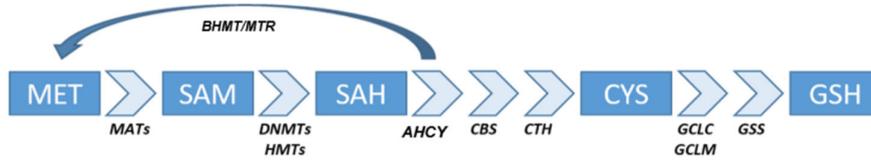


# **Are The Main Methionine Sources Equivalent For Fish Nutrition? A Focus On DL-Methionine (DL-MET) And Methionine Hydroxy Analog (MHA-Ca) Reveals Differences On Rainbow Trout Cell Lines Functions.**

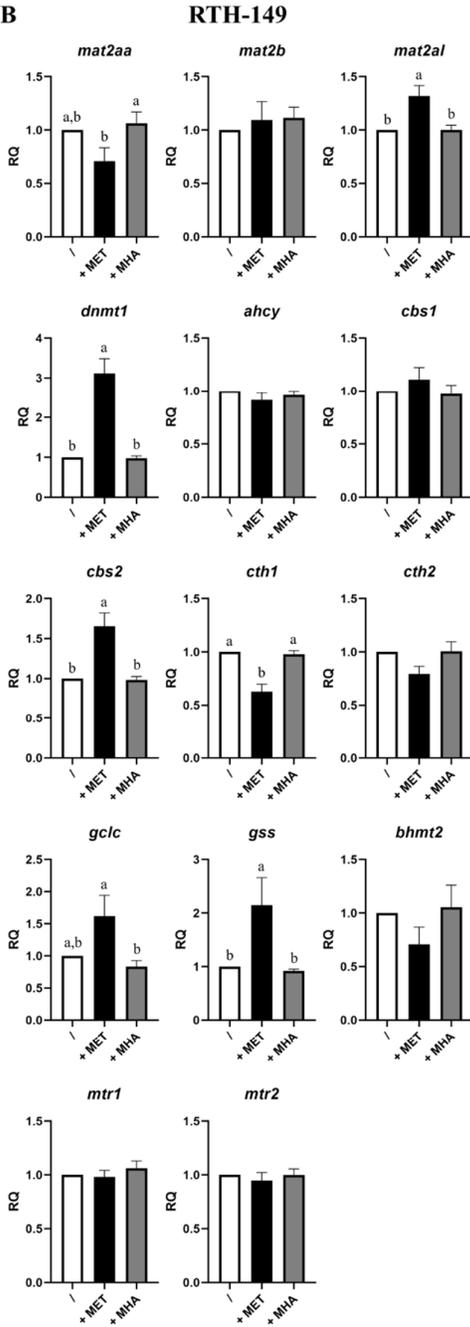
**Karine Pinel<sup>1</sup>, Cécile Heraud<sup>1</sup>, Guillaume Morin<sup>1</sup>, Karine Dias<sup>1</sup>, Annaëlle Marcé<sup>1</sup>, Linda Beauclair<sup>1</sup>, Stéphanie Fontagné-Dicharry<sup>1</sup>, Karthik Masagounder<sup>2</sup>, Martina Klüenemann<sup>2</sup>, Iban Seiliez<sup>1</sup> and Florian Beaumatin<sup>1,\*</sup>**

Supplementary figures

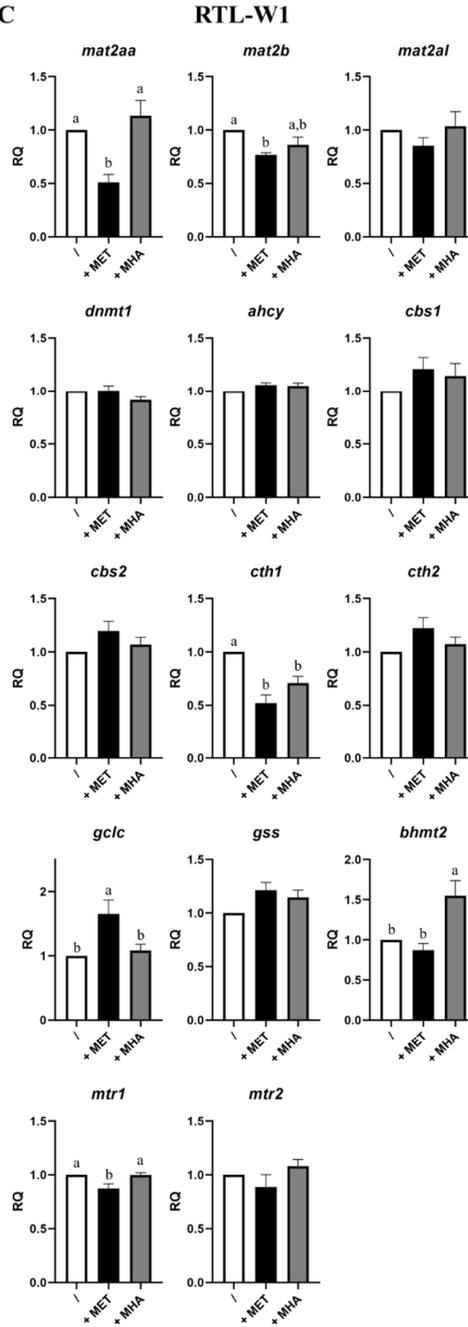
## A Simplified MET pathway



## B

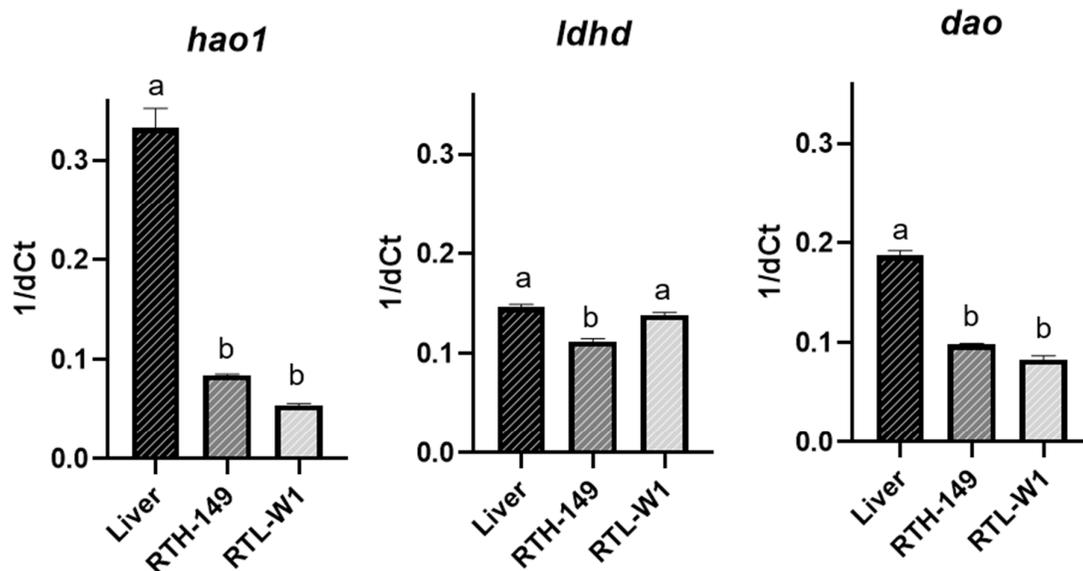


## C



Supplementary Figure S1 Impact of MET sources on the expression of methionine-related metabolism genes.

(A) Diagram showing a simplified methionine cycle, transsulfuration pathway and glutathione (GSH) synthesis. Abbreviations: MET, methionine; MAT, methionine adenosyltransferase; SAM, S-adenosyl L methionine; DNMT1, DNA methyltransferase 1, SAH, S-adenosylhomocysteine; AHCY, adenosylhomocysteinase (also known as SAHH for S-adenosylhomocysteine-hydrolase; BHMT, betaine-homocysteine S-methyltransferase; MTR, 5-methyltetrahydrofolate-homocysteine methyltransferase; CBS, cystathionine-beta-synthase; CTH, cystathionine gamma-lyase; CYS, cysteine; GCLC, glutamate-cysteine lyase catalytic subunit; GCLM, glutamate-cysteine ligase modifier subunit; GSS, glutathione synthetase; GSH, glutathione. (B, C) Methionine cycle analysis with gene expression assessed by RT-qPCR following treatments with MET-depleted media (/) supplemented with MET (+MET) or MHA (+MHA) for RTH-149 cells (B) (N=7) or RTL-W1 cells (C) (N=5). Conditions showing results statistically different from each other are presented using a different letter (one-way ANOVA with Tukey's post-hoc test).



Supplementary Figure S2 Impact of MET sources on gene expression for the oxidation reactions according to MET sources considered.

Hydroxyacid oxidase 1 (*hao1*), lactate dehydrogenase d (*ldhd*) and d-amino acid oxidase (*dao*) gene expression were assessed by RT-qPCR for both RTH-149 (N=3) and RTL-W1 (N=3) cell lines compared as in liver tissues (N=9) respectively. Conditions showing results statistically different from each other are presented using a different letter (one-way ANOVA with Tukey's post-hoc test).