Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 23:55:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081162.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_SRR3081162 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081162.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 23:55:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081162.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,348,994
Mapped reads	2,114,565 / 90.02%
Unmapped reads	234,429 / 9.98%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,045 / 0.81%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	75,799 / 3.23%
Duplication rate	2.79%
Clipped reads	908,554 / 38.68%

2.2. ACGT Content

Number/percentage of A's	40,223,013 / 28.23%
Number/percentage of C's	26,558,218 / 18.64%
Number/percentage of T's	44,386,510 / 31.15%
Number/percentage of G's	31,282,067 / 21.95%
Number/percentage of N's	42,910 / 0.03%
GC Percentage	40.59%

2.3. Coverage

Mean	0.046

Standard Deviation	0.3599

2.4. Mapping Quality

Mean Mapping Quality	46.28

2.5. Mismatches and indels

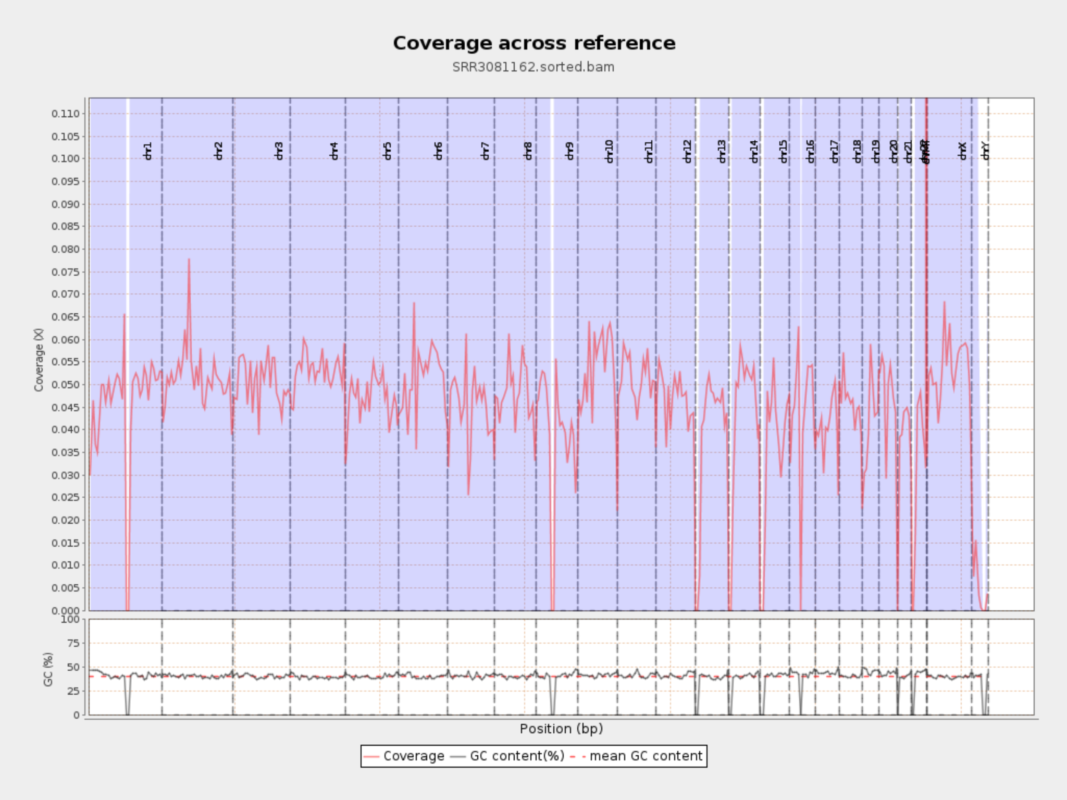
General error rate	0.84%
Mismatches	1,172,451
Insertions	11,115
Mapped reads with at least one insertion	0.52%
Deletions	33,173
Mapped reads with at least one deletion	1.55%
Homopolymer indels	47.28%

2.6. Chromosome stats

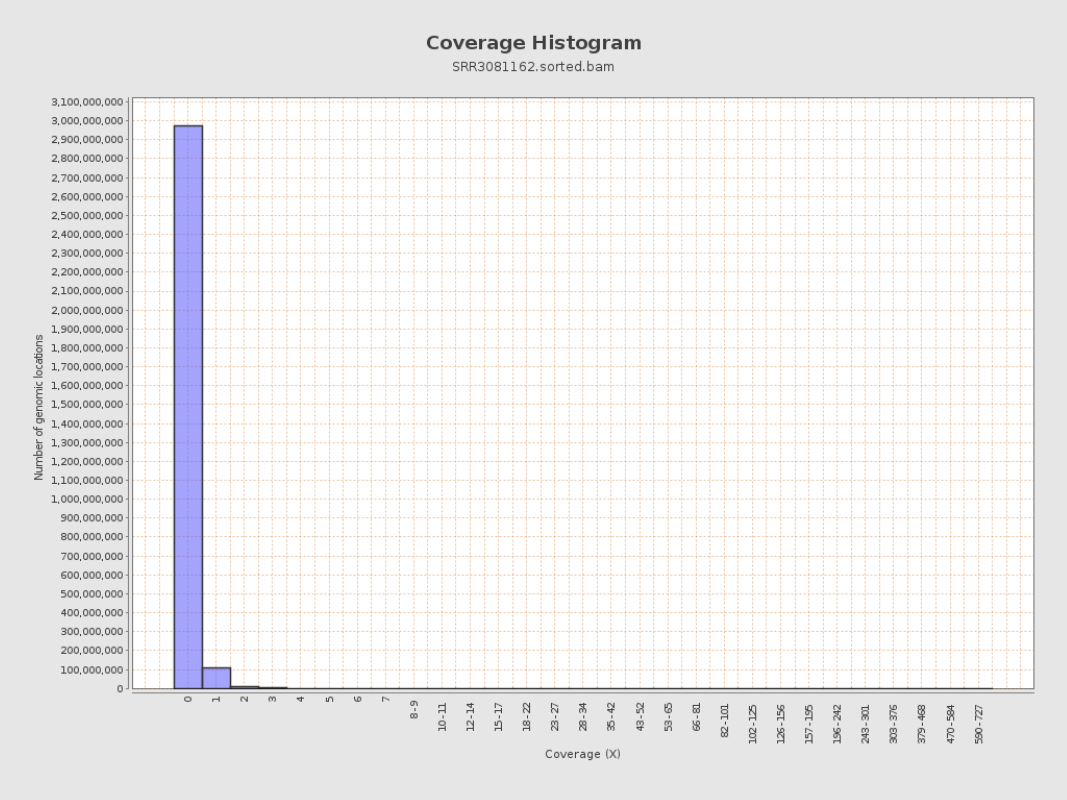
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11355092	0.0456	0.5686
chr2	243199373	12639660	0.052	0.4508
chr3	198022430	10024260	0.0506	0.2489
chr4	191154276	10171214	0.0532	0.2642
chr5	180915260	8577842	0.0474	0.2429
chr6	171115067	8807197	0.0515	0.3143
chr7	159138663	7213997	0.0453	0.4265

chr8	146364022	7015837	0.0479	0.4985
chr9	141213431	5427622	0.0384	0.3453
chr10	135534747	7349149	0.0542	0.3296
chr11	135006516	6885125	0.051	0.3509
chr12	133851895	6260363	0.0468	0.2462
chr13	115169878	4408083	0.0383	0.2169
chr14	107349540	4576576	0.0426	0.2558
chr15	102531392	3590917	0.035	0.2147
chr16	90354753	3993412	0.0442	0.2619
chr17	81195210	3283227	0.0404	0.2726
chr18	78077248	3625450	0.0464	0.6546
chr19	59128983	2477673	0.0419	0.4404
chr20	63025520	2965424	0.0471	0.25
chr21	48129895	1771803	0.0368	0.2297
chr22	51304566	1507437	0.0294	0.1895
chrMT	16571	24926	1.5042	1.4461
chrX	155270560	8277522	0.0533	0.284
chrY	59373566	316471	0.0053	0.1102

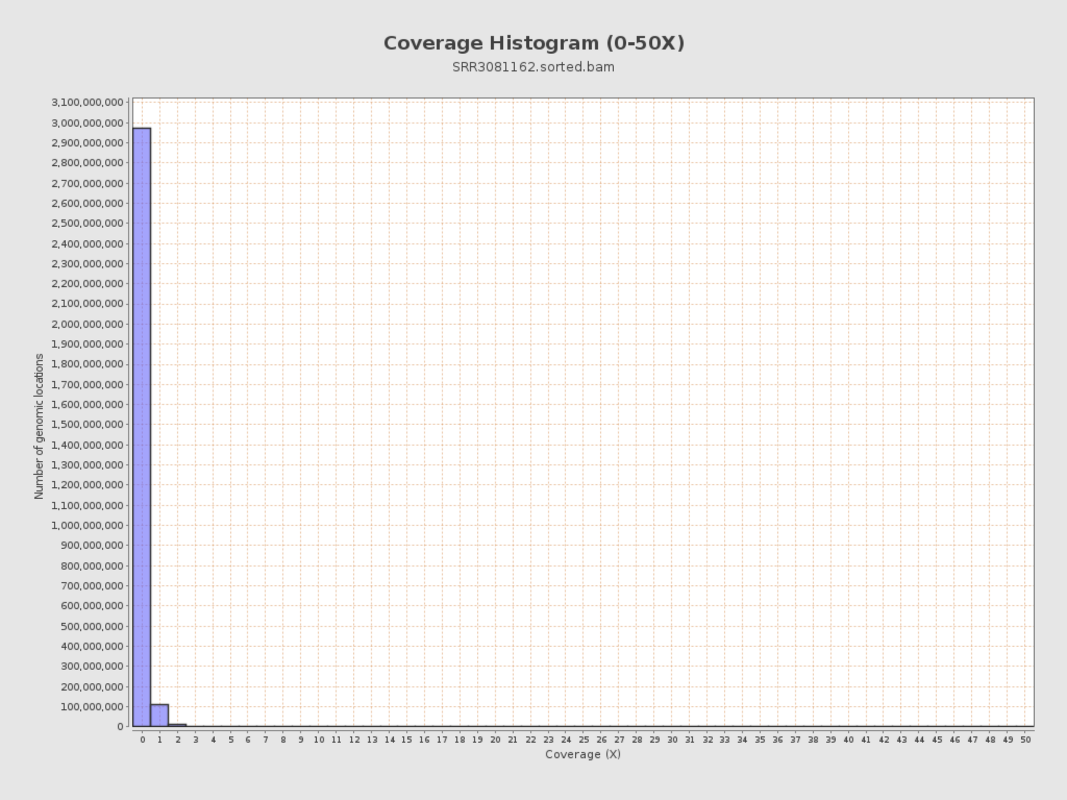
3. Results : Coverage across reference



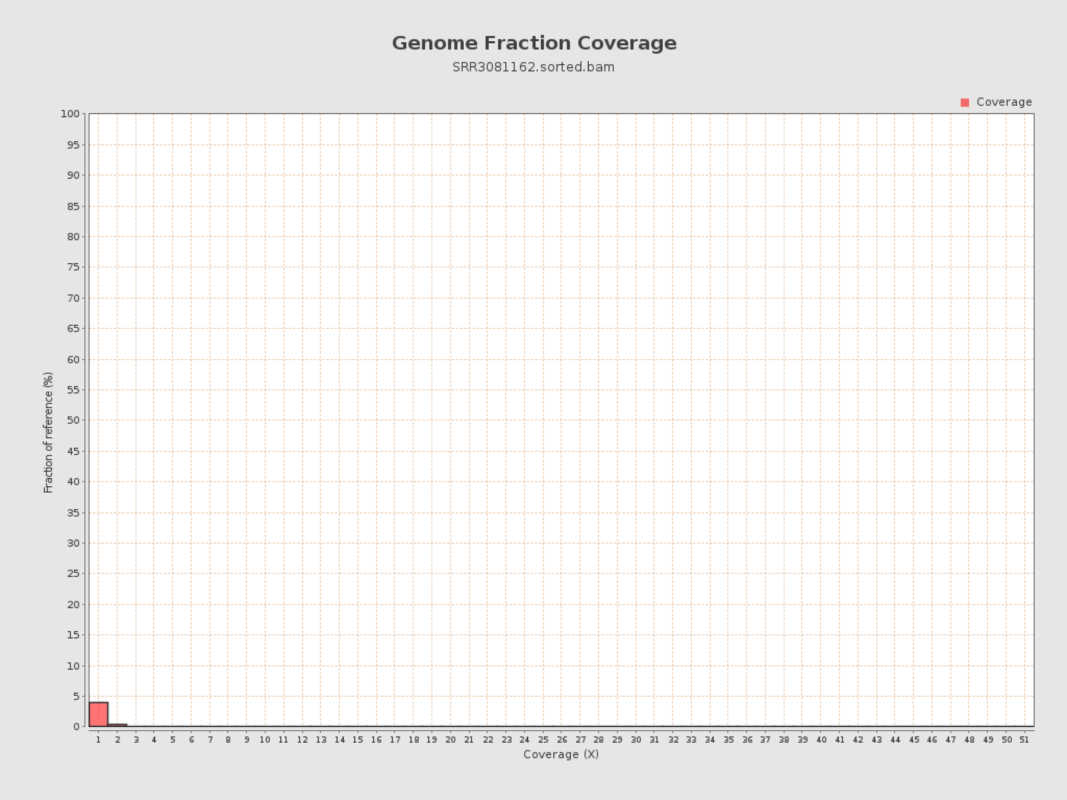
4. Results : Coverage Histogram



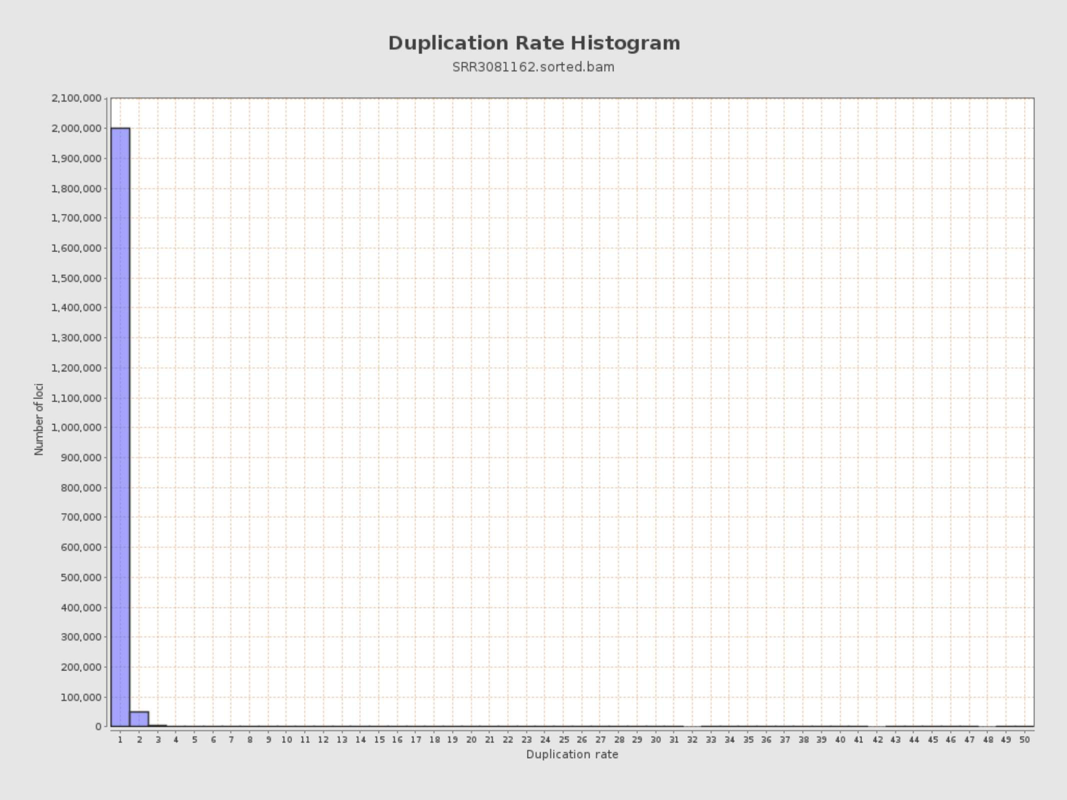
5. Results : Coverage Histogram (0-50X)



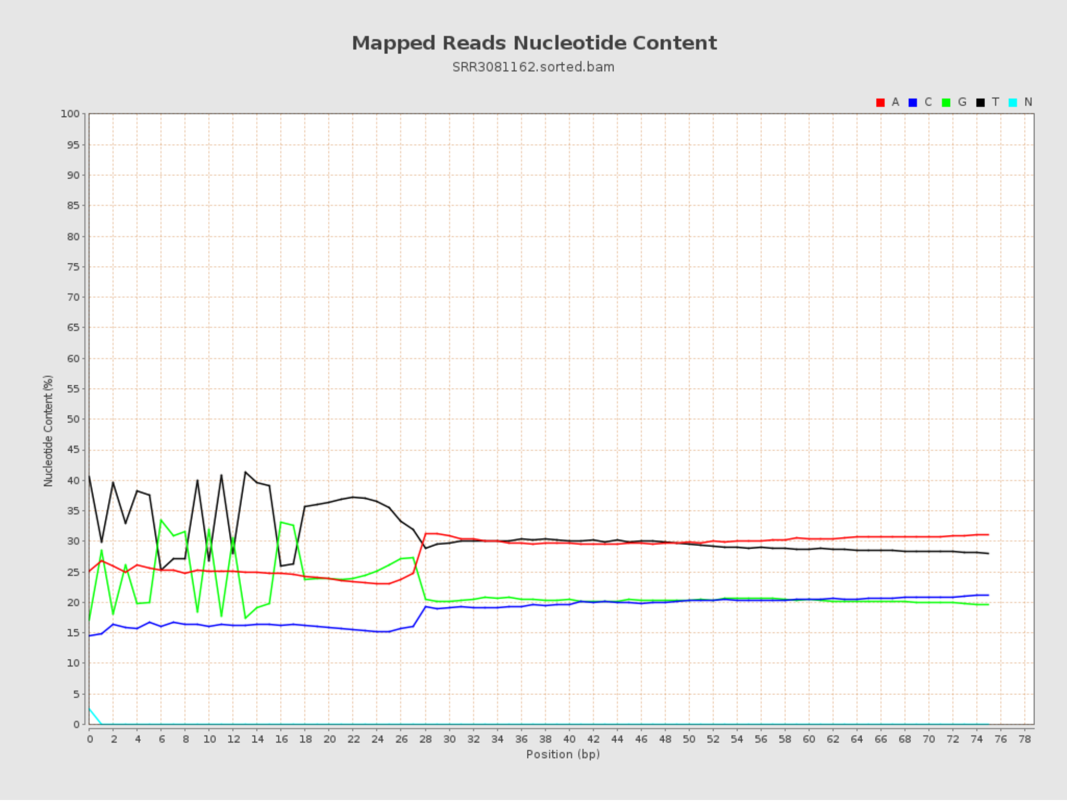
6. Results : Genome Fraction Coverage



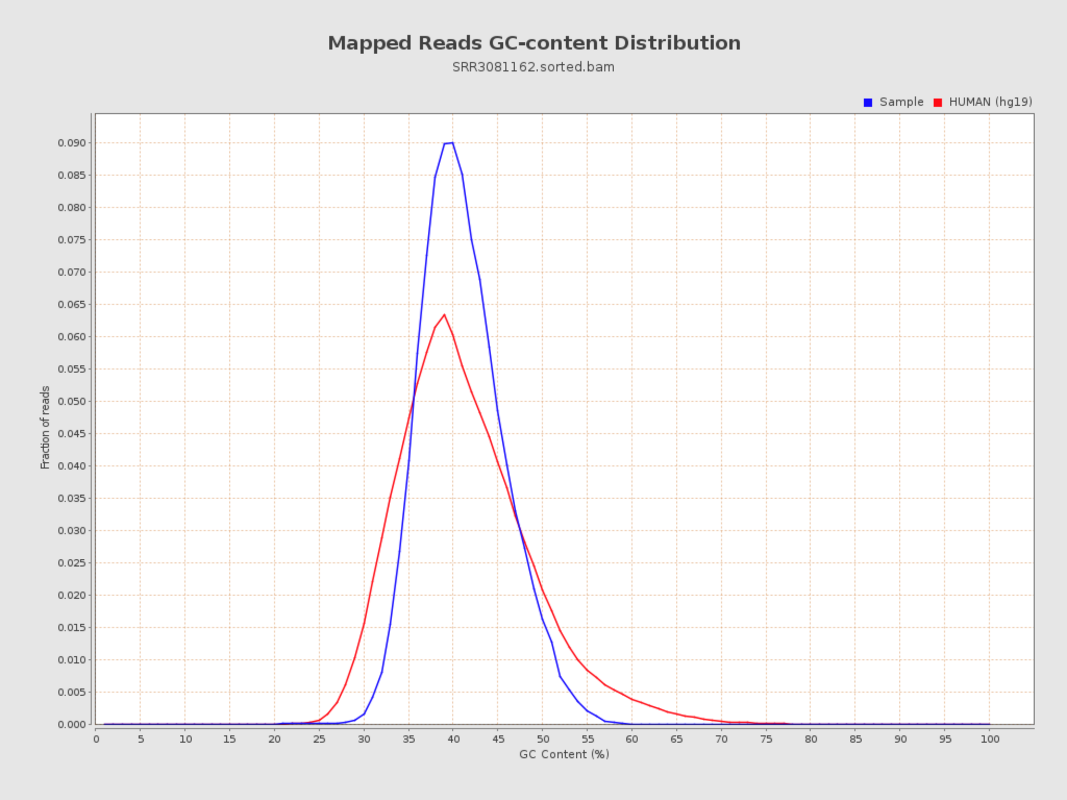
7. Results : Duplication Rate Histogram



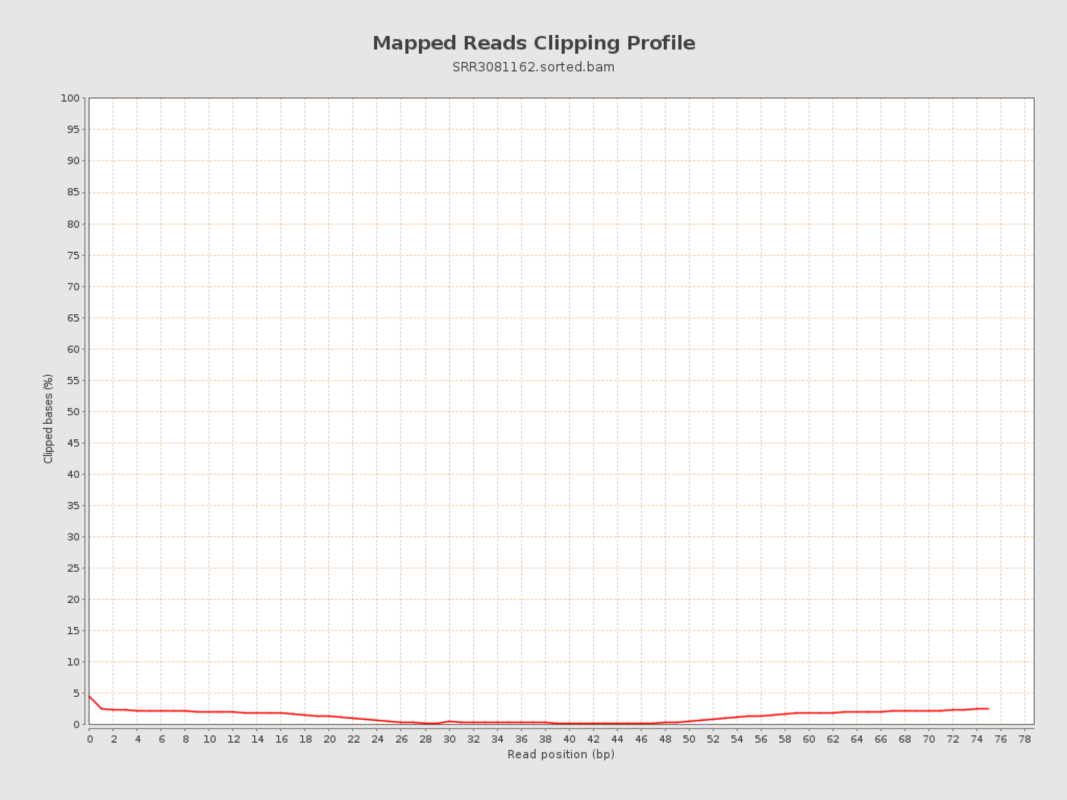
8. Results : Mapped Reads Nucleotide Content



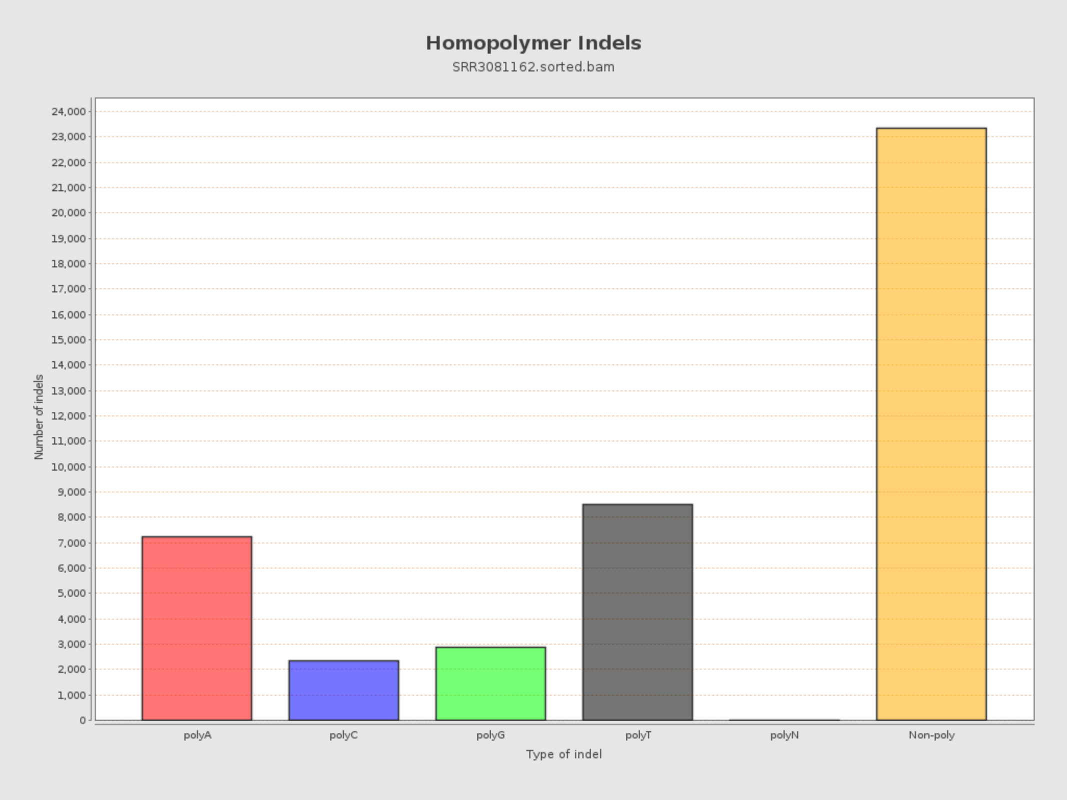
9. Results : Mapped Reads GC-content Distribution



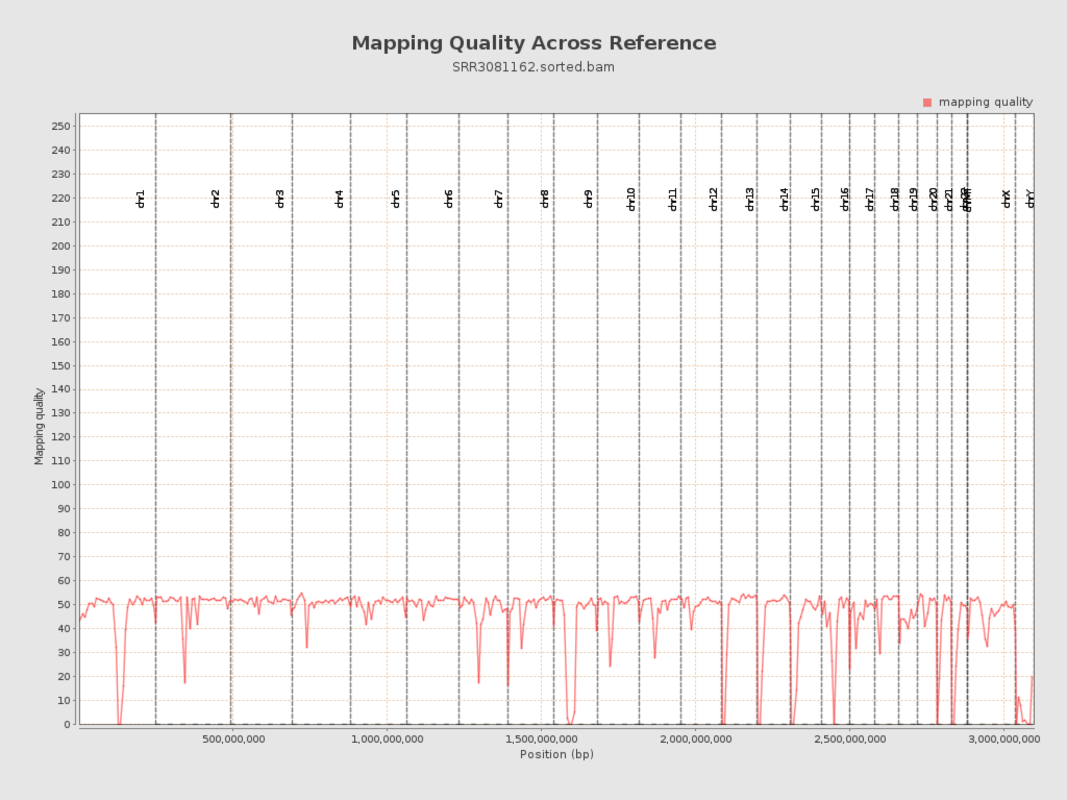
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram