

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 16:45:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068946.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_SRR6068946 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068946.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 16:45:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068946.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,724,349
Mapped reads	2,292,552 / 84.15%
Unmapped reads	431,797 / 15.85%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,258 / 0.63%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	105,311 / 3.87%
Duplication rate	3.41%
Clipped reads	966,387 / 35.47%

2.2. ACGT Content

Number/percentage of A's	43,178,498 / 28.07%
Number/percentage of C's	26,975,973 / 17.54%
Number/percentage of T's	50,989,408 / 33.15%
Number/percentage of G's	32,297,187 / 21%
Number/percentage of N's	382,853 / 0.25%
GC Percentage	38.53%

2.3. Coverage

Mean	0.0497

Standard Deviation	0.4582
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2.4. Mapping Quality

Mean Mapping Quality	43.89
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2.5. Mismatches and indels

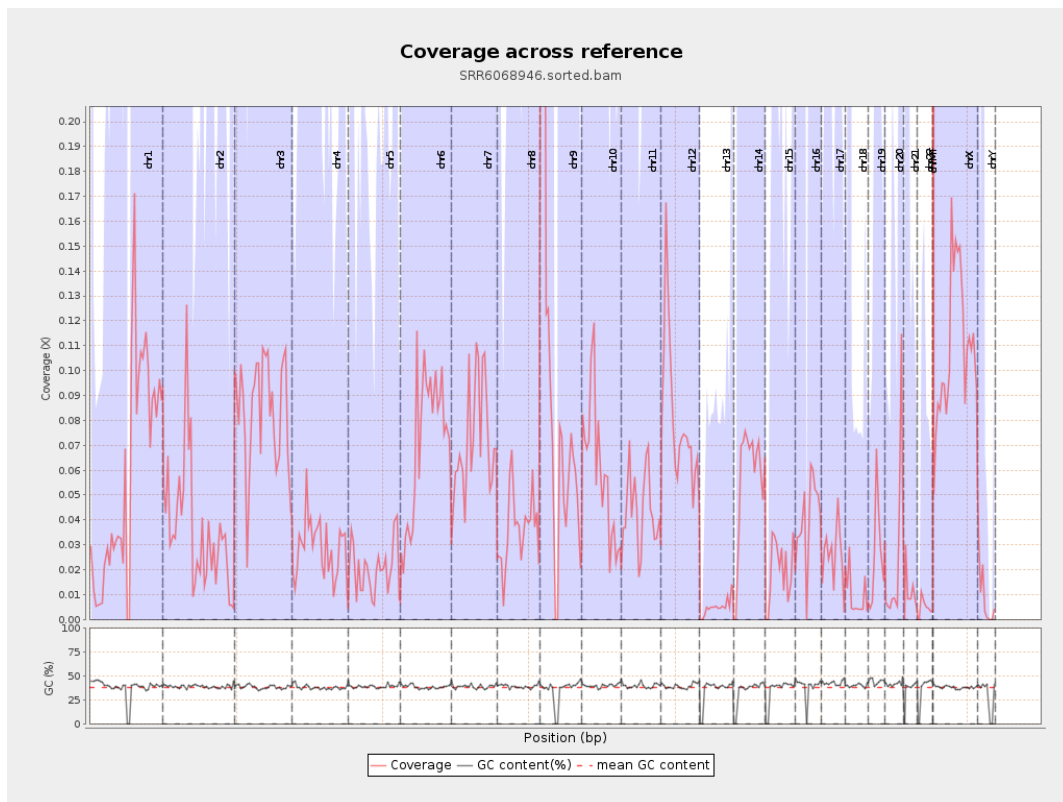
General error rate	1.13%
Mismatches	1,712,128
Insertions	14,115
Mapped reads with at least one insertion	0.61%
Deletions	41,139
Mapped reads with at least one deletion	1.77%
Homopolymer indels	48.31%

2.6. Chromosome stats

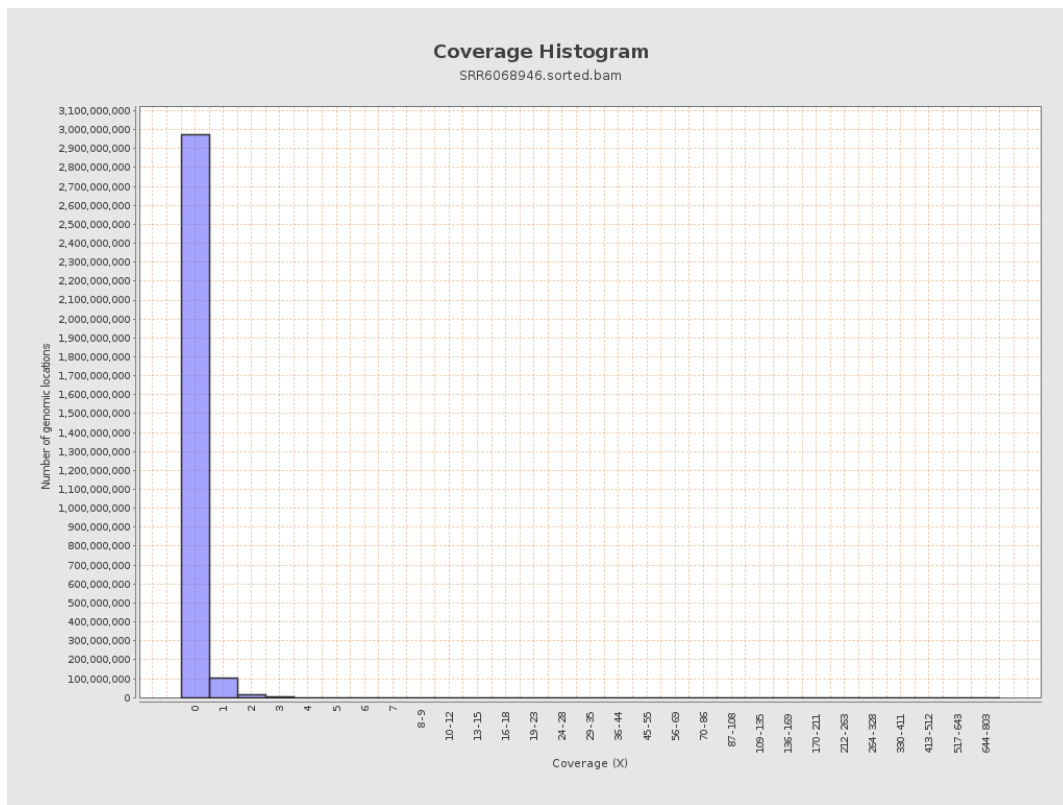
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	14047063	0.0564	0.6666
chr2	243199373	8738394	0.0359	0.3721
chr3	198022430	16577938	0.0837	0.3465
chr4	191154276	5438501	0.0285	0.2479
chr5	180915260	3608006	0.0199	0.1765
chr6	171115067	12237405	0.0715	0.4382
chr7	159138663	11417026	0.0717	0.6965

chr8	146364022	5305906	0.0363	0.5797
chr9	141213431	14181653	0.1004	0.5684
chr10	135534747	7935098	0.0585	0.5705
chr11	135006516	5944504	0.044	0.36
chr12	133851895	10826346	0.0809	0.345
chr13	115169878	588292	0.0051	0.1027
chr14	107349540	6016286	0.056	0.3268
chr15	102531392	2082105	0.0203	0.1634
chr16	90354753	3623081	0.0401	0.2956
chr17	81195210	2165225	0.0267	0.2212
chr18	78077248	744758	0.0095	0.6785
chr19	59128983	1588069	0.0269	0.3906
chr20	63025520	1708938	0.0271	0.2161
chr21	48129895	547777	0.0114	0.2217
chr22	51304566	244911	0.0048	0.0923
chrMT	16571	952755	57.4953	26.9204
chrX	155270560	16880414	0.1087	0.4576
chrY	59373566	491863	0.0083	0.1915

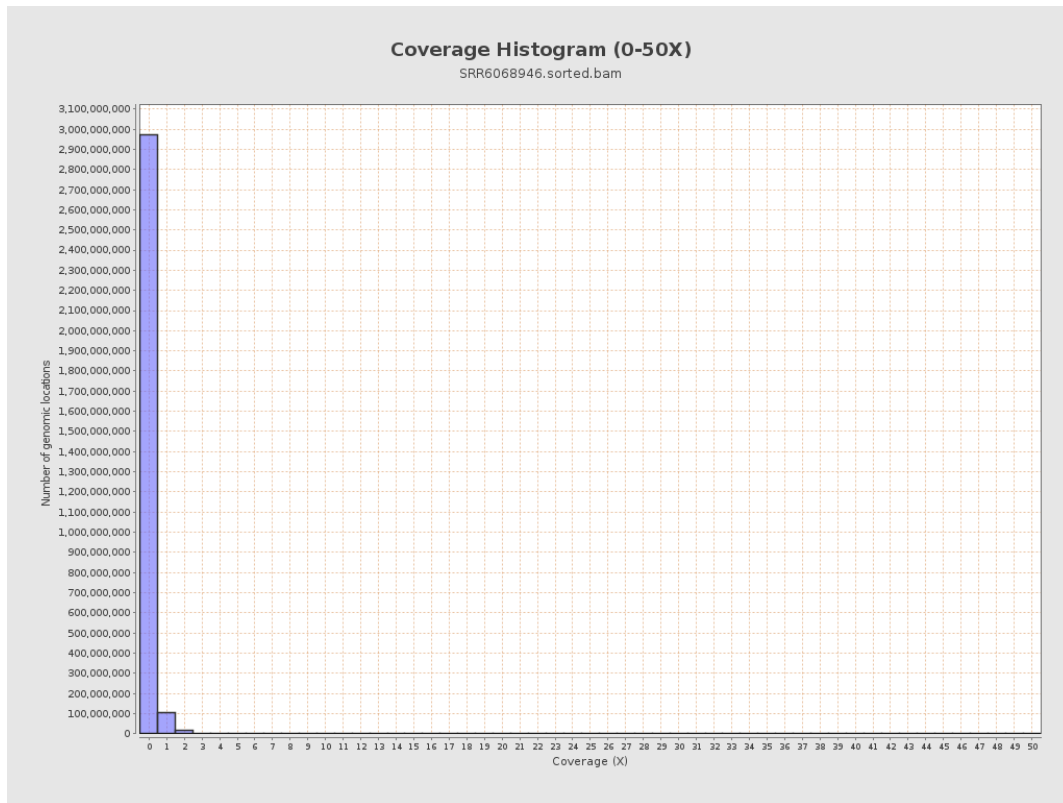
3. Results : Coverage across reference



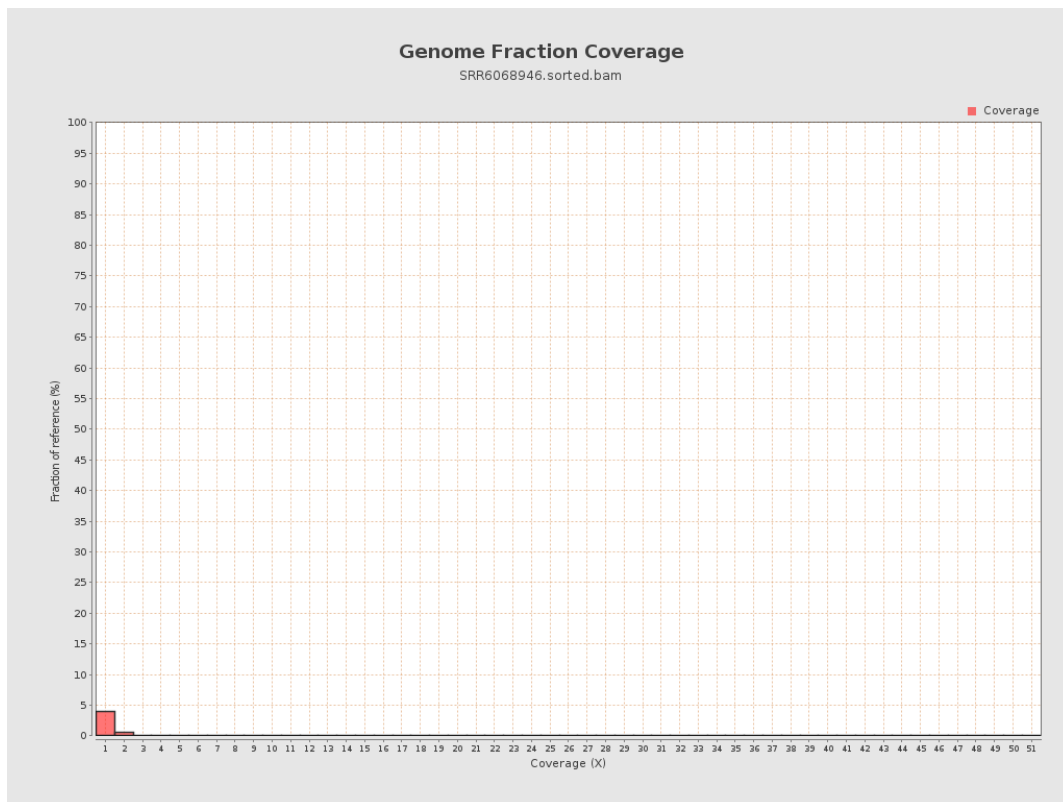
4. Results : Coverage Histogram



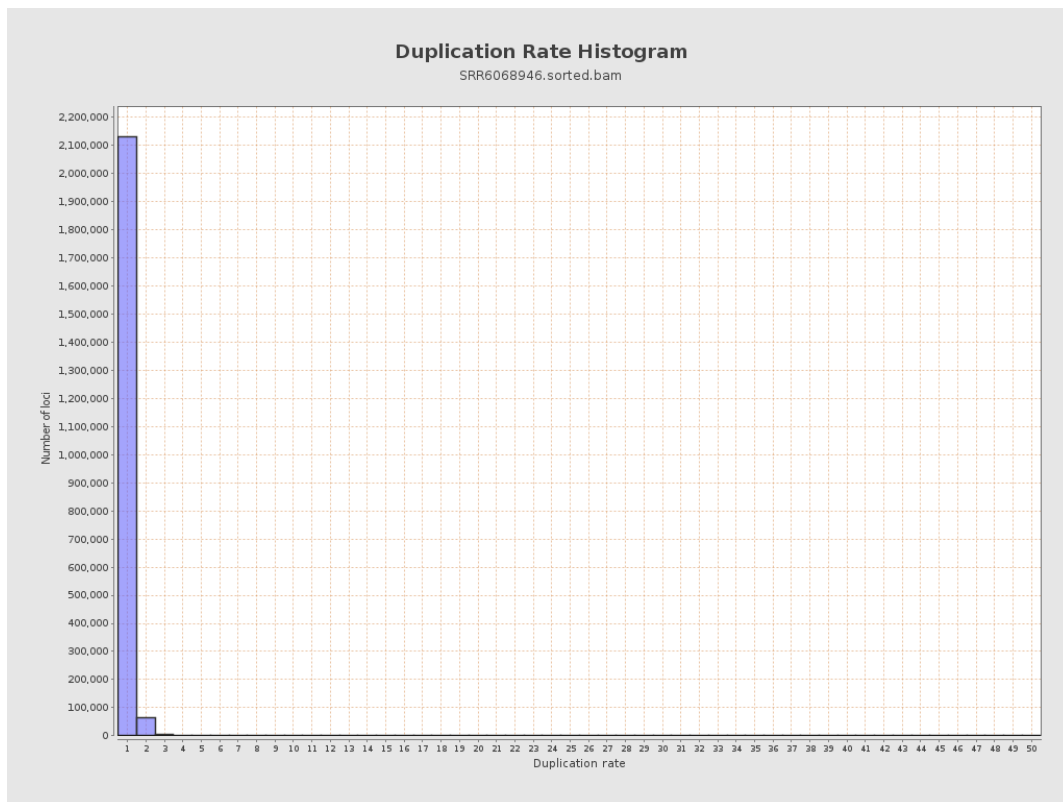
5. Results : Coverage Histogram (0-50X)



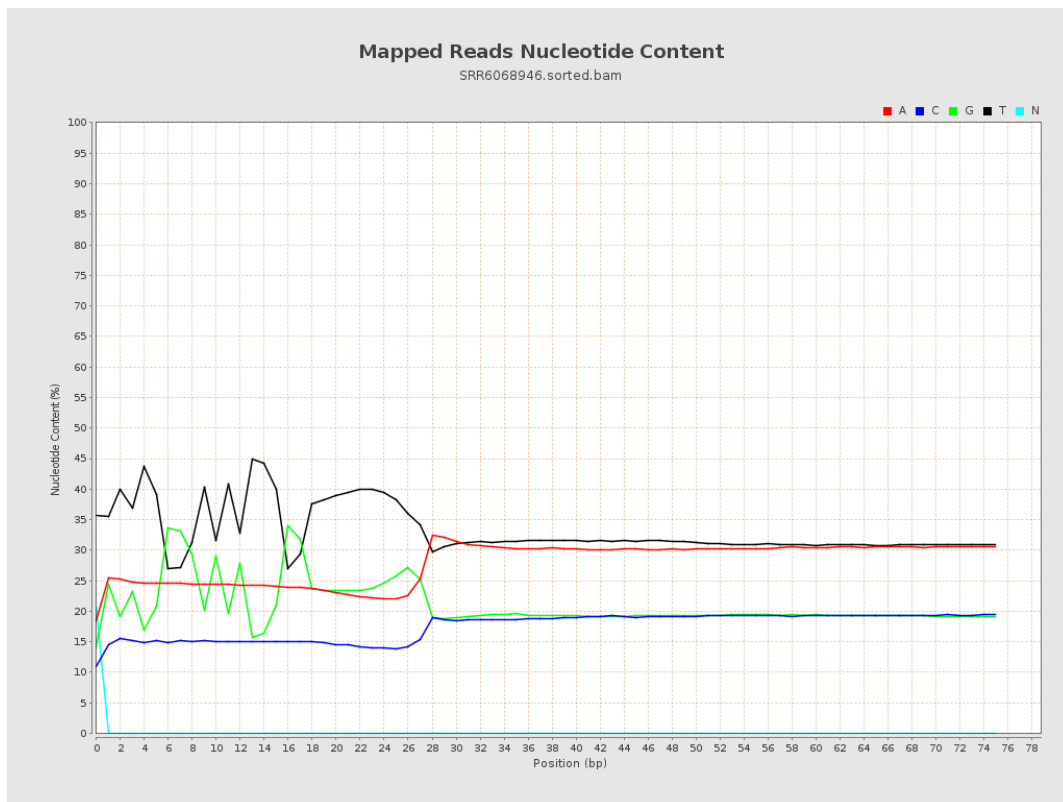
6. Results : Genome Fraction Coverage



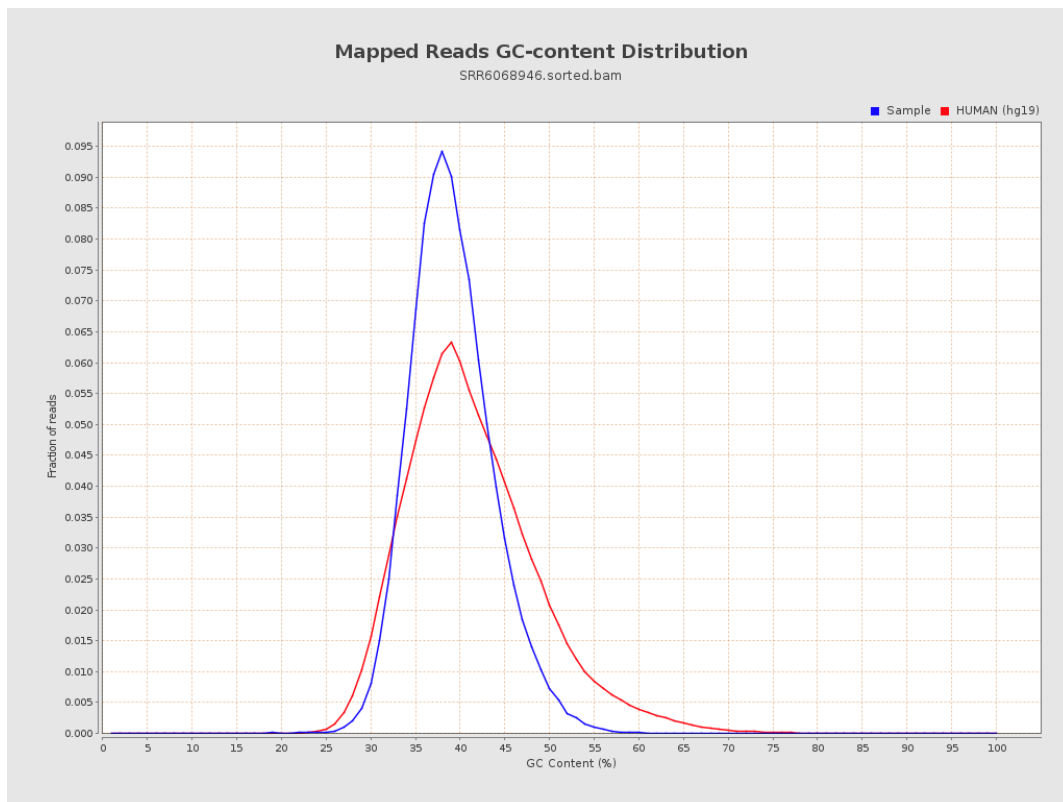
7. Results : Duplication Rate Histogram



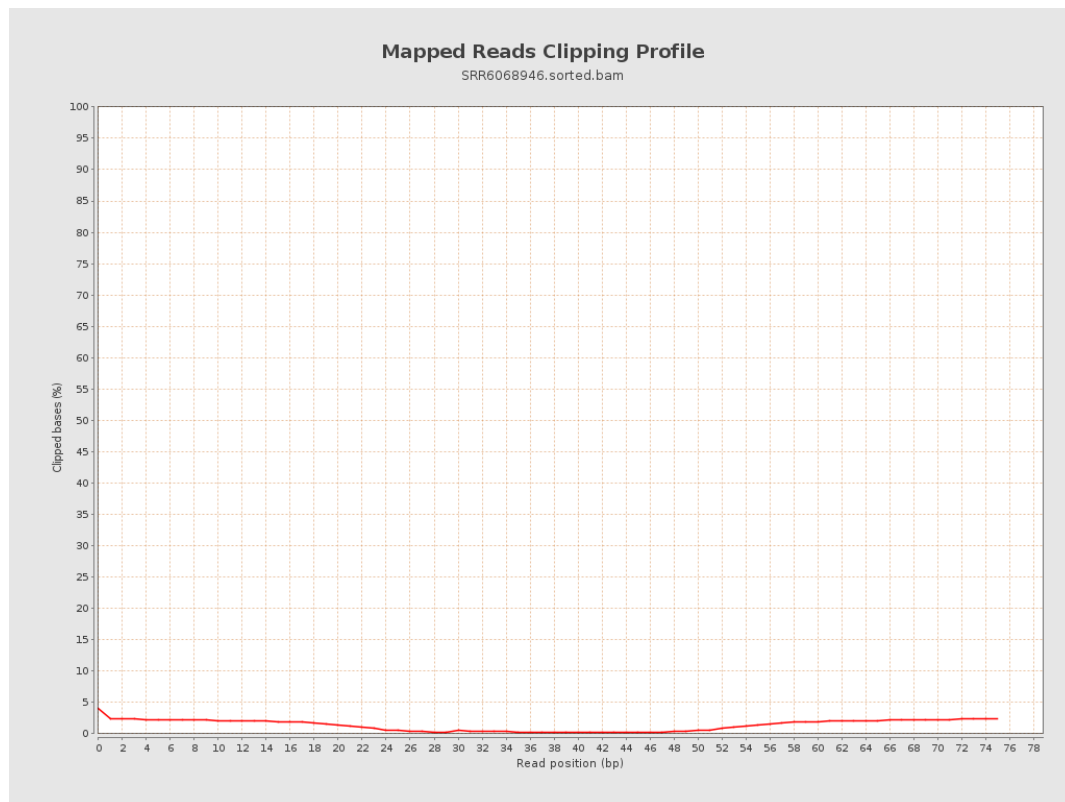
8. Results : Mapped Reads Nucleotide Content



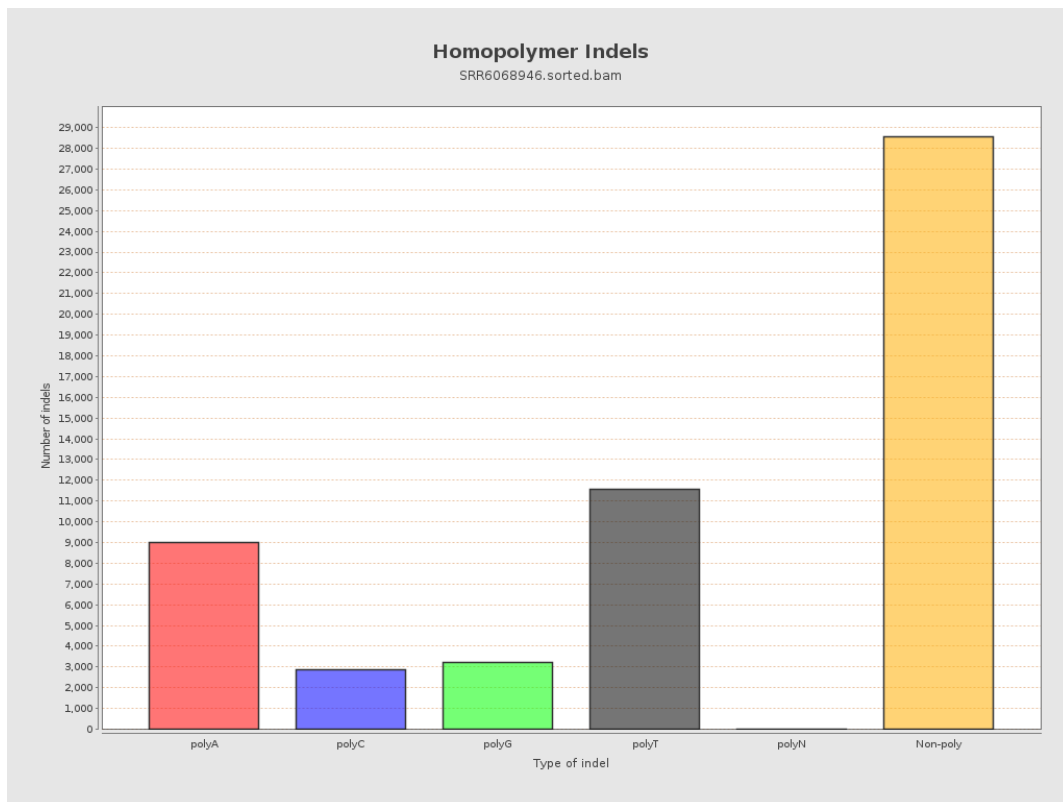
9. Results : Mapped Reads GC-content Distribution



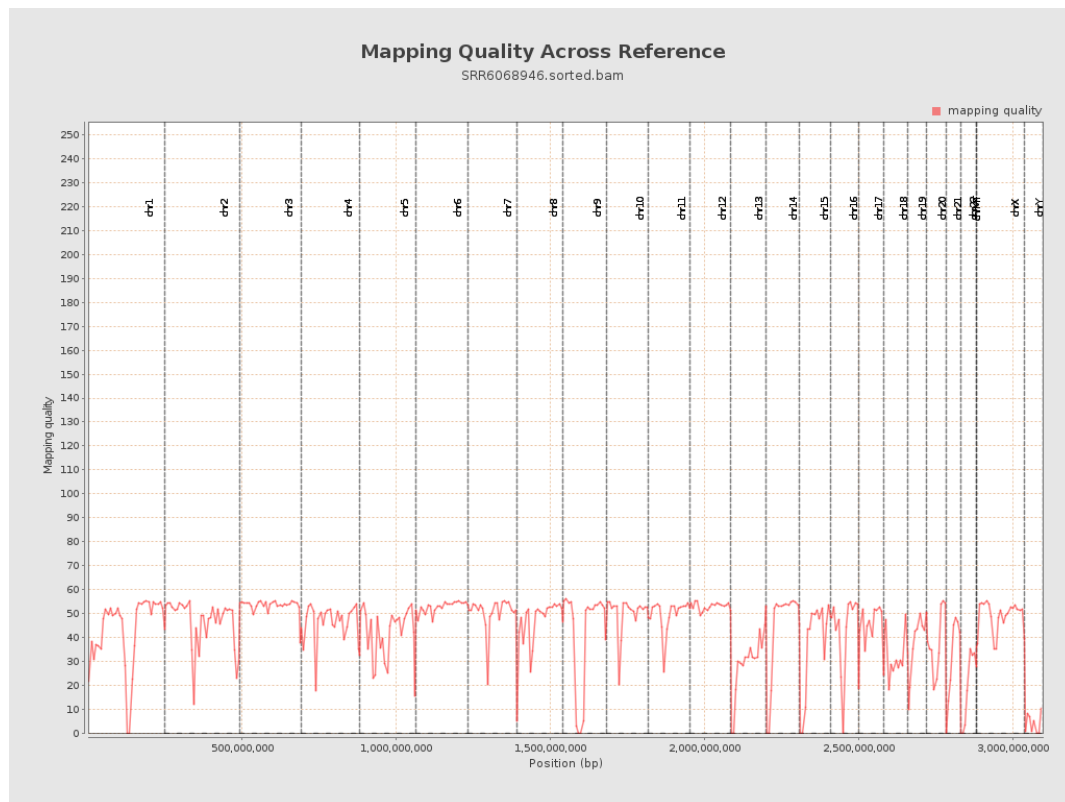
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

