Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 04:36:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237590.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_SRR6237590 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237590.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 04:36:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237590.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,636,554
Mapped reads	1,306,176 / 79.81%
Unmapped reads	330,378 / 20.19%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,861 / 0.42%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	78,772 / 4.81%
Duplication rate	4.21%
Clipped reads	816,229 / 49.87%

2.2. ACGT Content

Number/percentage of A's	21,157,506 / 25.91%
Number/percentage of C's	14,814,991 / 18.14%
Number/percentage of T's	24,962,694 / 30.56%
Number/percentage of G's	20,693,230 / 25.34%
Number/percentage of N's	45,012 / 0.06%
GC Percentage	43.48%

2.3. Coverage

Mean	0.0264

Standard Deviation	0.2724

2.4. Mapping Quality

Mean Mapping Quality	40.63

2.5. Mismatches and indels

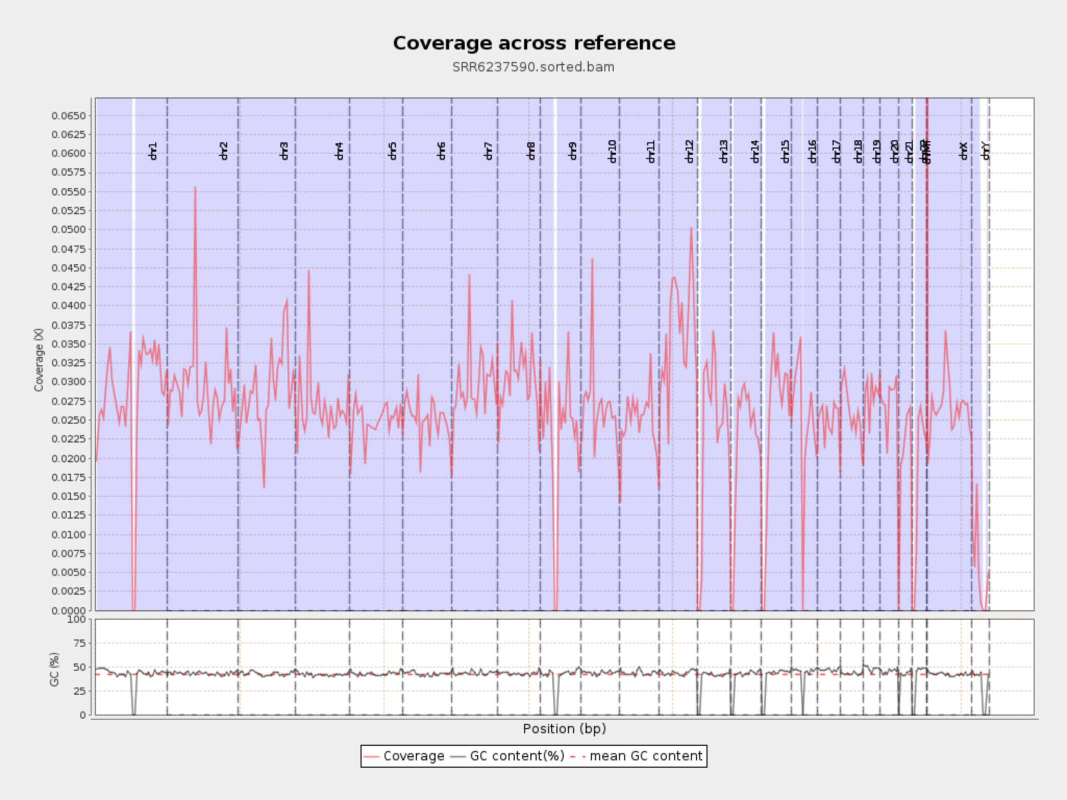
General error rate	1%
Mismatches	806,470
Insertions	7,559
Mapped reads with at least one insertion	0.57%
Deletions	29,242
Mapped reads with at least one deletion	2.21%
Homopolymer indels	46.42%

2.6. Chromosome stats

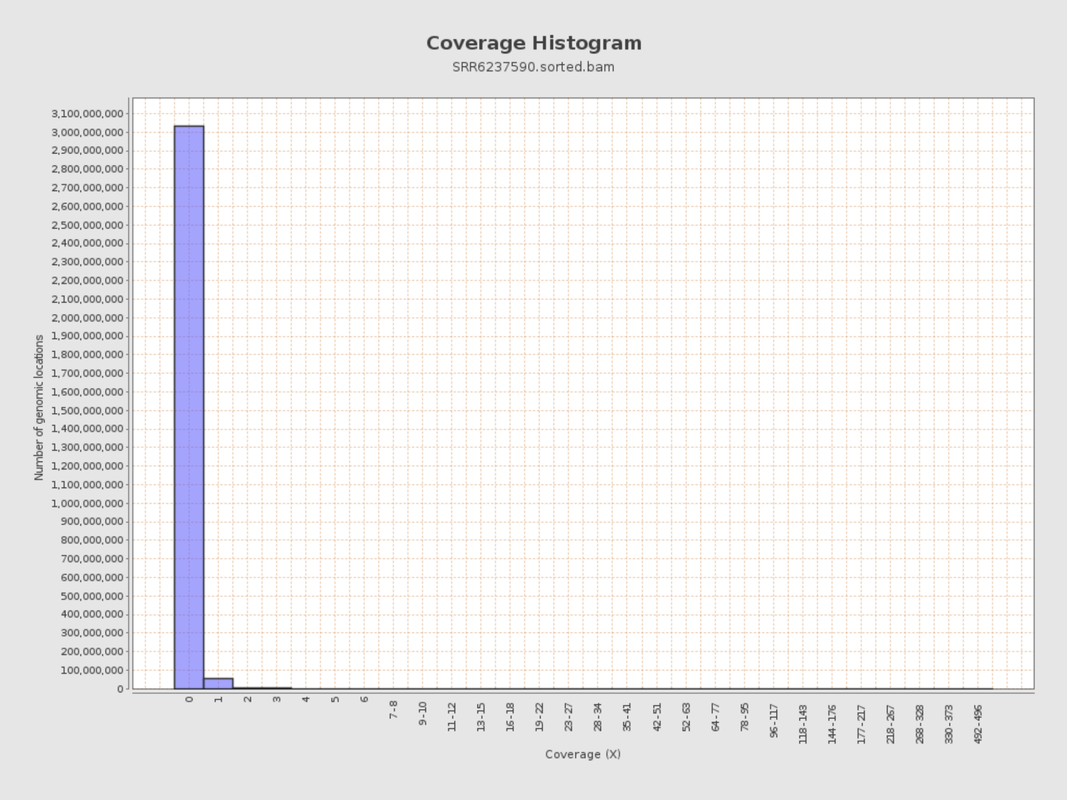
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6998853	0.0281	0.3215
chr2	243199373	7141706	0.0294	0.3867
chr3	198022430	5679187	0.0287	0.221
chr4	191154276	5126785	0.0268	0.229
chr5	180915260	4537768	0.0251	0.1995
chr6	171115067	4299628	0.0251	0.2195
chr7	159138663	4720739	0.0297	0.3851

chr8	146364022	4448781	0.0304	0.2759
chr9	141213431	3243246	0.023	0.2807
chr10	135534747	3610195	0.0266	0.2713
chr11	135006516	3398403	0.0252	0.3059
chr12	133851895	4916530	0.0367	0.2576
chr13	115169878	2693086	0.0234	0.2009
chr14	107349540	2330128	0.0217	0.2119
chr15	102531392	2517709	0.0246	0.2087
chr16	90354753	2220308	0.0246	0.2265
chr17	81195210	2035566	0.0251	0.2138
chr18	78077248	2053431	0.0263	0.3987
chr19	59128983	1655428	0.028	0.2697
chr20	63025520	1708197	0.0271	0.2215
chr21	48129895	983375	0.0204	0.2067
chr22	51304566	870913	0.017	0.1683
chrMT	16571	55889	3.3727	3.0281
chrX	155270560	4170965	0.0269	0.2261
chrY	59373566	304870	0.0051	0.141

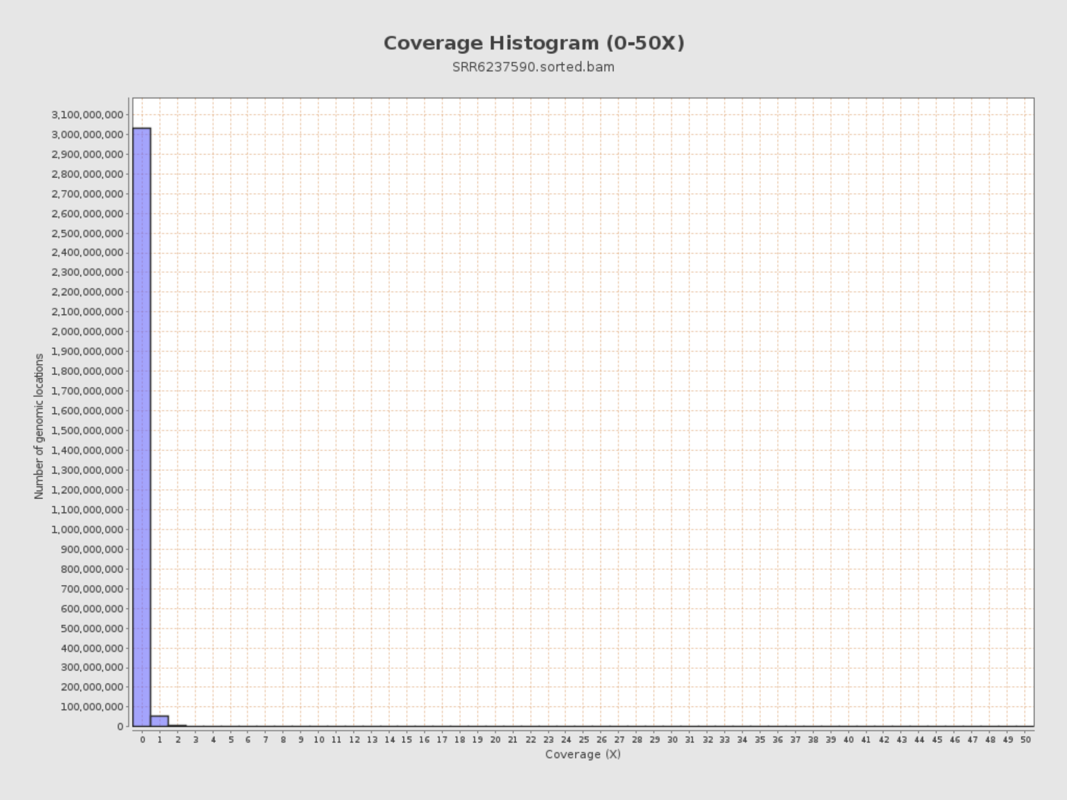
3. Results : Coverage across reference



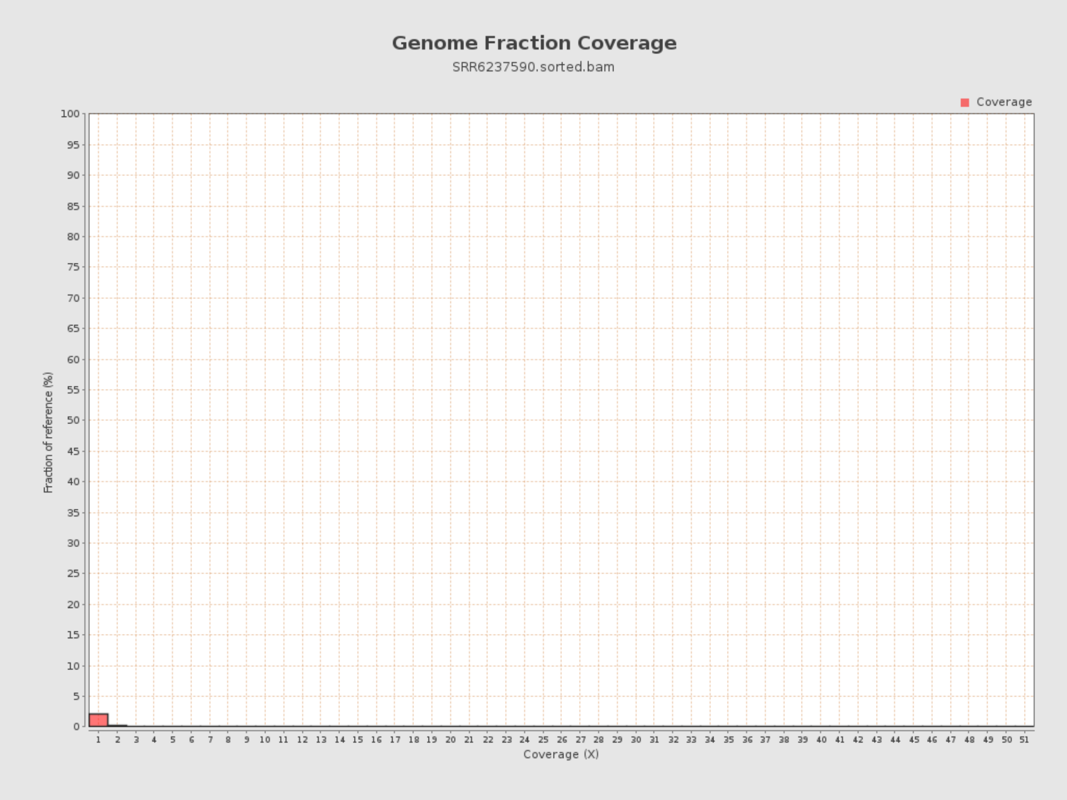
4. Results : Coverage Histogram



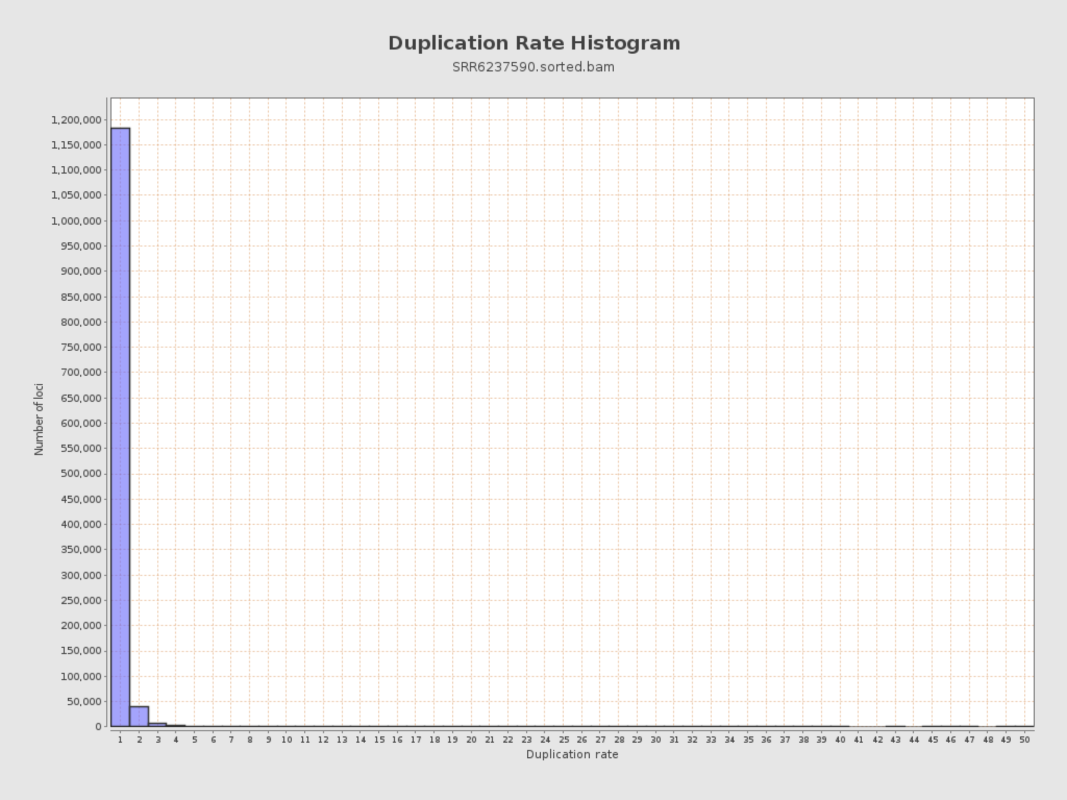
5. Results : Coverage Histogram (0-50X)



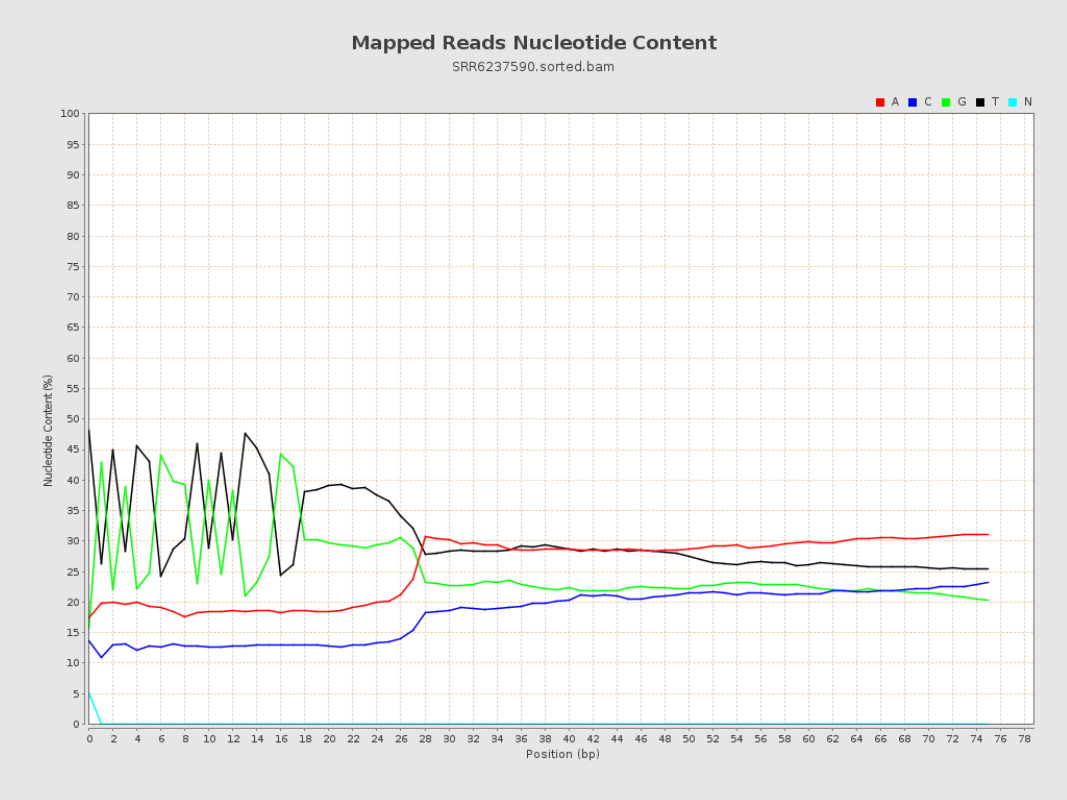
6. Results : Genome Fraction Coverage



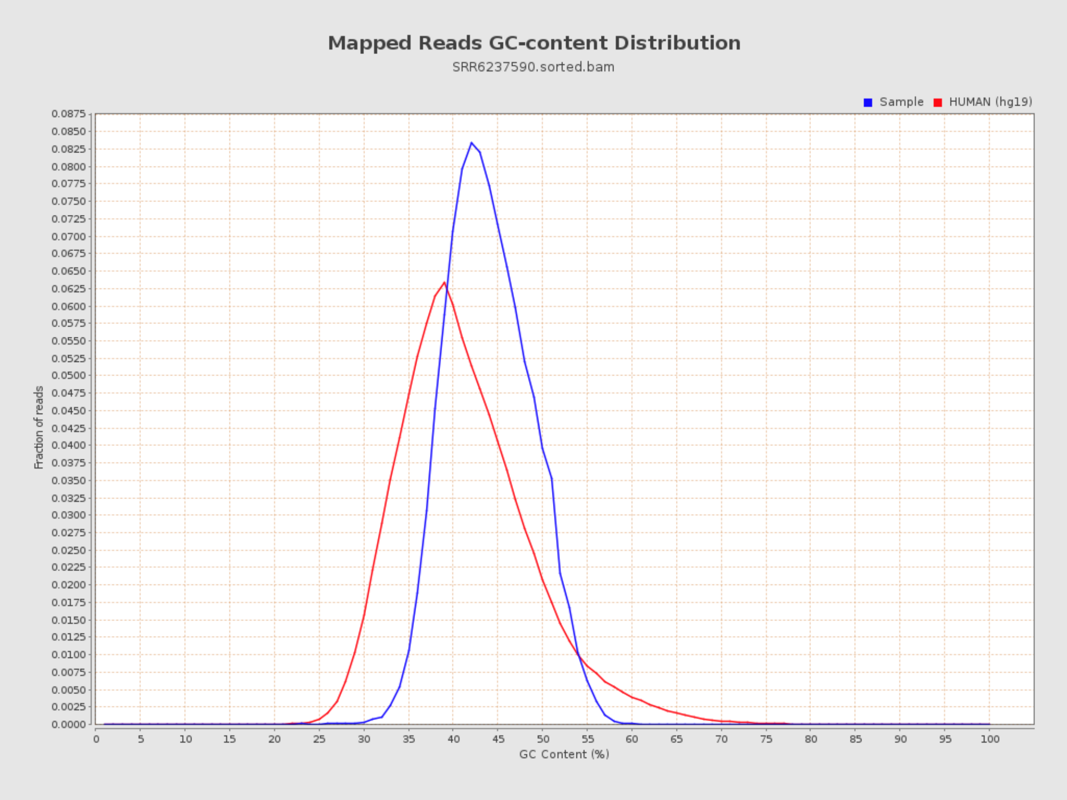
7. Results : Duplication Rate Histogram



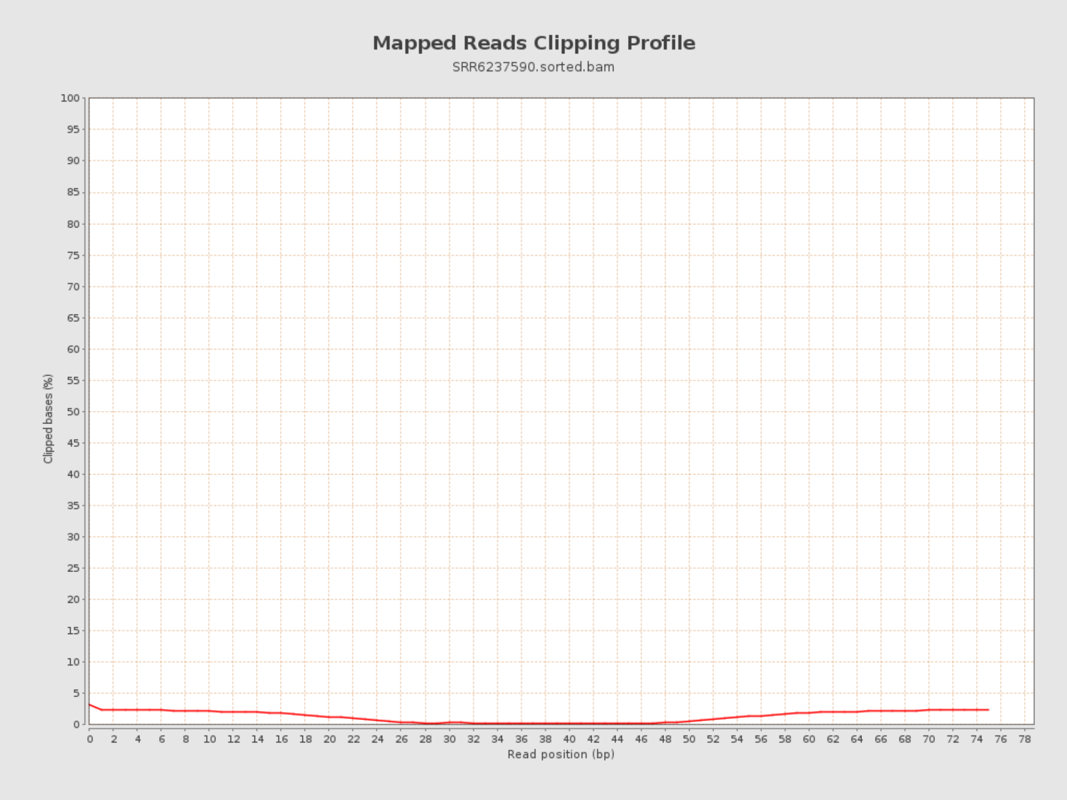
8. Results : Mapped Reads Nucleotide Content



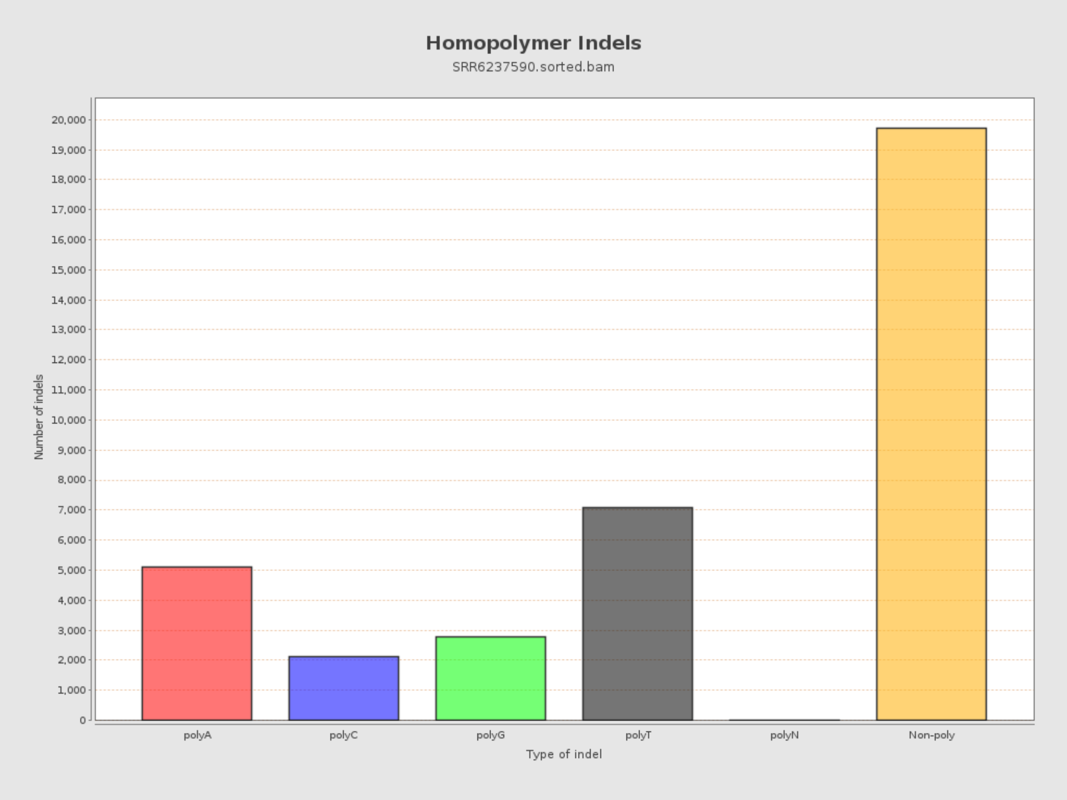
9. Results : Mapped Reads GC-content Distribution



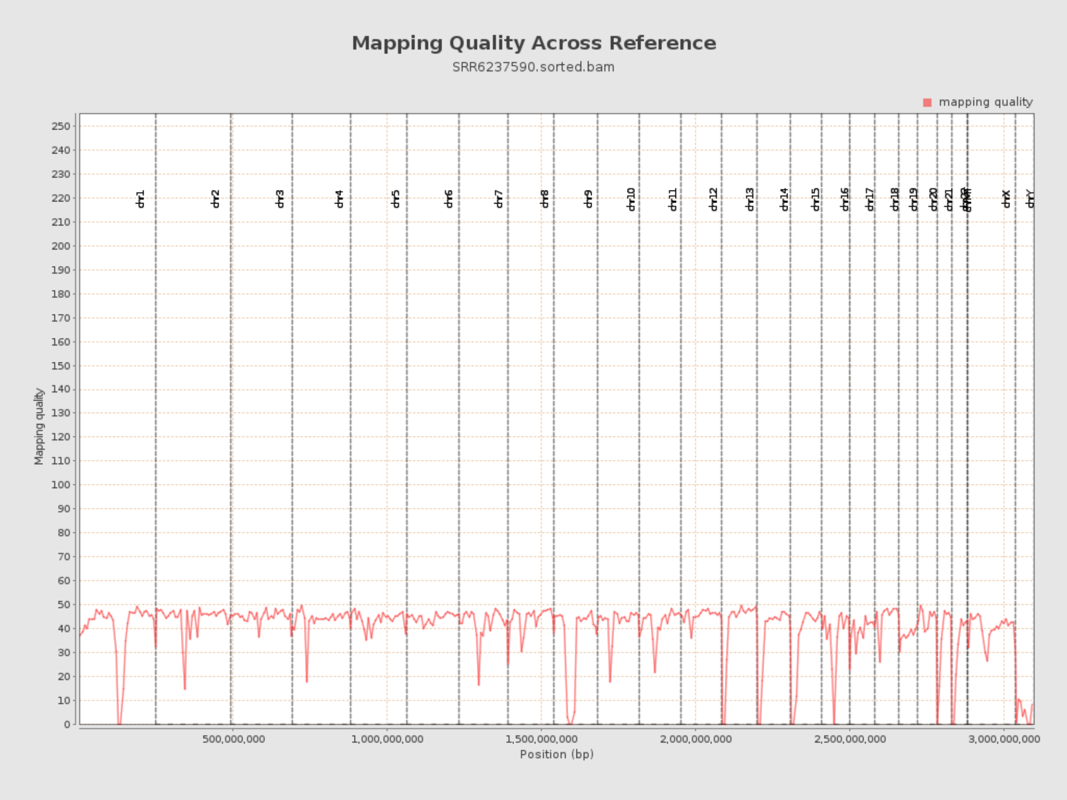
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram