Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 03:30:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237567.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_SRR6237567 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237567.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 03:30:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237567.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,442,790
Mapped reads	2,817,344 / 81.83%
Unmapped reads	625,446 / 18.17%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,647 / 0.6%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	197,627 / 5.74%
Duplication rate	5.24%
Clipped reads	1,836,217 / 53.34%

2.2. ACGT Content

Number/percentage of A's	46,921,722 / 26.99%
Number/percentage of C's	29,594,044 / 17.02%
Number/percentage of T's	56,268,151 / 32.37%
Number/percentage of G's	40,785,592 / 23.46%
Number/percentage of N's	280,153 / 0.16%
GC Percentage	40.48%

2.3. Coverage

Mean	0.0562

Standard Deviation	0.4962

2.4. Mapping Quality

Mean Mapping Quality	44.39

2.5. Mismatches and indels

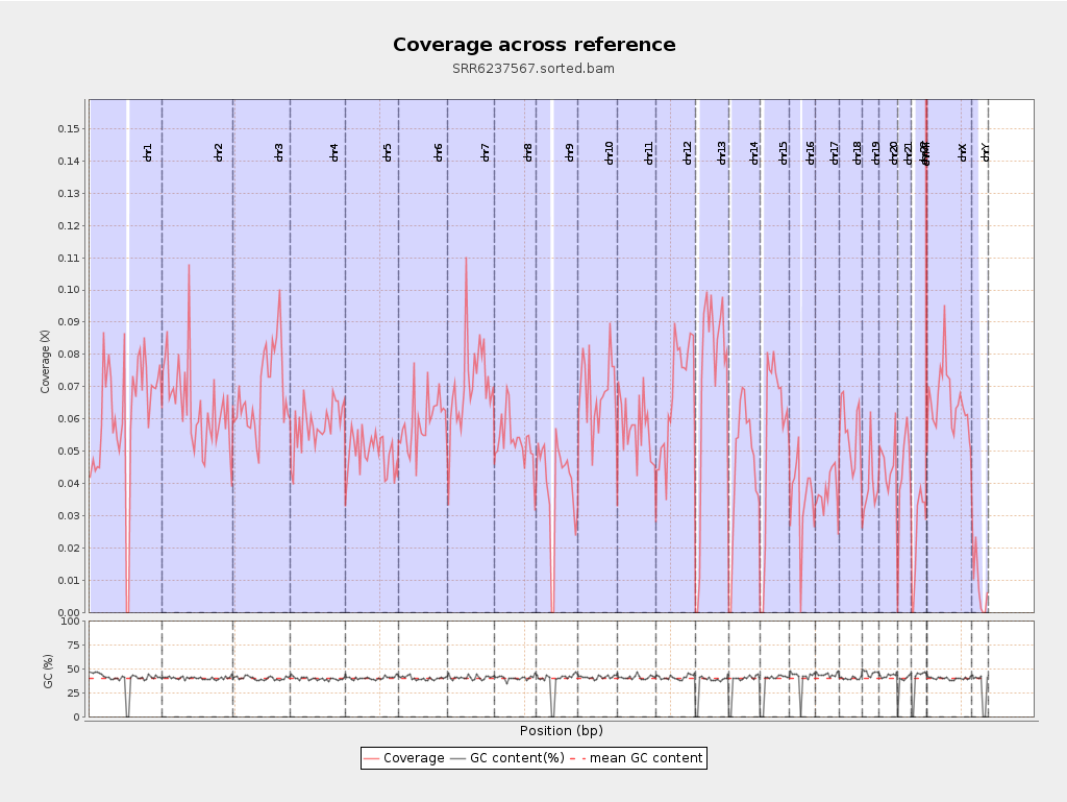
General error rate	0.93%
Mismatches	1,591,895
Insertions	14,696
Mapped reads with at least one insertion	0.52%
Deletions	59,415
Mapped reads with at least one deletion	2.08%
Homopolymer indels	47.86%

2.6. Chromosome stats

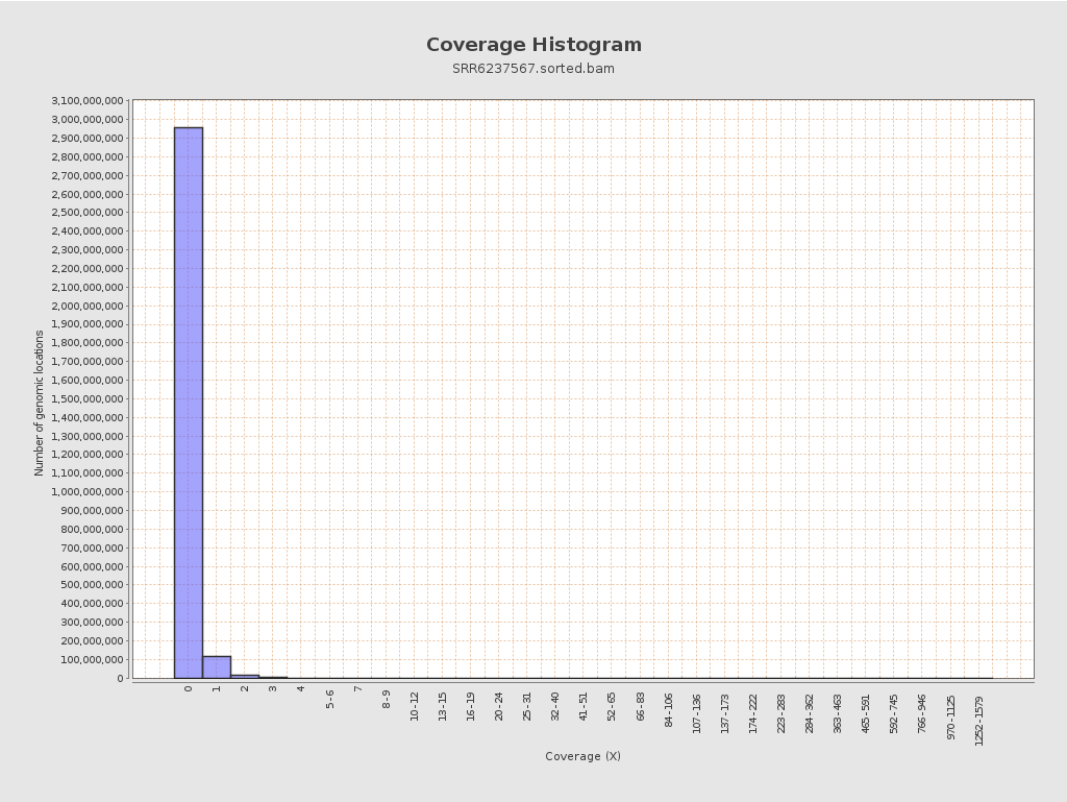
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	15273626	0.0613	0.7242
chr2	243199373	15561257	0.064	0.6235
chr3	198022430	13562803	0.0685	0.3347
chr4	191154276	11090234	0.058	0.3134
chr5	180915260	8959565	0.0495	0.2857
chr6	171115067	10112078	0.0591	0.3917
chr7	159138663	11311564	0.0711	0.7703

chr8	146364022	7755284	0.053	0.9537
chr9	141213431	5596498	0.0396	0.4094
chr10	135534747	9297032	0.0686	0.4371
chr11	135006516	7628079	0.0565	0.4274
chr12	133851895	9037979	0.0675	0.3377
chr13	115169878	8216441	0.0713	0.3336
chr14	107349540	4905964	0.0457	0.3028
chr15	102531392	5759120	0.0562	0.3128
chr16	90354753	3207448	0.0355	0.2724
chr17	81195210	3028853	0.0373	0.2713
chr18	78077248	4343435	0.0556	0.7198
chr19	59128983	2330505	0.0394	0.5093
chr20	63025520	2905612	0.0461	0.2939
chr21	48129895	2047007	0.0425	0.2822
chr22	51304566	1250135	0.0244	0.1958
chrMT	16571	115990	6.9996	5.585
chrX	155270560	10153487	0.0654	0.3774
chrY	59373566	494668	0.0083	0.1595

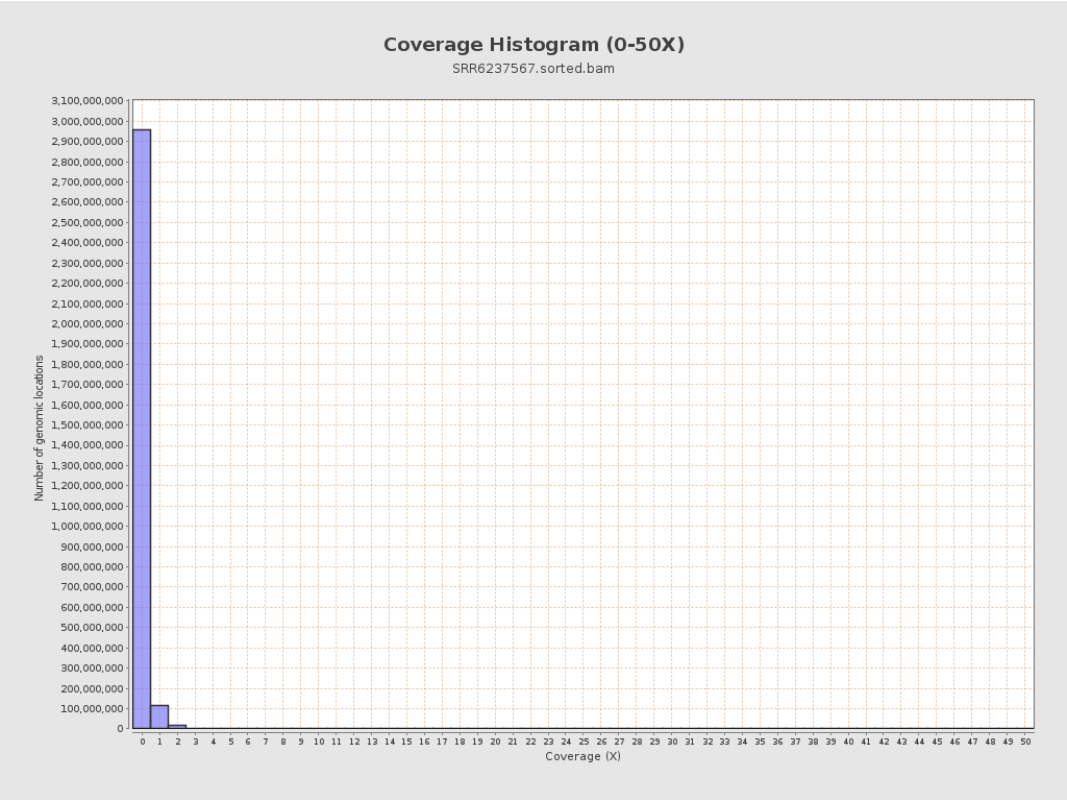
3. Results : Coverage across reference



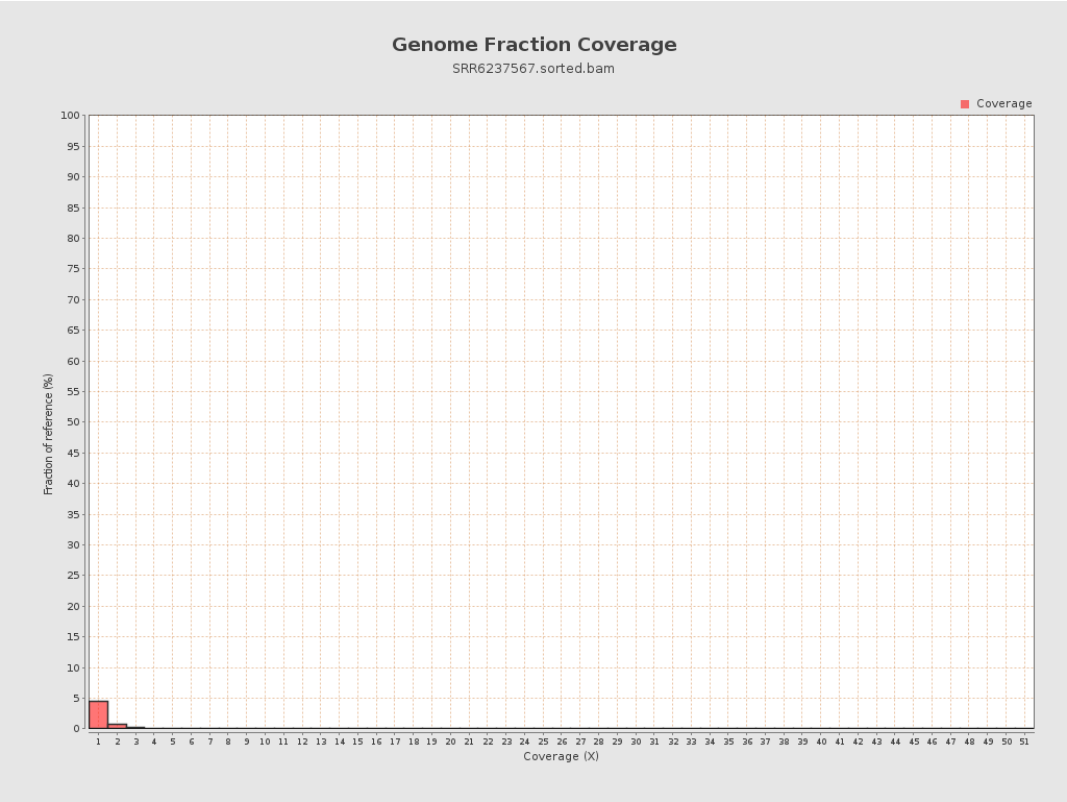
4. Results : Coverage Histogram



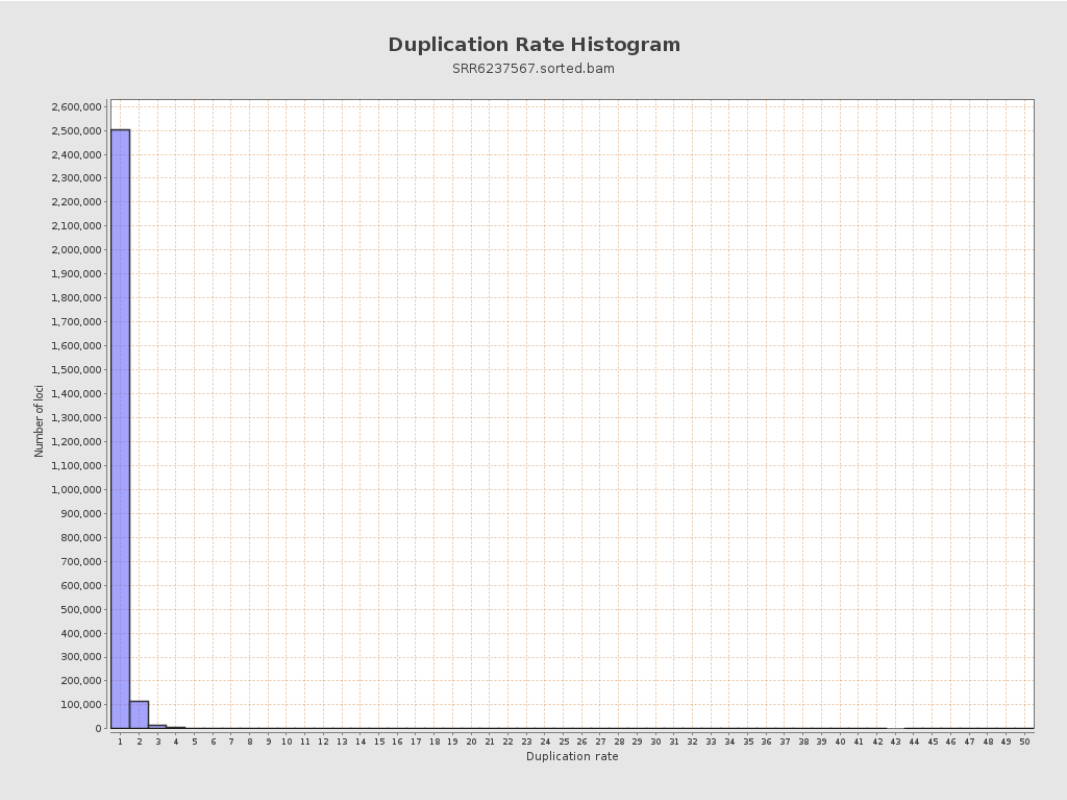
5. Results : Coverage Histogram (0-50X)



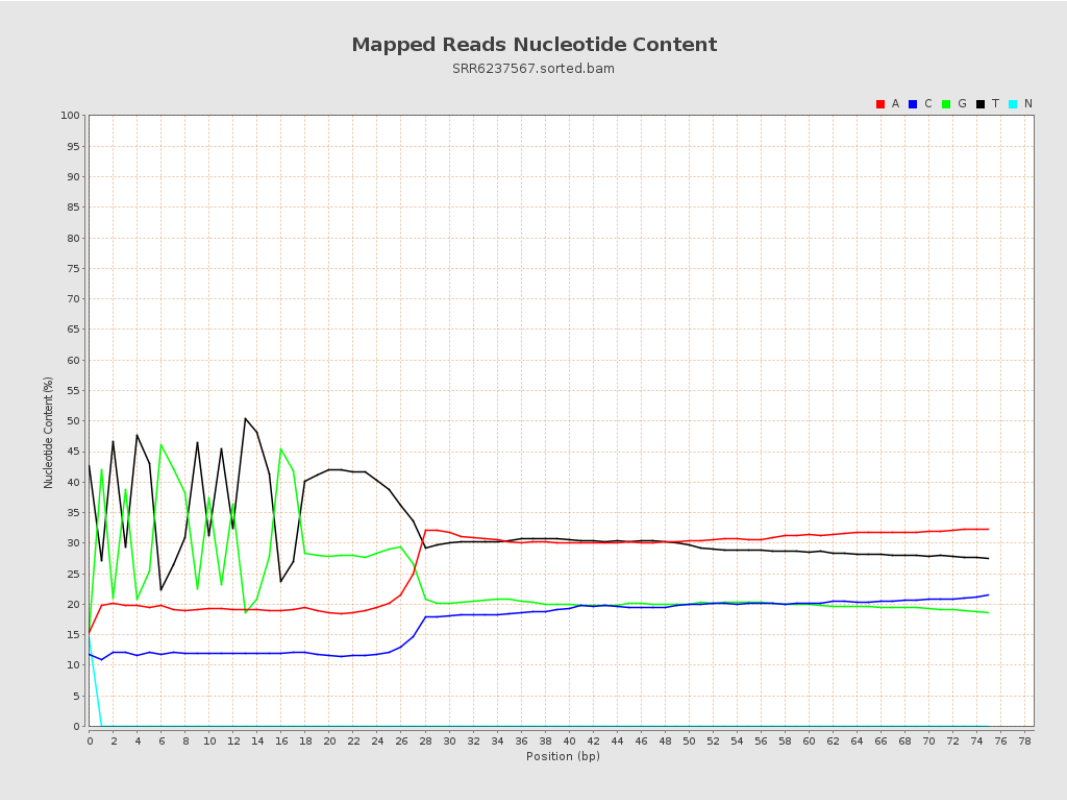
6. Results : Genome Fraction Coverage



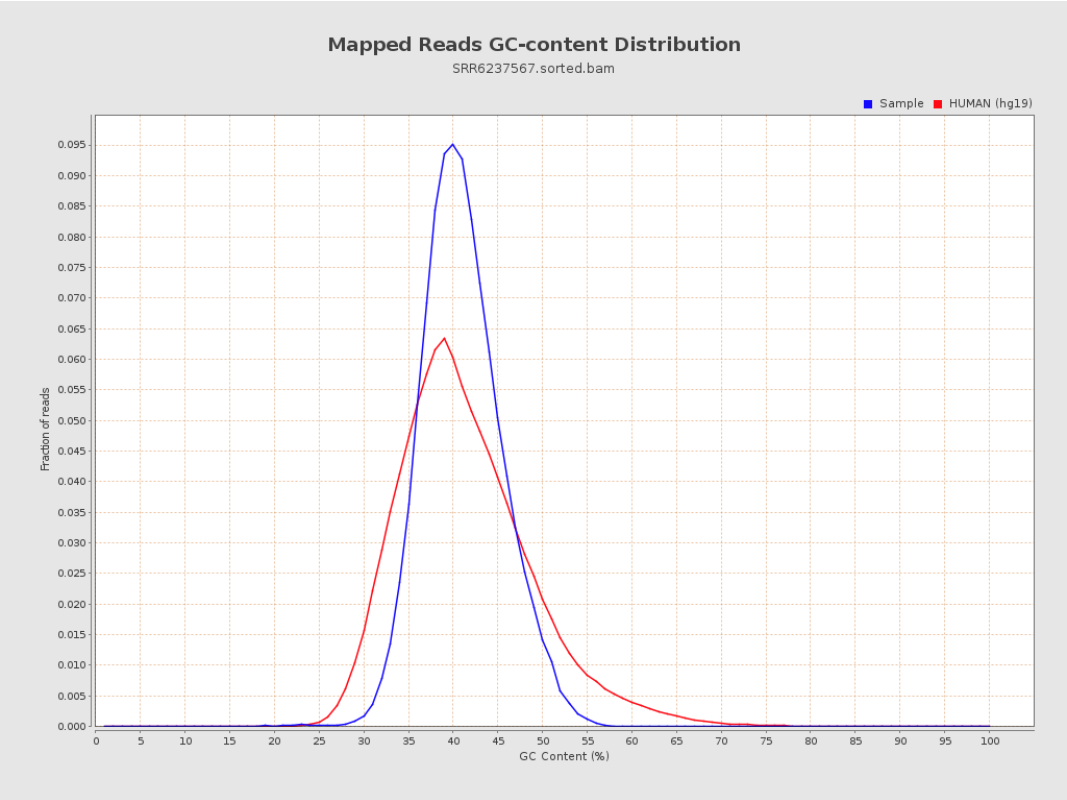
7. Results : Duplication Rate Histogram



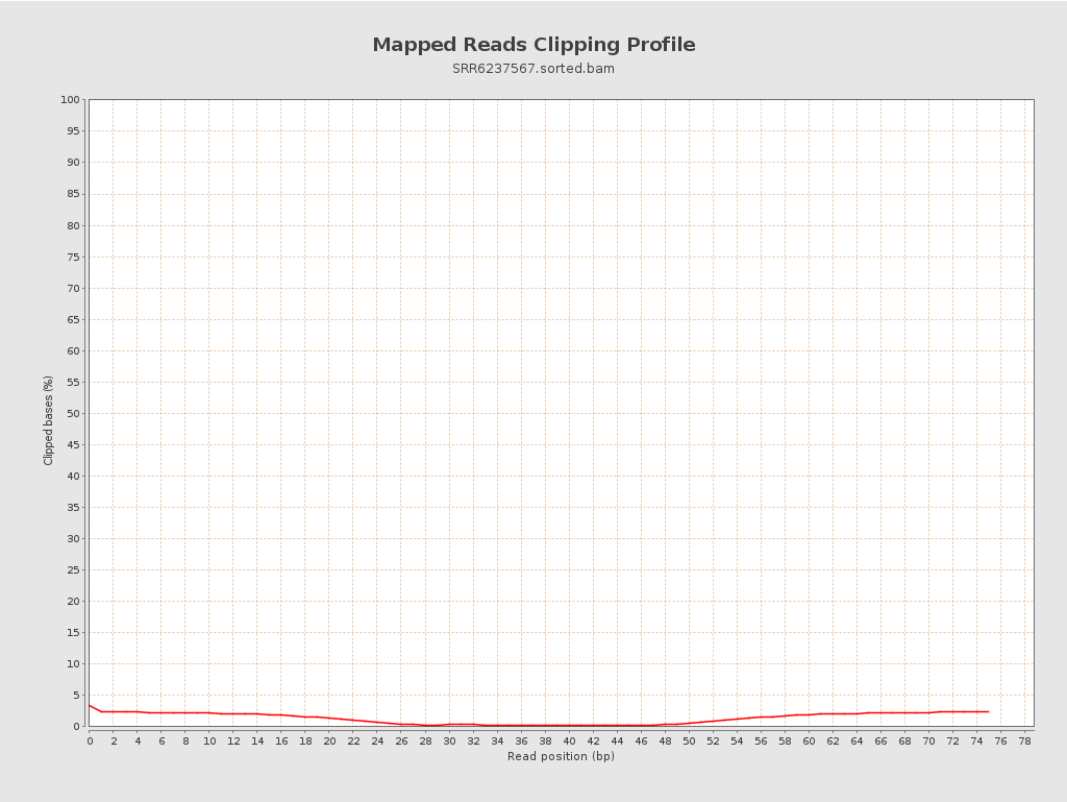
8. Results : Mapped Reads Nucleotide Content



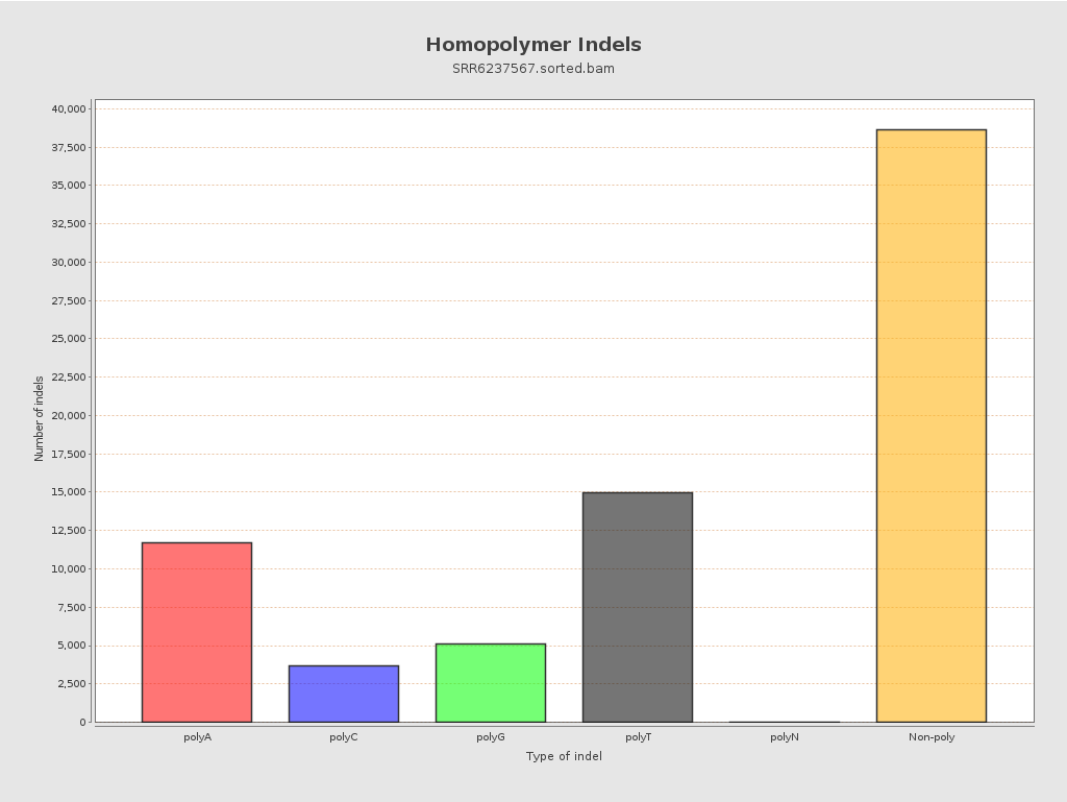
9. Results : Mapped Reads GC-content Distribution



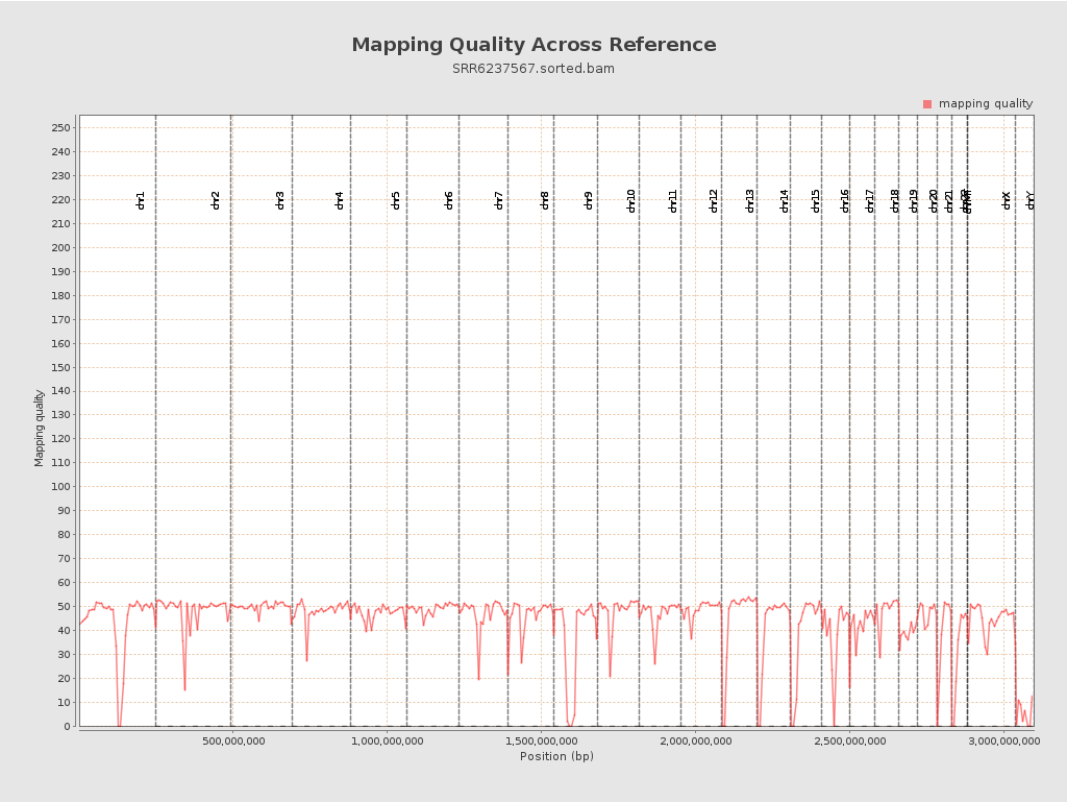
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram