



Sequencing Data Report

Project: F25A430000584_MUSukijR

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

Sample	Length	Q20(%)	Q30(%)	GC Content(%)	Total Reads	Total Bases
2_26_Rep1	150;150	98.12;98.04	93.78;93.4	44.43;44.39	28,603,666	8,581,099,800
2_26_Rep1_aux	150;150	97.28;98.22	91.23;93.84	43.04;43.11	32,207,661	9,662,298,300
2_26_Rep2	150;150	97.51;97.8	92.04;92.66	43.29;43.34	13,865,362	4,159,608,600
2_26_Rep2_aux	150;150	97.92;97.64	93.17;92.14	43.86;43.69	20,695,428	6,208,628,400
LBR2_11	150;150	98.51;98.47	95.02;94.41	37.9;38.42	6,355	1,906,500
LBR2_12	150;150	98.44;98.4	94.75;94.28	38.2;38.38	3,881	1,164,300
LBR2_13	150;150	98.55;98.51	94.98;94.55	38.05;38.62	3,683	1,104,900
LBR2_21	150;150	98.37;98.41	94.45;94.2	37.81;38.43	5,333	1,599,900
LBR2_22	150;150	98.48;98.42	94.8;94.27	37.89;38.36	4,887	1,466,100
LBR2_23	150;150	98.39;98.22	94.47;93.87	38.01;38.37	3,119	935,700
LBR2_31	150;150	98.25;98.42	93.98;94.33	38.17;38.43	3,264	979,200
LBR2_32	150;150	98.37;98.3	94.41;93.84	38.32;38.44	3,240	972,000
LBR2_33	150;150	98.26;98.37	94.15;94.13	38.23;38.37	3,646	1,093,800
LBR2_41	150;150	98.1;98.34	93.52;94.03	38.14;38.2	4,324	1,297,200
LBR2_42	150;150	98.35;98.33	94.43;94.02	38.05;38.34	4,310	1,293,000
LBR2_43	150;150	98.19;98.4	93.93;94.22	37.94;38.47	5,000	1,500,000
LBR2_51	150;150	98.2;98.39	93.9;94.22	38.25;38.36	4,623	1,386,900
LBR2_52	150;150	98.33;98.4	94.39;94.22	38.03;38.31	7,021	2,106,300
LBR2_53	150;150	98.41;98.23	94.55;93.78	38.31;38.29	2,478	743,400
LBR2_61	150;150	98.53;98.49	95.04;94.51	38.08;38.41	6,694	2,008,200
LBR2_62	150;150	98.37;98.44	94.48;94.26	37.94;38.31	6,791	2,037,300
LBR2_63	150;150	98.34;98.39	94.44;94.23	37.97;38.41	6,705	2,011,500
MoPh11_DR_Ac	150;150	98.03;97.12	93.6;91.13	49.95;50.02	15,187,194	4,556,158,200
MoPh11_DR_Cas	150;150	98.18;98.09	93.96;93.52	43.02;42.91	16,769,833	5,030,949,900
MoPh11_TR_Ac	150;150	97.48;96.82	91.92;90.19	49.12;49.22	15,608,473	4,682,541,900
MoPh11_TR_Cas	150;150	97.56;98.1	92.1;93.45	42.33;42.23	20,423,794	6,127,138,200
MoPh11_DR_Ac	150;150	97.99;96.92	92.1;90.5	49.16;49.24	16,657,106	4,997,121,900

Data Statistics

MoPh14_DR_Ac	150;150	97.65;97.94	92.37;93.0	42.96;43.1	11,168,499	3,350,549,700
MoPh14_DR_Cas	150;150	97.65;97.94	92.37;93.0	42.96;43.1	11,168,499	3,350,549,700
MoPh14_TR_Ac	150;150	98.1;97.25	93.77;91.43	49.46;49.43	20,679,329	6,203,798,700
MoPh14_TR_Cas	150;150	97.66;98.04	92.4;93.26	42.32;42.41	18,017,250	5,405,175,000
MoPh15_TR_Cas	150;150	97.2;97.08	90.95;90.15	42.09;42.17	5,627,146	1,688,143,800
MoPh7_DR_Cas	150;150	97.19;96.8	90.89;89.36	43.19;43.29	6,782,108	2,034,632,400
MoPh7_TR_Cas	150;150	97.78;97.96	92.73;93.0	41.9;41.91	18,975,023	5,692,506,900
MoPh7_VPR_Cas	150;150	97.97;97.75	93.21;92.36	42.04;42.14	15,686,267	4,705,880,100
Trih_1	150;150	96.78;98.32	89.8;94.04	42.03;42.18	107,782,591	32,334,777,300
Trih_2	150;150	98.31;98.72	94.36;95.36	41.47;41.92	178,611,113	53,583,333,900
brInt_a_R2	150;150	98.09;98.03	93.76;93.47	44.57;44.46	4,627,908	1,388,372,400
brLinker_Rep5_aux	150;150	96.78;98.32	89.84;94.25	44.79;44.72	40,809,159	12,242,747,700
brLinker_a_R3	150;150	97.7;97.6	92.62;92.14	44.23;44.15	5,848,413	1,754,523,900
brLinker_a_R4	150;150	97.03;97.16	90.43;90.57	45.98;46.12	4,903,179	1,470,953,700
brNTD_Rep6_aux	150;150	97.37;98.42	91.58;94.63	44.83;44.88	32,467,472	9,740,241,600
brNTD_a_R3	150;150	98.06;97.73	93.7;92.65	46.73;46.74	4,141,063	1,242,318,900
brNTD_a_R5	150;150	96.17;97.2	88.2;90.79	45.94;45.74	1,746,453	523,935,900
brRad21_Rep1	150;150	98.24;98.45	94.18;94.73	43.85;43.97	31,688,615	9,506,584,500
brRad21_Rep1_aux	150;150	98.2;98.0	94.03;93.29	44.09;43.94	23,851,227	7,155,368,100
brRad21_Rep2	150;150	98.24;98.45	94.18;94.68	43.62;43.88	25,697,302	7,709,190,600
brRad21_Rep2_aux	150;150	98.11;97.98	93.76;93.22	42.62;42.28	19,543,503	5,863,050,900
i_MoPh11_DR	150;150	97.31;97.48	91.56;91.83	46.23;46.43	8,492,433	2,547,729,900
i_MoPh11_TR	150;150	97.5;97.63	92.1;92.29	45.83;45.92	9,201,104	2,760,331,200
i_MoPh14_DR	150;150	97.32;97.2	91.58;91.02	46.45;46.55	9,188,883	2,756,664,900
i_MoPh14_TR	150;150	97.74;97.32	92.87;91.54	46.9;46.93	13,476,532	4,042,959,600
i_MoPh7_TR_Cas	150;150	97.38;97.45	91.82;91.72	44.83;44.86	7,896,731	2,369,019,300
targ_PandR_MSQ43RGPC	150;150	98.5;97.99	94.87;93.19	48.5;48.45	1,874,761	562,428,300
targ_PandR_MoPh11	150;150	98.45;98.48	94.77;94.76	44.31;44.06	334,091	100,227,300
targ_PandR_MoPh14	150;150	98.66;98.51	95.44;94.85	46.03;46.17	631,341	189,402,300
targ_PandR_MoPh15	150;150	98.49;98.43	94.94;94.62	45.68;46.01	391,874	117,562,200
targ_PandR_MoPh7	150;150	97.0;98.12	90.45;93.64	46.52;46.57	642,573	192,771,900

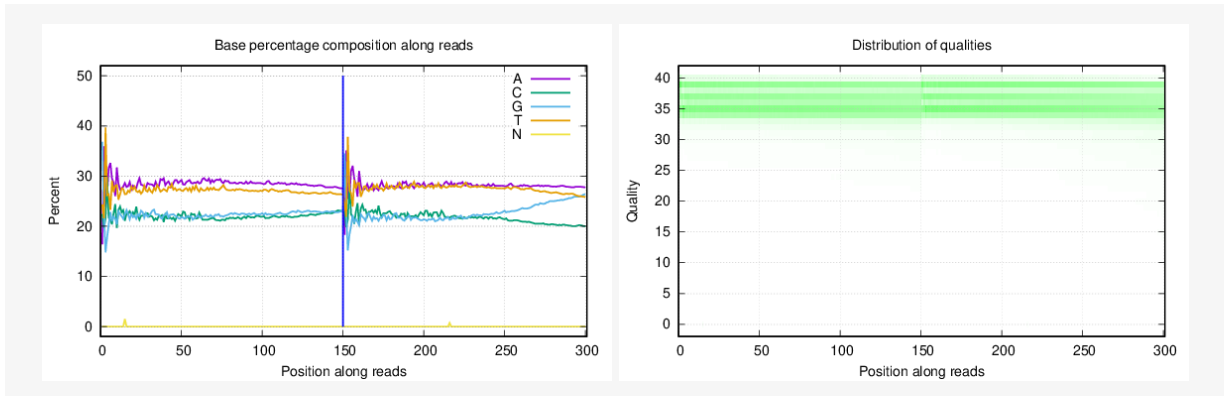
Table Format:

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

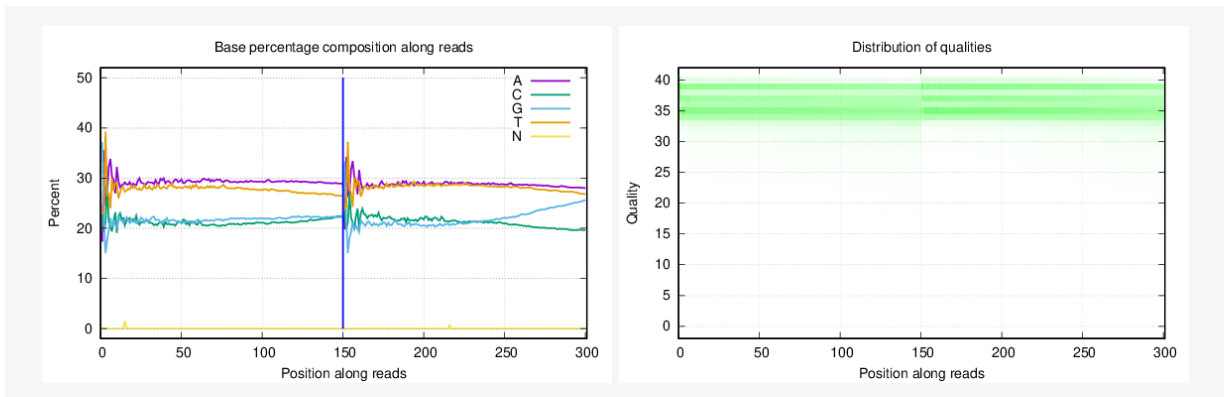
Data Quality Control

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.

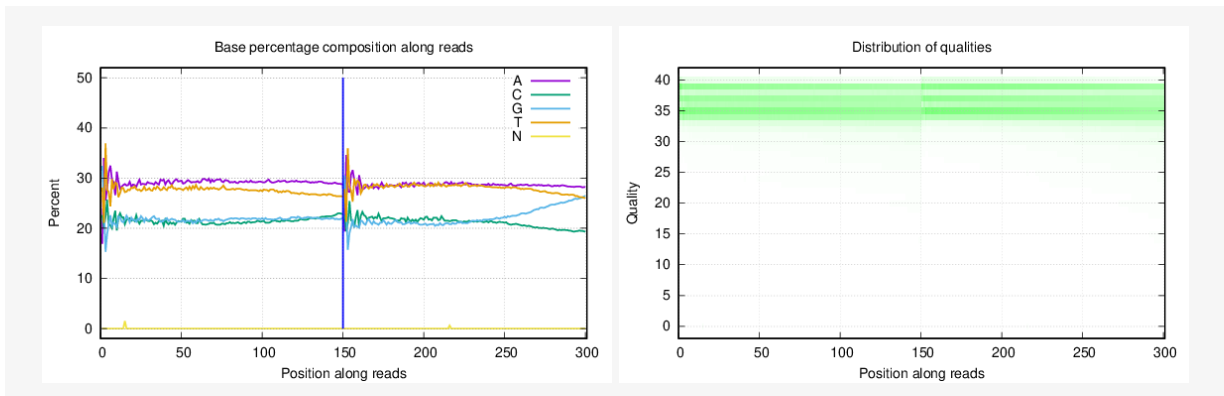
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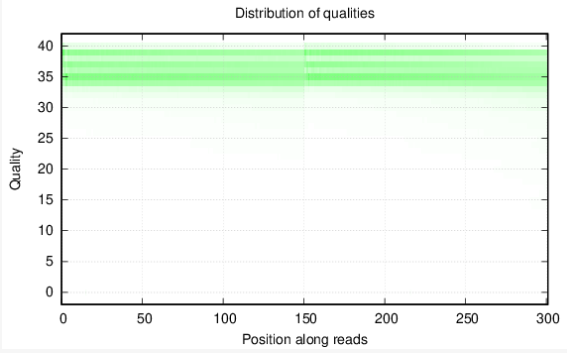
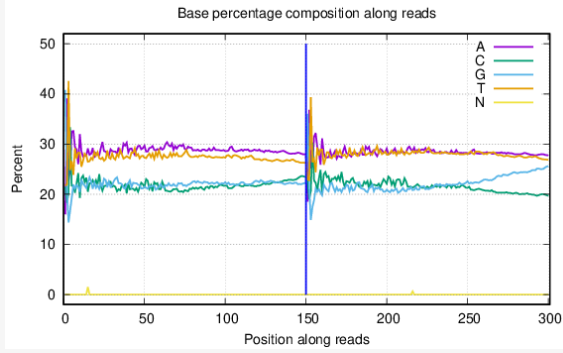
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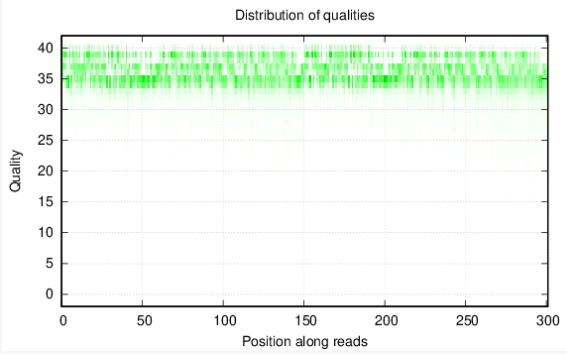
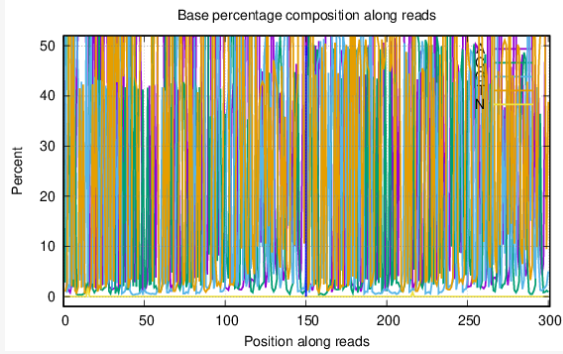
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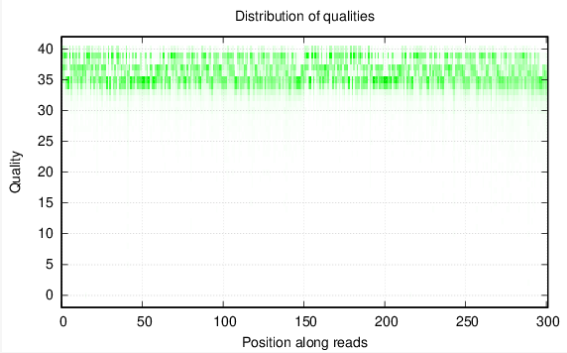
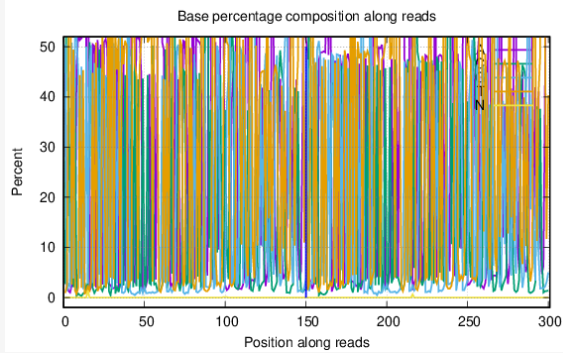
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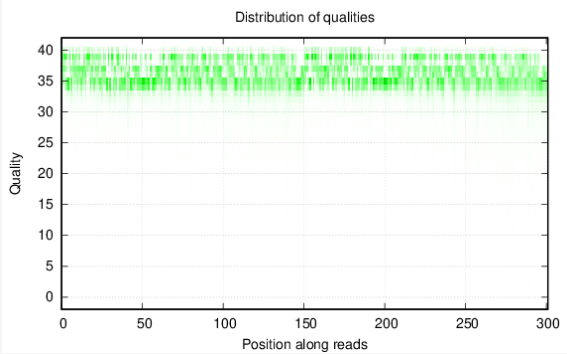
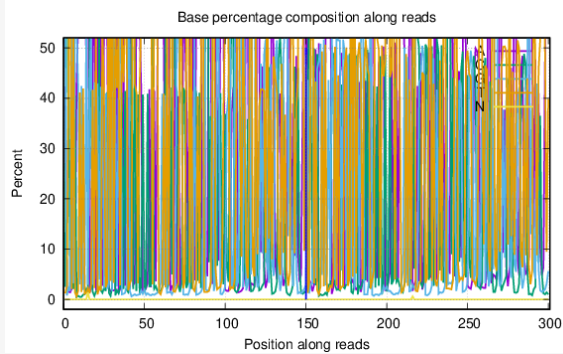
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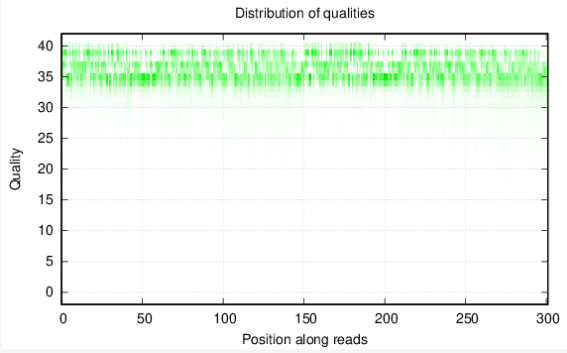
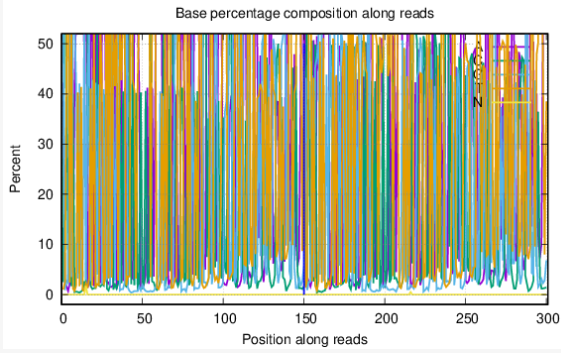
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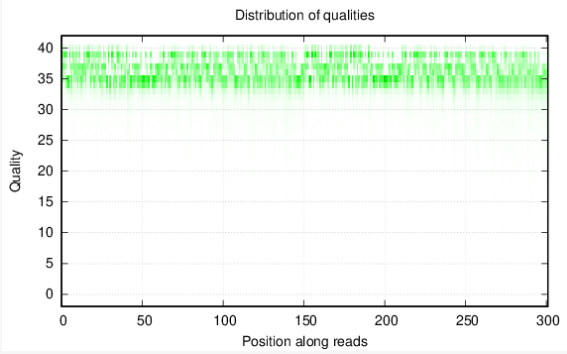
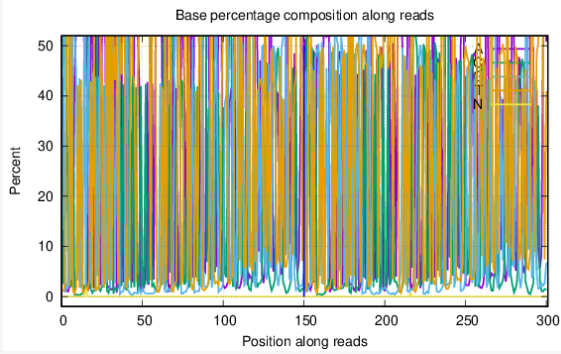
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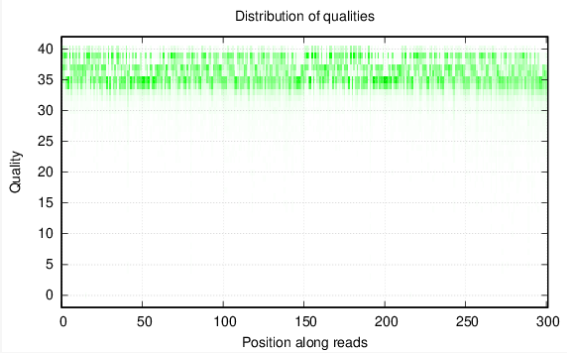
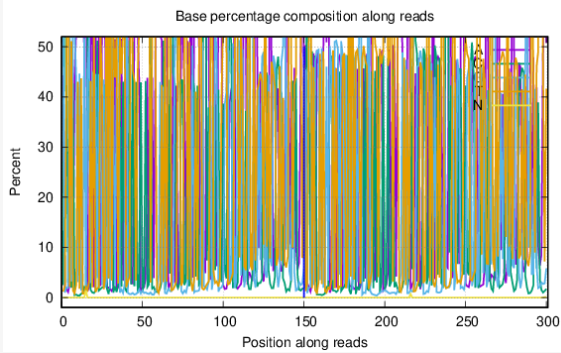
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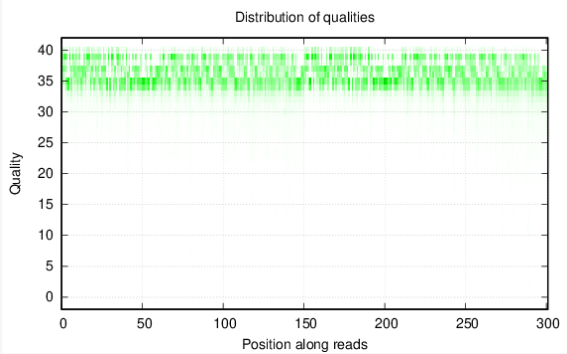
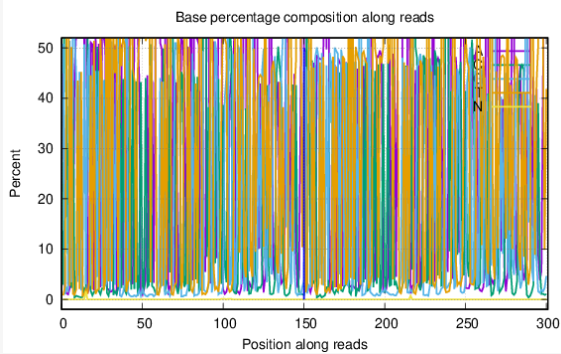
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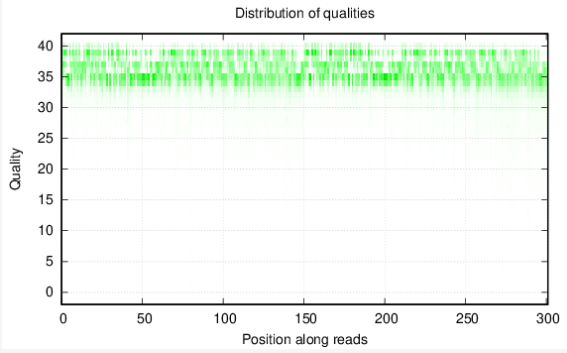
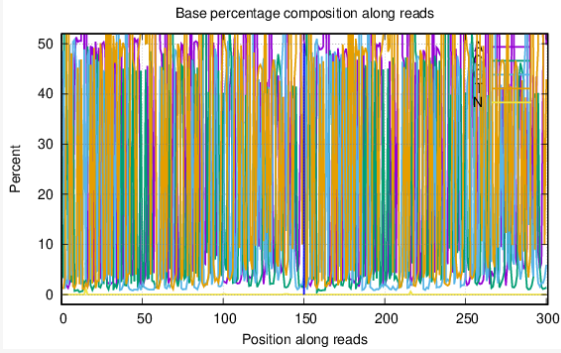
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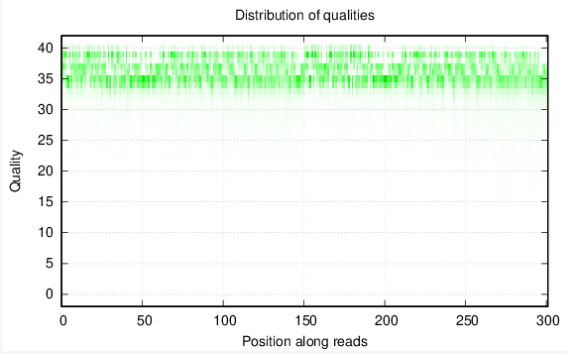
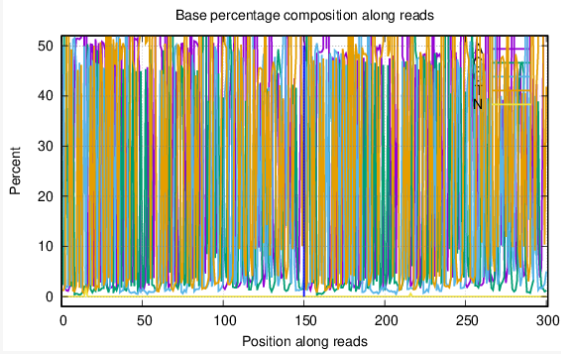
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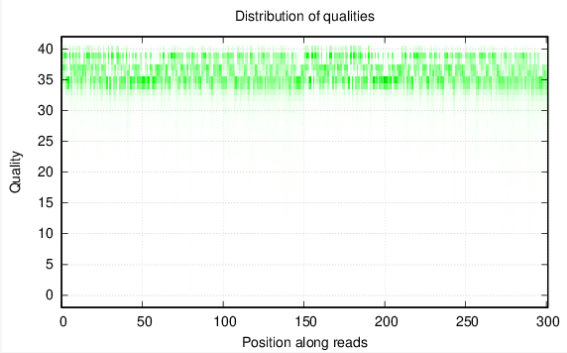
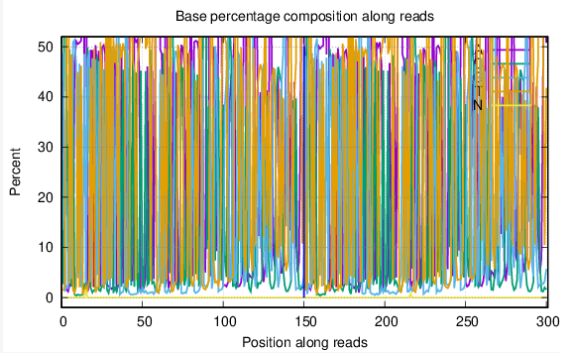
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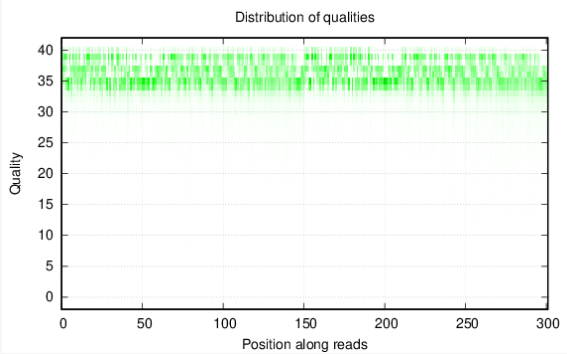
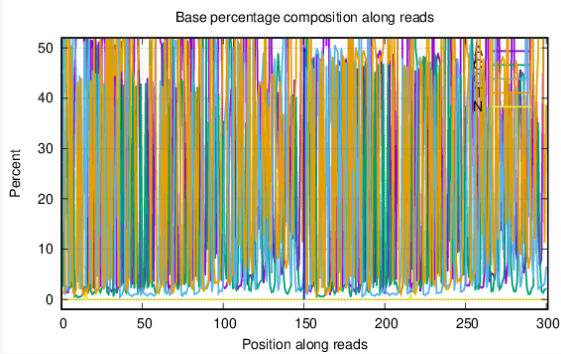
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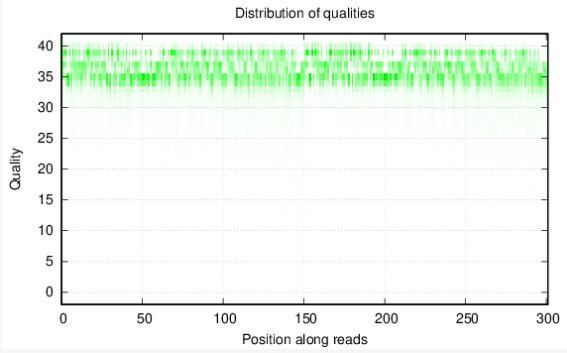
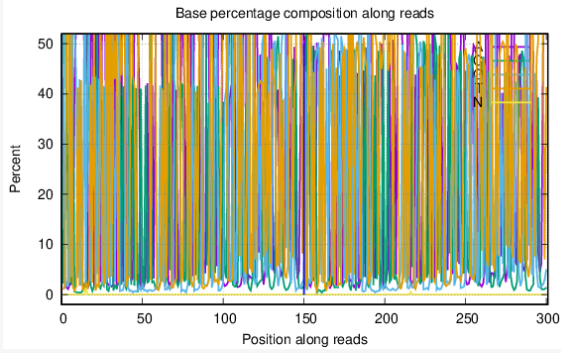
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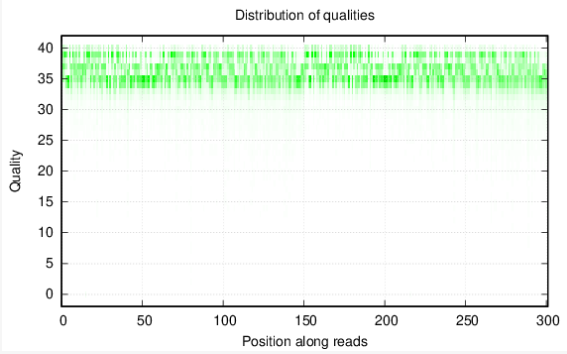
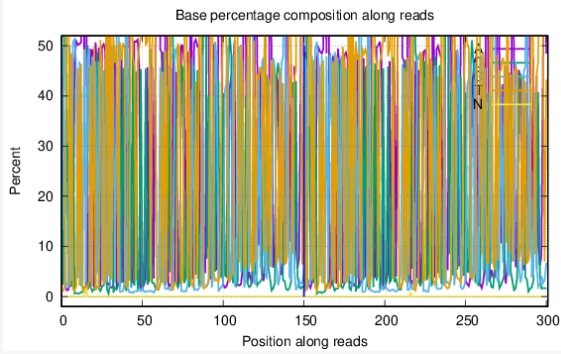
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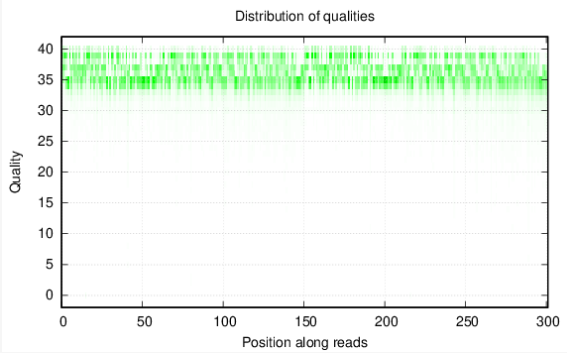
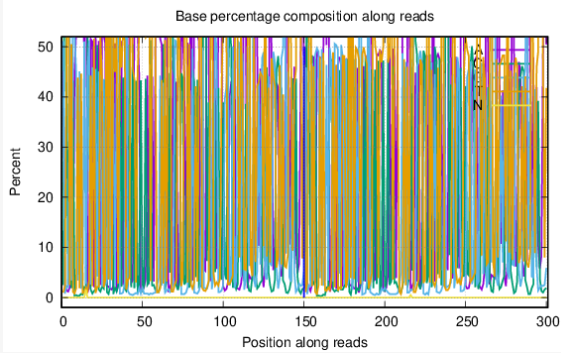
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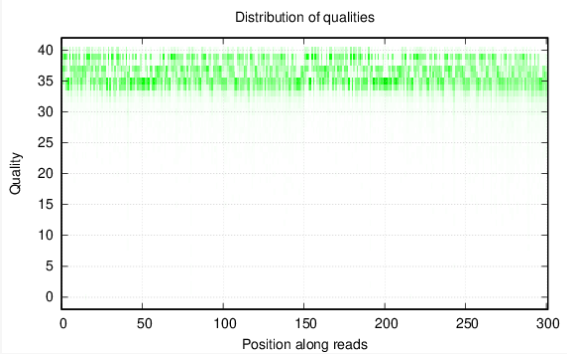
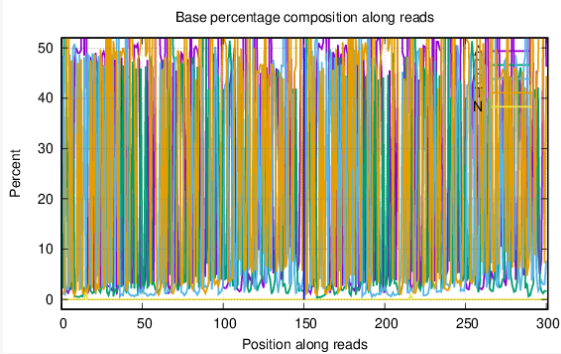
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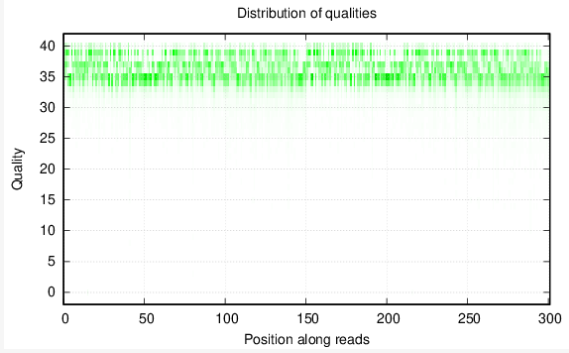
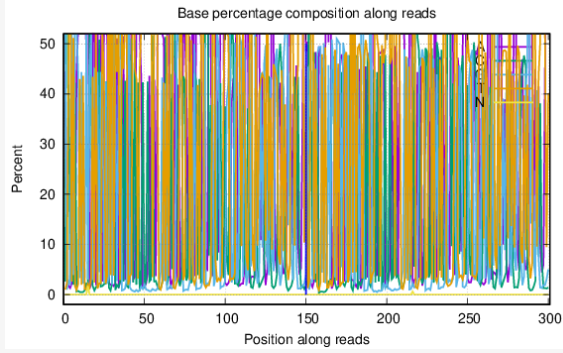
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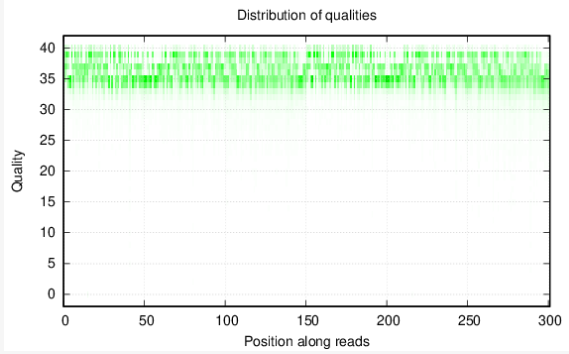
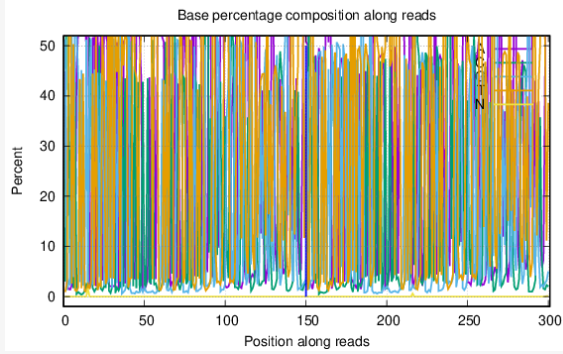
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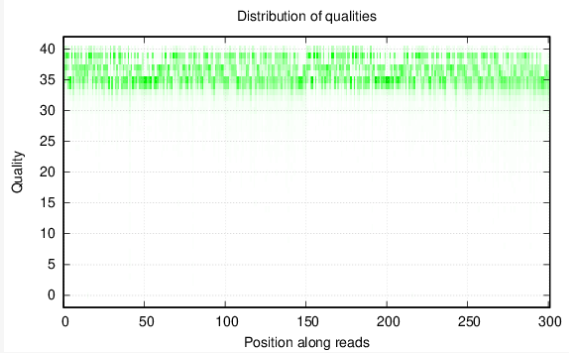
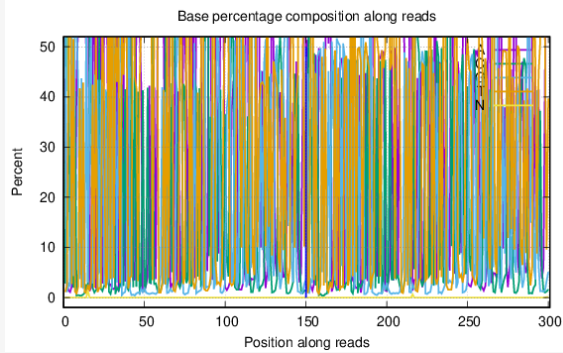
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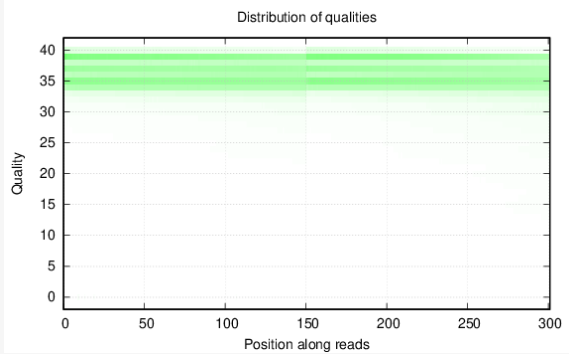
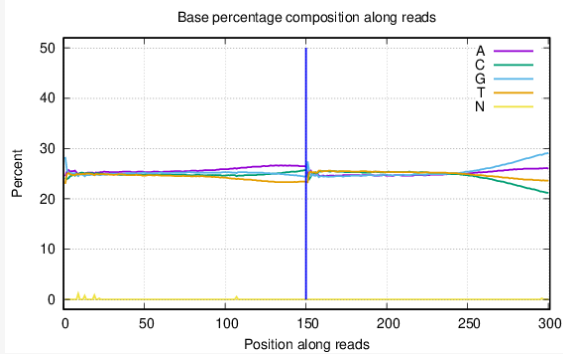
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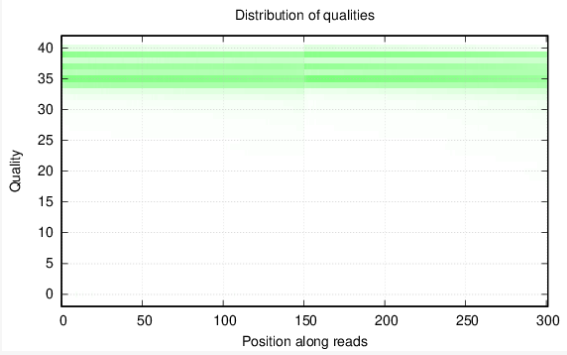
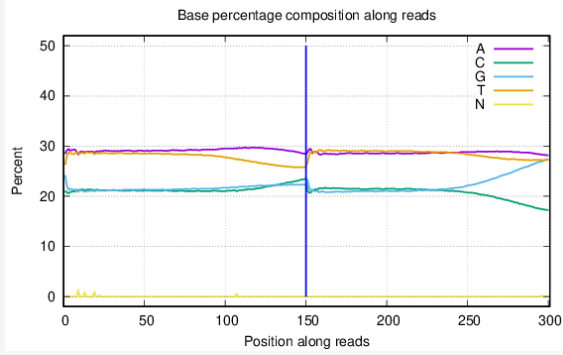
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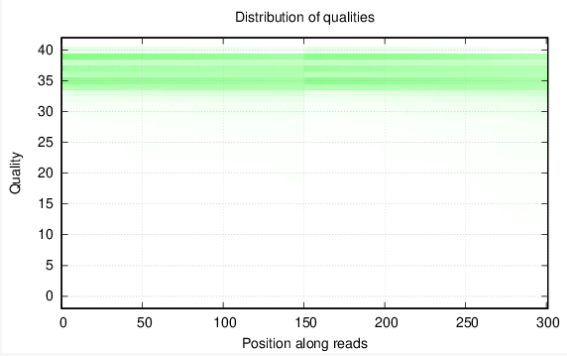
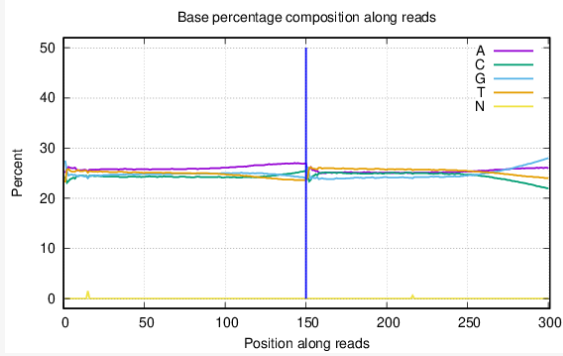
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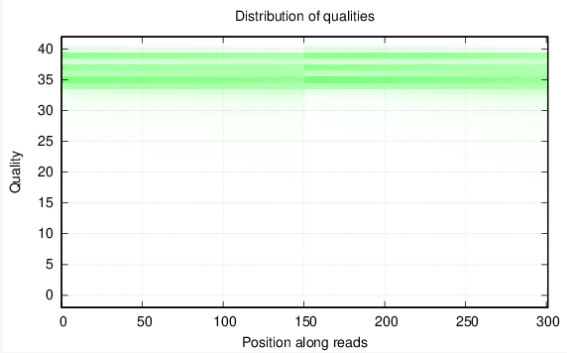
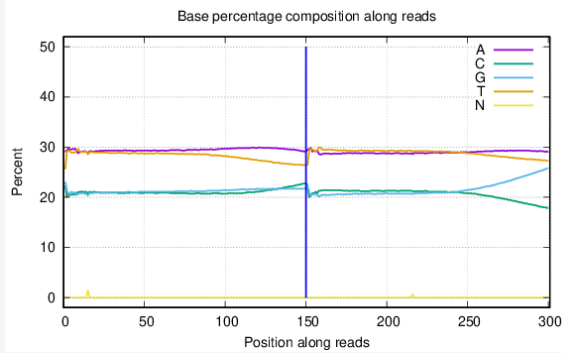
MoPh11_DR_Cas



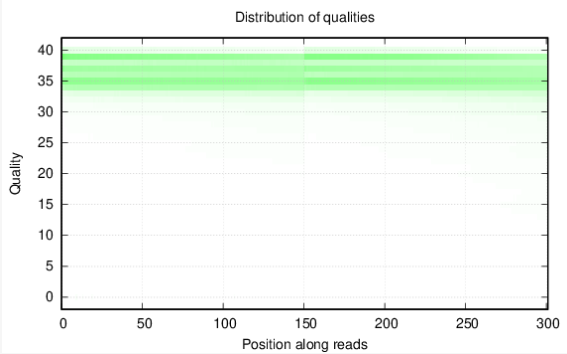
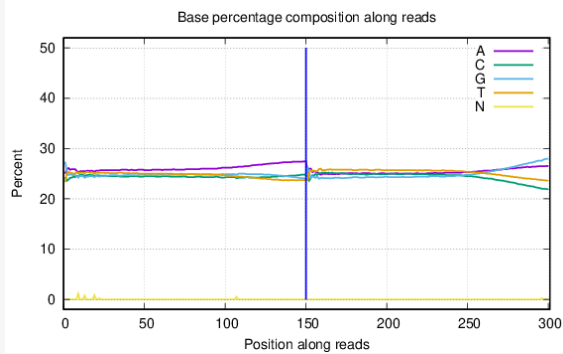
MoPh11_TR_Ac



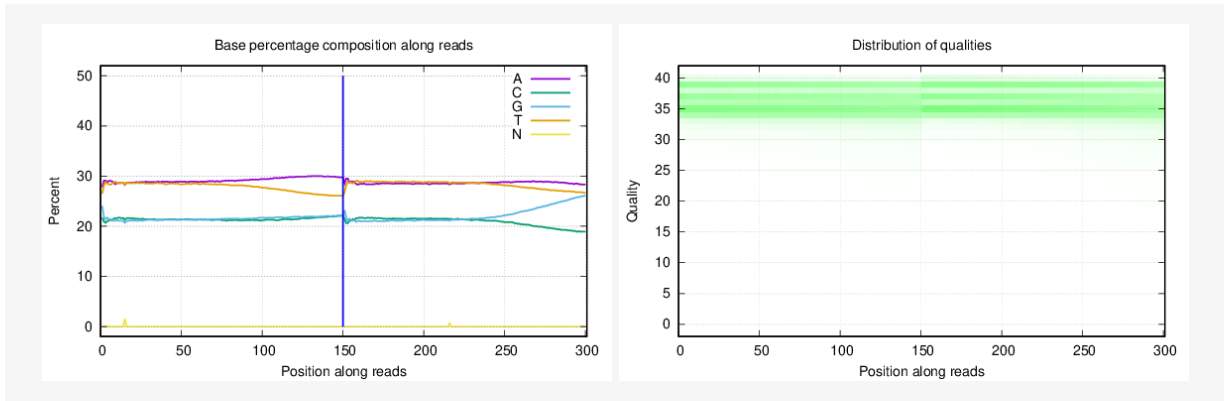
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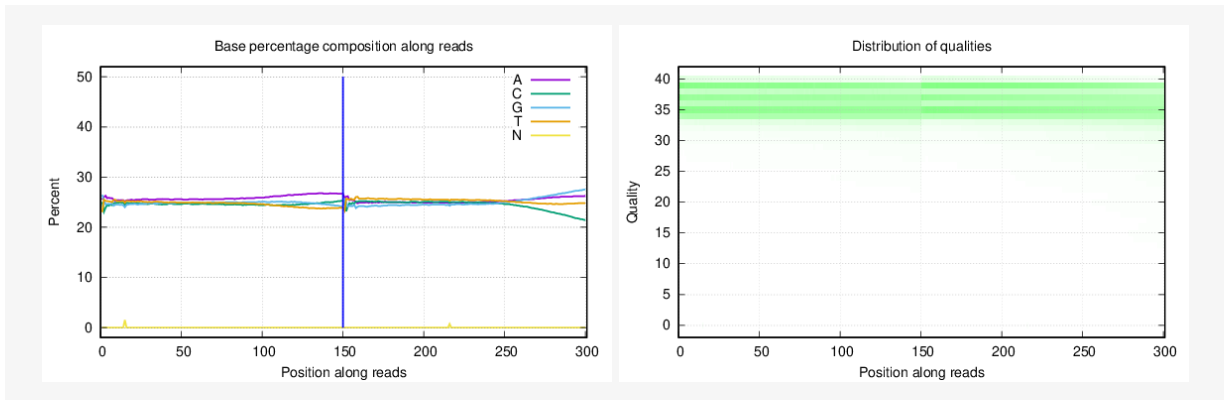
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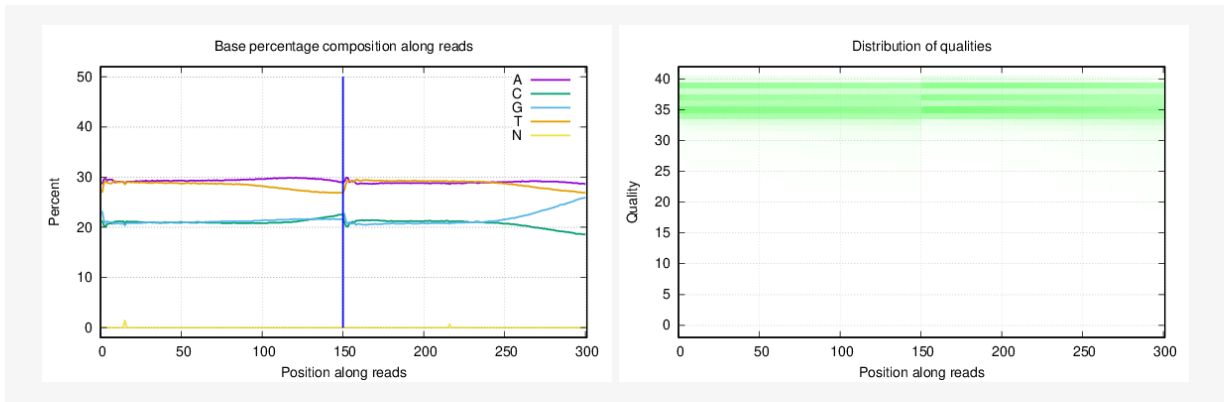
MoPh14_DR_Cas



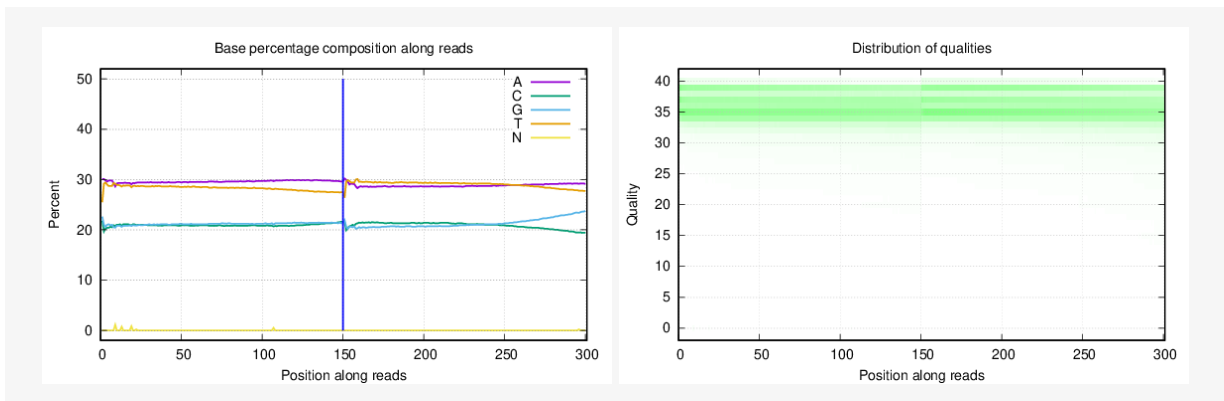
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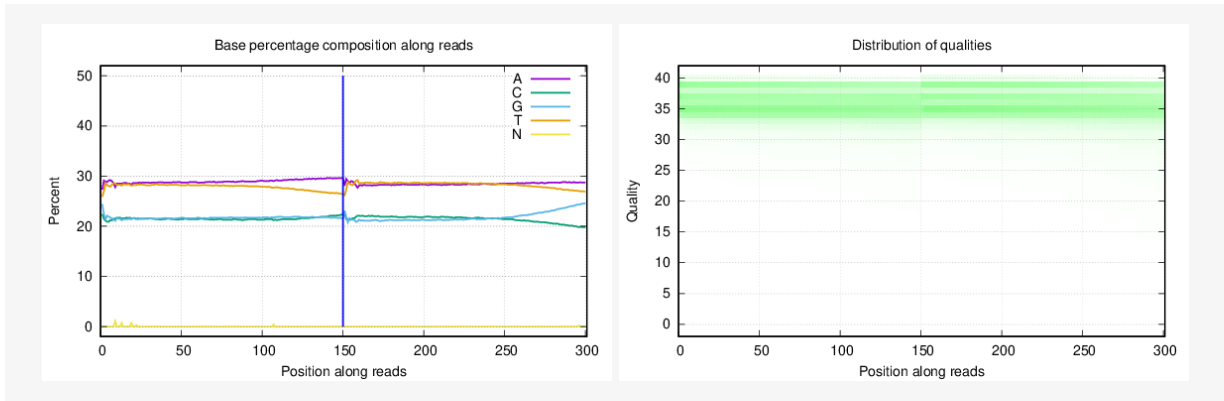
MoPh14_TR_Cas



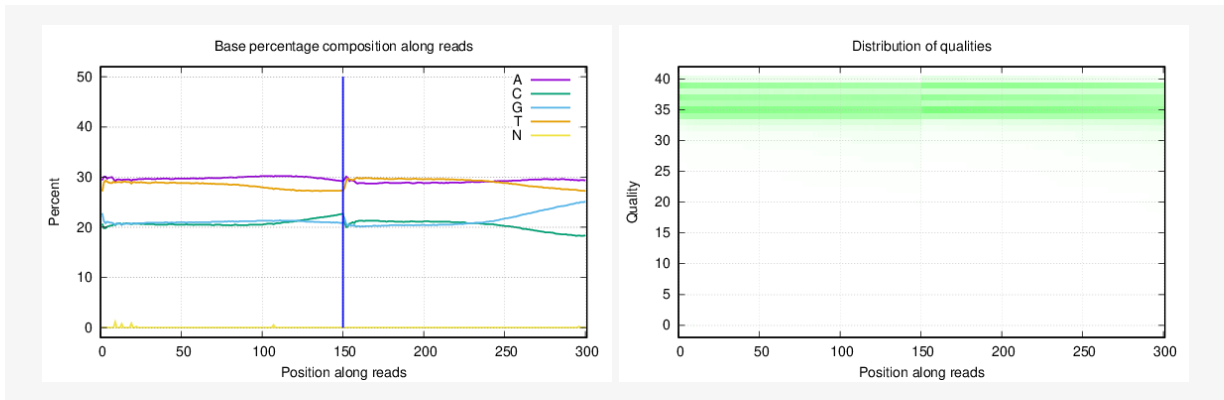
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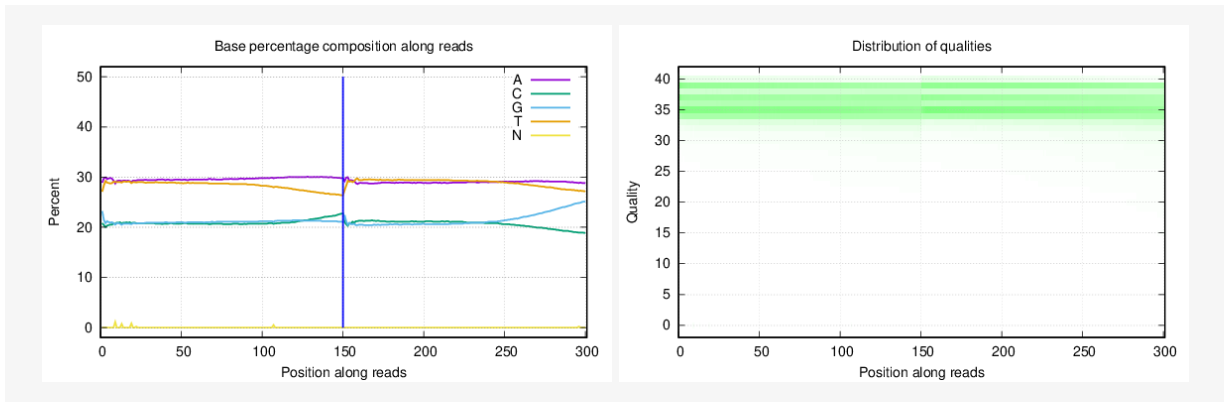
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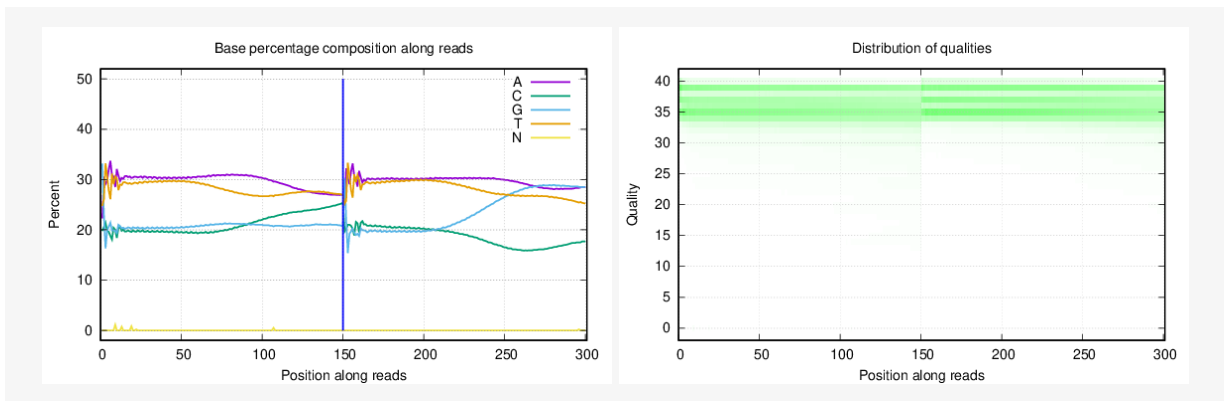
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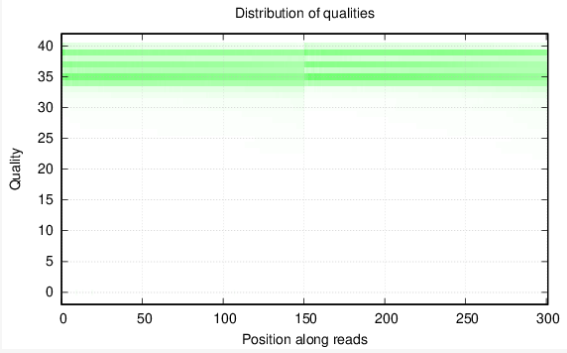
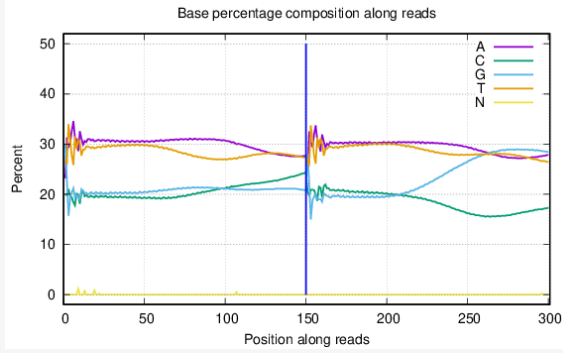
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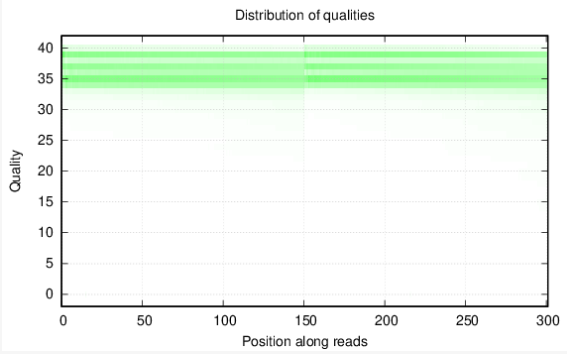
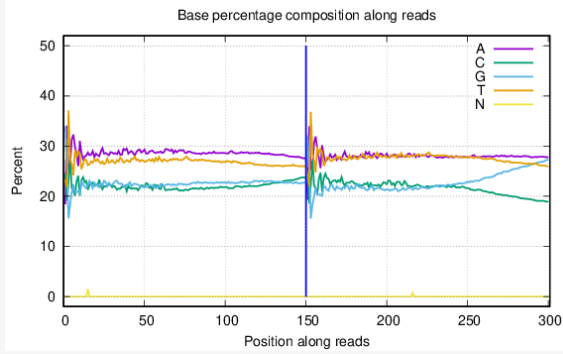
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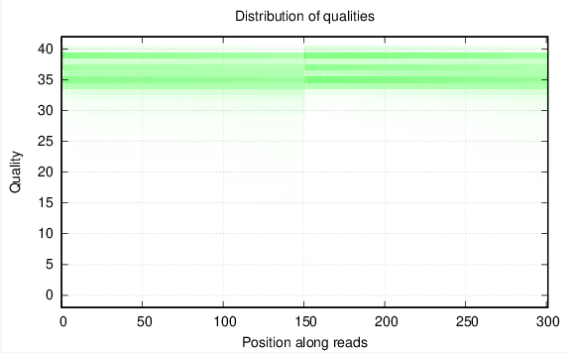
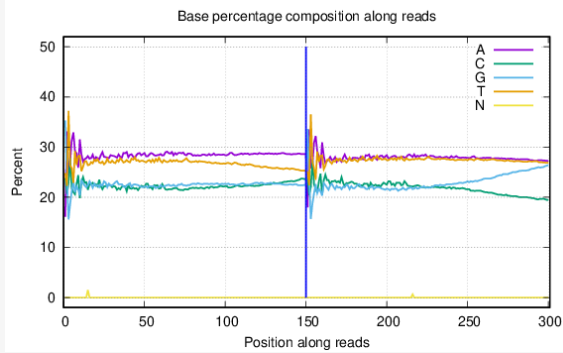
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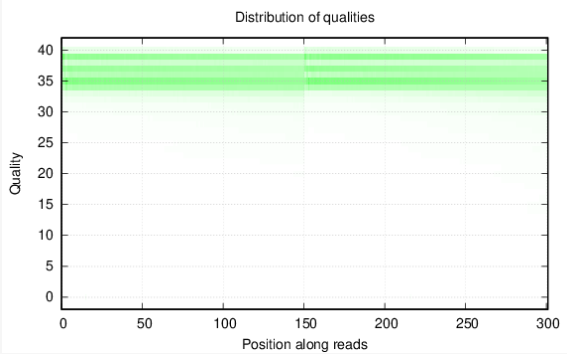
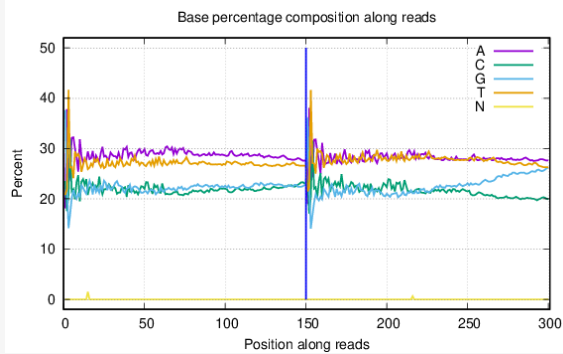
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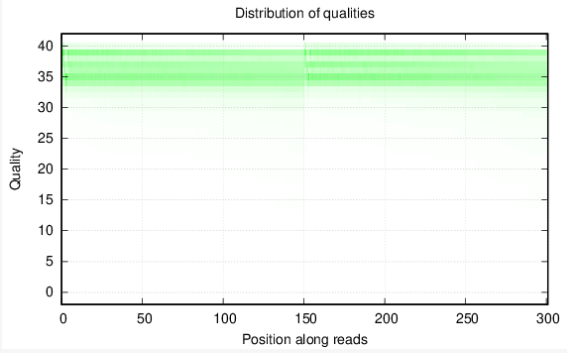
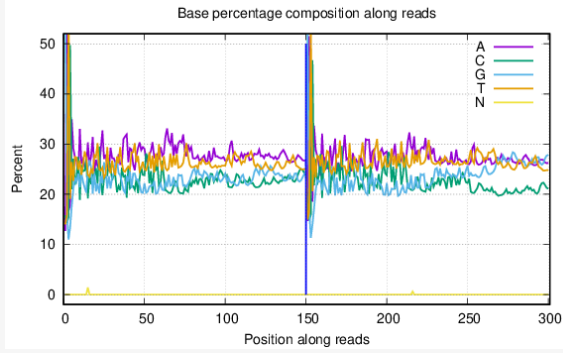
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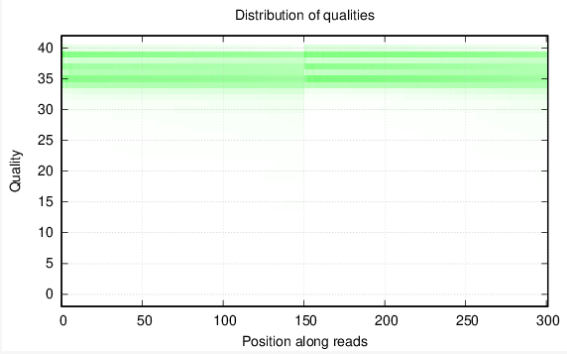
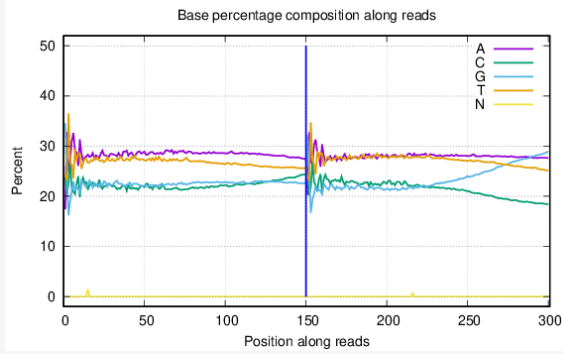
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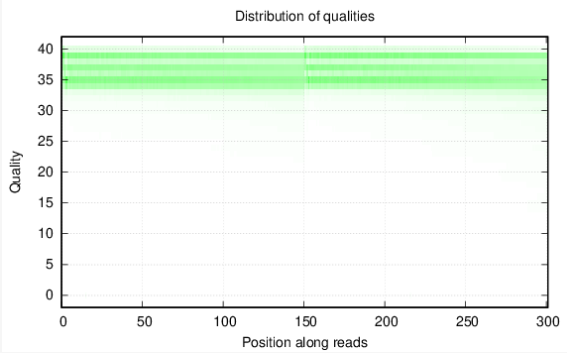
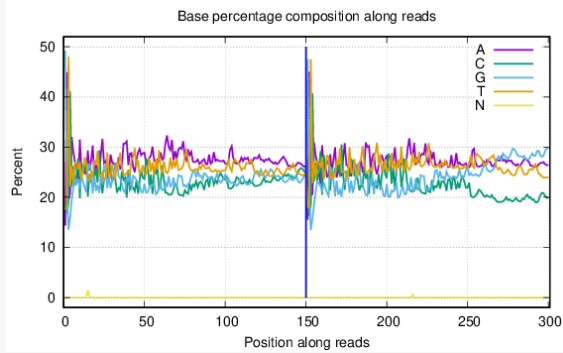
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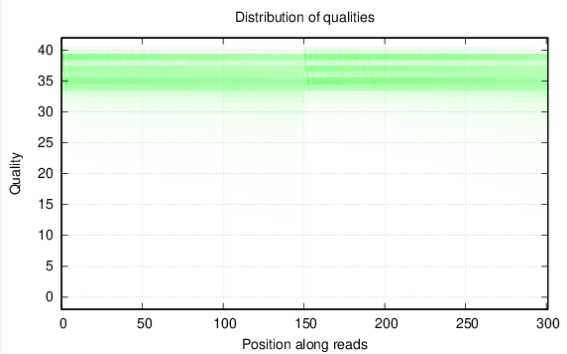
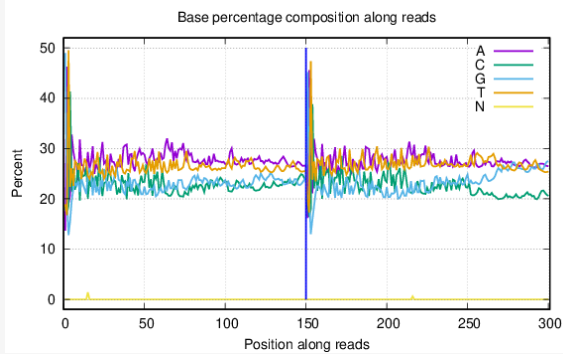
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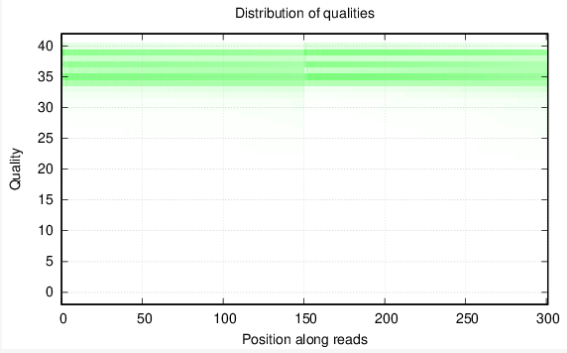
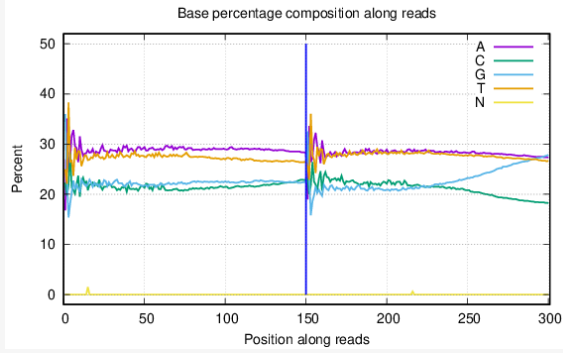
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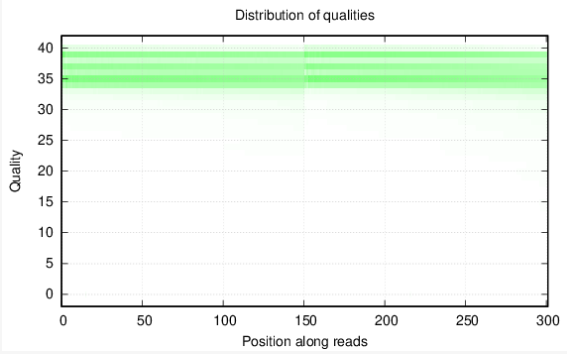
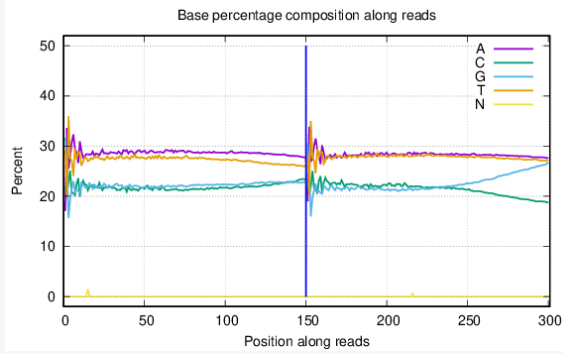
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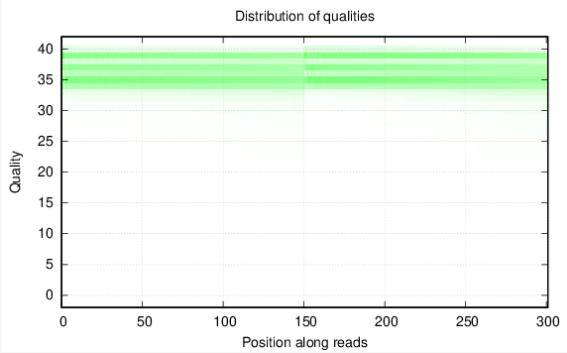
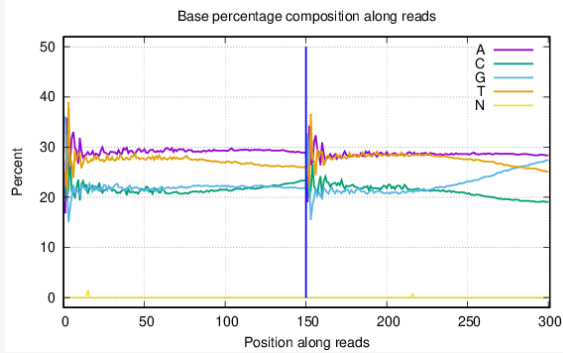
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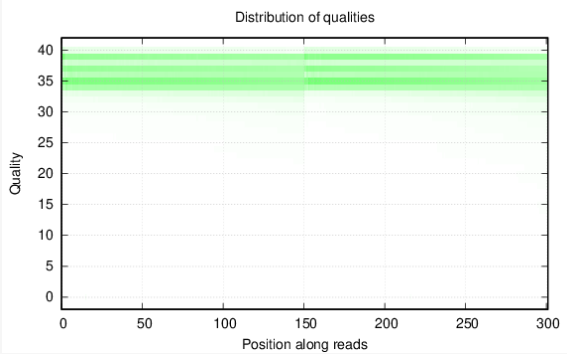
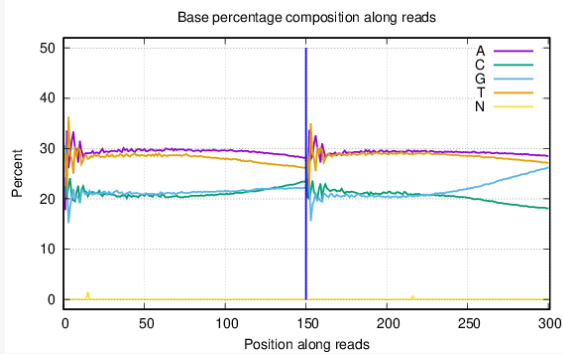
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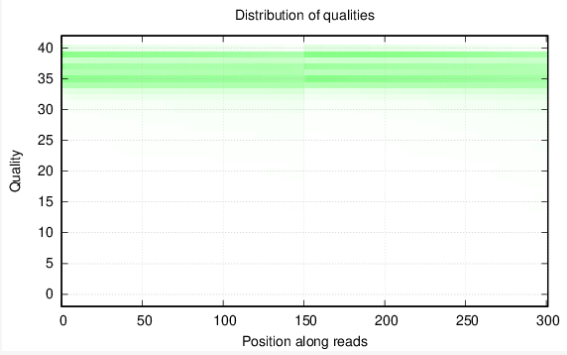
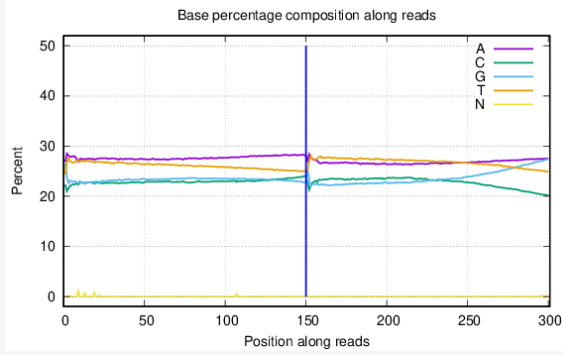
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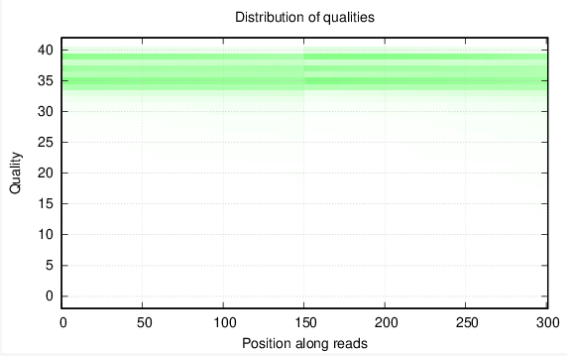
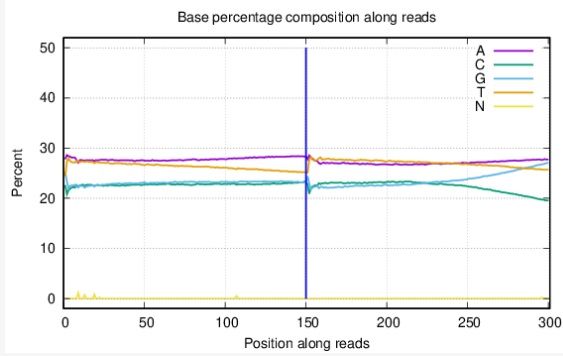
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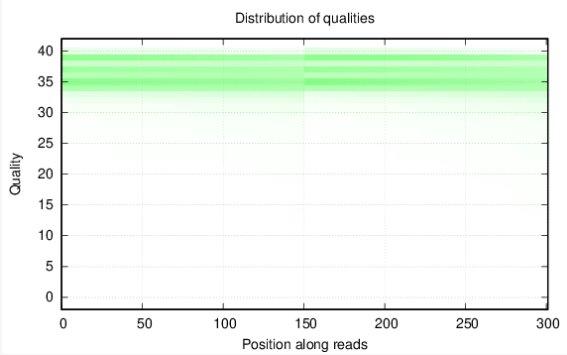
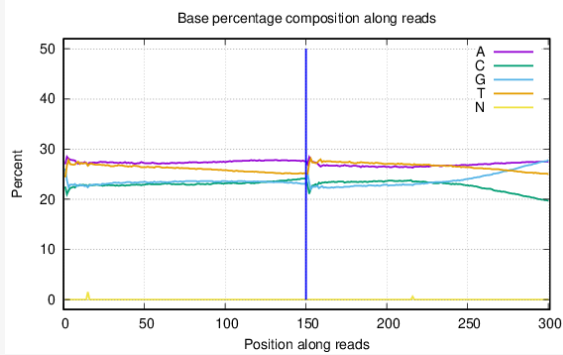
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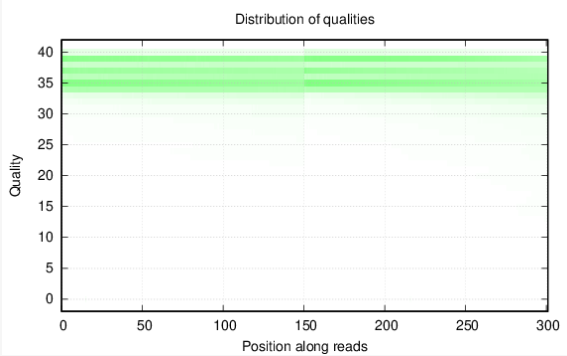
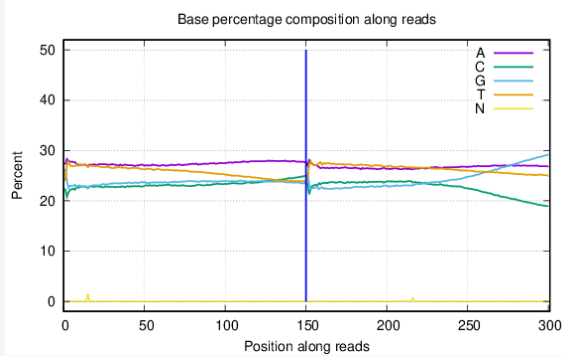
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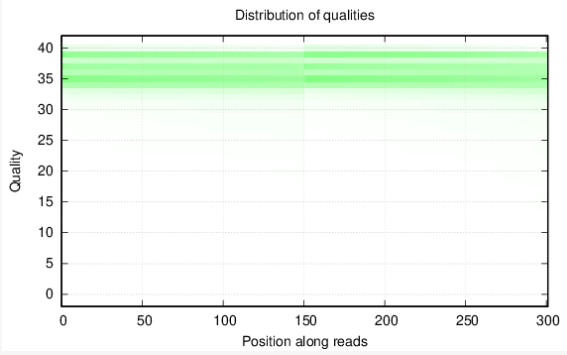
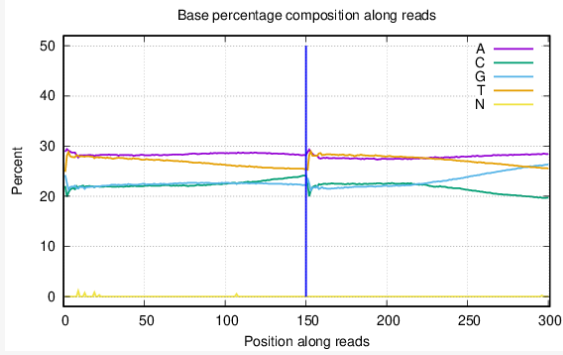
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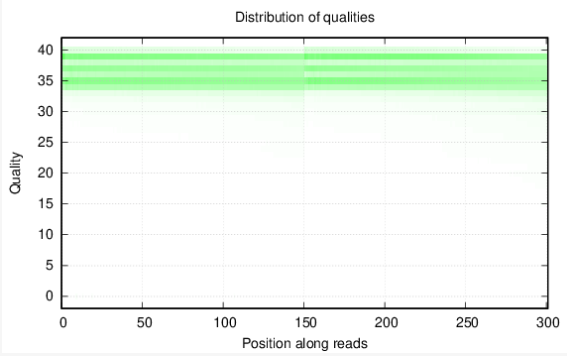
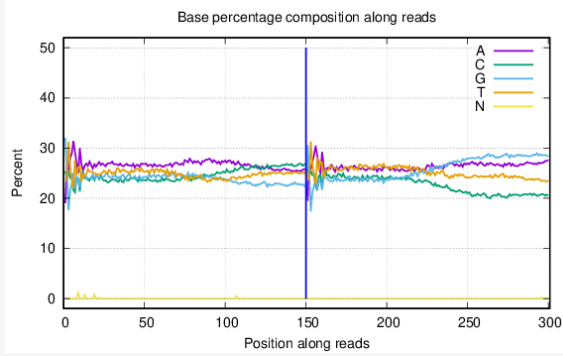
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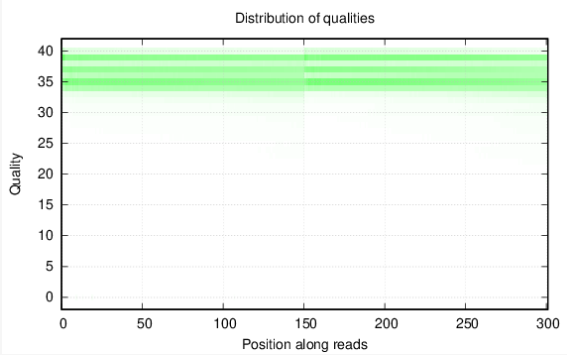
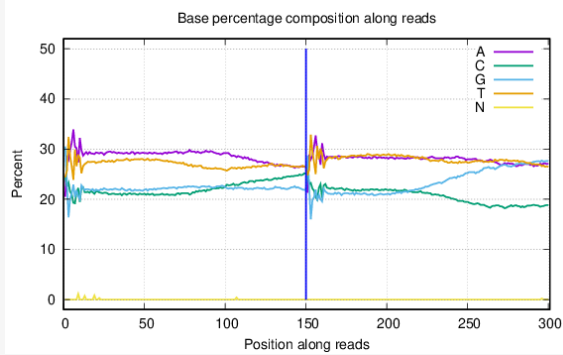
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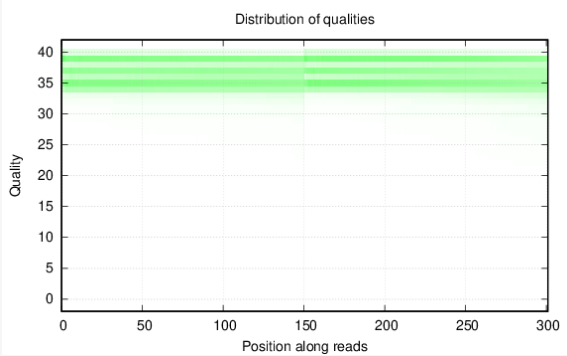
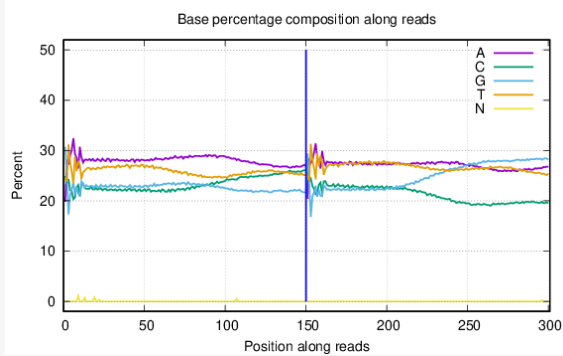
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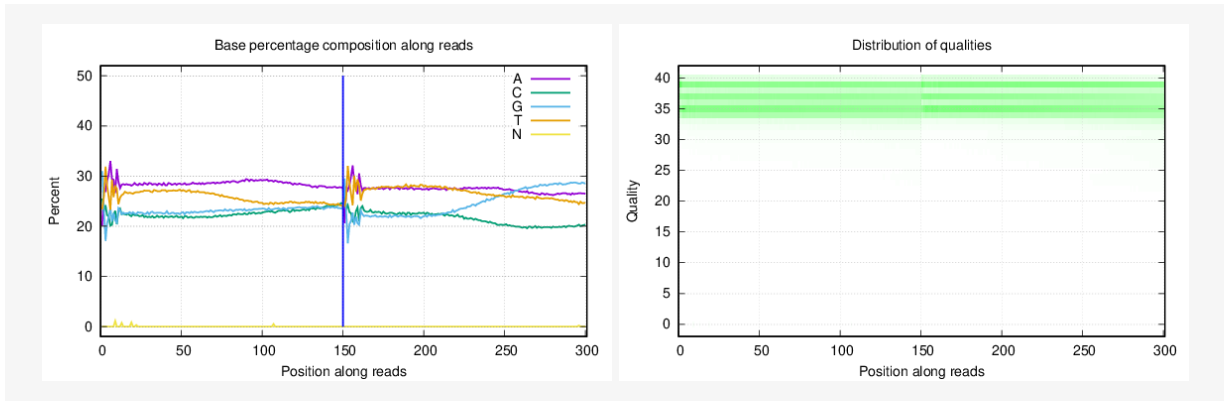
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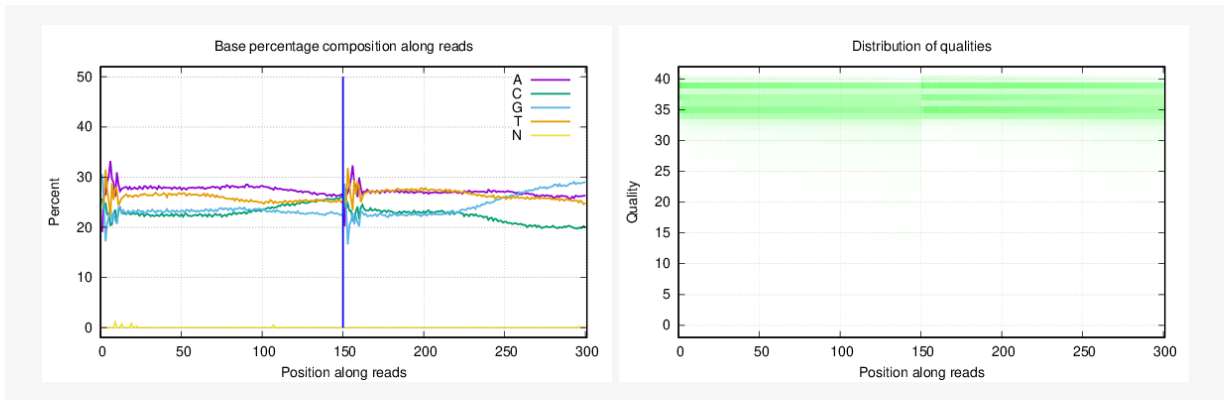
targ_PandR_MoPh14



targ_PandR_MoPh15



targ_PandR_MoPh7



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
+
FFFCFFFFFFFFDFEFFFFFFEF0FFFFFFEFFFFFFEFFFFFFEFCGFFFF
```

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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