

G			
Ythdc2	RIP &		Genes
CLIP ta	rget /		with m ⁶ A
genes			
	4 (140)	10,157	
			/

GO term	P (FDR)	Genes
meiotic nuclear division	0.036	Mei1, Tubgcp6, Mki67, Smc1a, Smc3, Smc1b
lateral element	0.011	Sycp2, Sycp1, Brca1, Smc3, Smc1b

Figure S2 (Supplement to Figure 1) YTHDC2 binds preferentially to m⁶A-marked RNA transcripts. (A) Gel shift assay measuring the dissociation (K_d, nM, indicated at the upper left corner of the gel) of FLAG-tagged YTHDC2 with methylated and unmethylated RNA probes. Protein concentrations are listed in nM. 4 nmol RNA probe was used. (B) In vitro probe pulldown assay of positive m⁶A-binding control YTHDF1 and negative m⁶A-binding control HUR in HeLa cells showing that YTHDF1 binds preferentially to probe with m⁶A, while HUR does not. GGYCU Probe sequence: 5'-CGUGGYCUGGCU-B-3' (Y=m⁶A or A, B=biotin) ACYGA Probe sequence: 5'-GAUACYGAGAAG-B-3' (Y=m⁶A or A, **B**=biotin). (C) In vitro probe pulldown assay of Ythdc2 in 16 d.p.p. mouse testes showing Ythdc2 binds preferentially to probe with m⁶A on GGACU. (D) Consensus motifs of biological replicates of Ythdc2 binding identified by HOMER of CLIP-seq of Ythdc2 in mouse testes. (E) Distribution of peak densities in CLIP-seq of Ythdc2 in mouse testes. (F) Overlap of Ythdc2 RIP-seq genes and genes containing m⁶A in young mouse testes. Targets of YTHDC2 are defined as genes enriched in the RIP: Log2(RIP/input) >= 1. Non-targets are defined as genes depleted in the RIP: Log2(RIP/input) <= -1. Genes with m⁶A are defined as genes enriched in the m⁶A IP: Log2(m⁶A IP/input) >= 2. **(G)** Overlap of genes common to Ythdc2 RIP-seg in 16 d.p.p. mice and Ythdc2 CLIP-seq in adult mice. 140/144 (97.2%) of genes contain m⁶A, a higher proportion than genes identified by Ythdc2 RIP-seq alone. (H) GO analysis of Ythdc2 RIP-seq genes; meiosis-related GO terms.