

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
K	150;150	95.17;81.77	88.83;67.66	5,535	1,660,500
MG	150;150	91.52;73.78	82.84;56.77	152	45,600
NB	150;150	93.03;79.60	86.91;65.21	11,709,467	3,512,840,100
NR_A1	150;150	95.90;83.21	90.68;69.87	9,594,276	2,878,282,800
NR_A10	150;150	96.82;88.17	92.66;77.73	31,254,517	9,376,355,100
NR_A11	150;150	96.50;88.29	92.22;78.00	29,965,214	8,989,564,200
NR_A8	150;150	96.08;85.42	91.31;73.14	11,431,843	3,429,552,900
P11	150;150	95.81;85.51	91.19;73.52	9,174,028	2,752,208,400
P12	150;150	96.89;87.81	92.81;77.19	5,667,321	1,700,196,300
VL_A13	150;150	96.58;86.80	92.34;75.53	5,880,245	1,764,073,500
VL_A14	150;150	96.47;85.77	92.12;73.91	4,360,273	1,308,081,900
VL_A15	150;150	97.16;83.21	92.94;69.65	3,385,976	1,015,792,800
VL_A19	150;150	97.01;88.06	92.90;77.33	7,779,267	2,333,780,100
VL_A2	150;150	96.77;87.38	92.60;76.26	9,387,426	2,816,227,800
VL_A3	150;150	97.19;84.36	92.98;71.42	3,515,697	1,054,709,100
VL_A4	150;150	96.63;86.34	92.40;74.90	4,327,839	1,298,351,700
VL_A5	150;150	95.31;86.47	90.76;75.49	5,665,395	1,699,618,500
VL_A6	150;150	96.99;85.08	92.65;72.42	306,665	91,999,500
VL_A7	150;150	97.14;83.42	92.57;69.30	502,575	150,772,500
VL_A9	150;150	97.30;84.25	92.89;70.57	514,293	154,287,900

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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