

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 10:38:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068108.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_SRR6068108 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068108.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 10:38:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068108.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,483,157
Mapped reads	3,291,029 / 94.48%
Unmapped reads	192,128 / 5.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,608 / 0.53%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	343,687 / 9.87%
Duplication rate	9%
Clipped reads	1,706,313 / 48.99%

2.2. ACGT Content

Number/percentage of A's	55,878,121 / 26.37%
Number/percentage of C's	37,495,161 / 17.69%
Number/percentage of T's	69,642,483 / 32.86%
Number/percentage of G's	48,871,150 / 23.06%
Number/percentage of N's	23,983 / 0.01%
GC Percentage	40.76%

2.3. Coverage

Mean	0.0685

Standard Deviation	0.663
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2.4. Mapping Quality

Mean Mapping Quality	44.87
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2.5. Mismatches and indels

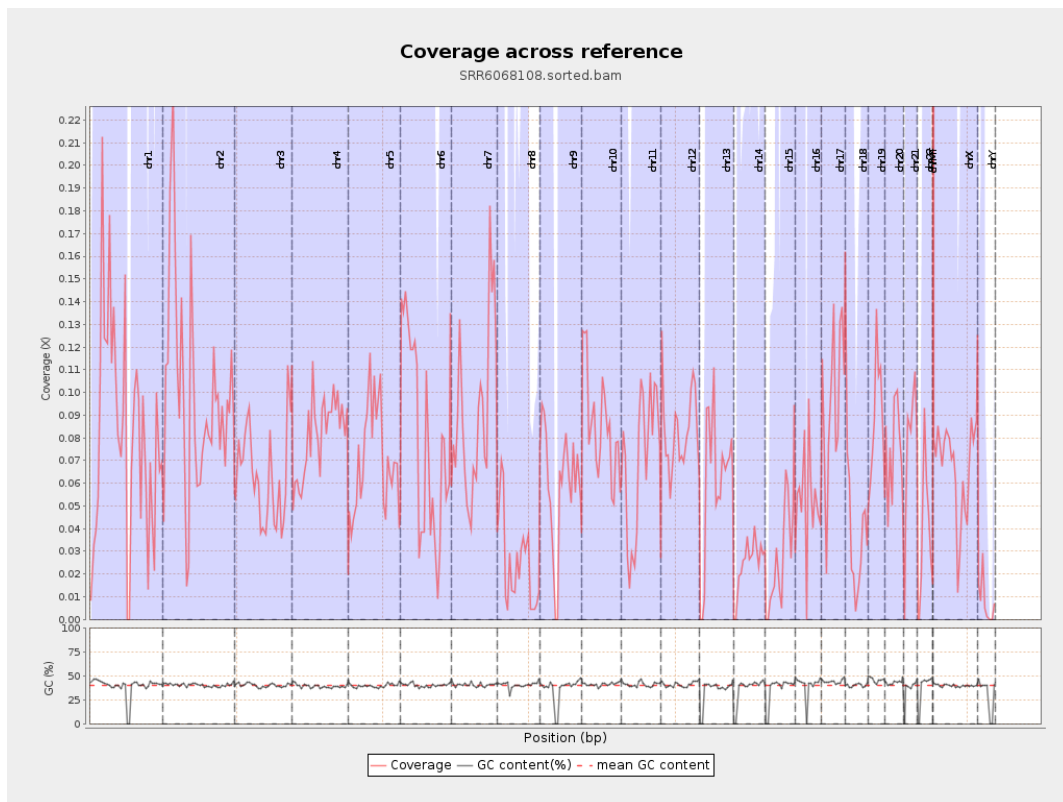
General error rate	0.55%
Mismatches	1,138,953
Insertions	13,601
Mapped reads with at least one insertion	0.41%
Deletions	51,508
Mapped reads with at least one deletion	1.55%
Homopolymer indels	45.53%

2.6. Chromosome stats

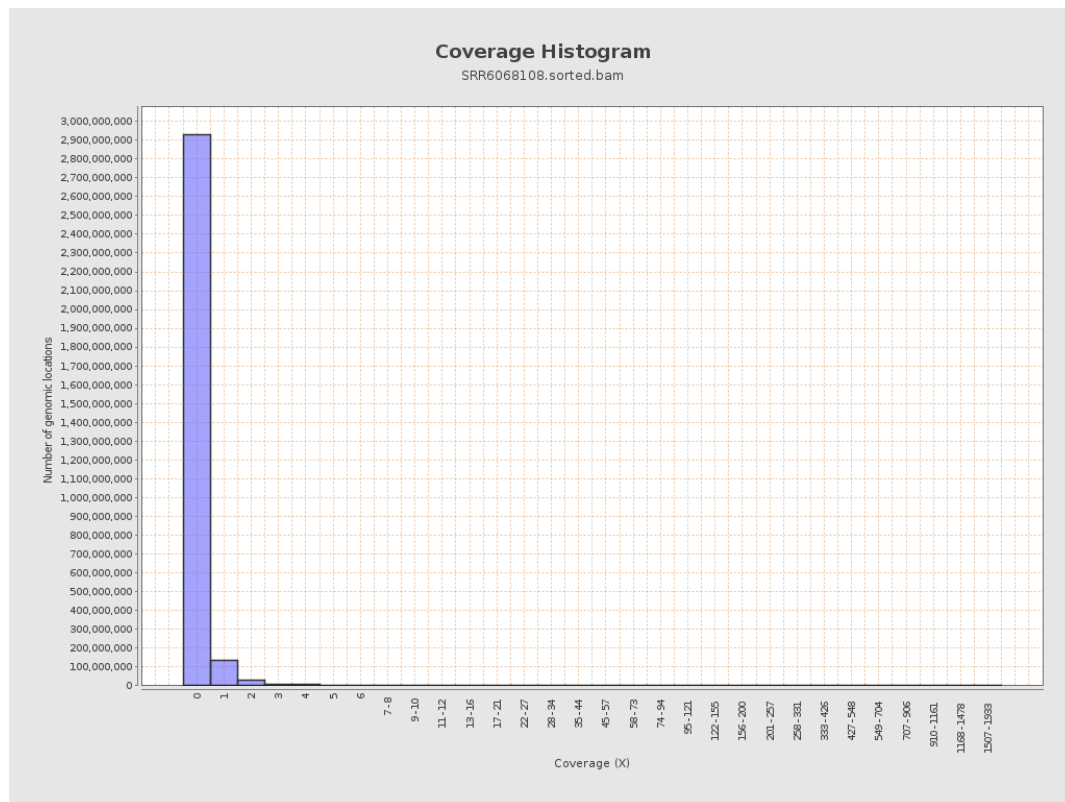
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	20131931	0.0808	1.5239
chr2	243199373	24201173	0.0995	0.9953
chr3	198022430	12527215	0.0633	0.3113
chr4	191154276	15547634	0.0813	0.3635
chr5	180915260	12590157	0.0696	0.3304
chr6	171115067	13628158	0.0796	0.4579
chr7	159138663	14275819	0.0897	0.4018

chr8	146364022	3565798	0.0244	0.7739
chr9	141213431	8348993	0.0591	0.5059
chr10	135534747	11620313	0.0857	0.5123
chr11	135006516	9453187	0.07	0.359
chr12	133851895	11236180	0.0839	0.3833
chr13	115169878	7036833	0.0611	0.33
chr14	107349540	2678650	0.025	0.288
chr15	102531392	2796508	0.0273	0.2495
chr16	90354753	4722286	0.0523	0.3307
chr17	81195210	7793840	0.096	0.3854
chr18	78077248	3166236	0.0406	0.921
chr19	59128983	5259444	0.0889	0.9809
chr20	63025520	4665680	0.074	0.3542
chr21	48129895	3661314	0.0761	0.358
chr22	51304566	1955123	0.0381	0.2363
chrMT	16571	130627	7.8829	5.2765
chrX	155270560	10536527	0.0679	0.3606
chrY	59373566	472754	0.008	0.3108

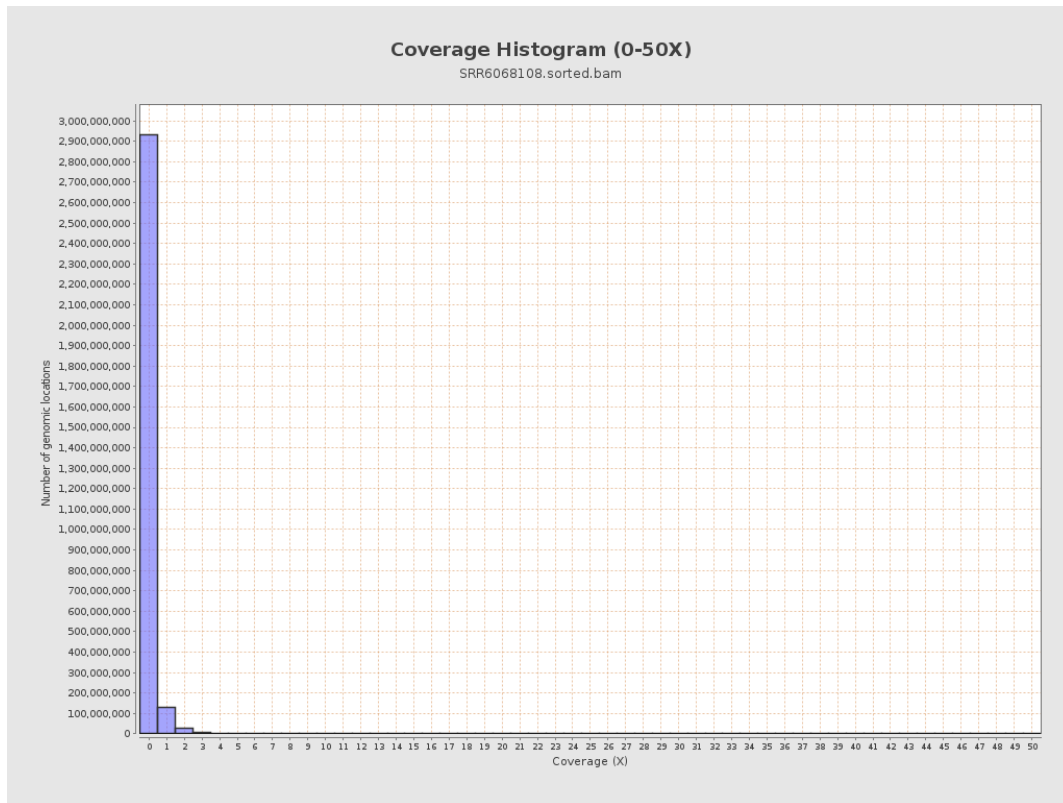
3. Results : Coverage across reference



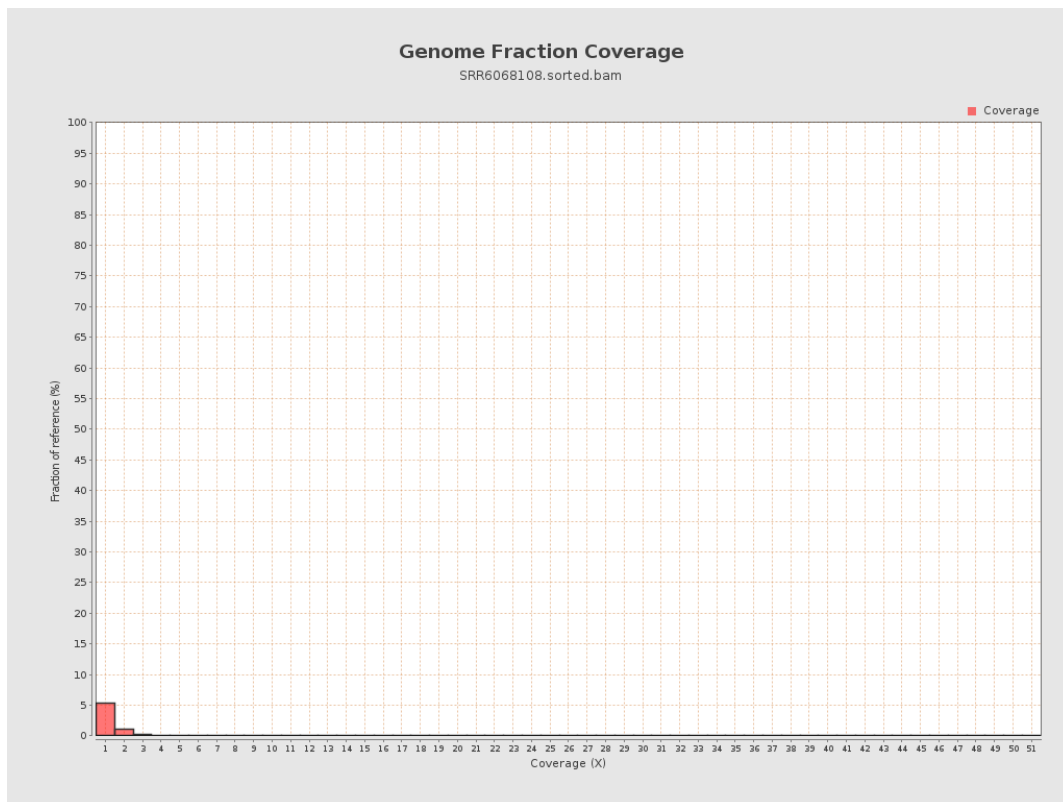
4. Results : Coverage Histogram



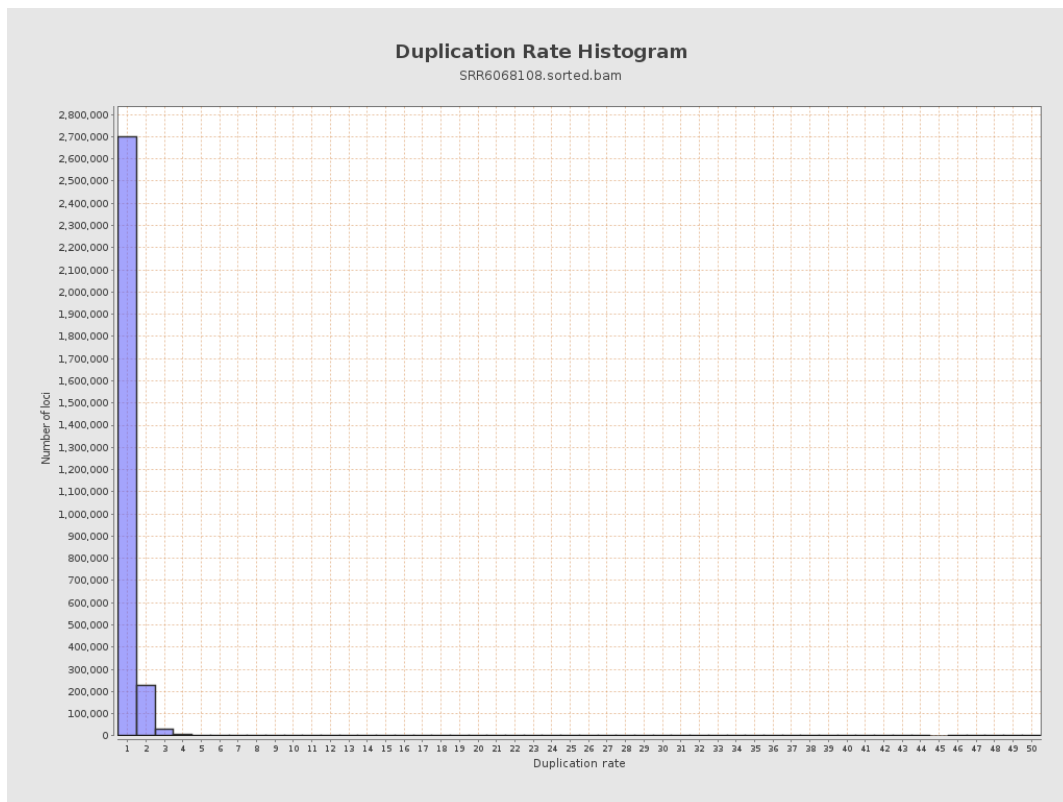
5. Results : Coverage Histogram (0-50X)



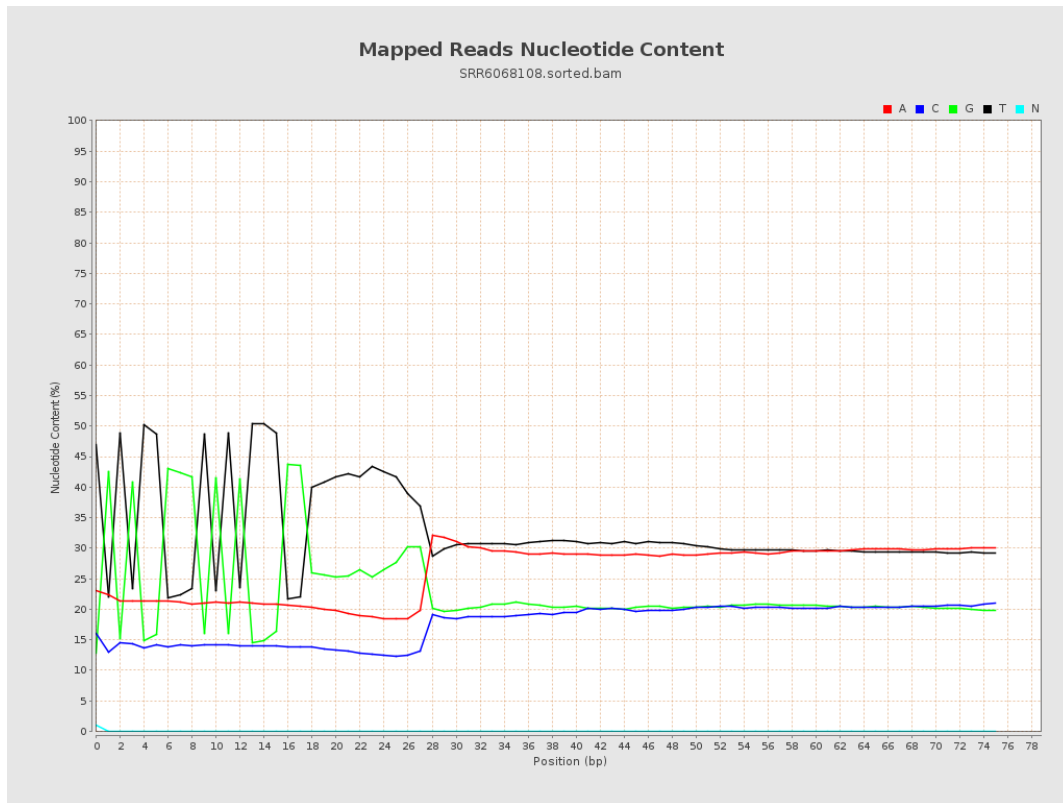
6. Results : Genome Fraction Coverage



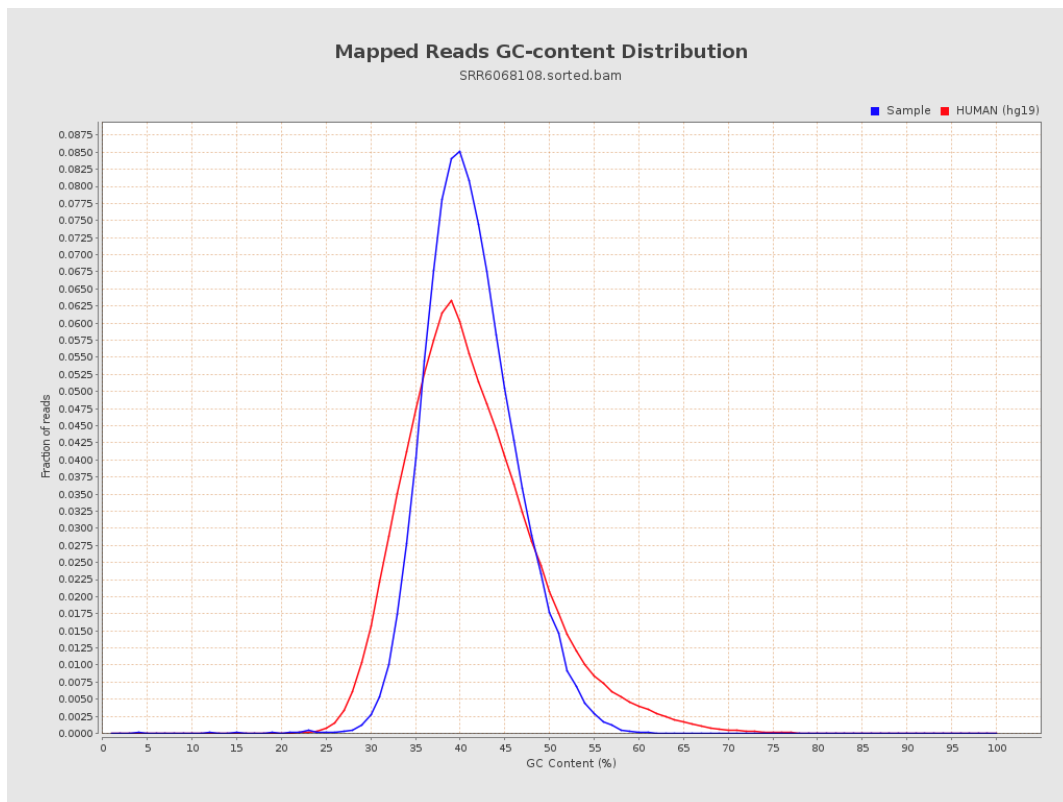
7. Results : Duplication Rate Histogram



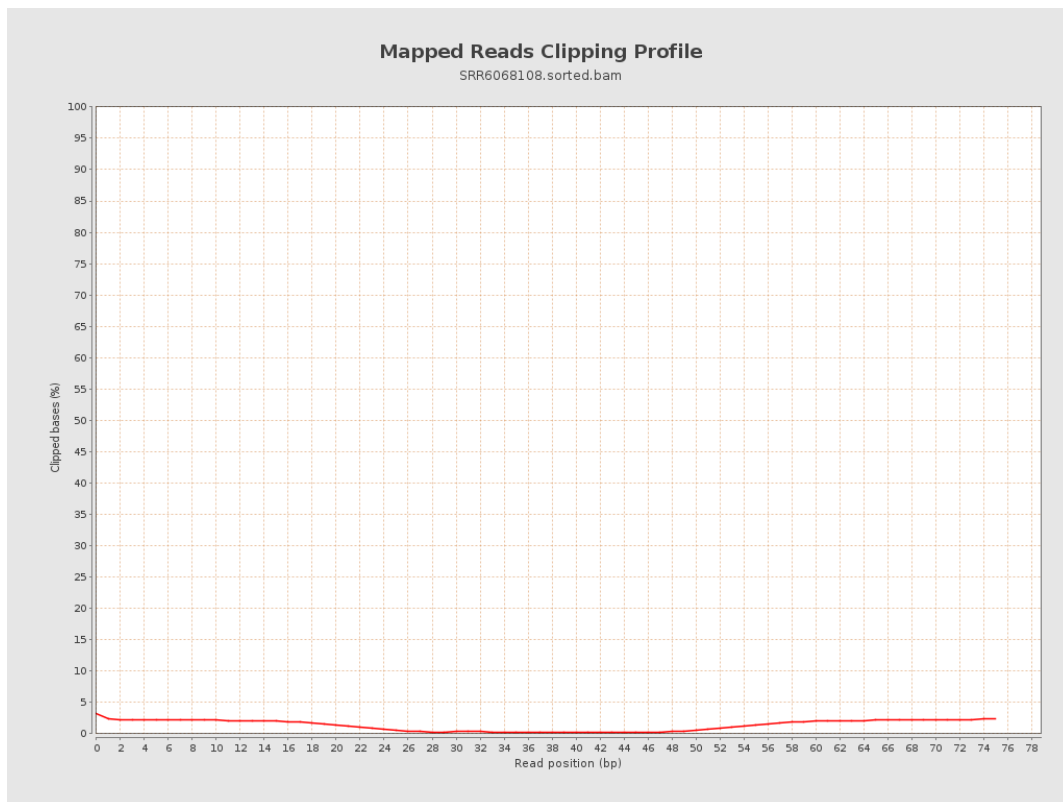
8. Results : Mapped Reads Nucleotide Content



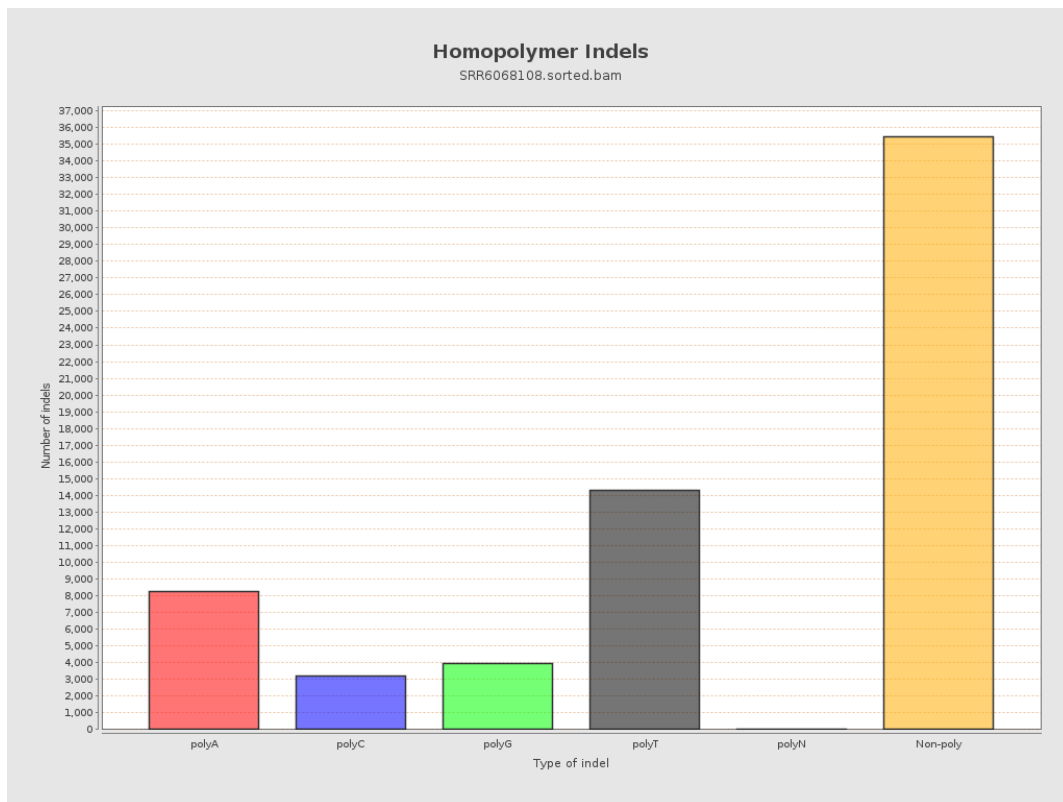
9. Results : Mapped Reads GC-content Distribution



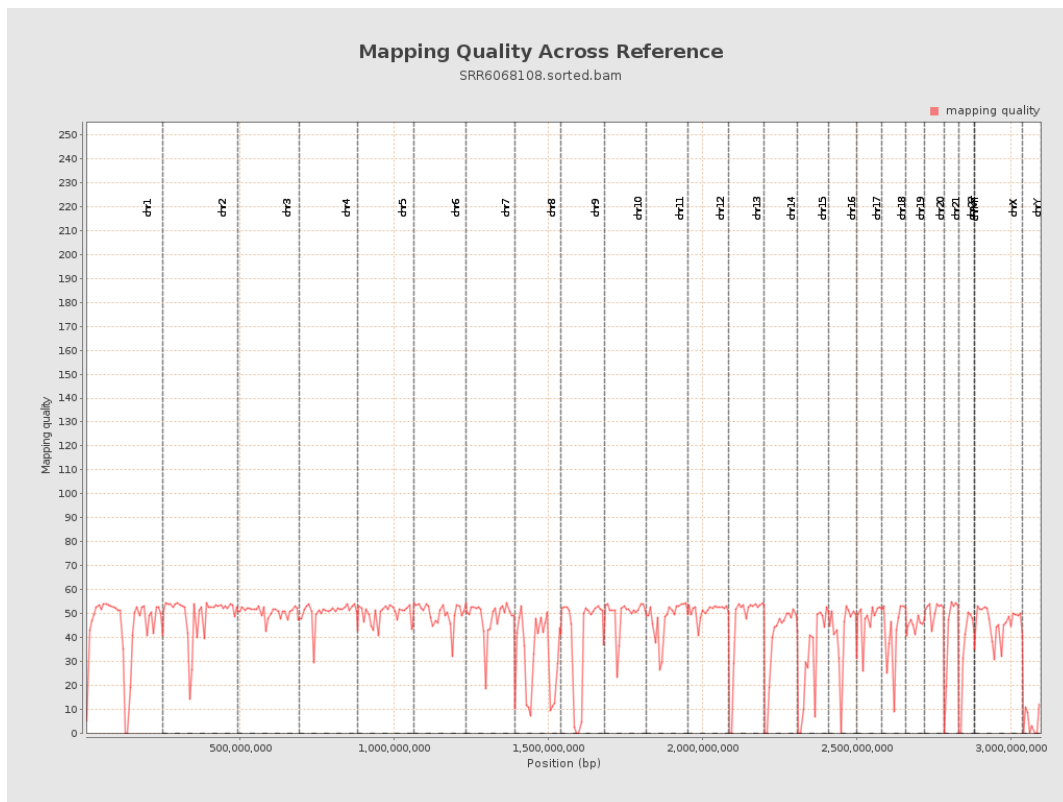
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

