

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 07:13:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549134.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_SRR1549134 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549134.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 07:13:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549134.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,459,767
Mapped reads	10,816,319 / 86.81%
Unmapped reads	1,643,448 / 13.19%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	581,242 / 4.66%
Duplication rate	4.25%
Clipped reads	537,736 / 4.32%

2.2. ACGT Content

Number/percentage of A's	125,859,017 / 29.31%
Number/percentage of C's	88,551,365 / 20.62%
Number/percentage of T's	126,836,031 / 29.54%
Number/percentage of G's	88,099,543 / 20.51%
Number/percentage of N's	94,356 / 0.02%
GC Percentage	41.14%

2.3. Coverage

Mean	0.1387
Standard Deviation	1.089

2.4. Mapping Quality

Mean Mapping Quality	44.04
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2.5. Mismatches and indels

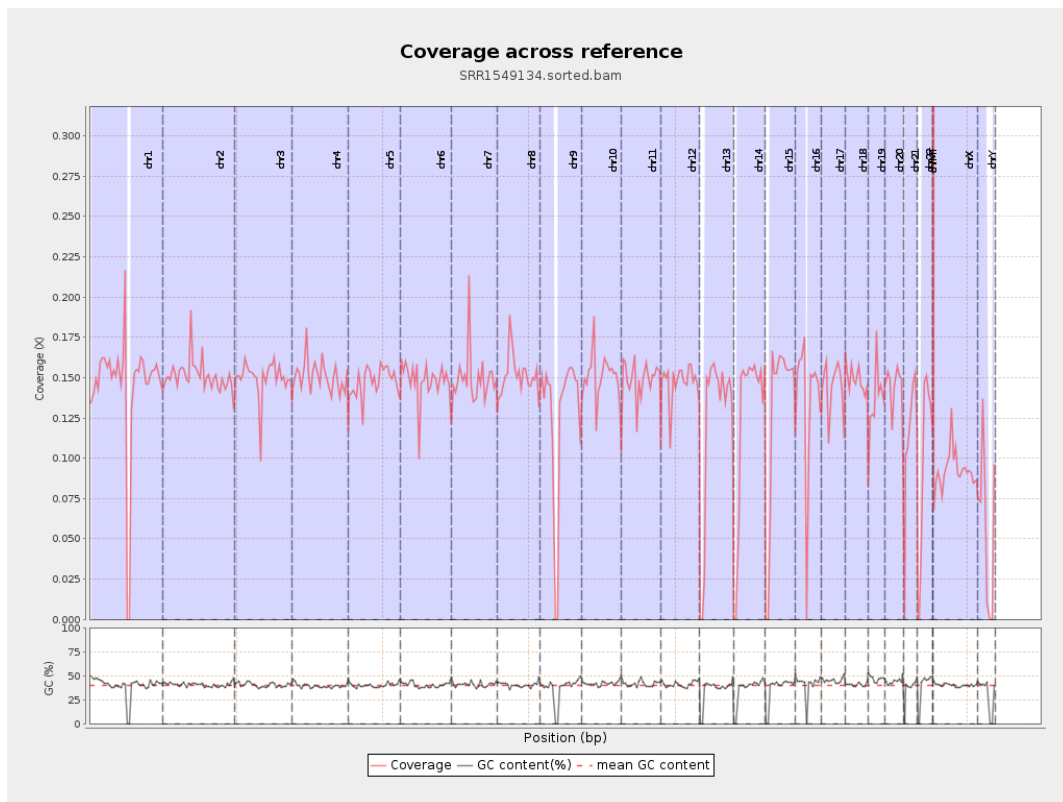
General error rate	0.32%
Mismatches	1,374,203
Insertions	10,760
Mapped reads with at least one insertion	0.1%
Deletions	32,714
Mapped reads with at least one deletion	0.3%
Homopolymer indels	45.39%

2.6. Chromosome stats

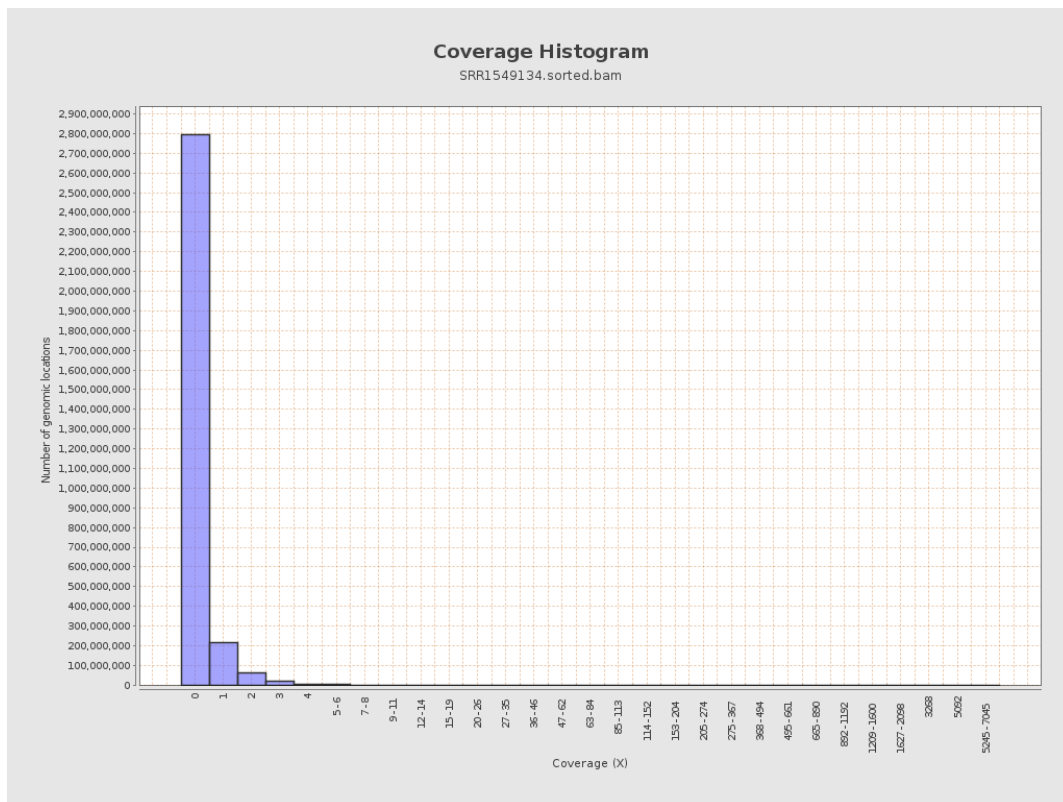
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	36054483	0.1447	1.6221
chr2	243199373	36780013	0.1512	0.7251
chr3	198022430	29616516	0.1496	0.5141
chr4	191154276	28885892	0.1511	0.5578
chr5	180915260	26629678	0.1472	0.5228
chr6	171115067	25354867	0.1482	0.559
chr7	159138663	23747035	0.1492	1.1234
chr8	146364022	22213916	0.1518	3.4669

chr9	141213431	17914871	0.1269	0.6676
chr10	135534747	20430381	0.1507	0.7491
chr11	135006516	20048916	0.1485	0.6706
chr12	133851895	19806765	0.148	0.5318
chr13	115169878	14119335	0.1226	0.4625
chr14	107349540	13486426	0.1256	0.5931
chr15	102531392	13143517	0.1282	0.4694
chr16	90354753	12096974	0.1339	0.5298
chr17	81195210	11819579	0.1456	0.5523
chr18	78077248	11594476	0.1485	1.3175
chr19	59128983	8122583	0.1374	1.3065
chr20	63025520	9100591	0.1444	0.5391
chr21	48129895	5505496	0.1144	0.5295
chr22	51304566	5014850	0.0977	0.4405
chrMT	16571	166939	10.0742	12.1746
chrX	155270560	14316085	0.0922	0.4968
chrY	59373566	3511520	0.0591	0.555

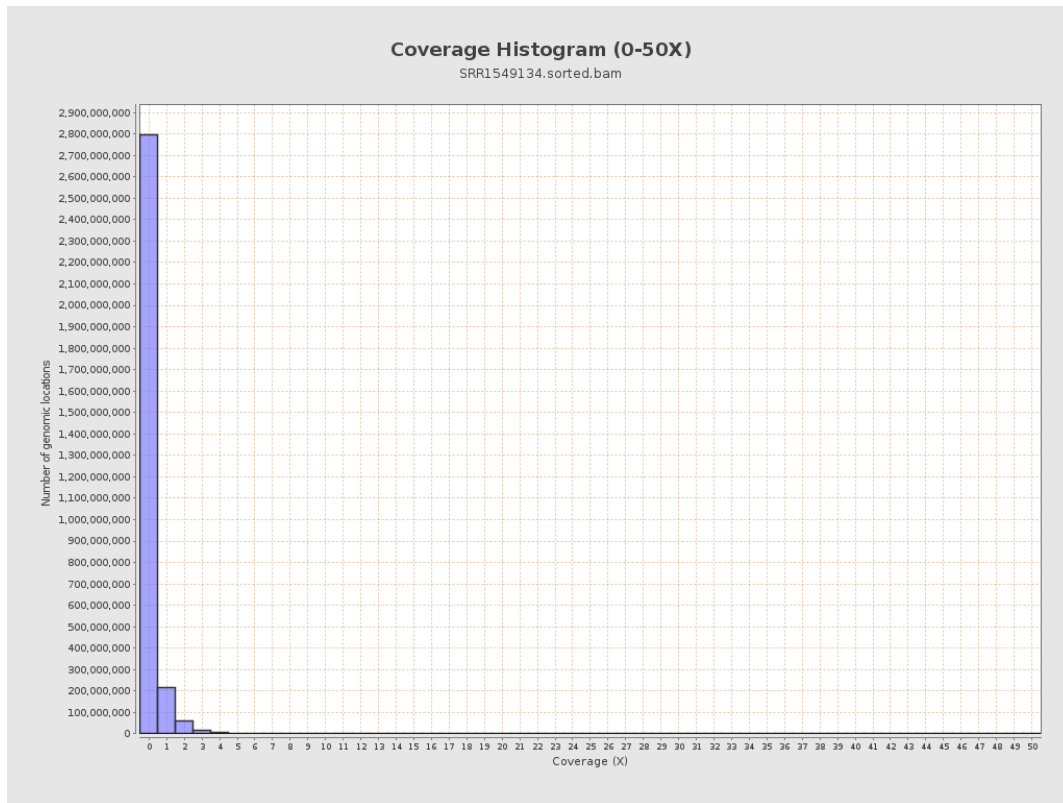
3. Results : Coverage across reference



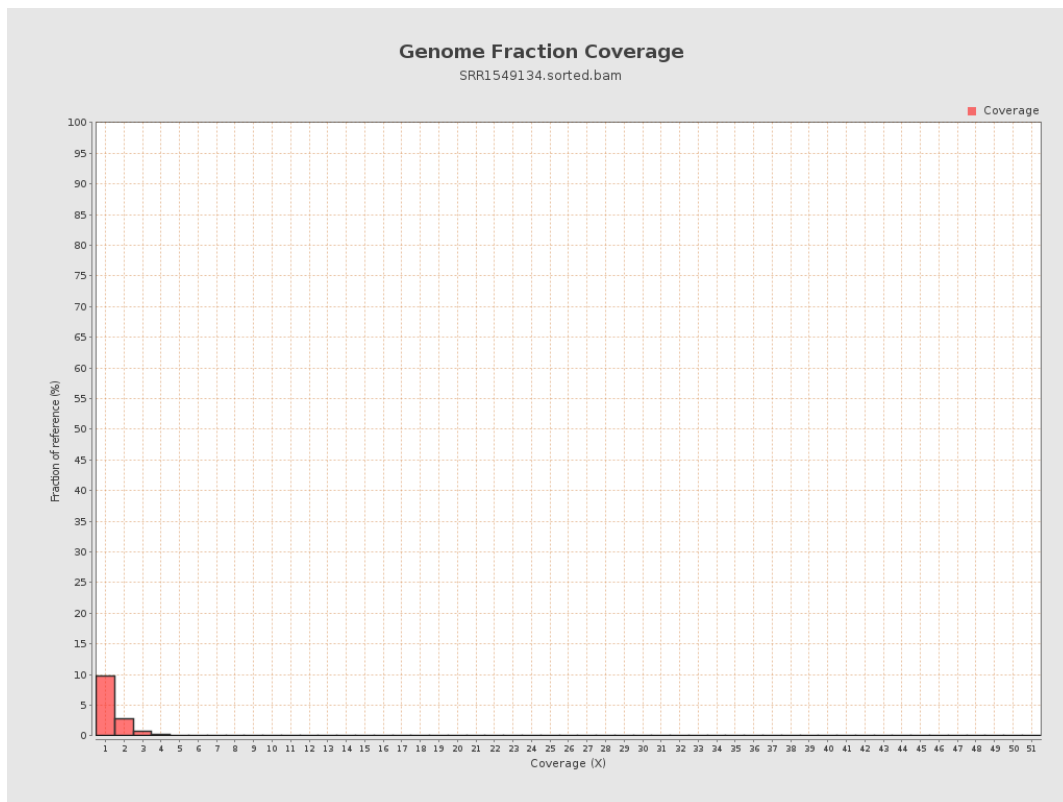
4. Results : Coverage Histogram



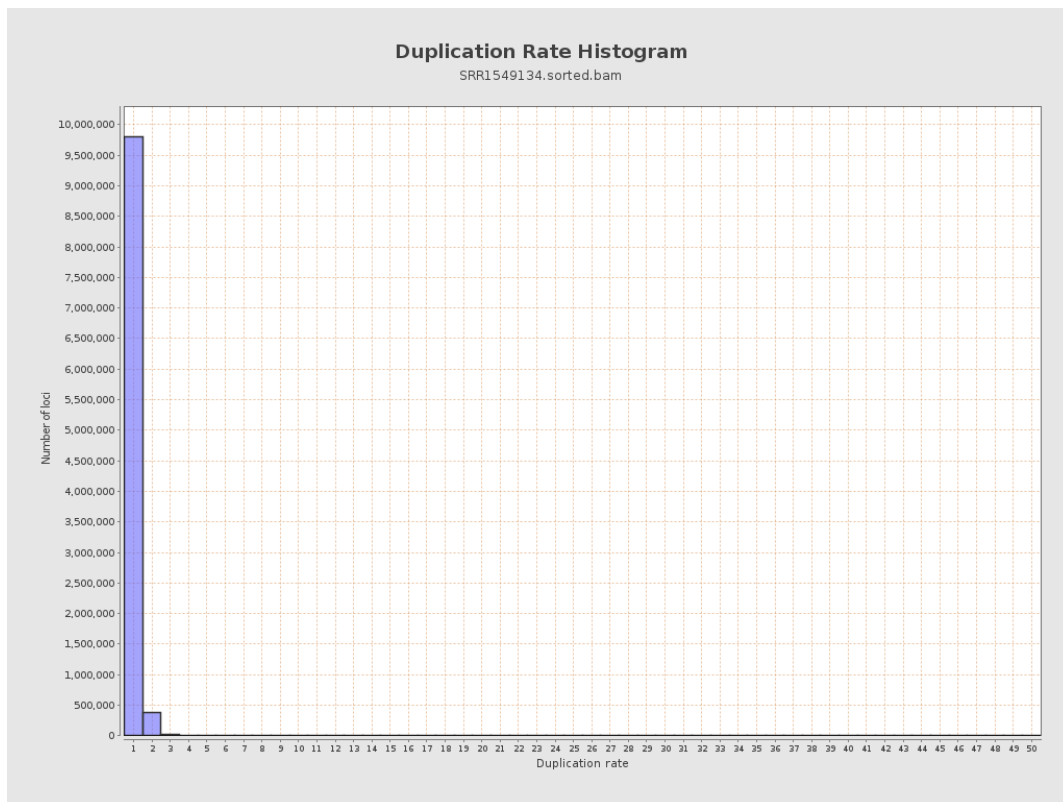
5. Results : Coverage Histogram (0-50X)



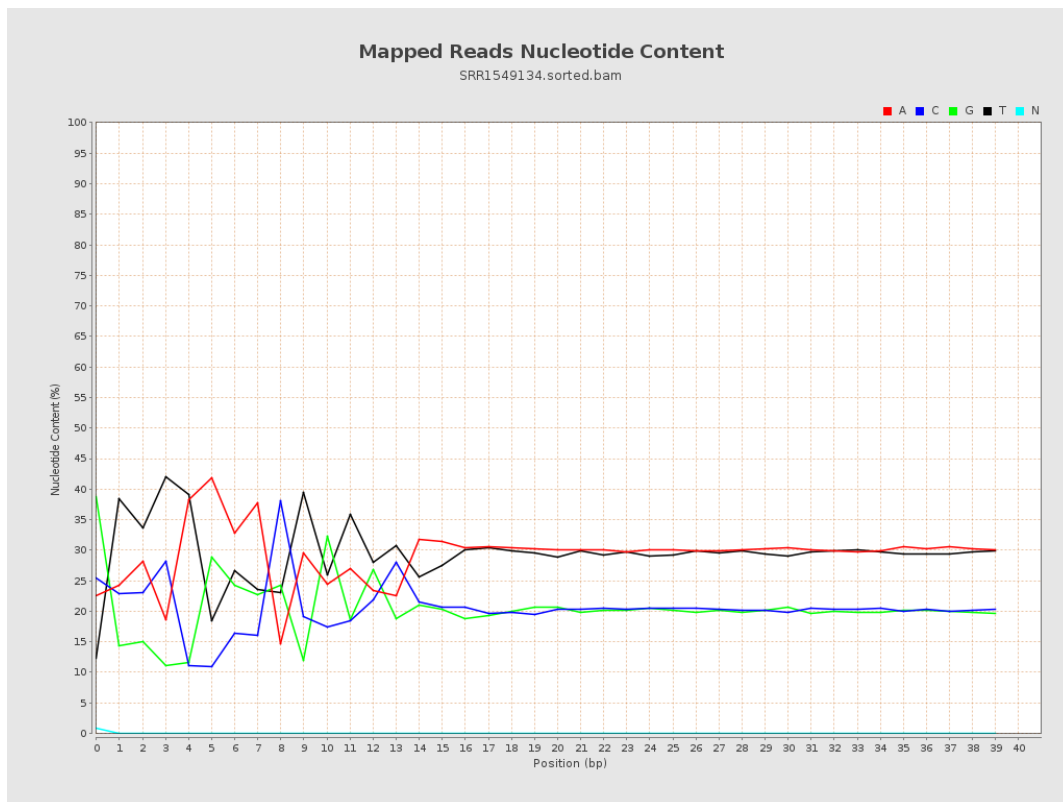
6. Results : Genome Fraction Coverage



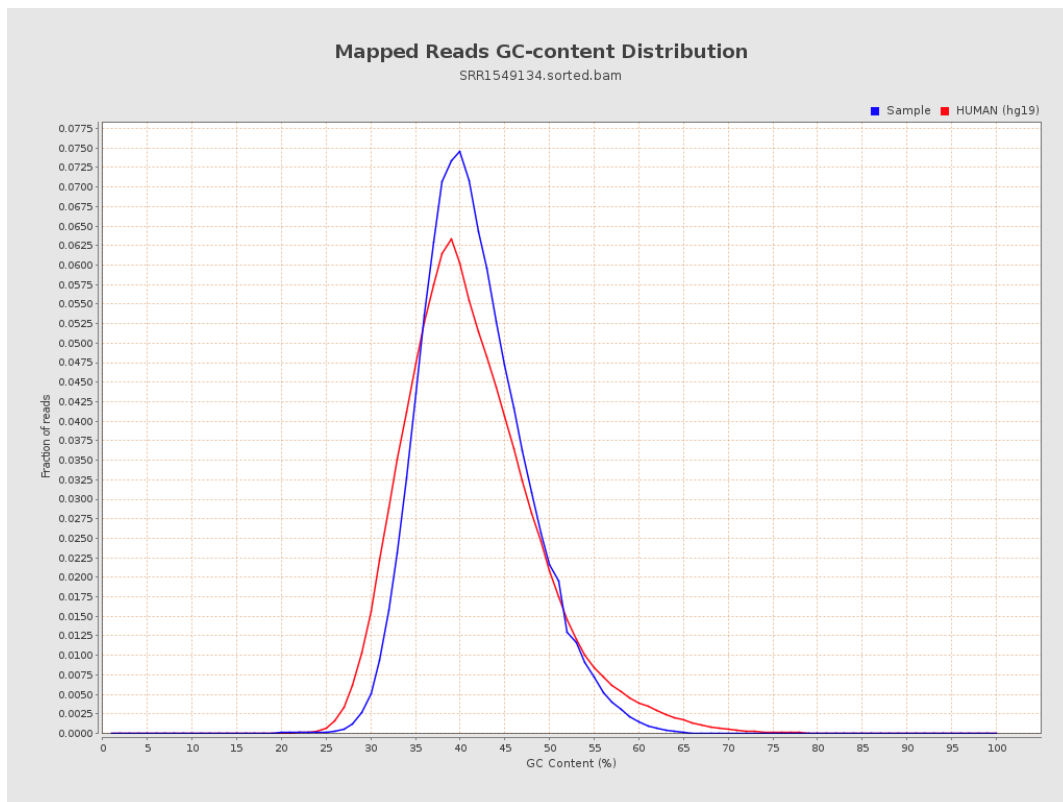
7. Results : Duplication Rate Histogram



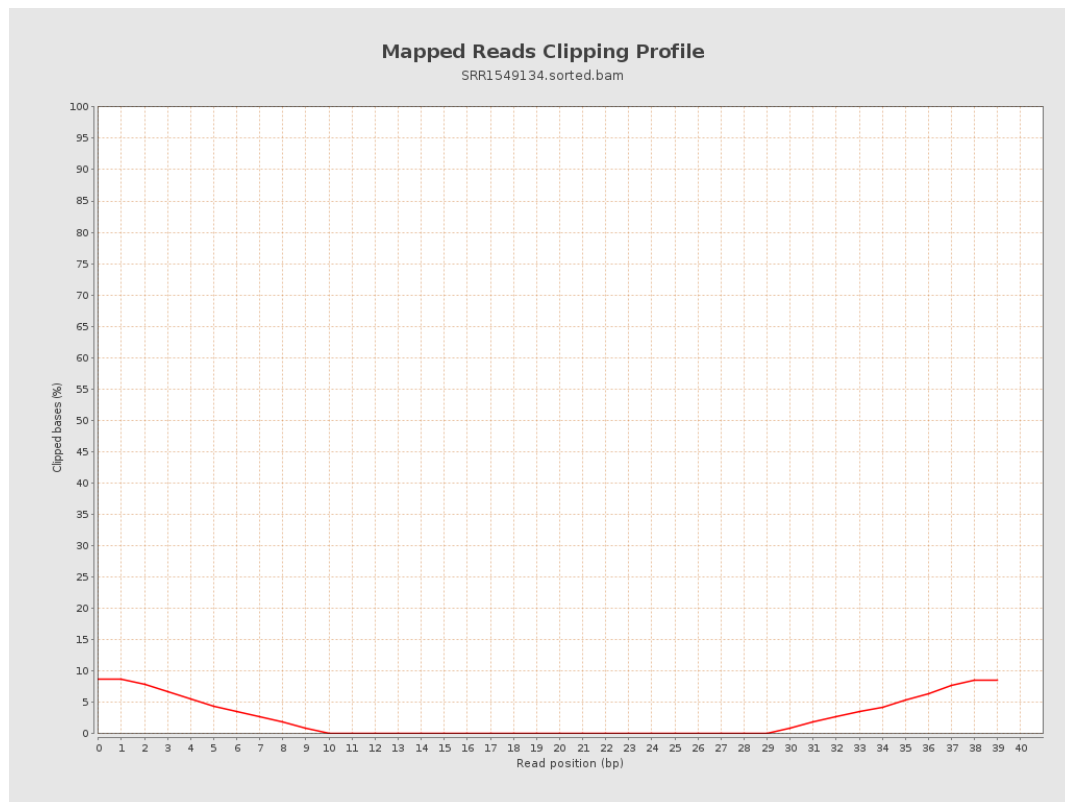
8. Results : Mapped Reads Nucleotide Content



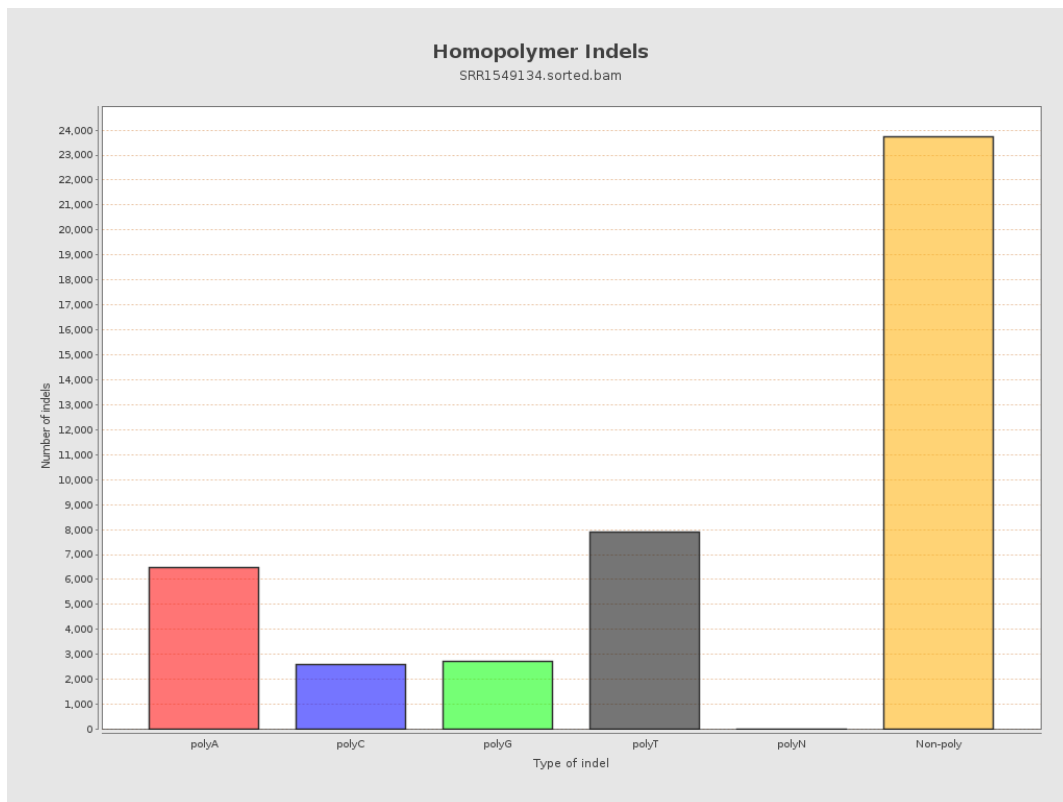
9. Results : Mapped Reads GC-content Distribution



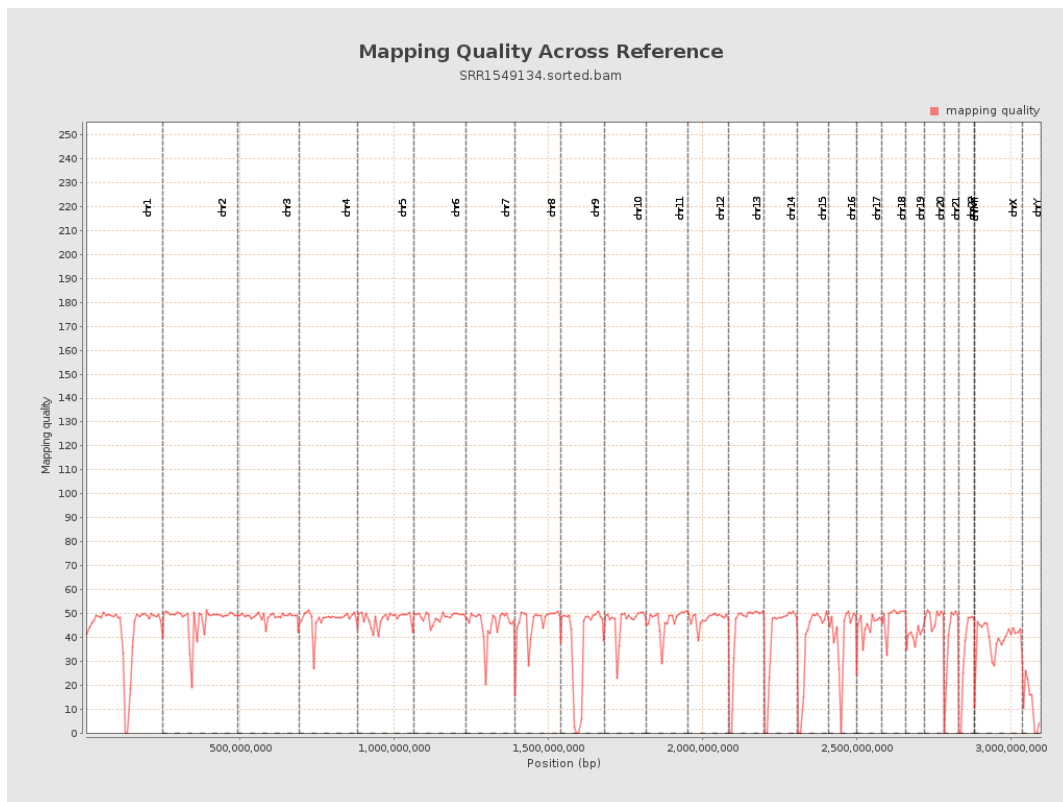
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

