Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/01 10:26:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472842.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_SRR3472842 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472842.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 01 10:26:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472842.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,393,458
Mapped reads	2,125,334 / 88.8%
Unmapped reads	268,124 / 11.2%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,377 / 0.52%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	72,559 / 3.03%
Duplication rate	2.69%
Clipped reads	1,060,053 / 44.29%

2.2. ACGT Content

Number/percentage of A's	36,834,448 / 26.55%
Number/percentage of C's	27,350,746 / 19.71%
Number/percentage of T's	41,825,029 / 30.15%
Number/percentage of G's	32,730,499 / 23.59%
Number/percentage of N's	2,907 / 0%
GC Percentage	43.3%

2.3. Coverage

Mean	0.0448

Standard Deviation	0.323

2.4. Mapping Quality

Mean Mapping Quality	44.95

2.5. Mismatches and indels

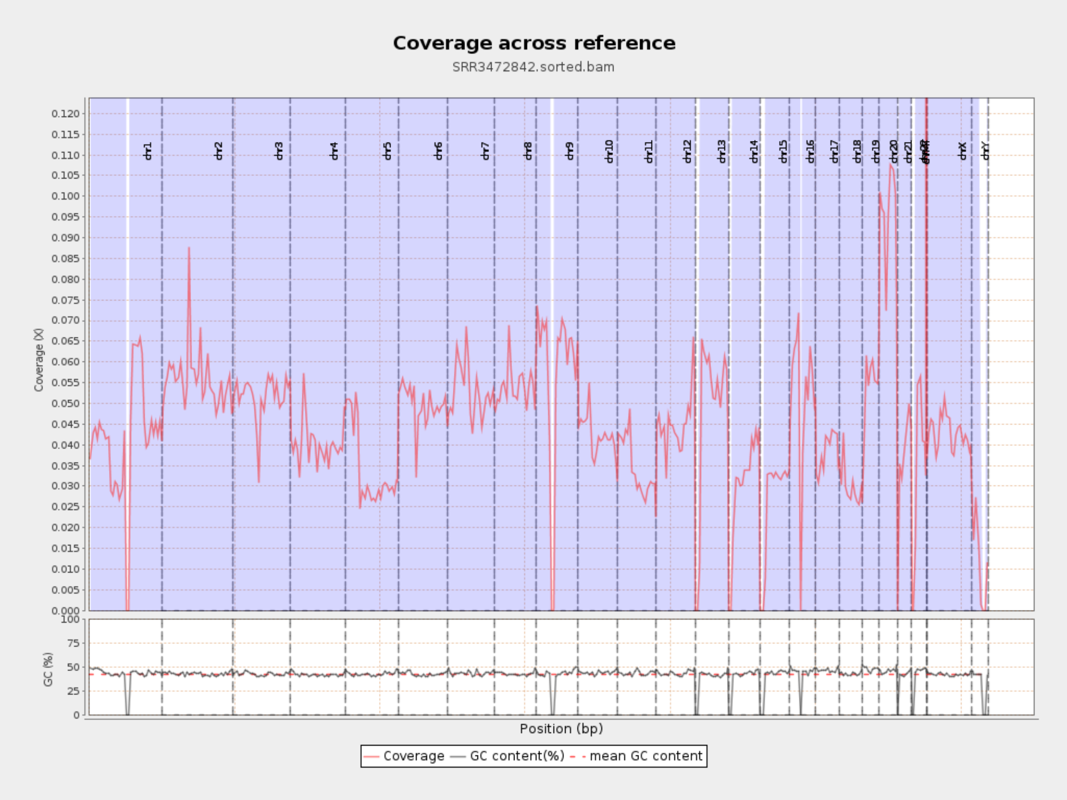
General error rate	0.85%
Mismatches	1,166,392
Insertions	10,501
Mapped reads with at least one insertion	0.49%
Deletions	31,324
Mapped reads with at least one deletion	1.46%
Homopolymer indels	45.81%

2.6. Chromosome stats

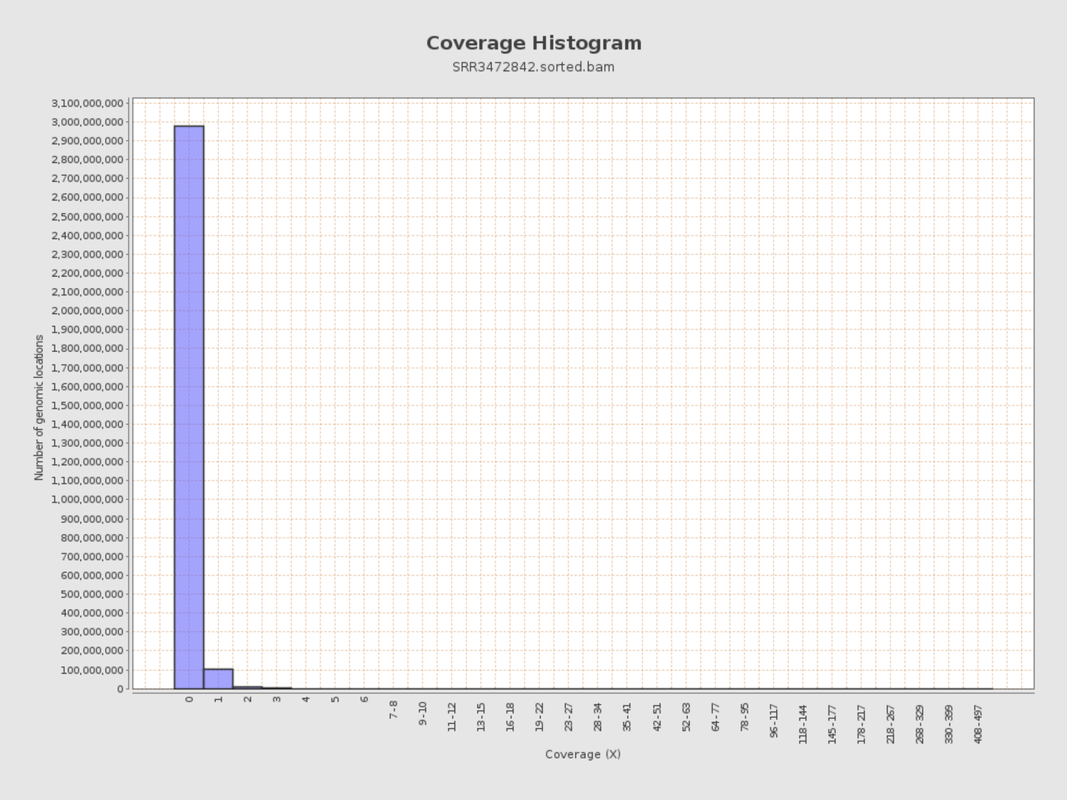
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10225105	0.041	0.4098
chr2	243199373	13613316	0.056	0.4522
chr3	198022430	10210722	0.0516	0.2542
chr4	191154276	7659091	0.0401	0.2433
chr5	180915260	6140588	0.0339	0.2072
chr6	171115067	8496227	0.0497	0.2688
chr7	159138663	8455462	0.0531	0.4358

chr8	146364022	7889568	0.0539	0.3339
chr9	141213431	7998083	0.0566	0.3733
chr10	135534747	5753364	0.0424	0.2996
chr11	135006516	4671959	0.0346	0.3147
chr12	133851895	6038318	0.0451	0.2447
chr13	115169878	5493353	0.0477	0.2518
chr14	107349540	3209477	0.0299	0.2186
chr15	102531392	2690922	0.0262	0.1883
chr16	90354753	4710785	0.0521	0.2778
chr17	81195210	3134725	0.0386	0.2377
chr18	78077248	2356849	0.0302	0.582
chr19	59128983	3198015	0.0541	0.3464
chr20	63025520	6039857	0.0958	0.3676
chr21	48129895	1763805	0.0366	0.2524
chr22	51304566	1676280	0.0327	0.2163
chrMT	16571	40809	2.4627	2.2988
chrX	155270560	6653127	0.0428	0.256
chrY	59373566	679473	0.0114	0.1518

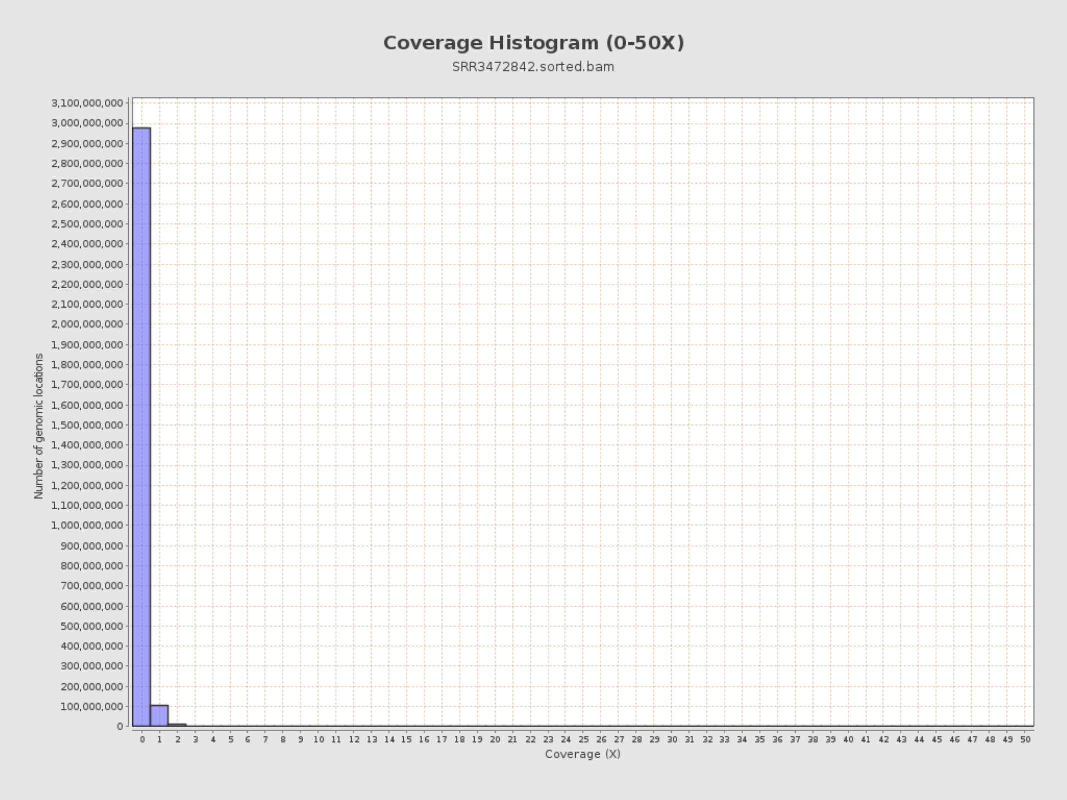
3. Results : Coverage across reference



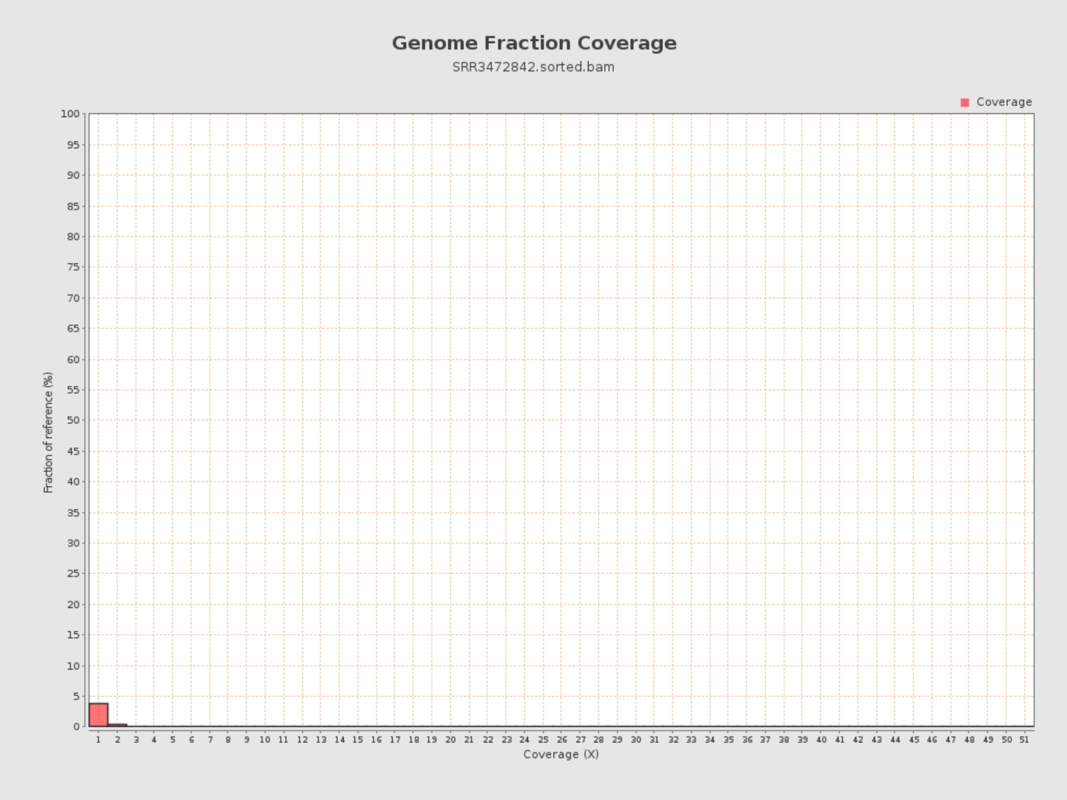
4. Results : Coverage Histogram



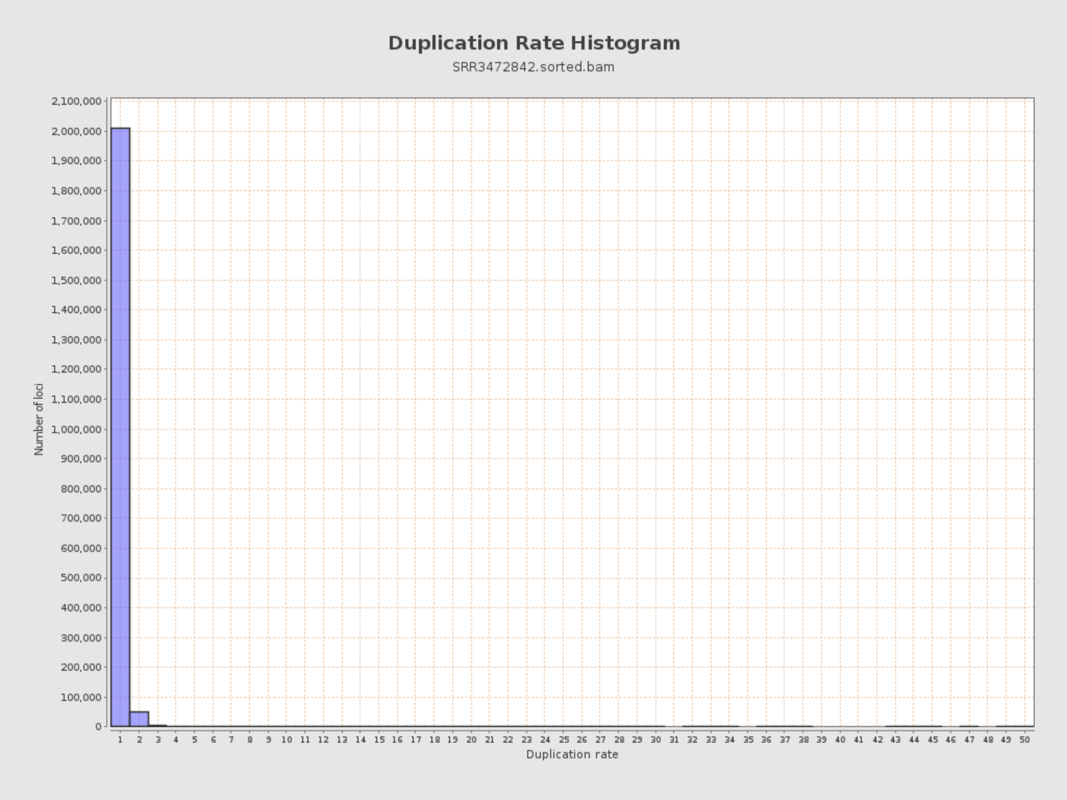
5. Results : Coverage Histogram (0-50X)



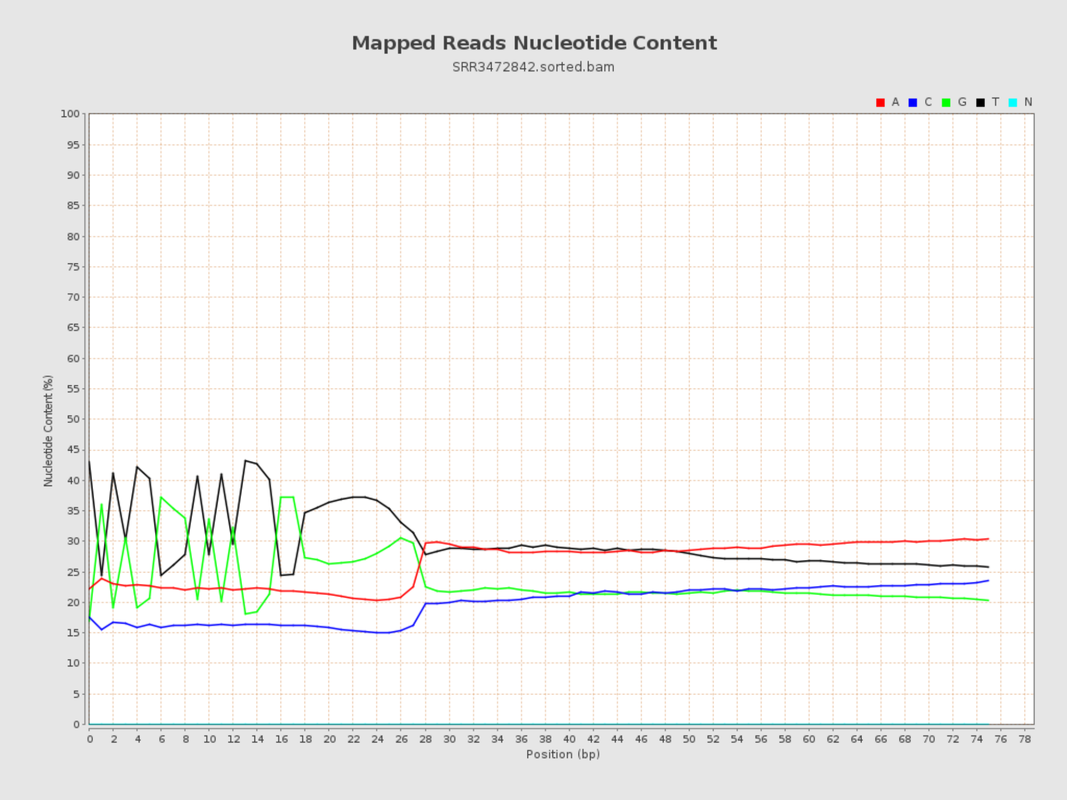
6. Results : Genome Fraction Coverage



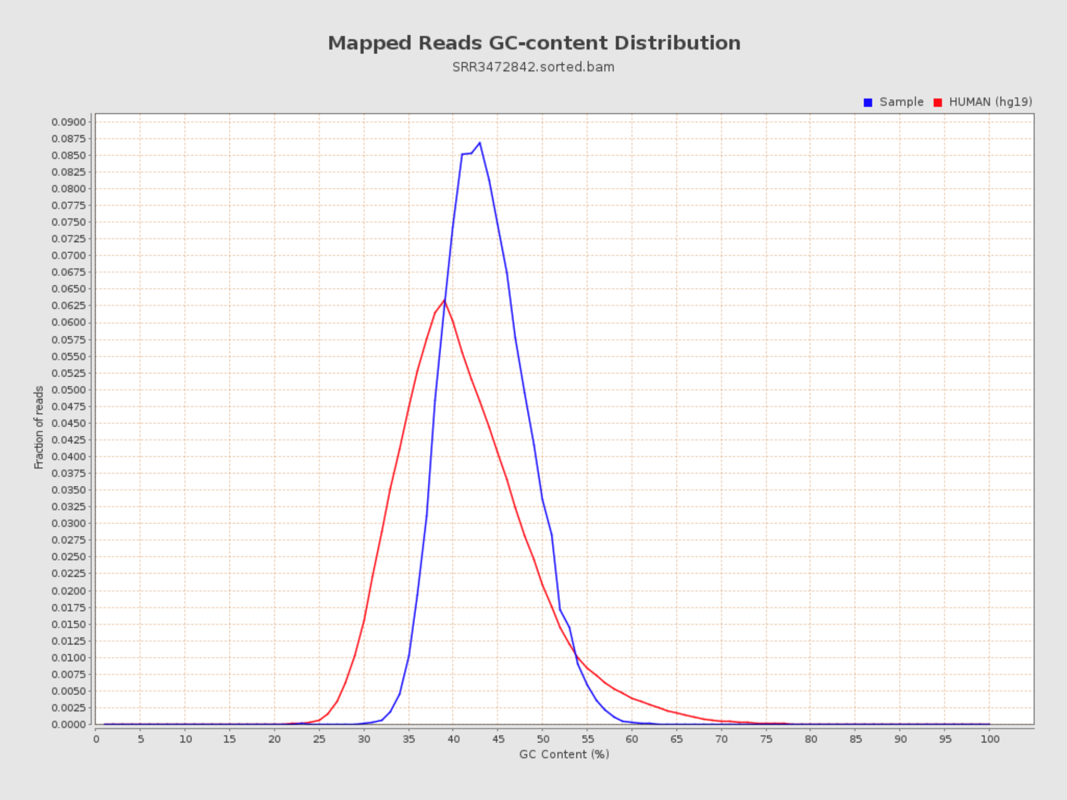
7. Results : Duplication Rate Histogram



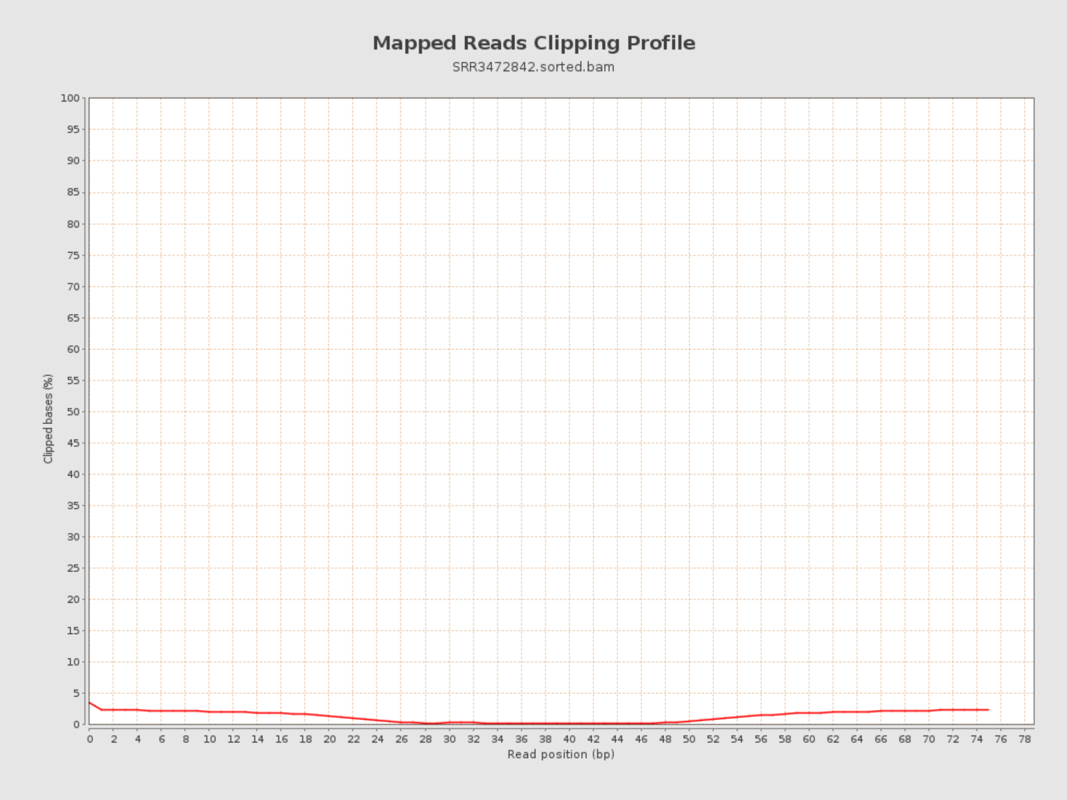
8. Results : Mapped Reads Nucleotide Content



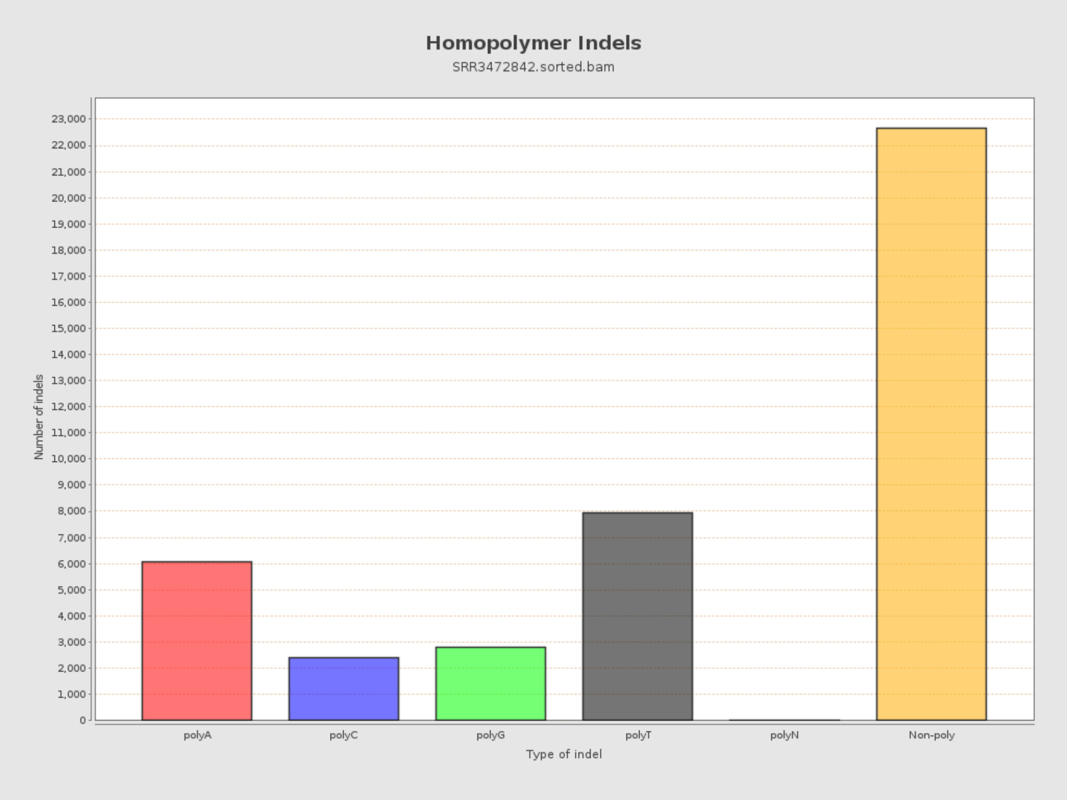
9. Results : Mapped Reads GC-content Distribution



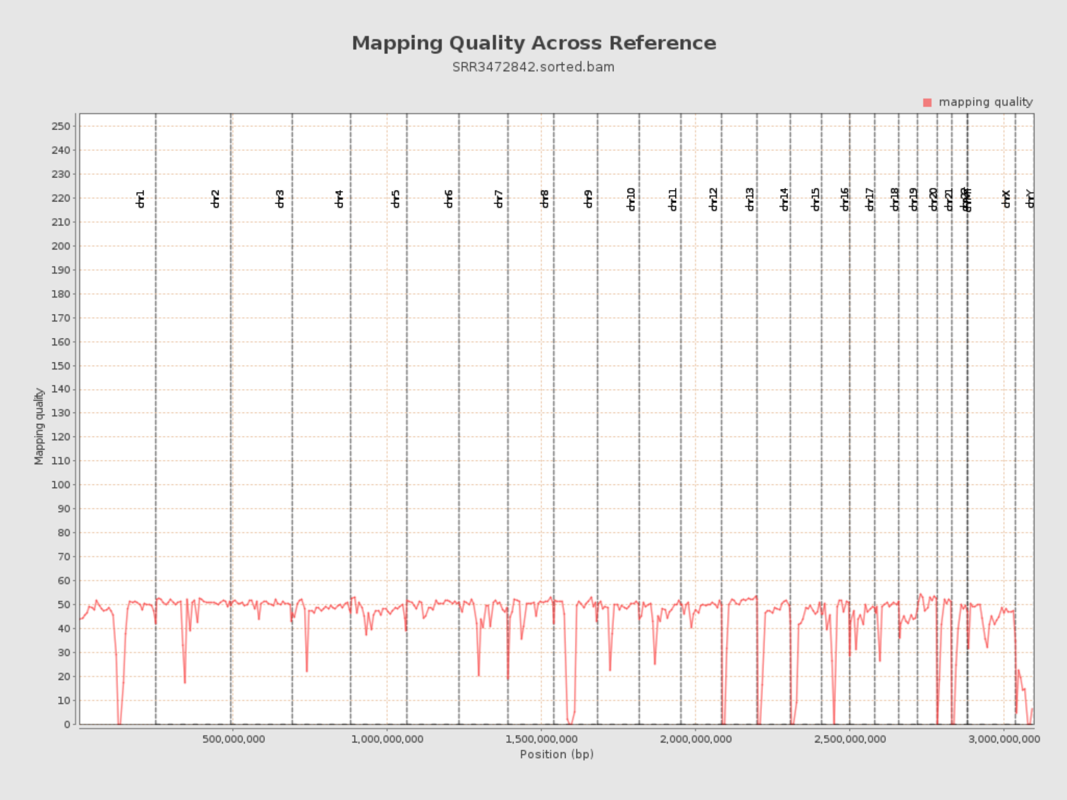
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram