

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 13:13:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234063.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_SRR6234063 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234063.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 13:13:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234063.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,598,178
Mapped reads	3,365,796 / 93.54%
Unmapped reads	232,382 / 6.46%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	38,583 / 1.07%
Read min/max/mean length	30 / 76 / 76.38
Duplicated reads (estimated)	464,944 / 12.92%
Duplication rate	5.53%
Clipped reads	1,205,493 / 33.5%

2.2. ACGT Content

Number/percentage of A's	60,283,700 / 26.03%
Number/percentage of C's	41,364,869 / 17.86%
Number/percentage of T's	65,088,983 / 28.1%
Number/percentage of G's	64,834,844 / 27.99%
Number/percentage of N's	48,724 / 0.02%
GC Percentage	45.85%

2.3. Coverage

Mean	0.0748

Standard Deviation	36.5247
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2.4. Mapping Quality

Mean Mapping Quality	46.02
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2.5. Mismatches and indels

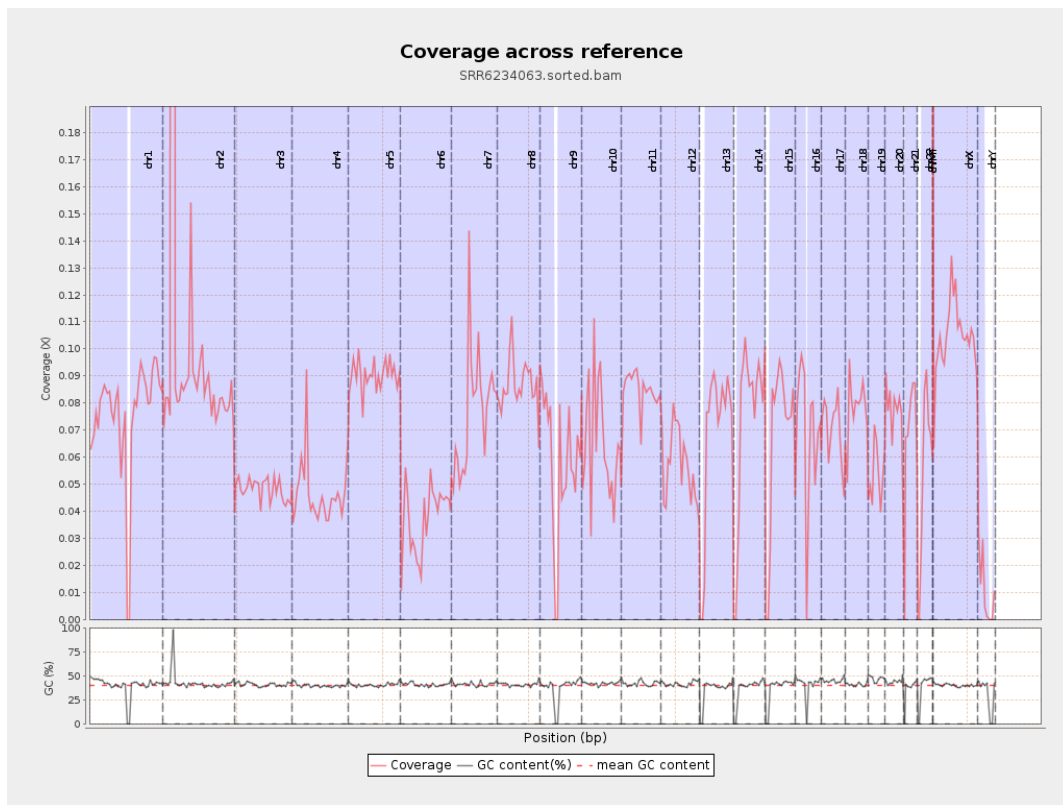
General error rate	0.68%
Mismatches	1,556,774
Insertions	15,654
Mapped reads with at least one insertion	0.46%
Deletions	50,522
Mapped reads with at least one deletion	1.49%
Homopolymer indels	46.52%

2.6. Chromosome stats

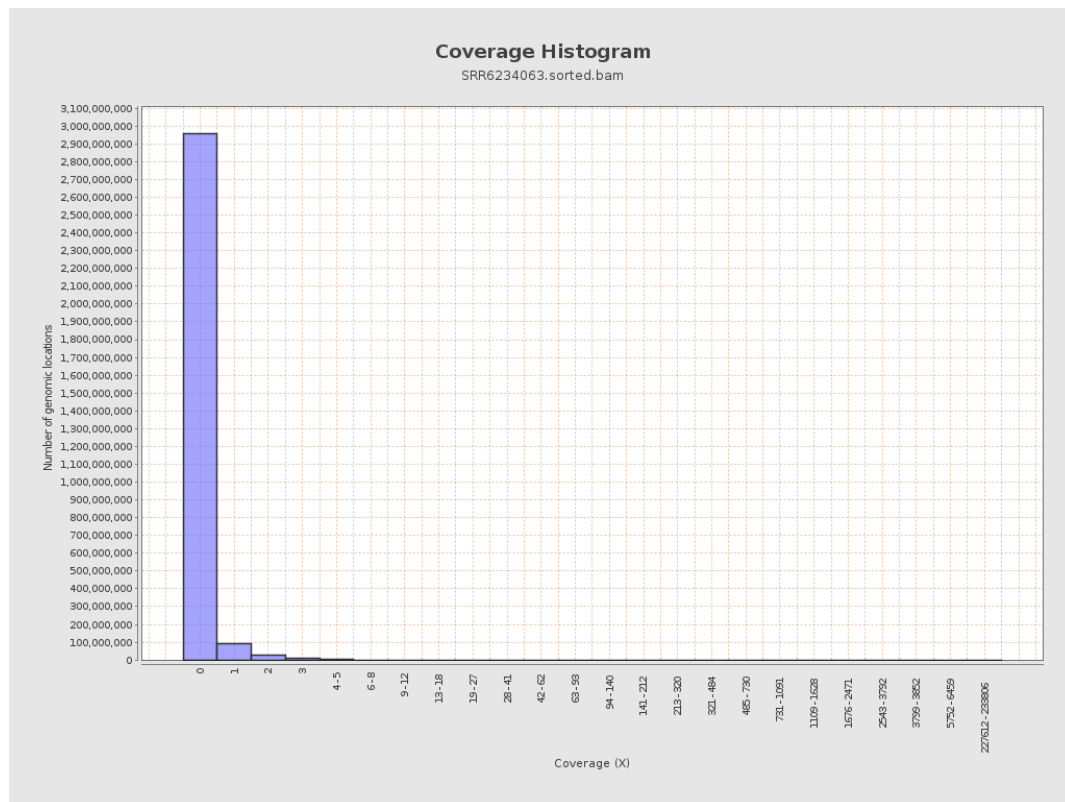
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	18851709	0.0756	0.8471
chr2	243199373	39091281	0.1607	130.2945
chr3	198022430	9489103	0.0479	0.3116
chr4	191154276	8880772	0.0465	0.3352
chr5	180915260	16335281	0.0903	0.4383
chr6	171115067	6398192	0.0374	0.2941
chr7	159138663	12241691	0.0769	1.0522

chr8	146364022	12684522	0.0867	0.8527
chr9	141213431	8144914	0.0577	0.5656
chr10	135534747	8833045	0.0652	0.5625
chr11	135006516	11402895	0.0845	0.8648
chr12	133851895	7662506	0.0572	0.351
chr13	115169878	7796920	0.0677	0.3739
chr14	107349540	7983290	0.0744	0.5274
chr15	102531392	6867405	0.067	0.3736
chr16	90354753	6124839	0.0678	0.4454
chr17	81195210	5778115	0.0712	0.5031
chr18	78077248	6103171	0.0782	1.3669
chr19	59128983	3211802	0.0543	0.6427
chr20	63025520	4880093	0.0774	0.4479
chr21	48129895	3315148	0.0689	0.4044
chr22	51304566	2791033	0.0544	0.337
chrMT	16571	6968	0.4205	0.9763
chrX	155270560	16206301	0.1044	0.5378
chrY	59373566	622921	0.0105	0.1987

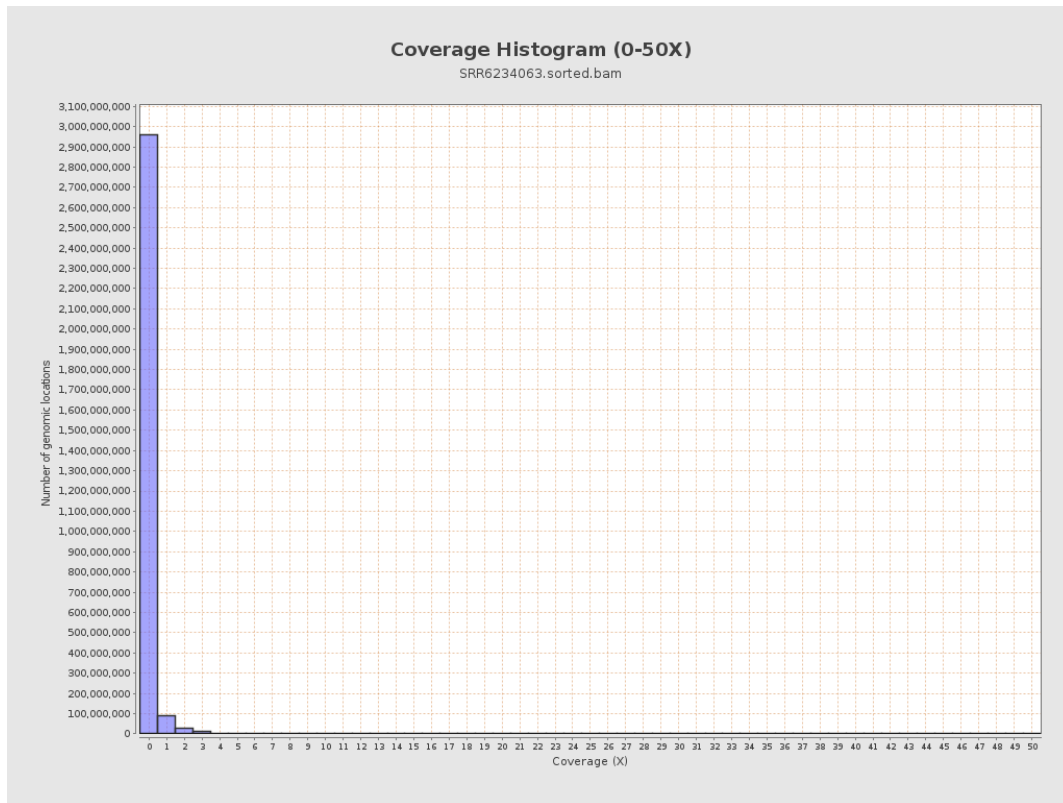
3. Results : Coverage across reference



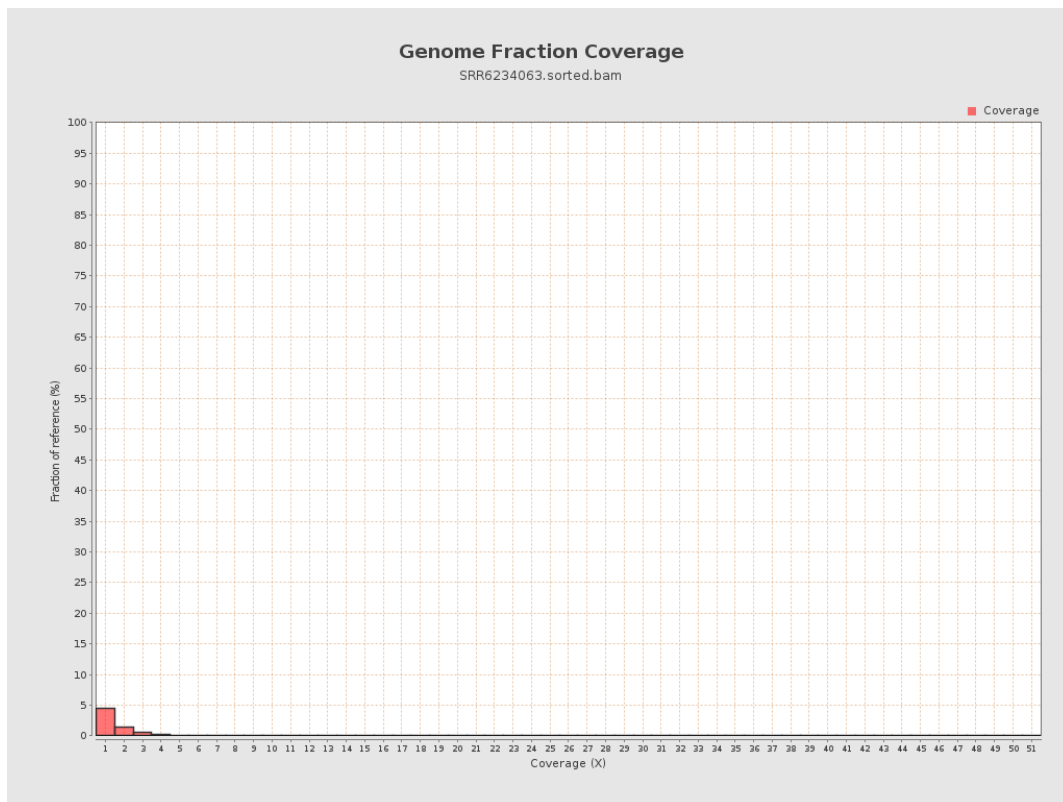
4. Results : Coverage Histogram



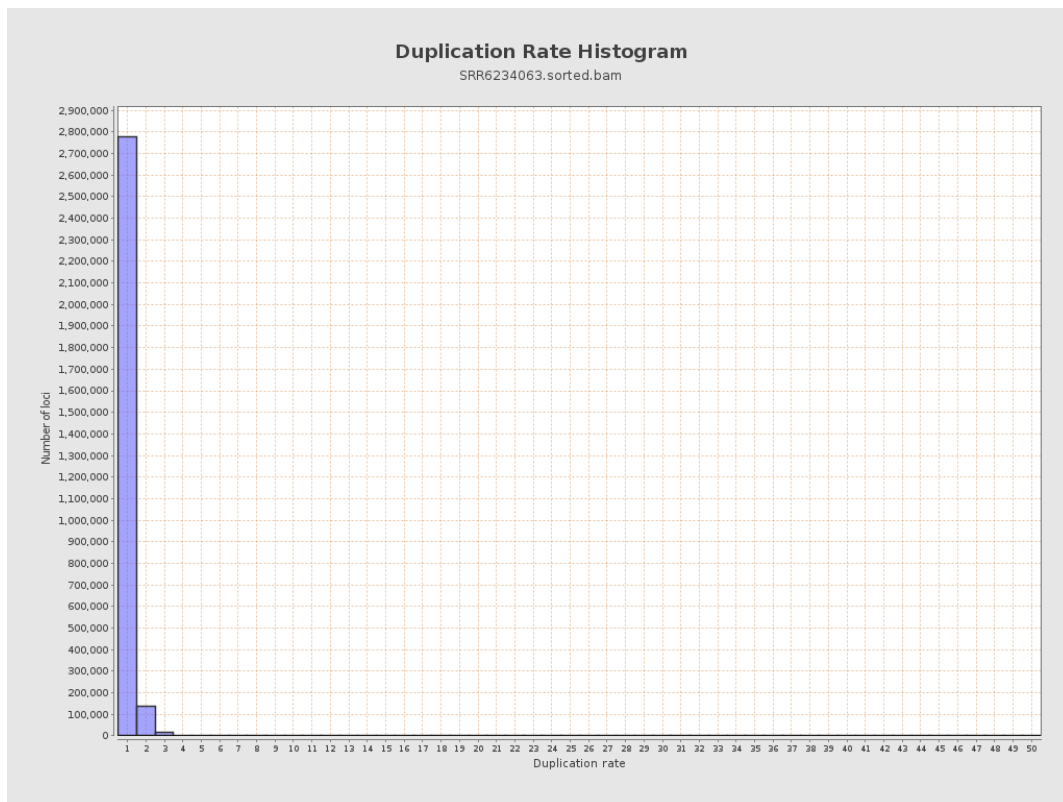
5. Results : Coverage Histogram (0-50X)



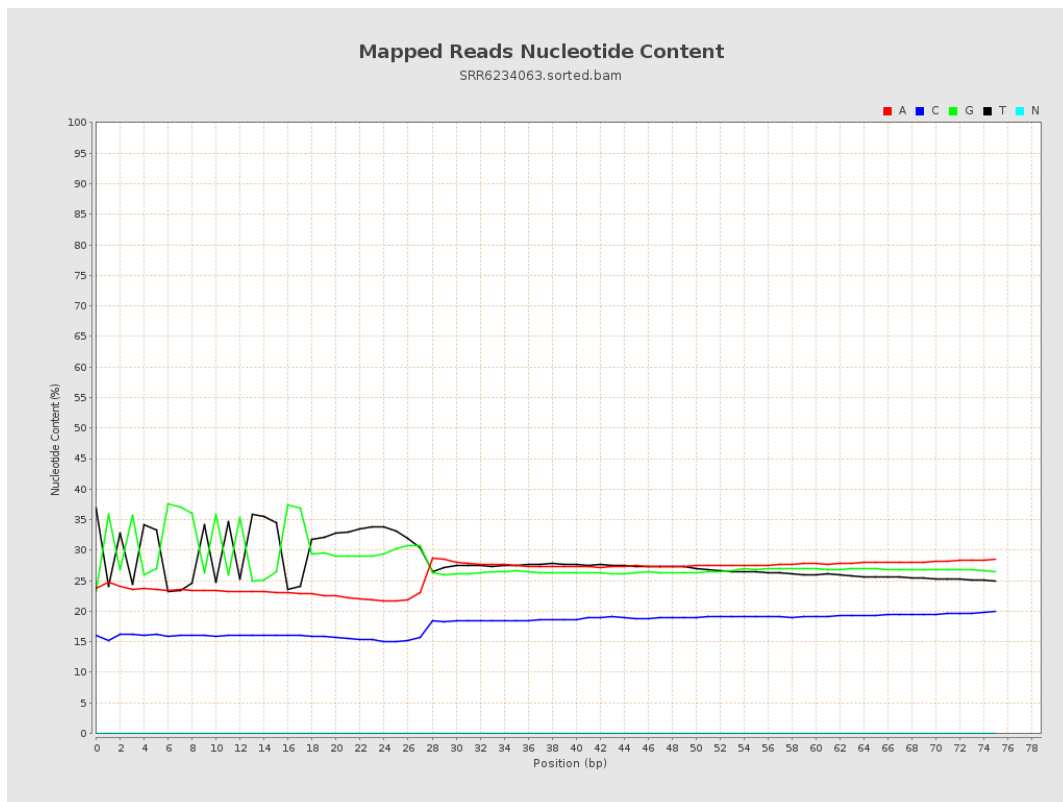
6. Results : Genome Fraction Coverage



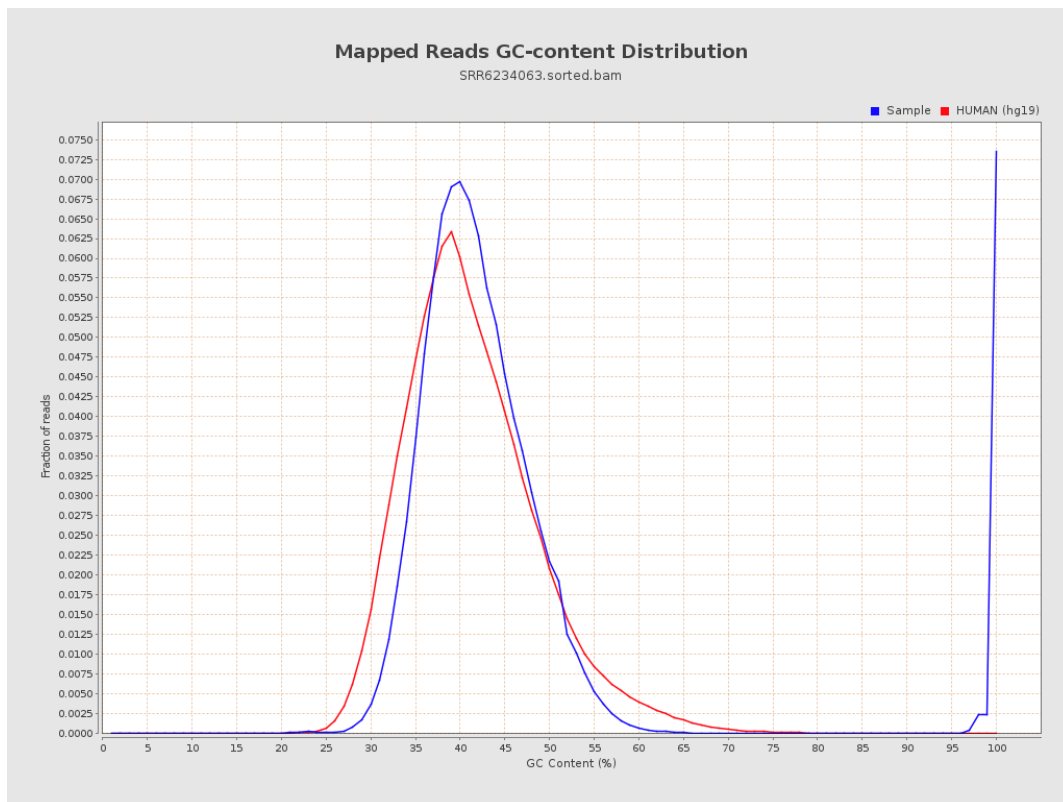
7. Results : Duplication Rate Histogram



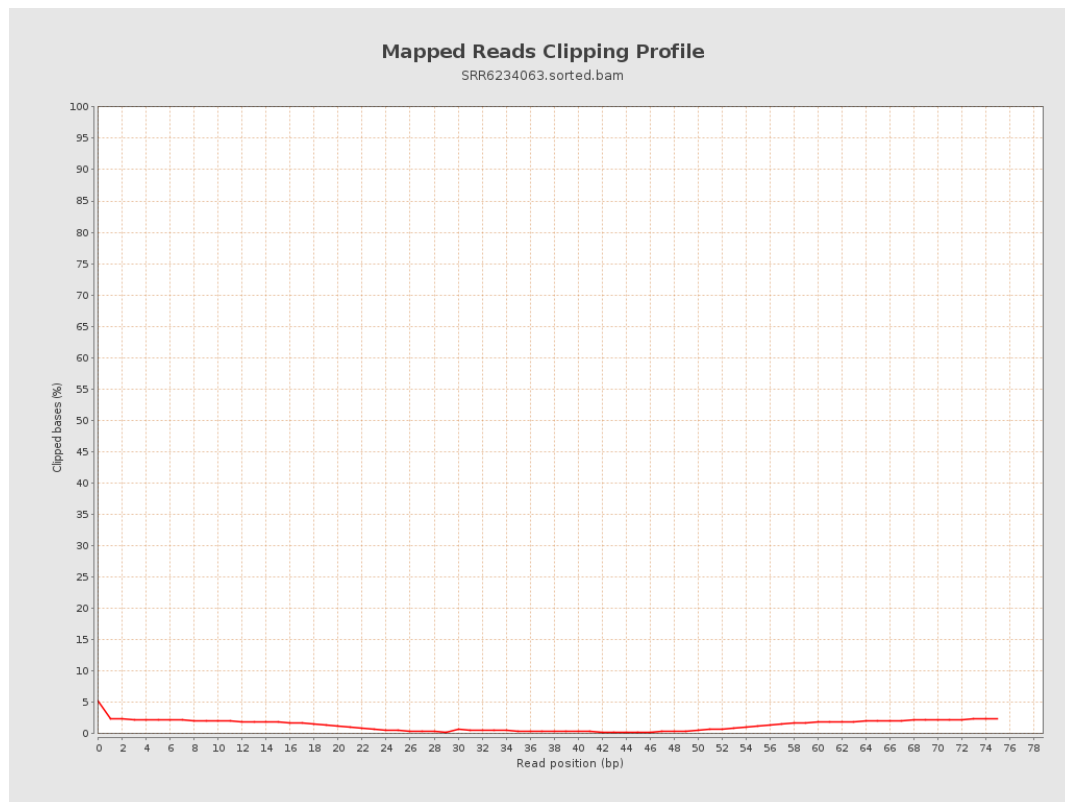
8. Results : Mapped Reads Nucleotide Content



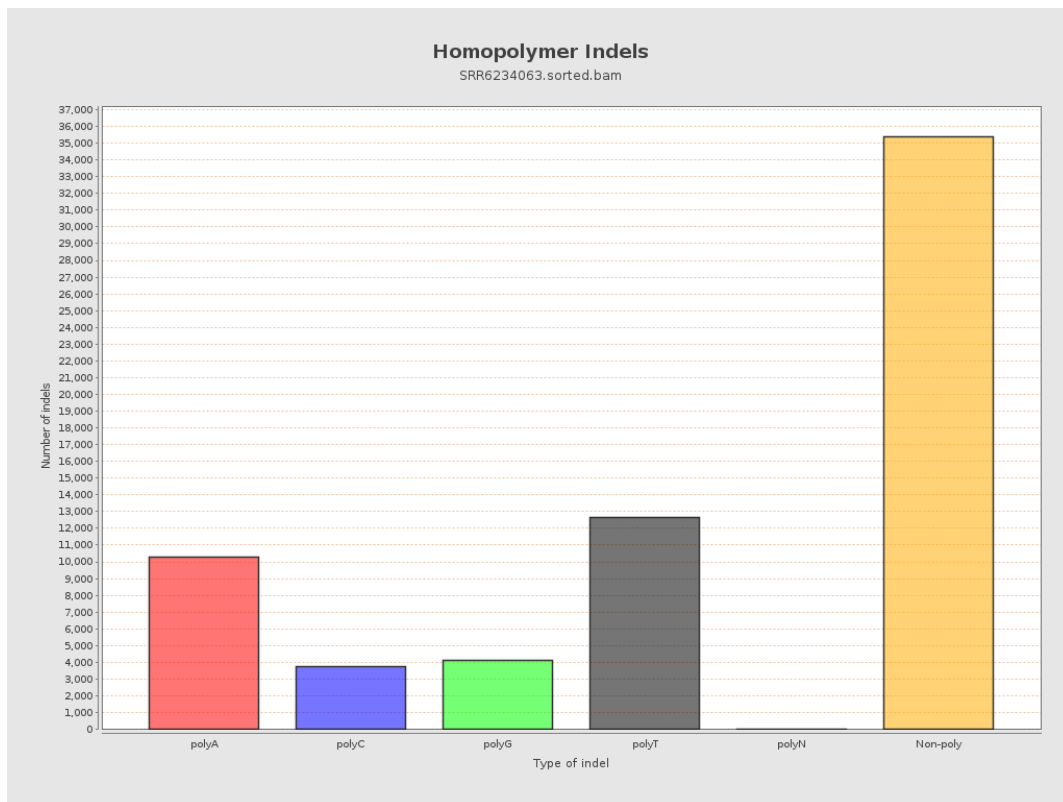
9. Results : Mapped Reads GC-content Distribution



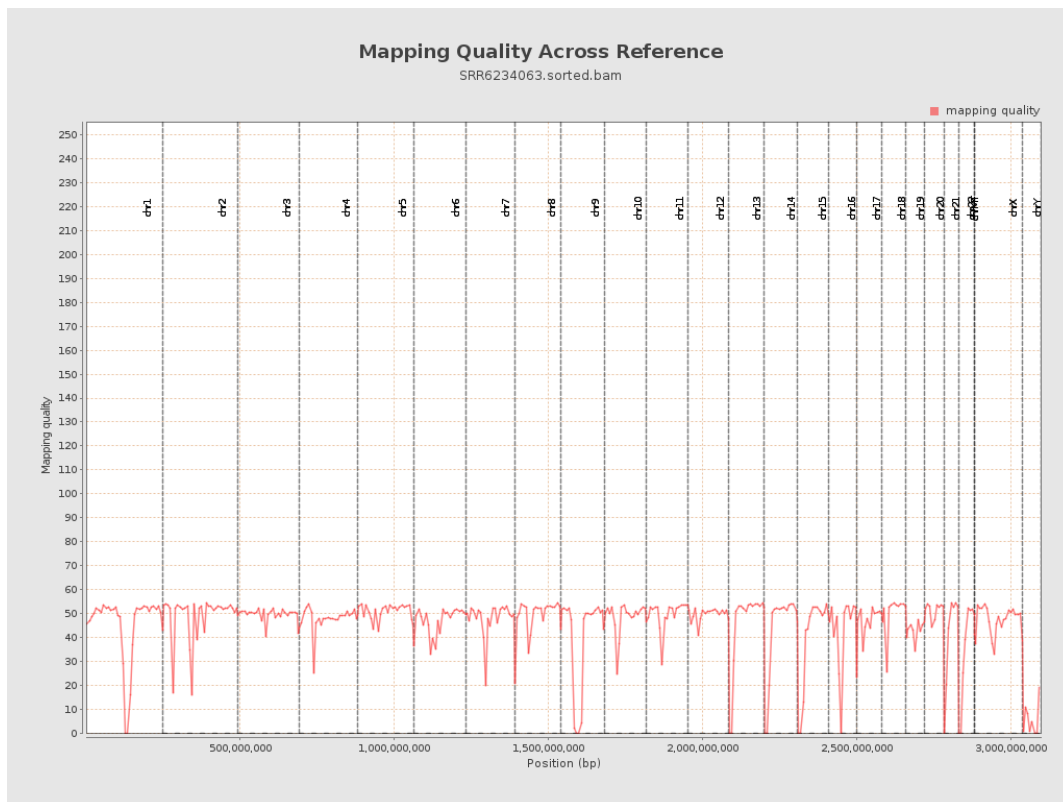
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

