

Table S1. Details of the genomes used in this study.

Species	Phyla	Website/source
<i>Amphimedon queenslandica</i>	Porifera	http://metazoa.ensembl.org/Amphimedon_queenslandica/Info/Index
<i>Xestospongia bergquistia</i>	Porifera	Data available from the authors on request
<i>Tethya wilhelma</i>	Porifera	http://tethya.spongebase.net/
<i>Ephydatia muelleri</i>	Porifera	https://spaces.facsci.ualberta.ca/ephybase/
<i>Oscarella carmela</i>	Porifera	http://compagen.unit.oist.jp/index.html
<i>Sycon ciliatum</i>	Porifera	http://compagen.unit.oist.jp/index.html
<i>Mnemiopsis leidyi</i>	Ctenophora	https://research.nhgri.nih.gov/mnemiopsis/
<i>Nematostella vectensis</i>	Cnidaria	https://www.ebi.ac.uk/ena/browser/view/GCA_000209225.1?show=blobtoolkit
<i>Acanthaster planci</i>	Echinoderm	https://marinegenomics.oist.jp/cots/viewer/info?project_id=46
<i>Strongylocentrotus purpuratus</i>	Echinoderm	https://www.ebi.ac.uk/ena/browser/view/GCA_000002235.4?show=blobtoolkit
<i>Branchiostoma floridae</i>	Chordata	https://mycocosm.jgi.doe.gov/Brafl1/Brafl1_home.html
<i>Ciona intestinalis</i>	Chordata	https://www.ebi.ac.uk/ena/browser/view/GCA_000224145.1
<i>Capitella teleta</i>	Annelida	https://www.ebi.ac.uk/ena/browser/view/GCA_000328365.1?show=blobtoolkit
<i>Lingula anatina</i>	Brachipoda	https://www.ebi.ac.uk/ena/browser/view/GCA_001039355.1
<i>Caenorhabditis elegans</i>	Nematoda	https://downloads.wormbase.org/releases/WS279/species/c_elegans/PRJNA13758/
<i>Drosophila melanogaster</i>	Arthropoda	https://flybase.org/ (release dmel_r6.32 (FB2020_01))
<i>Danio rerio</i>	Chordata	https://www.ncbi.nlm.nih.gov/grc/zebrafish
<i>Xenopus tropicalis</i>	Chordata	http://www.xenbase.org/
<i>Homo sapiens</i>	Chordata	https://www.ncbi.nlm.nih.gov/grc/human

Table S2. Details of sequences used from species for evolutionary comparison. Sequences were obtained from either the UniProt data base <https://www.uniprot.org/> or NCBI <https://www.ncbi.nlm.nih.gov/>

Species	Phylum	Gene ID	Uniprot accession
<i>Pseudanabaena.ABRG5-3</i>	Cyanobacteria	CuZnSOD	A0A2Z5WSM0
<i>Pseudanabaena.PCC7367</i>	Cyanobacteria	CuZnSOD	K9SG01
<i>Pseudanabaena.PCC7429</i>	Cyanobacteria	CuZnSOD	L8N810
<i>Pseudanabaena.SR411</i>	Cyanobacteria	CuZnSOD	A0A256BEG9
<i>Pseudanabaena.ABRG5-3.sodB</i>	Cyanobacteria	MnSOD	A0A2Z5WSL4
<i>Pseudanabaena.PCC7367</i>	Cyanobacteria	MnSOD	K9SFI2
<i>Pseudanabaena.PCC7429</i>	Cyanobacteria	MnSOD	L8MYC0
<i>Pseudanabaena.SR411</i>	Cyanobacteria	MnSOD	A0A256BCV0
<i>Gloeobacter.kilaeensis.JS1.SODC</i>	Cyanobacteria	CuZnSOD	U5QI46
<i>Gloeobacter.kilaeensis.JS1.GKIL_3379</i>	Cyanobacteria	CuZnSOD	U5QPK5
<i>Gloeobacter.violaceus.PCC7421.glr2170</i>	Cyanobacteria	CuZnSOD	Q7NIL3
<i>Gloeobacter.violaceus.PCC7421.glr1981</i>	Cyanobacteria	CuZnSOD	Q7NJ51
<i>Gloeobacter.violaceus.PCC7421.sodB</i>	Cyanobacteria	MnSOD	Q7NDA9
<i>Gloeobacter.kilaeensis.JS1.sodA</i>	Cyanobacteria	MnSOD	U5QI99
<i>Gloeobacter.violaceus.PCC7421.sodB</i>	Cyanobacteria	MnSOD	Q7NMT3
<i>Algoriphagus machipongonensis</i>	Bacteroidetes	MnSOD	A3HUU8
<i>Arabidopsis thaliana</i>	Spermatophyta	CuZnSOD_1	P24704
<i>Arabidopsis thaliana</i>	Spermatophyta	CuZnSOD_2	O78310
<i>Arabidopsis thaliana</i>	Spermatophyta	RBOHD	Q9FIJ0
<i>Arabidopsis thaliana</i>	Spermatophyta	RBOHF	O48538
<i>Arabidopsis thaliana</i>	Spermatophyta	RBOHC	O81210
<i>Arabidopsis thaliana</i>	Spermatophyta	RBOHB	Q9SBI0
<i>Arabidopsis thaliana</i>	Spermatophyta	RBOHA	O81209
<i>Arabidopsis thaliana</i>	Spermatophyta	RBOHE	O81211
<i>Podospora anserina</i>	Ascomycota (filamentous fungus)	CuZnSOD_1	Q711T9
<i>Podospora anserina</i>	Ascomycota (filamentous fungus)	CuZnSOD_2	B2ATY8
<i>Podospora anserina</i>	Ascomycota (filamentous fungus)	MnSOD_1	Q711T6
<i>Podospora anserina</i>	Ascomycota (filamentous fungus)	MnSOD_2	Q9C208
<i>Podospora anserina</i>	Ascomycota (filamentous fungus)	NOX3(C/D)	B2AAS7
<i>Podospora anserina</i>	Ascomycota (filamentous fungus)	NOX2 (A/B)	B2AL10
<i>Podospora anserina</i>	Ascomycota (filamentous fungus)	NOX1 (A/B)	B2AA06
<i>Phaeosphaeria nodorum</i>	Ascomycota (Sac fungi)	CuZnSOD_1	Q0UEY3
<i>Phaeosphaeria nodorum</i>	Ascomycota (Sac fungi)	CuZnSOD_2	Q0UPE0
<i>Phaeosphaeria nodorum</i>	Ascomycota (Sac fungi)	CuZnSOD_3	Q0UD72
<i>Phaeosphaeria nodorum</i>	Ascomycota (Sac fungi)	CuZnSOD_4	Q0UMZ2
<i>Chondrus crispus</i>	Red algae (Irish moss)	CuZnSOD_1	R7QQ00

<i>Chondrus crispus</i>	Red algae (Irish moss)	CuZnSOD_2	R7QRY5
<i>Chondrus crispus</i>	Red algae (Irish moss)	MnSOD_1	R7QCE3
<i>Chondrus crispus</i>	Red algae (Irish moss)	MnSOD_2	R7QI02
<i>Chondrus crispus</i>	Red algae (Irish moss)	NOX_rboh (C/D)	Q2FA46
<i>Pyropia yezoensis</i>	Red algae (glume blotch)	MnSOD	Q3YB09
<i>Pyropia yezoensis</i>	Red algae (glume blotch)	NOX_rboh (C/D)	Q2F9N3
<i>Dictyostelium discoideum</i>	Amoebozoa	CuZnSOD_1	Q55GQ5
<i>Dictyostelium discoideum</i>	Amoebozoa	CuZnSOD_2	Q54TU5
<i>Dictyostelium discoideum</i>	Amoebozoa	CuZnSOD_3	Q54G70
<i>Dictyostelium discoideum</i>	Amoebozoa	CuZnSOD_4	Q54TW8
<i>Dictyostelium discoideum</i>	Amoebozoa	MnSOD	Q55BJ9
<i>Dictyostelium discoideum</i>	Amoebozoa	NOXA	Q9XYS3
<i>Dictyostelium discoideum</i>	Amoebozoa	NOXB	Q86GL4
<i>Dictyostelium discoideum</i>	Amoebozoa	NOXC	Q54F44
<i>Fonticula alba</i>	Amoebozoa	CuZnSOD_1	A0A058ZE05
<i>Monosiga brevicollis</i>	Choanoflagellata	MnSOD	A9VBJ0
<i>Trichoplax adhaerens</i>	Placozoa	CuZnSOD	B3S9R7
<i>Trichoplax adhaerens</i>	Placozoa	MnSOD_1	Q55BJ9
<i>Trichoplax adhaerens</i>	Placozoa	MnSOD_2	B3SFQ5
<i>Trichoplax adhaerens</i>	Placozoa	MnSOD_3	B3SFI3
<i>Bombyx mori</i>	Arthropoda	BmSOD6 (Rsod)	A0A455R4Z2
			NCBI accession
<i>Monosiga brevicollis</i>	Choanoflagellata	NOX1(A/B)	XP_001746171.1
<i>Monosiga brevicollis</i>	Choanoflagellata	NOX2	XP_001748123.1
<i>Trichoplax adhaerens</i>	Placozoa	NOX_1(NOX5)	XP_002115436.1
<i>Trichoplax adhaerens</i>	Placozoa	NOX_2	XP_002112911.1

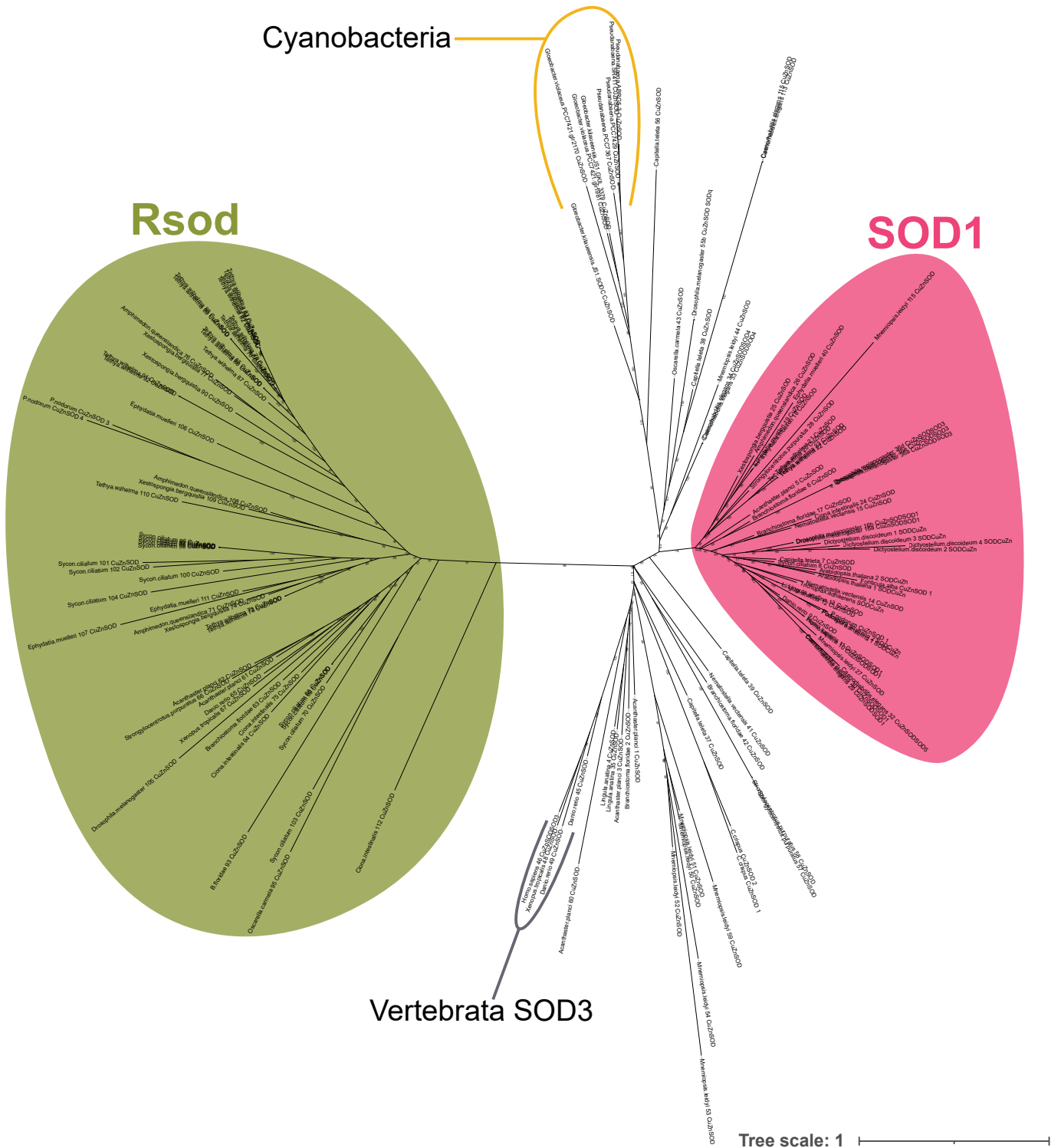


Figure S1. Maximum likelihood phylogenetic tree of CuZnSOD enzyme family. Black numbers on branches indicate bootstrap support. Filled in coloured shapes indicate monophyletic group; SOD1 (pink), and Rsod (green). SOD3 sequences from Vertebrata and CuZnSOD sequences from ancestral cyanobacteria, *Pseudanabaena* sp. and *Gloeobacter violaceus* [40] are indicated. Constructed based on edited alignment (Additional file 5), 1000 bb and the WAG+R5 evolutionary model.

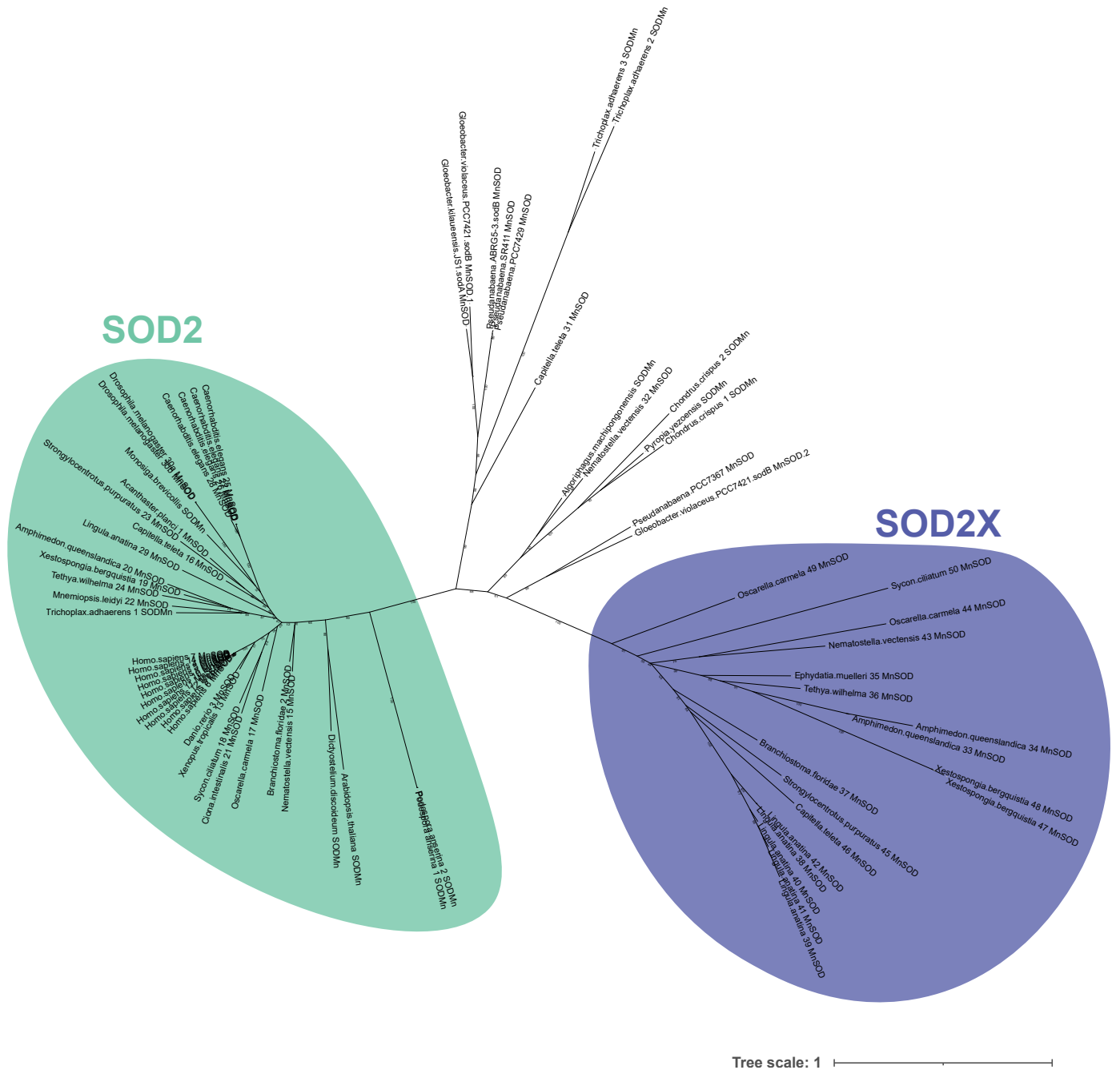


Figure S2. Maximum likelihood phylogenetic tree of MnSOD enzyme family. Black numbers on branches indicate bootstrap support. Filled in coloured shapes indicate monophyletic group; SOD2 (turquoise), and SOD2X (purple). Constructed based on edited alignment (Additional file 5), 1000 bb and the WAG+I+G4 evolutionary model.