

Table S1 RNAseq quality and filtering. Br- brain, Go- gonads, Mu- muscle; FB- female B+, Fb- female without B-, MB- male B+, Mb- male, B-. The numbers meaning the biological replicates.

RNAseq sample	Raw reads	Filtered reads	Filtered reads (%)
Br-FB-1	13,950,507	12,899,609	92.47
Br-FB-2	18,245,415	8,483,048	46.49
Br-FB-3	16,470,250	12,186,072	73.99
Br-Fb-1	16,038,123	11,730,340	73.14
Br-Fb-2	14,597,485	13,479,974	92.34
Br-Fb-3	19,878,364	11,544,813	58.08
Br-MB-1	15,599,135	11,757,289	75.37
Br-MB-2	14,950,748	9,883,886	66.11
Br-MB-3	18,418,396	13,734,438	74.57
Br-Mb-1	13,218,667	10,767,397	81.46
Br-Mb-2	13,396,271	11,236,968	83.88
Br-Mb-3	14,462,144	11,213,256	77.54
Go-FB-1	20,357,731	9,767,262	47.98
Go-FB-2	24,067,280	13,157,076	54.67
Go-FB-3	13,883,524	8,265,707	59.54
Go-Fb-1	13,684,230	7,858,365	57.43
Go-Fb-2	14,017,168	8,077,051	57.62
Go-Fb-3	19,560,926	11,616,614	59.39
Go-MB-1	15,985,926	6,640,759	41.54
Go-MB-2	16,173,228	6,600,334	40.81
Go-MB-3	24,888,369	9,741,359	39.14
Go-Mb-1	15,415,060	6,766,093	43.89
Go-Mb-2	19,567,332	7,383,530	37.73
Go-Mb-3	15,972,791	7,121,332	44.58
Mu-FB-1	23,788,846	9,221,077	38.76
Mu-FB-2	18,143,462	10,736,418	59.18
Mu-Fb-1	25,030,699	14,799,691	59.13
Mu-Fb-2	16,617,575	13,410,630	80.70
Mu-MB-1	20,630,448	11,569,042	56.08

Mu-MB-2	12,479,370	7,798,086	62.49
Mu-Mb-1	16,459,529	9,930,843	60.33
Mu-Mb-2	23,882,108	14,441,392	60.47

Table S2 Normalized reads mapped in the genome. Br- brain, Go- gonads, Mu- muscle; FB- female B+, Fb- female without B-, MB- male B+, Mb- male, B-

Sample	Total reads	Mapped reads	Mapped reads (%)
Br-Fb	26,342,977	23,205,950	88.09
Br-FB	25,399,499	22,663,007	89.23
Br-MB	24,911,453	21,800,249	87.51
Br-Mb	25,228,301	22,977,679	91.08
Go-FB	26,159,086	7,242,201	27.69
Go-Fb	23,217,731	6,435,588	27.72
Go-MB	19,020,567	4,457,475	23.44
Go-Mb	17,684,510	3,682,046	20.82
Mu-FB	15,590,884	11,077,022	71.05
Mu-Fb	22,503,951	19,735,616	87.70
Mu-MB	14,596,696	10,241,158	70.16
Mu-Mb	18,466,577	12,744,712	69.02

Table S3 miRbase fish database entries used to create the reference miRNA list.

Species	number of precursors	number of matures
<i>Astatotilapia burtoni</i>	298	236
<i>Cyprinus carpio</i>	134	146
<i>Danio rerio</i>	355	373
<i>Electrophorus electricus</i>	20	34
<i>Fugu rubripes</i>	131	108
<i>Gadus morhua</i>	401	516
<i>Hippoglossus hippoglossus</i>	39	36
<i>Ictalurus punctatus</i>	281	205
<i>Metriaclicma zebra</i>	256	184
<i>Neolamprologus brichardi</i>	251	182
<i>Oryzias latipes</i>	168	146
<i>Oreochromis niloticus</i>	812	695
<i>Pundamilia nyererei</i>	250	182
<i>Paralichthys olivaceus</i>	20	38
<i>Salmo salar</i>	371	497
<i>Tetraodon nigroviridis</i>	132	109

Table S4 Primers used to genomic PCR, genomic qPCR and RT-qPCR

Name	sequence
1B+read-novel-Fw	ATGACCGTTAATATCTGGGTG
1B+read-novel-Rv	TCCTAGTGGCCGAAAATGG
2B+read-novel-Fw	GCTCCCTTTGATAGCTCAGC
2B+read-novel-Rv	CAGCTTGAAGGGAGATGTTAGTG
3B+read-novel-Fw	GTATCGCTTCTCGGCCTTTT
3B+read-novel-Rv	CAATACCAGGTCGATGCGT
4B+read-novel-Fw	GGGAGCAATGTCACTTTTGTCT
4B+read-novel-Rv	ATTTTTATGAGCCGCAGCAG
5b-read-novel-Bbl-Fw	ATCAGGTGGGTGGTTGCTTTA
5b-read-novel-Bbl-Rv	ATGGCTCATCAGGACTACATGC
6b-read-novel-Bbl-Fw	CCAATCCCTCCTTTAGGTTTCAG
6b-read-novel-Bbl-Rv	TTCCTGTCAGGCCCCAAA
7b-read-novel-ctrl-Fw	AGATGTGAAGTACTCTGACTGCGA
7b-read-novel-ctrl-Rv	CTTGAAATGTAGCCTGGGTATAGC
8b-B+read-novel-Fw	AAGGTCTTCTCACCCAGTCTCC
8b-B+read-novel-Rv	CAGCAACCTCGGTGGAAAC
9b-B+read-novel-Fw	CCTCCTTGCTGCTGTGTTG
9b-B+read-novel-Rv	AAGTGAGGACGGCTGCTTG
10b-B+read-novel-Fw	ATCAGAAGGTCTGGTGGTTCG
10b-B+read-novel-Rv	ACAACCTAAGGACCCCAAAGC
HPRT-Fw-gen-ctrl	TCTGTGTGCTGAAAGGGGGC
HPRT-Rv-gen-ctrl	GCTCTCTGTGTGCTGAAAGG
Dicer_F	CCTGGACAGATACGCCTCTC
Dicer_R	GTCATTGAGGACCTGTTTGGAG
Drosha_F	GACCAAGTGGGAGACTCTACAG
Drosha_R	CTGAGTCGCTGCTGTAACCTG
UBCE_Fw	GTCCGTTTCAATCCCAACTT
UBCE_Rv	GTTCTCCGTCATCAGAGACT