

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 17:55:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230334.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_SRR6230334 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230334.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 17:55:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230334.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,026,904
Mapped reads	2,641,160 / 87.26%
Unmapped reads	385,744 / 12.74%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	33,158 / 1.1%
Read min/max/mean length	30 / 76 / 76.38
Duplicated reads (estimated)	414,975 / 13.71%
Duplication rate	10.88%
Clipped reads	1,233,222 / 40.74%

2.2. ACGT Content

Number/percentage of A's	49,280,417 / 28.06%
Number/percentage of C's	32,464,219 / 18.49%
Number/percentage of T's	55,655,542 / 31.7%
Number/percentage of G's	38,116,644 / 21.71%
Number/percentage of N's	77,184 / 0.04%
GC Percentage	40.2%

2.3. Coverage

Mean	0.0567

Standard Deviation	0.5957
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2.4. Mapping Quality

Mean Mapping Quality	45.87
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2.5. Mismatches and indels

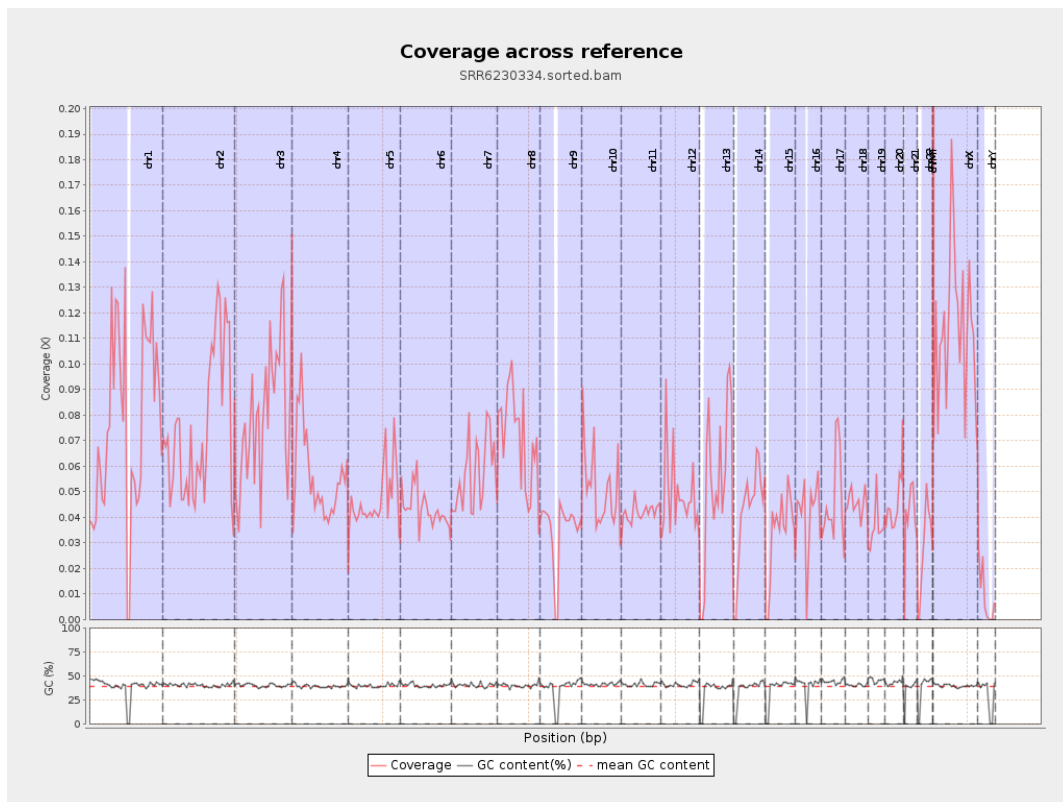
General error rate	0.86%
Mismatches	1,489,769
Insertions	14,346
Mapped reads with at least one insertion	0.54%
Deletions	47,524
Mapped reads with at least one deletion	1.78%
Homopolymer indels	46.61%

2.6. Chromosome stats

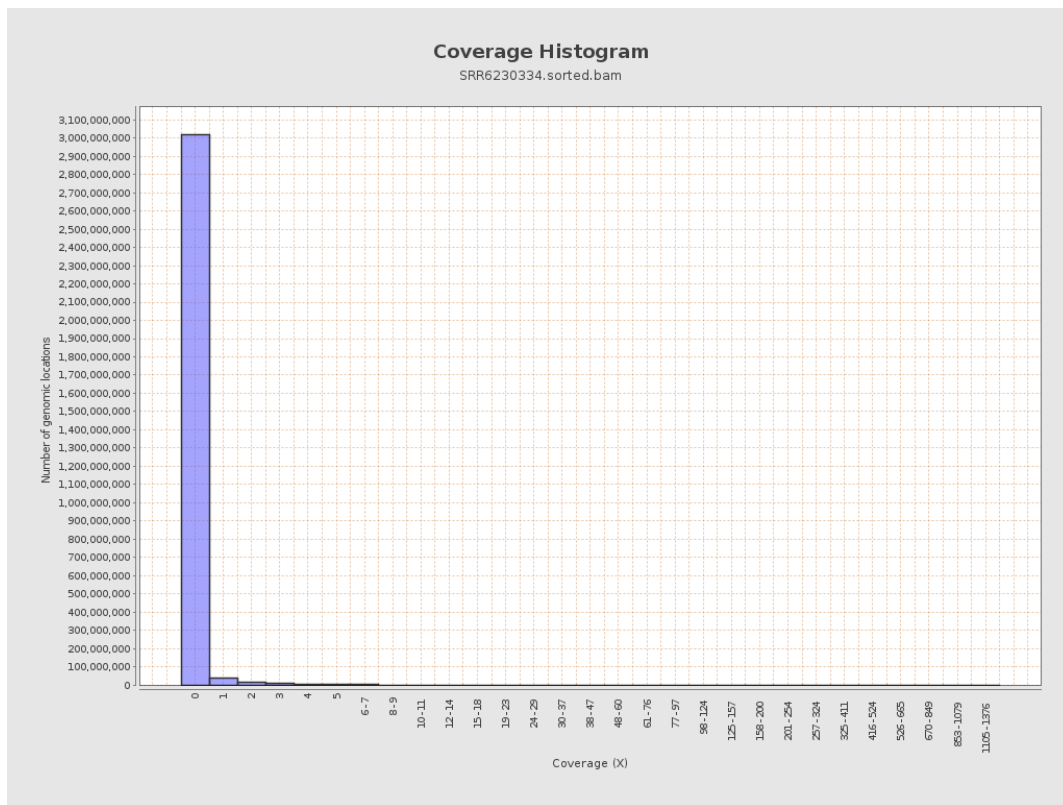
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	19017374	0.0763	1.0189
chr2	243199373	18378136	0.0756	0.6366
chr3	198022430	15929804	0.0804	0.545
chr4	191154276	10658328	0.0558	0.4603
chr5	180915260	8366813	0.0462	0.4055
chr6	171115067	7466006	0.0436	0.4437
chr7	159138663	9062815	0.0569	0.6098

chr8	146364022	10383288	0.0709	0.98
chr9	141213431	4974824	0.0352	0.4201
chr10	135534747	6914097	0.051	0.522
chr11	135006516	5645670	0.0418	0.4596
chr12	133851895	6487119	0.0485	0.4147
chr13	115169878	6305519	0.0547	0.452
chr14	107349540	4582114	0.0427	0.4022
chr15	102531392	3424321	0.0334	0.3378
chr16	90354753	3578815	0.0396	0.3792
chr17	81195210	3859365	0.0475	0.4244
chr18	78077248	3555216	0.0455	0.7334
chr19	59128983	2152088	0.0364	0.618
chr20	63025520	2877311	0.0457	0.4098
chr21	48129895	1899371	0.0395	0.3846
chr22	51304566	1482946	0.0289	0.3079
chrMT	16571	431509	26.04	23.0644
chrX	155270560	17713919	0.1141	0.6938
chrY	59373566	525129	0.0088	0.1831

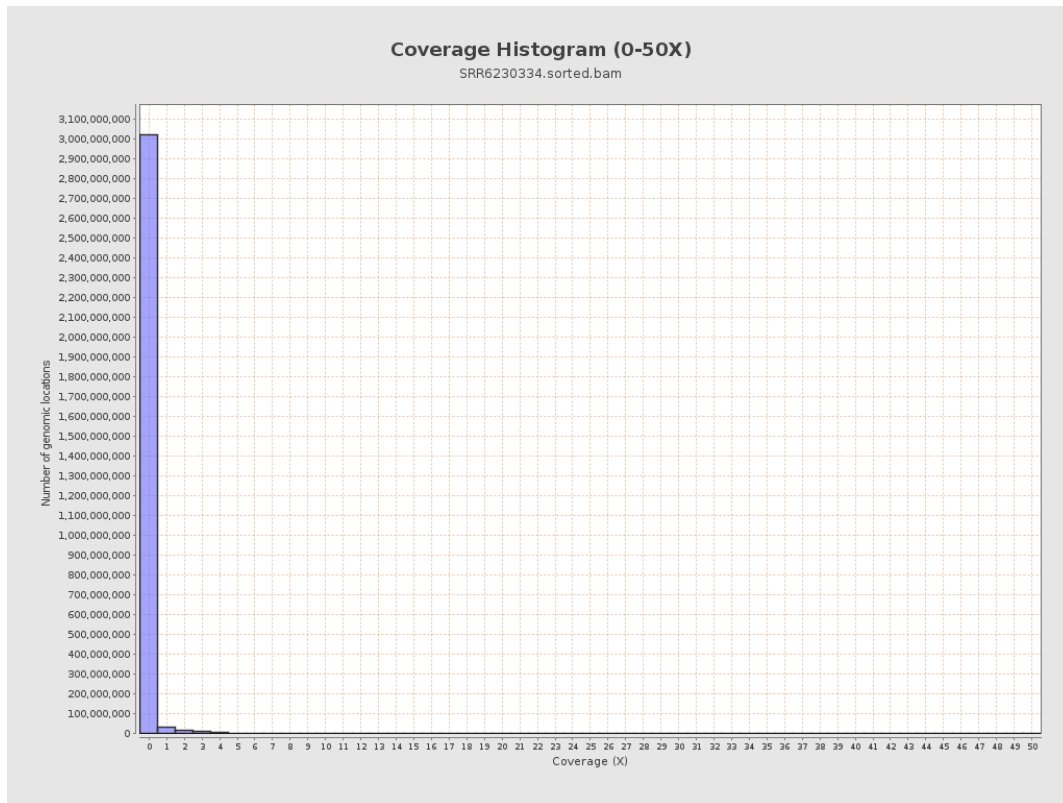
3. Results : Coverage across reference



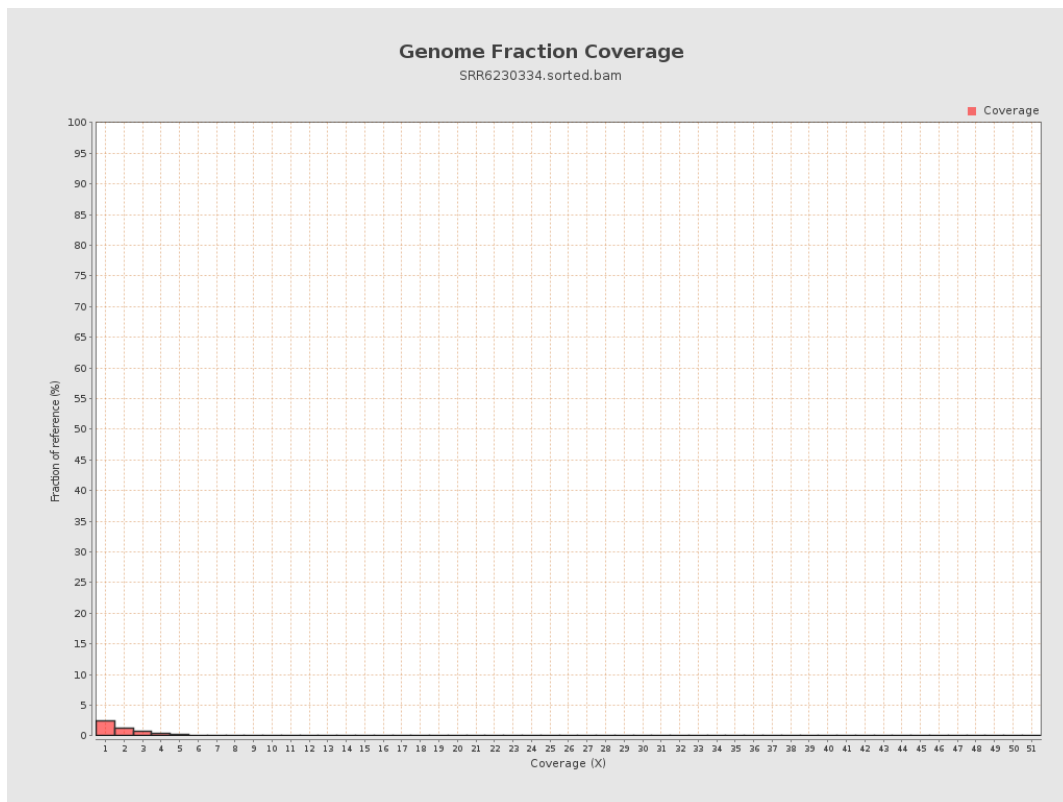
4. Results : Coverage Histogram



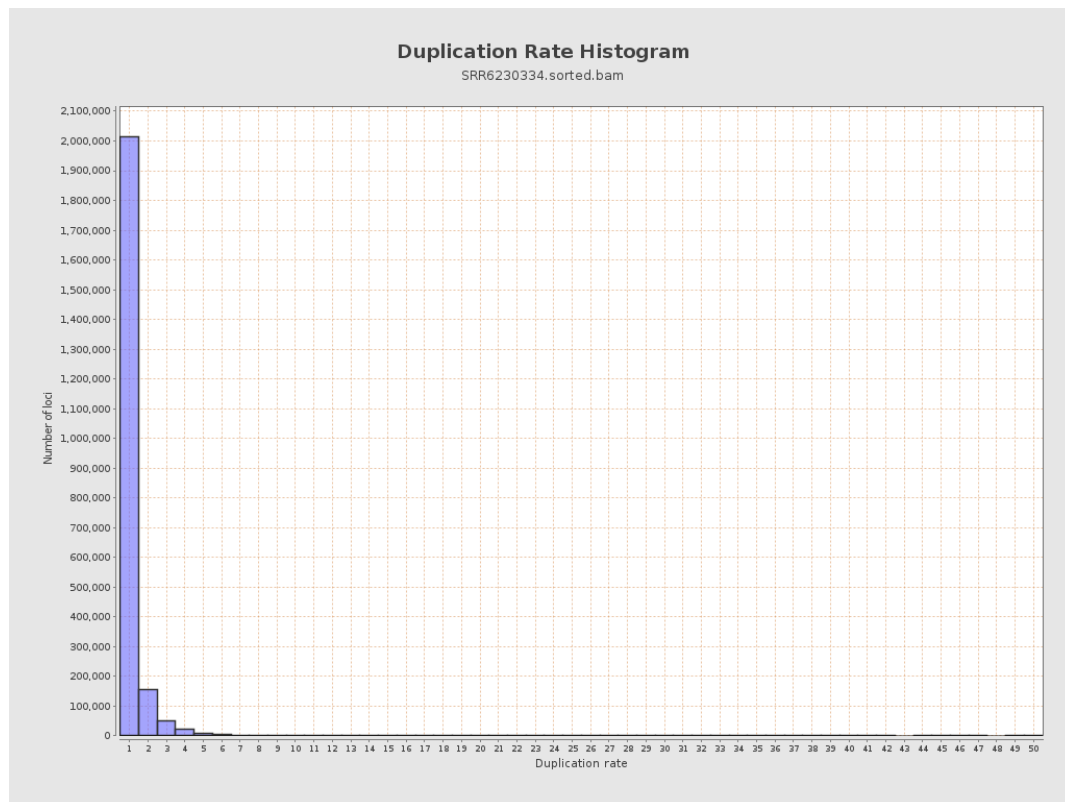
5. Results : Coverage Histogram (0-50X)



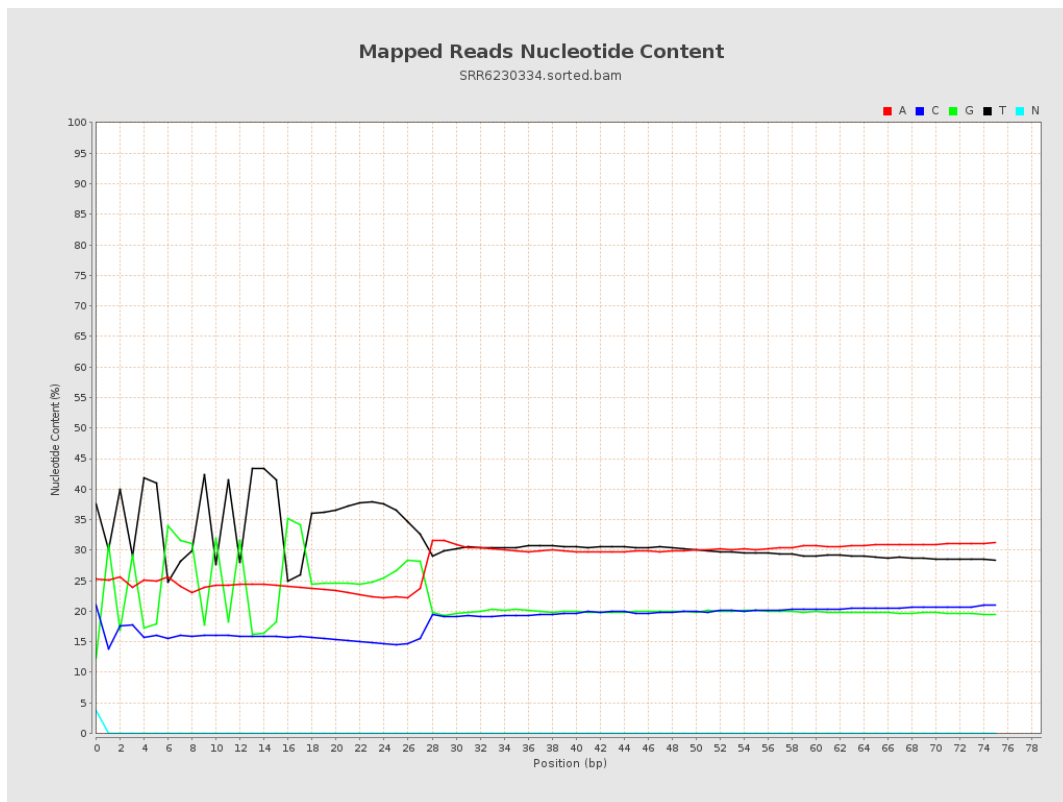
6. Results : Genome Fraction Coverage



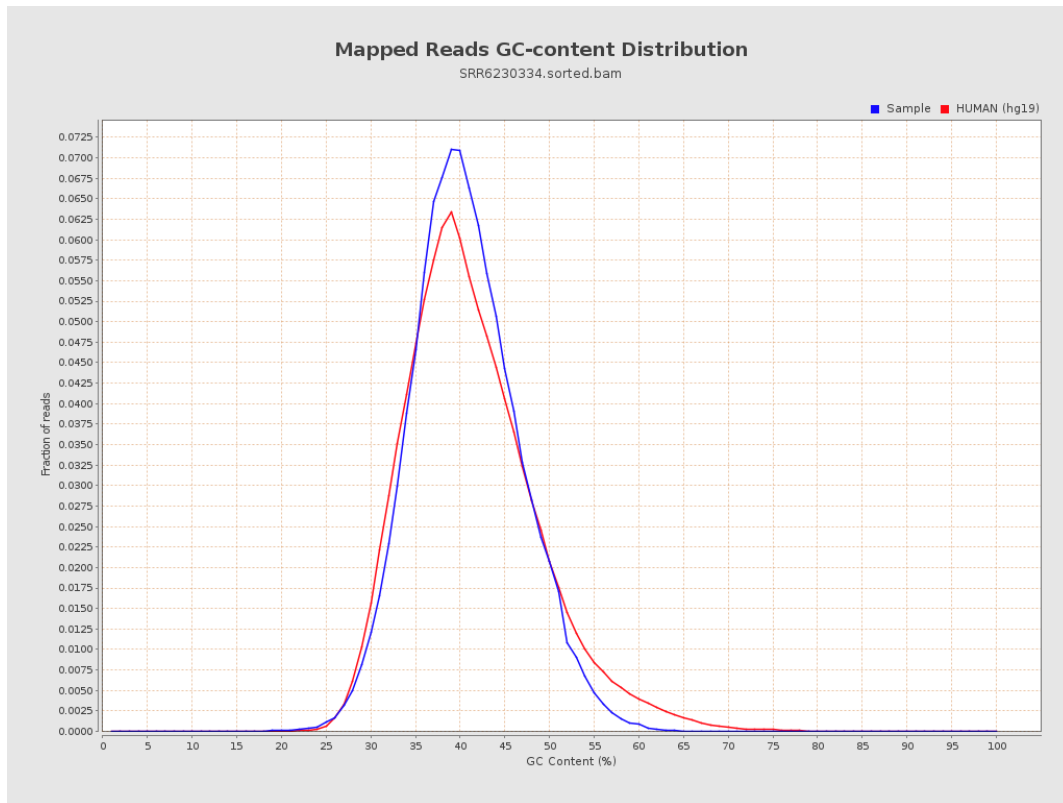
7. Results : Duplication Rate Histogram



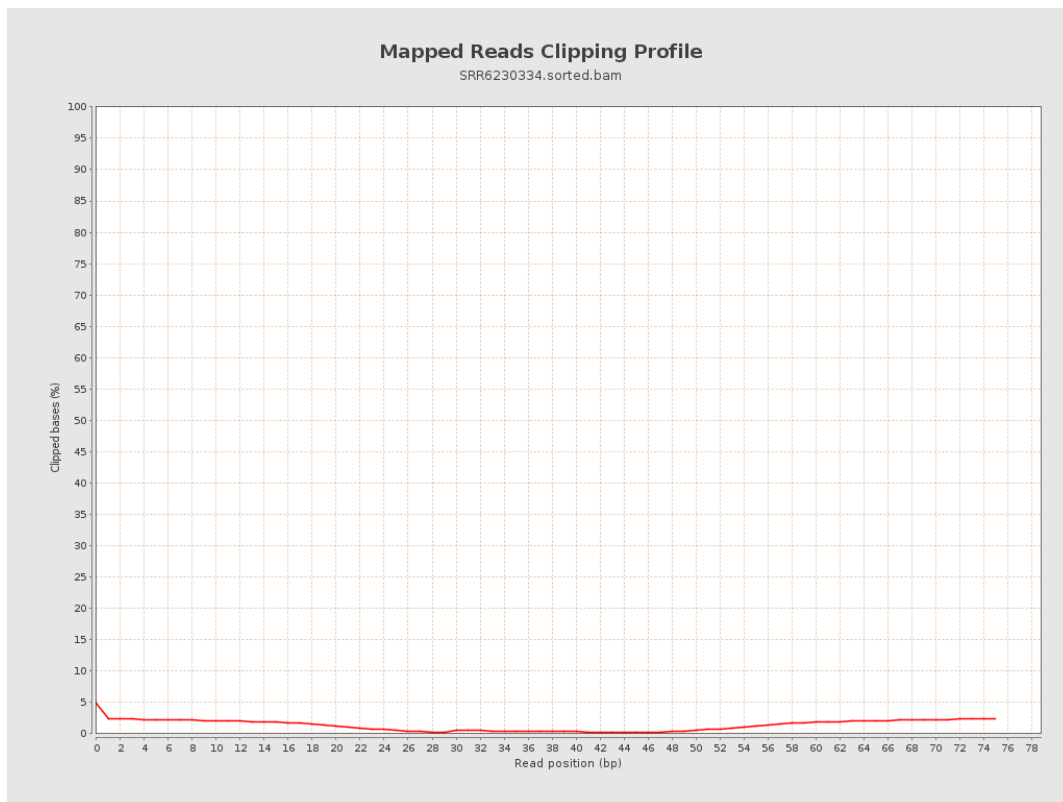
8. Results : Mapped Reads Nucleotide Content



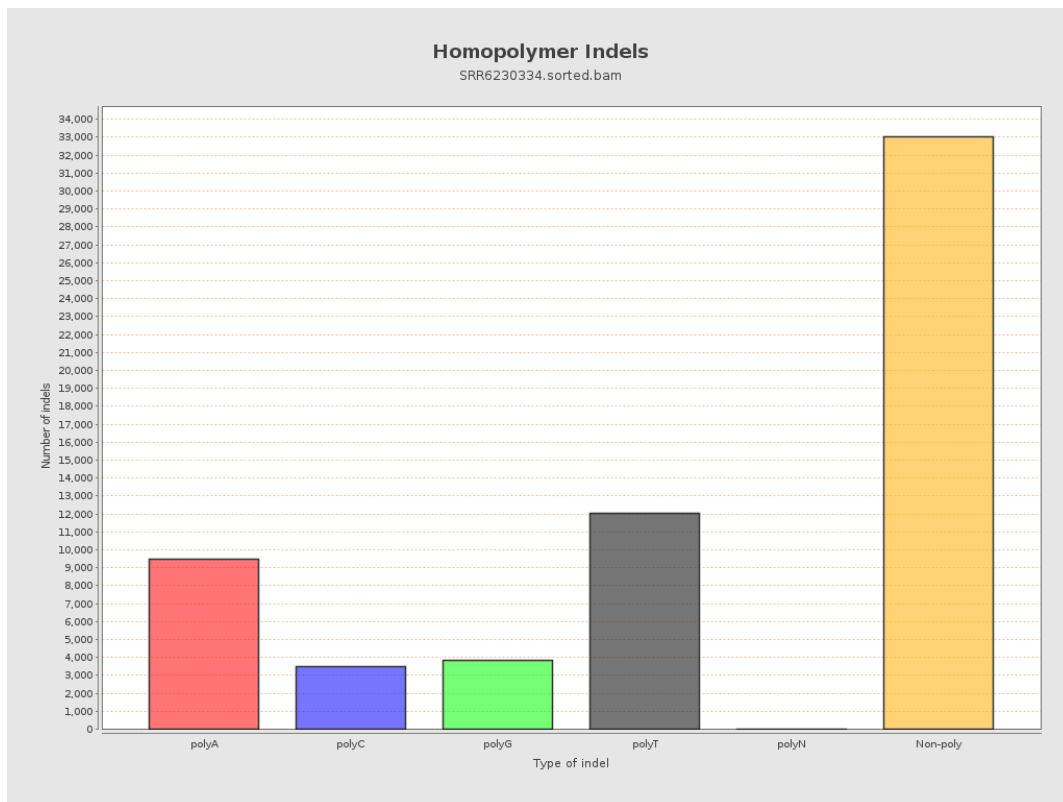
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

