Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 23:19:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237267.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_SRR6237267 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237267.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 23:19:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237267.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,030,819
Mapped reads	1,820,900 / 89.66%
Unmapped reads	209,919 / 10.34%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,720 / 0.58%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	97,264 / 4.79%
Duplication rate	4.15%
Clipped reads	765,464 / 37.69%

2.2. ACGT Content

Number/percentage of A's	34,654,062 / 28.38%
Number/percentage of C's	21,832,058 / 17.88%
Number/percentage of T's	39,450,800 / 32.31%
Number/percentage of G's	26,163,424 / 21.43%
Number/percentage of N's	1,974 / 0%
GC Percentage	39.31%

2.3. Coverage

Mean	0.0395

Standard Deviation	0.4097

2.4. Mapping Quality

Mean Mapping Quality	45.17

2.5. Mismatches and indels

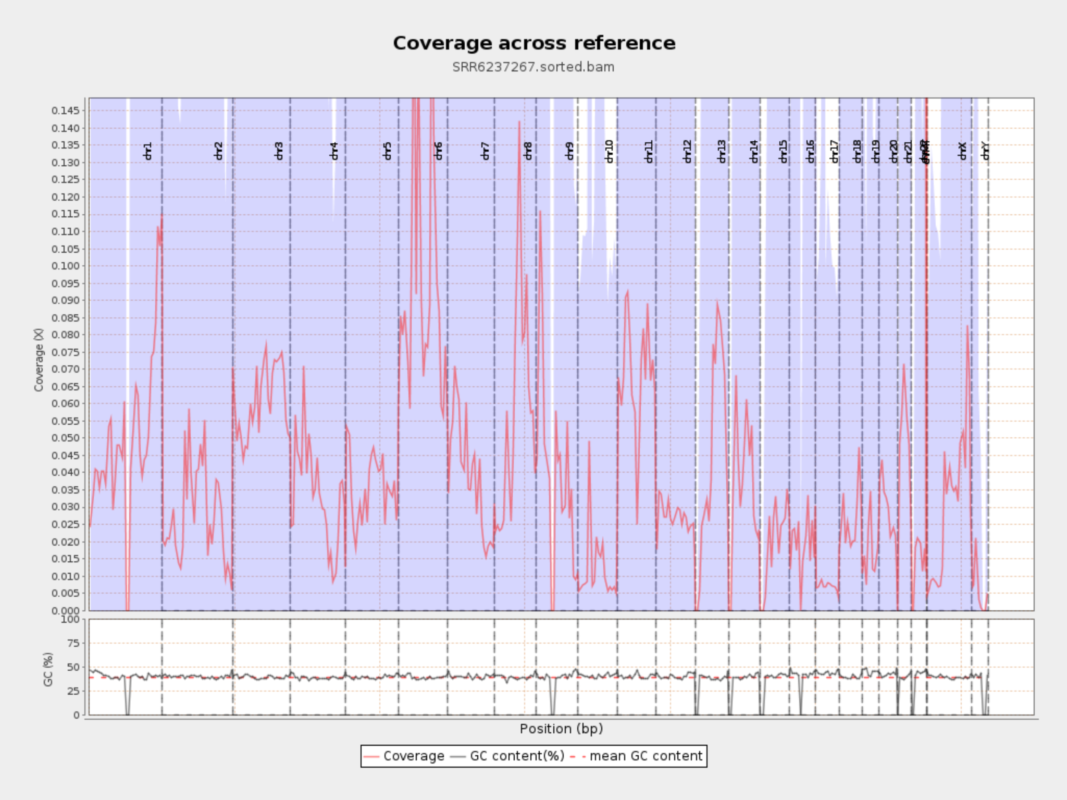
General error rate	0.79%
Mismatches	946,497
Insertions	9,715
Mapped reads with at least one insertion	0.53%
Deletions	35,487
Mapped reads with at least one deletion	1.93%
Homopolymer indels	46.52%

2.6. Chromosome stats

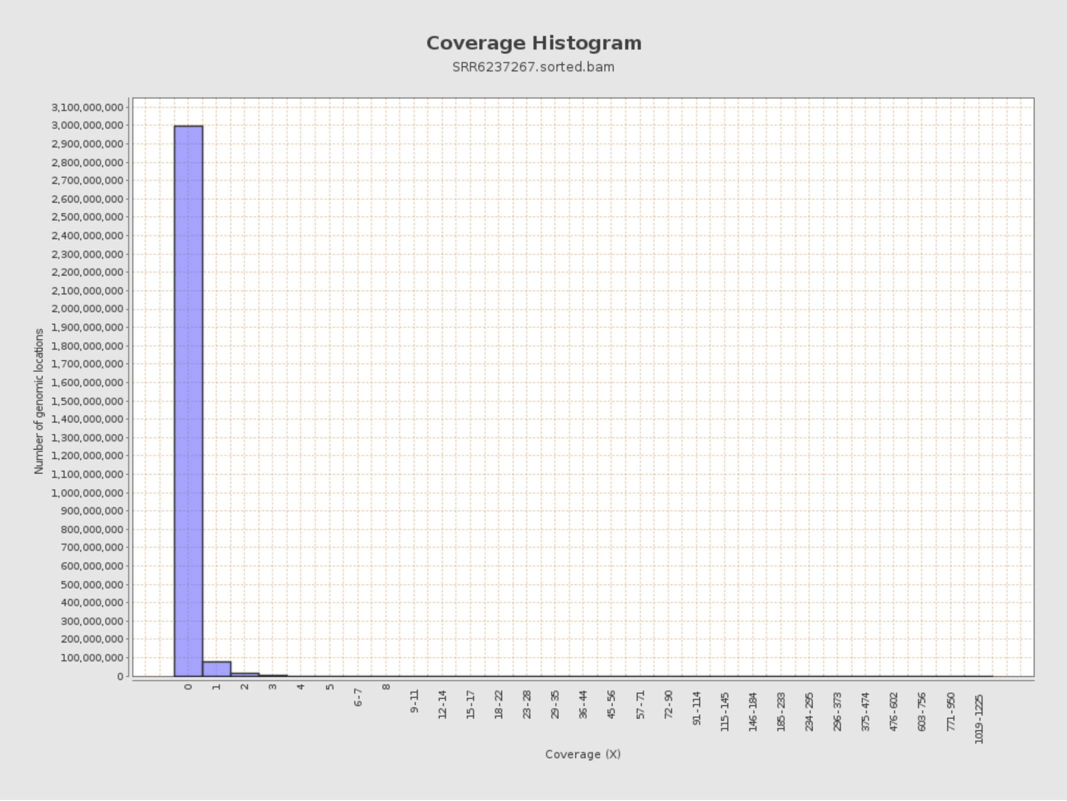
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12268165	0.0492	0.6315
chr2	243199373	6775396	0.0279	0.3432
chr3	198022430	12079131	0.061	0.2948
chr4	191154276	6507038	0.034	0.247
chr5	180915260	6415674	0.0355	0.2259
chr6	171115067	16410184	0.0959	0.7008
chr7	159138663	6280114	0.0395	0.3866

chr8	146364022	8441775	0.0577	0.7961
chr9	141213431	5857995	0.0415	0.3699
chr10	135534747	1634623	0.0121	0.2993
chr11	135006516	9117277	0.0675	0.4303
chr12	133851895	3628536	0.0271	0.2061
chr13	115169878	5182883	0.045	0.2535
chr14	107349540	3837043	0.0357	0.246
chr15	102531392	2011356	0.0196	0.1722
chr16	90354753	1741128	0.0193	0.2125
chr17	81195210	570737	0.007	0.1437
chr18	78077248	2087834	0.0267	0.681
chr19	59128983	1048781	0.0177	0.3653
chr20	63025520	1873888	0.0297	0.2126
chr21	48129895	2289747	0.0476	0.2877
chr22	51304566	706078	0.0138	0.1373
chrMT	16571	252429	15.2332	8.9721
chrX	155270560	4821368	0.0311	0.2284
chrY	59373566	325516	0.0055	0.1589

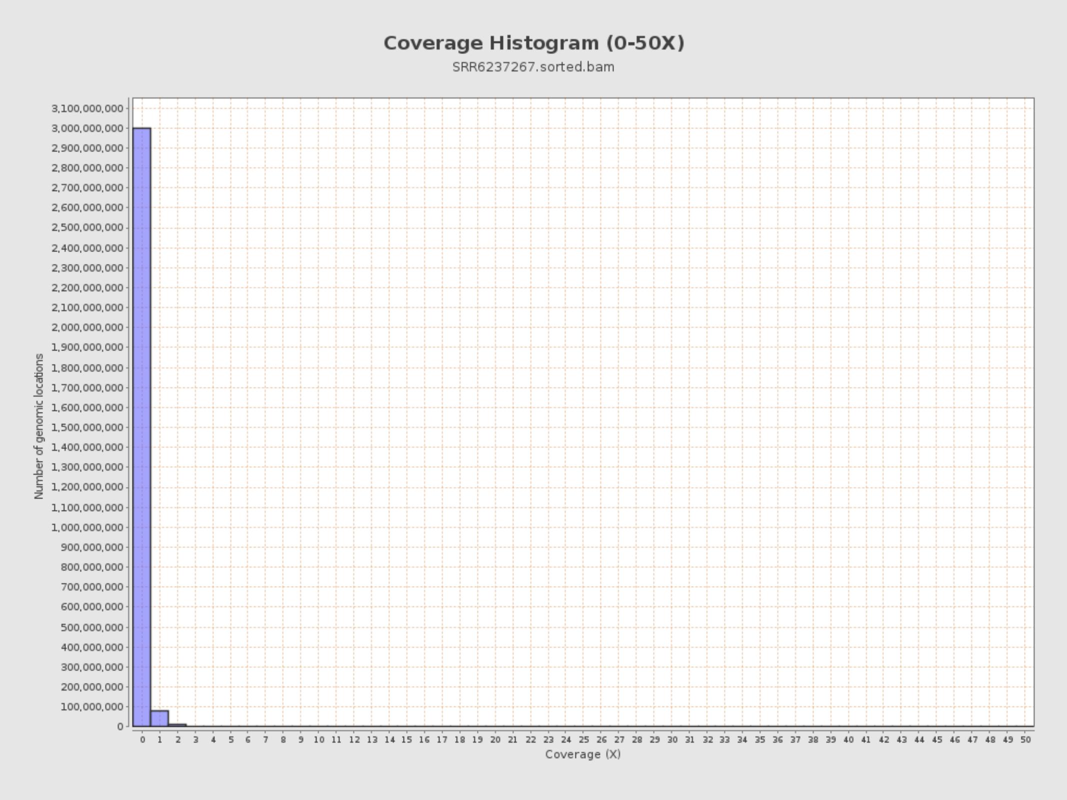
3. Results : Coverage across reference



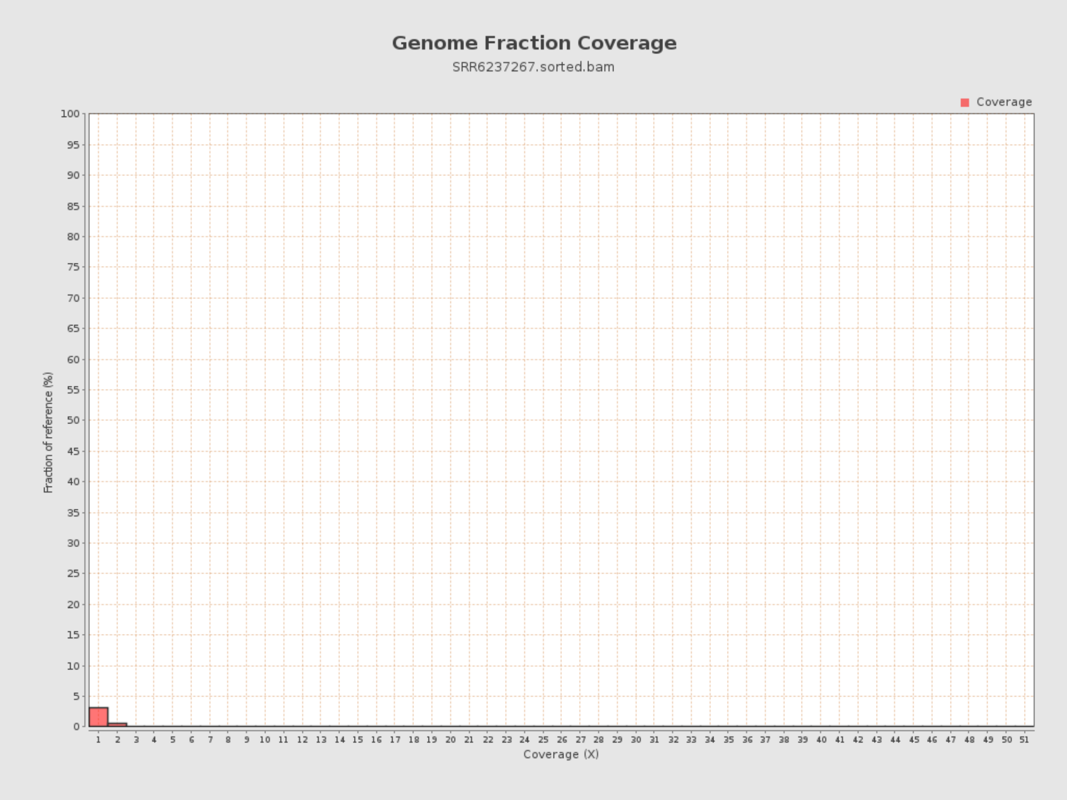
4. Results : Coverage Histogram



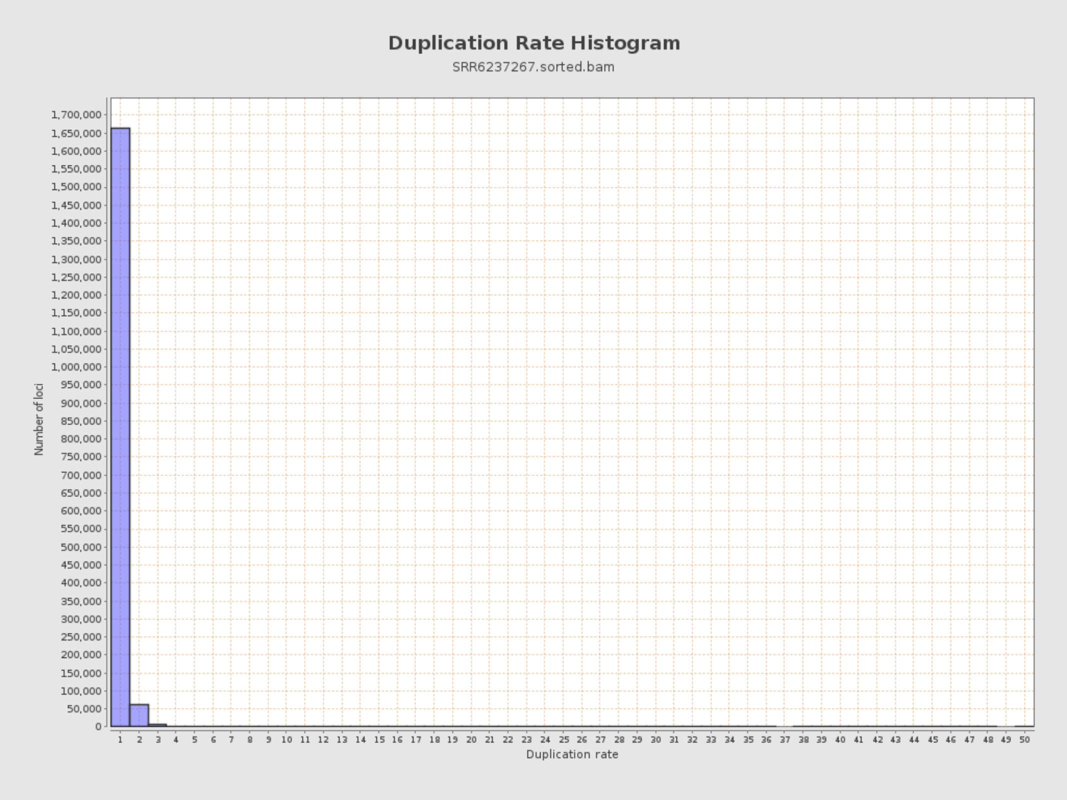
5. Results : Coverage Histogram (0-50X)



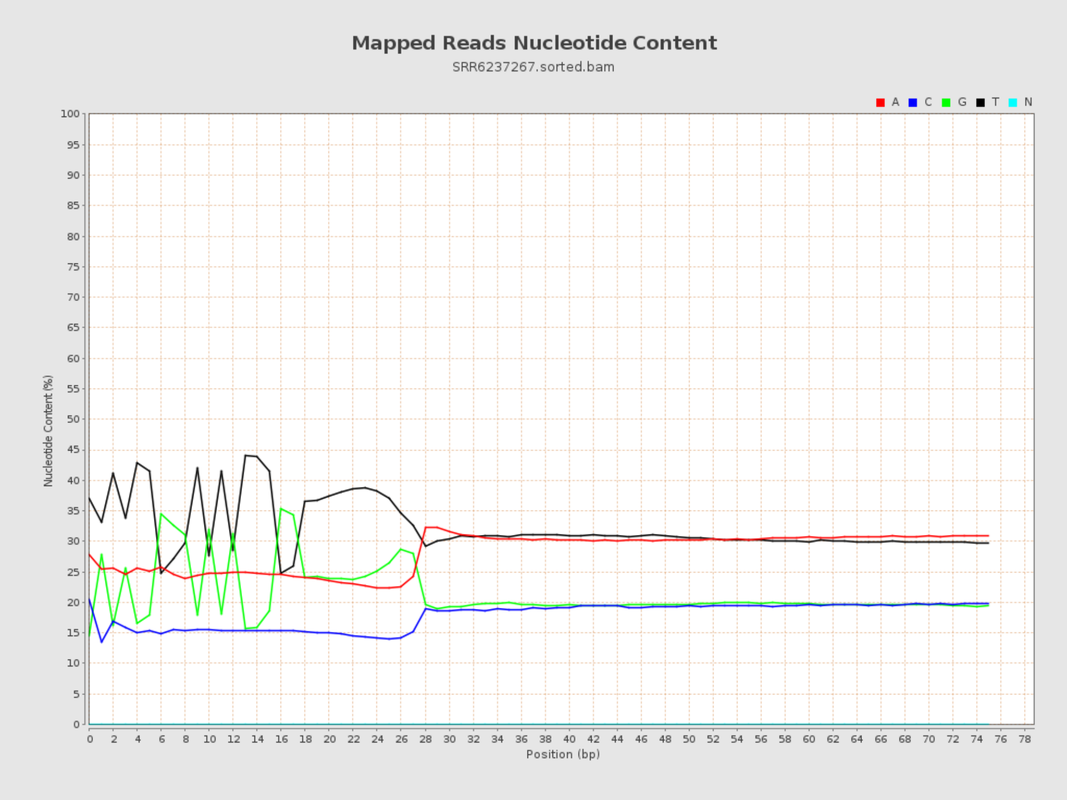
6. Results : Genome Fraction Coverage



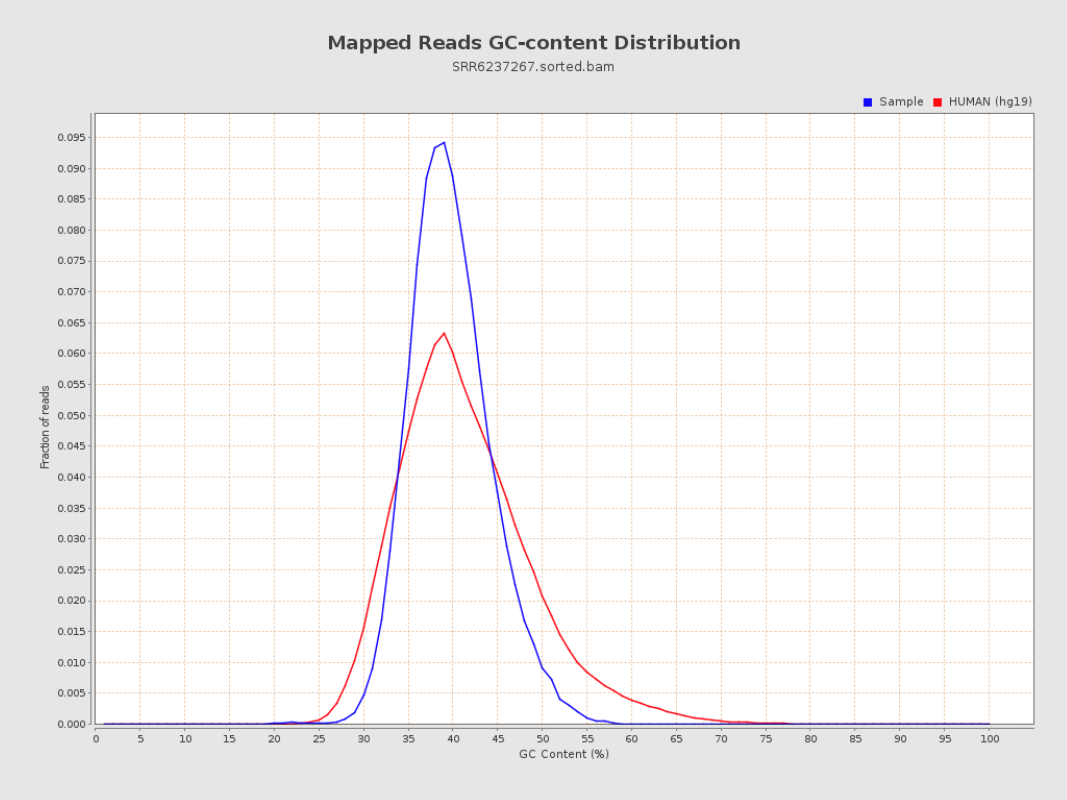
7. Results : Duplication Rate Histogram



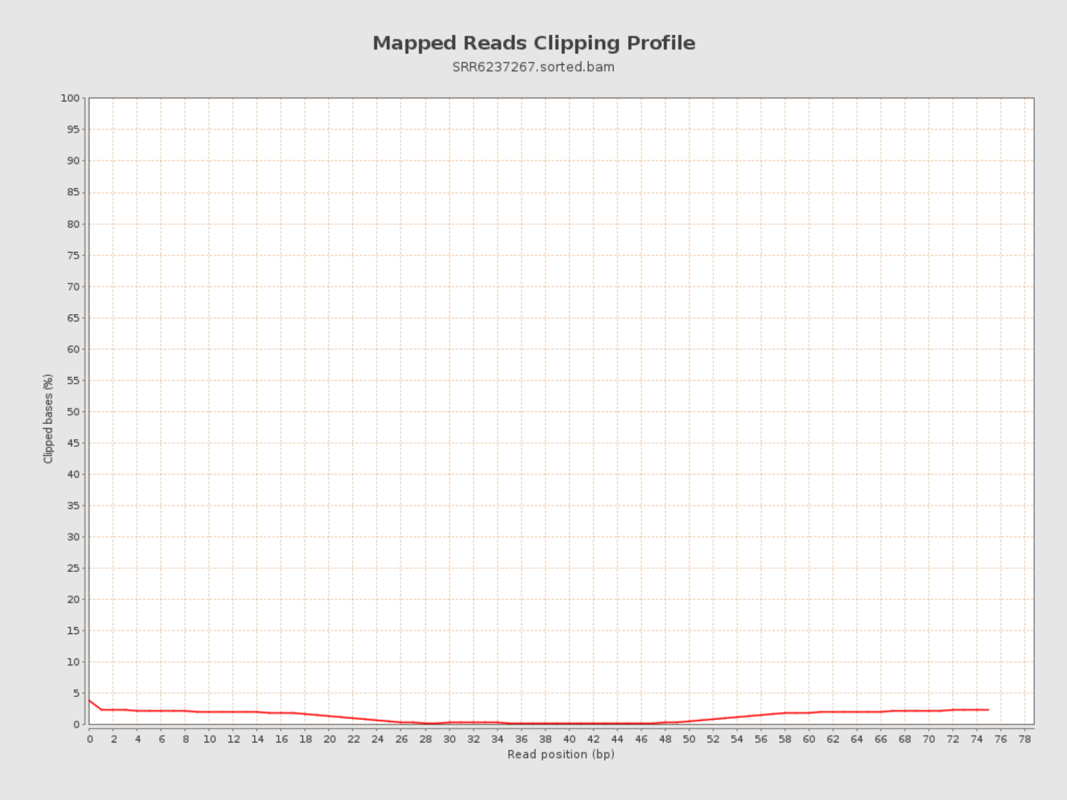
8. Results : Mapped Reads Nucleotide Content



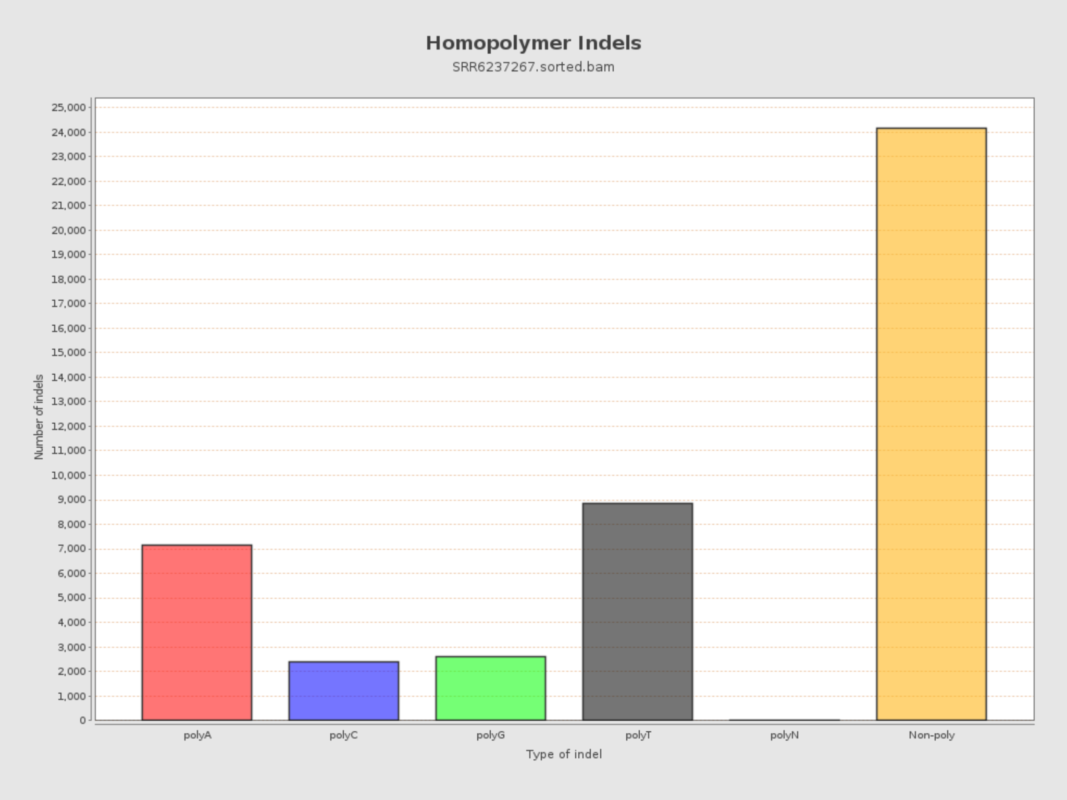
9. Results : Mapped Reads GC-content Distribution



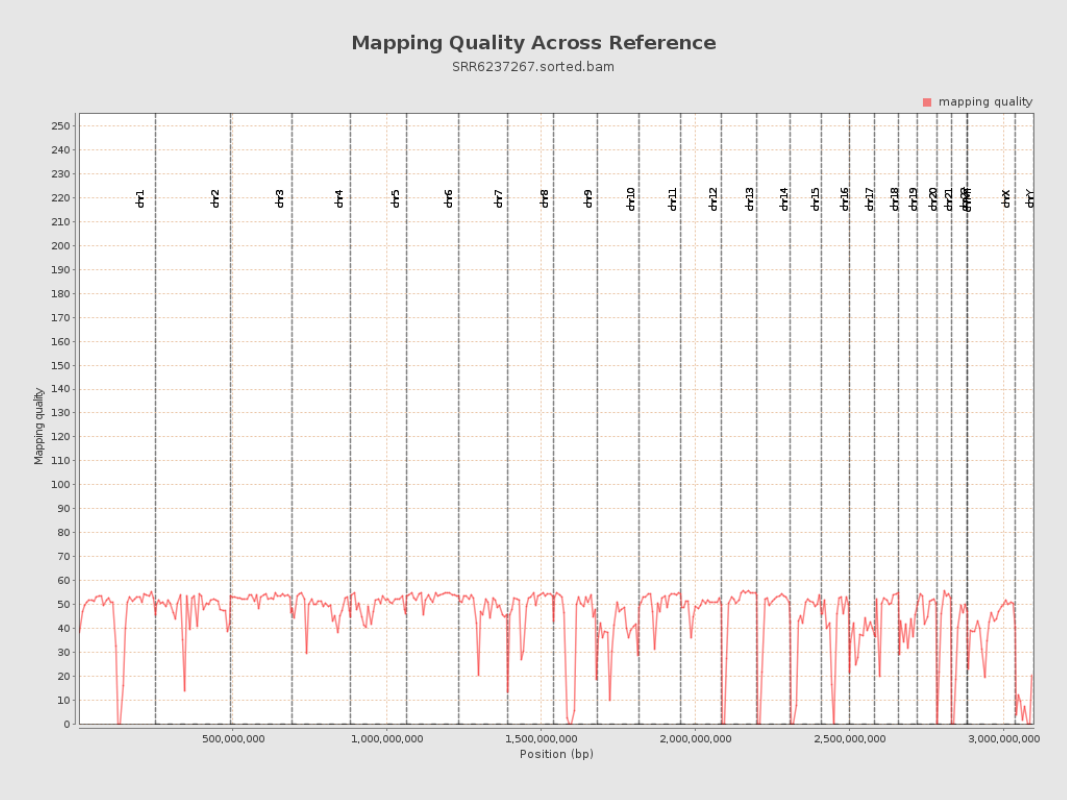
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram