**Table S1:** **Statistical analysis of the ratio of methylated to unmethylated CpGs in single copy DMR loci**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Locus** | **Methylation site** | **Modern*Bos taurus*** | **Mummified*Bos taurus*** | **Ancient*Bison priscus*** |
| **Chi-square** | **P-value** | **Chi-square** | **P-value** | **Chi-square** | **P-value** |
| PEG3 | 1 | 0.8 | 0.3711 | 0.8 | 0.3711 | 0.2 | 0.6547 |
| 2 | 0.8 | 0.3711 | 0.0 | 1.0000 | 1.8 | 0.1797 |
| 3 | 0.8 | 0.3711 | 0.2 | 0.6547 | 0.8 | 0.3711 |
| 4 | 1.8 | 0.1797 | 0.2 | 0.6547 | 1.8 | 0.1797 |
| NESP55 (proximal) | 1 | 0.2 | 0.6547 | 0.8 | 0.3711 | 0.8 | 0.3711 |
| 2 | 0.2 | 0.6547 | 0.2 | 0.6547 | 0.8 | 0.3711 |
| 3 | 0.8 | 0.3711 | 0.2 | 0.6547 | 0.8 | 0.3711 |
| 4 | 0.2 | 0.6547 | 0.8 | 0.3711 | 0.8 | 0.3711 |
| 5 | 0.2 | 0.6547 | 0.2 | 0.6547 | 1.8 | 0.1797 |
| 6 | 0.2 | 0.6547 | 0.0 | 1.0000 | 0.8 | 0.3711 |
| 7 | 0.2 | 0.6547 | 0.2 | 0.6547 | 9.8 | 0.0017\* |
| 8 | 0.2 | 0.6547 | 0.2 | 0.6547 | 0.8 | 0.3711 |
| 9 | 0.2 | 0.6547 | 0.2 | 0.6547 | 0.8 | 0.3711 |
| 10 | 0.0 | 1.0000 | 0.0 | 1.0000 | 0.8 | 0.3711 |
| 11 | 0.2 | 0.6547 | 0.0 | 1.0000 | 0.8 | 0.3711 |
| NESP55 (distal) | 1 | 1.8 | 0.1797 | 0.2 | 0.6547 | 0.0 | 1.0000 |
| 2 | 1.8 | 0.1797 | 0.2 | 0.6547 | 0.2 | 0.6547 |
| 3 | 1.8 | 0.1797 | 0.2 | 0.6547 | 0.2 | 0.6547 |
| 4 | 1.8 | 0.1797 | 0.8 | 0.3711 | 0.2 | 0.6547 |
| 5 | 1.8 | 0.1797 | 0.2 | 0.6547 | 0.2 | 0.6547 |

Chi-square: chi-square test of goodness of fit with 1 degree of freedom; P-value: two-tailed P-value, \*P < 0.01. Methylation sites are numbered in the order they appear in Figure 2.