Supplementary information for

Gene expression profiles in rice gametes and zygotes: Identification of gamete-enriched genes and fertilization-induced or -suppressed genes in zygotes

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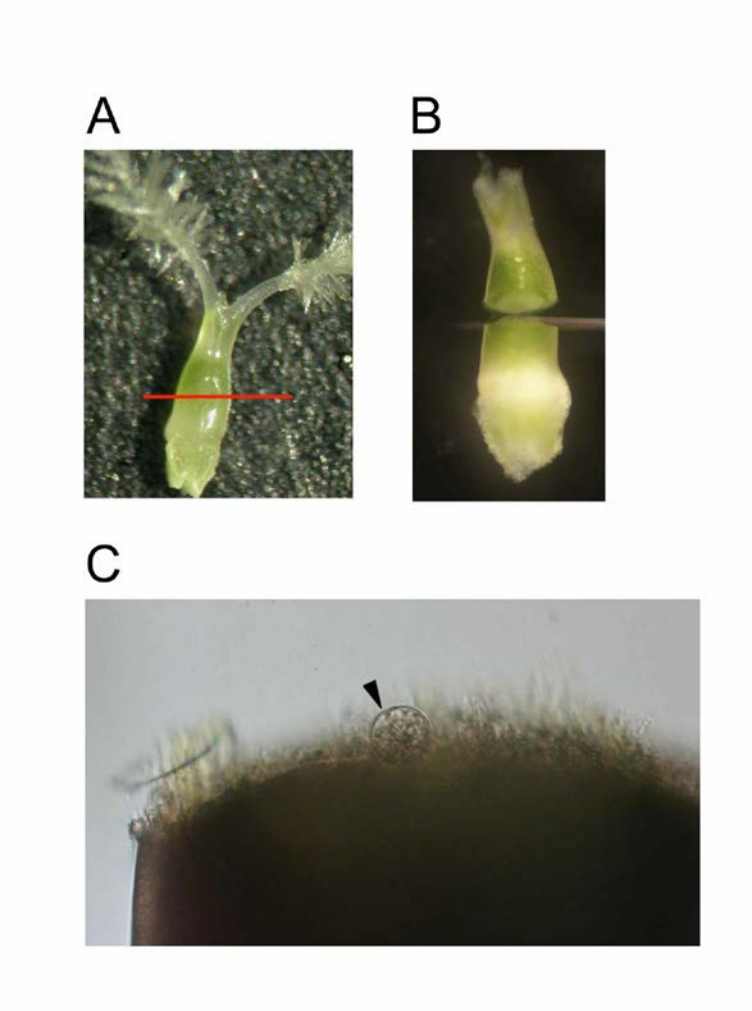

Fig. S1. Isolation of rice egg cells from ovaries. (A) Ovary harvested from a rice flower before flowering. The red line indicates the incision line for egg isolation. (B) Cut ovary. (C) Rice egg cell (arrowhead) being released from basal portion of the dissected ovary.

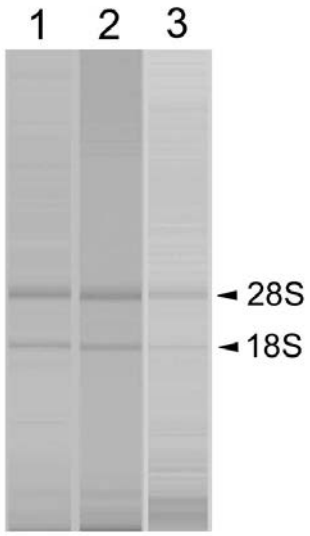

Fig. S2. Assessment of RNA extracted from rice gametes and zygotes. RNA bands corresponding to 28S and 18S RNAs were clearly visible in each sample. Lane 1, egg cells; lane 2, zygotes; lane 3, sperm cells.

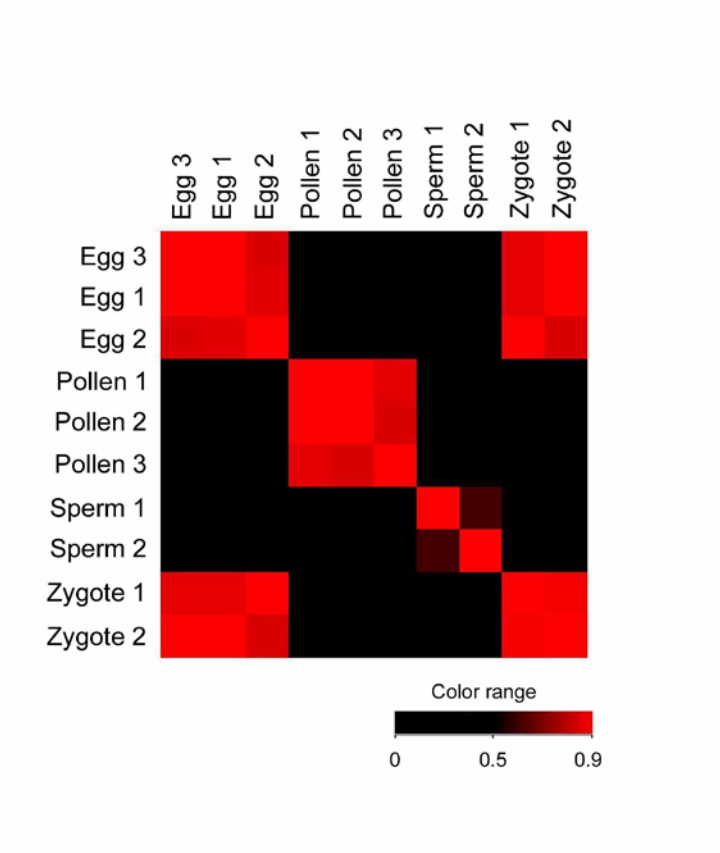

Fig. S3. Microarray correlation plot within and among rice cell types. Pearson's correlation coefficients among array chips are displayed as a heatmap ranging from black (coefficient = 0; no positive correlation) to saturated red (coefficient = 0.9). All replicate cell types had correlation coefficients of 0.86 or higher except sperm (0.62).

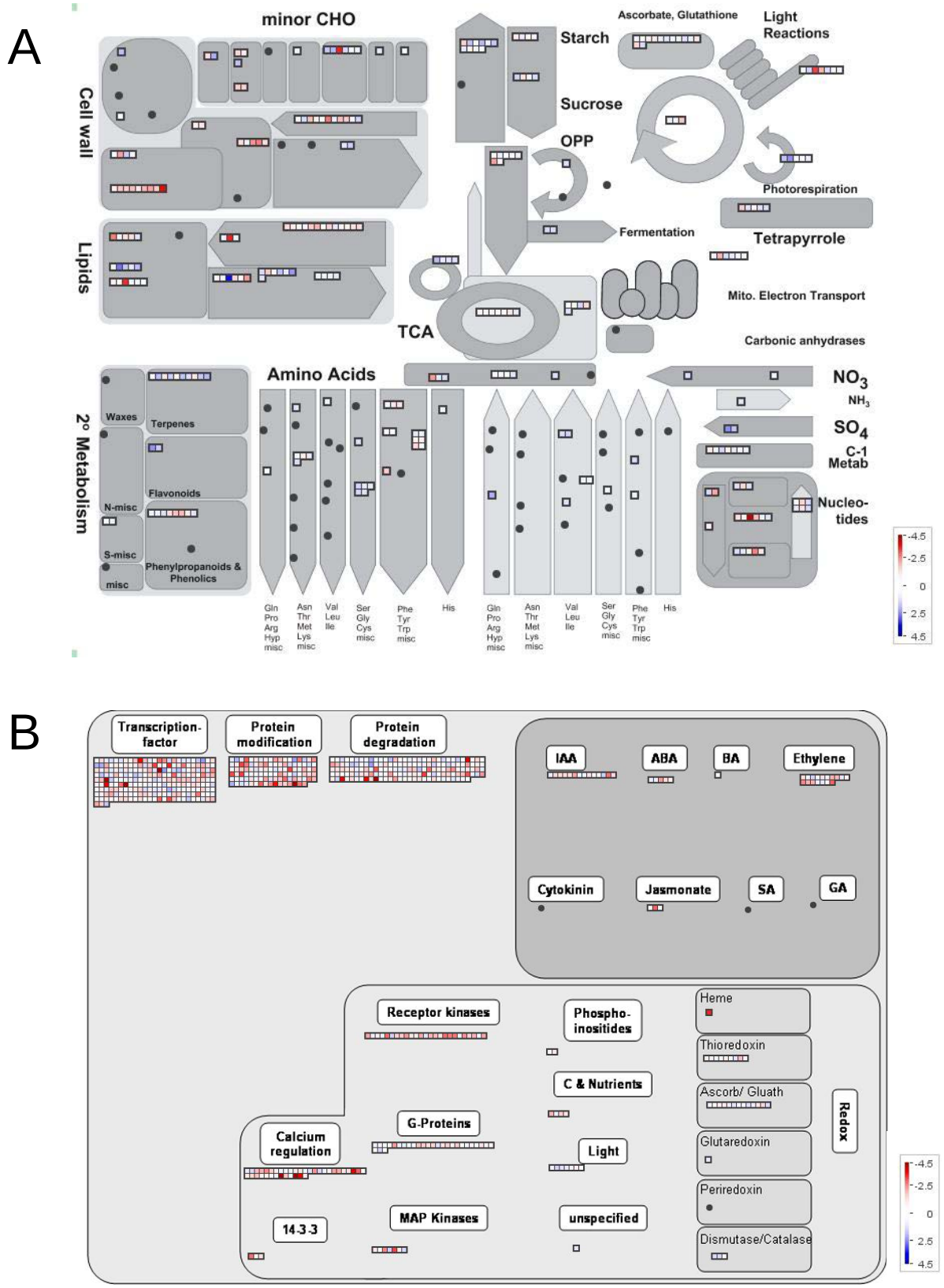

Fig. S4. Change of transcript levels in zygotes, compared to egg cells. Overview display of genes assigned to metabolism and regulation are presented in (A) and (B), respectively**.** The log2 fold changes between the egg cells and the zygotes was visualized using the MapMan software. Red and blue indicated up-regulated and down-regulated in zygotes after fertilization, respectively (see colour scale in panels).

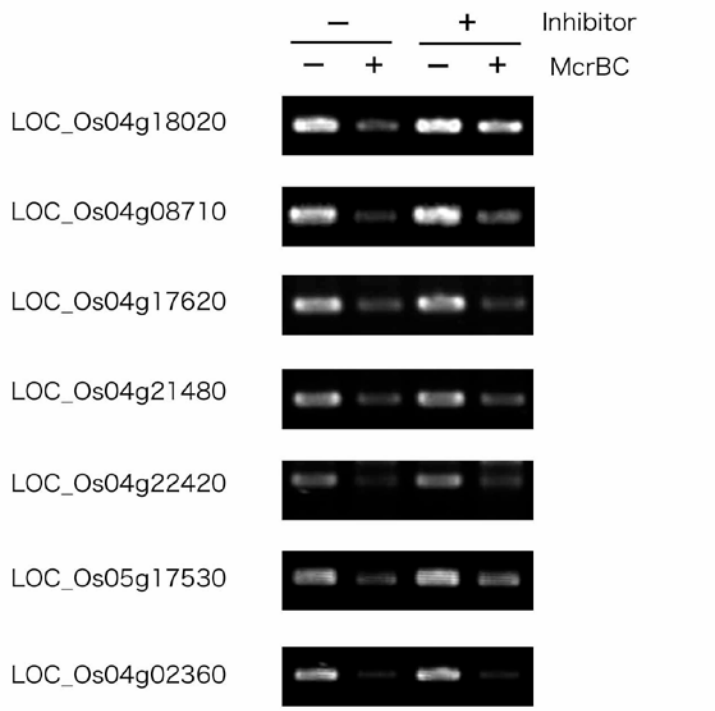

Fig. S5. Effects of MG108 on DNA methylation status on some transposon-related elements in cultured rice cells.

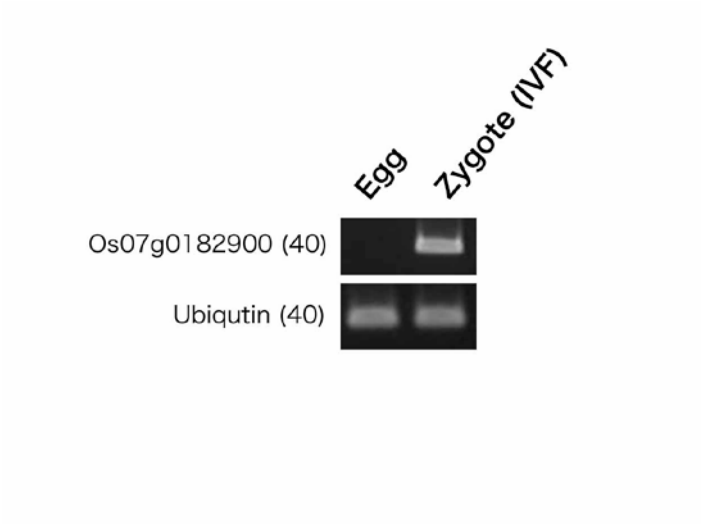

Fig. S6. Expression of a gene (Os07g0182900) putatively encoding DNA methyltransferase 1 (MET1) in rice egg cells and in vitro-produced zygotes. Semiquantitative RT-PCR was performed on total RNAs isolated from egg cells and zygotes cultured for 10 h after in vitro fusion using specific primers. Ubiquitin mRNA was used as an internal control. The numbers in parentheses indicate the number of PCR cycles. See Table S1 for primer sequences.