



Supplemental_Figure_S1: Validation of m⁶A immunoprecipitation transcripts
A. Relative methylation (left) and expression level (right) of targeted transcripts c-Myc, KLF, METTL3, hnRNPA2B1 and Oct4 quantified by MeRIP-qPCR (left) and qPCR (right) on a pool of oyster development. The dotted line represents the minimal value to consider an enrichment of m⁶A-RNA. **B.** Methylation (left) and expression level in TPM (right) of targeted transcripts c-Myc, KLF, METTL3, hnRNPA2B1 and Oct4 quantified by MeRIP-seq (left) and RNA-seq (left) on a pool of oyster development. Error bars represent the standard deviation.