





## 1 Data Statistics

Raw reads produced from sequencing machines contain dirty reads which contain adapters, unknown or low quality bases.

Table 1-1 Output Statistics of Raw Data

Sample	Length	Q20(%)	Q30(%)	Total Reads	Total Bases
A	150;150	95.21;84.56	89.02;71.89	352,262,909	105,678,872,700

Table Format:

1. Sample\_name: The name of sample
2. Q20 (%): The proportion of nucleotides with quality value larger than 20
3. Q30 (%): The proportion of nucleotides with quality value larger than 30
4. Total Reads: The total number of raw reads
5. Total Bases: The total nucleotides number of raw reads

## 2 Contact

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