

S5 Table. Proteins altered in LV and RV after transverse aortic constriction (TAC).

Primary protein name*	Swiss Prot ID	Protein name	LV 4d	LV 14d	LV 21d	LV 28d	LV 42d	LV 56d	RV 4d	RV 14d	RV 21d	RV 28d	RV 42d	RV 56d
6PGD	Q9DCD0	6-phosphogluconate dehydrogenase,decarboxylating	2.78	5.80	2.93	0.61	2.31	1.10	2.78	0.90	0.61	1.07	0.82	2.61
A1AG2	P07361	Alpha-1-acid glycoprotein 2	0.30	1.82	1.95	10.6	0.00	3.43	0.46	0.16	2.36	5.82	0.11	0.68
ACTN1	Q7TPR4	Alpha-actinin-1	0.99	1.45	0.95	1.78	1.40	2.30	1.19	1.71	2.19	1.74	1.20	2.33
ACTS	P68134	Actin, alpha skeletal muscle	1.37	6.31	4.44	4.99	5.70	5.31	0.92	1.88	2.50	2.83	2.05	5.09
ADA10	O35598	Disintegrin and metalloproteinase domain-containing protein 10	1.02	0.85	0.47	1.01	1.38	1.78	0.57	1.66	1.46	0.42	1.81	4.00
ANF	P05125	Atrial natriuretic factor	1.84	4.91	6.26	5.33	4.37	32.8	0.11	0.53	0.17	1.44	0.58	15.2
ANK1	Q02357	Ankyrin-1	1.28	0.32	1.72	2.11	0.12	0.40	0.67	1.31	0.76	0.79	1.55	0.50
ANK2	Q8C8R3	Ankyrin-2	1.07	0.40	3.11	0.71	0.83	0.86	1.14	1.12	0.44	0.65	1.36	0.91
ANXA1	P10107	Annexin A1	1.87	2.01	1.12	1.28	0.95	1.98	1.25	1.58	0.47	1.24	2.23	1.44
ANXA4	P97429	Annexin A4	1.22	4.06	1.36	1.36	1.79	2.07	1.25	1.49	2.01	0.54	1.38	1.27
BZW2	Q91VK1	Basic leucine zipper and W2 domain-containing protein 2	0.55	0.93	0.69	0.45	1.29	1.09	0.70	0.90	0.59	1.70	0.78	0.31
C1QBP	O35658	Complement component 1 Q subcomponent-binding protein. mitochondrial	4.00	0.31	0.76	0.73	0.22	0.37	0.72	0.92	1.08	2.74	1.45	0.61
CALM	P62204	Calmodulin	2.30	0.62	0.94	1.08	0.64	0.84	0.89	1.69	0.77	2.83	1.40	0.27
CAPZB	P47757	F-actin-capping protein subunit beta	3.01	1.76	7.46	0.65	1.13	0.60	0.36	0.09	0.41	2.93	15.7	7.26
CC138	Q0VF22	Coiled-coil domain-containing protein 138	0.57	0.79	0.14	0.81	0.70	1.04	1.63	5.91	1.31	0.65	0.37	0.55
CES1D	Q8VCT4	Carboxylesterase 1D	0.75	0.36	0.30	0.55	0.47	0.30	0.93	0.92	0.92	0.65	0.76	0.47
CHCH2	Q9D1L0	Coiled-coil-helix-coiled-coil-helix domain-containing protein 2, mitochondrial	1.04	1.70	9.96	1.07	2.88	0.51	0.67	0.04	0.44	9.16	7.95	7.62
CLN8	Q9QUK3	Protein CLN8	0.55	1.64	0.51	0.45	0.65	1.49	1.11	2.73	1.08	0.56	1.10	0.82
CN159	Q8BH86	UPF0317 protein C14orf159 homolog,mitochondrial	0.96	0.57	0.60	0.79	0.54	0.41	0.72	0.84	0.71	0.77	0.65	0.49
CND2	Q8C156	Condensin complex subunit 2	0.84	1.03	2.42	1.39	0.72	0.71	0.83	0.95	1.45	2.99	1.15	0.85

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CO1A2	Q01149	Collagen alpha-2(I) chain	0.59	2.38	1.57	1.14	1.21	1.65	1.31	1.16	0.97	0.46	1.12	1.14
CO4A1	P02463	Collagen alpha-1(IV) chain	1.20	1.78	2.66	1.09	1.01	1.19	0.74	0.44	0.92	1.59	2.26	1.49
COX1	P00397	Cytochrome c oxidase subunit 1	1.19	0.38	2.82	1.26	0.73	0.73	0.73	0.81	0.78	2.82	1.33	1.06
COX20	Q9D7J4	Cytochrome c oxidase protein 20 homolog	1.09	0.67	0.88	0.45	0.73	0.81	0.92	1.28	0.89	2.04	0.76	0.47
CP4AA	O88833	Cytochrome P450 4A10	1.70	0.88	0.66	1.95	0.49	0.94	1.06	1.06	1.73	0.47	1.22	0.46
CX6B1	P56391	Cytochrome c oxidase subunit 6B1	5.29	0.94	5.63	1.09	1.21	0.61	0.32	0.11	0.57	4.29	28.9	4.23
EIF3I	Q9QZD9	Eukaryotic translation initiation factor 3 subunit I	0.96	2.05	0.97	0.91	1.21	1.34	1.66	0.88	1.25	0.38	0.97	0.94
F210A	Q8BGY7	Protein FAM210A	0.84	1.04	0.45	0.24	0.51	0.48	1.12	0.76	0.51	1.19	1.21	0.46
FETUA	P29699	Alpha-2-HS-glycoprotein	1.42	1.39	4.00	0.83	1.27	0.78	0.46	0.42	0.65	2.46	5.22	1.77
FGF1	P61148	Heparin-binding growth factor 1	0.67	2.35	1.47	1.79	0.49	0.78	1.09	0.78	0.93	0.43	1.06	0.70
FHL1	P97447	Four and a half LIM domains protein 1	2.21	4.14	4.03	2.72	2.82	4.55	1.30	2.54	2.46	1.28	2.36	4.50
FHL2	O70433	Four and a half LIM domains protein 2	1.05	0.95	2.50	0.78	1.09	1.14	0.87	0.33	0.81	0.72	1.82	1.28
FINC	P11276	Fibronectin	1.89	1.86	1.89	2.13	0.79	2.31	2.24	1.40	2.61	1.15	0.81	0.67
FLNC	Q8VHX6	Filamin-C	1.73	2.13	2.10	2.11	1.95	2.78	1.28	1.65	1.72	1.89	1.40	2.44
FRIH	P09528	Ferritin heavy chain	0.48	0.39	0.45	0.51	0.45	0.50	0.71	0.84	0.66	0.68	0.66	0.45
GBB2	P62880	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	0.88	1.34	5.26	0.99	2.46	0.55	0.47	0.23	0.54	2.08	6.02	1.43
GCAB	P01864	Ig gamma-2A chain C region secreted form	0.77	0.88	1.48	3.27	0.49	0.96	0.36	0.70	2.25	4.07	0.45	0.87
GLRX5	Q80Y14	Glutaredoxin-related protein 5	0.98	1.17	10.4	1.28	1.07	0.77	0.31	0.08	0.48	1.51	7.09	4.96
GPDM	Q64521	Glycerol-3-phosphate dehydrogenase, mitochondrial	0.89	0.49	0.47	2.15	0.45	0.64	0.87	1.10	1.34	0.62	0.80	0.31
HBB1	P02088	Hemoglobin subunit beta-1	1.13	1.04	0.71	2.29	0.88	0.59	1.11	0.86	2.02	0.71	0.53	0.94
HPT	Q61646	Haptoglobin	0.31	0.25	1.79	7.65	0.09	1.49	0.48	0.31	1.29	3.10	0.22	1.44
HSPB6	Q5EBG6	Heat shock protein beta-6	2.34	2.27	1.98	1.97	2.06	1.94	0.96	1.29	1.46	1.58	2.46	1.96
IF5A1	P63242	Eukaryotic translation initiation factor 5A-1	1.19	1.48	9.32	0.56	0.60	0.74	0.72	1.00	1.43	2.08	0.53	0.35
IGG2B	P01867	Ig gamma-2B chain C region	0.63	1.31	1.46	2.41	0.34	1.26	0.50	0.73	1.77	2.10	0.47	1.15

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IGH1M	P01869	Ig gamma-1 chain C region, membrane-bound form	0.63	0.86	4.30	3.87	0.44	1.55	0.55	0.59	1.76	2.47	0.49	1.31
IGKC	P01837	Ig kappa chain C region	0.77	1.19	3.12	1.82	0.63	1.59	0.36	0.65	2.10	3.50	0.50	1.13
KAT1	Q8BTY1	Kynurenine--oxoglutarate transaminase 1	0.79	1.00	0.49	0.85	0.99	1.03	1.40	0.67	1.04	0.49	0.73	0.69
KCC1A	Q91YS8	Calcium/calmodulin-dependent protein kinase type 1	1.11	0.82	0.60	2.32	0.34	1.52	0.85	0.93	1.34	1.53	0.37	0.38
KV5A3	P01635	Ig kappa chain V-V region K2 (Fragment)	1.05	1.92	2.70	3.41	1.17	2.22	0.84	2.01	2.65	2.73	0.64	1.69
MLRA	Q9QVP4	Myosin regulatory light chain 2, atrial isoform	0.16	0.52	0.30	0.75	0.90	1.10	0.32	1.42	0.24	0.95	0.27	3.84
MUCM	P01873	Ig mu chain C region membrane-bound form	1.03	1000	0.29	0.83	1.42	0.68	2.45	2.00	1.94	1.32	1.20	0.52
MYH7	Q91Z83	Myosin-7	1.59	5.00	5.21	7.11	5.27	17.2	2.30	1.40	1.76	2.38	1.72	9.50
MYL1	P05977	Myosin light chain 1/3, skeletal muscle isoform	2.01	5.36	4.07	2.64	2.91	2.85	1.43	1.49	2.13	1.35	1.37	1.71
MYL4	P09541	Myosin light chain 4	0.21	0.43	0.55	0.63	0.96	1.03	0.31	1.45	0.21	1.06	0.48	4.36
NDUF4	Q9D1H6	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 4	0.82	0.52	0.91	1.55	0.37	0.97	0.72	0.72	0.67	1.84	0.37	0.30
NDUV3	Q8BK30	NADH dehydrogenase [ubiquinone] flavoprotein 3. mitochondrial	0.52	2.28	1.14	0.59	1.04	0.69	1.05	0.82	1.23	0.47	1.22	0.85
NU3M	P03899	NADH-ubiquinone oxidoreductase chain 3	4.03	1.21	5.35	0.73	1.18	0.59	0.36	0.15	0.47	2.76	18.3	5.52
PALLD	Q9ET54	Palladin	1.17	3.71	1.69	1.47	1.47	1.16	1.76	1.17	0.62	1.28	1.31	2.18
PDLI1	O70400	PDZ and LIM domain protein 1	1.01	2.32	1.59	1.70	1.87	1.65	1.23	1.00	1.73	1.37	1.63	2.41
PDP1	Q3UV70	[Pyruvate dehydrogenase [acetyl-transferring]]-phosphatase 1. mitochondrial	0.76	0.93	0.74	1.42	0.35	1.33	0.87	0.96	1.33	0.69	0.66	0.23
PGFS	Q9DB60	Prostaglandin F synthase	2.09	0.59	2.54	1.39	0.31	0.95	0.83	1.41	1.16	3.25	2.16	1.19
PKHO1	Q9JIY0	Pleckstrin homology domain-containing family O member 1	0.85	1.18	0.50	0.65	0.76	0.88	0.89	0.79	0.89	2.05	0.66	0.76
PLIN4	O88492	Perilipin-4	0.41	1.26	0.66	1.73	1.05	0.90	0.91	1.92	1.67	0.48	0.54	0.38
PTCD3	Q14C51	Pentatricopeptide repeat-containing protein 3, mitochondrial	1.89	0.58	0.61	2.43	1.29	1.02	0.66	0.67	2.12	1.02	1.03	0.50
PURB	O35295	Transcriptional activator protein Pur-beta	0.55	2.41	1.07	0.94	2.06	1.55	1.25	1.23	1.39	0.81	2.01	0.80
QCR10	Q9CPX8	Cytochrome b-c1 complex subunit 10	0.91	0.32	0.38	0.91	1.42	0.73	0.85	0.77	1.30	1.70	0.42	0.58
QCR6	P99028	Cytochrome b-c1 complex subunit 6, mitochondrial	6.50	1.12	5.53	1.03	1.36	0.54	0.40	0.15	0.79	2.70	37.9	2.87
RAB18	P35293	Ras-related protein Rab-18	3.36	1.66	0.62	1.26	0.75	1.14	1.28	1.22	1.40	1.11	0.38	1.95

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RAB6A	P35279	Ras-related protein Rab-6A	1.32	0.85	1.27	1.48	1.01	2.21	0.81	0.51	3.10	2.97	0.67	1.24
RBM46	P86049	Probable RNA-binding protein 46	1.32	20.3	0.21	1.31	1.10	4.21	17.5	0.05	0.33	1.04	0.64	1.29
RS15	P62843	40S ribosomal protein S15	4.60	0.78	0.90	0.91	0.41	0.98	1.27	1.35	0.99	3.10	1.73	0.60
RS3A	P97351	40S ribosomal protein S3a	1.48	1.13	2.06	1.24	0.87	0.86	0.77	0.42	0.82	1.11	2.56	2.08
SAA1	P05366	Serum amyloid A-1 protein	0.50	1000	5.65	1000	0.00	0.93	0.63	1.28	2.45	0.47	1.32	2.13
SIR3	Q8R104	NAD-dependent protein deacetylase sirtuin-3	1.98	0.96	0.43	0.42	0.12	0.90	1.09	2.16	1.09	2.70	0.69	0.55
SLMAP	Q3URD3	Sarcolemmal membrane-associated protein	1.08	1.73	2.00	1.51	1.54	2.05	1.30	1.71	2.23	1.64	1.77	2.50
SPT6H	Q62383	Transcription elongation factor SPT6	0.53	1.68	0.37	0.61	0.78	1.12	0.71	2.62	0.98	0.57	0.56	1.28
SSPN	Q62147	Sarcospan	0.45	1.00	2.29	0.63	1.25	0.78	1.37	0.70	0.95	0.40	1.33	1.58
SYNE1	Q6ZWR6	Nesprin-1	0.92	1.20	3.18	4.33	0.27	0.41	1.25	1.01	1.09	0.57	1.03	2.70
SYP2L	Q8BWB1	Synaptopodin 2-like protein	1.92	3.67	3.47	2.11	2.79	3.41	1.44	2.01	1.53	1.68	1.98	2.99
TBB2A	Q7TMM9	Tubulin beta-2A chain	1.45	2.77	2.54	1.92	1.68	3.45	1.35	1.65	1.47	0.92	1.64	2.29
TFR1	Q62351	Transferrin receptor protein 1	1.61	2.36	1.76	1.57	1.29	1.02	1.35	0.90	1.14	0.63	1.13	2.80
XIRP1	O70373	Xin actin-binding repeat-containing protein 1	1.94	3.17	2.99	2.13	3.22	3.81	1.27	1.71	1.61	1.10	1.32	2.45