

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 07:03:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240219.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_SRR6240219 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240219.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 07:03:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240219.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,601,901
Mapped reads	1,991,207 / 76.53%
Unmapped reads	610,694 / 23.47%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,714 / 0.8%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	229,833 / 8.83%
Duplication rate	8.89%
Clipped reads	965,197 / 37.1%

2.2. ACGT Content

Number/percentage of A's	37,484,279 / 28.45%
Number/percentage of C's	24,343,570 / 18.48%
Number/percentage of T's	41,859,424 / 31.77%
Number/percentage of G's	28,042,128 / 21.29%
Number/percentage of N's	12,414 / 0.01%
GC Percentage	39.76%

2.3. Coverage

Mean	0.0426

Standard Deviation	0.4552
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2.4. Mapping Quality

Mean Mapping Quality	46.64
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2.5. Mismatches and indels

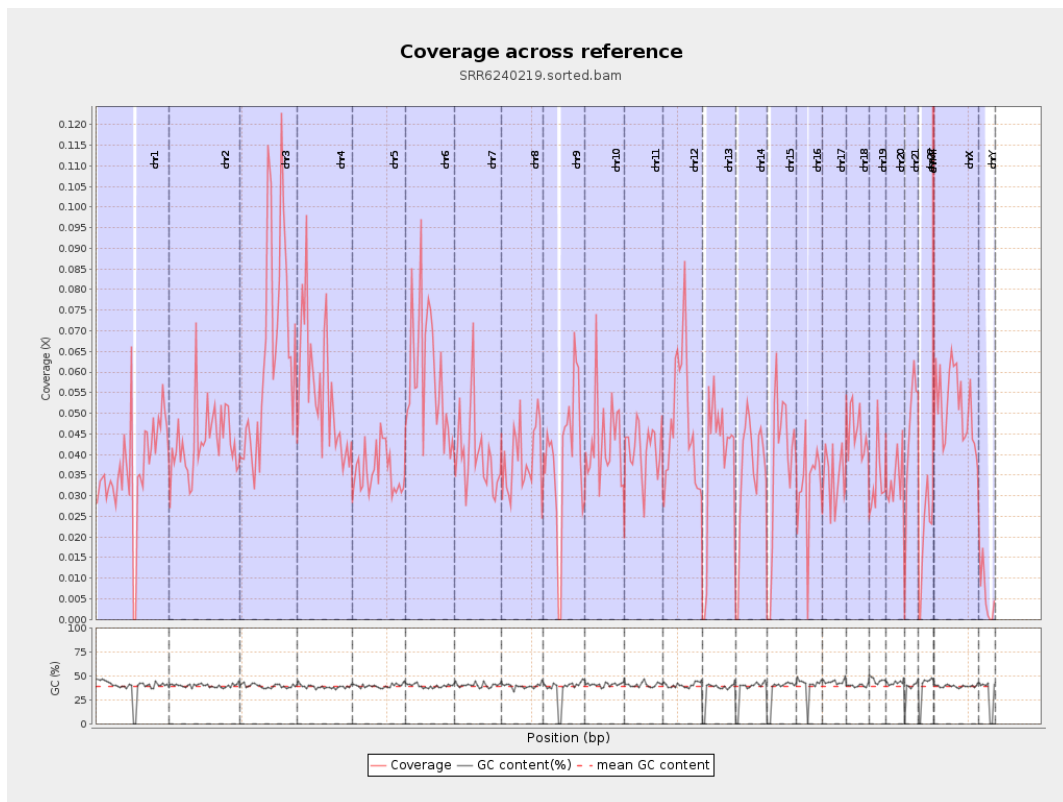
General error rate	0.8%
Mismatches	1,029,986
Insertions	9,707
Mapped reads with at least one insertion	0.48%
Deletions	29,732
Mapped reads with at least one deletion	1.48%
Homopolymer indels	47.34%

2.6. Chromosome stats

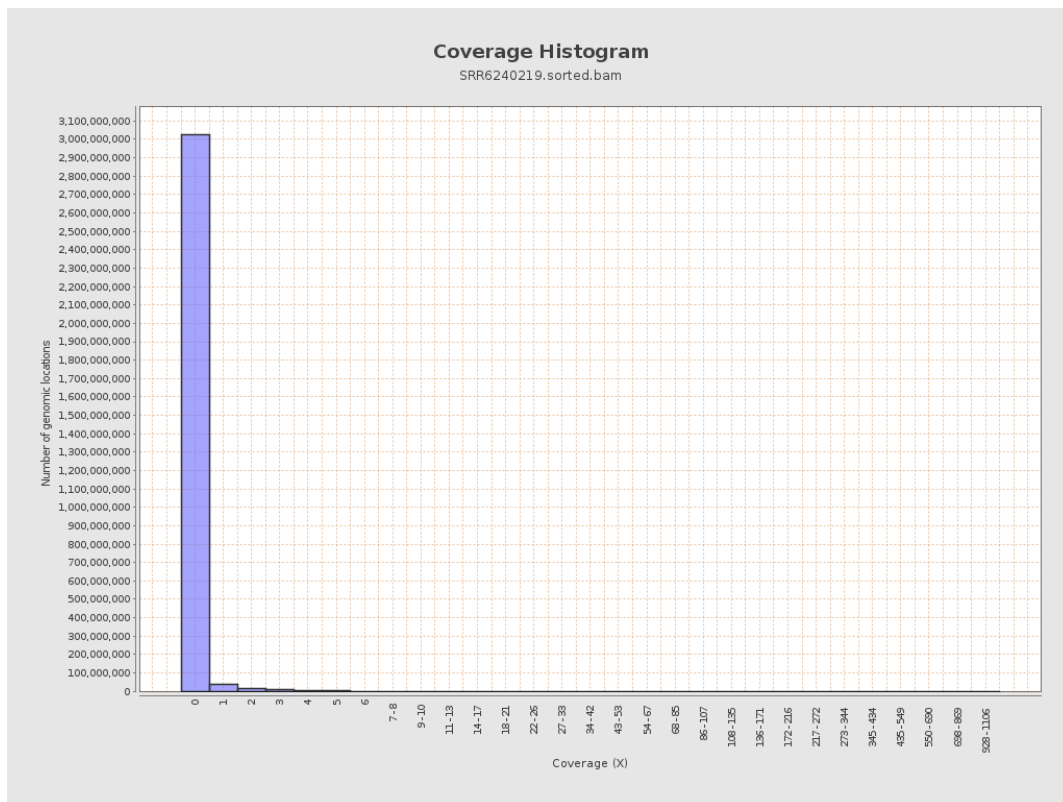
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	9186851	0.0369	0.6202
chr2	243199373	10479480	0.0431	0.469
chr3	198022430	12525181	0.0633	0.4268
chr4	191154276	10494308	0.0549	0.4055
chr5	180915260	6517865	0.036	0.3177
chr6	171115067	10014687	0.0585	0.4402
chr7	159138663	6394767	0.0402	0.4923

chr8	146364022	5670317	0.0387	0.7381
chr9	141213431	5629366	0.0399	0.4265
chr10	135534747	5824744	0.043	0.475
chr11	135006516	5531864	0.041	0.4865
chr12	133851895	6399506	0.0478	0.3676
chr13	115169878	4450293	0.0386	0.3298
chr14	107349540	3881850	0.0362	0.3329
chr15	102531392	3882149	0.0379	0.3251
chr16	90354753	2925587	0.0324	0.3172
chr17	81195210	2744694	0.0338	0.3327
chr18	78077248	3563984	0.0456	0.7258
chr19	59128983	2014303	0.0341	0.4519
chr20	63025520	2142610	0.034	0.3038
chr21	48129895	2176330	0.0452	0.3692
chr22	51304566	1004438	0.0196	0.2212
chrMT	16571	28841	1.7405	2.4871
chrX	155270560	7958342	0.0513	0.4053
chrY	59373566	351214	0.0059	0.1369

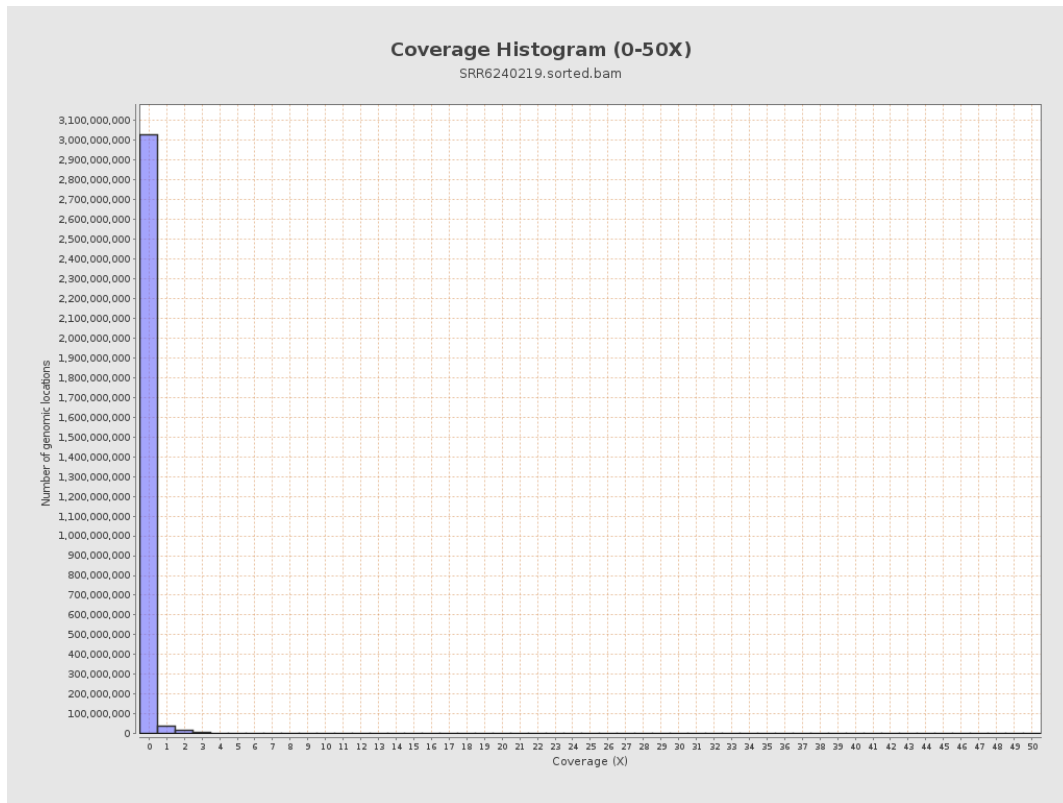
3. Results : Coverage across reference



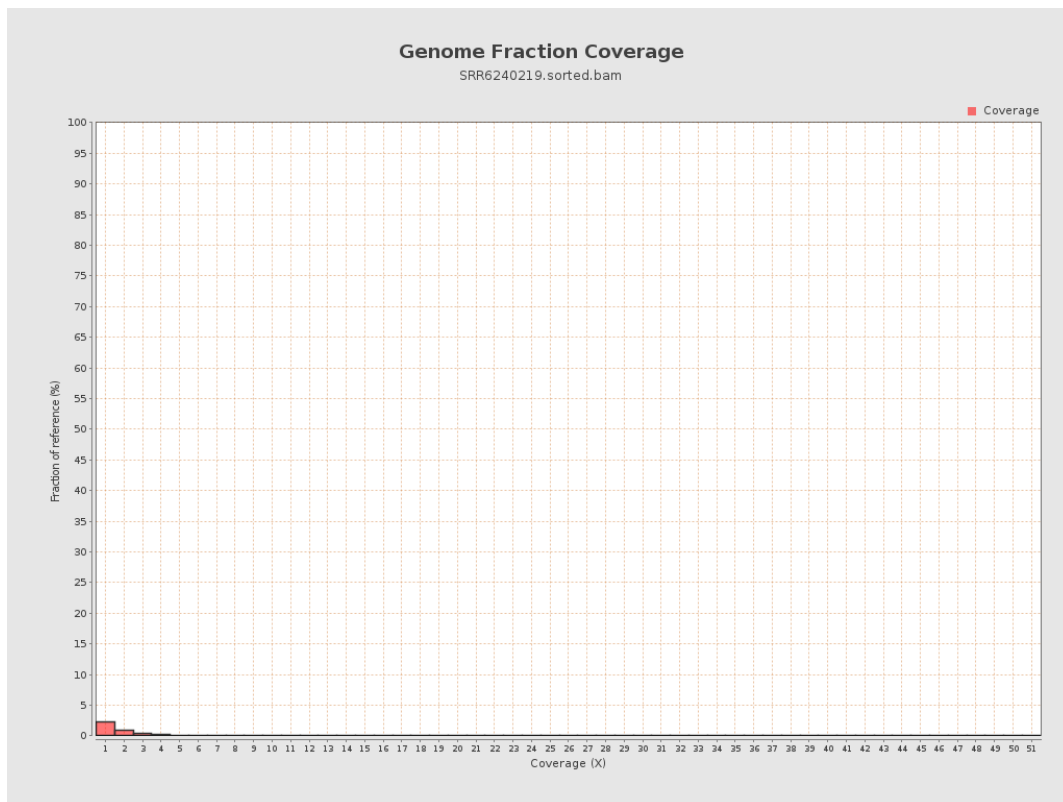
4. Results : Coverage Histogram



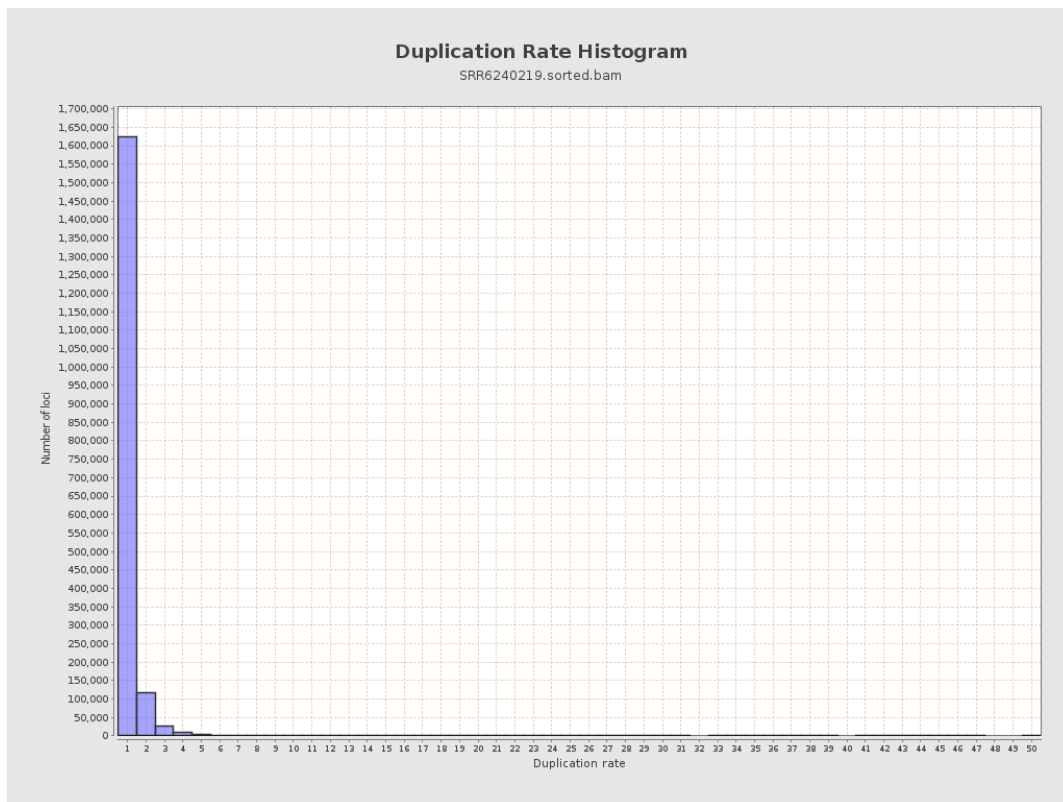
5. Results : Coverage Histogram (0-50X)



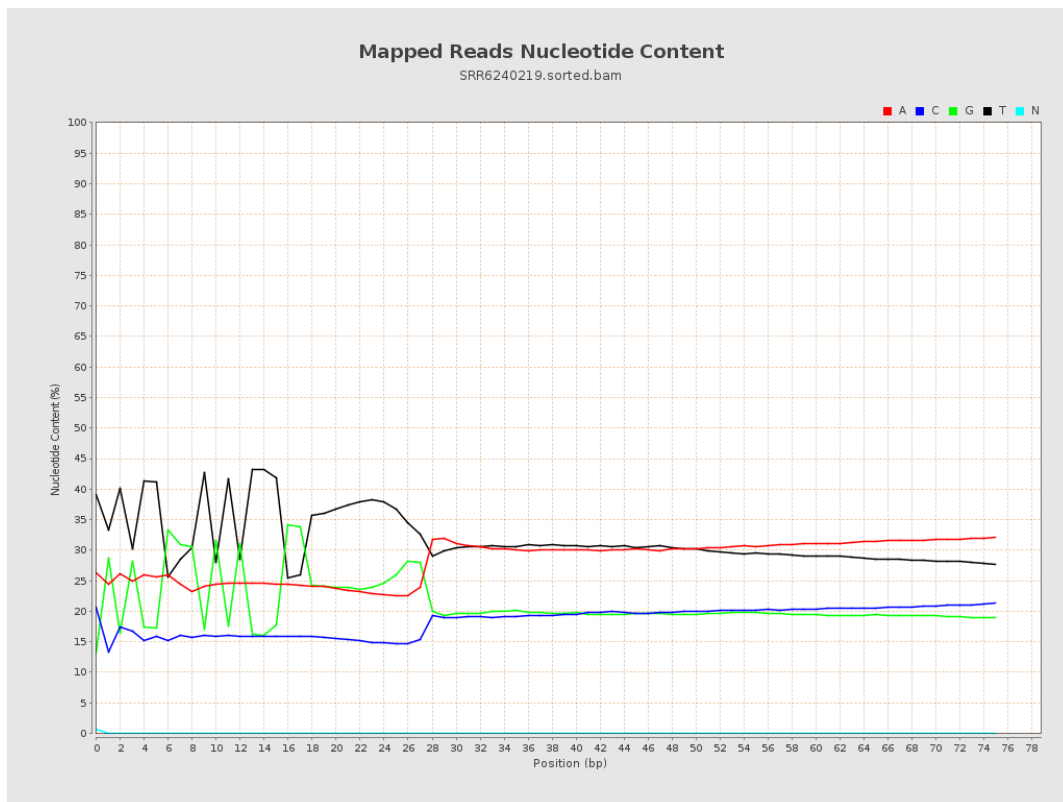
6. Results : Genome Fraction Coverage



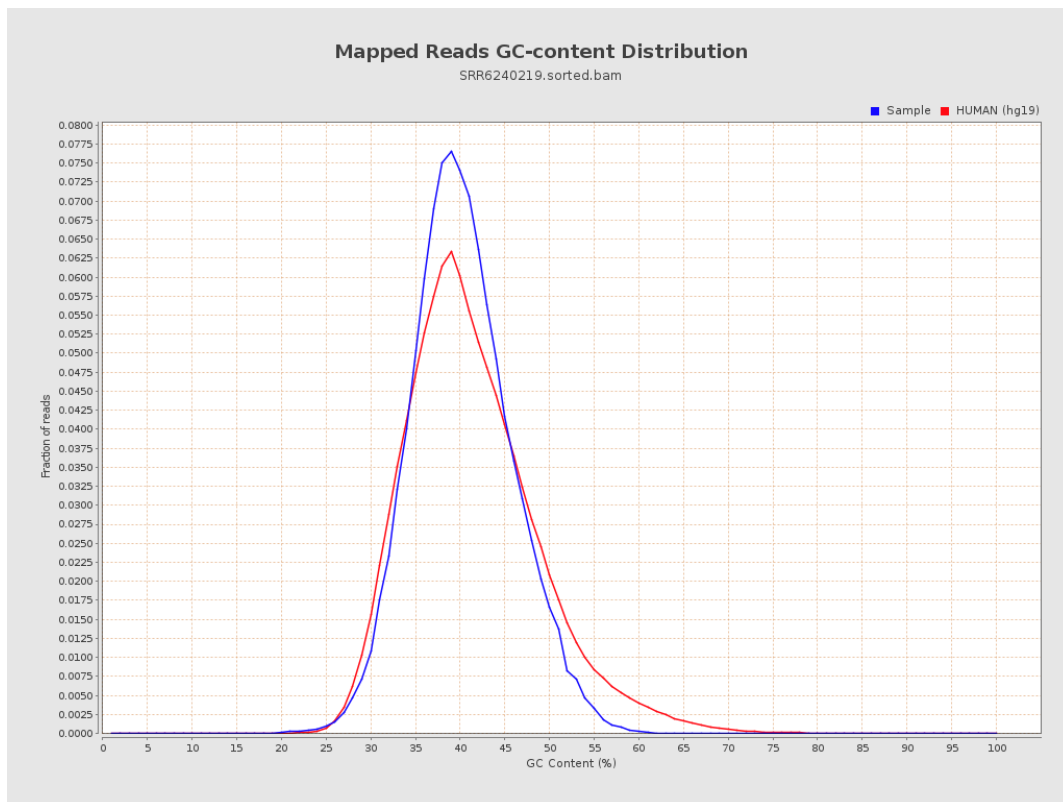
7. Results : Duplication Rate Histogram



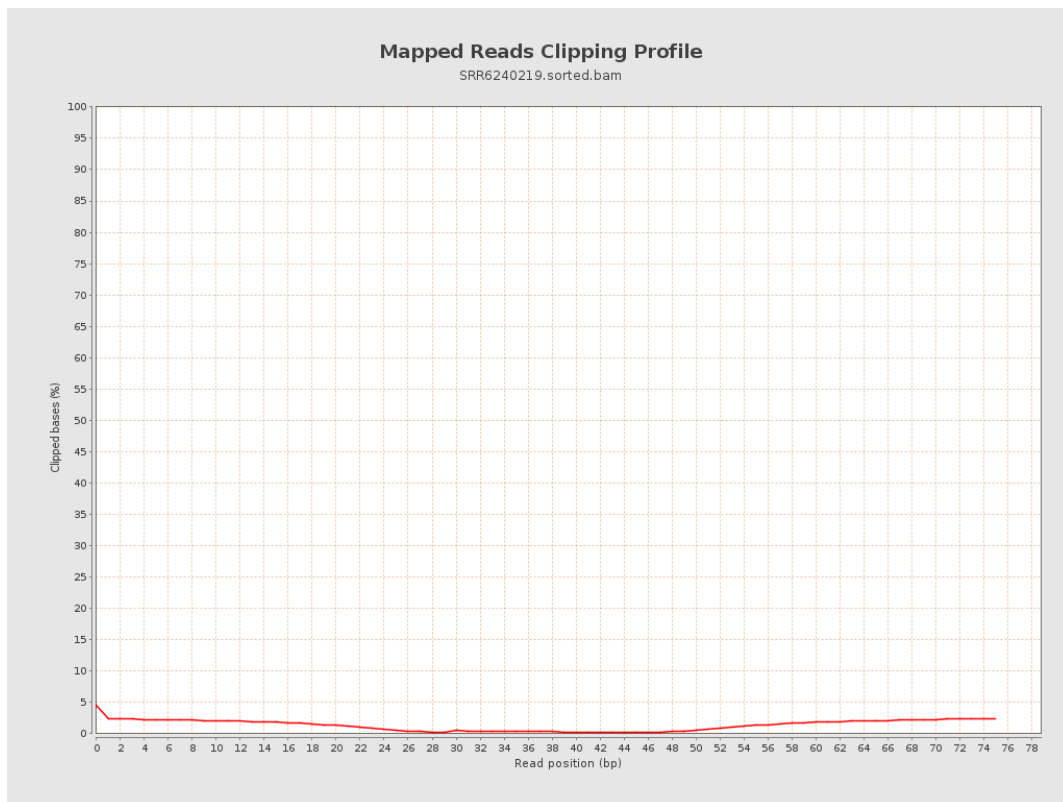
8. Results : Mapped Reads Nucleotide Content



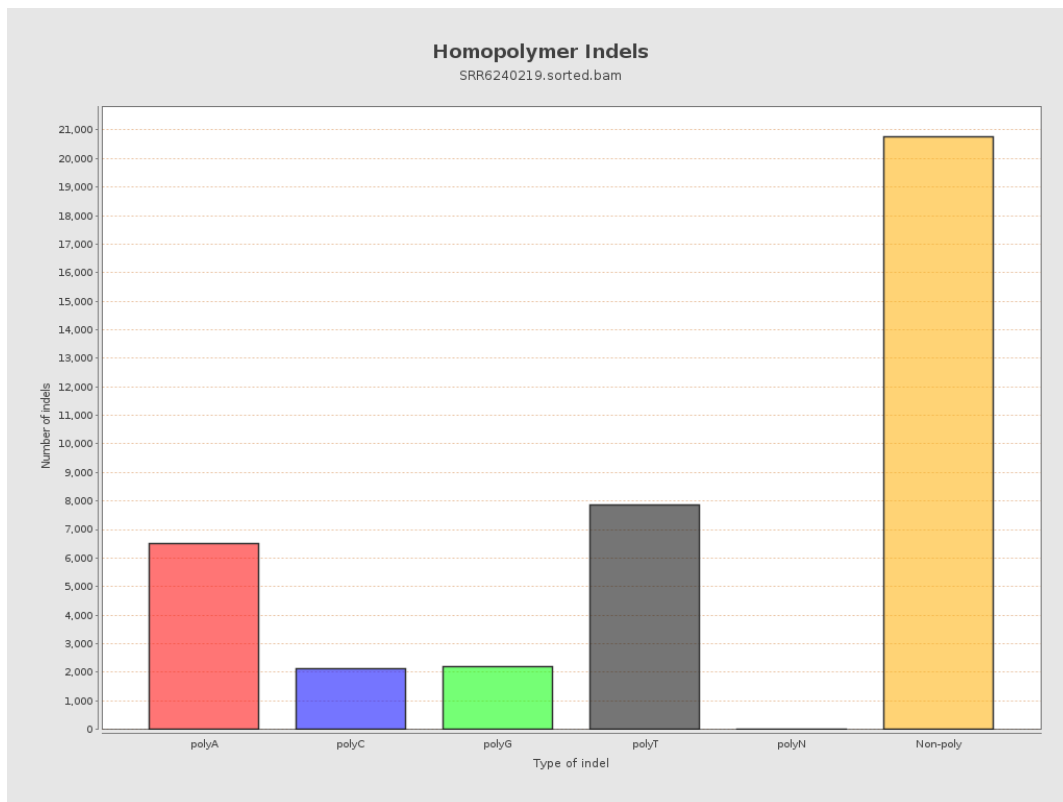
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

