

# PROTEOMICS

## Supporting Information for Proteomics

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**Differential expression profile of membrane proteins  
in zebrafish (*Danio rerio*) brain exposed to methyl parathion**

## Supporting Information

**Table S1.** Peptide information of membrane proteins identified by 1-DE-MS/MS

Band no.	Protein name	Identified peptides number	Peptide lists	
			Mass	Sequence
1	spectrin alpha 2	25	804.6203	LQQLFR
			847.6133	LHQFFR
			986.7389	IDGITIQR
			1015.7402	DLTGVQNL
			1085.8312	DLASVQALLR
			1139.7726	LNSYMLQR
			1185.8391	LAQFVEHWR
			1215.8549	ADLEKAWVQR
			1256.9241	GVIDTGNALIQR
			1259.886	WNQLLSNSAAR
			1262.8262	EANQQQQFNR
			1291.844	GACAGSEDAVKAR
			1444.0103	ENLLDEQGSIGLR
			1476.0101	LSDSLRLQQLFR
			1496.0254	MQHNLEQQIQAR
			1558.0468	EIPSAFDFVEFTR
			1558.0468	HEGFERDLAALGDK
			1617.0455	KHEAFETDFTVHR
			1634.061	QFQDAGHFDADNIR
			1634.061	HQLLEADISAHEDR
			1709.1595	AALEDSFHLQQFFR
			1811.2073	AKLDENSAFLQFNWK
			1897.3481	AGTFLAFEQFGQQLLAR
			1926.2667	SSLSSAEADFSQLAELDR
			2060.4114	DELITNWEQIQTLATER
2	spectrin, beta, non-erythrocytic	13	1130.6562	KQEMESHNK
			1130.6562	QEMESHNKK
			1139.6393	LMAHRDLQR
			1157.6974	MPLATSTDHGK
			1162.6176	ETWLSENQR
			1179.6656	SDLIDFDNLK
			1241.7637	TDSIQRHQK
			1242.7539	LEDLEVIQQR
			1263.6935	DEQSALVMVKK
			1502.7993	EVDDLEQWIAER
			1554.8604	AQWSHLEEASQLR

			1651.8964	LLEVELSGEQLPKPTK
			1747.9617	AVTEAWEGLQSATQTR
			1995.0955	AMTMPSPSSGEAGGV TMR
3	Pyruvate carboxylase	7	1338.9032	DRLHADSVNLAK
			1351.9352	EVFFELNGQLR
			1363.9325	IAEEFEVELER
			1501.9167	EYEELEENYQR
			1522.0472	GFQPD TGRIEVFR
			1621.1124	IEGRPGASLPSMDFK
			1705.1602	VVEIAPAFQLDPHLR
4	Hexokinase 1	4	1235.6676	QIAETLEEFR
			1250.7185	MAKEGLLFEGR
			1441.7664	LPLGFTFSFPCR
			1484.9296	SANLIAATLGAILTR
5	aconitase mitochondrial	2, 7	922.4873	EHAAL EPR
			1160.6478	GEIATLADENK
			1433.7771	AQFTVTPGSEQIR
			1556.8937	CTTDHISAAGPWLK
			1590.853	NLLTGEYSGVPDVAR
			1631.8536	FEPSSYINYDKLR
			1753.9176	IVYGHLLDDPAGQEIAR
6	ATPase, transporting, lysosomal subunit A-like	H+ V1 14	885.4413	LASFYER
			913.511	GVNIGALNR
			972.55	DPVKEGEAK
			1034.4911	GNEMSEVLR
			1147.5562	EHMGEILYR
			1262.6622	FTMVQVWPVR
			1269.6283	GVNIGALNRDLK
			1275.666	WDFTPINNLR
			1308.7257	VGHSELVGEIIR
			1316.6934	LPANHPLLTGQR
			1515.7999	TALVANTSNPVAAR
			1749.8619	EASIYTGITLSEYFR
			1781.8479	LAEMPADSGYPAYLGAR
			2058.1365	IKADYAQLLEDMQNSFR
7	synaptic vesicle membrane protein homolog	VAT-1 9	909.4312	DYVEEVR
			1120.6184	GYNLLKPMGK
			1166.5801	TRDYVEEVR
			1228.5481	APEEDTFTYR
			1398.6327	MCGLNFADLMAR
			1734.8116	IDSTYHLEQVGDAMR
			1807.9086	HEVISQGGVTHPIDYR
			2178.1091	TWYQQFSVHTLSLIQGNR
			2570.3469	GYNLLKPMGK LISYGAANMLAGQK

8	tubulin, beta 2	7	1053.6017	YLTVAAI FR
			1130.59	FPGQLNADLR
			1143.629	LAVNMVPFPR
			1229.5983	ISEQFTAMFR
			1266.729	ISEQFTAMFR
			1615.8121	AILVDLEPGTMDSVR
			1620.8325	LHFFMPGFAPLTSR
9	Mitochondrial ATP synthase beta subunit-1like	6	1385.7217	IMNVIGEPIDER
			1439.8069	VALTGLTVAEYFR
			1677.9698	LVLEVAQHLGENTVR
			1829.9518	IMDPNIVGTEHYDVAR
			1988.1317	AIAELGIYPAVDPLDSTSR
			2266.2444	IPSAVGYQPTLATDMGTMQER
10	Creatine kinase, brain b	5	862.4294	FGEILKR
			1198.6709	ELLDPVIEDR
			1230.5436	GFCLPPHCSR
			1572.7841	GFCLPPHCSRGER
			1978.8904	GTGGVDTA AVGGVFDISNADR
11	Bactin 1	3	1132.5482	GYSFTTTAER
			1198.7252	AVFPSIVGRPR
			1515.7793	IWHHTFYNELR
12	Ldhb protein	2	913.5568	IVVVTAGVR
			1685.8086	ELADELALVDVVEDR
13	guanine nucleotide binding protein (G protein), beta polypeptide 1, like	4	916.4677	EGNVRVSR
			1009.4814	AGVLAGHDNR
			1336.5731	IYAMHWGTDSR
			1523.6262	ELAGHTGYLSCCR
14	syntaxin binding protein 6-like	4	1045.542	RASQVLSER
			1132.552	SQWSVEQLR
			1314.6925	MKTSMTANQDR
			1354.6268	HFAEAAQRLALK
15	prohibitin		914.5545	NVPVITGSK
			1058.5553	QVAQQAER
			1149.5515	FDAGELITQR
			1366.7867	ILFRPVAGQLPR
			1444.6108	IFTSIGEDYDER
16	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondria	7	973.5195	QSAAIVQTR
			1018.5182	AASLVRVFR
			1486.7786	VVAEPVELAQEFR
			1551.7566	ILTDYGFEGHPFR
			1613.693	SLNVARQSAAIVQTR
			1707.7678	RILTDYGFEGHPFR

		2109.9753	EVWDMFGVFFTNHPDLR
17	ATP synthase, 5	973.5117	VLAKSTQAR
	H+ transporting,	983.5201	SMLFDAKR
	mitochondrial	1449.7128	NNVAMLLEINYR
	F0	1458.7198	SITPQQEKESIAK
	complex,	1527.7656	LDYQVELQNLHR
	subunit b,		
	isoform 1		
18	Myelin protein 2	1018.7079	LEFVGNPSR
	zero	1360.938	NPPDIGGHPSTIR

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**Table S2.** Peptide information of differentially expressed of membrane proteins identified by 2DE-MS/MS

Spot no.	Protein name	Identified peptides number	Peptide lists	
			Mass	Sequence
1	PREDICTED: 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide 2	11	903.4854	VISSIEQK
			932.4082	MKGDYYR
			948.4012	MKGDYYR
			1080.5258	YLAEVATGEK
			1189.6354	DSTLIMQLLR
			1205.6102	DSTLIMQLLR
			1236.6378	YLAEVATGEKR
			1245.5961	EHMQPThPIR
			1590.7323	SVTELNEALSNEER
			1812.7941	LAEQAERYDDMAAAMK
			1828.7808	LAEQAERYDDMAAAMK
2	ependymin	2	921.4847	ETLQFRK
			1955.861	VVSTGGHDLASGEFSYDSK
3	ependymin	3	921.4814	KETLQFR
			921.4814	ETLQFRK
			1955.8483	VVSTGGHDLASGEFSYDSK
4	ependymin	3	921.4852	ETLQFRK
			1955.8441	VVSTGGHDLASGEFSYDSK
			2299.0774	VVSTGGHDLASGEFSYDSKTNK
5	ubiquitin C-terminal hydrolase L1	3	865.4087	LYELDGR
			1395.6161	FLEATSGMSPAER
			2197.0022	IDGPVSHGPTKPDsfVMDAAR
6	guanine nucleotide binding protein (G protein), beta polypeptide 2	5	1009.502	AGVLAGHDNR
			1336.595	IYAMHWGTDSR
			1352.5836	IYAMHWGTDSR
			1353.6813	LIIWDSYTTNK
			1728.8564	SELEQLRQEAQLR
7	guanine nucleotide binding protein (G protein), beta polypeptide 1, like	3	1009.4805	AGVLAGHDNR
			1225.5917	LFVSGACDASAK
			1336.5704	IYAMHWGTDSR
8	SH3-domain GRB2-like 2	9	888.4938	EYVPKPR
			956.4836	RLDFDYK
			1044.5948	REYVPKPR
			1234.5299	AKMSMMSSMSK
			1315.7216	QAAEILQLSSK
			1320.5779	MSMMSSMSKIR
1390.6962	TTEYLQNPATR			

			1843.8385	ALYDFDPENEGELGFK
			2169.0129	GGDKGPGYTQTETTLGEAMQK
9	PREDICTED: keratin 8-like	8	1060.5634	KLLEGEESR
			1066.5164	AQYEEIASR
			1082.5994	FASFIDKVR
			1277.71	LALDIEIATYR
			1455.7988	IARIHSEMELIK
			1792.9916	DIHNTGLVKQEVVVK
			1851.927	MLETKWSVLQEQTSR
			2384.2529	EYQSLMNIKLALDIEIATYR
10	GDP dissociation inhibitor 2	13	938.4575	LYSESLAR
			1074.5905	MLLITQVTR
			1090.5767	MLLITQVTR
			1148.5803	FLMANGQLVR
			1179.563	IKLYSESLAR
			1193.658	KNDIFGDAADQ
			1312.6586	GRDWNVDLIPK
			1707.7155	MTGTEFDFAEMERK
			2141.0339	SPYLYPLYGLGELPQGFAR
			2236.0913	FLMANGQLVRMLLITQVTR
			2247.0137	NSYYGGESASITPLEDLFKR
			2279.1062	KFDLGQDVIDFTGHALALYR
			2533.1479	FVSISDLYSPTDVGSDSQIFISR
11	Keratin, cytoskeletal 18	I 26	951.4894	TTNVPTYR
			1002.5327	SEVNELRR
			1026.5215	ISSASYSGVR
			1041.6051	LVLQIDNAR
			1045.4698	GPDVHDYSR
			1059.543	VIDDTNLNR
			1065.5575	LEAEIATYR
			1092.4924	MAMQNLNDR
			1107.5906	RTTNVPTYR
			1116.6049	FQPIVDELRL
			1122.5538	IFDATTNNAR
			1158.6113	QGVEADITGLR
			1201.5709	RGPDVHDYSR
			1223.6631	VKYESELSIR
			1244.6998	FQPIVDELRLK
			1250.6488	KIFDATTNNAR
			1256.5688	NHDNEVMELR
			1265.6233	AASIYGGAGGQGTR
			1286.7063	QGVEADITGLRK
			1307.6876	VMTVTQTLVDGK
			1324.693	MKLEAEIATYR

			1418.6945	GQDLSQIMEEIR
			1434.6893	GQDLSQIMEEIR
			1602.881	SSTSQVPVSQVSIKR
			1999.0243	GNIQHQTQEYEALLNIK
			2823.4021	AWHESQITEVQVQVTQNTALQGAR
12	dihydrolipoamide S-succinyltransferase	14	852.5438	GLVVPVIR
			963.5375	EAVTFLRK
			999.502	LGFMSAFVK
			1042.5049	IKSVVEDPR
			1130.566	TINELGEKAR
			1309.6021	GVEGMNFADIEK
			1434.7369	HGIKLGFM SAFVK
			1478.6752	TPAFAESVTEGDVR
			1921.881	TPAFAESVTEGDVRWEK
			1979.9362	VEVRPMMYVALTYDHR
			1995.9282	VEVRPMMYVALTYDHR
			2038.0323	EIVYRDYVDISVAVATPK
			2148.0095	AAAYALTDQPAVNAVIDDTTK
			2211.0447	DYVDISVAVATPKGLVVPVIR
13	Sb:cb825 protein	9	1191.5625	LAPEYEEAATR
			1224.4395	LAPEYEEAATR
			1326.6757	HGIDGEGIILFR
			1356.6782	EVSDFISYLKR
			1454.7629	KHGIDGEGIILFR
			1515.715	FLQDYFDGNLKR
			1640.6888	IFRDGEDSGGYDGPR
			2384.1362	FSHDVSELGLDGSSGELPLVGIR
			2677.2126	YIGDRDASVVGFFADGGSAQGEFLK
14	Isocitrate dehydrogenase (NAD <sup>+</sup> ) alpha	15 3	918.489	LITEEASR
			938.4764	MSDGLFLR
			954.4713	MSDGLFLR
			1058.5266	TPIQWEER
			1066.5714	MSDGLFLRK
			1074.5902	LITEEASRR
			1178.6052	EVAENFKDVK
			1232.5946	IAEYAFEYAR
			1388.6957	RIAEYAFEYAR
			1392.7369	TPYTDVDLVTIR
			1523.7821	ANIMRMSDGLFLR
			1590.8785	TPIAAGHPSMNLLLR
			1606.8734	TPIAAGHPSMNLLLR
			1846.9587	DMANPTALLLSAVMMLR
			1862.9537	DMANPTALLLSAVMMLR
15	syntaxin binding	19	938.4764	KMPQYQK



	protein 1		957.5727	SQLIILDR
			960.5546	IMNDVIKK
			1036.5211	HYPYISTR
			1070.475	YDTSGIGDSR
			1145.6348	ALIVDQLSMR
			1161.6296	ALIVDQLSMR
			1210.6063	VSEQTYQLSR
			1215.6515	TQLKNPVMER
			1232.51	ADDPTMGEGPDK
			1268.6594	HIAEVSQEVTR
			1323.6759	TTMRDLSQMLK
			1475.6432	ADDPTMGEGPDKAR
			1493.7748	LDTKHYPYISTR
			1533.8132	HKHIAEVSQEVTR
			1799.9287	SVQTLINDFKDPHSK
			1822.9335	EVLHEDDDLWVALR
			2015.1536	AIVPILLDANVTTYDKIR
			2056.1326	REPLPSLEAIYLITPTDK
			2080.071	EKEVLHEDDDLWVALR
16	aldehyde dehydrogenase family, member A1	7 5	894.4768	TEGFIDGR
			1374.8024	VYGDIVAAPAKDR
			1435.8518	QVADAVDHGAVVVR
			1603.9412	FLVQTGIHDAFVEK
			1851.0511	LGHGSEPSTTQGPLINSR
			2234.2209	VSMELGGHAPFIVFDSAD VDK
			2250.1997	LGHGSEPSTTQGPLINSRAAEK
17	hypothetical LOC768289	protein 26	918.4899	ASIEQQSR
			1002.5977	TQITDLRR
			1062.5239	ATMQNLNDR
			1064.6398	LASYLDKVR
			1122.6135	LEQEIATYR
			1128.6044	QIREYYEK
			1166.6281	NHQEDLAALR
			1174.642	SLEAANATLER
			1198.7382	MSISIQTTSSK
			1215.6737	QSVEADIANLR
			1224.5967	EQEDWFKDK
			1294.726	KNHQEDLAALR
			1301.7466	IKFEHELVMR
			1310.6575	DYSHFWNTIK
			1317.7319	IKFEHELVMR
			1346.7031	AAENSLGDTEAR
			1371.7808	QSVEADIANLRR
			1379.7753	TRLEQEIATYR

				1382.6952	AHSVYGGSFGGSTR
				1855.0696	VLEEIRAHYENIIQK
				1879.0548	NATIHNANILLQIDNSK
				2005.1659	ASIEQQSRDYILLDDIK
				2199.1206	SSAAFPQKAHSVYGGSFGGSTR
				2227.175	ADLEMQIEGMQDELAFMKK
				2291.2532	TQVPGGTVTITTTTTGGTSSVQQR
				3331.8196	SLENQDIKTQVPGGTVTITTTTTGGTSSVQQR
18	Tu	translation	12	851.5378	EHLLAR
	elongation	factor,		1018.5923	GTVVSGTLER
	mitochondrial			1217.6427	AEAGDNMGALIR
				1449.835	AQVYILSKEEGGR
				1558.9668	LLEVIDGHIPLPSR
				1636.8508	SYEDIDNAPEEKAR
				1688.9214	SLDRAEAGDNMGALIR
				1746.9556	GITINASHVEYTTANR
				1746.9556	SIITGIEMFHKSLDR
				1838.9998	RGMVMIKPGSIQPHQK
				2119.1765	DLDKPFLMPVDGVYSIPGR
				2211.1956	QIGVQHVVVYINKADAVDDK
19	hypothetical	protein	8	1064.6237	LASYLDKVR
	LOC678611			1093.5499	REQEAWFK
				1160.6486	SRGGSTSFPHK
				1198.7235	NHQEEMAALR
				1287.7311	LKFEHEVVMR
				1320.6127	DYALLLDIKTR
				1438.731	THYENIIQKHR
				2286.1624	EVAHSTETIQT SRSQITELR
20	brain creatine kinase b		5	862.482	FGEILKR
				1179.5609	GGNMREVFNR
				1657.7762	TFLVWVNEEDHLR
				1845.8318	RLESGQSIDDLMPEQK
				1978.8768	GTGGVDTA AVGGVFDISNADR
21	mitochondrial	malate	3	1090.5813	LVADAMTELK
	dehydrogenase			1233.7202	IFGVTTLDIVR
				1503.7803	VEFPADQLSALTGR

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## Figure legends

**Figure S1.** Quantitative RT-PCR analysis of mRNA level in zebra?sh brain exposed to temperature stress. Quantitative RT-PCR was performed on cDNA using gene specific primers for *EPD*, *UCHLI*, *GNB2*, *GNB1L*, *GDI2*, *DLST*, *IDH3A*, *STXBP1*, *ALDH5A1*, *TUFM*, *MDH* and  *$\beta$ -actin*.  *$\beta$ -actin* was used as a control gene. Relative quantification of each gene expression level was normalized according to the  *$\beta$ -actin* gene expression. The PCR data of treatments was calibrated to the control values (control=1). (mean  $\pm$  SD, n=3), \* $P$ <0.05; \*\* $P$ <0.01.

**Figure S2.** Western blot analysis of STXBP1 expression level in zebra?sh brain exposed to temperature stress. Left panel: 50  $\mu$ g of protein was loaded onto a 12% SDS-PAGE and probed with antibody against STXBP1.  $\beta$ -actin was also measured as loading control and was used for data normalization; Right panel: the quantification of the signal has been analyzed by densitometric scanning. Band density was digitized, and mean  $\pm$  SD of the relative band intensity of STXBP1 (STXBP1/ $\beta$ -actin band intensity) from three independent experiments were shown.

**Figure S3.** Quantitative RT-PCR analysis of mRNA level in zebra?sh brain exposed to CdCl<sub>2</sub>. Quantitative RT-PCR was performed on cDNA using gene specific primers for *EPD*, *UCHLI*, *GNB2*, *GNB1L*, *GDI2*, *DLST*, *IDH3A*, *STXBP1*, *ALDH5A1*, *TUFM*, *MDH* and  *$\beta$ -actin*.  *$\beta$ -actin* was used as a control gene. Relative quantification of each gene expression level was normalized according to the  *$\beta$ -actin* gene expression. The PCR data of treatments was calibrated to the control values (control=1). (mean  $\pm$  SD, n=3), \* $P$ <0.05; \*\* $P$ <0.01.

**Figure S4.** Western blot analysis of STXBP1 expression level in zebra?sh brain exposed to CdCl<sub>2</sub>. Left panel: 50  $\mu$ g of protein was loaded onto a 12% SDS-PAGE and probed with antibody against STXBP1.  $\beta$ -actin was also measured as loading control and was used for data normalization; Right

panel: the quantification of the signal has been analyzed by densitometric scanning. Band density was digitized, and mean  $\pm$  SD of the relative band intensity of STXBP1 (STXBP1/ $\beta$ -actin band intensity) from three independent experiments were shown.

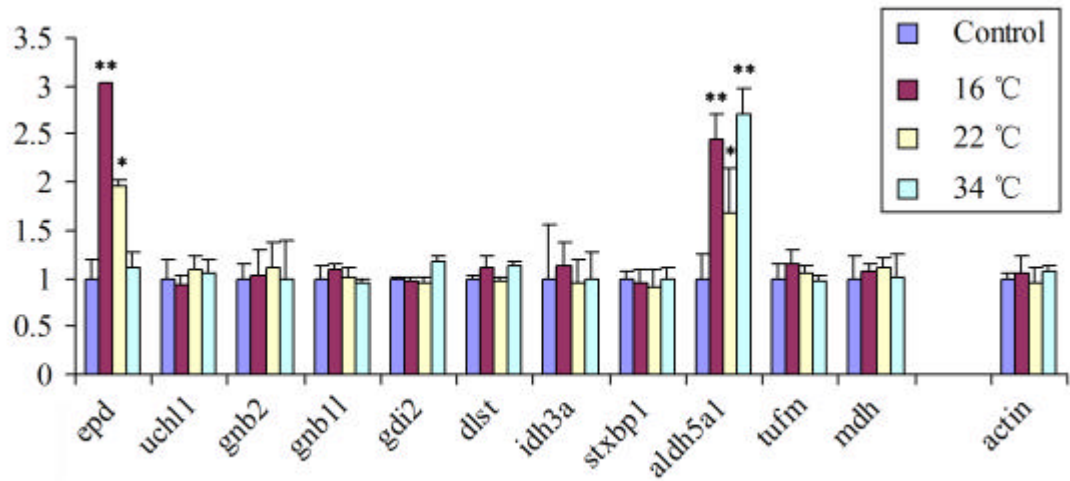


Figure S1

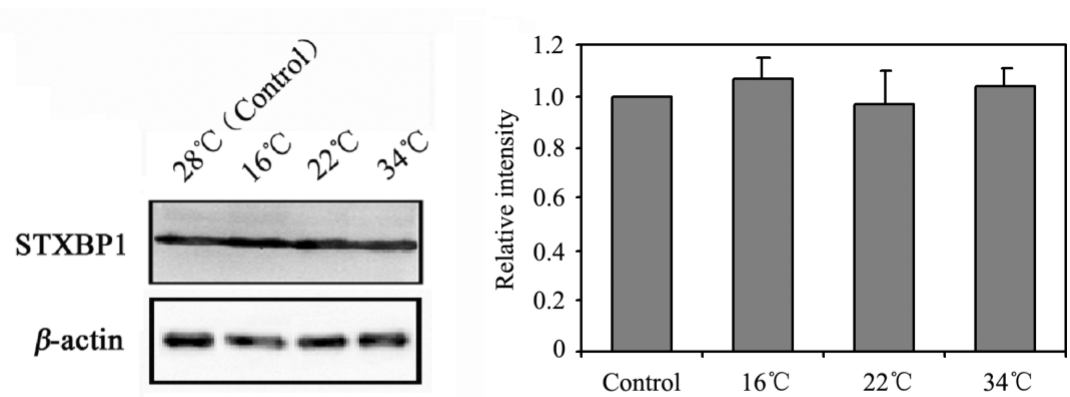


Figure S2

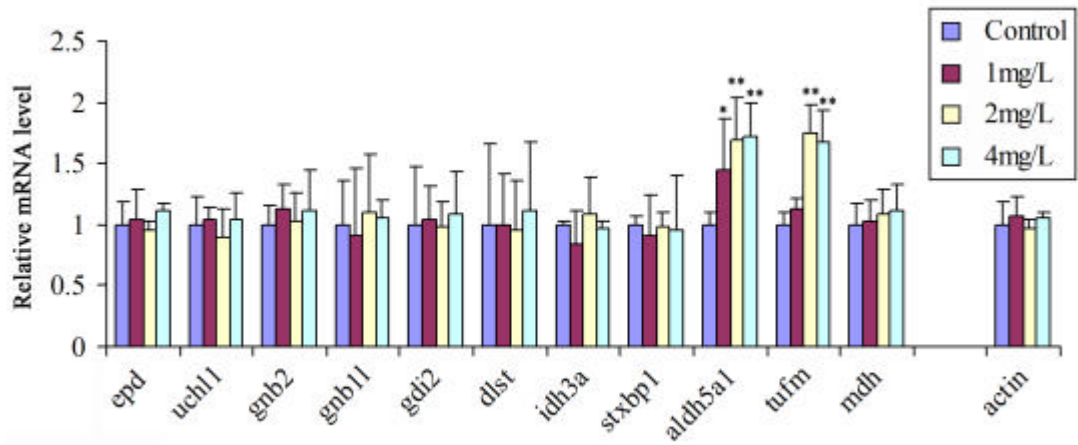


Figure S3

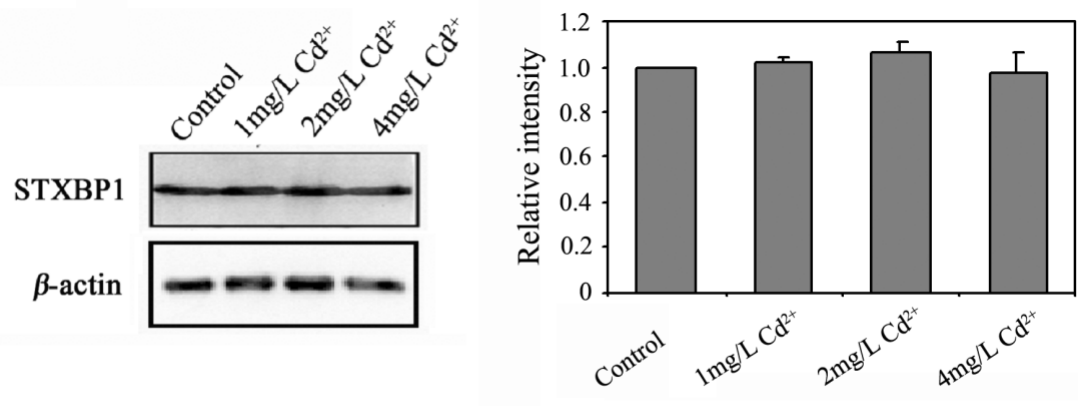


Figure S4