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| **Table S1 Details of the MethylC-Seq libraries.** |
| 　 | HL | LL |
| Read length (bp) | 90 | 90 |
| Data size (G) | 10.06  | 10.06  |
| Clean reads (M) | 114.44  | 114.44  |
| Mapped reads (M) | 87.15  | 88.58  |
| Mapped bases (Gb) | 7.66  | 7.79  |
| %Cytosines covered (at least one read) | 96.46% | 96.10% |
| %CG covered (at least one read) | 96.69% | 96.63% |
| %CHG covered (at least one read) | 96.96% | 96.91% |
| %CHH covered (at least one read) | 96.37% | 95.94% |
| Average depth of genome coverage (×) | 14.03  | 14.03  |
| Average read depth at cytosines (×) | 14.22  | 14.37  |
| Average read depth at CG-cytosines (×) | 19.35 | 19.95 |
| Average read depth at CHG-cytosines (×) | 16.78 | 17.51 |
| Average read depth at CHH-cytosines (×) | 13.34 | 13.24 |
| Genome average methylation level | 16.31% | 16.01% |
| CG average methylation level | 58.24% | 58.84% |
| CHG average methylation level | 30.01% | 29.79% |
| CHH average methylation level | 7.11% | 6.19% |