Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/01 08:26:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472821.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_SRR3472821 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472821.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 01 08:26:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472821.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,084,914
Mapped reads	1,193,967 / 57.27%
Unmapped reads	890,947 / 42.73%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,826 / 0.42%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	119,331 / 5.72%
Duplication rate	7.14%
Clipped reads	806,857 / 38.7%

2.2. ACGT Content

Number/percentage of A's	19,917,477 / 27.47%
Number/percentage of C's	13,862,024 / 19.12%
Number/percentage of T's	21,690,464 / 29.92%
Number/percentage of G's	17,029,006 / 23.49%
Number/percentage of N's	1,270 / 0%
GC Percentage	42.61%

2.3. Coverage

Mean	0.0234

Standard Deviation	0.2713

2.4. Mapping Quality

Mean Mapping Quality	41.91

2.5. Mismatches and indels

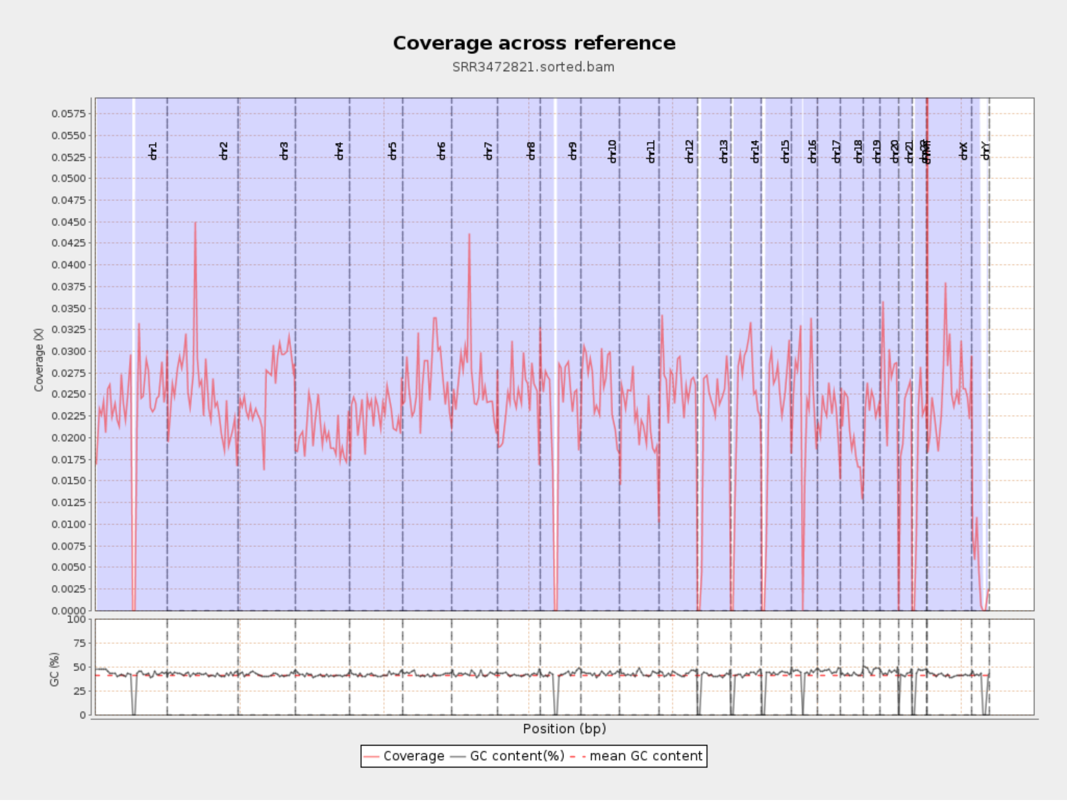
General error rate	0.98%
Mismatches	698,289
Insertions	5,621
Mapped reads with at least one insertion	0.47%
Deletions	22,567
Mapped reads with at least one deletion	1.87%
Homopolymer indels	47.68%

2.6. Chromosome stats

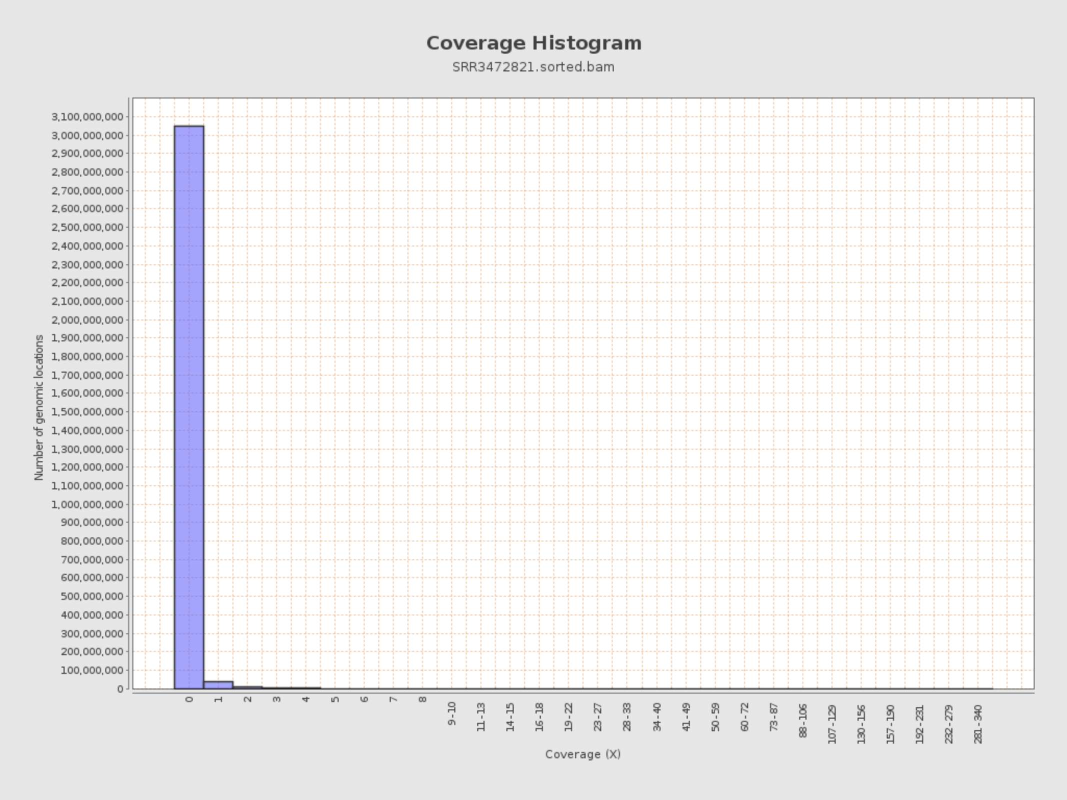
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5743730	0.023	0.3059
chr2	243199373	6112371	0.0251	0.3027
chr3	198022430	5119084	0.0259	0.2378
chr4	191154276	3882842	0.0203	0.2258
chr5	180915260	4144286	0.0229	0.2313
chr6	171115067	4586683	0.0268	0.2609
chr7	159138663	4217850	0.0265	0.3868

chr8	146364022	3562208	0.0243	0.2777
chr9	141213431	3201361	0.0227	0.2762
chr10	135534747	3516791	0.0259	0.2634
chr11	135006516	3008645	0.0223	0.2709
chr12	133851895	3525168	0.0263	0.2553
chr13	115169878	2432269	0.0211	0.2254
chr14	107349540	2488610	0.0232	0.2541
chr15	102531392	2237295	0.0218	0.2498
chr16	90354753	2076188	0.023	0.24
chr17	81195210	1837035	0.0226	0.2423
chr18	78077248	1563516	0.02	0.3637
chr19	59128983	1398095	0.0236	0.2747
chr20	63025520	1710708	0.0271	0.2601
chr21	48129895	1002454	0.0208	0.2275
chr22	51304566	867857	0.0169	0.2017
chrMT	16571	151962	9.1704	6.9555
chrX	155270560	3922164	0.0253	0.26
chrY	59373566	231596	0.0039	0.0958

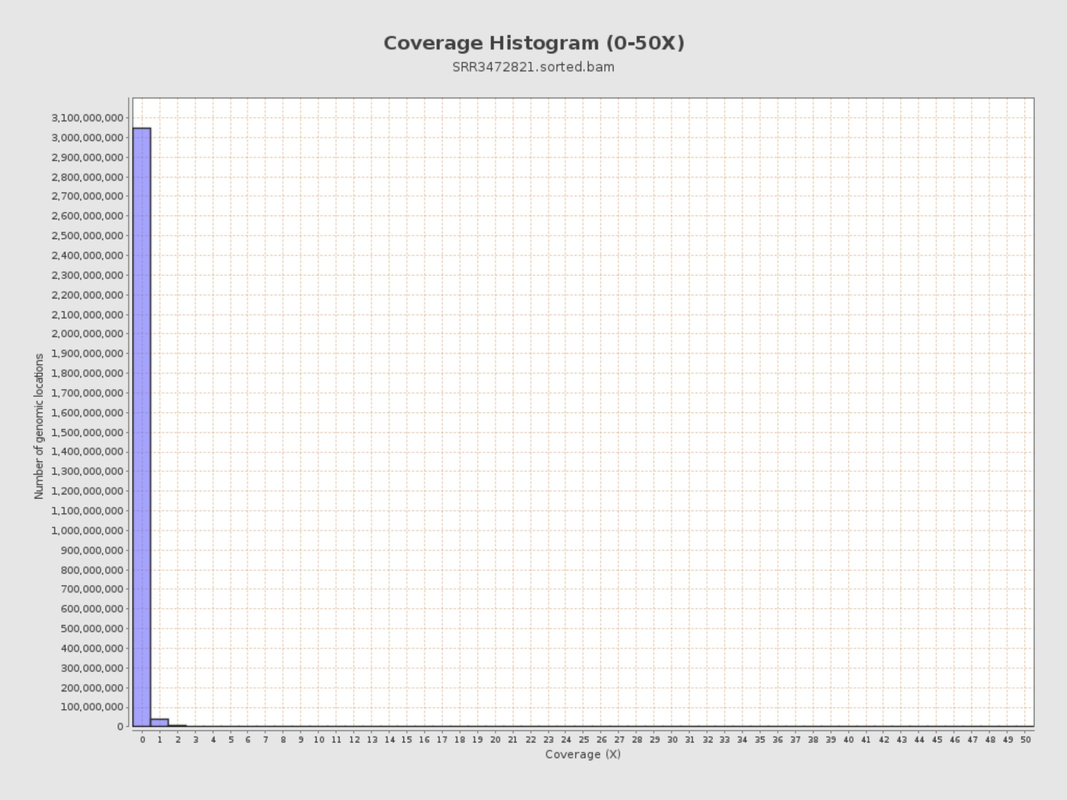
3. Results : Coverage across reference



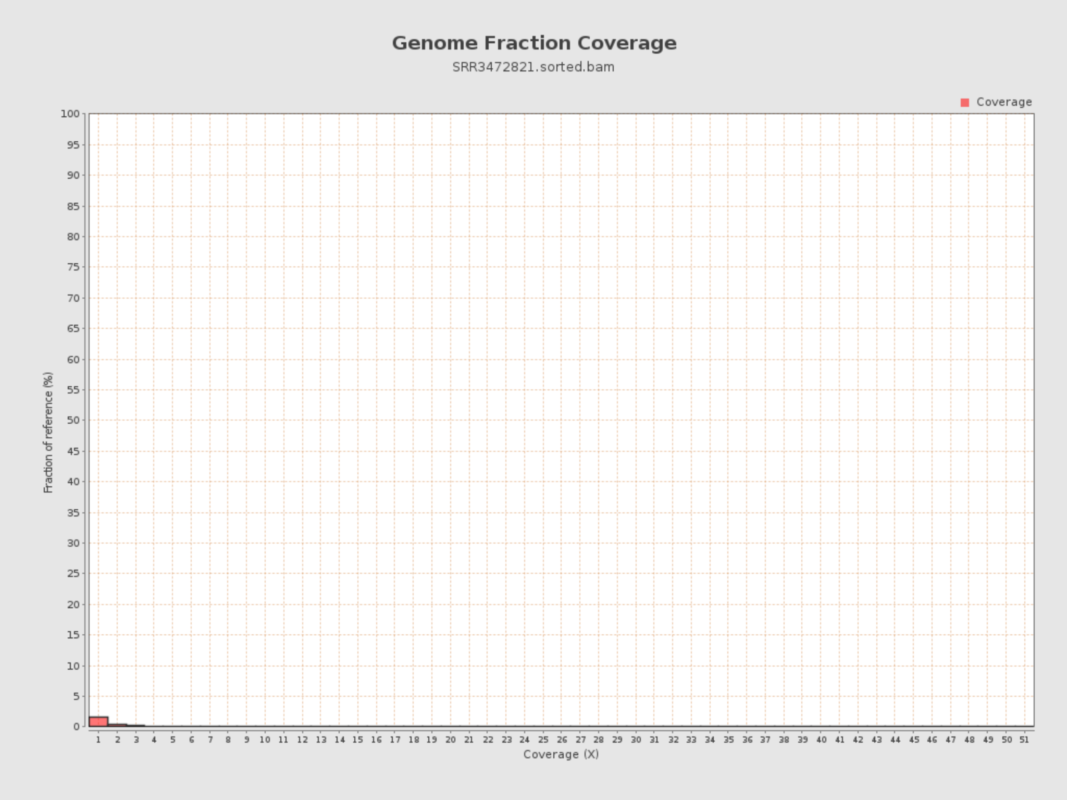
4. Results : Coverage Histogram



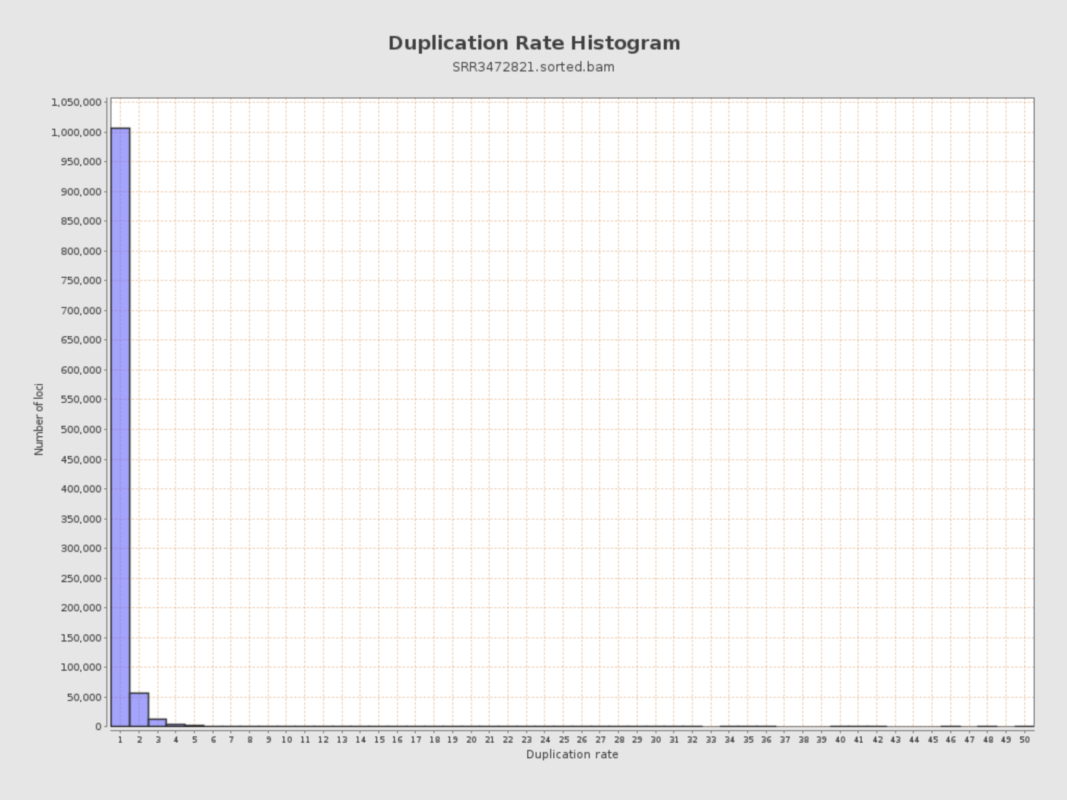
5. Results : Coverage Histogram (0-50X)



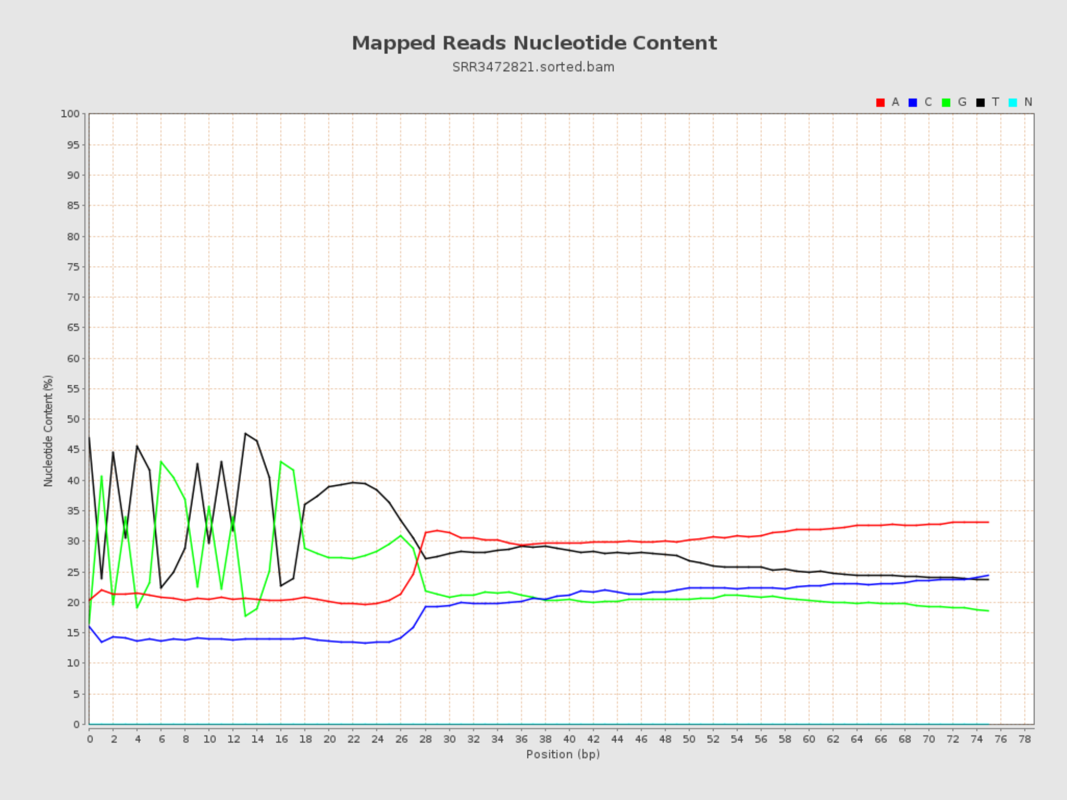
6. Results : Genome Fraction Coverage



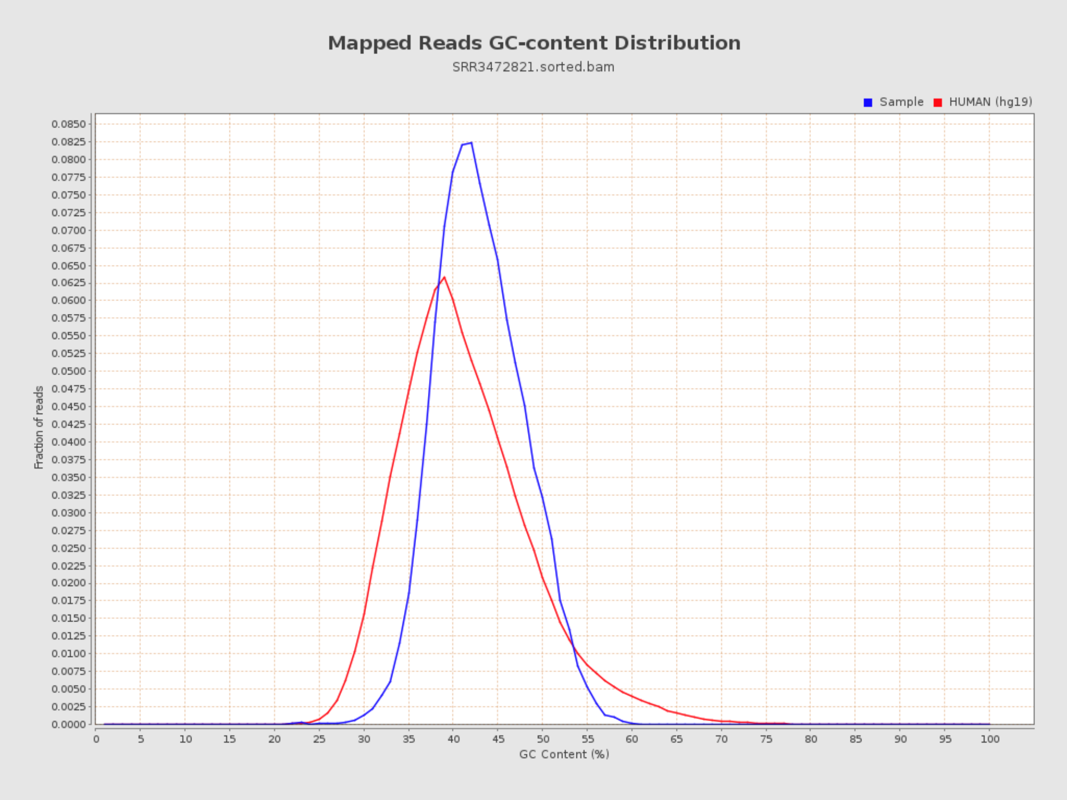
7. Results : Duplication Rate Histogram



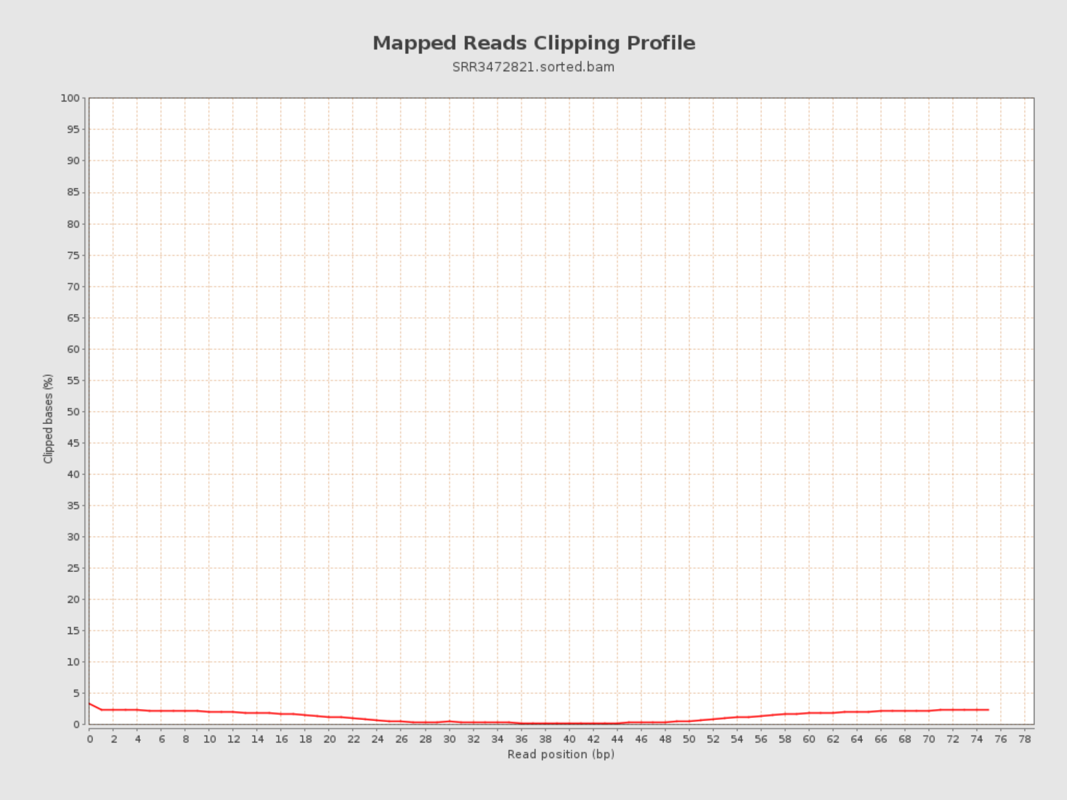
8. Results : Mapped Reads Nucleotide Content



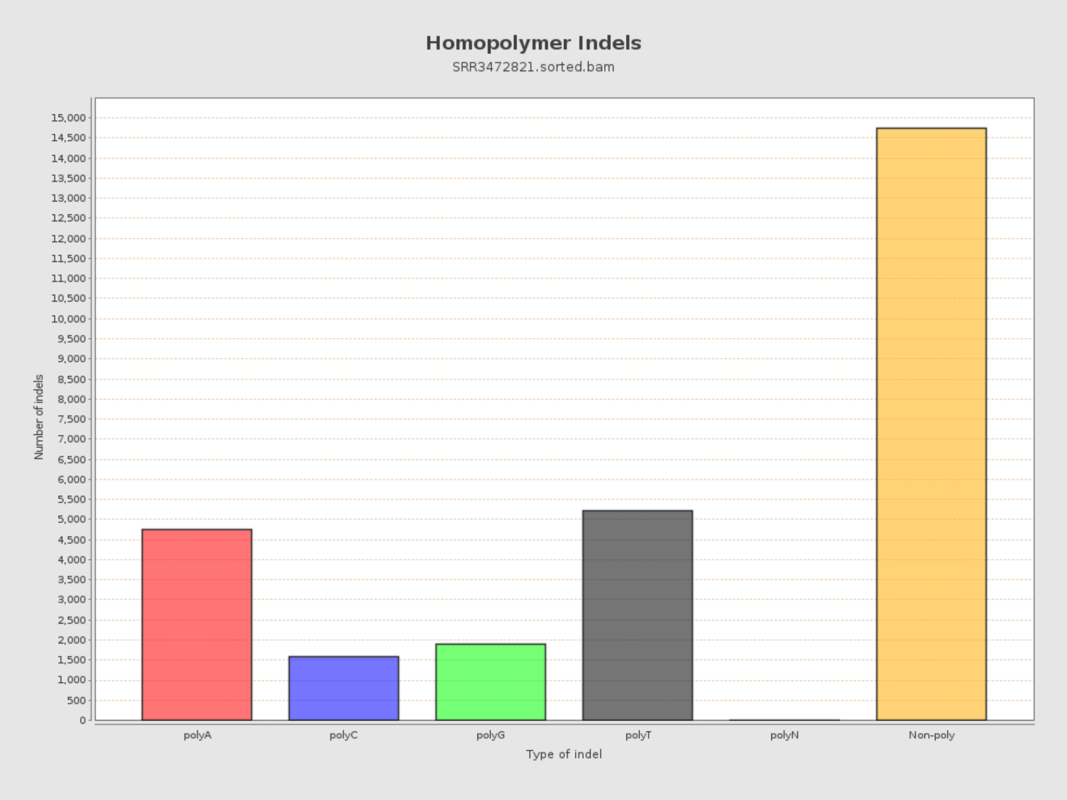
9. Results : Mapped Reads GC-content Distribution



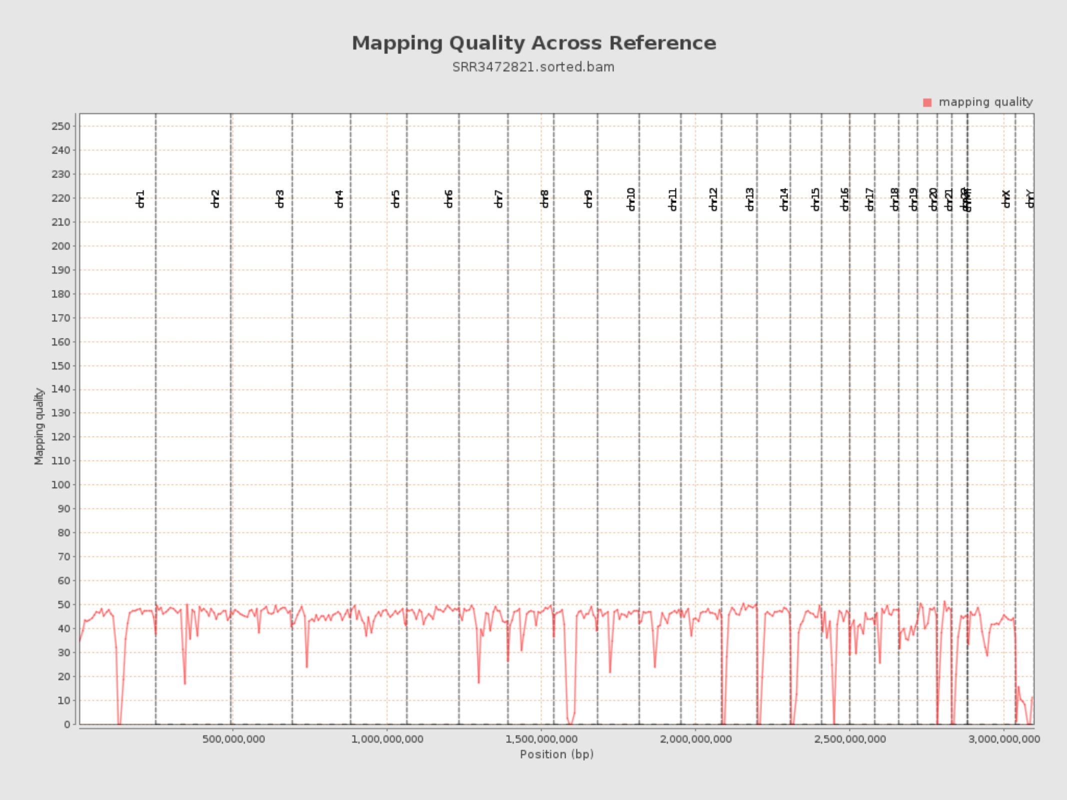
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram