Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 05:22:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237609.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_SRR6237609 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237609.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 05:22:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237609.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,196,337
Mapped reads	1,033,735 / 86.41%
Unmapped reads	162,602 / 13.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,687 / 0.48%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	56,869 / 4.75%
Duplication rate	4.76%
Clipped reads	563,850 / 47.13%

2.2. ACGT Content

Number/percentage of A's	17,714,881 / 26.88%
Number/percentage of C's	11,106,793 / 16.85%
Number/percentage of T's	22,007,013 / 33.39%
Number/percentage of G's	14,955,417 / 22.69%
Number/percentage of N's	120,601 / 0.18%
GC Percentage	39.55%

2.3. Coverage

Mean	0.0213

Standard Deviation	0.2005

2.4. Mapping Quality

Mean Mapping Quality	46.17

2.5. Mismatches and indels

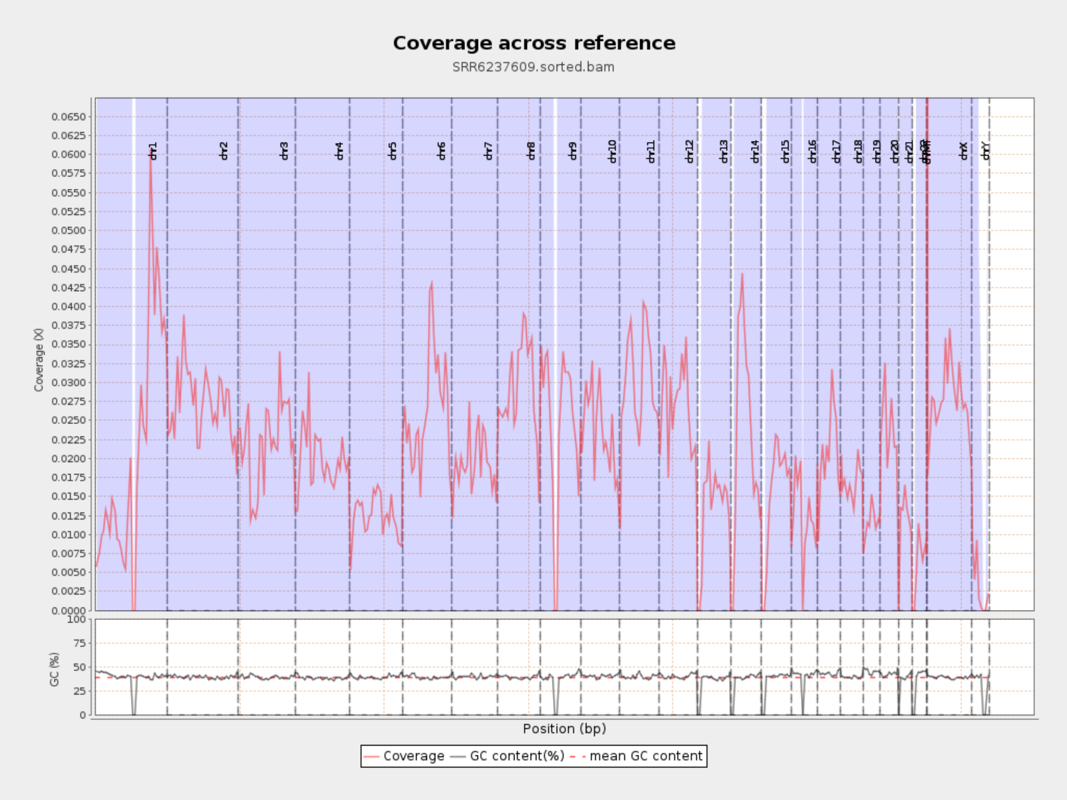
General error rate	0.89%
Mismatches	577,208
Insertions	5,405
Mapped reads with at least one insertion	0.52%
Deletions	21,851
Mapped reads with at least one deletion	2.08%
Homopolymer indels	46.57%

2.6. Chromosome stats

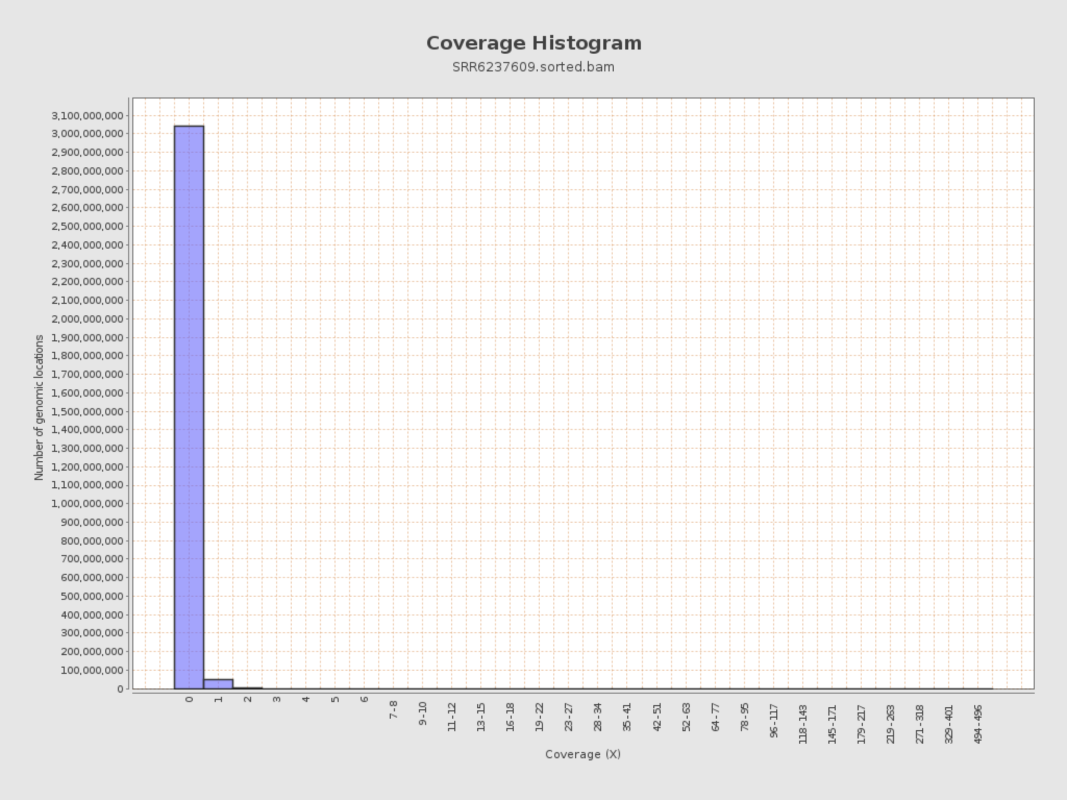
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5268124	0.0211	0.2026
chr2	243199373	6638478	0.0273	0.2914
chr3	198022430	4391361	0.0222	0.1715
chr4	191154276	3788262	0.0198	0.1711
chr5	180915260	2252538	0.0125	0.1271
chr6	171115067	4573942	0.0267	0.2144
chr7	159138663	3089197	0.0194	0.2096

chr8	146364022	4318147	0.0295	0.3072
chr9	141213431	3466189	0.0245	0.2094
chr10	135534747	3178799	0.0235	0.206
chr11	135006516	4063134	0.0301	0.2185
chr12	133851895	3608373	0.027	0.1915
chr13	115169878	1547489	0.0134	0.1363
chr14	107349540	2482094	0.0231	0.1776
chr15	102531392	1566145	0.0153	0.1433
chr16	90354753	1094727	0.0121	0.1325
chr17	81195210	1680930	0.0207	0.1721
chr18	78077248	1318026	0.0169	0.239
chr19	59128983	693254	0.0117	0.1473
chr20	63025520	1503967	0.0239	0.1784
chr21	48129895	576503	0.012	0.1333
chr22	51304566	328717	0.0064	0.0885
chrMT	16571	7673	0.463	0.8124
chrX	155270560	4321680	0.0278	0.1981
chrY	59373566	182383	0.0031	0.0841

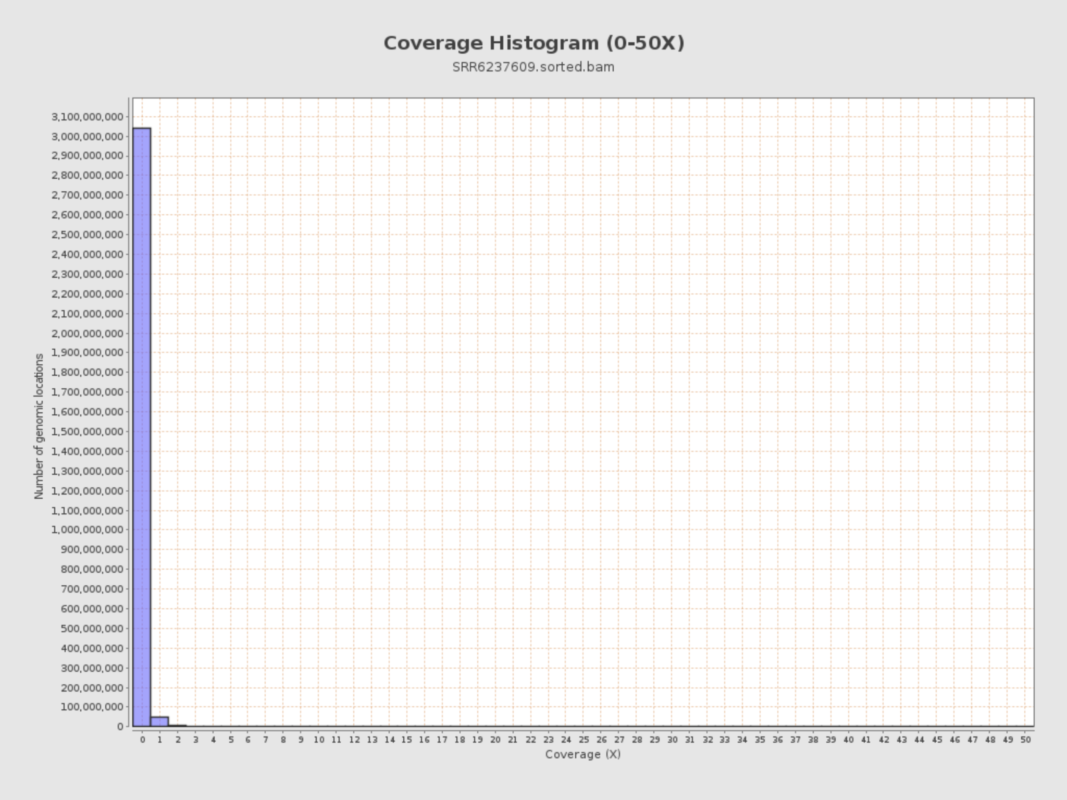
3. Results : Coverage across reference



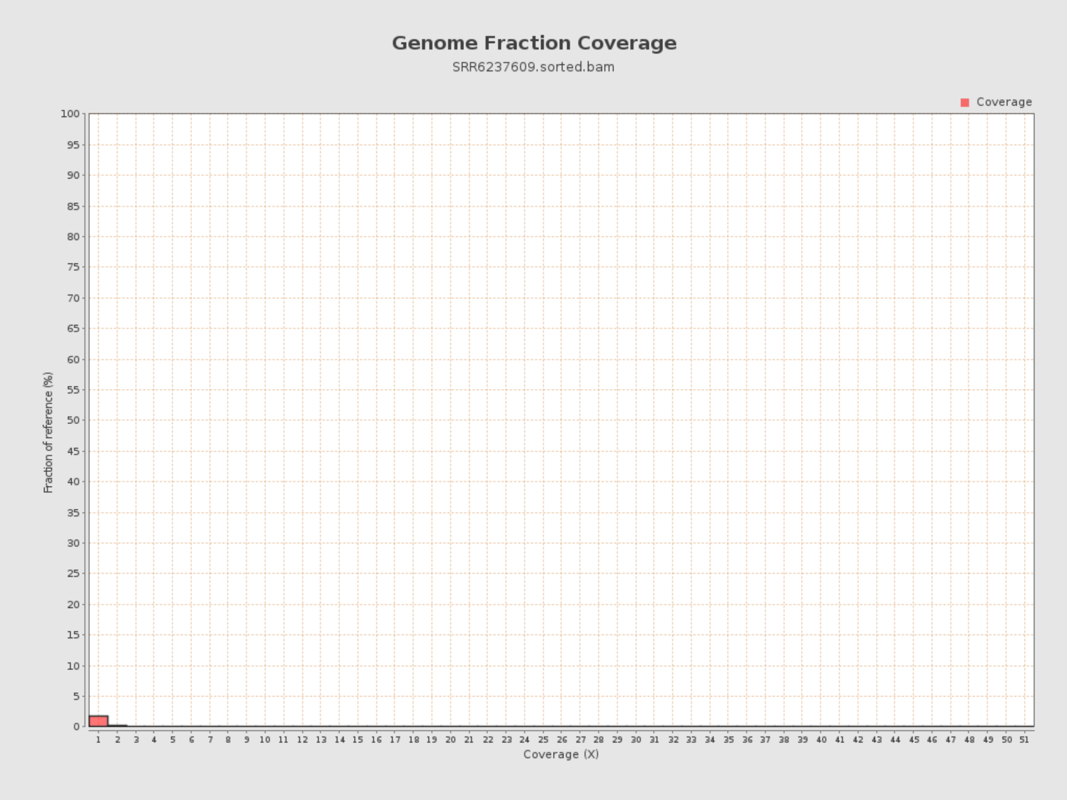
4. Results : Coverage Histogram



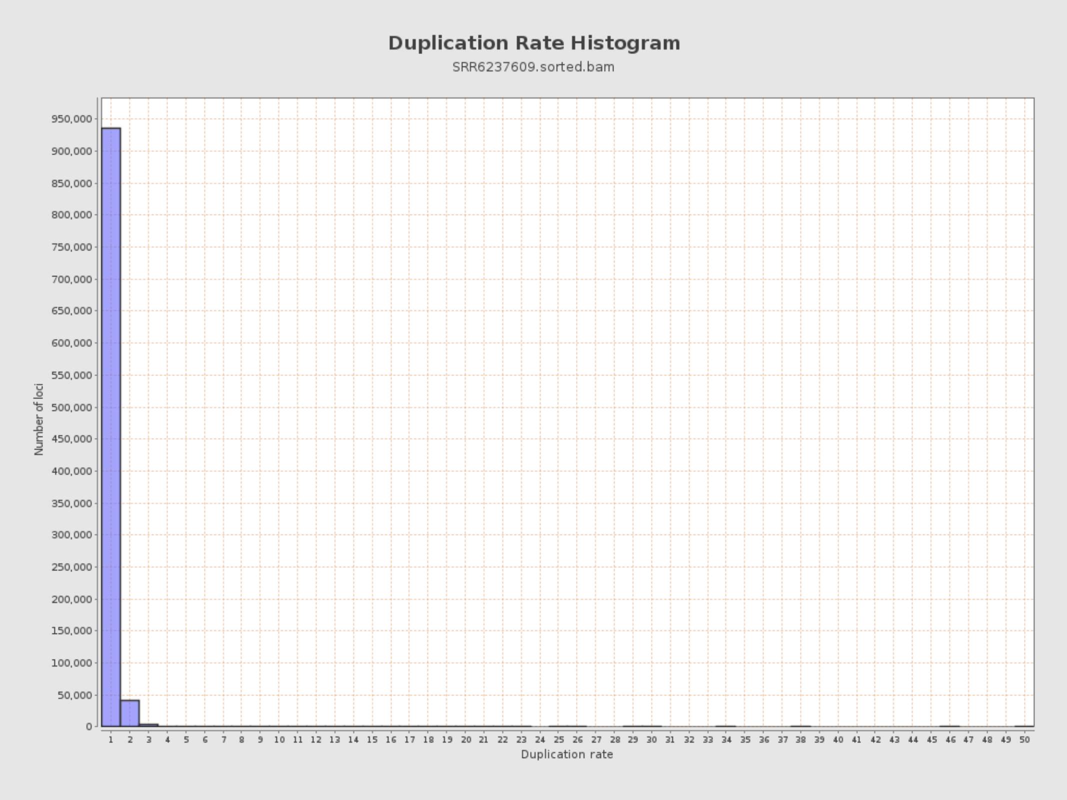
5. Results : Coverage Histogram (0-50X)



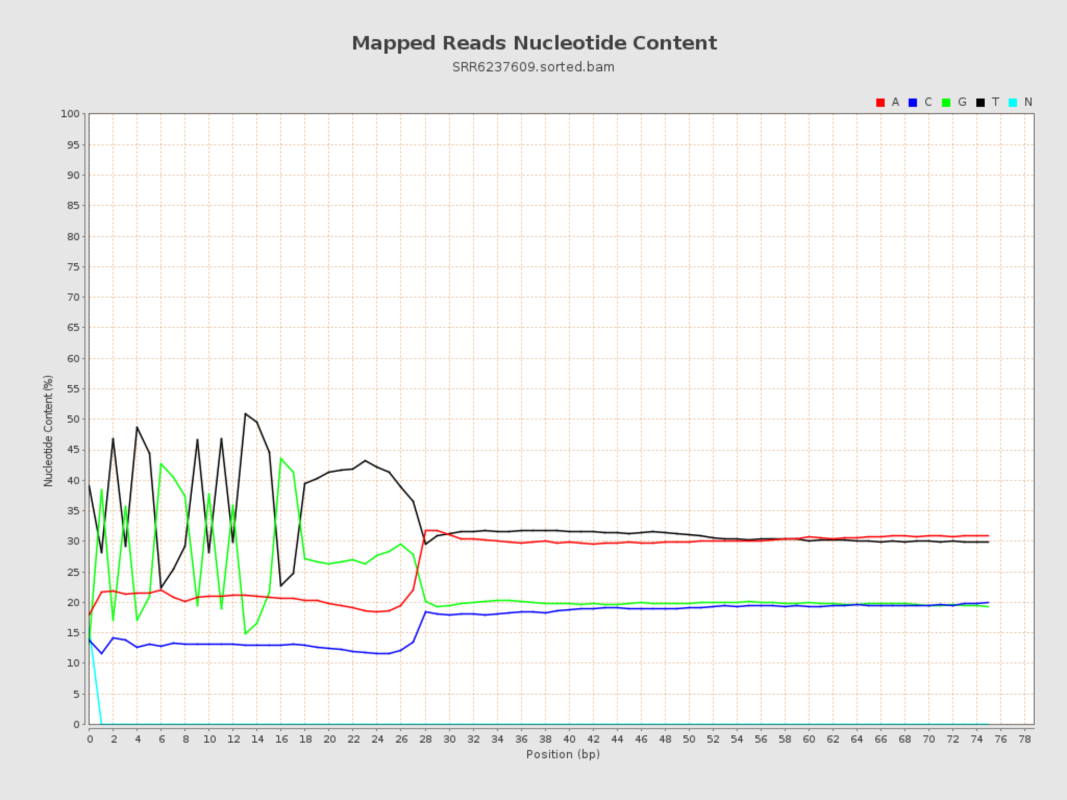
6. Results : Genome Fraction Coverage



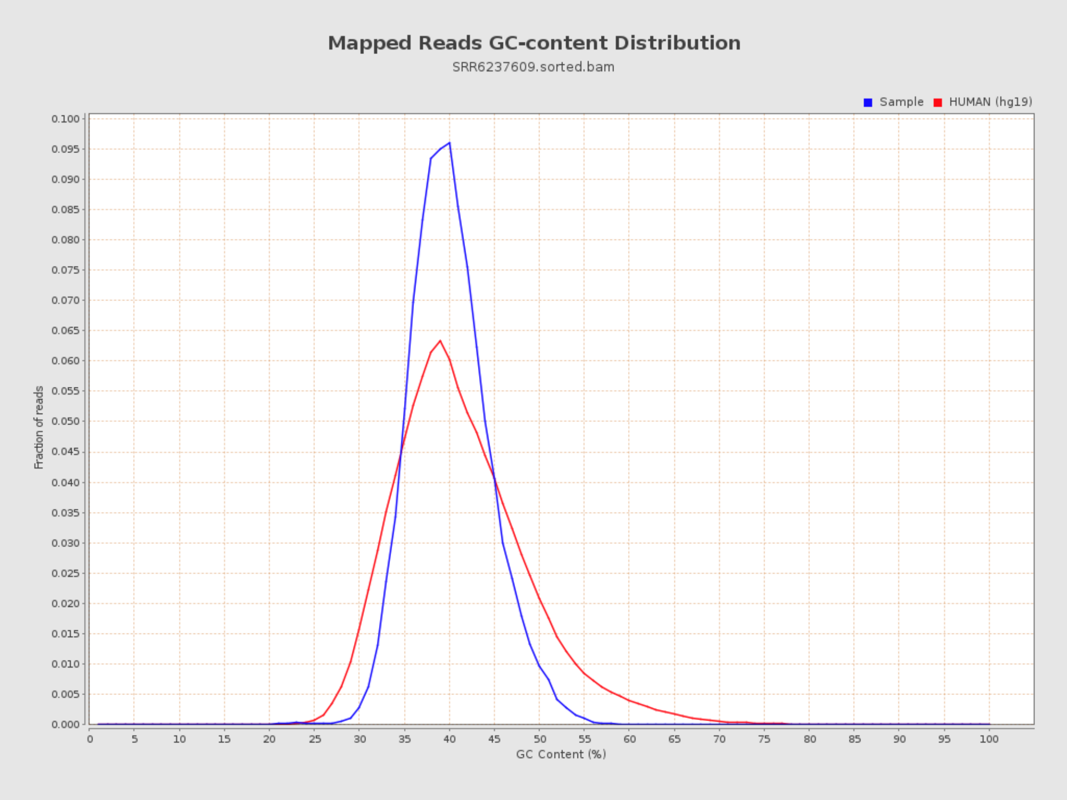
7. Results : Duplication Rate Histogram



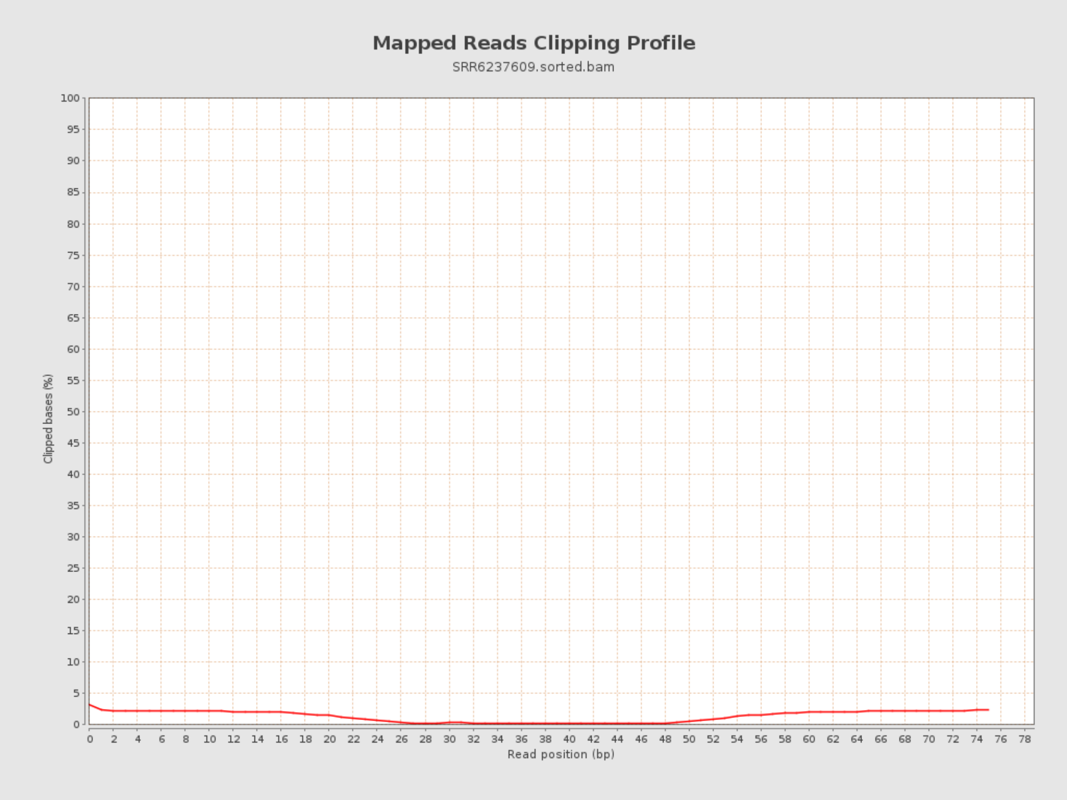
8. Results : Mapped Reads Nucleotide Content



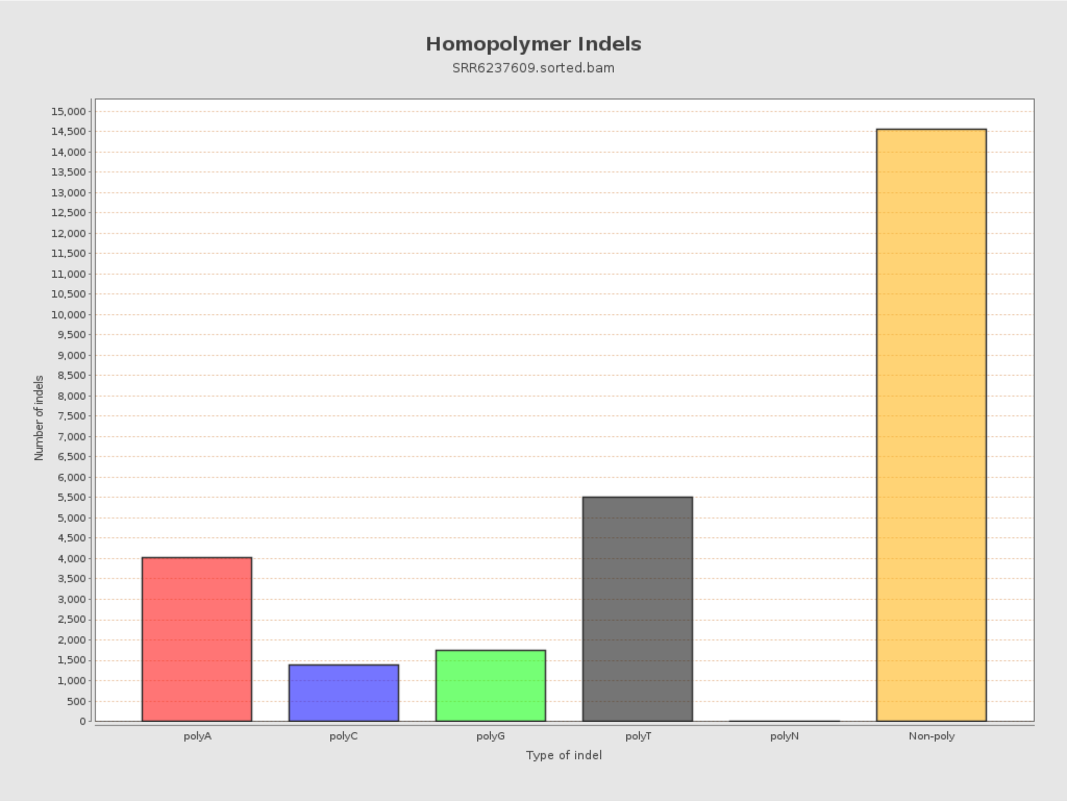
9. Results : Mapped Reads GC-content Distribution



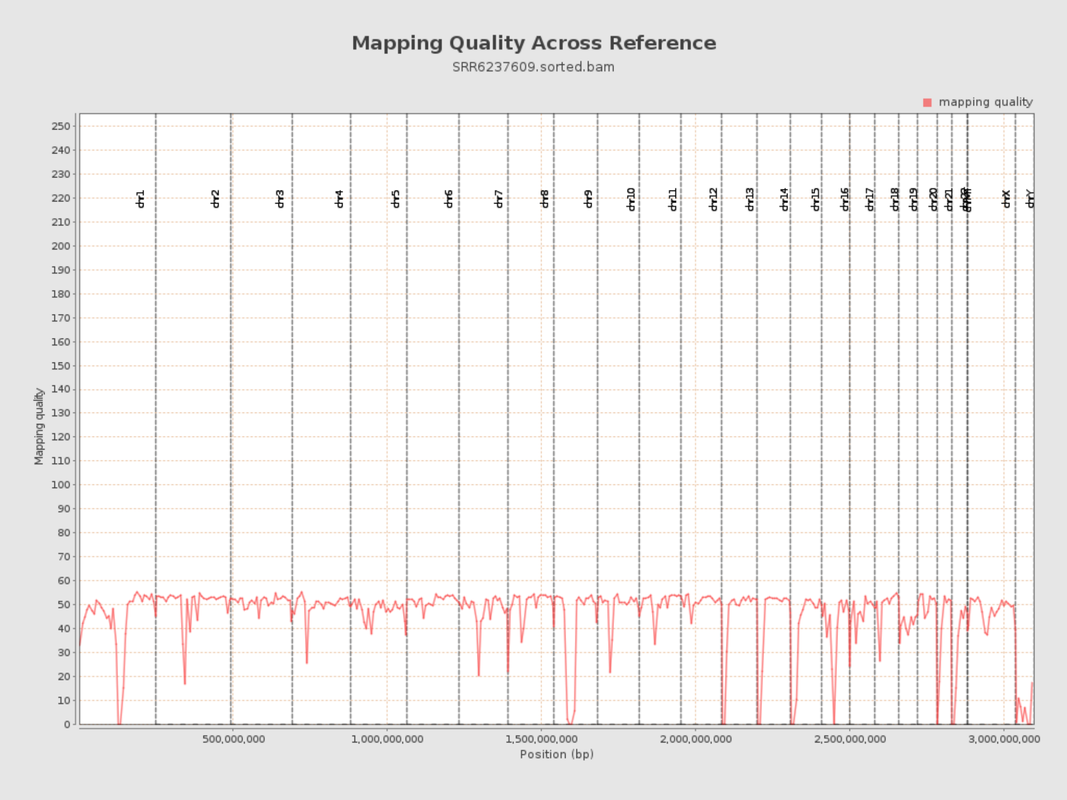
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram