FastQC Report

Wed 19 Dec 2012
174gm_A_NoIndex_L006_R2.fastq.gz

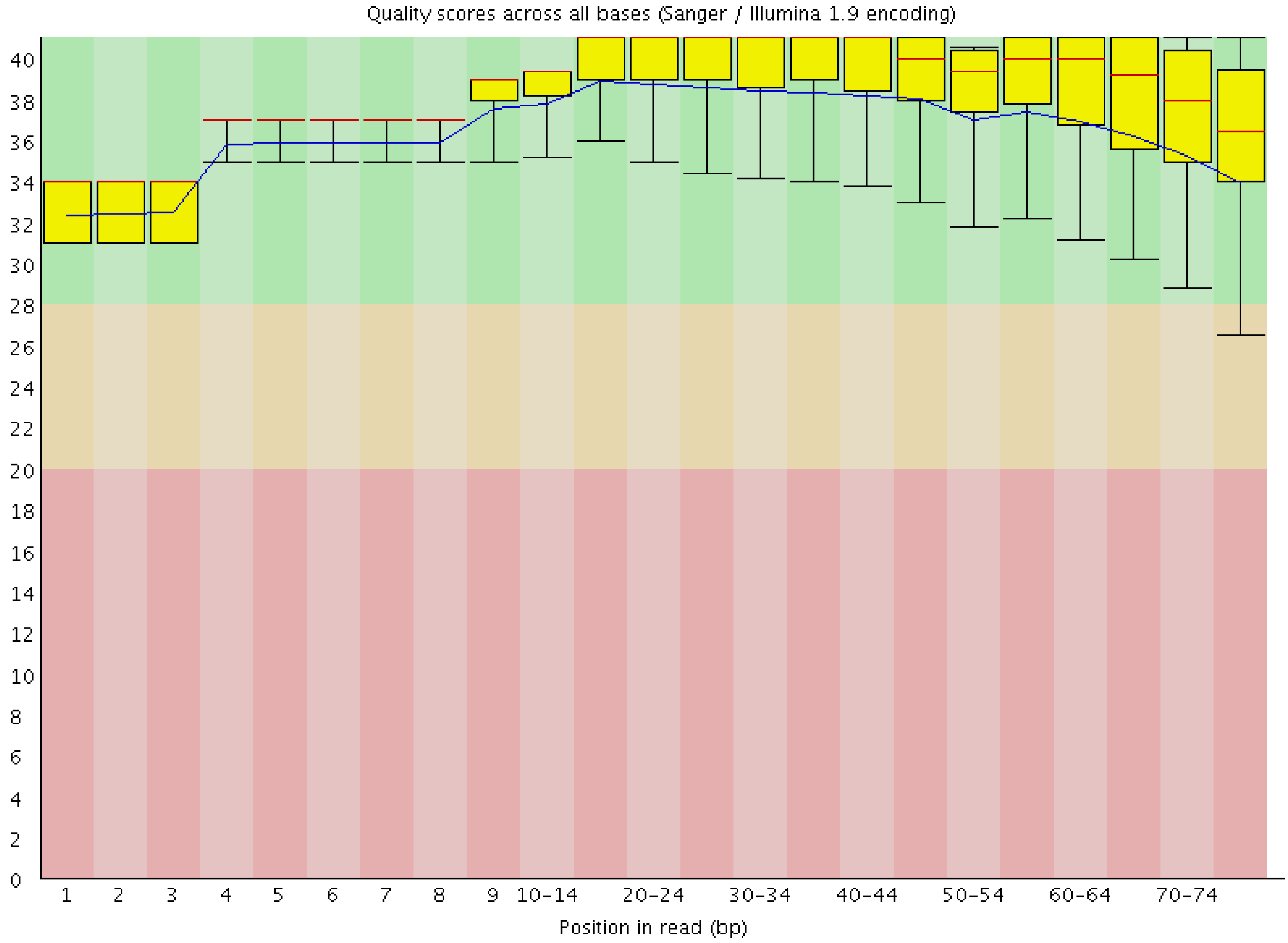
Summary

- ✓ Basic Statistics
- ✓ Per base sequence quality
- ✓ Per sequence quality scores
- ✗ Per base sequence content
- ! Per base GC content
- ! Per sequence GC content
- ✓ Per base N content
- ✓ Sequence Length Distribution
- ! Sequence Duplication Levels
- ✓ Overrepresented sequences
- ✗ Kmer Content

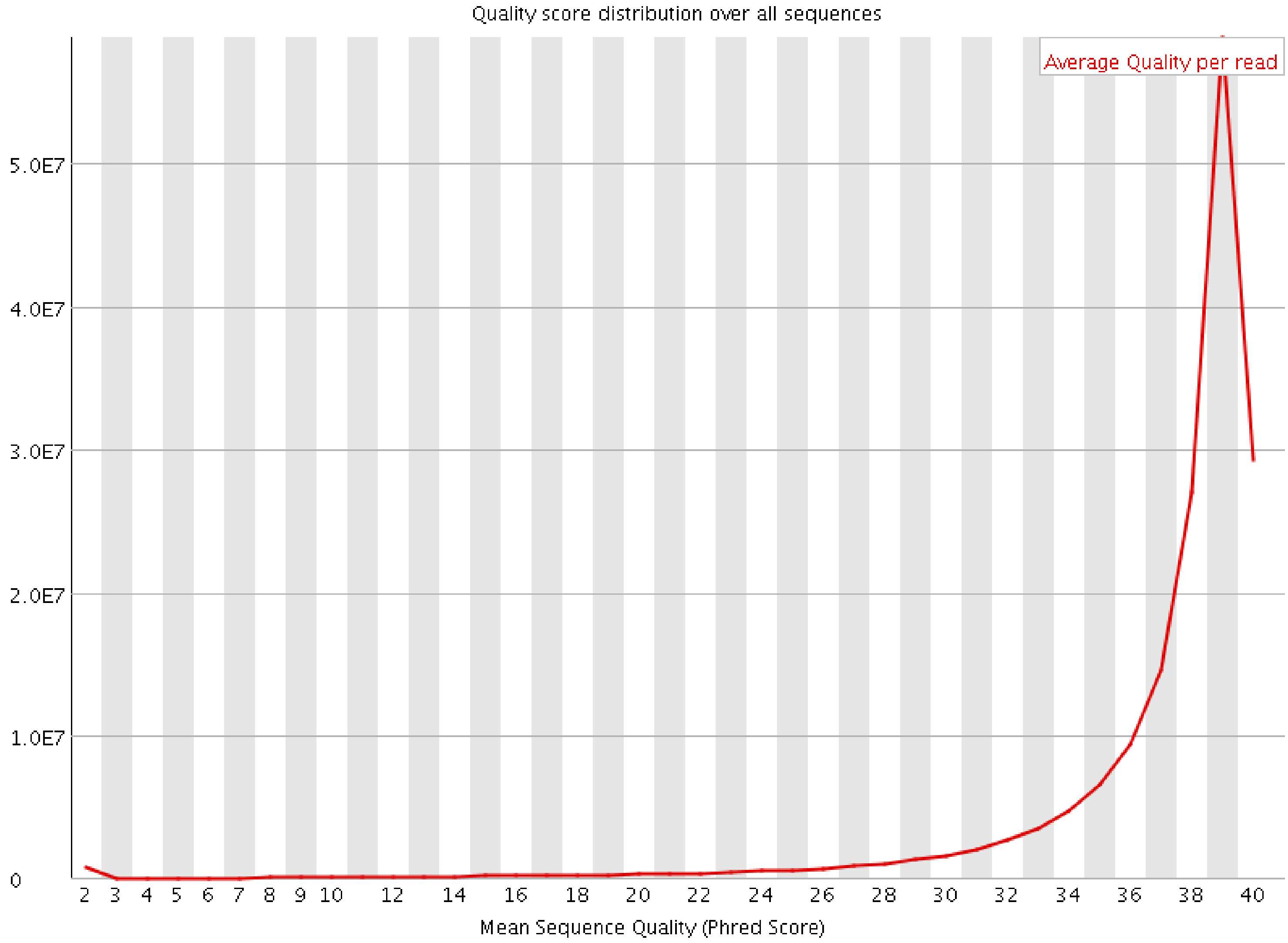
✓ Basic Statistics

Measure	Value
Filename	174gm_A_NoIndex_L006_R2_001.fastq.gz
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	171582441
Filtered Sequences	20032583
Sequence length	76
%GC	18

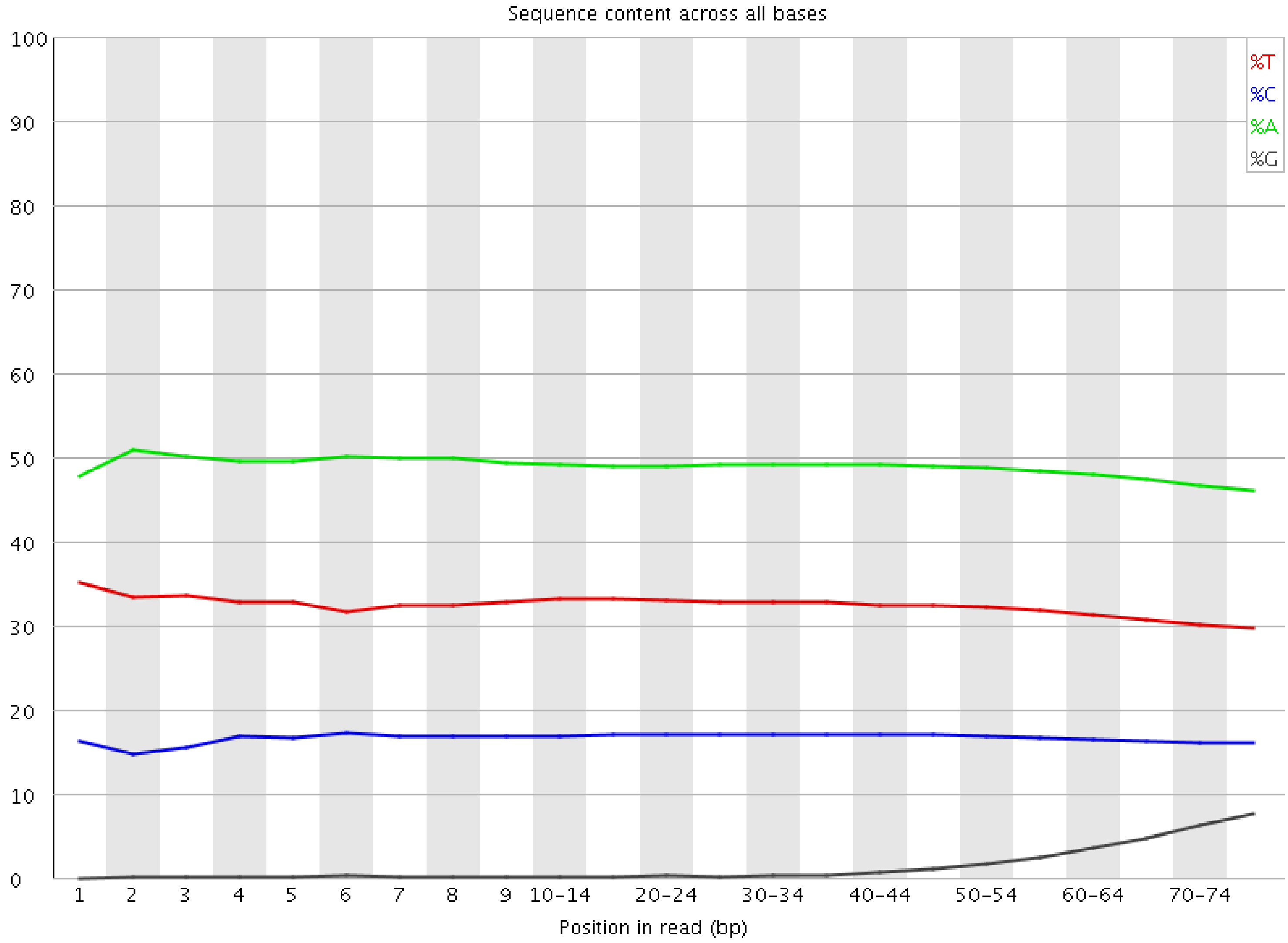
✓ Per base sequence quality



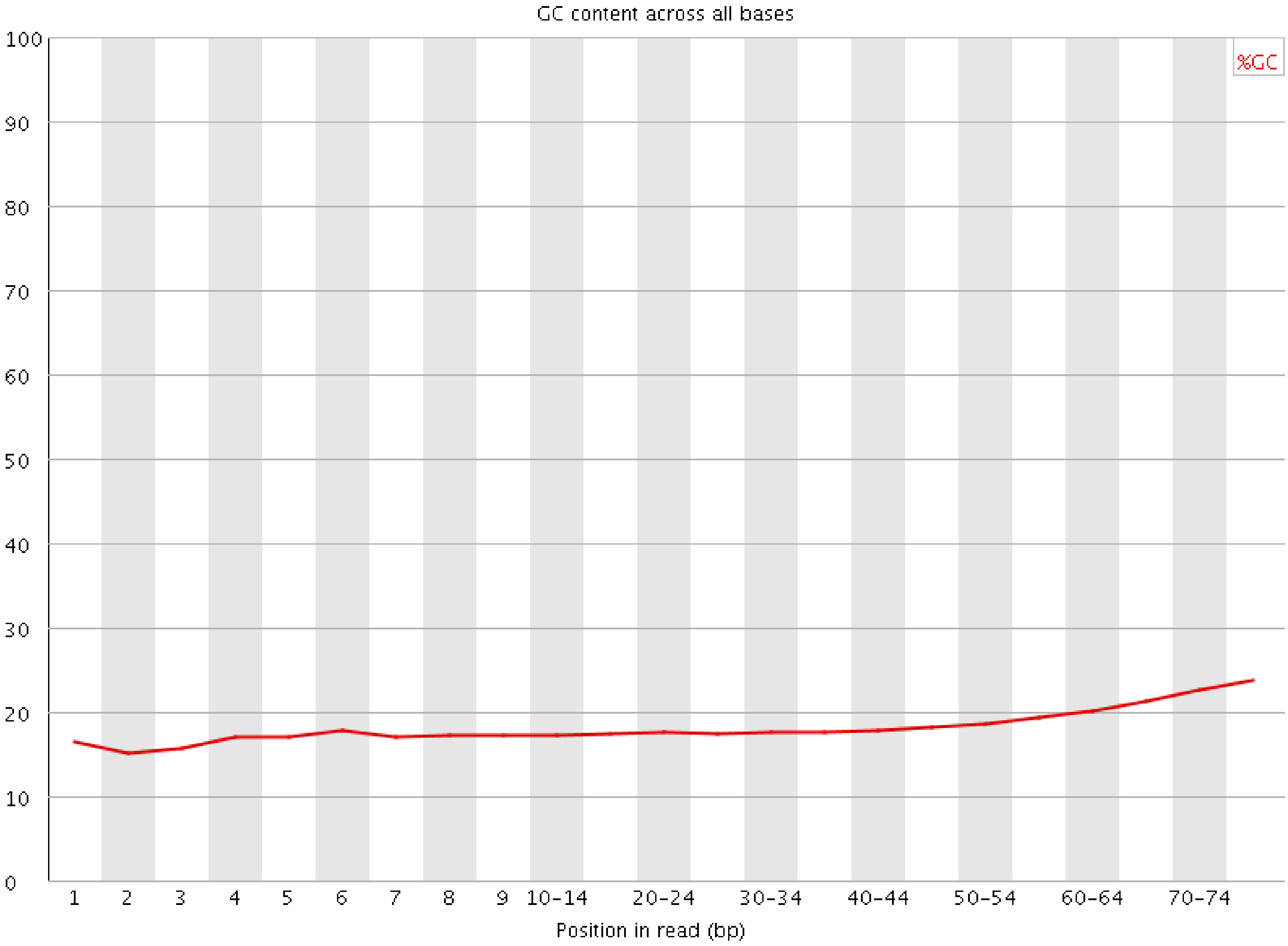
✓ Per sequence quality scores



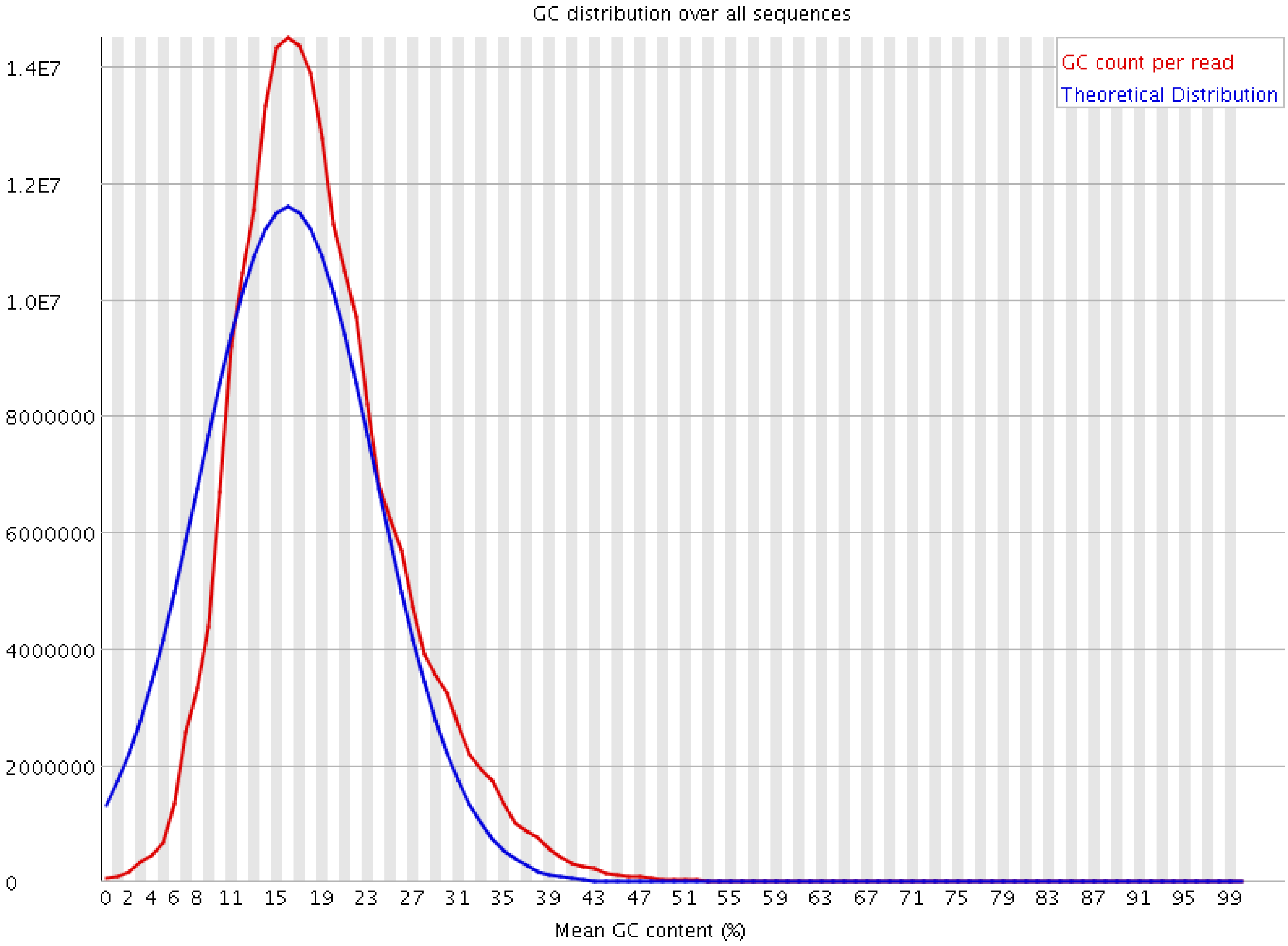
✗ Per base sequence content



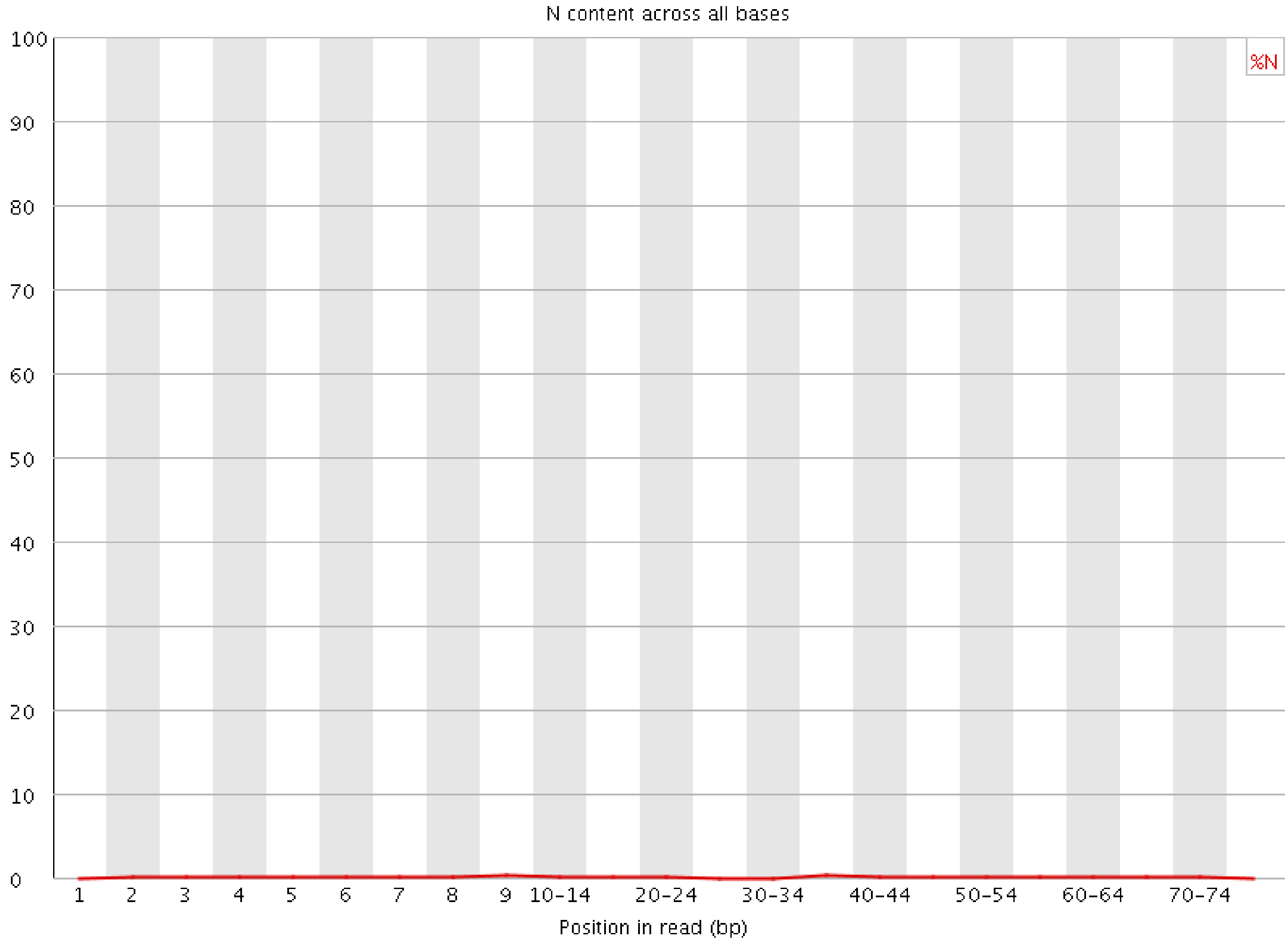
❗ Per base GC content



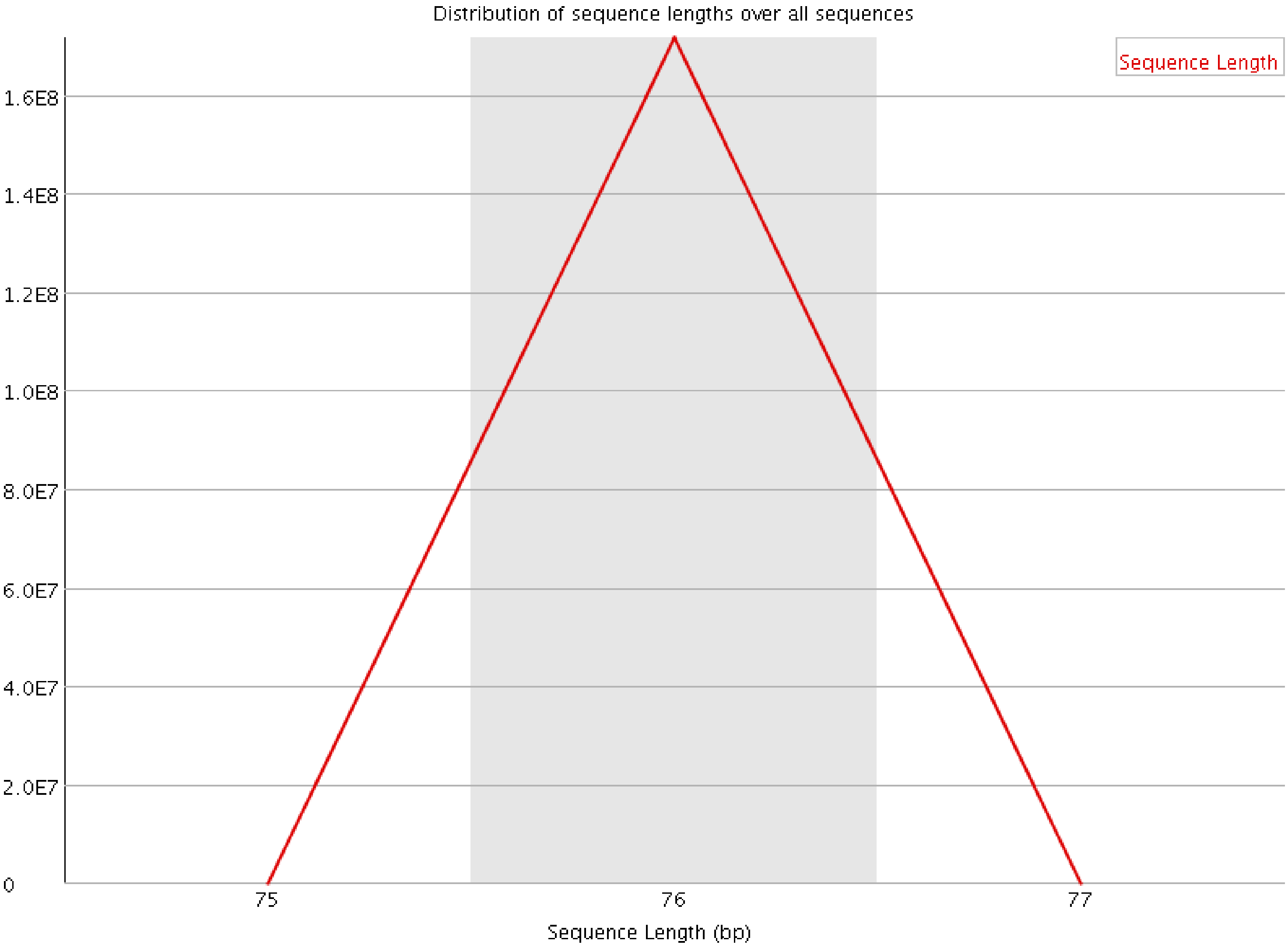
Per sequence GC content



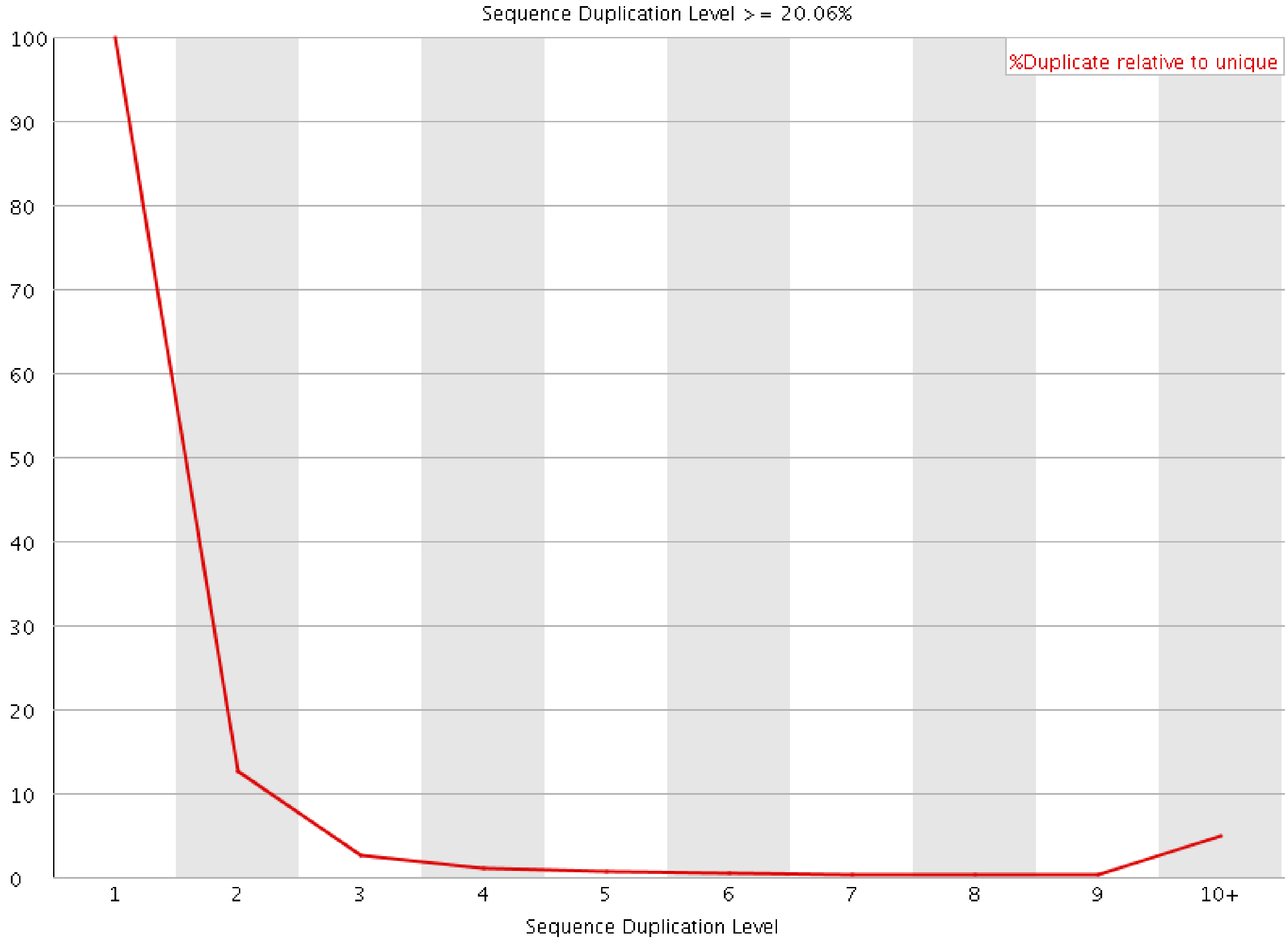
✓ Per base N content



✓ Sequence Length Distribution



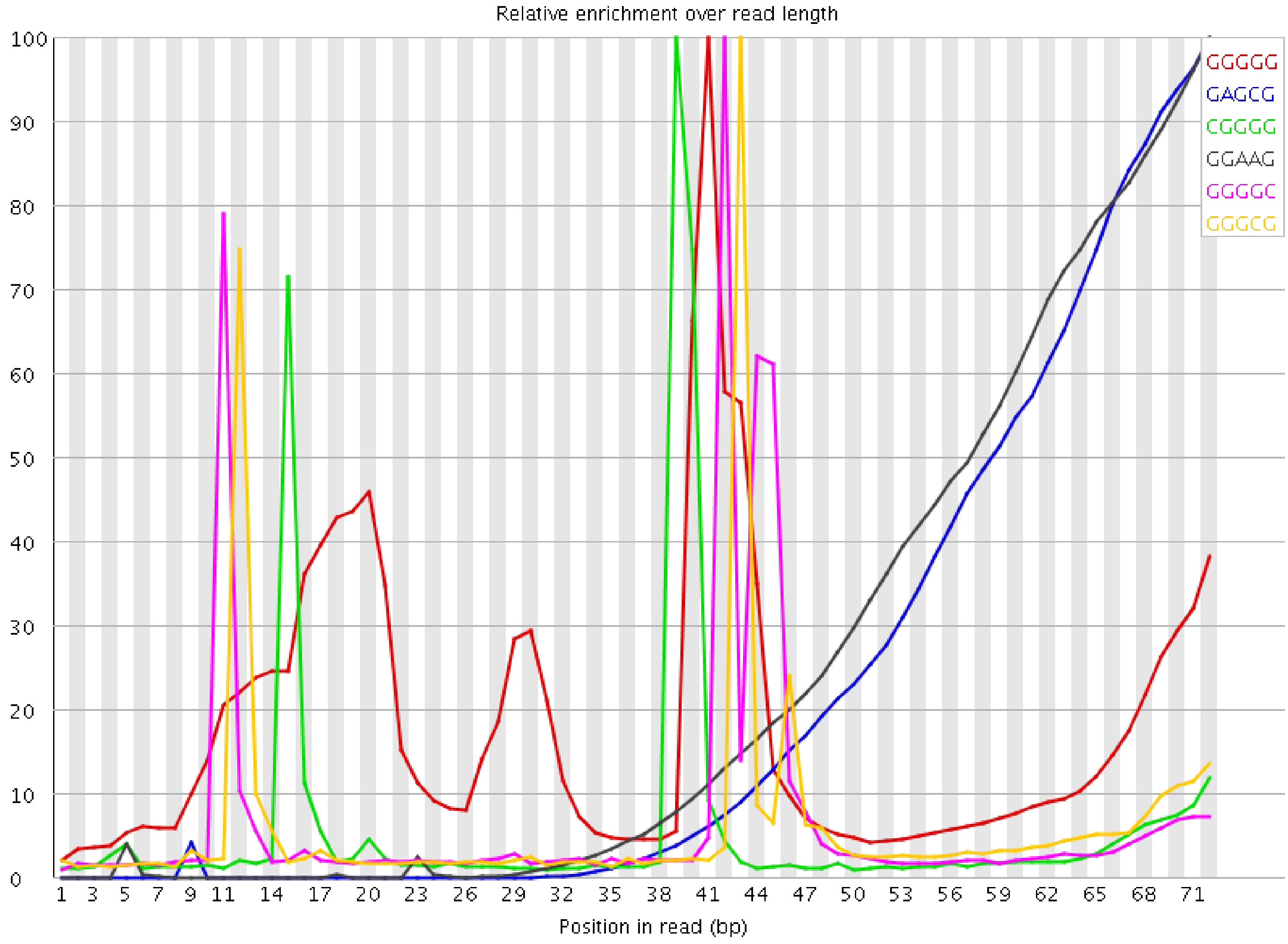
Sequence Duplication Levels



✓ Overrepresented sequences

No overrepresented sequences

✗ Kmer Content



Sequence	Count	Obs/Exp Overall	Obs/Exp Max	Max Obs/Exp Position
GGGGG	1470430	61084.34	341843.34	41
GAGCG	14643965	2415.3853	11359.559	72
CGGGG	247955	1101.6149	18436.523	39
GGAAG	19107165	1094.0151	4627.327	72
GGGGC	221220	982.83655	13668.534	42
GGGCG	198920	883.7621	14249.549	43
GGTGG	362950	843.0632	10537.728	72
GGCGG	150555	668.886	14154.308	13
GCGGG	140940	626.16846	14055.603	14
GTAGG	6945215	598.9214	3745.601	72
AGGGG	383215	591.0155	6633.149	28
GGGGA	359065	553.76996	8866.018	21
TAGGG	6314050	544.4928	3501.7385	72

GAGGG	277330	427.71375	4857.0283	27
GCGTC	12829540	340.85315	1714.8082	72
GGGAG	218980	337.72308	4255.6216	30
TGGGG	145180	337.22534	3153.4482	20
AGGGA	5811895	332.77057	2205.892	72
CGTCG	11985830	318.43756	1655.1895	72
GGGAA	5528620	316.55112	2130.4165	72
GGGGT	128410	298.2718	4113.9976	41
GTGGG	117080	271.95444	2214.944	19
GGGTG	105290	244.56845	2084.8347	43
GGAGG	152775	235.61804	3603.2603	18
GAGTG	2602620	224.43724	1959.0343	72
GATCG	24299310	224.10396	820.4318	72
ATCGG	22761360	209.91998	792.56854	72
TCGGA	21529705	198.56087	783.0041	72
GTCGT	10891575	151.28758	815.4043	72
TCGTG	10015580	139.11972	793.9742	72
CGTGT	9183370	127.56005	742.02893	72
AGCGT	13723025	126.56263	603.624	72
CGGAA	20407110	124.96261	507.97742	72
AGAGC	15978710	97.84537	444.6056	72
CGGTG	367570	91.31137	1337.9324	72
GTGTA	10447480	50.375977	330.6555	72
TCGGG	194335	48.276505	964.1055	38
TGTAG	9477720	45.69996	310.1067	72
AAGAG	20671395	43.940773	223.70648	72
GGTCG	173940	43.21	579.5441	72
GGCGC	89945	42.737133	1399.8507	44
GGGCC	88055	41.839108	827.2551	45
GAAGA	18180495	38.645916	165.46942	72
GCGCG	76245	36.22762	122.804016	72
CCGGG	75685	35.961536	808.8547	39
GCGGC	74020	35.17041	590.88007	11
CGGCG	72355	34.379295	586.017	12
GCCGG	67040	31.853886	552.4763	47

GTGGT	231265	30.036623	443.30316	72
GGCCG	61585	29.261955	331.37814	46
GTCGG	94880	23.569994	272.91867	13
AAGGG	340355	19.487638	213.49615	27
CGCGG	40300	19.148443	70.08032	15
CGCCG	323720	16.45013	209.64014	46
CGGGA	96530	15.921722	332.21796	4
CTCGG	598370	15.897396	209.86096	72
CGGGT	63830	15.856585	370.42877	15
GAGAG	248035	14.201693	98.97464	7
GGCGT	54780	13.608393	139.28078	13
CGTGG	54285	13.485425	118.698456	15
AGAGG	230300	13.186243	175.30621	26
GGGTC	52355	13.005975	330.5506	42
CGGGC	27295	12.969149	35.59984	42
GGAAA	5568205	11.836222	80.17751	72
GCGTG	46870	11.643398	132.7631	14
AGTGT	2338620	11.276431	97.87545	72
AGCGG	66325	10.93969	209.74323	10
GGGTA	125670	10.837166	192.46942	29
GAAGG	182170	10.430472	96.47737	72
GGTAG	118290	10.200751	173.07347	30
AGGGC	61735	10.182612	69.898735	11
GAAAG	4769775	10.139016	74.55352	72
TTGGG	76690	9.960472	95.040085	38
AGAGT	3056185	9.784409	78.81701	72
AGGGT	113215	9.763109	202.34413	28
AGATC	26962930	9.231951	35.73861	72
CCGCG	169780	8.627527	10.951615	48
GTGCG	31270	7.7680616	29.330425	72
GCGCC	149875	7.616036	151.93724	45
GGAGA	132290	7.5745025	151.94344	31
TCGCG	277215	7.3650026	11.772322	71
ACGGG	42910	7.077604	109.3006	3
CGACG	400110	7.0579505	10.984826	71

GTGTG	54145	7.032335	116.64642	72
CGCGC	133860	6.802219	8.707419	47
TGGGA	78415	6.762127	73.12199	4
CGCGA	383240	6.760363	7.461766	14
CCCCC	11325780	6.5828023	7.6132603	26
CGGAG	39365	6.4928894	64.309875	5
TCGGT	466100	6.474283	87.32546	72
CAGGG	38330	6.3221755	32.298798	72
GCGGT	24335	6.045276	23.327967	48
GTAGA	1884245	6.03243	56.46908	72
CGCGT	226520	6.0181465	11.73407	71
GCAGG	36325	5.99147	38.71106	72
GTTGG	44945	5.837442	79.83682	18
CTGGG	23205	5.7645626	121.400696	39
GGTGC	22195	5.513659	156.64548	44
TGTGG	42125	5.4711814	34.99394	40
AGGCG	32660	5.386962	45.027657	12
GGGTT	37510	4.871786	38.346954	16
GTCGC	182715	4.8543425	53.65512	44
ATGGG	56205	4.846844	38.10708	3
ACGCG	269685	4.7572503	5.323781	3
GTGGC	18970	4.712508	51.246502	45
GGTGT	35640	4.628911	19.261332	71
GGACG	27570	4.547414	37.404884	1
TGGGC	18100	4.4963837	106.93232	42
GGTTG	33905	4.40357	39.790337	17
GCCGT	160295	4.258692	83.82834	47
GACGG	25555	4.215059	37.539417	2
GGGCT	14825	3.6828115	24.15788	43
TGGTG	28255	3.6697502	25.44466	39
GGAGC	21990	3.627045	25.363111	44
GCCGC	71000	3.6079304	38.43338	47
GGGCA	21645	3.5701406	16.030079	70
GTGGA	41255	3.5576298	36.54572	16
GCCCG	69655	3.539583	52.90306	47

GAGGC	19880	3.2790205	32.30214	11
TGGCG	13095	3.2530468	21.1982	46
GGCAG	19270	3.1784067	12.4682865	72
TGGAG	36750	3.1691406	38.744102	17
TGCGG	12545	3.1164162	17.448954	40
GCTGG	12530	3.11269	10.750049	14
GATGG	35935	3.098859	18.9744	2
GGGAC	18340	3.0250118	14.199791	42
GGCTG	12005	2.98227	10.031798	13
GCGGA	17700	2.9194498	17.519659	16
AGGAG	50880	2.9132264	16.797491	72
TGGGT	22050	2.8638468	26.292616	42
GTCCG	107365	2.8524559	5.048272	13
GCGAG	15640	2.579672	11.755813	72
GAACG	420670	2.575966	7.2453265	72
GGCCC	49360	2.5082738	58.713146	46
GGATG	28665	2.4719293	19.059546	1
GGGAT	27970	2.4119964	23.3713	33
GAGGA	40985	2.3466704	15.920117	29
GACCG	128185	2.2611868	5.1177864	71
TGGTC	159530	2.2159245	38.145203	72
GCGAC	124380	2.1940663	6.7559857	71
TCTCG	1420725	2.1105423	14.694156	72
GAGCA	338005	2.0697682	9.572741	71
AGTGG	22815	1.9674542	13.037465	72
AGCGC	109480	1.93123	26.288101	72
CGAGG	11495	1.895993	11.70426	40
GAGGT	21975	1.8950168	11.803701	41
CGCCC	343155	1.8649259	7.8270316	46
AGGTG	21165	1.8251663	7.9612236	12
TAGAT	10116565	1.810989	8.029562	72
GTGAG	20400	1.7591964	11.237053	72
GGCGA	10635	1.754144	5.7616444	44
GCCGA	96410	1.7006748	6.0389643	47
GGTGA	19380	1.6712364	30.360949	31

AAGAT	13807315	1.6410997	5.655627	72
AAGCG	265645	1.6266727	7.401827	72
CAGAT	4714305	1.6141505	5.329566	72
TGAGG	17775	1.532829	6.3367167	40
GCGTA	159175	1.4680148	5.192066	71
CCCGG	28275	1.43682	10.8333645	38
GGAGT	16595	1.4310716	8.412937	34
CCGTG	53405	1.4188554	7.555148	72
TCGCC	496535	1.4108391	6.8823757	45
CGGCC	23755	1.2071322	8.068712	46
CCGGA	67770	1.1954645	15.46066	48
CGTGC	41710	1.1081445	6.436221	72
TCCGG	39080	1.0382711	37.973373	38
TTCGG	74625	1.0365659	19.257248	37
ACCGG	55905	0.9861656	5.812959	3
CGTAG	91425	0.8431805	5.195527	72
AGAGA	392155	0.8335961	5.2366776	71
CGTGA	81105	0.74800277	10.142067	72
GCCCC	133735	0.72680235	5.4837427	47
GATCT	1332150	0.6869681	6.387825	72
AAAGG	302740	0.64352834	8.011515	26
CCGGT	20900	0.5552678	7.9623227	49
AACGG	88625	0.54269373	6.0465646	2
GTGCC	17490	0.4646715	16.308176	45
TGCCG	14240	0.378326	11.526808	46
CGGAT	34255	0.31592178	7.9369807	49
TCTGG	15845	0.22009228	5.2122135	38
GGATC	23505	0.21677832	5.544605	50

Produced by FastQC (version 0.10.1)