

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 17:05:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549062.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_SRR1549062 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549062.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 17:05:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549062.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,841,248
Mapped reads	7,647,238 / 86.5%
Unmapped reads	1,194,010 / 13.5%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	275,764 / 3.12%
Duplication rate	2.21%
Clipped reads	368,187 / 4.16%

2.2. ACGT Content

Number/percentage of A's	90,516,839 / 29.81%
Number/percentage of C's	61,450,444 / 20.23%
Number/percentage of T's	90,515,582 / 29.81%
Number/percentage of G's	61,196,062 / 20.15%
Number/percentage of N's	5,600 / 0%
GC Percentage	40.39%

2.3. Coverage

Mean	0.0981
Standard Deviation	0.9791

2.4. Mapping Quality

Mean Mapping Quality	43.5
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2.5. Mismatches and indels

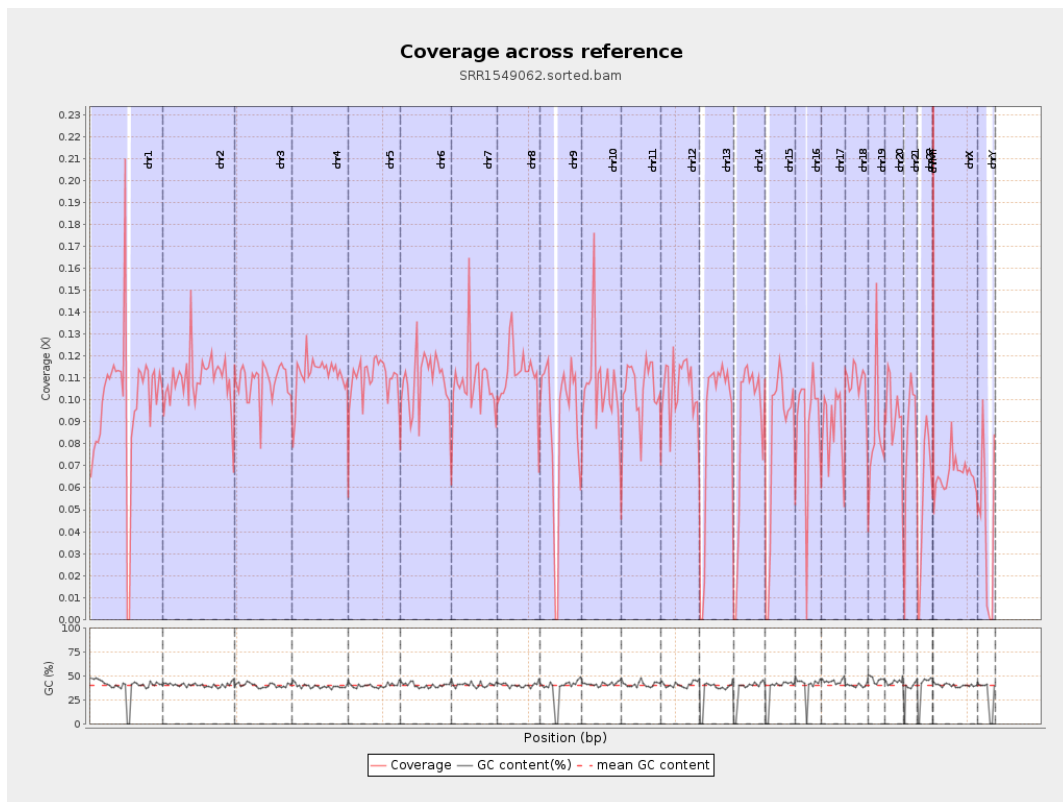
General error rate	0.32%
Mismatches	954,420
Insertions	7,638
Mapped reads with at least one insertion	0.1%
Deletions	23,094
Mapped reads with at least one deletion	0.3%
Homopolymer indels	44.32%

2.6. Chromosome stats

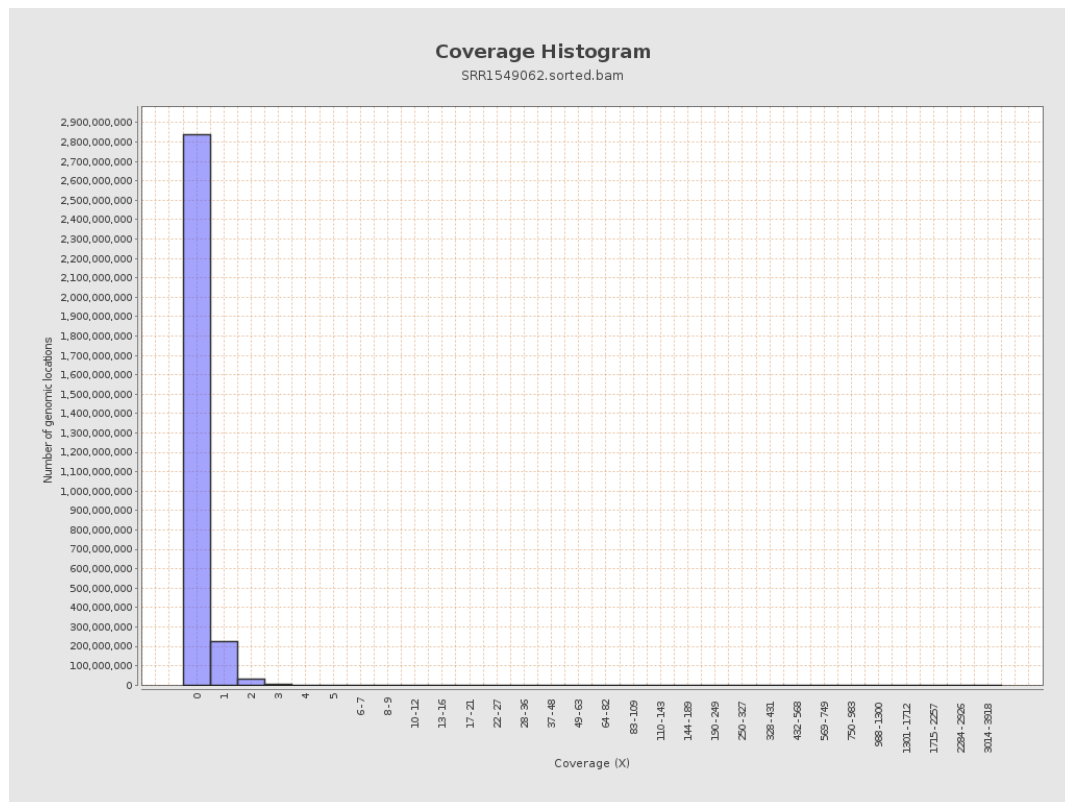
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	24626304	0.0988	2.3987
chr2	243199373	26570042	0.1093	0.6063
chr3	198022430	21463569	0.1084	0.3786
chr4	191154276	21378116	0.1118	0.4035
chr5	180915260	19807890	0.1095	0.3884
chr6	171115067	18729125	0.1095	0.4854
chr7	159138663	17043631	0.1071	0.8895
chr8	146364022	16324060	0.1115	1.9639

chr9	141213431	12754250	0.0903	0.5759
chr10	135534747	14410424	0.1063	0.7552
chr11	135006516	14104855	0.1045	0.5696
chr12	133851895	14123773	0.1055	0.3992
chr13	115169878	10341410	0.0898	0.3317
chr14	107349540	9388238	0.0875	0.3893
chr15	102531392	8406801	0.082	0.3202
chr16	90354753	7896677	0.0874	0.4237
chr17	81195210	7191027	0.0886	0.3933
chr18	78077248	8467417	0.1084	1.2556
chr19	59128983	5101263	0.0863	1.7824
chr20	63025520	5933435	0.0941	0.3648
chr21	48129895	3914523	0.0813	0.3892
chr22	51304566	2887715	0.0563	0.3008
chrMT	16571	17635	1.0642	1.5137
chrX	155270560	10226329	0.0659	0.4086
chrY	59373566	2605114	0.0439	0.4289

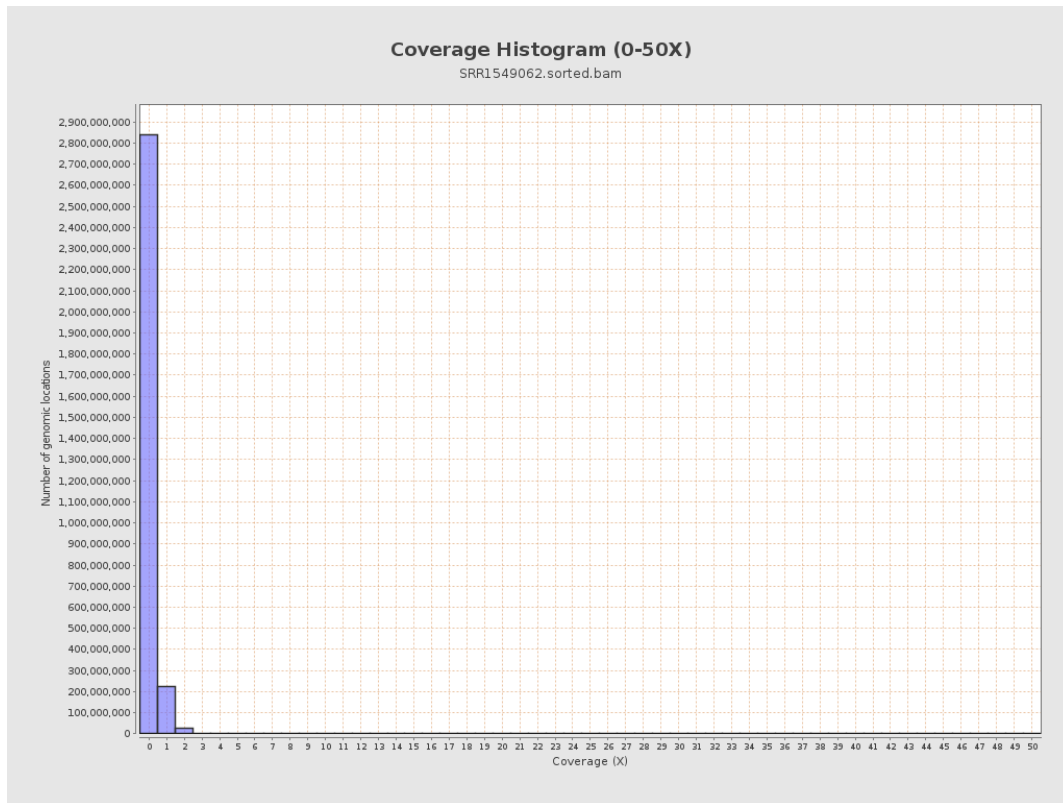
3. Results : Coverage across reference



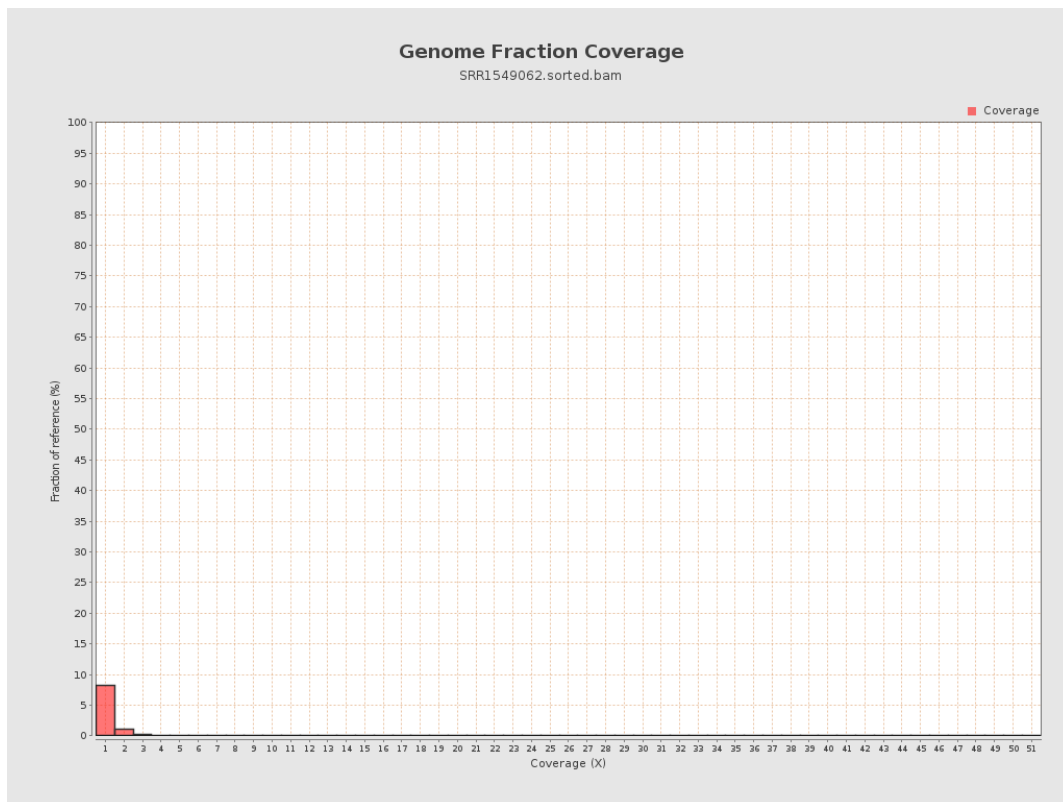
4. Results : Coverage Histogram



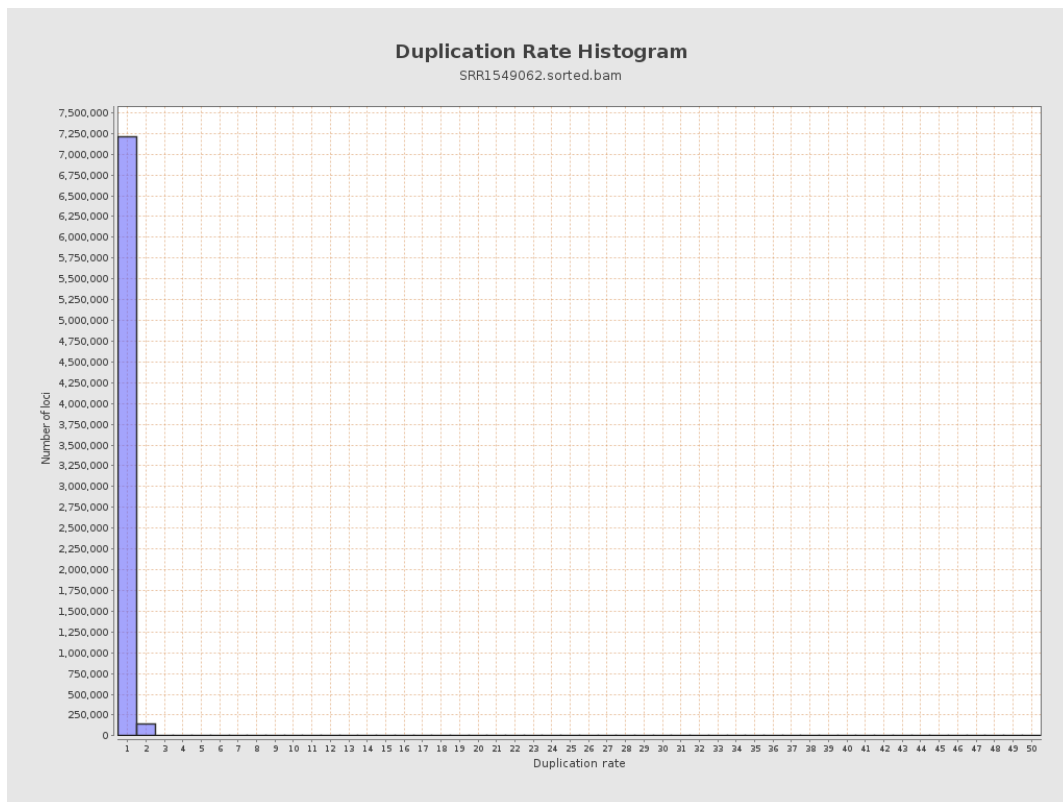
5. Results : Coverage Histogram (0-50X)



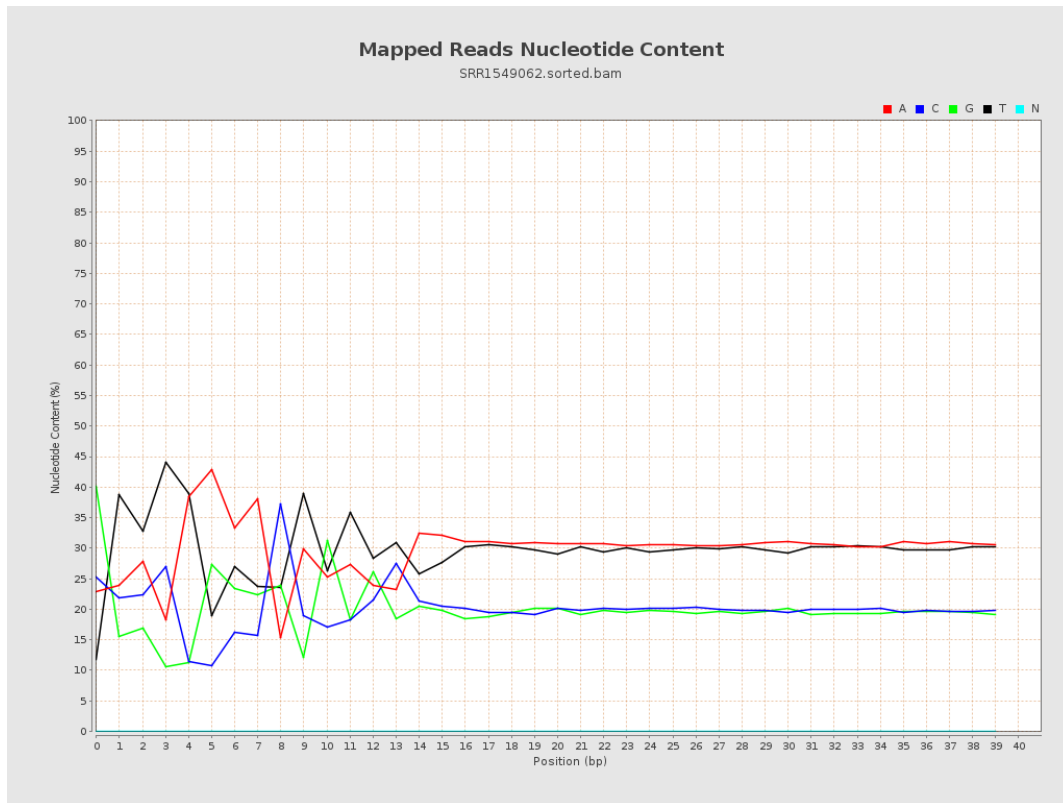
6. Results : Genome Fraction Coverage



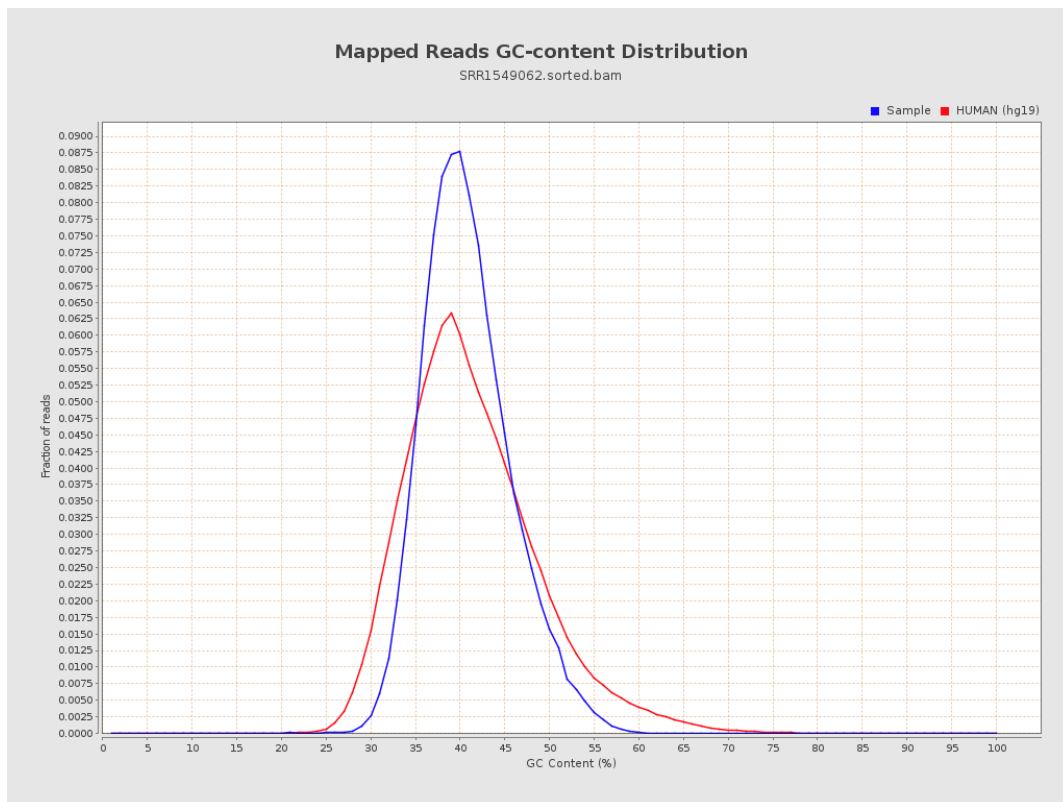
7. Results : Duplication Rate Histogram



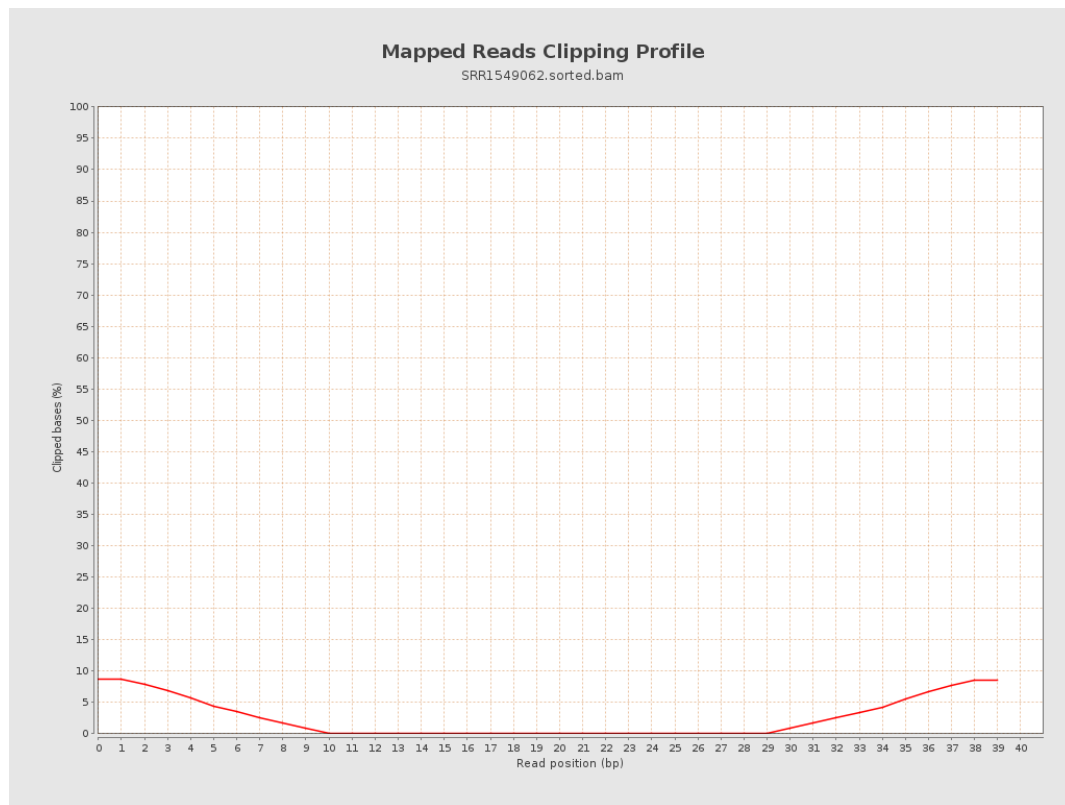
8. Results : Mapped Reads Nucleotide Content



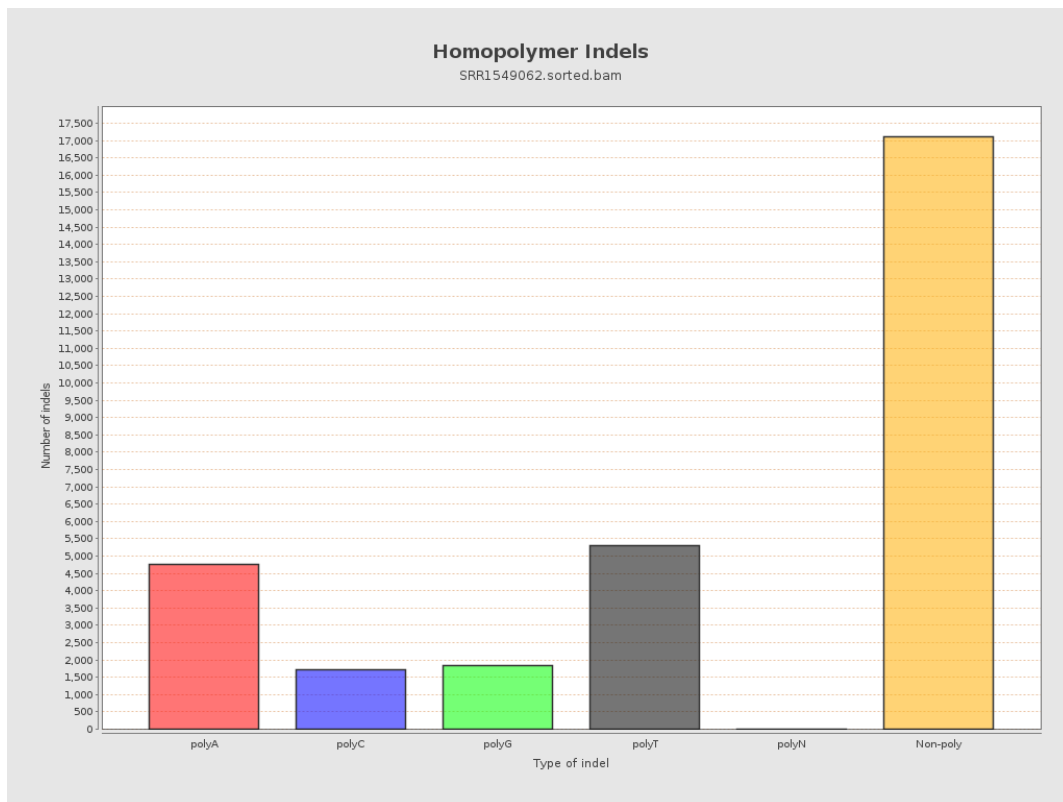
9. Results : Mapped Reads GC-content Distribution



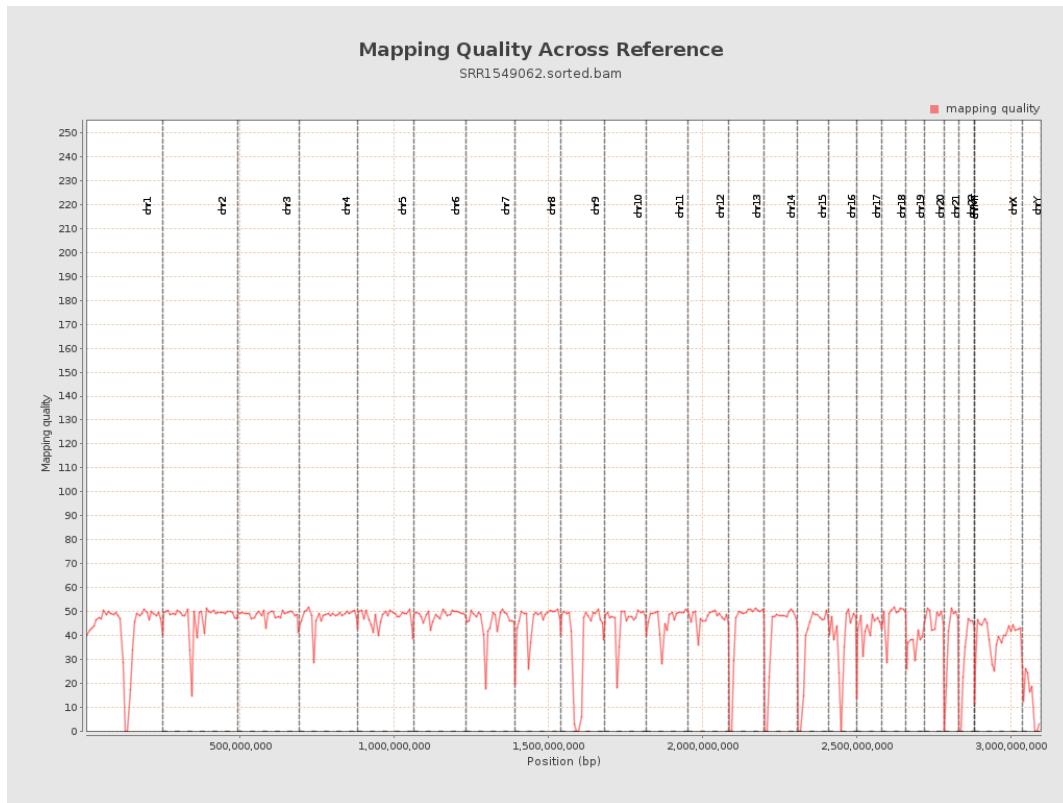
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

