|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Library | Methylated CpGs | | Unmethylated CpGs | |
| *Fam60a+/+* embryo 1 | 55,301,002 | 45.8% | 65,324,110 | 54.2% |
| *Fam60a+/+* embryo 2 | 43,690,864 | 46.0% | 51,193,421 | 54.0% |
| *Fam60a+/+* embryo 3 | 56,201,851 | 44.2% | 70,981,705 | 55.8% |
| *Fam60a-/-* embryo 1 | 57,123,330 | 45.9% | 67,350,896 | 54.1% |
| *Fam60a-/-* embryo 2 | 51,987,177 | 45.2% | 63,117,178 | 54.8% |
| *Fam60a-/-* embryo 3 | 51,817,415 | 44.1% | 65,716,556 | 55.9% |

Figure 8-supplement table 1

Methylation level of CpG sites in the captured DNA in three embryos of each genotype.