

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 21:28:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6236119.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_SRR6236119 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6236119.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 21:28:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6236119.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,709,959
Mapped reads	1,526,884 / 89.29%
Unmapped reads	183,075 / 10.71%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,012 / 0.64%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	73,220 / 4.28%
Duplication rate	3.46%
Clipped reads	549,927 / 32.16%

2.2. ACGT Content

Number/percentage of A's	30,103,422 / 28.8%
Number/percentage of C's	18,930,742 / 18.11%
Number/percentage of T's	33,632,648 / 32.17%
Number/percentage of G's	21,811,844 / 20.86%
Number/percentage of N's	63,279 / 0.06%
GC Percentage	38.97%

2.3. Coverage

Mean	0.0338

Standard Deviation	0.4496
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2.4. Mapping Quality

Mean Mapping Quality	46.69
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2.5. Mismatches and indels

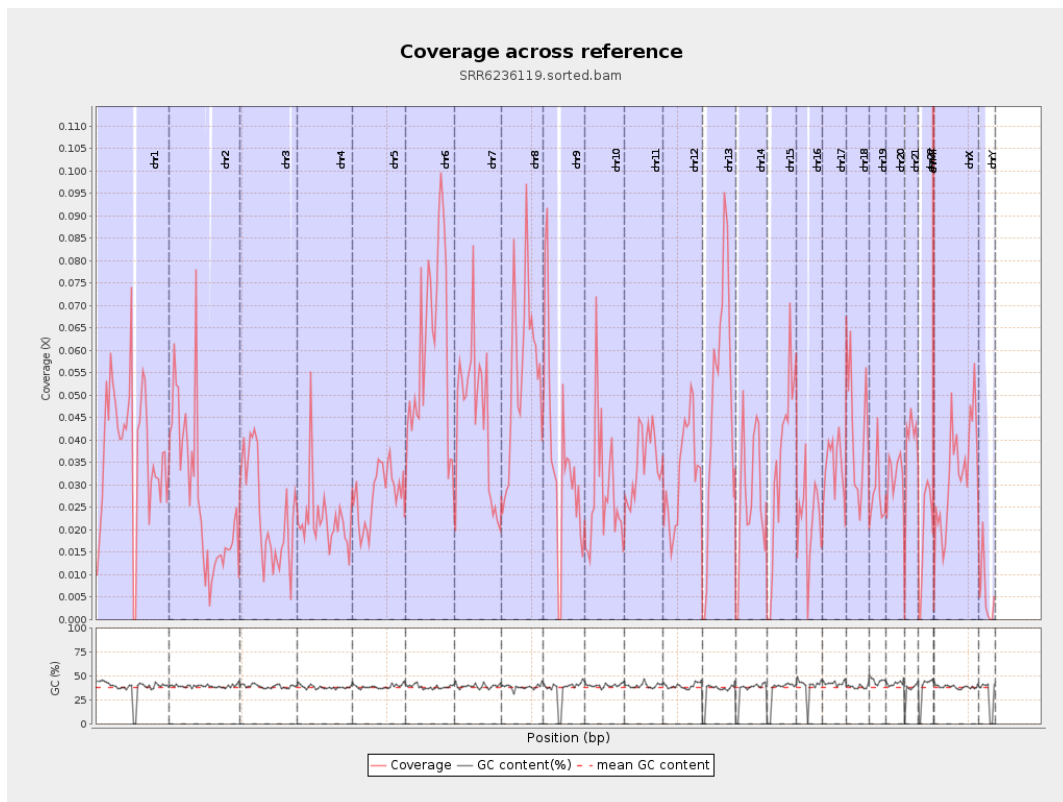
General error rate	0.89%
Mismatches	915,890
Insertions	8,810
Mapped reads with at least one insertion	0.57%
Deletions	36,204
Mapped reads with at least one deletion	2.34%
Homopolymer indels	45.88%

2.6. Chromosome stats

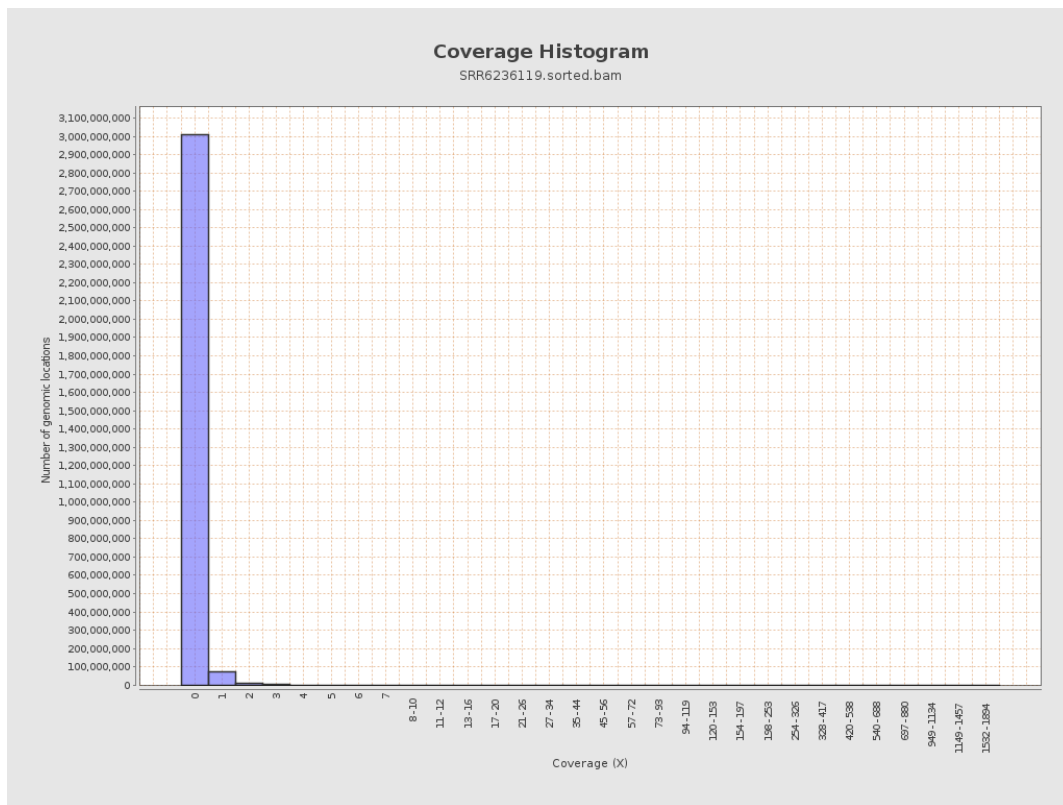
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	9356025	0.0375	0.6992
chr2	243199373	6601508	0.0271	0.3801
chr3	198022430	4650854	0.0235	0.1773
chr4	191154276	4240830	0.0222	0.2286
chr5	180915260	5065068	0.028	0.1973
chr6	171115067	10095484	0.059	0.3911
chr7	159138663	7123649	0.0448	0.4932

chr8	146364022	7881881	0.0539	1.275
chr9	141213431	4975928	0.0352	0.3506
chr10	135534747	3762281	0.0278	0.3358
chr11	135006516	4670729	0.0346	0.3089
chr12	133851895	4347102	0.0325	0.2139
chr13	115169878	5492545	0.0477	0.2567
chr14	107349540	2829669	0.0264	0.2013
chr15	102531392	3586361	0.035	0.2176
chr16	90354753	2027372	0.0224	0.2131
chr17	81195210	2733648	0.0337	0.2538
chr18	78077248	3262839	0.0418	0.6736
chr19	59128983	1668509	0.0282	0.4334
chr20	63025520	2021307	0.0321	0.2167
chr21	48129895	1835196	0.0381	0.262
chr22	51304566	1003786	0.0196	0.1598
chrMT	16571	35988	2.1717	2.0934
chrX	155270560	5024015	0.0324	0.2319
chrY	59373566	313384	0.0053	0.1805

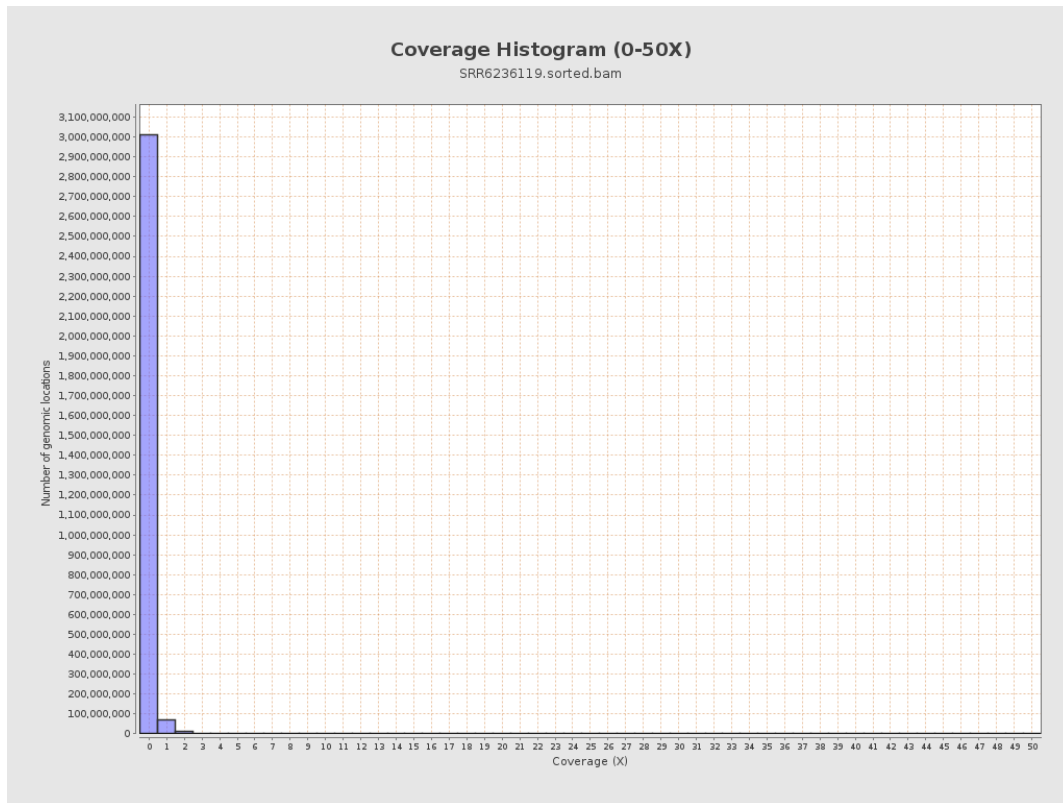
3. Results : Coverage across reference



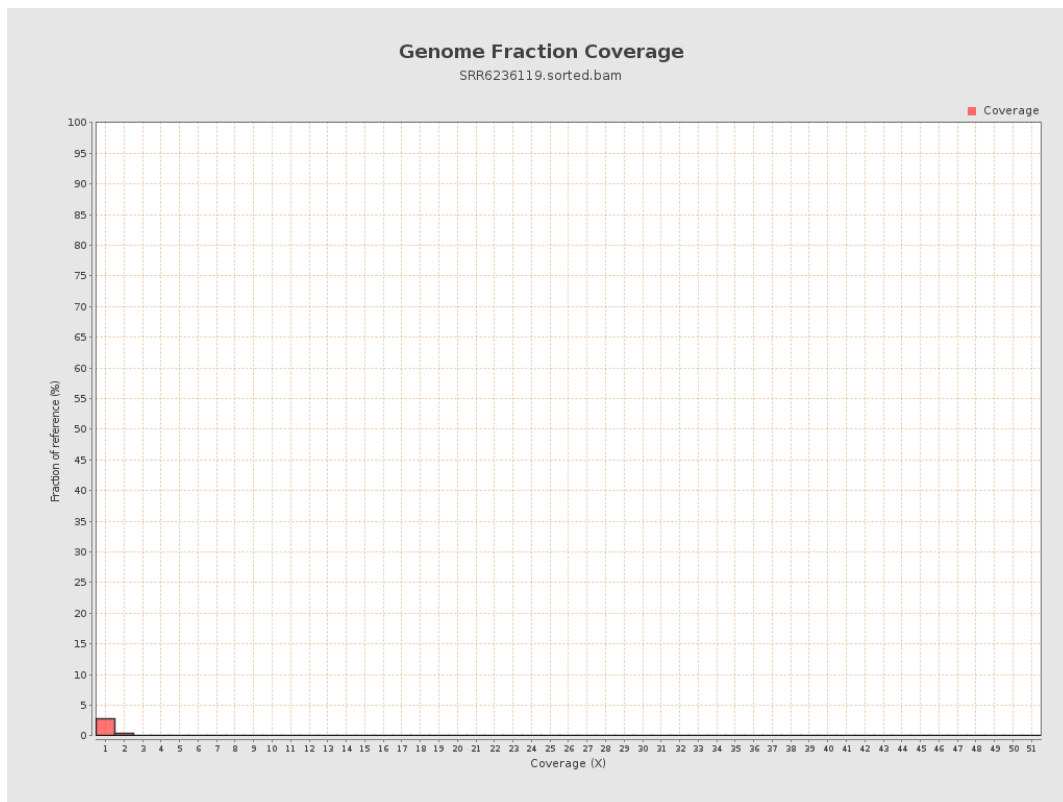
4. Results : Coverage Histogram



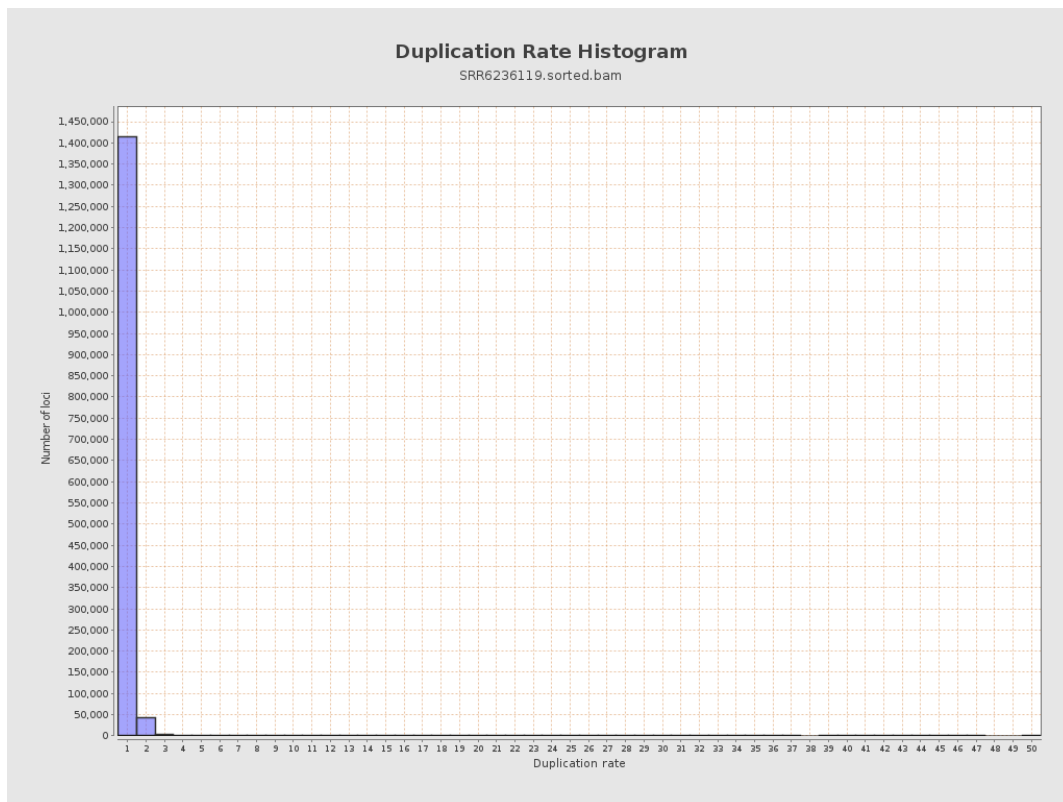
5. Results : Coverage Histogram (0-50X)



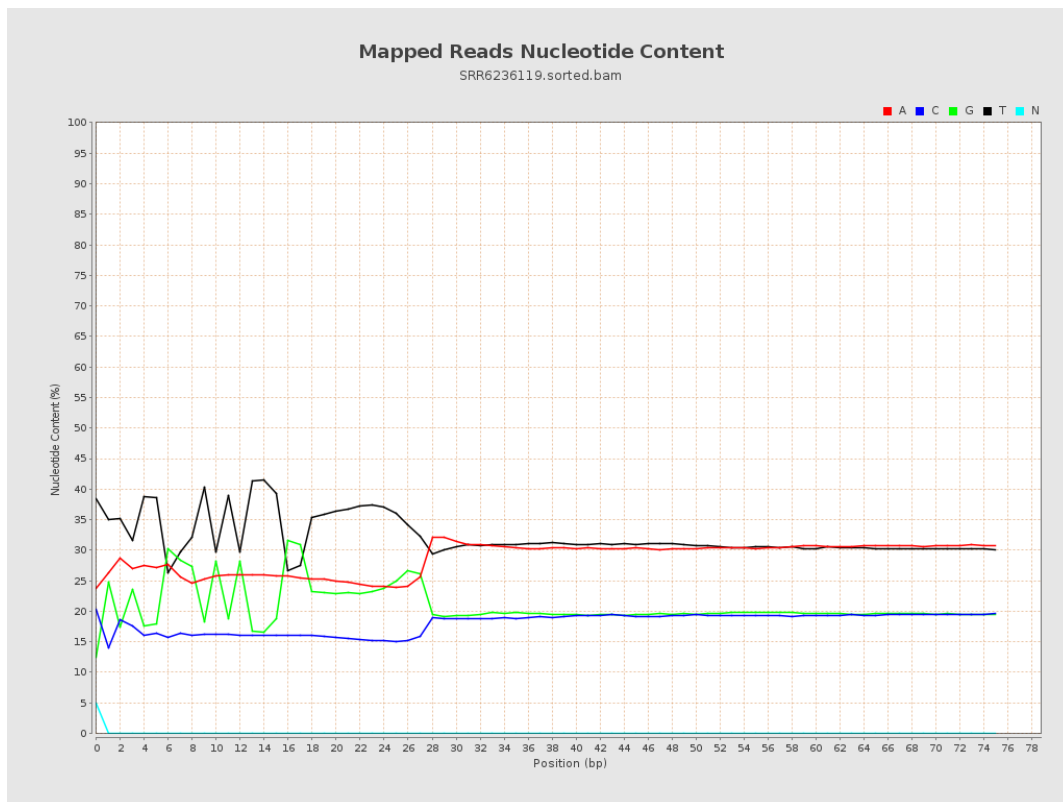
6. Results : Genome Fraction Coverage



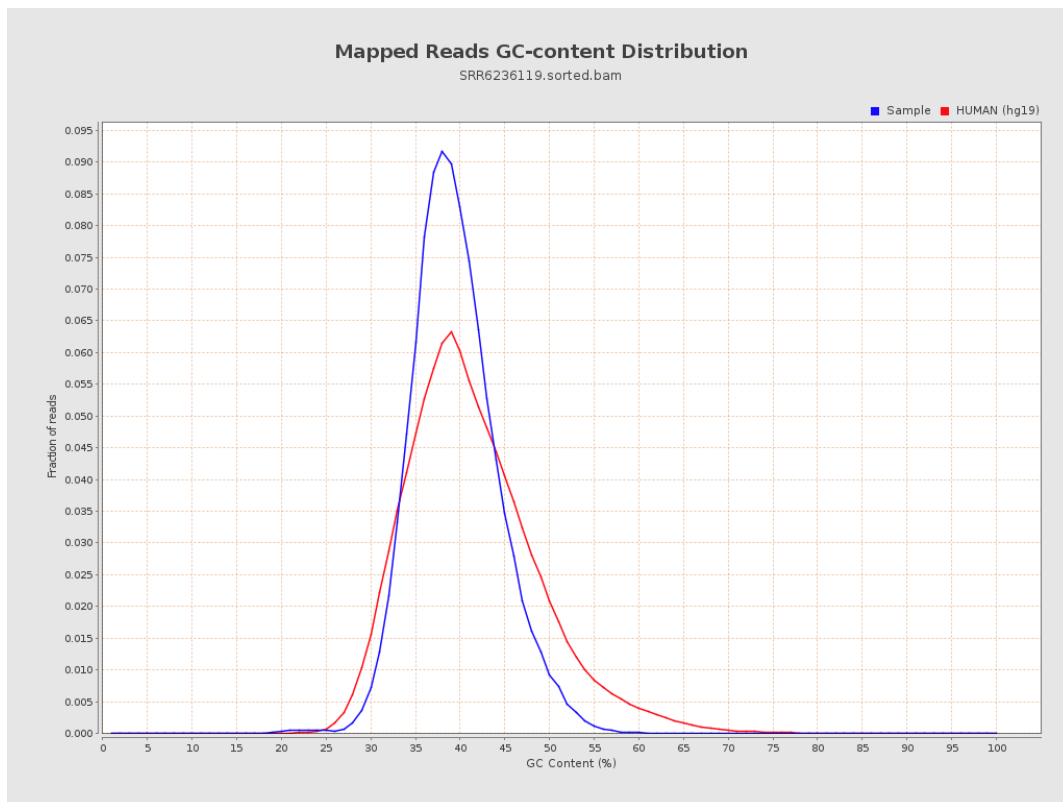
7. Results : Duplication Rate Histogram



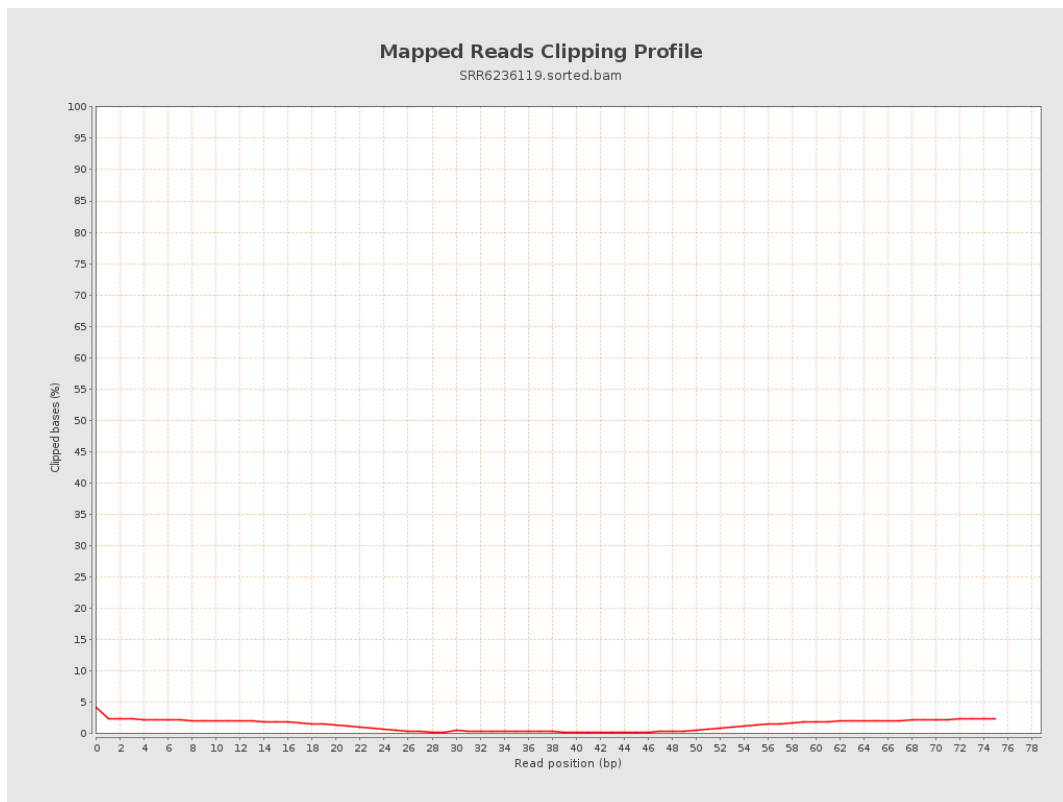
8. Results : Mapped Reads Nucleotide Content



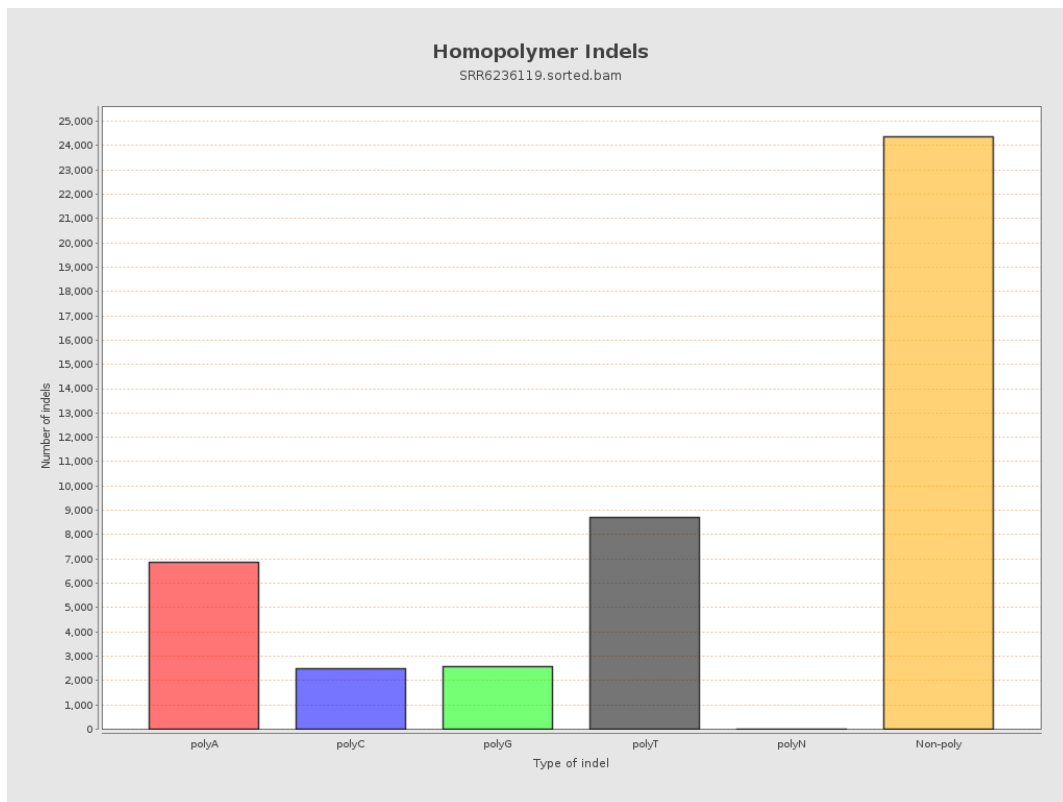
9. Results : Mapped Reads GC-content Distribution



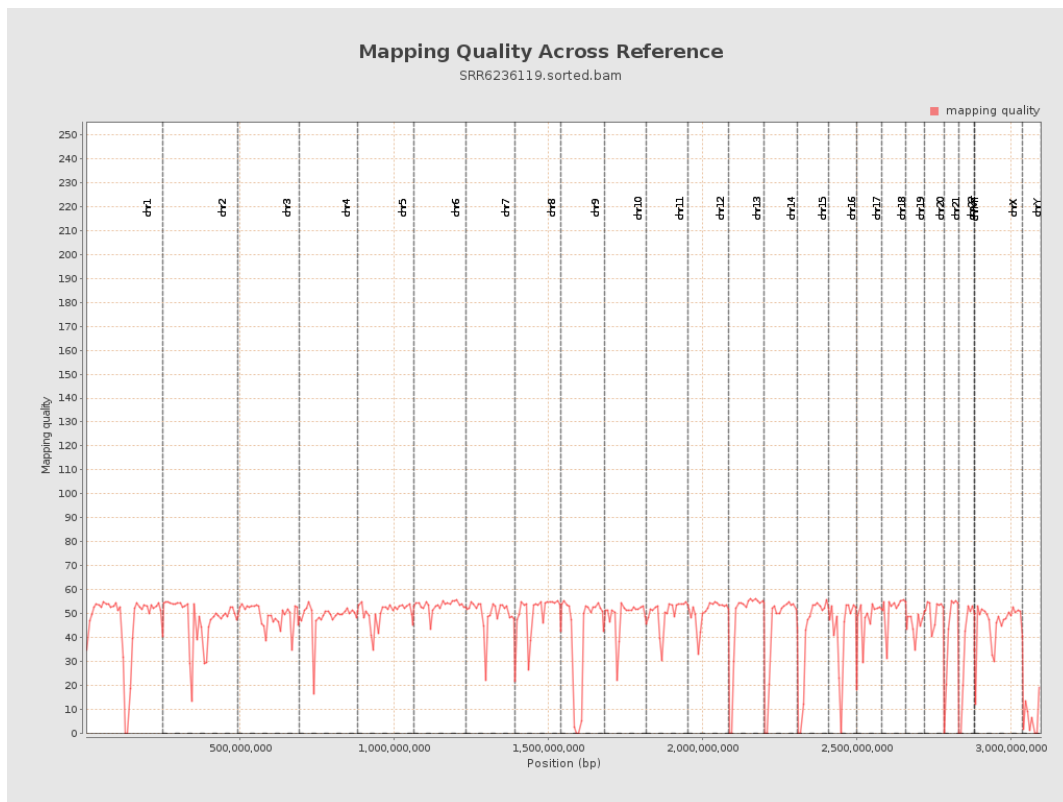
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

