**Supplementary Table S1. Mapping summary of GPS, WGBS, ChIP-seq and RNA-seq data.**

**a**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Sample** | **Sequenced reads for methylation detection** | **Filtered reads for methylation detection** | **Mapped reads** | **Bisulfite coverted rate** | **Mapped percenge** | **CpGs coverage\*** |
| **Liver** | 653,627,669 | 598,982,206 | 526,000,000 | 99.3% | 87.8% | 54,853,393 |
| **97L** | 878,411,580 | 748,255,993 | 586,104,435 | 99.0% | 78.3% | 55,111,920 |
| **LM3** | 508,351,384 | 317,418,209 | 205,850,382 | 98.2% | 64.9% | 48,025,765 |
| **Primary liver cancer** | 553,349,823 | 374,428,526 | 261,826,126 | 99.4% | 69.9% | 43,430,724 |
| hg19 CpG total sites number : 56434896 | | | |  |  |  |
| \* : CpGs covered ≥1 read | |  |  |  |  |  |

**b**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Sample** | **Sequenced reads for methylation detection** | **Filtered reads for methylation detection** | **Mapped reads** | **Bisulfite convertion rate** | **Mapped percentage** | **CpGs coverage\*** |
| **GPS Rep1** | 257,367,674 | 200,753,426 | 162,919,287 | 99.0% | 81.2% | 43,887,783 |
| **GPS Rep2** | 219,147,841 | 173,596,779 | 140,088,960 | 98.6% | 80.7% | 39,908,912 |
| **WGBS Rep1** | 453,695,287 | 368,467,266 | 238,202,894 | 99.7% | 64.6% | 39,805,038 |
| **WGBS Rep2** | 460,297,982 | 380,473,106 | 248,738,046 | 99.0% | 65.4% | 35,063,481 |
| hg19 CpG total sites number : 56434896 | | | |  |  |  |
| \* : CpGs covered ≥1 read | |  |  |  |  |  |

**c**

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| --- | --- | --- | --- | --- |
| **ChIP-seq Sample** | **Sequenced reads** | **Filtered reads** | **Mapped reads** | **Mapped percenge** |
| **97L-H3K27ac Rep1** | 89,976,316 | 82,687,300 | 65,069,193 | 78.7% |
| **97L-H3K27ac Rep2** | 75,266,698 | 72,937,498 | 60,335,036 | 82.7% |
| **97L-H3K36Me3 Rep1** | 32,417,586 | 30,634,050 | 21,862,609 | 71.4% |
| **97L-H3K36Me3 Rep2** | 87,910,880 | 85,810,390 | 62,626,474 | 73.0% |
| **97L-H3K4Me3 Rep1** | 42,469,270 | 37,624,052 | 30,905,450 | 82.1% |
| **97L-H3K4Me3 Rep2** | 114,150,042 | 110,202,626 | 89,630,580 | 81.3% |
| **LM3-H3K27ac Rep1** | 64,623,630 | 60,583,658 | 49,588,094 | 81.9% |
| **LM3-H3K27ac Rep2** | 68,338,794 | 66,697,966 | 54,592,462 | 81.9% |
| **LM3-H3K36Me3 Rep1** | 27,549,748 | 25,952,416 | 16,744,378 | 64.5% |
| **LM3-H3K36Me3 Rep2** | 91,376,088 | 88,864,462 | 63,302,398 | 71.2% |
| **LM3-H3K4Me3 Rep1** | 42,831,044 | 35,842,282 | 27,395,263 | 76.4% |
| **LM3-H3K4Me3 Rep2** | 99,816,872 | 96,314,594 | 56,587,461 | 58.8% |

**d**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **RNA-seq Sample** | **Sequenced reads** | **Filtered reads** | **Mapped reads** | **Mapped percenge** |
| **Liver RNA** | 202,852,458 | 155,171,914 | 86,680,447 | 55.9% |
| **LM3 RNA** | 133,633,086 | 100,052,812 | 46,349,621 | 46.3% |
| **primary liver cancer RNA** | 65,042,768 | 44,550,380 | 22,213,001 | 49.9% |
| **97L RNA Rep1** | 170,933,482 | 137,442,748 | 43,696,920 | 31.8% |
| **97L RNA Rep2** | 185,367,944 | 168,738,358 | 149,936,540 | 88.9% |