**RNA-seq mapping and differential gene expression**

RNA-seq data was mapped to the *Taeniopygia guttata* genome [1] version 3.2.4, downloaded from Ensembl release 88 – Mar 2017 [2]. Reads were first trimmed for adapters and quality using Cutadapt version 1.9.1 [3] supplied with TruSeq adapter sequences and the following options: --trim-n --max-n 0.1 -m 30 -q 20,20 -e 0.1 -O 3. Unusual per-base sequence content at the beginning and end of reads indicated further contamination, so an additional round of trimming was conducted using PRINSEQ version 0.20.4 [4] and the following options: -trim\_left 13 -trim\_right 2 -min\_len 30 -trim\_ns\_right 1. Before and after each round of trimming reads were assessed for quality using FastQC version 0.11.4 [5]. Trimmed reads were then mapped using Tophat2 version 2.1.1 [6] supplied with the *T. guttata* version 3.2.4 annotations and the following options: -F 0.1 --no-coverage-search --b2-very-sensitive --no-mixed --read-realign-edit-dist 0 -i 70 -M -I 500000 --library-type fr-firststrand. Mapping statistics can be found in supplementary table X.

Differential gene expression and FPKM values (Fragments Per Kilobase of transcript per Million mapped reads) was determined using the Cufflinks suite version 2.2.1 [7-9]. Protein coding gene and transcript expression was first quantified using Cuffquant with the following options: -b –M -u --library-type fr-firststrand. Differential gene expression was then determined using Cuffdiff2 and the following options: -L FCH,MCH,FTH,MTH,FCNT,MCNT,FTNT,MTNT --dispersion-method per-condition --library-norm-method geometric --min-reps-for-js-test 3 -b -M -u --library-type fr-firststrand. The –b options were provided with the *T. guttata* genome and a GFF file including mitochondrial, rRNA, pseudogenes, and other non-protein coding sequences was supplied with the –M option for masking. Cuffdiff2 performed all pair-wise comparisons, increasing the number of tests and affecting the multiple testing correction. As only the comparison of control and treatment between samples of matching sex and tissue were of interest; results were imported into R, comparisons not of interest were removed, and q-values (false discovery rate) were readjusted using the function p.adjust() and Benjamini-Hochberg Procedure [10]. Sample clustering, heatmaps, and plots of individual gene expression were made in R using CummeRbund [11] and ggplot2 [12].

**Gene ontology enrichment**

GO terms [13] for *T. guttata* were downloaded from ARK-Genomics [14]. Enrichment analysis was performed for each comparison in R with the topGO [15] package using the parentCHILD algorithm [16] and and F-statistic. GO terms were considered significant with a p-value of < 0.01.

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