Description of Additional Supplementary Files

File name: Supplementary Data 1
Description: Identification of hnRNPH1 interactors by mass spectrometry.

File name: Supplementary Data 2
Description: Total identified abnormal alternative splicing genes in *hnRNPH1* cKO pachytene spermatocytes by RNA-Seq. To detect valid alternative splicing events, those with false discovery rate (FDR) < 0.05 and |△PSI|> 10% were categorized as differential alternative splicing events. A two-sided likelihood-ratio test was performed and adjustments were made for multiple comparisons.

File name: Supplementary Data 3
Description: Total identified abnormal alternative splicing genes in *hnRNPH1* cKO round spermatids by RNA-Seq. Total identified abnormal alternative splicing genes in *hnRNPH1* cKO pachytene spermatocytes by RNA-Seq. To detect valid alternative splicing events, those with false discovery rate (FDR) < 0.05 and |△PSI|> 10% were categorized as differential alternative splicing events. A two-sided likelihood-ratio test was performed and adjustments were made for multiple comparisons.

File name: Supplementary Data 4
Description: Total identified differentially expressed genes between *hnRNPH1* cKO and control pachytene spermatocytes by RNA-Seq.

File name: Supplementary Data 5
Description: Total identified differentially expressed genes between hnRNPH1 cKO and control round spermatids by RNA-Seq.

File name: Supplementary Data 6
Description: Total identified abnormal alternative splicing genes in *Ptbp2* cKO testes by analysis of published RNA-Seq data. Total identified abnormal alternative splicing genes in *hnRNPH1* cKO pachytene spermatocytes by RNA-Seq. To detect valid alternative splicing events, those with false discovery rate (FDR) < 0.05 and |△PSI|> 10% were categorized as differential alternative splicing events. A two-sided likelihood-ratio test was performed and adjustments were made for multiple comparisons.

File name: Supplementary Data 7
Description: Total identified hnRNPH1-binding target genes by analysis of published ChIP-seq data. A two-sided likelihood-ratio test was performed and adjustments were made for multiple comparisons.

File name: Supplementary Data 8

Description: Total identified hnRNPH1-binding target genes by RIP-seq using isolated germ cells of P28 testes.

File name: Supplementary Data 9

Description: Primer sequences are used in this study.

File name: Supplementary Data 10

Description: Antibodies used in this study.