

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 20:51:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013309.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_SRR6013309 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013309.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 20:51:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013309.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,242,803
Mapped reads	2,779,537 / 85.71%
Unmapped reads	463,266 / 14.29%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,399 / 0.6%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	109,401 / 3.37%
Duplication rate	2.83%
Clipped reads	1,417,046 / 43.7%

2.2. ACGT Content

Number/percentage of A's	49,806,901 / 27.49%
Number/percentage of C's	34,314,151 / 18.94%
Number/percentage of T's	55,868,883 / 30.84%
Number/percentage of G's	41,122,702 / 22.7%
Number/percentage of N's	40,998 / 0.02%
GC Percentage	41.64%

2.3. Coverage

Mean	0.0586

Standard Deviation	0.4976
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2.4. Mapping Quality

Mean Mapping Quality	44.75
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2.5. Mismatches and indels

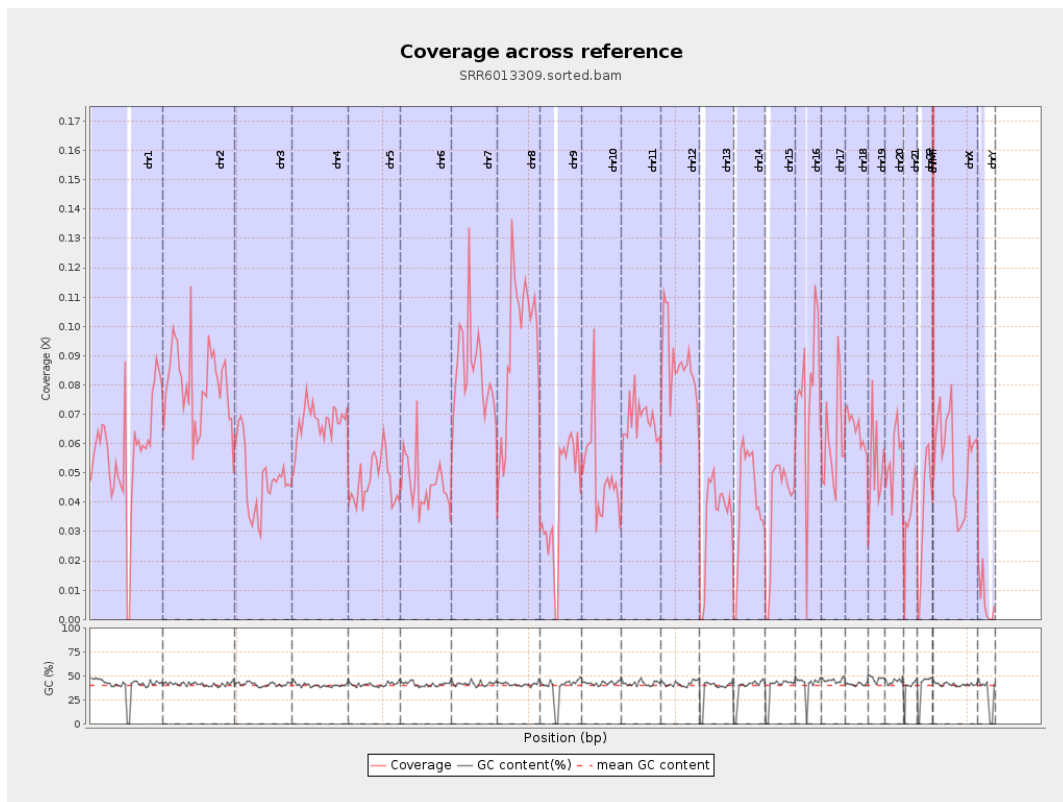
General error rate	0.88%
Mismatches	1,563,095
Insertions	12,700
Mapped reads with at least one insertion	0.45%
Deletions	60,808
Mapped reads with at least one deletion	2.16%
Homopolymer indels	43.19%

2.6. Chromosome stats

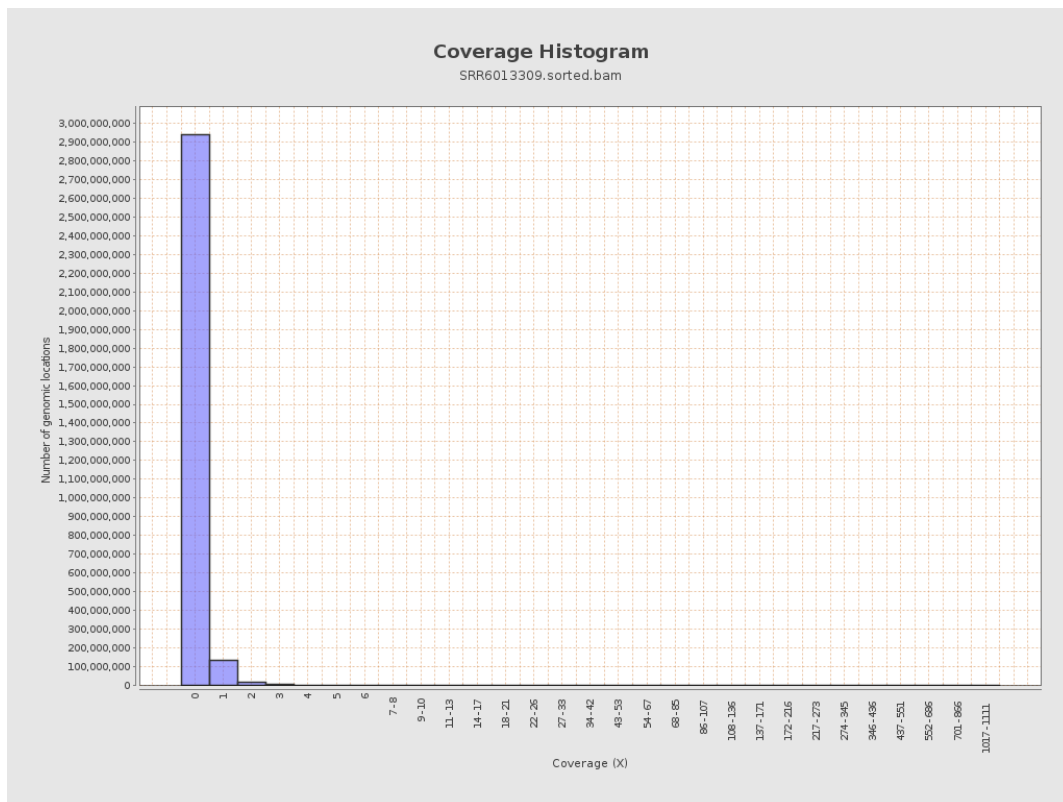
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	14272477	0.0573	0.8956
chr2	243199373	19414701	0.0798	0.6033
chr3	198022430	9440485	0.0477	0.247
chr4	191154276	12877364	0.0674	0.3208
chr5	180915260	8556791	0.0473	0.2475
chr6	171115067	7970324	0.0466	0.3736
chr7	159138663	13377080	0.0841	0.9021

chr8	146364022	13730457	0.0938	0.5409
chr9	141213431	5848856	0.0414	0.3902
chr10	135534747	6626289	0.0489	0.5531
chr11	135006516	9102227	0.0674	0.3932
chr12	133851895	11747597	0.0878	0.3403
chr13	115169878	3939058	0.0342	0.2132
chr14	107349540	4408482	0.0411	0.2614
chr15	102531392	3973795	0.0388	0.2215
chr16	90354753	6801280	0.0753	0.3555
chr17	81195210	4906551	0.0604	0.3507
chr18	78077248	5078726	0.065	0.6586
chr19	59128983	3128587	0.0529	0.78
chr20	63025520	3422959	0.0543	0.2713
chr21	48129895	1737832	0.0361	0.2482
chr22	51304566	1877181	0.0366	0.2143
chrMT	16571	143508	8.6602	5.5102
chrX	155270560	8490593	0.0547	0.3211
chrY	59373566	386850	0.0065	0.1809

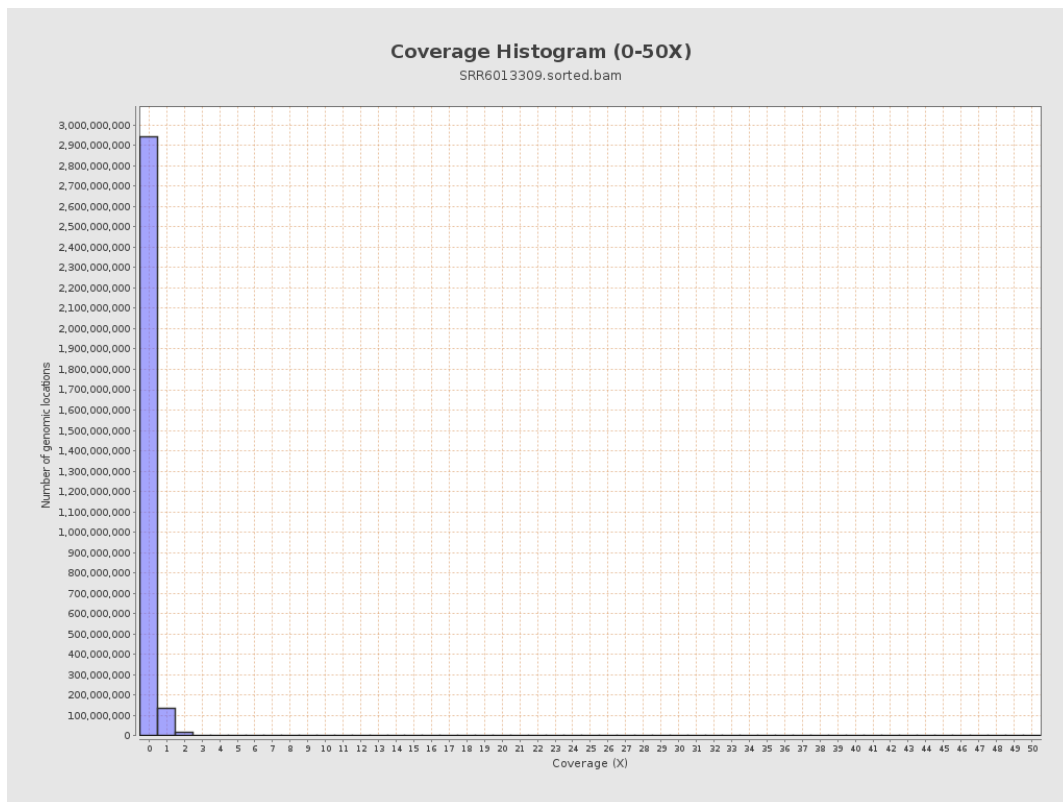
3. Results : Coverage across reference



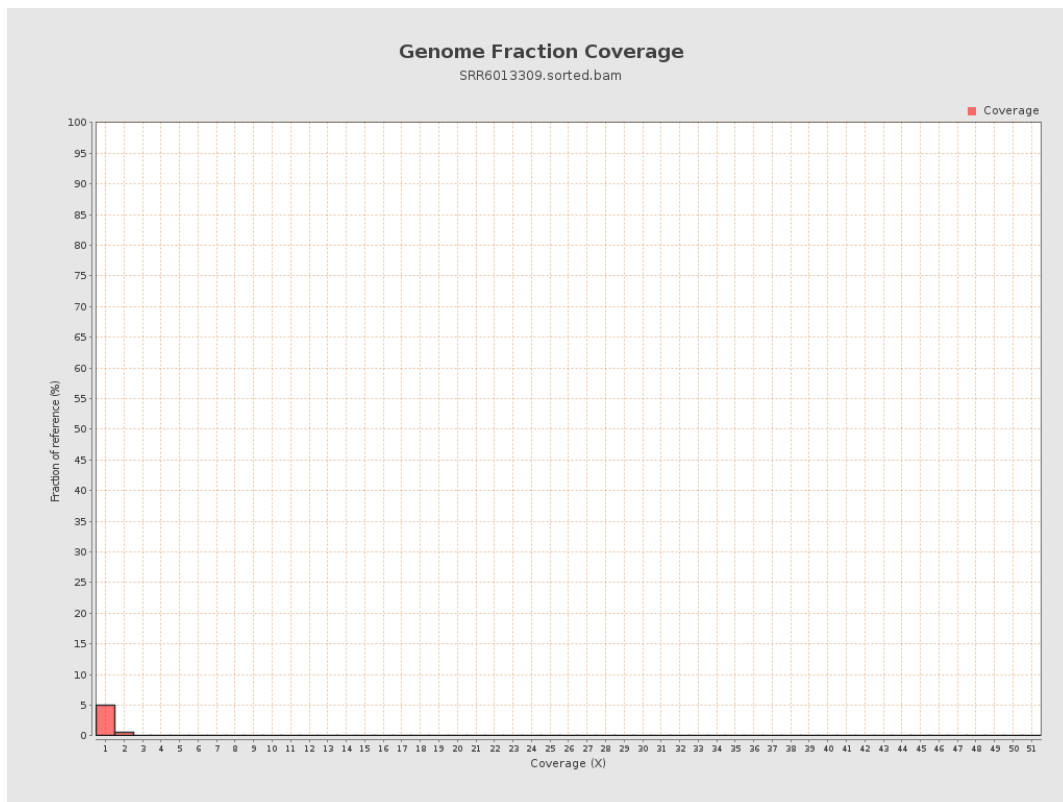
4. Results : Coverage Histogram



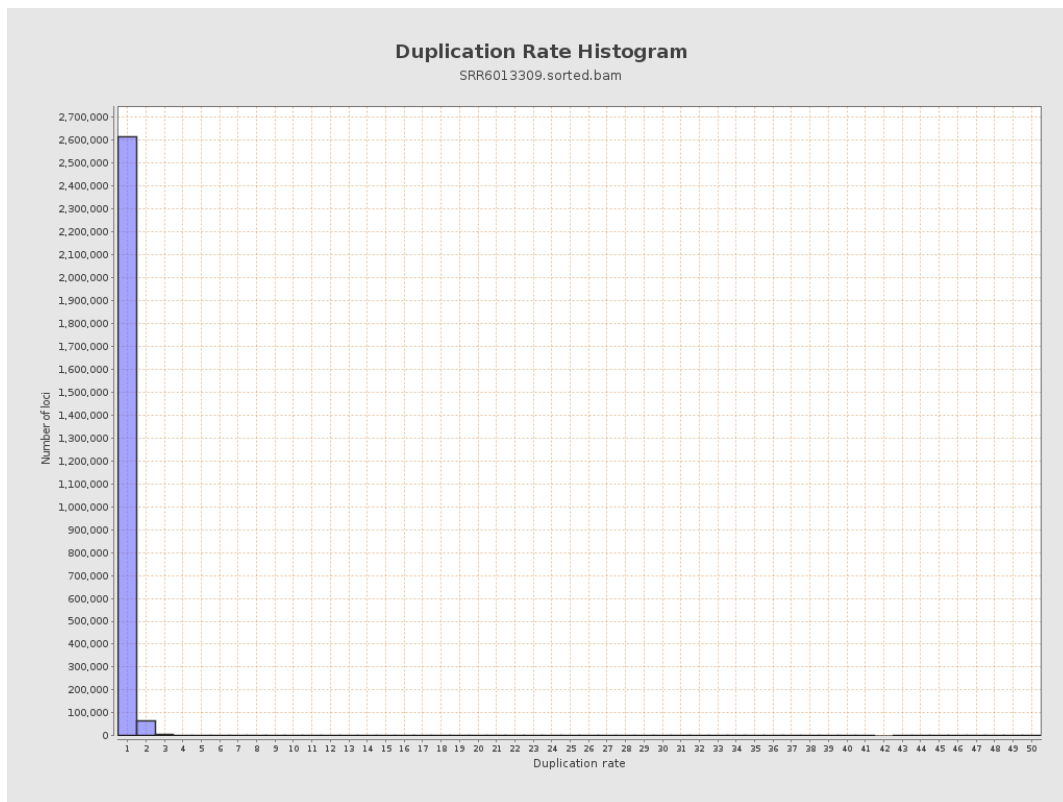
5. Results : Coverage Histogram (0-50X)



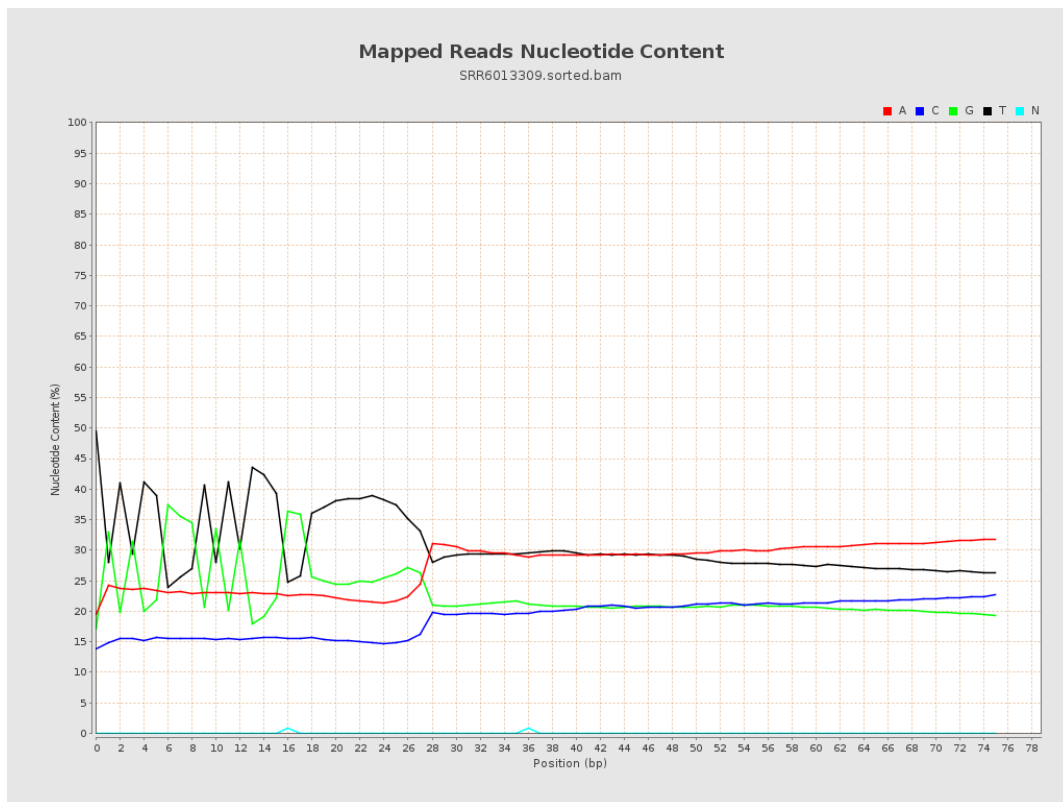
6. Results : Genome Fraction Coverage



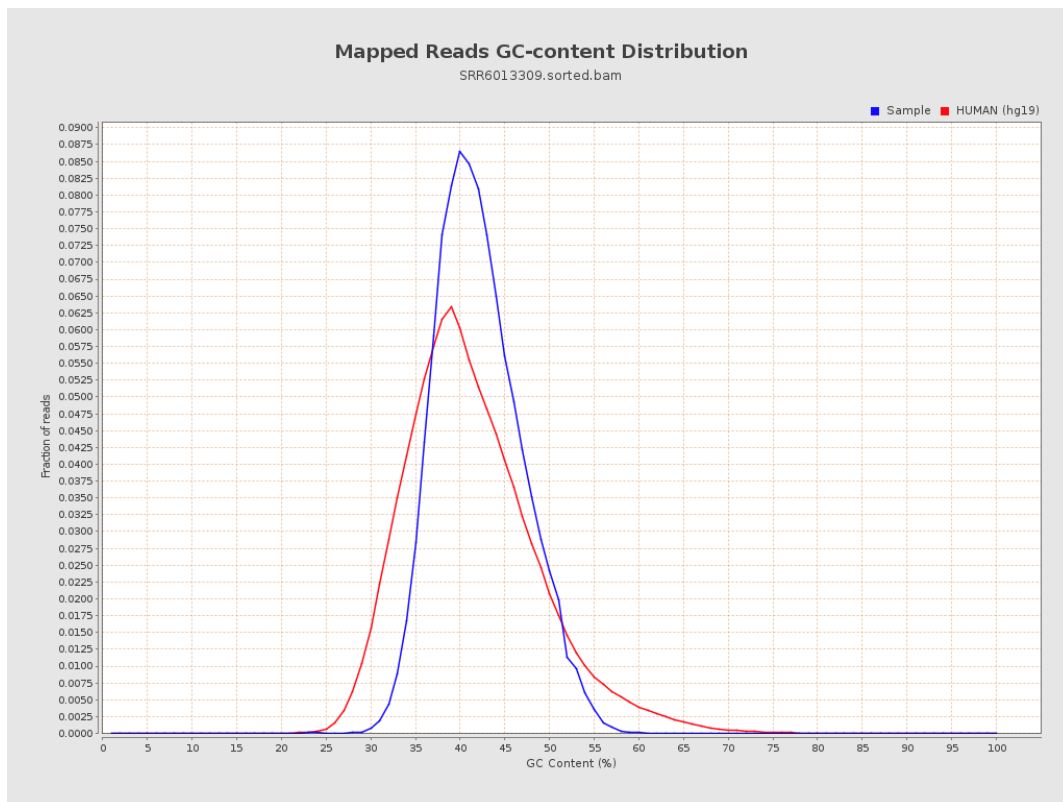
7. Results : Duplication Rate Histogram



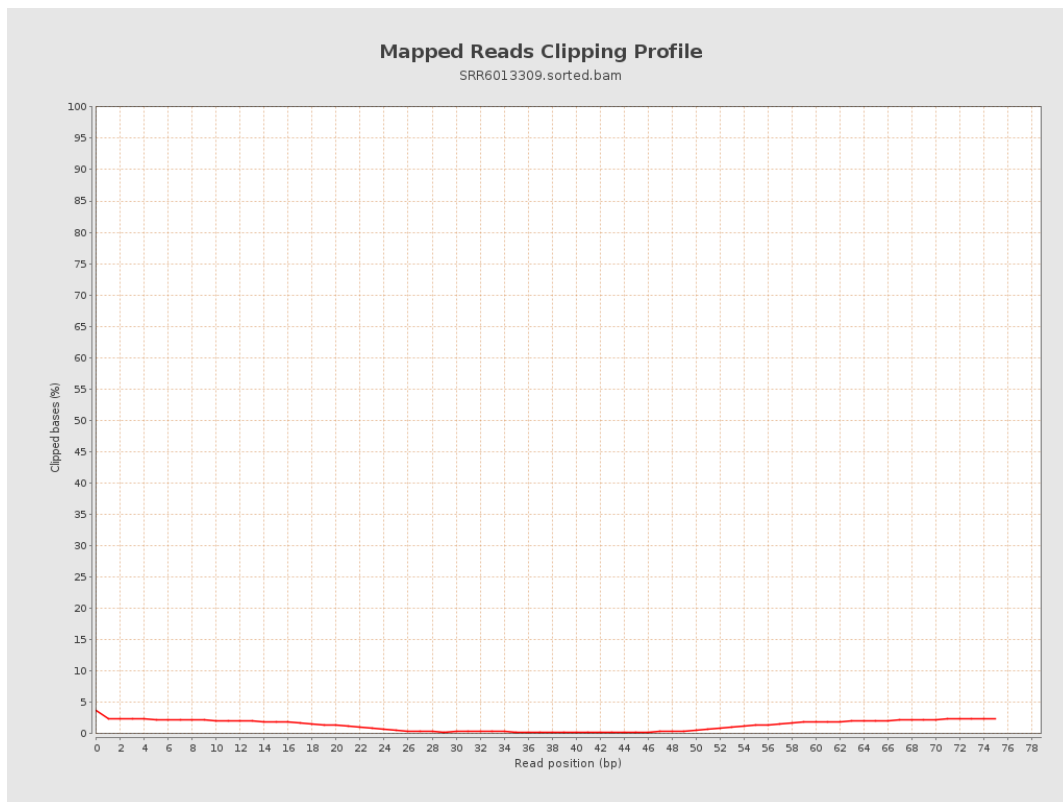
8. Results : Mapped Reads Nucleotide Content



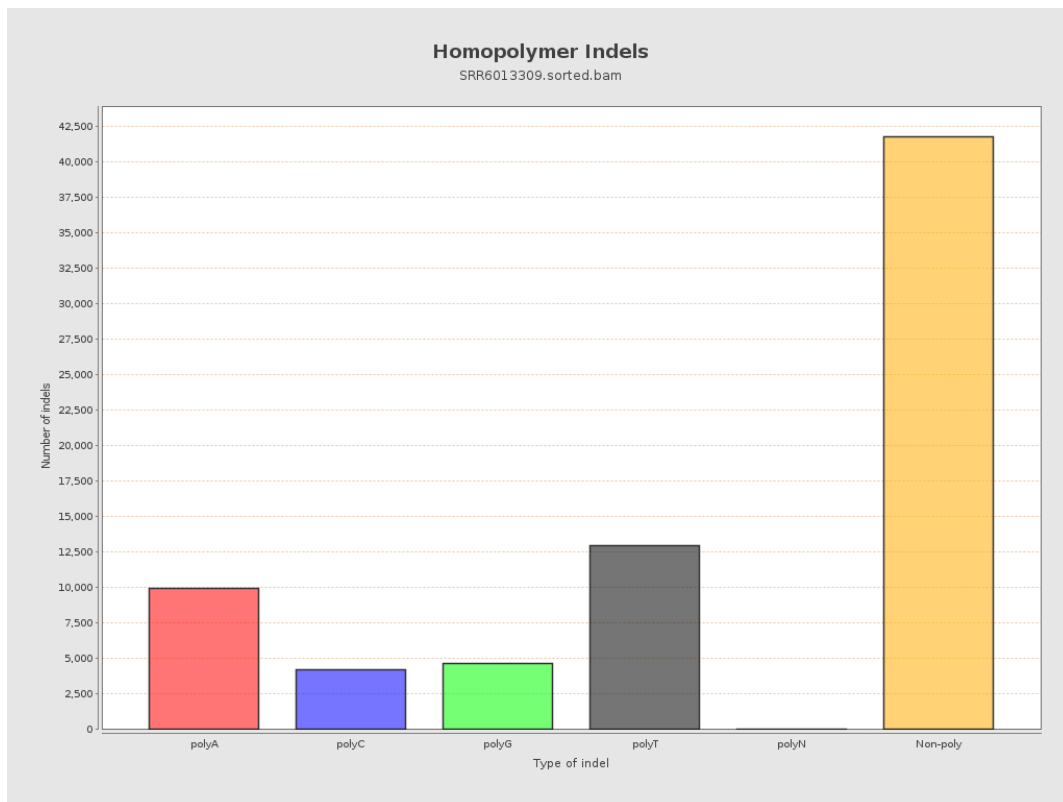
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

