Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 00:54:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237296.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_SRR6237296 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237296.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 00:54:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237296.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,581,504
Mapped reads	5,223,993 / 93.59%
Unmapped reads	357,511 / 6.41%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	36,600 / 0.66%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	390,031 / 6.99%
Duplication rate	4.93%
Clipped reads	1,474,650 / 26.42%

2.2. ACGT Content

Number/percentage of A's	109,042,770 / 29.46%
Number/percentage of C's	71,779,317 / 19.39%
Number/percentage of T's	113,343,506 / 30.62%
Number/percentage of G's	75,980,273 / 20.53%
Number/percentage of N's	6,371 / 0%
GC Percentage	39.92%

2.3. Coverage

Mean	0.1196

Standard Deviation	1.4302

2.4. Mapping Quality

Mean Mapping Quality	46.41

2.5. Mismatches and indels

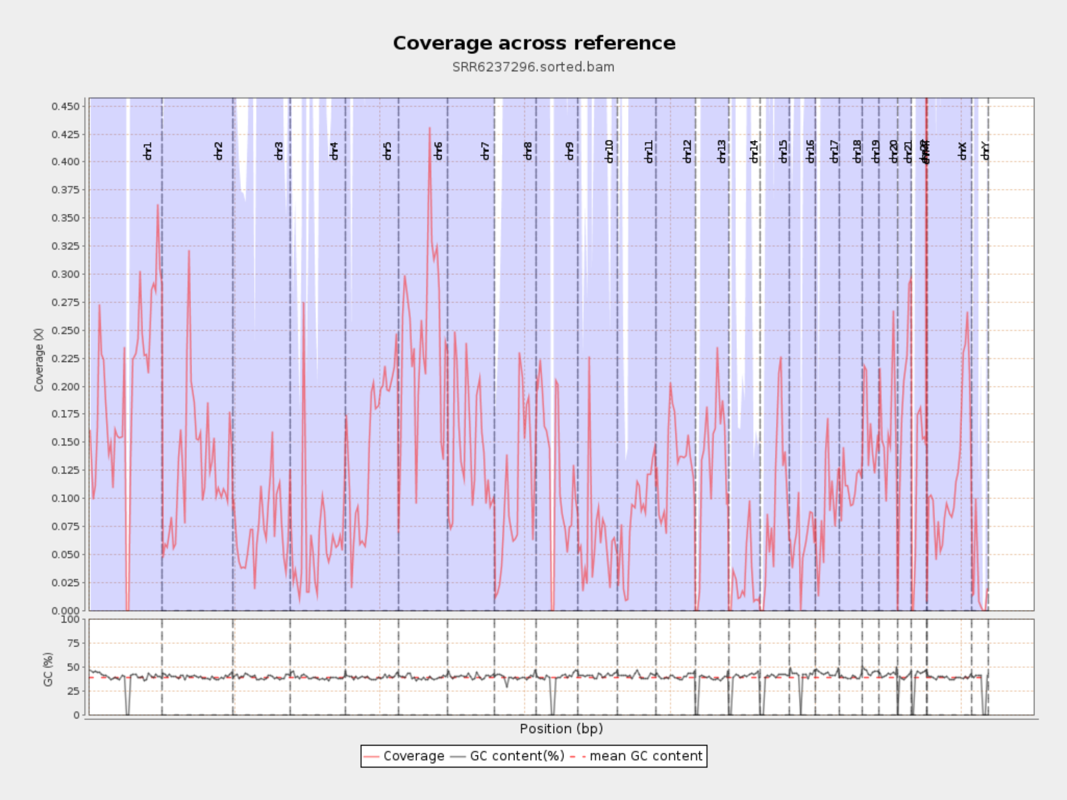
General error rate	0.8%
Mismatches	2,855,951
Insertions	36,533
Mapped reads with at least one insertion	0.69%
Deletions	94,158
Mapped reads with at least one deletion	1.78%
Homopolymer indels	47.46%

2.6. Chromosome stats

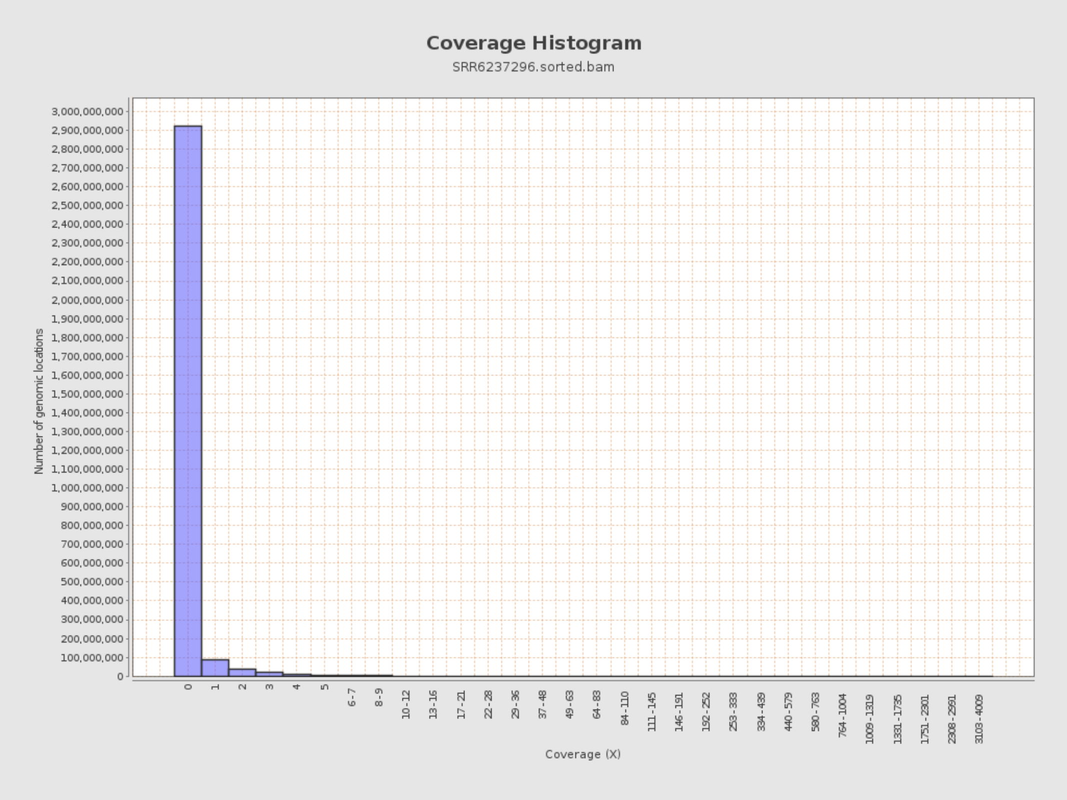
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	49101729	0.197	2.3545
chr2	243199373	31177751	0.1282	1.8063
chr3	198022430	14307260	0.0723	0.4784
chr4	191154276	11332998	0.0593	1.3787
chr5	180915260	26847038	0.1484	0.7353
chr6	171115067	41385986	0.2419	1.1586
chr7	159138663	23127319	0.1453	1.4841

chr8	146364022	15045116	0.1028	2.8449
chr9	141213431	17236688	0.1221	1.2435
chr10	135534747	8526239	0.0629	2.0314
chr11	135006516	11174376	0.0828	0.7505
chr12	133851895	17744278	0.1326	0.7035
chr13	115169878	14810008	0.1286	0.6519
chr14	107349540	2652450	0.0247	0.5421
chr15	102531392	9565850	0.0933	0.5416
chr16	90354753	5678983	0.0629	0.7268
chr17	81195210	7418750	0.0914	0.6602
chr18	78077248	8675203	0.1111	2.1062
chr19	59128983	9555959	0.1616	1.2979
chr20	63025520	10425366	0.1654	0.8524
chr21	48129895	9224541	0.1917	1.3111
chr22	51304566	5800275	0.1131	0.5869
chrMT	16571	31280	1.8876	2.2022
chrX	155270560	18287777	0.1178	0.6733
chrY	59373566	1192007	0.0201	1.3017

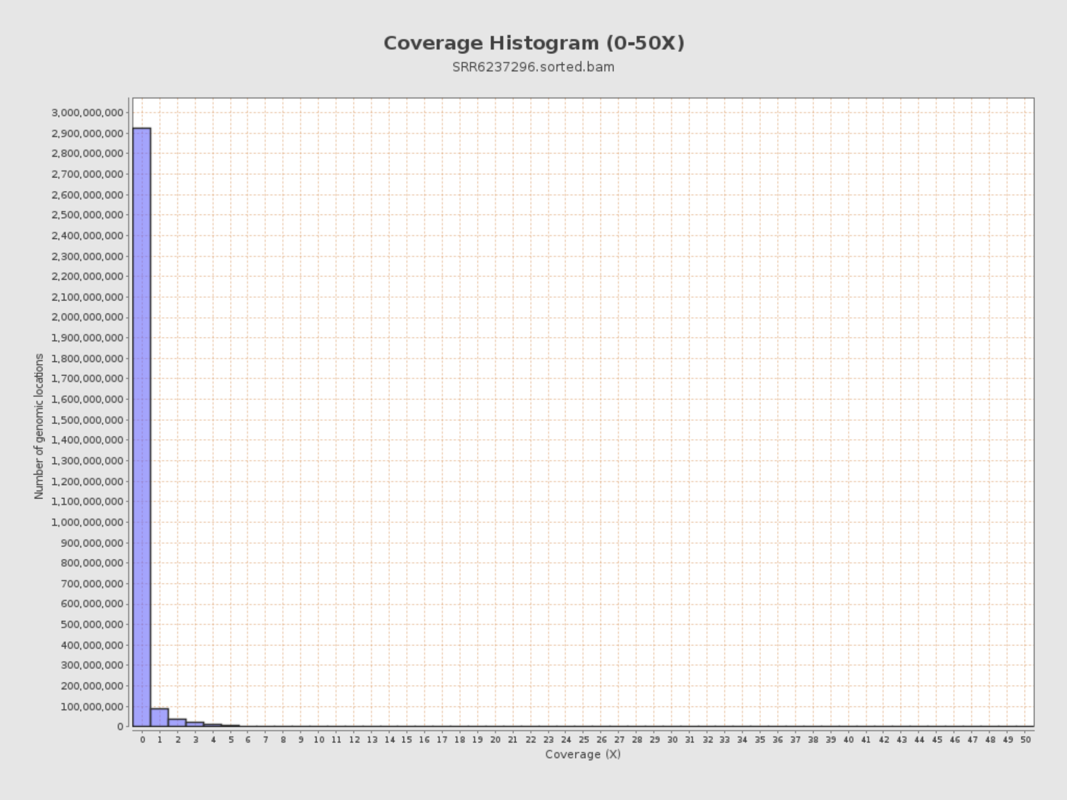
3. Results : Coverage across reference



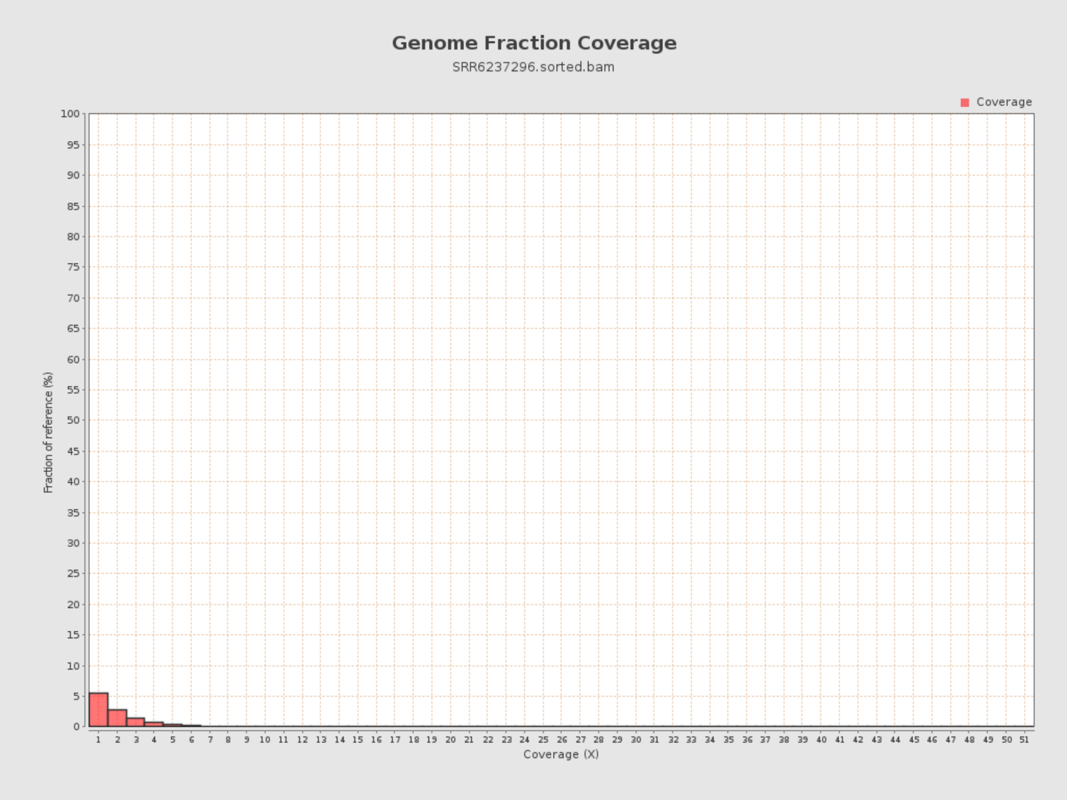
4. Results : Coverage Histogram



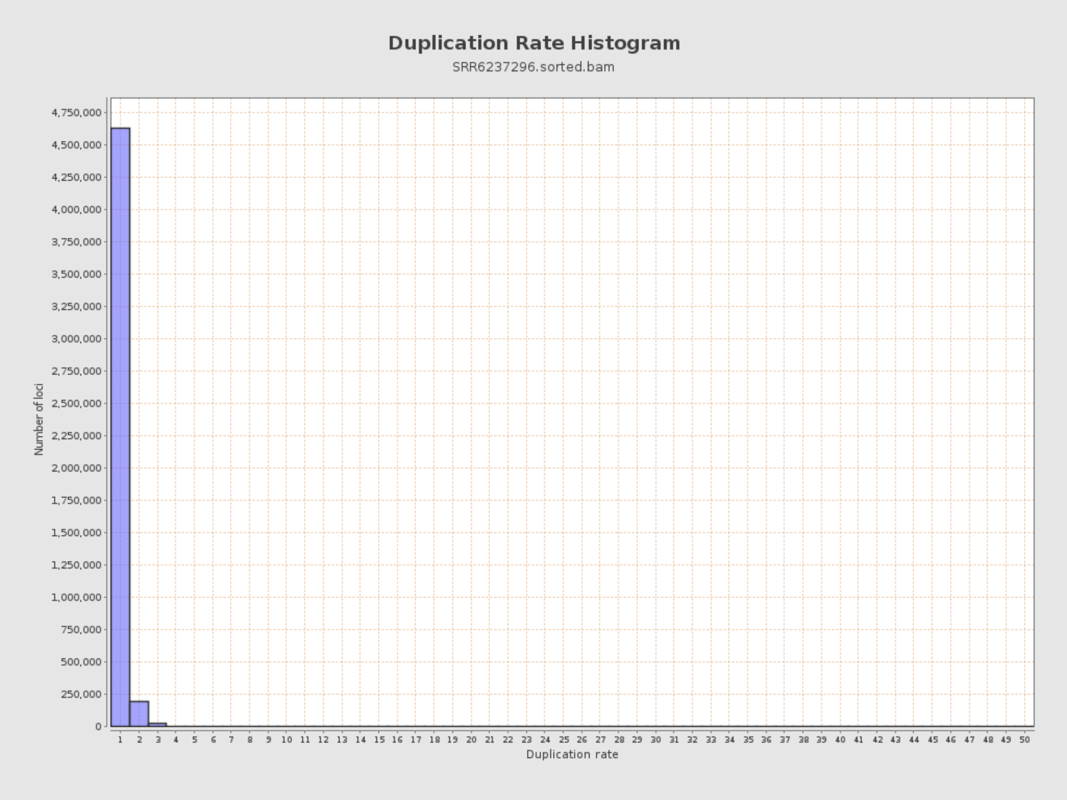
5. Results : Coverage Histogram (0-50X)



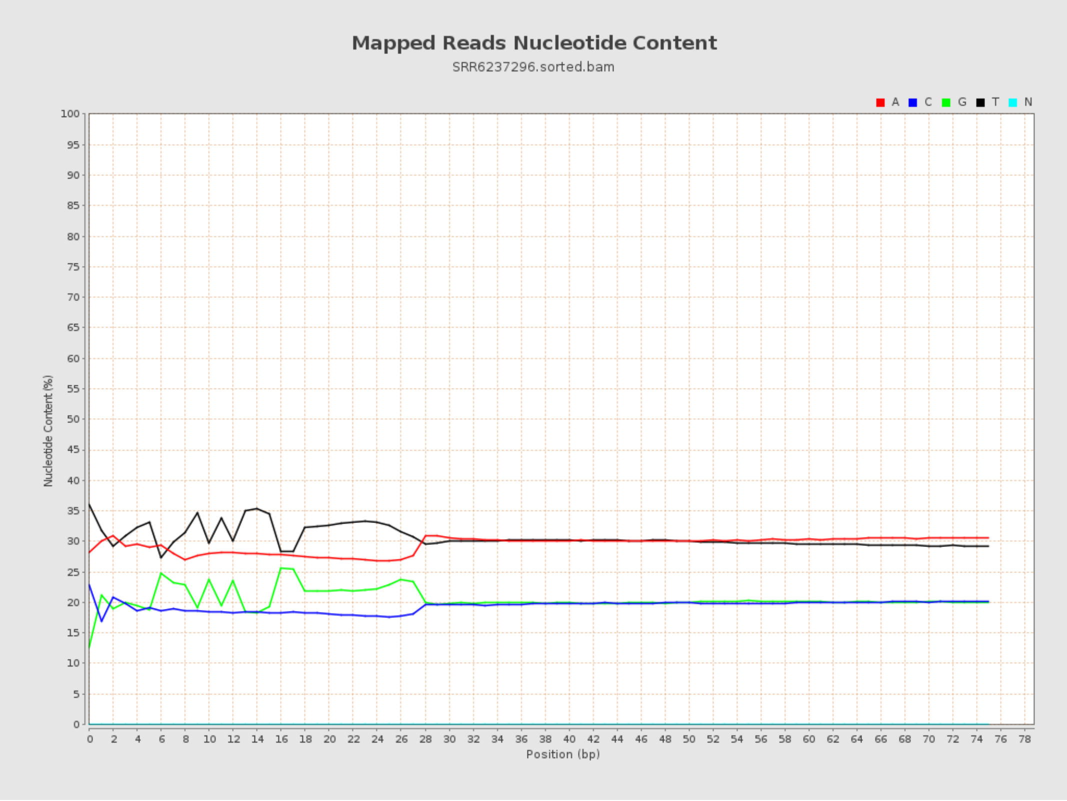
6. Results : Genome Fraction Coverage



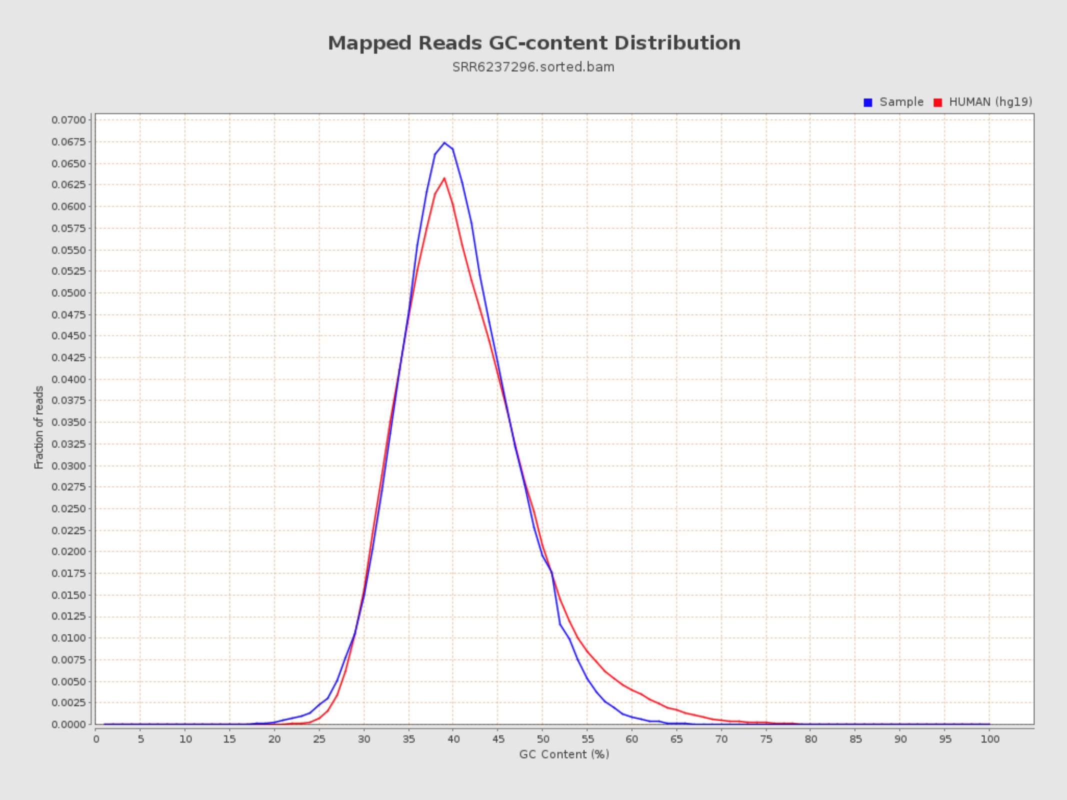
7. Results : Duplication Rate Histogram



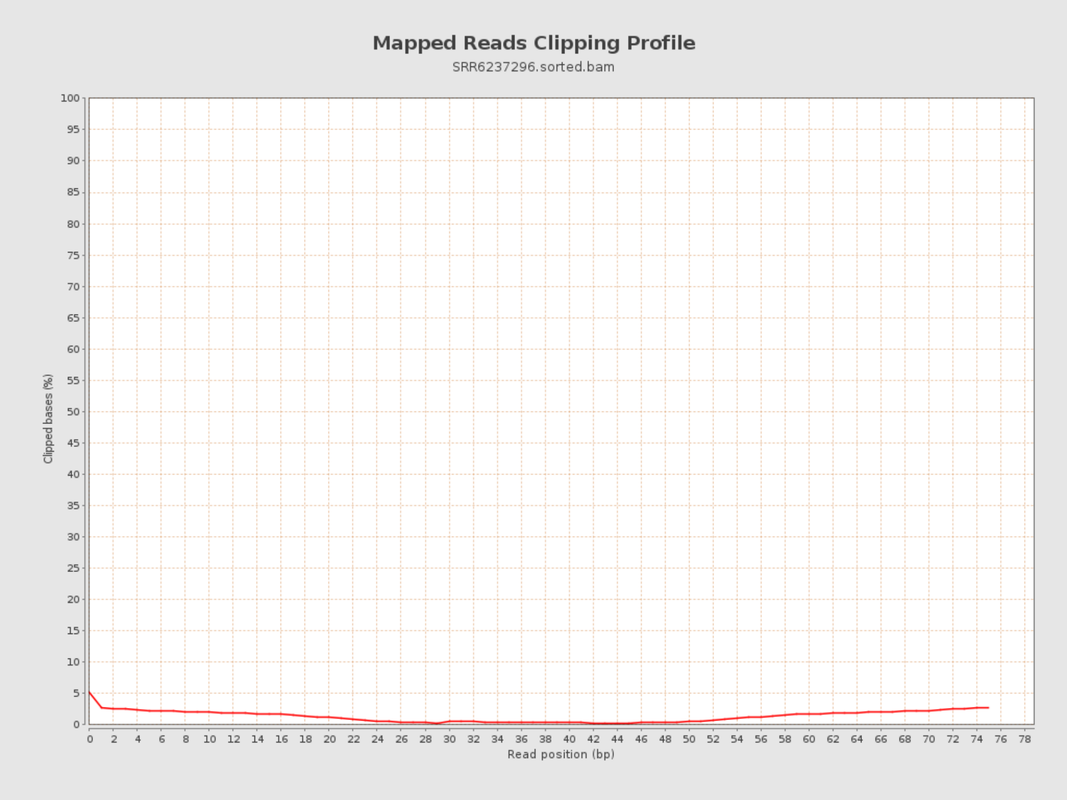
8. Results : Mapped Reads Nucleotide Content



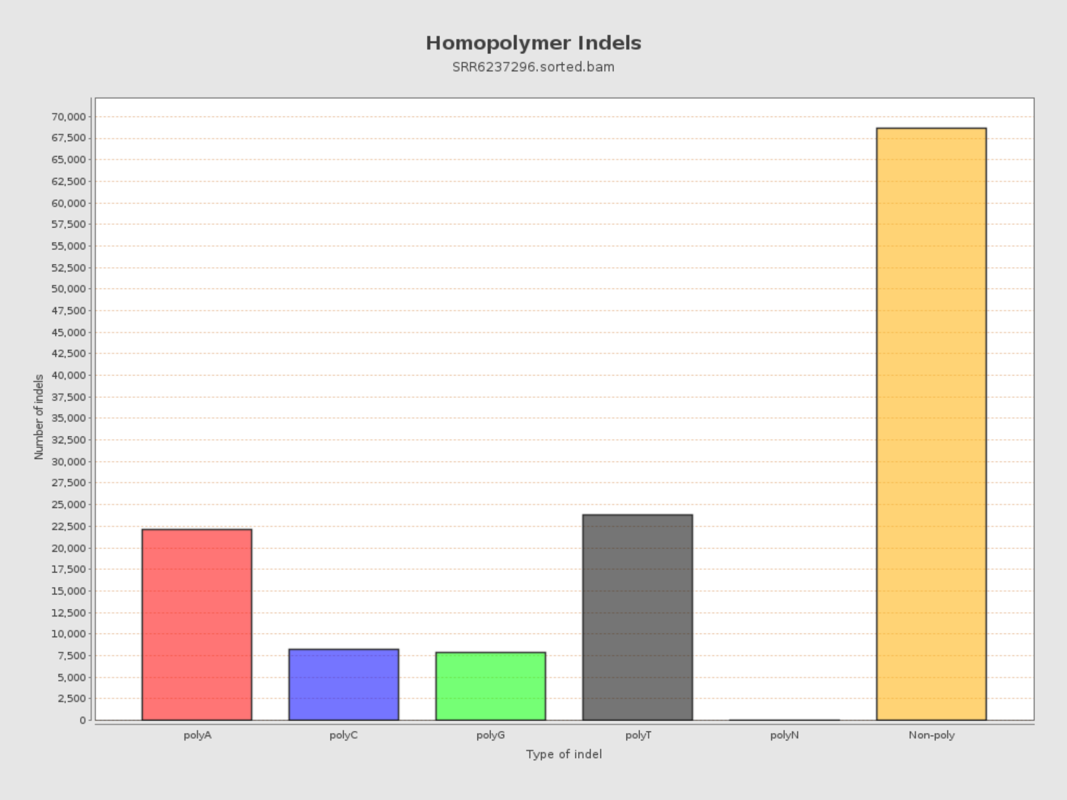
9. Results : Mapped Reads GC-content Distribution



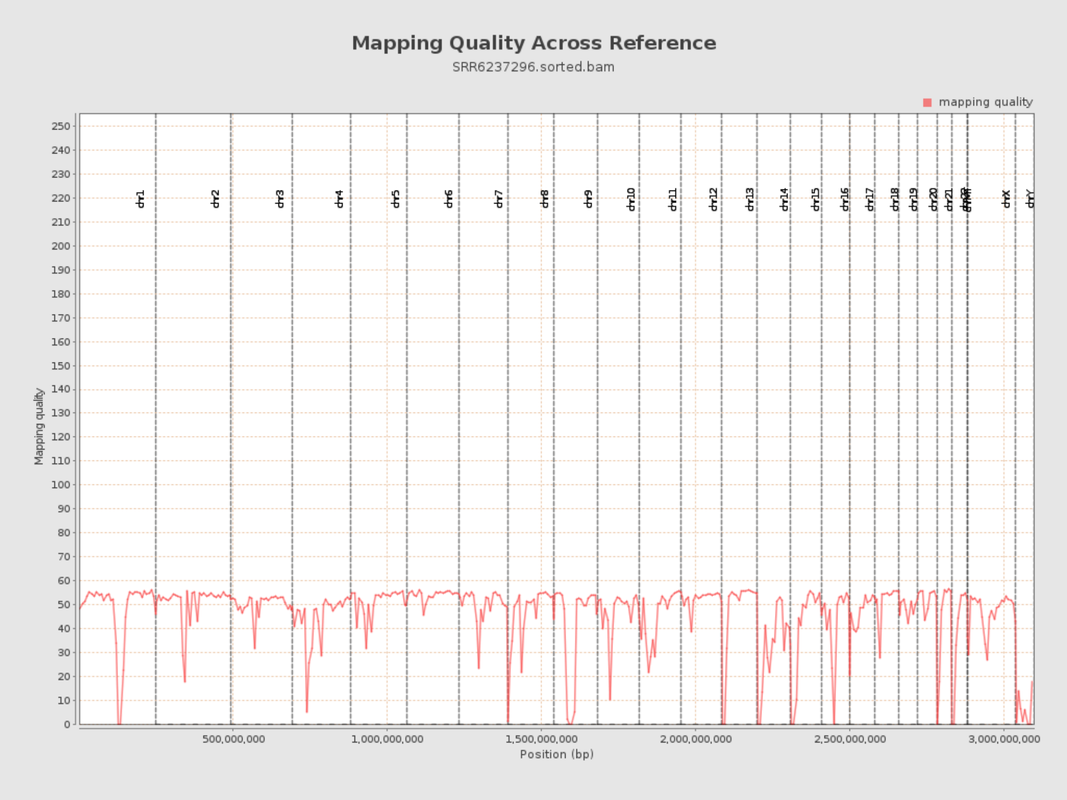
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram