Sequencing Data Report

Project: F25A430000584_MUSxylmR

Date: 2026.1.12

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

Sample	Length	Q20(%)	Q30(%)	GC Content(%)	Total Reads	Total Bases
10A2	150;150	96.04;98.9	88.79;95.65	52.35;44.92	216	64,800
142_A1_R1_786	150;150	96.31;98.25	89.76;93.96	53.56;44.33	213	63,900
142_A1_R2_786	150;150	95.62;98.92	87.79;95.25	53.63;44.44	109	32,700
143_A2_R1	150;150	96.19;98.8	89.16;95.08	52.5;44.06	149	44,700
143_A2_R2	150;150	96.17;98.42	89.02;93.92	53.06;47.65	160	48,000
143_A2_R3	150;150	96.07;98.61	88.98;95.73	52.74;46.26	151	45,300
186_M2_R1	150;150	94.35;98.81	84.76;95.52	53.03;44.62	349	104,700
1_25_A1	150;150	94.29;98.89	85.16;95.99	53.93;44.55	329	98,700
1_25_M0	150;150	95.16;98.62	87.15;94.66	53.3;45.2	143	42,900
2_26_Rep1	150;150	97.36;98.74	91.72;95.6	44.63;44.63	115,012	34,503,600
2_26_Rep1_aux	150;150	96.3;98.92	88.82;96.16	43.31;43.36	132,723	39,816,900
2_26_Rep2	150;150	96.72;98.52	90.0;94.89	43.57;43.61	52,387	15,716,100
2_26_Rep2_aux	150;150	97.06;98.53	90.81;94.84	44.12;43.97	91,574	27,472,200
CMAH	150;150	95.76;99.22	87.12;96.81	41.44;42.25	1,338	401,400
Embr10_CN10_x6	150;150	97.13;98.6	91.66;96.32	53.5;53.62	1,022,486	306,745,800
Embr10_inv_x5p1	150;150	98.0;99.06	93.37;96.59	51.92;51.86	1,676,601	502,980,300
Embr11_CN2_x6	150;150	96.21;98.61	89.24;96.49	53.34;53.44	372,624	111,787,200
Embr17_CN12_x6	150;150	97.13;98.6	91.86;96.48	53.21;53.41	1,611,282	483,384,600
Embr17_inv_x5p1	150;150	98.17;99.08	93.9;96.73	51.57;51.52	2,099,129	629,738,700
Embr19_CN5_x6	150;150	97.87;98.73	94.01;96.64	52.73;52.91	419,972	125,991,600
Embr19_inv_x5p1	150;150	97.71;98.92	92.47;96.14	51.79;51.78	1,385,413	415,623,900
GGTA1	150;150	95.34;98.86	86.72;95.98	35.2;34.85	580	174,000
GGTA2	150;150	95.94;98.37	87.79;94.45	35.13;34.93	939	281,700
H3K27Ac2	150;150	94.51;98.5	84.16;94.68	45.68;45.68	30,858,848	9,257,654,400
HCT_13_1	150;150	98.45;98.86	94.64;95.8	49.15;46.99	1,344,301	403,290,300
HCT_13_2	150;150	98.57;98.92	95.08;96.02	49.58;47.01	2,382,030	714,609,000
HCT_13_3	150;150	97.93;97.68	92.78;91.53	46.64;46.96	644,558	193,367,400

HCT_15_1	150;150	98.22;98.14	93.75;93.14	47.48;46.47	607,689	182,306,700
HCT_15_2	150;150	98.15;97.53	93.47;90.88	45.61;46.93	413,841	124,152,300
HCT_15_3	150;150	98.29;97.99	93.94;93.0	47.48;46.98	260	78,000
HCT_7_1	150;150	98.46;99.0	94.74;96.26	49.46;46.65	1,562,032	468,609,600
HCT_7_2	150;150	98.24;98.52	93.91;94.43	48.12;46.49	863,814	259,144,200
HCT_7_3	150;150	98.4;98.83	94.48;95.59	48.69;46.51	768,734	230,620,200
HEKM272_1_1	150;150	99.04;97.89	96.68;92.95	65.89;64.74	46,249	13,874,700
HEKM272_1_2	150;150	98.97;97.95	96.5;93.0	65.88;64.69	32,161	9,648,300
HEKM272_1_3	150;150	98.77;98.05	95.83;93.29	65.91;64.71	56,007	16,802,100
HEKM272_2_1	150;150	98.92;97.92	96.34;92.92	65.88;64.69	65,518	19,655,400
HEKM272_2_2	150;150	98.97;98.02	96.47;93.16	65.88;64.7	97,643	29,292,900
HEKM272_2_3	150;150	98.91;97.95	96.28;93.02	65.86;64.67	55,209	16,562,700
HEKM272_3_1	150;150	98.98;97.96	96.57;93.12	65.79;64.62	43,428	13,028,400
HEKM272_3_2	150;150	98.86;97.79	96.12;92.6	65.83;64.66	37,493	11,247,900
HEKM272_3_3	150;150	98.8;98.06	95.92;93.32	65.85;64.66	46,147	13,844,100
HEKM272_5_1	150;150	98.81;97.78	95.99;92.57	65.73;64.57	48,223	14,466,900
HEKM272_5_2	150;150	99.0;97.97	96.58;93.07	65.77;64.59	68,552	20,565,600
HEKM272_5_3	150;150	98.86;97.96	96.15;93.06	65.71;64.51	38,152	11,445,600
HEKM272_6_1	150;150	98.93;98.03	96.37;93.26	65.78;64.58	44,005	13,201,500
HEKM272_6_2	150;150	98.99;97.93	96.6;92.95	65.81;64.63	48,217	14,465,100
HEKM272_6_3	150;150	99.06;97.95	96.82;93.07	65.81;64.63	44,475	13,342,500
HEKM301_1_1	150;150	98.76;99.47	95.94;98.02	50.59;50.66	19,516	5,854,800
HEKM301_1_2	150;150	98.7;99.51	95.75;98.17	50.62;50.67	13,026	3,907,800
HEKM301_1_3	150;150	98.24;99.39	94.34;97.72	50.62;50.67	7,594	2,278,200
HEKM301_1_3_1	150;150	98.68;99.49	95.69;98.06	50.59;50.63	17,153	5,145,900
HEKM301_1_3_2	150;150	98.03;99.43	93.68;97.81	50.55;50.63	18,047	5,414,100
HEKM301_1_3_3	150;150	98.68;99.49	95.73;98.08	50.59;50.63	19,085	5,725,500
HEKM301_2_1	150;150	98.61;99.4	95.43;97.75	50.62;50.67	21,817	6,545,100
HEKM301_2_2	150;150	98.22;99.41	94.35;97.75	50.59;50.66	31,075	9,322,500
HEKM301_2_3	150;150	98.57;99.41	95.33;97.8	50.61;50.66	33,653	10,095,900
HEKM301_3_1	150;150	98.71;99.41	95.79;97.78	50.58;50.63	43,245	12,973,500

HEKM301_3_2	150;150	98.5;99.41	95.12;97.79	50.59;50.64	29,347	8,804,100
HEKM301_3_3	150;150	98.54;99.4	95.33;97.75	50.61;50.66	10,919	3,275,700
HEKM301_5_1	150;150	98.7;99.39	95.75;97.76	50.58;50.63	29,543	8,862,900
HEKM301_5_2	150;150	98.08;99.33	93.82;97.54	50.53;50.62	28,478	8,543,400
HEKM301_5_3	150;150	98.86;99.42	96.33;97.86	50.55;50.61	33,013	9,903,900
HEKM301_6_1	150;150	98.8;99.38	96.08;97.73	50.57;50.63	28,807	8,642,100
HEKM301_6_2	150;150	98.66;99.4	95.68;97.77	50.64;50.69	25,444	7,633,200
HEKM301_6_3	150;150	98.37;99.33	94.76;97.49	50.77;50.82	8,816	2,644,800
HEKM5_1_1	150;150	94.51;88.03	84.89;70.47	57.65;56.49	21,722	6,516,600
HEKM5_1_2	150;150	94.47;87.79	84.73;69.91	57.66;56.53	34,912	10,473,600
HEKM5_1_3	150;150	93.19;88.73	82.0;71.48	57.79;56.46	34,720	10,416,000
HEKM5_2_1	150;150	94.9;88.13	85.73;70.59	57.58;56.48	15,725	4,717,500
HEKM5_2_2	150;150	93.52;88.35	82.66;71.03	57.73;56.5	20,656	6,196,800
HEKM5_2_3	150;150	93.78;88.09	83.28;70.52	57.72;56.47	15,660	4,698,000
HEKM5_3_1	150;150	95.62;87.44	87.4;69.63	57.34;56.34	22,823	6,846,900
HEKM5_3_2	150;150	96.15;87.91	88.51;70.24	57.33;56.39	30,887	9,266,100
HEKM5_3_3	150;150	94.24;88.79	84.12;71.76	57.56;56.37	21,143	6,342,900
HEKM5_5_1	150;150	95.91;87.75	87.95;70.12	57.24;56.29	15,532	4,659,600
HEKM5_5_2	150;150	95.25;87.92	86.4;70.37	57.16;56.16	11,948	3,584,400
HEKM5_5_3	150;150	95.35;87.66	86.67;69.93	57.26;56.24	8,418	2,525,400
HEKM5_6_1	150;150	95.29;87.78	86.51;70.15	57.33;56.31	42,585	12,775,500
HEKM5_6_2	150;150	96.01;87.18	88.13;69.11	57.18;56.33	19,553	5,865,900
HEKM5_6_3	150;150	95.61;87.27	87.21;69.23	57.34;56.4	20,505	6,151,500
HEKS30_1_2	150;150	98.57;99.59	95.31;98.35	47.3;48.02	135,123	40,536,900
HEKS30_1_3	150;150	98.57;99.56	95.35;98.27	47.3;48.02	84,072	25,221,600
HEKS30_1_4	150;150	98.35;99.59	94.63;98.34	47.3;48.01	90,588	27,176,400
HEKS30_2_2	150;150	98.54;99.54	95.26;98.21	47.31;48.03	46,923	14,076,900
HEKS30_2_3	150;150	98.5;99.58	95.1;98.33	47.31;48.02	81,463	24,438,900
HEKS30_2_4	150;150	98.6;99.6	95.39;98.38	47.33;48.02	23,952	7,185,600
HEKS30_3_2	150;150	98.38;99.59	94.77;98.37	47.3;48.02	62,244	18,673,200
HEKS30_3_3	150;150	98.55;99.6	95.24;98.41	47.32;48.02	40,005	12,001,500
HEKS30_3_4	150;150	98.42;99.6	94.85;98.4	47.32;48.02	33,294	9,988,200

HEKS30_5_2	150;150	98.51;99.63	95.16;98.51	47.31;48.02	23,512	7,053,600
HEKS30_5_3	150;150	98.53;99.63	95.1;98.5	47.31;48.02	24,970	7,491,000
HEKS30_5_4	150;150	98.63;99.63	95.49;98.5	47.34;48.01	9,942	2,982,600
HEKS30_6_2	150;150	98.44;99.62	94.88;98.48	47.31;48.02	49,764	14,929,200
HEKS30_6_3	150;150	98.49;99.6	94.97;98.4	47.32;48.02	38,112	11,433,600
HEKS30_6_4	150;150	98.6;99.63	95.41;98.48	47.31;48.02	42,343	12,702,900
HEKS53_1_3_1	150;150	97.9;99.44	92.95;97.86	39.86;41.08	67,723	20,316,900
HEKS53_1_3_2	150;150	98.04;99.5	93.39;98.08	40.2;41.29	42,892	12,867,600
HEKS53_1_3_3	150;150	98.29;99.47	94.24;97.93	39.87;41.11	64,639	19,391,700
HEKS53_3_1	150;150	97.8;99.5	92.69;98.02	39.49;40.75	67,720	20,316,000
HEKS53_3_2	150;150	98.23;99.49	94.09;98.05	39.58;40.83	68,025	20,407,500
HEKS53_3_3	150;150	98.22;99.52	94.0;98.15	39.61;40.79	47,716	14,314,800
HEKS53_3_3_1	150;150	98.13;99.49	93.75;98.03	40.1;41.25	90,101	27,030,300
HEKS53_3_3_2	150;150	98.19;98.18	93.75;93.29	46.73;46.11	872,503	261,750,900
HEKS53_3_3_3	150;150	98.23;99.52	93.96;98.13	39.73;40.97	45,295	13,588,500
L1T2G1D	150;150	95.71;94.52	86.16;80.84	54.11;57.3	1,128,080	338,424,000
L2R2TGA	150;150	97.88;98.35	92.99;94.19	50.95;52.59	539,742	161,922,600
L2R2TGC	150;150	97.3;99.25	91.44;97.27	48.82;50.5	601,387	180,416,100
L2RT2GD	150;150	94.57;94.65	83.4;81.44	50.66;55.8	159,802	47,940,600
L2RTGA	150;150	97.93;98.56	93.38;94.96	52.0;53.16	443,041	132,912,300
L2RTGB	150;150	98.27;99.38	94.45;97.86	51.69;52.11	810,392	243,117,600
L2RTGC	150;150	96.74;99.31	89.83;97.47	48.57;50.48	1,017,513	305,253,900
LRT2GD	150;150	95.93;93.97	86.93;78.57	50.22;55.49	131,726	39,517,800
MoPh11	150;150	97.14;99.05	91.15;96.77	44.72;45.0	170,996	51,298,800
MoPh14	150;150	98.24;99.11	94.31;96.94	44.55;44.88	235,530	70,659,000
MoPh15	150;150	96.7;98.7	89.83;95.29	43.38;43.38	41,706,609	12,511,982,700
MoPh15_input	150;150	96.1;98.55	88.43;95.04	42.42;42.52	29,281,073	8,784,321,900
MoPh7	150;150	96.29;98.62	88.75;95.07	45.34;45.49	35,272,515	10,581,754,500
MoPh7_input	150;150	96.65;98.47	89.83;94.75	42.98;43.06	28,881,871	8,664,561,300
P228	150;150	97.62;98.46	92.3;94.78	54.56;54.51	37,770,873	11,331,261,900
P230	150;150	98.08;98.62	93.6;95.25	53.79;53.9	18,898,298	5,669,489,400

P231	150;150	98.43;98.86	94.8;96.12	54.35;54.52	26,361,163	7,908,348,900
P232	150;150	97.7;98.45	92.52;94.72	54.34;54.04	24,533,753	7,360,125,900
P233	150;150	97.81;98.75	92.85;95.72	54.29;54.39	43,769,504	13,130,851,200
P234	150;150	97.75;98.57	92.65;95.07	53.92;53.98	44,350,801	13,305,240,300
P235	150;150	97.23;98.69	91.09;95.53	54.06;54.34	26,314,708	7,894,412,400
P236	150;150	97.71;98.68	92.53;95.46	53.94;54.02	37,398,991	11,219,697,300
P237	150;150	97.74;98.65	92.64;95.38	54.22;53.89	25,712,025	7,713,607,500
P238	150;150	97.99;98.84	93.43;96.05	53.7;53.55	28,321,243	8,496,372,900
P239	150;150	97.91;98.67	93.08;95.48	54.57;54.51	23,466,917	7,040,075,100
P240	150;150	97.79;98.81	92.79;95.94	53.56;53.89	26,660,813	7,998,243,900
PARP_KO_r1	150;150	97.51;99.0	92.18;96.51	44.63;44.52	38,760,534	11,628,160,200
PARP_KO_r2	150;150	96.22;99.16	88.6;97.05	44.4;44.5	36,690,803	11,007,240,900
PARP_WT_r1	150;150	95.74;99.17	87.37;97.13	45.23;45.22	27,106,160	8,131,848,000
PARP_WT_r2	150;150	98.34;99.21	94.57;97.27	44.9;45.1	36,657,078	10,997,123,400
R1_1-25	150;150	97.51;97.41	92.54;91.75	49.76;49.75	301,693	90,507,900
R2_149-4	150;150	96.52;96.83	89.63;89.96	48.86;48.86	163,413	49,023,900
R3_149-1-o-14	150;150	96.16;95.88	89.08;86.17	48.65;48.49	74,825	22,447,500
S1_1-25	150;150	96.93;97.33	90.72;91.43	51.22;51.4	206,157	61,847,100
S2_149-4	150;150	96.7;97.22	90.19;91.15	48.84;48.94	109,286	32,785,800
S3_149-1-o-14	150;150	96.43;96.96	89.4;90.22	49.57;49.67	96,206	28,861,800
SIX_10A2_2	150;150	95.85;98.86	88.37;95.61	53.88;44.02	2,221	666,300
SIX_10A3_1	150;150	95.64;99.12	87.92;96.38	53.77;44.13	2,048	614,400
SIX_10MMG2	150;150	95.79;99.01	88.16;96.1	54.08;44.77	1,545	463,500
SIX_142	150;150	97.27;98.86	91.16;95.79	42.95;42.96	2,922	876,600
SIX_142R2_119	150;150	97.3;98.85	91.15;95.58	43.05;43.07	2,759	827,700
SIX_142R2_119_RT	150;150	97.03;98.86	90.41;95.55	43.07;43.07	2,915	874,500
SIX_143	150;150	97.89;99.09	92.91;96.43	43.27;43.25	2,687	806,100
SIX_186M2_R1	150;150	95.99;99.03	88.96;96.13	54.06;43.8	1,559	467,700
SIX_3A2_1	150;150	95.65;98.87	87.99;95.76	54.47;44.53	1,387	416,100
TK	150;150	97.09;97.42	90.69;91.36	47.89;47.69	12,244,047	3,673,214,100
TM_I	150;150	97.76;97.63	92.68;93.02	52.27;52.24	22,027,001	6,608,100,300

Trih1	150;150	96.63;99.03	89.49;96.08	34.56;34.66	122,879,353	36,863,805,900
Trih2	150;150	96.53;99.18	89.45;96.79	38.18;38.09	150,541,901	45,162,570,300
Ufa_134	150;150	96.38;95.66	87.31;81.84	54.22;55.11	714	214,200
Ufa_28	150;150	96.3;95.28	87.63;81.31	54.45;54.82	343	102,900
brLinker_Rep5_aux	150;150	95.88;98.99	87.77;96.44	44.92;44.83	168,501	50,550,300
brNTD_Rep6_aux	150;150	96.56;99.0	89.6;96.56	44.93;44.96	125,382	37,614,600
brRad21_Rep1	150;150	97.55;98.98	92.33;96.49	43.92;44.04	113,919	34,175,700
brRad21_Rep1_aux	150;150	97.53;98.7	92.2;95.5	44.26;44.14	92,436	27,730,800
brRad21_Rep2	150;150	97.59;98.98	92.45;96.46	43.87;44.16	120,197	36,059,100
brRad21_Rep2_aux	150;150	97.5;98.69	92.11;95.45	42.8;42.47	77,731	23,319,300
cmv_ori_2_wo_bpd	150;150	97.46;99.24	92.17;97.44	44.87;44.2	352,766	105,829,800
cmv_ori_4_bpd	150;150	97.59;99.06	92.46;96.75	44.03;44.44	208,863	62,658,900
dpn_1_bpd	150;150	96.26;99.35	88.86;97.88	45.81;45.77	171,309	51,392,700
dpn_1_wo_bpd	150;150	98.23;99.34	94.45;97.86	45.23;44.67	418,221	125,466,300
hCTCF_R4	150;150	95.1;96.06	84.66;85.94	46.08;46.22	4,107,477	1,232,243,100
hCTCF_a_R4	150;150	95.15;96.29	84.78;86.65	45.5;45.59	8,075,963	2,422,788,900
i1_1-25	150;150	96.08;96.77	88.73;89.94	44.14;44.45	435,219	130,565,700
i2_149-4	150;150	96.08;96.58	88.85;89.43	44.23;44.13	181,052	54,315,600
i3_149-1-o-14	150;150	96.66;96.91	90.13;90.29	44.14;43.84	174,112	52,233,600
i_MoPh15_TR	150;150	94.65;98.07	84.55;93.25	45.16;45.13	14,459,383	4,337,814,900
mES1-2_CNb25_x6	150;150	97.28;98.78	92.03;96.83	53.09;53.25	4,463,103	1,338,930,900
mES1-2_inv_x5p1	150;150	97.95;99.02	93.18;96.49	51.67;51.68	4,557,375	1,367,212,500
mES1-3_CN4_x6	150;150	96.84;98.47	91.21;96.15	53.18;53.31	351,355	105,406,500
mES1-6_CNb25_x6	150;150	97.35;98.66	92.49;96.42	53.13;53.21	4,429,980	1,328,994,000
mES1-6_inv_x5p1	150;150	97.9;99.14	93.06;96.9	51.55;51.45	4,057,417	1,217,225,100
mES2-2_CNb25_x6	150;150	96.45;98.67	90.03;96.53	52.07;52.12	7,524,480	2,257,344,000
mES2-2_inv_x5	150;150	98.04;99.1	93.48;96.73	49.61;49.61	3,236,038	970,811,400
mES2-8_CN22_x6	150;150	97.3;98.46	92.44;96.08	53.3;53.52	2,567,114	770,134,200
mES5-5_CN16_x6	150;150	96.75;98.66	90.54;96.43	53.06;53.24	1,877,145	563,143,500
mix_1_TA_STAG2	150;150	97.18;98.72	90.96;94.79	33.82;33.96	114,167	34,250,100
mix_2_TA_STAG2	150;150	97.41;98.89	91.63;95.41	32.28;32.23	135,266	40,579,800
rigs_11	150;150	96.68;99.4	90.03;97.68	50.45;51.43	58,415	17,524,500

rigs_14	150;150	96.05;99.51	88.27;98.03	49.67;49.97	107,526	32,257,800
rigs_17	150;150	97.24;99.48	91.4;98.0	49.86;50.16	174,462	52,338,600
rigs_2	150;150	97.26;99.55	91.5;98.23	49.73;50.89	264,285	79,285,500
rigs_mysticseq	150;150	97.82;98.84	92.91;96.27	45.57;45.68	550	165,000

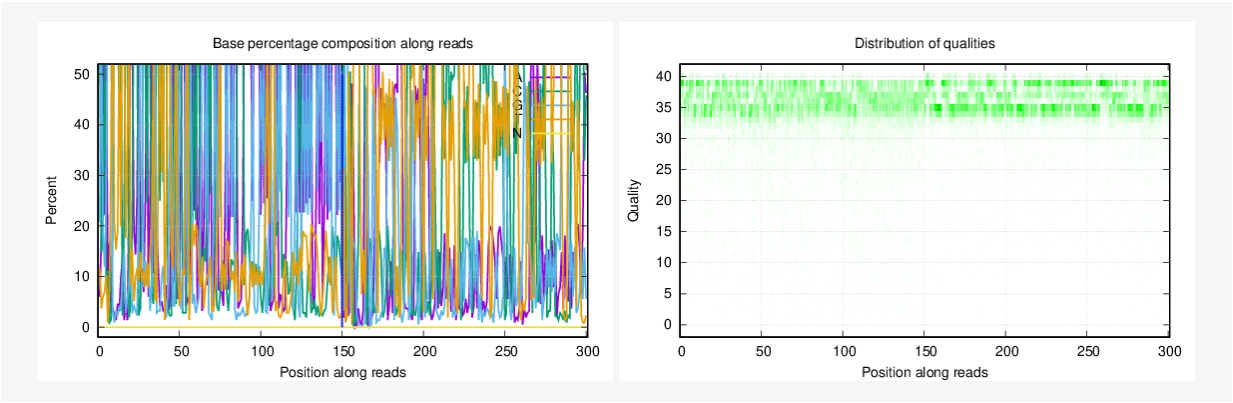
Table Format:

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

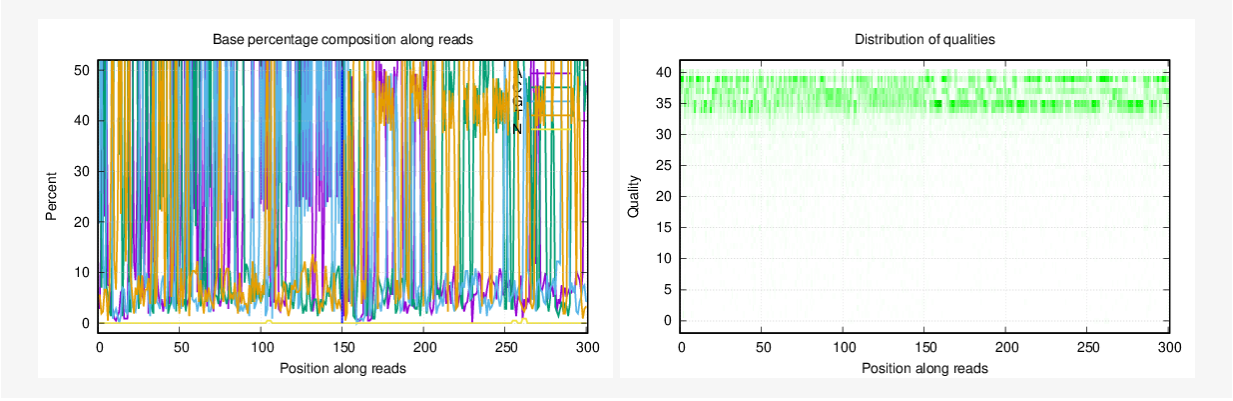
Data Quality Control

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.

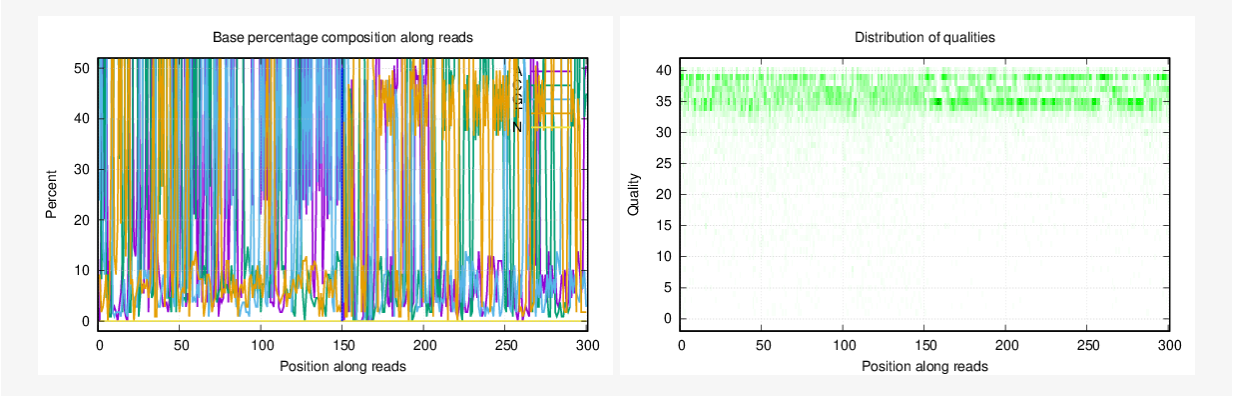
10A2



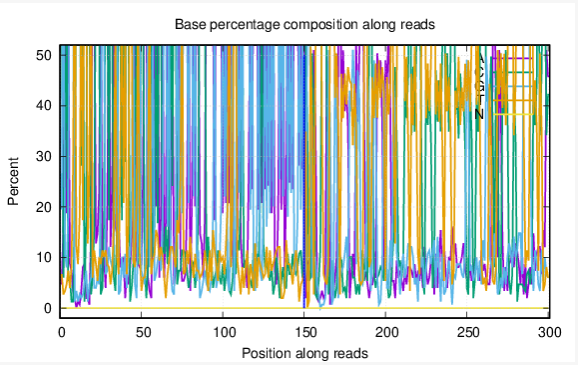
142_A1_R1_786

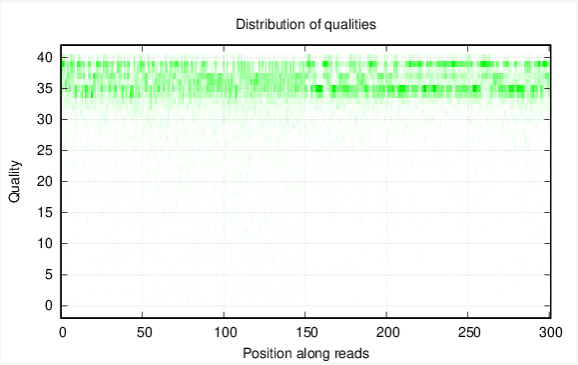


142_A1_R2_786

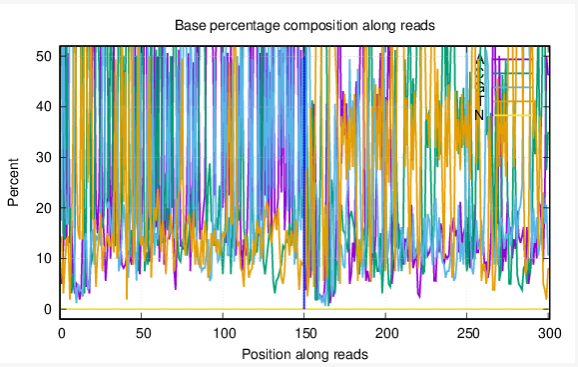


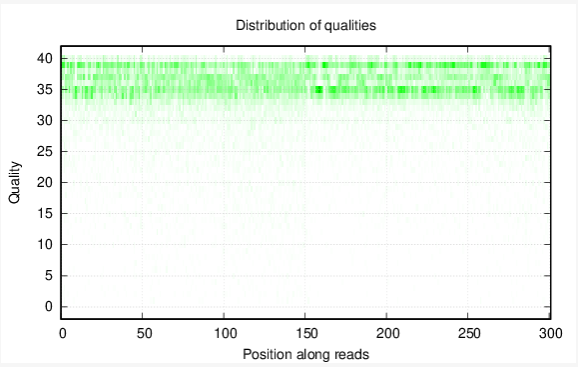
143_A2_R1



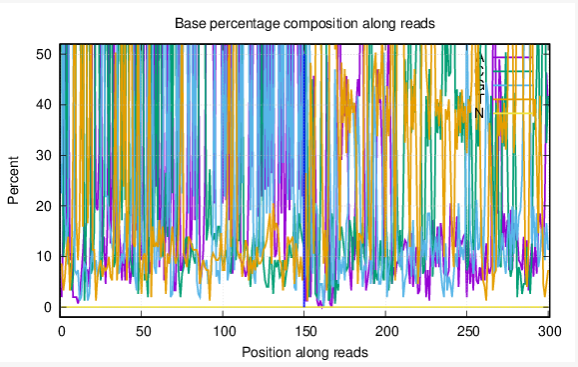


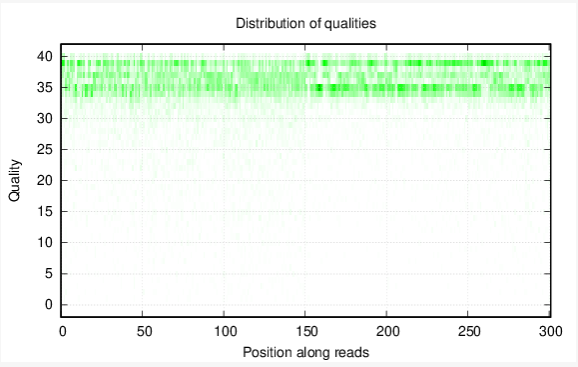
143_A2_R2



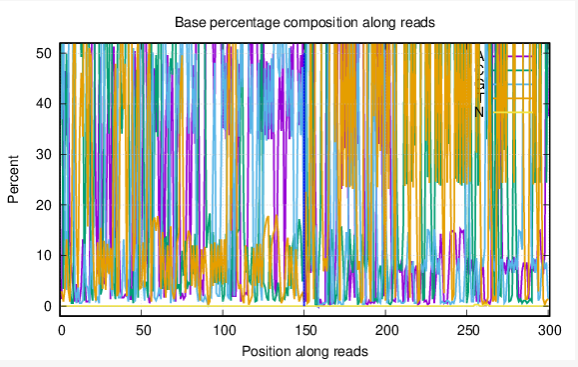


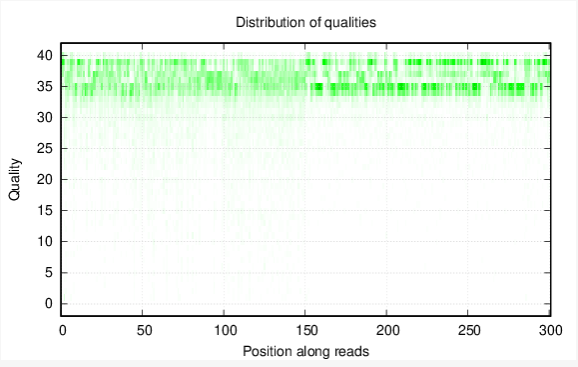
143_A2_R3



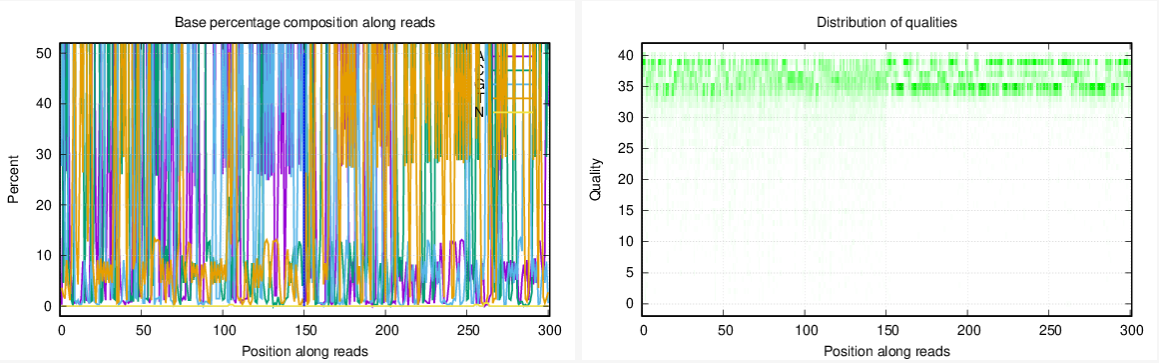


186_M2_R1

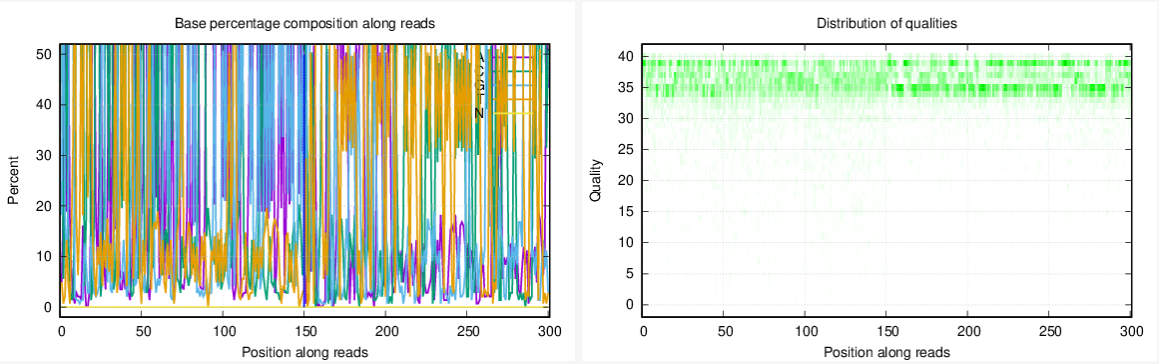




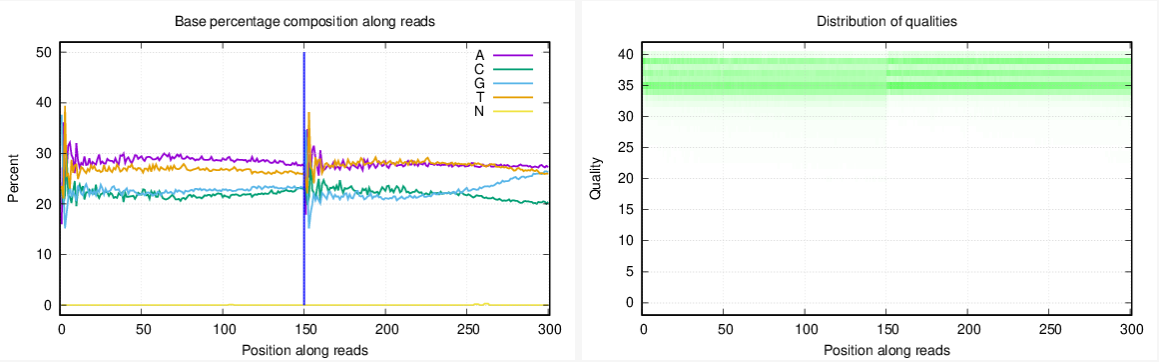
1_25_A1



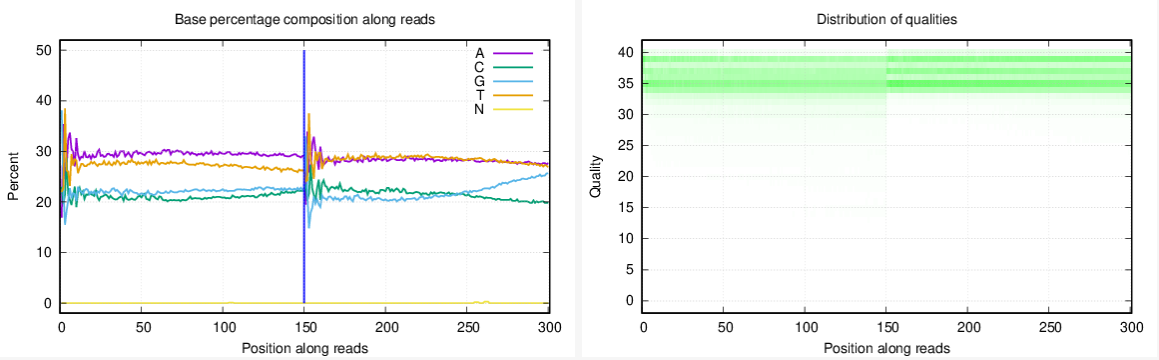
1_25_M0



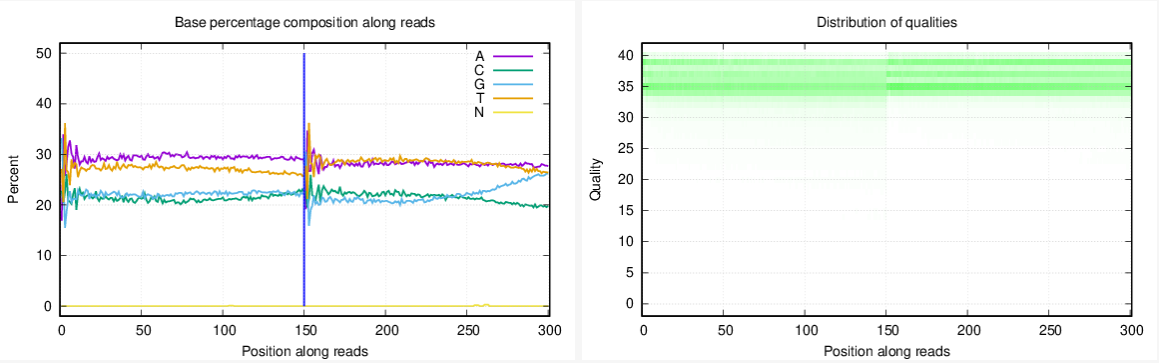
2_26_Rep1



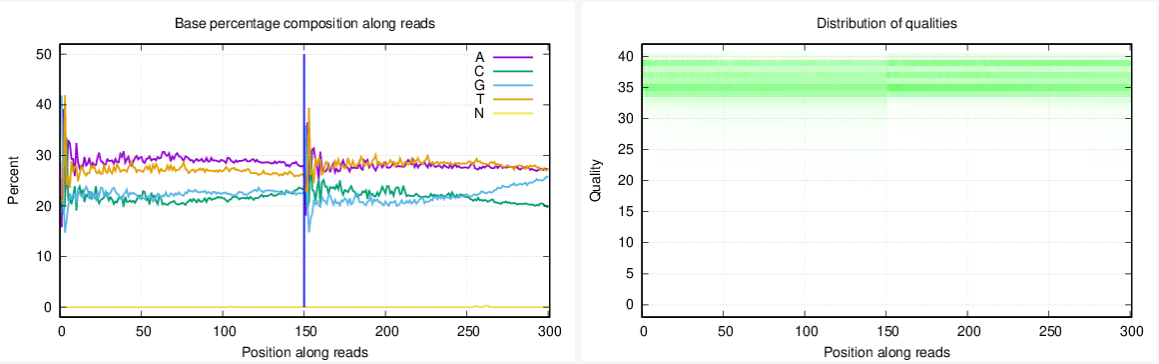
2_26_Rep1_aux



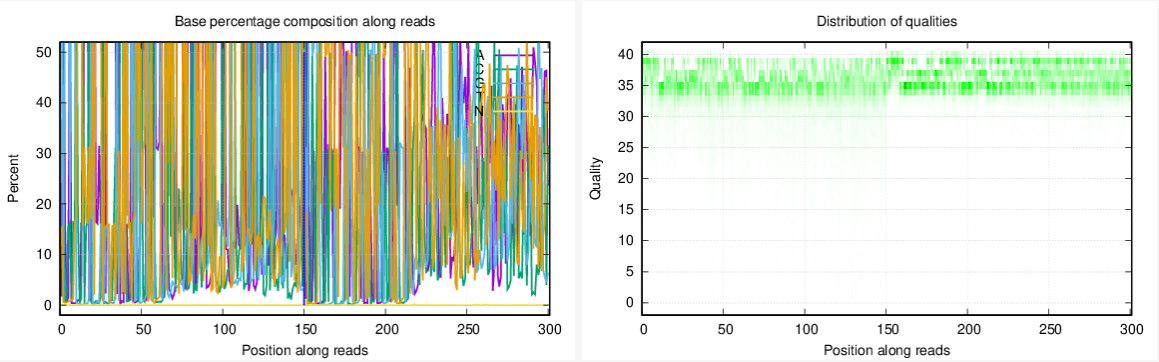
2_26_Rep2



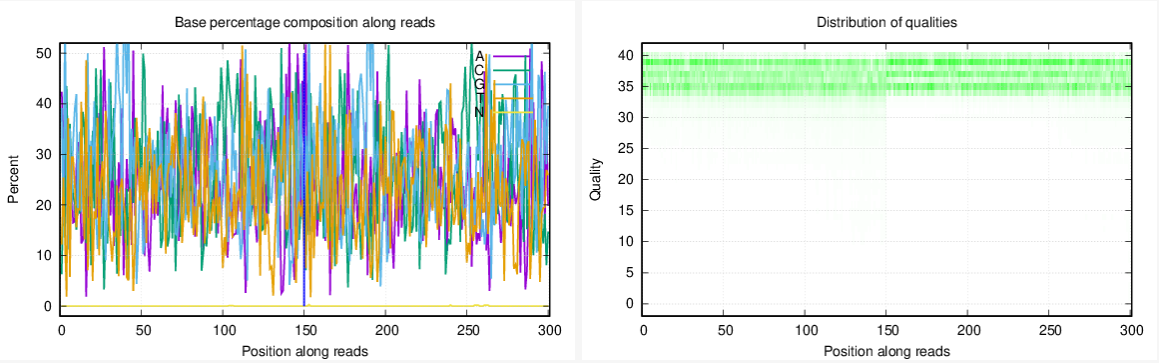
2_26_Rep2_aux



CMAH



Embr10_CN10_x6



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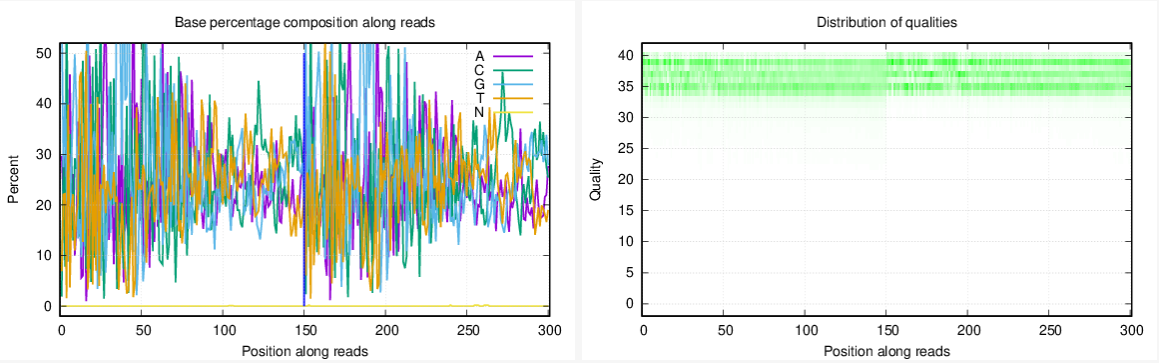
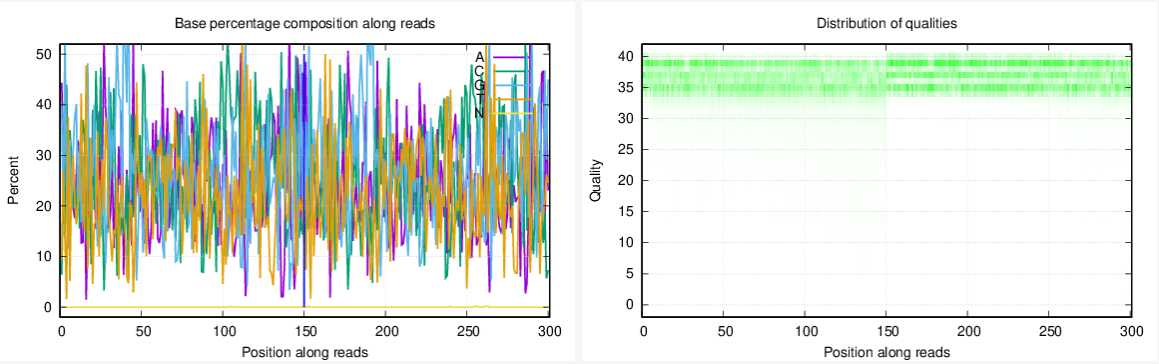
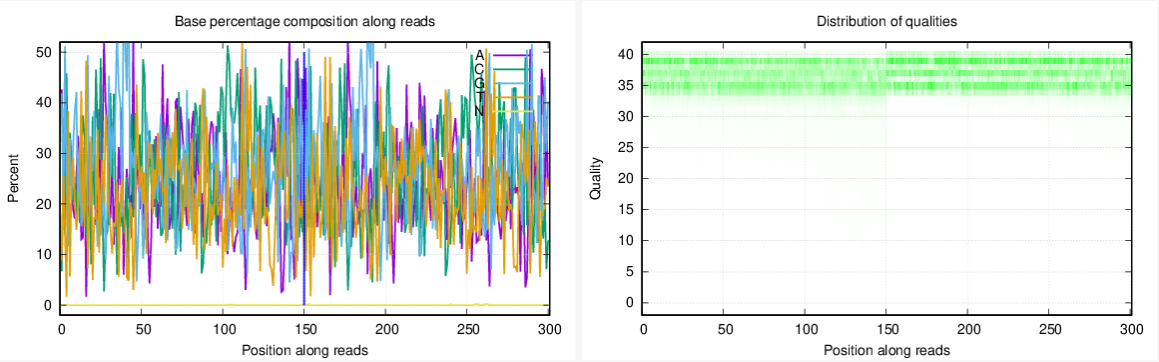


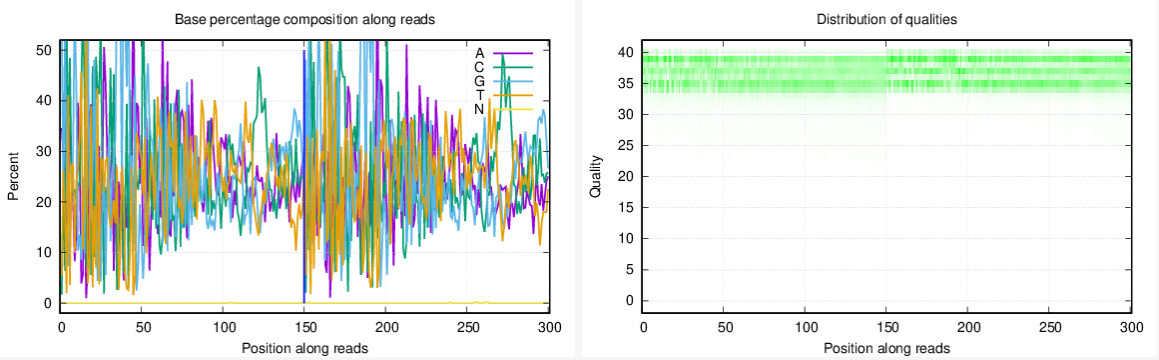
Embr11_CN2_x6



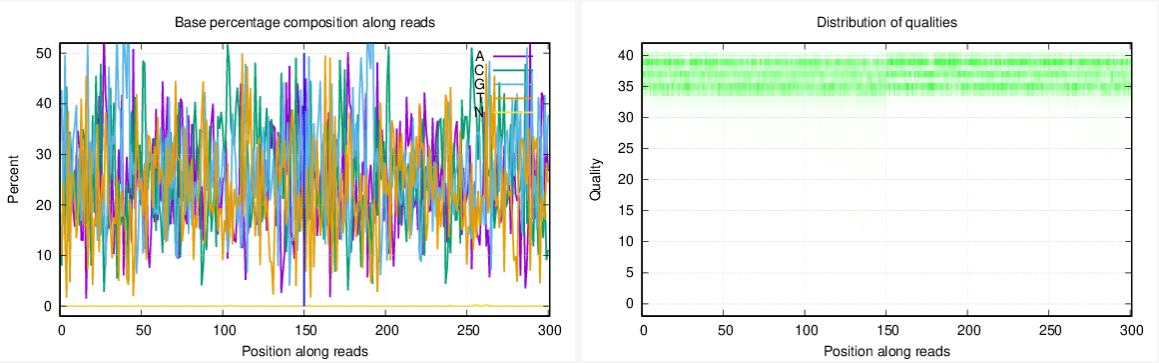
Embr17_CN12_x6



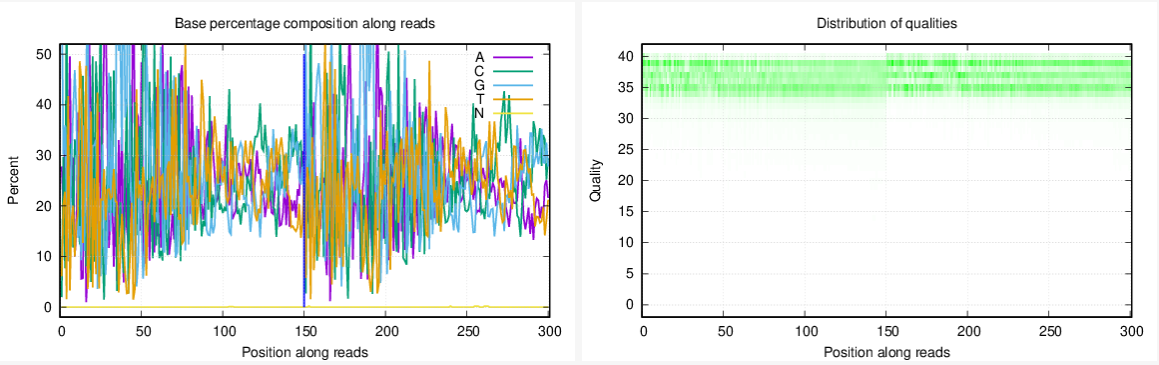
Embr17_inv_x5p1



Embr19_CN5_x6



Embr19_inv_x5p1



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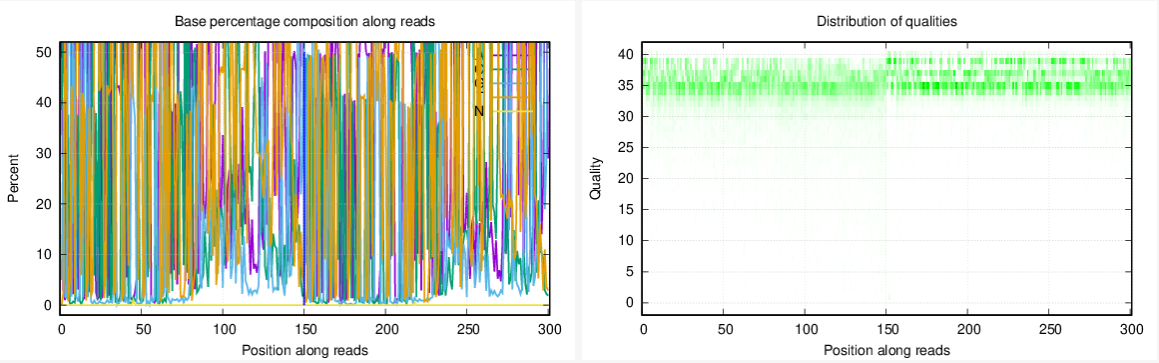
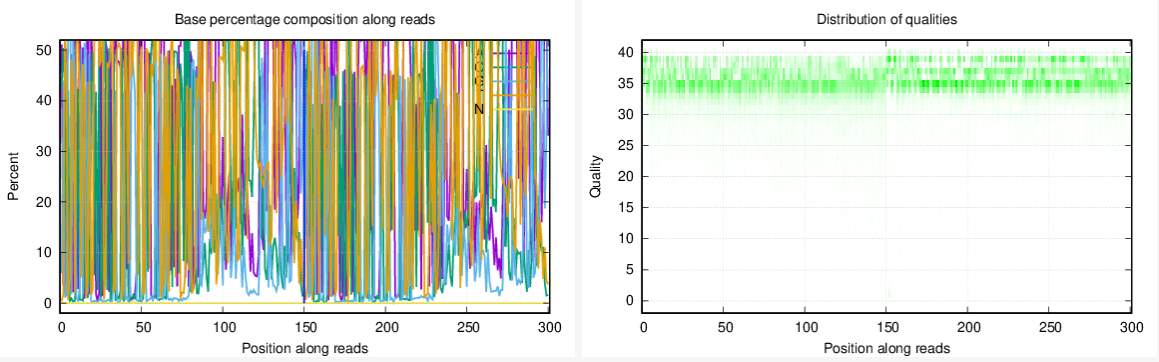


GGTA2



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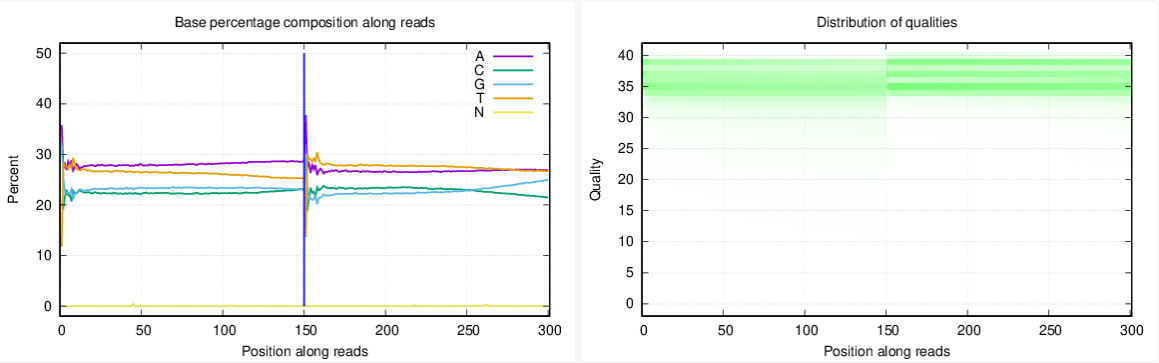
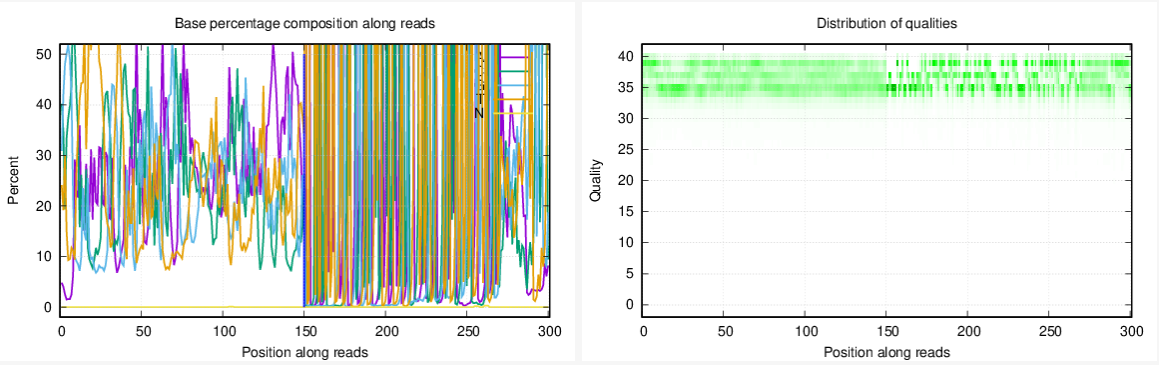


HCT_13_1



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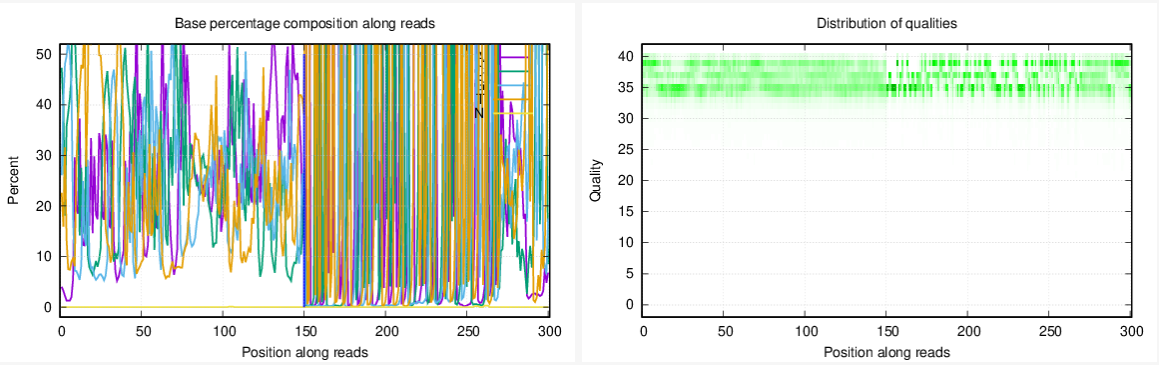

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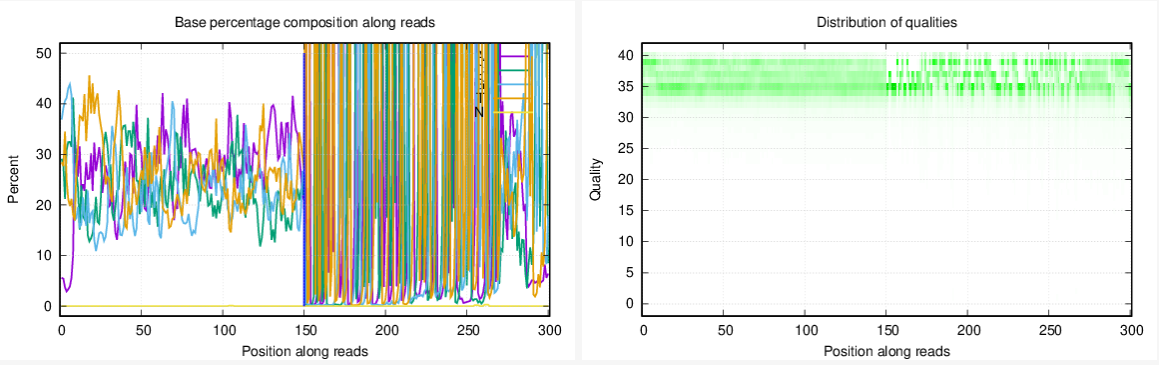

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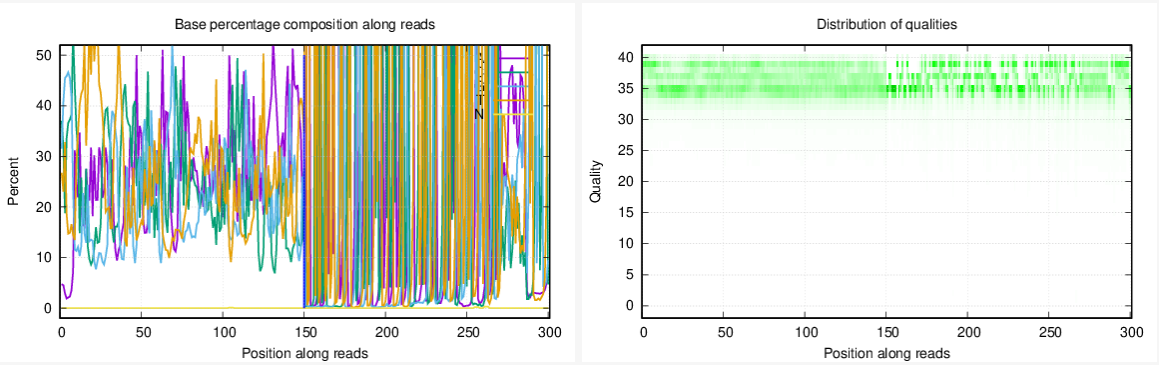

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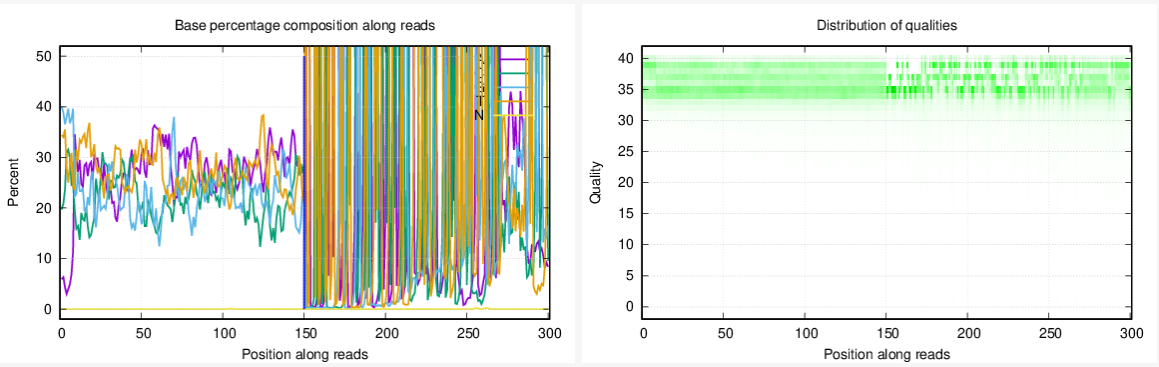

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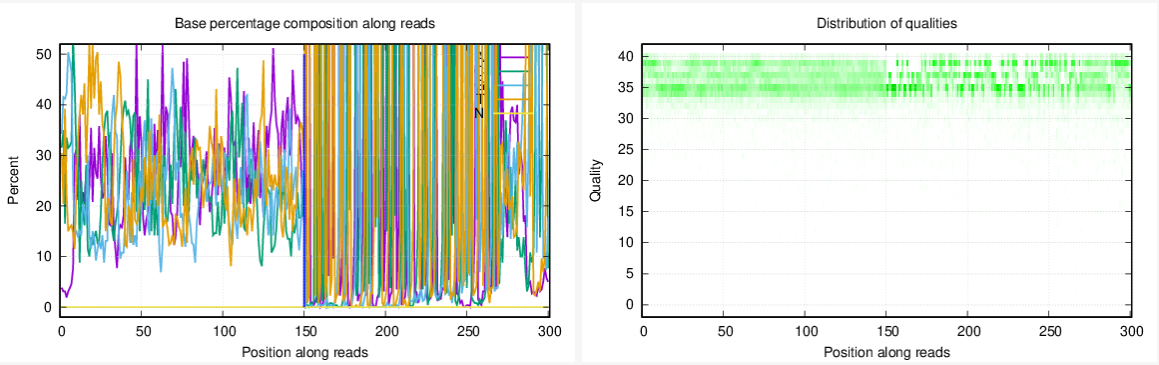
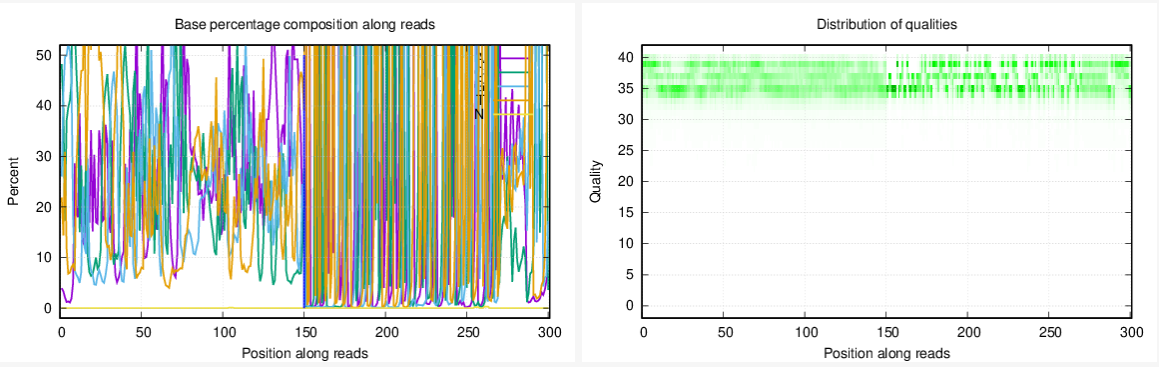
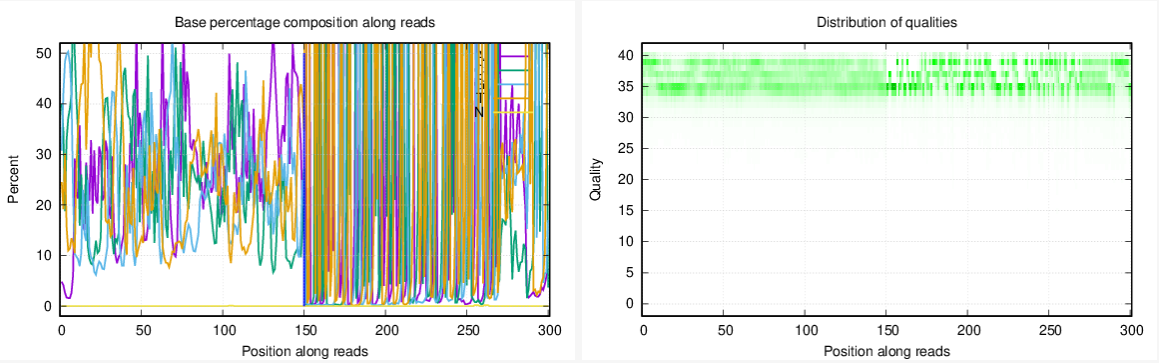


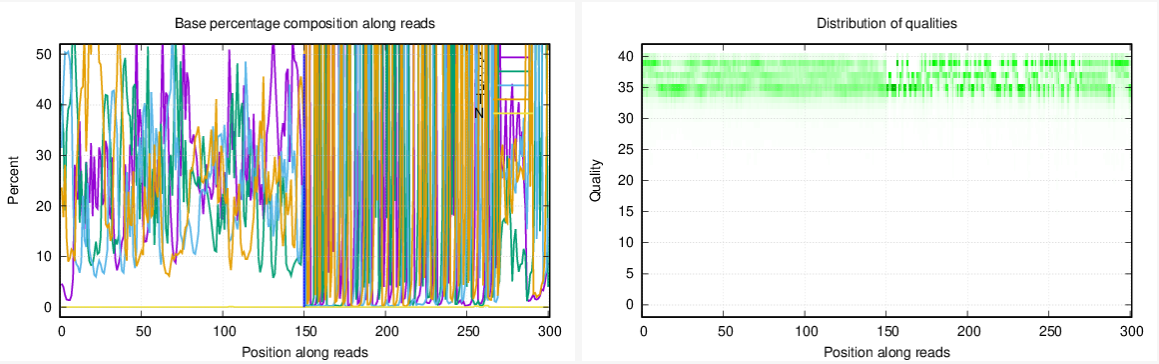
HCT_7_1



HCT_7_2



HCT_7_3



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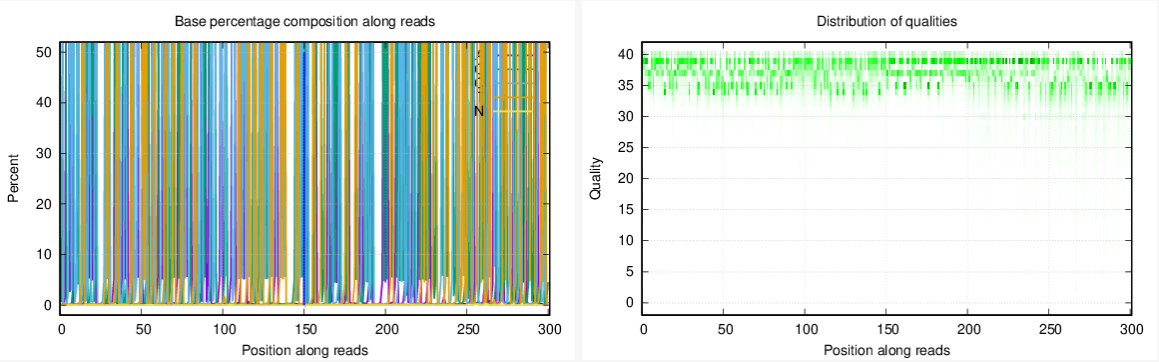

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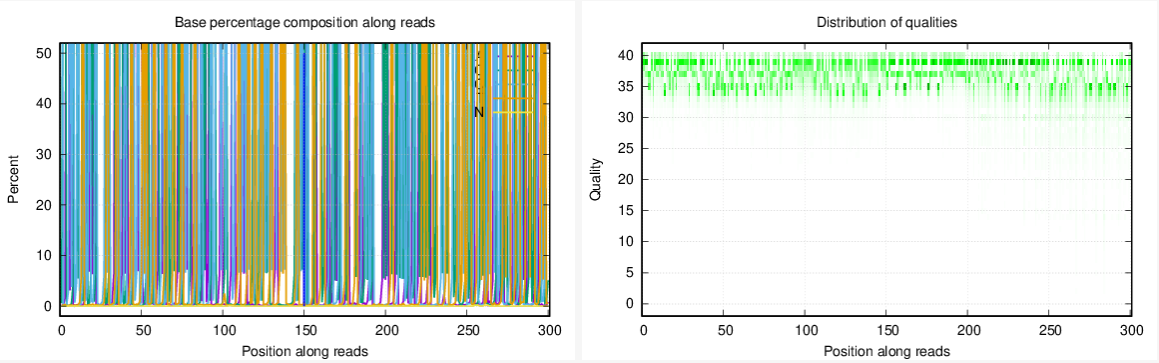

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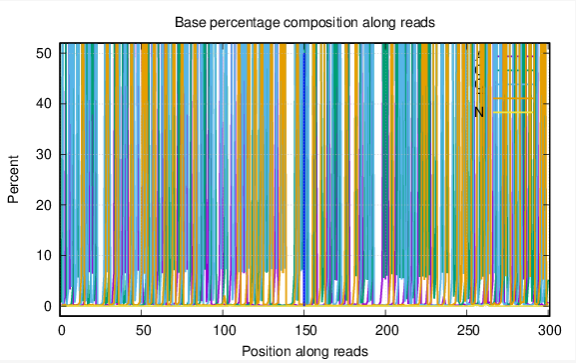

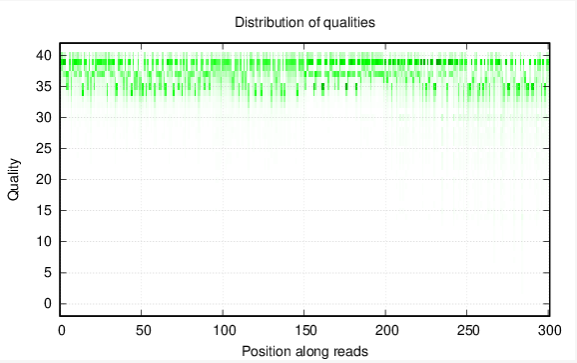

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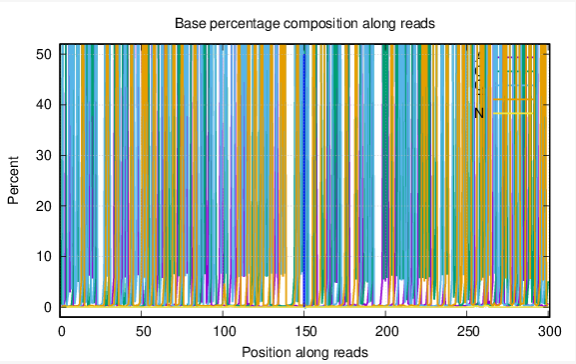

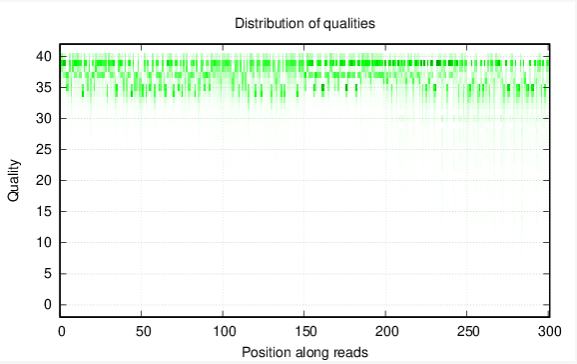

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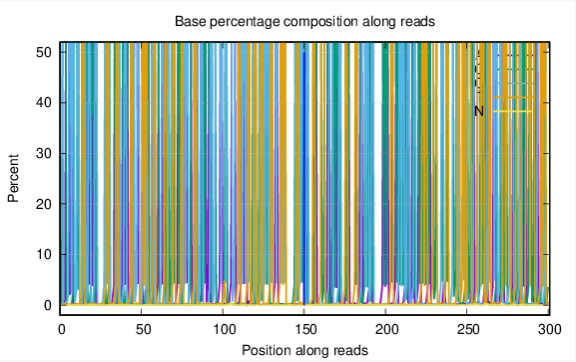

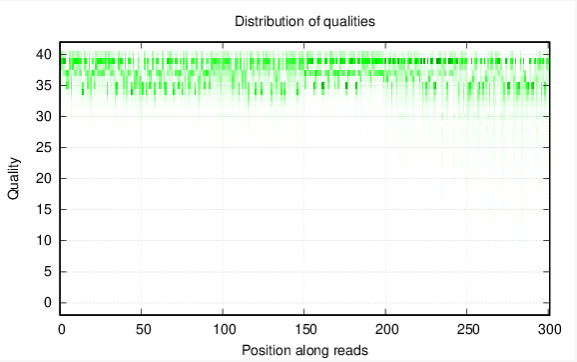

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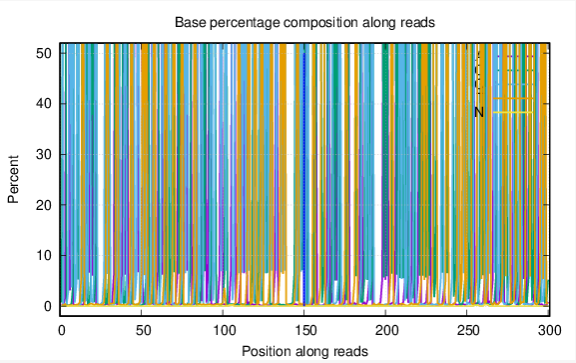
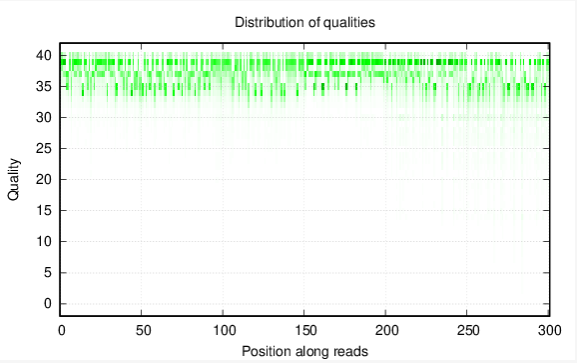
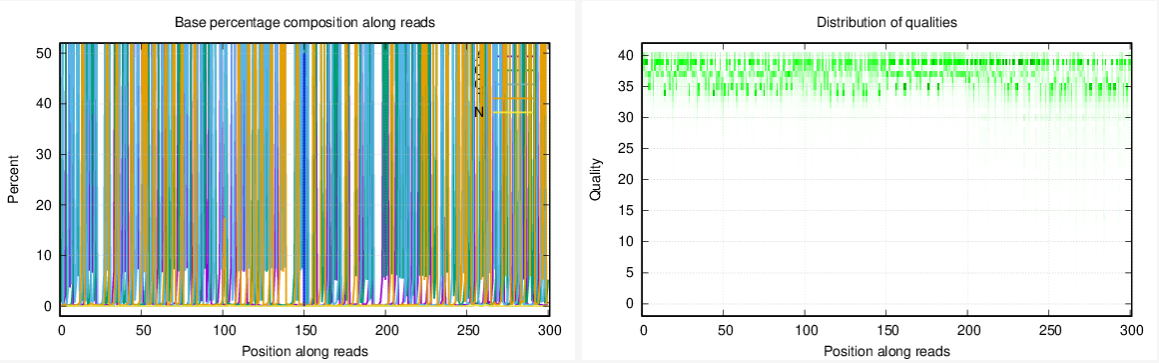




HEKM272_3_1



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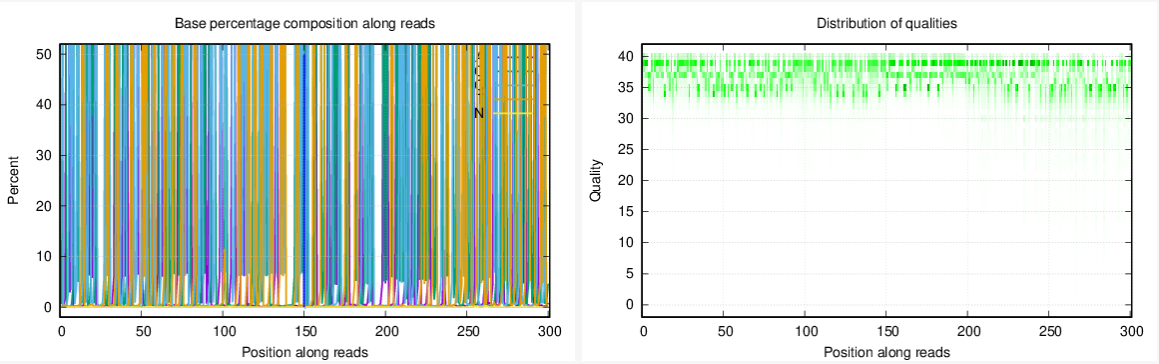

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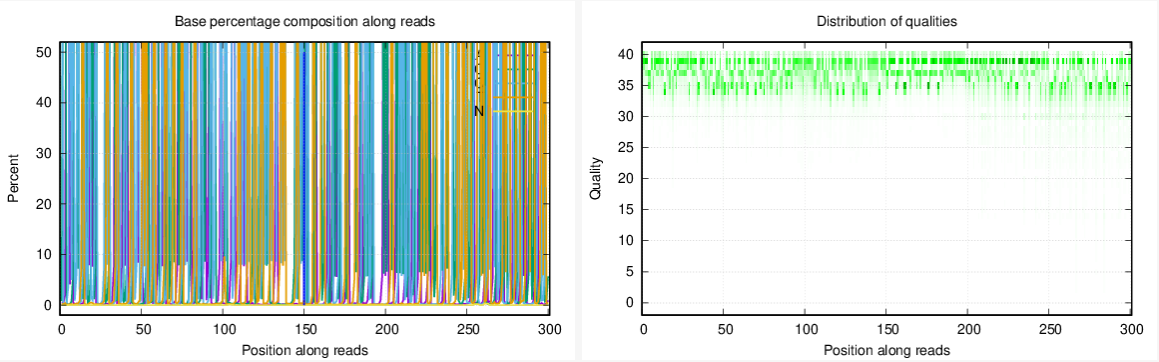

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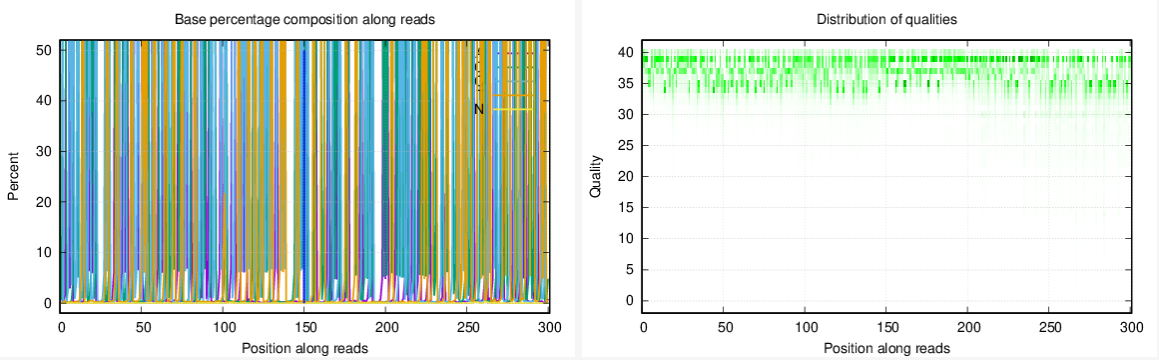
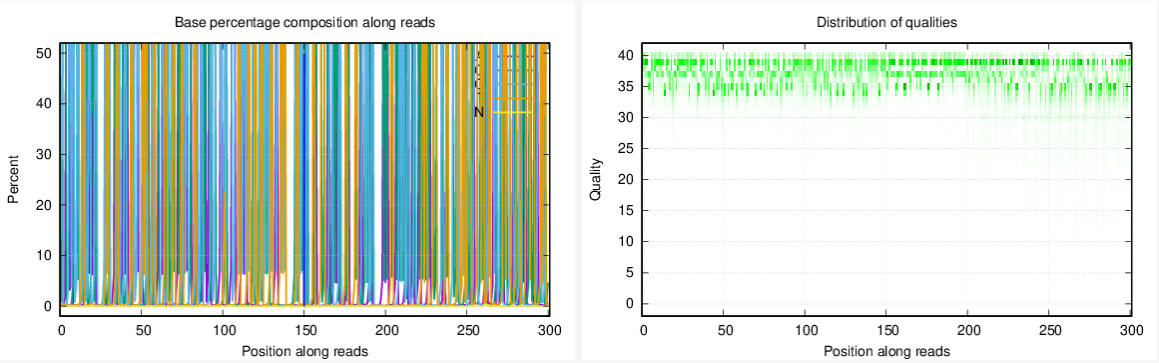


HEKM272_5_2



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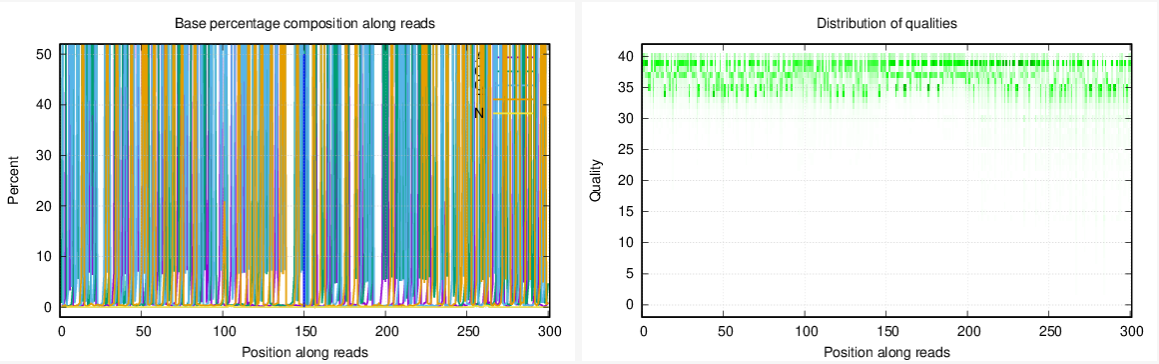

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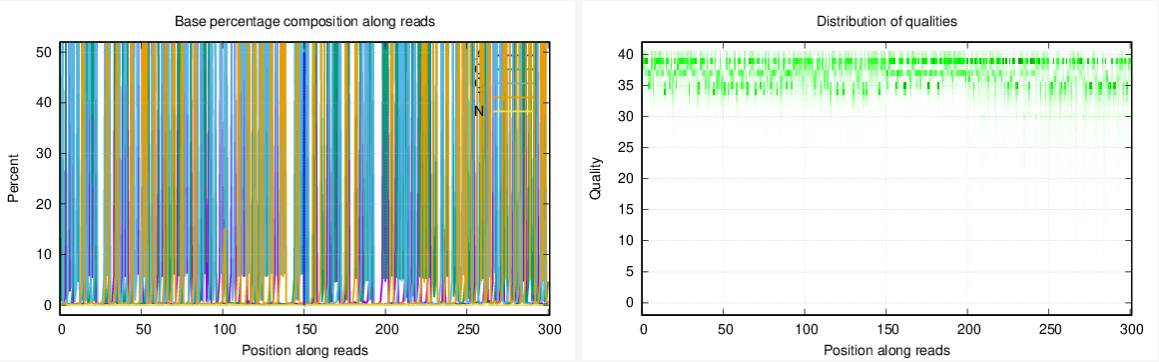

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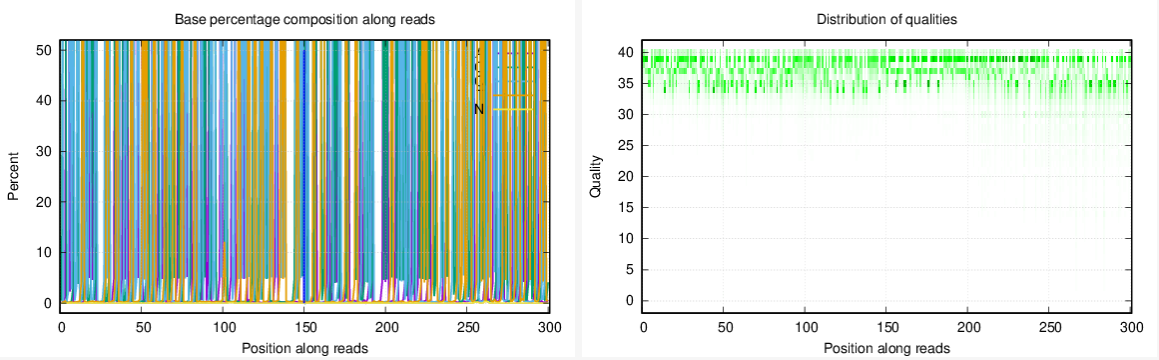

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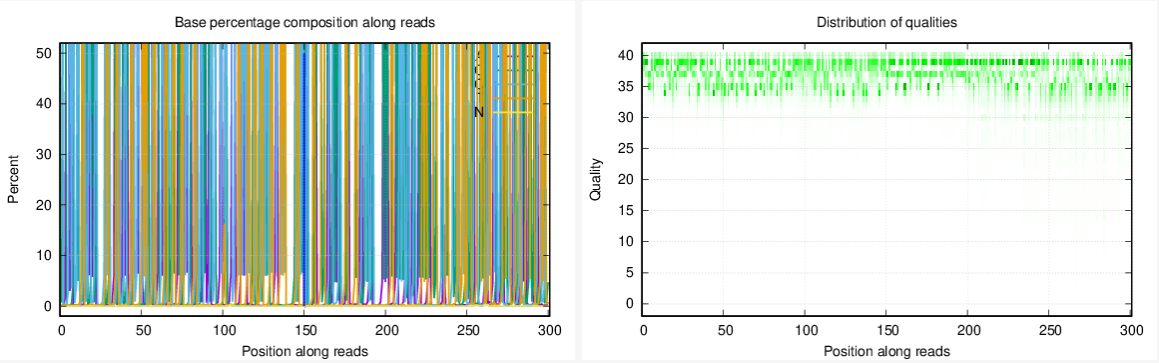

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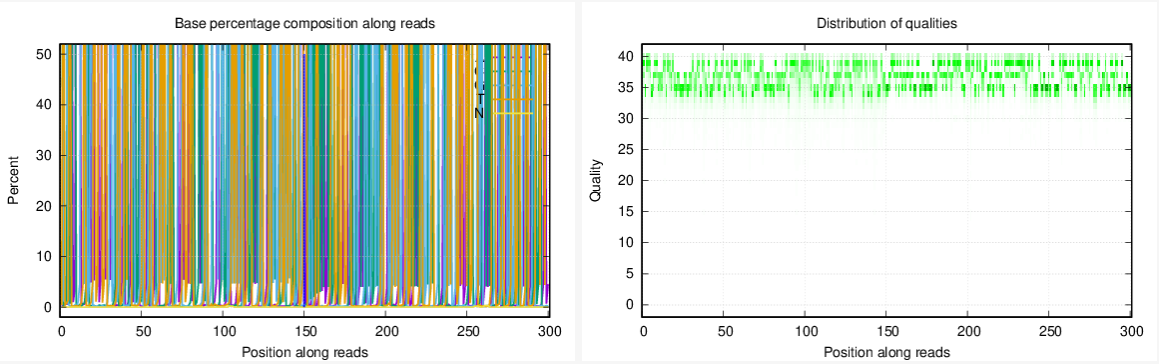

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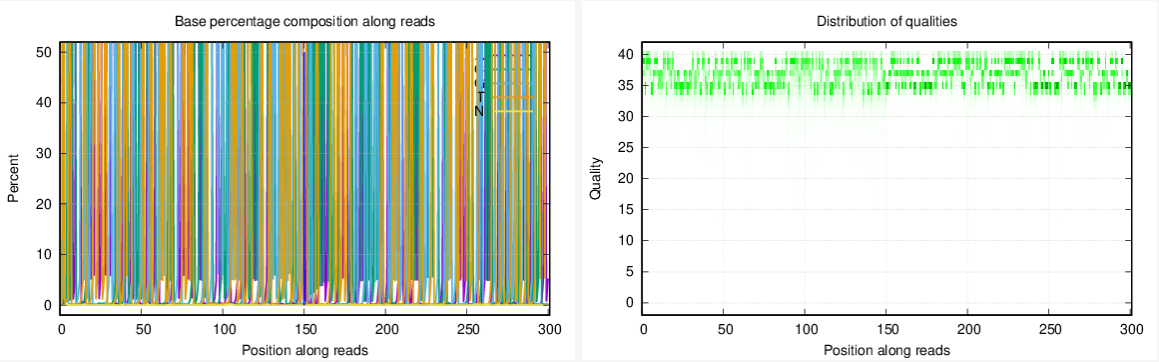

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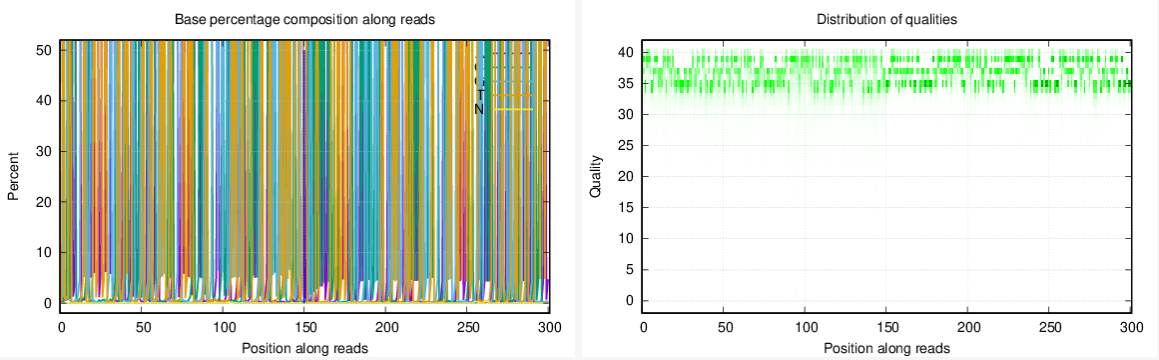

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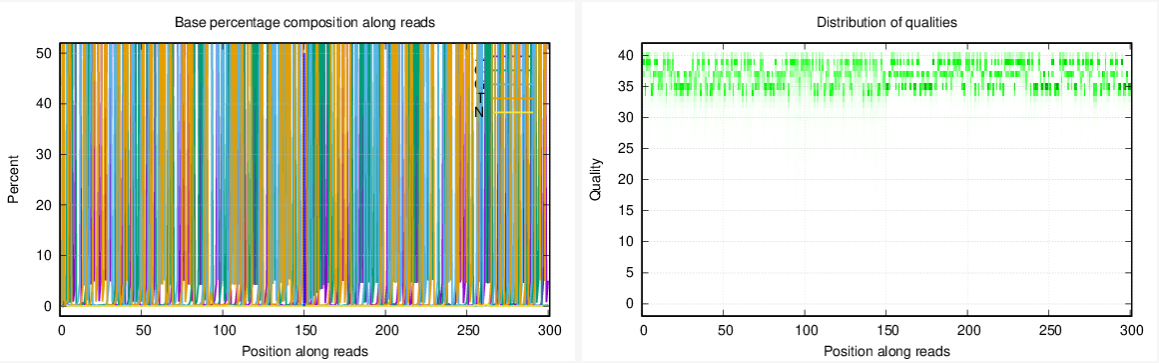

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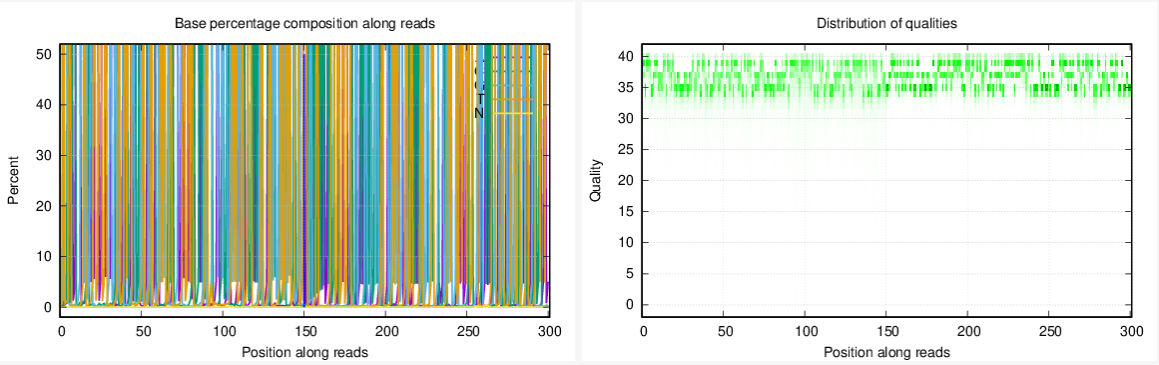

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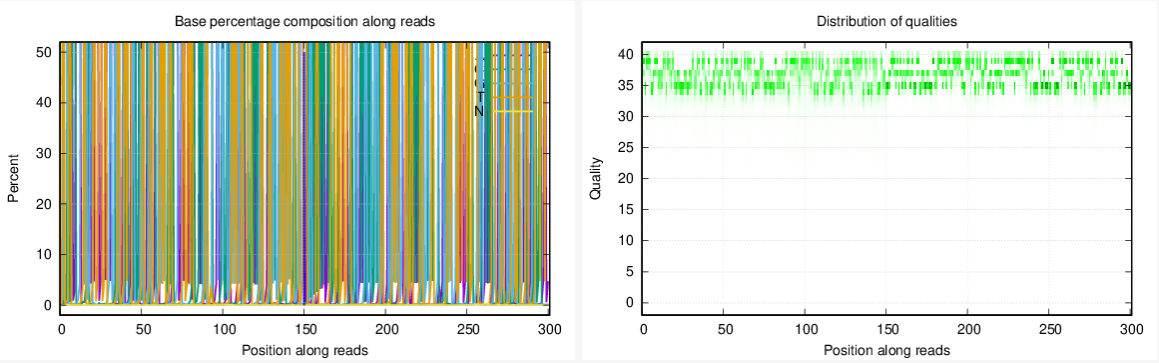

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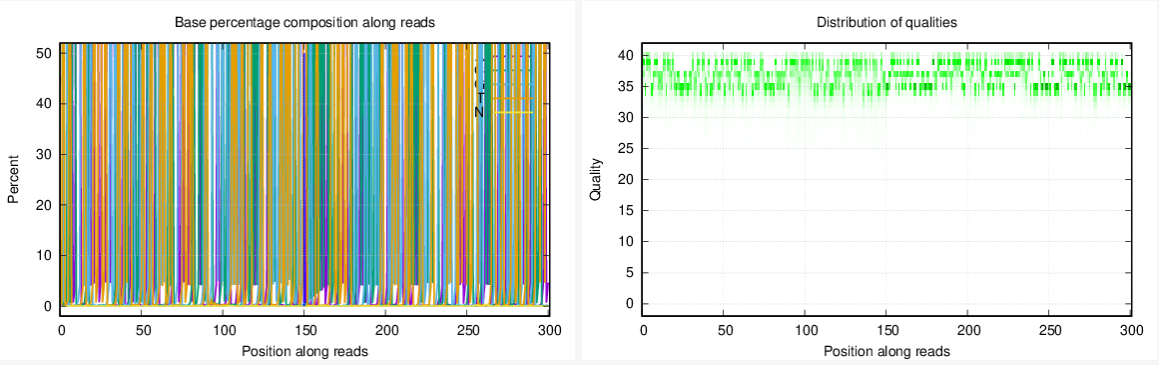

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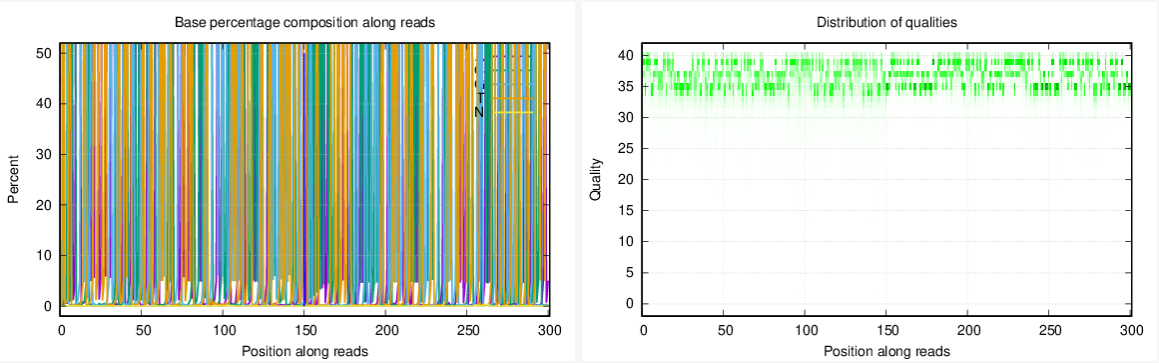

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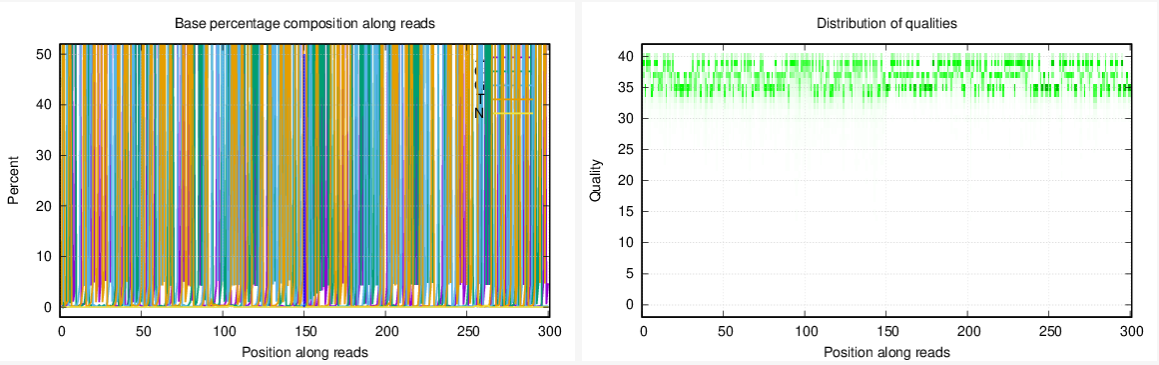

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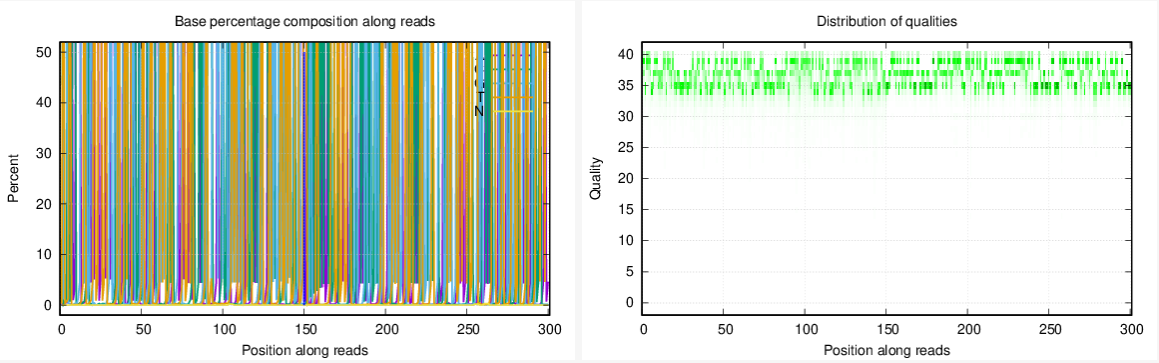

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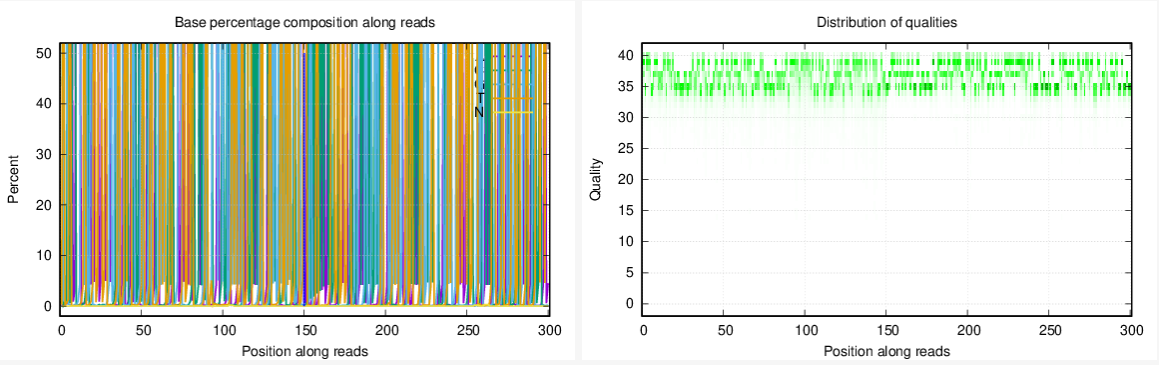

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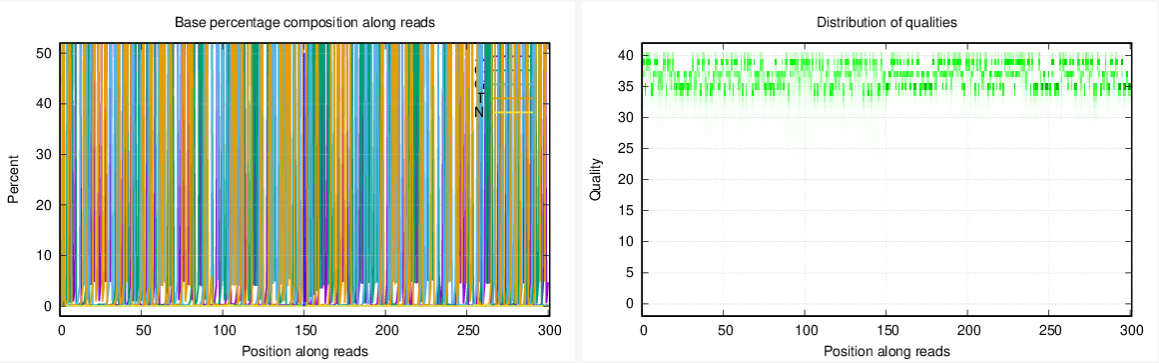

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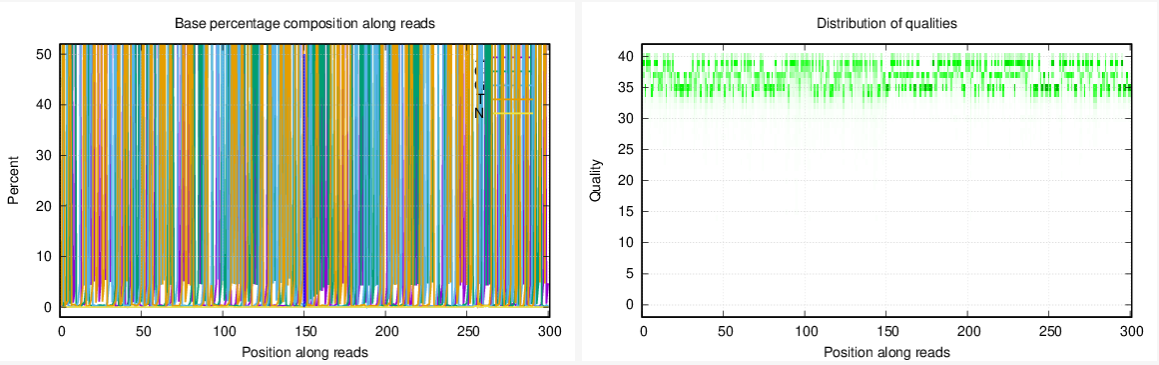

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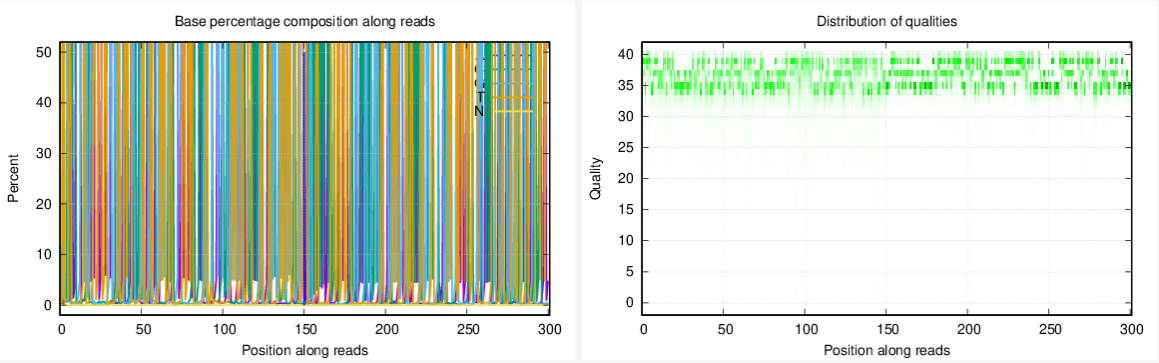

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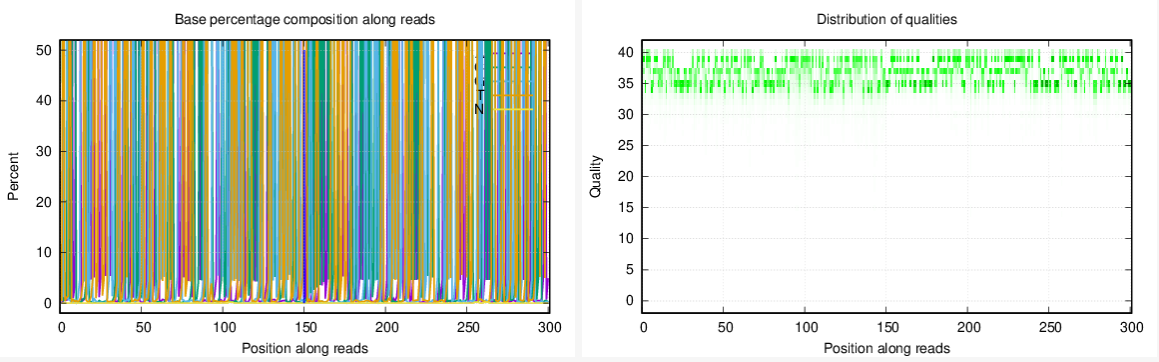

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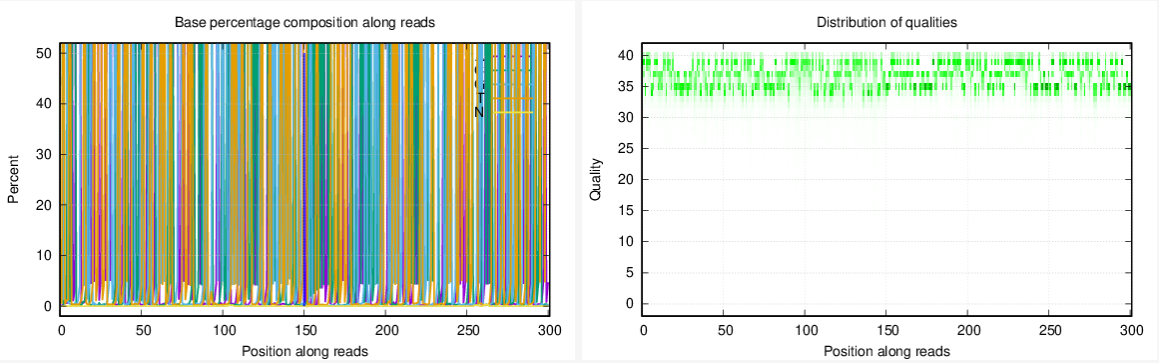

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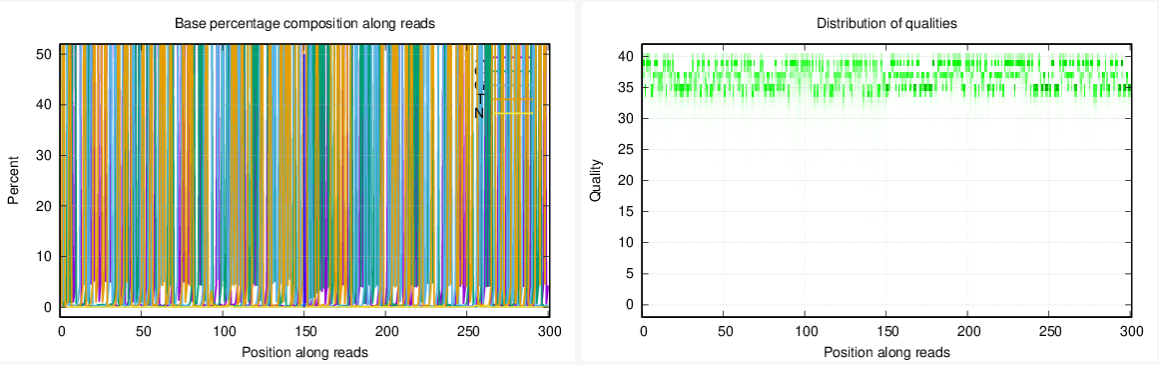

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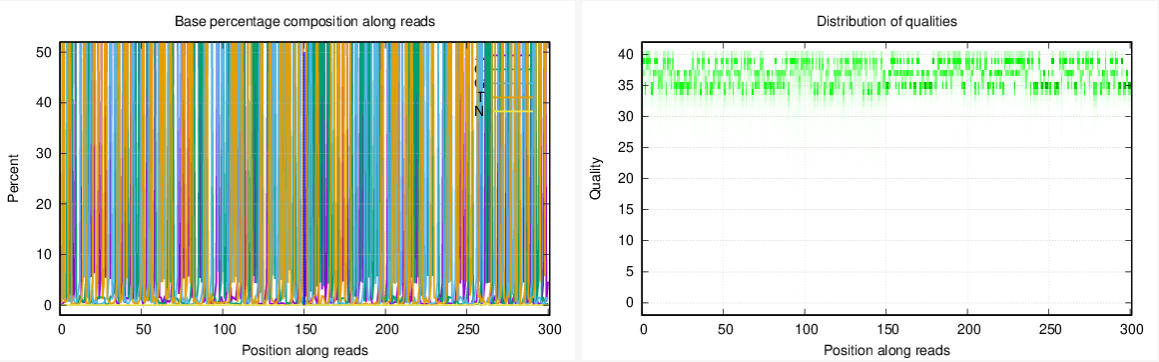

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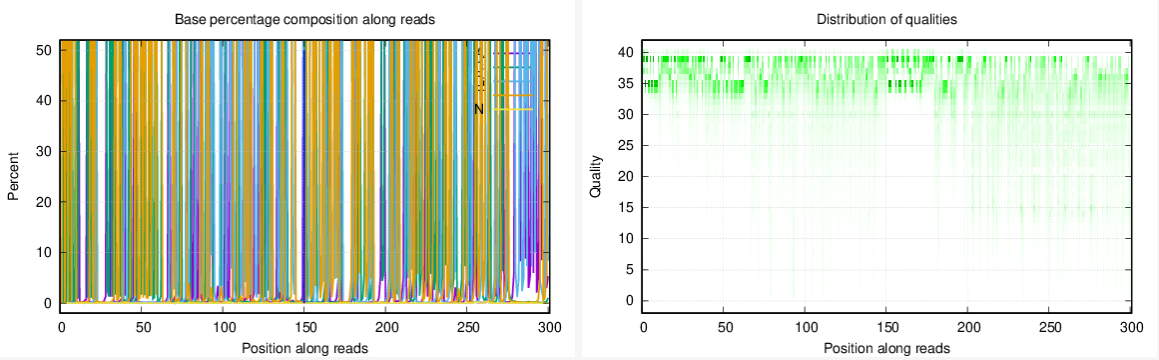

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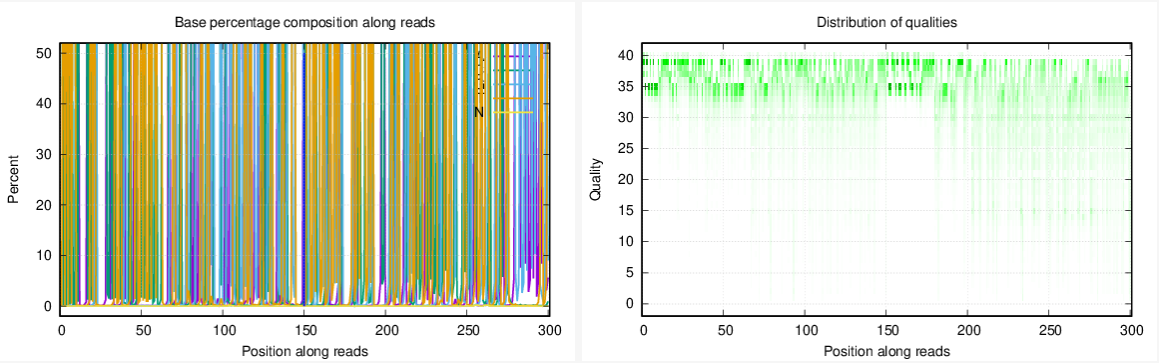

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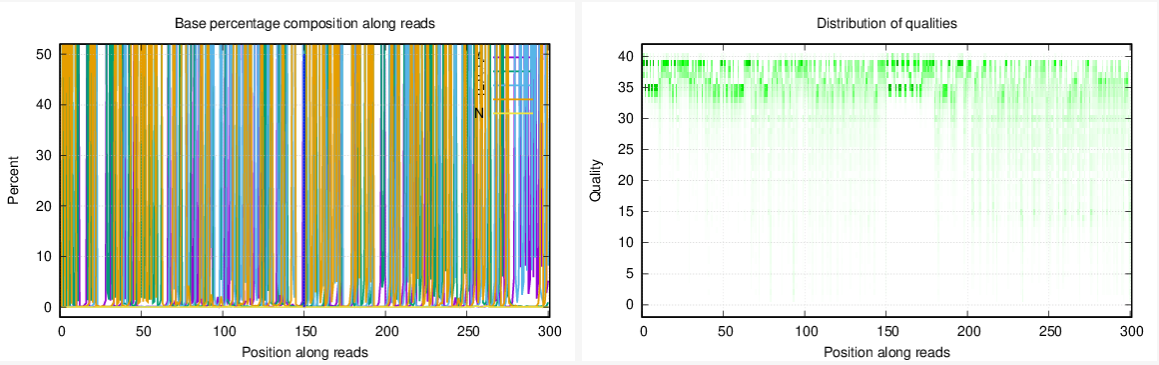

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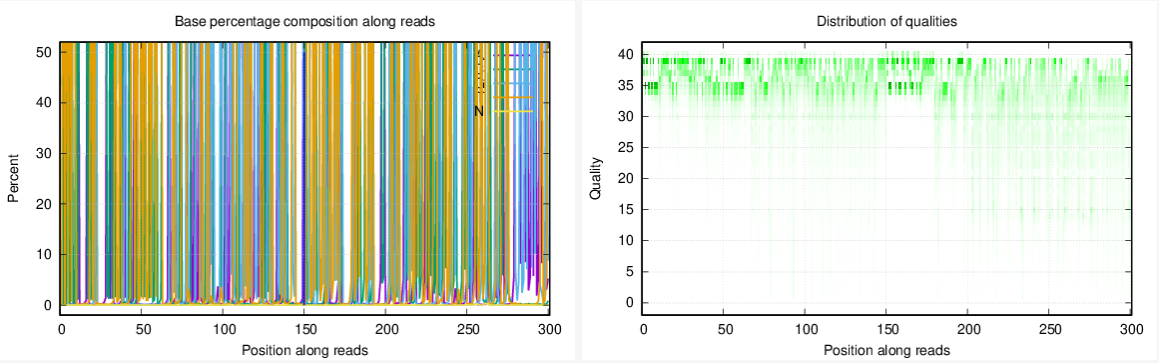

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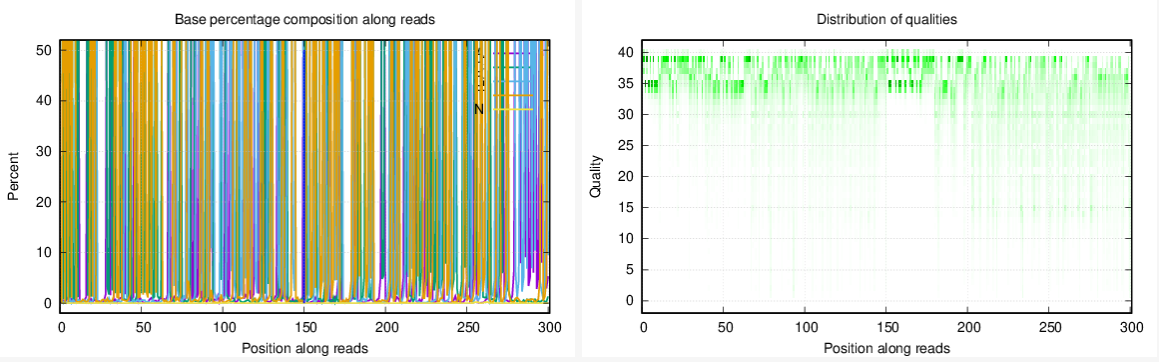

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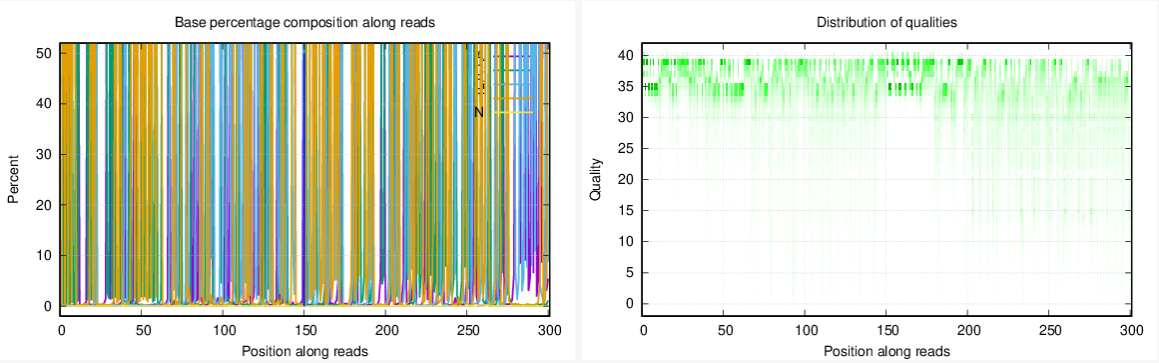

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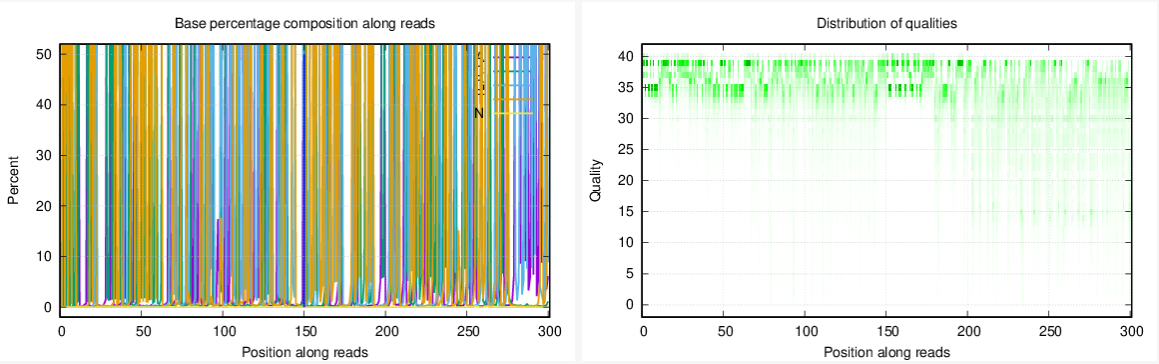

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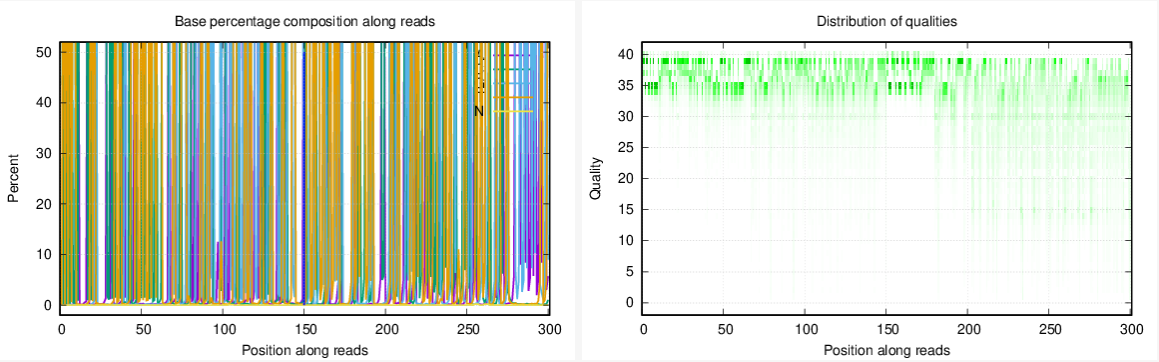

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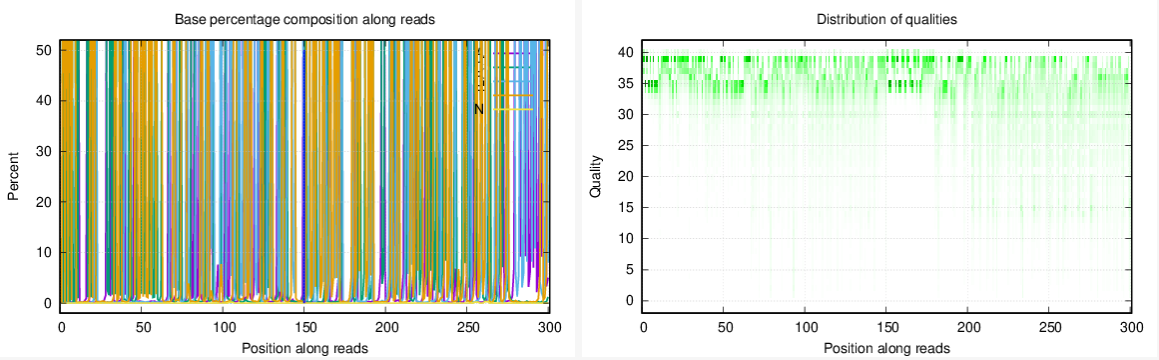

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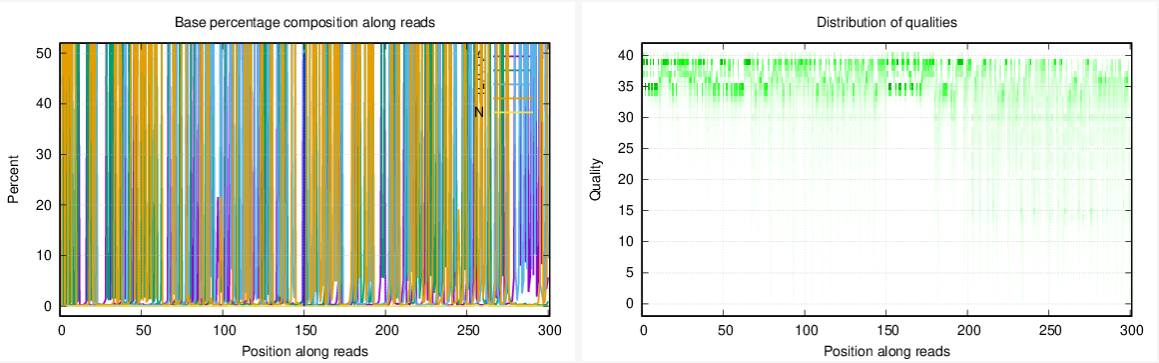

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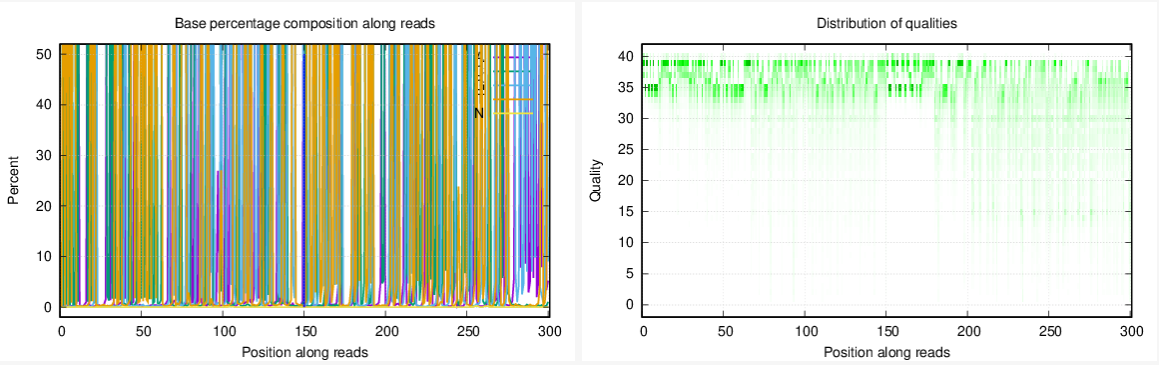

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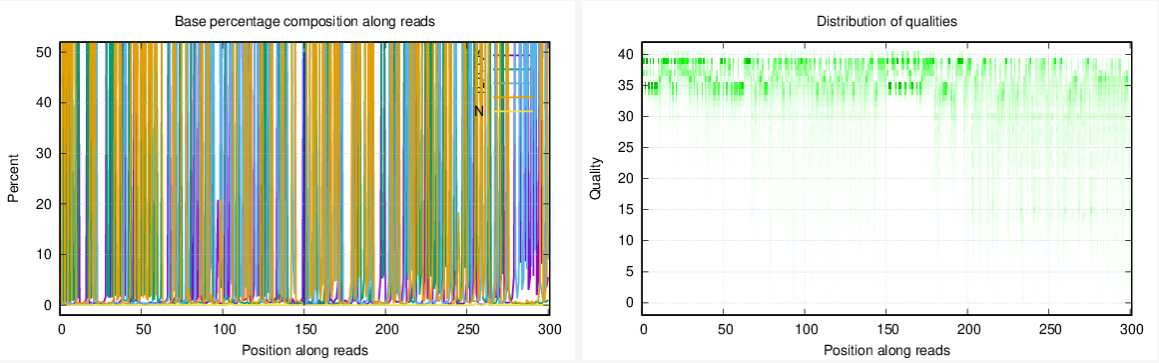

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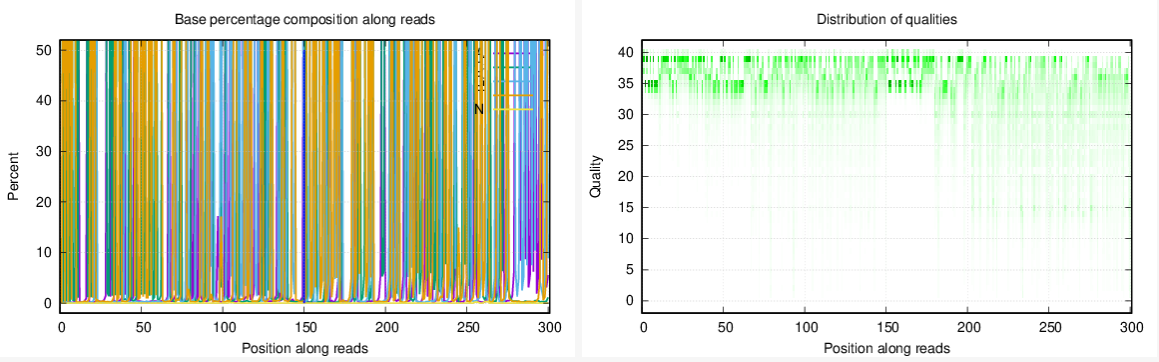

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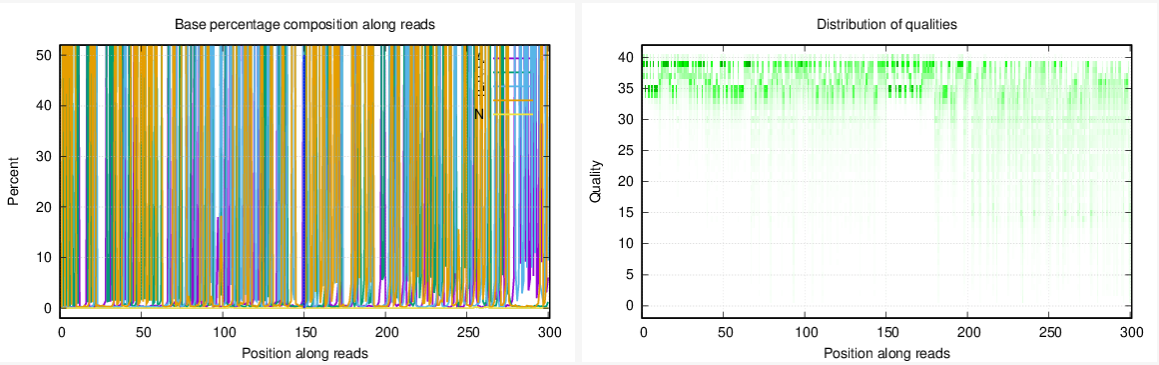

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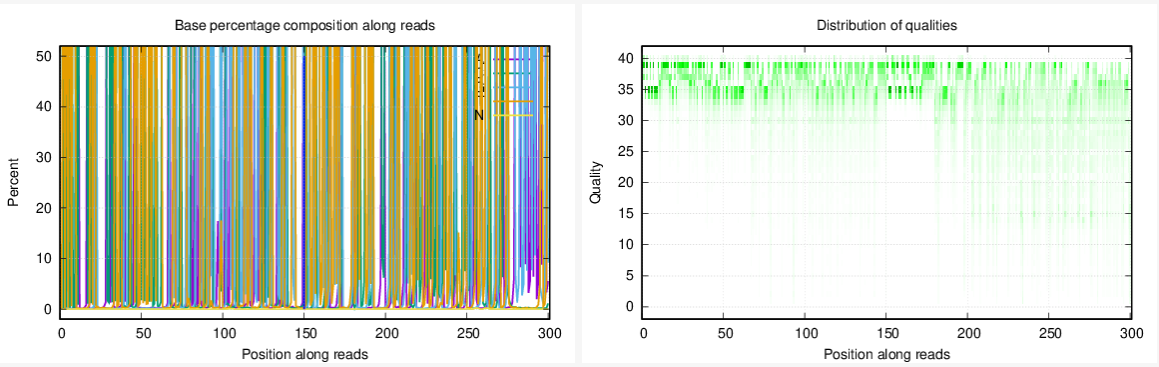

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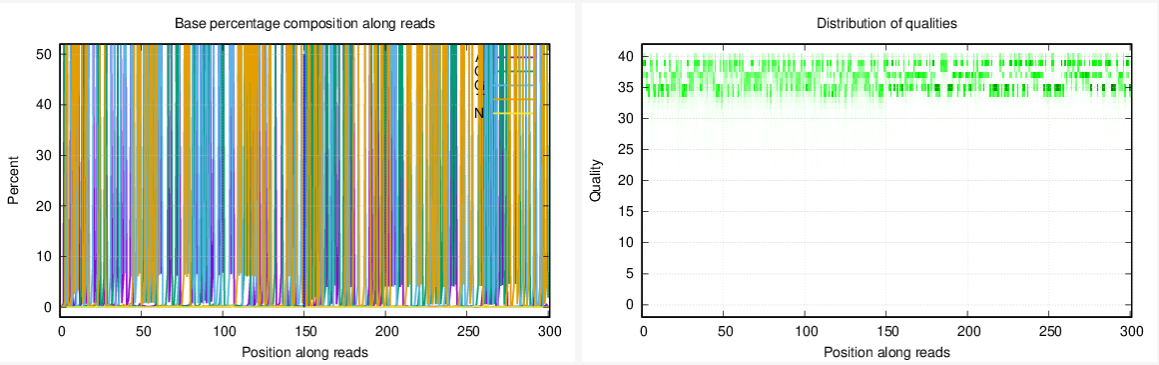

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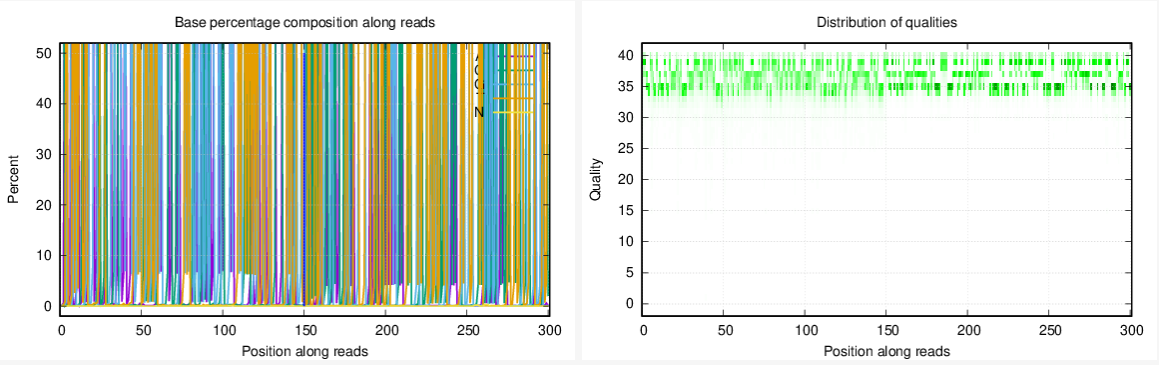

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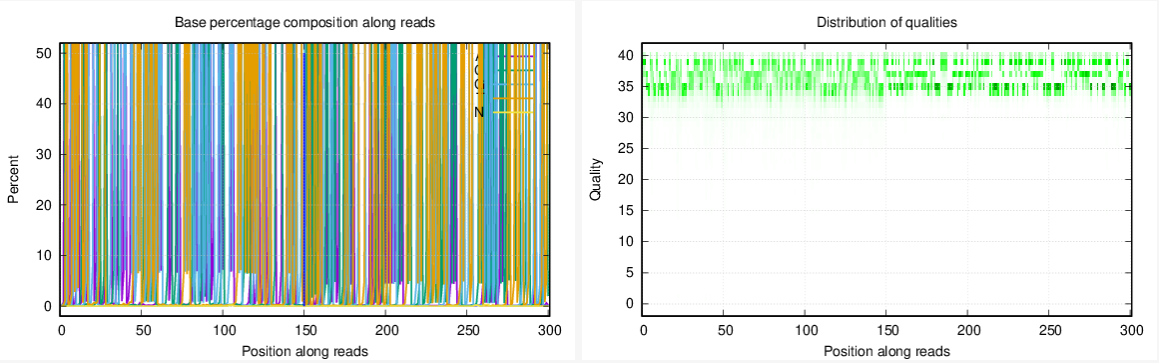

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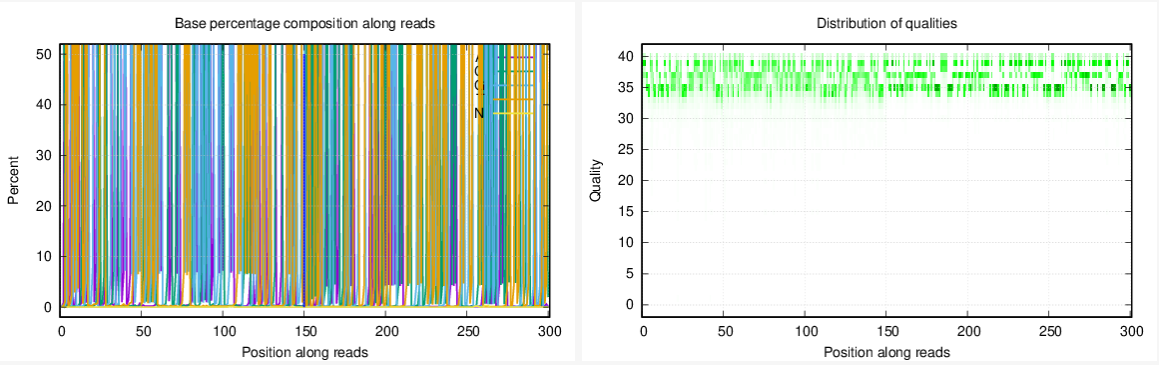

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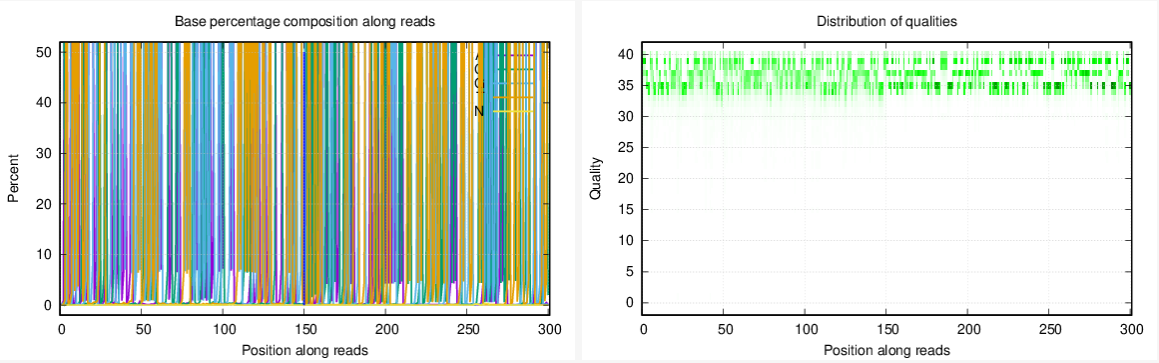

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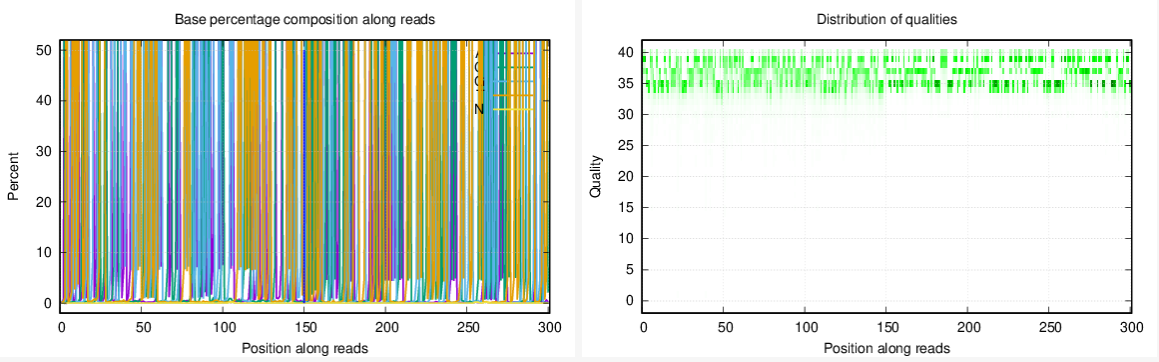

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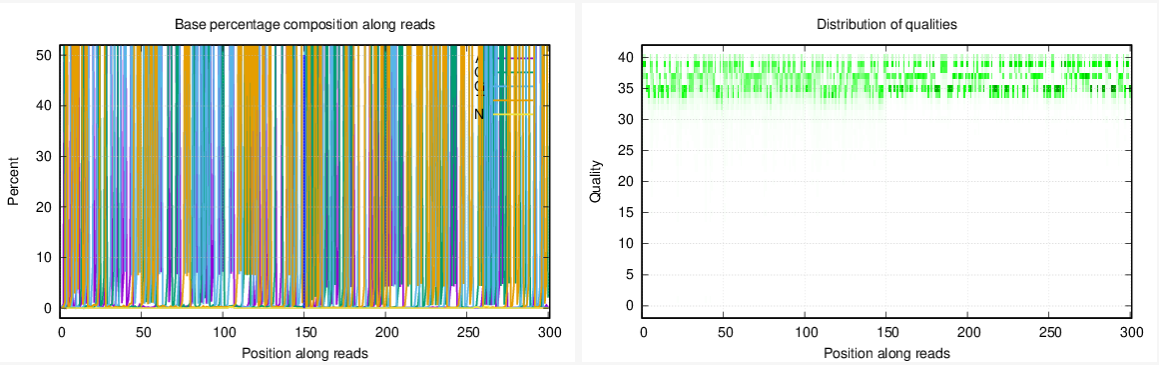

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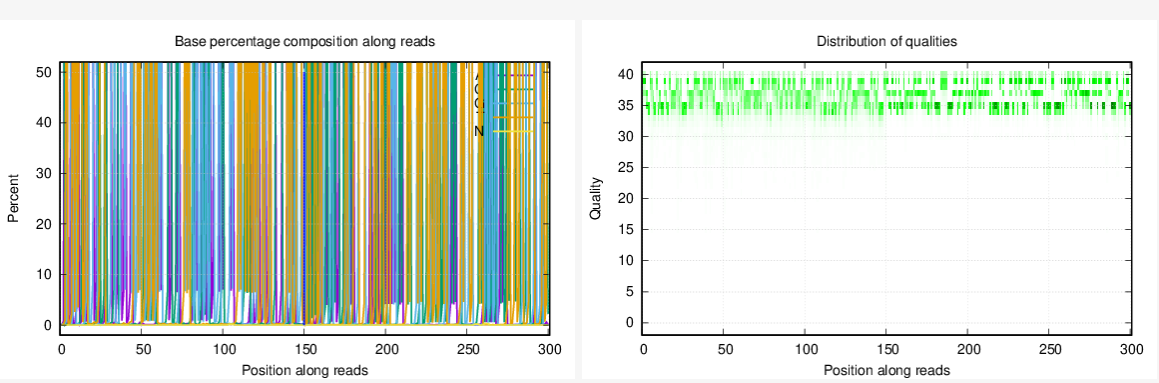

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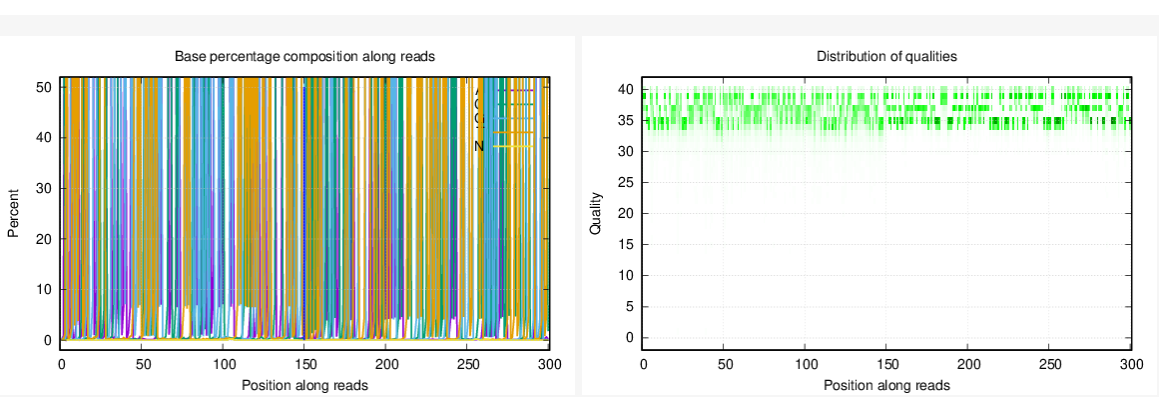

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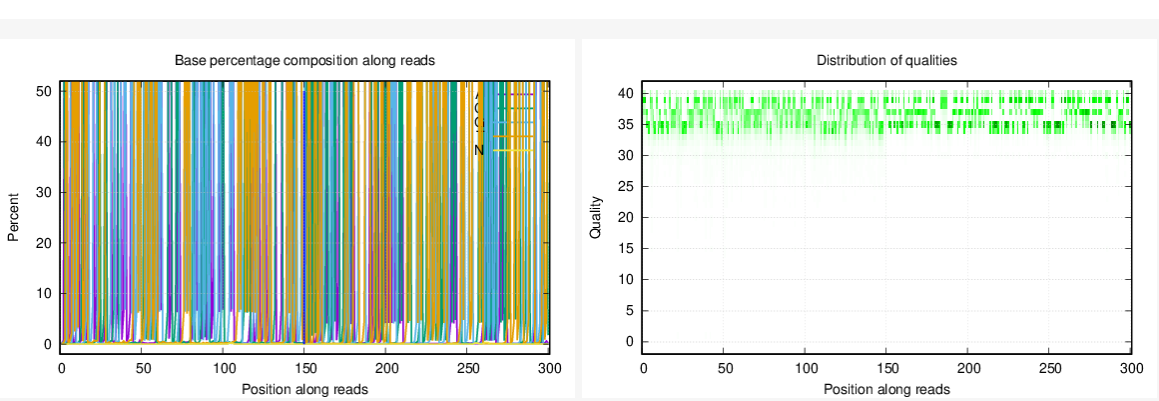

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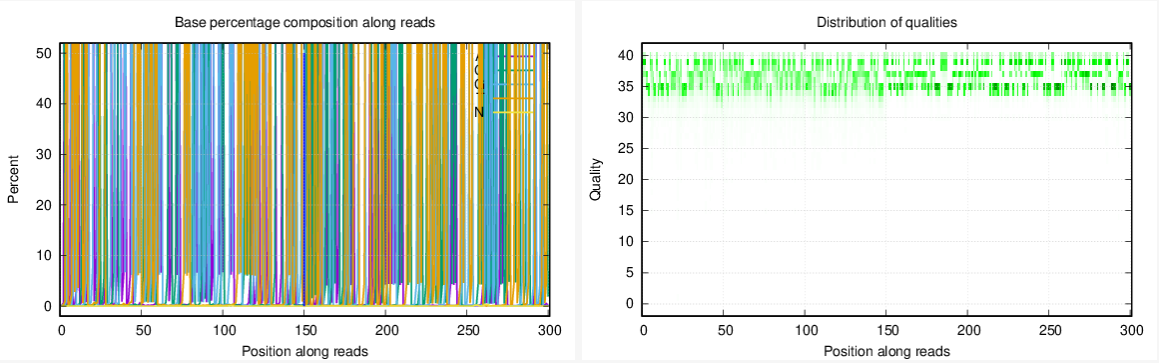

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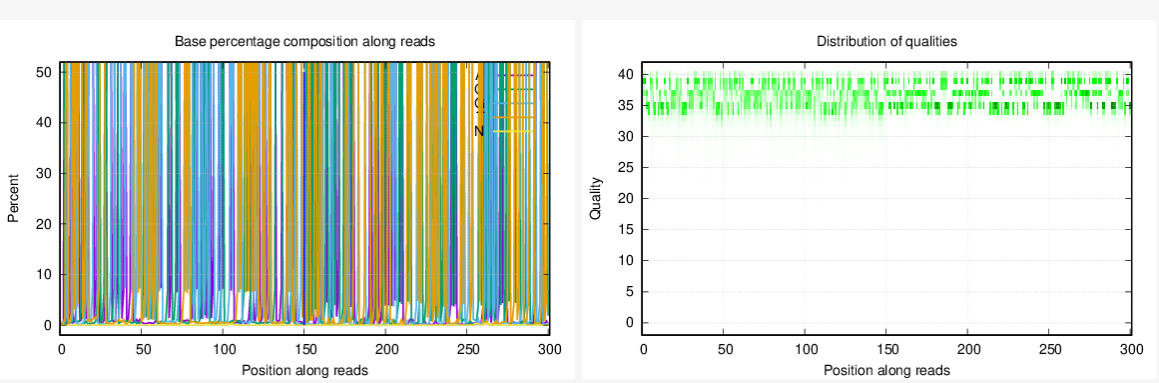

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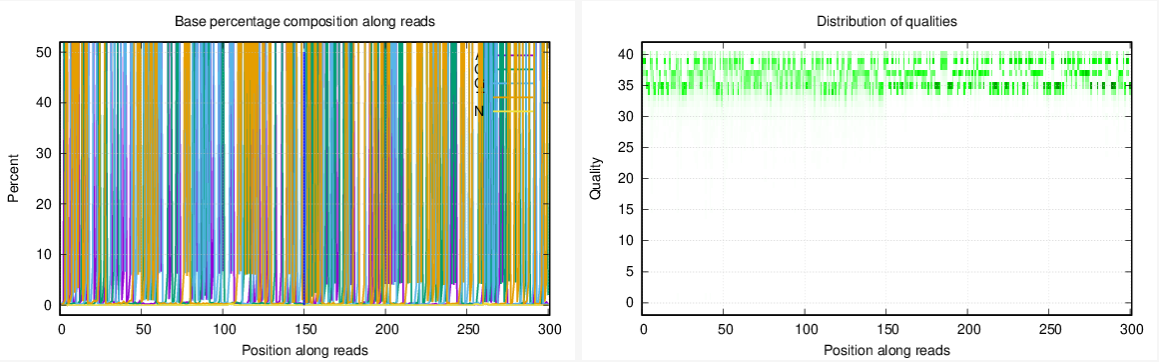

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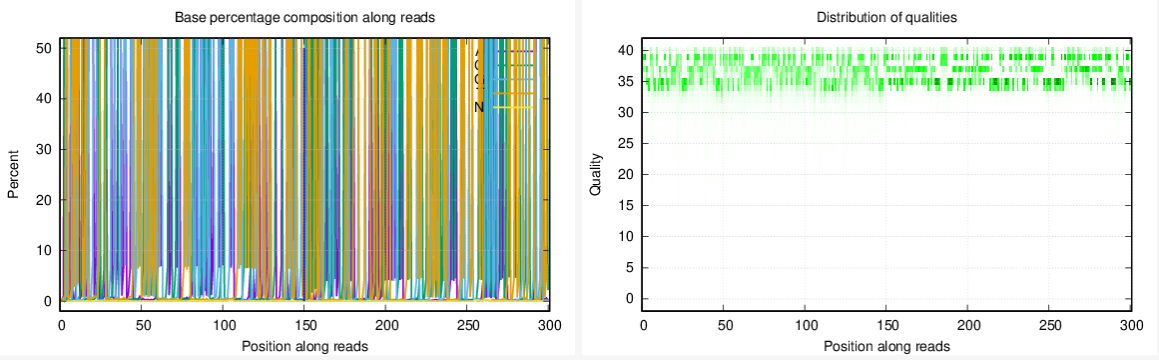

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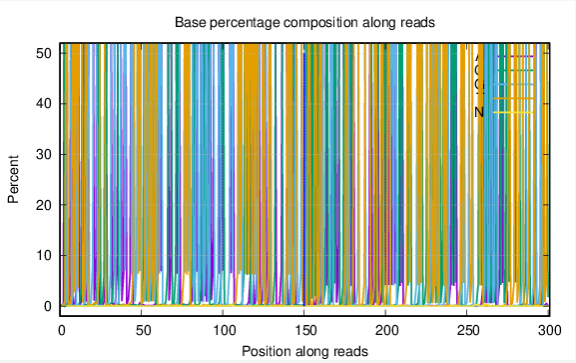

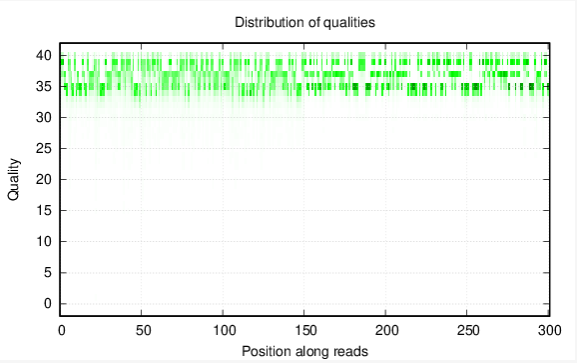

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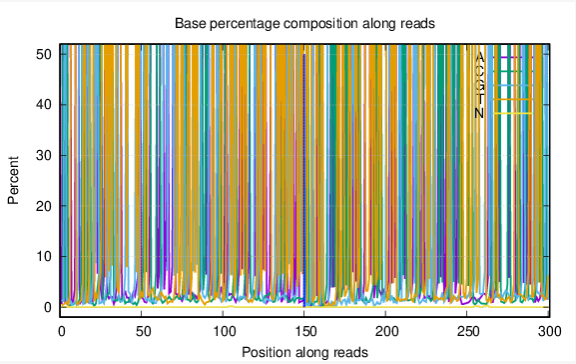

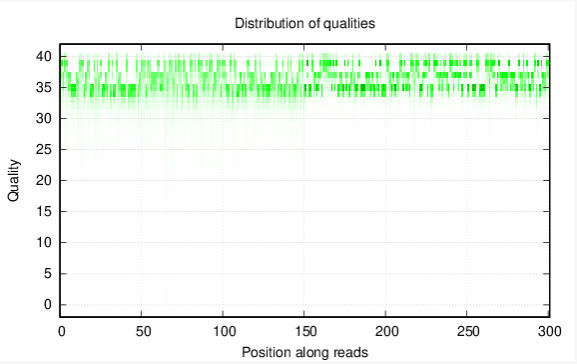

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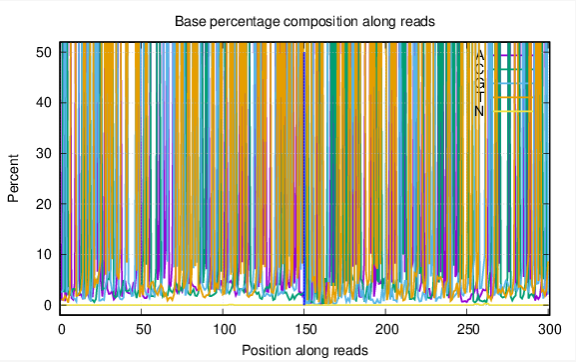

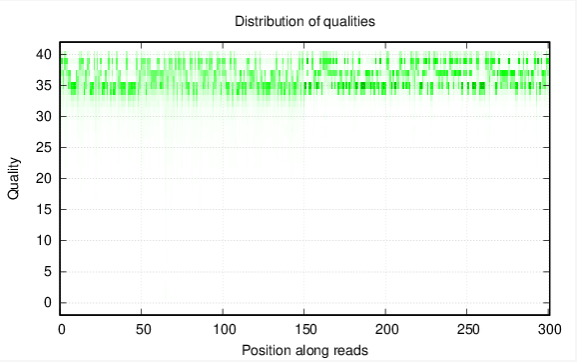

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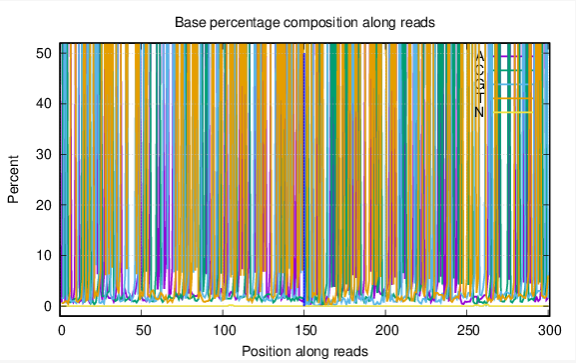

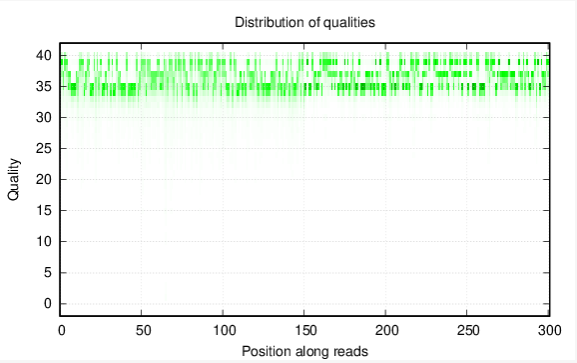

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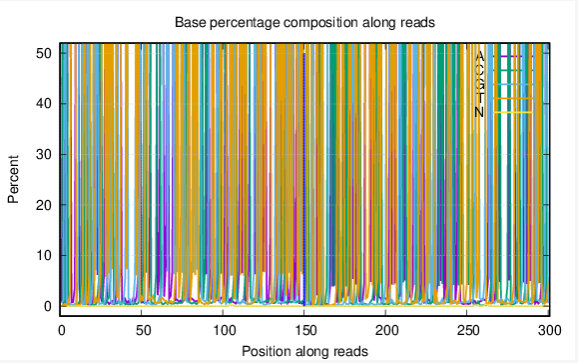

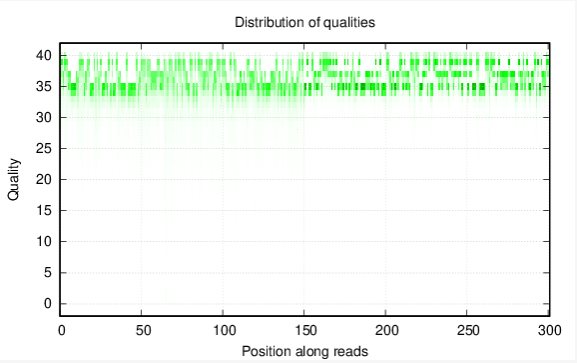

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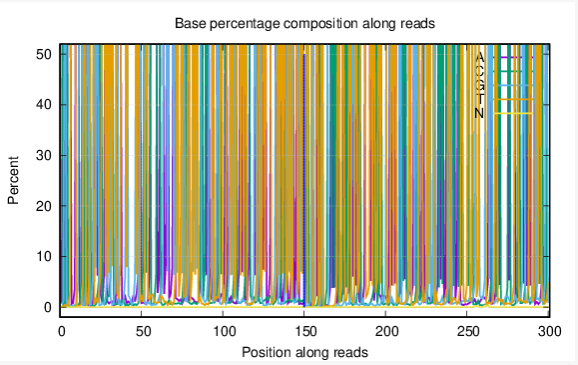

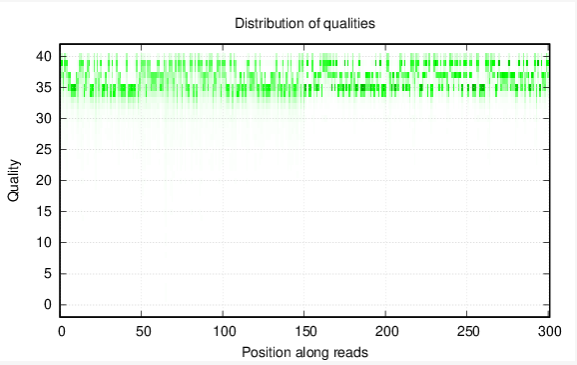

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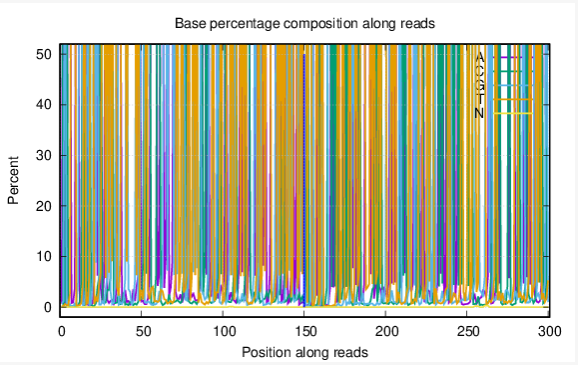

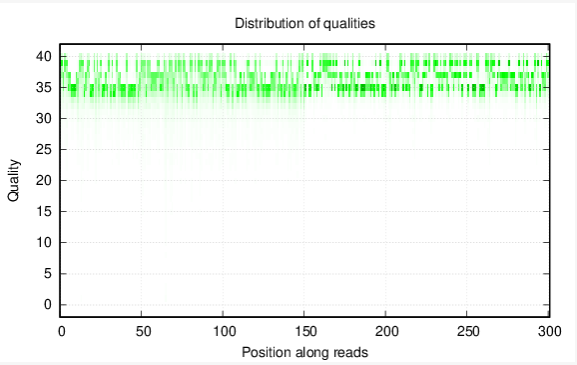

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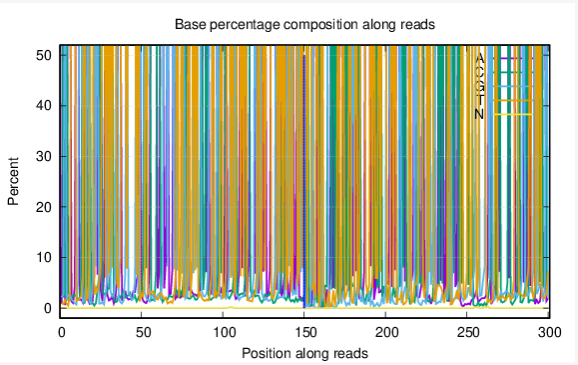

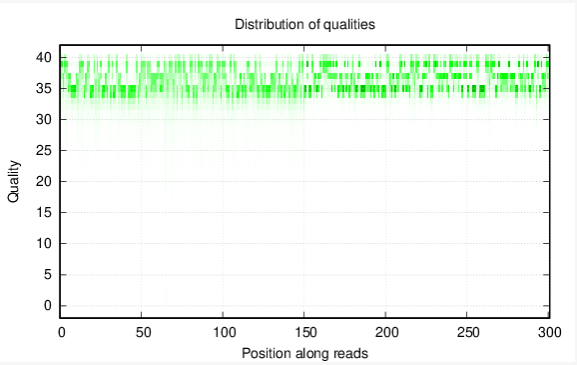

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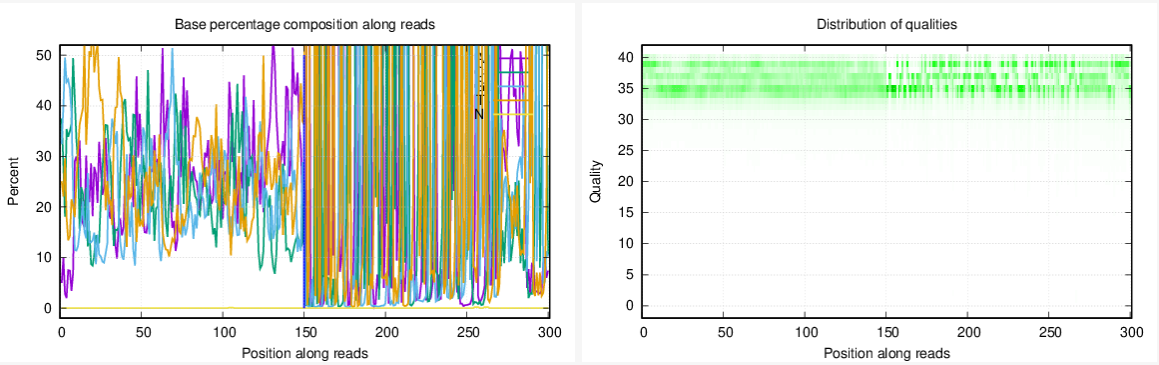

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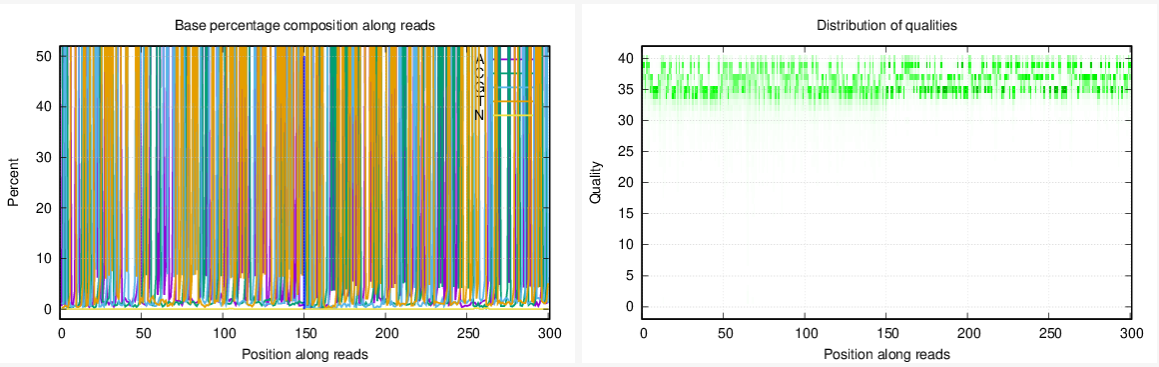

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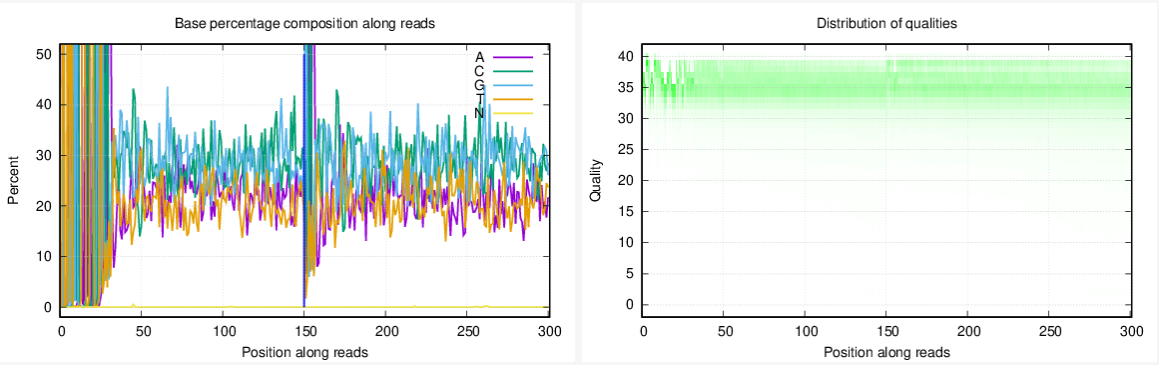

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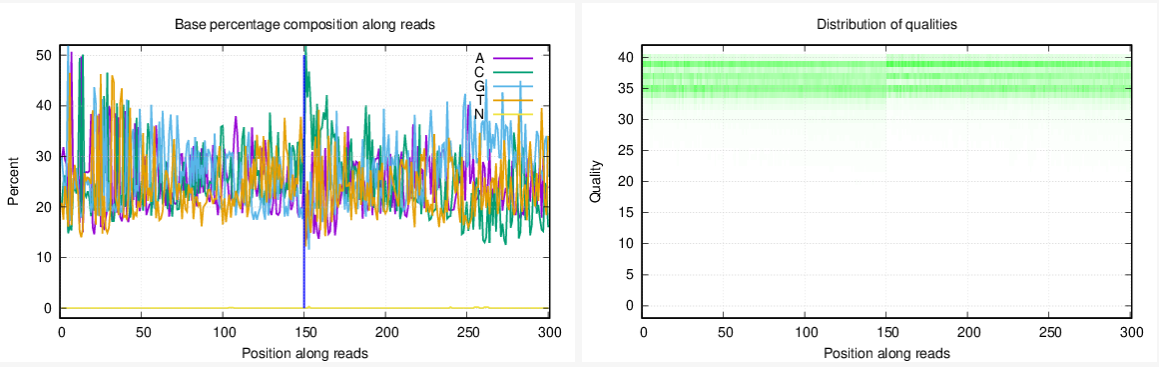

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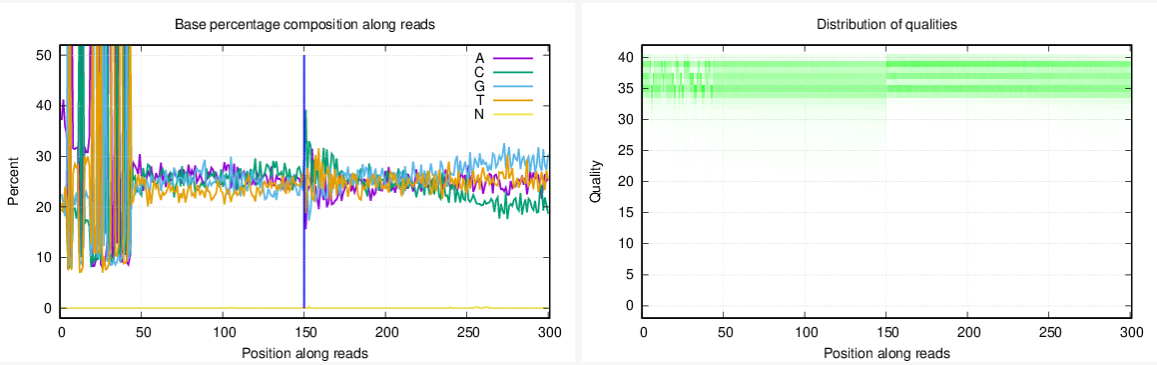

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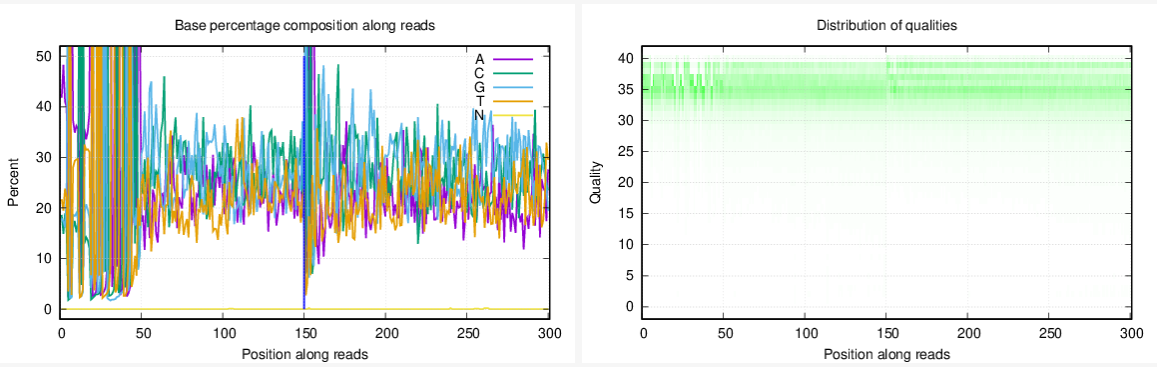

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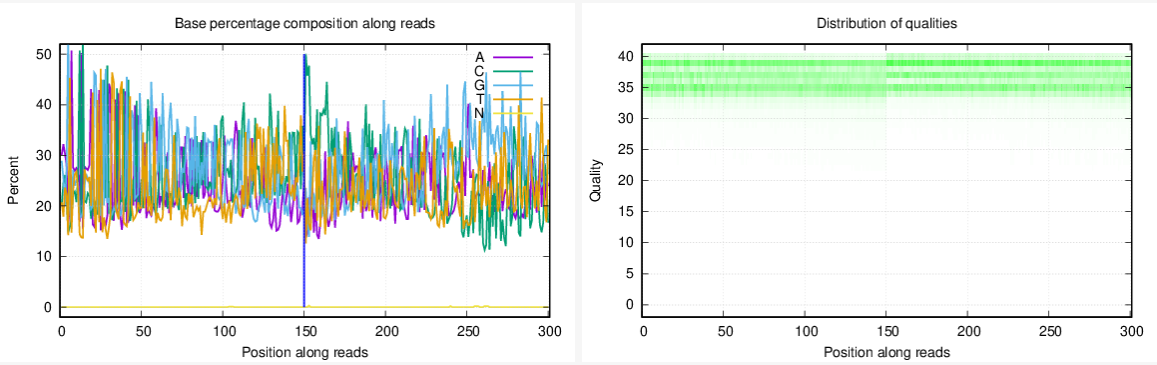

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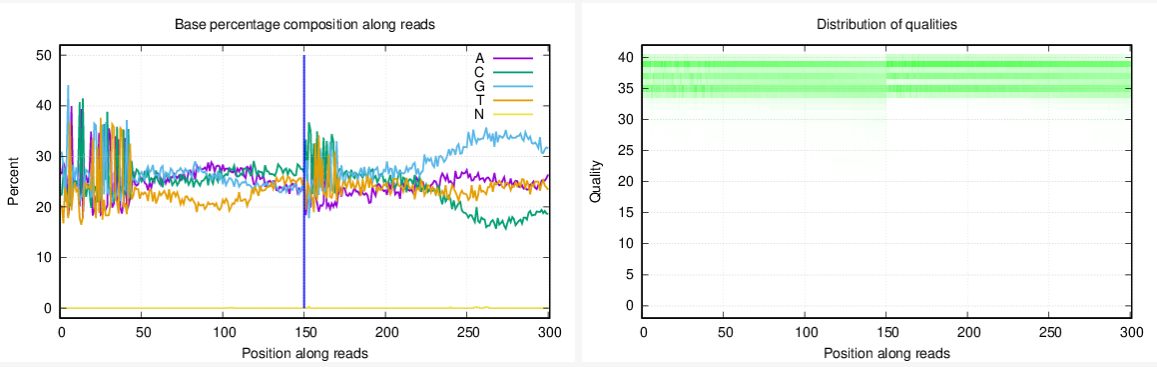

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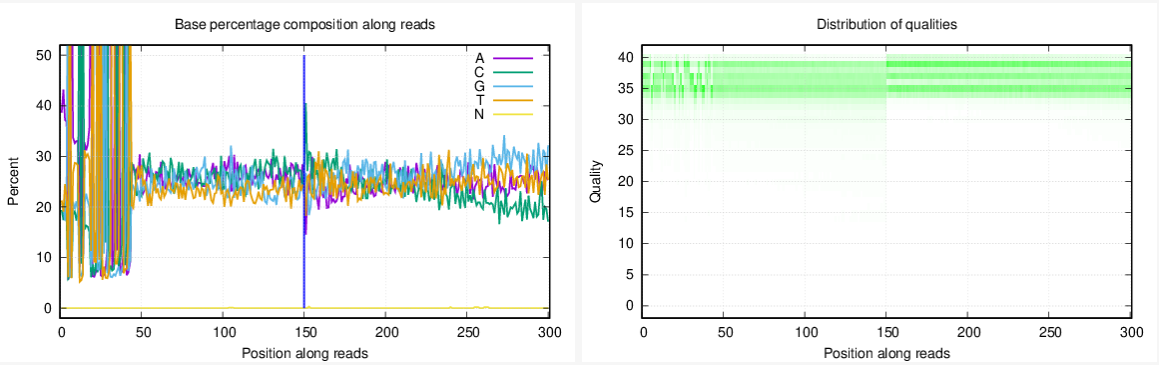

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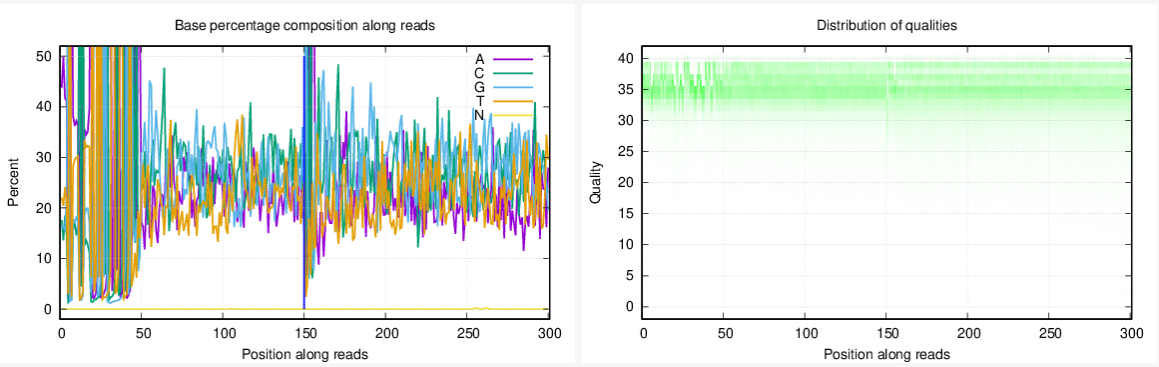

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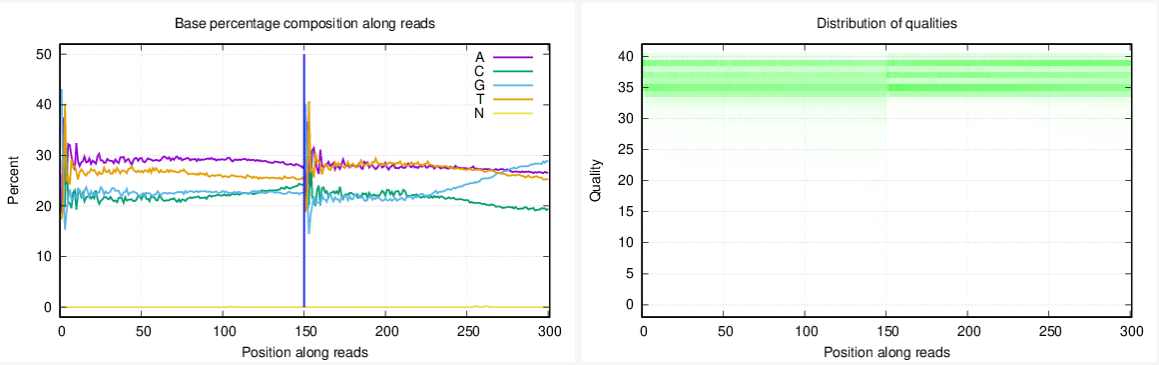

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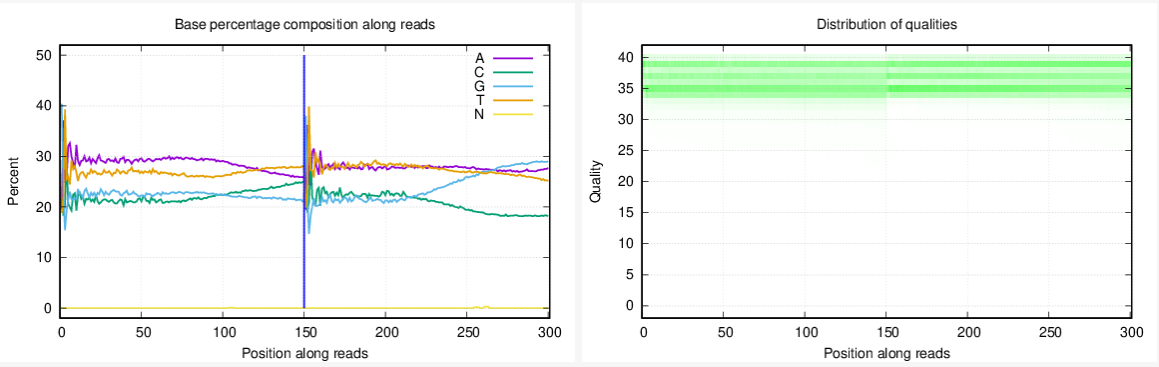

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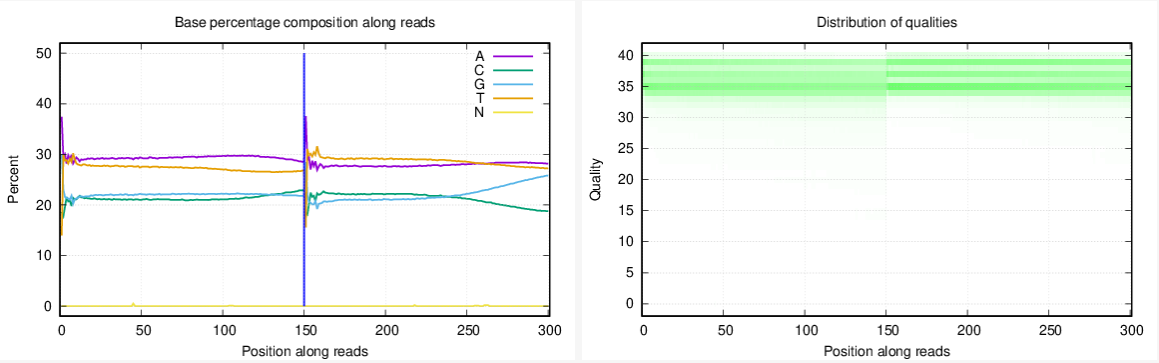

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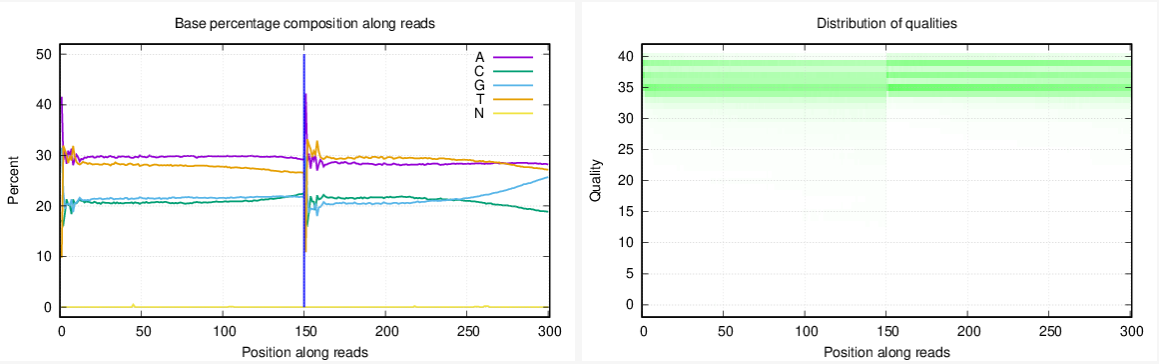

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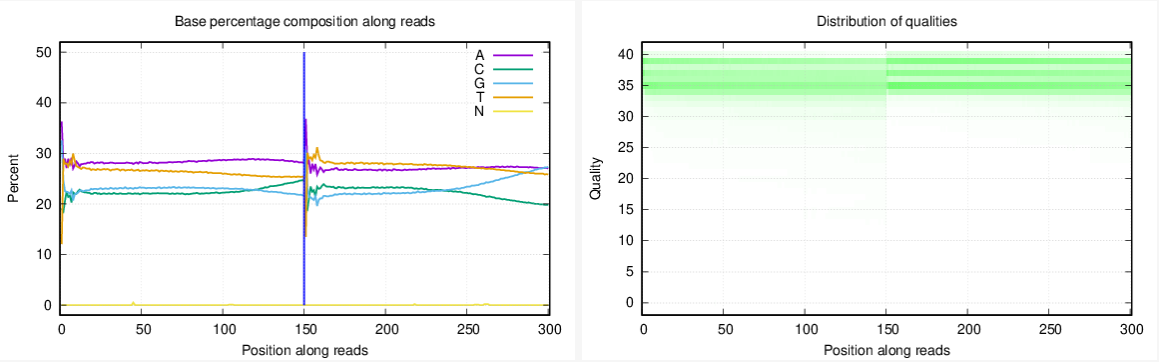

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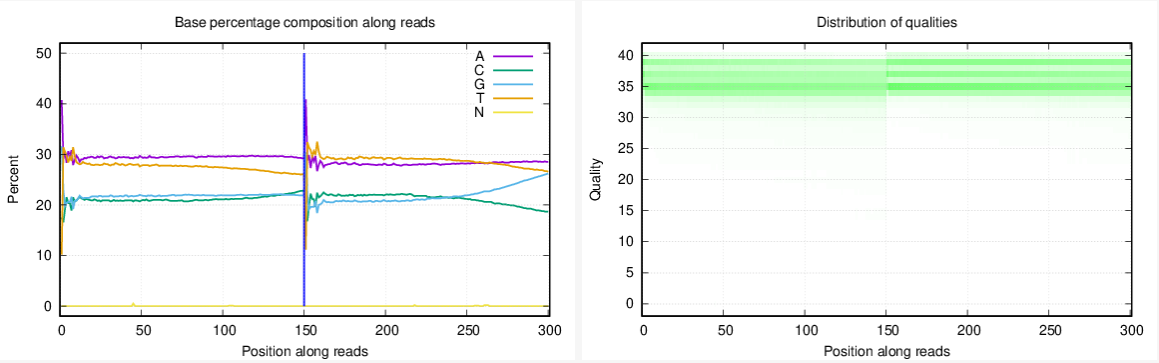

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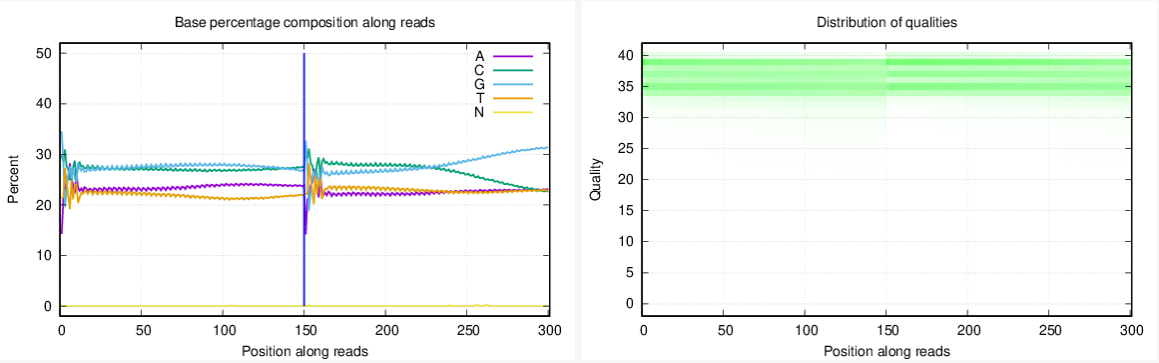

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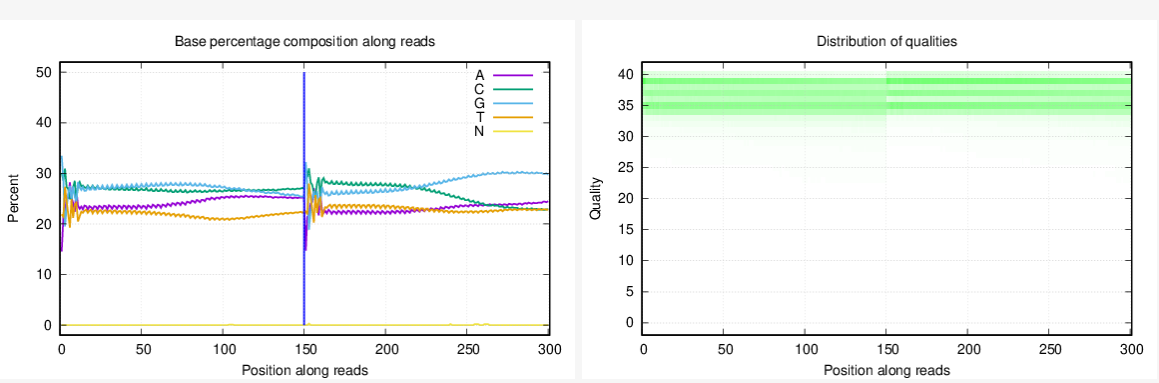

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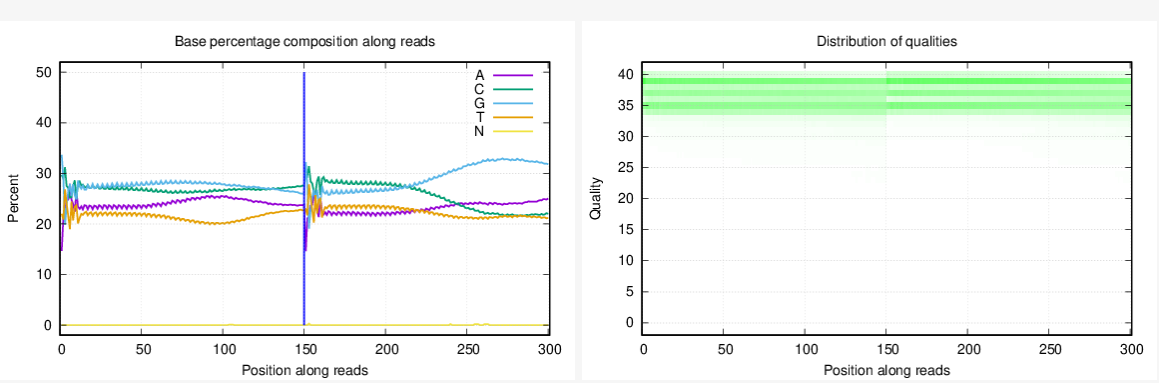

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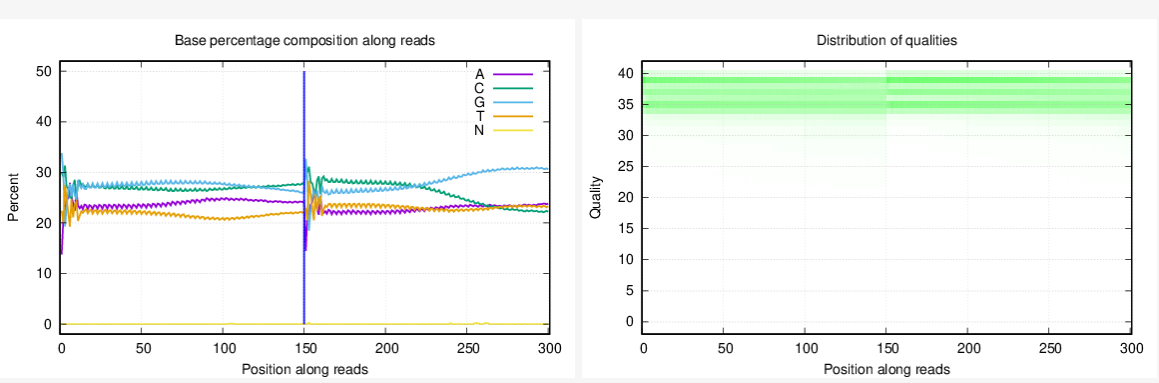

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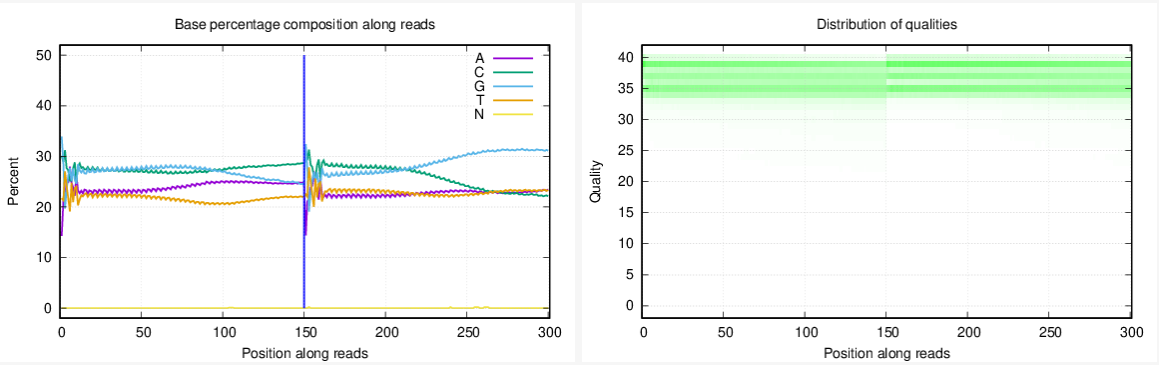

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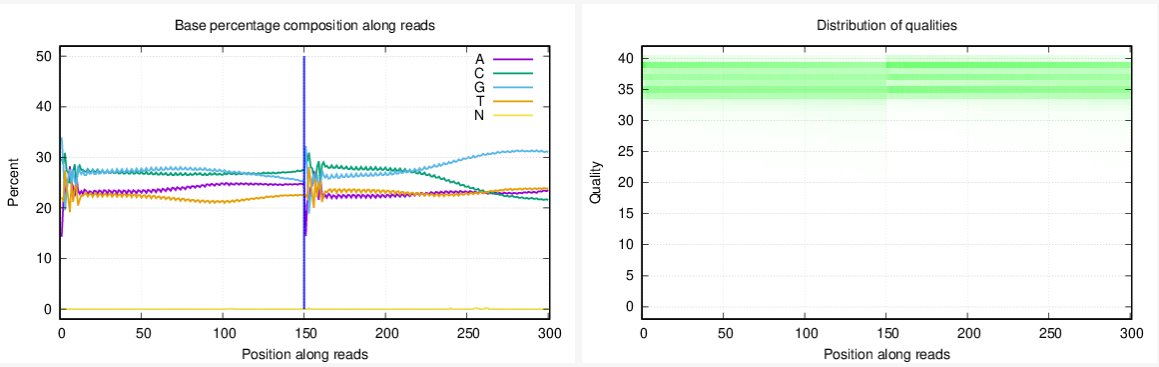

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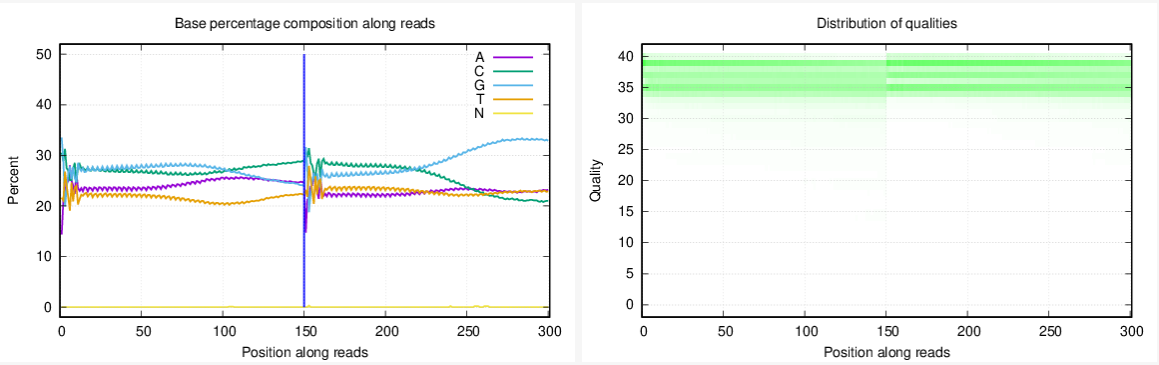

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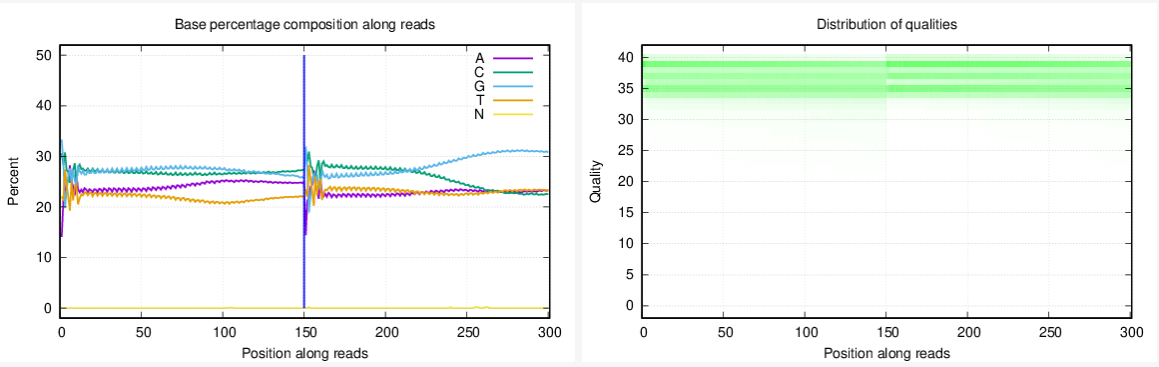

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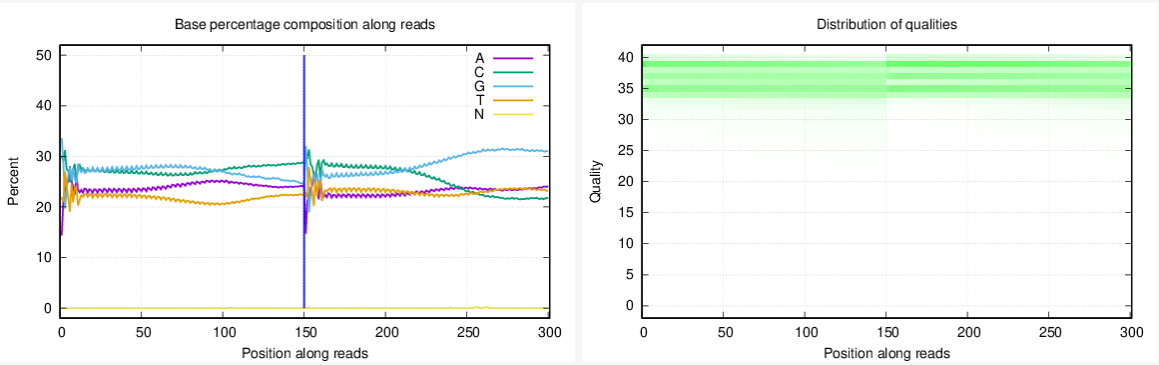

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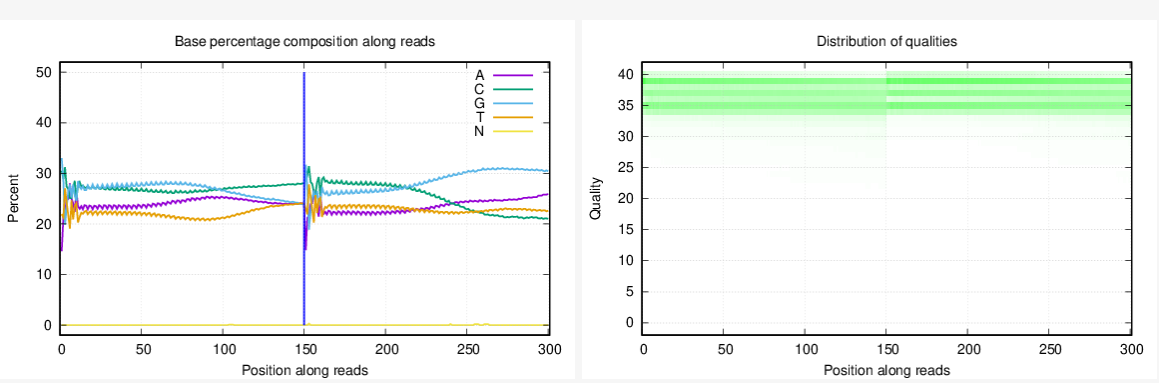

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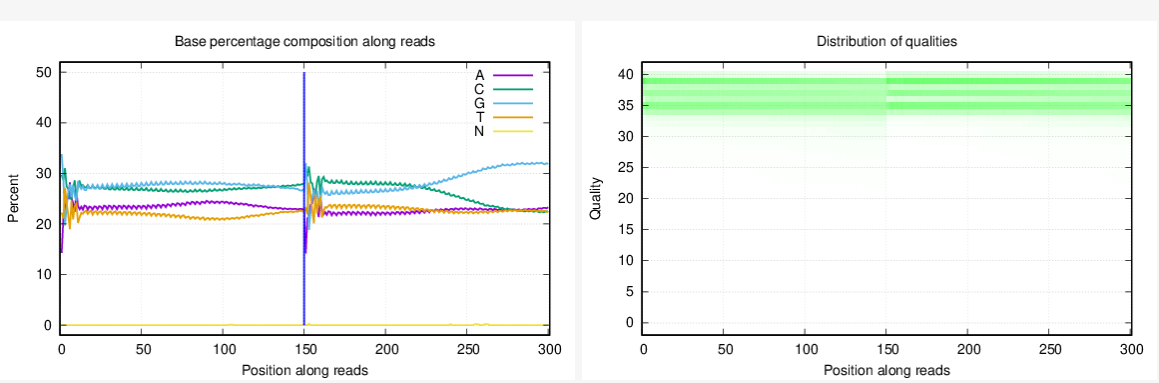

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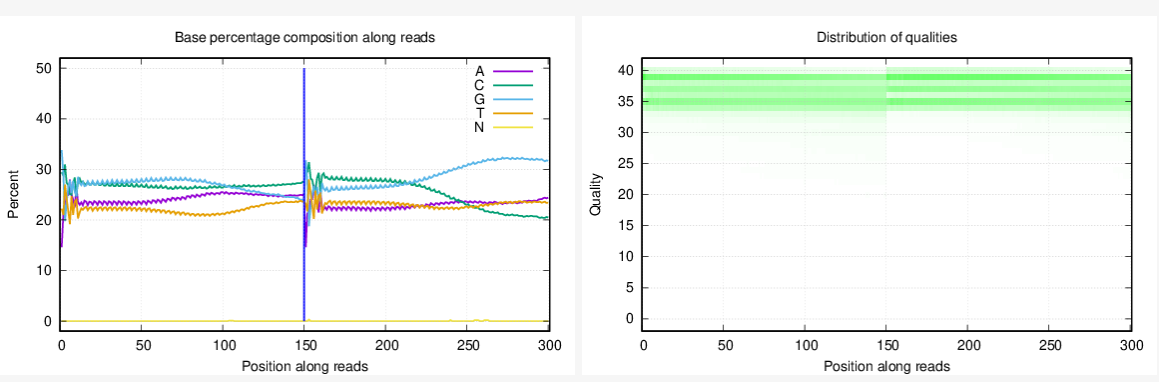

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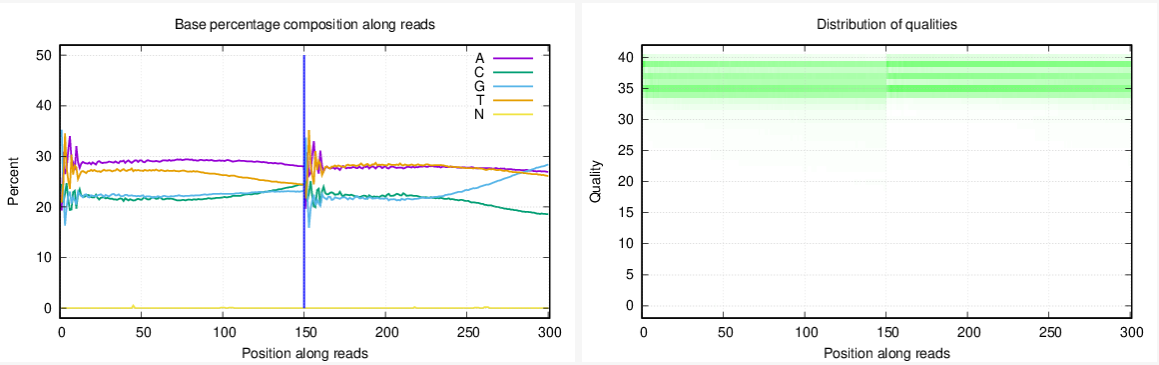

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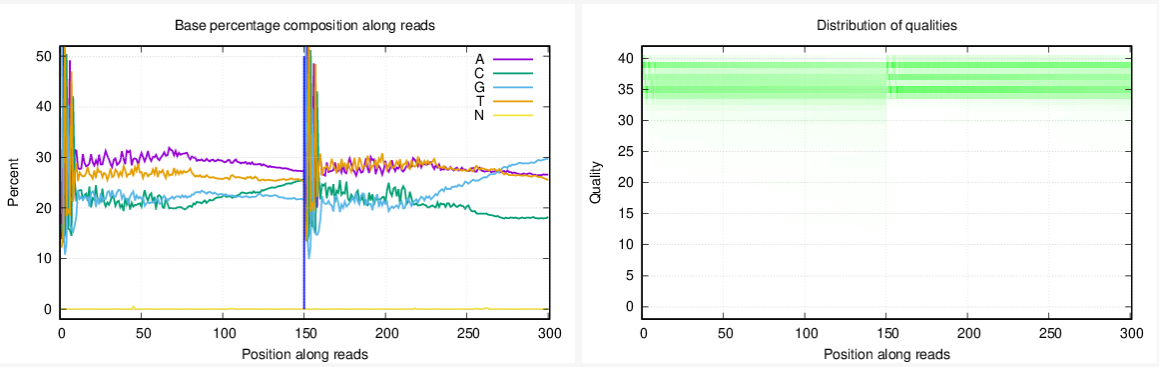

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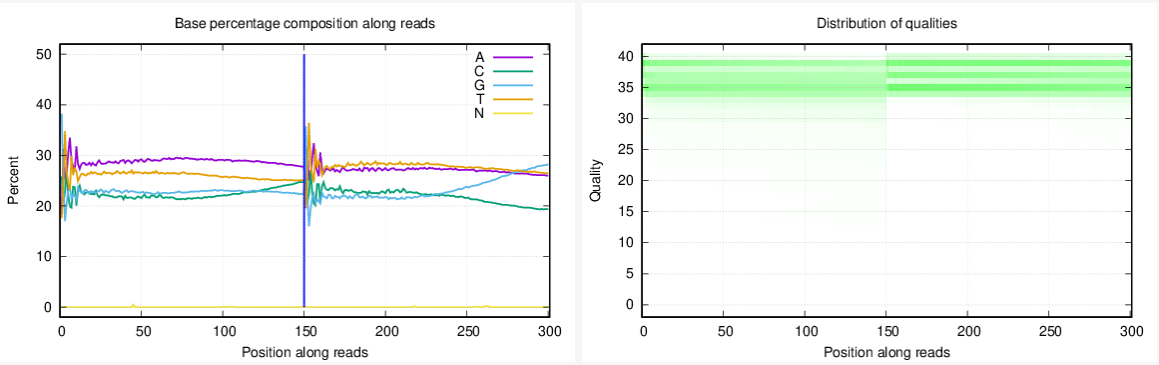

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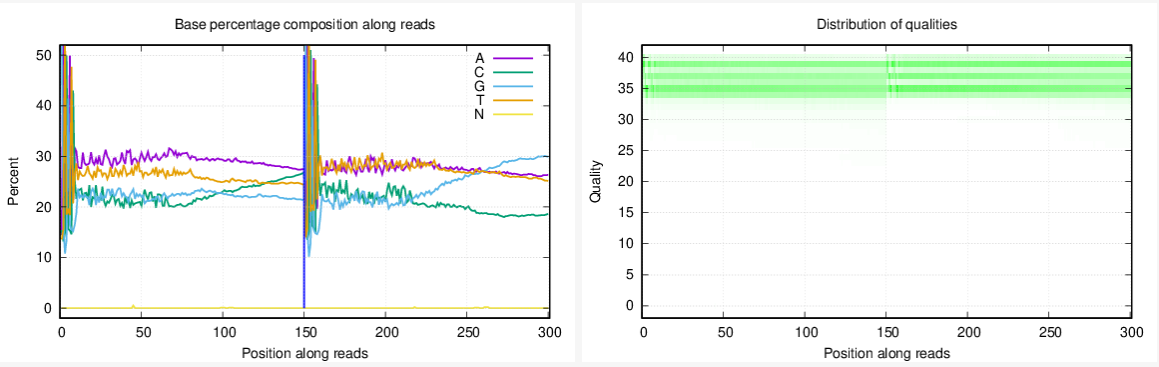
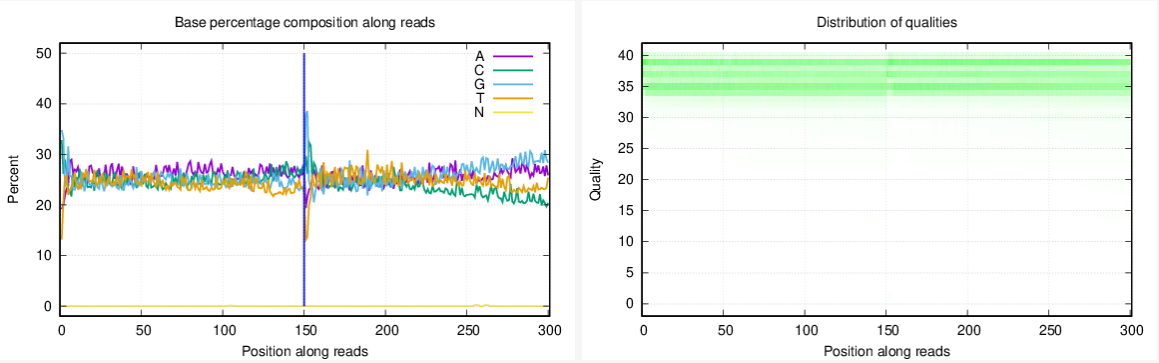
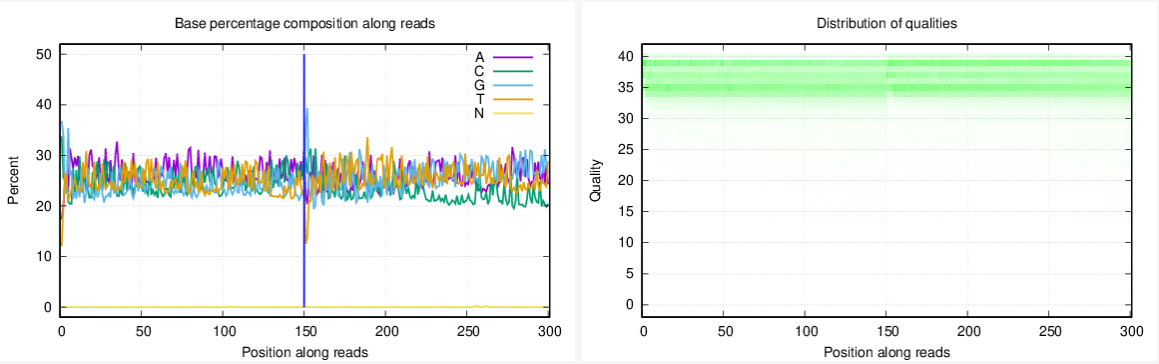


R1_1-25



R2_149-4



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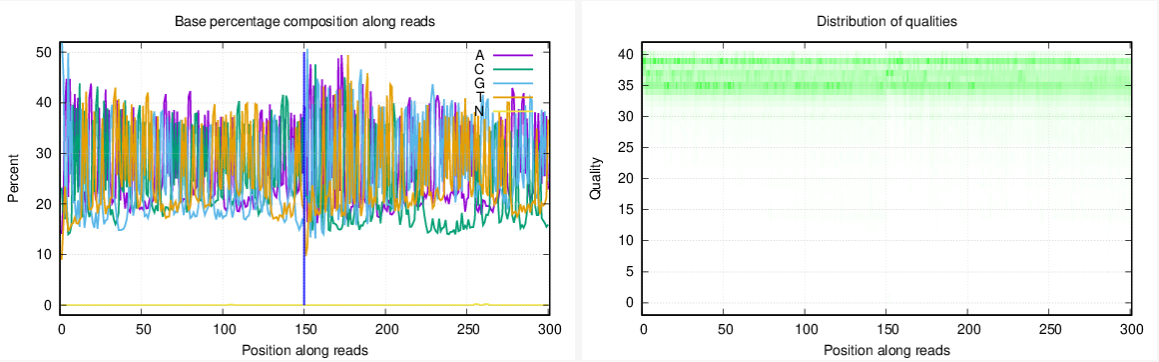

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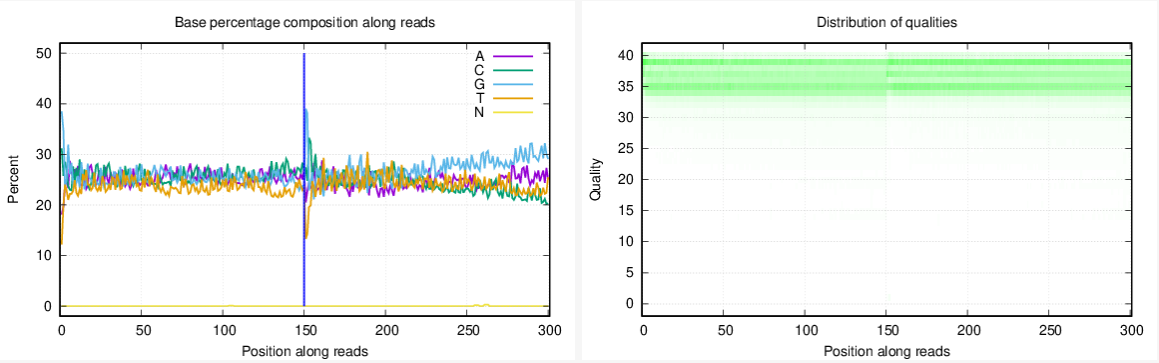

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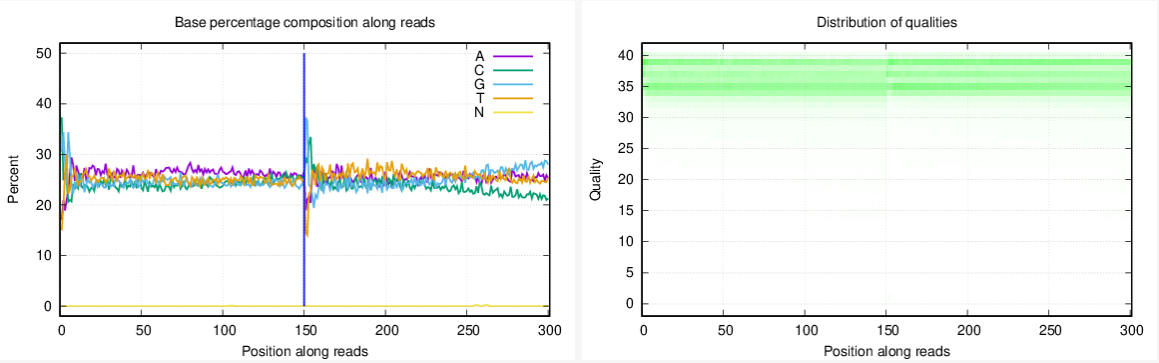

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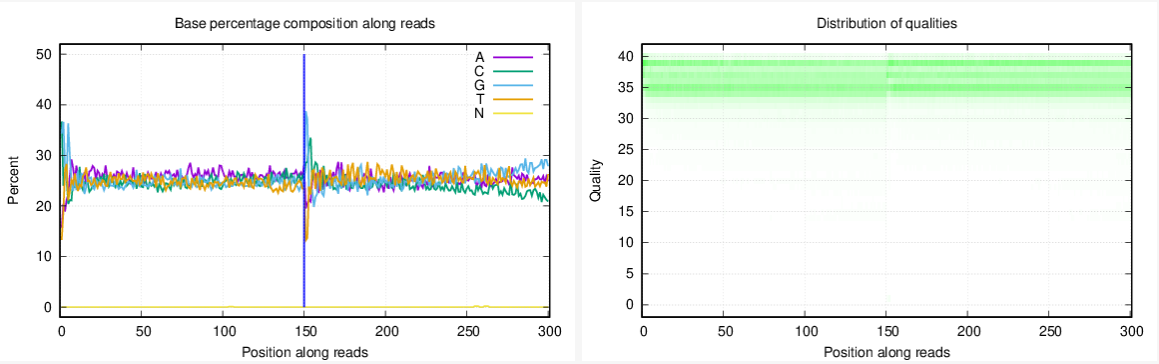

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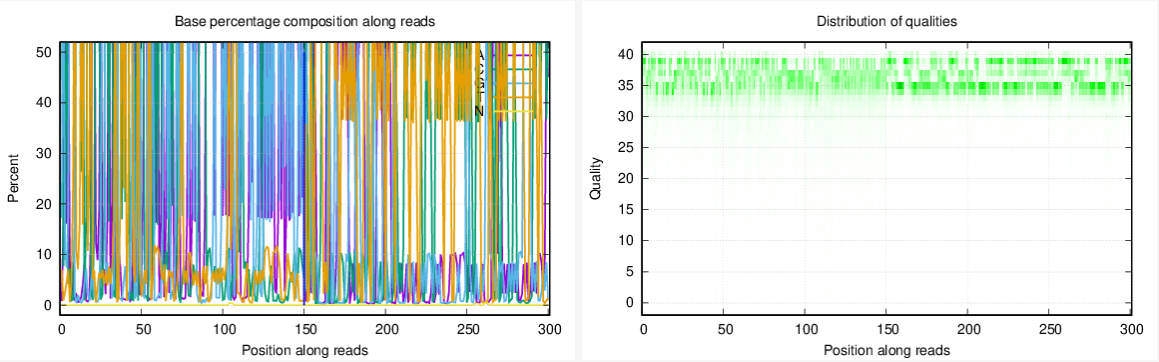

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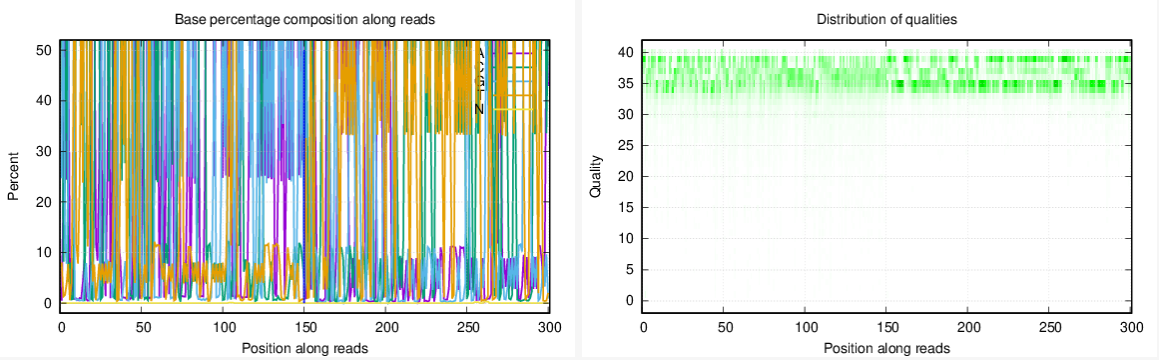

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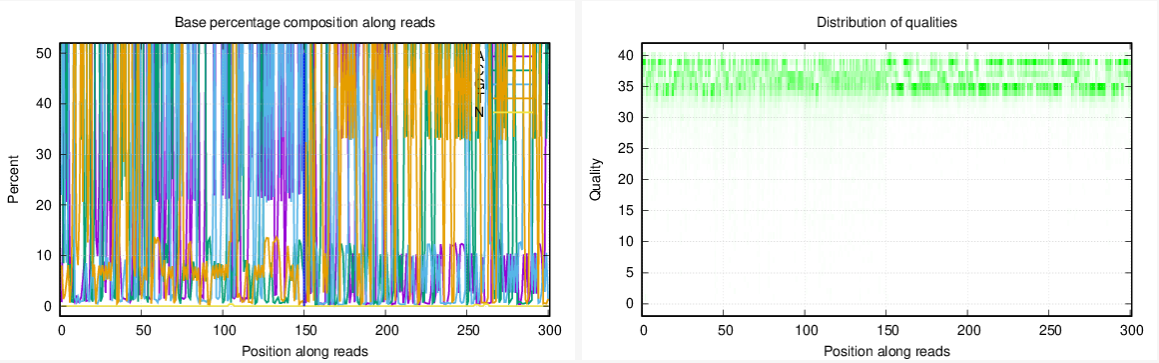
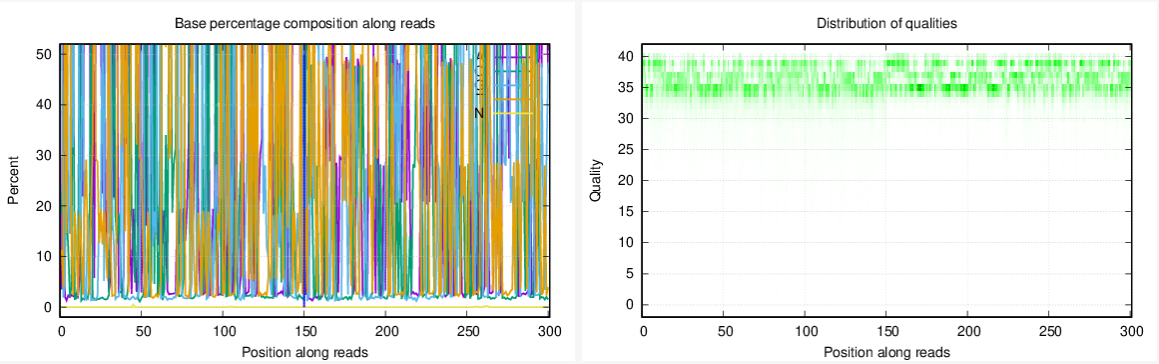


SIX_142



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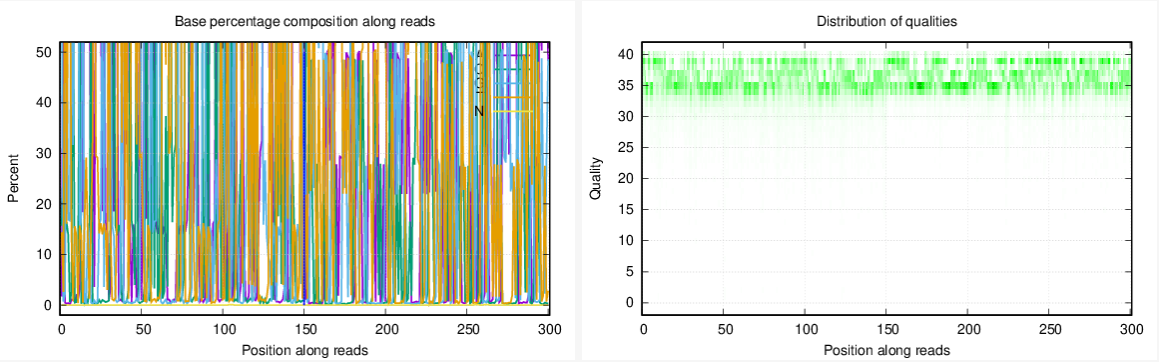

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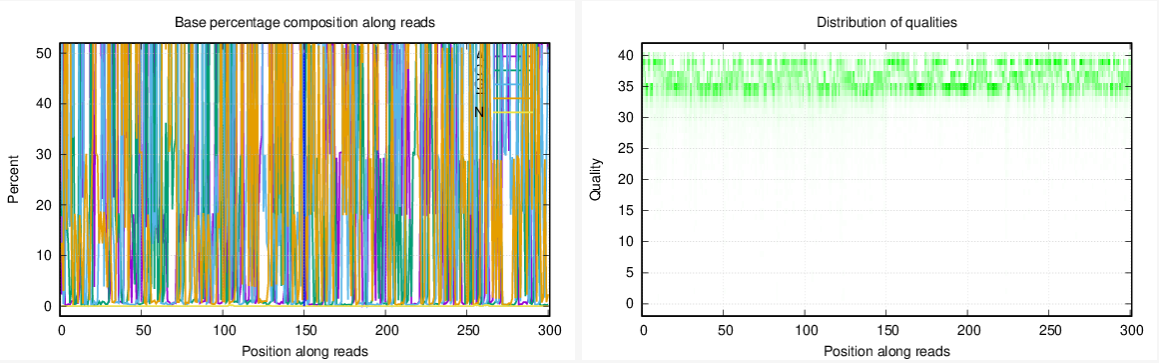
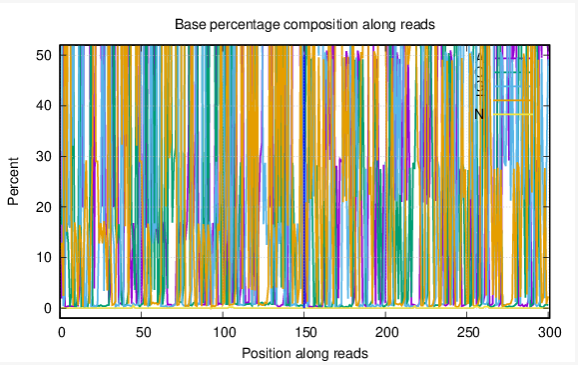
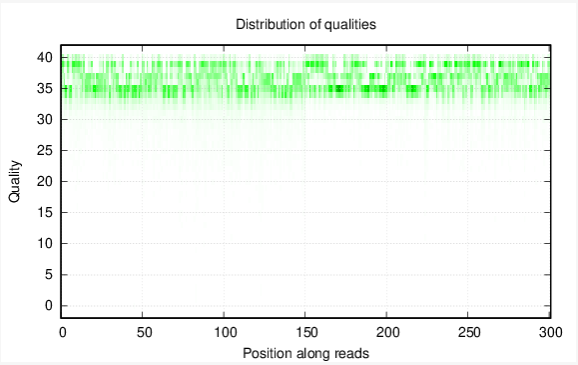


SIX_143





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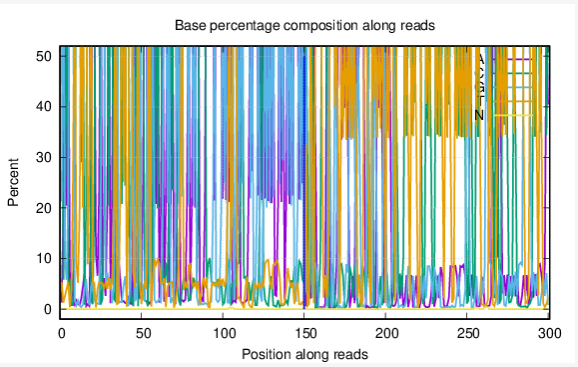

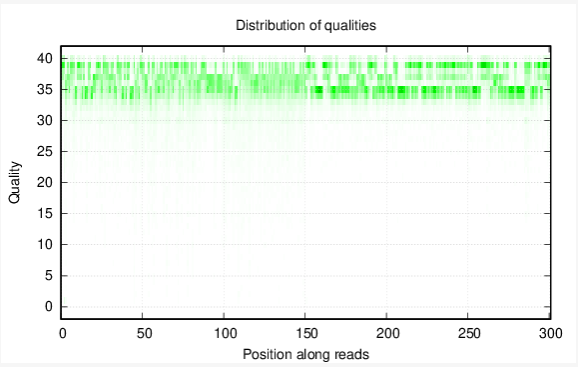

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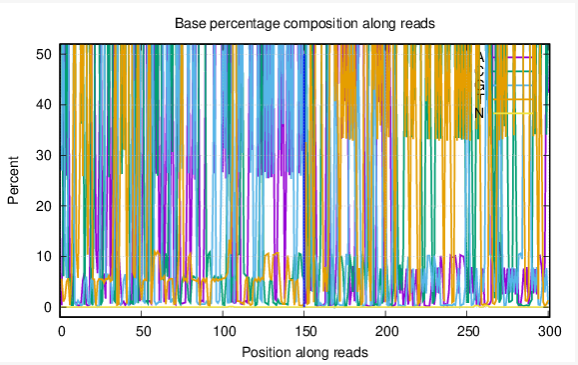

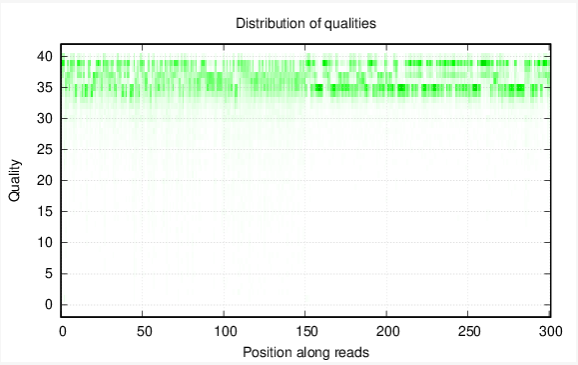

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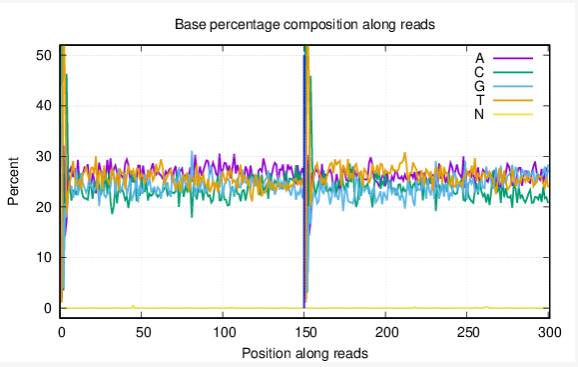

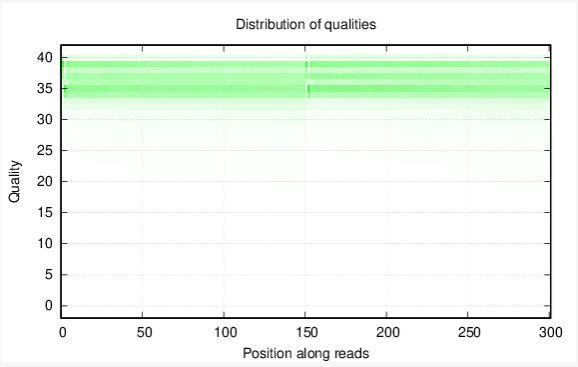

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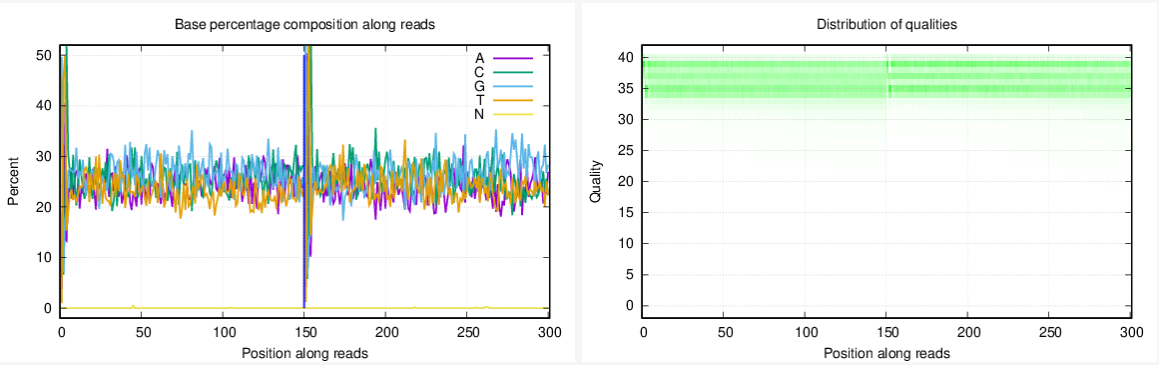

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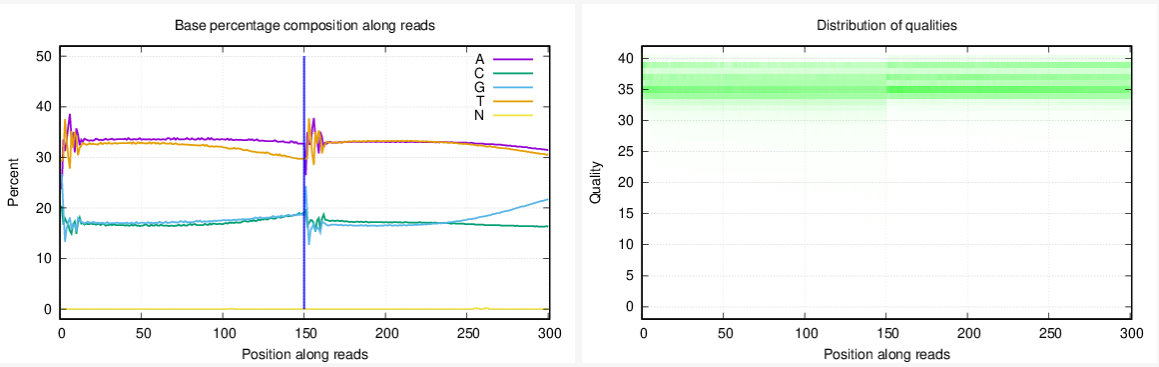

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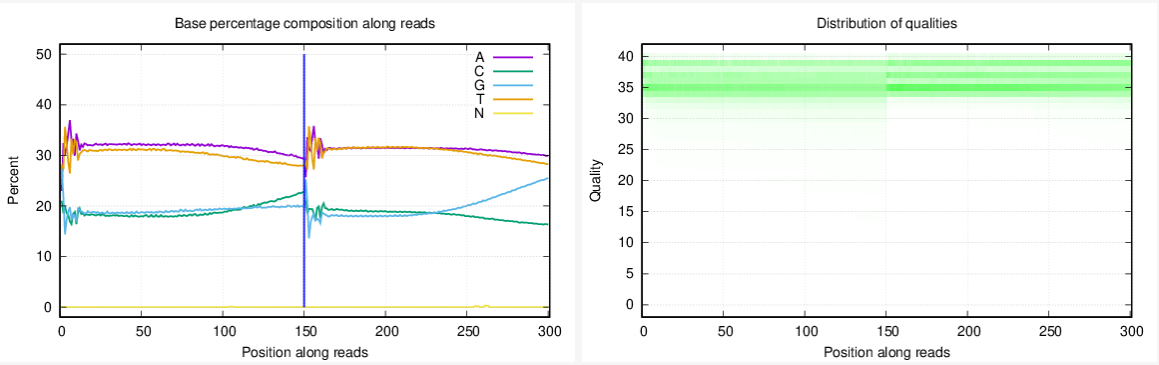

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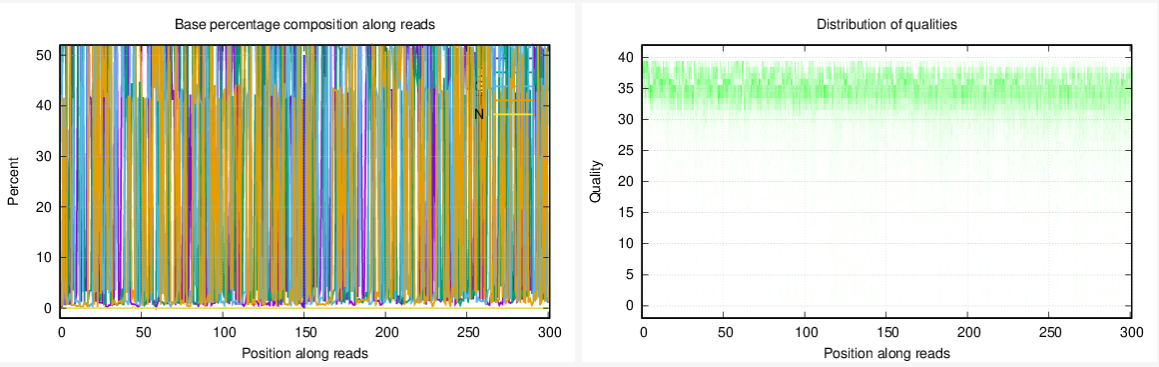

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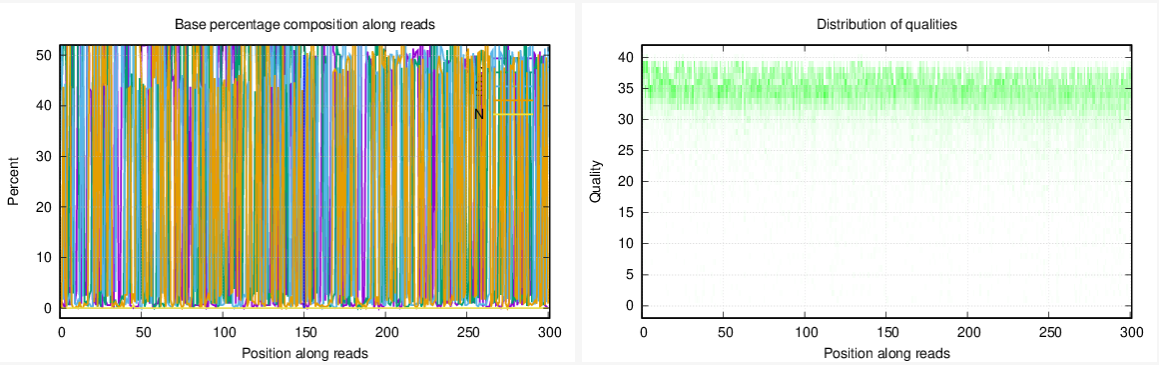

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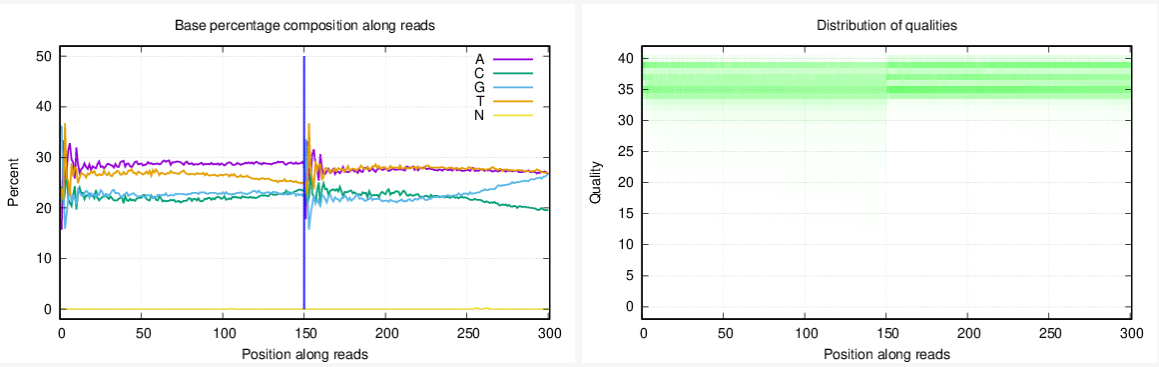

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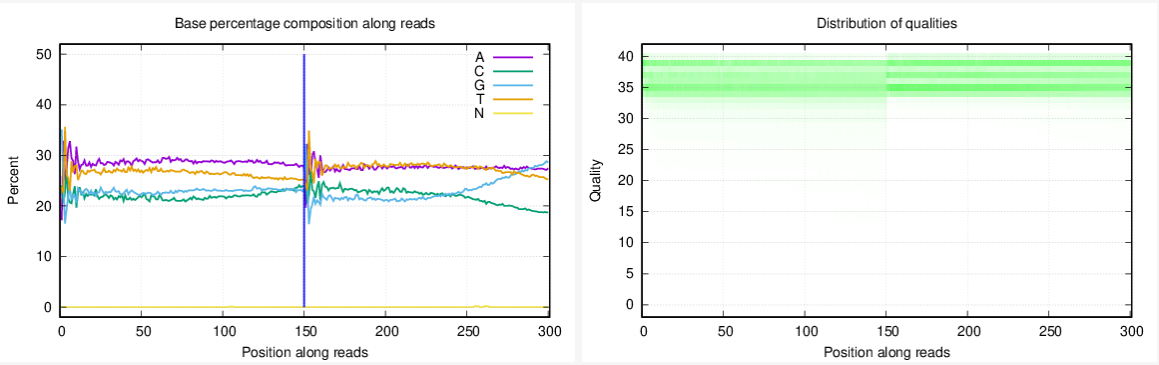

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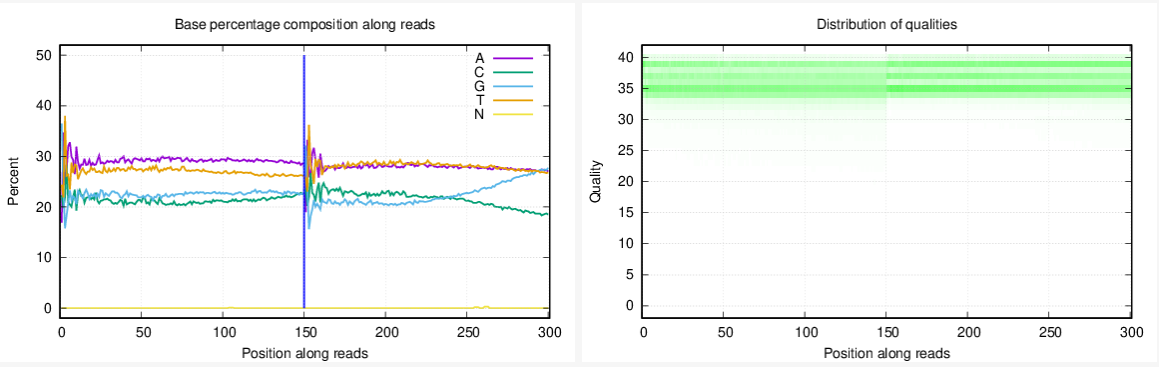

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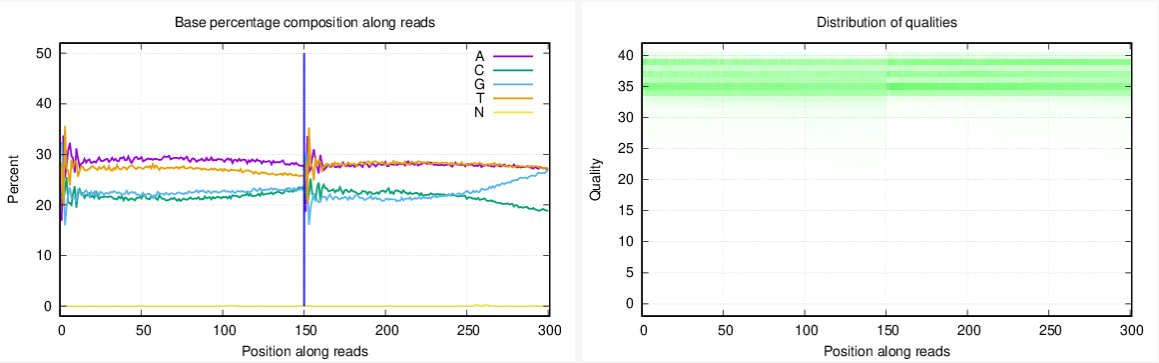

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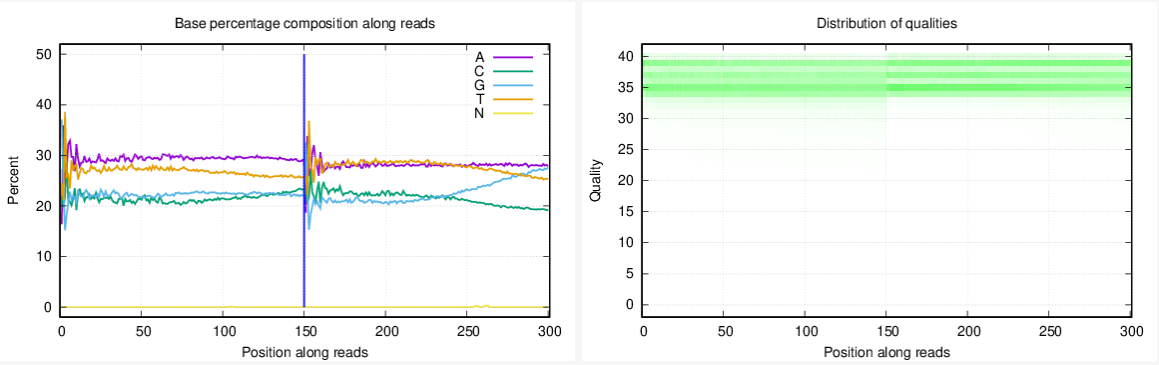

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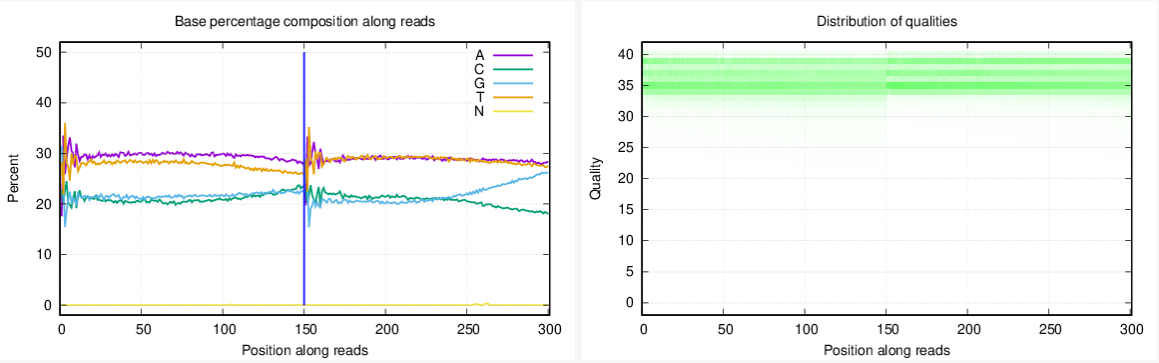

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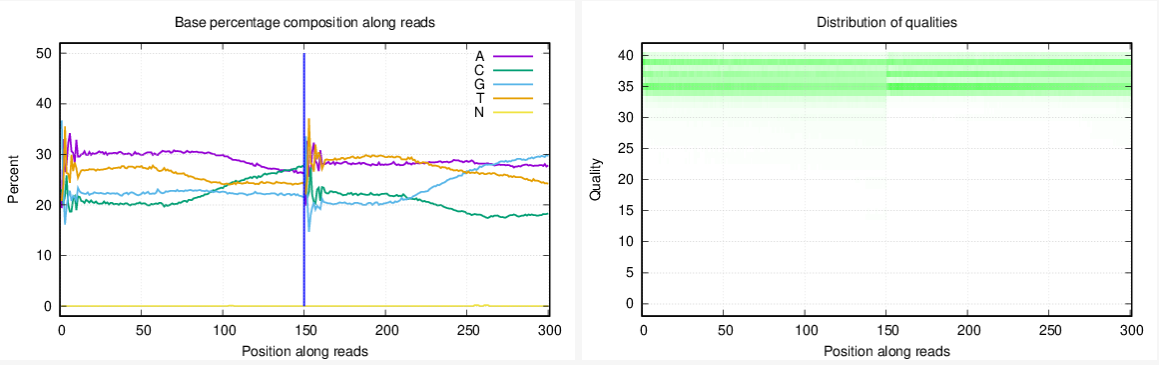

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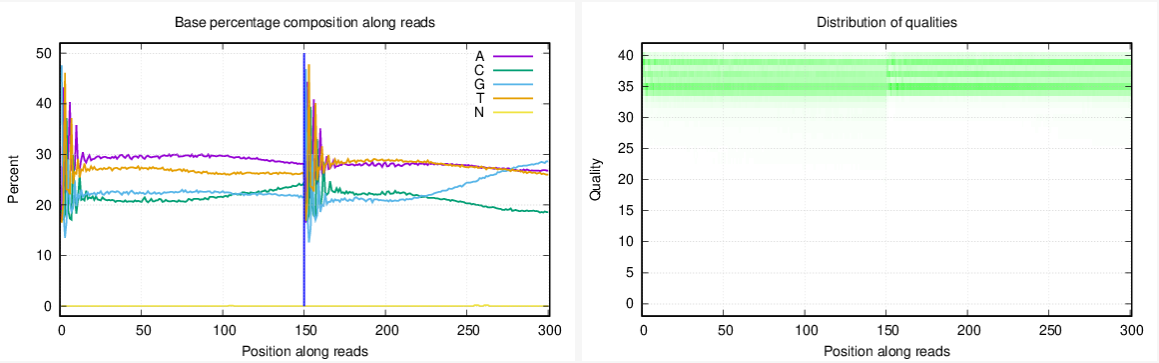
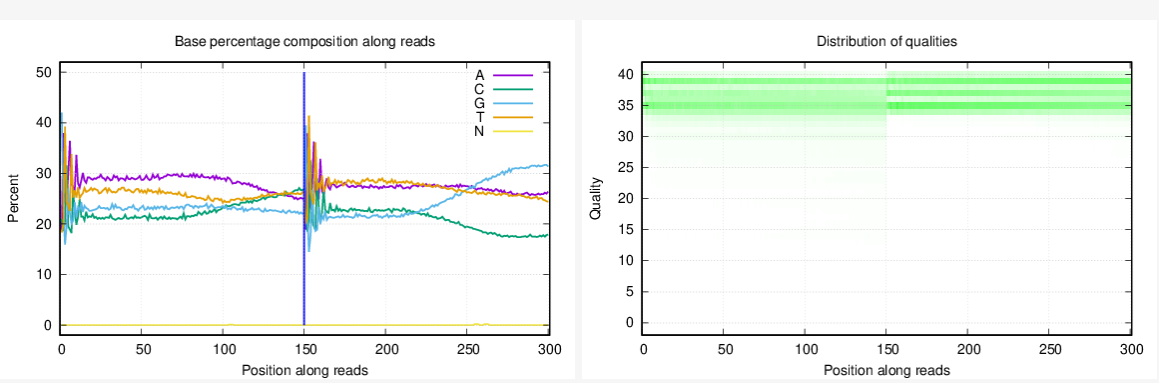


dpn_1_bpd



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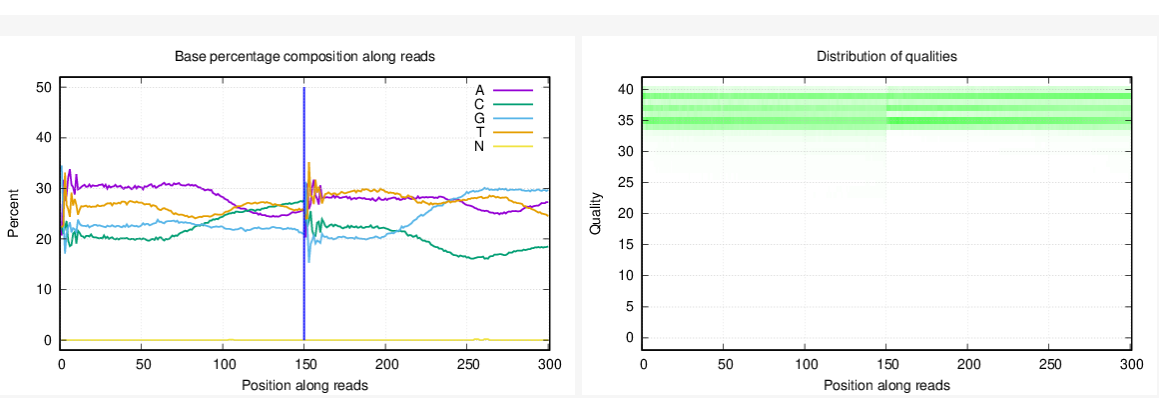

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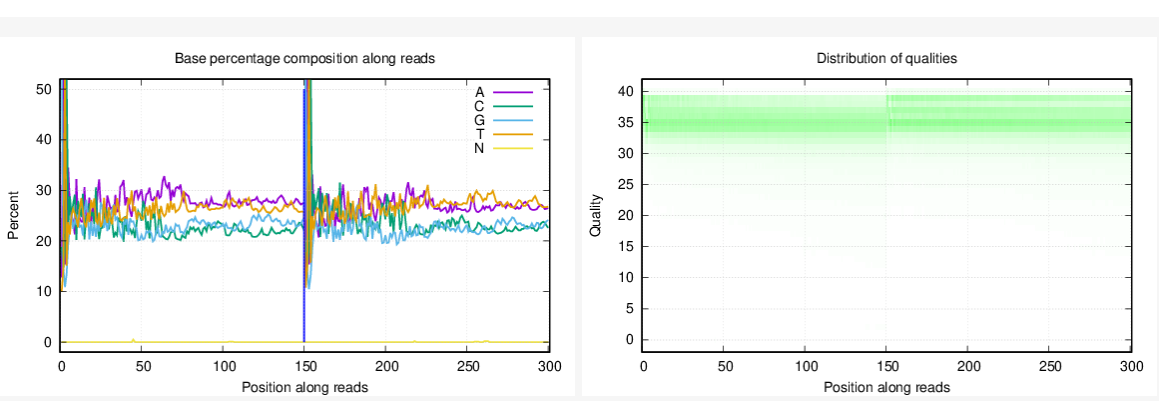

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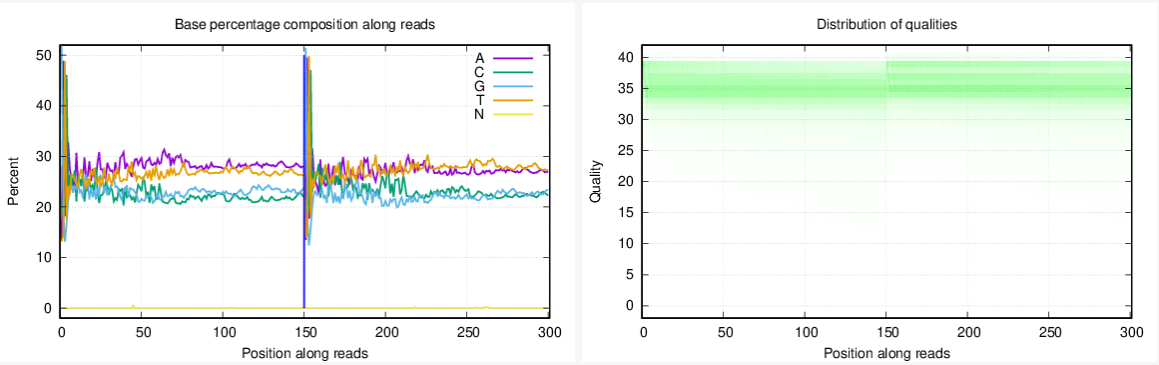

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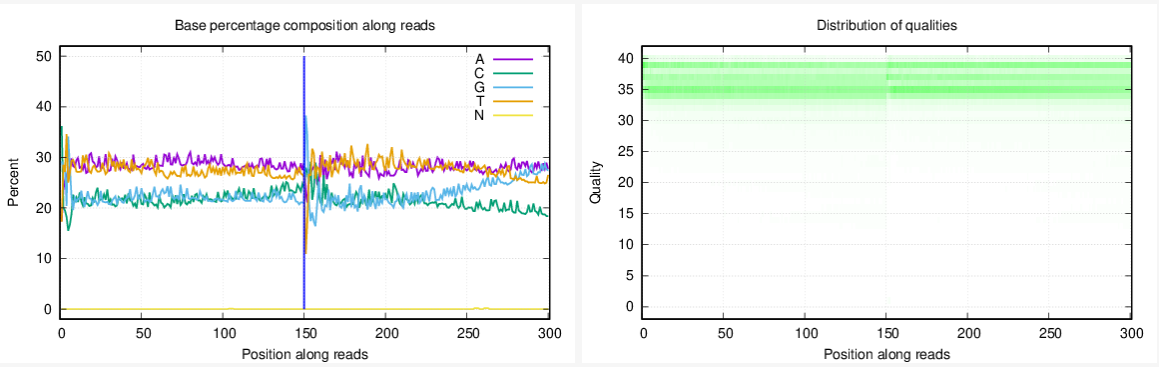

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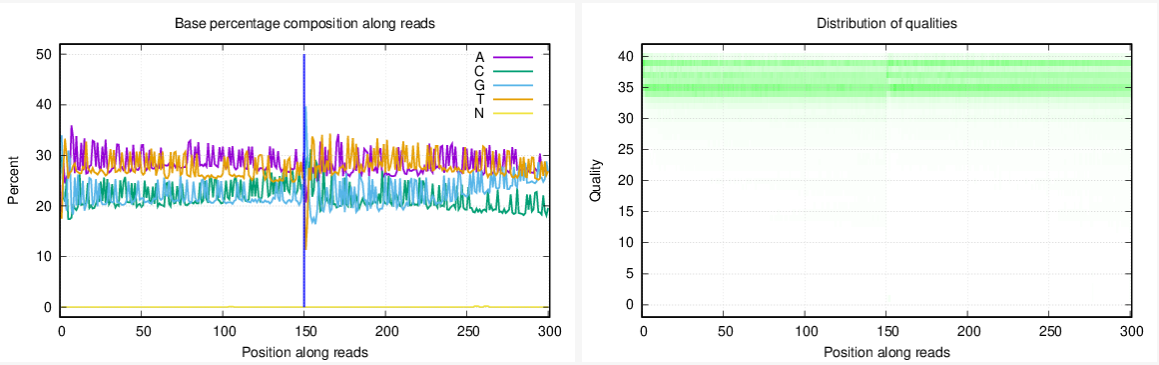

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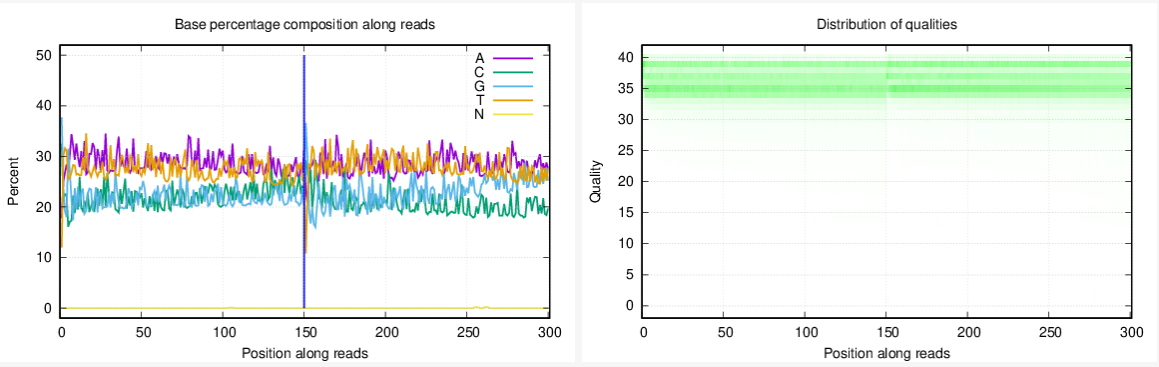

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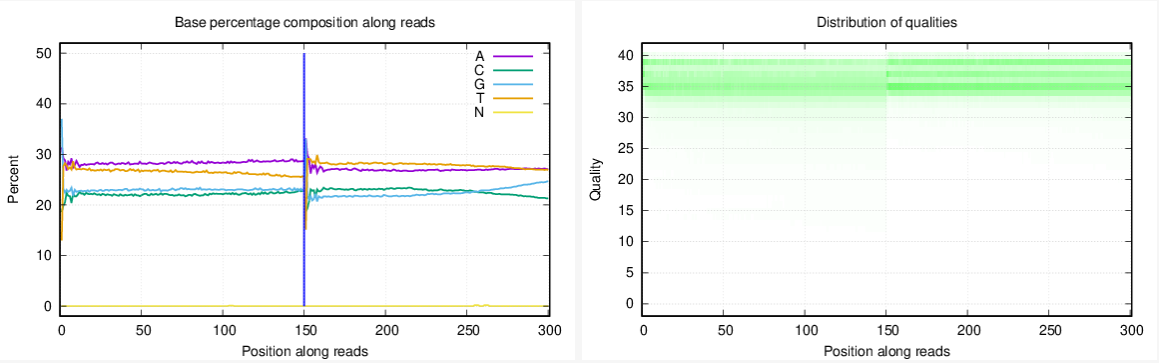

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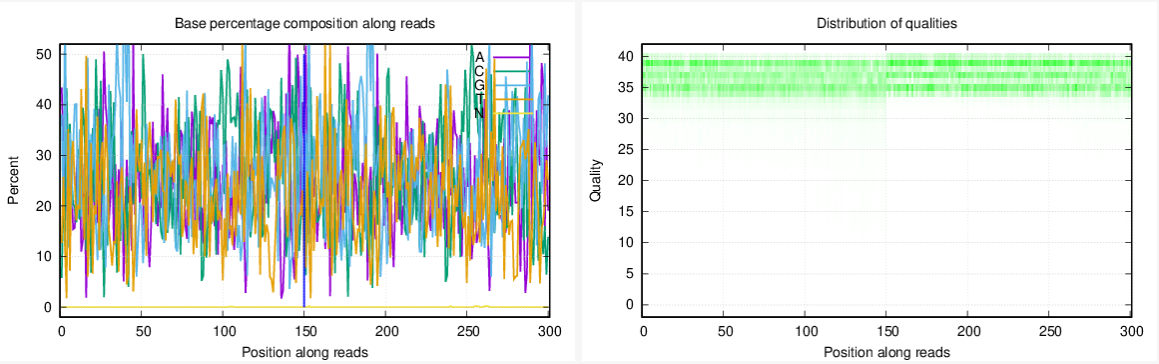

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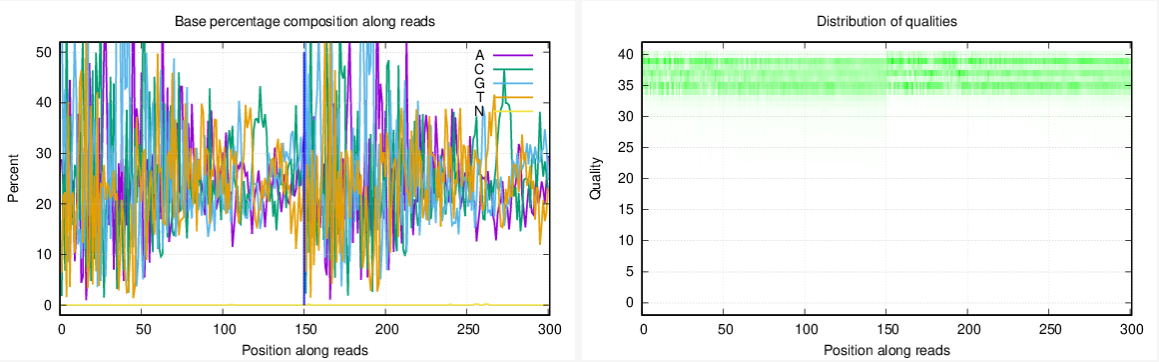

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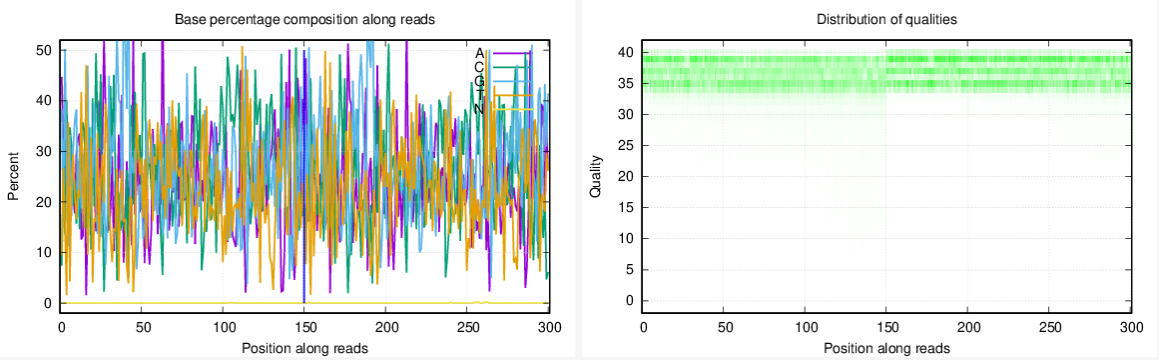

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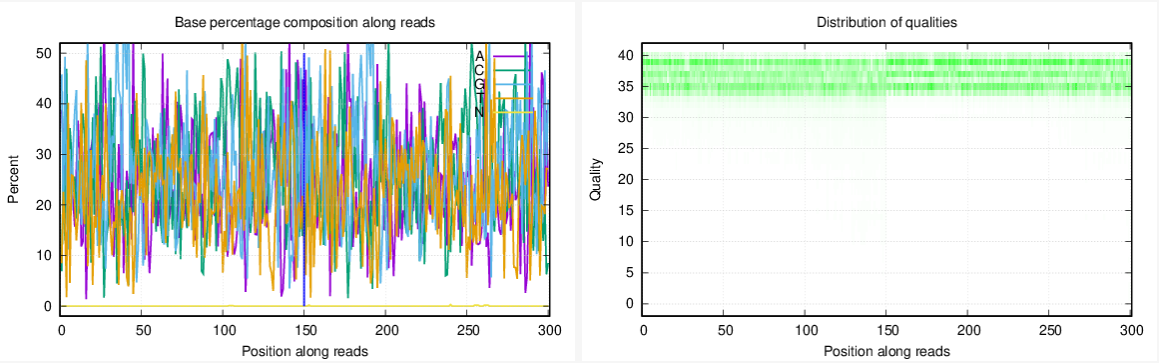

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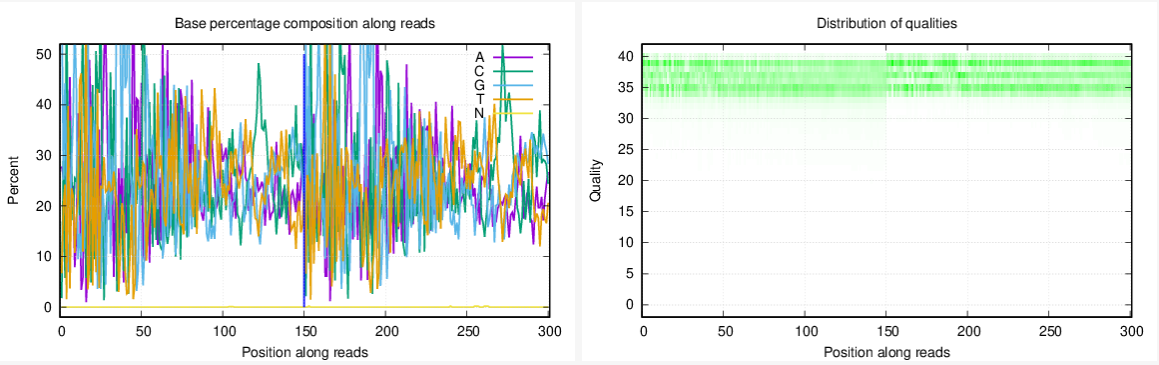

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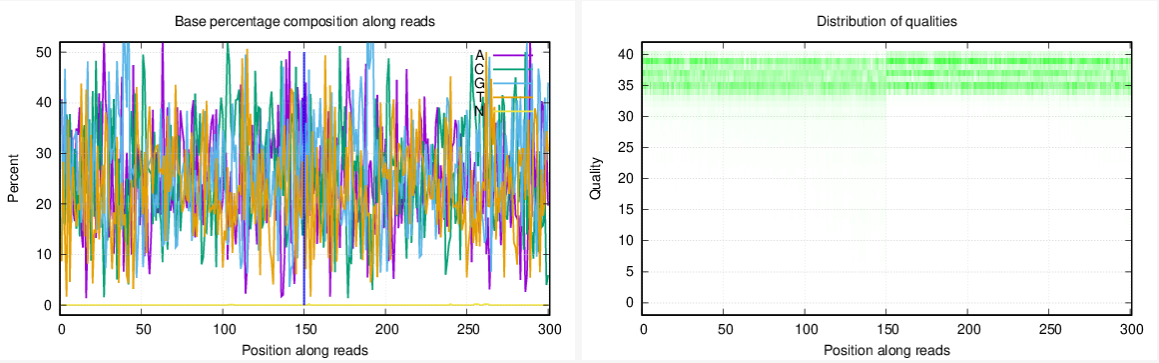

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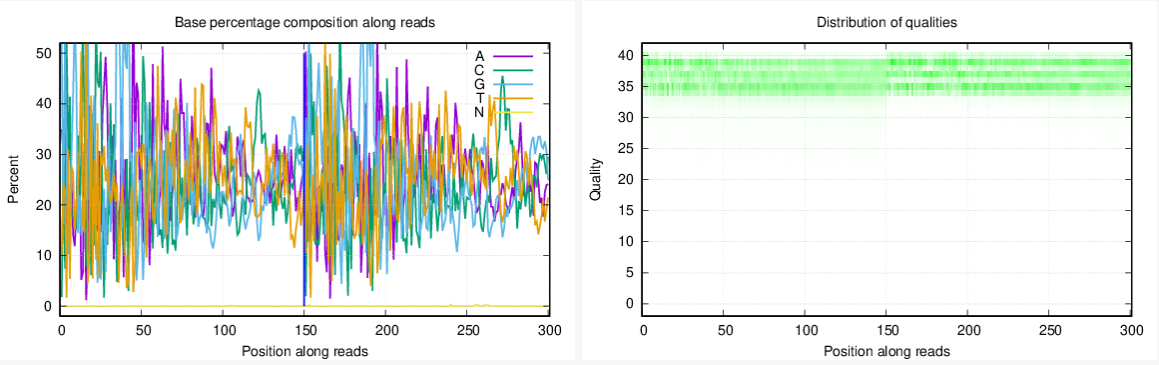

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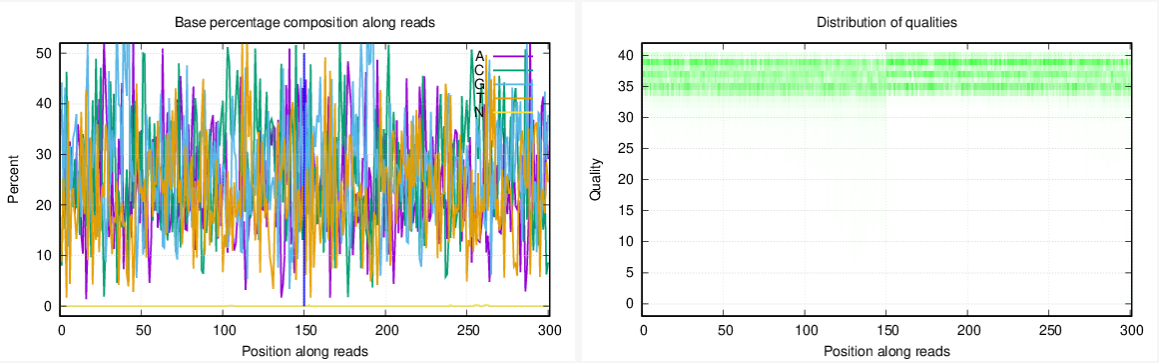

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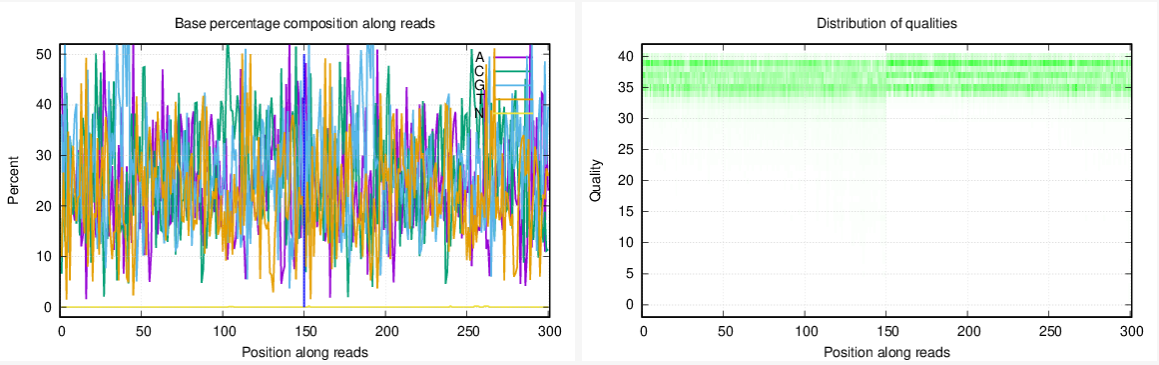
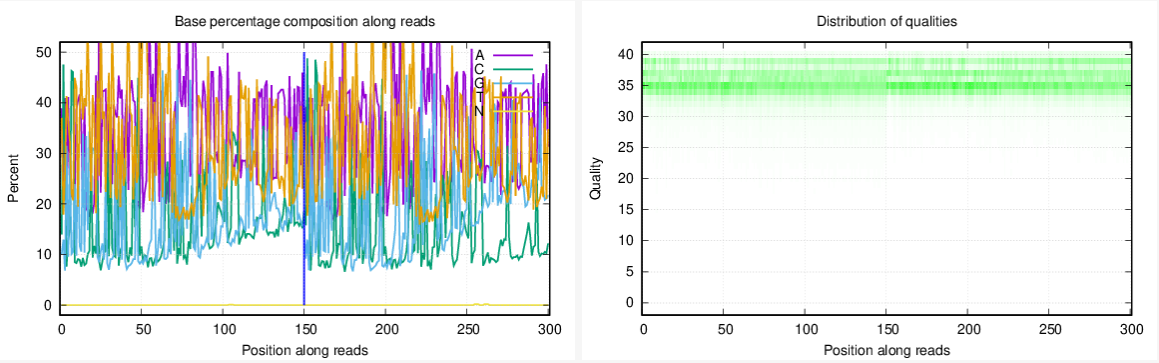


mix_1_TA_STAG2



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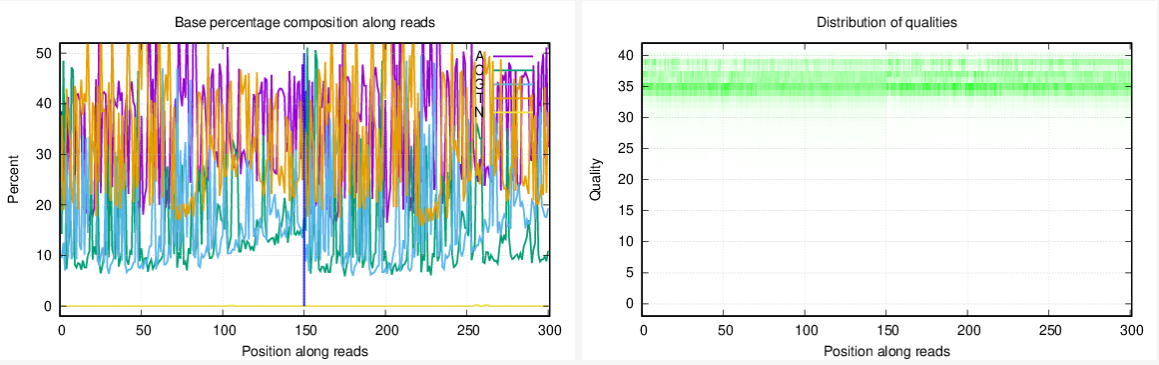
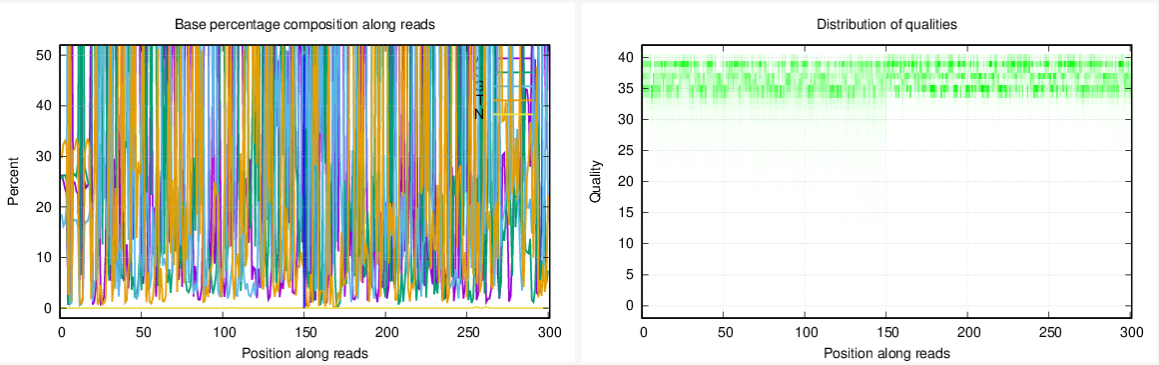
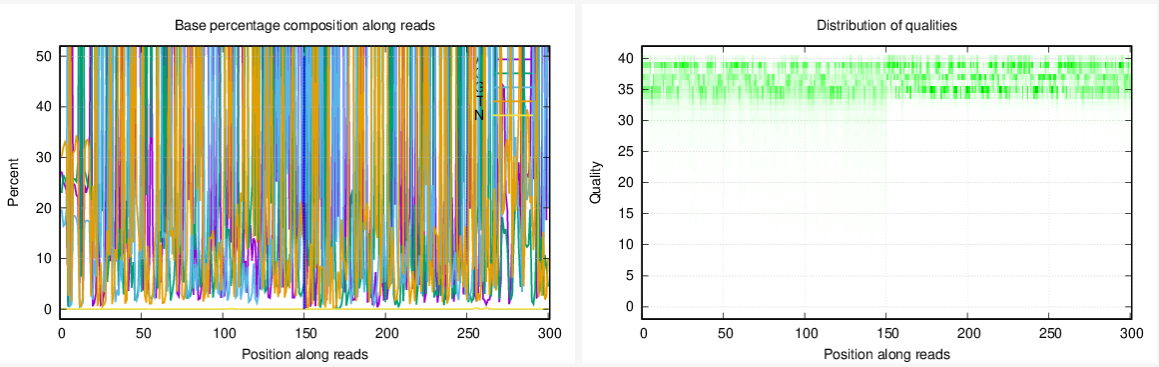


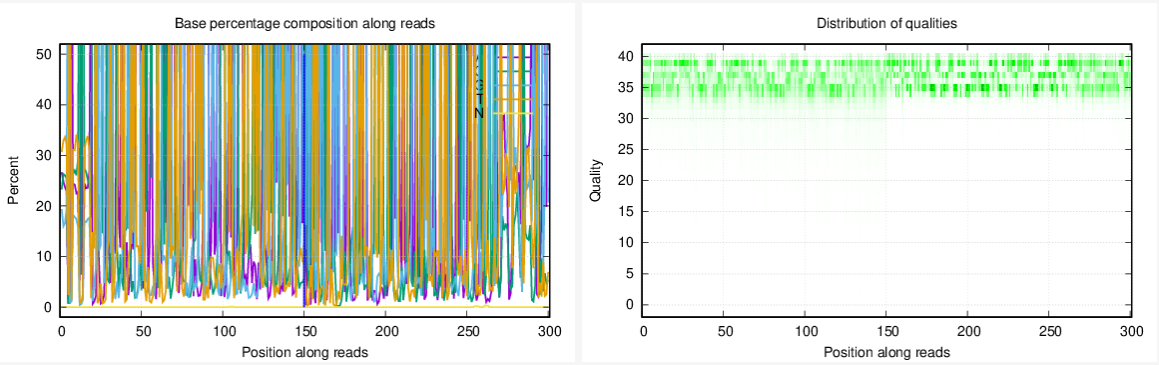
rigs_11



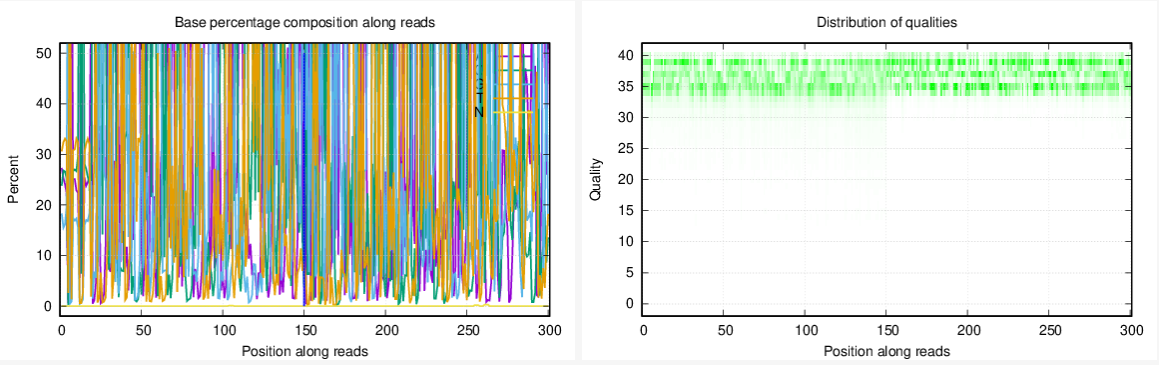
rigs_14



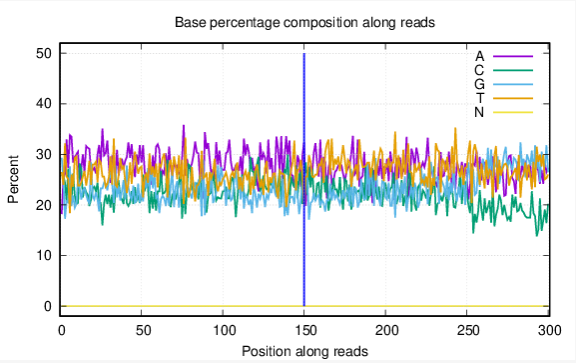
rigs_17

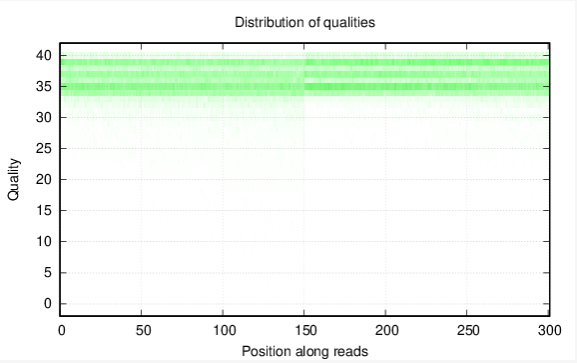


rigs_2



rigs_mysticseq





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	?

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