Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/01 07:25:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472809.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_SRR3472809 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472809.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 01 07:25:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472809.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,663,090
Mapped reads	2,083,708 / 78.24%
Unmapped reads	579,382 / 21.76%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,988 / 0.79%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	85,912 / 3.23%
Duplication rate	2.99%
Clipped reads	1,216,967 / 45.7%

2.2. ACGT Content

Number/percentage of A's	34,890,402 / 26.46%
Number/percentage of C's	27,067,516 / 20.52%
Number/percentage of T's	38,492,897 / 29.19%
Number/percentage of G's	31,428,672 / 23.83%
Number/percentage of N's	2,553 / 0%
GC Percentage	44.35%

2.3. Coverage

Mean	0.0426

Standard Deviation	0.3414

2.4. Mapping Quality

Mean Mapping Quality	42.46

2.5. Mismatches and indels

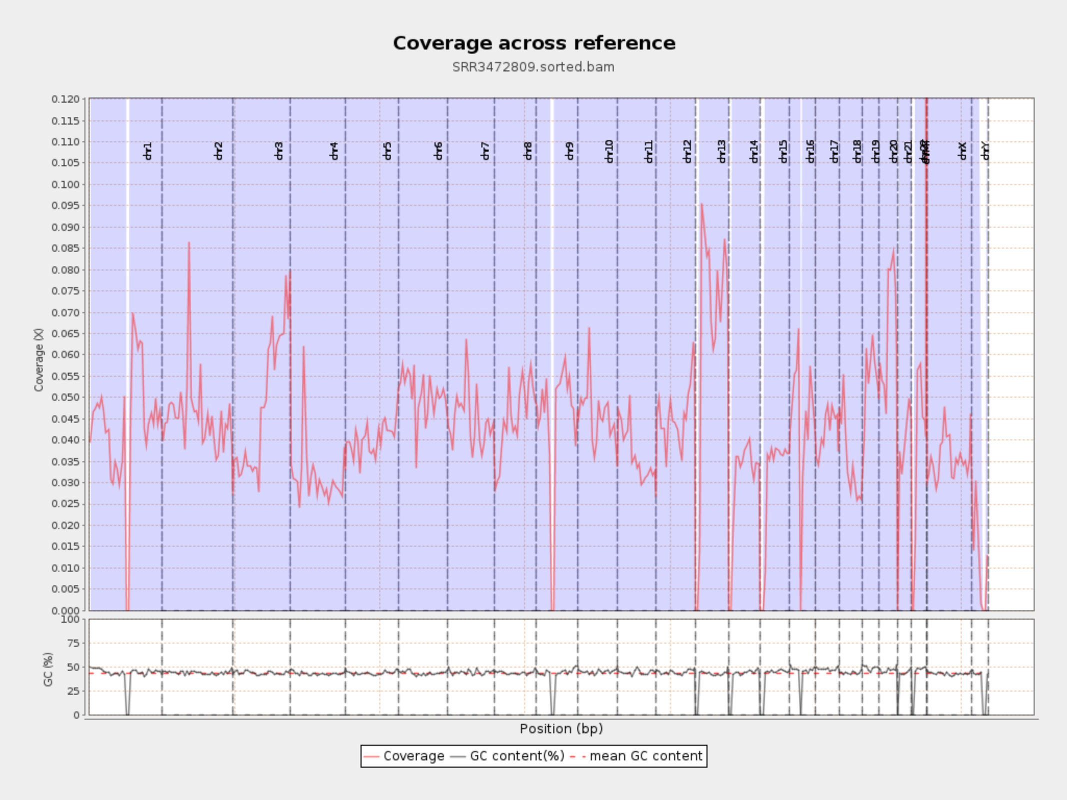
General error rate	0.9%
Mismatches	1,165,506
Insertions	10,762
Mapped reads with at least one insertion	0.51%
Deletions	31,283
Mapped reads with at least one deletion	1.48%
Homopolymer indels	43.76%

2.6. Chromosome stats

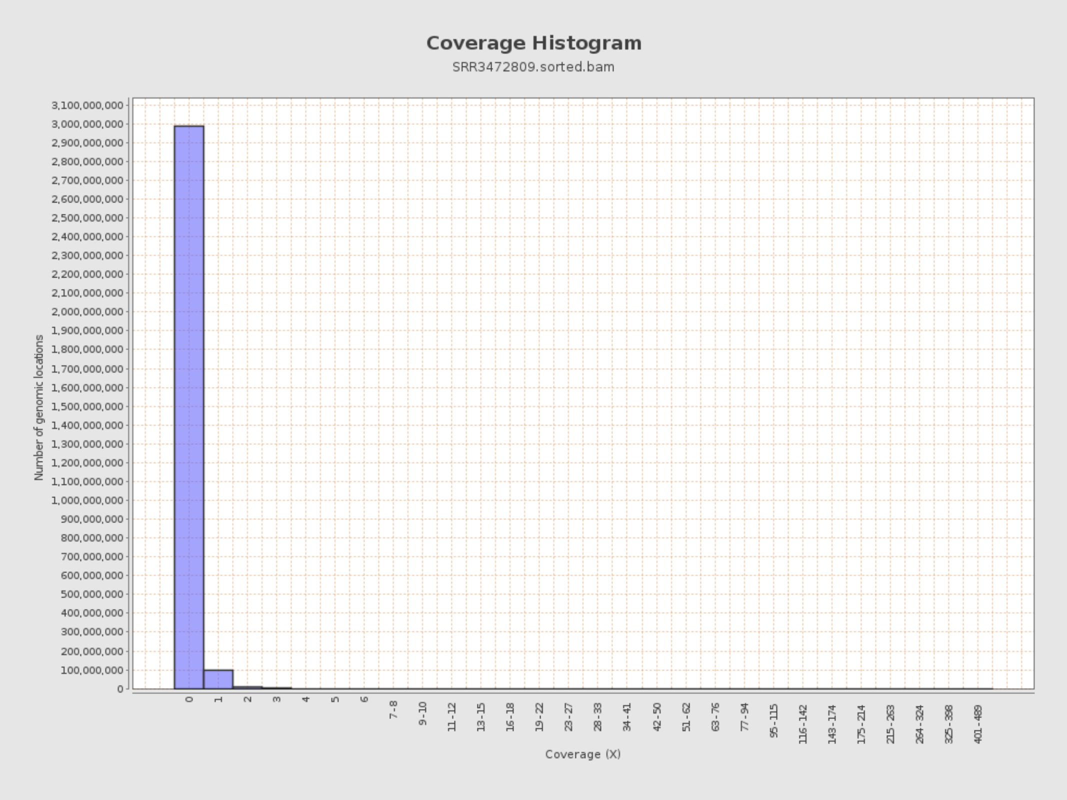
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10743022	0.0431	0.4529
chr2	243199373	11173986	0.0459	0.4739
chr3	198022430	9493069	0.0479	0.256
chr4	191154276	5973351	0.0312	0.2435
chr5	180915260	7286224	0.0403	0.2362
chr6	171115067	8684918	0.0508	0.2894
chr7	159138663	7145171	0.0449	0.4183

chr8	146364022	6632313	0.0453	0.3132
chr9	141213431	6220502	0.0441	0.3616
chr10	135534747	6234258	0.046	0.3633
chr11	135006516	4948633	0.0367	0.3477
chr12	133851895	6117770	0.0457	0.2547
chr13	115169878	7527955	0.0654	0.3033
chr14	107349540	3203388	0.0298	0.2399
chr15	102531392	3031623	0.0296	0.2264
chr16	90354753	4078964	0.0451	0.2842
chr17	81195210	3430731	0.0423	0.2608
chr18	78077248	2759750	0.0353	0.653
chr19	59128983	3212052	0.0543	0.3791
chr20	63025520	4186428	0.0664	0.3203
chr21	48129895	1775146	0.0369	0.2652
chr22	51304566	1794191	0.035	0.2273
chrMT	16571	102056	6.1587	4.7028
chrX	155270560	5516641	0.0355	0.2613
chrY	59373566	666730	0.0112	0.1732

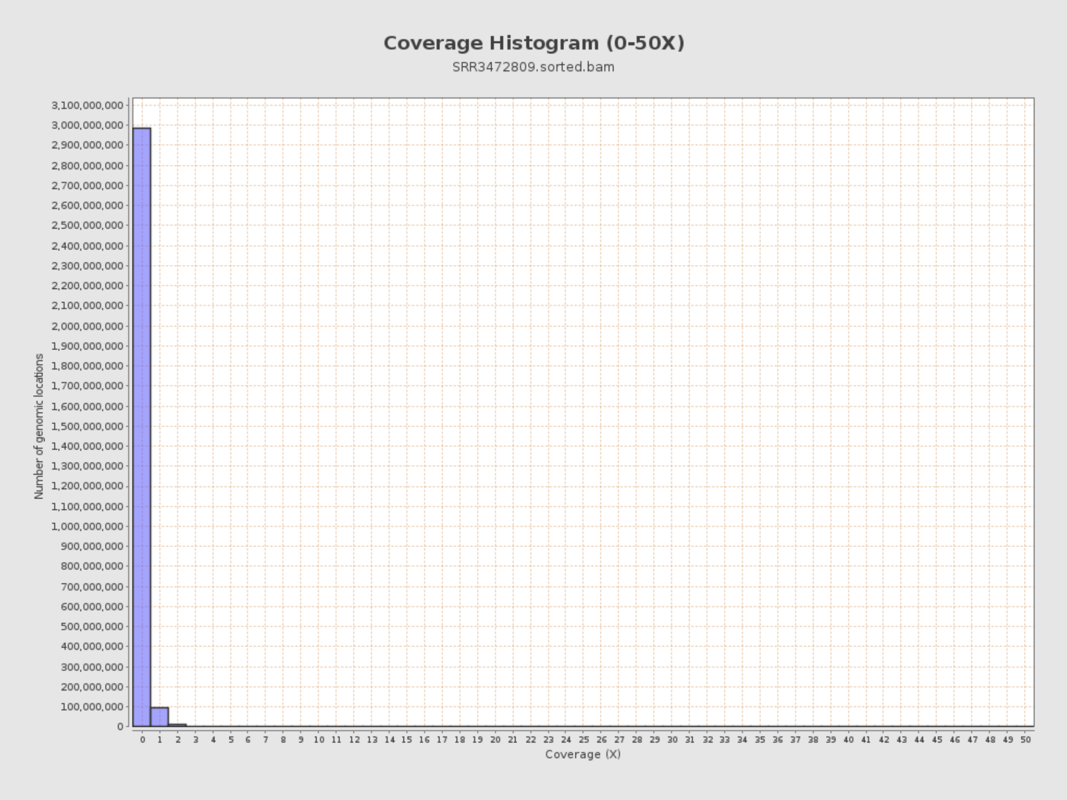
3. Results : Coverage across reference



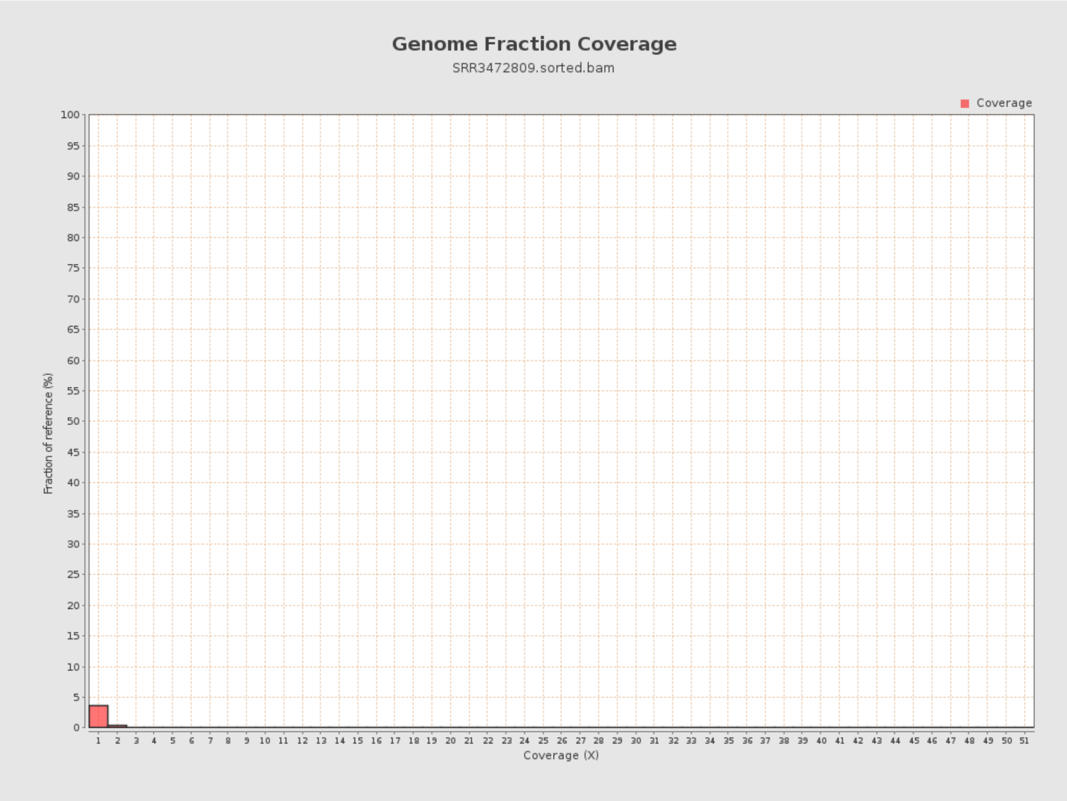
4. Results : Coverage Histogram



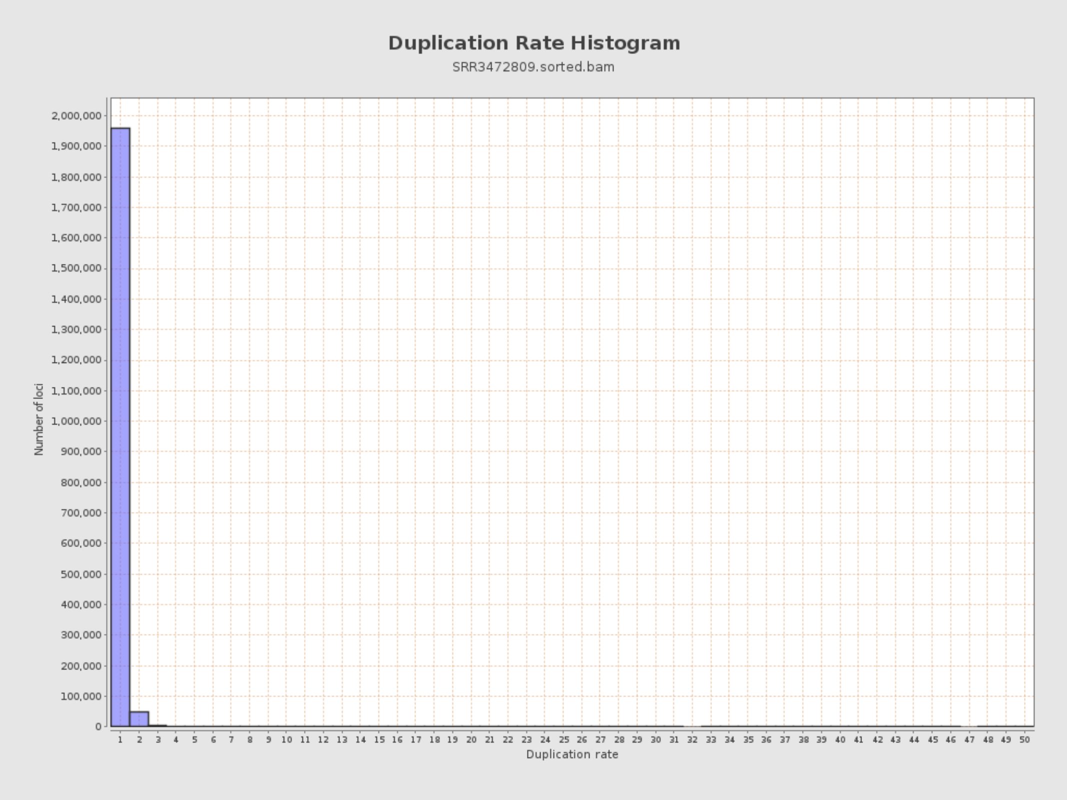
5. Results : Coverage Histogram (0-50X)



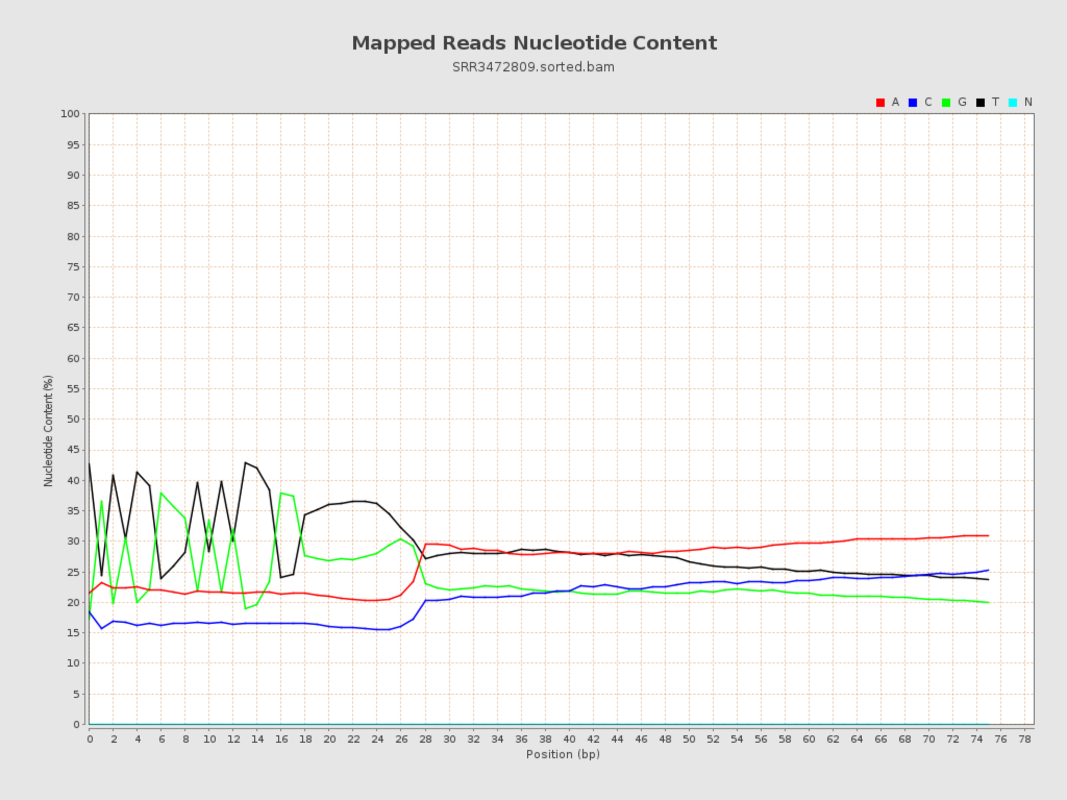
6. Results : Genome Fraction Coverage



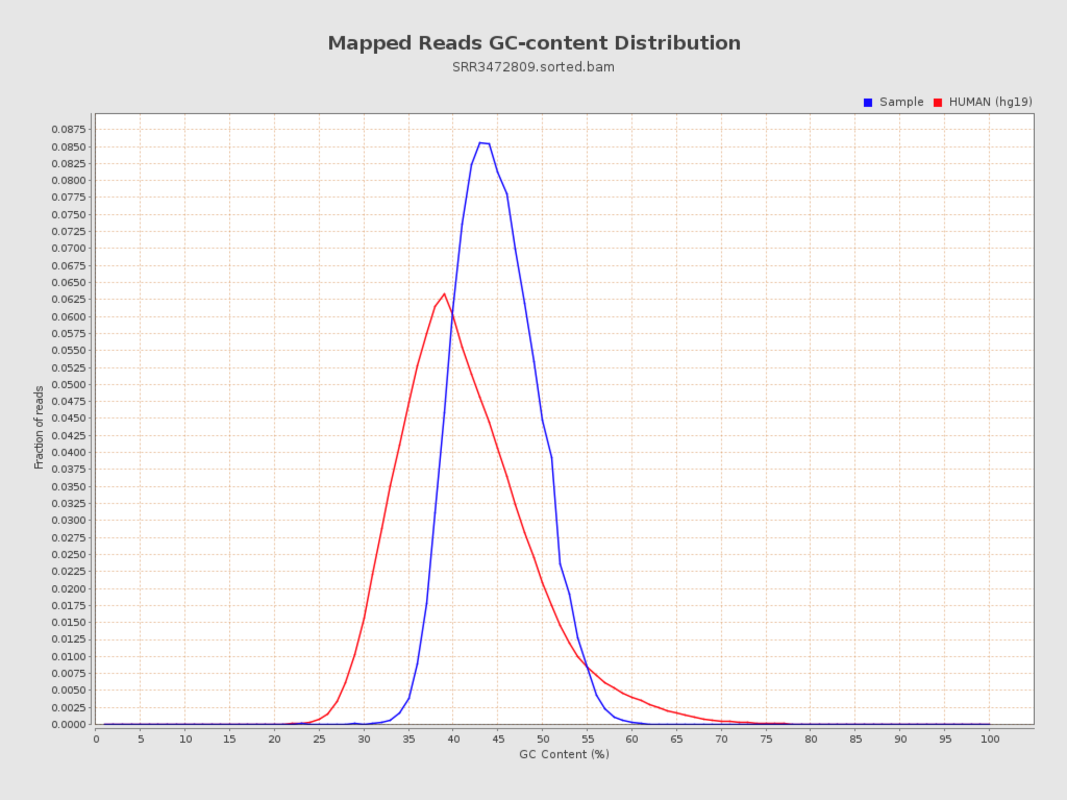
7. Results : Duplication Rate Histogram



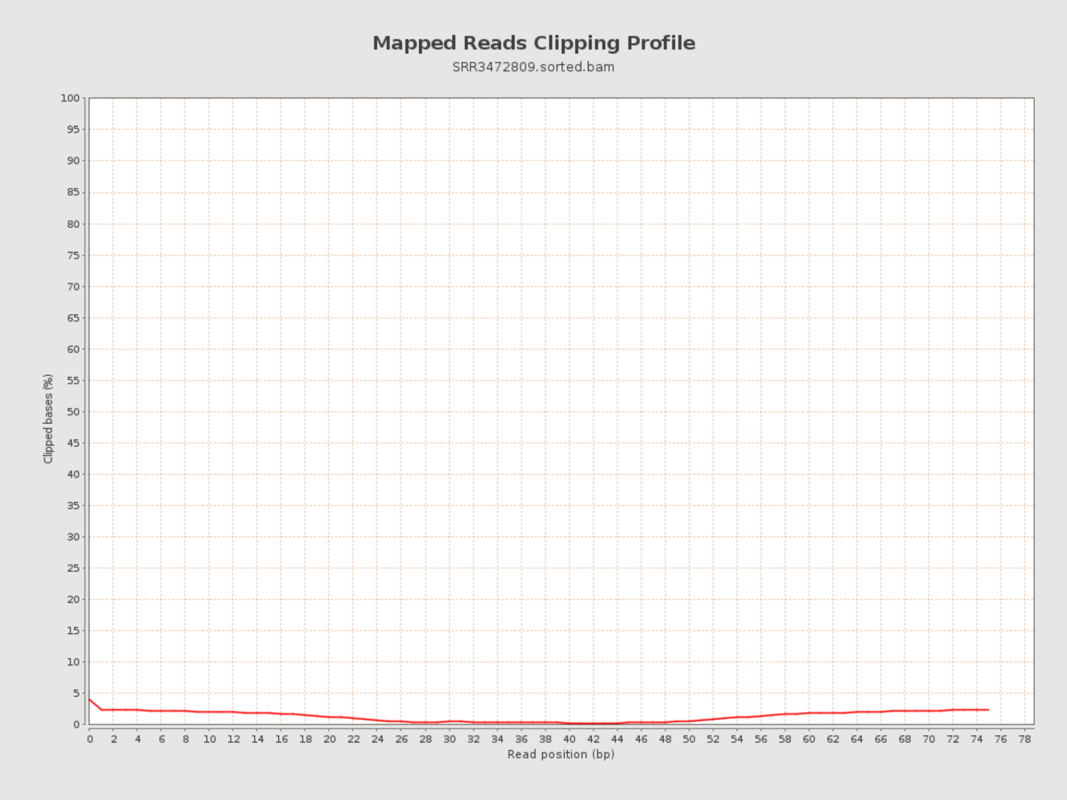
8. Results : Mapped Reads Nucleotide Content



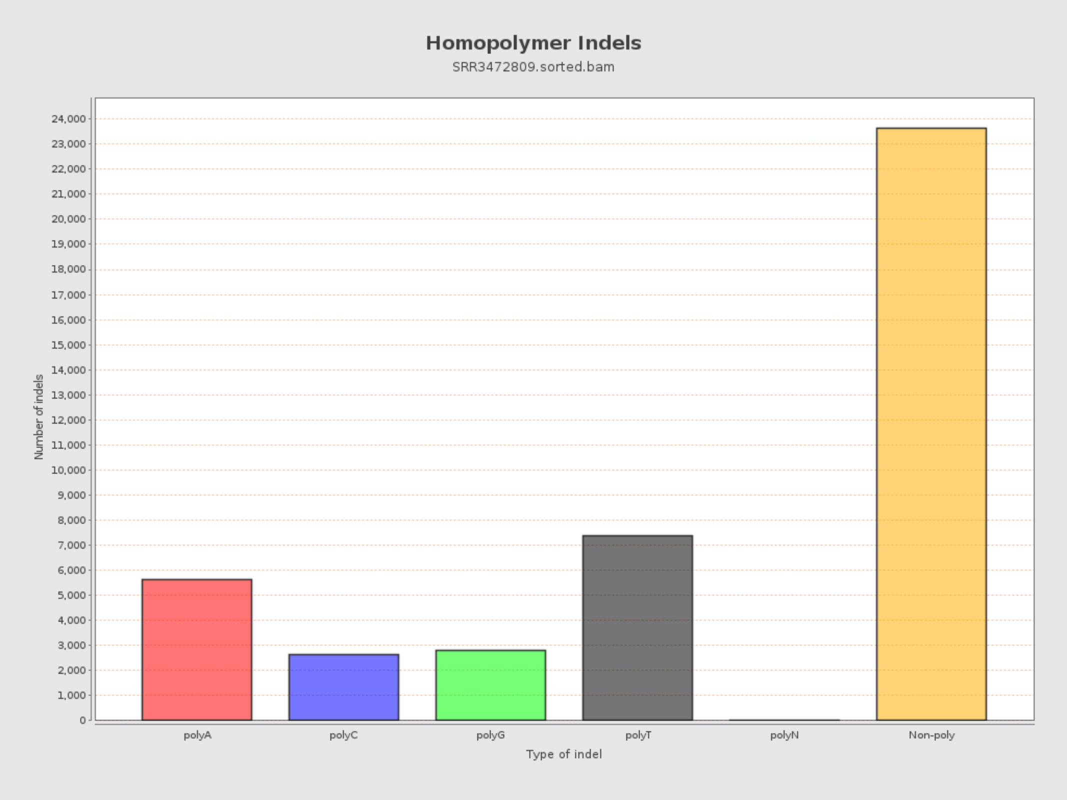
9. Results : Mapped Reads GC-content Distribution



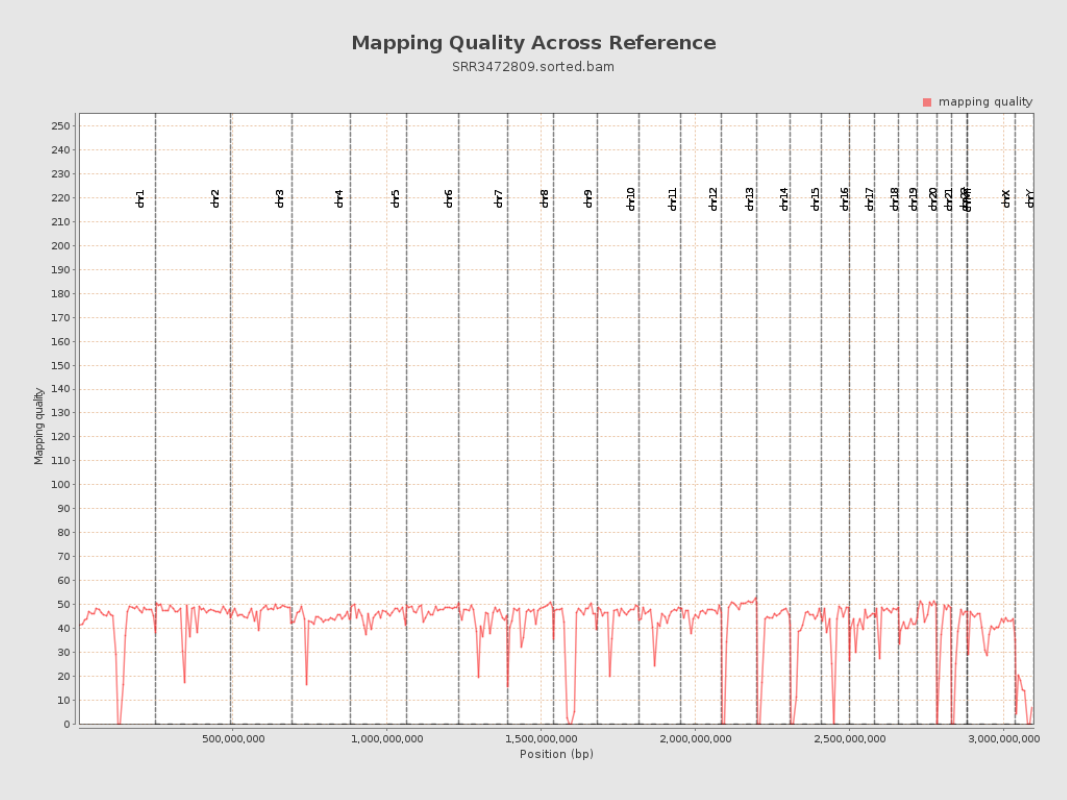
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram