Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 10:12:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068103.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_SRR6068103 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068103.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 10:12:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068103.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,074,430
Mapped reads	3,896,589 / 95.64%
Unmapped reads	177,841 / 4.36%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,265 / 0.57%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	441,238 / 10.83%
Duplication rate	9.4%
Clipped reads	1,814,171 / 44.53%

2.2. ACGT Content

Number/percentage of A's	70,061,155 / 27.35%
Number/percentage of C's	45,606,406 / 17.8%
Number/percentage of T's	83,782,029 / 32.7%
Number/percentage of G's	56,718,232 / 22.14%
Number/percentage of N's	30,286 / 0.01%
GC Percentage	39.94%

2.3. Coverage

Mean	0.0828

Standard Deviation	0.9027

2.4. Mapping Quality

Mean Mapping Quality	46.72

2.5. Mismatches and indels

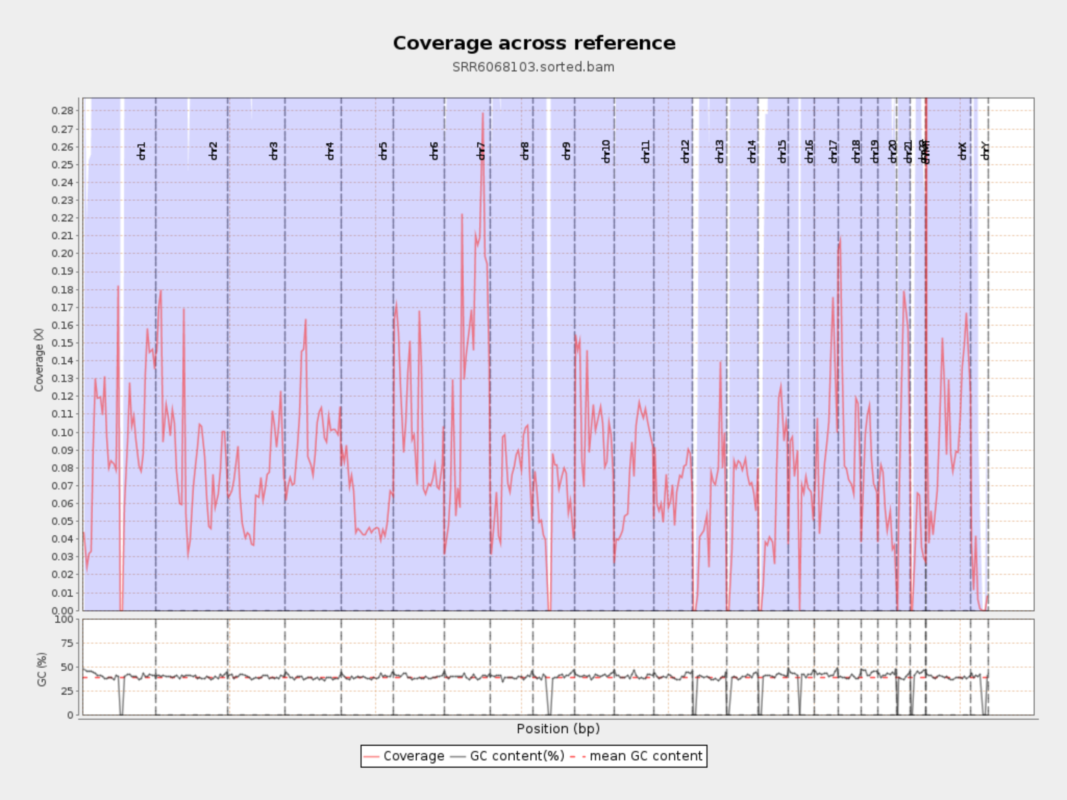
General error rate	0.56%
Mismatches	1,410,423
Insertions	17,100
Mapped reads with at least one insertion	0.44%
Deletions	65,521
Mapped reads with at least one deletion	1.66%
Homopolymer indels	45.42%

2.6. Chromosome stats

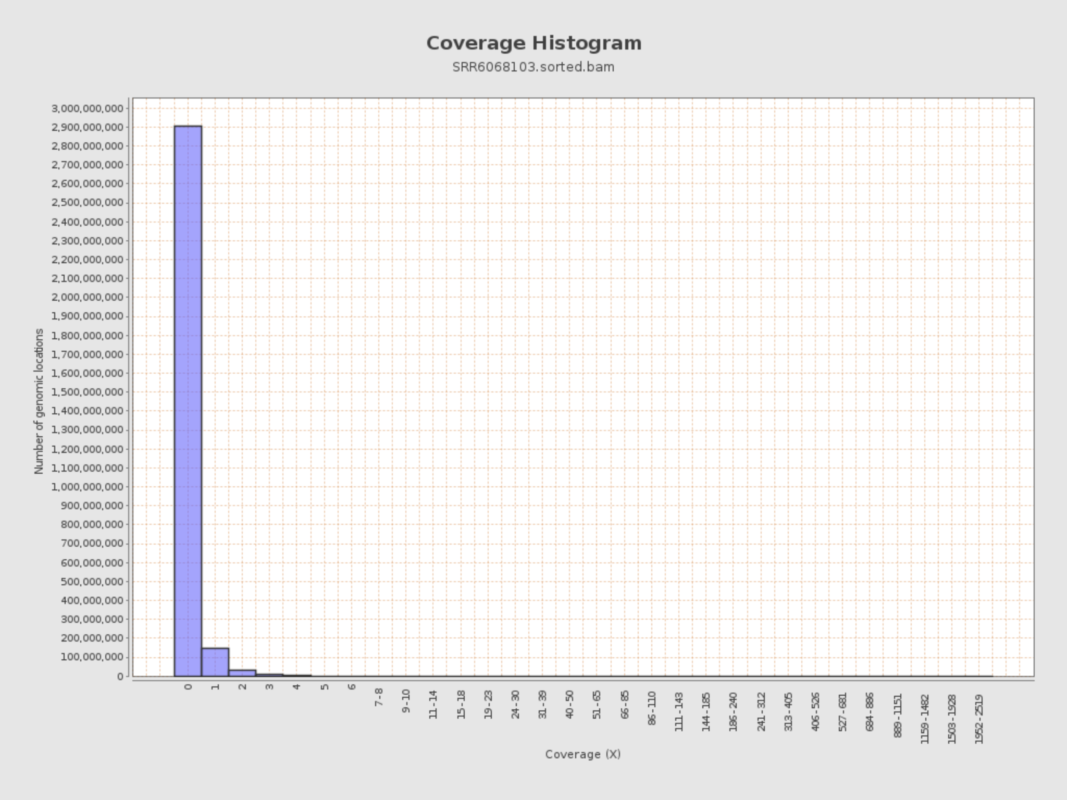
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	23391774	0.0938	2.0234
chr2	243199373	21747659	0.0894	0.8732
chr3	198022430	14133098	0.0714	0.3417
chr4	191154276	19034236	0.0996	0.4288
chr5	180915260	10086137	0.0558	0.3122
chr6	171115067	17851107	0.1043	0.5244
chr7	159138663	22304148	0.1402	1.6411

chr8	146364022	10855365	0.0742	1.321
chr9	141213431	8119711	0.0575	0.663
chr10	135534747	14556037	0.1074	0.6387
chr11	135006516	10750805	0.0796	0.4739
chr12	133851895	9332156	0.0697	0.3832
chr13	115169878	6573184	0.0571	0.3153
chr14	107349540	6795650	0.0633	0.3923
chr15	102531392	5867821	0.0572	0.3219
chr16	90354753	6047036	0.0669	0.3707
chr17	81195210	8301256	0.1022	0.4349
chr18	78077248	8436081	0.108	1.1629
chr19	59128983	4937355	0.0835	1.2638
chr20	63025520	3473370	0.0551	0.3297
chr21	48129895	5519283	0.1147	0.4618
chr22	51304566	1750480	0.0341	0.2265
chrMT	16571	157472	9.5029	6.2598
chrX	155270560	15571626	0.1003	0.4956
chrY	59373566	720288	0.0121	0.4825

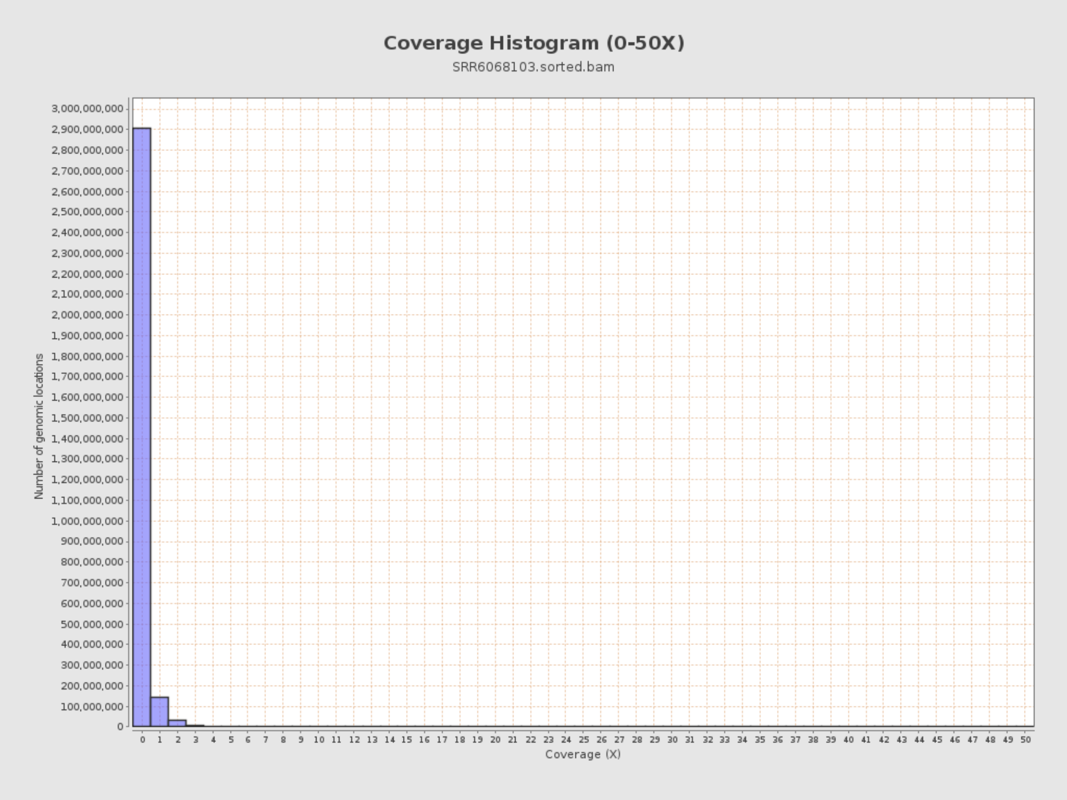
3. Results : Coverage across reference



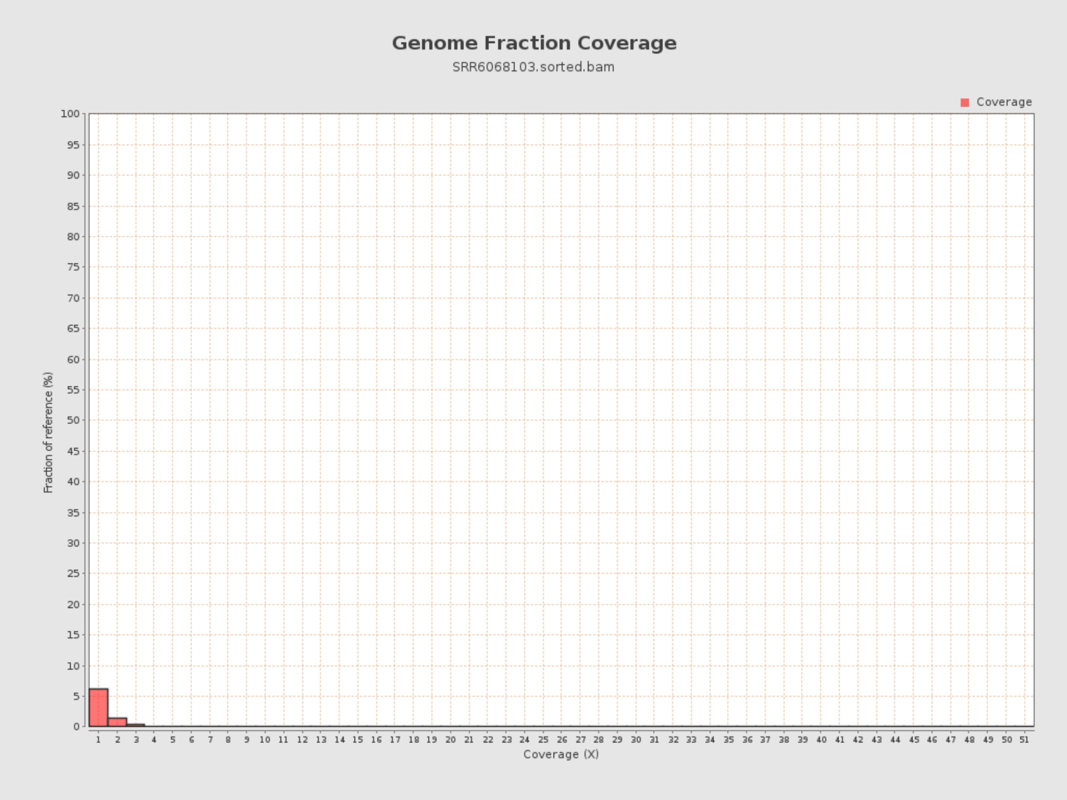
4. Results : Coverage Histogram



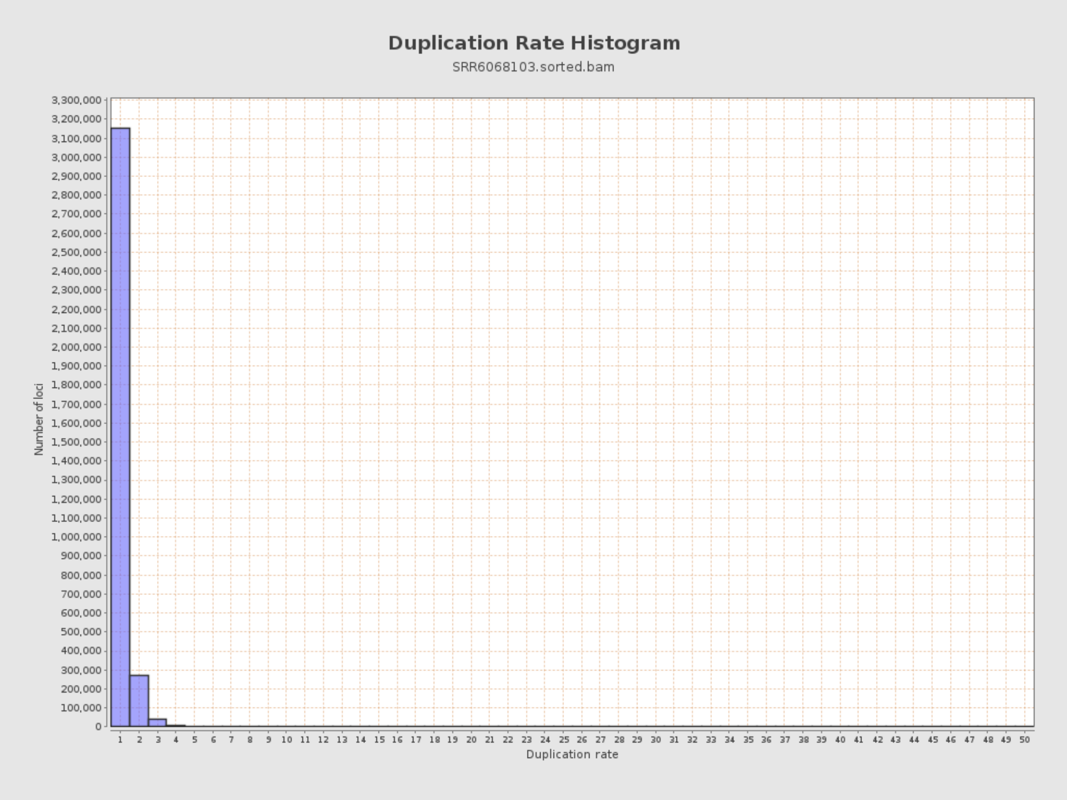
5. Results : Coverage Histogram (0-50X)



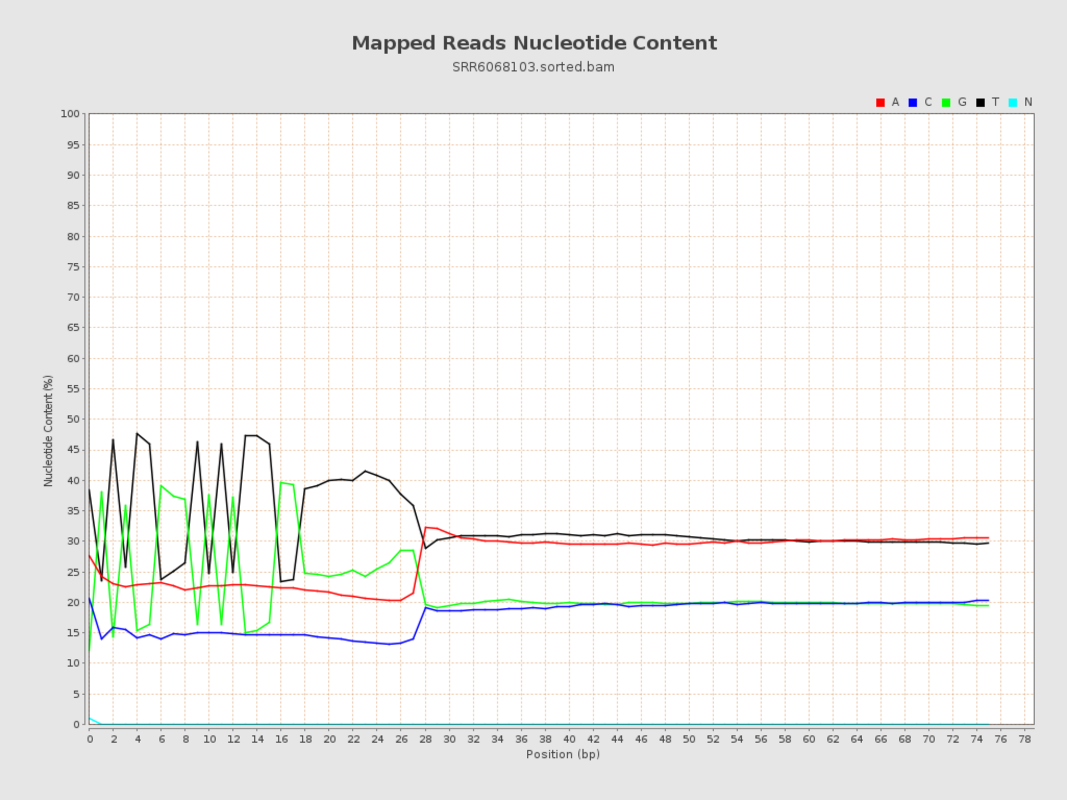
6. Results : Genome Fraction Coverage



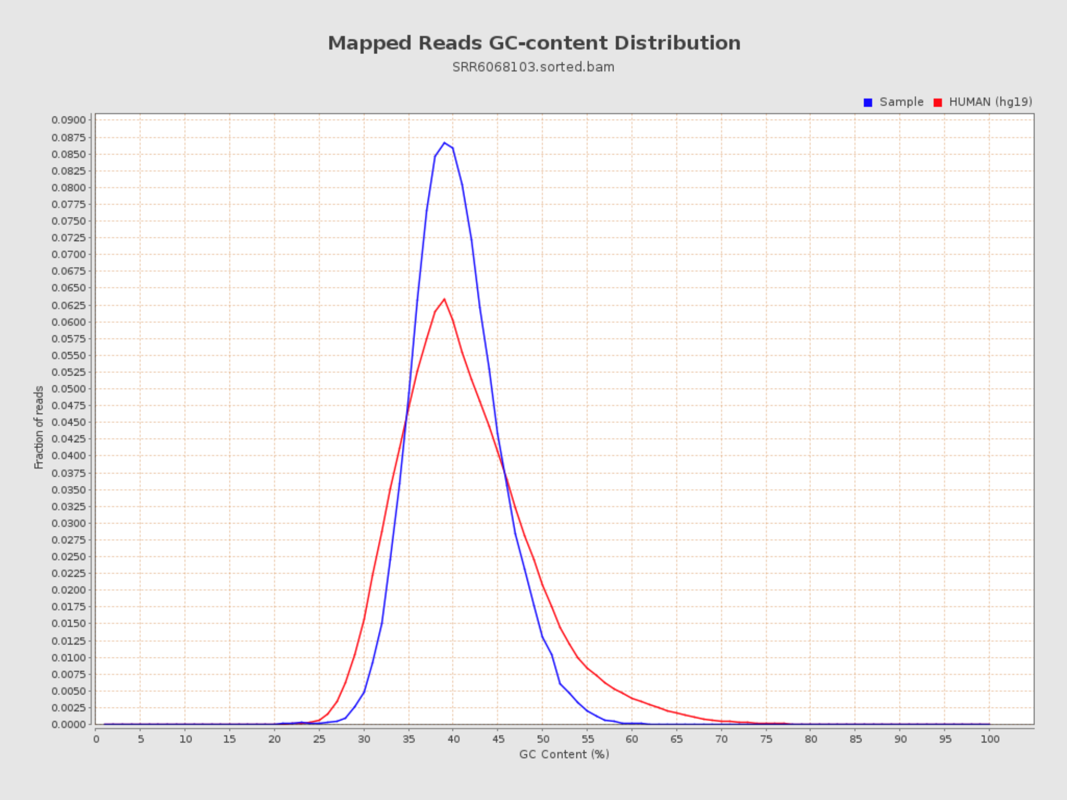
7. Results : Duplication Rate Histogram



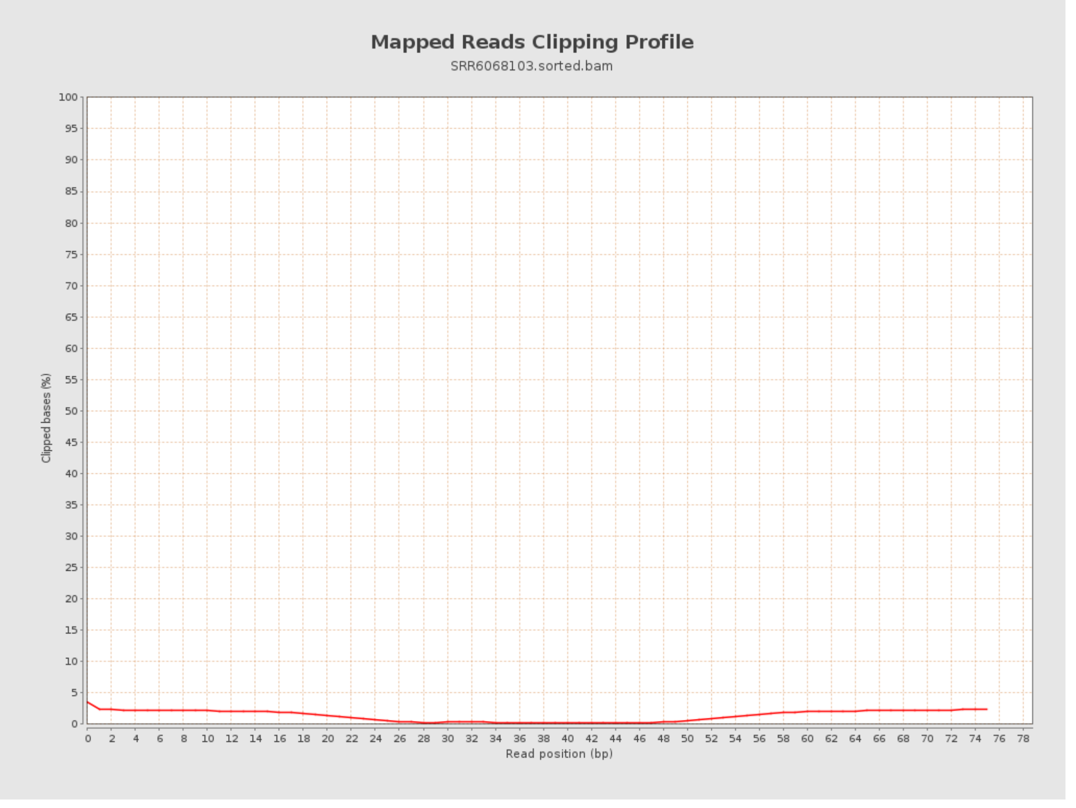
8. Results : Mapped Reads Nucleotide Content



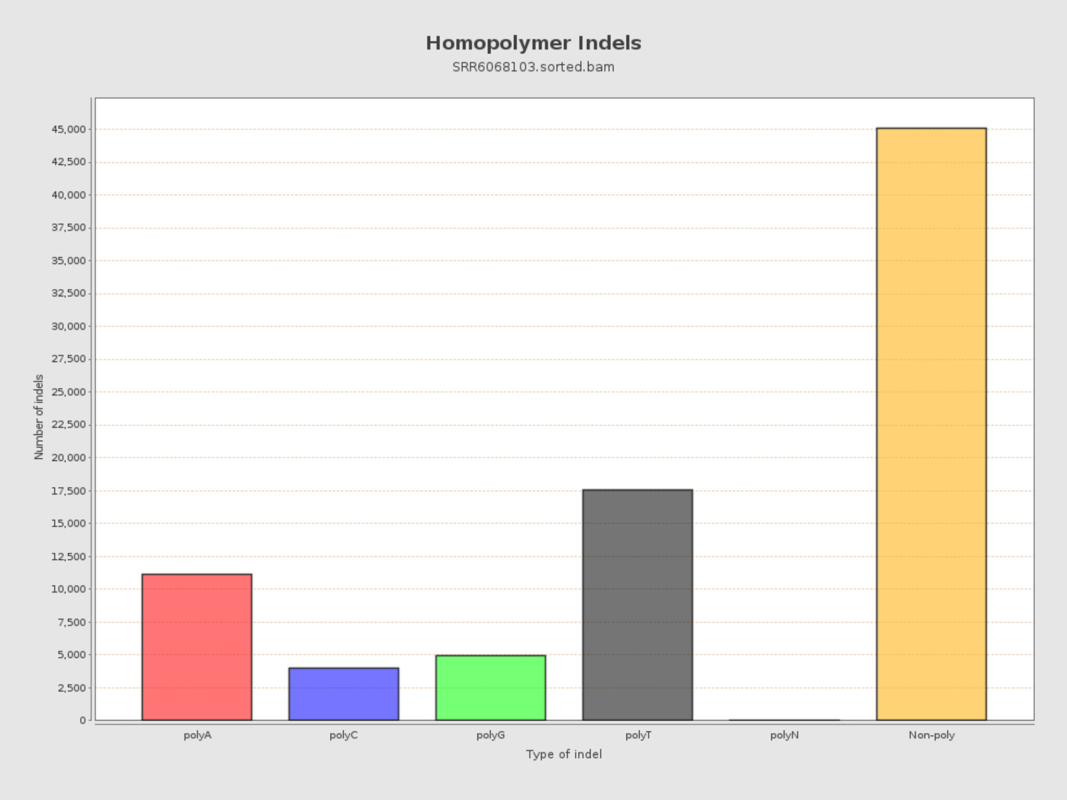
9. Results : Mapped Reads GC-content Distribution



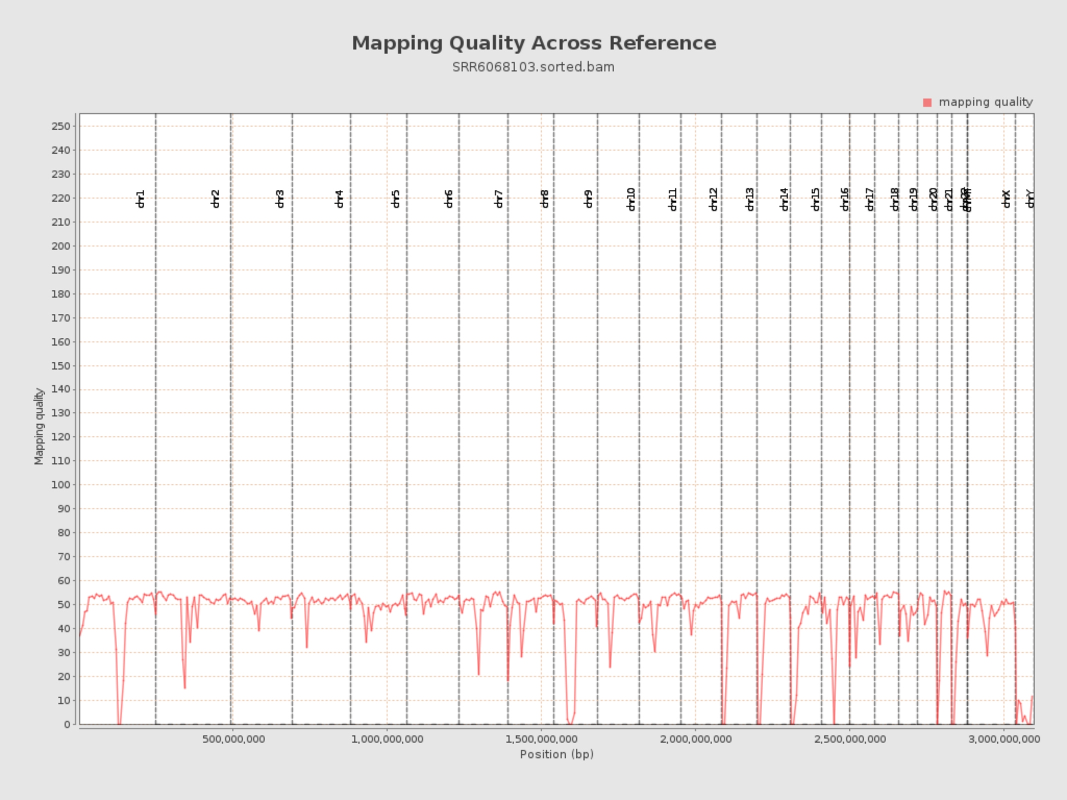
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram