Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 09:08:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237854.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_SRR6237854 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237854.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 09:08:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237854.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,532,376
Mapped reads	3,350,969 / 94.86%
Unmapped reads	181,407 / 5.14%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	34,340 / 0.97%
Read min/max/mean length	30 / 76 / 76.34
Duplicated reads (estimated)	334,733 / 9.48%
Duplication rate	6.9%
Clipped reads	632,596 / 17.91%

2.2. ACGT Content

Number/percentage of A's	75,241,693 / 30.62%
Number/percentage of C's	48,199,093 / 19.62%
Number/percentage of T's	74,001,747 / 30.12%
Number/percentage of G's	47,819,150 / 19.46%
Number/percentage of N's	433,449 / 0.18%
GC Percentage	39.08%

2.3. Coverage

Mean	0.0794

Standard Deviation	1.5432

2.4. Mapping Quality

Mean Mapping Quality	48.01

2.5. Mismatches and indels

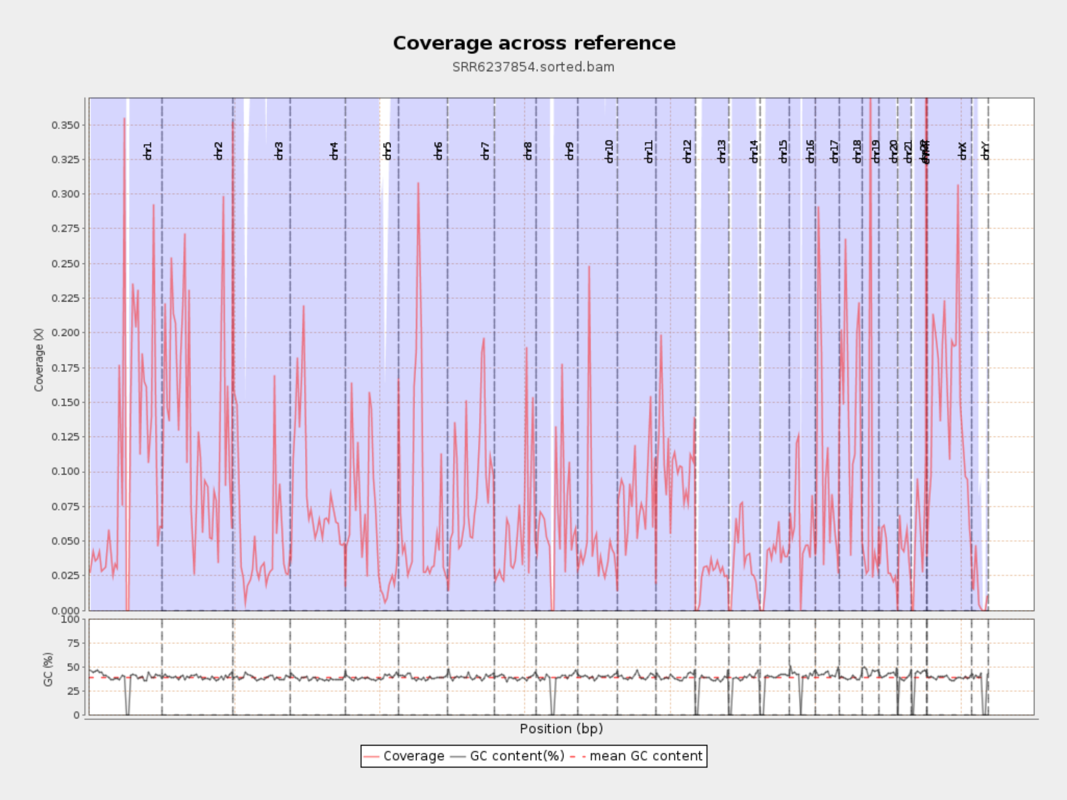
General error rate	0.94%
Mismatches	2,260,324
Insertions	19,651
Mapped reads with at least one insertion	0.58%
Deletions	67,688
Mapped reads with at least one deletion	2%
Homopolymer indels	45.64%

2.6. Chromosome stats

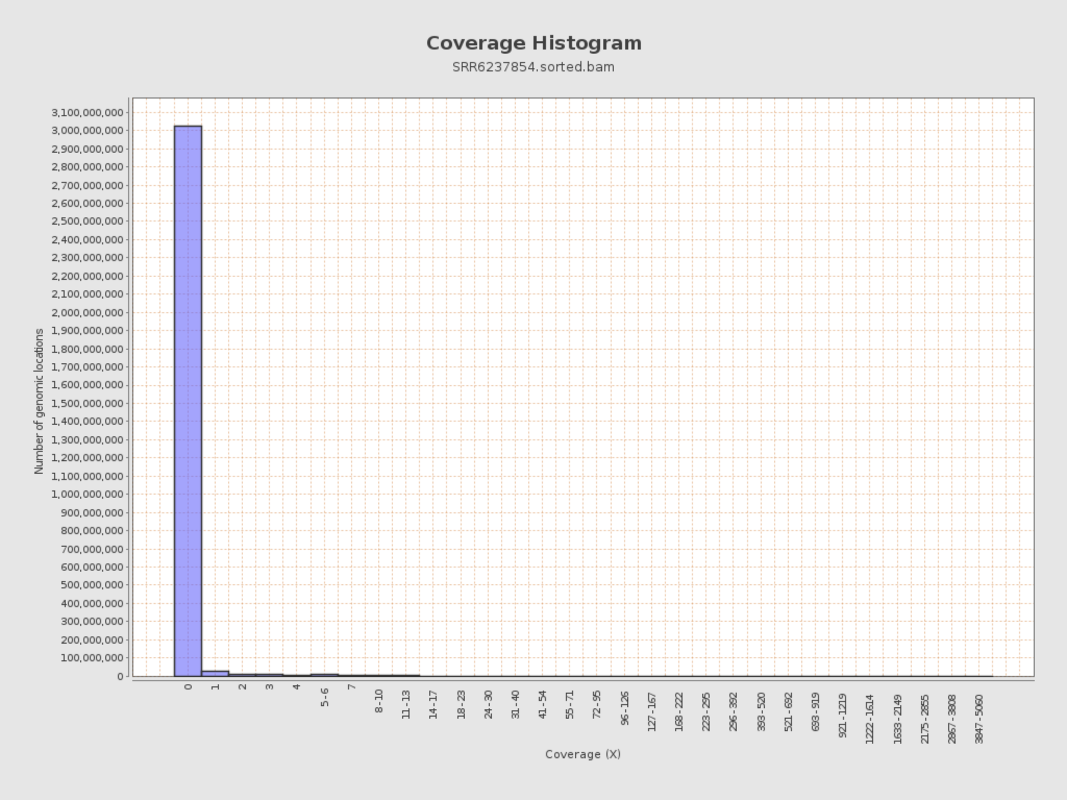
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	25703595	0.1031	3.9079
chr2	243199373	32912082	0.1353	1.5285
chr3	198022430	10851179	0.0548	0.6892
chr4	191154276	16358335	0.0856	0.8126
chr5	180915260	10973410	0.0607	0.639
chr6	171115067	13002214	0.076	0.756
chr7	159138663	14533668	0.0913	1.4284

chr8	146364022	8491457	0.058	1.0289
chr9	141213431	9052688	0.0641	1.2447
chr10	135534747	6883573	0.0508	1.5803
chr11	135006516	10859597	0.0804	1.023
chr12	133851895	14147546	0.1057	0.8553
chr13	115169878	2828010	0.0246	0.3767
chr14	107349540	3800135	0.0354	0.5587
chr15	102531392	3622665	0.0353	0.4678
chr16	90354753	5519185	0.0611	0.8761
chr17	81195210	7840563	0.0966	1.085
chr18	78077248	12419433	0.1591	2.5446
chr19	59128983	4745487	0.0803	2.2203
chr20	63025520	2344002	0.0372	0.5108
chr21	48129895	2022649	0.042	0.5691
chr22	51304566	2616439	0.051	0.5809
chrMT	16571	35162	2.1219	3.1168
chrX	155270560	23558740	0.1517	1.2239
chrY	59373566	695324	0.0117	0.3883

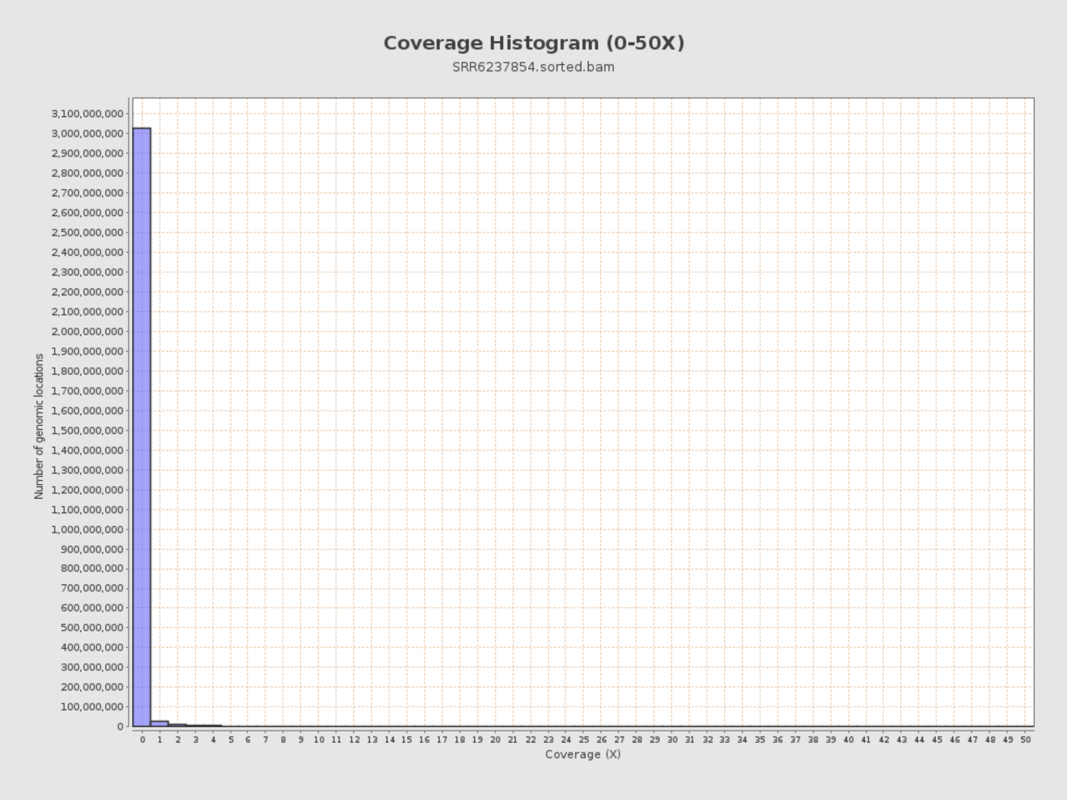
3. Results : Coverage across reference



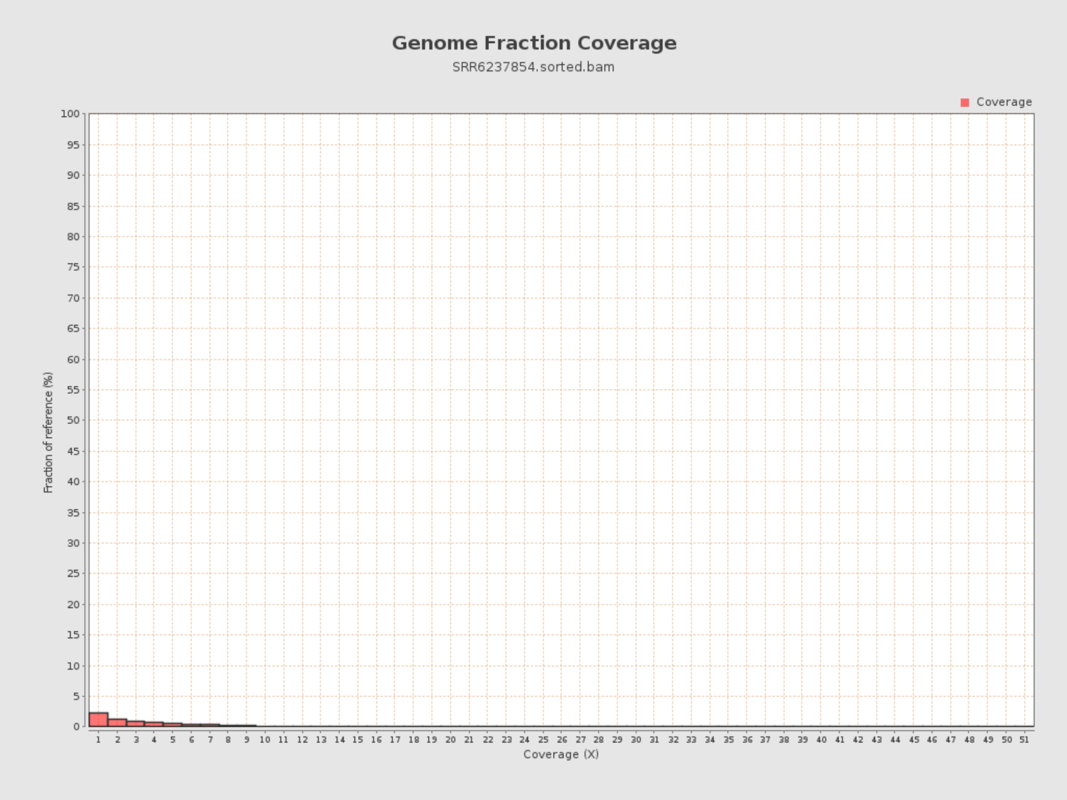
4. Results : Coverage Histogram



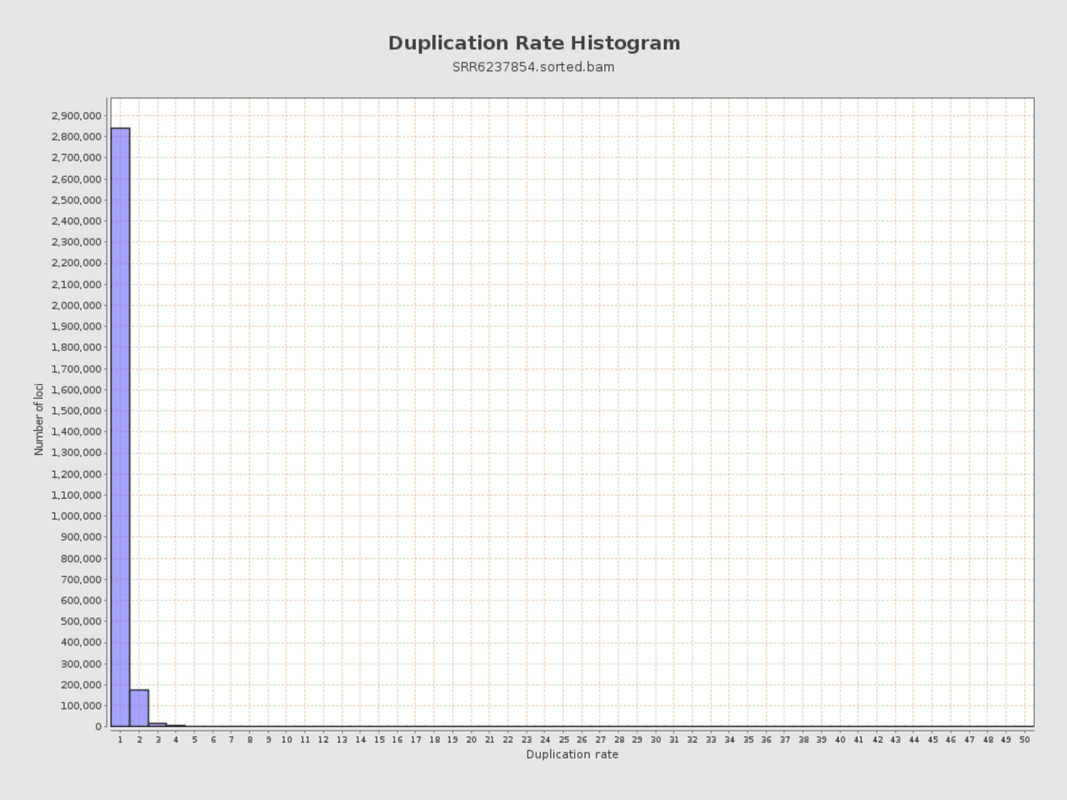
5. Results : Coverage Histogram (0-50X)



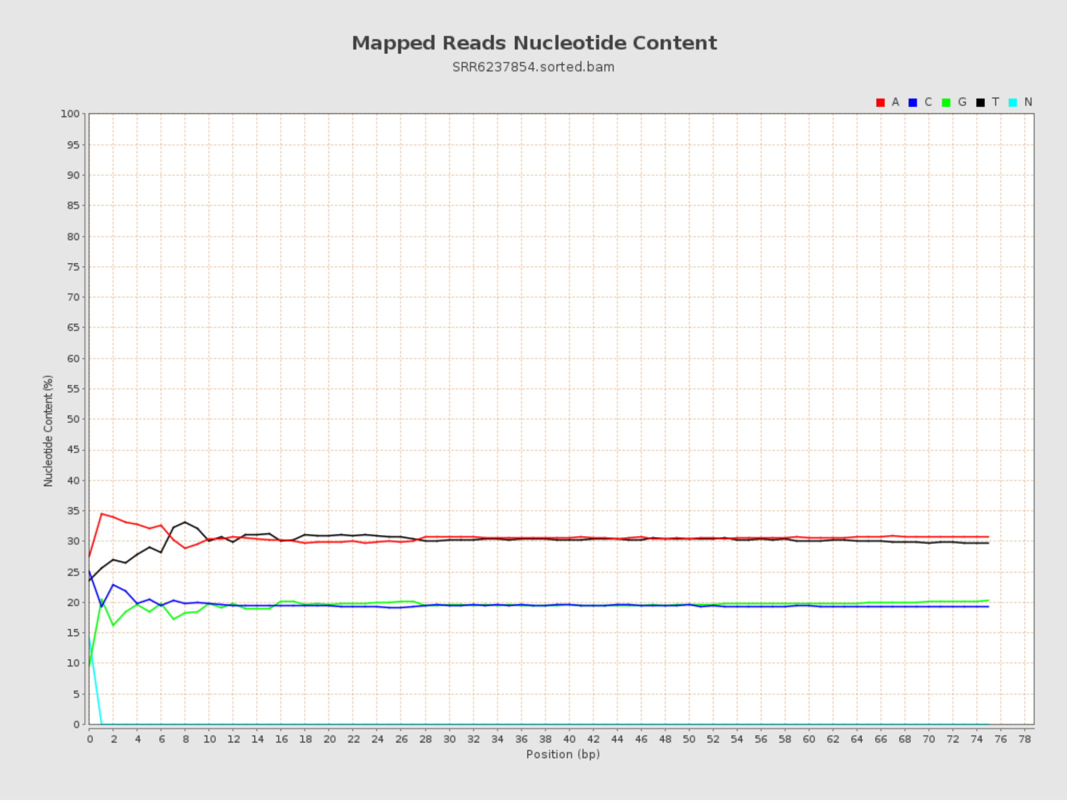
6. Results : Genome Fraction Coverage



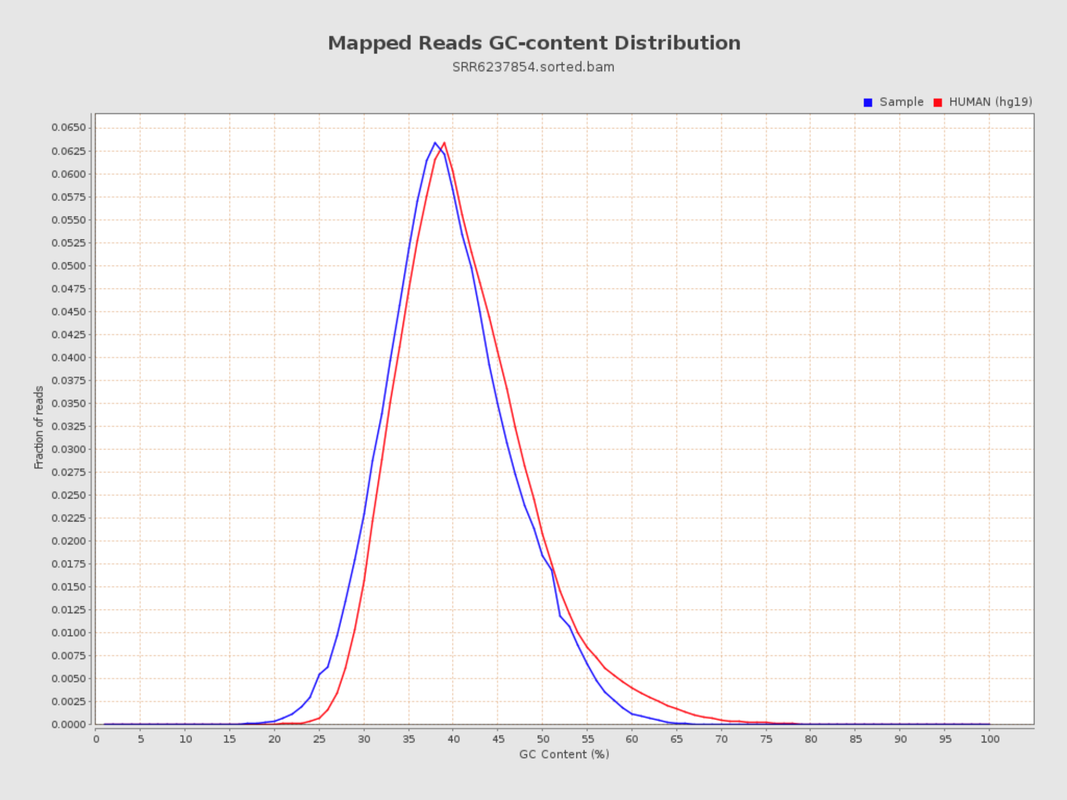
7. Results : Duplication Rate Histogram



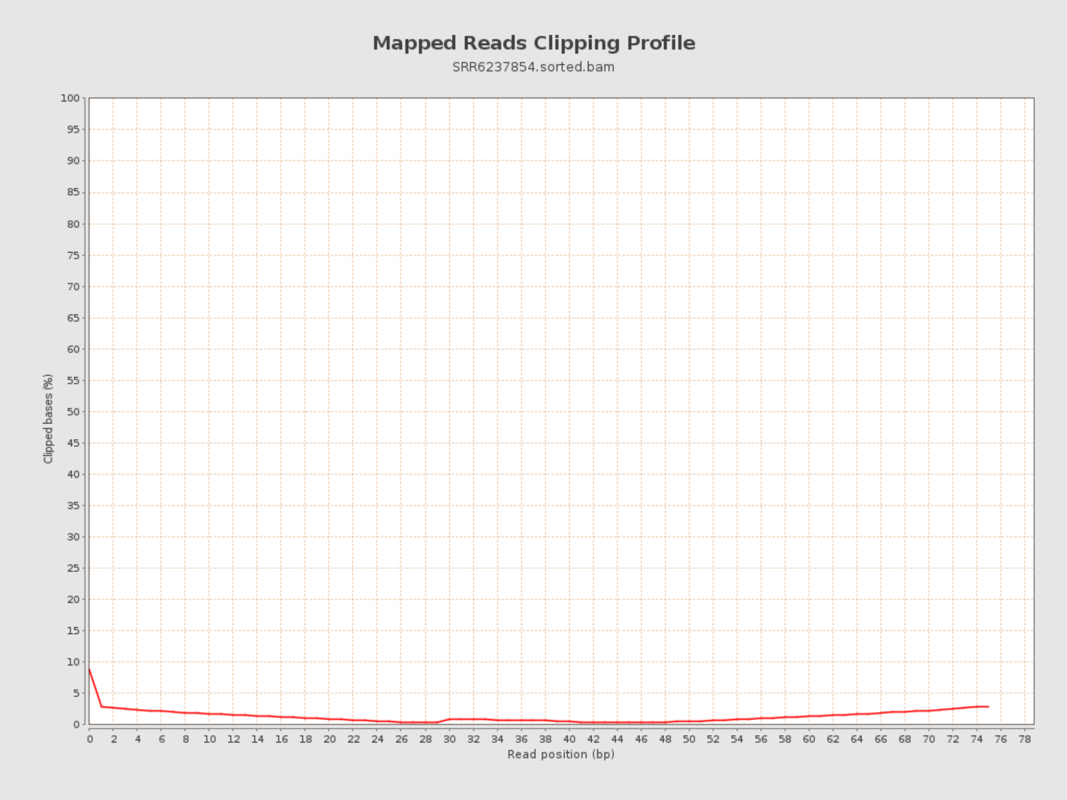
8. Results : Mapped Reads Nucleotide Content



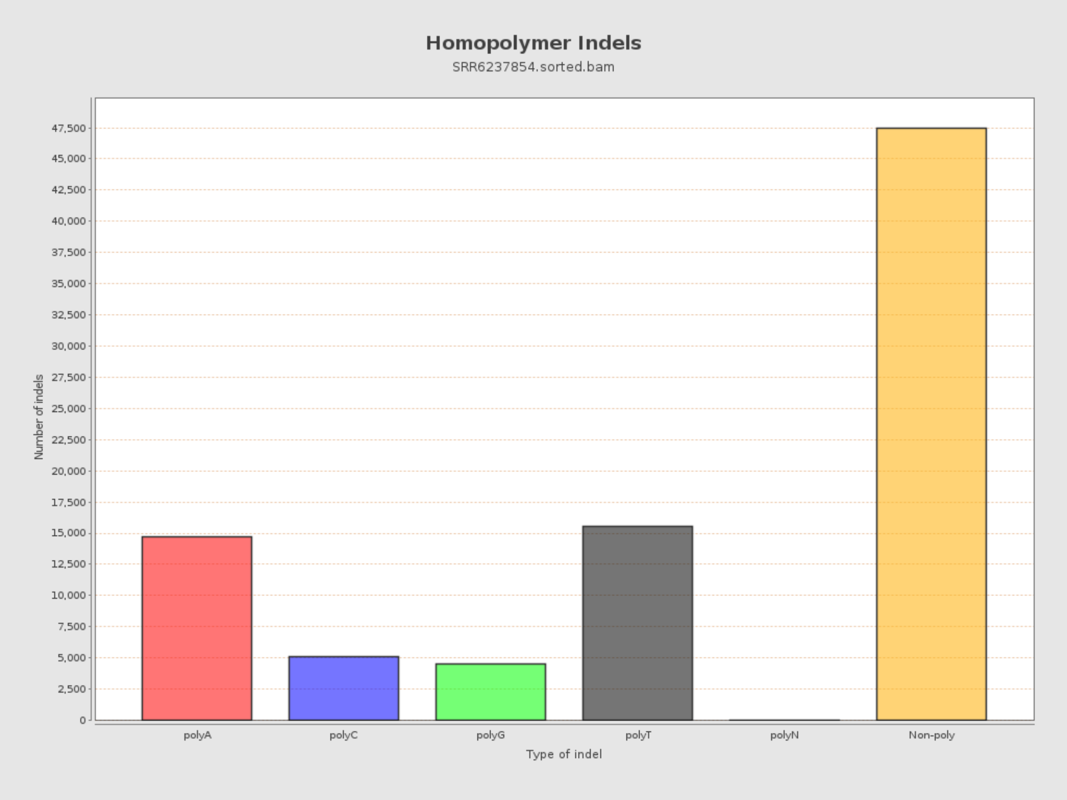
9. Results : Mapped Reads GC-content Distribution



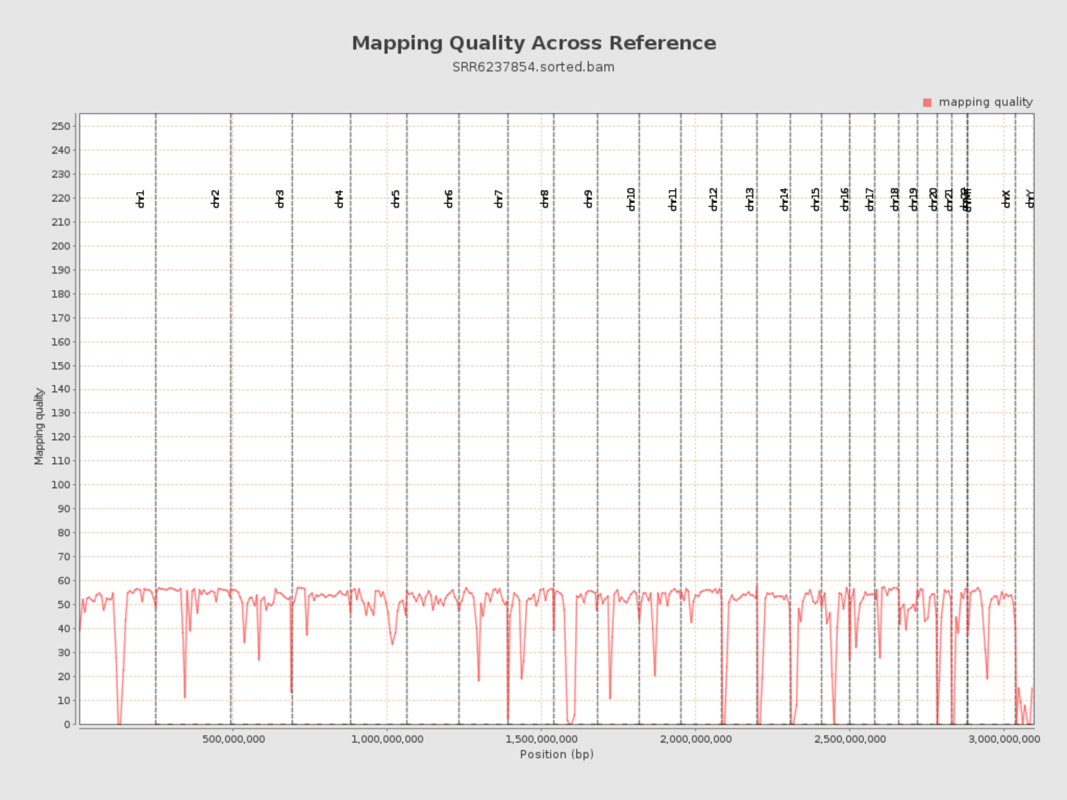
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram