



Sequencing Data Report

Project: F20FTSEUHT0946-02_MUSyxjsR

Date: 2024.12.9

Note: For Research Use Only.



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Data Statistics

Raw reads produced from sequencer contain adapters, unknown or low quality bases.

There are 107 samples in this project, the statistics of fastq data is shown below.

Sample	Length	Q20(%)	Q30(%)	GC Content(%)	Total Reads	Total Bases
4C_pct_cmv_prc2_6	150;150	97.94;95.13	93.69;87.15	49.42;49.04	31,058	9,317,400
4C_pct_cmv_prc2_7	150;150	97.85;95.81	93.49;88.73	43.79;43.87	756	226,800
4C_pct_cmv_prc2_dm6_nla_6	150;150	98.12;95.98	94.28;89.19	46.45;47.03	102,262	30,678,600
4C_pct_cmv_prc2_dm6_nla_7	150;150	98.17;95.67	94.37;88.51	48.66;48.85	72,801	21,840,300
4C_lig2_dm6_nla_2	150;150	97.86;96.51	93.56;90.24	45.01;45.48	199,715	59,914,500
4C_lig2_dm6_nla_5	150;150	98.09;96.19	94.13;89.62	47.36;47.46	76,564	22,969,200
63-1_C16_1	150;150	97.96;97.18	93.80;90.77	42.45;39.01	1,048	314,400
63-1_C16_2	150;150	97.79;97.37	93.44;91.90	43.08;40.95	2,643	792,900
63-1_C21_1	150;150	97.80;97.19	93.51;91.14	42.47;39.01	1,642	492,600
63-1_C21_2	150;150	97.64;97.56	93.22;92.33	43.04;40.99	1,668	500,400
63-2_A30_1	150;150	98.00;97.25	93.88;91.08	42.44;39.27	1,621	486,300
63-2_A30_2	150;150	97.74;97.39	93.34;91.87	43.06;41.25	2,213	663,900
Bag3_K	150;150	97.95;95.53	93.74;87.67	43.50;43.55	54,180	16,254,000
C1	150;150	100.00;99.33	98.67;98.00	44.00;44.67	1	300
C10	150;150	95.83;92.00	88.42;82.58	55.25;54.08	8	2,400
C13	150;150	94.67;92.09	88.00;78.90	59.01;58.09	37,962	11,388,600
C18	150;150	0.00;98.00	0.00;93.33	57.33;57.33	1	300
C5	150;150	98.02;96.76	93.84;90.22	47.05;46.81	18,064	5,419,200
C9	150;150	96.00;90.33	91.00;79.33	80.33;81.00	2	600
D2	150;150	98.31;97.08	94.75;91.32	47.75;47.94	88,618	26,585,400
Ezh1_K	150;150	97.71;95.09	92.96;86.55	44.10;44.19	45,023	13,506,900
Ezh2_K3110	150;150	97.94;95.60	93.69;87.86	42.55;42.64	57,567	17,270,100
Ezh3_K	150;150	97.51;95.66	92.49;87.94	42.91;42.88	43,591	13,077,300
HCT+aux	150;150	98.35;98.43	95.09;95.10	36.44;39.53	29,600	8,880,000
HCT-aux	150;150	98.76;98.55	96.20;95.51	36.60;39.54	32,389	9,716,700
Hep	150;150	98.69;98.04	95.94;94.26	49.80;49.60	160,667	48,200,100
Maks_App2510	150;150	98.18;97.48	95.11;93.44	49.19;49.64	736,745	221,023,500
NBC143_B1	150;150	97.99;95.95	93.59;88.45	43.45;43.45	6,357,600	1,877,383,700

Data Statistics

NPC143_R1	150;150	97.69;95.83	92.89;88.43	43.43;43.43	6,231,009	1,811,282,100
NPC143_R1_in	150;150	97.64;95.83	92.89;88.39	41.69;41.73	6,187,246	1,856,173,800
NPC143_R2	150;150	97.85;95.73	93.47;88.16	43.71;43.74	3,448,359	1,034,507,700
NPC143_R2_in	150;150	97.63;96.04	92.87;88.94	42.17;42.15	4,596,496	1,378,948,800
NPC146_7_R1	150;150	97.77;96.48	93.33;90.14	43.16;43.20	11,315,447	3,394,634,100
NPC146_7_R1_in	150;150	98.01;96.89	94.00;91.28	42.25;42.31	10,614,544	3,184,363,200
NPC146_7_R2	150;150	98.06;96.61	94.15;90.46	43.69;43.77	11,299,667	3,389,900,100
NPC146_7_R2_in	150;150	96.94;96.84	90.99;91.14	42.92;42.95	9,131,725	2,739,517,500
NPC149_1_R1	150;150	97.97;96.59	93.89;90.47	42.82;42.87	16,652,100	4,995,630,000
NPC149_1_R1_in	150;150	97.93;96.62	93.79;90.61	43.35;43.44	7,120,970	2,136,291,000
NPC149_1_R2	150;150	98.20;96.73	94.53;90.85	42.85;42.93	17,211,470	5,163,441,000
NPC149_1_R2_in	150;150	98.05;97.07	94.21;91.84	43.25;43.28	11,618,035	3,485,410,500
NPC27110_R1	150;150	97.68;95.27	92.98;86.99	44.29;44.33	7,026,112	2,107,833,600
NPC27110_R1_in	150;150	97.69;95.98	93.05;88.80	42.05;42.09	6,695,204	2,008,561,200
NPC27110_R2	150;150	97.70;95.68	93.09;88.06	43.69;43.73	8,953,091	2,685,927,300
NPC27110_R2_in	150;150	97.60;96.16	92.91;89.31	42.64;42.71	5,907,707	1,772,312,100
NPC_63-1C16_pp1	150;150	99.42;97.66	98.12;93.52	55.15;55.70	34,351	10,305,300
NPC_63-1C16_pp2	150;150	98.65;97.89	95.73;93.99	58.64;63.11	25,987	7,796,100
NPC_63-1C21_pp1	150;150	99.39;97.80	97.96;94.14	55.16;55.51	222,310	66,693,000
NPC_63-1C21_pp2	150;150	98.60;97.64	95.61;93.32	57.36;62.26	15,562	4,668,600
NPC_63-2A30_pp1	150;150	97.31;97.72	93.62;93.65	58.73;61.05	10,817	3,245,100
NPC_63-2A30_pp2	150;150	97.94;97.95	95.39;94.41	53.94;54.14	16,839	5,051,700
NPC_63-2A32_pp1	150;150	98.72;98.02	95.95;94.30	60.84;63.84	33,508	10,052,400
NPC_63-2A32_pp1_2	150;150	98.71;97.84	95.90;93.86	60.06;62.85	13,423	4,026,900
NPC_63-2A32_pp2	150;150	99.08;97.54	97.12;93.50	55.39;55.53	173,346	52,003,800
NPC_63-2A32_pp2_2	150;150	99.40;97.59	98.06;93.60	55.60;56.05	111,574	33,472,200
NPC_63-2_A24_1	150;150	97.85;97.32	93.72;91.22	42.51;38.78	1,525	457,500
NPC_63-2_A24_2	150;150	97.97;97.29	93.95;91.68	43.04;40.72	2,994	898,200
NPC_63-2_A25_1	150;150	97.91;97.09	93.78;90.73	42.43;38.71	2,316	694,800
NPC_63-2_A25_2	150;150	97.96;97.35	94.00;91.81	43.04;40.70	4,794	1,438,200
NPC_63-2_A32_1	150;150	97.54;97.33	92.77;91.21	42.47;39.09	1,404	421,200
NPC_63-2_A32_2	150;150	97.78;97.35	93.48;91.83	43.11;41.06	2,165	649,500
NPC_63-2_C13_1	150;150	98.12;97.36	94.16;91.40	42.44;38.74	1,545	463,500

Data Statistics

NPC_63-2_C13_2	150;150	98.04;97.36	94.10;91.77	43.05;40.78	2,546	763,800
NPC_63-2_C19_1	150;150	97.85;97.54	93.59;91.96	42.45;38.96	1,347	404,100
NPC_63-2_C19_2	150;150	98.14;97.53	94.60;92.47	43.08;40.90	3,054	916,200
NPC_63-2C13_pp1	150;150	99.38;97.64	97.95;93.69	55.35;55.44	226,848	68,054,400
NPC_63-2C13_pp1_2	150;150	99.46;97.76	98.16;93.97	55.57;55.97	195,331	58,599,300
NPC_63-2C13_pp2	150;150	98.67;97.98	95.83;94.16	58.87;62.93	46,079	13,823,700
NPC_63-2C13_pp2_2	150;150	98.49;97.91	95.40;93.96	59.39;64.07	36,145	10,843,500
NPC_63-2C19_pp1	150;150	99.05;98.17	97.20;95.17	54.65;55.04	123,481	37,044,300
NPC_63-2C19_pp2	150;150	96.61;97.51	92.85;92.99	53.17;56.21	7,219	2,165,700
R1	150;150	96.70;92.90	91.17;83.07	58.57;58.27	20	6,000
R8	150;150	95.78;92.11	90.17;80.06	62.00;61.89	12	3,600
Sach2_K2110	150;150	98.67;96.97	95.87;91.49	50.45;50.52	85,118	25,535,400
Shur1_K	150;150	97.92;95.78	93.66;88.31	42.73;42.81	53,837	16,151,100
Shur2_K	150;150	97.75;95.29	93.13;87.01	43.04;43.10	58,634	17,590,200
Tok1_K	150;150	97.85;95.24	93.41;86.87	42.56;42.60	53,453	16,035,900
Vor2_K	150;150	98.55;96.55	95.46;90.26	52.49;52.44	75,355	22,606,500
iP146_7_R1	150;150	96.77;96.27	90.50;89.63	44.14;44.15	11,580,278	3,474,083,400
iP146_7_R1_in	150;150	97.77;96.61	93.35;90.49	42.08;42.12	9,769,210	2,930,763,000
iP146_7_R2	150;150	98.04;96.76	94.12;90.98	44.41;44.45	15,611,545	4,683,463,500
iP146_7_R2_in	150;150	97.98;97.01	93.95;91.63	42.98;43.04	14,496,936	4,349,080,800
iP149_1_R1	150;150	97.52;95.64	92.49;87.91	42.61;42.65	12,430,524	3,729,157,200
iP149_1_R1_in	150;150	97.52;95.55	92.55;87.60	42.10;42.11	6,336,241	1,900,872,300
iP149_1_R2	150;150	97.64;96.66	92.86;90.66	43.63;43.67	20,135,848	6,040,754,400
iP149_1_R2_in	150;150	98.10;97.12	94.29;91.92	43.05;43.11	12,184,922	3,655,476,600
iP181_R1	150;150	97.84;96.25	93.51;89.59	43.61;43.62	15,957,963	4,787,388,900
iP181_R1_in	150;150	97.73;96.45	93.23;90.09	42.53;42.62	10,813,559	3,244,067,700
iP181_R2	150;150	97.70;95.68	93.10;88.13	44.30;44.33	12,903,084	3,870,925,200
iP181_R2_in	150;150	97.70;96.10	93.10;89.09	41.86;41.88	10,218,270	3,065,481,000
iP1_25_R1	150;150	97.91;96.04	93.66;89.06	44.02;44.07	10,833,371	3,250,011,300
iP1_25_R1_in	150;150	97.75;96.60	93.30;90.53	42.60;42.65	6,734,687	2,020,406,100
iP1_25_R2	150;150	97.78;95.94	93.31;88.75	43.72;43.72	15,051,047	4,515,314,100
iP1_25_R2_in	150;150	97.79;95.96	93.36;88.77	42.32;42.33	7,323,393	2,197,017,900
iP63-1C16_dd1	150;150	98.44;97.84	95.23;93.89	57.09;63.66	26.282	7.884.600

Data Statistics

Sample	Length	Q20 (%)	Q30 (%)	GC Content (%)	Total Reads	Total Bases
iP63-1C16_pp2	150;150	99.40;97.79	98.05;94.12	55.19;55.73	49,795	14,938,500
iP63-1C5_pp1	150;150	98.53;97.59	95.46;93.33	59.14;61.49	15,992	4,797,600
iP63-1C5_pp2	150;150	99.38;97.80	97.97;94.25	55.17;55.77	130,914	39,274,200
iP63-2A30_pp1	150;150	99.26;98.33	97.66;95.54	54.77;55.25	177,663	53,298,900
iP63-2A30_pp2	150;150	98.38;97.84	95.03;93.87	57.93;62.93	14,292	4,287,600
iP63-2A32_pp1	150;150	99.52;97.65	98.40;93.79	56.36;56.54	69,466	20,839,800
iP63-2A32_pp2	150;150	98.63;97.12	95.61;92.23	57.75;60.36	4,558	1,367,400
iP63-2C19_pp1	150;150	99.18;97.71	97.73;93.75	56.53;55.65	55,103	16,530,900
iP63-2C19_pp2	150;150	97.55;97.85	93.71;93.99	56.67;61.99	13,797	4,139,100
iP63-2C13_pp1	150;150	99.46;97.18	98.19;92.61	56.80;56.03	149,326	44,797,800
iP63-2C13_pp1_2	150;150	99.57;97.26	98.53;92.75	56.81;56.59	119,491	35,847,300
iP63-2C13_pp2	150;150	98.63;97.92	95.79;94.11	59.25;63.18	31,902	9,570,600
iP63-2C13_pp2_2	150;150	98.57;98.05	95.48;94.39	59.71;63.85	25,180	7,554,000
worm_rigs	150;150	99.06;98.24	97.16;94.90	55.85;54.86	178,913	53,673,900

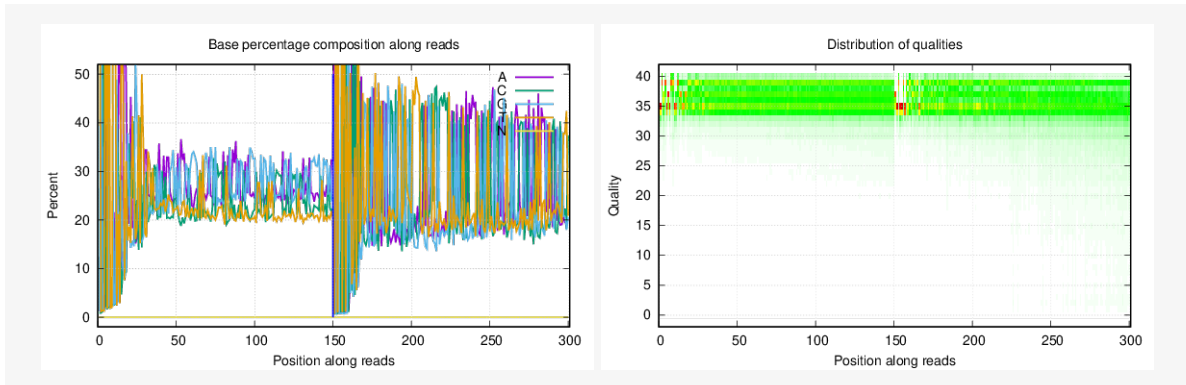
Table Format:

1. Sample: The name of sample
2. Length: The Length of 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. GC Content(%): The proportion of bases G and C
6. Total Reads: The total number of read pairs
7. Total Bases: The total nucleotides number of reads

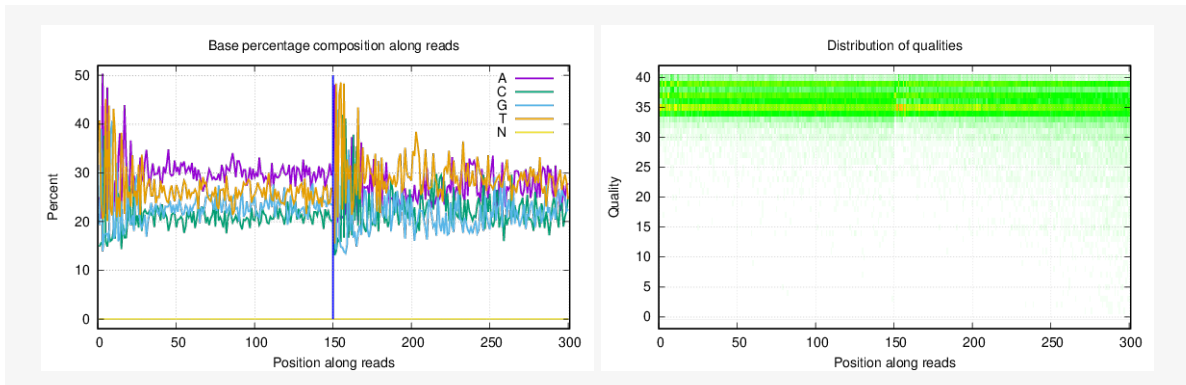
Data Quality Control

The distribution of base percentage and qualities along reads in data filtering are shown as following(If a sample has multiple lanes, only one of them will be displayed). The left picture is base percentage distribution along reads the sample, the right picture is distribution of qualities along reads of the sample.

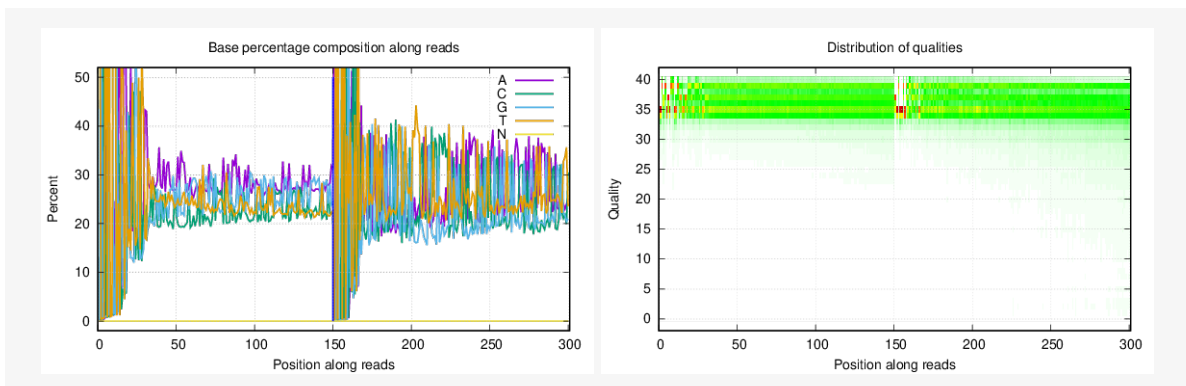
4C_pct_cmV_prc2_6



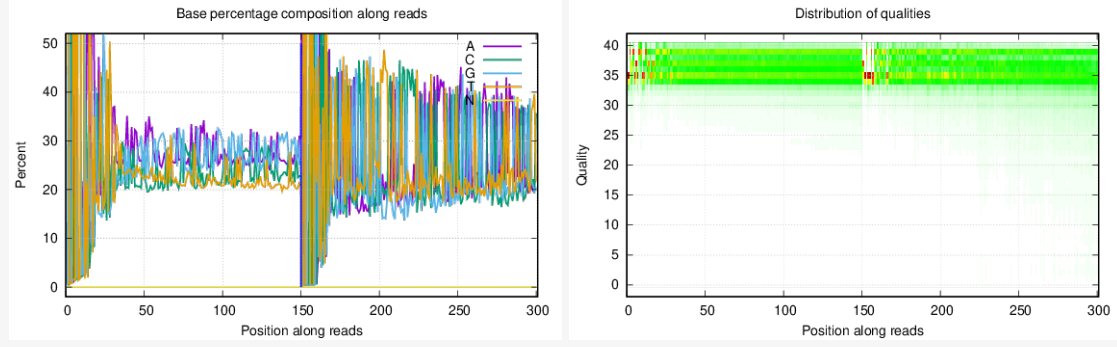
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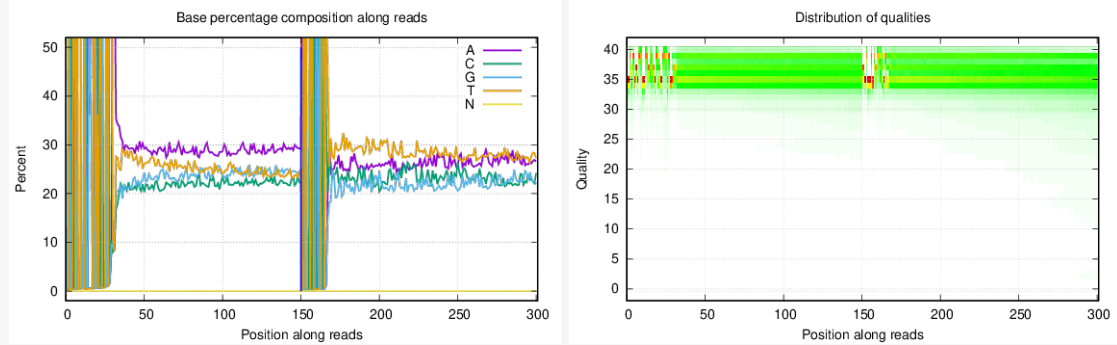
4C_pct_cmV_prc2_dm6_nla_6



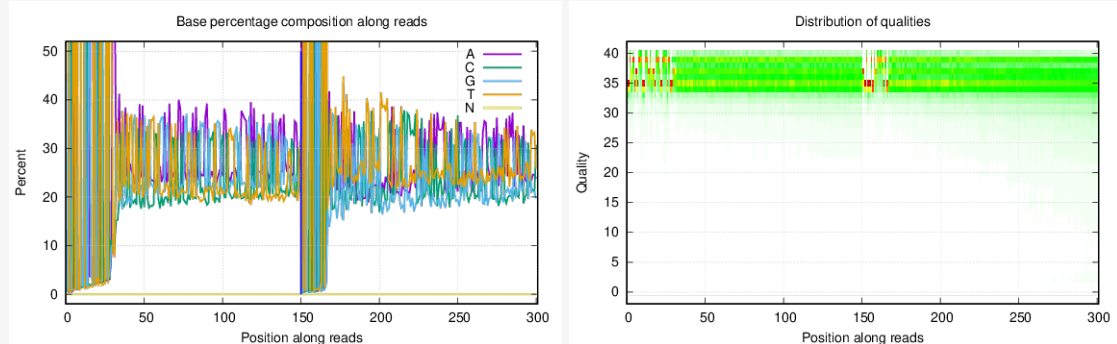
4C_pct_cmV_prc2_dm6_nla_7



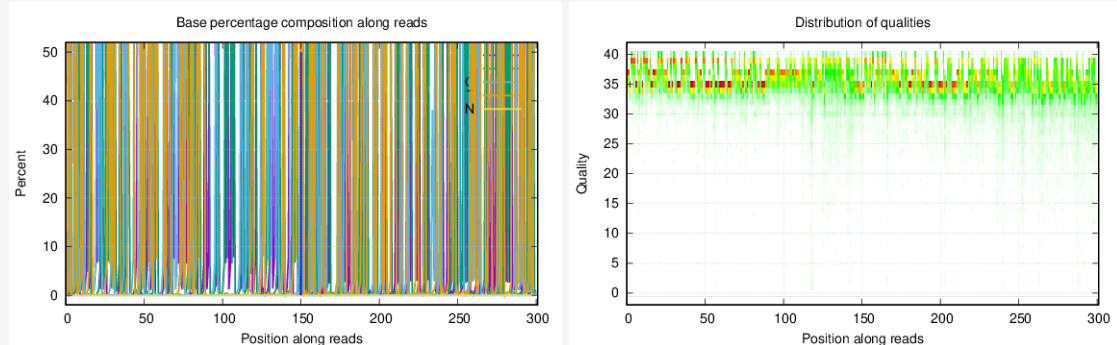
4C_lig2_dm6_nla_2



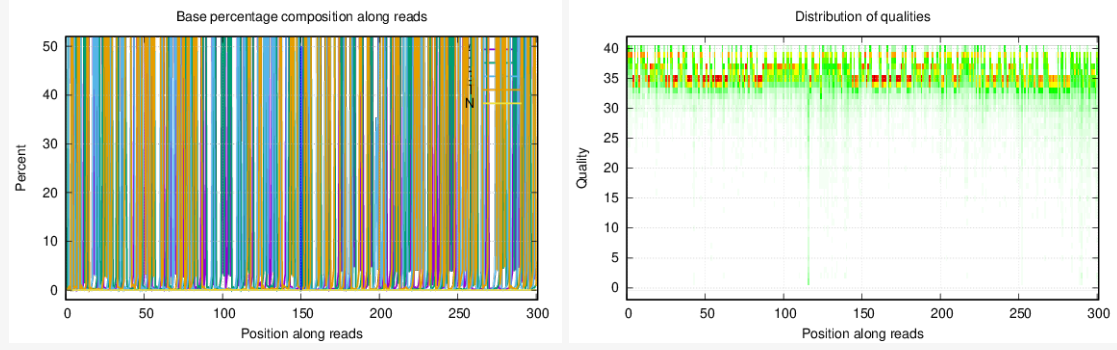
4C_lig2_dm6_nla_5



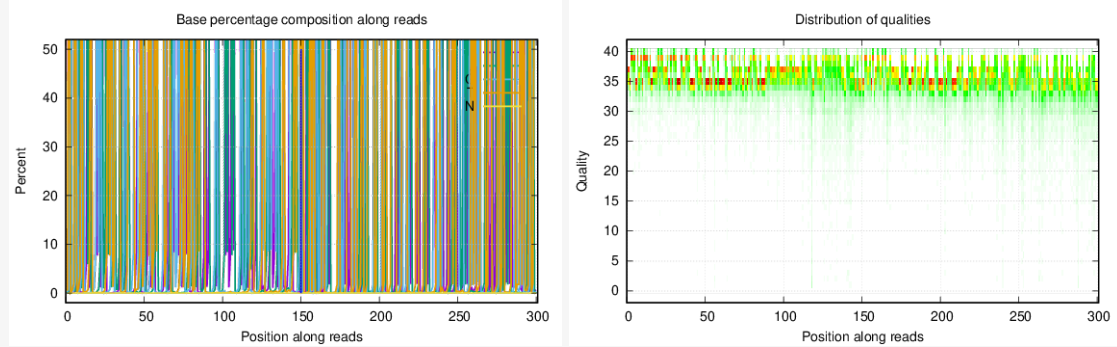
63-1_C16_1



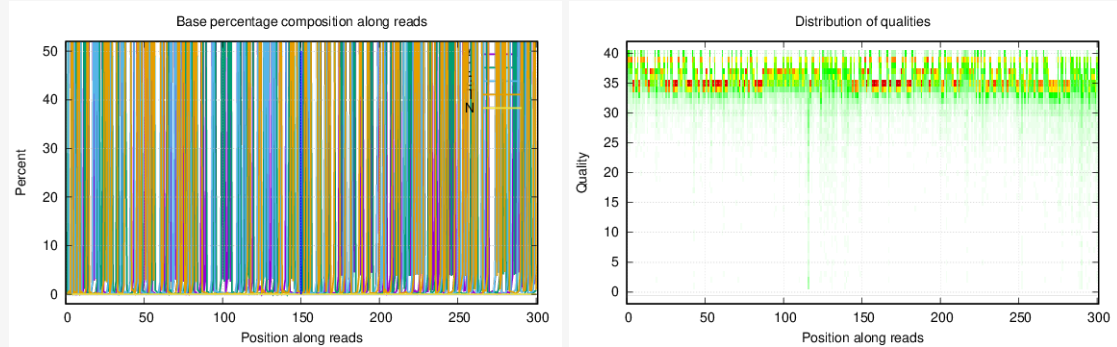
63-1_C16_2



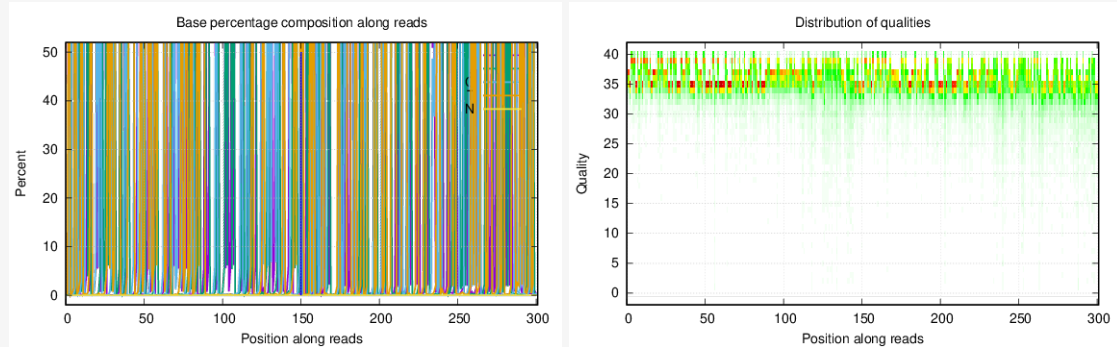
63-1_C21_1



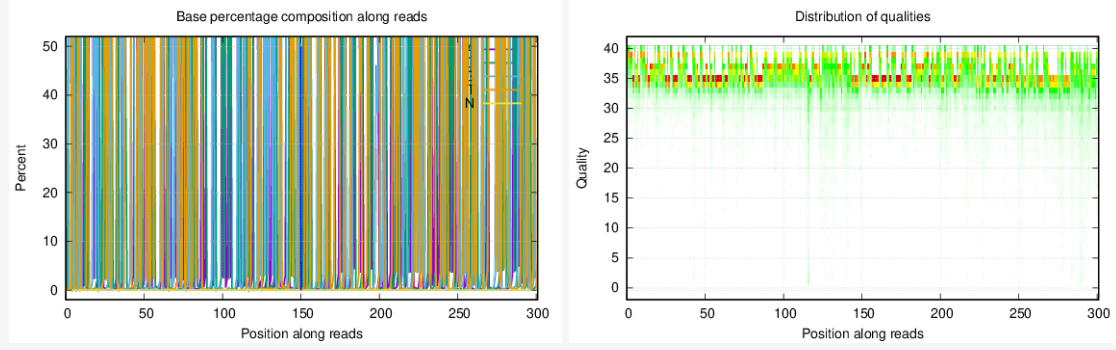
63-1_C21_2



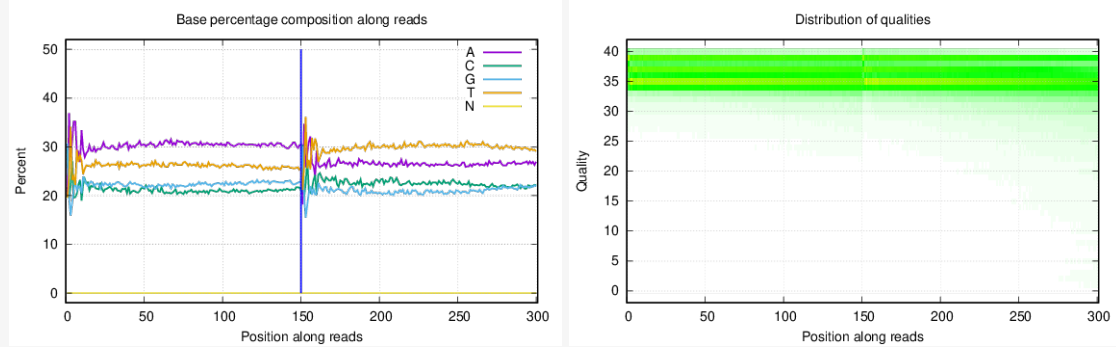
63-2_A30_1



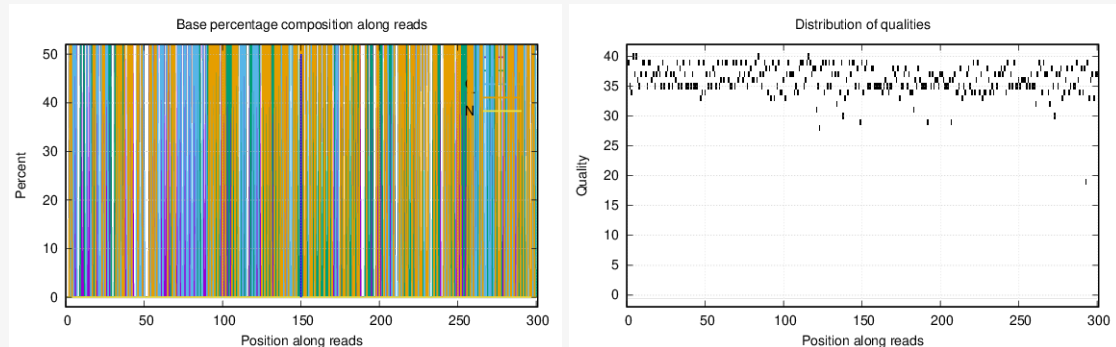
63-2_A30_2



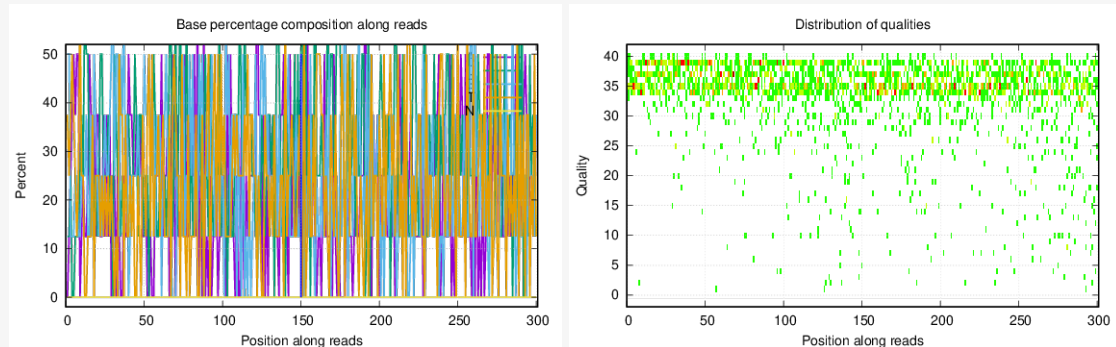
Bag3_K



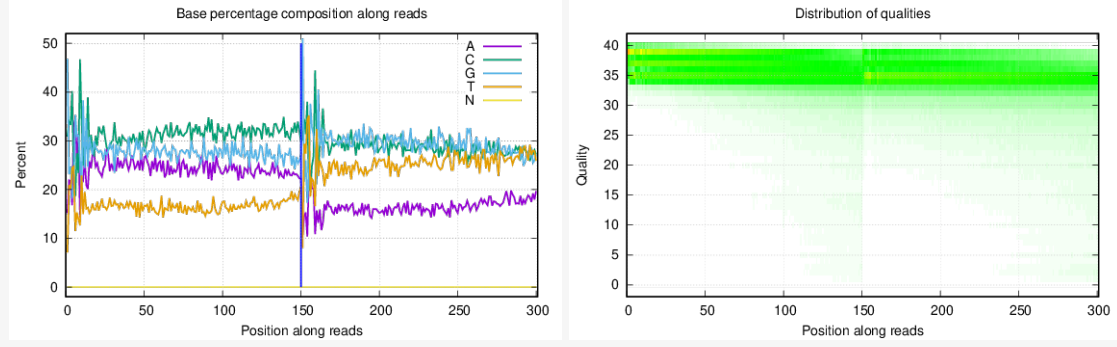
C1



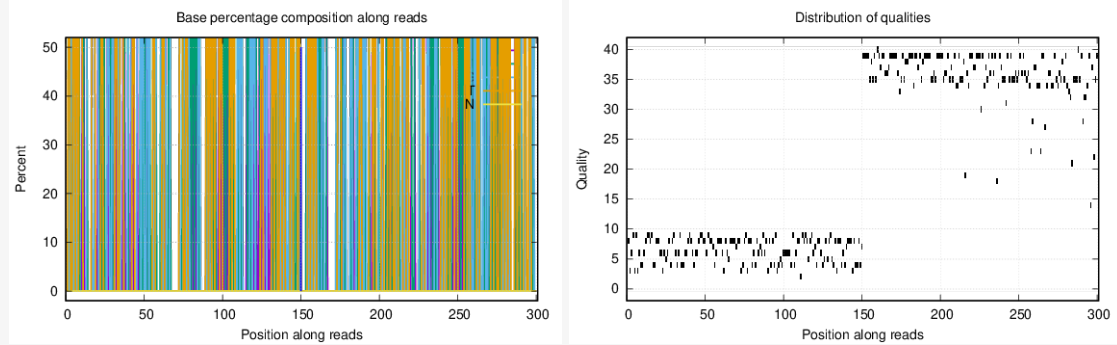
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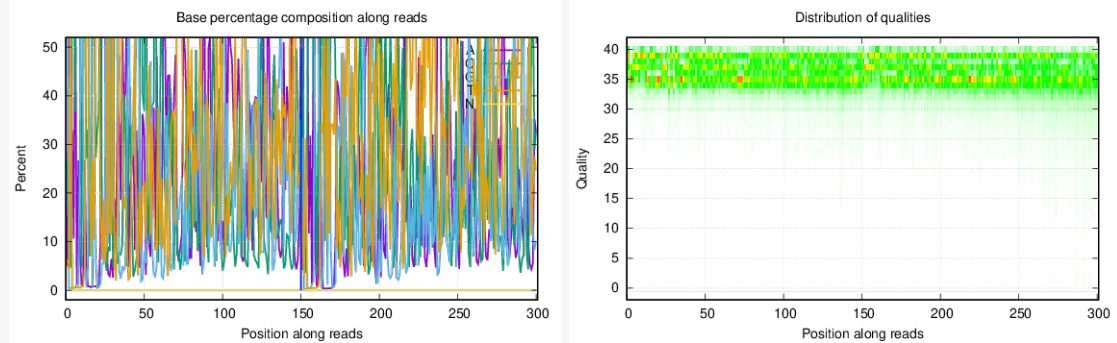
C13



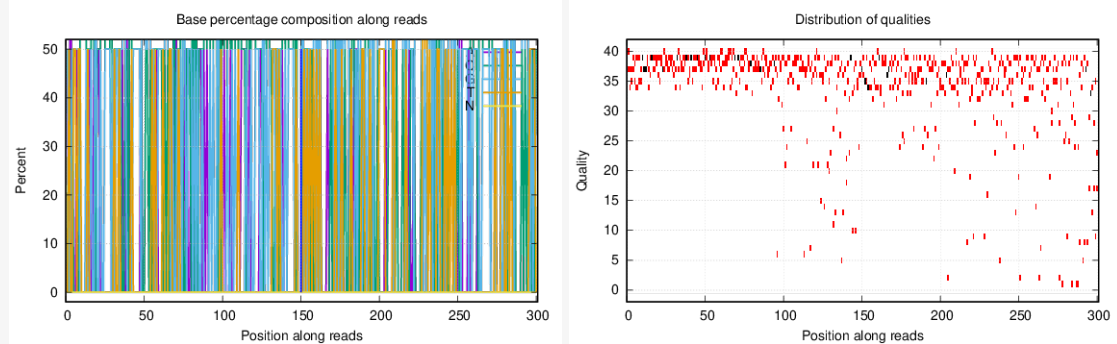
C18



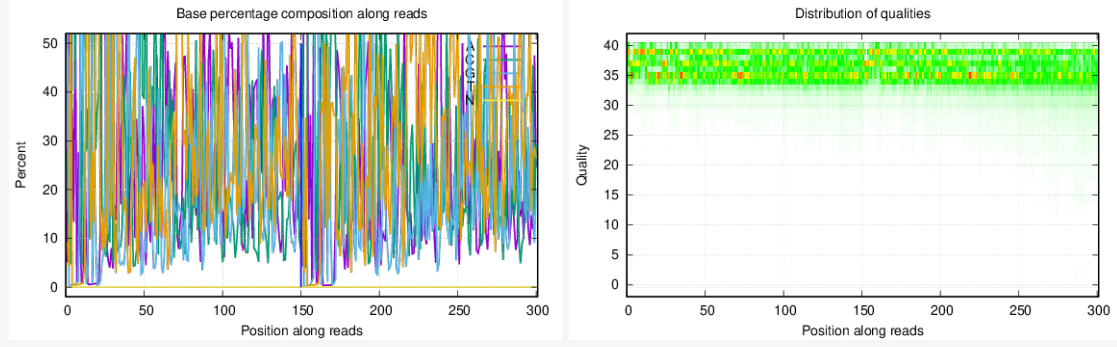
C5



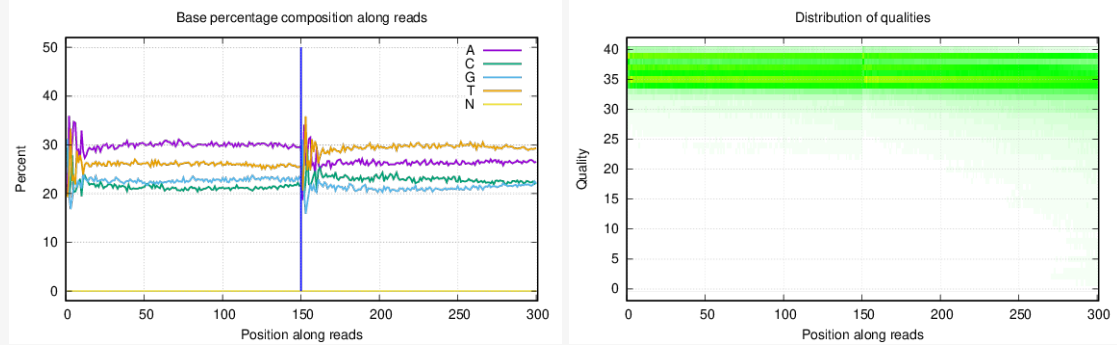
C9



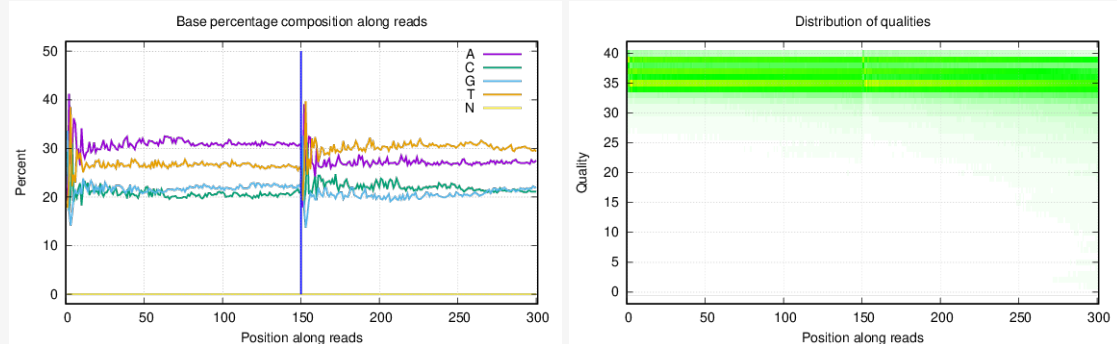
D2



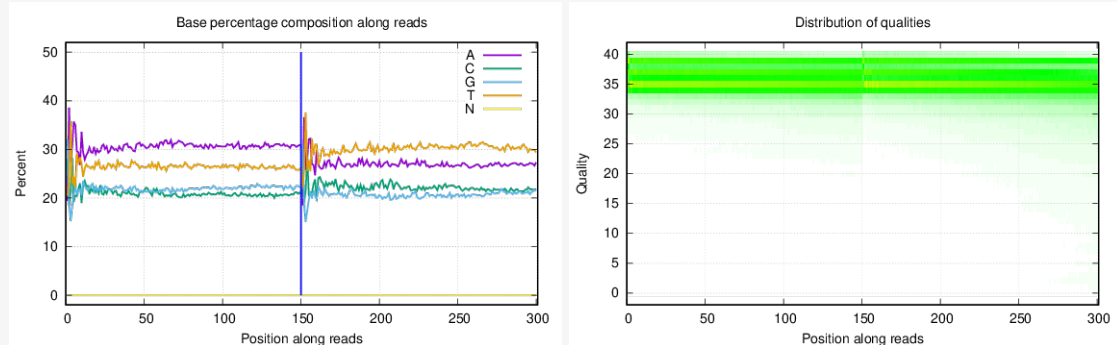
Ezh1_K



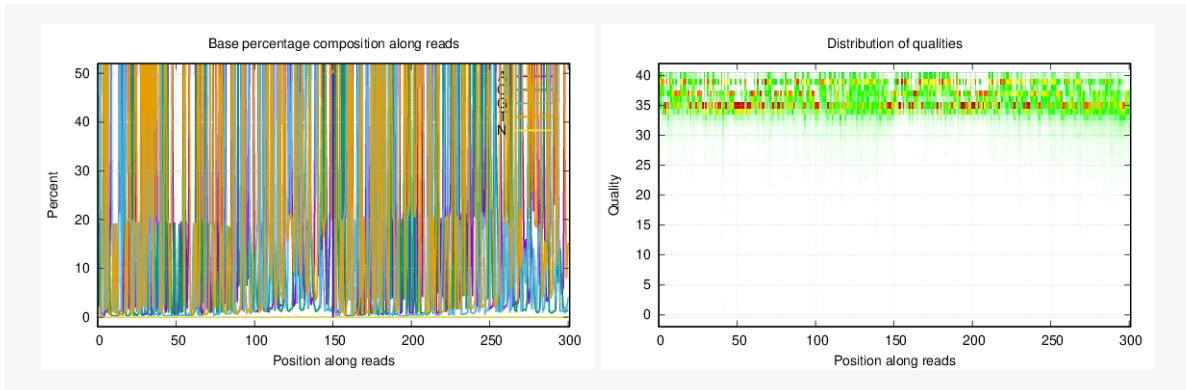
Ezh2_K3110



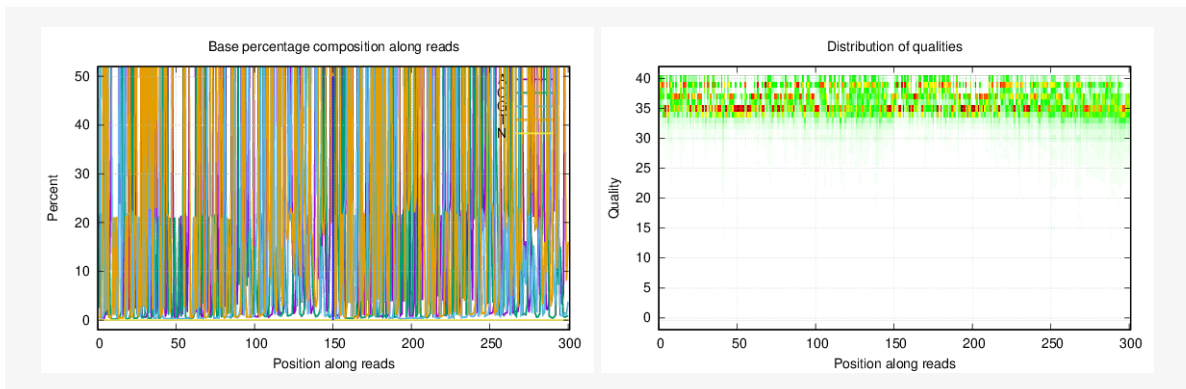
Ezh3_K



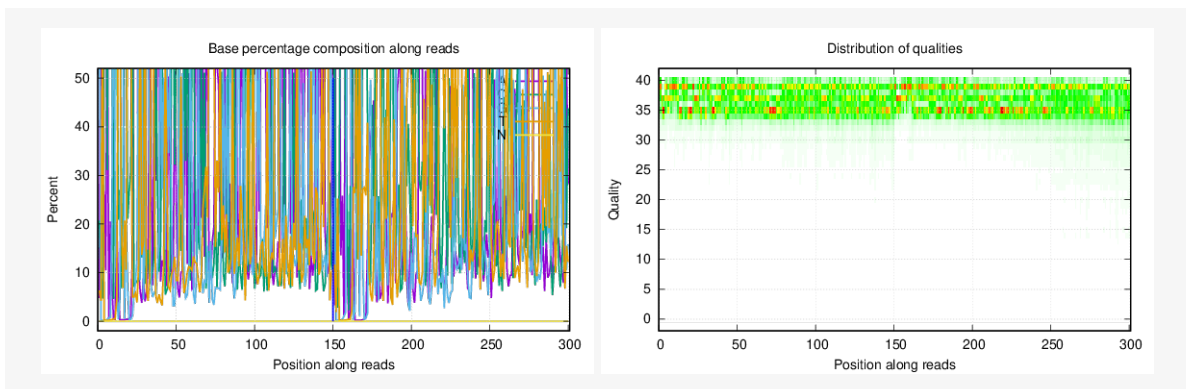
HCT+aux



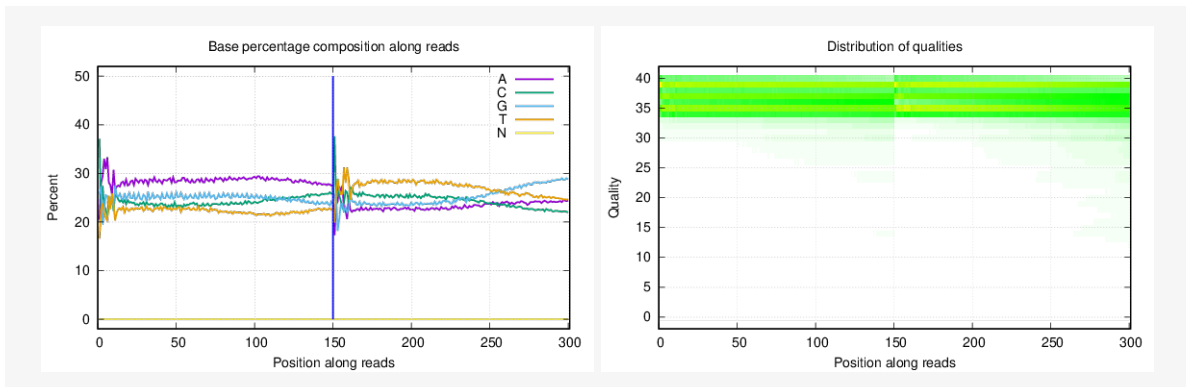
HCT-aux



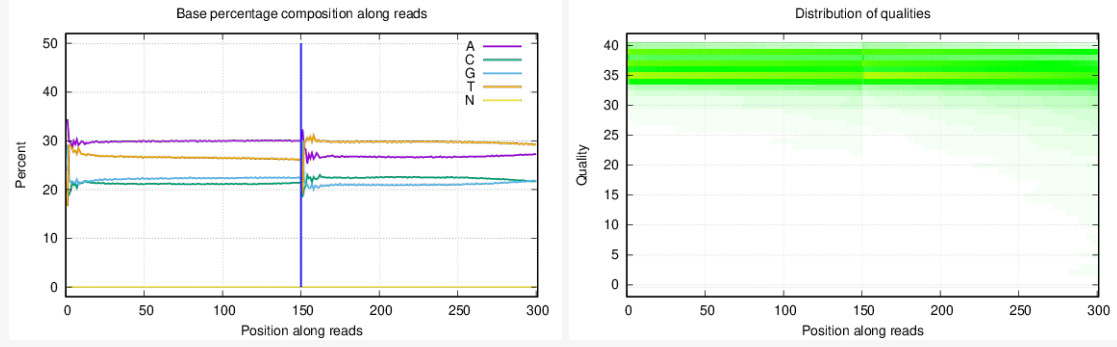
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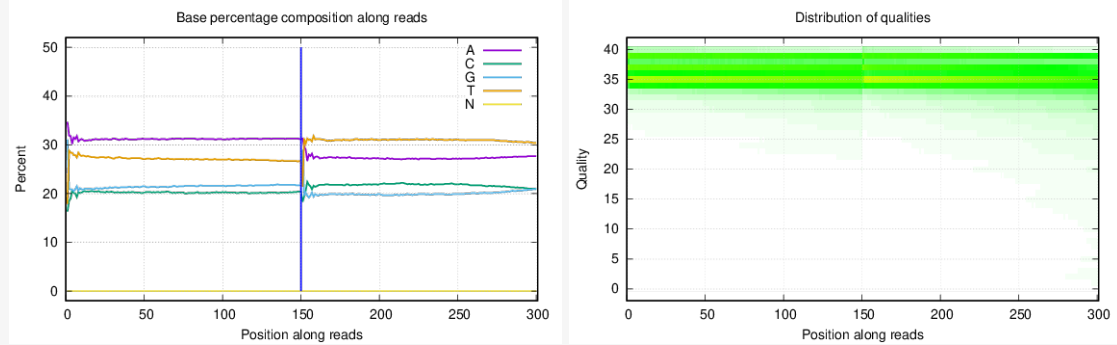
Maks_App2510



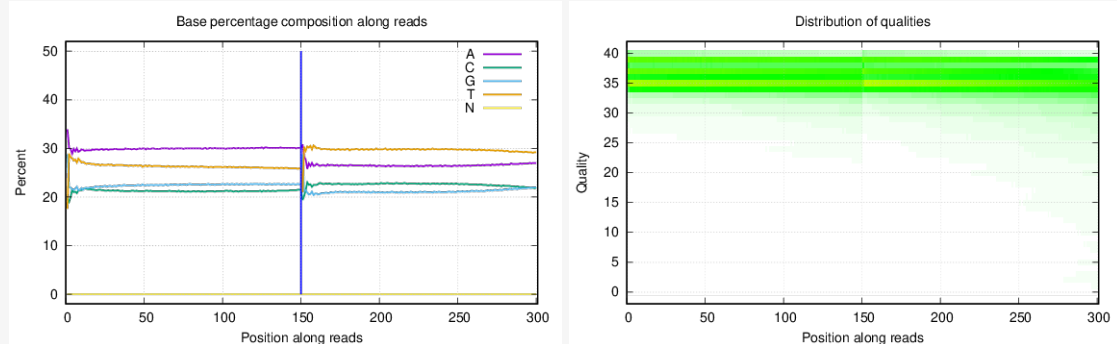
NPC143_R1



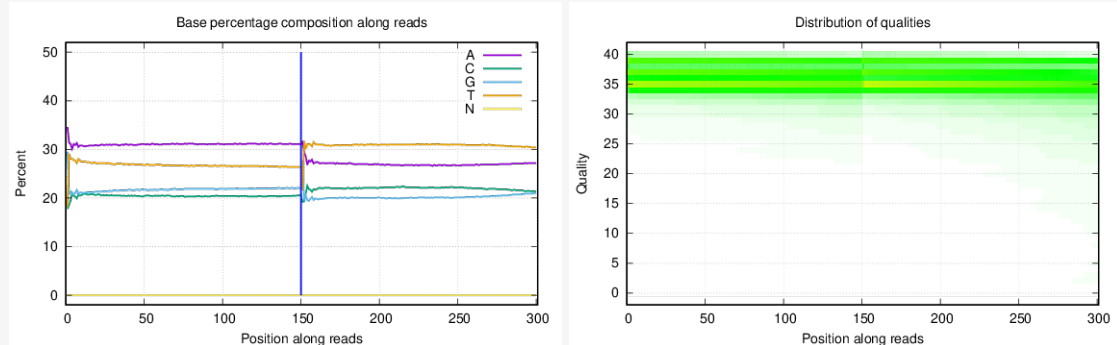
NPC143_R1_in



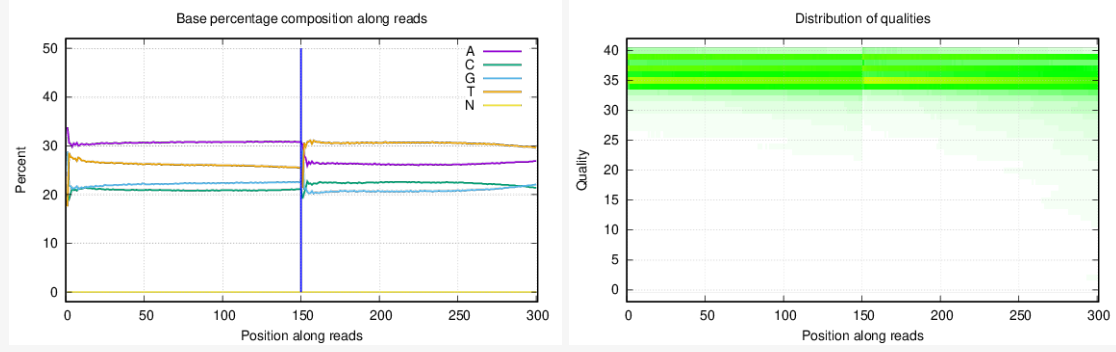
NPC143_R2



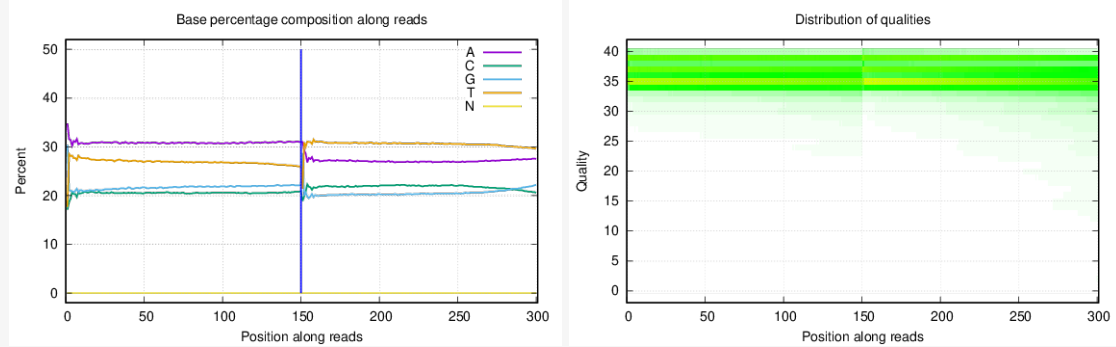
NPC143_R2_in



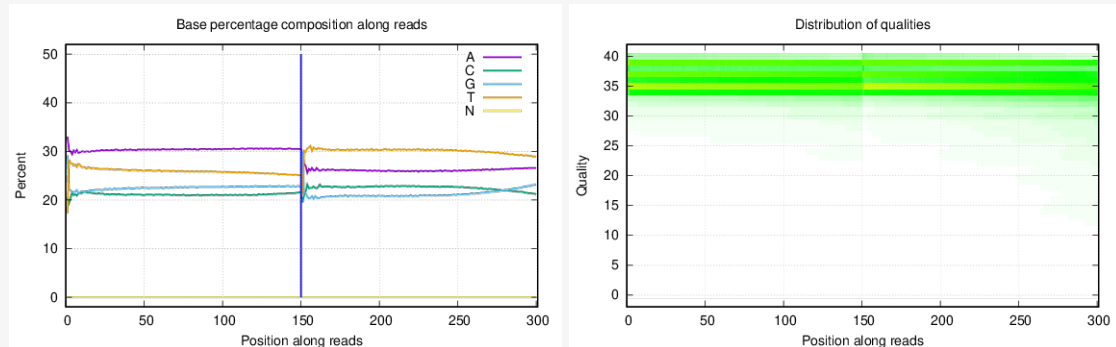
NPC146_7_R1



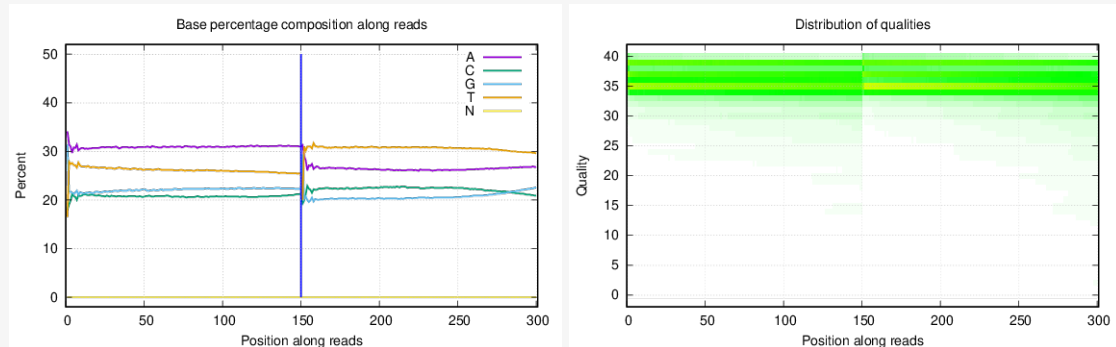
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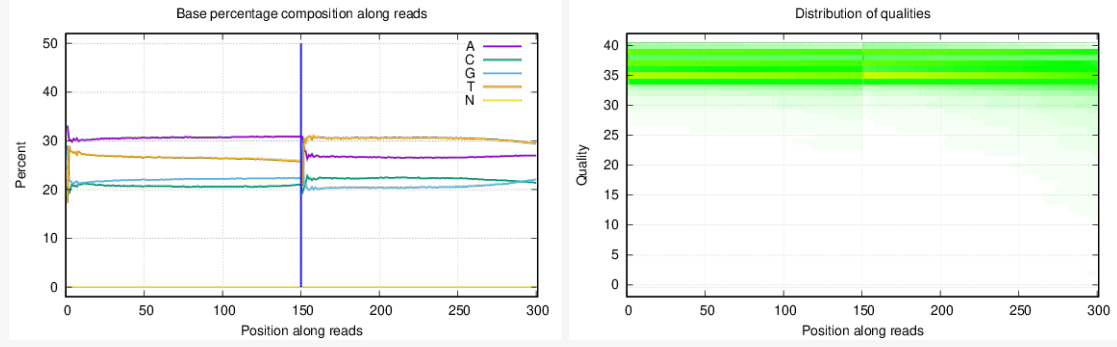
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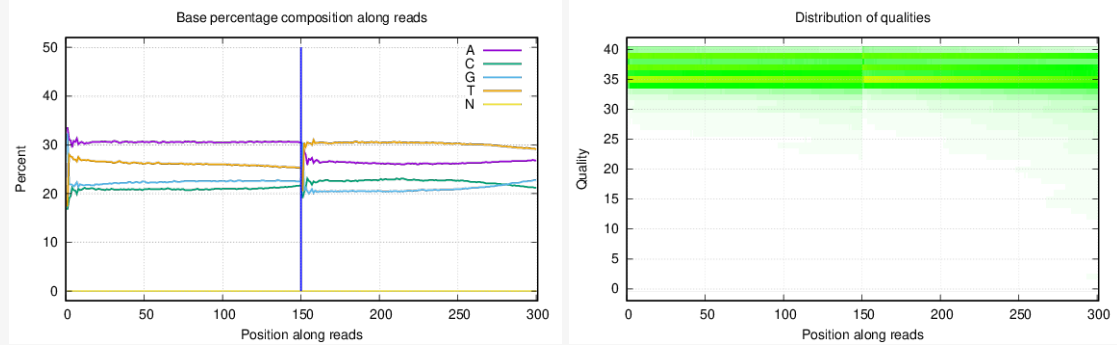
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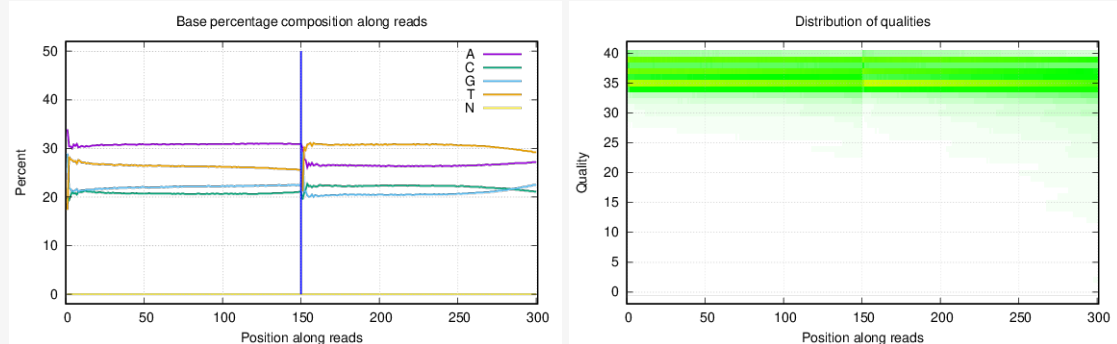
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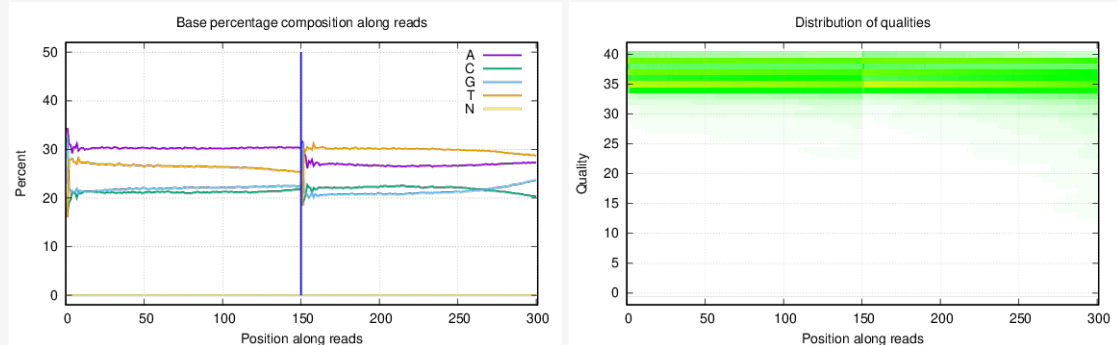
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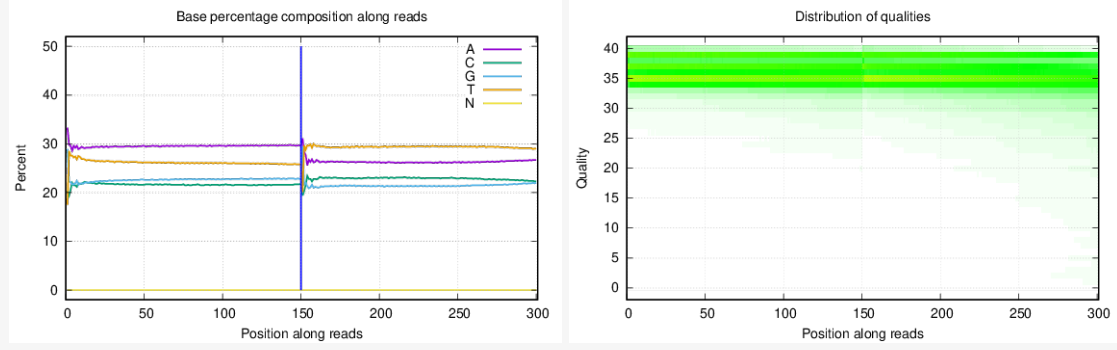
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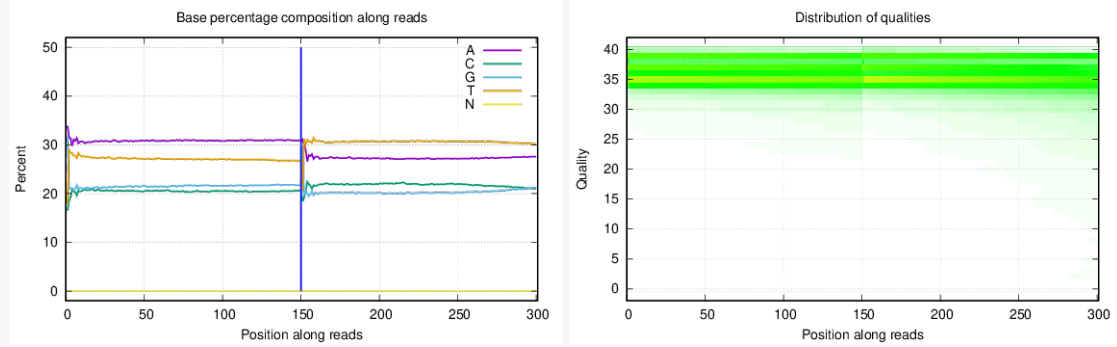
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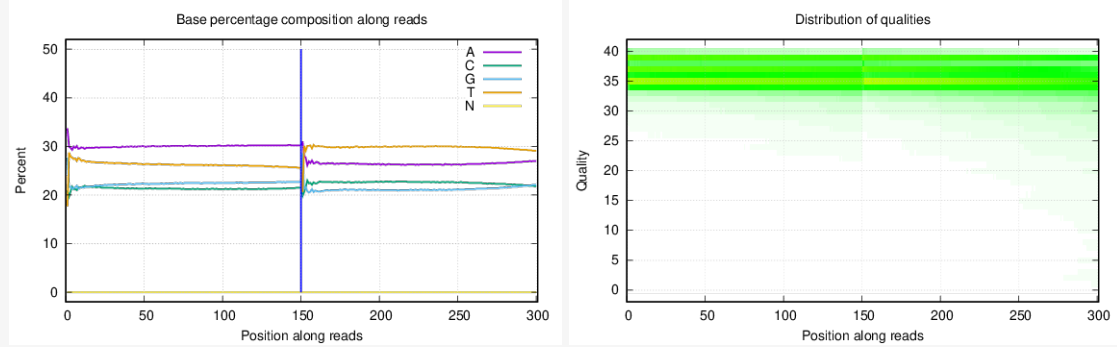
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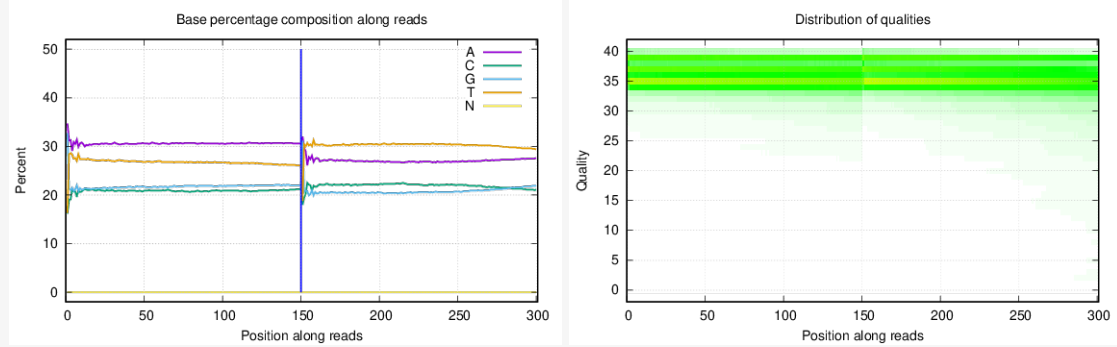
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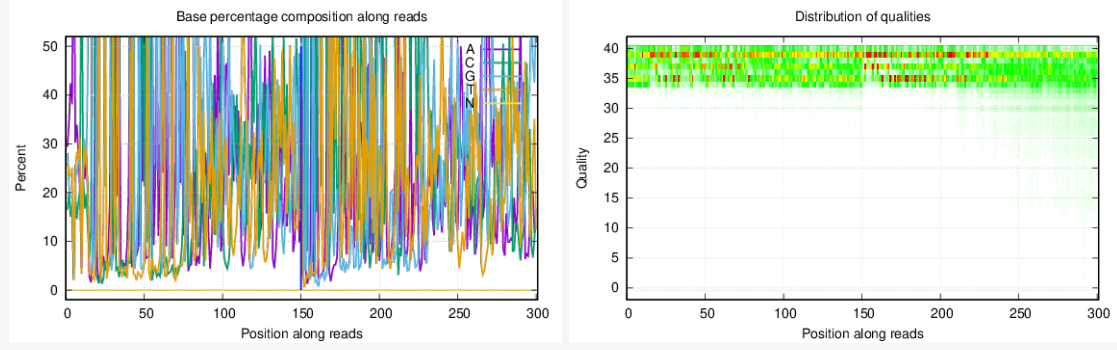
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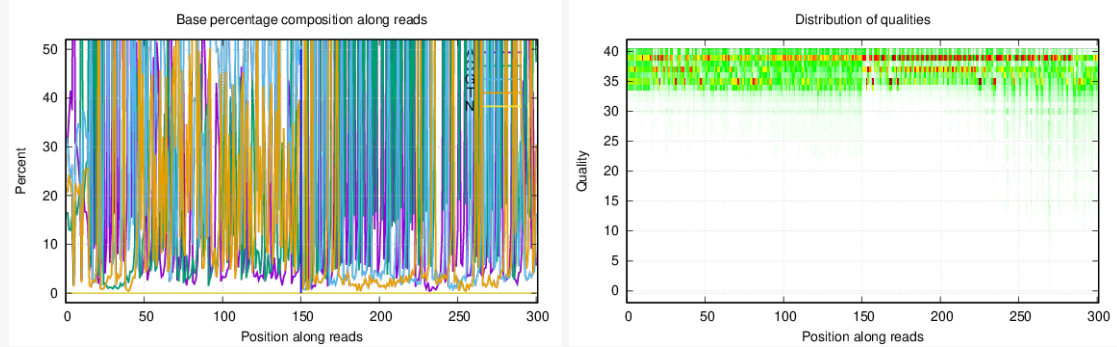
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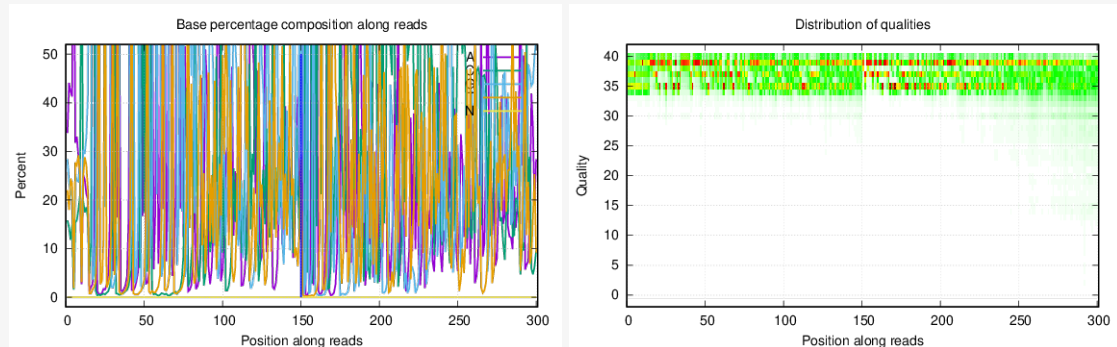
NPC_63-1C16_pp1



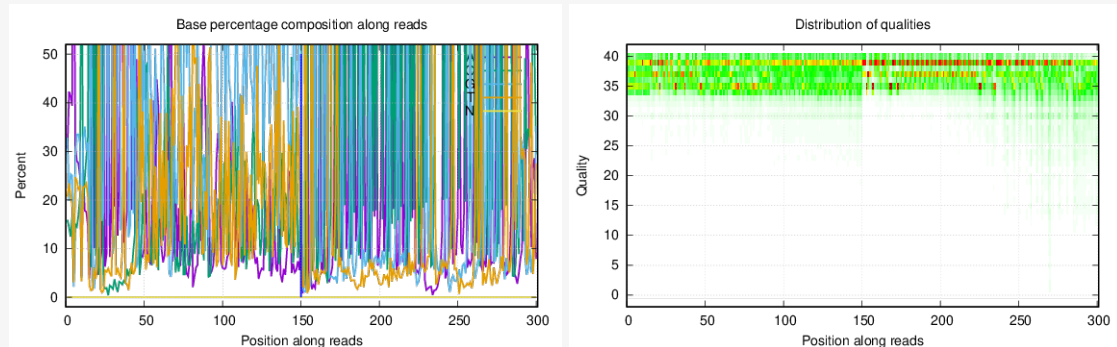
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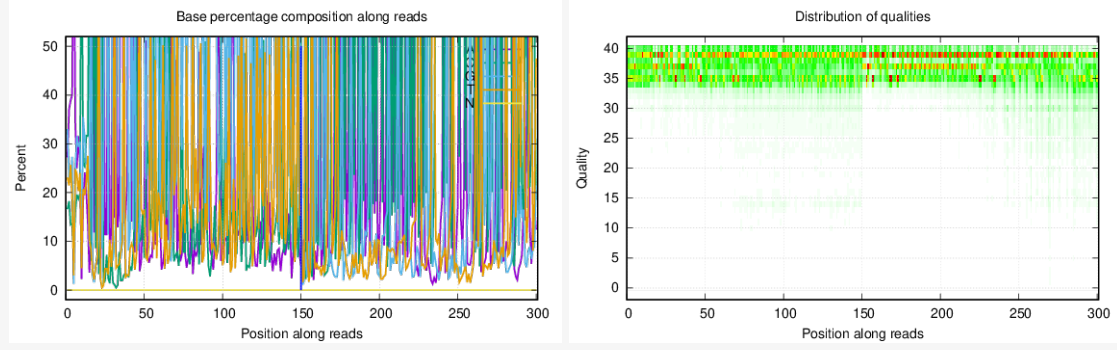
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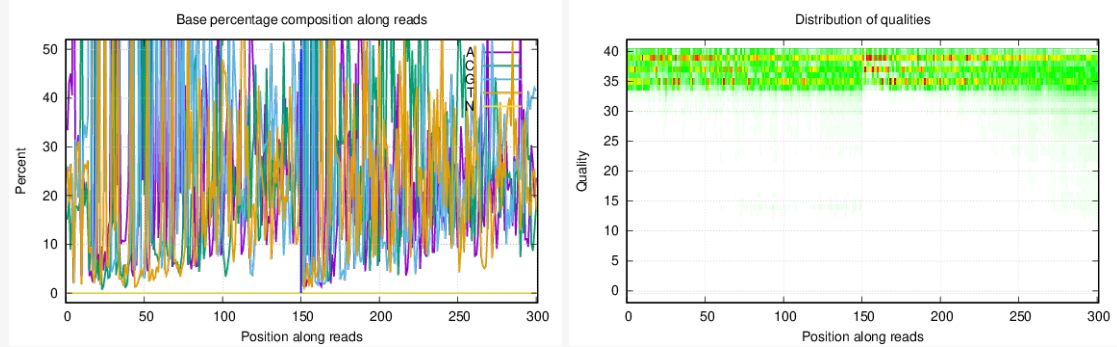
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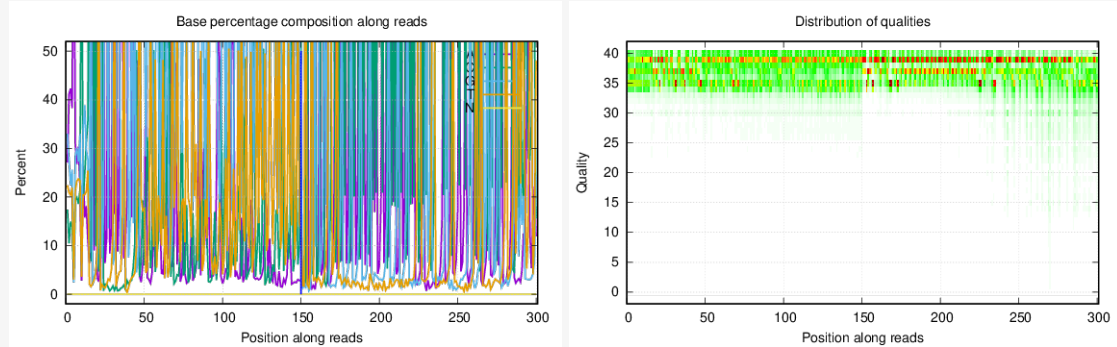
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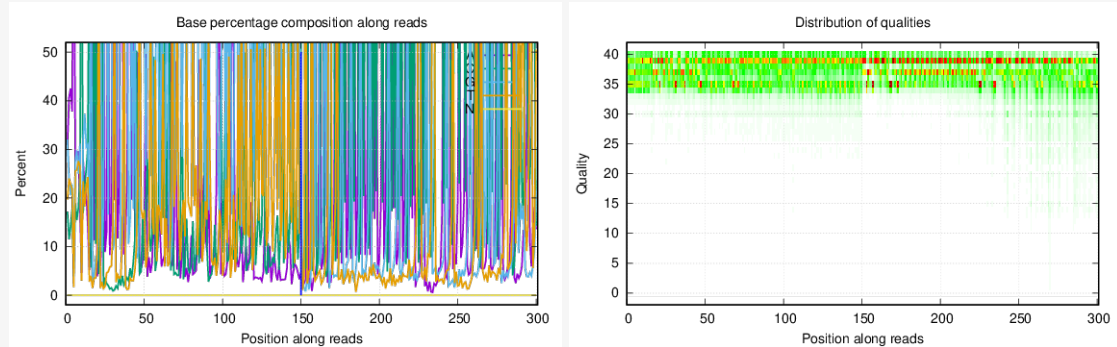
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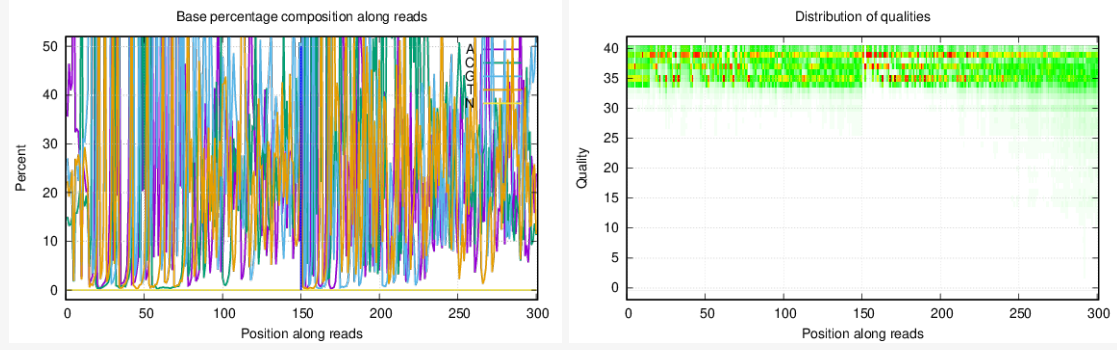
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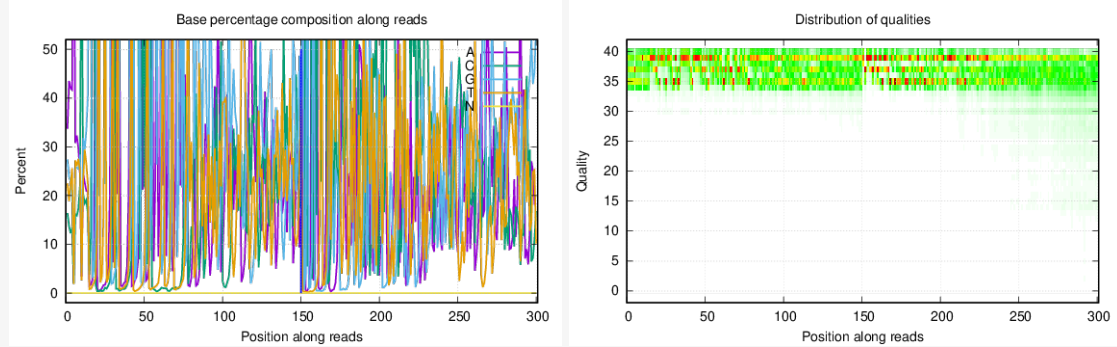
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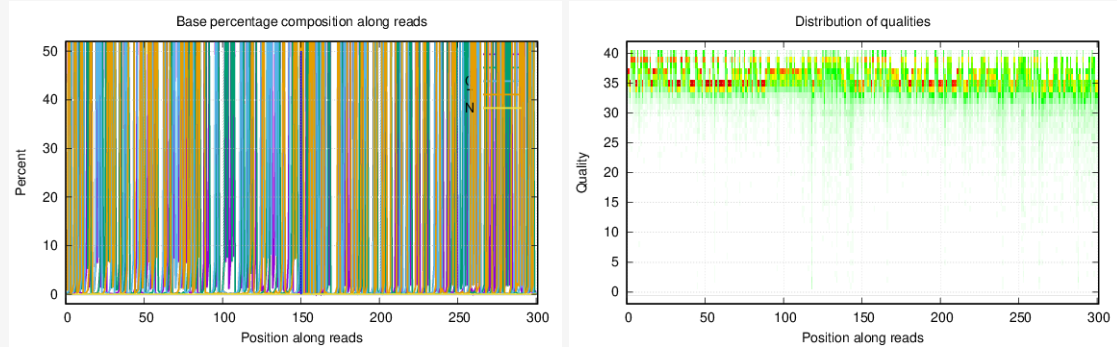
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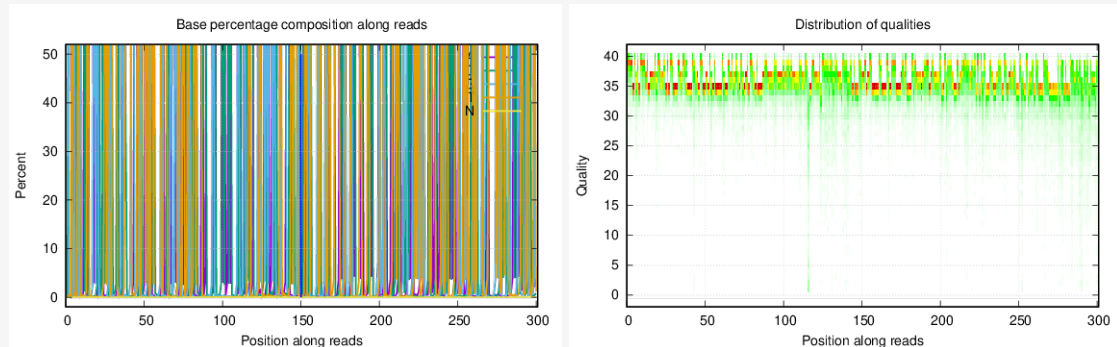
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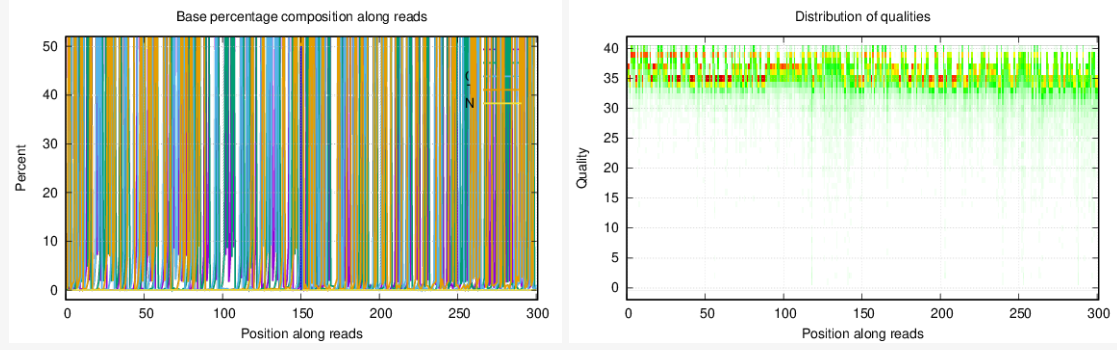
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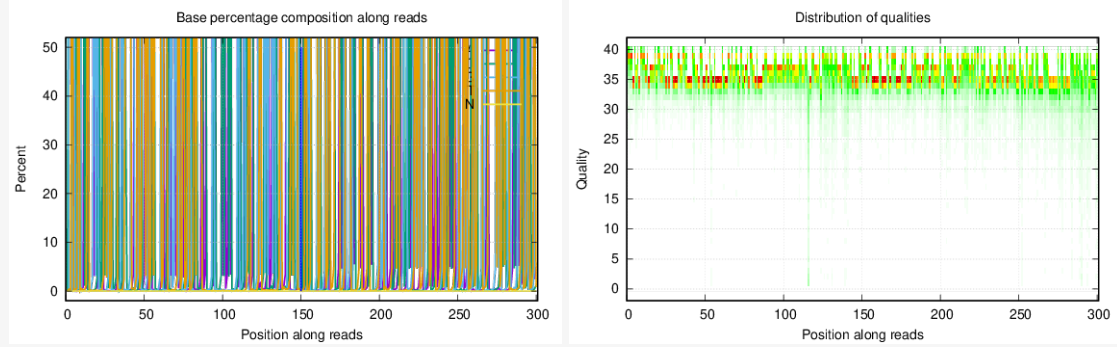
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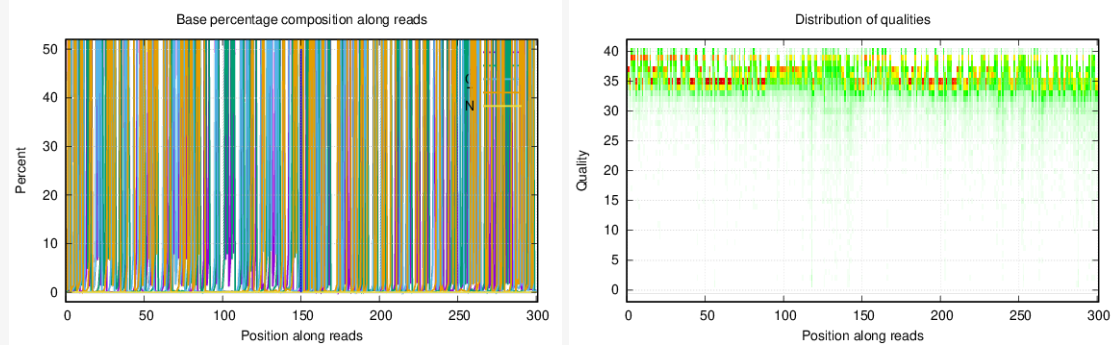
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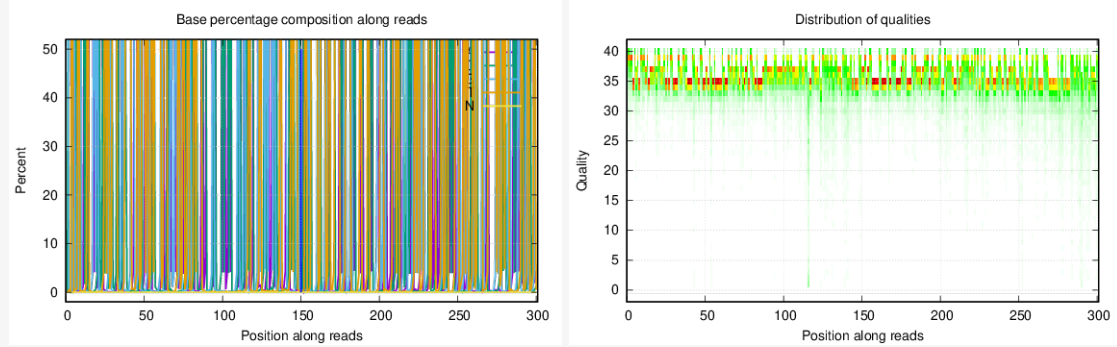
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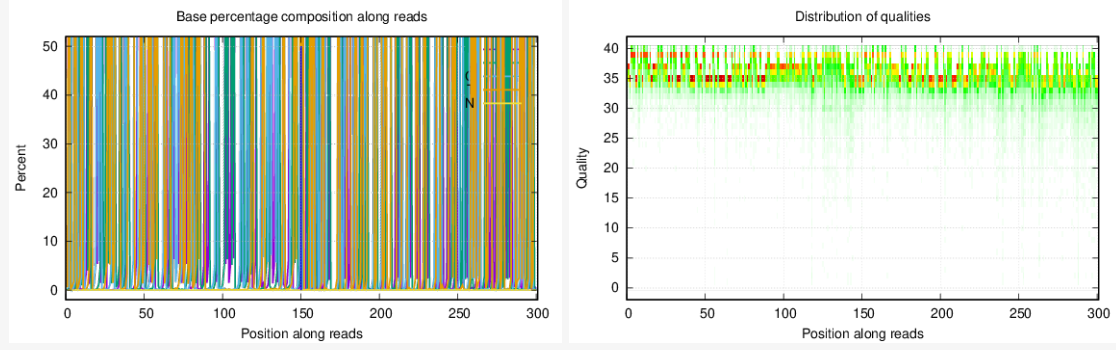
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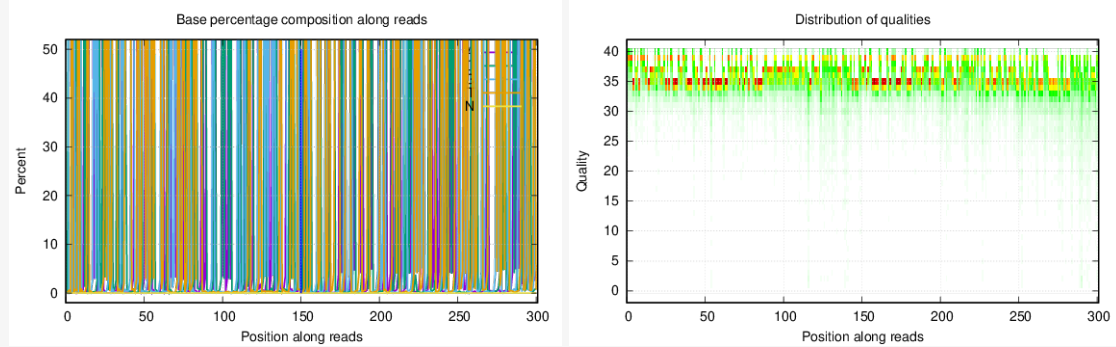
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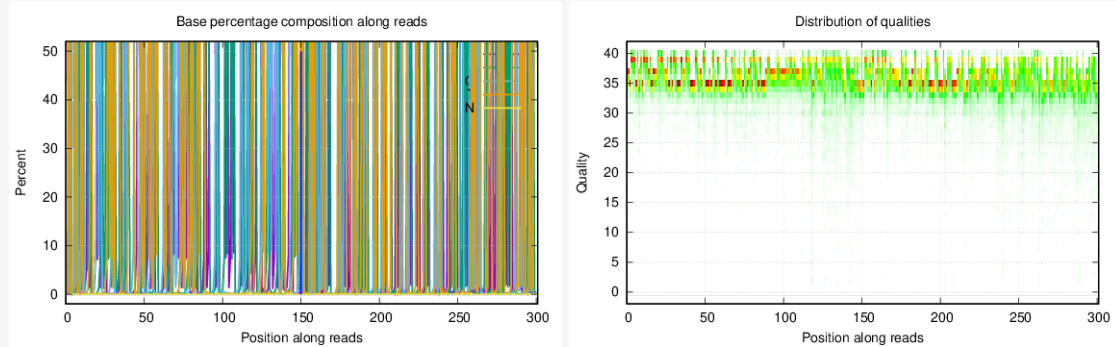
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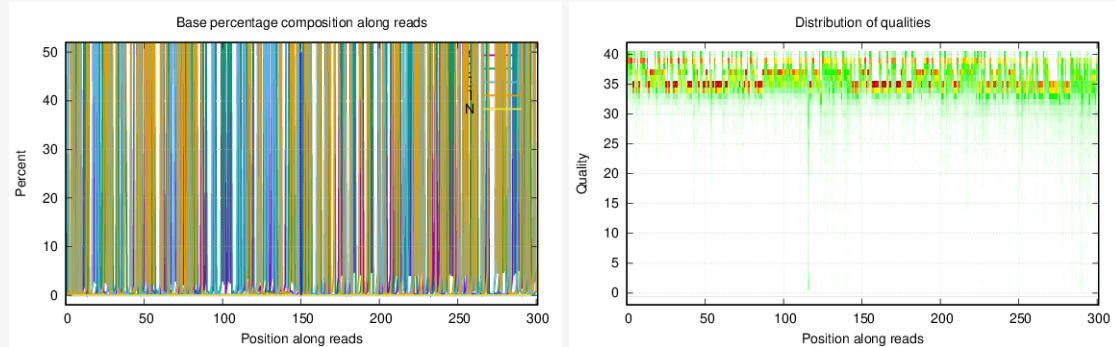
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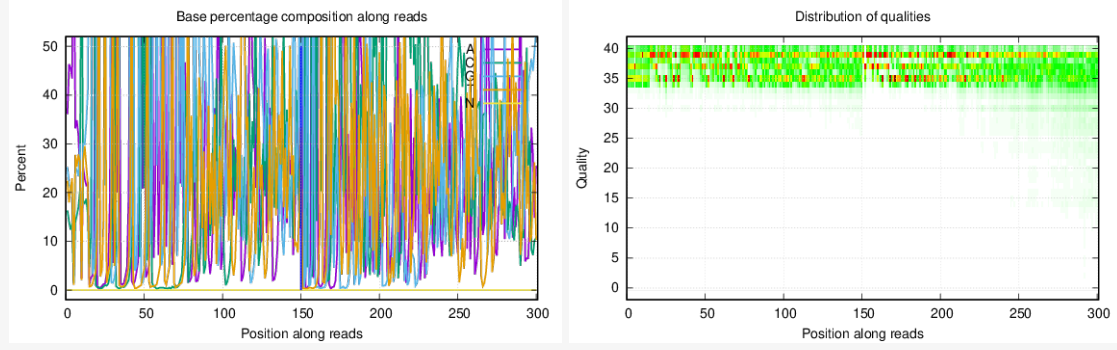
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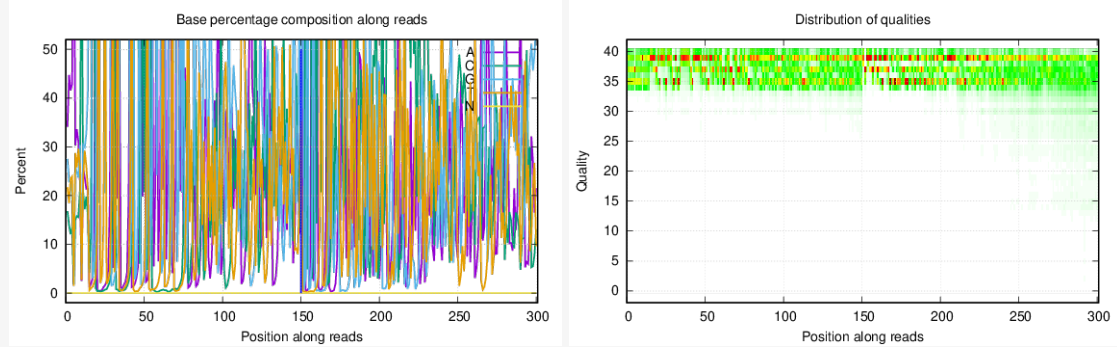
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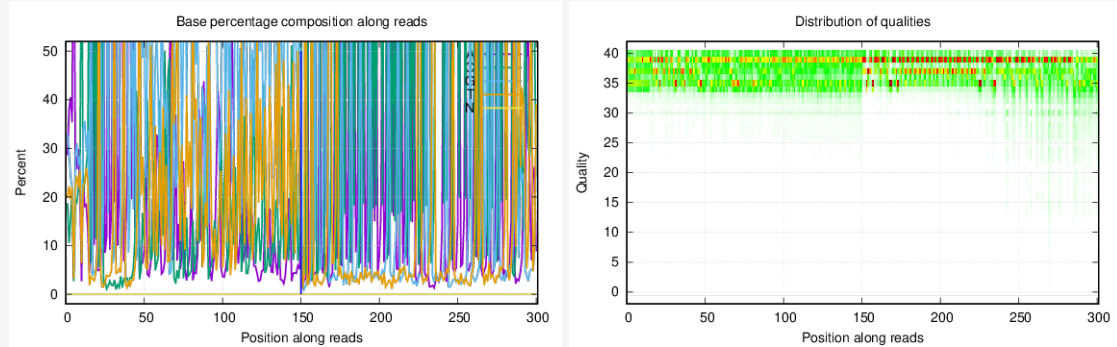
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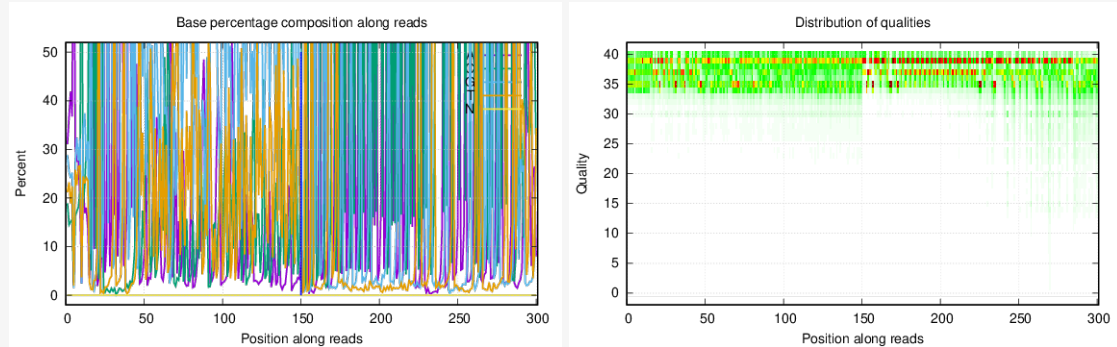
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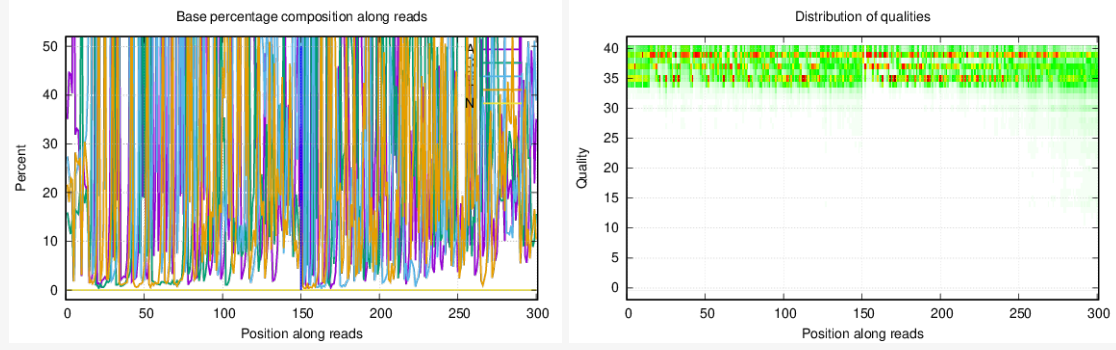
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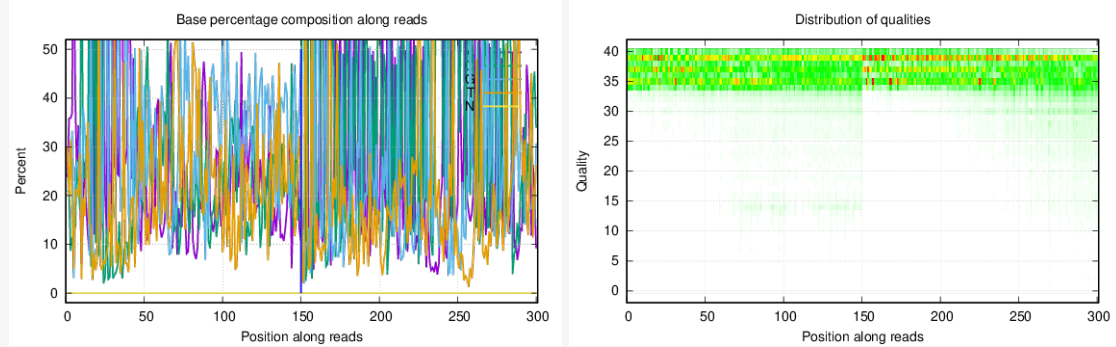
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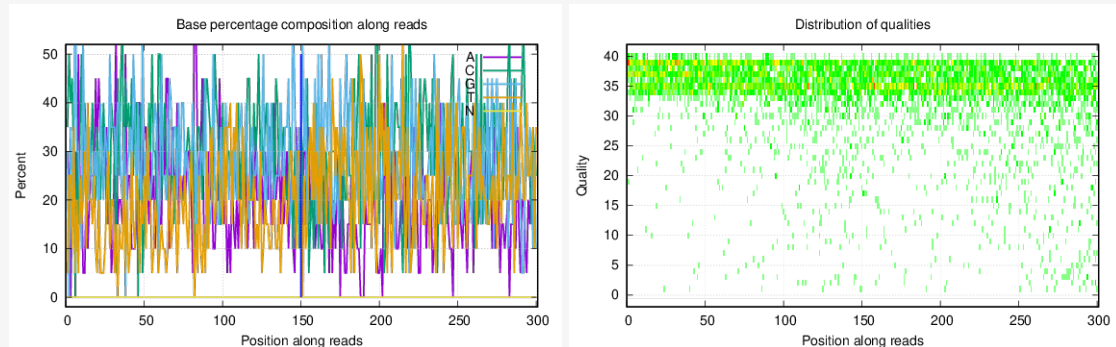
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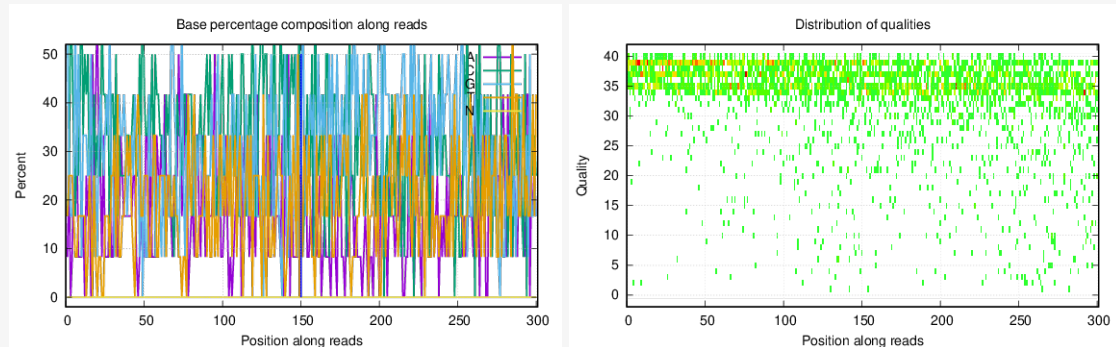
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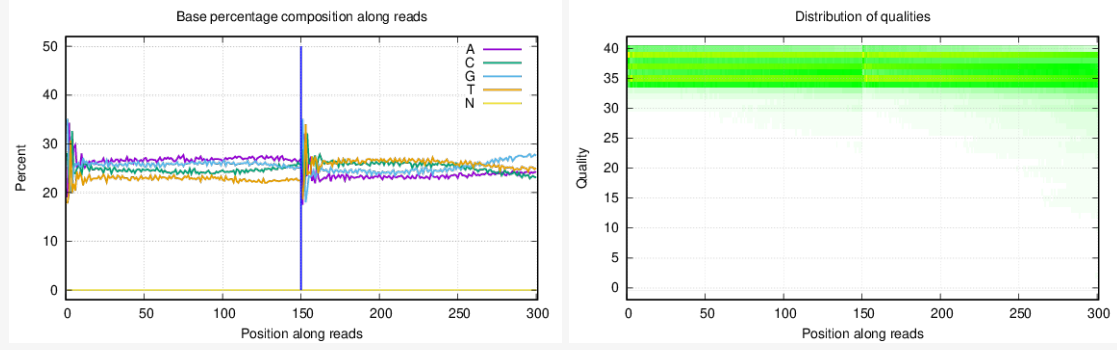
R1



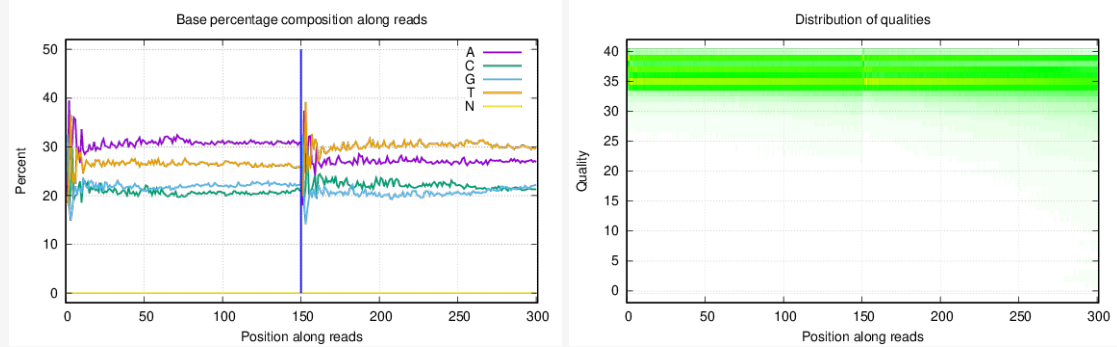
R8



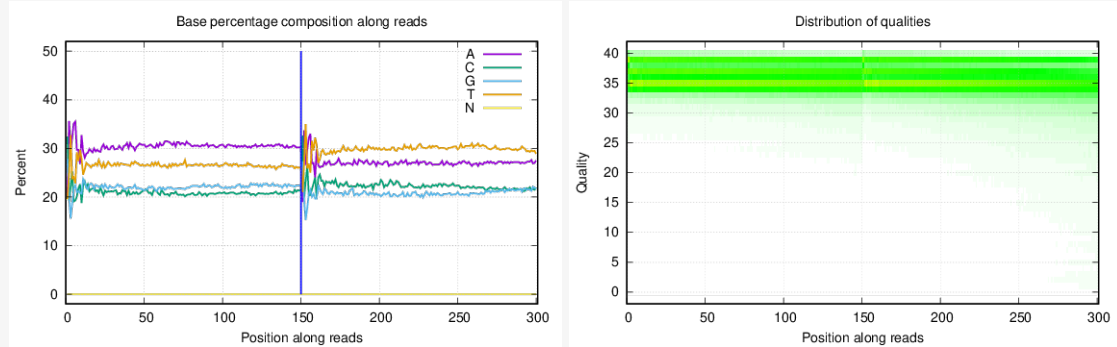
Sach2_K2110



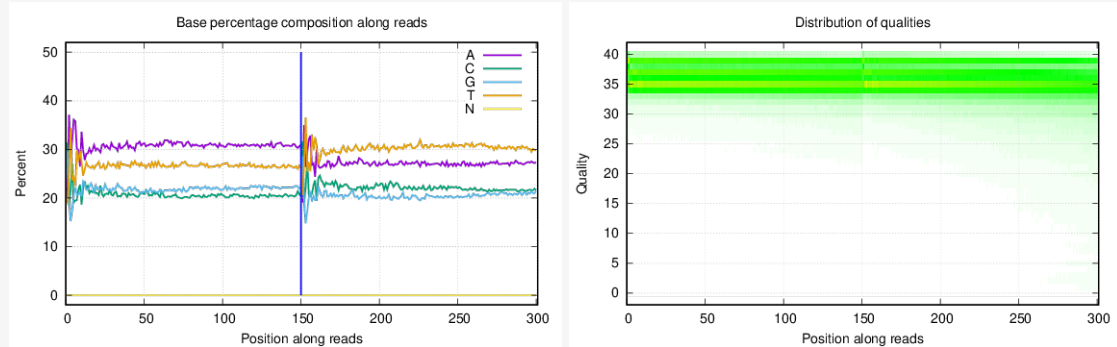
Shur1_K



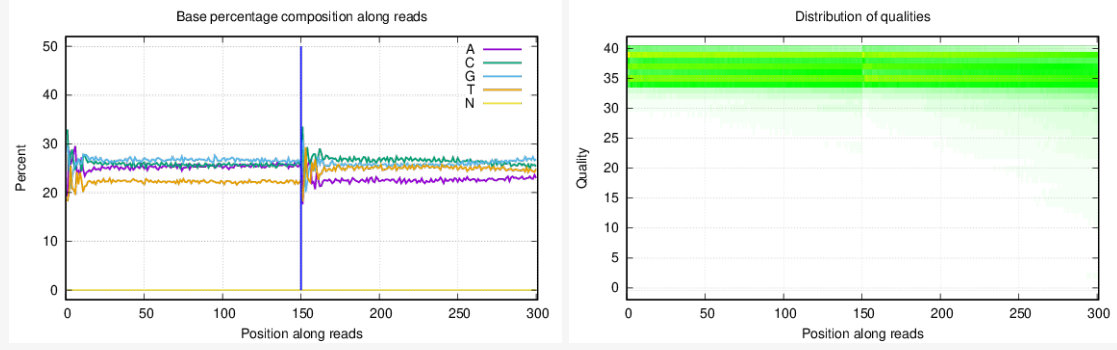
Shur2_K



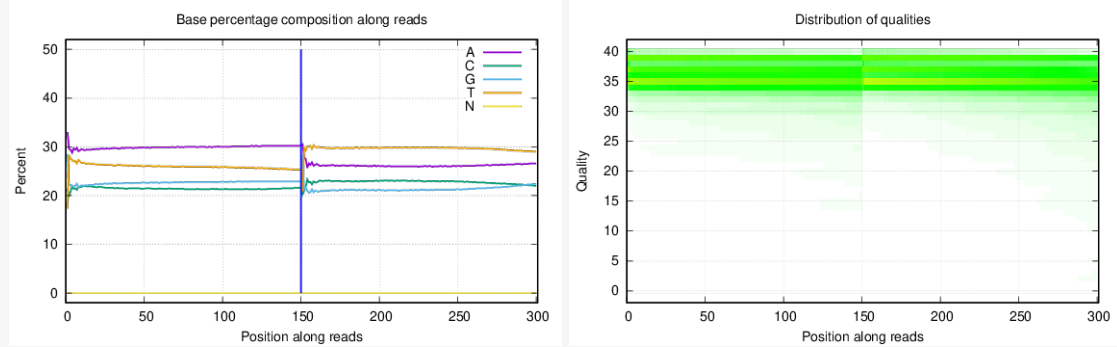
Tok1_K



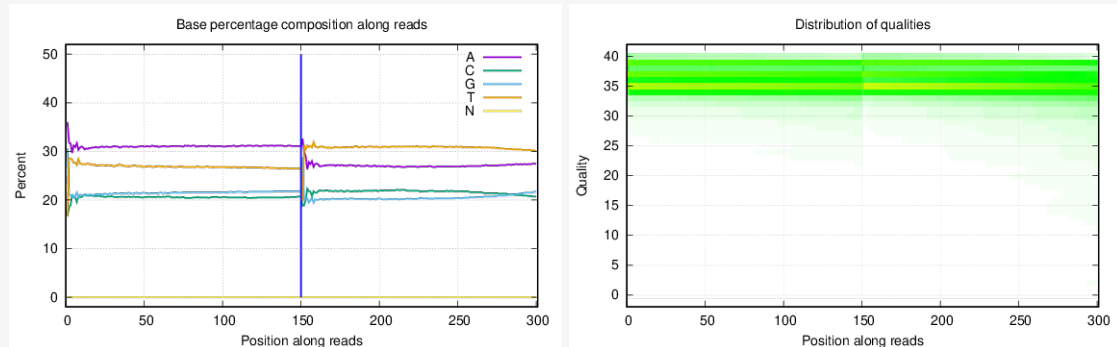
Vor2_K



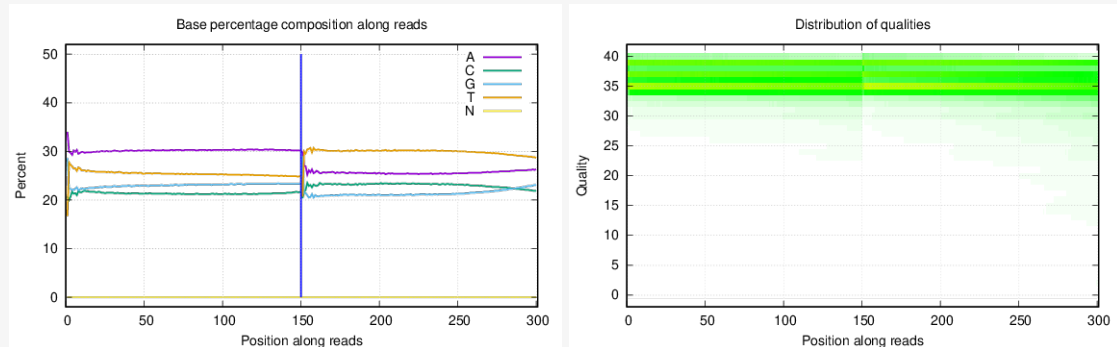
iP146_7_R1



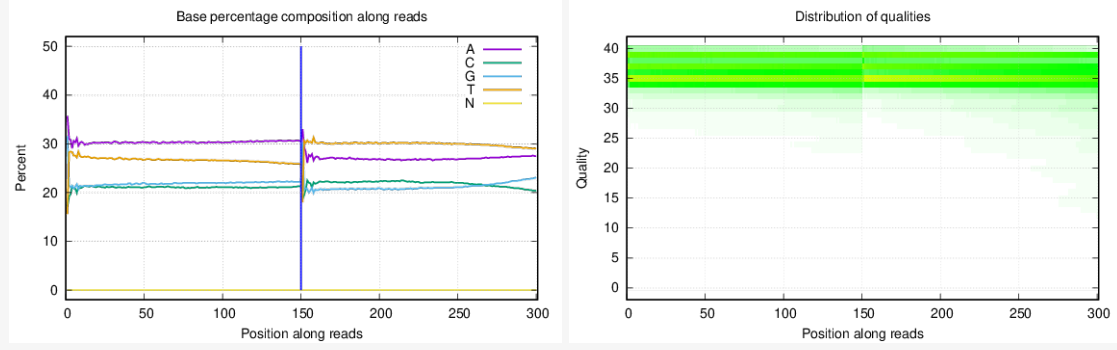
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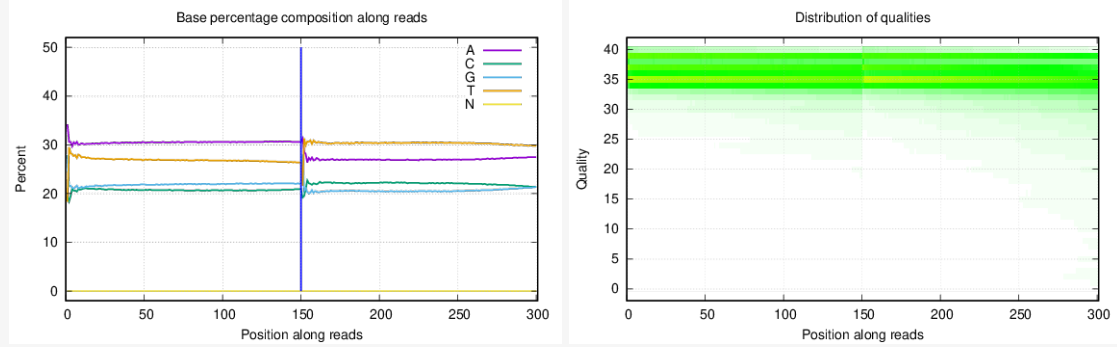
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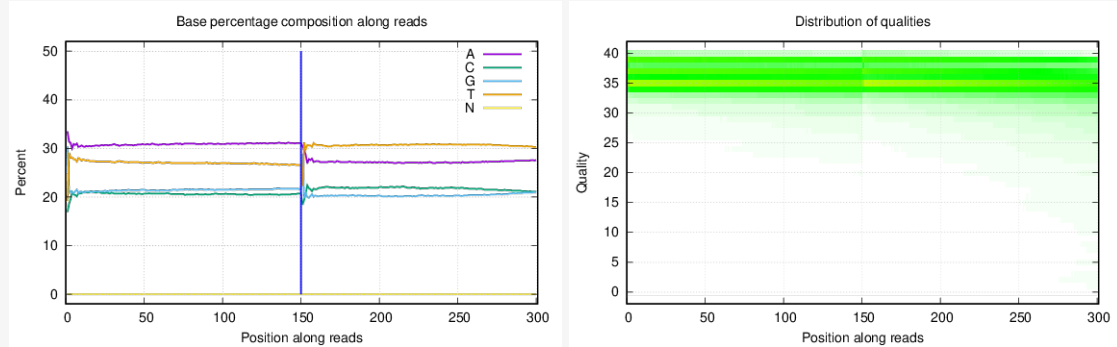
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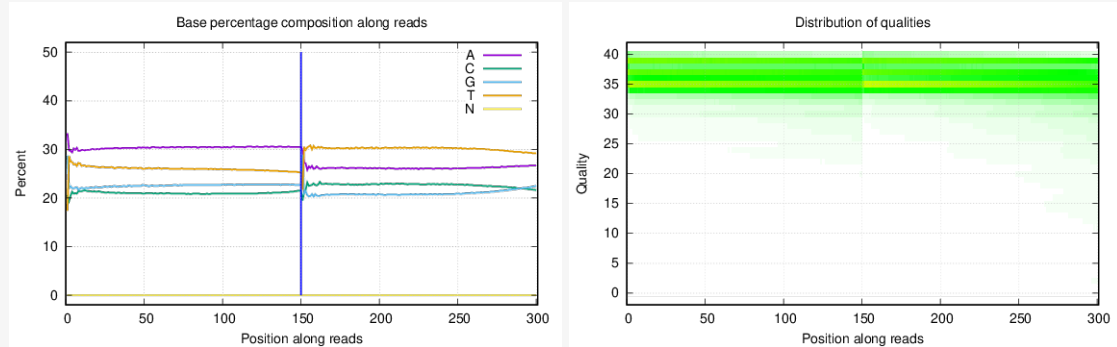
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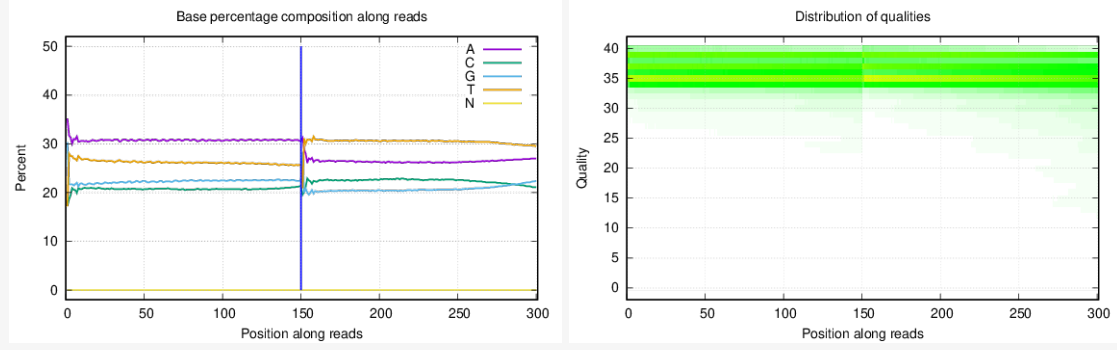
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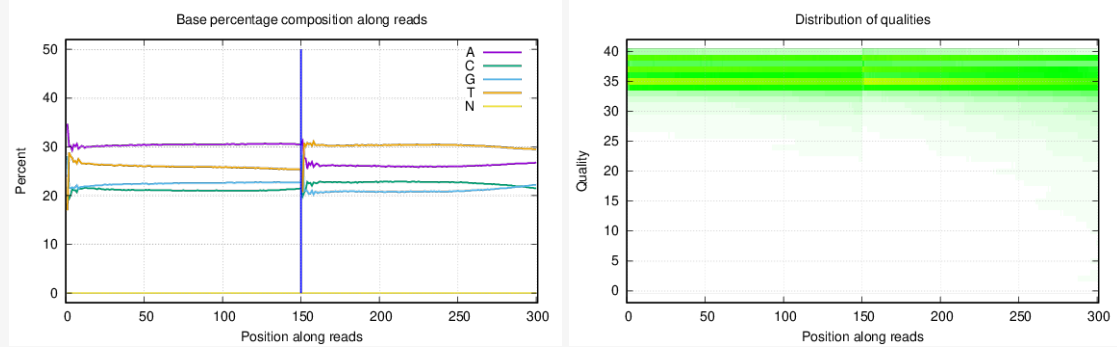
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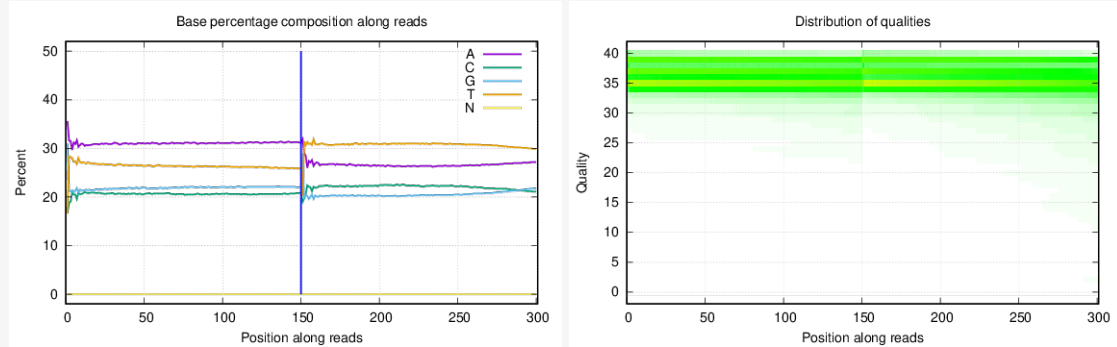
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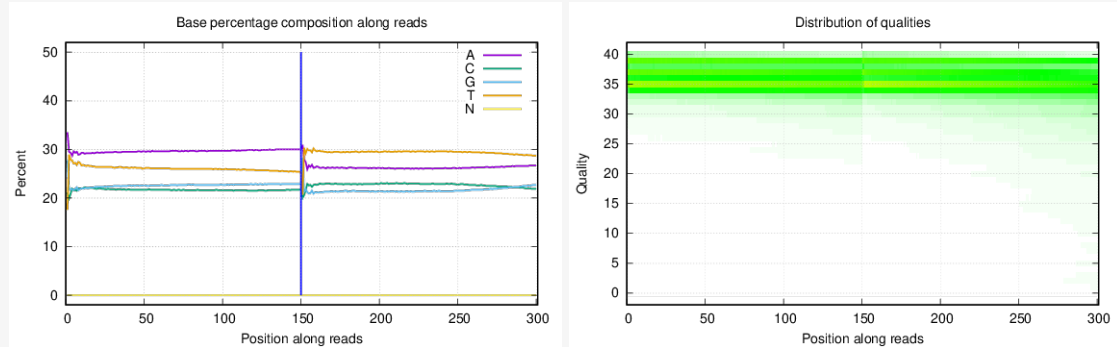
iP181_R1



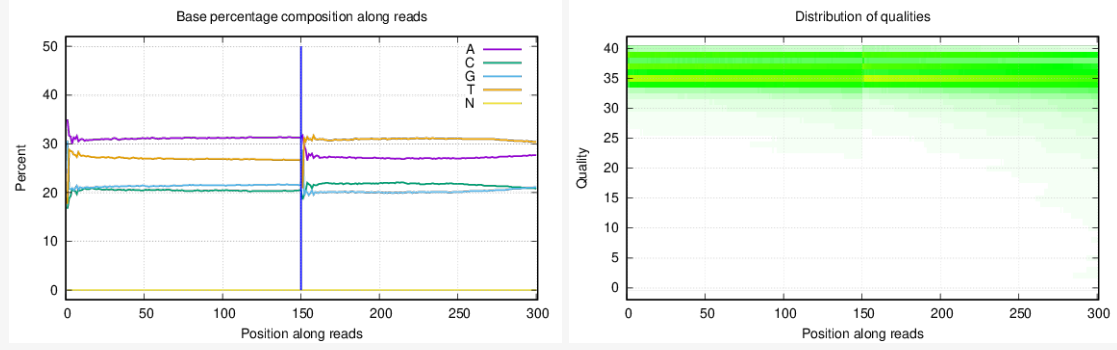
iP181_R1_in



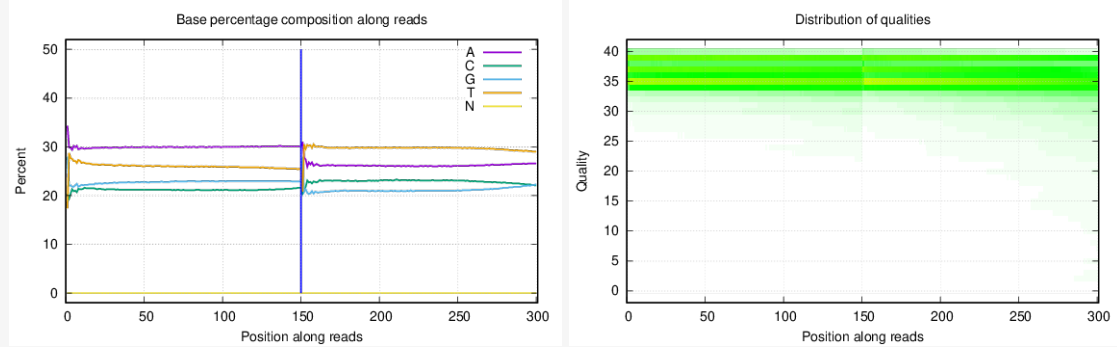
iP181_R2



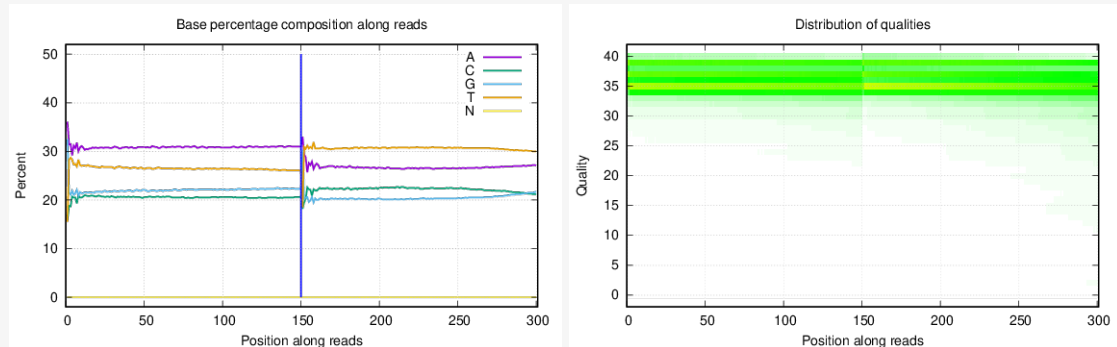
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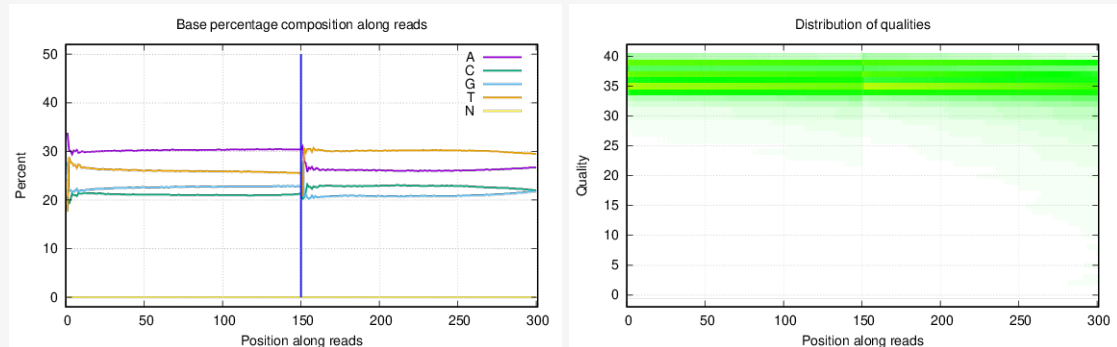
iP1_25_R1



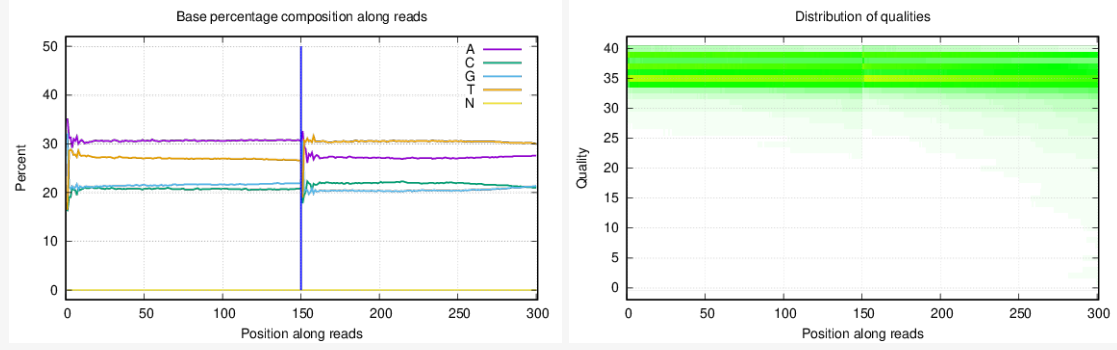
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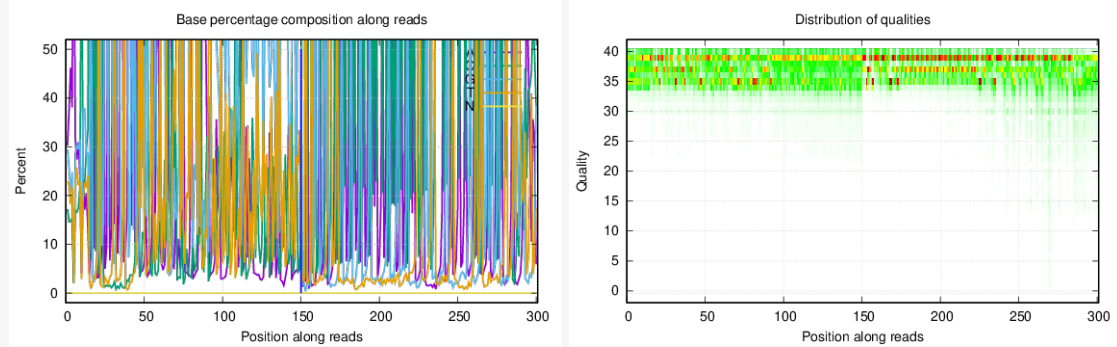
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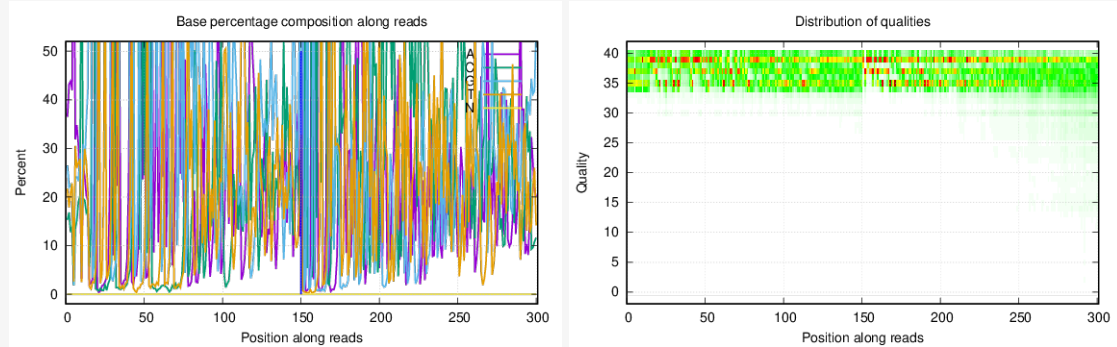
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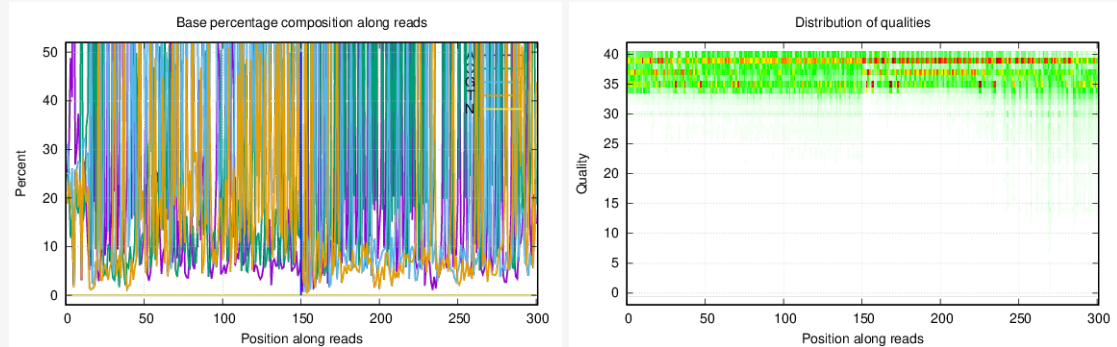
iP63-1C16_pp1



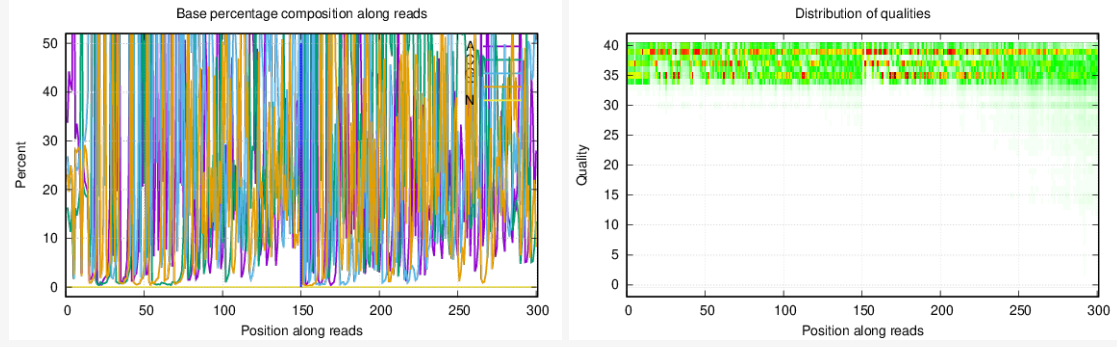
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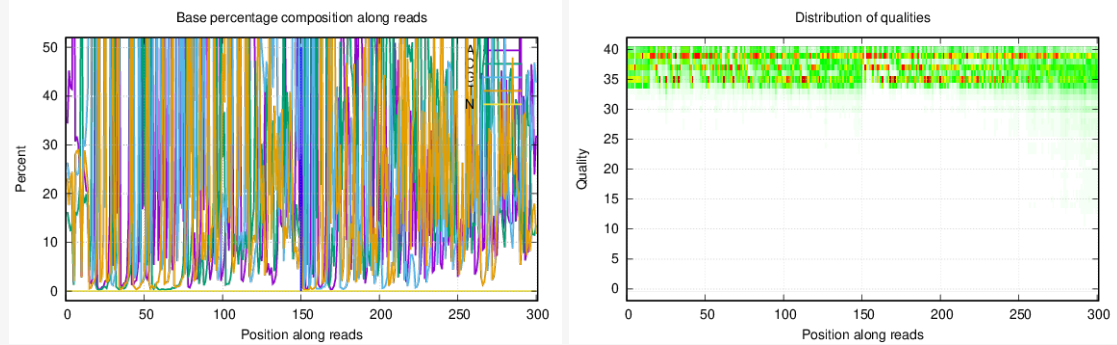
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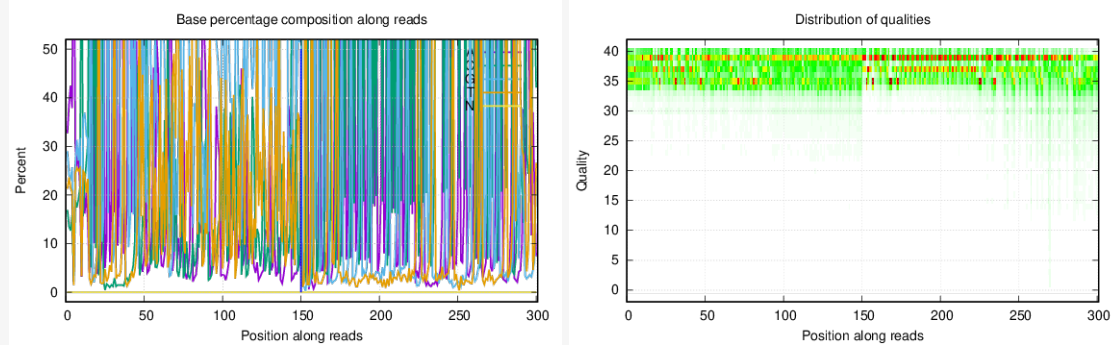
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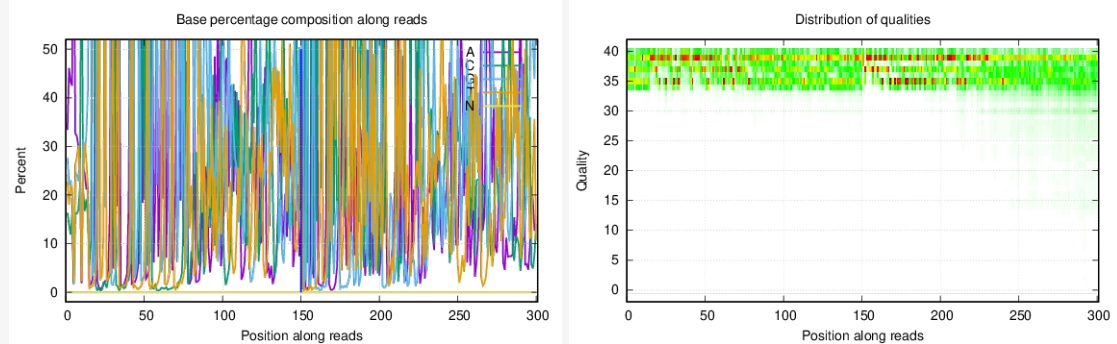
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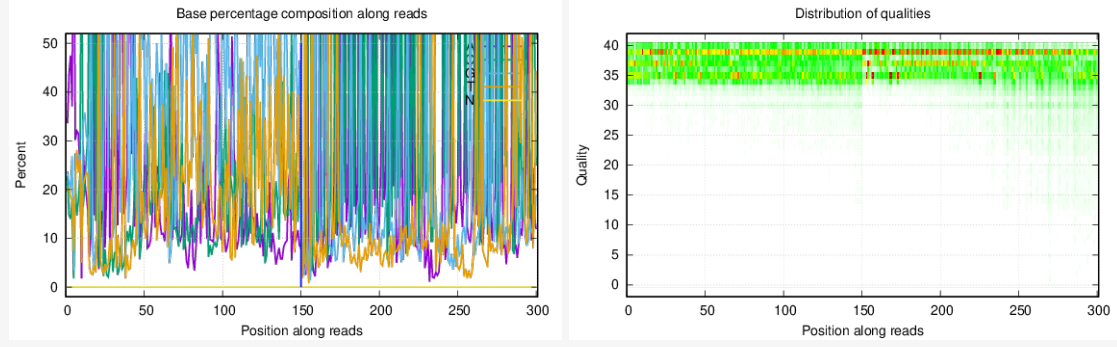
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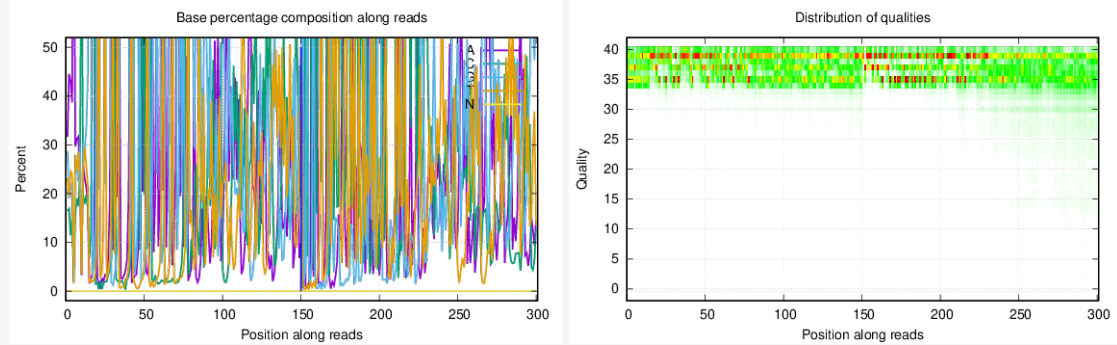
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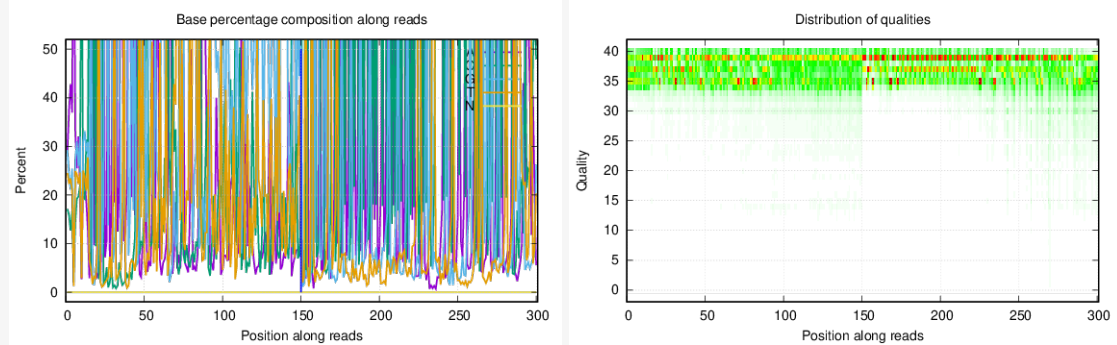
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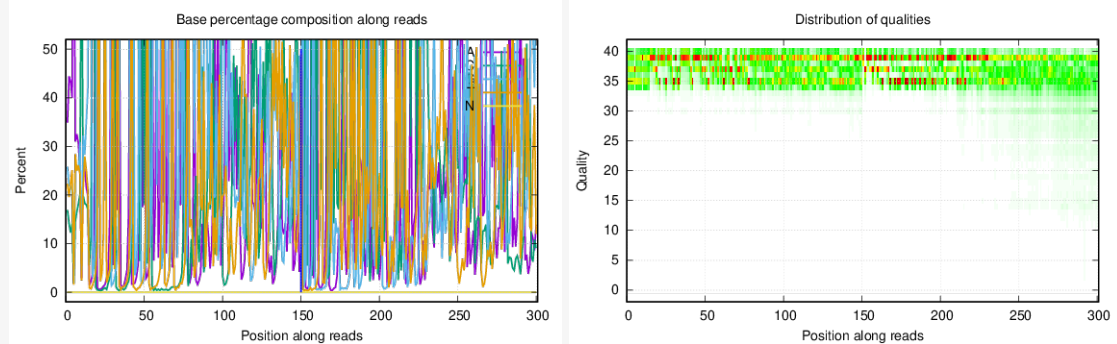
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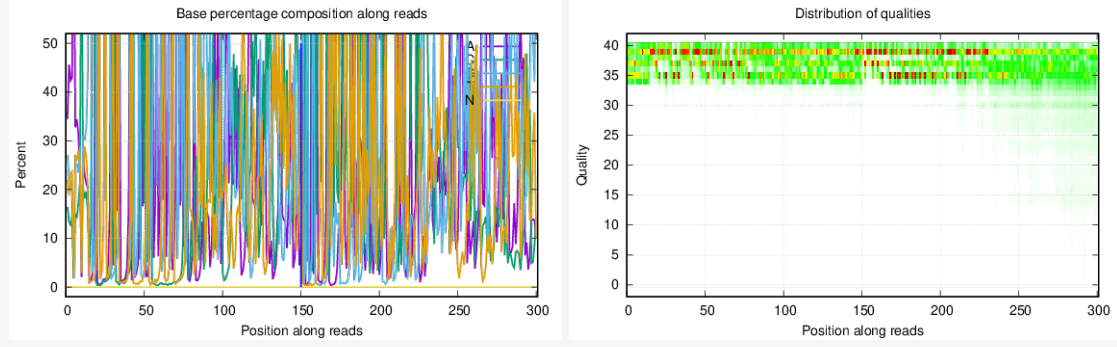
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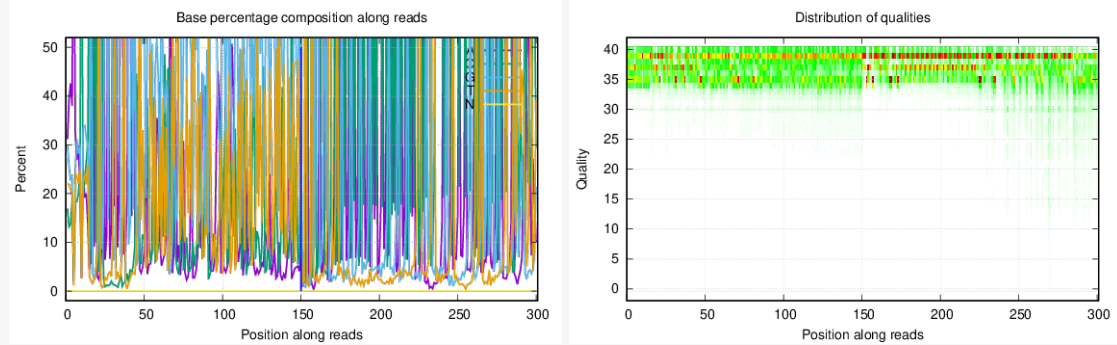
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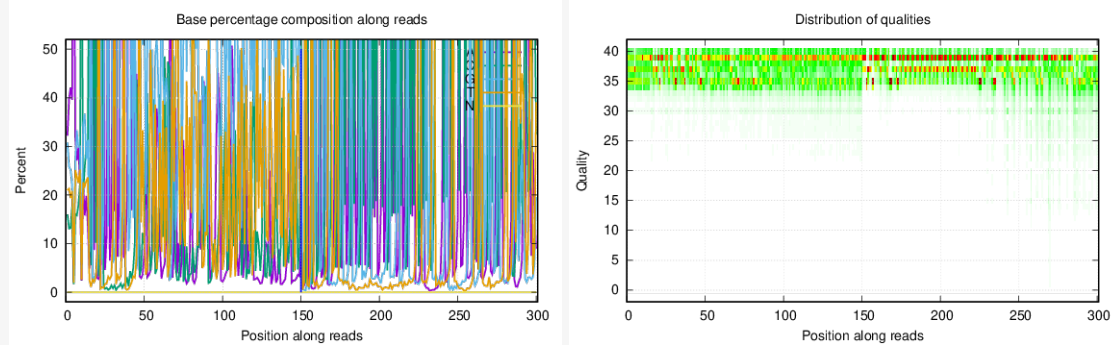
iP63-2C13_pp1_2



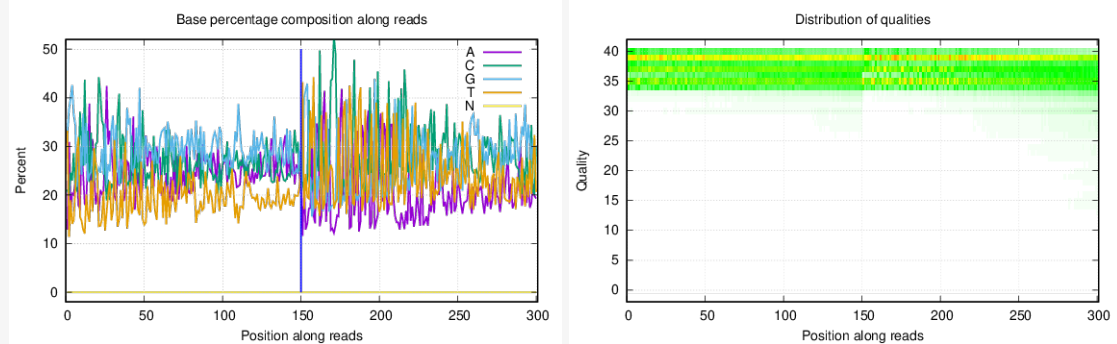
iP63-2C13_pp2



iP63-2C13_pp2_2



worm_rigs



Help Document

The original image data is transferred into sequence data via base calling, which is defined as raw data or raw reads and saved as FASTQ file. Each entry in a FASTQ files consists of 4 lines:

1. A sequence identifier with information about the sequencing run and the cluster. The exact contents of this line vary by based on the BCL to FASTQ conversion software used.
2. The sequence (the base calls; A, C, T, G and N).
3. A separator, which is simply a plus (+) sign.
4. The base call quality scores. These are Phred +33 encoded, using ASCII characters to represent the numerical quality scores.

Here is an example of a single entry in a FASTQ file:

```
@V300029029L1C001R0010000210/1
GCGACCCCAGGTCAGTCGGGACTACCCGCTGAAGTCGGAGGCCAAGCGGT
+
FFFCFFFFFFFFDFEFFFFFFEF0FFFFFFEFFFFFFEFFFFFFECGFFFF
```

The relationship between DNBSEQ sequencer sequencing error rate and the sequencing quality value is shown in the following formula. Specifically, if the sequencing error rate is denoted as "E", DNBSEQ sequencer base quality value is denoted as "sQ", the relationship is as follows:

$$sQ = -10 \log_{10} E$$

Sequencing error rate	Sequencing quality value	Character of Phred +33 quality system
5%	13	.
1%	20	5
0.1%	30	?



Omics For All

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