Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 16:58:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068950.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_SRR6068950 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068950.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 16:58:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068950.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,138,963
Mapped reads	1,721,125 / 80.47%
Unmapped reads	417,838 / 19.53%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,329 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	61,799 / 2.89%
Duplication rate	2.16%
Clipped reads	895,915 / 41.89%

2.2. ACGT Content

Number/percentage of A's	29,466,706 / 26.4%
Number/percentage of C's	19,337,976 / 17.33%
Number/percentage of T's	36,860,754 / 33.03%
Number/percentage of G's	25,676,877 / 23.01%
Number/percentage of N's	264,300 / 0.24%
GC Percentage	40.33%

2.3. Coverage

Mean	0.0361

Standard Deviation	0.4435

2.4. Mapping Quality

Mean Mapping Quality	44.06

2.5. Mismatches and indels

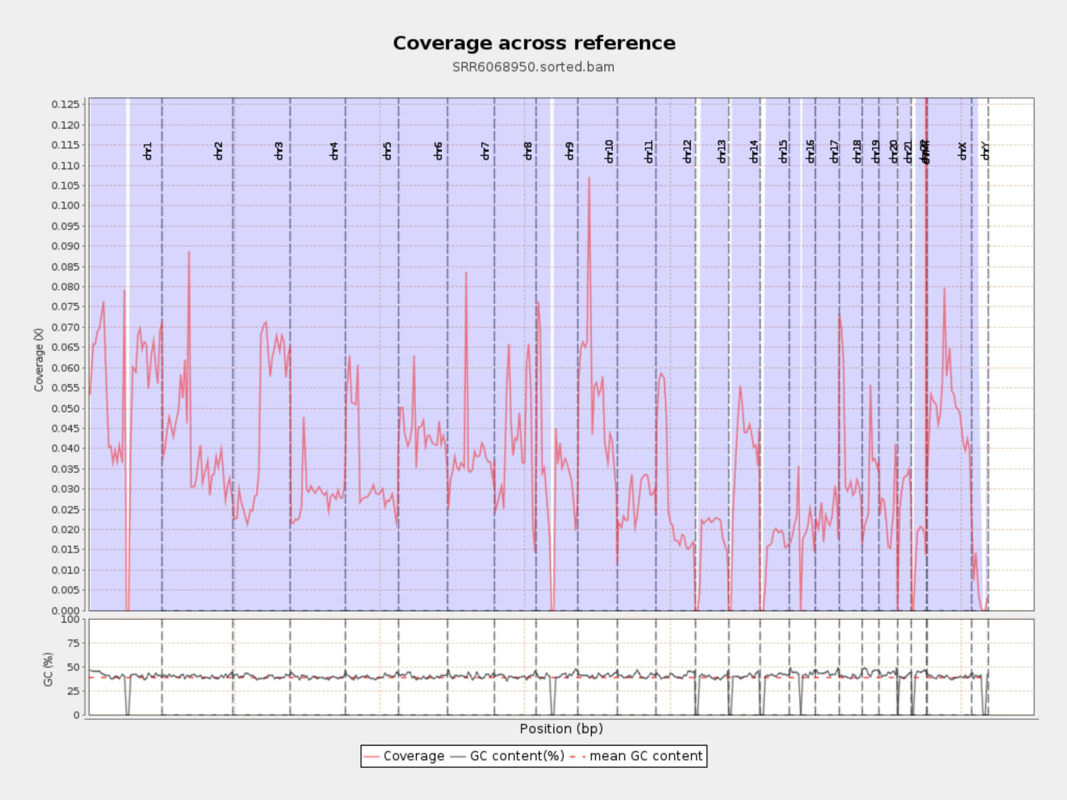
General error rate	0.98%
Mismatches	1,070,503
Insertions	10,634
Mapped reads with at least one insertion	0.61%
Deletions	29,991
Mapped reads with at least one deletion	1.73%
Homopolymer indels	47.92%

2.6. Chromosome stats

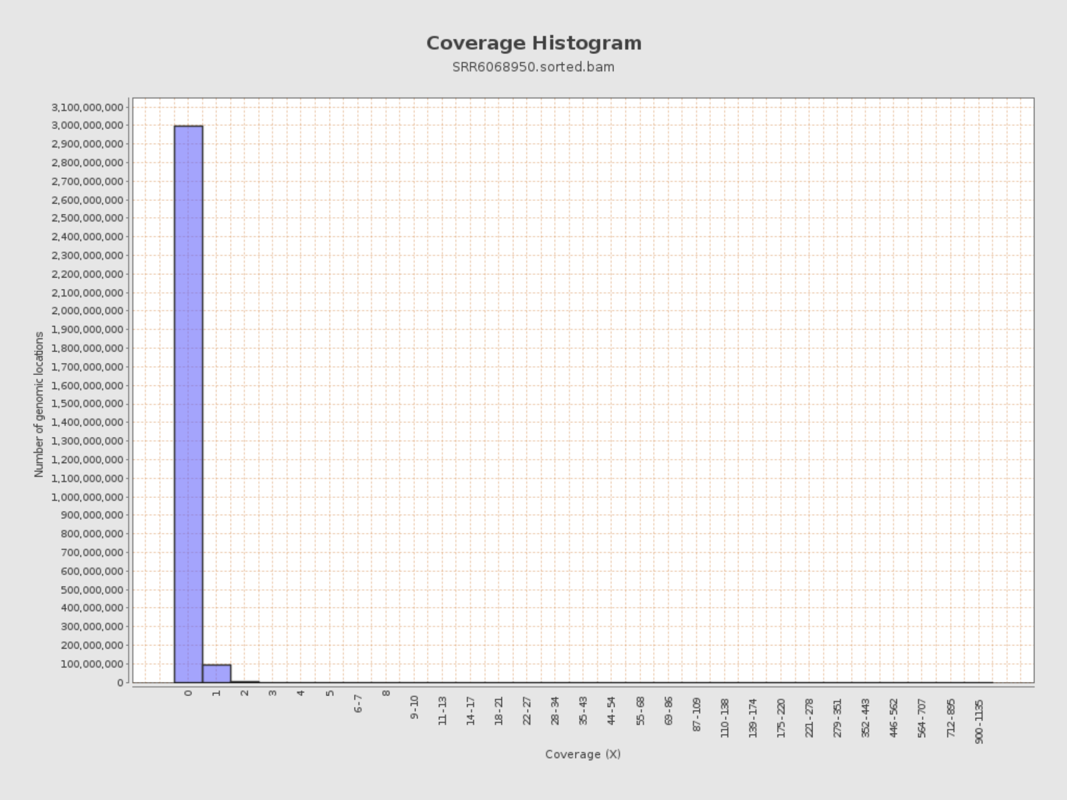
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13657668	0.0548	0.9319
chr2	243199373	9911108	0.0408	0.4293
chr3	198022430	9151736	0.0462	0.2467
chr4	191154276	5408034	0.0283	0.208
chr5	180915260	6293452	0.0348	0.2038
chr6	171115067	7538882	0.0441	0.3187
chr7	159138663	6104986	0.0384	0.6647

chr8	146364022	5929196	0.0405	0.6238
chr9	141213431	4790885	0.0339	0.4074
chr10	135534747	7416507	0.0547	0.54
chr11	135006516	3651765	0.027	0.3049
chr12	133851895	3775029	0.0282	0.1961
chr13	115169878	1996783	0.0173	0.1397
chr14	107349540	4012207	0.0374	0.2362
chr15	102531392	1477446	0.0144	0.1289
chr16	90354753	1775740	0.0197	0.1998
chr17	81195210	1861280	0.0229	0.1788
chr18	78077248	3062976	0.0392	0.6635
chr19	59128983	1920153	0.0325	0.5848
chr20	63025520	1593403	0.0253	0.1924
chr21	48129895	1343809	0.0279	0.2091
chr22	51304566	721470	0.0141	0.1292
chrMT	16571	185149	11.1731	6.988
chrX	155270560	7773351	0.0501	0.3034
chrY	59373566	303370	0.0051	0.1244

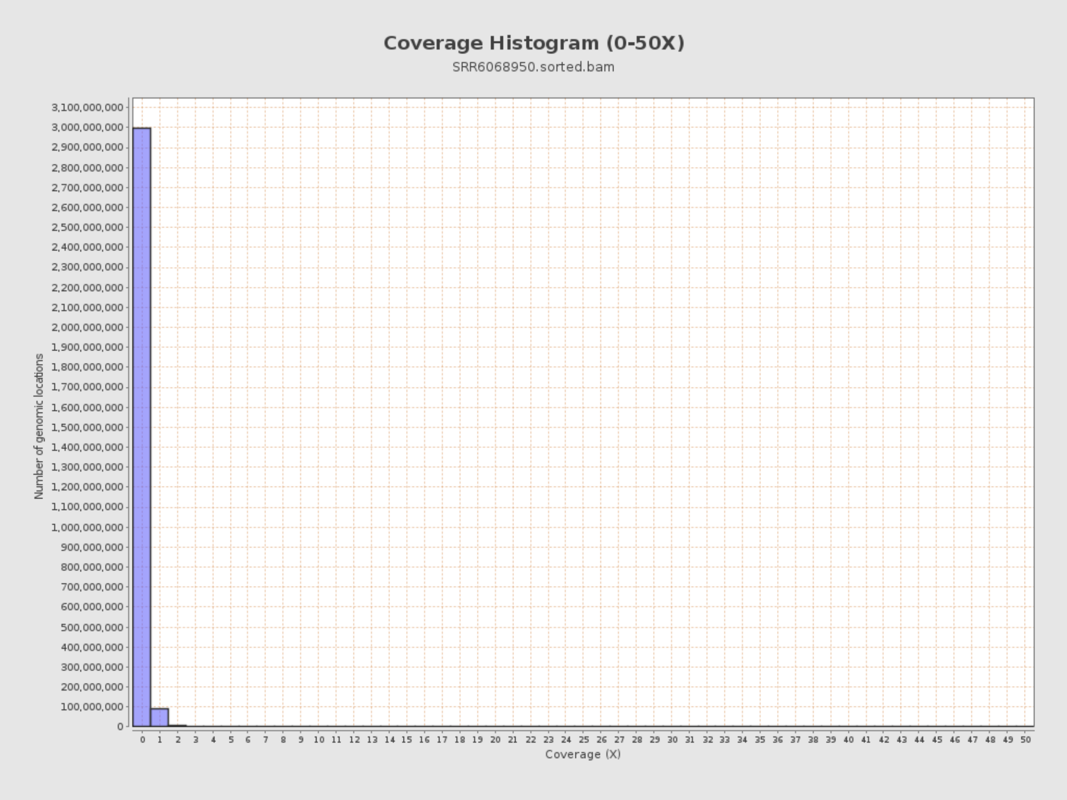
3. Results : Coverage across reference



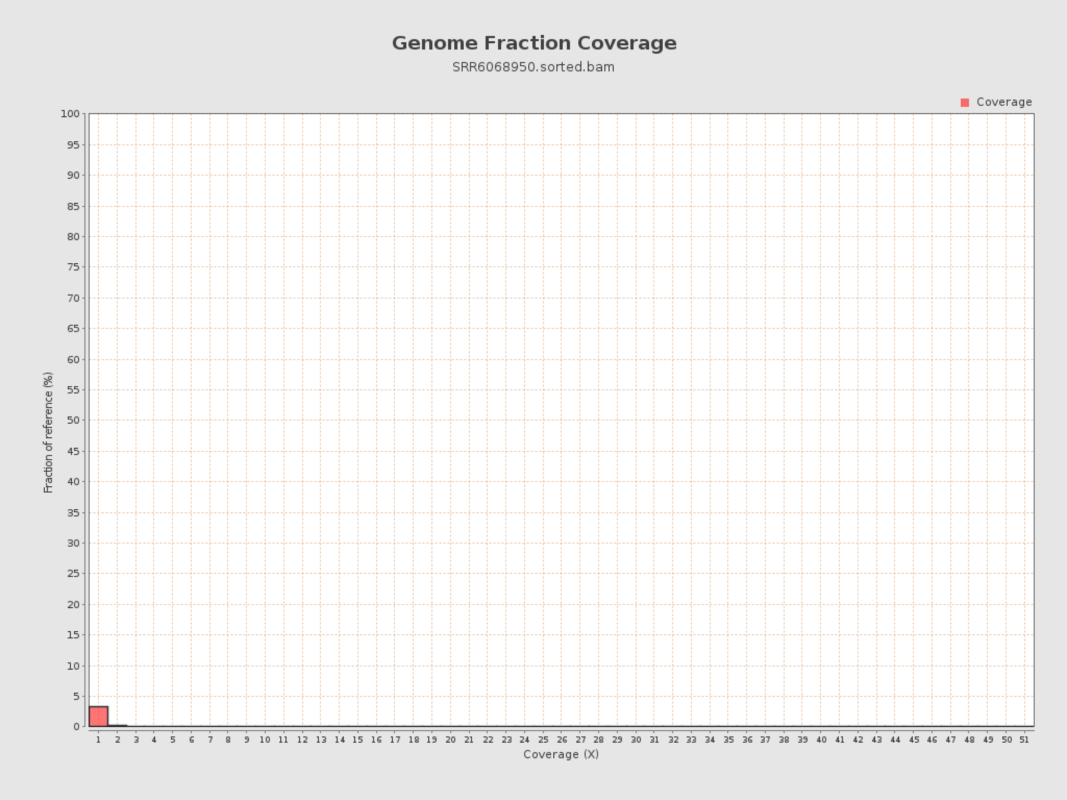
4. Results : Coverage Histogram



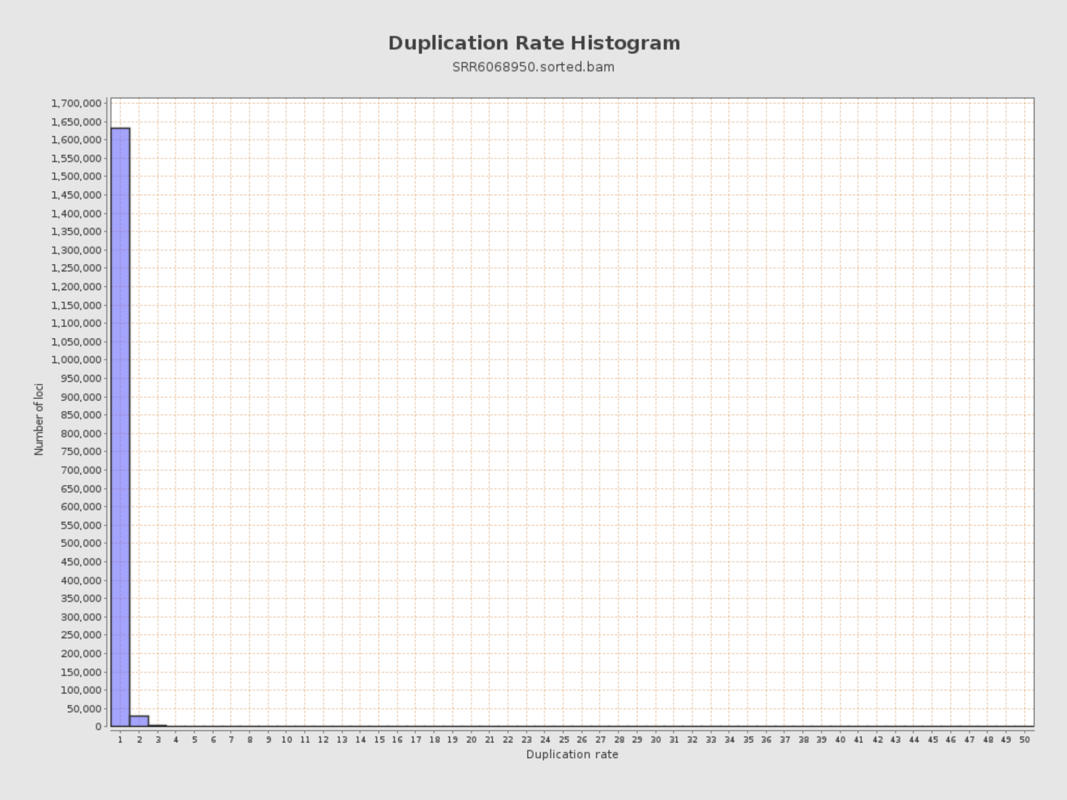
5. Results : Coverage Histogram (0-50X)



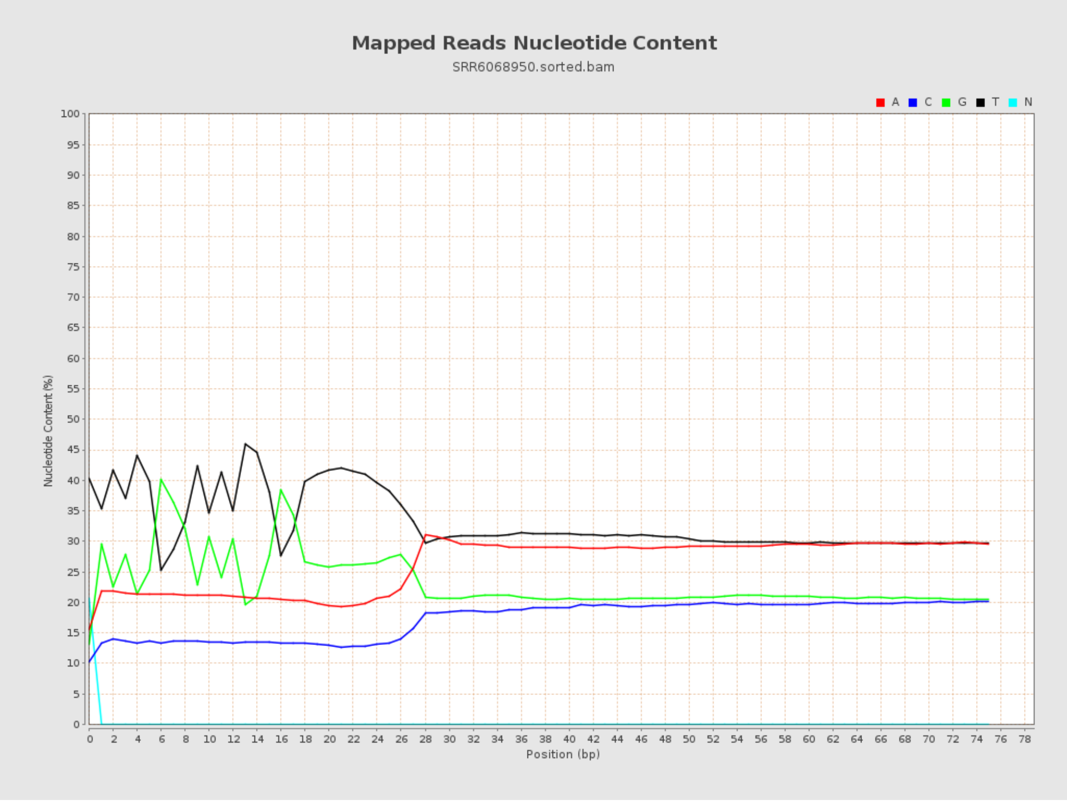
6. Results : Genome Fraction Coverage



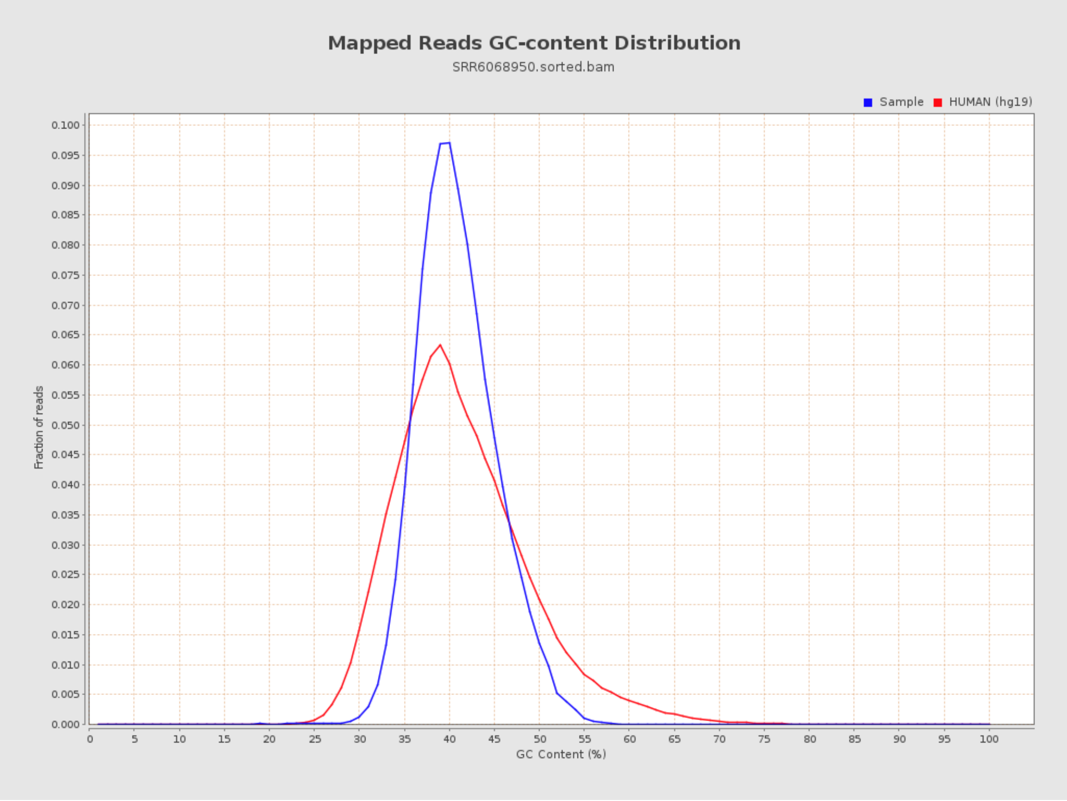
7. Results : Duplication Rate Histogram



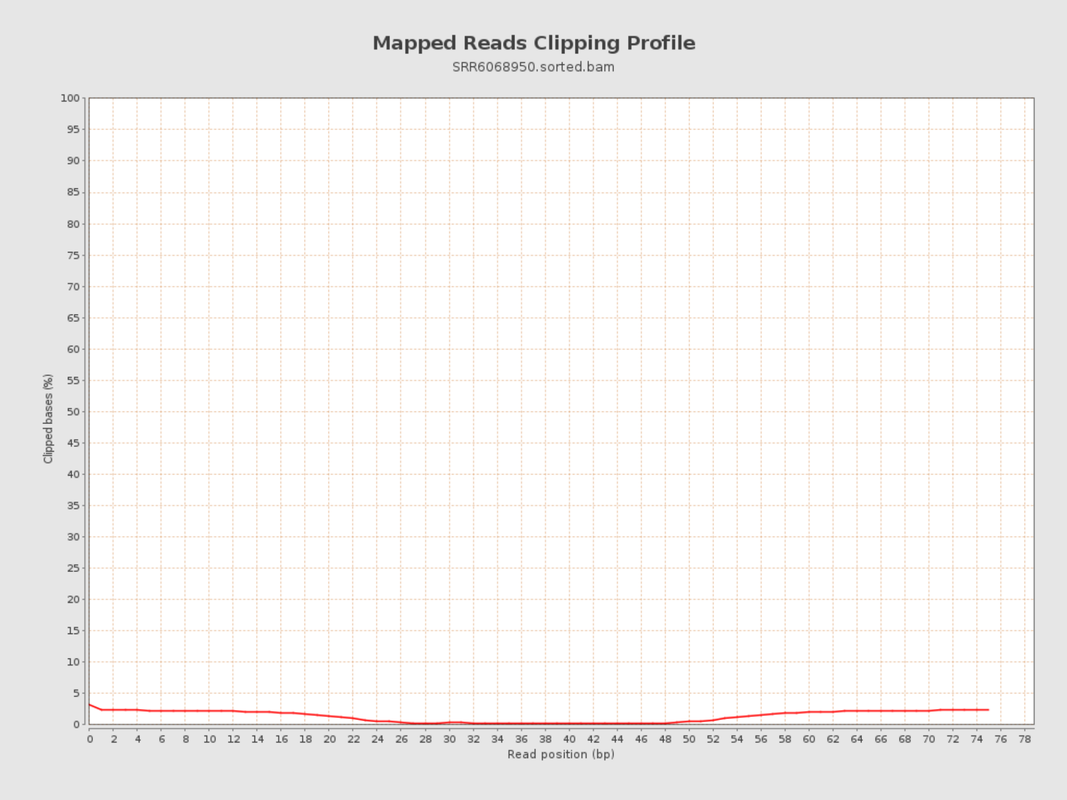
8. Results : Mapped Reads Nucleotide Content



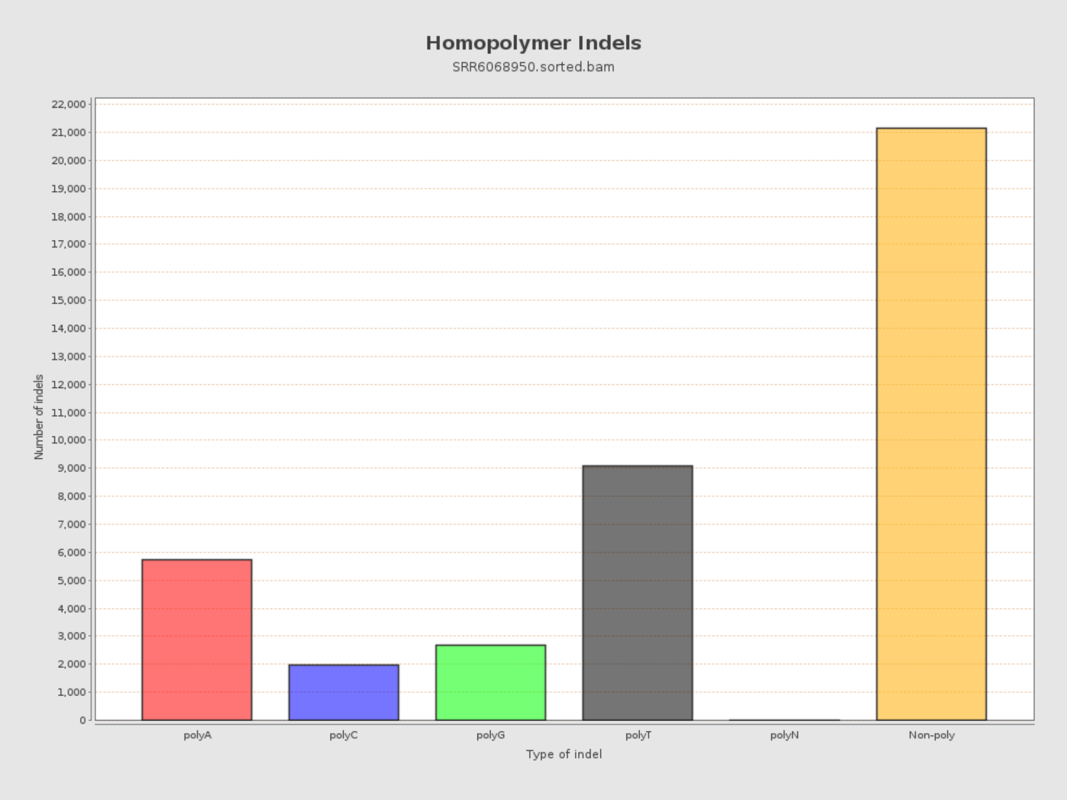
9. Results : Mapped Reads GC-content Distribution



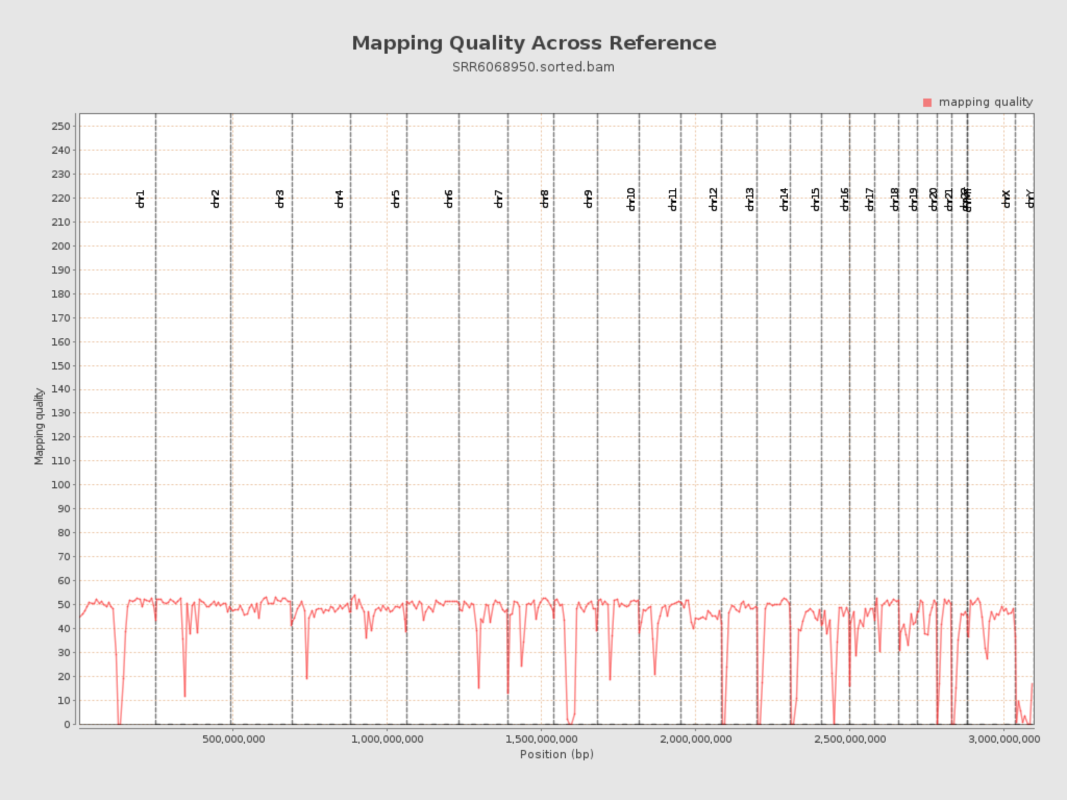
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram