Role of methionine adenosyltransferase 2A in bovine preimplantation development and its associated genomic regions

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Supplementary figure legends

Figure S1. Nuclear localization of MAT2A in bovine blastocyst cells. (A) Immunofluorescence image of MAT2A protein in blastocyst cells. Nuclei showing more abundant MAT2A compared with the cytoplasm are indicated by arrowheads. (B) Nuclear counterstaining with propidium iodide. (C) Merged image of (A) and (B). Scale bar represents 50 μm.

Figure S2. Identification of MAT2A-ChIP specific peaks in duplicated ChIP-seq (Rep 1 and Rep 2). (A) 39 peaks (intersection) are specific for MAT2A-ChIP samples against Input in both replicates. (B) 59 peaks (intersection) are specific for MAT2A-ChIP samples against IgG control in both replicates. (C) The union of these peaks makes 76 MAT2A-ChIP specific peaks with 22 overlapping peaks.

Figure S3. Hierarchical tree graph of overrepresented GO terms in biological process generated by Singular Enrichment Analysis (SEA) of agriGO (http://bioinfo.cau.edu.cn/agriGO/). The first line in each significant box represents the GO term ID with the adjusted P-value in parentheses, followed by the lines indicating the term definition. In the last line of the significant box, the first pair of numerals represents the number of genes associated with the GO term and that of all genes in the query list and the second pair of numerals represents those in the *Bos taurus* database. The degree of colour saturation of the boxes is positively correlated with the enrichment level of the term: yellow, <0.05; orange, <5e-03 - <5e-09; and red, <5e-10. Solid, dashed, and dotted lines represent two, one and zero enriched terms at both ends connected by the line, respectively.

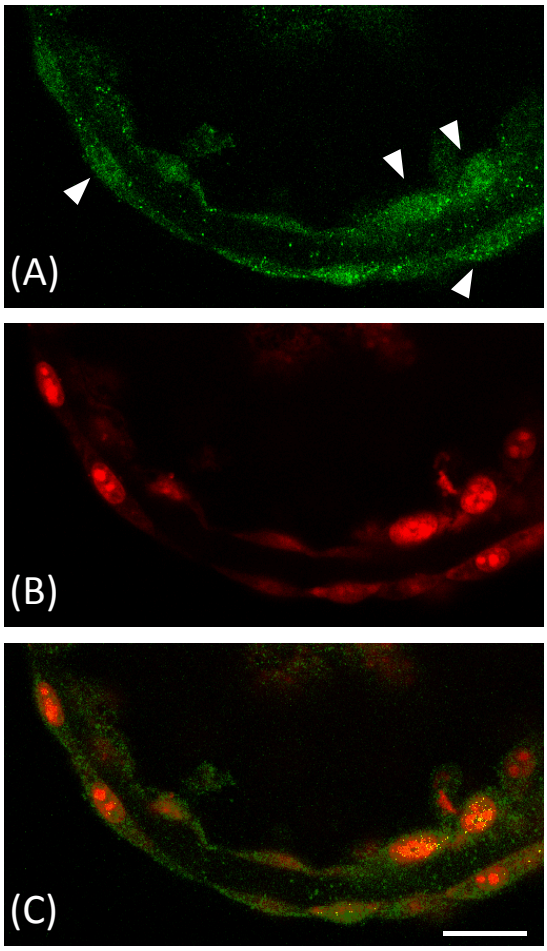
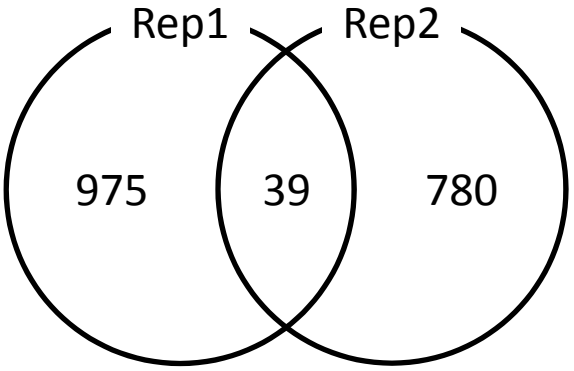


Figure S1

(A)

MAT2A-ChIP specific against

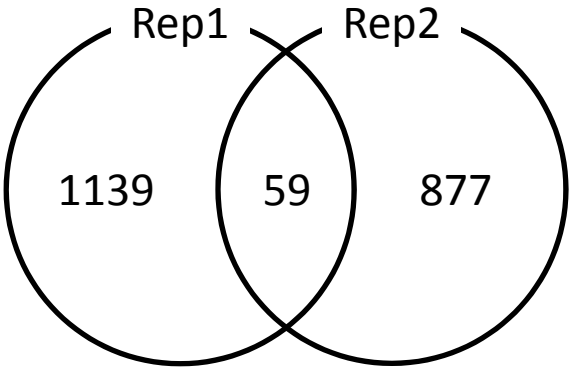
Input



(B)

MAT2A-ChIP specific against

IgG control



(C)

76 MAT2A-ChIP specific peaks

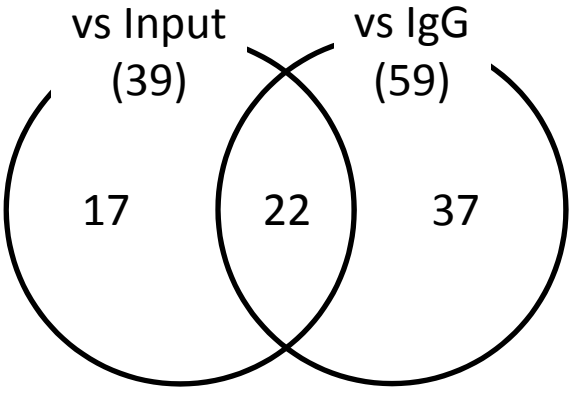


Figure S2

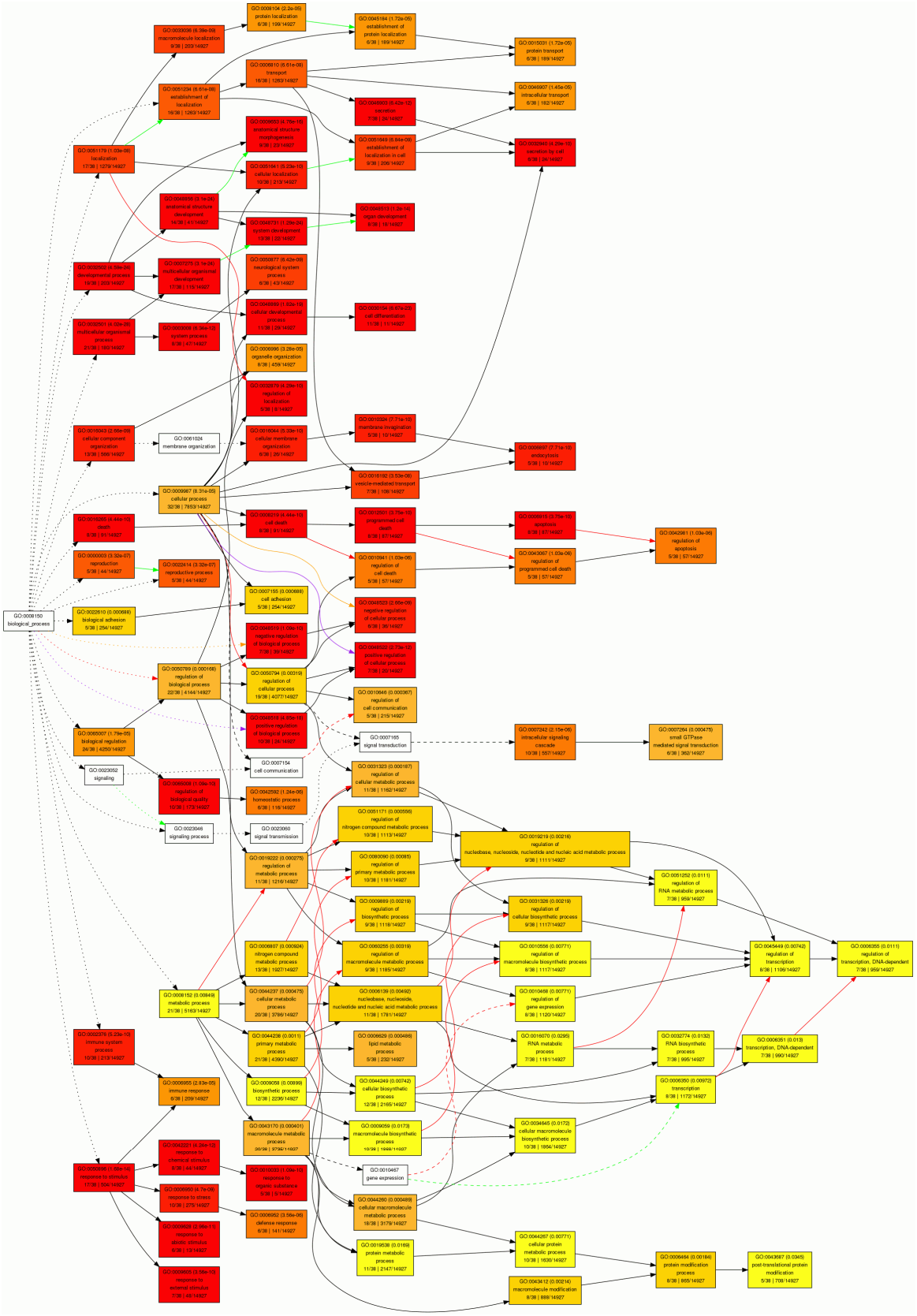

GO:0008150 biological_process
GO:0033036 (6.39e-09) macromolecule localization 9/38 | 203/14927
GO:0006104 (2.2e-05) protein localization 6/38 | 199/14927
GO:0045184 (1.72e-05) establishment of protein localization 6/38 | 189/14927
GO:0015031 (1.72e-05) protein transport 6/38 | 189/14927
GO:0051234 (6.61e-09) establishment of localization 16/38 | 1263/14927
GO:0006810 (6.61e-08) transport 16/38 | 1283/14927
GO:0046907 (1.45e-05) intracellular transport 6/38 | 182/14927
GO:0051179 (1.03e-08) localization 17/38 | 1279/14927
GO:0009953 (4.75e-16) anatomical structure morphogenesis 9/38 | 231/14927
GO:0051641 (5.23e-10) cellular localization 10/38 | 313/14927
GO:0048856 (3.1e-24) anatomical structure development 16/38 | 41/14927
GO:0048731 (1.29e-26) system development 13/38 | 22/14927
GO:0048519 (1.2e-14) organ development 8/38 | 18/14927
GO:0022502 (4.56e-24) developmental process 19/38 | 269/14927
GO:0007275 (3.1e-24) multicellular organismal development 17/38 | 115/14927
GO:0050877 (6.42e-09) neurological system process 6/38 | 43/14927
GO:0032501 (6.02e-28) multicellular organismal process 21/38 | 193/14927
GO:0044699 (1.82e-13) cellular developmental process 11/38 | 29/14927
GO:0030154 (6.67e-22) cell differentiation 11/38 | 31/14927
GO:0003008 (6.34e-12) system process 8/38 | 67/14927
GO:0006996 (3.26e-05) organelle organization 8/38 | 459/14927
GO:0032879 (4.29e-10) regulation of localization 5/38 | 9/14927
GO:0016043 (2.66e-09) cellular component organization 13/38 | 566/14927
GO:0061024 membrane organization
GO:0016044 (5.33e-10) cellular membrane organization 6/38 | 29/14927
GO:0010324 (7.71e-10) membrane invagination 5/38 | 10/14927
GO:0006897 (7.71e-10) endocytosis 5/38 | 10/14927
GO:0016192 (3.53e-08) vesicle-mediated transport 7/38 | 108/14927
GO:0009987 (6.31e-05) cellular process 32/38 | 7853/14927
GO:0008219 (4.44e-10) cell death 8/38 | 91/14927
GO:0012501 (3.75e-10) programmed cell death 8/38 | 87/14927
GO:0006915 (3.75e-10) apoptosis 8/38 | 87/14927
GO:0042981 (1.03e-06) regulation of apoptosis 5/38 | 57/14927
GO:0043067 (1.03e-06) regulation of programmed cell death 5/38 | 57/14927
GO:0016265 (4.44e-10) death 8/38 | 91/14927
GO:0000003 (3.32e-07) reproduction 5/38 | 44/14927
GO:0022414 (3.32e-07) reproductive process 5/38 | 44/14927
GO:0010941 (1.03e-06) regulation of cell death 5/38 | 57/14927
GO:0048523 (2.66e-09) negative regulation of cellular process 6/38 | 39/14927
GO:0048522 (3.73e-10) positive regulation of cellular process 7/38 | 29/14927
GO:0007155 (0.000688) cell adhesion 5/38 | 254/14927
GO:0022610 (0.000688) biological adhesion 5/38 | 254/14927
GO:0048519 (1.09e-10) negative regulation of biological process 7/38 | 39/14927
GO:0050789 (0.000166) regulation of biological process 22/38 | 4144/14927
GO:0050794 (0.00319) regulation of cellular process 19/38 | 4077/14927
GO:0010646 (0.000367) regulation of cell communication 5/38 | 215/14927
GO:0048518 (4.85e-18) positive regulation of biological process 10/38 | 24/14927
GO:0065007 (1.79e-05) biological regulation 24/38 | 4250/14927
GO:0007165 signal transduction
GO:0007242 (2.15e-06) intracellular signaling cascade 10/38 | 557/14927
GO:0007264 (0.000475) small GTPase mediated signal transduction 6/38 | 362/14927
GO:0023052 signaling
GO:0007154 cell communication
GO:0031323 (0.000167) regulation of cellular metabolic process 11/38 | 1162/14927
GO:0065008 (1.03e-10) regulation of biological quality 10/38 | 173/14927
GO:0042592 (1.24e-06) homeostatic process 6/38 | 116/14927
GO:0023046 signaling process
GO:0023060 signal transmission
GO:0051171 (0.000556) regulation of nitrogen compound metabolic process 10/38 | 1119/14927
GO:0019219 (0.00216) regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process 9/38 | 1111/14927
GO:0019222 (0.000275) regulation of metabolic process 11/38 | 1219/14927
GO:0080090 (0.00985) regulation of primary metabolic process 10/38 | 1181/14927
GO:0051252 (0.0111) regulation of RNA metabolic process 7/38 | 959/14927
GO:0009889 (0.00219) regulation of biosynthetic process 9/38 | 1116/14927
GO:0031326 (0.00219) regulation of cellular biosynthetic process 9/38 | 1117/14927
GO:0006807 (0.000304) nitrogen compound metabolic process 13/38 | 1927/14927
GO:0060255 (0.00319) regulation of macromolecule metabolic process 9/38 | 1185/14927
GO:0010556 (0.00771) regulation of macromolecule biosynthetic process 8/38 | 1117/14927
GO:0045449 (0.00742) regulation of transcription 8/38 | 1109/14927
GO:0006355 (0.0111) regulation of transcription, DNA-dependent 7/38 | 959/14927
GO:0044237 (0.000475) cellular metabolic process 20/38 | 3789/14927
GO:0006139 (0.00492) nucleobase, nucleoside, nucleotide and nucleic acid metabolic process 11/38 | 1781/14927
GO:0010468 (0.00771) regulation of gene expression 8/38 | 1120/14927
GO:0008152 (0.00949) metabolic process 21/38 | 5163/14927
GO:0044238 (0.0011) primary metabolic process 21/38 | 4390/14927
GO:0006629 (0.000488) lipid metabolic process 5/38 | 232/14927
GO:0016070 (0.0295) RNA metabolic process 7/38 | 1181/14927
GO:0032774 (0.0132) RNA biosynthetic process 7/38 | 995/14927
GO:0006351 (0.013) transcription, DNA-dependent 7/38 | 990/14927
GO:0009058 (0.00999) biosynthetic process 12/38 | 2290/14927
GO:0044249 (0.00742) cellular biosynthetic process 12/38 | 2165/14927
GO:0006350 (0.00973) transcription 8/38 | 1172/14927
GO:0043170 (0.000401) macromolecule metabolic process 20/38 | 3736/14927
GO:0009059 (0.0173) macromolecule biosynthetic process 10/38 | 1668/14927
GO:0034645 (0.0172) cellular macromolecule biosynthetic process 10/38 | 1854/14927
GO:0010467 gene expression
GO:0044260 (0.000499) cellular macromolecule metabolic process 18/38 | 3179/14927
GO:0044267 (0.00771) cellular protein metabolic process 10/38 | 1630/14927
GO:0019538 (0.0169) protein metabolic process 11/38 | 2147/14927
GO:0006464 (0.00184) protein modification process 8/38 | 955/14927
GO:0043687 (0.0345) post-translational protein modification 5/38 | 708/14927
GO:0043412 (0.00214) macromolecule modification 8/38 | 889/14927
GO:0002376 (5.23e-10) immune system process 10/38 | 213/14927
GO:0006955 (2.83e-05) immune response 6/38 | 259/14927
GO:0050896 (1.88e-14) response to stimulus 17/38 | 506/14927
GO:0042221 (4.24e-12) response to chemical stimulus 8/38 | 44/14927
GO:0006950 (4.7e-06) response to stress 10/38 | 275/14927
GO:0009628 (2.96e-11) response to abiotic stimulus 6/38 | 13/14927
GO:0009605 (3.56e-10) response to external stimulus 7/38 | 48/14927
GO:0010033 (1.09e-10) response to organic substance 5/38 | 5/14927
GO:0006952 (3.56e-06) defense response 6/38 | 141/14927

Figure S3

Table S3. The primer pairs used for validation of ChIP-seq peaks.

Peak ID	Primer sequences	
Peak 468	Forward	GGGTAGTTCCCCAAAGGCTG
	Reverse	CAAGGGCTGGGGCATGTAAT
Peak 1232	Forward	CAGCAGTCAGGCACCACTC
	Reverse	CTGCCCAGCTTCTAGCGT
Peak 1485	Forward	AAGTCAACACGAAGGGGCA
	Reverse	GGTTGAGGCATGGAACTCCG
Peak 1639	Forward	TTTGGTCTCTCTGTGCAGCTT
	Reverse	CCTGCTGTCTTATGGAGGGC
Peak 1723	Forward	TTCTGCCCTCTGACATGATTC
	Reverse	CAGATTGGACTGAAAGGACCA
Peak 2043	Forward	TAAGCACCTGGTGAACTGAG
	Reverse	TATTACGTGGCGTGTCAGG
GAPDH promoter *	Forward	TGTTATATCCTTGCGGCAGCTT
	Reverse	AGCACTGCGGGAGAGTAGTAAACT

* Herrmann D et al., Epigenetics 2013 8(3): 281-289 doi:10.4161/epi.23899