Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 00:36:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237291.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_SRR6237291 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237291.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 00:36:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237291.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,691,510
Mapped reads	2,500,426 / 92.9%
Unmapped reads	191,084 / 7.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,439 / 0.61%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	119,429 / 4.44%
Duplication rate	3.12%
Clipped reads	743,720 / 27.63%

2.2. ACGT Content

Number/percentage of A's	51,756,082 / 29.43%
Number/percentage of C's	33,610,049 / 19.11%
Number/percentage of T's	54,336,948 / 30.9%
Number/percentage of G's	36,138,970 / 20.55%
Number/percentage of N's	2,913 / 0%
GC Percentage	39.67%

2.3. Coverage

Mean	0.0568

Standard Deviation	0.6795

2.4. Mapping Quality

Mean Mapping Quality	46

2.5. Mismatches and indels

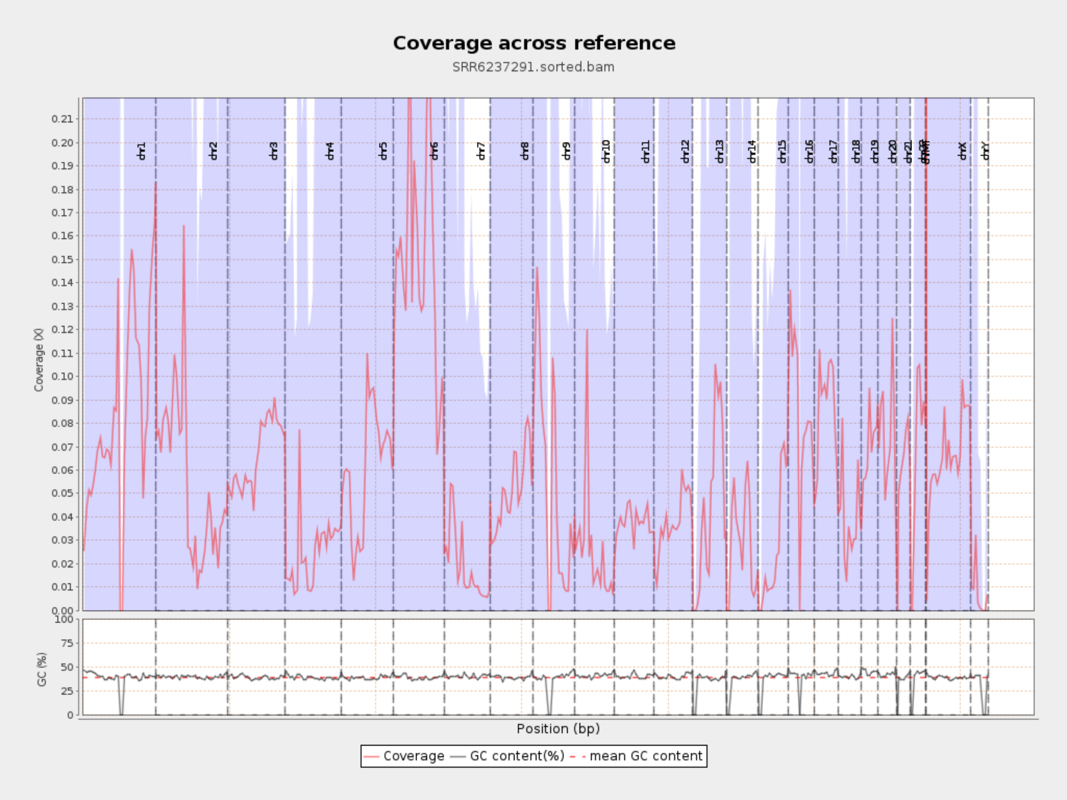
General error rate	0.83%
Mismatches	1,427,984
Insertions	15,048
Mapped reads with at least one insertion	0.6%
Deletions	55,986
Mapped reads with at least one deletion	2.21%
Homopolymer indels	45.9%

2.6. Chromosome stats

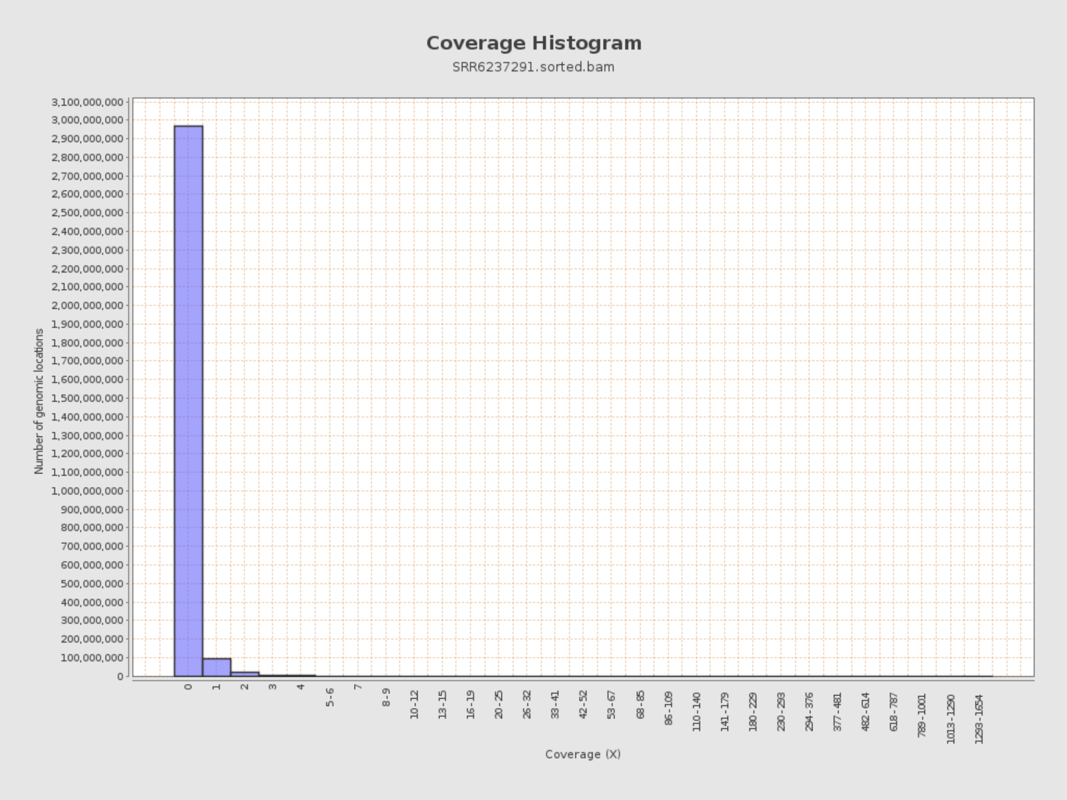
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	20951795	0.0841	1.3875
chr2	243199373	13494480	0.0555	0.6978
chr3	198022430	13151656	0.0664	0.3421
chr4	191154276	4805383	0.0251	0.3632
chr5	180915260	11057490	0.0611	0.3327
chr6	171115067	26215332	0.1532	1.0506
chr7	159138663	2948016	0.0185	0.4382

chr8	146364022	7635868	0.0522	0.5904
chr9	141213431	7711631	0.0546	0.6734
chr10	135534747	3441631	0.0254	0.662
chr11	135006516	5112086	0.0379	0.4704
chr12	133851895	5019033	0.0375	0.2747
chr13	115169878	5063563	0.044	0.2717
chr14	107349540	3207995	0.0299	0.2967
chr15	102531392	2572449	0.0251	0.2038
chr16	90354753	7486801	0.0829	0.4797
chr17	81195210	7105328	0.0875	0.5751
chr18	78077248	3036324	0.0389	1.3905
chr19	59128983	4082443	0.069	0.9202
chr20	63025520	4864138	0.0772	0.3772
chr21	48129895	2887799	0.06	0.426
chr22	51304566	3385024	0.066	0.3291
chrMT	16571	102599	6.1915	4.8944
chrX	155270560	10144492	0.0653	0.3954
chrY	59373566	460999	0.0078	0.3317

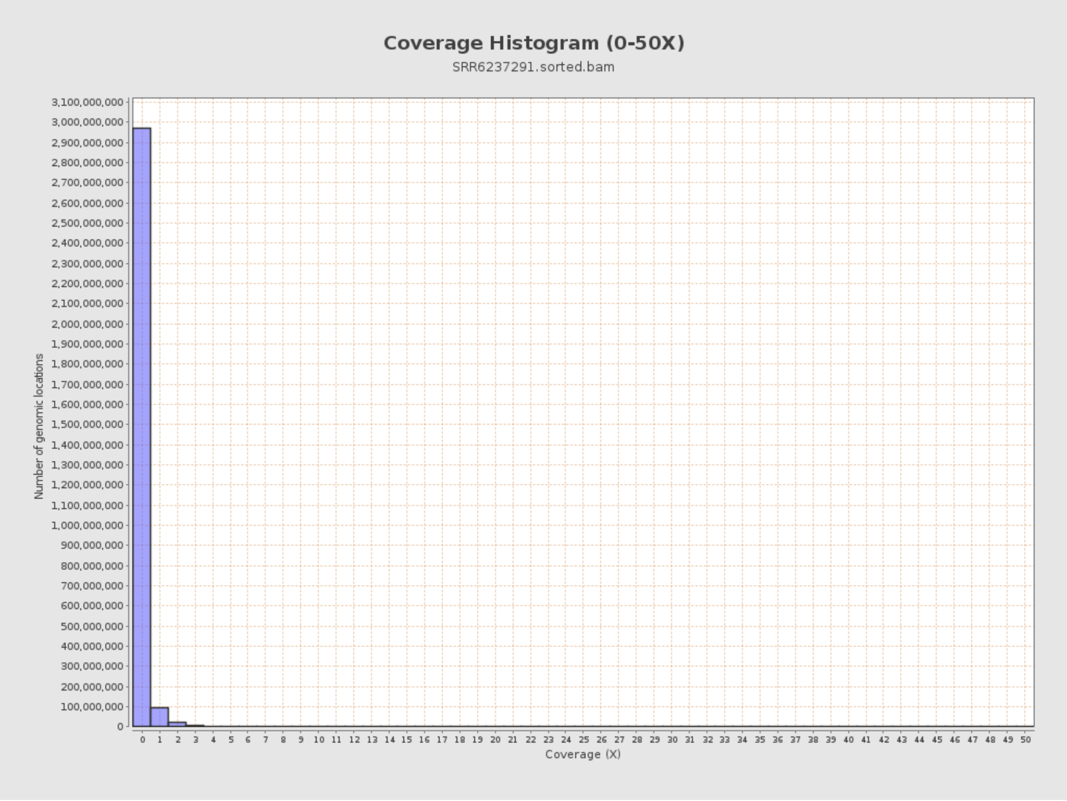
3. Results : Coverage across reference



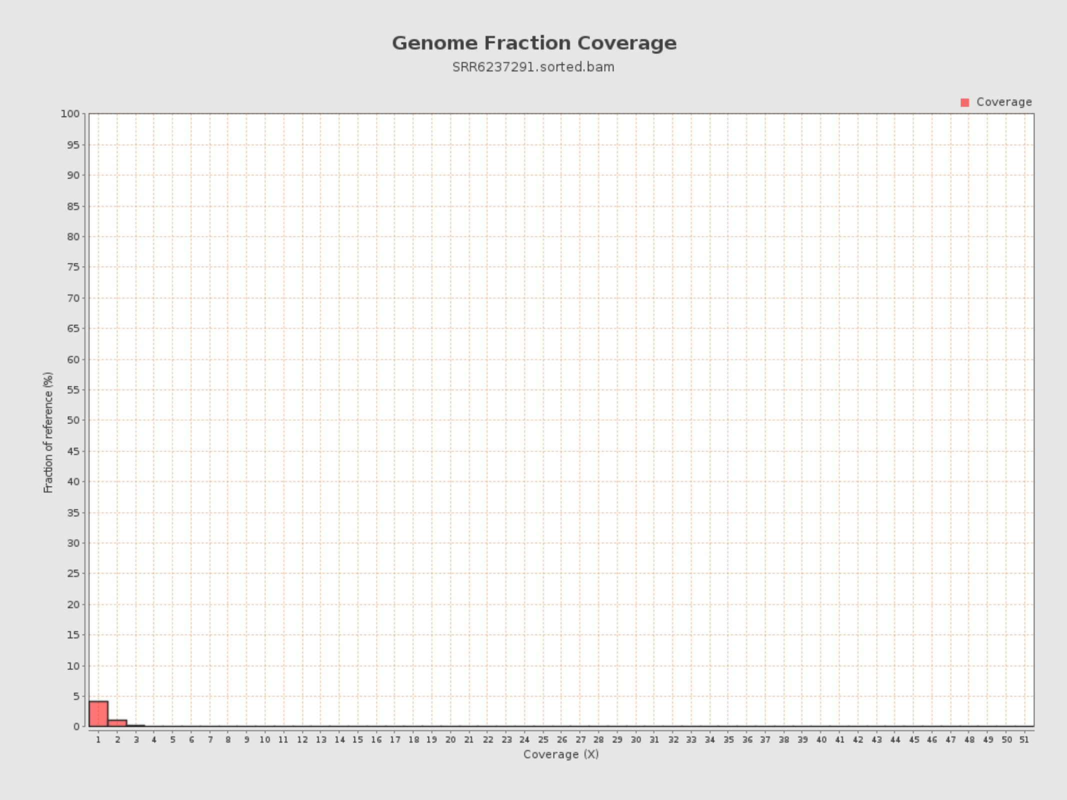
4. Results : Coverage Histogram



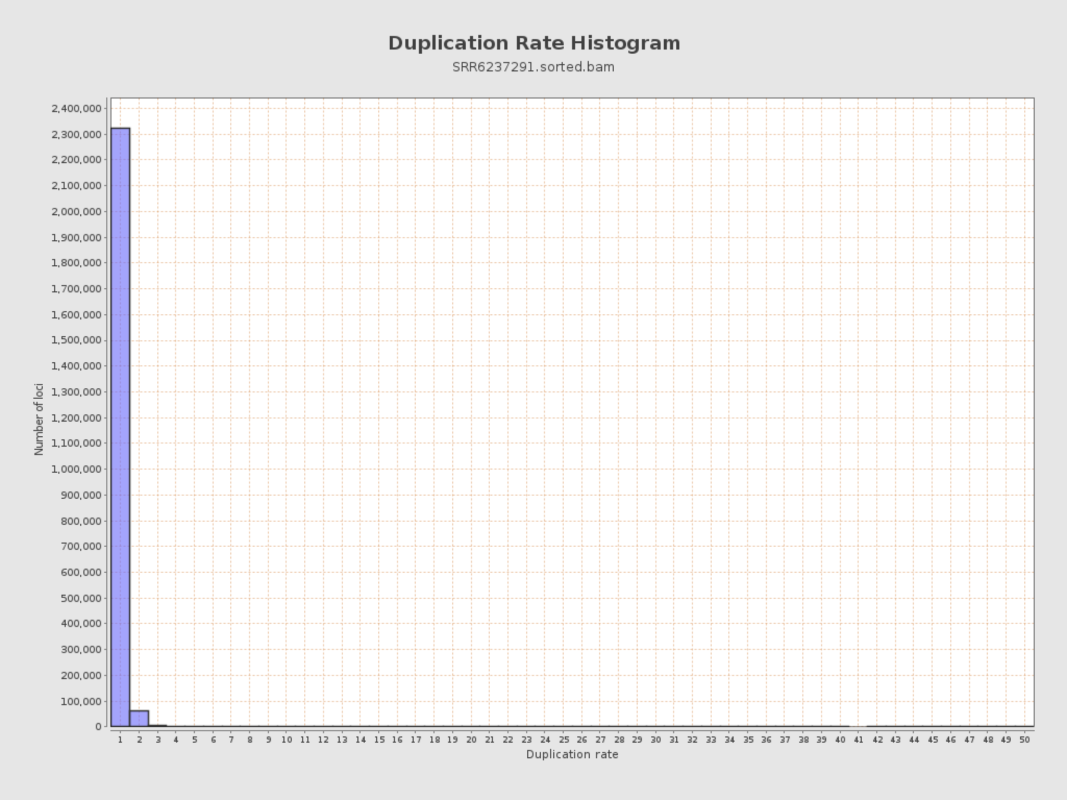
5. Results : Coverage Histogram (0-50X)



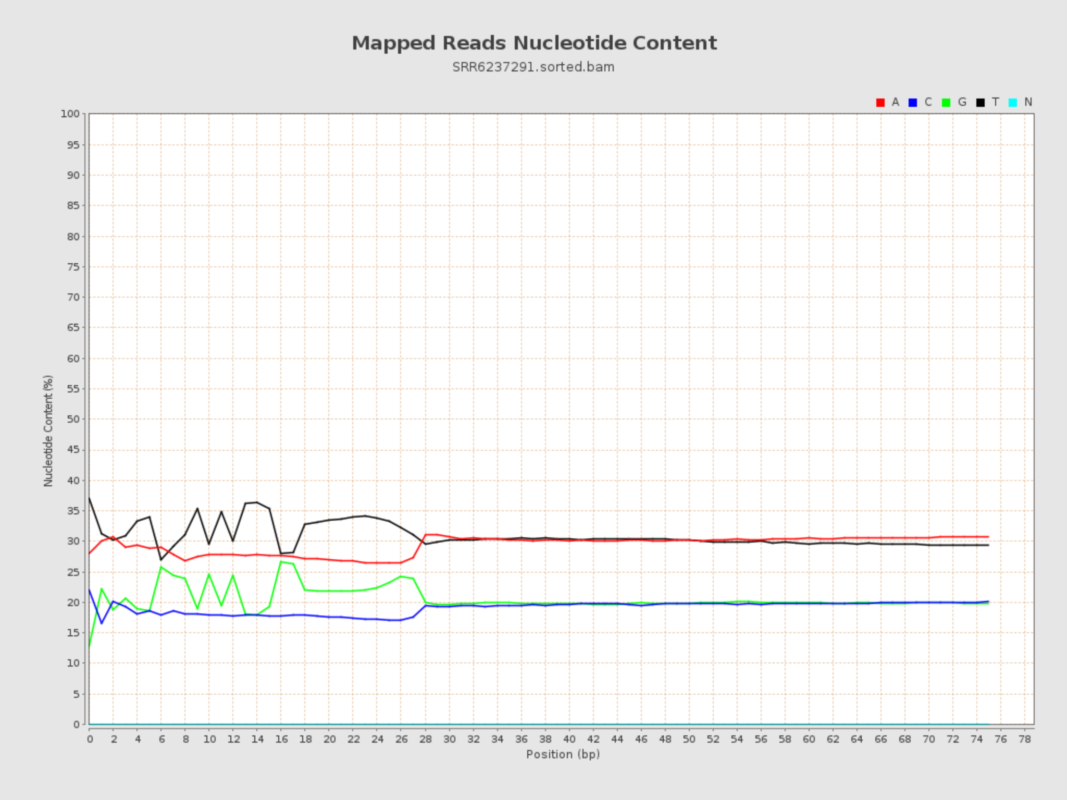
6. Results : Genome Fraction Coverage



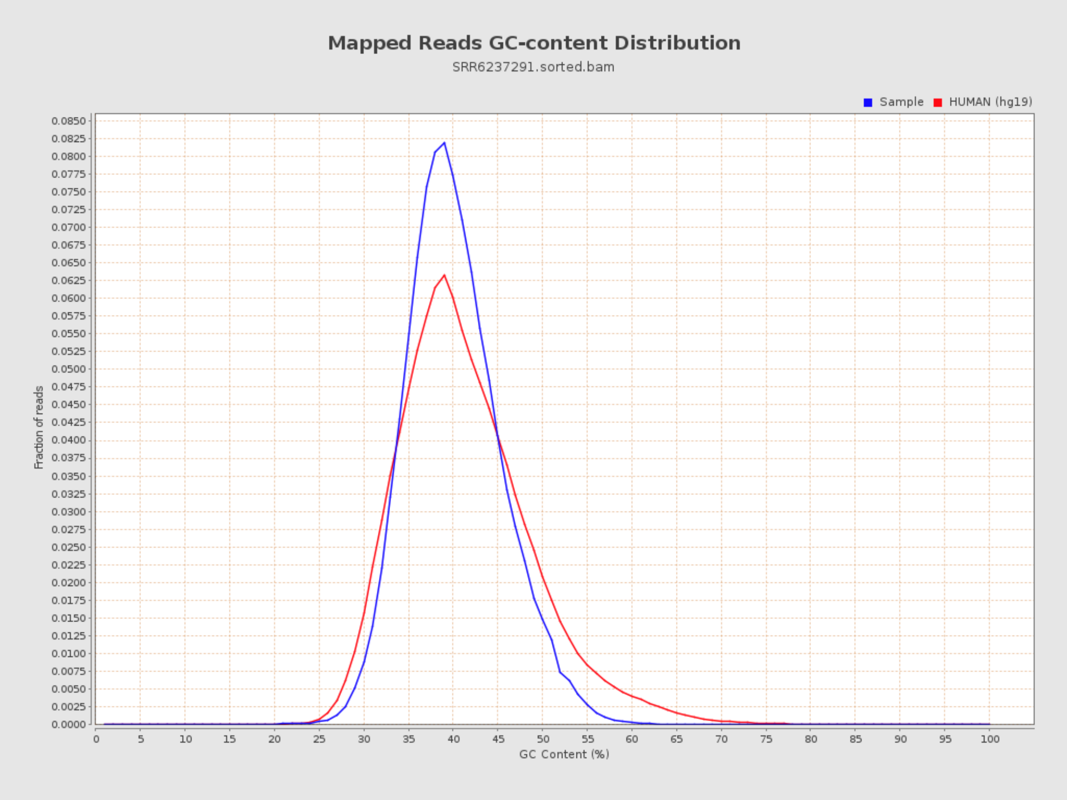
7. Results : Duplication Rate Histogram



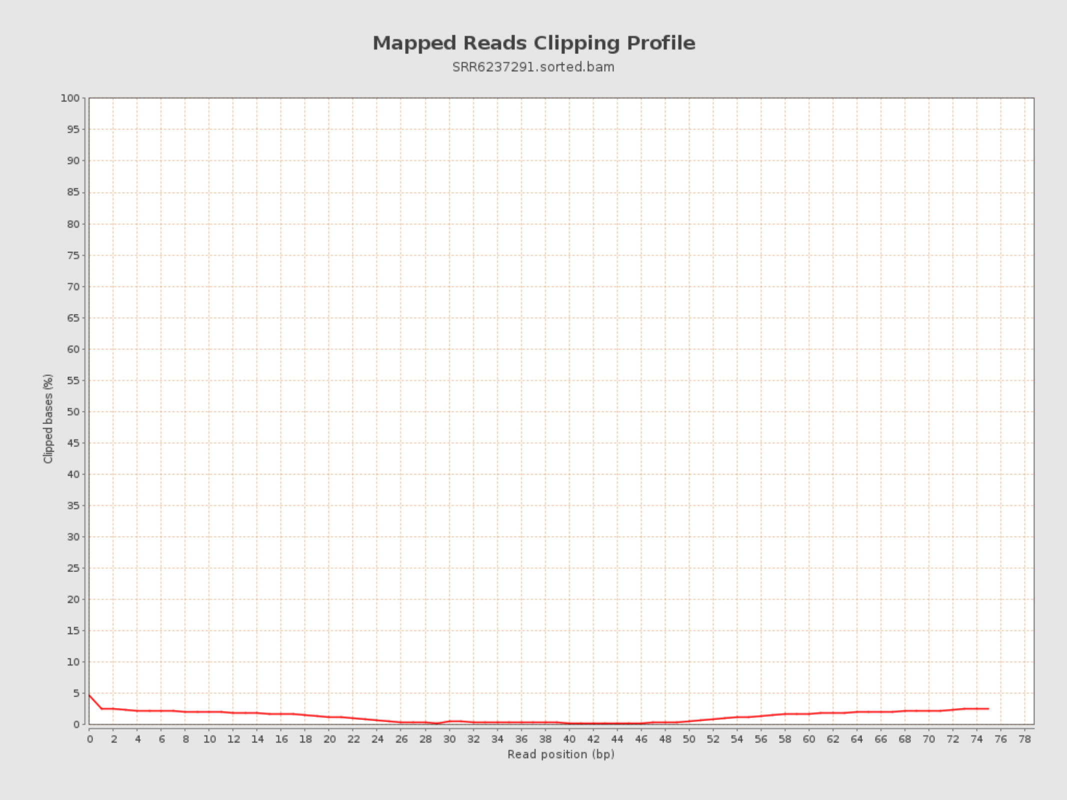
8. Results : Mapped Reads Nucleotide Content



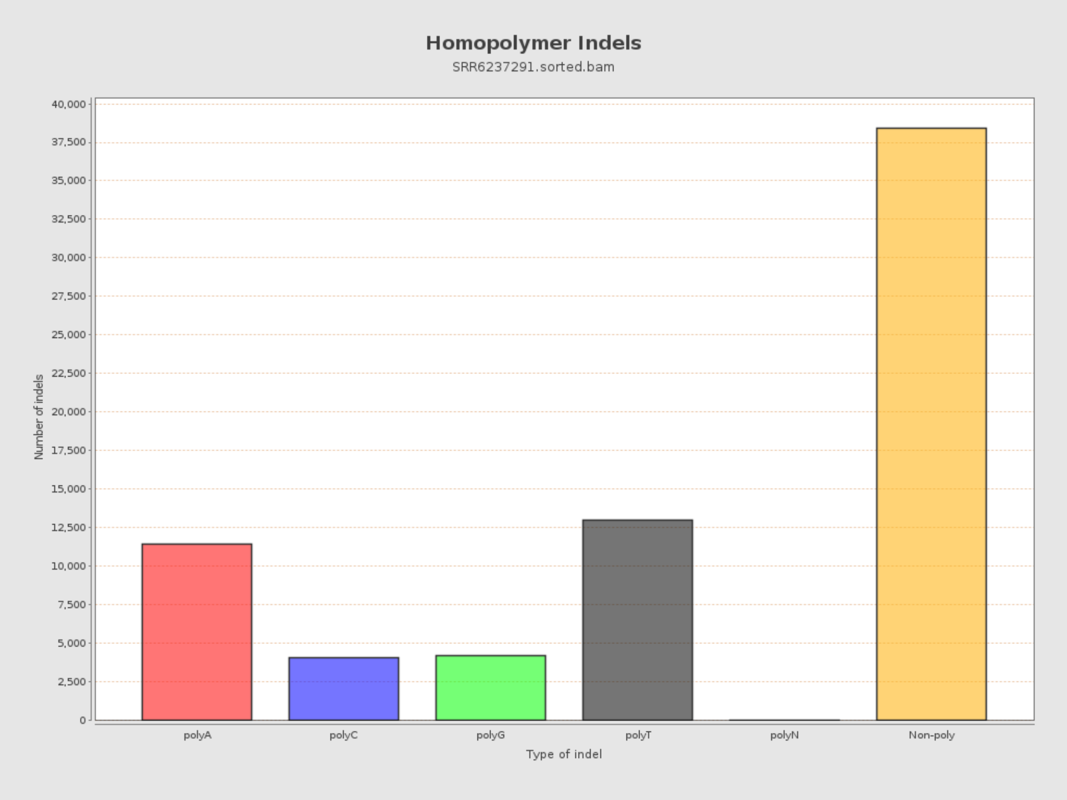
9. Results : Mapped Reads GC-content Distribution



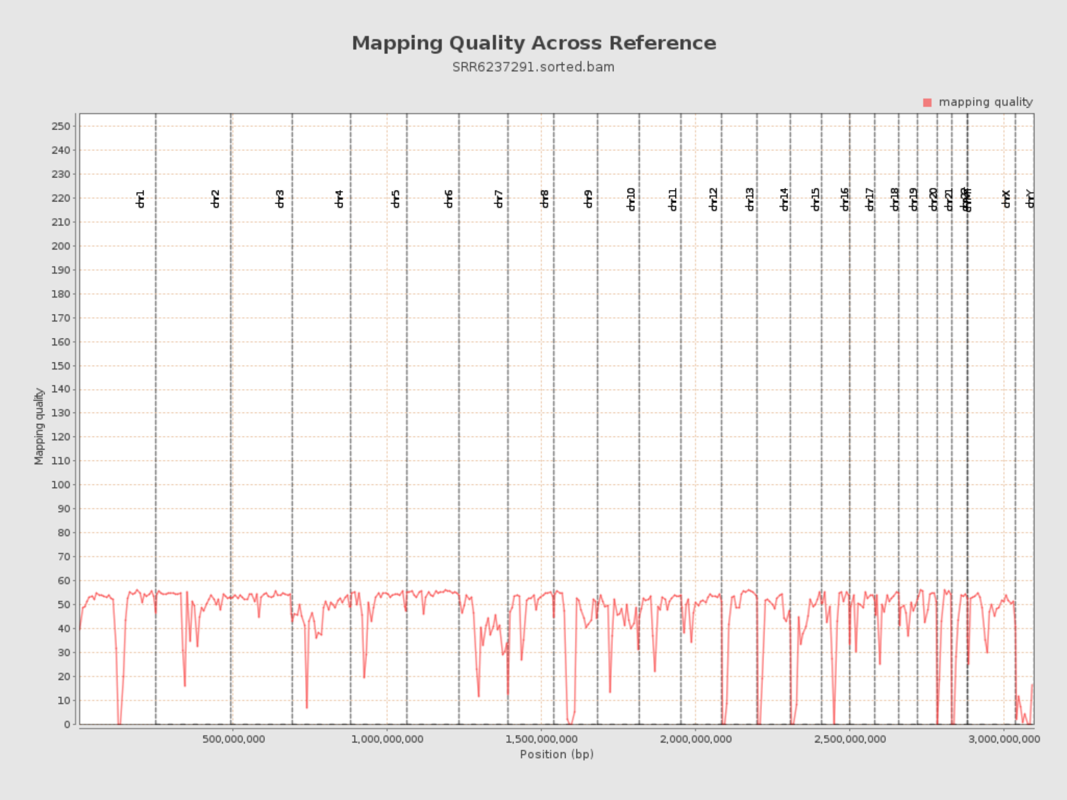
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram