Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 23:22:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237268.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_SRR6237268 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237268.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 23:22:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237268.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,507,372
Mapped reads	2,198,093 / 87.67%
Unmapped reads	309,279 / 12.33%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,792 / 0.71%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	127,208 / 5.07%
Duplication rate	4.78%
Clipped reads	1,012,970 / 40.4%

2.2. ACGT Content

Number/percentage of A's	40,817,791 / 28.03%
Number/percentage of C's	26,056,221 / 17.89%
Number/percentage of T's	47,106,719 / 32.35%
Number/percentage of G's	31,650,731 / 21.73%
Number/percentage of N's	2,352 / 0%
GC Percentage	39.62%

2.3. Coverage

Mean	0.0471

Standard Deviation	0.3825

2.4. Mapping Quality

Mean Mapping Quality	44.69

2.5. Mismatches and indels

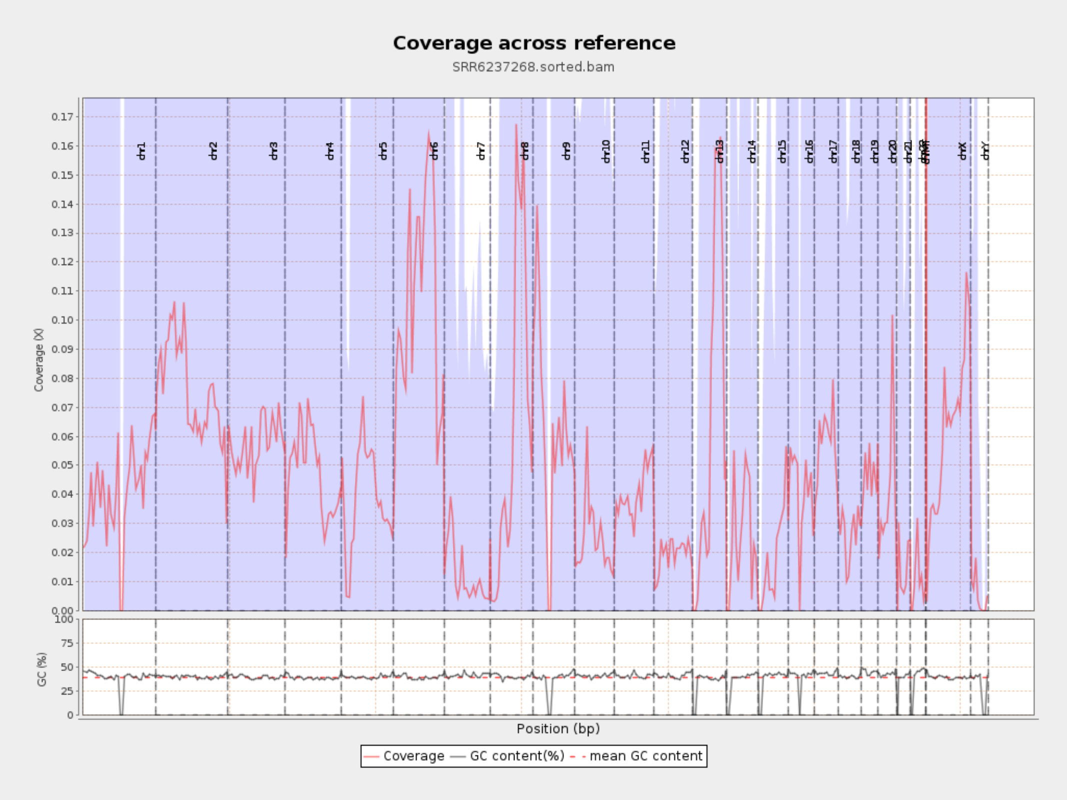
General error rate	0.77%
Mismatches	1,095,742
Insertions	10,284
Mapped reads with at least one insertion	0.46%
Deletions	39,080
Mapped reads with at least one deletion	1.76%
Homopolymer indels	47.05%

2.6. Chromosome stats

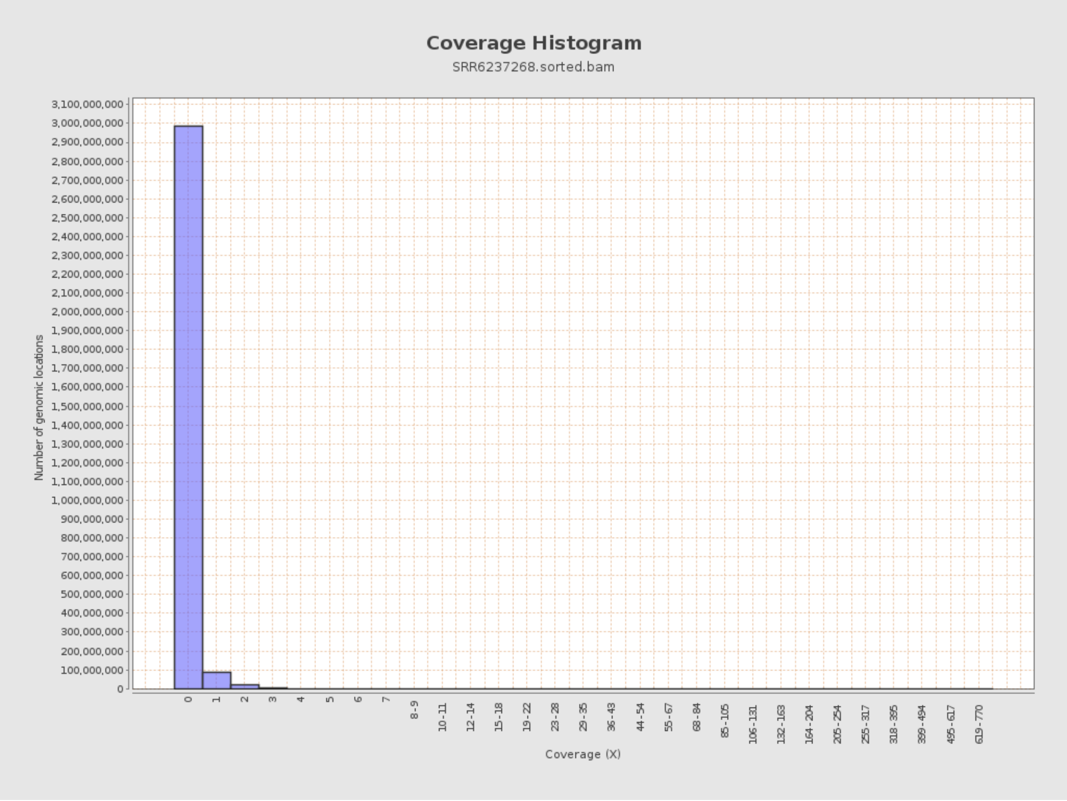
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10263564	0.0412	0.6255
chr2	243199373	18632876	0.0766	0.4849
chr3	198022430	11350858	0.0573	0.2948
chr4	191154276	9025095	0.0472	0.2987
chr5	180915260	7059904	0.039	0.2456
chr6	171115067	18630185	0.1089	0.53
chr7	159138663	1931799	0.0121	0.1573

chr8	146364022	9378830	0.0641	0.5529
chr9	141213431	8969275	0.0635	0.4207
chr10	135534747	3287079	0.0243	0.3246
chr11	135006516	5403372	0.04	0.2986
chr12	133851895	2576830	0.0193	0.186
chr13	115169878	7571611	0.0657	0.325
chr14	107349540	2786655	0.026	0.2347
chr15	102531392	1939968	0.0189	0.1741
chr16	90354753	3589668	0.0397	0.2718
chr17	81195210	4712836	0.058	0.3239
chr18	78077248	2067251	0.0265	0.5654
chr19	59128983	2715888	0.0459	0.426
chr20	63025520	2683356	0.0426	0.2618
chr21	48129895	716691	0.0149	0.2133
chr22	51304566	511666	0.01	0.1191
chrMT	16571	66434	4.0091	3.177
chrX	155270560	9506052	0.0612	0.3326
chrY	59373566	324065	0.0055	0.1598

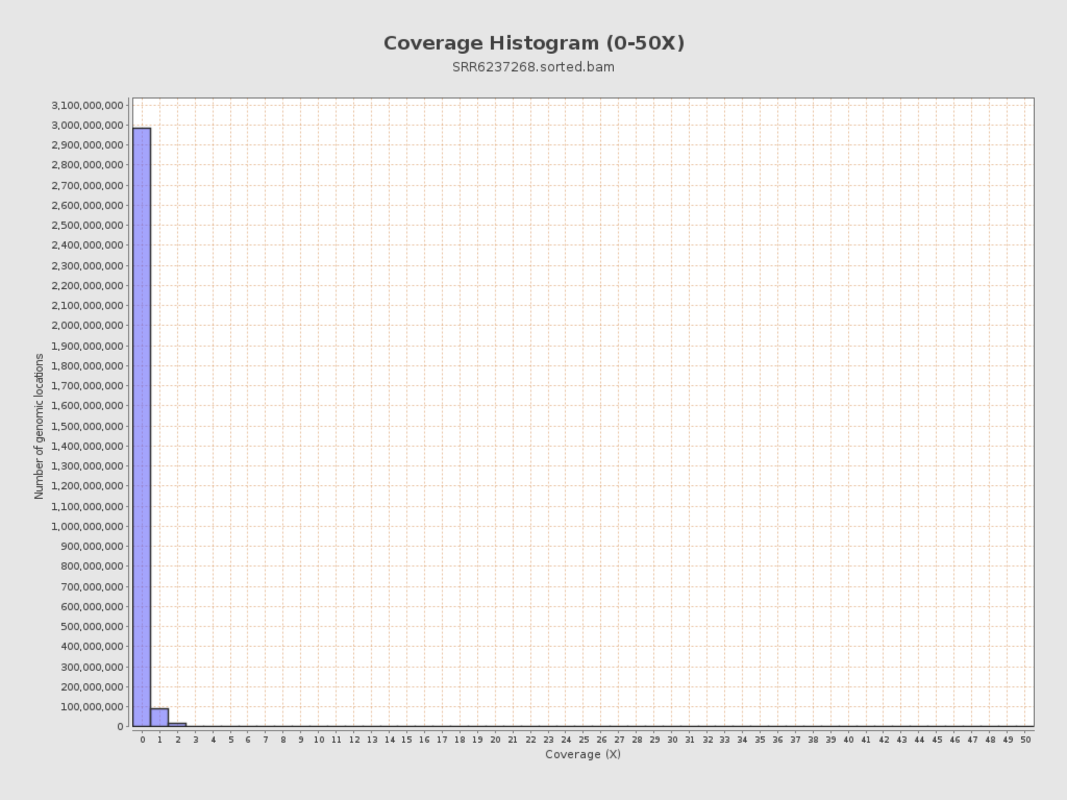
3. Results : Coverage across reference



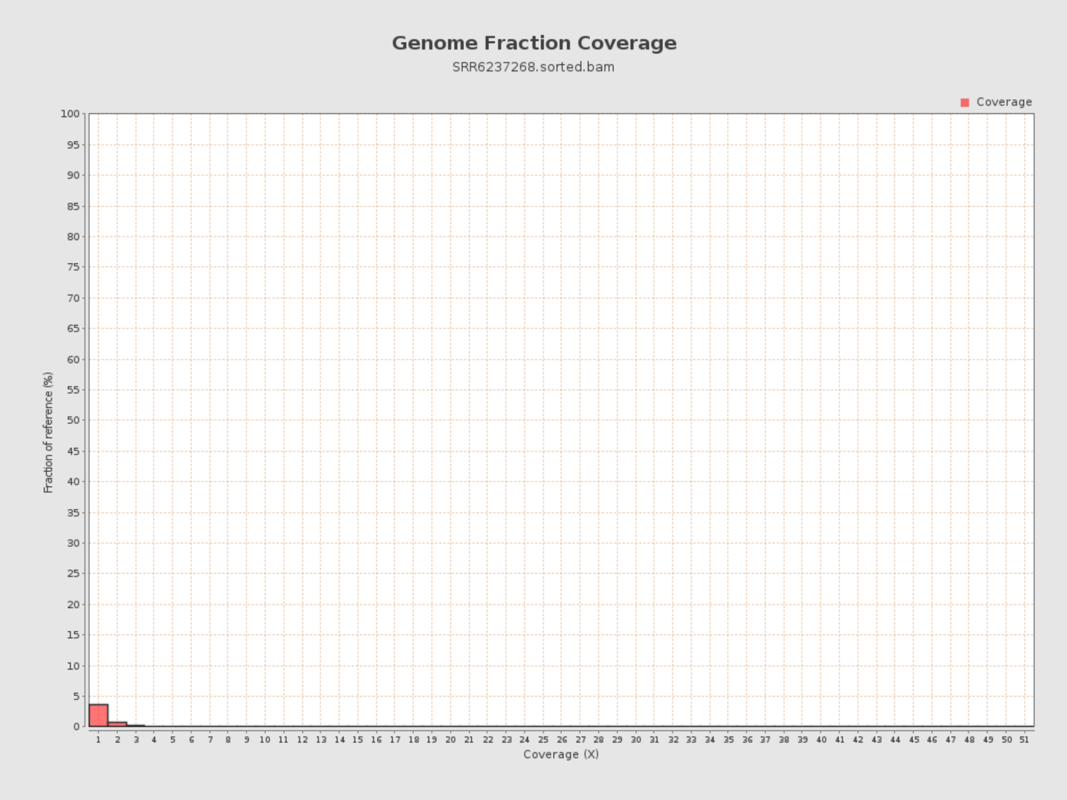
4. Results : Coverage Histogram



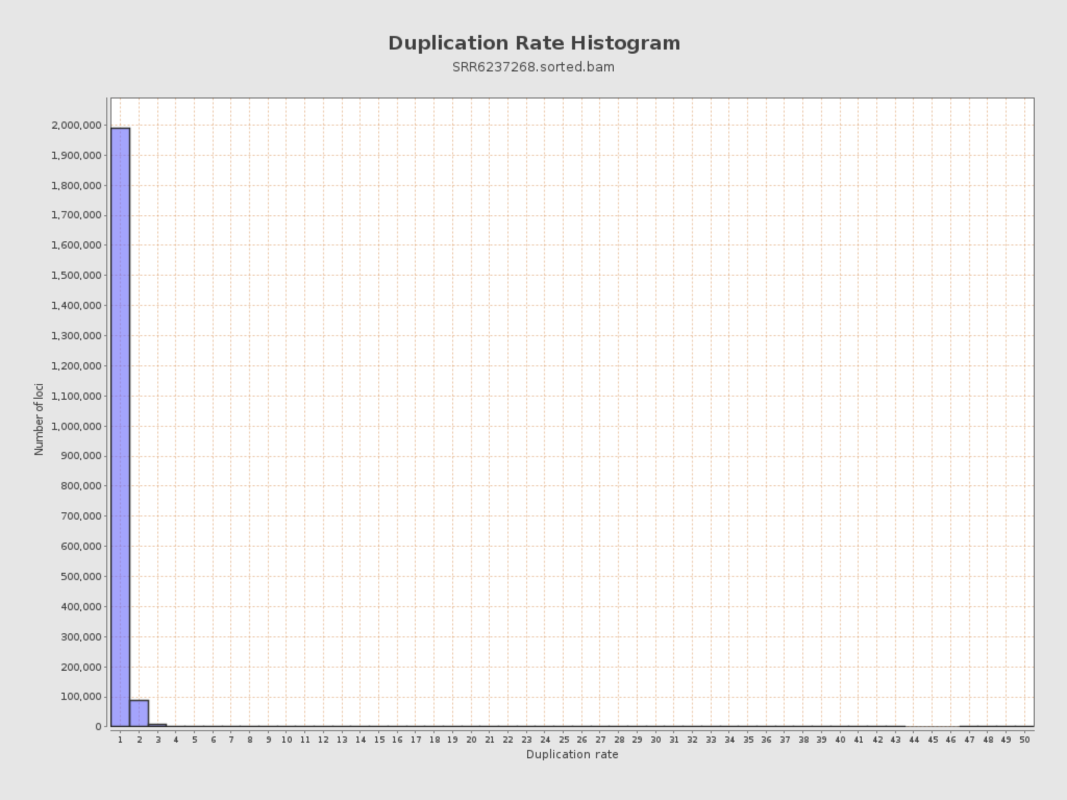
5. Results : Coverage Histogram (0-50X)



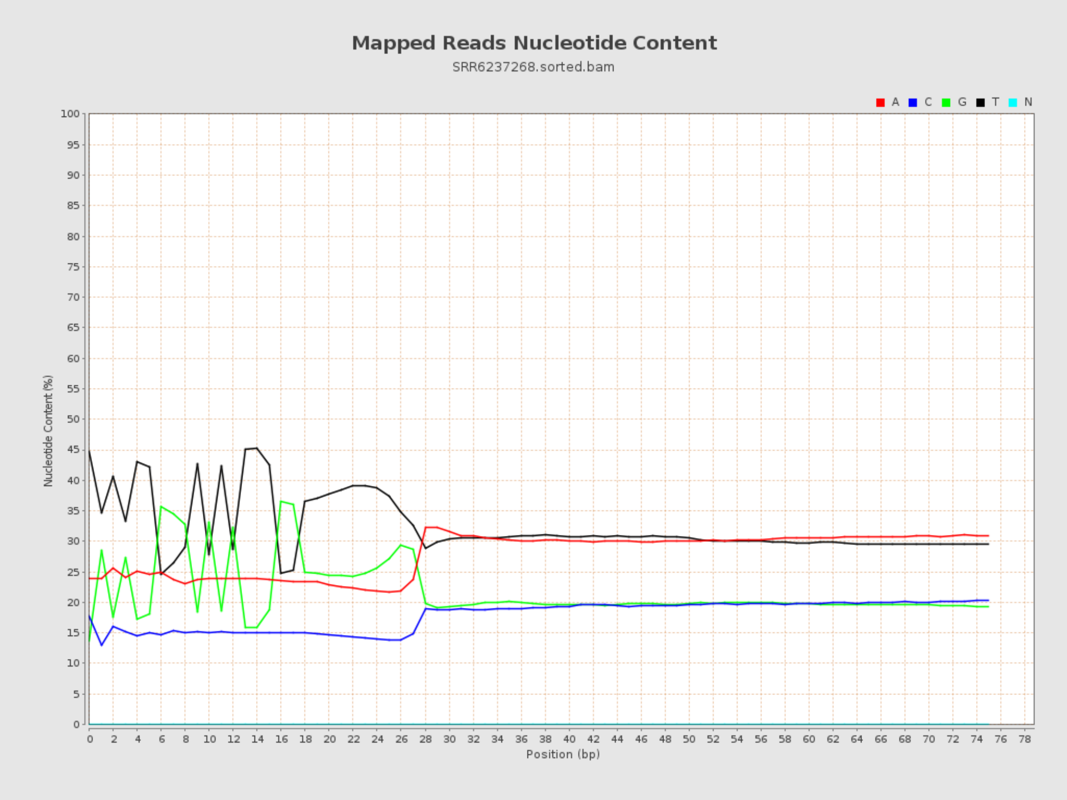
6. Results : Genome Fraction Coverage



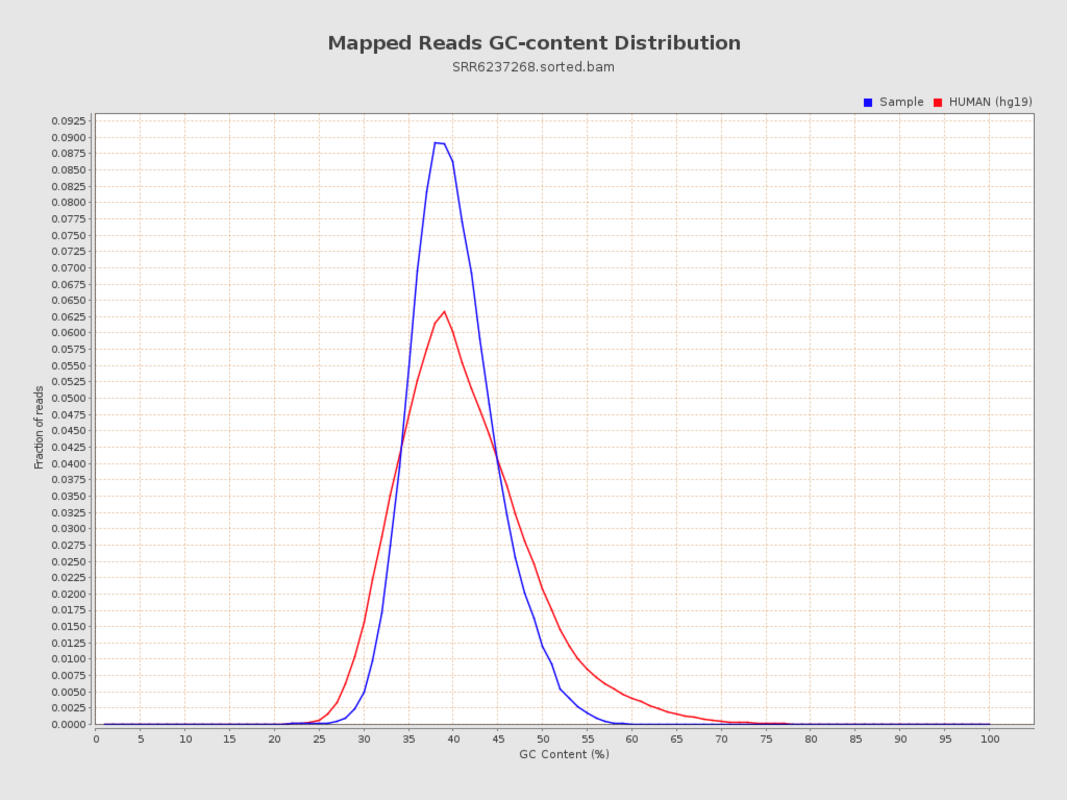
7. Results : Duplication Rate Histogram



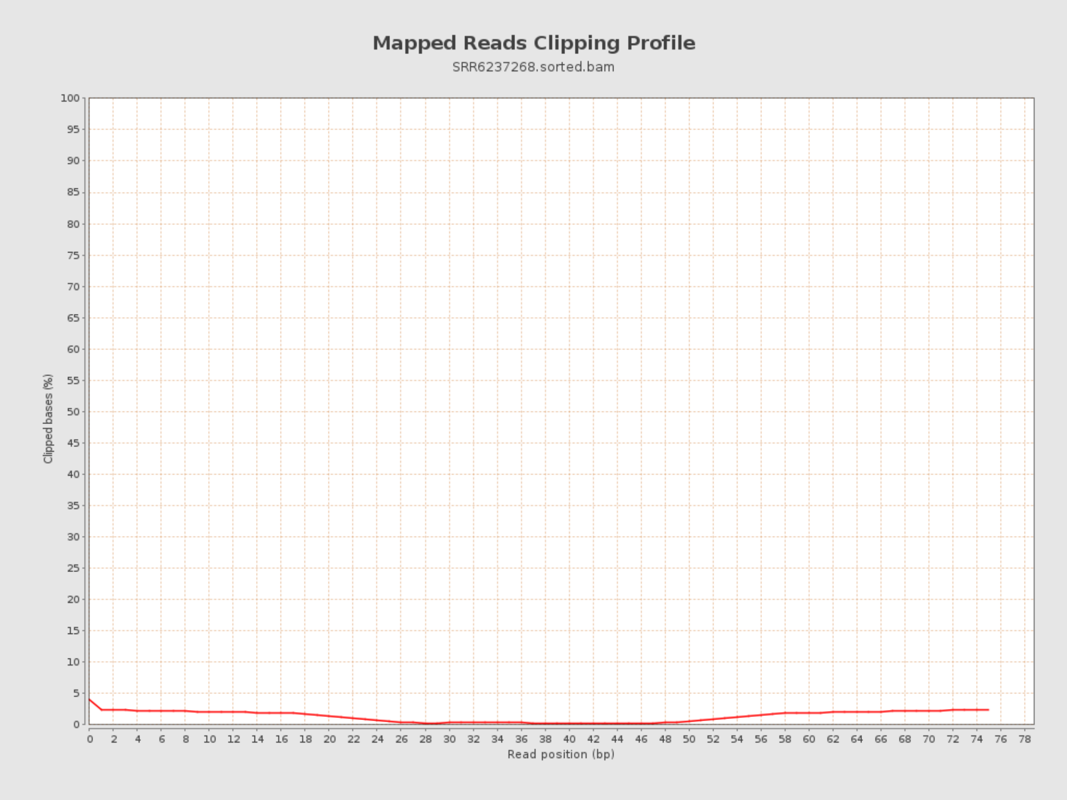
8. Results : Mapped Reads Nucleotide Content



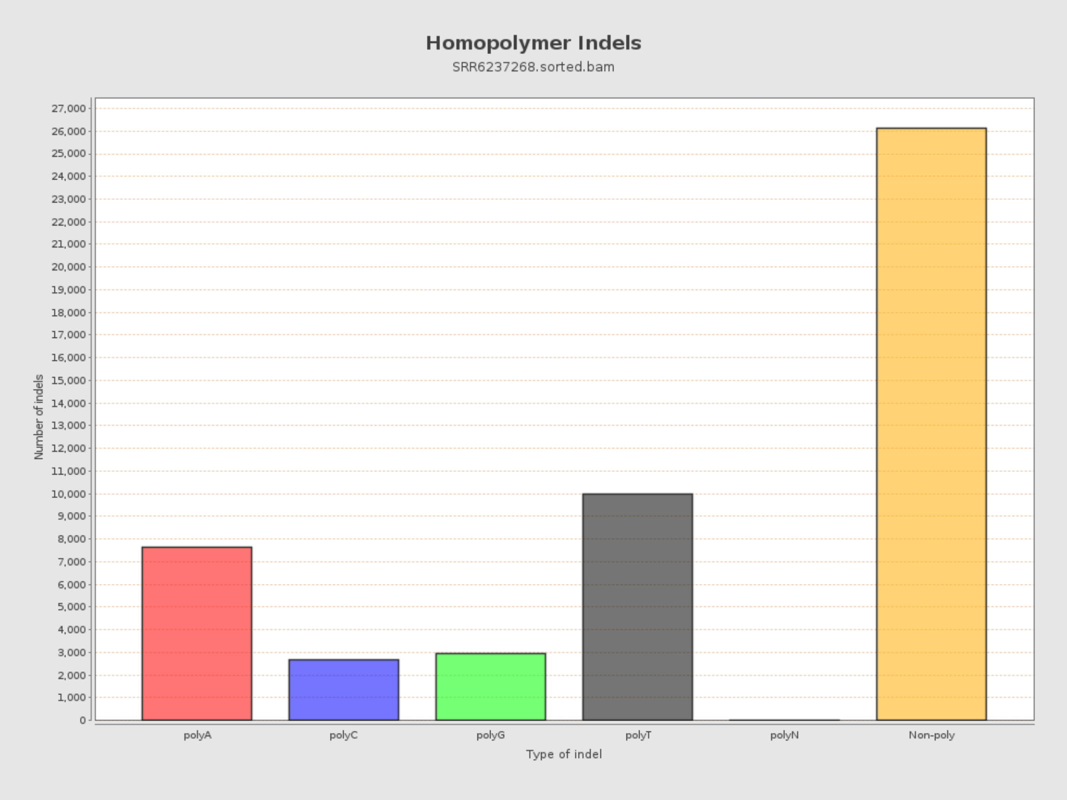
9. Results : Mapped Reads GC-content Distribution



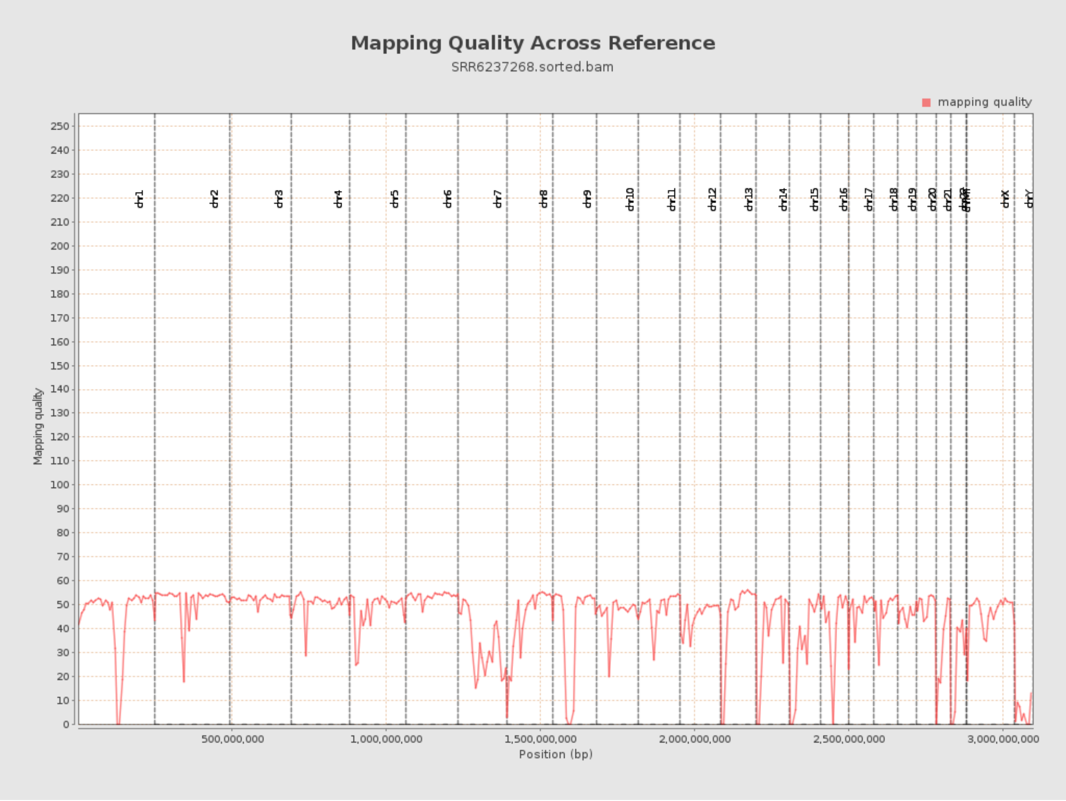
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram