

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 17:26:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549064.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_SRR1549064 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549064.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 17:26:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549064.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,152,142
Mapped reads	9,683,492 / 86.83%
Unmapped reads	1,468,650 / 13.17%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	458,587 / 4.11%
Duplication rate	2.38%
Clipped reads	559,533 / 5.02%

2.2. ACGT Content

Number/percentage of A's	113,997,569 / 29.69%
Number/percentage of C's	78,296,521 / 20.39%
Number/percentage of T's	114,018,985 / 29.69%
Number/percentage of G's	77,696,838 / 20.23%
Number/percentage of N's	7,318 / 0%
GC Percentage	40.62%

2.3. Coverage

Mean	0.1241
Standard Deviation	1.6924

2.4. Mapping Quality

Mean Mapping Quality	41.39
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2.5. Mismatches and indels

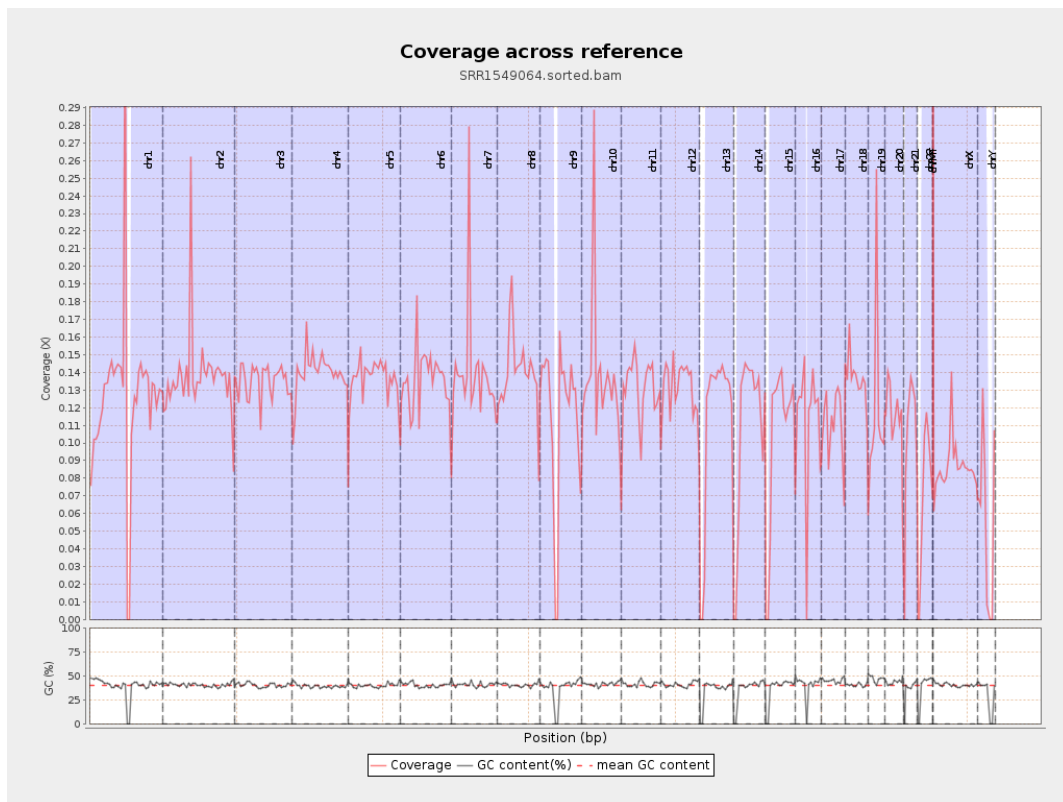
General error rate	0.35%
Mismatches	1,335,563
Insertions	11,053
Mapped reads with at least one insertion	0.11%
Deletions	30,630
Mapped reads with at least one deletion	0.32%
Homopolymer indels	42.8%

2.6. Chromosome stats

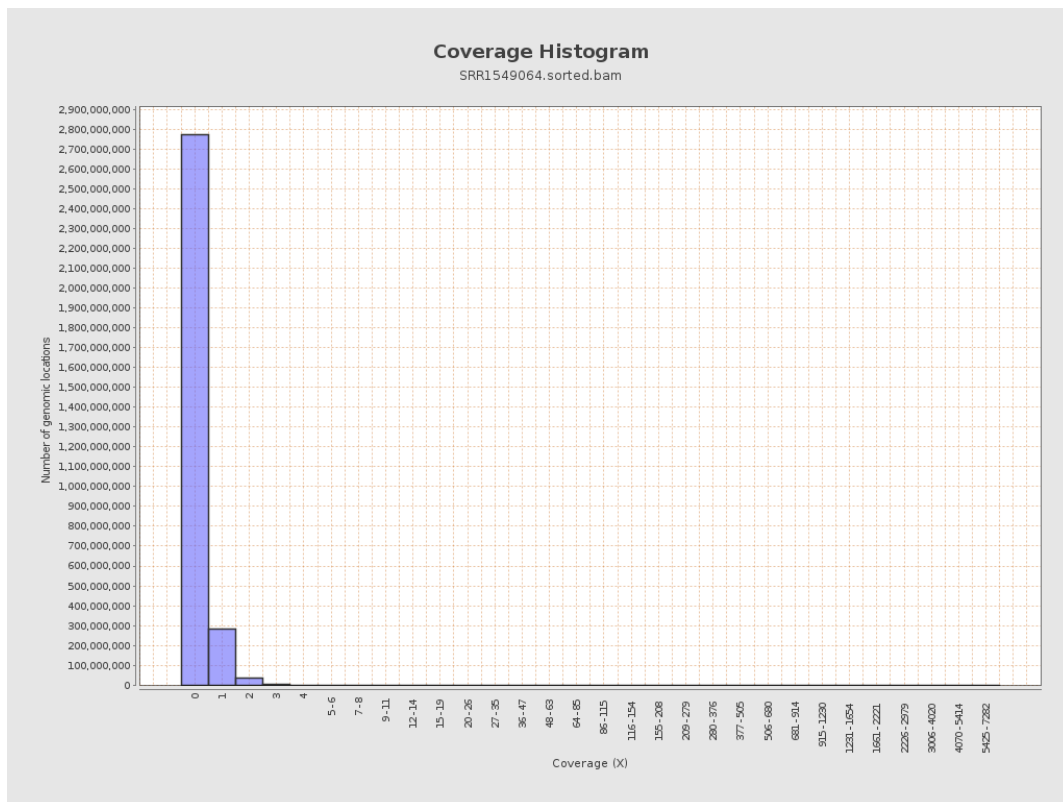
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	31422905	0.1261	4.636
chr2	243199373	33540810	0.1379	1.0772
chr3	198022430	26756868	0.1351	0.446
chr4	191154276	26785704	0.1401	0.4868
chr5	180915260	24590718	0.1359	0.4709
chr6	171115067	23326392	0.1363	0.6307
chr7	159138663	22049020	0.1386	1.6234
chr8	146364022	20498918	0.1401	2.0631

chr9	141213431	16311928	0.1155	0.9788
chr10	135534747	18575723	0.1371	1.3236
chr11	135006516	17671738	0.1309	0.9156
chr12	133851895	17611016	0.1316	0.5302
chr13	115169878	12875667	0.1118	0.365
chr14	107349540	11804468	0.11	0.5118
chr15	102531392	10560719	0.103	0.3646
chr16	90354753	9974311	0.1104	0.6116
chr17	81195210	9069781	0.1117	0.4852
chr18	78077248	10728163	0.1374	2.3509
chr19	59128983	7100151	0.1201	3.6882
chr20	63025520	7345408	0.1165	0.4587
chr21	48129895	4962135	0.1031	0.5373
chr22	51304566	3635219	0.0709	0.3522
chrMT	16571	10309	0.6221	0.9885
chrX	155270560	13424948	0.0865	0.6706
chrY	59373566	3422525	0.0576	0.5536

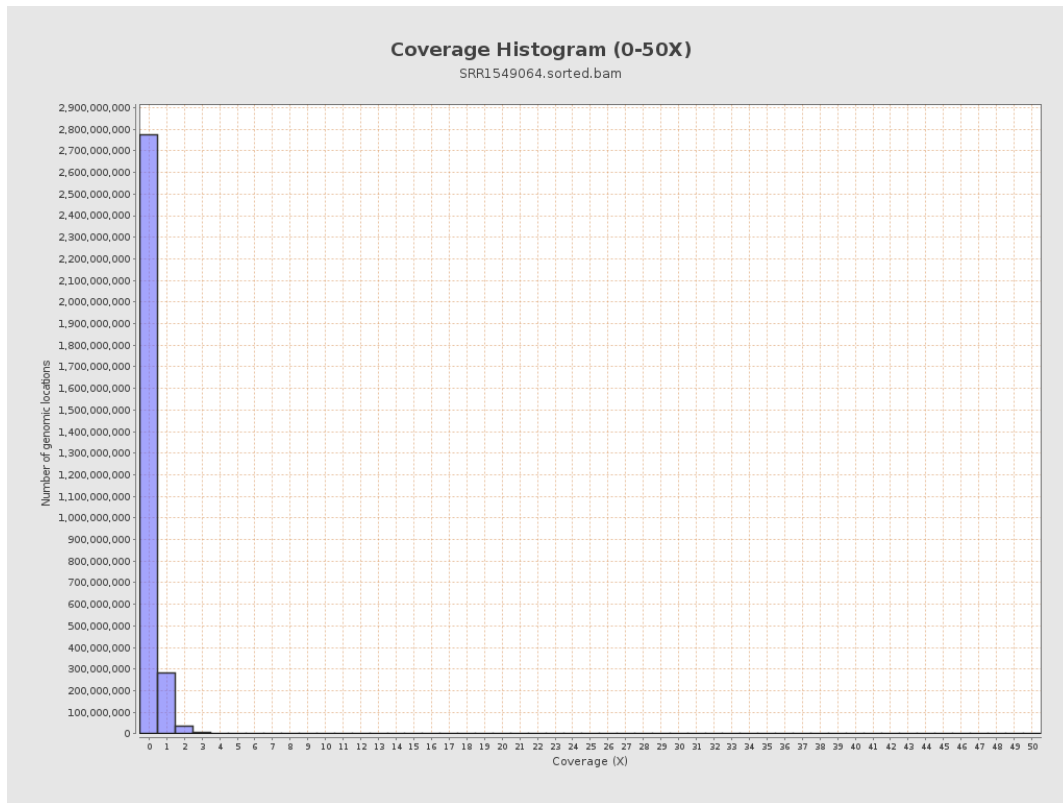
3. Results : Coverage across reference



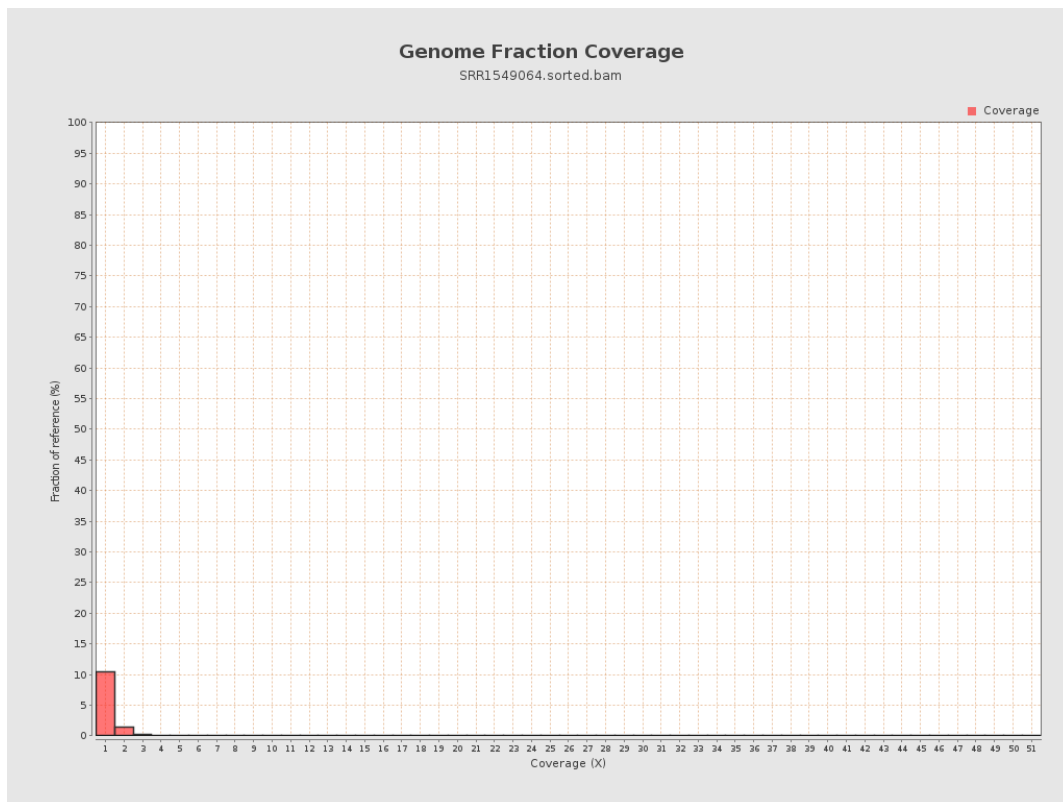
4. Results : Coverage Histogram



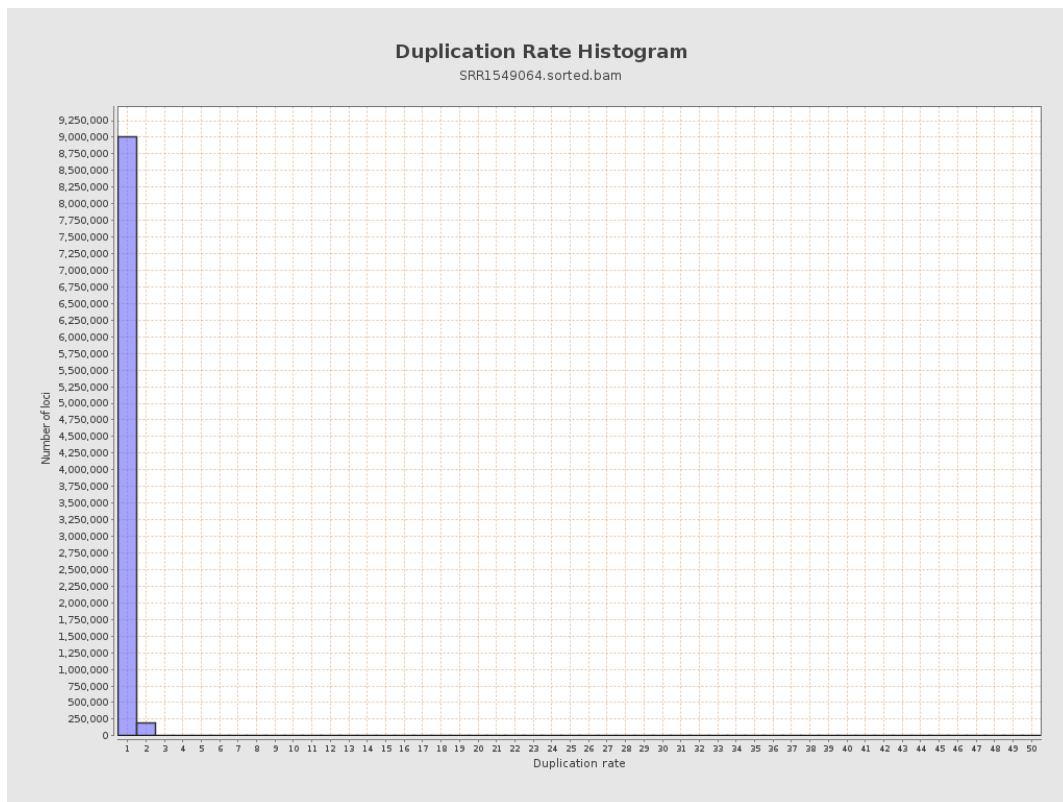
5. Results : Coverage Histogram (0-50X)



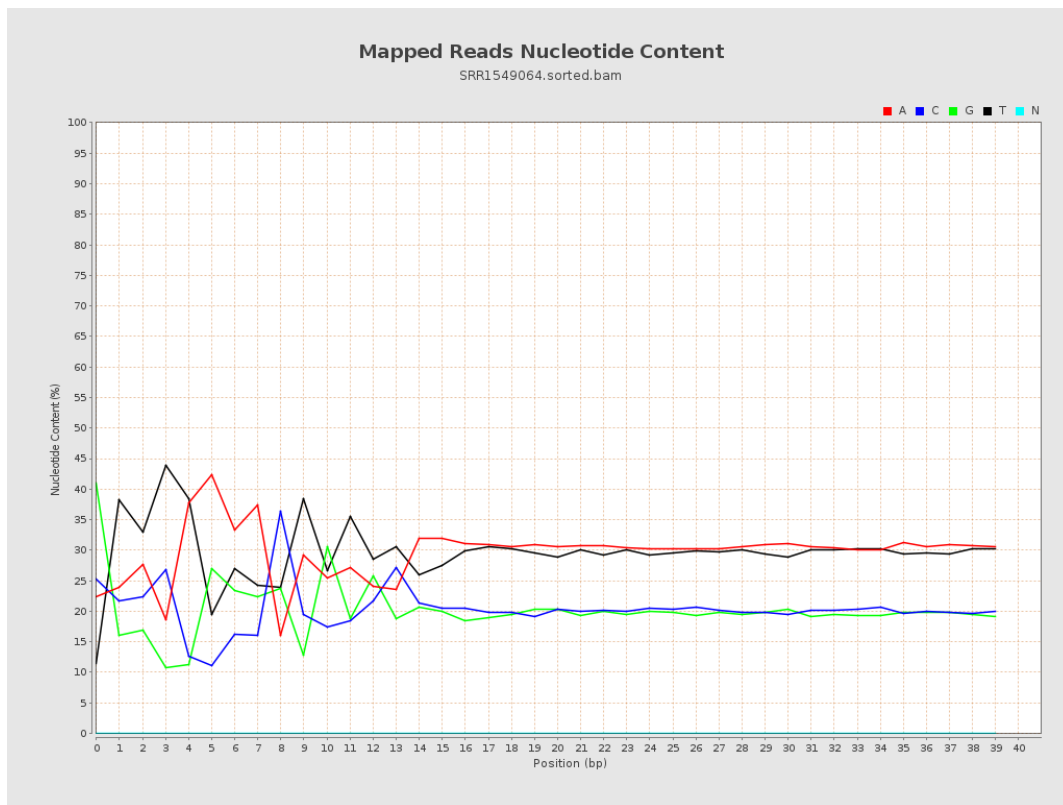
6. Results : Genome Fraction Coverage



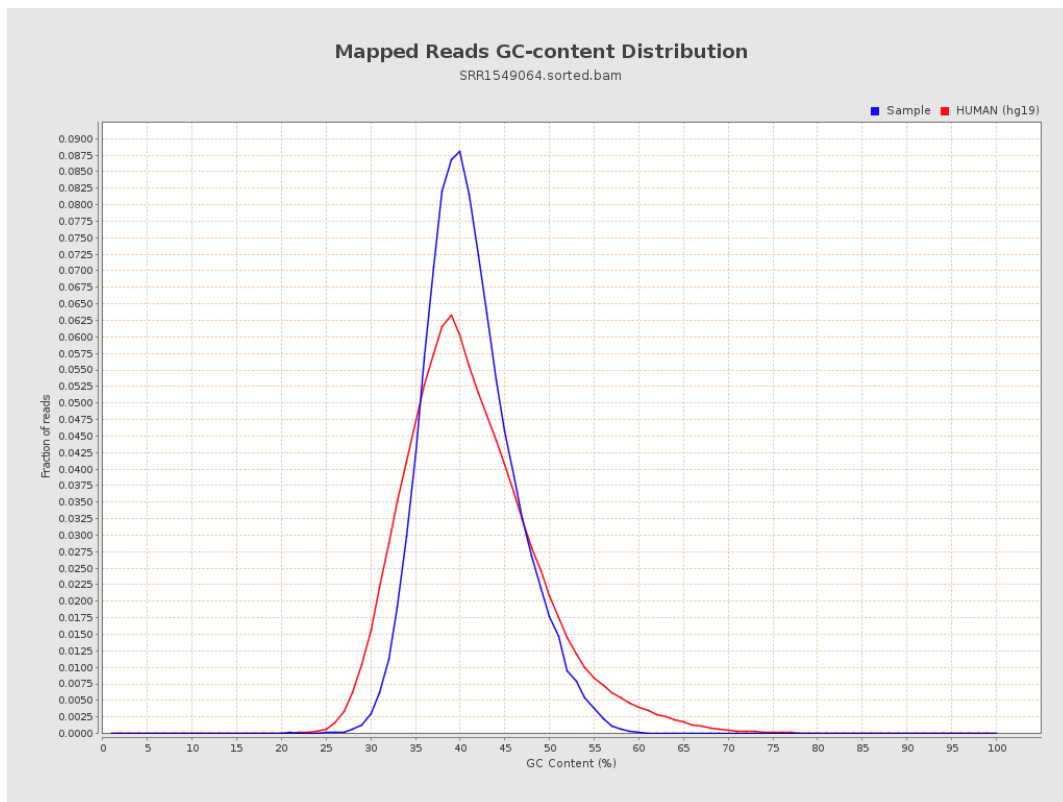
7. Results : Duplication Rate Histogram



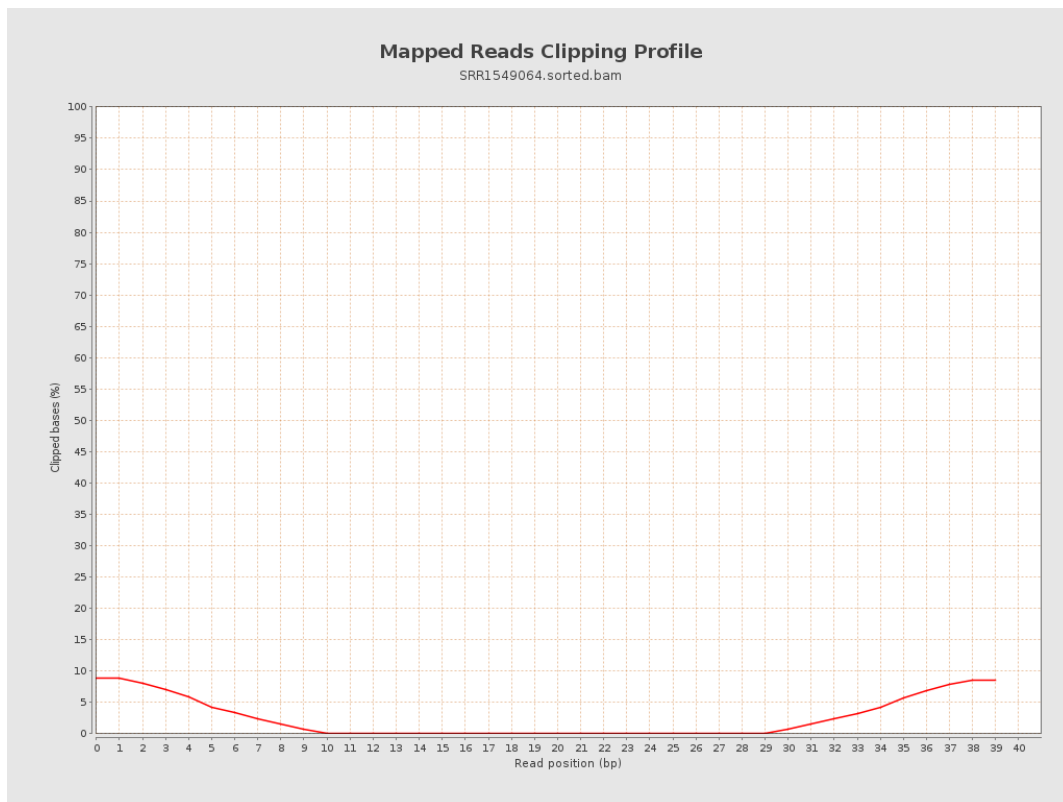
8. Results : Mapped Reads Nucleotide Content



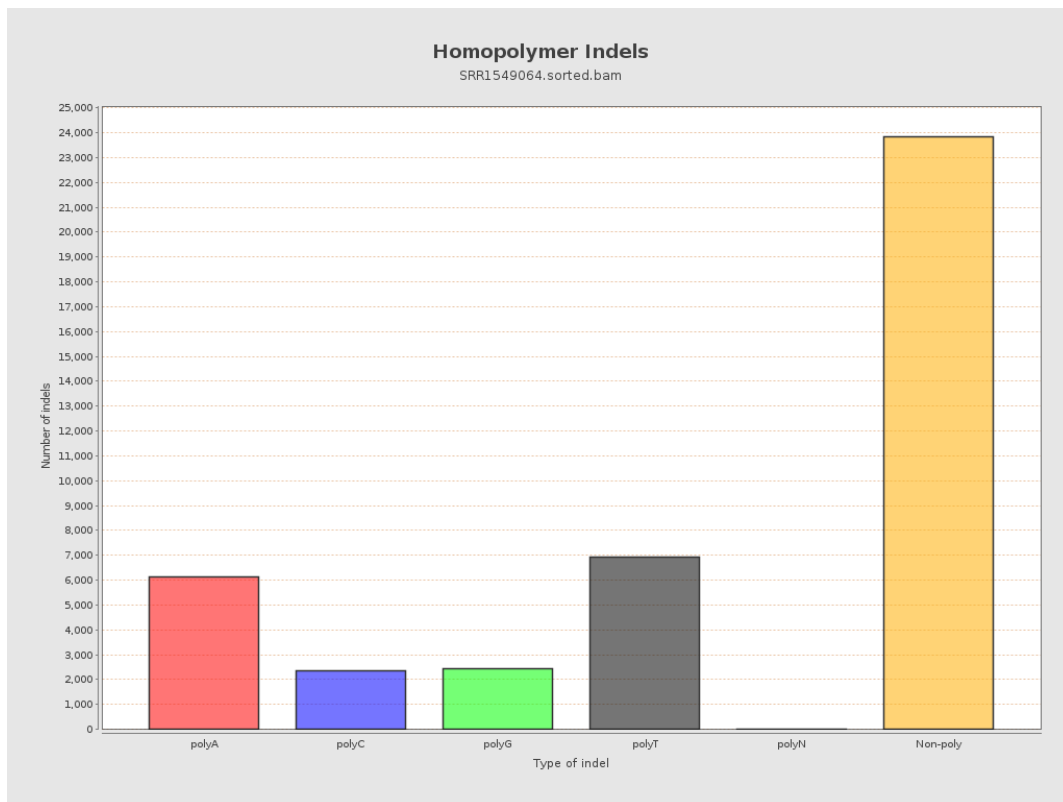
9. Results : Mapped Reads GC-content Distribution



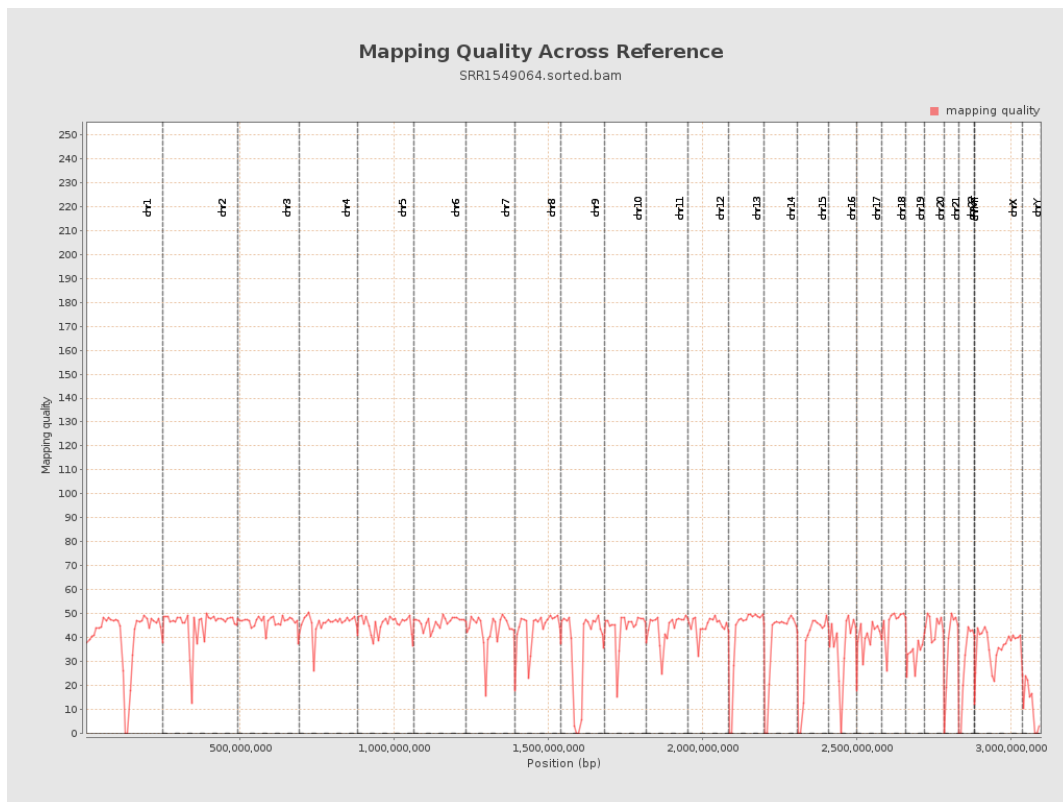
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

