

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 09:51:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068097.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_SRR6068097 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068097.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 09:51:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068097.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,631,557
Mapped reads	2,205,679 / 83.82%
Unmapped reads	425,878 / 16.18%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,936 / 0.83%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	264,516 / 10.05%
Duplication rate	9.39%
Clipped reads	1,208,935 / 45.94%

2.2. ACGT Content

Number/percentage of A's	38,567,832 / 27.23%
Number/percentage of C's	25,443,232 / 17.96%
Number/percentage of T's	45,697,952 / 32.27%
Number/percentage of G's	31,921,196 / 22.54%
Number/percentage of N's	2,691 / 0%
GC Percentage	40.5%

2.3. Coverage

Mean	0.0458

Standard Deviation	0.4484
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2.4. Mapping Quality

Mean Mapping Quality	43.27
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2.5. Mismatches and indels

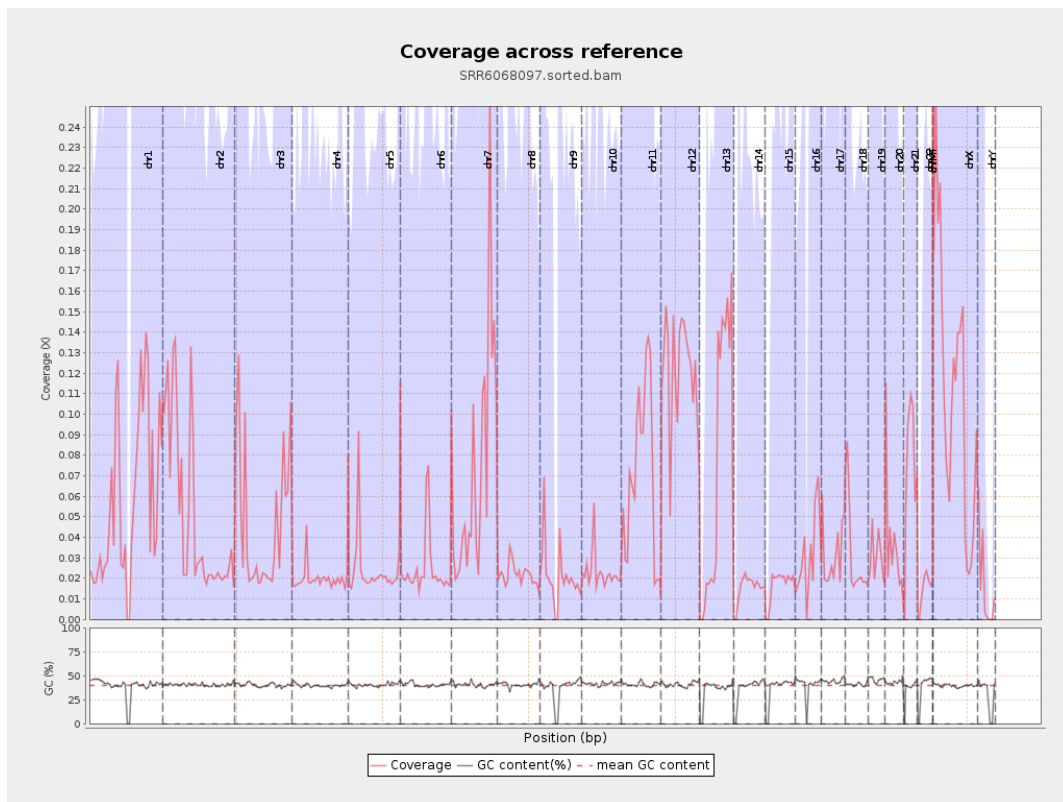
General error rate	0.8%
Mismatches	1,108,479
Insertions	10,938
Mapped reads with at least one insertion	0.49%
Deletions	35,662
Mapped reads with at least one deletion	1.6%
Homopolymer indels	46.6%

2.6. Chromosome stats

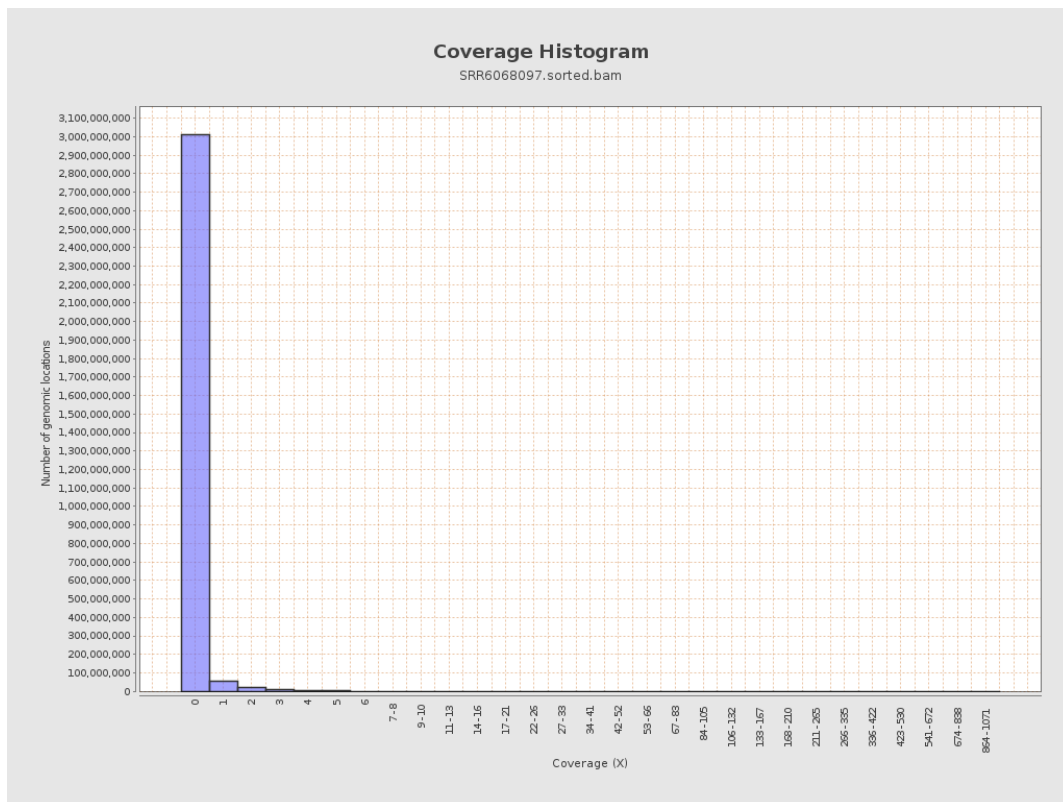
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	14410562	0.0578	0.5008
chr2	243199373	12454115	0.0512	0.674
chr3	198022430	9060961	0.0458	0.3299
chr4	191154276	3759935	0.0197	0.2463
chr5	180915260	4553154	0.0252	0.2464
chr6	171115067	4228462	0.0247	0.2799
chr7	159138663	11536695	0.0725	0.4829

chr8	146364022	3180818	0.0217	0.5993
chr9	141213431	2989639	0.0212	0.3587
chr10	135534747	3085662	0.0228	0.3855
chr11	135006516	9650186	0.0715	0.6743
chr12	133851895	16345863	0.1221	0.537
chr13	115169878	8784819	0.0763	0.4299
chr14	107349540	1647192	0.0153	0.2022
chr15	102531392	1699322	0.0166	0.2235
chr16	90354753	2745762	0.0304	0.2962
chr17	81195210	2551708	0.0314	0.3314
chr18	78077248	2462890	0.0315	0.6052
chr19	59128983	1799619	0.0304	0.3282
chr20	63025520	2243103	0.0356	0.2947
chr21	48129895	3567289	0.0741	0.4499
chr22	51304566	734469	0.0143	0.1754
chrMT	16571	61486	3.7105	3.4846
chrX	155270560	17241605	0.111	0.5383
chrY	59373566	894627	0.0151	0.5262

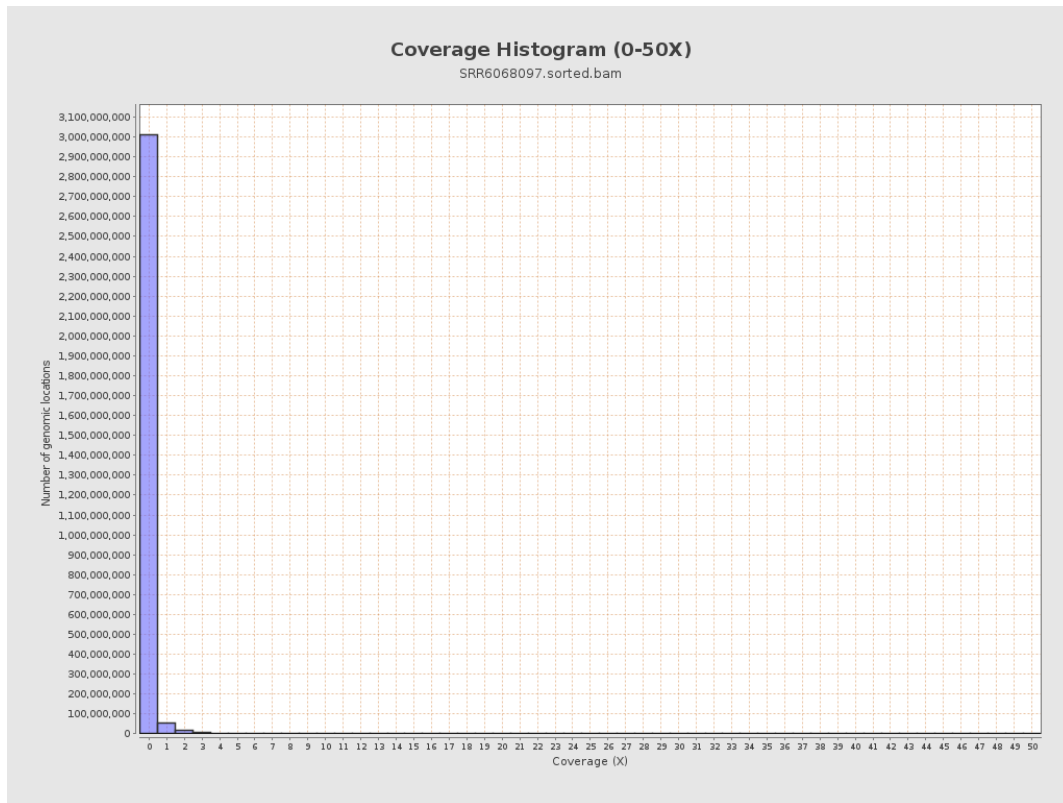
3. Results : Coverage across reference



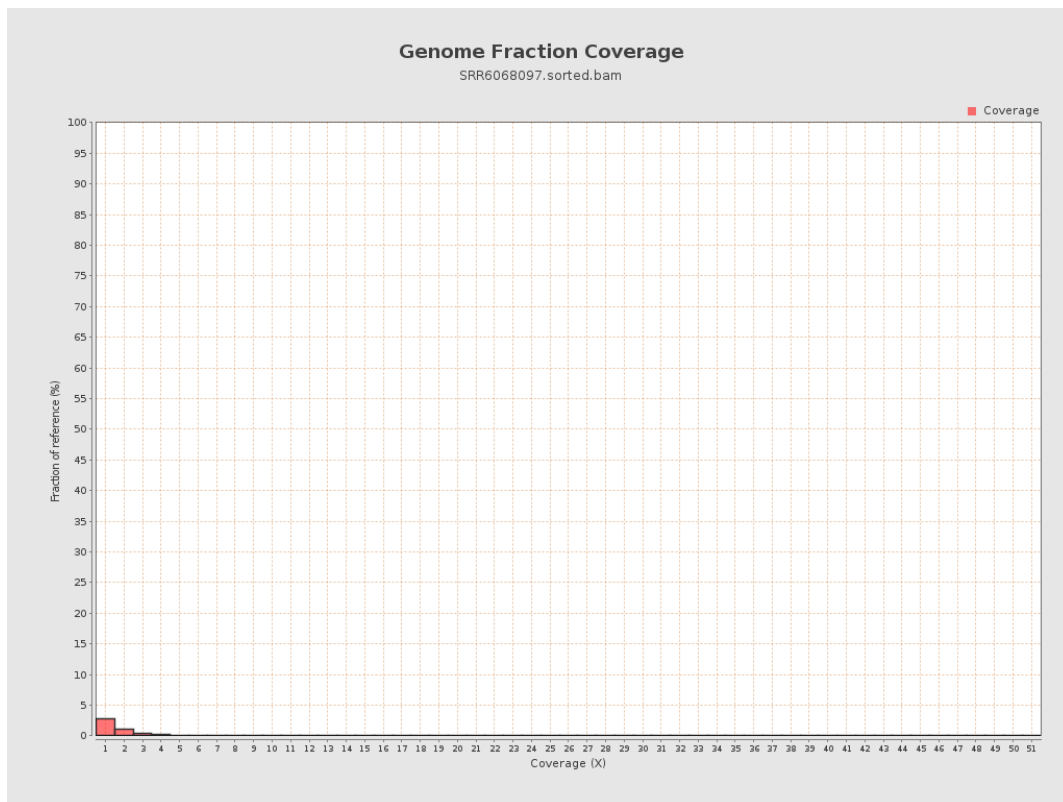
4. Results : Coverage Histogram



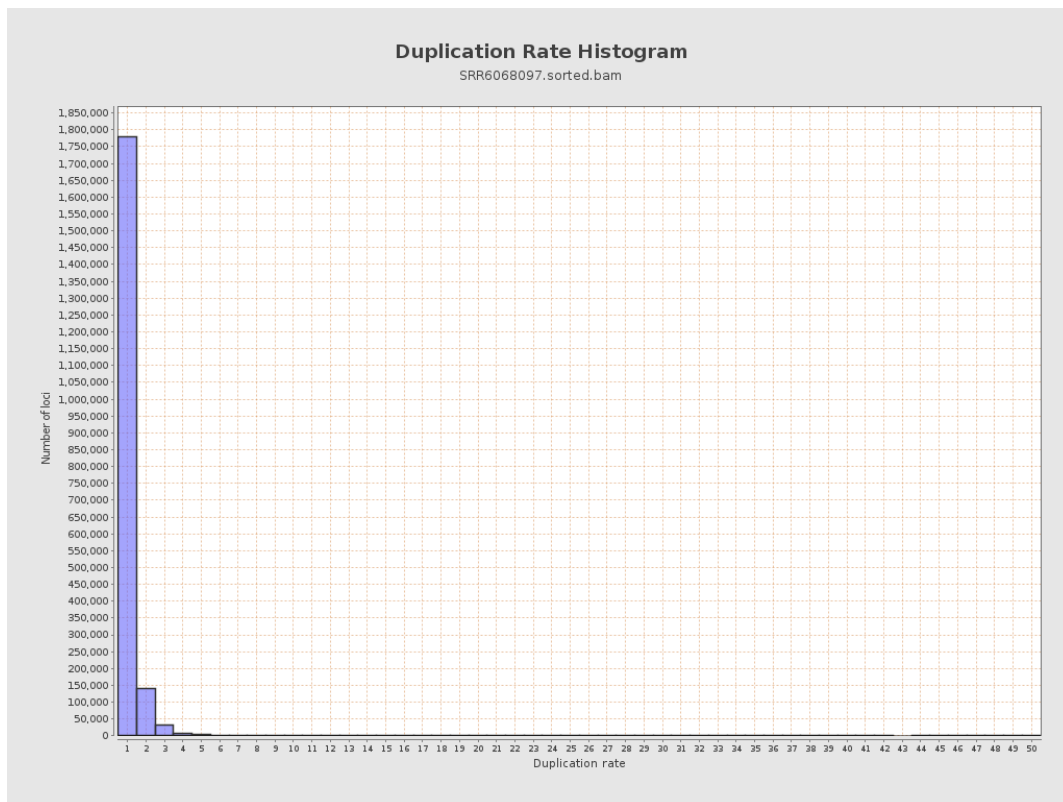
5. Results : Coverage Histogram (0-50X)



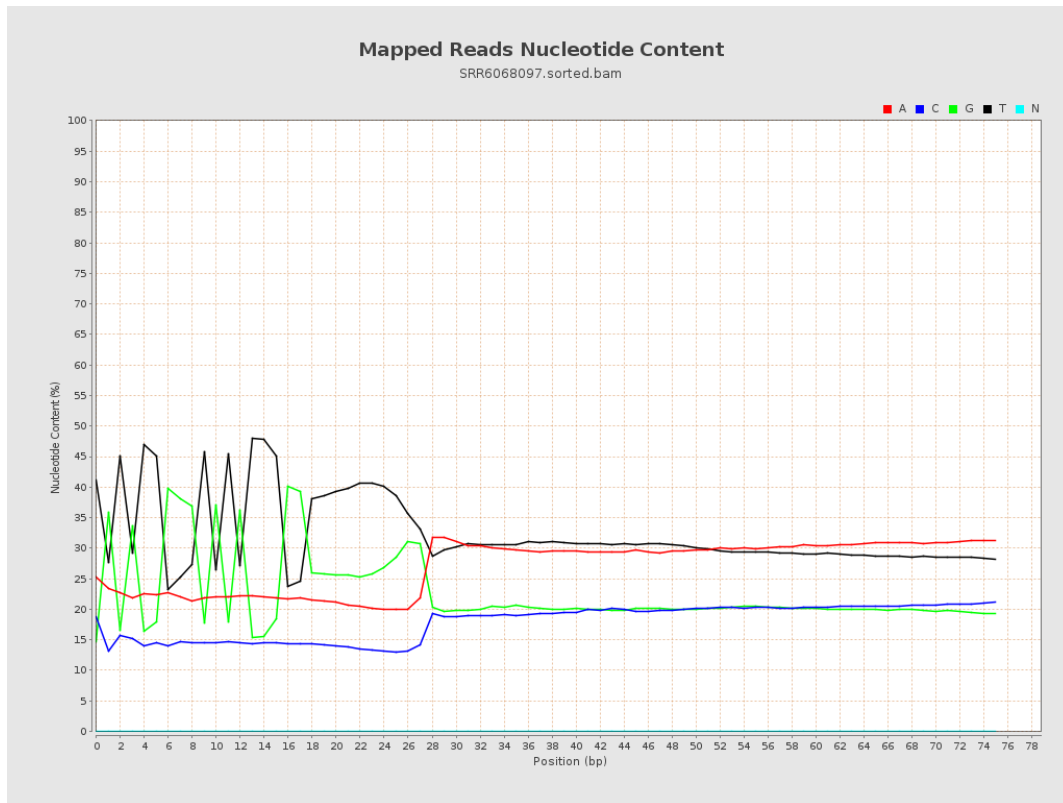
6. Results : Genome Fraction Coverage



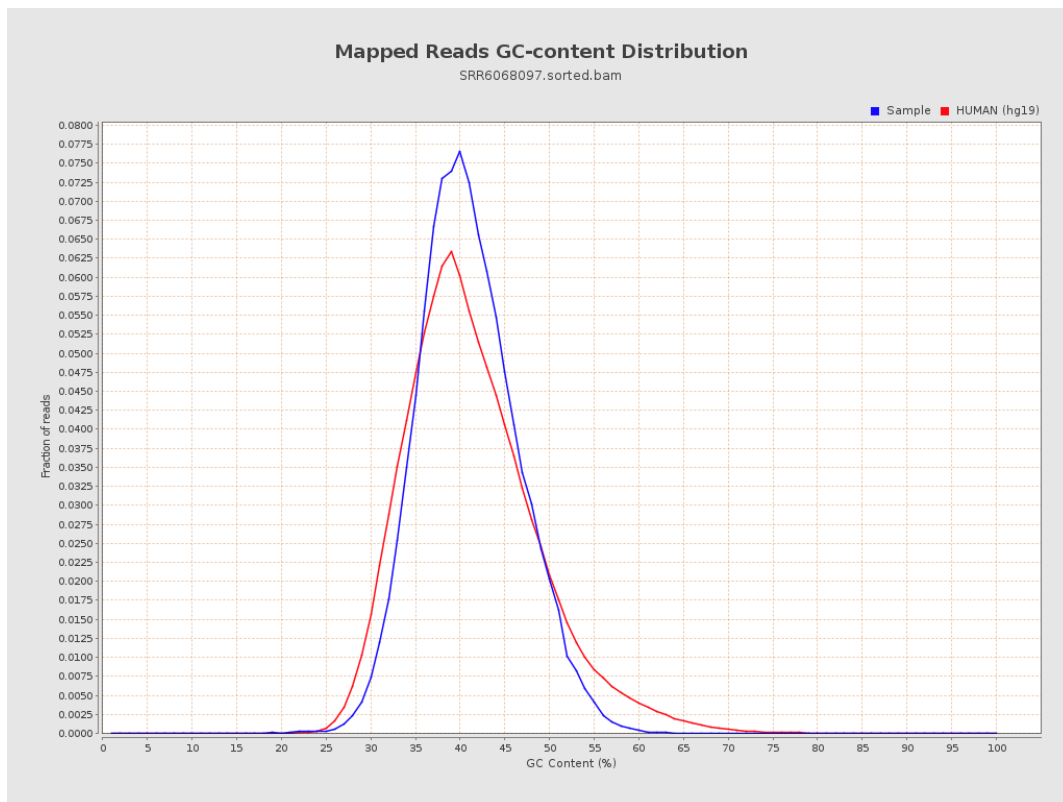
7. Results : Duplication Rate Histogram



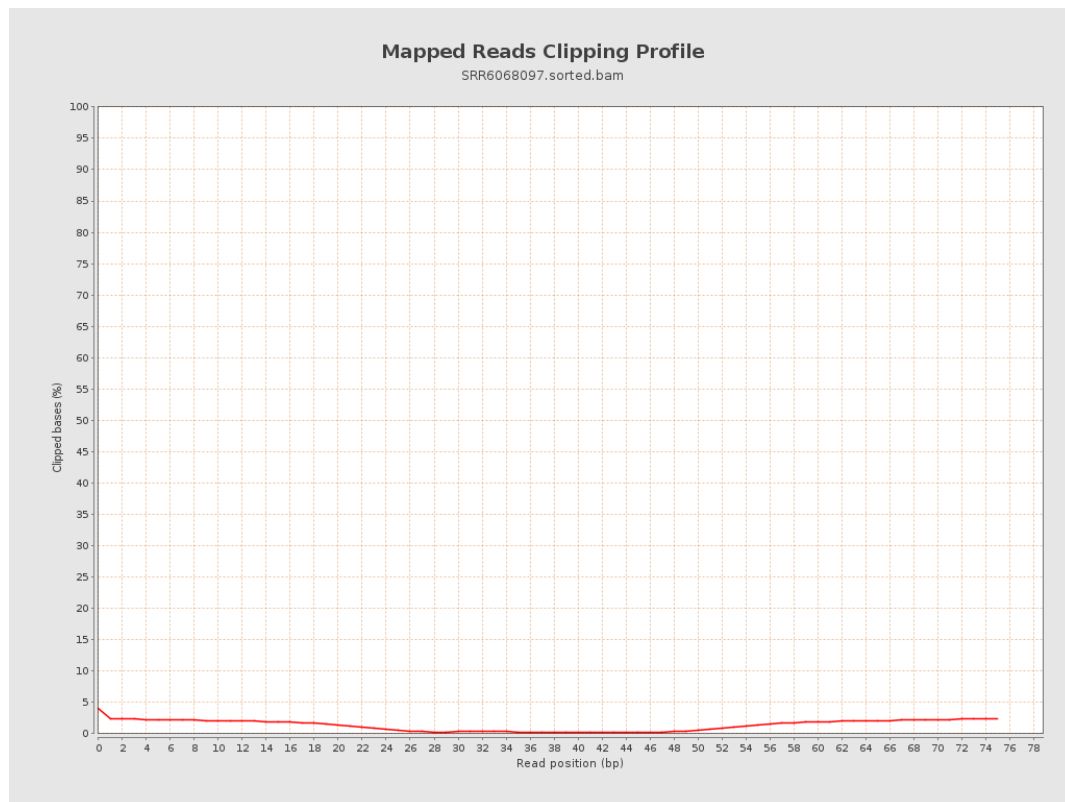
8. Results : Mapped Reads Nucleotide Content



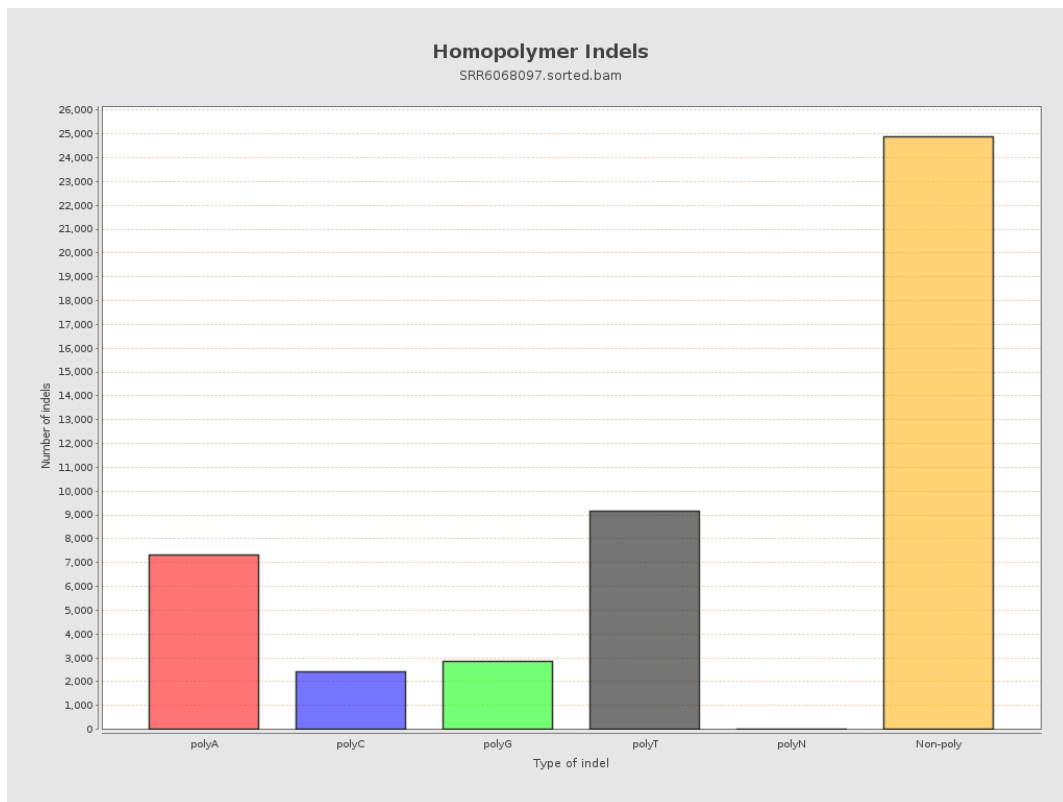
9. Results : Mapped Reads GC-content Distribution



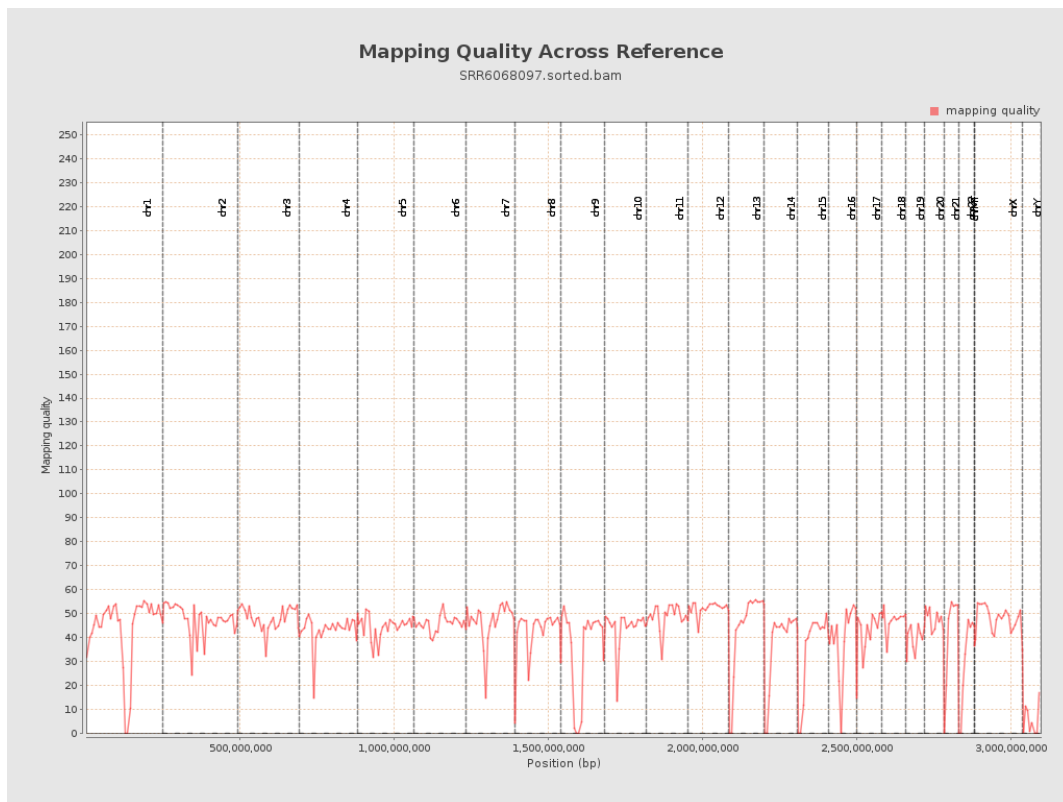
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

