

Sequencing Data Report

Project: F25A430000584_MUSoxkgR

Date: 2025.10.22

Note: For Research Use Only.



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Data Statistics

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

There are 186 samples in this project, the statistics of fastq data is shown below.

Sample	Length	Q20(%)	Q30(%)	GC Content(%)	Total Reads	Total Bases
06SnBl1	150;150	99.53;98.61	98.29;95.3	54.99;56.73	54,036	16,210,800
07SnBl1	150;150	99.31;98.61	97.61;95.24	56.32;56.11	276,846	83,053,800
1	150;150	97.49;97.31	91.81;91.36	45.59;45.49	17,278,867	5,183,660,100
146-1_5v1	150;150	98.06;98.03	93.52;93.52	48.26;48.35	563,007	168,902,100
146_1_1v1	150;150	97.21;98.32	90.92;94.25	44.52;44.51	618,606	185,581,800
146_1_1v6	150;150	98.23;98.6	93.48;94.97	45.52;45.61	266	79,800
146_1_6v1	150;150	98.19;98.16	93.91;93.82	46.04;46.03	681,397	204,419,100
146_1_o_10	150;150	97.63;98.33	92.17;94.31	45.09;45.26	1,116,458	334,937,400
146_1_o_8	150;150	97.96;97.98	93.22;93.25	45.96;45.99	257,125	77,137,500
149-1_20v6	150;150	97.98;98.23	93.23;94.06	46.53;47.01	1,051,599	315,479,700
149-1_6v1	150;150	98.15;97.88	93.79;93.03	47.84;47.74	240,083	72,024,900
149-4_3v1	150;150	98.38;98.42	94.55;94.67	46.34;46.36	1,253,216	375,964,800
149-4_7v6	150;150	98.21;98.37	94.02;94.55	45.88;45.74	547,488	164,246,400
149_1_1v1	150;150	98.11;98.21	93.63;93.91	45.13;45.07	1,839,369	551,810,700
149_1_o_14	150;150	97.59;97.89	92.03;92.92	45.63;45.8	322,058	96,617,400
149_1_o_17	150;150	97.88;98.01	92.95;93.31	45.56;45.64	665,984	199,795,200
149_4_o_14	150;150	97.89;97.96	92.94;92.99	44.77;44.88	965,158	289,547,400
149_4_o_2	150;150	97.92;97.86	93.03;92.75	45.77;45.84	2,098,263	629,478,900
149_4_o_4	150;150	97.44;98.18	91.57;93.76	44.32;44.43	1,016,057	304,817,100
14_t_vec_stag2	150;150	96.5;96.55	89.23;87.07	49.18;48.59	38,883	11,664,900
1_2	150;150	98.18;98.38	93.94;94.34	45.41;45.41	25,450,591	7,635,177,300
2	150;150	97.63;97.61	92.28;92.39	44.73;44.69	20,055,748	6,016,724,400
23_t_vec_stag2	150;150	96.66;96.65	89.42;87.46	48.6;48.16	34,970	10,491,000
25G	150;150	97.69;98.01	92.56;93.77	39.21;39.05	19,233,709	5,770,112,700
25M	150;150	97.82;97.91	93.05;93.7	40.23;40.15	25,543,858	7,663,157,400
26_t_vec_stag2	150;150	96.18;96.32	88.31;85.97	48.61;48.19	25,908	7,772,400
28_t_vec_stag2	150;150	96.26;96.45	88.33;86.59	48.82;48.36	32,078	9,623,400
2_t_vec_stag2	150;150	96.18;96.08	88.19;85.41	47.9;47.34	32,202	9,660,600

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3	150;150	97.46;97.17	91.74;91.2	44.82;44.75	14,375,128	4,312,538,400
31G	150;150	97.43;97.71	91.87;92.86	43.58;43.41	17,828,751	5,348,625,300
31M	150;150	97.6;97.65	92.45;92.99	41.69;41.57	17,484,000	5,245,200,000
31_t_vec_stag2	150;150	96.37;96.9	88.81;88.25	48.67;48.3	33,311	9,993,300
39_t_vec_stag2	150;150	96.11;96.63	87.76;87.18	48.18;47.86	34,638	10,391,400
3G	150;150	97.4;97.49	91.78;92.33	40.55;40.36	19,118,948	5,735,684,400
3M	150;150	97.91;98.1	93.32;94.11	40.2;40.07	21,146,439	6,343,931,700
4	150;150	93.9;95.01	83.69;86.31	41.48;41.19	3,577	1,073,100
43_t_vec_stag2	150;150	96.23;96.36	88.27;86.3	49.35;48.95	31,889	9,566,700
4C_PFA_2_4day_6_lig	150;150	96.89;97.73	89.88;92.28	45.01;45.95	463,121	138,936,300
4C_outside_pl_1_CMV_1	150;150	97.9;98.42	93.32;94.62	41.7;42.43	1,086,476	325,942,800
4C_outside_pl_1_CMV_2	150;150	97.79;98.39	93.01;94.51	41.64;42.4	1,306,193	391,857,900
4C_outside_pl_2_Bgl	150;150	97.36;97.9	91.7;92.82	42.07;42.09	753,764	226,129,200
4C_outside_pl_2_CMV_Bgl_Afe	150;150	97.6;96.91	92.38;90.13	53.77;55.51	689,387	206,816,100
4_1	150;150	98.09;98.2	93.67;93.82	46.11;46.22	22,114,153	6,634,245,900
4_t_vec_stag2	150;150	96.77;96.64	89.75;87.26	49.21;48.88	36,380	10,914,000
5	150;150	93.32;91.73	80.94;76.76	45.25;45.03	24,809	7,442,700
6	150;150	97.81;97.45	92.71;91.77	45.18;45.03	16,927,550	5,078,265,000
60_t_vec_stag2	150;150	96.41;96.78	88.76;87.68	47.22;46.8	34,408	10,322,400
62_t_vec_stag2	150;150	96.28;96.64	88.42;87.24	49.03;48.81	28,461	8,538,300
7	150;150	97.57;97.54	92.06;92.12	45.3;45.2	18,690,083	5,607,024,900
8G	150;150	97.31;97.3	91.65;92.23	39.91;39.74	13,883,233	4,164,969,900
8M	150;150	97.45;97.55	91.88;92.5	40.15;40.03	17,921,554	5,376,466,200
8_t_vec_stag2	150;150	96.21;96.24	88.35;85.86	48.84;48.41	39,973	11,991,900
BOV-3	150;150	98.43;97.37	94.93;91.74	60.09;60.82	4,290	1,287,000
B_1	150;150	97.76;97.59	92.49;92.46	45.34;45.16	6,151,561	1,845,468,300
B_1_2	150;150	98.4;98.73	94.53;95.53	45.18;45.2	7,707,651	2,312,295,300
B_2	150;150	97.87;97.86	92.89;93.38	44.48;44.37	6,661,810	1,998,543,000
B_25G	150;150	97.91;98.24	93.11;94.66	39.1;38.79	6,574,655	1,972,396,500
B_25M	150;150	98.04;98.12	93.64;94.55	40.01;39.83	8,972,368	2,691,710,400
B_3	150;150	97.69;97.39	92.3;92.09	44.59;44.45	5,014,077	1,504,223,100
B_31G	150;150	97.67;98.02	92.46;93.98	43.24;42.95	6,132,912	1,839,873,600
B_31M	150;150	97.92;97.88	92.99;92.88	41.27;41.16	5,022,466	1,776,720,800

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B_31M	150;150	97.82;97.88	92.99;93.89	41.37;41.10	3,922,400	1,110,139,800
B_3G	150;150	97.62;97.72	92.3;93.25	40.4;40.13	6,392,144	1,917,643,200
B_3M	150;150	98.16;98.34	93.97;95.04	40.05;39.84	7,236,214	2,170,864,200
B_4	150;150	92.28;94.5	80.36;85.47	41.23;40.53	1,505	451,500
B_4_1	150;150	98.32;98.56	94.29;95.03	45.87;46.01	6,759,665	2,027,899,500
B_5	150;150	96.33;94.67	88.77;85.46	43.52;43.36	2,534	760,200
B_6	150;150	98.06;97.74	93.35;92.88	44.95;44.77	5,622,216	1,686,664,800
B_7	150;150	97.83;97.74	92.73;92.99	45.12;44.96	7,018,287	2,105,486,100
B_8G	150;150	97.57;97.4	92.3;92.87	39.75;39.43	5,001,980	1,500,594,000
B_8M	150;150	97.65;97.77	92.37;93.39	40.0;39.8	6,441,086	1,932,325,800
B_L2_7	150;150	95.97;95.22	88.37;86.84	44.28;44.14	3,345	1,003,500
B_LK	150;150	91.16;91.95	76.91;78.79	43.28;43.04	2,985	895,500
B_R2.7	150;150	97.47;97.63	92.14;92.98	45.34;45.41	1,239	371,700
B_RK	150;150	97.7;97.57	92.65;92.88	43.86;43.77	6,110	1,833,000
Cen_B7	150;150	97.51;97.14	91.72;89.95	45.54;45.54	16,948,536	5,084,560,800
Cen_B8	150;150	97.46;97.38	91.69;90.86	45.64;45.8	10,902,694	3,270,808,200
EBS1.1	150;150	99.26;98.22	97.45;94.0	56.8;57.03	17,051	5,115,300
HCT_13_1	150;150	98.59;98.32	95.03;94.25	49.35;46.98	1,176,978	353,093,400
HCT_13_1_k	150;150	98.72;98.67	95.53;95.5	49.79;47.17	1,282,655	384,796,500
HCT_13_2	150;150	98.62;98.37	95.17;94.47	49.7;47.0	1,382,952	414,885,600
HCT_13_2_k	150;150	98.81;98.73	95.86;95.75	49.63;47.1	862,075	258,622,500
HCT_13_3	150;150	98.23;97.14	93.7;89.96	47.11;46.97	382,674	114,802,200
HCT_13_3_k	150;150	98.69;98.68	95.45;95.57	49.62;47.08	452,991	135,897,300
HCT_13_k_w_o	150;150	98.64;98.46	95.24;94.69	49.73;47.02	1,342,001	402,600,300
HCT_15_1	150;150	98.41;97.73	94.33;92.01	47.98;46.49	323,915	97,174,500
HCT_15_2	150;150	98.44;97.06	94.37;89.53	46.25;46.99	220,877	66,263,100
HCT_15_2_k	150;150	98.76;98.78	95.7;95.87	49.2;46.59	736,584	220,975,200
HCT_15_3	150;150	98.6;98.42	95.01;94.37	49.09;46.69	3,095	928,500
HCT_15_3_k	150;150	99.09;99.05	96.72;96.47	48.9;47.0	435	130,500
HCT_7_1	150;150	98.62;98.51	95.17;94.86	49.51;46.6	944,328	283,298,400
HCT_7_1_k	150;150	99.05;99.06	96.69;96.83	48.67;46.96	1,797,522	539,256,600
HCT_7_2	150;150	98.53;98.02	94.78;93.02	48.38;46.47	786,133	235,839,900
HCT_7_2_k	150;150	99.06;99.08	96.74;96.9	48.47;46.97	1,213,479	364,043,700

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HCT_7_3	150;150	98.51;98.18	94.74;93.61	48.71;46.5	1,025,074	307,522,200
HCT_7_3_k	150;150	98.84;98.83	95.94;96.05	48.79;46.82	1,066,254	319,876,200
L1T1G1A	150;150	95.9;88.72	85.97;58.87	44.13;47.35	10,970	3,291,000
L1T1G1B	150;150	97.51;97.5	91.84;91.26	44.81;45.34	362,383	108,714,900
L1T1G1C	150;150	97.09;97.86	90.63;92.47	46.16;47.17	452,021	135,606,300
L1T1G1D	150;150	97.72;96.26	92.44;87.28	55.81;58.18	27,386	8,215,800
L1T2G1D	150;150	97.12;92.93	90.37;76.57	54.6;57.28	16,003	4,800,900
L2_7	150;150	91.82;91.99	80.2;80.05	42.3;41.99	4,666	1,399,800
LK	150;150	92.16;93.23	78.59;80.76	43.66;43.17	10,194	3,058,200
LepBo-22	150;150	98.89;98.07	96.5;93.79	54.04;53.69	1,645	493,500
MBS_22	150;150	97.38;97.34	91.56;90.65	41.5;41.65	1,636,926	491,077,800
MBS_33	150;150	97.5;97.3	92.07;90.73	42.48;42.74	2,115,438	634,631,400
MBS_77	150;150	97.41;97.38	91.78;90.94	42.25;42.39	1,517,435	455,230,500
MBS_88	150;150	97.38;97.38	91.6;90.7	41.59;41.7	1,064,705	319,411,500
MI-4	150;150	97.45;98.05	92.16;93.98	44.06;44.15	6,117	1,835,100
MI-5	150;150	96.99;97.27	90.5;90.85	49.24;48.96	21,665	6,499,500
Mam-1	150;150	99.33;98.78	97.67;95.79	56.24;56.57	37,881	11,364,300
Mam-2	150;150	99.41;98.38	97.95;94.41	57.88;56.02	25,780	7,734,000
Mam-5	150;150	98.46;98.32	94.86;94.42	56.9;58.63	26,971	8,091,300
MamAf-2	150;150	98.69;97.15	95.57;91.08	62.79;62.76	1,200,032	360,009,600
MamFar-1	150;150	98.9;97.89	96.27;93.37	57.98;58.5	212,662	63,798,600
MamKan-1	150;150	98.93;97.15	96.35;90.81	60.19;59.68	12,761	3,828,300
MamKoz-1	150;150	93.47;85.73	81.87;64.0	48.53;47.87	5	1,500
MamKra1-1	150;150	99.06;97.97	96.85;93.59	54.06;54.65	212,651	63,795,300
MamKra2-1	150;150	98.67;97.85	95.69;93.07	55.28;54.46	1,346,517	403,955,100
MoPh11_enr.v2	150;150	96.83;97.72	89.79;92.48	45.32;45.53	14,606,659	4,381,997,700
MoPh14_enr.v2	150;150	97.86;97.76	92.94;92.62	45.57;45.35	11,451,855	3,435,556,500
MoPh15_enr.v2	150;150	97.67;97.77	92.36;92.56	45.19;45.12	10,219,014	3,065,704,200
MoPh7_enr.v2	150;150	97.2;98.0	90.85;93.41	45.24;46.24	13,186,115	3,955,834,500
Novo-1	150;150	98.66;98.56	95.67;95.3	51.03;50.49	1,001,064	300,319,200
P217	150;150	98.05;97.91	93.47;93.18	48.78;48.69	35,507,698	10,652,309,400
P218	150;150	98.56;98.4	95.14;94.83	50.25;50.13	34,148,459	10,244,537,700
P219	150;150	98.08;98.02	93.57;93.53	48.56;48.65	34,233,770	10,270,131,000

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P220	150;150	98.58;98.33	95.19;94.67	49.12;49.7	37,974,149	11,392,244,700
P221	150;150	98.58;98.32	95.15;94.61	48.72;49.06	41,045,237	12,313,571,100
P222	150;150	98.22;98.28	94.0;94.36	48.5;48.66	40,569,655	12,170,896,500
P223	150;150	98.66;98.19	95.41;94.12	49.2;48.65	44,698,119	13,409,435,700
P224	150;150	98.46;98.42	94.79;94.9	47.78;48.18	24,664,242	7,399,272,600
P225	150;150	98.79;98.5	95.88;95.12	48.81;48.61	26,513,486	7,954,045,800
P225R	150;150	97.85;97.51	92.83;91.84	49.37;49.44	13,779,192	4,133,757,600
P226	150;150	98.94;98.53	96.34;95.24	49.89;49.42	29,140,713	8,742,213,900
P227	150;150	97.89;97.82	92.92;92.76	47.3;47.45	26,566,820	7,970,046,000
PARP_KO_r1	150;150	98.88;98.83	96.15;96.11	45.56;45.64	12,077,226	3,623,167,800
PARP_WT_r1	150;150	98.98;98.77	96.51;95.99	46.71;46.86	11,728,867	3,518,660,100
PEM_seq_aux	150;150	99.44;97.11	98.33;91.44	52.34;52.33	12	3,600
PEM_seq_ctr	150;150	97.03;96.81	92.0;90.46	49.96;50.41	33	9,900
R2.7	150;150	97.45;97.51	92.12;92.32	44.8;44.81	4,800	1,440,000
RK	150;150	97.68;97.82	92.66;93.32	44.89;44.92	9,853	2,955,900
SP-dCas9-VPR_1	150;150	95.87;95.32	87.38;82.99	54.3;54.2	1,345	403,500
SP-dCas9-VPR_2	150;150	96.02;95.72	87.96;84.18	52.51;52.51	48,731	14,619,300
SP-dCas9-VPR_3	150;150	95.66;94.72	86.69;80.24	53.18;53.1	2,634	790,200
SP-dCas9-VPR_4	150;150	96.32;95.92	88.7;85.1	51.68;51.55	10,899	3,269,700
StyelaC10_R4	150;150	98.1;98.08	94.06;93.93	45.26;45.07	21,024,682	6,307,404,600
StyelaC10_a_R4	150;150	98.11;98.24	94.05;94.37	44.62;44.78	26,983,610	8,095,083,000
TK	150;150	97.64;96.77	92.22;89.85	48.26;48.05	361,080	108,324,000
TM_I	150;150	97.96;96.66	93.22;90.48	52.48;52.38	727,266	218,179,800
Uru-3	150;150	98.34;98.58	94.56;95.32	44.84;45.02	10,676,426	3,202,927,800
VspGus-2	150;150	99.27;98.97	97.58;96.76	48.31;49.19	2,329,095	698,728,500
Vsplma-1	150;150	99.03;98.14	96.69;93.93	57.91;58.76	3,001,544	900,463,200
Vsplma-3	150;150	98.91;97.98	96.26;93.39	58.07;57.55	1,147,083	344,124,900
Vsplma-4	150;150	99.07;98.03	96.81;93.51	57.7;56.87	719,813	215,943,900
VspKur-1	150;150	99.03;97.88	96.67;93.24	57.46;58.65	800,999	240,299,700
VspZap-3	150;150	99.14;98.28	97.02;94.34	57.94;58.19	2,445,466	733,639,800
VspZap-3_tr	150;150	99.05;98.17	96.8;93.98	57.4;57.99	1,561,387	468,416,100
VspZap-4	150;150	98.59;97.95	95.25;93.34	59.37;58.97	3,926,565	1,177,969,500
Vvulma-1	150;150	98.61;97.15	95.3;91.04	60.2;60.51	5,577.880	1.673.364.000

Data Statistics						
Feature	100,000	200,000	300,000	400,000	500,000	1,000,000
VvuMan-1	150;150	0.0;98.67	0.0;96.67	64.67;64.67	1	300
Y226A_R1	150;150	97.19;96.78	91.21;89.28	42.46;42.74	16,895,585	5,068,675,500
brInt_R2	150;150	98.01;97.95	93.74;93.62	45.96;46.15	28,949,271	8,684,781,300
brInt_a_R1	150;150	98.12;97.73	93.72;92.54	47.37;47.64	29,185,634	8,755,690,200
brInt_a_R2	150;150	97.94;98.08	93.58;93.93	44.26;44.17	21,874,900	6,562,470,000
brLinker_R3	150;150	97.05;98.53	90.96;95.32	45.5;45.56	24,045,543	7,213,662,900
brLinker_R4	150;150	97.83;97.68	93.13;92.36	44.47;44.62	24,000,651	7,200,195,300
brLinker_a_R3	150;150	97.62;97.7	92.69;92.71	44.02;43.99	12,546,199	3,763,859,700
brLinker_a_R4	150;150	97.14;97.31	91.17;91.28	45.83;46.06	24,461,150	7,338,345,000
brNTD_R3	150;150	98.44;98.3	95.01;94.63	46.21;45.65	33,044,270	9,913,281,000
brNTD_R5	150;150	97.9;97.51	93.0;91.74	47.08;47.32	30,906,136	9,271,840,800
brNTD_a_R3	150;150	98.04;97.72	93.9;92.96	46.42;46.48	16,315,597	4,894,679,100
brNTD_a_R5	150;150	96.64;97.52	89.18;91.58	45.87;45.8	22,096,409	6,628,922,700
eGFP	150;150	96.93;97.3	90.9;90.01	53.41;53.45	384	115,200
lenti_sgRNA_zeo_backbone	150;150	96.36;96.17	88.88;86.06	51.34;51.04	9,911	2,973,300
mutE14K_R3	150;150	97.4;98.08	91.93;93.81	44.35;44.24	36,689,055	11,006,716,500
mutE14K_R4	150;150	97.65;97.26	92.54;90.97	44.77;44.8	14,543,200	4,362,960,000
mutE14K_a_R3	150;150	97.33;98.07	91.75;93.86	44.78;44.77	28,898,725	8,669,617,500
mutE14K_a_R4	150;150	97.58;97.29	92.45;91.34	46.26;46.21	18,060,737	5,418,221,100
mutG261S_R5	150;150	97.8;97.5	93.08;91.88	45.06;44.89	24,019,731	7,205,919,300
mutG261S_R6	150;150	97.51;97.6	92.25;92.14	44.52;44.55	17,114,171	5,134,251,300
mutG261S_a_R5	150;150	97.36;96.9	91.73;89.88	45.67;45.75	10,418,342	3,125,502,600
mutG261S_a_R6	150;150	97.2;97.34	91.3;91.31	44.38;44.5	21,746,682	6,524,004,600
rigs_11	150;150	98.18;98.58	93.97;95.02	50.1;51.26	30,750	9,225,000
rigs_14	150;150	98.05;98.69	93.56;95.4	49.25;49.73	34,930	10,479,000
rigs_17	150;150	98.23;98.62	94.17;95.29	49.57;49.94	47,906	14,371,800
rigs_2	150;150	98.41;98.91	94.71;96.05	49.56;50.74	39,580	11,874,000

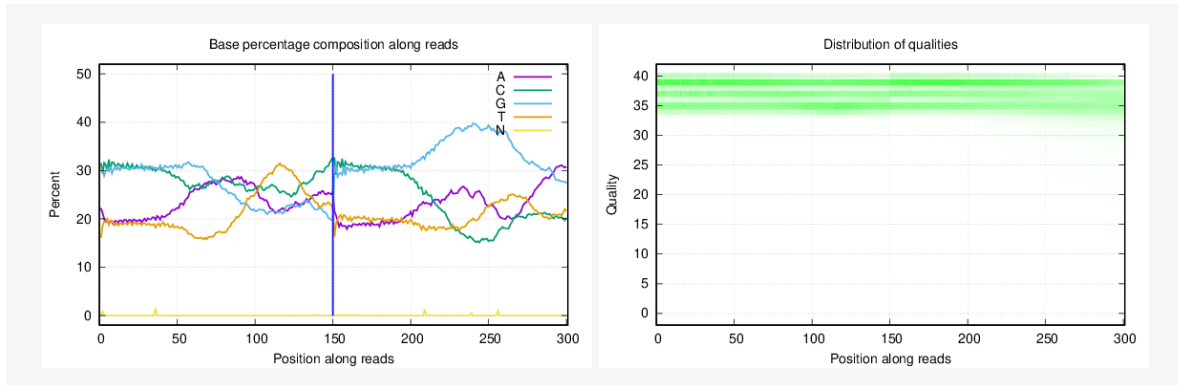
Table Format:

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

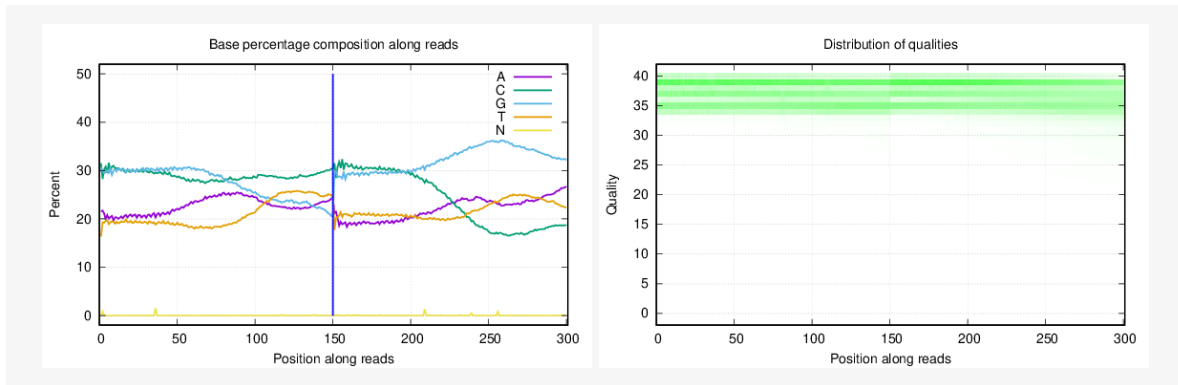
Data Quality Control

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.

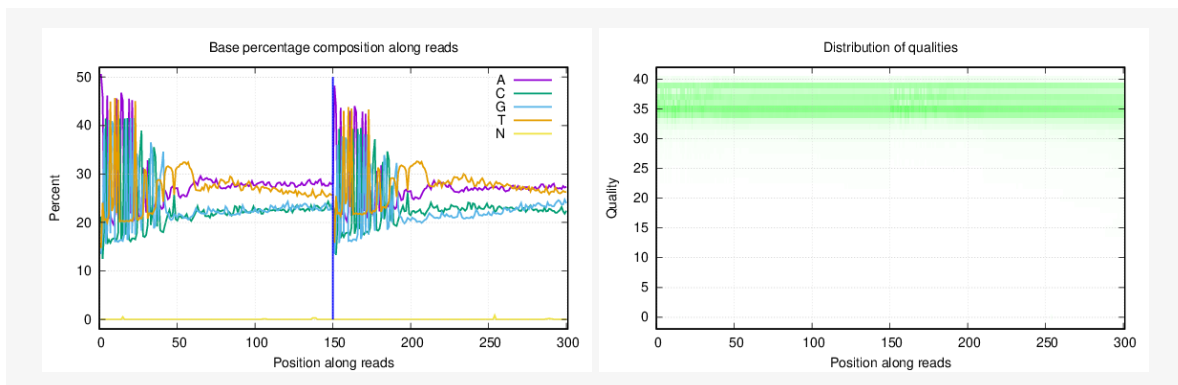
06SnBl1



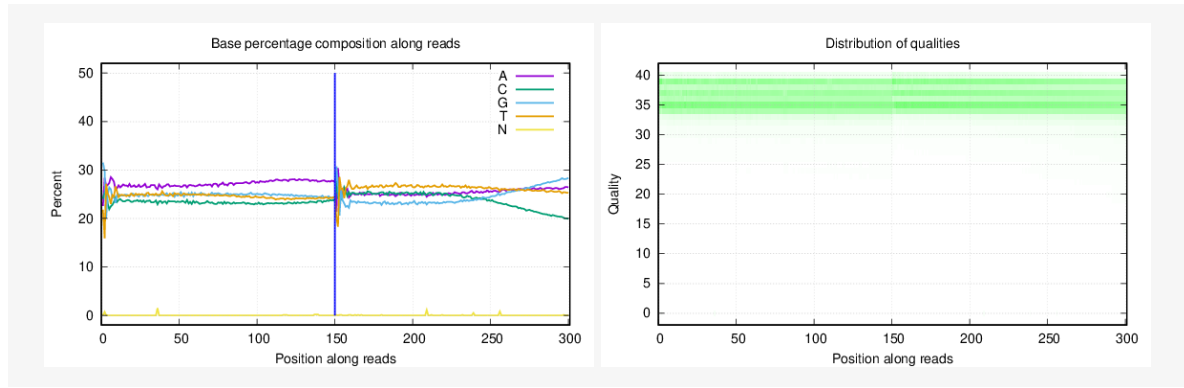
07SnBl1



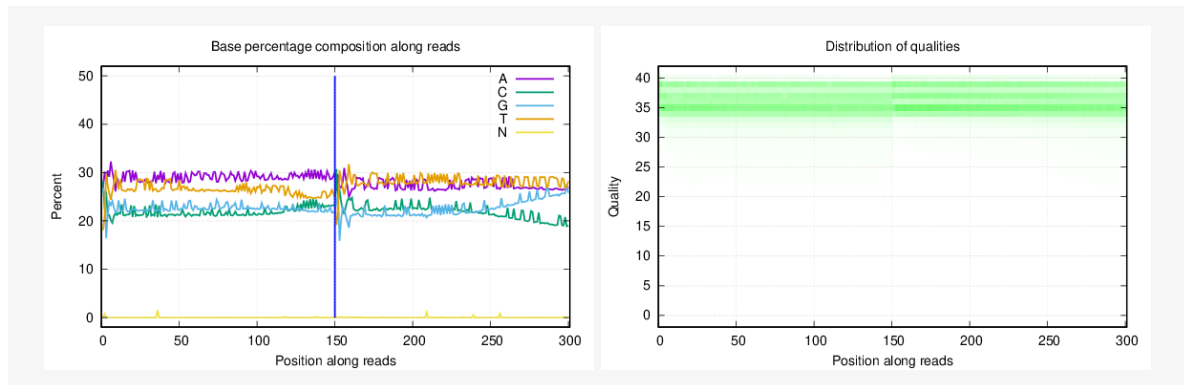
1



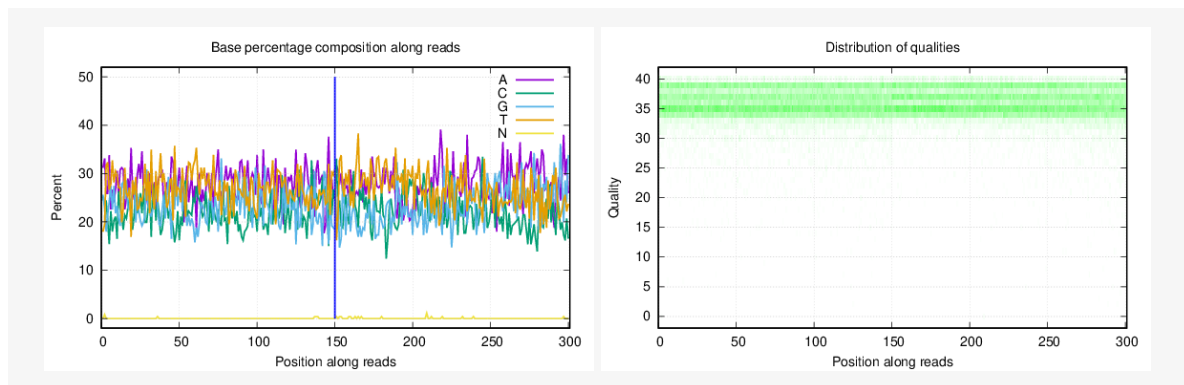
146-1_5v1



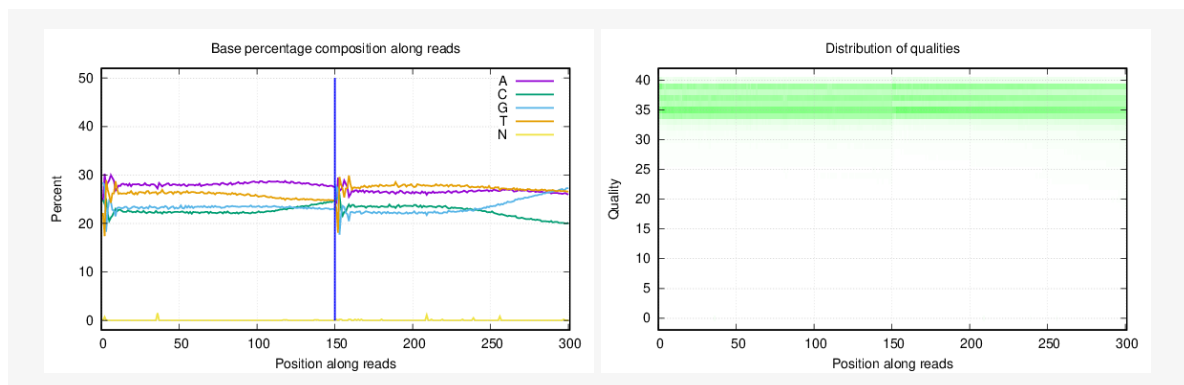
146_1_1v1



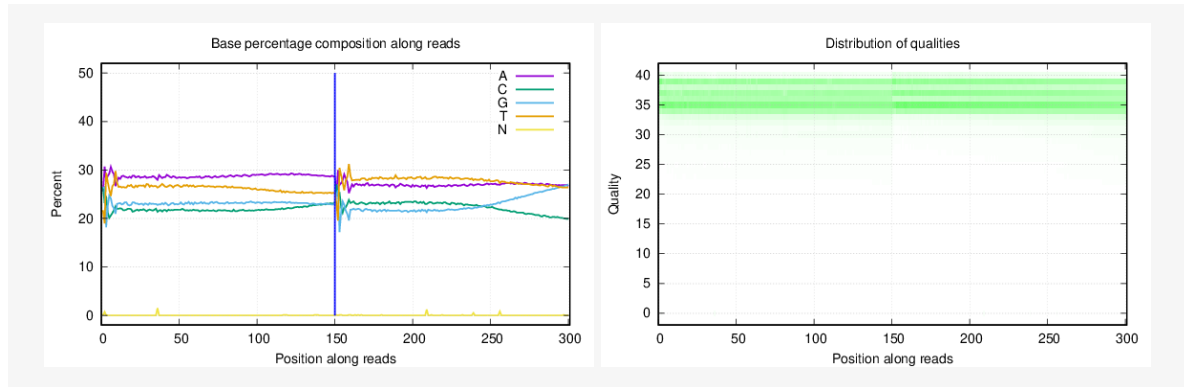
146_1_1v6



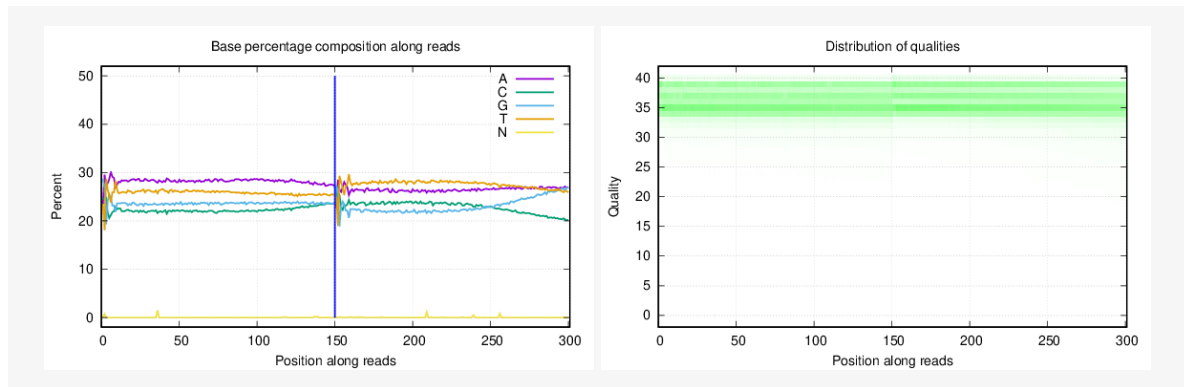
146_1_6v1



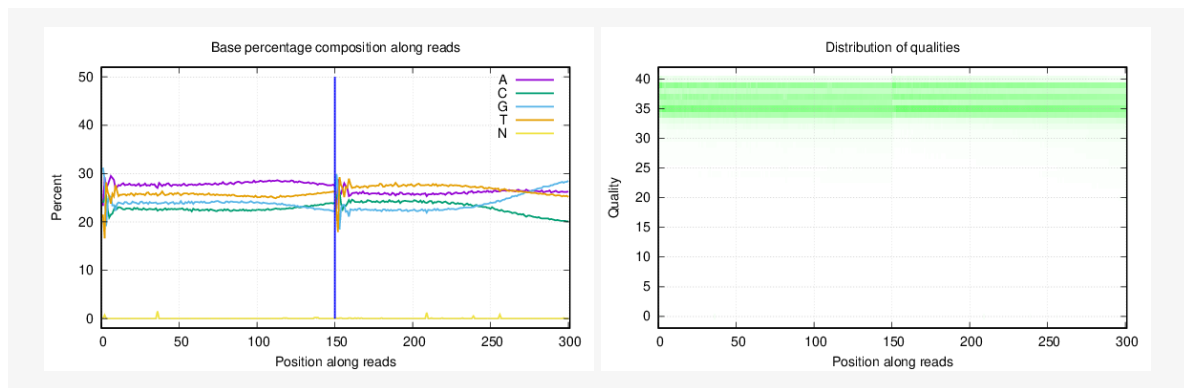
146_1_o_10



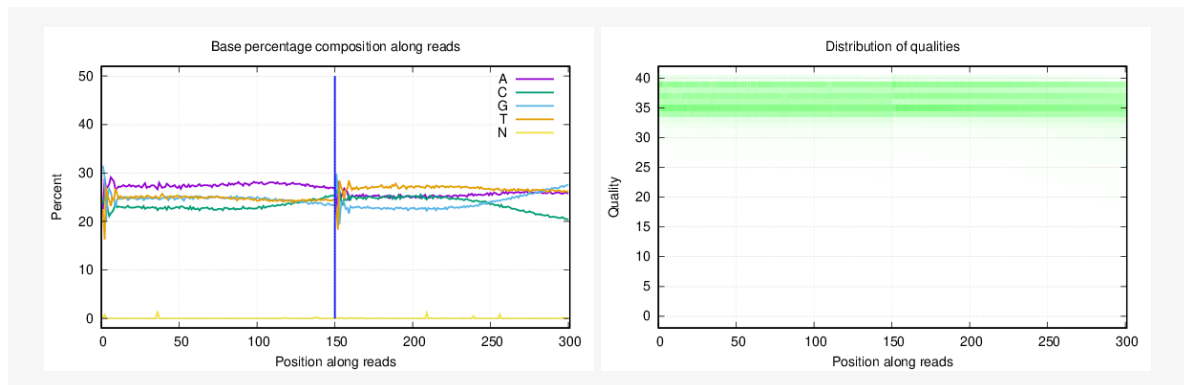
146_1_o_8



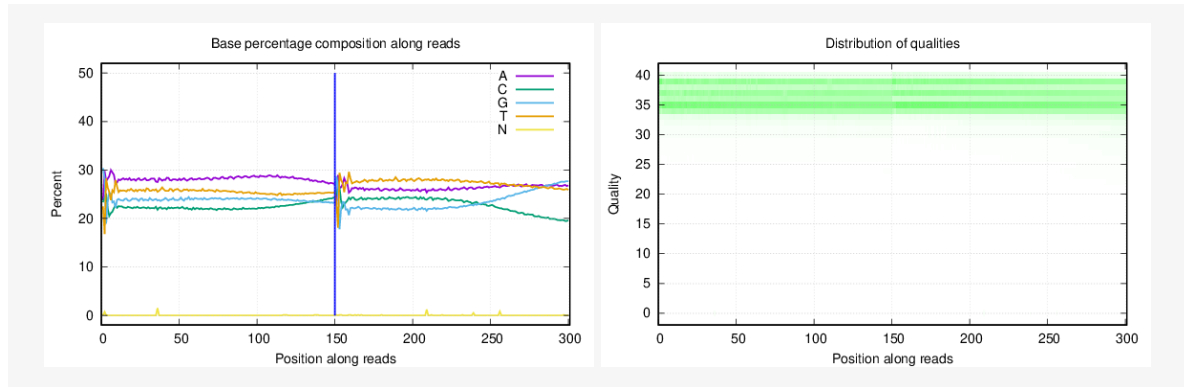
149-1_20v6



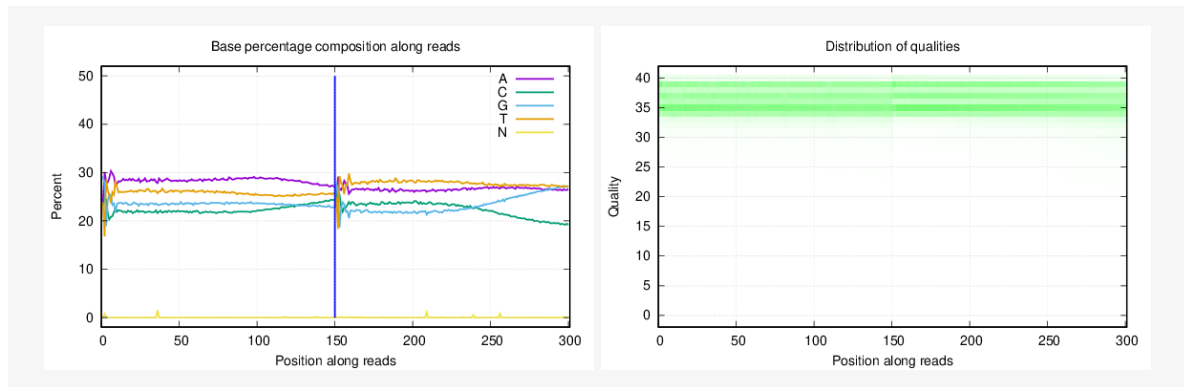
149-1_6v1



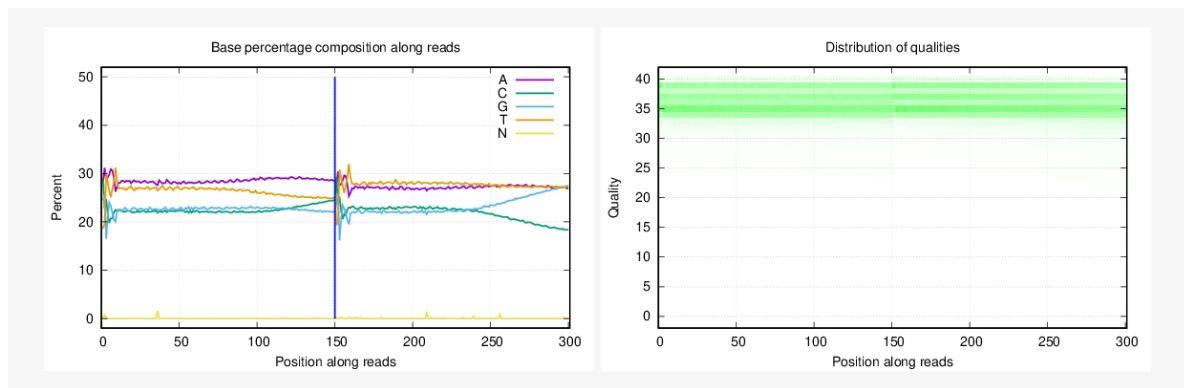
149-4_3v1



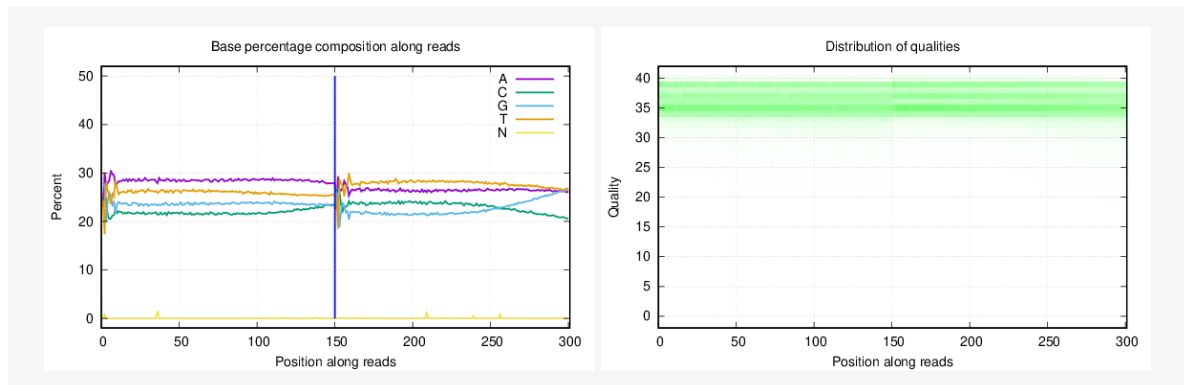
149-4_7v6



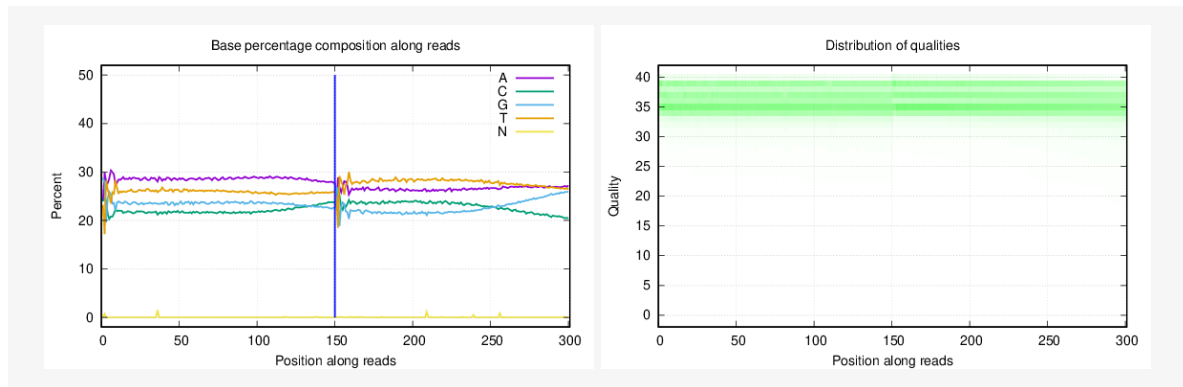
149_1_1v1



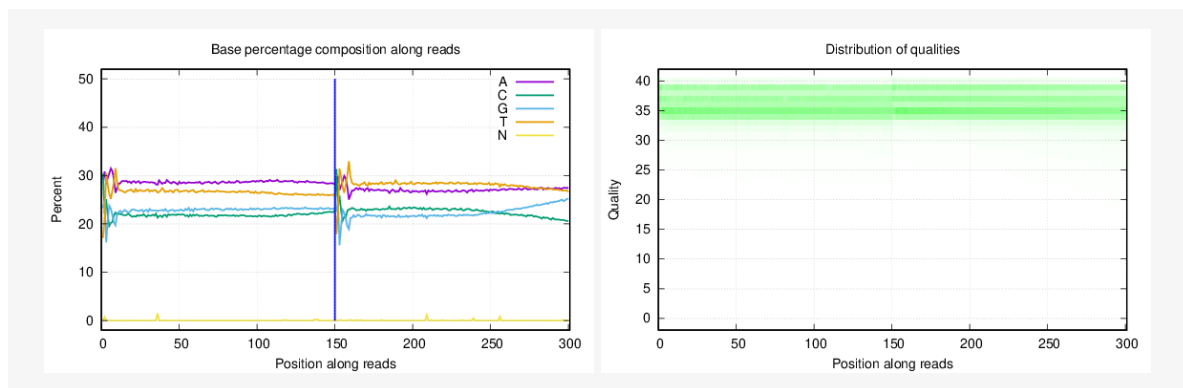
149_1_o_14



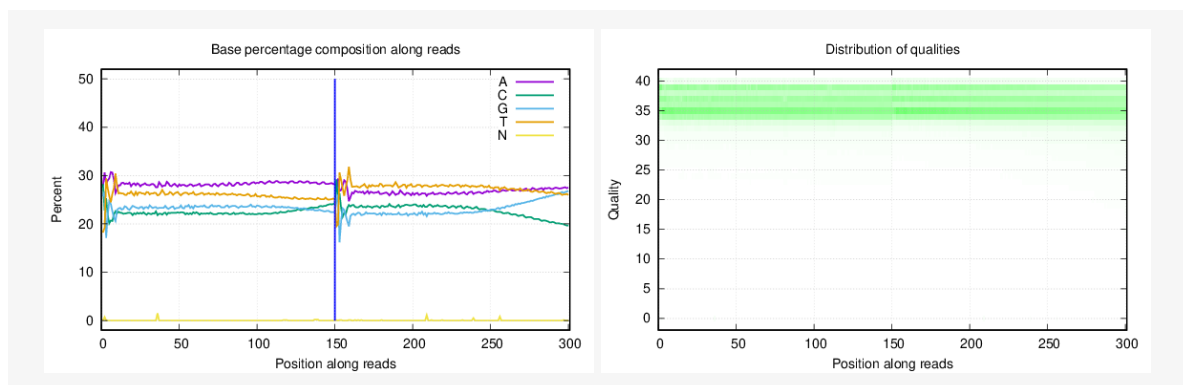
149_1_o_17



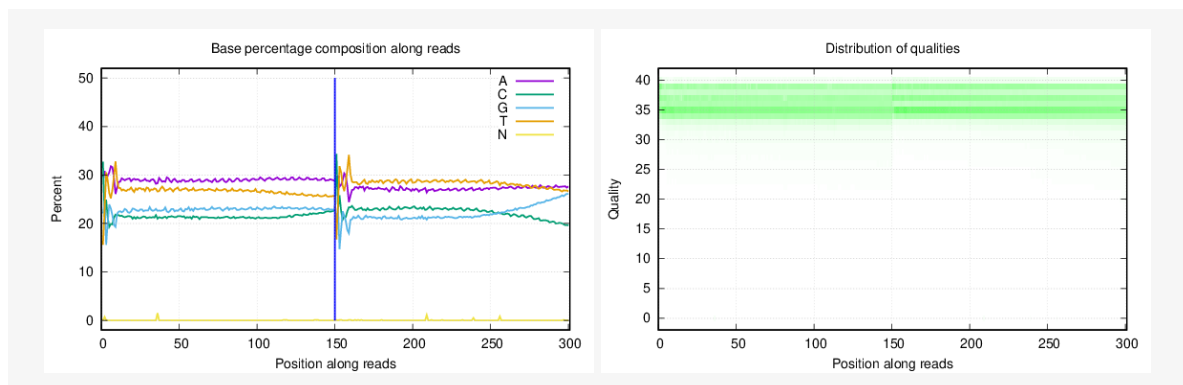
149_4_o_14



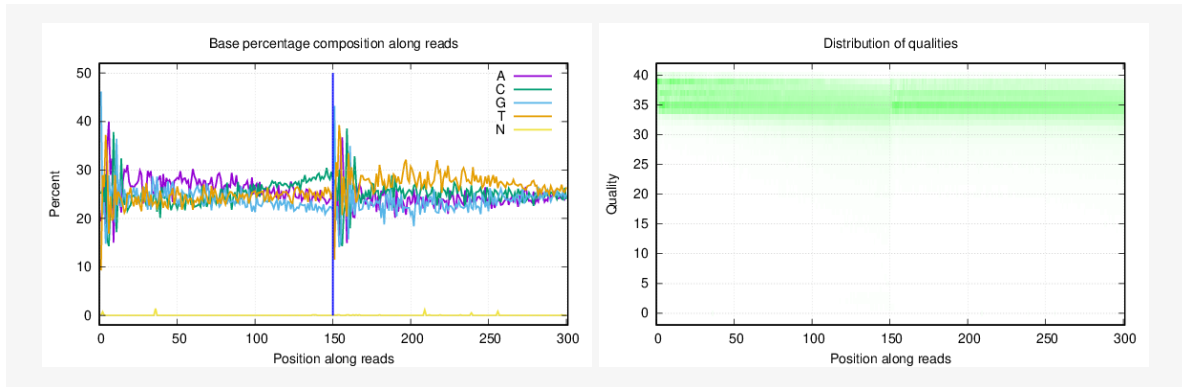
149_4_o_2



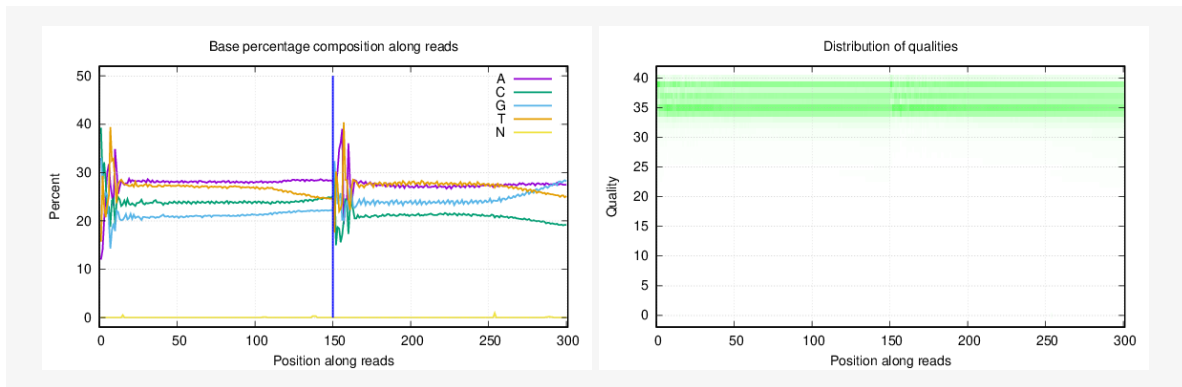
149_4_o_4



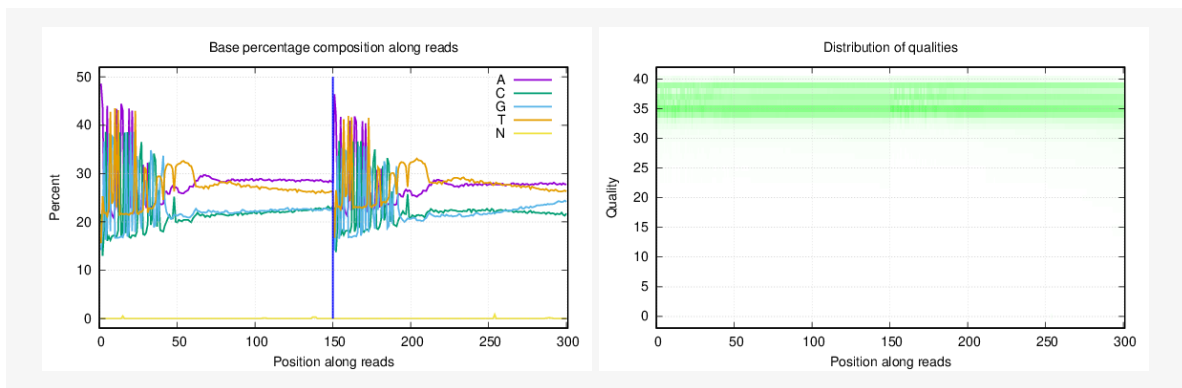
14_t_vec_stag2



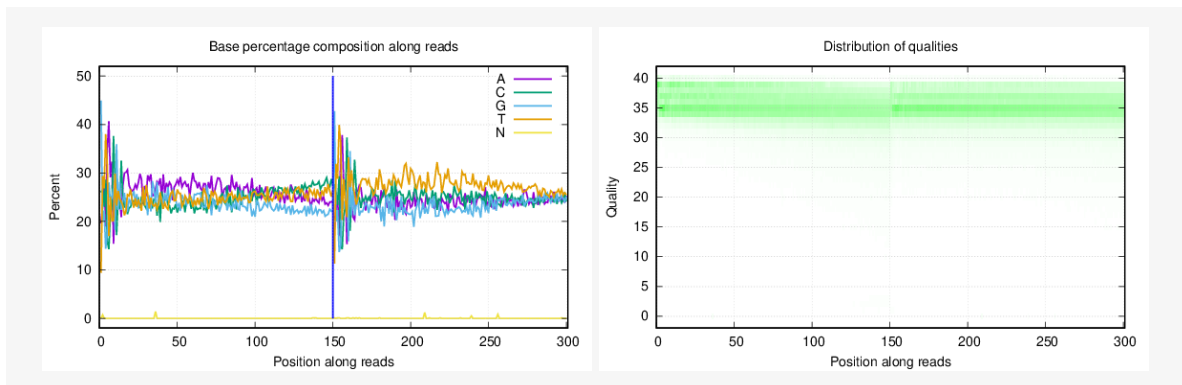
1_2



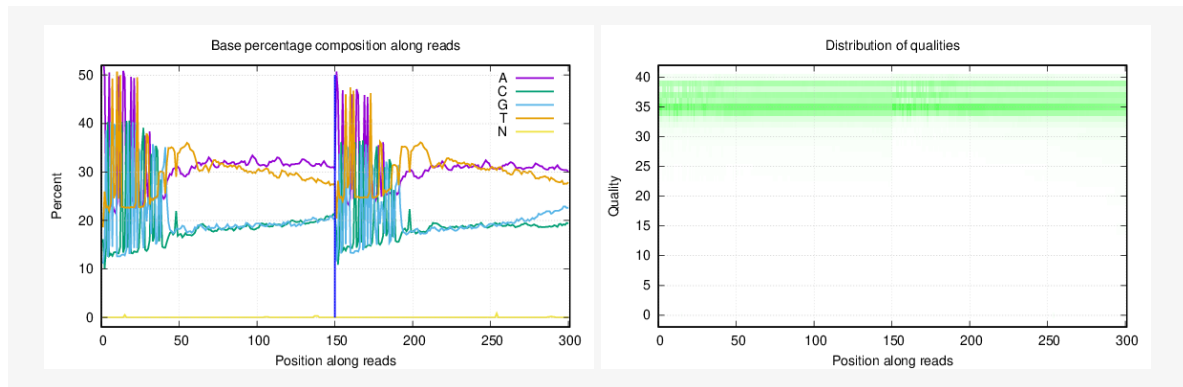
2



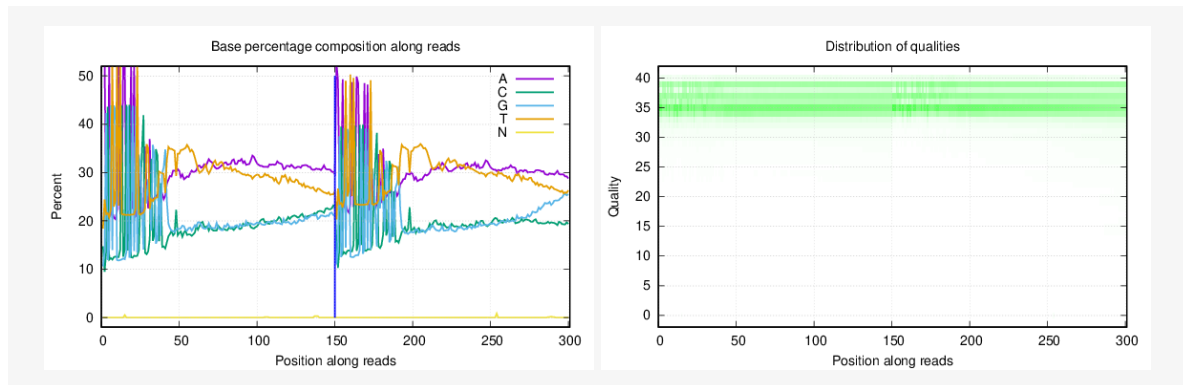
23_t_vec_stag2



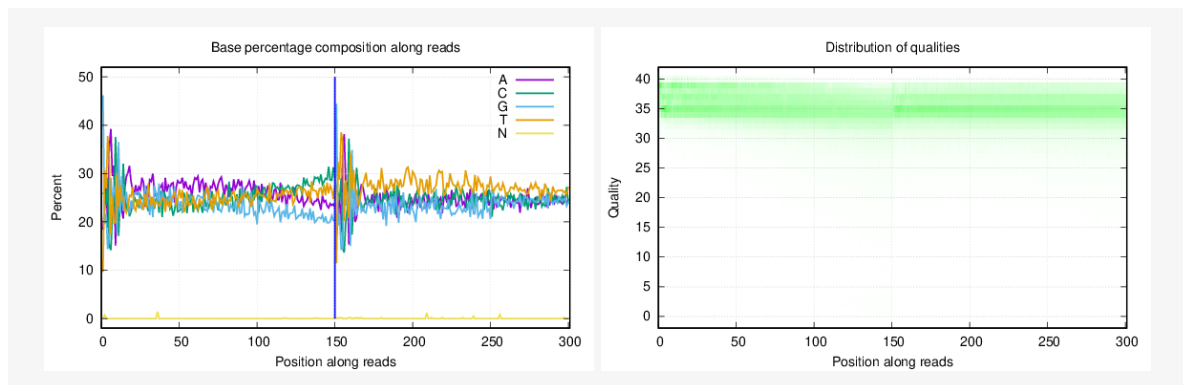
25G



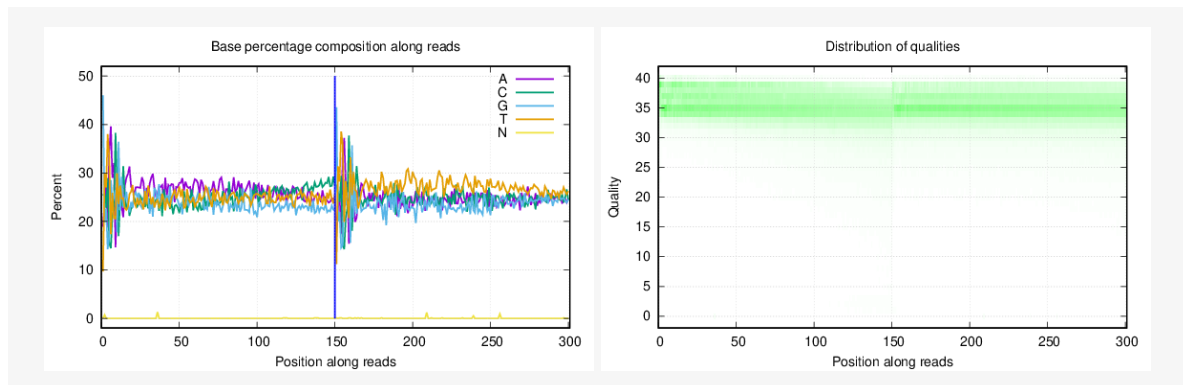
25M



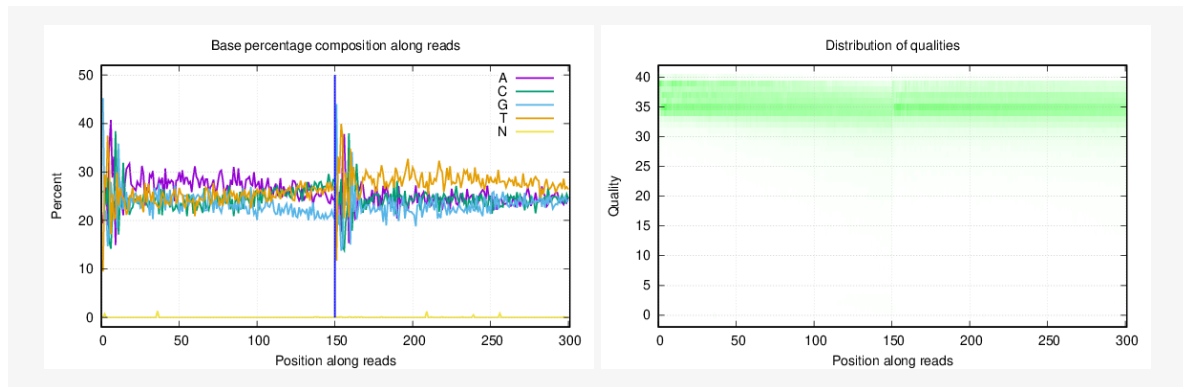
26_t_vec_stag2



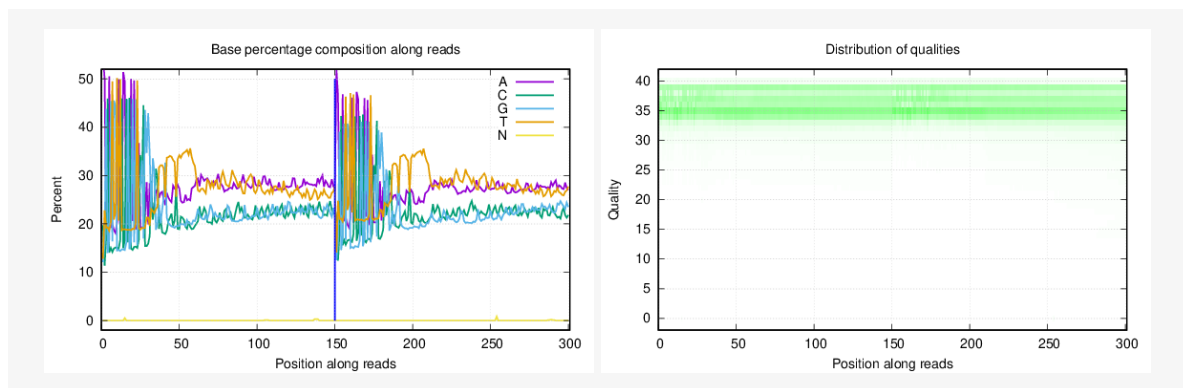
28_t_vec_stag2



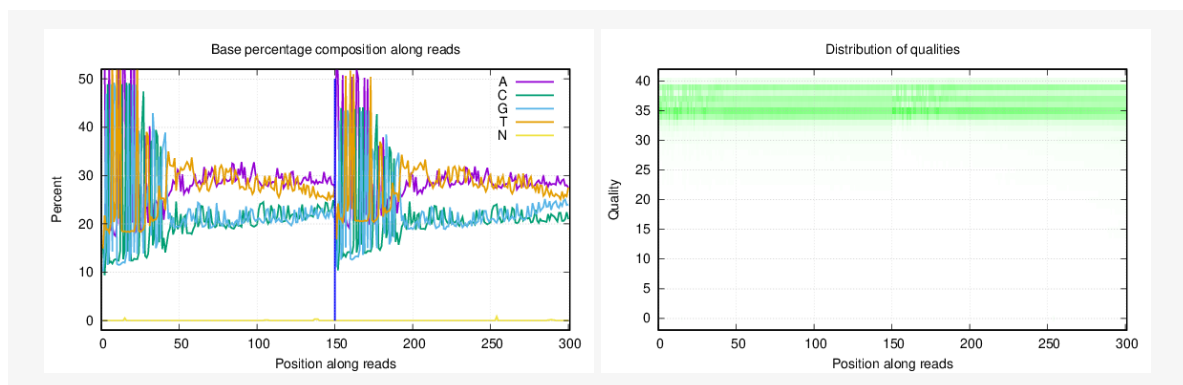
2_t_vec_stag2



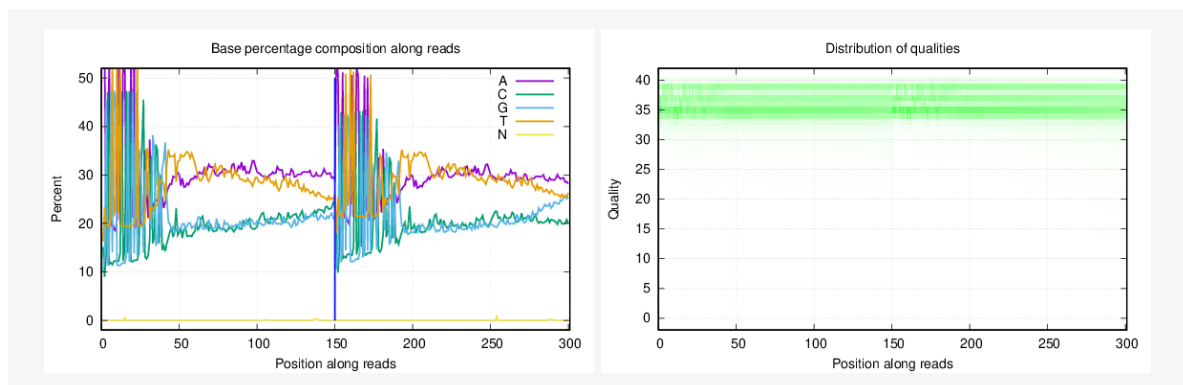
3



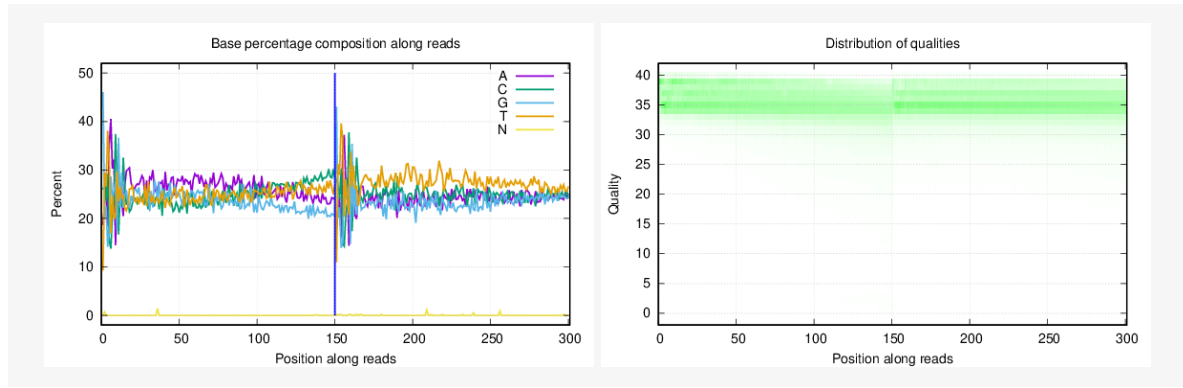
31G



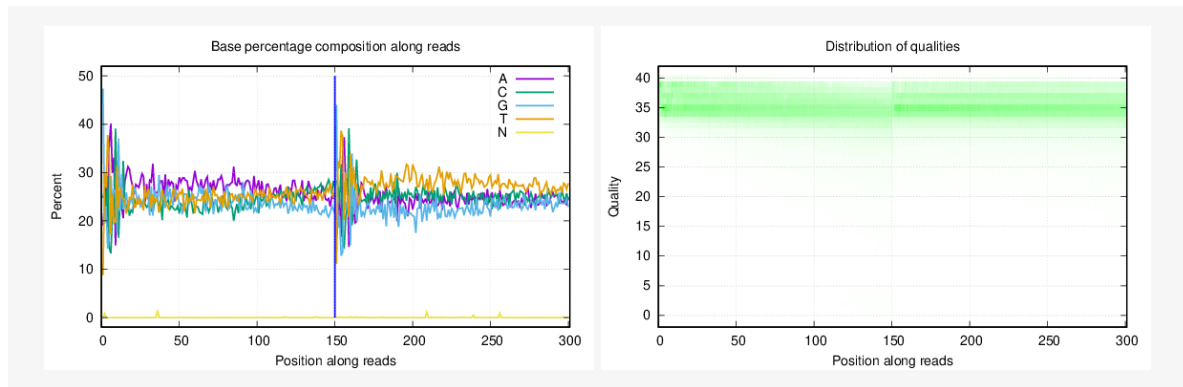
31M



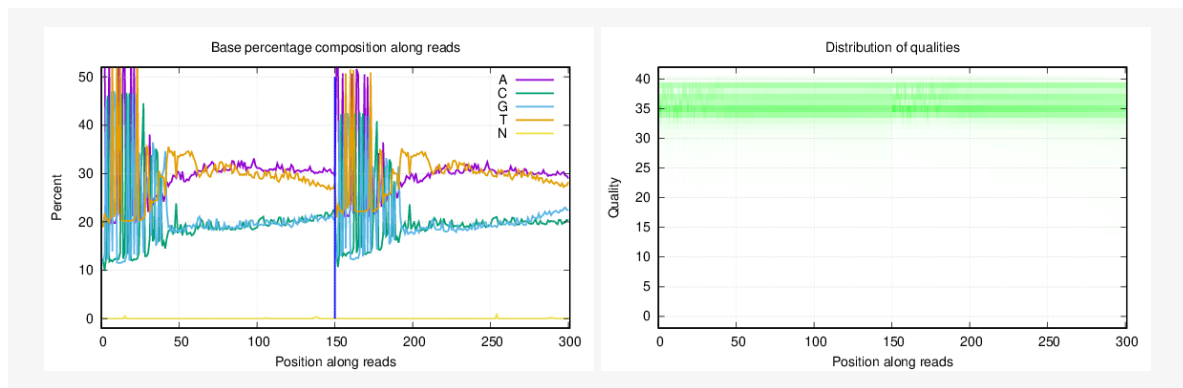
31_t_vec_stag2



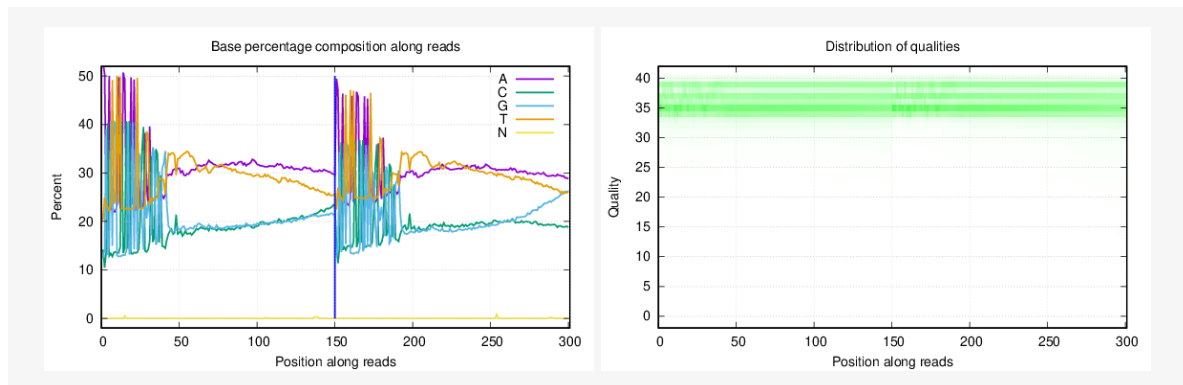
39_t_vec_stag2



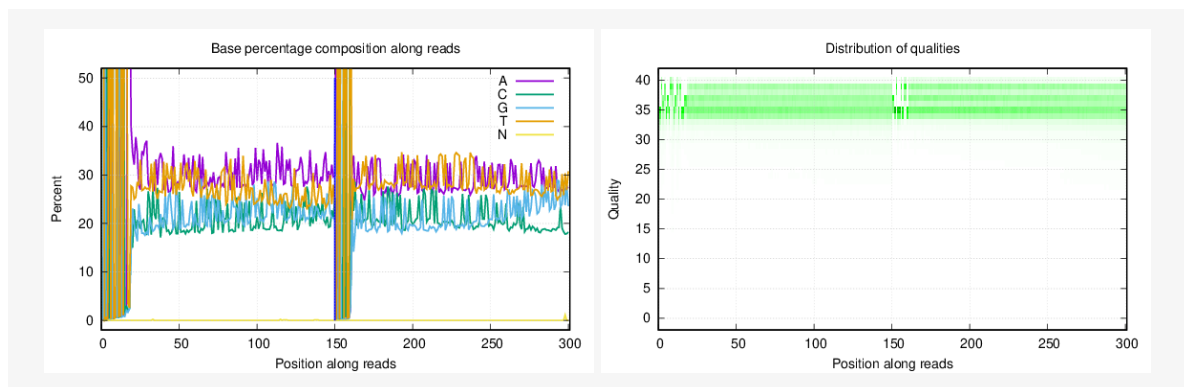
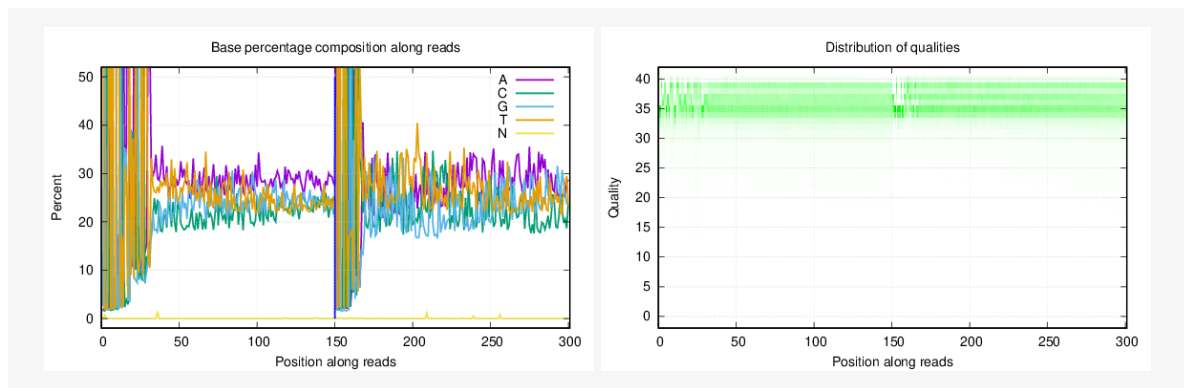
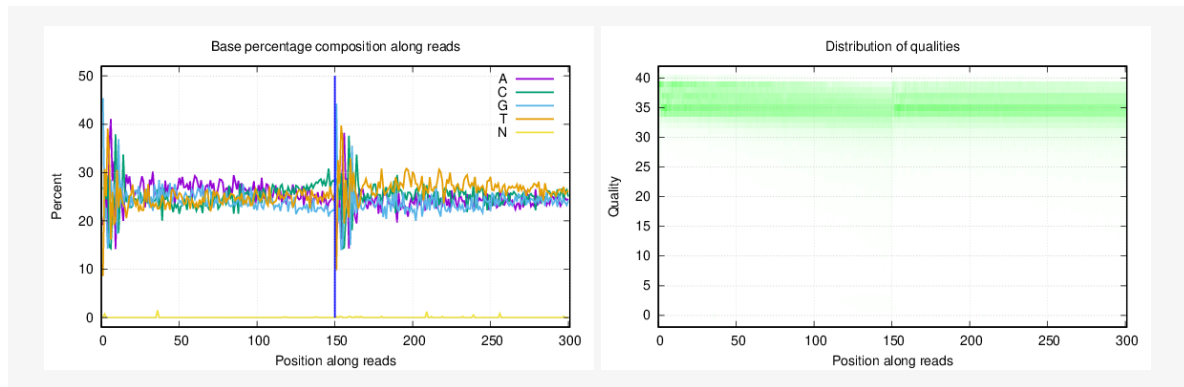
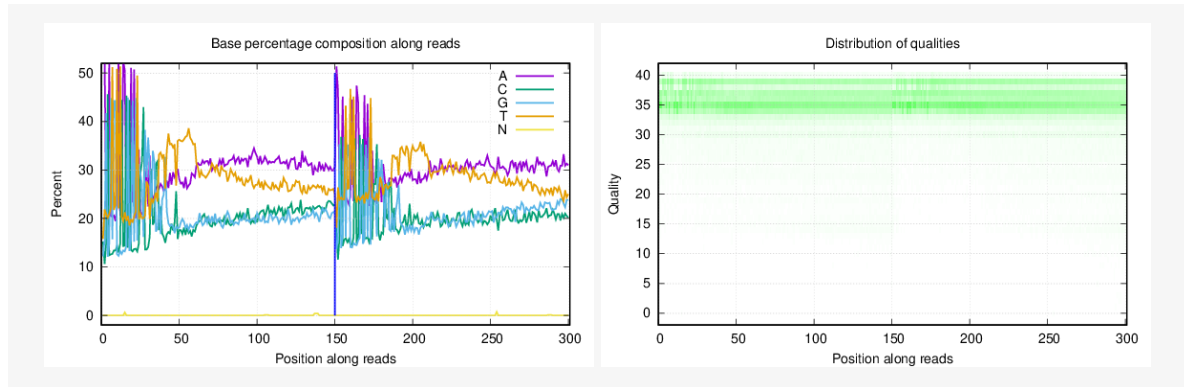
3G

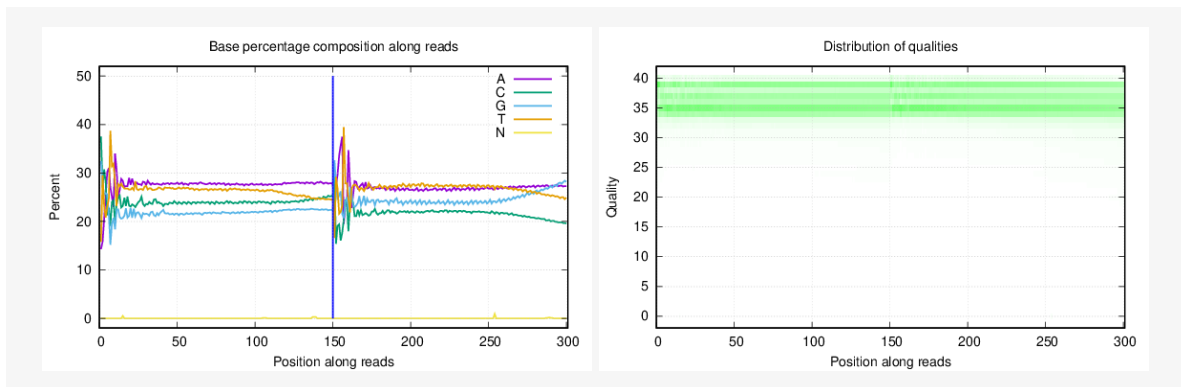
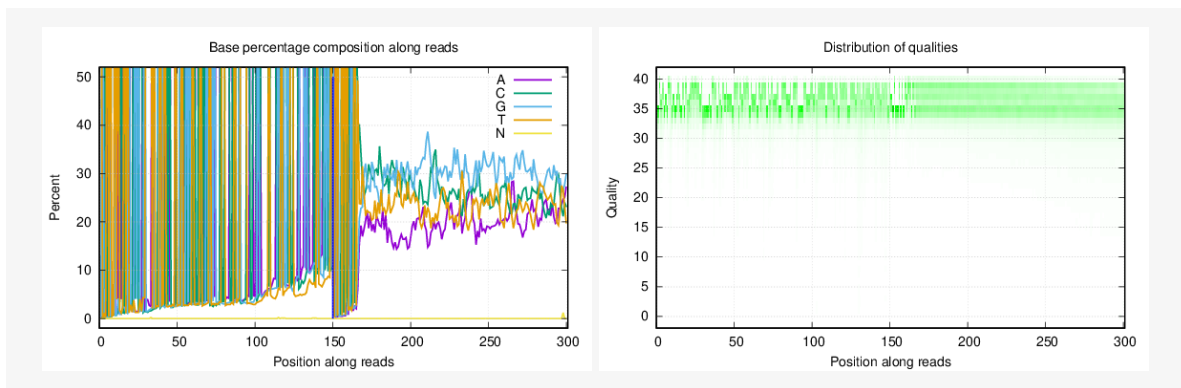
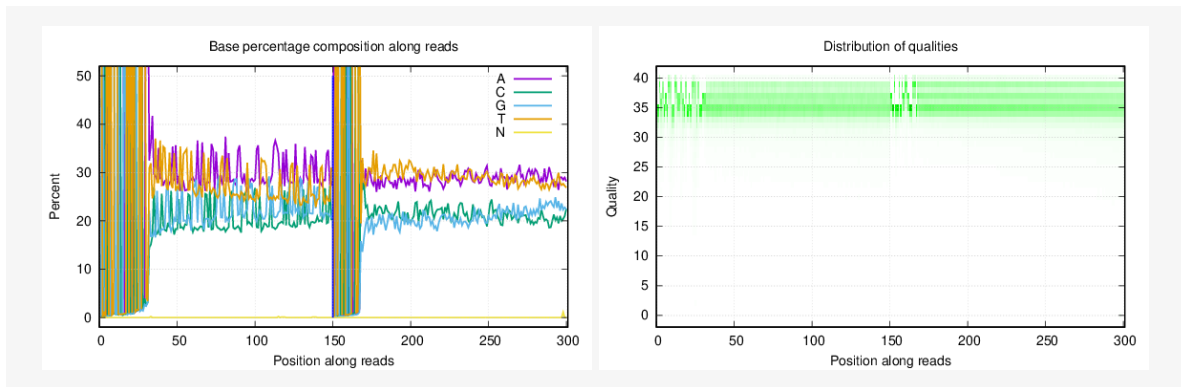
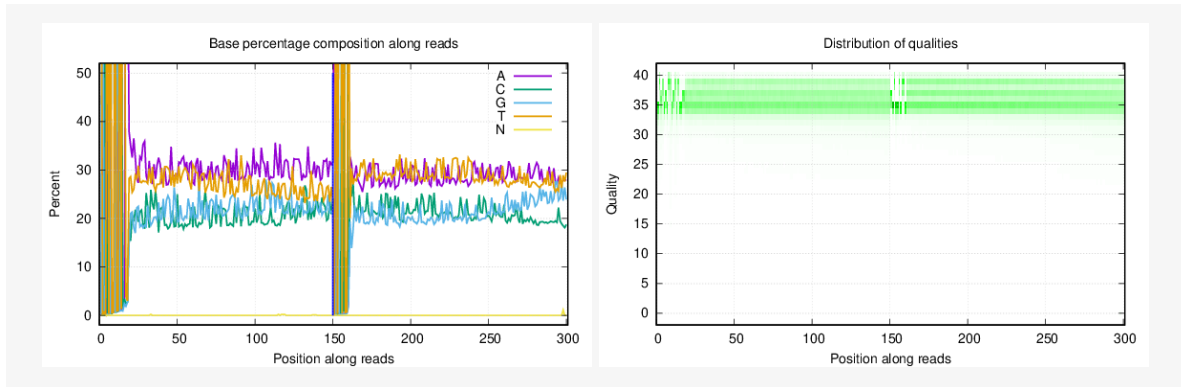


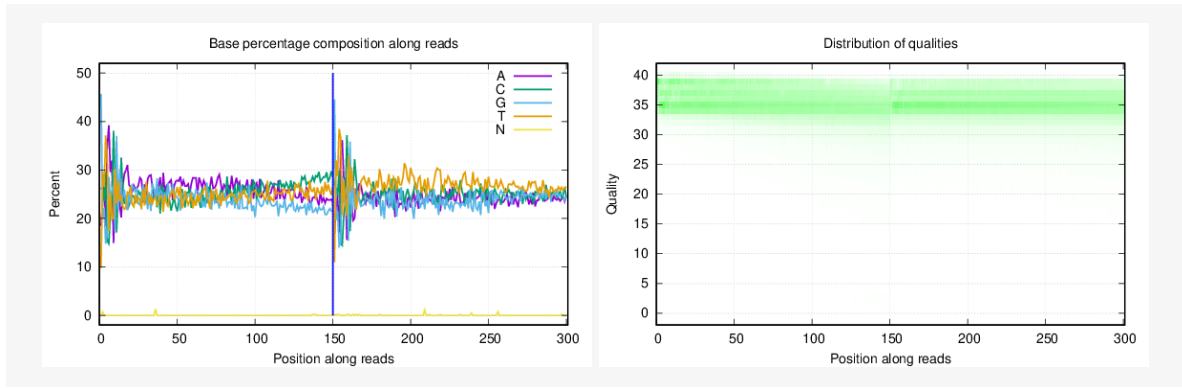
3M



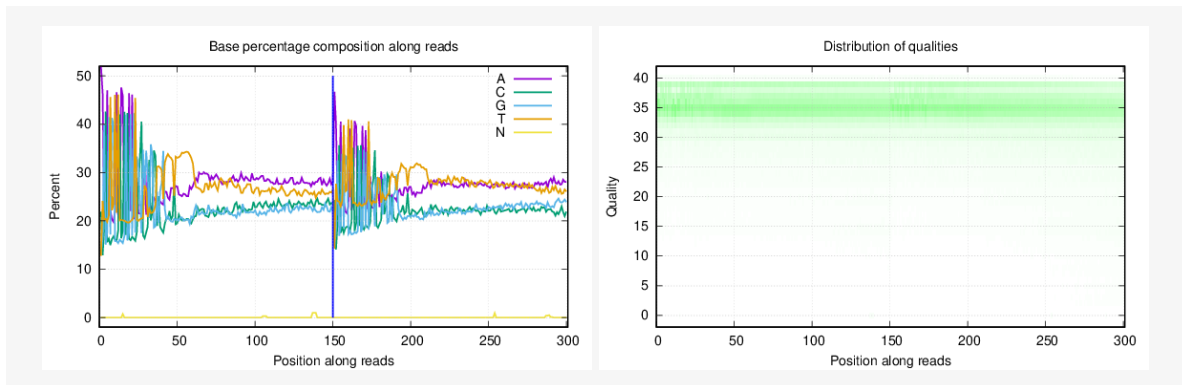
4



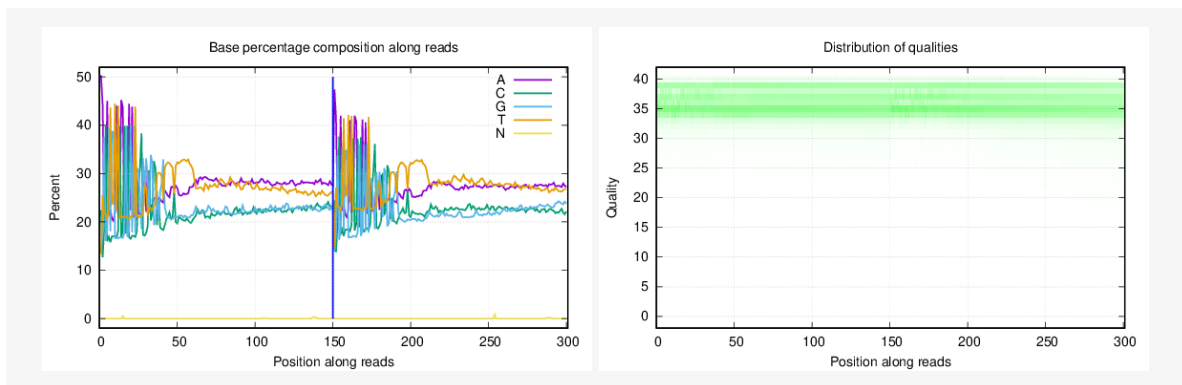




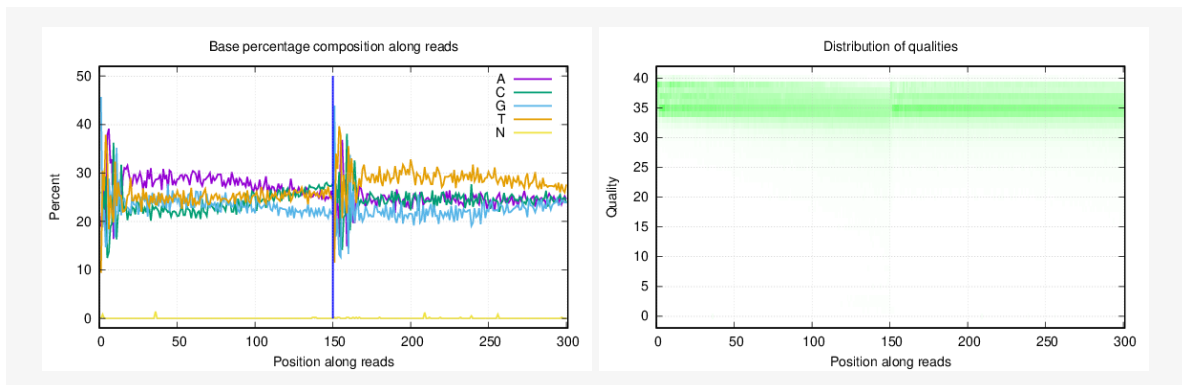
5



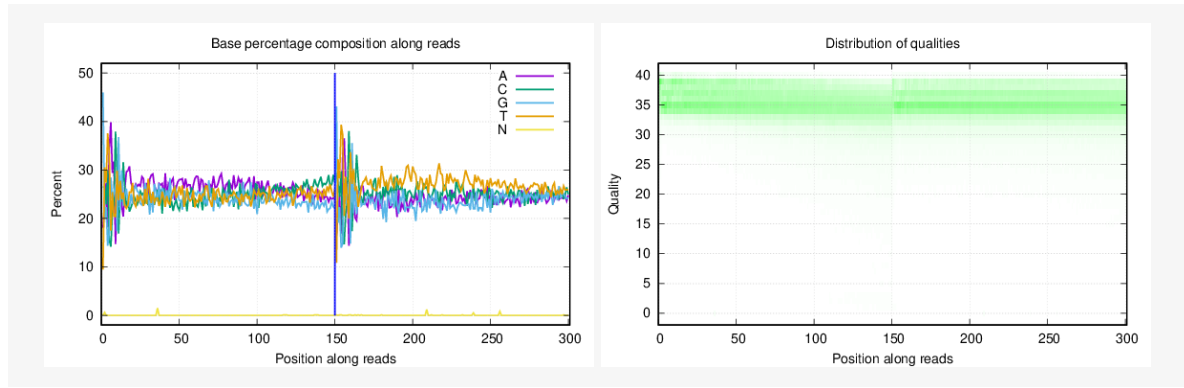
6



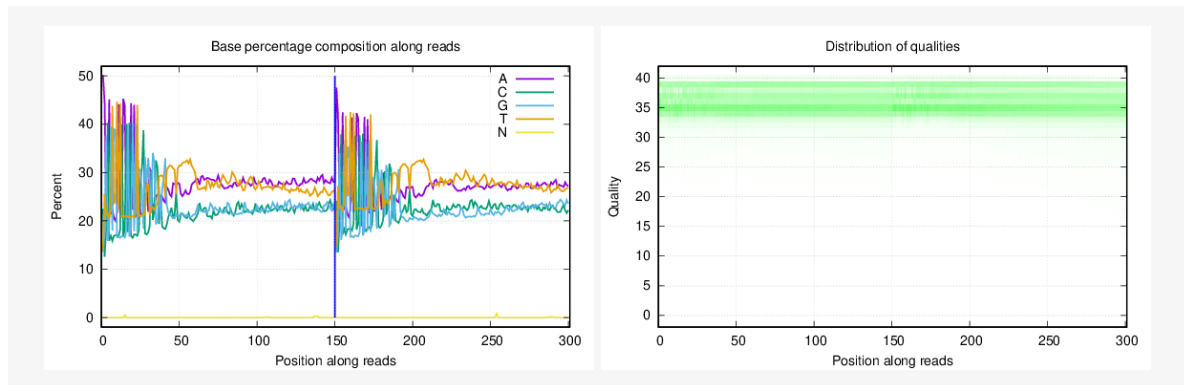
60_t_vec_stag2



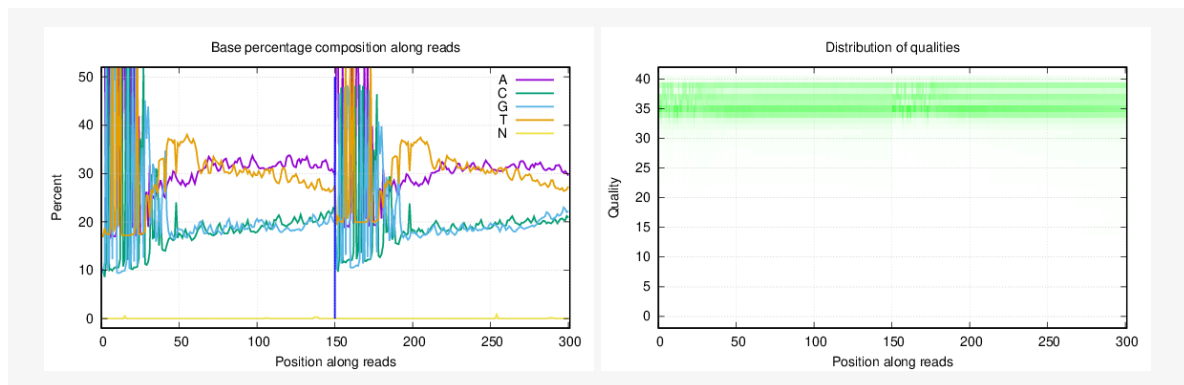
62_t_vec_stag2



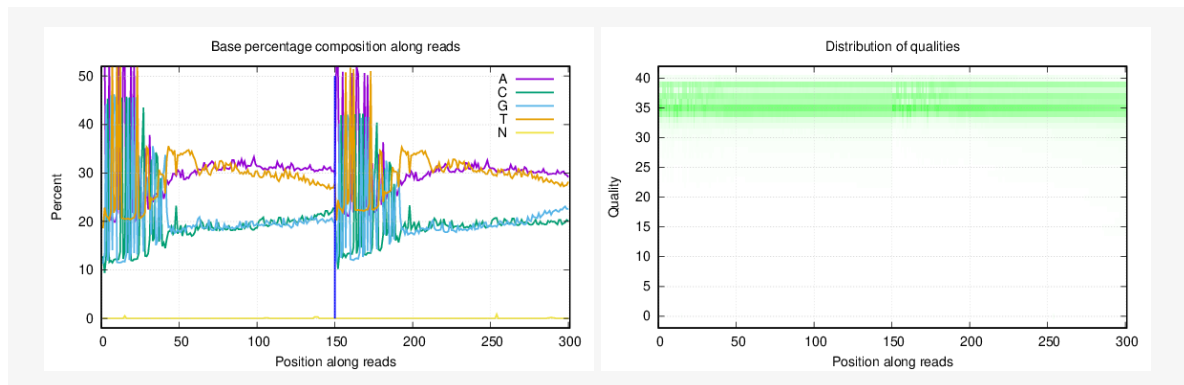
7



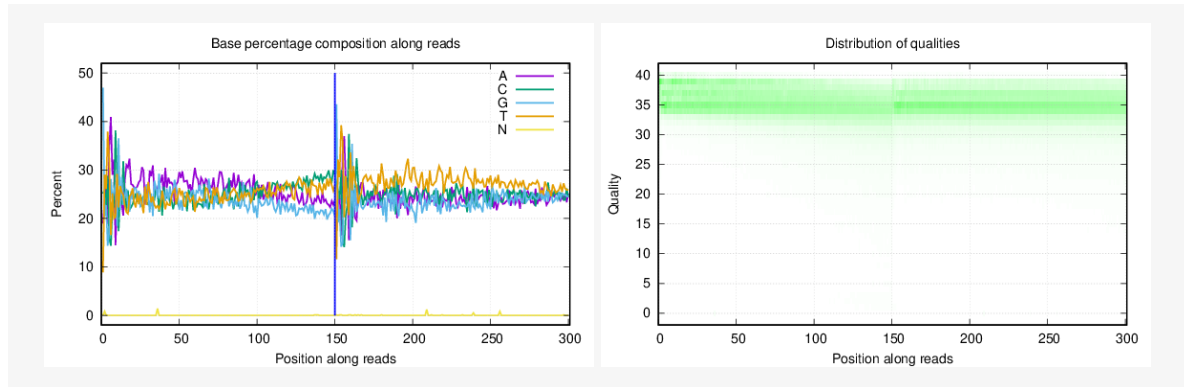
8G



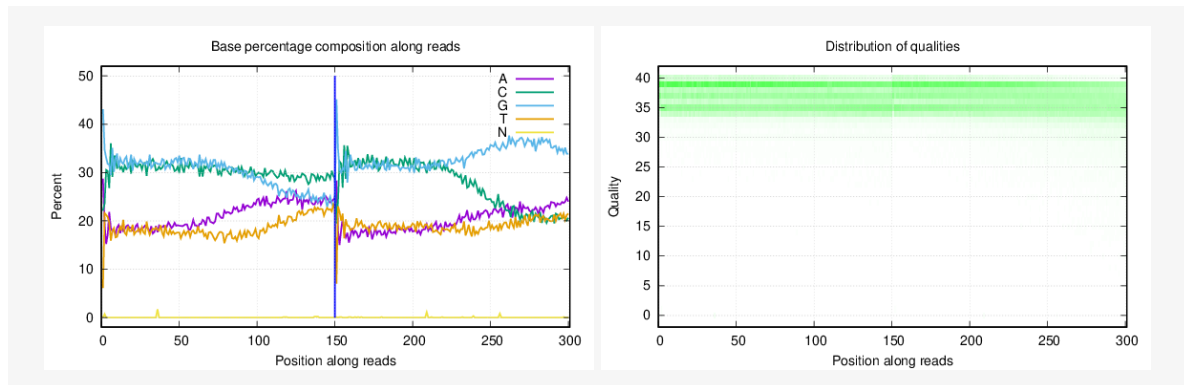
8M



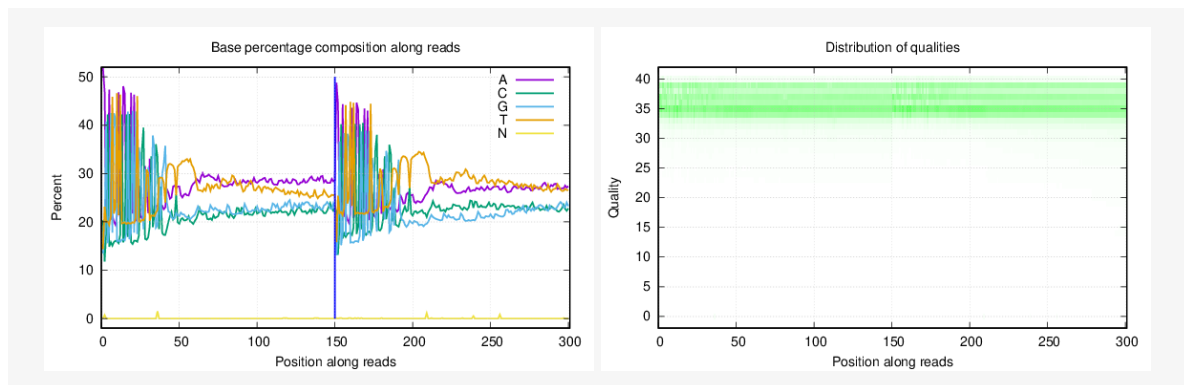
8_t_vec_stag2



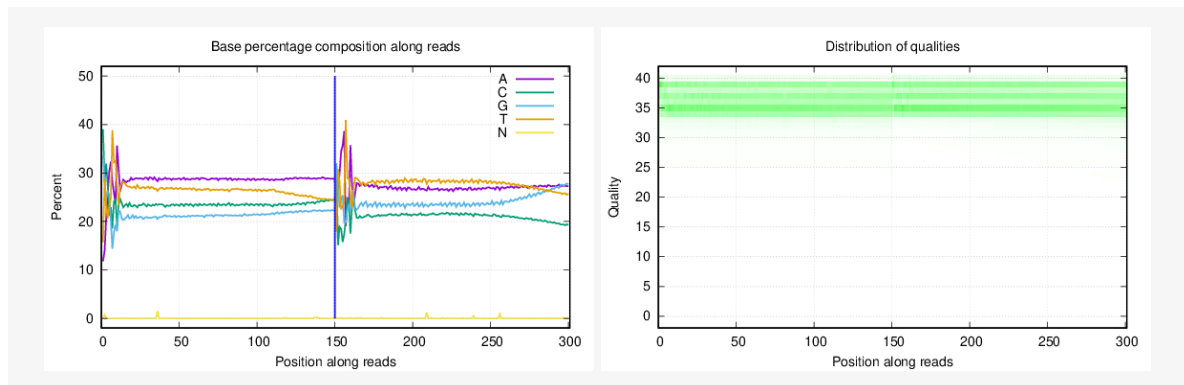
BOV-3



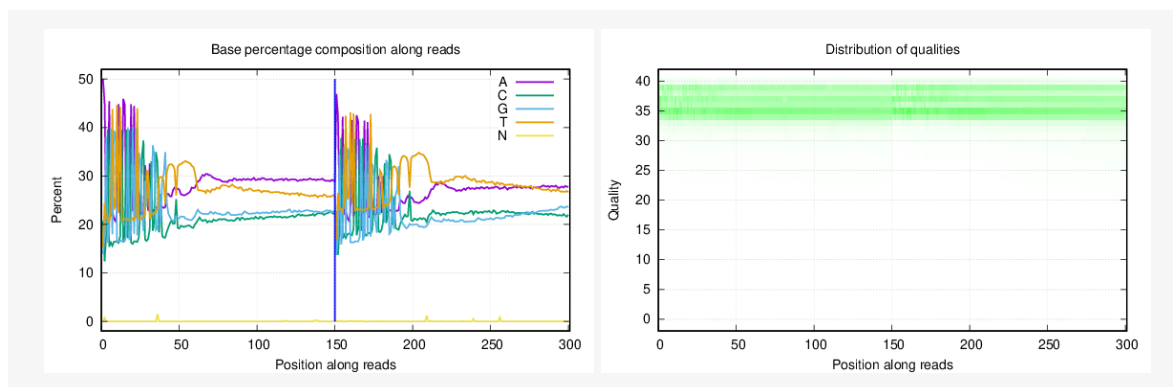
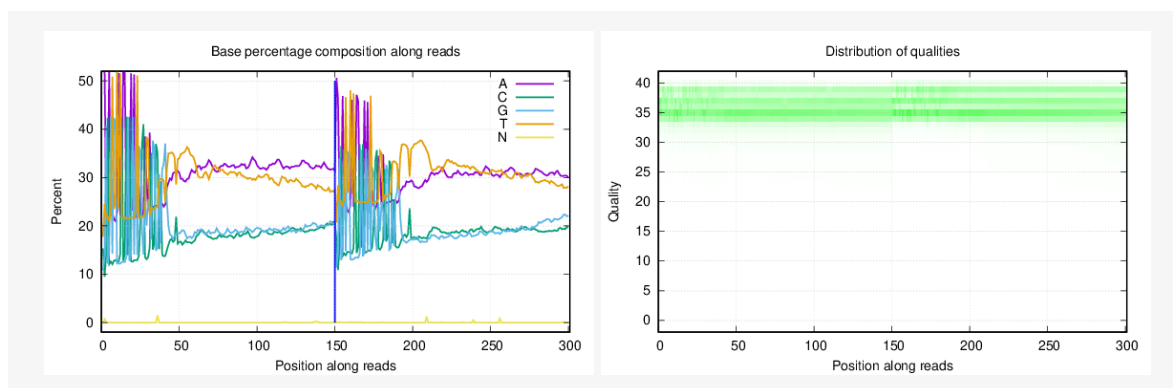
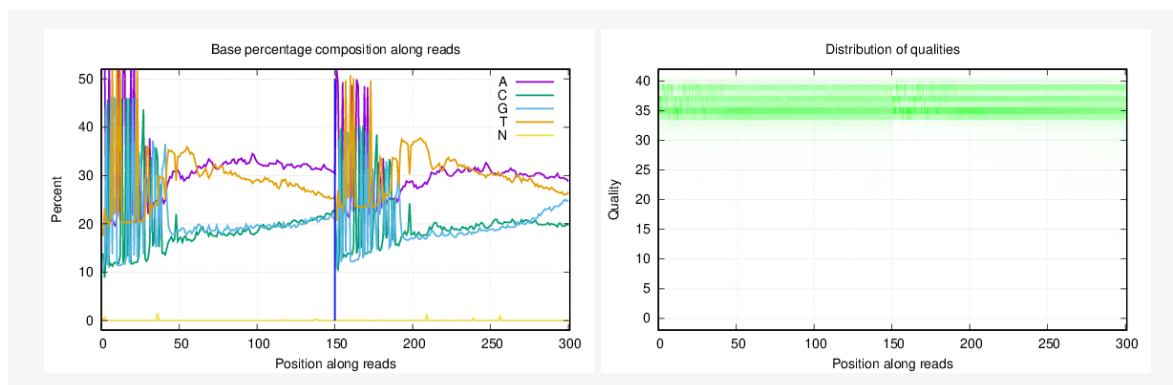
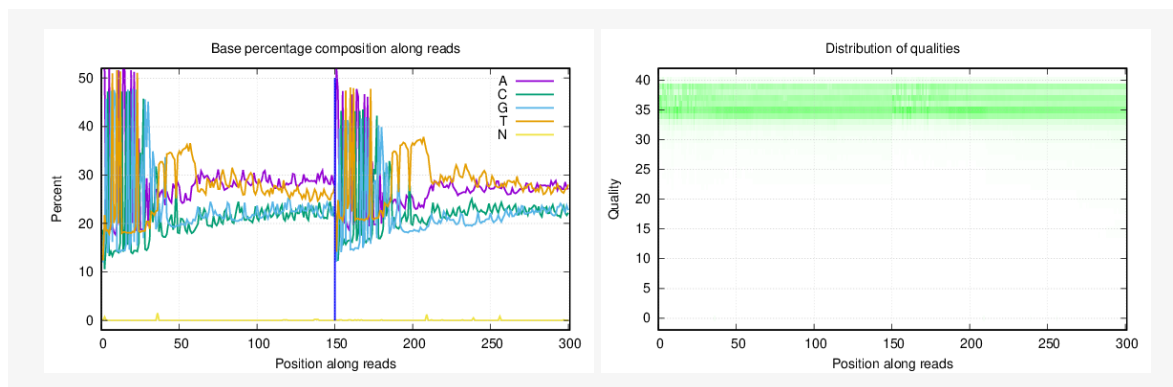
B_1

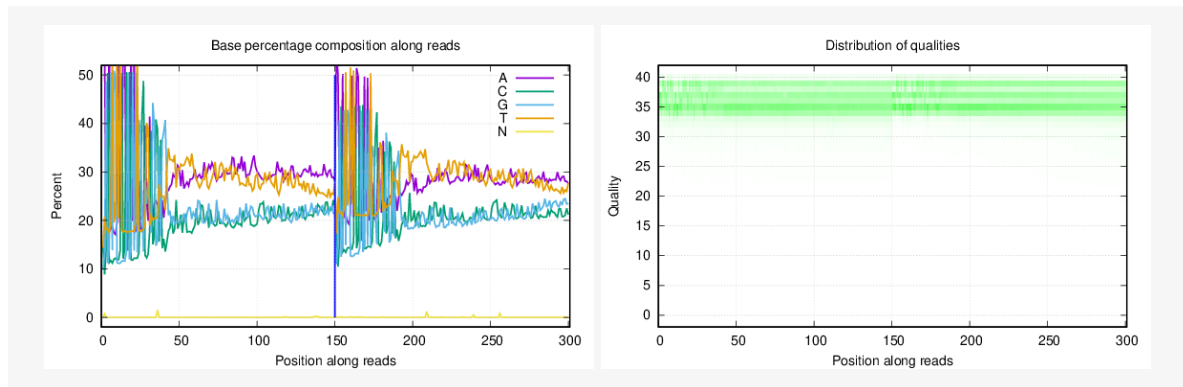


B_1_2

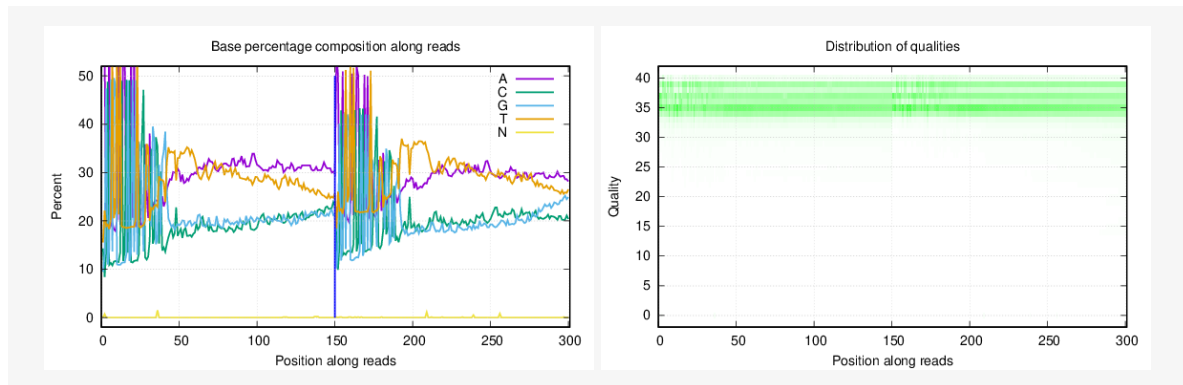


B_2

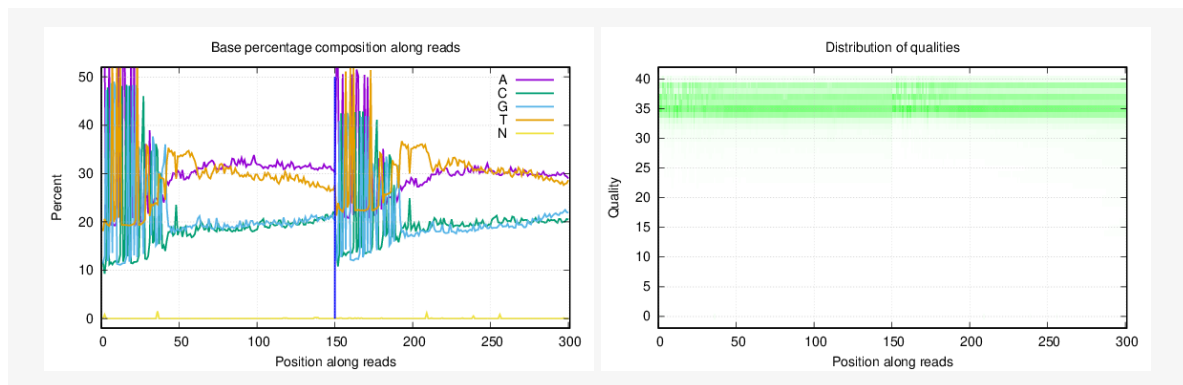
**B_25G****B_25M****B_3****B_31G**



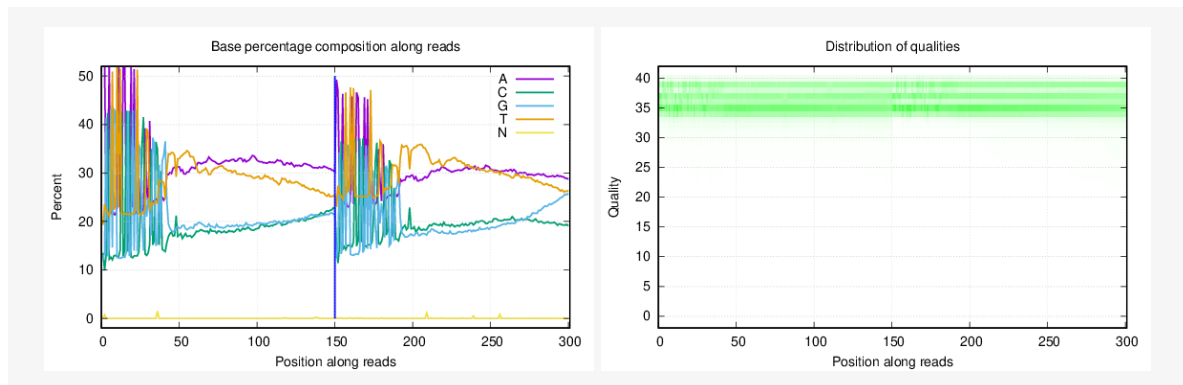
B_31M



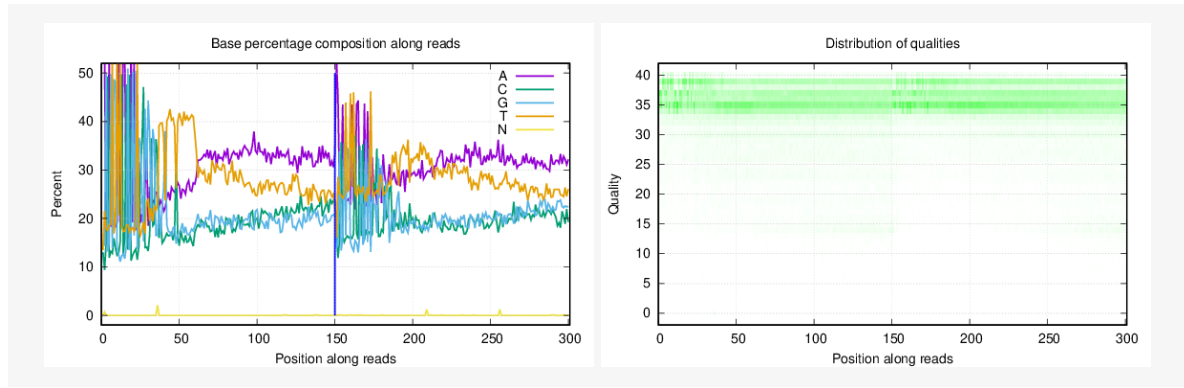
B_3G



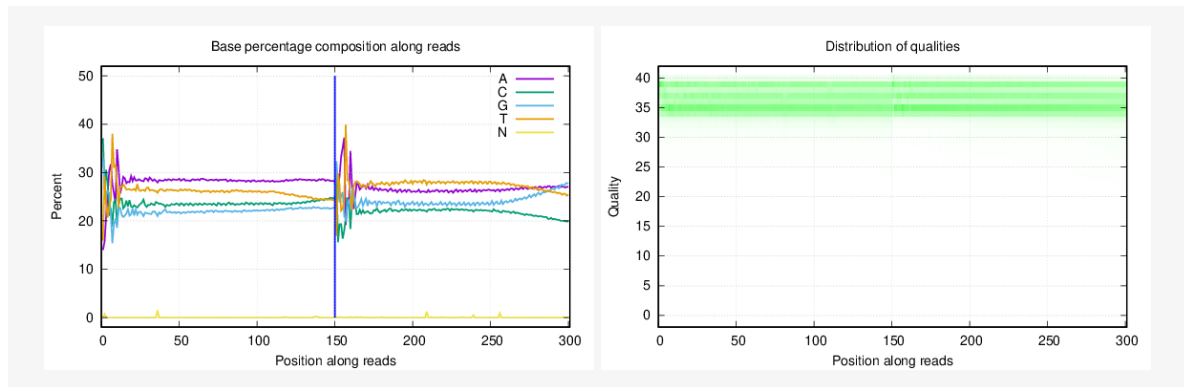
B_3M



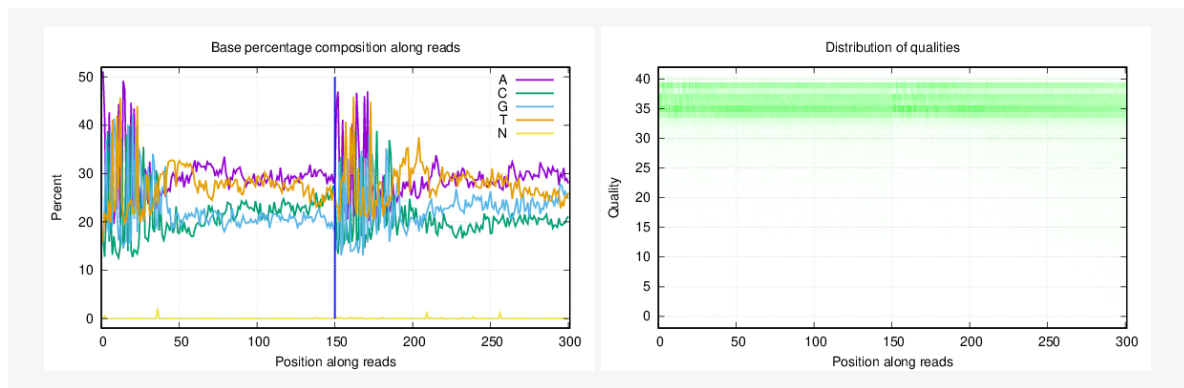
B_4



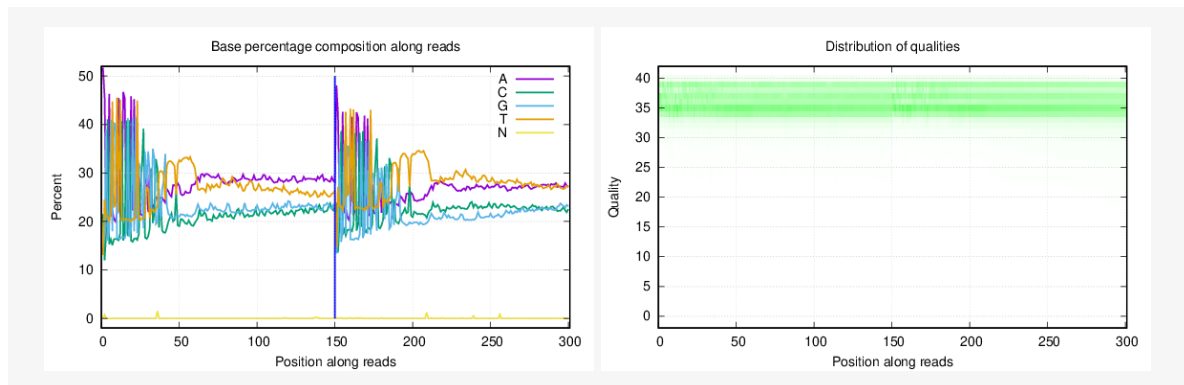
B_4_1



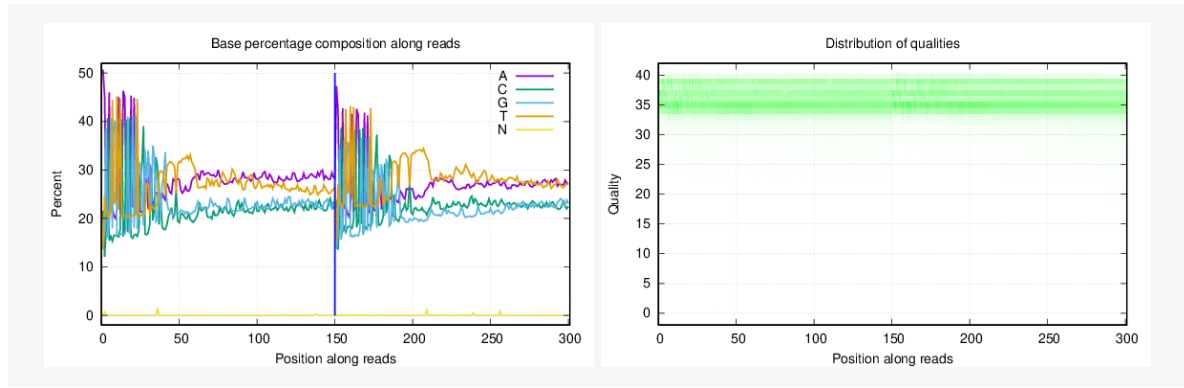
B_5



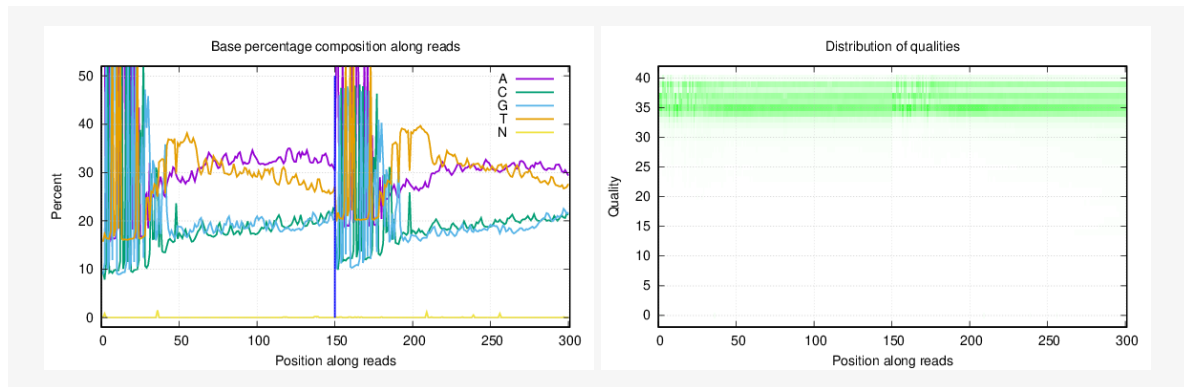
B_6



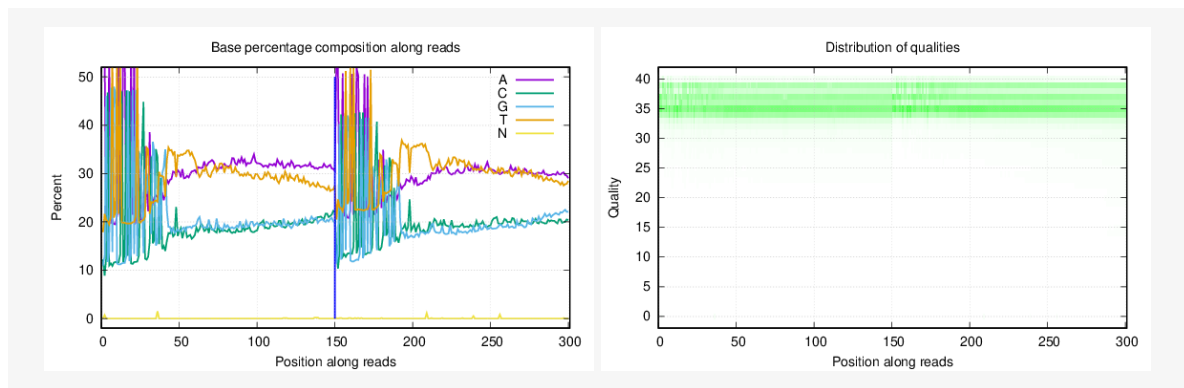
B_7



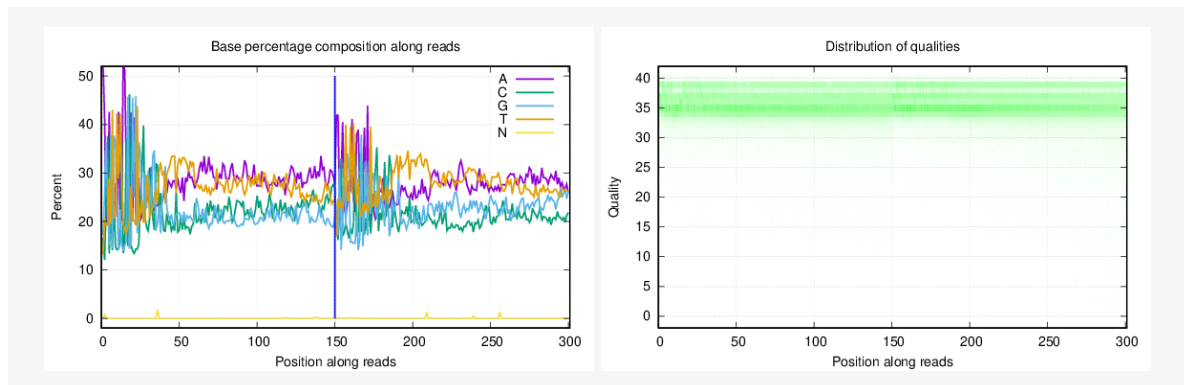
B_8G



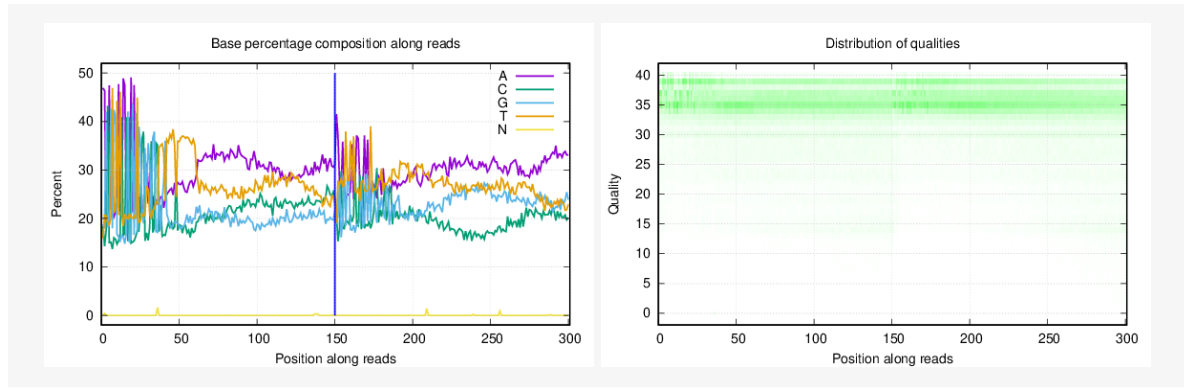
B_8M



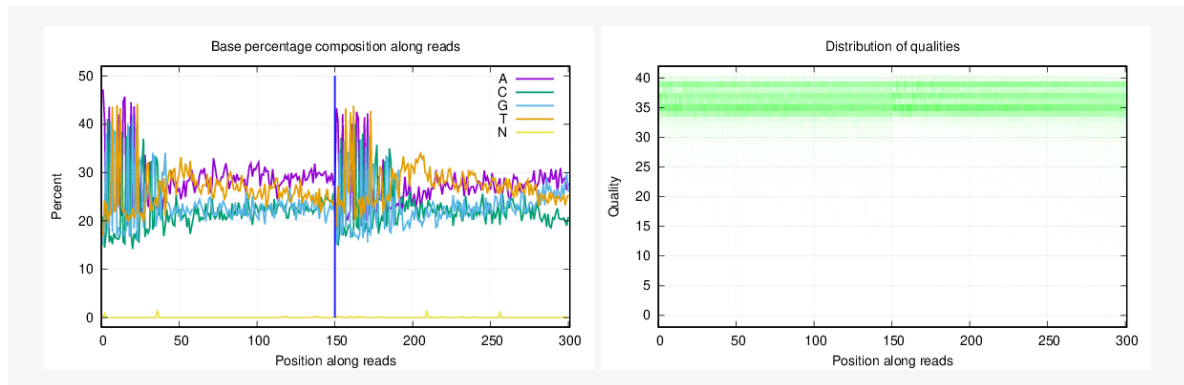
B_L2_7



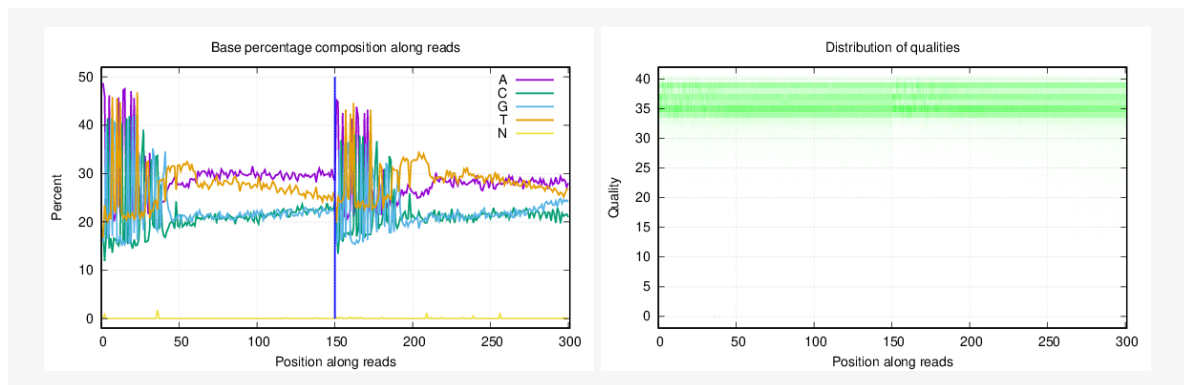
B_LK



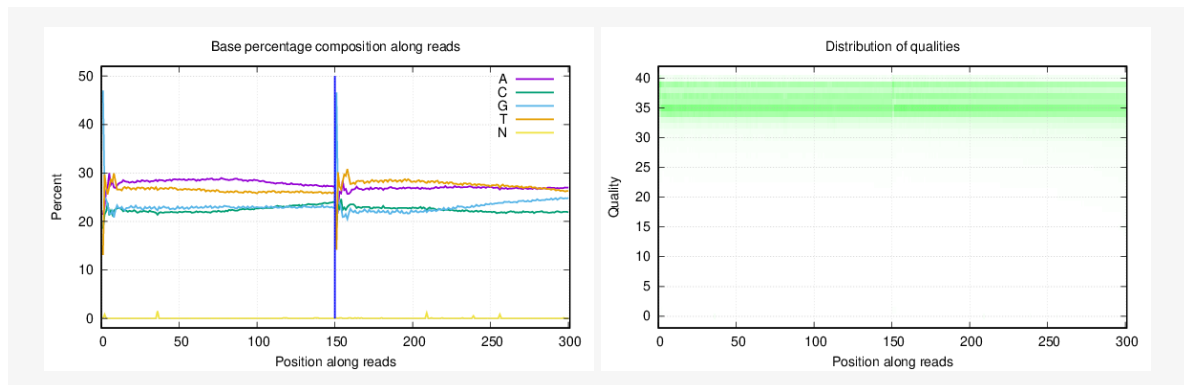
B_R2.7



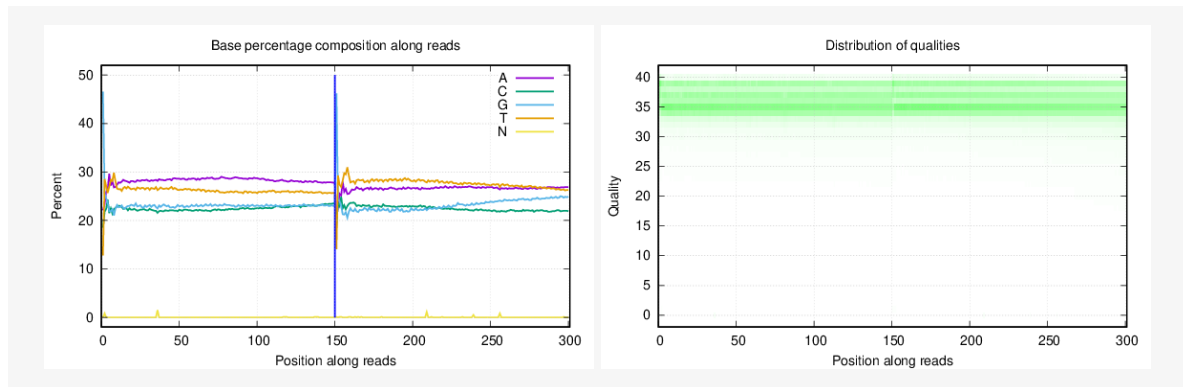
B_RK



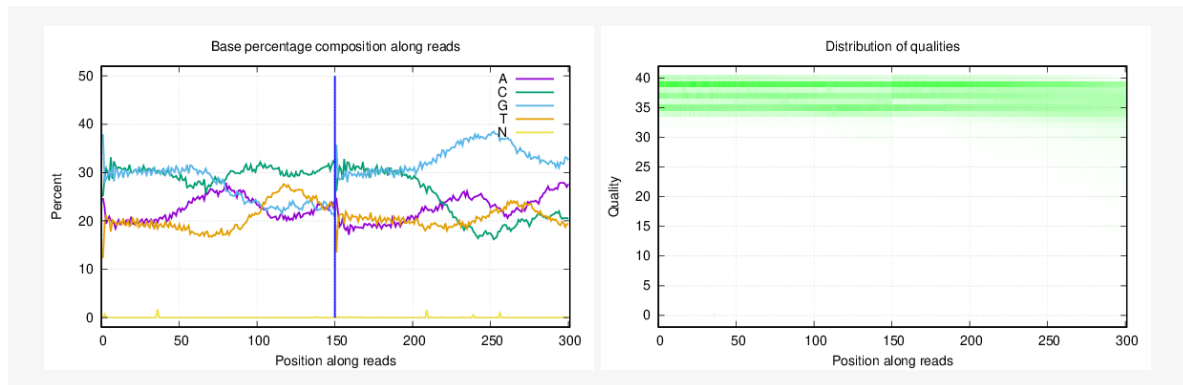
Cen_B7



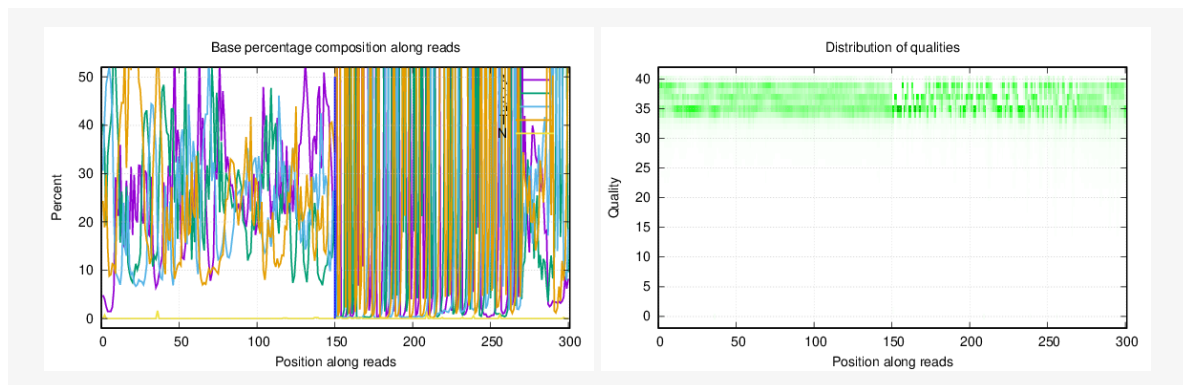
Cen_B8



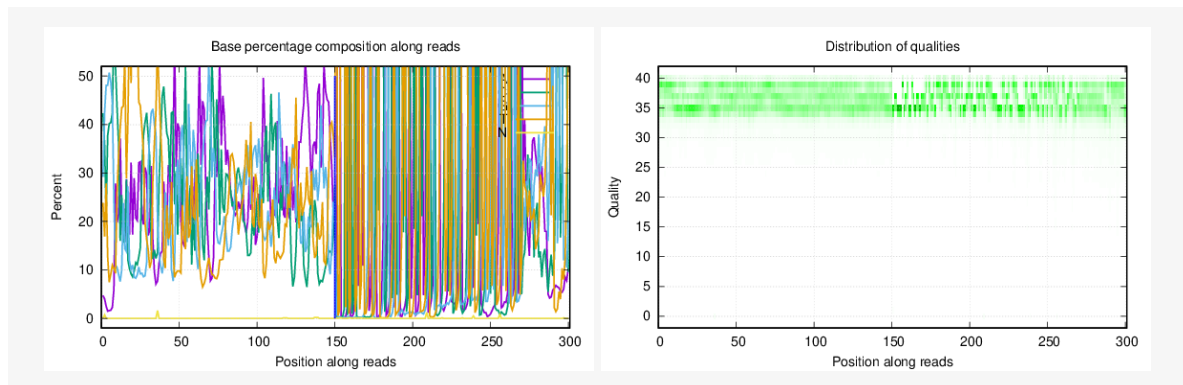
EBS1.1



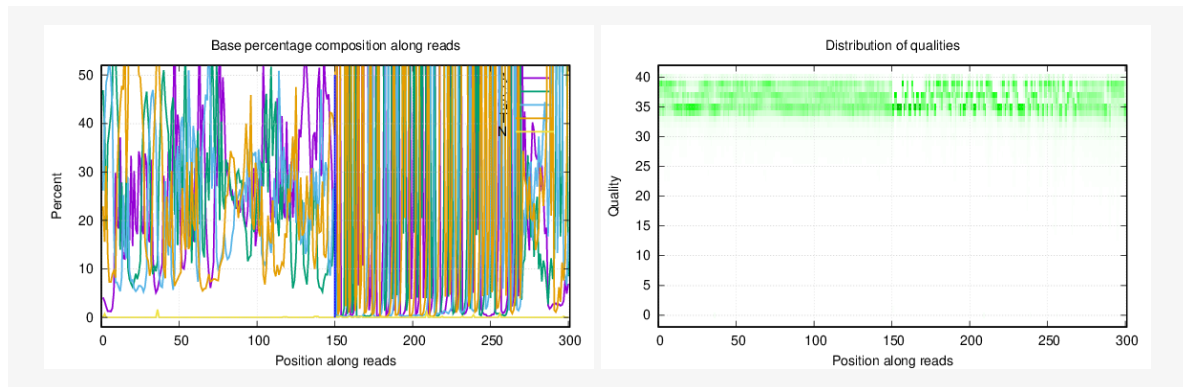
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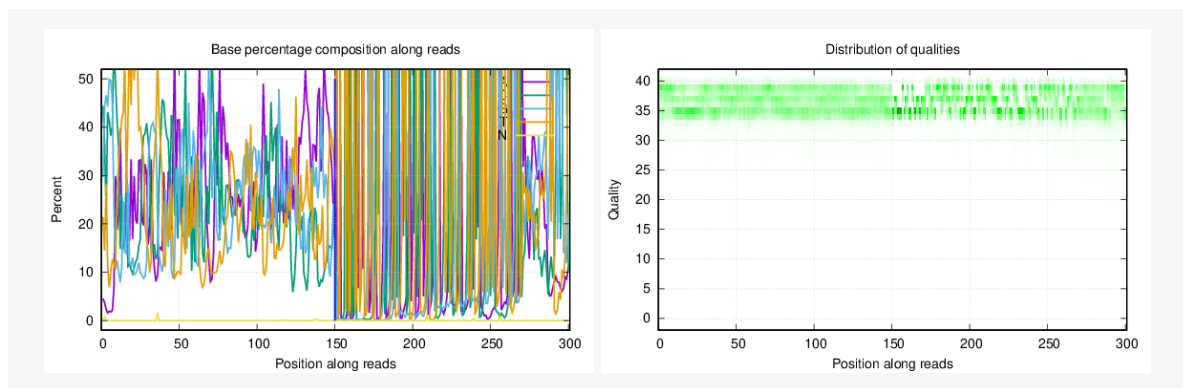
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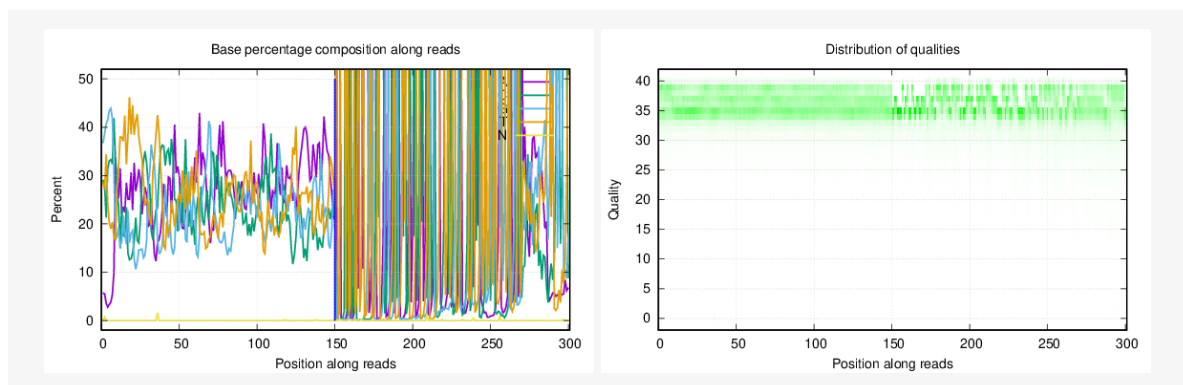
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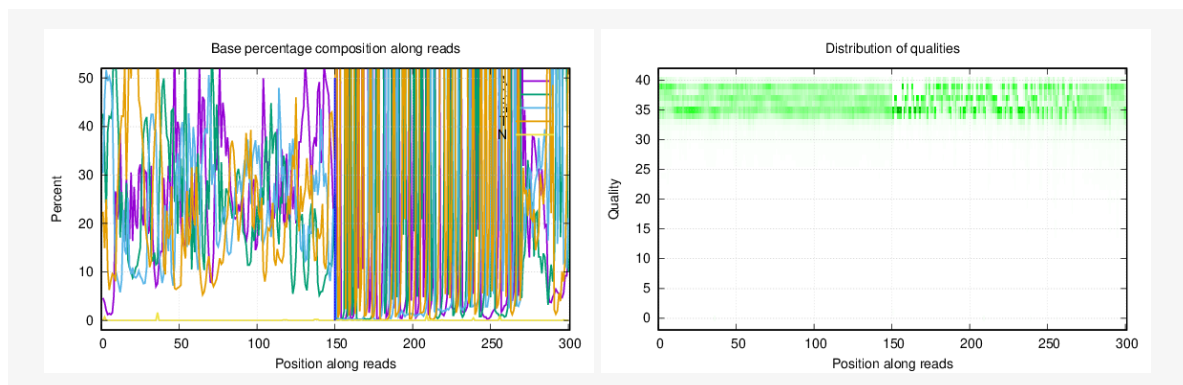
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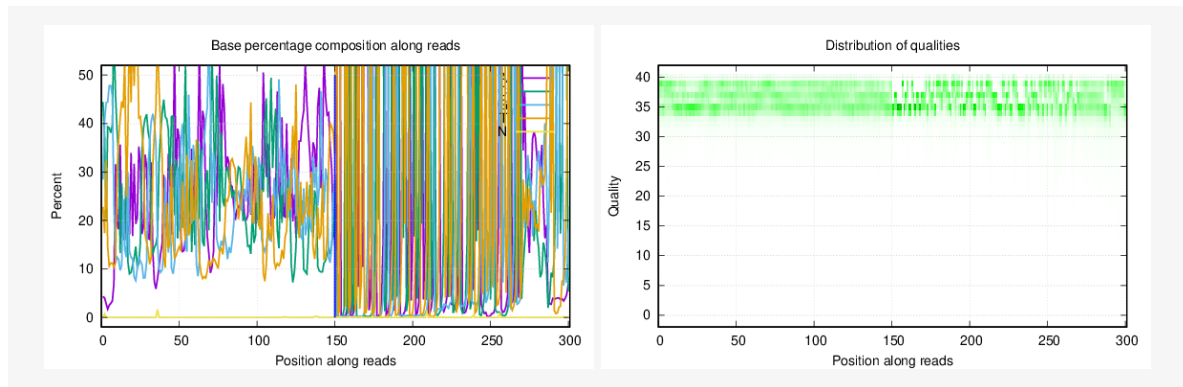
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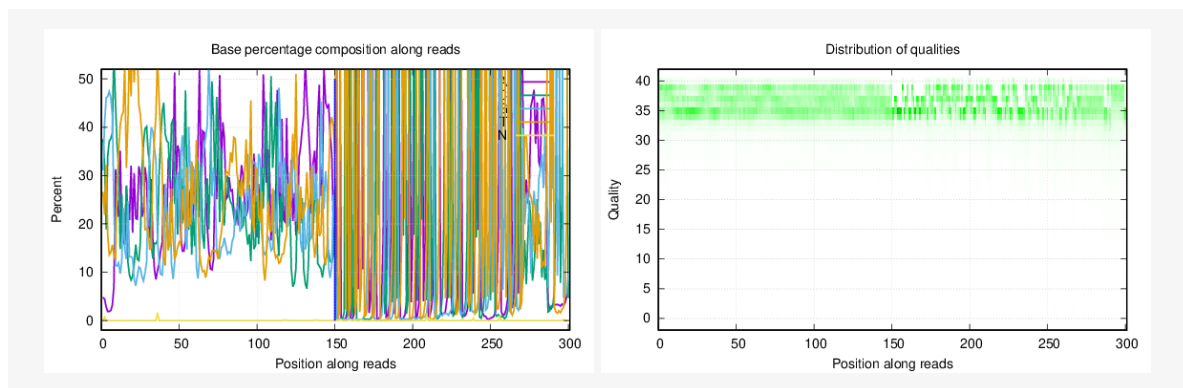
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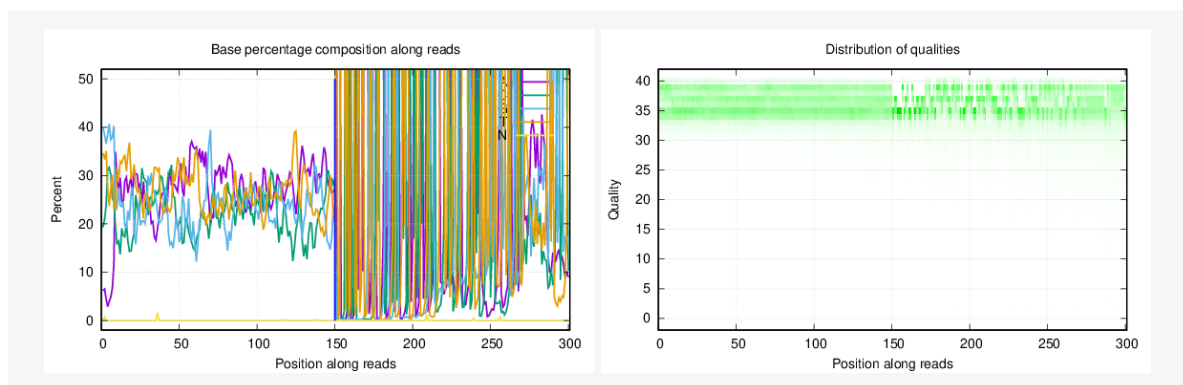
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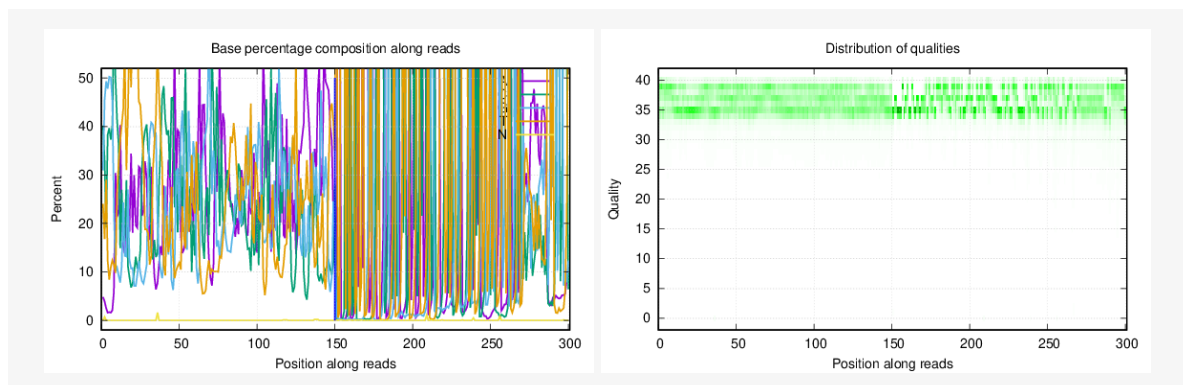
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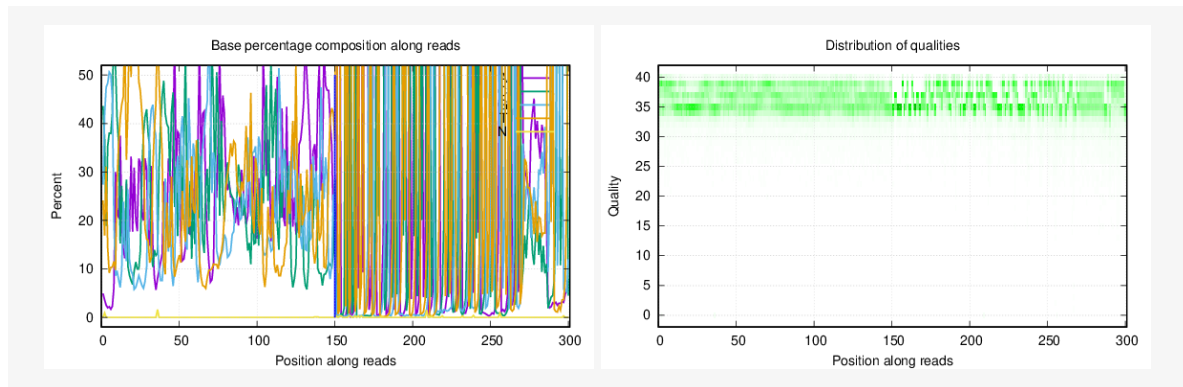
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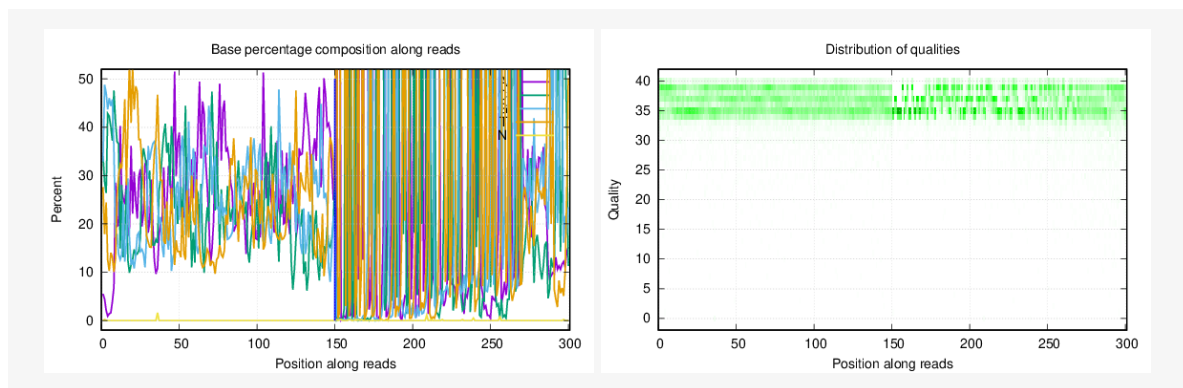
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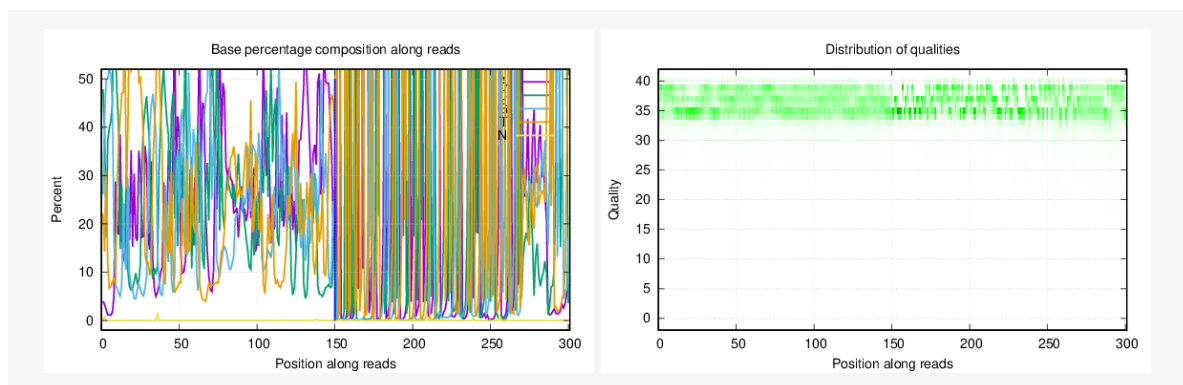
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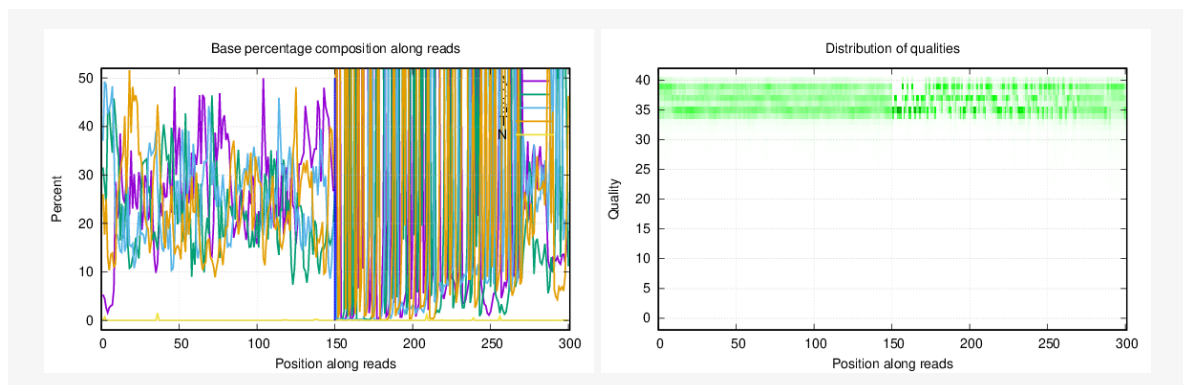
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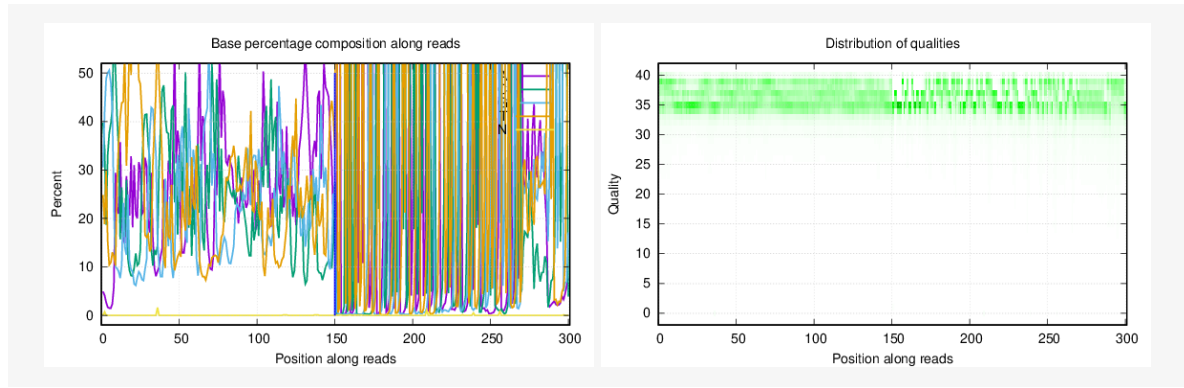
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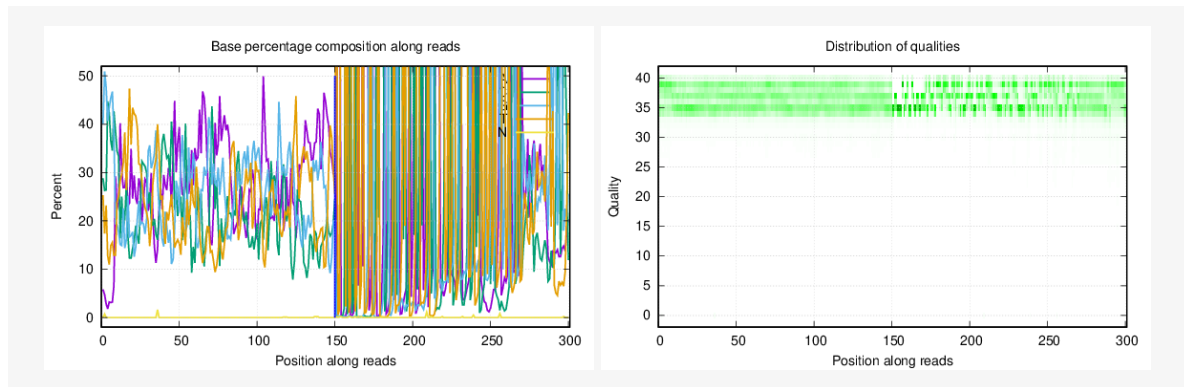
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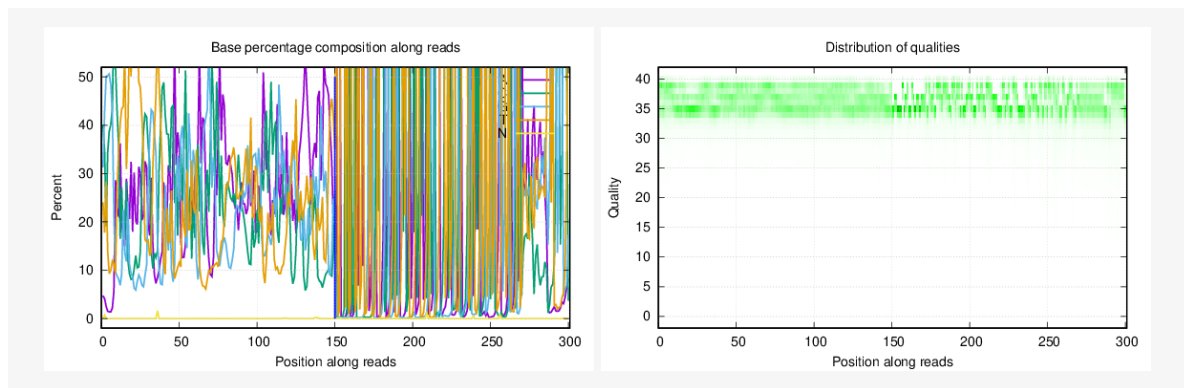
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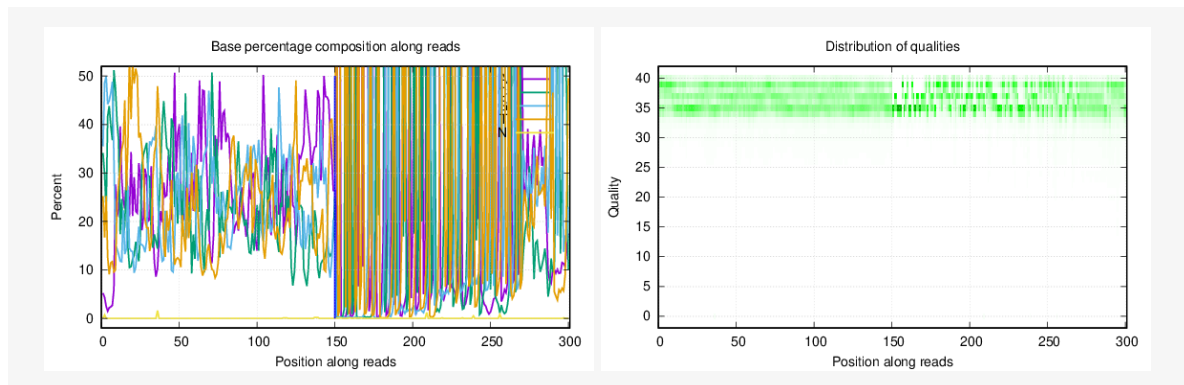
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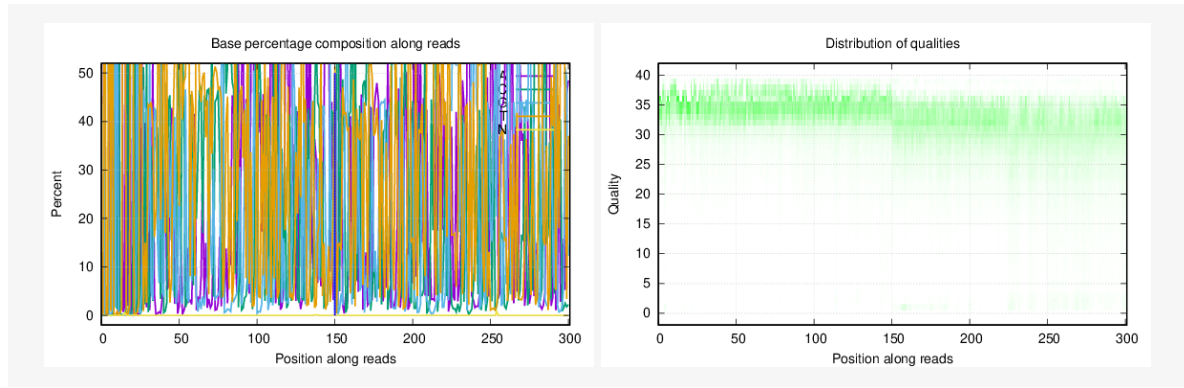
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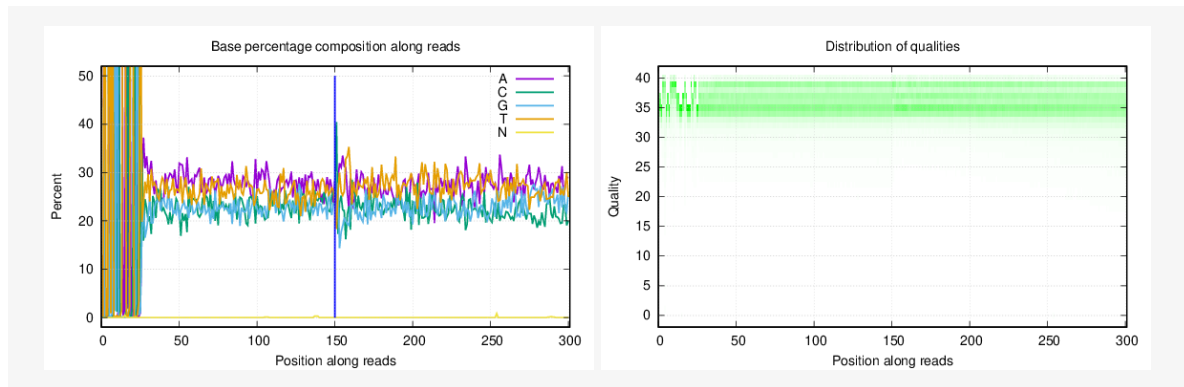
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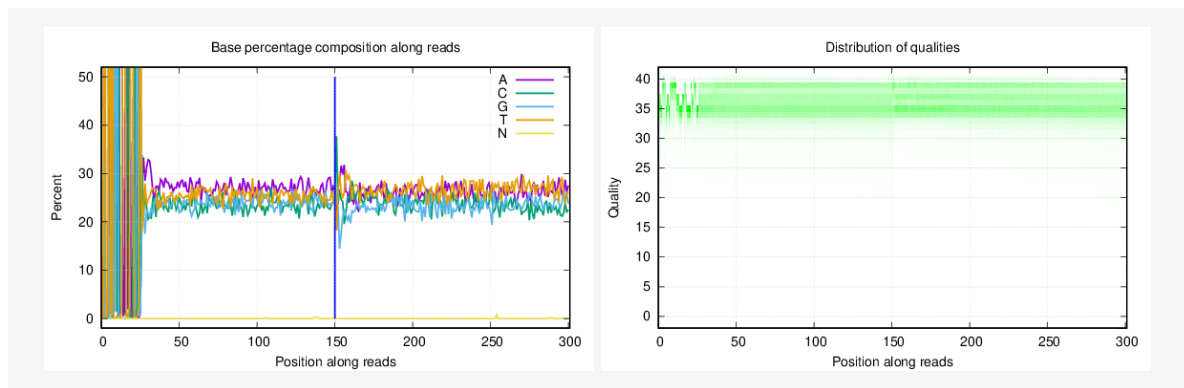
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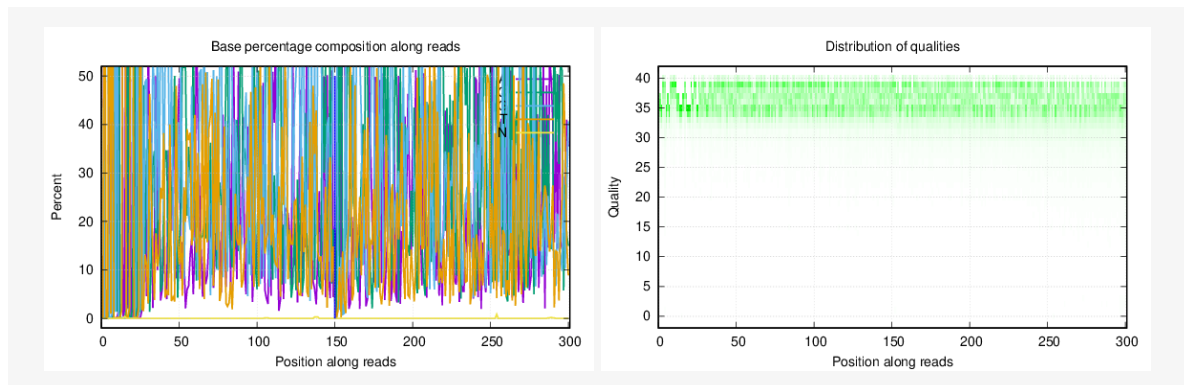
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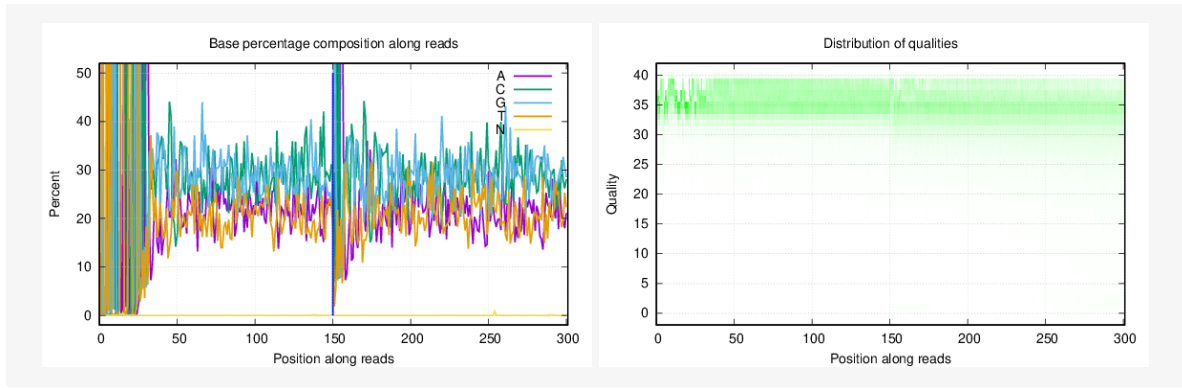
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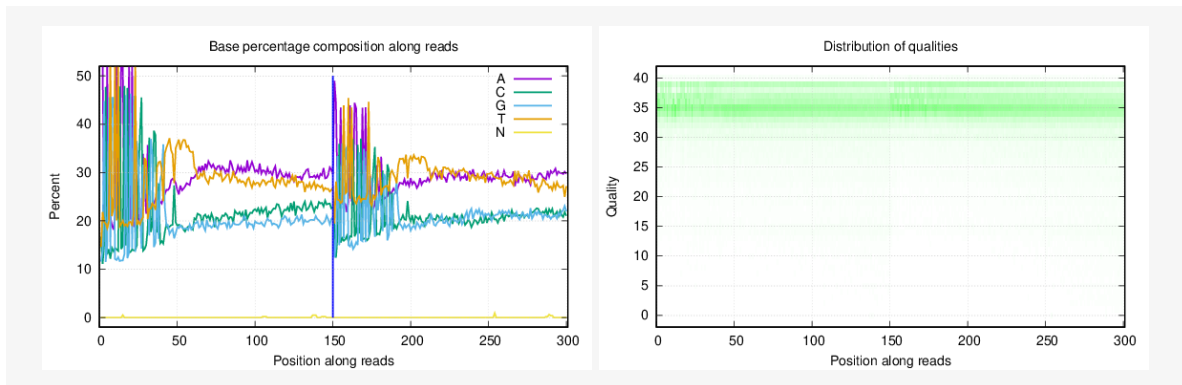
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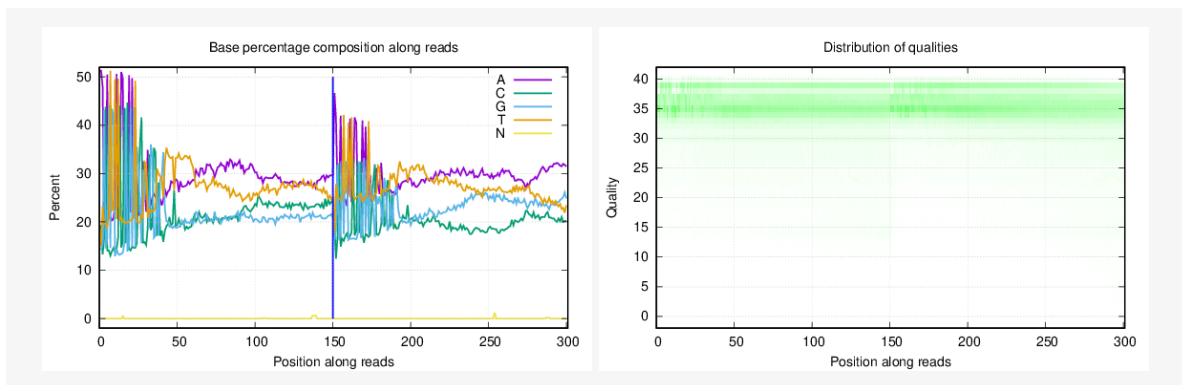
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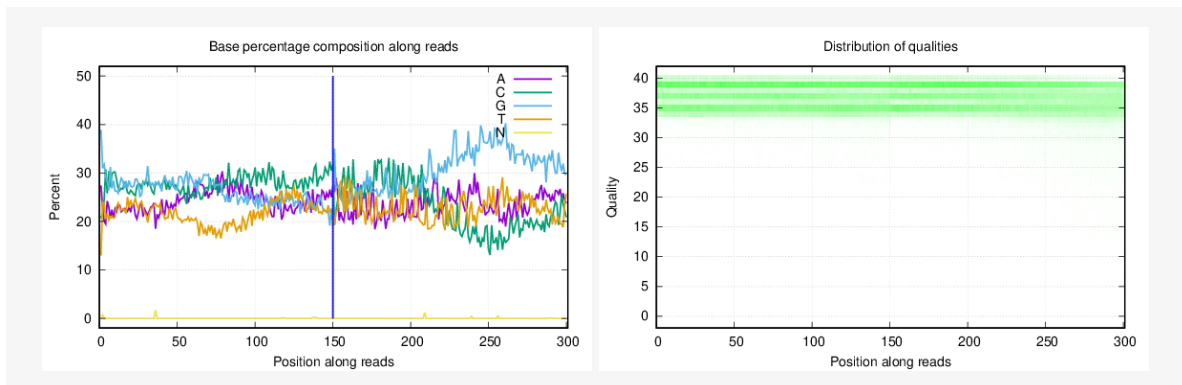
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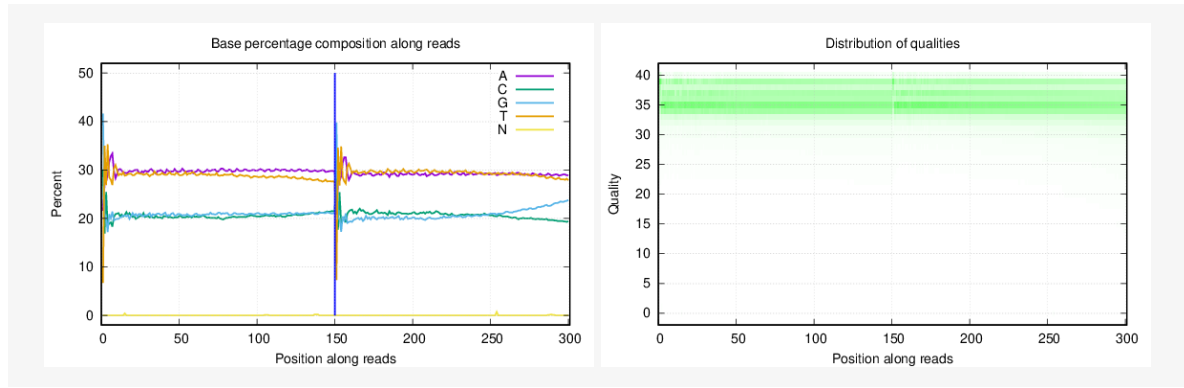
LK



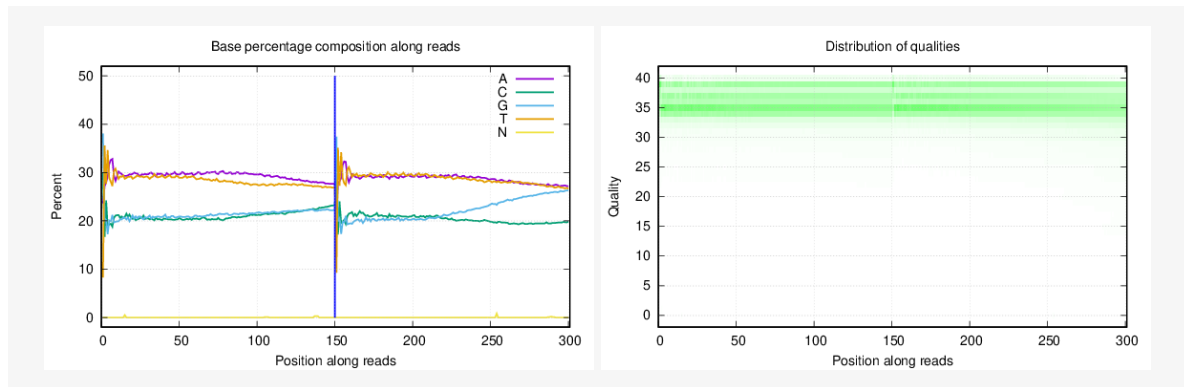
LepBo-22



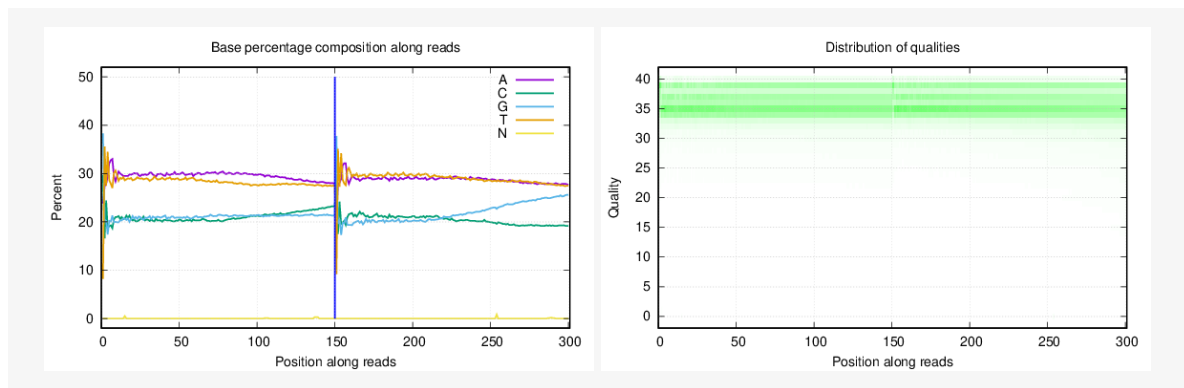
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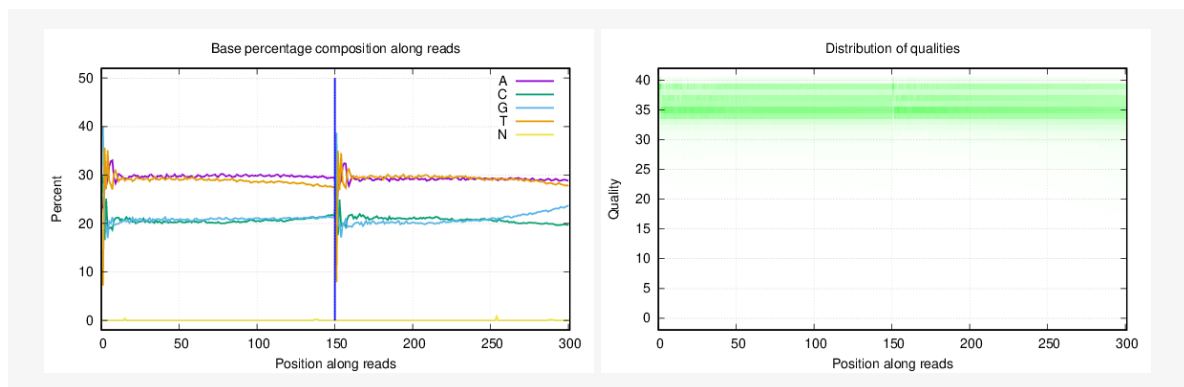
MBS_33



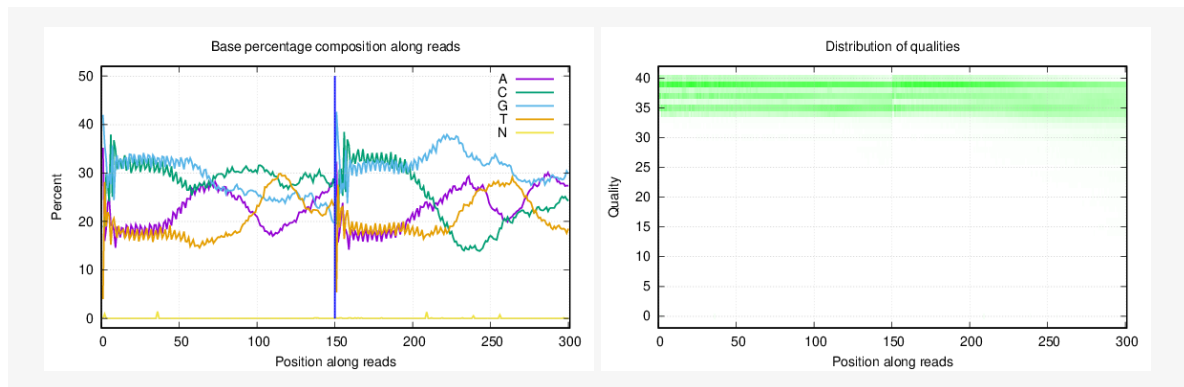
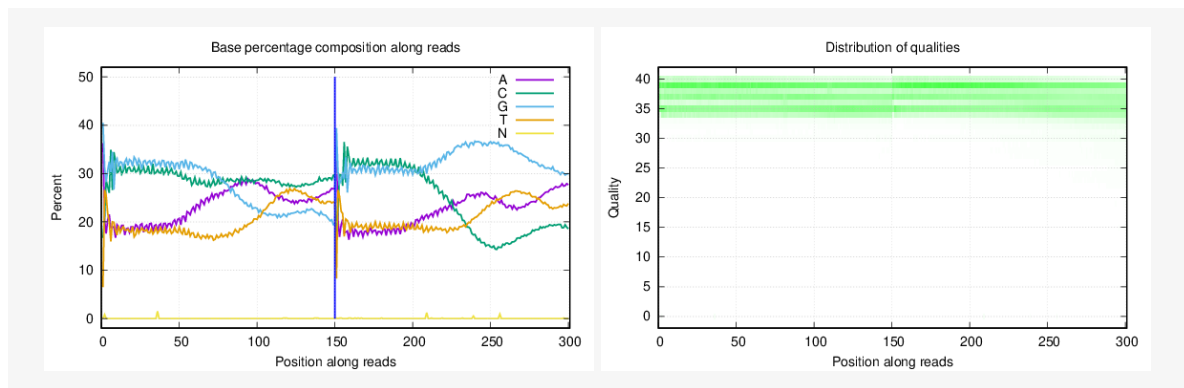
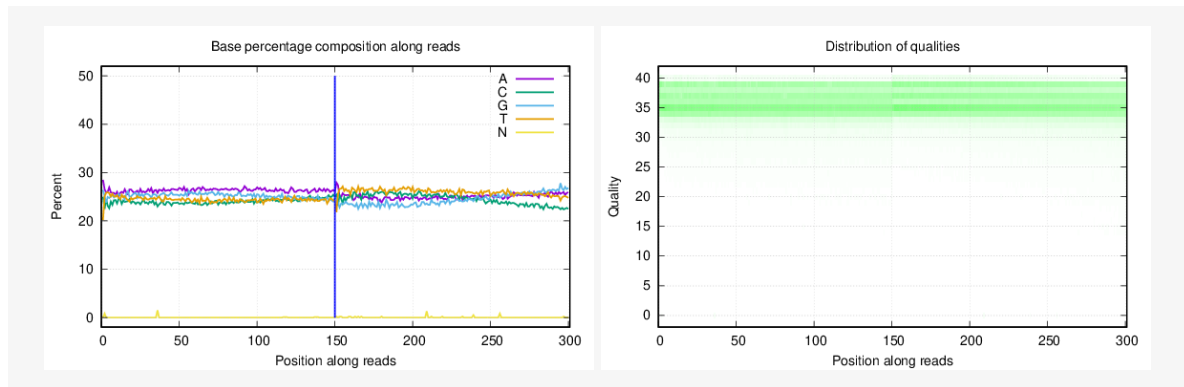
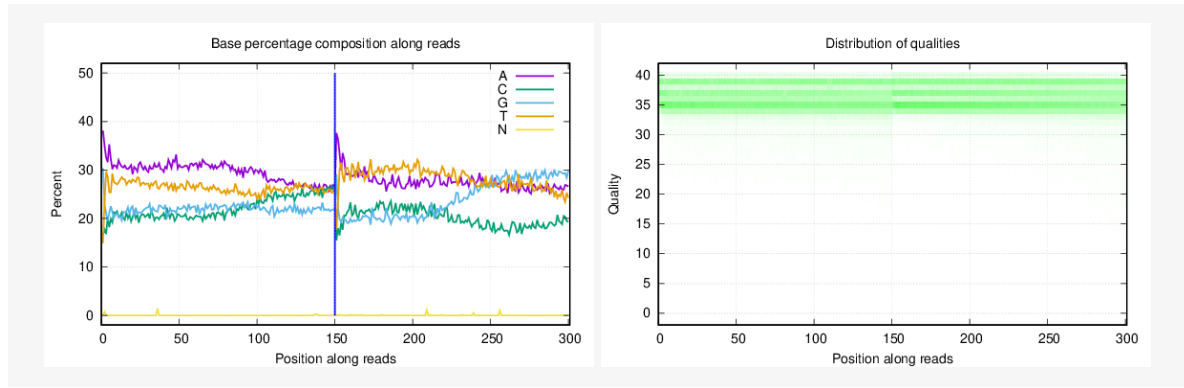
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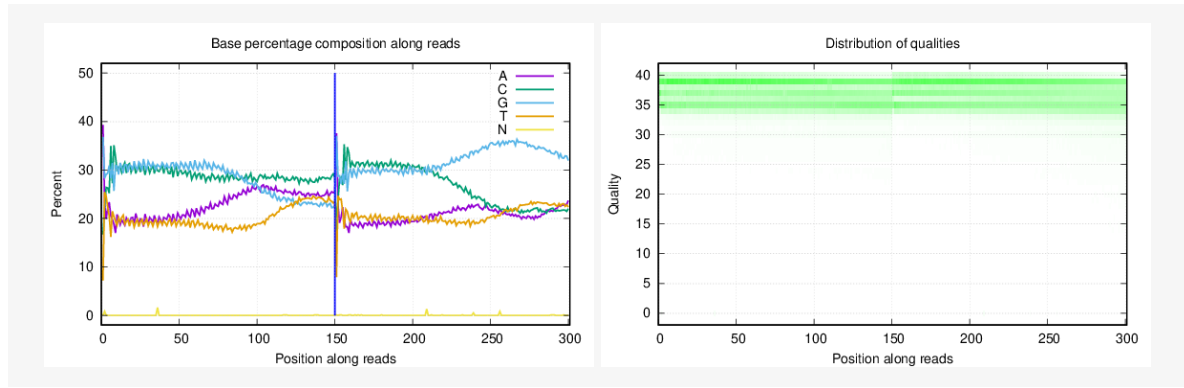


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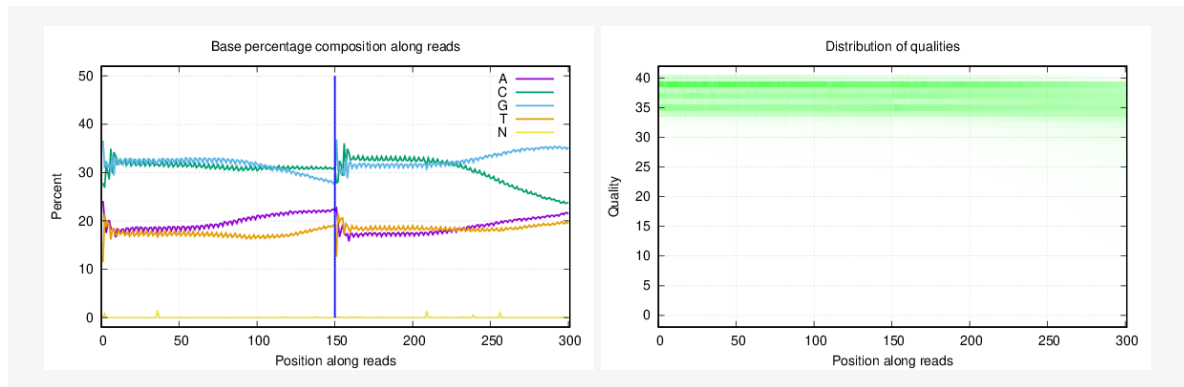


MI-4

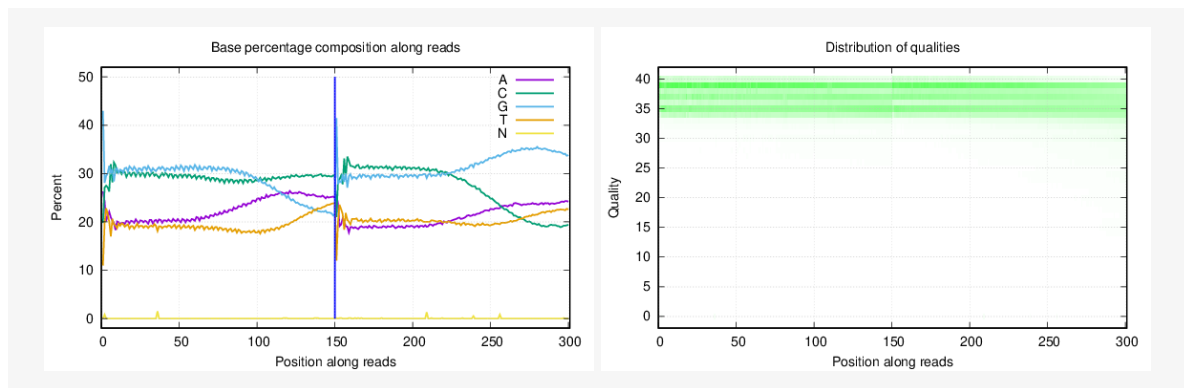




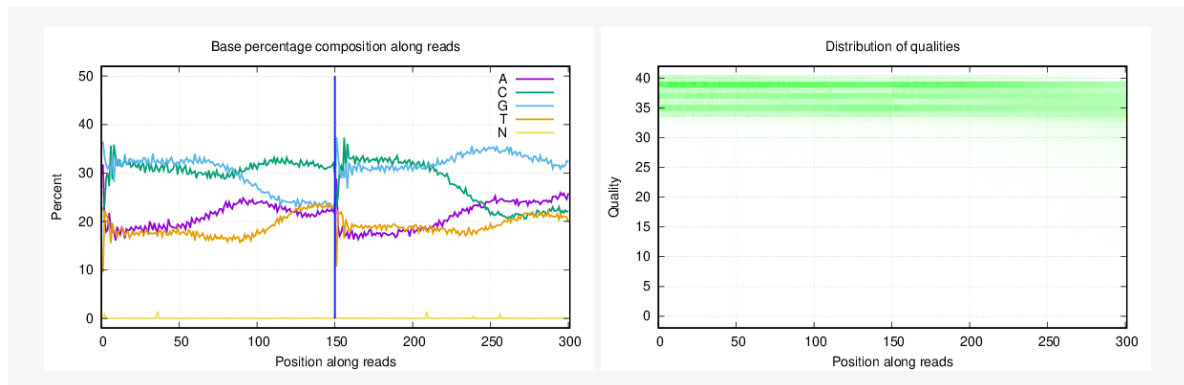
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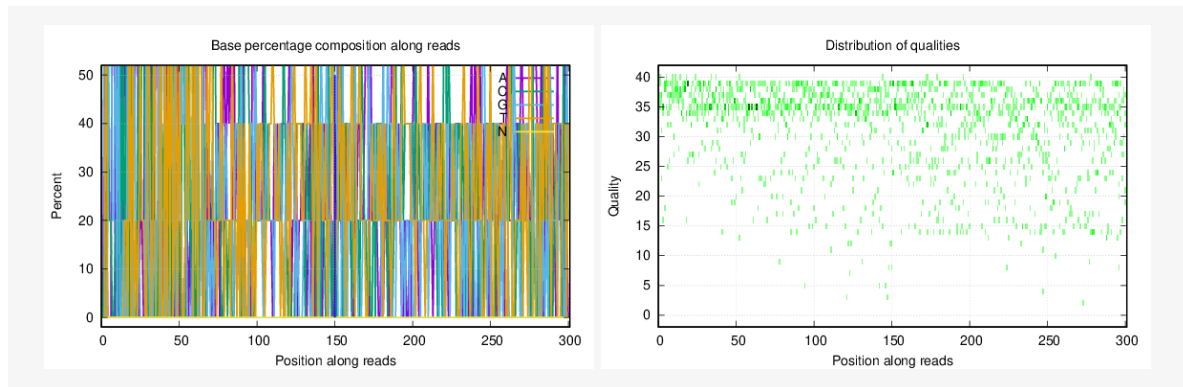
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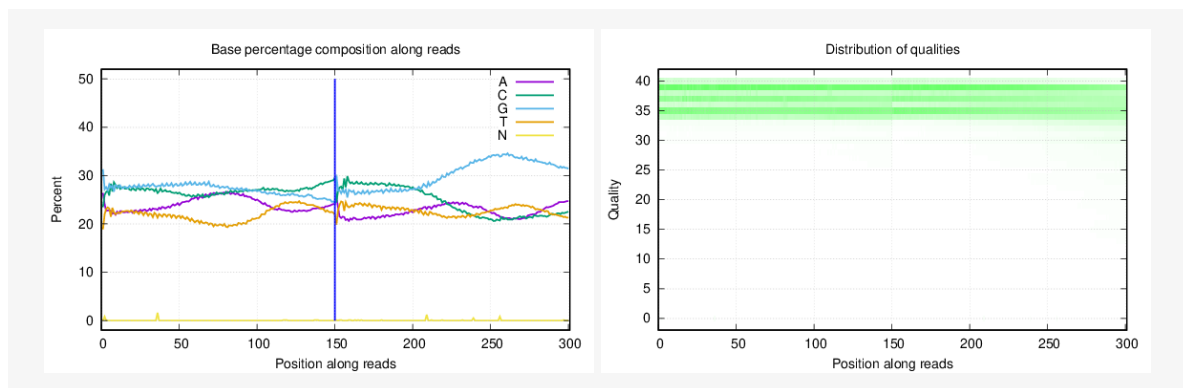
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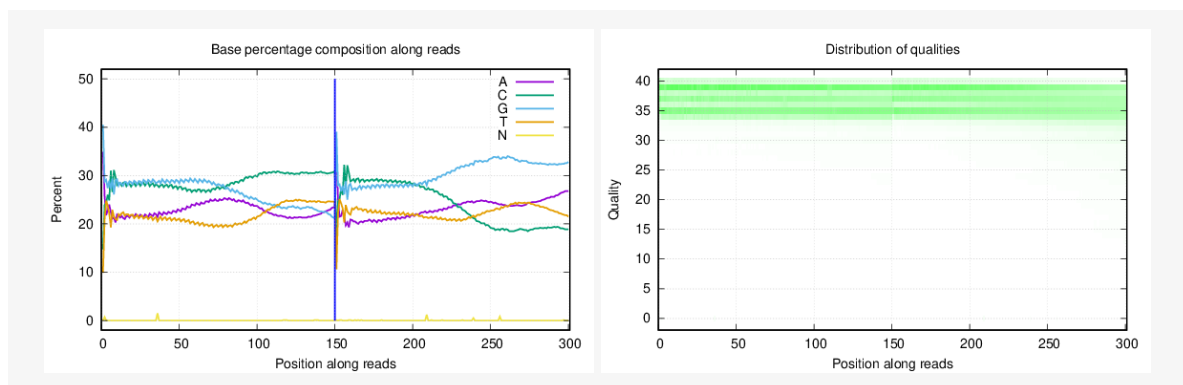
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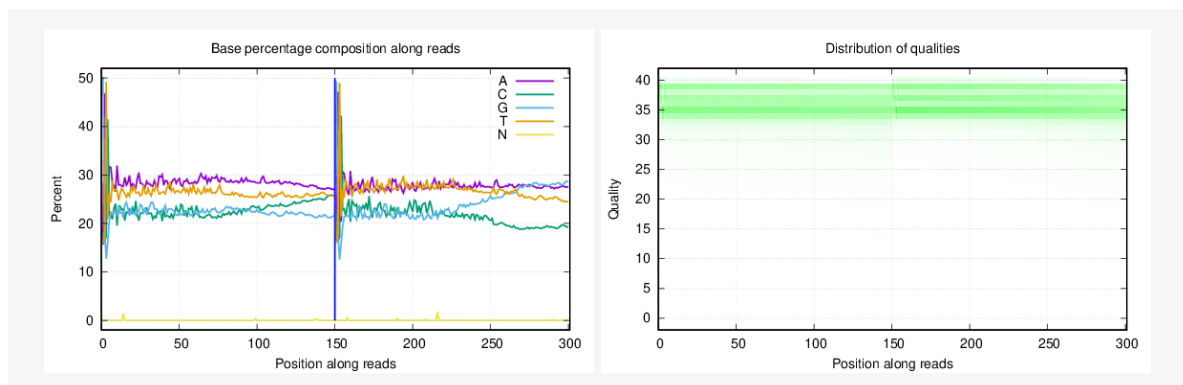
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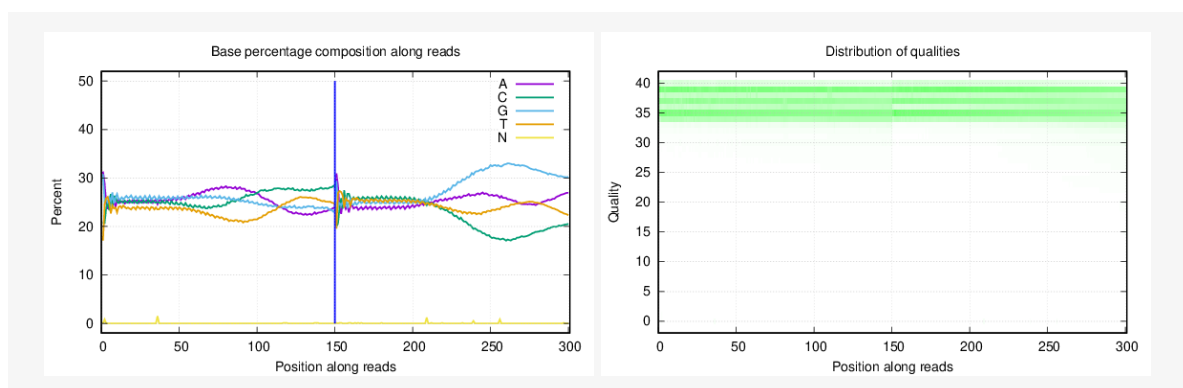
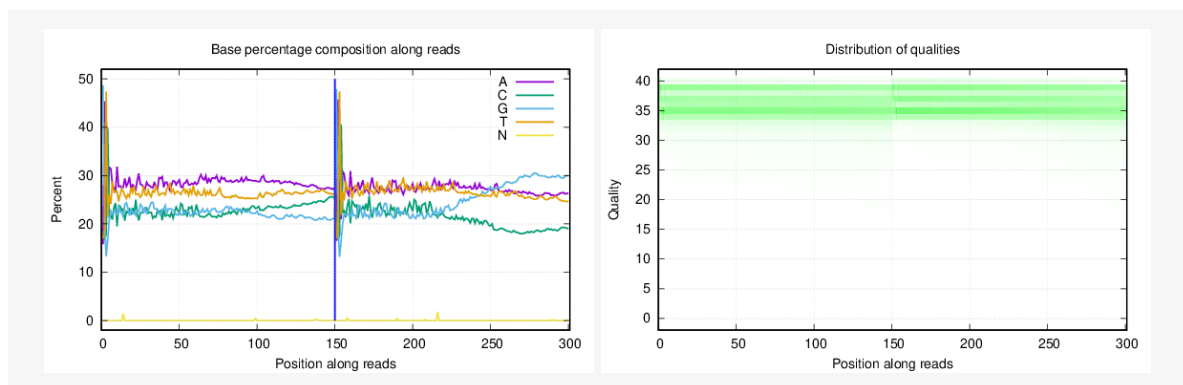
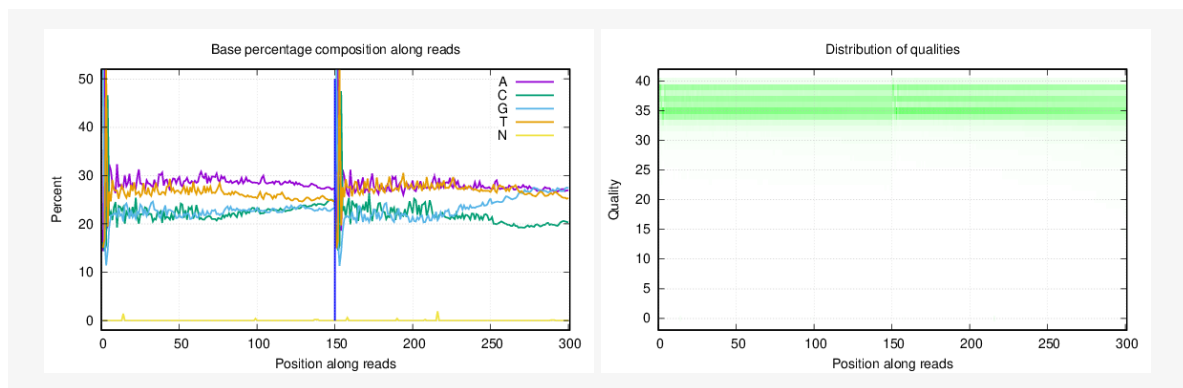
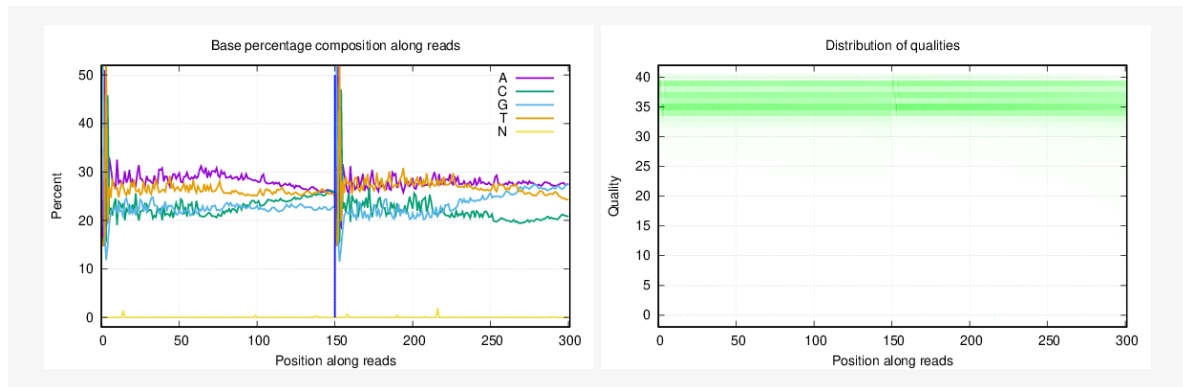
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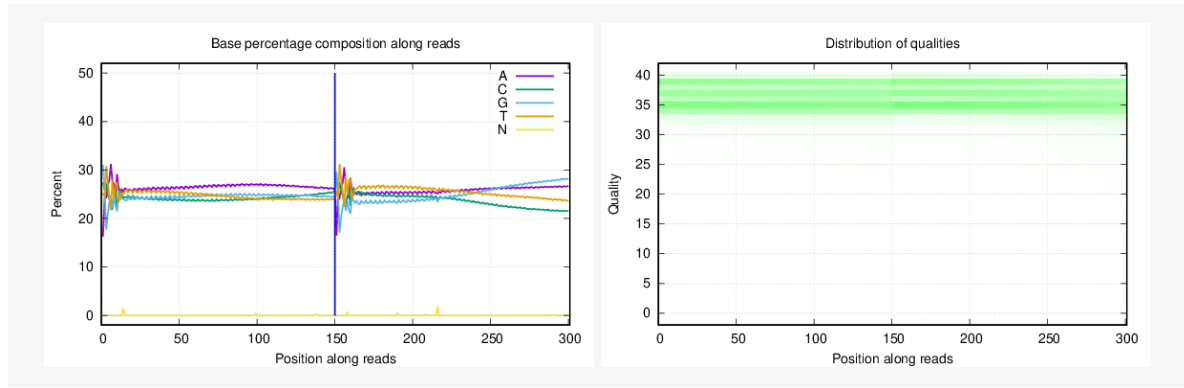


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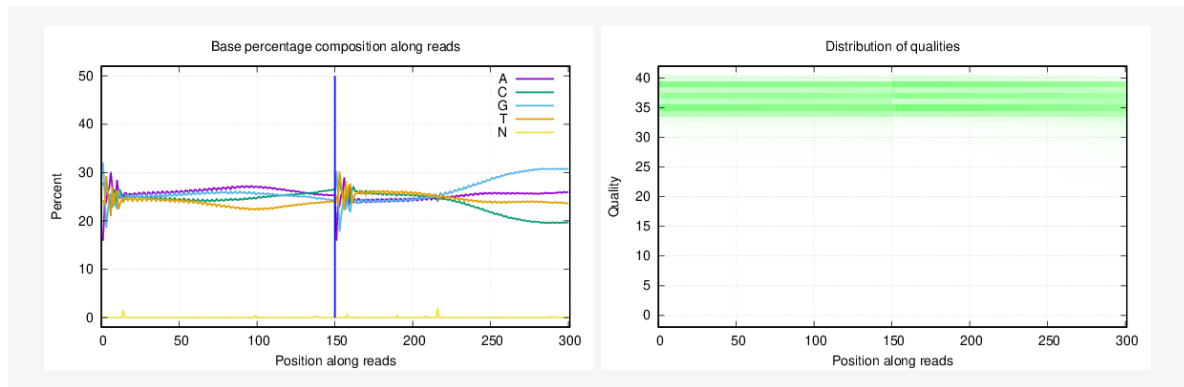


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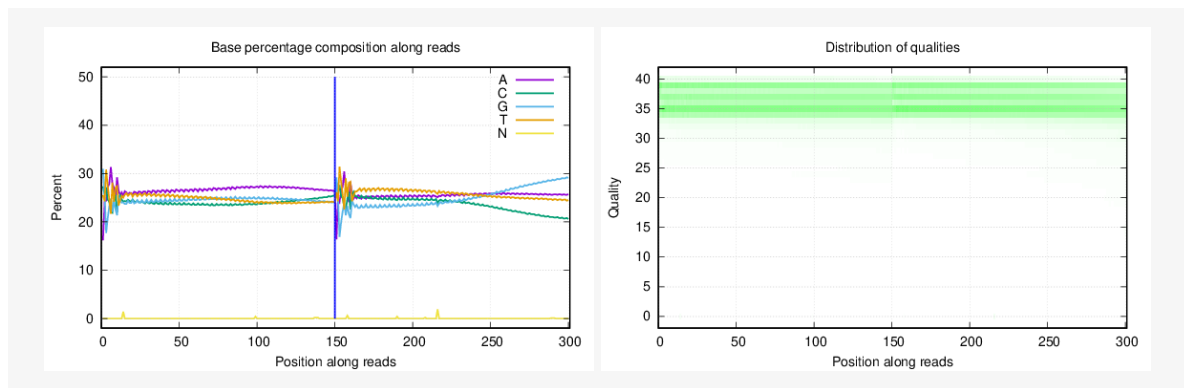




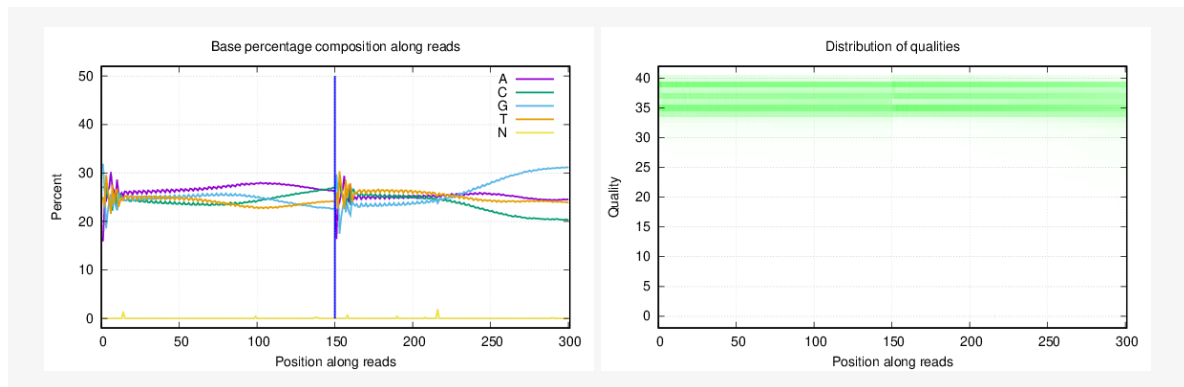
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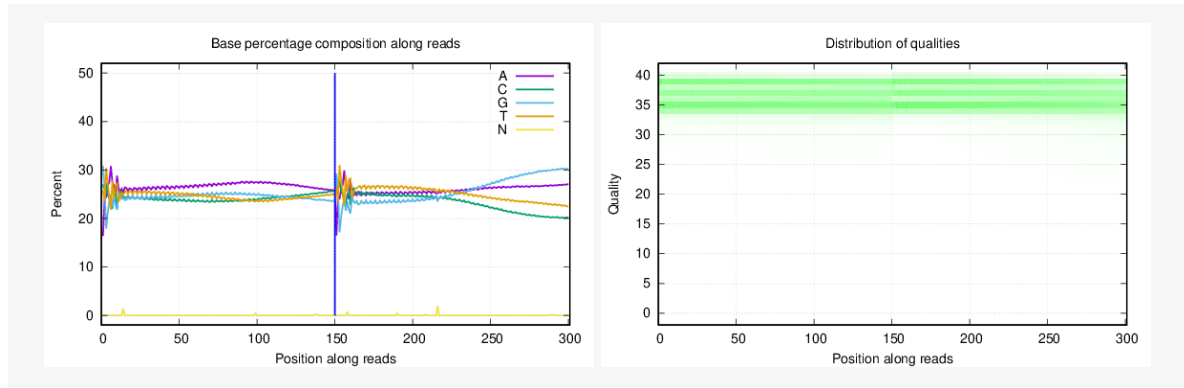
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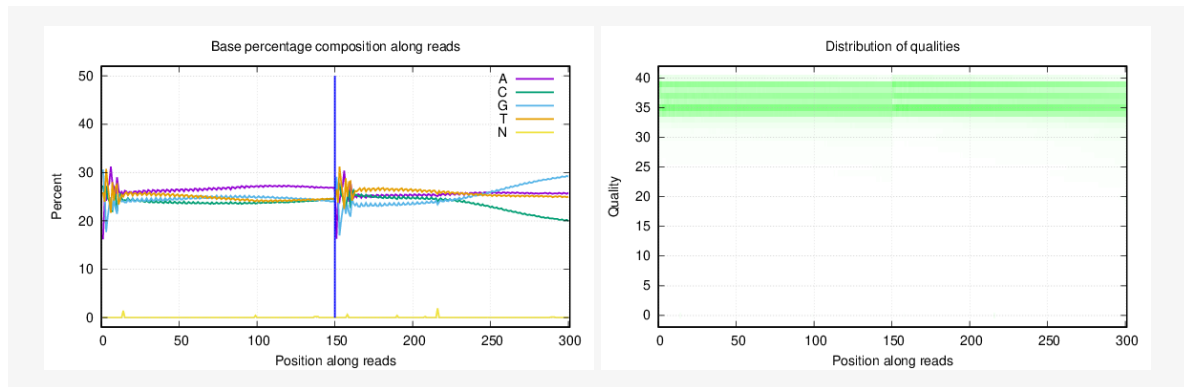
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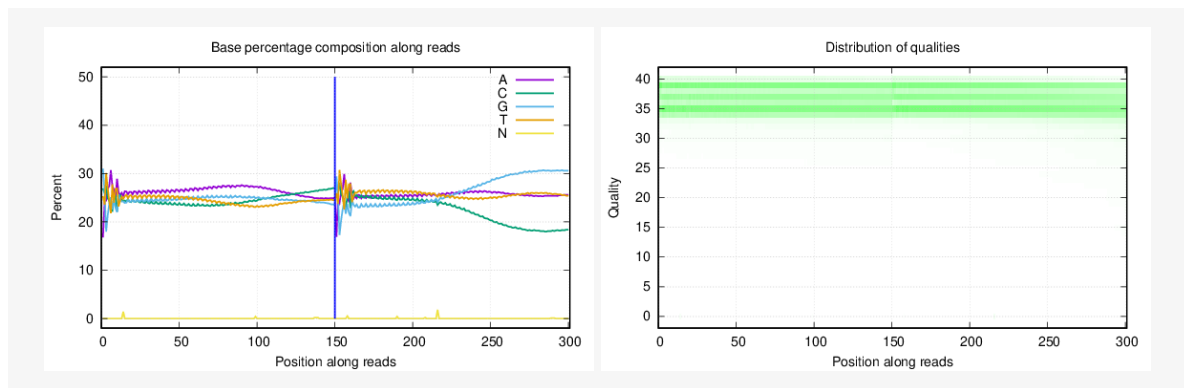
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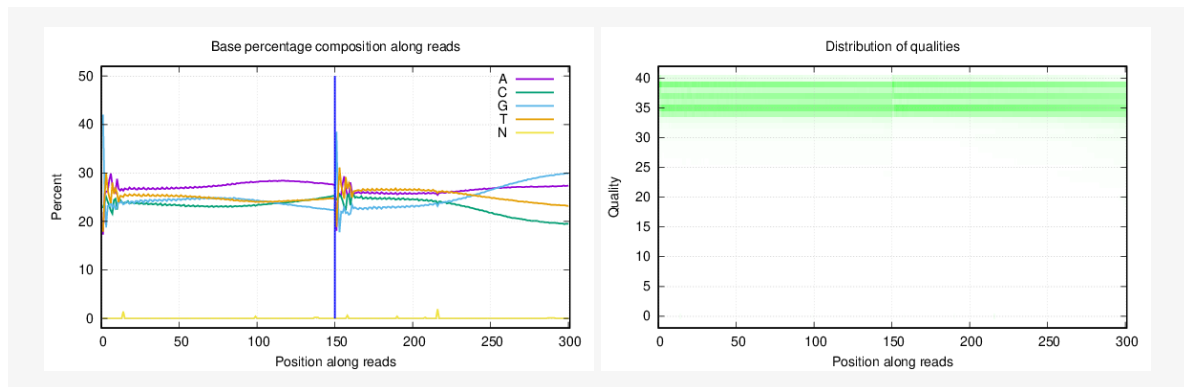
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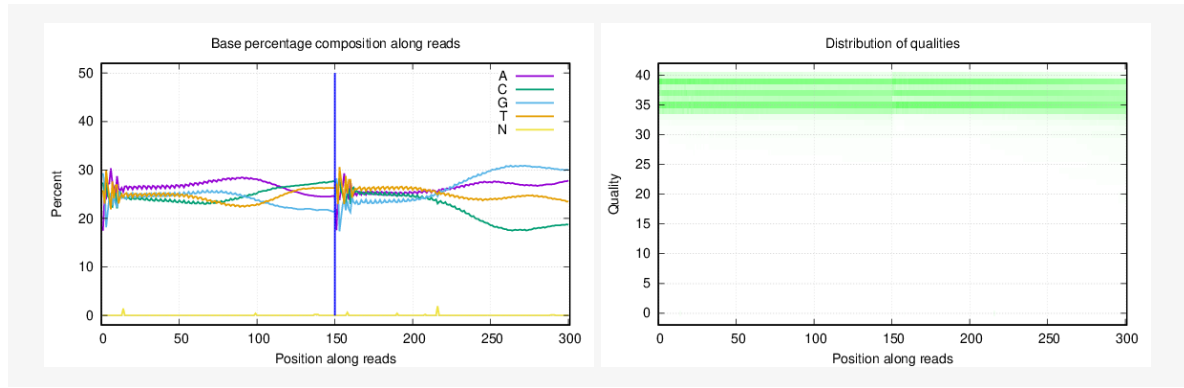
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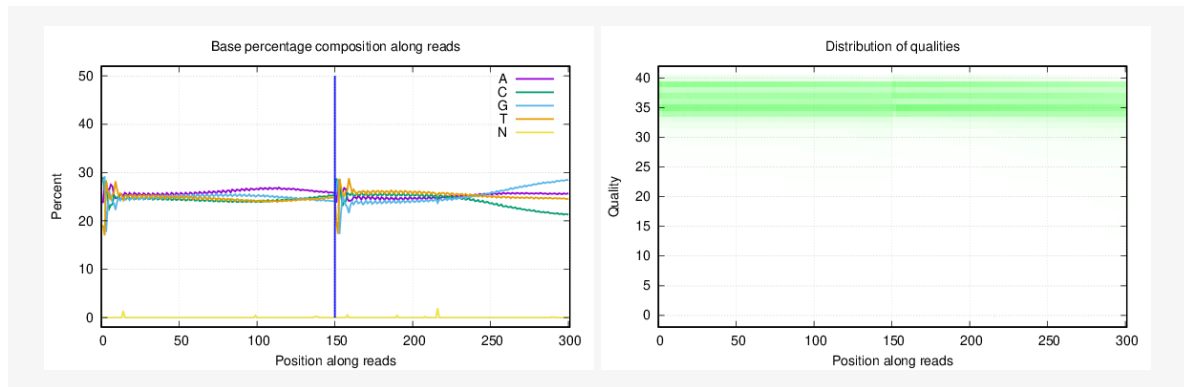
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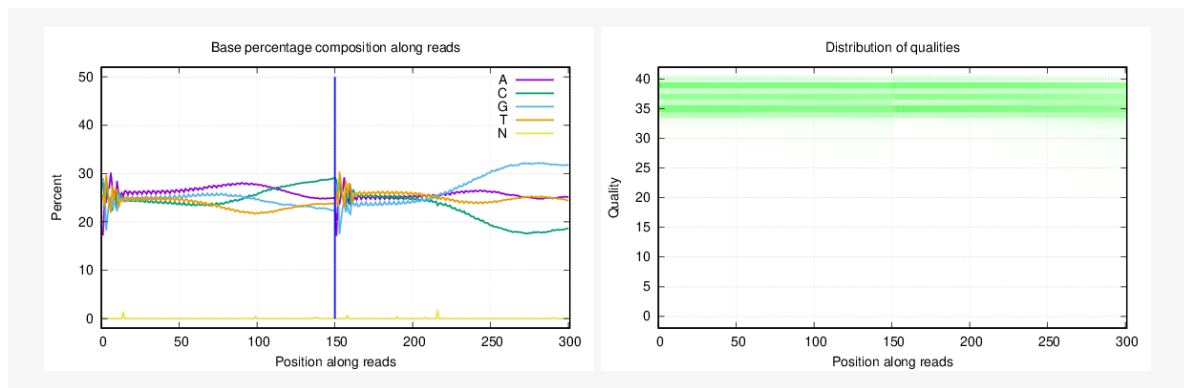
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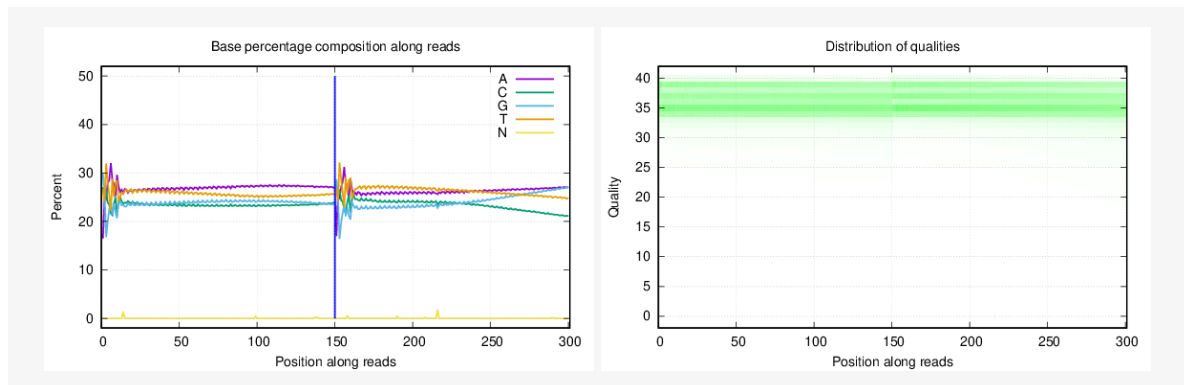
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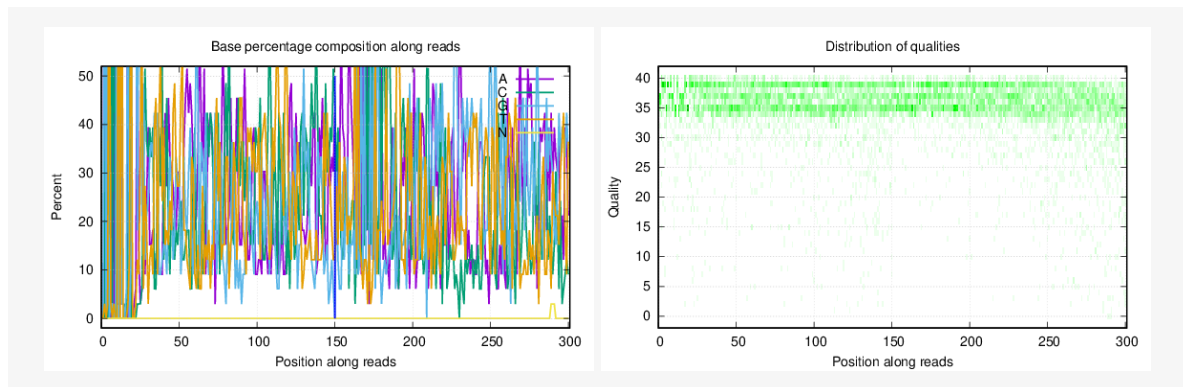
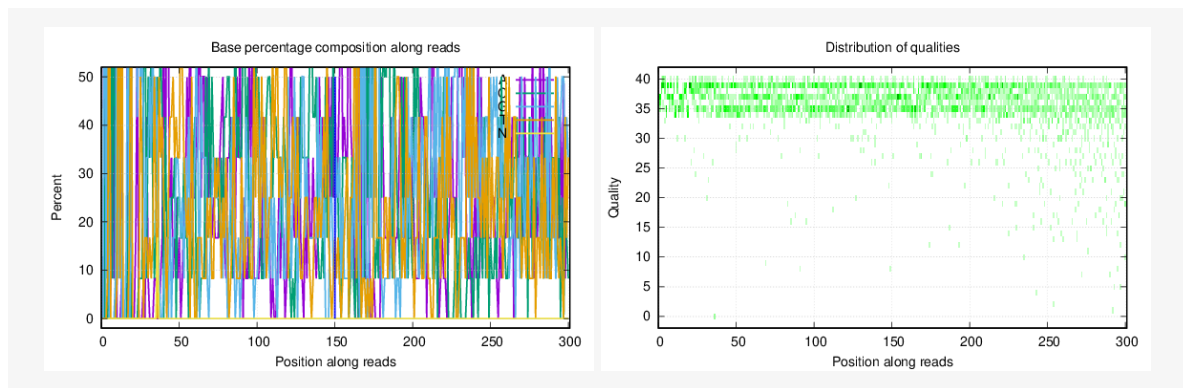
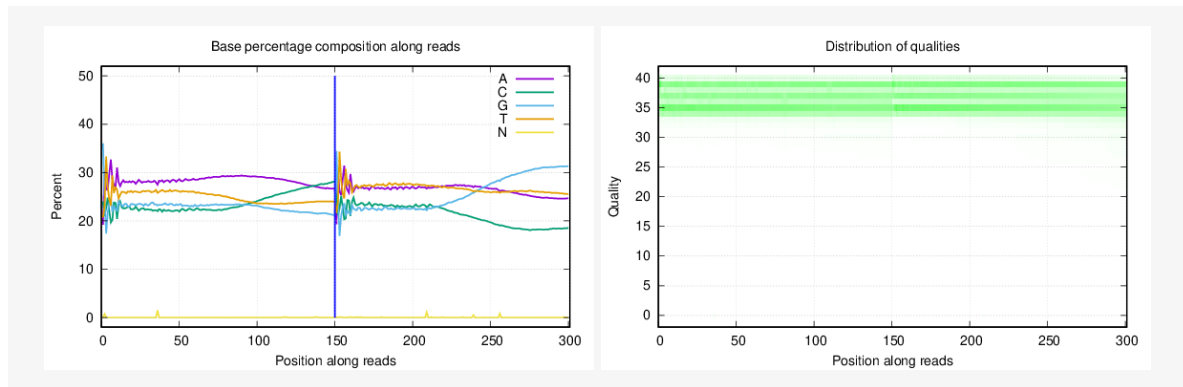
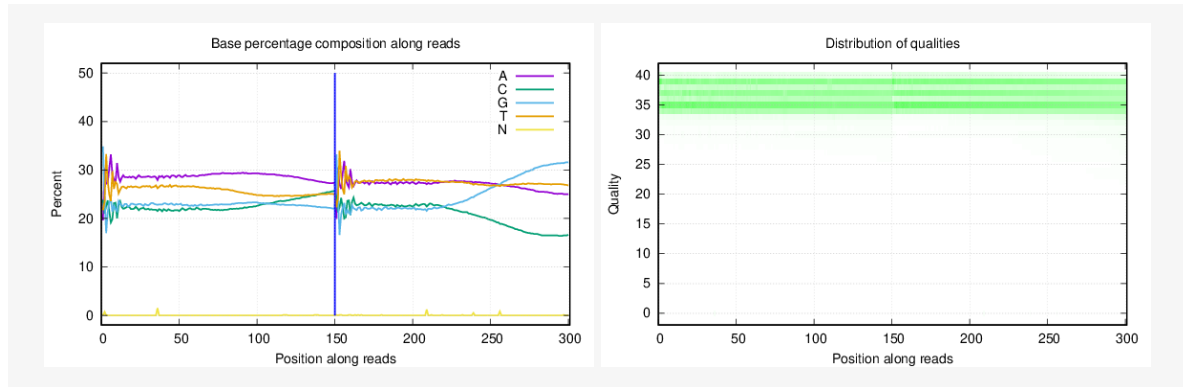
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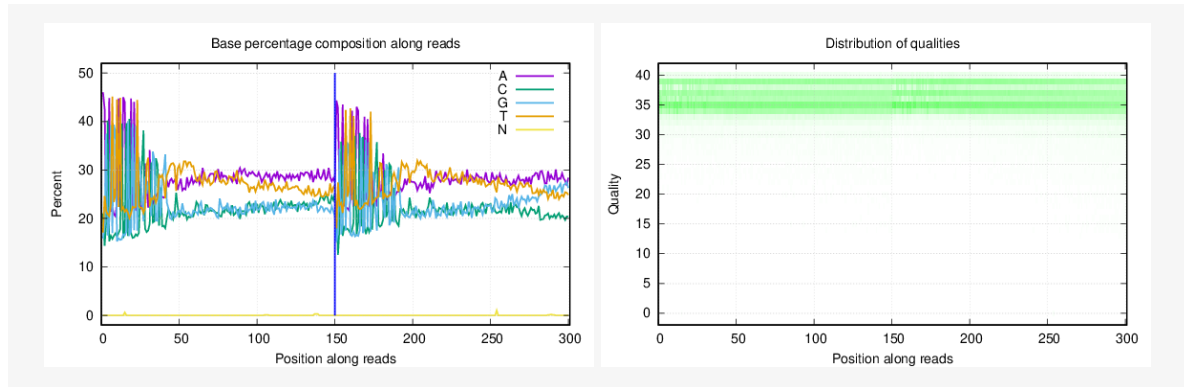


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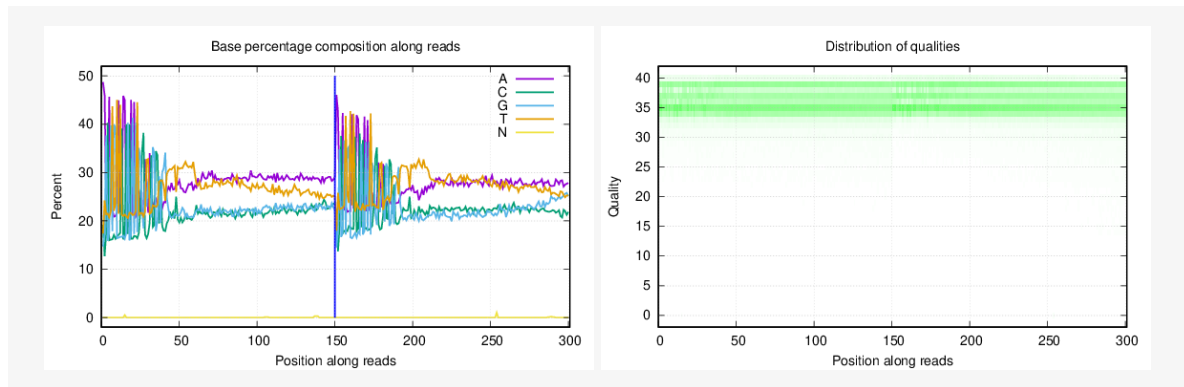


PARP_KO_r1

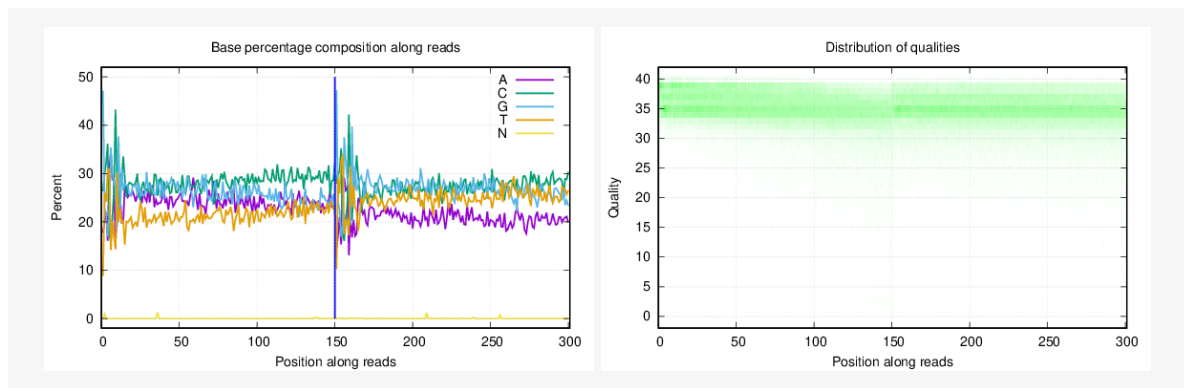




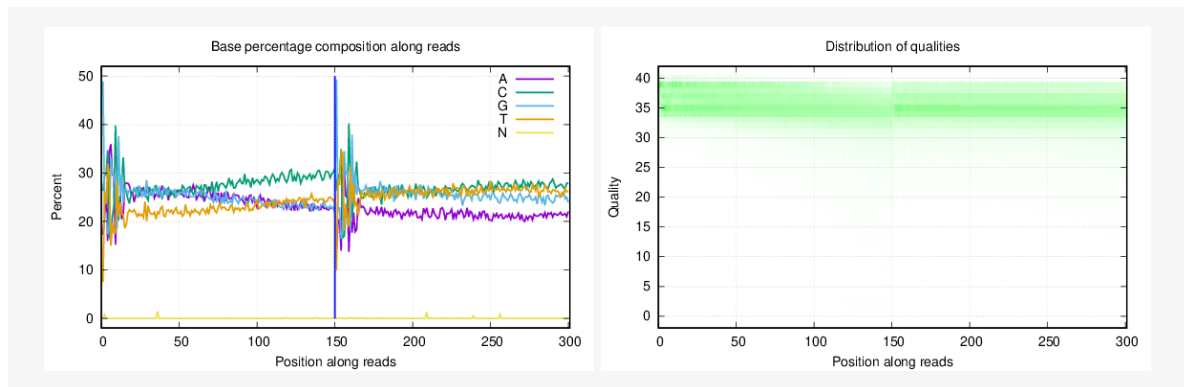
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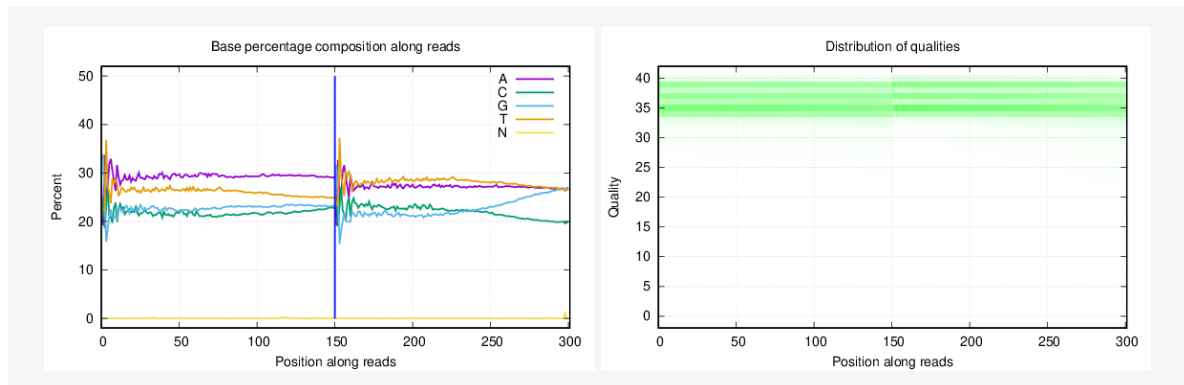
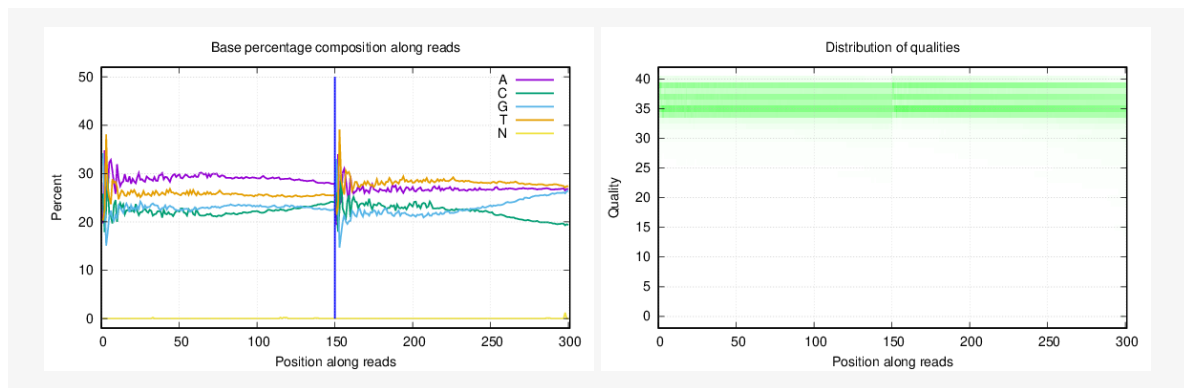
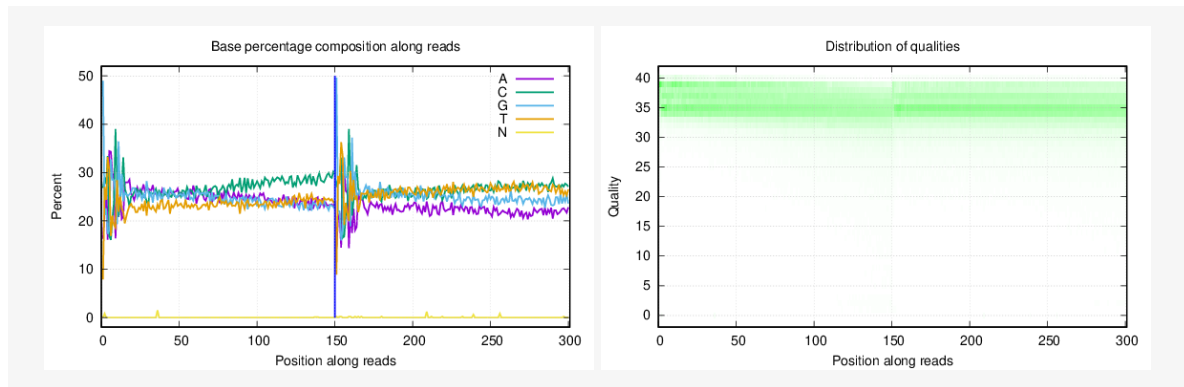
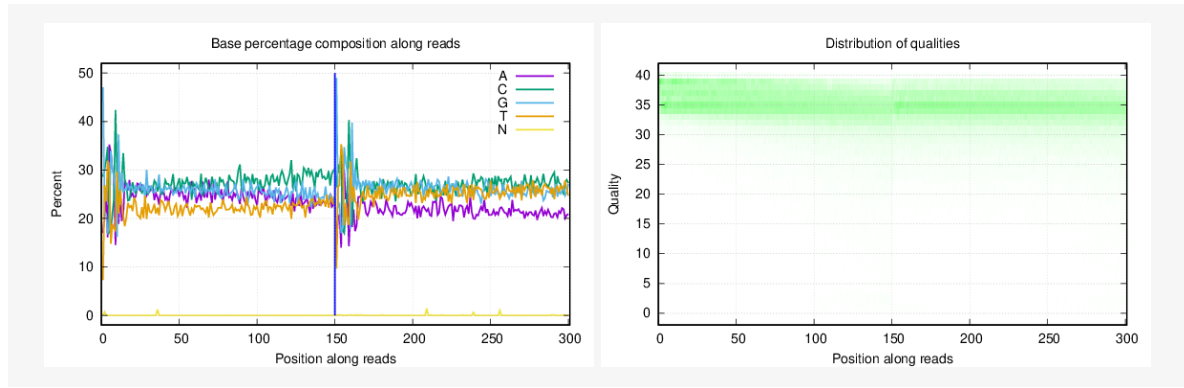
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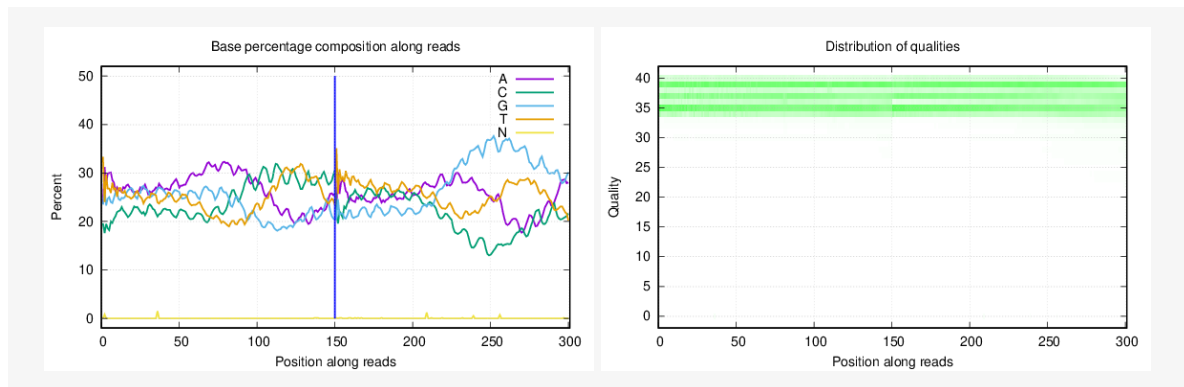
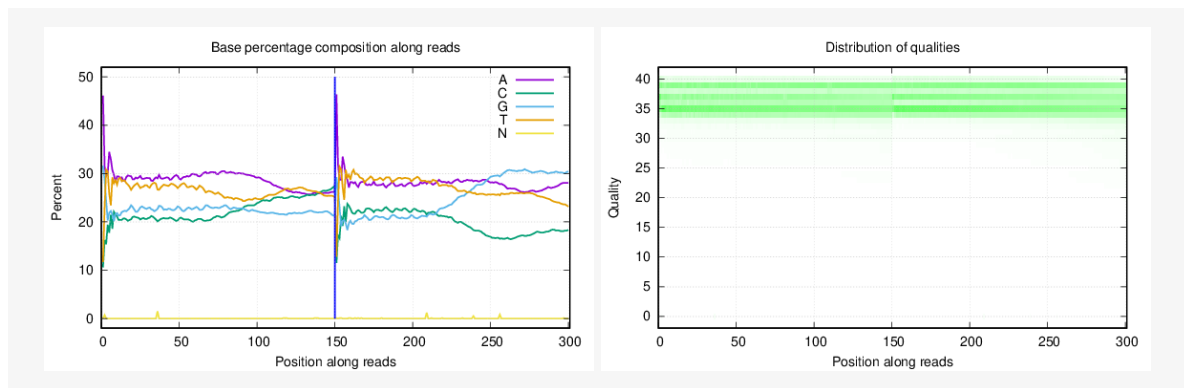
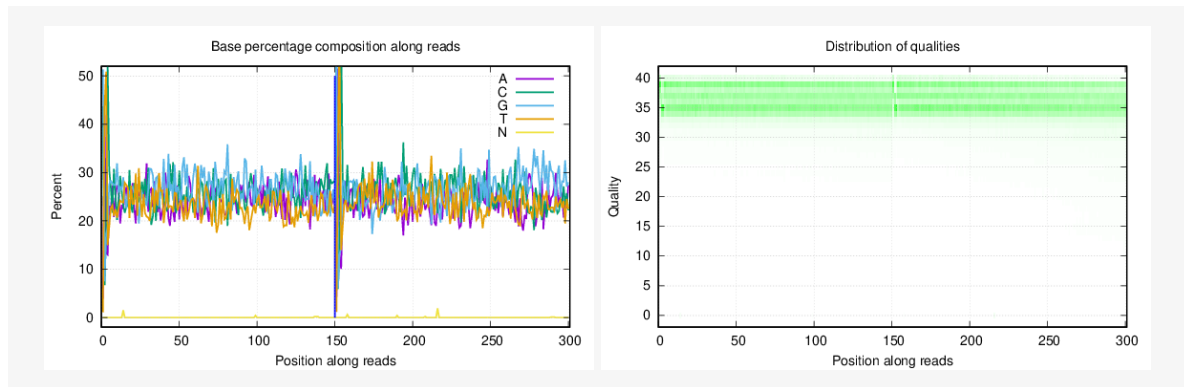
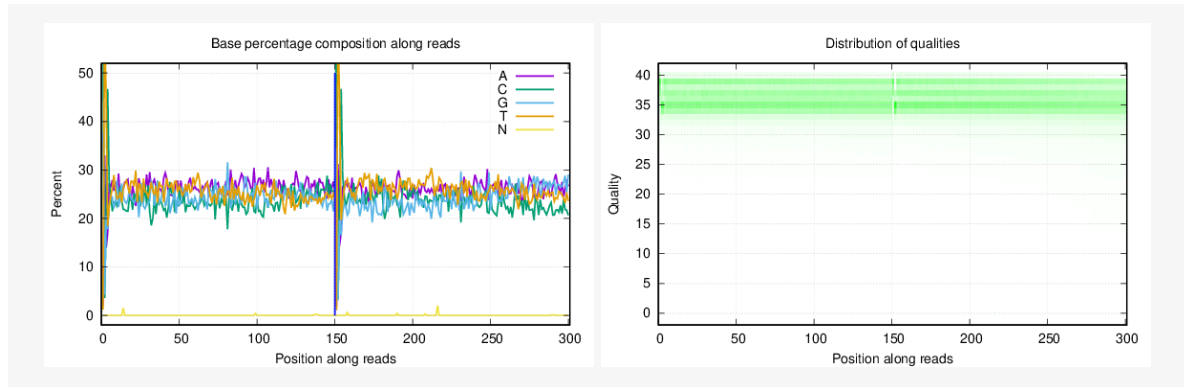


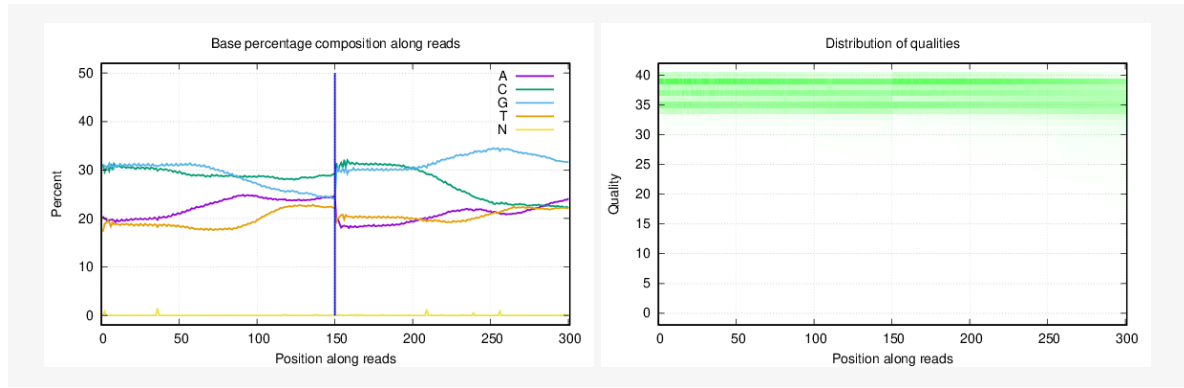
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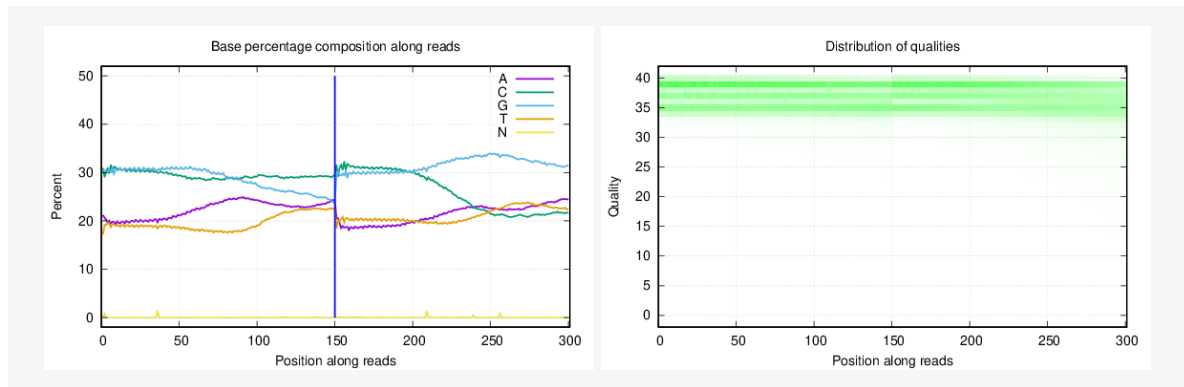
SP-dCas9-VPR_3



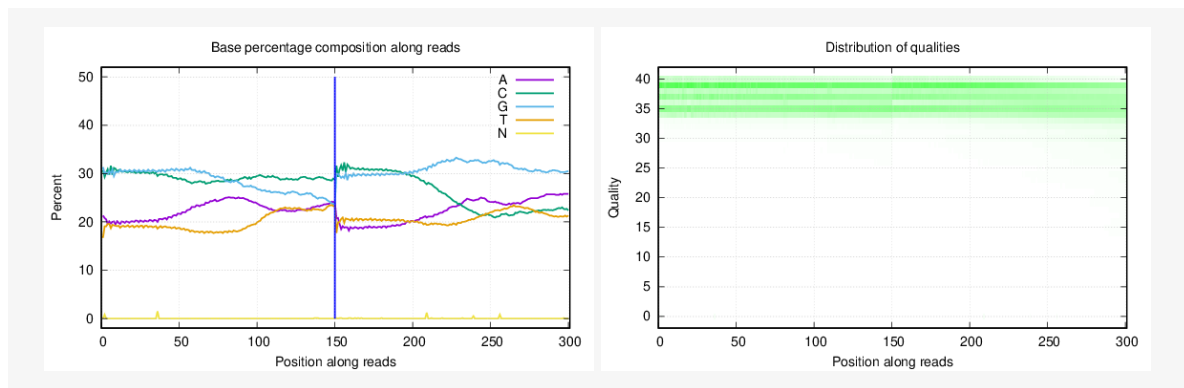




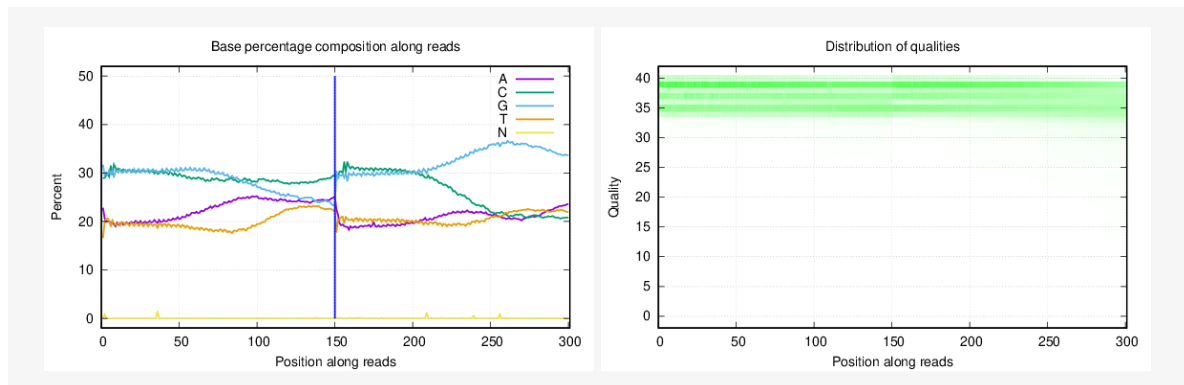
Vsplma-3



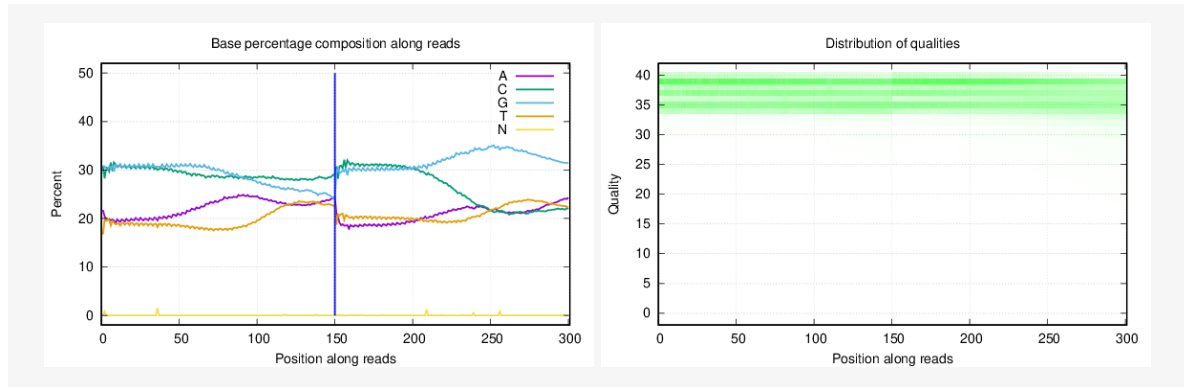
Vsplma-4



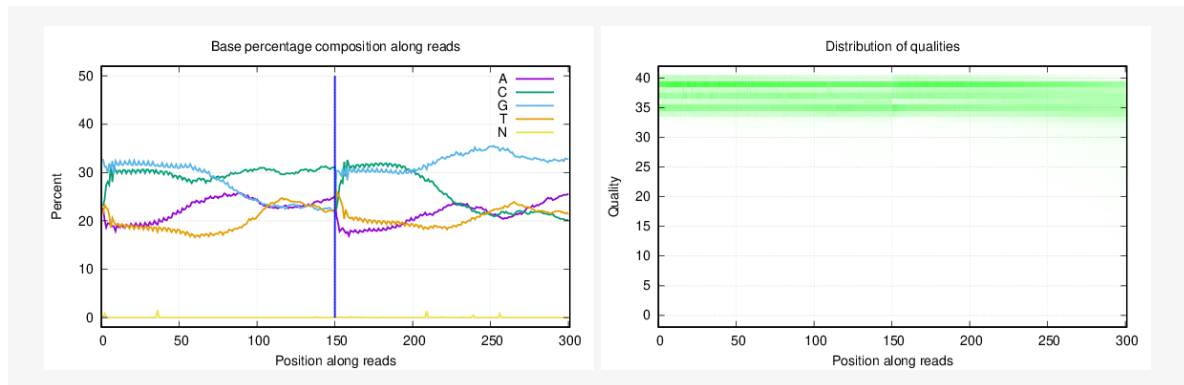
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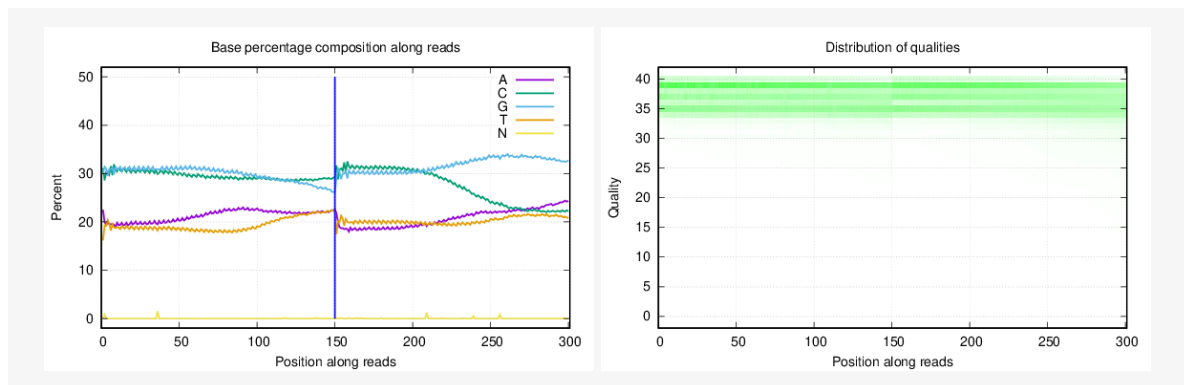
VspZap-3



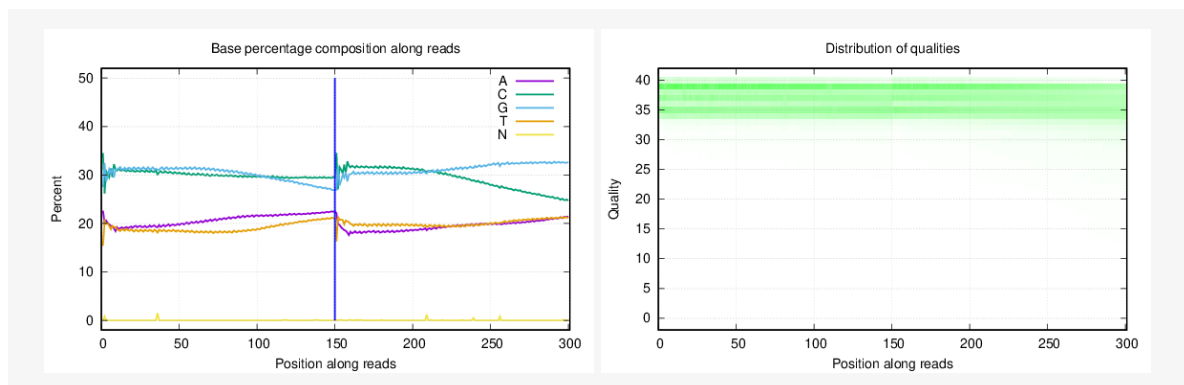
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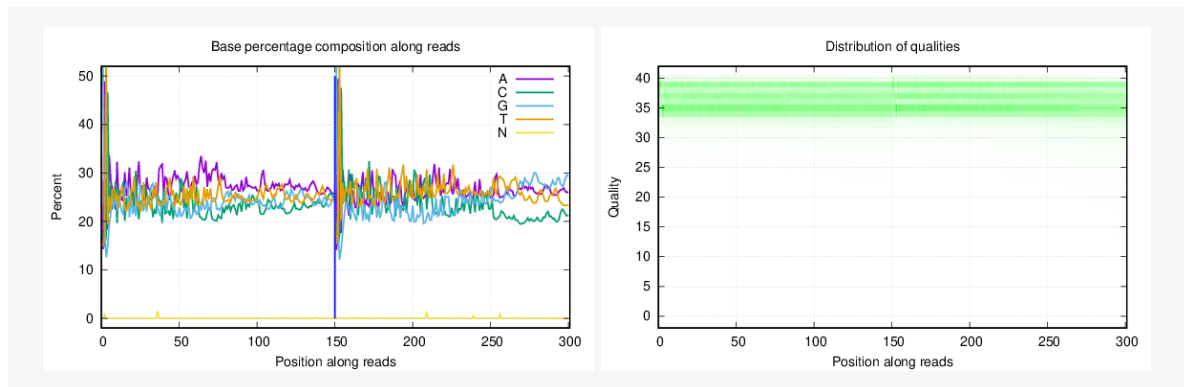
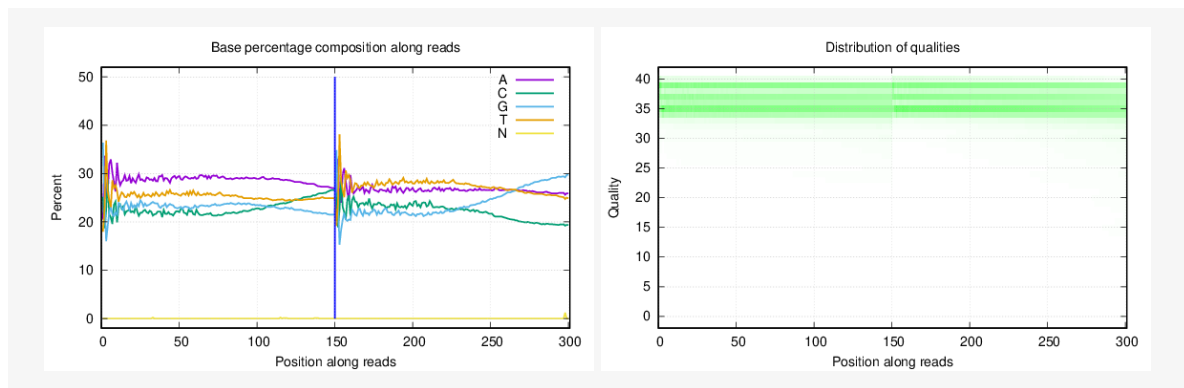
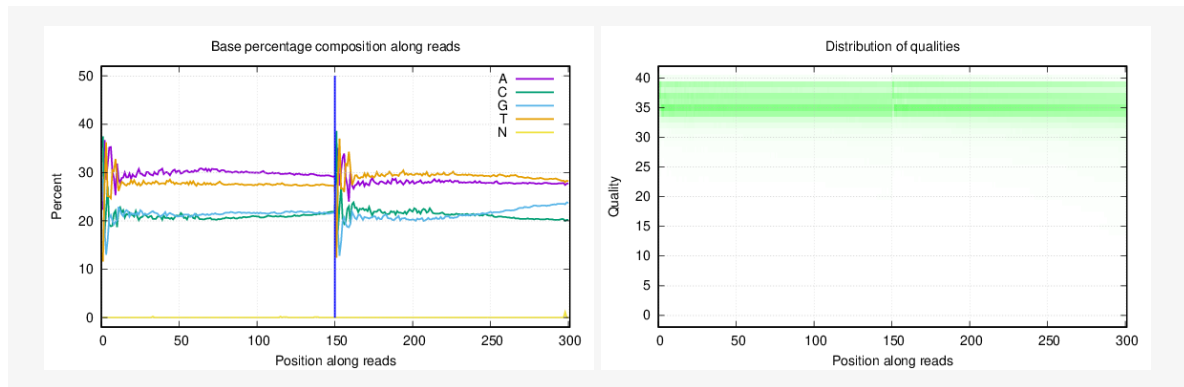
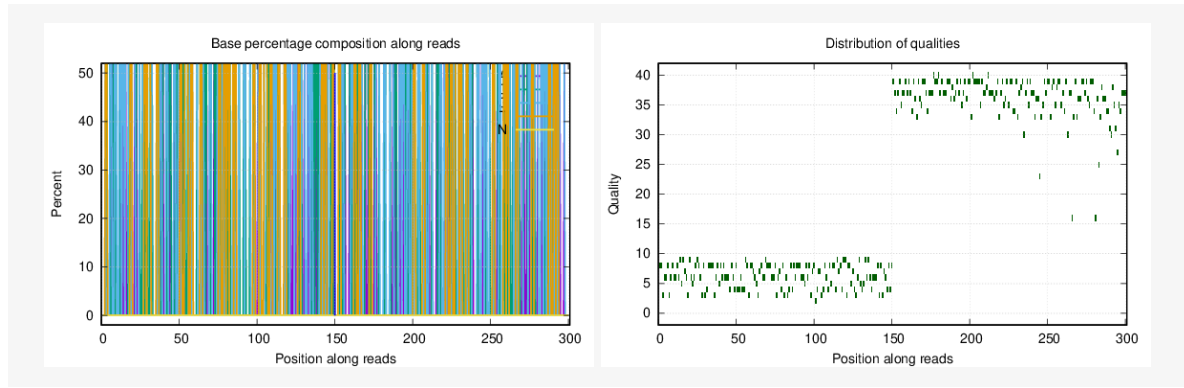
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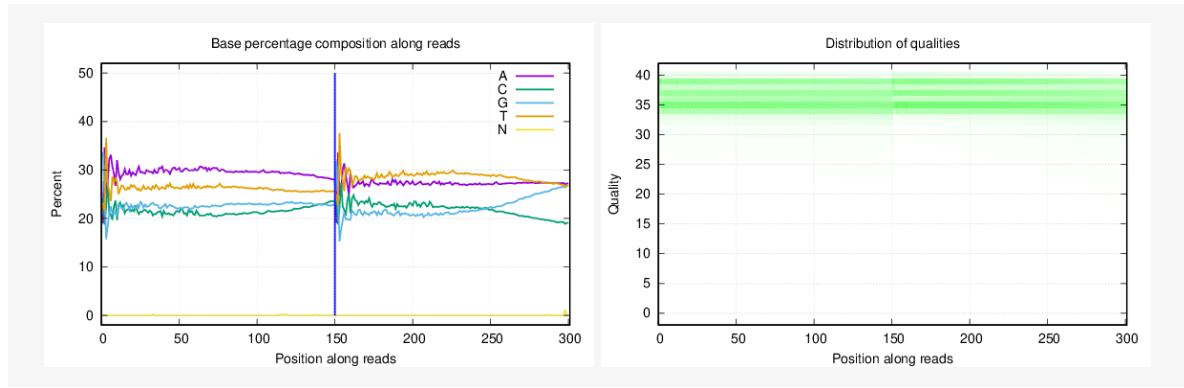


Vvulma-1

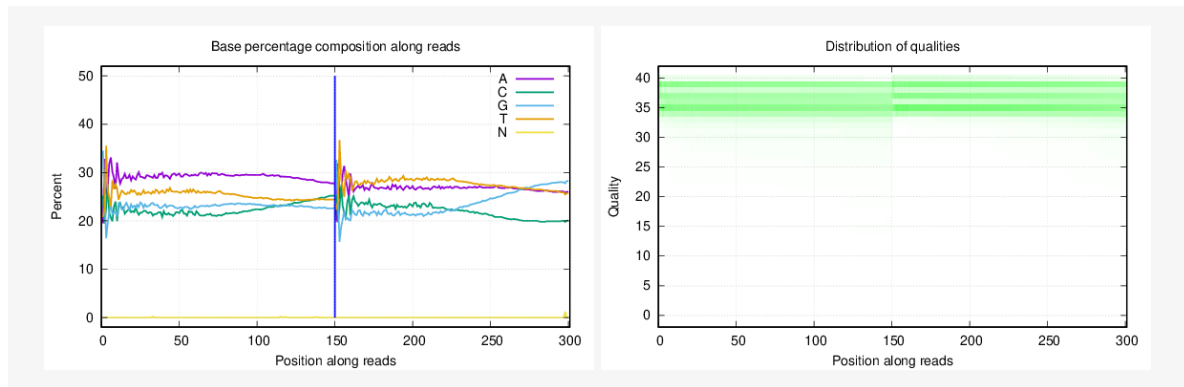


VvuMan-1

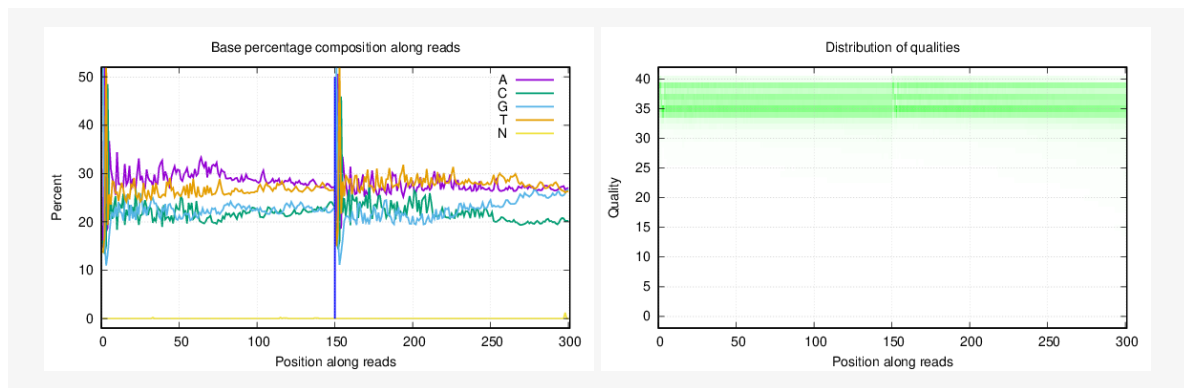




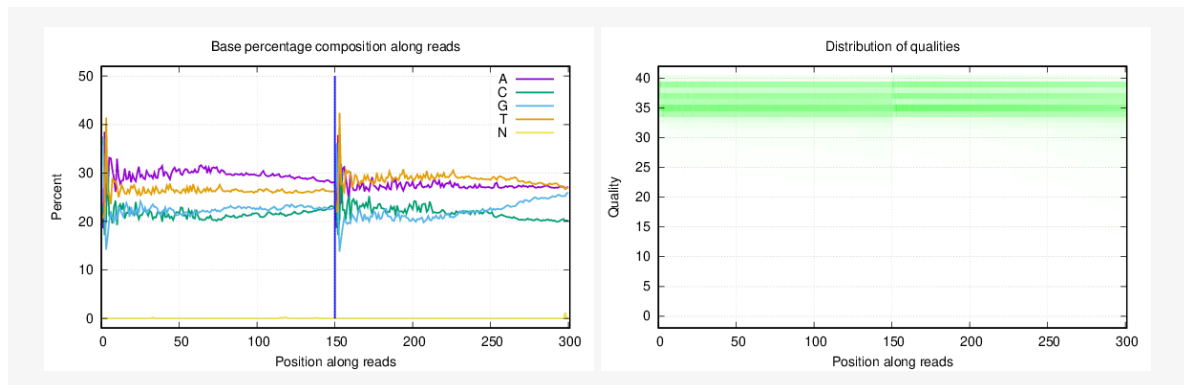
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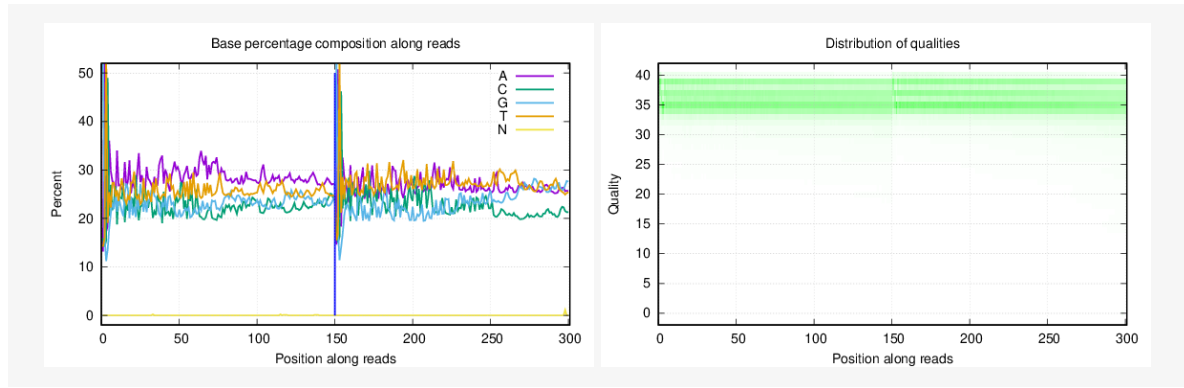
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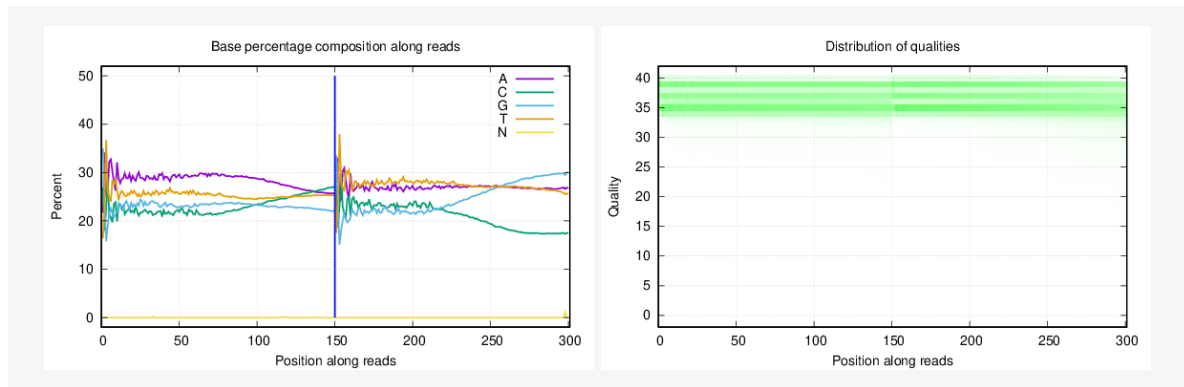
brLinker_a_R3



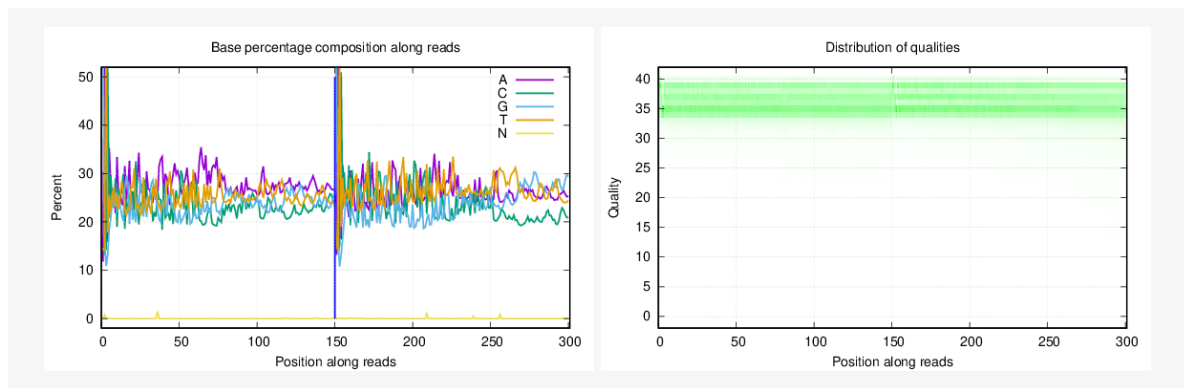
brLinker_a_R4



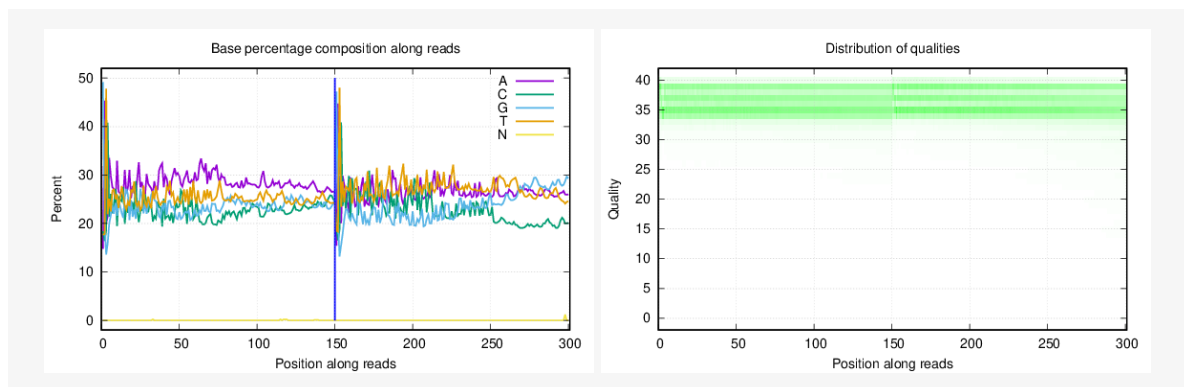
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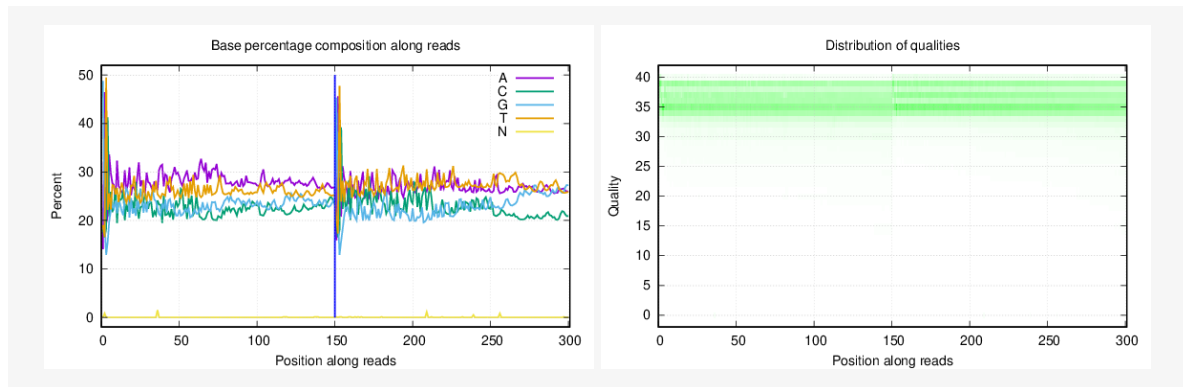
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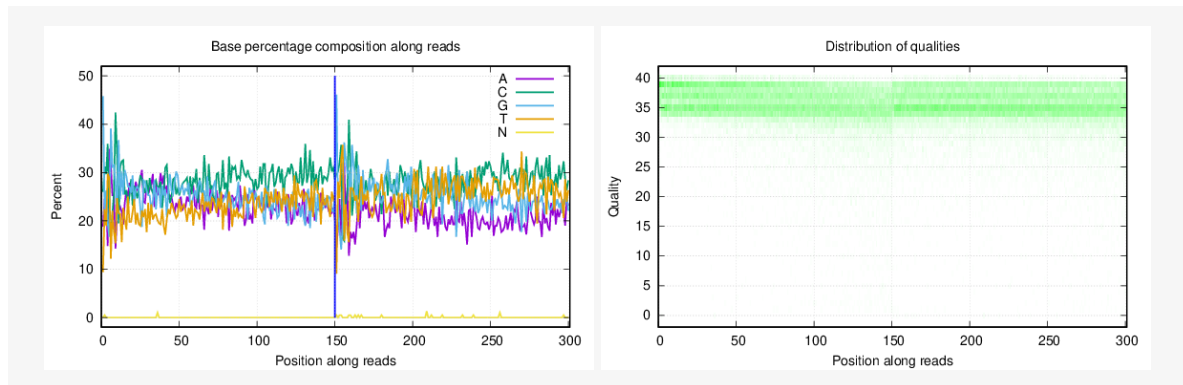
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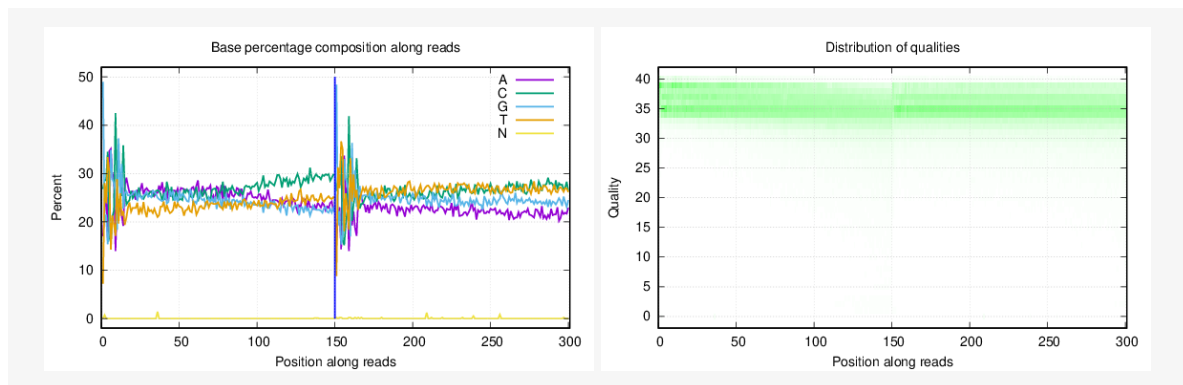
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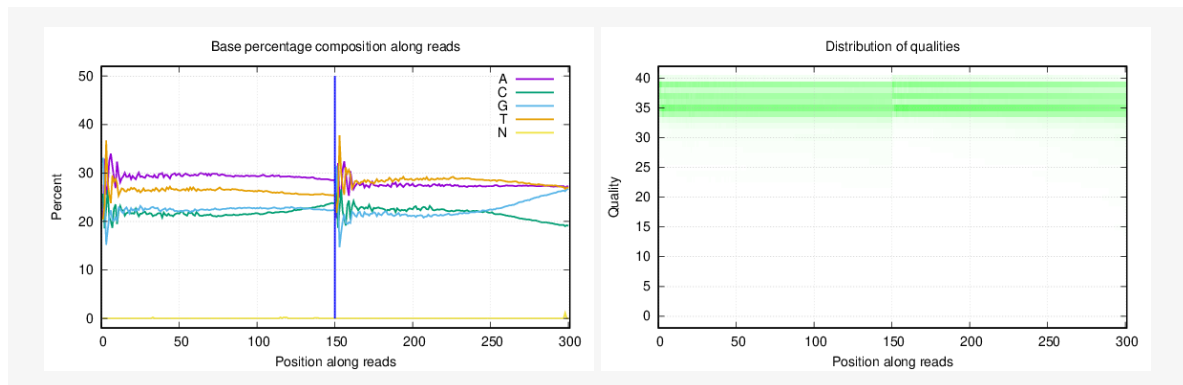
eGFP



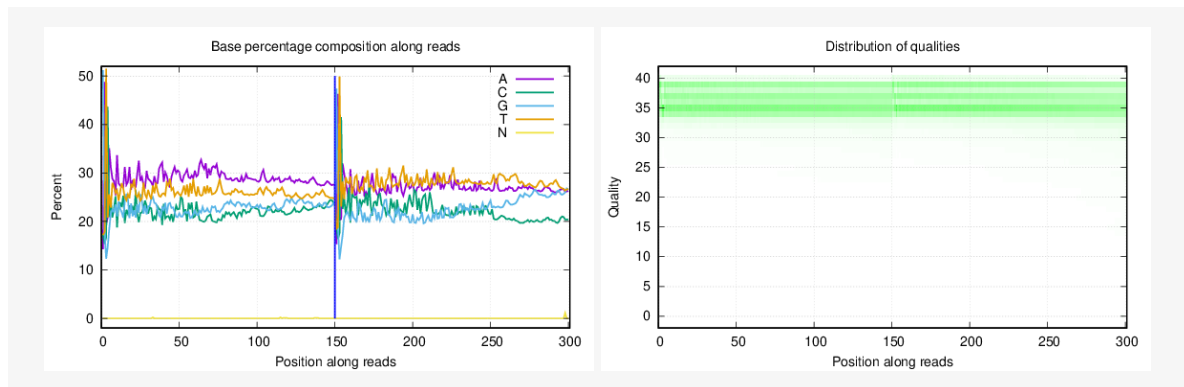
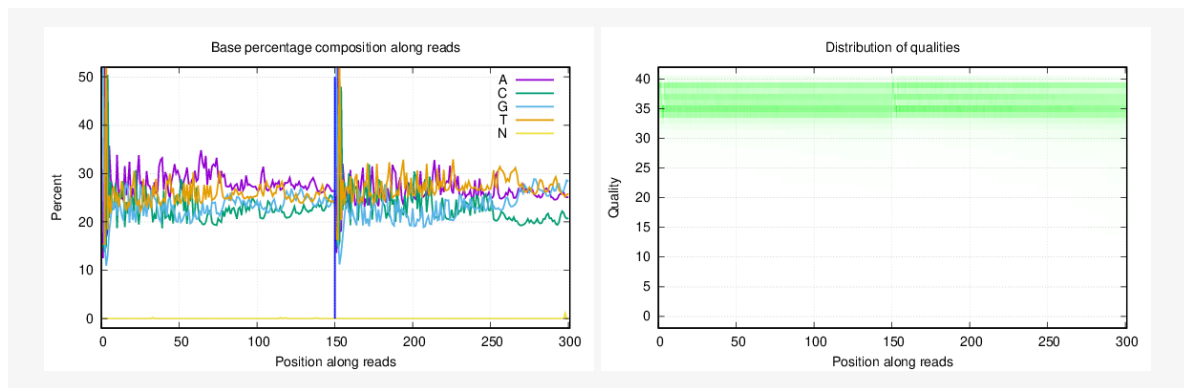
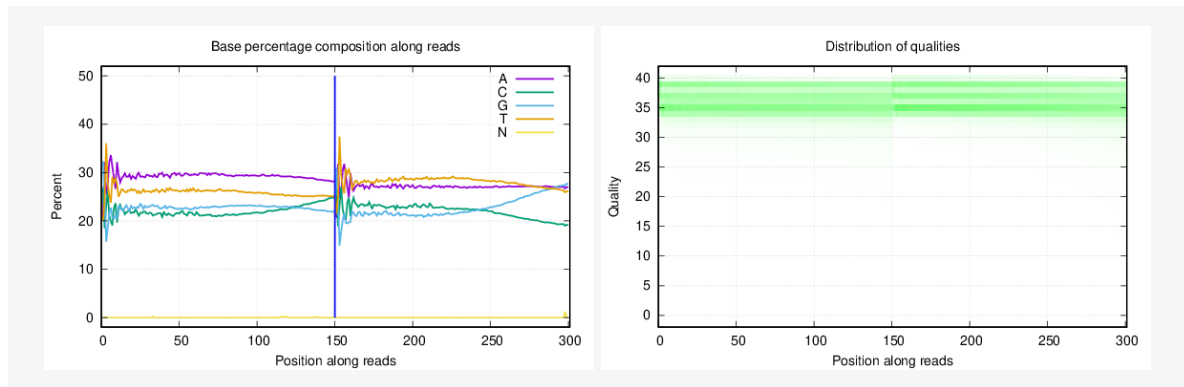
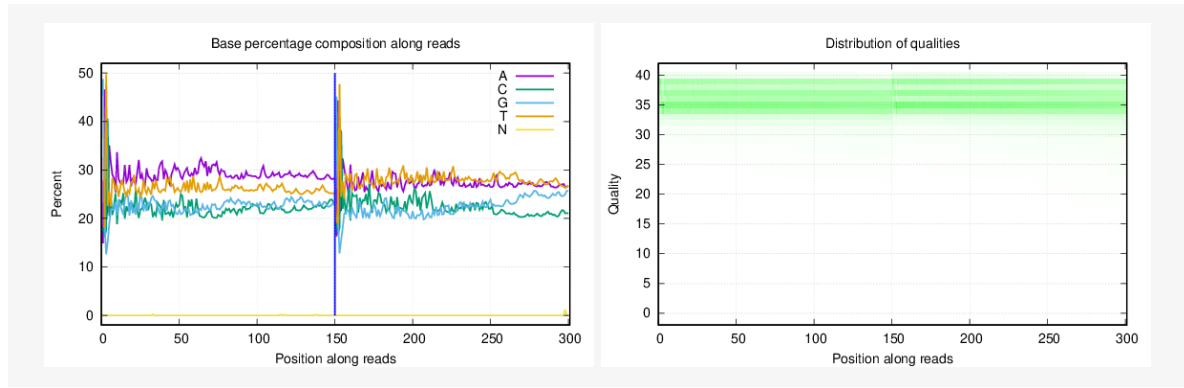
lenti_sgRNA_zeo_backbone

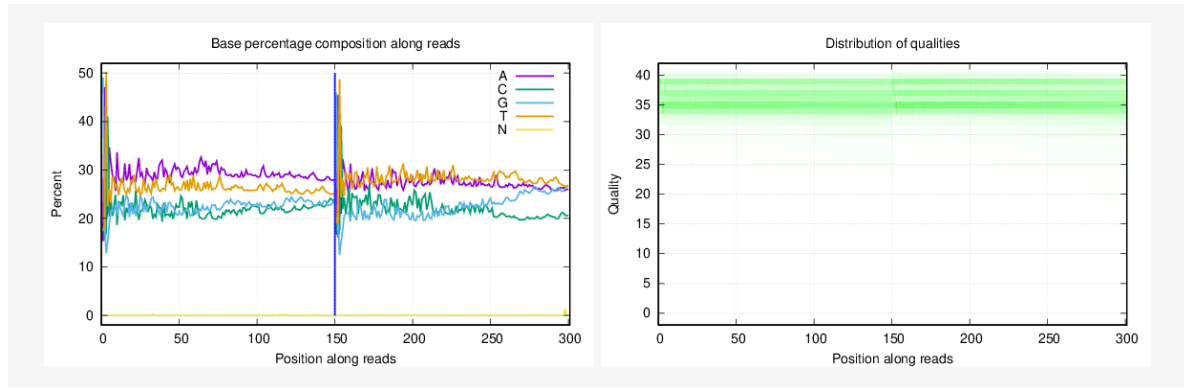


mutE14K_R3

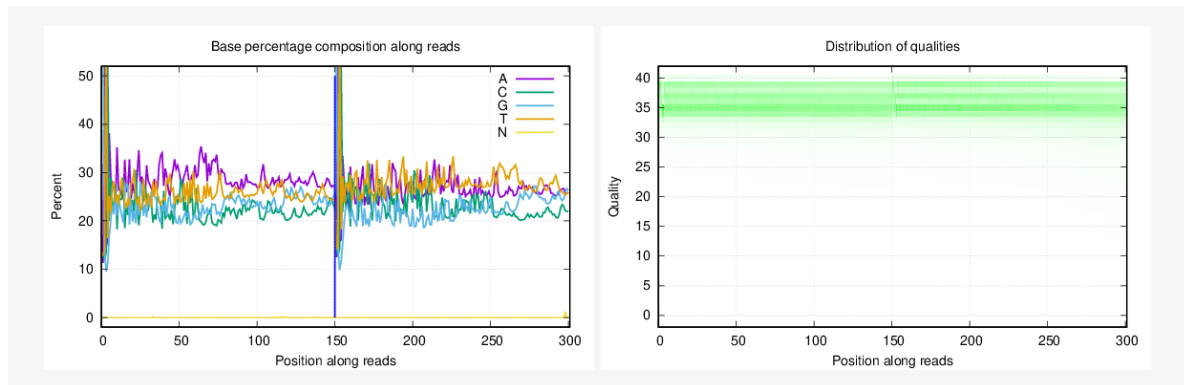


mutE14K_R4

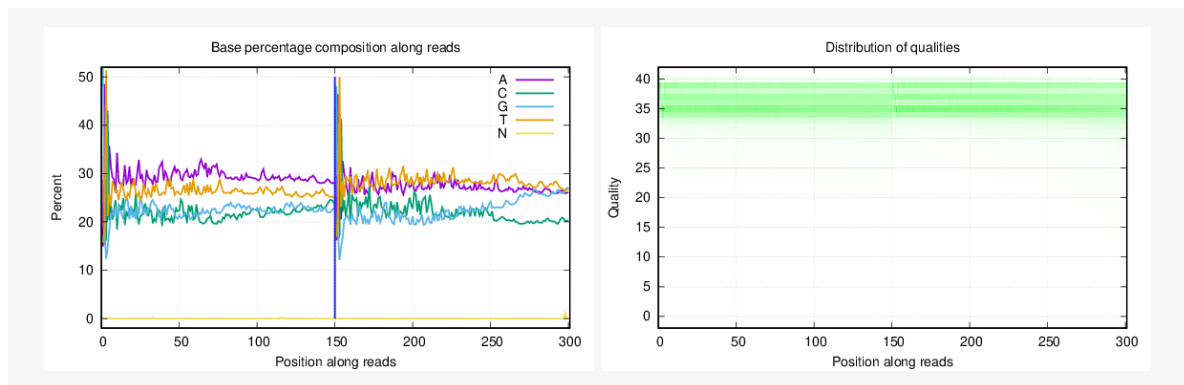




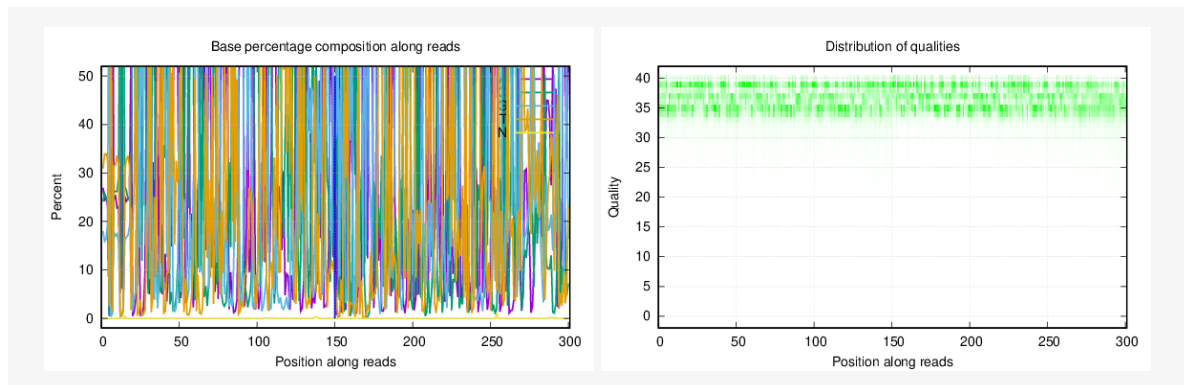
mutG261S_a_R5



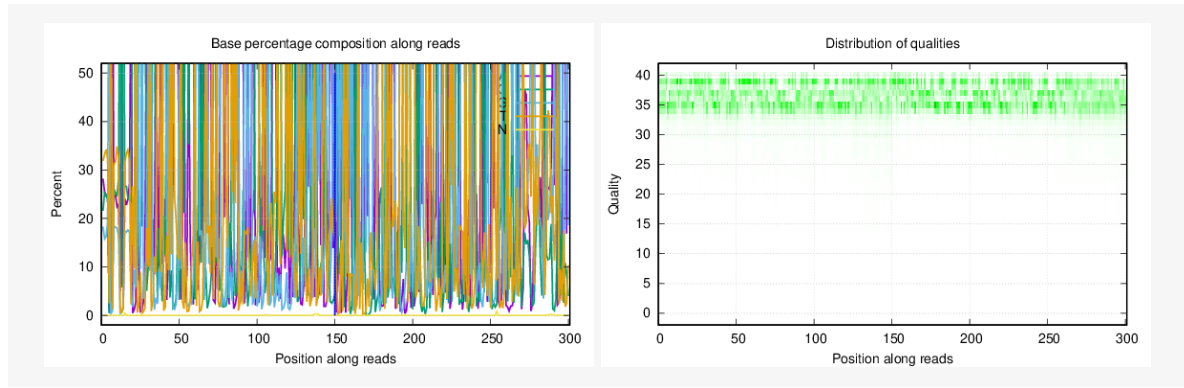
mutG261S_a_R6



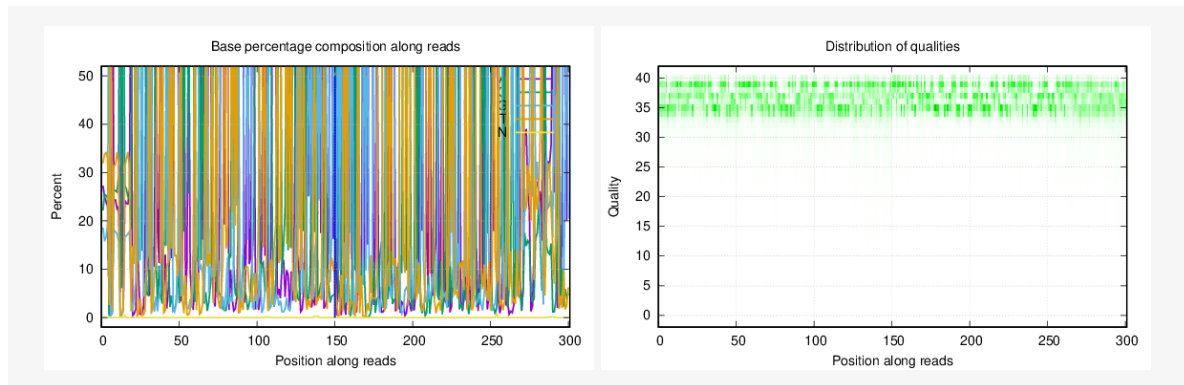
rigs_11



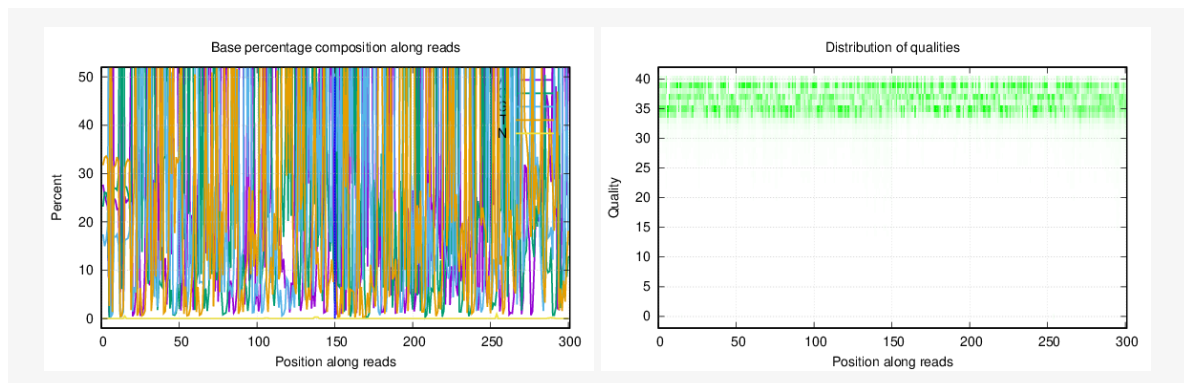
rigs_14



rigs_17



rigs_2



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
+
FFFFFFFFFFFDFFFEFFEF0FFFEFFFFFEFFFFFEFCGFFFF
```

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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