

**Supplementary Table S5.** Functional analysis of differentially methylated genes in liver tissue of F3 generation animals derived from early embryos exposed to the combination of multiple ovulations, vitrification and embryo transfer (MOVET) and naturally-conceived (NC).

| Type <sup>+</sup> | Category* | Term  | Count | p-value |
|-------------------|-----------|---|-------|---------|
| Hypo              | BP        | Regulation of apoptotic process   | 2     | 0.09    |
| Hypo              | CC        | Cell cortex   | 2     | 0.08    |
| Hypo              | CC        | Recycling endosome  | 2     | 0.09    |
| Hypo              | KEGG      | Endocytosis   | 3     | 0.04    |
| Hypo              | KEGG      | Glycerolipid metabolism   | 2     | 0.09    |
| Hyper             | BP        | DNA damage response, signal transduction by p53 class mediator resulting in transcription of p21 class mediator | 2     | 0.03    |
| Hyper             | BP        | Cell aging  | 2     | 0.04    |
| Hyper             | BP        | Positive regulation of transcription from RNA polymerase II promoter  | 5     | 0.04    |
| Hyper             | BP        | Response to gamma radiation   | 2     | 0.06    |
| Hyper             | BP        | Intrinsic apoptotic signalling pathway in response to endoplasmic reticulum stress                              | 2     | 0.06    |
| Hyper             | BP        | Establishment of protein localization   | 2     | 0.07    |
| Hyper             | CC        | Transcription factor complex  | 4     | 0.01    |
| Hyper             | CC        | Cytosol   | 7     | 0.01    |
| Hyper             | CC        | Growth cone   | 2     | 0.08    |
| Hyper             | KEGG      | Huntington's disease  | 4     | 0.03    |
| Hyper             | KEGG      | Natural killer cell mediated cytotoxicity   | 3     | 0.05    |
| Hyper             | KEGG      | Transcriptional misregulation in cancer   | 3     | 0.10    |

+ Type is referred to the epigenetic status of the gene: hypomethylated (hypo) or hypermethylated (hyper). \*Functional analysis was referred to the GO term annotation according to the biological process (BP), cellular component (CC) and molecular function (MF) classification, and the KEGG pathways in which they are involved. Red denotes statistical differences at  $p < 0.05$ .