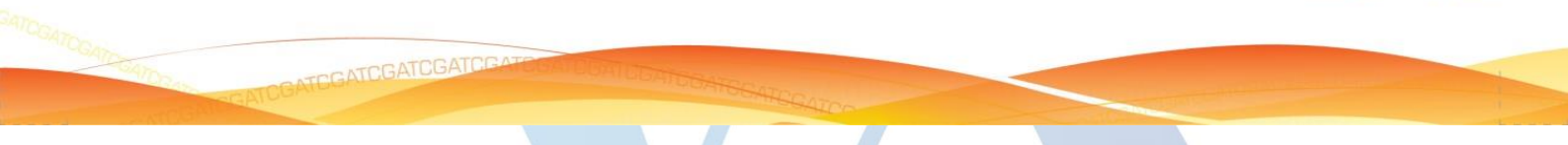


BGI Bioinformatics Report for Re-sequencing



Nov 8, 2019



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1 Basic Biologic Analysis

1.1 Output Statistics

1.1.1 Data Statistic

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
2	150;150	98.66;96.35	96.53;92.64	118,177,982	17,726,697,300
4	150;150	98.80;96.58	96.48;92.40	51,044,524	7,656,678,600
5	150;150	98.53;97.13	96.42;94.17	277,539,854	41,630,978,100
6	150;150	98.77;96.53	96.71;92.87	31,694,210	4,754,131,500
7	150;150	98.58;97.17	96.43;94.16	242,150,432	36,322,564,800
15	150;150	98.70;97.05	96.47;93.65	122,806,280	18,420,942,000
19	150;150	98.61;97.20	96.46;94.24	120,778,976	18,116,846,400

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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