Table S1. Primers used in this study.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Primer name |  | Sequences (5' to 3') | Primer name |  | Sequences (5' to 3') |
| Genotyping  sex | Forward | GTCAAAGGCGTCTTCCTCACTT | ***enpep*** | Forward | ATGCCATCAGTCAGCAGCTT |
| Reverse | ACAGTGTCTCCGTGGAGTTAAA | Reverse | TCCCAGACGATGTAGTCGGT |
| β-actin | Forward | GAGAGGTTCCGTTGCCCAGAG | ***smox*** | Forward | CTCCCAGTATGGATGAGGTGTC |
| Reverse | CAGACAGCACAGTGTTGGCGT | Reverse | CTGATGCTGCGCTGAGTAGTT |
| *spata5l1x3* | Forward | AGAGAGCCACAGTCTGACCA | ***arg1*** | Forward | ACCTCTCGGCCAAAGTGAAG |
| Reverse | ACGGGTGTCGTTGGGTTTAG | Reverse | GCCCTCCAACTACAGGTGTC |
| *ckap4* | Forward | CACACAGACACTCGAAGGCT | ***sam*** | Forward | AGTTGTCCGTGACACCATCC |
| Reverse | GTCTGGACACCCGTTTGGAT | Reverse | TCCAATGTCCTCCTCGTTGC |
| *dan4lx2* | Forward | GGCACAACTTGCTACACGTC | ***srm*** | Forward | TGGTGGAATCGGTGGTTCTG |
| Reverse | AGCCTGCTGTCCACTTCAAA | Reverse | AGGCATCCTGGTTCTGCTTC |
| *ccnb1* | Forward | GTGACAGACAGGGCCTACAC | ***gss*** | Forward | TGTTTCAATCTGACTCTGGACCTT |
| Reverse | CTTCTGAGGAACTGCAGGGG | Reverse | TTATTCCTGTTCCTGGGCTTTT |
| *cbln1l* | Forward | GCTCTTCTGCCGTCTTGTCT | ***enoph1*** | Forward | CTGACGGGACGGGTTTAACA |
| Reverse | GTGTCCTACGTGCTGTGTCA | Reverse | AAACCTCCGGAACCATCGAC |
| *lcnl* | Forward | GTACTCAAGACGCCAGTGCT | ***fbxo25x1*** | Forward | TGTCGGAGATGTGTGTGAGC |
| Reverse | TGGGACTGGATAGACAGCGA | Reverse | GTTGAGTGCTTCACCAAGCG |
| *per1l* | Forward | GGAGAAGTGGAAGCGTTGGA | ***bmal1x1*** | Forward | AACTATTGTCGGTTATCTTCCCC |
| Reverse | GCTAAGGTCCTTGAAGCGGT | Reverse | CTCTTTACTCCGCAGCACTTTT |
| *adcy1l* | Forward | TCCATCGCCAACTTCAACGA | ***cbslx2*** | Forward | AGGTCAGACCCTCAGATGCT |
| Reverse | AGGCAGTTGTAGGAACCAGC | Reverse | ATCATGCACCACCAGAGCAA |
| *loxhd1* | Forward | TGGATCGTGTGGAAGTCACG | ***fmo5l*** | Forward | GGTCATCGGCATCGGTAACT |
| Reverse | GGGTAGAGGACCCTGGTGAT | Reverse | GCAGCAGTTTGAACAGGACG |
| *cycsl* | Forward | CCCAGTGCCATACAGTGGAG | ***glul*** | Forward | GGAGTGGGAGCAGATAAGGC |
| Reverse | CCTCATCCCAGATGATGCCC | Reverse | TGAAGGATGAAGCGGGCAAT |
| *cbln1l* | Forward | GCTCTTCTGCCGTCTTGTCT | ***elovl6l*** | Forward | GATCAGCTGACGGGGTTCAA |
| Reverse | GTGTCCTACGTGCTGTGTCA | Reverse | AGCTTCACAGTCAGCACCTC |
| *crhr1* | Forward | GGAGGAGAAGACGAAGTCGC | ***fads2*** | Forward | GCCTGGCTGATGATATGGCA |
| Reverse | CCAACGAATCCAACGCTTCC | Reverse | GCAACAAGTGATTCCAGCGG |
| *scgnlx2* | Forward | AAAGCCCTGATGGGTCACTG | ***hsd17b7l*** | Forward | ATGCAGCACAGAGATGGGAC |
| Reverse | GGATGTTGTGAGGGTCCGTT | Reverse | AGGAGAACAGCCCCTGGTTA |
| *caln1l* | Forward | AACCGGATCGATCAACGAGG | ***cyp450 3a40*** | Forward | TGGGATGCGATTTGCTCTGT |
| Reverse | TGGTGGAACGGCATCTTCTC | Reverse | ACGTGGCACCATCTTCAGTT |
| *adcy1l* | Forward | CTGCGGCTGGACTATCTCTG | ***hadhb*** | Forward | TGCAGGCCAGATAATGGCAA |
| Reverse | CAAGACTCCAACCTGAGCGT | Reverse | GTGTGCCACCGTGGTTACTA |
| *rsbn1l* | Forward | ACTGTCAACAACCACCATCCC | ***tymp*** | Forward | CGCTGAGTGATGAGGAGGTC |
| Reverse | AAGCCAGCTCATCAGCGTAG | Reverse | TGGCCATGACATCACTTCCC |
| *cdca3* | Forward | CACCAACAAAACCAGAGGCG | ***got1*** | Forward | ACAGATGAAGGTCAGCCGTG |
| Reverse | GTACGATCGATGCCTGCTGA | Reverse | ATCTGAACTCAGGCAAGCCC |
| *fstl* | Forward | CCAGCACAAAGGAGGCCTAA | ***fasn*** | Forward | CCGGATACGCTGTGCATTTG |
| Reverse | CGGCCGCAAGGTAAATCAAG | Reverse | AAGACACCCCAACGTCCATC |
| *cdc20* | Forward | CCGTTAGAAACAGCAAACAAAT | ***fads2a*** | Forward | TCTTTCTTGTGGGACCACCG |
| Reverse | TAGCCATTCAGTGACATAGACCAG | Reverse | ACCTGACGAAGGTGATGAGC |
| *pmf1l* | Forward | TGAGAAGCAGCCTGATGAAGC | ***sams*** | Forward | AGTTGTCCGTGACACCATCC |
| Reverse | GTGCTGGCGAATCTGGTAAAA | Reverse | TCCAATGTCCTCCTCGTTGC |
| *chac1l* | Forward | GCCCTCGTCTACATCGCTAC | ***hgf*** | Forward | AATGTGCCCTTCTACACGCA |
| Reverse | CTGCCAGGCGGATCAAGTAT | Reverse | AGTGCACCGCTGGATTTACA |
| *gadd45bl* | Forward | AGCCGGAACCAATGACTCAG | ***gys2*** | Forward | TTCAACTCCAGGAACGACCG |
| Reverse | ATGCAAAGCAGAAGCGCAAA | Reverse | ACAGGTTGGTGGTCACACTG |
| *cbsl* | Forward | TCCTGGAGCAGTGCGATGGT | ***spock2xl*** | Forward | TGCAATGCTGTCAGGCTGTA |
| Reverse | ATGGAGCCTTCTGGGTCAACA | Reverse | ACATCAATGGCACAGCGGTA |
| *ctsbl* | Forward | GTCGAGGCGATATCCGACAG | ***ldlr*** | Forward | AGAATTCAGCTGCCTGGACC |
| Reverse | AGCCCATGCCACATTCATCA | Reverse | TCACAGTCTGCCTCGTTGTC |

Table S2. Statistics of golden pompano transcriptome sequencing data.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Sample | Clean Base | Clean Read | Q20 (%) | Q30 (%) | GC (%) |
| Hy-A1 | 6,670,945,084 | 22,327,022 | 98.09 | 94.92 | 45.34 |
| Hy-A2 | 6,174,803,378 | 20,664,971 | 98.17 | 95.14 | 45.37 |
| Hy-A3 | 5,800,526,836 | 19,416,132 | 97.97 | 94.72 | 45.22 |
| Hy-B1 | 6,086,908,682 | 20,384,163 | 98.31 | 95.39 | 45.47 |
| Hy-B2 | 6,521,726,696 | 21,839,911 | 98.00 | 94.73 | 45.26 |
| Hy-B3 | 5,935,701,768 | 19,865,252 | 97.99 | 94.74 | 45.40 |
| Hy-C1 | 6,834,331,250 | 22,873,543 | 98.10 | 94.92 | 45.26 |
| Hy-C2 | 6,432,758,472 | 21,532,193 | 98.16 | 95.06 | 45.37 |
| Hy-C3 | 6,006,345,080 | 20,099,115 | 97.95 | 94.61 | 45.46 |
| Go-A1 | 6,330,127,620 | 21,180,886 | 98.17 | 95.18 | 47.49 |
| Go-A2 | 6,072,144,546 | 20,320,418 | 98.03 | 94.91 | 47.93 |
| Go-A3 | 6,197,091,822 | 20,725,608 | 98.01 | 94.76 | 47.96 |
| Go-B1 | 6,708,235,612 | 22,431,646 | 98.16 | 95.14 | 48.47 |
| Go-B2 | 5,954,803,486 | 19,915,480 | 98.18 | 95.22 | 49.03 |
| Go-B3 | 5,968,865,680 | 19,957,681 | 98.29 | 95.47 | 48.34 |
| Go-C1 | 6,300,908,920 | 21,054,317 | 98.19 | 95.06 | 50.37 |
| Go-C2 | 6,245,529,888 | 20,903,553 | 98.10 | 95.11 | 47.26 |
| Go-C3 | 6,701,929,110 | 22,414,969 | 98.24 | 95.31 | 48.59 |
| L-A1 | 8,677,107,292 | 28,979,556 | 98.36 | 95.53 | 49.43 |
| L-A2 | 6,926,336,152 | 23,133,692 | 98.45 | 95.74 | 49.36 |
| L-A3 | 6,311,035,430 | 21,091,758 | 98.54 | 95.86 | 49.55 |
| L-B1 | 6,200,145,536 | 20,707,076 | 98.37 | 95.51 | 49.18 |
| L-B2 | 6,372,020,478 | 21,283,071 | 98.03 | 94.56 | 49.46 |
| L-B3 | 6,068,629,174 | 20,273,109 | 98.05 | 94.62 | 48.96 |
| L-C1 | 6,455,381,174 | 21,561,221 | 98.26 | 95.06 | 49.88 |
| L-C2 | 6,526,339,290 | 21,797,800 | 98.14 | 94.73 | 49.14 |
| L-C3 | 6,327,113,848 | 21,136,088 | 97.80 | 94.05 | 49.03 |