Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 10:14:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472843.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_SRR3472843 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472843.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 10:14:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472843.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,055,687
Mapped reads	1,686,166 / 82.02%
Unmapped reads	369,521 / 17.98%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,051 / 0.54%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	45,297 / 2.2%
Duplication rate	2.19%
Clipped reads	909,319 / 44.23%

2.2. ACGT Content

Number/percentage of A's	29,208,942 / 27%
Number/percentage of C's	21,442,565 / 19.82%
Number/percentage of T's	32,168,789 / 29.74%
Number/percentage of G's	25,342,802 / 23.43%
Number/percentage of N's	2,212 / 0%
GC Percentage	43.25%

2.3. Coverage

Mean	0.035

Standard Deviation	0.2482

2.4. Mapping Quality

Mean Mapping Quality	44.11

2.5. Mismatches and indels

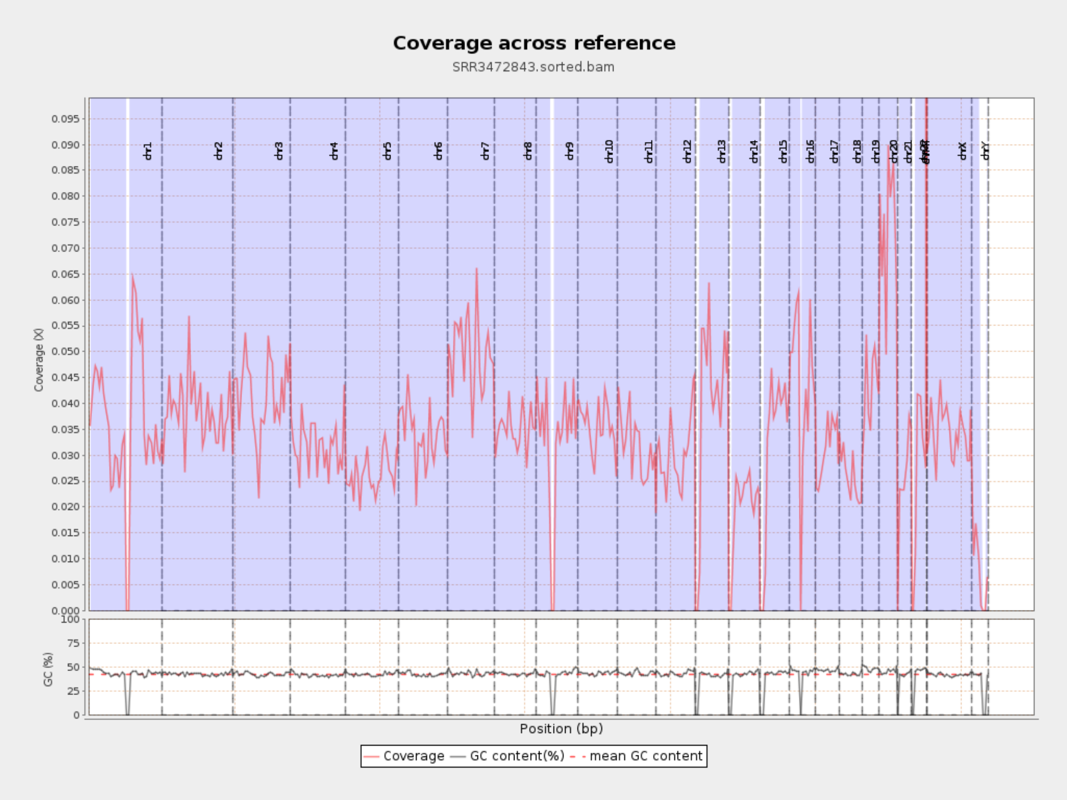
General error rate	0.81%
Mismatches	856,721
Insertions	8,213
Mapped reads with at least one insertion	0.48%
Deletions	24,670
Mapped reads with at least one deletion	1.45%
Homopolymer indels	46.39%

2.6. Chromosome stats

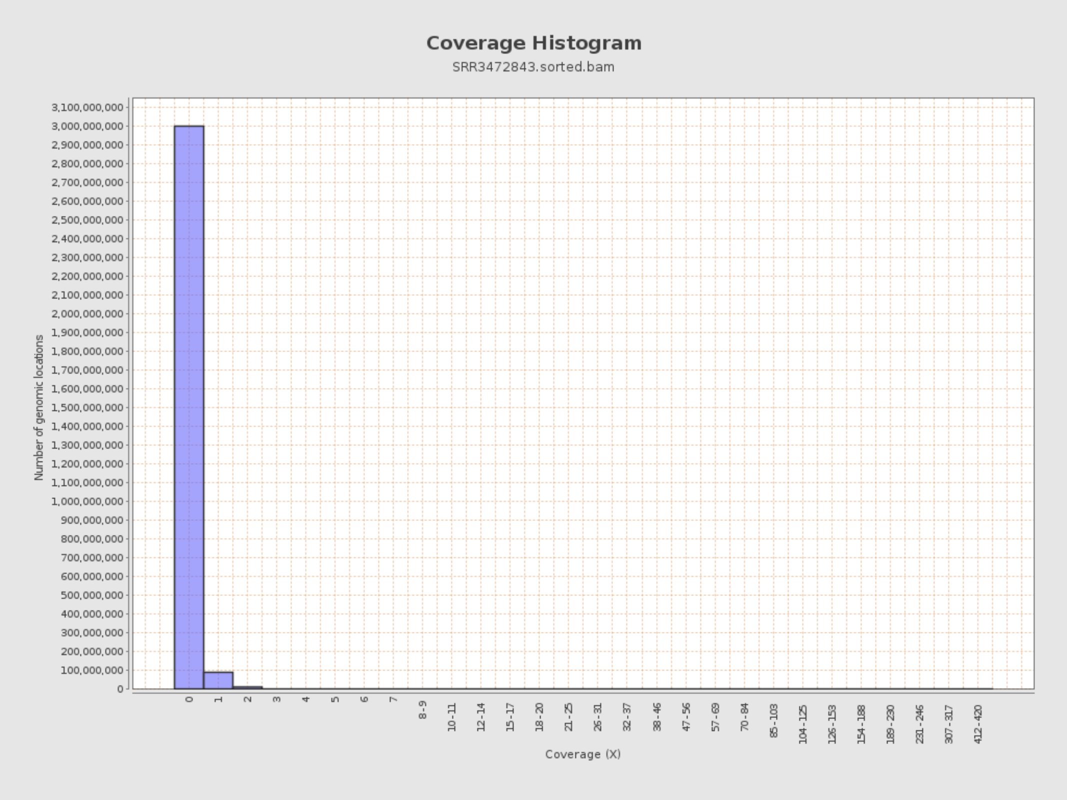
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8985570	0.0361	0.2681
chr2	243199373	9375620	0.0386	0.3381
chr3	198022430	8181949	0.0413	0.2245
chr4	191154276	6082050	0.0318	0.2022
chr5	180915260	4781286	0.0264	0.1796
chr6	171115067	5861613	0.0343	0.2175
chr7	159138663	7913931	0.0497	0.3383

chr8	146364022	5118498	0.035	0.241
chr9	141213431	4535784	0.0321	0.2527
chr10	135534747	4821524	0.0356	0.2316
chr11	135006516	4313233	0.0319	0.2442
chr12	133851895	4078669	0.0305	0.1927
chr13	115169878	4554947	0.0395	0.228
chr14	107349540	2083603	0.0194	0.1635
chr15	102531392	3271190	0.0319	0.207
chr16	90354753	3995444	0.0442	0.2506
chr17	81195210	2546756	0.0314	0.2037
chr18	78077248	2024277	0.0259	0.355
chr19	59128983	2534874	0.0429	0.2574
chr20	63025520	4659364	0.0739	0.3093
chr21	48129895	1230712	0.0256	0.1906
chr22	51304566	1271542	0.0248	0.18
chrMT	16571	196765	11.8741	8.0558
chrX	155270560	5343403	0.0344	0.2174
chrY	59373566	446668	0.0075	0.1068

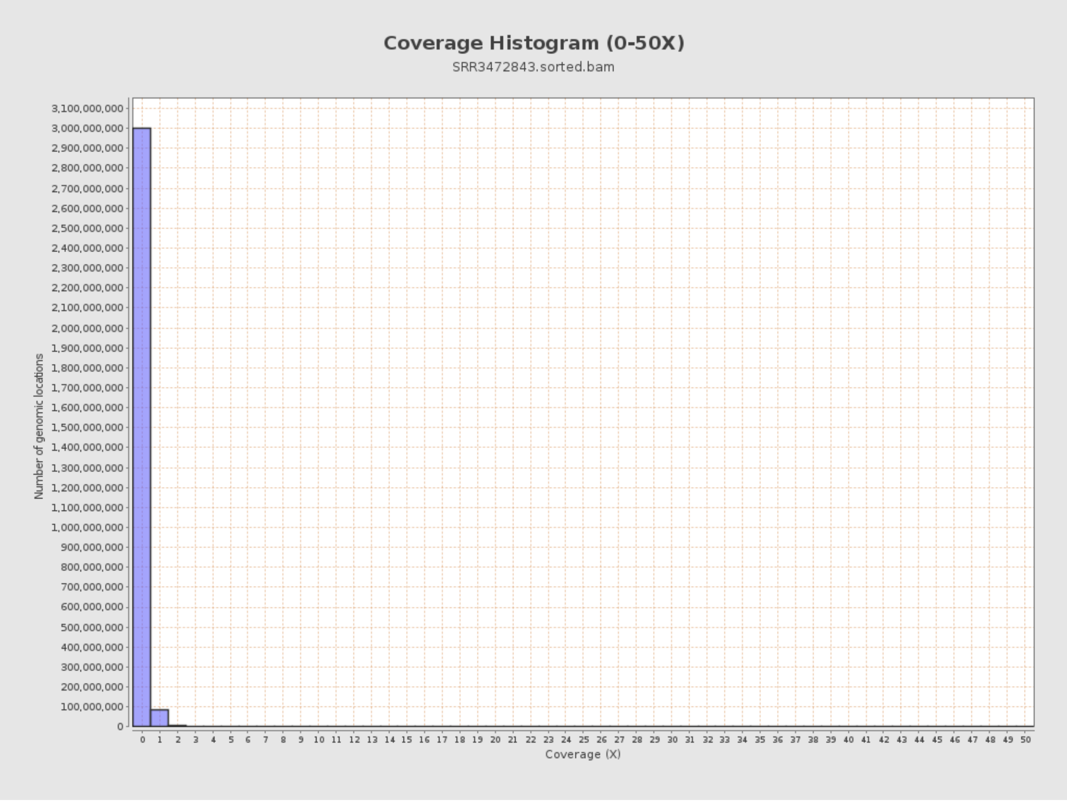
3. Results : Coverage across reference



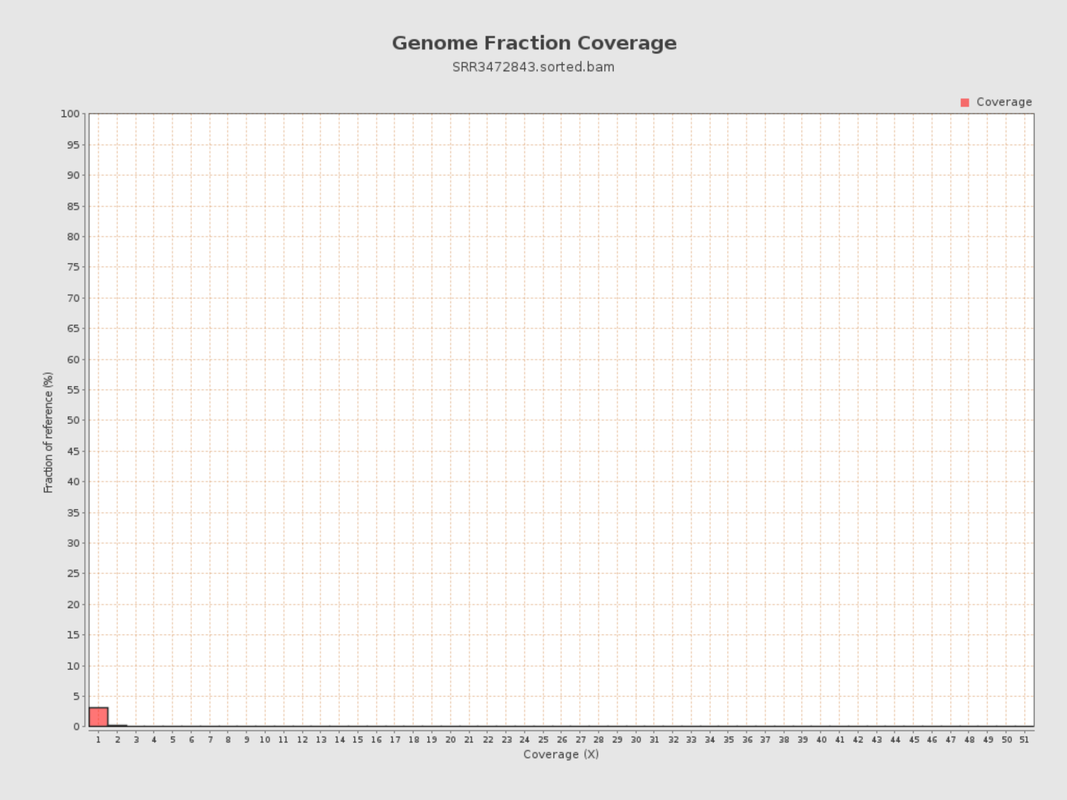
4. Results : Coverage Histogram



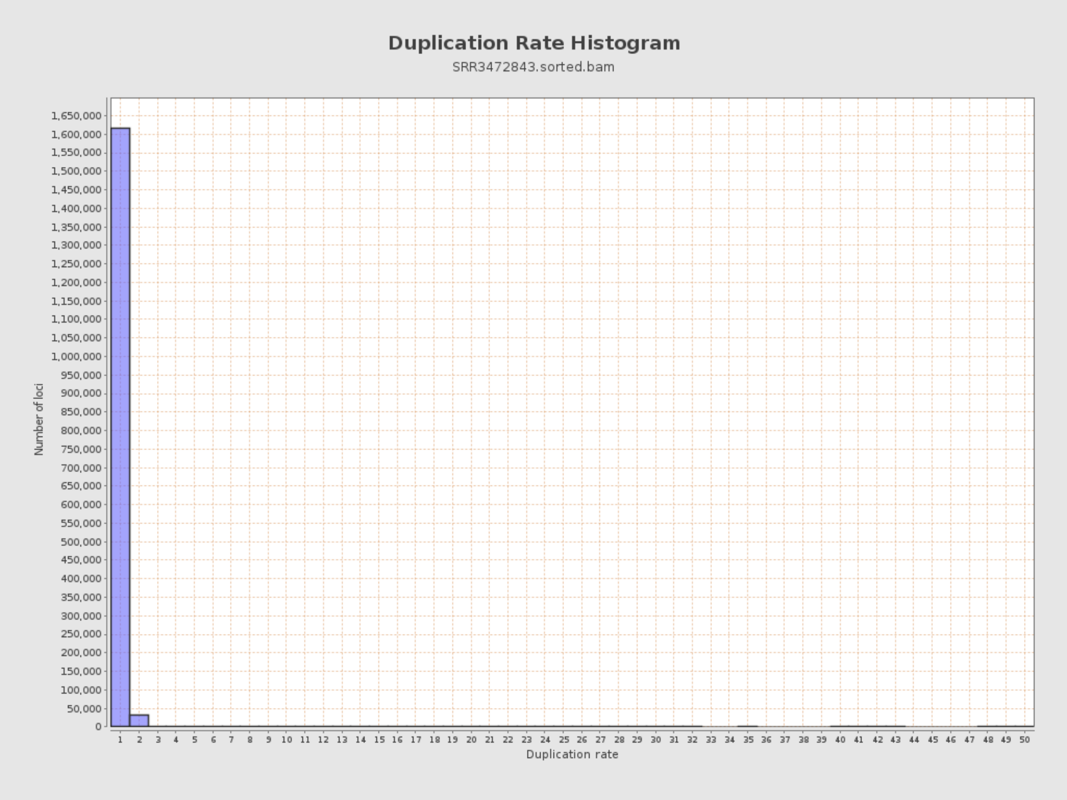
5. Results : Coverage Histogram (0-50X)



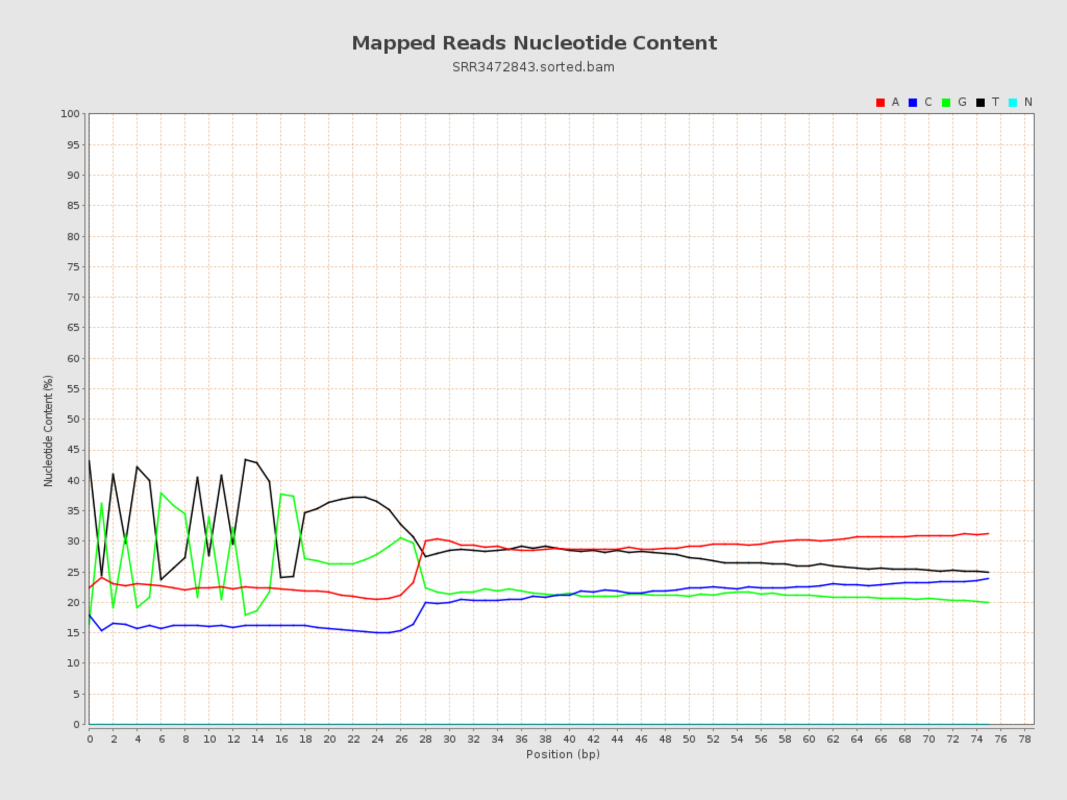
6. Results : Genome Fraction Coverage



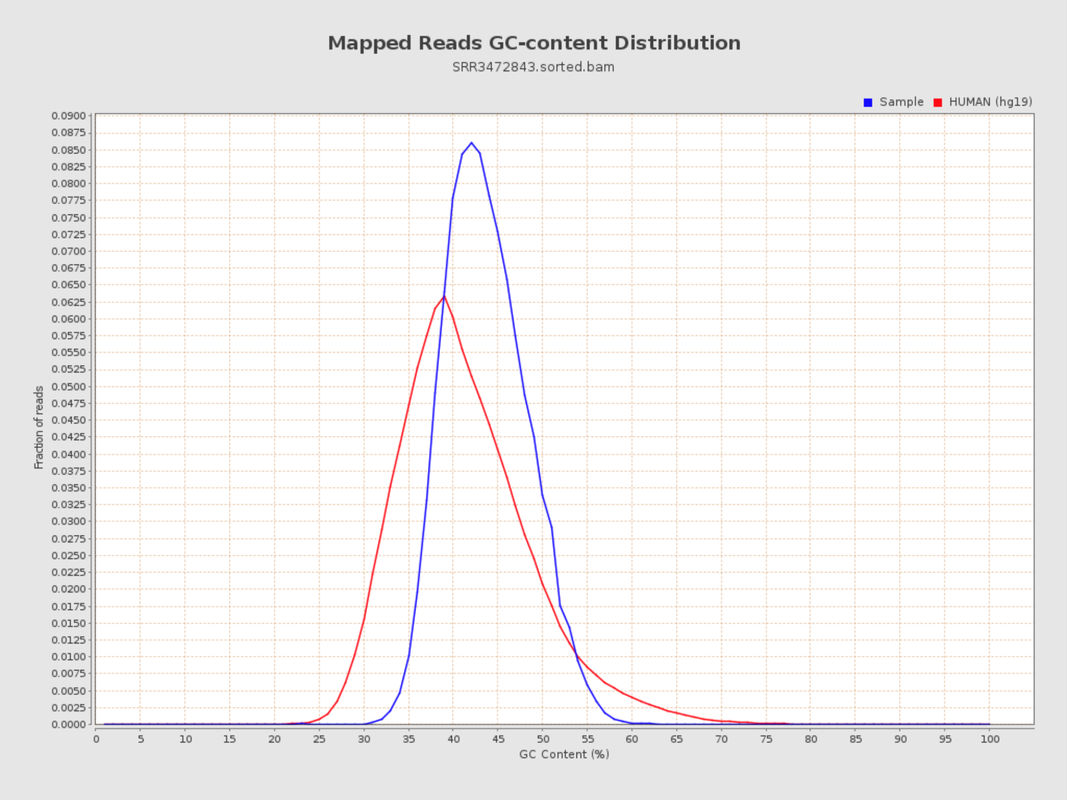
7. Results : Duplication Rate Histogram



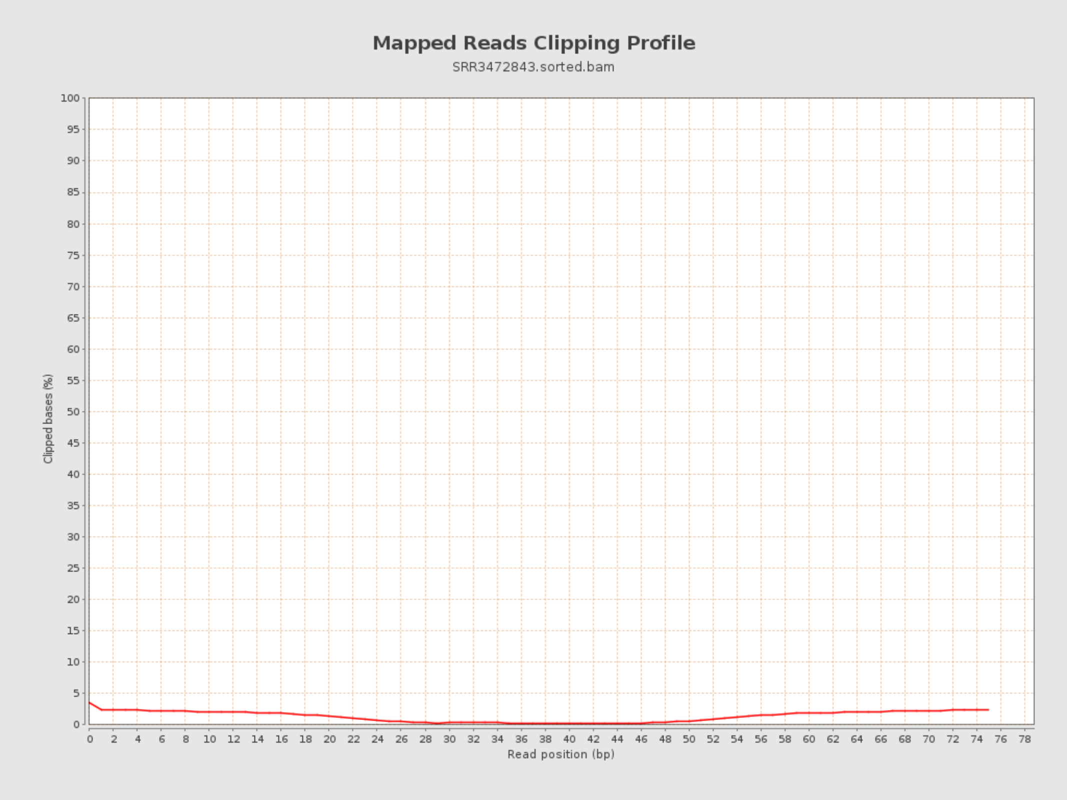
8. Results : Mapped Reads Nucleotide Content



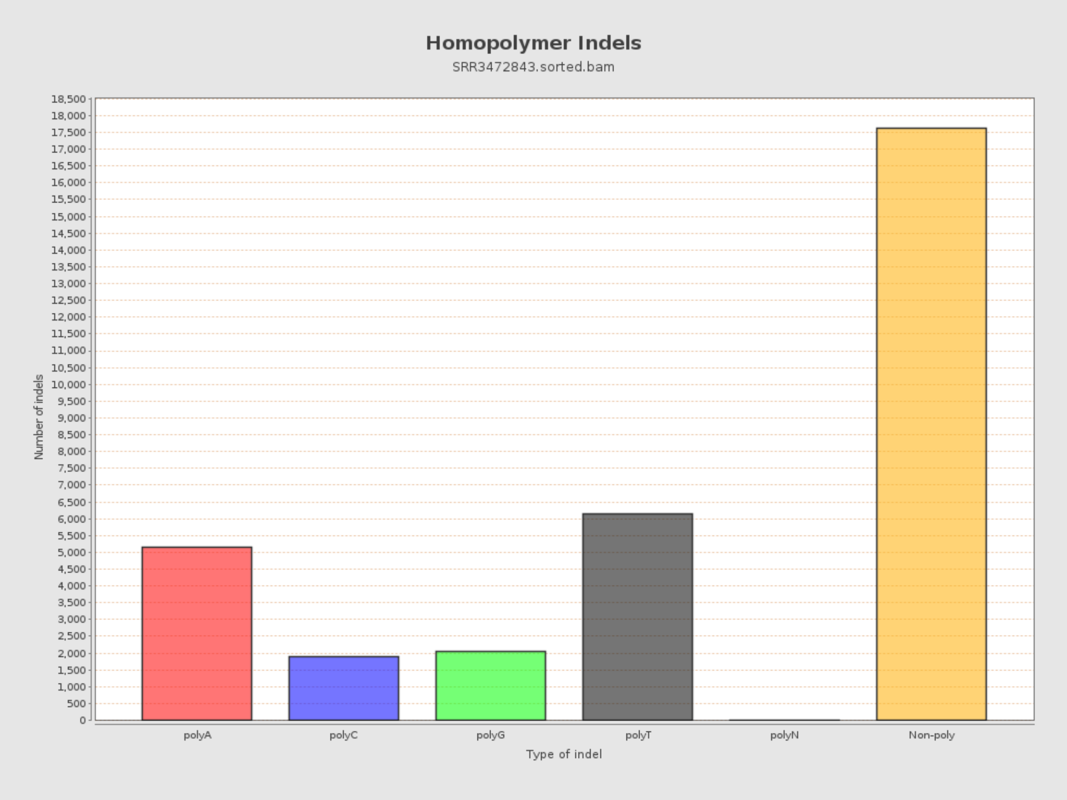
9. Results : Mapped Reads GC-content Distribution



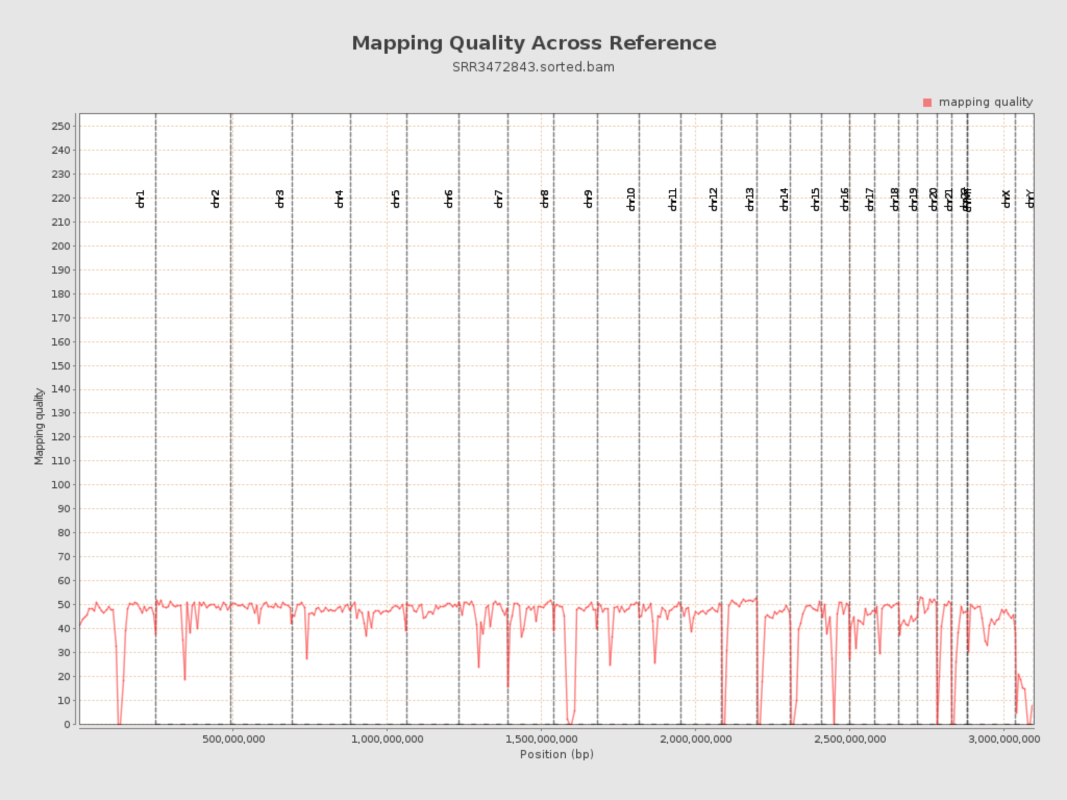
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram