$	0.046	-2.60	0.060	-1.77
492						6.9	9	6.8	15.94	53	7/16	$1.7x10^{-10}$	0.053	-3.06	0.062	-1.89
747						7.06	10	6.8	15.94	64	8/15	5.4×10^{-12}	0.056	-2.53	0.044	-1.71
751						7.07	9	6.8	15.94	56	8/21	$2.1x10^{-7}$	0.054	-3.16	0.057	-2.00
480	P69905	HBA1	3642675	hemoglobin subunit alpha 1	1	7.93	9	8.7	15.30	75	7/11	8.0×10^{-9}	0.042	-2.45	0.044	-1.70
488	P02042	HBD	3360417	hemoglobin subunit delta	1	7.6	9	8.0	16.15	80	11/26	6.0×10^{-12}	0.044	-2.58	0.045	-1.76
117	Q8WUP2	FBLIM1	2322036	filamin-binding LIM protein 1	2	5.56	53	9.7	32.24	44	20/36	2.1×10^{-15}	0.012	-1.17		-1.03
122						5.43	52	9.7	32.24	37	8/17	2.6×10^{-11}		1.02	0.021	1.13
322	Q9Y696	CLIC4	2325593	chloride intracellular channel protein 4	1	5.43	18	5.5	28.98	34	8/19	1.4×10^{-7}		-1.06		-1.17
123	P08670	VIM	3236958	vimentin	8	5.09	52	5.1	53-69	48	21/50	2.1×10^{-7}	0.005	-1.17		1.08
164						5	41	5.1	53.69	40	19/41	$1.6x10^{-12}$		1.08		1.07
165						5.08	41	5.1	53.69	38	17/33	$5.5x10^{-14}$		1.13		1.13
166						5.04	41	5.1	53.69	38	13/41	6.8×10^{-7}		-1.08		1.06
170						4.85	39	5.1	53.69	21	9/28	8.0×10^{-7}	0.009	1.36		-1.10
171						4.82	39	5.1	53.69	26	12/37	$1.45x10^{-6}$		1.24		-1.21
175						4.78	37	5.1	53.69	24	14/41	$5.2x10^{-7}$	0.014	1.31		-1.07
193						4.68	35	5.1	53.69	25	14/51	$8.1x10^{-8}$	0.001	1.36		1.22
241	A8MVM2	MFAP4	3748798	microfibrillar-associated protein 4	2	4.79	26	5.4	29.00	18	6/63	0.046	0.021	-1.20		-1.03
245						4.88	26	5.4	29.06	17	6/25	4.5×10^{-3}	0.015	-1.18		1.04
262	Q69YN4	KIAA1429	3145020	KIAA1429 protein	1	5.68	25	6.0	122.55	4	4/16	0.24	0.025	1.31	0.015	1.18
267	Q7Z532	OGN	3214800	osteoglycin OG	3	5.08	25	5.3	34.25	28	14/52	$4.7x10^{-12}$	0.046	-1.27	0.027	-1.35
269						5.2	24	5.3	34.25	28	13/43	$6.7x10^{-12}$	0.041	-1.23	0.032	-1.26
272						5.36	24	5.3	34.25	28	12/46	$1.5x10^{-7}$	0.032	-1.16	0.008	-1.16
148	Q9GZM7	TINAGL1	2328320	tubulointerstitial nephritis antigen-like isoform 3	2	6.03	43	6.5	41.53	30	8/19	7.4×10^{-8}	0.032	1.25		1.02
149						6.15	43	6.5	41.53	31	8/30	7.2×10^{-11}		1.01	0.031	1.14
230	Q53GG5	PDLIM3	2796951	PDZ and LIM domain protein 3 isoform b	1	7.27	27	8.0	34.72	43	9/44	2.4×10^{-5}		-1.00		1.04
451	P02766	TTR	3783565	Transthyretin	1	5.45	10	5.5	15.99	50	6/19	$5.0x10^{-6}$		-1.20	0.005	-1.21
102	P34931	HSPA1L	2949450	HSP70-1 (heat shock protein)	3	5.43	59	5.5	70.31	17	9/40	3.0×10^{-5}	0.035	-1.25		-1.07
106						5.37	59	5.5	70.31	25	13/40	1.9×10^{-10}	0.020	-1.20		-1.06
107						5.32	59	5.5	70.31	18	8/35	8.4×10^{-5}		-1.11		-1.04
119	P13645	KRT10		keratin, type I cytoskeletal 10	3	4.9	53	5.1	58.81	23	13/52	6.8×10^{-7}	0.027	-1.24		-1.02
222						7.28	28	5.1	58.81	22	11/50	3.6×10^{-7}	0.049	1.37		1.15
252						5.73	26	5.1	58.81	18	10/26	7.4×10^{-10}	0.005	1.19	0.020	1.19
223	P04259	KRT6B		keratin, type II cytoskeletal 6B	1	6.95	28	8.3	60.05	14	8/45	4.0×10^{-3}	0.052	1.28		1.15

D = Dilated
C = Non-dilated

[a] ABS (loading)-ABS(jack-knife conf intervall) protein expression data, dilated higher (green), non-dilated higher (blue), TAV

[b] Difference in average mean protein spot expression between the groups indicated

[c] ABS (loading)-ABS(jack-knife conf intervall) protein expression data, dilated higher (green), non-dilated higher (blue), BAV

Supplemental Table 4. Summary of identification measures for 35 proteins from LC-MS/MS. All three pools for pool specific variables from the analysis are included.

						Pool 1					Pool 2					Pool 3				
Accession	Gene name	Protein name	MW [kDa]	calc. pI	# AAs	ΣCoverage	Σ# Proteins	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	ΣCoverage	Σ# Proteins	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	ΣCoverage	Σ# Proteins	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs
P12814	ACTN1	Alpha-actinin-1	103.0	5.41	892	57.85	2	1	40	258	58.30	3	22	39	249	51.23	22	20	38	237
O43707	ACTN4	Alpha-actinin-4	104.8	5.44	911	56.97	4	24	40	251	60.48	4	26	42	233	53.02	16	24	41	219
P02768	ALB	Serum albumin	69.3	6.28	609	74.71	2	47	47	631	75.04	2	49	49	747	76.35	2	50	50	782
P04083	ANXA1	Annexin A1	38.7	7.02	346	62.72	1	16	16	80	60.98	1	17	17	73	54.05	1	15	15	62
P09525	ANXA4	Annexin A4	35.9	6.13	319	5.02	1	2	2	6	11.29	3	3	4	8	4.39	1	2	2	4
P08758	ANXA5	Annexin A5	35.9	5.05	320	51.88	1	12	12	80	53.75	3	14	15	81	54.69	1	14	14	79
P02743	APCS	Serum amyloid P-component	25.4	6.54	223	33.18	1	8	8	81	34.08	1	9	9	88	34.08	1	9	9	87
Q9Y696	CLIC4	Chloride intracellular channel protein 4	28.8	5.59	253	30.83	1	5	5	15	20.55	1	3	3	7	25.30	1	4	4	9
P06733	ENO1	Alpha-enolase	47.1	7.39	434	62.67	12	23	24	164	55.76	5	20	22	105	56.22	6	21	21	101
Q8WUP2	FBLIM1	Isoform 3 of Filamin-binding LIM protein 1	30.7	8.02	276	12.32	3	4	4	14	10.87	3	3	3	9	3.62	3	2	2	6
P02675	FGB	Fibrinogen beta chain	55.9	8.27	491	20.16	1	9	9	22	38.49	1	16	16	56	33.81	1	15	15	60
P02679	FGG	Isoform Gamma-A of Fibrinogen gamma chain	49.5	6.09	437	26.54	4	9	9	28	30.89	4	11	11	35	29.29	2	10	10	36
P04406	GAPDH	Glyceraldehyde-3-phosphate dehydrogenase	36.0	8.46	335	63.28	1	16	16	188	61.49	1	15	15	174	58.21	1	14	14	117
P06396	GSN	Isoform 2 of Gelsolin	80.6	5.85	731	41.86	2	26	26	127	38.03	2	20	20	88	32.97	2	22	22	113
P69905	HBA1	Hemoglobin subunit alpha	15.2	8.68	142	55.63	2	7	7	310	64.08	2	8	8	355	64.08	2	8	8	602
P68871	HBB	Hemoglobin subunit beta	16.0	7.28	147	78.91	4	6	12	416	78.91	4	6	12	350	78.91	4	6	12	458
P02042	HBD	Hemoglobin subunit delta	16.0	8.05	147	70.75	4	4	10	153	70.07	4	4	10	153	78.91	4	5	11	228
P04792	HSPB1	Heat shock protein beta-1	22.8	6.40	205	79.51	1	14	14	114	79.51	1	13	13	102	83.41	1	15	15	102
P00338	LDHA	L-lactate dehydrogenase A chain	36.7	8.27	332	43.37	6	12	13	60	41.57	6	9	10	54	35.54	6	9	10	44
P09382	LGALS1	Galectin-1	14.7	5.50	135	77.78	1	9	9	98	77.78	1	9	9	72	46.67	1	7	7	56
P60660	MYL6	Myosin light polypeptide 6	16.9	4.65	151	66.89	6	10	10	137	66.89	6	10	10	104	66.89	6	10	10	91
P24844	MYL9	Myosin regulatory light polypeptide 9	19.8	4.92	172	66.28	1	4	10	126	62.21	1	4	9	110	66.28	1	4	10	135
Q99497	PARK7	Protein DJ-1	19.9	6.79	189	46.03	1	6	6	15	38.10	1	5	5	17	38.10	1	5	5	13
Q53GG5	PDLIM3	Isoform 2 of PDZ and LIM domain protein 3	34.3	7.71	316	31.96	3	5	5	12	19.62	3	4	4	9	28.80	3	5	5	13
Q01995	TAGLN	Transgelin	22.6	8.84	201	81.09	1	20	21	389	78.11	1	19	20	317	83.58	1	20	21	300
P37802	TAGLN2	Transgelin-2	22.4	8.25	199	63.32	1	11	12	111	67.34	1	12	13	109	66.83	1	11	12	97
P02787	TF	Transferrin	77.0	7.12	698	55.30	1	30	32	144	58.45	1	32	33	165	55.30	1	31	32	147
P21980	TGM2	Protein-glutamine gamma-glutamyltransferase 2	77.3	5.22	687	24.75	3	12	12	48	16.59	3	9	9	41	16.01	3	9	9	30
Q9GZM7	TINAGL1	Tubulointerstitial nephritis antigen-like	52.4	6.99	467	14.13	2	5	5	16	12.63	2	4	4	18	6.21	2	2	2	7
P07951	TPM2	Isoform 2 of Tropomyosin beta chain	33.0	4.67	284	84.86	3	8	41	459	77.82	3	9	37	347	79.58	3	8	38	427
P02766	TTR	Transthyretin	15.9	5.76	147	13.61	7	3	3	9	28.57	7	3	3	10	12.93	7	2	2	5
P07437	TUBB	Tubulin beta chain	49.6	4.89	444	51.13	5	3	15	107	43.69	6	3	13	95	43.69	5	3	13	89
P08670	VIM*	Vimentin	53.6	5.12	466	80.26	51	41	45	939	80.90	29	46	47	873	79.83	59	43	44	947
P31946	YWHAB	Isoform Short of 14-3-3 protein beta/alpha	27.8	4.83	244	27.46	5	2	7	58	19.26	5	1	5	46	19.26	8	1	5	36
P63104	YWHAZ	14-3-3 protein zeta/delta	27.7	4.79	245	40.00	1	5	9	59	41.22	1	6	9	50	31.43	3	4	7	44

Supplemental Table 5. Loadings and jack-knife (JK) confidence intervals for the 35 proteins from LC-MS/MS analysis for both TAV and BAV OPLS-DA models, where dilated and non-dilated have been added as a Y variable. Only those proteins present in 2D gel analsyis were extracted from LC-MS/MS data set.

			TAV model		
Gene	**Protein accession number**	**Loading value [a]**	**jack-knife (JK) confidence interval[b]**	**ABS(Loading value)-ABS(JK)[c]**	**Significant probe set = 1[d]**
ACTN1	P12814	0.083	0.189	-0.106	0
ACTN4	O43707	0.170	0.178	-0.008	0
ALB	P02768	-0.046	0.251	-0.204	0
ANXA1	P04083	0.110	0.263	-0.153	0
ANXA4	P09525	-0.096	0.155	-0.059	0
ANXA5	P08758	-0.094	0.203	-0.108	0
APCS	P02743	-0.167	0.213	-0.046	0
CLIC4	Q9Y696	0.068	0.221	-0.153	0
ENO1	P06733	0.240	0.132	0.108	1
FBLIM1	Q8WUP2	0.105	0.210	-0.105	0
FGB	P02675	0.057	0.272	-0.215	0
FGG	P02679	0.100	0.265	-0.165	0
GAPDH	P04406	0.191	0.162	0.029	1
GSN	P06396	-0.143	0.216	-0.073	0
HBA1	P69905	-0.303	0.101	0.202	1
HBB	P68871	-0.290	0.144	0.146	1
HBD	P02042	-0.287	0.150	0.136	1
HSPB1	P04792	0.035	0.234	-0.199	0
LDHA	P00338	0.291	0.165	0.126	1
LGALS1	P09382	0.171	0.165	0.005	1
MYL6	P60660	0.207	0.148	0.059	1
MYL9	P24844	0.083	0.190	-0.107	0
PARK7	Q99497	0.267	0.075	0.191	1
PDLIM3	Q53GG5	0.132	0.194	-0.062	0
TAGLN	Q01995	0.115	0.181	-0.067	0
TAGLN2	P37802	0.294	0.111	0.183	1
TF	P02787	0.063	0.241	-0.178	0
TGM2	P21980	0.068	0.286	-0.218	0
TINAGL1	Q9GZM7	0.115	0.209	-0.094	0
TPM2	P07951	-0.041	0.190	-0.149	0
TTR	P02766	0.031	0.219	-0.187	0
TUBB	P07437	0.296	0.134	0.162	1
VIM	P08670	-0.061	0.265	-0.204	0
YWHAB	P31946	-0.022	0.221	-0.199	0
YWHAZ	P63104	0.205	0.122	0.082	1

			BAV model		
Gene	**Protein accession number**	**Loading value [a]**	**jack-knife (JK) confidence interval[b]**	**ABS(Loading value)-ABS(JK)[c]**	**Significant probe set = 1[d]**
ACTN1	P12814	-0.231	0.116	0.115	1
ACTN4	O43707	0.255	0.094	0.161	1
ALB	P02768	-0.083	0.181	-0.097	0
ANXA1	P04083	0.158	0.234	-0.075	0
ANXA4	P09525	-0.110	0.174	-0.064	0
ANXA5	P08758	0.001	0.169	-0.168	0
APCS	P02743	-0.075	0.202	-0.127	0
CLIC4	Q9Y696	0.061	0.237	-0.176	0
ENO1	P06733	0.207	0.089	0.117	1
FBLIM1	Q8WUP2	0.223	0.142	0.082	1
FGB	P02675	0.058	0.210	-0.152	0
FGG	P02679	0.071	0.206	-0.135	0
GAPDH	P04406	0.089	0.204	-0.115	0
GSN	P06396	0.194	0.145	0.049	1
HBA1	P69905	-0.250	0.052	0.198	1
HBB	P68871	-0.214	0.091	0.123	1
HBD	P02042	-0.209	0.096	0.113	1
HSPB1	P04792	0.155	0.174	-0.018	0
LDHA	P00338	0.078	0.221	-0.143	0
LGALS1	P09382	0.240	0.077	0.163	1
MYL6	P60660	0.263	0.069	0.194	1
MYL9	P24844	0.244	0.091	0.152	1
PARK7	Q99497	0.231	0.073	0.158	1
PDLIM3	Q53GG5	0.106	0.146	-0.040	0
TAGLN	Q01995	0.257	0.073	0.184	1
TAGLN2	P37802	0.239	0.148	0.091	1
TF	P02787	-0.023	0.160	-0.137	0
TGM2	P21980	0.081	0.174	-0.092	0
TINAGL1	Q9GZM7	0.102	0.151	-0.049	0
TPM2	P07951	0.179	0.140	0.039	1
TTR	P02766	-0.136	0.138	-0.002	0
TUBB	P07437	0.065	0.236	-0.171	0
VIM	P08670	-0.144	0.196	-0.052	0
YWHAB	P31946	-0.062	0.174	-0.112	0
YWHAZ	P63104	0.206	0.103	0.103	1

[a] Loading value from OPLS-DA model with controls vs dilated

[b] Jack-Knife confidence interval derived from cross-validation in OPLS-DA models

[c] Subtracting the jack-knife confidence intervals from the corresponding loading values, if positive indicates significance

[d] If the subtracting jack-knife cofidence interval from the corresponding loading is positive (significant), and indicated with 1, and if negative (non-singnificant), it is indicated with 0

Supplemental Table 6. Loadings and jack-knife (JK) confidence intervals for the 43 genes for both TAV and BAV OPLS-DA models, where dilated and non-dilated have been added as a Y variable.

TAV model						BAV model					
Gene	**Affymetrix ID**	**Loading value [a]**	**jack-knife (JK) confidence interval[b]**	**ABS(Loading value)-ABS(JK)[c]**	**Significant probe set = 1[d]**	**Gene**	**Affymetrix ID**	**Loading value [a]**	**jack-knife (JK) confidence interval[b]**	**ABS(Loading value)-ABS(JK)[c]**	**Significant probe set = 1[d]**
HBB	3360401	-0.29	0.08	0.21	1	HBB	3360401	-0.39	0.14	0.25	1
MYL6	3417457	-0.26	0.23	0.03	1	FGG	2790652	-0.31	0.18	0.13	1
APCS	2362651	-0.20	0.18	0.02	1	LGALS1	3944882	-0.30	0.10	0.20	1
FGG	2790652	-0.17	0.14	0.03	1	MYL6	3417457	-0.27	0.13	0.13	1
HBD	3360417	-0.16	0.14	0.02	1	PARK7	2318736	-0.24	0.16	0.08	1
YWHAZ	3146898	-0.12	0.08	0.03	1	HBD	3360417	-0.15	0.14	0.02	1
LDHA	3322775	0.12	0.08	0.04	1	TINAGL1	2328320	0.14	0.11	0.03	1
TUBB	2901913	0.16	0.14	0.02	1	HSPA1L	2949450	0.14	0.12	0.02	1
YWHAB	3886639	0.18	0.14	0.03	1	FBLIM1	2322036	0.16	0.09	0.07	1
YWHAQ	2539869	0.19	0.15	0.04	1	HSPB1	3009399	0.18	0.12	0.06	1
TINAGL1	2328320	0.22	0.16	0.05	1	TUBB	2901913	0.21	0.11	0.10	1
TAGLN2	2439842	0.22	0.10	0.12	1	ACTN1	3569814	0.23	0.13	0.10	1
ACTN1	3569814	0.22	0.15	0.07	1	ACTN4	3832643	0.28	0.11	0.16	1
ENO1	2395490	0.25	0.13	0.12	1	MFAP4	3748798	0.31	0.22	0.09	1
ACTN4	3832643	0.28	0.11	0.18	1	ANXA1	3174816	-0.12	0.23	-0.12	0
MFAP4	3748798	0.32	0.10	0.22	1	GAPDH	3402625	-0.10	0.24	-0.13	0
LGALS1	3944882	-0.20	0.23	-0.03	0	TAGLN2	2439842	-0.09	0.17	-0.08	0
HBA1	3642675	-0.17	0.21	-0.03	0	YWHAZ	3146898	-0.09	0.21	-0.12	0
GAPDH	3402625	-0.15	0.20	-0.05	0	ANXA4	2487412	-0.09	0.31	-0.22	0
PARK7	2318736	-0.14	0.21	-0.07	0	PDLIM3	2796951	-0.08	0.23	-0.15	0
ANXA1	3174816	-0.12	0.15	-0.03	0	FGB	2748542	-0.07	0.26	-0.19	0
OGN	3214800	-0.10	0.18	-0.08	0	MYL12B	3776449	-0.05	0.16	-0.11	0
FGB	2748542	-0.08	0.18	-0.10	0	TTR	3783565	-0.03	0.28	-0.25	0
TAGLN	3350830	-0.08	0.26	-0.18	0	ANXA5	2784027	-0.02	0.29	-0.28	0
HSPA1L	2949450	-0.06	0.25	-0.18	0	APCS	2362651	-0.01	0.26	-0.24	0
VIM	3236958	-0.06	0.20	-0.14	0	OGN	3214800	-0.01	0.16	-0.15	0
HSPB1	3009399	-0.02	0.22	-0.20	0	CLIC4	2325593	-0.01	0.28	-0.28	0
ALB	2731192	-0.02	0.17	-0.15	0	LDHA	3322775	0.00	0.16	-0.15	0
TTR	3783565	0.01	0.06	-0.05	0	VIM	3236958	0.01	0.13	-0.13	0
TF	2643217	0.03	0.20	-0.17	0	ALB	2731192	0.01	0.10	-0.09	0
CLIC4	2325593	0.03	0.26	-0.23	0	KIAA1429	3145020	0.01	0.23	-0.22	0
FBLIM1	2322036	0.03	0.21	-0.17	0	TAGLN	3350830	0.02	0.12	-0.10	0
TPM2	3204721	0.04	0.21	-0.17	0	TPM2	3204721	0.03	0.19	-0.16	0
ANXA4	2487412	0.07	0.19	-0.12	0	HSP90AB1	2908474	0.04	0.29	-0.25	0
GSN	3187686	0.08	0.12	-0.04	0	GSN	3187686	0.07	0.22	-0.15	0
MYL12B	3776449	0.08	0.16	-0.08	0	YWHAB	3886639	0.07	0.21	-0.13	0
KIAA1429	3145020	0.09	0.21	-0.12	0	YWHAQ	2539869	0.08	0.21	-0.13	0
ANXA5	2784027	0.10	0.16	-0.07	0	HBA1	3642675	0.08	0.25	-0.17	0
MYL9	3883921	0.11	0.22	-0.11	0	TF	2643217	0.12	0.22	-0.10	0
PDLIM3	2796951	0.11	0.23	-0.12	0	ACTA2	3299504	0.12	0.12	0.00	0
ACTA2	3299504	0.11	0.16	-0.04	0	MYL9	3883921	0.15	0.22	-0.07	0
HSP90AB1	2908474	0.12	0.20	-0.07	0	ENO1	2395490	0.18	0.21	-0.02	0
TGM2	3905145	0.14	0.18	-0.04	0	TGM2	3905145	0.19	0.20	-0.002	0

[a] Loading value from OPLS-DA model with controls vs dilated

[b] Jack-Knife confidence interval derived from cross-validation in OPLS-DA models

[c] Subtracting the jack-knife confidence intervals from the corresponding loading values, if positive indicates significance

[d] If the subtracting jack-knife cofidence interval from the corresponding loading is positive (significant), and indicated with 1, and if negative (non-singnificant), it is indicated with 0

Supplemental Table 7. Loadings and jack-knife (JK) confidence intervals for the 393 probe sets for both TAV and BAV OPLS-DA models, where dilated and non-dilated have been added as a Y variable.

TAV model

Probe set ID	Affymetrix ID	Loading value [a]	jack-knife (JK) confidence interval[b]	ABS(Loading value)-ABS(JK)[c]	Significant probe set = 1[d]
ACTN1_21	3569871	-0.128	0.042	0.085	1
GSN_5	3187729	-0.126	0.042	0.084	1
TGM2_16	3905184	-0.112	0.043	0.070	1
OGN_8	3214813	-0.110	0.023	0.087	1
GSN_6	3187731	-0.110	0.065	0.045	1
TPM2_13	3204742	-0.108	0.066	0.042	1
HBD_2	3360423	-0.106	0.045	0.061	1
ACTN1_22	3569908	-0.104	0.035	0.069	1
ACTA2_3	3299513	-0.103	0.047	0.056	1
MYL9_1	3883922	-0.101	0.039	0.062	1
ACTN4_1	3832644	-0.099	0.067	0.031	1
OGN_10	3214815	-0.097	0.046	0.051	1
GSN_7	3187735	-0.092	0.075	0.017	1
YWHAB_3	3886644	-0.091	0.035	0.056	1
TINAGL1_13	2328363	-0.090	0.040	0.050	1
GSN_8	3187739	-0.090	0.042	0.048	1
TINAGL1_15	2328365	-0.090	0.083	0.007	1
ACTN1_15	3569849	-0.089	0.024	0.066	1
KIAA1429_28	3145067	-0.089	0.031	0.058	1
TGM2_17	3905187	-0.089	0.076	0.012	1
KIAA1429_26	3145060	-0.088	0.044	0.044	1
PDLIM3_10	2796976	-0.086	0.040	0.046	1
ACTN4_7	3832688	-0.086	0.063	0.023	1
MFAP4_2	3748801	-0.085	0.069	0.016	1
HBB_3	3360405	-0.081	0.064	0.017	1
GSN_2	3187720	-0.081	0.051	0.030	1
ANXA4_14	2487454	-0.081	0.035	0.047	1
PDLIM3_11	2796978	-0.080	0.048	0.032	1
GSN_3	3187721	-0.079	0.055	0.024	1
TF_12	2643264	-0.077	0.051	0.026	1
ENO1_2	2395499	-0.075	0.064	0.012	1
HSPB1_3	3009406	-0.074	0.063	0.012	1
ACTN1_18	3569860	-0.074	0.030	0.044	1
PDLIM3_12	2796986	-0.073	0.051	0.021	1
TGM2_15	3905180	-0.071	0.055	0.015	1
LDHA_1	3322777	-0.070	0.058	0.013	1
ANXA5_13	2784072	-0.070	0.066	0.004	1
MFAP4_8	3748807	-0.070	0.061	0.009	1
TGM2_14	3905179	-0.068	0.056	0.012	1
MFAP4_6	3748805	-0.068	0.056	0.012	1
HBB_1	3360403	-0.065	0.038	0.027	1
FBLIM1_3	2322047	-0.065	0.054	0.010	1
KIAA1429_31	3145076	-0.063	0.048	0.015	1
ACTN4_5	3832685	-0.062	0.057	0.005	1
YWHAB_6	3886652	-0.061	0.048	0.014	1
YWHAB_5	3886650	-0.060	0.047	0.013	1
FGG_5	2790662	-0.057	0.027	0.030	1
FBLIM1_5	2322051	-0.055	0.036	0.019	1
YWHAQ_4	2539900	-0.054	0.040	0.014	1
GSN_10	3187742	-0.052	0.044	0.008	1
HSPA1L_3	2949453	-0.046	0.036	0.010	1
ANXA4_7	2487431	-0.046	0.042	0.004	1
ANXA5_10	2784065	-0.040	0.037	0.004	1
ANXA5_11	2784066	-0.038	0.023	0.014	1
FGG_8	2790667	0.043	0.042	0.001	1
ACTN1_1	3569819	0.045	0.042	0.003	1
ACTN1_12	3569841	0.046	0.030	0.016	1
TAGLN_11	3350846	0.048	0.033	0.015	1
TPM2_9	3204737	0.048	0.041	0.007	1
VIM_8	3236987	0.049	0.033	0.016	1
TAGLN_5	3350840	0.049	0.032	0.017	1
GSN_14	3187751	0.051	0.025	0.026	1
VIM_13	3236999	0.053	0.048	0.004	1
HBD_3	3360426	0.056	0.047	0.009	1
KIAA1429_18	3145051	0.056	0.040	0.016	1
ANXA5_2	2784038	0.057	0.052	0.005	1
ANXA4_15	2487456	0.058	0.045	0.013	1
ACTN1_2	3569820	0.061	0.051	0.010	1
YWHAB_2	3886643	0.064	0.062	0.002	1
HBB_2	3360404	0.065	0.057	0.009	1
TGM2_4	3905150	0.066	0.066	0.000	1
LDHA_2	3322803	0.068	0.048	0.020	1
OGN_5	3214807	0.068	0.049	0.019	1
TAGLN_7	3350842	0.069	0.063	0.006	1
YWHAB_10	3886658	0.069	0.065	0.004	1
KIAA1429_10	3145036	0.070	0.068	0.002	1
ALB_6	2731207	0.071	0.033	0.038	1
TF_16	2643273	0.072	0.023	0.049	1
ACTA2_6	3299521	0.072	0.049	0.023	1
HSPB1_4	3009407	0.073	0.027	0.047	1
ANXA1_9	3174850	0.076	0.063	0.013	1
ACTN4_9	3832690	0.077	0.053	0.023	1
ACTN4_13	3832702	0.077	0.029	0.048	1
TF_20	2643279	0.078	0.070	0.008	1
FBLIM1_8	2322061	0.078	0.070	0.008	1
VIM_9	3236988	0.078	0.077	0.002	1
MFAP4_4	3748803	0.079	0.052	0.027	1
PDLIM3_6	2796967	0.081	0.036	0.045	1
TINAGL1_9	2328356	0.081	0.054	0.027	1
TGM2_1	3905146	0.083	0.058	0.025	1
ACTN1_3	3569821	0.085	0.031	0.054	1
KIAA1429_9	3145035	0.086	0.049	0.037	1
OGN_1	3214802	0.087	0.050	0.037	1
MFAP4_5	3748804	0.087	0.048	0.039	1
TGM2_6	3905152	0.089	0.037	0.051	1
ACTN1_11	3569840	0.090	0.074	0.015	1
ACTN1_13	3569842	0.091	0.055	0.036	1
MYL9_3	3883929	0.095	0.033	0.062	1
TINAGL1_11	2328360	0.095	0.062	0.033	1
ACTN1_9	3569835	0.097	0.049	0.048	1
GSN_16	3187756	0.101	0.058	0.043	1
GSN_19	3187764	0.101	0.034	0.068	1
GSN_20	3187765	0.103	0.053	0.050	1
HBB_5	3360413	0.104	0.059	0.045	1
OGN_4	3214806	0.105	0.060	0.045	1
KIAA1429_8	3145034	0.107	0.056	0.051	1

BAV model

Probe set ID	Affymetrix ID	Loading value [a]	jack-knife (JK) confidence interval[b]	ABS(Loading value)-ABS(JK)[c]	Significant probe set = 1[d]
TINAGL1_15	2328365	-0.174	0.092	0.082	1
ACTA2_1	3299507	-0.156	0.073	0.082	1
HBD_2	3360423	-0.149	0.054	0.096	1
YWHAB_1	3886640	-0.136	0.084	0.052	1
FBLIM1_5	2322051	-0.135	0.080	0.055	1
HBB_1	3360403	-0.122	0.056	0.066	1
FBLIM1_3	2322047	-0.119	0.061	0.059	1
ANXA4_15	2487456	-0.117	0.074	0.043	1
TF_12	2643264	-0.111	0.052	0.059	1
TPM2_1	3204722	-0.107	0.052	0.055	1
KIAA1429_18	3145051	-0.107	0.089	0.018	1
ACTN1_20	3569864	-0.106	0.039	0.068	1
TF_20	2643279	-0.104	0.055	0.048	1
ACTN1_22	3569908	-0.102	0.051	0.051	1
GSN_2	3187720	-0.100	0.056	0.044	1
GSN_3	3187721	-0.099	0.054	0.045	1
LGALS1_3	3944897	-0.099	0.078	0.020	1
TINAGL1_13	2328363	-0.098	0.074	0.024	1
VIM_15	3237001	-0.097	0.091	0.006	1
KIAA1429_29	3145069	-0.093	0.036	0.057	1
ALB_1	2731194	-0.093	0.046	0.047	1
PARK7_5	2318755	-0.092	0.052	0.040	1
ACTN4_1	3832644	-0.088	0.060	0.028	1
TPM2_13	3204742	-0.087	0.054	0.033	1
KIAA1429_13	3145042	-0.087	0.070	0.017	1
TF_8	2643251	-0.087	0.076	0.011	1
KIAA1429_1	3145023	-0.083	0.049	0.034	1
ENO1_2	2395499	-0.081	0.073	0.008	1
MYL9_1	3883922	-0.081	0.079	0.002	1
HBB_3	3360405	-0.080	0.075	0.005	1
HSPA1L_2	2949452	-0.080	0.053	0.027	1
MYL6_2	3417476	-0.079	0.049	0.030	1
TF_1	2643237	-0.077	0.047	0.030	1
PDLIM3_11	2796978	-0.074	0.067	0.008	1
ANXA4_9	2487439	-0.073	0.044	0.029	1
PDLIM3_12	2796986	-0.071	0.034	0.037	1
OGN_10	3214815	-0.071	0.028	0.043	1
KIAA1429_28	3145067	-0.070	0.053	0.017	1
VIM_16	3237002	-0.068	0.030	0.039	1
YWHAQ_1	2539873	-0.065	0.063	0.002	1
YWHAZ_2	3146941	-0.065	0.053	0.011	1
TINAGL1_1	2328342	-0.055	0.034	0.022	1
MFAP4_2	3748801	-0.055	0.052	0.002	1
MFAP4_3	3748802	-0.054	0.043	0.011	1
YWHAB_3	3886644	-0.051	0.047	0.003	1
ACTN4_14	3832703	-0.049	0.041	0.008	1
ACTN1_18	3569860	-0.048	0.040	0.009	1
VIM_17	3237003	-0.045	0.034	0.011	1
FGG_7	2790664	-0.045	0.042	0.003	1
MFAP4_1	3748799	-0.040	0.027	0.013	1
OGN_9	3214814	-0.037	0.021	0.016	1
YWHAB_8	3886656	0.034	0.030	0.004	1
ACTN4_16	3832719	0.036	0.032	0.004	1
FGG_13	2790678	0.039	0.035	0.004	1
ANXA4_2	2487420	0.041	0.022	0.019	1
APCS_6	2362658	0.041	0.040	0.001	1
PDLIM3_6	2796967	0.042	0.036	0.006	1
PARK7_2	2318747	0.044	0.032	0.013	1
MYL6_1	3417469	0.048	0.041	0.007	1
VIM_8	3236987	0.049	0.044	0.005	1
KIAA1429_11	3145039	0.051	0.050	0.001	1
GSN_11	3187744	0.053	0.039	0.014	1
ANXA4_5	2487428	0.058	0.037	0.021	1
ANXA4_4	2487427	0.058	0.054	0.005	1
ACTN1_13	3569842	0.059	0.028	0.031	1
TPM2_4	3204728	0.060	0.031	0.029	1
OGN_2	3214804	0.062	0.042	0.020	1
TF_21	2643280	0.063	0.062	0.001	1
TGM2_2	3905147	0.063	0.055	0.007	1
VIM_9	3236988	0.064	0.041	0.023	1
TF_18	2643275	0.066	0.065	0.001	1
PDLIM3_13	2796987	0.066	0.061	0.005	1
HBD_4	3360427	0.068	0.038	0.030	1
ANXA4_7	2487431	0.069	0.053	0.016	1
MFAP4_5	3748804	0.069	0.067	0.002	1
ACTN4_10	3832693	0.071	0.036	0.036	1
TINAGL1_10	2328358	0.079	0.049	0.029	1
HBD_3	3360426	0.079	0.054	0.025	1
KIAA1429_16	3145048	0.081	0.057	0.024	1
ANXA1_9	3174850	0.086	0.084	0.002	1
VIM_6	3236977	0.086	0.062	0.025	1
LDHA_2	3322803	0.089	0.084	0.004	1
TINAGL1_12	2328362	0.091	0.061	0.031	1
ALB_7	2731209	0.093	0.073	0.019	1
TPM2_8	3204734	0.093	0.074	0.019	1
GSN_17	3187758	0.094	0.069	0.025	1
ACTN1_12	3569841	0.096	0.053	0.043	1
VIM_10	3236991	0.098	0.070	0.028	1
TINAGL1_9	2328356	0.100	0.064	0.036	1
ACTA2_9	3299534	0.104	0.050	0.054	1
TINAGL1_11	2328360	0.109	0.029	0.079	1
GSN_15	3187753	0.119	0.044	0.075	1
FBLIM1_7	2322060	0.126	0.065	0.061	1
FBLIM1_8	2322061	0.128	0.053	0.075	1
ACTN4_18	3832721	0.130	0.050	0.080	1
KIAA1429_9	3145035	0.135	0.054	0.081	1
HBB_5	3360413	0.143	0.048	0.095	1
ANXA5_5	2784046	-0.101	0.105	-0.004	0
ENO1_1	2395498	-0.085	0.089	-0.004	0
FGB_6	2748564	-0.075	0.095	-0.019	0
LDHA_1	3322777	-0.070	0.085	-0.015	0
FGB_11	2748569	-0.066	0.101	-0.035	0
HSPB1_3	3009406	-0.061	0.096	-0.035	0
KIAA1429_22	3145055	-0.060	0.067	-0.007	0
TGM2_17	3905187	-0.060	0.097	-0.037	0
ACTN1_21	3569871	-0.059	0.101	-0.042	0

ACTN4_20	3832723	0.111	0.031	0.080	1
GSN_17	3187758	0.112	0.044	0.068	1
ACTN1_4	3569822	0.114	0.030	0.083	1
GSN_15	3187753	0.119	0.039	0.080	1
OGN_3	3214805	0.125	0.058	0.067	1
FBLIM1_7	2322060	0.129	0.044	0.085	1
TPM2_1	3204722	-0.072	0.085	-0.013	0
ACTN4_12	3832699	-0.067	0.074	-0.007	0
FGB_11	2748569	-0.067	0.075	-0.008	0
TF_9	2643252	-0.065	0.080	-0.014	0
YWHAB_1	3886640	-0.065	0.070	-0.004	0
KIAA1429_29	3145069	-0.065	0.068	-0.003	0
ACTA2_8	3299531	-0.064	0.067	-0.003	0
APCS_3	2362655	-0.063	0.090	-0.027	0
PARK7_5	2318755	-0.062	0.068	-0.007	0
FBLIM1_2	2322044	-0.061	0.070	-0.009	0
VIM_16	3237002	-0.056	0.064	-0.008	0
VIM_12	3236997	-0.056	0.058	-0.003	0
TF_21	2643280	-0.054	0.057	-0.003	0
ALB_8	2731211	-0.053	0.066	-0.012	0
ACTN4_6	3832686	-0.052	0.078	-0.026	0
TPM2_12	3204741	-0.052	0.071	-0.019	0
PDLIM3_13	2796987	-0.051	0.060	-0.009	0
ALB_16	2731229	-0.051	0.055	-0.004	0
TF_19	2643277	-0.050	0.062	-0.013	0
VIM_2	3236971	-0.049	0.053	-0.003	0
TF_5	2643244	-0.049	0.060	-0.011	0
GSN_11	3187744	-0.049	0.079	-0.031	0
CLIC4_1	2325626	-0.049	0.055	-0.006	0
KIAA1429_13	3145042	-0.048	0.057	-0.009	0
TF_15	2643268	-0.047	0.065	-0.018	0
YWHAZ_3	3146954	-0.047	0.070	-0.023	0
TTR_3	3783581	-0.046	0.058	-0.012	0
ANXA1_4	3174836	-0.044	0.050	-0.005	0
TAGLN_1	3350832	-0.044	0.059	-0.015	0
ANXA1_1	3174831	-0.044	0.052	-0.008	0
KIAA1429_4	3145028	-0.043	0.064	-0.021	0
ANXA1_7	3174845	-0.043	0.050	-0.007	0
GSN_1	3187708	-0.043	0.058	-0.015	0
ACTN1_17	3569859	-0.041	0.054	-0.013	0
FBLIM1_1	2322038	-0.041	0.053	-0.012	0
ACTN1_20	3569864	-0.040	0.068	-0.028	0
OGN_9	3214814	-0.040	0.049	-0.009	0
KIAA1429_30	3145071	-0.040	0.066	-0.026	0
TPM2_6	3204730	-0.040	0.079	-0.040	0
APCS_6	2362658	-0.039	0.070	-0.031	0
ACTN1_16	3569850	-0.039	0.075	-0.037	0
TF_6	2643248	-0.039	0.049	-0.010	0
TAGLN_6	3350841	-0.038	0.040	-0.001	0
TAGLN_3	3350837	-0.038	0.078	-0.040	0
KIAA1429_20	3145053	-0.038	0.054	-0.016	0
TGM2_5	3905151	-0.038	0.058	-0.020	0
ANXA4_3	2487423	-0.037	0.053	-0.015	0
VIM_7	3236980	-0.037	0.051	-0.014	0
ANXA4_11	2487443	-0.037	0.051	-0.014	0
MFAP4_1	3748799	-0.036	0.047	-0.011	0
FGB_6	2748564	-0.035	0.071	-0.036	0
FGG_6	2790663	-0.035	0.050	-0.016	0
YWHAZ_2	3146941	-0.034	0.052	-0.017	0
HSPA1L_2	2949452	-0.034	0.059	-0.025	0
VIM_1	3236968	-0.034	0.066	-0.032	0
ALB_3	2731198	-0.034	0.064	-0.030	0
ACTN4_4	3832684	-0.034	0.038	-0.004	0
LGALS1_2	3944893	-0.033	0.068	-0.035	0
VIM_5	3236975	-0.033	0.073	-0.040	0
FGG_1	2790655	-0.032	0.097	-0.065	0
KIAA1429_21	3145054	-0.032	0.065	-0.033	0
FGG_7	2790664	-0.032	0.065	-0.033	0
ANXA4_1	2487413	-0.031	0.054	-0.023	0
CLIC4_2	2325627	-0.030	0.070	-0.040	0
TINAGL1_1	2328342	-0.030	0.036	-0.005	0
KIAA1429_12	3145040	-0.029	0.069	-0.040	0
TINAGL1_7	2328353	-0.028	0.057	-0.029	0
FGG_14	2790679	-0.027	0.040	-0.013	0
ENO1_3	2395503	-0.027	0.087	-0.060	0
VIM_3	3236972	-0.026	0.029	-0.003	0
ACTN1_7	3569832	-0.026	0.078	-0.053	0
VIM_17	3237003	-0.026	0.049	-0.023	0
FBLIM1_4	2322048	-0.025	0.067	-0.042	0
ANXA4_2	2487420	-0.025	0.079	-0.055	0
KIAA1429_17	3145050	-0.024	0.048	-0.023	0
ALB_10	2731214	-0.024	0.044	-0.019	0
ALB_4	2731201	-0.024	0.064	-0.040	0
ALB_2	2731195	-0.024	0.079	-0.055	0
TF_7	2643249	-0.023	0.034	-0.011	0
TPM2_10	3204738	-0.023	0.042	-0.018	0
ACTA2_7	3299527	-0.023	0.061	-0.038	0
OGN_6	3214809	-0.022	0.055	-0.032	0
HSPA1L_6	2949457	-0.022	0.049	-0.027	0
ACTN1_10	3569836	-0.022	0.069	-0.047	0
ANXA5_8	2784050	-0.021	0.058	-0.037	0
TF_2	2643240	-0.021	0.065	-0.044	0
YWHAB_4	3886649	-0.021	0.029	-0.008	0
ANXA5_5	2784046	-0.021	0.089	-0.069	0
OGN_2	3214804	-0.020	0.040	-0.020	0
MFAP4_9	3748809	-0.019	0.037	-0.017	0
GSN_4	3187722	-0.018	0.079	-0.060	0
TAGLN_2	3350833	-0.018	0.064	-0.045	0
TINAGL1_5	2328351	-0.018	0.054	-0.036	0
TGM2_9	3905167	-0.018	0.075	-0.057	0
ANXA4_8	2487434	-0.017	0.057	-0.040	0
ALB_14	2731225	-0.017	0.051	-0.034	0
FGB_10	2748568	-0.017	0.104	-0.088	0
ANXA4_4	2487427	-0.016	0.069	-0.053	0
ACTN4_14	3832703	-0.016	0.094	-0.079	0
YWHAQ_3	2539899	-0.015	0.052	-0.036	0
TINAGL1_2	2328344	-0.015	0.074	-0.059	0
TTR_4	3783587	-0.015	0.080	-0.065	0
ACTN1_19	3569862	-0.015	0.029	-0.014	0
ACTN4_2	3832645	-0.014	0.060	-0.046	0
ANXA5_4	2784045	-0.013	0.068	-0.054	0
ACTN4_16	3832719	-0.013	0.050	-0.037	0
FGG_11	2790675	-0.013	0.055	-0.042	0
FGG_1	2790655	-0.059	0.074	-0.015	0
FGG_3	2790658	-0.059	0.063	-0.004	0
APCS_3	2362655	-0.058	0.085	-0.027	0
ACTN4_5	3832685	-0.058	0.058	0.000	0
ALB_11	2731218	-0.057	0.073	-0.016	0
TGM2_9	3905167	-0.057	0.107	-0.049	0
ACTN1_2	3569820	-0.057	0.068	-0.011	0
KIAA1429_24	3145057	-0.056	0.069	-0.013	0
MYL9_5	3883931	-0.056	0.059	-0.003	0
ACTN1_5	3569825	-0.053	0.096	-0.043	0
ACTA2_3	3299513	-0.053	0.076	-0.023	0
ANXA4_14	2487454	-0.053	0.092	-0.039	0
FGG_17	2790684	-0.052	0.054	-0.002	0
PDLIM3_1	2796954	-0.051	0.091	-0.040	0
GSN_7	3187735	-0.051	0.060	-0.009	0
TGM2_16	3905184	-0.049	0.095	-0.046	0
TINAGL1_7	2328353	-0.046	0.061	-0.015	0
TINAGL1_2	2328344	-0.045	0.103	-0.059	0
FGB_2	2748554	-0.044	0.081	-0.037	0
KIAA1429_19	3145052	-0.044	0.067	-0.024	0
TTR_3	3783581	-0.043	0.089	-0.046	0
HSPA1L_6	2949457	-0.042	0.081	-0.038	0
TPM2_9	3204737	-0.042	0.095	-0.054	0
FGG_2	2790657	-0.041	0.102	-0.061	0
ANXA1_6	3174840	-0.041	0.049	-0.008	0
TGM2_15	3905180	-0.040	0.079	-0.039	0
TINAGL1_3	2328347	-0.040	0.081	-0.041	0
ANXA1_5	3174838	-0.039	0.104	-0.065	0
FBLIM1_6	2322053	-0.038	0.041	-0.003	0
ANXA5_13	2784072	-0.038	0.069	-0.031	0
ACTN4_7	3832688	-0.037	0.069	-0.032	0
ACTN1_8	3569834	-0.034	0.074	-0.040	0
PDLIM3_2	2796955	-0.034	0.094	-0.060	0
TAGLN_1	3350832	-0.034	0.081	-0.047	0
ACTN4_19	3832722	-0.034	0.049	-0.015	0
ANXA4_3	2487423	-0.033	0.065	-0.031	0
FBLIM1_4	2322048	-0.033	0.048	-0.014	0
ANXA4_12	2487446	-0.033	0.058	-0.025	0
HBB_4	3360411	-0.033	0.097	-0.064	0
OGN_8	3214813	-0.032	0.059	-0.027	0
TPM2_12	3204741	-0.032	0.056	-0.024	0
TINAGL1_6	2328352	-0.032	0.033	-0.001	0
PDLIM3_4	2796959	-0.031	0.035	-0.003	0
ACTN1_3	3569821	-0.031	0.033	-0.002	0
ACTN1_7	3569832	-0.031	0.040	-0.010	0
TTR_2	3783579	-0.031	0.083	-0.053	0
TAGLN_2	3350833	-0.030	0.075	-0.045	0
YWHAB_5	3886650	-0.030	0.101	-0.071	0
GSN_4	3187722	-0.029	0.089	-0.059	0
TF_11	2643257	-0.029	0.105	-0.075	0
ALB_13	2731223	-0.029	0.047	-0.018	0
ALB_8	2731211	-0.029	0.069	-0.041	0
PARK7_4	2318754	-0.029	0.069	-0.040	0
VIM_2	3236971	-0.029	0.043	-0.014	0
TGM2_13	3905177	-0.027	0.066	-0.039	0
ANXA5_1	2784037	-0.027	0.072	-0.045	0
CLIC4_1	2325626	-0.026	0.092	-0.065	0
ACTN1_16	3569850	-0.026	0.105	-0.079	0
MFAP4_8	3748807	-0.026	0.058	-0.032	0
FGB_8	2748566	-0.026	0.044	-0.019	0
FGG_14	2790679	-0.025	0.064	-0.039	0
GSN_1	3187708	-0.025	0.108	-0.082	0
PDLIM3_10	2796976	-0.025	0.055	-0.030	0
OGN_7	3214810	-0.025	0.074	-0.049	0
ALB_10	2731214	-0.025	0.072	-0.047	0
TF_15	2643268	-0.024	0.034	-0.010	0
KIAA1429_21	3145054	-0.024	0.055	-0.031	0
TAGLN_10	3350845	-0.022	0.061	-0.039	0
GSN_13	3187747	-0.021	0.047	-0.026	0
ACTN4_2	3832645	-0.021	0.038	-0.018	0
KIAA1429_25	3145058	-0.020	0.060	-0.039	0
PDLIM3_9	2796971	-0.020	0.033	-0.013	0
ACTA2_6	3299521	-0.020	0.083	-0.063	0
OGN_11	3214816	-0.018	0.066	-0.048	0
ANXA5_11	2784066	-0.018	0.028	-0.010	0
ANXA4_11	2487443	-0.018	0.058	-0.040	0
ACTN4_15	3832708	-0.017	0.070	-0.053	0
APCS_5	2362657	-0.017	0.090	-0.073	0
GSN_5	3187729	-0.017	0.046	-0.029	0
ANXA1_2	3174832	-0.016	0.046	-0.030	0
VIM_5	3236975	-0.016	0.030	-0.014	0
TF_14	2643267	-0.016	0.045	-0.029	0
VIM_11	3236993	-0.016	0.085	-0.069	0
YWHAZ_1	3146904	-0.015	0.030	-0.015	0
GSN_9	3187741	-0.015	0.064	-0.049	0
ANXA1_11	3174857	-0.014	0.048	-0.034	0
HSPB1_4	3009407	-0.014	0.026	-0.012	0
ACTN1_6	3569830	-0.013	0.066	-0.053	0
VIM_14	3237000	-0.013	0.031	-0.018	0
YWHAQ_4	2539900	-0.013	0.091	-0.078	0
KIAA1429_27	3145066	-0.012	0.061	-0.049	0
ANXA1_3	3174835	-0.011	0.077	-0.066	0
ACTA2_7	3299527	-0.011	0.050	-0.039	0
TGM2_1	3905146	-0.010	0.056	-0.045	0
KIAA1429_23	3145056	-0.010	0.070	-0.060	0
TAGLN_6	3350841	-0.010	0.090	-0.080	0
GSN_6	3187731	-0.010	0.039	-0.029	0
ACTN4_13	3832702	-0.010	0.061	-0.051	0
TF_2	2643240	-0.010	0.082	-0.073	0
YWHAQ_2	2539883	-0.009	0.079	-0.070	0
TAGLN_11	3350846	-0.009	0.106	-0.096	0
TF_19	2643277	-0.009	0.106	-0.097	0
FGG_8	2790667	-0.008	0.090	-0.082	0
ANXA4_8	2487434	-0.008	0.105	-0.097	0
FGG_4	2790659	-0.007	0.118	-0.111	0
VIM_12	3236997	-0.007	0.047	-0.040	0
FBLIM1_1	2322038	-0.007	0.064	-0.057	0
FGG_6	2790663	-0.006	0.042	-0.036	0
FGB_1	2748550	-0.005	0.063	-0.058	0
TAGLN_3	3350837	-0.005	0.038	-0.033	0
ALB_14	2731225	-0.005	0.049	-0.045	0
TPM2_6	3204730	-0.004	0.106	-0.102	0
TPM2_10	3204738	-0.004	0.061	-0.058	0

TF_11	2643257	-0.013	0.059	-0.047	0	FGG_10	2790672	-0.003	0.074	-0.072	0
ANXA5_6	2784047	-0.012	0.061	-0.049	0	ACTN1_14	3569846	-0.002	0.064	-0.062	0
FGG_15	2790681	-0.012	0.093	-0.081	0	HBB_2	3360404	-0.002	0.054	-0.052	0
FGB_5	2748562	-0.012	0.068	-0.056	0	PDLIM3_3	2796957	-0.002	0.051	-0.048	0
LGALS1_3	3944897	-0.012	0.075	-0.063	0	FGB_10	2748568	-0.002	0.059	-0.056	0
ANXA5_12	2784068	-0.012	0.033	-0.021	0	MYL9_2	3883926	-0.002	0.038	-0.036	0
TAGLN_9	3350844	-0.012	0.047	-0.035	0	ALB_9	2731212	-0.001	0.098	-0.097	0
ACTN4_17	3832720	-0.011	0.040	-0.029	0	HSPA1L_1	2949451	-0.001	0.048	-0.047	0
FGG_17	2790684	-0.011	0.102	-0.092	0	TGM2_11	3905173	-0.001	0.086	-0.086	0
ANXA4_6	2487429	-0.010	0.062	-0.052	0	GSN_14	3187751	0.000	0.054	-0.054	0
PARK7_3	2318751	-0.010	0.073	-0.063	0	TPM2_11	3204739	0.000	0.079	-0.079	0
TPM2_7	3204732	-0.010	0.072	-0.062	0	TGM2_14	3905179	0.000	0.052	-0.052	0
ENO1_1	2395498	-0.010	0.064	-0.054	0	ALB_12	2731220	0.000	0.060	-0.060	0
ALB_11	2731218	-0.010	0.068	-0.058	0	TF_4	2643243	0.000	0.059	-0.058	0
KIAA1429_25	3145058	-0.009	0.073	-0.063	0	TF_9	2643252	0.000	0.084	-0.083	0
ALB_13	2731223	-0.009	0.072	-0.063	0	TAGLN_8	3350843	0.001	0.053	-0.052	0
ACTN1_14	3569846	-0.009	0.064	-0.055	0	GSN_10	3187742	0.001	0.073	-0.072	0
ALB_9	2731212	-0.009	0.078	-0.069	0	PARK7_1	2318743	0.001	0.076	-0.075	0
TAGLN_8	3350843	-0.008	0.077	-0.069	0	ANXA1_4	3174836	0.001	0.078	-0.077	0
VIM_11	3236993	-0.007	0.095	-0.088	0	ENO1_6	2395510	0.001	0.055	-0.054	0
ANXA5_7	2784049	-0.007	0.054	-0.047	0	ACTN4_20	3832723	0.002	0.048	-0.047	0
TF_13	2643265	-0.007	0.079	-0.072	0	MFAP4_7	3748806	0.002	0.045	-0.044	0
LGALS1_1	3944888	-0.006	0.076	-0.070	0	KIAA1429_7	3145033	0.002	0.068	-0.067	0
FGG_16	2790683	-0.006	0.071	-0.065	0	ENO1_4	2395504	0.002	0.074	-0.072	0
TGM2_13	3905177	-0.006	0.053	-0.047	0	KIAA1429_4	3145028	0.003	0.104	-0.101	0
FGB_7	2748565	-0.006	0.059	-0.053	0	FGB_4	2748560	0.003	0.047	-0.045	0
FGG_10	2790672	-0.006	0.048	-0.042	0	TGM2_4	3905150	0.003	0.036	-0.033	0
MYL9_2	3883926	-0.006	0.096	-0.090	0	ANXA5_6	2784047	0.003	0.057	-0.054	0
KIAA1429_11	3145039	-0.006	0.067	-0.061	0	FGG_12	2790677	0.006	0.088	-0.083	0
KIAA1429_1	3145023	-0.005	0.088	-0.083	0	VIM_1	3236968	0.006	0.099	-0.093	0
MYL6_1	3417469	-0.005	0.034	-0.029	0	TAGLN_4	3350838	0.006	0.037	-0.031	0
HSPA1L_5	2949456	-0.005	0.073	-0.068	0	HSPA1L_5	2949456	0.006	0.067	-0.061	0
TINAGL1_14	2328364	-0.004	0.077	-0.073	0	MFAP4_9	3748809	0.007	0.028	-0.021	0
ACTN4_18	3832721	-0.004	0.048	-0.044	0	KIAA1429_3	3145026	0.007	0.081	-0.074	0
YWHAB_9	3886657	-0.004	0.058	-0.054	0	APCS_4	2362656	0.007	0.074	-0.067	0
TF_17	2643274	-0.004	0.037	-0.034	0	ANXA5_3	2784039	0.007	0.030	-0.023	0
TAGLN_10	3350845	-0.002	0.097	-0.095	0	YWHAB_6	3886652	0.007	0.109	-0.101	0
KIAA1429_16	3145048	-0.002	0.050	-0.049	0	ACTN4_3	3832683	0.007	0.048	-0.040	0
ANXA1_5	3174838	-0.001	0.077	-0.075	0	OGN_3	3214805	0.008	0.063	-0.055	0
TF_8	2643251	-0.001	0.070	-0.068	0	ACTN4_9	3832690	0.008	0.061	-0.053	0
YWHAQ_2	2539883	-0.001	0.048	-0.047	0	FGG_9	2790670	0.009	0.047	-0.039	0
FGG_4	2790659	-0.001	0.064	-0.064	0	ACTN1_4	3569822	0.009	0.054	-0.045	0
HSPB1_1	3009402	0.000	0.066	-0.065	0	FGG_15	2790681	0.009	0.077	-0.068	0
ALB_12	2731220	0.000	0.050	-0.050	0	TPM2_7	3204732	0.009	0.076	-0.067	0
PARK7_1	2318743	0.000	0.085	-0.085	0	ACTA2_8	3299531	0.010	0.055	-0.045	0
FBLIM1_6	2322053	0.000	0.045	-0.045	0	HSPA1L_3	2949453	0.010	0.040	-0.030	0
ACTN1_6	3569830	0.000	0.072	-0.072	0	ANXA5_10	2784065	0.010	0.061	-0.051	0
ACTN1_5	3569825	0.001	0.077	-0.076	0	ALB_3	2731198	0.011	0.045	-0.034	0
ENO1_5	2395505	0.002	0.074	-0.072	0	YWHAB_10	3886658	0.011	0.042	-0.032	0
OGN_7	3214810	0.002	0.047	-0.045	0	ANXA4_10	2487441	0.011	0.022	-0.011	0
APCS_4	2362656	0.002	0.078	-0.076	0	OGN_6	3214809	0.011	0.058	-0.046	0
KIAA1429_19	3145052	0.002	0.034	-0.032	0	TTR_4	3783587	0.011	0.084	-0.073	0
TF_18	2643275	0.002	0.063	-0.061	0	TGM2_5	3905151	0.012	0.058	-0.046	0
TGM2_12	3905175	0.003	0.056	-0.053	0	ACTN4_8	3832689	0.012	0.058	-0.046	0
TINAGL1_8	2328355	0.003	0.089	-0.086	0	ENO1_3	2395503	0.013	0.078	-0.066	0
PDLIM3_5	2796962	0.003	0.078	-0.074	0	PDLIM3_7	2796968	0.013	0.064	-0.051	0
MYL9_4	3883930	0.003	0.037	-0.034	0	TGM2_12	3905175	0.013	0.063	-0.049	0
ACTN4_15	3832708	0.003	0.064	-0.060	0	TPM2_2	3204723	0.014	0.051	-0.037	0
ACTN4_3	3832683	0.005	0.076	-0.071	0	ALB_6	2731207	0.014	0.089	-0.075	0
PDLIM3_4	2796959	0.006	0.073	-0.067	0	TF_6	2643248	0.014	0.080	-0.066	0
GSN_9	3187741	0.006	0.092	-0.086	0	TTR_5	3783588	0.015	0.059	-0.045	0
TINAGL1_6	2328352	0.006	0.051	-0.045	0	ACTA2_2	3299508	0.015	0.042	-0.027	0
ANXA1_2	3174832	0.007	0.040	-0.033	0	ALB_15	2731228	0.015	0.071	-0.056	0
ANXA4_13	2487453	0.007	0.051	-0.044	0	ACTN4_17	3832720	0.016	0.065	-0.049	0
ANXA1_3	3174835	0.007	0.064	-0.057	0	ANXA1_8	3174847	0.017	0.042	-0.025	0
ANXA1_6	3174840	0.008	0.041	-0.033	0	ANXA4_13	2487453	0.017	0.072	-0.055	0
GSN_18	3187761	0.008	0.070	-0.062	0	ACTN1_17	3569859	0.017	0.111	-0.094	0
PDLIM3_8	2796969	0.008	0.058	-0.049	0	HBD_1	3360419	0.018	0.074	-0.056	0
ANXA4_5	2487428	0.008	0.075	-0.067	0	TGM2_8	3905165	0.019	0.064	-0.045	0
FGG_2	2790657	0.009	0.049	-0.040	0	VIM_3	3236972	0.019	0.058	-0.039	0
TPM2_11	3204739	0.009	0.051	-0.042	0	KIAA1429_17	3145050	0.019	0.055	-0.036	0
ANXA4_10	2487441	0.009	0.071	-0.061	0	ANXA5_9	2784059	0.020	0.071	-0.051	0
HSPB1_2	3009405	0.009	0.076	-0.067	0	TF_16	2643273	0.020	0.064	-0.045	0
FGB_1	2748550	0.011	0.080	-0.069	0	ACTN4_4	3832684	0.020	0.061	-0.041	0
TPM2_2	3204723	0.011	0.054	-0.043	0	GSN_18	3187761	0.020	0.055	-0.035	0
ANXA5_9	2784059	0.011	0.035	-0.024	0	OGN_4	3214806	0.021	0.068	-0.047	0
TGM2_3	3905149	0.011	0.098	-0.086	0	ANXA5_12	2784068	0.021	0.049	-0.028	0
ANXA5_1	2784037	0.013	0.056	-0.044	0	ACTN1_15	3569849	0.021	0.059	-0.038	0
ALB_7	2731209	0.013	0.085	-0.072	0	GSN_19	3187764	0.022	0.068	-0.046	0
FGB_9	2748567	0.013	0.081	-0.067	0	KIAA1429_12	3145040	0.022	0.063	-0.041	0
ANXA1_10	3174853	0.014	0.076	-0.062	0	ANXA5_2	2784038	0.022	0.060	-0.037	0
KIAA1429_6	3145031	0.014	0.093	-0.079	0	ACTN1_1	3569819	0.023	0.048	-0.025	0
FGG_9	2790670	0.015	0.083	-0.068	0	YWHAB_2	3886643	0.023	0.091	-0.067	0
ALB_1	2731194	0.016	0.091	-0.075	0	ACTA2_5	3299520	0.023	0.050	-0.027	0
TF_14	2643267	0.016	0.101	-0.086	0	ANXA4_1	2487413	0.024	0.083	-0.059	0
TINAGL1_3	2328347	0.016	0.059	-0.044	0	YWHAB_4	3886649	0.024	0.075	-0.051	0
ACTN4_10	3832693	0.016	0.042	-0.026	0	YWHAZ_3	3146954	0.024	0.058	-0.034	0
HBD_4	3360427	0.016	0.043	-0.027	0	YWHAB_7	3886655	0.024	0.049	-0.025	0
ANXA1_11	3174857	0.017	0.063	-0.046	0	HSPB1_1	3009402	0.024	0.062	-0.038	0
FGG_12	2790677	0.017	0.070	-0.053	0	ACTN1_19	3569862	0.024	0.094	-0.070	0
TAGLN_4	3350838	0.017	0.062	-0.045	0	TAGLN_5	3350840	0.024	0.037	-0.013	0
TF_10	2643254	0.018	0.088	-0.071	0	GSN_20	3187765	0.025	0.041	-0.016	0
TGM2_10	3905168	0.018	0.071	-0.054	0	OGN_5	3214807	0.026	0.083	-0.057	0
TPM2_8	3204734	0.018	0.048	-0.030	0	OGN_12	3214817	0.026	0.057	-0.030	0
APCS_1	2362652	0.019	0.062	-0.043	0	TGM2_7	3905162	0.027	0.127	-0.100	0
FGB_3	2748555	0.019	0.050	-0.030	0	ANXA1_7	3174845	0.027	0.058	-0.031	0
ACTN1_8	3569834	0.020	0.067	-0.047	0	KIAA1429_14	3145043	0.028	0.092	-0.064	0
OGN_12	3214817	0.020	0.090	-0.071	0	FGG_11	2790675	0.028	0.097	-0.069	0
MFAP4_7	3748806	0.020	0.034	-0.015	0	TTR_1	3783578	0.028	0.088	-0.059	0
TTR_2	3783579	0.021	0.062	-0.041	0	TF_7	2643249	0.029	0.050	-0.021	0
ACTA2_1	3299507	0.022	0.056	-0.034	0	ACTN4_6	3832686	0.029	0.069	-0.040	0
TF_1	2643237	0.022	0.054	-0.032	0	VIM_13	3236999	0.030	0.069	-0.040	0
KIAA1429_22	3145055	0.022	0.059	-0.037	0	TPM2_5	3204729	0.030	0.063	-0.033	0
ALB_5	2731206	0.022	0.070	-0.047	0	ACTN4_11	3832694	0.031	0.067	-0.036	0
TPM2_3	3204727	0.023	0.082	-0.058	0	FBLIM1_2	2322044	0.031	0.071	-0.039	0
HBB_4	3360411	0.024	0.050	-0.027	0	HSPA1L_4	2949455	0.032	0.059	-0.028	0
GSN_12	3187745	0.024	0.055	-0.031	0	TAGLN_7	3350842	0.032	0.061	-0.029	0
VIM_15	3237001	0.024	0.048	-0.024	0	APCS_1	2362652	0.032	0.043	-0.011	0
ACTN4_11	3832694	0.025	0.052	-0.027	0	ACTN4_12	3832699	0.032	0.066	-0.034	0
TINAGL1_10	2328358	0.025	0.049	-0.024	0	TF_10	2643254	0.032	0.097	-0.065	0
YWHAB_7	3886655	0.025	0.064	-0.039	0	GSN_16	3187756	0.032	0.105	-0.072	0
MYL6_2	3417476	0.025	0.035	-0.010	0	FGB_7	2748565	0.033	0.089	-0.056	0
ACTA2_5	3299520	0.026	0.069	-0.043	0	KIAA1429_10	3145036	0.034	0.053	-0.019	0

ANXA5_3	2784039	0.026	0.045	-0.019	0	OGN_1	3214802	0.034	0.076	-0.042	0
ALB_15	2731228	0.026	0.053	-0.027	0	TINAGL1_5	2328351	0.034	0.056	-0.022	0
PDLIM3_3	2796957	0.027	0.059	-0.031	0	MYL9_4	3883930	0.035	0.091	-0.056	0
FGG_13	2790678	0.027	0.097	-0.070	0	HSPB1_2	3009405	0.035	0.058	-0.023	0
FGG_3	2790658	0.028	0.067	-0.039	0	ANXA5_8	2784050	0.035	0.056	-0.021	0
TTR_5	3783588	0.028	0.072	-0.043	0	LGALS1_1	3944888	0.035	0.083	-0.048	0
VIM_4	3236974	0.029	0.062	-0.033	0	VIM_7	3236980	0.035	0.109	-0.074	0
PDLIM3_2	2796955	0.029	0.058	-0.029	0	ANXA1_10	3174853	0.036	0.068	-0.032	0
TGM2_8	3905165	0.030	0.066	-0.036	0	MFAP4_4	3748803	0.036	0.060	-0.024	0
KIAA1429_14	3145043	0.030	0.071	-0.041	0	PARK7_3	2318751	0.036	0.056	-0.020	0
ANXA4_9	2487439	0.030	0.046	-0.016	0	TF_17	2643274	0.037	0.079	-0.042	0
HSPA1L_1	2949451	0.030	0.080	-0.050	0	KIAA1429_15	3145045	0.038	0.055	-0.018	0
TF_3	2643241	0.030	0.040	-0.009	0	KIAA1429_31	3145076	0.038	0.062	-0.024	0
ACTN4_8	3832689	0.031	0.039	-0.008	0	GSN_8	3187739	0.038	0.108	-0.070	0
TINAGL1_4	2328349	0.032	0.084	-0.052	0	APCS_2	2362653	0.039	0.081	-0.042	0
HBD_1	3360419	0.032	0.059	-0.027	0	ANXA1_1	3174831	0.039	0.073	-0.034	0
TF_4	2643243	0.033	0.083	-0.051	0	KIAA1429_6	3145031	0.039	0.053	-0.013	0
ACTA2_2	3299508	0.033	0.079	-0.047	0	TGM2_3	3905149	0.039	0.043	-0.003	0
PDLIM3_7	2796968	0.033	0.057	-0.024	0	ALB_2	2731195	0.039	0.088	-0.048	0
APCS_5	2362657	0.033	0.070	-0.036	0	KIAA1429_2	3145024	0.040	0.042	-0.002	0
KIAA1429_3	3145026	0.034	0.085	-0.052	0	FGG_16	2790683	0.040	0.065	-0.026	0
KIAA1429_5	3145030	0.034	0.047	-0.014	0	KIAA1429_30	3145071	0.040	0.077	-0.037	0
GSN_13	3187747	0.034	0.089	-0.055	0	ACTN1_10	3569836	0.040	0.045	-0.005	0
TTR_1	3783578	0.034	0.069	-0.035	0	VIM_4	3236974	0.043	0.089	-0.046	0
ACTA2_4	3299517	0.034	0.044	-0.010	0	GSN_12	3187745	0.043	0.067	-0.024	0
YWHAB_8	3886656	0.035	0.044	-0.009	0	CLIC4_2	2325627	0.044	0.075	-0.031	0
YWHAZ_1	3146904	0.036	0.060	-0.024	0	ANXA4_6	2487429	0.045	0.069	-0.025	0
FGB_2	2748554	0.036	0.052	-0.016	0	KIAA1429_20	3145053	0.045	0.048	-0.003	0
MYL9_5	3883931	0.037	0.040	-0.003	0	ALB_16	2731229	0.046	0.101	-0.055	0
KIAA1429_2	3145024	0.037	0.063	-0.025	0	TGM2_10	3905168	0.046	0.087	-0.041	0
ANXA4_12	2487446	0.037	0.058	-0.020	0	FGB_9	2748567	0.047	0.103	-0.056	0
PARK7_4	2318754	0.037	0.067	-0.030	0	MYL9_3	3883929	0.047	0.073	-0.027	0
TPM2_5	3204729	0.038	0.047	-0.009	0	KIAA1429_8	3145034	0.047	0.058	-0.011	0
FGB_8	2748566	0.038	0.058	-0.020	0	KIAA1429_5	3145030	0.048	0.072	-0.025	0
PARK7_2	2318747	0.038	0.048	-0.009	0	ANXA5_4	2784045	0.048	0.054	-0.006	0
PDLIM3_1	2796954	0.038	0.054	-0.016	0	TINAGL1_14	2328364	0.048	0.085	-0.036	0
VIM_6	3236977	0.038	0.070	-0.032	0	TPM2_3	3204727	0.049	0.075	-0.027	0
TGM2_11	3905173	0.039	0.047	-0.009	0	KIAA1429_26	3145060	0.049	0.065	-0.016	0
KIAA1429_23	3145056	0.040	0.082	-0.043	0	FGB_5	2748562	0.050	0.082	-0.033	0
FGB_4	2748560	0.040	0.076	-0.036	0	FGB_3	2748555	0.050	0.062	-0.012	0
KIAA1429_7	3145033	0.040	0.053	-0.012	0	TF_13	2643265	0.050	0.077	-0.027	0
ENO1_4	2395504	0.041	0.068	-0.027	0	TINAGL1_8	2328355	0.050	0.087	-0.037	0
TGM2_2	3905147	0.041	0.066	-0.025	0	MFAP4_6	3748805	0.050	0.098	-0.048	0
OGN_11	3214816	0.042	0.069	-0.026	0	TAGLN_9	3350844	0.050	0.107	-0.057	0
VIM_14	3237000	0.042	0.053	-0.011	0	TF_5	2643244	0.050	0.076	-0.026	0
KIAA1429_24	3145057	0.043	0.066	-0.024	0	PDLIM3_8	2796969	0.051	0.051	-0.001	0
APCS_2	2362653	0.043	0.051	-0.007	0	TF_3	2643241	0.052	0.073	-0.021	0
ANXA1_8	3174847	0.047	0.079	-0.032	0	YWHAQ_3	2539899	0.056	0.087	-0.030	0
HSPA1L_4	2949455	0.047	0.075	-0.028	0	ENO1_5	2395505	0.057	0.061	-0.004	0
KIAA1429_15	3145045	0.048	0.051	-0.003	0	ANXA5_7	2784049	0.059	0.097	-0.038	0
ENO1_6	2395510	0.048	0.082	-0.034	0	ACTN1_11	3569840	0.062	0.073	-0.011	0
YWHAQ_1	2539873	0.051	0.060	-0.009	0	PDLIM3_5	2796962	0.062	0.082	-0.020	0
ACTA2_9	3299534	0.054	0.059	-0.005	0	ACTA2_4	3299517	0.065	0.067	-0.002	0
PDLIM3_9	2796971	0.056	0.056	-0.001	0	TINAGL1_4	2328349	0.067	0.107	-0.041	0
TPM2_4	3204728	0.058	0.063	-0.005	0	ALB_4	2731201	0.068	0.085	-0.017	0
KIAA1429_27	3145066	0.058	0.065	-0.007	0	TGM2_6	3905152	0.071	0.094	-0.023	0
VIM_10	3236991	0.069	0.074	-0.005	0	LGALS1_2	3944893	0.074	0.092	-0.018	0
ACTN4_19	3832722	0.072	0.077	-0.005	0	ALB_5	2731206	0.074	0.081	-0.007	0
TGM2_7	3905162	0.074	0.088	-0.014	0	FGG_5	2790662	0.075	0.094	-0.019	0
TINAGL1_12	2328362	0.075	0.075	-0.001	0	ACTN1_9	3569835	0.075	0.093	-0.018	0
MFAP4_3	3748802	0.076	0.085	-0.008	0	YWHAB_9	3886657	0.075	0.090	-0.015	0

[a] Loading value from OPLS-DA model with controls vs dilated

[b] Jack-Knife confidence interval derived from cross-validation in OPLS-DA models

[c] Subtracting the jack-knife confidence intervals from the corresponding loading values, if positive indicates significance

[d] If the subtracting jack-knife cofidence interval from the corresponding loading is positive (significant), and indicated with 1, and if negative (non-singnificant), it is indicated with 0

Supplemental Table 8. Genes showing correlation with protein expression in TAV and BAV based on multivariate statistics.

TAV

				Protein expression	Gene expression	Exon expression	
Gene name	**Meta probe set ID**	**Protein accession number**	**No of protein spots***	CvsD[a]	CvsD[b]	CvsD[c]	Total no of probe sets/gene
ACTN1	3569814	P12814	2	0.051	0.070	12	22
ACTN4	3832643	O43707	5	0.063	0.178	6	20
ENO1	2395490	P06733	3	0.025	0.122	1	6
HBB	3360401	P68871	7	0.053	0.211	4	5
HBD	3360417	P02042	1	0.044	0.023	2	4
LDHA	3322775	P00338	1	0.022	0.041	2	2
TINAGL1	2328320	Q9GZM7	2	0.032	0.055	4	15
TUBB	2901913	P07437	3	0.037	0.020	na	na
YWHAB	3886639	P31946	2	0.076	0.030	5	10
YWHAQ	2539869	P27348	1	0.050	0.038	1	4

BAV

				Protein expression	Gene expression	Exon expression	
Gene name	**Meta probe set ID**	**Protein accession number**	**No of protein spots***	CvsD[a]	CvsD[b]	CvsD[c]	Total no of probe sets/gene
ACTN1	3569814	P12814	2	0.049	0.096	5	22
ACTN4	3832643	O43707	5	0.086	0.163	5	20
FBLIM1	2322036	Q8WUP2	2	0.021	0.067	4	8
HBB	3360401	P68871	7	0.057	0.253	3	5
HBD	3360417	P02042	1	0.045	0.017	3	4
HSPB1	3009399	P04792	2	0.044	0.063	0	4
TINAGL1	2328320	Q9GZM7	2	0.031	0.028	7	15
TUBB	2901913	P07437	3	0.045	0.102	na	

[a] ABS (loading)-ABS(jack-knife conf intervall) protein expression data, dilated higher (green), non-dilated higher (blue)

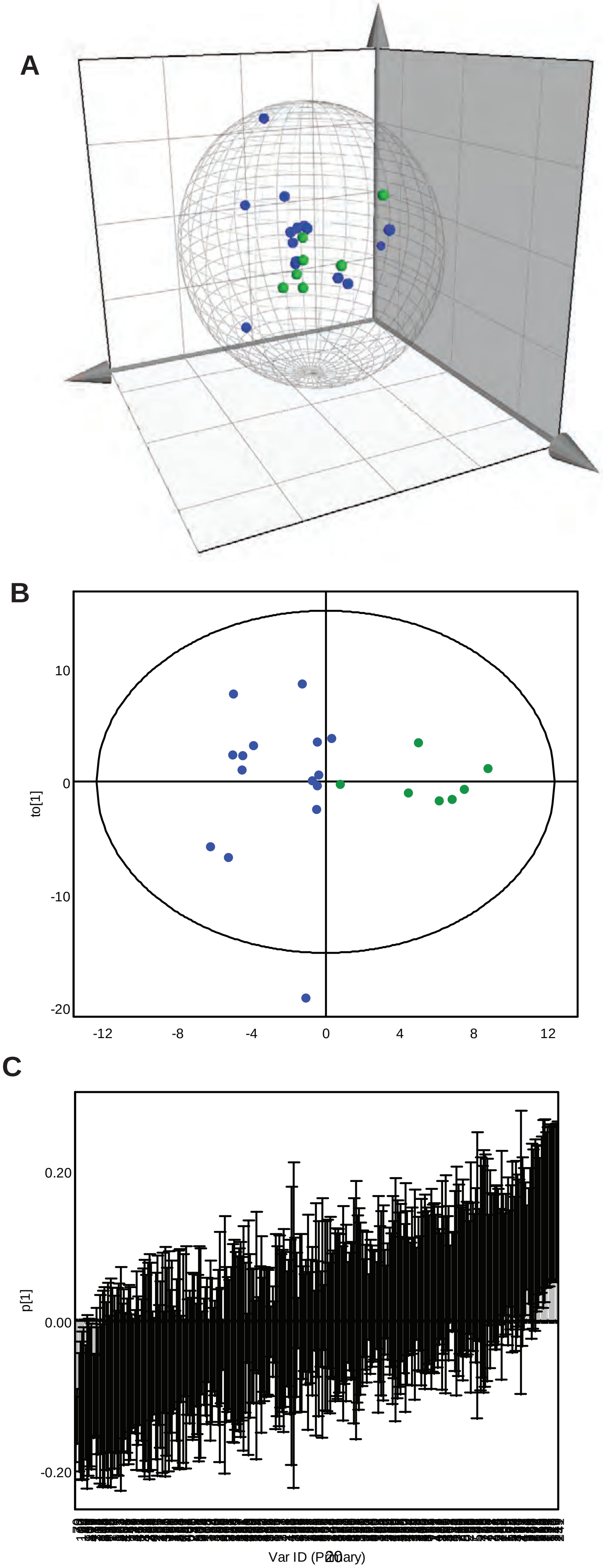
[b] ABS (loading)-ABS(jack-knife conf intervall) meta probe set array expression data

[c] ABS (loading)-ABS(jack-knife conf intervall) probe set array expression data

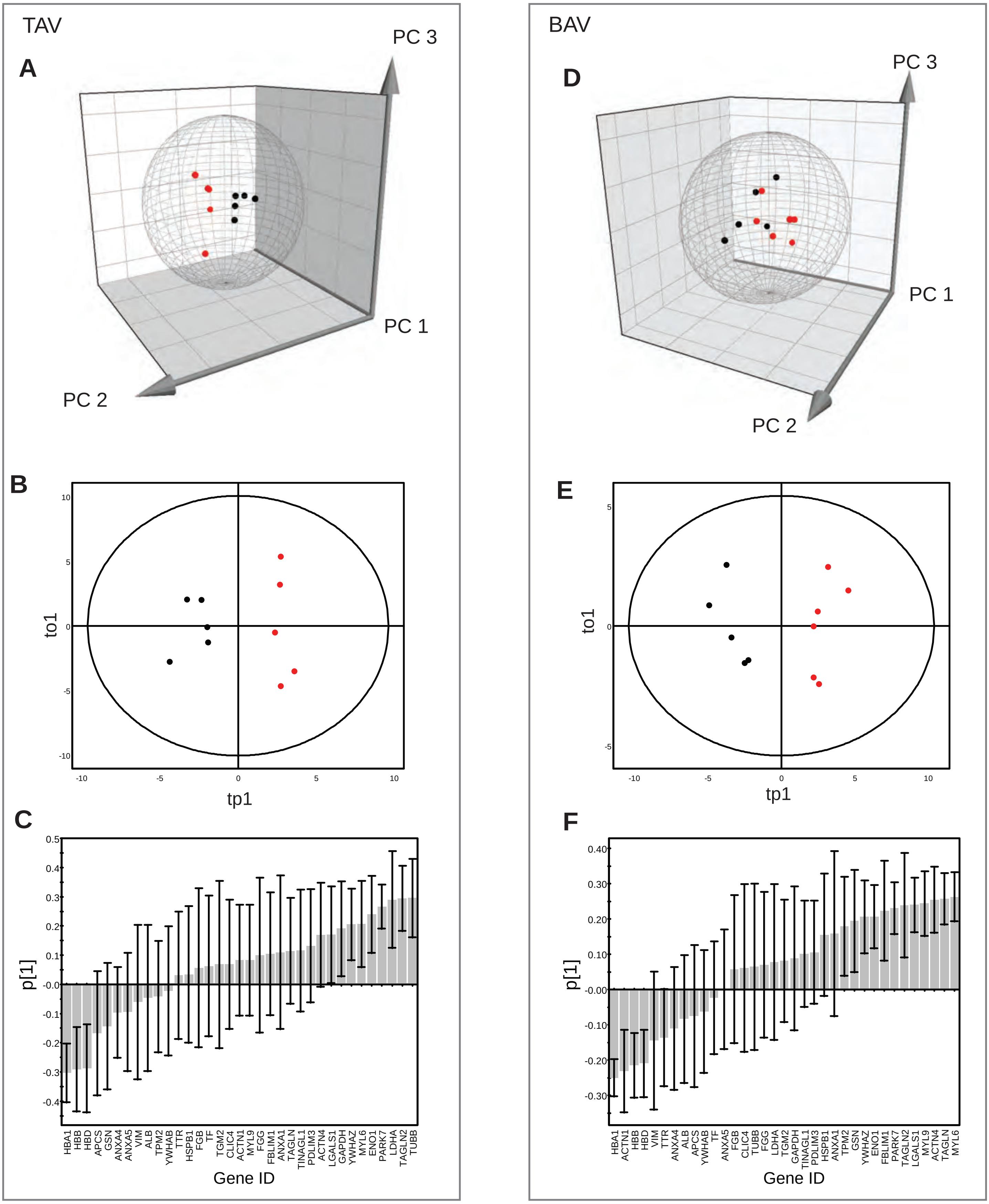
na not analyzed due to not present at core level or only one exon

* Number of protein spots identified on the gel

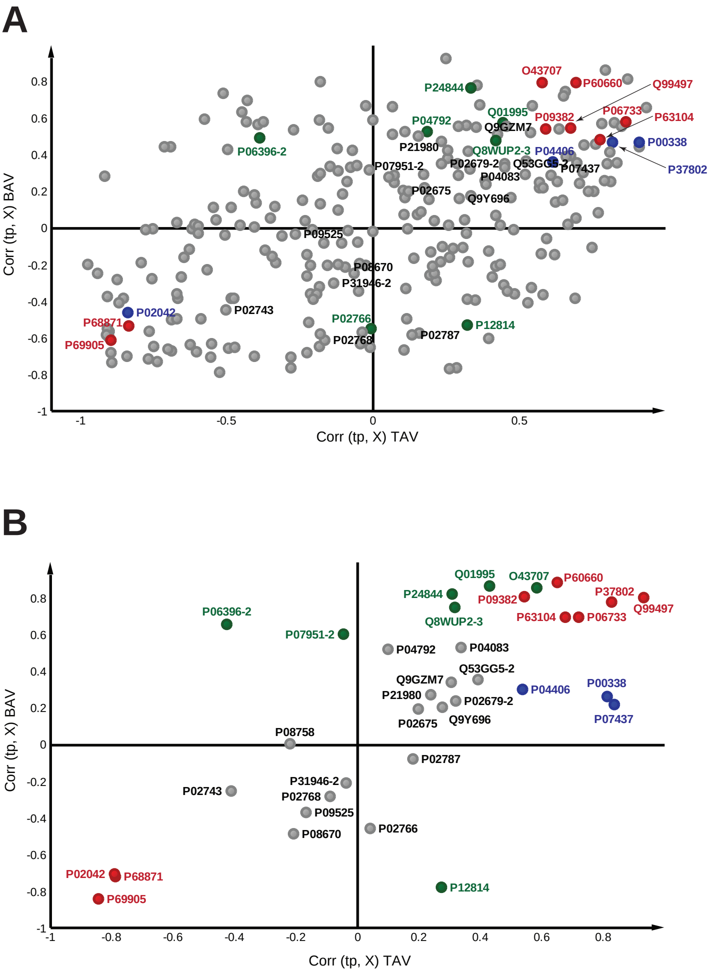
Supplemental Figure 1



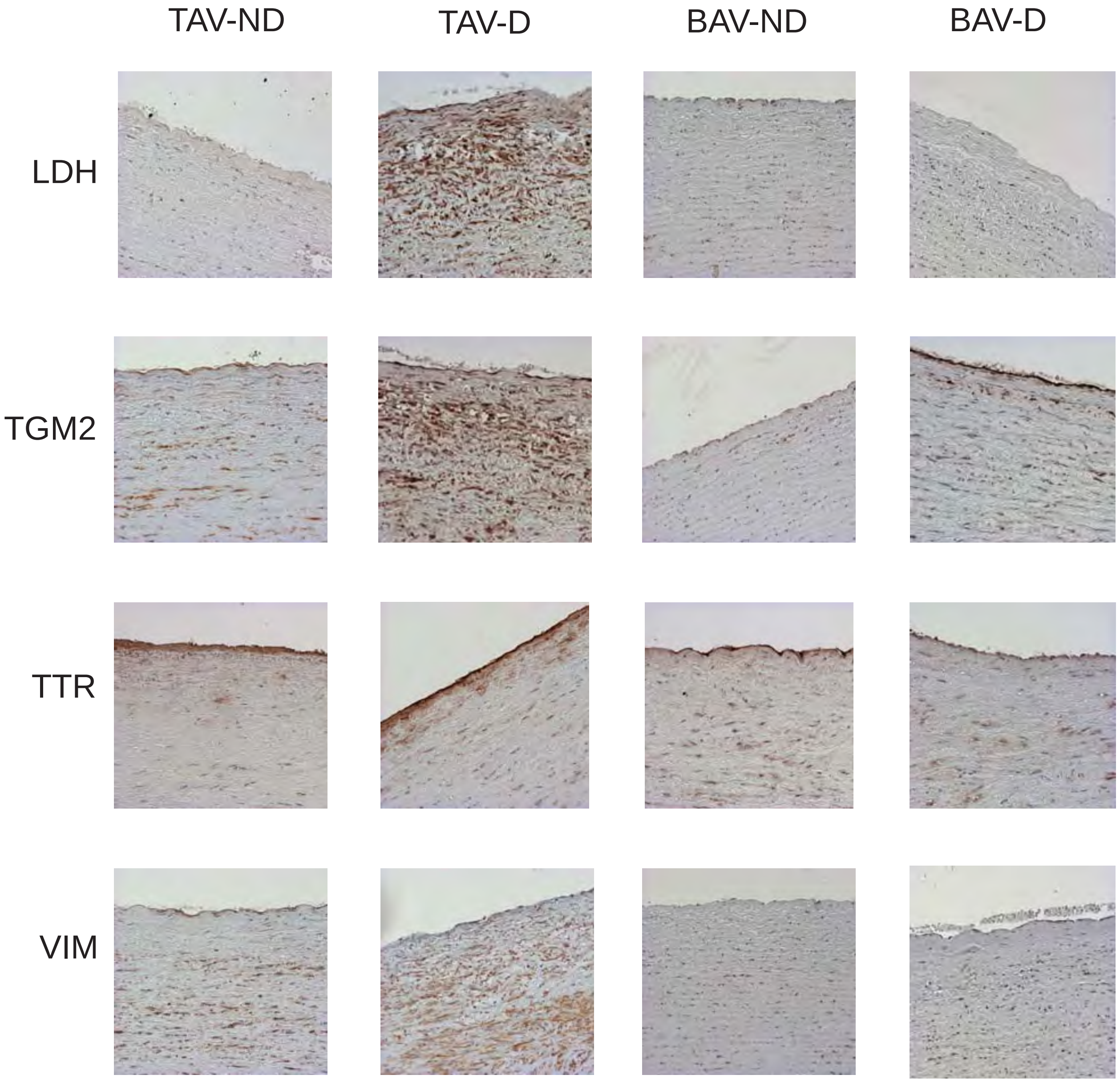
Supplemental Figure 2



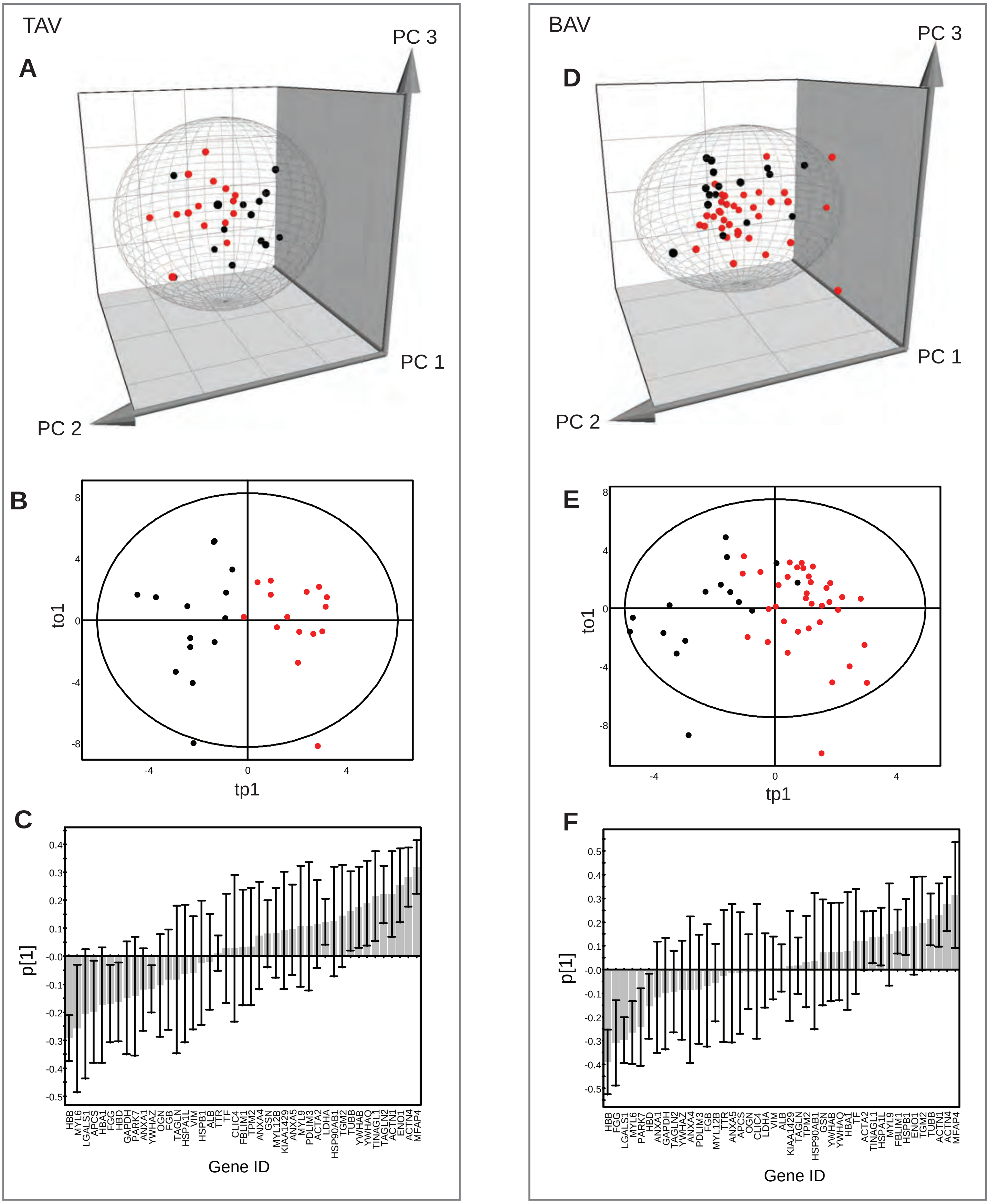
Supplemental Figure 3



Supplemental Figure 4



Supplemental Figure 5



Supplemental Figure 6