

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 08:45:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549140.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_SRR1549140 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549140.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 08:45:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549140.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,749,171
Mapped reads	10,345,268 / 88.05%
Unmapped reads	1,403,903 / 11.95%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	499,341 / 4.25%
Duplication rate	3.68%
Clipped reads	528,048 / 4.49%

2.2. ACGT Content

Number/percentage of A's	117,310,402 / 28.57%
Number/percentage of C's	87,596,159 / 21.33%
Number/percentage of T's	118,359,930 / 28.82%
Number/percentage of G's	87,295,479 / 21.26%
Number/percentage of N's	91,177 / 0.02%
GC Percentage	42.59%

2.3. Coverage

Mean	0.1327
Standard Deviation	0.7958

2.4. Mapping Quality

Mean Mapping Quality	43.05
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2.5. Mismatches and indels

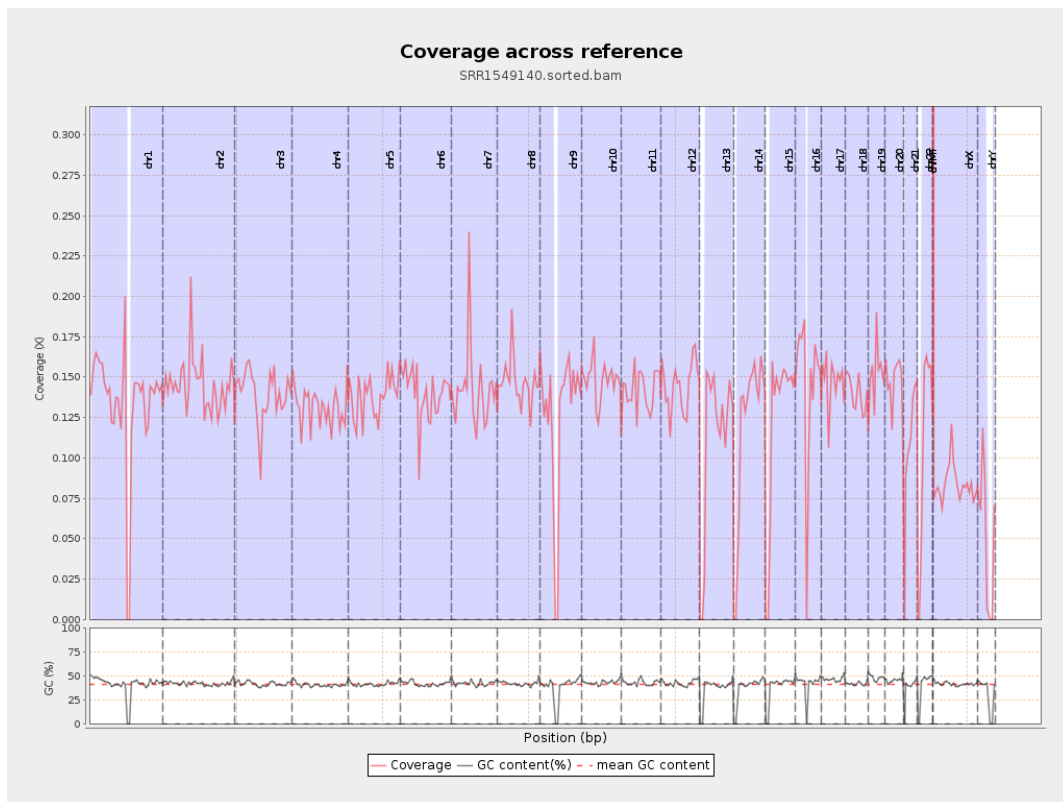
General error rate	0.32%
Mismatches	1,309,304
Insertions	10,437
Mapped reads with at least one insertion	0.1%
Deletions	31,281
Mapped reads with at least one deletion	0.3%
Homopolymer indels	46.41%

2.6. Chromosome stats

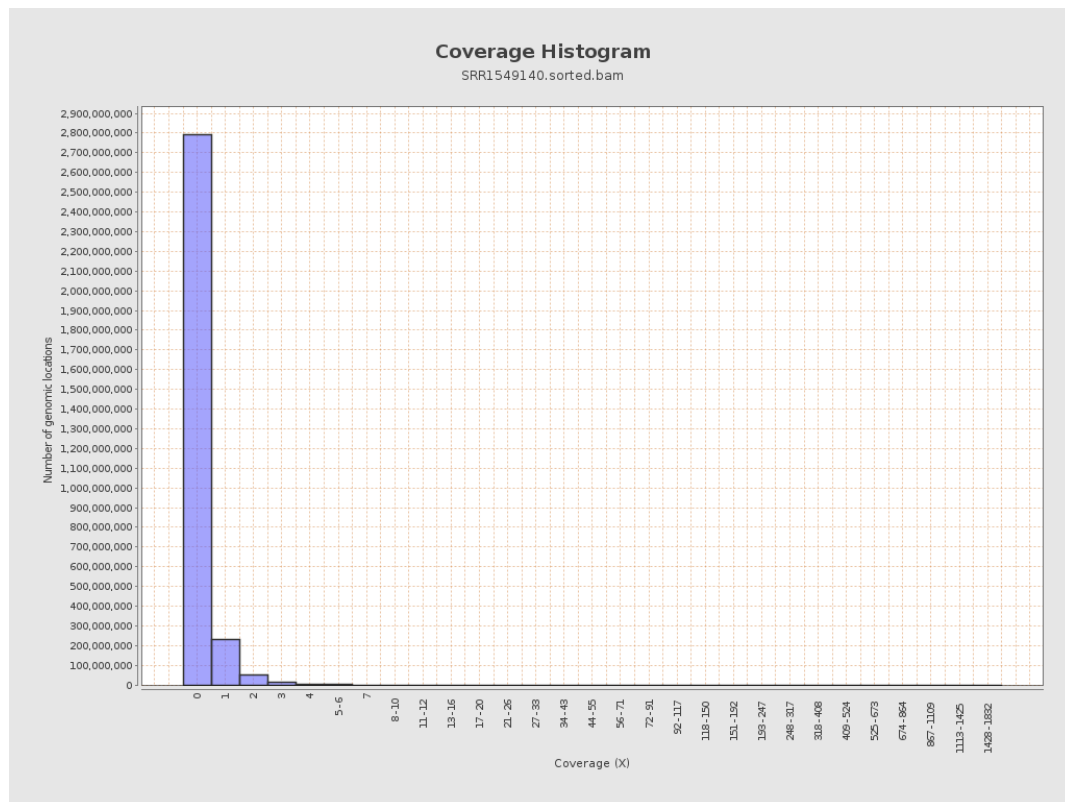
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	33461174	0.1342	1.44
chr2	243199373	35379138	0.1455	0.764
chr3	198022430	27532157	0.139	0.4827
chr4	191154276	25147275	0.1316	0.4824
chr5	180915260	25143852	0.139	0.5012
chr6	171115067	23918307	0.1398	0.5824
chr7	159138663	22788603	0.1432	1.2977
chr8	146364022	21399748	0.1462	0.7168

chr9	141213431	17704839	0.1254	0.7131
chr10	135534747	20014704	0.1477	0.7263
chr11	135006516	19121644	0.1416	0.7025
chr12	133851895	19456670	0.1454	0.5225
chr13	115169878	12948318	0.1124	0.427
chr14	107349540	12969239	0.1208	0.6126
chr15	102531392	12416786	0.1211	0.4407
chr16	90354753	12962490	0.1435	0.5476
chr17	81195210	12005498	0.1479	0.5502
chr18	78077248	10906479	0.1397	1.5598
chr19	59128983	9036669	0.1528	1.2908
chr20	63025520	9286113	0.1473	0.5308
chr21	48129895	5263775	0.1094	0.5151
chr22	51304566	5516376	0.1075	0.4563
chrMT	16571	159153	9.6043	12.814
chrX	155270560	13028321	0.0839	0.5096
chrY	59373566	3125362	0.0526	0.4011

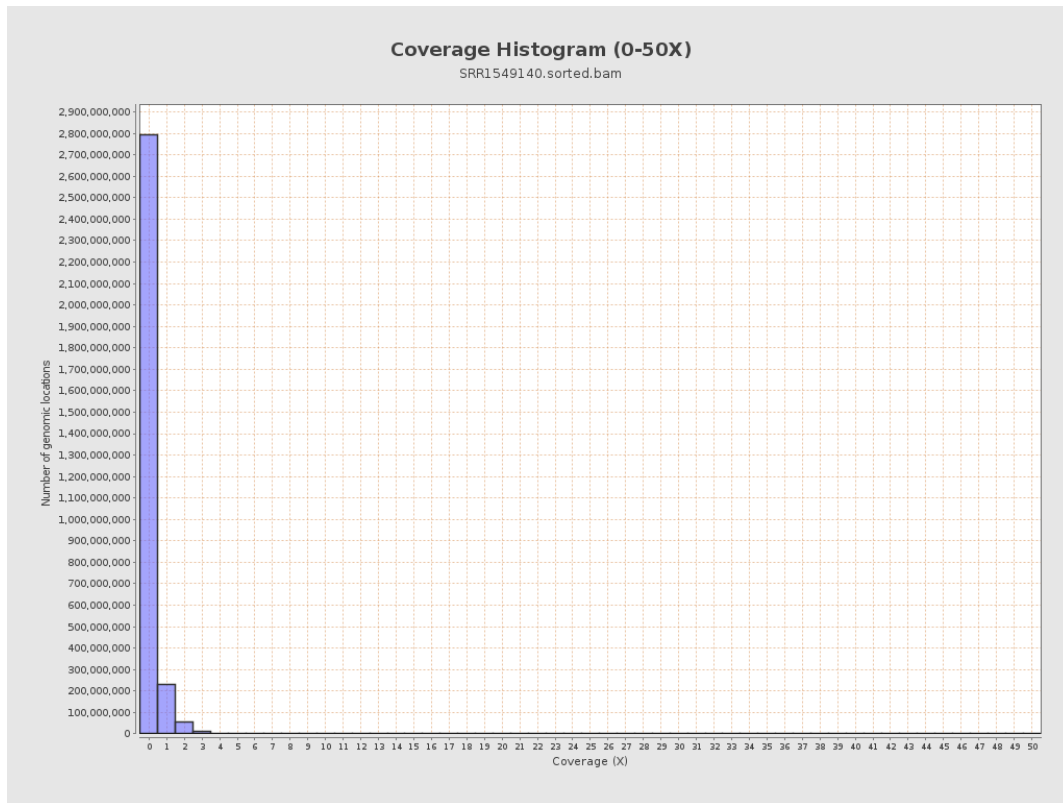
3. Results : Coverage across reference



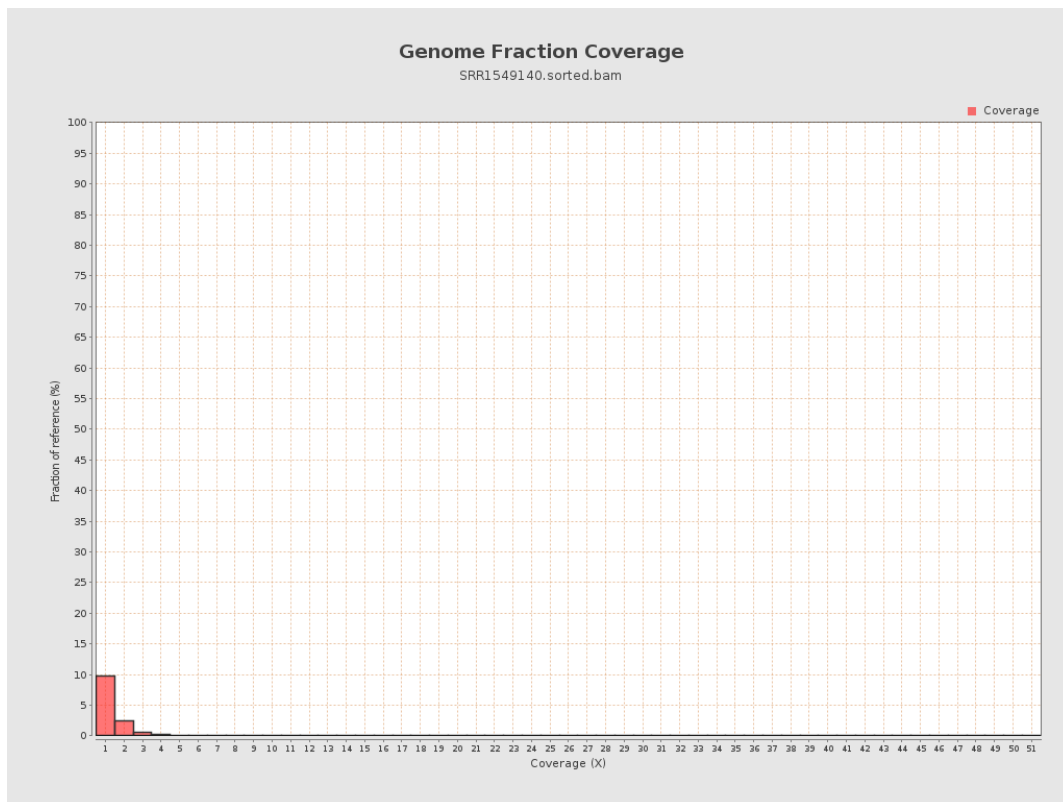
4. Results : Coverage Histogram



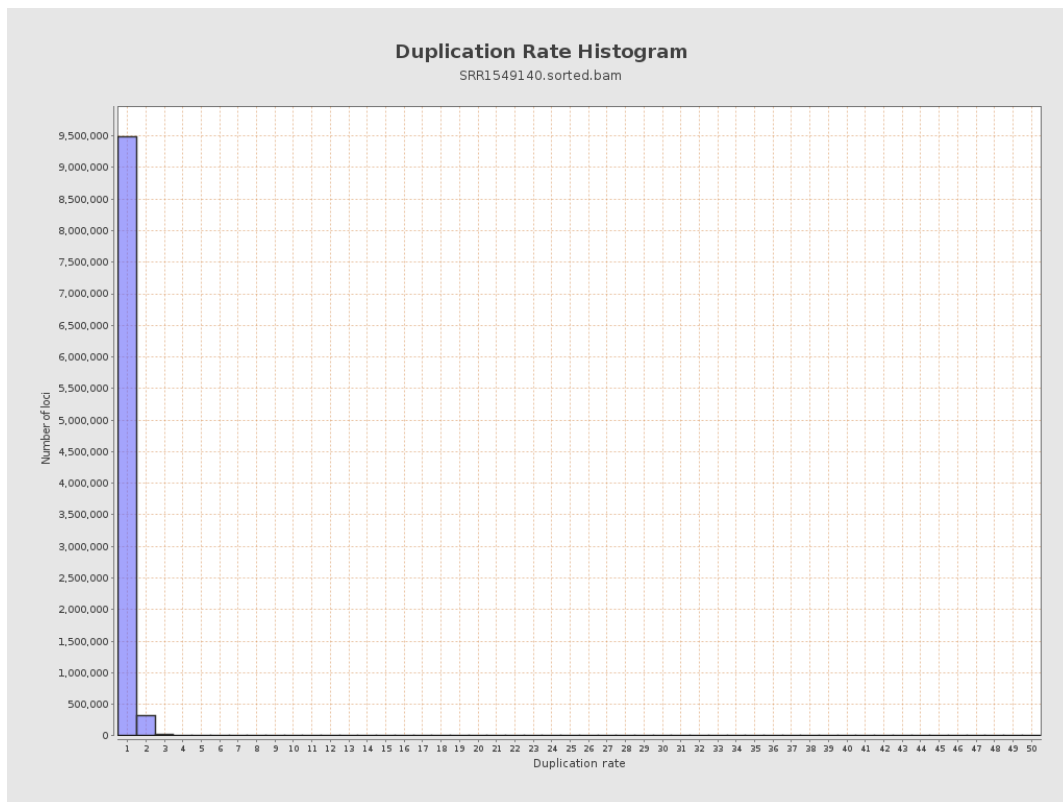
5. Results : Coverage Histogram (0-50X)



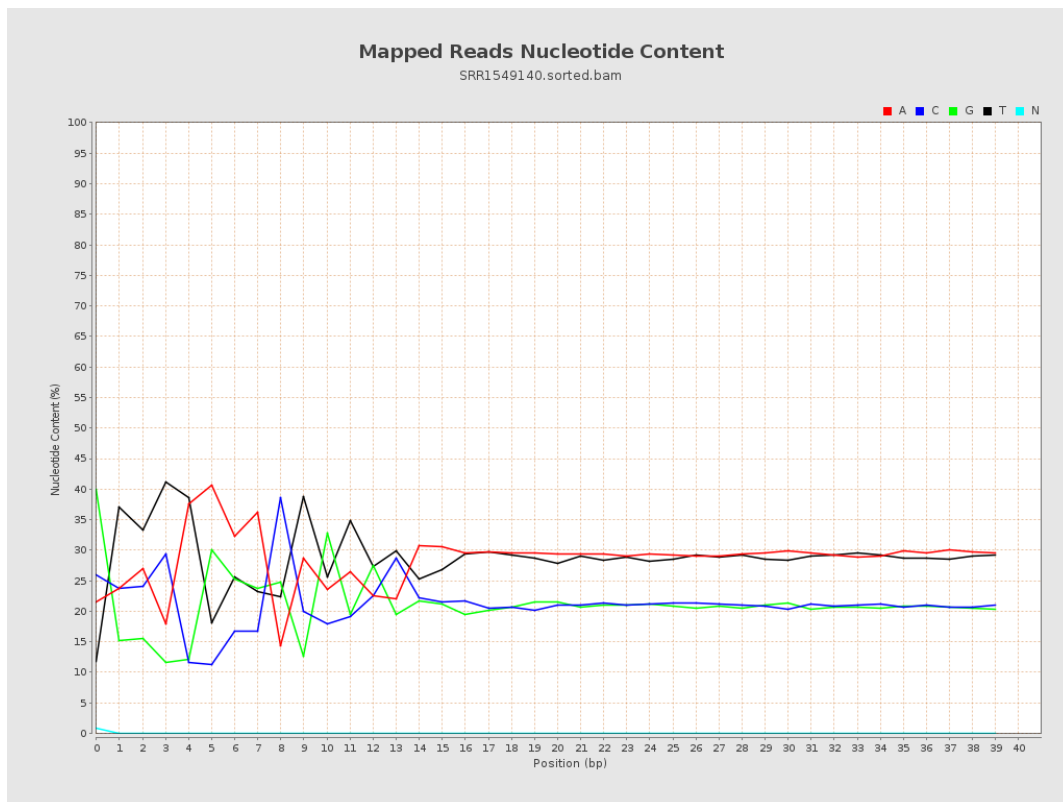
6. Results : Genome Fraction Coverage



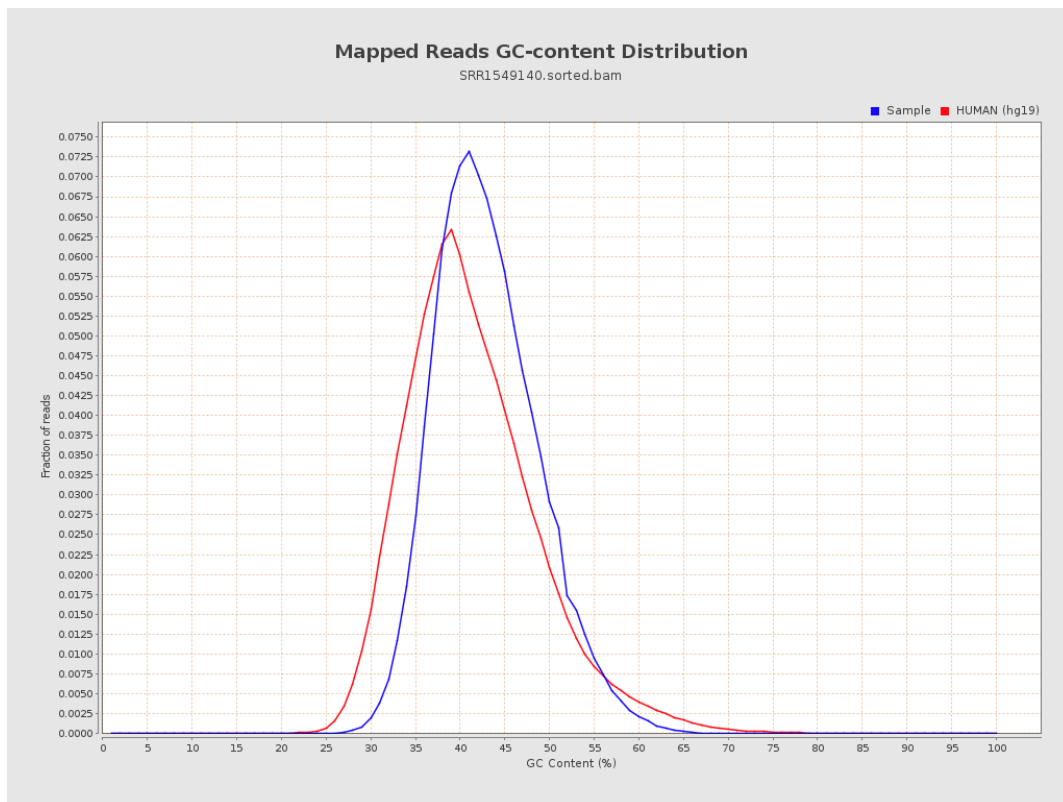
7. Results : Duplication Rate Histogram



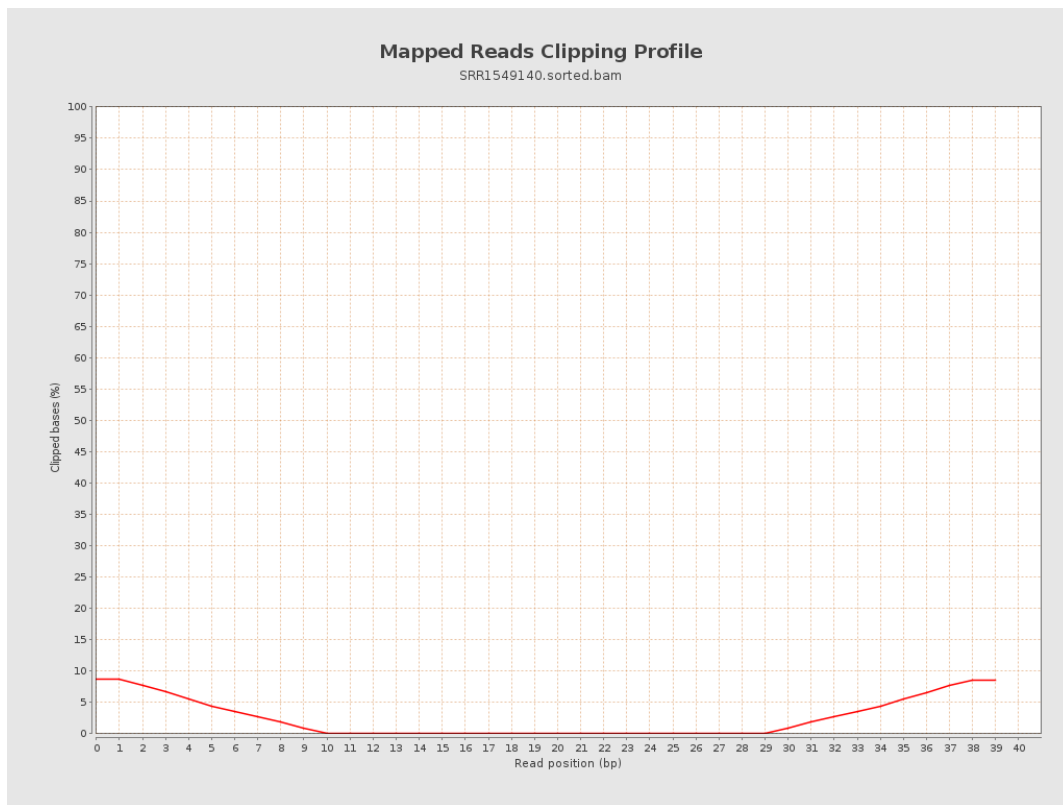
8. Results : Mapped Reads Nucleotide Content



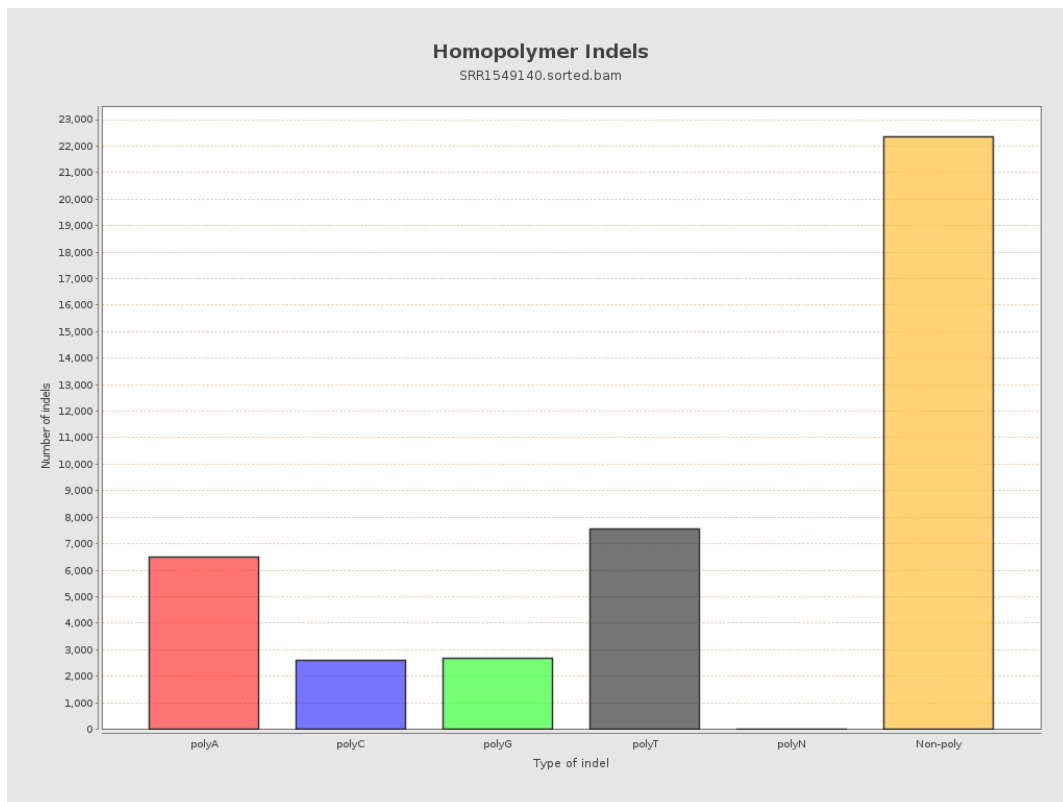
9. Results : Mapped Reads GC-content Distribution



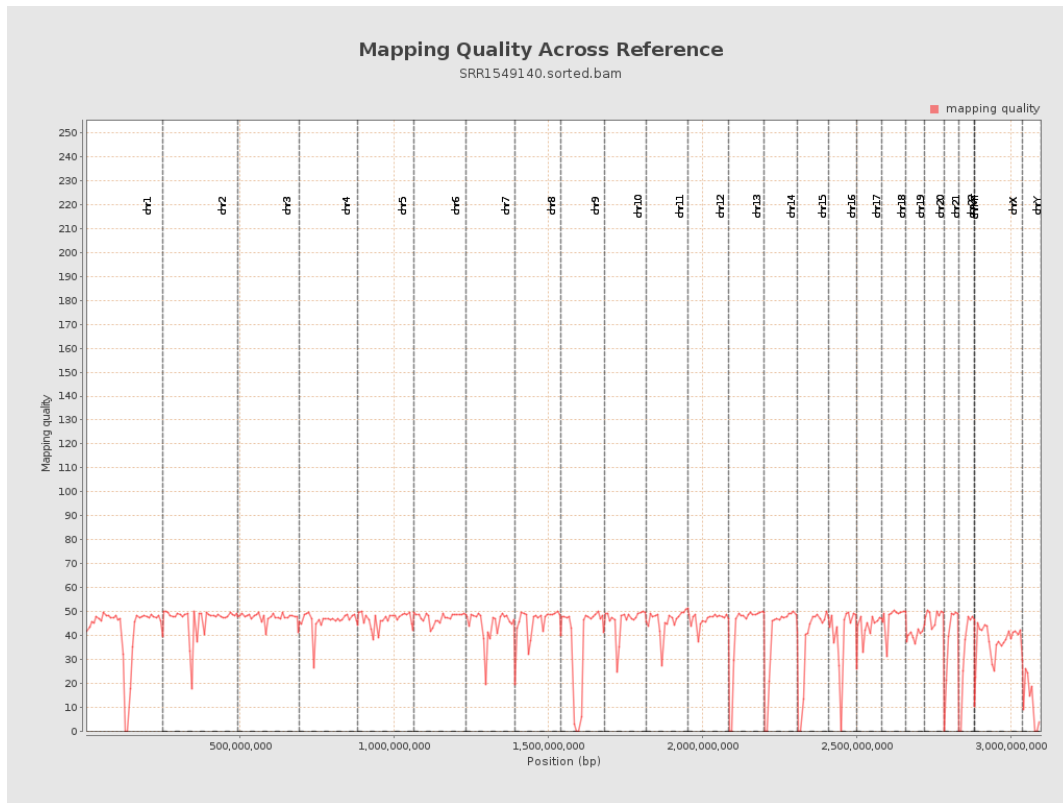
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

