

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 23:21:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549089.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_SRR1549089 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549089.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 23:20:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549089.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,073,567
Mapped reads	7,116,068 / 88.14%
Unmapped reads	957,499 / 11.86%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	227,467 / 2.82%
Duplication rate	2.21%
Clipped reads	336,878 / 4.17%

2.2. ACGT Content

Number/percentage of A's	83,788,071 / 29.64%
Number/percentage of C's	57,852,152 / 20.47%
Number/percentage of T's	84,766,711 / 29.99%
Number/percentage of G's	56,189,677 / 19.88%
Number/percentage of N's	68,368 / 0.02%
GC Percentage	40.35%

2.3. Coverage

Mean	0.0913
Standard Deviation	0.6565

2.4. Mapping Quality

Mean Mapping Quality	44.33
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2.5. Mismatches and indels

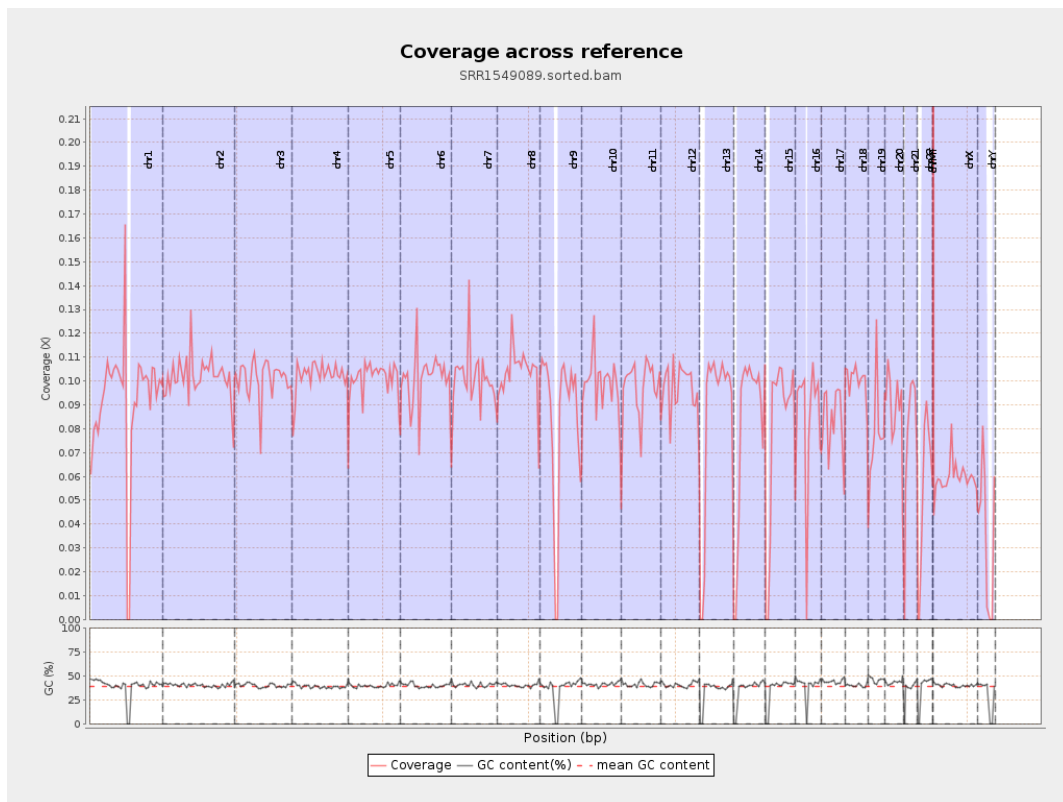
General error rate	0.4%
Mismatches	1,113,564
Insertions	6,425
Mapped reads with at least one insertion	0.09%
Deletions	21,385
Mapped reads with at least one deletion	0.3%
Homopolymer indels	45.27%

2.6. Chromosome stats

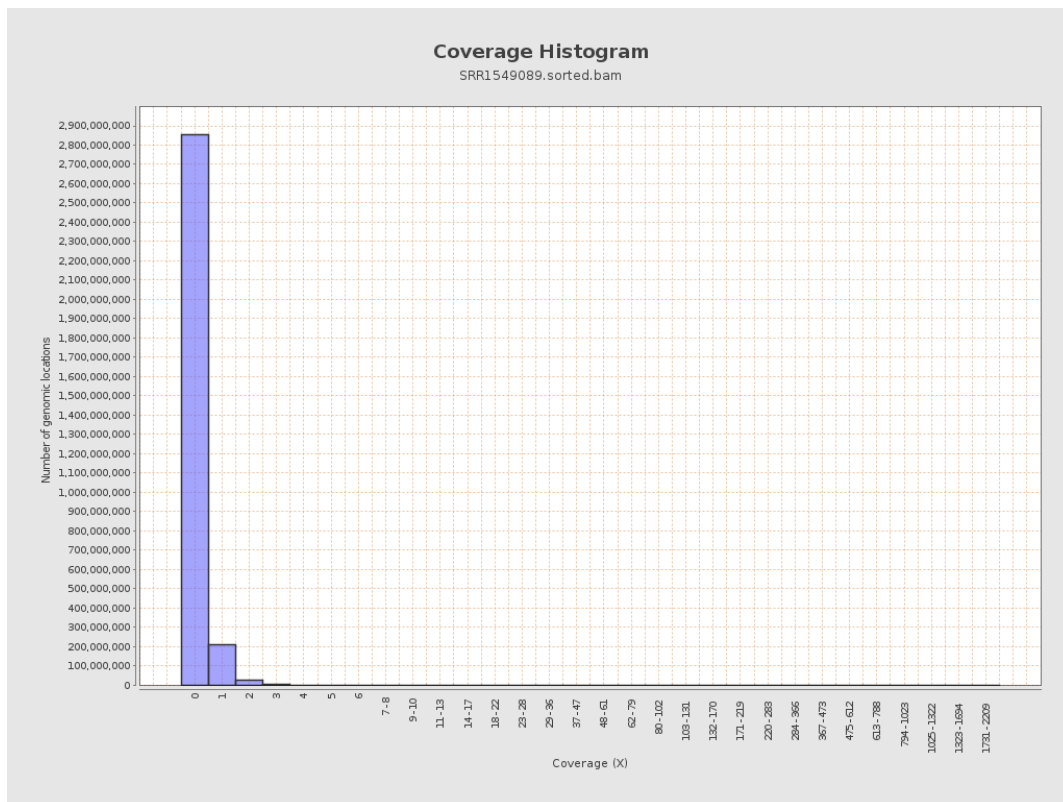
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	22897141	0.0919	1.5638
chr2	243199373	24765262	0.1018	0.512
chr3	198022430	20017717	0.1011	0.3626
chr4	191154276	19550828	0.1023	0.3702
chr5	180915260	18252146	0.1009	0.372
chr6	171115067	17352491	0.1014	0.4743
chr7	159138663	16013529	0.1006	0.7562
chr8	146364022	15156520	0.1036	0.6785

chr9	141213431	11968227	0.0848	0.4876
chr10	135534747	13423215	0.099	0.5385
chr11	135006516	13168592	0.0975	0.5152
chr12	133851895	12995309	0.0971	0.3715
chr13	115169878	9771036	0.0848	0.3236
chr14	107349540	8805379	0.082	0.3689
chr15	102531392	8106612	0.0791	0.3136
chr16	90354753	7489983	0.0829	0.375
chr17	81195210	6830209	0.0841	0.373
chr18	78077248	7860496	0.1007	0.9611
chr19	59128983	4665760	0.0789	1.1822
chr20	63025520	5670919	0.09	0.3498
chr21	48129895	3672356	0.0763	0.3579
chr22	51304566	2831156	0.0552	0.2953
chrMT	16571	18359	1.1079	1.5882
chrX	155270560	9207487	0.0593	0.3493
chrY	59373566	2201344	0.0371	0.3246

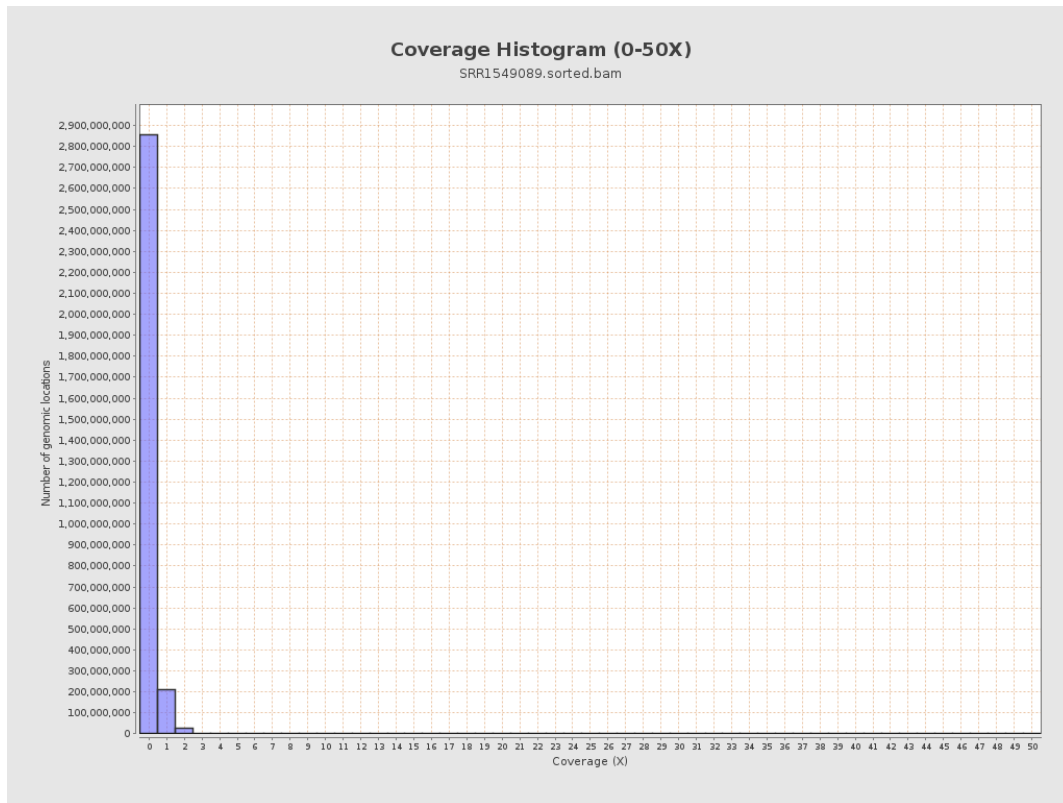
3. Results : Coverage across reference



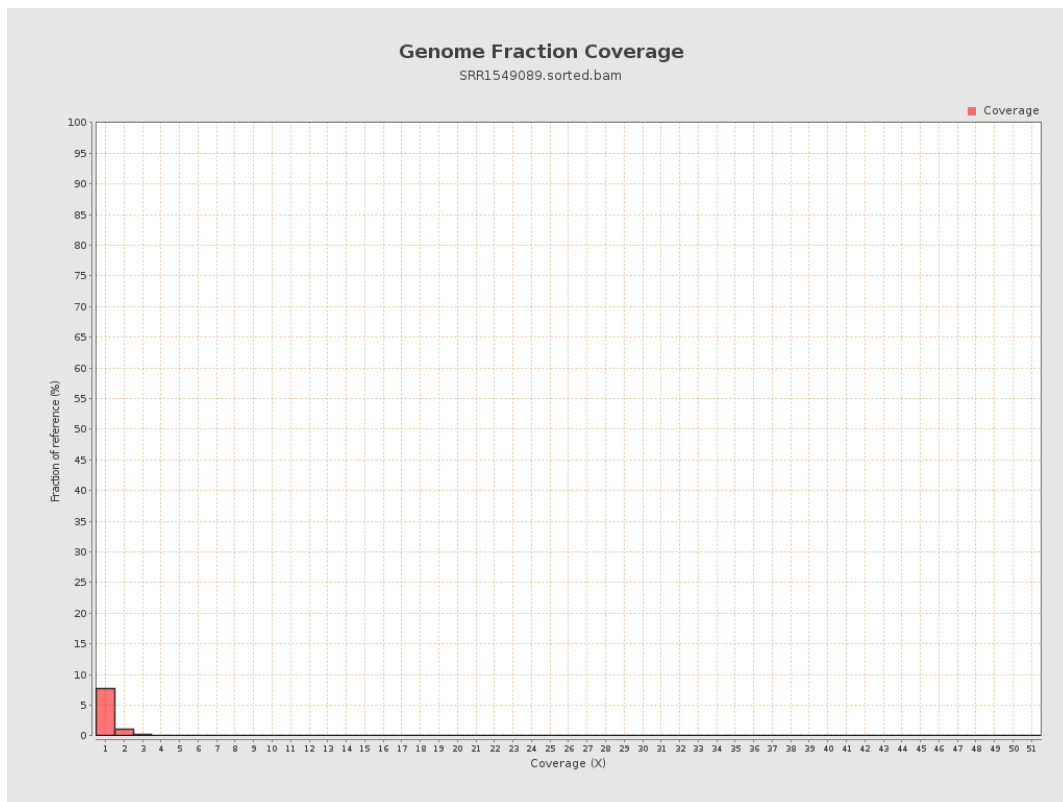
4. Results : Coverage Histogram



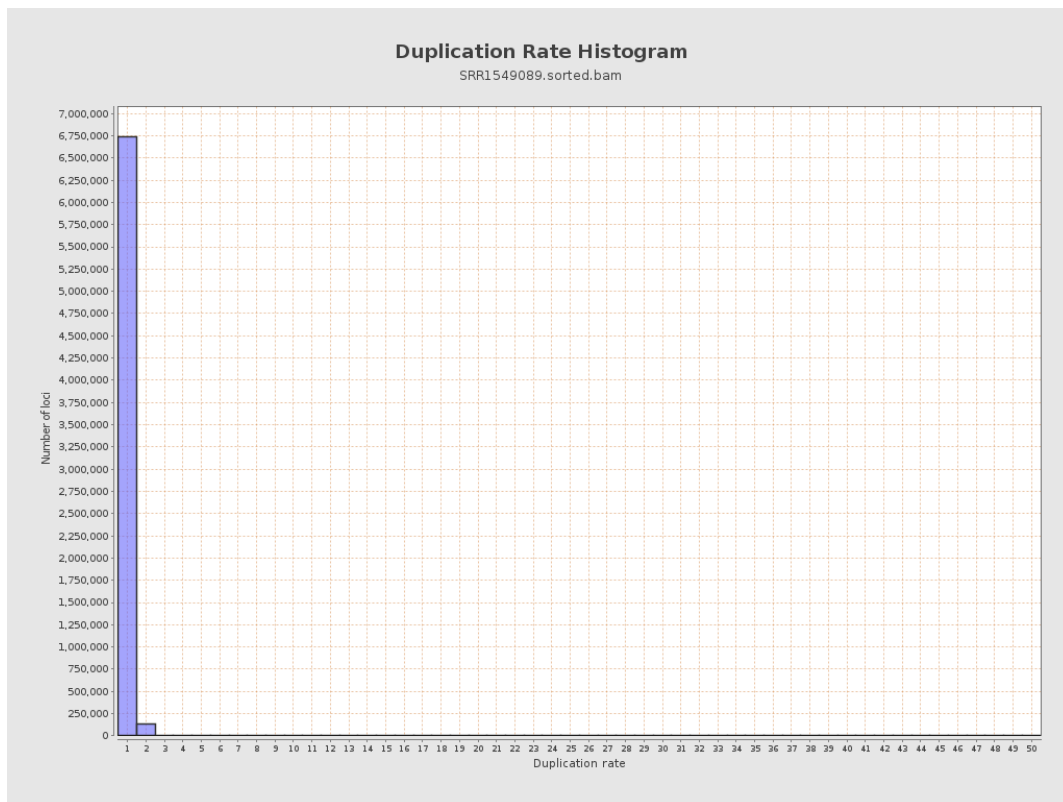
5. Results : Coverage Histogram (0-50X)



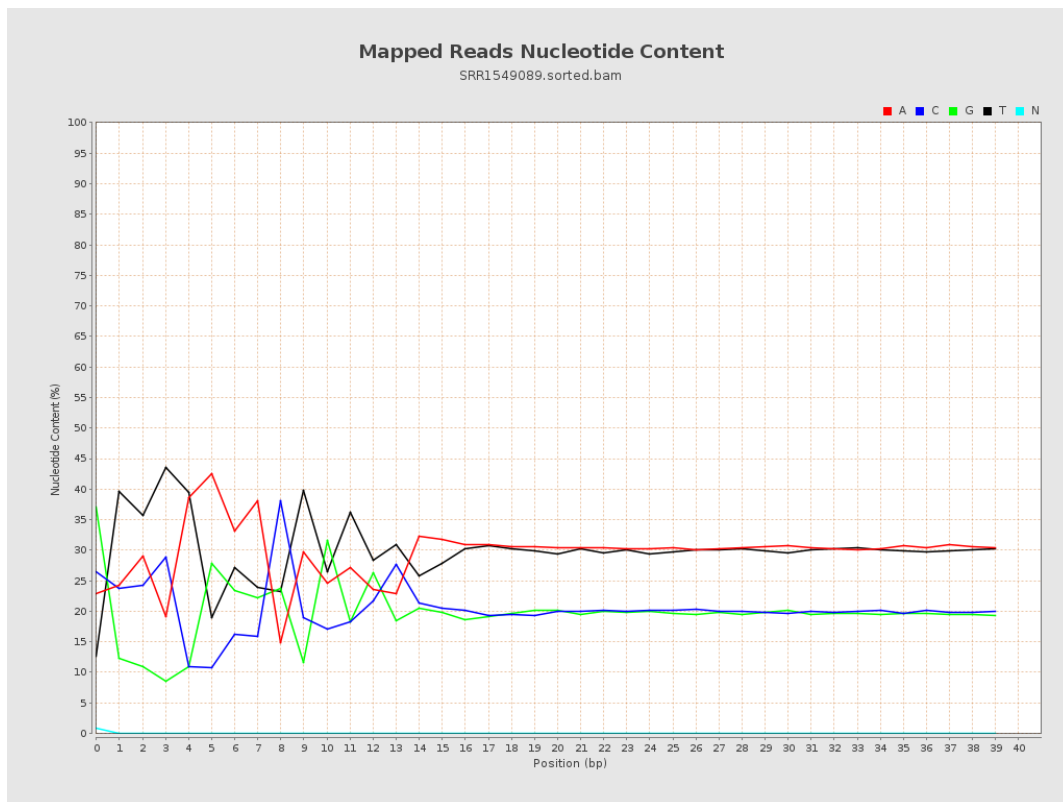
6. Results : Genome Fraction Coverage



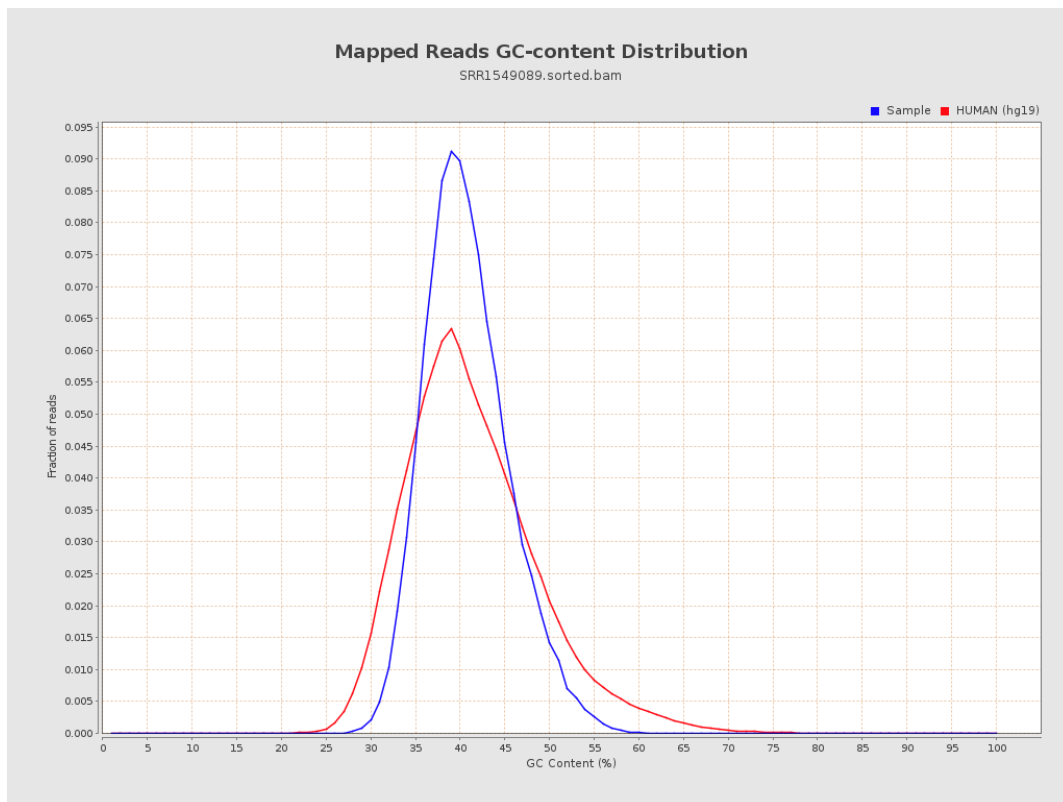
7. Results : Duplication Rate Histogram



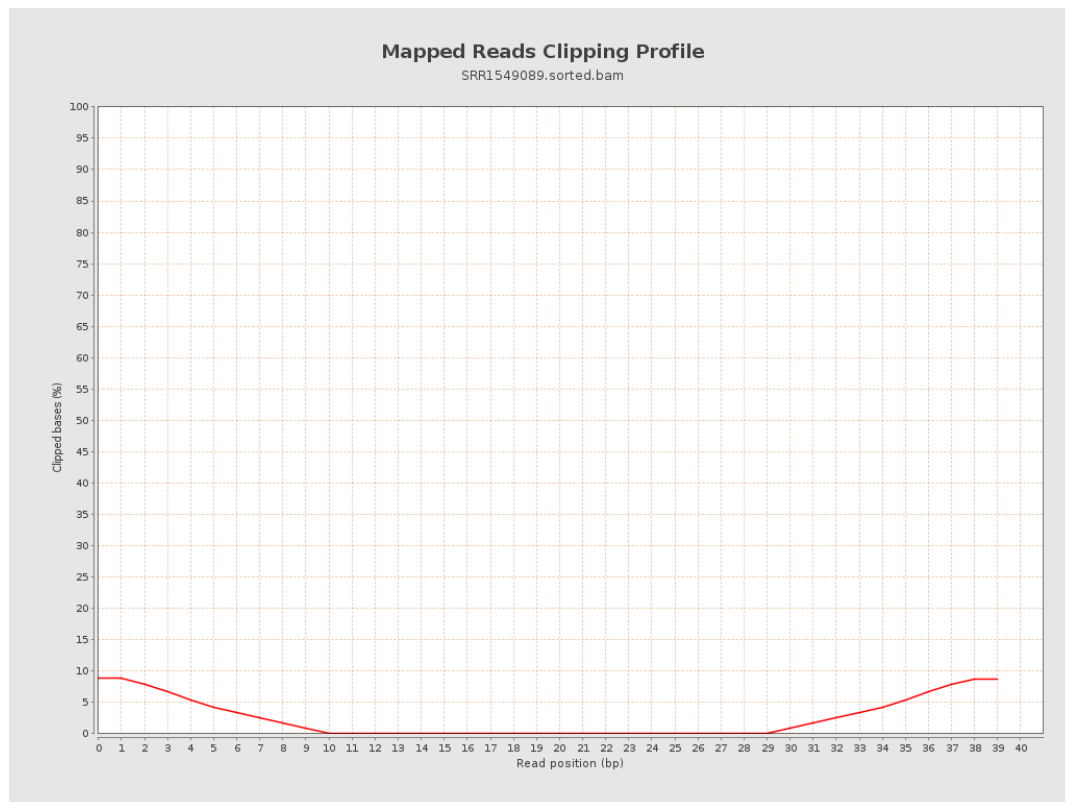
8. Results : Mapped Reads Nucleotide Content



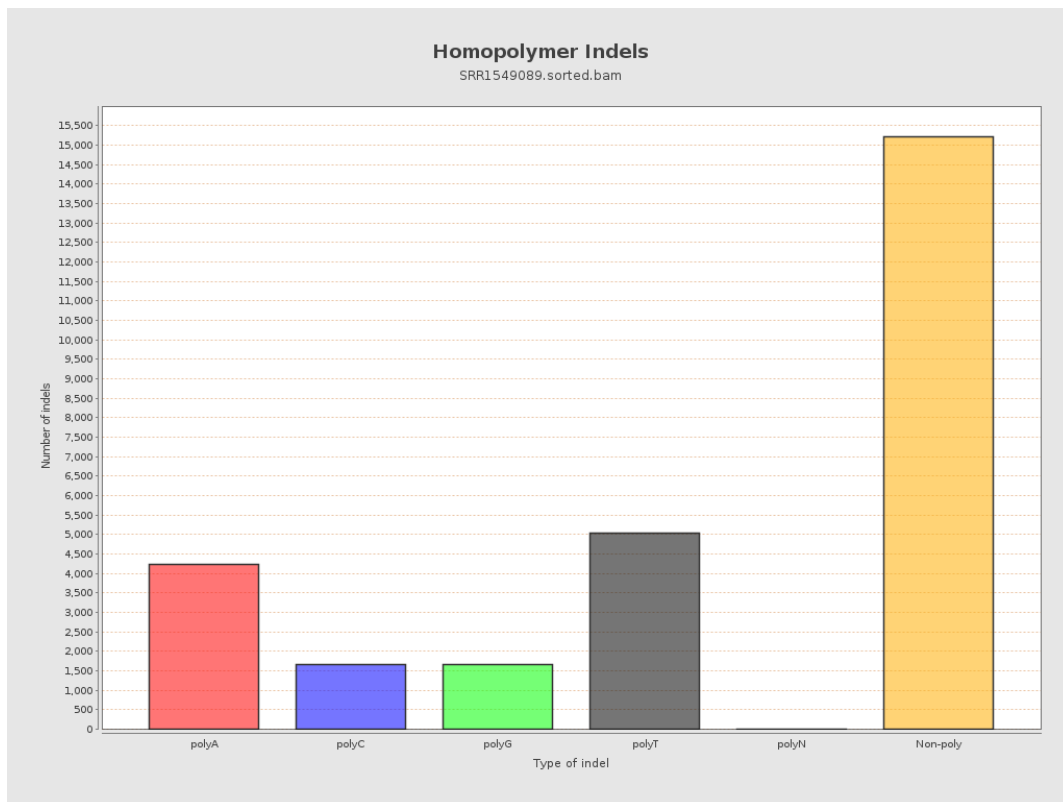
9. Results : Mapped Reads GC-content Distribution



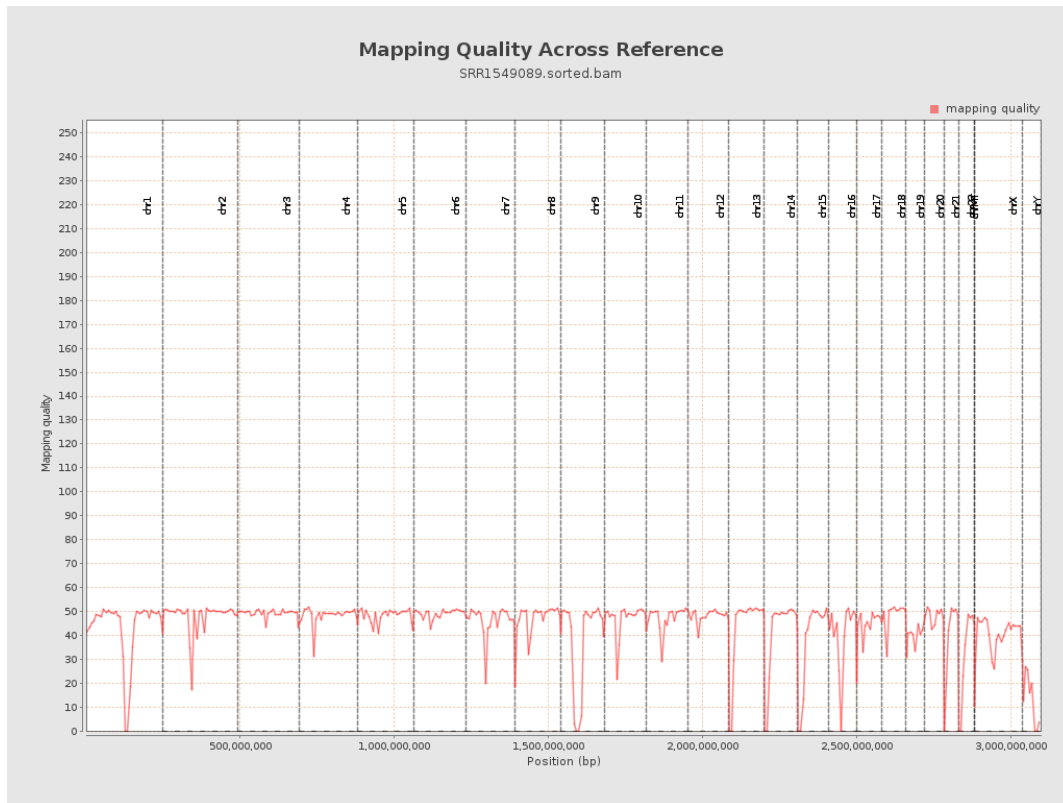
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

