



Fig. S1. Comparison of genomic architecture between mRNAs and lncRNAs. (A) Box plot indicating expression level of total mRNAs and lncRNAs by $\log_{10}(\text{TPM} + 1)$. (B) Distribution of transcript lengths of mRNAs and lncRNAs. The x axis represents the length of transcripts, and the y axis represents composing proportion. (C) Distribution of the number of exons in mRNAs and lncRNAs. Single-exon lncRNAs were filtered out from the pig genome.

Table S1 Summary of clean reads after Filtering and Mapping to the reference genome

Sample	Total Clean R	Mapped reads	Percentage of	Percentage of	Clean Data Q:	Clean Data Q:	GC Content (%)
PP_1	89,134,050	83,988,897	94.23%	54.06%	96.55	91.88	54.45
PP_2	89,761,138	84,554,534	94.20%	59.20%	96.6	92.05	51.96
PP_3	89,870,702	84,589,878	94.12%	54.77%	96.46	91.78	53.61
IP_1	89,626,552	84,574,219	94.36%	58.56%	96.75	92.33	52.52
IP_2	89,357,710	84,599,747	94.68%	64.33%	96.88	92.6	50.84
IP_3	88,835,098	84,306,217	94.90%	56.81%	96.75	92.3	53.75