

Table S1: Precursor miRNA sequences of each species used in the analyses and their respective nomenclature according to the evolutionary relationship provided by the Bayesian phylogenetic trees.

[Click here to Download Table S1](#)

Table S2: Quantitative PCR primer sequences. Genes are as follow: *slow myhc* (*slow myosin heavy chain*); *fast myhc* (*fast myosin heavy chain*); *sox6* (*(sex determining region Y)-box 6*); *six1* (*six homeobox 1*); *glut4* (*insulin-responsive glucose transporter type 4*); *lamtor3* (*late endosomal/lysosomal adaptor, mapk and mtor activator 3*); *ragd* (*ras related GTP binding D*); *rptor* (*regulatory associated protein of mtor complex 1*); *mafbx* (*muscle atrophy f-box protein*); *pgc1a* (*peroxisome proliferator-activated receptor gamma coactivator 1 alpha*); *ckma* (*creatine kinase, m-type a*); *ckmb* (*creatine kinase, m-type b*); *myog* (*myogenin*); *rpl13* (*ribosomal protein L13*); *rpl19* (*ribosomal protein L19*); *omy-mir-133a-1a*, *omy-mir-133a-1b*, *omy-mir-133a-2* (precursor sequences of rainbow trout mir-133 paralogues); *omy-mir-499aa+ab*, *omy-mir-499ab*, *omy-mir-499ba*, *omy-mir-499bb* (precursor sequences of rainbow trout mir-499 paralogues); *omy-mir-206-1* (precursor sequence of rainbow trout mir-206); and *U6 snRNA* (*U6 small nuclear RNA*). Accession code based on rainbow trout genome in Genoscope (<https://www.genoscope.cns.fr/trout/>) (Berthelot et al., 2014) or NCBI (<http://www.ncbi.nlm.nih.gov>) database.

Gene	Primers (5' to 3')	Tm (°C)	Accession code
<i>slow myhc</i>	F: AGTCCGCAAGATTCAGCAT R: GCCGACATCACAACCTCTTGA	81	AF211172.1
<i>fast myhc</i>	F: GGCCAAGAAGGCTATCACTG R: GCCAGATTCTCAGCCTCATC	84	Z48794.1
<i>sox6</i>	F: TGGGAGAGGATGATGGAAAG R: CCCAGGATCTTGCTGATGTT	85	XM_021566535.1
<i>six1</i>	F: TCCCTCTGGATATCGGCGTT R: AGAAAACGACCGAGCCTCTC	83	XM_021574266.1
<i>glut4</i>	F: GTGCCAGGCTTATTGTCCATATTC R: TAGAGAAGATGGCCACCGACAG	85	XM_021615262.1
<i>lamtor3</i>	F: TCACCATGGACTGGGGGTTA R: TGC GTTATCATTG CCACTTTG	79	NM_001160681.1
<i>ragd</i>	F: AGGGGGTTTCGAAGTACACC R: TGAAACCACCTCCGTCTTCG	80	XM_021573884.1
<i>rptor</i>	F: CCATCGACAAGATGAGACGA R: CCTGGGGAGACAGAGACAGA	86	XM_021557184.1
<i>mafbx</i>	F: CAGGAGCCCCGAGTGACTTTT R: ATCAAATGCACCATCACCCCT	76	NM_001193326.1
<i>pgc1a</i>	F: AACCTGAGAGATGACGGGGA R: GTGTGTCCGTTTTCAAGGGC	78	XM_021617116.1
<i>ckma</i>	F: GTGGGTGGAGTGTTTCGACAT R: TCCACCATGAGCTTGACACC	82	XM_021623857.1
<i>ckmb</i>	F: AGCACACACCCCAAGTTTGA R: CAGAAGATCCCAGACGGTCA	84	XM_021617754.1

<i>myog</i>	F: AGCAACACCTCAGACCACTG R: AGGAGGTCTCGTTGCTGTA	75	NM_001124727.1
<i>rpl13</i>	F: CACCATTGGCATCTCTGTTG R: AGTGCTGTCTCCCTTCTTGG	85	scaffold_1560 chrUn_26:11288161..11308160
<i>rpl19</i>	F: GAGAAGACGACGCAGGATTC R: CAAGTGAAGGCACACAGGAA	80	scaffold_1008 chrUn_1:27789918..27809917
<i>omy-mir-133a-1a</i>	F: AGTGAACCCCAATGCTTT R: GGGACCAAATCCATTCAAGA	73	scaffold_1560 chrUn:390576274..390581273
<i>omy-mir-133a-1b</i>	F: GACAAACACCTAATGCCTTG R: GGGACCAAATCCATTCAAGA	73	scaffold_79929 chrUn:366226605..366231604
<i>omy-mir-133a-2</i>	F: TTCACACCAAAAATGCTTT R: GGGACCAAATCCATTGAACA	71	scaffold_1154 chrUn:346363877..346368876
<i>omy-mir-499aa+ab</i>	F: CTGAGAAGGAGACAGTTAAGACTTG R: AGAGTGGAGCCAGCAGAGAC	74	scaffold_984 chrUn_17:42432554..42452553
<i>omy-mir-499ab</i>	F: AGGAGACAGTTAAGACTTGC R: TGAGAATGGAGCCAGCAC	74	scaffold_116 chrUn_7:18225955..18230954
<i>omy-mir-499ba</i>	F: GAGGGAAGTAGTTAAGACTTG R: CTAAAGTGATGTTTCATGAGT	70	scaffold_347 chrUn_9:20331061..20336060
<i>omy-mir-499bb</i>	F: GAGGGAAGTAGTTAAGACTTA R: CTAAAGTGATGTTTCATGAGC	70	scaffold_1915 chrUn_16:304245..309244
<i>omy-mir-206-1</i>	F: TCGTTGCCTCCTGTGAAGAC R: CTCCATTCCCCTTGTAACCA	76	scaffold_13810 chrUn:893645720..893645918
<i>U6 snRNA</i>	F: GGCTTCGGCAGCACATATAC R: AACGCTTCACGATTTTGC	77	scaffold_15039 chrUn:278113300..278133299

T_m, melting temperature; F, forward; R, reverse.

Table S3: Rainbow trout miRNAs similarity. Percentage of similarity between miRNAs paralogues identified in rainbow trout.

Paralogue	Nucleotide similarity
<i>omy-mir-133a-1a</i> vs <i>omy-mir-133a-1b</i>	97%
<i>omy-mir-133a-1a</i> vs <i>omy-mir-133a-2</i>	93%
<i>omy-mir-133a-1b</i> vs <i>omy-mir-133a-2</i>	92%
<i>omy-mir-499aa</i> vs <i>omy-mir-499ab</i>	96%
<i>omy-mir-499ba</i> vs <i>omy-mir-499bb</i>	97%

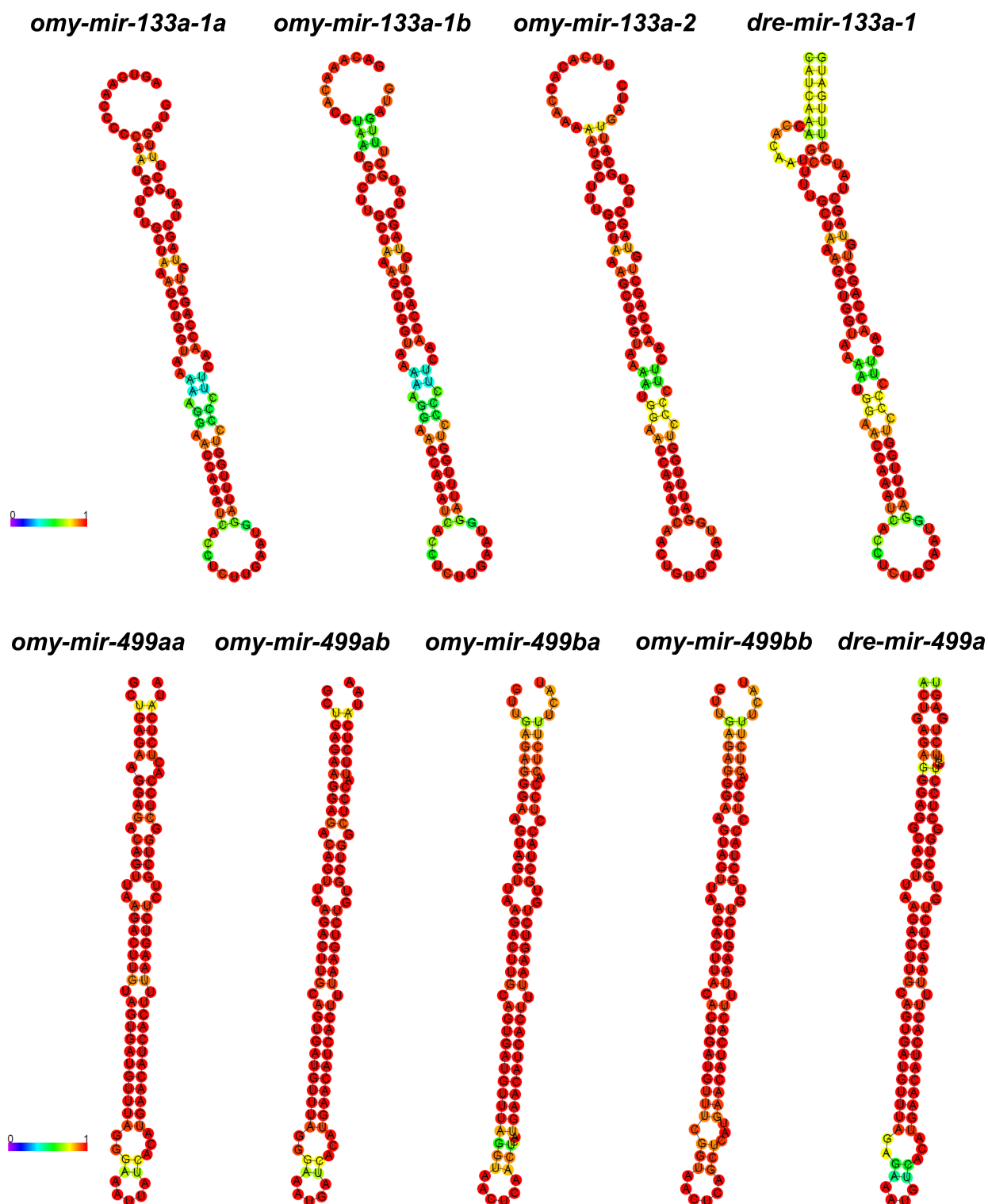


Figure S1: Predicted secondary structures of the identified miRNA precursor sequences. The precursor sequences of the mir-133 and mir-499 paralogues were submitted to minimum free energy (MFE) prediction of the optimal secondary structures in dot-bracket notation. Base pair probabilities are color coded 0-1, with higher numbers corresponding to higher confidence. Secondary structures of zebrafish *dre-mir-133a-1* and *dre-mir-499a* precursor sequences are shown only for comparative purposes.

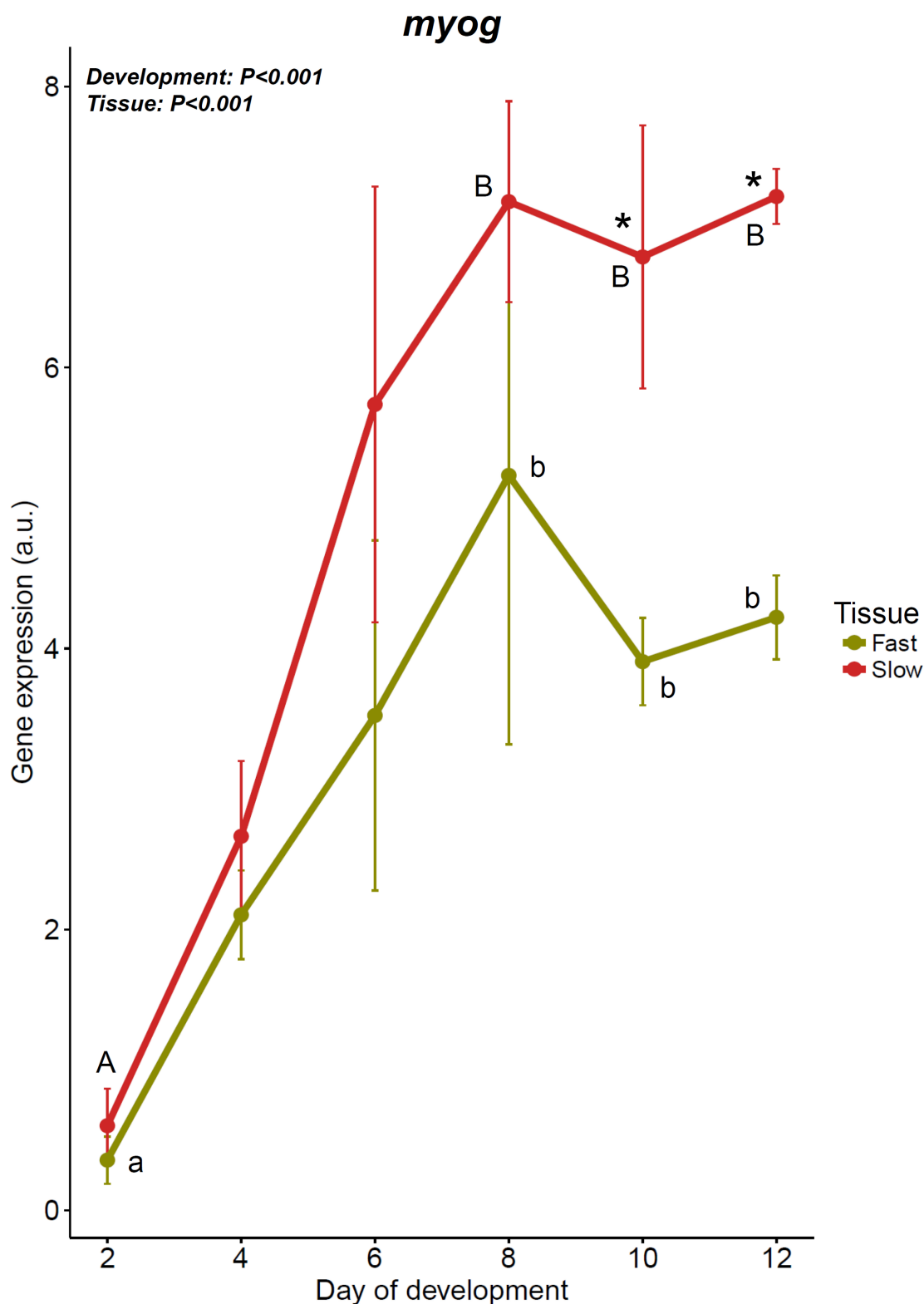


Figure S2: Myogenin expression in rainbow trout fast and slow myoblast cell culture.

Myogenin (*myog*) expression in slow and fast myoblast cell culture at days 2, 4, 6, 8, 10 and 12 of development. Values represent mean \pm SE (n=4 independent cell cultures; a.u.= arbitrary units). The P-values of the tissue of origin (*tissue*) and the day of development (*development*) are shown in the left corner of the graph. Asterisks indicate significant differences between means of slow myoblasts and fast myoblasts cell cultures, and different letters (upper case for slow and lower case for fast) indicate significant differences between means of days of development ($P < 0.05$).

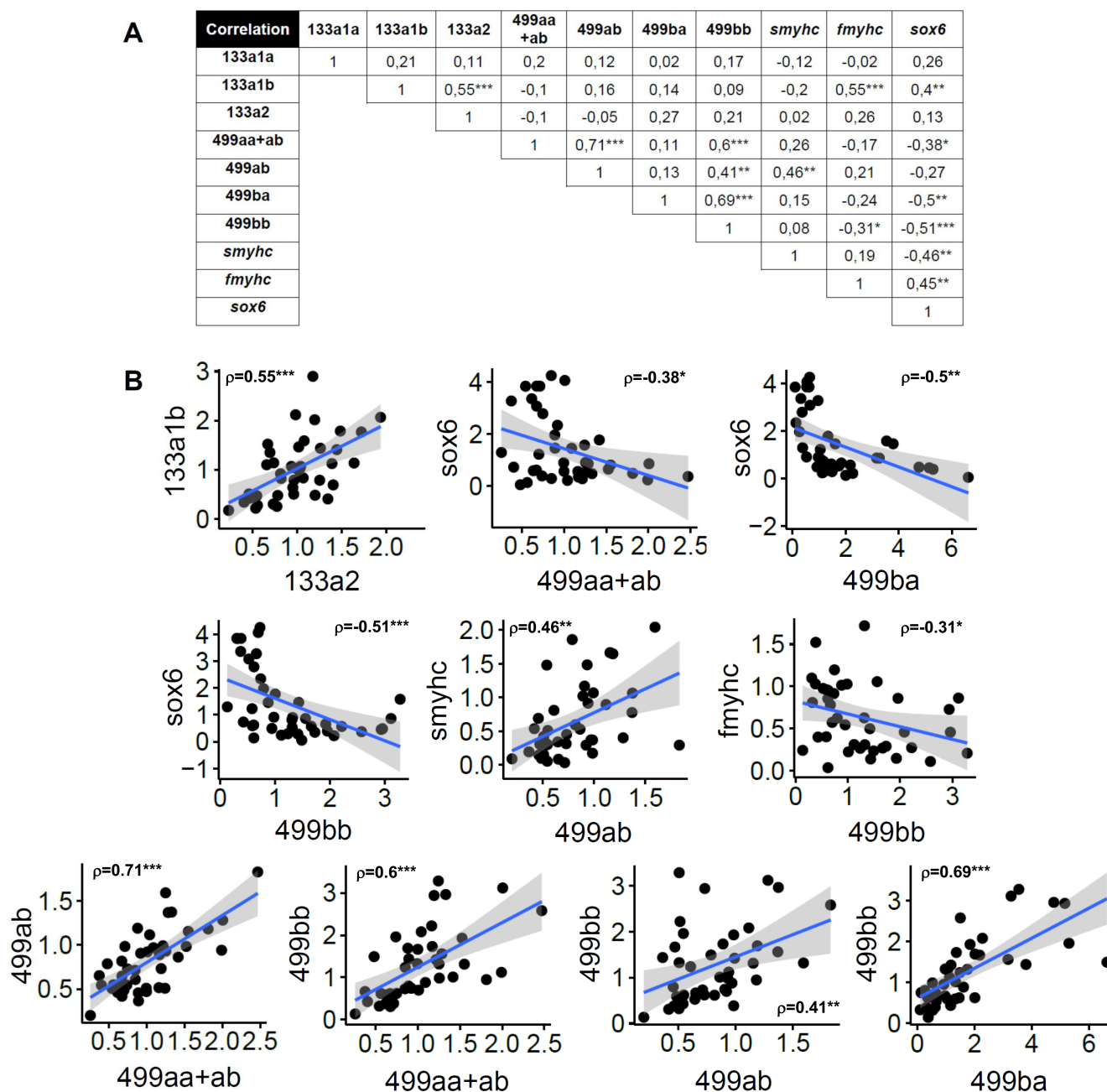


Figure S3: Correlation of rainbow trout miRNAs and mRNAs expression. (A) Pearson's correlation (ρ) index between the expression of *omy-mir-133* and *omy-mir-499* paralogues, and *smyhc*, *fmyhc* and *sox6* mRNAs. (B) Plot char between gene expression values for *omy-mir-133a-1b* vs *omy-mir-133a-2*, *omy-mir-499aa+ab* vs *sox6*, *omy-mir-499ba* vs *sox6*, *omy-mir-499bb* vs *sox6*, *omy-mir-499ab* vs *smyhc*, *omy-mir-499bb* vs *fmyhc*, *omy-mir-499aa+ab* vs *omy-mir-499ab*, *omy-mir-499aa+ab* vs *omy-mir-499bb*, *omy-mir-499ab* vs *omy-mir-499bb* and *omy-mir-499ba* vs *omy-mir-499bb*. Pearson correlation and p-value are indicated in the corners of the plot graphs. Significant differences between gene correlations are indicated with one (P<0.05), two (P<0.01) or three (P<0.001) asterisks.