Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 08:54:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084268.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_SRR3084268 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084268.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 08:54:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084268.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,941,321
Mapped reads	1,592,892 / 82.05%
Unmapped reads	348,429 / 17.95%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,161 / 0.52%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	54,115 / 2.79%
Duplication rate	2.72%
Clipped reads	886,616 / 45.67%

2.2. ACGT Content

Number/percentage of A's	29,119,234 / 28.69%
Number/percentage of C's	19,157,348 / 18.88%
Number/percentage of T's	30,888,536 / 30.44%
Number/percentage of G's	22,318,217 / 21.99%
Number/percentage of N's	1,092 / 0%
GC Percentage	40.87%

2.3. Coverage

Mean	0.0328

Standard Deviation	0.2726

2.4. Mapping Quality

Mean Mapping Quality	45.62

2.5. Mismatches and indels

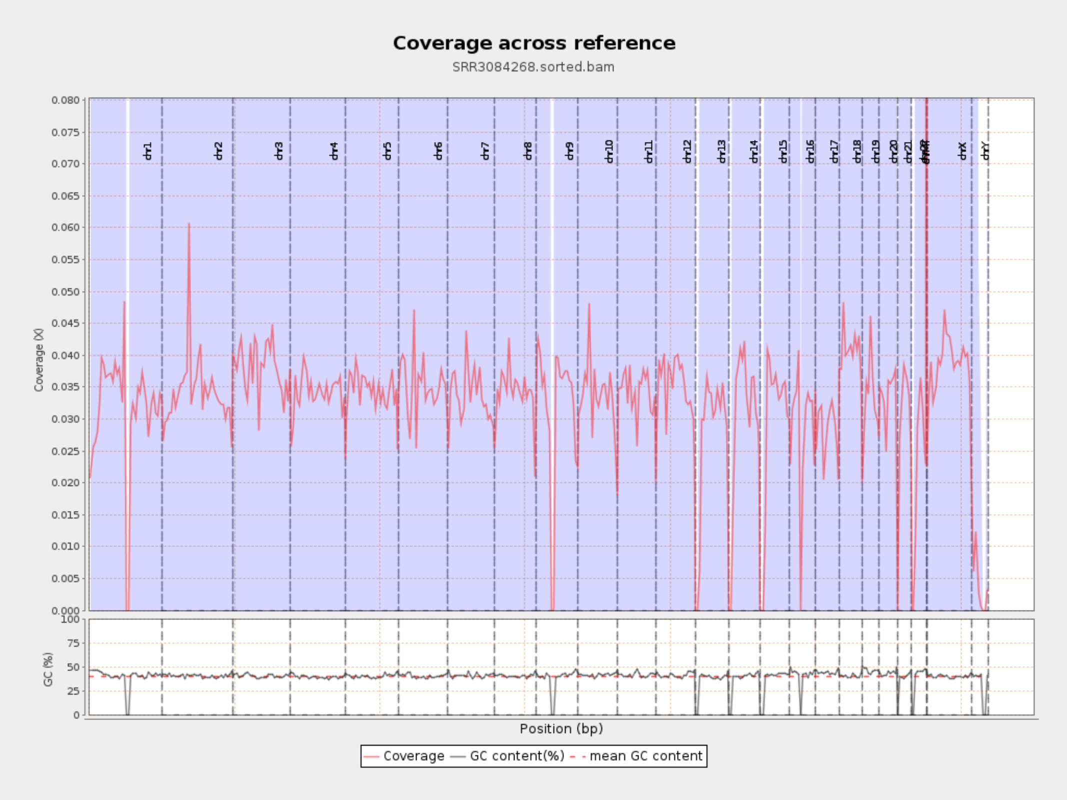
General error rate	0.87%
Mismatches	867,961
Insertions	8,013
Mapped reads with at least one insertion	0.5%
Deletions	22,371
Mapped reads with at least one deletion	1.39%
Homopolymer indels	45.68%

2.6. Chromosome stats

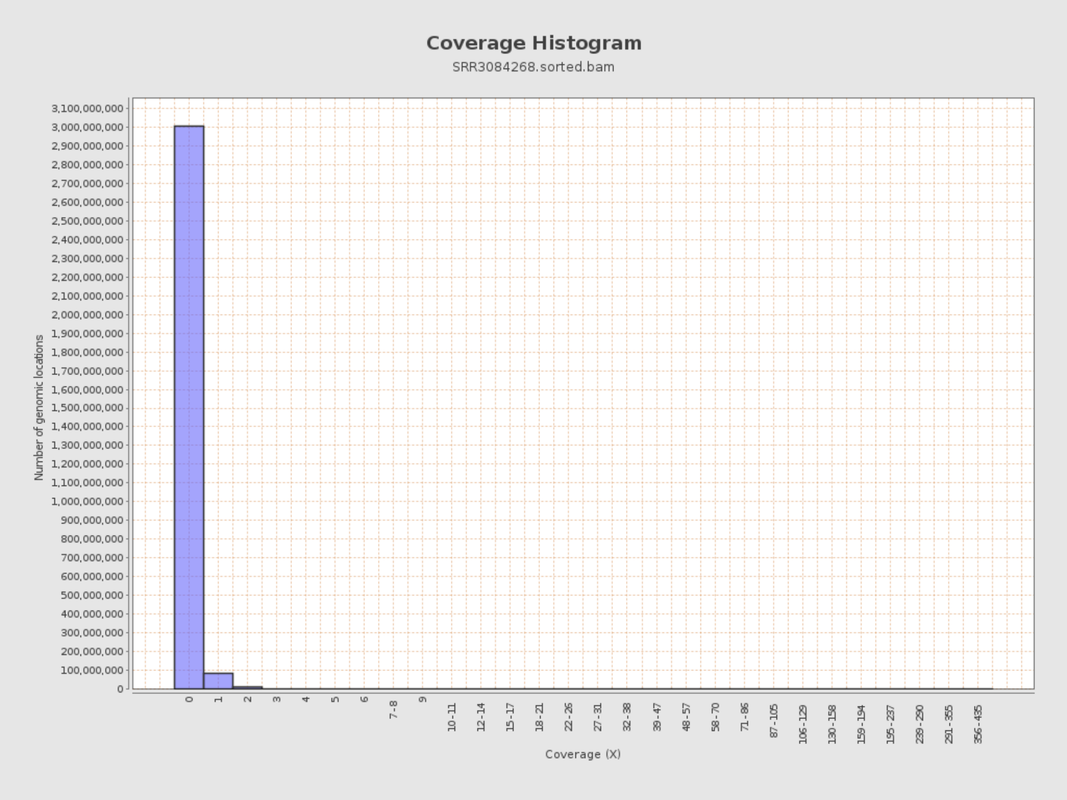
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7862080	0.0315	0.406
chr2	243199373	8376859	0.0344	0.3514
chr3	198022430	7545705	0.0381	0.2142
chr4	191154276	6527234	0.0341	0.2091
chr5	180915260	6255497	0.0346	0.2043
chr6	171115067	6029980	0.0352	0.2446
chr7	159138663	5413830	0.034	0.2813

chr8	146364022	4998449	0.0342	0.2934
chr9	141213431	4473734	0.0317	0.2672
chr10	135534747	4603007	0.034	0.2724
chr11	135006516	4602360	0.0341	0.2441
chr12	133851895	4723283	0.0353	0.2085
chr13	115169878	3096840	0.0269	0.1816
chr14	107349540	3193143	0.0297	0.2047
chr15	102531392	2951179	0.0288	0.1898
chr16	90354753	2578976	0.0285	0.2145
chr17	81195210	2266297	0.0279	0.1906
chr18	78077248	3213445	0.0412	0.5612
chr19	59128983	1991504	0.0337	0.3161
chr20	63025520	2102328	0.0334	0.206
chr21	48129895	1426284	0.0296	0.1964
chr22	51304566	1074684	0.0209	0.1571
chrMT	16571	5660	0.3416	0.5966
chrX	155270560	5958317	0.0384	0.2348
chrY	59373566	249397	0.0042	0.0915

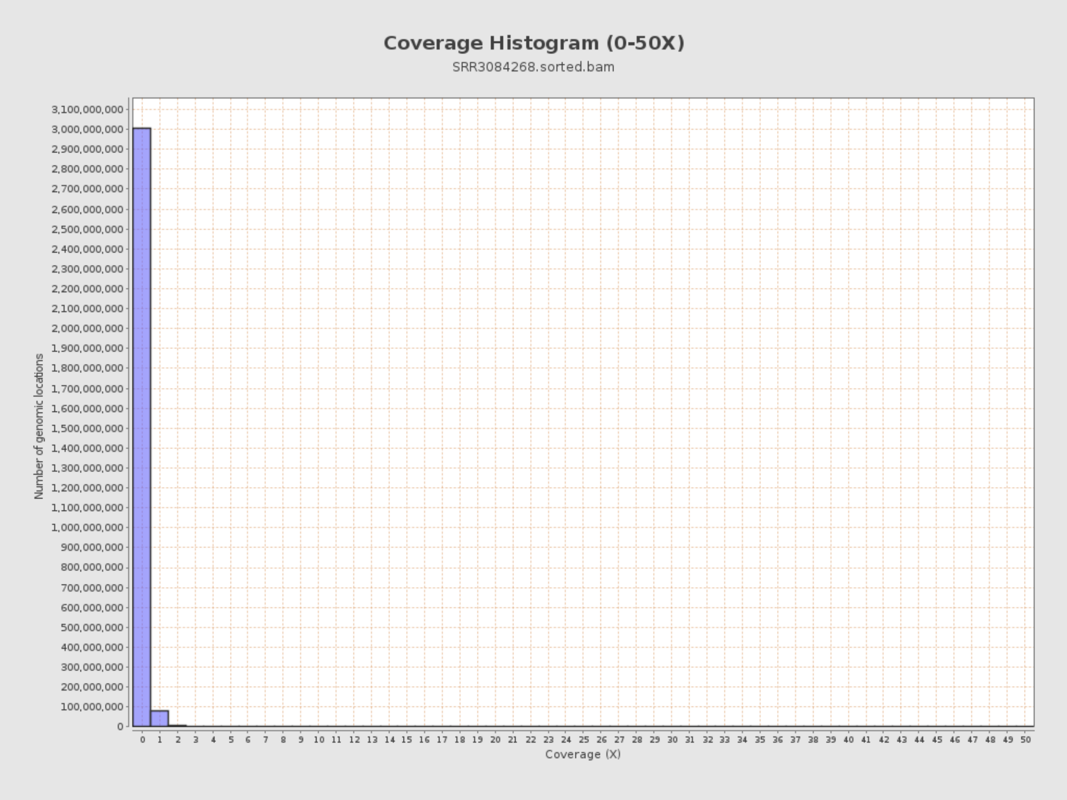
3. Results : Coverage across reference



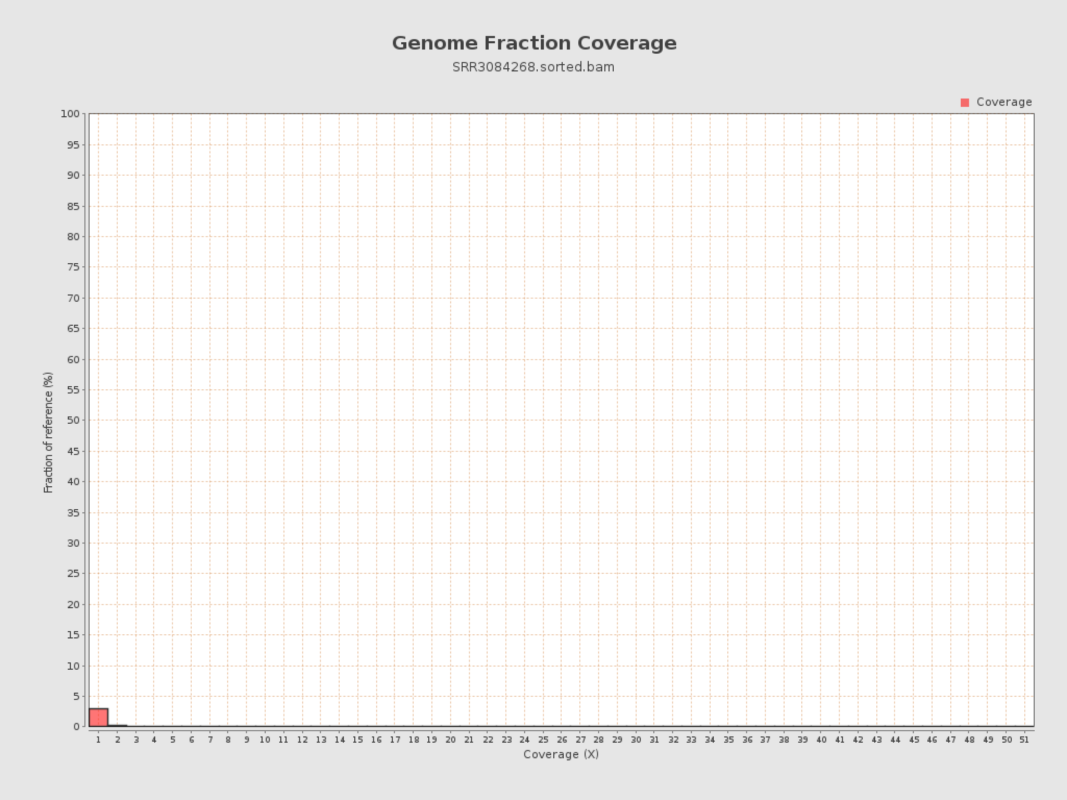
4. Results : Coverage Histogram



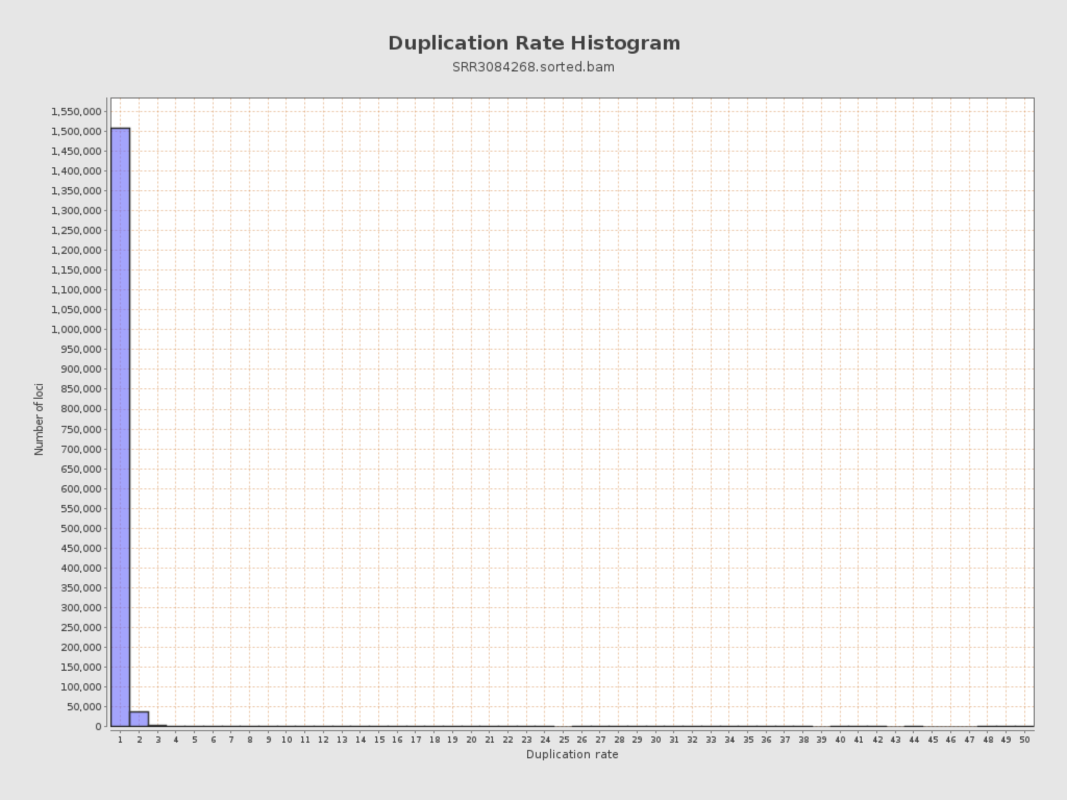
5. Results : Coverage Histogram (0-50X)



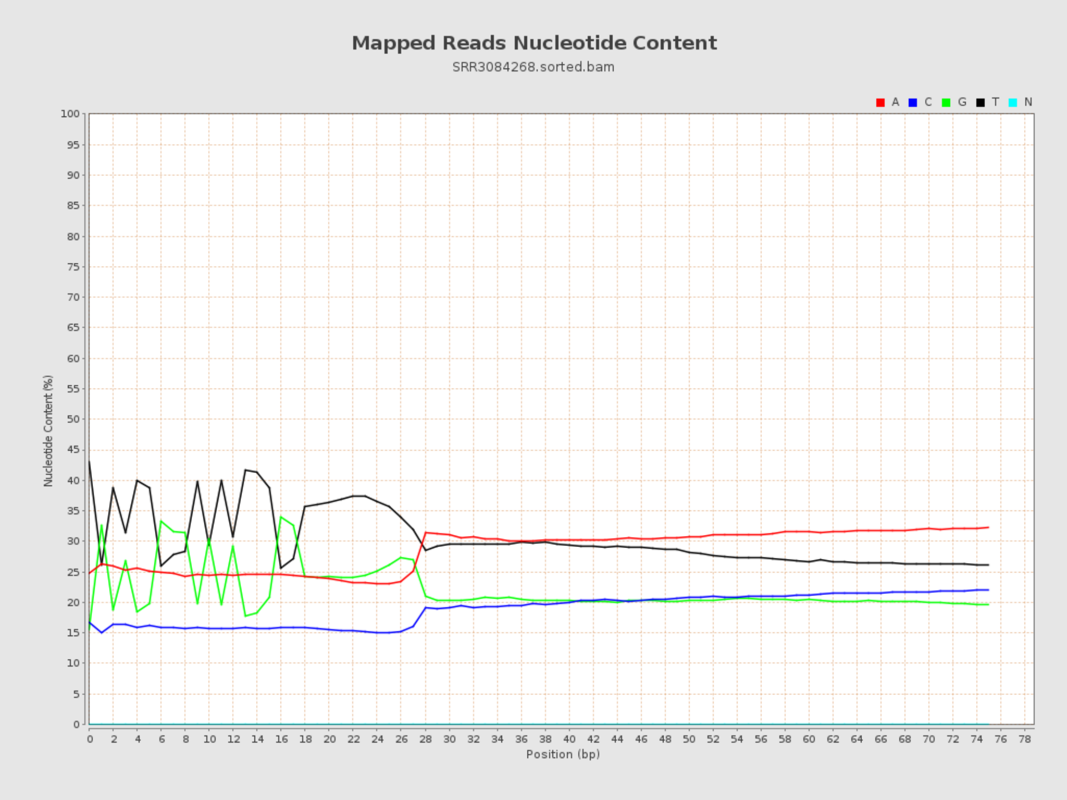
6. Results : Genome Fraction Coverage



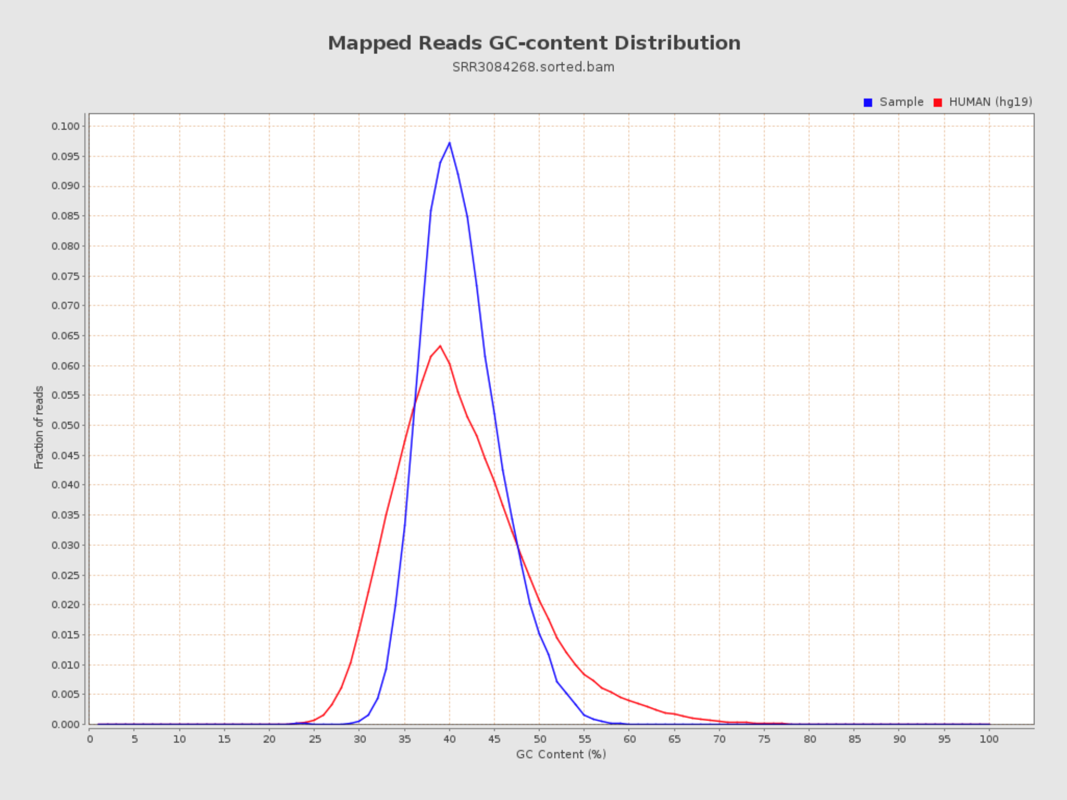
7. Results : Duplication Rate Histogram



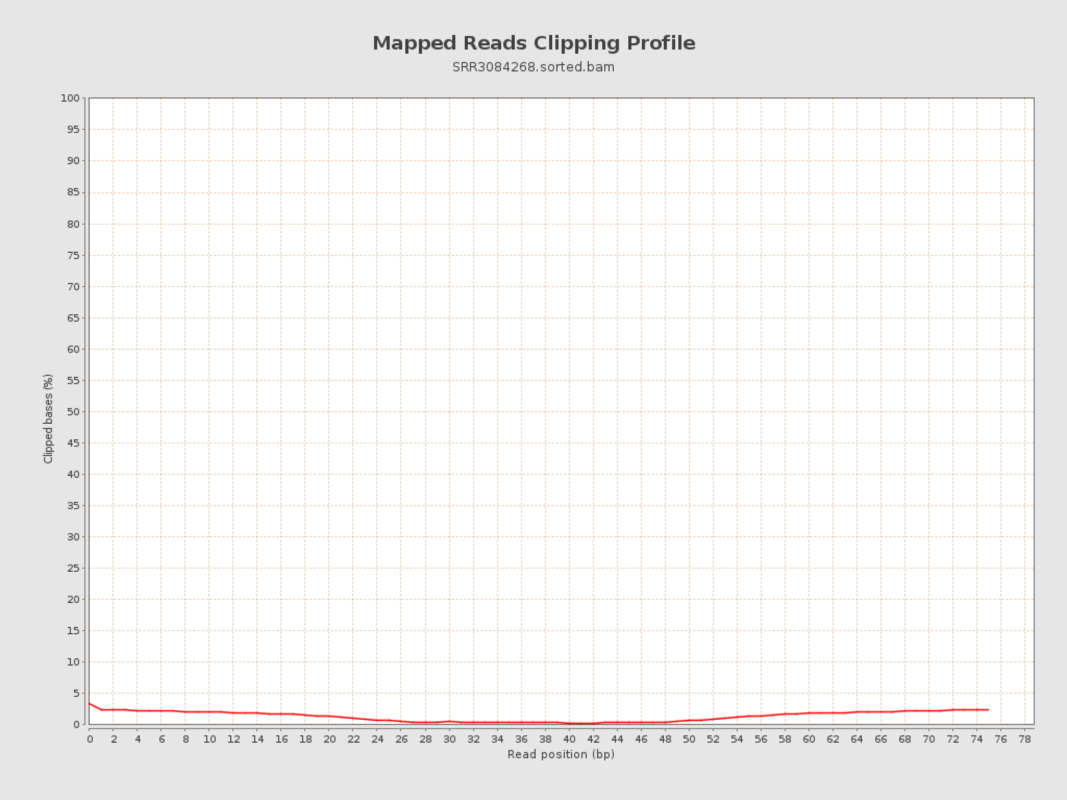
8. Results : Mapped Reads Nucleotide Content



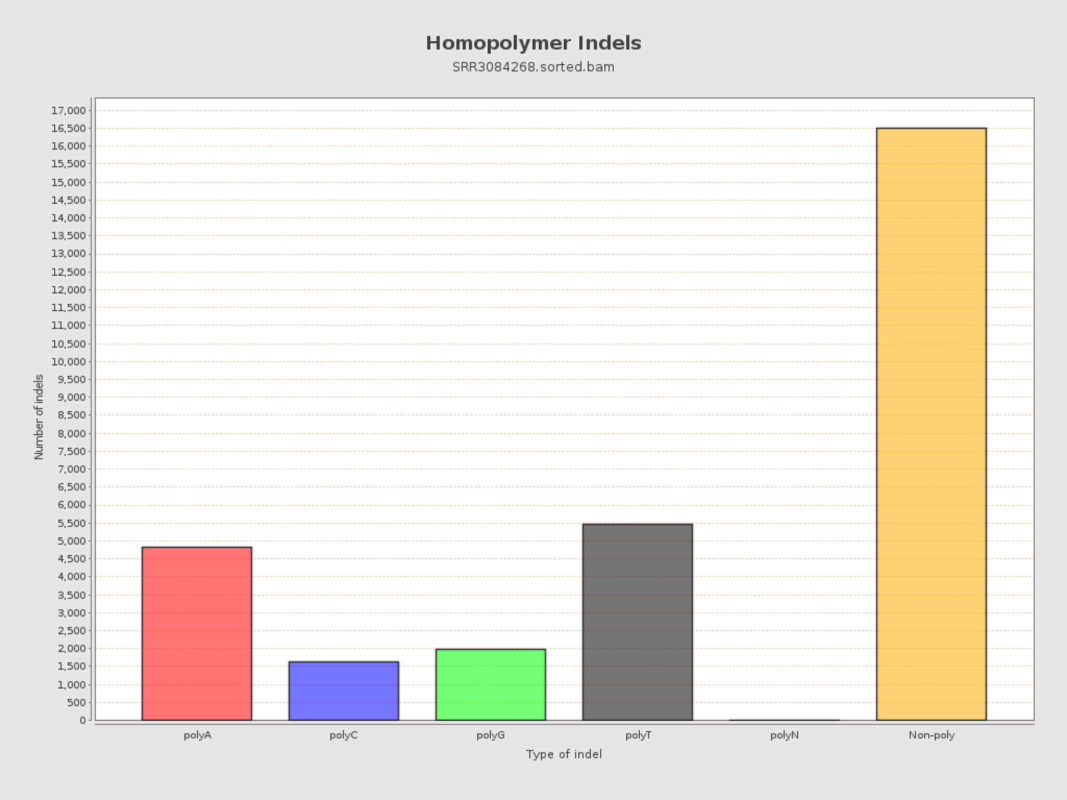
9. Results : Mapped Reads GC-content Distribution



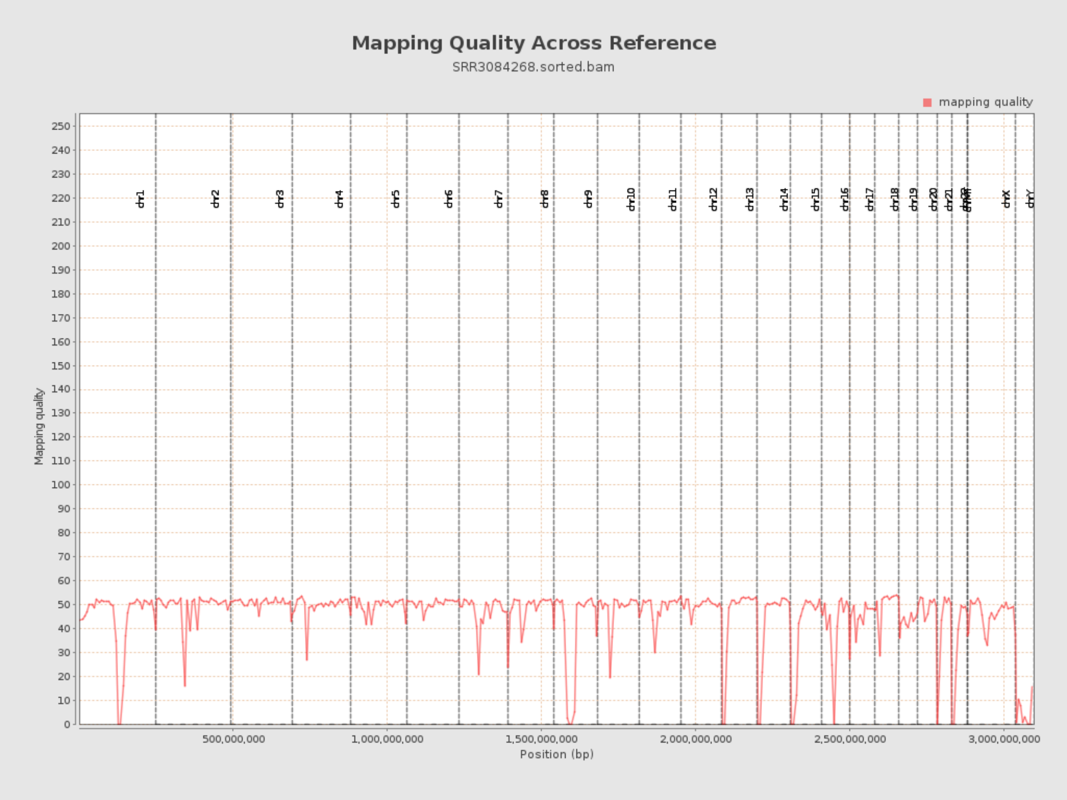
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram