Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 04:34:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237589.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_SRR6237589 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237589.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 04:34:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237589.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,192,530
Mapped reads	849,648 / 71.25%
Unmapped reads	342,882 / 28.75%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,809 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	37,572 / 3.15%
Duplication rate	3.34%
Clipped reads	515,791 / 43.25%

2.2. ACGT Content

Number/percentage of A's	14,548,493 / 27.35%
Number/percentage of C's	9,128,934 / 17.16%
Number/percentage of T's	16,627,466 / 31.25%
Number/percentage of G's	12,802,221 / 24.06%
Number/percentage of N's	95,510 / 0.18%
GC Percentage	41.22%

2.3. Coverage

Mean	0.0172

Standard Deviation	0.1877

2.4. Mapping Quality

Mean Mapping Quality	44.16

2.5. Mismatches and indels

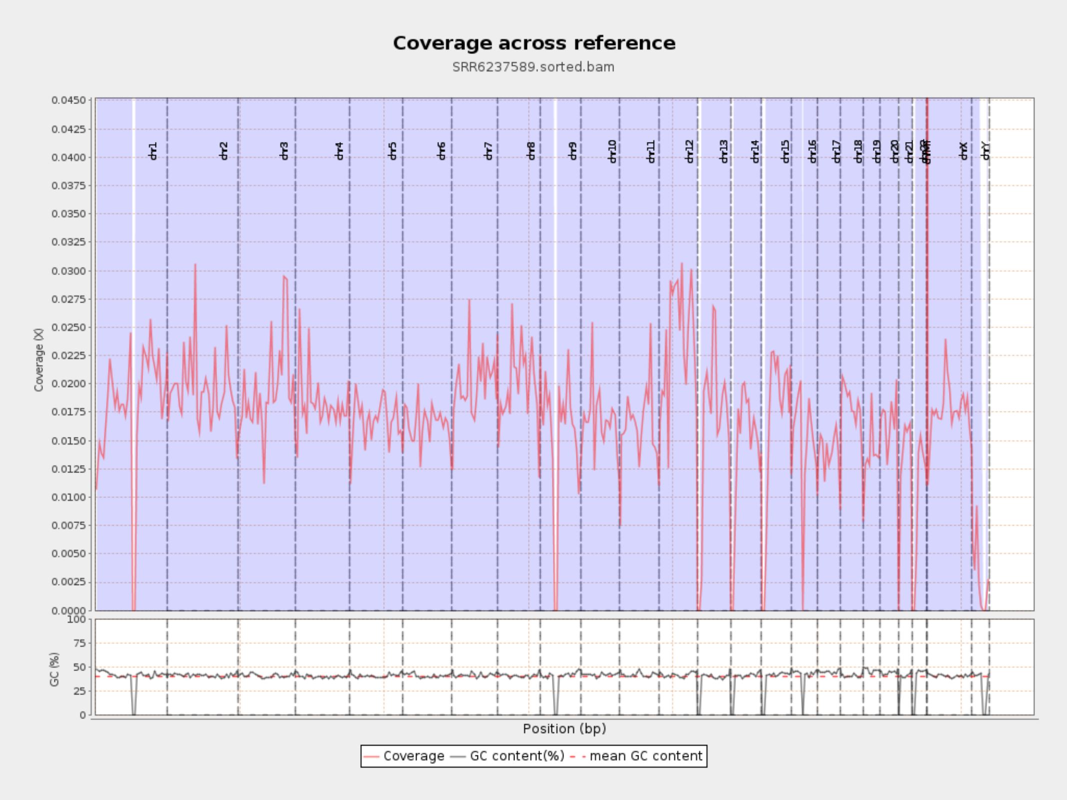
General error rate	1.07%
Mismatches	562,188
Insertions	4,790
Mapped reads with at least one insertion	0.56%
Deletions	19,924
Mapped reads with at least one deletion	2.32%
Homopolymer indels	47.89%

2.6. Chromosome stats

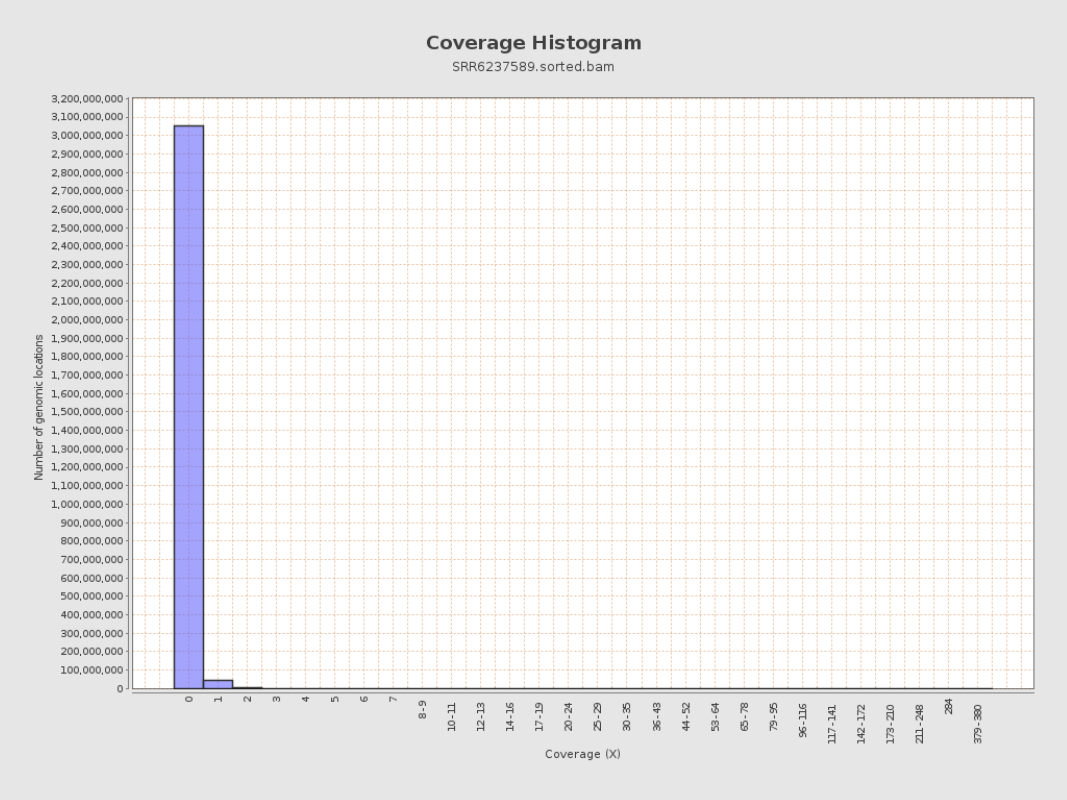
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4470209	0.0179	0.2267
chr2	243199373	4754678	0.0196	0.2501
chr3	198022430	3845505	0.0194	0.1655
chr4	191154276	3473382	0.0182	0.1605
chr5	180915260	3062271	0.0169	0.1486
chr6	171115067	2814165	0.0164	0.1629
chr7	159138663	3182472	0.02	0.2472

chr8	146364022	2910555	0.0199	0.2037
chr9	141213431	2162505	0.0153	0.1944
chr10	135534747	2263716	0.0167	0.1746
chr11	135006516	2231399	0.0165	0.1906
chr12	133851895	3186635	0.0238	0.1877
chr13	115169878	1855381	0.0161	0.1504
chr14	107349540	1499607	0.014	0.1464
chr15	102531392	1680732	0.0164	0.153
chr16	90354753	1322470	0.0146	0.1514
chr17	81195210	1138228	0.014	0.1407
chr18	78077248	1422454	0.0182	0.2986
chr19	59128983	821356	0.0139	0.1716
chr20	63025520	1042473	0.0165	0.1519
chr21	48129895	637633	0.0132	0.1427
chr22	51304566	491177	0.0096	0.1145
chrMT	16571	40796	2.4619	2.1191
chrX	155270560	2753575	0.0177	0.1596
chrY	59373566	171963	0.0029	0.0776

3. Results : Coverage across reference

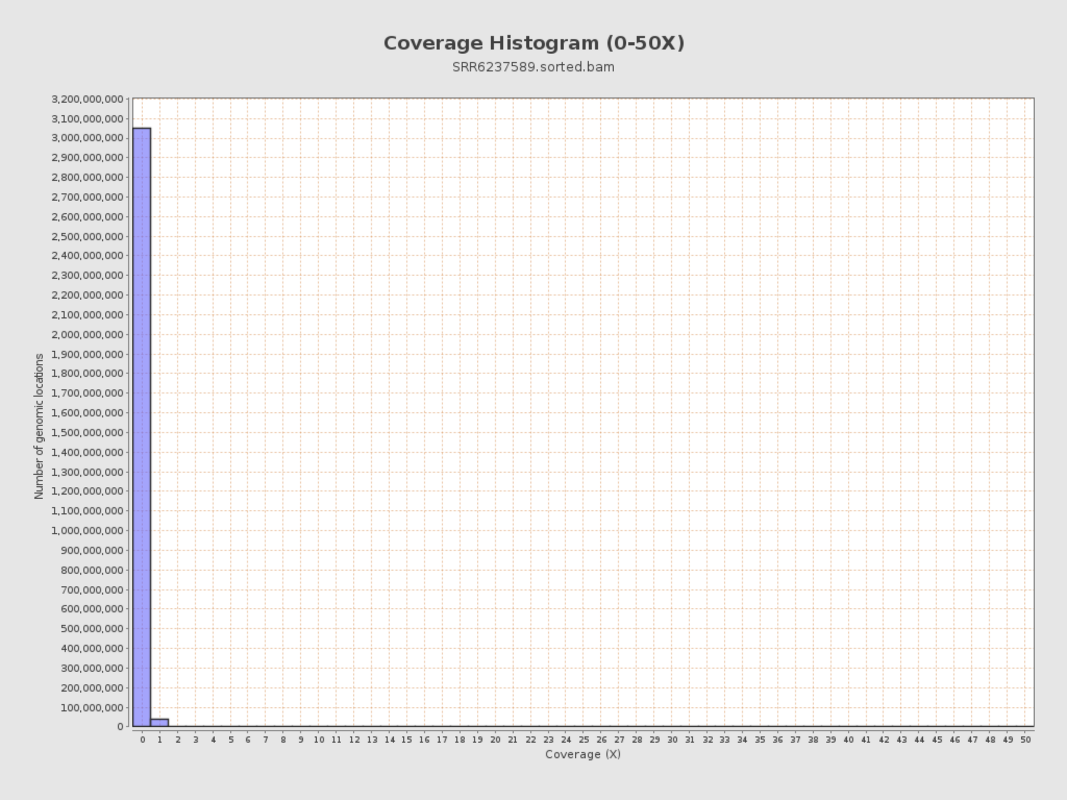


4. Results : Coverage Histogram

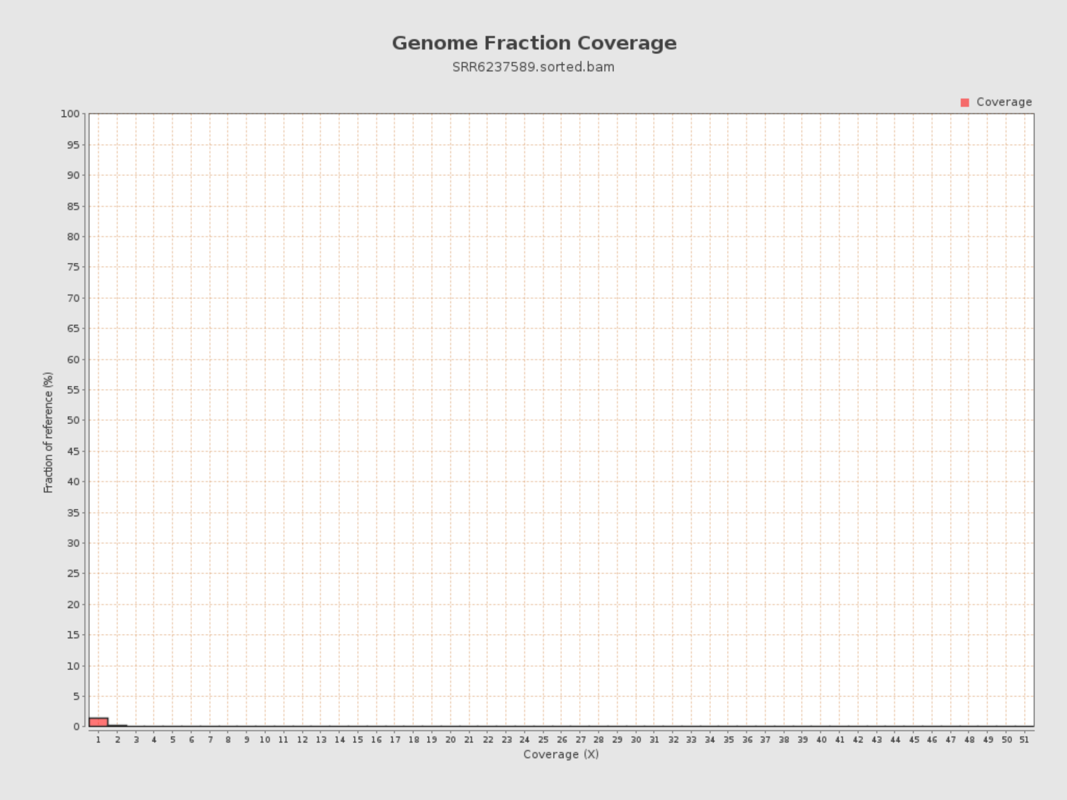


"

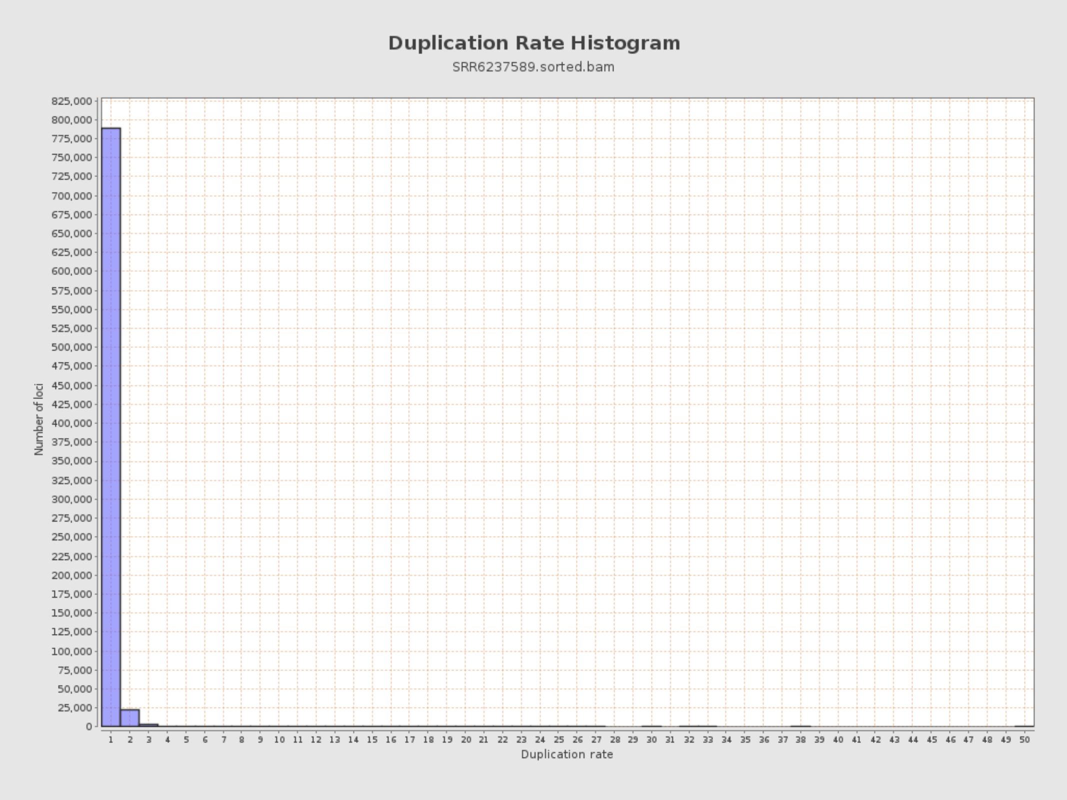
5. Results : Coverage Histogram (0-50X)



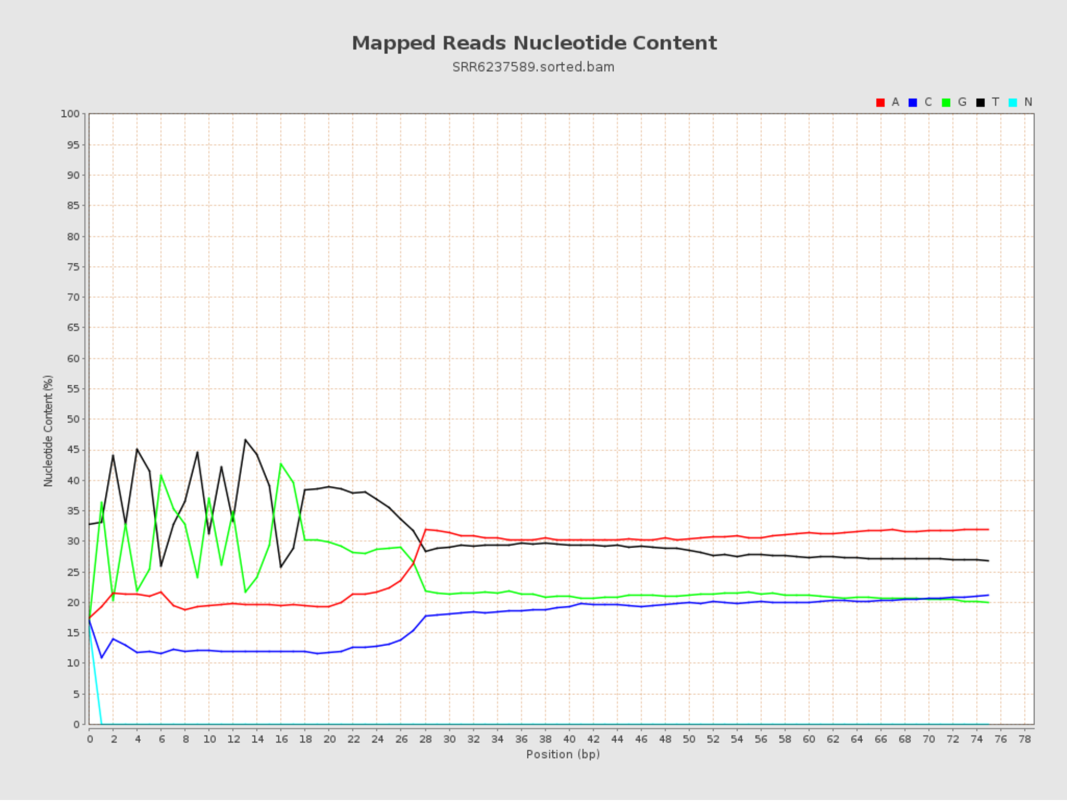
6. Results : Genome Fraction Coverage



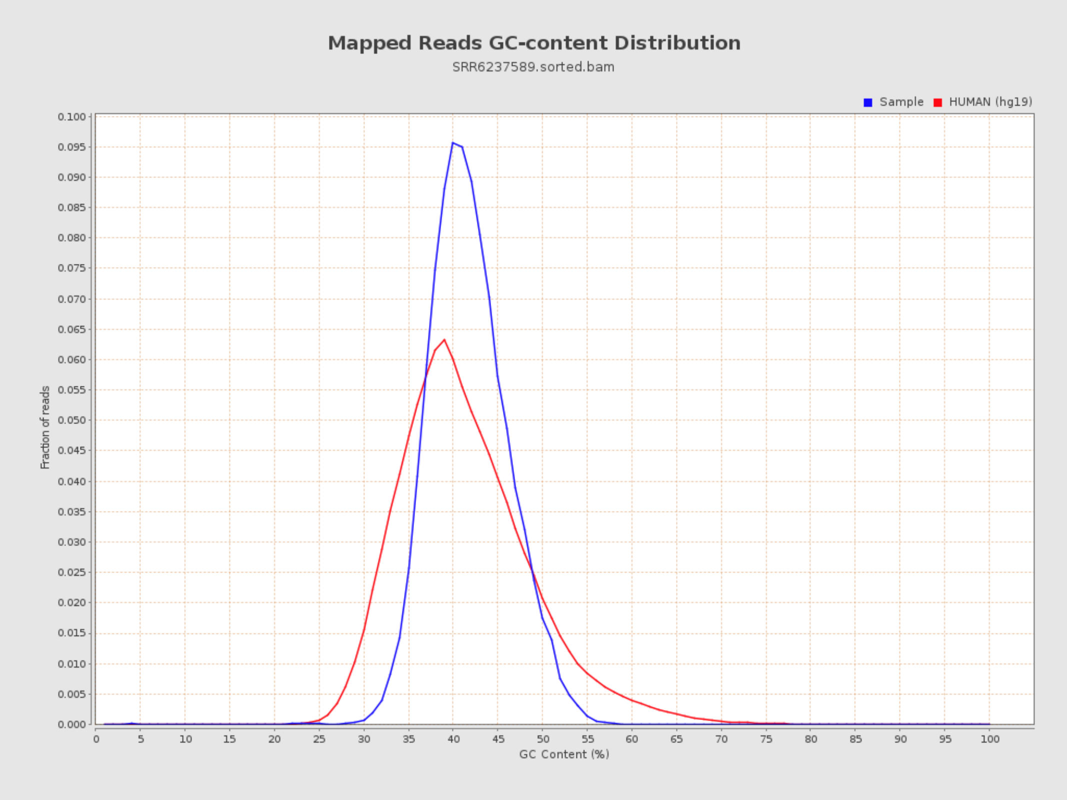
7. Results : Duplication Rate Histogram



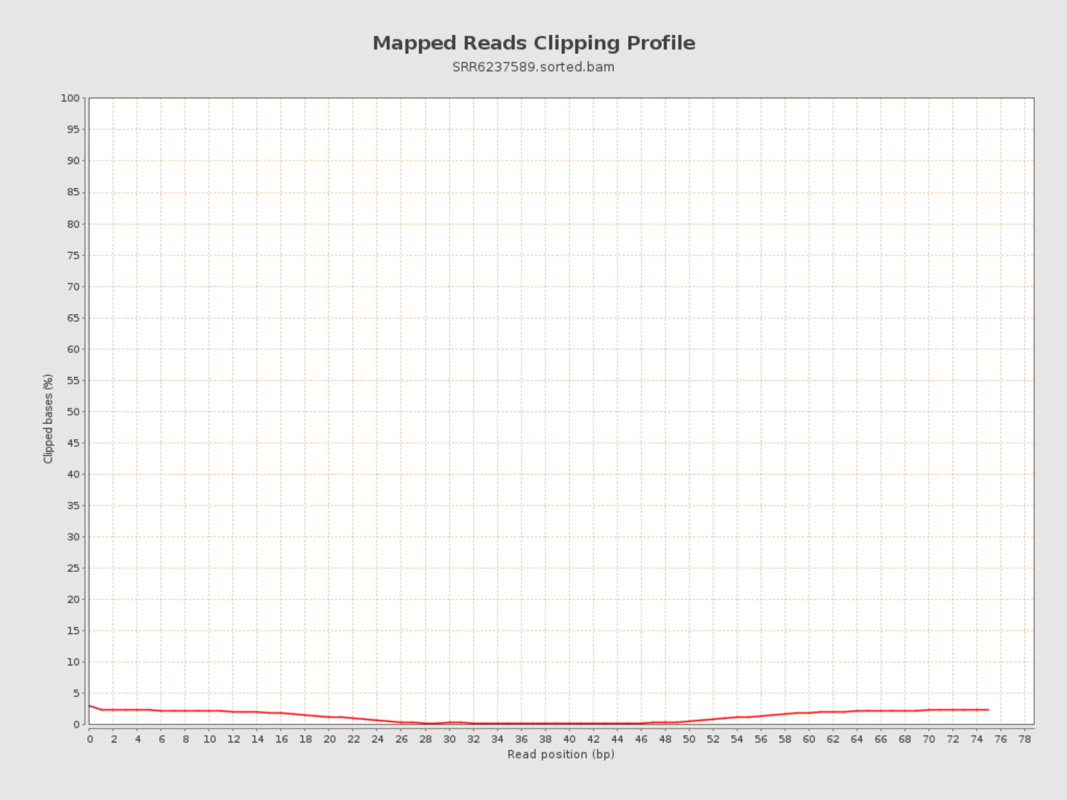
8. Results : Mapped Reads Nucleotide Content



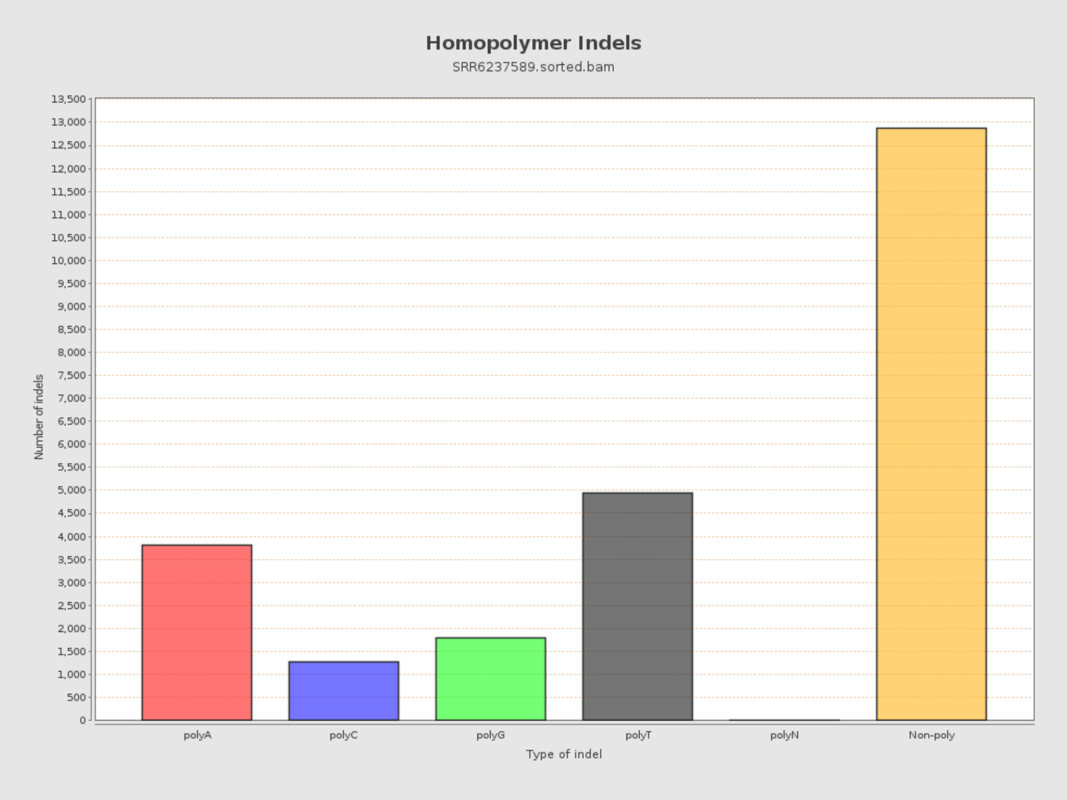
9. Results : Mapped Reads GC-content Distribution



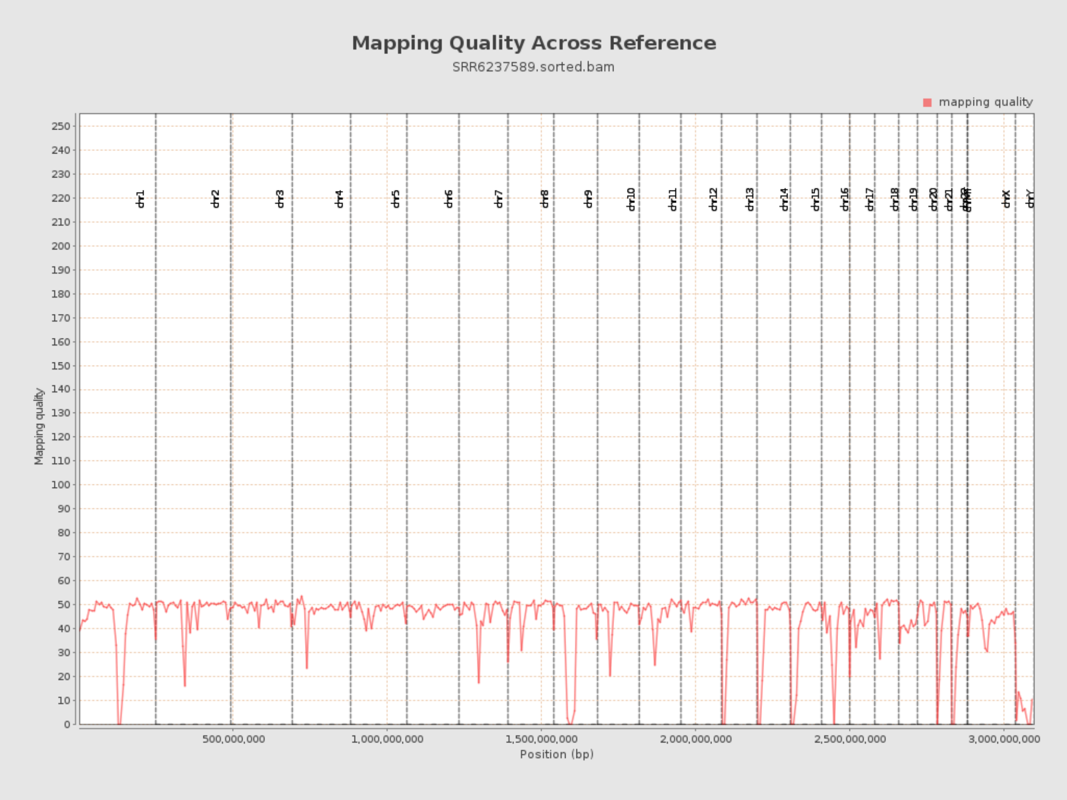
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram