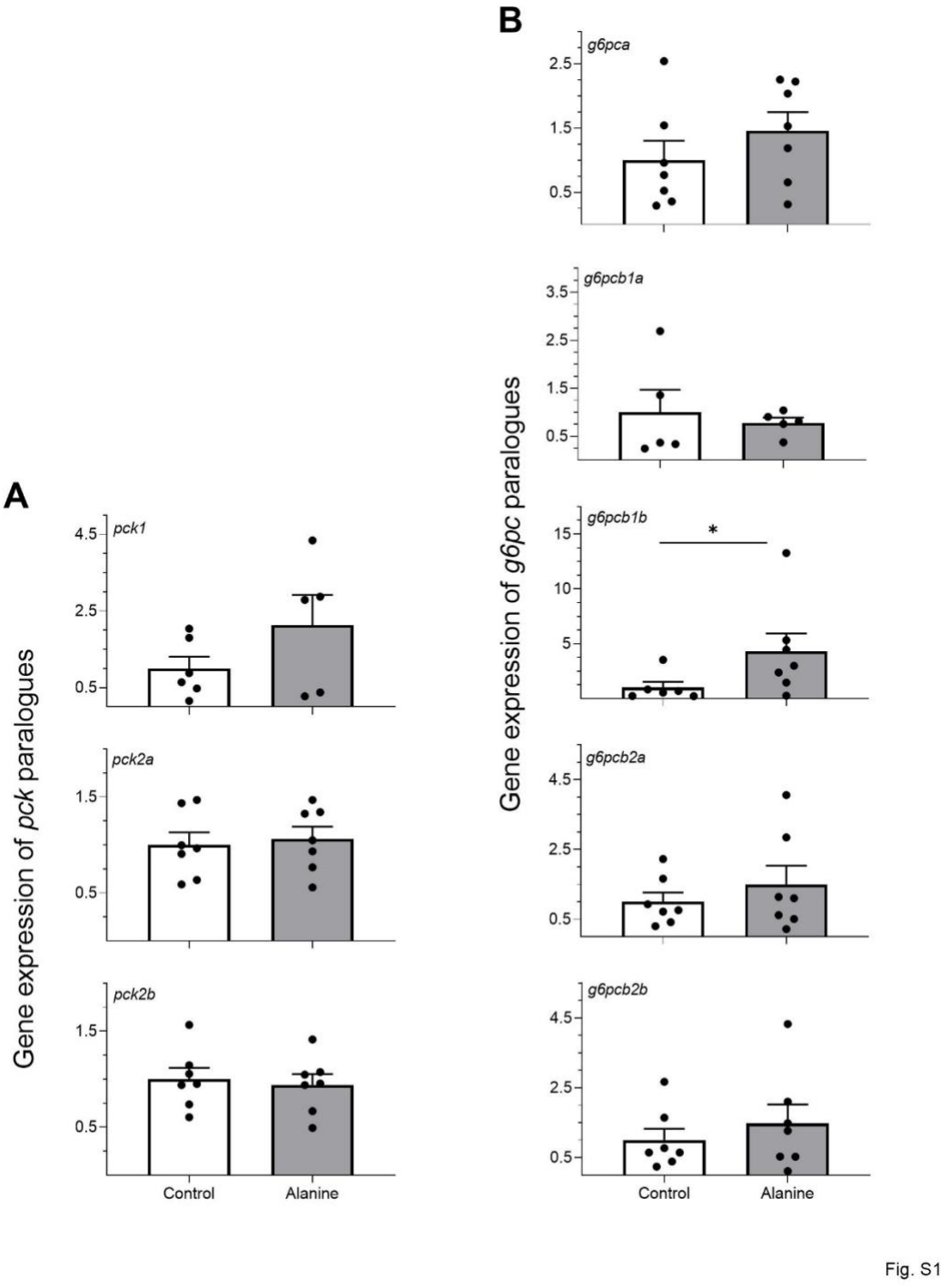

Fig. S1. Liver relative mRNA abundance of (A) phosphoenolpyruvate carboxykinase (*pck*) and (B) glucose-6-phosphatase (*g6pc*) paralogues in the control and alanine-infused rainbow trout. Data were normalized by the reference gene *β-actin*. The mean + s.e.m. are represented (N=5-7). Filled circles represent individual data points. Data were analyzed using two-tailed t-test and means significantly different from control are indicated by an asterisk ($p<0.05$).

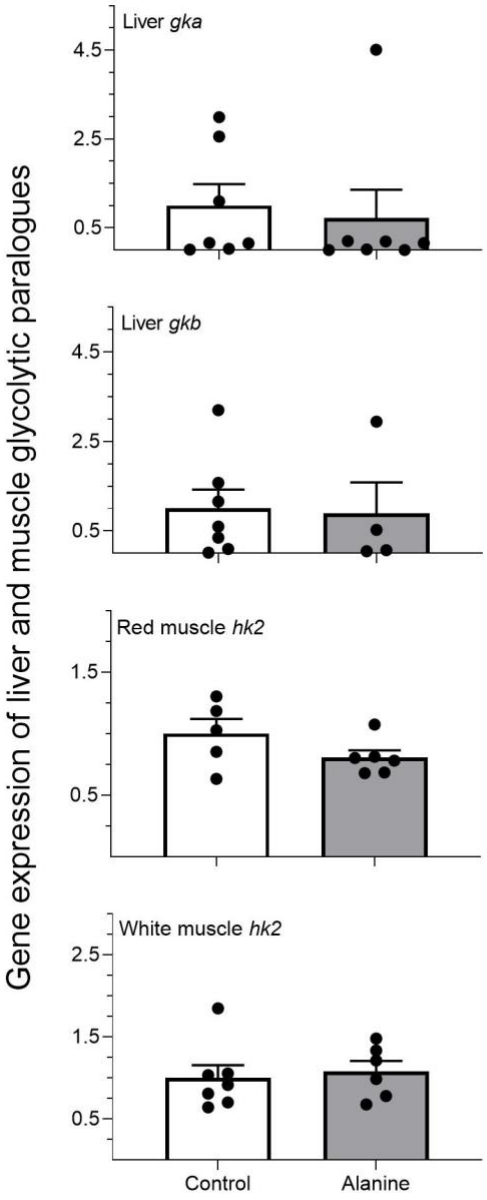

Fig. S2

Fig. S2. Relative mRNA abundance of glucokinase (*gk*) in the liver and hexokinase 2 (*hk2*) in the red and white muscle in the control and alanine-infused rainbow trout. Data were normalized by the reference gene *β-actin* for the liver and *ef1α* for red and white muscle. The mean + s.e.m. are represented (N=4-7). Filled circles represent individual data points. Data were analyzed using two-tailed t-test. Alanine had no effect on the measured glycolytic mRNA transcript abundance ($p>0.05$).

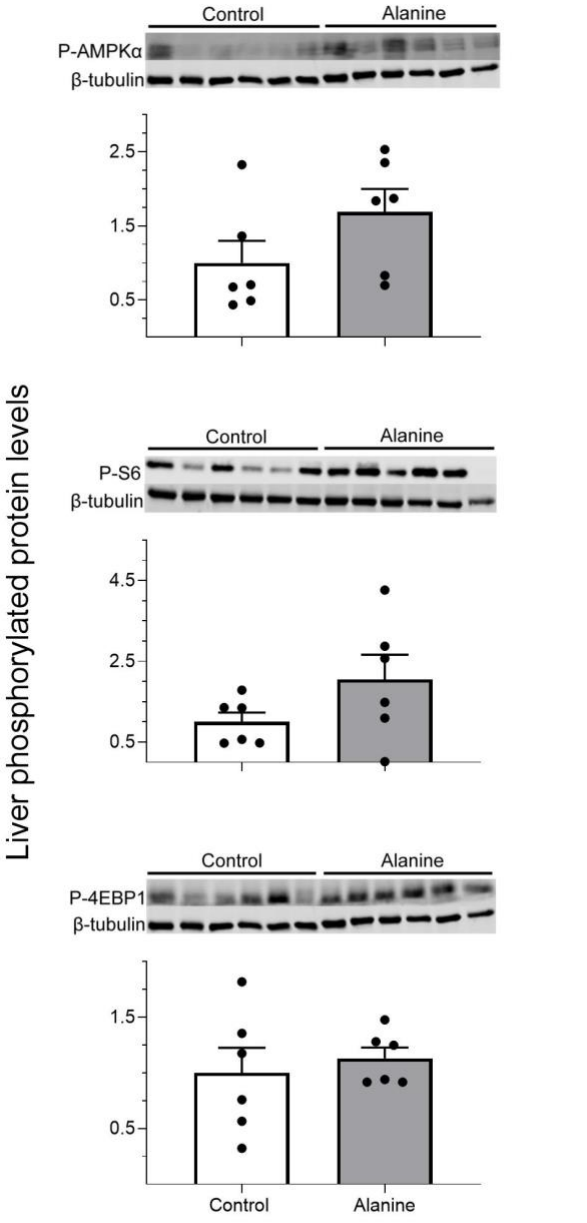

Fig. S3

Fig. S3. Liver relative abundance of phosphorylated AMPKα (at T172), ribosomal protein S6 (S6; at S235/236) and eukaryotic translation initiation factor 4E binding protein 1 (4EBP1; at T37/46) in the control and the alanine-infused groups. Data were normalized by β-tubulin and are represented as fold changes relative to the control group. The western blot of each phosphorylated protein is shown on top of its figure. The mean + s.e.m. are represented (N=6). Filled circles represent individual data points. Data were analyzed using two-tailed t-test. Alanine had no effect on the phosphorylated level of these proteins in the liver ($p>0.05$).

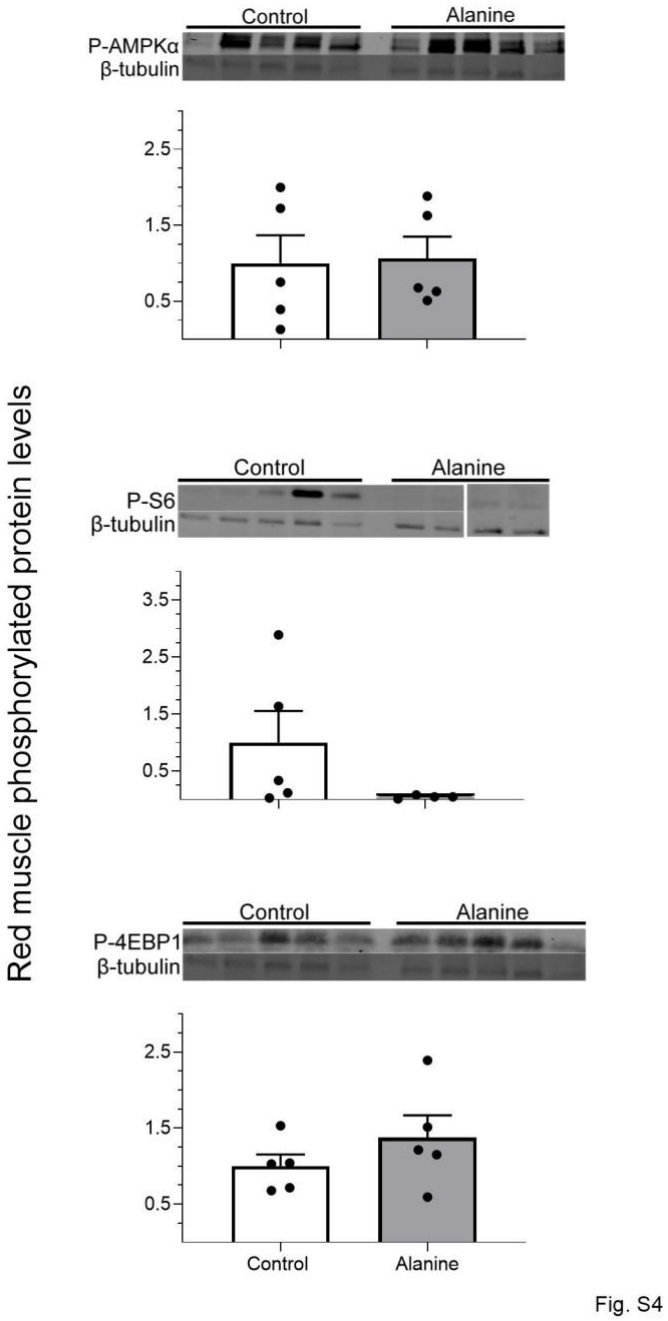

Fig. S4. Red muscle relative levels of phosphorylated AMPKα (at T172), S6 (at S235/236) and 4EBP1 (at T37/46) in the control and the alanine-infused groups. Data were normalized by β-tubulin and are represented as fold changes relative to the control group. The western blot of each phosphorylated protein is shown on top of its figure. The mean + s.e.m. are represented (N=4-5). Filled circles represent individual data points. Data were analyzed using two-tailed t-test. Alanine had no effect on the phosphorylated level of these proteins in the red muscle ($p>0.05$). A white space indicates the removal of a lane (outlier).

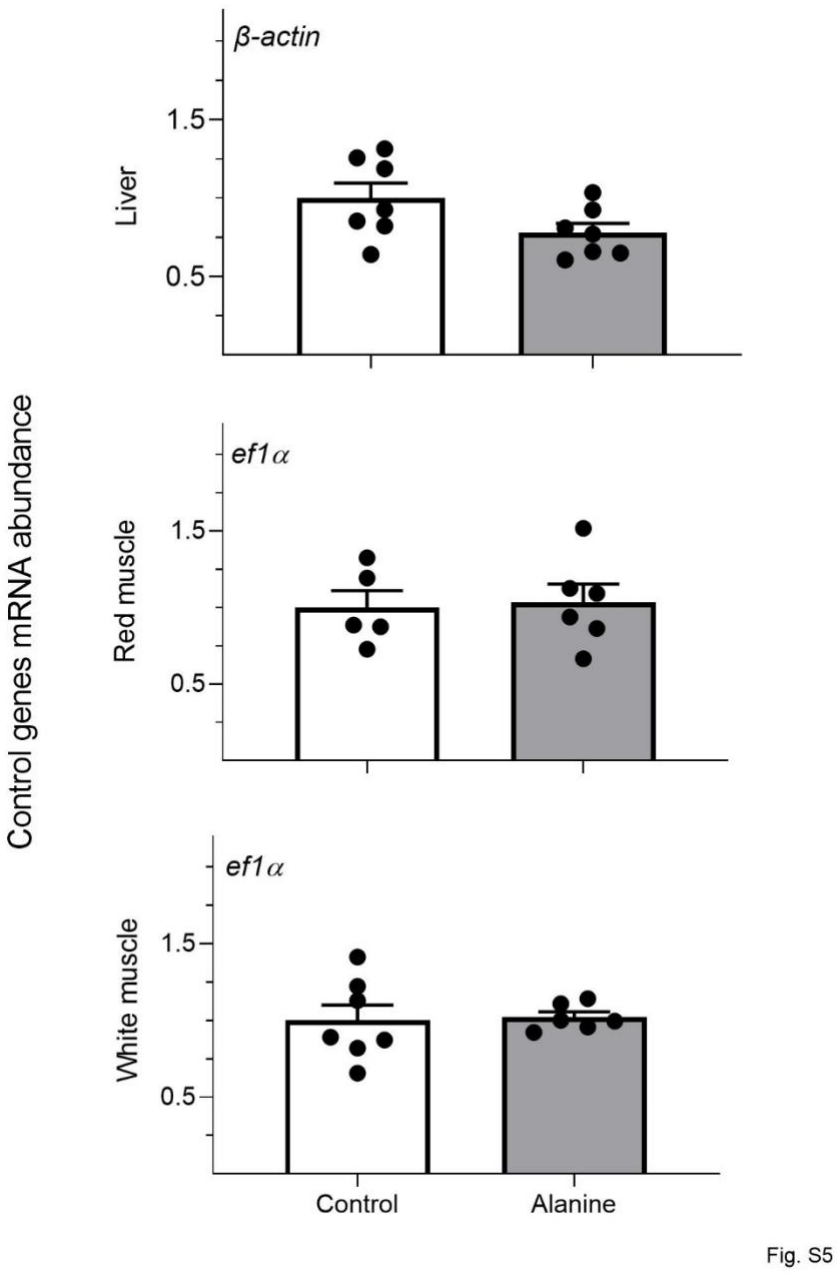

Fig. S5. Relative mRNA abundance of the control genes *β-actin* in the liver and elongation factor 1α (*ef1α*) in the muscle of the control and alanine-infused rainbow trout. Data points are relative to the control group for each gene. The mean + s.e.m. are represented (N=5-7). Filled circles represent individual data points. Data were analyzed using two-tailed t-test. Alanine had no effect on the measured mRNA transcript abundance of the control genes ($p>0.05$).

Table S1. Primer pair conditions used for mRNA quantification by real-time RT PCR.

mRNA	Primer sequence (5' to 3')	Annealing temperature °C	Efficiency %, R^2	Reference
pck1	F: ACAGGGTGAGGCAGATGTAGG R: CTAGTCTGTGGAGGTCTAAGGGC	55	91.9, 0.995	Marandel et al., 2015
pck2a	F: ACAATGAGATGATGTGACTGCA R: TGCTCCATCACCTACAACCT	55	90.4, 0.997	Marandel et al., 2015
pck2b	F: AGTAGGAGCAGGGACAGGAT R: CCGTTCAGCAAAGGTTAGGC	55	102.8, 0.989	Marandel et al., 2019
g6pca	F: GATGGCTTGACGTTCTCCT R: AGATCCAGGAGAGTCCTCC	55	91.9, 0.995	Marandel et al., 2015
g6pcb1a	F: GCAAGGTCCAAAGATCAGGC R: GCCAATGTGAGATGTGATGGG	59	105.9, 0.975	Marandel et al., 2015
g6pcb1b	F: GCTACAGTGCTCTCCTTCTG R: TCACCCCATAGCCCTGAAA	55	91.6, 0.997	Marandel et al., 2015
g6pcb2a	F: ATCGGACAATACACACAGAACT R: CAACTGATCTATAGCTGCTGCCT	54	91.3, 0.994	Marandel et al., 2015
g6pcb2b	F: CCTCTGCTCTTCTGACGTAG R: TGTCCATGGCTGCTCTCTAG	55	92.3, 0.985	Marandel et al., 2015
gka	F: CTGCCCACCTACGTCTGT R: GTCATGGCGTCCTCAGAGAT	54	96.3, 0.993	Marandel et al., 2015
gkb	F: TCTGTGCTAGAGACAGCCC R: CATTTTGACGCTGGACTCCT	57	90.9, 0.993	Marandel et al., 2015
hk2	F: TGAAAAGGGACATGCAGAGA R: GGCCCTAAAAGCAAGGAAA	58	92.3-96.1,0.992-0.988	Designed
glut4a	F: CATCTTTGCAGTGCTCCTTG R: CAGCTCTGTACTCTGCTTGC	56	106.1-101.1, 0.997-0.982	Liu et al., 2017
glut4b	F: TCGGCTTTGGCTTCCAATATG R: GTTTGCTGAAGGTGTTGGAG	56	101.4-106.2, 0.995-0.996	Liu et al., 2017
β-actin	F: AGAGCTACGAGCTGCCTGAC R: GTGTTGGCGTACAGGTCCTT	60	90.4, 0.996	Moltesen et al., 2016
ef1α	F: CACATCGCCTGCAAGTTT R: GAAGCTCTCCACACACATGG	58	106.6-110.1, 0.985-0.988	Designed

F and R represent forward and reverse primer sequences, respectively. Primer sequences for *hk2* and ***ef1α*** was designed using Primer 3 algorithm. The efficiency and R^2 values are presented for both the red and white muscle *glut4a*, *glut4b*, *hk2* and *ef1α*. The reference genes for the liver and muscle are ***β-actin*** and ***ef1α,*** respectively.