

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 17:01:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068951.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_SRR6068951 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068951.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 17:01:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068951.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,473,671
Mapped reads	2,015,461 / 81.48%
Unmapped reads	458,210 / 18.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,334 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	89,003 / 3.6%
Duplication rate	3.51%
Clipped reads	1,091,776 / 44.14%

2.2. ACGT Content

Number/percentage of A's	34,848,392 / 26.88%
Number/percentage of C's	21,964,303 / 16.94%
Number/percentage of T's	43,966,273 / 33.92%
Number/percentage of G's	28,537,395 / 22.02%
Number/percentage of N's	306,324 / 0.24%
GC Percentage	38.96%

2.3. Coverage

Mean	0.0419

Standard Deviation	0.3551
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2.4. Mapping Quality

Mean Mapping Quality	47.43
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2.5. Mismatches and indels

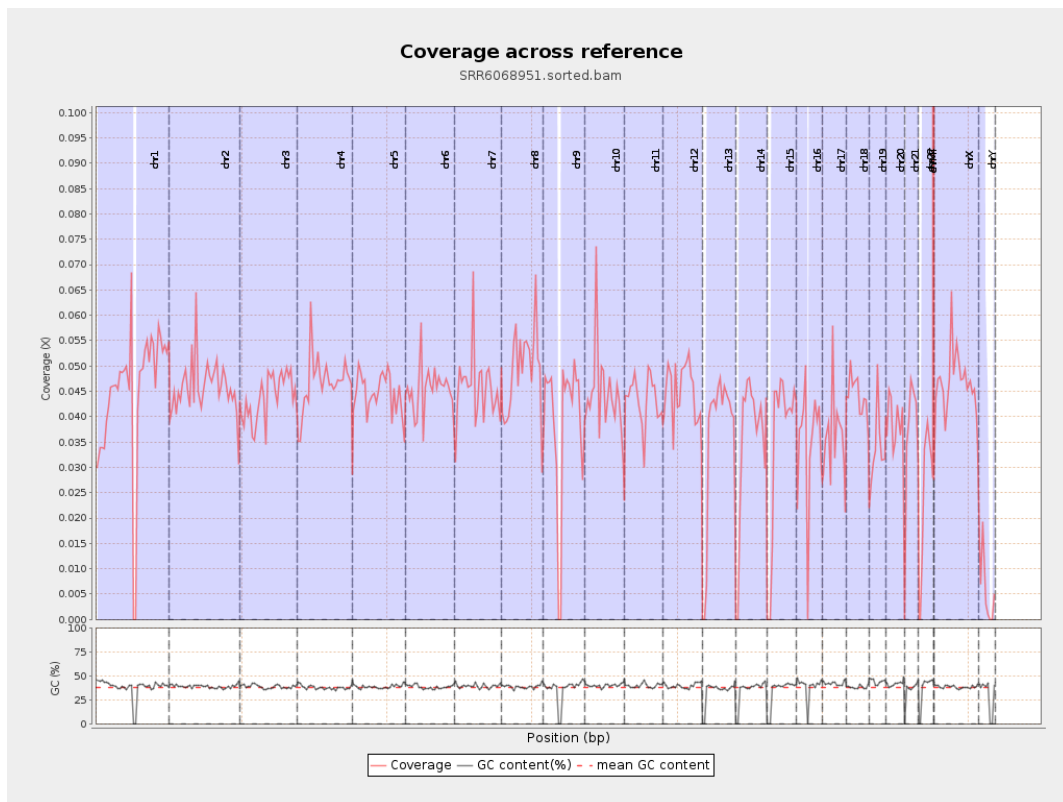
General error rate	1.07%
Mismatches	1,367,758
Insertions	11,497
Mapped reads with at least one insertion	0.57%
Deletions	35,558
Mapped reads with at least one deletion	1.74%
Homopolymer indels	48.73%

2.6. Chromosome stats

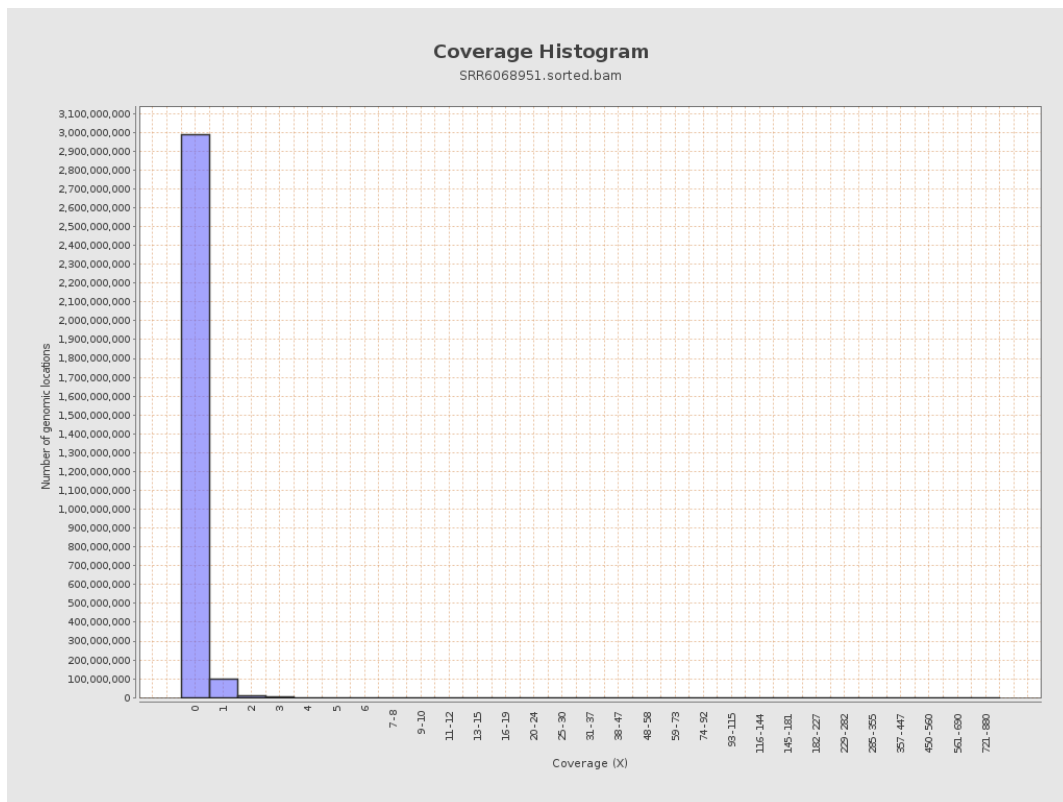
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	11198521	0.0449	0.591
chr2	243199373	11155845	0.0459	0.3553
chr3	198022430	8685567	0.0439	0.2386
chr4	191154276	8924866	0.0467	0.2651
chr5	180915260	8075372	0.0446	0.2414
chr6	171115067	7756890	0.0453	0.286
chr7	159138663	7284714	0.0458	0.4776

chr8	146364022	7161704	0.0489	0.5863
chr9	141213431	5495355	0.0389	0.3483
chr10	135534747	6033938	0.0445	0.3633
chr11	135006516	5817162	0.0431	0.297
chr12	133851895	6016653	0.045	0.2456
chr13	115169878	4101837	0.0356	0.2142
chr14	107349540	3729732	0.0347	0.224
chr15	102531392	3607370	0.0352	0.2144
chr16	90354753	3147767	0.0348	0.2364
chr17	81195210	2913479	0.0359	0.2302
chr18	78077248	3454493	0.0442	0.5667
chr19	59128983	2015567	0.0341	0.3966
chr20	63025520	2429186	0.0385	0.2309
chr21	48129895	1763976	0.0367	0.2386
chr22	51304566	1236477	0.0241	0.1736
chrMT	16571	146849	8.8618	6.0641
chrX	155270560	7181911	0.0463	0.2743
chrY	59373566	345007	0.0058	0.141

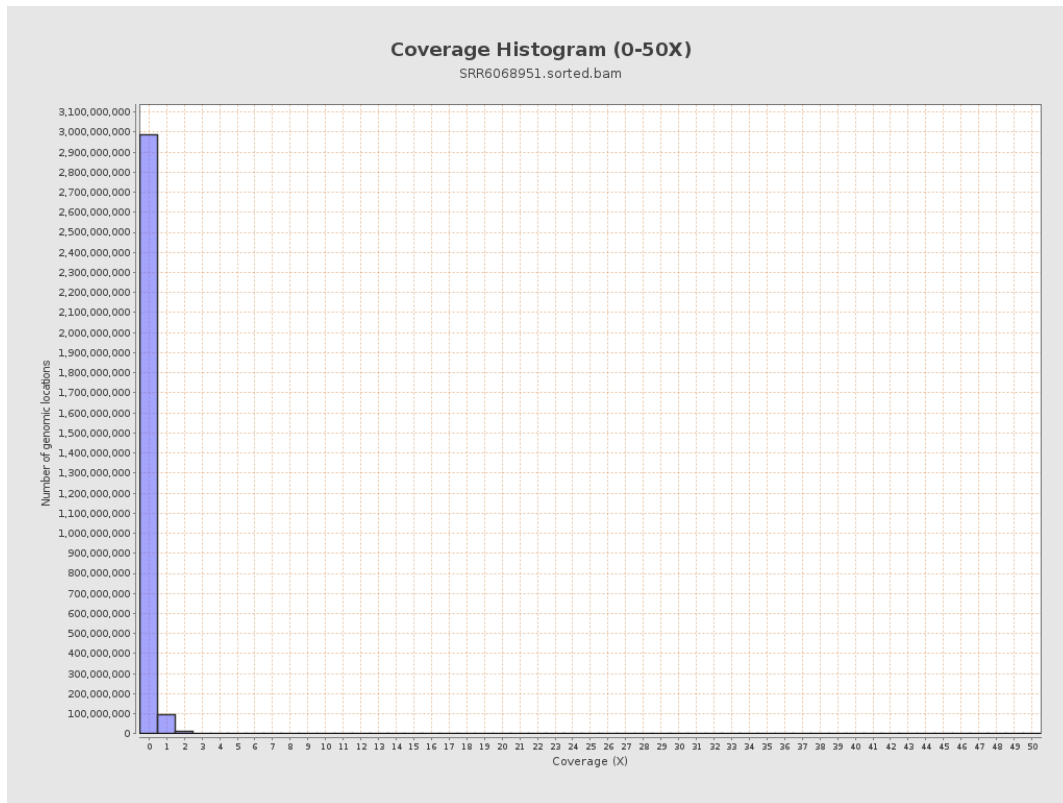
3. Results : Coverage across reference



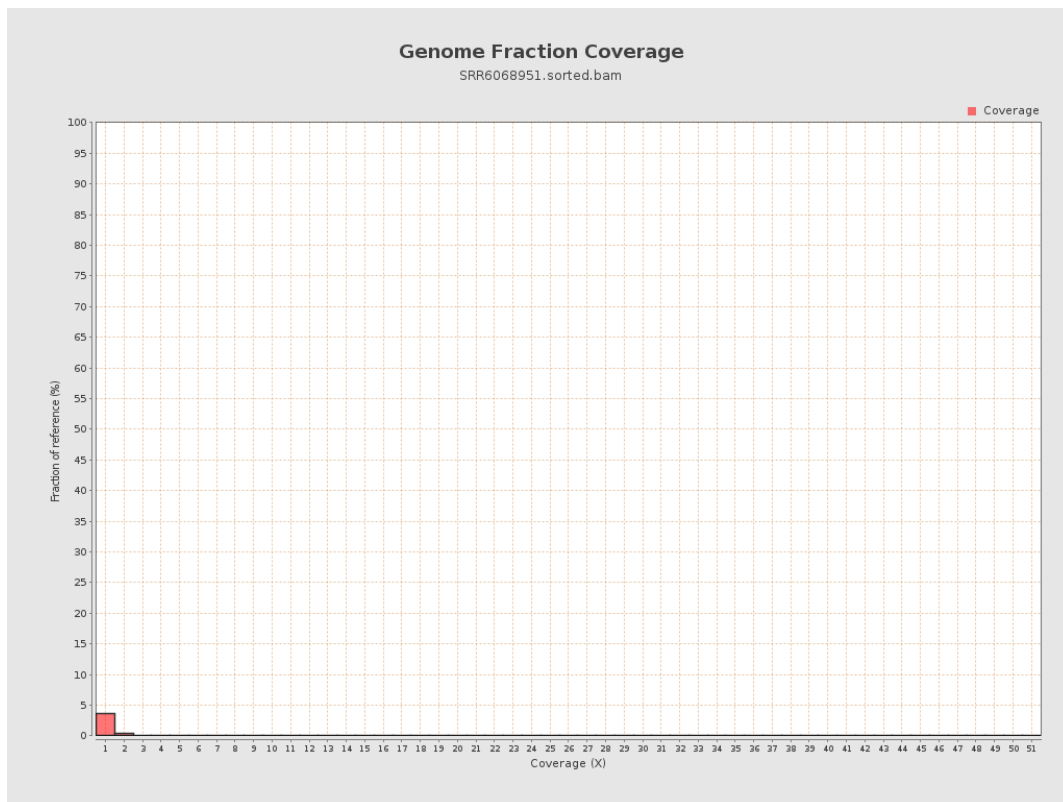
4. Results : Coverage Histogram



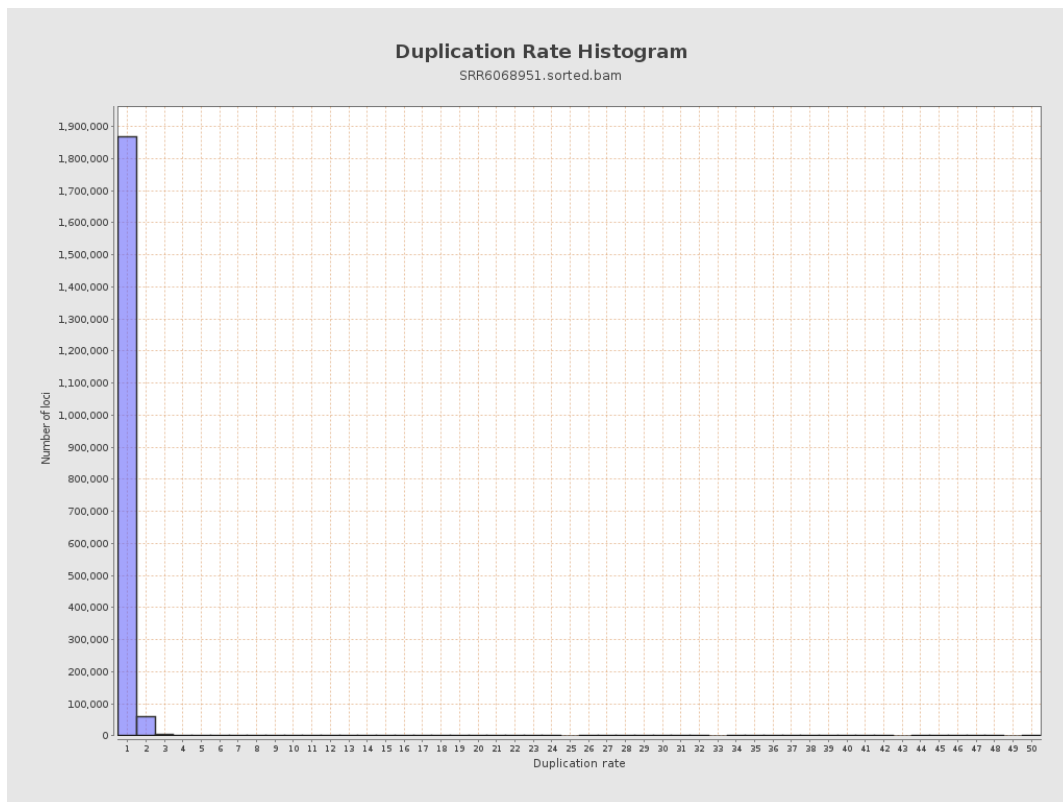
5. Results : Coverage Histogram (0-50X)



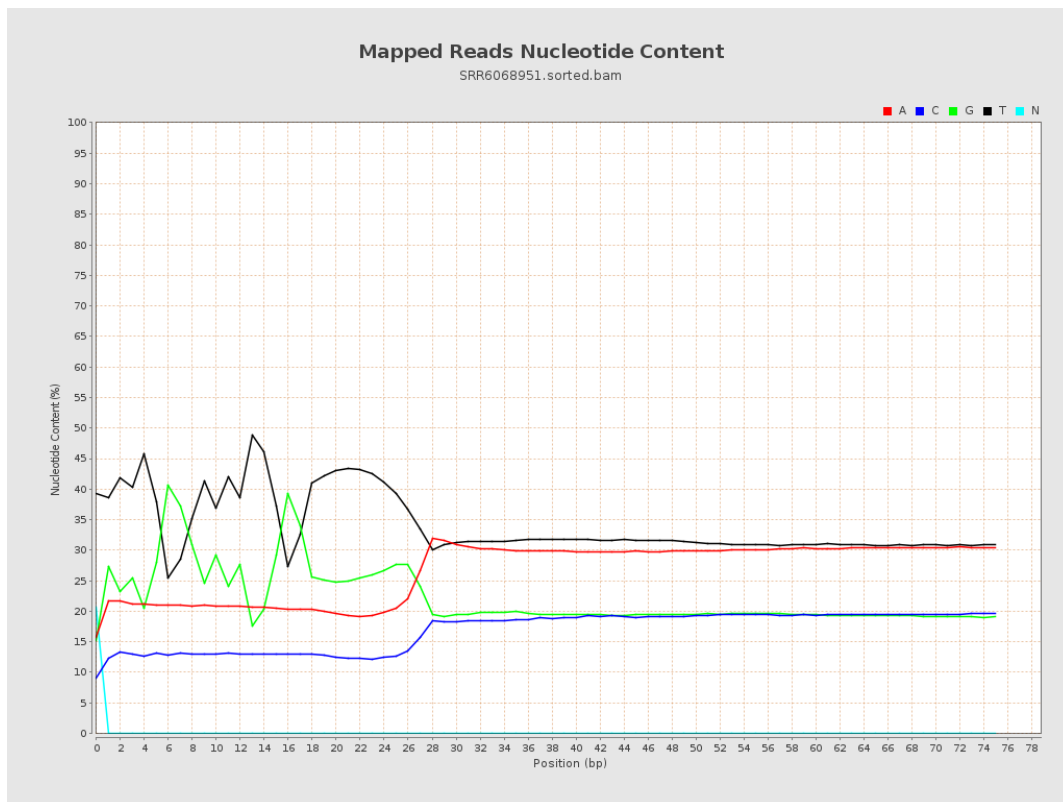
6. Results : Genome Fraction Coverage



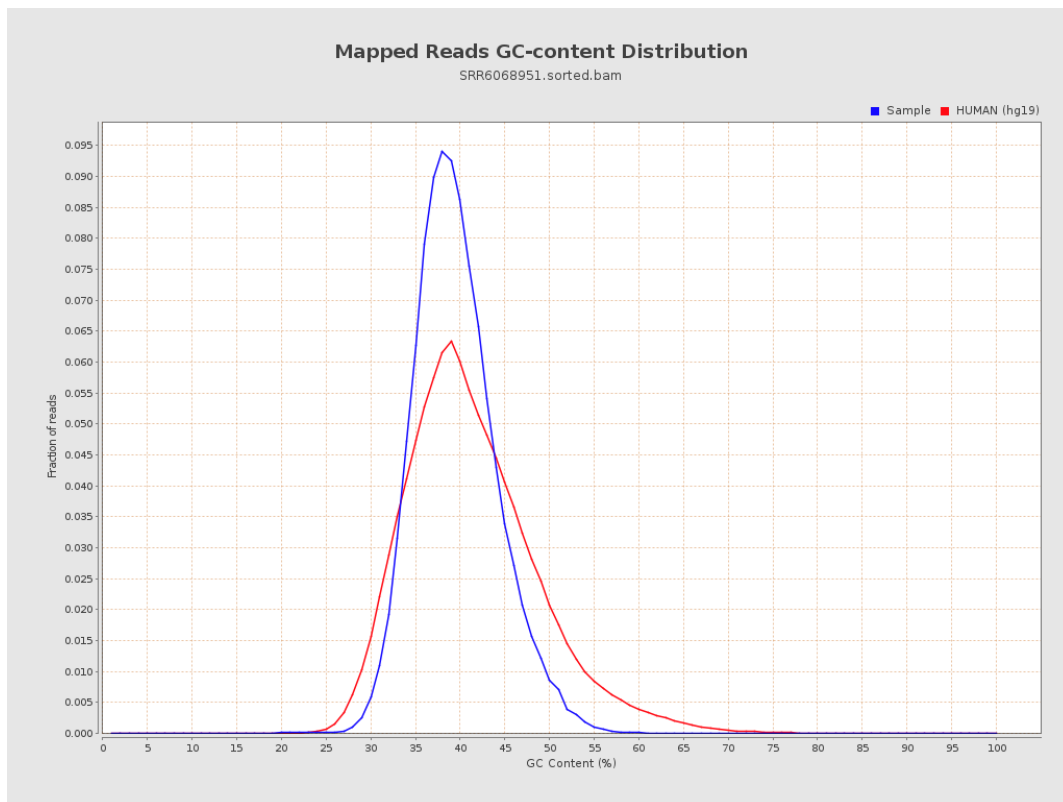
7. Results : Duplication Rate Histogram



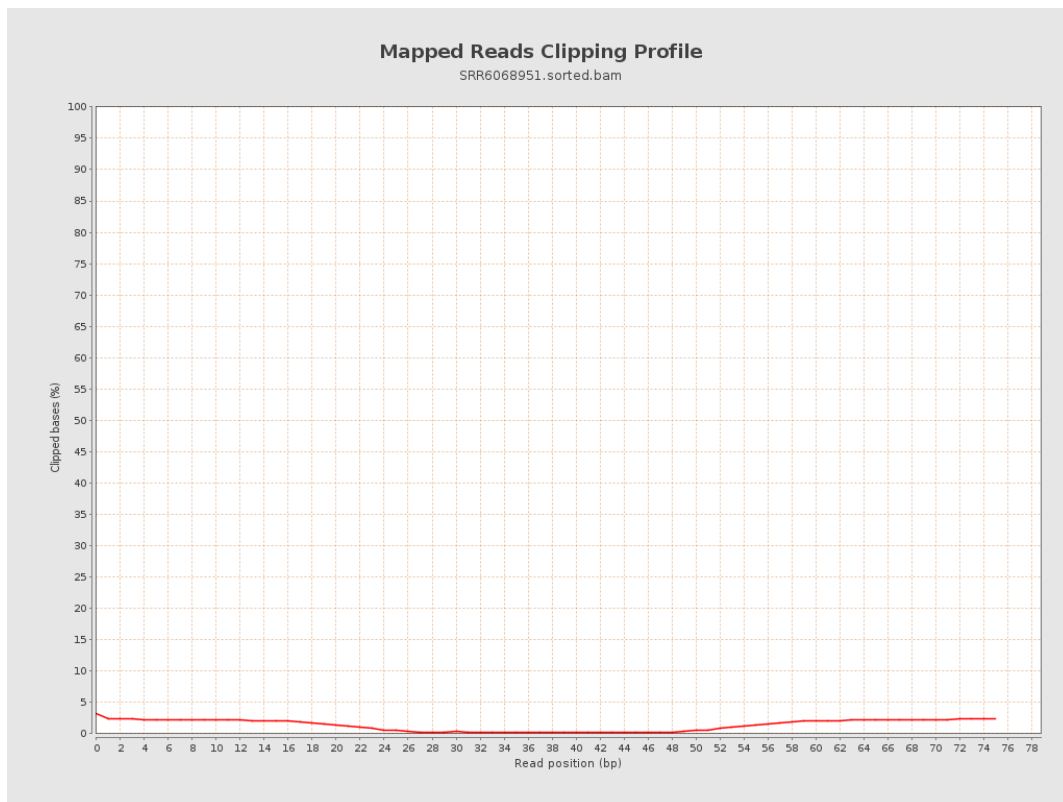
8. Results : Mapped Reads Nucleotide Content



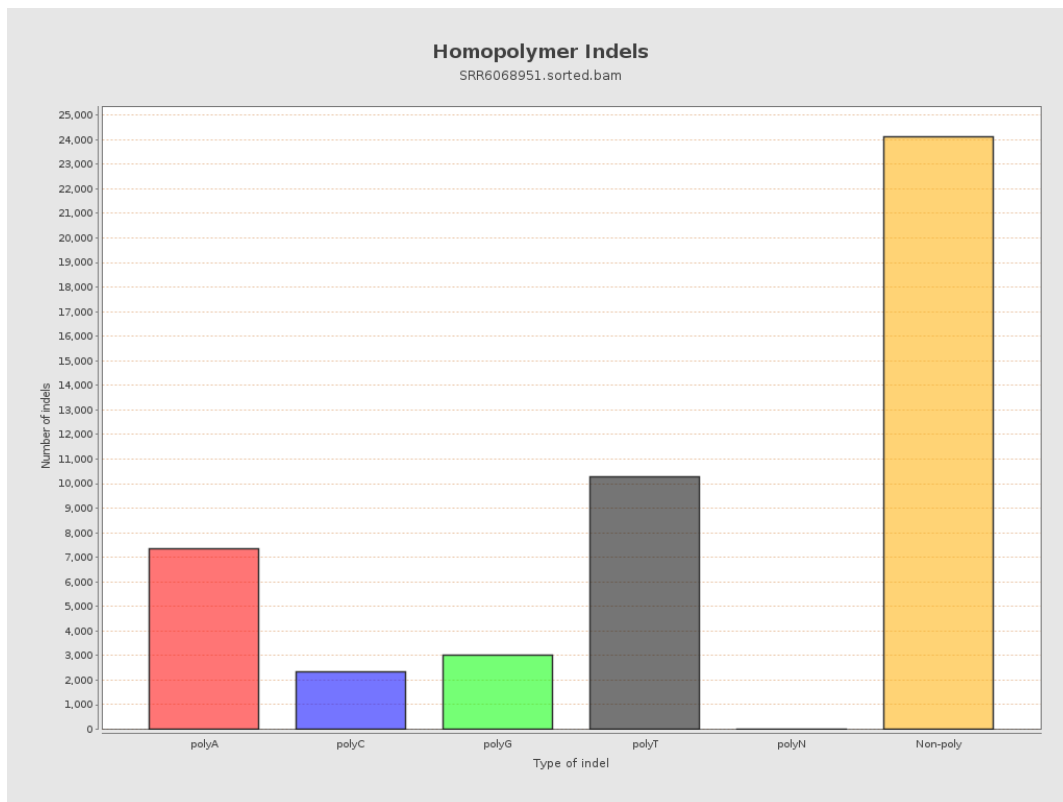
9. Results : Mapped Reads GC-content Distribution



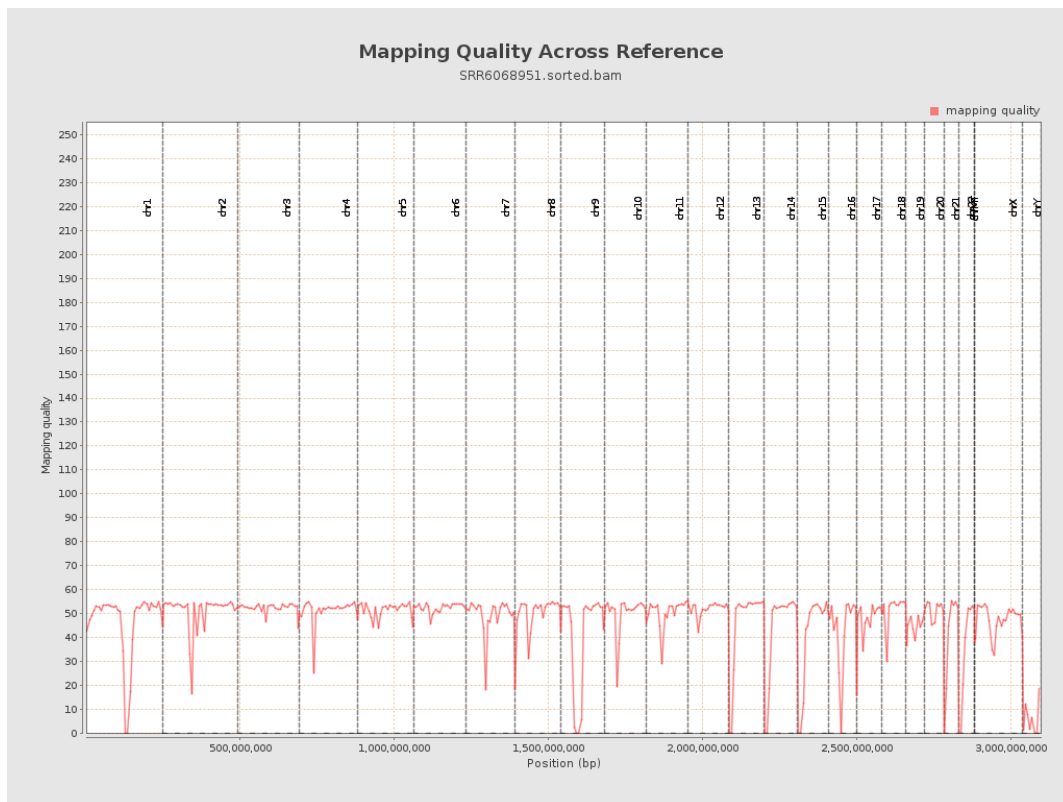
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

