

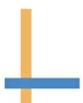


# Sequencing Data Report

Project: F26A430000218\_MUSmyglR

Date: 2026.3.24

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 84 samples in this project, the statistics of fastq data is shown below.

Sample	Length	Q20(%)	Q30(%)	GC Content(%)	Total Reads	Total Bases
10nm_1	150;150	98.71;98.92	95.44;96.09	45.25;44.91	75,033,511	22,510,053,300
10nm_2	150;150	98.28;98.79	94.06;95.64	44.33;44.62	90,764,710	27,229,413,000
13_1_k2	150;150	99.17;99.19	97.08;97.06	50.36;47.12	17,309	5,192,700
13_2_k2	150;150	99.47;99.48	98.29;98.01	49.79;47.28	104	31,200
13_3_k2	150;150	99.0;99.04	96.52;96.63	50.6;47.16	3,718	1,115,400
15_1_k2	150;150	99.19;99.16	97.08;97.04	49.96;46.57	6,240	1,872,000
15_2_k2	150;150	99.17;99.16	97.07;97.05	50.02;46.7	3,609	1,082,700
15_3_k2	150;150	99.26;99.37	97.36;97.57	49.91;46.59	6,429	1,928,700
15_gLBR	150;150	99.14;99.26	96.97;97.29	49.42;46.26	19,015	5,704,500
7_2_k2	150;150	99.17;99.27	97.11;97.32	50.26;46.94	19,020	5,706,000
7_3_k2	150;150	99.1;99.19	96.9;97.06	50.22;46.81	14,898	4,469,400
Aux_1	150;150	98.22;98.69	93.86;95.31	43.89;43.72	49,229,211	14,768,763,300
Aux_2	150;150	98.36;98.93	94.29;96.14	44.47;44.53	66,134,657	19,840,397,100
B1	150;150	97.67;99.02	92.66;96.34	35.23;34.53	1,956	586,800
B1_1	150;150	97.95;99.1	93.44;96.64	35.6;34.77	1,879	563,700
B1_10	150;150	97.87;98.96	93.06;96.36	35.64;34.92	1,230	369,000
B1_12	150;150	97.61;99.09	92.7;96.53	35.67;34.96	804	241,200
B1_3	150;150	97.44;98.74	92.23;95.77	41.9;42.13	425	127,500
B1_6	150;150	97.75;99.29	93.32;97.08	37.25;36.1	193	57,900
B1_7	150;150	97.89;98.76	93.34;95.78	36.44;35.4	526	157,800
B2	150;150	98.48;99.29	95.02;97.54	40.68;40.76	1,735	520,500
B2_11	150;150	97.38;98.41	91.96;94.89	44.81;45.53	1,452	435,600
B2_14	150;150	98.11;98.97	94.15;96.73	40.69;40.71	743	222,900
B2_3	150;150	98.13;99.11	94.15;97.08	39.17;39.27	701	210,300
B2_6	150;150	98.04;99.34	94.09;97.57	43.67;43.01	779	233,700
B2_7	150;150	98.11;99.32	94.44;97.53	39.38;39.58	832	249,600
B2_8	150;150	98.06;99.12	93.72;97.01	37.41;37.5	2,301	690,300

## Data Statistics

MBS22_PCR1	150;150	97.8;98.37	93.14;94.64	42.81;43.05	484,605	145,381,500
MBS45_PCR3	150;150	97.94;98.46	93.51;94.92	43.38;43.22	770,000	231,000,000
MBS64_PCR4	150;150	97.7;98.4	92.73;94.68	42.79;42.87	834,491	250,347,300
MBS66_PCR2	150;150	97.68;98.28	92.7;94.35	43.15;43.18	600,998	180,299,400
MBS76	150;150	97.62;98.44	92.54;94.78	40.92;41.03	699,558	209,867,400
NPC149_1_STAG2	150;150	96.93;98.48	90.4;94.89	41.64;41.67	14,826,798	4,448,039,400
NPC1_25_STAG2	150;150	97.93;98.68	93.3;95.58	42.55;42.59	18,411,134	5,523,340,200
OE	150;150	0.0;0.0	0.0;0.0	47.33;46.67	1	300
P244	150;150	99.08;99.22	96.8;97.19	45.36;45.22	29,923,450	8,977,035,000
P245	150;150	98.69;99.25	95.42;97.3	44.51;44.89	40,385,193	12,115,557,900
RAD21_1	150;150	99.09;99.09	96.72;96.71	46.05;45.95	89,303,211	26,790,963,300
RAD21_2	150;150	97.16;98.59	90.55;94.98	44.82;44.82	62,296,305	18,688,891,500
T12_23	150;150	97.51;97.35	91.61;91.2	45.79;45.88	1,194	358,200
T12_31	150;150	98.71;99.31	95.48;97.47	45.47;45.82	1,939	581,700
T12_33	150;150	97.76;98.33	92.48;94.55	44.17;44.42	144	43,200
TM_II	150;150	98.81;98.08	96.03;94.77	51.92;51.95	938,346	281,503,800
TM_III	150;150	98.68;98.39	95.66;95.26	50.36;50.56	1,082,436	324,730,800
T_L	150;150	98.62;98.18	95.44;94.6	51.52;51.23	862,723	258,816,900
To_1	150;150	98.48;98.34	94.65;94.5	45.64;45.34	1,305	391,500
To_11	150;150	98.85;99.53	95.86;98.09	46.64;46.71	801	240,300
To_9	150;150	98.77;99.23	95.63;97.0	46.8;46.73	36,346,077	10,903,823,100
Trih_3	150;150	97.53;98.76	92.03;95.64	46.74;46.84	203,123,703	60,937,110,900
Trih_4	150;150	98.64;98.82	95.19;95.35	43.74;42.93	138,431,124	41,529,337,200
brCTCF_FLAG	150;150	97.77;98.14	92.76;93.83	42.4;42.43	15,130,376	4,539,112,800
hCTCF_FLAG	150;150	97.75;98.47	92.73;94.89	42.5;42.57	17,523,850	5,257,155,000
i_MoPh15_TR_Cas	150;150	96.89;97.45	90.13;90.88	45.83;45.91	4,868,412	1,460,523,600
i_MoPh7_DR_Cas	150;150	96.13;97.28	87.75;90.28	46.69;46.7	3,873,019	1,161,905,700
i_MoPh7_VPR_Cas	150;150	96.88;97.72	90.05;91.98	45.85;45.85	7,010,351	2,103,105,300
i_NPC149_1_STAG2	150;150	97.91;98.38	93.39;94.81	42.94;42.96	12,666,602	3,799,980,600
i_NPC1_25_STAG2	150;150	97.99;98.21	93.63;94.43	44.4;44.5	18,188,338	5,456,501,400
i_brCTCF_FLAG	150;150	97.8;98.21	92.97;94.2	44.07;44.27	12,226,444	3,667,933,200

Data Statistics

i_hCTCF_FLAG	150;150	98.07;98.36	93.78;94.72	44.5;44.57	17,326,245	5,197,873,500
mutG261S_a_R5	150;150	97.72;97.44	92.54;91.75	45.65;45.7	1,919,896	575,968,800
mutR29W_R4	150;150	98.28;98.3	94.43;94.53	45.74;45.63	2,097,683	629,304,900
mutY226A_a_R1	150;150	97.23;97.05	91.03;90.35	42.69;42.9	2,537,407	761,222,100
mutY226A_a_R3	150;150	97.05;98.5	90.68;95.13	46.68;46.73	1,952,111	585,633,300
rigs2_11	150;150	98.41;99.15	94.43;96.73	49.45;50.62	44,725	13,417,500
rigs2_14	150;150	98.51;99.13	94.72;96.73	49.1;49.91	63,840	19,152,000
rigs2_17	150;150	98.42;99.13	94.44;96.71	49.96;50.82	86,603	25,980,900
rigs2_19_1	150;150	98.36;99.05	94.25;96.5	49.91;50.91	20,093	6,027,900
rigs2_19_2	150;150	98.35;99.03	94.24;96.38	50.03;51.35	46,480	13,944,000
rigs2_2	150;150	98.48;99.08	94.64;96.47	49.94;51.7	77,004	23,101,200
rigs2_20	150;150	98.21;98.89	93.76;95.81	49.46;52.02	34,631	10,389,300
rigs2_3	150;150	98.54;99.18	94.83;96.84	49.68;50.76	123,866	37,159,800
rigs2_5	150;150	97.97;99.12	93.01;96.63	49.32;50.42	82,805	24,841,500
rigs_total_11	150;150	97.94;98.52	92.6;94.23	54.34;41.55	12,219	3,665,700
rigs_total_11v2	150;150	97.85;98.42	92.4;93.96	54.72;41.75	9,801	2,940,300
rigs_total_13	150;150	98.01;98.42	92.87;94.05	53.96;41.36	49,026	14,707,800
rigs_total_13v2	150;150	98.19;98.57	93.42;94.46	54.31;41.39	52,920	15,876,000
rigs_total_14	150;150	98.19;98.3	93.39;93.59	53.59;41.3	42,881	12,864,300
rigs_total_15	150;150	97.93;98.26	92.56;93.36	53.98;41.3	17,940	5,382,000
rigs_total_17	150;150	98.52;98.62	94.48;94.76	54.16;44.73	46,507	13,952,100
rigs_total_2	150;150	97.98;98.46	92.74;94.11	54.42;41.3	33,121	9,936,300
rigs_total_20	150;150	98.07;98.49	92.93;94.1	53.79;41.3	55,194	16,558,200
rigs_total_3	150;150	98.13;98.49	93.21;94.19	53.44;41.33	53,594	16,078,200
rigs_total_5	150;150	98.0;98.57	92.83;94.49	53.65;41.31	46,240	13,872,000
rigs_total_5v2	150;150	98.16;98.66	93.32;94.71	53.59;41.3	30,769	9,230,700

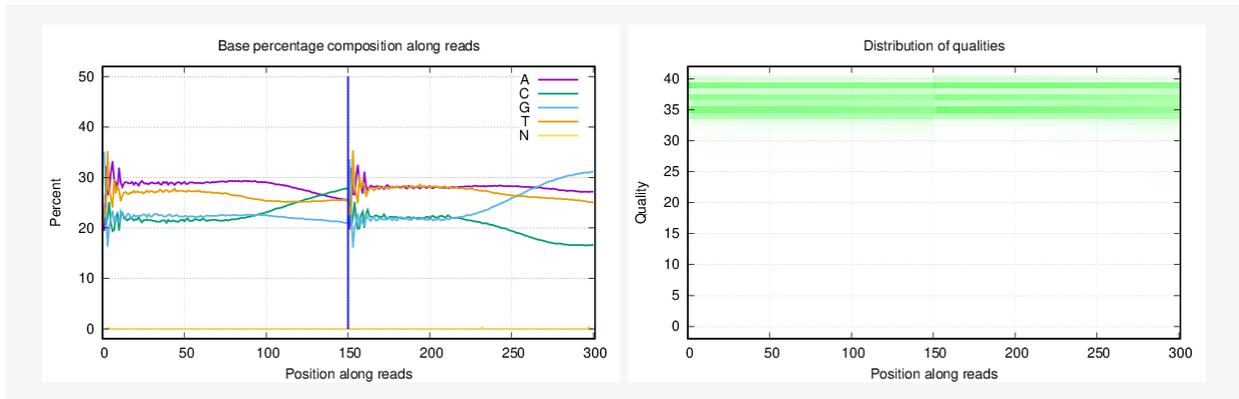
Table Format:

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

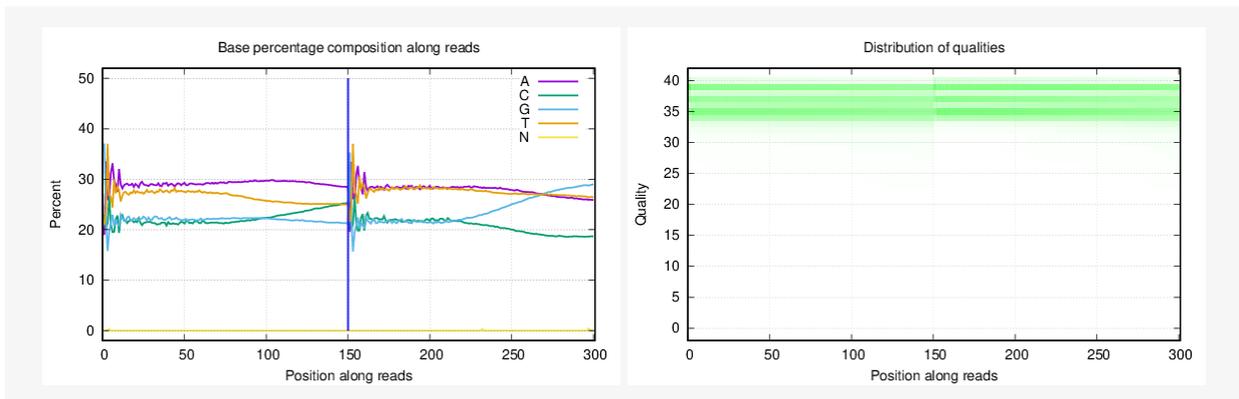
# Data Quality Control

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.

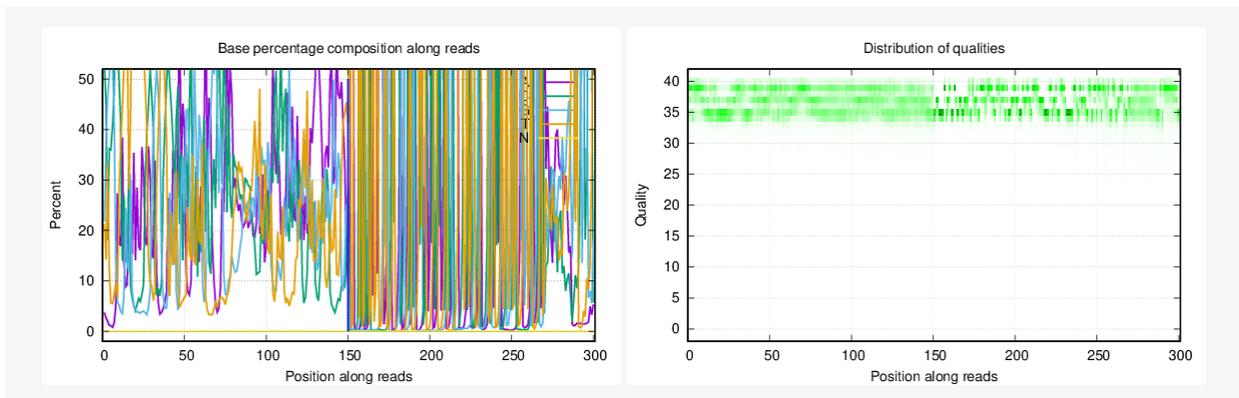
10nm\_1



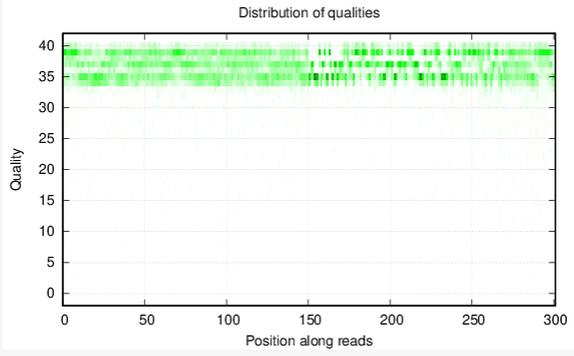
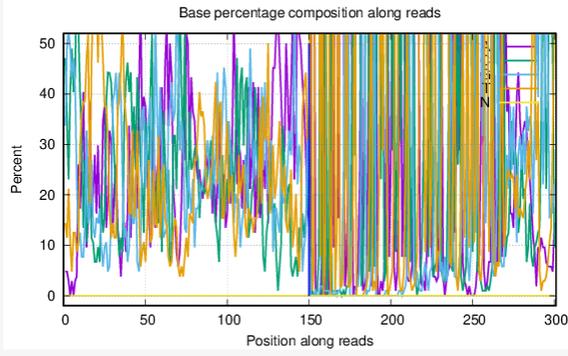
10nm\_2



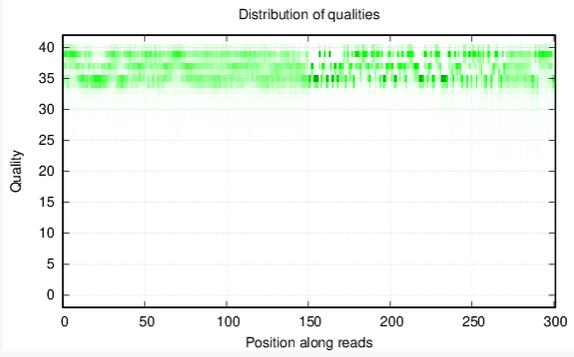
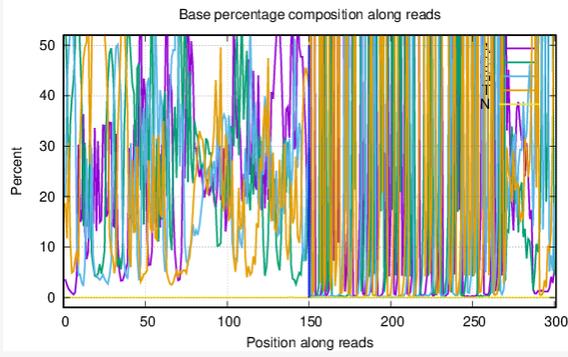
13\_1\_k2



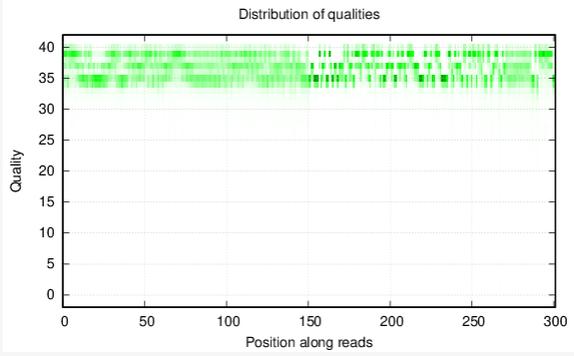
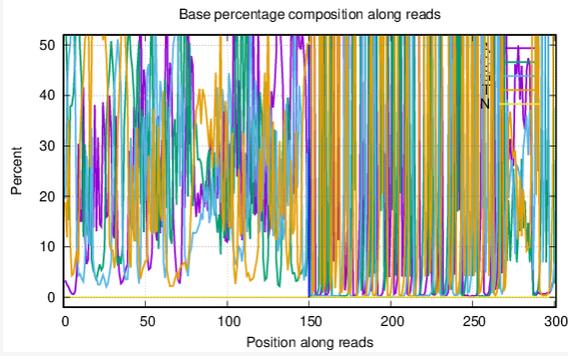
13\_2\_k2



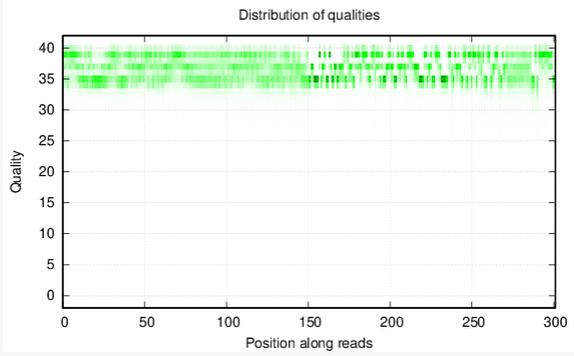
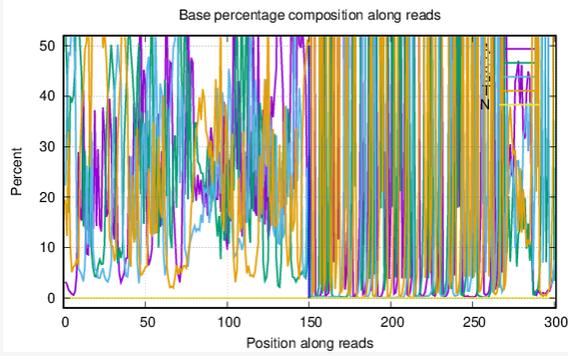
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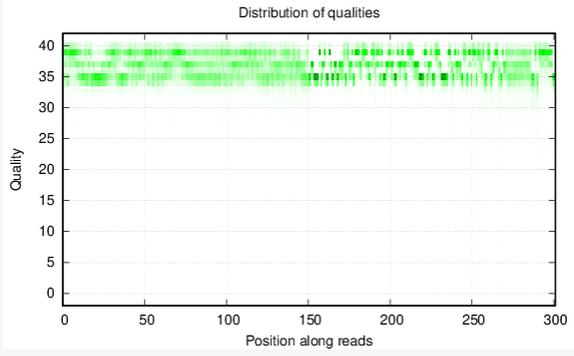
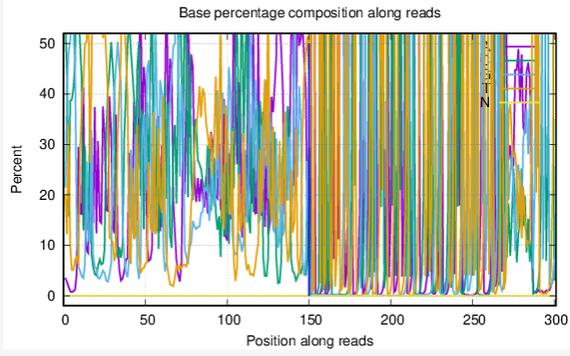
15\_1\_k2



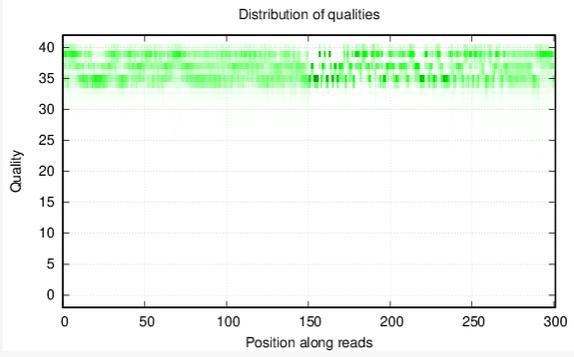
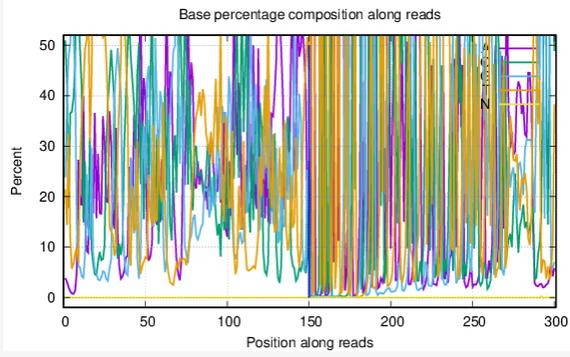
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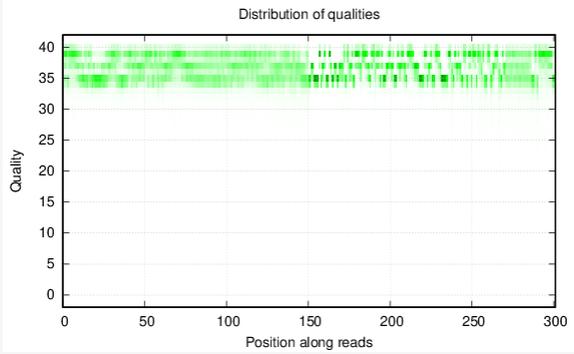
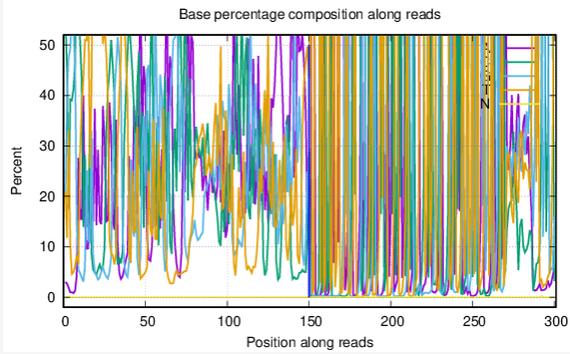
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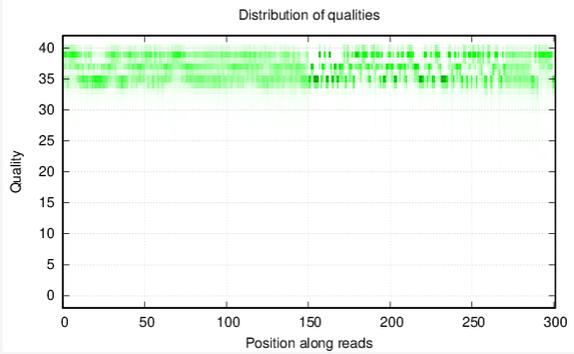
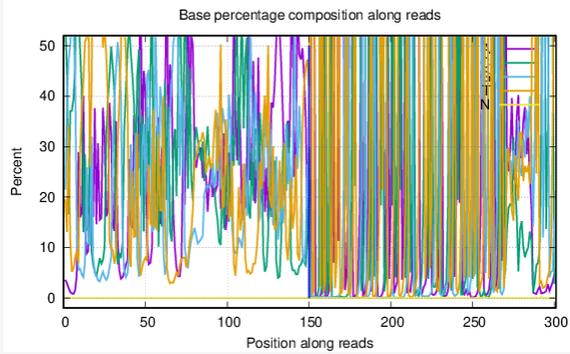
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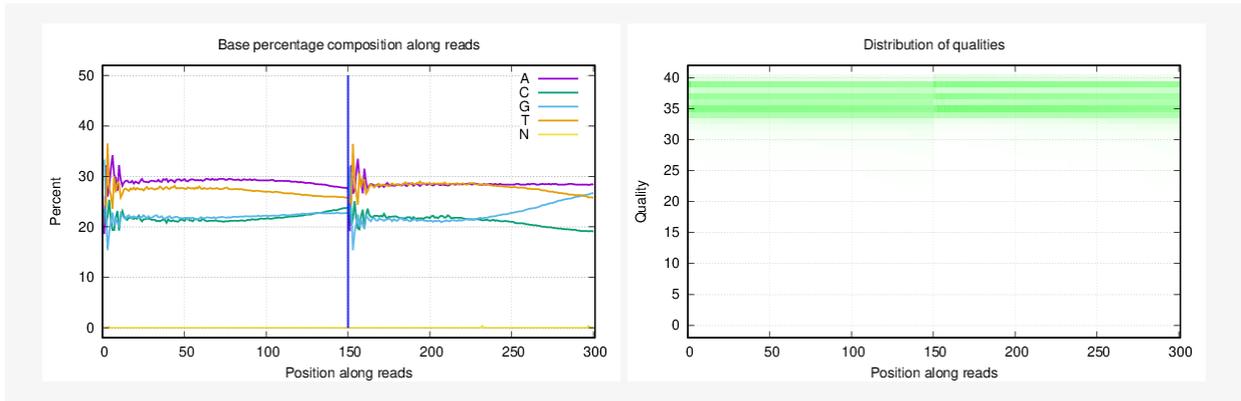
7\_2\_k2



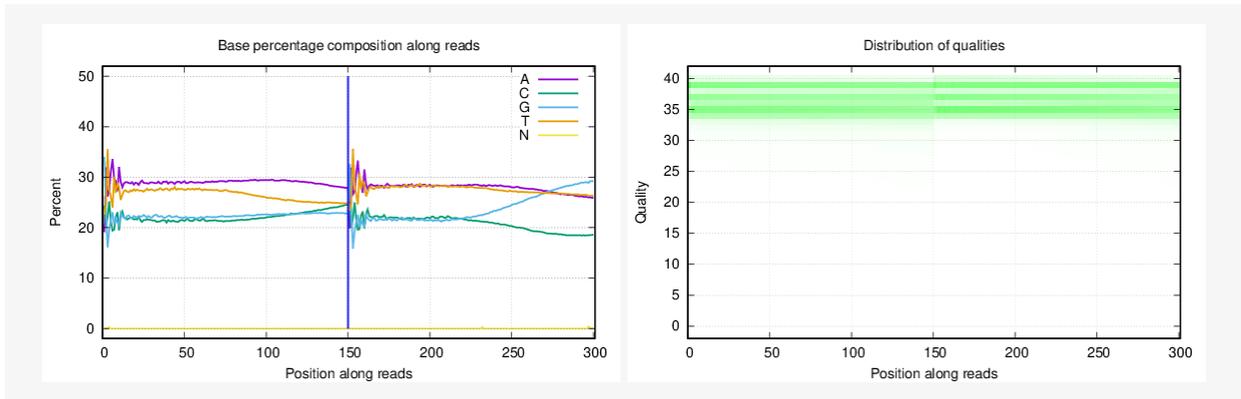
7\_3\_k2



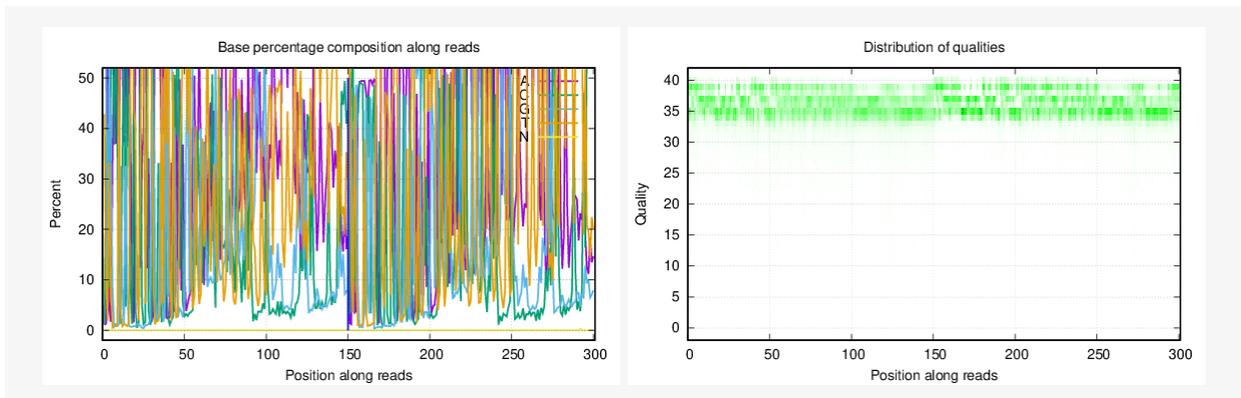
Aux\_1



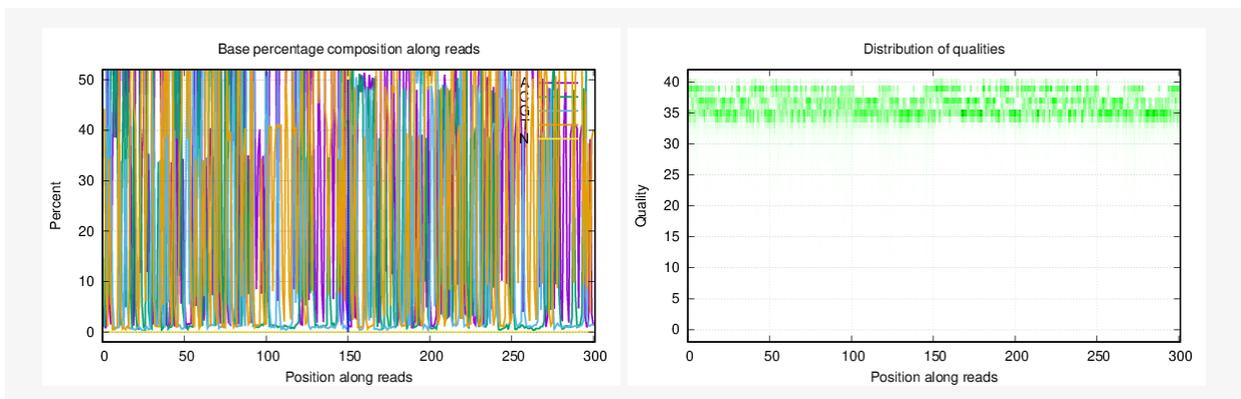
Aux\_2



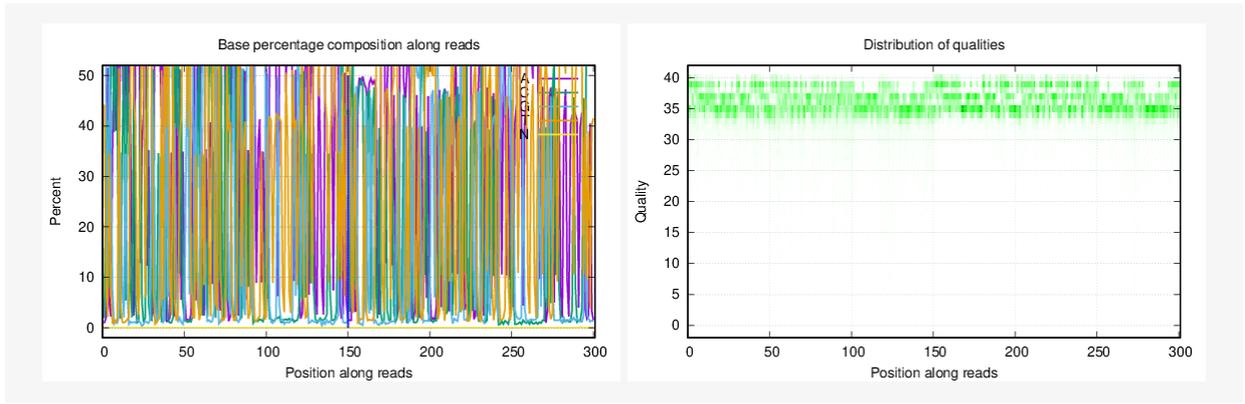
B1



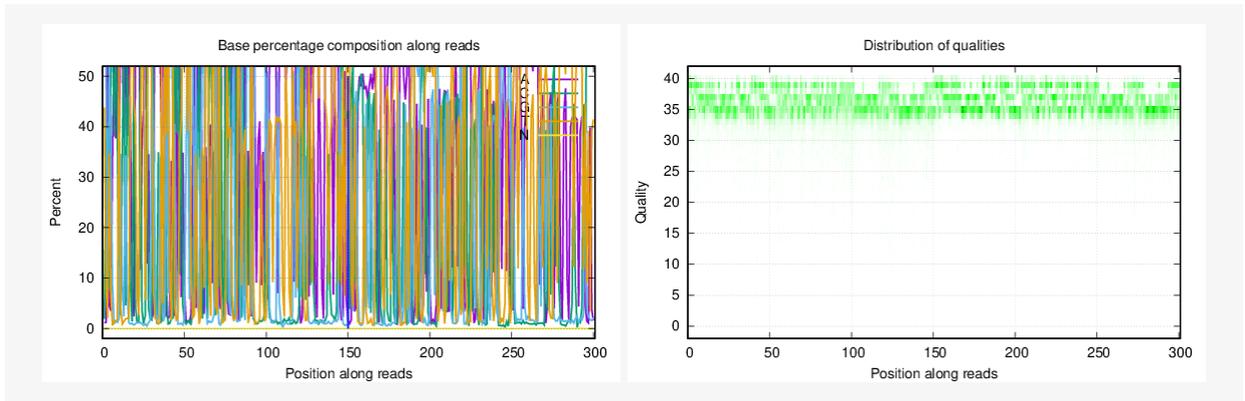
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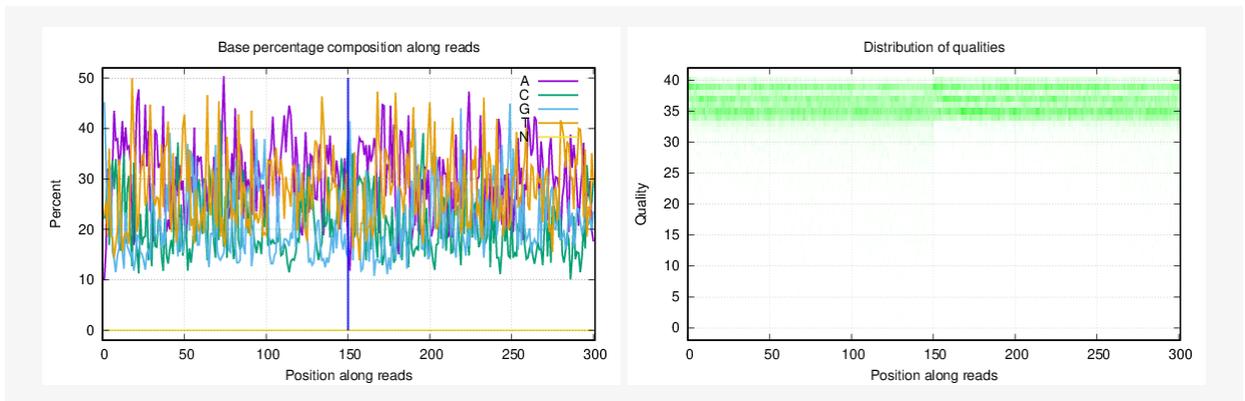
B1\_10



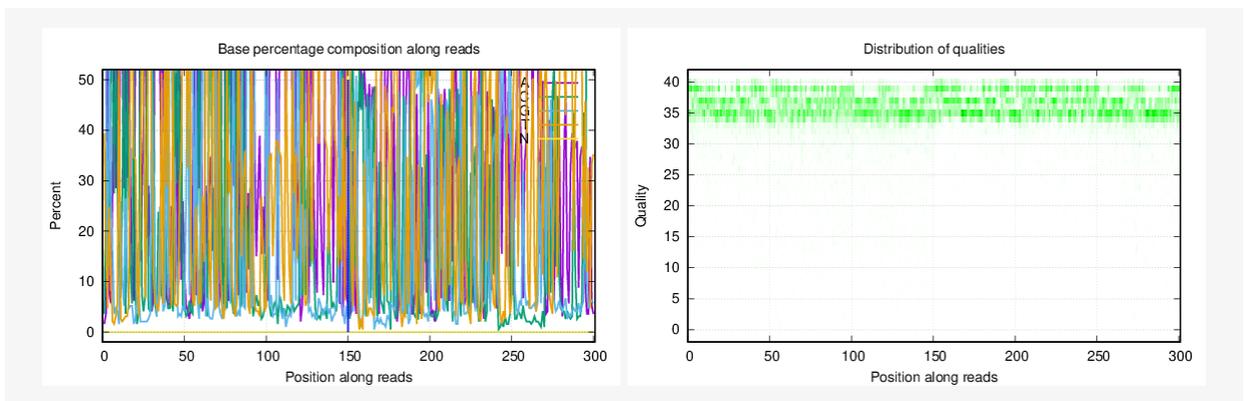
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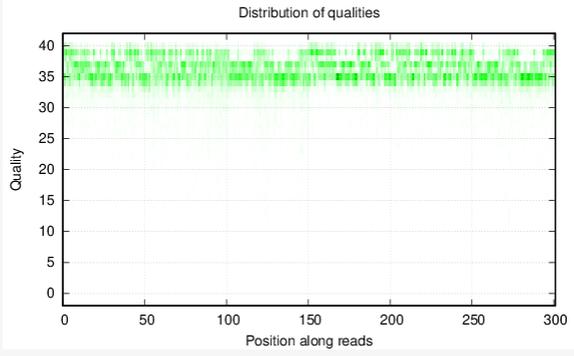
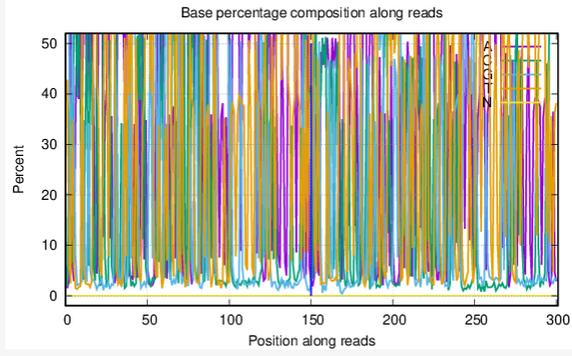
B1\_3



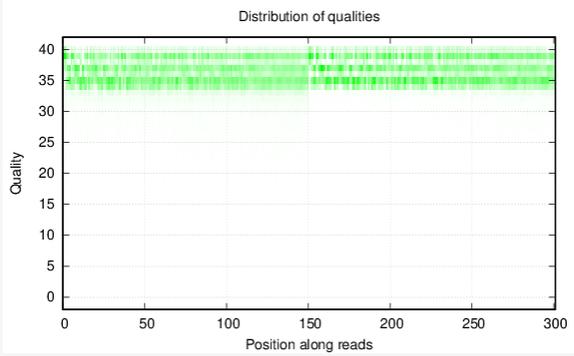
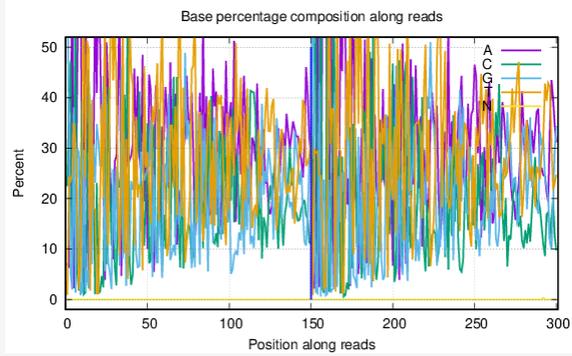
B1\_6



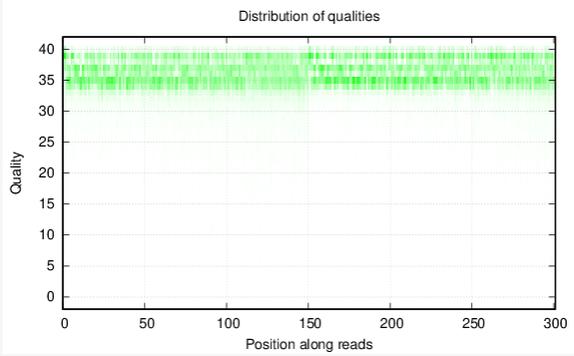
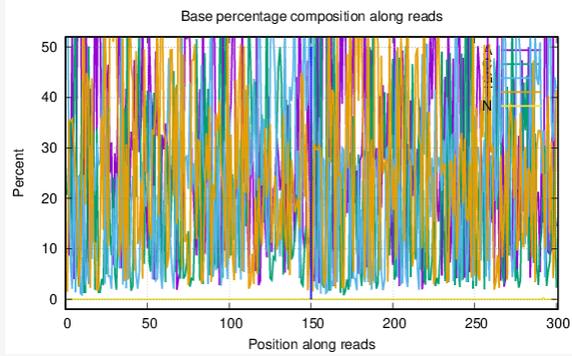
B1\_7



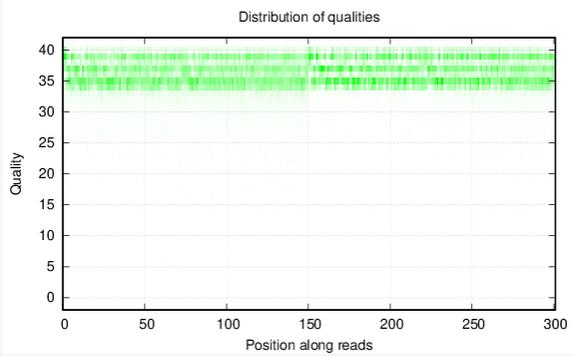
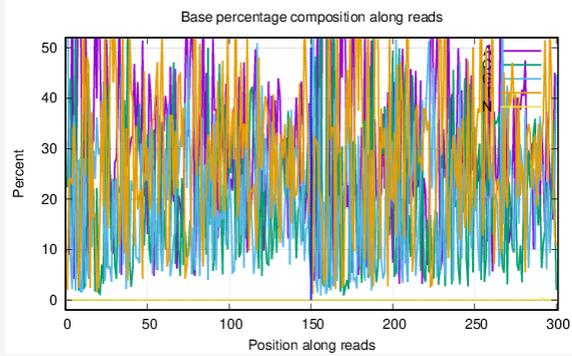
B2



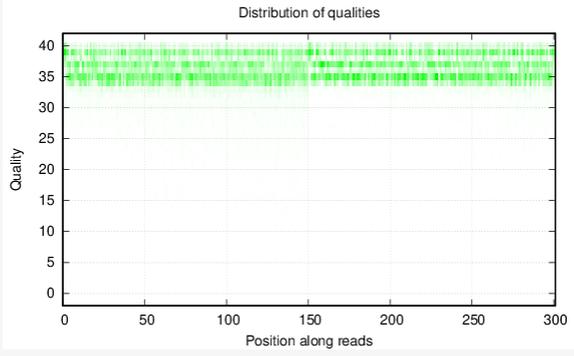
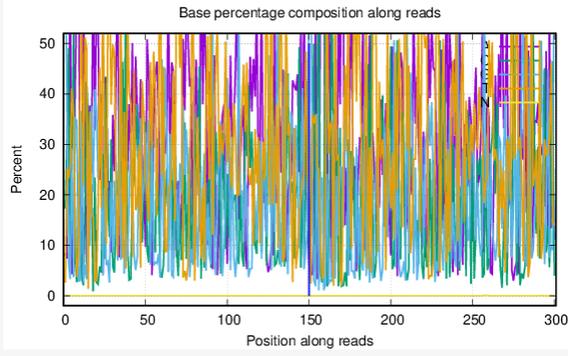
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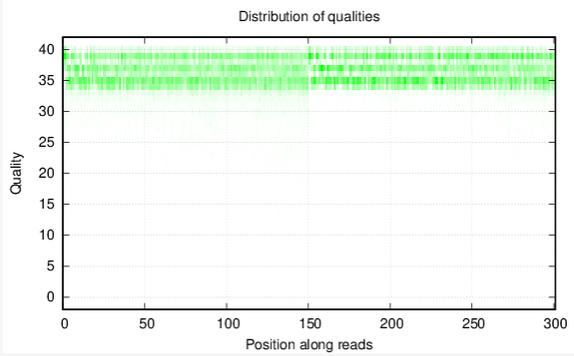
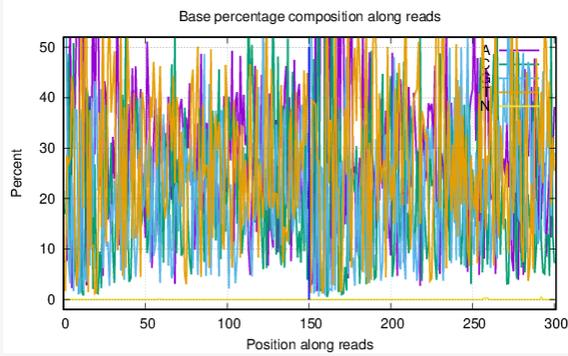
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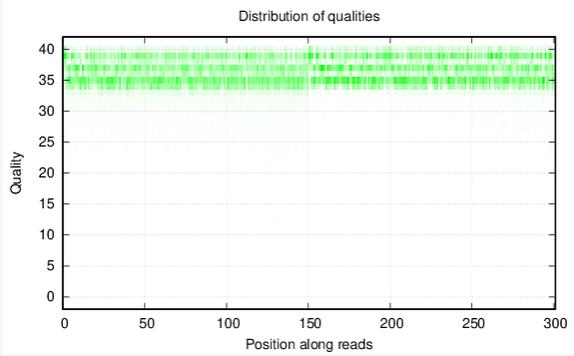
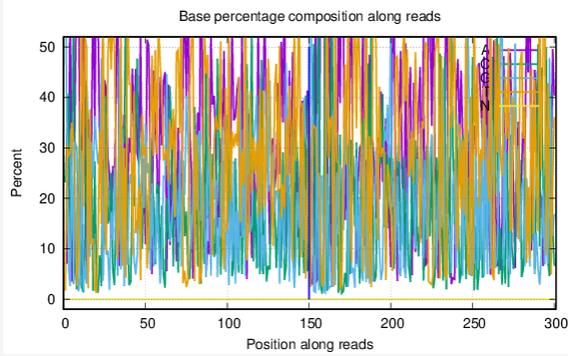
B2\_3



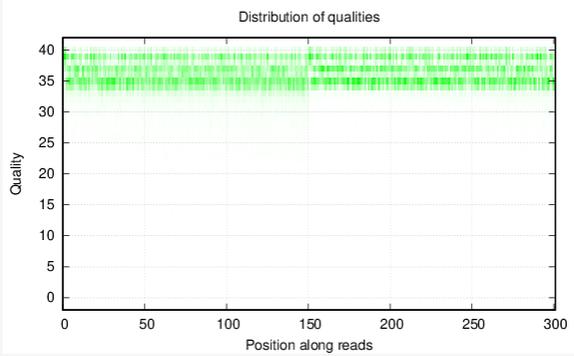
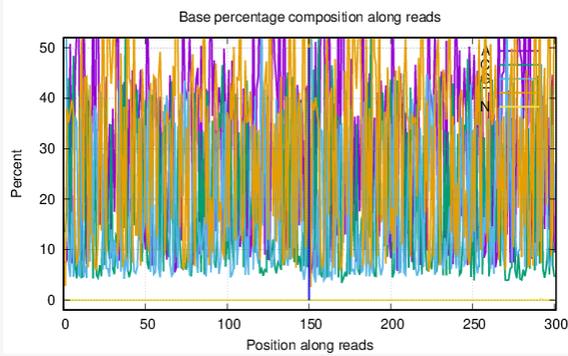
B2\_6



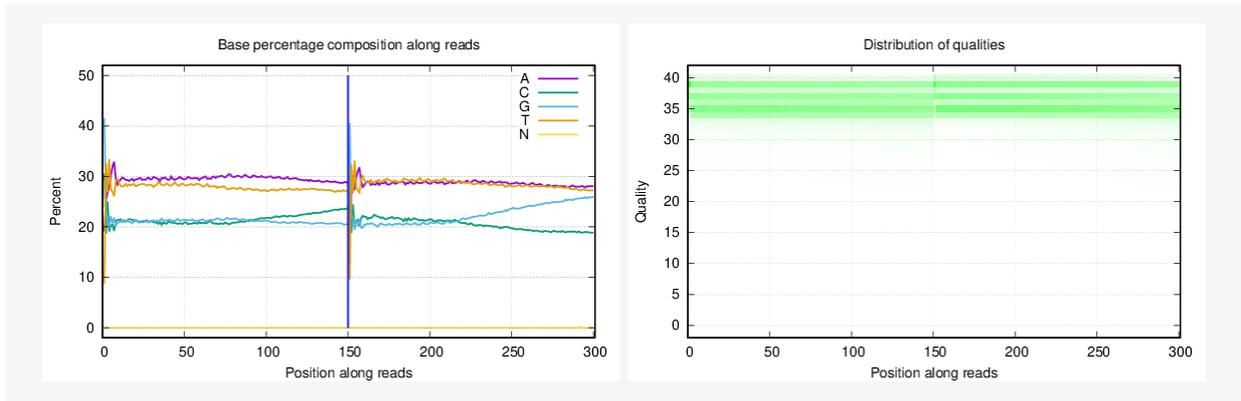
B2\_7



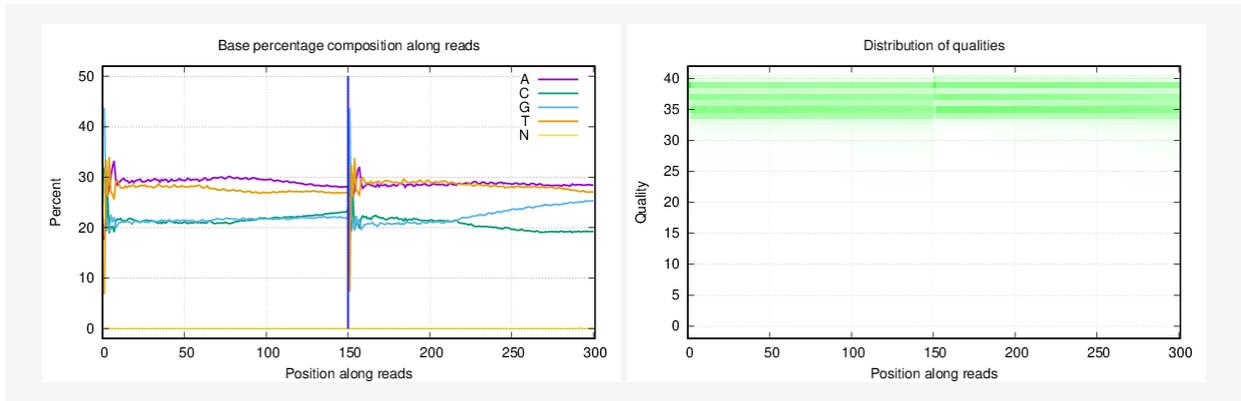
B2\_8



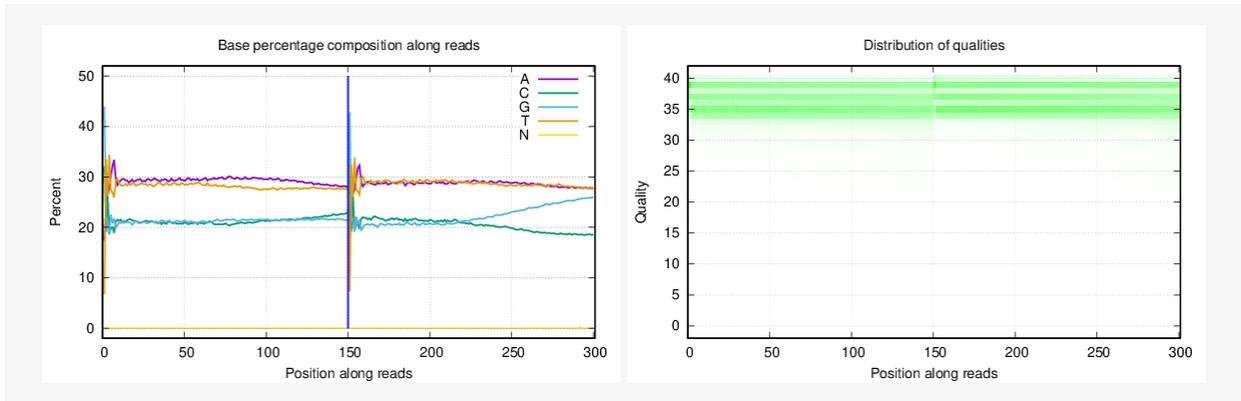
MBS22\_PCR1



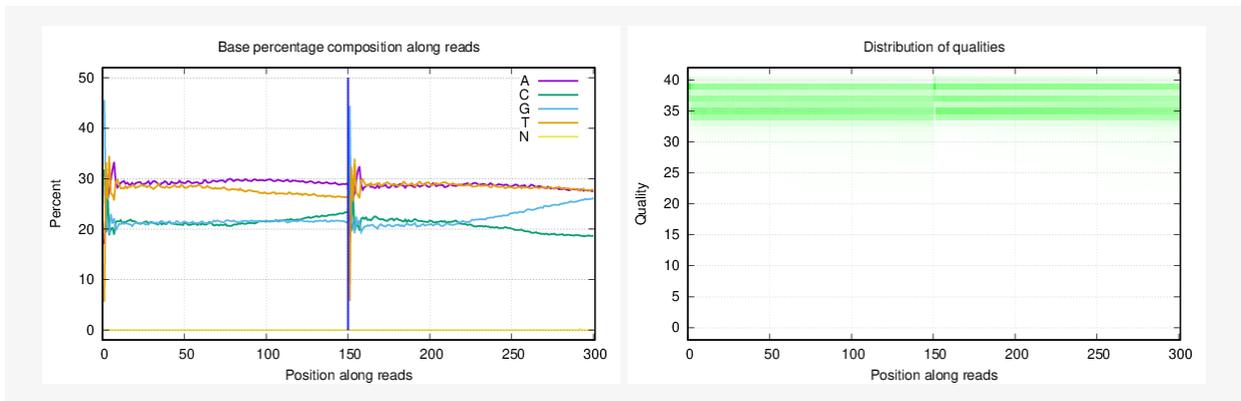
MBS45\_PCR3



MBS64\_PCR4

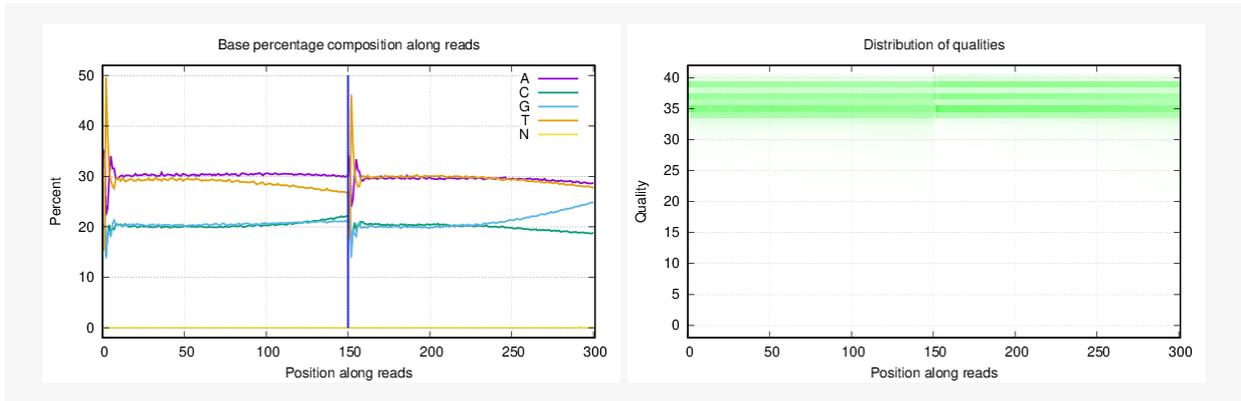


MBS66\_PCR2

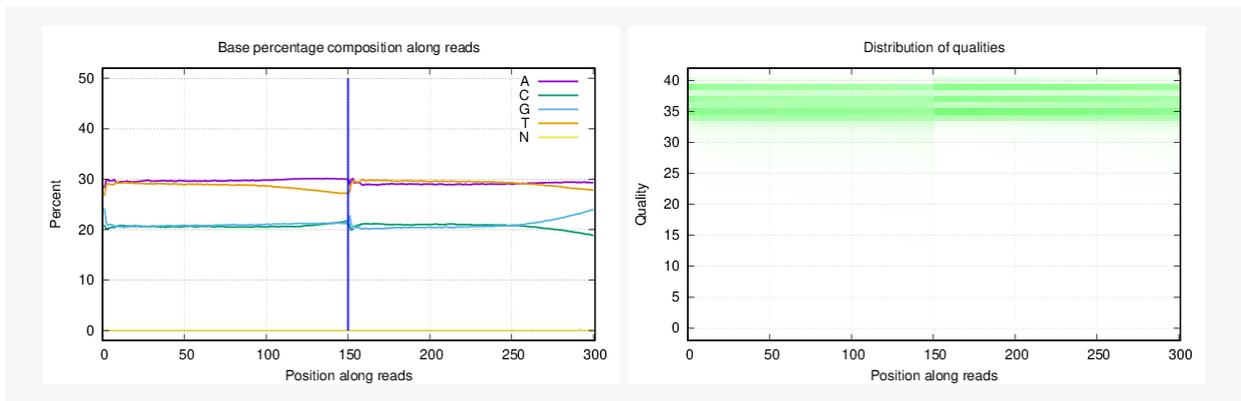


MBS76

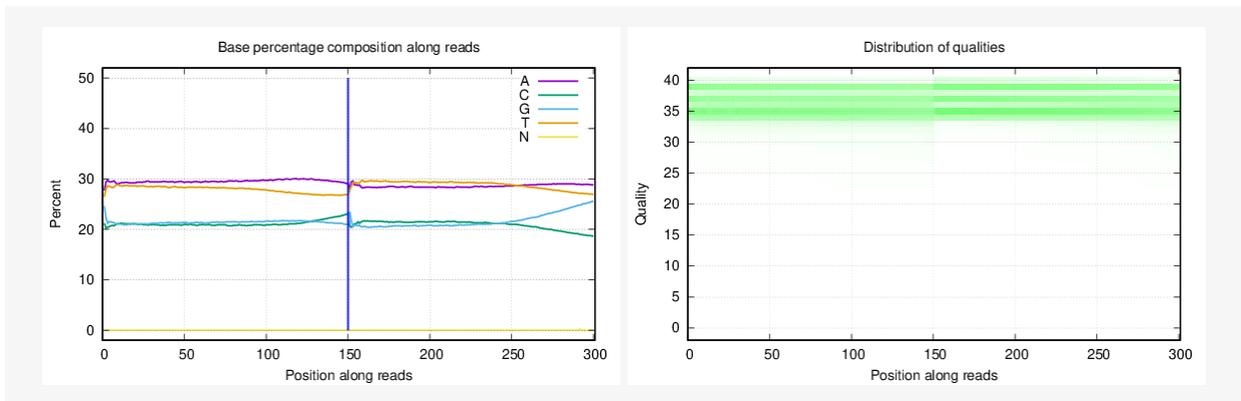
# Data Quality Control



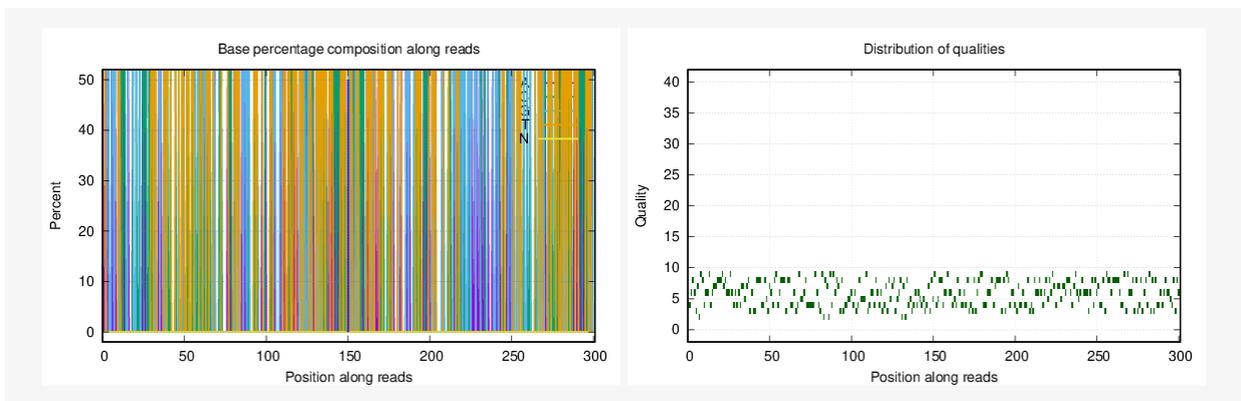
NPC149\_1\_STAG2



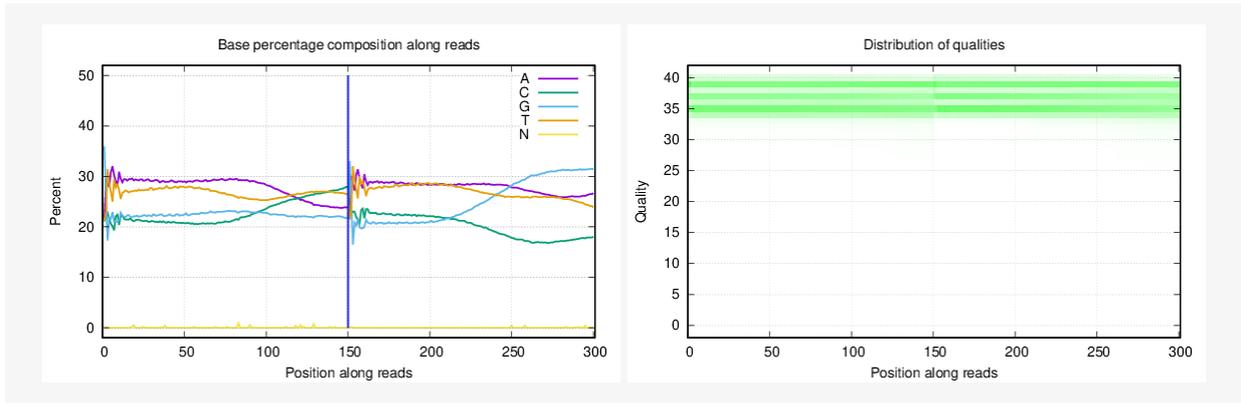
NPC1\_25\_STAG2



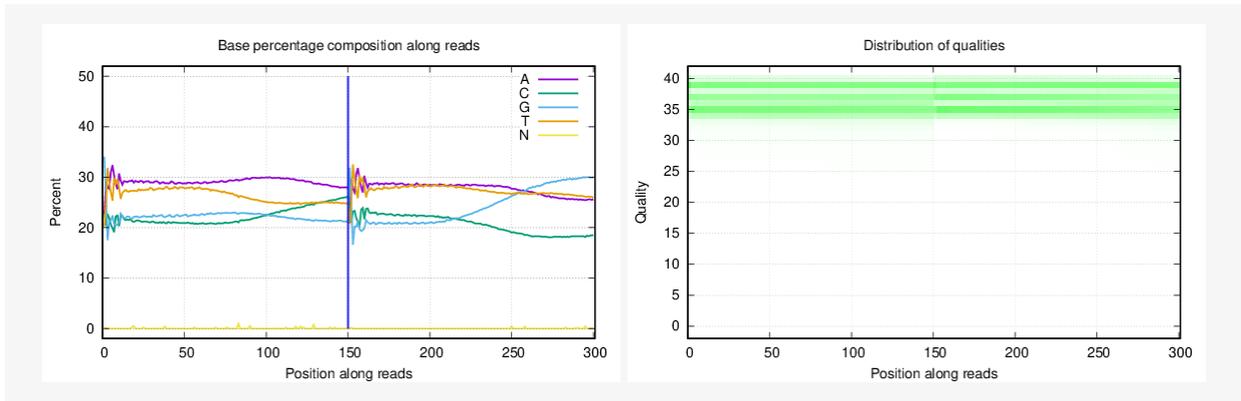
OE



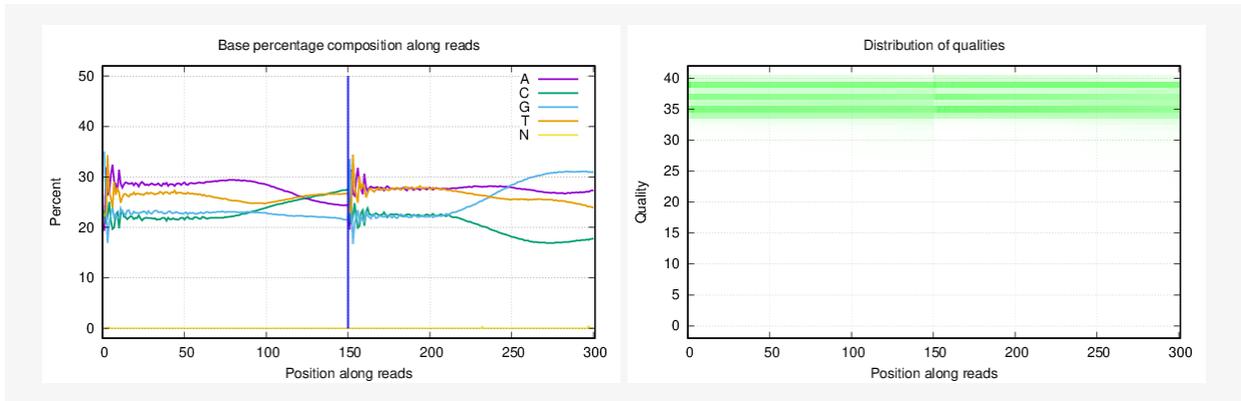
P244



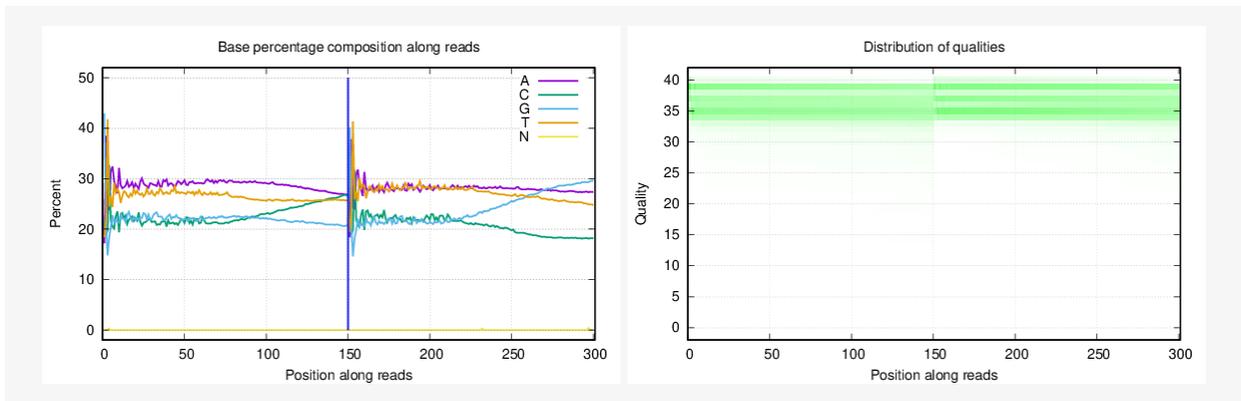
P245



RAD21\_1

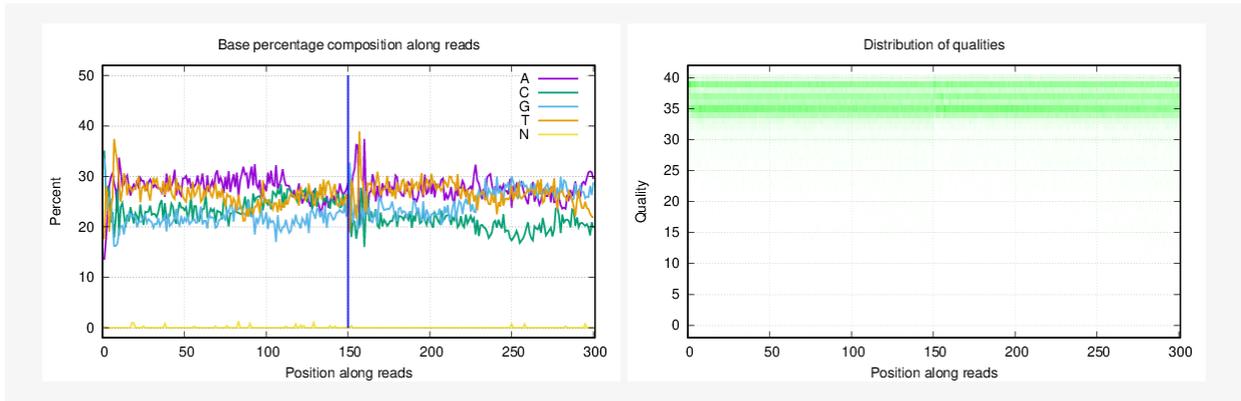


RAD21\_2

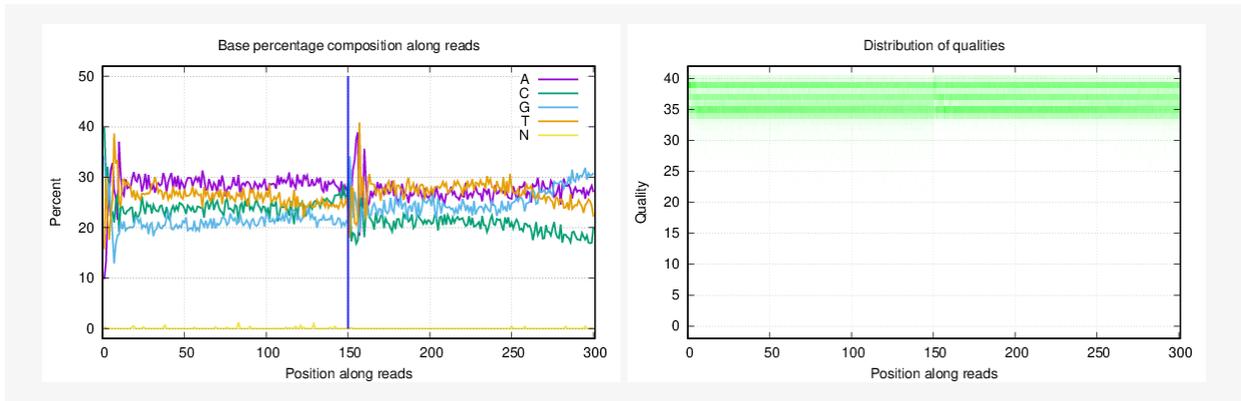


T12\_23

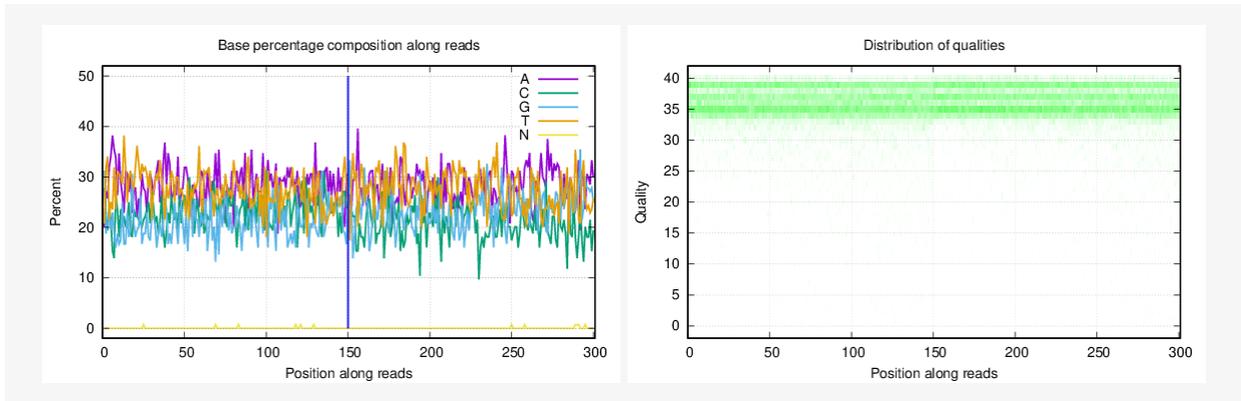
# Data Quality Control



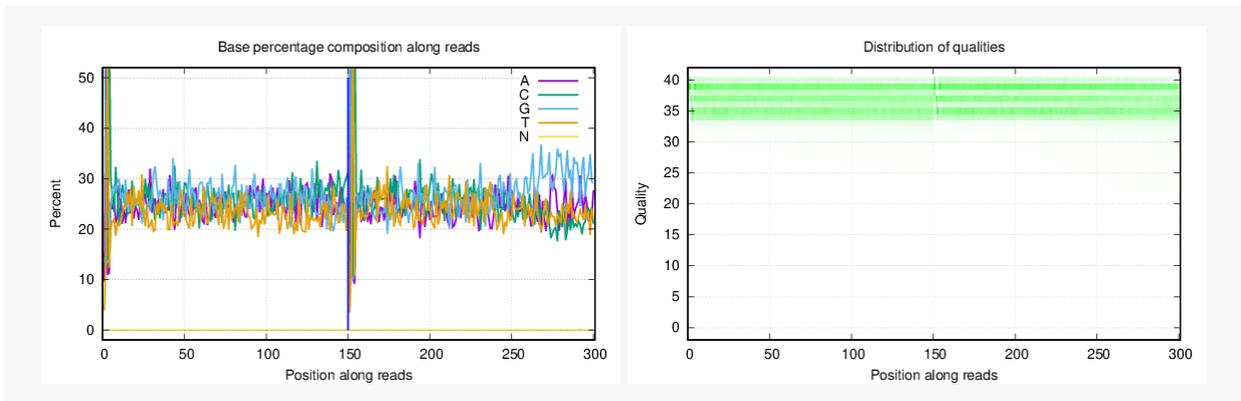
T12\_31



T12\_33

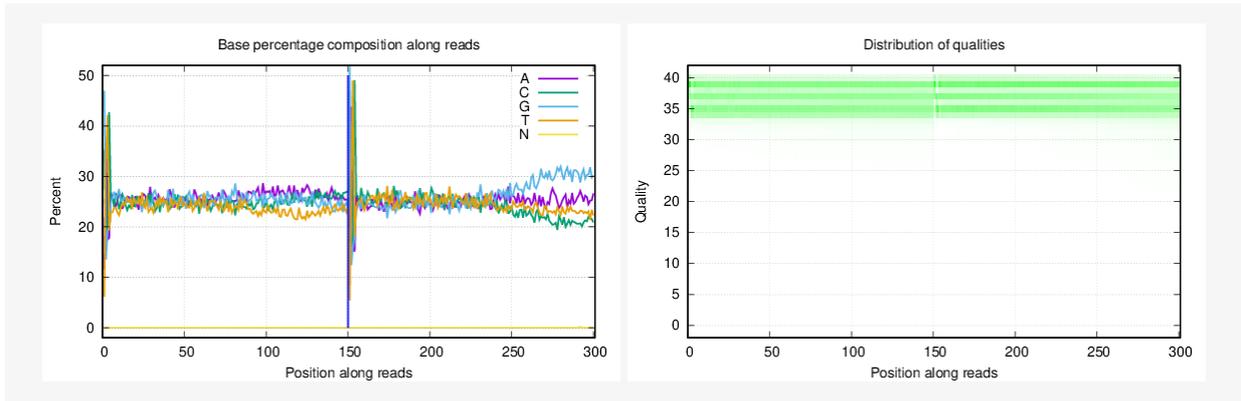


TM\_II

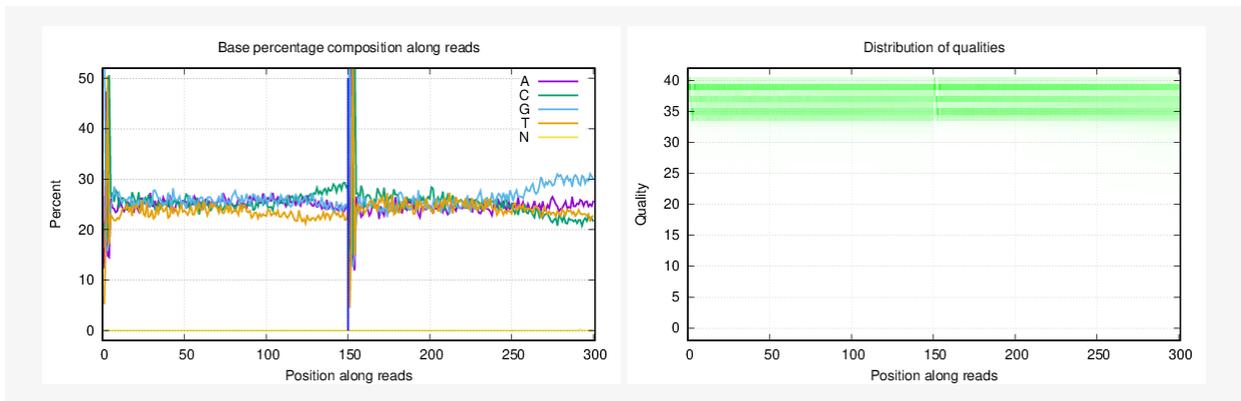


TM\_III

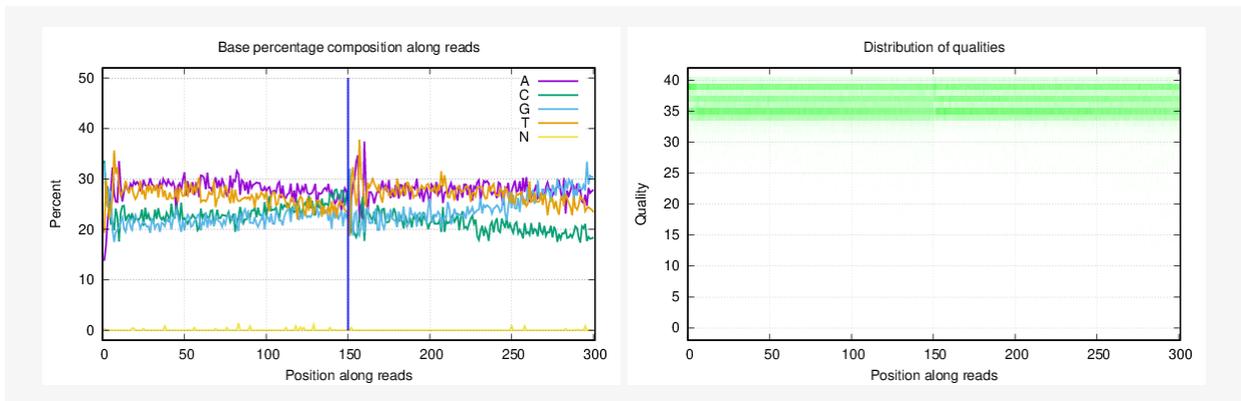
# Data Quality Control



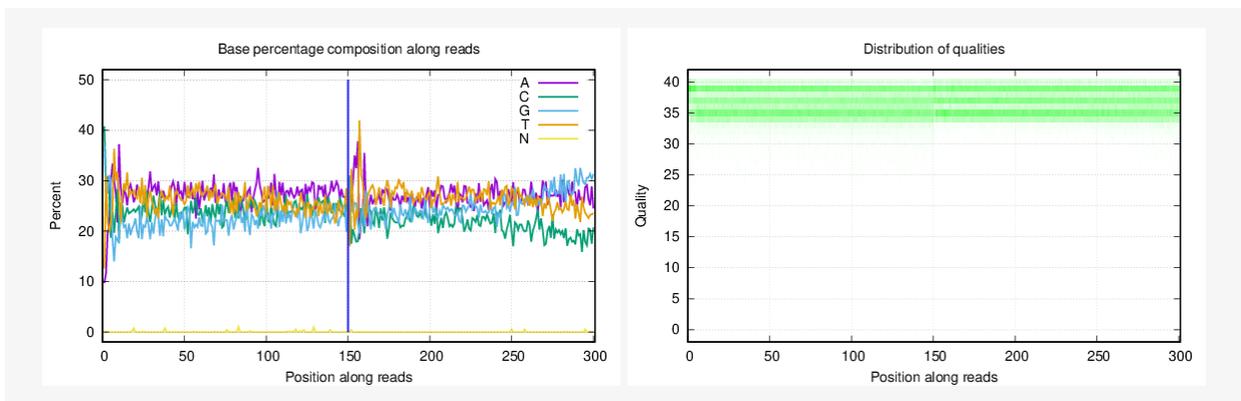
T\_L



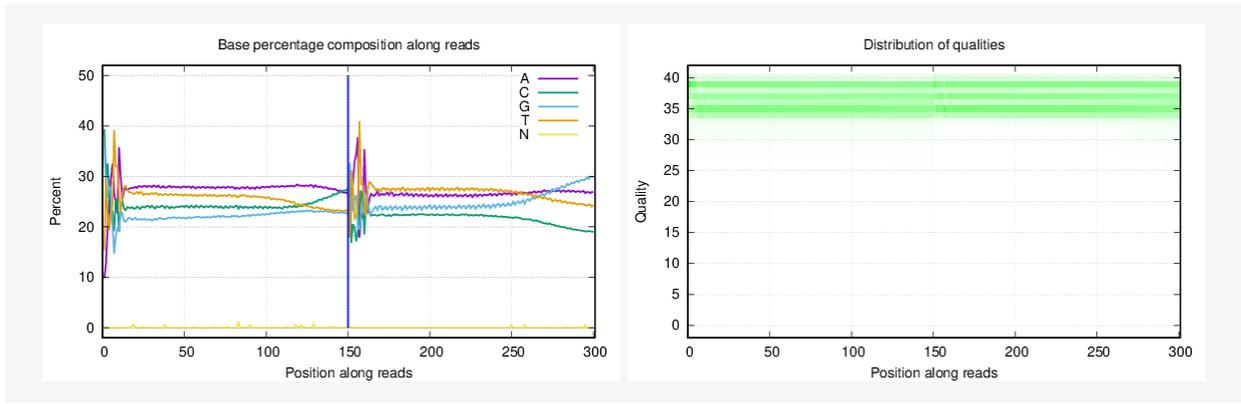
To\_1



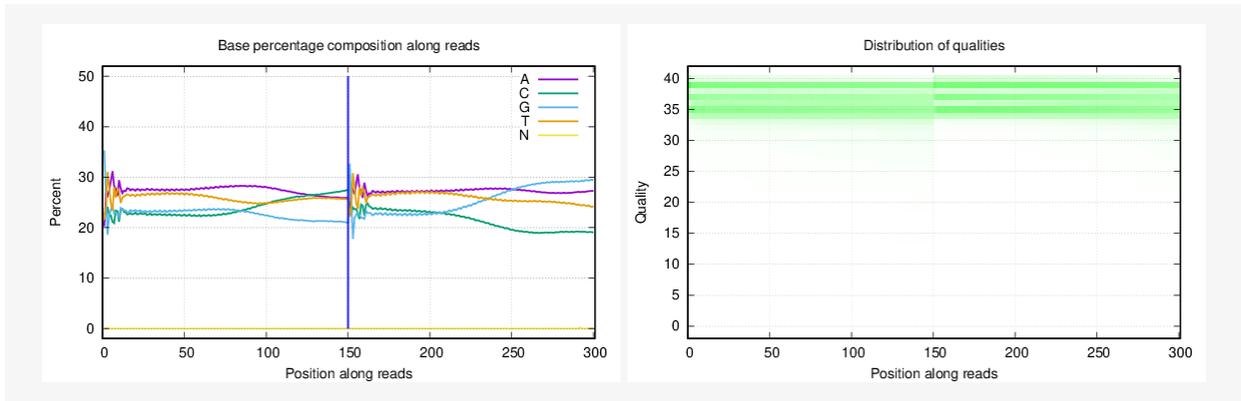
To\_11



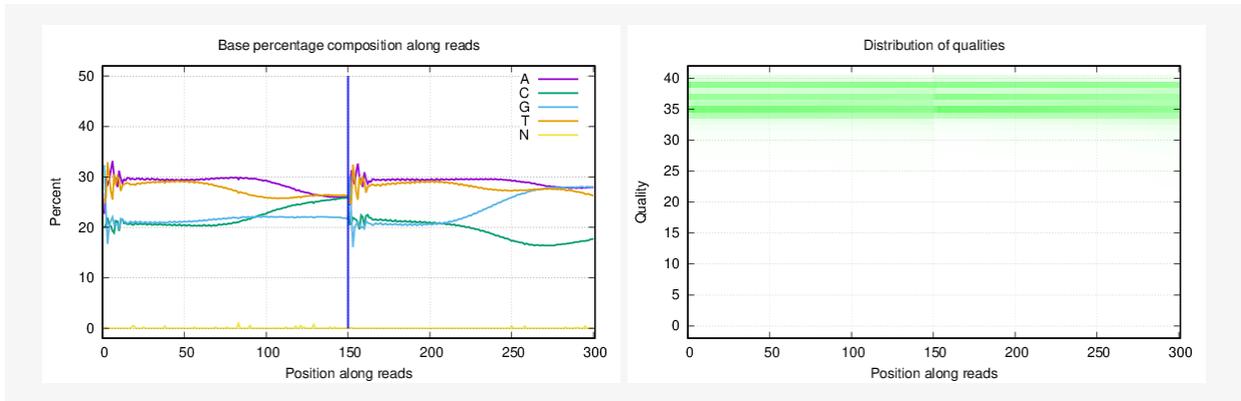
To\_9



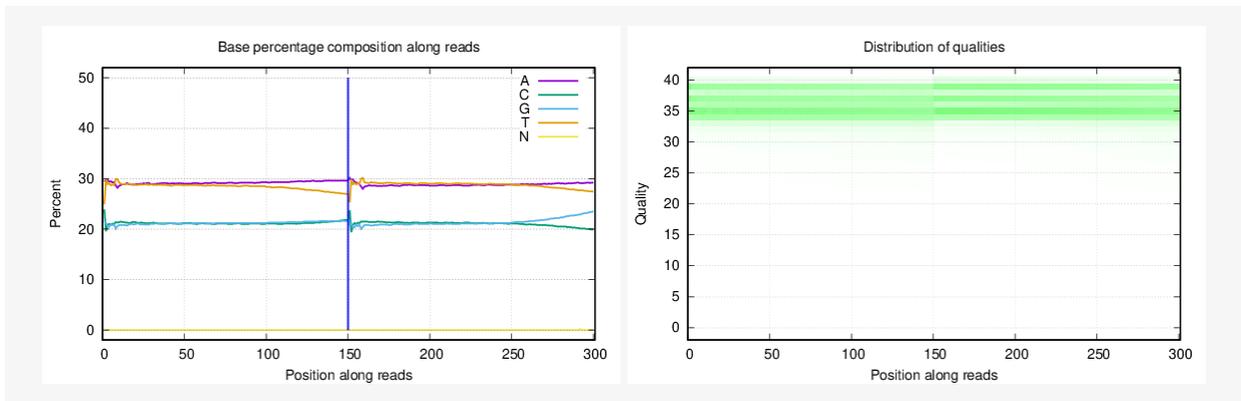
Trih\_3



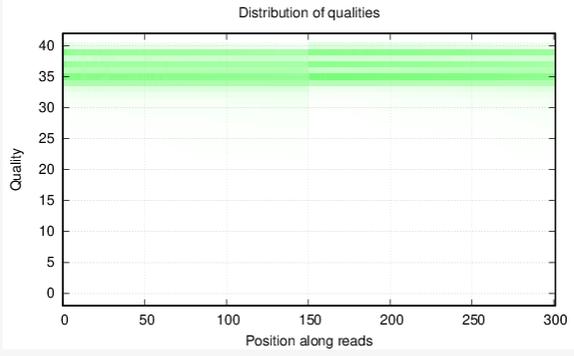
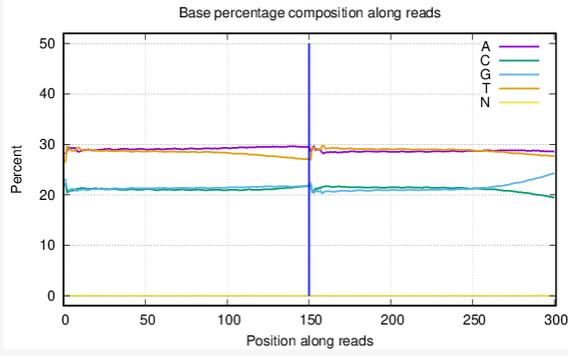
Trih\_4



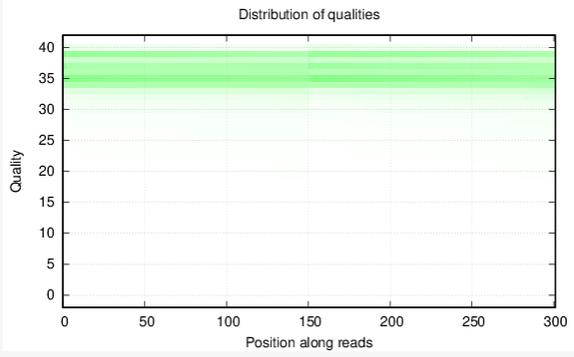
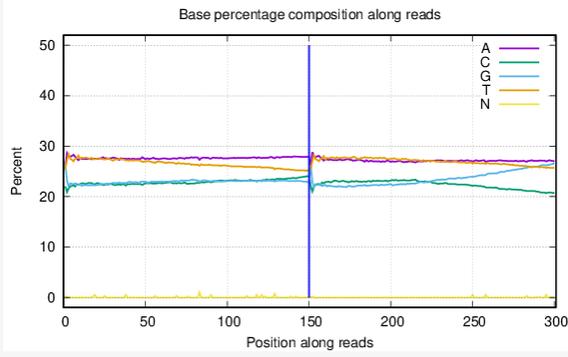
brCTCF\_FLAG



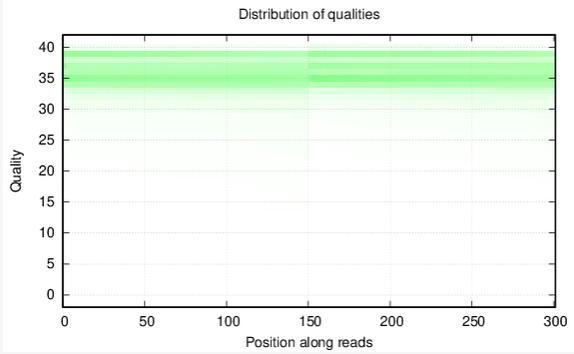
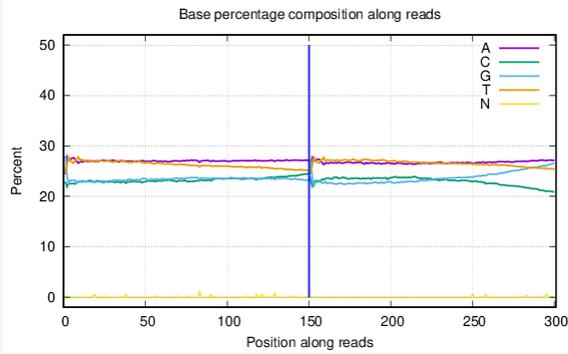
hCTCF\_FLAG



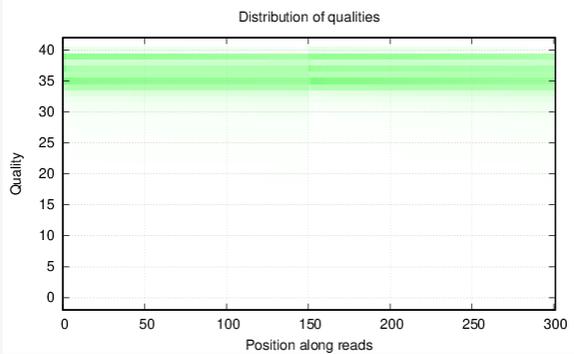
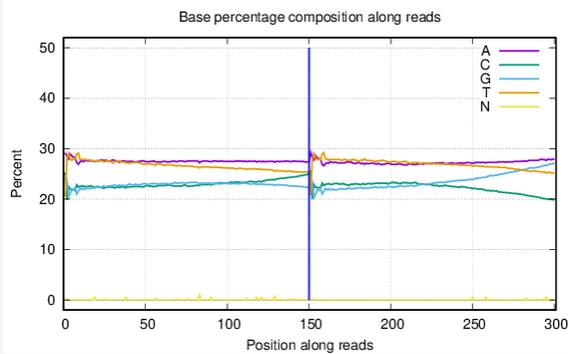
**i\_MoPh15\_TR\_Cas**



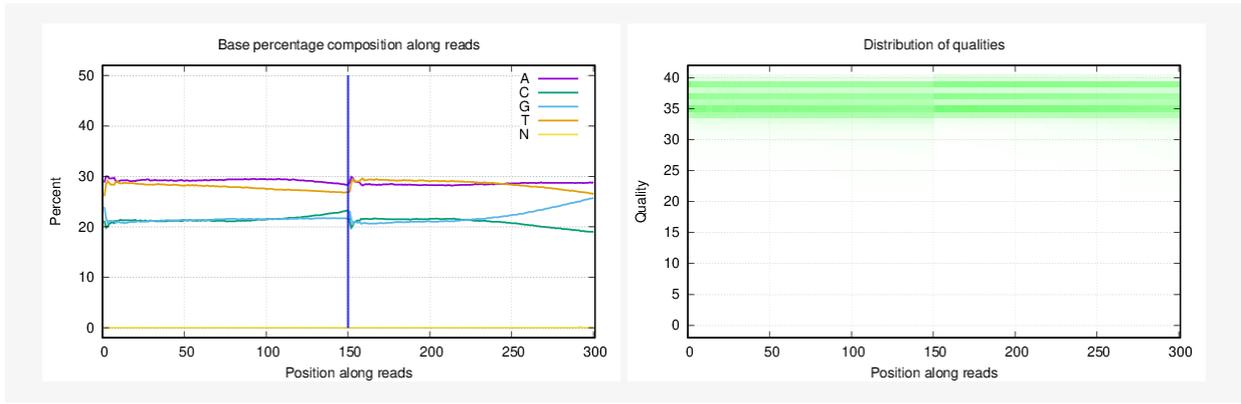
**i\_MoPh7\_DR\_Cas**



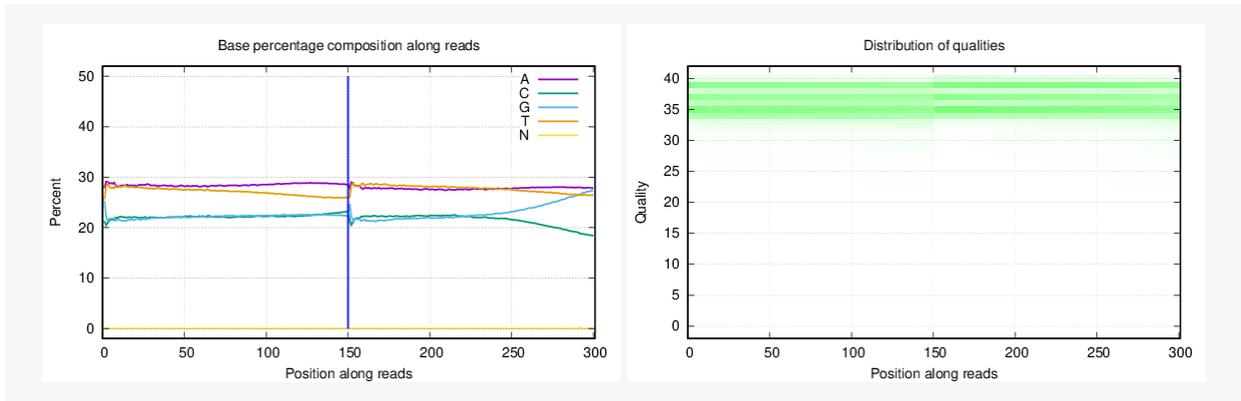
**i\_MoPh7\_VPR\_Cas**



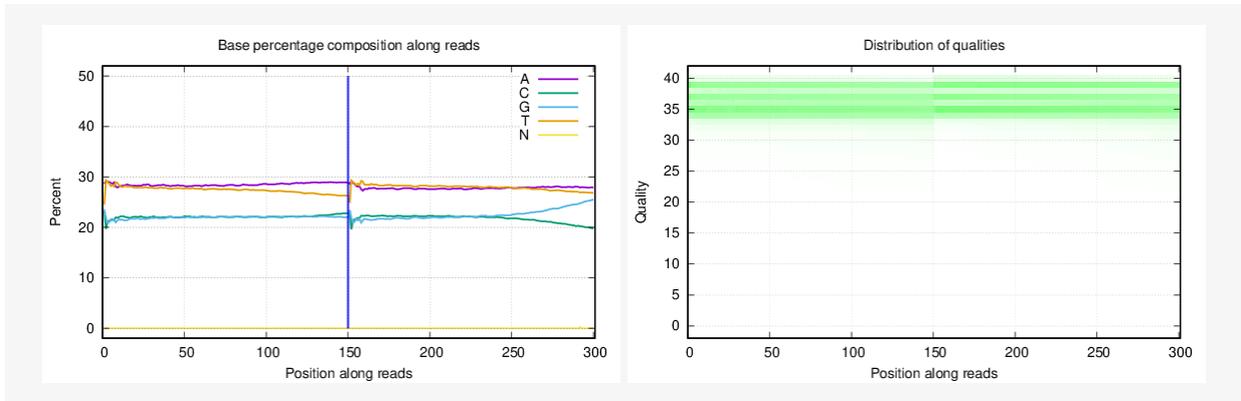
**i\_NPC149\_1\_STAG2**



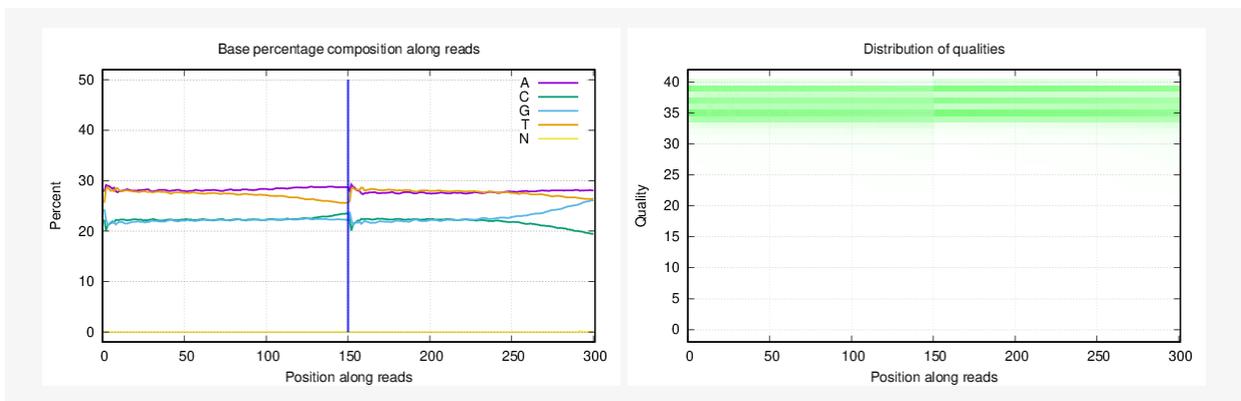
**i\_NPC1\_25\_STAG2**



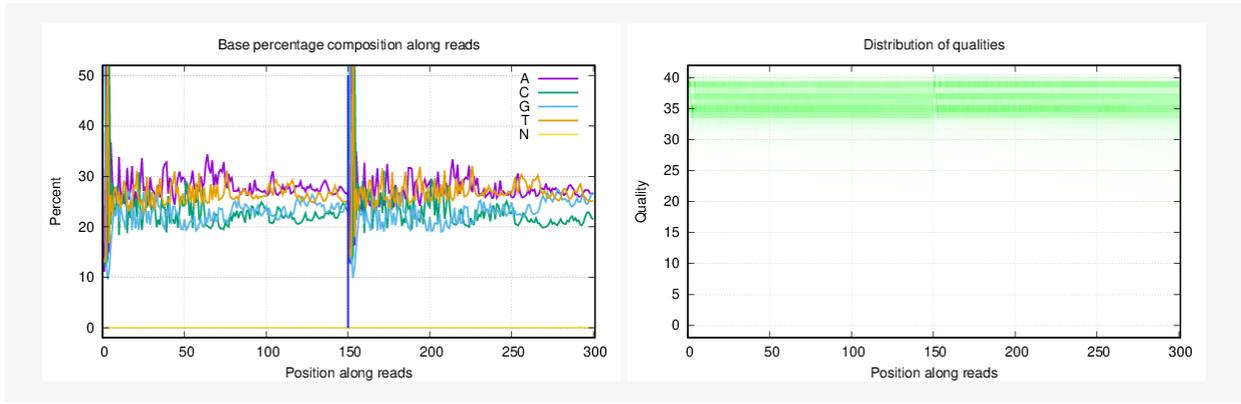
**i\_brCTCF\_FLAG**



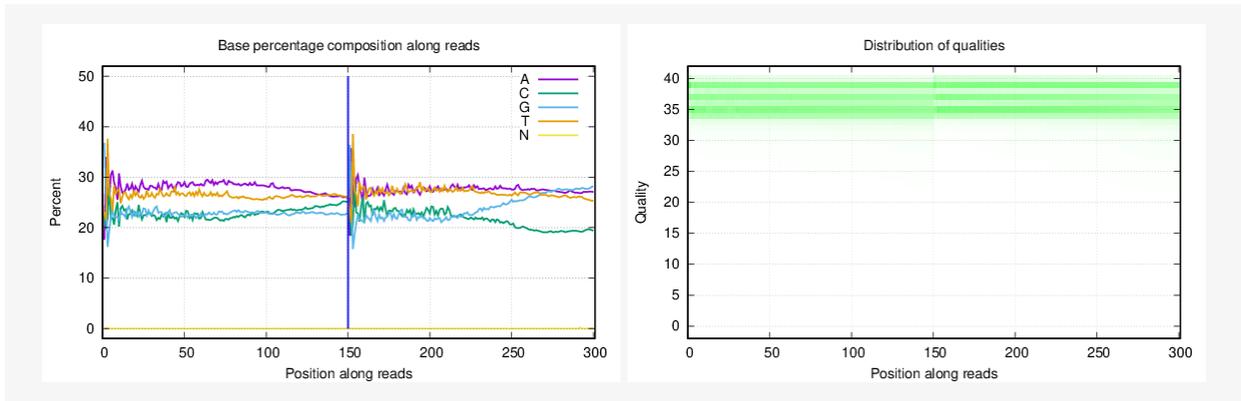
**i\_hCTCF\_FLAG**



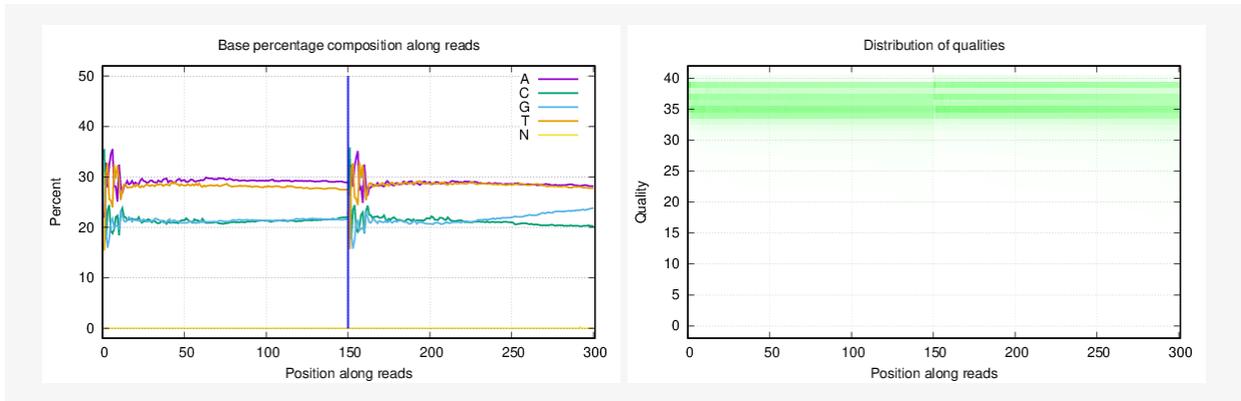
**mutG261S\_a\_R5**



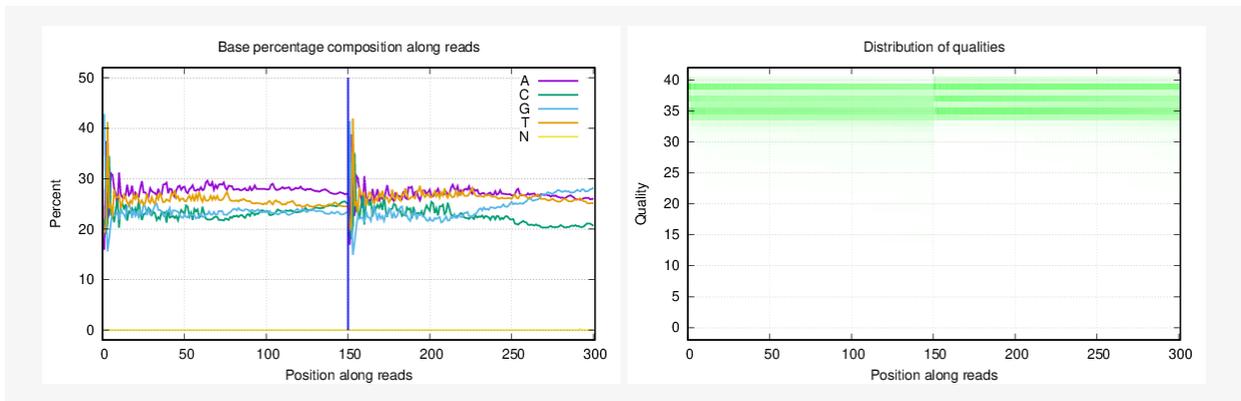
**mutR29W\_R4**



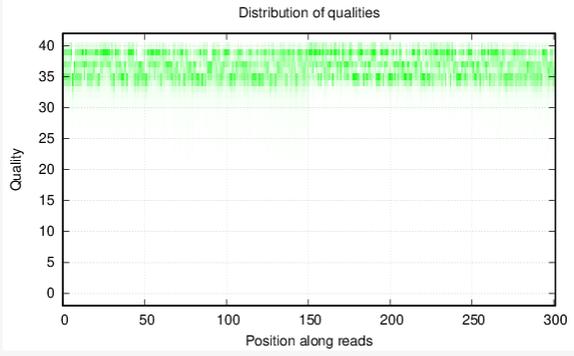
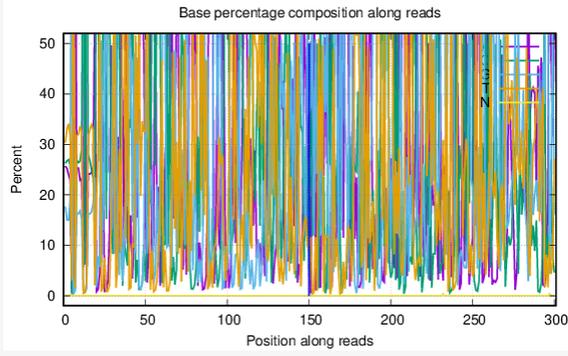
**mutY226A\_a\_R1**



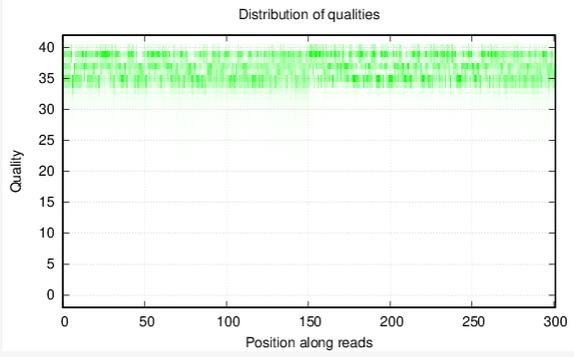
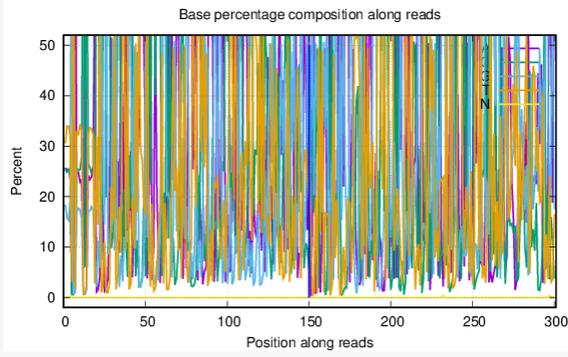
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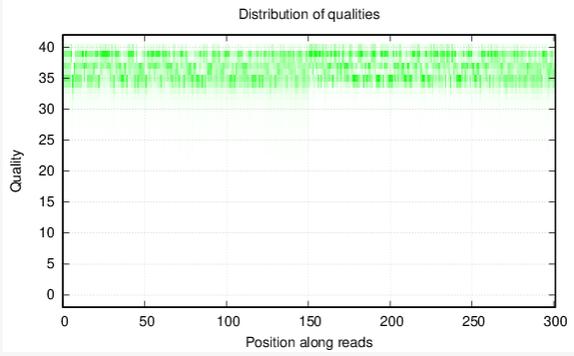
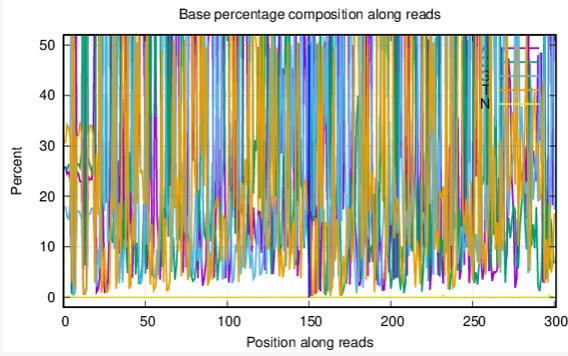
**rigs2\_11**



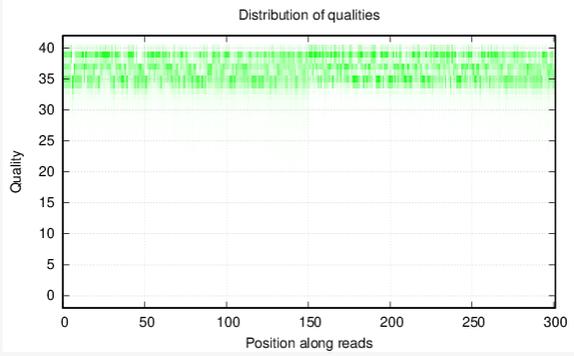
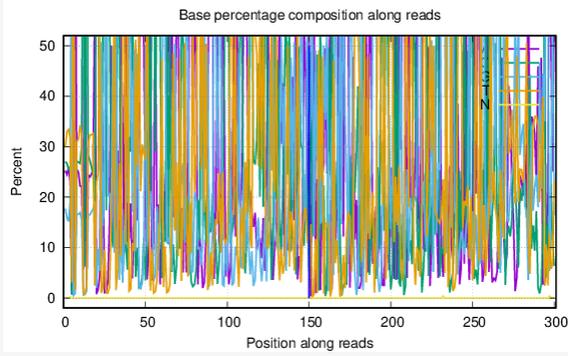
rigs2\_14



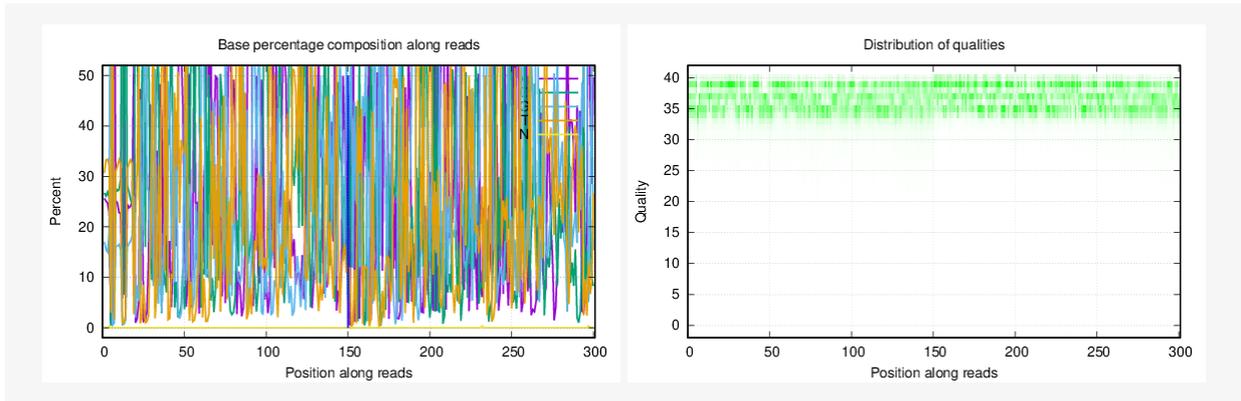
rigs2\_17



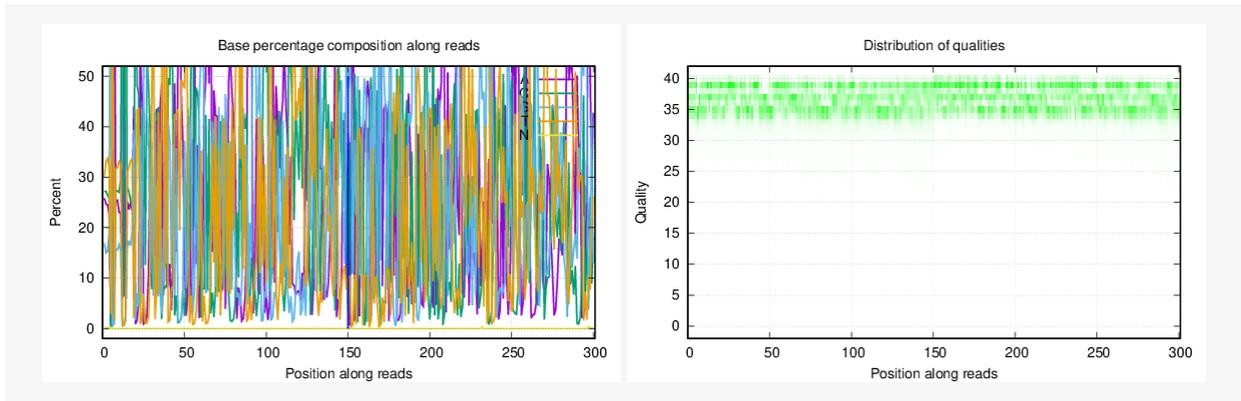
rigs2\_19\_1



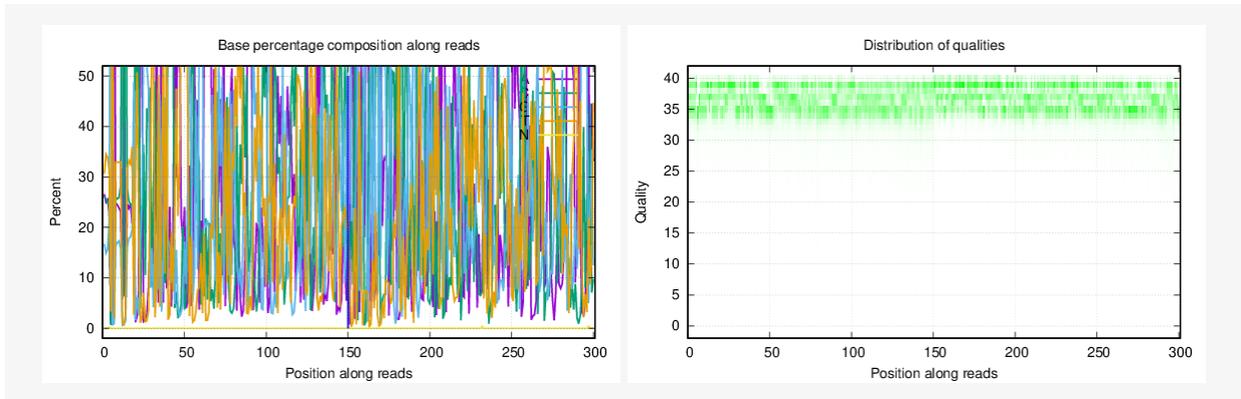
rigs2\_19\_2



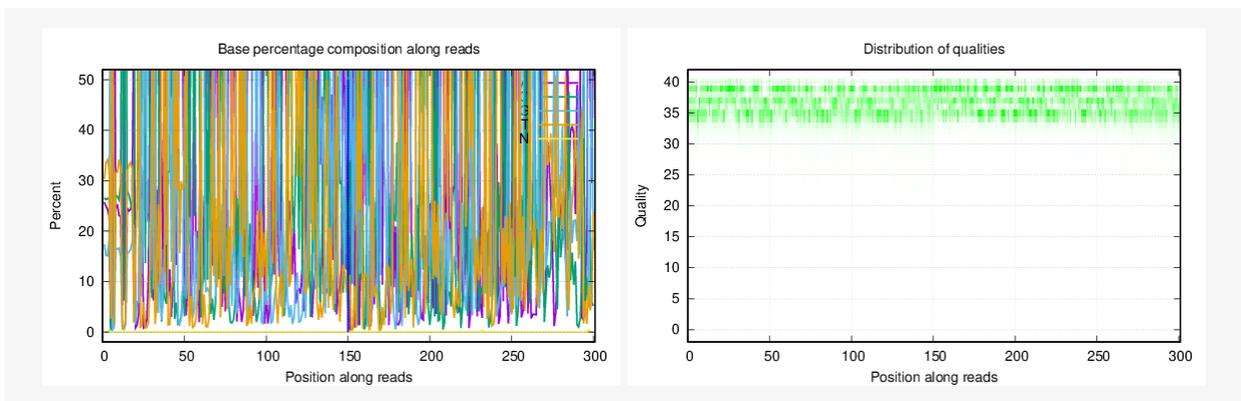
rigs2\_2



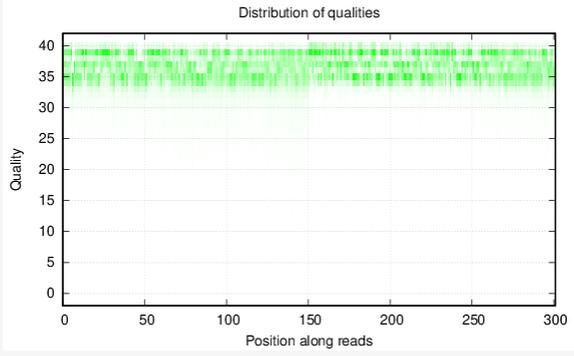
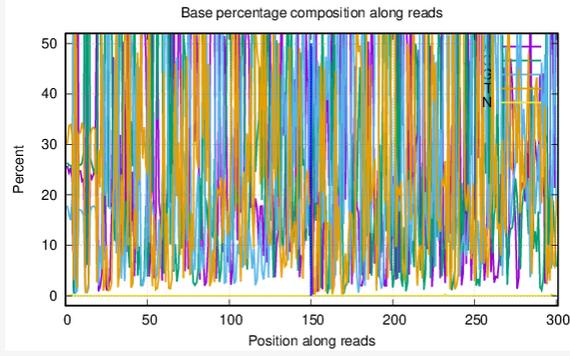
rigs2\_20



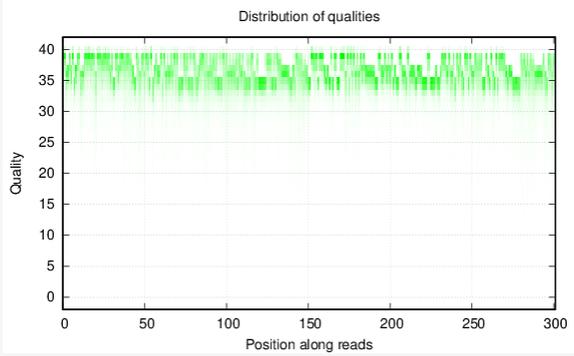
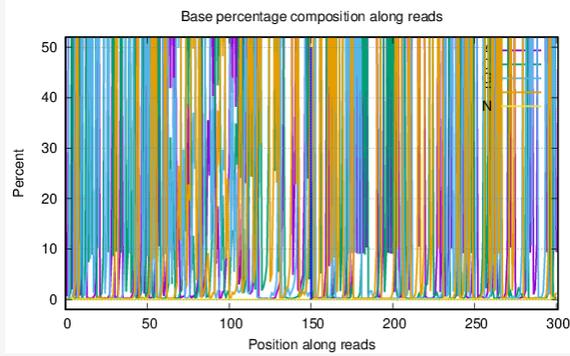
rigs2\_3



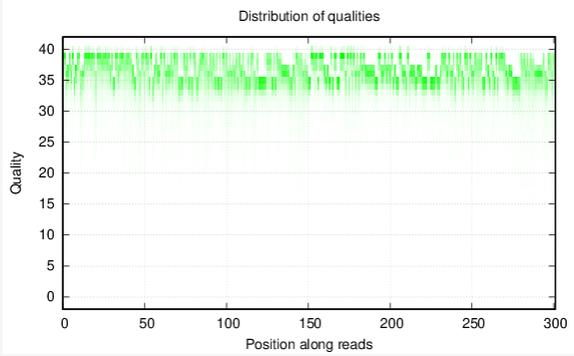
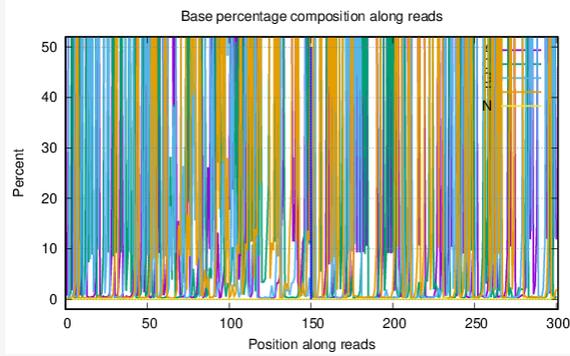
rigs2\_5



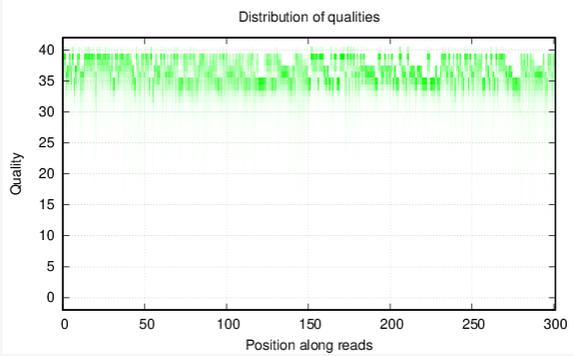
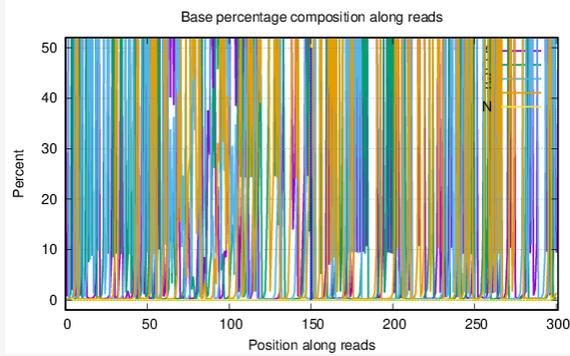
**rigs\_total\_11**



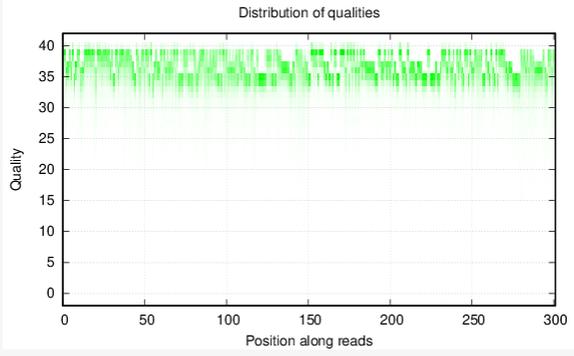
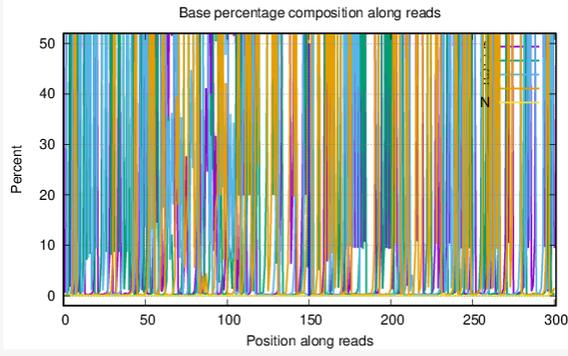
**rigs\_total\_11v2**



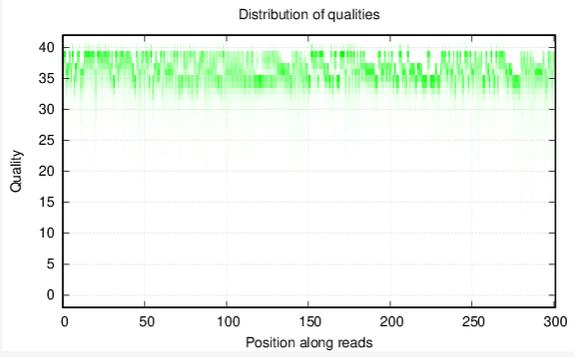
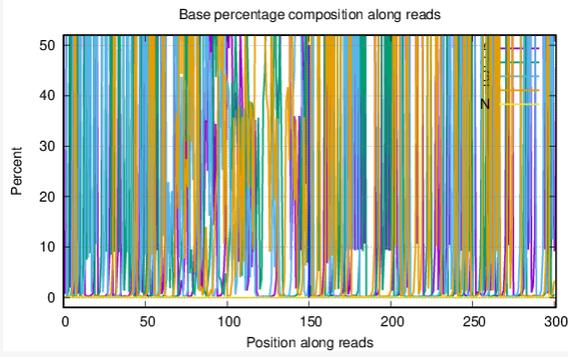
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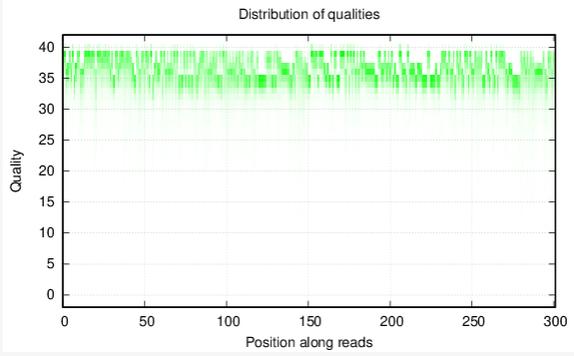
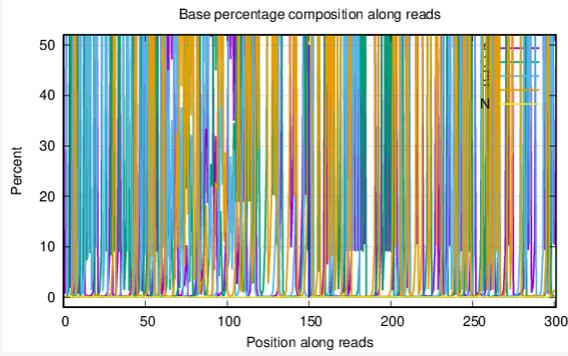
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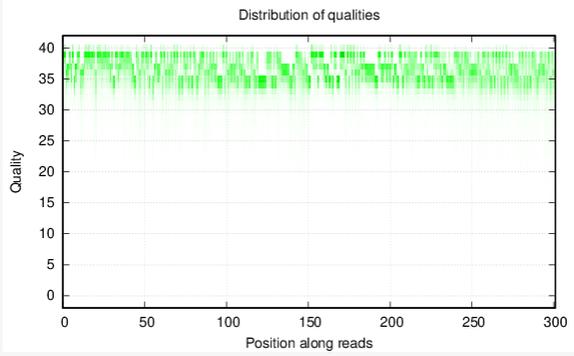
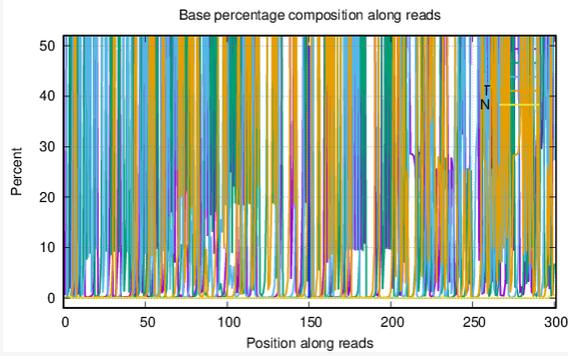
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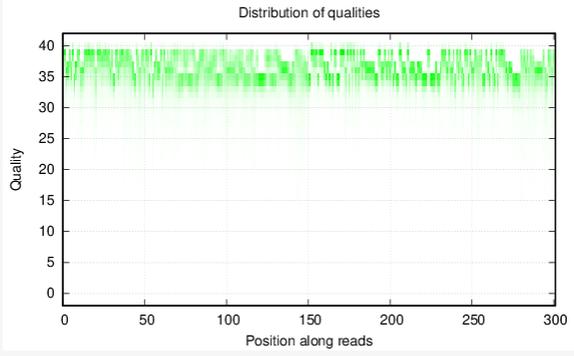
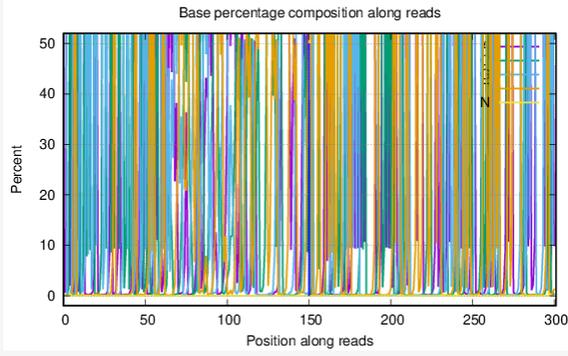
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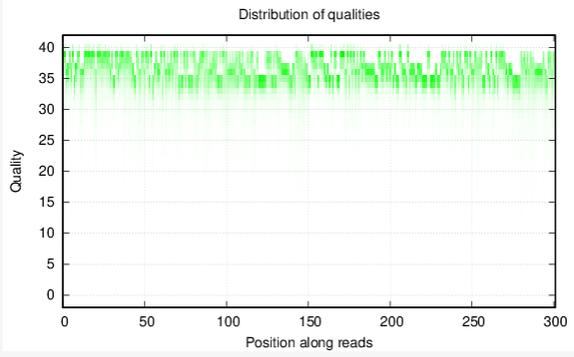
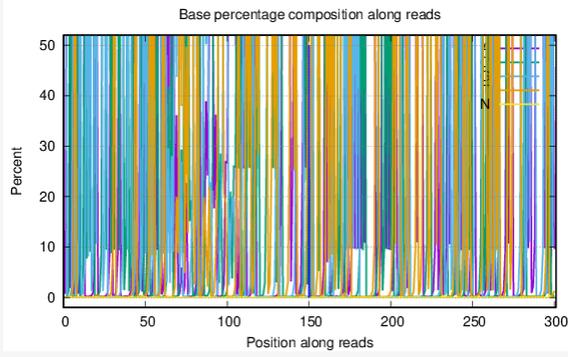
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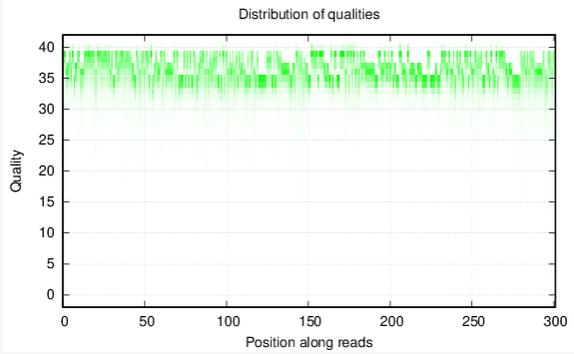
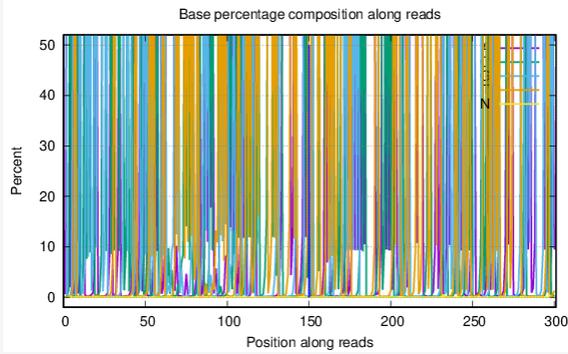
**rigs\_total\_2**



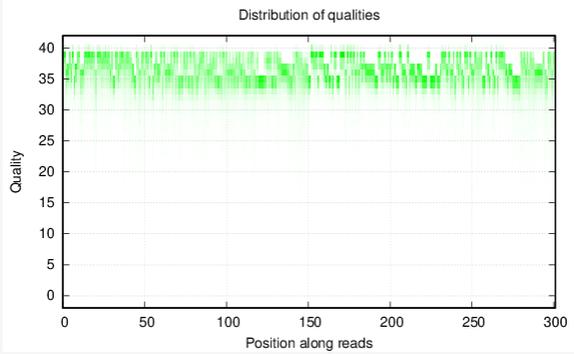
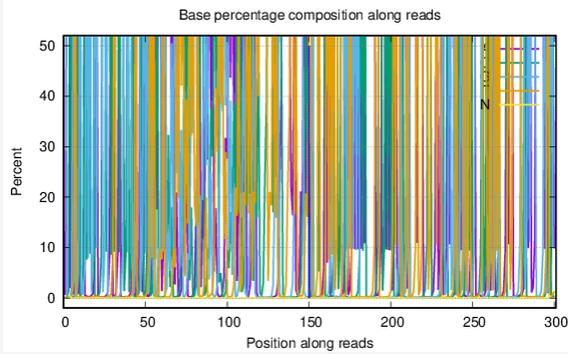
**rigs\_total\_20**



**rigs\_total\_3**

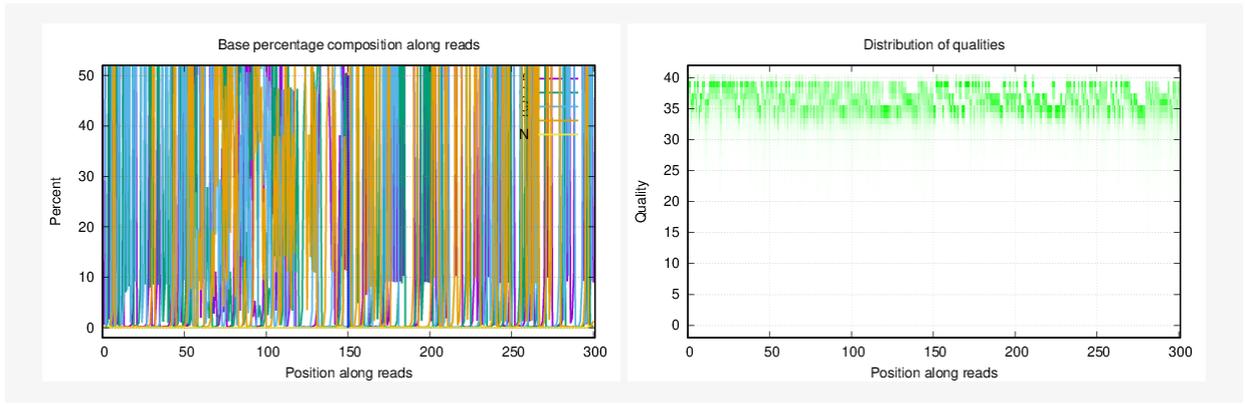


**rigs\_total\_5**



**rigs\_total\_5v2**

# Data Quality Control



## 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
+
FFFCFFFFFFFFDFEFFFFFFEF0FFFFFFFFFFFFFFFFEFCGFFFF
```

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	?

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E-mail: [info@bgi.com](mailto:info@bgi.com)

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