Co-expression network analysis predicts a key role of microRNAs in the adaptation of the porcine skeletal muscle to nutrient supply

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ADDITIONAL FIGURES:

Additional Fig. 1: Sequencing depth obtained for samples analyzed in each one of the two contrasts (AL-T0/AL-T1 and AL-T0/AL-T2).
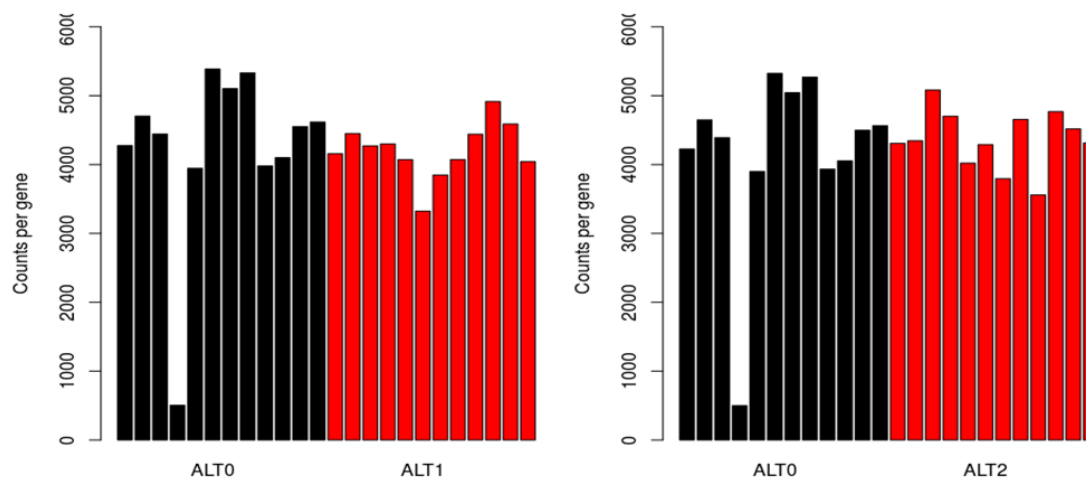
Additional Fig. 2: Joint Principal Component Analysis (PCA) clustering of *gluteus medius* skeletal muscle samples (11 AL-T0, 12 AL-T1 and 12 AL-T2 samples) according to the expression profiles of **(A)** mRNAs, **(B)** microRNAs and **(C)** lincRNAs.
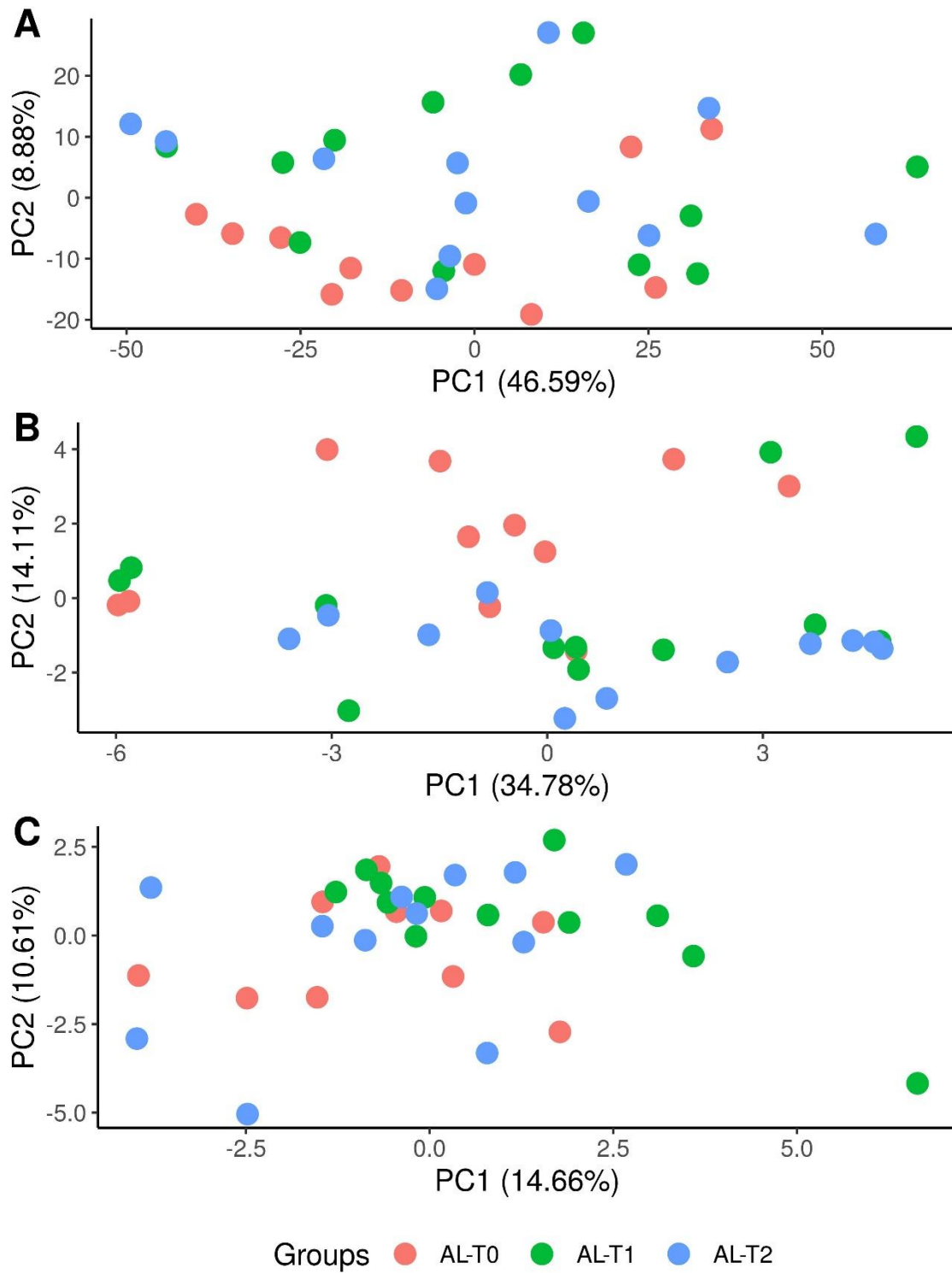
Additional Fig. 3: Phylogenetically conserved 7mer-8m predicted binding sites in the 3'- UTR of the pig *PDK4* gene for **(A)** ssc-miR-148a-3p and **(B)** ssc-miR-493-5p porcine miRNAs. The TargetScan software was used for generating conservation graphs across the investigated mammalian species. Red nucleotides show complementary matching base-pairs between the seed of the mature miRNA and the 3'UTR of the pig *PDK4* gene.
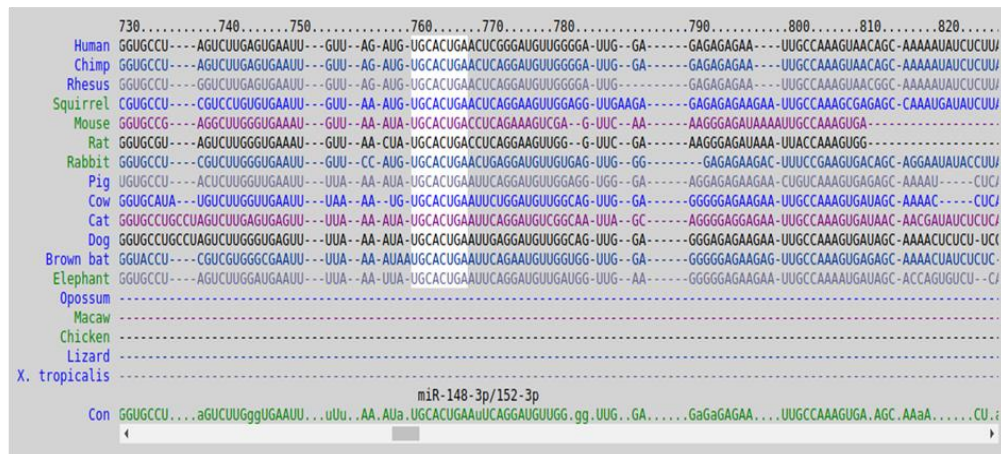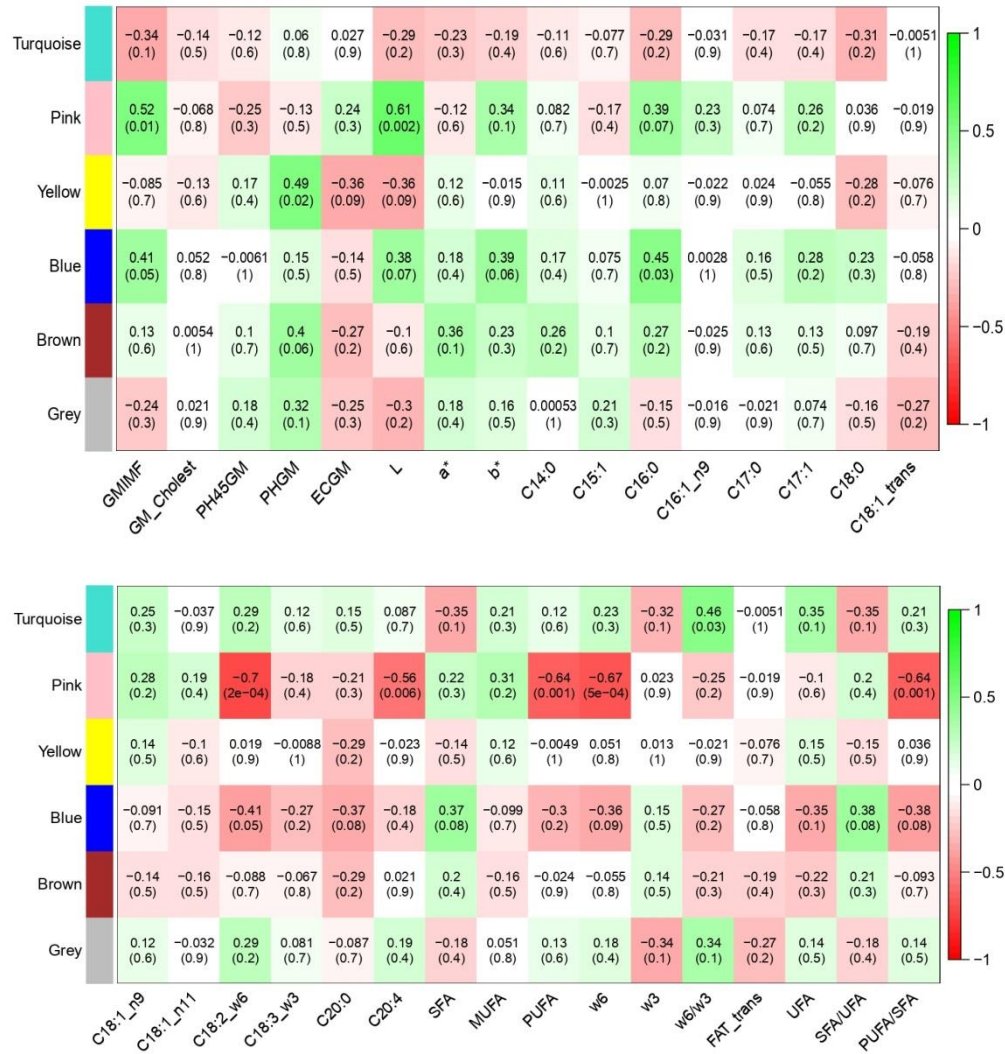
Additional Fig. 4: Gene co-expression module association with meat quality and fatty acids composition traits in the AL-T0/AL-T1 contrast as determined with the WGCNA tool.

Additional Fig. 5: Gene co-expression module association with meat quality and fatty acids composition traits in the AL-T0/AL-T2 contrast as determined with the WGCNA tool.