Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 20:46:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084969.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_SRR3084969 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084969.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 20:46:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084969.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,552,002
Mapped reads	2,379,634 / 93.25%
Unmapped reads	172,368 / 6.75%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,204 / 0.95%
Read min/max/mean length	30 / 76 / 76.33
Duplicated reads (estimated)	98,119 / 3.84%
Duplication rate	2.65%
Clipped reads	766,514 / 30.04%

2.2. ACGT Content

Number/percentage of A's	49,607,731 / 29.77%
Number/percentage of C's	30,664,212 / 18.4%
Number/percentage of T's	52,658,351 / 31.6%
Number/percentage of G's	33,665,026 / 20.2%
Number/percentage of N's	24,789 / 0.01%
GC Percentage	38.61%

2.3. Coverage

Mean	0.0538

Standard Deviation	0.662

2.4. Mapping Quality

Mean Mapping Quality	48.28

2.5. Mismatches and indels

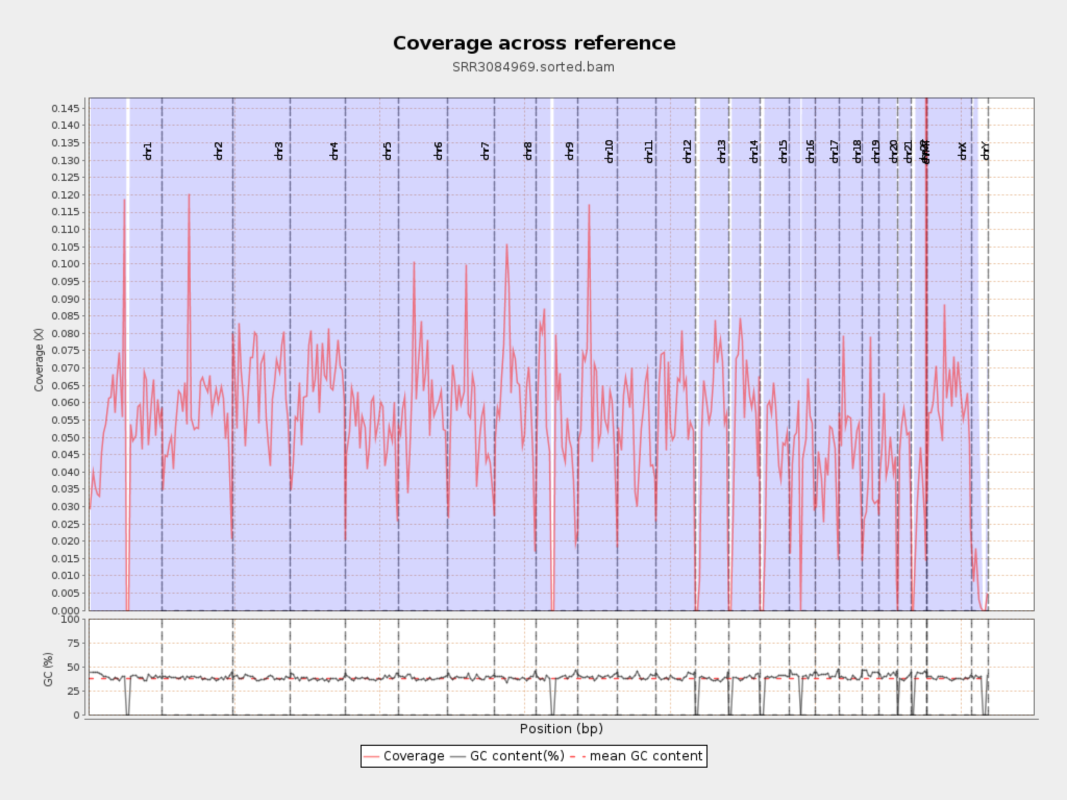
General error rate	0.86%
Mismatches	1,401,153
Insertions	13,880
Mapped reads with at least one insertion	0.58%
Deletions	38,872
Mapped reads with at least one deletion	1.62%
Homopolymer indels	47.69%

2.6. Chromosome stats

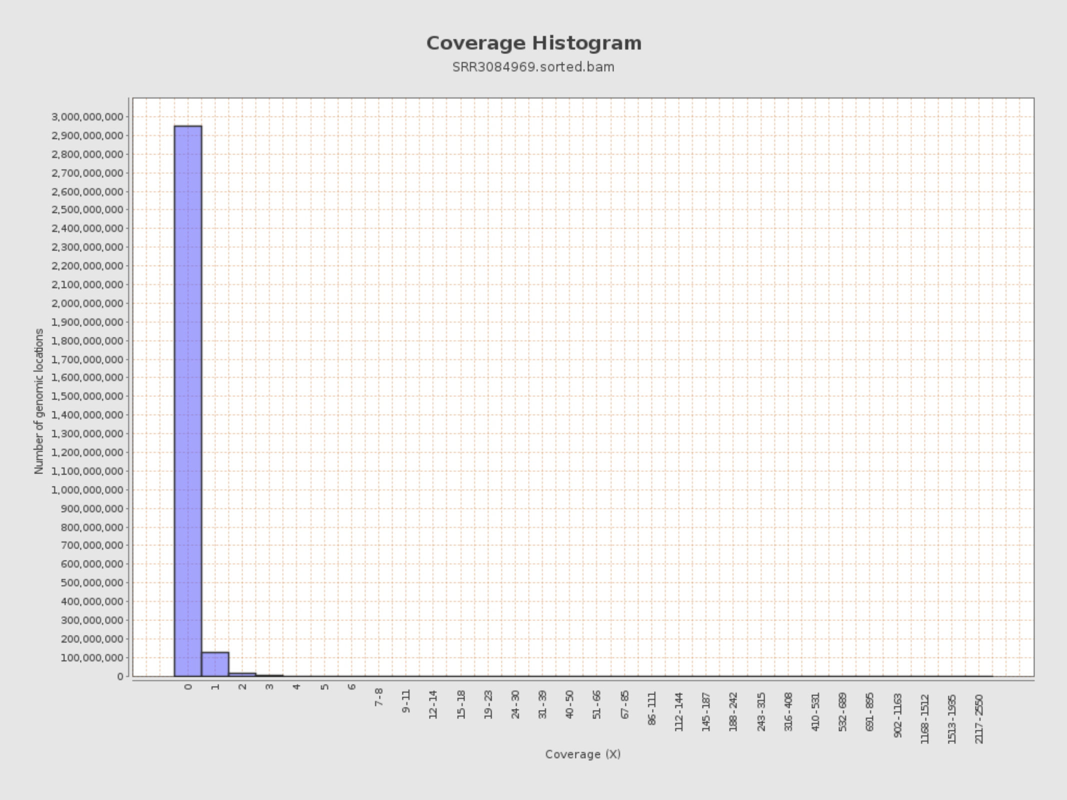
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13111678	0.0526	1.3524
chr2	243199373	13943430	0.0573	0.5692
chr3	198022430	12972539	0.0655	0.2886
chr4	191154276	12418664	0.065	0.2866
chr5	180915260	9443541	0.0522	0.2583
chr6	171115067	10468784	0.0612	0.4497
chr7	159138663	8968150	0.0564	0.5394

chr8	146364022	9310715	0.0636	1.5552
chr9	141213431	7204282	0.051	0.5421
chr10	135534747	8352561	0.0616	0.5841
chr11	135006516	6991055	0.0518	0.5253
chr12	133851895	7961014	0.0595	0.2848
chr13	115169878	6084650	0.0528	0.2508
chr14	107349540	5807277	0.0541	0.2945
chr15	102531392	4347667	0.0424	0.2258
chr16	90354753	3995884	0.0442	0.3209
chr17	81195210	3140057	0.0387	0.2791
chr18	78077248	4099360	0.0525	1.115
chr19	59128983	2168447	0.0367	0.8564
chr20	63025520	2762231	0.0438	0.2508
chr21	48129895	2142821	0.0445	0.2743
chr22	51304566	1251016	0.0244	0.17
chrMT	16571	28909	1.7446	1.5238
chrX	155270560	9371179	0.0604	0.3426
chrY	59373566	337545	0.0057	0.1425

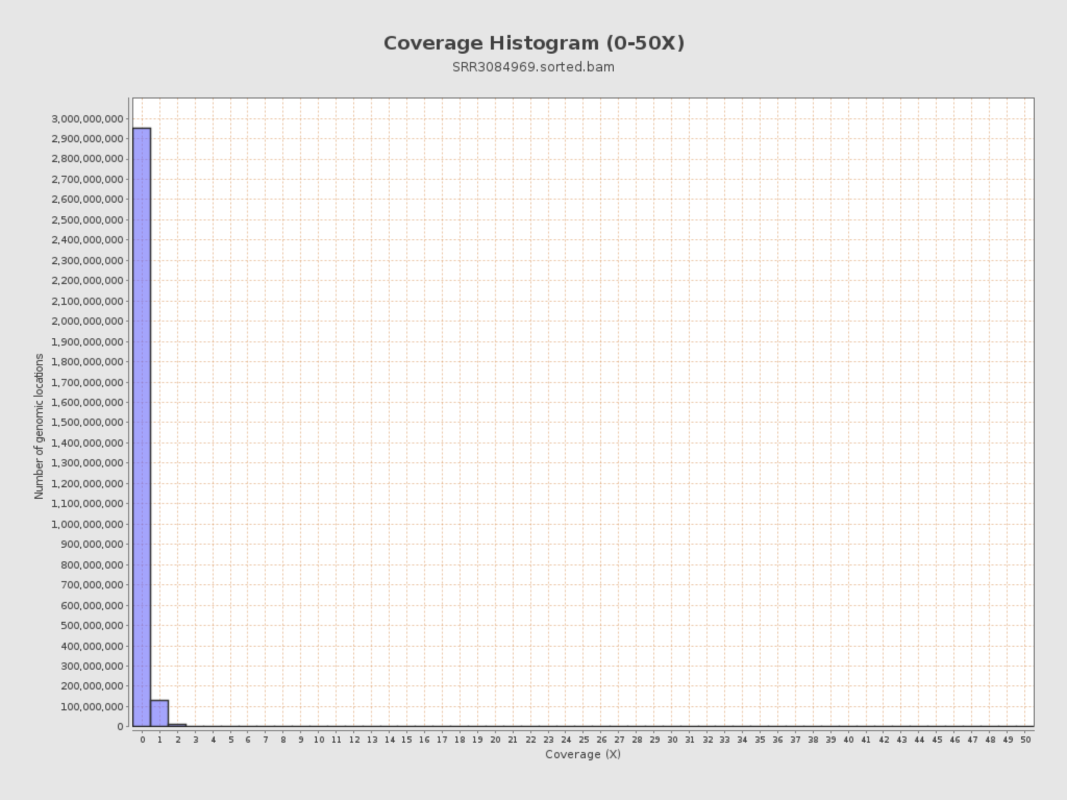
3. Results : Coverage across reference



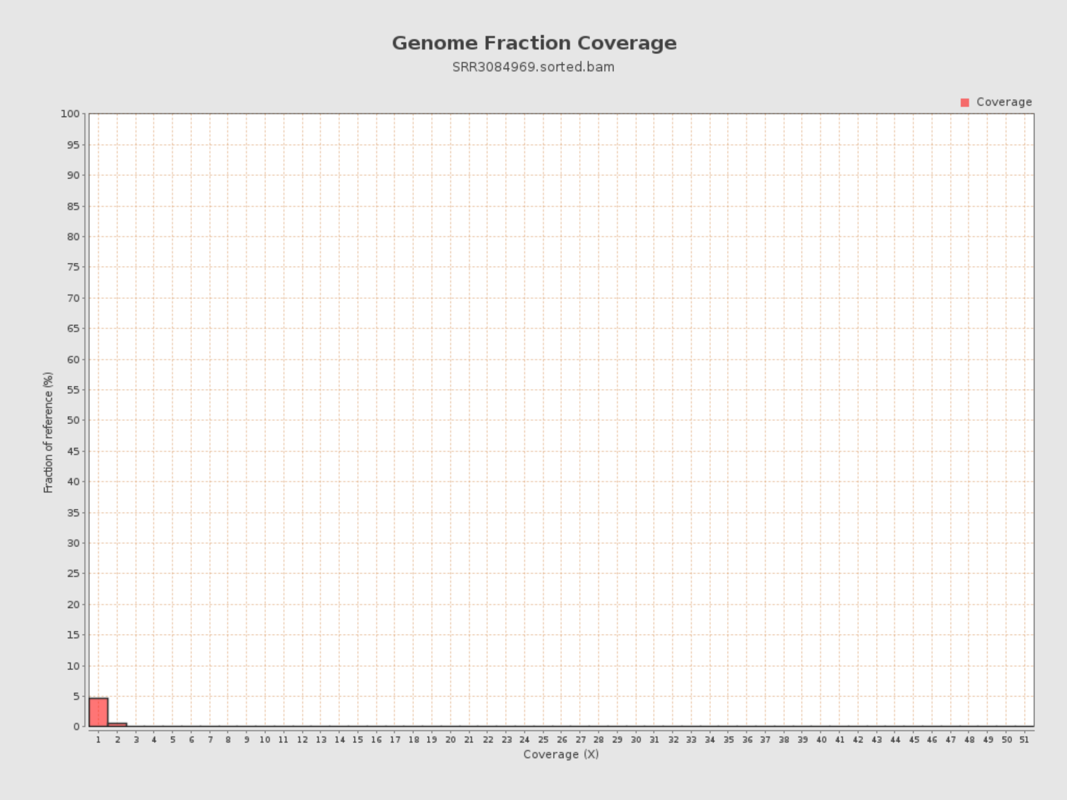
4. Results : Coverage Histogram



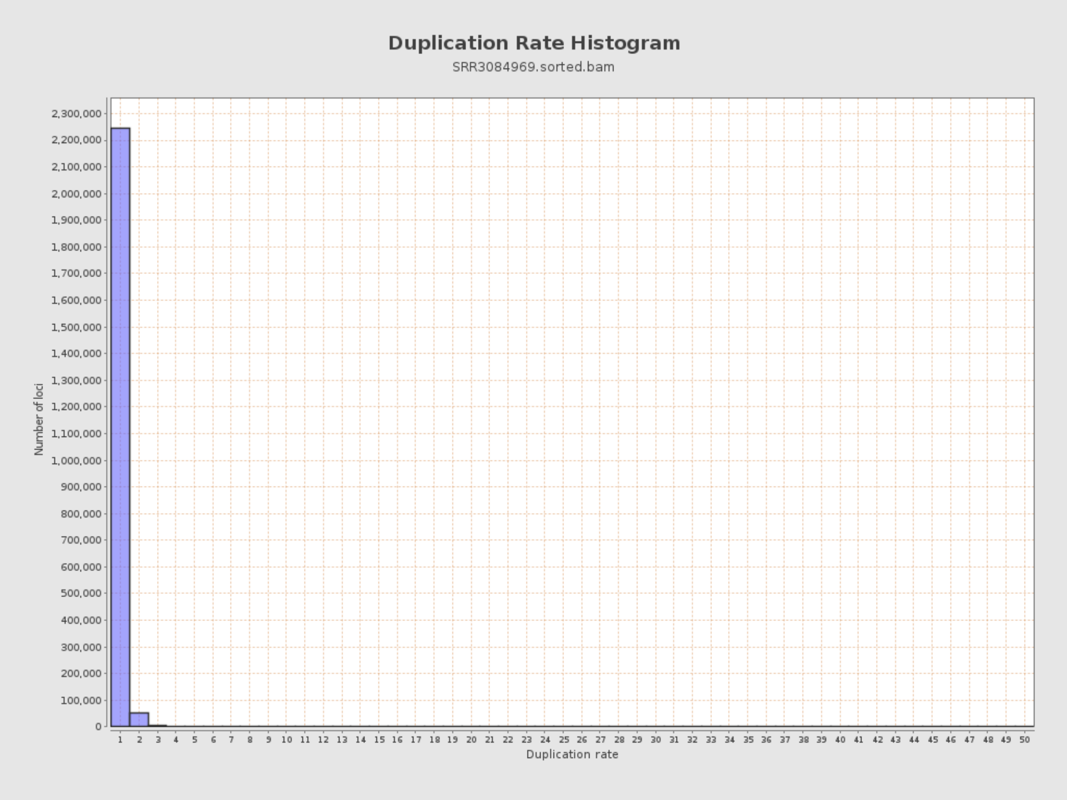
5. Results : Coverage Histogram (0-50X)



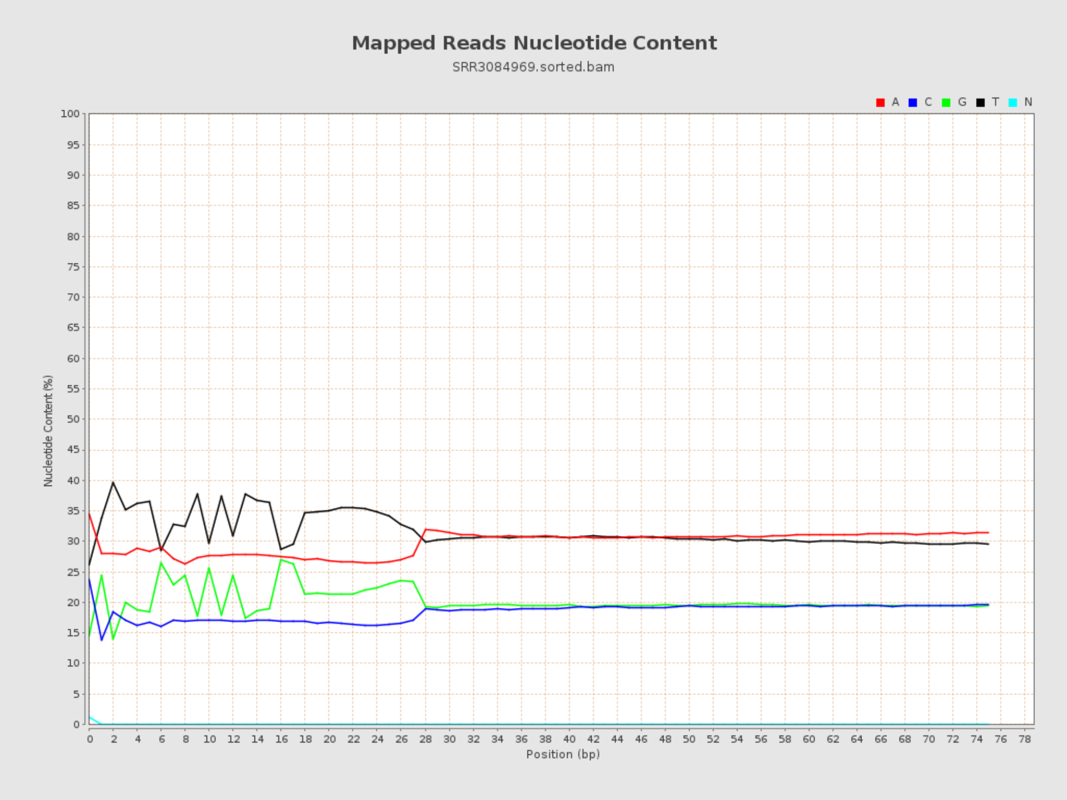
6. Results : Genome Fraction Coverage



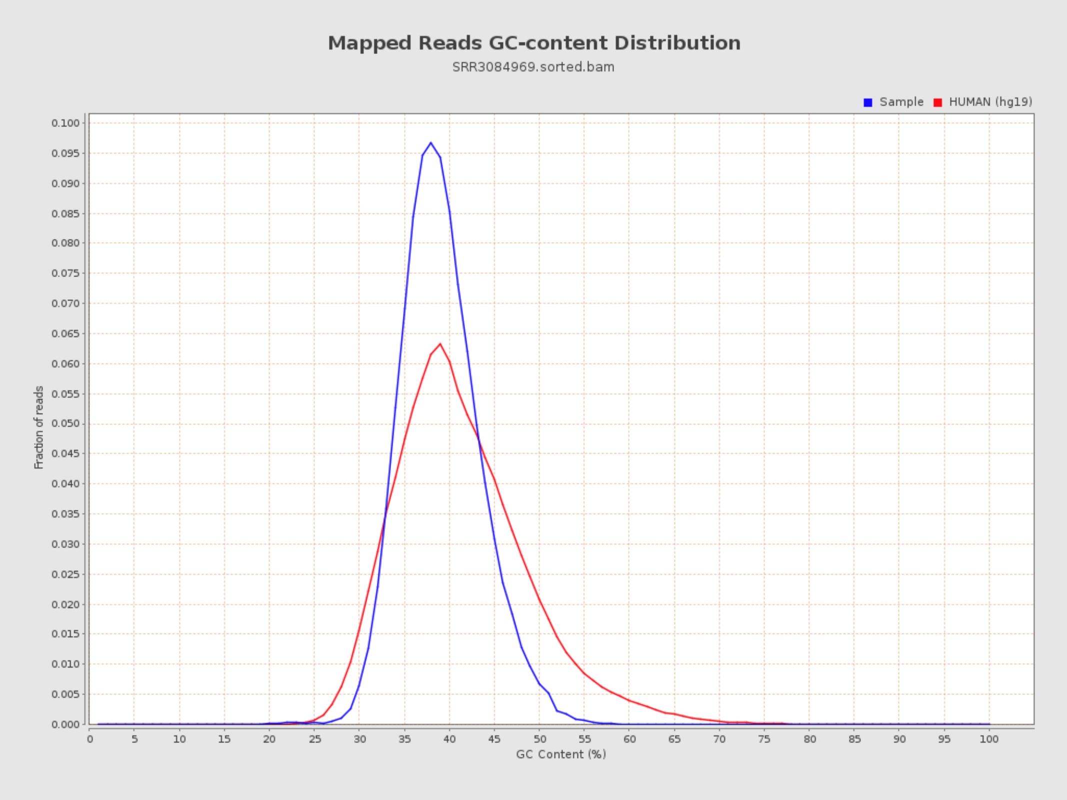
7. Results : Duplication Rate Histogram



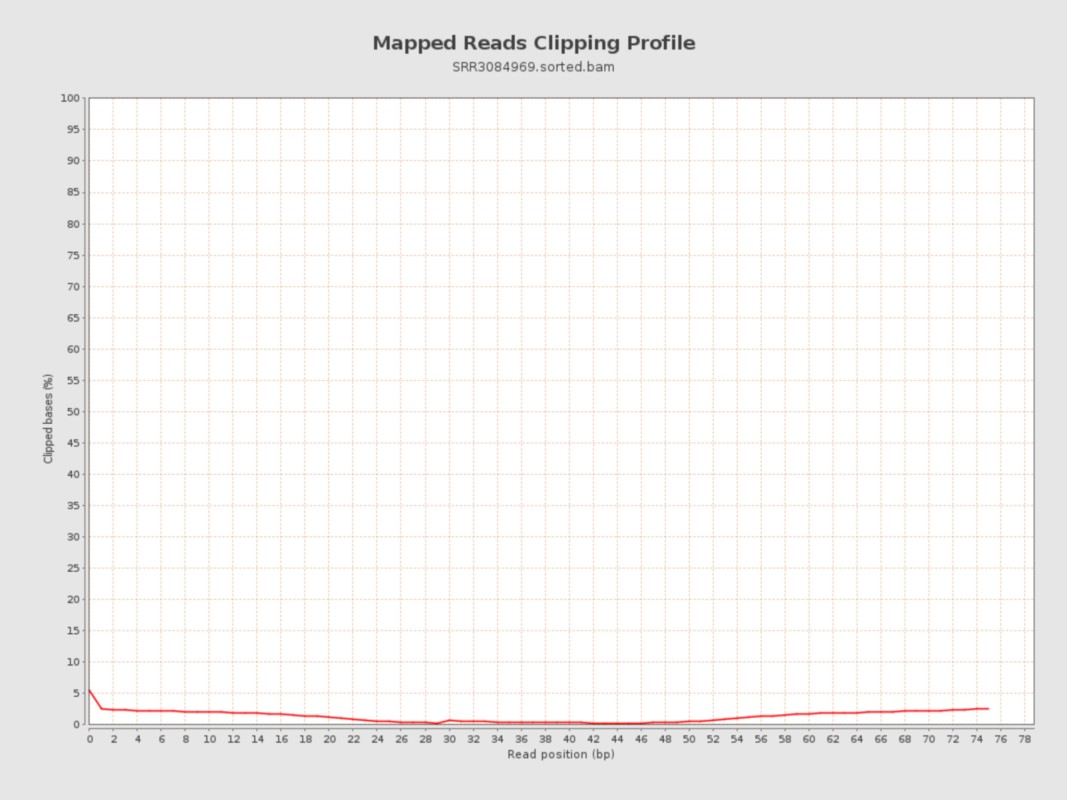
8. Results : Mapped Reads Nucleotide Content



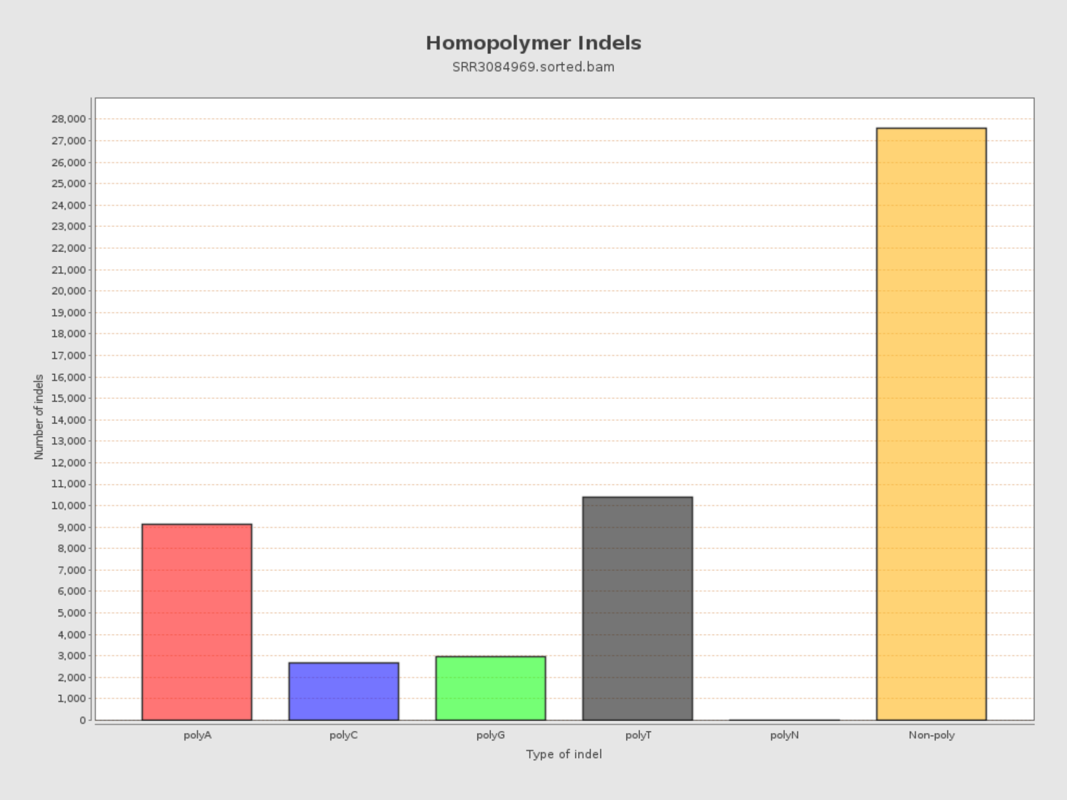
9. Results : Mapped Reads GC-content Distribution



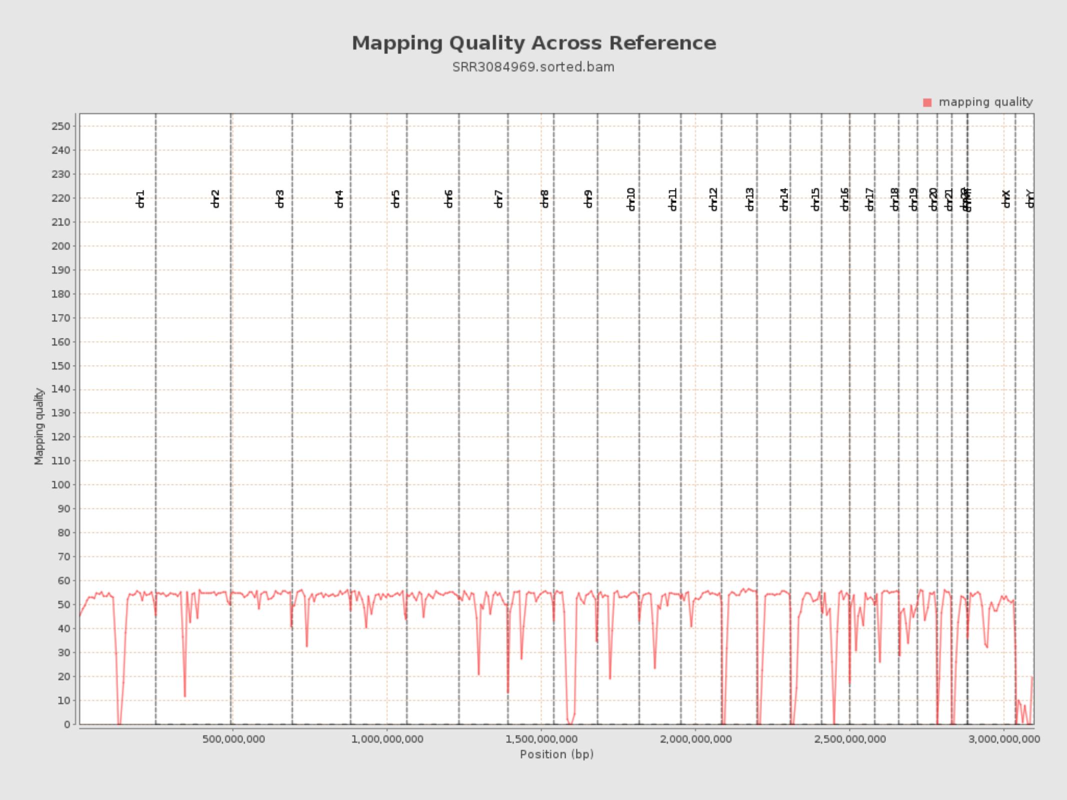
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram