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Characterization of conserved and novel miRNAs using deep sequencing and prediction of miRNA targets in Crucian carp (*Carassiusauratus*)

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1. Introduction

MicroRNAs (miRNAs) are an abundant class of non-coding small RNAs with approximately 22 nts in length (Bartel, 2004; Chua et al., 2009). MiRNA derived from approximately 70-nts long stem-loop pre-miRNAs through a sequential processing by two RNase III enzymes, Drosha and Dicer (Denli et al., 2004; Friedlander et al., 2014; Voinnet, 2009). MiRNA regulate gene expression at post-transcriptional levels by binding to either perfect or imperfect complementary in the 3'UTRs of targets, and trigger either the degradation of the targets or inhibit their translation (Kumar et al., 2012; Ott et al., 2011). An increasing amount of evidence showed that miRNAs might have potentially enormous importance in the regulation of many fundamental biological processes, such as organ development, cell proliferation, differentiation, apoptosis, organogenesis, signal transduction, immune responses and metabolism and so on (Ambros, 2004; Huang et al., 2011; Kumarswamy et al., 2011; Roy, 2016). Since the first miRNA (lin-4) was discovered in *Caenorhabditis elegans* (Lee et al., 1993), numerous miRNAs have been identified in a wide range of organisms including animals, plants and viruses through plasmid vector cloning, computational prediction, northern blotting, microarray assay and sequencing technology in recent years. Up to now, 28,645 mature miRNAs from 223 species have been discovered and deposited in the public available miRNA database miRBase (http://www.mirbase.org/, Release 21, 2014). Recently, deep sequencing technologies has become the standard approach to identify miRNAs in organisms for which small RNAs have not been characterized or novel miRNAs that might not be detected using traditional methods (Li et al., 2011; Li et al., 2016; Rahmann et al., 2013; Sha et al., 2014). This powerful strategy provides insight into the identification of conserved miRNAs as well as low-abundance or species-specific (novel) miRNAs, especially for animal species whose genomes have not been fully sequenced.