Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 17:08:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234118.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_SRR6234118 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234118.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 17:08:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234118.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	633,067
Mapped reads	416,931 / 65.86%
Unmapped reads	216,136 / 34.14%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,522 / 0.24%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	6,575 / 1.04%
Duplication rate	1.31%
Clipped reads	190,223 / 30.05%

2.2. ACGT Content

Number/percentage of A's	7,842,195 / 28.62%
Number/percentage of C's	4,548,049 / 16.6%
Number/percentage of T's	8,864,289 / 32.35%
Number/percentage of G's	6,141,889 / 22.41%
Number/percentage of N's	4,593 / 0.02%
GC Percentage	39.01%

2.3. Coverage

Mean	0.0089

Standard Deviation	0.1072

2.4. Mapping Quality

Mean Mapping Quality	45.38

2.5. Mismatches and indels

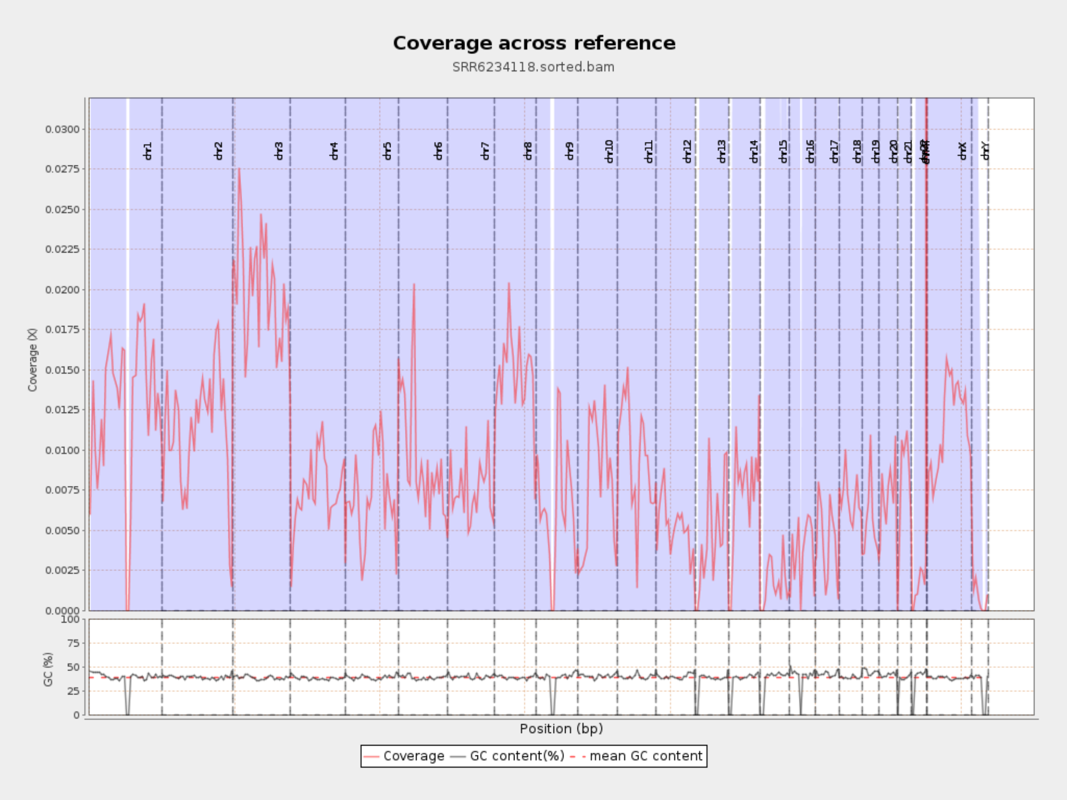
General error rate	0.95%
Mismatches	256,299
Insertions	2,097
Mapped reads with at least one insertion	0.5%
Deletions	7,742
Mapped reads with at least one deletion	1.83%
Homopolymer indels	46.68%

2.6. Chromosome stats

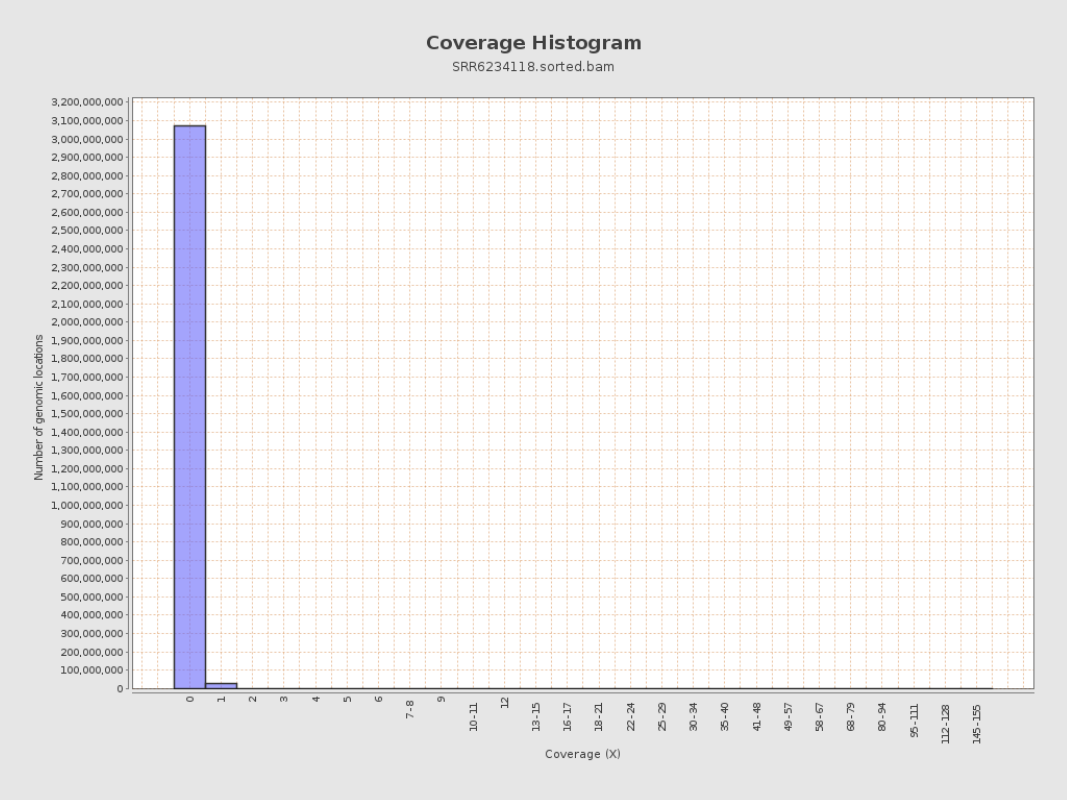
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3178170	0.0128	0.1477
chr2	243199373	2753196	0.0113	0.1229
chr3	198022430	3988113	0.0201	0.1483
chr4	191154276	1434444	0.0075	0.0898
chr5	180915260	1292133	0.0071	0.087
chr6	171115067	1648267	0.0096	0.1107
chr7	159138663	1203818	0.0076	0.1156

chr8	146364022	2161995	0.0148	0.158
chr9	141213431	913244	0.0065	0.0851
chr10	135534747	1064278	0.0079	0.099
chr11	135006516	1304424	0.0097	0.1036
chr12	133851895	692496	0.0052	0.0742
chr13	115169878	543048	0.0047	0.0709
chr14	107349540	756315	0.007	0.0876
chr15	102531392	180607	0.0018	0.0441
chr16	90354753	335878	0.0037	0.0634
chr17	81195210	337943	0.0042	0.0667
chr18	78077248	550296	0.007	0.1102
chr19	59128983	331245	0.0056	0.0849
chr20	63025520	457973	0.0073	0.0883
chr21	48129895	378242	0.0079	0.0921
chr22	51304566	73101	0.0014	0.0387
chrMT	16571	8084	0.4878	0.892
chrX	155270560	1772067	0.0114	0.1124
chrY	59373566	54974	0.0009	0.0327

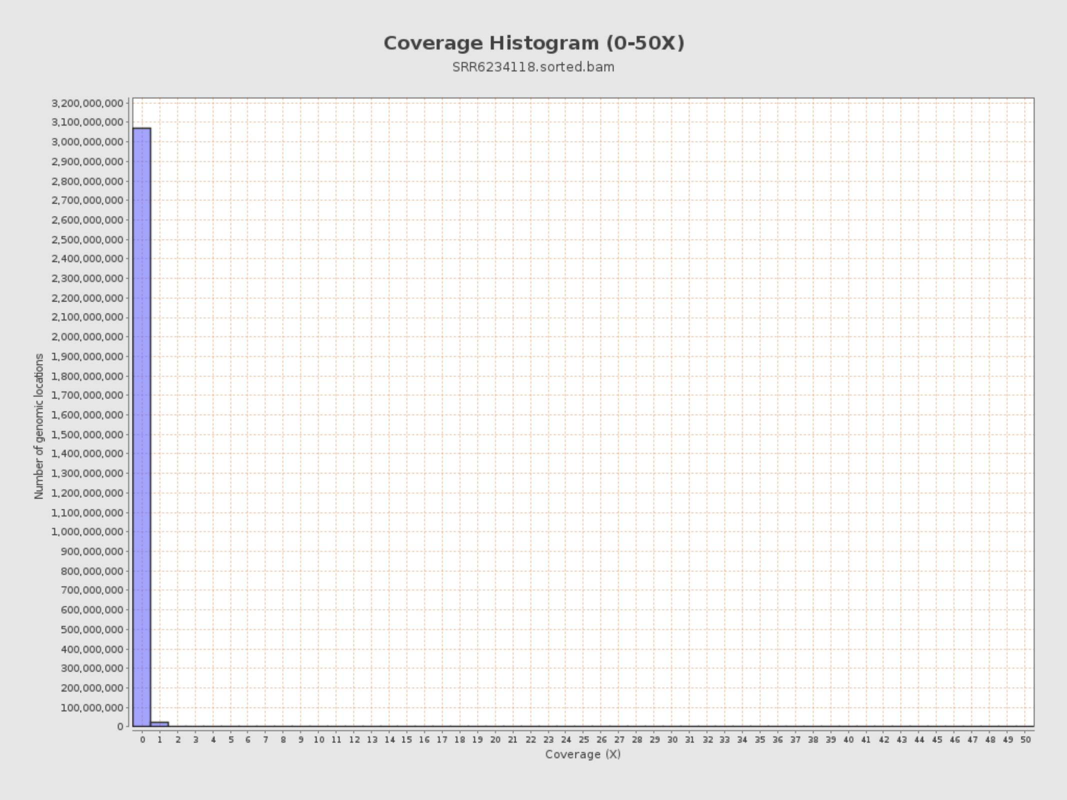
3. Results : Coverage across reference



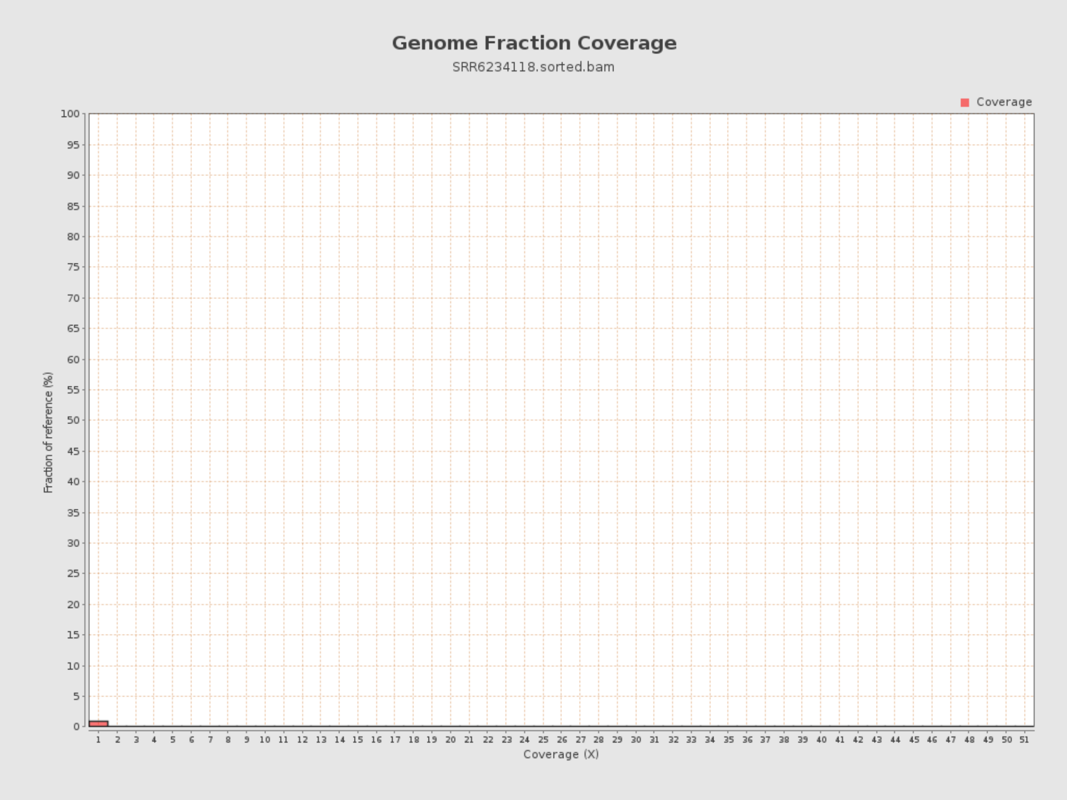
4. Results : Coverage Histogram



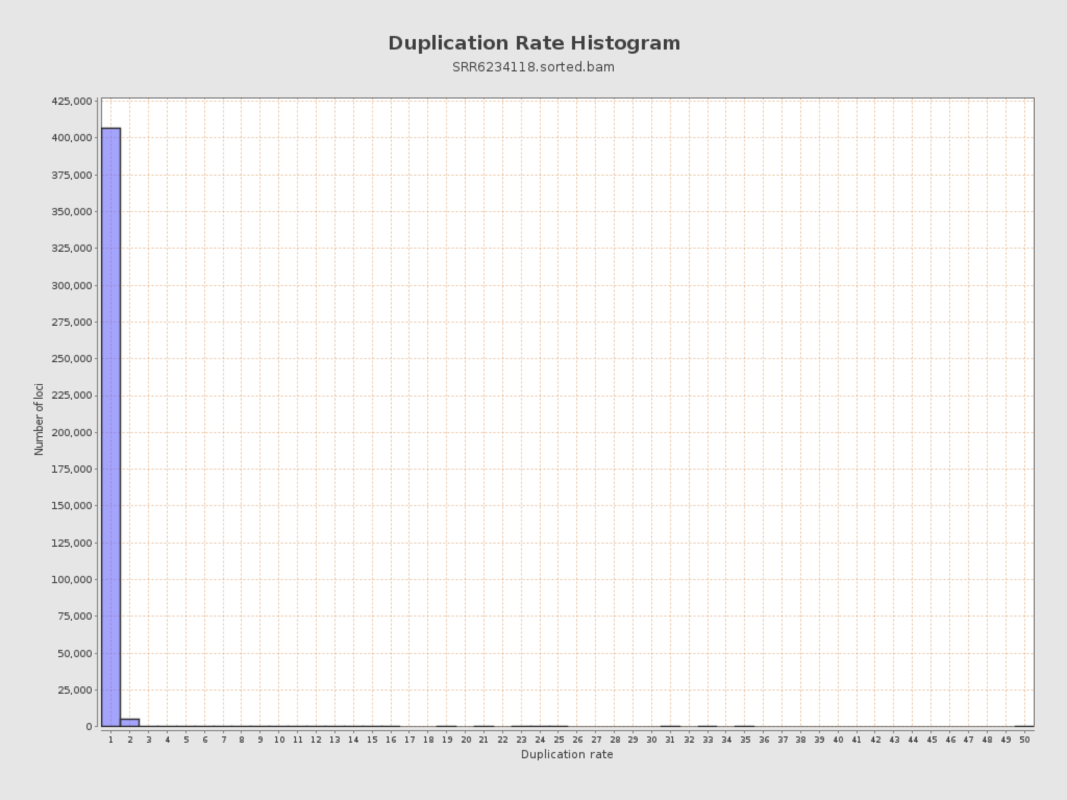
5. Results : Coverage Histogram (0-50X)



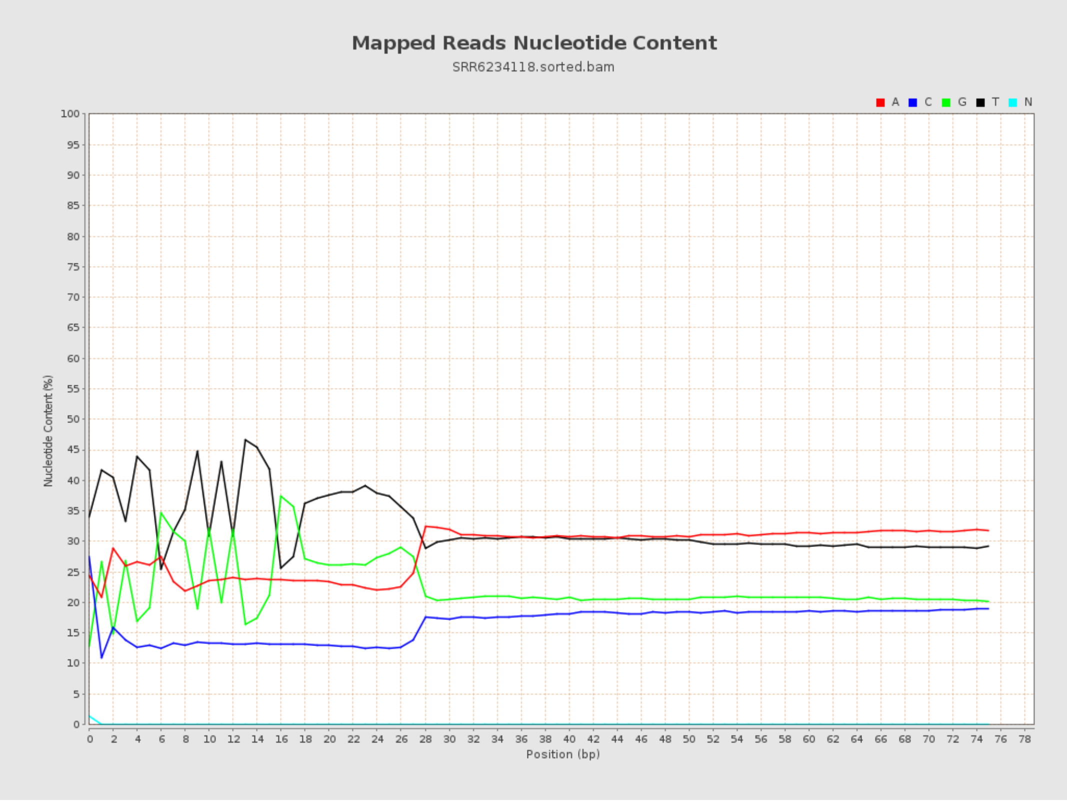
6. Results : Genome Fraction Coverage



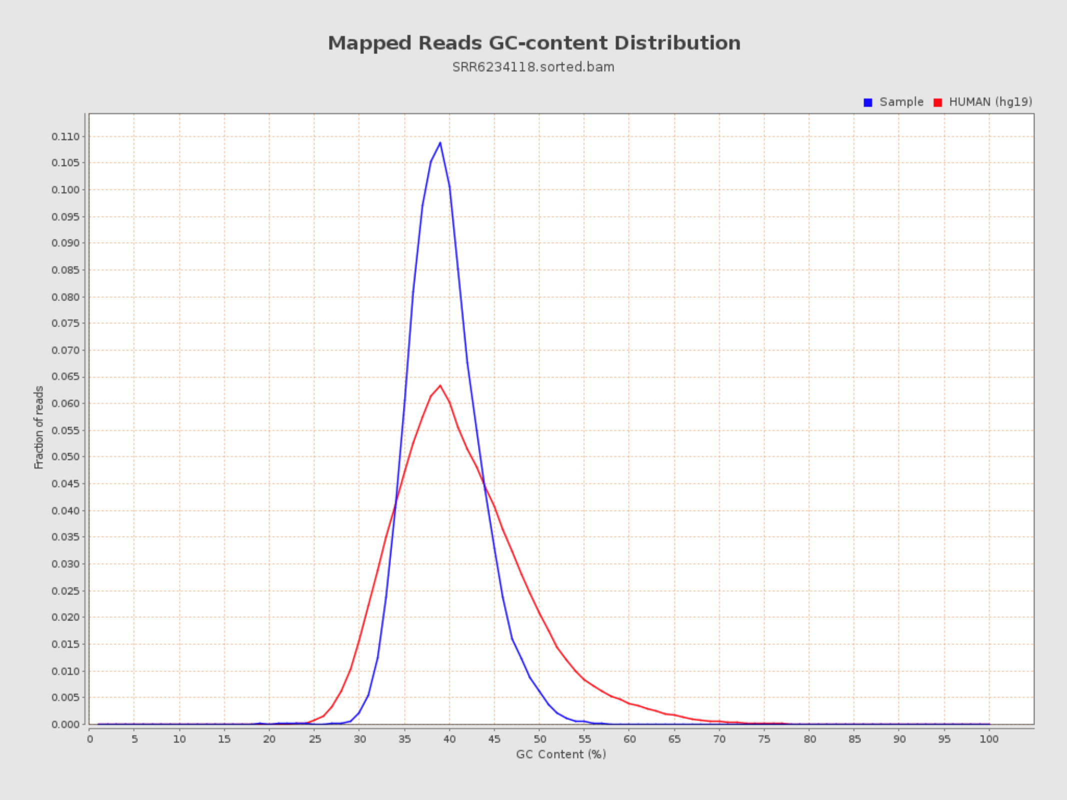
7. Results : Duplication Rate Histogram



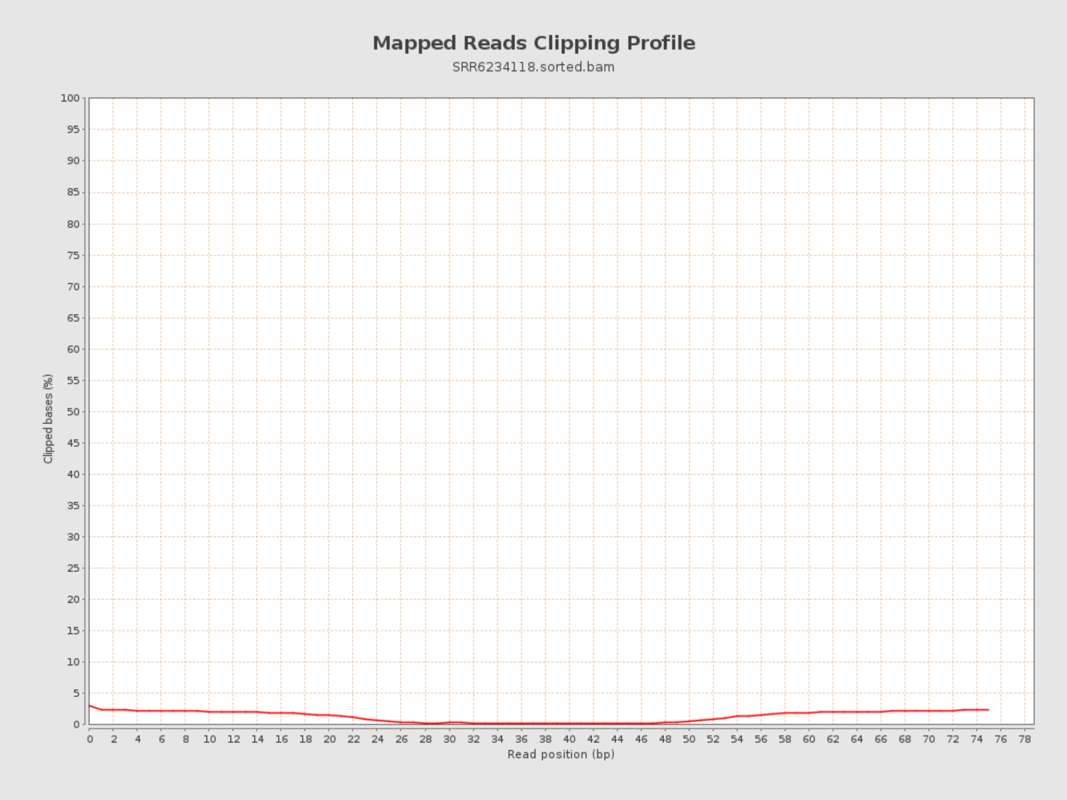
8. Results : Mapped Reads Nucleotide Content



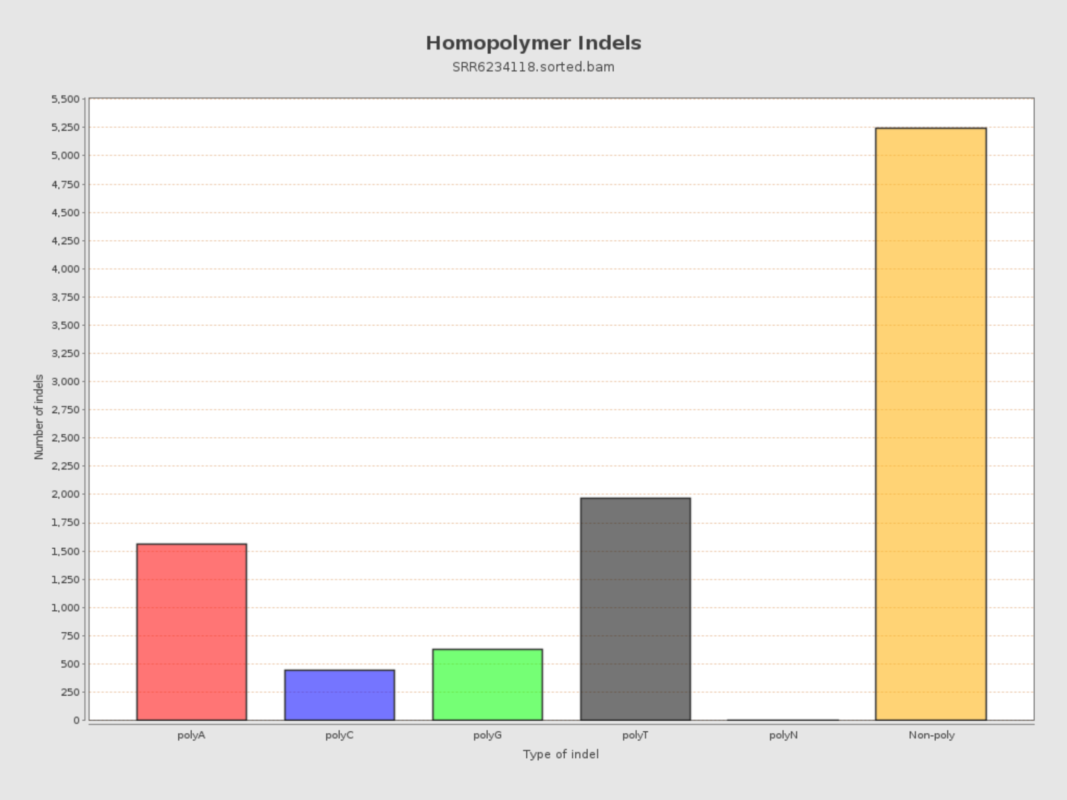
9. Results : Mapped Reads GC-content Distribution



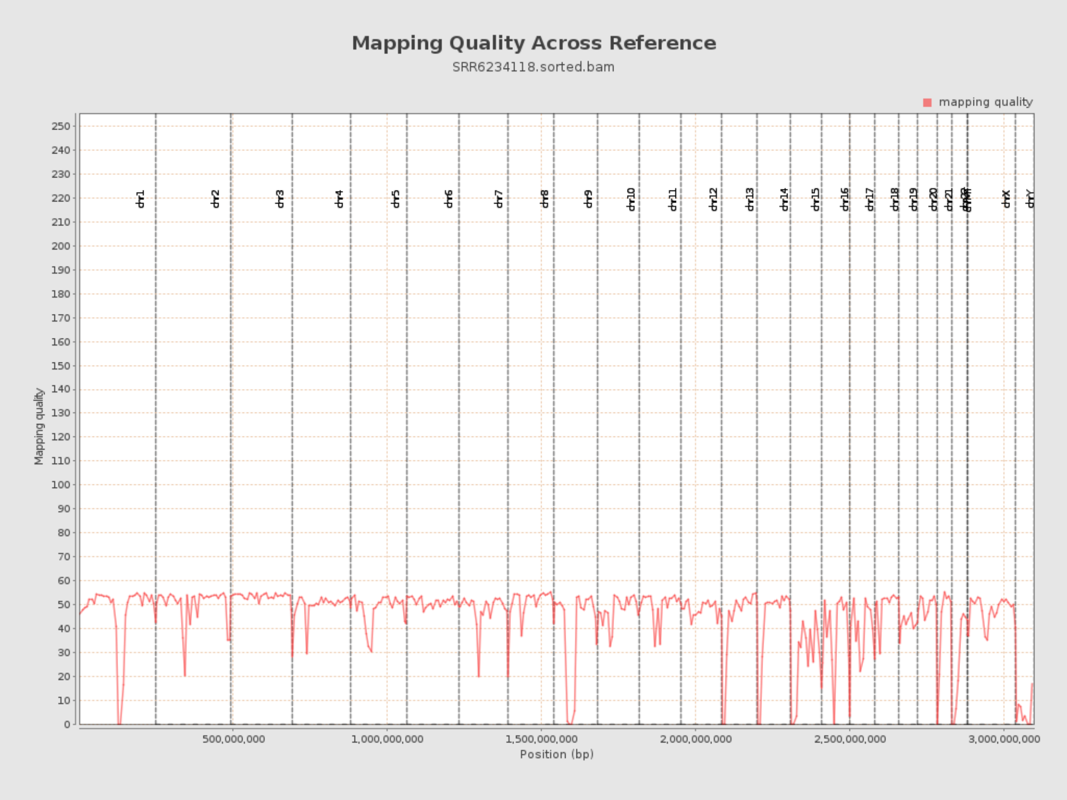
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram