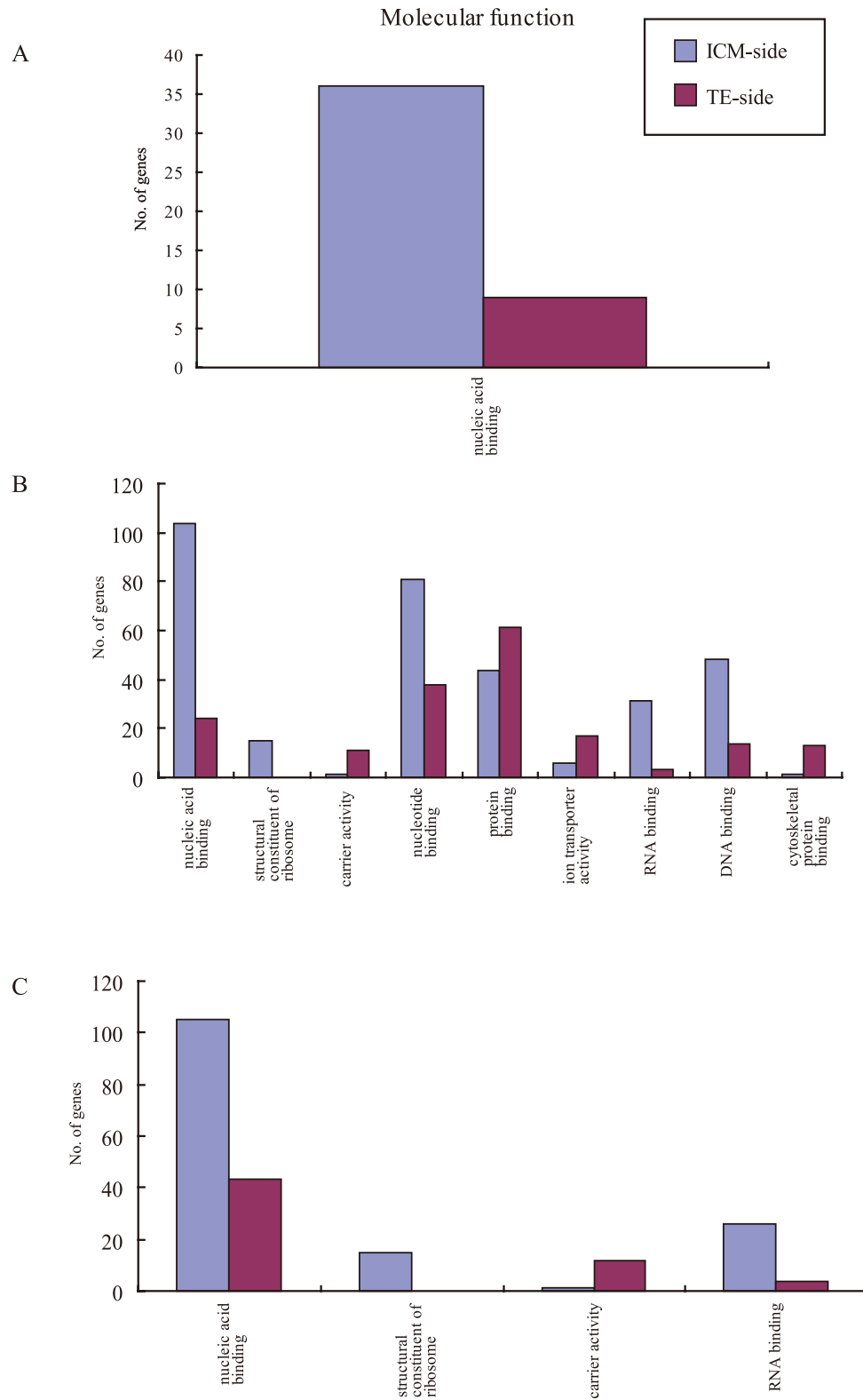




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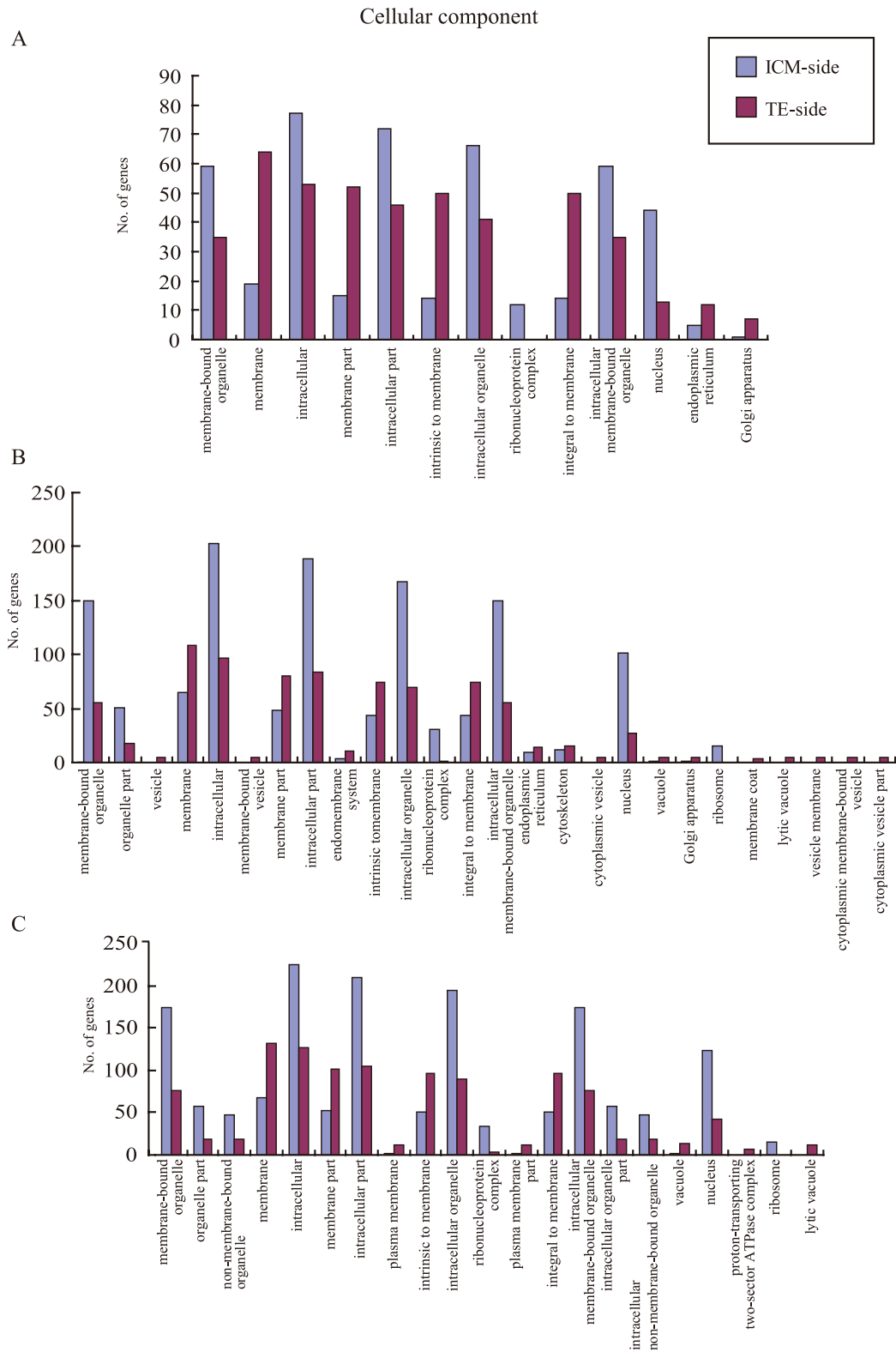
Title	Comparing spatial expression dynamics of bovine blastocyst under three different procedures : in-vivo, in-vitro derived, and somatic cell nuclear transfer embryos
Author(s)	Nagatomo, Hiroaki; Akizawa, Hiroki; Sada, Ayari et al.
Citation	Japanese Journal of Veterinary Research, 63(4), 159-171
Issue Date	2015-11
DOI	https://doi.org/10.14943/jjvr.63.4.159
Doc URL	https://hdl.handle.net/2115/60304
Type	departmental bulletin paper
File Information	JJVR63-4 p.159-171 Suppl. figure.pdf, Supplemental Figure



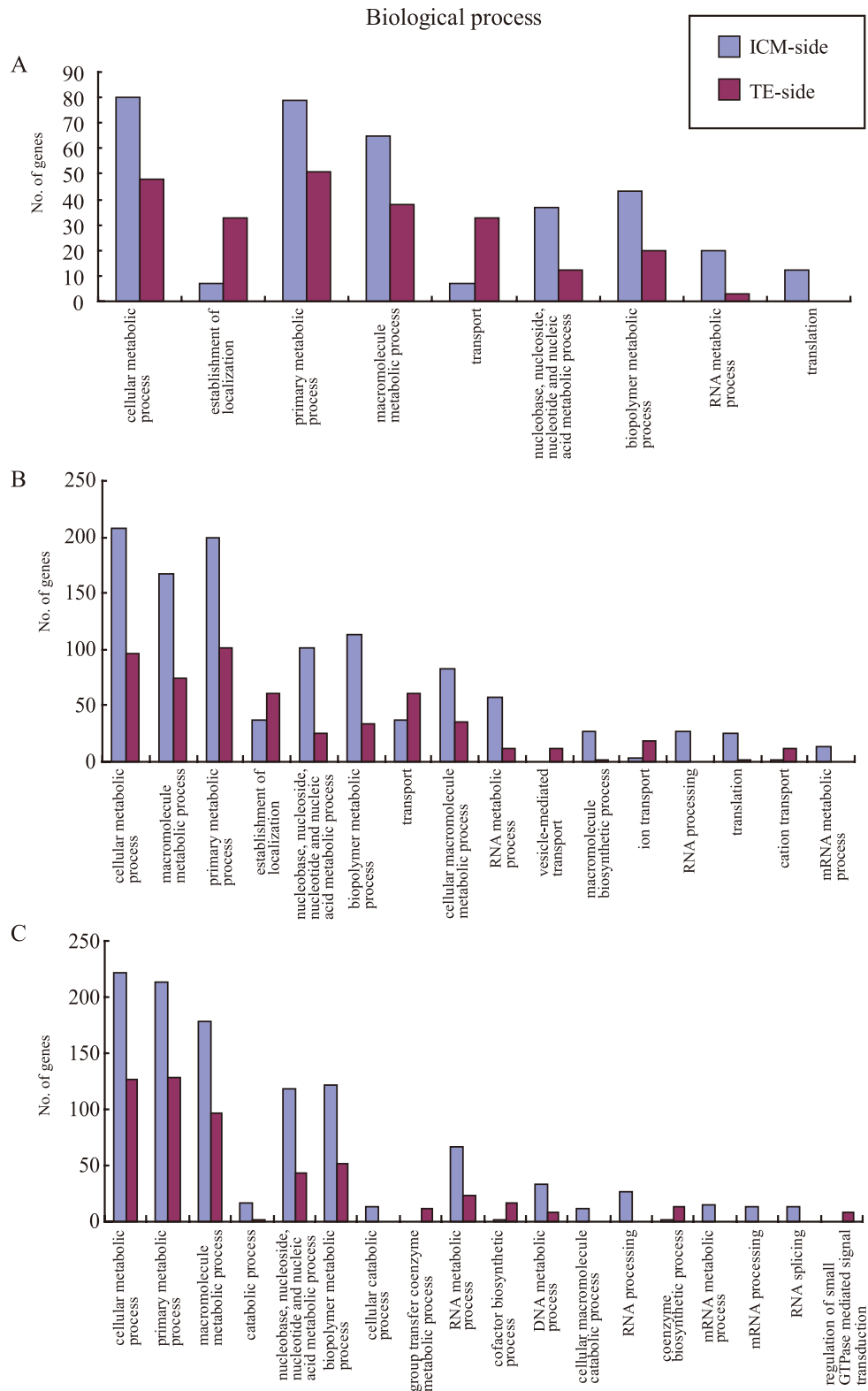


Supplemental figure 1. Biological roles of the genes differentially expressed in ICM-side and TE-side samples in the molecular function category. The top GO categories were defined based on the probe sets differentially expressed between ICM-side and TE-side samples from in vivo- (A), in vitro-derived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

Gene expression analyses in bovine blastocysts

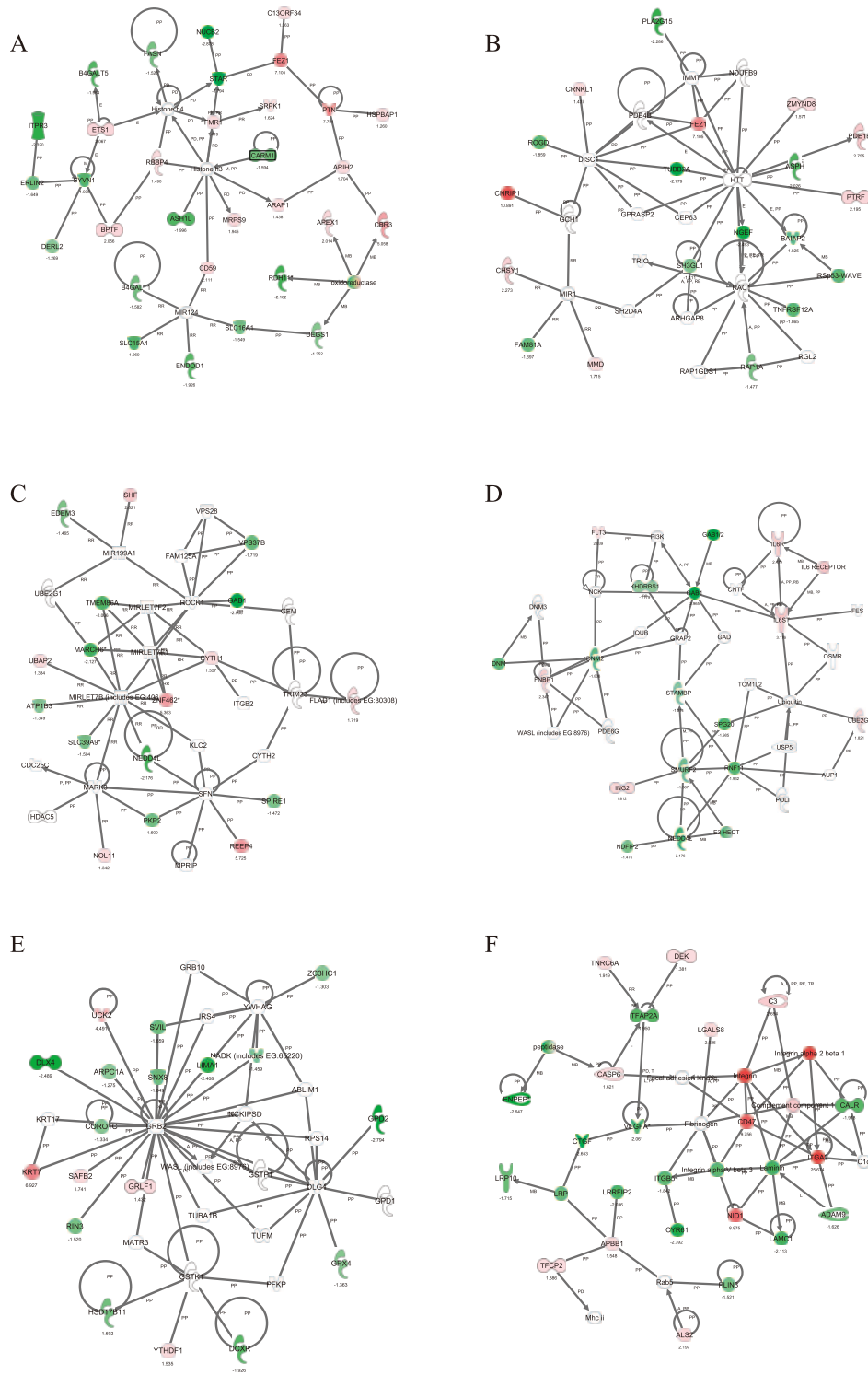


Supplemental figure 2. Biological roles of the genes differentially expressed in ICM-side and TE-side samples in the cellular component category. The top GO categories were defined based on the probe sets differentially expressed between ICM-side and TE-side samples from in vivo- (A), in vitro-derived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



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 $P < 0.05$.

Gene expression analyses in bovine blastocysts

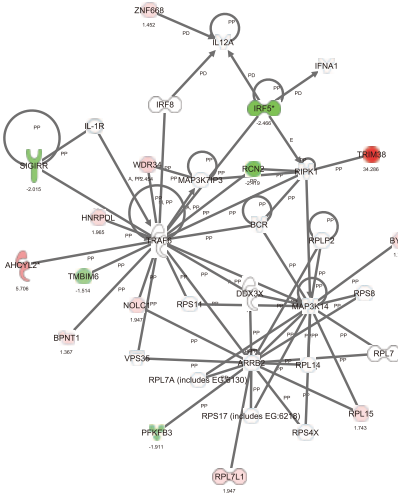


Supplemental figure 4. Functional networks of genes that are expressed exclusively in the ICM- and TE-side samples from in vivo-derived blastocysts. We constructed 16 functional networks by integrating 984 genes expressed in the in vivo-derived blastocysts, as shown in Fig. 2C. Genes marked in red and 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)).

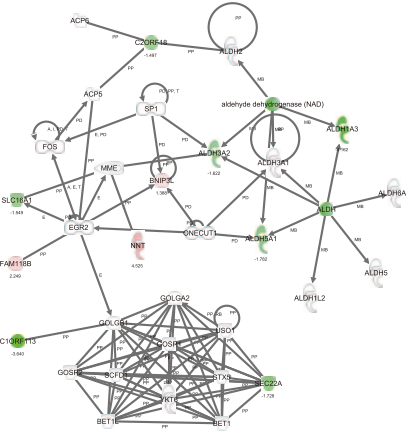


Gene expression analyses in bovine blastocysts

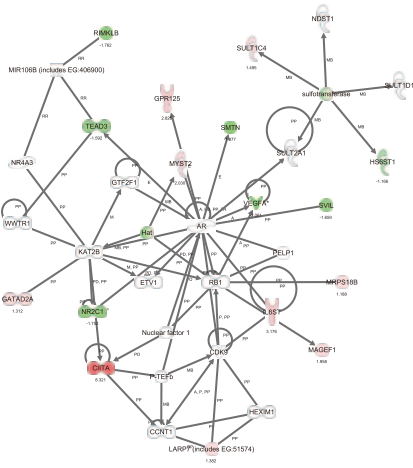
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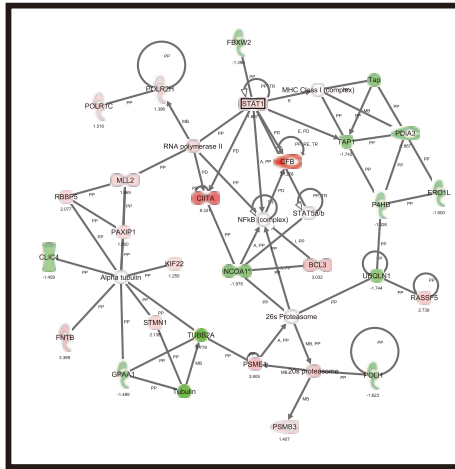
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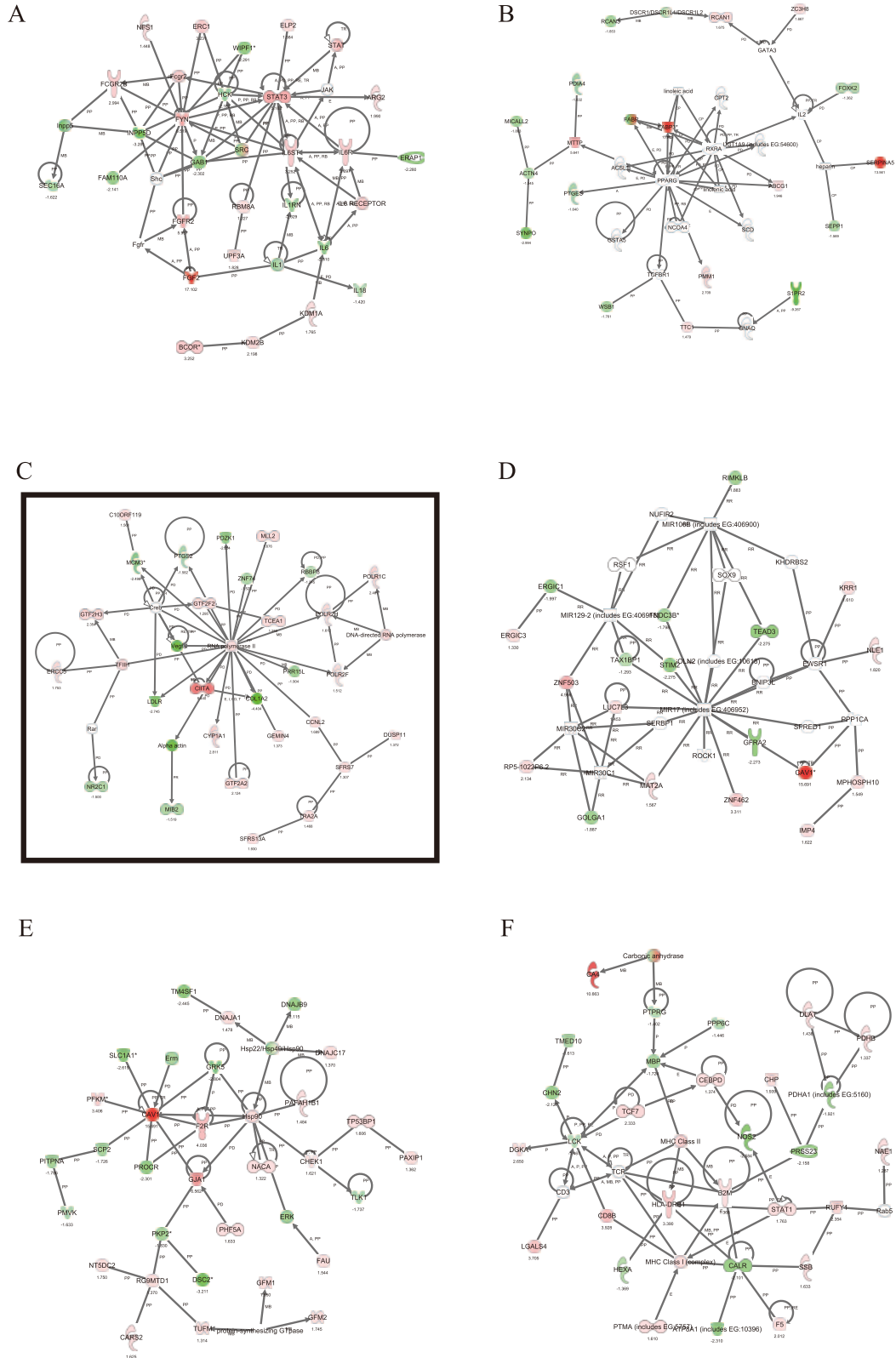


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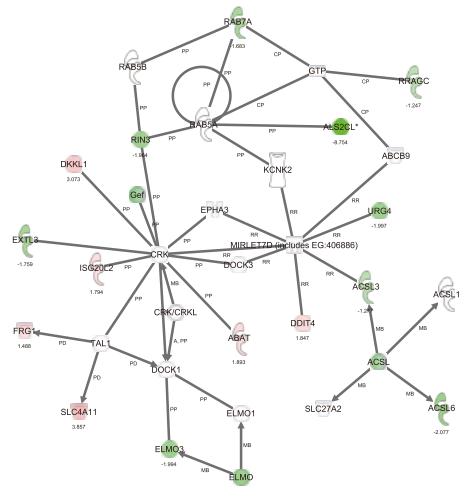




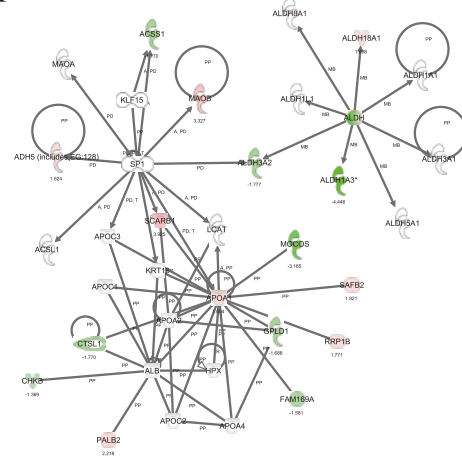
Supplemental figure 5. Functional networks of genes that are expressed exclusively in the ICM- and TE-side samples in in vitro-derived blastocysts. We constructed 21 functional networks by integrating 2279 genes expressed in the in vitro-derived blastocysts, as shown in Fig. 2C.

Gene expression analyses in bovine blastocysts

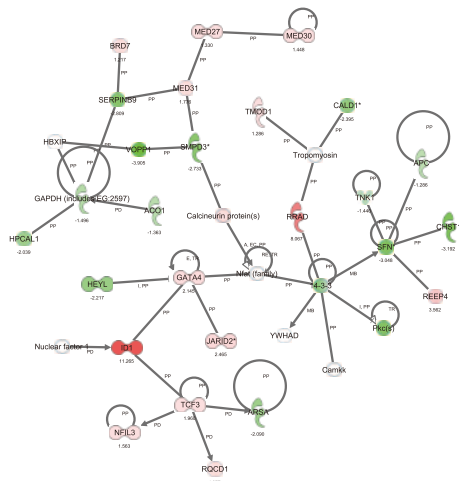
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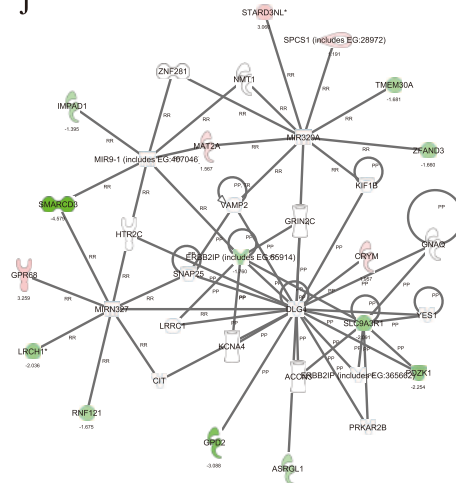
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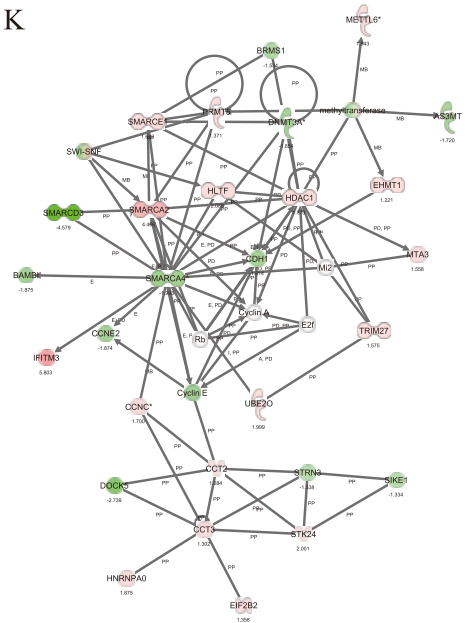
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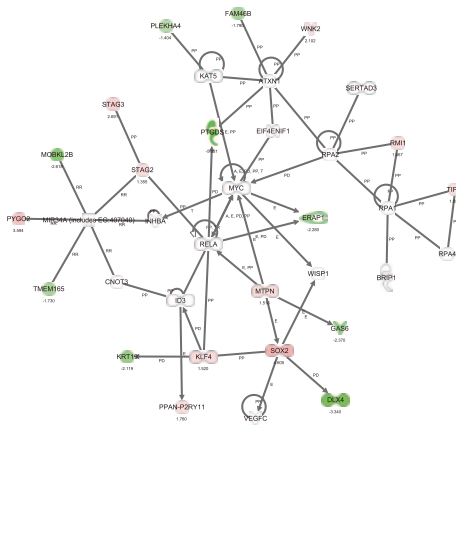
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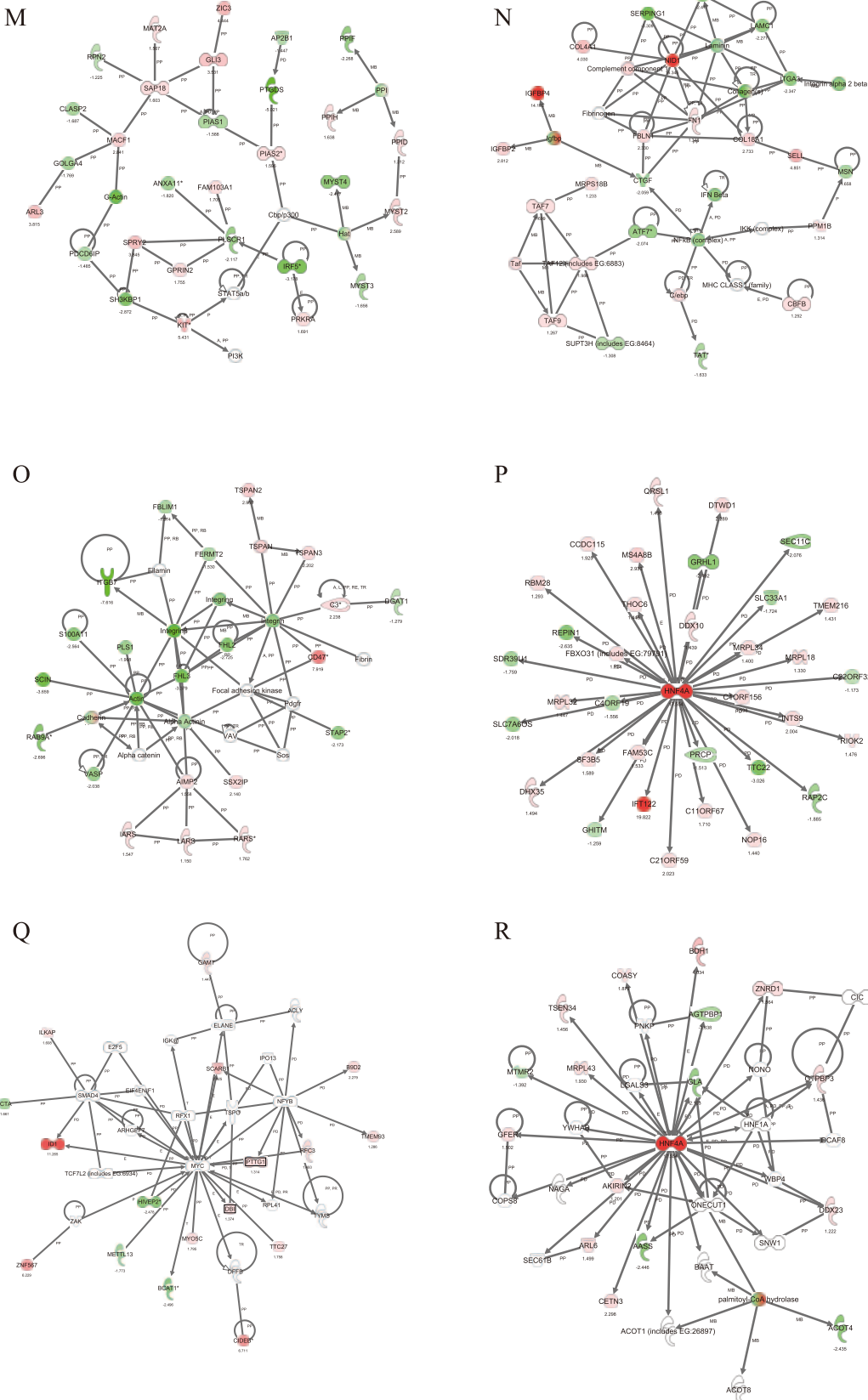


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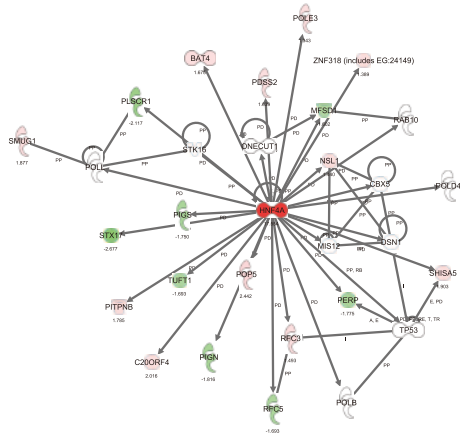


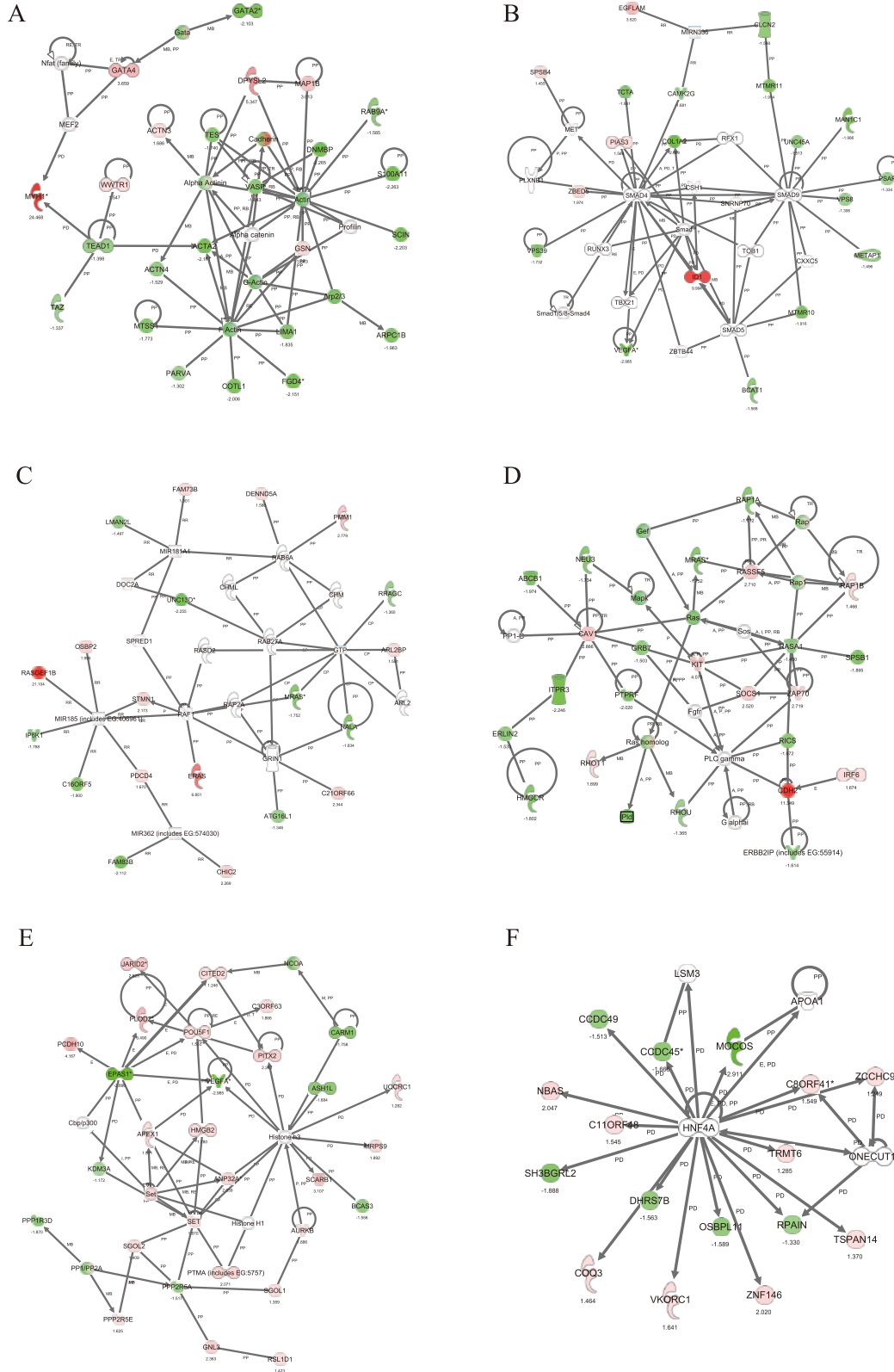
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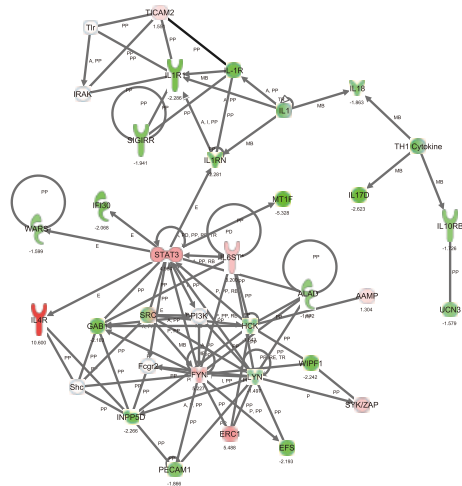




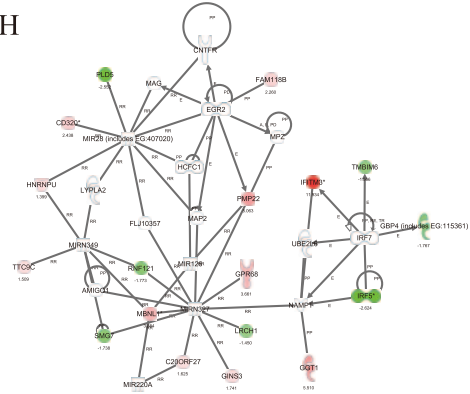
Supplemental figure 6. Functional networks of genes that are expressed exclusively in the ICM- and TE-side samples from SCNT blastocysts. We constructed 14 functional networks by integrating 2599 genes expressed in SCNT blastocysts as shown in Fig. 2C.

Gene expression analyses in bovine blastocysts

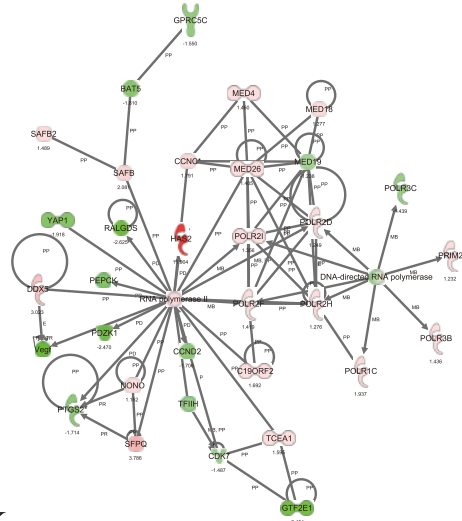
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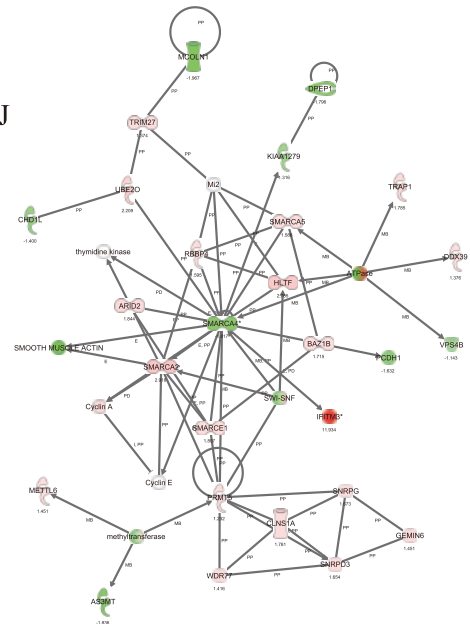
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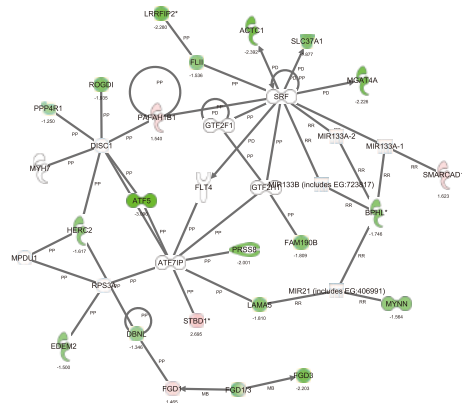
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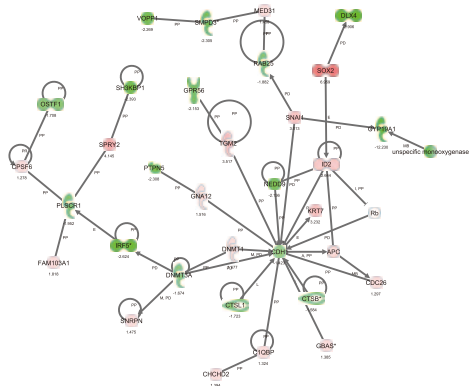
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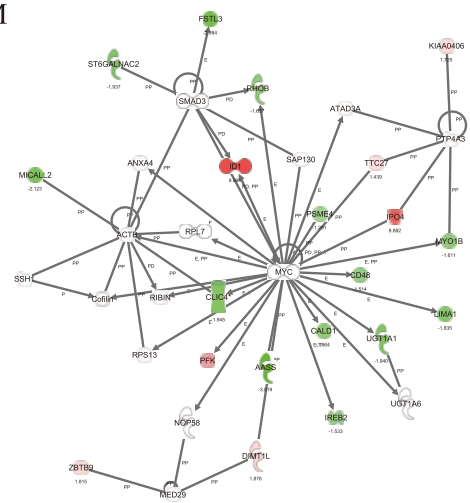
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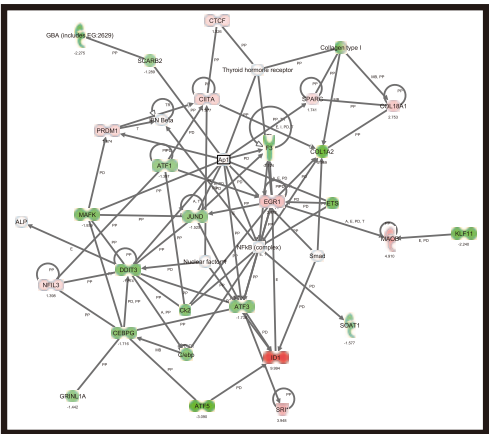
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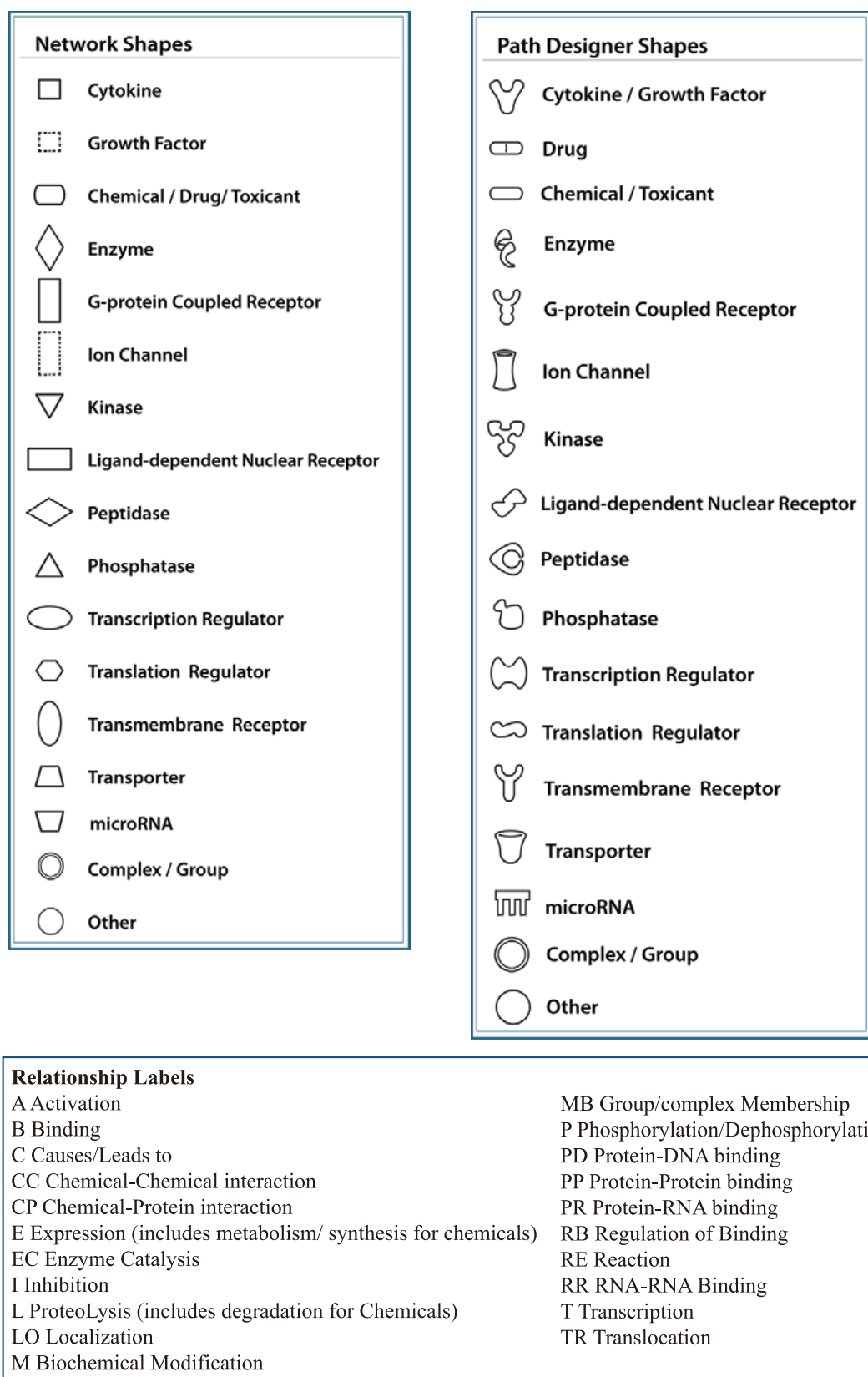


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N





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