**Supplementary File 6. Sequencing statistics of Sox2 ChIP-seq samples generated in this study, related to Figure 6-7**

All samples were sequenced on a HiSeq 1500 (Illumina) sequencing platform in 76bp paired-end mode.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| No. | Hours of DOX treatment | Replicateno. | Sequencedreads | Mapped reads | Duplicates（%） |
| 1 | 0h | 1 | 31,157,808 | 26,708,870 | 8.0 |
| 2 | 2 | 30,358,437 | 26,105,044 | 8.0 |
| 3 | 3h | 1 | 29,224,107 | 25,024,914 | 8.0 |
| 4 | 2 | 23,143,269 | 19,813,671 | 8.0 |
| 5 | 6h | 1 | 32,774,215 | 28,167,501 | 8.0 |
| 6 | 2 | 26,661,227 | 22,987,161 | 7.0 |
| 7 | 9h | 1 | 29,314,133 | 25,170,019 | 9.0 |
| 8 | 2 | 25,428,443 | 21,723,313 | 8.0 |
| 9 | 12h | 1 | 26,165,258 | 22,383,270 | 9.0 |
| 10 | 2 | 24,258,711 | 20,855,734 | 8.0 |
| 11 | 15h | 1 | 26,728,664 | 22,835,623 | 8.0 |
| 12 | 2 | 24,926,639 | 21,369,856 | 9.0 |