**Supplementary Table 1**

**Top ten candidate DMRs (Differentially methylated regions) associated with daughter fertility**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **DMR** | **Chromosome** | **start** | **end** | **location** | **gene** | **direction** | **length** |
| 1 | Chr1 | 328001 | 328500 | intron | ENSBTAG00000006648 | hyper | 500bp |
| 2 | Chr1 | 379101 | 379700 | CDS | ENSBTAG00000006648 | hyper | 600bp |
| 3 | Chr15 | 1092601 | 1093400 | CDS | ENSBTAG00000046387 | hypo | 800bp |
| 4 | Chr16 | 11333201 | 11334000 | Distal intergenic | ENSBTAG00000502589 | hypo | 800bp |
| 5 | Chr18 | 57249301 | 57249800 | Promoter | ENSBTAG00000060266 | hypo | 500bp |
| 6 | ChrX | 123940101 | 123940600 | Distal intergenic | ENSBTAG00000051616 | hypo | 500p |
| 7 | ChrX | 123948001 | 123948700 | Distal intergenic | ENSBTAG00000051616 | hypo | 700bp |
| 8 | ChrX | 124021501 | 124022200 | Distal intergenic | ENSBTAG00000038660 | hypo | 700bp |
| 9 | Chr14 | 13777101 | 13777800 | intron | ENSBTAG00000052622 | hypo | 700bp |
| 10 | Chr21 | 33024301 | 33025100 | downstream | ENSBTAG00000516472 | hypo | 800bp |

**Notes:** The absolute methylation difference was higher than 15% (q <1.1e-26). CDS (coding DNA sequence)

**Supplementary Figure 1** The size distribution of the identified DMRs.

**Supplementary figure 2**

The pantothenate pathway that is predicted via the enriched reproduction GO term

**Supplementary figure 3**

The information of the genes that covered at least one DMR that associated with bull and daughter fertility. There are 60 genes overlapped (BF: bull fertility, DF: daughter fertility, DMGs (genes that covered at least one DMRs (q<0.05)).

**Supplementary file 1**

The information of sperm-derived differentially methylated cytosines associated with daughter fertility. Sheet1. The methylation difference was higher than 20% and q <0.01 between the high daughter fertility and low daughter fertility groups, a total of 252 CG was listed. Sheet 2. The information of the samples used for sequencing.

**Supplementary file 2**

The conversion rate of the samples. The conversion rate of the enzyme was calculated by three imprinting genes, namely, KCNQ1, SNRPN, and H19.

**Supplementary file 3**

The function cluster of the genes covered at least one DMR (q<0.05) that was associated with bull fertility and daughter fertility. All the genes were classified into 7 clusters based on their function annotation via uploading to DAVID.

**Supplementary file 4**

Sheet1-Sheet2.The 791 genes covered at least one DMCs (q<0.05) and their annotation. Sheet 3: The seven functional clusters of the genes that covered at least one DMCs(q<0.05).

**Supplementary file 5**

Sheet 1.355 Genes that covered at least one DMR (q<0.05) and associated with daughter fertility. Sheet 2. The functional classification of the genes that contain at least one DMR (q<0.05). Sheet3. The information of the 37 genes associated with the development process (genes covered at least one DMR (q<0.05))

**Supplementary file 6**

X chromosome-link genes (a total of 27 genes) that covered at least one DMR and their functional classification.