Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 23:11:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237264.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_SRR6237264 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237264.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 23:11:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237264.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,722,918
Mapped reads	2,468,648 / 90.66%
Unmapped reads	254,270 / 9.34%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,283 / 0.78%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	149,597 / 5.49%
Duplication rate	4.55%
Clipped reads	832,564 / 30.58%

2.2. ACGT Content

Number/percentage of A's	50,653,588 / 29.5%
Number/percentage of C's	31,894,955 / 18.57%
Number/percentage of T's	54,099,019 / 31.5%
Number/percentage of G's	35,075,998 / 20.43%
Number/percentage of N's	3,093 / 0%
GC Percentage	39%

2.3. Coverage

Mean	0.0555

Standard Deviation	0.6402

2.4. Mapping Quality

Mean Mapping Quality	42.8

2.5. Mismatches and indels

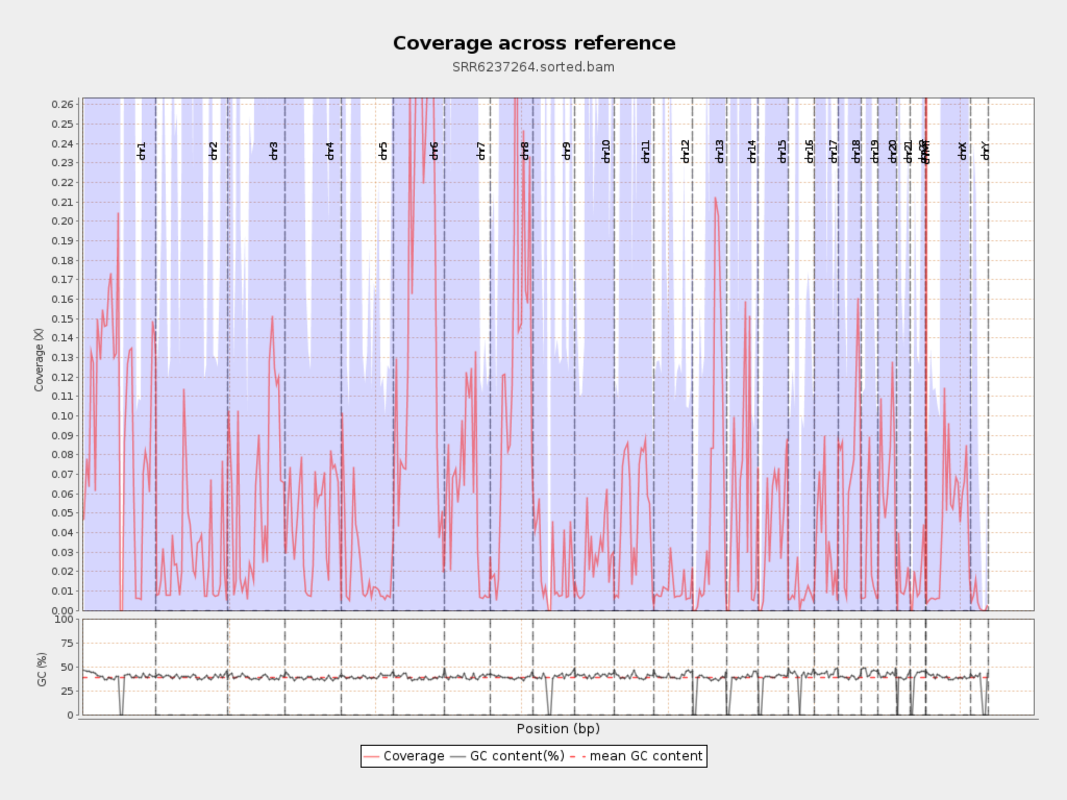
General error rate	0.79%
Mismatches	1,340,847
Insertions	12,064
Mapped reads with at least one insertion	0.48%
Deletions	50,558
Mapped reads with at least one deletion	2.02%
Homopolymer indels	46.24%

2.6. Chromosome stats

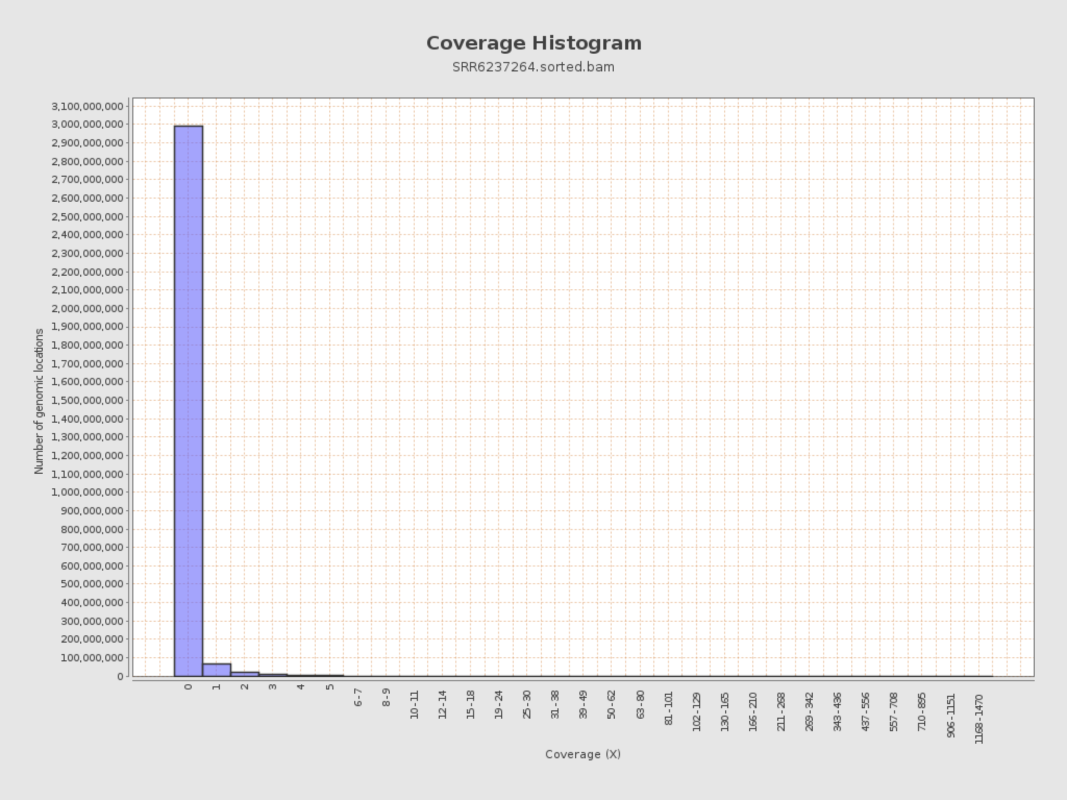
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	24827175	0.0996	1.3294
chr2	243199373	6805756	0.028	0.5822
chr3	198022430	11712145	0.0591	0.3756
chr4	191154276	8986357	0.047	0.3245
chr5	180915260	4184857	0.0231	0.2338
chr6	171115067	29937786	0.175	1.1478
chr7	159138663	9462671	0.0595	0.5786

chr8	146364022	18412019	0.1258	0.7753
chr9	141213431	2958470	0.021	0.4448
chr10	135534747	3637403	0.0268	0.4591
chr11	135006516	6791943	0.0503	0.5185
chr12	133851895	1490154	0.0111	0.1688
chr13	115169878	7575729	0.0658	0.3914
chr14	107349540	5676403	0.0529	0.3595
chr15	102531392	4613635	0.045	0.3139
chr16	90354753	757681	0.0084	0.2401
chr17	81195210	2937023	0.0362	0.516
chr18	78077248	6036449	0.0773	1
chr19	59128983	1565831	0.0265	0.7712
chr20	63025520	4747385	0.0753	0.4092
chr21	48129895	760235	0.0158	0.1927
chr22	51304566	822483	0.016	0.1791
chrMT	16571	152879	9.2257	5.9376
chrX	155270560	6694880	0.0431	0.368
chrY	59373566	267380	0.0045	0.1197

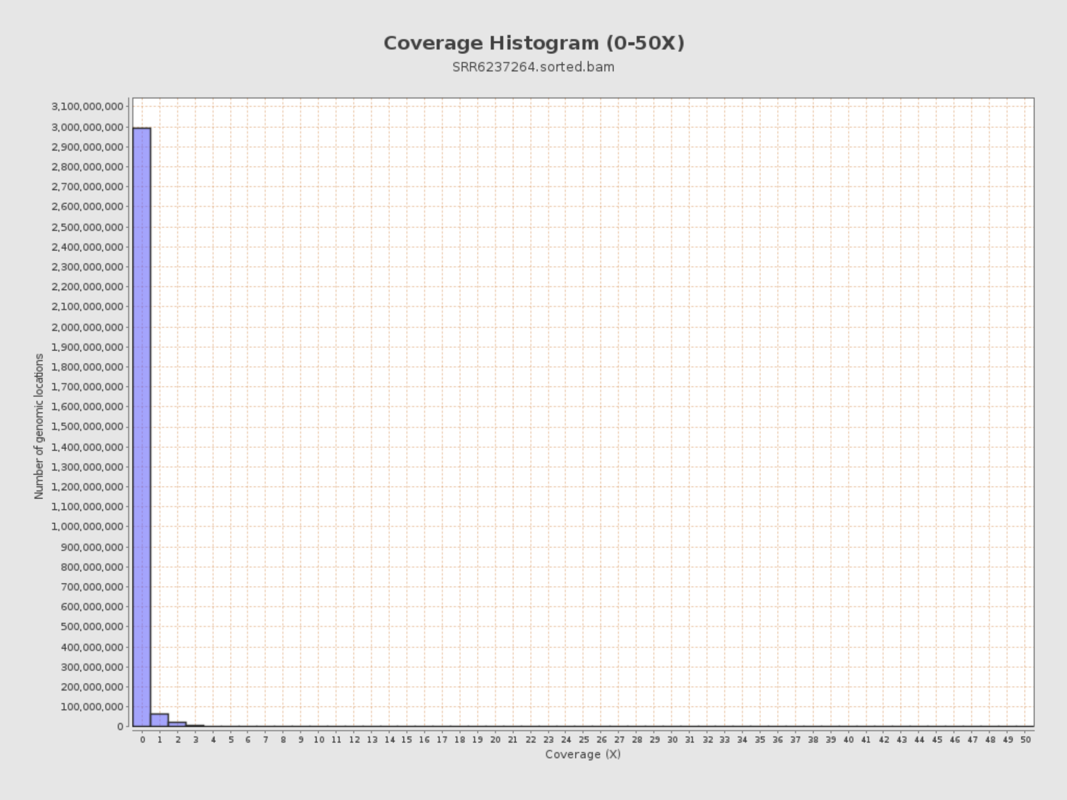
3. Results : Coverage across reference



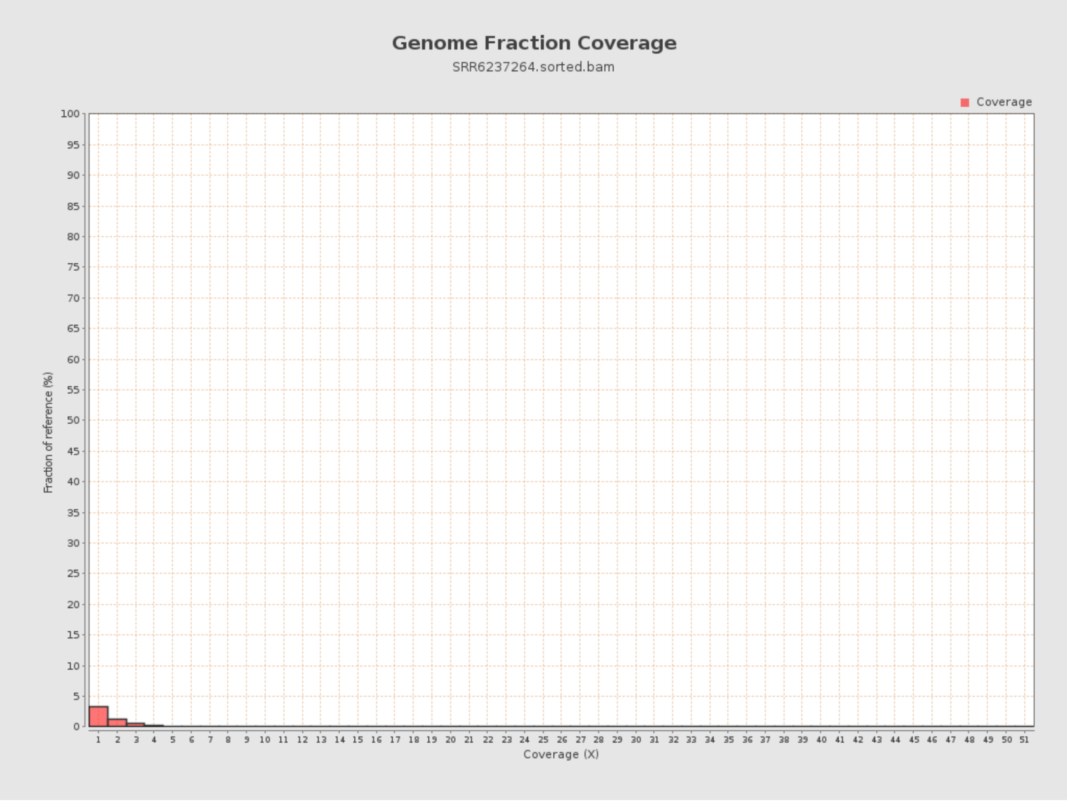
4. Results : Coverage Histogram



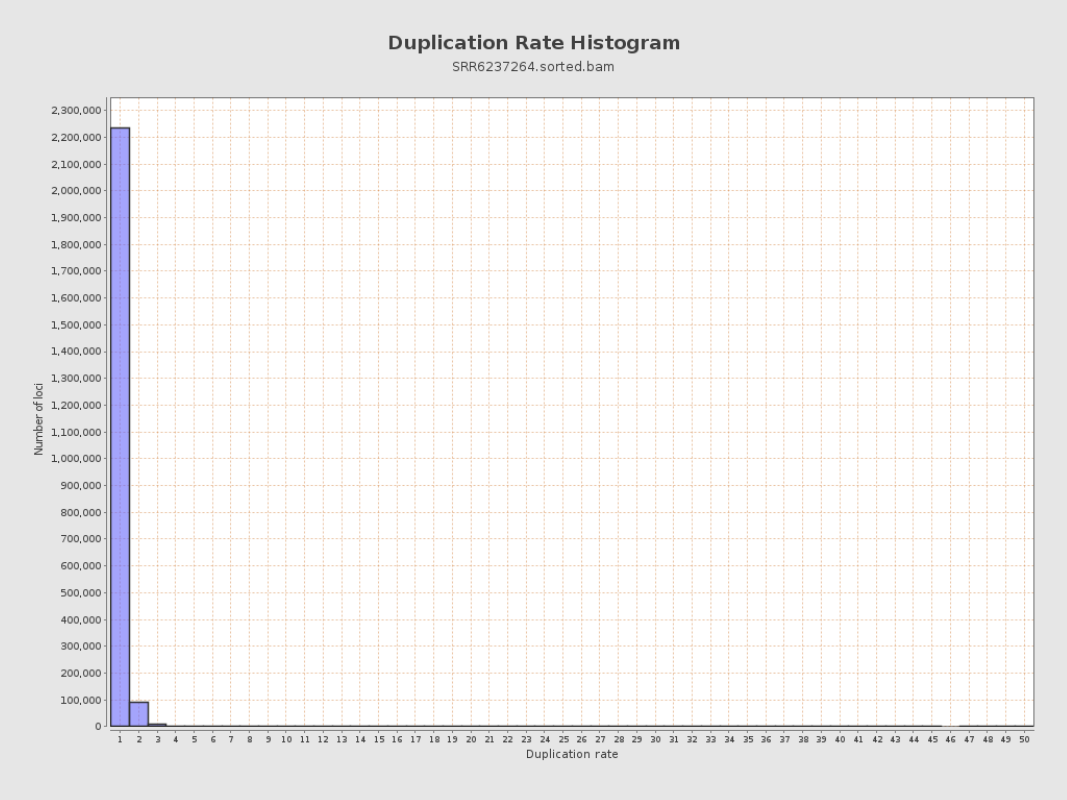
5. Results : Coverage Histogram (0-50X)



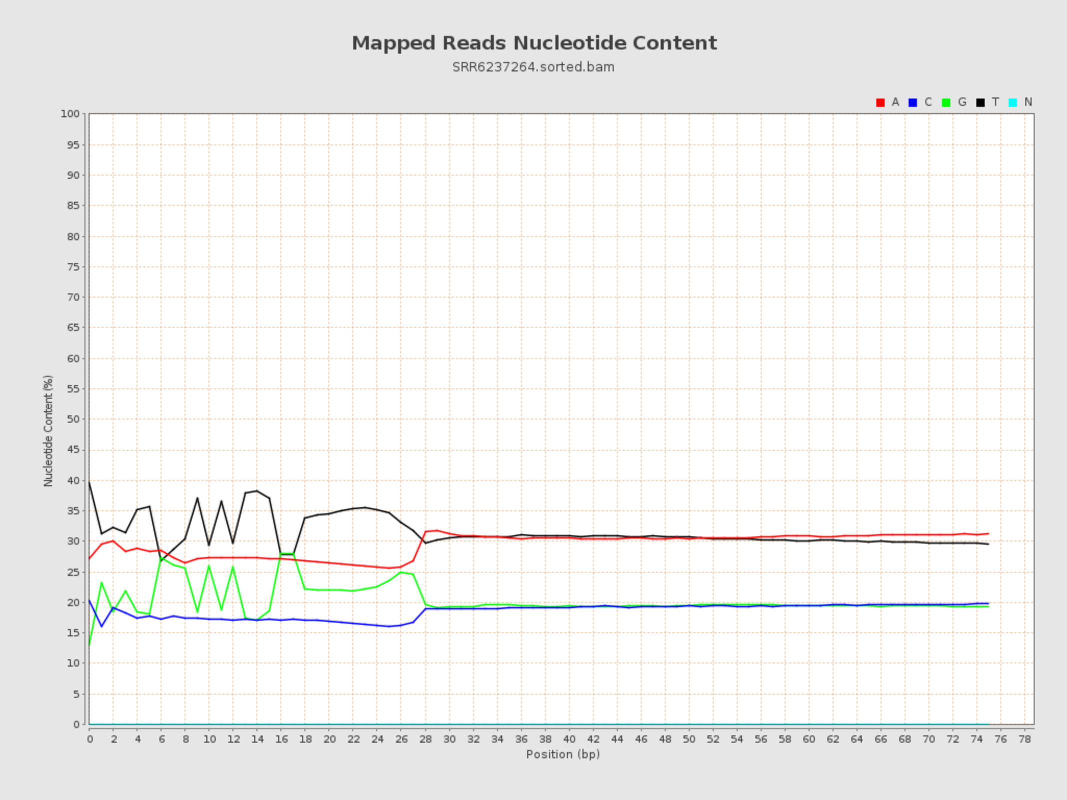
6. Results : Genome Fraction Coverage



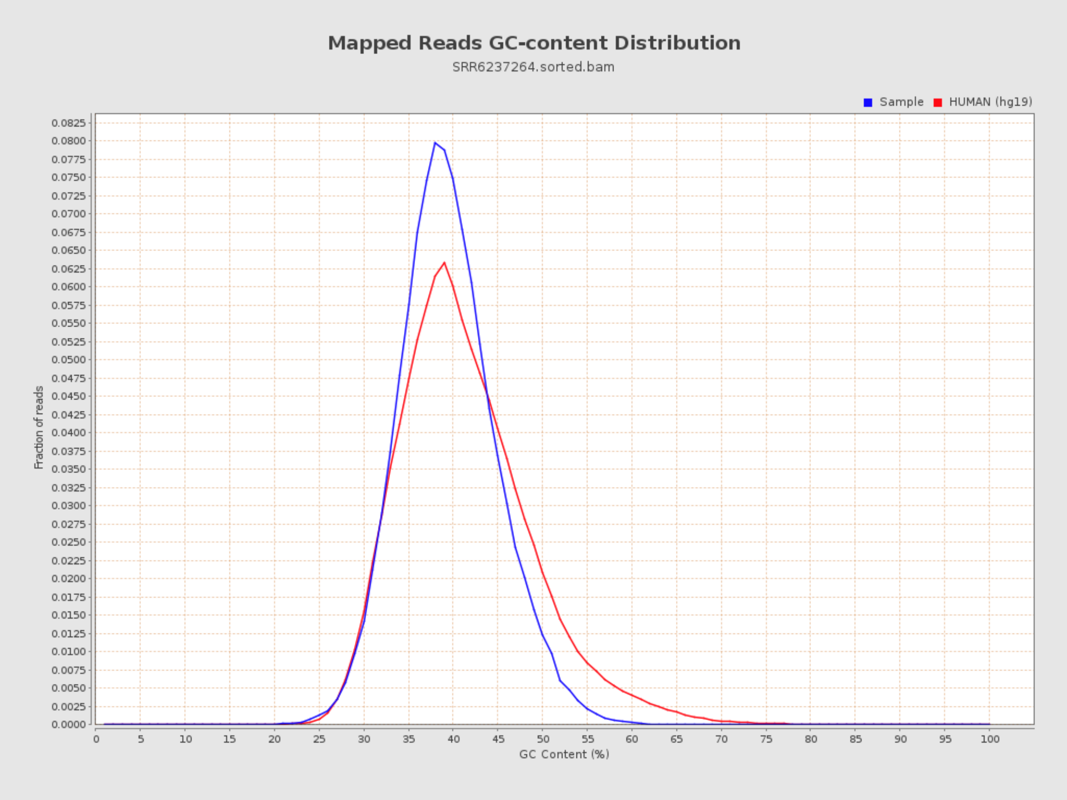
7. Results : Duplication Rate Histogram



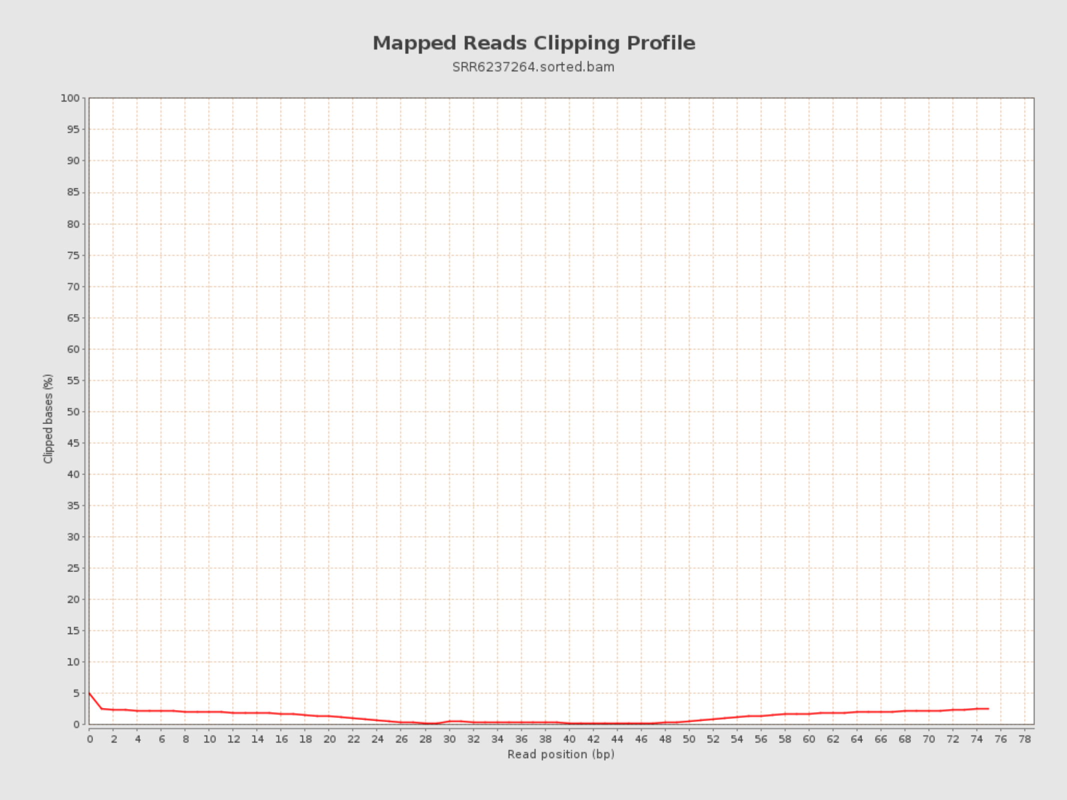
8. Results : Mapped Reads Nucleotide Content



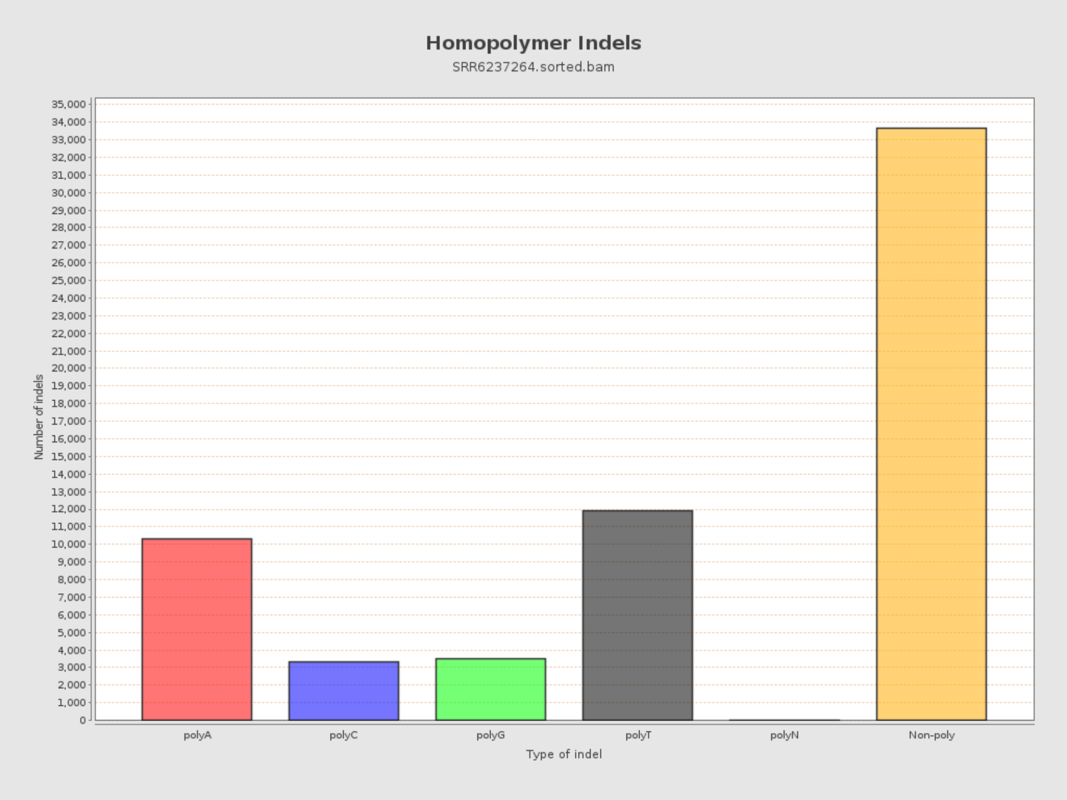
9. Results : Mapped Reads GC-content Distribution



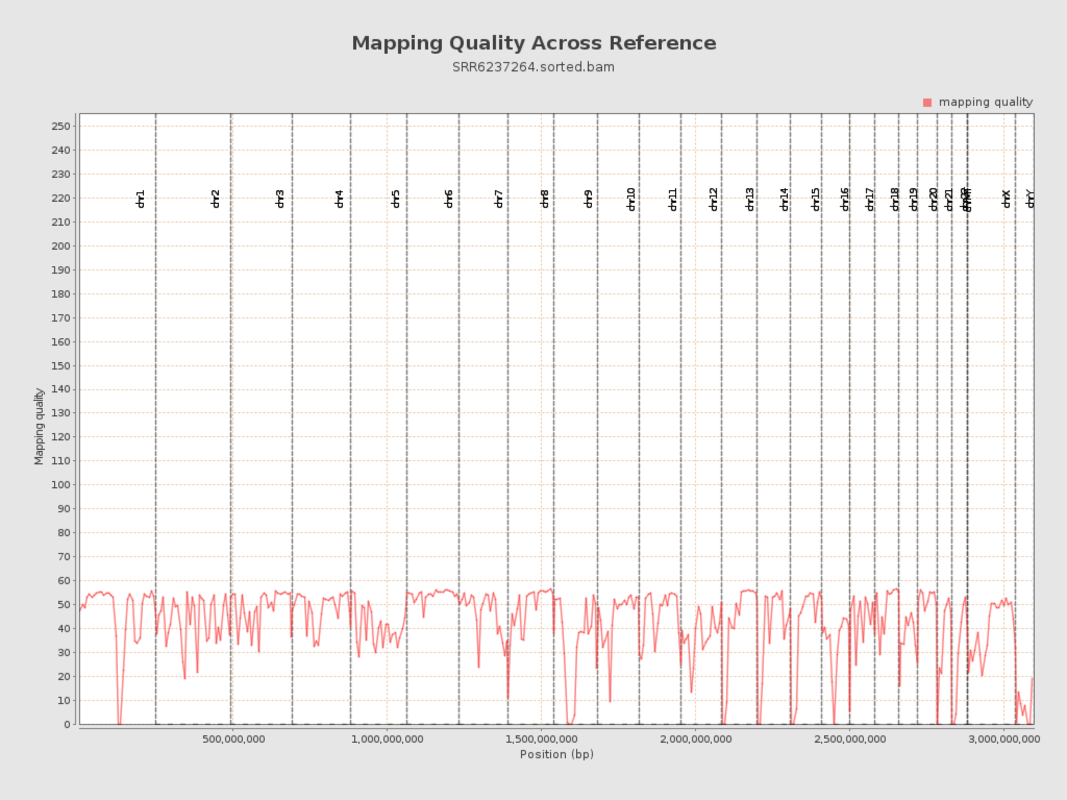
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram