Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 02:13:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237319.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_SRR6237319 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237319.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 02:13:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237319.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,038,373
Mapped reads	2,658,723 / 87.5%
Unmapped reads	379,650 / 12.5%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	27,185 / 0.89%
Read min/max/mean length	30 / 76 / 76.31
Duplicated reads (estimated)	818,893 / 26.95%
Duplication rate	20.49%
Clipped reads	1,677,167 / 55.2%

2.2. ACGT Content

Number/percentage of A's	41,568,150 / 25.21%
Number/percentage of C's	28,757,590 / 17.44%
Number/percentage of T's	54,896,022 / 33.29%
Number/percentage of G's	39,670,016 / 24.06%
Number/percentage of N's	17,515 / 0.01%
GC Percentage	41.49%

2.3. Coverage

Mean	0.0533

Standard Deviation	0.7345

2.4. Mapping Quality

Mean Mapping Quality	43.6

2.5. Mismatches and indels

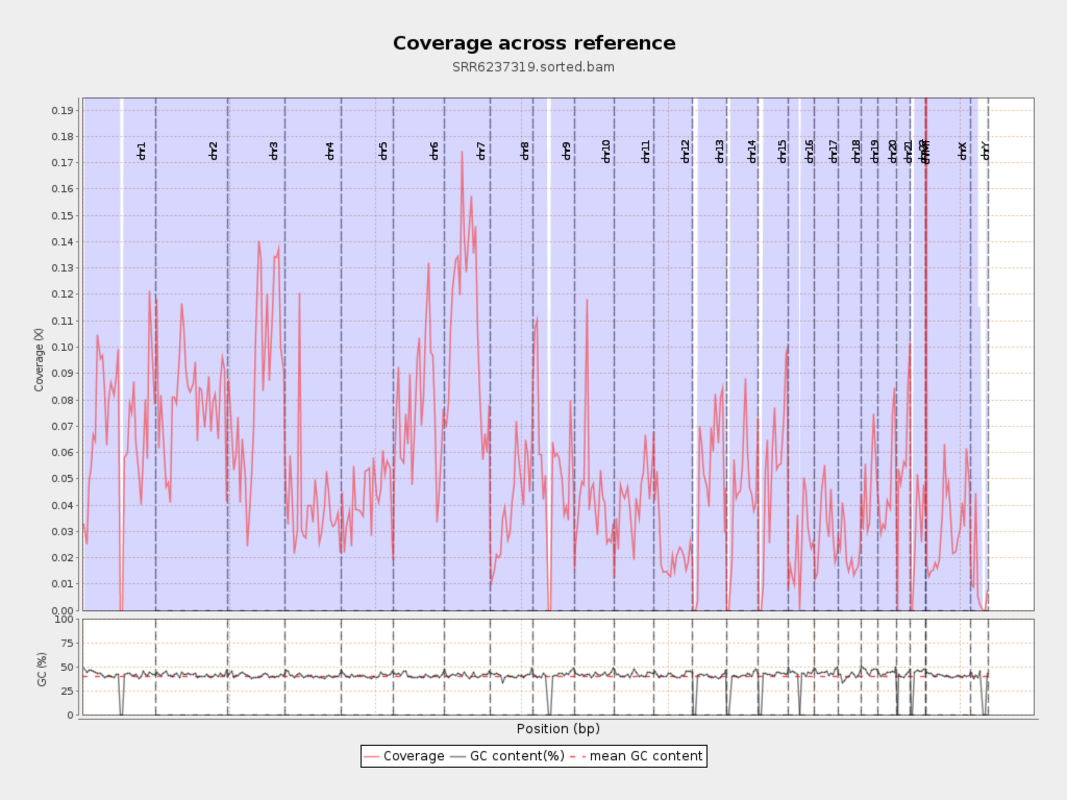
General error rate	0.63%
Mismatches	999,297
Insertions	13,421
Mapped reads with at least one insertion	0.5%
Deletions	43,456
Mapped reads with at least one deletion	1.61%
Homopolymer indels	43.84%

2.6. Chromosome stats

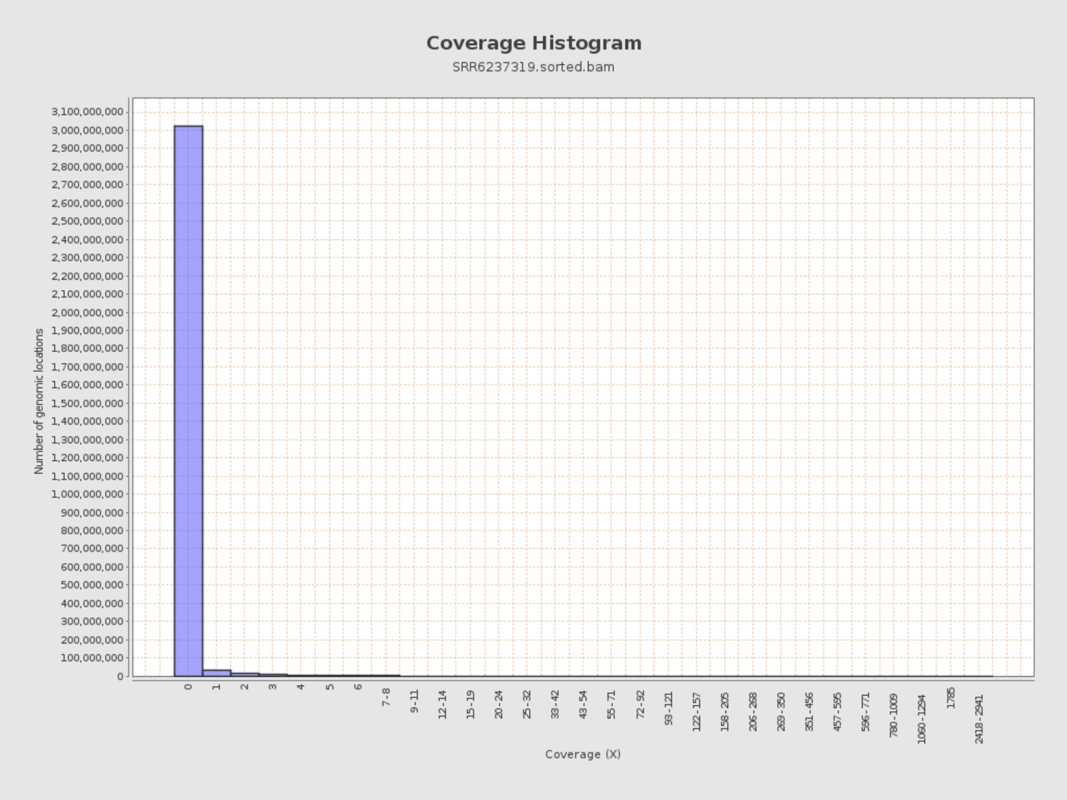
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16982442	0.0681	0.666
chr2	243199373	19428008	0.0799	1.4982
chr3	198022430	17012935	0.0859	0.5584
chr4	191154276	7588703	0.0397	0.6271
chr5	180915260	7738868	0.0428	0.4031
chr6	171115067	13110038	0.0766	0.6695
chr7	159138663	17704601	0.1113	1.1517

chr8	146364022	5830478	0.0398	0.7398
chr9	141213431	7484298	0.053	0.4957
chr10	135534747	5796595	0.0428	0.8529
chr11	135006516	5720808	0.0424	0.4398
chr12	133851895	3050634	0.0228	0.3259
chr13	115169878	5854025	0.0508	0.4998
chr14	107349540	4561918	0.0425	0.413
chr15	102531392	5155787	0.0503	0.444
chr16	90354753	2186165	0.0242	0.3526
chr17	81195210	2494833	0.0307	0.3829
chr18	78077248	1741069	0.0223	1.2741
chr19	59128983	2771118	0.0469	0.4973
chr20	63025520	3004013	0.0477	0.4454
chr21	48129895	2819653	0.0586	0.5793
chr22	51304566	1488297	0.029	0.3373
chrMT	16571	21803	1.3157	2.2135
chrX	155270560	4859963	0.0313	0.3824
chrY	59373566	579555	0.0098	0.5011

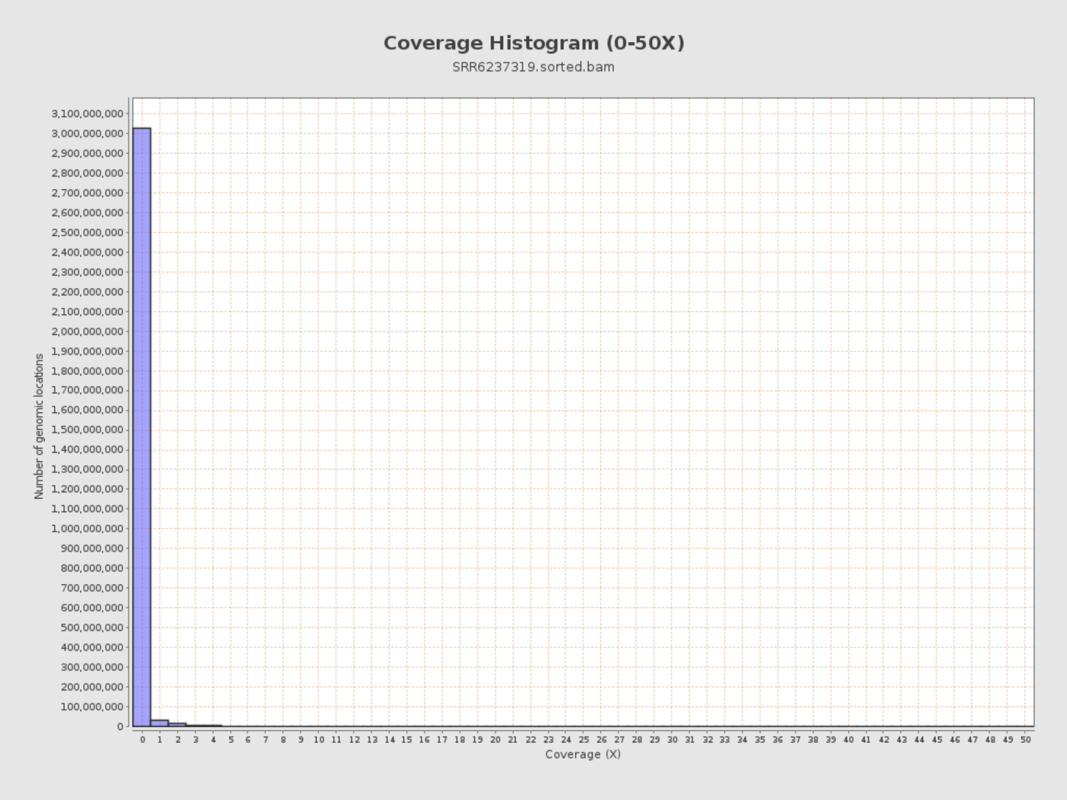
3. Results : Coverage across reference



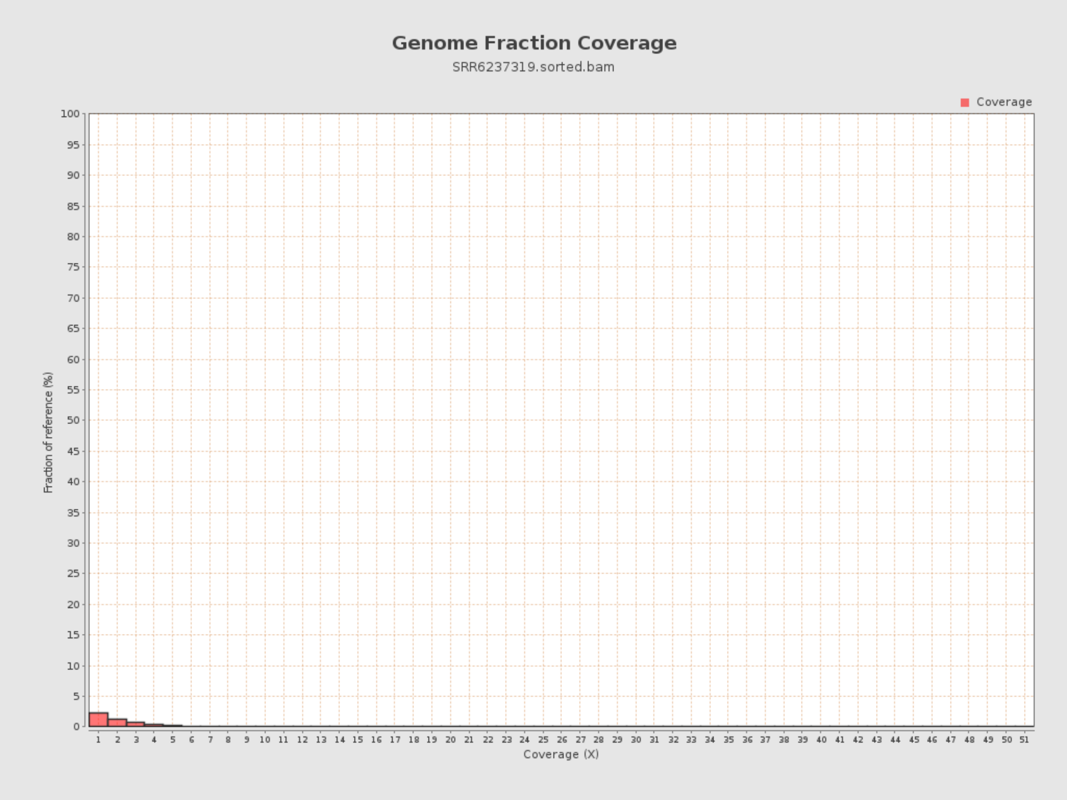
4. Results : Coverage Histogram



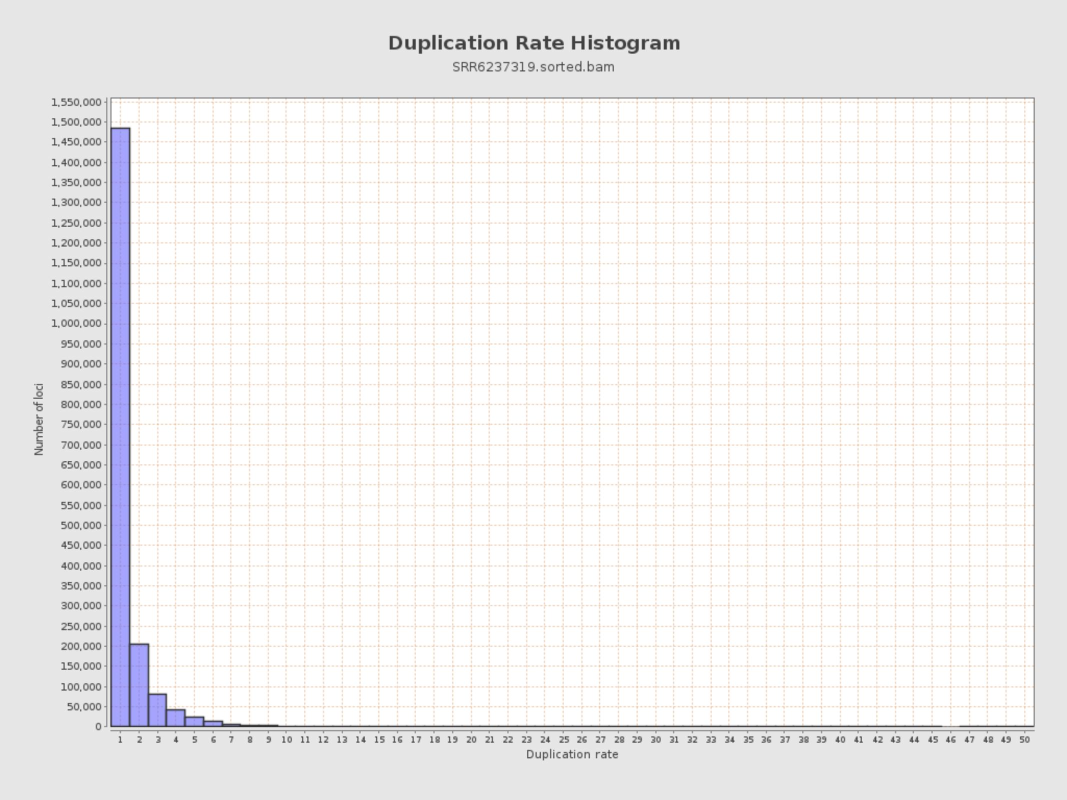
5. Results : Coverage Histogram (0-50X)



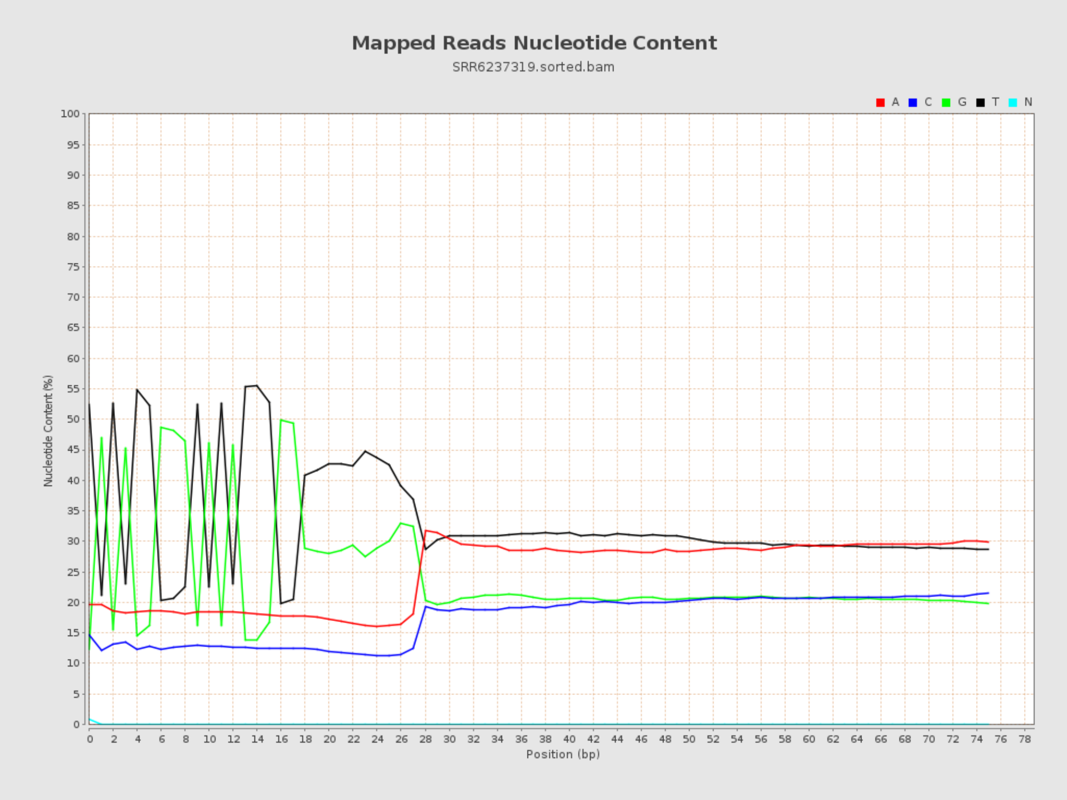
6. Results : Genome Fraction Coverage



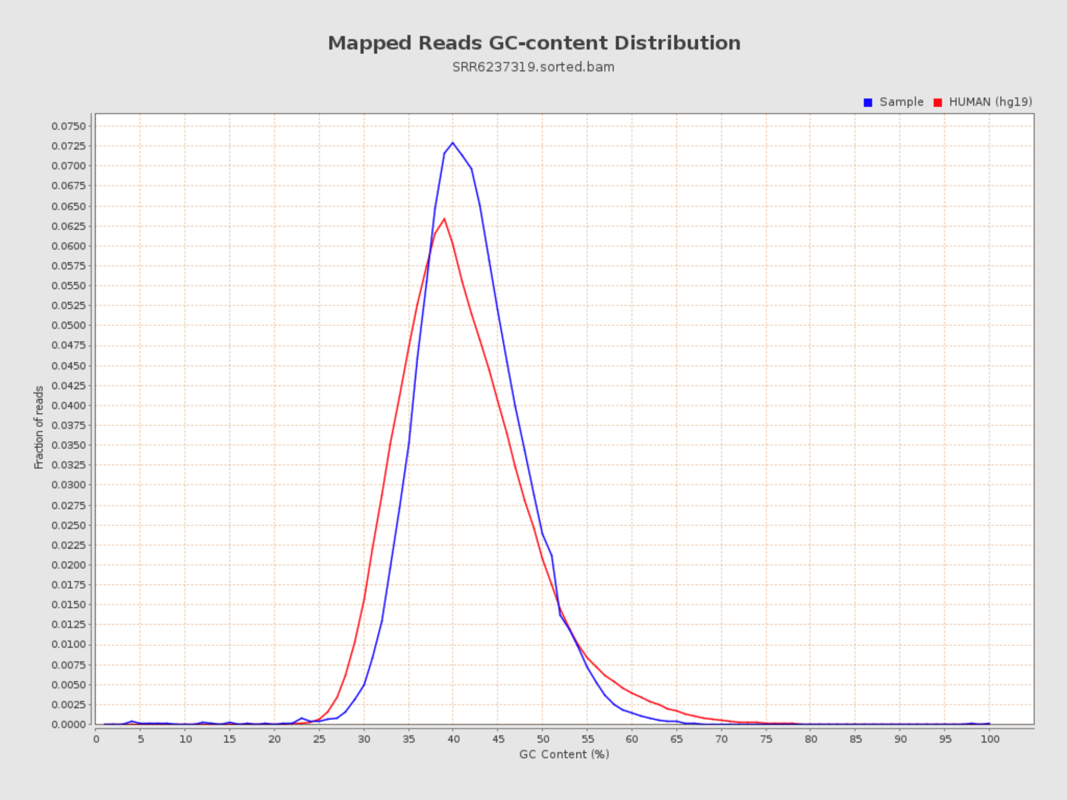
7. Results : Duplication Rate Histogram



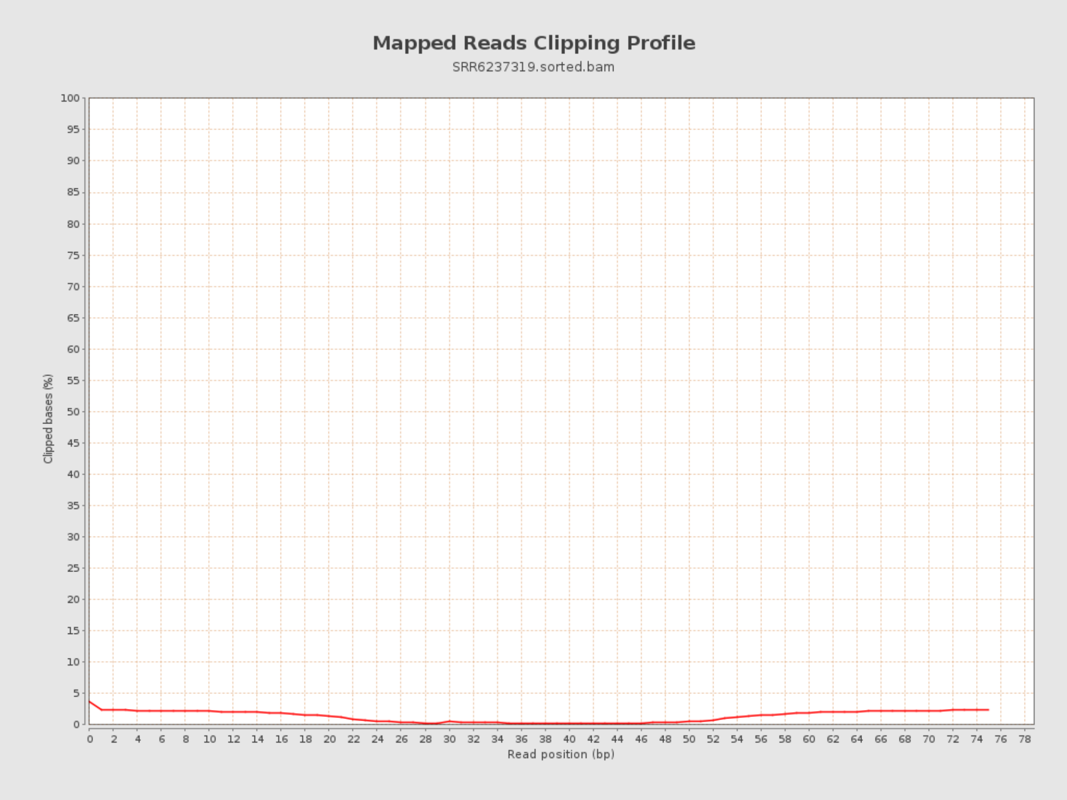
8. Results : Mapped Reads Nucleotide Content



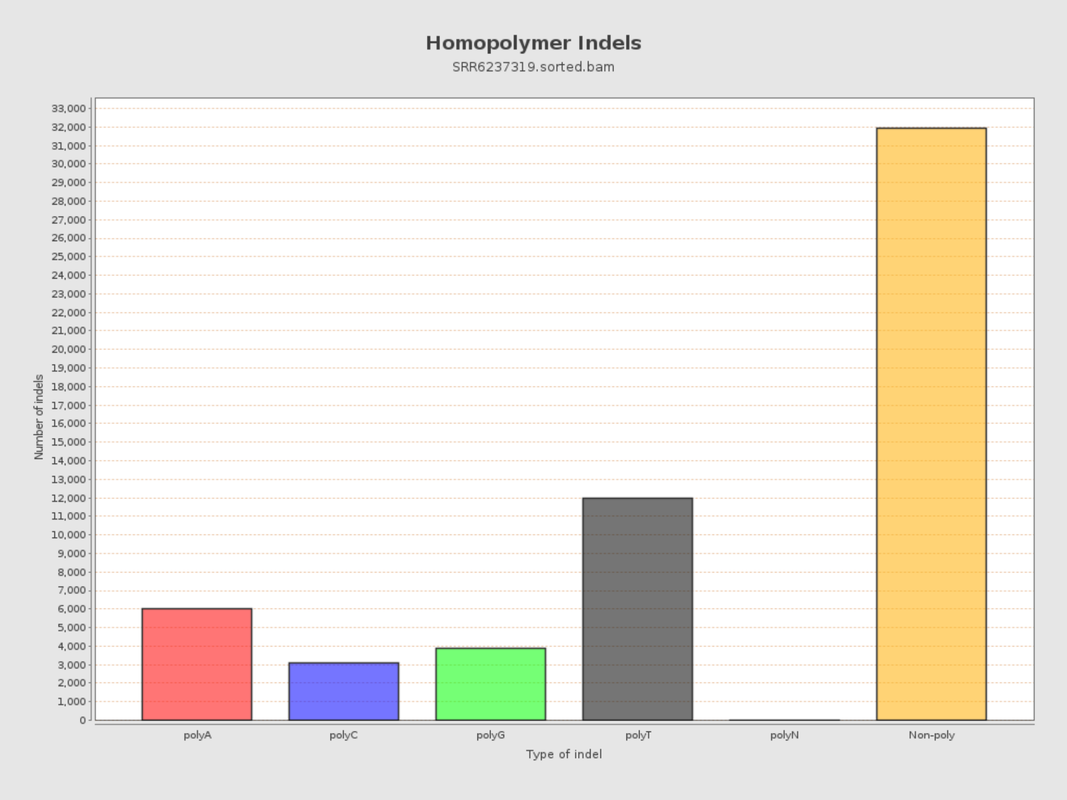
9. Results : Mapped Reads GC-content Distribution



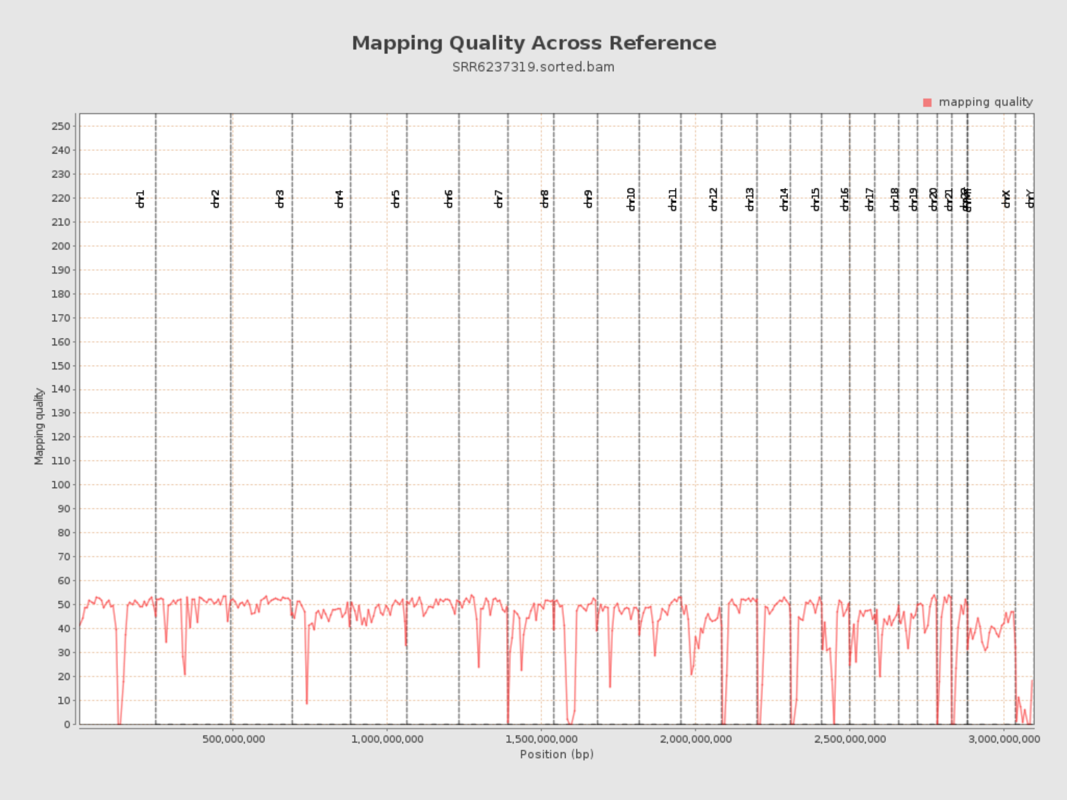
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram