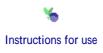
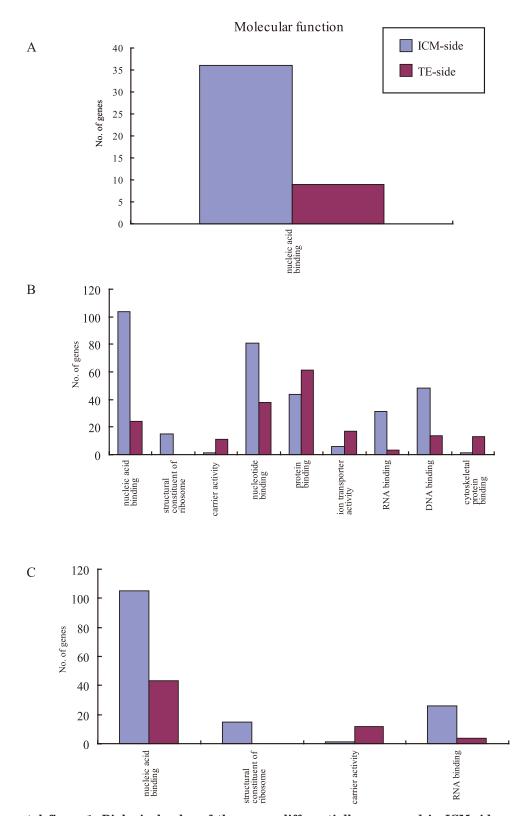


HOKKAIDO UNIVERSITY

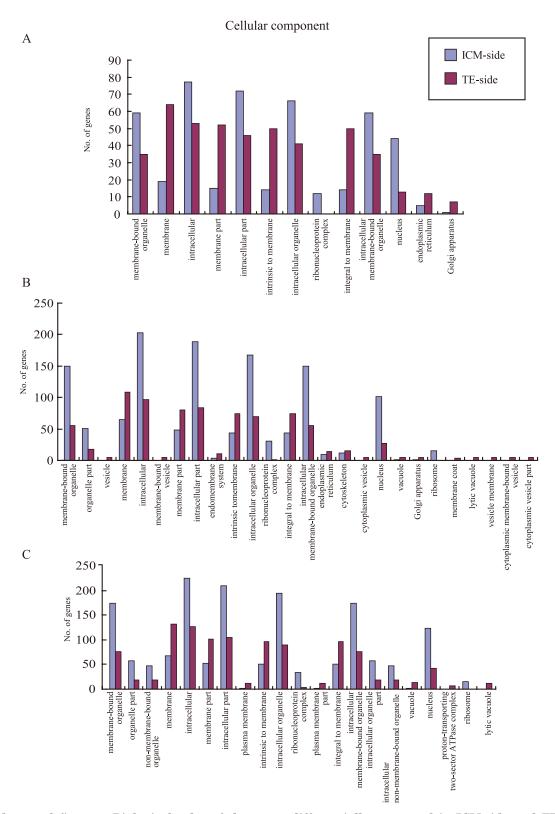
Title	Comparing spatial expression dynamics of bovine blastocyst under three different procedures : in-vivo, in-vitro derived, and somatic cell nuclear transfer embryos
Author(s)	Nagatomo, Hiroaki; Akizawa, Hiroki; Sada, Ayari; Kishi, Yasunori; Yamanaka, Ken-ichi; Takuma, Tetsuya; Sasaki, Keisuke; Yamauchi, Nobuhiko; Yanagawa, Yojiro; Nagano, Masashi; Kono, Tomohiro; Takahashi, Masashi; Kawahara, Manabu
Citation	Japanese Journal of Veterinary Research, 63(4), 159-171
Issue Date	2015-11
DOI	10.14943/jjvr.63.4.159
Doc URL	http://hdl.handle.net/2115/60304
Туре	bulletin (article)
Additional Information	There are other files related to this item in HUSCAP. Check the above URL.
File Information	JJVR63-4 p.159-171 Suppl. figure.pdf (Supplemental Figure)





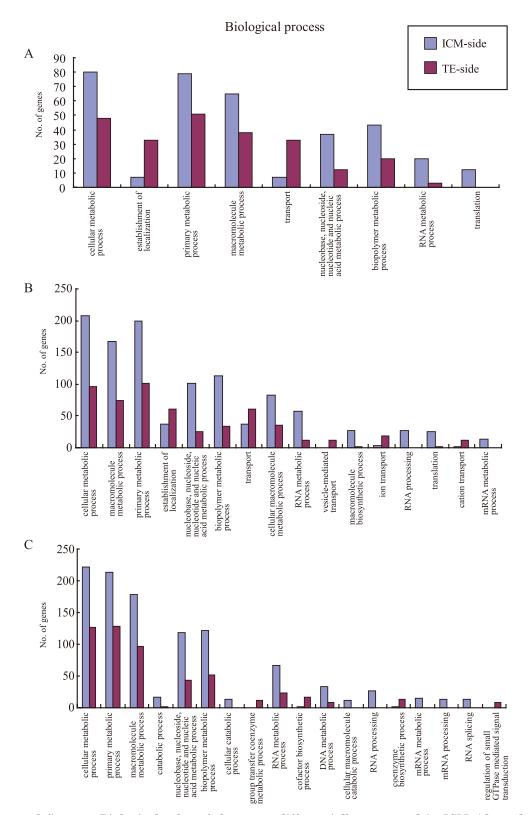
Supplemental figure 1. Biological roles of the genes differentially expressed in ICM-side and TE-side samples in the molecular function category. The top GO categories were defined based on the probe sets differentially expressed between ICM-side and TE-side samples from in vivo- (A), in vitro-derived (B), and SCNT (C) blastocysts. Differences were considered significant at a level of P < 0.05.

## Gene expression analyses in bovine blastocysts

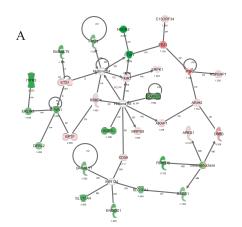


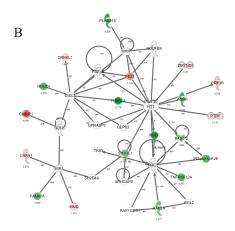
Supplemental figure 2. Biological roles of the genes differentially expressed in ICM-side and TE-side samples in the cellular component category. The top GO categories were defined based on the probe sets differentially expressed between ICM-side and TE-side samples from in vivo- (A), in vitro-derived (B), and SCNT (C) blastocysts. Differences were considered significant at a level of P < 0.05.

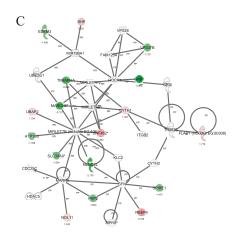
## Hiroaki Nagatomo et al.

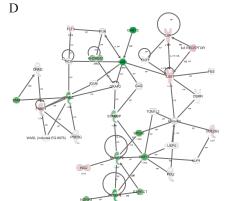


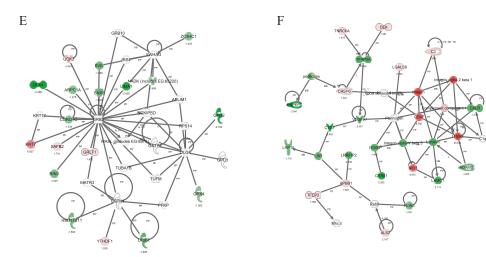
Supplemental figure 3. Biological roles of the genes differentially expressed in ICM-side and TE-side samples in the biological process category. The top GO categories were defined based on the probe sets differentially expressed between ICM-side and TE-side samples from in vivo- (A), in vitro-derived (B), and SCNT (C) blastocysts. Differences were considered significant at a level of P < 0.05.



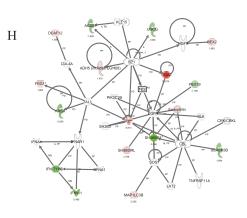


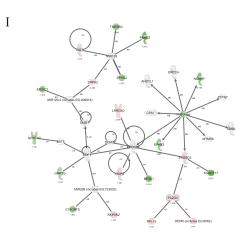


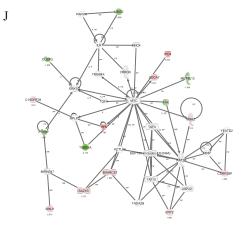




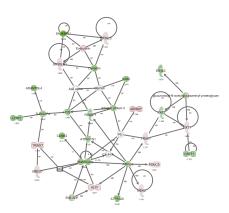
**Supplemental figure 4. Functional networks of genes that are expressed exclusively in the ICM- and TE-side samples from in vivo-derived blastocysts.** We constructed 16 functional networks by integrating 984 genes expressed in the in vivo-derived blastocysts, as shown in Fig. 2C. Genes marked in red and green are upregulated and downregulated in the ICM-side sample, respectively. Conversely, upregulated and downregulated genes in the TE-side sample are represented by green and red, respectively. The network is displayed graphically as nodes (gene or gene product) and edges (the biological relationships between nodes, including the functional or physical interactions (refer to Supplemental figure 7).

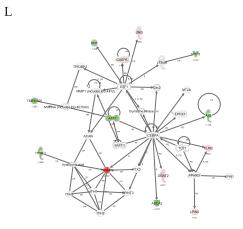


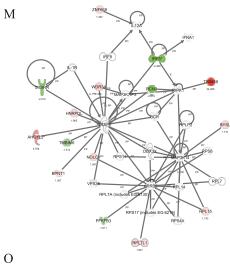


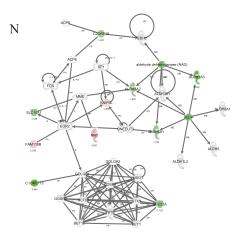




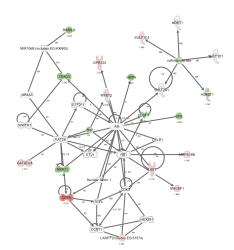


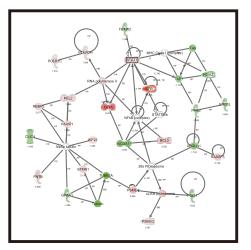


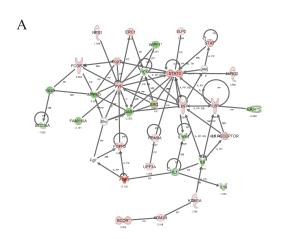


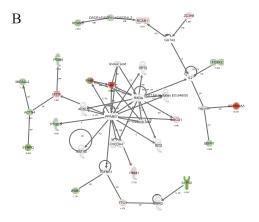


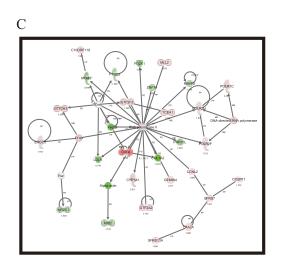
Р

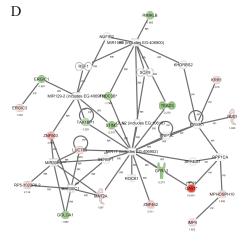




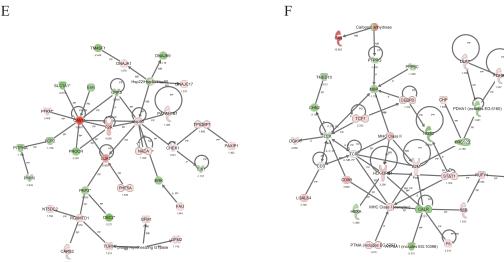






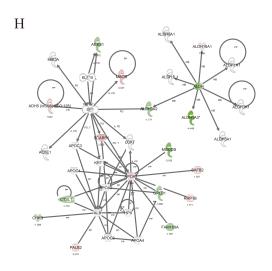


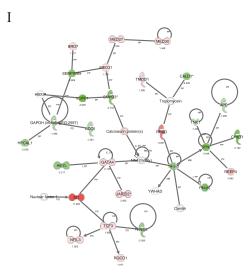
Е

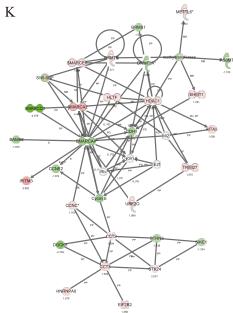


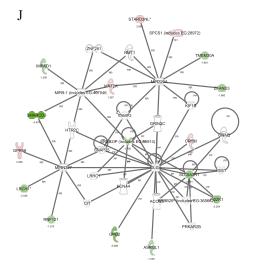
Supplemental figure 5. Functional networks of genes that are expressed exclusively in the ICM- and TE-side samples in in vitro-derived blastocysts. We constructed 21 functional networks by integrating 2279 genes expressed in the in vitro-derived blastocysts, as shown in Fig. 2C.

## Gene expression analyses in bovine blastocysts

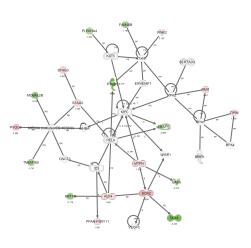




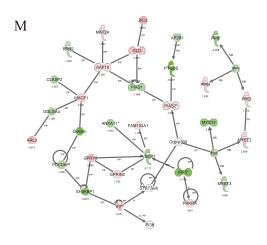


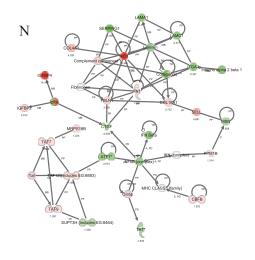


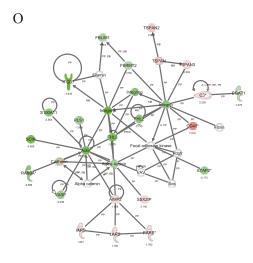
L

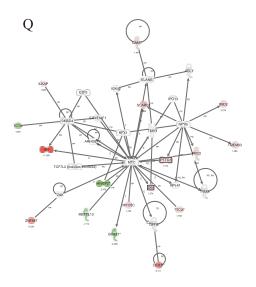


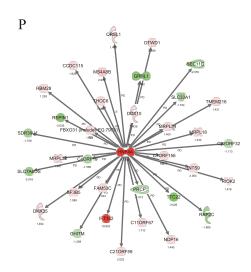
G

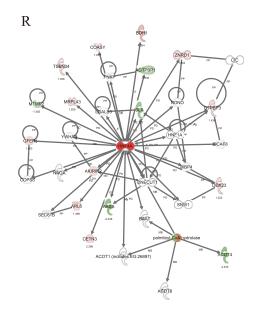




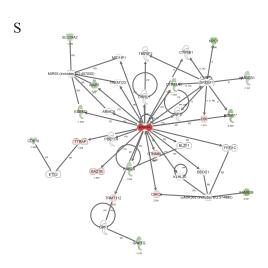


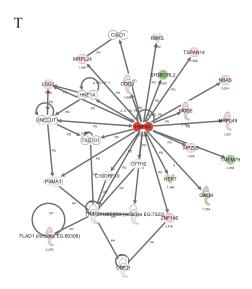




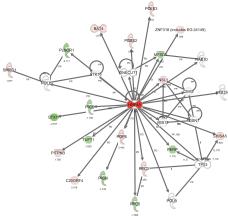


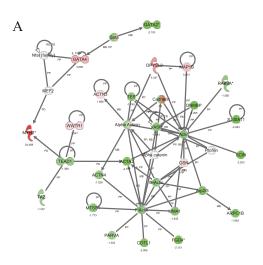
## Gene expression analyses in bovine blastocysts

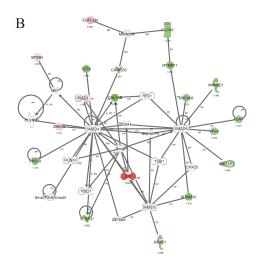


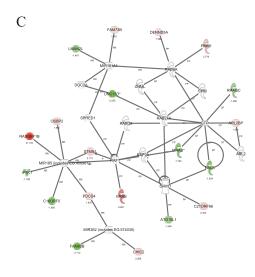


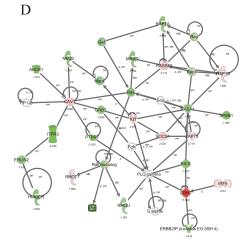
U

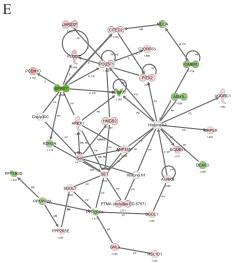


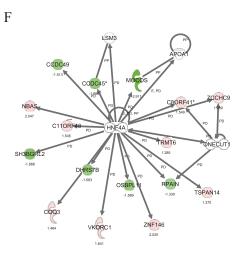




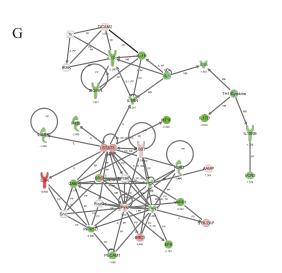




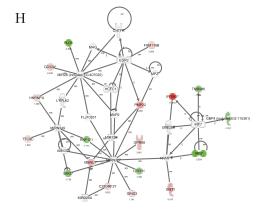


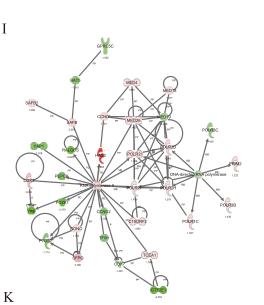


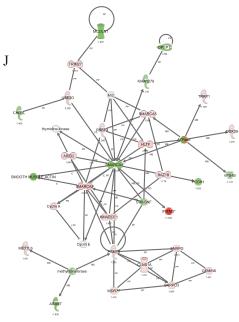
Supplemental figure 6. Functional networks of genes that are expressed exclusively in the ICM- and TE-side samples from SCNT blastocysts. We constructed 14 functional networks by integrating 2599 genes expressed in SCNT blastocysts as shown in Fig. 2C.



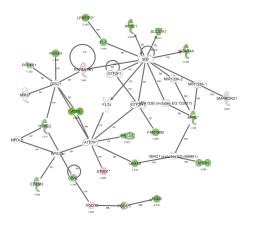
Ι

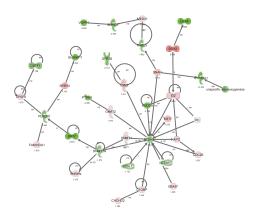




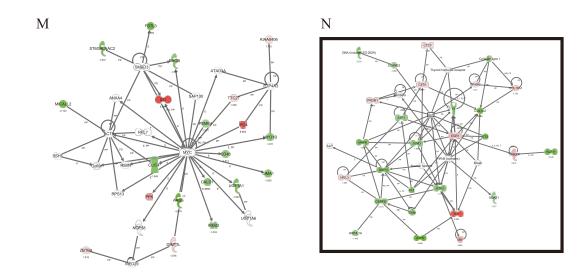


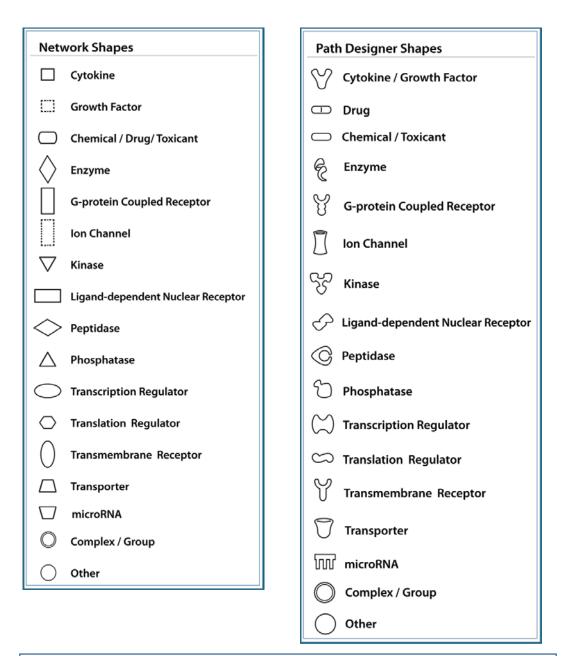
L





Hiroaki Nagatomo et al.





Relationship Labels		
AActivation	MB Group/complex Membership	
B Binding	P Phosphorylation/Dephosphorylation	
C Causes/Leads to	PD Protein-DNA binding	
CC Chemical-Chemical interaction	PP Protein-Protein binding	
CP Chemical-Protein interaction	PR Protein-RNA binding	
E Expression (includes metabolism/ synthesis for chemicals)	RB Regulation of Binding	
EC Enzyme Catalysis	RE Reaction	
I Inhibition	RR RNA-RNA Binding	
L ProteoLysis (includes degradation for Chemicals)	T Transcription	
LO Localization	TR Translocation	
M Biochemical Modification		

Supplemental figure 7. Node types and relationship labels in a network constructed by the IPA.