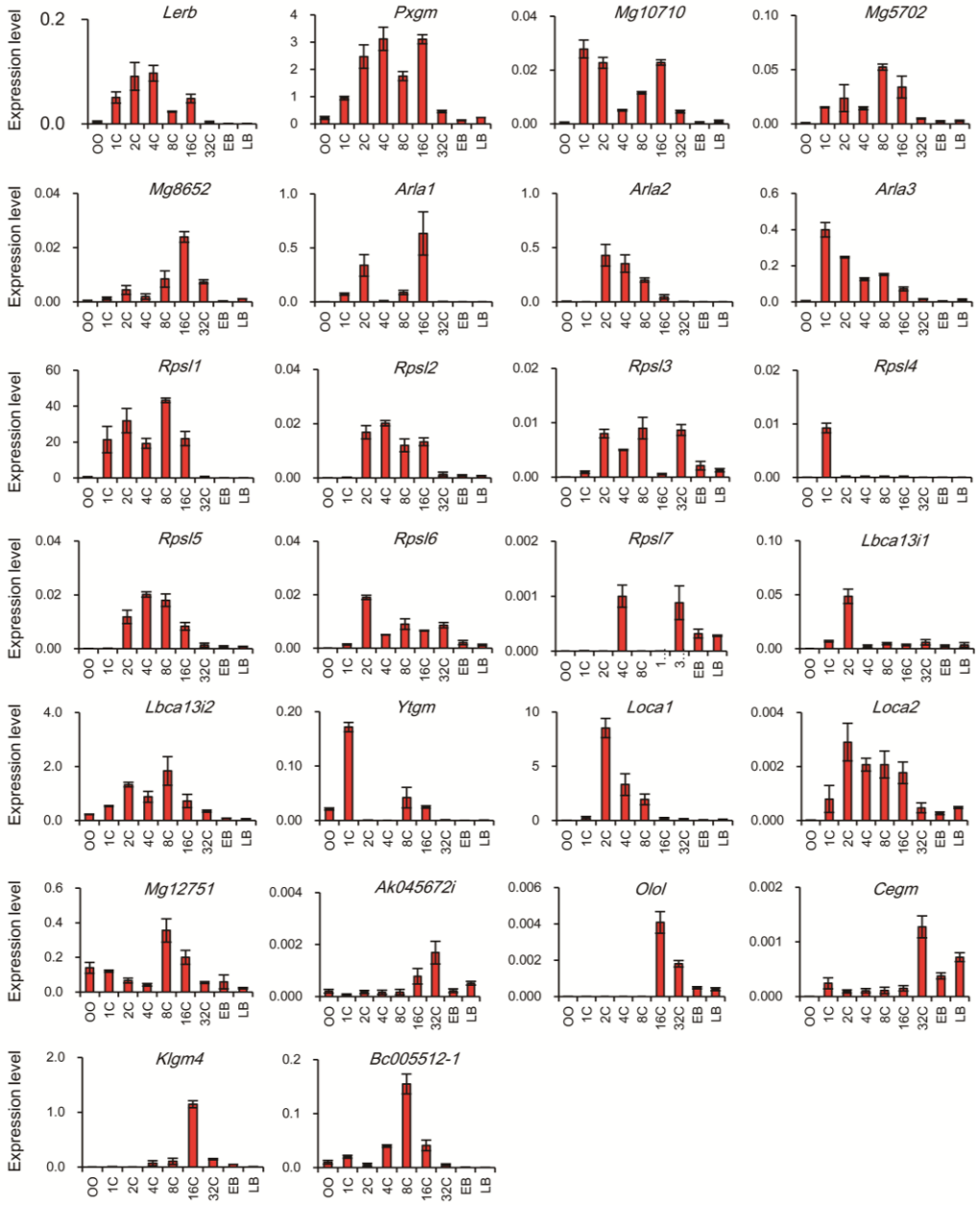
Appendix

This Appendix file contains the following contents:

Contents	
Supplementary Figures	Appendix Figure S1, S2, S3, S4, and S5

Figure S1



Appendix Figure S1. Expression pattern of the other novel transcripts, except *LincGET* and *Dyei,* in preimplantation embryos

The expression pattern of the other novel transcripts, except *LincGET* and *Dyei,* in preimplantation embryos was confirmed by SG-qPCR. OO, oocyte. 1C, zygote stage. 2C, 2-cell stage. 4C, 4-cell stage. 8C, 8-cell stage. 16C, 16-cell stage. 32C, 32-cell stage. EB, early blastocyst stage. LB, late blastocyst stage. The error bars represent s.e.m.. For each stage about 100 embryos were used for each experiment and three experimental replicates were performed.

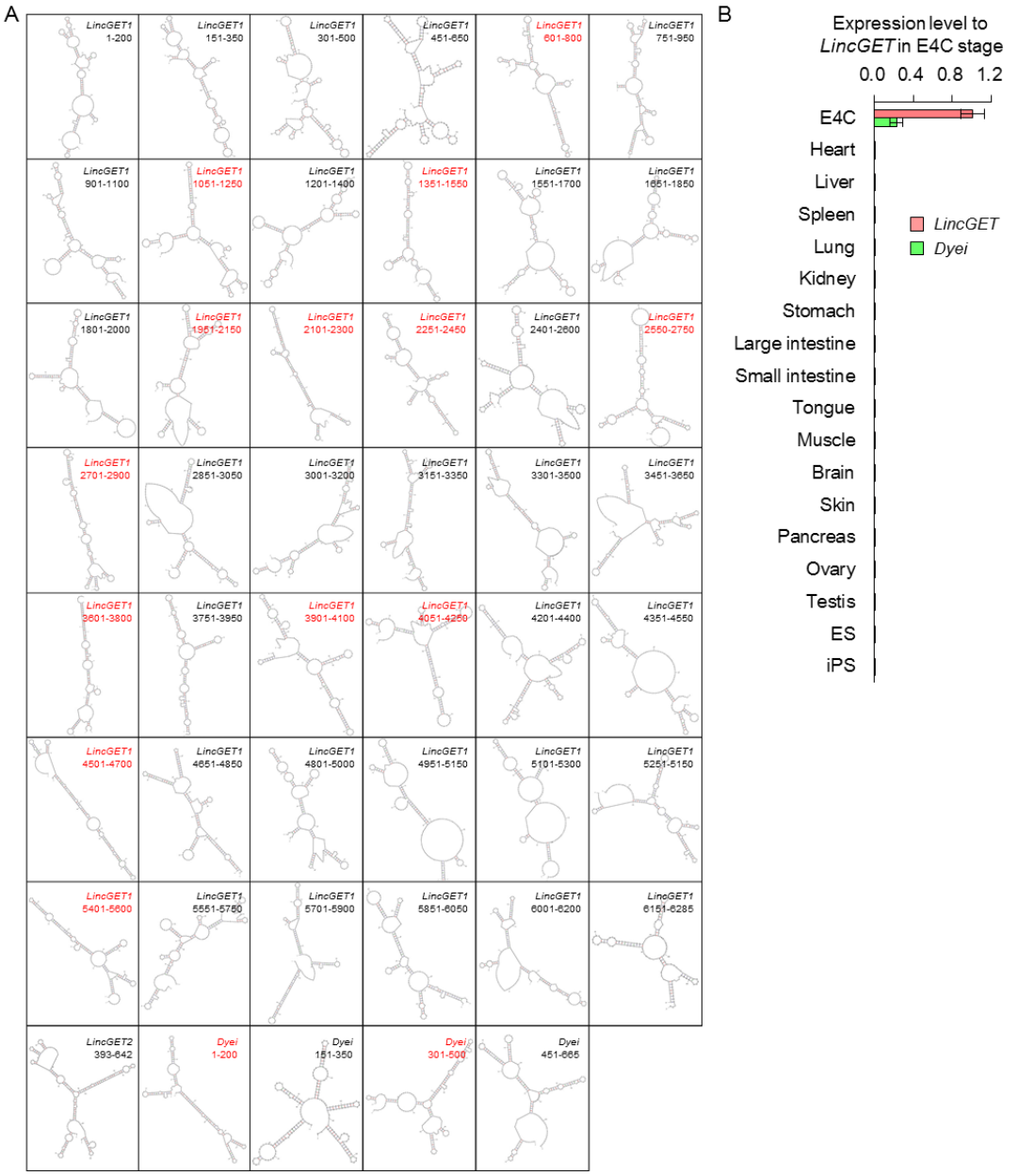
Figure S2

Appendix Figure S2. *LincGET* and *Dyei* are 2- to 4-cell embryo-specific transcripts without coding potential

A. Expression pattern of *LincGET* and *Dyei* in preimplantation embryos was confirmed by SYBR Green qPCR. The results show that *LincGET* is highly expressed in 2-cell to 4-cell embryos and *Dyei* is highly expressed in 4-cell embryos. OO, oocyte. 1C, zygote stage. 2C, 2-cell stage. 4C, 4-cell stage. 8C, 8-cell stage. 16C, 16-cell stage. 32C, 32-cell stage. EB, early blastocyst stage. LB, late blastocyst stage. The error bars represent s.e.m.. For each stage about 50 embryos were used for each experiment and three experimental replicates were performed.

B. Multiple short unconserved ORFs can be predicted in *LincGET* and *Dyei* showing no coding potential. ORFs were analyzed by NCBI ORF Finder (http://www.ncbi.nlm.nih.gov/projects/gorf/).

Figure S3

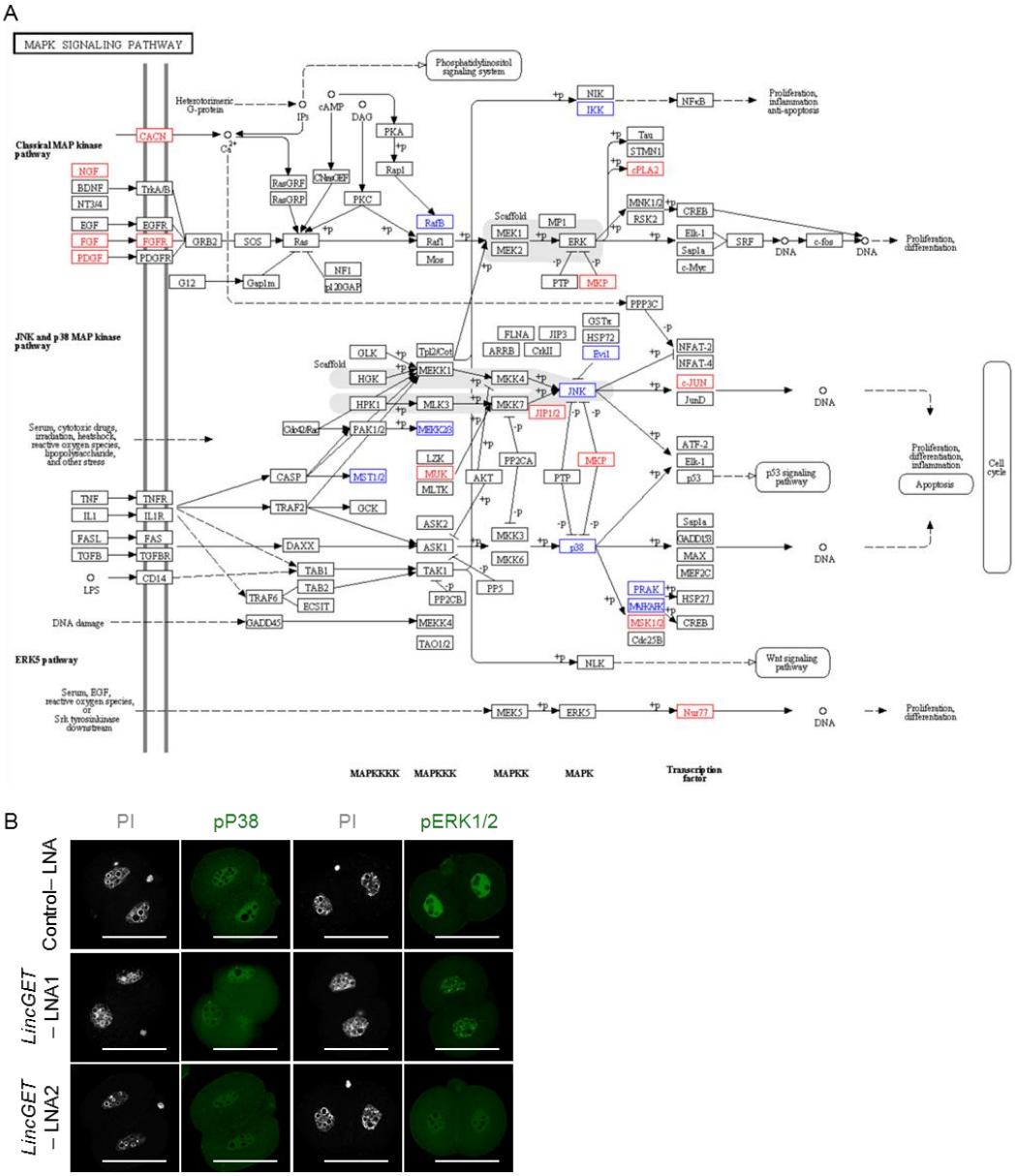


Appendix Figure S3. Secondary structure and expression pattern analysis of *LincGET* and *Dyei*

A. The analysis of *LincGET* and *Dyei* secondary structure by Mfold web server version 3.2 did not reveal obvious stem loops. Each structure shown here refers to 200 nt fragments at every 50th nucleotide spanning the entire *LincGET* sequence. Fragments tested by miRNA reverse Northern blot (Figure 1E) are shown in red.

B. Both *LincGET* and *Dyei* are undetectable in various tissues, mouse ESCs, and mouse iPSCs. 4C, 4-cell stage. Three experimental replicates were performed, and the error bars represent s.e.m..

Figure S4

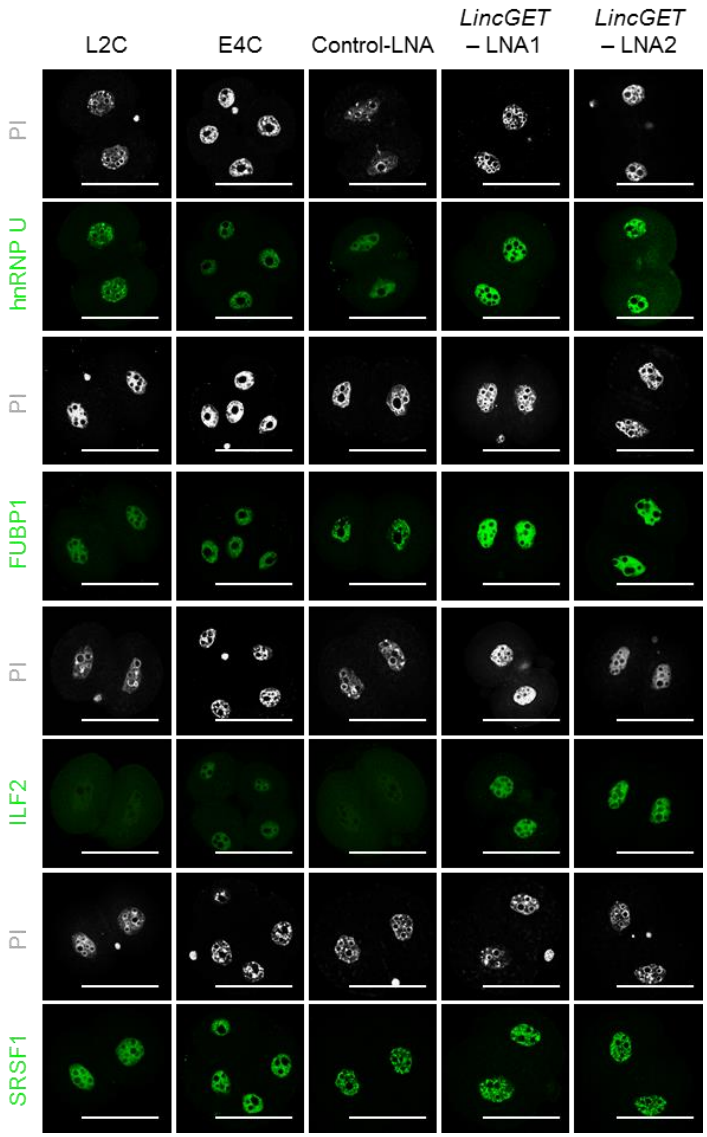


Appendix Figure S4. *LincGET* depletion results in the inhibition of the MAPK signaling pathway

A. *LincGET* depletion results in the inhibition of the MAPK signaling pathway. Up-regulated genes are shown in red, while down-regulated genes are shown in blue.

B. Immunofluorescence indicated that the phosphorylation level of p38 and ERK1/2 decreased dramatically in *LincGET*-depleted 2C. Embryos injected with LNA were collected at phCG 48 hours at the late 2-cell stage for IF analysis. Scale bar, 50 μm. Three experimental replicates were performed, and about 15 embryos were used in each group.

Figure S5



Appendix Figure S5. *LincGET* decreases the protein level of hnRNP U, FUBP1, and ILF2

IF staining of hnRNP U, FUBP1, ILF2, and SRSF1 in normal L2C, E4C, and embryos injected with Control-LNA or *LincGET*-LNA. The results showed that hnRNP U, FUBP1, ILF2, and SRSF1are all present in the nuclei of 2- to 4-cell embryos, and the levels of hnRNP U, FUBP1, and ILF2 increased significantly after *LincGET* depletion. Normal L2C and 4-cell embryos were collected at phCG 48 hours and 54 hours, respectively. Embryos injected with LNA were collected at phCG 48 hours. Scale bar, 50 μm. Three experimental replicates were performed and about 15 embryos were used in each group.