**Table S2.** Alignment of RNA-Seq reads.

Aligned reads to the *A. anguilla* genome using TopHat and quantifications of the aligned reads using HTseq. The alignments to the original pro-opiomelanocortin (*pomc*) and secretogranin III copy 1 (*scg3a*) are included, as well as the new alignments after the manual re-annotation of these genes. Percentages of aligned reads are relative to the total sequenced number of reads. All other percentages are relative to the number of aligned reads.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | **Silver eel 1** | **Silver eel 2** | **Silver eel 3** | **Silver eel 4** | **Yellow eel** | **Mature eel** |
| Reads | 2 x 34 979 211 | 2 x 12 868 247 | 2 x 8 115 788 | 2 x 8 265 310 | 2 x 32 610 312 | 2 x 29 733 953 |
| Aligned reads1 | 31 559 019(90.2%) | 12 437 924(96.7%) | 7 834 849(96.5%) | 8 036 605(97.2%) | 29 400 983(90.2%) | 24 688 357(83.0%) |
| Quantified reads, original | 22 147 534(70.2%) | 8 591 952(69.1%) | 5 625 555(71.8%) | 5 629 873(70.1%) | 19 877 926(67.6%) | 16 646 953(67.4%) |
| Quantified reads, annotated only2 | 19 797 190(62.7%) | 7 748 716(62.3%) | 5 144 679(65.7%) | 5 153 350(64.1%) | 17 179 534(58.4%) | 13 759 075(55.7%) |
| Original *pomc* alignments | 7 264 700(23.0%) | 1 753 463(14.1%) | 1 598 406(20.4%) | 1 345 307(16.7%) | 3 271 467(11.1%) | 1 411 832(5.7%) |
| New *pomc* alignments | 9 506 165(30.1%) | 2 174 308(17.5%) | 1 956 854(25.0%) | 1 675 734(20.9%) | 4 334 693(14.7%) | 1 900 682(7.7%) |
| Original *scg3a* alignments | 469 540(1.5%) | 164 911(1.3%) | 112 601(1.4%) | 100 525(1.3%) | 516 365(1.8%) | 314 118(1.3%) |
| New *scg3a* alignments | 1 091 385(3.5%) | 361 987(2.9%) | 237 805(3.0%) | 216 715(2.7%) | 1 069 095(3.6%) | 644 190(2.6%) |

1 Where at least one read of the pair aligns

2 Reads with no functional annotation removed from original alignments