



Bond, Iacobazzi, Abdul-Ghani, S., Ghorbel, Heesom, George, Caputo, Suleiman, & Tulloh (2018). The cardiac proteome in patients with congenital ventricular septal defect: A comparative study between right atria and right ventricles. *Journal of Proteomics*. Advance online publication. <https://doi.org/10.1016/j.jprot.2018.03.022>

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[10.1016/j.jprot.2018.03.022](https://doi.org/10.1016/j.jprot.2018.03.022)

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Supplementary Information

Supplementary Table A: Significantly changed proteins between the right atria (RA) and right ventricle (RV) of infants with ventricular septal defect (VSD).

Accession #	Gene ID	Description	Mean		SEM		Fold Change	p-value	log ₂ [fold change]	-log ₁₀ [p-value]
			RA	RV	RA	RV	RA/RV			
P13929	ENO3	Beta-enolase	0.50	1.25	0.07	0.21	0.40	0.02	-1.32	1.70
Q6ZP09	-	cDNA FLJ26763 fis, clone PRS02632, highly similar to COCHLIN	0.62	1.27	0.09	0.25	0.49	0.02	-1.03	1.70
B2RD40	-	cDNA, FLJ96442, highly similar to Homo sapiens copine II (CPNE2), mRNA	0.68	1.36	0.15	0.15	0.50	0.04	-1.00	1.43
Q9UKE5	TNIK	TRAF2 and NCK-interacting protein kinase	1.04	1.99	0.14	0.22	0.52	0.02	-0.93	1.72
Q6FHU0	PSMB8	Proteasome subunit beta type (Fragment)	1.04	1.95	0.10	0.34	0.53	0.03	-0.91	1.48
A0A024RAL3	ZFYVE16	Zinc finger, FYVE domain containing 16, isoform CRA_a	0.90	1.67	0.09	0.23	0.54	0.05	-0.90	1.33
Q9NPG3	UBN1	Ubinuclein-1	1.00	1.81	0.14	0.32	0.55	0.03	-0.86	1.46
A6NI28	ARHGAP42	Rho GTPase-activating protein 42	0.90	1.61	0.14	0.34	0.56	0.03	-0.84	1.56
F5GX99	CLPB	Caseinolytic peptidase B protein homolog	0.86	1.52	0.14	0.34	0.57	0.03	-0.82	1.52
Q8TEA1	NSUN6	Putative methyltransferase NSUN6	1.14	2.01	0.47	0.56	0.57	0.05	-0.82	1.33
Q13325	IFIT5	Interferon-induced protein with tetratricopeptide repeats 5	0.91	1.56	0.14	0.14	0.58	0.03	-0.78	1.57
Q9NQ88	TIGAR	Fructose-2,6-bisphosphatase TIGAR	0.86	1.46	0.07	0.22	0.59	0.03	-0.76	1.55
E9PQ73	FAT3	Protocadherin Fat 3	1.01	1.70	0.04	0.21	0.59	0.02	-0.75	1.61
P78310	CXADR	Coxsackievirus and adenovirus receptor	0.82	1.36	0.14	0.07	0.60	0.01	-0.74	2.18
Q9P1A0	NDUFS1	NDUFS1 protein	0.87	1.41	0.12	0.17	0.62	0.01	-0.69	2.09
Q14315	FLNC	Filamin-C	0.76	1.22	0.09	0.06	0.62	0.02	-0.69	1.64
Q8NI37	PPTC7	Protein phosphatase PTC7 homolog	1.01	1.62	0.10	0.16	0.62	0.02	-0.69	1.80
E7EVA0	MAP4	Microtubule-associated protein	0.87	1.40	0.05	0.12	0.62	0.00	-0.69	2.39
Q96L96	ALPK3	Alpha-protein kinase 3	0.81	1.31	0.10	0.12	0.62	0.04	-0.68	1.40

O15173	PGRMC2	Membrane-associated progesterone receptor component 2	1.09	1.73	0.04	0.12	0.63	0.01	-0.67	2.28
Q8N122	RPTOR	Regulatory-associated protein of mTOR	0.92	1.45	0.06	0.21	0.63	0.03	-0.66	1.49
P26447	S100A4	Protein S100-A4	0.77	1.22	0.12	0.20	0.63	0.04	-0.66	1.40
P53582	METAP1	Methionine aminopeptidase 1	0.88	1.37	0.10	0.15	0.64	0.05	-0.64	1.34
O95218	ZRANB2	Zinc finger Ran-binding domain-containing protein 2	0.95	1.48	0.10	0.27	0.64	0.04	-0.63	1.36
Q9UM22	EPDR1	Mammalian ependymin-related protein 1	0.99	1.53	0.07	0.20	0.65	0.03	-0.63	1.48
O14907	TAX1BP3	Tax1-binding protein 3	1.21	1.87	0.13	0.20	0.65	0.01	-0.62	1.92
O00151	PDLIM1	PDZ and LIM domain protein 1	0.89	1.36	0.07	0.19	0.65	0.03	-0.61	1.47
K7EMU8	DNMT1	DNA (cytosine-5)-methyltransferase 1	0.63	0.96	0.03	0.10	0.66	0.02	-0.61	1.68
F8VPF7	HVCN1	Voltage-gated hydrogen channel 1 (Fragment)	1.21	1.83	0.16	0.26	0.66	0.04	-0.60	1.41
Q96CT7	CCDC124	Coiled-coil domain-containing protein 124	0.98	1.48	0.09	0.19	0.66	0.04	-0.60	1.36
V5T7C5	LDB3	LIM domain binding 3 transcript variant 8	0.90	1.36	0.06	0.12	0.66	0.00	-0.60	2.50
Q5TA31	RNF187	E3 ubiquitin-protein ligase RNF187	1.21	1.83	0.19	0.13	0.66	0.02	-0.59	1.69
Q9BQ48	MRPL34	39S ribosomal protein L34, mitochondrial	1.01	1.53	0.07	0.18	0.66	0.02	-0.59	1.71
E9PMI6	CLNS1A	Methylosome subunit pICln	1.18	1.78	0.18	0.27	0.66	0.02	-0.59	1.81
Q9Y4D7	PLXND1	Plexin-D1	0.92	1.37	0.11	0.15	0.67	0.00	-0.58	2.52
P43897	TSFM	Elongation factor Ts, mitochondrial	0.94	1.40	0.12	0.09	0.67	0.00	-0.58	2.79
B2RE63	-	cDNA, FLJ93742, highly similar to Homo sapiens kelch repeat and BTB (POZ) domain containing 10(KBTBD10), mRNA	0.86	1.28	0.07	0.14	0.67	0.05	-0.57	1.32
B7Z9B7	-	cDNA FLJ54732, moderately similar to Sorbin and SH3 domain-containing protein 1	0.93	1.38	0.06	0.18	0.67	0.03	-0.57	1.58
B4DGU4	CTNNB1	Catenin beta-1	0.84	1.25	0.09	0.07	0.67	0.03	-0.57	1.50
Q5BKX8	MURC	Muscle-related coiled-coil protein	0.98	1.45	0.03	0.12	0.68	0.01	-0.56	1.95
B2R6J3	-	cDNA, FLJ92974, highly similar to Homo sapiens methylmalonic aciduria (cobalamin deficiency) type B(MMAB), mRNA	0.92	1.35	0.12	0.22	0.68	0.04	-0.56	1.38

B4DEN6	-	cDNA FLJ55549, highly similar to 3-ketoacyl-CoA thiolase, peroxisomal (EC 2.3.1.16)	0.98	1.44	0.05	0.12	0.68	0.01	-0.56	1.96
Q96HY7	DHTKD1	Probable 2-oxoglutarate dehydrogenase E1 component DHKTD1, mitochondrial	0.96	1.41	0.07	0.17	0.68	0.05	-0.55	1.33
H0YIV9	-	Uncharacterized protein (Fragment)	1.10	1.62	0.06	0.15	0.68	0.03	-0.55	1.50
A8K6A5	-	cDNA FLJ77742, highly similar to Homo sapiens integrin, alpha 5 (fibronectin receptor, alpha polypeptide), mRNA	1.17	1.71	0.05	0.13	0.68	0.02	-0.55	1.67
Q6UWS5	PET117	Protein PET117 homolog, mitochondrial	1.13	1.65	0.17	0.26	0.68	0.03	-0.55	1.48
O15050	TRANK1	TPR and ankyrin repeat-containing protein 1	1.14	1.66	0.31	0.37	0.68	0.04	-0.55	1.41
B2R8K8	-	cDNA, FLJ93949, highly similar to Homo sapiens NIMA (never in mitosis gene a)-related kinase 7 (NEK7), mRNA	1.00	1.45	0.10	0.18	0.69	0.04	-0.54	1.38
Q6IAA8	LAMTOR1	Ragulator complex protein LAMTOR1	1.08	1.58	0.06	0.16	0.69	0.02	-0.54	1.69
A0A087WTU3	TEX264	Testis-expressed sequence 264 protein	1.38	2.01	0.07	0.21	0.69	0.04	-0.54	1.38
B3KTX0	-	cDNA FLJ38893 fis, clone NOVAR1000091, highly similar to COLORECTAL MUTANT CANCER PROTEIN	1.12	1.63	0.16	0.13	0.69	0.00	-0.54	2.32
Q8WW22	DNAJA4	DnaJ homolog subfamily A member 4	1.00	1.45	0.09	0.15	0.69	0.00	-0.54	2.30
B4DDC9	-	cDNA FLJ59448, highly similar to Trifunctional enzyme subunit beta, mitochondrial	1.28	1.85	0.13	0.13	0.69	0.01	-0.53	1.91
Q9BR63	FARSB	FARSB protein (Fragment)	0.96	1.39	0.09	0.12	0.69	0.02	-0.53	1.74
B2RBJ8	QRSL1	Glutamyl-tRNA(Gln) amidotransferase subunit A, mitochondrial	1.12	1.61	0.09	0.16	0.69	0.02	-0.53	1.69
A5YKK6	CNOT1	CCR4-NOT transcription complex subunit 1	0.82	1.19	0.05	0.14	0.69	0.04	-0.53	1.37
P30837	ALDH1B1	Aldehyde dehydrogenase X, mitochondrial	1.02	1.47	0.09	0.13	0.69	0.03	-0.53	1.59
Q9BT30	ALKBH7	Alpha-ketoglutarate-dependent dioxygenase alkB homolog 7, mitochondrial	1.10	1.59	0.10	0.22	0.70	0.04	-0.52	1.37
P21964	COMT	Catechol O-methyltransferase	0.97	1.39	0.07	0.16	0.70	0.04	-0.52	1.45
Q5QP19	NFS1	NFS1 nitrogen fixation 1 (<i>S. cerevisiae</i>), isoform CRA_b	0.94	1.35	0.05	0.14	0.70	0.02	-0.52	1.67
A8K1E1	-	cDNA FLJ75589, highly similar to Homo sapiens mutS homolog 3 (<i>E. coli</i>) (MSH3), mRNA	0.79	1.12	0.11	0.13	0.70	0.03	-0.52	1.51
Q9UHA4	LAMTOR3	Ragulator complex protein LAMTOR3	0.85	1.21	0.12	0.10	0.70	0.00	-0.52	2.39

O75131	CPNE3	Copine-3	0.97	1.38	0.10	0.08	0.70	0.00	-0.51	2.93
Q6QN92	-	Mitochondrial glycine cleavage system H-protein (Fragment)	1.01	1.44	0.08	0.15	0.70	0.01	-0.51	1.91
E7EV43	RWDD4	RWD domain-containing protein 4	1.18	1.67	0.07	0.20	0.70	0.02	-0.51	1.61
B1ALH6	PHYH	Phytanoyl-CoA dioxygenase, peroxisomal	0.90	1.27	0.12	0.05	0.71	0.03	-0.50	1.50
P50461	CSRP3	Cysteine and glycine-rich protein 3	0.83	1.17	0.07	0.06	0.71	0.01	-0.50	1.92
Q9Y285	FARSA	Phenylalanine--tRNA ligase alpha subunit	1.02	1.44	0.05	0.15	0.71	0.03	-0.50	1.56
Q9UL25	RAB21	Ras-related protein Rab-21	1.02	1.43	0.04	0.17	0.71	0.05	-0.50	1.34
P51648	ALDH3A2	Fatty aldehyde dehydrogenase	0.88	1.23	0.08	0.08	0.71	0.04	-0.49	1.36
P49840	GSK3A	Glycogen synthase kinase-3 alpha	0.97	1.36	0.10	0.10	0.71	0.04	-0.49	1.44
P35968	KDR	Vascular endothelial growth factor receptor 2	0.90	1.27	0.11	0.04	0.71	0.05	-0.49	1.33
X6R886	PLPP7	Inactive phospholipid phosphatase 7	0.70	0.98	0.05	0.05	0.71	0.01	-0.49	1.96
P83111	LACTB	Serine beta-lactamase-like protein LACTB, mitochondrial	0.94	1.33	0.11	0.11	0.71	0.05	-0.49	1.33
Q8NAN7	-	cDNA FLJ35062 fis, clone OCBBF2019195, highly similar to VERY LOW-DENSITY LIPOPROTEIN RECEPTOR	0.95	1.34	0.07	0.18	0.71	0.05	-0.49	1.32
Q9NP74	PALMD	Palmdelphin	0.99	1.39	0.07	0.10	0.71	0.03	-0.49	1.51
A0A0A0MR33	GSTZ1	Maleylacetoacetate isomerase	1.02	1.42	0.10	0.19	0.72	0.04	-0.48	1.40
B5BUI8	DUSP3	Dual specificity phosphatase 3 (Fragment)	0.98	1.37	0.08	0.08	0.72	0.01	-0.48	2.18
P53370	NUDT6	Nucleoside diphosphate-linked moiety X motif 6	0.96	1.34	0.13	0.13	0.72	0.01	-0.48	1.94
A0A0S2Z5P5	MCMBP	Chromosome 10 open reading frame 119, isoform CRA_c (Fragment)	0.94	1.30	0.10	0.16	0.72	0.02	-0.48	1.71
L0R6Q1	SLC35A4	Alternative protein SLC35A4	1.03	1.43	0.05	0.11	0.72	0.04	-0.48	1.45
Q9UDY4	DNAJB4	DnaJ homolog subfamily B member 4	1.00	1.39	0.11	0.14	0.72	0.02	-0.48	1.65
Q9HA77	CARS2	Probable cysteine--tRNA ligase, mitochondrial	1.04	1.45	0.11	0.18	0.72	0.00	-0.48	2.39
Q9P0P8	C6orf203	Uncharacterized protein C6orf203	1.01	1.41	0.10	0.18	0.72	0.03	-0.48	1.46
A0A024RD99	GRSF1	G-rich RNA sequence binding factor 1, isoform CRA_a	1.19	1.65	0.08	0.11	0.72	0.05	-0.47	1.30

Q99584	S100A13	Protein S100-A13	1.06	1.46	0.07	0.06	0.72	0.03	-0.47	1.54
A0A087X020	SBDS	Ribosome maturation protein SBDS	0.93	1.28	0.09	0.12	0.72	0.03	-0.47	1.53
P11177	PDHB	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	1.02	1.41	0.04	0.07	0.72	0.00	-0.47	2.45
Q9BVJ8	HEXA	HEXA protein (Fragment)	0.84	1.16	0.11	0.19	0.72	0.03	-0.47	1.53
P82932	MRPS6	28S ribosomal protein S6, mitochondrial	1.17	1.62	0.06	0.20	0.72	0.05	-0.46	1.33
A0A024QZY0	BPHL	Biphenyl hydrolase-like (Serine hydrolase breast epithelial mucin-associated antigen), isoform CRA_d	1.06	1.46	0.08	0.11	0.72	0.02	-0.46	1.81
A0A0D9SGF6	SPTAN1	Spectrin alpha chain, non-erythrocytic 1	1.04	1.44	0.05	0.09	0.73	0.05	-0.46	1.33
B2REA4	PRDM1	PR domain zinc finger protein 1 (Fragment)	1.00	1.37	0.13	0.16	0.73	0.03	-0.46	1.55
B7ZAF6	SUCLA2	Succinyl-CoA ligase subunit beta	1.01	1.39	0.06	0.09	0.73	0.03	-0.46	1.48
A5YM53	ITGAV	ITGAV protein	0.94	1.29	0.06	0.10	0.73	0.01	-0.46	1.86
Q9HIK6	MESDC1	Mesoderm development candidate 1	0.72	0.98	0.03	0.07	0.73	0.02	-0.46	1.82
P27144	AK4	Adenylate kinase 4, mitochondrial	1.06	1.45	0.12	0.16	0.73	0.00	-0.46	2.44
B2R7G6	-	cDNA, FLJ93437, highly similar to Homo sapiens histidyl-tRNA synthetase-like (HARSL), mRNA	1.01	1.39	0.05	0.14	0.73	0.04	-0.46	1.36
Q05BS8	SFRS2IP	SFRS2IP protein (Fragment)	1.04	1.43	0.06	0.06	0.73	0.01	-0.45	2.06
B4E3T6	-	cDNA FLJ56405, highly similar to Epidermal growth factor receptor kinase substrate 8	1.20	1.64	0.14	0.14	0.73	0.02	-0.45	1.70
Q96HS1	PGAM5	Serine/threonine-protein phosphatase PGAM5, mitochondrial	0.87	1.19	0.06	0.14	0.73	0.02	-0.45	1.76
Q9NUJ1	ABHD10	Mycophenolic acid acyl-glucuronide esterase, mitochondrial	0.96	1.31	0.12	0.09	0.73	0.00	-0.45	2.36
B4DJX1	-	Acetyltransferase component of pyruvate dehydrogenase complex	0.94	1.28	0.07	0.09	0.74	0.00	-0.44	3.00
Q05639	EEF1A2	Elongation factor 1-alpha 2	0.92	1.25	0.11	0.12	0.74	0.01	-0.44	2.26
Q5JTJ3	COA6	Cytochrome c oxidase assembly factor 6 homolog	1.17	1.59	0.07	0.15	0.74	0.02	-0.44	1.68
B4DR53	-	Anion exchange protein	1.07	1.44	0.23	0.21	0.74	0.05	-0.44	1.34
Q96DB5	RMDN1	Regulator of microtubule dynamics protein 1	1.01	1.37	0.07	0.09	0.74	0.01	-0.43	1.91

Q969S3	ZNF622	Zinc finger protein 622	1.04	1.40	0.14	0.14	0.74	0.00	-0.43	2.82
Q08380	LGALS3BP	Galectin-3-binding protein	0.92	1.24	0.10	0.13	0.74	0.00	-0.43	2.41
A8MXV4	NUDT19	Nucleoside diphosphate-linked moiety X motif 19	0.97	1.31	0.13	0.18	0.74	0.01	-0.43	1.97
B7Z499	-	cDNA FLJ50571, highly similar to Myotubularin (EC 3.1.3.48)	0.93	1.25	0.11	0.08	0.74	0.01	-0.43	1.88
Q8N0Z2	ABRA	Actin-binding Rho-activating protein	1.00	1.34	0.06	0.09	0.75	0.03	-0.42	1.56
Q9BXW7	CECR5	Cat eye syndrome critical region protein 5	0.98	1.31	0.12	0.14	0.75	0.03	-0.42	1.47
P13804	ETFA	Electron transfer flavoprotein subunit alpha, mitochondrial	1.06	1.42	0.07	0.12	0.75	0.02	-0.42	1.80
Q99447	PCYT2	Ethanolamine-phosphate cytidyltransferase	1.05	1.41	0.07	0.09	0.75	0.02	-0.42	1.63
B3KSN3	-	cDNA FLJ36686 fis, clone UTERU2008027, highly similar to ATP-binding cassette sub-family B member 8, mitochondrial	1.00	1.34	0.07	0.12	0.75	0.04	-0.42	1.41
B1AK13	HMGCL	3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase (Hydroxymethylglutaricaciduria), isoform CRA_b	1.01	1.35	0.09	0.04	0.75	0.00	-0.41	2.49
Q8IWX7	UNC45B	Protein unc-45 homolog B	1.01	1.34	0.09	0.13	0.75	0.03	-0.41	1.60
P82909	MRPS36	28S ribosomal protein S36, mitochondrial	1.14	1.52	0.04	0.14	0.75	0.04	-0.41	1.41
B2R673	-	cDNA, FLJ92818, highly similar to Homo sapiens pyruvate dehydrogenase complex, component X (PDHX), mRNA	1.08	1.43	0.11	0.09	0.75	0.00	-0.41	3.08
Q9BSH4	TACO1	Translational activator of cytochrome c oxidase 1	1.11	1.48	0.09	0.14	0.75	0.02	-0.41	1.61
B2RA56	-	Nicalin	0.94	1.25	0.07	0.13	0.75	0.01	-0.41	2.04
A3KMH1	VWA8	von Willebrand factor A domain-containing protein 8	1.12	1.49	0.14	0.14	0.75	0.04	-0.41	1.42
O43819	SCO2	Protein SCO2 homolog, mitochondrial	1.05	1.40	0.09	0.07	0.75	0.01	-0.41	2.20
Q9UQ90	SPG7	Paraplegin	1.01	1.35	0.11	0.13	0.75	0.05	-0.41	1.30
Q9HCC0	MCCC2	Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial	1.07	1.42	0.08	0.06	0.75	0.02	-0.41	1.80
Q7Z434	MAVS	Mitochondrial antiviral-signaling protein	1.17	1.55	0.05	0.16	0.75	0.04	-0.41	1.37
P30405	PPIF	Peptidyl-prolyl cis-trans isomerase F, mitochondrial	1.11	1.47	0.07	0.07	0.75	0.00	-0.41	5.64

Q5T440	IBA57	Putative transferase CAF17, mitochondrial	1.20	1.58	0.07	0.10	0.75	0.02	-0.41	1.74
P30084	ECHS1	Enoyl-CoA hydratase, mitochondrial	1.02	1.35	0.07	0.09	0.75	0.00	-0.41	3.18
B7Z6G7	-	cDNA FLJ53098, highly similar to Tryptophanyl-tRNA synthetase, mitochondrial (EC 6.1.1.2)	1.01	1.33	0.08	0.15	0.75	0.01	-0.41	2.09
P35221	CTNNA1	Catenin alpha-1	1.00	1.32	0.08	0.07	0.76	0.00	-0.40	2.48
A8JZZ8	-	cDNA FLJ77826, highly similar to Homo sapiens BCS1-like (yeast), mRNA	1.07	1.42	0.09	0.18	0.76	0.04	-0.40	1.37
B2RAQ8	-	cDNA, FLJ95058, highly similar to Homo sapiens carnitine palmitoyltransferase 1A (liver) (CPT1A),nuclear gene encoding mitochondrial protein, mRNA	1.05	1.38	0.09	0.15	0.76	0.02	-0.40	1.68
P21399	ACO1	Cytoplasmic aconitate hydratase	1.01	1.34	0.06	0.12	0.76	0.02	-0.40	1.70
Q9H078	CLPB	Caseinolytic peptidase B protein homolog	1.12	1.47	0.16	0.23	0.76	0.01	-0.40	1.91
P14621	ACYP2	Acylphosphatase-2	1.16	1.52	0.13	0.07	0.76	0.04	-0.40	1.37
Q96C19	EFHD2	EF-hand domain-containing protein D2	0.91	1.19	0.09	0.07	0.76	0.02	-0.40	1.74
Q9Y305	ACOT9	Acyl-coenzyme A thioesterase 9, mitochondrial	1.06	1.39	0.07	0.12	0.76	0.00	-0.39	2.31
H3BNK2	LYRM1	LYR motif-containing protein 1	1.01	1.32	0.06	0.03	0.76	0.01	-0.39	2.07
Q99797	MIPEP	Mitochondrial intermediate peptidase	1.05	1.37	0.02	0.09	0.76	0.01	-0.39	1.94
C9JIG7	TSGA13	Testis-specific gene 13 protein (Fragment)	0.91	1.19	0.07	0.07	0.76	0.03	-0.39	1.60
P0DMM9	SULT1A3	Sulfotransferase 1A3	1.04	1.36	0.13	0.18	0.76	0.03	-0.39	1.57
A0A0A0MT39	SCN5A	Sodium channel protein	1.04	1.36	0.06	0.12	0.76	0.03	-0.39	1.50
H7C4K3	ITGB1	Integrin beta-1 (Fragment)	1.02	1.33	0.08	0.16	0.76	0.05	-0.39	1.33
A6NDG6	PGP	Glycerol-3-phosphate phosphatase	0.89	1.16	0.04	0.08	0.76	0.00	-0.39	2.60
Q7Z4Y4	AK3	GTP:AMP phosphotransferase AK3, mitochondrial	1.20	1.57	0.09	0.17	0.77	0.04	-0.39	1.44
A0A0K0K1H7	HEL-S-284	Aconitate hydratase, mitochondrial	1.10	1.44	0.08	0.13	0.77	0.04	-0.39	1.38
A0A024QZR0	LRRC20	Leucine rich repeat containing 20, isoform CRA_a	0.97	1.26	0.07	0.09	0.77	0.01	-0.38	1.83
O95363	FARS2	Phenylalanine--tRNA ligase, mitochondrial	1.20	1.56	0.13	0.15	0.77	0.00	-0.38	2.70

Supplementary Table B: Significantly changed phosphoproteins between the right atria (RA) and right ventricle (RV) of infants with ventricular septal defect (VSD). Sequence: the amino acid sequence detected during MS/MS analysis. Protein Phosphosite: the letters S, T and Y represent phosphorylation at serine, threonine and tyrosine respectively, and the number indicates the position of the modification in the protein.

Accession #	Gene ID	Protein Names	Sequence	Protein Phosphosite	Mean		SEM		Fold Change RA/RV	p-value	log2[fold change]	-log10 [p-value]
					RA	RV	RA	RV				
A0JLR8	EIF5B	EIF5B protein (Fragment)	kWDGsEEDEDNSk	S164	1.26	2.50	0.18	0.42	0.50	0.05	-0.99	1.34
Q6ZS32	-	cDNA FLJ45870 fis, clone OCBBF3005330, highly similar to FYVE finger-containing phosphoinositide kinase (EC 2.7.1.68) (Fragment)	fDDSDtEQIAEEGDDNLak	T109	0.86	1.70	0.35	0.60	0.51	0.05	-0.98	1.33
B4DEN3	-	cDNA FLJ61101, highly similar to Eukaryotic translation initiation factor 5	eAEEEssGGEEDEDENIE VVYSk	S151, S152	0.87	1.50	0.06	0.21	0.58	0.04	-0.78	1.37
H0Y8T1	SGCA	Alpha-sarcoglycan (Fragment)	vDsAQVPLILDQH	S150	0.85	1.41	0.12	0.20	0.61	0.02	-0.72	1.67
Q59EZ3	-	Insulin-like growth factor 2 receptor variant (Fragment)	aLSSLHGDDQDsEDEVLTIPeVvk	S2332	1.01	1.65	0.13	0.12	0.61	0.03	-0.70	1.56
Q96AT1	KIAA1143	Uncharacterized protein KIAA1143	iQPQPPDEDGDHsDkeDEQPQVVVLk	S50	0.97	1.58	0.14	0.07	0.61	0.02	-0.70	1.63
B7Z255	-	Glycogen [starch] synthase (EC 2.4.1.11)	rAscTSSTSGSk	S331	0.61	0.98	0.11	0.14	0.62	0.00	-0.70	2.53
Q2M3C7	SPHKAP	A-kinase anchor protein SPHKAP	gGDTAVSACQIHSDsLDTR	S83	0.59	0.94	0.16	0.21	0.62	0.01	-0.68	1.93
B4E3Q9	-	cDNA FLJ59659, highly similar to Vinculin	gQGSsPVAmQk	S253	0.91	1.46	0.12	0.15	0.62	0.03	-0.68	1.47

P12270	TPR	Nucleoprotein TPR	tDGFAEAIHsPQVAGVPR	S2155	1.36	2.16	0.32	0.41	0.63	0.01	-0.67	1.85
B4DTX5	-	cDNA FLJ60072, highly similar to Homo sapiens sorbin and SH3 domain containing 1 (SORBS1), transcript variant 6, mRNA	sATAsPQQPQAQQR	S668	1.02	1.61	0.11	0.13	0.64	0.00	-0.65	2.70
O76041	NEBL	Nebulette	sHsSSTFGTGLGDDR	S885	0.45	0.70	0.09	0.10	0.64	0.01	-0.65	2.11
E7EW31	PROB1	Proline-rich basic protein 1	eAQQQFTEPAFISPLPPGP AsPAAVPR	S150	0.91	1.42	0.06	0.16	0.64	0.04	-0.65	1.41
B4DQQ2	-	cDNA FLJ54127, highly similar to Heterogeneous nuclear ribonucleoproteins C	mESEGGADDSAEEGDLLD DDDNE DRGDDQV k	S155	0.99	1.53	0.11	0.11	0.65	0.03	-0.63	1.59
A0A0U1RQ K4	ADPRH L1	[Protein ADP- ribosylarginine] hydrolase-like protein 1	qQsHQAEETPQPGDAGk	S1382	0.89	1.37	0.07	0.10	0.65	0.03	-0.61	1.59
A0A0U1RR M0	ERC1	ELKS/Rab6- interacting/CAST family member 1 (Fragment)	vEPSSQsPGRsPR	S17, S21	1.10	1.65	0.07	0.16	0.67	0.02	-0.58	1.74
Q5T481	RBM20	RNA-binding protein 20	eAEFsDPENTR	S876	0.91	1.35	0.09	0.15	0.67	0.04	-0.57	1.42
Q15772	SPEG	Striated muscle preferentially expressed protein kinase	gsPVLAMR	S2448	0.99	1.42	0.07	0.15	0.70	0.04	-0.51	1.36
M0QZ43	HRC	Sarcoplasmic reticulum histidine- rich calcium-binding protein	sHEEDDNDDDDVsTEYGH QAHR	S311	1.10	1.56	0.06	0.17	0.71	0.02	-0.50	1.70
A0A0C4DG G1	PACSIN 3	Protein kinase C and casein kinase substrate in neurons	gGRsPDEVTLTSIVPTR	S319	0.71	0.99	0.07	0.11	0.72	0.03	-0.48	1.58

protein 3 (Fragment)												
Q5VST9	OBSCN	Obscurin (EC 2.7.11.1) (Obscurin-RhoGEF) (Obscurin-myosin light chain kinase) (Obscurin-MLCK)	IQVPGGDsDEDSk	S5563	0.60	0.83	0.06	0.10	0.72	0.03	-0.47	1.60
B4DEF0	CASQ2	Calsequestrin	iNTEDDDEDNDDDDNsDE EDNDDSDDDDE	S339	1.19	1.64	0.20	0.26	0.73	0.01	-0.46	1.85
Q15111	PLCL1	Inactive phospholipase C-like protein 1	IPSDPDVLEGEVtDEDEEA EMSR	T556	0.95	1.30	0.17	0.19	0.73	0.02	-0.46	1.62
Q03135	CAV1	Caveolin-1	qVyDAHTk	Y42	1.37	1.81	0.16	0.07	0.76	0.01	-0.40	1.85
B4E0X8	-	cDNA FLJ61021, highly similar to Far upstream element-binding protein 1	qQAAYYAQTsPQGmPQHP PAPQGQ	S630	1.03	1.35	0.14	0.11	0.77	0.03	-0.38	1.51

Supplementary Table C: Significant canonical pathways (IPA Canonical Pathway analysis). The $-\log(p\text{-value})$ is calculated by the Fisher's exact test right-tailed, and the ratio was calculated by the number of expressed proteins divided by the total number of proteins that make up the pathway.

Ingenuity Canonical Pathway	$-\log(p\text{-value})$	Ratio	Molecules
tRNA Charging	6.44	0.158	WARS2, FARS2, CARS2, HARS2, FARSA, FARSB
TCA Cycle II (Eukaryotic)	4.62	0.174	SUCLA2, DHTKD1, ACO2, ACO1
Dopamine Degradation	4.14	0.133	ALDH1B1, COMT, ALDH3A2, SULT1A3/SULT1A4
Sertoli Cell-Sertoli Cell Junction Signaling	3.48	0.041	ITGB1, SORBS1, CTNNA1, ITGA5, GSK3A, SPTAN1, CTNNB1
Acetyl-CoA Biosynthesis I (Pyruvate Dehydrogenase Complex)	3.08	0.333	DLAT, PDHB
Fatty Acid β -oxidation I	2.84	0.100	ECHS1, ACAA1, HADHB
Leucine Degradation I	2.71	0.222	HMGCL, MCCC2
Caveolar-mediated Endocytosis Signaling	2.70	0.056	ITGB1, FLNC, ITGAV, ITGA5
Noradrenaline and Adrenaline Degradation	2.64	0.086	ALDH1B1, COMT, ALDH3A2
Ketogenesis	2.62	0.200	HADHB, HMGCL
Isoleucine Degradation I	2.32	0.143	ECHS1, HADHB
Histamine Degradation	2.26	0.133	ALDH1B1, ALDH3A2
Oxidative Ethanol Degradation III	2.15	0.118	ALDH1B1, ALDH3A2
Virus Entry via Endocytic Pathways	2.14	0.039	ITGB1, FLNC, ITGA5, CXADR
Alanine Biosynthesis III	2.12	1.000	NFS1
Valine Degradation I	2.10	0.111	ECHS1, HADHB
Fatty Acid α -oxidation	2.10	0.111	ALDH1B1, ALDH3A2
Putrescine Degradation III	2.06	0.105	ALDH1B1, ALDH3A2
Tryptophan Degradation X (Mammalian, via Tryptamine)	2.01	0.100	ALDH1B1, ALDH3A2
Ethanol Degradation IV	1.97	0.095	ALDH1B1, ALDH3A2
Serotonin Degradation	1.91	0.047	ALDH1B1, ALDH3A2, SULT1A3/SULT1A4
PTEN Signaling	1.91	0.034	ITGB1, ITGA5, GSK3A, KDR
PI3K/AKT Signaling	1.86	0.033	ITGB1, ITGA5, GSK3A, CTNNB1
L-DOPA Degradation	1.83	0.500	COMT
L-glutamine Biosynthesis II (tRNA-dependent)	1.83	0.500	QRSL1
Ethanol Degradation II	1.62	0.063	ALDH1B1, ALDH3A2
3-phosphoinositide Degradation	1.56	0.026	PLPP7, MTM1, PGAM5, PPTC7

NF- κ B Activation by Viruses	1.56	0.035	ITGB1, ITGAV, ITGA5
2-ketoglutarate Dehydrogenase Complex	1.53	0.250	DHTKD1
Phenylethylamine Degradation I	1.53	0.250	ALDH3A2
Molybdenum Cofactor Biosynthesis	1.53	0.250	NFS1
Reelin Signaling in Neurons	1.49	0.033	ITGB1, ITGA5, VLDLR
Mitochondrial Dysfunction	1.45	0.024	NDUFS1, CPT1A, ACO2, ACO1
Rapoport-Luebering Glycolytic Shunt	1.43	0.200	TIGAR
Tyrosine Degradation I	1.43	0.200	GSTZ1
Germ Cell-Sertoli Cell Junction Signaling	1.41	0.024	ITGB1, SORBS1, CTNNA1, CTNNB1
Glycine Cleavage Complex	1.35	0.167	GCSH
Paxillin Signaling	1.30	0.027	ITGB1, ITGAV, ITGA5

Supplementary Table D: Calcium signalling proteins used in analysis.

Protein Symbol	Protein Name
ADCY6	Adenylate cyclase type 6
AKAP9	A-kinase anchor protein 9
ATP2A2	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2
ATP2B1	Calcium-transporting ATPase
ATP2B4	Calcium-transporting ATPase
CAMK2B	Calcium/calmodulin-dependent protein kinase type II subunit beta
CAMK2D	Calcium/calmodulin-dependent protein kinase type II subunit delta
CASQ2	Calsequestrin-2
HRC	Sarcoplasmic reticulum histidine-rich calcium-binding protein
JPH2	Junctophilin-2
PKIA	cAMP-dependent protein kinase inhibitor alpha
PLN	Cardiac phospholamban
PPP1CA	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit
PPP1R12B	Protein phosphatase 1 regulatory subunit
PPP1R12C	Protein phosphatase 1, regulatory (Inhibitor) subunit 12C
PPP1R14A	Protein phosphatase 1 regulatory subunit 14A
PPP1R14C	Protein phosphatase 1 regulatory subunit 14C
PPP1R2	Protein phosphatase inhibitor 2

PPP1R21	Protein phosphatase 1 regulatory subunit 21
PPP1R3A	Protein phosphatase 1 regulatory subunit 3A
PPP1R3G	Protein phosphatase 1 regulatory subunit 3G
PRKACA	cAMP-dependent protein kinase catalytic subunit alpha
PRKACB	cAMP-dependent protein kinase catalytic subunit beta
PRKAR1A	cAMP-dependent protein kinase type I-alpha regulatory subunit
PRKAR1B	cAMP-dependent protein kinase type I-beta regulatory subunit
RYR2	Ryanodine receptor 2
SLC8A1	Sodium/calcium exchanger 1
SRL	Sarcalumenin
TNNC1	Troponin C, slow skeletal and cardiac muscles
TNNI1	Troponin I, slow skeletal muscle
TNNI3	Mutant cardiac troponin I
TNNT2	Troponin T, cardiac muscle