

Supplementary Information

Table S1. Primers used for fragment cloning, rapid amplification of cDNA ends, and quantitative real-time polymerase chain reaction analyses of *M. nipponense* catalase (*cat*), glutathione S-transferase (*gst*), Cu/Zn-superoxide dismutase (*sod*), and glutathione peroxidase (*gpx*).

Primer Name	Primer Sequence (5' to 3')	Remark	Reference
<i>cat</i> -F	CGCAGGTGCCTTGGATAC	<i>cat</i> fragment	
<i>cat</i> -R	GCCTTCTCCGCACTCAAAT	cloning	
<i>cat</i> -5gsp1	GTCTCGGATAAAGAACACGGGT		
<i>cat</i> -5gsp2	AGCAATAGGTGTCTTCTTCCCAA	<i>cat</i> 5'-RACE	
<i>cat</i> -3gsp1	CGTGTCTTATCCGAGACCCT		
<i>cat</i> -3gsp2	ACCAGGTCAACCATCCTTTCTC	<i>cat</i> 3'-RACE	
<i>gst</i> -F	CTTCCCCAACCTCCCTACTA	<i>gst</i> fragment	
<i>gst</i> -R	CGACGCCATGTACTTCTTGAT	cloning	
<i>gst</i> -5gsp1	CACCAAGCATACCAAGGGTTGTT		
<i>gst</i> -5gsp2	TTCTCAGATTCACTGCTTGCACAA	<i>gst</i> 5'-RACE	
<i>gst</i> -3gsp1	TGAATCTGAGAAAGTCCGTGTTG		
<i>gst</i> -3gsp2	AGCAATAGGTGTCTTCTTCCCAA	<i>gst</i> 3'-RACE	
5'-RACE Outer Primer	CATGGCTACATGCTGACAGCCTA	<i>cat</i> gene	
5'-RACE Inner Primer	CGCGGATCCACAGCCTACTGATGATCAGTCGATG	walking	
3'-RACE Outer Primer	TACCGTCGTTCCACTAGTGATT	<i>gst</i> gene	
3'-RACE Inner Primer	CGCGGATCCTCCACTAGTGATTCACTATAGG	walking	
<i>cat</i> -qRT-F	GAACCTGGGATTGGTTGGCA		
<i>cat</i> -qRT-R	GGTCCGAGAAAAGGATGGTG	<i>cat</i> qRT-PCR	This study
<i>gst</i> -qRTF	GAACCTGGGATTGGTTGGCA		
<i>gst</i> -qRTTR	GGTCCGAGAAAAGGATGGTG	<i>gst</i> qRT-PCR	This study
Cu/Zn-sod-qRT-F	AGTTTCAGCCGTCTGTTCG	Cu/Zn-sod	Accession number:
Cu/Zn-sod-qRT-R	CACAGTGCTTACATCACCCCTTA	qRT-PCR	JX045662
<i>gpx</i> -qRT-F	CCTGGCTTCCCCTGTAACC		Accession number:
<i>gpx</i> -qRT-R	ACCGAGTCATCCGAAGGCA	<i>gpx</i> qRT-PCR	HQ651155
β -actin-qRTF	AATGTGTGACGACGAAGTAG	β -actin	
β -actin-qRTTR	GCCTCATCACCGACATAA	qRT-PCR	Sun <i>et al.</i> 2015 [26]

1 gaaaagtctgggagtgagtgaggatcgtgacacagacaacacagcagtcgtcacacagacggtagtgcggactgaaggata
M P R D R A A E Q L N E F K K
91 cttttaaaagtctcaagtgtatccacggcttatccacg[ATGCCCTCGCAGACAGCTGCCAGCAACTGAACGAGTCAGAAG
K Q T T P E V L T T S Q G C P A D K L N S P T V G P R G P
181 AAGCAGACGACTCTGAAGTCTTAACAACCTCGAAGGATGTCCCCCTGGCAGACAAAGCTCAATTCCCGACAGTGGGTCAGAGGTCTC
I L L Q D I Q L L D E M A H F D R E I P E R V V H A K G A
271 ATCCTCTGCAGGATATCCAACCTCTGGACGAGATGGCCACTTCGACAGGGAGCGATCCCGAGAGAGTAGTCAGCTAACGGGCTC
G A F G H F E V T H D I T K Y C R A N I F S E I G K K T P I
361 GGTGCCCTGGACACTTCGAAGTCACCATGACATTACGAAGTATTGAGAGGCCAACATATTCACTGAGATTGGAGAAGAACCTATT
A V R F S T V G G E S G S A D T A R D P R G F A V K F Y T E
451 GCTGTAAGATTCTACTGTAGGAGGTGAAAGTGGTCTGCAGACACGGCTAGGGATCCTCGTGGCTCGCTGCAAGTTACACCGAA
E G N W D L V G N N T P V F F I R D P I L F P S L I H T Q K
541 GAAGGAACTGGGATTGGTGGCAACAACACCCGTCTTATCCAGACCCCTATTCTTCCCTCACTCATCCACACTCAGAAG
R N P A T H L K D P D M F W D F I T L R P E T T H Q V T I L
631 AGGAATCCAGCAACACCTGAAGGACCCGACATGTTCTGGACTTCATAACCTGAGACCCGACCAGTCACCATCCTT
F S D R G T P D G Y R H M N G Y G S H T F K L V N T E G K A
721 TTCTCGGACCGAGGTACTCTGTAGGCTACAGGCATATGAATGGTTAGGTTCTCACACTTCAAGCTGGTAATACTGAGGGAAAAGCC
V Y C K F H Y K T D Q G I R N L S A E K A D D L A G T D P D
811 GTTACTGAAATTCACTACAAGACTGACCAAGGAATCAGAAATTGAGCGGGAGAAGGGCAGACTTAGCTGGAACTGACCTGAC
Y A I R D L Y N A I E G G D Y P S Y T M Y I Q V M T Y E E A
901 TATGCTATTCTGTAGTGTACAACGTATTGAGGCGGAGACTACCCATCATATACTATGACATCCAGGTTAGCATATGAAGGGCT
E K H R F N P F D L T K V W P H K D F P L I P V G R L T F D
991 GAGAAGCACCGGTCATCTTCACTTGACCAAGTGTGGCCACACAAGGATTCCCTCATCCCTGGGACGCCACTTTGAC
R N P R N Y F E V E Q I A F F S P A N M V P G I E A S P D K
1081 AGAAATCTAGGAACTACTTGTAGGAGGTGAAAGATGGCTTCTCCAGAAATATGGTCCCTGGCATGAAGCATACCCGACAAG
M L Q G R L F S Y N D T H R H R L G A N Y T Q I P V N C P Y
1171 ATGTTGCAAGGACGCCATTCTCTACAATGACACCCATGCCATAGGCTGGCGCAAACACTACAGATACTGTCAATTGCTTAT
R S R A R N Y Q R D G P M T V D Y N Q E S A P N Y F P N S F
1261 CGCTCTGTCTAGGAACTACAGCGAGATGGCCAATGACCGTCGATTACACCCAGGAAAGTGCTCCAACTACTTCCAAACAGCTC
S G P M D C K R H S E S T F T C S T D V N R Y N S G D E D N
1351 TCTGGACCTATGGATTGTAAAAGGCATTAGTCCACTTCACTTGCTGCCAGGACGTTAACAGCGGGCATGAAGATAAC
F T Q A G N L F R H V M N E E R Q R L V S N I A G H L V N
1441 TTACTCAAGCTGGTAACCTGTTAGCATGTAACGAAGAGGAACGCCAGCGCTAGTCAGCAACATTGCTGGTACCTCGTGAAC
A Q K F L Q D R A I N N F S Q A D P E Y G G A G I R R A L E K
1531 GCACAGAAGTCTCTGCAAGATCGGCCATCAACAACTTCAGCAGGCTAGTCAGCAACAGCTGATCCTGAGTACGGTGTGAAATT
L Q K A A A S H P V N L V A A P A S N A K L
1621 CTACAGAAGGCAGCAGCGTCTACCCGTGAACTTGTAGCTGCTCTGCTTCAATGCCAAGCTATAaaaaaaaaaaaaaa

Figure S1. Nucleotide and amino acid sequences of the full length cDNA of the *M. nippone* catalase (*cat*) gene. The translated amino acid sequence is shown in standard one-letter code below the nucleotide sequence. The initiation codon and stop codon are indicated in the box.

Figure S2. Nucleotide and amino acid sequences of the full length cDNA for glutathione S-transferase (*gst*) in *M. nippонense*. The translated amino acid sequence is shown in standard one-letter code below the nucleotide sequence. The initiation codon and stop codon are indicated in the box. The polyadenylation signal is shaded light gray.

<i>M. nipponense</i>	MP--RDRAAEQLNEFKKKQ--TTPVEVLTSQQCPLADKLNLSPTVGRGPILLQDQIQLLDE	56
<i>M. rosenbergii</i>	MP--RDCKCAEQLTDPKKQQ--TAPDNLTTSIGCPLADKLNLSLTGPRGPILLQDQIQLLDE	56
<i>F. chinensis</i>	MP--RDCKCAEQLTDPKKQQ--TAPDNLTTSIGCPLADKLNLSLTGPRGPILLQDQIQLLDE	56
<i>L. vannamei</i>	MP--RDCKCAEQLNDFKKQQ--TAPDNLTTSIGCPLADKLNLSLTGPRGPILLQDQIQLLDE	56
<i>P. trituberculatus</i>	MP--RDKAAEQLNEFKKSQ--TNPDPVLTGHCPLSDKLNLSLTGPRGPILLQDQIQLLDE	56
<i>H. sapiens</i>	MADSRDPASDQMHQWKEQRRAQKADVLTTGAGNPGDKLNLTVGPRGPILLVQDVFTDE	60
<i>M. musculus</i>	MSDSRDPASDQMHQWKEQRASQRPDVLTTGGNP1GDKLNTAGSRGPILLVQDVFTDE	60
<i>D. rerio</i>	MADDREKSTDQMLWKEGRGSQRPDVLTTGAGVP1GDKLNAATAGPRGPILLVQDVFTDE	60
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<i>M. nipponense</i>	MAHFDRERIPERVVAHKAGAGFGYFEVTHDIITKCYCRANI FSEIGKKTPIAVRFSTVGGES	116
<i>M. rosenbergii</i>	MAHFDRERIPERVVAHKAGAGFGYFEVTHDIITKCYCRANI FSEIGKKTPIAVRFSTVGGES	116
<i>F. chinensis</i>	MAHFDRERIPERVVAHKAGAGFGYFEVTHDIITKCYCAAMFSEIGKQTPIAVRYSTVGGES	116
<i>L. vannamei</i>	MAHFDRERIPERVVAHKAGAGFGYFEVTHDIISKYCYKAALFSEIGKRTPLAIFRFSTVGGES	116
<i>P. trituberculatus</i>	MAHFDRERIPERVVAHKAGAGFGYFEVTHDIISQYTAKAFISEIGKRTPLAIFRFSTVGGES	116
<i>H. sapiens</i>	MAHFDRERIPERVVAHKAGAGFGYFEVTHDIITKYSKAKVFEHIGKKTPIAVRFSTVAGES	120
<i>M. musculus</i>	MAHFDRERIPERVVAHKAGAGFGYFEVTHDIITRYSKAKVFEHIGKRTPIAVRFSTVAGES	120
<i>D. rerio</i>	MAHFDRERIPERVVAHKAGAGFGYFEVTHDIITRYSKAKVFEHVGKTPPIAVRFSTVAGEA	120
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<i>M. nipponense</i>	GSADTARDPRGFAVKFYTEEGNWDLVGNTPVPFLRDPILFPSLIIHTQKRNPATHLKDPD	176
<i>M. rosenbergii</i>	GSADTARDPRGFAVKFYTEEGNWDLVGNTPVPFLRDPILFPSLIIHTQKRNPATHLKDPD	176
<i>F. chinensis</i>	GSADTARDPRGFAVKFYTEEGNWDLVGNTPVPFLRDPILFPSLIIHTQKRNPATHLKDA	176
<i>L. vannamei</i>	GSTDARDPRGFAVKFYTEEGNWDLVGNTPVPFLRDPILFPSLIIHTQKRNPATHLKCD	176
<i>P. trituberculatus</i>	GSADTARDPRGFAVKFYTEEGNWDLVGNTPVPFLRDPILFPSLIIHTQKRNPATHLKDA	176
<i>H. sapiens</i>	GSADTVRDPRGFAVKFYTEDGNWDLVGNTPVPFLRDPILFPSLIIHSQKRNPQTHLKDPD	180
<i>M. musculus</i>	GSADTVRDPRGFAVKFYTEDGNWDLVGNTPVPFLRDPILFPSLIIHSQKRNPQTHLKDPD	180
<i>D. rerio</i>	GSSDTVDPRGFAVKFYTEDGNWDLVGNTPVPFLRDPILFPSLIIHSQKRNPQTHLKDPD	180
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<i>M. nipponense</i>	MFWDFITLRPETTTHQVTILFSDRGTPDGYRHMGNGSHTFKLVNTEGKAVYCKFYHTDQ	236
<i>M. rosenbergii</i>	MFWDFITLRPETTTHQVTILFSDRGTPDGYRHMGNGSHTFKLVNAEGKAVYCKFYHTDQ	236
<i>F. chinensis</i>	MFWDFISLRPETTTHQVSFLFSDRGTPDGYRHMGNGSHTFKLVNAKGAEAVYCKFYHTDQ	236
<i>L. vannamei</i>	MFWDFISLRPETTTHQVSFLFSDRGTPDGYRHMGNGSHTFKLVNAKGAEAVYCKFYHTDQ	236
<i>P. trituberculatus</i>	MFWDFISLRPETTTHQVSFLFSDRGTPDGYRHMGNGSHTFKLVNANGEAVYCKFYHTDQ	240
<i>H. sapiens</i>	MWDFWSLRPESLHQVSFLFSDRGIPDGHRHMNGNGSHTFKLVNADGEAVYCKFYHTDQ	240
<i>M. musculus</i>	MWDFWSLRPESLHQVSFLFSDRGIPDGHRHMNGNGSHTFKLVNAQQPVYCKFYHTDQ	240
<i>D. rerio</i>	MWDFWSLRPESLHQVSFLFSDRGIPDGHRHMNGNGSHTFKLVNAQQPVYCKFYHTDQ	240
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<i>M. nipponense</i>	GIRNLSAEKADDLAGTDPDYAIRDLYNAIEGDDYPSYTMYIQVMTYEEAEKHRNPFPDLT	296
<i>M. rosenbergii</i>	GIRNLSAEKADDIAGTDPDYAIRDLYNAIEGDDYPSYTLYIQVMTYEEAEKHRNPFPDLT	296
<i>F. chinensis</i>	GIKCLCSKKADELAGSDPDYATRDLYNAISSGDYPSYTMYIQVMTFEEAEKWKFNFPFDLT	296
<i>L. vannamei</i>	GIKCLSAERADFLAGSDPDYAIRDLYNAISGNYPSYTMYIQVMTYEEQAEKWEEFNFPFDLT	296
<i>P. trituberculatus</i>	GKLNLSVEDAARLSQEDPDYGRDLFNAITAKGKPYTFLYIQVMTPNQAAETFPFPNPFDLT	300
<i>H. sapiens</i>	GKLNLPVGEAGRLAQEDPDYGLRDLFNAIANGNYPSTWFLYIQVMTFEEAETFPFPNPFDLT	300
<i>M. musculus</i>	GKNIPIVEEADRLAATDPDYSIRDLYNAIANGNPFSTWFLYIQVMTFEEAENWKWNPFDLT	300
<i>D. rerio</i>	*****: : ***: : ***: : ***: : ***: : ***: : ***: : ***: : ***: : ***: :	
<i>M. nipponense</i>	KWPWHKDFFPLIPVGRLTFRDRNPRNFAVEQIAFSPANMVPGIEASPDKMLQGRLFSYND	356
<i>M. rosenbergii</i>	KWPWHKEFFPLIPVGRLTFRDRNPKNYFAVEQIAFSPANMVPGIEASPDKMLQGRLFSYND	356
<i>F. chinensis</i>	KWPWHDEFFPLIPVGRLTFRDRNPKNYFAVEQIAFSPANMVPGIEASPDKMLQGRLFSYND	356
<i>L. vannamei</i>	KWPWHGEFFPLIPVGRLTFRDRNPKNYFAVEQIAFSSANMVPGIEASPDKMLQGRLFSYND	356
<i>P. trituberculatus</i>	KWPWHADFFPLIPVGRITLDRDNAQNYFAVEQIAFSPANLVPGIEPSPDKMLQGRLFSYND	356
<i>H. sapiens</i>	KWPWHDYPLIPVGRKLVLNRRNPVNYFAVEQIAFDPNSNMPPGIEASPDKMLQGRLFAAPD	360
<i>M. musculus</i>	KWPWHDYPLIPVGRKLVLNKNPVPVNYFAVEQIAFDPNSNMPPGIEASPDKMLQGRLFAAPD	360
<i>D. rerio</i>	KWWSHKEFFPLIPVGRFVLNRNRPVNYFAVEQIAFDPNSNMPPGIEASPDKMLQGRLFSYPD	360
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<i>M. nipponense</i>	THRHRGLANYTQIPVNCPYRSRARNYQRDGMPTVDYDQEASPNYPNSFSGPMDCRKHSE	416
<i>M. rosenbergii</i>	THRHRGLANYTQIPVNCPYRSRARNYQRDGMPTVDYDQEASPNYPNSFSGPMDCRKHSE	416
<i>F. chinensis</i>	THRHRGLANYTQIPVNCPYRARTKNYQRDGMPCVDDNGEASPNYPNSFSGPMDCRKHTA	416
<i>L. vannamei</i>	THRHRGLANYTQIPVNCPYRARTRNYQRDGMPCVDDNGEASPNYPNSFSGPMDCRKHTA	416
<i>P. trituberculatus</i>	THRHRGLANYHQIPVNCPYRARPNQYQRDGMPCVDDNGEASPNYPNSFSGPMDCRKQFEG	416
<i>H. sapiens</i>	THRHRGLANYHQIPVNCPYRARVANYQRDGMPCMEHDNOGGAPNPYPPNSFGAPEQOQPSALE	420
<i>M. musculus</i>	THRHRGLCPNYLIPVNCPYRARVANYQRDGMPCVDDNGEASPNYPNSFSGPMDCRKQFEG	420
<i>D. rerio</i>	THRHRGLCPNYLIPVNCPYTRVNTQVRFTYTKVLNEERKRLCENIAAGHLKDAQIFLQKKAVK	420
	THRHRGLANYLQLPVNCPRYTRVNTQVRFTYTKVLNEERKRLCENIAAGHLKDAQIFLQKKAVK	420
	*****: : ***: : ***: : ***: : ***: : ***: : ***: : ***: : ***: : ***: :	
<i>M. nipponense</i>	STFTCSTDVNRYNSQEDDNFTQAGNLFRHVMMEEERQRLVSNIAGHLVNAQKFLQDRAIN	476
<i>M. rosenbergii</i>	STFACSTDVSYRN5ADEFNFTQAGNLFRQVMNEERQRLVSNIAGHLVNAQKFLQDRAIN	476
<i>F. chinensis</i>	PKFSVADVDRYNSADEFNFTQAGNLFRQVMNEERQRLVSNIAGHLVNAQKFLQDRAIN	476
<i>L. vannamei</i>	PKFSVADVDRYNSADEFNFTQAGNLFRQVMNEERQRLVSNIAGHLVNAQKFLQDRAIN	476
<i>P. trituberculatus</i>	PKFSVADVDRYNSADEFNFTQAGNLFRQVMNEERQRLVSNIAGHLVNAQKFLQDRAIN	476
<i>H. sapiens</i>	PKFKLAGDMVRYNSADEFNFTQAGNLFRQVMNEERQRLVSNIAGHLVNAQKFLQDRAIN	476
<i>M. musculus</i>	HS1QYSGEVRPRFTANDNDNTQVRFTYTKVLNEERKRLCENIAAGHLKDAQIFLQKKAVK	480
<i>D. rerio</i>	HSVQCAVDVKRFRNSANEDNTQVRFTYTKVLNEERKRLCENIAAGHLKDAQIFLQKKAVK	480
	SKCKVSPDVARYNSADDNNTQVRFTYTKVLNEERKRLCENIAAGHLKDAQIFLQKKAVK	480
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<i>M. nipponense</i>	NFSQADPEYAGIRRALKQAAASHPVNLAAPASNAKL-----	517
<i>M. rosenbergii</i>	NFSQADPEYAGVRRSLEKLQKAAS-QPLNVLQASNAKL-----	517
<i>F. chinensis</i>	NFTQADPEYAGIRRALKQAAQASSKTHI QALAASSNGAKL-----	520
<i>L. vannamei</i>	NFTQADPEYAGIRRALKQAAQASSKTHI QALAASSNGAKL-----	505
<i>P. trituberculatus</i>	NFSQACPEYAGIERSALNRIKAQSSNSAIIHAVAASNAKL-----	517
<i>H. sapiens</i>	NFTDVHPDYGARIQALLDKYNAEKPKNIAHTYTQAGSHMAAKGKANL-----	527
<i>M. musculus</i>	NLMAVHSYGNRVQALLDKHNAEGKNTVHYSRGGSAVAASAKM-----	526
<i>D. rerio</i>		

Figure S3. Comparison of the *M. nipponense* catalase (CAT) amino acid sequences among vertebrates and invertebrates. Accession numbers of the sequences used to compare the amino acid residues are as follows: *Danio rerio*, NM130912; *Homo sapiens*, AY028632; *Hyriopsis cumingii*, HM188565; *Eriocheir sinensis*, GU361618; *Macrobrachium rosenbergii*, HQ668089; and *Litopenaeus vannamei*, JX162772. The CAT proximal heme-ligand signature is framed. Shaded region indicates amino acid residues combined with coenzyme (NADPH). Underline indicates CAT proximal active signature site. Asterisks indicate positions where all sequences share the same amino acid residues.

<i>H. sapiens</i>	-----MPMILGYWDIRGLAHAIRLLLEYTDSSYEKKYTMGDAPDYD 42
<i>M. musculus</i>	SQCSHRRPVDSVSGTSIMPMTLGYWDIRGLAHAIRLLLEYTGSSEEEKRYTMGDAPDYD 60
<i>C. carpio</i>	-----MAVKLAYWDIRGLAQPIRLLLEYTGTKEYEKFYTCGEAPNYD 42
<i>D. rerio</i>	-----MAMKLAYWDIRGLAQPIRLLLEYTGTKEYEKFYTCGEAPNYD 42
<i>O. niloticus</i>	-----MPMTLAYWDIRGLAQPIRLLLEYTGEEYEDKYYVCGEAPNYD 42
<i>M. nipponense</i>	-----MSPTLAYWNIRGLAQPIRLLLEYTGTEFEDKMYECGPAPKFD 42
<i>C. ariakensis</i>	-----MPALGYWKIRGLAQPVRLNNVGEEFDDVQYEQGDAPEFS 41
<i>P. nana</i>	-----MAPRGFYWNLQQLGQASRLLAFTGTEHEDEVLDIA----H 37
* * :	
<i>H. sapiens</i>	RSQWLNEKFKLGLDFPNLPYLIDGAHKITQSNAILCYIARKHNLCGETEEKIRVDILEN 102
<i>M. musculus</i>	RSQWLSEKFKLGLDFPNLPYLIDGSHKITQSNAILRYIARKHNLCGETEEKIRVDILEN 120
<i>C. carpio</i>	KSCWFNEKDQLGMDFPNLPYLEDGDTKVQNSNAIMRYIARKHNLCGETDEAQMRVDILEN 102
<i>D. rerio</i>	KSCWFNEKSQKLMDFPNLPYLEDGDRKIVQNSNAIMRYIARKHNLCGETEEQMRVDILEN 102
<i>O. niloticus</i>	KTCWIDVKNKLGLDFPNLPYLLDGDRKITQNSNAIMRYIARKHDLGKGETEDEKVRVDIEN 102
<i>M. nipponense</i>	KSCWFDIKYSLGLDFPNLPYYIDGGDVKVTQNSNAIMRYIARKHDLGKGETEDEKVRVDIEN 102
<i>C. ariakensis</i>	RDAWLSVKNTLGLAFPNLPYYIDGDIKVTQNSNISLRYIGDKHGLGKTPKEKVDCDMMVE 101
<i>P. nana</i>	REVWMDKKFNLGLDFPNLPYYIDQDVKLTQSNAILRYLGRKNLYGKNAIEAGTIDMLID 97
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<i>H. sapiens</i>	QTMDNHMQLGMICYNPEFEKLKPYLEELPEKLYSEFLGKRPWFAGNKITFVDFLVYD 162
<i>M. musculus</i>	QAMDVSQNQLARVCYSPDFEKLKVEYLEQLPCMVKLFQSFLGQRTWVGEKITFVDFLAYD 180
<i>C. carpio</i>	QAMDFRNGFVQLCYG-DFDKNKTCTYCEKLPGLKQFSDFLGDRKWFA GDKITFVDFIMYE 161
<i>D. rerio</i>	QAMDFRNGFVQLCYL-DFDKNKSSEKLSGTQKQFSDFLGDRKWFA GDKITFVDFIMYE 161
<i>O. niloticus</i>	QSMDFRNGFVRLCYT-NFDEMPPDYLKTLPTNLQKQFSDFLGDRKWFA GDKITFVDFIMYE 161
<i>M. nipponense</i>	QSMDFRNGFVRLCYV-DFDTQKQTYLEALPTTLKLFSTFLGEQPWYAGDNITIFVDFIMYE 161
<i>C. ariakensis</i>	NAMDFRNGVVRLCYNDYEKIKDDYFANVKDKLQKFDTFLGDKPWFAGDNITICDFFPMYE 161
<i>P. nana</i>	EAQDIKMALIKTATSPDFENVKGDHIKAMEQKLKIVSDFLGNKKFFMGDEVTIGDFAMID 157
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<i>H. sapiens</i>	VLDLHRIFEPKCLDAFPNLKDFLSRFEGLEKISAYMKSSRFLPRPVFSKMAVGWNK-- 218
<i>M. musculus</i>	ILDHLIIFEPTCLDAFPNLKDFVARFEVLKRISAYMKTTSRFLRTPLYTKVATWGNK-- 236
<i>C. carpio</i>	LLDQHRMFEPECLDDYENLRSFLDRFESLEKIVEYMSKNFKMTPVNNKMAKGWNKKE 219
<i>D. rerio</i>	LLDQHRMFEPACLDDFKNLRCFLDHFESLEKIAEYMSKNRFMETPVNNKMAKGWNKKE 219
<i>O. niloticus</i>	LLDQHRLFDSDKCLDDFKNLTDFLNRFEALEKIAAYMKSPrFMKAPINNKMAKGWNK-- 217
<i>M. nipponense</i>	LIDQHQLQDPNLKDFKNLEDFQKRFEELEPKKYMMASSRFMKSPLNNKMAKGWNK-- 216
<i>C. ariakensis</i>	LLDQHRLMKPGILDDYPNLAKFVERENLPKIKAYMASDKFMAPPINNKVAGFK---- 215
<i>P. nana</i>	ALSWHQIFADLMGKFPNLVAFIDNFKALDKIKAFYEGPKHFKLVLPPMFPWHGQ--- 212
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Figure S4. Comparison of *M. nipponense* glutathione S-transferase (GST) amino acid sequences among vertebrates and invertebrates. Accession numbers of the sequences used to compare amino acid residues are as follows: *Homo sapiens*, M63509; *Mus musculus*, X65021; *Cyprinus carpio*, DQ411212; *Oreochromis niloticus*, EU107284; *Crassostrea ariakensis*, EU908270 and *Paracyclops nana*, HQ115574. “■” indicate G-sites and “◆” indicate H-sites. Symbols below the amino acid sequences indicate invariant (*), strongly conserved (:) or conserved residues (.).