Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 02:39:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237326.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_SRR6237326 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237326.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 02:39:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237326.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,866,743
Mapped reads	2,621,138 / 91.43%
Unmapped reads	245,605 / 8.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	30,695 / 1.07%
Read min/max/mean length	30 / 76 / 76.37
Duplicated reads (estimated)	562,876 / 19.63%
Duplication rate	17.01%
Clipped reads	1,671,834 / 58.32%

2.2. ACGT Content

Number/percentage of A's	41,772,190 / 25.66%
Number/percentage of C's	28,338,336 / 17.41%
Number/percentage of T's	54,120,129 / 33.24%
Number/percentage of G's	38,562,340 / 23.69%
Number/percentage of N's	17,583 / 0.01%
GC Percentage	41.09%

2.3. Coverage

Mean	0.0526

Standard Deviation	0.5669

2.4. Mapping Quality

Mean Mapping Quality	43.29

2.5. Mismatches and indels

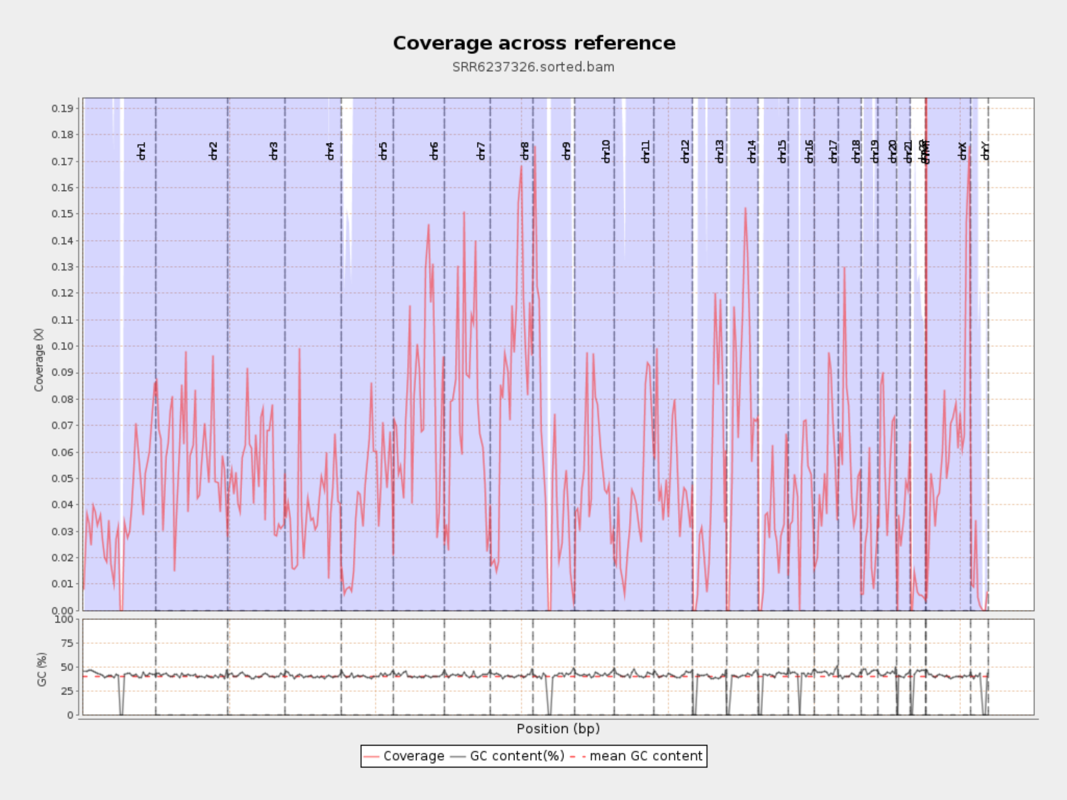
General error rate	0.59%
Mismatches	934,633
Insertions	11,812
Mapped reads with at least one insertion	0.45%
Deletions	41,687
Mapped reads with at least one deletion	1.57%
Homopolymer indels	43.28%

2.6. Chromosome stats

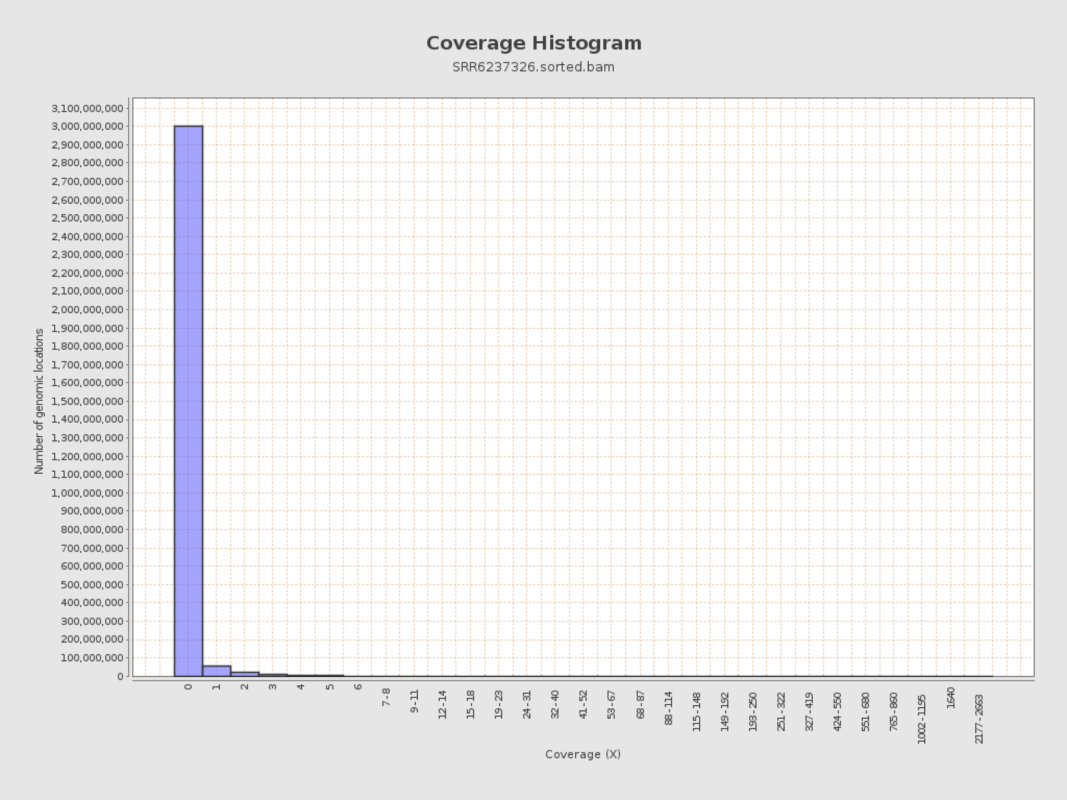
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9093311	0.0365	0.3774
chr2	243199373	14456084	0.0594	1.2688
chr3	198022430	10340871	0.0522	0.3605
chr4	191154276	7382479	0.0386	0.4392
chr5	180915260	7457826	0.0412	0.3205
chr6	171115067	13887157	0.0812	0.5963
chr7	159138663	12146163	0.0763	0.4963

chr8	146364022	12736965	0.087	0.7241
chr9	141213431	7460699	0.0528	0.4416
chr10	135534747	7188709	0.053	0.5918
chr11	135006516	5721609	0.0424	0.3622
chr12	133851895	6767999	0.0506	0.3604
chr13	115169878	5386768	0.0468	0.3888
chr14	107349540	8746246	0.0815	0.4569
chr15	102531392	3040703	0.0297	0.292
chr16	90354753	3917905	0.0434	0.3532
chr17	81195210	4143486	0.051	0.3816
chr18	78077248	4894701	0.0627	0.9338
chr19	59128983	1447443	0.0245	0.3305
chr20	63025520	3823094	0.0607	0.4023
chr21	48129895	1789403	0.0372	0.3595
chr22	51304566	304105	0.0059	0.1102
chrMT	16571	23437	1.4143	2.2104
chrX	155270560	10234764	0.0659	0.4291
chrY	59373566	491461	0.0083	0.3398

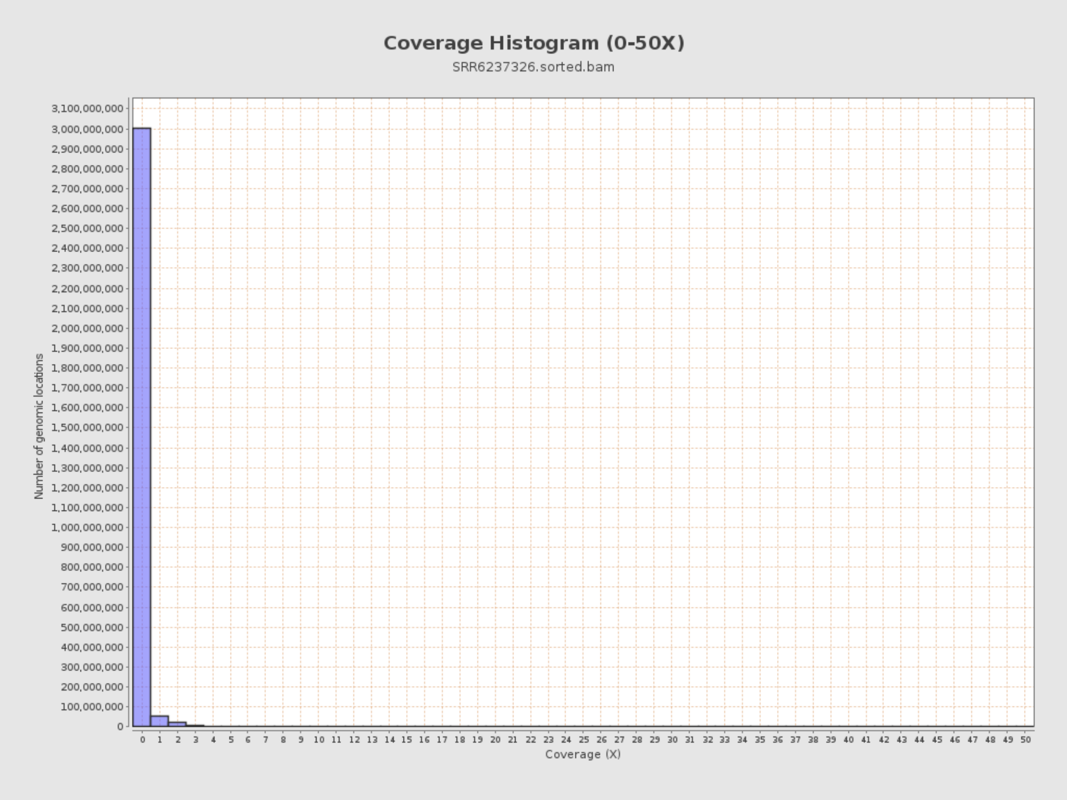
3. Results : Coverage across reference



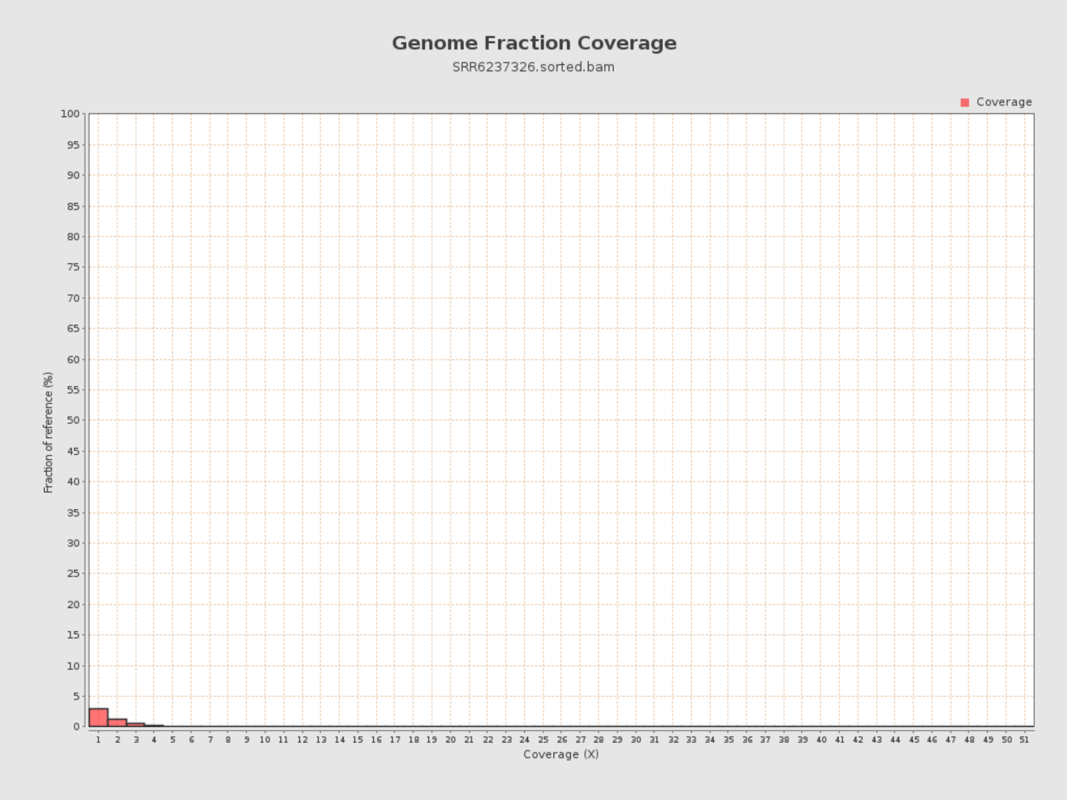
4. Results : Coverage Histogram



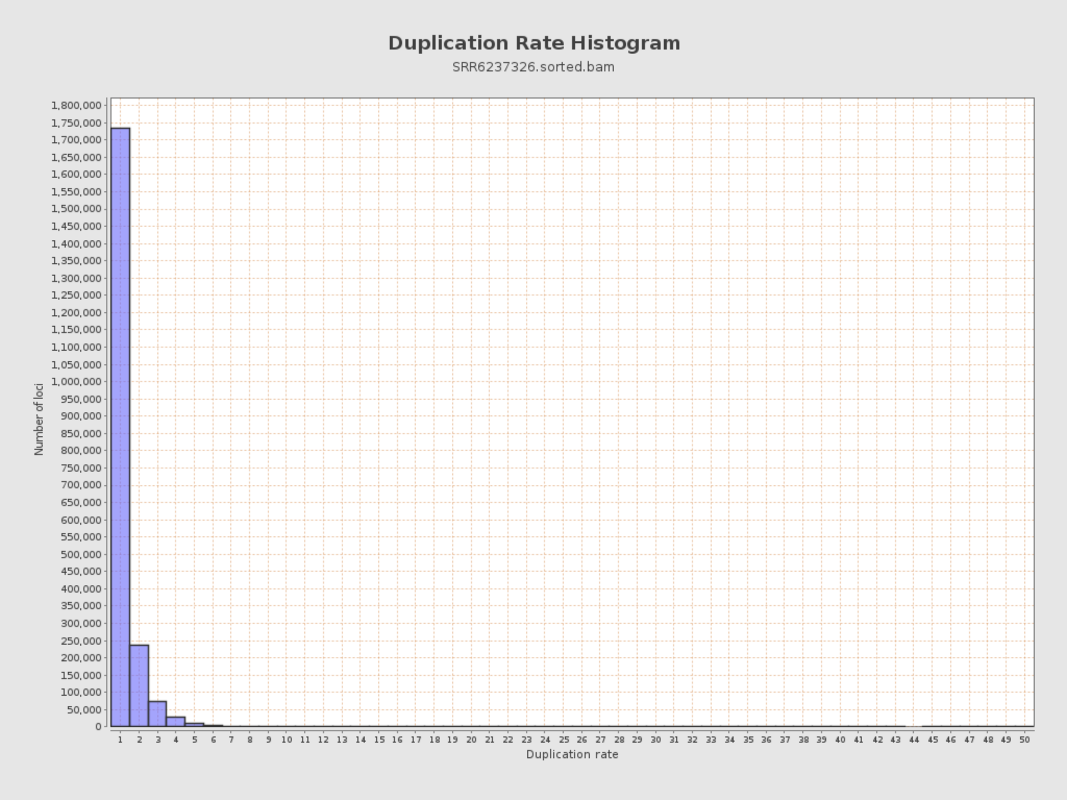
5. Results : Coverage Histogram (0-50X)



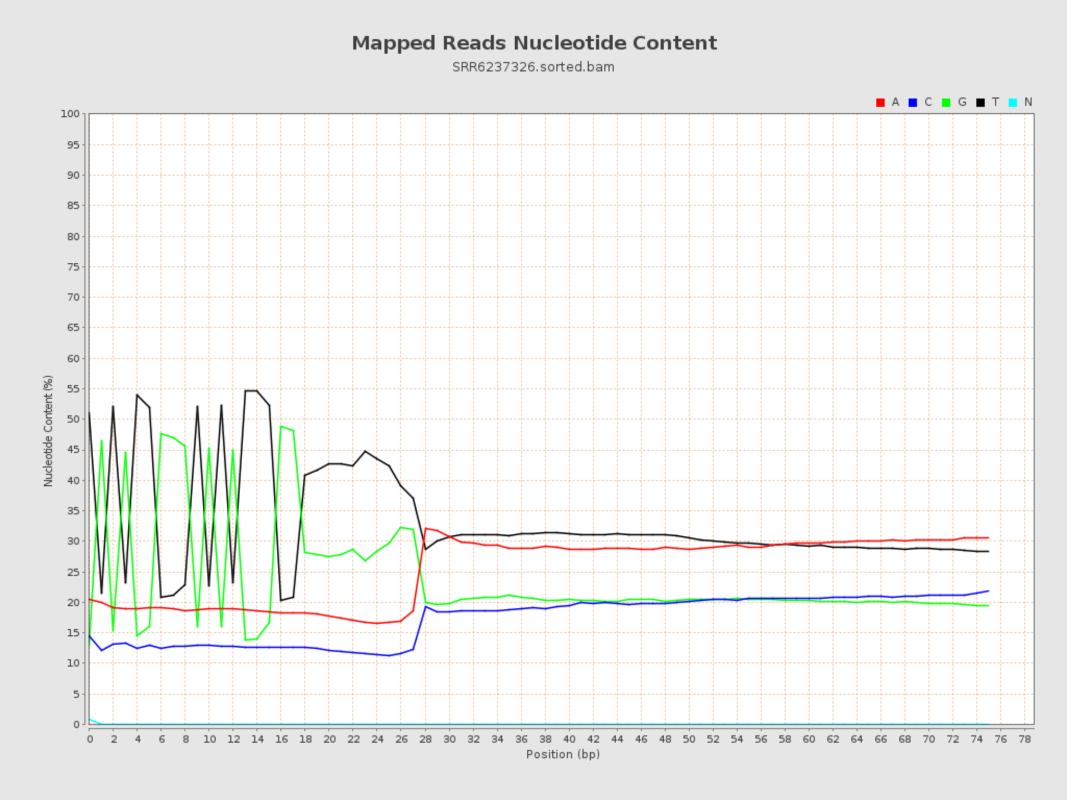
6. Results : Genome Fraction Coverage



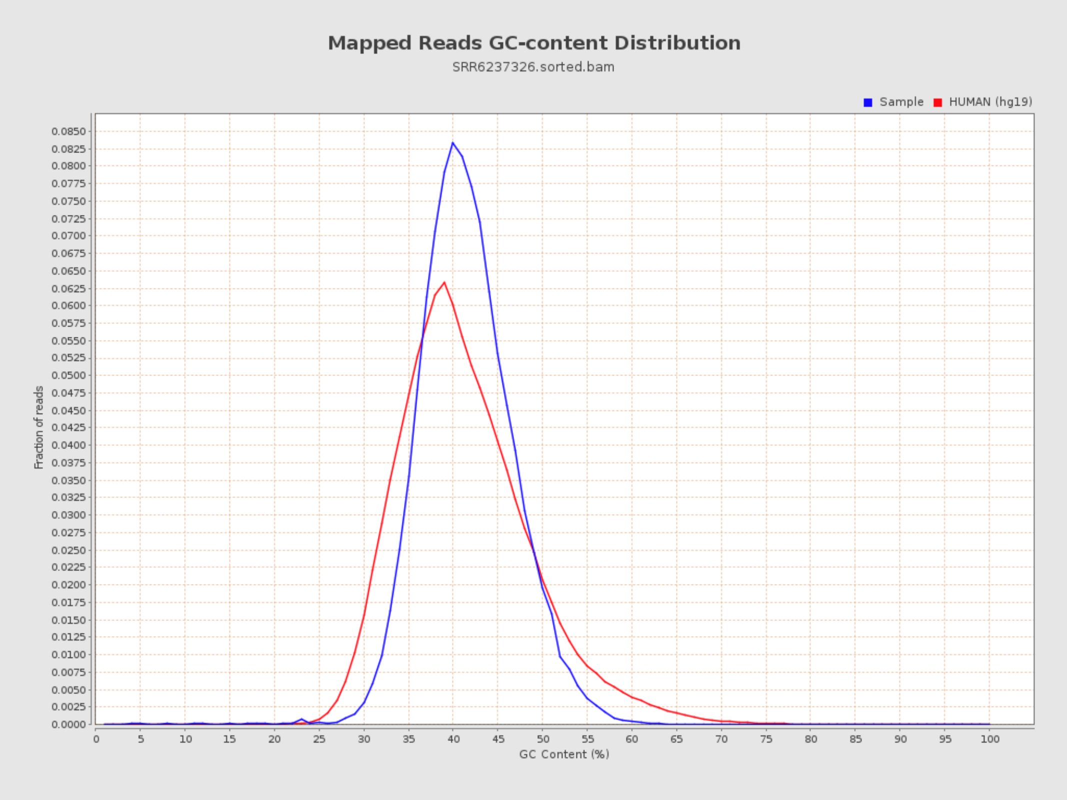
7. Results : Duplication Rate Histogram



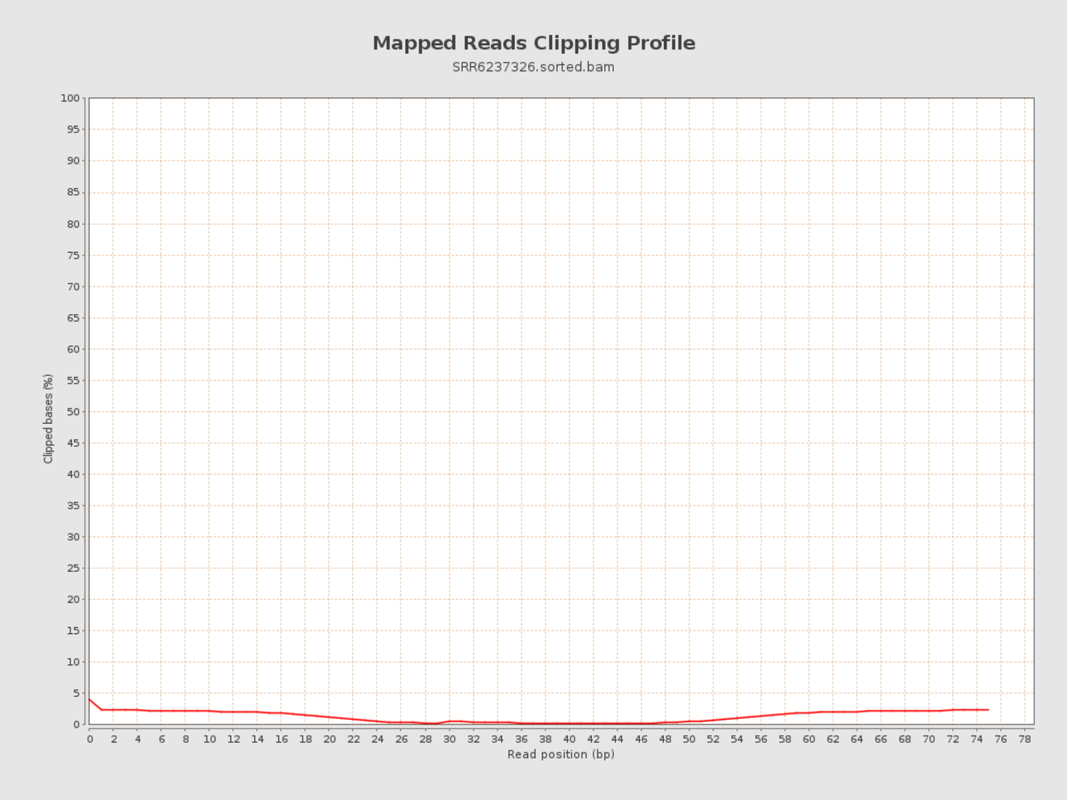
8. Results : Mapped Reads Nucleotide Content



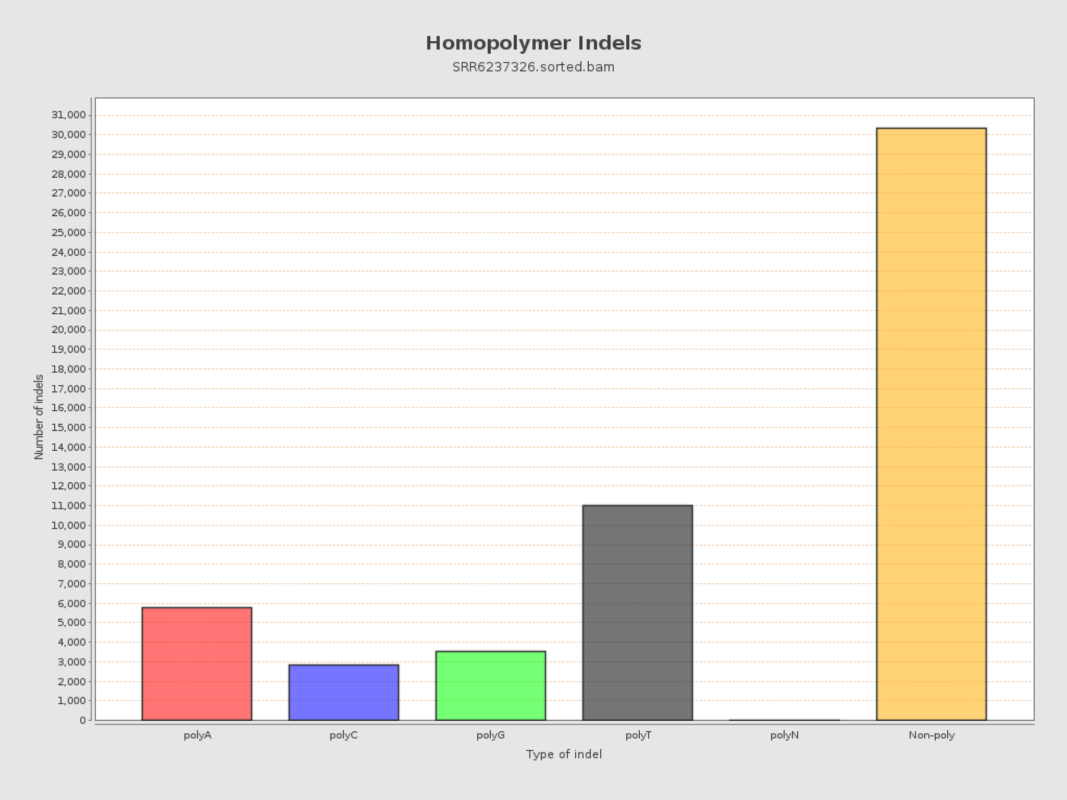
9. Results : Mapped Reads GC-content Distribution



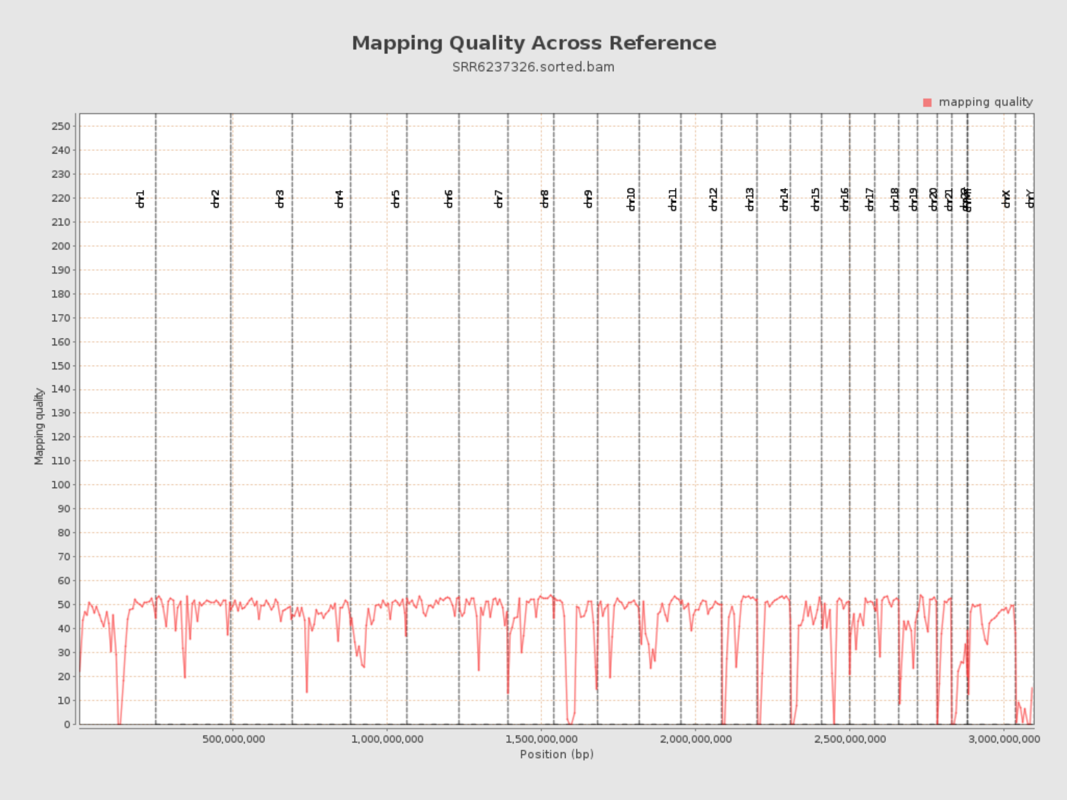
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram