Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 17:36:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068962.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_SRR6068962 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068962.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 17:36:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068962.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,024,988
Mapped reads	1,652,951 / 81.63%
Unmapped reads	372,037 / 18.37%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,375 / 0.27%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	128,194 / 6.33%
Duplication rate	6.41%
Clipped reads	1,038,002 / 51.26%

2.2. ACGT Content

Number/percentage of A's	26,783,372 / 26.05%
Number/percentage of C's	16,699,967 / 16.24%
Number/percentage of T's	35,103,640 / 34.14%
Number/percentage of G's	23,991,539 / 23.33%
Number/percentage of N's	237,012 / 0.23%
GC Percentage	39.58%

2.3. Coverage

Mean	0.0332

Standard Deviation	0.3097

2.4. Mapping Quality

Mean Mapping Quality	46.32

2.5. Mismatches and indels

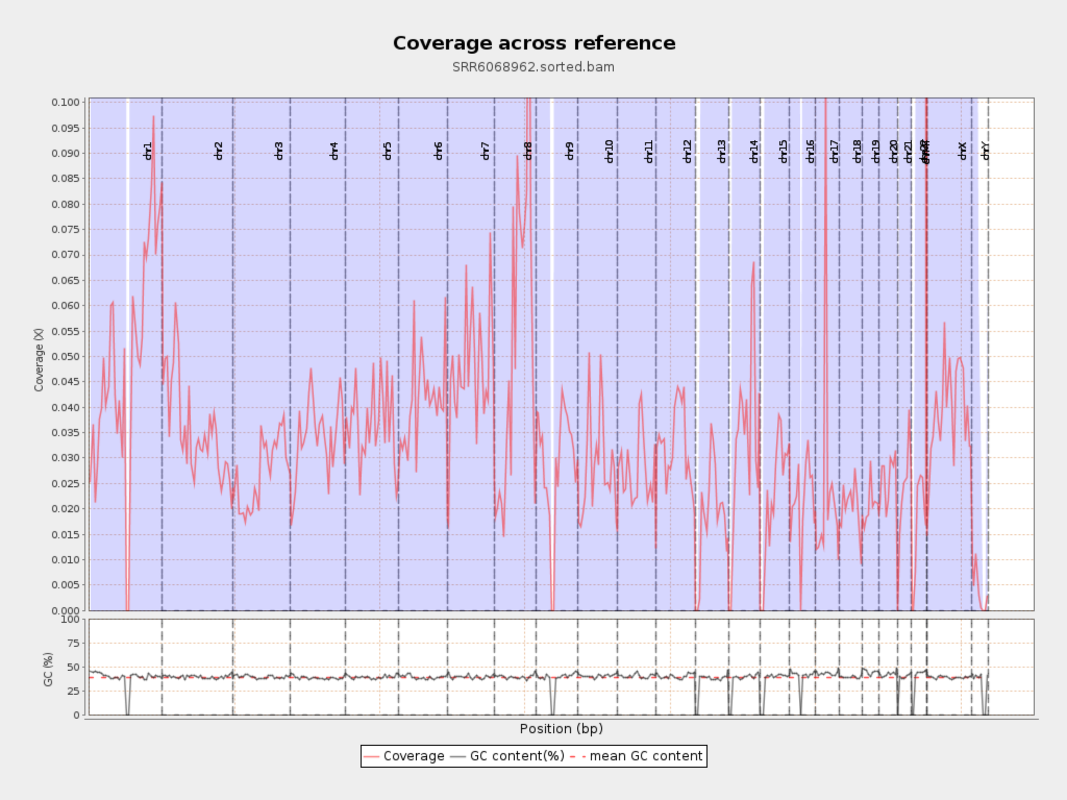
General error rate	0.99%
Mismatches	1,002,861
Insertions	8,301
Mapped reads with at least one insertion	0.5%
Deletions	34,324
Mapped reads with at least one deletion	2.05%
Homopolymer indels	49.79%

2.6. Chromosome stats

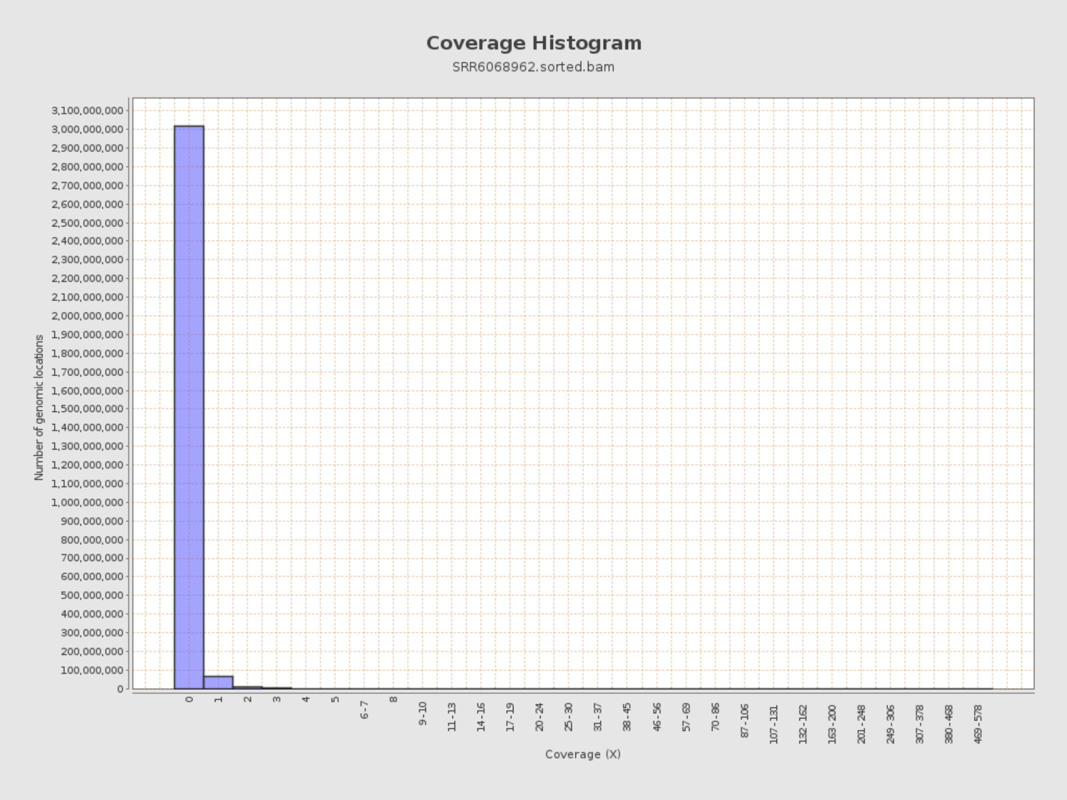
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12274796	0.0492	0.4464
chr2	243199373	8682665	0.0357	0.2919
chr3	198022430	5342272	0.027	0.2065
chr4	191154276	6539337	0.0342	0.2416
chr5	180915260	6694598	0.037	0.2407
chr6	171115067	6983980	0.0408	0.3414
chr7	159138663	7669600	0.0482	0.587

chr8	146364022	7885054	0.0539	0.4418
chr9	141213431	4020726	0.0285	0.2936
chr10	135534747	3903776	0.0288	0.274
chr11	135006516	3746320	0.0277	0.2353
chr12	133851895	4352289	0.0325	0.2307
chr13	115169878	2147861	0.0186	0.1719
chr14	107349540	3551171	0.0331	0.2311
chr15	102531392	2262574	0.0221	0.1861
chr16	90354753	1959859	0.0217	0.1909
chr17	81195210	2066630	0.0255	0.2215
chr18	78077248	1602024	0.0205	0.3679
chr19	59128983	1222627	0.0207	0.3221
chr20	63025520	1621652	0.0257	0.2047
chr21	48129895	1118600	0.0232	0.198
chr22	51304566	836743	0.0163	0.1567
chrMT	16571	114437	6.9059	5.1548
chrX	155270560	6050578	0.039	0.2737
chrY	59373566	218626	0.0037	0.0901

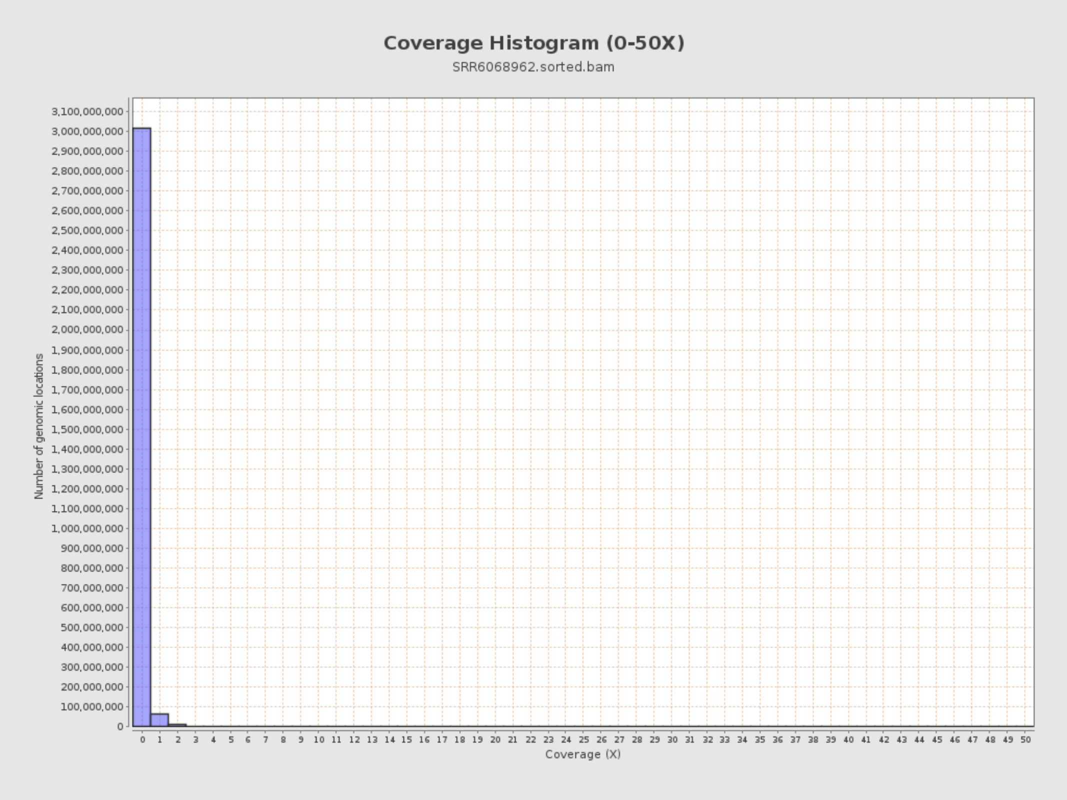
3. Results : Coverage across reference



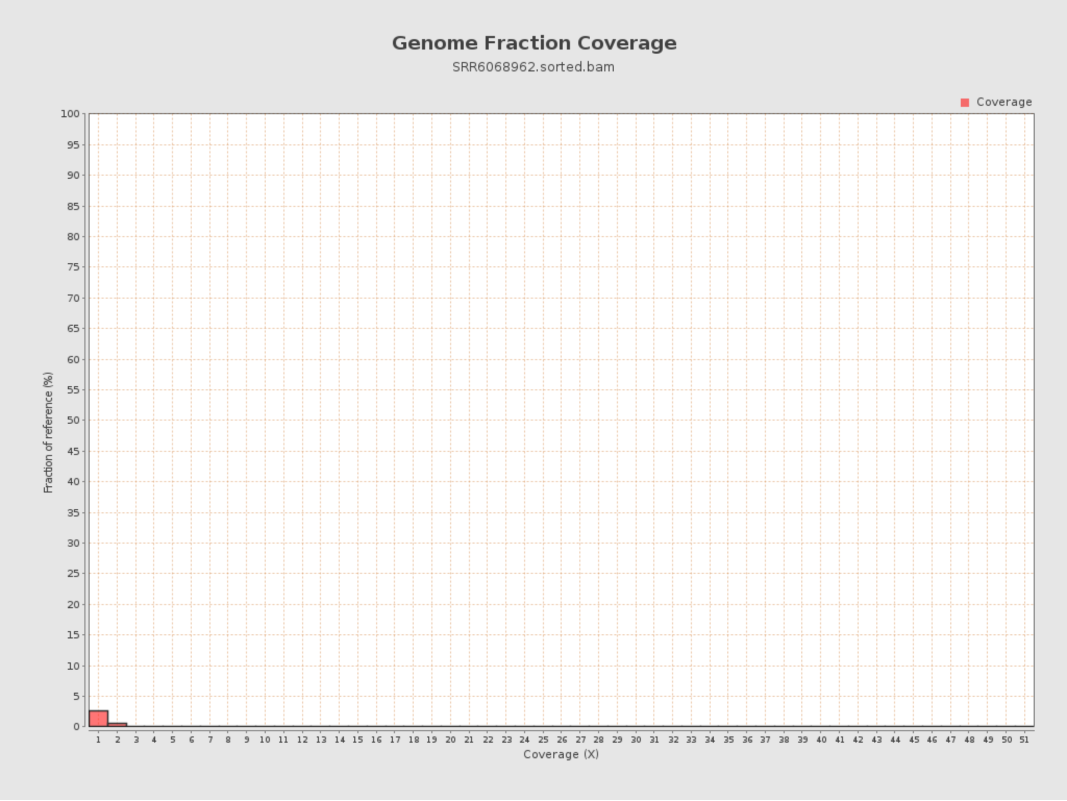
4. Results : Coverage Histogram



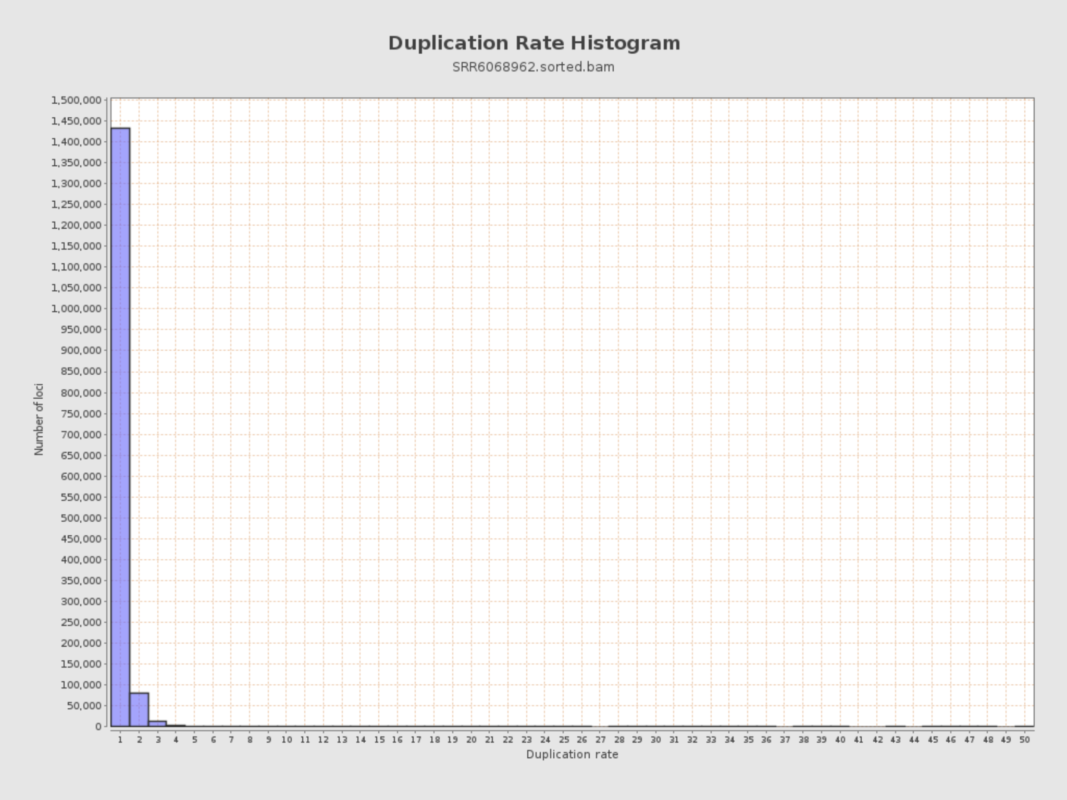
5. Results : Coverage Histogram (0-50X)



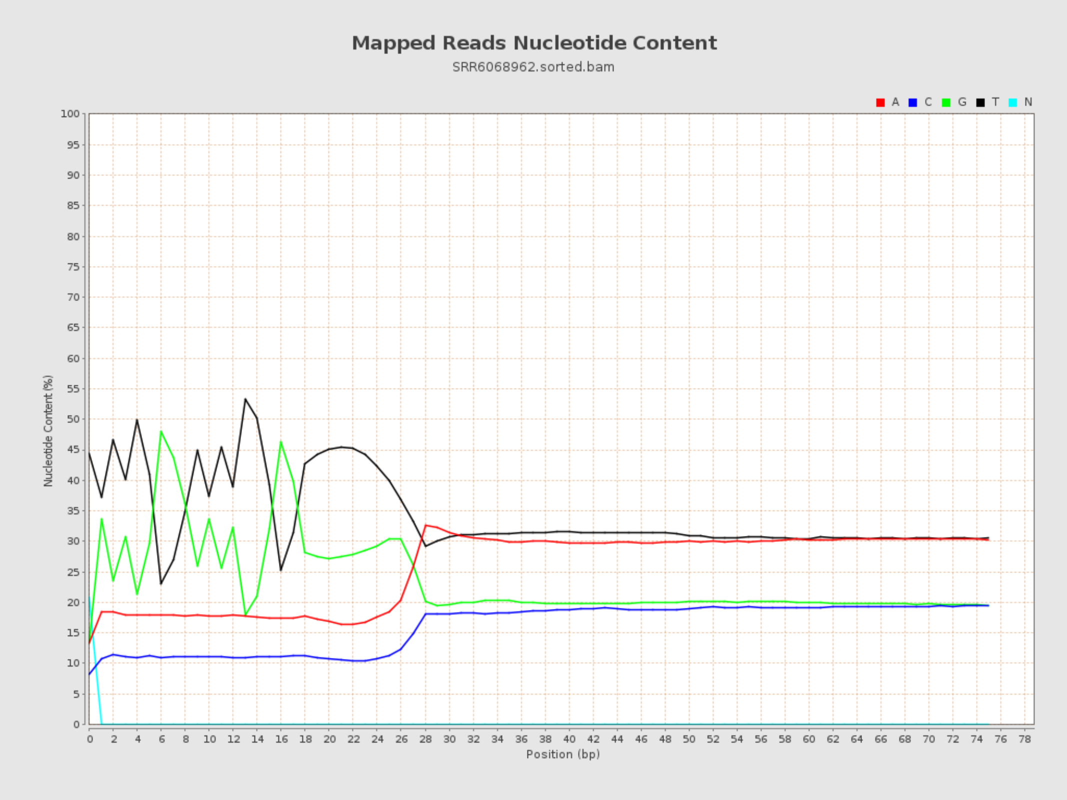
6. Results : Genome Fraction Coverage



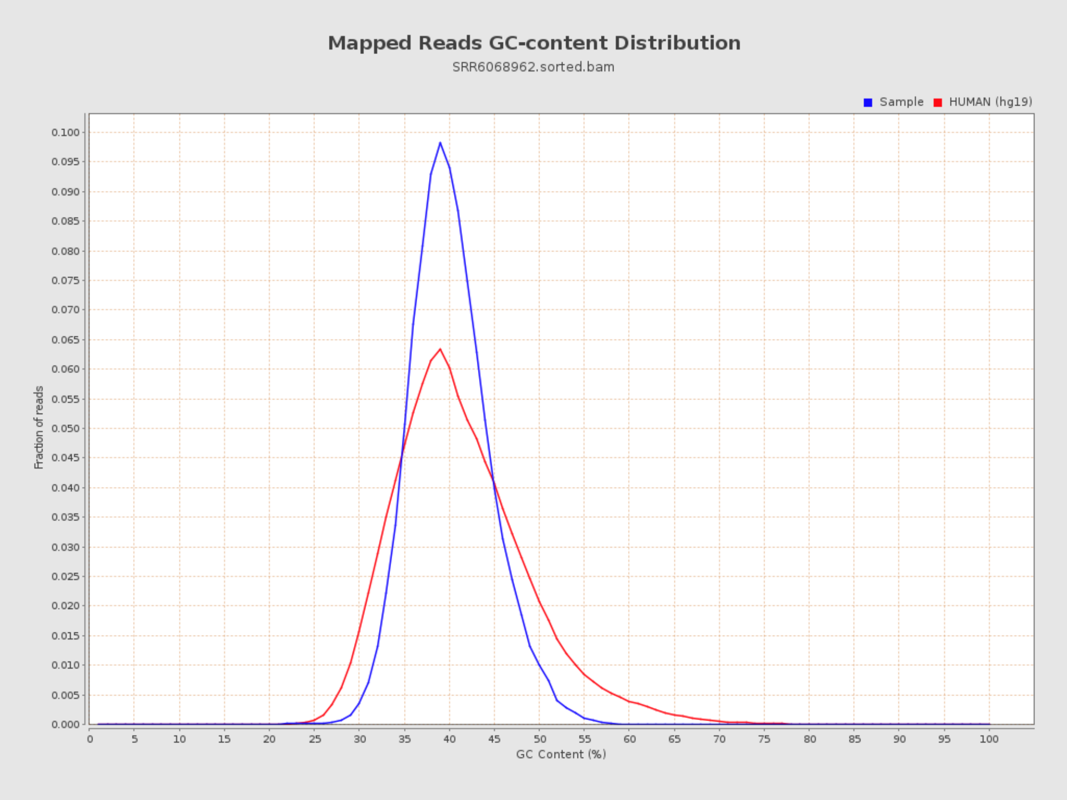
7. Results : Duplication Rate Histogram



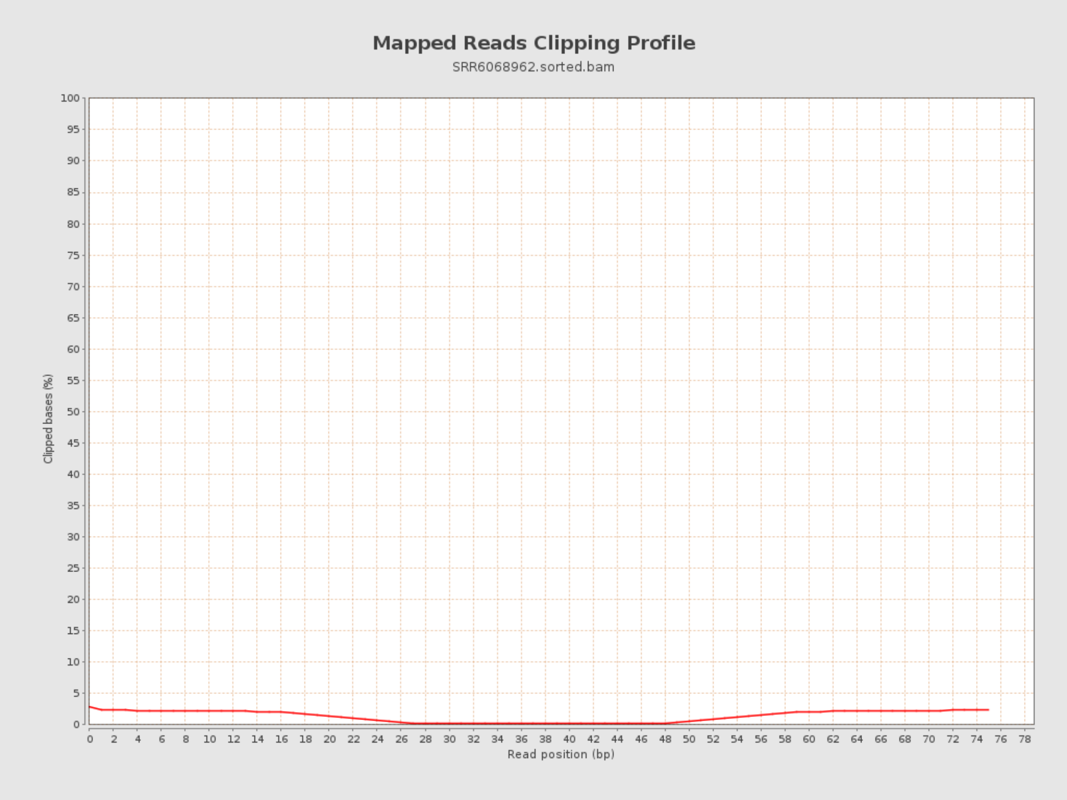
8. Results : Mapped Reads Nucleotide Content



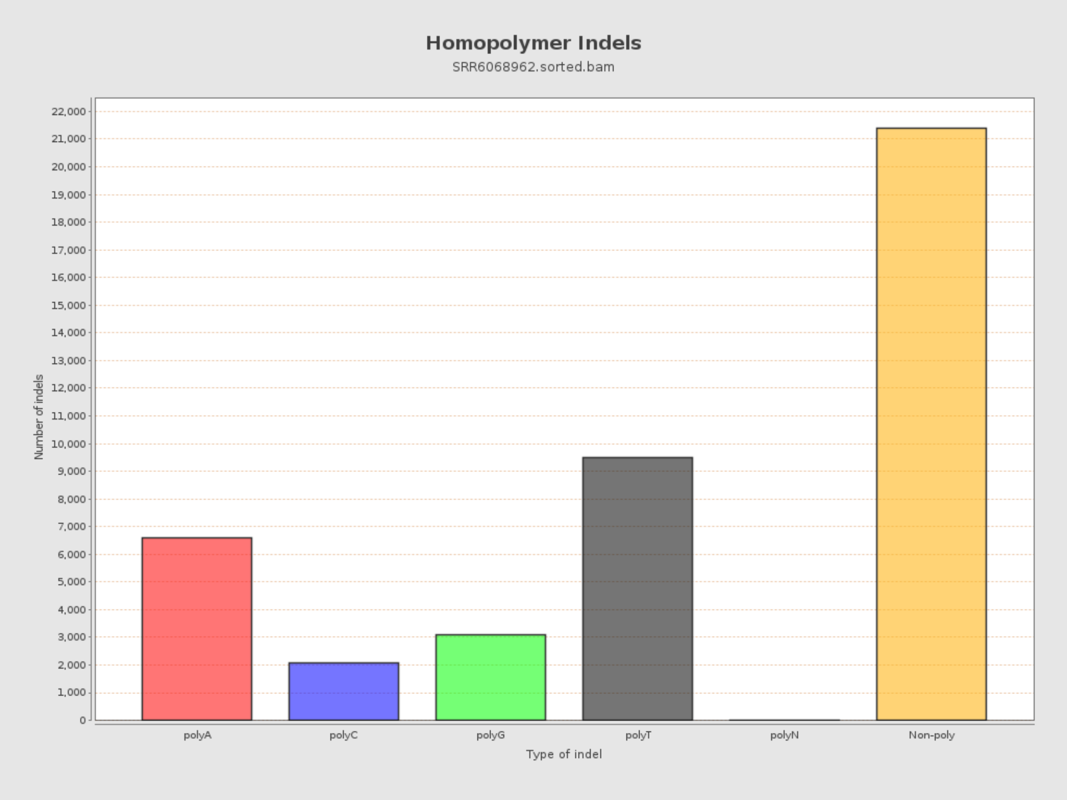
9. Results : Mapped Reads GC-content Distribution



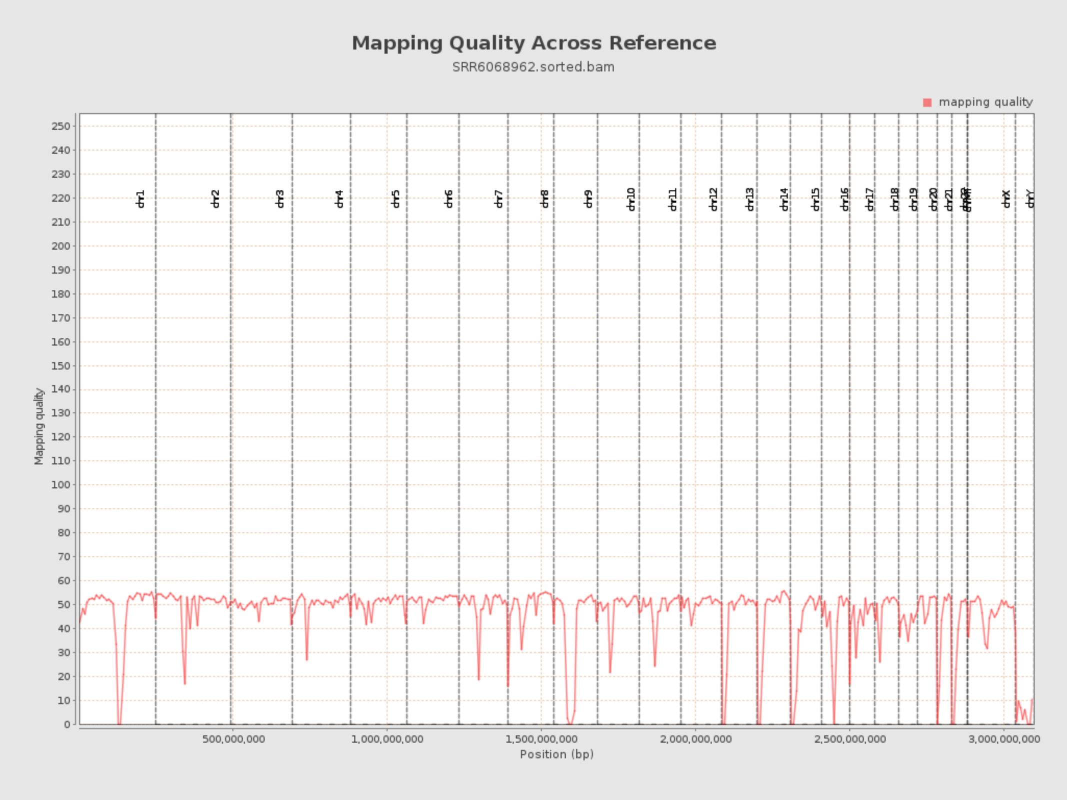
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram