**Table S1. Primers for RT-qPCR**

|  |  |  |  |
| --- | --- | --- | --- |
| Primers | Forward primer sequence (5′–3′) | Reverse primer sequence (5′–3′) | Note |
| *PxSOD3* | CTTCTCGCGCTCAACAGATAAACAT | CTAATTACAAAATTCCGATGACGCC | Gene clone |
| *PxSOD5* | TACTTGTTTAACTGGTTGTGCGAAT | TCATCCGTTGACGTATCCGATGACGC | Gene clone |
| *PxSOD3q* | TCGGCGACTTGGGTAACATC | GGCCCTGCCGAGTATATTGT | RT-qPCR |
| *PxSOD5q* | GTGGAAACATCACGGGACTG | TTCCGAGATCTCCGATGTGA | RT-qPCR |
| *α-Tubulin* | TGGCAGGTTCAAAACAAGCG | TCGATGGTGCCCTCAATGTT | RT-qPCR |
| *β-Tubulin* | AAGGAAGCCGAATCATGCGA | CGGATACTTTTGGCGAGGGT | RT-qPCR |

**Table S2. Insect SODs used for phylogenetic analysi**

|  |  |  |
| --- | --- | --- |
| SOD name | Accession No. | Sequence |
| PxSOD1 | OR469741 | MSAKAVCVVKGENVSGTIWFEQTQGDGSVKVTGSVSGLTPGLHGFHVHEFGDTTNGCISAGAHFNPHGKDHGGPDSDIRHVGDLGNINAGSDGVGKVDLSDKFISLCGPMNIIGRTLVVHADPDDLGVGGHELSKTTGNAGARVACGVIGIAKI |
| PxSOD2 | OR469742 | MAVLEANVSFLYPISLHYLVGNMFATNRIYTVMRLGIRMKHSLPELPYELNALEPIISREIMFLHHQKHHATYINNFNAAEEKLALATSKSDINTIISLAPVLRFNGGGHINHTIFWKNLSPNGGEPSKELCAAINTCFGSFDNMKTQLSNAAVGIQGSGWGWLSYNKTSKRLQIATCSNQDPLEGTTGLIPLFGIDVWEHAYYLQYKNVRADYVKAIFEIANWCDISERFAKASC |
| PxSOD3 | PQ333015 | MFRYLITLALLAAACAEEYKAIVHLVGTAQSVTGNVTFTQEEAGKPVHVDGIVVGLAPGKHGFHVHAKGDLTGGCLTTSGHFNPENKKHGAPDDKERHVGDLGNIVANHDGIARFSLDDSIISLCGSHNILGRAVVVHASEDDLGKGGHEDSLTTGHAGARVACGVIGIL |
| PxSOD5 | OR469743 | MEPFAYNVRPLLASATLLPNAGNGRAAGGDAETEAESVTPGPVYGELVFSQTLPPGGHVIVRGNITGLTPGKHAIHVHEYGDTRKGCESAGGHFNPYQLHHGAPHDAIRHIGDLGNIVAGDDGTAEVKILDPLLSLLPGPRGIVGRSIVIHAMEDDLGRADTVDSQTSGSAGARIACGVIGYVNG |
| BmSOD2 | NP\_001037299 | MLMSQRIGSLIRVAGASRQKHTLPELPYEYNALEPVISREIMSLHHSKHHATYINNLNVAEEKLAQAQAKGDIDTIINLAPALKFNGGGHINHSIFWHNLSPNGGKPSDVLTKAVEKDFGSWDNIKNQLSTASVAVQGSGWGWLGYNKQMKKLQIATCQNQDPLQATTGLVPLFGIDVWEHAYYLQYKNVRADYVKAIFDVANWNDISQRYEKALK |
| BmSOD5 | BBD33996 | MNLRGYLLFGQFLWLVAVLNGKTLQGIPGYGRNLIIKSLPAIEDYQSPVYEVYMEPYLYALGQTTYPLNDNRAEKQIDLSMAPHHAPGLQAVVHLIADEESGVSGDLIFTQIVPNGPVTIEGNVTGLAPGLHGLHVHQTGNIKDNCKEIGPHFFGYYGRHGGPRDPIRHVGDLGNIKAEEEATLNLKIVDHLISLAGPRSVVGRSIAISKSEDDYGRASTEDSALTGTSGPAVACGIIGYLH |
| BmSOD4 | BBD33995 | MAIVTIIVFVFLCVFTSGTNGENRVAVAHLVSGKITGTIVFTETSEGLHITGTITGLPAGRYGFHVHALGDTSTCDAAGPHFDPEGNNHGGPDHNVRHVGDLGNVVFVGNQEPVATVNFVDRLITLRGKNNIIGRTLVLHEQEDDLGLGGHELSLTTGNAGPRVACGVIGIRSPVVWNSAVTSFPLIVLYVLAAVFLLFLN |
| BmSOD1 | NP\_001037084 | MPAKAVCVLRGDVSGTVFFDQQDEKSPVVVSGEVQGLTKGKHGFHVHEFGDNTNGCTSAGAHFNPEKQDHGGPSSAVRHVGDLGNIEAIEDSGVTKVSIQDSQISLHGPNSIIGRTLVVHADPDDLGLGGHELSKTTGNAGGRIACGVIGLAKI |
| BmCCS | BBD33998 | MVSDQSCCNKILGVVRLQQTAEGPLVADGSIDGLSPGRHGLHVYESGDLSQGCNSIGGHYNPSGGPHGGPGDPPDRRHAGDLGNITADANGRAAFRIVDDVLKVWDVIGRSMDVTERGDDCGRGDGTSRVDGNSGPILACGIIARSAGIFQNPKRICACDGVVVWDERDKPLAGSGRRGQGDCAPSEGGCCGKAGKTTKGSNNKGGRCGAGDSGGGNGKTCCKV |
| HaSOD1 | XP\_021192583 | MPAKAVCVLKGDVTGTVYFAQKDENSAVVLTGEVHGLKQGKHGFHVHEFGDNTNGCTSAGAHFNPLKLEHGAPDSAVRHVGDLGNIEASGTGATQVNIQDKLISLSGPHSIIGRTLVVHADPDDLGAGGHELSKTTGNAGARIACGVIGLAQV |
| HaSOD2 | XP\_021192374 | MFAKRRFLLTSAVNAVRQKHTLPELPYEYSALEPVISREIMSLHHSKHHATYINNLNAAEEKLAQAQAKGDISTVISLAPGLKFNGGGHINHTIFWQNLSPNGGKPSGLLTQAIEKDFGSWDNMKNQLAAASVGVQGSGWGWLGYNKQMKKLQIATCQNQDPLQATTGLIPLFGIDVWEHAYYLQYKNVRADYVKAIFDVANWGDVSKRFEAAVN |
| HaSOD | XP\_021185298 | MNLRLHVFFGQFLWLLAALNGKTIQGIPGYGRNLLIKTLPAIEDYQSNIYEVFMEPYLYEFGHQVLPPGNRAEKQIEYVIPQRSPGLQAIVHLQADEESGVEGDLIFTQVVPNGPVTIEGNITGLAAGLHGIHVHQTGAVKDDCKEIGPHFLAFYGRHGGPRDNVRHVGDLGNIKAEEGPVSVRIIDHLISLAGPRSIVGRSLAISKGEDDYGRASTEDSALTGTSGPAIACGIIGYLH |
| HaCCS | XP\_063899484 | MLTSKLEVLVDFGPTVDDAILNKTLNELKSQDGVKEAVFKDGAILVETSLPSTDVLDMVKKTSGKRAVLQGFGETQSAVAMVSSQSCCGSQVLGVIRFQQAAAGPLLADGSIDGLATGPHALHVHSSGDLTQGCDSLGEHYNPTGAPHGGPNDPSDRRHAGDLGNIVADETGRATFRIIDEVLKVSDIIGRSVAVTERRDDLGRGSSPTSKIDGDSGKPVACGIIARSAGIFQNPKRICACDGVVVWDEKDRPLAGKGRRTEEKTEKKCCSNH |
| CcSOD1 | XP\_044739591 | MALAAVAVVKGDVVKGVIHFNQSKPEDPITITGQVEGLTEGLHGFHVHEFGDTTNGCISAGPHFNPHKKDHGGPSDAVRHAGDLGNIVADGSGVGKVNITDKQISLFPGPLNIIGRTLVVHADPDDLGKGGHELSLTTGNAGARVACGVIGVAAPK |
| CcSOD3 | XP\_044734675 | MNQFVIAIFVLFGTILTANGQEAVKATVKLIGSIEGNITFTQAAYGLPVQVEGVILGLAPNSQHGFHVHQSGDITGGCGSTGGHFNPENQNHGAPNAAVRHVGDLGNVQANANGVAQFSFADHLISLCAGPHSIIGRAIVVHAGVDDLGLGGNADSLKTGNAGGRLACGVIGLASAKTCAGDGSGVSGLKPTVFTMVTVIFAMILKSL |
| CcSOD | XP\_044732007 | MIVKFLSVTSILLVNYVVKTSVSSPSLKQVDRSLHVRSLPPINGIQSNIYEVYMEPYGFELGPILASAVIRPNGGNLSGGKQDAANVGIKVKGELLLRQTHPPHGPVQIVGNITGLPPGLHGFHVHQFGDIREGCTSCGEHFNPFMVPHAGKNDPIRHVGDLGNILADAEGKAEVNVMDSYLTLKHGPRSIIGRAIVIHELADDLGRGHTAQSVQSGSSGKRLACGIIAHVN |
| AcSOD1 | XP\_016917119 | MTKAVCVLQGEVKGTIFFEQPESTNSVKVTGQVTGLKKGLHGFHVHEFGDNTNGCTSAGAHFNPLGKDHGGPDSDIRHVGDLGNIEADASGIANVNITDKTIQLQGPHSVIGRTLVVHADPDDLGKGGVELSKTTGNAGARLACGVIGITKV |
| AcCCS | XP\_061928345 | MTTTKIEFAVNMTCQKCVDLVRNTLTGIDGIENIDISLENNNVIVETNLPYSIIQEKIEQSGKKAVLKGYGDTSSAVTMLGGNSGYTVNNKIMGVIRFAQTPDGCLIDGTIDGLTPGEHGIHIHECGDISQGCDSVGEHFNPNNTIHGGPKDDIFKRHVGDLGNIMVNDFGRATFRMIDKVIEIADIIGRSLVITEKPDDLGRGTNPESKIDGNSGNKLACGIIARSSTLFQNTKKICACDGLTLWDERDKTFTNKYDYSKSSNNCTVF |
| OcSOD1 | QFZ96020 | MTIKAVCVLNGEQVKGTVHFEQEGANSPVKVTGEITGLTKGLHGFHVHEFGDNTNGCMSAGAHFNPHSKDHAGPEDSDRHVGDLGNVEAGGDGVAKVNISDKIISLTGDHNVIGRTLVVHADPDDLGRGGHELSKTTGNAGARVACGVIGIAKA |
| OcSOD2 | QFZ96018 | MLACRRSALTFIRCNANVMSAEKREKHTLPDLPYDYNALEPVISAEIMKLHHSKHHATYVNNLNVAEEKLQEAKSKNDISTIISLAPALKFNGGGHINHTIFWQNLSPCGGSAEGELLEAIKRDFGSLENMKTKLSAAAVGVQGSGWGWLGYNKETQKLQLAACANQDPLQATTGLIPLFGIDVWEHAYYLQYKNVRPDYVKAIFDIVNWKDVSERYAKAKCN |
| DmSOD1 | NP\_476735 | MVVKAVCVINGDAKGTVFFEQESSGTPVKVSGEVCGLAKGLHGFHVHEFGDNTNGCMSSGPHFNPYGKEHGAPVDENRHLGDLGNIEATGDCPTKVNITDSKITLFGADSIIGRTVVVHADADDLGQGGHELSKSTGNAGARIGCGVIGIAKV |
| DmSOD2 | CAA45418 | IICREIMELHHQKHHQTYVNNLNAAEEQLEEAKSKSDTTKLIQLAPALRFNGGGHINHTIFWQNLSPNKTQPSDDLKKAIESQWKSLEEFKKEVTTLTVAVQGSGWGWLGFNKKSGKLQLAALPNQDPLEASTGLIPLFGIDV |
| DmCCS | AAK07691 | MSSIKIEFAVQMRRGDESYAGALRSALDGVGQVEIDTQEGRVIIQTQRPWSEIQDKIEATGVRAVLSGFGGQSAVALINTTGSVVDKTPIQGVVRFTTITADKKPGVVVDGVVDGLSPGLHGLHIHESGDTSAGCSSVGEHYNPRQSPHGSPAAGAEERHAGDLGNIRADENGRATFRFVDPVLEVWDIIGRAVVLTANADDLGRGGNDQSLIDGNSGERIACGIIARSAGILENFKRICACDGVTLWDERNKPLAGKDRSQKL |
| TcSOD1 | EFA02790 | MPTKAVCVLNGEVKGTIFFTQENGKAPVQVTGEVSGLKKGLHGFHIHEFGDNTNGCISAGAHFNPHGKDHGGPTHDVRHVGDLGNIEAGGDGVAKVGITDKFISLEGEHSIIGRTLVVHADPDDLGQGGHELSKTTGNAGARLACGVVGITKA |
| TcSOD2 | EFA09191 | MFALRRLATAPLAGSRAAHSLPELPYAYEALEPVISRDIMCLHHSKHHQTYVTNLNAAEEKLKAALSKGDISTAISLEPALRFNGGGHLNHSIFWQNLSPESTQPSDALKKAIEDSFGGVQQLKDQLSASSIGVQGSGWGWLGYCSKSGKLKIATCANQDPLQATTGLVPLLGIDVWEHAYYLQYKNVRADYVKAIFEIVNWKDVSQRFEKAKSC |
| TcSOD3 | EFA10685 | MFKLFVLALCATATLATVEKAIVCLKSGDIDGKITFTQTAEGVQVEGVINGLPKGKHGFHIHEKGALGDSCKDAGGHFNPDKKDHGAPEDAVRHVGDLGNIIADDKKVAHVNISDKIISLNGEHSIIGRAVVVHEGEDDLGKGNFNDSKTTGHAGARLVCGVIGIASDGTETCPEGPGNIAISTTGNYFLLFTGLYTLFLNLRF |
| TcSOD | EFA10684 | MFKSVVFLCTLVTIKNVQSASMQTLAVRNALYQVPGLGNRPLIIKMYPGVENYQSDLYEVYAEPYTFDLRAASAVALIQGEGESAAKGEIVFFQRHPPNGPILVRGNLTDLPPGKHGLHIHQSGDLRQGCDKLGPHFNPYLLQHGGPSDPVRHVGDLGNIEVEEDGSVEFNIADPLLSLMGGPRGIVGRSIVISGNPDDLGRGGTAESLVNGDSGKPIACGVIAYIK |

**Table S3. Secreted SODs identified in *Protohermes xanthodes***

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Gene name | ORF length (bp/aa) | Mw (kDa) | *pI* | Subcellular location | Accession Number |
| *PxSOD3* | 513 / 170 | 17.61 | 6.07 | Extracellular | PQ333015 |
| *PxSOD5* | 735 / 244 | 25.44 | 5.61 | Extracellular | OR469743 |