Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 23:26:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237269.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_SRR6237269 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237269.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 23:26:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237269.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,365,065
Mapped reads	3,118,905 / 92.68%
Unmapped reads	246,160 / 7.32%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,033 / 0.68%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	165,242 / 4.91%
Duplication rate	3.71%
Clipped reads	772,509 / 22.96%

2.2. ACGT Content

Number/percentage of A's	67,820,976 / 30.34%
Number/percentage of C's	42,290,969 / 18.92%
Number/percentage of T's	69,597,893 / 31.13%
Number/percentage of G's	43,854,986 / 19.62%
Number/percentage of N's	4,006 / 0%
GC Percentage	38.53%

2.3. Coverage

Mean	0.0723

Standard Deviation	0.7817

2.4. Mapping Quality

Mean Mapping Quality	45.96

2.5. Mismatches and indels

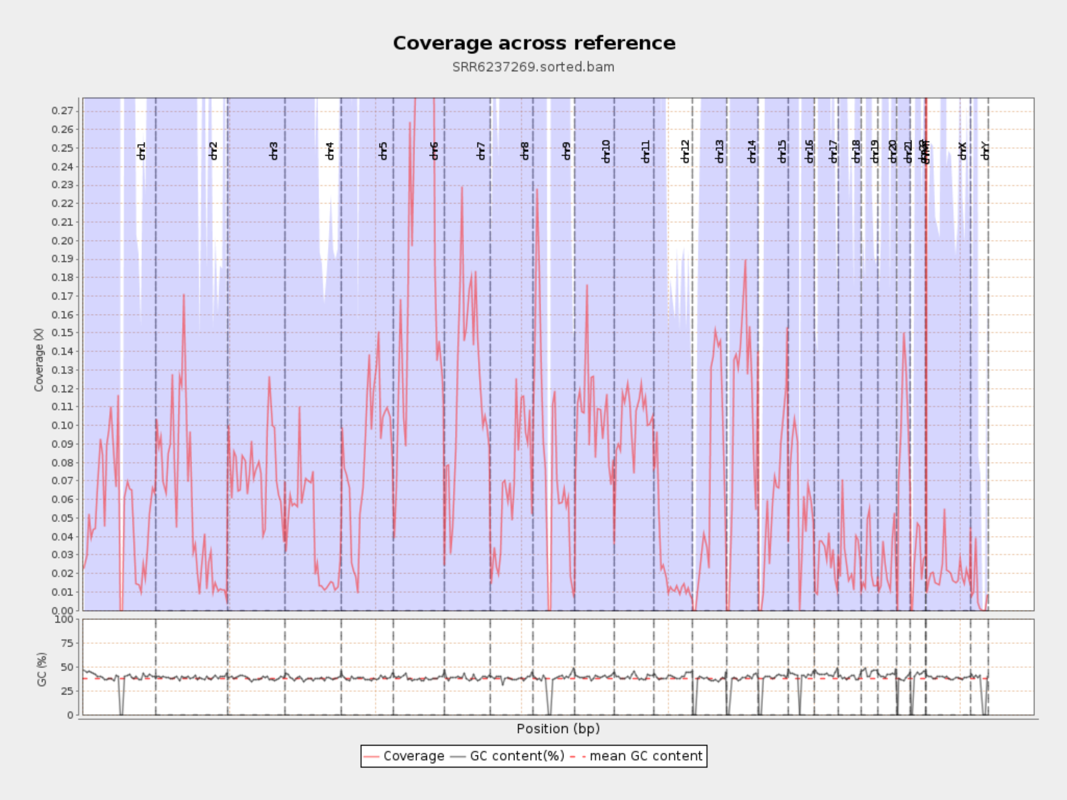
General error rate	0.8%
Mismatches	1,744,847
Insertions	18,567
Mapped reads with at least one insertion	0.59%
Deletions	68,432
Mapped reads with at least one deletion	2.16%
Homopolymer indels	45.81%

2.6. Chromosome stats

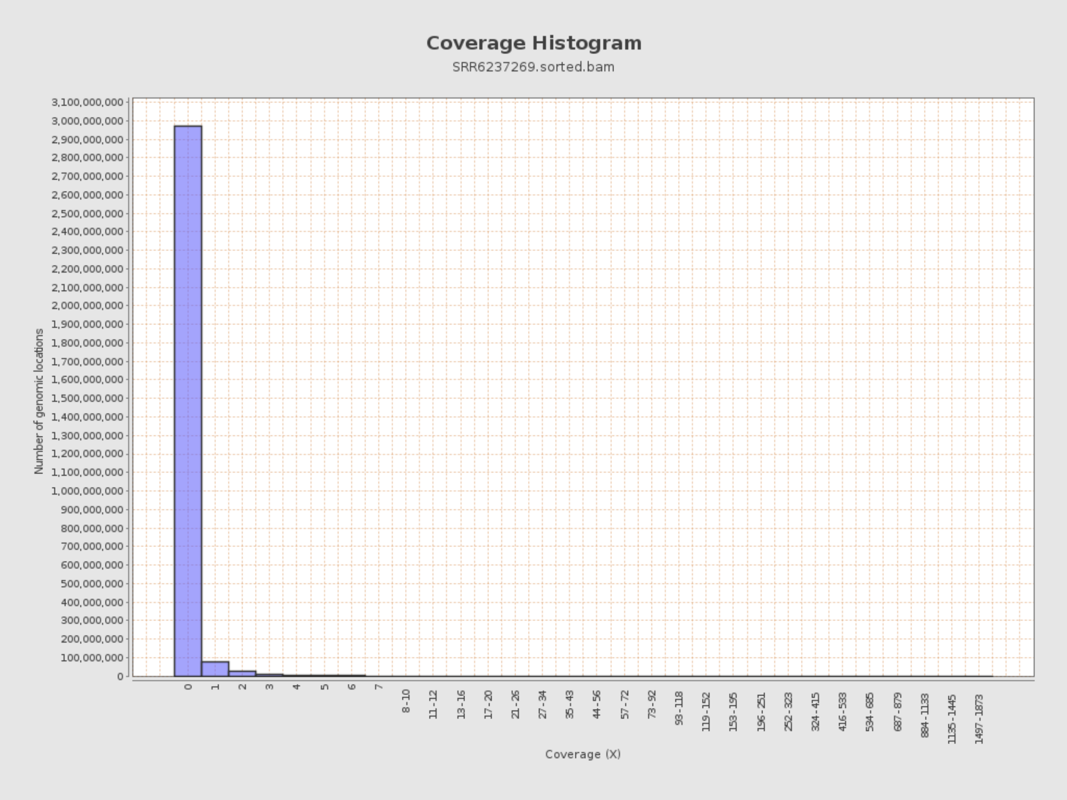
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13129114	0.0527	0.8848
chr2	243199373	14166820	0.0583	0.7214
chr3	198022430	14951999	0.0755	0.4442
chr4	191154276	7833116	0.041	0.4464
chr5	180915260	15325547	0.0847	0.4731
chr6	171115067	37132193	0.217	1.1089
chr7	159138663	19504222	0.1226	1.574

chr8	146364022	10008472	0.0684	1.255
chr9	141213431	11600657	0.0821	0.73
chr10	135534747	14282404	0.1054	0.9078
chr11	135006516	13867329	0.1027	0.7557
chr12	133851895	3173535	0.0237	0.2833
chr13	115169878	8156200	0.0708	0.4294
chr14	107349540	11705865	0.109	0.581
chr15	102531392	5990878	0.0584	0.3844
chr16	90354753	5396371	0.0597	0.4987
chr17	81195210	2134861	0.0263	0.4156
chr18	78077248	2356349	0.0302	1.3808
chr19	59128983	1441921	0.0244	0.6542
chr20	63025520	1671645	0.0265	0.2913
chr21	48129895	4566937	0.0949	0.586
chr22	51304566	1325336	0.0258	0.2437
chrMT	16571	253382	15.2907	11.2106
chrX	155270560	3184795	0.0205	0.295
chrY	59373566	530611	0.0089	0.3732

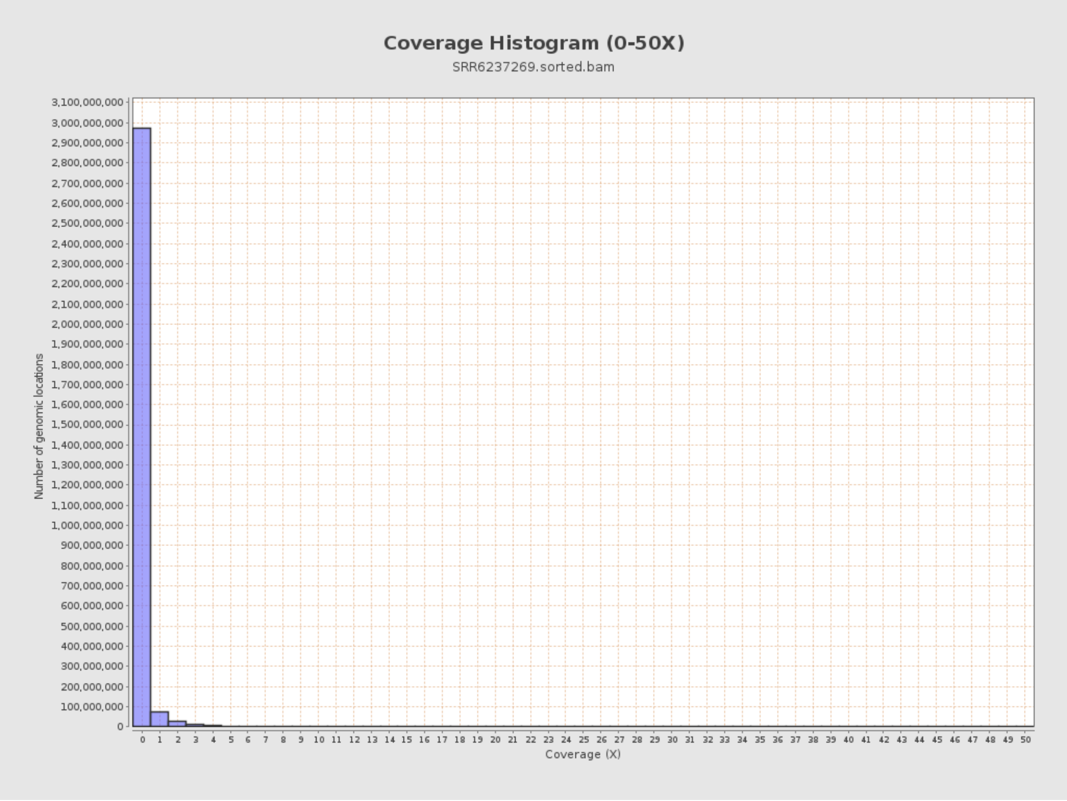
3. Results : Coverage across reference



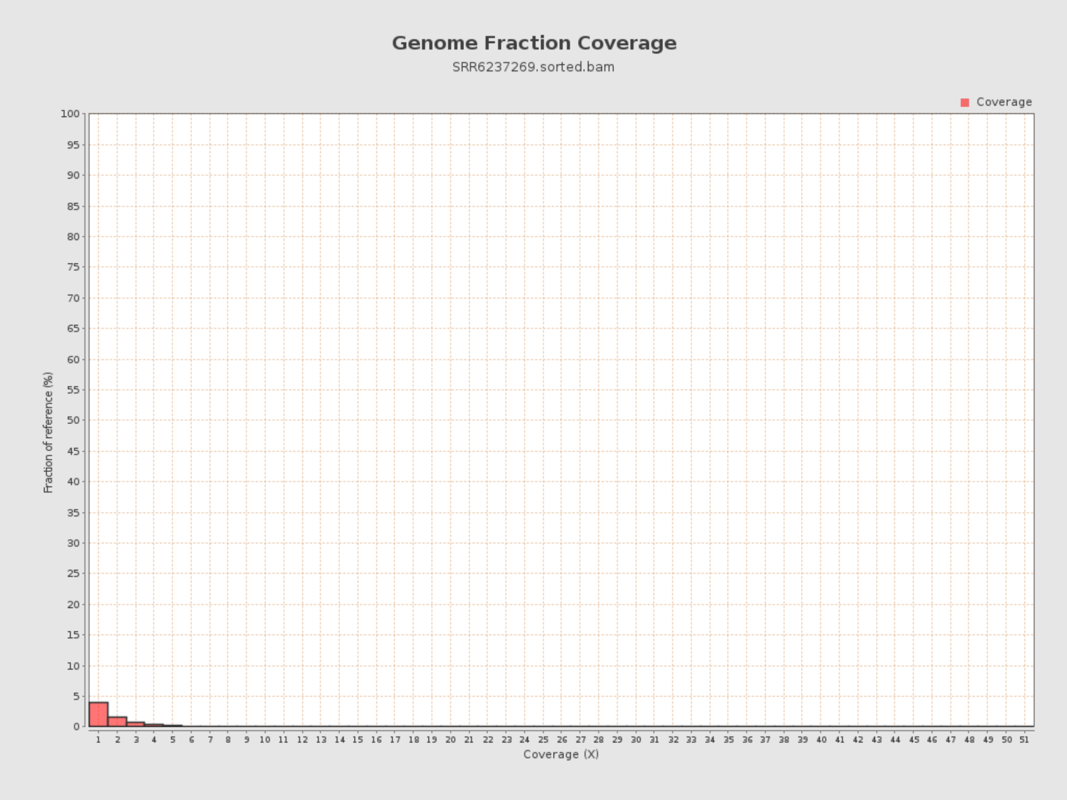
4. Results : Coverage Histogram



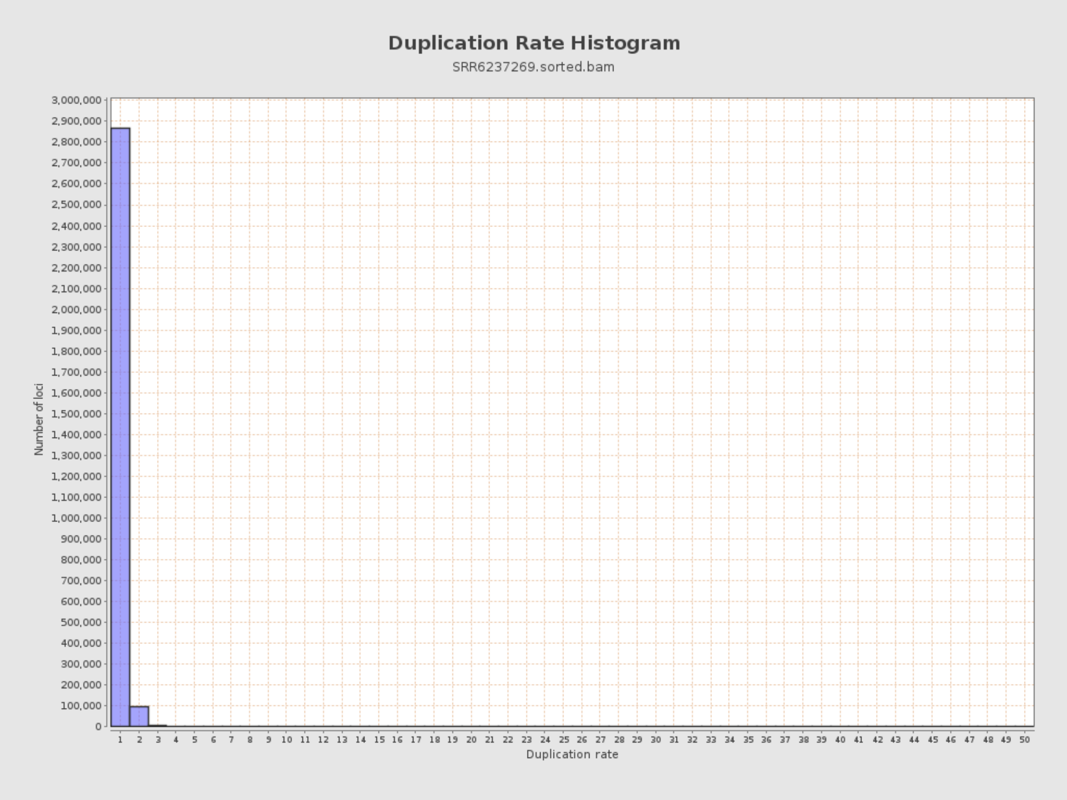
5. Results : Coverage Histogram (0-50X)



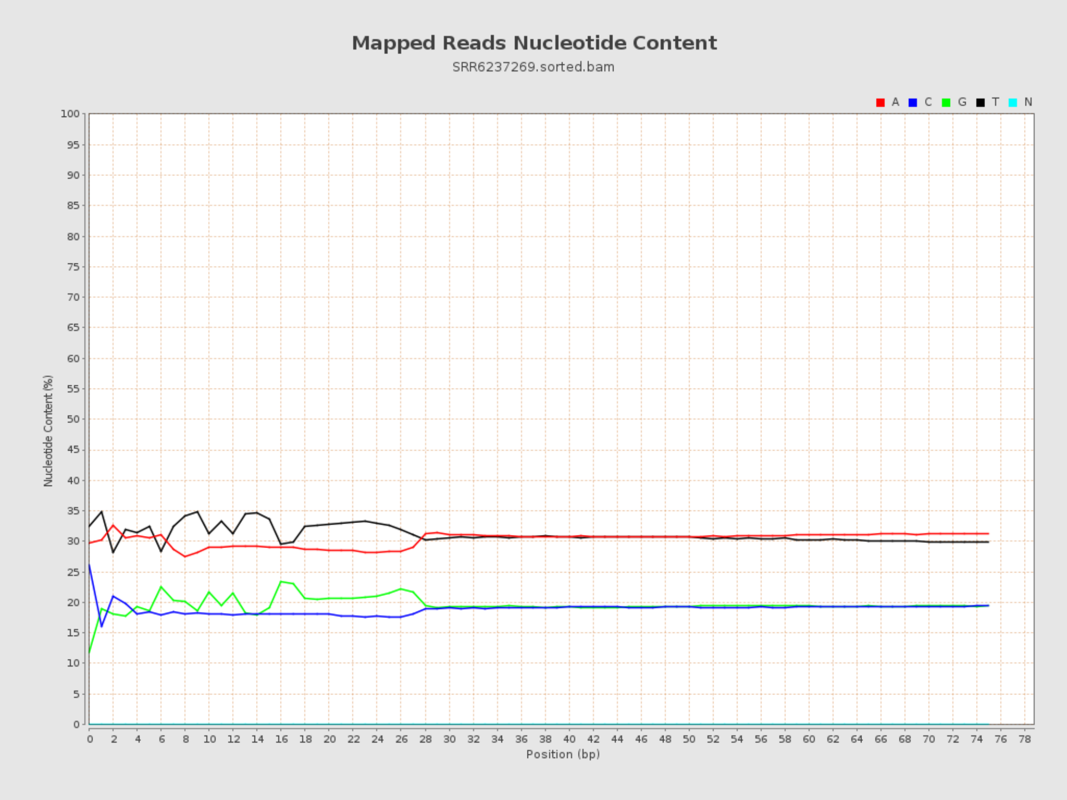
6. Results : Genome Fraction Coverage



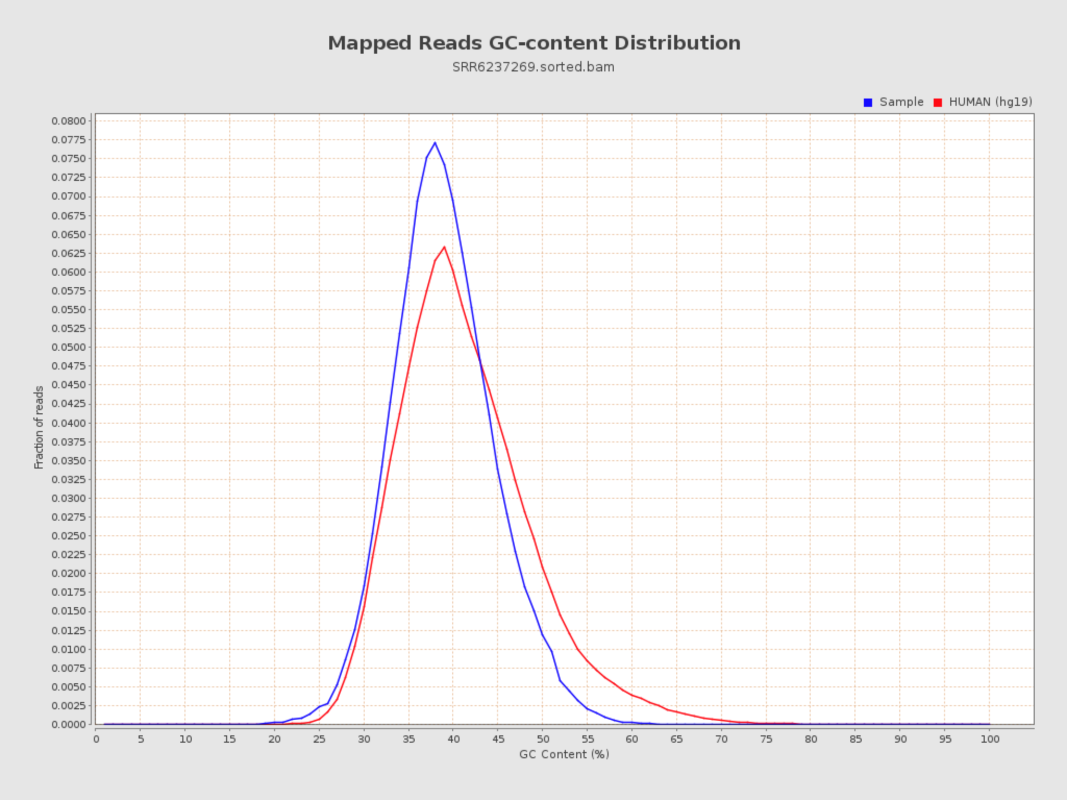
7. Results : Duplication Rate Histogram



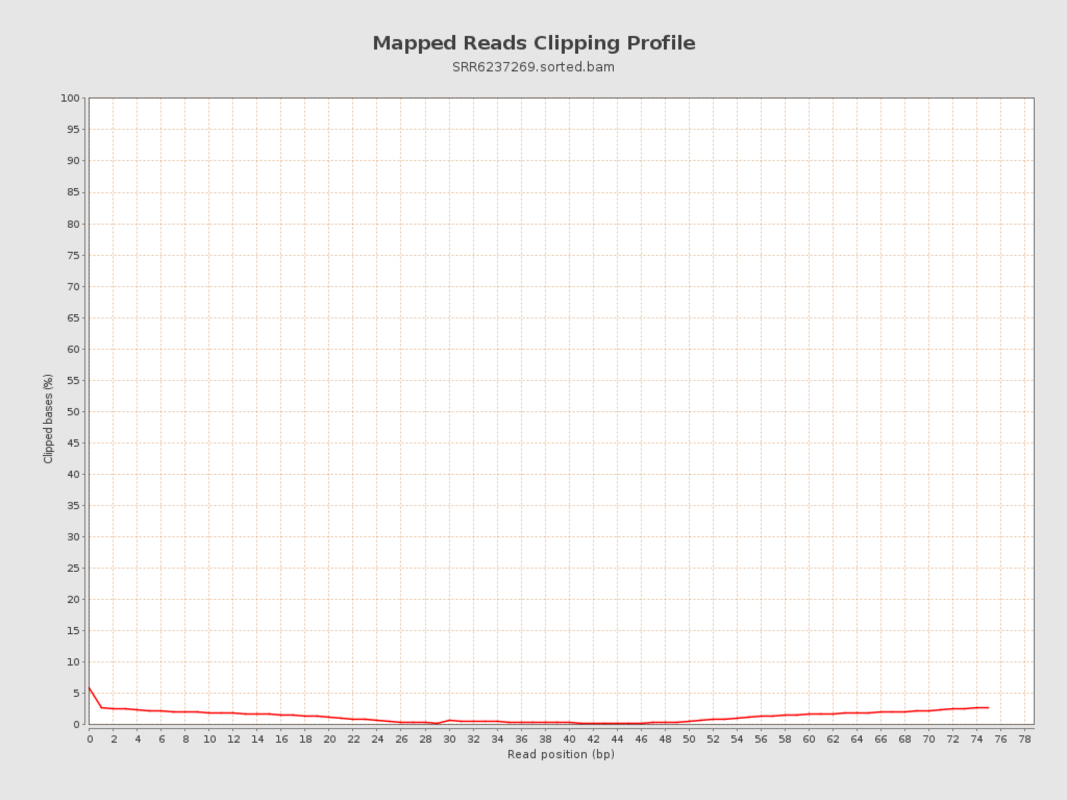
8. Results : Mapped Reads Nucleotide Content



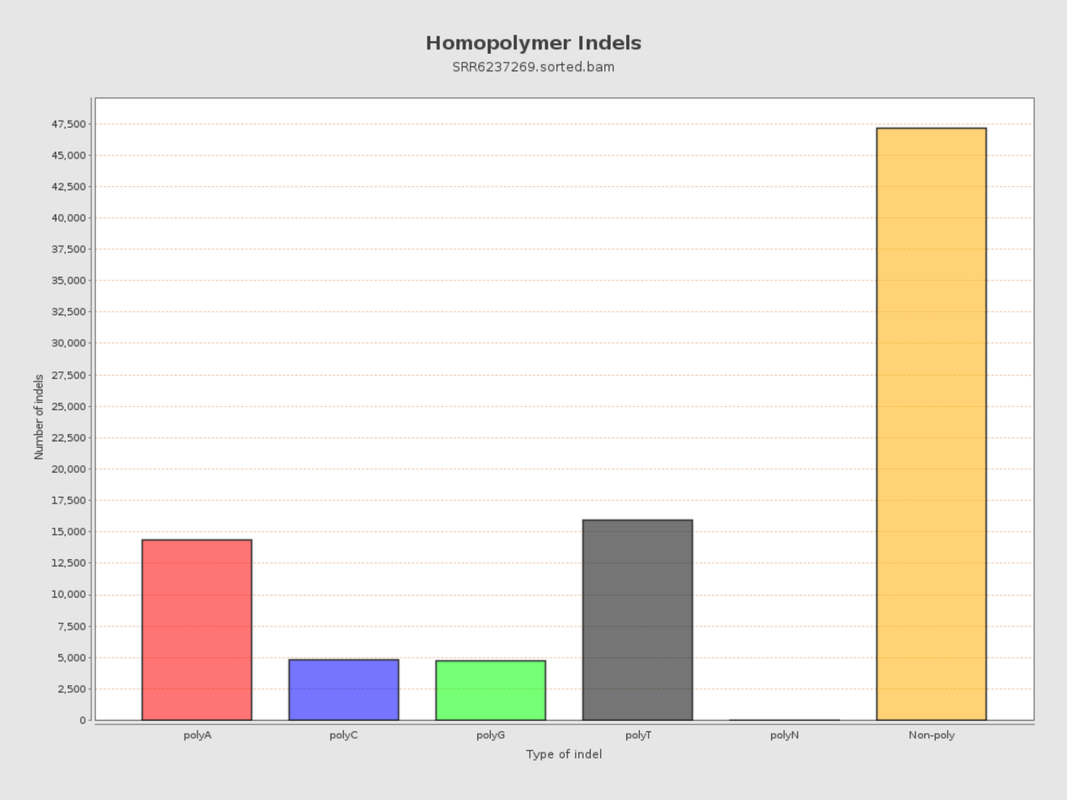
9. Results : Mapped Reads GC-content Distribution



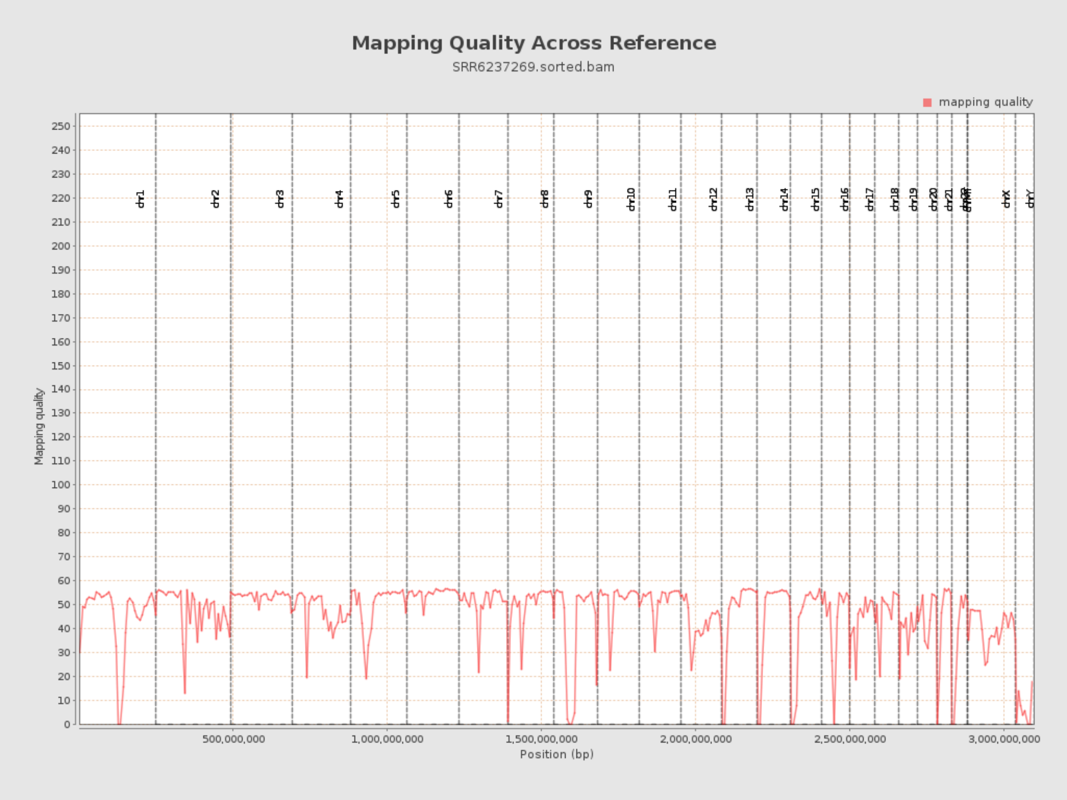
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram