

S4 Table. Species included in comparative analysis.

Species name	Common name	Phylum	Genome span (Mb)	Scaffold N50 (kb)	Number of genes ¹	Accession
<i>Aplysia californica</i>	California sea hare	Mollusca	927.3	91.7 kb	21,312	GCA_000002075.1 [1]
<i>Biomphalaria glabrata</i>	Freshwater snail	Mollusca	916.4	48.1 kb	28,551	GCA_000457365.1 [2]
<i>Caenorhabditis elegans</i>	Roundworm	Nematoda	100.3	17.5 kb	20,222	GCF_000002985.6 [3]
<i>Capitella teleta</i>	Annelid worm	Annelida	333.3	188.4 kb	32,175	GCA_000328365.1 [4]
<i>Crassostrea gigas</i>	Pacific oyster	Mollusca	557.7	401.7 kb	26,101	GCA_000297895.1 [5]
<i>Drosophila melanogaster</i>	Fruit fly	Arthropoda	143.7	25,286.9 kb	13,931	GCA_000001215.4 [6]
<i>Helobdella robusta</i>	Leech	Annelida	235.4	3,060.2 kb	23,432	GCA_000326865.1 [4]
<i>Intoschia linei</i>	NA	Orthonectida	41.6	26.3 kb	8,724	GCA_001642005.1 [7]
<i>Lingula anatina</i>	Lampshell	Brachiopoda	425.5	294.5 kb	34,105	GCA_001039355.1 [8]
<i>Lottia gigantea</i>	Owl limpet	Mollusca	359.5	1,870.1 kb	23,349	GCA_000327385.1 [4]

<i>Octopus bimaculoides</i>	Octopus	Mollusca	2338.2	475.2 kb	33,609	GCA_001194135.1 [9]
<i>Ramazzottius varieornatus</i>	Water bear	Tardigrada	55.8	474.0 kb	19,521	GCA_001949185.1 [10]
<i>Schistosoma haematobium</i>	Blood fluke	Platyhelminthes	375.9	317.5 kb	13,073	GCA_000699445.1 [11]

¹Inferred from Ensembl Metazoa or the literature.

References

1. Broad Institute [Internet]. [cited 2016]. Available: <https://www.broadinstitute.org/aplysia/aplysia-genome-project>
2. Adema CM, Hillier LW, Jones CS, Loker ES, Knight M, Minx P, et al. Whole genome analysis of a schistosomiasis-transmitting freshwater snail. *Nat Commun.* 2017;8: 15451.
3. C. elegans Sequencing Consortium. Genome sequence of the nematode *C. elegans*: a platform for investigating biology. *Science.* 1998;282: 2012–2018.
4. Simakov O, Marletaz F, Cho S-J, Edsinger-Gonzales E, Havlak P, Hellsten U, et al. Insights into bilaterian evolution from three spiralian genomes. *Nature.* 2013;493: 526–531.
5. Zhang G, Fang X, Guo X, Li L, Luo R, Xu F, et al. The oyster genome reveals stress adaptation and complexity of shell formation. *Nature.* 2012;490: 49–54.
6. Adams MD, Celiker SE, Holt RA, Evans CA, Gocayne JD, Amanatides PG, et al. The genome sequence of *Drosophila melanogaster*. *Science.* 2000;287: 2185–2195.
7. Mikhailov KV, Slyusarev GS, Nikitin MA, Logacheva MD, Penin AA, Aleoshin VV, et al. The Genome of *Intosha linea* Affirms Orthonectids as Highly Simplified Spiraliens. *Curr Biol.* 2016;26: 1768–1774.
8. Luo Y-J, Takeuchi T, Koyanagi R, Yamada L, Kanda M, Khalturina M, et al. The *Lingula* genome provides insights into brachiopod evolution and the origin of phosphate biomineralization. *Nat Commun.* 2015;6: 8301.
9. Albertin CB, Simakov O, Mitros T, Wang ZY, Pungor JR, Edsinger-Gonzales E, et al. The octopus genome and the evolution of cephalopod neural and morphological novelties. *Nature.* 2015;524: 220–224.
10. Hashimoto T, Horikawa DD, Saito Y, Kuwahara H, Kozuka-Hata H, Shin-I T, et al. Extremotolerant tardigrade genome and improved radiotolerance of human cultured cells by tardigrade-unique protein. *Nat Commun.* 2016;7: 12808.
11. Young ND, Jex AR, Li B, Liu S, Yang L, Xiong Z, et al. Whole-genome sequence of *Schistosoma haematobium*. *Nat Genet.* 2012;44: 221–225.

15. Young ND, Jex AR, Li B, Liu S, Yang L, Xiong Z, et al. Whole-genome sequence of *Schistosoma haematobium*. *Nat Genet*. 2012;44: 221–225.