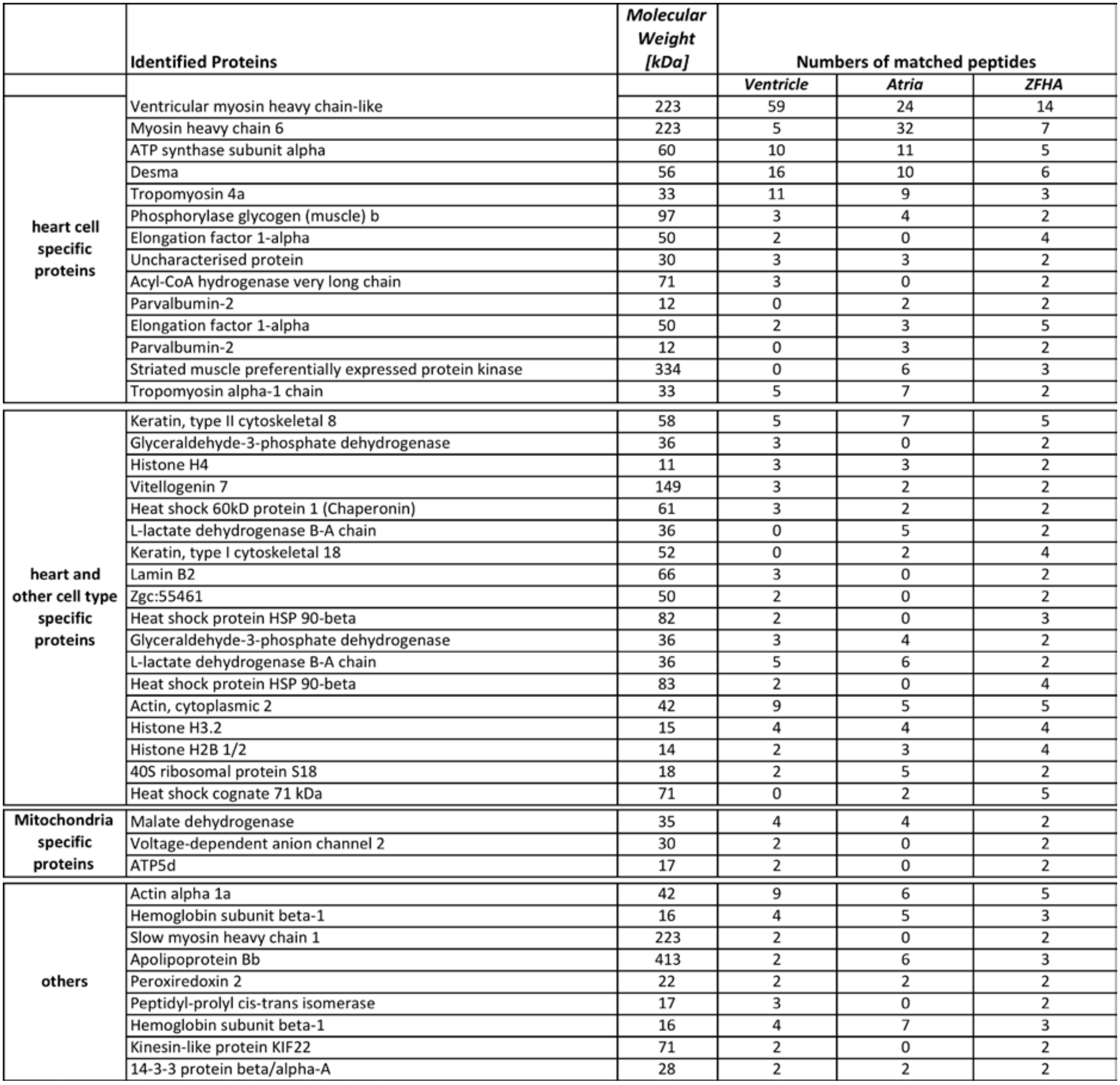
Table S1. Proteins Identified using LC-MS in adult zebrafish ventricle and atria, and in ZFHA.



	Identified Proteins	***Molecular Weight [kDa]***	**Numbers of matched peptides**		
			Ventricle	***Atria***	***ZFHA***
heart cell specific proteins	Ventricular myosin heavy chain-like	223	59	24	14
	Myosin heavy chain 6	223	5	32	7
	ATP synthase subunit alpha	60	10	11	5
	Desma	56	16	10	6
	Tropomyosin 4a	33	11	9	3
	Phosphorylase glycogen (muscle) b	97	3	4	2
	Elongation factor 1-alpha	50	2	0	4
	Uncharacterised protein	30	3	3	2
	Acyl-CoA hydrogenase very long chain	71	3	0	2
	Parvalbumin-2	12	0	2	2
	Elongation factor 1-alpha	50	2	3	5
	Parvalbumin-2	12	0	3	2
	Striated muscle preferentially expressed protein kinase	334	0	6	3
	Tropomyosin alpha-1 chain	33	5	7	2
heart and other cell type specific proteins	Keratin, type II cytoskeletal 8	58	5	7	5
	Glyceraldehyde-3-phosphate dehydrogenase	36	3	0	2
	Histone H4	11	3	3	2
	Vitellogenin 7	149	3	2	2
	Heat shock 60kD protein 1 (Chaperonin)	61	3	2	2
	L-lactate dehydrogenase B-A chain	36	0	5	2
	Keratin, type I cytoskeletal 18	52	0	2	4
	Lamin B2	66	3	0	2
	Zgc:55461	50	2	0	2
	Heat shock protein HSP 90-beta	82	2	0	3
	Glyceraldehyde-3-phosphate dehydrogenase	36	3	4	2
	L-lactate dehydrogenase B-A chain	36	5	6	2
	Heat shock protein HSP 90-beta	83	2	0	4
	Actin, cytoplasmic 2	42	9	5	5
	Histone H3.2	15	4	4	4
	Histone H2B 1/2	14	2	3	4
	40S ribosomal protein S18	18	2	5	2
	Heat shock cognate 71 kDa	71	0	2	5
Mitochondria specific proteins	Malate dehydrogenase	35	4	4	2
	Voltage-dependent anion channel 2	30	2	0	2
	ATP5d	17	2	0	2
others	Actin alpha 1a	42	9	6	5
	Hemoglobin subunit beta-1	16	4	5	3
	Slow myosin heavy chain 1	223	2	0	2
	Apolipoprotein Bb	413	2	6	3
	Peroxiredoxin 2	22	2	2	2
	Peptidyl-prolyl cis-trans isomerase	17	3	0	2
	Hemoglobin subunit beta-1	16	4	7	3
	Kinesin-like protein KIF22	71	2	0	2
	14-3-3 protein beta/alpha-A	28	2	2	2

Data are from pooled samples of n= 6 adult ventricle, n=5 adult atria and n=20 ZFHAs after 3 days in culture. The number of matched peptides shows how many peptides were used to identify the protein in the sample. The greater the number of matches the more certain the identification. 1 match is a possible identification, 2 – 3 matches a probable identification, 4 and over almost certain identification. There were 44 peptides with 2 or more matches and these were identified against both Swissprot and DANRE databases (see methods for details).