Sequencing Data Report

Project: F25A430000584_MUStxenR
Date: 2025.5.3
Note: For Research Use Only.

BGI Genomics Co.,Ltd.

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Data Statistics

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

There are 224 samples in this project, the statistics of fastq data is shown below.

Sample	Length	Q20(%)	Q30(%)	GC Content(%)	Total Reads	Total Bases
12	150;150	99.36;98.52	95.18;94.33	45.69;45.77	33,438,491	10,031,547,300
17	150;150	99.42;98.69	95.62;95.0	45.43;45.54	40,179,648	12,053,894,400
1771	150;150	96.95;97.26	87.23;91.65	52.91;52.14	19	5,700
19646	150;150	99.75;98.87	98.42;95.48	50.11;50.45	53	15,900
21	150;150	99.43;98.79	95.65;95.31	45.2;45.28	35,834,418	10,750,325,400
22	150;150	99.45;98.79	95.76;95.32	45.03;45.1	34,160,008	10,248,002,400
23	150;150	99.48;98.86	96.02;95.54	45.07;45.13	35,374,513	10,612,353,900
2322	150;150	99.73;98.81	97.6;95.46	56.36;56.19	3,509	1,052,700
24	150;150	99.48;99.02	96.03;96.21	45.77;45.87	44,046,646	13,213,993,800
25	150;150	99.48;98.93	96.05;95.85	45.61;45.68	37,519,242	11,255,772,600
4	150;150	99.4;98.67	95.5;94.98	45.31;45.38	23,595,753	7,078,725,900
42	150;150	99.27;98.0	95.68;93.23	50.87;51.03	720	216,000
4Cplasmid_lig_adapt_0_24_6	150;150	99.23;99.14	94.02;96.34	44.29;45.17	50,782,403	15,234,720,900
4Cplasmid_lig_adapt_0_24_7	150;150	99.25;98.78	94.06;94.86	43.97;44.5	7,483,812	2,245,143,600
4Cplasmid_lig_adapt_16_7_6	150;150	99.28;98.83	94.27;95.08	43.64;44.23	19,350	5,805,000
4Cplasmid_lig_adapt_16_7_7	150;150	99.6;99.16	96.51;96.69	49.58;49.61	1,177,321	353,196,300
5	150;150	99.39;98.67	95.45;94.97	44.69;44.78	25,510,479	7,653,143,700
6	150;150	99.38;98.69	95.34;94.97	44.77;44.87	40,153,465	12,046,039,500
7	150;150	98.53;96.18	91.3;88.11	45.48;45.67	26,886	8,065,800
74C_R3	150;150	99.38;98.24	94.59;92.78	43.51;43.62	26,174,022	7,852,206,600
8	150;150	99.35;98.5	95.08;94.21	45.01;45.12	34,445,630	10,333,689,000
87C_R5	150;150	99.44;98.15	94.97;92.41	44.12;44.17	11,834,965	3,550,489,500
87T_R5	150;150	99.49;98.37	95.37;93.28	43.07;43.1	51,569,546	15,470,863,800
Blank-Sn-1	150;150	99.66;98.53	97.19;94.61	57.89;58.16	965	289,500
Blank-Sn-2	150;150	99.16;99.29	94.0;96.87	48.91;46.79	58	17,400
CMV-PCR-Nla_3	150;150	99.54;98.47	95.89;93.75	50.76;51.58	746,620	223,986,000
CMV-PCR-Nla_Kl_3dtransf_4	150;150	99.45;98.28	95.28;93.04	51.0;51.79	713,606	214,081,800
CV4_CV3-9	150;150	99.75;98.61	97.43;94.82	60.22;60.37	280	84,000

CV7_CV3-7	150;150	99.74;98.68	97.64;94.95	60.19;60.5	59,785	17,935,500
Cen_B3	150;150	99.47;98.81	96.04;95.41	46.3;46.2	12,651,082	3,795,324,600
Cen_B4	150;150	99.43;98.83	95.8;95.46	45.36;45.51	85,883,268	25,764,980,400
Cen_B5	150;150	99.2;98.68	94.66;94.96	49.46;49.98	6,014,408	1,804,322,400
Cen_B6	150;150	99.33;98.66	95.23;94.75	50.07;50.42	6,742,820	2,022,846,000
Cen_P	150;150	99.44;99.03	96.0;96.26	45.95;46.08	107,171,213	32,151,363,900
Cen_Po	150;150	99.36;98.63	95.41;94.69	45.05;45.08	54,751,927	16,425,578,100
CoIne-1	150;150	99.59;99.24	96.81;97.12	48.55;48.39	12,483	3,744,900
CoIne-2	150;150	99.6;99.23	96.96;97.14	49.11;48.4	21,317	6,395,100
CoIne-3	150;150	99.38;99.08	95.44;96.53	43.78;43.9	206	61,800
CoIne-4	150;150	98.63;98.04	92.3;92.22	48.6;48.4	764	229,200
CusBog-1	150;150	99.57;99.2	96.82;97.0	49.4;48.32	70,745	21,223,500
CusBur-1	150;150	99.63;98.57	96.86;94.96	58.18;57.76	275	82,500
CusCha09-1	150;150	99.67;98.61	97.72;94.68	50.07;51.05	38	11,400
CusKon-1	150;150	99.45;97.36	94.77;92.22	54.33;54.98	61	18,300
CusKras-1	150;150	99.48;99.15	96.45;96.74	52.02;52.38	541	162,300
CusTash-1	150;150	99.61;99.03	97.04;96.04	56.99;56.22	2,415	724,500
CusUst-1	150;150	99.71;99.01	97.38;96.1	54.92;54.37	1,156	346,800
CusUst-2	150;150	99.75;98.51	96.83;94.74	50.8;50.82	56	16,800
EB3_13_26	150;150	99.2;98.47	93.86;93.61	42.14;41.42	12,835	3,850,500
EB3_149_3	150;150	99.06;98.69	93.17;94.33	42.42;42.07	3,077	923,100
EB3_149_4	150;150	99.19;98.47	93.81;93.53	41.32;40.88	12,739	3,821,700
EB3_151_4	150;150	99.0;98.36	92.83;93.16	41.13;40.4	4,823	1,446,900
EB3_1_25	150;150	99.08;98.35	93.43;93.09	39.71;39.59	3,902	1,170,600
EB3_6_4	150;150	99.23;98.73	94.38;94.7	45.19;44.86	12,234	3,670,200
EB3_7_4	150;150	98.94;98.17	92.44;92.37	40.93;40.43	2,328	698,400
EB6_149_1	150;150	99.24;98.95	93.97;95.51	43.91;43.63	13,457	4,037,100
EB6_149_2	150;150	99.01;98.55	92.81;94.0	40.56;40.32	1,484	445,200
EB6_149_3	150;150	99.18;99.07	93.32;95.99	45.9;45.51	2,610	783,000
EB6_181	150;150	99.07;98.81	93.14;94.99	42.94;41.91	7,452	2,235,600
EB6_1_25	150;150	99.09;98.64	93.4;94.28	40.69;40.71	3,854	1,156,200
EB6_7_4	150;150	99.18;98.74	93.72;94.73	43.45;42.8	2,205	661,500
EBA1_25	150;150	99.47;98.64	96.3;94.81	56.56;55.99	612	183,600

EBC1_25	150;150	98.81;97.82	92.5;92.33	48.78;49.82	12,330	3,699,000
EBM2_25	150;150	99.76;99.3	97.65;97.09	52.31;53.12	6,790	2,037,000
EBS1	150;150	99.08;99.29	93.88;97.21	51.3;51.09	2,690	807,000
EBS2	150;150	99.44;98.68	96.27;94.66	49.35;48.61	98	29,400
EBS3	150;150	98.75;97.66	90.93;93.33	52.05;50.98	6,799	2,039,700
EKB_1_25	150;150	99.85;98.18	98.43;93.43	61.21;61.55	253	75,900
EKB_2_25	150;150	99.61;99.41	96.74;97.58	46.22;48.0	25,650	7,695,000
Ezh3_K	150;150	99.25;97.97	93.48;91.41	42.5;42.52	5,332,506	1,599,751,800
FerKra1-1	150;150	99.65;98.11	96.54;93.25	53.84;53.58	327	98,100
FerLoko-1	150;150	99.45;98.97	96.37;96.04	48.17;48.74	507	152,100
FerPre-1	150;150	99.03;95.77	93.79;85.69	53.9;53.67	26	7,800
FerTik-1_1	150;150	99.09;98.97	93.81;96.71	46.86;47.58	4,319	1,295,700
FerTik-3_1	150;150	99.15;99.36	94.09;97.5	47.49;49.25	50,378	15,113,400
FerTik-4_1	150;150	99.24;98.63	94.12;94.71	49.57;48.66	181	54,300
FerTik-5	150;150	99.5;98.24	95.72;94.37	53.74;54.4	468	140,400
FerTsag-2	150;150	99.76;99.45	97.77;97.76	47.04;48.7	4,504	1,351,200
FerTsag-5	150;150	99.34;99.61	95.04;98.33	45.34;45.34	45,109	13,532,700
IP10_2	150;150	99.29;98.42	94.0;93.03	44.96;44.84	2,136	640,800
IP142	150;150	99.41;98.68	94.7;94.29	46.09;45.58	1,239	371,700
IP146_1	150;150	98.92;98.21	92.17;92.34	44.97;44.32	463	138,900
IP146_7	150;150	99.47;99.05	95.34;95.98	45.42;45.42	9,205	2,761,500
IP149_1	150;150	99.35;98.71	94.83;94.85	46.63;46.22	856	256,800
IP149_3	150;150	99.02;98.36	92.74;93.01	42.3;41.97	1,570	471,000
IP149_4	150;150	99.21;98.73	93.65;94.67	44.51;44.13	8,401	2,520,300
IP151_4	150;150	99.25;98.98	94.0;95.85	45.71;45.58	13,187	3,956,100
IP7_4	150;150	99.22;98.47	93.82;93.59	43.78;43.58	1,756	526,800
IP_146_2	150;150	99.32;98.78	94.68;94.92	44.31;43.66	7,486	2,245,800
IP_181	150;150	99.11;98.53	93.37;93.85	42.66;42.12	4,216	1,264,800
ITAF1_25	150;150	99.11;98.5	93.11;93.43	44.52;43.49	1,561	468,300
LBA1_25	150;150	99.21;97.48	94.44;92.08	52.0;52.41	159,938	47,981,400
LBC1_25	150;150	99.43;99.0	95.56;96.29	54.31;54.38	3,818	1,145,400
LBM2_25	150;150	99.53;98.86	96.7;95.37	56.43;54.43	99	29,700
LBS1	150;150	99.38;98.45	95.64;94.74	53.14;54.12	102	30,600

LBS2	150;150	99.37;98.44	95.23;94.56	49.64;51.33	2,110	633,000
LBS3	150;150	99.13;96.76	93.99;90.3	52.96;53.77	2,487	746,100
LepBo-22-1-1	150;150	99.56;99.24	96.68;97.12	46.12;46.86	26,197,584	7,859,275,200
LepOgor-2-1	150;150	99.72;99.67	97.6;98.51	43.42;43.44	4,657	1,397,100
LepOgor-4-1	150;150	99.26;99.56	94.01;97.95	50.92;51.57	116	34,800
LepOgor-5-1	150;150	99.39;98.55	96.5;93.48	59.3;58.14	47	14,100
LepSid-1	150;150	99.38;98.49	95.64;94.33	60.7;61.2	52,269	15,680,700
LepSid-1-2	150;150	99.53;98.59	97.04;93.97	54.63;54.21	103	30,900
LepVoron-1	150;150	99.61;99.04	96.68;96.89	53.32;53.83	84	25,200
MSQ43_H2A199Ub_r1	150;150	99.55;98.58	96.12;94.31	46.43;46.62	14,816,302	4,444,890,600
MSQ43_H3K27Ac_r1	150;150	99.44;97.86	94.7;91.01	46.99;47.06	13,231,886	3,969,565,800
MSQ43_H3K27Ac_r2	150;150	99.5;98.16	95.3;92.35	46.79;46.92	18,198,587	5,459,576,100
MSQ_Chip-Seq_1	150;150	99.27;98.66	94.43;94.53	44.38;44.44	69,716,617	20,914,985,100
MSQ_Chip-Seq_2	150;150	99.58;98.7	96.19;94.63	45.93;46.0	72,946,923	21,884,076,900
MSQ_Chip-Seq_3	150;150	99.47;98.49	95.44;93.68	43.65;43.7	77,624,778	23,287,433,400
MSQ_Chip-Seq_4	150;150	99.04;98.36	93.02;93.16	43.57;43.56	49,473,900	14,842,170,000
MSQ_Chip-Seq_5	150;150	99.48;98.62	95.71;94.35	44.33;44.49	60,153,581	18,046,074,300
MSQ_Chip-Seq_6	150;150	99.52;98.58	95.81;94.13	44.22;44.32	62,447,530	18,734,259,000
MSQ_Chip-Seq_7	150;150	99.58;98.72	96.23;94.8	45.56;45.66	70,950,028	21,285,008,400
MSQ_Chip-Seq_8	150;150	99.58;98.83	96.35;95.24	45.24;45.31	78,934,234	23,680,270,200
MaYak-1	150;150	99.82;99.57	98.35;98.1	47.48;47.48	28,053	8,415,900
MaYak-10	150;150	99.78;98.83	98.56;95.28	44.89;45.83	12	3,600
MaYak-11	150;150	99.44;98.92	95.61;95.82	50.31;50.17	118,117	35,435,100
MaYak-12	150;150	99.59;99.18	96.38;96.73	49.65;49.67	7,447	2,234,100
MaYak-13	150;150	99.64;98.52	96.95;94.4	59.86;60.08	1,935,138	580,541,400
MaYak-14	150;150	99.67;98.71	96.69;94.5	59.68;60.53	126	37,800
MaYak-15	150;150	98.95;98.91	92.33;95.89	50.44;50.87	409	122,700
MaYak-16	150;150	99.97;98.89	98.5;95.53	54.33;56.06	24	7,200
MaYak-17	150;150	99.68;99.13	97.01;96.65	55.38;55.53	1,080	324,000
MaYak-18	150;150	99.32;97.54	95.11;92.06	51.41;51.96	989	296,700
MaYak-19	150;150	99.72;99.6	97.43;98.26	48.2;46.38	4,614	1,384,200
MaYak-2	150;150	98.39;96.34	91.69;90.74	50.73;50.38	176	52,800
MaYak-20	150:150	99.61:98.42	97.11:94.57	50.04:51.3	126	37.800

MaYak-21	150;150	99.4;98.46	95.6;94.61	50.34;51.44	1,093	327,900
MaYak-22	150;150	99.55;99.1	96.55;96.57	50.38;51.65	14,873	4,461,900
MaYak-3	150;150	99.61;98.43	96.73;94.53	54.18;54.93	15,439	4,631,700
MaYak-6	150;150	99.52;97.62	92.95;92.48	50.86;50.38	7	2,100
MaYak-7	150;150	99.72;99.42	97.74;97.75	44.48;44.21	1,641	492,300
MaYak-8	150;150	99.31;97.56	95.12;90.28	48.3;47.51	57	17,100
MaYak-9	150;150	99.17;99.45	93.34;97.68	44.87;46.21	58,759	17,627,700
MaYak-_4	150;150	97.07;96.13	85.41;86.15	48.32;48.14	1,193	357,900
MaYak-_5	150;150	99.69;99.66	97.31;98.53	41.79;42.3	21,778	6,533,400
MoPh11_H3K27Ac_r1	150;150	99.52;98.47	95.85;93.83	43.87;43.97	16,536,875	4,961,062,500
MoPh11_H3K27Ac_r2	150;150	99.17;98.36	93.81;93.35	44.01;44.11	14,029,346	4,208,803,800
MoPh14_H2A199Ub_r1	150;150	99.38;98.32	94.77;93.07	43.11;43.09	16,116,449	4,834,934,700
MoPh14_H3K27Ac_r1	150;150	99.5;98.28	95.59;92.95	45.04;45.12	19,753,175	5,925,952,500
MoPh7_H2A199Ub_r1	150;150	99.09;98.56	93.33;94.1	43.36;43.4	21,700,911	6,510,273,300
MoPh7_H3K9me3_r1	150;150	99.41;98.21	94.69;92.67	41.47;41.51	11,470,492	3,441,147,600
Neon1203_1_B4	150;150	98.55;98.5	91.87;94.39	54.29;52.33	23,318	6,995,400
Neon1203_1_CM	150;150	99.35;98.31	94.87;93.38	41.74;42.89	17,159	5,147,700
Neon1203_1_GG	150;150	99.0;98.68	94.04;94.97	36.13;36.4	10,098	3,029,400
Neon1203_2_B4	150;150	98.31;98.46	90.76;94.17	56.73;53.74	17,426	5,227,800
Neon1203_2_CM	150;150	99.61;99.2	96.75;96.73	42.71;43.28	25,265	7,579,500
Neon1203_2_GG	150;150	99.0;98.65	93.76;94.84	35.68;35.92	13,344	4,003,200
Neon1203_3_B4	150;150	98.1;98.44	89.88;94.27	56.79;53.63	9,677	2,903,100
Neon1203_3_CM	150;150	99.19;98.37	93.87;93.74	41.77;42.74	29,309	8,792,700
Neon1203_4_B4	150;150	98.76;98.51	92.46;94.38	56.26;53.66	17,823	5,346,900
Neon1203_4_CM	150;150	99.59;98.1	96.85;93.53	55.47;56.12	336,346	100,903,800
Neon1203_4_GG	150;150	98.83;98.71	93.51;95.04	35.67;36.16	12,534	3,760,200
Neon1203_5_CM	150;150	99.24;98.44	94.25;93.94	41.88;42.92	18,577	5,573,100
Neon1203_5_GG	150;150	98.9;98.54	93.72;94.5	35.62;36.02	11,295	3,388,500
Neon1203_7_B4	150;150	98.59;98.46	91.68;94.18	56.31;53.65	22,955	6,886,500
Neon1203_7_CM	150;150	99.25;98.37	94.19;93.74	41.77;42.83	27,077	8,123,100
Neon1203_7_GG	150;150	98.85;98.69	93.84;95.1	35.72;36.21	15,667	4,700,100
Neon1203_8_AAVS	150;150	99.43;98.32	94.67;93.24	54.77;54.83	16,841	5,052,300
OvoAf4-1	150:150	99.45:97.59	95.27:93.34	55.16:55.12	63	18.900

OvoBerez-1	150;150	99.44;97.88	95.15;93.24	51.76;51.77	102	30,600
OvoKul-1	150;150	99.77;97.92	97.83;93.1	64.38;63.84	11,889	3,566,700
OvoVKame-1	150;150	99.18;98.87	94.49;95.95	54.76;55.19	162	48,600
OvoVKame-2	150;150	99.54;98.09	95.53;93.69	50.48;50.95	101	30,300
OvoVKame-3	150;150	98.42;96.9	91.49;89.26	54.16;53.8	129	38,700
OvoVKame-4	150;150	99.61;98.83	96.81;95.83	51.59;52.53	306	91,800
P192	150;150	99.41;98.21	95.02;92.81	51.09;51.13	33,239,523	9,971,856,900
P198	150;150	99.44;98.24	95.14;92.91	51.09;51.04	37,581,738	11,274,521,400
P202	150;150	99.56;98.32	95.96;93.18	50.01;49.89	35,578,792	10,673,637,600
P203	150;150	99.51;98.08	95.45;92.17	52.34;52.5	26,480,230	7,944,069,000
P204	150;150	99.21;98.34	93.69;93.26	49.07;49.1	20,932,171	6,279,651,300
P205	150;150	99.46;98.36	95.22;93.31	48.91;48.97	27,337,149	8,201,144,700
P206	150;150	99.4;98.29	94.91;93.09	49.39;49.22	33,390,963	10,017,288,900
P207	150;150	99.53;98.18	95.74;92.54	48.55;48.57	21,796,143	6,538,842,900
P208	150;150	99.47;98.28	95.32;92.99	49.11;49.1	38,429,642	11,528,892,600
P209	150;150	99.52;98.13	95.57;92.4	51.88;51.95	31,652,395	9,495,718,500
P210	150;150	99.53;98.33	95.7;93.19	48.5;48.47	29,117,568	8,735,270,400
Pet1_K	150;150	99.42;98.23	94.71;92.58	42.64;42.74	11,778,626	3,533,587,800
Pig_6	150;150	99.39;98.74	95.13;94.91	44.93;45.04	614,094,672	184,228,401,600
PriKob-1	150;150	99.68;99.24	97.24;96.98	45.08;45.55	3,939	1,181,700
PriPre3-1	150;150	99.14;98.8	93.6;95.87	48.44;47.97	197	59,100
PrzBerel89-1	150;150	99.37;98.64	95.2;95.08	49.04;48.82	381	114,300
PrzVKam-1	150;150	99.72;98.77	97.51;95.15	54.91;55.76	1,783	534,900
SanSol-1	150;150	99.25;98.12	95.09;93.86	51.7;50.98	1,208	362,400
Shur1_e	150;150	98.79;97.39	91.85;90.98	45.64;45.57	1,131	339,300
Shur2_K	150;150	99.34;97.95	93.9;91.28	42.73;42.77	6,527,976	1,958,392,800
Tok1_K	150;150	99.41;98.54	95.55;94.51	46.3;46.28	2,661	798,300
VcoBel-1	150;150	99.06;99.39	93.79;97.35	37.47;37.53	5,637	1,691,100
VspIme-1	150;150	97.55;97.74	88.92;92.68	54.22;54.44	75	22,500
VspZap-1	150;150	99.73;98.82	97.53;94.99	55.76;55.79	359,260	107,778,000
VvuMoh-1	150;150	96.57;96.33	80.43;84.29	47.71;46.1	14	4,200
VvuPod3-2	150;150	99.59;99.49	96.81;97.93	43.15;43.67	2,929	878,700
brLinker_a_R1	150;150	99.13;96.72	92.05;86.16	50.11;50.08	1,224,336	367,300,800

d2_cb_1	150;150	99.41;98.49	94.91;93.71	43.34;43.22	181,429,596	54,428,878,800
d2_cb_2	150;150	99.41;98.62	94.99;94.27	43.52;43.54	206,048,257	61,814,477,100
d2_kid_1	150;150	99.22;98.56	93.9;94.1	42.72;42.72	107,766,103	32,329,830,900
d2_kid_2	150;150	99.39;98.56	94.92;94.1	42.66;42.54	248,070,802	74,421,240,600
d2_liv_1	150;150	99.29;98.55	94.19;94.01	42.9;42.99	112,048,283	33,614,484,900
d2_liv_2	150;150	99.3;98.53	94.33;93.91	43.08;43.08	156,177,633	46,853,289,900
d4_cb_1	150;150	99.33;98.65	94.6;94.44	43.76;43.95	43,892,259	13,167,677,700
d4_cb_2	150;150	99.48;98.42	95.47;93.45	44.01;43.94	203,808,821	61,142,646,300
d4_kid_1	150;150	99.41;98.53	95.14;94.04	43.19;43.12	59,830,017	17,949,005,100
d4_kid_2	150;150	98.98;98.62	92.87;94.46	43.38;43.3	132,298,687	39,689,606,100
d4_liv	150;150	99.4;98.63	94.97;94.34	42.85;42.8	48,985,795	14,695,738,500
ench3-PCR-Dpn_3	150;150	99.24;97.55	93.66;90.49	49.52;49.61	340,288	102,086,400
ench3-PCR-Dpn_Kl_1	150;150	97.36;95.28	81.59;83.51	52.13;52.79	26	7,800
ench3-PCR-Dpn_Kl_2	150;150	99.26;97.5	93.87;90.59	52.04;52.71	468,211	140,463,300
hCTCF_R4	150;150	99.2;97.29	92.33;88.36	45.91;45.93	4,127,372	1,238,211,600
hCTCF_a_R4	150;150	99.28;97.2	92.96;87.94	45.24;45.22	6,565,774	1,969,732,200
mCherry_sR	150;150	99.36;98.39	94.63;93.31	41.57;41.62	30,651,204	9,195,361,200
wgs-CMV-PCR-Nla_3	150;150	99.43;98.56	95.05;93.94	42.33;42.2	96,810	29,043,000
wgs-CMV-PCR-Nla_Kl_1	150;150	99.44;98.52	95.18;93.77	42.1;42.27	25,437	7,631,100
wgs-CMV-PCR-Nla_Kl_2	150;150	99.52;98.56	95.77;94.01	42.31;42.2	22,205	6,661,500
wgs-CMV-PCR-Nla_Kl_3dtransf_4	150;150	99.47;98.82	95.53;95.07	42.41;42.53	31,646	9,493,800
wgs-ench3-PCR-Dpn_3	150;150	99.45;98.65	95.29;94.3	42.75;42.51	48,638	14,591,400
wgs-ench3-PCR-Dpn_Kl_1	150;150	98.93;98.55	92.48;93.97	43.16;43.2	52,233	15,669,900
wgs-ench3-PCR-Dpn_Kl_2	150;150	99.45;98.33	95.09;92.93	41.73;41.74	45,108	13,532,400
wgs-ench3-PCR-Dpn_Kl_3dtransf_4	150;150	99.57;98.61	96.02;94.26	42.92;43.15	45,772	13,731,600
wo-RAD21_E	150;150	99.66;92.68	96.78;65.85	42.45;42.61	2,344	703,200
wo-RAD21_K	150;150	99.7;92.68	96.87;65.86	40.3;40.74	4,828	1,448,400
wt_cb_1	150;150	99.18;98.69	93.67;94.61	43.58;43.67	61,411,124	18,423,337,200
wt_cb_2	150;150	99.48;98.59	95.54;94.17	43.65;43.61	156,711,638	47,013,491,400
wt_kid	150;150	99.44;98.45	95.1;93.61	43.16;42.95	103,264,239	30,979,271,700
wt_liv	150;150	99.45;98.6	95.2;94.21	43.07;43.22	132,927,242	39,878,172,600

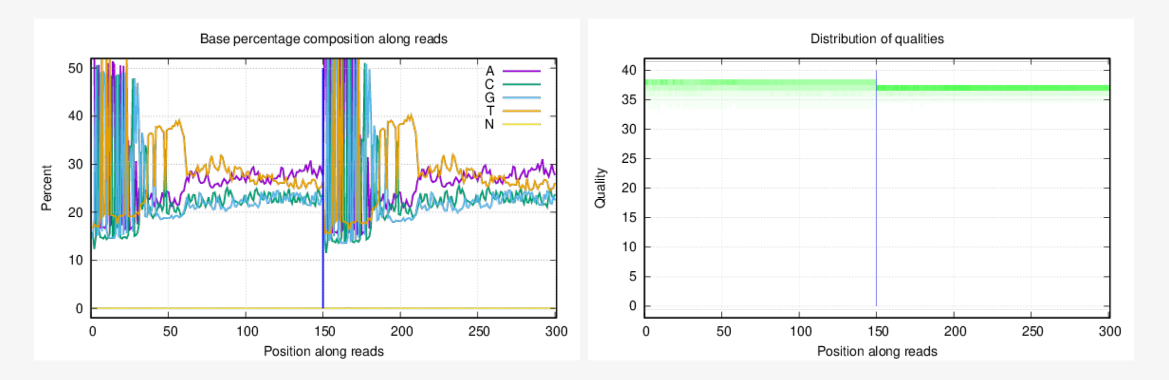
Table Format:

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.

12



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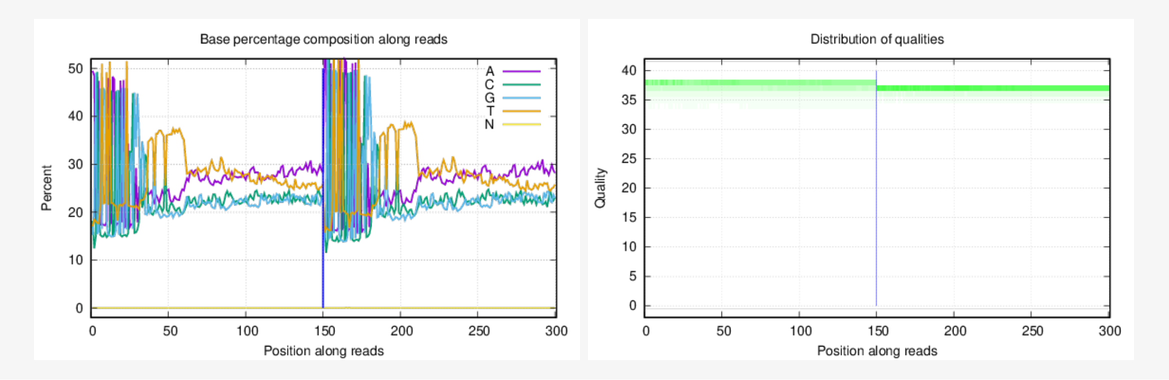

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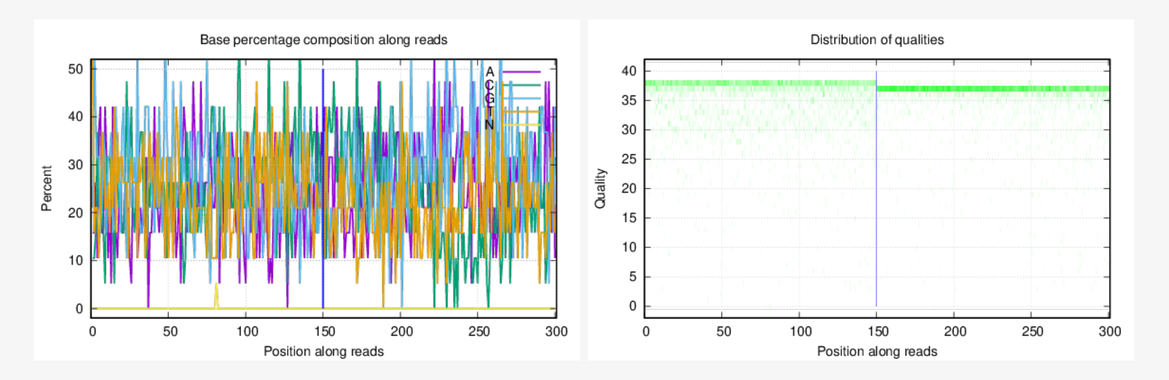
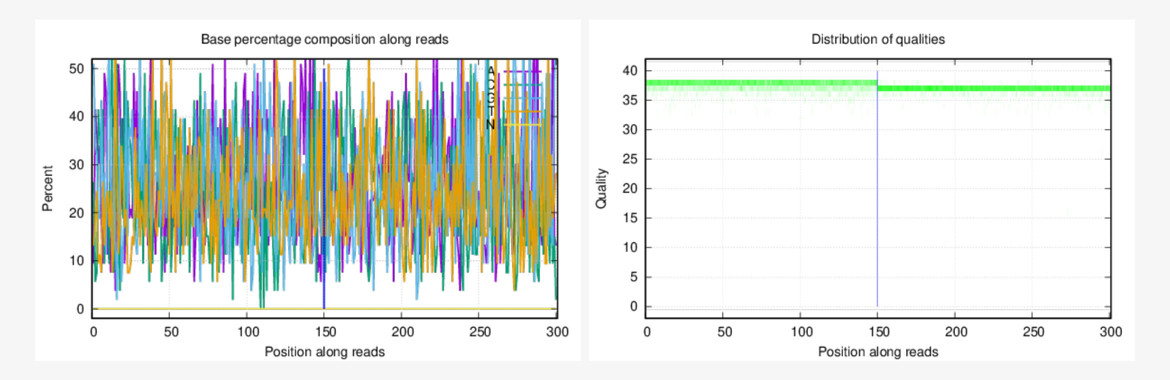


19646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Position along reads
A
C
G
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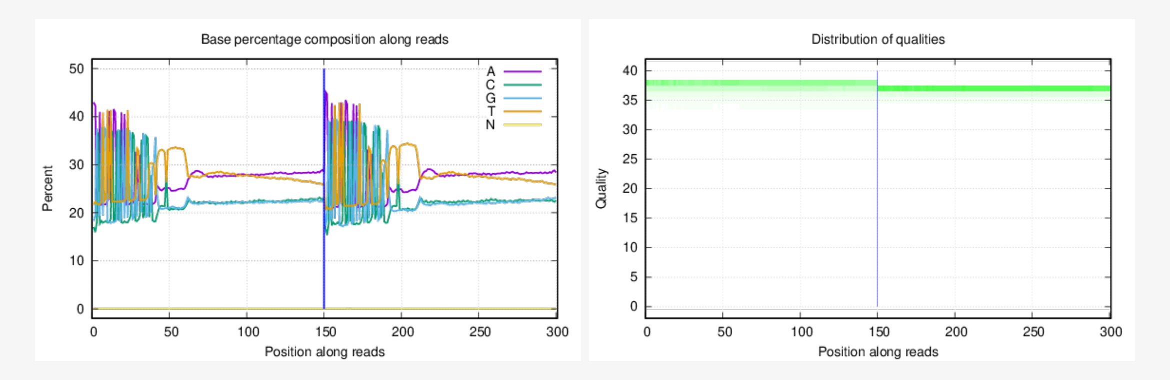
Distribution of qualities
Quality
0
5
10
15
20
25
30
35
40
Position along reads

21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Position along reads
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Distribution of qualities
Quality
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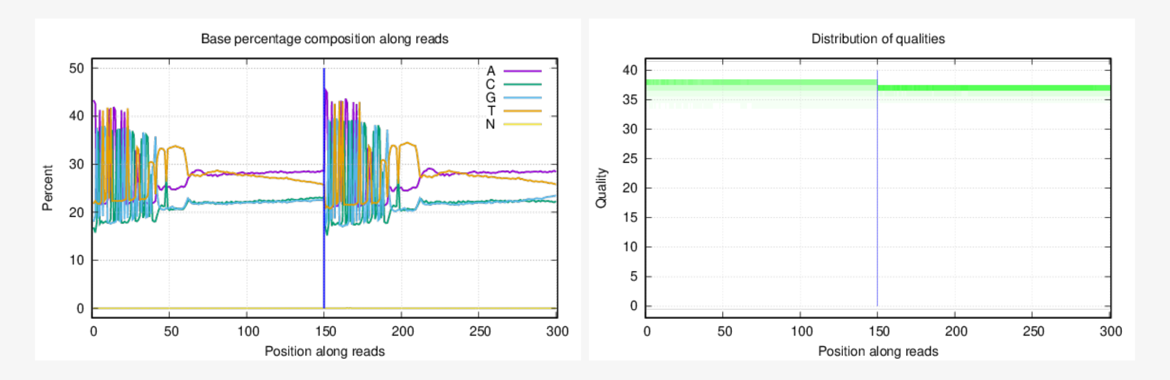
Position along reads

22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Distribution of qualities
Quality
0
5
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15
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25
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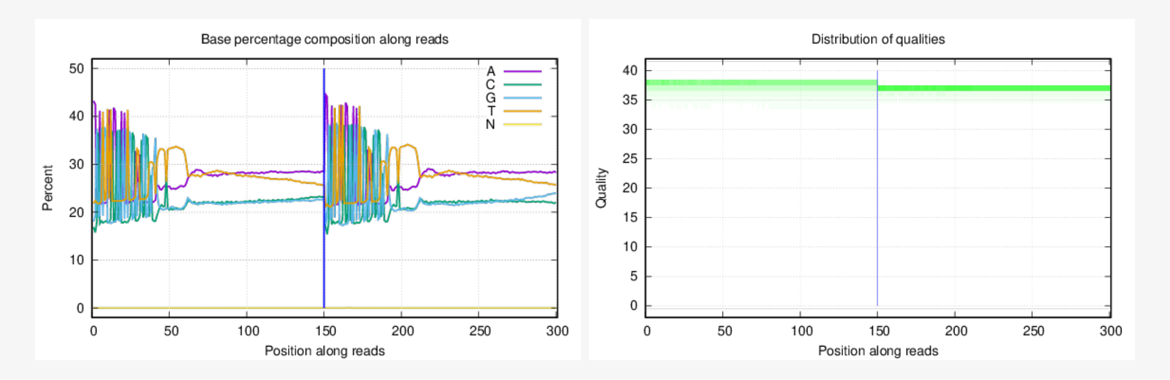
40
Position along reads

23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Position along reads
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Distribution of qualities
Quality
0
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25
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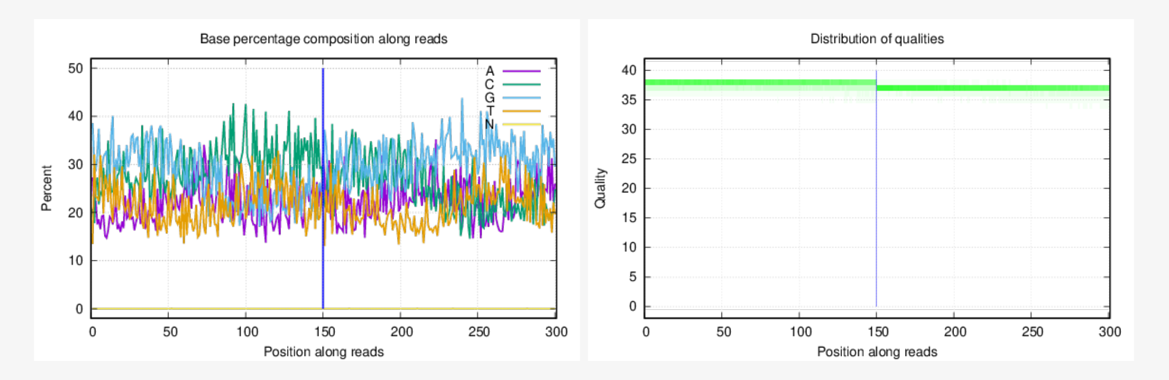
40
Position along reads

2322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Position along reads
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Distribution of qualities
Quality
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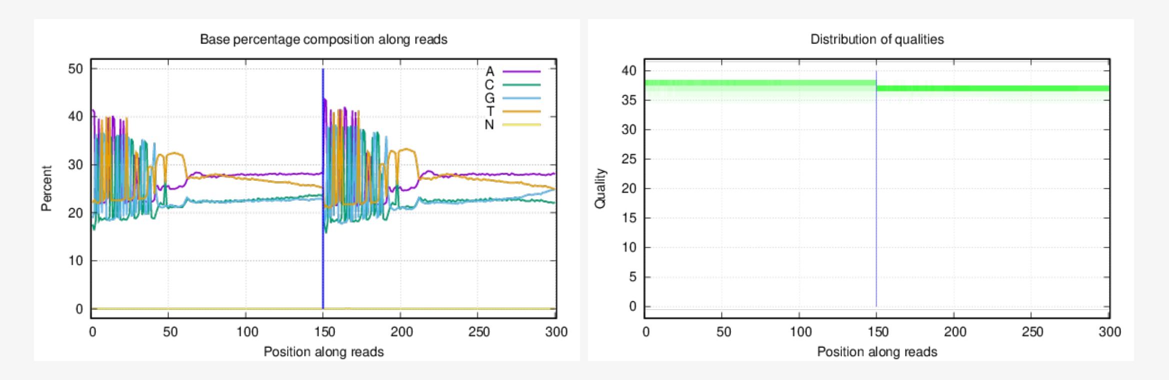
24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Distribution of qualities
Quality

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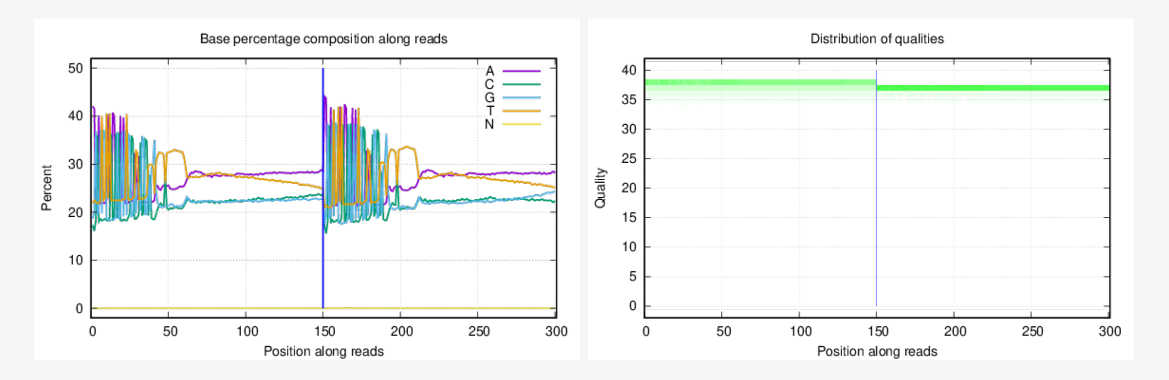
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Distribution of qualities
Quality

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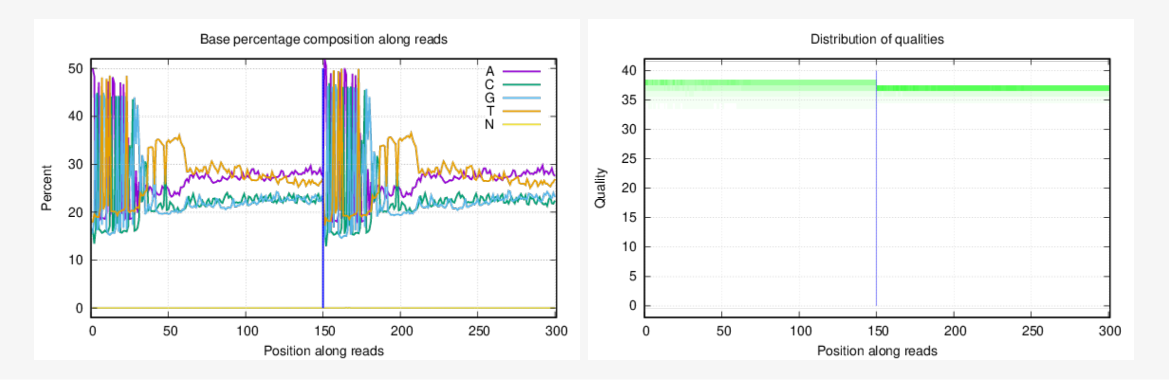
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Position along reads
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Distribution of qualities
Quality

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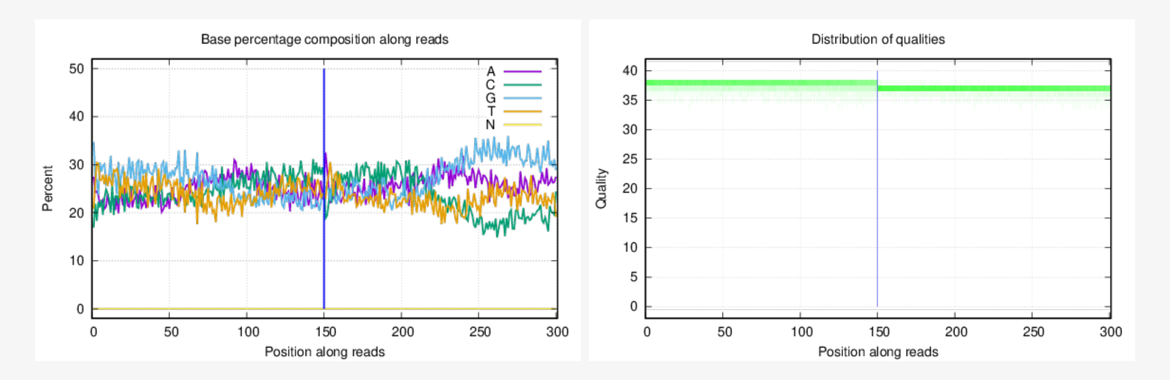

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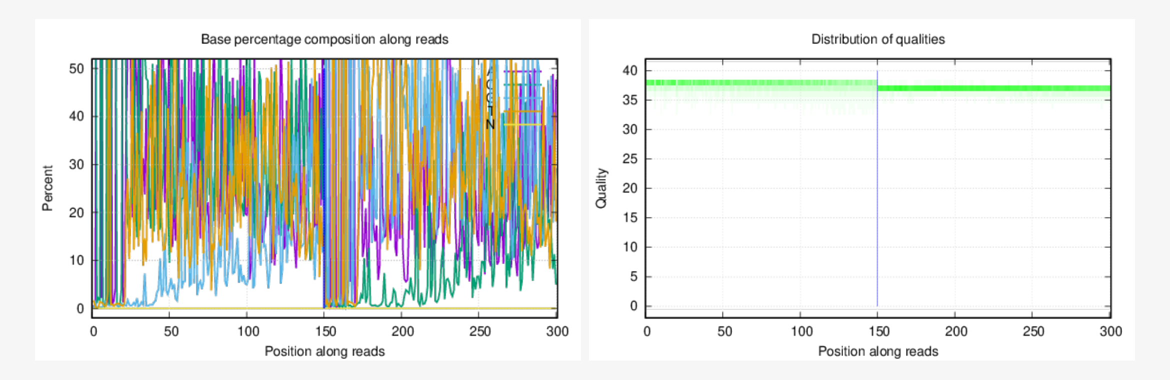

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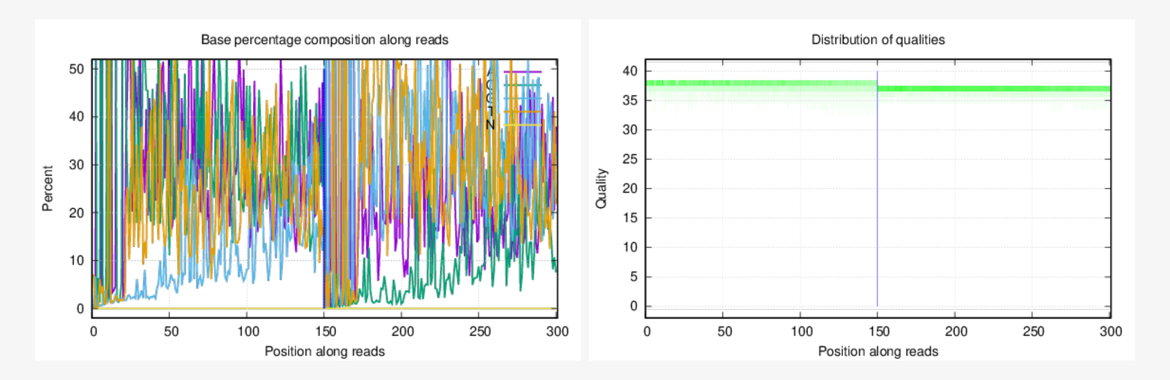

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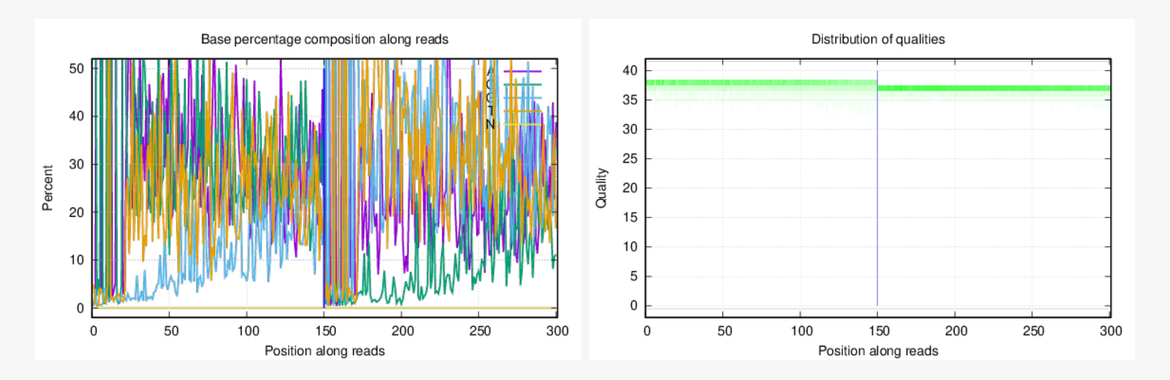

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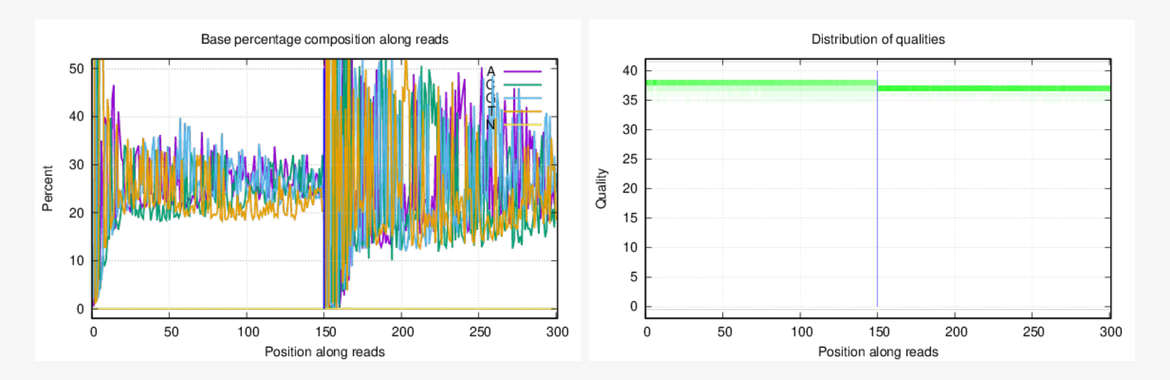
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Position along reads
Distribution of qualities
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Position along reads

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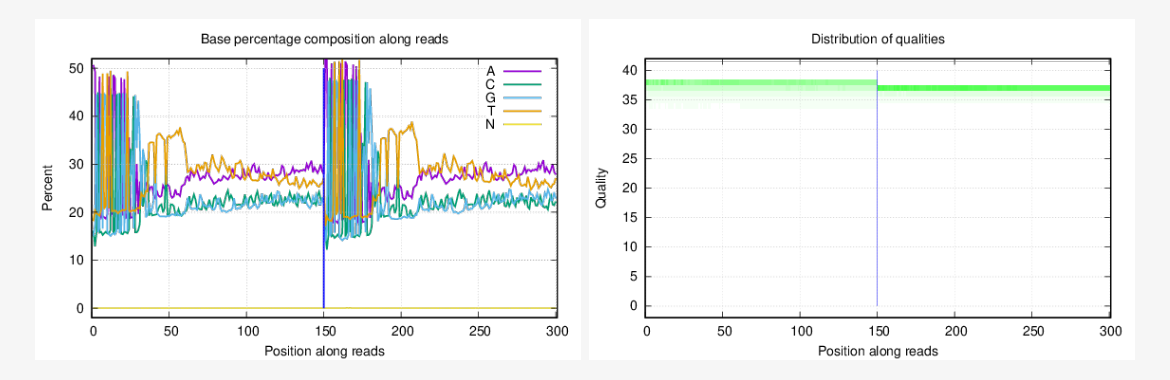
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Position along reads
Distribution of qualities
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Position along reads

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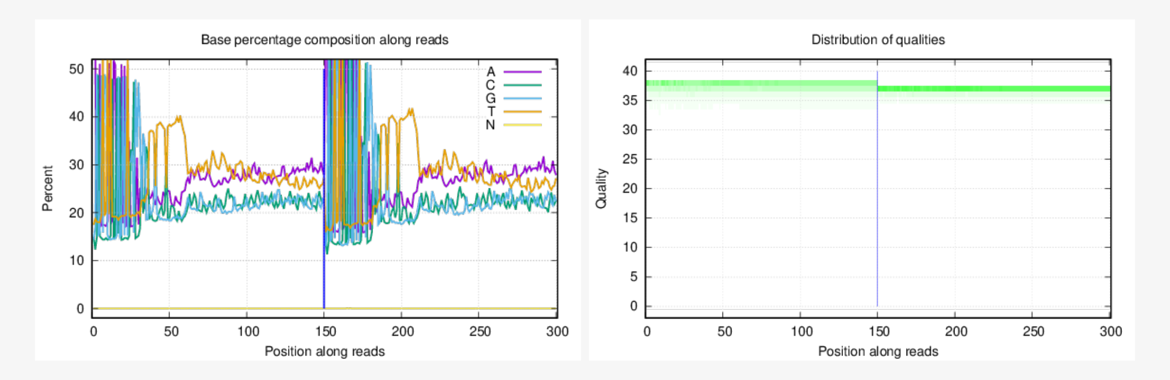
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Distribution of qualities
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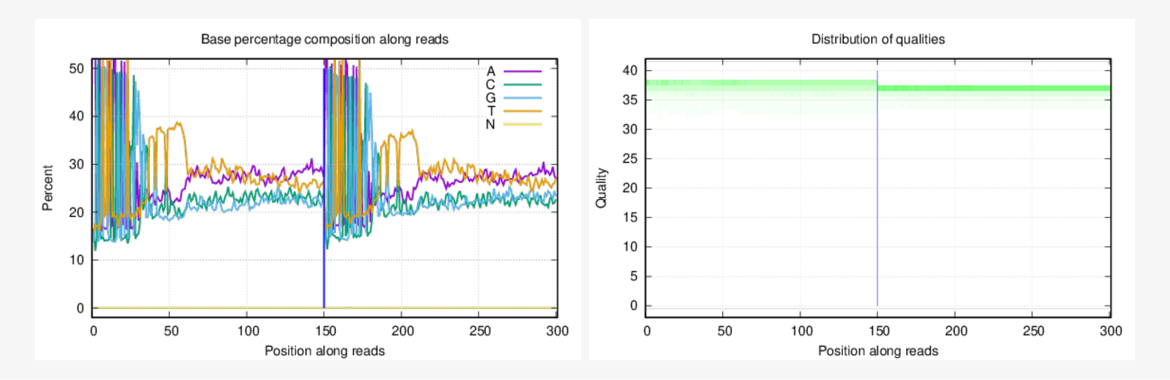
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Position along reads
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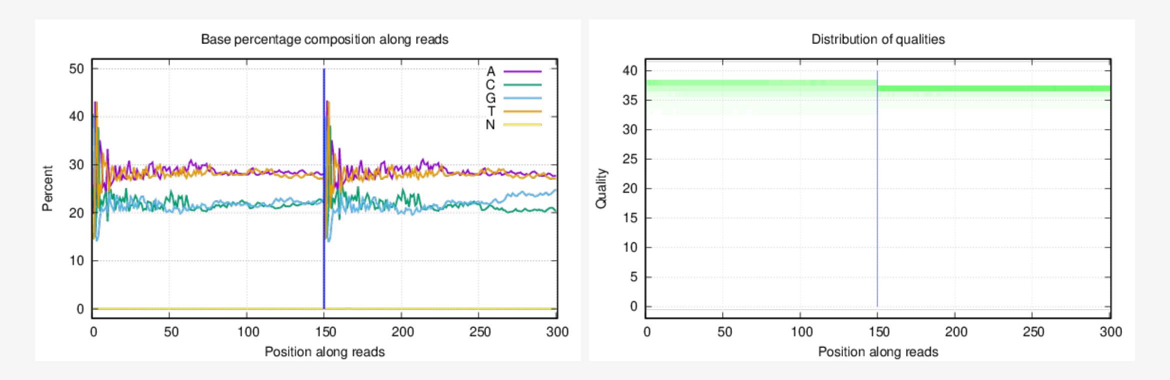
74C_R3



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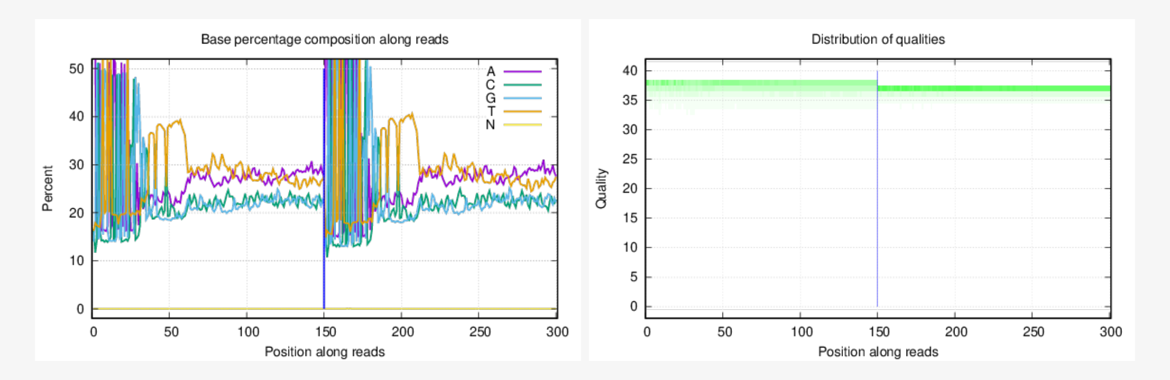

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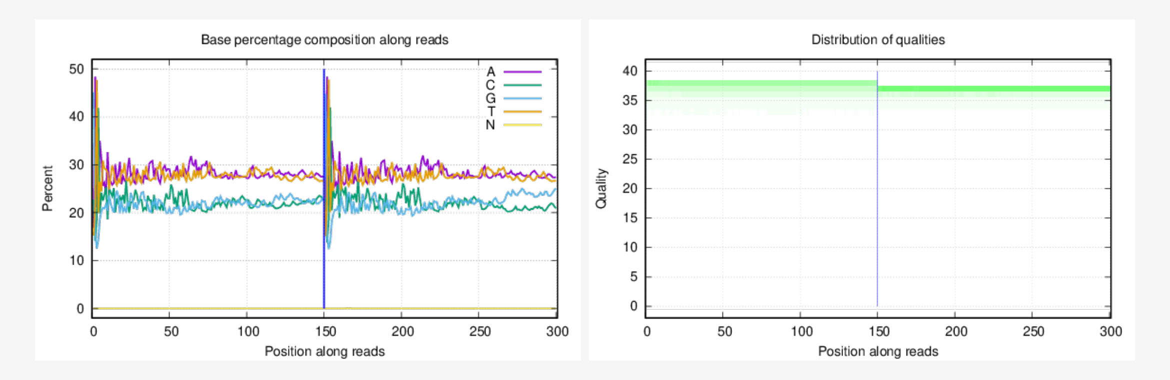

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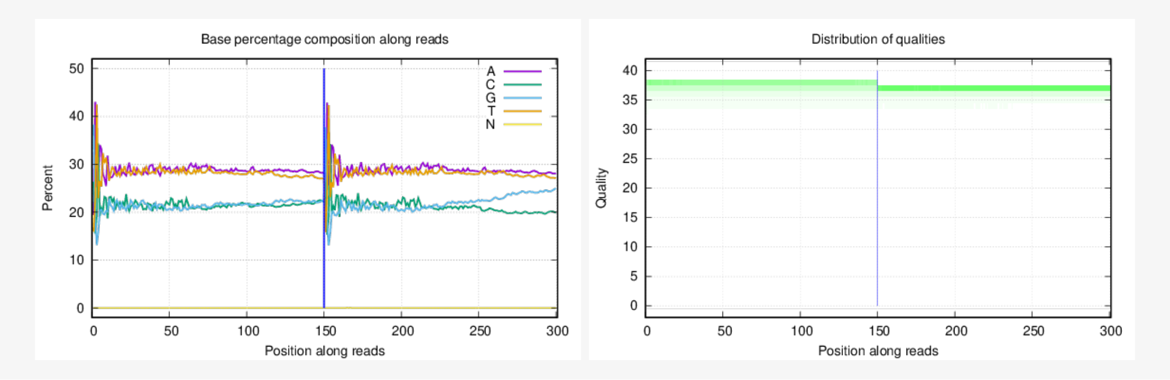

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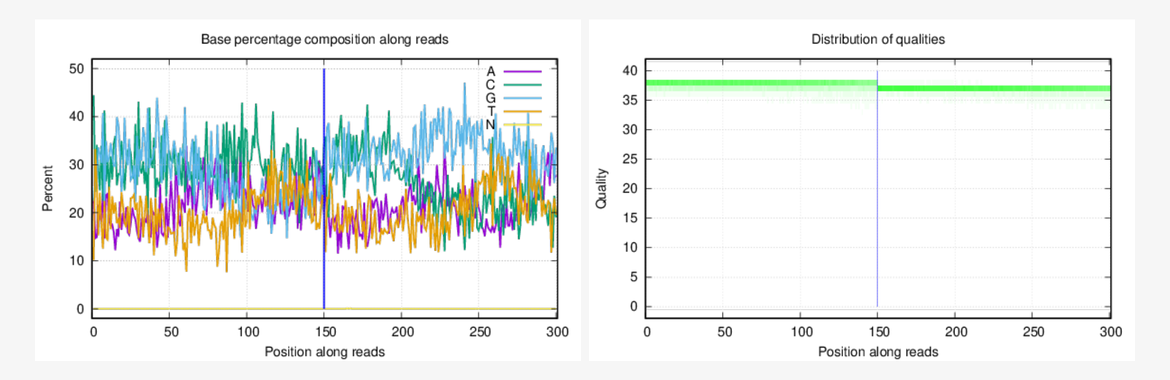

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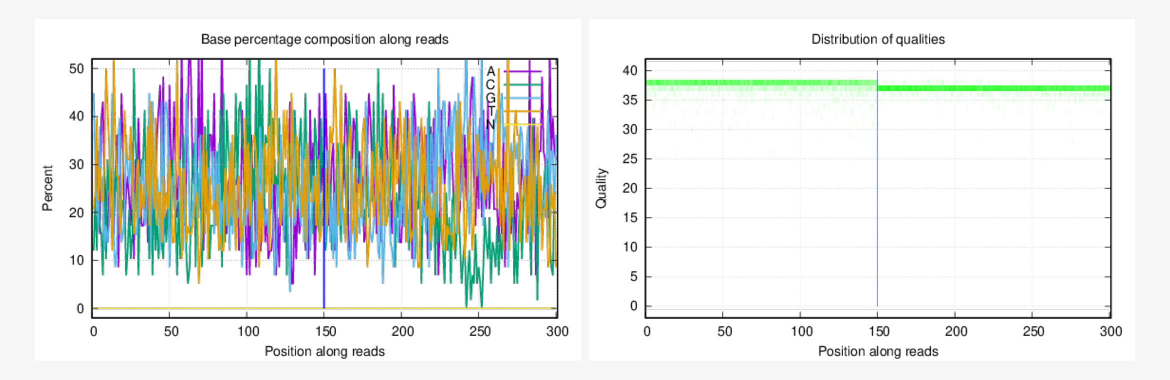
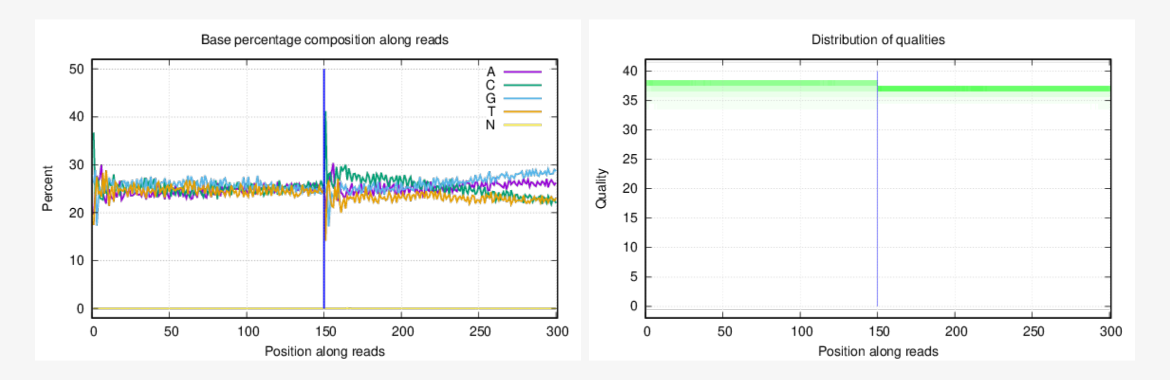


CMV-PCR-Nla_3



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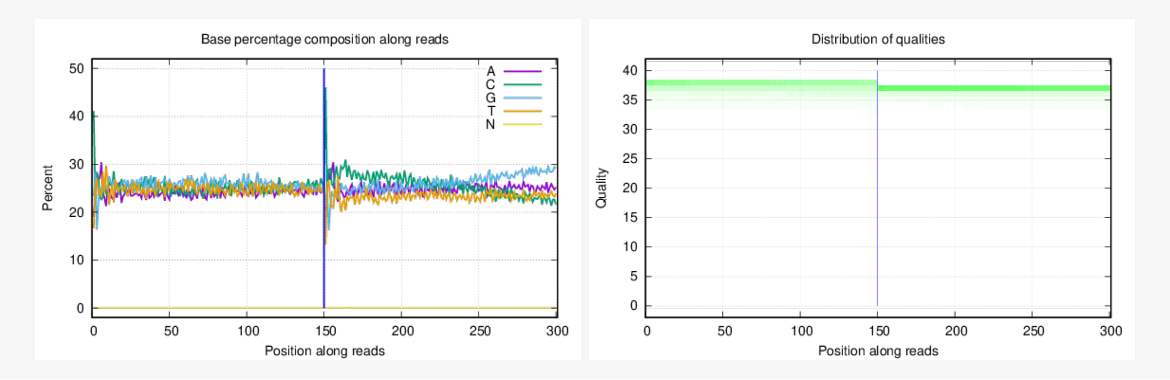

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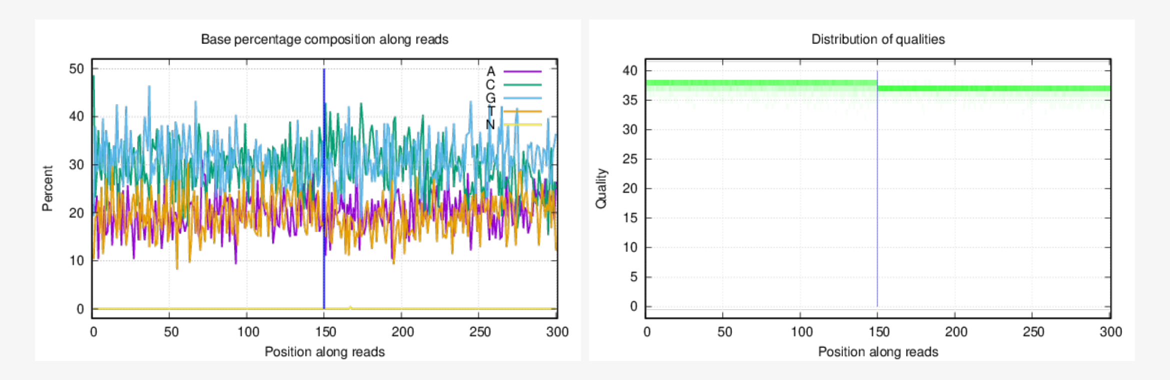
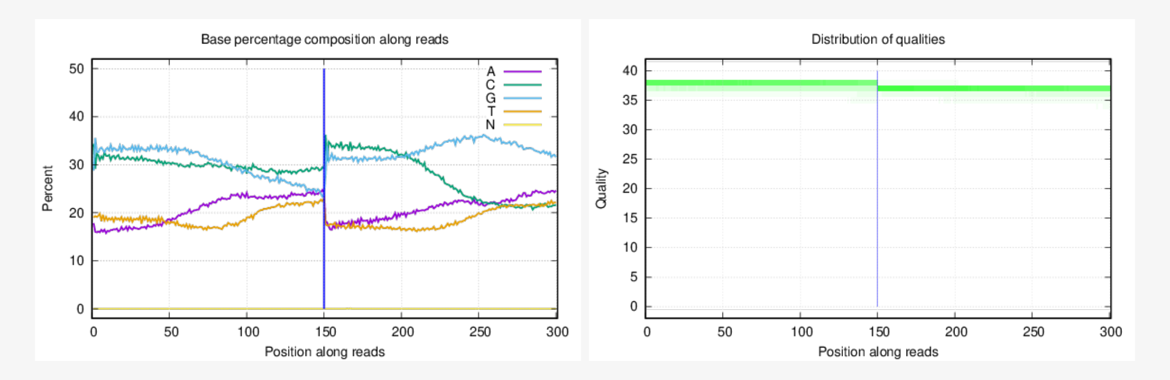
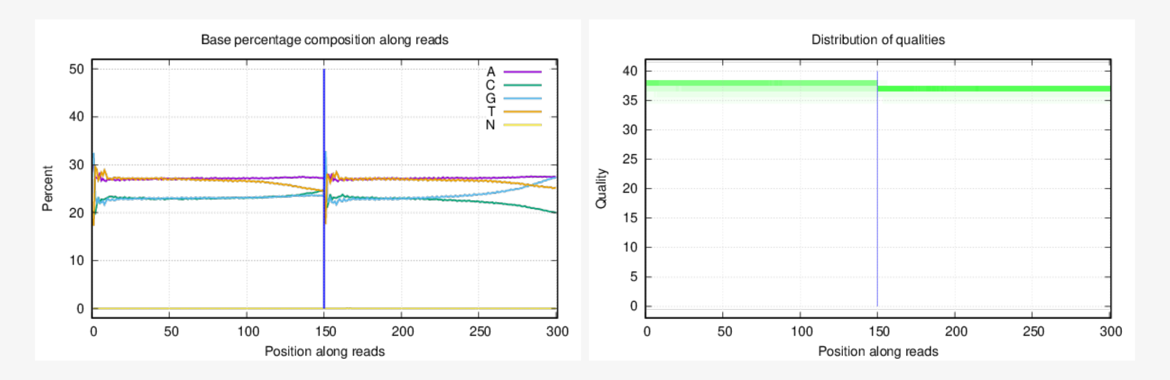


CV7_CV3-7



Cen_B3



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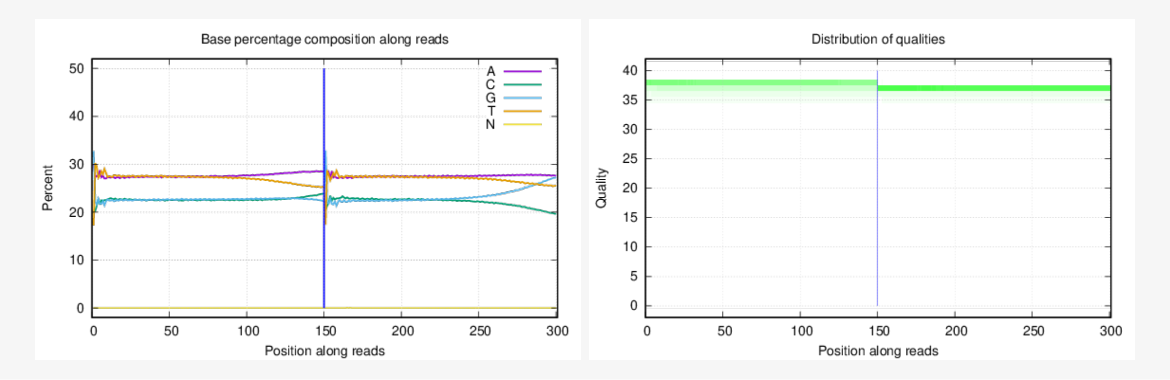

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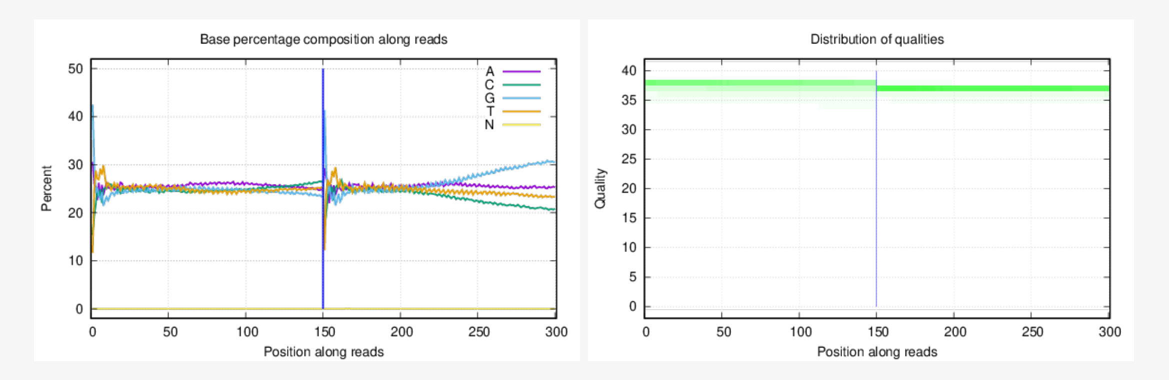

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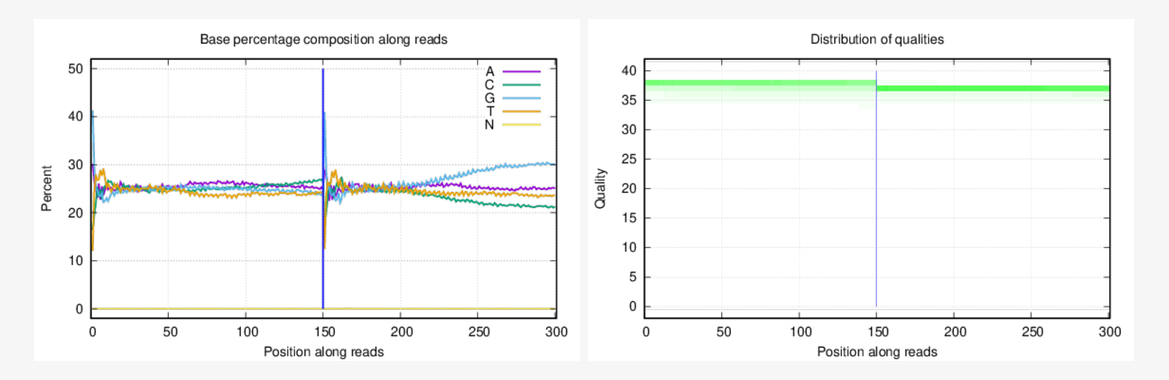

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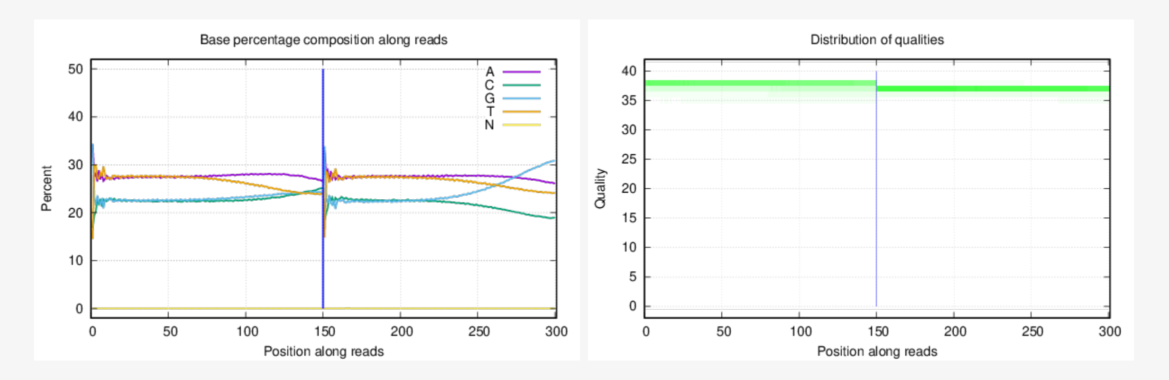

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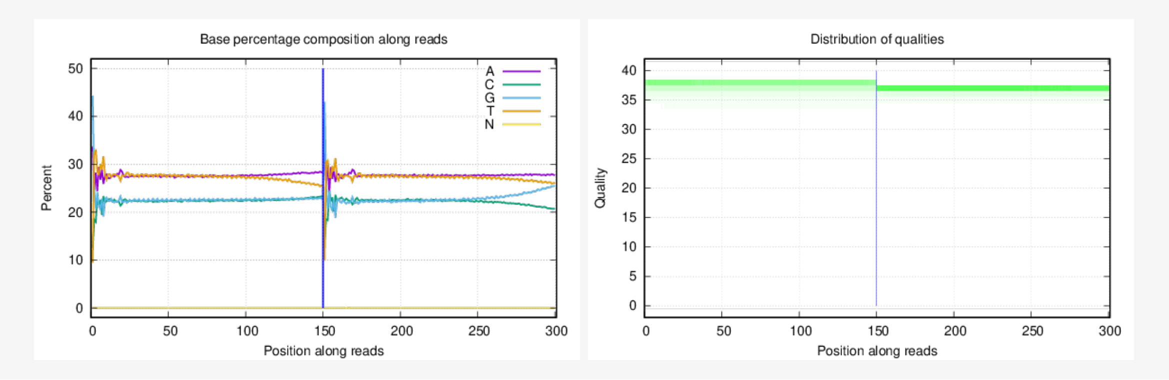

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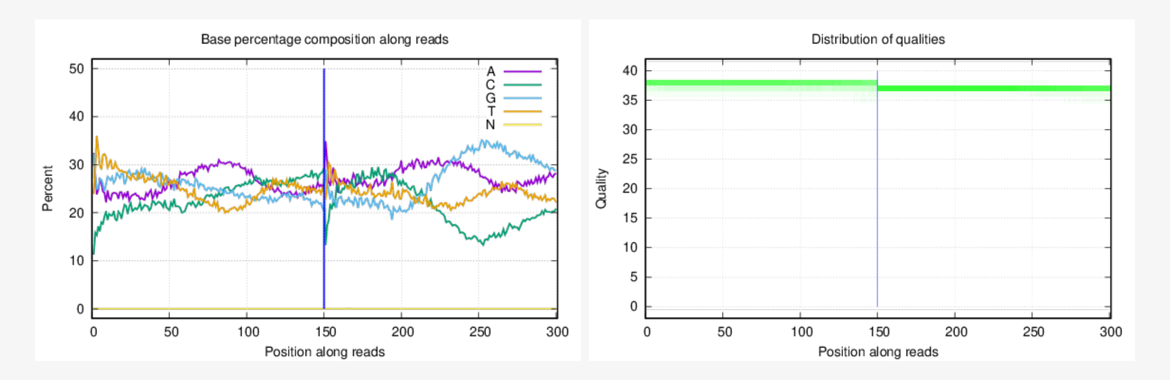

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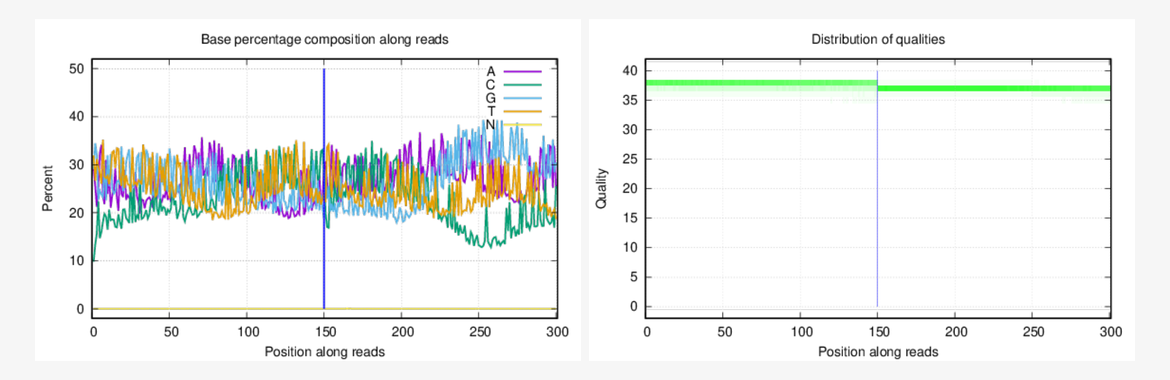

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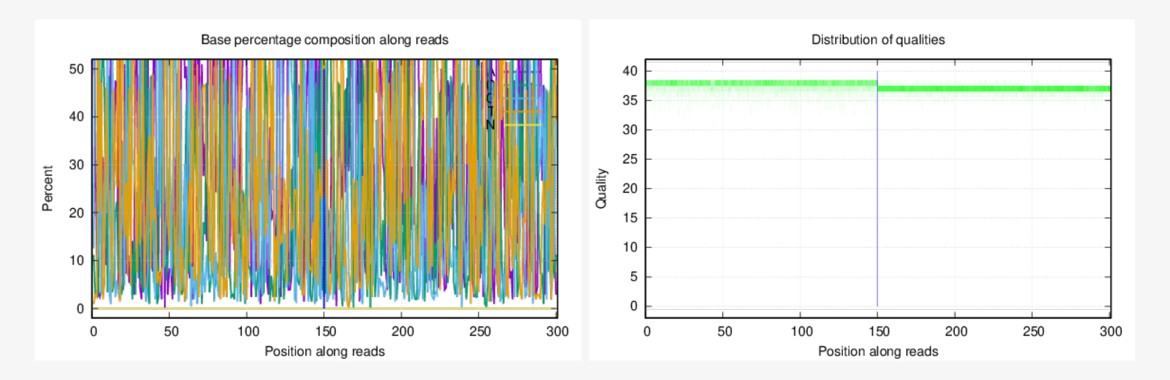
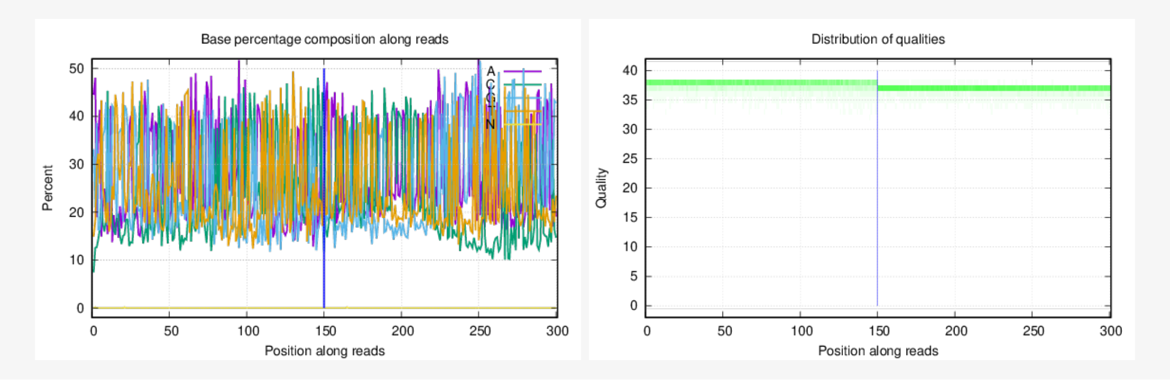


Colne-4



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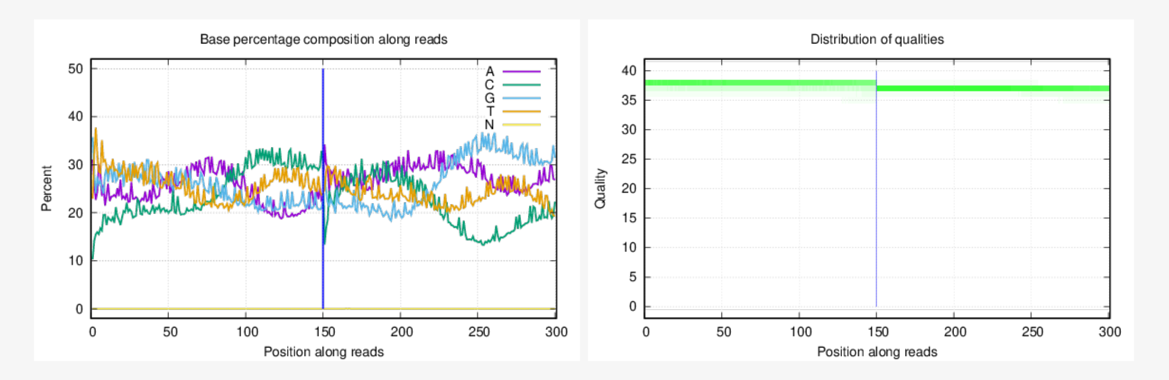

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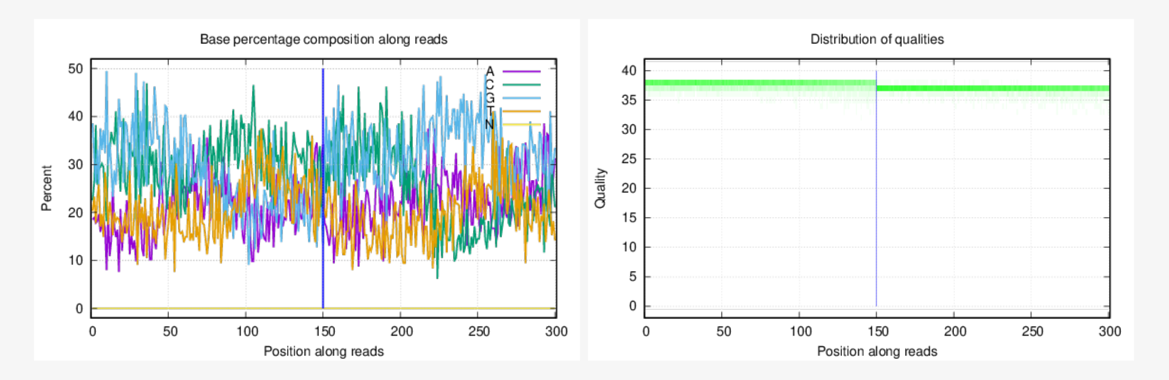

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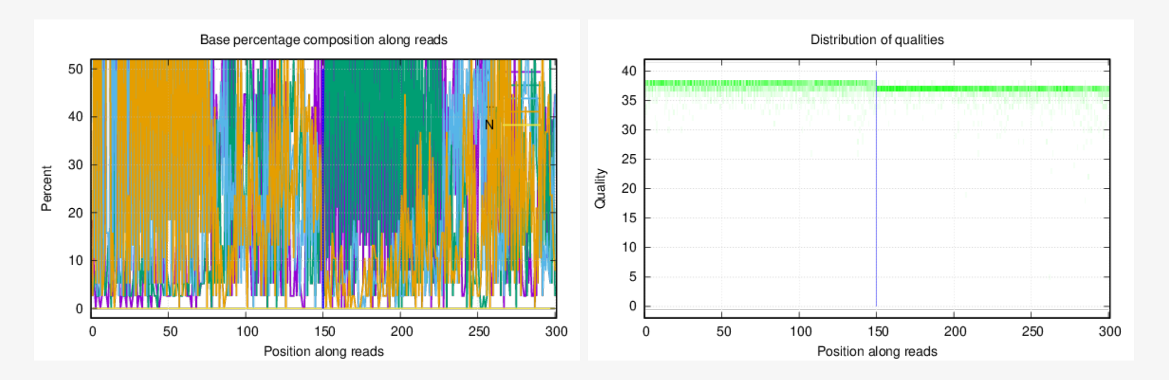

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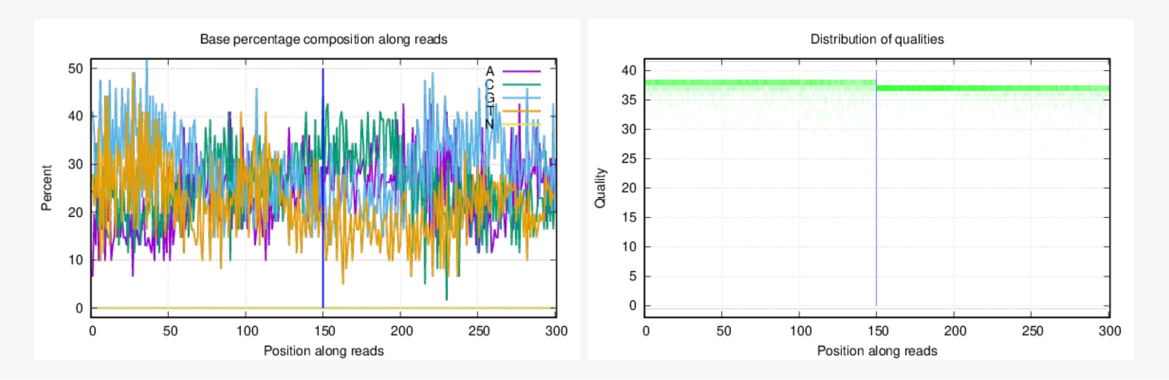

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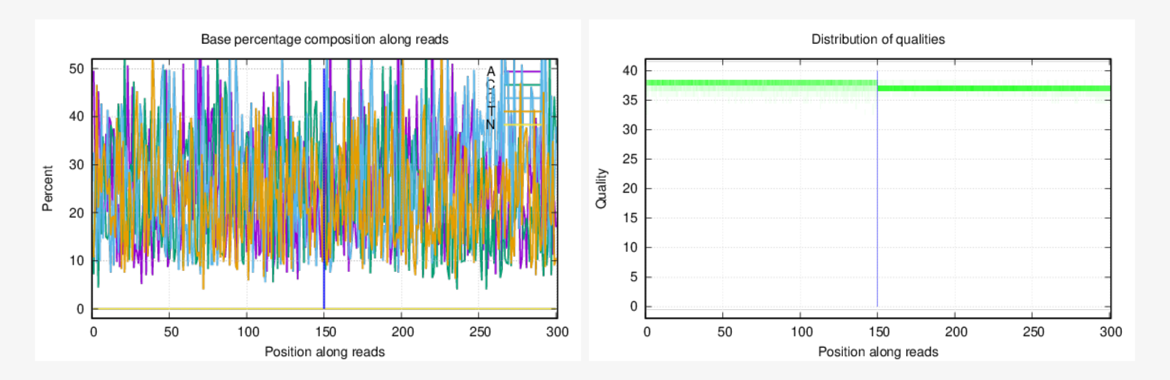

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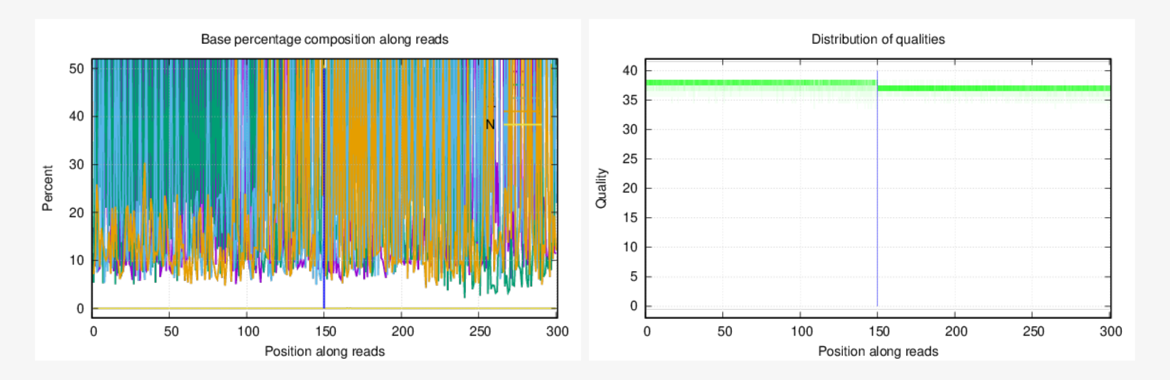

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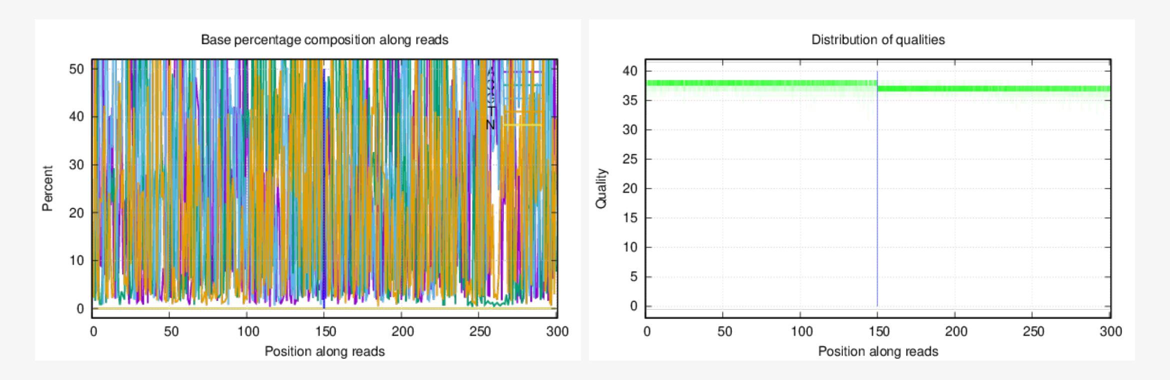

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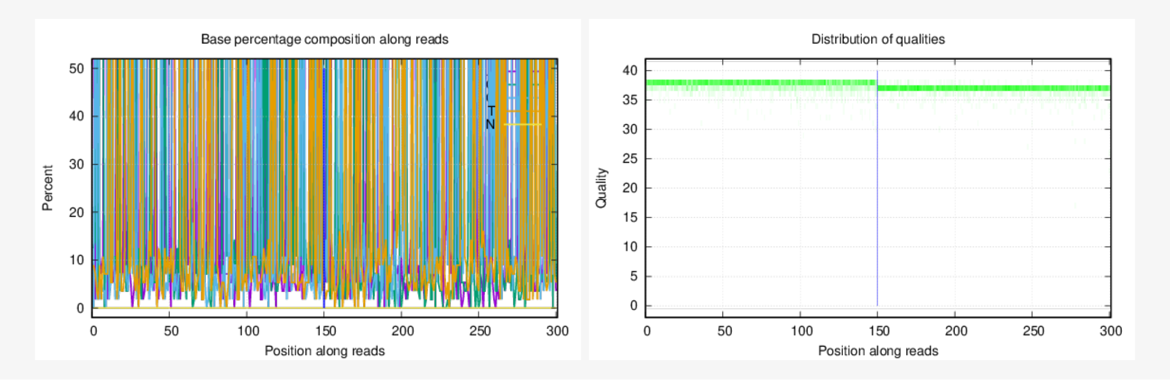

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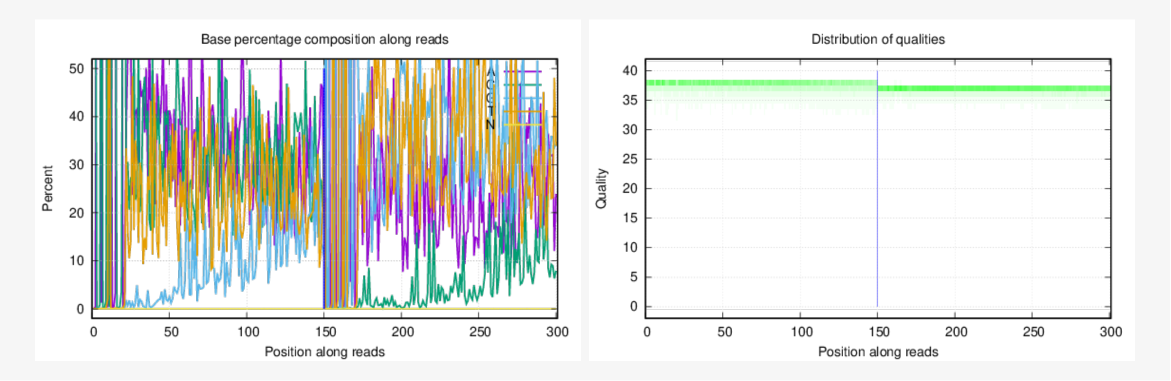

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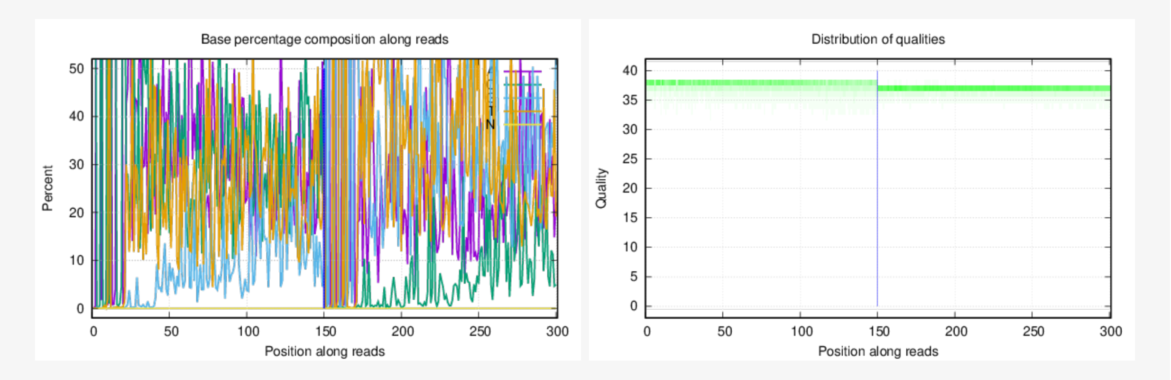

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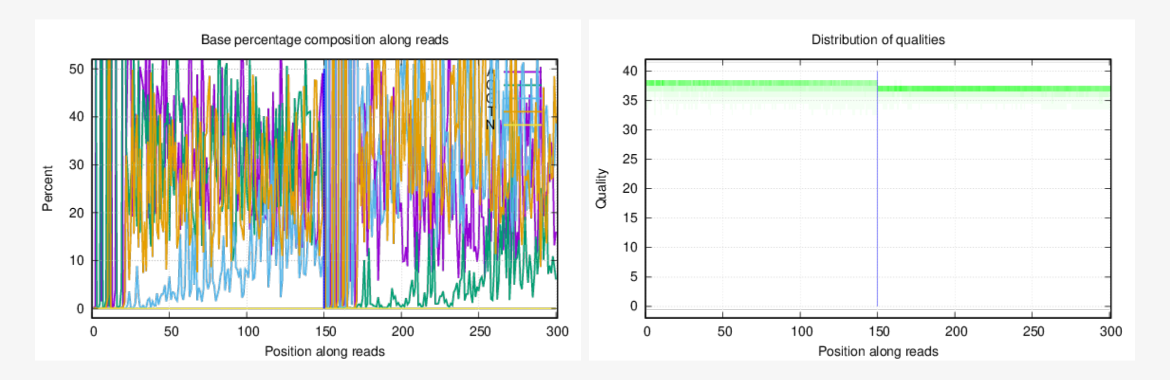

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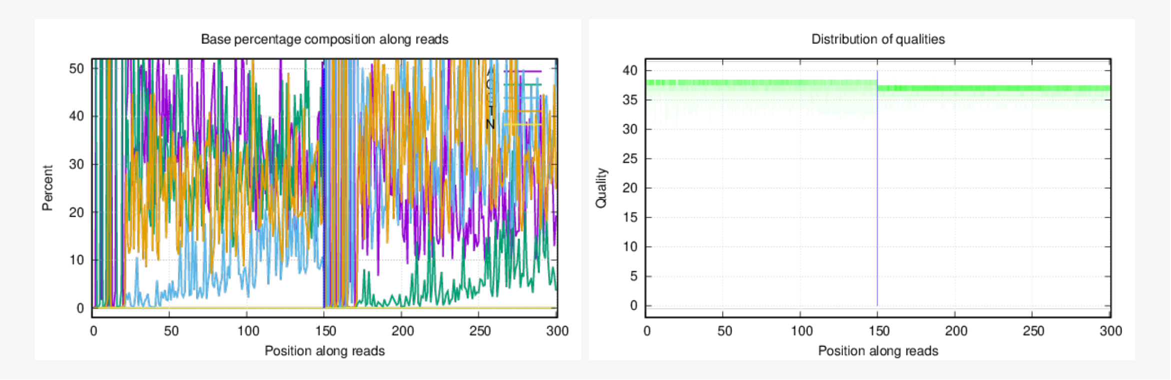

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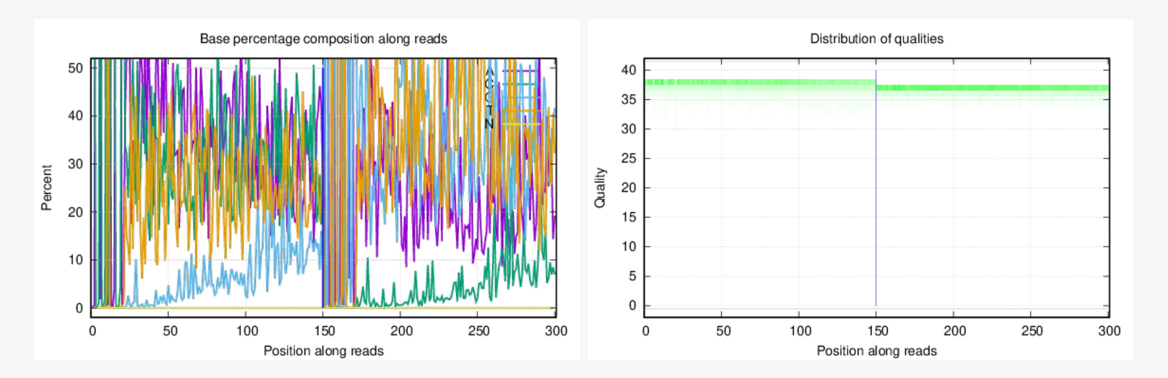

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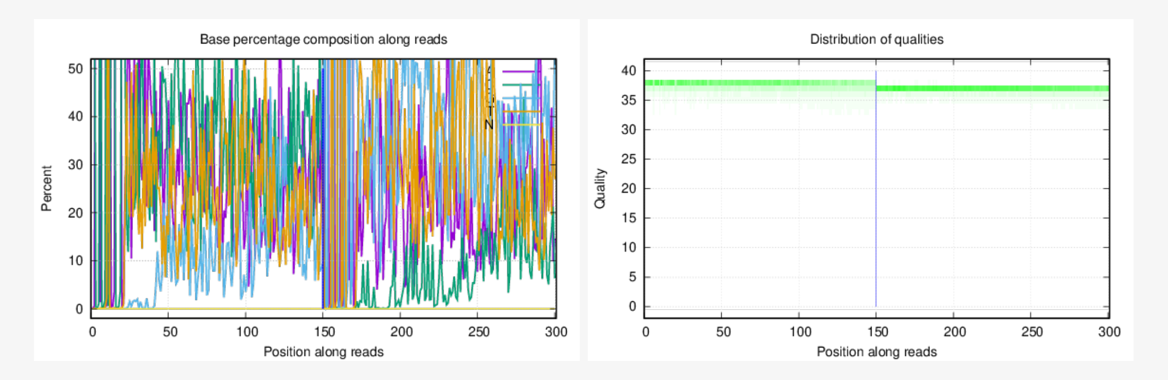

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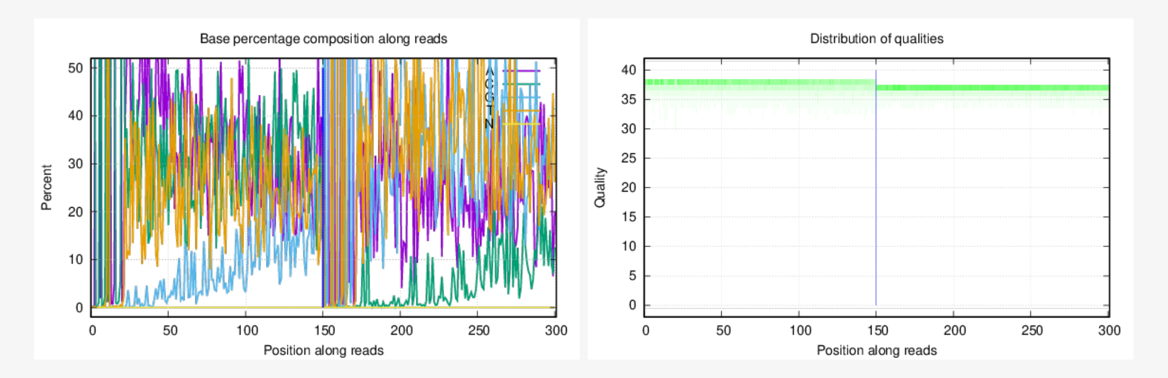

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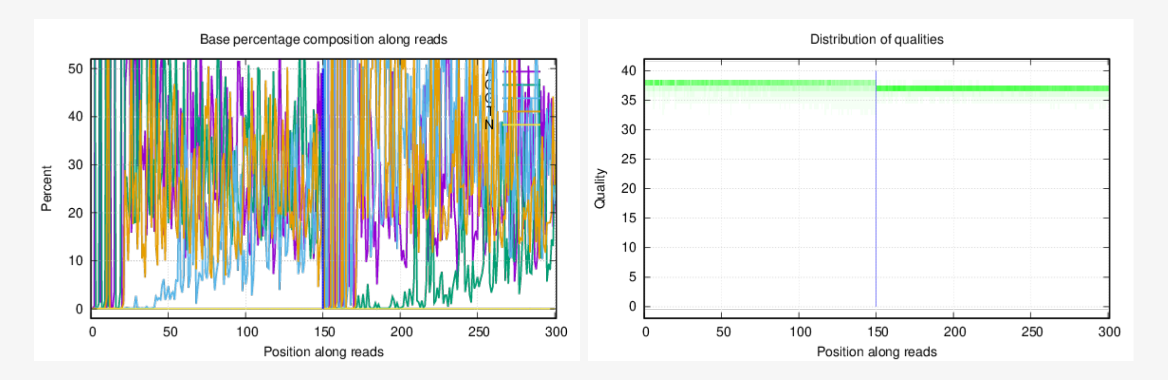

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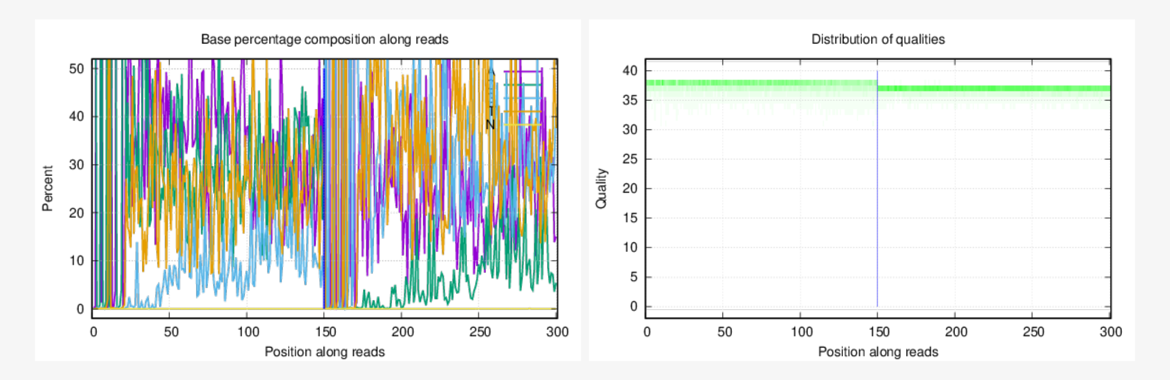

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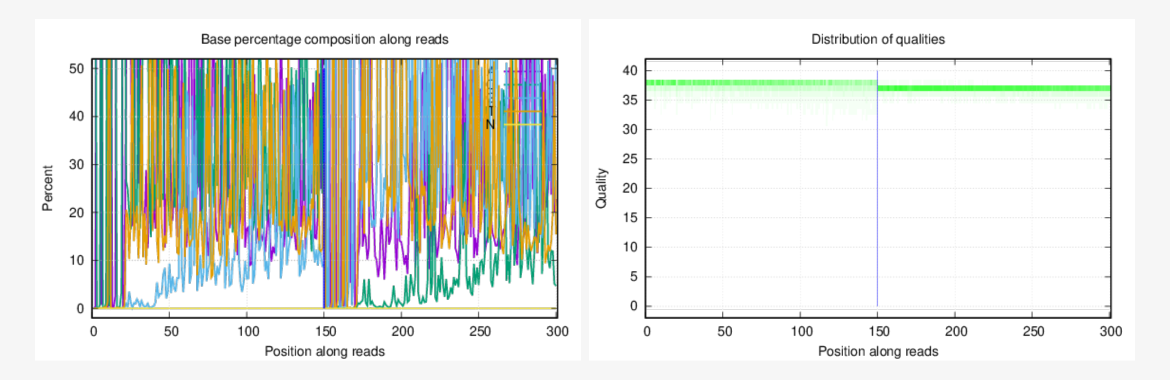

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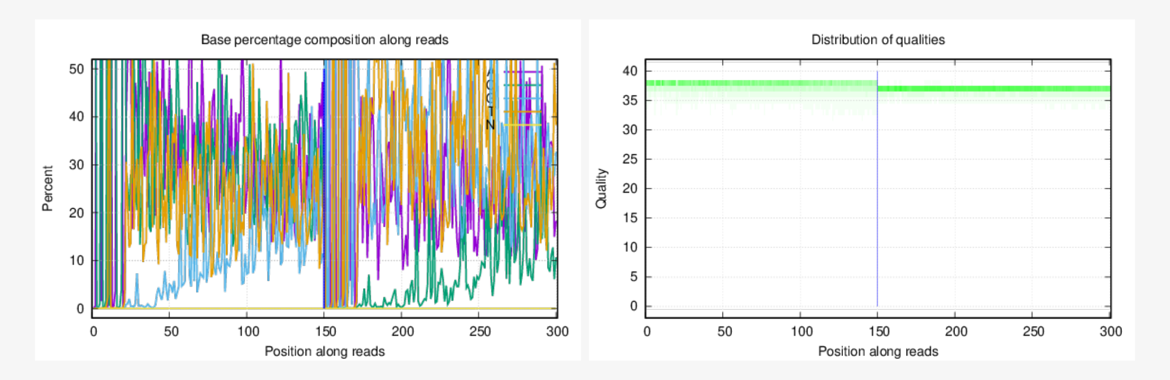

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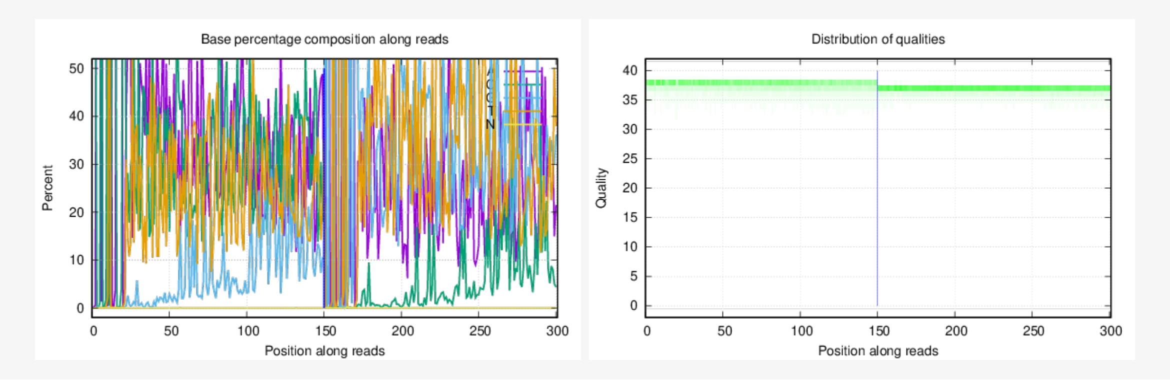

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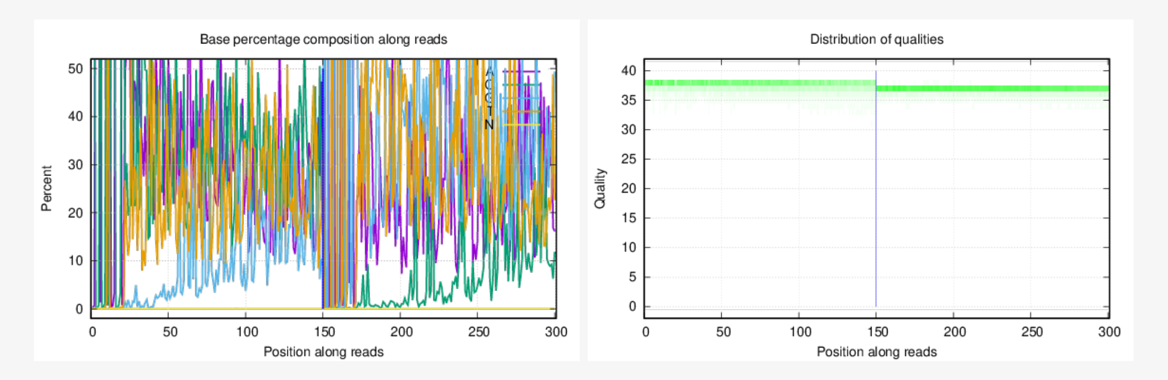

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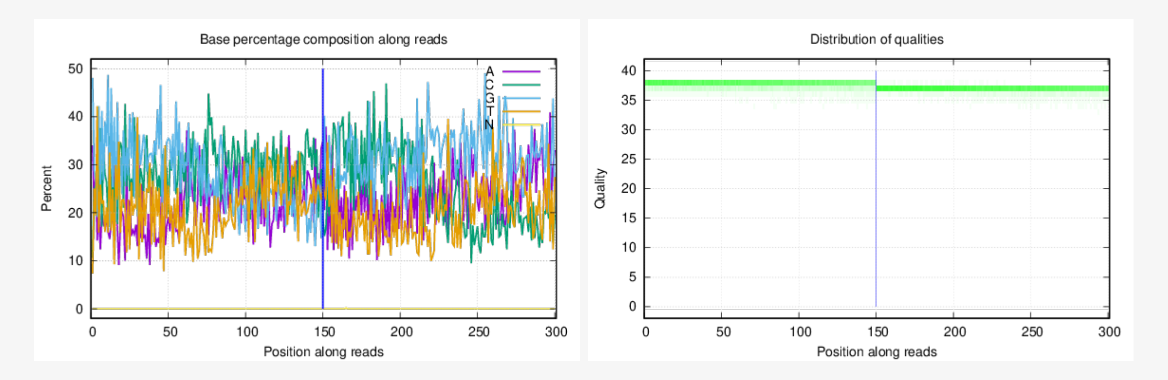

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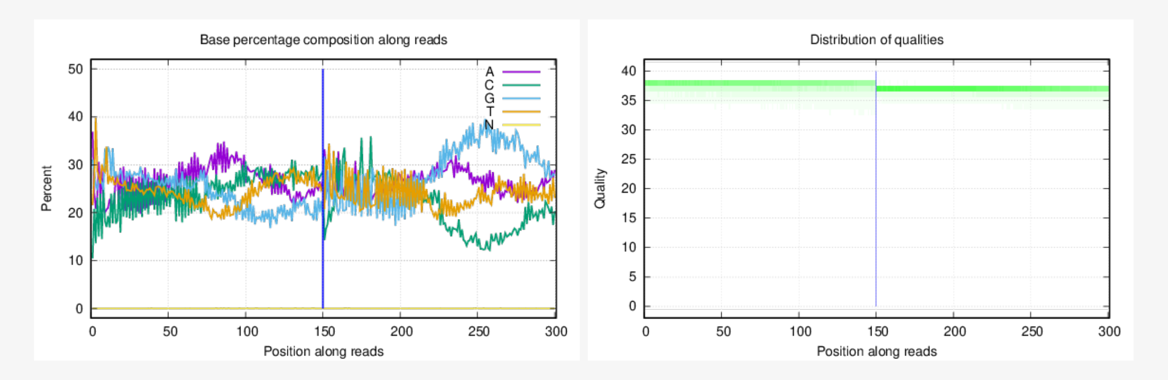

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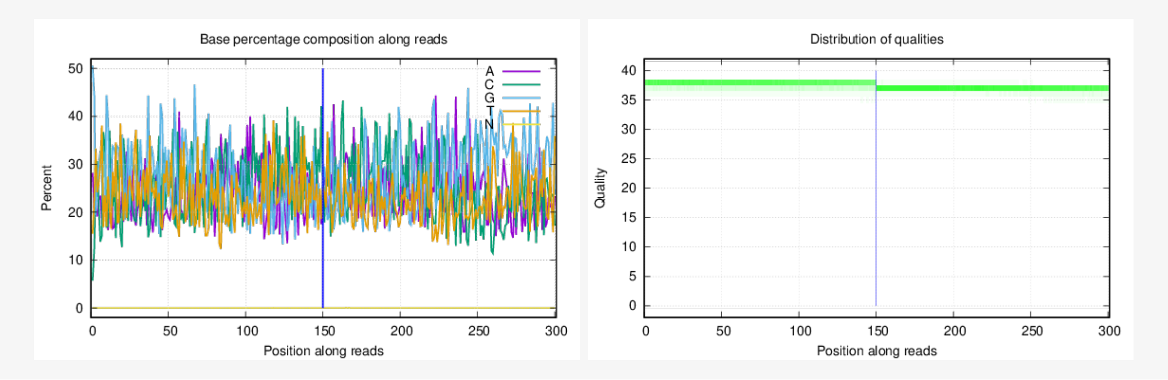

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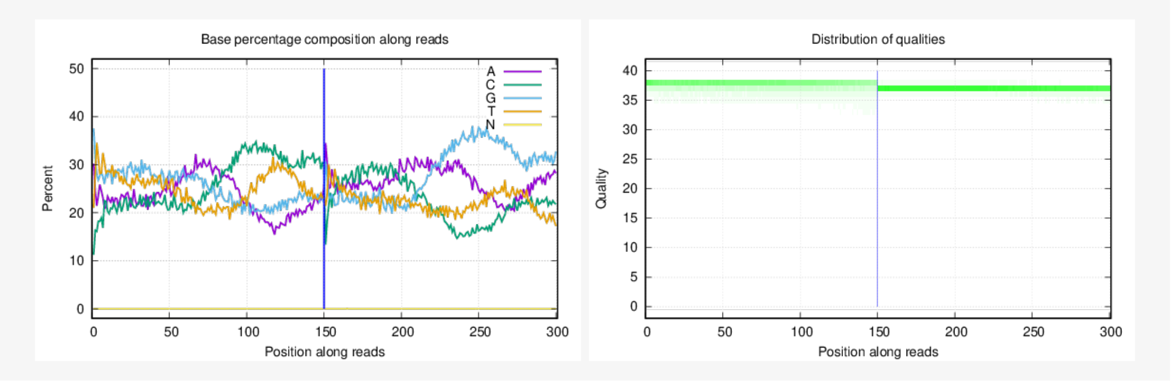

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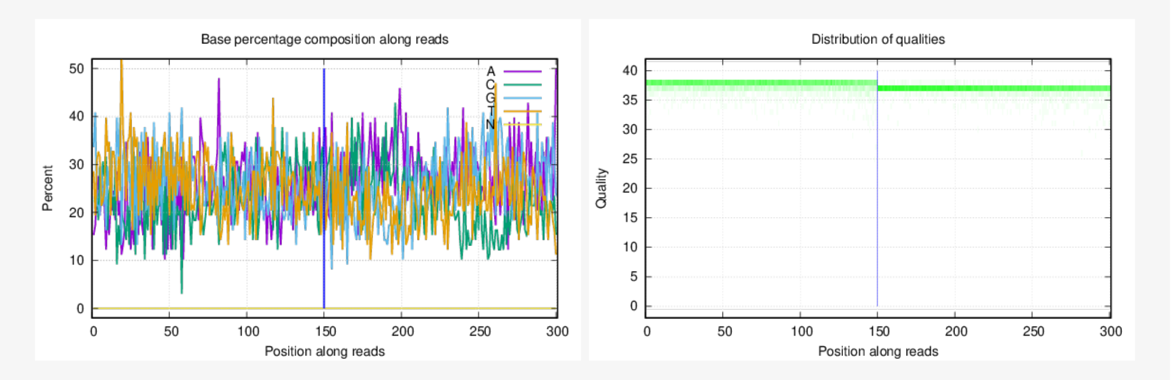

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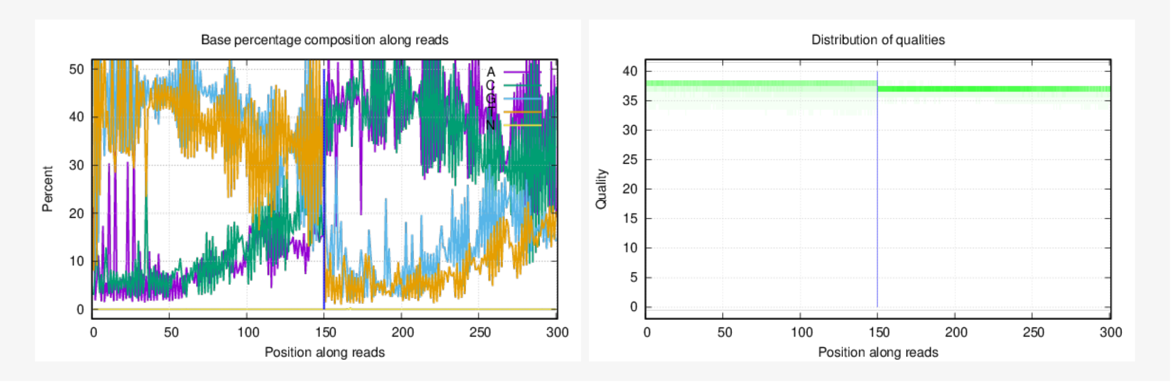

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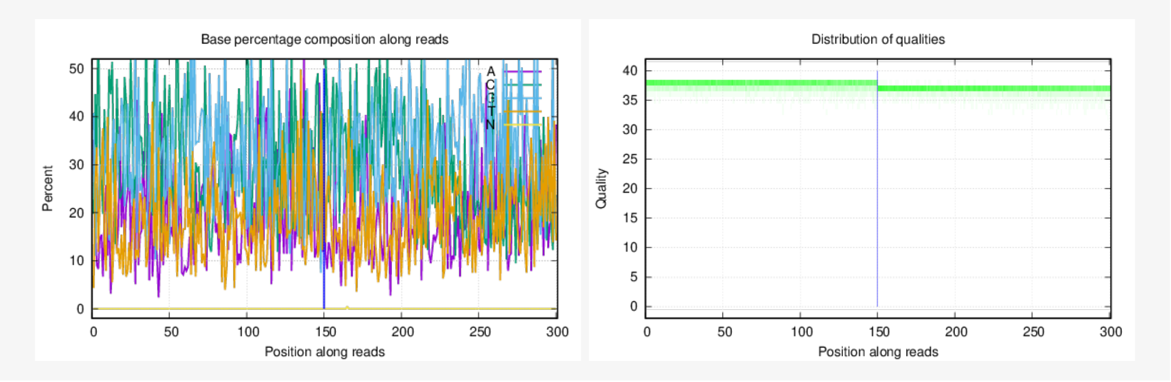

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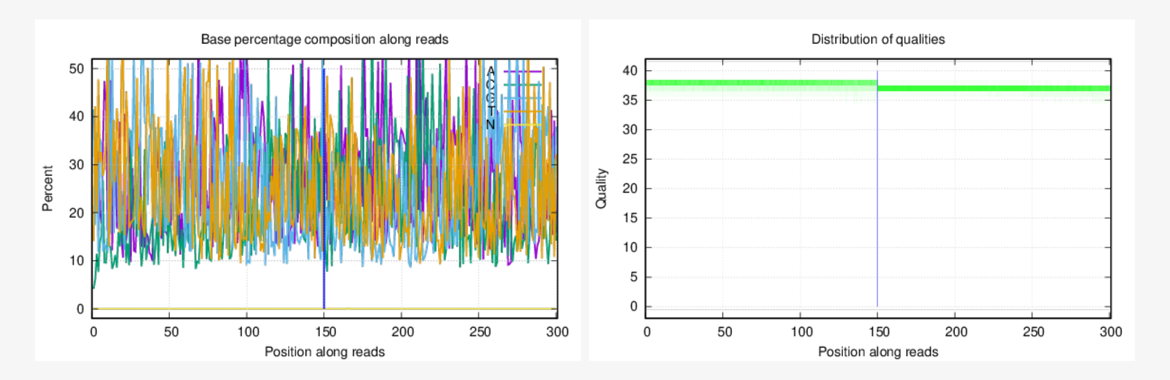

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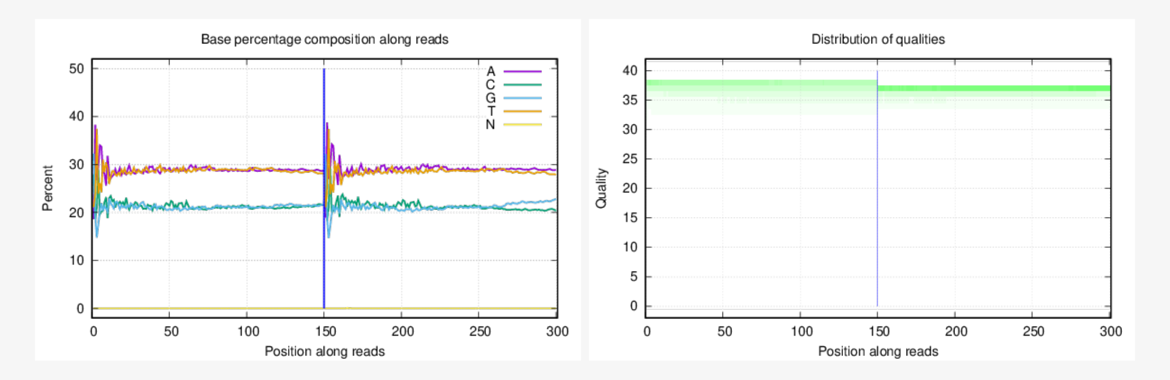

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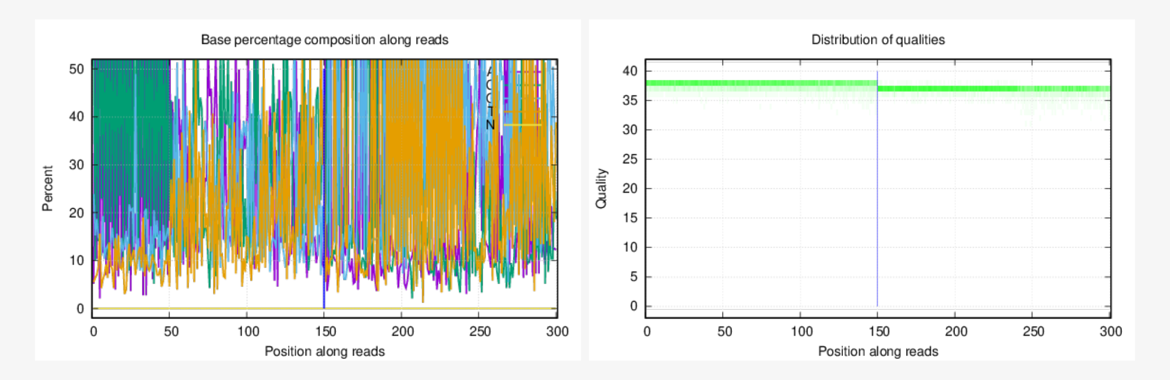

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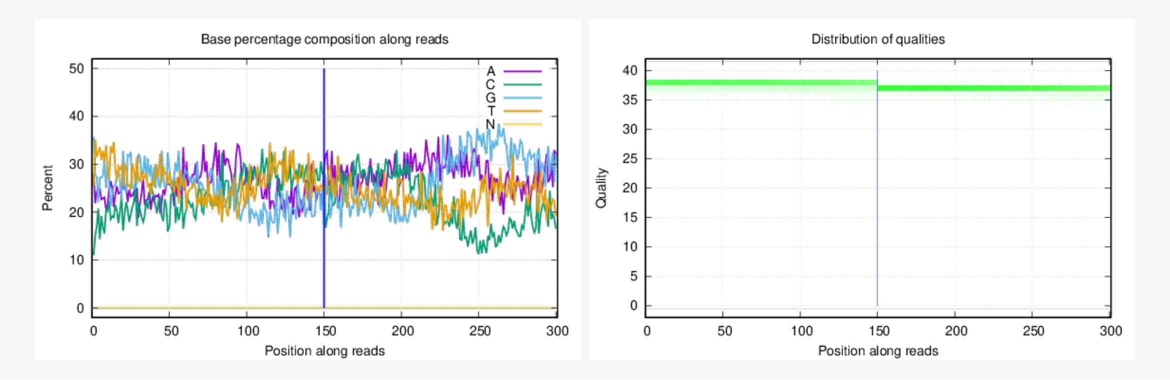

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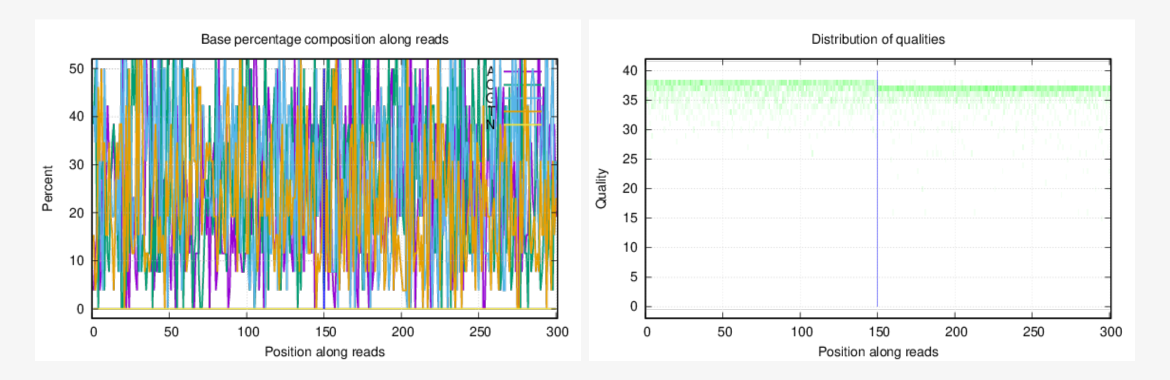

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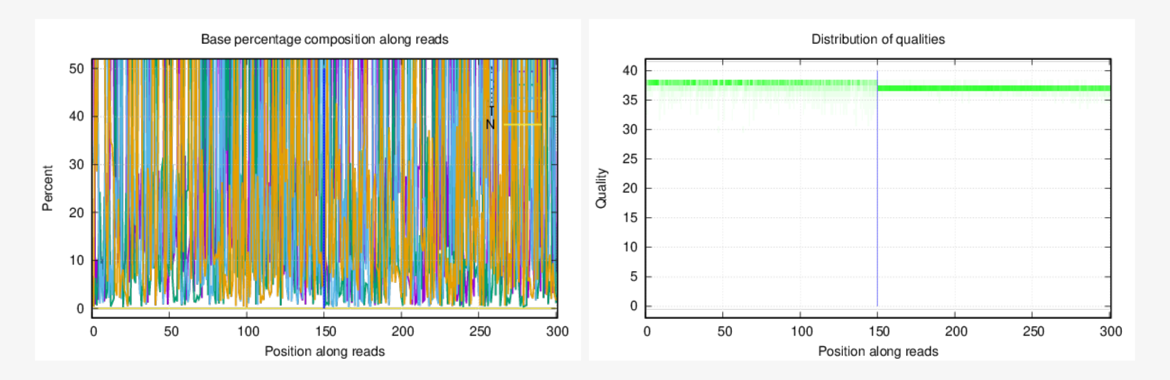

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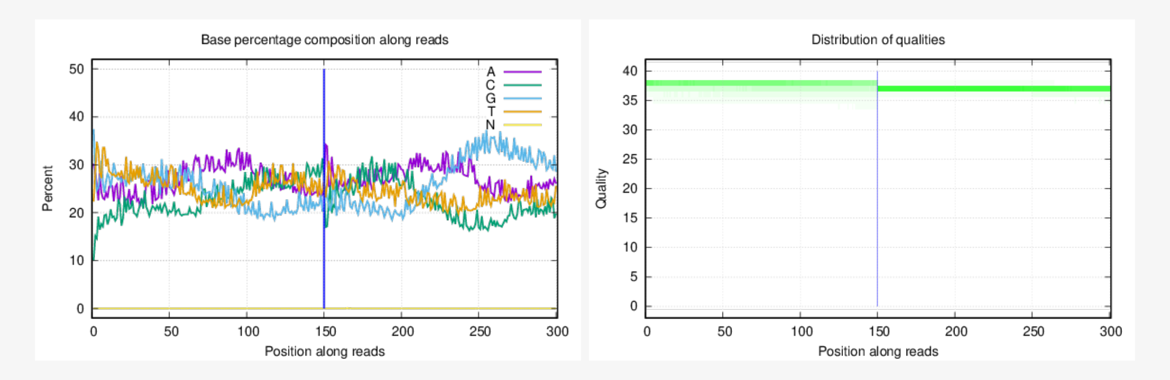

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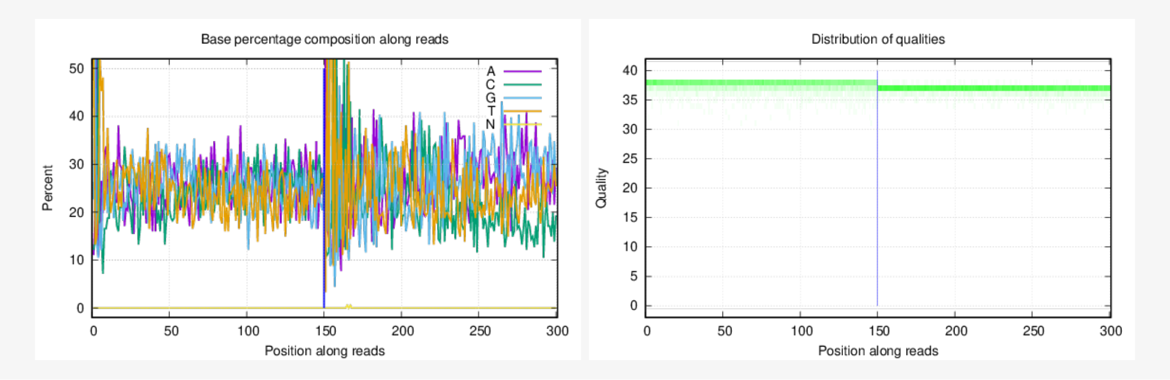

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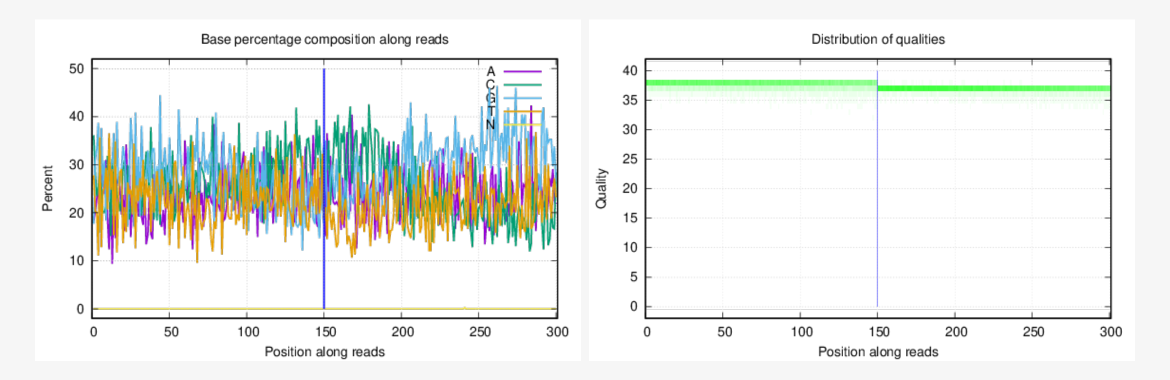

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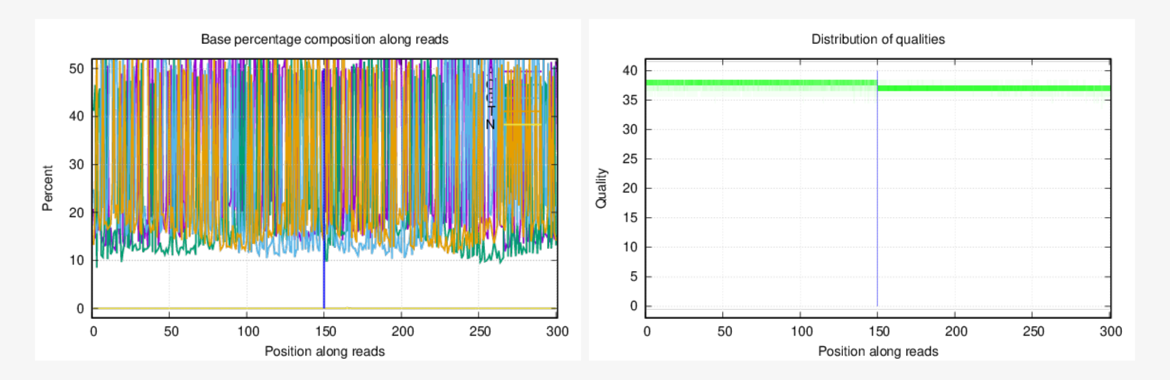

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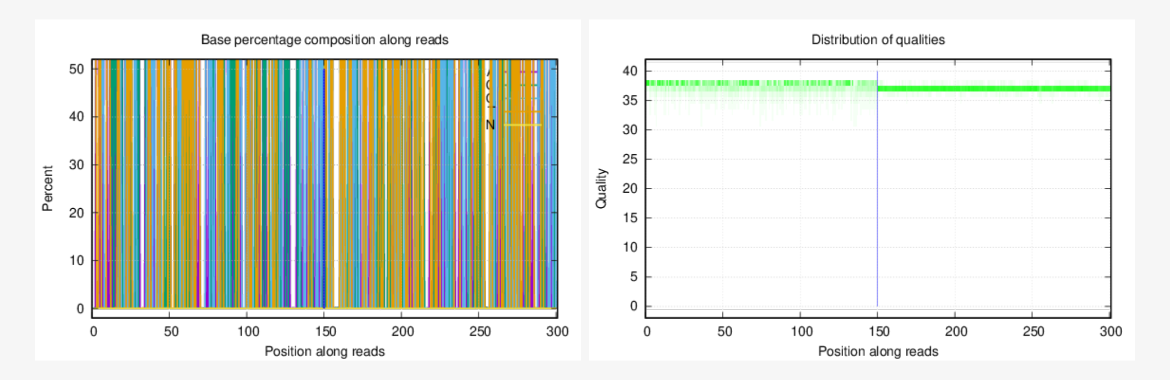

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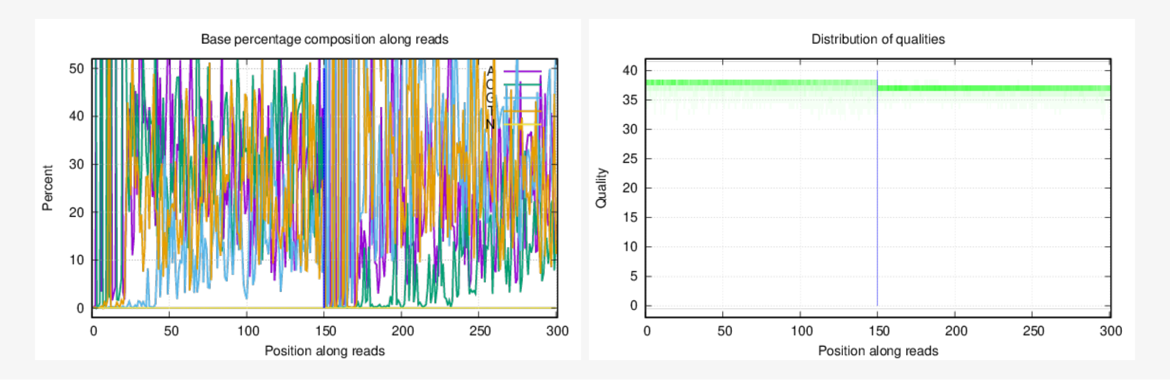
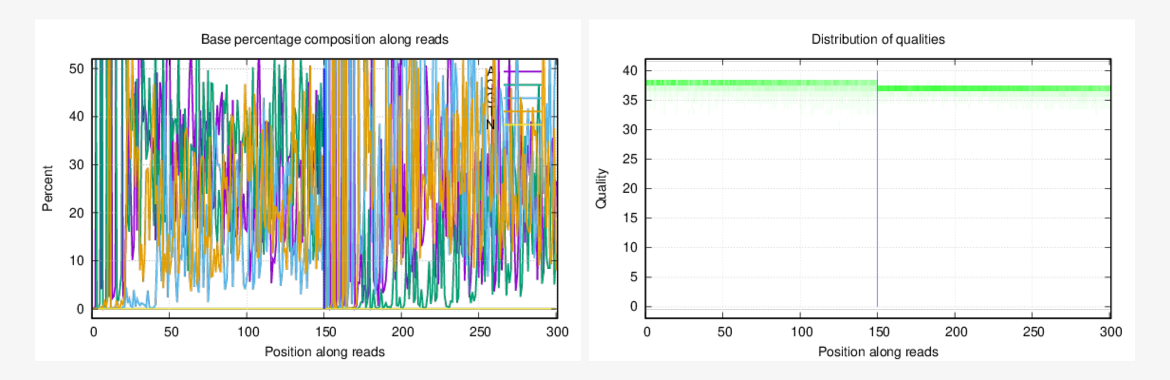
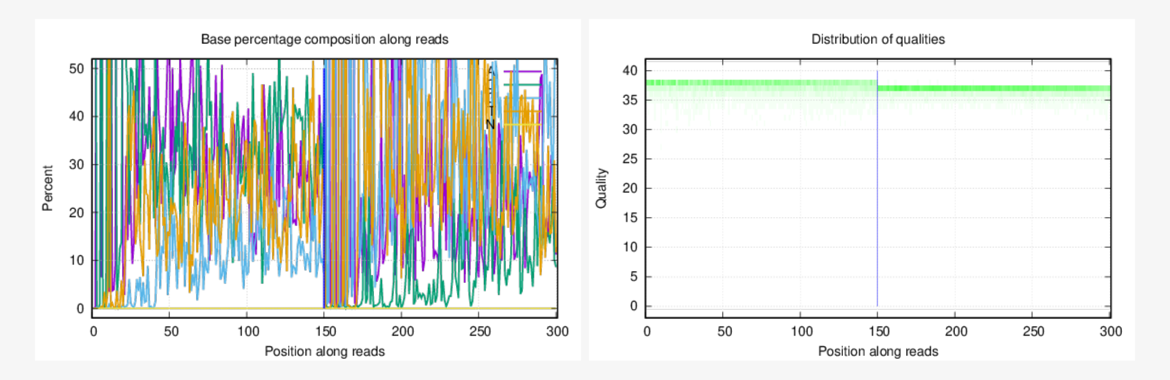


IP142



IP146_1



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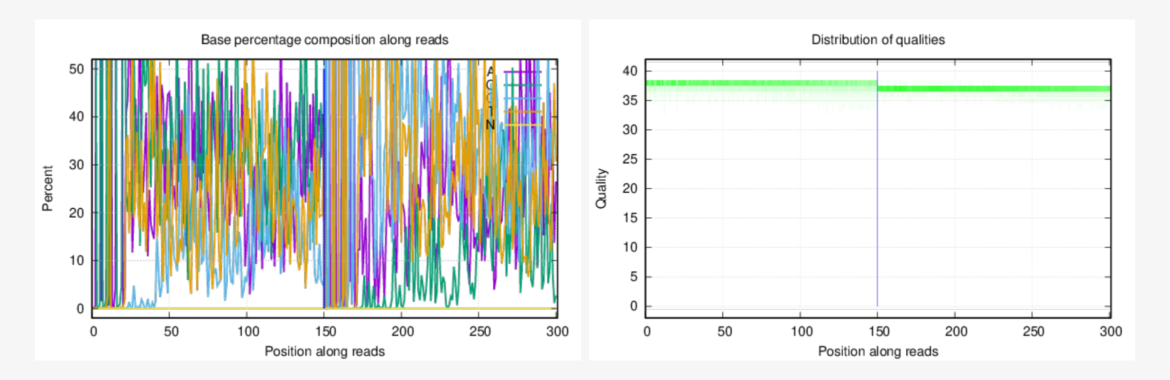

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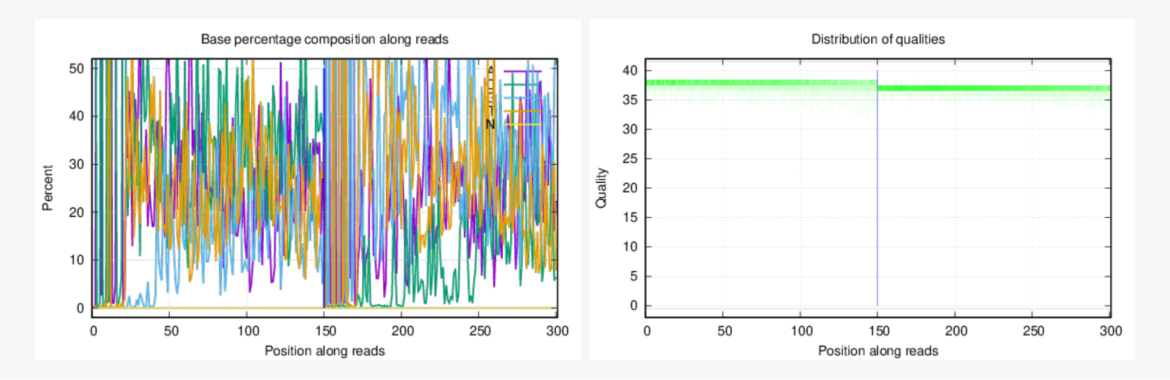

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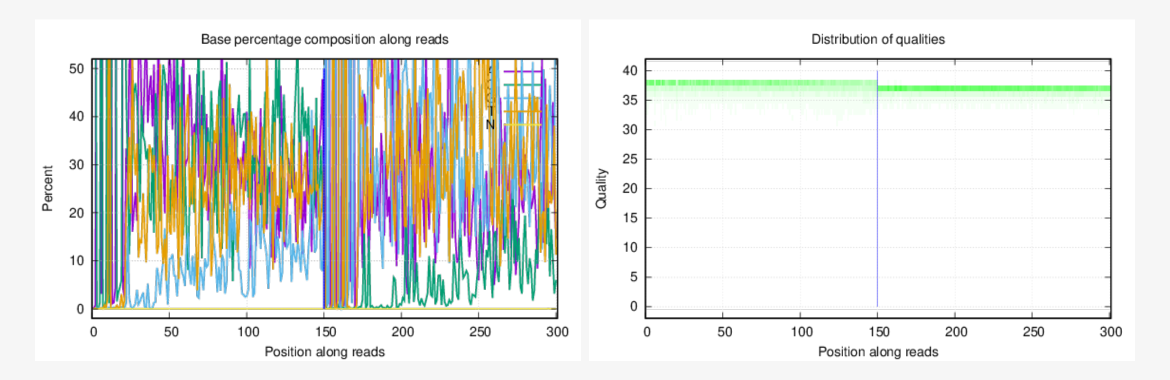

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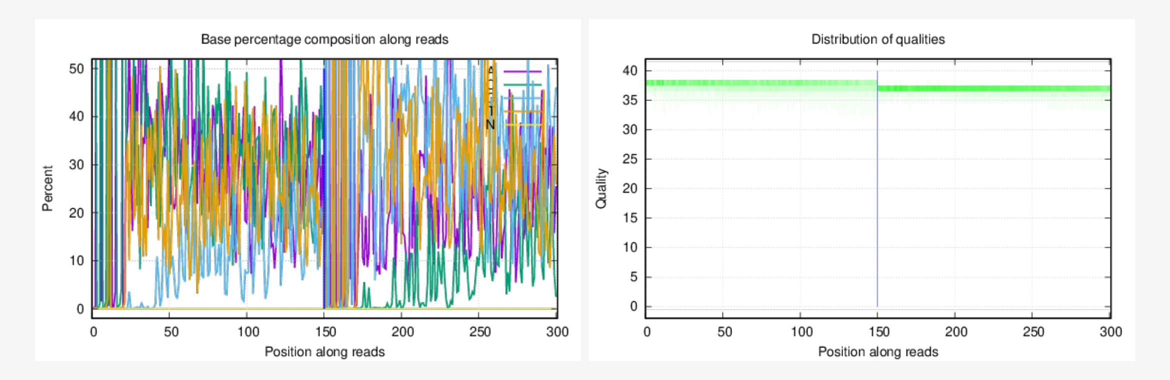

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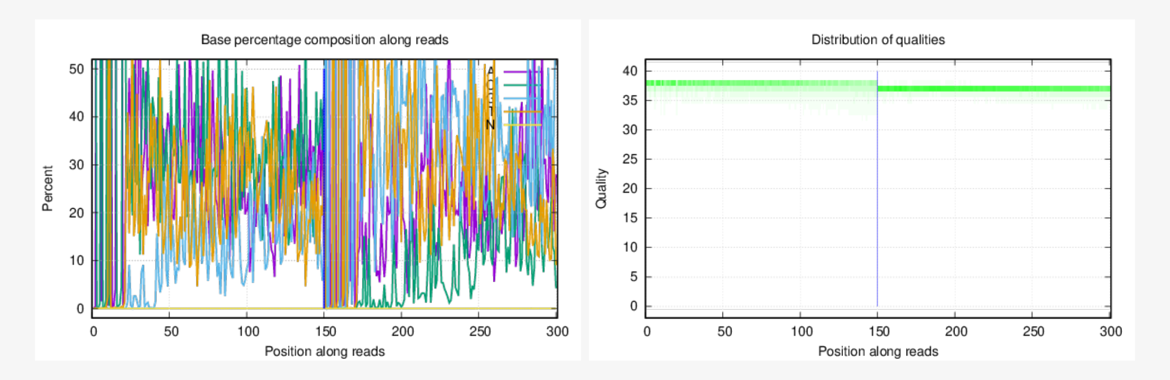

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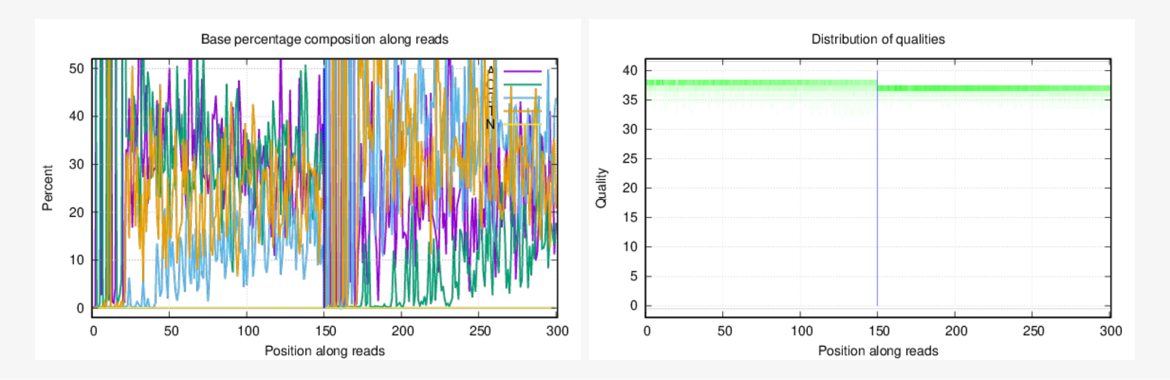

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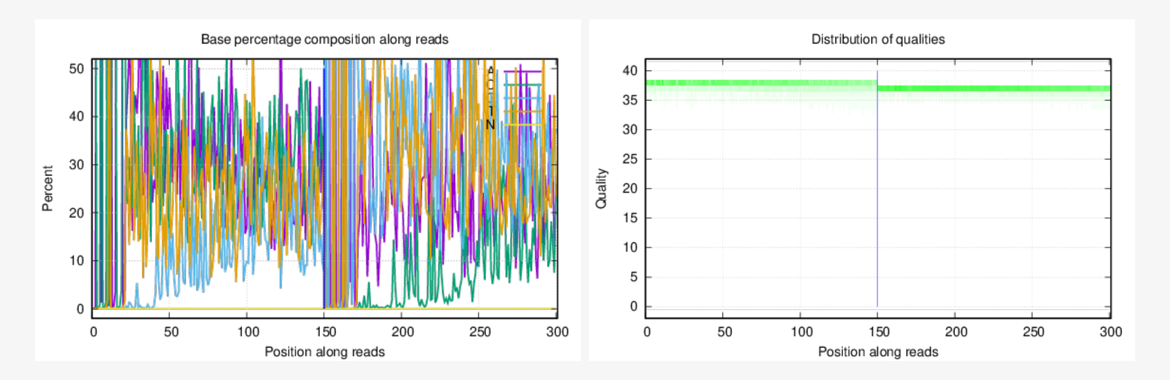

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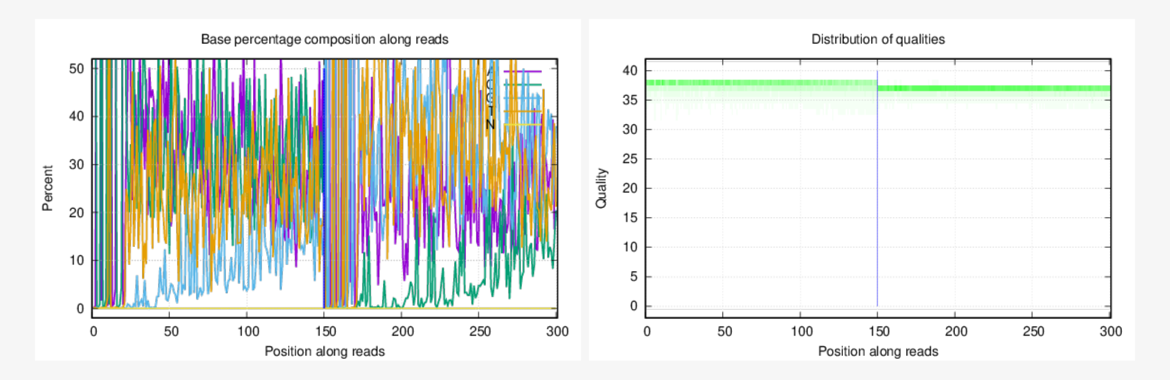

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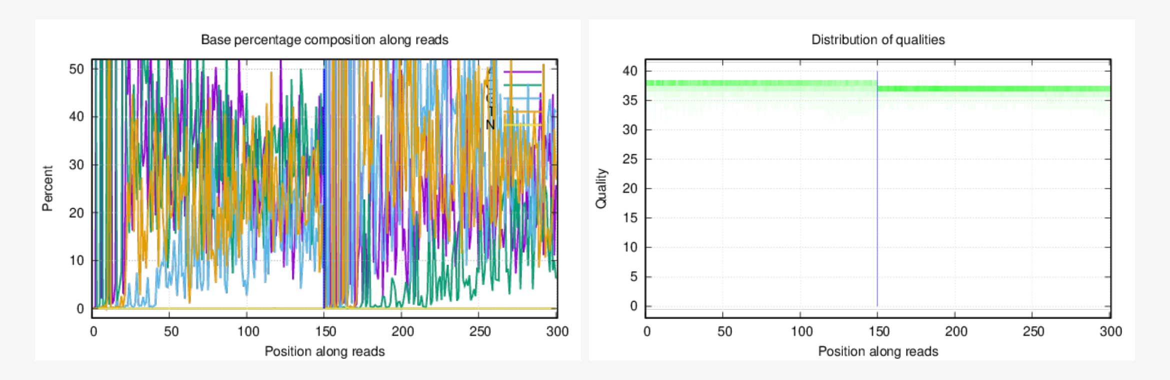

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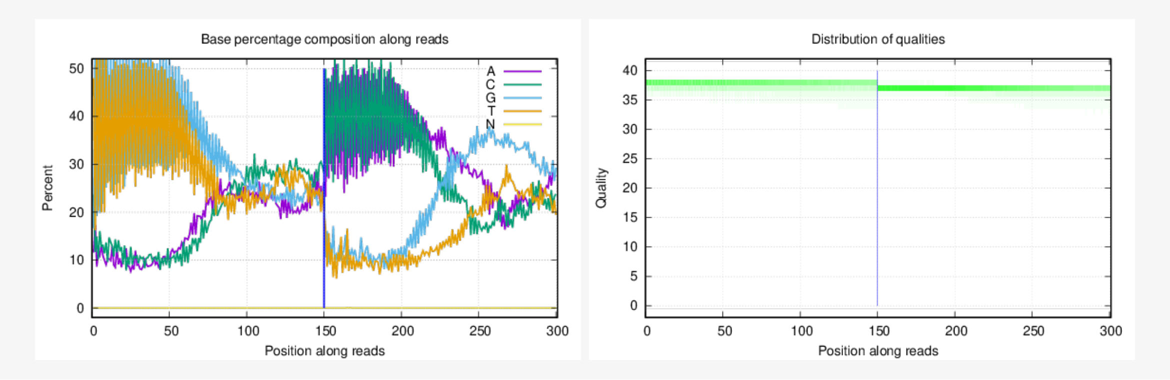

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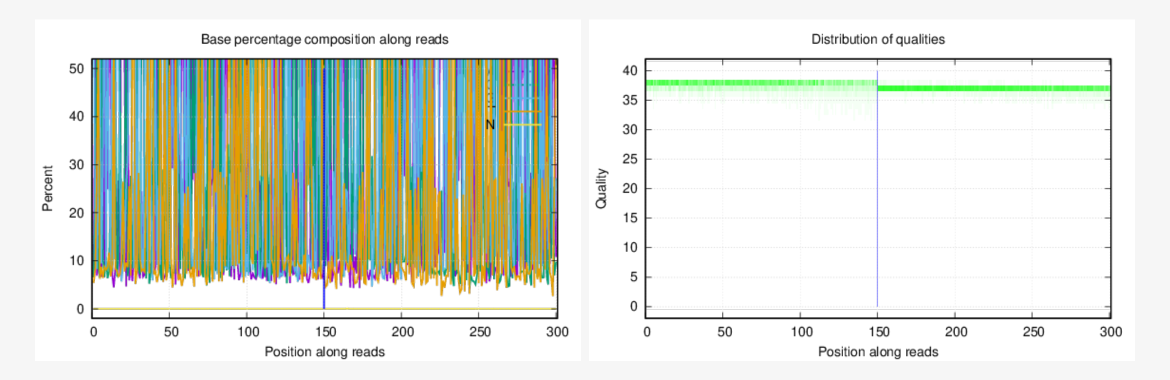

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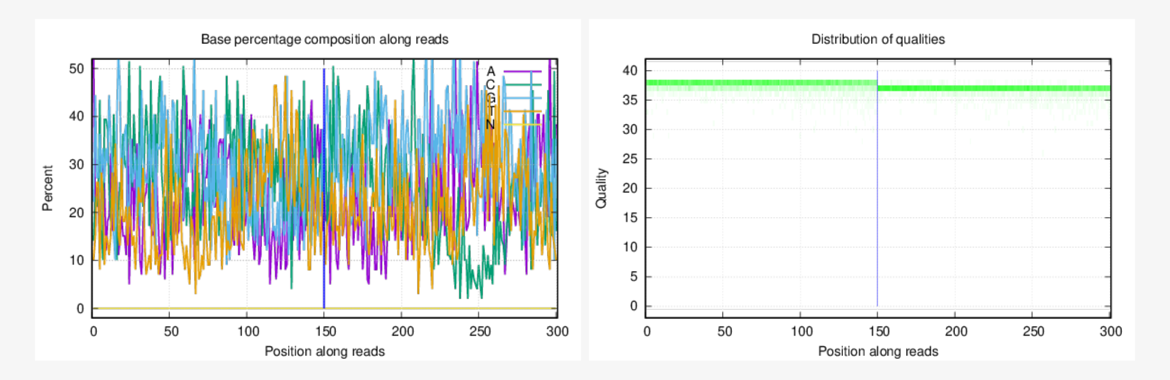

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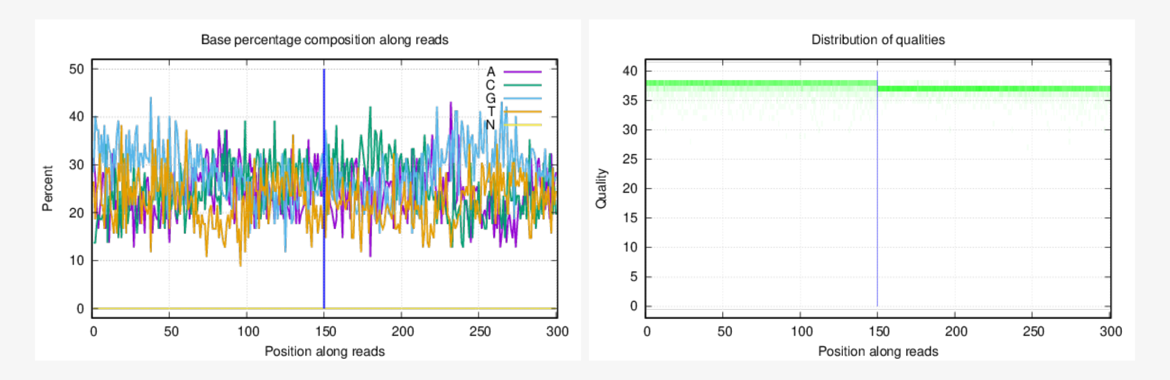

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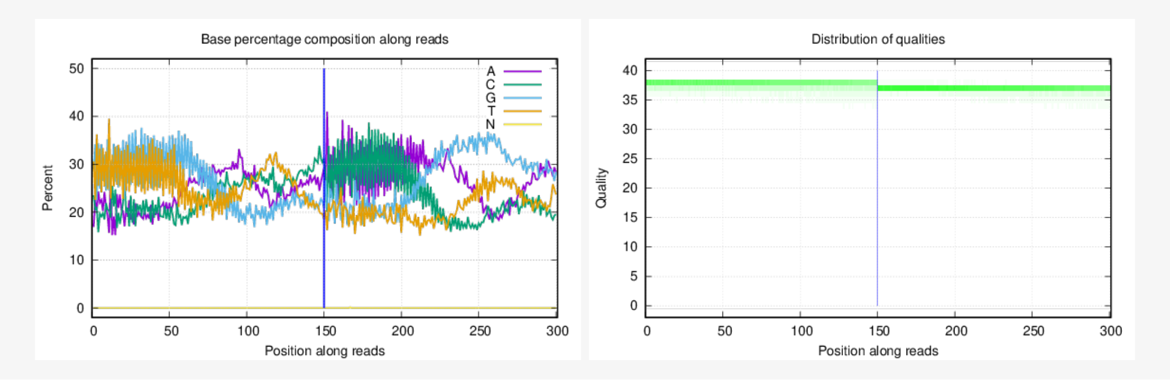

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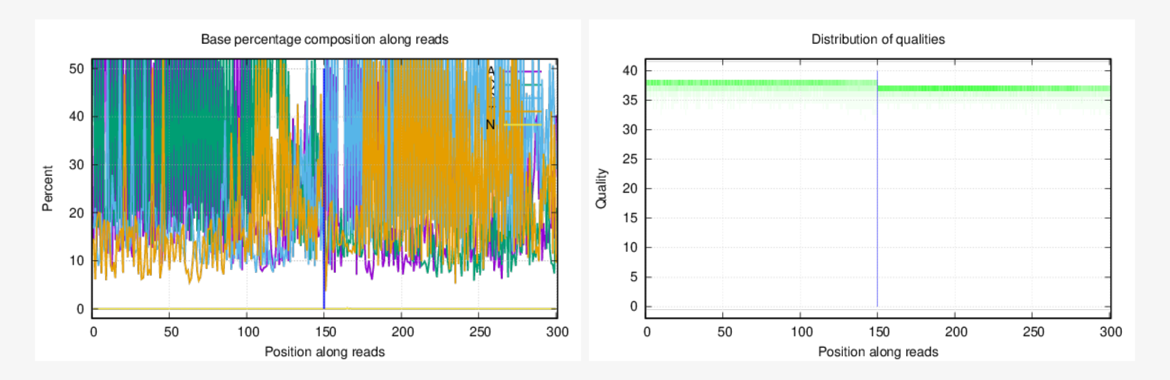

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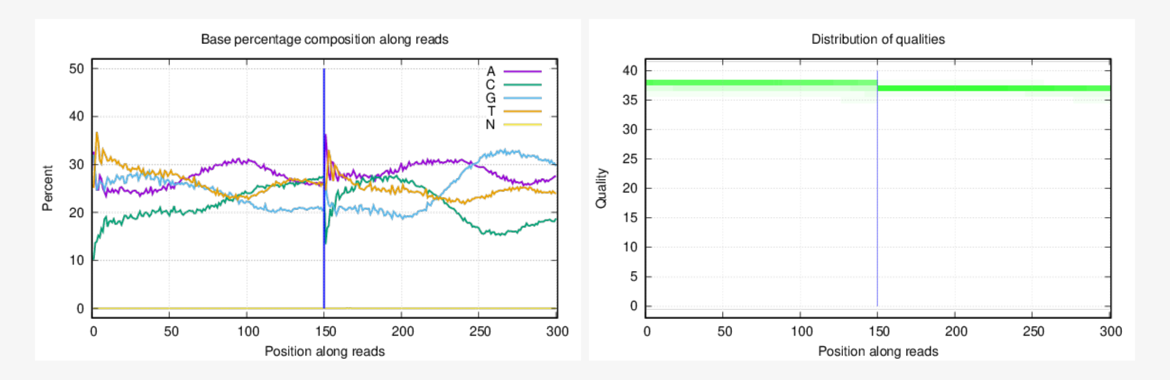

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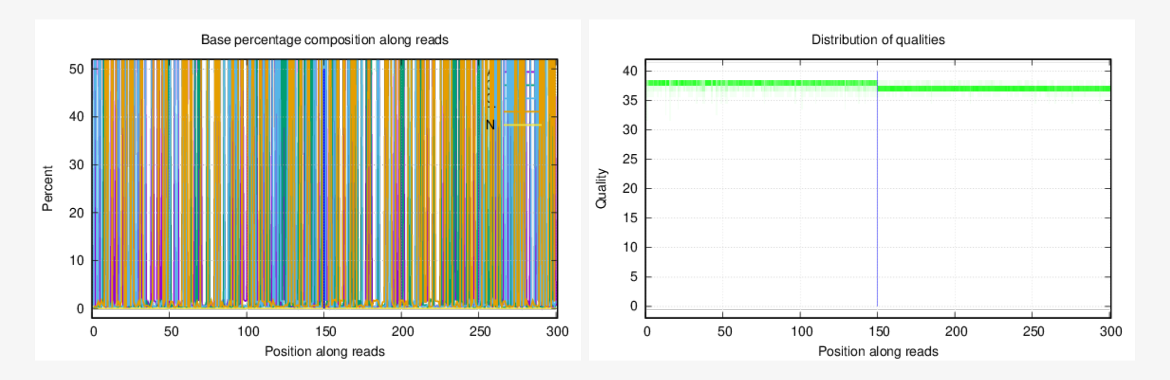

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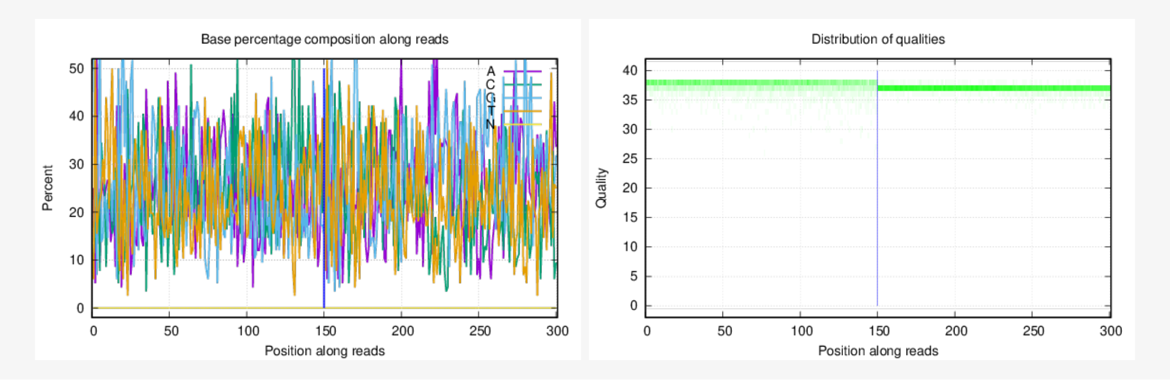

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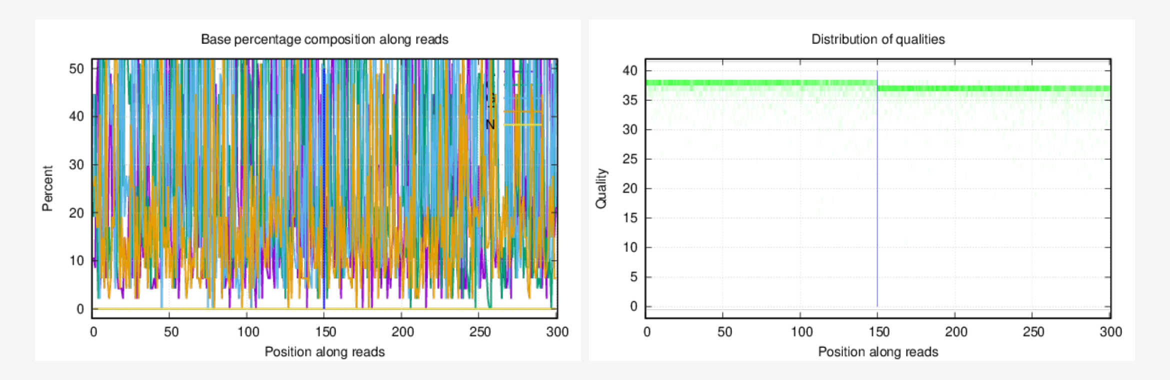

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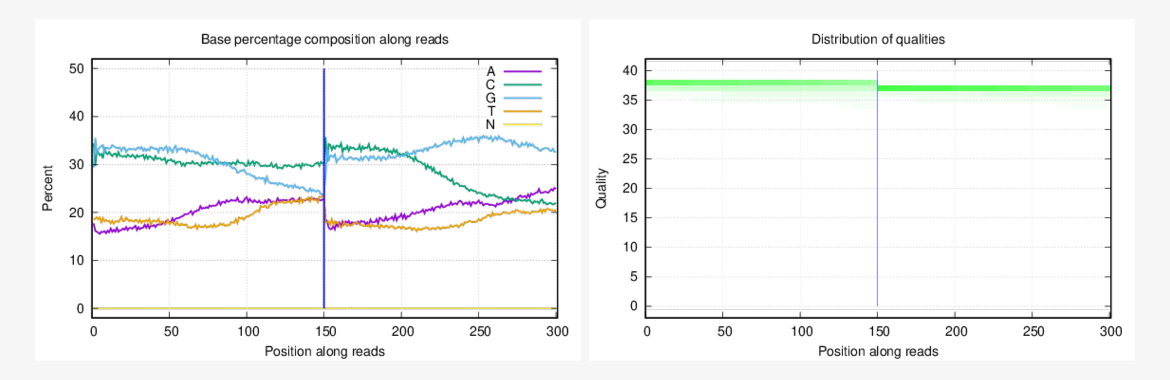

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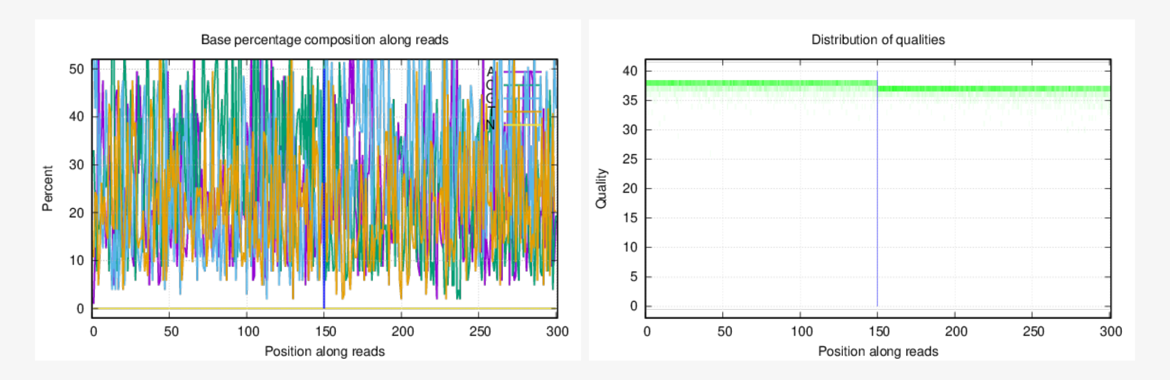

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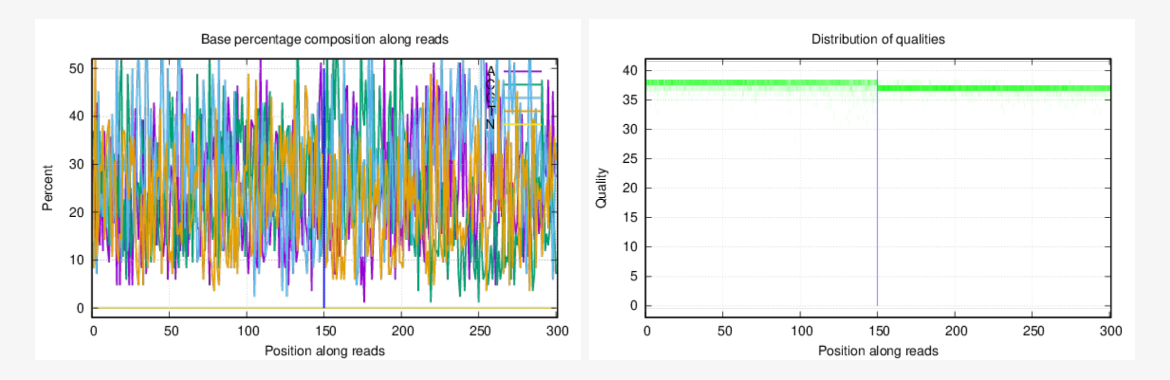

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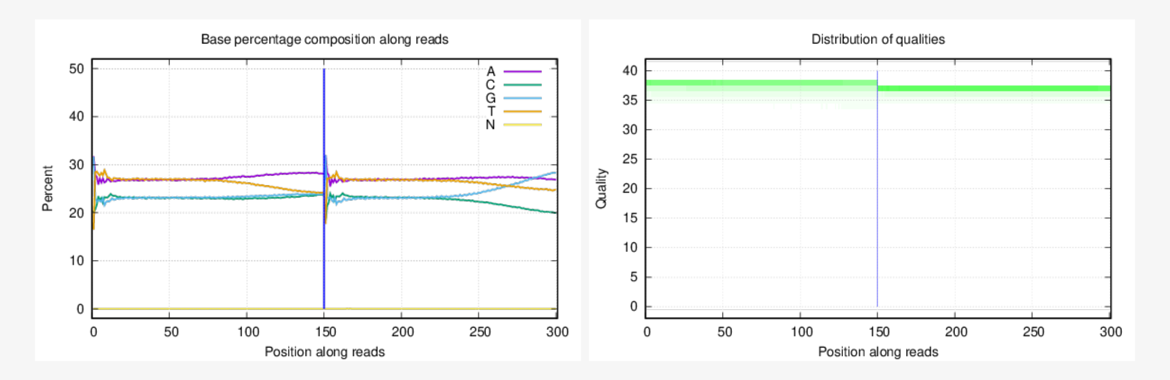

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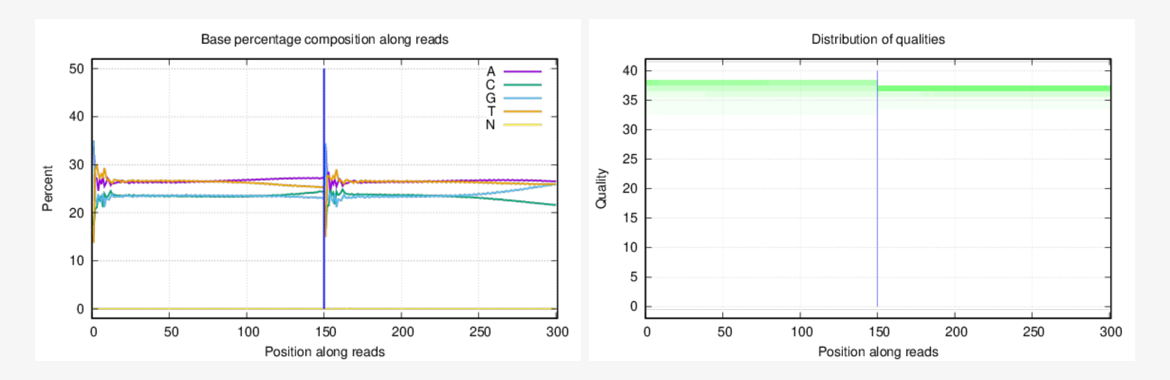

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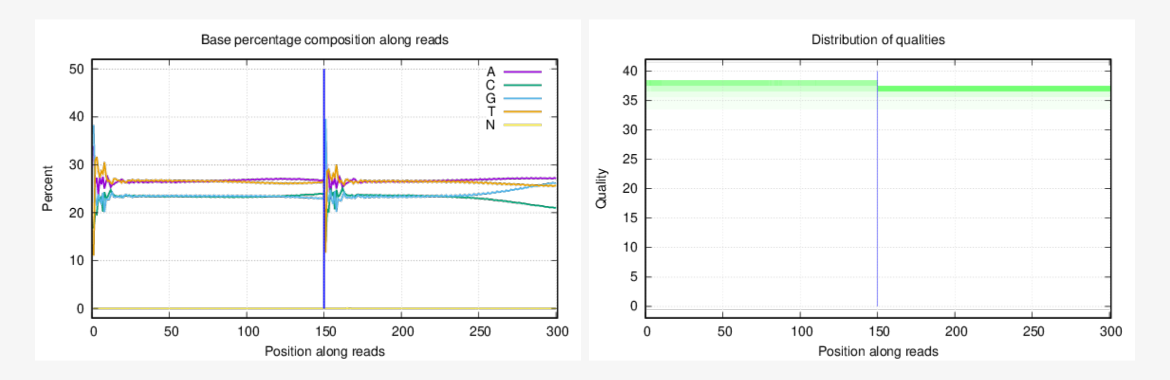

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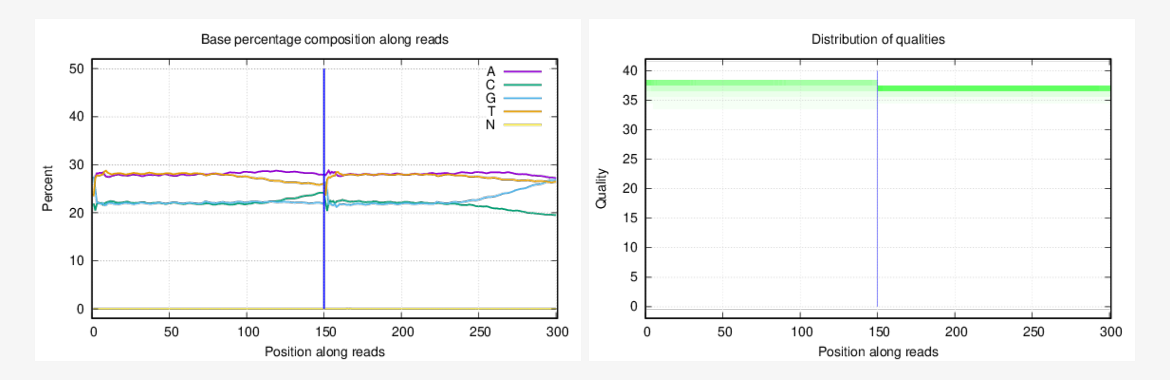

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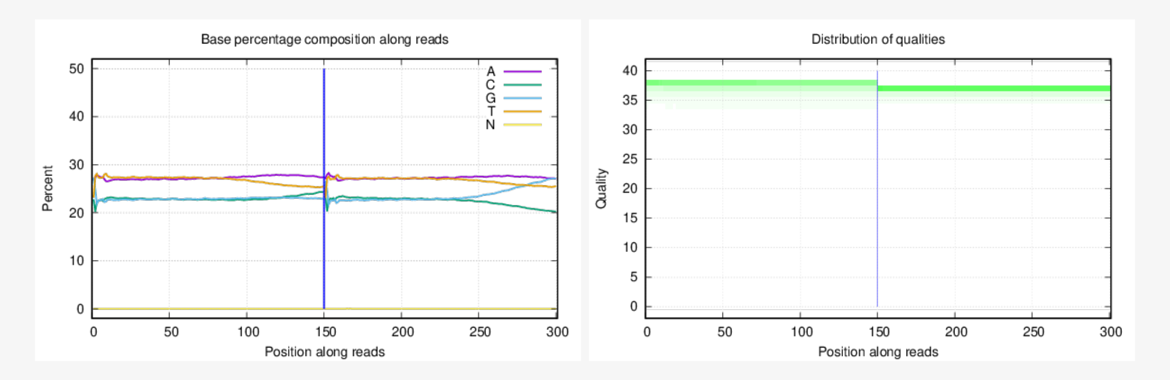

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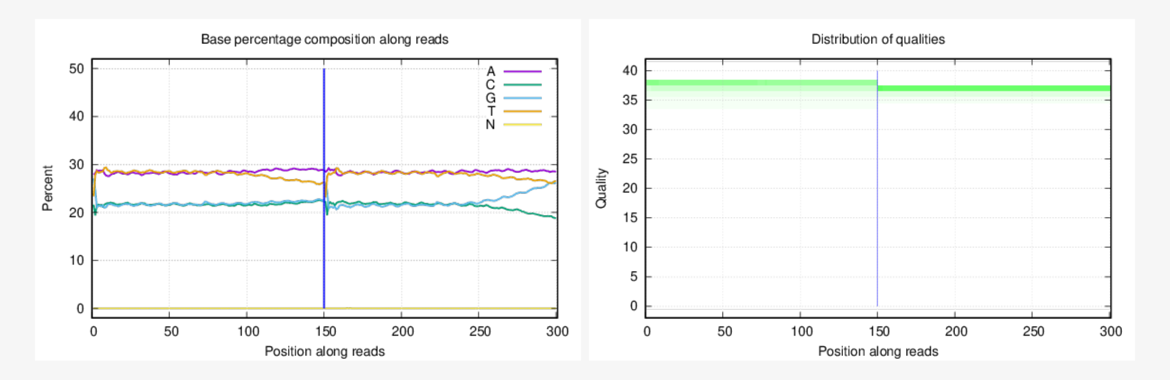

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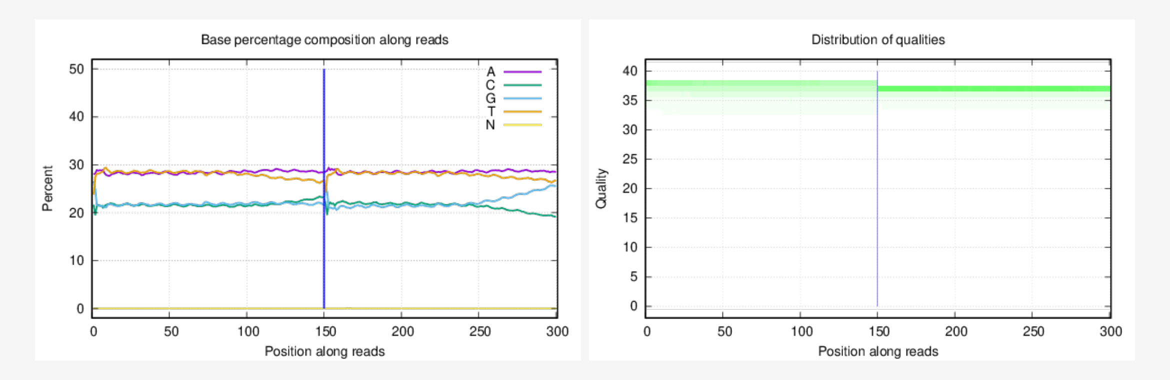

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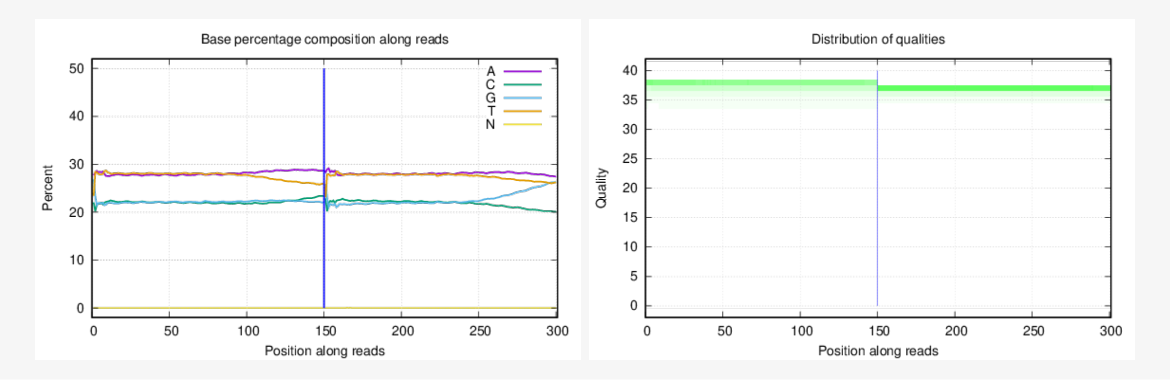

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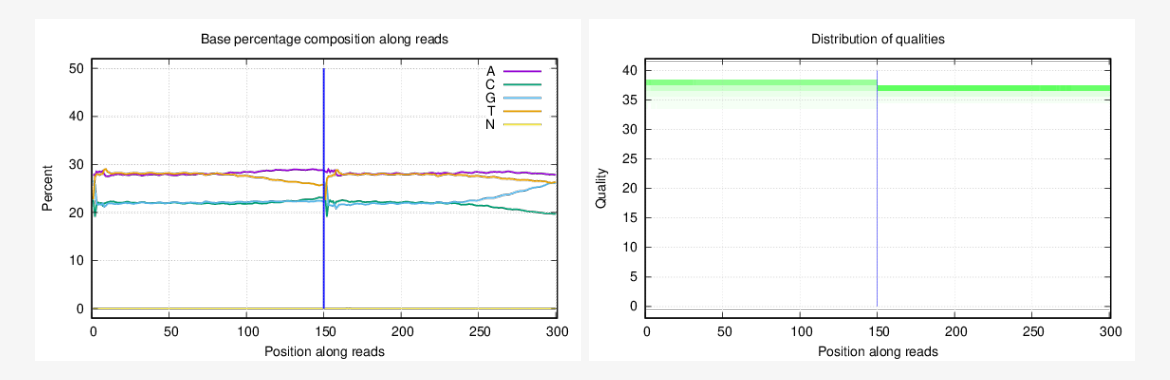

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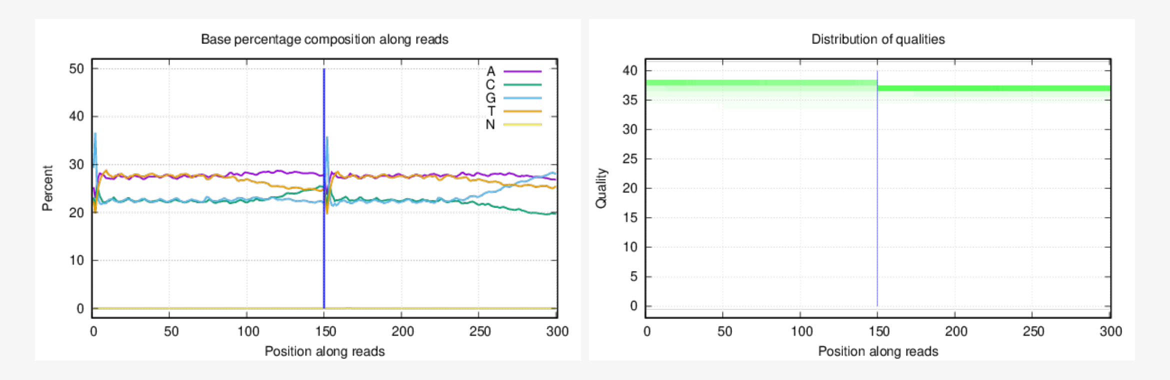

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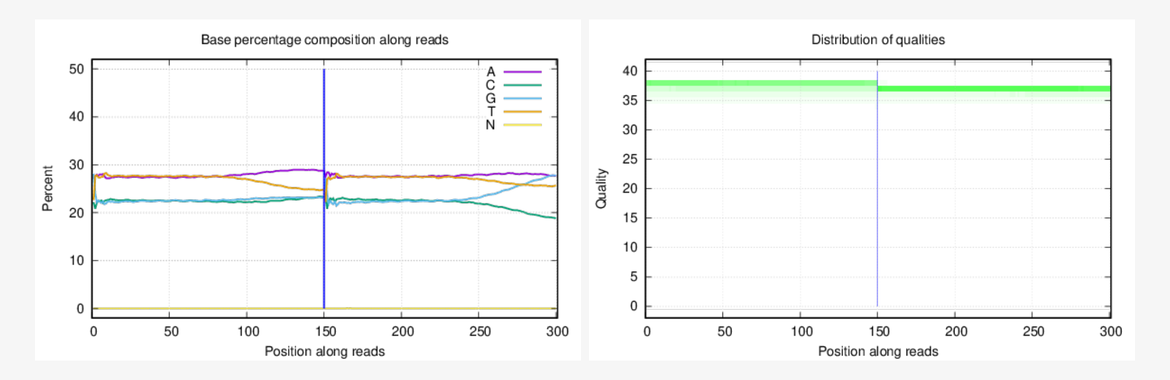

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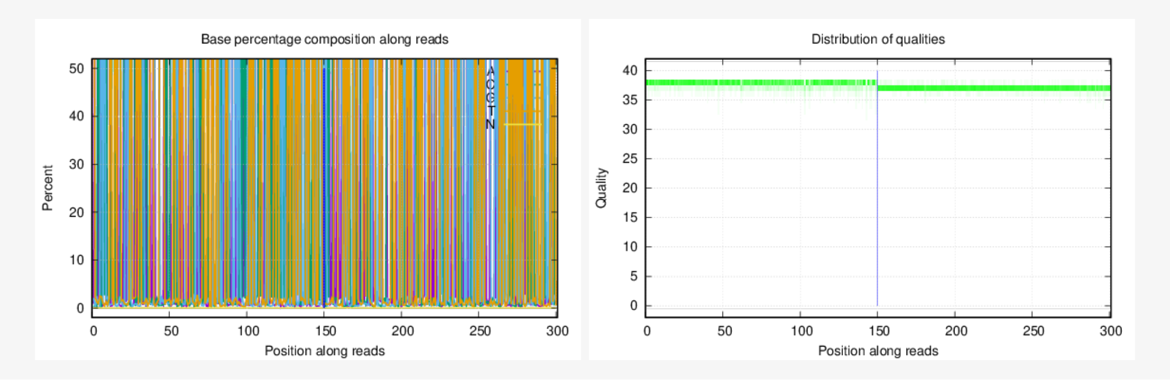

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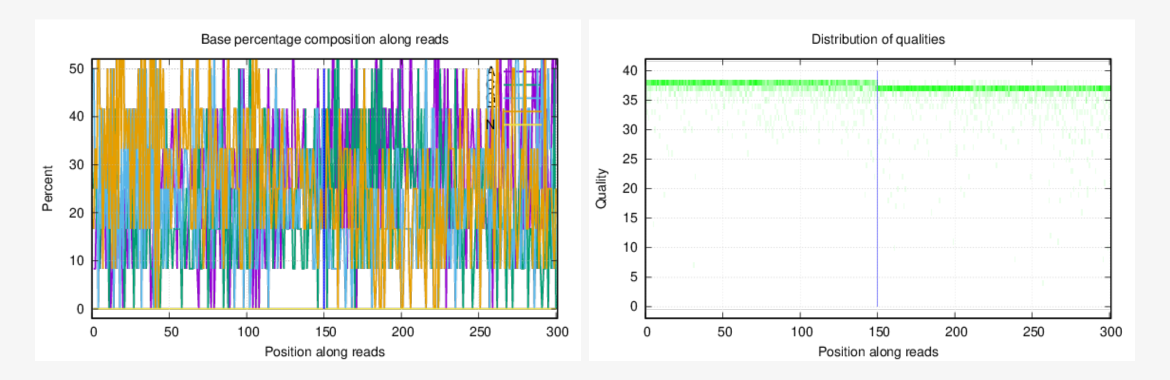

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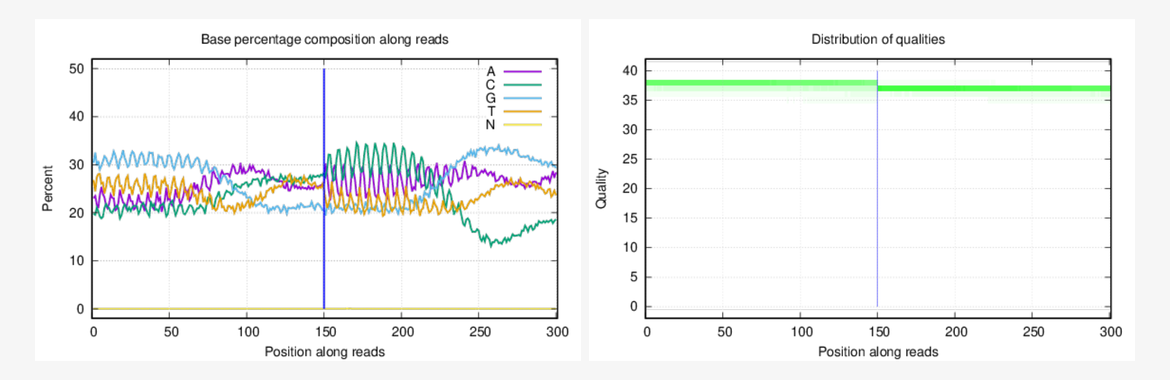

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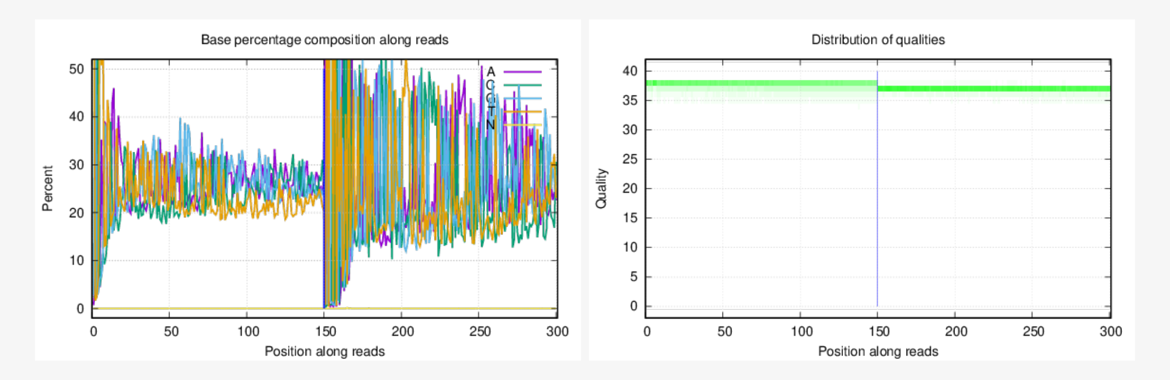

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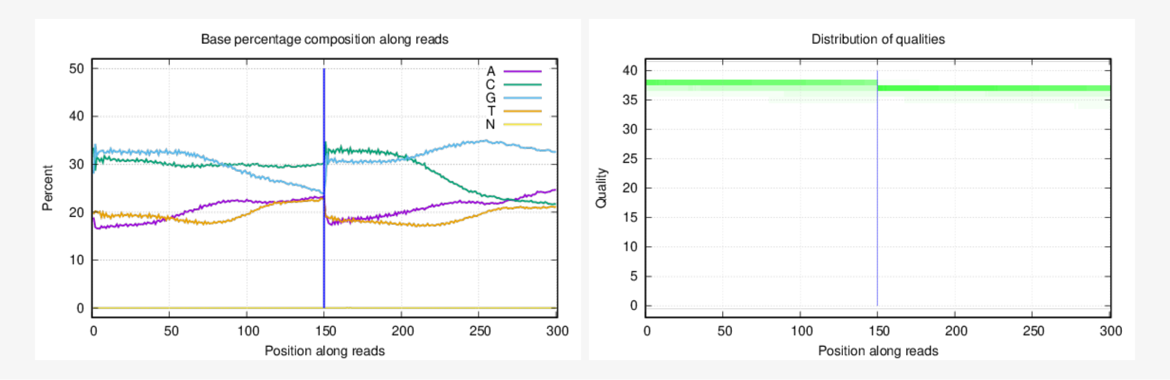

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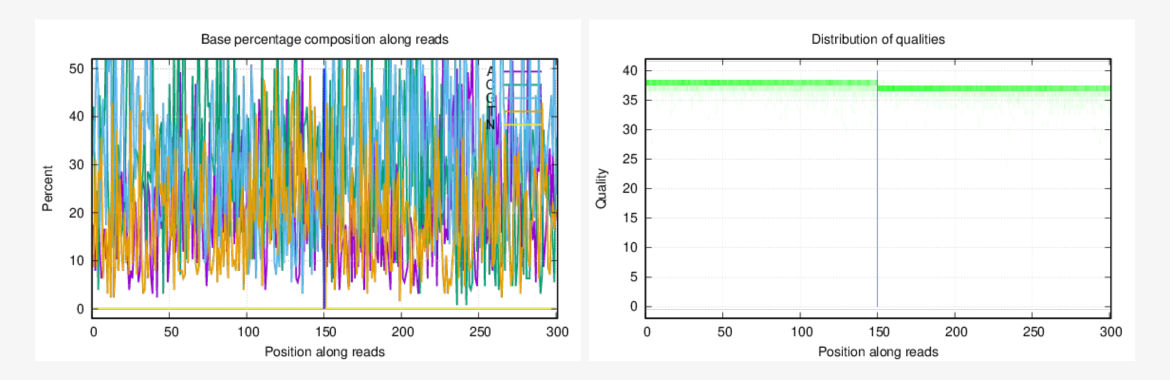

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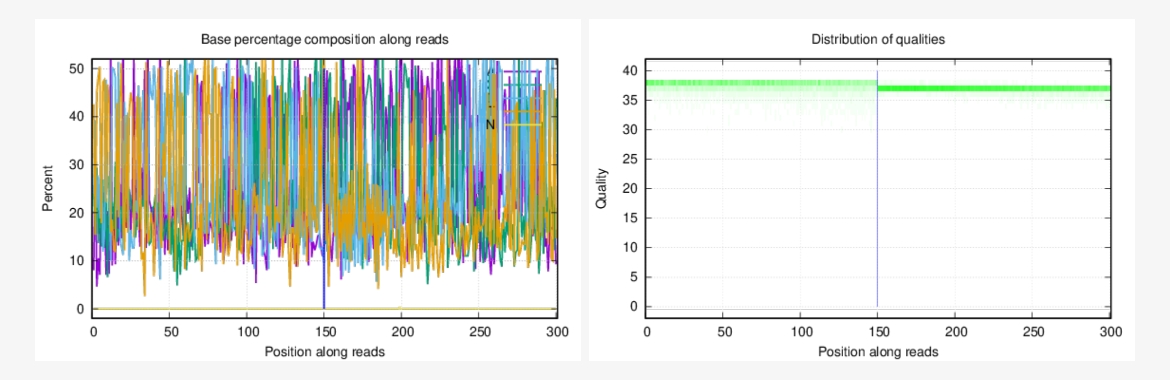

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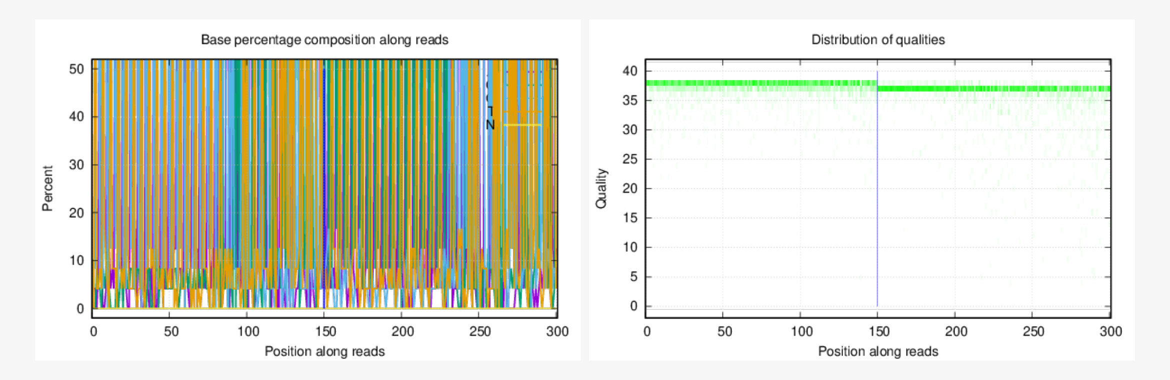

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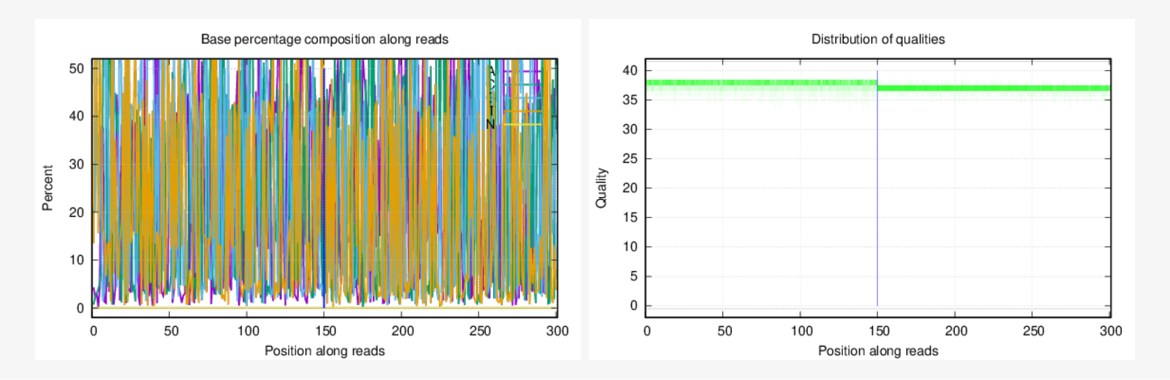

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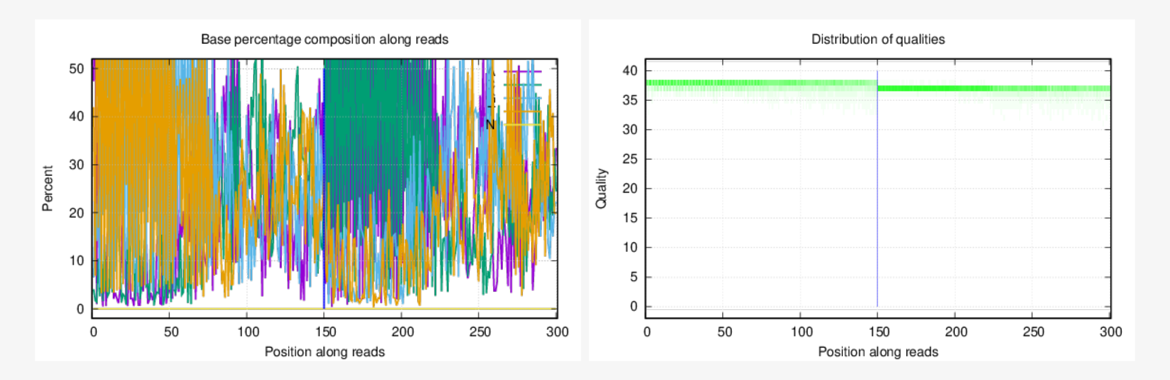

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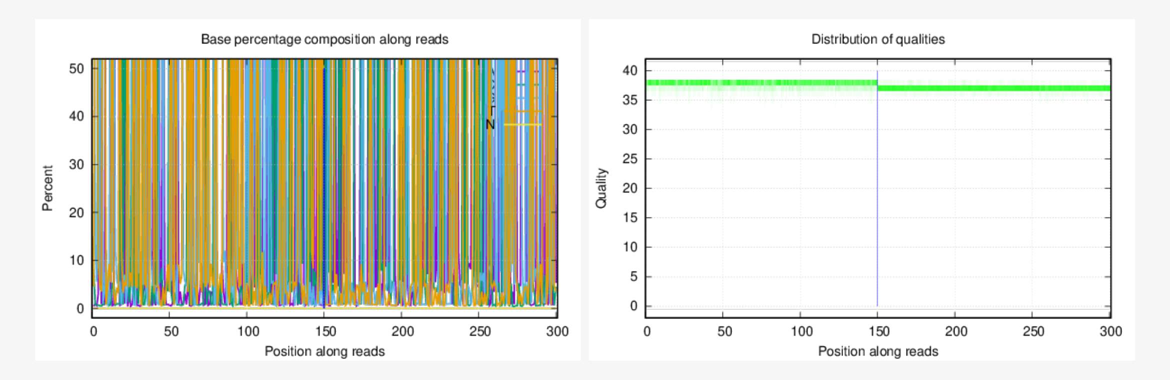

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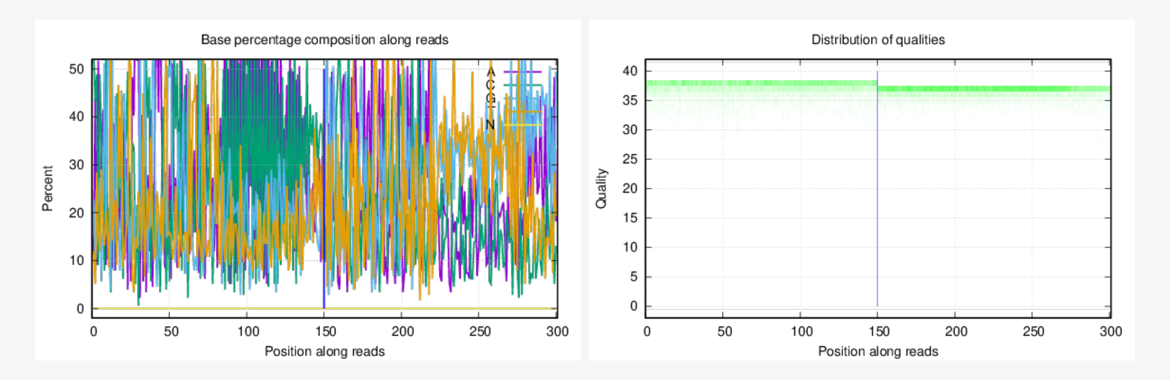

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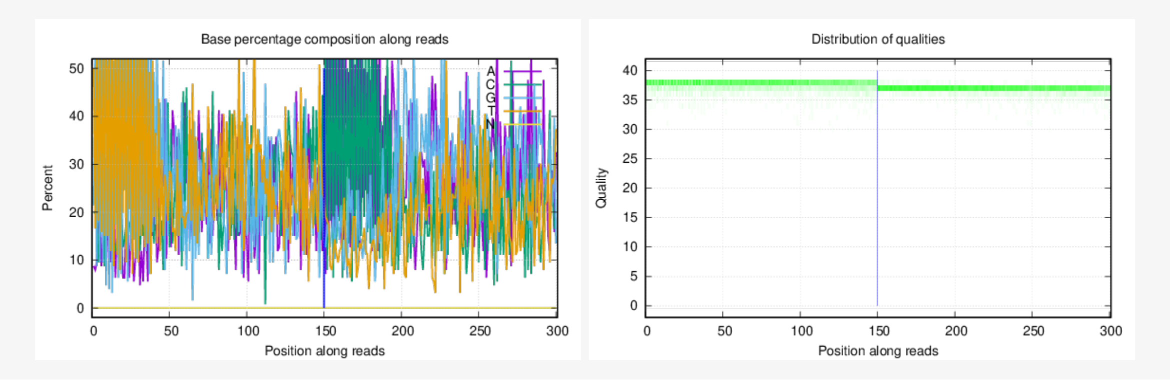

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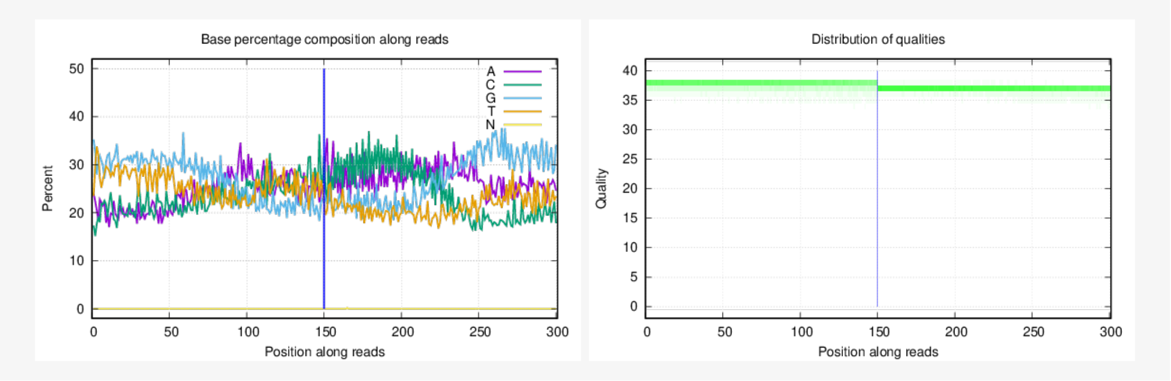

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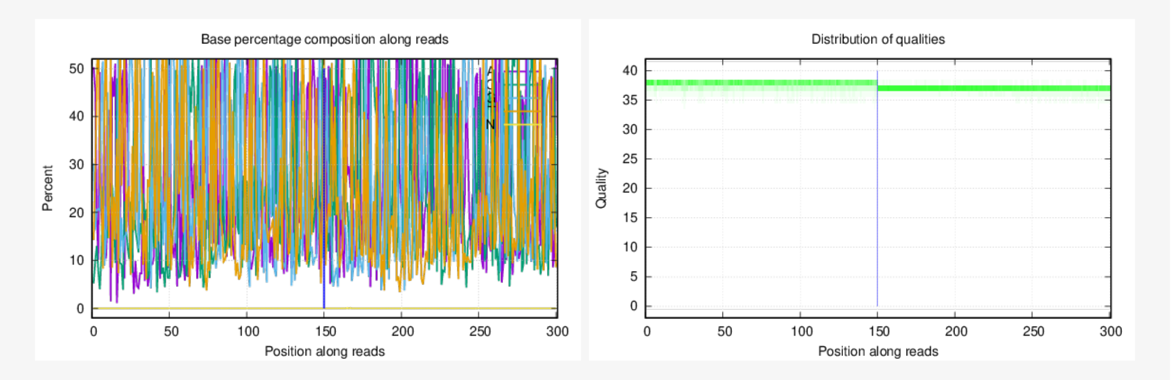

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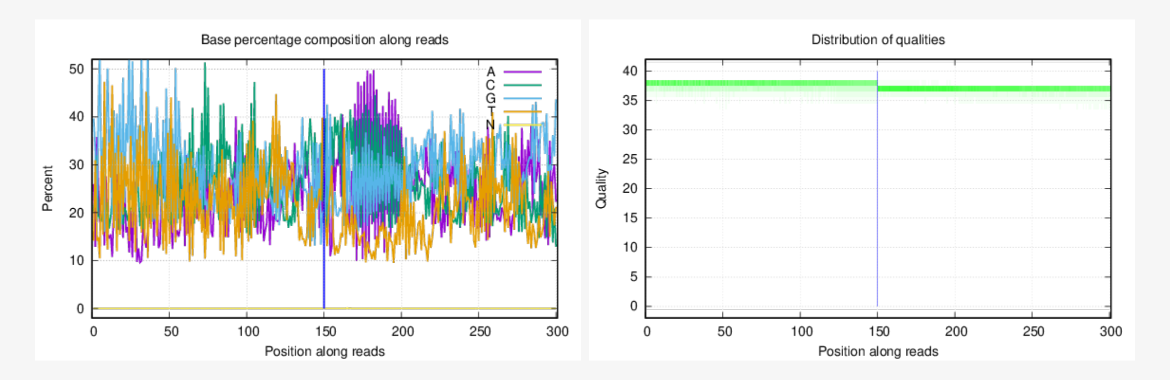

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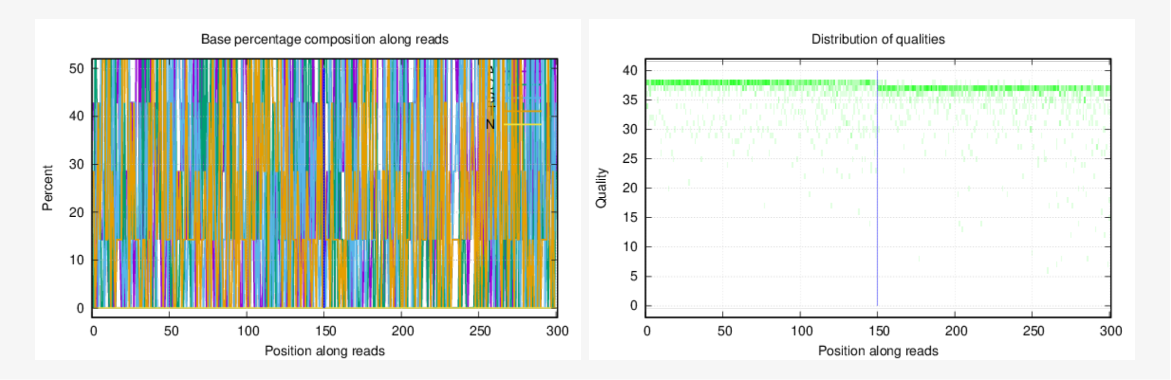

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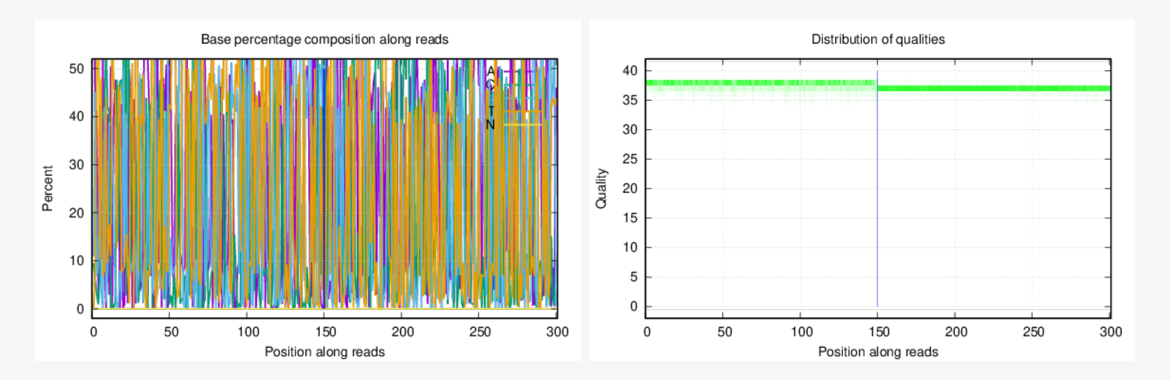

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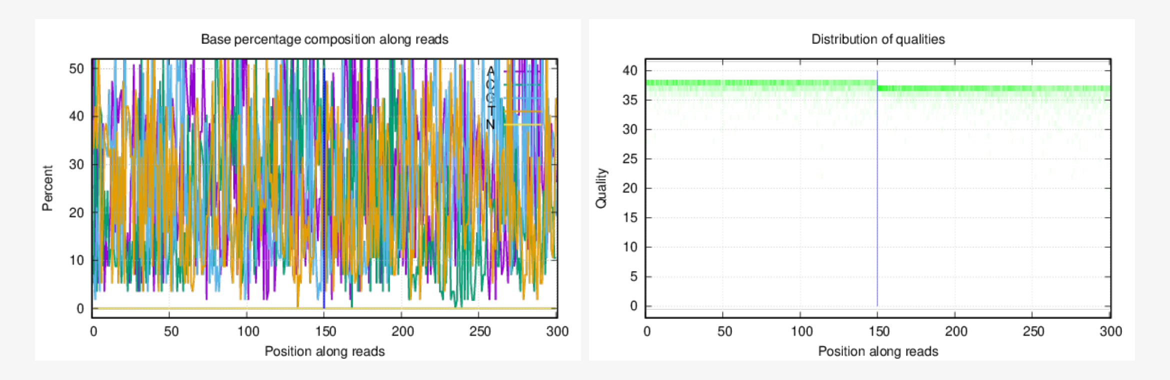

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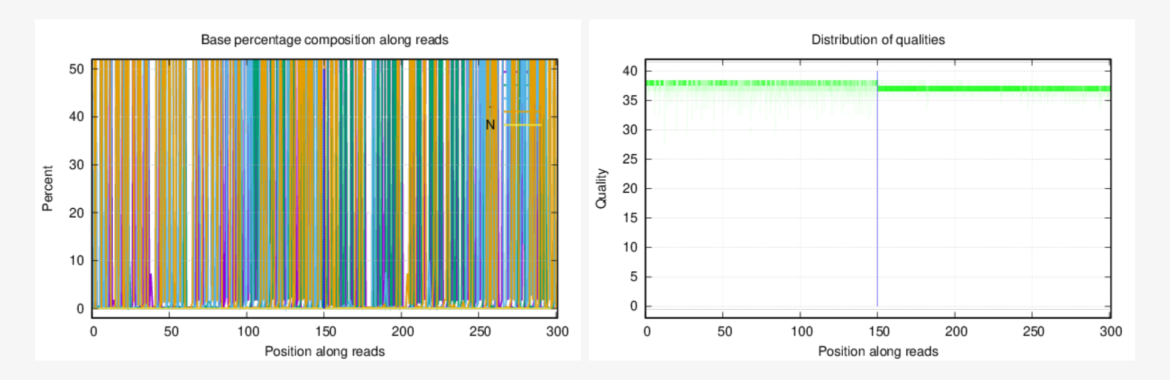

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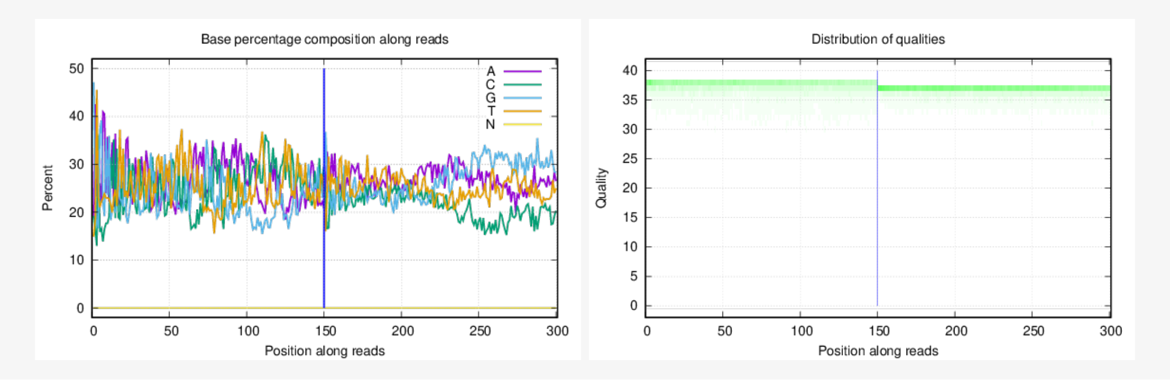

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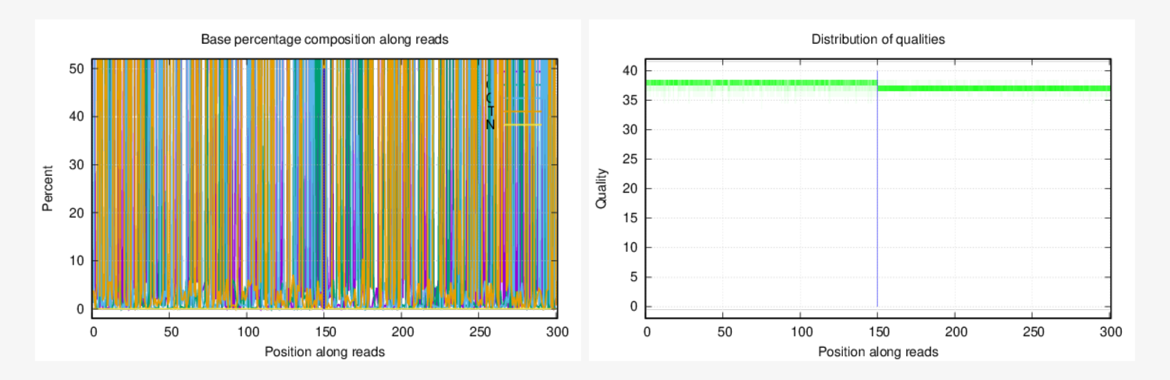

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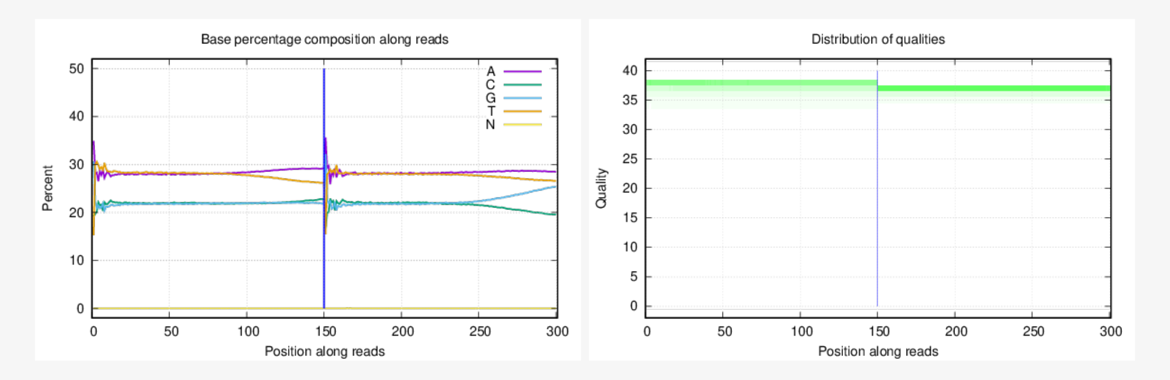

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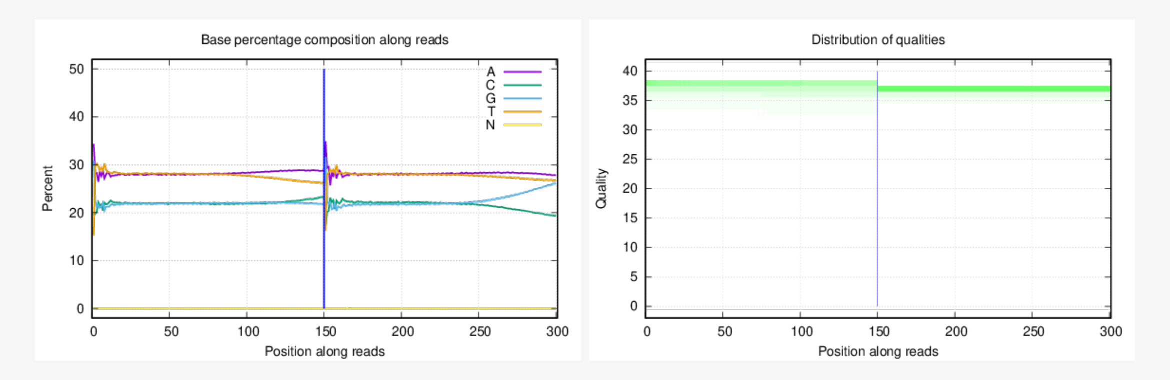

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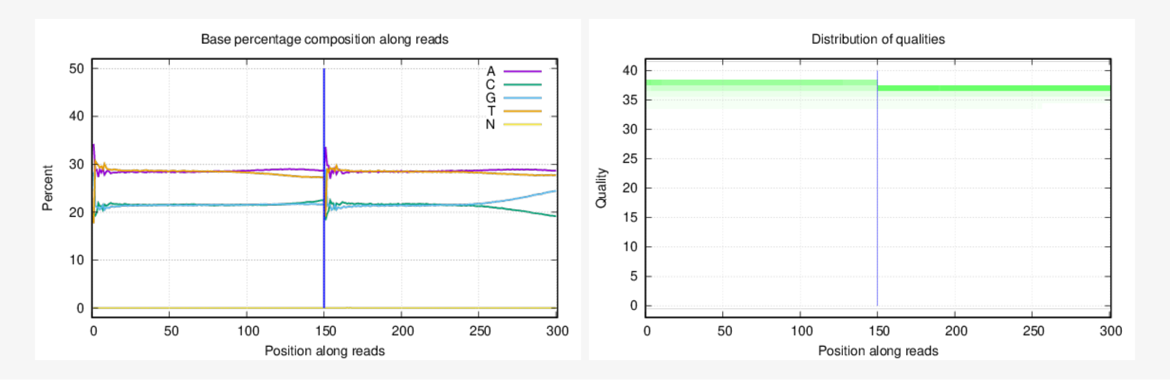

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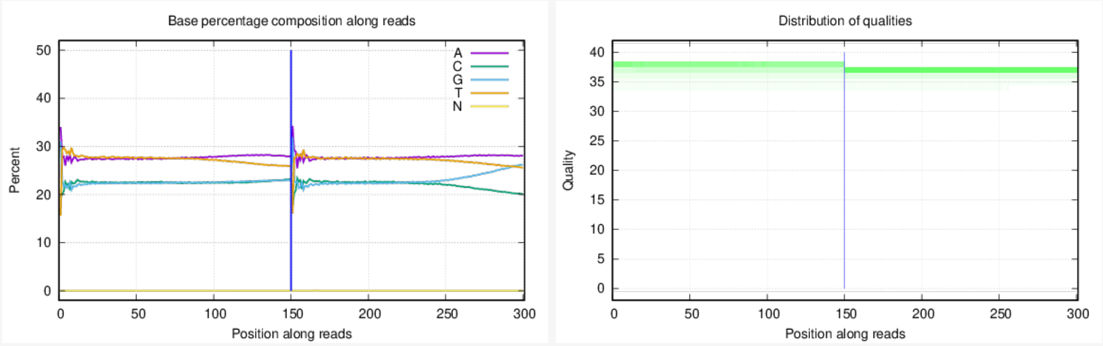

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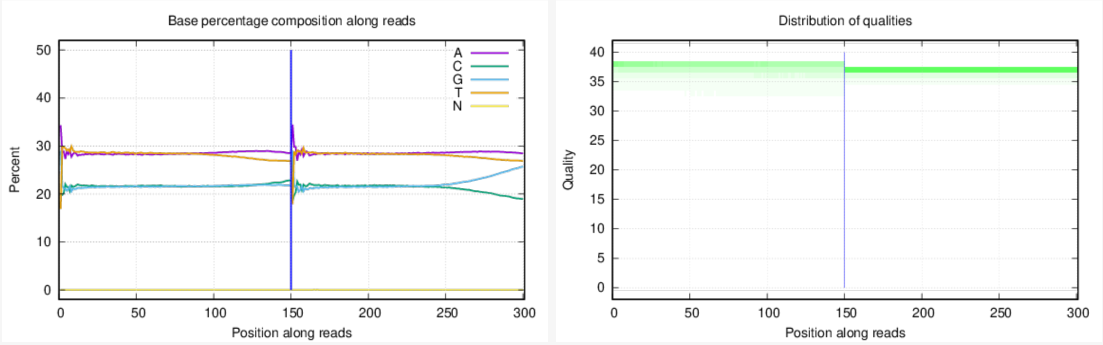

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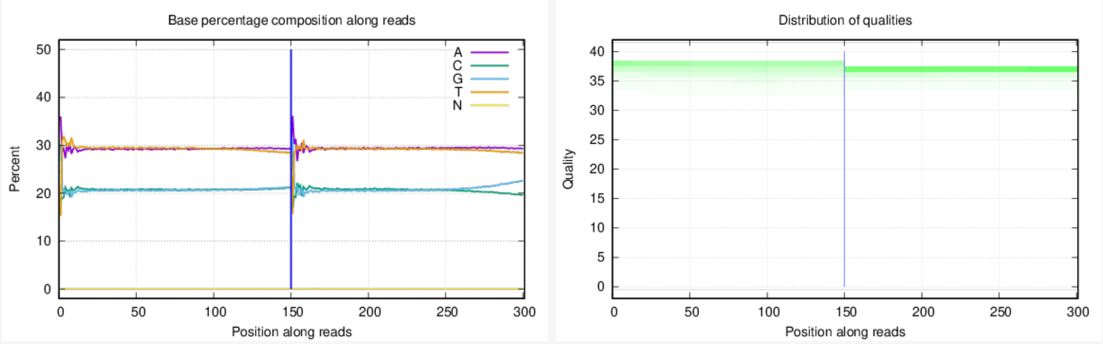

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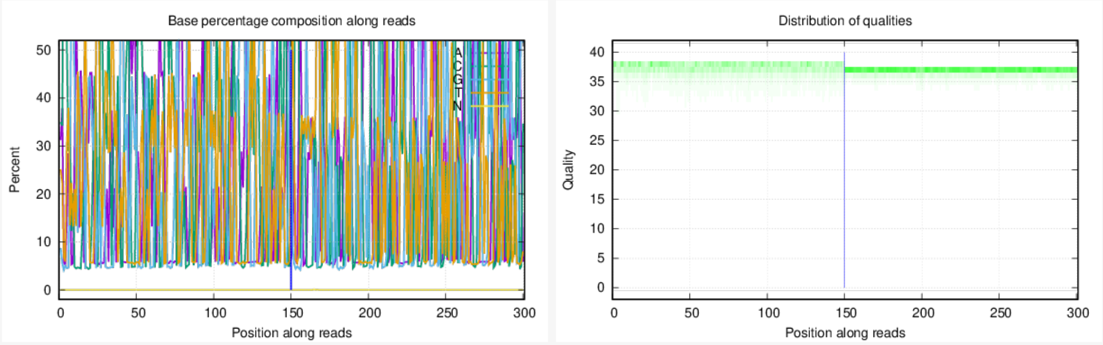

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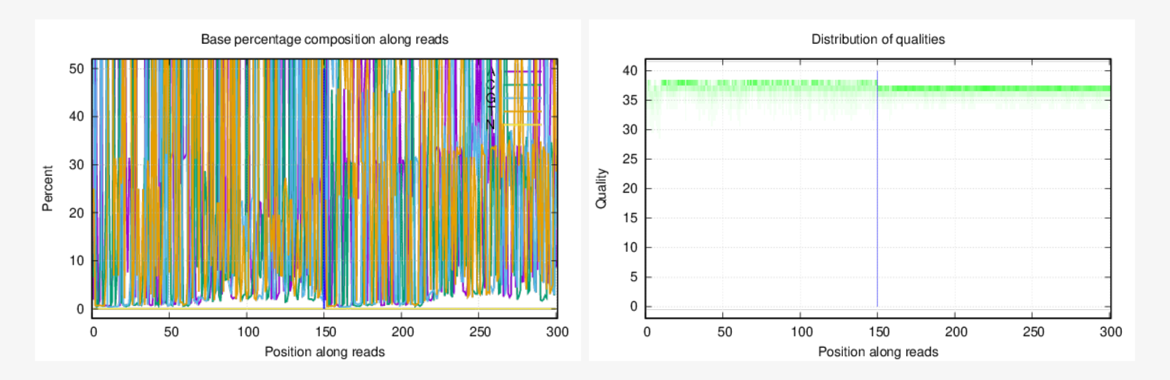

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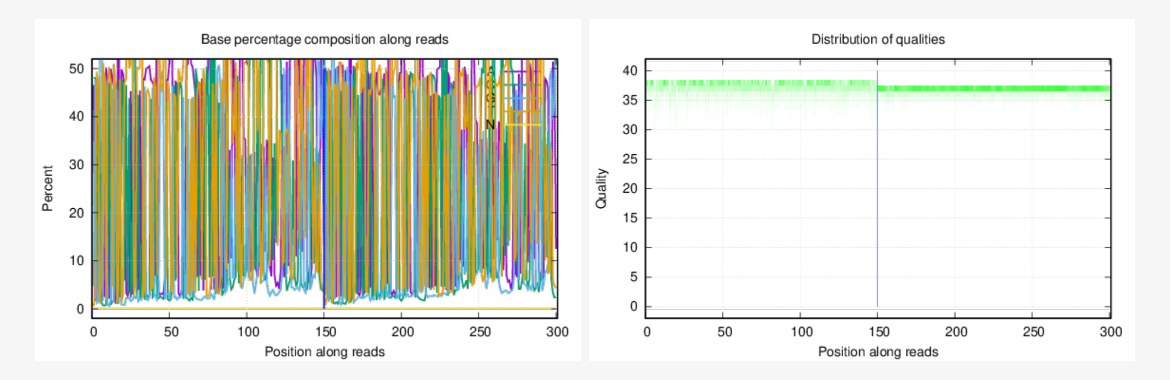

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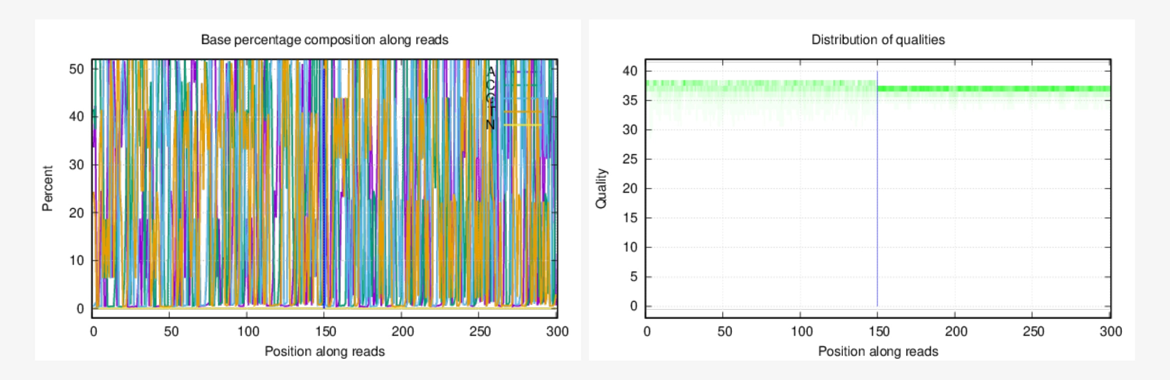

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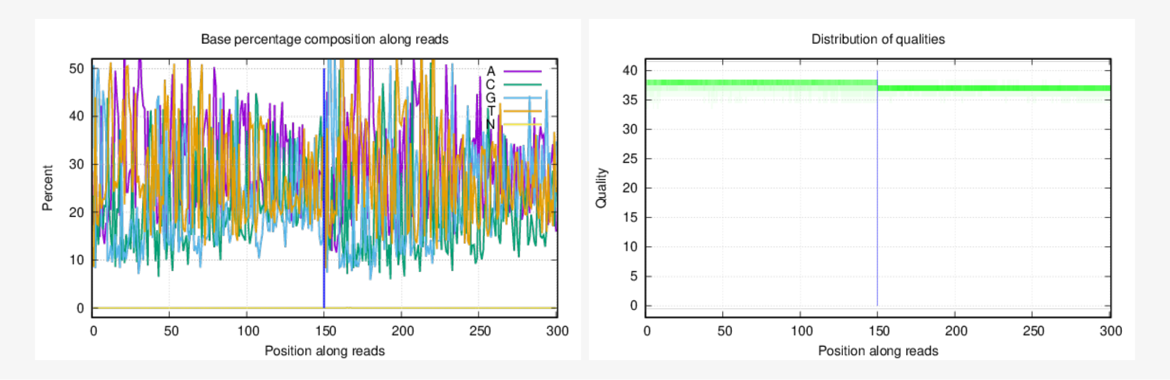

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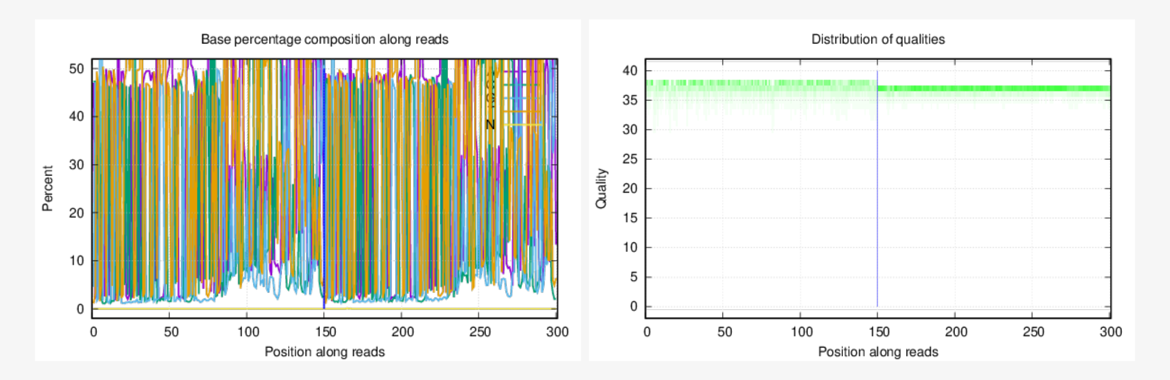

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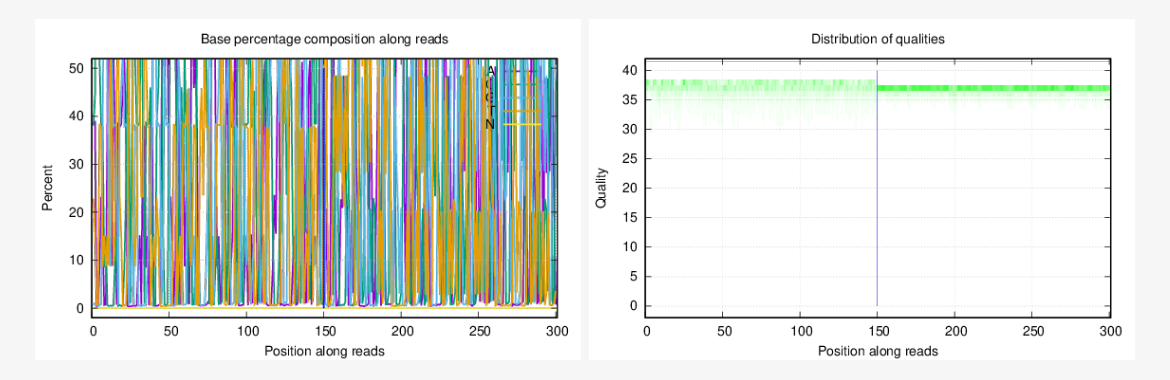

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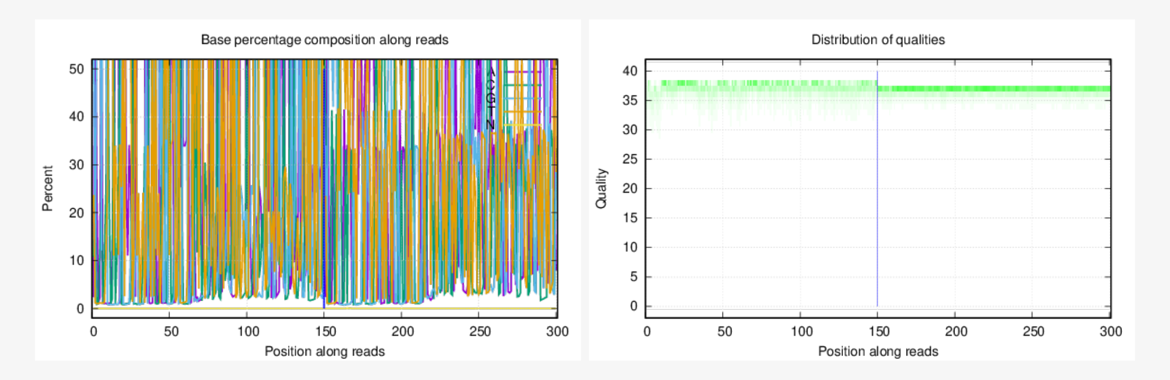

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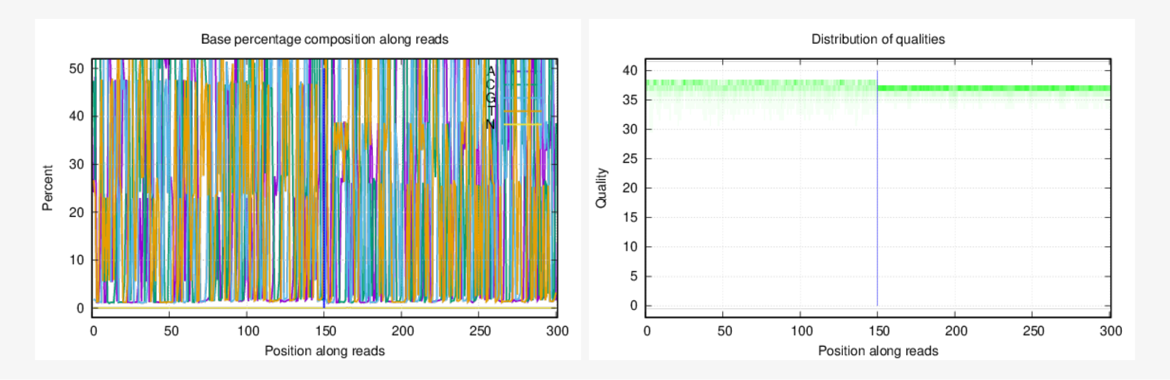

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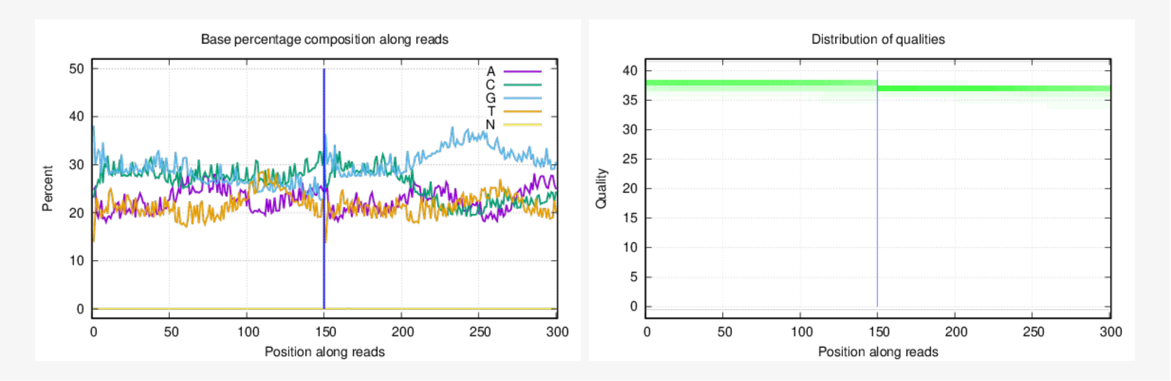

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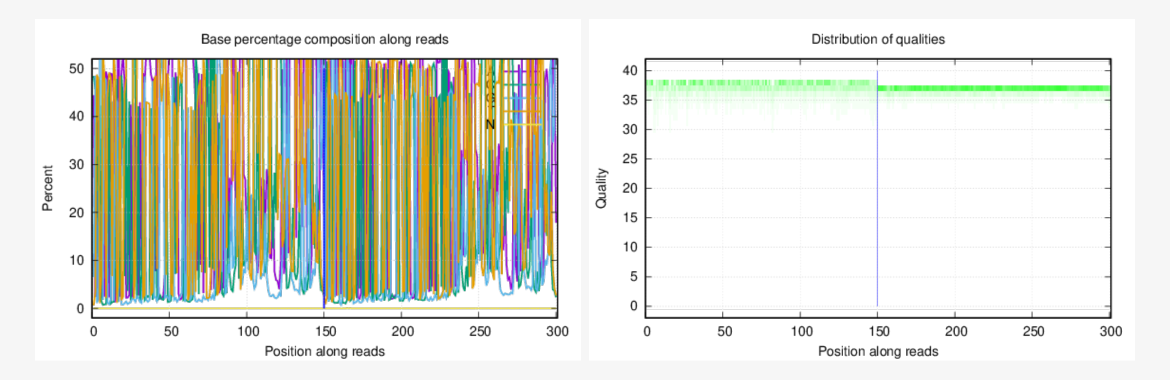

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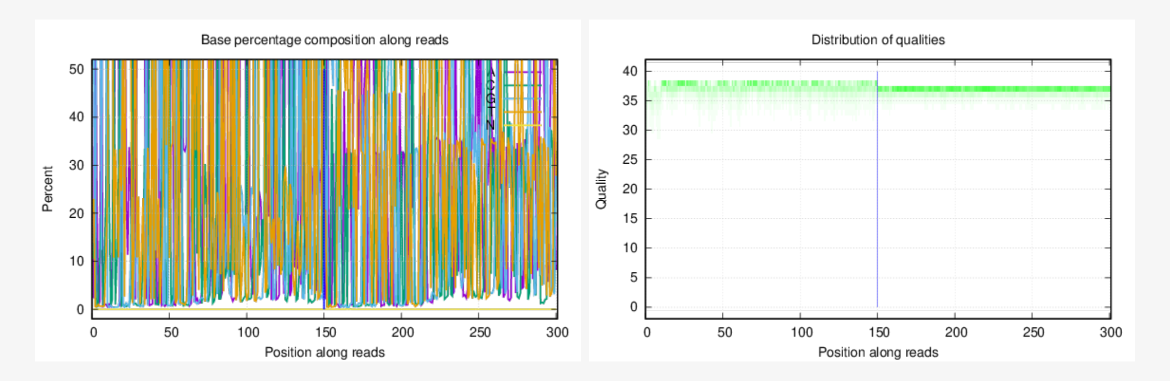

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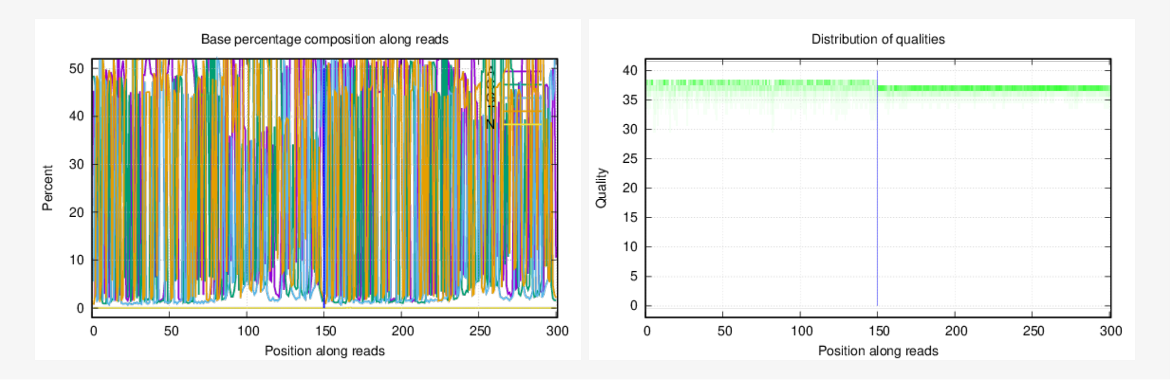

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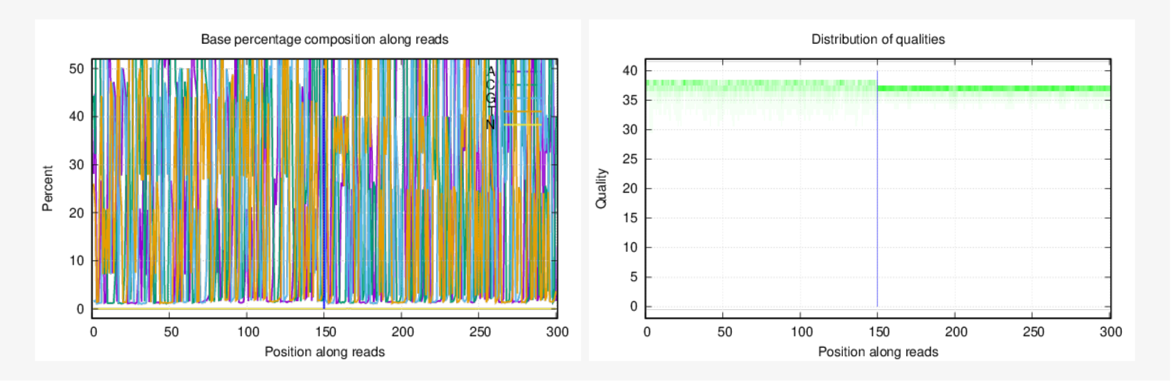

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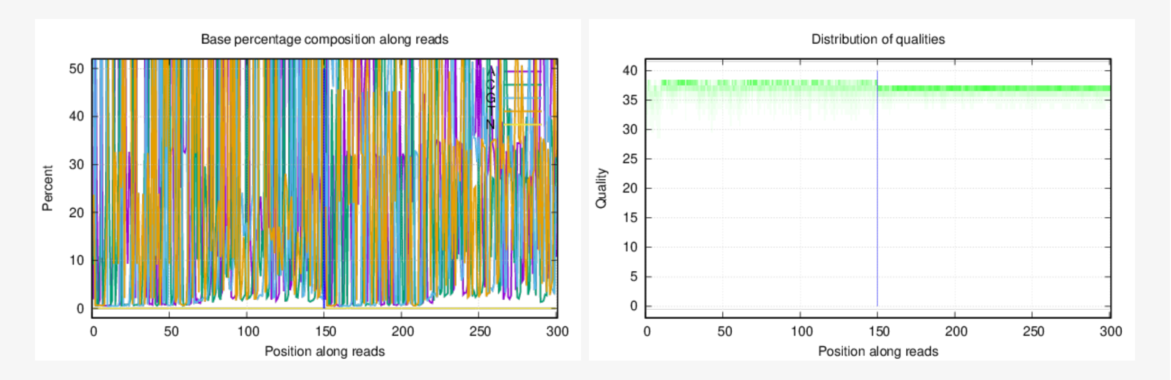

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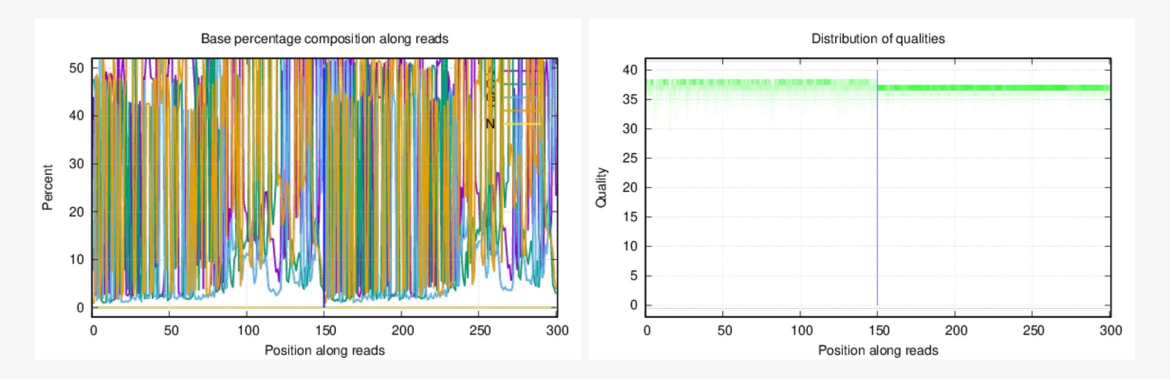

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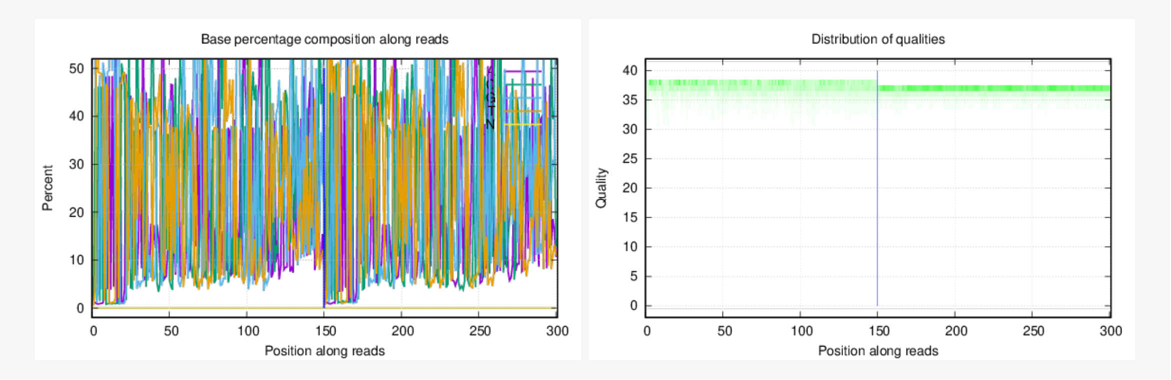

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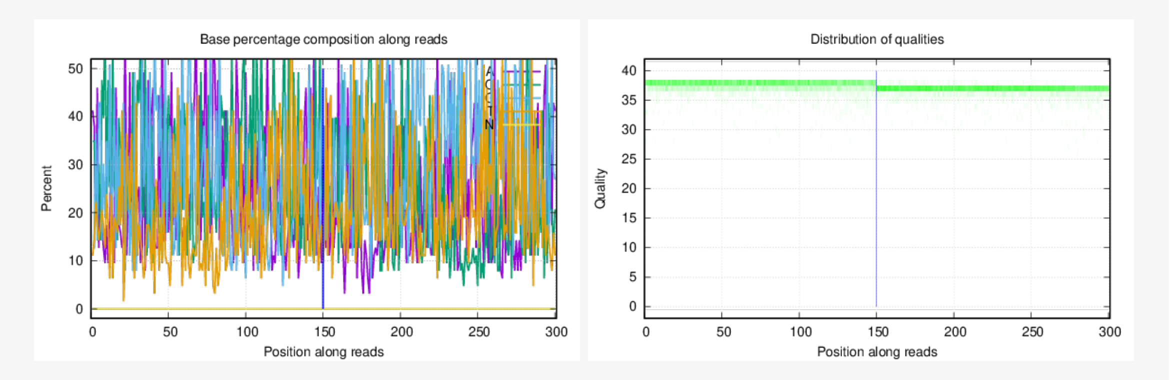

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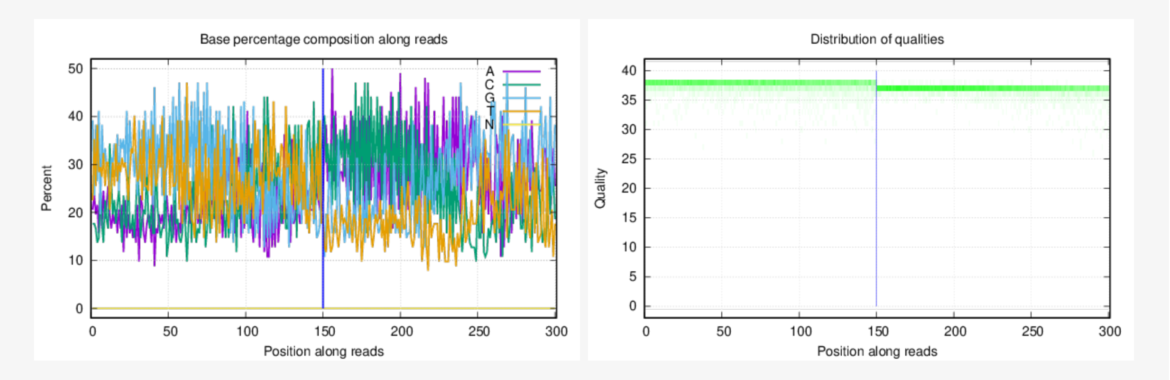

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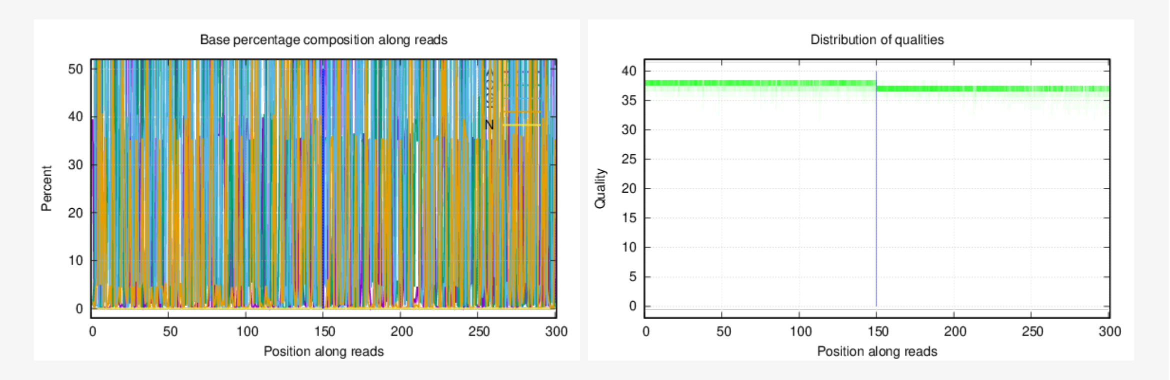

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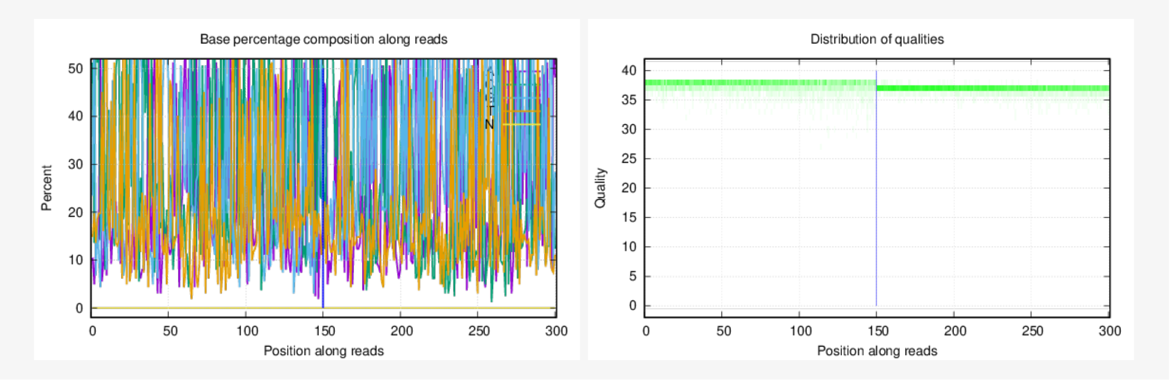

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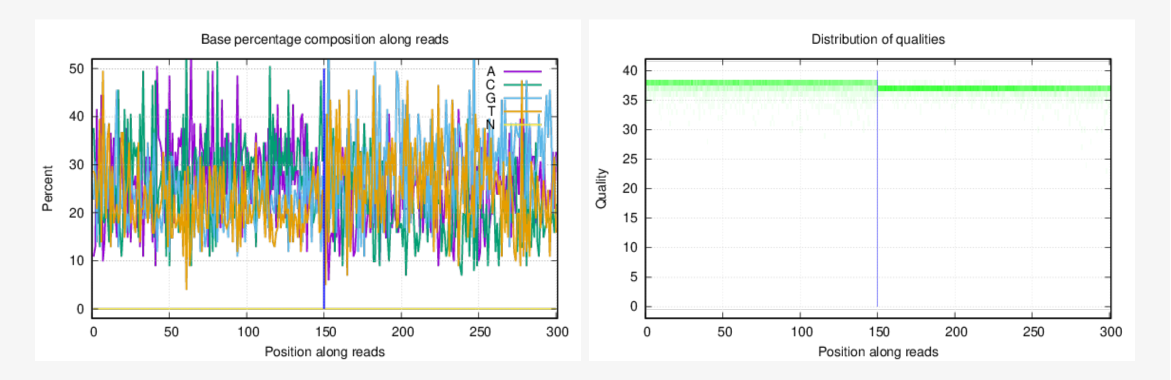

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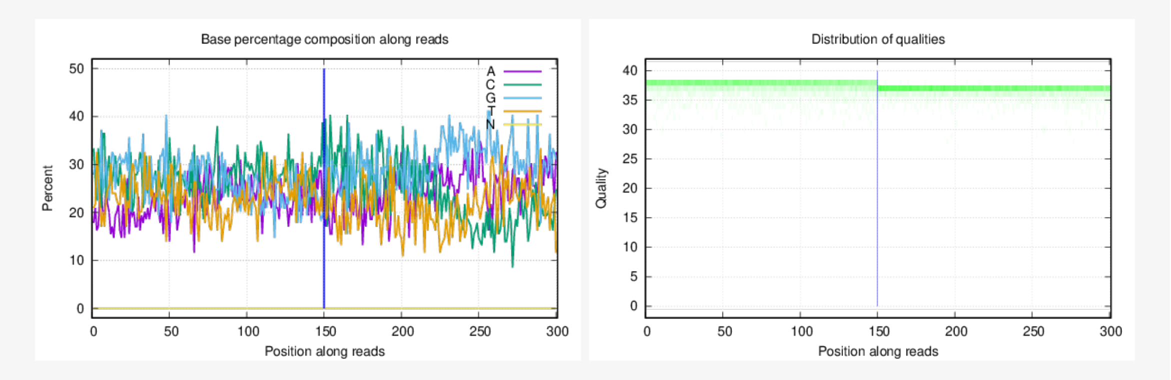

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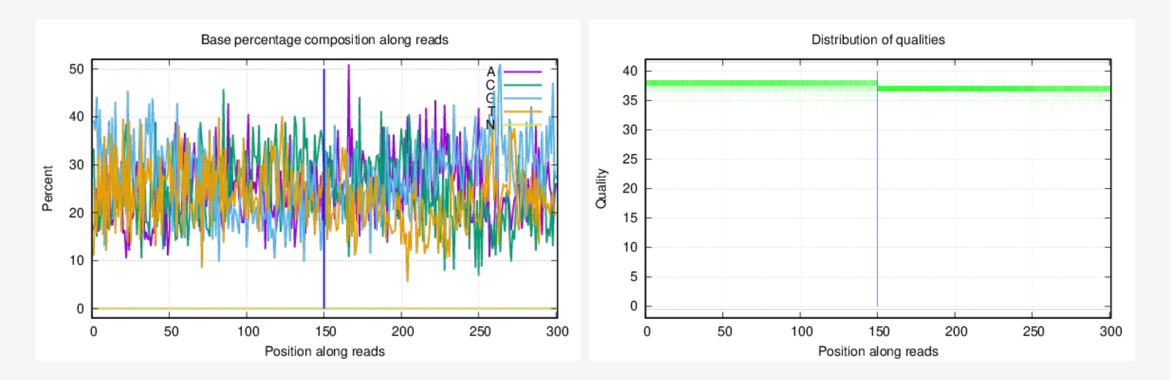

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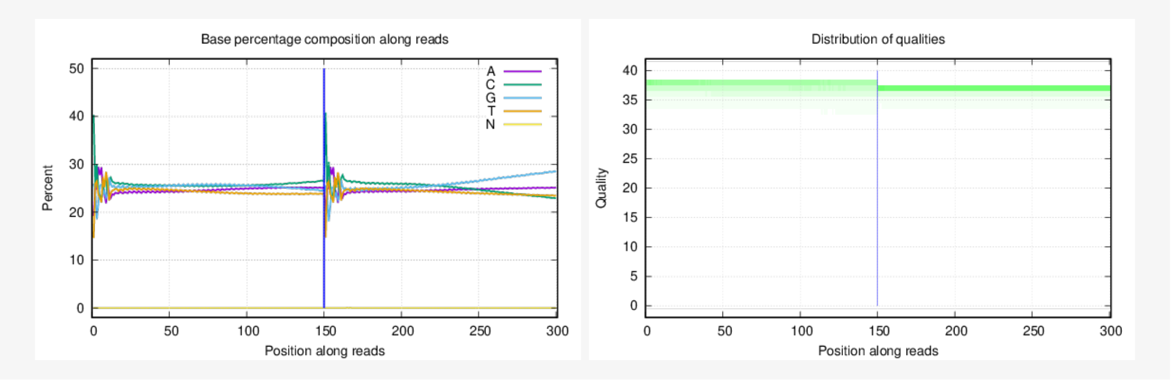

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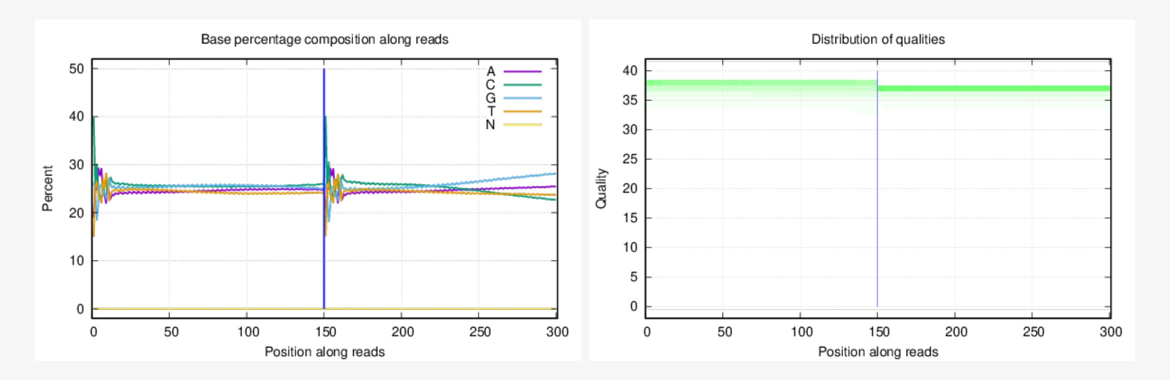

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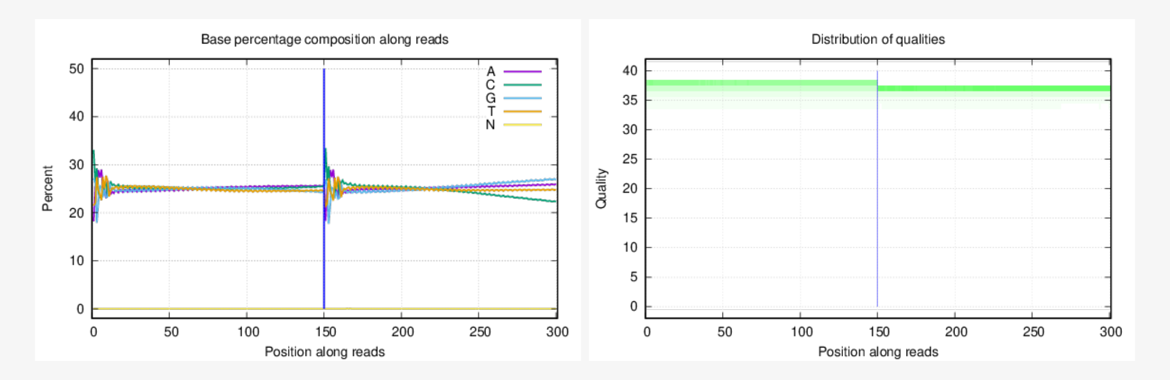

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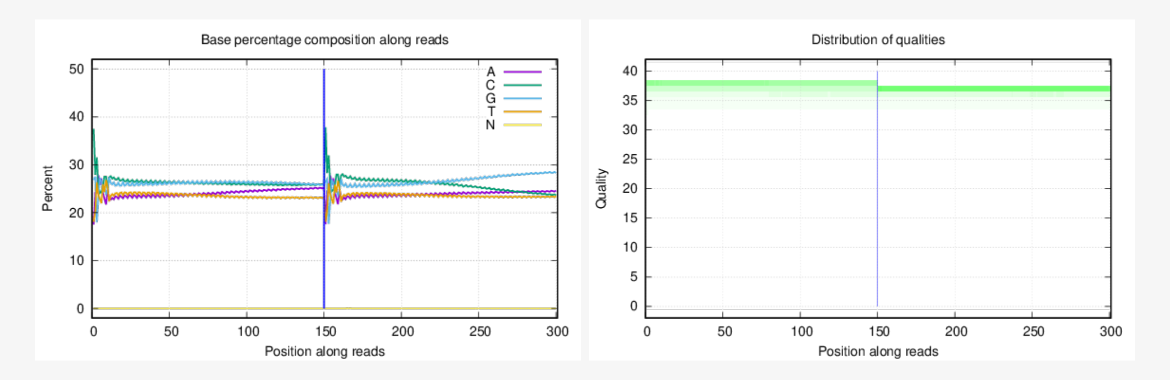

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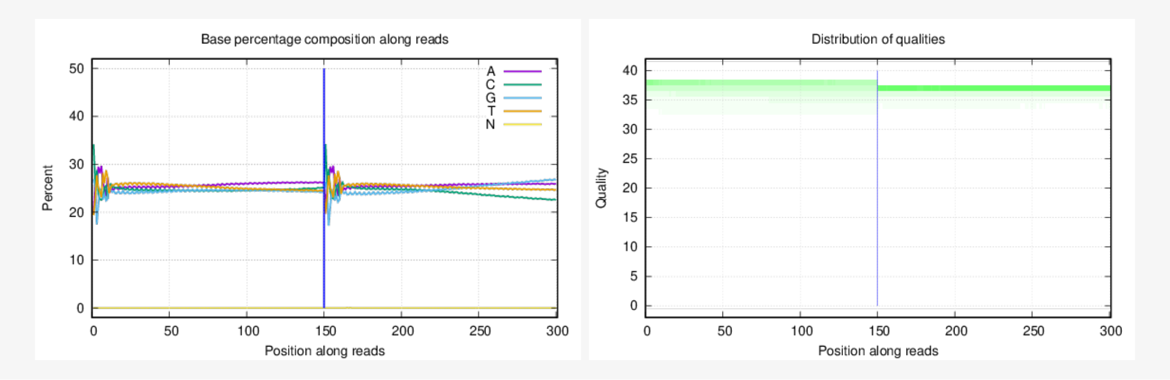

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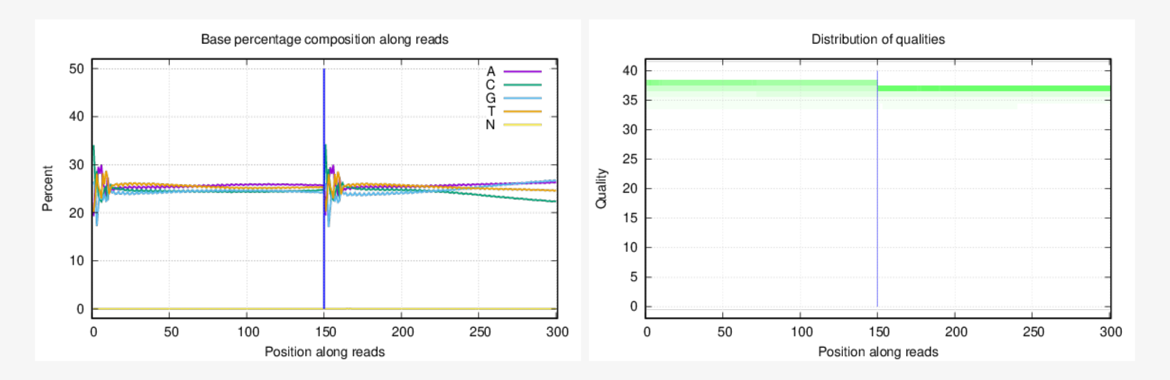

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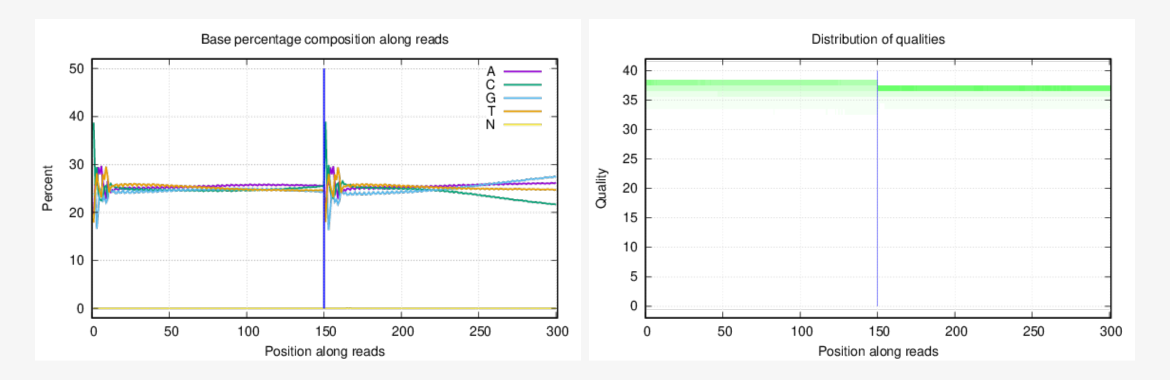

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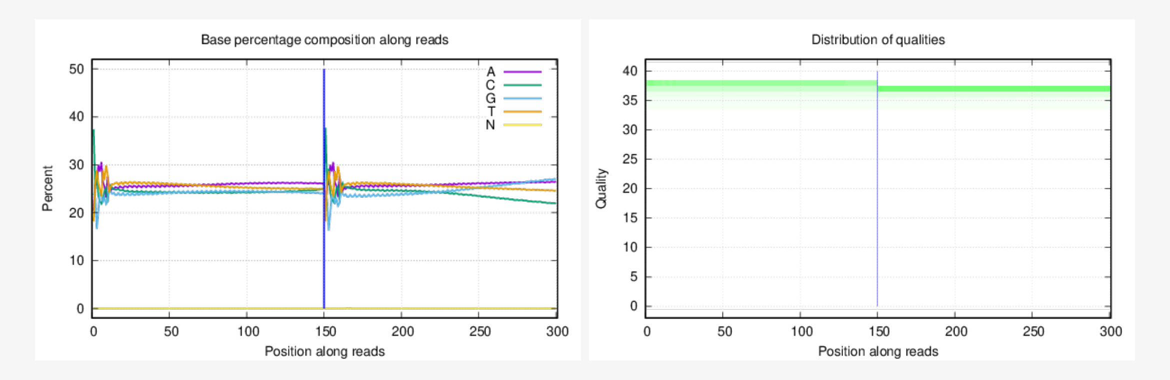

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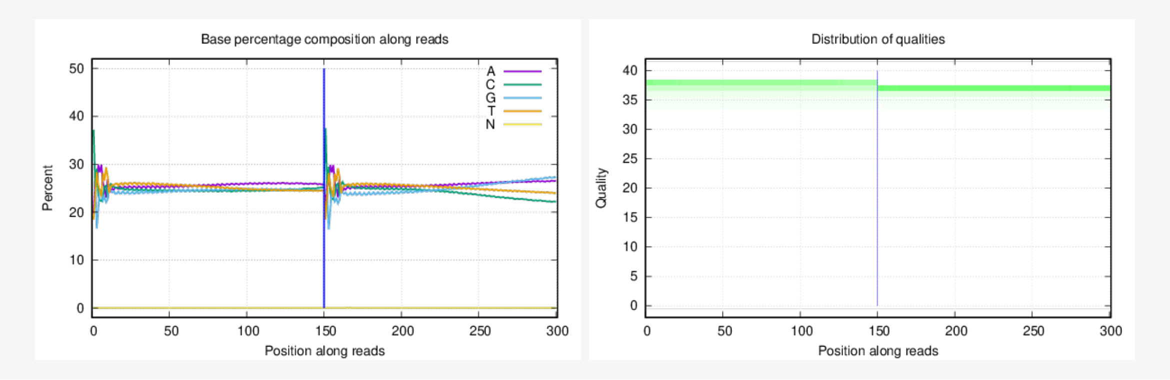

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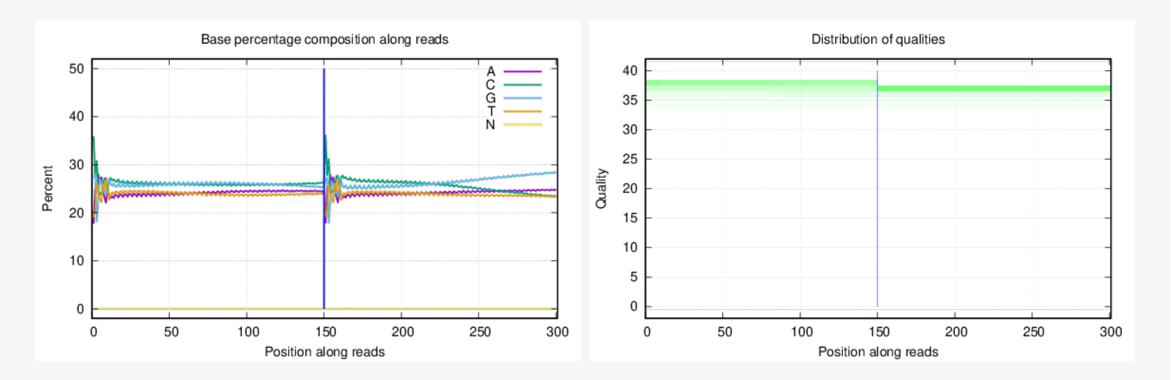

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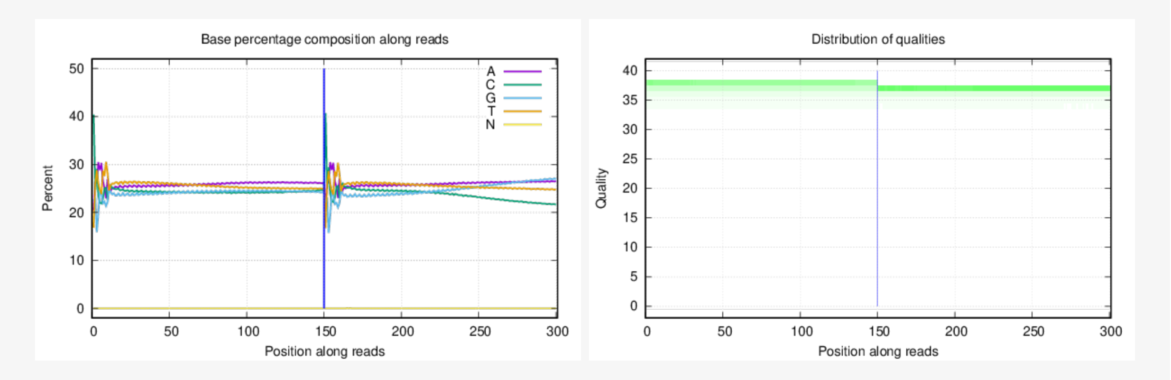

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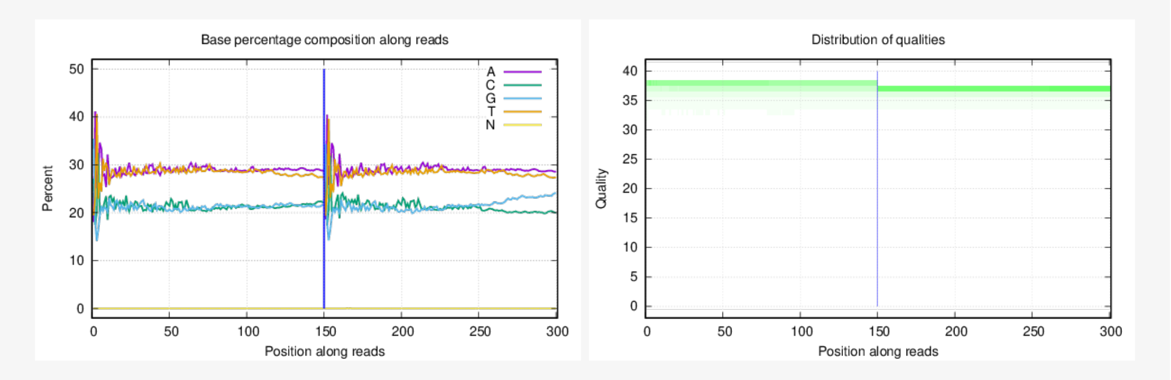

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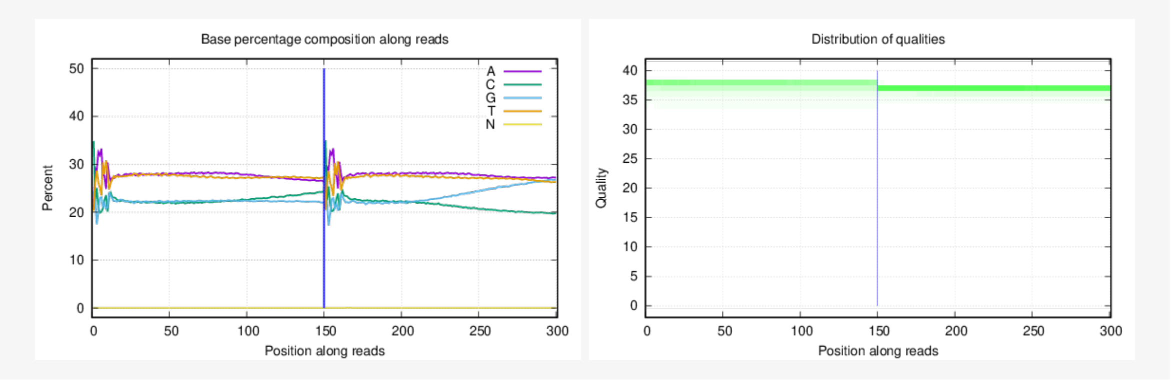

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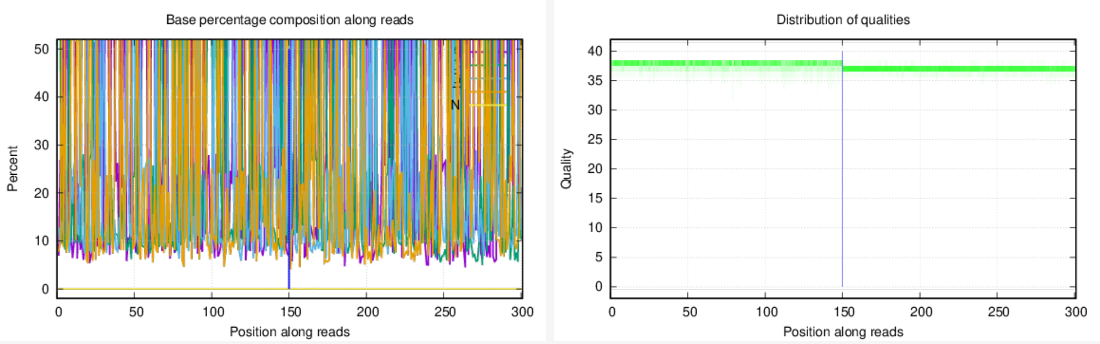

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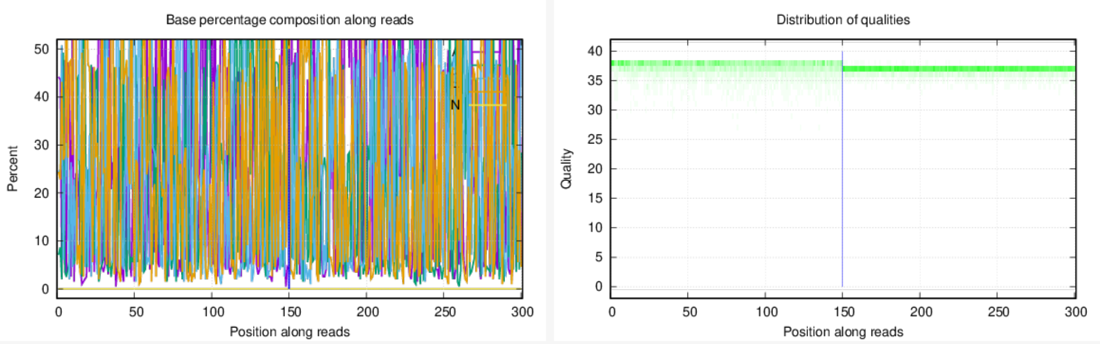

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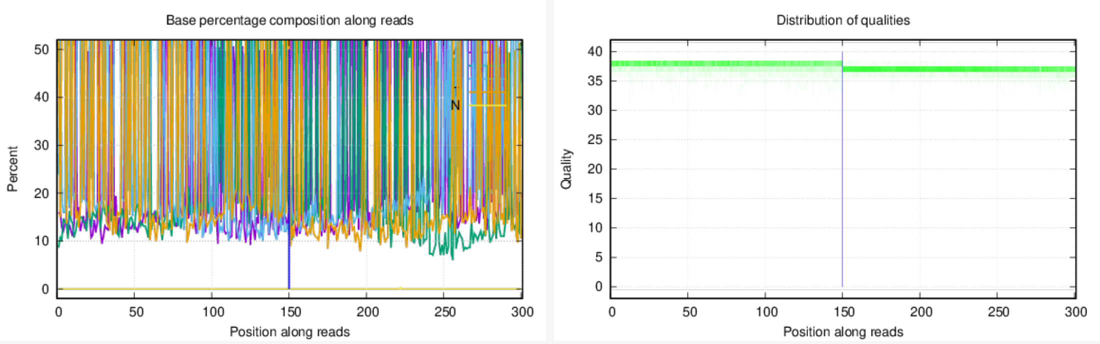

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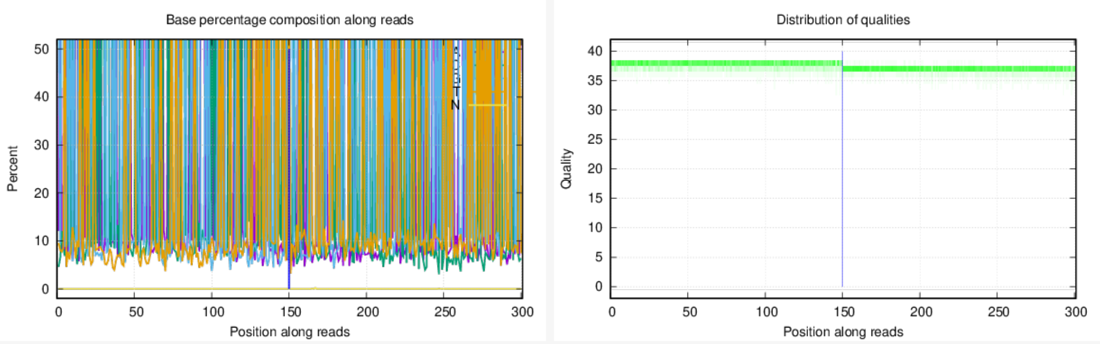

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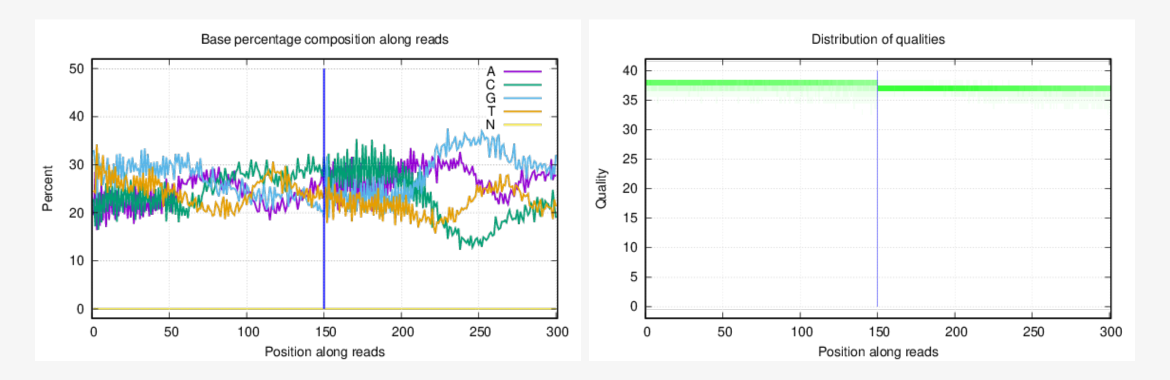

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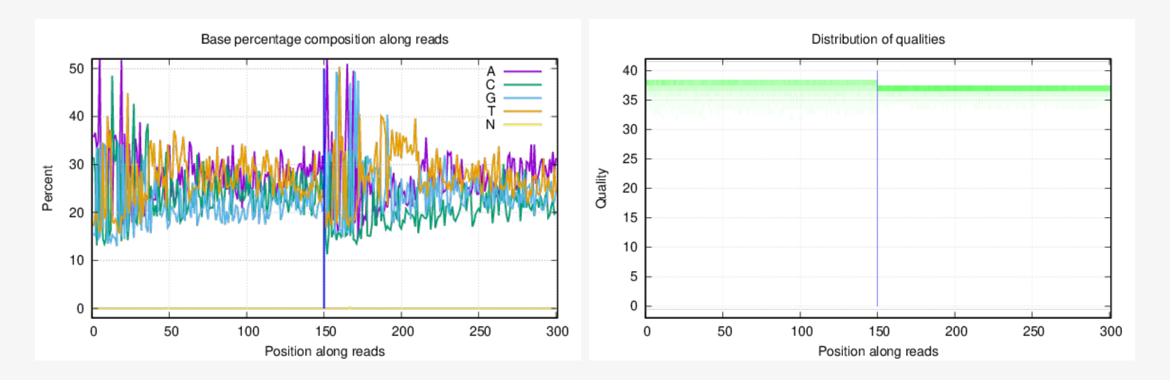

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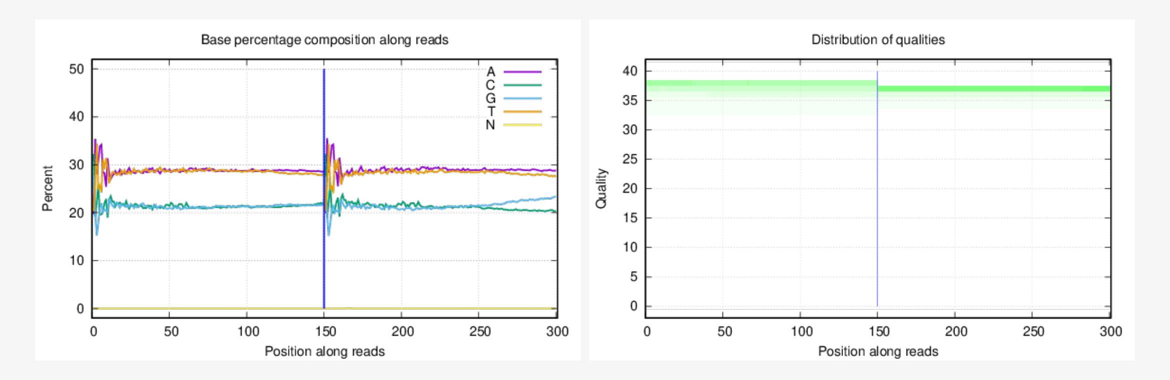

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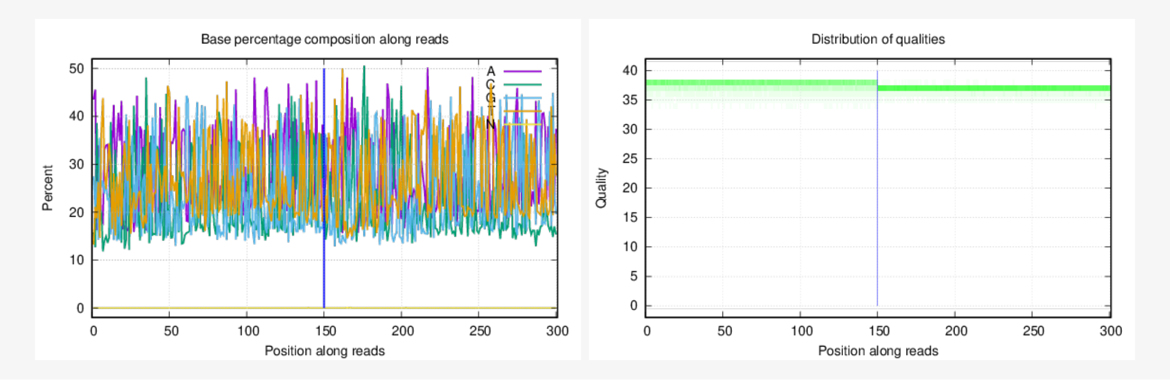

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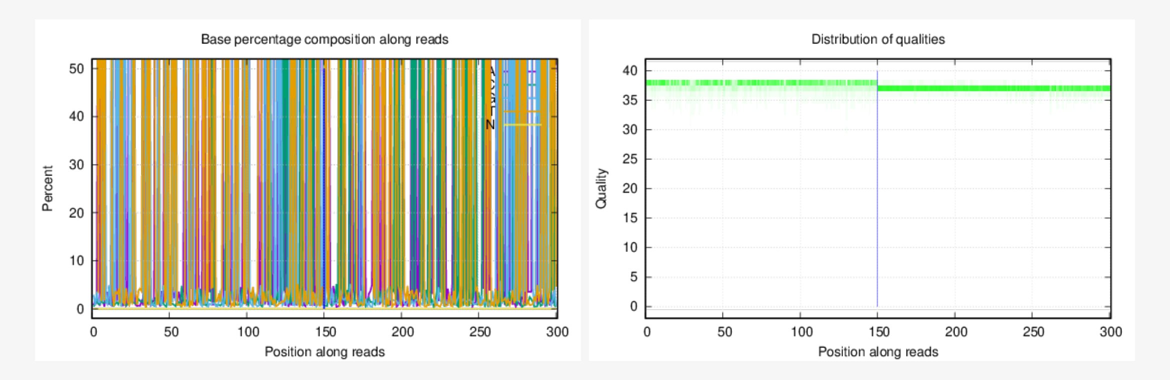

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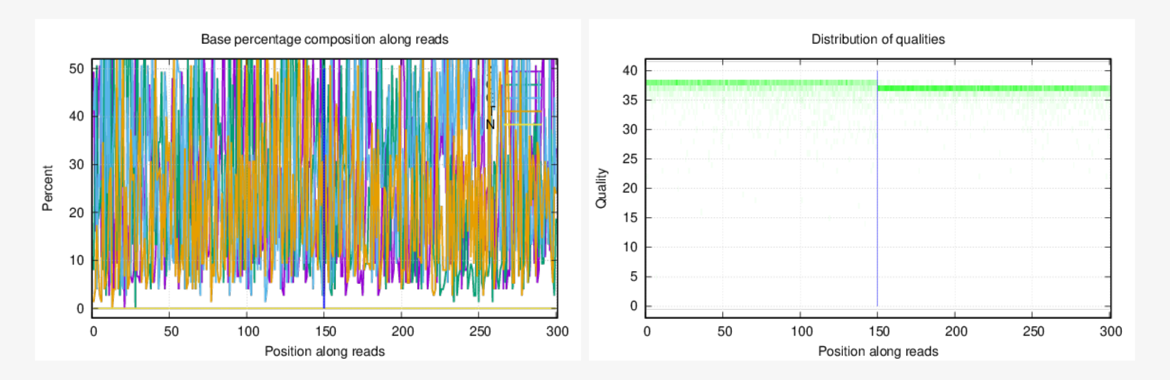

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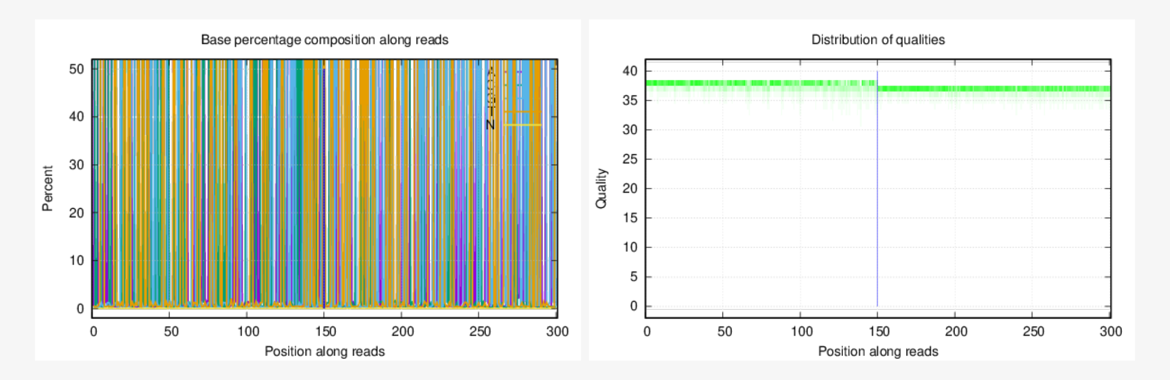

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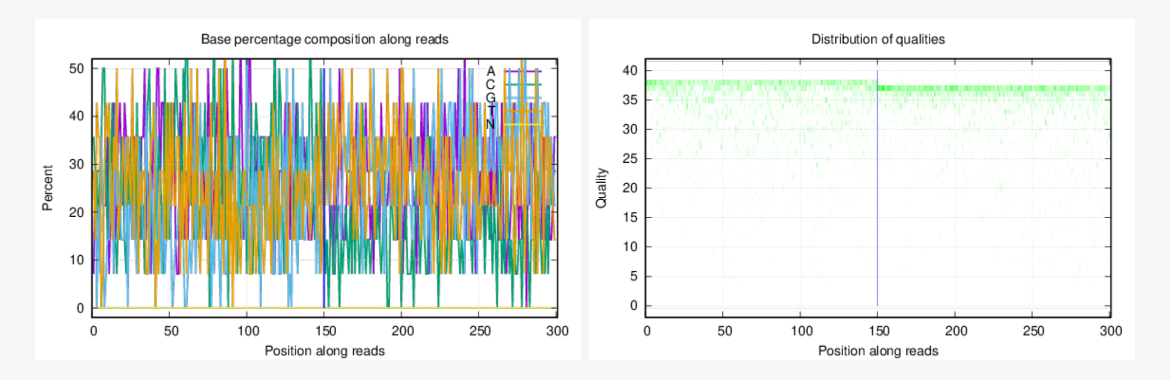

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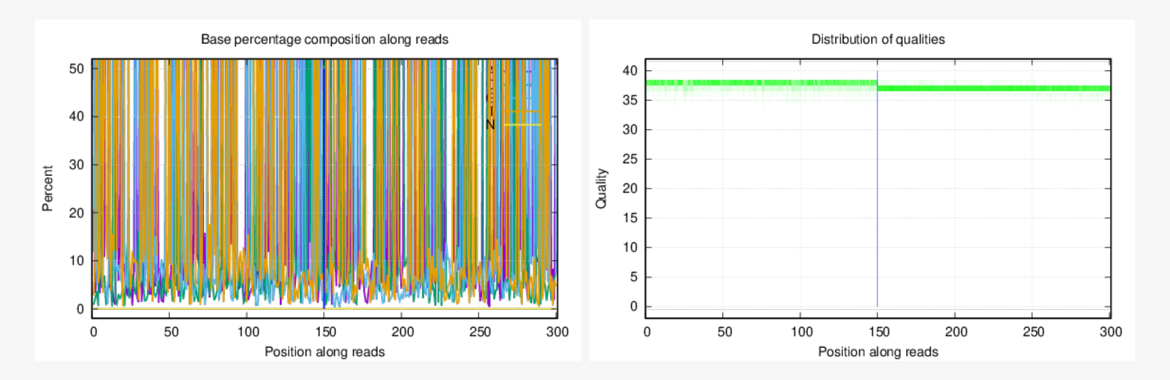

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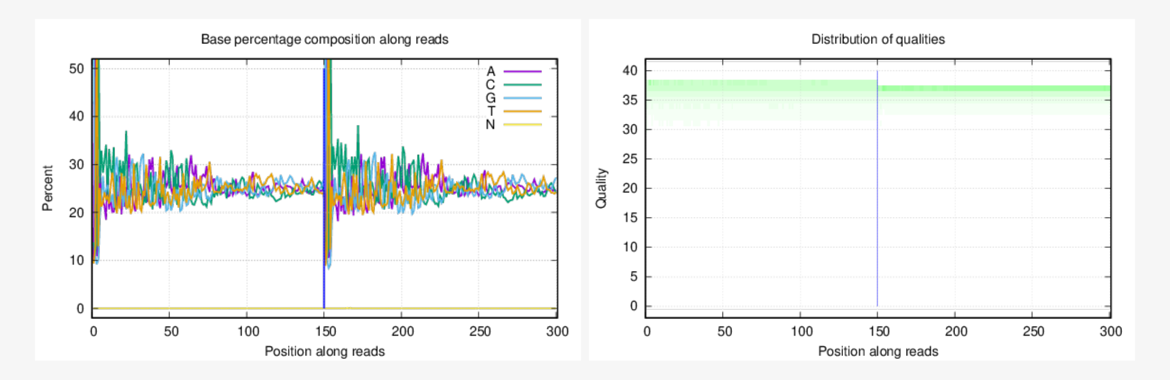

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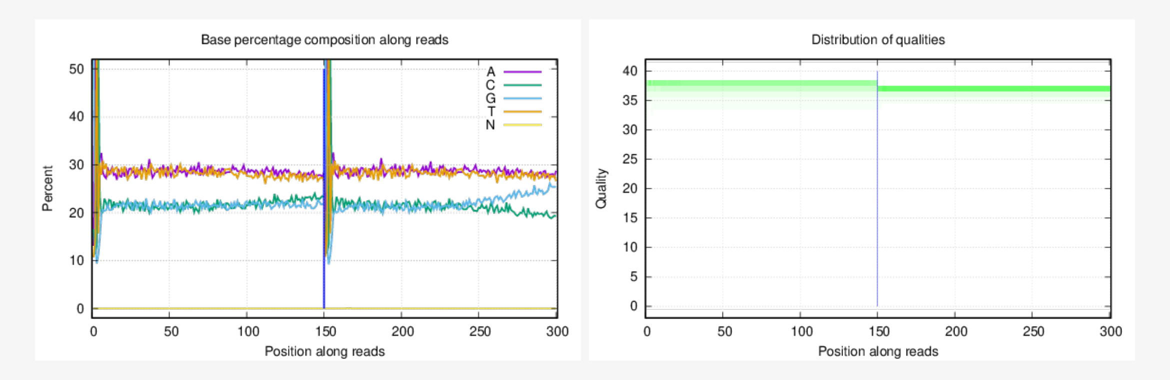

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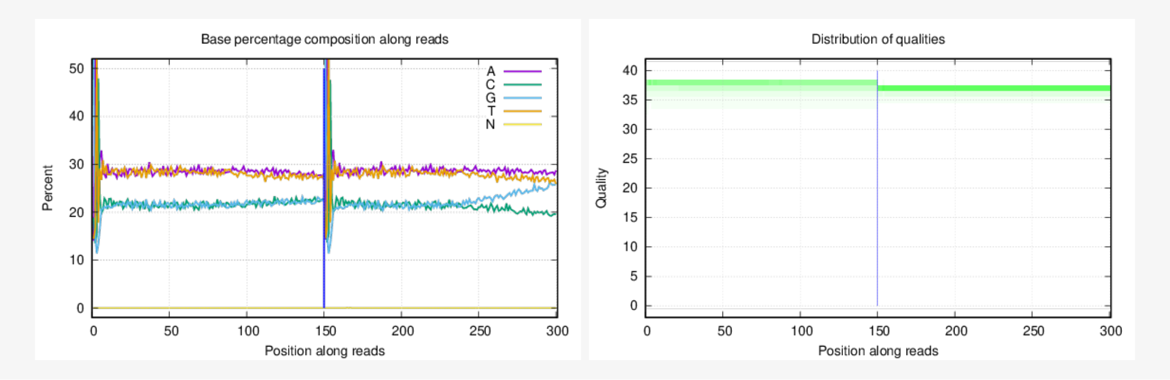

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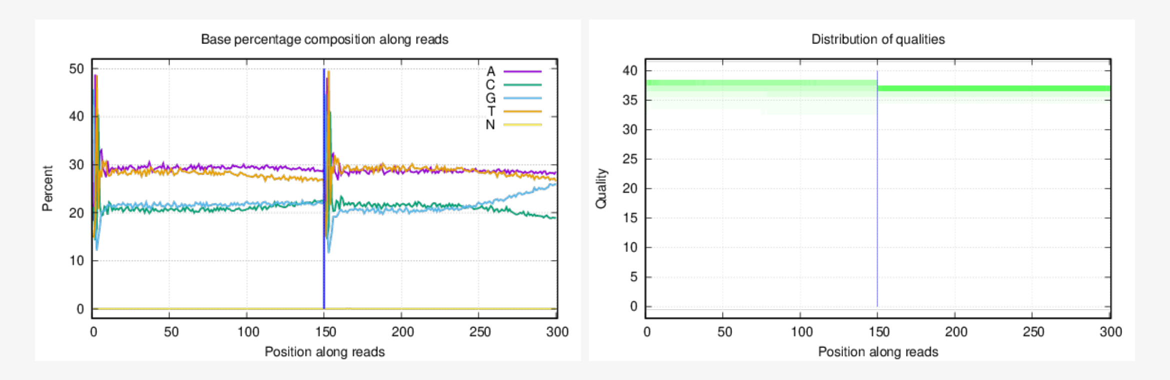

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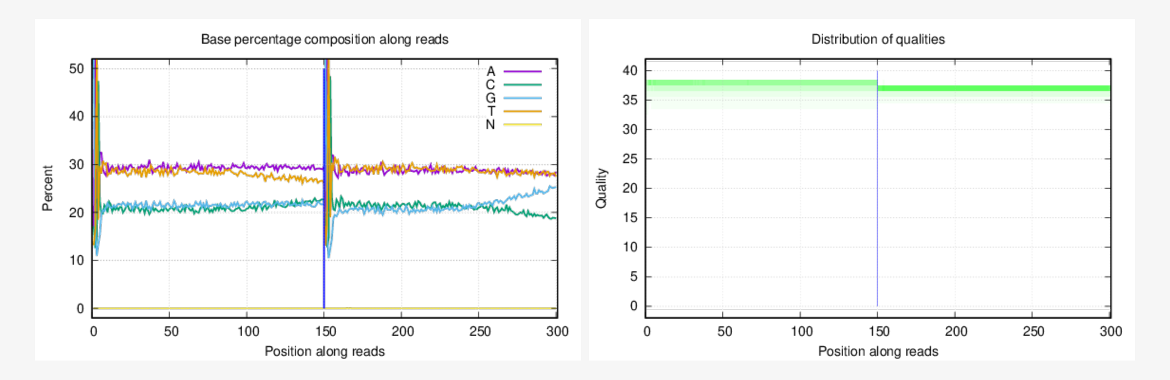

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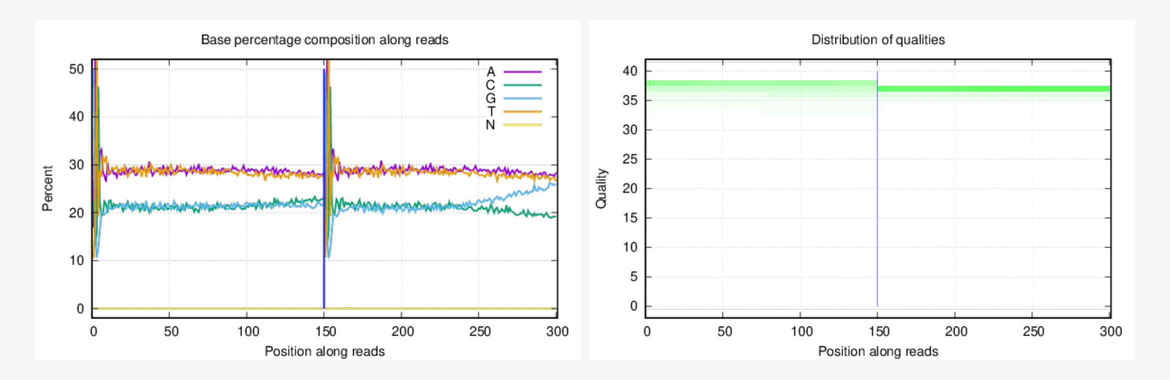

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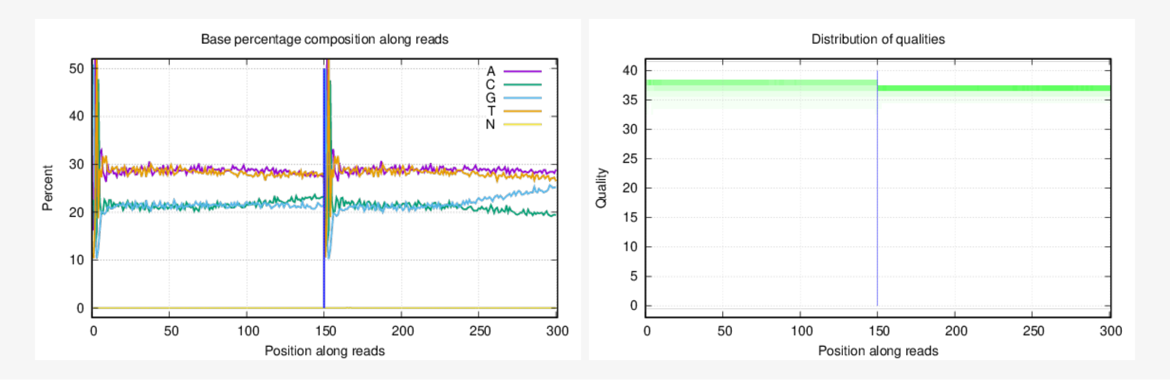

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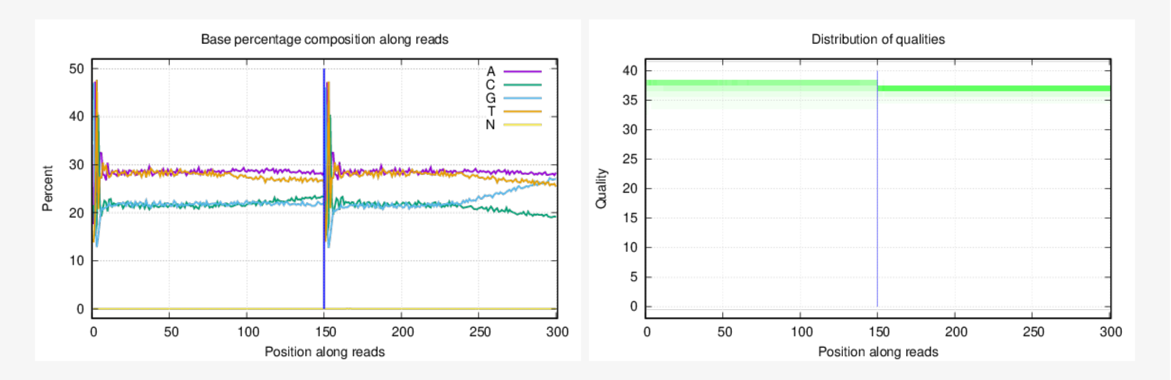

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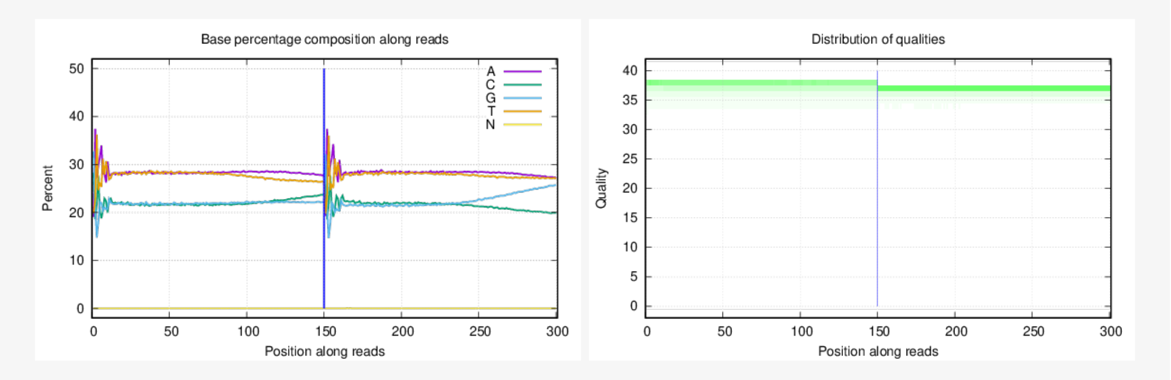

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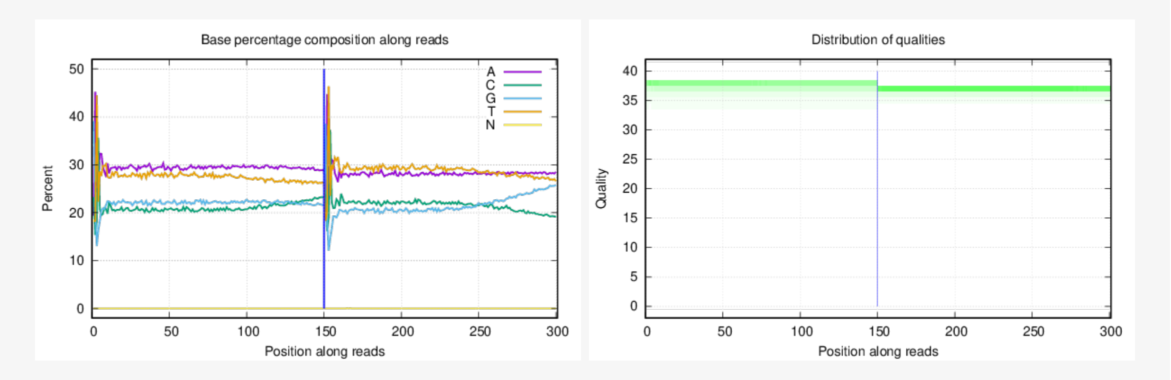

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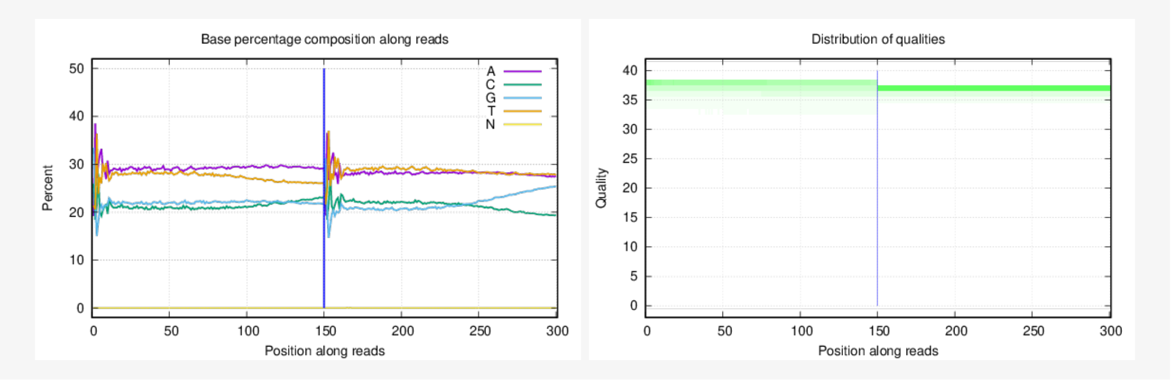

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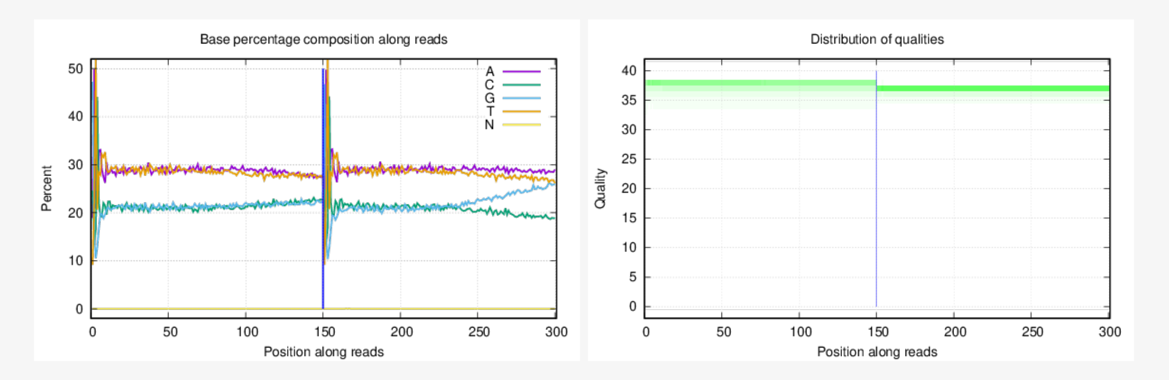

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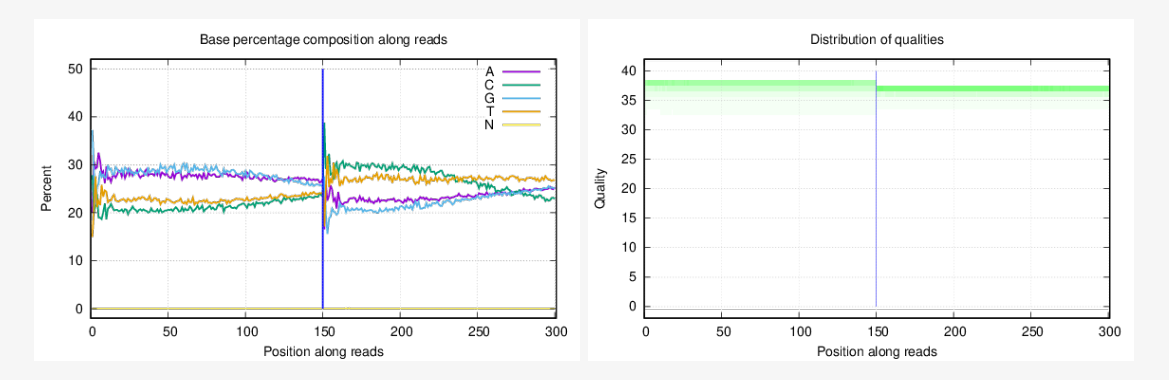

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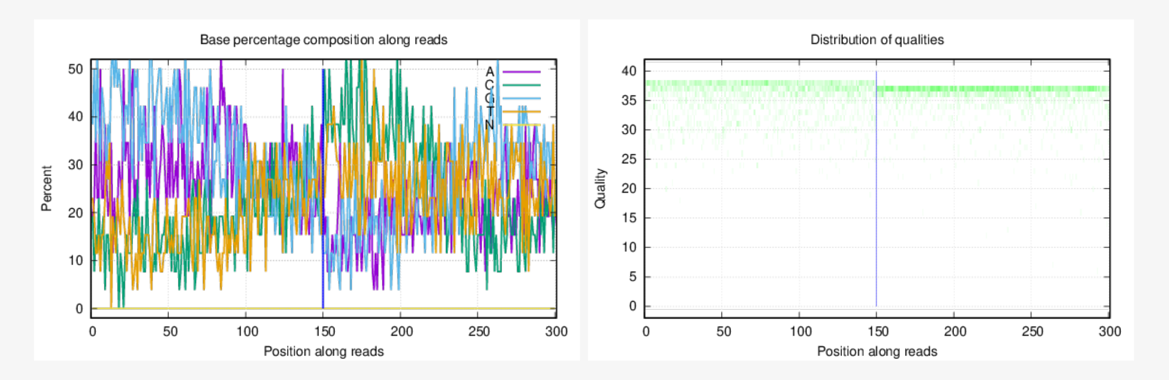

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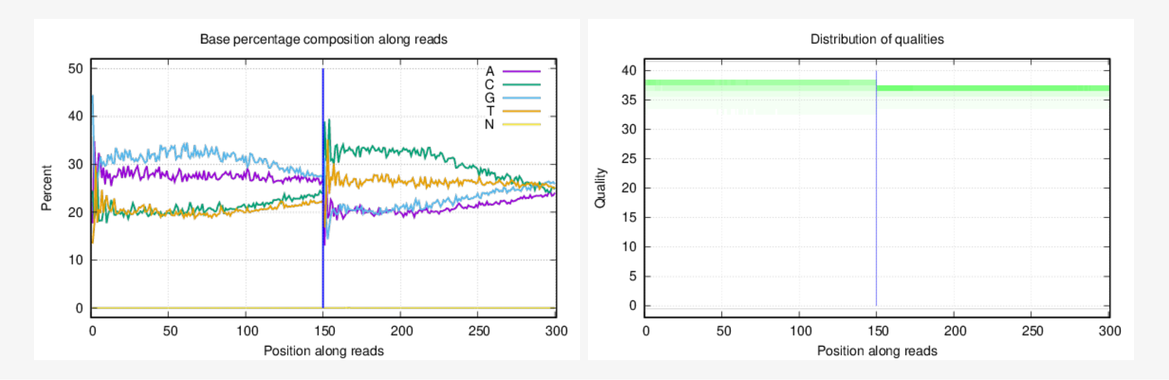

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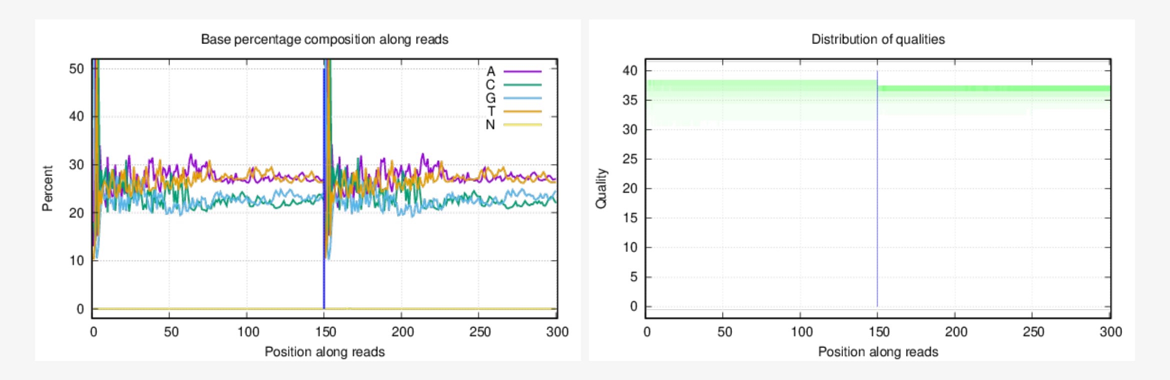

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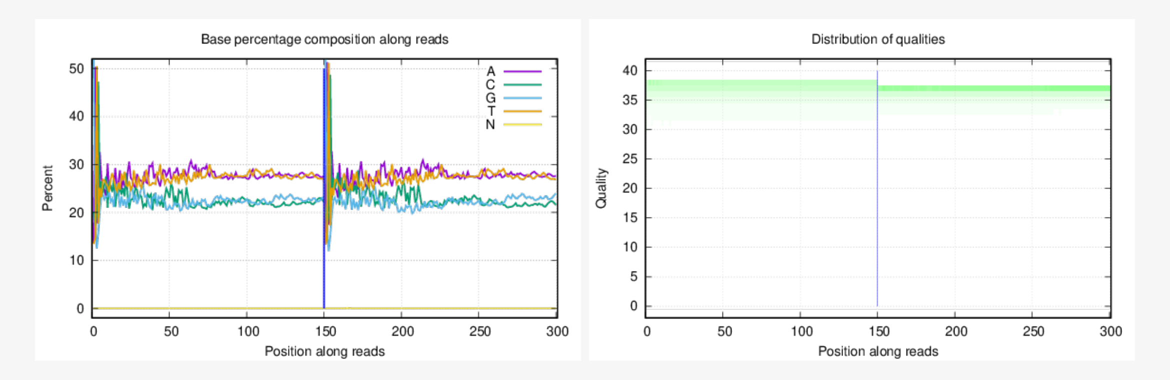

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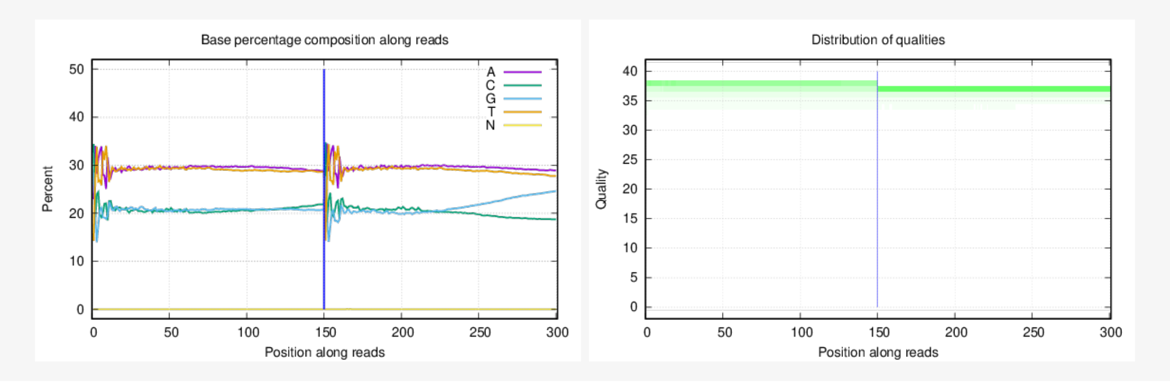

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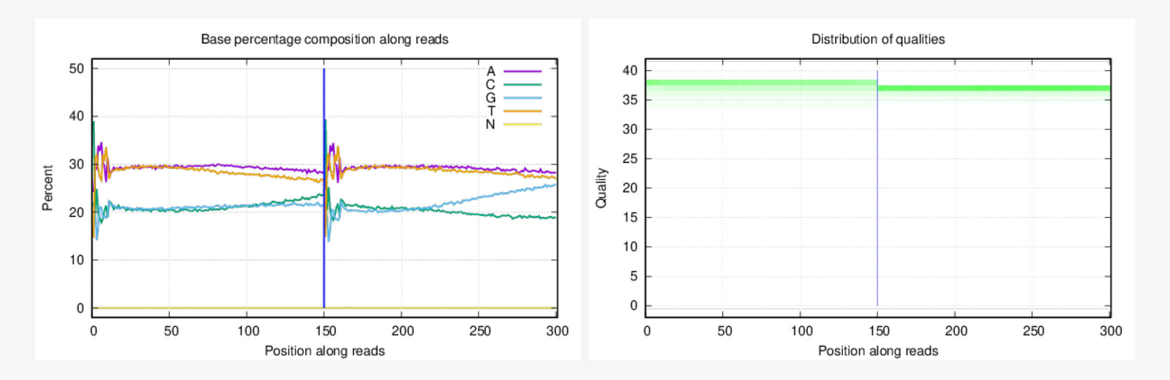

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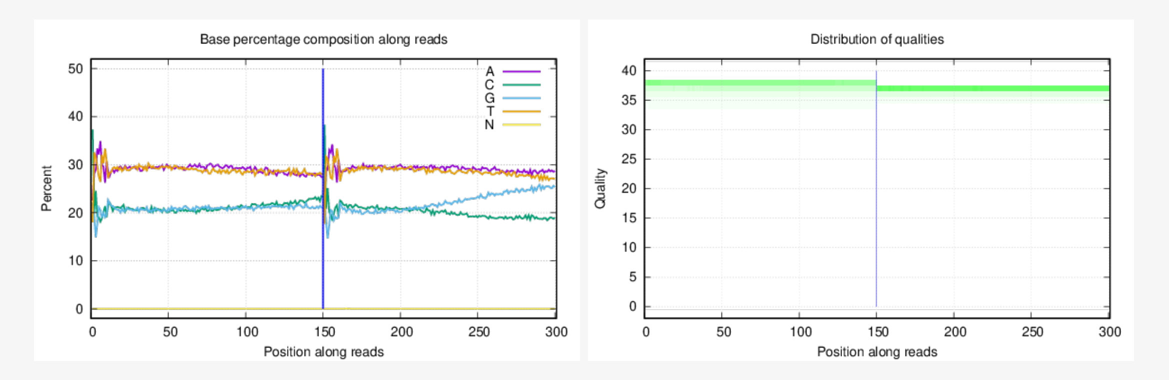

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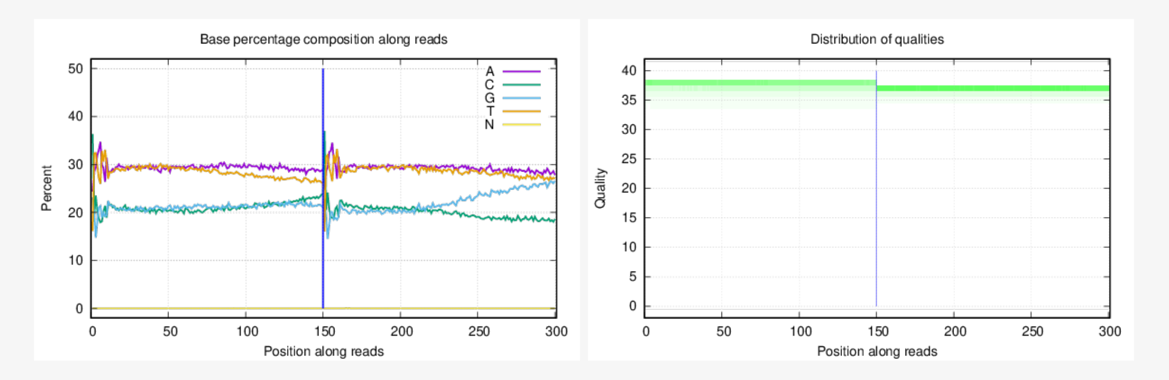

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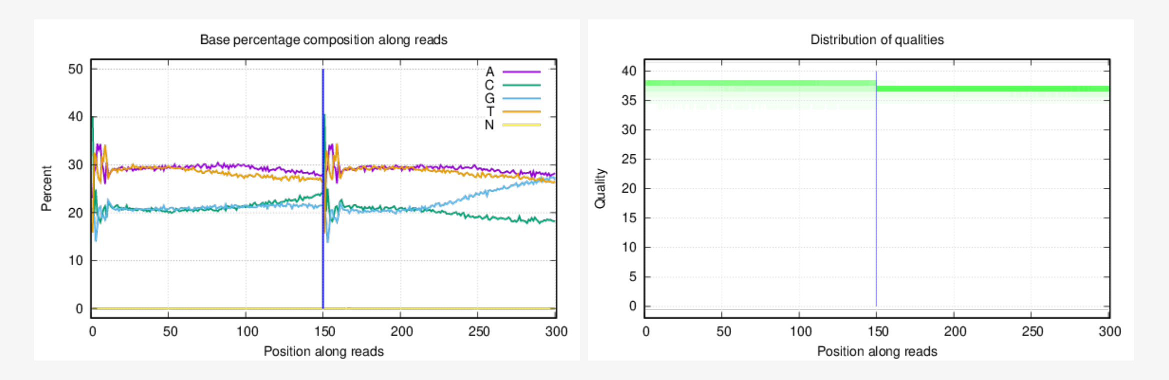

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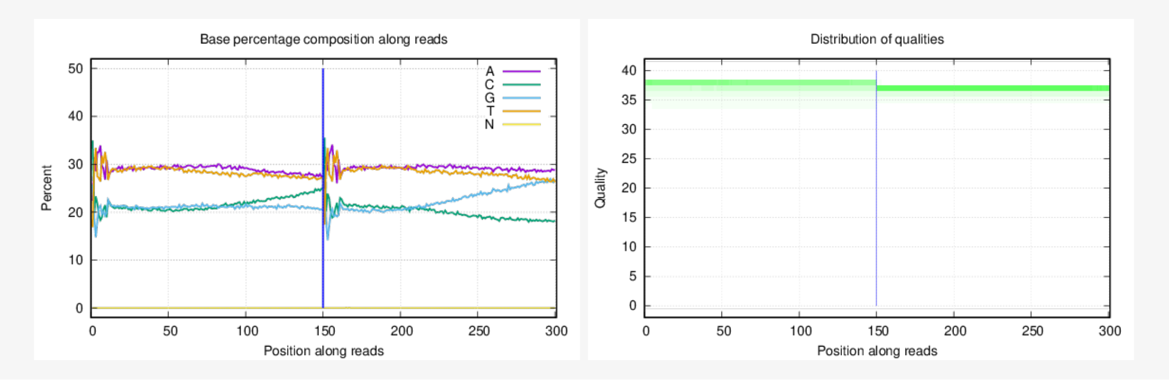

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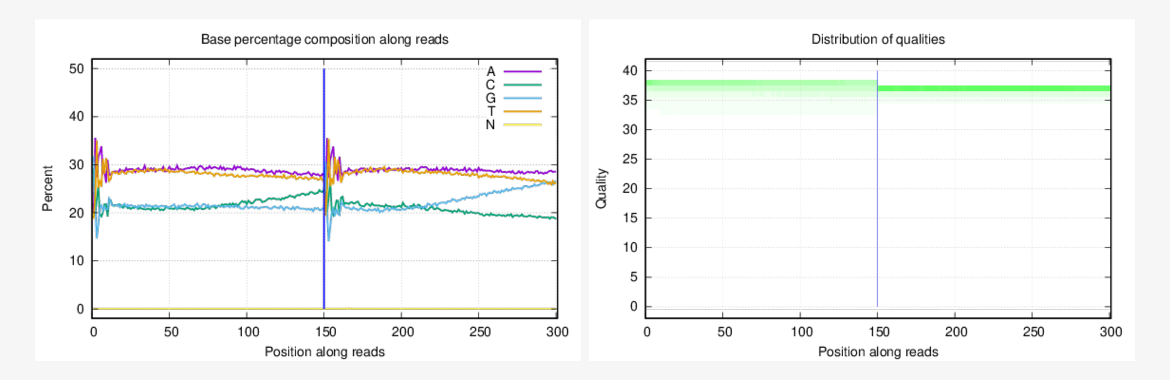

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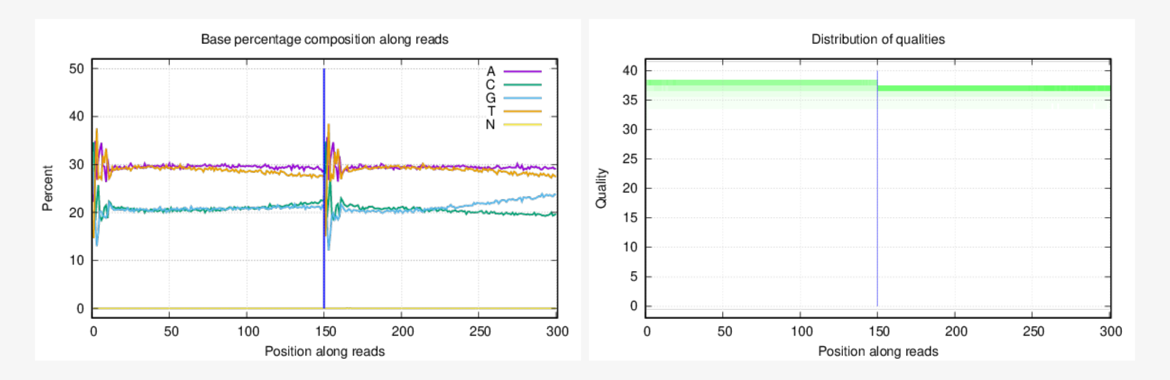

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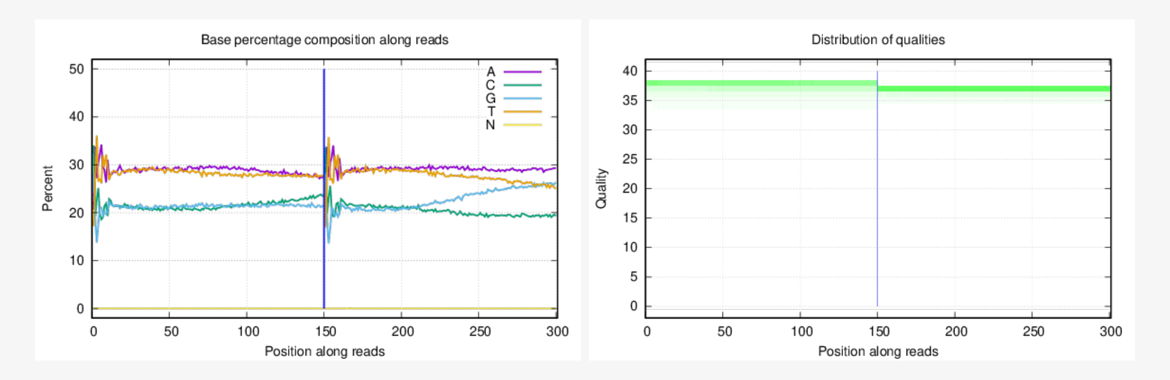

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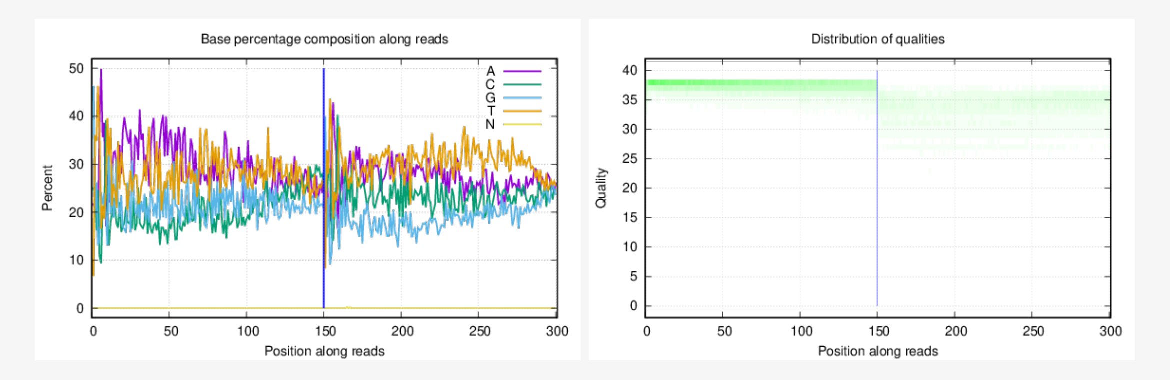

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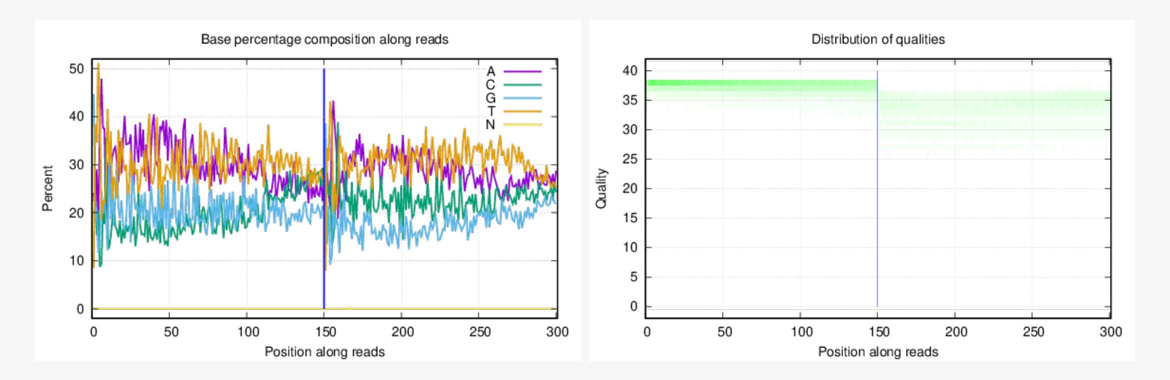

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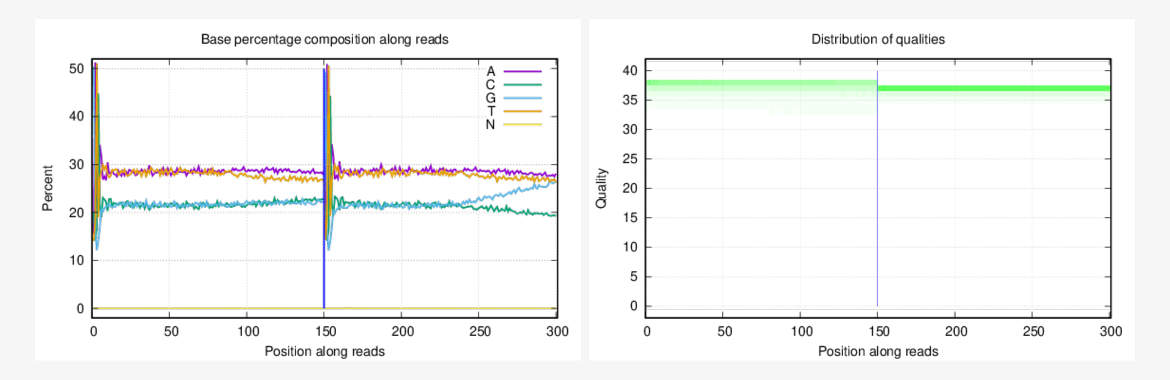

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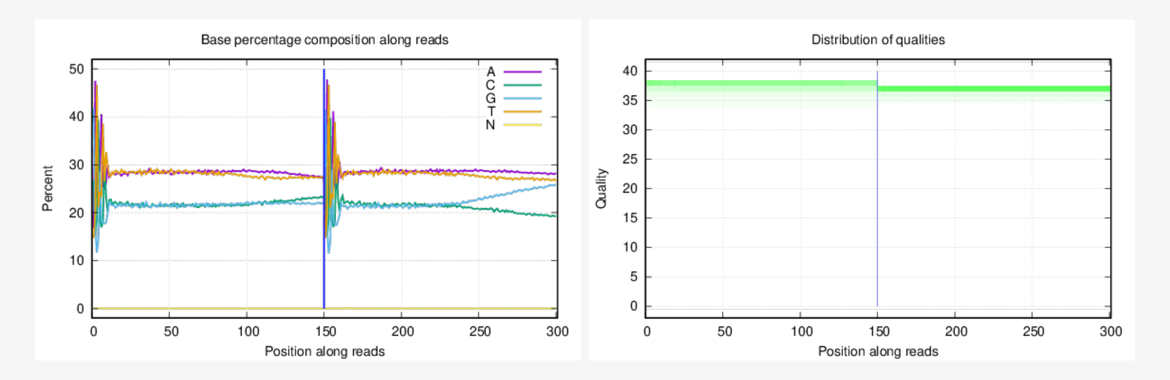

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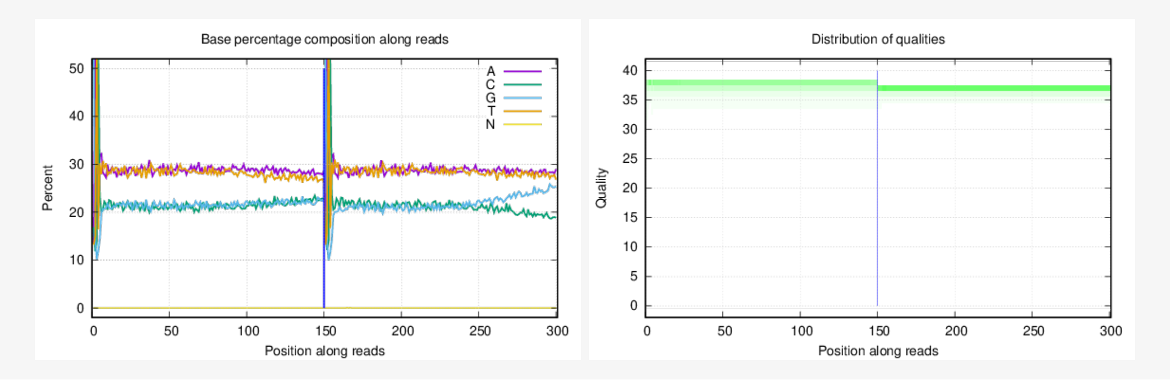

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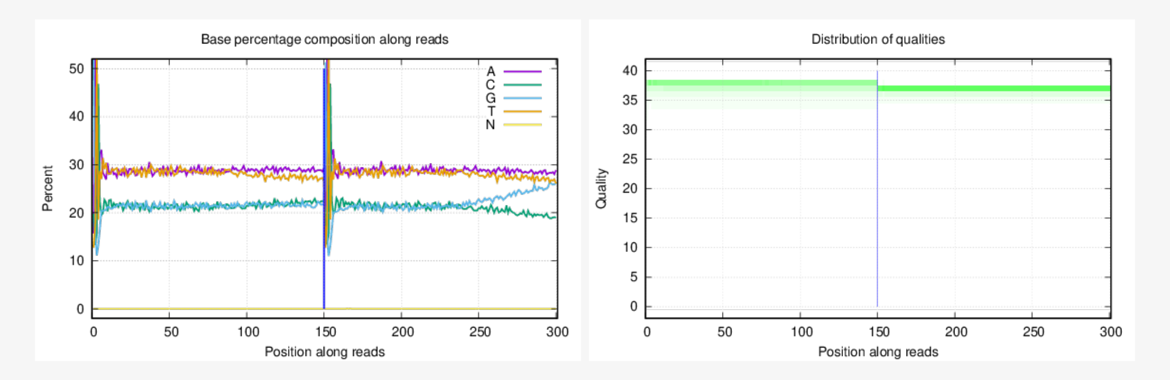
Base percentage composition along reads
Percent
50
40
30
20
10
0
0
50
100
150
200
250
300
Position along reads
A
C
G
T
N
Distribution of qualities
Quality
40
35
30
25
20
15
10
5
0
0
50
100
150
200
250
300
Position along reads

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
+
FFFCFFFFFFFFFDFEFFFFEFEF0FFFFEFFFFFFFEFFFFFECGFFFF
```

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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