Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 04:04:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237579.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_SRR6237579 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237579.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 04:04:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237579.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,143,042
Mapped reads	953,451 / 83.41%
Unmapped reads	189,591 / 16.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,361 / 0.47%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	44,813 / 3.92%
Duplication rate	3.38%
Clipped reads	589,391 / 51.56%

2.2. ACGT Content

Number/percentage of A's	15,367,490 / 25.64%
Number/percentage of C's	10,884,293 / 18.16%
Number/percentage of T's	18,419,355 / 30.74%
Number/percentage of G's	15,216,908 / 25.39%
Number/percentage of N's	37,758 / 0.06%
GC Percentage	43.56%

2.3. Coverage

Mean	0.0194

Standard Deviation	0.2157

2.4. Mapping Quality

Mean Mapping Quality	40.09

2.5. Mismatches and indels

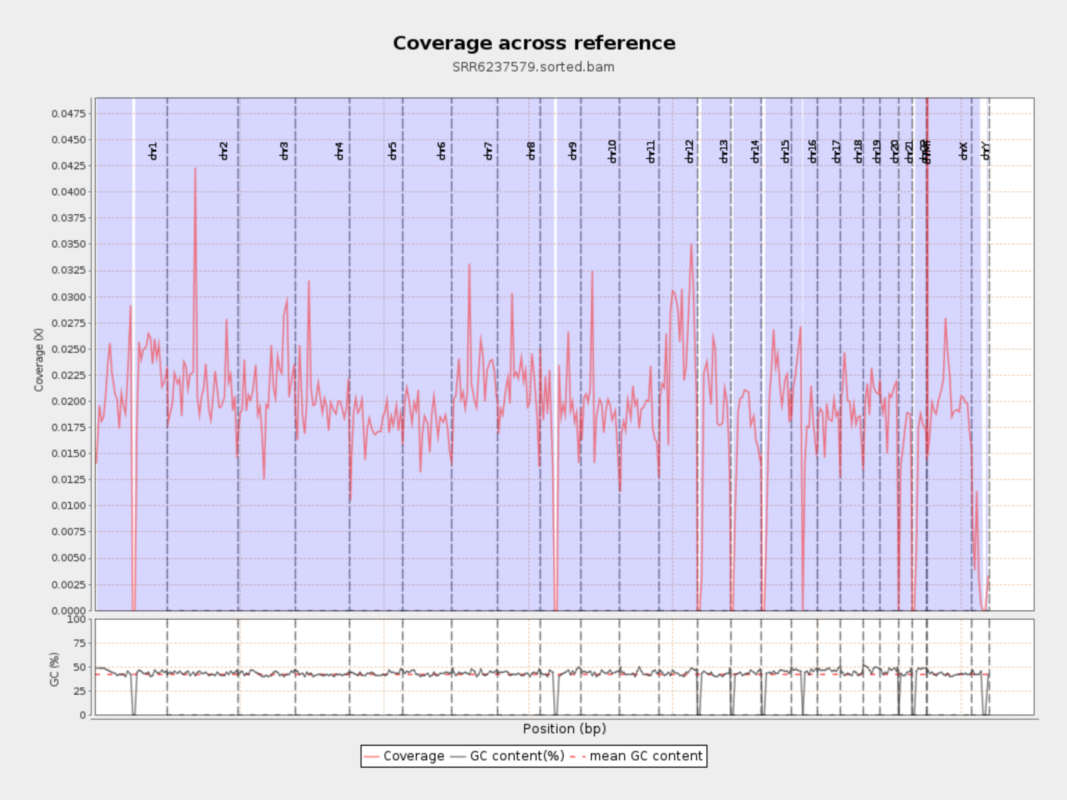
General error rate	0.97%
Mismatches	568,880
Insertions	5,591
Mapped reads with at least one insertion	0.58%
Deletions	21,107
Mapped reads with at least one deletion	2.18%
Homopolymer indels	46.75%

2.6. Chromosome stats

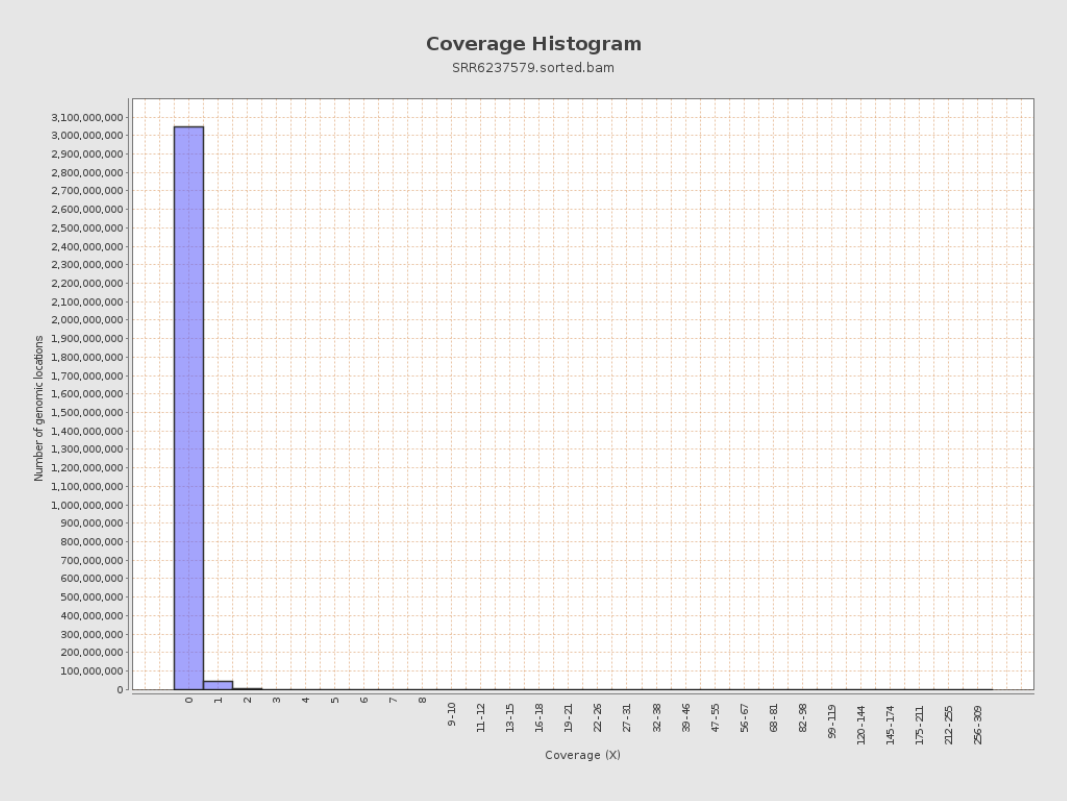
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5200041	0.0209	0.2816
chr2	243199373	5270784	0.0217	0.2859
chr3	198022430	4213756	0.0213	0.1775
chr4	191154276	3847275	0.0201	0.179
chr5	180915260	3258153	0.018	0.1588
chr6	171115067	3099106	0.0181	0.1736
chr7	159138663	3533360	0.0222	0.3005

chr8	146364022	3121708	0.0213	0.2112
chr9	141213431	2478690	0.0176	0.2321
chr10	135534747	2620827	0.0193	0.2121
chr11	135006516	2525643	0.0187	0.2319
chr12	133851895	3470815	0.0259	0.2006
chr13	115169878	1984015	0.0172	0.1599
chr14	107349540	1675271	0.0156	0.1737
chr15	102531392	1834478	0.0179	0.1692
chr16	90354753	1636458	0.0181	0.1807
chr17	81195210	1480992	0.0182	0.1703
chr18	78077248	1526292	0.0195	0.3139
chr19	59128983	1219490	0.0206	0.2193
chr20	63025520	1225282	0.0194	0.1743
chr21	48129895	724154	0.015	0.1621
chr22	51304566	627606	0.0122	0.1333
chrMT	16571	55830	3.3691	3.014
chrX	155270560	3117833	0.0201	0.1821
chrY	59373566	212867	0.0036	0.0941

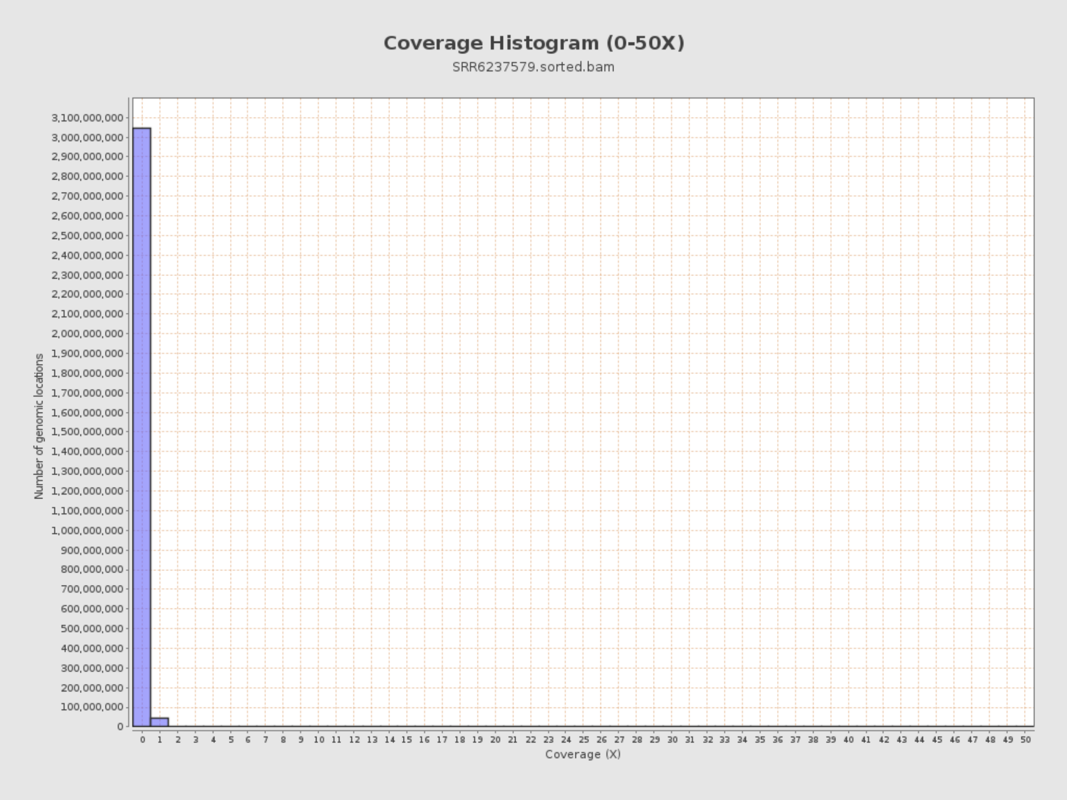
3. Results : Coverage across reference



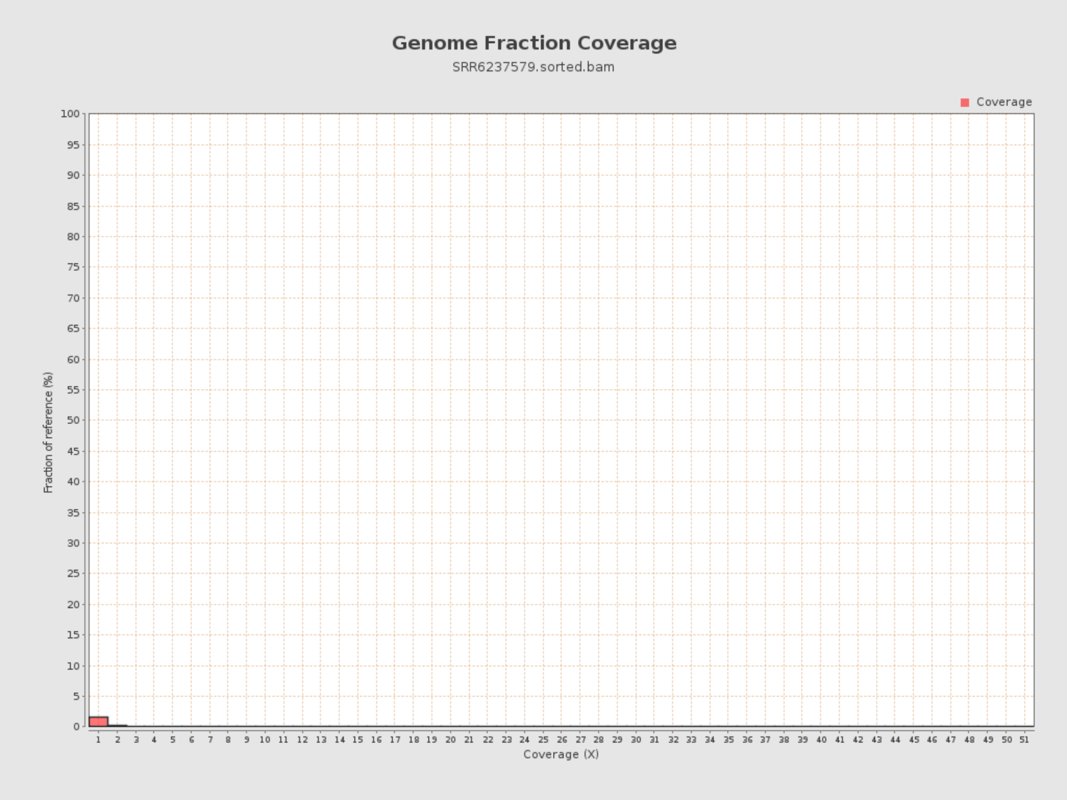
4. Results : Coverage Histogram



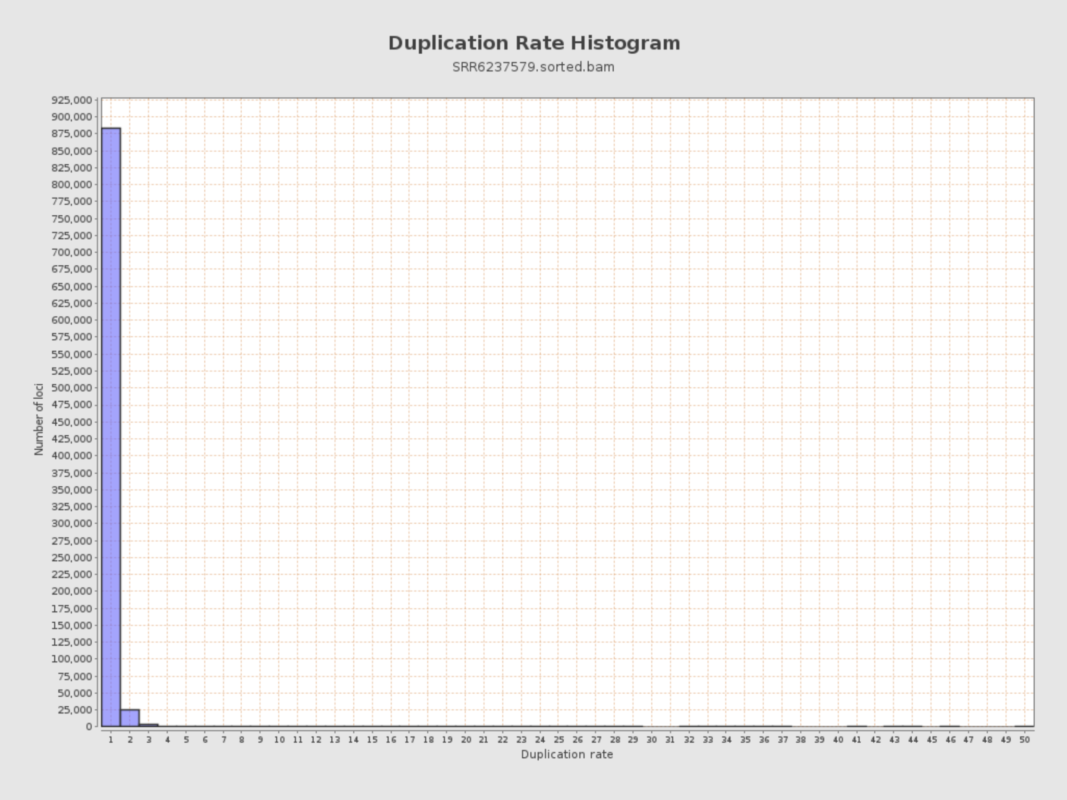
5. Results : Coverage Histogram (0-50X)



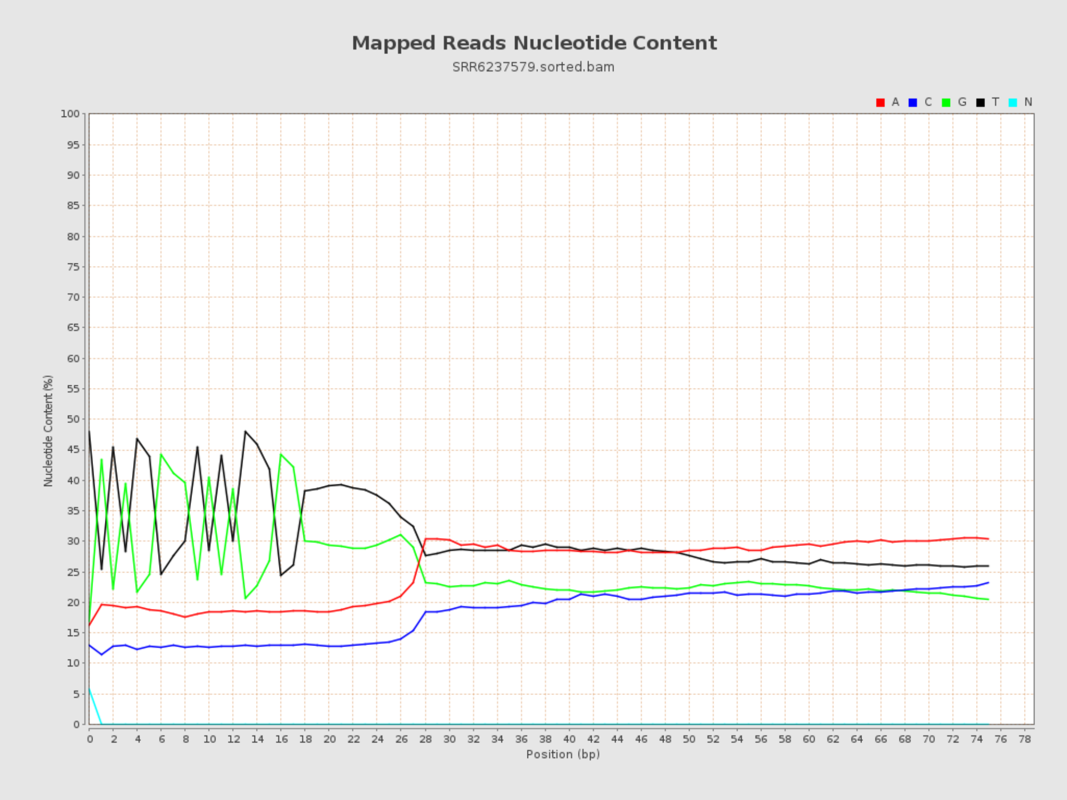
6. Results : Genome Fraction Coverage



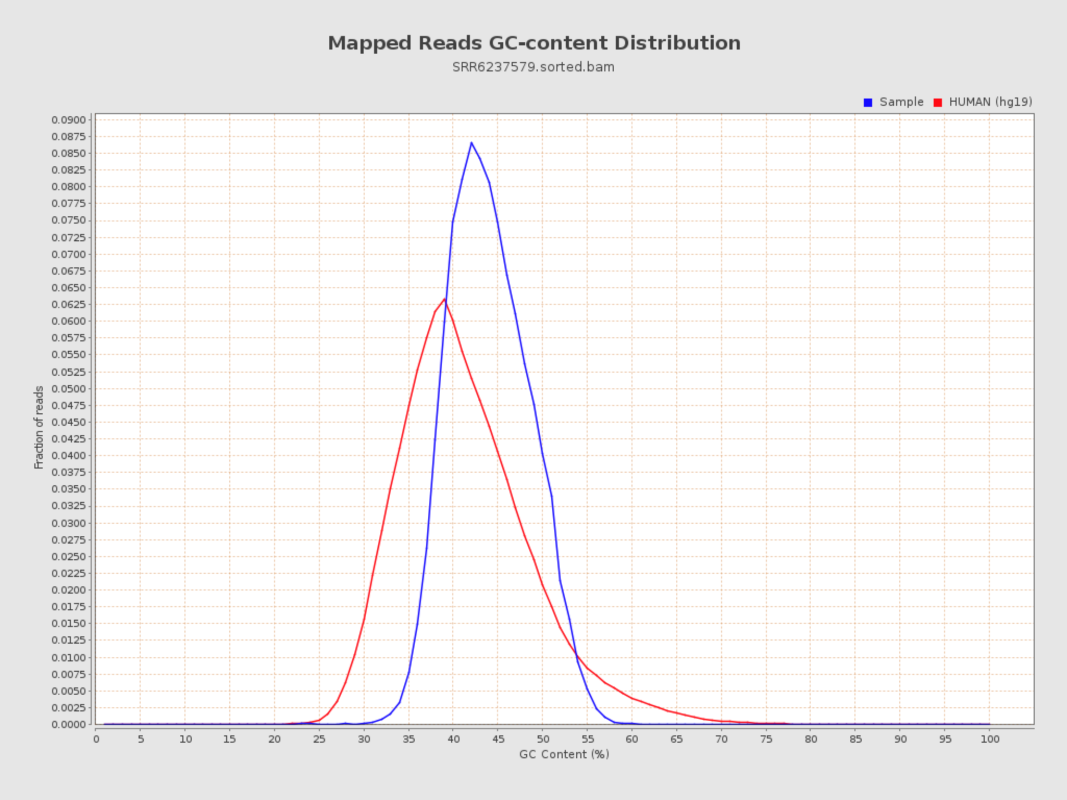
7. Results : Duplication Rate Histogram



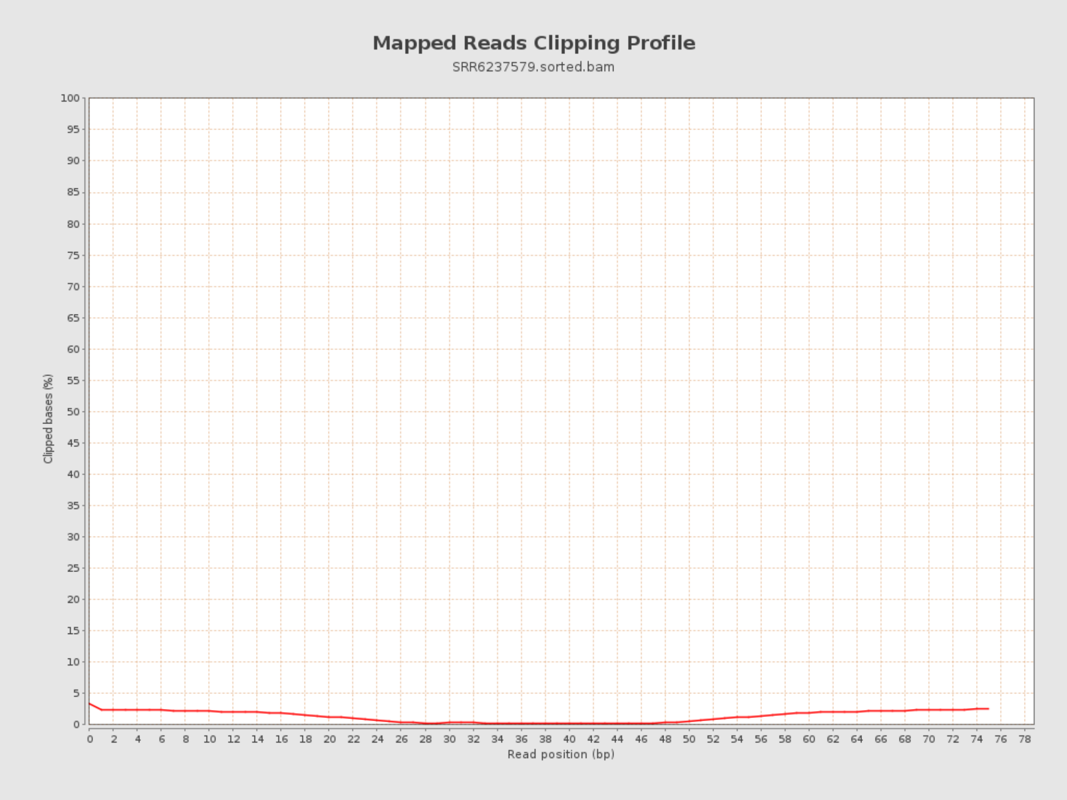
8. Results : Mapped Reads Nucleotide Content



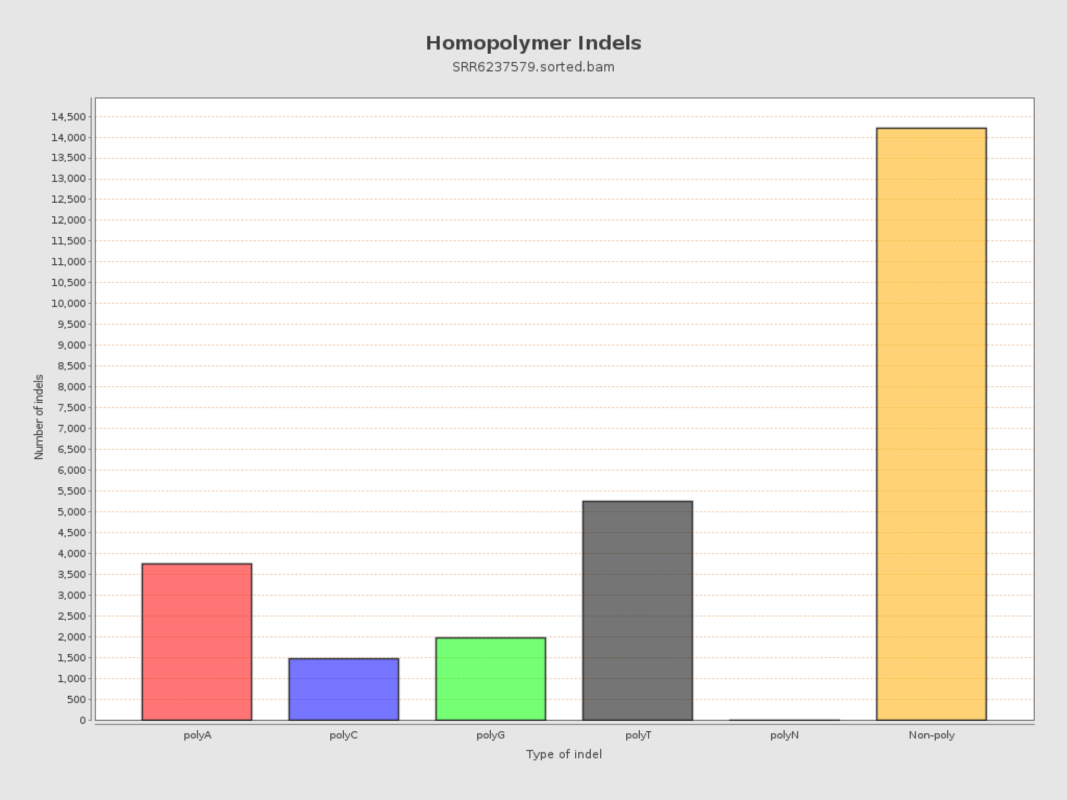
9. Results : Mapped Reads GC-content Distribution



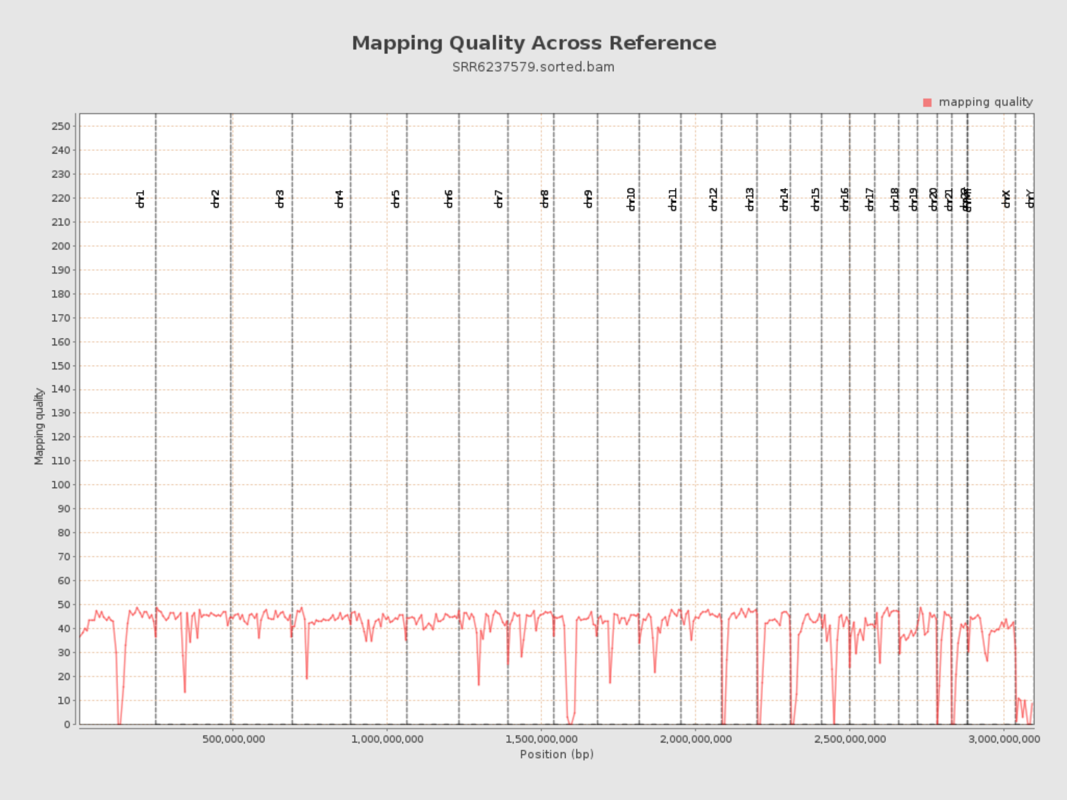
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram