Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 07:59:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237831.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_SRR6237831 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237831.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 07:59:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237831.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,721,626
Mapped reads	1,316,448 / 76.47%
Unmapped reads	405,178 / 23.53%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,599 / 0.79%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	266,594 / 15.49%
Duplication rate	12.89%
Clipped reads	639,978 / 37.17%

2.2. ACGT Content

Number/percentage of A's	23,556,420 / 27.26%
Number/percentage of C's	15,981,071 / 18.49%
Number/percentage of T's	27,315,545 / 31.61%
Number/percentage of G's	19,417,419 / 22.47%
Number/percentage of N's	140,703 / 0.16%
GC Percentage	40.97%

2.3. Coverage

Mean	0.0279

Standard Deviation	0.4347

2.4. Mapping Quality

Mean Mapping Quality	45.4

2.5. Mismatches and indels

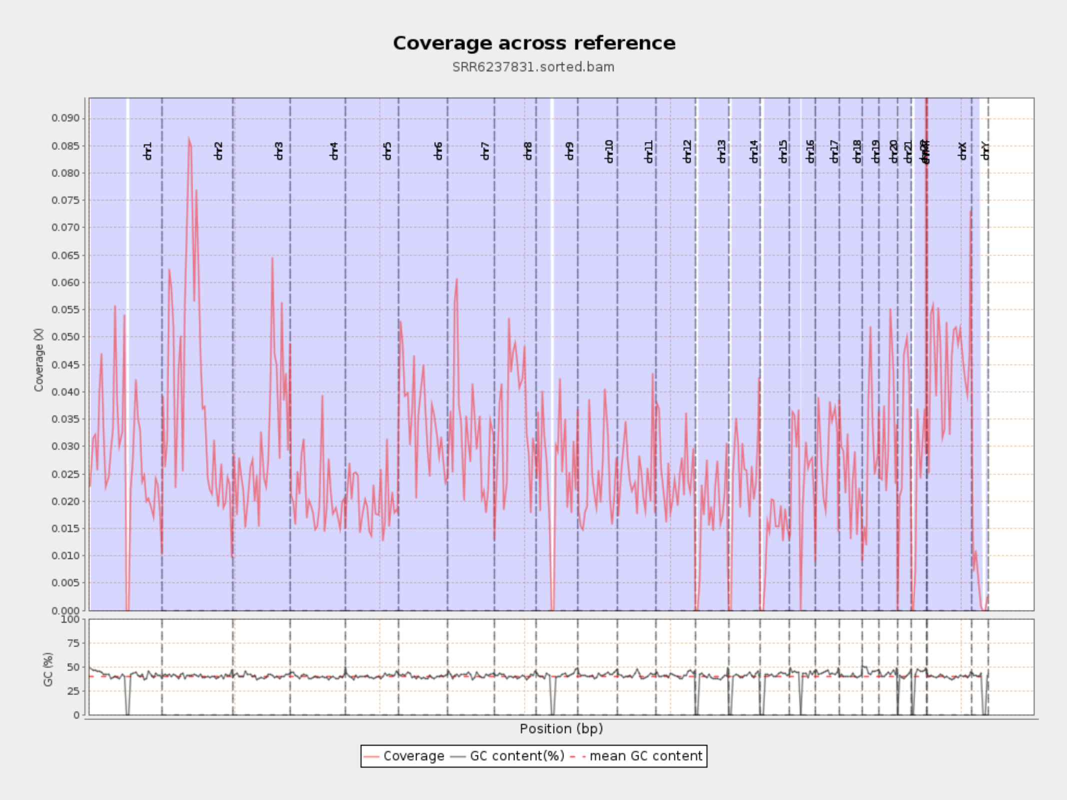
General error rate	0.86%
Mismatches	734,046
Insertions	5,912
Mapped reads with at least one insertion	0.45%
Deletions	22,264
Mapped reads with at least one deletion	1.67%
Homopolymer indels	46.65%

2.6. Chromosome stats

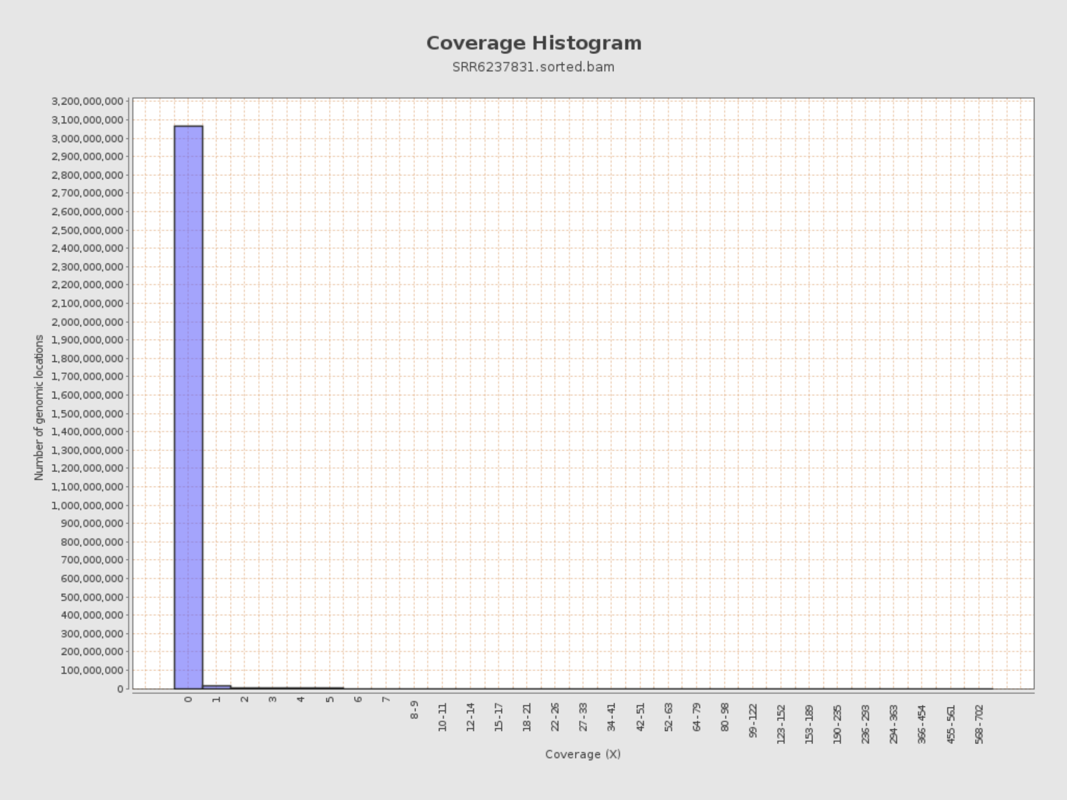
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6998618	0.0281	0.7155
chr2	243199373	9899752	0.0407	0.5555
chr3	198022430	6072512	0.0307	0.3951
chr4	191154276	3958447	0.0207	0.3127
chr5	180915260	3596656	0.0199	0.3052
chr6	171115067	6011026	0.0351	0.4447
chr7	159138663	5207658	0.0327	0.4261

chr8	146364022	5208185	0.0356	0.4568
chr9	141213431	3521731	0.0249	0.3775
chr10	135534747	3145891	0.0232	0.3752
chr11	135006516	3362266	0.0249	0.3644
chr12	133851895	3369235	0.0252	0.3483
chr13	115169878	2009825	0.0175	0.302
chr14	107349540	2449794	0.0228	0.3383
chr15	102531392	1383502	0.0135	0.2546
chr16	90354753	2309470	0.0256	0.3641
chr17	81195210	2333952	0.0287	0.3881
chr18	78077248	1897972	0.0243	0.5029
chr19	59128983	1695046	0.0287	0.4501
chr20	63025520	2060014	0.0327	0.4144
chr21	48129895	1494224	0.031	0.3976
chr22	51304566	1112807	0.0217	0.3272
chrMT	16571	80970	4.8862	4.5236
chrX	155270560	6988034	0.045	0.494
chrY	59373566	282094	0.0048	0.1368

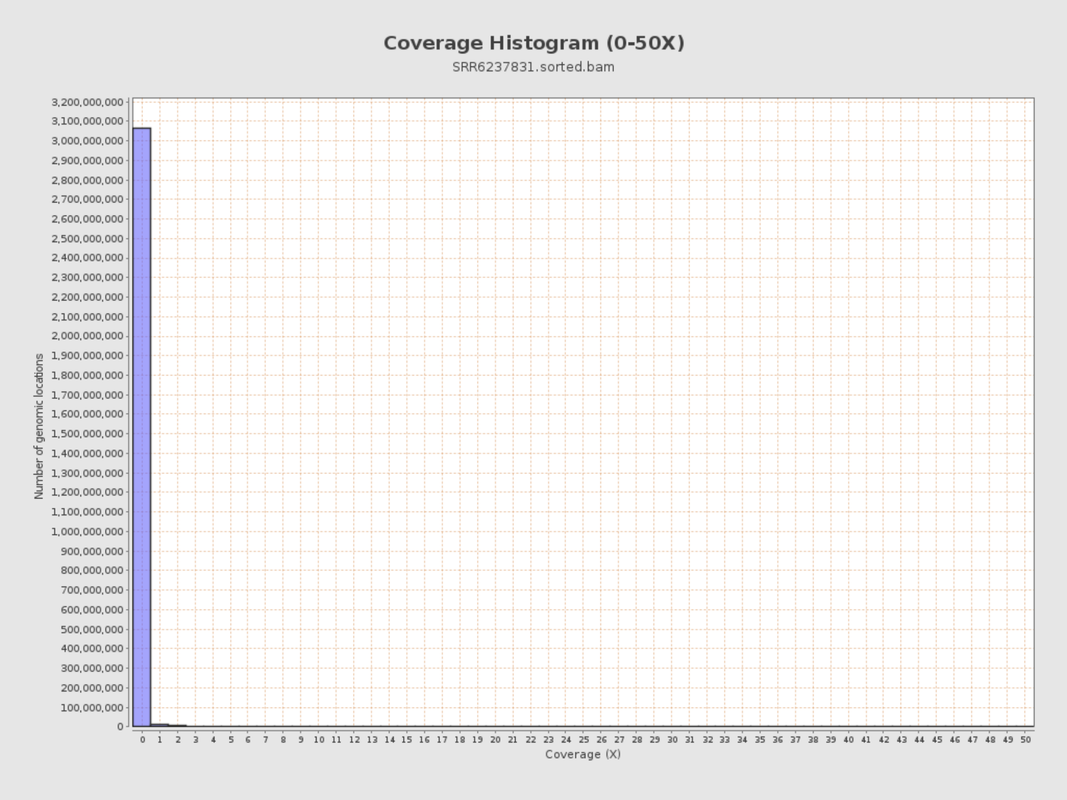
3. Results : Coverage across reference



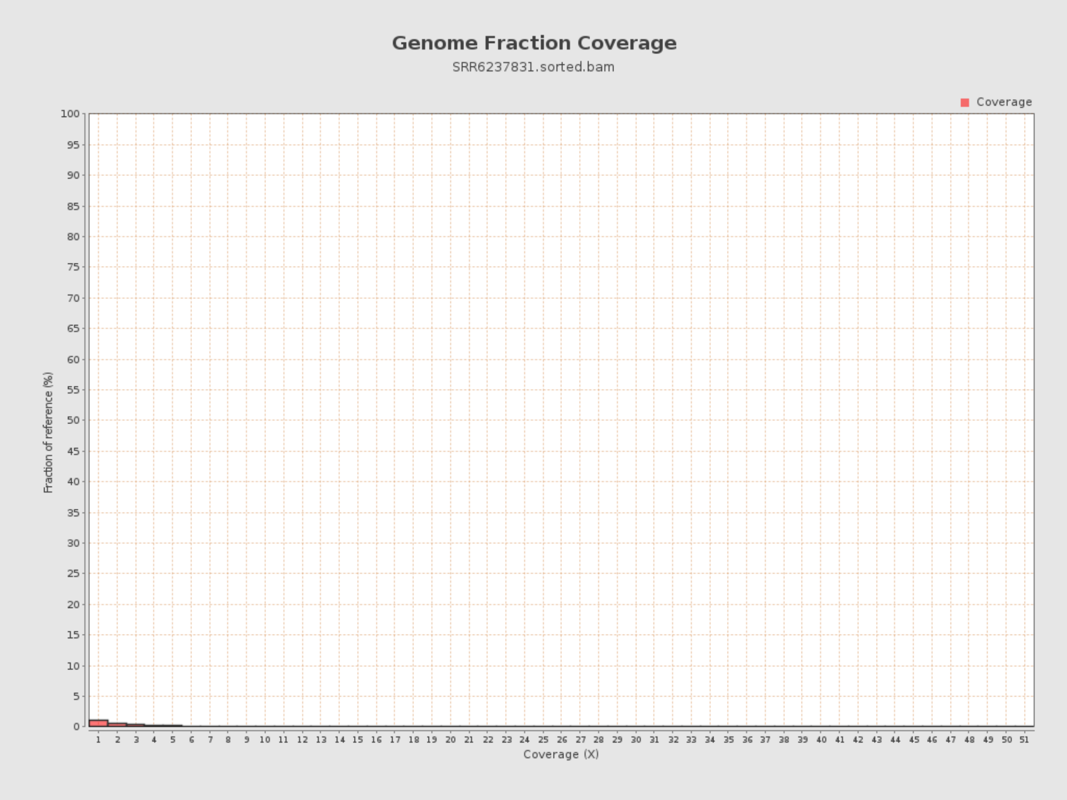
4. Results : Coverage Histogram



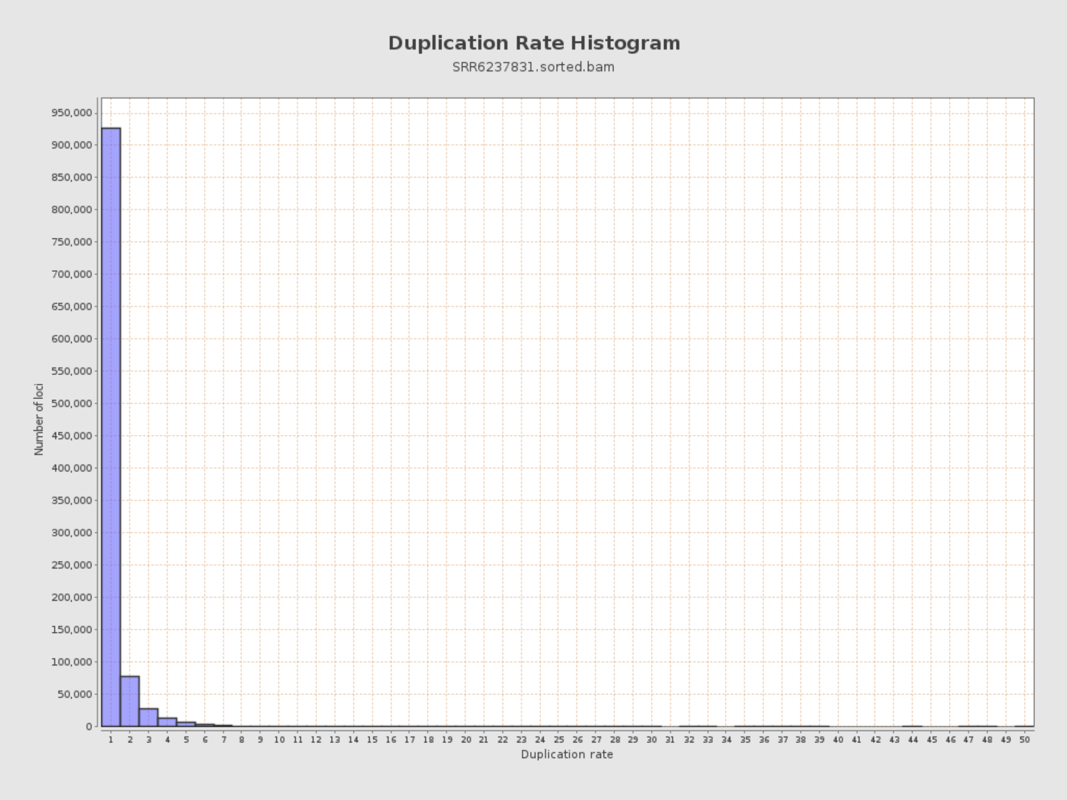
5. Results : Coverage Histogram (0-50X)



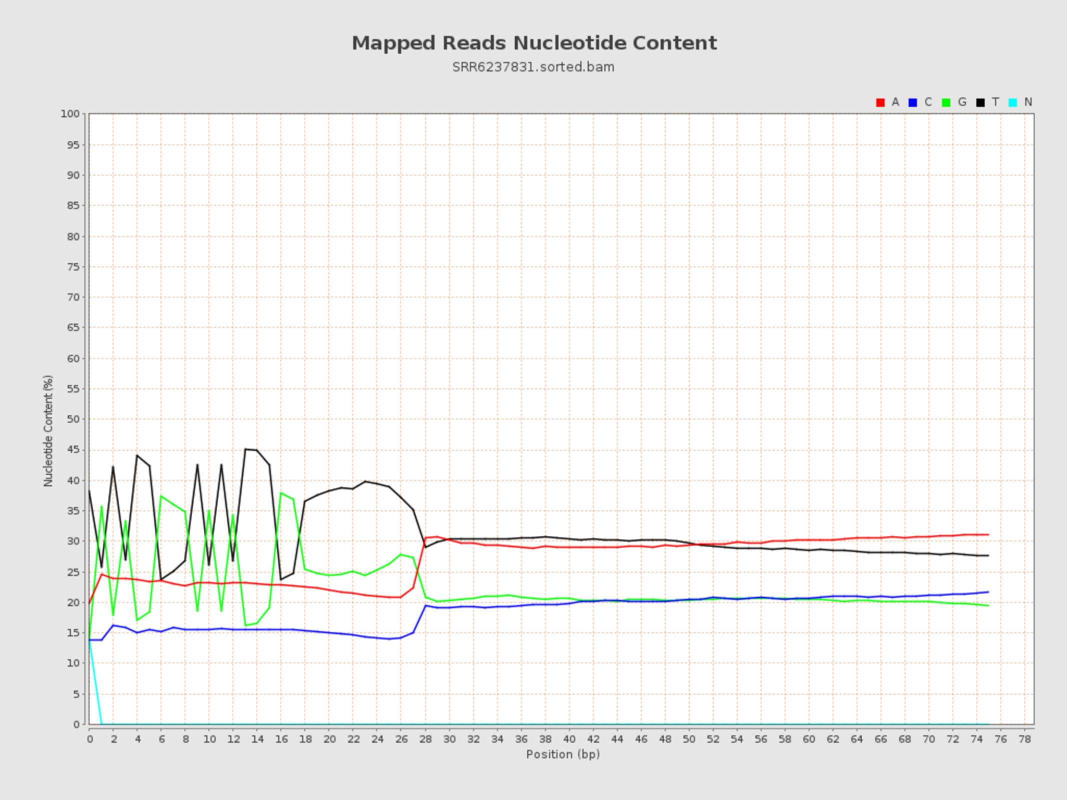
6. Results : Genome Fraction Coverage



7. Results : Duplication Rate Histogram



8. Results : Mapped Reads Nucleotide Content



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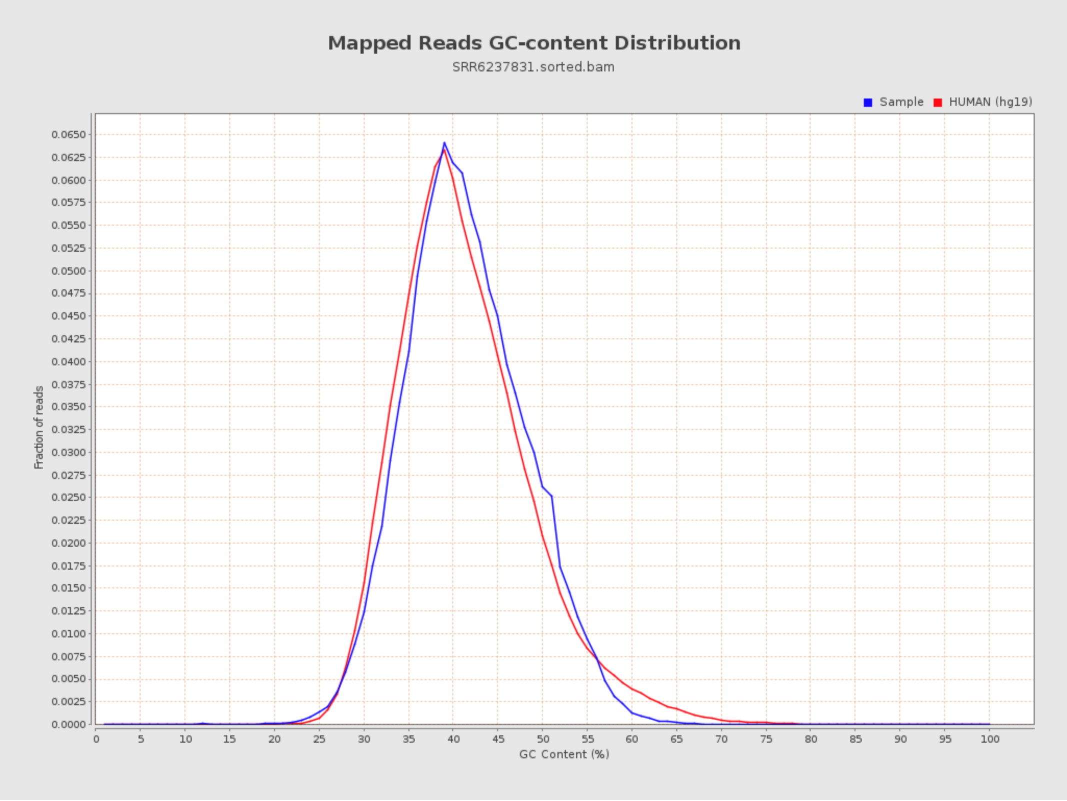
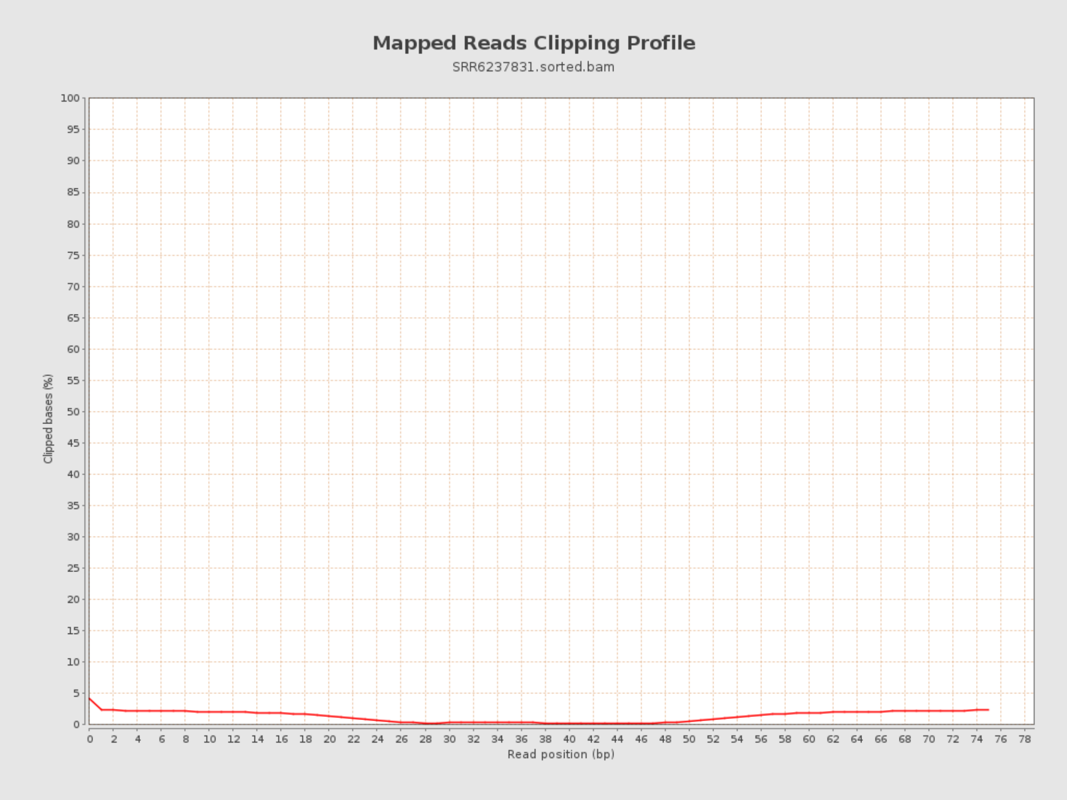
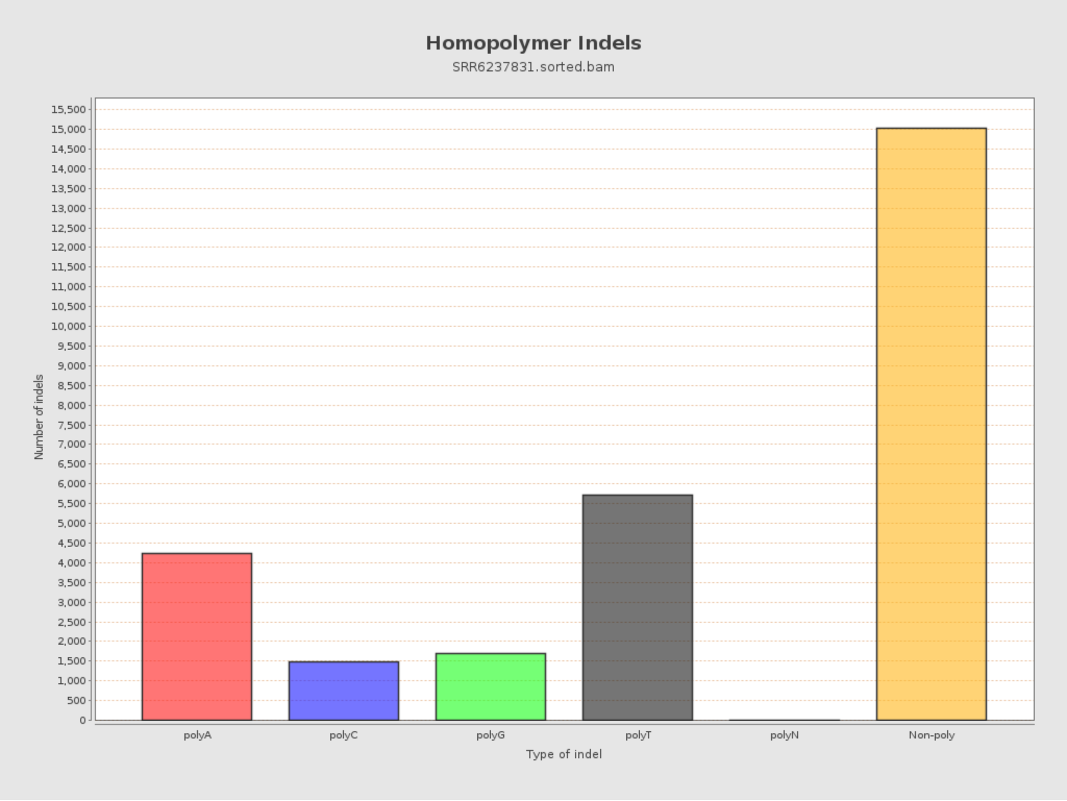
9. Results : Mapped Reads GC-content Distribution



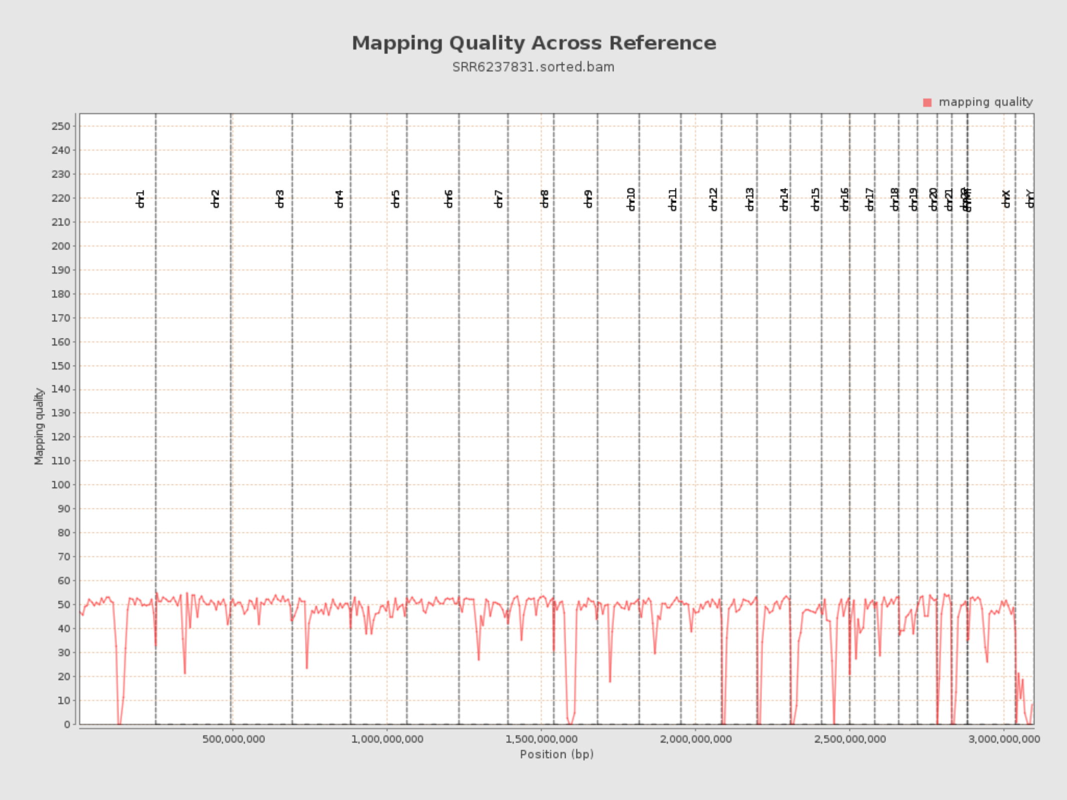
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram