

**Supplementary information, Table S5** Deep sequencing analysis of transcriptome in elongating spermatids

Libraries	Small RNAs		Long Transcripts	
Unique reads	1,095,891		18,574,777	
Total reads	5,983,095		36,194,541	
miRNA	406,086	6.79%	13,874	0.06%
ncRNA	20,829	0.35%	23,895	0.11%
mRNA	228,166	3.81%	15,809,096	71.7%
Intron	133,520	2.23%	2,037,927	9.25%
TE	930,823	15.56%	1,151,068	5.23%
Intergenic regions	4,263,671	71.26%	2,989,641	13.6%