



BGI Bioinformatics Report for Sequencing

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● Results

1 Data Statistics

Raw reads produced from sequencing machines contain dirty reads which contain adapters, unknown or low quality bases. The output statistics of raw data is shown below:

Sample	Length	Q20(%)	Q30(%)	Total Reads	Total Bases
P26	150;150	96.98;94.72	89.38;85.30	44,618,032	13,385,409,600
P31	150;150	97.16;94.04	89.89;83.84	33,392,522	10,017,756,600
P32	150;150	96.97;94.19	89.28;84.15	31,850,565	9,555,169,500
P35	150;150	97.13;94.31	89.82;84.45	38,415,716	11,524,714,800
P36	150;150	96.76;93.88	88.86;83.61	37,163,417	11,149,025,100
P37	150;150	97.14;93.32	89.92;82.46	50,365,354	15,109,606,200
P38	150;150	96.99;93.40	89.54;82.63	51,605,033	15,481,509,900
P39	150;150	97.21;94.44	90.04;84.72	39,255,360	11,776,608,000
P40	150;150	97.06;93.73	89.66;83.27	37,048,863	11,114,658,900
TAF3	150;150	97.22;94.27	90.04;84.24	34,568,455	10,370,536,500
TAF4	150;150	97.04;94.05	89.65;83.99	31,740,599	9,522,179,700
TAF9	150;150	96.74;94.01	88.78;83.77	37,631,195	11,289,358,500

Table Format:

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

2 Contact

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