Identification and functional analysis of long intergenic noncoding RNA genes in porcine pre-implantation embryonic development

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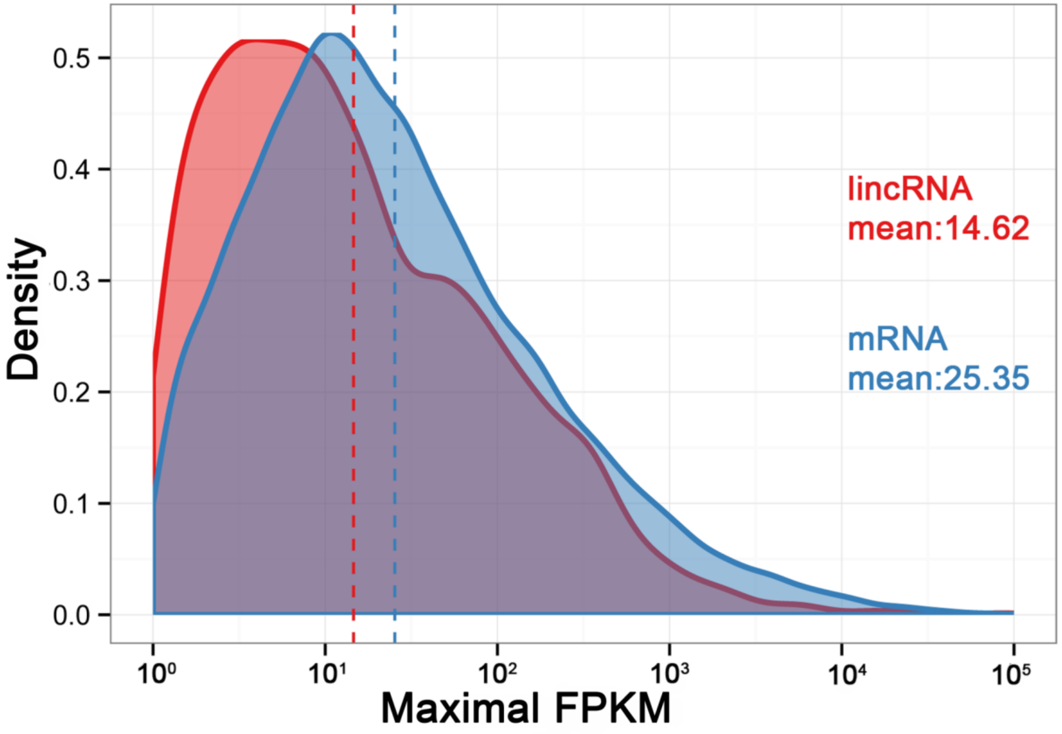
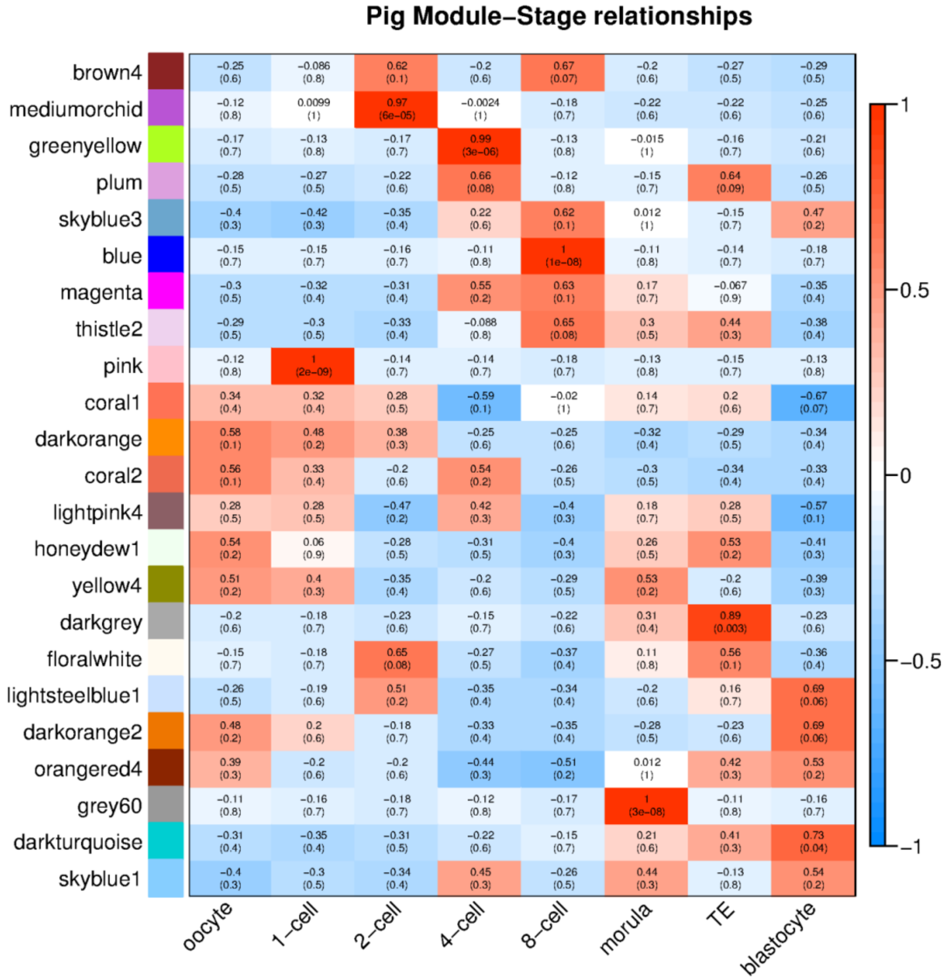
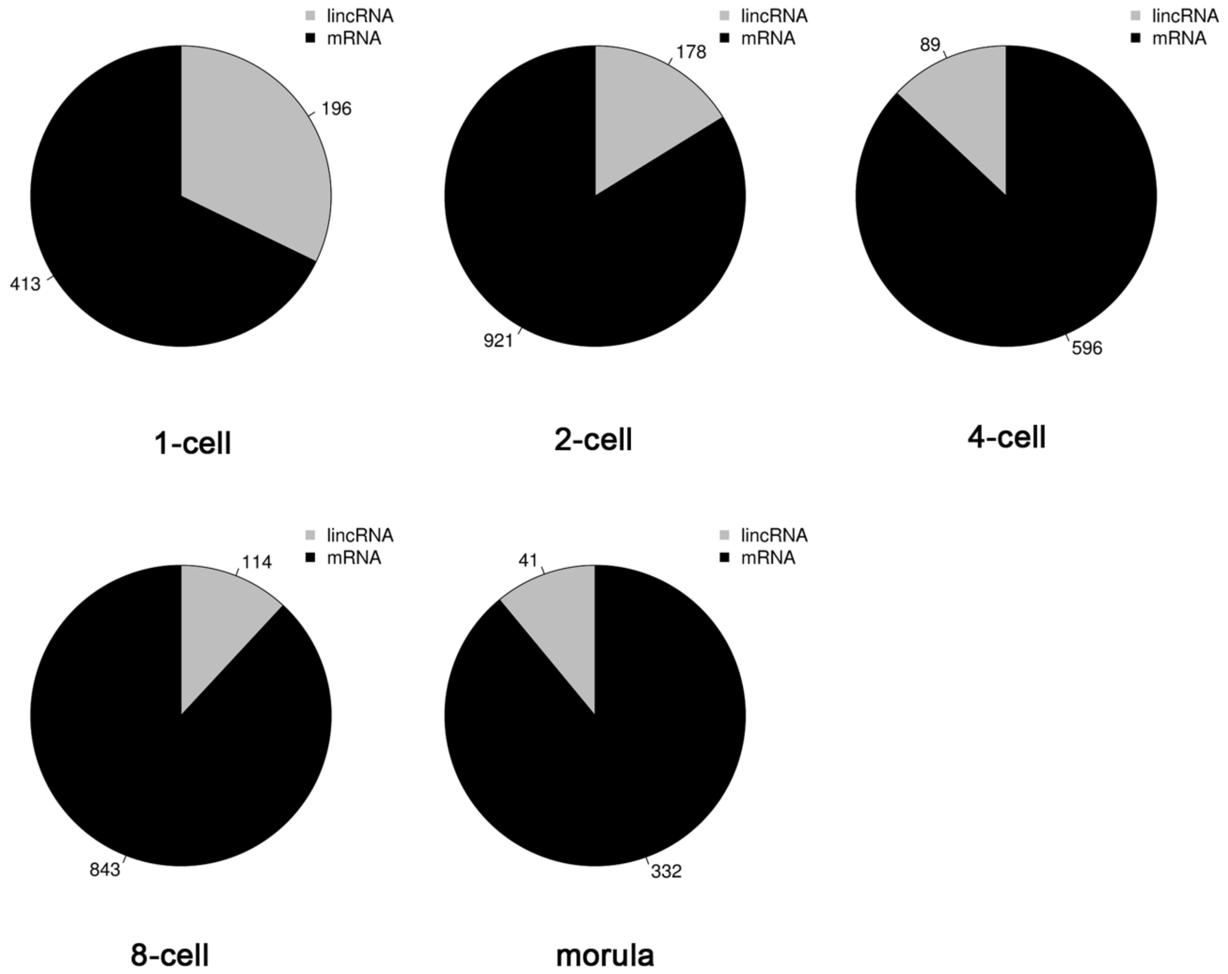


Supplementary Figure S1. Distribution of maximal expression level of lincRNAs and mRNAs across five RNA-seq datasets.

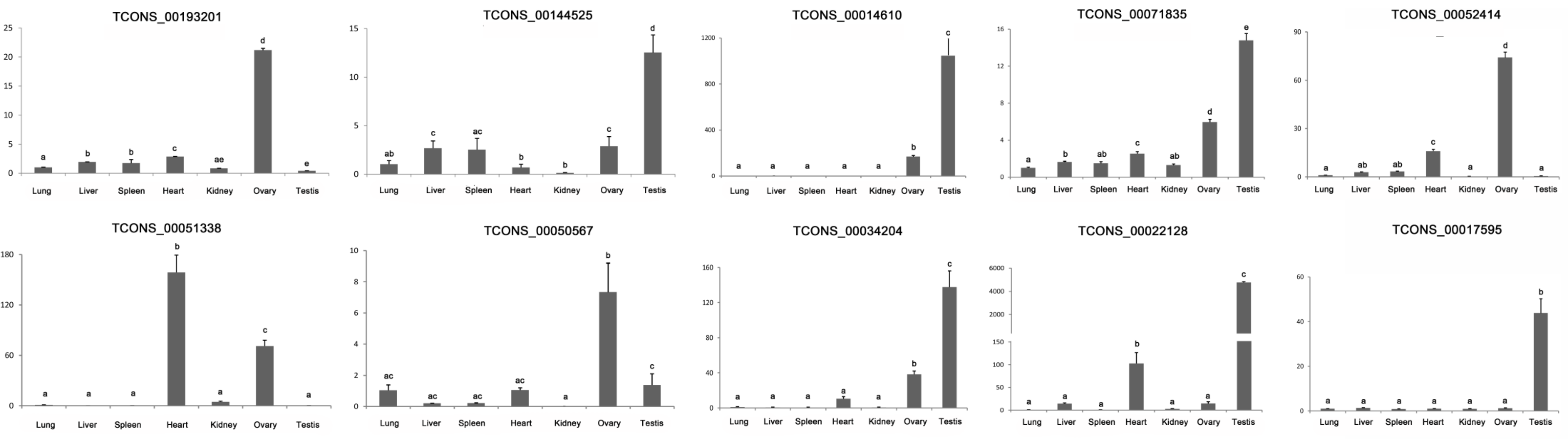


	oocyte	1–cell	2–cell	4–cell	8–cell	morula	TE	blastocyte
brown4	−0.25 (0.6)	−0.086 (0.8)	0.62 (0.1)	−0.2 (0.6)	0.67 (0.07)	−0.2 (0.6)	−0.27 (0.5)	−0.29 (0.5)
mediumorchid	−0.12 (0.8)	0.0099 (1)	0.97 (6e−05)	−0.0024 (1)	−0.18 (0.7)	−0.22 (0.6)	−0.22 (0.6)	−0.25 (0.6)
greenyellow	−0.17 (0.7)	−0.13 (0.8)	−0.17 (0.7)	0.99 (3e−06)	−0.13 (0.8)	−0.015 (1)	−0.16 (0.7)	−0.21 (0.6)
plum	−0.28 (0.5)	−0.27 (0.5)	−0.22 (0.6)	0.66 (0.08)	−0.12 (0.8)	−0.15 (0.7)	0.64 (0.09)	−0.26 (0.5)
skyblue3	−0.4 (0.3)	−0.42 (0.3)	−0.35 (0.4)	0.22 (0.6)	0.62 (0.1)	0.012 (1)	−0.15 (0.7)	0.47 (0.2)
blue	−0.15 (0.7)	−0.15 (0.7)	−0.16 (0.7)	−0.11 (0.8)	1 (1e−08)	−0.11 (0.8)	−0.14 (0.7)	−0.18 (0.7)
magenta	−0.3 (0.5)	−0.32 (0.4)	−0.31 (0.4)	0.55 (0.2)	0.63 (0.1)	0.17 (0.7)	−0.067 (0.9)	−0.35 (0.4)
thistle2	−0.29 (0.5)	−0.3 (0.5)	−0.33 (0.4)	−0.088 (0.8)	0.65 (0.08)	0.3 (0.5)	0.44 (0.3)	−0.38 (0.4)
pink	−0.12 (0.8)	1 (2e−09)	−0.14 (0.7)	−0.14 (0.7)	−0.18 (0.7)	−0.13 (0.8)	−0.15 (0.7)	−0.13 (0.8)
coral1	0.34 (0.4)	0.32 (0.4)	0.28 (0.5)	−0.59 (0.1)	−0.02 (1)	0.14 (0.7)	0.2 (0.6)	−0.67 (0.07)
darkorange	0.58 (0.1)	0.48 (0.2)	0.38 (0.3)	−0.25 (0.6)	−0.25 (0.6)	−0.32 (0.4)	−0.29 (0.5)	−0.34 (0.4)
coral2	0.56 (0.1)	0.33 (0.4)	−0.2 (0.6)	0.54 (0.2)	−0.26 (0.5)	−0.3 (0.5)	−0.34 (0.4)	−0.33 (0.4)
lightpink4	0.28 (0.5)	0.28 (0.5)	−0.47 (0.2)	0.42 (0.3)	−0.4 (0.3)	0.18 (0.7)	0.28 (0.5)	−0.57 (0.1)
honeydew1	0.54 (0.2)	0.06 (0.9)	−0.28 (0.5)	−0.31 (0.5)	−0.4 (0.3)	0.26 (0.5)	0.53 (0.2)	−0.41 (0.3)
yellow4	0.51 (0.2)	0.4 (0.3)	−0.35 (0.4)	−0.2 (0.6)	−0.29 (0.5)	0.53 (0.2)	−0.2 (0.6)	−0.39 (0.3)
darkgrey	−0.2 (0.6)	−0.18 (0.7)	−0.23 (0.6)	−0.15 (0.7)	−0.22 (0.6)	0.31 (0.4)	0.89 (0.003)	−0.23 (0.6)
floralwhite	−0.15 (0.7)	−0.18 (0.7)	0.65 (0.08)	−0.27 (0.5)	−0.37 (0.4)	0.11 (0.8)	0.56 (0.1)	−0.36 (0.4)
lightsteelblue1	−0.26 (0.5)	−0.19 (0.6)	0.51 (0.2)	−0.35 (0.4)	−0.34 (0.4)	−0.2 (0.6)	0.16 (0.7)	0.69 (0.06)
darkorange2	0.48 (0.2)	0.2 (0.6)	−0.18 (0.7)	−0.33 (0.4)	−0.35 (0.4)	−0.28 (0.5)	−0.23 (0.6)	0.69 (0.06)
orangered4	0.39 (0.3)	−0.2 (0.6)	−0.2 (0.6)	−0.44 (0.3)	−0.51 (0.2)	0.012 (1)	0.42 (0.3)	0.53 (0.2)
grey60	−0.11 (0.8)	−0.16 (0.7)	−0.18 (0.7)	−0.12 (0.8)	−0.17 (0.7)	1 (3e−08)	−0.11 (0.8)	−0.16 (0.7)
darkturquoise	−0.31 (0.4)	−0.35 (0.4)	−0.31 (0.5)	−0.22 (0.6)	−0.15 (0.7)	0.21 (0.6)	0.41 (0.3)	0.73 (0.04)
skyblue1	−0.4 (0.3)	−0.3 (0.5)	−0.34 (0.4)	0.45 (0.3)	−0.26 (0.5)	0.44 (0.3)	−0.13 (0.8)	0.54 (0.2)

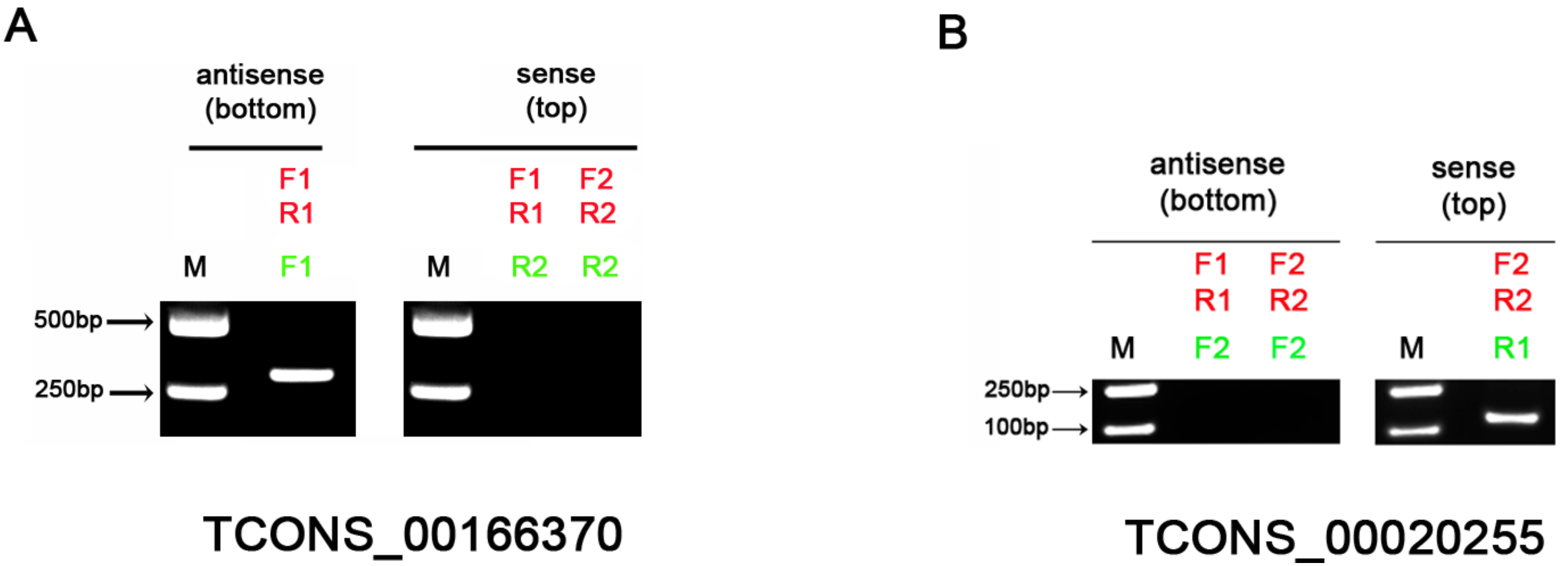
Supplementary Figure S2. Module development stage correlation. Each row corresponds to a module eigengene, column to each development stage. Each cell contains the corresponding correlation and *p*-value. The table is color-coded by correlation according to the color legend.



Supplementary Figure S3. The ratio of mRNAs and lincRNAs in module.



Supplementary Figure S4. The expression of eight hub lincRNAs from 4-cell stage-specific module in porcine different tissues. Results are presented as mean values ± SEM. Different letters indicate significant differences (*p*<0.05).



Supplementary Figure S5. SSRT-PCR result of *TCONS_00166370* and *TCONS_00020255*. It shows that *TCONS_00166370* is transcribed from the bottom strand, and *TCONS_00020255* are the from the top strand.