Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 04:40:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237592.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_SRR6237592 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237592.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 04:40:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237592.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,238,000
Mapped reads	951,710 / 76.87%
Unmapped reads	286,290 / 23.13%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,638 / 0.37%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	41,106 / 3.32%
Duplication rate	3.21%
Clipped reads	589,580 / 47.62%

2.2. ACGT Content

Number/percentage of A's	16,126,904 / 27.23%
Number/percentage of C's	10,366,209 / 17.5%
Number/percentage of T's	18,488,372 / 31.21%
Number/percentage of G's	14,141,978 / 23.87%
Number/percentage of N's	110,724 / 0.19%
GC Percentage	41.38%

2.3. Coverage

Mean	0.0191

Standard Deviation	0.208

2.4. Mapping Quality

Mean Mapping Quality	43.19

2.5. Mismatches and indels

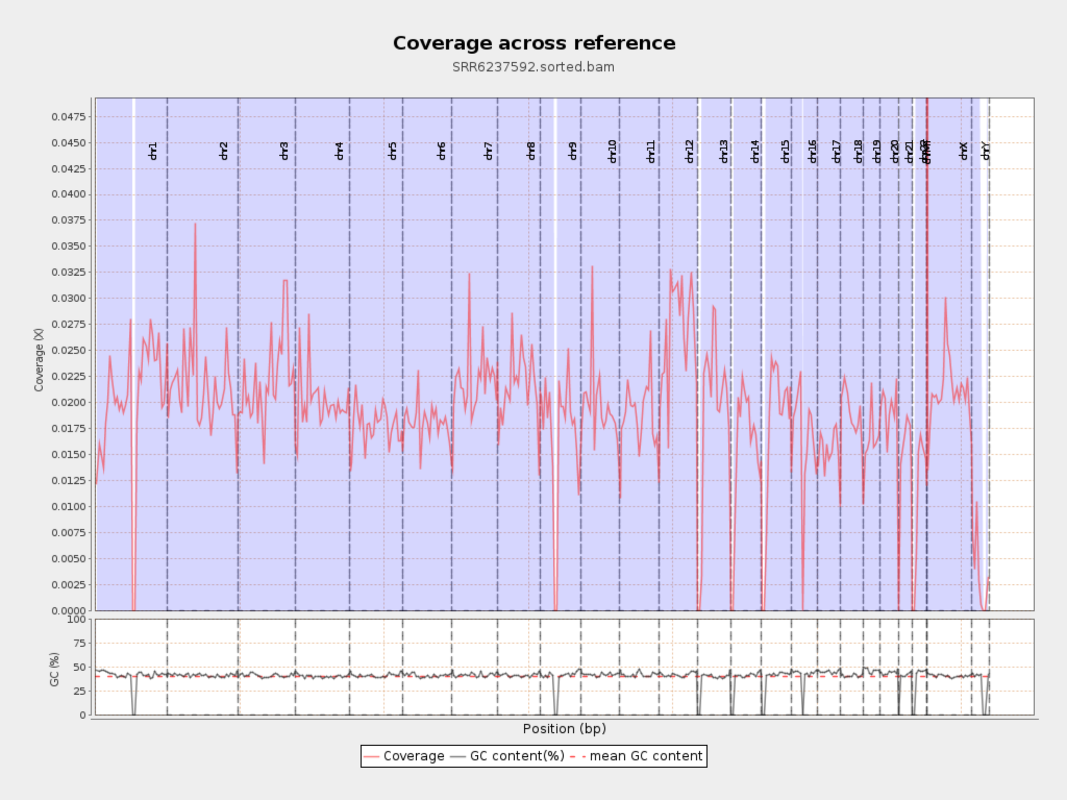
General error rate	1.02%
Mismatches	591,749
Insertions	5,672
Mapped reads with at least one insertion	0.59%
Deletions	21,621
Mapped reads with at least one deletion	2.24%
Homopolymer indels	47.62%

2.6. Chromosome stats

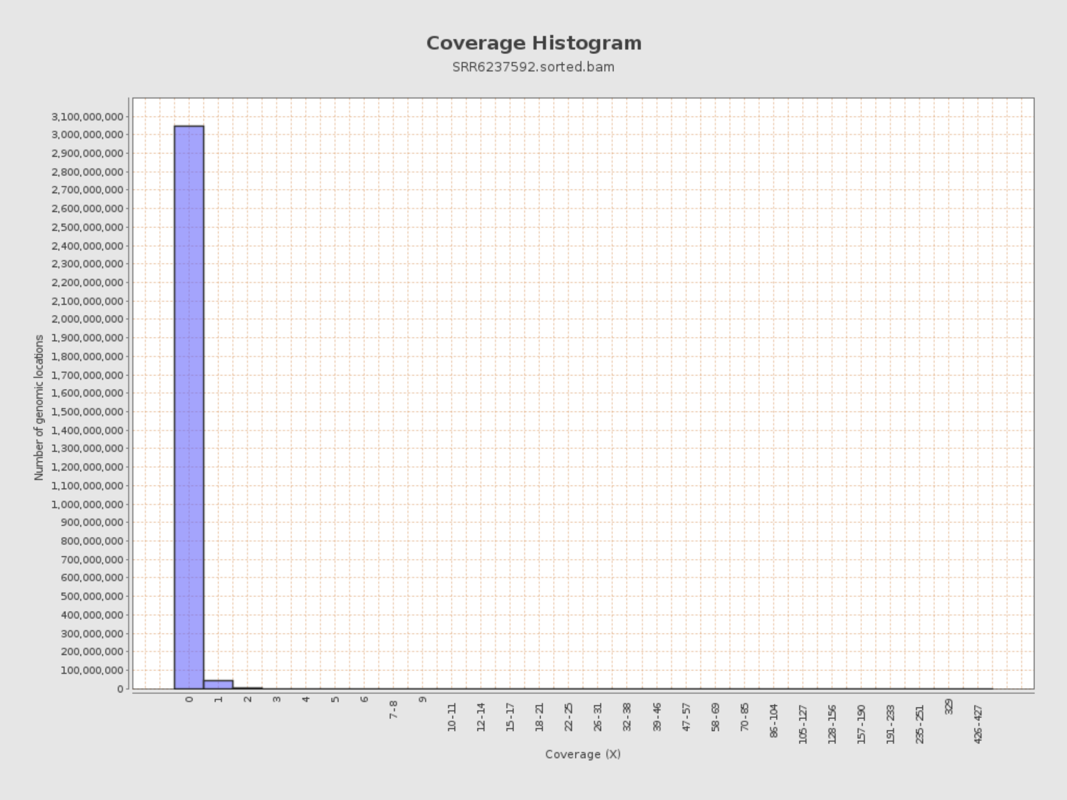
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4993370	0.02	0.2524
chr2	243199373	5229084	0.0215	0.2883
chr3	198022430	4368136	0.0221	0.175
chr4	191154276	3812681	0.0199	0.1701
chr5	180915260	3235581	0.0179	0.1529
chr6	171115067	3081289	0.018	0.1756
chr7	159138663	3499781	0.022	0.2879

chr8	146364022	3150424	0.0215	0.2258
chr9	141213431	2363006	0.0167	0.2036
chr10	135534747	2655124	0.0196	0.1973
chr11	135006516	2557664	0.0189	0.2103
chr12	133851895	3596587	0.0269	0.198
chr13	115169878	2149992	0.0187	0.1643
chr14	107349540	1642478	0.0153	0.1585
chr15	102531392	1760539	0.0172	0.155
chr16	90354753	1445992	0.016	0.1604
chr17	81195210	1249493	0.0154	0.1538
chr18	78077248	1488024	0.0191	0.3556
chr19	59128983	975815	0.0165	0.1936
chr20	63025520	1204357	0.0191	0.1662
chr21	48129895	711623	0.0148	0.1499
chr22	51304566	550741	0.0107	0.1207
chrMT	16571	49336	2.9772	2.5047
chrX	155270560	3297548	0.0212	0.1763
chrY	59373566	201189	0.0034	0.0885

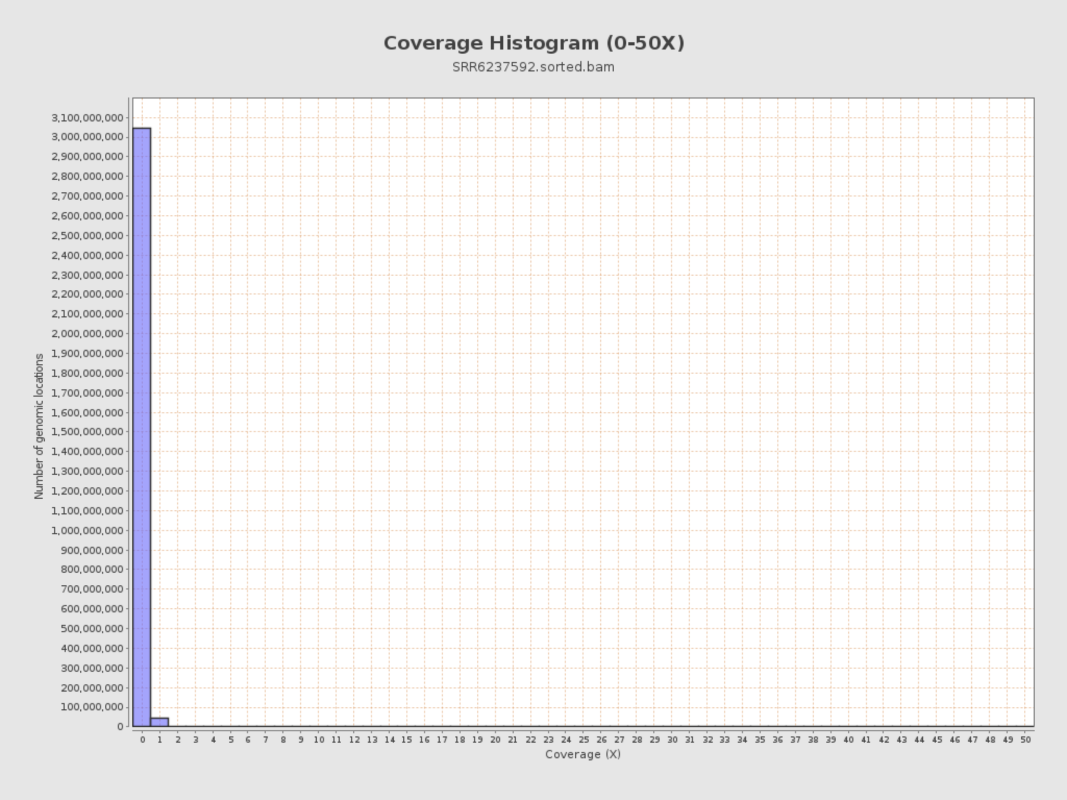
3. Results : Coverage across reference



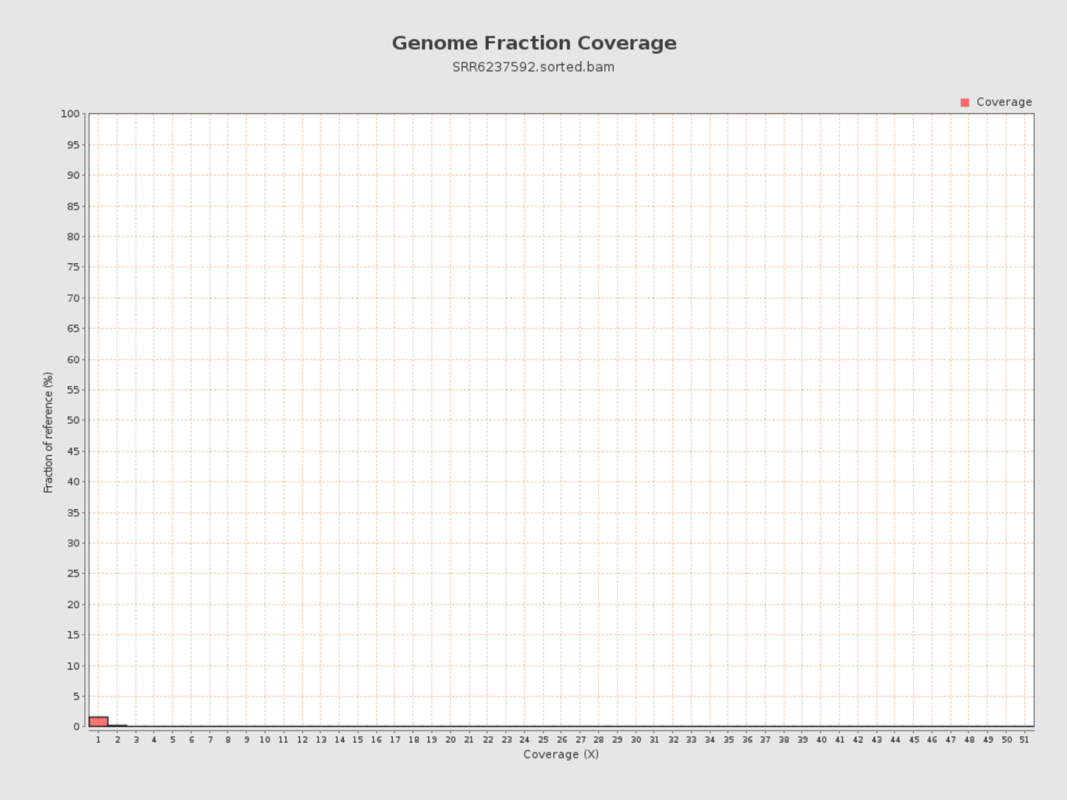
4. Results : Coverage Histogram



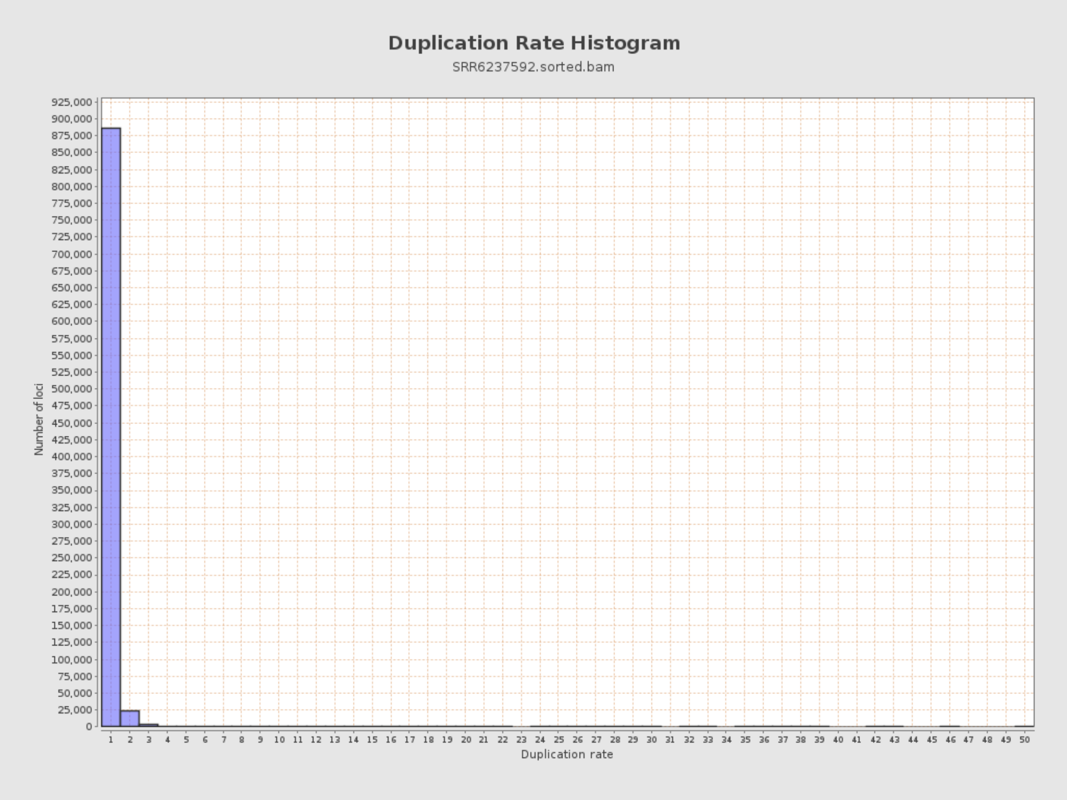
5. Results : Coverage Histogram (0-50X)



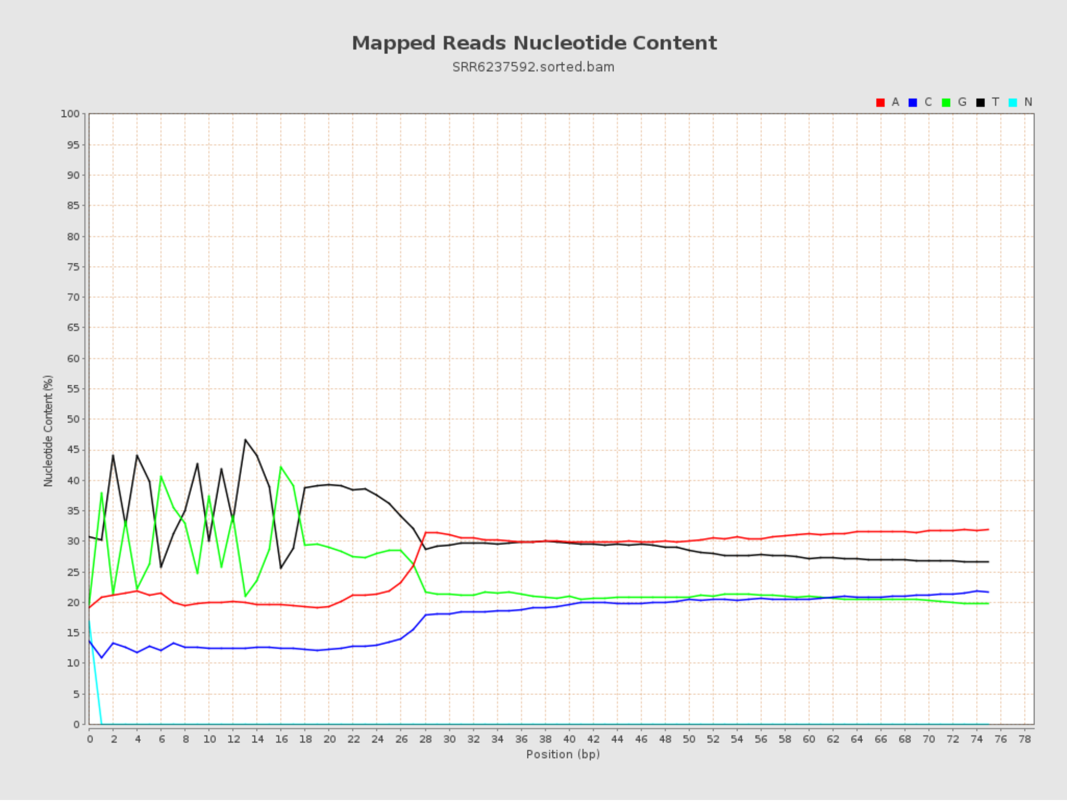
6. Results : Genome Fraction Coverage



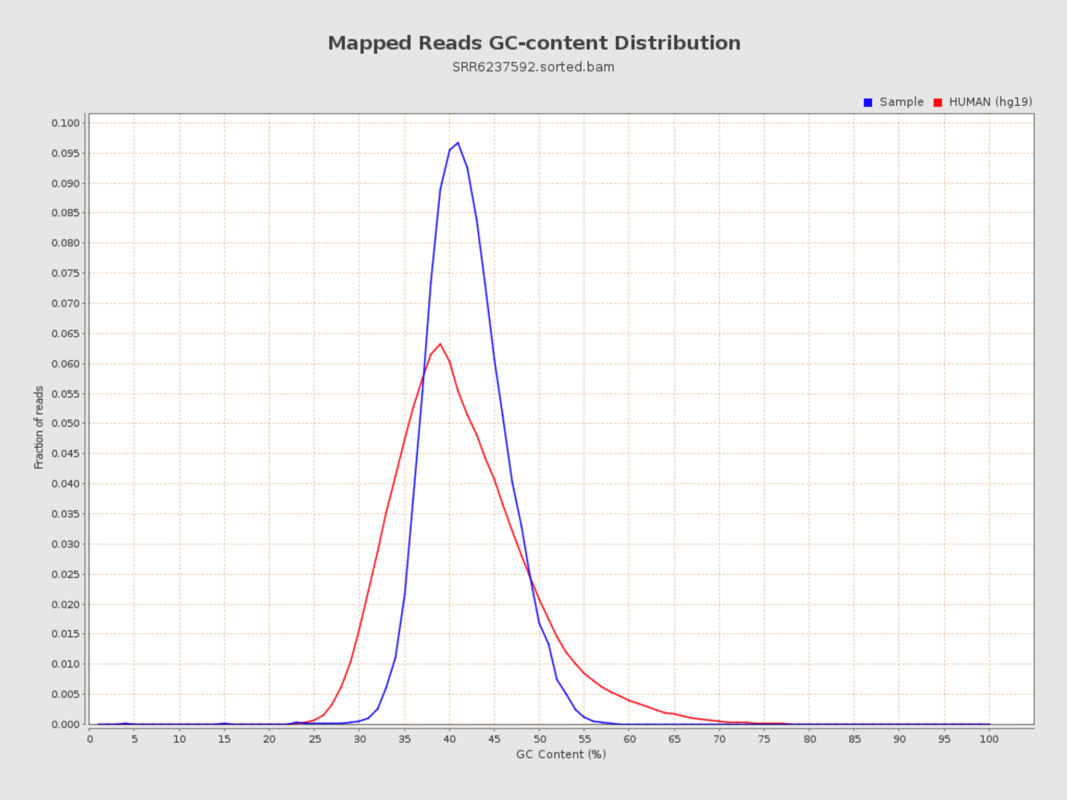
7. Results : Duplication Rate Histogram



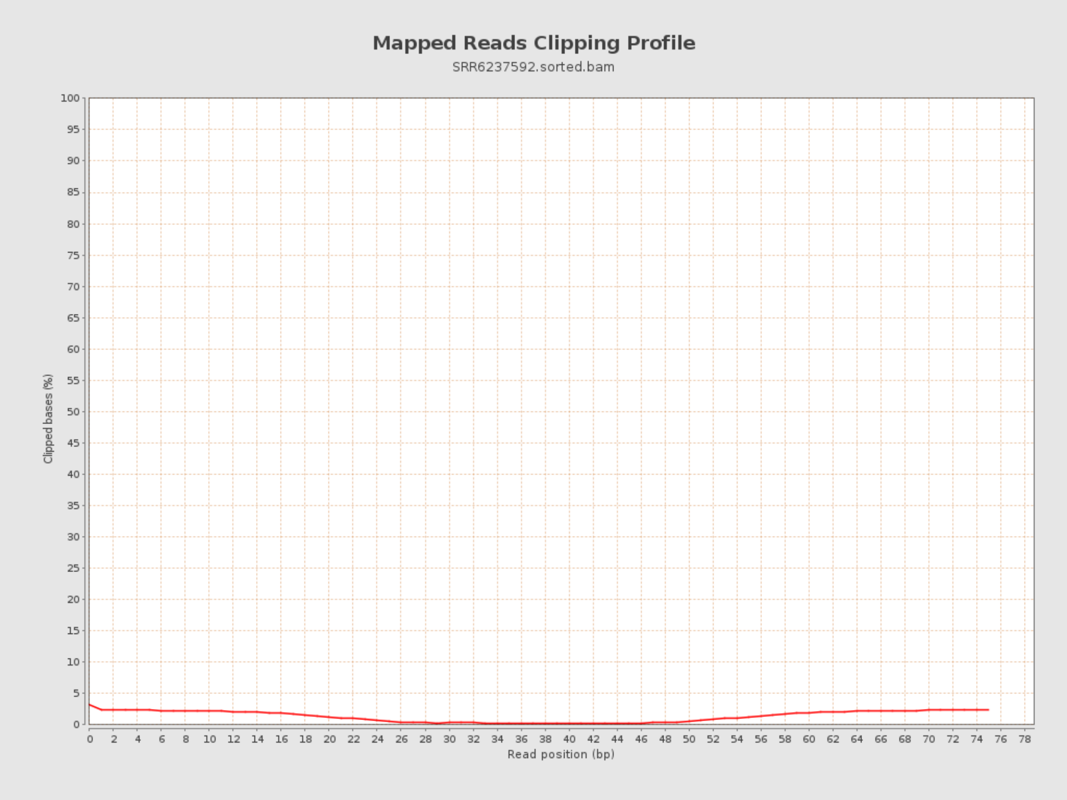
8. Results : Mapped Reads Nucleotide Content



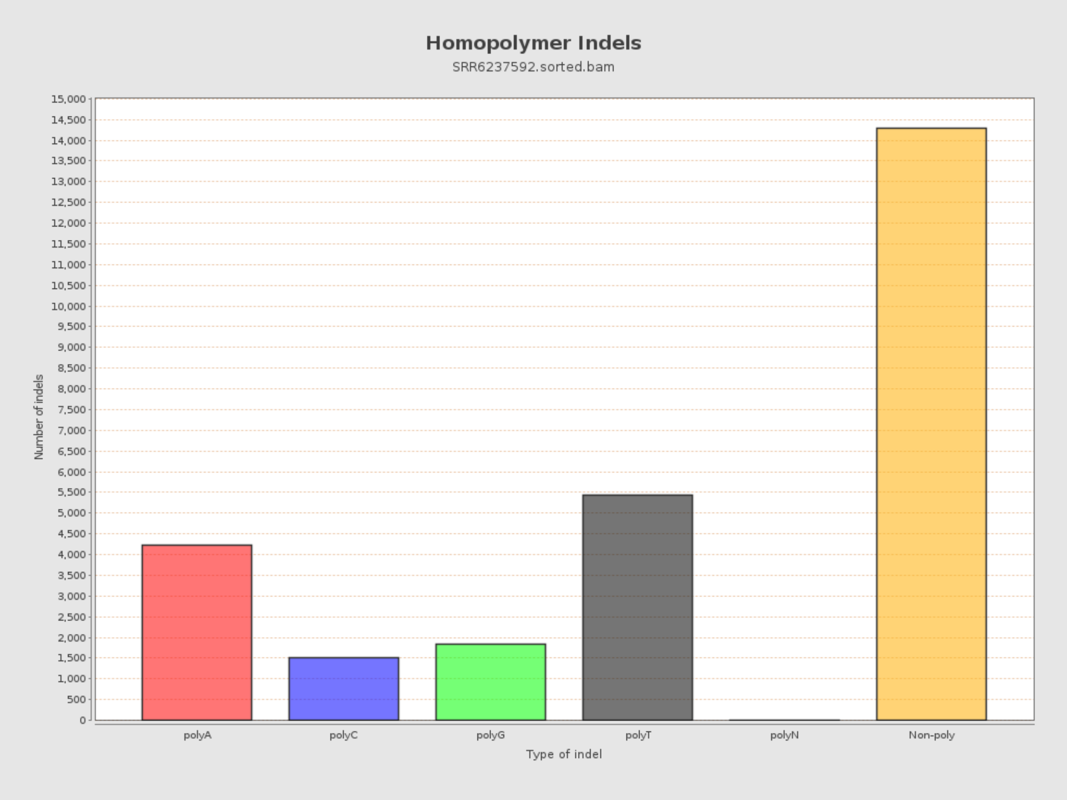
9. Results : Mapped Reads GC-content Distribution



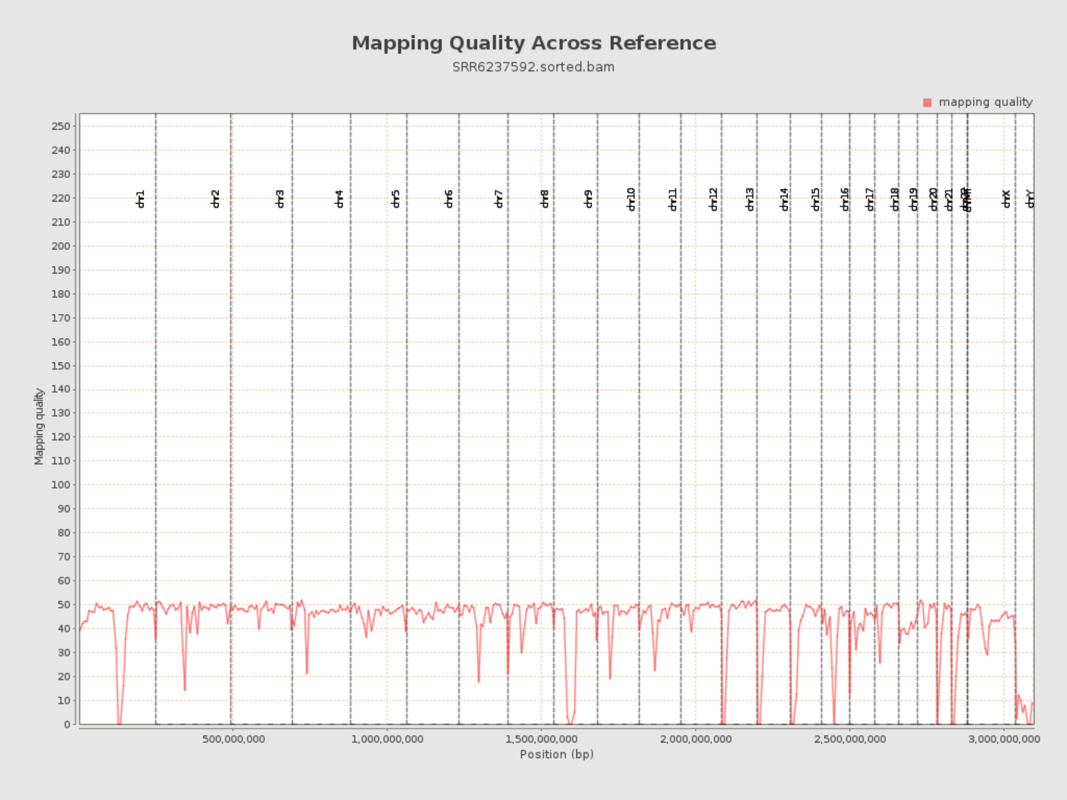
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram