**S2 Table. Sequencing and analytical pipelines of ChIP-Seq used in ENCODE and Roadmap.**

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|  | **ENCODE (HAIB lab)** | **Roadmap (Tsankov *et al.* [41])** |
| Read length | 25-50 bp | 25-36 bp |
| Layout | Single | Single/Paired |
| Platform | Genome Analyzer | HiSeq2000 |
| Mapping | Eland/Bowtie | MAQ/Bowtie2 |
| Filtering multiple mapped reads | Yes | No |
| Peak calling | SPP peak caller with calculation of IDR (Irreproducible Discovery Rate) | MACS |
| Using input control for peak calling | Yes | No |