

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 14:07:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549044.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_SRR1549044 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549044.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 14:07:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549044.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,441,396
Mapped reads	3,730,009 / 83.98%
Unmapped reads	711,387 / 16.02%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	120,118 / 2.7%
Duplication rate	2.52%
Clipped reads	337,035 / 7.59%

2.2. ACGT Content

Number/percentage of A's	40,233,667 / 27.31%
Number/percentage of C's	32,879,486 / 22.32%
Number/percentage of T's	41,297,197 / 28.03%
Number/percentage of G's	32,894,444 / 22.33%
Number/percentage of N's	1,134 / 0%
GC Percentage	44.65%

2.3. Coverage

Mean	0.0476
Standard Deviation	0.3408

2.4. Mapping Quality

Mean Mapping Quality	36.07
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2.5. Mismatches and indels

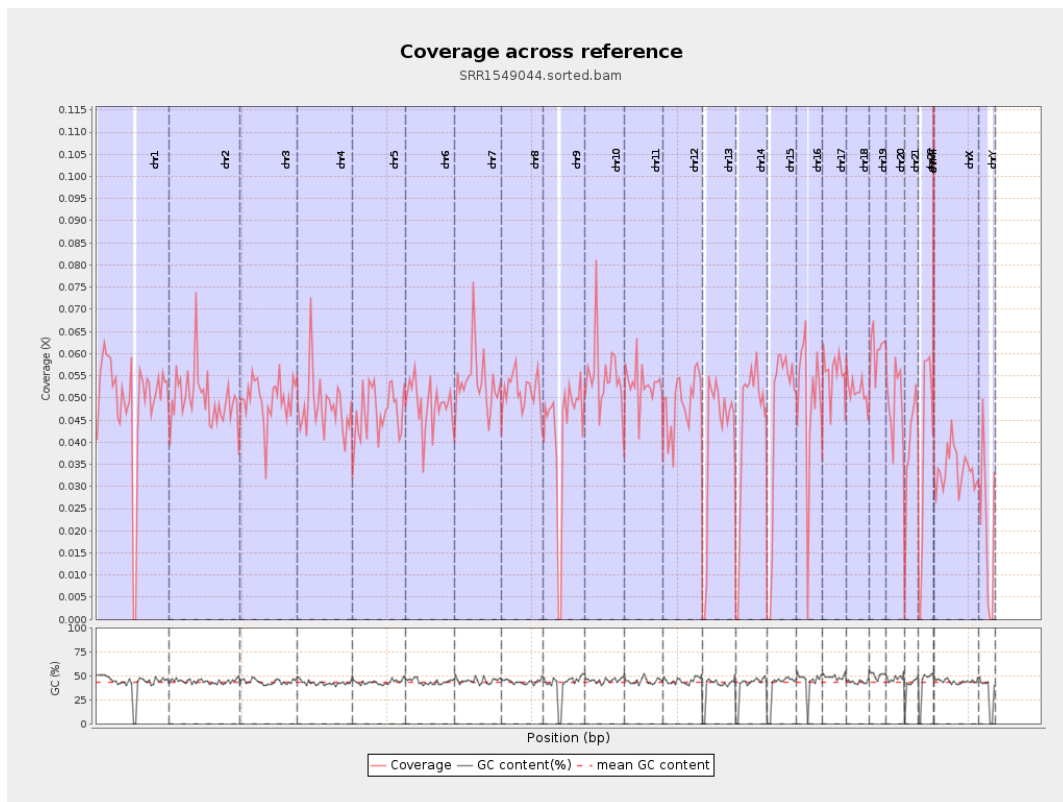
General error rate	0.3%
Mismatches	437,799
Insertions	5,147
Mapped reads with at least one insertion	0.14%
Deletions	10,268
Mapped reads with at least one deletion	0.28%
Homopolymer indels	38.22%

2.6. Chromosome stats

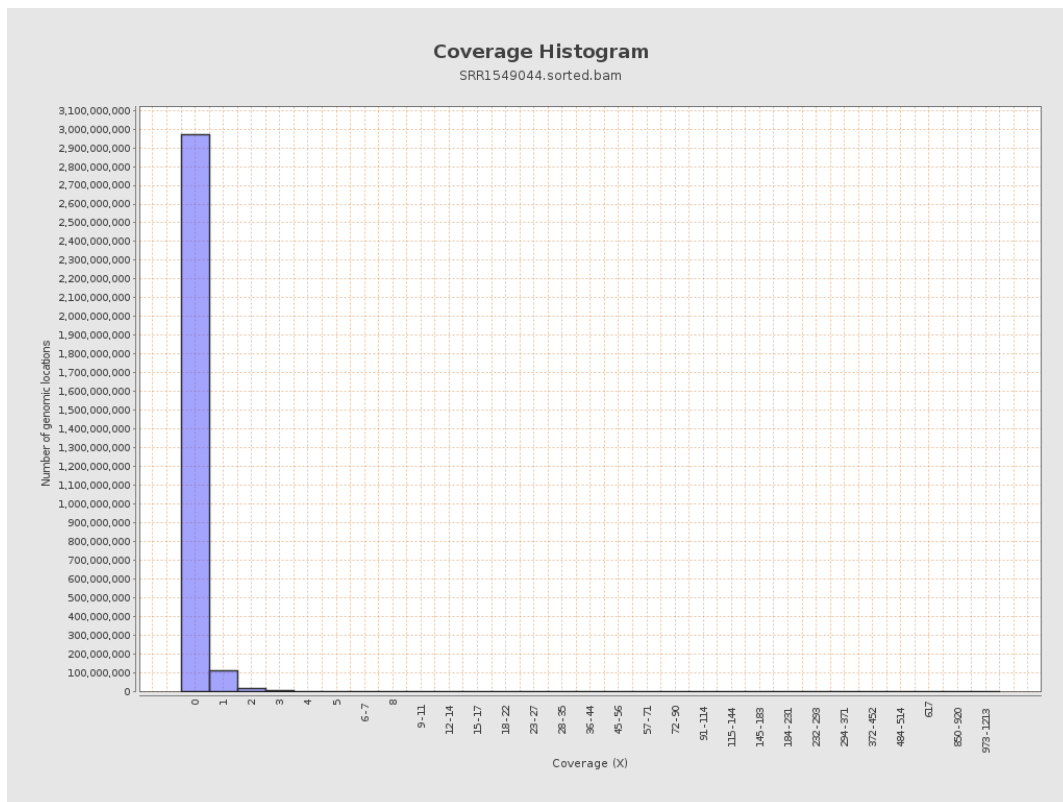
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	12245225	0.0491	0.4473
chr2	243199373	12127843	0.0499	0.3495
chr3	198022430	9839859	0.0497	0.2535
chr4	191154276	9145271	0.0478	0.273
chr5	180915260	8472707	0.0468	0.2471
chr6	171115067	8269422	0.0483	0.2563
chr7	159138663	8576658	0.0539	0.3821
chr8	146364022	7548438	0.0516	0.655

chr9	141213431	5999451	0.0425	0.3342
chr10	135534747	7437355	0.0549	0.3443
chr11	135006516	7121205	0.0527	0.2955
chr12	133851895	6549903	0.0489	0.2543
chr13	115169878	4688054	0.0407	0.2288
chr14	107349540	4684157	0.0436	0.2513
chr15	102531392	4618874	0.045	0.2424
chr16	90354753	4489733	0.0497	0.275
chr17	81195210	4506573	0.0555	0.2721
chr18	78077248	4033749	0.0517	0.5334
chr19	59128983	3602401	0.0609	0.4882
chr20	63025520	3051781	0.0484	0.2585
chr21	48129895	1874202	0.0389	0.2672
chr22	51304566	1977416	0.0385	0.3061
chrMT	16571	2709	0.1635	0.4302
chrX	155270560	5262351	0.0339	0.2357
chrY	59373566	1193786	0.0201	0.2319

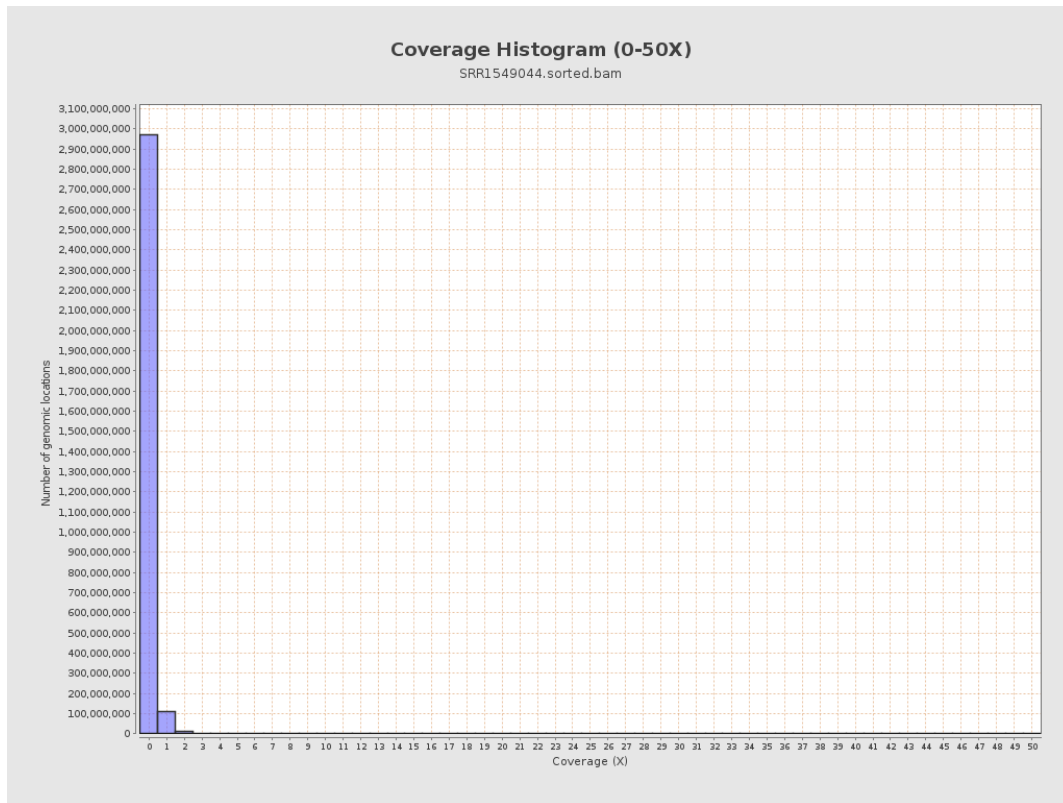
3. Results : Coverage across reference



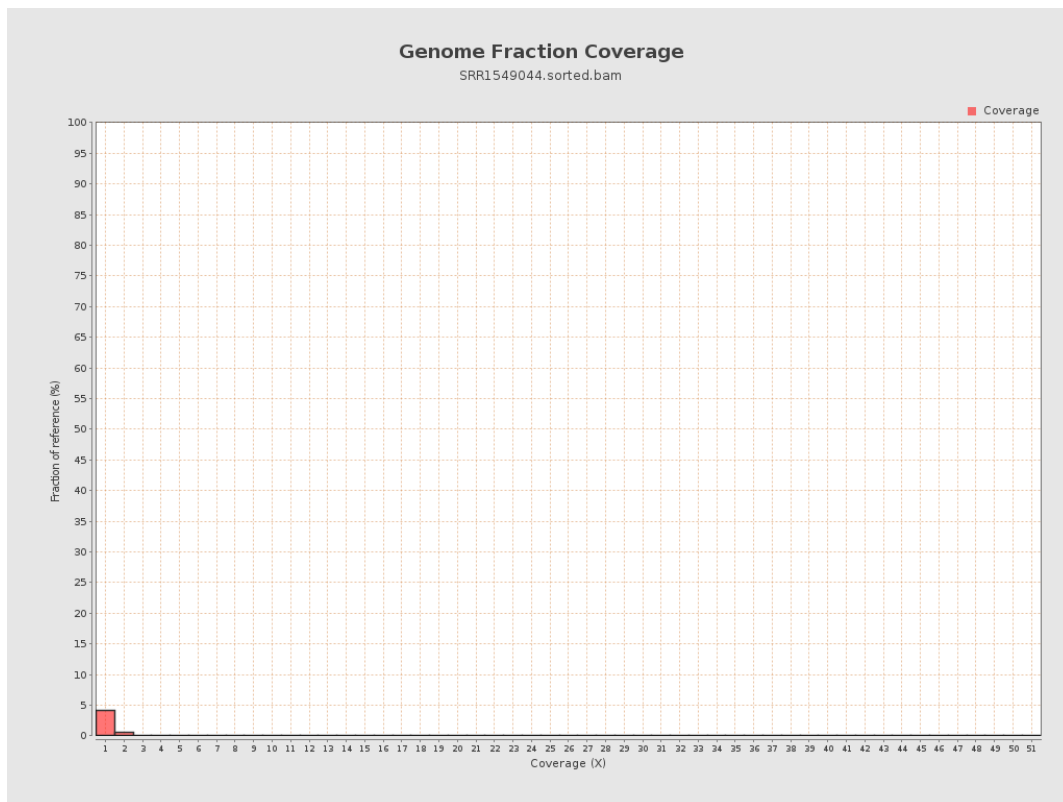
4. Results : Coverage Histogram



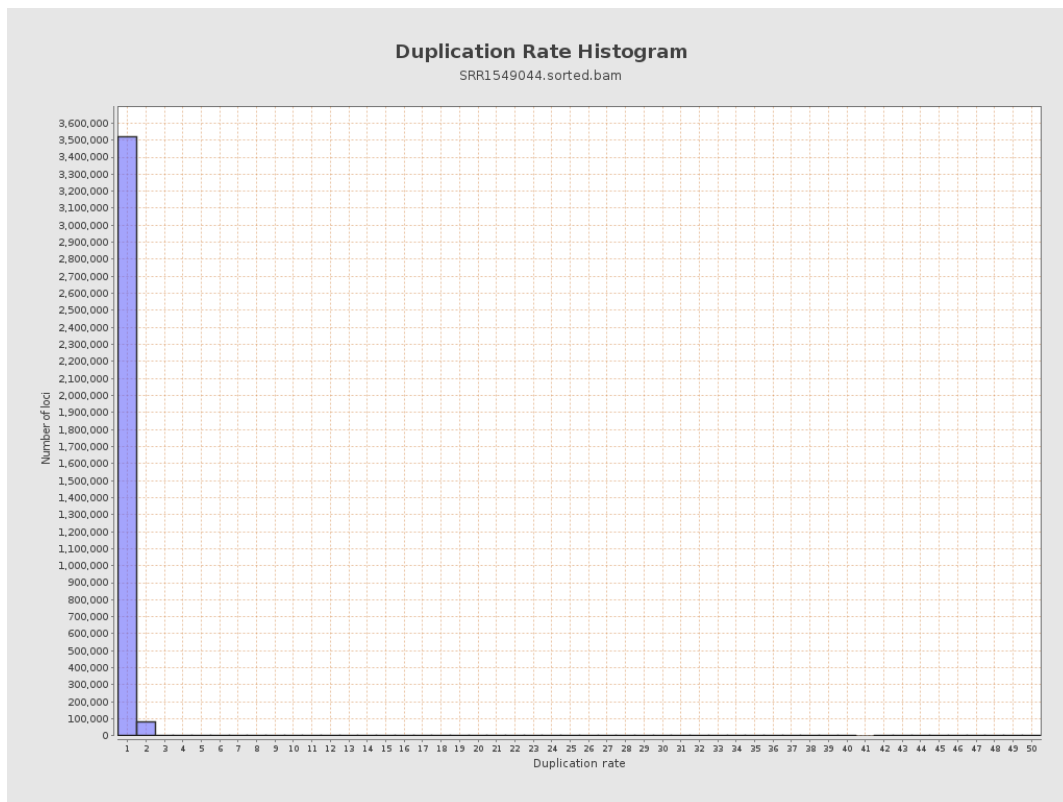
5. Results : Coverage Histogram (0-50X)



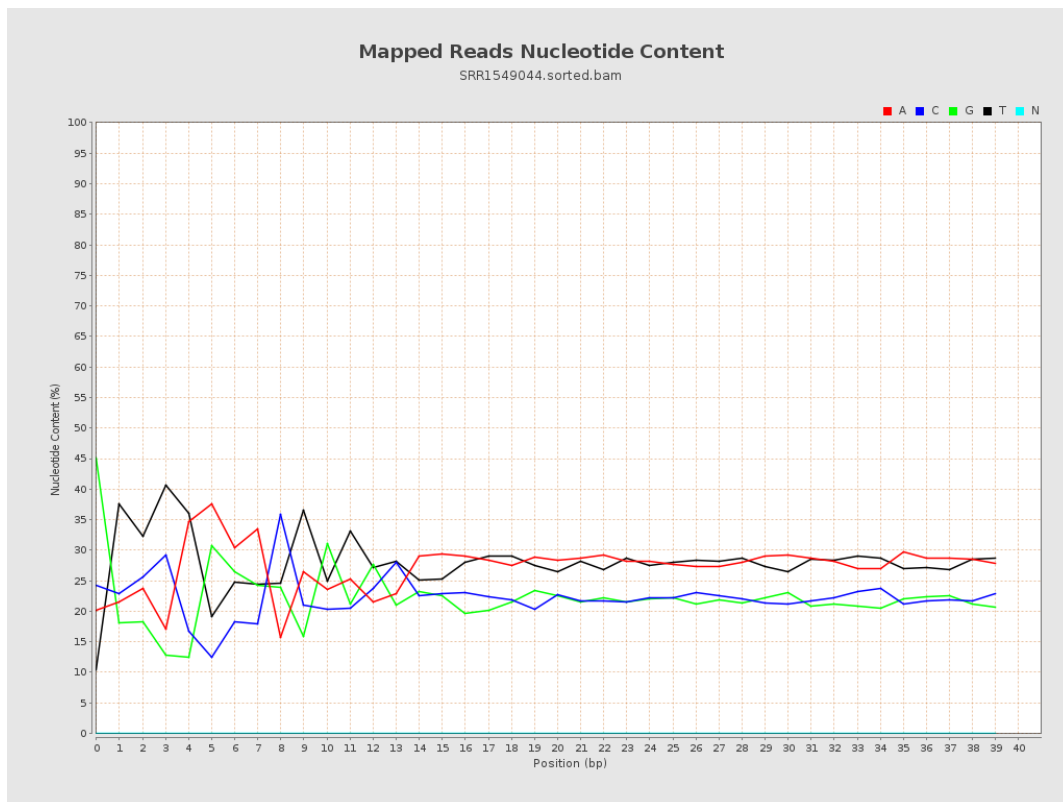
6. Results : Genome Fraction Coverage



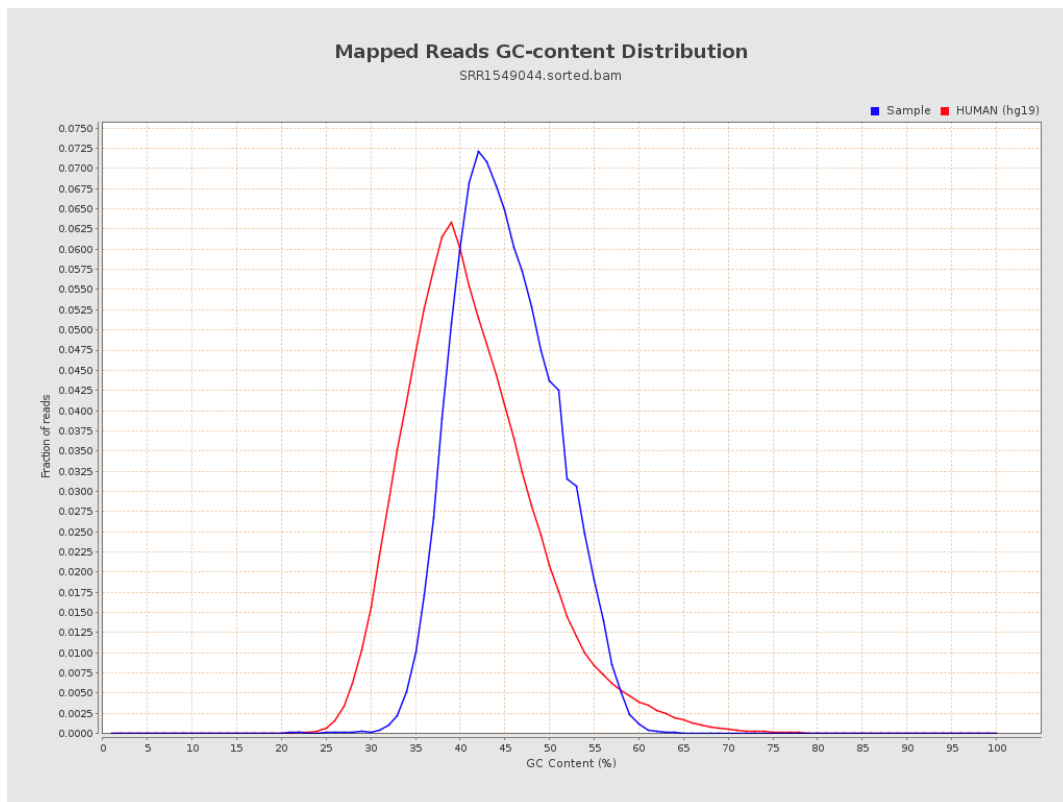
7. Results : Duplication Rate Histogram



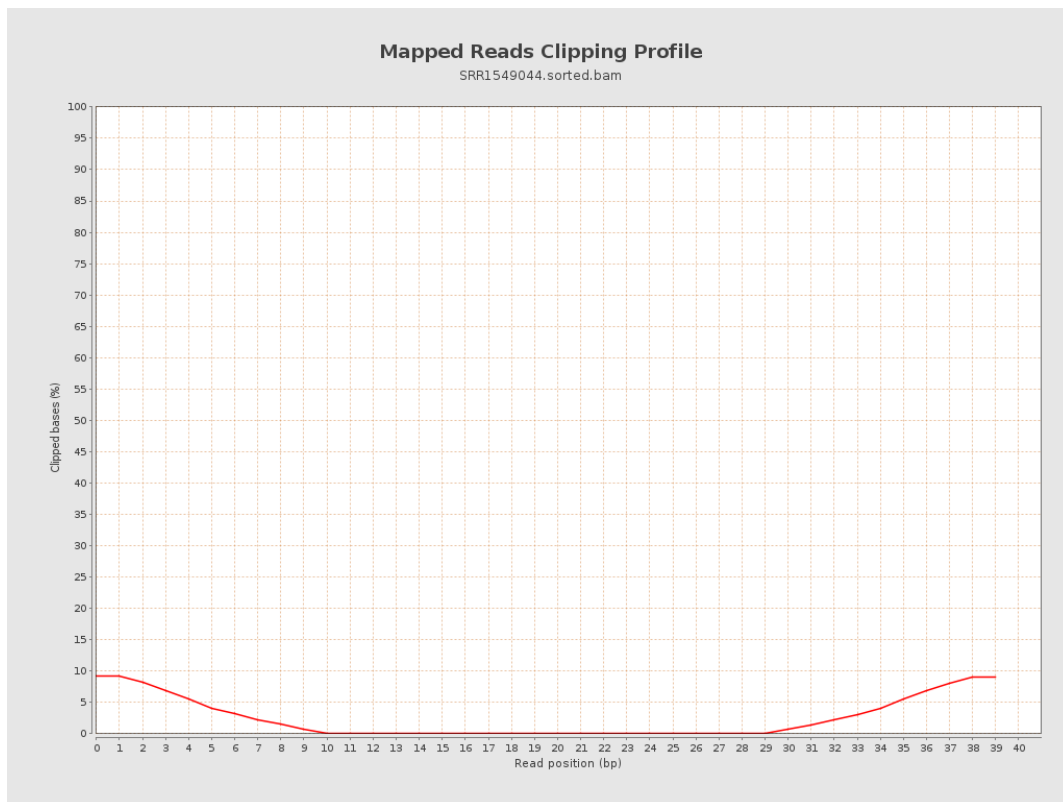
8. Results : Mapped Reads Nucleotide Content



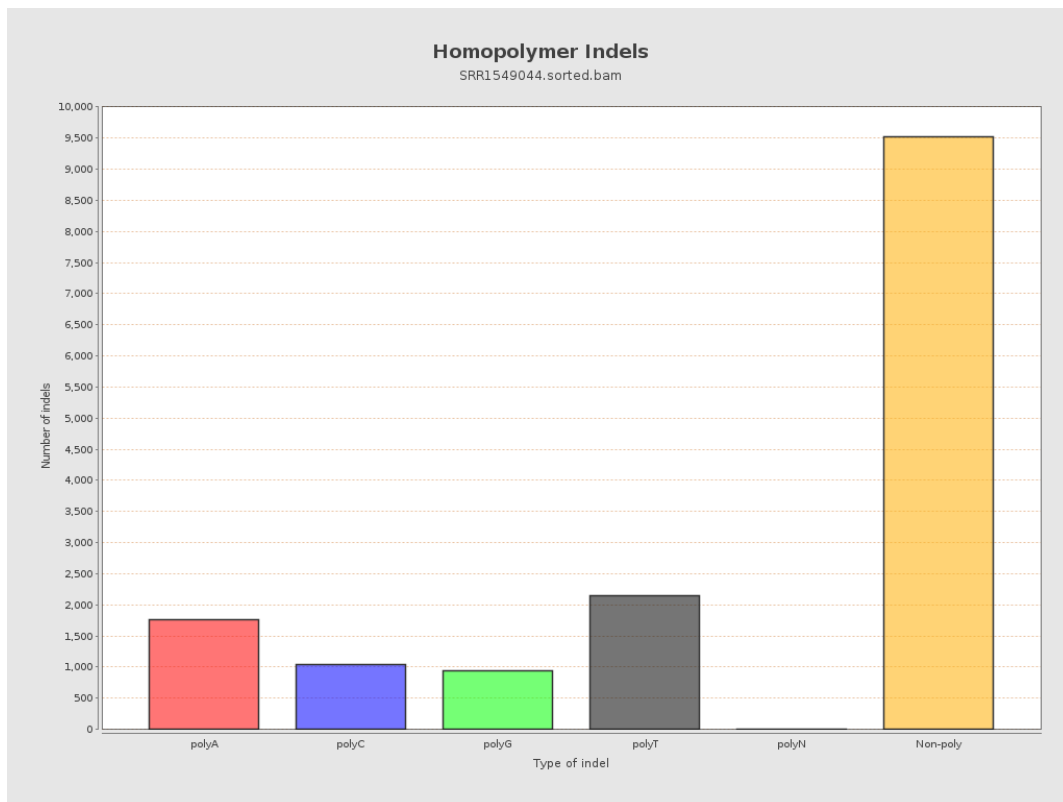
9. Results : Mapped Reads GC-content Distribution



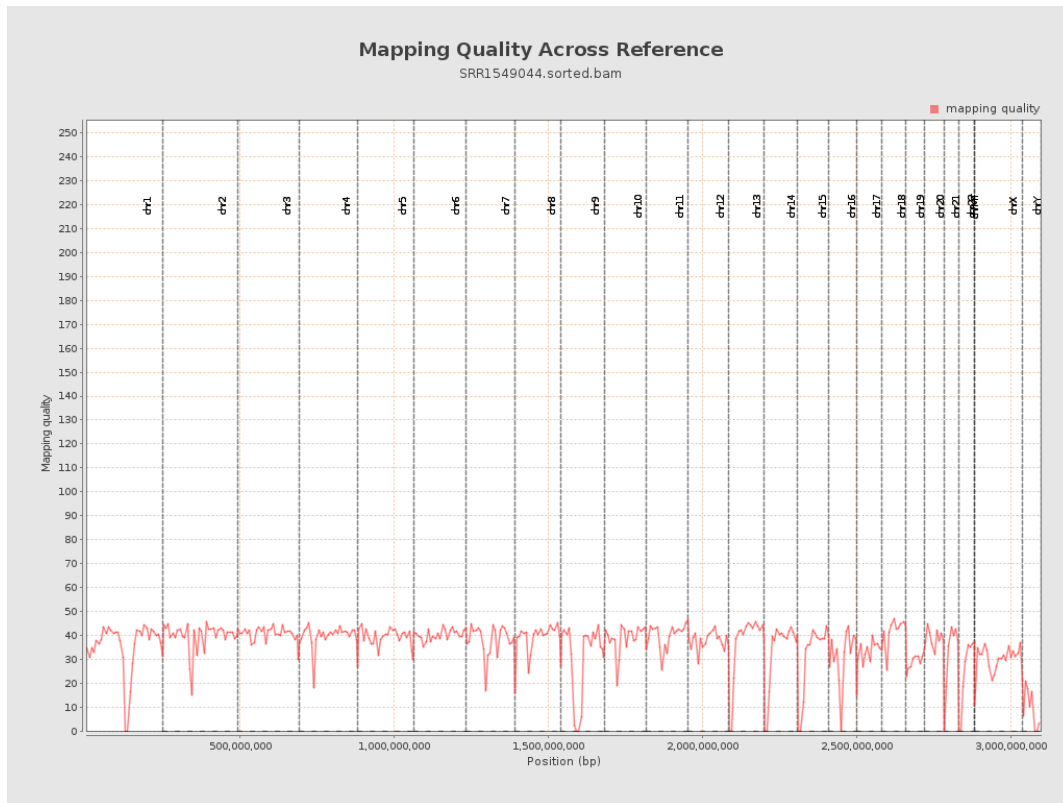
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

