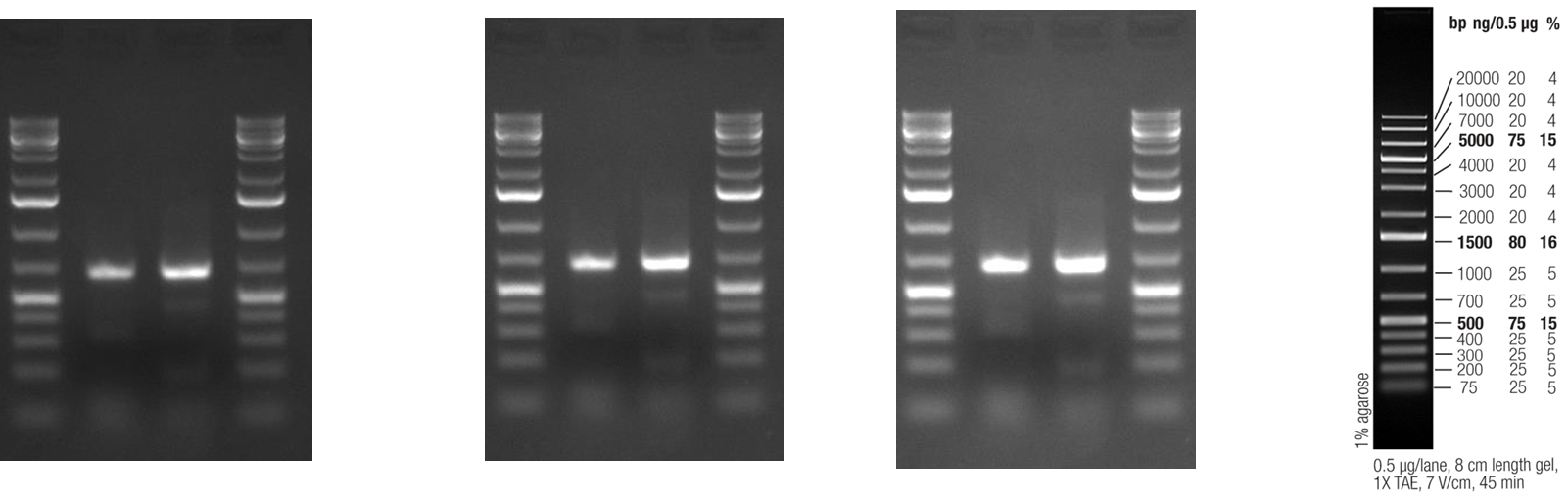
**Supplementary text S2: Amplification of Mexican tetra *HAA* by RT-PCR**

Total RNA samples of gill (sample 1) and a mix of internal organs (sample 2) of a Mexican tetra were converted to cDNA and then subjected to PCR experiments. The primers used for PCR amplification were *Asme-HAA 5’UTR.F1* and *Asme-HAA 3’UTR.R1* designed at the5’ and 3’ untranslated regions of *Asme-HAA*, respectively, as indicated by the Transcriptome Shotgun Assembly (TSA) sequence report GFIF01006274. For either sample, the only clear band that was amplified was 659 bp as expected from the GFIF01006274 report, and no longer bands were detected (A). Sequence analysis revealed that these bands contained two, presumably allelic sequences, which only show one silent nucleotide difference in the *Asme-HAA* coding sequence and were named *Asme-HAA*\*01 and *Asme-HAA*\*02 [for their alignment see (B)]. These sequences were deposited in GenBank as accessions LC494124 and LC494125. The amino acid sequence encoded by these sequences is shown in main text Fig. 4. The experiment confirms that *Asme-HAA* lacks an 1 exon sequence, as also indicated by TSA report GFIF01006274 and by genomic sequence information (see main text Fig. 3).

(A) *Agarose gel electrophoresis of RT-PCR amplified Asme-HAA fragments*

 1 2

700 bp -

1000 bp -

500 bp -

(B) *Alignment of the Asme-HAA\*01 and \*02 nucleotide sequences, with encoded amino acids above the second nucleotides of codons*

  M  V  S  A  E  M  L  W  M  M  M  L  V  F  L  G  G  S  P  L    
*Asme-HAA*\*01 1 ATGGTTTCTGCAGAGATGCTGTGGATGATGATGCTGGTGTTTCTGGGTGGTTCCCCACTC 60

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*Asme-HAA*\*02 1 ATGGTTTCTGCAGAGATGCTGTGGATGATGATGCTGGTGTTTCTGGGTGGTTCCCCACTC 60

 WAFPLAPPPGVVECEYAGRR    
*Asme-HAA*\*01 61 TGGGCTTTTCCTTTAGCTCCGCCCCCGGGCGTGGTTGAATGTGAGTATGCTGGTCGGCGG 120

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*Asme-HAA*\*02 61 TGGGCTTTTCCTTTAGCTCCGCCCCCGGGCGTGGTTGAATGTGAGTATGCTGGTCGGCGG 120

 VELLRDRVRVEGRDVLVLNQ    
*Asme-HAA*\*01 121 GTGGAGCTGCTGAGGGACCGGGTTCGGGTGGAGGGTCGGGATGTCCTGGTGCTGAATCAG 180

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*Asme-HAA*\*02 121 GTGGAGCTGCTGAGGGACCGGGTTCGGGTGGAGGGTCGGGATGTCCTGGTGCTGAATCAG 180

  VNHTWTMLVTEPAQLDLQQI    
*Asme-HAA*\*01 181 GTAAATCACACCTGGACGATGTTGGTAACAGAACCGGCTCAGCTGGACCTGCAGCAGATC 240

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*Asme-HAA*\*02 181 GTAAATCACACCTGGACGATGTTGGTAACAGAACCGGCTCAGCTGGACCTGCAGCAGATC 240

 LQECTDLKKKMLNYNQTTTG    
*Asme-HAA*\*01 241 CTGCAGGAGTGTACAGACCTGAAGAAGAAGATGCTCAATTACAACCAGACTACAACAGGC 300

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*Asme-HAA*\*02 241 CTGCAGGAGTGTACAGACCTGAAGAAGAAGATGCTCAATTACAACCAGACTACAACAGGC 300

 VSVFGVVATLLAALLFVGFV    
*Asme-HAA*\*01 301 GTCTCTGTTTTTGGAGTGGTGGCGACGCTTCTGGCAGCTTTATTGTTCGTTGGTTTTGTT 360

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*Asme-HAA*\*02 301 GTCTCTGTTTTTGGAGTGGTGGCGACGCTTCTGGCAGCTTTATTGTTCGTTGGTTTTGTT 360

 LLSFKYPEYVGVGGVLGSII    
*Asme-HAA*\*01 361 TTACTGAGCTTTAAGTATCCAGAATATGTCGGAGTCGGAGGTGTTTTGGGCTCCATCATC 420

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*Asme-HAA*\*02 361 TTACTGAGCTTTAAGTATCCAGAATATGTCGGAGTCGGAGGTGTTTTGGGCTCCATCATC 420

 HYPPHSQKEKEKGRSENVPP    
*Asme-HAA*\*01 421 CACTATCCTCCTCATTCTCAGAAAGAAAAAGAAAAAGGACGGTCTGAAAACGTTCCTCCA 480

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*Asme-HAA*\*02 421 CACTATCCTCCTCATTCTCAGAAAGAAAAAGAAAAAGGACGATCTGAAAACGTTCCTCCA 480

A N V S P Y \*

*Asme-HAA*\*01 481 GCTAATGTCTCTCCTTACTGA 501

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*Asme-HAA*\*02 481 GCTAATGTCTCTCCTTACTGA 501