|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Ens87** | **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 |   |  |
|   | Ciona savignyi | Ciona savignyi | Csa | CSAV 2.0 |   |  |
|   | Caenorhabditis elegans | Caenorhabditis elegans | Cel | WBcel235 |   |  |
|   | Chicken | Gallus gallus | Gga | Gallus\_gallus-5.0 |   |  |
|   | Chinese softshell turtle | Pelodiscus sinensis | Psi | PelSin\_1.0 |   |  |
|   | Coelacanth | Latimeria chalumnae | Lch | LatCha1 | LatCha1 |  |
|   | Fruitfly | Drosophila melanogaster | Dme | BDGP6 |   |  |
|   | Human | Homo sapiens | Hsa | GRCh38.p7 |   |  |
|   | Medaka | Oryzias latipes | Ola | HdrR |   |  |
|   | Purple sea urchin | Strongylocentrotus purpuratus | Spu | Spur\_4.2 |   |  |
|   | 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 sequence name** | **Comments/Annotation notes** |
| Human | ATL1 | 14: 50.53m | ENSG00000198513  | ENST00000441560.6 | Hsa.14 |   |
|   | ATL2 | 2: 38.29m | ENSG00000119787 | ENST00000378954.8 | Hsa.2 |   |
|   | ATL3 | 11: 63.62m | ENSG00000184743 | ENST00000398868.7 | Hsa.11 |   |
| Chicken |   | 5: 58.00m | ENSGALG00000012339 | ENSGALT00000020162.5 | Gga.5 |   |
|   |   | 3: 16.43m | ENSGALG00000037289 | ENSGALT00000065464.1 | Gga.3 |   |
| Anole lizard |   | Scaffold GL343890.1: 68.89k | ENSACAG00000002701 | ENSACAT00000002836.3 | Aca.GL343890 |   |
|   |   | 1: 254.16m | ENSACAG00000014506 | ENSACAT00000014651.3 | Aca.1 |   |
| Coelacanth  | Scaffold JH126849.1: 676.04k | ENSLACG00000012098 | ENSLACT00000013840.1 | Lch.JH126849 |   |
|   |   | Scaffold JH126593.1: 88.70k | ENSLACG00000003585 | ENSLACT00000004062.2 | Lch.JH126593 |   |
| Spotted gar  | LG7: 12.07m | ENSLOCG00000011885 | ENSLOCT00000014646.1 | Loc.LG7 |   |
|   |  | LG16: 4.55m | ENSLOCG00000015787 | ENSLOCT00000019475.1 | Loc.LG16 |   |
|   |   |  LG28: 118.01k | ENSLOCG00000000849 | ENSLOCT00000000956.1 | Loc.LG28 |   |
| Zebrafish | atl1 | 13: 36.64m | ENSDARG00000060481 | ENSDART00000111832.4 | Dre.13.2 |   |
|   | atl2 | 13: 7.95m | ENSDARG00000057719 | ENSDART00000080460.6 | Dre.13.1 |   |
|   | atl3 | 14: 30.43m | ENSDARG00000004270 | ENSDART00000023054.9 | Dre.14 |   |
| Amphioxus  | NW\_003101444.1:1.84m | XP\_002596876.1 |   | Bfl.NW\_003101444 | oct-09 |
| Fruitfly | atl | 3R: 24.63m | FBgn0039213 | FBtr0084657 | Dme.3R |   |
| Caenorhabditis elegans | IV: 2.79m | WBGene00021868 | Y54G2A.2b | Cel.IV |   |
|  |  |  |  |  |  |  |
| **Species** | **HGNC,ZFIN or FlyBase name** | **Chromosome/scaffold locations** | **Ensembl ID or NCBI accession number** | **Transcript ID** | **Assigned sequence name** | **Comments/Annotation notes** |
| Human | EHD1 | 11: 64.85m | ENSG00000110047 | ENST00000320631.7 | Hsa.11 |   |
|   | EHD2 | 19: 47.71m | ENSG00000024422 | ENST00000263277.7 | Hsa.19 |   |
|   | EHD3 | 2: 31.23m | ENSG00000013016 | ENST00000322054.9 | Hsa.2 |   |
|   | EHD4 | 15: 41.90m | ENSG00000103966  | ENST00000220325.8 | Hsa.15 |   |
| Chicken |   | Scaffold NT\_465842.1:0.05k | XP\_015129283.1 |   | Gga.scaffold | jan-16, manually edited |
|   |  | 3: 7.72m | ENSGALG00000009086 | ENSGALT00000014784.3 | Gga.3 |   |
|   |   | 5: 25.30m | ENSGALG00000008950 | ENSGALT00000014555.4 | Gga.5 |   |
| Anole lizard |   | NW\_003342544.1:0.02m | XP\_003230702.2 |   | Aca.NW\_003342544 | may-16 |
|   |  | 1: 40.55m | ENSACAG00000014864 | ENSACAT00000014952.3 | Aca.1.1 |   |
|   |  | 1: 250.59m | ENSACAG00000007103 | ENSACAT00000007133.2 | Aca.1.2 |   |
|   |   | NW\_003339612.1 :0.09m | XP\_003229733.2 |   | Aca.NW\_003339612 | may-16 |
| Chinese softshell turtle |   | Scaffold JH212639.1: 172.05k | ENSPSIG00000005727 | ENSPSIT00000006245.1 | Psi.JH212639 |   |
|   |  | Scaffold JH207369.1: 2.77m | ENSPSIG00000017757 | ENSPSIT00000020163.1 | Psi.JH207369 |   |
|   |   | Scaffold JH210682.1: 460.57k | ENSPSIG00000016990 | ENSPSIT00000019278.1 | Psi.JH210682 |   |
| Coelacanth  | Scaffold JH126593.1: 2.81m | ENSLACG00000018148 | ENSLACT00000020794.1 | Lch.Jh126593 | manually edited |
|   |  | Scaffold JH126578.1: 3.07m | ENSLACG00000018332  | ENSLACT00000021006.1 | Lch.JH126578 | manually edited |
|   |  | Scaffold JH128897.1: 108.39k | ENSLACG00000004089 | ENSLACT00000004631.1 | Lch.JH128897 | manually edited |
|   |   | Scaffold JH126639.1: 2.39m | ENSLACG00000017804 | ENSLACT00000020398.1 | Lch.JH126639 | manually edited |
| Spotted Gar  | LG28: 160.66k | ENSLOCG00000000924 |  ENSLOCT00000001034.1 | Loc.LG28 | manually edited |
|   |  | LG2: 62.19m | ENSLOCG00000014200 | ENSLOCT00000017525.1 | Loc.LG2 | manually edited |
|   |  | LG1: 46.26m | ENSLOCG00000016786  |  ENSLOCT00000020785.1 | Loc.LG1 |   |
|   |   | LG7: 6.14m | ENSLOCG00000009774 | ENSLOCT00000011963.1 | Loc.LG7 |   |
| Zebrafish | ehd1a | 14: 46.45m | ENSDARG00000098853 | ENSDART00000173209.1 | Dre.14 |   |
|   | ehd1b | 10: 27.11m | ENSDARG00000014793 | ENSDART00000012717.7 | Dre.10 |   |
|   | ehd2a | 5: 61.31m | ENSDARG00000035137 | ENSDART00000050885.4 | Dre.5 |   |
|   | ehd2b | 18: 44.66m | ENSDARG00000040362 | ENSDART00000059063.3 | Dre.18 |   |
|   | ehd3 | 20: 38.30m | ENSDARG00000007869 | ENSDART00000022694.6 | Dre.20 |   |
|   | ehd4 | 17:29.19m | XP\_698033.4 |   | Dre.17 | jun-17 |
| Ciona intestinalis |   | 2: 2.68m | ENSCING00000005231 | ENSCINT00000010754.3 | Cin.2 |   |
| Ciona savignyi |   | reftig\_219: 187.05k | ENSCSAVG00000000028 | ENSCSAVT00000000059.1 | Csa.ref219 |   |
| Caenorhabditis elegans | V: 6.21m | WBGene00004373 | W06H8.1a | Cel.V |   |
| Fruitfly | Past1 | 3R: 12.70m | FBgn0016693 | FBtr0082654 | Dme.3R |   |
|  |  |  |  |  |  |  |
| **Species** | **HGNC,ZFIN or FlyBase name** | **Chromosome/scaffold locations** | **Ensembl ID or NCBI accession number** | **Transcript ID** | **Assigned sequence name** | **Comments/Annotation notes** |
| Human | FERMT1 | 20: 6.07m | ENSG00000101311 | ENST00000217289.8 | Hsa.20 |   |
|   | FERMT2 | 14: 52.86m | ENSG00000073712 | ENST00000343279.8 | Hsa.14 |   |
|   | FERMT3 | 11: 64.21m | ENSG00000149781 | ENST00000279227.9 | Hsa.11 |   |
| Chicken |   | 3: 15.31m | ENSGALG00000008827 | ENSGALT00000014344.5 | Gga.3 |   |
|   |   |  5: 58.40m | ENSGALG00000012425 | ENSGALT00000020309.5 | Gga.5 |   |
| Chinese softshell turtle | Scaffold JH210532.1: 49.20k | ENSPSIG00000008127 | ENSPSIT00000009189.1  | Psi.JH210532 |   |
|   |  | Scaffold JH206845.1: 2.39m | ENSPSIG00000014143 | ENSPSIT00000016041.1 | Psi.JH206845 |   |
|   |   | Scaffold JH212622.1: 456.01k | ENSPSIG00000005395 | ENSPSIT00000005845.1 | Psi.2JH12622 |   |
| Coelacanth  | Scaffold JH126648.1: 1445.85k | ENSLACG00000016076 | ENSLACT00000018382.1 | Lch.JH126648 |   |
|   |  | Scaffold JH126564.1: 7.75m | ENSLACG00000019103 | ENSLACT00000021880.1 | Lch.JH126564 |   |
|   |   | Scaffold JH126593.1: 1785.83k | ENSLACG00000016877 | ENSLACT00000019317.1 | Lch.JH126593 |   |
| Spotted gar  | LG1: 34.61m | ENSLOCG00000016445 | ENSLOCT00000020347.1 | Loc.LG1 |   |
|   |  | LG7: 12.89m | ENSLOCG00000012153 | ENSLOCT00000014982.1 | Loc.LG7 |   |
|   |   | LG28: 537.85k | ENSLOCG00000001364 | ENSLOCT00000001550.1 | Loc.LG28 | manually edited |
| Zebrafish | fermt1 | 20: 45.87m | ENSDARG00000052652 | ENSDART00000074546.5 | Dre.20 |   |
|   | fermt2 | 17: 50.62m | ENSDARG00000020242 | ENSDART00000049464.7 | Dre.17 |   |
|   | fermt3a | 5: 66.08m | ENSDARG00000079267 | ENSDART00000113077.3 | Dre.5 |   |
|   | fermt3b | 14: 46.92m | ENSDARG00000030938 | ENSDART00000047716.6 | Dre.14 |   |
| Ciona intestinalis |   | 1:8.43m | XP\_009862486.1 |   | Cin.1 | oct-16 |
| Fruitfly | Fit2 | 3L: 17.02m | FBgn0036688 | FBtr0075275 | Dme.3L.2 |   |
|   | Fit1 | 3L: 4.10m | FBgn0035498 | FBtr0073210  | Dme.3L.1 |   |
| Caenorhabditis elegans | V: 14.69m | WBGene00006836 | C47E8.7.2 | Cel.V |   |
|  |  |  |  |  |  |  |
| **Species** | **HGNC,ZFIN or FlyBase name** | **Chromosome/scaffold locations** | **Ensembl ID or NCBI accession number** | **Transcript ID** | **Assigned sequence name** | **Comments/Annotation notes** |
| Human | JAG2 | 14: 105.14m | ENSG00000184916 | ENST00000331782.7 | Hsa.14 |   |
|   | JAG1 | 20: 10.64m | ENSG00000101384 | ENST00000254958.9 | Hsa.20 |   |
| Chicken |   | 3: 13.51m | ENSGALG00000009020 | ENSGALT00000014678.6 | Gga.3 |   |
|   |   | 5: 52.20m | ENSGALG00000011696 | ENSGALT00000021553.4 | Gga.5 |   |
| Coelacanth | JH126795.1: 11.26k | ENSLACG00000001168 | ENSLACT00000001314.1 | Lch.JH126795 |   |
|   |   | JH126564.1: 775.13k | ENSLACG00000012867 | ENSLACT00000014718.1 | Lch.JH126564 |   |
| Spotted gar  | LG16: 6.35m | ENSLOCG00000015958 | ENSLOCT00000019689.1 | LocLG16 |   |
|   |  | LG2: 66.41m | ENSLOCG00000014652 | ENSLOCT00000018067.1 | Loc.LG2 | assigned family member name in tree: JAG3 |
|   |  | LG7: 7.81m | ENSLOCG00000010321 | ENSLOCT00000012701.1 | Loc.LG7 |   |
| Zebrafish | jag1a | 1: 50.46m | ENSDARG00000030289 | ENSDART00000137172.2 | Dre.1 |   |
|   | jag2a | 13: 33.38m | ENSDARG00000014246 | ENSDART00000025007.8 | Dre.13.1 |   |
|   | jag1b | 13: 35.21m | ENSDARG00000013168 | ENSDART00000019323.6 | Dre.13.2 |   |
|   | CABZ01040999.1 | 18: 35.30m | ENSDARG00000068104 | ENSDART00000098297.4 | Dre.18 | Assigned gene name in this study: jag3 |
|   | jag2b | 20: 21.49m | ENSDARG00000021389 | ENSDART00000024922.6 | Dre.20 |   |
| Ciona intestinalis |   | 11: 5.04m | ENSCING00000021217 | ENSCINT00000031505.1 | Cin.11 |   |
| Ciona savignyi |   | reftig\_13: 1628.86k | ENSCSAVG00000006943 | ENSCSAVT00000011971.1 | Csa.ref13 |   |
| Fruitfly |   | 3R: 27.17m | FBgn0004197 | FBtr0085128 | Dme.3R |   |
|  |  |  |  |  |  |  |
| **Species** | **HGNC,ZFIN or FlyBase name** | **Chromosome/scaffold locations** | **Ensembl ID or NCBI accession number** | **Transcript ID** | **Assigned sequence name** | **Comments/Annotation notes** |
| Human | LTBP1 |  2: 32.95m | ENSG00000049323  | ENST00000418533.6 | Hsa.2 |   |
|   | LTBP2 | 14: 74.50m | ENSG00000119681 | ENST00000261978.8  | Hsa.14 |   |
|   | LTBP3 | 11: 65.54m | ENSG00000168056  | ENST00000322147.8 | Hsa.11 |   |
|   | LTBP4 | 19: 40.59m | ENSG00000090006  | ENST00000204005.13 | Hsa.19 |   |
| Chicken |   | 5: 37.97m | ENSGALG00000010448 | ENSGALT00000017012.5 | Gga.5 |   |
|   |   | 3: 31.21m | ENSGALG00000010258  | ENSGALT00000080003.1 | Gga.3 |   |
| Anole lizard |   | NW\_003340183.1:0.04m | XP\_008122757.1 |   | Aca.NW\_003340183 | may-16, manually edited |
|   |  | LGf: 1900.62k | ENSACAG00000003759 | ENSACAT00000003884.3 | Aca.LGf |   |
|   |  | 1: 231.43m | ENSACAG00000009007 | ENSACAT00000009266.3 | Aca.1.2 |   |
|   |   | 1: 22.97m | ENSACAG00000016494 | ENSACAT00000016615.3 | Aca.1.1 |   |
| Coelacanth  | Scaffold JH126663.1: 1780.03k | ENSLACG00000016869  | ENSLACT00000019309.1 | Lch.JH126663 |   |
|   |  | Scaffold JH128017.1: 47.88k | ENSLACG00000002385  | ENSLACT00000002686.1 | Lch.JH128017 | manually edited |
|   |  | Scaffold JH126700.1: 531.11k | ENSLACG00000010764 | ENSLACT00000012320.1 | Lch.JH126700 |   |
|   |   | NW\_005819014.1:4.28m | XP\_014341338.1 |   | Lch.NW\_005819014 | OCT-2015 |
| Spotted Gar | LG2:64.22m | XP\_015196417.1 |   | Loc.LG2 | jan-16 |
|   |  | LG7: 8.92m | ENSLOCG00000010749 | ENSLOCT00000013204.1 | Loc.LG7 |   |
|   |  | LG16: 16.61m | ENSLOCG00000016686 | ENSLOCT00000020650.1 | Loc.LG16 |   |
|   |   | LG28:3.62m | XP\_015194379.1 |   | Loc.LG28 | jan-16, manually edited |
| Zebrafish | ltbp4 | 18: 49.01m | ENSDARG00000099137 | ENSDART00000160702.1 | Dre.18 | Assigned gene name in this study: ltbp4 |
|   | ltbp3 | 5: 36.92m | ENSDARG00000035682 | ENSDART00000048107.7 | Dre.5 |   |
|   | ltbp1 | 17: 22.94m | ENSDARG00000056922 | ENSDART00000079460.5 | Dre.17 |   |
| Medaka |   | 22: 13.25m | ENSORLG00000016691 | ENSORLT00000020883.1 | Ola.22 |   |
| Fruitfly |   | 4: 215.01k | FBgn0051999 | FBtr0089144 | Dme.4 |   |
| Caenorhabditis elegans | IV: 9.54m | WBGene00001403 | F56H11.1g | Cel.IV |   |
|   |   |  III: 7.63m | WBGene00022816 | ZK783.1k | Cel.III |   |
| Human | FBLN1 | 22: 45.50m | ENSG00000077942 | ENSG00000077942 | Hsa.FBLN1 |   |
|   | FBLN2 | 3: 13.55m | ENSG00000163520 | ENST00000295760.11 | Hsa.FBLN2 |   |
|   | FBLN5 | 14: 91.87m | ENSG00000140092 | ENST00000342058.8 | Hsa.FBLN5 |   |
|   | EFEMP1 | 2: 55.87m | ENSG00000115380 | ENST00000394555.6 | Hsa.EFEMP1 |   |
|   | EFEMP2 | 11: 65.87m | ENSG00000172638 | ENST00000307998.10 | Hsa.EFEMP2 |   |
|  |  |  |  |  |  |  |
| **Species** | **HGNC,ZFIN or FlyBase name** | **Chromosome/scaffold locations** | **Ensembl ID or NCBI accession number** | **Transcript ID** | **Assigned sequence name** | **Comments/Annotation notes** |
| Human | MERTK | 2: 111.90m | ENSG00000153208 | ENST00000421804.6 | Hsa.2 |   |
|   | TYRO3 | 15: 41.56m | ENSG00000092445 | ENST00000263798.7 | Hsa.15 |   |
|   | AXL | 19: 41.22m | ENSG00000167601 | ENST00000359092.7 | Hsa.19 |   |
| Chicken |   | 3: 3.20m | ENSGALG00000008257 | ENSGALT00000013438.4 | Gga.3 |   |
|   |   | 5: 24.92m | ENSGALG00000008631 | ENSGALT00000014067.5 | Gga.5 |   |
| Anole lizard |   | GL343437.1: 208.91k | ENSACAG00000005886 | ENSACAT00000006091.3 | Aca.GL343437 |   |
|   |  | LGf: 3.52m | ENSACAG00000003874 | ENSACAT00000003990.3 | Aca.LGf |   |
|   |   | 1: 41.10m | ENSACAG00000014118 | ENSACAT00000014314.3 | Aca.1 |   |
| Coelacanth | JH128421.1: 230.21k | ENSLACG00000006674 | ENSLACT00000007591.1 | Lch.JH128421 | assigned family member name in tree: novel |
|   |  | JH126731.1: 429.73k | ENSLACG00000009552 | ENSLACT00000010931.1 | Lch.JH126731 |   |
|   |  | JH130650.1: 27.74k | ENSLACG00000001709 | ENSLACT00000001925.1 | Lch.JH130650 | *manually edited* |
|   |   | JH126578.1: 2.53m | ENSLACG00000017950 | ENSLACT00000020563.1 | Lch.JH126578 |   |
| Spotted gar  | LG16: 15.18m | ENSLOCG00000016537 | ENSLOCT00000020464.1 | Loc.LG16 |   |
|   |  | LG2: 61.92m | ENSLOCG00000014171 | ENSLOCT00000017488.1 | Loc.LG2 | *manually edited* |
|   |   | LG7: 11.69m | ENSLOCG00000011682 | ENSLOCT00000014385.1 | Loc.LG7 |   |
| Zebrafish | tyro3 | 17: 10.35m | ENSDARG00000005356 | ENSDART00000140391.2 | Dre.17 |   |
|   | mertka | 13: 47.33m | ENSDARG00000074695 | ENSDART00000109266.3 | Dre.13 |   |
|   | AXL | 15:0.05m | XP\_017206598.2 |  | Dre.15 | may-17. Described as AXL at Ensembl and NCBI |
|   | si:ch73-40a2.1 | 7: 17.82m | ENSDARG00000105521 | ENSDART00000173689.1 | Dre.7 | assigned family member name in synteny figure and tree: novel |
| Ciona intestinalis |   | 14: 149.24k | ENSCING00000000360 | ENSCINT00000027120.2 | Cin.14 |   |
| Ciona savignyi |   | reftig\_49: 261.92k | ENSCSAVG00000007251 | ENSCSAVT00000012473.1 | Csa.ref49 |   |
| Caenorhabditis elegans | X: 6.55m | WBGene00020504 | T14E8.1a | Cel.X |   |
|  |  |  |  |  |  |  |
| **Species** | **HGNC,ZFIN or FlyBase name** | **Chromosome/scaffold locations** | **Ensembl ID or NCBI accession number** | **Transcript ID** | **Assigned sequence name** | **Comments/Annotation notes** |
| Human | NRXN1 |  2: 49.92m | ENSG00000179915 | ENST00000404971.5 | Hsa.2 |   |
|   | NRXN2 | 11: 64.61m | ENSG00000110076 | ENST00000377559.7 | Hsa.11 |   |
|   | NRXN3 | 14: 78.17m | ENSG00000021645 | ENST00000635466.1 | Hsa.14 |   |
| Chicken |   | 3: 6.56m | ENSGALG00000009107 | ENSGALT00000047522.1 | Gga.3 |   |
|   |   | 5:39.57m | NP\_001258852.1 |   | Gga.5 | oct-17 |
| Chinese softshell turtle | NW\_005853176.1:0.91m | XP\_006116042.1 |   | Psi.NW\_005853176 | nov-15 |
|   |  | NW\_005854898.1:1.36m | XP\_014428577.1 |  | Psi.NW\_005854898 | nov-15 |
|   |   | JH211041.1: 591.14k | ENSPSIG00000003726 | ENSPSIT00000003973.1 | Psi.JH211041 |   |
| Coelacanth  | JH126696.1: 1879.38k | ENSLACG00000017041 | ENSLACT00000019509.1 | Lch.JH126696 | *short* |
|   |  | JH126618.1: 75.29k | ENSLACG00000003239 | ENSLACT00000003669.1 | Lch.JH126618 | *manually edited,short* |
|   |  | JH126618.1: 539.47k | ENSLACG00000010836 | ENSLACT00000012400.1 |  |  |
|   |  | JH129271.1: 97.62k | ENSLACG00000003804 | ENSLACT00000004310.1 | Lch.JH129271 | *short* |
|   |  | JH127406.1: 291.56k | ENSLACG00000007669 | ENSLACT00000008743.1 | Lch.JH127406 | *short* |
|   |   | NW\_005819260.1:0.44m | XP\_005995332.1 |   | Lch.NW\_005819260 | oct-15 |
| Spotted gar  | LG7: 2.03m | ENSLOCG00000008835 | ENSLOCT00000010797.1 | Loc.LG7 |   |
|   |  | LG16: 11.51m | ENSLOCG00000016276 | ENSLOCT00000020112.1 | Loc.LG16 |   |
|   |  | LG28: 2.48m | ENSLOCG00000002397 | ENSLOCT00000002886.1 | Loc.LG28 | manually edited |
|   |   | LG28: 3.02m | ENSLOCG00000002471 | ENSLOCT00000002909.1 |   | manually edited |
| Zebrafish | nrwn3a | 17:16.91m | NP\_001073478.1 |   | Dre.17 | dec-17 |
|   | nrxn3b | 20: 5.52m | ENSDARG00000062693 | ENSDART00000090934.5 | Dre.20 |   |
|   | nrxn1a | 12: 24.22m | ENSDARG00000061647 | ENSDART00000093094.6 | Dre.12 |   |
|   | nrxn1b | 13: 602.74k | ENSDARG00000063635 | ENSDART00000149547.2 | Dre.13 |   |
|   | nrxn2a | 21: 27.60m | ENSDARG00000061454 | ENSDART00000141629.2 | Dre.21 |   |
|   | nrxn2b | 7:0.43m | NP\_001073453.1 |   | Dre.7 | aug-17 |
| Ciona intestinalis |   | 3: 962.05k | ENSCING00000005088 | ENSCINT00000010501.3 | Cin.3 |   |
| Fruitfly | Nrx-1  | 3R: 22.47m | FBgn0038975 | FBtr0334610 | Dme.3R |   |
|  |  |  |  |  |  |  |
| **Species** | **HGNC,ZFIN or FlyBase name** | **Chromosome/scaffold locations** | **Ensembl ID or NCBI accession number** | **Transcript ID** | **Assigned sequence name** | **Comments/Annotation notes** |
| Human | PLD3 | 19: 40.35m | ENSG00000105223 | ENST00000356508.9 | Hsa.19 |   |
|   | PLD4 | 14: 104.92m | ENSG00000166428 | ENST00000392593.8 | Hsa.14 |   |
|   | PLD5 | 1: 242.08m | ENSG00000180287  | ENST00000536534.6 | Hsa.1 |   |
| Chicken |   | Scaffold NT\_465812.1:0.01m  | XP\_015129279.1 |   | Gga.scaffold | jan-16 |
|   |  | 3: 35.58m | ENSGALG00000010737 | ENSGALT00000047039.1 | Gga.3 |   |
|   |  | 5: 51.87m | ENSGALG00000011646 | ENSGALT00000019035.6  | Gga.5 |   |
| Chinese softshell turtle | Scaffold JH208232.1: 42.70k | ENSPSIG00000008356 | ENSPSIT00000009316.1 | Psi.JH208232 |   |
|   |  | Scaffold JH211376.1: 990.76k | ENSPSIG00000009358 | ENSPSIT00000010449.1 | Psi.JH211376 |   |
|   |  | Scaffold JH212505.1: 55.98k | ENSPSIG00000004919 | ENSPSIT00000005308.1 | Psi.JH212505 |   |
|   |   | Scaffold JH206113.1: 49.05k | ENSPSIG00000003872 | ENSPSIT00000004138.1 | Psi.JH206113 | assigned family member name in tree: pld7 |
| Coelacanth | Scaffold JH126593.1: 228.36k | ENSLACG00000006642 | ENSLACT00000007554.1 | Lch.JH126593 | assigned family member name in tree: pld7 |
|   |  | Scaffold JH126986.1: 327.52k | ENSLACG00000008209 | ENSLACT00000009378.1 | Lch.JH126986 |   |
|   |  | Scaffold JH126564.1: 350.31k | ENSLACG00000008533 | ENSLACT00000009752.1 | Lch.JH126564 | manually edited |
|   |   | Scaffold JH126663.1: 2.50m | ENSLACG00000017919 | ENSLACT00000020531.1 | Lch.JH126663 |   |
| Spotted gar  | LG28: 699.07k | ENSLOCG00000001445  | ENSLOCT00000001659.1 | Loc.LG28 | Assigned gene name in this study: pld7 |
|   |  | LG16: 76.54k | ENSLOCG00000015383  | ENSLOCT00000018963.1 | Loc.LG16 |   |
|   |  |  LG7: 16.44m | ENSLOCG00000012785 | ENSLOCT00000015762.1 | Loc.LG7 |   |
|   |  | LG2: 67.62m | ENSLOCG00000014810 | ENSLOCT00000018266.1 | Loc.LG2 |   |
| Zebrafish | si:dkeyp-110e4.6 | 14: 26.13m | ENSDARG00000061845 | ENSDART00000088677.5 | Dre.14 | Assigned gene name in this study: pld7 |
|   | si:ch211-194e18.2 | 6: 6.24m | ENSDARG00000063257 | ENSDART00000092257.5 | Dre.6 |   |
|   | pld3 | 18: 46.27m | ENSDARG00000068199 | ENSDART00000131724.1 | Dre.18 |   |
|   | pld4 | 17:1.63m | XP\_021322934.1 |   | Dre.17 | jun-17, manually edited |
| Amphioxus | NW\_003101358.1:1.01m | XP\_002589021.1 |  | Bfl.NW\_003101358.1 | oct-09 |
|   |   | NW\_003101358.1:1.07m | XP\_002589028.1 |   | Bfl.NW\_003101358.2 | oct-09 |
| Fruitfly | CG43345 | 2L: 21.17m | FBgn0263050 | FBtr0346589 | Dme.2L.1 |   |
|   | CG9248 | 2L: 21.16m | FBgn0032923 | FBtr0343870 | Dme.2L.2 |   |
| Caenorhabditis elegans | V: 5.49m | WBGene00020256 | T05C3.6a | Cel.V.1 |   |
|   |  |  II: 7.19m | WBGene00017124 | E04F6.4 | Cel.II |   |
|   |  | V: 18.57m | WBGene00013080 | Y51A2D.13b | Cel.V.3 |   |
|   |   | V: 7.19m | WBGene00017316 | F09G2.8b | Cel.V.2 |   |
|  |  |  |  |  |  |  |
| **Species** | **HGNC,ZFIN or FlyBase name** | **Chromosome/scaffold locations** | **Ensembl ID or NCBI accession number** | **Transcript ID** | **Assigned sequence name** | **Comments/Annotation notes** |
| Human | PRKD1 | 14: 29.58m | ENSG00000184304 | ENST00000415220.6 | Hsa.14 |   |
|   | PRKD2 | 19: 46.67m | ENSG00000105287  | ENST00000433867.5 | Hsa.19 |   |
|   | PRKD3 | 2: 37.25m | ENSG00000115825  | ENST00000379066.5 | Hsa.2 |   |
| Chicken |   | 5: 33.85m | ENSGALG00000009900 | ENSGALT00000057736.2 | Gga.5 | edited manually  |
|   |   | 3: 33.63m | ENSGALG00000010612 | ENSGALT00000017268.4 | Gga.3 |   |
| Chinese softshell turtle | Scaffold JH207692.1: 8.54k | ENSPSIG00000016551 | ENSPSIT00000018815.1 | Psi.JH207692 | edited manually  |
|   |  | Scaffold JH208684.1: 208.22k | ENSPSIG00000010601 | ENSPSIT00000012146.1 | Psi.JH208684 | edited manually  |
|   |  | Scaffold JH212505.1: 3.64m | ENSPSIG00000006040 | ENSPSIT00000006690.1 | Psi.JH212505 | edited manually  |
|   |   | Scaffold JH207378.1: 335.67k | ENSPSIG00000007942 | ENSPSIT00000008981.1 | Psi.JH207378 | Assigned family member name in tree : PRKD4 |
| Coelacanth  | Scaffold JH128496.1: 178.03k | ENSLACG00000005649 | ENSLACT00000006419.1 | Lch.JH128496 | edited manually  |
|   |  | Scaffold JH127173.1: 150.88k | ENSLACG00000005076 | ENSLACT00000005762.1 | Lch.JH127173 | edited manually  |
|   |   | Scaffold JH126749.1: 590.35k | ENSLACG00000011315 | ENSLACT00000012945.1 | Lch.JH126749 | edited manually  |
| Spotted gar  | LG7: 5.50m | ENSLOCG00000009700 | ENSLOCT00000011878.1 | Loc.LG7 |   |
|   |  | LG2: 68.48m | ENSLOCG00000014916 | ENSLOCT00000018401.1 | Loc.LG2 | edited manually  |
|   |  | LG1: 50.25m | ENSLOCG00000016864 | ENSLOCT00000020882.1 | Loc.LG1 |   |
|   |   | LG28: 881.06k | ENSLOCG00000001570 | ENSLOCT00000001812.1 | Loc.LG28 | Assigned gene name in this study: PRKD4 |
| Zebrafish | prkd1 | 17: 28.87m | ENSDARG00000075949 | ENSDART00000153937.2 | Dre.17.1 |   |
|   | prkd2 | 15:11.77m |  XP\_021322000.1 |  | Dre.15 | jun-17 |
|   | prkd3 | 17: 42.34m |  ENSDARG00000079967 | ENSDART00000112765.3 | Dre.17.2 |   |
|   | zgc:175248 | 7: 6.88m  | NP\_001170925.1 |   | Dre.7 | Assigned gene name in this study: prkd4 |
| Ciona intestinalis |   | 2: 1376.49k | ENSCING00000011582  | ENSCINT00000022313.2 | Cin.2 |   |
|   |   | 4: 5.33m | ENSCING00000005266 | ENSCINT00000010841.3 | Cin.4 |   |
| Ciona savignyi |   | reftig\_19: 2.68m | ENSCSAVG00000009881 | ENSCSAVT00000016979.1 | Csa.ref19 |   |
|   |   | reftig\_15: 2.05m | ENSCSAVG00000009491 | ENSCSAVT00000016306.1 | Csa.ref15 |   |
| Fruitfly | PKD | 3R: 18.30m |  FBgn0038603 | FBtr0330313 | Dme.3R |   |
| Caenorhabditis elegans | I: 13.64m | WBGene00012352 | W09C5.5 | Cel.I |   |
|   |   | V: 16,75m | WBGene00012019  | T25E12.4f | Cel.V |   |
|  |  |  |  |  |  |  |
| **Species** | **HGNC,ZFIN or FlyBase name** | **Chromosome/scaffold locations** | **Ensembl ID or NCBI accession number** | **Transcript ID** | **Assigned sequence name** | **Comments/Annotation notes** |
| Human | PROX1 | 1: 213.98m | ENSG00000117707 | ENST00000366958.8 | Hsa.1 |   |
|   | PROX2 | 14: 74.85m | ENSG00000119608  | ENST00000556489.3  | Hsa.14 |   |
| Chicken |   | 5: 38.13m | XP\_015143173.1  |   | Gga.5 | nov-15 |
|   |   | 3: 21.31m | ENSGALG00000009791 | ENSGALT00000015927.5 | Gga.3 |   |
| Chinese softshell turtle | scaffold NW\_005857314.1: 0.10m  | XP\_014432861.1 |   | Psi.NW\_005857314 | nov-15 |
|   |  | scaffold NW\_005859004.1: 0.50m  | XP\_006136626.1 |  | Psi.NW\_005859004 | nov-15., manually edited. Assigned family member name in tree : PROX3 |
|   |   | scaffold NW\_005853657.1: 6.51m  | XP\_014426287.1 |   | Psi.NW\_005853657 | Nov-15. manually edited |
| Coelacanth  | Scaffold JH127021.1: 896.11k | ENSLACG00000013691 | ENSLACT00000015662.1  | Lch.JH127021 | manually edited  |
|   |   | Scaffold JH126565.1: 5.25m | ENSLACG00000018909 | ENSLACT00000021660.1 | Lch.JH126565 |   |
| Spotted gar  | LG1: 44.46m | ENSLOCG00000016698 | ENSLOCT00000020666.1 | Loc.LG1 |   |
|   |  | LG7: 8.79m | ENSLOCG00000010701 | ENSLOCT00000013140.1  | Loc.LG7 |   |
|   |   | LG28: 1980.83k | ENSLOCG00000002197  | ENSLOCT00000002563.1 | Loc.LG28 | Assigned gene name in this study: prox3  |
| Zebrafish | prox1b | 7: 19.68m | ENSDARG00000088810  | ENSDART00000127669.3 | Dre.7 | Assigned gene name in this study: prox3 |
|   | prox1a | 17: 32.87m | ENSDARG00000055158  | ENSDART00000172016.1 | Dre.17.1 | Assigned gene name in this study: prox1 |
|   | prox2 | 17: 52.41m | ENSDARG00000041952 | ENSDART00000114931.3 | Dre.17.2 |  |
| Ciona intestinalis |   | 4: 528.34k | ENSCING00000008999 |  ENSCINT00000018262.3 | Cin.4.1 |   |
|   |   | 4: 543.58k | ENSCING00000013650 | ENSCINT00000025222.2 | Cin.4.2 |   |
| Ciona savignyi |   | reftig\_15: 1373.97k |  ENSCSAVG00000007613 |  ENSCSAVT00000013114.1 | Csa.ref15 |   |
| Caenorhabditis elegans | III: 8.07m |  WBGene00000448 | K12H4.1 | Cel.III |   |
|  |  |  |  |  |  |  |
| **Species** | **HGNC,ZFIN or FlyBase name** | **Chromosome/scaffold locations** | **Ensembl ID or NCBI accession number** | **Transcript ID** | **Assigned sequence name** | **Comments/Annotation notes** |
| Human | PRPH2 | 6: 42.70m | ENSG00000112619 | ENST00000230381.6 | Hsa.6. |   |
|   | ROM1 | 11: 62.61m | ENSG00000149489 | ENST00000278833.3 | Hsa.11 |   |
| Chicken |   | 3: 23.09m | ENSGALG00000009909 | ENSGALT00000016117.2 | Gga.3 |   |
|   |   | 5: 25.97m | ENSGALG00000009185 | ENSGALT00000014960.1 | Gga.5 | Assigned gene name in this study: PRPH2L |
| Coelacanth  | Scaffold JH126942.1: 768.29k | ENSLACG00000012811 | ENSLACT00000014656.1 | Lch.JH126942 |   |
|   |  | Scaffold JH126593.1: 329.42k | ENSLACG00000008239 | ENSLACT00000009410.1 | Lch.JH126593 |   |
|   |   | Scaffold JH129987.1: 138.23k | ENSLACG00000004767 | ENSLACT00000005409.1 | Lch.JH129987 | Assigned family member name in tree: PRPH2L |
| Spotted gar  | LG16: 14.47m | ENSLOCG00000016479 | ENSLOCT00000020394.1 | Loc.LG16 |   |
|   |  | LG28: 273.81k | ENSLOCG00000001099 | ENSLOCT00000001243.1 | Loc.LG28 |   |
|   |  | LG7: 17.74m | ENSLOCG00000012939 | ENSLOCT00000015964.1 | Loc.LG7 | Assigned gene name in this study: PRPH2L |
| Zebrafish | prph2a | 12: 34.80m | ENSDARG00000038018 | ENSDART00000055415.5 | Dre.12 |   |
|   | prph2b | 13: 3.12m | ENSDARG00000014840 | ENSDART00000020671.8 | Dre.13 |   |
|   | rom1a | 5: 66.45m | ENSDARG00000019752 | ENSDART00000011295.8 | Dre.5 |   |
|   | rom1b | 14: 46.69m | ENSDARG00000026926 | ENSDART00000105461.3 | Dre.14 |   |
|   | prph2l | 20: 27.49m | ENSDARG00000021345 | ENSDART00000010584.4 | Dre.20 | Assigned gene name in this study: prph2lb |
|   | zmp:0000000545 | 17: 39.93m | ENSDARG00000013134 | ENSDART00000002217.4 | Dre.17 | Assigned gene name in this study: prph2la |
| Amphioxus  | NW\_003101360.1:0.48m | XP\_002589165.1 |   | Bfl.NW\_003101360 | oct-09 |
| Purple sea urchin |   | NW\_011992578.1:0.22m | XP\_011677540.1 |   | Spu.NW\_011992578 | mar-15 |
|   |   | NW\_011992578.1:0.23m | XP\_001197913.1 |   | Spu.NW\_011992578 | mar-15 |
|  |  |  |  |  |  |  |
| **Species** | **HGNC,ZFIN or FlyBase name** | **Chromosome/scaffold locations** | **Ensembl ID or NCBI accession number** | **Transcript ID** | **Assigned sequence name** | **Comments/Annotation notes** |
| Human | PYGB | 20: 25.25m | ENSG00000100994  | ENST00000216962.8 | Hsa.20 |   |
|   | PYGL | 14: 50.86m | ENSG00000100504 | ENST00000216392.7 | Hsa.14 |   |
|   | PYGM | 11: 64.75m | ENSG00000068976  | ENST00000164139.3 | Hsa.11 |   |
| Chicken |   | 3: 4.19m | ENSGALG00000008508  | ENSGALT00000039933.2 | Gga.3 |   |
|   |   | 5: 58.10m | ENSGALG00000012365 | ENSGALT00000020196.6 | Gga.5 |   |
| Anole lizard |   | Scaffold GL343850.1: 12.75k | ENSACAG00000013595 | ENSACAT00000014006.3 | Aca.GL343850 | manually edited |
|   |  | 1: 254.33m | ENSACAG00000013998 | ENSACAT00000014189.3 | Aca.1 | manually edited |
|   |   | Scaffold GL344430.1: 9.77k | ENSACAG00000005131 | ENSACAT00000005240.3 | Aca.GL344430 | manually edited |
| Coelacanth  | NW\_005819966.1: 0.39m rev | XP\_014348577.1 |   | Lch.NW\_005819966 | oct-15. manually edited |
|   |  | NW\_005819042.1: 3.46m fwd | XP\_014354239.1 |  | Lch.NW\_005819042 | oct-15. manually edited |
|   |   | Scaffold JH126849.1: 954.96k | ENSLACG00000014055  | ENSLACT00000016073.1 | Lch.JH126849 | manually edited |
| Spotted gar  | LG16: 17.17m | ENSLOCG00000016769  | ENSLOCT00000020772.1 | Loc.LG16 |   |
|   |  | LG28: 1823.12k | ENSLOCG00000002115 | ENSLOCT00000002469.1 | Loc.LG28 | manually edited  |
|   |   | LG7: 12.17m | ENSLOCG00000011949 | ENSLOCT00000014731.1 | Loc.LG7 | manually edited  |
| Zebrafish | pygma | 21: 28.41m | ENSDARG00000055518 |  ENSDART00000077871.4 | Dre.21 |   |
|   | pygmb | 7: 22.55m | ENSDARG00000013317  | ENSDART00000127467.2 | Dre.7 |   |
|   | pygl | 13: 36.72m | ENSDARG00000002197 | ENSDART00000149011.1 | Dre.13 |   |
|   | pygb | 17: 21.11m | ENSDARG00000002021  |  ENSDART00000022830.8 | Dre.17 |   |
| Ciona intestinalis |   | Scaffold HT000068.1: 3.10k rev | ENSCING00000006480 | ENSCINT00000013376.3 | Cin.HT000068 |   |
| Ciona savignyi |   | reftig 56: 1.06m fwd | ENSCSAVG00000000173 | ENSCSAVT00000000313.1 | Csa.ref56 |   |
| Amphioxus  | NW\_003101565.1: 3.46m rev | XP\_002613320.1 |   | Bfl.NW\_003101565 | oct-09 |
| Caenorhabditis elegans | V: 3.58m | WBGene00020696 | T22F3.3b.3 | Cel.V |   |
| Fruitfly | GlyP | Dme.2L |  FBgn0004507 | FBtr0077828 | Dme.2L |   |
|  |  |  |  |  |  |  |
| **Species** | **HGNC,ZFIN or FlyBase name** | **Chromosome/scaffold locations** | **Ensembl ID or NCBI accession number** | **Transcript ID** | **Assigned sequence name** | **Comments/Annotation notes** |
| Human | SLC24A3 | 20: 19.21m | ENSG00000185052 | ENST00000328041.10 | Hsa.20 |   |
|   | SLC24A4 | 14: 92.32m | ENSG00000140090 | ENST00000532405.5 | Hsa.14 |   |
| Chicken |   | 3: 3.98m | ENSGALG00000008445 | ENSGALT00000013756.5 | Gga.3 |   |
|   |   | 5: 44.71m | ENSGALG00000010793 | ENSGALT00000017553.5 | Gga.5 |   |
| Coelacanth  | JH126565.1: 6.65m | ENSLACG00000019037 | ENSLACT00000021807.1 | Lch.JH126565 |   |
|   |  | JH127769.1: 171.94k | ENSLACG00000005528 | ENSLACT00000006284.1 | Lch.JH127769 |   |
| Spotted gar  | LG28: 3.53m | ENSLOCG00000002679 | ENSLOCT00000003170.1 | Loc.LG28 | Assigned gene name in this study: SLC2416 |
|   |  | LG16: 10.12m | ENSLOCG00000016155 | ENSLOCT00000019947.1 | Loc.LG16 |   |
|   |  | LG7: 32.71m | ENSLOCG00000014107 | ENSLOCT00000017416.1 | Loc.LG7 |   |
| Zebrafish | slc24a4a | 17: 38.84m | ENSDARG00000015425 | ENSDART00000141177.1 | Dre.17 |   |
|   | slc24a4b | 20: 50.31m | ENSDARG00000067509 | ENSDART00000031139.8 | Dre.20 |   |
|   | slc24a3 | 13: 26.94m | ENSDARG00000006760 | ENSDART00000146227.1 | Dre.13 |   |
|   |  | 7: 71.80m | ENSDARG00000041086 | ENSDART00000017763.8 | Dre.7 | Assigned gene name in this study: slc24a6b |
|   | si:ch73-335m24.5 | 14: 33.56m | ENSDARG00000036383 | ENSDART00000112438.5 | Dre.14 | Assigned gene name in this study: slc24a6a |
| Ciona intestinalis |   | Scaffold HT000052.1: 81.93k | ENSCING00000001025 | ENSCINT00000001908.3 | Cin.HT000052 |   |
| Ciona savignyi |   | reftig\_1596: 4.26k | ENSCSAVG00000003510 | ENSCSAVT00000005949.1 | Csa.ref1596 |   |
| Amphioxus  | NW\_003101527.1:0.53m | XP\_002606620.1 |   | Bfl.NW\_003101527 | oct-2009 |
|   |  | NW\_003101373.1:0.46m | XP\_002590091.1  |  | Bfl.NW\_003101373 | oct-2009 |
|   |   | NW\_003101410.1:0.79m | XP\_002593527.1  |   | Bfl.NW\_003101410 | oct-2009 |
| Fruitfly | zyd |  X: 23.02m | FBgn0265767 | FBtr0301133 | Dme.X.1 |   |
|   | CG12061 | X: 23.04m | FBgn0040031 | FBtr0332625 | Dme.X.2 |   |
|   | CG17167 | X: 23.07m | FBgn0039941 | FBtr0300807 | Dme.X.3 |   |
|   | CG1090 | 3R: 4.36m | FBgn0037238 | FBtr0335201 | Dme.3R |   |
| Human | SLC24A5 | 15: 48.12m | ENSG00000188467 | ENST00000341459.7 | Hsa.SLC24A5 |   |
|   | SLC24A1 | 15: 65.61m | ENSG00000074621 | ENST00000261892.10 | Hsa.SLC24A1 |   |
|   | SLC24A2 | 9: 19.51m | ENSG00000155886 | ENST00000341998.6 | Hsa.SLC24A2 |   |
|  |  |  |  |  |  |  |
| **Species** | **HGNC,ZFIN or FlyBase name** | **Chromosome/scaffold locations** | **Ensembl ID or NCBI accession number** | **Transcript ID** | **Assigned sequence name** | **Comments/Annotation notes** |
| Human | SPTB | 14: 64.75m | ENSG00000070182 | ENST00000389722.7 | Hsa.14 |   |
|   | SPTBN4 | 19: 40.47m | ENSG00000160460 | ENST00000598249.5 | Hsa.19 |   |
|   | SPTBN2 | 11: 66.69m | ENSG00000173898 | ENST00000309996.6 | Hsa.11 |   |
|   | SPTBN1 |  2: 54.46m | ENSG00000115306 | ENST00000356805.8 | Hsa.2 |   |
| Chicken |   | 3: 2.70m | ENSGALG00000029512 | ENSGALT00000057896.1 | Gga.3 |   |
|   |  | Scaffold AADN04004592.1: 1,366 | ENSGALG00000041560 | ENSGALT00000076960.1 | Gga.AADN04004592.1 | manually edited |
|   |  | 5: 311.49k | ENSGALG00000036805 | ENSGALT00000056882.1 | Gga.5 |   |
|   |   | Scaffold NT\_464134.1:0.07m | XP\_015128474.1 |   | Gga.NT\_464134 | jan-16 |
| Anolis lizard |   | 1: 263.40m | ENSACAG00000011972 | ENSACAT00000012304.3 | Aca.1.2 |   |
|   |  | GL343961.1: 63.38k | ENSACAG00000007494 | ENSACAT00000007763.3 | Aca.GL343961 |   |
|   |  | LGf: 2.00m | ENSACAG00000003147 | ENSACAT00000003648.3 | Aca.LGf |   |
|   |   | 1: 93.84m | ENSACAG00000009068 | ENSACAT00000009339.3 | Aca.1.1 |   |
| Coelacanth  | JH126660.1: 1911.64k | ENSLACG00000017110 | ENSLACT00000019589.1 | Lch.JH126660 |   |
|   |  | JH126663.1: 2.19m | ENSLACG00000017554 | ENSLACT00000020107.1 | Lch.JH126663 |   |
|   |  | JH126593.1: 3.17m | ENSLACG00000018388 | ENSLACT00000021069.1 | Lch.JH126593 |   |
|   |   | JH127271.1: 900.75k | ENSLACG00000013725 | ENSLACT00000015698.1 | Lch.JH127271 |   |
| Spotted gar  | LG16: 2.28m | ENSLOCG00000015528 | ENSLOCT00000019156.1 | Loc.LG16 |   |
|   |  | LG28: 2.29m | ENSLOCG00000002333 | ENSLOCT00000002734.1 | Loc.LG28 | manually edited |
|   |  | LG28: 2.30m | ENSLOCG00000002344 | ENSLOCT00000002752.1 |
|   |  | LG2: 64.33m | ENSLOCG00000014564 | ENSLOCT00000017962.1 | Loc.LG2 |   |
|   |  | LG7: 19.70m | ENSLOCG00000013491 | ENSLOCT00000016682.1 | Loc.LG7 |   |
| Zebrafish | sptb | 17: 38.62m | ENSDARG00000030490 | ENSDART00000040627.5 | Dre.17 |   |
|   | si:ch73-262h23.4  | 18: 46.03m | ENSDARG00000092624 | ENSDART00000078561.5 | Dre.18 | Assigned gene name in this study: sptbn4b |
|   | si:dkey-27p18.5 | 5: 21.96m | ENSDARG00000068624 | ENSDART00000133174.1 | Dre.5.1 | Assigned gene name in this study: sptbn4a |
|   | sptbn2 | 5: 37.05m | ENSDARG00000053956 | ENSDART00000162929.1 | Dre.5.2 |   |
|   | sptbn1 | 11: 42.84m | ENSDARG00000102883 | ENSDART00000164700.1 | Dre.11 |   |
| Ciona intestinalis |   | 3: 5.13m | ENSCING00000008947 | ENSCINT00000018184.3 | Cin.3 |   |
| Ciona savignyi |   | reftig\_1: 4.53m | ENSCSAVG00000011411 | ENSCSAVT00000019668.1 | Csa.ref1 |   |
| Fruitfly | beta-Spec | X: 17.66m | FBgn0250788 | FBtr0334404 | Dme.X |   |
| Caenorhabditis elegans | V: 6.88m | WBGene00006803 | K11C4.3c | Cel.V |   |
|  |  |  |  |  |  |  |
| **Species** | **HGNC,ZFIN or FlyBase name** | **Chromosome/scaffold locations** | **Ensembl ID or NCBI accession number** | **Transcript ID** | **Assigned sequence name** | **Comments/Annotation notes** |
| Human | TGFB1 | 19: 41.30m | ENSG00000105329 | ENST00000221930.5 | Hsa.19 |   |
|   | TGFB2 | 1: 218.35m | ENSG00000092969 | ENST00000366930.8 | Hsa.1 |   |
|   | TGFB3 | 14: 75.96m | ENSG00000119699 | ENST00000238682.7 | Hsa.14 |   |
| Chicken |   | 3: 19.37m | ENSGALG00000009612 | ENSGALT00000031945.4 | Gga.3 |   |
|   |  | 5: 38.50m | ENSGALG00000010346  | ENSGALT00000037707.4 | Gga.5 |   |
|   |   | 32: 24.39k  | NP\_001305385.1 |   | Gga.32 | aug-17 |
| Anole lizard |   | Chromosome LGf: 3.76m  | ENSACAG00000023287 | ENSACAT00000027756.2 | Aca.LGf |   |
|   |  | Chromosome 1: 242.49m  | ENSACAG00000001183 | ENSACAT00000001108.3 | Aca.1.2 |   |
|   |   | Chromsome 1: 21.99m  | ENSACAG00000017020 | ENSACAT00000017101.3 | Aca.1.1 |   |
| Coelacanth  | Scaffold JH126578.1: 2.81m | ENSLACG00000018146 | ENSLACT00000020792.1 | Lch.JH126578 |   |
|   |  | Scaffold JH127048.1: 240.06k | ENSLACG00000006847 | ENSLACT00000007797.1 | Lch. JH127048 |   |
|   |  | Scaffold JH126565.1: 1664.07k | ENSLACG00000016642 | ENSLACT00000019045.1 | Lch.JH126565 |   |
|   |   | Scaffold JH126593.1: 1968.39k | ENSLACG00000017213 | ENSLACT00000019712.1 | Lch.JH126593 | Assigned family member name in tree: TGFB5 |
| Spotted gar  | LG2: 61.85m | ENSLOCG00000014160 | ENSLOCT00000017474.1 | Loc.LG2 |   |
|   |  | LG28: 402.53k | ENSLOCG00000001175 | ENSLOCT00000001332.1 | Loc.LG28 | manually edited. Assigned gene name in this study: TGFB5 |
|   |  | LG1: 18.27m | ENSLOCG00000015921 | ENSLOCT00000019635.1 | Loc.LG1 |   |
|   |  | LG7: 8.44m | ENSLOCG00000010588 | ENSLOCT00000013005.1 | Loc.LG7 |   |
| Zebrafish | tgfb1a | 15: 2.81m | ENSDARG00000041502  | ENSDART00000060839.2 | Dre.15 |   |
|   | tgfb1b | 21: 21.58m | ENSDARG00000034895  | ENSDART00000134907.1 | Dre.21 |   |
|   | tgfb2l | 14: 8.46m | ENSDARG00000071879 | ENSDART00000106671.4 | Dre.14 | Assigned gene name in this study: tgfb5 |
|   | tgfb3 | 17: 51.99m | ENSDARG00000019367 | ENSDART00000019766.8 | Dre.17 |   |
|   | tgfb2 | 16: 2.75m  | NP\_919366.1 |  | Dre.16 | dec-18 |
| Ciona intestinalis |   | 3: 6.26m | ENSCING00000008565 | ENSCINT00000017469.3 | Cin.3 |   |
| Ciona savignyi |   | reftig\_107: 917.85k | ENSCSAVG00000002907  | ENSCSAVT00000004952.1 | Csa.ref107 |   |
| Fruitfly | daw | 2L: 2.81m |  FBgn0031461 | FBtr0335151 | Dme.2L |   |