

Ens84	Common name	Scientific name	Abbreviation	Assembly Ensembl	Assembly NCBI
	Anole lizard	Anolis carolinensis	Aca	AnoCar2.0	AnoCar2.0
	Amphioxus	Branchiostoma floridae	Bfl		GCA_000003815.1 Version 2
	Ciona intestinalis	Ciona intestinalis	Cin	KH	KH
	Ciona savignyii	Ciona savignyii	Csa	CSAV 2.0	
	Caenorhabditis elegans	Caenorhabditis elegans	Cel	WBcel235	
	Chicken	Gallus gallus	Gga	Galgal4	
	Chinese softshell turtle	Pelodiscus sinensis	Psi	PelSin_1.0	PelSin_1.0
	Coelacanth	Latimeria chalumnae	Lch	LatCha1	LatCha1
	Fruitfly	Drosophila melanogaster	Dme	BDGP6	
	Human	Homo sapiens	Hsa	GRCh38.p5	
	Spotted gar	Lepisosteus oculatus	Loc	LepOcu1	LepOcu1
	Zebrafish	Danio rerio	Dre	GRCz10	GRCz11

Species	HGNC_ZFIN or FlyBase name	Chromosome/scaffold locations	Ensembl ID or NCBI accession number	Transcript ID	Assigned taxa ID	Comments/Annotation notes
Human	ANP32E	1: 150.22m	ENSG00000143401	ENST00000563931	Hsa_1_ANP32E	
	ANP32B	9: 97.98m	ENSG00000136938	ENST00000339399	Hsa_9_ANP32B	
	ANP32D	12: 48.47m	ENSG00000139223	ENST00000266594		contains no introns, pseudogene
	ANP32A	15: 68.78m	ENSG00000140350	ENST00000465139	Hsa_15_ANP32A	
Chicken		10: 18.73m	ENSGALG00000080954	ENSGALT0000013068	Gga_10	
		25: 29.85k	ENSGALG00000013464	ENSGALT0000021945	Gga_25	
		28: 1712.02k	ENSGALG00000001580	ENSGALT0000002401	Gga_28	assigned family member name in syntenic figure and tree: novel
Anole lizard		GL343544: 0.24m	ENSACAG00000004336	ENSACAT00000004337	Aca_scaffoldGL343544	manually edited
		GL343671: 0.26m	ENSACAG00000001378	ENSACAT00000013866	Aca_scaffoldGL343671	
		GL343697: 0.23m	ENSACAG00000008040	ENSACAT00000008066	Aca_scaffoldGL343697	
Coelacanth		JH126613: 1: 550.96k	ENSLACG00000010958	ENSLACT00000012531	Lch_scaffoldJH126613	assigned family member name in tree: novel
		JH126917: 1: 987.06k	ENSLACG00000014232	ENSLACT00000016269	Lch_scaffoldJH126917	
		JH127275: 1: 590.71k	ENSLACG00000011320	ENSLACT00000012950	Lch_scaffoldJH127275	
		JH127010: 1: 467.00k	ENSLACG00000010064	ENSLACT00000011527	Lch_scaffoldJH127010	
Spotted gar		LG19: 1869.47k	ENSLOC00000001045	ENSLOCT00000001178	Loc_LG19	manually edited, assigned family member name in syntenic figure and tree: novel
		LG24: 7.98m	ENSLOC00000008924	ENSLOCT00000010502	Loc_LG24	
		LG3: 43.74m	ENSLOC000000013972	ENSLOCT00000017254	Loc_LG3	manually edited
		LG4: 50.37m	ENSLOC00000011941	ENSLOCT00000014714	Loc_LG4	
Zebrafish	anp32b	1: 25.97m	ENSNDARG00000023330	ENSNDART00000102500	Dre_1_anp32b	
	anp32a	7: 33.07m	ENSNDARG00000006487	ENSNDART00000008785	Dre_7_anp32a	
	anp32e	19: 42.76m	ENSNDARG00000054804	ENSNDART00000070599	Dre_19_anp32e	
Ciona intestinalis		3: 3.10m	ENSCING00000001232	ENSCINT00000002382	Cin_3	
Ciona savignyii		reflitg_1: 4.88m	ENSCSAVG00000011549	ENSCSAVT00000019911	Csa_ref1	
Fruitfly	Mapmodulin	2R: 17.87m	FBgn0034282	FBtr0113091	Dme_2R	

Species	HGNC_ZFIN or FlyBase name	Chromosome/scaffold locations	Ensembl ID or NCBI accession number	Transcript ID	Assigned taxa ID	Comments/Annotation notes
Human	APH1A	1: 150.27m	ENSG00000117362	ENST00000360244	Hsa_1_APH1A	
	APH1B	15: 63.28m	ENSG00000138613	ENST00000261879	Hsa_15_APH1B	
Chicken		25: 1569.58k	ENSGALG00000028838	ENSGALT00000043142	Gga_25	
		Z: 9.08m	ENSGALG00000002578	ENSGALT00000004064	Gga_Z	assigned family member name in tree: APH1
Chinese softshell turtle		NW_005857372.1: 74.67k	XP_006131171.1		Psi_scaffoldNW005857372	nov-15. Assigned family member name in tree: APH1
		NW_005853750.1: 0.29m	XP_014426560.1		Psi_scaffoldNW005853750	nov-15
Coelacanth		JH126577: 1: 673.63k	ENSLACG00000012093	ENSLACT00000013835	Lch_scaffoldJH126577	assigned family member name in tree: APH1
		JH127392: 1: 511.27k	ENSLACG00000010519	ENSLACT00000012043	Lch_scaffoldJH127392	
		JH127746: 1: 358.87k	ENSLACG00000008646	ENSLACT00000009881	Lch_scaffoldJH127746	
Spotted gar		LG2: 22.24m	ENSLOC000000007436	ENSLOCT00000009032	Loc_LG2	assigned family member name in syntenic figure and tree: APH1
		LG24: 5.04m	ENSLOC00000006674	ENSLOCT00000008068	Loc_LG24	
		LG3: 54.36m	ENSLOC00000014889	ENSLOCT00000018364	Loc_LG3	
Zebrafish	aph1b	7: 28.91m	ENSNDARG00000005612	ENSNDART00000008096	Dre_7_aph1b	
	zgc:114200	10: 6.38m	ENSNDARG00000100633	ENSNDART00000170548	Dre_10_aph1	assigned gene name in this study: aph1
Ciona intestinalis		14: 1440.45k	ENSCING00000002845	ENSCINT00000005808	Cin_14	
Ciona savignyii		reflitg_49: 2.64m	ENSCSAVG00000009986	ENSCSAVT00000017157	Csa_ref49	
Fruitfly	aph-1	2L: 2.77m	FBgn0031458	FBtr0077716	Dme_2L	

Species	HGNC_ZFIN or FlyBase name	Chromosome/scaffold locations	Ensembl ID or NCBI accession number	Transcript ID	Assigned taxa ID	Comments/Annotation notes
Human	AQP10	1: 154.32m	ENSG00000143595	ENST00000324978	Hsa_1_AQP10	
	AQP7	9: 33.38m	ENSG00000165269	ENST00000297988	Hsa_9_AQP7	
	AQP3	9: 33.44m	ENSG00000165272	ENST00000297991	Hsa_9_AQP3	
	AQP9	15: 58.14m	ENSG00000103569	ENST00000219919	Hsa_15_AQP9	
Chicken		25: 2.15m	XP_015154084.1		Gga_25	jan-16
		Z: 6.99m	ENSGALG00000018534	ENSGALT00000003866	Gga_Z_1	
		Z: 7.05m	ENSGALG00000002452	ENSGALT00000003868	Gga_Z_2	
Coelacanth		10: 6.57m	ENSGALG00000004261	ENSGALT00000006776	Gga_10	
		JH127649: 1: 7.64k	ENSLACG000000010114	ENSLACT00000001143	Lch_scaffoldJH127649_1	
		JH127649: 1: 100.95k	ENSLACG00000003909	ENSLACT00000004434	Lch_scaffoldJH127649_2	
Spotted gar		JH127034: 1: 519.94k	ENSLACG000000022342	ENSLACT000000026673	Lch_scaffoldJH127034	
		LG24: 6.05m	ENSLOC000000007547	ENSLOCT000000009170	Loc_LG24_1	
		LG2: 12.99m	ENSLOC00000005015	ENSLOCT00000006068	Loc_LG2	
Zebrafish		LG3: 41.58m	ENSLOC00000013583	ENSLOCT00000016782	Loc_LG3	
	aqp10a	16: 22.37m	ENSNDARG00000007086	ENSNDART00000124718	Dre_16_aqp10a	
	aqp10b	19: 7.89m	ENSNDARG00000058678	ENSNDART000000081592	Dre_19_aqp10b	
	aqp7	21: 11.92m	ENSNDARG00000026787	ENSNDART00000123522	Dre_21_aqp7	
	aqp3a	5: 42.41m	ENSNDARG00000003808	ENSNDART00000009182	Dre_5_aqp3a	
	aqp3b	21: 16.94m	ENSNDARG00000069518	ENSNDART00000101241	Dre_21_aqp3b	
Amphioxus		7: 30.10m	ENSNDARG00000053480	ENSNDART00000075513	Dre_7_aqp9b	
		NW_003101541.1	XP_002609960.1		Bfl_scaffoldNW003101541	Jul-16
C elegans		NW_003101512.1	XP_002604987.1		Bfl_scaffoldNW003101512	Jul-16
		II: 9.28m	WBGene00000170	C01G6.1a.1	Cel_II_2	
		II: 7.24m	WBGene00000169	F32A5.5a	Cel_II_1	
		IV: 10.96m	WBGene00000171	Y69E1A.7a	Cel_IV	
		X: 3.03m	WBGene00000175	M02F4.8.1	Cel_X_1	
	X: 4.70m	WBGene00000176	K02G10.7b	Cel_X_2		

Species	HGNC_ZFIN or FlyBase name	Chromosome/scaffold locations	Ensembl ID or NCBI accession number	Transcript ID	Assigned taxa ID	Comments/Annotation notes
Human	ARHGEF2	1: 155.95m	ENSG00000116584	ENST00000361247	Hsa_1_ARHGEF2	
	AKAP13	15: 85.39m	ENSG00000170776	ENST00000361243	Hsa_15_AKAP13	
	ARHGEF28	5: 73.63m	ENSG00000214944	ENST00000545377	Hsa_5_ARHGEF28	
	ARHGEF18	19: 7.40m	ENSG00000104880	ENST00000359820	Hsa_19_ARHGEF18	
Chicken		10: 13.47m	XP_015147538.1		Gga_10	
		Z: 24.43m	ENSGALG00000014923	ENSGALT00000024069	Gga_Z	
		28: 3.84m	ENSGALG00000003572	ENSGALT00000005655	Gga_28	
Chinese softshell turtle		JH206249: 6.61m	ENSPSIG00000005876	ENSPSIT00000006449	Psi_scaffoldJH206249	
Coelacanth		JH127704: 1: 267.79k	ENSLACG000000007285	ENSLACT00000008297	Lch_scaffoldJH127704	
		NW_005819199.1: 0.97m	XP_014342695.1		Lch_scaffoldNW005819199	
		JH127918: 1: 205.34k	ENSLACG00000006187	ENSLACT00000007026	Lch_scaffoldJH127918	
		JH128563: 1: 276.48k	ENSLACG00000007446	ENSLACT00000008478	Lch_scaffoldJH128563	
Spotted gar		LG24: 5.73m	ENSLOC000000007365	ENSLOCT00000008956	Loc_LG24	
		LG3: 50.05m	ENSLOC00000014508	ENSLOCT00000017889	Loc_LG3	
		LG2: 44.92m	ENSLOC00000011032	ENSLOCT00000013576	Loc_LG24	
		LG19: 6.08m	ENSLOC00000004244	ENSLOCT00000005082	Loc_LG19	
Zebrafish	arhgef1a	19: 11.12m	ENSNDARG00000040380	ENSNDART00000059102	Dre_19_arhgef1a	assigned gene name in this study: arhgef2a
	arhgef2	16: 6.92m	ENSNDARG00000075819	ENSNDART00000078306	Dre_16_arhgef2b	assigned gene name in this study: arhgef2b
	si:dkey-172h23.2	7: 14.84m	ENSNDARG00000023868	ENSNDART00000173072	Dre_7_ahap13a	assigned gene name in this study: akap13a

Coelacanth		JH126577.1: 3.30m JH128820.1: 729 JH128139.1: 168.36k	ENSLACG00000018435 ENSLACG00000000213 ENSLACG00000005455	ENSLACT00000021122 ENSLACT0000000238 ENSLACT00000006202	Lch_scaffoldJH126577 Lch_scaffoldJH128820 Lch_scaffoldJH128139
Spotted gar		LG3: 41.95m LG2: 17.56m LG24: 9.25m	ENSLOC00000013672 ENSLOC00000006743 ENSLOC00000009056	ENSLOCT00000016883 ENSLOCT00000008158 ENSLOCT00000011057	Loc_LG3 Loc_LG2 LG24
Zebrafish	mtmr10 mtmr12 mtmr11	7: 30.45m 5: 40.50m 16: 46.03m	ENSARG00000010601 ENSARG00000059817 ENSARG000000069755	ENSART000000085716 ENSART000000083561 ENSART000000101753	Dre_7_mtmr10 Dre_5_mtmr12 Dre_16_mtmr11
Amphioxus		NW_003101420.1	XP_002594546.1		Bfl_scaffoldNW003101420
Ciona intestinalis		HT000074.1: 230.30k	ENSCING00000024080	ENSCINT00000036049	Cin_HT000074
Fruitley		X: 14.83m	FBgn0030582	FBtr0073946	Dme_X

Species	HGNC_ZFIN or FlyBase name	Chromosome/scaffold locations	Ensembl ID or NCBI accession number	Transcript ID	Assigned taxa ID	Comments/Annotation notes
Human	MYO1E	15: 59.13m	ENSG00000157483	ENST0000028235	Hsa_15_MYO1E	
	MYO1F	19: 8.52m	ENSG00000142347	ENST00000338257	Hsa_10_MYO1F	
Chicken		10: 6.23m 28: 1.74m	ENSGALG00000004150 NP_990585.1	ENSGALT00000006599	Gga_10 Gga_28	16-apr
Anole lizard		Contig AAWZ0037949: 0.30k GL343573: 0.13m GL343616: 0.31m	ENSACAG00000016910 ENSACAG00000015242 ENSACAG00000000455	ENSACAT00000017027 ENSACAT00000015351 ENSACAT00000000711	Aca_contigAAWZ0037949 Aca_scaffoldGL343573 Aca_scaffoldGL343616	assigned family member name in synteny figure and tree: MYO11
Coelacanth		JH127474.1: 193.50k JH126613.1: 471.79k	ENSLACG00000005949 ENSLACG00000010079	ENSLACT00000006762 ENSLACT00000011542	Lch_scaffoldJH127474 Lch_scaffoldJH126613	assigned family member name in synteny figure and tree: MYO11
Spotted gar		LG3: 41.83m LG19: 1886.03k LG24: 7.70m	ENSLOC00000013657 ENSLOC00000001068 ENSLOC00000008426	ENSLOCT00000016876 ENSLOCT0000001223 ENSLOCT00000010268	Loc_LG3 Loc_LG19 Loc_LG24	manually edited assigned family member name in synteny figure and tree: MYO11
Zebrafish	myo1f myo1ea myo1eb	8: 20.22m 7: 30.36m 16: 38.25m	ENSARG00000078734 XP_005168983.1 NP_956930.1	ENSART00000148304	Dre_8_myo1f Dre_7_myo1e Dre_16_myo1f	jun-16. Assigned gene name in this study: myo1e jun-16. Assigned gene name in this study: myo1f
Ciona intestinalis		Scaffold HT000104.1: 44.64k	ENSCING00000003718	ENSCINT00000007773	Cin_scaffoldHT000104	
C elegans		I: 8.85m	WBGene00002035	F29D10.4	Cel_I	

Species	HGNC_ZFIN or FlyBase name	Chromosome/scaffold locations	Ensembl ID or NCBI accession number	Transcript ID	Assigned taxa ID	Comments/Annotation notes
Human	PEAR1	1: 156.89m	ENSG00000187800	ENST00000292357	Hsa_1_PEAR1	
	MEGF11	15: 65.90m	ENSG00000157890	ENST00000422354	Hsa_15_MEGF11	
	MEGF10	5: 127.29m	ENSG00000145794	ENST00000274473	Hsa_5_MEGF10	
Chicken		25: 404.20k Z: 56.17m 10: 17.67m	ENSGALG00000028622 ENSGALG00000014699 ENSGALG00000007631	ENSGALT00000045144 ENSGALT00000023694 ENSGALT00000012349	Gga_25 Gga_Z Gga_10	
Coelacanth		NW_005819113.1: 1.45m NW_005819856.1: 0.47m NW_005819068.1: 0.42m		XP_014341393.1 XP_014348032.1 XP_014340580.1	Lch_scaffoldNW005819113 Lch_scaffoldNW005819856 Lch_scaffoldNW005819068	oct-15 oct-15 oct-15
Spotted gar		LG24: 8.52m LG3: 42.95m LG2: 26.54m	ENSLOC00000008463	ENSLOCT00000010314	Loc_LG24 Loc_LG3 Loc_LG2	jan-16 jan-16
Zebrafish	pear1 megf11 megf10	16: 30.48m 18: 19.14m 10: 16.11m	ENSARG00000006753 XP_009291879.1 ENSARG00000017229	ENSART00000137977 XP_009291879.1 ENSART00000154835	Dre_16_pear1 Dre_18_megf11 Dre_10_megf10	jun-17
Amphioxus		NW_003101452.1: 0.13 NW_003101570.1: 2.79m		XP_002597880.1 XP_002613914.1	Bfl_scaffoldNW003101452 Bfl_scaffoldNW003101570	oct-09 oct-09
Fruitley	drpr	3L: 1715.80k	FBgn0027594	FBtr0334079	Dme_3L	
C elegans		II: 11.85m	WBGene00000415	Y47H9C.4a	Cel_II	

Species	HGNC_ZFIN or FlyBase name	Chromosome/scaffold locations	Ensembl ID or NCBI accession number	Transcript ID	Assigned taxa ID	Comments/Annotation notes
Human	SV2A	1: 149.90m	ENSG00000159164	ENST00000369146	Hsa_1_SV2A	
	SV2B	15: 91.10m	ENSG00000185518	ENST00000330276	Hsa_15_SV2B	
	SV2C	5: 76.08m	ENSG00000122012	ENST00000502798	Hsa_5_SV2C	
Chicken		25: 0.94m 10: 13.70m Z: 23.45m	XP_015153832.1 ENSGALG00000006859 ENSGALG00000014967	ENSGALT00000011103 ENSGALT00000032846	Gga_25 Gga_10 Gga_Z	jan-16
Coelacanth		JH126664.1: 237.84k JH126693.1: 5.71k JH126756.1: 1560.36k	ENSLACG00000006807 ENSLACG00000012173 ENSLACG00000000841 ENSLACG00000016393	ENSLACT00000007747 ENSLACT00000013924 ENSLACT00000000951 ENSLACT00000018752	Lch_scaffoldJH126664 Lch_scaffoldJH126750 Lch_scaffoldJH126693 Lch_scaffoldJH126756	manually edited
Spotted gar		LG24: 9.15m LG3: 49.90m LG2: 14.25m LG3: 55.57m	ENSLOC00000009018 ENSLOC00000014500 ENSLOC00000005520 ENSLOC00000015007	ENSLOCT00000011026 ENSLOCT00000017882 ENSLOCT00000006675 ENSLOCT00000018508	Loc_LG24 Loc_LG3_1 Loc_LG2 Loc_LG3_2	
Zebrafish	sv2a sv2ba sv2bb sv2c sv2	16: 46.14m 7: 15.02m 25: 10.94m 5: 45.39m 25: 5.92m	ENSARG00000059945 ENSARG00000057427 ENSARG000000060711 ENSARG00000059997 ENSARG00000091833	ENSART000000083919 ENSART00000124676 ENSART00000154748 ENSART00000084024 ENSART00000128816	Dre_16_sv2a Dre_7_sv2ba Dre_25_2_sv2bb Dre_5_sv2ca Dre_25_1_sv2	manually edited. Assigned gene name in this study: sv2ca
Amphioxus		NW_003101517.1: 0.69m NW_003101517.1: 0.67m		XP_002805503.1 XP_002805502.1	Bfl_scaffoldNW003101517 Bfl_scaffoldNW003101517	oct-09. Manually edited, sequences combined.
Ciona intestinalis		14: 2.46m	ENSCING00000000453	ENSCINT00000000831	Cin_14	
Ciona savignyi		ref1g_76: 2.07m	ENSCSAVG00000008201	ENSCSAVT00000014155	Csa_ref76	
Fruitley		X: 6.72m	FBgn0029896	FBtr0079885	Dme_X	
Human	SVOP1	7: 138.59m	ENSG00000157703	ENST00000419765	Hsa_7_SVOP1	
Chicken		1: 56.51m	ENSGALG00000012812	ENSGALT00000020903	Gga_1	
Spotted gar		LG8: 46.34m	ENSLOC00000016932	ENSLOCT00000020969	Loc_LG8	
Human	SVOP	12: 108.91m	ENSG00000166111	ENST000000610966	Hsa_12_SVOP1	
Chicken		15: 6.61m	ENSGALG00000004970	ENSGALT00000007970	Gga_15	
Spotted gar		LG20: 6.17m	ENSLOC00000004555	ENSLOCT00000005455	Loc_LG20	