

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 18:07:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549069.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_SRR1549069 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549069.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 18:07:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549069.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,806,250
Mapped reads	8,505,300 / 86.73%
Unmapped reads	1,300,950 / 13.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	303,211 / 3.09%
Duplication rate	2.46%
Clipped reads	385,406 / 3.93%

2.2. ACGT Content

Number/percentage of A's	99,824,605 / 29.54%
Number/percentage of C's	69,220,636 / 20.49%
Number/percentage of T's	99,820,455 / 29.54%
Number/percentage of G's	69,029,735 / 20.43%
Number/percentage of N's	6,297 / 0%
GC Percentage	40.91%

2.3. Coverage

Mean	0.1092
Standard Deviation	0.9533

2.4. Mapping Quality

Mean Mapping Quality	43.97
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2.5. Mismatches and indels

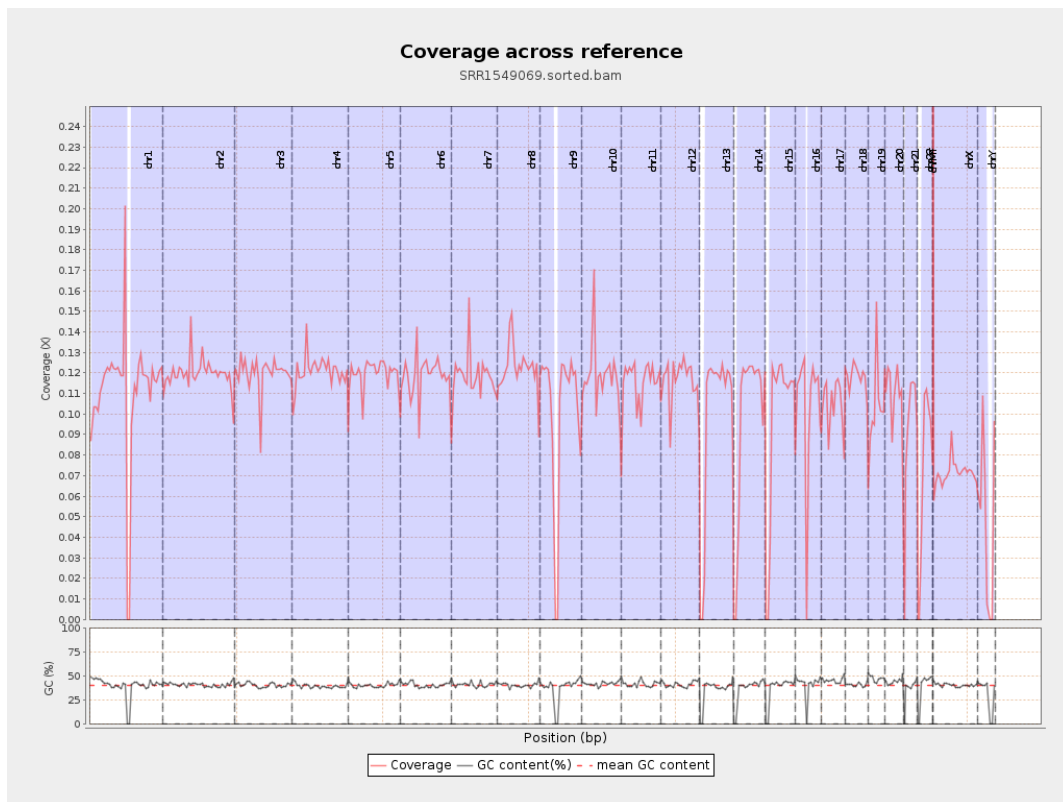
General error rate	0.31%
Mismatches	1,040,782
Insertions	8,082
Mapped reads with at least one insertion	0.09%
Deletions	27,831
Mapped reads with at least one deletion	0.33%
Homopolymer indels	44.49%

2.6. Chromosome stats

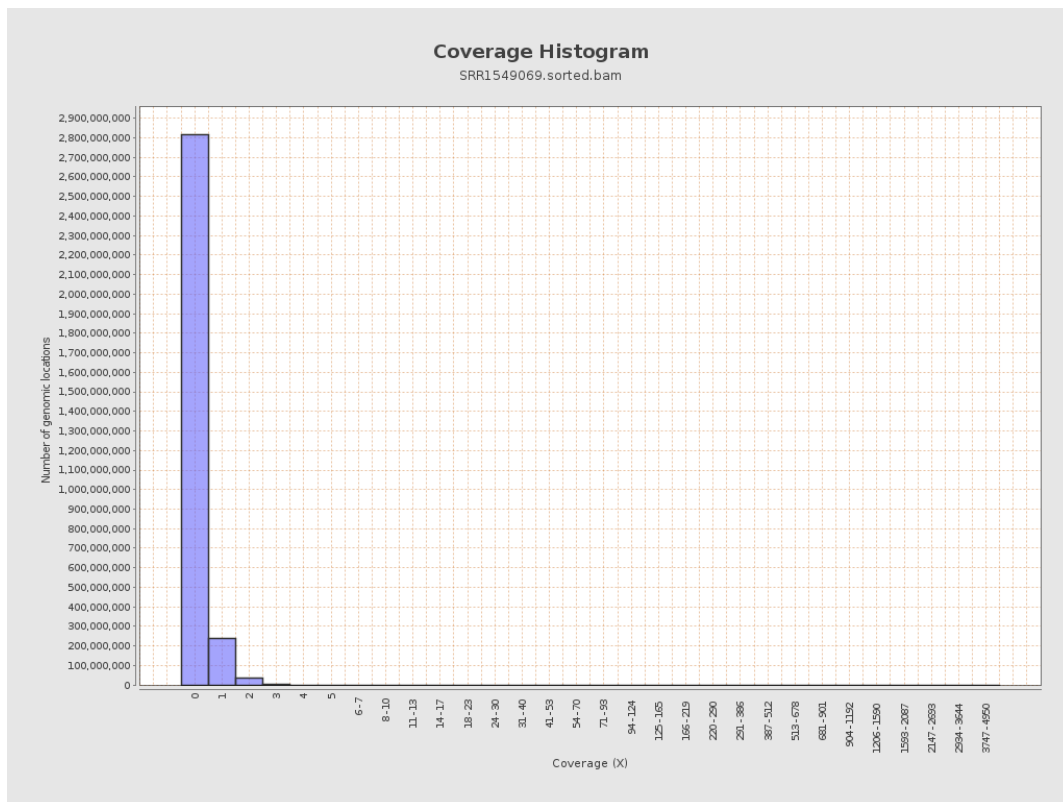
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	27647417	0.1109	2.0752
chr2	243199373	29129368	0.1198	0.5822
chr3	198022430	23740430	0.1199	0.4004
chr4	191154276	23138786	0.121	0.4391
chr5	180915260	21584881	0.1193	0.4045
chr6	171115067	20356018	0.119	0.4805
chr7	159138663	18815957	0.1182	0.7916
chr8	146364022	17934852	0.1225	2.4511

chr9	141213431	14353906	0.1016	0.5393
chr10	135534747	16099760	0.1188	0.6702
chr11	135006516	15610892	0.1156	0.5625
chr12	133851895	15616234	0.1167	0.4133
chr13	115169878	11383700	0.0988	0.3558
chr14	107349540	10551988	0.0983	0.4077
chr15	102531392	9769040	0.0953	0.3509
chr16	90354753	9192713	0.1017	0.4257
chr17	81195210	8543315	0.1052	0.4087
chr18	78077248	9243641	0.1184	1.1204
chr19	59128983	6200180	0.1049	1.5229
chr20	63025520	6914468	0.1097	0.3957
chr21	48129895	4412567	0.0917	0.4184
chr22	51304566	3698962	0.0721	0.3447
chrMT	16571	9273	0.5596	0.976
chrX	155270560	11062189	0.0712	0.3871
chrY	59373566	2927110	0.0493	0.4925

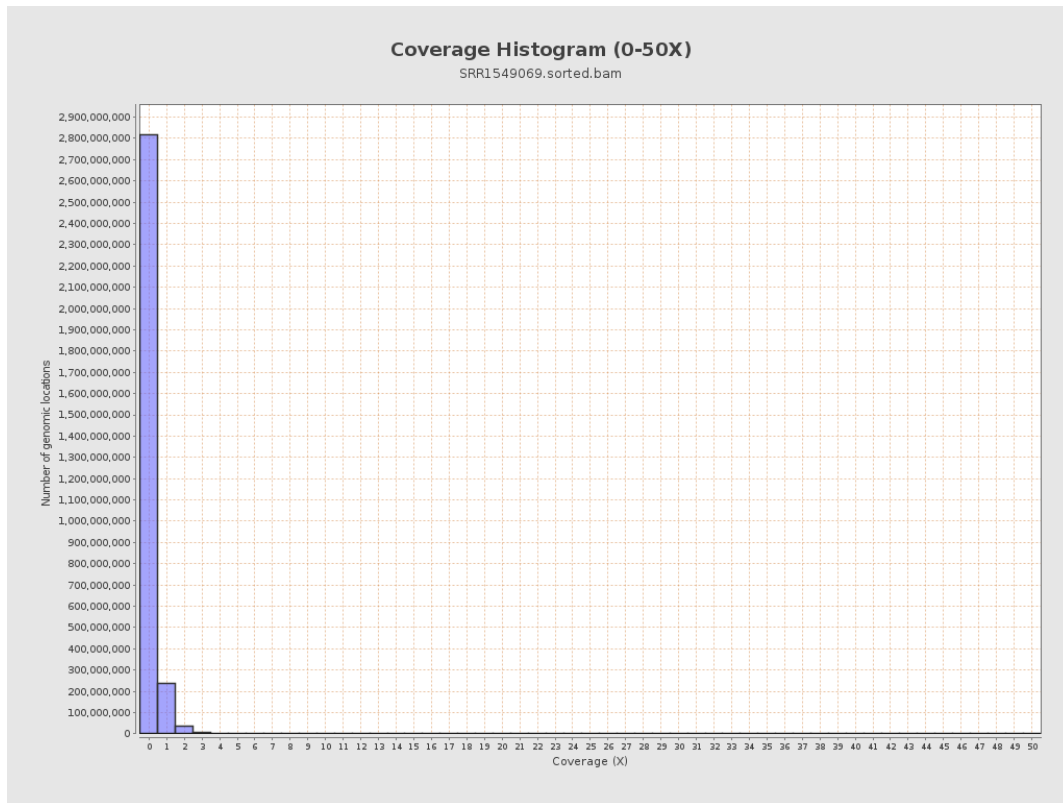
3. Results : Coverage across reference



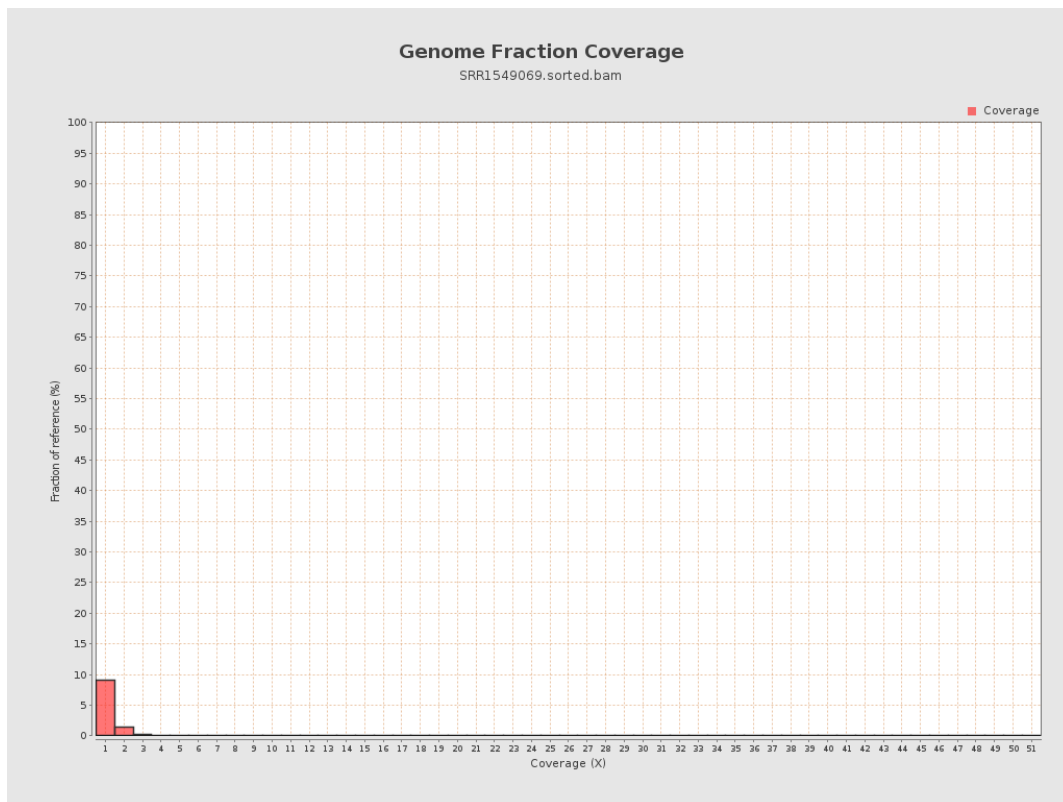
4. Results : Coverage Histogram



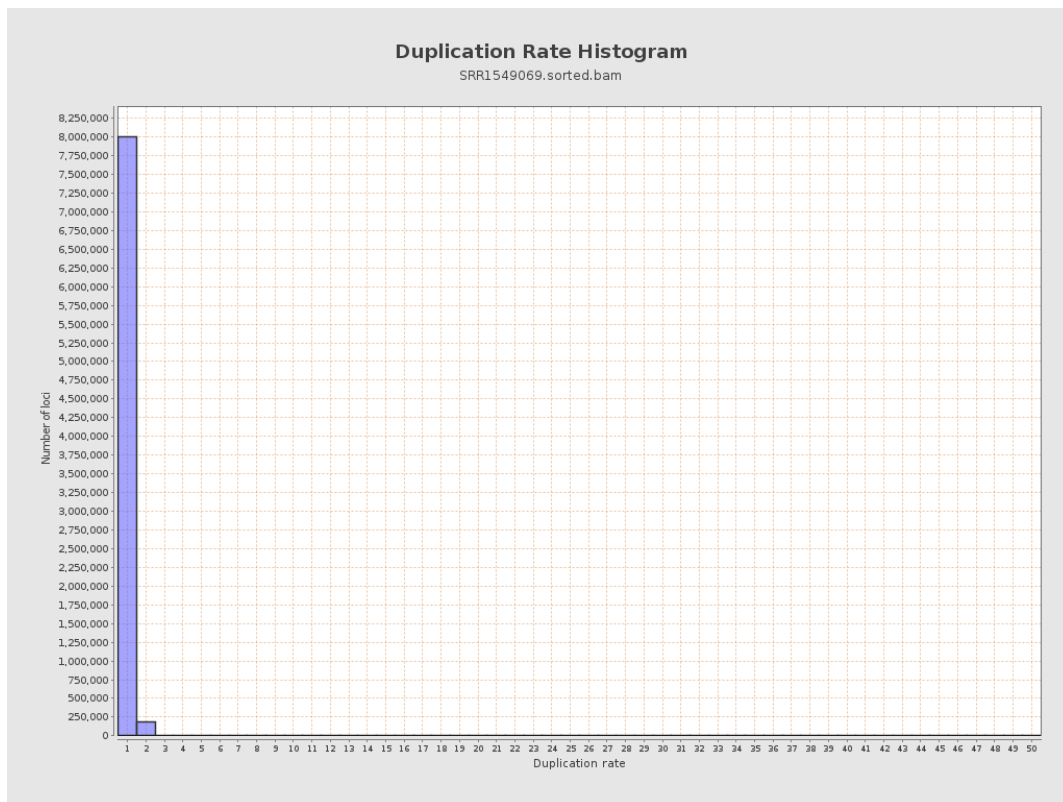
5. Results : Coverage Histogram (0-50X)



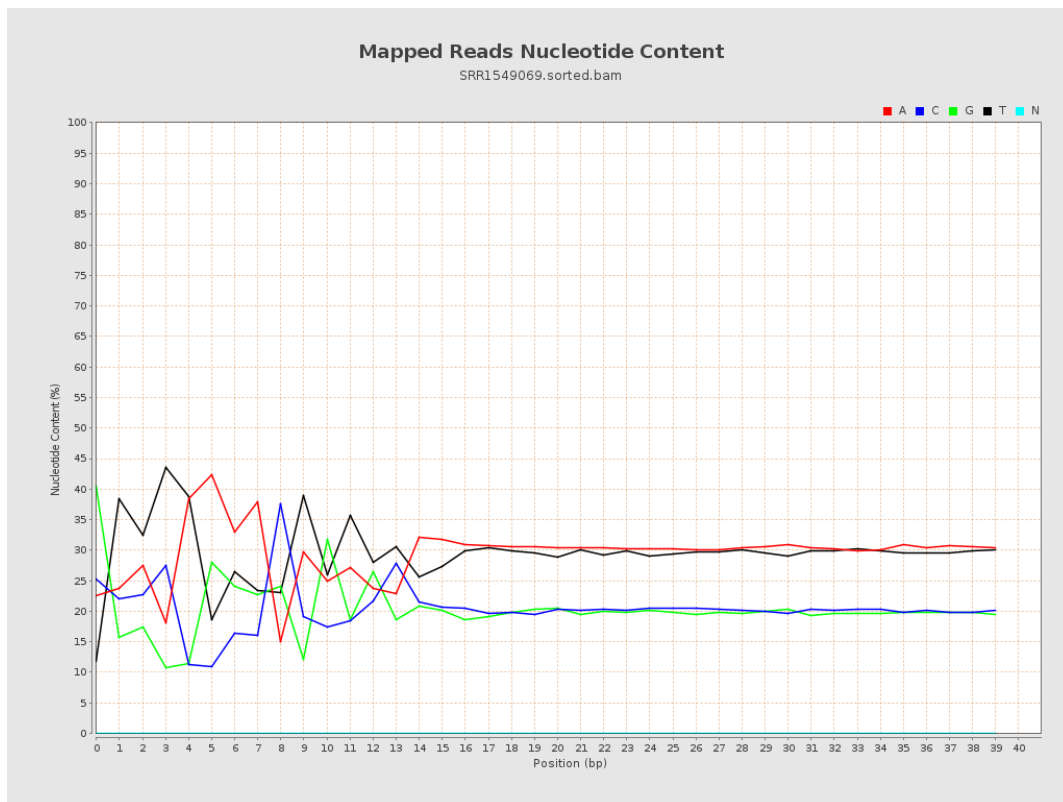
6. Results : Genome Fraction Coverage



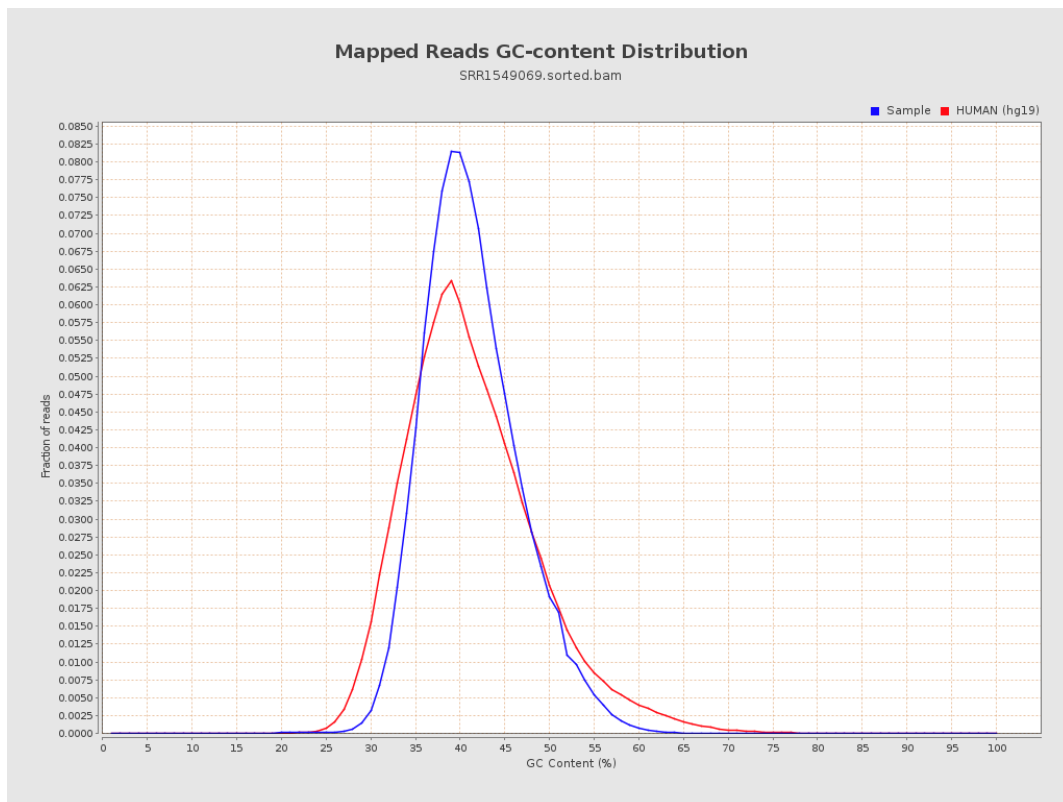
7. Results : Duplication Rate Histogram



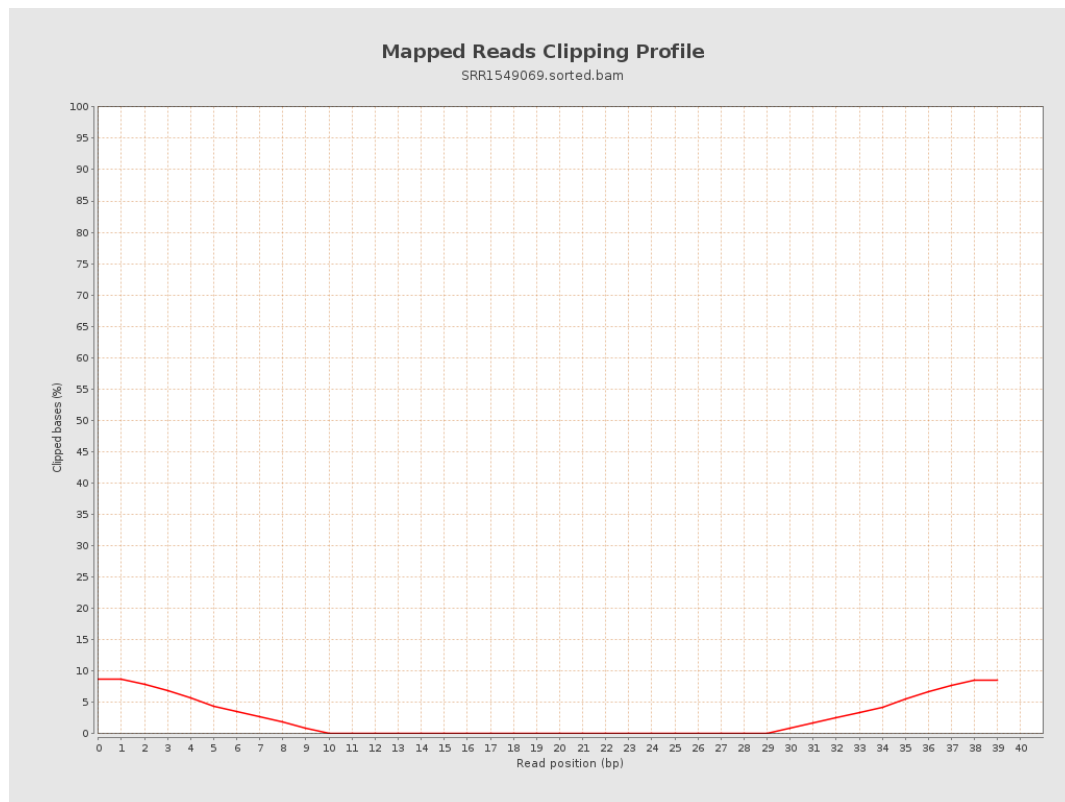
8. Results : Mapped Reads Nucleotide Content



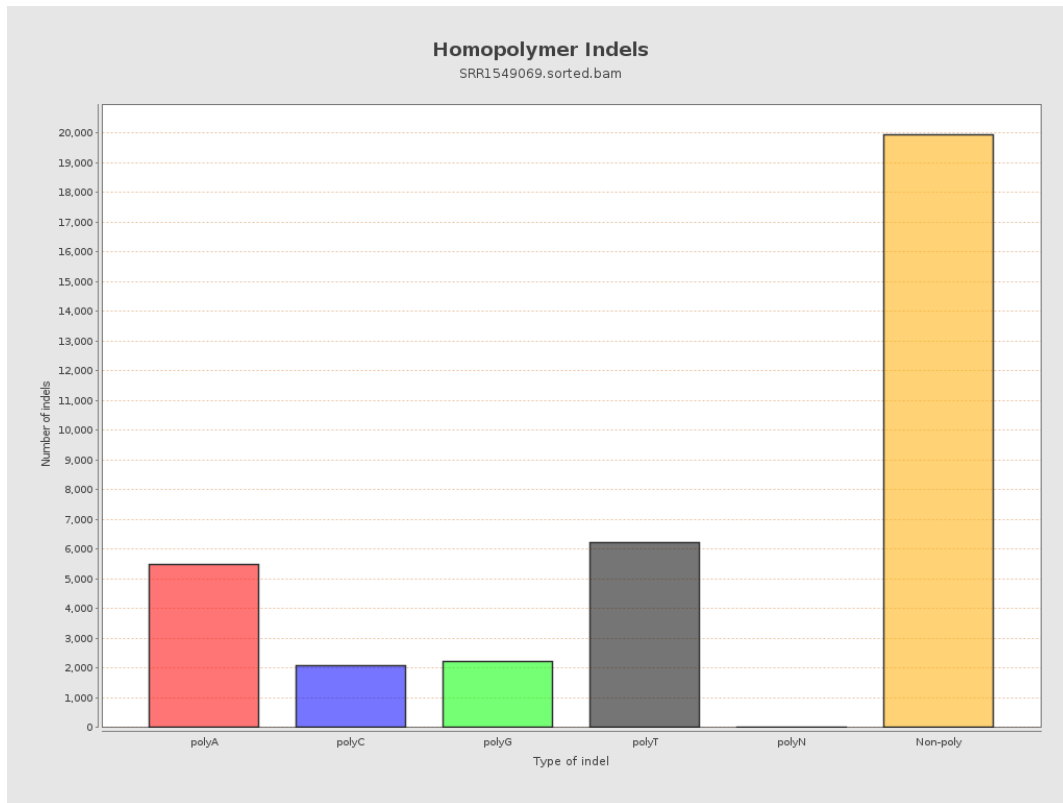
9. Results : Mapped Reads GC-content Distribution



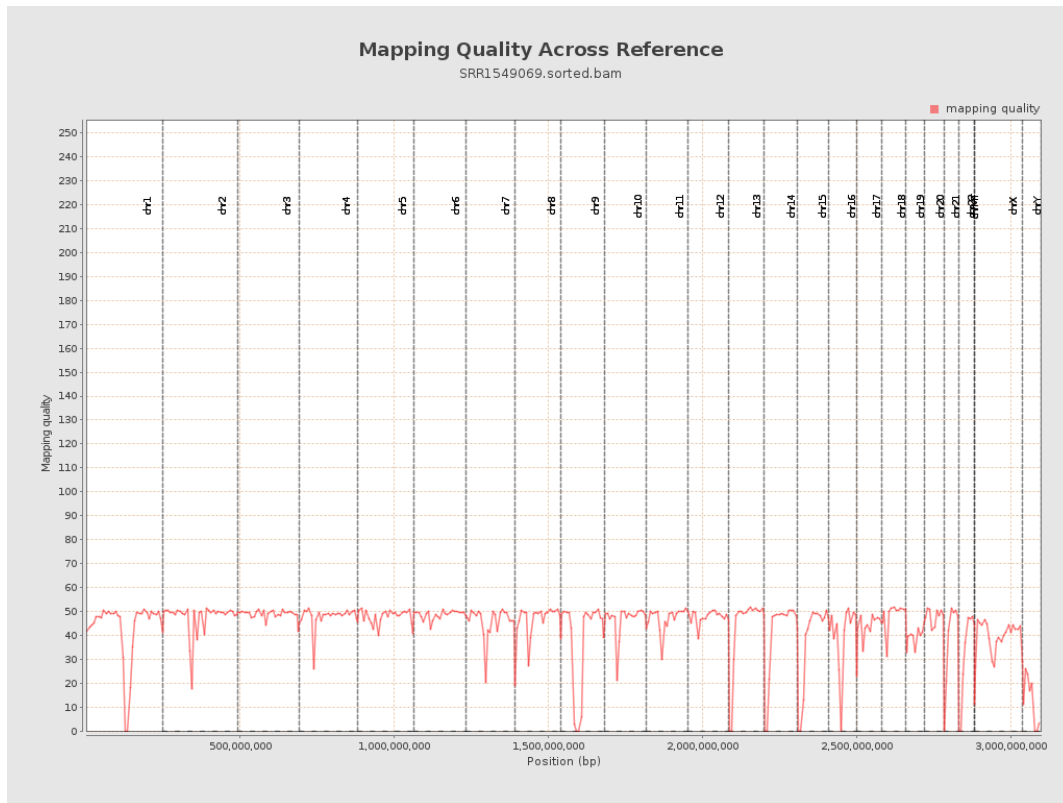
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

