



BGI Bioinformatics Report for Sequencing

2021/6/22



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Table of Contents

Results	3
1 Data Statistics	3
2 Contact	3



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
CapF-1	150;150	95.73;94.53	87.02;85.32	36,260,578	10,878,173,400
CapF-2	150;150	95.66;94.79	86.74;85.93	37,908,695	11,372,608,500
CapF-3	150;150	95.79;95.20	87.16;86.92	46,789,360	14,036,808,000
CapF-4	150;150	95.15;93.82	85.66;83.81	31,502,444	9,450,733,200
CapF-5	150;150	95.37;94.63	85.92;85.44	35,826,542	10,747,962,600
CapF-6	150;150	95.82;95.10	87.19;86.58	44,063,239	13,218,971,700
HapSA1	150;150	96.91;96.76	89.09;89.51	54,099,880	16,229,964,000
NR7	150;150	96.61;96.29	88.45;88.82	5,812,622	1,743,786,600
O102	150;150	97.39;92.84	90.55;81.53	37,261,761	11,178,528,300
O103	150;150	97.29;92.41	90.28;80.81	30,924,281	9,277,284,300
VL5	150;150	95.41;92.91	86.19;81.98	14,070,690	4,221,207,000
VL6	150;150	96.59;96.65	88.77;89.57	21,731,211	6,519,363,300
VL7	150;150	95.15;91.39	85.63;78.74	11,966,669	3,590,000,700
VL8	150;150	96.04;96.08	87.49;88.13	16,486,657	4,945,997,100

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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