Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 01:11:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819121.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR1819121 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819121.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 01:11:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819121.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,384,388
Mapped reads	1,263,100 / 91.24%
Unmapped reads	121,288 / 8.76%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,616 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	55,212 / 3.99%
Duplication rate	3.33%
Clipped reads	1,264,903 / 91.37%

2.2. ACGT Content

Number/percentage of A's	18,596,648 / 25.32%
Number/percentage of C's	14,406,846 / 19.61%
Number/percentage of T's	22,972,674 / 31.27%
Number/percentage of G's	17,479,372 / 23.8%
Number/percentage of N's	1,004 / 0%
GC Percentage	43.41%

2.3. Coverage

Mean	0.0237

Standard Deviation	0.2379

2.4. Mapping Quality

Mean Mapping Quality	44.74

2.5. Mismatches and indels

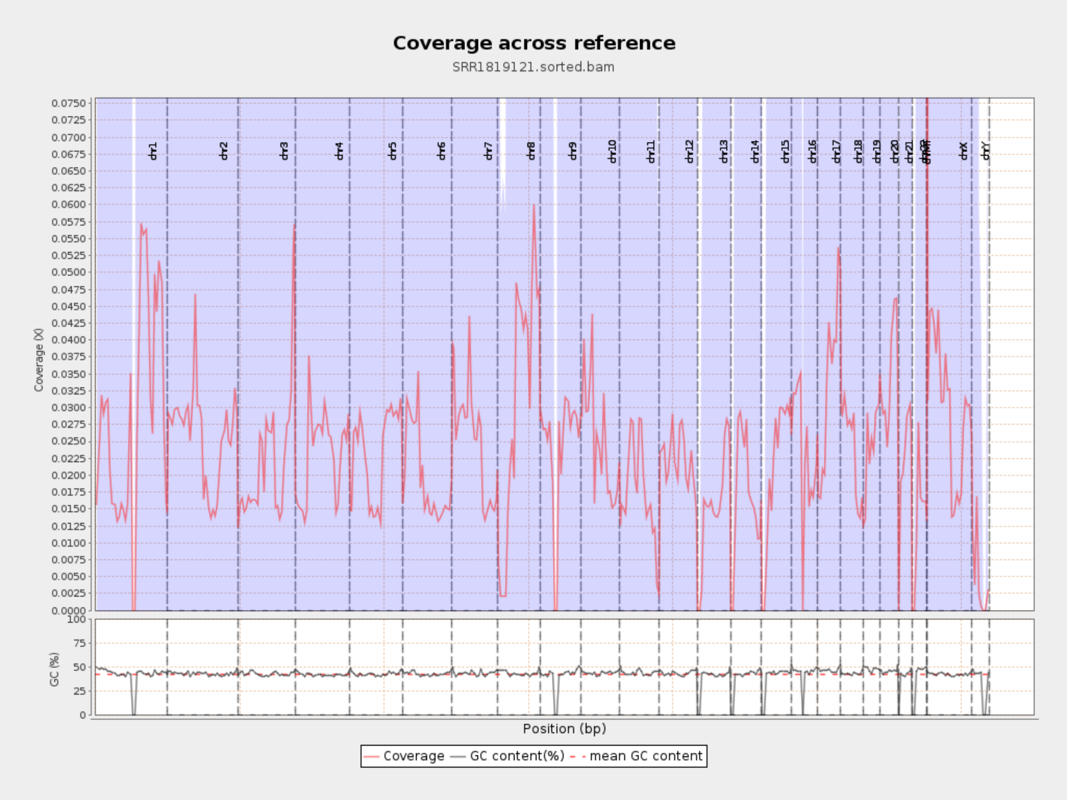
General error rate	0.52%
Mismatches	375,253
Insertions	4,834
Mapped reads with at least one insertion	0.38%
Deletions	13,618
Mapped reads with at least one deletion	1.07%
Homopolymer indels	43.74%

2.6. Chromosome stats

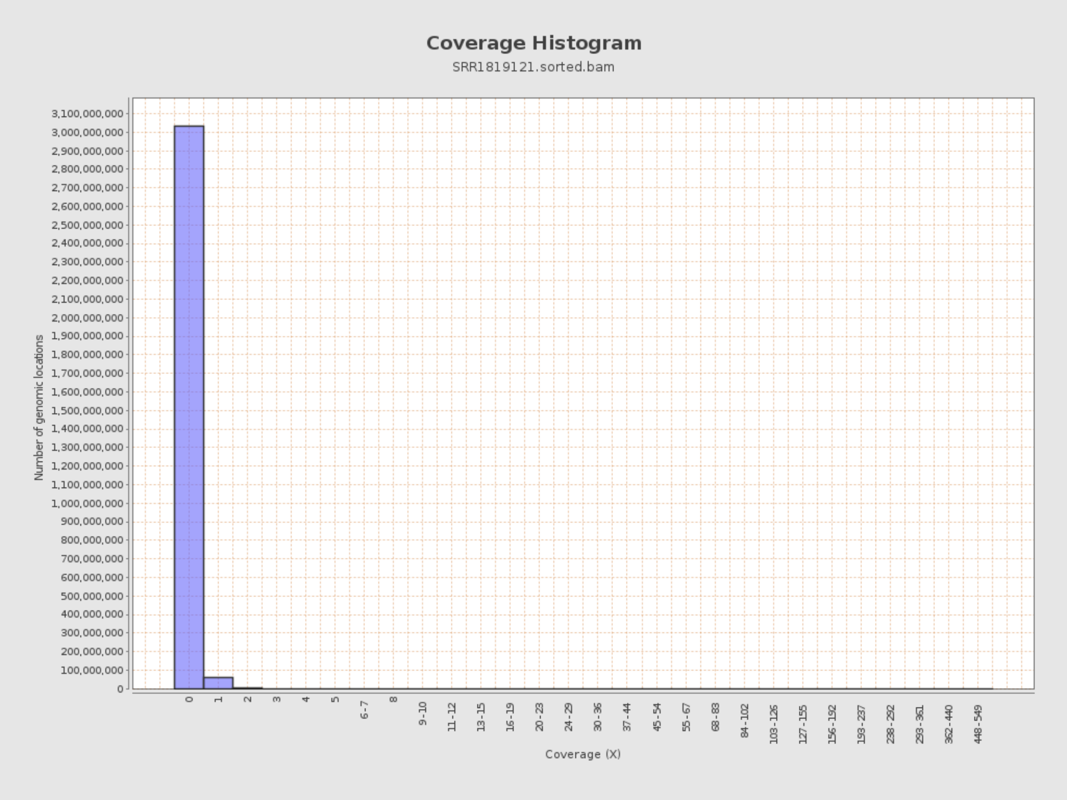
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7095229	0.0285	0.4115
chr2	243199373	6321754	0.026	0.2871
chr3	198022430	4345747	0.0219	0.1625
chr4	191154276	4462256	0.0233	0.1888
chr5	180915260	4254412	0.0235	0.1684
chr6	171115067	3383015	0.0198	0.1859
chr7	159138663	4027403	0.0253	0.3025

chr8	146364022	4540950	0.031	0.2464
chr9	141213431	3396872	0.0241	0.2194
chr10	135534747	3429281	0.0253	0.2372
chr11	135006516	2412168	0.0179	0.2133
chr12	133851895	3004595	0.0224	0.1664
chr13	115169878	1780704	0.0155	0.1366
chr14	107349540	1815058	0.0169	0.1466
chr15	102531392	2140627	0.0209	0.1594
chr16	90354753	2096820	0.0232	0.1778
chr17	81195210	2692044	0.0332	0.2074
chr18	78077248	1867230	0.0239	0.3585
chr19	59128983	1451390	0.0245	0.3071
chr20	63025520	2197729	0.0349	0.2059
chr21	48129895	1079829	0.0224	0.1803
chr22	51304566	693173	0.0135	0.1275
chrMT	16571	12094	0.7298	0.9377
chrX	155270560	4708024	0.0303	0.2072
chrY	59373566	270757	0.0046	0.1488

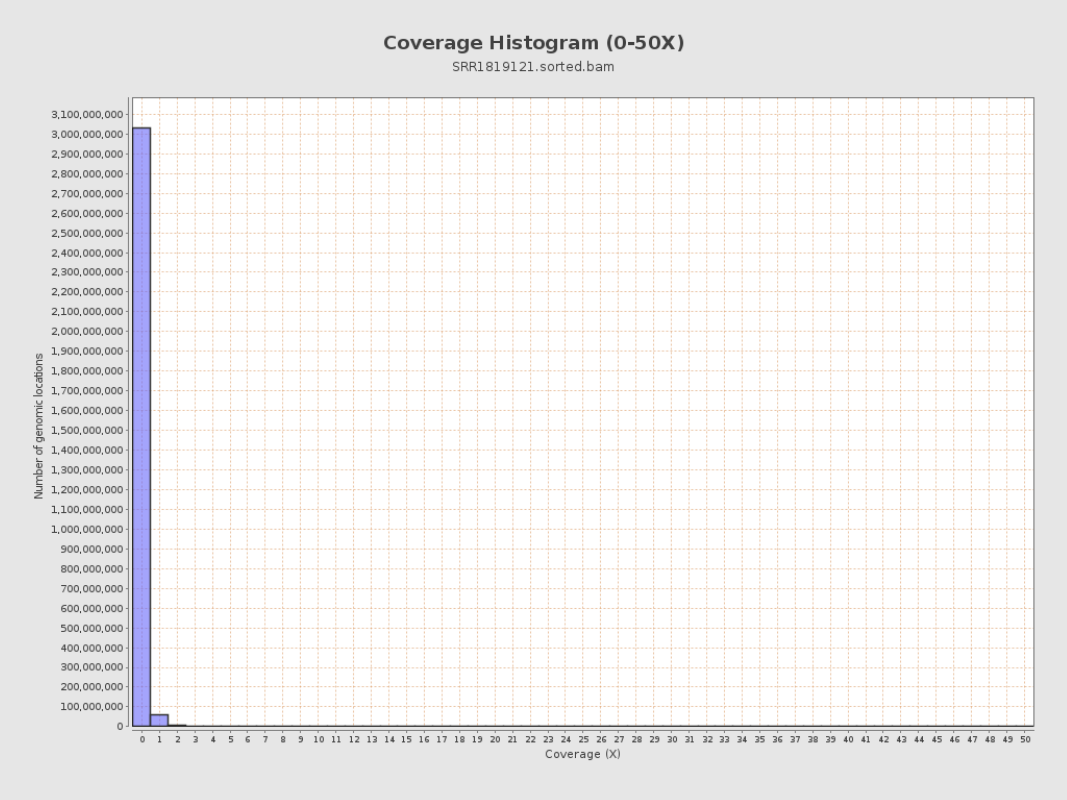
3. Results : Coverage across reference



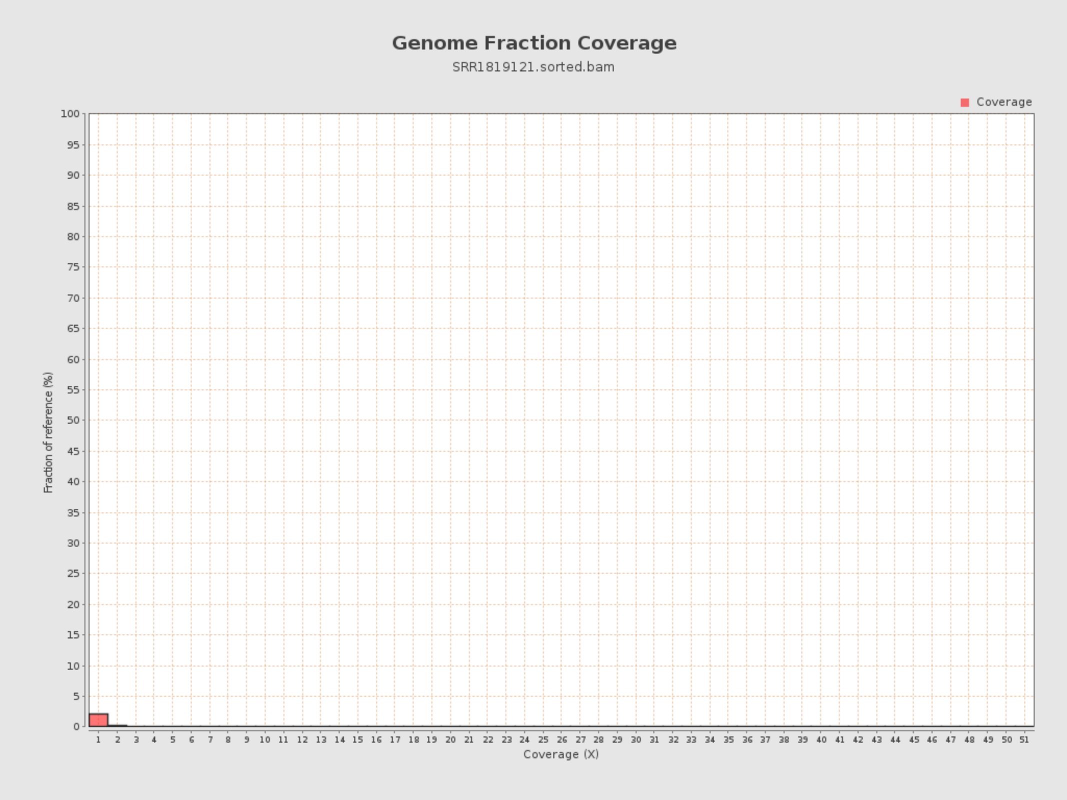
4. Results : Coverage Histogram



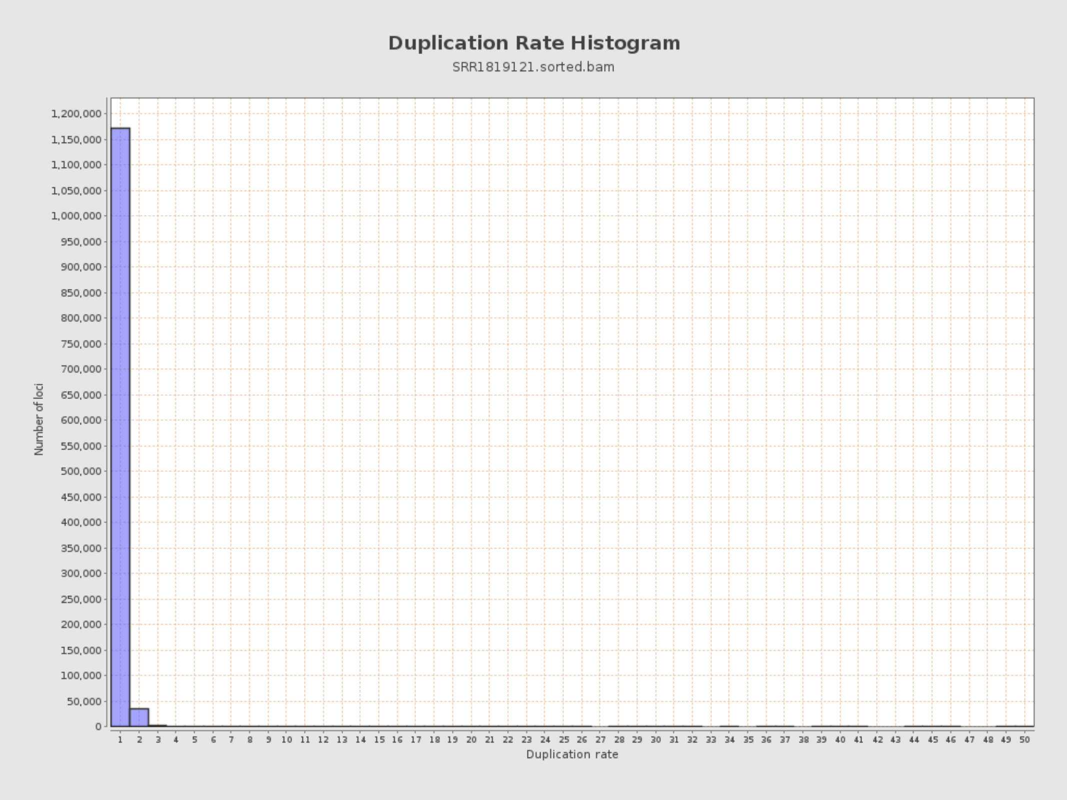
5. Results : Coverage Histogram (0-50X)



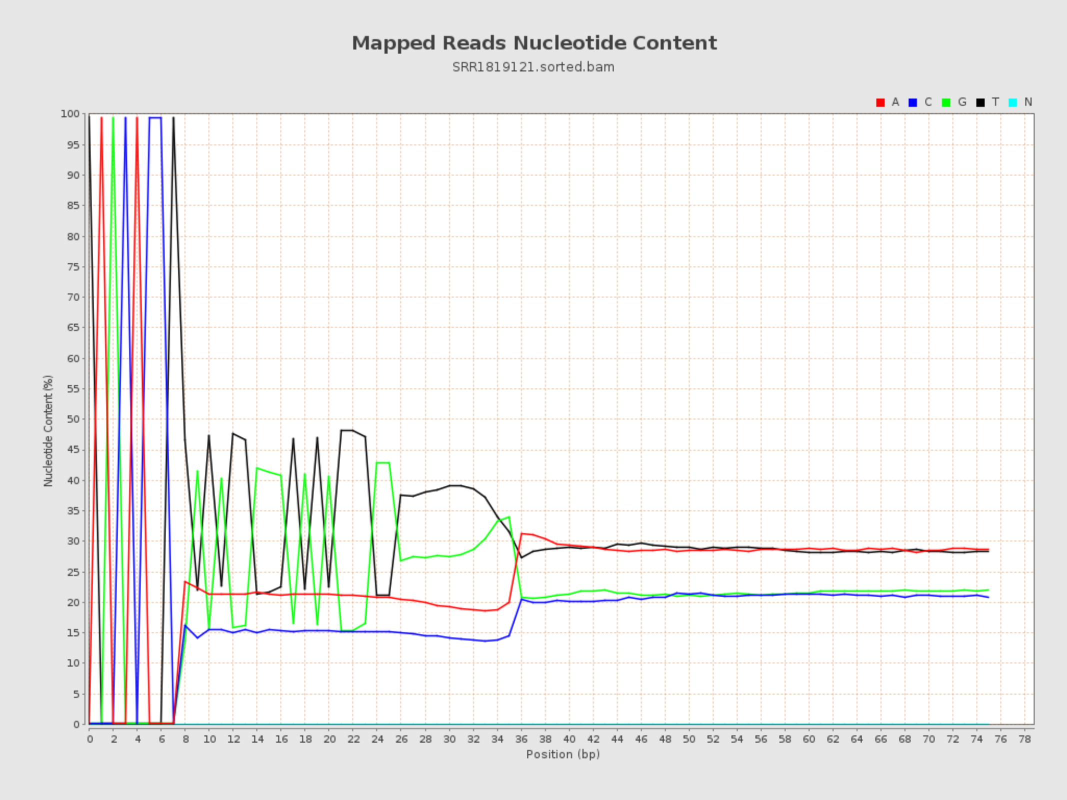
6. Results : Genome Fraction Coverage



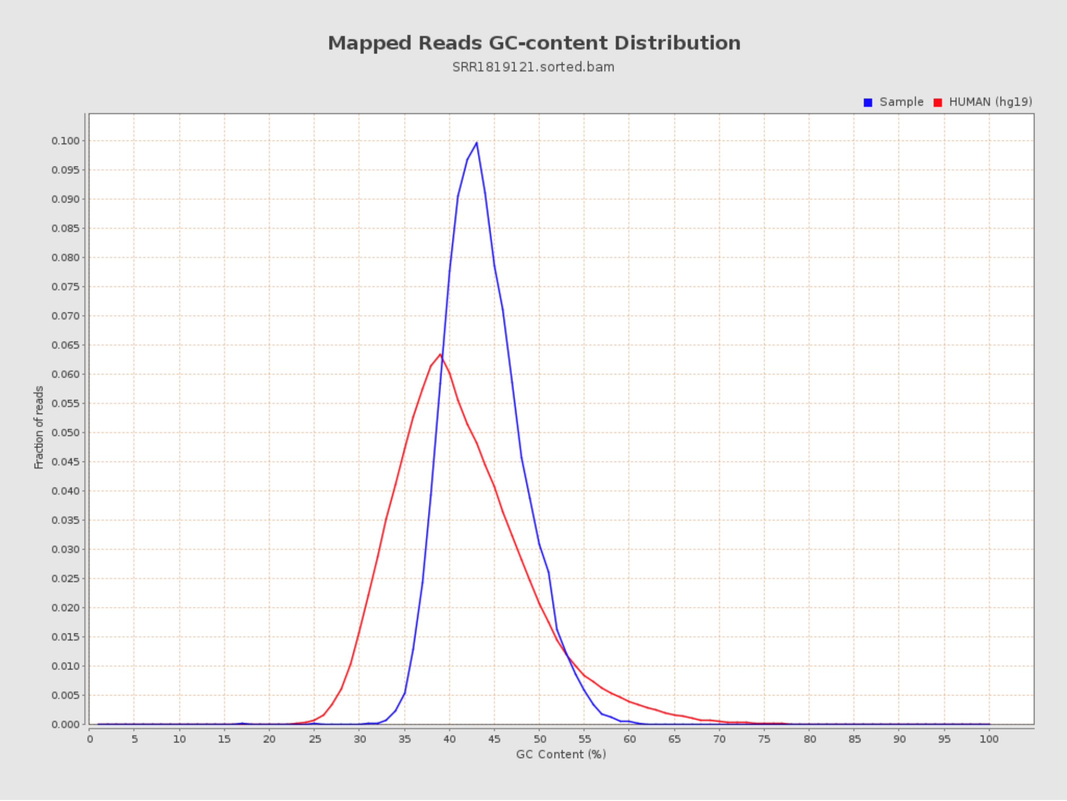
7. Results : Duplication Rate Histogram



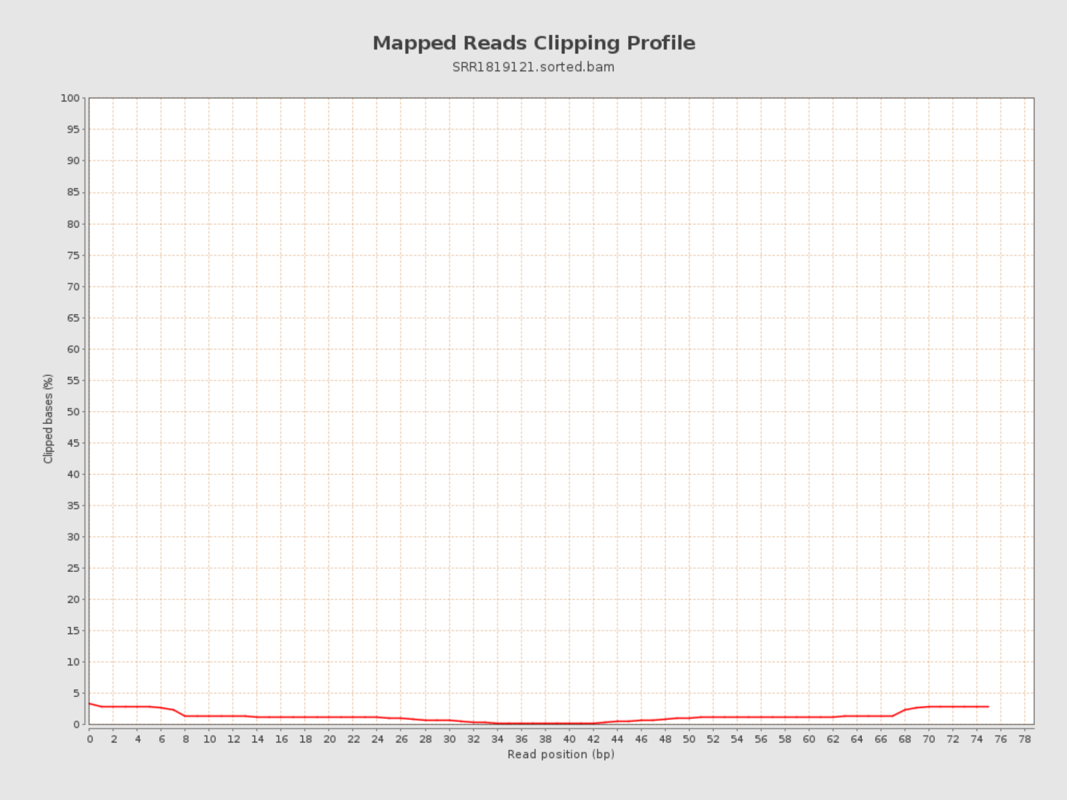
8. Results : Mapped Reads Nucleotide Content



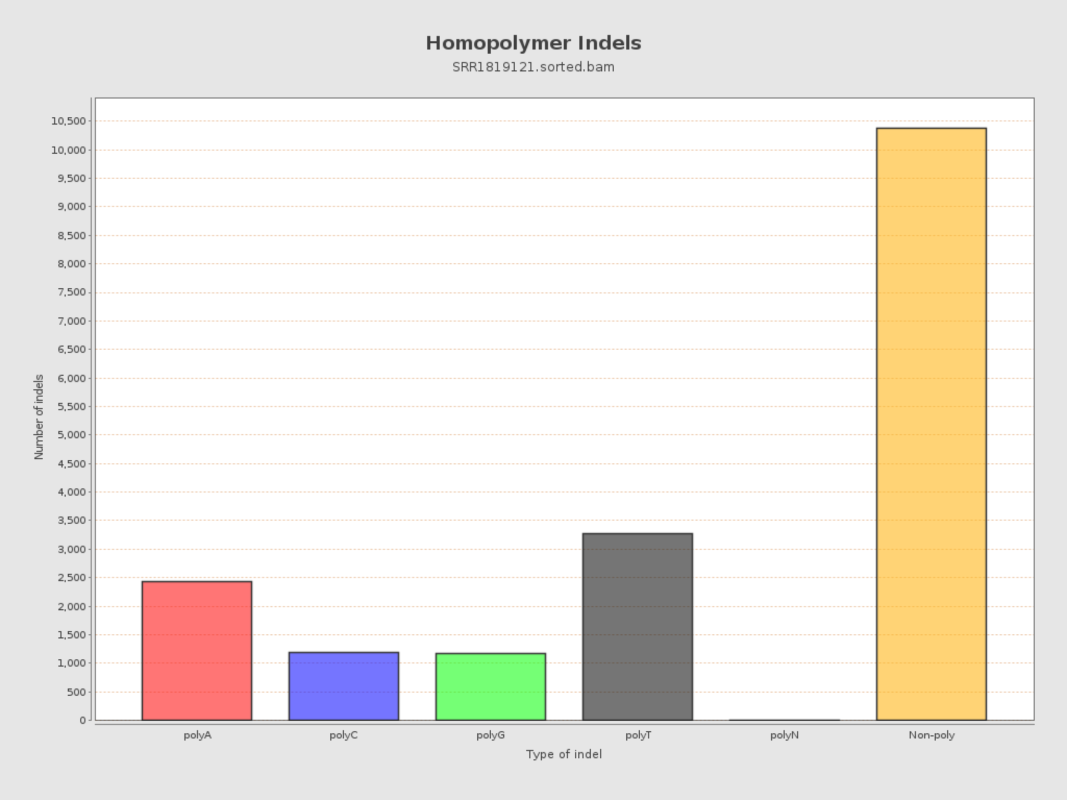
9. Results : Mapped Reads GC-content Distribution



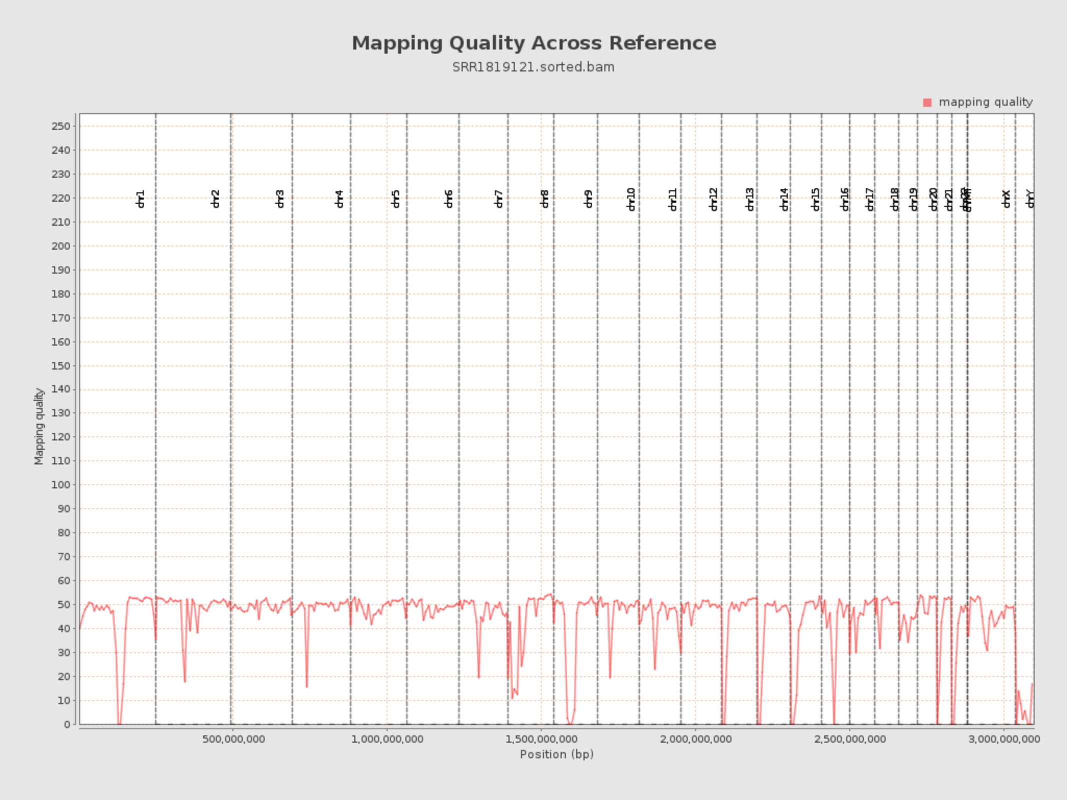
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram