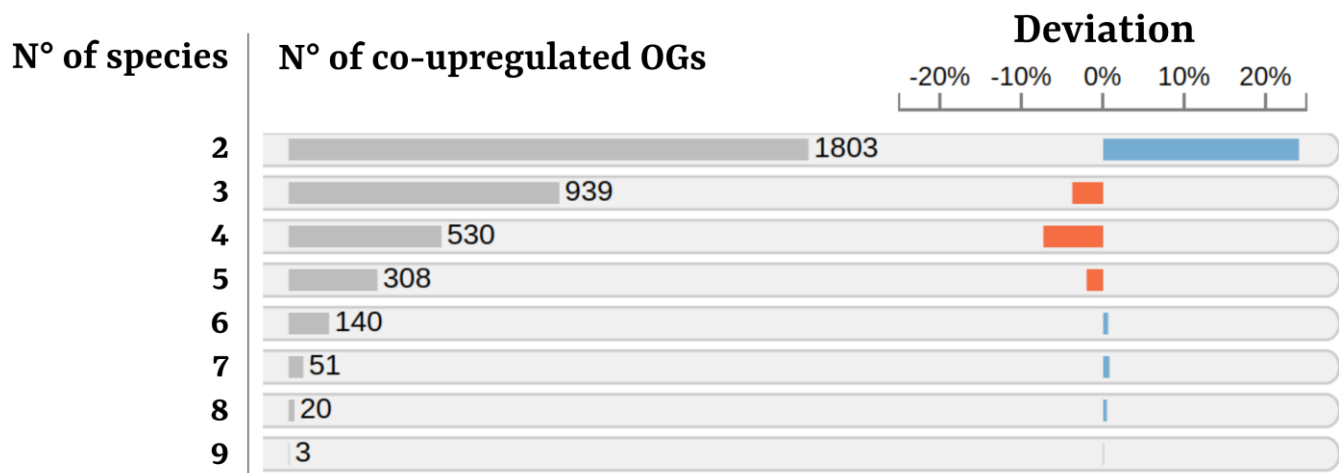


Additional Information

	<i>Caenorhabditis elegans</i>	<i>Danio rerio</i>	<i>Drosophila melanogaster</i>	<i>Ephydatia fluviatilis</i>	<i>Haliotis rufescens</i>	<i>Nematostella vectensis</i>	<i>Ruditapes philippinarum</i>	<i>Schmidtea mediterranea</i>	<i>Xenopus tropicalis</i>	
Nanos	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	IPR024161
	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	IPR008705
	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	IPR038129
Vasa	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	IPR001650
	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	IPR011545
	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	IPR014001
	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	IPR014014
	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	IPR027417
	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	IPR000629
Piwi	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	IPR036397
	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	IPR003100
	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	IPR036085
	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	IPR003165
	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	IPR012337
Boule	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	IPR037366
	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	IPR000504
	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	IPR034988
	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	IPR012677
	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	IPR035979
Bruno	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	IPR000504
	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	IPR034196
	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	IPR012677
	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	IPR035979
Pumilio	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	IPR033133
	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	IPR033712
	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	IPR011989
	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	IPR016024
	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	IPR001313
Tudor	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	Light blue	IPR002999

Additional file 1: Figure S1. GMP genes-associated IPR codes in germline-related samples. The table represents presence (light blue) or absence (light grey) in different species (columns) of IPR codes annotated for some representative GMP genes (whose transcript upregulation is depicted in Figure 2 of the main text). Considering associated domains and families rather than whole sequence homology improved the signal: for instance, virtually all domains belonging to *vasa* are biased in germline-related samples of all species, even if we could not observe *vasa* homologue upregulation for *C. elegans* and *H. rufescens* (Figure 2 of the main text).



Additional file 1: Figure S2. Counts of co-upregulated OGs for all combinations of species. Each row represents the number of OGs that included upregulated germline-related transcripts in a precise number of species (from 2 to 9). For example, first row: 1803 OGs included germline-related upregulated sequences belonging to 2 species only (counting any possible 2-species combination). On the right the deviation from expected random distributions for the combinations of the corresponding number of species is reported: positive deviation from expectation is depicted in blue, negative deviation in red. For instance: the number of observed co-upregulated OGs in 4 species (any 4 species and only 4 species) was lower than expected; the number of observed co-upregulated OGs in 8 species (any 8 species and only 8 species) was higher than expected.

Additional file 1: Figure S3 (figure in previous page). Co-enriched GO terms (Biological Processes) in 6 or more species. The table represents presence (light blue) or absence (light grey) in different species (columns) of GO terms enriched in more than 2/3 of the data set.

	<i>Caenorhabditis elegans</i>	<i>Danio rerio</i>	<i>Drosophila melanogaster</i>	<i>Ephydatia fluviatilis</i>	<i>Haliotis rufescens</i>	<i>Nematostella vectensis</i>	<i>Ruditapes philippinarum</i>	<i>Schmidtea mediterranea</i>	<i>Xenopus tropicalis</i>	
GO:0003678	Light Blue	Light Blue	Light Blue	Light Blue	Light Grey	Light Blue	Light Blue	Light Blue	Light Blue	DNA helicase activity
GO:0003684	Light Blue	Light Grey	Light Blue	Light Blue	Light Grey	Light Grey	Light Blue	Light Blue	Light Blue	damaged DNA binding
GO:0004386	Light Blue	Light Blue	Light Blue	Light Blue	Light Grey	Light Blue	Light Blue	Light Blue	Light Blue	helicase activity
GO:0004518	Light Blue	Light Blue	Light Blue	Light Blue	Light Grey	Light Blue	Light Blue	Light Blue	Light Blue	nuclease activity
GO:0004519	Light Blue	Light Blue	Light Blue	Light Blue	Light Grey	Light Blue	Light Blue	Light Blue	Light Blue	endonuclease activity
GO:0004527	Light Blue	Light Blue	Light Blue	Light Blue	Light Grey	Light Blue	Light Blue	Light Blue	Light Blue	exonuclease activity
GO:0008094	Light Grey	Light Blue	Light Blue	Light Blue	Light Grey	Light Blue	Light Blue	Light Blue	Light Blue	DNA-dependent ATPase activity
GO:0008170	Light Grey	Light Blue	Light Blue	Light Blue	Light Grey	Light Blue	Light Blue	Light Blue	Light Blue	N-methyltransferase activity
GO:0008173	Light Grey	Light Blue	Light Blue	Light Blue	Light Grey	Light Blue	Light Blue	Light Blue	Light Blue	RNA methyltransferase activity
GO:0008276	Light Grey	Light Blue	Light Blue	Light Blue	Light Grey	Light Blue	Light Blue	Light Blue	Light Blue	protein methyltransferase activity
GO:0008536	Light Grey	Light Grey	Light Blue	Light Blue	Light Grey	Light Blue	Light Blue	Light Blue	Light Blue	Ran GTPase binding
GO:0008757	Light Grey	Light Blue	Light Blue	Light Blue	Light Grey	Light Blue	Light Blue	Light Blue	Light Blue	S-adenosylmethionine-dependent methyltransferase activity
GO:0009982	Light Grey	Light Blue	Light Blue	Light Blue	Light Grey	Light Blue	Light Blue	Light Blue	Light Blue	pseudouridine synthase activity
GO:0016273	Light Grey	Light Blue	Light Blue	Light Blue	Light Grey	Light Blue	Light Blue	Light Blue	Light Blue	arginine N-methyltransferase activity
GO:0016274	Light Grey	Light Blue	Light Blue	Light Blue	Light Grey	Light Blue	Light Blue	Light Blue	Light Blue	protein-arginine N-methyltransferase activity
GO:0030983	Light Blue	Light Grey	Light Blue	Light Blue	Light Grey	Light Blue	Light Blue	Light Blue	Light Blue	mismatched DNA binding
GO:0043139	Light Grey	Light Blue	Light Grey	Light Blue	Light Grey	Light Blue	Light Blue	Light Blue	Light Blue	5'-3' DNA helicase activity
GO:0140097	Light Blue	Light Blue	Light Blue	Light Grey	Light Grey	Light Blue	Light Blue	Light Blue	Light Blue	catalytic activity, acting on DNA

Additional file 1: Figure S4. Co-enriched GO terms (Molecular Functions) in 6 or more species. The table represents presence (light blue) or absence (light grey) in different species (columns) of GO terms enriched in more than 2/3 of the data set.

	<i>Caenorhabditis elegans</i>	<i>Danio rerio</i>	<i>Drosophila melanogaster</i>	<i>Ephydatia fluviatilis</i>	<i>Haliotis rufescens</i>	<i>Nematostella vectensis</i>	<i>Ruditapes philippinarum</i>	<i>Schmidtea mediterranea</i>	<i>Xenopus tropicalis</i>	
IPR000253										Forkhead-associated (FHA) domain
IPR000398										Thymidylate synthase
IPR000504										RNA recognition motif domain
IPR001352										Ribonuclease HII/HIII
IPR001357										BRCT domain
IPR001494										Importin-beta, N-terminal domain
IPR003750										Putative RNA methyltransferase
IPR004582										Checkpoint protein Rad17/Rad24
IPR004584										DNA repair protein Rad50, eukaryotes
IPR004803										tRNA-guanine transglycosylase
IPR005550										Kinetochore protein Ndc80
IPR006084										XPG/Rad2 endonuclease
IPR006085										XPG, N-terminal
IPR006086										XPG-I domain
IPR006133										DNA-directed DNA polymerase, family B, exonuclease domain
IPR006166										ERCC4 domain
IPR006554										Helicase-like, DEXD box c2 type
IPR007019										Surfeit locus 6
IPR007146										Sas10/Utp3/C1D
IPR007174										Las1
IPR007185										DNA polymerase alpha/delta/epsilon, subunit B
IPR007238										DNA primase large subunit, eukaryotic/archaeal
IPR007252										Nuclear pore protein 84/107
IPR007287										Soft-like protein
IPR007502										Helicase-associated domain
IPR007807										Helicase domain
IPR007846										RNA-recognition motif (RRM) Nup35-type domain
IPR007857										Protein arginine N-methyltransferase PRMT5
IPR008048										DNA replication licensing factor Mcm5
IPR008049										DNA replication licensing factor Mcm6
IPR008705										Nanos/Xcat2
IPR008918										Helix-hairpin-helix motif, class 2
IPR009361										RZZ complex, subunit Zw10
IPR010666										Zinc finger, GRF-type
IPR010920										LSM domain superfamily
IPR011023										Nop2p
IPR011145										Scavenger mRNA decapping enzyme, N-terminal
IPR011760										Pseudouridine synthase, TruD, insertion domain
IPR011989										Armadillo-like helical
IPR011990										Tetratricopeptide-like helical domain superfamily
IPR012677										Nucleotide-binding alpha-beta plait domain superfamily
IPR012978										Uncharacterised domain NUC173
IPR013026										Tetratricopeptide repeat-containing domain
IPR013083										Zinc finger, RING/FYVE/PHD-type
IPR013346										Ribonucleotide reductase, class 1, alpha subunit
IPR013562										tRNA(Met) cytidine acetyltransferase TmcA, N-terminal
IPR013748										Replication factor C, C-terminal
IPR013763										Cyclin-like
IPR013876										TFIIH p62 subunit, N-terminal
IPR014013										Helicase superfamily 1/2, ATP-binding domain, DinG/Rad3-type
IPR015088										Zinc finger, DNA-directed DNA polymerase, family B, alpha
IPR015163										Cdc6, C-terminal
IPR015408										Zinc finger, Mcm10/DnaG-type
IPR016558										DNA primase, large subunit, eukaryotic
IPR017389										Nucleoporin, NUP53
IPR019136										Transcription factor IIIC subunit 5, HTH domain
IPR019496										Nuclear fragile X mental retardation-interacting protein 1, conserved domain
IPR019544										Tetratricopeptide, SHNi-TPR domain
IPR019734										Tetratricopeptide repeat
IPR020103										Pseudouridine synthase, catalytic domain superfamily
IPR020472										G-protein beta WD-40 repeat
IPR020568										Ribosomal protein S5 domain 2-type fold
IPR020588										DNA recombination and repair protein RecA-like, ATP-binding domain
IPR020795										Origin recognition complex, subunit 3
IPR020796										Origin recognition complex, subunit 5
IPR022043										Chromatin assembly factor 1 subunit A
IPR022100										Minichromosome loss protein Mcl1, middle region
IPR023211										DNA polymerase, palm domain superfamily
IPR023273										RNA (C5-cytosine) methyltransferase, NOP2
IPR023451										Thymidylate synthase/dCMP hydroxymethylase domain
IPR024166										Ribosomal RNA assembly KRR1
IPR024567										Ribonuclease HII/HIII domain
IPR024576										Ribosomal RNA methyltransferase Spb1, domain of unknown function DUF381
IPR024639										DNA polymerase epsilon subunit B, N-terminal
IPR024647										DNA polymerase alpha catalytic subunit, N-terminal domain
IPR024790										Anaphase-promoting complex subunit 4 long domain
IPR026851										DNA replication ATP-dependent helicase/nuclease Dna2
IPR027408										PNPase/RNase PH domain superfamily
IPR027973										Protein of unknown function DUF4602
IPR028077										Ubiquitin/SUMO-activating enzyme ubiquitin-like domain
IPR028589										AdoMet-dependent tRNA methyltransferase Spb1-like
IPR029026										tRNA (guanine-N1-)methyltransferase, N-terminal
IPR029028										Alpha/beta knot methyltransferases
IPR029190										Ribosomal RNA-processing protein 14/surfeit locus protein 6, C-terminal domain
IPR029448										Fanconi anaemia protein FANCD2
IPR030475										Ribonucleotide reductase small subunit, active site
IPR031341										Ribosomal RNA small subunit methyltransferase F, N-terminal
IPR032682										Condensin complex subunit 1, C-terminal
IPR033310										Mms4/EME1/EME2
IPR033809										USP39
IPR033909										Ribonucleotide reductase small subunit
IPR034159										SF3B4, RNA recognition motif 2
IPR035247										PRMT5, TIM barrel domain
IPR035248										PRMT5, oligomerisation domain
IPR035979										RNA-binding domain superfamily
IPR036236										Zinc finger C2H2 superfamily
IPR036279										5'-3' exonuclease, C-terminal domain superfamily
IPR036322										WD40-repeat-containing domain superfamily
IPR036345										Exoribonuclease, PH domain 2 superfamily
IPR036390										Winged helix DNA-binding domain superfamily
IPR036855										Zinc finger, CCH-type superfamily
IPR036926										Thymidylate synthase/dCMP hydroxymethylase superfamily
IPR037624										Nuclear pore complex protein Nup133-like
IPR037626										Nucleoporin Nup37
IPR037942										RuvB-like helicase 2
IPR038256										DNA polymerase alpha, zinc finger domain superfamily
IPR038273										Ndc80 domain superfamily
IPR040184										Minichromosome maintenance protein 10
IPR040454										Transcription factor IIIC subunit Tfc1/Sfc1
IPR043519										Nucleotidyltransferase superfamily

Additional file 1: Figure S6 (figure in previous page). Co-enriched IPR codes in 6 species. The table represents presence (light blue) or absence (light grey) in different species (columns). Code annotation that refer to strictly DNA-related or proliferative activities are highlighted in bold. Codes associated to DNA repair are highlighted in red.

Additional file 1: Table S1. Species in the data set and accession codes of Genome assemblies.

When the proteome was retrieved from an online source different from NCBI, the whole accession link is present. Phyla are in alphabetical order, with the four non-Metazoa phyla at the bottom of the table.

Phylum	Species	Genome code / database
ANNELIDA	<i>Capitella teleta</i>	GCA_000328365.1
	<i>Dimorphilus gyrocoliliatus</i>	GCA_904063045.1
	<i>Helobdella robusta</i>	GCF_000326865.1
	<i>Owenia fusiformis</i>	GCA_903813345.1
ARTHROPODA	<i>Aphis gossypii</i>	GCF_004010815.1
	<i>Apis mellifera</i>	GCF_003254395.2
	<i>Centruroides sculpturatus</i>	GCF_000671375.1
	<i>Cloeon dipterum</i>	GCA_902829235.1
	<i>Cryptotermes secundus</i>	GCF_002891405.2
	<i>Ctenocephalides felis</i>	GCF_003426905.1
	<i>Daphnia magna</i>	GCF_003990815.1
	<i>Dermatophagoides pteronyssinus</i>	GCF_001901225.1
	<i>Drosophila melanogaster</i>	GCF_000001215.4
	<i>Eurytemora affinis</i>	GCF_000591075.1
	<i>Folsomia candida</i>	GCF_002217175.1
	<i>Hyalella azteca</i>	GCF_000764305.1
	<i>Ixodes scapularis</i>	GCF_002892825.2
	<i>Lepeophtheirus salmonis</i>	GCF_016086655.3
	<i>Limulus polyphemus</i>	GCF_000517525.1
	<i>Nymphon striatum</i>	GCA_016618385.1
	<i>Parasteatoda tepidariorum</i>	GCF_000365465.2
	<i>Penaeus vannamei</i>	GCF_003789085.1
	<i>Sitophilus oryzae</i>	GCF_002938485.1
<i>Tetranychus urticae</i>	GCF_000239435.1	
<i>Varroa destructor</i>	GCF_002443255.1	
BRACHIPODA	<i>Lingula anatina</i>	GCF_001039355.2

BRIOZOA	<i>Bugula neritina</i>	GCA_010799875.2
CHORDATA	<i>Acipenser ruthenus</i>	GCF_010645085.1
	<i>Amblyraja radiata</i>	GCF_010909765.1
	<i>Branchiostoma floridae</i>	GCF_000003815.2
	<i>Ciona intestinalis</i>	GCF_000224145.3
	<i>Danio rerio</i>	GCF_000002035.6
	<i>Gallus gallus</i>	GCF_000002315.6
	<i>Gekko japonicus</i>	GCF_001447785.1
	<i>Homo sapiens</i>	GCF_000001405.39
	<i>Oikopleura dioica</i>	GCA_000209555.1
	<i>Petromyzon marinus</i>	GCF_010993605.1
	<i>Styela clava</i>	GCF_013122585.1
	<i>Xenopus tropicalis</i>	GCF_000004195.4
CNIDARIA	<i>Acropora digitifera</i>	GCF_000222465.1
	<i>Actinia tenebrosa</i>	GCF_009602425.1
	<i>Aurelia aurita</i>	https://marinegenomics.oist.jp/aurelia_aurita/
	<i>Clytia hemisphaerica</i>	http://ftp.ensemblgenomes.org/pub/metazoa/release-52/fasta/clytia_hemisphaerica_gca902728285
	<i>Dendronephthya gigantea</i>	GCF_004324835.1
	<i>Exaiptasia diaphana</i>	GCF_001417965.1
	<i>Henneguya salminicola</i>	GCA_009887335.1
	<i>Hydra vulgaris</i>	GCF_000004095.1
	<i>Morbakka virulenta</i>	https://marinegenomics.oist.jp/morbakka_virulenta/
	<i>Myxobolus squamalis</i>	GCA_010108815.1
	<i>Nematostella vectensis</i>	GCF_000209225.1
	<i>Orbicella faveolata</i>	GCF_002042975.1
	<i>Pocillopora damicornis</i>	GCF_003704095.1
	<i>Stylophora pistillata</i>	GCF_002571385.1
	<i>Thelohanellus kitauei</i>	GCA_000827895.1
CTENOPHORA	<i>Hormiphora californiensis</i>	https://github.com/conchoecia/hormiphora
	<i>Mnemiopsis leidyi</i>	https://research.nhgri.nih.gov/mnemiopsis
ECHINODERMATA	<i>Anneissia japonica</i>	GCF_011630105.1
	<i>Apostichopus japonicus</i>	GCA_002754855.1
	<i>Asterias rubens</i>	GCF_902459465.1
	<i>Strongylocentrotus purpuratus</i>	GCF_000002235.5
HEMICHORDATA	<i>Ptychodera flava</i>	https://marinegenomics.oist.jp/acornworm/
	<i>Saccoglossus kowalevskii</i>	GCF_000003605.2
MOLLUSCA	<i>Aplysia californica</i>	GCF_000002075.1
	<i>Biomphalaria glabrata</i>	GCF_000457365.1
	<i>Crassostrea gigas</i>	GCF_902806645.1
	<i>Lottia gigantea</i>	GCF_000327385.1
	<i>Mizuhopecten yessoensis</i>	GCF_002113885.1
	<i>Octopus bimaculoides</i>	GCF_001194135.1
	<i>Pomacea canaliculata</i>	GCF_003073045.1
NEMATODA	<i>Aphelenchus avenae</i>	GCA_020875895.1
	<i>Brugia malayi</i>	GCF_000002995.3

	<i>Bursaphelenchus okinawaensis</i>	GCA_904066225.2
	<i>Caenorhabditis elegans</i>	GCF_000002985.6
	<i>Loa loa</i>	GCF_000183805.1
	<i>Necator americanus</i>	GCF_000507365.1
	<i>Plectus sambesii</i>	GCA_002796945.1
	<i>Strongyloides ratti</i>	GCF_001040885.1
	<i>Trichinella spiralis</i>	GCF_000181795.1
NEMERTEA	<i>Notospermus geniculatus</i>	https://marinegenomics.oist.jp/nge_v2/
ORTHONECTIDA	<i>Intoshia linei</i>	GCA_001642005.1
PHORONIDA	<i>Phoronis australis</i>	https://marinegenomics.oist.jp/pau_v2/
PLACOZOA	<i>Trichoplax adhaerens</i>	GCF_000150275.1
	<i>Trichoplax spH2</i>	GCA_003344405.1
PLATYHELMINTHES	<i>Dibothriocephalus latus</i>	GCA_900617775.1
	<i>Echinococcus granulosus</i>	GCF_000524195.1
	<i>Fasciola hepatica</i>	GCA_002763495.2
	<i>Macrostomum lignano</i>	GCA_002269645.1
	<i>Opisthorchis viverrini</i>	GCF_000715545.1
	<i>Protopolystoma xenopodis</i>	GCA_900617795.1
	<i>Schistosoma mansoni</i>	GCF_000237925.1
	<i>Schmidtea mediterranea</i>	(MSG.1)
PORIFERA	<i>Amphimedon queenslandica</i>	GCF_000090795.1
	<i>Ephydatia muelleri</i>	https://spaces.facsce.ualberta.ca/ephybase/
PRIAPULIDA	<i>Priapulul caudatus</i>	GCF_000485595.1
MESOOZOA	<i>Dicyema japonicum</i>	GCA_011109175.1
ROTIFERA	<i>Adineta ricciae</i>	GCA_905250095.1
	<i>Brachionus calyciflorus</i>	GCA_905250105.1
	<i>Didymodactylos carnosus</i>	GCA_905250885.1
	<i>Rotaria socialis</i>	GCA_905332285.1
TARDIGRADA	<i>Hypsibius dujardini</i>	GCA_002082055.1
	<i>Ramazzottius varieornatus</i>	GCA_001949185.1
XENACOELOMORPHA	<i>Praesagittifera naikaiensis</i>	http://gigadb.org/dataset/100564
	<i>Xenoturbella bocki</i>	https://figshare.com/articles/dataset/Genome_of_Xenoturbella_bocki/
CHOANOFLLAGELLATA	<i>Monosiga brevicollis</i>	http://ftp.ensemblgenomes.org/pub/protists/release-52/fasta/protists_choanoflagellida1_collection/monosiga_brevicollis_mx1_gca_000002865/
	<i>Salpingoeca rosetta</i>	GCA_000188695.1
FILASTEREA	<i>Capsaspora owczarzaki</i>	GCF_000151315.2
ICHTHYOSPOREA	<i>Chromosphaera perkinsii</i>	https://figshare.com/articles/dataset/Genome_-_Chromosphaera_perkinsii/
	<i>Ichthyophonus hoferi</i>	https://figshare.com/articles/dataset/Genome_-_Ichthyophonus_hoferi/
	<i>Pirum gemmata</i>	https://figshare.com/articles/dataset/Genome_-_Pirum_gemmata/
	<i>Sphaeroforma arctica</i>	GCF_001186125.1
PLURIFORMEA	<i>Corallochytrium limacisporum</i>	https://figshare.com/articles/dataset/Genome_-_Corallochytrium_limacisporum/