

PART ONE

Table SMO. Dataset collection for the genome projects of 461 eukaryotic species

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Genome-wide features of introns are evolutionary decoupled among themselves and from genome size throughout Eukarya.

<https://www.biorxiv.org/content/early/2018/03/18/283549>

Number	Relative taxonomic order	Species name	Abbreviation	Kingdom	Estimated genome size (published)	Assembled genome size (available file)	Genome sequence status (published)	Number of protein-coding genes (published)	Number of protein-coding genes (available file)	Database collection	Reference for genome publication	Download sequence link
1	1	<i>Thecamonas trahens</i>	tht	Protist	28.68	28.68	assembly	10,543	10544	ensembl	The Broad Institute: https://protists.ensembl.org/Thecamonas_trahens_atcc_50062_gca_000142905/info/Annotation/#assembly Dudin O., et al. (2019). A unicellular relative of animals generates a layer of polarized cells by actomyosin-dependent cellularization. <i>eLife</i> 8:e49801.	https://protists.ensembl.org/Thecamonas_trahens_atcc_50062_gca_000142905/info/index.html
2	2	<i>Sphaeroforma arctica</i>	sar	Protist	121.59	121.59	assembly	18,213	18319	genbank	Sebé-Pedrós A., et al. (2016). The Dynamic Regulatory Genome of Capsaspora and the Origin of Animal Multicellularity. <i>Cell</i> , 165: 1224-1237.	https://www.ncbi.nlm.nih.gov/bioproject/?term=PRJDB8474
3	3	<i>Capsaspora owczarzaki</i>	cow	Protist	28.00	27.97	assembly	8,657	8758	broadi	Fairclough S.R., et al. (2013). Premetazoan genome evolution and the regulation of cell differentiation in the choanoflagellate <i>Salpingoeca rosetta</i> . <i>Genome Biology</i> , 14:R15.	http://www.broadinstitute.org/annotation/genome/multicellularity_project/GenomeDescriptions.html#%3C%3ECapsaspora_owczarzaki%3C%3E_ATCC_30864
4	4	<i>Salpingoeca rosetta</i>	sro	Protist	55.00	55.44	assembly	11,629	11629	broadi	King N., et al. (2008). The genome of the choanoflagellate <i>Monosiga brevicollis</i> and the origin of metazoans. <i>Nature</i> , 451:783-8.	http://genome.jgi-psf.org/Monbr1/Monbr1.home.html
5	5	<i>Monosiga brevicollis</i>	mbr	Protist	41.60	41.63	assembly	9,196	9196	jgi	Ryan J.F., et al. (2013). The Genome of the Ctenophore <i>Mnemiopsis leidyi</i> and Its Implications for Cell Type Evolution. <i>Science</i> , 342(6164): 1242592.	http://research.ncbi.nih.gov/mnemiopsis/
6	6	<i>Mnemiopsis leidyi</i>	mle	Metazoa	303.18	155.88	assembly	16,645	16058	ensembl	Srivastava M., et al. (2010). The <i>Amphimedon queenslandica</i> genome and the evolution of animal complexity. <i>Nature</i> , 466: 720-726.	http://metazoa.ensembl.org/Amphimedon_queenslandica/info/Index.html
7	7	<i>Amphimedon queenslandica</i>	aqu	Metazoa	167.00	166.68	assembly	24,743	29883	jgi	Srivastava M., et al. (2010). The Trichoplax genome and the nature of placozoans. <i>Nature</i> 454: 955-960.	http://genome.jgi-psf.org/Triad1/Triad1.home.html
8	8	<i>Trichoplax adhaerens</i>	tad	Metazoa	39.12	105.63	assembly	11,520	11518	coge	Shinzato C., et al. (2014). Using the <i>Acropora digitifera</i> genome to understand coral responses to environmental change. <i>Nature</i> 476: 320-323.	https://www.ncbi.nlm.nih.gov/genome/annotation_euk/Acropora_digitifera100/
9	9	<i>Acropora digitifera</i>	adi	Metazoa	420.00	412.16	assembly	23,700	24910	oistip	Putnam N.H., et al. (2007). Sea anemone genome reveals ancestral eumetazoan gene repertoire and genomic organization. <i>Science</i> , 317: 86-94.	http://genome.jgi-psf.org/Nemve1/Nemve1.home.html
10	10	<i>Nematostella vectensis</i>	nve	Metazoa	224.94	356.61	assembly	27,273	27273	jgi	Chapman J.A., et al. (2010). The dynamic genome of <i>Hydra</i> . <i>Nature</i> , 464: 592-596.	https://research.ncbi.nih.gov/hydra/
11	11	<i>Hydra magnipapillata</i> (<i>Hydra vulgaris</i>)	hma	Metazoa	1,050.00	852.16	assembly	20,000	20000	metazome	Yang Y., et al. (2014). The genome of the myxosporean <i>Thelohanellus kitai</i> shows adaptations to nutrient acquisition within its fish host. <i>Genome Biol Evol</i> . 6: 3182-98.	https://www.ncbi.nlm.nih.gov/assembly/GCA_000827895.1/
12	12	<i>Thelohanellus kitai</i>	tki	Metazoa	188.50	150.35	assembly	16,638	15020	ensembl	Flot J.F., et al. (2013). Genetic evidence for ameiotic evolution in the bdelloid rotifer <i>Adinetina vaga</i> . <i>Nature</i> , 500: 453-457.	http://www.genoscope.cns.fr/adinet/a/gbrowse/adinet/
13	13	<i>Adinetina vaga</i>	ava	Metazoa	244.50	218.07	assembly	49,300	49300	genoscope	Wang X., et al. (2011). The draft genome of the carcinogenic human liver fluke <i>Clonorchis sinensis</i> . <i>Genome Biology</i> 12:R107. Huang Y., et al. (2013). The Carcinogenic Liver Fluke, <i>Clonorchis sinensis</i> : New Assembly, Rerannotation and Analysis of the Genome and Characterization of Tissue Transcriptomes. <i>PLoS ONE</i> , 8(1): e54732.	https://www.ncbi.nlm.nih.gov/genome/?term=txid79923[Organism:noexp]
14	14	<i>Clonorchis sinensis</i>	cls	Metazoa	644.00	536.8	assembly	16,258	13634	coge	Berriman M., et al. (2009). The genome of the blood fluke <i>Schistosoma mansoni</i> . <i>Nature</i> , 460: 352-8.	http://www.sanger.ac.uk/resources/downloads/helminths/schistosoma-mansoni.html
15	15	<i>Schistosoma mansoni</i>	sma	Metazoa	254.28	364.53	chromosomes	11,809	8564	sanger	Simakov O., et al. (2013). Insights into bilaterian evolution from three spiralian genomes. <i>Nature</i> , 493: 526-31.	http://www.sanger.ac.uk/resources/downloads/helminths/schistosoma-mansoni.html
16	16	<i>Helobdella robusta</i>	hro	Metazoa	352.08	235.38	assembly	32,389	23432	jgi	Simakov O., et al. (2013). Insights into bilaterian evolution from three spiralian genomes. <i>Nature</i> , 493: 526-31.	http://genome.jgi-psf.org/Helro1/Helro1.download.ftp.html
17	17	<i>Capitella teleta</i>	cte	Metazoa	324.00	333.72	assembly	23,400	32415	jgi	Simakov O., et al. (2013). Insights into bilaterian evolution from three spiralian genomes. <i>Nature</i> , 493: 526-31.	http://genome.jgi-psf.org/Capca1/Capca1.download.ftp.html
18	18	<i>Octopus bimaculoides</i>	oct	Metazoa	2,700.00	2338.19	assembly	33,638	33609	ensembl	Albertin C., et al. (2015). The octopus genome and the evolution of cephalopod neural and morphological novelties. <i>Nature</i> , 524: 220-224.	http://metazoa.ensembl.org/Octopus_bimaculoides/info/Index.html
19	19	<i>Pinctada fucata</i>	pfu	Metazoa	1,150.00	815.3	assembly	23,257	33306	oistip	Takeuchi T., et al. (2016). Bivalve-specific gene expansion in the pearl oyster genome: implications of adaptation to a sessile lifestyle. <i>Zoological Letters</i> , 2:3. Takeuchi T., et al. (2012). Draft Genome of the Pearl Oyster <i>Pinctada fucata</i> : A Platform for Understanding Bivalve Biology. <i>DNA Res</i> . 19: 117-130.	http://marinegenomics.oist.jp/pearl/viewer/download?project_id=20
20	20	<i>Crassostrea gigas</i>	cgi	Metazoa	637.00	557.72	assembly	28,027	26089	ensembl	Zhang G., et al. (2012). The oyster genome reveals stress adaptation and complexity of shell formation. <i>Nature</i> , 490: 49-54.	http://metazoa.ensembl.org/Crassostrea_gigas/info/Index.html
21	21	<i>Biomphalaria glabrata</i>	bg1	Metazoa	929.10	916.43	assembly	14,423	14141	vectorbase	Adema C.M., et al. (2017). Whole genome analysis of a schistosomiasis-transmitting freshwater snail. <i>Nature Communications</i> , 8:15451.	https://www.vectorbase.org/organisms/biomphalaria-glabrata
22	22	<i>Lottia gigantea</i>	lgi	Metazoa	420.54	359.51	assembly	23,800	23851	jgi	Simakov O., et al. (2013). Insights into bilaterian evolution from three spiralian genomes. <i>Nature</i> , 493: 526-31.	http://genome.jgi-psf.org/Lotgi1/Lotgi1.download.ftp.html
23	23	<i>Trichinella spiralis</i>	tsp	Metazoa	71.30	63.53	assembly	15,808	15461	ensembl	Mitreva M., et al. (2011). The draft genome of the parasitic nematode <i>Trichinella spiralis</i> . <i>Nature Genetics</i> , 43: 228-235.	https://www.ncbi.nlm.nih.gov/bioproject/PRJNA12603
24	24	<i>Pristionchus pacificus</i>	prp	Metazoa	166.26	169.75	assembly	23,500	29201	ensembl	Dieterich C., et al. (2008). The <i>Pristionchus pacificus</i> genome provides a unique perspective on nematode lifestyle and parasitism. <i>Nat Genet</i> , 40: 1193-8.	http://www.pristionchus.org/cgi-bin/index.pl
25	25	<i>Caenorhabditis elegans</i>	cel	Metazoa	92.91	100.27	chromosomes	19,099	20532	ensembl	The <i>C. elegans</i> Sequencing Consortium. (1998). Genome sequence of the nematode <i>C. elegans</i> : a platform for investigating biology. <i>Science</i> , 282: 2012-8.	http://www.sanger.ac.uk/research/projects/caenorhabditisgenomics/
26	26	<i>Strongyloides ratti</i>	srt	Metazoa	43.15	43.15	assembly	12,451	12449	ensembl	Hunt V., et al. (2016). The genomic basis of parasitism in the <i>Strongyloides</i> clade of nematodes. <i>Nature Genetics</i> , 48: 299-307.	http://www.sanger.ac.uk/resources/downloads/helminths/strongyloides-ratti.html

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27	27	<i>Ascaris suum</i>	asu	Metazoa	244.50	272.78	assembly	18,500	18542	gigadb	Jex A., et al. (2011). <i>Ascaris suum</i> draft genome. <i>Nature</i> , 479: 529–533.	http://parasite.wormbase.org/Ascaris_suum_prjna80881/info/Index/	
28	28	<i>Loa loa</i>	loa	Metazoa	91.40	86.81	assembly	14,907	16281	coge	Desjardins C., et al. (2013). Genomics of <i>Loa loa</i> , a Wolbachia-free filarial parasite of humans. <i>Nature Genetics</i> , 45: 495–500.	https://www.ncbi.nlm.nih.gov/bioproject/PRJNA37757	
29	29	<i>Brugia malayi</i>	bma	Metazoa	107.58	94.14	assembly	11,500	13439	ensembl	Ghedin E., et al. (2007). Draft genome of the filarial nematode parasite <i>Brugia malayi</i> . <i>Science</i> , 317:1756-60.	http://tools.neb.com/wolbachia/	
30	30	<i>Ixodes scapularis</i>	isc	Metazoa	2,100.00	1765.38	assembly	20,467	20486	vectorbase	Gulia-Nuss M., et al. (2015). Genomic insights into the <i>Ixodes scapularis</i> tick vector of Lyme disease. <i>Nature Communications</i> 7, Article number: 10507.	http://gsc.jcvi.org/projects/msc/ixodes_scapularis/	
31	31	<i>Metaseiulus occidentalis</i>	mcc	Metazoa	90.00	151.7	assembly	18,338	11430	genbank	Hoy M., et al. (2016). Genome sequencing of the phytoseiid predatory mite <i>Metaseiulus occidentalis</i> reveals completely attenuated Hox genes and super-dynamic intron evolution. <i>Genome Biol Evol</i> , 8: 1762-1775.	https://www.ncbi.nlm.nih.gov/assembly/GCF_000255335.2	
32	32	<i>Tetranychus urticae</i>	tur	Metazoa	78.24	90.82	assembly	18,414	18224	ensembl	Grbic M., et al. (2011). The genome of <i>Tetranychus urticae</i> reveals herbivorous pest adaptation. <i>Nature</i> , 478: 487–492.	http://metazoa.ensembl.org/Tetranychus_urtriae/info/Index	
33	33	<i>Stegodyphus mimosarum</i>	smm	Metazoa	2,738.70	2738.7	assembly	27,235	27135	ensembl	Sanggaard K., et al. (2014). Spider genomes provide insight into composition and evolution of venom and silk. <i>Nature Communications</i> 5, Article number: 3765.	http://metazoa.ensembl.org/Stegodyphus_mimosarum/info/Index	
34	34	<i>Sarcopeltis scabiei</i>	sas	Metazoa	98.00	56.25	assembly	10,471	10458	ensembl	Rider Jr S., et al. (2015). Draft genome of the scabies mite. <i>Parasites & Vectors</i> , 2015:585.	http://metazoa.ensembl.org/Sarcopeltis_scabiei/info/Index	
35	35	<i>Strigamia maritima</i>	stm	Metazoa	290.00	176.21	assembly	14,992	14992	ensembl	Chipman A., et al. (2014). The First Myriapod Genome Sequence Reveals Conservative Arthropod Gene Content and Genome Organisation in the Centipede <i>Strigamia maritima</i> . <i>PLoS Biol</i> , 12(11): e1002005.	http://metazoa.ensembl.org/Strigamia_maritima/info/Index	
36	36	<i>Lingula anatina</i>	lgn	Metazoa	426.49	425.49	assembly	27,068	34105	ensembl	Luo Y., et al. (2015). The Lingula genome provides insights into brachiopod evolution and the origin of phosphate biomineralization. <i>Nature Communications</i> 6, Article number: 8301.	http://metazoa.ensembl.org/Lingula_anatina/info/Index	
37	37	<i>Daphnia pulex</i>	dpp	Metazoa	234.72	197.26	assembly	30,907	30895	jgi	Colbourne J., et al. (2011). The Ecoresponsive Genome of <i>Daphnia pulex</i> . <i>Science</i> , 331: 555-561.	http://genome.jgi-psf.org/Dappu1/Dappu1.info.html	
38	38	<i>Acyrtosiphon pisum</i>	api	Metazoa	517.00	464.3	assembly	10,249	10249	coge	The International Aphid Genomics Consortium (2010). Genome Sequence of the Pea Aphid <i>Acyrtosiphon pisum</i> . <i>PLoS Biol</i> , 8(2): e1000313.	http://www.aphidbase.com/	
39	39	<i>Nilaparvata lugens</i>	nil	Metazoa	1,200.00	1128.52	assembly	27,571	36724	insectbase	Xue J., et al. (2014). Genomic analysis of the rice pest brown planthopper and its endosymbionts reveal complex complementary contributions for host adaptation. <i>Genome Biology</i> , 15:521.	https://www.ncbi.nlm.nih.gov/assembly/GCF_000757685.1/	
40	40	<i>Diaphorina citri</i>	dic	Metazoa	485.71	485.71	assembly	25,600	19311	CitrusGreening	Saha S., et al. (2017). Improved annotation of the insect vector of citrus greening disease: biocuration by a diverse genomic community. <i>Journal Database</i> , 2017:391079.	https://citrusgreening.org/ftp/genomes/Diaphorina_citri/assembly/DIACI_v2.0/	
41	41	<i>Rhodnius prolixus</i>	rpr	Metazoa	702.65	702.65	assembly	17,143	15426	vectorbase	Mesquita R.D., et al. (2015). Genome of <i>Rhodnius prolixus</i> , an insect vector of Chagas disease, reveals unique adaptations to hematophagy and parasite infection. <i>Proc Natl Acad Sci U S A</i> , 112: 14936-41.	https://www.vectorbase.org/genomes	
42	42	<i>Pediculus humanus</i>	phu	Metazoa	107.58	110.78	assembly	10,773	10773	coge	Kirkness E., et al. (2010). Genome sequences of the human body louse and its primary endosymbiont provide insights into the permanent parasitic lifestyle. <i>Proc Natl Acad Sci U S A</i> , 107: 12168-12173.	https://www.ncbi.nlm.nih.gov/assembly/Pediculus-humanus	
43	43	<i>Locusta migratoria</i>	loc	Metazoa	6,300.00	6905.71	assembly	17,307	17586	locustbase	Wang X., et al. (2013). The locust genome provides insight into swarming formation and long-distance flight. <i>Nature Communications</i> 5, Article number: 2957.	https://www.ncbi.nlm.nih.gov/bioproject/PRJNA185471	
44	44	<i>Zootermopsis nevadensis</i>	zoo	Metazoa	567.24	485.01	assembly	15,876	14610	ensembl	Terrapon N., et al. (2013). Molecular traces of alternative social organization in a termite genome. <i>Nature Communications</i> 5, Article number: 3636.	http://www.nature.com/ncomms/2014/140520/ncomms4636/full/ncomms4636.html	
45	45	<i>Nasonia vitripennis</i>	nvi	Metazoa	332.52	191.72	chromosomes	9,159	10842	coge	Werren J., et al. (2010). Functional and Evolutionary Insights from the Genomes of Three Parasitoid Nasonia Species. <i>Science</i> , 327: 343-348.	http://metazoa.ensembl.org/Nasonia_vitripennis/info/Index	
46	46	<i>Ceratosolen solmsi</i>	cso	Metazoa	294.00	277.06	assembly	11,412	9823	genbank	Xiao J.H., et al. (2013). Obligate mutualism within a host drives the extreme specialization of a fig wasp genome. <i>Genome Biology</i> , 14:R141.	https://www.ncbi.nlm.nih.gov/genome/?term=id326594Organism=noexp	
47	47	<i>Athalia rosae</i>	aro	Metazoa	163.84	163.84	assembly	12,074	10950	i5k	Oeyen J.P., et al. (2020). Savvy Genomes Reveal Evolutionary Acquisitions That Fostered the Mega-Radiation of Parasitoid and Eusocial Hymenoptera. <i>Genome Biology and Evolution</i> , 12(7): 1099–1188.	https://www.ncbi.nlm.nih.gov/assembly/GCF_000344095.2/	
48	48	<i>Micropeltis demolitor</i>	mde	Metazoa	247.00	250.53	assembly	18586	12377	genbank	Burke G.R., et al. (2018). Whole Genome Sequence of the Parasitoid Wasp <i>Micropeltis demolitor</i> That Harbors an Endogenous Virus Mutualist. <i>G3 (Bethesda)</i> 8(9):2875-2880.	https://www.ncbi.nlm.nih.gov/assembly/GCF_000572035.2	
49	49	<i>Fopius arisanus</i>	foa	Metazoa	153.63	153.63	assembly	10,991	10991	insectbase	Geib S.M., et al. (2017). Whole Genome Sequencing of the Braconid Parasitoid <i>Wopius arisanus</i> , an Important Biocontrol Agent of Pest Tepidit Fruit Flies. <i>G3 (Bethesda)</i> 7:2407-2411.	https://gold.igv.doe.gov/project?id=103389	
50	50	<i>Harpegnathos saltator</i>	hsl	Metazoa	296.70	296.78	assembly	18,564	18518	hymenopteradb	Bonasio R., et al. (2010). Genomic Comparison of the Ants <i>Camponotus floridanus</i> and <i>Harpegnathos saltator</i> . <i>Science</i> , 329: 1068-1071.	https://www.ncbi.nlm.nih.gov/genome/?term=id10380Organism=noexp	
51	51	<i>Camponotus floridanus</i>	cfl	Metazoa	224.94	234.88	assembly	17,064	17015	hymenopteradb	Bonasio R., et al. (2010). Genomic Comparison of the Ants <i>Camponotus floridanus</i> and <i>Harpegnathos saltator</i> . <i>Science</i> , 329: 1068-1071.	https://www.ncbi.nlm.nih.gov/genome/?term=id104421Organism=noexp	
52	52	<i>Megachile rotundata</i>	mro	Metazoa	330.00	272.66	assembly	10,788	10788	genbank	Kapheim K.M., et al. (2015). Social evolution: Genomic signatures of evolutionary transitions from solitary to group living. <i>Science</i> , 348(6239):1139-43.	https://www.ncbi.nlm.nih.gov/genome/annotation_euk/Megachile_rotundata/101/	
53	53	<i>Bombus terrestris</i>	bte	Metazoa	274.00	216.85	assembly	10,587	8333	coge	Sadd B., et al. (2015). The genomes of two key bumblebee species with primitive eusocial organization. <i>Genome Biology</i> , 16:76.	https://www.hgsi.bcm.edu/arthropods/bumble-bee-genome-project	
54	54	<i>Apis mellifera</i>	ame	Metazoa	262.00	219.63	chromosomes	10,157	9131	coge	Weinstock G.M., et al. (2006). Insights into social insects from the genome of the honeybee <i>Apis mellifera</i> . <i>Nature</i> , 443: 931-949.	http://genomevolution.org/CeGee/OrganismView.pl?org_desc=Eukaryota	
55	55	<i>Cerapachys biroi</i>	ceb	Metazoa	212.83	212.83	assembly	17,263	12148	genbank	Oxley P., et al. (2014). The Genome of the Clonal Raider Ant <i>Cerapachys biroi</i> . <i>Curr Biol</i> , 24: 451-458.	http://hymenopteragenome.org/cerapachys/	
56	56	<i>Linepithema humile</i>	ihu	Metazoa	254.28	219.81	assembly	16,331	16048	hymenopteradb	Smith C., et al. (2011). Draft genome of the globally widespread and invasive Argentine ant (<i>Linepithema humile</i>). <i>Proc Natl Acad Sci U S A</i> , 108: 5673-5678.	https://hymenoptera.elisklab.missouri.edu/genome_fasta	
57	57	<i>Pogonomyrmex barbatus</i>	pba	Metazoa	235.00	235.36	assembly	17,177	17177	hymenopteradb	Smith C., et al. (2010). Draft genome of the red harvester ant <i>Pogonomyrmex barbatus</i> . <i>Proc Natl Acad Sci U S A</i> , 108: 5667-5672.	https://hymenoptera.elisklab.missouri.edu/ant_genomes/pogo	
58	58	<i>Solenopsis invicta</i>	sin	Metazoa	484.20	352.69	assembly	16,569	17177	hymenopteradb	Wurn Y., et al. (2011). The genome of the fire ant <i>Solenopsis invicta</i> . <i>Proc Natl Acad Sci U S A</i> , 108: 5679-5684.	https://hymenoptera.elisklab.missouri.edu/ant_genomes/solenopsis	
59	59	<i>Wasmannia auropunctata</i>	wau	Metazoa	324.12	324.12	assembly	13,668	13668	hymenopteradb	Okinawa Institute of Science and Technology: https://www.ncbi.nlm.nih.gov/genome/annotation_euk/Wasmannia_auropunctata/100/ ; https://hymenoptera.elisklab.missouri.edu/genome_fasta	https://hymenoptera.elisklab.missouri.edu/genome_fasta	
60	60	<i>Acromyrmex echinatior</i>	aec	Metazoa	335.00	297.52	assembly	17,278	17277	hymenopteradb	Nygaard S., et al. (2011). The genome of the leaf-cutting ant <i>Acromyrmex echinatior</i> suggests key adaptations to advanced social life and fungus farming. <i>Genome Res</i> , 21: 1339-1348.	https://www.ncbi.nlm.nih.gov/bioproject/PRJNA62733	
61	61	<i>Atta cephalotes</i>	ace	Metazoa	303.18	317.67	assembly	18,093	18062	hymenopteradb	Suen G., et al. (2011). The Genome Sequence of the Leaf-Cutter Ant <i>Atta cephalotes</i> Reveals Insights into Its Obligate Symbiotic Lifestyle. <i>PLoS Genet</i> , 7(2): e1002007.	https://hymenoptera.elisklab.missouri.edu/genome_fasta	
62	62	<i>Vollenhovia emeryi</i>	vem	Metazoa	287.90	287.9	assembly	14,870	14870	hymenopteradb	Smith C.R., et al. (2015). How Do Genomes Create Novel Phenotypes? Insights from the Loss of the Worker Caste in Ant Social Parasites. <i>Mol Biol Evol</i> , 32(11):2919-31.	https://hymenoptera.elisklab.missouri.edu/genome_fasta	
63	63	<i>Tribolium castaneum</i>	tct	Metazoa	202.94	228.75	assembly	16,404	16525	ensembl	Richards S., et al. (2008). The genome of the model beetle and pest <i>Tribolium castaneum</i> . <i>Nature</i> , 452: 949-55.	https://hgsc.bcm.edu/arthropods/ed-flour-beetle-genome-project/-text-The%20Triboliumcastaneum%20castaneum%20Genome%20Sequence%20Genetic%20Model%20of%20the%20Flour%20Beetle%20Coeloptera	

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64	64	<i>Dendroctonus ponderosae</i>	dpn	Metazoa	208.00	252.85	assembly	13088	13088	ensembl	Kelting C., et al. (2013). Draft genome of the mountain pine beetle, <i>Dendroctonus ponderosae</i> Hopkins, a major forest pest. <i>Genome Biology</i> , 14:R27.	http://metazoa.ensembl.org/Dendroctonus_ponderosae/info/index	
65	65	<i>Plutella xylostella</i>	pxy	Metazoa	343.00	394.06	assembly	18,100	18071	gigadb	You M., et al. (2013). A heterozygous moth genome provides insights into herbivory and detoxification. <i>Nature Genetics</i> , 45: 220–225.	http://iae.fafu.edu.cn/DBM/	
66	66	<i>Bombyx mori</i>	bmo	Metazoa	513.45	480.78	assembly	14,300	14623	silkdb	Xia Q., et al. (2004). A draft sequence for the genome of the domesticated silkworm (<i>Bombyx mori</i>). <i>Science</i> , 306: 1937–40. & Mita K., et al. (2004). The genome sequence of silkworm, <i>Bombyx mori</i> . <i>DN A Res.</i> , 11: 27–35.	http://www.sciencemag.org/content/306/5703.abstract & http://dnaresearch.oxfordjournals.org/content/11/1/27.abstract	
67	67	<i>Manduca sexta</i>	msx	Metazoa	384.40	384.4	assembly	15,451	15542	insectbase	Kanost M.R., et al. (2016). Multifaceted biological insights from a draft genome sequence of the tobacco hornworm moth, <i>Manduca sexta</i> . <i>Insect Biochem Mol Biol.</i> , 76:118–147.	https://hgsc.bcm.edu/arthropods/tobacco-hornworm-genome-project	
68	68	<i>Operophtera brumata</i>	opb	Metazoa	638.21	638.21	assembly	16,912	16912	wageningen	Derkx M.F.L., et al. (2015). The Genome of Winter Moth (<i>Operophtera brumata</i>) Provides a Genomic Perspective on Sexual Dimorphism and Phenology. <i>Genome Biol Evol.</i> , 7(8):2321–2332.	https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4558862/	
69	69	<i>Chilo suppressalis</i>	chu	Metazoa	372.38	372.38	assembly	10,221	10132	insectbase	Ma W., et al. (2020). A chromosome-level genome assembly reveals the genetic basis of cold tolerance in a notorious rice insect pest, <i>Chilo suppressalis</i> . <i>Mol Ecol Resour.</i> , 20(1):268–282.	http://ento.njau.edu.cn/ChiloDB	
70	70	<i>Papilio glaucus</i>	pgl	Metazoa	376.00	375.99	assembly	15,695	15692	wageningen	Cong Q., et al. (2015). Tiger Swallowtail Genome Reveals Mechanisms for Speciation and Caterpillar Chemical Defense. <i>Cell Rep.</i> , 10(6):910–919.	https://www.ncbi.nlm.nih.gov/genome/?term=txid4577[Organism]:noexp]	
71	71	<i>Papilio polytes</i>	ppo	Metazoa	227.01	227.01	assembly	15,700	12165	genbank	Nishikawa H., et al. (2015). A genetic mechanism for female-limited Batesian mimicry in <i>Papilio</i> butterfly. <i>Nature Genetics</i> , 47:405–409.	https://www.ncbi.nlm.nih.gov/bioproject/291535	
72	72	<i>Lerema accius</i>	lac	Metazoa	310.00	298.17	assembly	17,400	17411	wageningen	Cong Q., et al. (2015). Skipper genome sheds light on unique phenotypic traits and phylogeny. <i>BMC Genomics</i> , 16:639.	http://prodatab.swmed.edu/LepDB/	
73	73	<i>Phoebeis sennae</i>	phs	Metazoa	345.44	345.44	assembly	16,500	16493	wageningen	Cong Q., et al. (2016). Speciation in Cloudless Sulphurs Gleaned from Complete Genomes. <i>Genome Biol Evol.</i> , 8: 915–931.	http://prodatab.swmed.edu/LepDB/pse/index.html	
74	74	<i>Calycopis cecrops</i>	cce	Metazoa	760.00	728.79	assembly	14,379	16456	wageningen	Cong Q., et al. (2016). Complete genomes of Hairstreak butterflies, their speciation, and nucleo-mitochondrial incongruence. <i>Scientific Reports</i> 6, Article number: 24863.	http://prodatab.swmed.edu/LepDB/cce/index.html	
75	75	<i>Danaus plexippus</i>	dpl	Metazoa	272.85	272.85	assembly	16,866	16254	ensembl	Zhan S., et al. (2011). The Monarch Butterfly Genome Yields Insights into Long-Distance Migration. <i>Cell</i> , 147: 1171–1185.	http://metazoa.ensembl.org/Danaus_plexippus/info/Index	
76	76	<i>Heliconius melpomene</i>	hme	Metazoa	293.40	273.79	assembly	12,669	12669	butterflydb	The Heliconius Genome Consortium (2012). Butterly genome reveals promiscuous exchange of mimicry adaptations among species. <i>Nature</i> , 487: 94–98.	http://monarchbase.umassmed.edu/resource.html	
77	77	<i>Melitaea cinxia</i>	mcx	Metazoa	389.89	389.89	assembly	16,667	16674	ensembl	Ahola V., et al. (2014). The Glanville fritillary genome retains an ancient karyotype and reveals selective chromosomal fusions in Lepidoptera. <i>Nature Communications</i> 5, Article number: 4737.	http://metazoa.ensembl.org/Melitaea_cinxia/info/Index	
78	78	<i>Phlebotomus papatasii</i>	ppt	Metazoa	363.77	363.77	assembly	11,164	11164	vectorbase	Washington University Genome Sequencing Center: https://www.ncbi.nlm.nih.gov/genome/109997/genome_assembly_id=39903 ; BCM-HGSC: https://www.hgsc.bcm.edu/arthropods/sand-fly-genome-project ;	https://vectorbase.org/vectorbase/apprecord/dataset/TMPTX_ppaplsraeliGenomeAssociatedData	
79	79	<i>Lutzomyia longipalpis</i>	llp	Metazoa	154.23	154.23	assembly	10,110	10110	vectorbase	Adams M.D., et al. (2000). The genome sequence of <i>Drosophila melanogaster</i> . <i>Science</i> , 287(5461):2185–95.	http://www.fruitfly.org/	
80	80	<i>Drosophila melanogaster</i>	dme	Metazoa	180.00	168.72	chromosomes	13,601	13937	ensembl	Holt R.A., et al. (2002). The Genome Sequence of the Malaria Mosquito <i>Anopheles gambiae</i> . <i>Science</i> , 298(5591):129–149.	https://www.ncbi.nlm.nih.gov/bioproject/?term=AAAB01000001	
81	81	<i>Anopheles gambiae</i>	aga	Metazoa	264.06	248.15	chromosomes	14,000	12446	coge	Marinotti O., et al. (2013). The Genome of <i>Anopheles darlingi</i> , the main neotropical malaria vector. <i>Nucl. Acids Res.</i> , 41(15):7387–7400.	http://labinfo.lncc.br/index.php/anopheles-darlingi	
82	82	<i>Anopheles darlingi</i>	ada	Metazoa	200.49	113.51	assembly	10,481	11430	coge	Nene V., et al. (2007). Genome Sequence of <i>Aedes aegypti</i> , a Major Arbovirus Vector. <i>Science</i> , 316(5832):1718–1723.	http://metazoa.ensembl.org/Aedes_aegypti/info/Index	
83	83	<i>Aedes aegypti</i>	aae	Metazoa	942.14	959.49	assembly	17,391	15141	coge	Peng C., et al. (2011). A Draft Genome Assembly of <i>Culex pipiens pallens</i> (Diptera: Culicidae) Using PacBio Sequencing. <i>Genome Biology and Evolution</i> , 13(3): evab005.	http://www.broadinstitute.org/annotation/genome/culex_pipiens.4/Home.html	
84	84	<i>Culex pipiens</i>	cpq	Metazoa	528.12	579.04	assembly	20,330	18883	coge	Kelley J., et al. (2013). Compact genome of the Antarctic midge is likely an adaptation to an extreme environment. <i>Nature Communications</i> 5, Article number: 4611.	http://metazoa.ensembl.org/Belgica_antarctica/info/Index	
85	85	<i>Belgica antarctica</i>	ban	Metazoa	105.00	89.57	assembly	13517	13510	ensembl	International Glossina Genome Initiative. (2014). Genome Sequence of the Tsetse Fly (<i>Glossina morsitans</i>): Vector of African Trypanosomiasis. <i>Science</i> , 344(6182):380–386.	http://www.vectorbase.org/genomes	
86	86	<i>Glossina morsitans</i>	gmr	Metazoa	528.12	366.2	assembly	12,354	12301	vectorbase	Scott J., et al. (2014). Genome of the house fly, <i>Musca domestica</i> L., a global vector of diseases with adaptations to a septi environment. <i>Genome Biology</i> , 15:466.	https://www.ncbi.nlm.nih.gov/assembly/GCF_000371365.1	
87	87	<i>Musca domestica</i>	mud	Metazoa	870.42	750.4	assembly	15,345	14402	genbank	Anstead C., et al. (2015). <i>Lucilia cuprina</i> genome unlocks parasitic fly biology to underpin future interventions. <i>Nature Communications</i> 6, Article number: 7344.	https://www.hgsc.bcm.edu/arthropods/sheep-blowfly-genome-project	
88	88	<i>Lucilia cuprina</i>	lcu	Metazoa	470.00	434.13	assembly	14,544	14452	ensembl	Zhao C., et al. (2015). A Massive Expansion of Effector Genes Underlies Gall-Formation in the Wheat Pest <i>Metylolla destructor</i> . <i>Curr Biol</i> , 25(9):613–620.	https://www.hgsc.bcm.edu/arthropods/hessian-fly-genome-project	
89	89	<i>Metylolla destructor</i>	myd	Metazoa	185.25	185.25	assembly	20,163	17355	insectbase	Noor lab at Duke: https://www.ncbi.nlm.nih.gov/genome/15767/genome_assembly_id=235253	http://metazoa.ensembl.org/Megaselia scalaris/info/Index	
90	90	<i>Megaselia scalaris</i>	msc	Metazoa	540.00	490.07	assembly	11,461	11461	ensembl	Simakov O., et al. (2015). Hemichordate genomes and deuterostome origins. <i>Nature</i> , 527(7619):459–65.	http://marinegenomics.oist.jp/acornworm/viewer?project_id=33	
91	91	<i>Ptychoderma flava</i>	pfl	Metazoa	1,228.70	1228.7	assembly	18,556	34638	oistjp	Simakov O., et al. (2015). Hemichordate genomes and deuterostome origins. <i>Nature</i> , 527(7619):459–65.	https://groups.oist.jp/molgenu/hemichordate-genomes,+https://www.hgsc.bcm.edu/other-invertebrates/acorn-worm-genome-project	
92	92	<i>Saccoglossus kowalevskii</i>	sko	Metazoa	757.64	757.64	assembly	19,270	11119	metazome	Sea Urchin Genome Sequencing Consortium, et al. (2006). The genome of the sea urchin <i>Strongylocentrotus purpuratus</i> . <i>Science</i> , 314(5801):941–52.	http://genome.ucsc.edu/cgi-bin/hgGateway?org=S.+purpuratus&db=stRur2	
93	93	<i>Strongylocentrotus purpuratus</i>	spu	Metazoa	870.42	912.55	assembly	23,300	28836	coge	Putman N.H., et al. (2008). The amphioxus genome and the evolution of the chordate karyotype. <i>Nature</i> , 453:1064–71.	http://genome.jgi-psf.org/Brafl1/Brafl1.home.html	
94	94	<i>Branchiostoma floridae</i>	bfl	Metazoa	522.00	521.9	assembly	21,900	28621	coge	Hee-Chan S., et al. (2001). Miniature Genome in the Marine Chordate <i>Oikopleura dioica</i> . <i>Science</i> , 294(5551):2506.	http://www.genoscope.cns.fr/externe/GenomeBrowser/Oikopleura/	
95	95	<i>Oikopleura dioica</i>	odi	Metazoa	68.46	70.47	assembly	15,000	17152	coge	Dehal P., et al. (2002). The draft genome of <i>Ciona intestinalis</i> : insights into chordate and vertebrate origins. <i>Science</i> , 298:2157–67.	http://genome.jgi-psf.org/Cioin2/Cioin2.home.html	
96	96	<i>Ciona intestinalis</i>	cin	Metazoa	195.60	115.21		15,852	16658	ensembl	Small K.S., et al. (2007). A haplome alignment and reference sequence of the highly polymorphic <i>Ciona savignyi</i> genome. <i>Genome Biol.</i> , 8(3): R41. Vinson J., et al., (2005). Assembly of polymorphic genomes: algorithms and application to <i>C. savignyi</i> . <i>Genome Research</i> , 15:1127–1135.	http://www.ensembl.org/Ciona_savignyi/info/Index	
97	97	<i>Ciona savignyi</i>	csg	Metazoa	174.00	177	assembly	11,616	11616	ensembl	Smith J., et al. (2012). Sequencing of the sea lamprey (<i>Petromyzon marinus</i>) genome provides insights into vertebrate evolution. <i>Nature Genetics</i> , 45: 415–421.	http://www.ensembl.org/Petromyzon_marinus/info/Index	
98	98	<i>Petromyzon marinus</i>	pma	Metazoa	2,019.57	885.55	assembly	26,046	10415	ensembl	Howe K., et al. (2013). The zebrafish reference genome sequence and its relationship to the human genome. <i>Nature</i> , 496: 498–503.	http://www.ensembl.org/Danio_reio/info/Index & http://zfin.org/cgi-bin/webdriver?Ival=aa-ZDB_home.asp & http://www.sanger.ac.uk/Projects/D_reio/	
99	99	<i>Danio rerio</i>	dre	Metazoa	1,817.12	1412.45	chromosomes	26,206	26237	ensembl	McGaugh S., et al. (2014). The catfish genome reveals candidate genes for eye loss. <i>Nature Communications</i> 5, Article number: 5307.	http://www.ensembl.org/Astyanax_mexicanus/info/Annotation	
100	100	<i>Astyanax mexicanus</i>	amx	Metazoa	1,190.00	1191.24	assembly	23,042	23650	genbank	Rondeau E., et al. (2014). The Genome and Linkage Map of the Northern Pike (<i>Esox lucius</i>): Conserved Synteny Revealed between the Salmonid Sister Group and the Neoteleoste. <i>PLoS ONE</i> , 9(7): e102089.	http://journals.plos.org/plosone/article?id=10.1371/journal.pone.0102089	
101	101	<i>Esox lucius</i>	elu	Metazoa	1,120.00	877.81	chromosomes	23,811	24136	genbank			

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102	102	<i>Gadus morhua</i>	gmo	Metazoa	909.54	832.11	assembly	22,154	20095	ensembl	Star B., et al. (2011). The genome sequence of Atlantic cod reveals a unique immune system. <i>Nature</i> , 477(7363):207-10.	http://ftp.ensembl.org/pub/current_fasta/gadus_morhua/	
103	103	<i>Tetraodon nigroviridis</i>	tni	Metazoa	420.54	358.6	chromosomes	27,918	19602	ensembl	Jailion O., et al. (2004). Genome duplication in the teleost fish Tetraodon nigroviridis reveals the early vertebrate proto-karyotype. <i>Nature</i> , 431:946-57.	http://www.ensembl.org/Tetraodon_nigroviridis/info/Index.html & http://www.genoscope.cns.fr/externe/tetranew/ ; http://moma.ki.au.dk/genome-mirror/cgi-bin/hgGateway?db=tetNig2	
104	104	<i>Takifugu rubripes (Fugu rubripes)</i>	tru	Metazoa	391.20	393.3	assembly	18,523	18523	ensembl	Aparicio S., et al. (2002). Whole-Genome Shotgun Assembly and Analysis of the Genome of Fugu rubripes. <i>Science</i> , 295(5585):1301-1310.	http://www.ensembl.org/Takifugu_rubripes/info/Index.html	
105	105	<i>Gasterosteus aculeatus</i>	gac	Metazoa	530.00	461.52	chromosomes	20,787	20787	ensembl	Jones F., et al. (2012). The genomic basis of adaptive evolution in threespine sticklebacks. <i>Nature</i> , 484: 55-61.	http://www.ensembl.org/Gasterosteus_aculeatus/info/Index.html ; http://broadinstitute.org/models/stickleback	
106	106	<i>Cynoglossus semilaevis</i>	cys	Metazoa	626.90	470.18	chromosomes	21,516	21474	genbank	Chen S., et al. (2013). Whole-genome sequence of a flatfish provides insights into ZW sex chromosome evolution and adaptation to a benthic lifestyle. <i>Nature Genetics</i> , 46: 253-260.	https://www.ncbi.nlm.nih.gov/bioproject/251742	
107	107	<i>Larimichthys crocea</i>	lcr	Metazoa	743.00	648.39	assembly	25,401	22274	genbank	Xiao S., et al. (2015). Gene map of large yellow croaker (<i>Larimichthys crocea</i>) provides insights into teleost genome evolution and conserved regions associated with growth. <i>Scientific Reports</i> 5, Article number: 18661.	https://www.ncbi.nlm.nih.gov/bioproject/354443	
108	108	<i>Oryzias latipes</i>	ola	Metazoa	1,009.79	868.98	chromosomes	20,141	19699	ensembl	Kasahara M., et al. (2007). The medaka draft genome and insights into vertebrate genome evolution. <i>Nature</i> , 447: 714-719.	http://www.ensembl.org/Oryzias_latipes/info/Index.html ; http://genome.ucsc.edu/cgi-bin/hgGateway?db=oryLat2	
109	109	<i>Xiphophorus maculatus</i>	xma	Metazoa	885.09	729.68	assembly	20,366	20379	ensembl	Schardt M., et al. (2013). The genome of the platyfish, <i>Xiphophorus maculatus</i> , provides insights into evolutionary adaptation and several complex traits. <i>Nature Genetics</i> , 45: 567-572.	http://www.ensembl.org/Xiphophorus_maculatus/info/Annotation.html	
110	110	<i>Notothenia coriiceps</i>	nco	Metazoa	636.60	636.6	assembly	47,712	24776	genbank	Shin S., et al. (2014). The genome sequence of the Antarctic bullhead notothen reveals evolutionary adaptations to a cold environment. <i>Genome Biology</i> , 15:468.	https://www.ncbi.nlm.nih.gov/bioproject/?term=66471	
111	111	<i>Oreochromis niloticus</i>	oni	Metazoa	1,060.00	927.38	assembly	24,559	21437	ensembl	Brawand D., et al. (2014). The genomic substrate for adaptive radiation in African cichlid fish. <i>Nature</i> , 513: 375-381.	https://www.ncbi.nlm.nih.gov/bioproject/?term=PRJNA59571	
112	112	<i>Neolamprologus brichardi</i>	neb	Metazoa	847.89	847.89	assembly	20,119	22678	genbank	Brawand D., et al. (2014). The genomic substrate for adaptive radiation in African cichlid fish. <i>Nature</i> , 513: 375-381.	https://www.ncbi.nlm.nih.gov/bioproject/232513	
113	113	<i>Astatotilapia burtoni</i>	abu	Metazoa	950.00	831.41	assembly	23436	23604	genbank	Brawand D., et al. (2014). The genomic substrate for adaptive radiation in African cichlid fish. <i>Nature</i> , 513: 375-381.	https://www.ncbi.nlm.nih.gov/bioproject/220165	
114	114	<i>Pundamilia nyererei</i>	pyn	Metazoa	830.13	830.13	assembly	20611	22854	genbank	Brawand D., et al. (2014). The genomic substrate for adaptive radiation in African cichlid fish. <i>Nature</i> , 513: 375-381.	https://www.ncbi.nlm.nih.gov/bioproject/220167	
115	115	<i>Metriaclima zebra</i>	mze	Metazoa	849.60	849.6	assembly	21673	23135	genbank	Brawand D., et al. (2014). The genomic substrate for adaptive radiation in African cichlid fish. <i>Nature</i> , 513: 375-381.	https://www.ncbi.nlm.nih.gov/bioproject/?term=PRJNA60369	
116	116	<i>Latimeria chalumnae</i>	ich	Metazoa	3,134.39	2860.58	assembly	19,569	19569	ensembl	Amemiya C., et al. (2013). The African coelacanth genome provides insights into tetrapod evolution. <i>Nature</i> , 496: 311-316.	https://www.ncbi.nlm.nih.gov/genome/?term=txid7897[Organism:noexp]	
117	117	<i>Nanorana parkeri</i>	npa	Metazoa	2,300.00	2071.74	assembly	23,408	22972	gigadb	Sun Y., et al. (2015). Whole-genome sequence of the Tibetan frog <i>Nanorana parkeri</i> and the comparative evolution of tetrapod genomes. <i>Proc Natl Acad Sci U S A</i> , 112(11): E1257-E1262.	https://www.ncbi.nlm.nih.gov/bioproject/344660	
118	118	<i>Xenopus laevis</i>	xla	Metazoa	3,110.04	2746.82	assembly	45,099	43025	coge	Session A.M., et al. (2016). Genome evolution in the allotetraploid frog <i>Xenopus laevis</i> . <i>Nature</i> , 538:336-343.	http://genome.jgi-psf.org/Xentr4/Xentr4.info.html & http://www.xenbase.org/other/statistics.do	
119	119	<i>Xenopus tropicalis</i>	xtr	Metazoa	1,700.00	1511.74	assembly	21,000	18442	ensembl	Hellsten U., et al. (2010). The Genome of the Western Clawed Frog <i>Xenopus tropicalis</i> . <i>Science</i> , 328(5978):633-636.	http://www.ensembl.org/Xenopus_tropicalis/info/Index.html	
120	120	<i>Ophisaurus gracilis</i>	ogr	Metazoa	1,710.00	1781.36	assembly	19,513	19513	gigadb	Song B., et al. (2015). A genome draft of the legless anguid lizard, <i>Ophisaurus gracilis</i> . <i>GigaScience</i> , 4:17.	http://gigadb.org/dataset/100119	
121	121	<i>Pogona vitticeps</i>	pov	Metazoa	1,816.12	1816.12	assembly	19,406	19406	gigadb	Georges A., et al. (2015). High-coverage sequencing and annotated assembly of the genome of the Australian dragon lizard <i>Pogona vitticeps</i> . <i>GigaScience</i> , 4:45.	http://iae.canberra.edu.au/html/pogona-genome.php , http://gigadb.org/dataset/100166	
122	122	<i>Anolis carolinensis</i>	acr	Metazoa	2,242.00	1799.13	chromosomes	17,472	18596	ensembl	Alföldi J., et al. (2011). The genome of the green anole lizard and a comparative analysis with birds and mammals. <i>Nature</i> , 477(7366): 587-591.	http://www.anoliscogenome.org/ ; http://www.broadinstitute.org/anolis/anolis-genome-project	
123	123	<i>Python molurus</i>	pmo	Metazoa	1,422.70	1435.03	assembly	18,761	19120	genbank	Castro T., et al. (2011). Sequencing the genome of the Burmese python (<i>Python molurus pimbura</i>) as a model for studying extreme adaptations in snakes. <i>Genome Biology</i> , 12:406.	https://www.ncbi.nlm.nih.gov/bioproject/238085	
124	124	<i>Ophiophagus hannah</i>	oha	Metazoa	1,475.00	1594.07	assembly	18,387	18444	genbank	Vonk F., et al. (2013). The king cobra genome reveals dynamic gene evolution and adaptation in the snake venom system. <i>Proc Natl Acad Sci U S A</i> , 110(51):20651-20656.	https://www.ncbi.nlm.nih.gov/assembly/GCA_000516915.1/	
125	125	<i>Chelonia mydas</i>	cmy	Metazoa	2,581.92	2236.14	assembly	19,633	19633	gigadb	Wang X., et al. (2013). The draft genomes of soft-shell turtle and green sea turtle yield insights into the development and evolution of the turtle-specific body plan. <i>Nature Genetics</i> 45, 701-706.	http://gigadb.org/dataset/100085	
126	126	<i>Pelodiscus sinensis</i>	psi	Metazoa	2,210.00	2202.47	assembly	18,188	18188	ensembl	Wang X., et al. (2013). The draft genomes of soft-shell turtle and green sea turtle yield insights into the development and evolution of the turtle-specific body plan. <i>Nature Genetics</i> 45, 701-706.	http://www.ensembl.org/Pelodiscus_sinensis/info/Index.html	
127	127	<i>Chrysemys picta (Chrysemys picta bellii)</i>	chp	Metazoa	2,738.40	2365.75	chromosomes	21,796	21180	genbank	Shaffer H., et al. (2013). The western painted turtle genome, a model for the evolution of extreme physiological adaptations in a slowly evolving lineage. <i>Genome Biology</i> , 14:R28.	http://pre.ensembl.org/Chrysemys_picta_bellii/info/Index.html	
128	128	<i>Alligator mississippiensis</i>	ami	Metazoa	2,274.00	2174.24	assembly	23,323	18152	genbank	St John J., et al. (2012). Sequencing three crocodilian genomes to illuminate the evolution of archosaurs and amniotes. <i>Genome Biol</i> , 13:415.	http://crocdatabases.org	
129	129	<i>Crocodylus porosus</i>	crc	Metazoa	2,718.84	2123.47	assembly	13,321	13329	crocgenomes	St John J., et al. (2012). Sequencing three crocodilian genomes to illuminate the evolution of archosaurs and amniotes. <i>Genome Biol</i> , 13:415.	http://www.crocgenomes.org/downloads.html	
130	130	<i>Gavialis gangeticus</i>	gag	Metazoa	2,882.66	2882.66	assembly	14,043	14047	crocgenomes	St John J., et al. (2012). Sequencing three crocodilian genomes to illuminate the evolution of archosaurs and amniotes. <i>Genome Biol</i> , 13:415.	http://www.crocgenomes.org/downloads.html	
131	131	<i>Struthio camelus</i>	scl	Metazoa	1,225.03	1225.03	assembly	16,178	14577	genbank	Zhang G., et al. (2014). Comparative genomic data of the Avian Phylogenomics Project. <i>Gigascience</i> , 3:26.	http://avianbase.narf.ac.uk/Struthio_camelus/Info/Index.html , http://gigadb.org/dataset/101013 ,	
132	132	<i>Tinamus guttatus</i>	tgt	Metazoa	1,047.06	1047.06	assembly	15,788	15723	genbank	Zhang G., et al. (2014). Comparative genomic data of the Avian Phylogenomics Project. <i>Gigascience</i> , 3:26.	http://avianbase.narf.ac.uk/Tinamus_guttatus/Info/Index.html , http://gigadb.org/dataset/101014	
133	133	<i>Anas platyrhynchos (Anas platyrhynchos domestica)</i>	apl	Metazoa	1,650.86	1105.05	assembly	15,065	20648	gigadb	Huang Y., et al. (2013). The duck genome and transcriptome provide insight into an avian influenza virus reservoir species. <i>Nature Genetics</i> 45, 776-783. Zhang G., et al. (2014). Comparative genomic data of the Avian Phylogenomics Project. <i>Gigascience</i> , 3:26.	http://www.ensembl.org/Anas_platyrhynchos/Info/Index.html	
134	134	<i>Meleagris gallopavo</i>	mga	Metazoa	1,431.14	1061.98	chromosomes	16,051	14125	ensembl	Dalloul RA., et al. (2010). Multi-platform next-generation sequencing of the domestic turkey (<i>Meleagris gallopavo</i>): genome assembly and analysis. <i>PLoS Biol</i> , 8:e1000475. Zhang G., et al. (2014). Comparative genomic data of the Avian Phylogenomics Project. <i>Gigascience</i> , 3:26.	http://www.ensembl.org/Meleagris_gallopavo/Info/Index.html	
135	135	<i>Gallus gallus</i>	gga	Metazoa	1,222.50	1046.92	chromosomes	16,516	15508	ensembl	Hillier LW., et al. (2004). Sequence and comparative analysis of the chicken genome provide unique perspectives on vertebrate evolution. <i>Nature</i> , 432:695-716. Zhang G., et al. (2014). Comparative genomic data of the Avian Phylogenomics Project. <i>Gigascience</i> , 3:26.	http://www.ensembl.org/Gallus_gallus/Info/Index.html & http://genome.ucsc.edu/cgi-bin/hgGateway?org=chicken & http://www.genome.gov/11008054	
136	136	<i>Columba livia</i>	cli	Metazoa	1,435.22	1107.97	assembly	15,392	14725	genbank	Shapiro M., et al. (2013). Genomic Diversity and Evolution of the Head Crest in the Rock Pigeon. <i>Science</i> , 339(6123):1063-1067. Zhang G., et al. (2014). Comparative genomic data of the Avian Phylogenomics Project. <i>Gigascience</i> , 3:26.	http://www.ensembl.org/Columba_livia/Info/Index.html	

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137	137	<i>Cuculus canorus</i>	cuc	Metazoa	1,153.89	1153.89	assembly	15,889	14727	genbank	Zhang G., et al. (2014). Comparative genomic data of the Avian Phylogenomics Project. Gigascience, 3:26.	http://gigadb.org/dataset/101009 , http://avianbase.narf.ac.uk/Cuculus_canorus/info/index	
138	138	<i>Calypte anna</i>	ann	Metazoa	1,105.68	1105.68	assembly	16,000	14543	genbank	Zhang G., et al. (2014). Comparative genomic data of the Avian Phylogenomics Project. Gigascience, 3:26.	http://avianbase.narf.ac.uk/Calypte_anna/info/index , http://gigadb.org/dataset/101004 , http://avianbase.narf.ac.uk/Calypte_anna/info/index	
139	139	<i>Chaetura pelagica</i>	cpl	Metazoa	1,119.19	1119.19	assembly	15,373	14111	genbank	Zhang G., et al. (2014). Comparative genomic data of the Avian Phylogenomics Project. Gigascience, 3:26.	http://gigadb.org/dataset/101005 , http://avianbase.narf.ac.uk/Chaetura_pelagica/info/index	
140	140	<i>Opisthomodus hoazin</i>	oho	Metazoa	1,203.71	1203.71	assembly	15,702	13333	genbank	Zhang G., et al. (2014). Comparative genomic data of the Avian Phylogenomics Project. Gigascience, 3:26.	http://gigadb.org/dataset/101011 , http://avianbase.narf.ac.uk/Opisthomodus_hoazin/info/index	
141	141	<i>Charadrius vociferus</i>	cvo	Metazoa	1,219.86	1219.86	assembly	16,856	14465	genbank	Zhang G., et al. (2014). Comparative genomic data of the Avian Phylogenomics Project. Gigascience, 3:26.	http://gigadb.org/dataset/101007	
142	142	<i>Nipponia nippon</i>	nni	Metazoa	1,223.85	1223.85	assembly	16,756	15018	genbank	Zhang G., et al. (2014). Comparative genomic data of the Avian Phylogenomics Project. Gigascience, 3:26.	http://avianbase.narf.ac.uk/Nipponia_nippon/info/index	
143	143	<i>Egretta garzetta</i>	ega	Metazoa	1,206.48	1206.48	assembly	14,140	14127	genbank	Zhang G., et al. (2014). Comparative genomic data of the Avian Phylogenomics Project. Gigascience, 3:26.	http://gigadb.org/dataset/100005 , http://avianbase.narf.ac.uk/Egretta_garzetta/info/index	
144	144	<i>Aptenodytes forsteri</i>	afo	Metazoa	1,390.00	1254.35	assembly	16,070	14767	genbank	Zhang G., et al. (2014). Comparative genomic data of the Avian Phylogenomics Project. Gigascience, 3:26.	http://gigadb.org/dataset/100006 , http://avianbase.narf.ac.uk/Aptenodytes_forsteri/info/index	
145	145	<i>Pygoscelis adeliae</i>	pya	Metazoa	1,250.00	1216.6	assembly	15,270	13734	genbank	Zhang G., et al. (2014). Comparative genomic data of the Avian Phylogenomics Project. Gigascience, 3:26.	http://gigadb.org/dataset/100006 , http://avianbase.narf.ac.uk/Pygoscelis_adeliae/info/index	
146	146	<i>Falco cherrug</i>	fch	Metazoa	1,189.00	1177.9	assembly	16,204	15998	gigadb	Zhan X., et al. (2013). Peregrine and saker falcon genome sequences provide insights into evolution of a predatory lifestyle. <i>Nature Genetics</i> , 45: 563–566.	http://gigadb.org/dataset/100075	
147	147	<i>Melopsittacus undulatus</i>	mun	Metazoa	1,339.86	1117.36	assembly	15,470	15470	gigadb	Zhang G., et al. (2014). Comparative genomic data of the Avian Phylogenomics Project. Gigascience, 3:26.	http://gigadb.org/dataset/100059 , http://pre.ensembl.org/Melopsittacus_undulatus/info/index	
148	148	<i>Manacus vitellinus</i>	mvi	Metazoa	1,145.85	1145.85	assembly	15,285	14040	genbank	Zhang G., et al. (2014). Comparative genomic data of the Avian Phylogenomics Project. Gigascience, 3:26.	http://gigadb.org/dataset/100005 , http://avianbase.narf.ac.uk/Manacus_vitellinus/info/index	
149	149	<i>Corvus brachyrhynchos</i>	cob	Metazoa	1,242.06	1091.31	assembly	16,562	14350	genbank	Zhang G., et al. (2014). Comparative genomic data of the Avian Phylogenomics Project. Gigascience, 3:26.	http://gigadb.org/dataset/100006 , http://avianbase.narf.ac.uk/Corvus_brachyrhynchos/info/index	
150	150	<i>Taeniopygia guttata</i>	tgu	Metazoa	1,222.50	1195.8	chromosomes	17,475	17488	ensembl	Warren W.C., et al. (2010). The genome of a songbird. <i>Nature</i> , 463:536–539.	http://www.ncbi.nlm.nih.gov/genome/17510	
151	151	<i>Serinus canaria</i>	sca	Metazoa	1,152.08	1152.08	assembly	18,818	14756	genbank	Frankl-Vilches C., et al. (2015). Using the canary genome to decipher the evolution of hormone-sensitive gene regulation in seasonal singing birds. <i>Genome Biology</i> , 16:19.	http://www.ncbi.nlm.nih.gov/genome/17510	
152	152	<i>Zonotrichia albicollis</i>	zal	Metazoa	1,339.86	1052.6	assembly	14,389	13802	genbank	Huyhn L., et al. (2010). Contrasting population genetic patterns within the white-throated sparrow genome (<i>Zonotrichia albicollis</i>). <i>BMC Genetics</i> , 11:96.	http://www.ncbi.nlm.nih.gov/genome/17510	
153	153	<i>Ficedula albicollis</i>	fil	Metazoa	1,130.00	1118.33	assembly	15,395	15540	genbank	Ellgren H., et al. (2012). The genomic landscape of species divergence in Ficedula flycatchers. <i>Nature</i> , 491: 756–760.	http://www.ncbi.nlm.nih.gov/genome/17510	
154	154	<i>Pseudopodoces humilis</i>	phm	Metazoa	1,045.65	1045.65	assembly	16,998	16998	gigadb	Cai Q., et al. (2013). Genome sequence of ground tit <i>Pseudopodoces humilis</i> and its adaptation to high altitude. <i>Genome Biology</i> , 14:R29.	http://www.ncbi.nlm.nih.gov/genome/17510	
155	155	<i>Geospiza fortis</i>	gfo	Metazoa	1,065.29	1065.29	assembly	16,286	13946	genbank	Zhang G., et al. (2014). Comparative genomic data of the Avian Phylogenomics Project. Gigascience, 3:26.	http://gigadb.org/dataset/100040	
156	156	<i>Picoides pubescens</i>	ppu	Metazoa	1,167.32	1167.32	assembly	15,576	14136	genbank	Zhang G., et al. (2014). Comparative genomic data of the Avian Phylogenomics Project. Gigascience, 3:26.	http://www.ncbi.nlm.nih.gov/genome/17510	
157	157	<i>Haliaeetus leucocephalus</i>	hle	Metazoa	1,178.41	1178.41	assembly	16,526	15212	genbank	Zhang G., et al. (2014). Comparative genomic data of the Avian Phylogenomics Project. Gigascience, 3:26.	http://www.ncbi.nlm.nih.gov/genome/17510	
158	158	<i>Aquila chrysaetos</i>	aqc	Metazoa	1,369.20	1192.73	assembly	16,571	15637	genbank	Doyle J., et al. (2013). he Genome Sequence of a Widespread Apex Predator, the Golden Eagle (<i>Aquila chrysaetos</i>). <i>PLoS ONE</i> , 9(4): e95599.	http://www.ncbi.nlm.nih.gov/genome/17510	
159	159	<i>Ornithorhynchus anatinus</i>	oan	Metazoa	2,992.68	2073.13	chromosomes	18,527	21698	ensembl	Warren W.C., et al. (2008). Genome analysis of the platypus reveals unique signatures of evolution. <i>Nature</i> , 453:175–183.	http://www.ncbi.nlm.nih.gov/genome/17510	
160	160	<i>Macropus eugenii</i>	meu	Metazoa	2,900.00	2955.77	assembly	15290	15290	ensembl	Renfree M.B., et al. (2011). Genome sequence of an Australian kangaroo, <i>Macropus eugenii</i> , provides insight into the evolution of mammalian reproduction and development. <i>Genome Biology</i> 12, Article number: R81.	http://www.ncbi.nlm.nih.gov/genome/17510	
161	161	<i>Sarcophilus harrisii</i>	sha	Metazoa	3,550.14	3174.69	assembly	18,775	18788	ensembl	Murchison E.P., et al. (2012). Genome Sequencing and Analysis of the Tasmanian Devil and Its Transmissible Cancer. <i>Cell</i> , 148(4):780-91.	http://www.ncbi.nlm.nih.gov/genome/17510	
162	162	<i>Monodelphis domestica</i>	mdd	Metazoa	3,550.00	3605.61	chromosomes	18,648	21327	ensembl	Milkesen T.S., et al. (2007). Genome of the marsupial Monodelphis domestica reveals innovation in non-coding sequences. <i>Nature</i> , 447(7141):167-77.	http://www.ncbi.nlm.nih.gov/genome/17510	
163	163	<i>Loxodonta africana</i>	laf	Metazoa	4,342.32	3196.74	assembly	20,033	20033	ensembl	The Broad Institute: https://www.broadinstitute.org/elephant/elephant-genome-project ;	http://www.ncbi.nlm.nih.gov/genome/17510	
164	164	<i>Myotis lucifugus</i>	mlu	Metazoa	2,542.80	2034.58	assembly	19,728	19728	ensembl	The Broad Institute: https://www.broadinstitute.org/brown-bat/little-brown-bat-genome-project ;	http://www.ncbi.nlm.nih.gov/genome/17510	
165	165	<i>Pteropus alecto</i>	pal	Metazoa	2,030.00	2032.4	assembly	21,392	21392	gigadb	Zhang G., et al. (2013). Comparative Analysis of Bat Genomes Provides Insight into the Evolution of Flight and Immunity. <i>Science</i> , 339(6118):456-460.	http://gigadb.org/dataset/100066	
166	166	<i>Equus caballus</i>	eca	Metazoa	3,149.16	2474.91	chromosomes	20,322	20449	ensembl	Wade C.M., et al. (2009). Genome Sequence, Comparative Analysis, and Population Genetics of the Domestic Horse. <i>Science</i> , 326(5954):865-867.	http://www.ncbi.nlm.nih.gov/genome/17510	
167	167	<i>Camelus ferus (Camelus bactrianus ferus)</i>	cfe	Metazoa	2,327.64	2009.18	assembly	20,821	18364	genbank	The Bactrian Camels Genome Sequencing and Analysis Consortium (2011). Genome sequences of wild and domestic bactrian camels. <i>Nature Communications</i> 3, Article number: 1202.	http://www.ncbi.nlm.nih.gov/genome/17510	
168	168	<i>Sus scrofa</i>	ssc	Metazoa	3,097.82	2808.51	chromosomes	21,640	21629	ensembl	Groenen M.A., et al. (2012). Analyses of pig genomes provide insight into porcine demography and evolution. <i>Nature</i> , 491:393-8.	http://www.sanger.ac.uk/resources/downloads/othervertebrates/pig.html	
169	169	<i>Bos taurus</i>	bta	Metazoa	3,537.10	2670.41	chromosomes	22,000	19994	ensembl	Elsik C.G., et al. (2009). The genome sequence of taurine cattle: a window to ruminant biology and evolution. <i>Science</i> , 324:522-8.	http://www.ncbi.nlm.nih.gov/genome/17510	
170	170	<i>Ovis aries</i>	oar	Metazoa	3,007.35	2571.06	chromosomes	24,430	20306	csiro	Jian Y., et al. (2014). The sheep genome illuminates biology of the rumen and lipid metabolism. <i>Science</i> , 344(6188):1168-1173.	http://www.ncbi.nlm.nih.gov/genome/17510	
171	171	<i>Capra hircus</i>	chi	Metazoa	3,168.72	2664.28	chromosomes	20,620	22172	gigadb	Dong Y., et al. (2013). Sequencing and automated whole-genome optical mapping of the genome of a domestic goat (<i>Capra hircus</i>). <i>Nature Biotechnology</i> , 31: 135–141.	http://www.ncbi.nlm.nih.gov/genome/17510	
172	172	<i>Balaenoptera acutorostrata</i>	bac	Metazoa	2,442.00	2442.89	assembly	20,605	20605	wgc	Yim H.S., et al. (2014). Minke whale genome and aquatic adaptation in cetaceans. <i>Nature Genetics</i> , 46: 88–92.	http://www.ncbi.nlm.nih.gov/genome/17510	
173	173	<i>Lipotes vexillifer</i>	lve	Metazoa	3,823.98	2429.2	assembly	22,168	18877	genbank	Zhou Z., et al. (2013). Baiji genomes reveal low genetic variability and new insights into secondary aquatic adaptations. <i>Nature Communications</i> 4, Article number: 2708.	http://www.ncbi.nlm.nih.gov/genome/17510	
174	174	<i>Orcinus orca</i>	oor	Metazoa	2,373.00	2372.9	assembly	18,142	18129	genbank	Foote A., et al. (2015). Convergent evolution of the genomes of marine mammals. <i>Nature Genetics</i> , 47: 272–275.	http://www.ncbi.nlm.nih.gov/genome/17510	

Dataset_461_genomes_eukaryotes													
175	175	<i>Canis familiaris</i>	cfa	Metazoa	3,051.36	2410.96	chromosomes	19,300	19856	ensembl	Kirkness E.F., et al. (2003). The dog genome: survey sequencing and comparative analysis. <i>Science</i> , 301:1898-903. Lindblad-Toh K., et al. (2005). Genome sequence, comparative analysis and haplotype structure of the domestic dog. <i>Nature</i> , 438:803-19.	http://www.ensembl.org/Canis_familiaris/info/Index ; http://www.genome.gov/11008069	
176	176	<i>Ailuropoda melanoleuca</i>	aml	Metazoa	2,300.00	2299.49	assembly	21,001	19343	ensembl	Li R., et al. (2010). The sequence and de novo assembly of the giant panda genome. <i>Nature</i> , 463:311-7.	http://www.ensembl.org/Ailuropoda_melanoleuca/info/Index ; http://smilieblast.usc.edu/cgi-bin/nhgGateway?org=Panda&db=ailMe1&hsid=4004	
177	177	<i>Panthera tigris</i>	ptg	Metazoa	2,523.24	2391.07	assembly	20,226	18298	genbank	Cho Y., et al. (2013). The tiger genome and comparative analysis with lion and snow leopard genomes. <i>Nature Communications</i> 4, Article number: 2433	https://www.ncbi.nlm.nih.gov/genome?LinkName=bioproject_genome&from_uid=182708	
178	178	<i>Felis catus</i>	fca	Metazoa	3,039.62	2455.52	chromosomes	19,493	19493	ensembl	Tamazian G., et al. (2014). Annotated features of domestic cat – <i>Felis catus</i> genome. <i>Gigascience</i> , 3:13.	http://www.ensembl.org/Felis_catus/info/Index ; http://genome.wustl.edu/genomes/detail/felis-catus/	
179	179	<i>Oryctolagus cuniculus</i> (<i>Oryctolagus cuniculus cuniculus</i>)	ocu	Metazoa	3,491.46	2737.47	chromosomes	19,081	19018	ensembl	Carneiro M., et al. (2014). Rabbit genome analysis reveals a polygenic basis for phenotypic change during domestication. <i>Science</i> , 345:1074-1079.	http://www.ensembl.org/Oryctolagus_cuniculus/info/Index ; http://broadinstitute.org/scientific-community/science/projects/mammals-models/rabbit/rabbit-genome-project ; http://ensembl.fugse.org/Oryctolagus_cuniculus/index.html	
180	180	<i>Ictidomys tridecemlineatus</i>	itr	Metazoa	2,478.39	2478.39	assembly	18,826	18826	ensembl	The Broad Institute: http://software.broadinstitute.org/allpaths-lg/blog/?p=361 ; The Broad Institute: https://www.broadinstitute.org/guinea-pig/guinea-pig-genome-project ;	http://www.ensembl.org/Ictidomys_tridecemlineatus/info/Index	
181	181	<i>Cavia porcellus</i>	cpo	Metazoa	3,364.32	2723.2	assembly	18,095	18673	ensembl	Gibbs R.A., et al. (2004). Genome sequence of the Brown Norway rat yields insights into mammalian evolution. <i>Nature</i> , 428:493-521.	http://www.ensembl.org/Rattus_norvegicus/info/Index ; http://www.ebi.ac.uk/2car/genomes/eukaryotes/Rattus_norvegicus.html	
182	182	<i>Rattus norvegicus</i>	rno	Metazoa	3,286.08	2909.68	chromosomes	20,973	22941	ensembl	Waterston R.H., et al. (2002). Initial sequencing and comparative analysis of the mouse genome. <i>Nature</i> , 420:520-62.	http://www.ensembl.org/Mus_musculus/info/Index ; http://genome.ucsc.edu/cgi-bin/hgGateway?org=mouse ; http://www.ebi.ac.uk/2car/genomes/eukaryotes/Mus_musculus.html	
183	183	<i>Mus musculus</i>	mmu	Metazoa	3,227.40	2730.86	chromosomes	22,011	23056	ensembl	Fan Y., et al. (2012). Genome of the Chinese tree shrew. <i>Nature Communications</i> 4, Article number: 1426	http://www.gigadb.org/dataset/100072	
184	184	<i>Tupaia chinensis</i> (<i>Tupaia belangeri chinensis</i>)	tch	Metazoa	2,861.79	2861.79	assembly	22,063	22688	gigadb	Larsen P.A., et al., 2017. Hybrid de novo genome assembly and centromere characterization of the gray mouse lemur (<i>Microcebus murinus</i>). <i>BMC Biol.</i> , 15: 110.	http://www.ensembl.org/Microcebus_murinus/info/Index	
185	185	<i>Microcebus murinus</i>	mmr	Metazoa	3,051.36	2910.1	assembly	18,182	16319	ensembl	Gibbs R.A., et al. (2007). Evolutionary and biomedical insights from the rhesus macaque genome. <i>Science</i> , 316:222-34.	http://www.ensembl.org/Macaca_mulatta/info/Index ; http://genome.wustl.edu/genomes/detail/macaca-mulatta/	
186	186	<i>Macaca mulatta</i>	mml	Metazoa	3,290.97	3097.16	chromosomes	23,088	21905	ensembl	The Marmoset Genome Sequencing and Analysis Consortium, (2014). The common marmoset genome provides insight into primate biology and evolution. <i>Nature Genetics</i> , 46: 850-857.	http://www.ensembl.org/Callithrix_jacchus/info/Index	
187	187	<i>Callithrix jacchus</i>	cja	Metazoa	3,354.54	2914.96	chromosomes	20,993	20993	ensembl	Locke D.P., et al. (2011). Comparative and demographic analysis of orangutan genomes. <i>Nature</i> , 469:529-533.	http://genome.wustl.edu/genomes/detail/pongo-abelli/ ; http://www.ensembl.org/Pongo_abelli/info/Index	
188	188	<i>Pongo abelli</i>	pon	Metazoa	3,703.36	3446.75	chromosomes	20,068	20424	ensembl	Scally A., et al. (2012). Insights into hominid evolution from the gorilla genome sequence. <i>Nature</i> , 483:169-75.	http://www.ensembl.org/Gorilla_gorilla/info/Index ; http://www.sanger.ac.uk/resources/downloads/gorilla/	
189	189	<i>Gorilla gorilla</i>	ggo	Metazoa	3,442.56	3040.66	chromosomes	20,962	20962	ensembl	Chimpanzee Sequencing and Analysis Consortium. (2005). Initial sequence of the chimpanzee genome and comparison with the human genome. <i>Nature</i> , 437:69-87.	http://www.ensembl.org/Pan_troglodytes/info/Index	
190	190	<i>Pan troglodytes</i>	pan	Metazoa	3,594.15	3309.56	chromosomes	19,829	18759	ensembl	Lander E.S., et al. (2001). Initial sequencing and analysis of the human genome. <i>Nature</i> , 409:860-921. Venter J.C., et al. (2001). The sequence of the human genome. <i>Science</i> , 291:1304-51.	http://www.ensembl.org/Homo_sapiens/info/Index ; http://genome.wustl.edu/genomes/detail/homo-sapiens/	
191	191	<i>Homo sapiens</i>	hsa	Metazoa	3,423.00	3101.79	chromosomes	21,494	23080	ensembl	Nakamura Y., et al. (2013). The First Symbiont-Free Genome Sequence of Marine Red Alga, <i>Susaburi-nori</i> (<i>Pyropia yezoensis</i>). <i>PLoS ONE</i> , 8(3): e57122.	https://www.ncbi.nlm.nih.gov/genome?LinkName=bioproject_genome&from_uid=589917	
192	1	<i>Pyropia yezoensis</i>	pye	Protist	43.48	43.48	assembly	10,327	10327	nrifs	Collén J., et al. (2013). Genome structure and metabolic features in the red seaweed <i>Chondrus crispus</i> shed light on evolution of the Archaeplastida. <i>Proc Natl Acad Sci U S A</i> , 110 (13) 5247-5252.	http://www.ebi.ac.uk/ena/data/view/HG001459-HG002383	
193	2	<i>Chondrus crispus</i>	ccr	Protist	105.00	104.8	assembly	9,606	9807	ncbi	Schönknecht G., et al. (2013). Gene Transfer from Bacteria and Archaea Facilitated Evolution of an Extremophilic Eukaryote. <i>Science</i> , 339:1207-1210.	http://www.ebi.ac.uk/ena/data/search?query=galdieria%20sulphuraria	
194	3	<i>Galdieria sulphuraria</i>	gsu	Protist	14.00	13.71	assembly	6,623	6622	ebi	Matsuizaki M., et al. (2004). Genome sequence of the ultrasmall unicellular red alga <i>Cyanidioschyzon merolae</i> 10D. <i>Nature</i> , 428:653-7. Nozaki H., et al. (2007). A 100%-complete sequence reveals unusually simple genomic features in the hot-spring red alga <i>Cyanidioschyzon merolae</i> . <i>BMC Biology</i> , 5:28.	http://merolae.biols.u-tokyo.ac.jp/download/ ; http://ftp.ensemblgenomes.org/pub/plants/release-16/fasta/cyanidioschyzon_merolae/	
195	4	<i>Cyanidioschyzon merolae</i>	cme	Protist	16.50	16.55	chromosomes	5,331	4997	utkyo	Worden A.Z., et al. (2009). Green evolution and dynamic adaptations revealed by genomes of the marine picoeukaryotes <i>Micromonas</i> . <i>Science</i> , 324: 268-72.	http://genome.jgi.doe.gov/pages/dynamicOrganismDownload.jsf?organism=MicropC3 ; http://ftp.jgi-psf.org/pub/compgen/phytozome/v9.0/Mpusilla_CCMP1545/	
196	5	<i>Micromonas pusilla</i>	mpu	Viridiplantae	24.50	21.95	chromosomes	10,575	10660	phytozome	Worden A.Z., et al. (2009). Green evolution and dynamic adaptations revealed by genomes of the marine picoeukaryotes <i>Micromonas</i> . <i>Science</i> , 324: 268-72.	http://bioinformatics.psb.ugent.be/gdb/bathycoctus/RELEASE_15ju2011/	
197	6	<i>Micromonas spRCC299</i>	mic	Viridiplantae	21.10	20.99	chromosomes	10,056	10103	phytozome	Moreau H., et al (2012). Gene functionalities and genome structure in <i>Bathycoccus prasinus</i> reflect cellular specializations at the base of the green lineage. <i>Genome Biology</i> , 13:R74.	https://mycoscom.jgi.doe.gov/OstRCC809_2/OstRCC809_2.info.html	
198	7	<i>Bathycoccus prasinos</i>	bpr	Viridiplantae	9.78	15.01	chromosomes	7,847	7807	beg	Palenik B., et al. (2007). The tiny eukaryote <i>Ostreococcus</i> provides genomic insights into the paradox of plankton speciation. <i>Proc Natl Acad Sci U S A</i> , 104(18):7705-7710.	http://ftp.jgi-psf.org/pub/compgen/phytozome/v9.0/Creinhardtii/ ; http://ftp.ensemblgenomes.org/pub/plants/release-16/fasta/chlamydomonas_reinhardtii/ ; http://ftp.plantgdb.org/download/Genomes/CrGDB/	
199	8	<i>Ostreococcus sp</i>	osp	Viridiplantae	13.30	13.3	chromosomes	7,492	7492	jgi	Merchant S.S., et al. (2007). The Chlamydomonas genome reveals the evolution of key animal and plant functions. <i>Science</i> , 318(5848):245-50.	http://genome.jgi.doe.gov/Volca1/Volca1.download.ftp.html	
200	9	<i>Chlamydomonas reinhardtii</i>	cre	Viridiplantae	118.00	111.1	chromosomes	15,143	17737	phytozome	Prochnik S.E., et al. (2010). Genomic Analysis of Organismal Complexity in the Multicellular Green Alga <i>Volvox carteri</i> . <i>Science</i> , 329(5988):223-6.	http://genome.jgi.doe.gov/ChlNC64A_1/ChlNC64A_1.download.ftp.html	
201	10	<i>Volvox carteri</i>	vcn	Viridiplantae	138.00	131.16	assembly	14,520	14971	phytozome	Blanc G., et al. (2010). The <i>Chlorella variabilis</i> NC64A genome reveals adaptation to photosymbiosis, coevolution with viruses, and cryptic sex. <i>Plant cell</i> , 22(9):2943-55.	https://www.ncbi.nlm.nih.gov/genome/13660?genome_assembly_id=59306	
202	11	<i>Chlorella variabilis</i>	cva	Viridiplantae	46.20	46.16	assembly	9,791	9791	jgi	Pombert J.F., et al. (2014). A Lack of Parasite Reduction in the Obligate Parasitic Green Alga <i>Helicosporidium</i> . <i>PLoS Genet</i> 10(5):e1004355.	http://genome.jgi-psf.org/Coc_C169_1/Coc_C169_1.download.ftp.html	
203	12	<i>Helicosporidium sp</i>	hel	Viridiplantae	17.00	12.37	assembly	6035	6033	genbank	Blanc G., et al (2012). The genome of the polar eukaryotic microalga <i>Coccomyxa subellipsoidea</i> reveals traits of cold adaptation. <i>Genome Biol.</i> , 13(S):R39.	http://genome.jgi.doe.gov/Aspho1/Aspho1.download.ftp.html	
204	13	<i>Coccomyxa subellipsoidea</i>	csu	Viridiplantae	48.80	48.95	assembly	9,851	9629	jgi	Armao D., et al. (2019). The lichen symbiosis re-reviewed through the genomes of <i>Cladonia grayi</i> and its algal partner <i>Asterochloris glomerata</i> . <i>MC Genomics</i> 20, Article number: 605.	http://ftp.ncbi.nlm.nih.gov/genomes/Phyta/Phyta1_1/Phyta1_1.download.ftp.html	
205	14	<i>Asterochloris sp (Asterochloris glomerata)</i>	asp	Viridiplantae	56.14	56.14	assembly	10,025	7159	jgi	Rensing S.A., et al (2008). The Physcomitrella genome reveals evolutionary insights into the conquest of land by plants. <i>Science</i> , 319(5859):54-9.	http://ftp.ncbi.nlm.nih.gov/genomes/Phyta/Phyta1_1/Phyta1_1.download.ftp.html	
206	15	<i>Physcomitrella patens</i>	ppa	Viridiplantae	518.00	479.99	assembly	35,938	32273	phytozome		http://ftp.ncbi.nlm.nih.gov/genomes/Phyta/Phyta1_1/Phyta1_1.download.ftp.html ; http://ftp.ensemblgenomes.org/pub/plants/release-16/fasta/physcomitella_patens/ ; http://genome.jgi.doe.gov/Physp1_1/Physp1_1.download.ftp.html ; http://ftp.plantgdb.org/download/Genomes/PpGDB/	

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207	16	<i>Selaginella moellendorffii</i>	smo	Viridiplantae	127.00	212.5	assembly	22,285	22285	phytozome	Banks JA, et al. (2011). The Selaginella genome identifies genetic changes associated with the evolution of vascular plants. <i>Science</i> 332:960-3.	ftp://ftp.jgi-psf.org/pub/compgen/phytozome/v9.0/Sselaginella_moellendorffii/ ; http://ftp.ensemblgenomes.org/pub/plants/current/fasta/selaginella_moellendorffii/ ; http://ftp.plantfdb.org/download/Genomes/SmGDB/ ; https://www.ncbi.nlm.nih.gov/genome/?term=txid352[Organism:ncexp]	
208	17	<i>Pinus taeda</i>	pnt	Viridiplantae	22,564.68	22564.68	assembly	84,446	50172	pinegenome	Neale D.B., et al. (2014). Decoding the massive genome of loblolly pine using haploid DNA and novel assembly strategies. <i>Genome Biology</i> 15, Article number: R59.	http://www.ncbi.nlm.nih.gov/genome/?term=txid352[Organism:ncexp]	
209	18	<i>Amborella trichopoda</i>	atr	Viridiplantae	868.00	706.33	assembly	17,106	27313	ensembl	Amborella Genome Project. (2013). The Amborella Genome and the Evolution of Flowering Plants. <i>Science</i> , 342(6165):1241089	http://www.amborella.org	
210	19	<i>Spirodela polyrhiza</i>	spi	Viridiplantae	158.00	145.2	assembly	19,623	19623	rutgers	Wang W., et al. (2014). The Spirodela polyrhiza genome reveals insights into its neotropical reduction fast growth and aquatic lifestyle. <i>Nature Communications</i> 5, Article number: 3311	http://www.mobot.org/jwcross/duckweed/duckweed.htm	
211	20	<i>Phalaenopsis equestris</i>	peq	Viridiplantae	1,086.21	1086.21	assembly	29,431	29431	beg	Cai J., et al. (2015). The genome sequence of the orchid Phalaenopsis equestris. <i>Nature Genetics</i> , 47: 65–72.	https://www.ncbi.nlm.nih.gov/genome/11403	
212	21	<i>Phoenix dactylifera</i>	pda	Viridiplantae	658.00	381.56	assembly	28,890	28889	coge	Al-Dous E.K., et al. (2011). De novo genome sequencing and comparative genomics of date palm (<i>Phoenix dactylifera</i>). <i>Nature Biotechnology</i> , 29: 521–527.	http://qatar-weill.cornell.edu/research/datepalmGenome/download.html	
213	22	<i>Elaeis guineensis</i>	egu	Viridiplantae	1,839.00	1535.02	chromosomes	34,802	25893	genbank	Singh R., et al. (2013). Oil palm genome sequence reveals divergence of interfertile species in Old and New worlds. <i>Nature</i> , 500: 335–339.	https://www.ncbi.nlm.nih.gov/genome/2669	
214	23	<i>Musa acuminata</i>	mac	Viridiplantae	611.00	472.96	chromosomes	36,542	36519	cirad	D'Hont A., et al. (2012) The draft genome of the fast-growing non-timber forest species moso bamboo (<i>Phyllostachys heterocycla</i>). <i>Nature Genetics</i> , 45: 456–461.	http://ftp.ensemblgenomes.org/pub/plants/release-16/fasta/musa_acuminata/ ; http://banana-genome.cirad.fr/download.php	
215	24	<i>Phyllostachys heterocycla</i>	phe	Viridiplantae	2,075.00	2051.72	assembly	31,987	31987	bamboogdb	Peng Z., et al. (2013). The draft genome of the fast-growing non-timber forest species moso bamboo (<i>Phyllostachys heterocycla</i>). <i>Nature Genetics</i> , 45: 456–461.	http://www.bamboogdb.org	
216	25	<i>Brachypodium distachyon</i>	bdi	Viridiplantae	355.00	271.92	chromosomes	25,532	26552	phytozome	The International Brachypodium Initiative. (2010) Genome sequencing and analysis of the model grass <i>Brachypodium distachyon</i> . <i>Nature</i> 463, 763–768.	ftp://ftp.jgi-psf.org/pub/compgen/phytozome/v9.0/Bdistachyon/ ; http://ftp.ensemblgenomes.org/pub/plants/release-16/fasta/brachypodium_m_distachyon/ ; http://ftp.ncbi.nlm.nih.gov/genomes/Brachypodium_distachyon/ ; http://ftp.plantfdb.org/download/Genomes/BdGDB/	
217	26	<i>Hordeum vulgare</i>	hvu	Viridiplantae	5,428.00	4582.03	chromosomes	26,159	24212	mips	The International Barley Genome Sequencing Consortium (IBSC) (2012). A physical, genetic and functional sequence assembly of the barley genome. <i>Nature</i> , 491: 711–716.	http://ftp.ensemblgenomes.org/pub/plants/release-16/fasta/hordeum_vulgare/ ; http://ftp.mips.heidelberg-muenchen.de/plants/barley/public_data/genes/	
218	27	<i>Aegilops tauschii</i>	ata	Viridiplantae	4,360.00	3313.65	assembly	42,828	33849	ensembl	Jia J., et al. (2013). <i>Aegilops tauschii</i> draft genome sequence reveals a gene repertoire for wheat adaptation. <i>Nature</i> , 496: 91–95.	http://plants.ensembl.org/Aegilops_tauschii/info/Index	
219	28	<i>Triticum urartu</i>	tut	Viridiplantae	4,817.00	3747.05	assembly	34879	33424	ensembl	Ling H.Q., et al. (2013). Draft genome of the wheat A-genome progenitor <i>Triticum urartu</i> . <i>Nature</i> , 496: 87–90.	http://plants.ensembl.org/Triticum_urartu/info/Index	
220	29	<i>Oryza sativa</i>	osa	Viridiplantae	489.00	373.18	chromosomes	37,544	57781	phytozome	International Rice Genome Sequencing Project. (2005). The map-based sequence of the rice genome. <i>Nature</i> , 436:793-800.	ftp://ftp.jgi-psf.org/pub/compgen/phytozome/v9.0/Osativa/ ; http://ftp.ensemblgenomes.org/pub/plants/current/fasta/orza_sativa/ ; http://ftp.plantfdb.org/download/Genomes/OsGDB/ ; http://genome.jgi.doe.gov/Sorbi1/Sorbi1.download.ftp.html ; http://ftp.ensemblgenomes.org/pub/plants/current/fasta/orza_sativa/ ; http://ftp.jgi-psf.org/pub/compgen/phytozome/v9.0/Sbicolor/ ; http://ftp.plantfdb.org/download/Genomes/SbGDB/	
221	30	<i>Sorghum bicolor</i>	sbi	Viridiplantae	734.00	738.54	chromosomes	27,640	34496	phytozome	Paterson A.H., et al. (2009). The Sorghum bicolor genome and the diversification of grasses. <i>Nature</i> , 457(7229):551-6.	http://ftp.ensemblgenomes.org/pub/plants/current/fasta/sorghum_bicolor/ ; http://ftp.jgi-psf.org/pub/compgen/phytozome/v9.0/Sbicolor/ ; http://ftp.plantfdb.org/download/Genomes/SbGDB/	
222	31	<i>Zea mays</i>	zma	Viridiplantae	2,665.00	2065.72	chromosomes	32,540	63331	phytozome	Schnable P.S., et al. (2009). The B73 maize genome: complexity, diversity, and dynamics. <i>Science</i> , 326:1112-5.	http://ftp.ensemblgenomes.org/pub/plants/current/fasta/zea_mays/ ; http://ftp.jgi-psf.org/pub/compgen/phytozome/v9.0/zmays/ ; http://ftp.plantfdb.org/download/Genomes/ZmGDB/	
223	32	<i>Panicum virgatum</i>	pvi	Viridiplantae	1,358.08	1358.08	assembly	55598	65878	phytozome	Sharma M.K., et al. (2012). A Genome-Wide Survey of Switchgrass Genome Structure and Organization. <i>PLoS ONE</i> , 7(4): e33892.	https://phytozome-next.jgi.doe.gov/info/Pvirgatum_v4_1	
224	33	<i>Setaria italica</i>	sit	Viridiplantae	513.00	405.74	assembly	38,801	35471	phytozome	Zhang G., et al. (2012). Genome sequence of foxtail millet (<i>Setaria italica</i>) provides insights into grass evolution and biotic potential. <i>Nature Biotechnology</i> , 30: 549–554.	ftp://ftp.jgi-psf.org/pub/compgen/phytozome/v9.0/Sitalica/ ; http://ftp.ensemblgenomes.org/pub/plants/current/fasta/setaria_italica/	
225	34	<i>Aquilegia coerulea</i>	aco	Viridiplantae	301.98	301.98	assembly	30023	24823	phytozome	Filioli D.L., et al. (2018). The <i>Aquilegia</i> genome provides insight into adaptive radiation and reveals an extraordinarily polymorphic chromosome with a unique history. <i>Elife</i> , 7:e36426.	https://phytozome-next.jgi.doe.gov/info/Acoerulea_v3_1	
226	35	<i>Nelumbo nucifera</i>	nnu	Viridiplantae	929.00	804.48	assembly	26,685	24613	genbank	Ming R., et al. (2013). Genome of the long-living sacred lotus (<i>Nelumbo nucifera</i> Gaertn.). <i>Genome Biology</i> , 14:R41.	https://www.ncbi.nlm.nih.gov/genome/14095	
227	36	<i>Beta vulgaris</i>	bvu	Viridiplantae	758.00	568.98	assembly	27,421	74184	mpg	Dohm J., et al. (2014). The genome of the recently domesticated crop plant sugar beet (<i>Beta vulgaris</i>). <i>Nature</i> , 505: 546–549.	http://bvsq.molgen.mpg.de/index.shtml	
228	37	<i>Actinidia chinensis</i>	ach	Viridiplantae	758.00	631.45	chromosomes	39,040	39040	cornell	Huang S., et al. (2013). Draft genome of the kiwifruit <i>Actinidia chinensis</i> . <i>Nature Communications</i> 4, Article number: 2640.	http://bioinfo.bti.cornell.edu/cgi-bin/kiwi/home.cgi	
229	38	<i>Coffea canephora</i>	cof	Viridiplantae	710.00	569.91	chromosomes	25,574	25574	coffeegenome	Denoed F., et al. (2014). The coffee genome provides insight into the convergent evolution of caffeine biosynthesis. <i>Science</i> , 345(6201):1181-1184.	http://coffee-genome.org/coffeacanephora	
230	39	<i>Mimulus guttatus</i>	mgu	Viridiplantae	321.73	321.73	assembly	28140	26718	phytozome	Hellsten U., et al. (2013). Fine-scale variation in meiotic recombination in <i>Mimulus</i> inferred from population shotgun sequencing. <i>Proc Natl Acad Sci U S A</i> , 110(48):19478–19482.	https://phytozome-next.jgi.doe.gov/info/Mguttatus_v2_0	
231	40	<i>Sesamum indicum</i>	ssi	Viridiplantae	369.00	274.91	assembly	27,148	23811	genbank	Zhang H., et al. (2013). Genome sequencing of the important oilseed crop <i>Sesamum indicum</i> . <i>Genome Biology</i> , 14:401.	http://sesamegenome.org	
232	41	<i>Genlisea aurea</i>	gau	Viridiplantae	63.00	43.36	assembly	17,755	17685	genbank	Leushkin E., et al. (2013). The miniature genome of a carnivorous plant <i>Genlisea aurea</i> contains a low number of genes and short non-coding sequences. <i>BMC Genomics</i> , 14:476.	http://genlisea.org/about	
233	42	<i>Utricularia gibba</i>	ugi	Viridiplantae	88.00	81.88	assembly	28500	28494	coge	Ibarra-Laclette E., et al. (2013). Architecture and evolution of a minute plant genome. <i>Nature</i> , 498: 94–98.	http://genomevolution.org/CoGe/OrganismView.pl?oid=36222	
234	43	<i>Nicotiana tabacum</i>	nta	Viridiplantae	5,061.00	3729.08	assembly	61780	40129	solgenomics	Siero N., et al. (2014). The tobacco genome sequence and its comparison with those of tomato and potato. <i>Nature Communications</i> 5, Article number: 3833.	https://solgenomics.net/organism/941/view	
235	44	<i>Capsicum annuum</i>	cap	Viridiplantae	3,090.00	2753.5	chromosomes	34,476	30242	snu	Kim S., et al. (2013). Genome sequence of the hot pepper provides insights into the evolution of pungency in Capsicum species. <i>Nature Genetics</i> , 46: 270–278.	http://peppersequence.genomics.cn/page/species/index.jsp	
236	45	<i>Solanum melongena</i>	sme	Viridiplantae	833.11	833.11	assembly	34916	35119	kazusa	Hirakawa H., et al. (2014). Draft Genome Sequence of Eggplant (<i>Solanum melongena</i> L.): the Representative Solanum Species Indigenous to the Old World. <i>DNA Res</i> , 21(6): 649-660.	http://eggplant.kazusa.or.jp	
237	46	<i>Solanum lycopersicum</i>	sly	Viridiplantae	900.00	781.67	chromosomes	34,727	34727	phytozome	The Tomato Genome Consortium (2012). The tomato genome sequence provides insights into fleshy fruit evolution. <i>Nature</i> , 485: 635-641.	https://www.ncbi.nlm.nih.gov/genome/?term=AEKE00000000	
238	47	<i>Solanum tuberosum</i>	stu	Viridiplantae	856.00	791.61	chromosomes	39,031	35119	phytozome	Xu X., et al. (2011). Genome sequence and analysis of the tuber crop potato. <i>Nature</i> , 475(7355):189-95.	ftp://ftp.jgi-psf.org/pub/compgen/phytozome/v9.0/Stuberous/ ; http://ftp.ensemblgenomes.org/pub/plants/current/fasta/solanum_tuberosum/	
239	48	<i>Vitis vinifera</i>	vvi	Viridiplantae	475.00	486.2	chromosomes	30,434	26346	phytozome	Jalilov O., et al. (2007). The grapevine genome sequence suggests ancestral hexaploidization in major angiosperm phyla. <i>Nature</i> , 449: 463-467.	http://ftp.jgi-psf.org/pub/compgen/phytozome/v9.0/Vvinifera/	
240	49	<i>Eucalyptus grandis</i>	egr	Viridiplantae	640.00	691.3	chromosomes	36376	36376	phytozome	Myburg A. et al. (2014). The genome of <i>Eucalyptus grandis</i> . <i>Nature</i> , 510: 356–362.	http://web.up.ac.za/eucagen/viewnews.aspx?id=36	

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241	50	<i>Citrus clementina</i>	ccl	Viridiplantae	301.40	295.55	assembly	24,533	25385	coge	Wu G., et al. (2014). Sequencing of diverse mandarin, pummelo and orange genomes reveals complex history of admixture during citrus domestication. <i>Nature Biotechnology</i> , 32: 656-662.	https://www.citrusgenomedb.org/species/clementina/genome1.0
242	51	<i>Citrus sinensis</i>	csi	Viridiplantae	367.00	319.23	assembly	29,445	25379	phytozome	Xu Q., et al. (2012). The draft genome of sweet orange (<i>Citrus sinensis</i>). <i>Nature Genetics</i> , 45: 59-66.	http://citrus.hzau.edu.cn/orange/download/data.php ; ftp://ftp.ncbi.nih.gov/genbank/genomes/Eukaryotes/plants/Citrus_sinesis/ ; ftp://ftp.jgi-psf.org/pub/compgen/phytozome/v9.0/Citrus_sinensis/ ; http://bioinfo.wsu.edu/www/citrusgenomedb.org/Citrus_sinensis/
243	52	<i>Theobroma cacao</i>	tca	Viridiplantae	430.00	327.35	chromosomes	28,798	28672	cocoagendb	Argout X., et al. (2011). The genome of <i>Theobroma cacao</i> . <i>Nature Genetics</i> , 43: 101-108.	http://ftp.jgi-psf.org/pub/compgen/phytozome/v9.0/Tcacao/ ; http://cocoagendb.cirad.fr/gbrowse/download.html ; http://bioinformatics.psu.ugent.be/plaza/download/index
244	53	<i>Gossypium raimondii</i>	gra	Viridiplantae	880.00	761.41	chromosomes	40,976	40976	phytozome	Wang K., et al. (2012). The draft genome of a diploid cotton <i>Gossypium raimondii</i> . <i>Nature Genetics</i> , 44: 1098-1103.	http://ftp.jgi-psf.org/pub/compgen/phytozome/v9.0/Graimondii/ ; http://cpn.genomics.org.cn/page/species/download.jsp
245	54	<i>Carica papaya</i>	cpp	Viridiplantae	367.00	342.68	assembly	24,746	27769	phytozome	Ming R., et al. (2008). The draft genome of the transgenic tropical fruit tree papaya (<i>Carica papaya</i> Linnaeus). <i>Nature</i> , 452(7190):991-6.	http://ftp.jgi-psf.org/pub/compgen/phytozome/v9.0/Cpapaya/ ; http://ftp.plantgdb.org/download/Genomes/CpGDB/
246	55	<i>Tarenaya hassleriana</i>	tah	Viridiplantae	293.00	249.93	assembly	28,917	26997	genbank	Cheng S., et al. (2013). The <i>Tarenaya hassleriana</i> genome provides insight into reproductive trait and genome evolution of crucifers. <i>Plant Cell</i> , 25(8):2813-30.	https://www.ncbi.nlm.nih.gov/genome/17630
247	56	<i>Aethionema arabicum</i>	aar	Viridiplantae	240.00	199.43	assembly	23,167	37839	brassicadb	Haudry A., et al. (2013). An atlas of over 90,000 conserved noncoding sequences provides insight into crucifer regulatory regions. <i>Nature Genetics</i> , 45: 891-898.	https://plantcode.cup.uni-freiburg.de/aetar_db/
248	57	<i>Thellungiella halophila</i> (<i>Thellungiella salsuginosa</i> , <i>Eutrema salsugineum</i>)	tha	Viridiplantae	260.00	243.12	assembly	28,457	26351	phytozome	Yang R., et al. (2013). The Reference Genome of the Halophytic Plant <i>Eutrema salsugineum</i> . <i>Front Plant Sci</i> , 4:46.	http://ftp.jgi-psf.org/pub/compgen/phytozome/v9.0/Thalophila/
249	58	<i>Brassica rapa</i>	brp	Viridiplantae	468.00	283.82	chromosomes	41,174	41018	phytozome	Brassica rapa Genome Sequencing Project Consortium. (2011). The genome of the mesopolyploid crop species <i>Brassica rapa</i> . <i>Nat Genet</i> , 43(10):1035-9.	ftp://ftp.ensemblgenomes.org/pub/plants/release-16/fasta/brassica_rapa/ ; http://ftp.jgi-psf.org/pub/compgen/phytozome/v9.0/Brapa/
250	59	<i>Sisymbrium irio</i>	sir	Viridiplantae	262.00	259.49	assembly	28,917	49956	brassicadb	Haudry A., et al. (2013). An atlas of over 90,000 conserved noncoding sequences provides insight into crucifer regulatory regions. <i>Nature Genetics</i> , 45: 891-898.	https://www.ncbi.nlm.nih.gov/genome/17728
251	60	<i>Leavenworthia alabamica</i>	lal	Viridiplantae	316.00	174.2	assembly	30,343	38676	brassicadb	Haudry A., et al. (2013). An atlas of over 90,000 conserved noncoding sequences provides insight into crucifer regulatory regions. <i>Nature Genetics</i> , 45: 891-898.	https://www.ncbi.nlm.nih.gov/genome/?term=txid310722[orgn]
252	61	<i>Capsella rubella</i>	cru	Viridiplantae	215.00	134.83	assembly	26,521	26521	phytozome	Slote T., et al. (2013). The <i>Capsella rubella</i> genome and the genomic consequences of rapid mating system evolution. <i>Nature Genetics</i> , 45: 831-835.	http://ftp.jgi-psf.org/pub/compgen/phytozome/v9.0/Crubbella/
253	62	<i>Camelina sativa</i>	cam	Viridiplantae	785.00	641.36	chromosomes	89,418	81485	genbank	Kagale S., et al. (2014). The emerging biofuel crop <i>Camelina sativa</i> retains a highly undifferentiated hexaploid genome structure. <i>Nature Communications</i> 5, Article number: 3706.	http://camelagenomics.org/index.php?a=view
254	63	<i>Arabidopsis thaliana</i>	ath	Viridiplantae	156.00	119.15	chromosomes	25,498	27416	phytozome	Arabidopsis Genome Initiative. (2000). Analysis of the genome sequence of the flowering plant <i>Arabidopsis thaliana</i> . <i>Nature</i> , 408(6814):796-815.	https://www.ncbi.nlm.nih.gov/genome/?term=txid3702[Organism]:noexp
255	64	<i>Arabidopsis lyrata</i>	aly	Viridiplantae	245.00	206.67	chromosomes	32,670	32667	jgi	Hu T.T., et al. (2011). The <i>Arabidopsis lyrata</i> genome sequence and the basis of rapid genome size change. <i>Nat Genet</i> , 43:476-81.	https://www.ncbi.nlm.nih.gov/genome/?term=arabidopsis+lyrata
256	65	<i>Populus trichocarpa</i>	ptr	Viridiplantae	484.00	417.14	chromosomes	45,555	41377	plantgdb	Tuskan G.A., et al. (2006). The Genome of Black Cottonwood, <i>Populus trichocarpa</i> (Torr. & Gray). <i>Science</i> , 313 (5793):1596-1604.	http://ftp.jgi-psf.org/pub/compgen/phytozome/v9.0/Ptrichocarpa/ ; http://ftp.ensemblgenomes.org/pub/plants/release-16/fasta/populus_trichocarpa/ ; http://ftp.plantgdb.org/download/Genomes/PGDB/ ; http://genome.jgi.doe.gov/Poptr1_1/Poptr1_1_download ftp.html
257	66	<i>Linum usitatissimum</i>	lus	Viridiplantae	373.60	318.25	assembly	43,384	43471	phytozome	Wang Z., et al. (2012). The genome of flax (<i>Linum usitatissimum</i>) assembled de novo from short shotgun sequence reads. <i>Plant J</i> , 72(3): 461-473.	https://www.ncbi.nlm.nih.gov/genome/?term=linum+usatissimum
258	67	<i>Manihot esculenta</i>	mes	Viridiplantae	742.00	532.51	assembly	33033	30666	phytozome	Bredeson J.V., et al. (2016). Sequencing wild and cultivated cassava and related species reveals extensive interspecific hybridization and genetic diversity. <i>Nat Biotechnol</i> , 34: 562-570. Wang W., et al. (2014). Cassava genome from a wild ancestor to cultivated varieties. <i>Nature Communications</i> 5, Article number: 5110.	http://ftp.jgi-psf.org/pub/compgen/phytozome/v9.0/Mesculenta/ ; http://genome.jgi.doe.gov/cassava/cassava.download ftp.html
259	68	<i>Ricinus communis</i>	rcu	Viridiplantae	320.00	350.63	assembly	31,237	31221	phytozome	Chan A.P., et al. (2010). Draft genome sequence of the oilseed species <i>Ricinus communis</i> . <i>Nat Biotechnol</i> , 28:951-6.	http://ftp.jgi-psf.org/pub/compgen/phytozome/v9.0/Rcommunis/ ; http://bioinformatics.psu.ugent.be/plaza/download/index
260	69	<i>Lotus japonicus</i>	lja	Viridiplantae	465.00	301.34	chromosomes	34,245	37971	kazusa	Sato S., et al. (2008). Genome Structure of the Legume, <i>Lotus japonicus</i> . <i>DNA Research</i> , 15(4):227-39.	https://www.ncbi.nlm.nih.gov/genome/?term=lotus+japonicus
261	70	<i>Medicago truncatula</i>	mtr	Viridiplantae	465.00	418.58	chromosomes	47,845	44135	phytozome	Young N.D., et al. (2011). The <i>Medicago</i> genome provides insight into the evolution of rhizobial symbioses. <i>Nature</i> , 480:520-4.	https://www.ncbi.nlm.nih.gov/genome/?term=medicago+truncatula
262	71	<i>Cicer arietinum</i>	car	Viridiplantae	929.00	532.29	chromosomes	28,269	28269	gigadb	Varshney R., et al. (2013). Draft genome sequence of chickpea (<i>Cicer arietinum</i>) provides a resource for trait improvement. <i>Nature Biotechnology</i> , 31: 240-246.	https://www.ncbi.nlm.nih.gov/genome/?term=cicer+arietinum
263	72	<i>Cajanus cajan</i>	cca	Viridiplantae	856.00	605.78	chromosomes	48,680	48680	icrisat	Varshney R.K., et al. (2012). Draft genome sequence of pigeonpea (<i>Cajanus cajan</i>), an orphan legume crop of resource-poor farmers. <i>Nature Biotechnology</i> , 30(1):83-9.	https://www.ncbi.nlm.nih.gov/genome/?term=cajanus+cajan
264	73	<i>Glycine max</i>	gma	Viridiplantae	1,100.00	973.34	chromosomes	46,430	54175	phytozome	Schmutz J., et al. (2010). Genome sequence of the paleopolyploid soybean. <i>Nature</i> , 463(7278):178-83.	http://phytozome-next.jgi.doe.gov/info/Allyrate_v2_1#:~:text=Overview,a%620single%20individual%20was%20obtained.
265	74	<i>Phaseolus vulgaris</i>	pvu	Viridiplantae	587.00	521.08	chromosomes	28,217	27197	phytozome	Schmutz J., et al. (2014). A reference genome for common bean and genome-wide analysis of dual domestications. <i>Nature Genetics</i> , 46: 707-713.	https://phytozome-next.jgi.doe.gov/Phytozome_v2_1
266	75	<i>Citrullus lanatus</i>	cla	Viridiplantae	425.00	355.25	chromosomes	23,440	23440	cugedb	Guo S., et al. (2013). The draft genome of watermelon (<i>Citrullus lanatus</i>) and resequencing of 20 diverse accessions. <i>Nature Genetics</i> , 45: 51-58.	http://www.icugi.org/pub/genome/watermelon/v1/
267	76	<i>Cucumis melo</i>	cml	Viridiplantae	454.00	375.49	assembly	27,427	27427	melonomics	Garcí-Mas J., et al. (2012). The Genome of melon (<i>Cucumis melo</i> L.). <i>Proc Natl Acad Sci U S A</i> , 109(29):11872-7.	https://melonomics.net/files/Genome/
268	77	<i>Cucumis sativus</i>	csa	Viridiplantae	367.00	203.06	assembly	26,682	21503	phytozome	Huang S., et al. (2009). The genome of the cucumber, <i>Cucumis sativus</i> L. <i>Nature Genetics</i> , 41: 1275-1281.	http://ftp.jgi-psf.org/pub/compgen/phytozome/v9.0/Csativus/ ; http://ftp.plantgdb.org/download/Genomes/CsGDB/ ; http://ftp.jgi-psf.org/pub/compgen/phytozome/v9.0/Csativus/
269	78	<i>Fragaria vesca</i>	fve	Viridiplantae	241.00	206.89	chromosomes	34,809	32831	phytozome	Shulaev V., et al. (2011). The genome of the woodland strawberry (<i>Fragaria vesca</i>). <i>Nature genetics</i> , 43: 109-116.	http://www.rosaceae.org/projects/strawberry_genome/v1.1/assembly
270	79	<i>Prunus mume</i>	pmu	Viridiplantae	280.00	237.2	chromosomes	31,390	31390	bjfu	Zhang Q., et al. (2012). The genome of <i>Prunus mume</i> . <i>Nature Communications</i> 3, Article number: 1318.	http://prunusmumegenome.bjfu.edu.cn/
271	80	<i>Prunus persica</i>	ppe	Viridiplantae	269.00	227.25	chromosomes	27852	27864	phytozome	The International Peach Genome Initiative, Verde I., et al. (2013). The high-quality draft genome of peach (<i>Prunus persica</i>) identifies unique patterns of genetic diversity, domestication and genome evolution. <i>Nature Genetics</i> , 45:487-494. Ahmad R., et al. (2011). Whole genome sequencing of peach (<i>Prunus persica</i> L.) for SNP identification and selection. <i>BMC Genomics</i> 2011, 12:569.	http://ftp.jgi-psf.org/pub/compgen/phytozome/v9.0/Ppersica/
272	81	<i>Malus domestica</i>	mdo	Viridiplantae	792.00	609.31	chromosomes	57,386	58960	gdr	Velasco R., et al. (2010). The genome of the domesticated apple (<i>Malus × domestica</i> Borkh.). <i>Nature Genetics</i> , 42: 833-839.	https://www.rosaceae.org/species/malus_x_domestica/
273	82	<i>Pyrus bretschneideri</i>	pyb	Viridiplantae	527.00	508.97	chromosomes	42,812	42369	gigadb	Wu J., et al. (2013). The genome of the pear (<i>Pyrus bretschneideri</i> Rehd.). <i>Genome Res</i> , 23: 396-408.	http://gigadb.org/dataset/100083