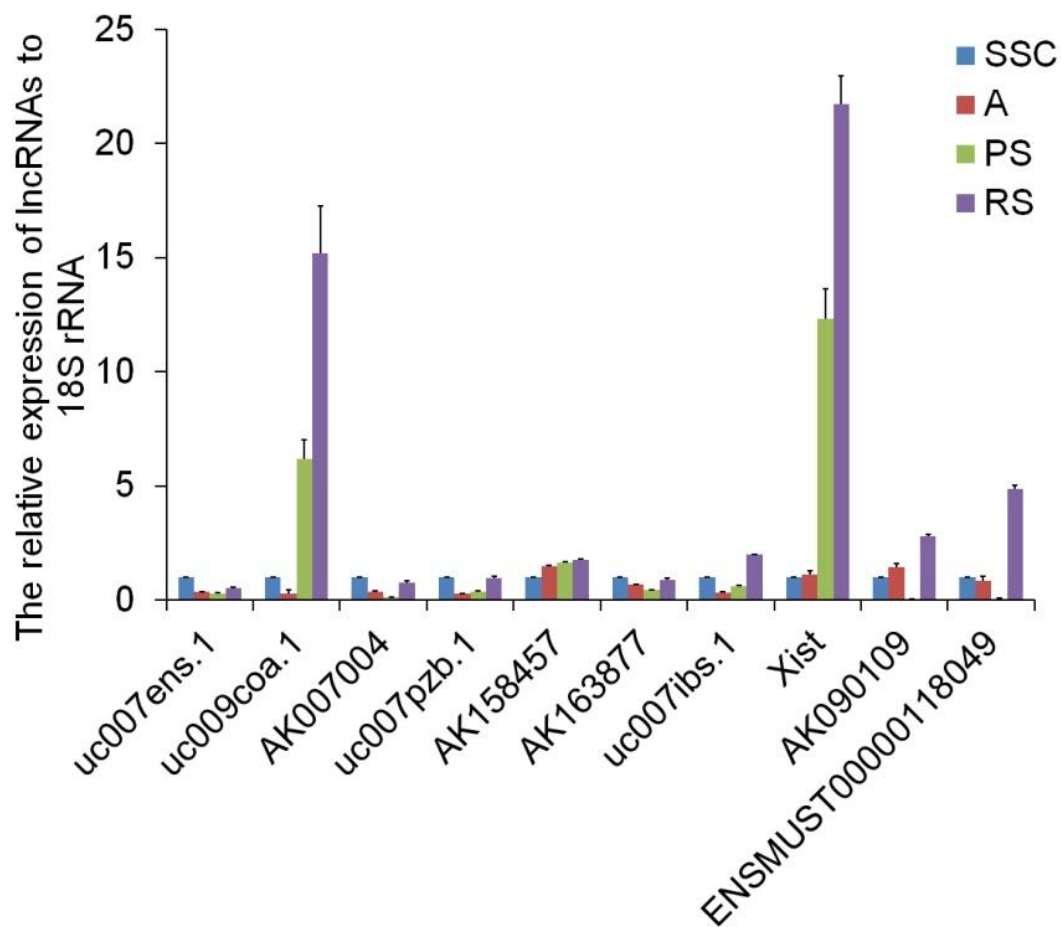


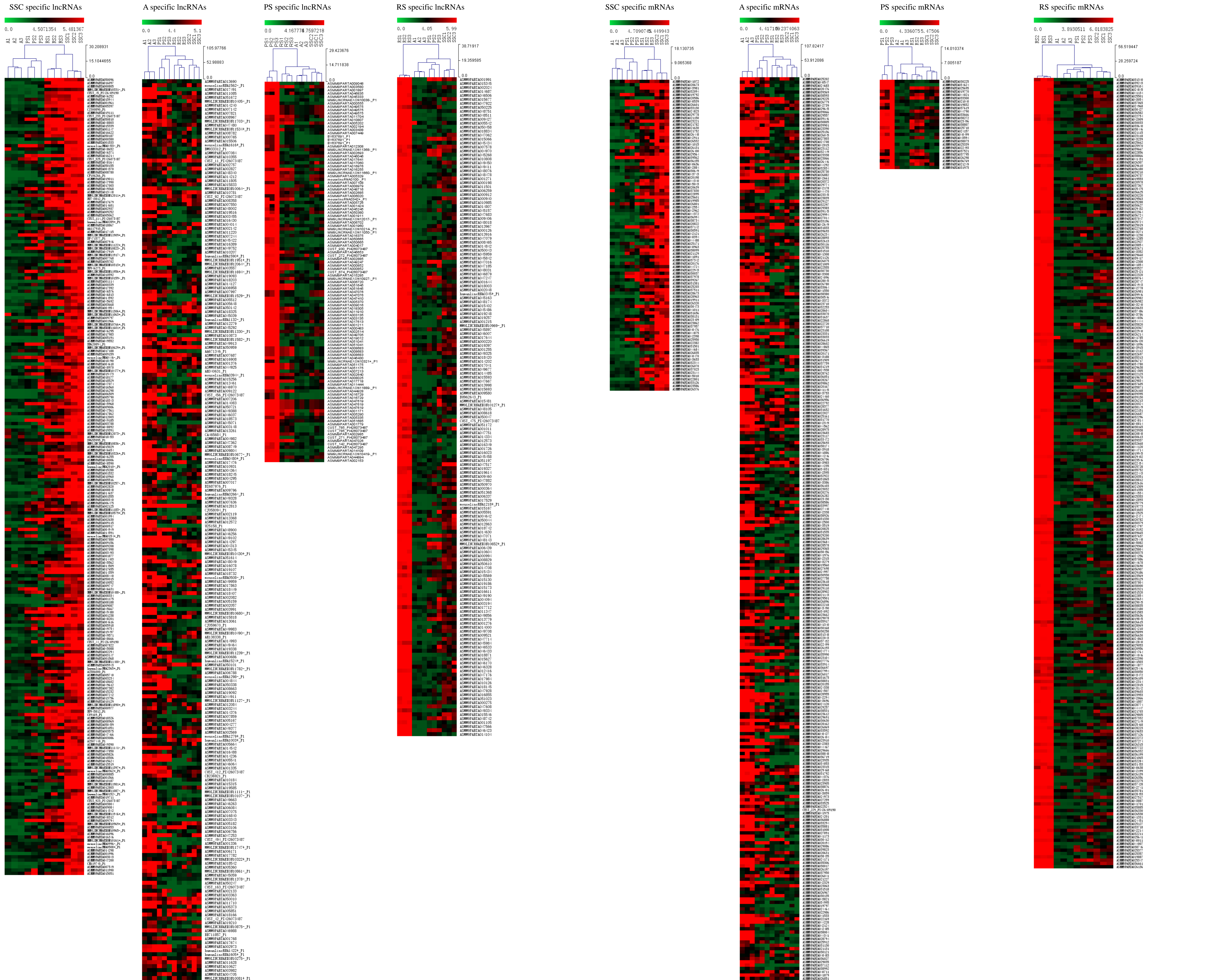
Sequential expression of long noncoding RNA as mRNA gene expression in specific stages of mouse spermatogenesis

Meng Liang, Wenqing Li, Hui Tian, Tao Hu, Lu Wang, Yu Lin, Yulei Li, Hefeng Huang & Fei Sun

Supplemental Figure S1. Total RNA was extracted from isolated male germ cells and then subjected to real-time PCR analysis for lncRNAs (uc007ens.1, uc009coa.1, AK007004, uc007pzb.1, AK158457, AK163877, uc007ibs.1, Xist, AK090109, ENSMUST00000118049) expression. These lncRNAs expression levels were normalized to endogenous 18S rRNA. Data shown are the mean \pm SEM of three separate experiments performed in triplicate.



Supplemental Figure S2. The clustered heat map showed these specific lncRNAs/mRNAs.



Supplemental Figure S3. Enriched biological process GO terms among changed genes. A, Up-regulated genes in A versus SSC. B, Down-regulated genes in A versus SSC. C, Up-regulated genes in PS versus A. D, Down-regulated genes in PS versus A. E, Up-regulated genes in RS versus PS. F, Down-regulated genes in RS versus PS.

