|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Ens87** | **Common name** | **Scientific name** | **Abbrevation** | **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 | ABTB2 | 11: 34.15m | ENSG00000166016 | ENST00000435224.2 | Hsa.11 |  |
|  | BTBD11 | 12: 107.32m | ENSG00000151136 | ENST00000280758.9 | Hsa.12 |  |
| Chicken |  | 5: 18.54m | XP\_423445.3 |  | Gga.5 |  |
|  |  | 1: 53.59m | XP\_015143383.1 |  | Gga.1 |  |
| Coelacanth | | JH127313.1: 161.11k | ENSLACG00000005390 | ENSLACT00000006125.2 | Lch.JH127313 |  |
|  |  | JH126576.1: 456.45k | ENSLACG00000009938 | ENSLACT00000011383.2 | Lch.JH126576 | assigned family member name in tree: novel |
|  |  | JH126600.1: 662.20k | ENSLACG00000012005 | ENSLACT00000013736.1 | Lch.JH126600 | manually edited |
|  |  | JH126600.1: 459.41k | ENSLACG00000009924 | ENSLACT00000011366.1 |  | manually edited |
| Spotted gar | | LG3: 36.86m | ENSLOCG00000012541 | ENSLOCT00000015480.1 | Loc.LG3 | assigned family member name in synteny figure and tree: novel |
|  |  | LG8: 4.10m | ENSLOCG00000015275 | ENSLOCT00000018831.1 | Loc.LG8 |  |
|  |  | LG27: 4.83m | ENSLOCG00000001988 | ENSLOCT00000002321.1 | Loc.LG27 |  |
| Zebrafish | abtb2a | 7: 49.00m | ENSDARG00000059751 | ENSDART00000083389.6 | Dre.7 |  |
|  | abtb2b | 25: 24.52m | ENSDARG00000062000 | ENSDART00000089113.5 | Dre.25 |  |
|  | btbd11a | 4: 11.81m | ENSDARG00000063255 | ENSDART00000092250.6 | Dre.4 |  |
|  | btbd11b | 18: 14.99m | ENSDARG00000063040 | ENSDART00000172273.1 | Dre.18 |  |
| Amphioxus |  | NW\_003101534.1:5.73m | XP\_002608561.1 |  | Bfl.NW\_003101534 |  |
| Fruitfly | CG43980 | 3L: 21.64m | FBgn0264711 | FBtr0333974 | Dme.3L |  |
|  |  |  |  |  |  |  |
| **Species** | **HGNC,ZFIN or FlyBase name** | **Chromosome/scaffold locations** | **Ensembl ID or NCBI accession number** | **Transcript ID** | **Assigned sequence name** | **Comments/Annotation notes** |
| Human | ARHGAP1 | 11: 46.68m | ENSG00000175220 | ENST00000311956.8 | Hsa.11 |  |
|  | ARHGAP8 | 22: 44.75m | ENSG00000241484 | ENST00000356099.10 | Hsa.22 |  |
| Chicken |  | 5: 23.45m | ENSGALG00000042357 | ENSGALT00000079282.1 | Gga.5 |  |
|  |  | 1: 69.90m | ENSGALG00000019261 | ENSGALT00000022983.4 | Gga.1 |  |
| Coelacanth | | JH126568.1: 4.57m | ENSLACG00000018798 | ENSLACT00000021536.1 | Lch.JH126568 | manually edited |
|  |  | NW\_005819187.1:0.88m | XP\_005993733.1 |  | Lch.NW\_005819187 | oct-15 |
| Spotted gar | | LG27: 12.31m | ENSLOCG00000005713 | ENSLOCT00000006907.1 | Loc.LG27 |  |
|  |  | LG8: 37.24m | ENSLOCG00000016538 | ENSLOCT00000020461.1 | Loc.LG8 |  |
| Zebrafish | arhgap1 | 7: 38.49m | ENSDARG00000024324 | ENSDART00000036461.5 | Dre.7 |  |
| Cave fish |  | Scaffold KB882095.1: 168.85k | ENSAMXG00000008329 | ENSAMXT00000008559.1 | Ame.KB882095 |  |
|  |  | Scaffold KB882086.1: 3.08m | ENSAMXG00000021366 | ENSAMXT00000021997.1 | Ame.KB882086 |  |
| Ciona intestinalis | | 2: 1207.59k | ENSCING00000011599 | ENSCINT00000022340.2 | Cin.2 |  |
| Ciona savignyi | | reftig\_19: 2.37m | ENSCSAVG00000009237 | ENSCSAVT00000015908.1 | Csa.ref19 |  |
| Fruitfly | RhoGAP68F | 3L: 12.14m | FBgn0036257 | FBtr0075997 | Dme.3L |  |
| Caenorhabditis elegans | | II: 11.46m | WBGene00012203 | W02B12.8a | Cel.II |  |
|  |  |  |  |  |  |  |
| **Species** | **HGNC,ZFIN or FlyBase name** | **Chromosome/scaffold locations** | **Ensembl ID or NCBI accession number** | **Transcript ID** | **Assigned sequence name** | **Comments/Annotation notes** |
| Human | CREB3L1 | 11: 46.28m | ENSG00000157613 | ENST00000621158.4 | Hsa.11 |  |
|  | CREB3L2 | 7: 137.87m | ENSG00000182158 | ENST00000330387.10 | Hsa.7 |  |
| Chicken |  | 5: 23.70m | ENSGALG00000008393 | ENSGALT00000013673.3 | Gga.5 |  |
|  |  | 1: 57.41m | ENSGALG00000012877 | ENSGALT00000021004.5 | Gga.1 |  |
| Coelacanth | | JH126568.1: 3.62m | ENSLACG00000018569 | ENSLACT00000021277.1 | Lch.JH126568 |  |
|  |  | JH126628.1: 350.69k | ENSLACG00000008535 | ENSLACT00000009754.1 | Lch.JH126628 |  |
| Spotted gar | | LG27: 12.11m | ENSLOCG00000005600 | ENSLOCT00000006770.1 | Loc.LG27 |  |
|  |  | LG8: 49.54m | ENSLOCG00000017109 | ENSLOCT00000021177.1 | Loc.LG8 | manually edited |
| Zebrafish | creb3l1 | 7: 38.63m | ENSDARG00000015793 | ENSDART00000172251.1 | Dre.7 |  |
|  | creb3l2 | 4: 4.70m | ENSDARG00000063563 | ENSDART00000092984.4 | Dre.4 |  |
| Ciona intestinalis | | Scaffold HT000025.1: 3.65k | ENSCING00000005364 | ENSCINT00000011026.3 | Cin.HT000025 |  |
| Ciona savignyi | | reftig\_19: 1732.56k | ENSCSAVG00000008562 | ENSCSAVT00000014819.1 | Csa.ref19 |  |
| Fruitfly | CrebA | 3L: 15.54m | FBgn0004396 | FBtr0075557 | Dme.3L |  |
| Caenorhabditis elegans | | II: 5.18m | WBGene00016162 | C27D6.4c | Cel.II |  |
|  |  |  |  |  |  |  |
| **Species** | **HGNC,ZFIN or FlyBase name** | **Chromosome/scaffold locations** | **Ensembl ID or NCBI accession number** | **Comments/Annotation notes** |  |  |
| Human | CRY1 | 12: 106.99m | ENSG00000008405 |  |  |  |
|  | CRY2 | 11: 45.85m | ENSG00000121671 |  |  |  |
| Chicken |  | 1: 53.64m | ENSGALG00000012638 |  |  |  |
|  |  | 5: 23.95m | ENSGALG00000008436 |  |  |  |
| Spotted gar | | JH591436.1: 96.77k | ENSLOCG00000014655 |  |  |  |
|  |  | LG3: 32.90m | ENSLOCG00000011417 | Assigned gene name in synteny figure: CRY3 |  |  |
|  |  | LG8: 4.05m | ENSLOCG00000015272 |  |  |  |
| Zebrafish | cry2 | 25: 13.75m | ENSDARG00000102403 |  |  |  |
|  | cry1ba | 8: 21.19m | ENSDARG00000069074 | Assigned gene name in this study: cry3a |  |  |
|  | cry1bb | 22: 748.82k | ENSDARG00000091131 | Assigned gene name in this study: cry3b |  |  |
|  | cry1aa | 4: 12.01m | ENSDARG00000045768 | Assigned gene name in this study: cry1a |  |  |
|  | cry1ab | 18: 15.14m | ENSDARG00000011583 | Assigned gene name in this study: cry1b |  |  |
|  |  |  |  |  |  |  |
| Reference for phylogenetic analysis and assigned gene names of the CRY family: | | |  |  |  |  |
| Haug, M.F., Gesemann, M., Lazović, V., and Neuhauss, S.C.F. (2015). Eumetazoan Cryptochrome Phylogeny and Evolution. Genome Biol Evol *7*, 601–619 | | | | | |  |
|  |  |  |  |  |  |  |
| **Species** | **HGNC,ZFIN or FlyBase name** | **Chromosome/scaffold locations** | **Ensembl ID or NCBI accession number** | **Transcript ID** | **Assigned sequence name** | **Comments/Annotation notes** |
| Human | DGKI | 7: 137.38m | ENSG00000157680 | ENST00000288490.9 | Hsa.7 |  |
|  | DGKZ | 11: 46.33m | ENSG00000149091 | ENST00000454345.5 | Hsa.11 |  |
| Chicken |  | 1: 57.49m | ENSGALG00000012890 | ENSGALT00000021020.5 | Gga.1 |  |
|  |  | 5: 23.65m | ENSGALG00000008380 | ENSGALT00000038374.3 | Gga.5 |  |
| Coelacanth | | JH126568.1: 4.02m | ENSLACG00000018674 | ENSLACT00000021394.1 | Lch.JH126568 |  |
|  |  | JH126628.1: 638.23k | ENSLACG00000011803 | ENSLACT00000013500.1 | Lch.JH126628 | manually edited |
| Spotted gar | | LG8: 49.59m | ENSLOCG00000017111 | ENSLOCT00000021183.1 | Loc.LG8 | manually edited |
|  |  | LG27: 11.92m | ENSLOCG00000005570 | ENSLOCT00000006752.1 | Loc.LG27 |  |
| Zebrafish | dgki | 4: 4.61m | ENSDARG00000063578 | ENSDART00000093005.5 | Dre.4 |  |
|  | dgkza | 7: 38.69m | ENSDARG00000014439 | ENSDART00000093009.5 | Dre.7 |  |
|  | dgkzb | 25: 7.66m | ENSDARG00000076025 | ENSDART00000155016.1 | Dre.25 |  |
| Ciona intestinalis | | 14: 2.60m | ENSCING00000003441 | ENSCINT00000007047.3 | Cin.14 |  |
|  |  | 4: 3.98m | ENSCING00000008888 | ENSCINT00000018087.3 | Cin.4 |  |
| Ciona savignyi | | reftig\_76: 1870.70k | ENSCSAVG00000008009 | ENSCSAVT00000013813.1 | Csa.ref76 |  |
|  |  | reftig\_90: 179.73k | ENSCSAVG00000009376 | ENSCSAVT00000016110.1 | Csa.ref90 |  |
| Fruitfly | rdgA | X: 8.91m | FBgn0261549 | FBtr0302660 | Dme.X |  |
| Caenorhabditis elegans | | II: 6.46m | WBGene00019428 | K06A1.6 | Cel.II |  |
|  |  |  |  |  |  |  |
| **Species** | **HGNC,ZFIN or FlyBase name** | **Chromosome/scaffold locations** | **Ensembl ID or NCBI accession number** | **Transcript ID** | **Assigned sequence name** | **Comments/Annotation notes** |
| Human | MYBPC1 | 12: 101.57m | ENSG00000196091 | ENST00000361466.6 | Hsa.12 |  |
|  | MYBPHL | 1: 109.29m | ENSG00000221986 | ENST00000357155.1 | Hsa.1.1 |  |
|  | MYBPC3 | 11: 47.33m | ENSG00000134571 | ENST00000545968.5 | Hsa.11 |  |
|  | MYBPC2 | 19: 50.43m | ENSG00000086967 | ENST00000357701.5 | Hsa.19 |  |
|  | MYBPH | 1: 203.17m | ENSG00000133055 | ENST00000255416.8 | Hsa.1.2 |  |
| Chicken |  | 1:55.65m | XP\_015143170.1 |  | Gga.1 | jan-16 |
|  |  | 26: 1001.41k | ENSGALG00000000164 | ENSGALT00000040700.4 | Gga.26 |  |
|  |  | 5: 22.98m | ENSGALG00000008148 | ENSGALT00000032650.4 | Gga.5 |  |
| Anole lizard | | 6: 79.59m | ENSACAG00000012342 | ENSACAT00000012500.3 | Aca.6 |  |
|  |  | 1: 43.90m | XP\_008103421.2 |  | Aca.1 | may-16 |
|  |  | 4: 133.15m | ENSACAG00000004704 | ENSACAT00000004779.2 | Aca.4 |  |
|  |  | 5:17.24m | XP\_008108767.1 |  | Aca.5 | may-16 |
| Coelacanth | | JH127380.1: 83.40k | ENSLACG00000003430 | ENSLACT00000003888.1 | Lch.JH127380 |  |
|  |  | JH126576.1: 821.40k | ENSLACG00000013194 | ENSLACT00000015097.1 | Lch.JH126576 |  |
|  |  | JH126568.1: 5.51m | ENSLACG00000018941 | ENSLACT00000021699.1 | Lch.JH126568 |  |
|  |  | JH126644.1: 1323.14k | ENSLACG00000015666 | ENSLACT00000017917.1 | Lch.JH126644 |  |
| Spotted gar |  | *JH591442.1: 155.01k* | *ENSLOCG00000000775* | *ENSLOCT00000000861.1* |  | *too short not included in alignment* |
|  |  | LG27: 12.85m | ENSLOCG00000006281 | ENSLOCT00000007615.1 | Loc.LG27 |  |
|  |  | LG3: 23.56m | ENSLOCG00000009756 | ENSLOCT00000011949.1 | Loc.LG3 |  |
|  |  | LG8: 2.64m | ENSLOCG00000015188 | ENSLOCT00000018724.1 | Loc.LG8 |  |
| Zebrafish | mybpc1 | 4: 17.74m | ENSDARG00000045560 | ENSDART00000066996.4 | Dre.4 |  |
|  | mybpha | 23: 6.14m | ENSDARG00000058799 | ENSDART00000139834.1 | Dre.23 |  |
|  | mybphb | 6: 55.02m | ENSDARG00000003081 | ENSDART00000122794.2 | Dre.6 |  |
|  | mybpc3 | 7: 31.57m | ENSDARG00000011615 | ENSDART00000174217.1 | Dre.7 |  |
|  | mybpc2a | 3: 30.13m | ENSDARG00000030157 | ENSDART00000121883.3 | Dre.3 |  |
|  | mybpc2b | 24: 38.37m | ENSDARG00000021265 | ENSDART00000105672.4 | Dre.24 |  |
| Ciona intestinalis | | 1: 2.00m | ENSCING00000004377 | ENSCINT00000009061.3 | Cin.1 |  |
| Ciona savignyi | | reftig\_14: 840.05k | ENSCSAVG00000010522 | ENSCSAVT00000018078.1 | Csa.ref14 |  |
| Fruitfly | CG14964 | 3L: 3.17m | FBgn0035410 | FBtr0307018 | Dme.3L |  |
| Human | IGSF22 | 11: 18.70m | ENSG00000179057 | ENST00000513874.5 | Hsa.IGSF22 |  |
|  | IGFN1 | 1: 201.19m | ENSG00000163395 | ENST00000295591.12 | Hsa.IGFN1 |  |
|  | MYOM1 | 18: 3.07m | ENSG00000101605 | ENST00000356443.8 | Hsa.MYOM1 |  |
|  | MYOM2 | 8: 2.05m | ENSG00000036448 | ENST00000262113.8 | Hsa.MYOM2 |  |
|  | MYOM3 | 1: 24.06m | ENSG00000142661 | ENST00000374434.3 | Hsa.MYOM3 |  |
| Amphioxus |  | NW\_003101518.1: 2.24m | XP\_002605775.1 |  | Bfl.NW\_003101518 | oct-09 |
|  |  |  |  |  |  |  |
| **Species** | **HGNC,ZFIN or FlyBase name** | **Chromosome/scaffold locations** | **Ensembl ID or NCBI accession number** | **Transcript ID** | **Assigned sequence name** | **Comments/Annotation notes** |
| Human | NAV1 | 1: 201.62m | ENSG00000134369 | ENST00000367296.8 | Hsa.1 |  |
|  | NAV2 | 11: 19.35m | ENSG00000166833 | ENST00000349880.8 | Hsa.11 |  |
|  | NAV3 | 12: 77.32m | ENSG00000067798 | ENST00000397909.6 | Hsa.12 |  |
| Chicken |  | 5:1.70m | XP\_004941374.1 |  | Gga.5 | jan-16 |
|  |  | 1: 38.67m | ENSGALG00000010311 | ENSGALT00000016778.5 | Gga.1 |  |
|  |  | 26:0.61m | XP\_015154353.1 |  | Gga.26 | jan-16 |
| Coelacanth | | NW\_005819268.1:0.78m | XP\_014343595.1 |  | Lch.NW\_005819268 | oct-15 |
|  |  | NW\_005819385.1:0.32m | XP\_014344647.1 |  | Lch.NW\_005819385 | oct-15 |
|  |  | JH127285.1: 11.60k | ENSLACG00000001187 | ENSLACT00000001335.1 | Lch.JH127285 |  |
| Spotted gar | | LG3: 23.60m | ENSLOCG00000009769 | ENSLOCT00000011965.1 | Loc.LG3 |  |
|  |  | LG27: 10.09m | ENSLOCG00000004849 | ENSLOCT00000005843.1 | Loc.LG27 |  |
|  |  | LG8: 29.60m | ENSLOCG00000016281 | ENSLOCT00000020119.1 | Loc.LG8 |  |
| Zebrafish | nav1b | 6: 54.87m | ENSDARG00000058771 | ENSDART00000113331.3 | Dre.6 |  |
|  |  | 23: 5.94m | ENSDARG00000078011 | ENSDART00000115403.3 | Dre.23 |  |
|  | nav2a | 7: 16.55m | ENSDARG00000073688 | ENSDART00000173541.1 | Dre.7 |  |
|  | nav2b | 25: 14.41m | ENSDARG00000001879 | ENSDART00000160462.1 | Dre.25 |  |
|  | nav3 | 4: 21.09m | ENSDARG00000005476 | ENSDART00000005847.8 | Dre.4 |  |
| Amphioxus |  | NW\_003101540.1: 220.56m |  | XP\_002609491.1 | Bfl.NW\_003101540 | oct-09, manually edited |
|  |  | NW\_003101540.1: 232.81m |  | XP\_002609492.1 | oct-09, manually edited |
| Fruitfly | sick | 2L: 19.80m | FBgn0263873 | FBtr0329845 | Dme.2L |  |
| Caenorhabditis elegans | | II: 11.06m | WBGene00006788 | F45E10.1c | Cel.II |  |
|  |  |  |  |  |  |  |
| **Species** | **HGNC,ZFIN or FlyBase name** | **Chromosome/scaffold locations** | **Ensembl ID or NCBI accession number** | **Transcript ID** | **Assigned sequence name** | **Comments/Annotation notes** |
| Human | NELL1 | 11: 20.67m | ENSG00000165973 | ENST00000357134.9 | Hsa.11 |  |
|  | NELL2 | 12: 44.51m | ENSG00000184613 | ENST00000429094.6 | Hsa.12 |  |
| Chicken |  | 1: 30.34m | ENSGALG00000009601 | ENSGALT00000038787.4 | Gga.1 |  |
|  |  | 5: 2.20m | ENSGALG00000003777 | ENSGALT00000005993.5 | Gga.5 |  |
| Coelacanth | | JH126716.1: 1989.65k | ENSLACG00000017255 | ENSLACT00000019760.1 | Lch.JH126716 |  |
|  |  | JH126936.1: 904.27k | ENSLACG00000013745 | ENSLACT00000015720.1 | Lch.JH126936 | manually edited |
|  |  | JH126936.1: 1162.57k | ENSLACG00000015057 | ENSLACT00000017211.1 | manually edited |
| Spotted gar | | LG27: 10.35m | ENSLOCG00000004971 | ENSLOCT00000006006.1 | Loc.LG27 |  |
|  |  | LG8: 35.39m | ENSLOCG00000016436 | ENSLOCT00000020336.1 | Loc.LG8 |  |
| Zebrafish | nell2a | 25: 558.24k | ENSDARG00000090690 | ENSDART00000126863.2 | Dre.25 |  |
|  | nell2b | 4: 14.25m | ENSDARG00000062797 | ENSDART00000091151.5 | Dre.4 |  |
| Stickleback | | groupII: 20.13m | ENSGACG00000017098 | ENSGACT00000022628.1 | Gac.II |  |
|  |  | groupXIX: 5.40m | ENSGACG00000004004 | ENSGACT00000005280.1 | Gac.XIX |  |
| Amphioxus |  | NW\_017803998.1:2.57m | XP\_019633163.1 |  | Bfl.NW\_017803998 |  |
| Caenorhabditis elegans | | X: 10.01m | WBGene00008952 | F19C6.3 | 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 | PPFIA1 | 11: 70.27m | ENSG00000131626 | ENST00000253925.11 | Hsa.11 |  |
|  | PPFIA2 | 12: 81.26m | ENSG00000139220 | ENST00000549396.5 | Hsa.12 |  |
|  | PPFIA3 | 19: 49.12m | ENSG00000177380 | ENST00000334186.8 | Hsa.19 |  |
|  | PPFIA4 | 1: 203.03m | ENSG00000143847 | ENST00000367240.6 | Hsa.1 |  |
| Chicken |  | 5: 17.84m | ENSGALG00000035774 | ENSGALT00000053972.1 | Gga.5 |  |
|  |  | 1: 40.20m | ENSGALG00000010958 | ENSGALT00000054646.1 | Gga.1 |  |
|  |  | 26: 944.39k | ENSGALG00000000217 | ENSGALT00000000287.5 | Gga.26 |  |
| Anole lizard | | GL343283.1: 0.11m | ENSACAG00000003711 | ENSACAT00000003896.3 | Aca.GL343284 |  |
|  |  | 4: 133.33m | ENSACAG00000004833 | ENSACAT00000004914.3 | Aca.4 |  |
|  |  | 5: 36.50m | ENSACAG00000014550 | ENSACAT00000014705.3 | Aca.5 |  |
|  |  | 6: 79.91m | ENSACAG00000013088 | ENSACAT00000013249.3 | Aca.6 |  |
| Coelacanth | | JH126862.1: 275.87k | ENSLACG00000007439 | ENSLACT00000008467.1 | Lch.JH126862 |  |
|  |  | JH126851.1: 904.80k | ENSLACG00000013750 | ENSLACT00000015725.1 | Lch.JH126851 |  |
|  |  | JH130138.1: 52.91k | ENSLACG00000002574 | ENSLACT00000002904.1 | Lch.JH130138 |  |
|  |  | JH126576.1: 1128.03k | ENSLACG00000014912 | ENSLACT00000017049.1 | Lch.JH126576 |  |
| Spotted gar | | LG27: 11.09m | ENSLOCG00000005197 | ENSLOCT00000006281.1 | Loc.LG27 |  |
|  |  | LG8: 30.86m | ENSLOCG00000016312 | ENSLOCT00000020174.1 | Loc.LG8 |  |
|  |  | LG3: 29.56m | ENSLOCG00000010689 | ENSLOCT00000013142.1 | Loc.LG3 |  |
| Zebrafish | ppfia3 | 3: 29.91m | ENSDARG00000077053 | ENSDART00000153562.2 | Dre.3 |  |
|  | ppfia1 | 18:50.94m | NP\_001104714.1 |  | Dre.18 |  |
|  | ppfia4 | 11: 22.21m | ENSDARG00000053205 | ENSDART00000112567.3 | Dre.11 |  |
|  | ppfia2 | 4: 22.24m | ENSDARG00000013000 | ENSDART00000142140.1 | Dre.4 |  |
| Ciona intestinalis | | Scaffold HT000098.1: 459.49k | ENSCING00000006030 | ENSCINT00000012503.3 | Cin.HT000098 |  |
| Ciona savignyi | | reftig\_489: 160.55k | ENSCSAVG00000001250 | ENSCSAVT00000002163.1 | Csa.ref489 |  |
| Fruitfly | Liprin-alpha | 2L: 6.72m | FBgn0046704 | FBtr0329943 | Dme.2L |  |
| Caenorhabditis elegans | | X: 10.55m | WBGene00006364 | F59F5.6 | 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 | RASSF7 | 11: 560.40k | ENSG00000099849 | ENST00000397583.7 | Hsa.11 |  |
|  | RASSF8 | 12: 25.96m | ENSG00000123094 | ENST00000405154.6 | Hsa.12 |  |
| Chicken |  | 1:67.55m | XP\_416437.2 |  | Gga.1 | jan-16 |
|  |  | 5: 15.89m | ENSGALG00000044251 | ENSGALT00000011134.6 | Gga.5 |  |
| Anole lizard | | GL343349: 1.01m | ENSACAG00000000388 | ENSACAT00000000374.3 | Aca.GL343349 |  |
|  |  | 1: 74.53m | ENSACAG00000014995 | ENSACAT00000015019.3 | Aca.1 |  |
| Coelacanth | | JH126587.1: 3.31m | ENSLACG00000018442 | ENSLACT00000021129.1 | Lch.JH126587 | assigned family member name in tree: RASSF11 |
|  |  | JH126580.1: 2.92m | ENSLACG00000018230 | ENSLACT00000020892.2 | Lch.JH126580 |  |
|  |  | JH127283.1: 859.80k | ENSLACG00000013466 | ENSLACT00000025618.1 | Lch.JH127283 |  |
| Spotted gar | | LG8: 4.77m | ENSLOCG00000015329 | ENSLOCT00000018894.1 | Loc.LG8 |  |
|  |  | LG27: 68.92k | ENSLOCG00000000536 | ENSLOCT00000000636.1 | Loc.LG27 |  |
|  |  | LG3: 28.57m | ENSLOCG00000010433 | ENSLOCT00000012814.1 | Loc.LG3 | assigned family member name in tree: RASSF11 |
| Zebrafish | si:ch211-261n11.3 | 8:22.52m | XP\_021334229.1 |  | Dre.8 | sep -17 , assigned gene name in this study:rassf11 |
|  | rassf8b | 4: 20.79m | ENSDARG00000045485 | ENSDART00000066895.3 | Dre.4 |  |
|  | rassf8a | 25: 31.05m | ENSDARG00000045596 | ENSDART00000067039.4 | Dre.25.2 |  |
|  | rassf7a | 25: 25.36m | ENSDARG00000079917 | ENSDART00000112330.3 | Dre.25.1 |  |
|  | rassf7b | 7: 49.38m | ENSDARG00000003193 | ENSDART00000025451.6 | Dre.7 |  |
| Ciona intestinalis | | Scaffold HT000075.1: 354.35k | ENSCING00000007050 | ENSCINT00000014493.3 | Cin.HT000075 |  |
| Fruitfly | RASSF8 | 3R: 25.66m | FBgn0261986 | FBtr0084898 | Dme.3R |  |
| Caenorhabditis elegans | | X: 4.91m | WBGene00019403 | K05B2.2a | 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 | SHANK1 | 19: 50.66m | ENSG00000161681 | ENST00000293441.5 | Hsa.19 |  |
|  | SHANK2 | 11: 70.47m | ENSG00000162105 | ENST00000601538.5 | Hsa.11 |  |
|  | SHANK3 | 22: 50.67m | ENSG00000251322 | ENST00000445220.5 | Hsa.22 |  |
| Chicken |  | 1: 393.74k | ENSGALG00000039165 | ENSGALT00000052302.1 | Gga.1 | manually edited |
|  |  | 1: 155.62k | ENSGALG00000033919 | ENSGALT00000080172.1 | manually edited |
|  |  | 5:17.92m | XP\_015142368.1 |  | Gga.5 | jan-16 |
| Anole lizard | | 6: 79.30m | ENSACAG00000012124 | ENSACAT00000012209.3 | Aca.6 |  |
|  |  | NW\_003338830.1:0.24m | XP\_008115586.1 |  | Aca.NW\_003338830 |  |
|  |  | GL343837.1: 74.61k | ENSACAG00000000095 | ENSACAT00000027586.2 | Aca.GL343837 |  |
| Coelacanth | | JH126644.1: 84.57k | ENSLACG00000003467 | ENSLACT00000003926.1 | Lch.JH126644 |  |
|  |  | JH126862.1: 138.17k | ENSLACG00000004766 | ENSLACT00000005408.1 | Lch.JH126862 |  |
|  |  | JH128886.1: 115.38k | ENSLACG00000004253 | ENSLACT00000004825.1 | Lch.JH128886 |  |
| Spotted gar | | LG27: 11.16m | ENSLOCG00000005253 | ENSLOCT00000006340.1 | Loc.LG27 |  |
|  |  | LG8:43.08m | XP\_015208638.1 |  | Loc.LG8 | jan-16 |
| Zebrafish | shank3b | 4: 9.55m | ENSDARG00000063054 | ENSDART00000145613.2 | Dre.4 |  |
|  | shank3a | 18:7.66m | XP\_017207498.1 |  | Dre.18.1 | jun-17 |
|  | shank1 | 3:30.70m | XP\_021329733.1 |  | Dre.3 | jun-17 |
|  | shank2 | 25: 14.07m | ENSDARG00000062325 | ENSDART00000145387.1 | Dre.25 | Assigned gene name in this study: shank2b |
|  | si:ch1073-450f2.1 | 18: 50.97m | ENSDARG00000102443 | ENSDART00000174109.1 | Dre.18.2 | Assigned gene name in this study: shank2a |
| Amphioxus |  | NW\_003101532.1:2.80m | XP\_002607814.1 |  | Bfl.NW\_003101532 | oct-09 |
| Fruitfly | Prosap | 2R: 14.06m | FBgn0040752 | FBtr0087601 | Dme.2R |  |
| Caenorhabditis elegans | | II: 11.38m | WBGene00006444 | C33B4.3c | Cel.II |  |