Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 08:32:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237843.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_SRR6237843 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237843.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 08:32:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237843.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,336,057
Mapped reads	1,966,570 / 84.18%
Unmapped reads	369,487 / 15.82%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,789 / 0.46%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	93,328 / 4%
Duplication rate	3.53%
Clipped reads	1,102,311 / 47.19%

2.2. ACGT Content

Number/percentage of A's	34,211,841 / 27.45%
Number/percentage of C's	22,233,774 / 17.84%
Number/percentage of T's	40,075,340 / 32.15%
Number/percentage of G's	28,008,516 / 22.47%
Number/percentage of N's	112,082 / 0.09%
GC Percentage	40.31%

2.3. Coverage

Mean	0.0403

Standard Deviation	0.3927

2.4. Mapping Quality

Mean Mapping Quality	45.14

2.5. Mismatches and indels

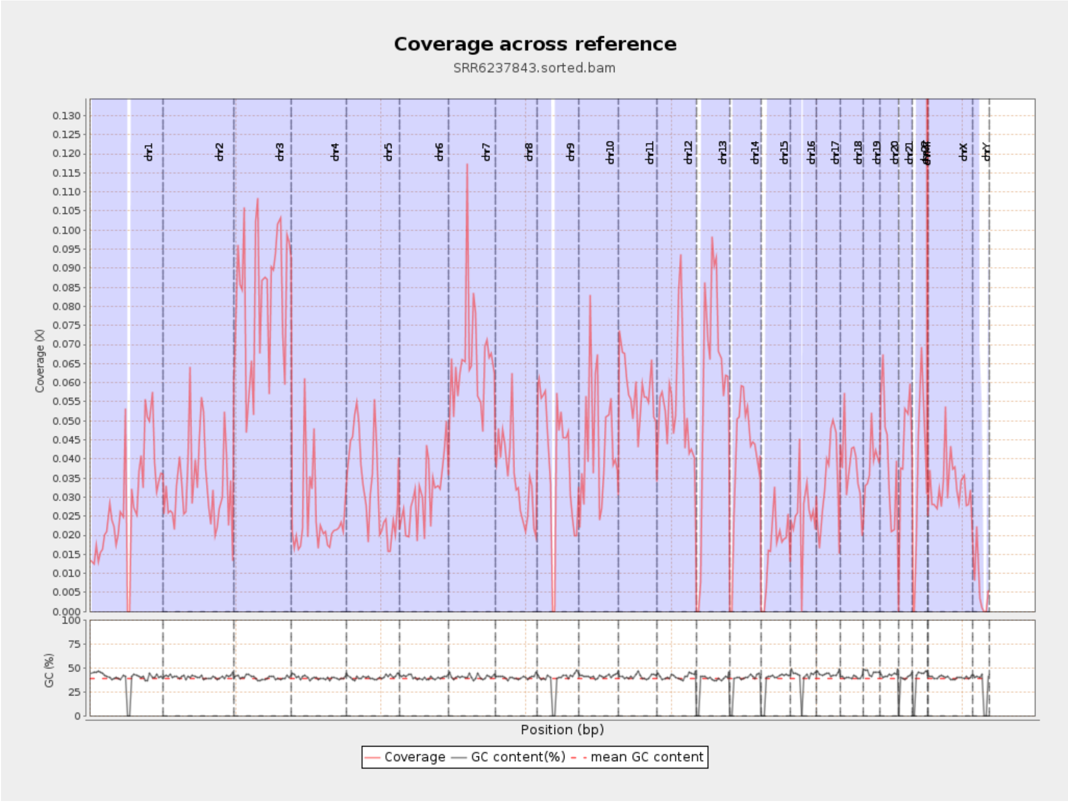
General error rate	0.83%
Mismatches	1,014,092
Insertions	11,244
Mapped reads with at least one insertion	0.57%
Deletions	32,788
Mapped reads with at least one deletion	1.65%
Homopolymer indels	47.27%

2.6. Chromosome stats

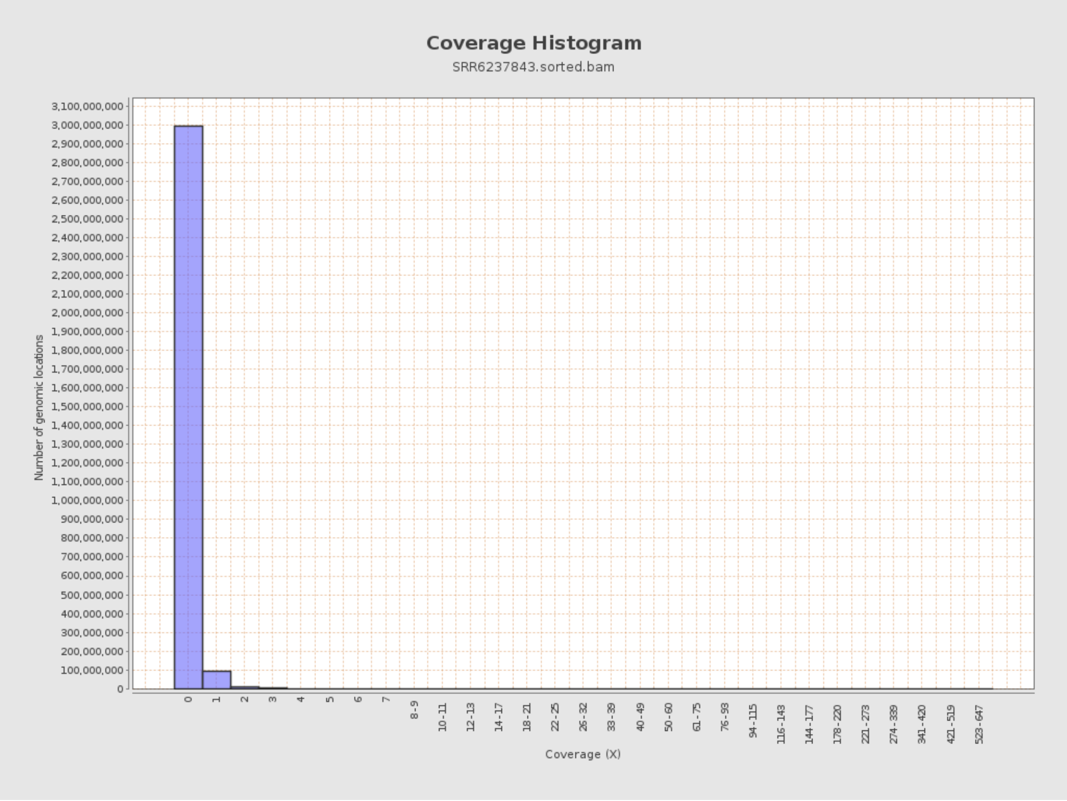
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6990094	0.028	0.494
chr2	243199373	8110492	0.0333	0.4189
chr3	198022430	16286856	0.0822	0.3308
chr4	191154276	4636408	0.0243	0.2333
chr5	180915260	5990202	0.0331	0.2119
chr6	171115067	5249377	0.0307	0.2202
chr7	159138663	10543471	0.0663	0.8112

chr8	146364022	5140670	0.0351	0.3895
chr9	141213431	5520936	0.0391	0.4473
chr10	135534747	6000182	0.0443	0.4332
chr11	135006516	7705758	0.0571	0.3775
chr12	133851895	7264671	0.0543	0.2822
chr13	115169878	6873223	0.0597	0.2799
chr14	107349540	4364974	0.0407	0.2925
chr15	102531392	1716072	0.0167	0.1495
chr16	90354753	2283486	0.0253	0.2577
chr17	81195210	2778453	0.0342	0.2623
chr18	78077248	2976585	0.0381	0.7897
chr19	59128983	2281357	0.0386	0.3967
chr20	63025520	2513264	0.0399	0.2555
chr21	48129895	2054707	0.0427	0.2901
chr22	51304566	1835210	0.0358	0.2162
chrMT	16571	88940	5.3672	4.1737
chrX	155270560	5116073	0.0329	0.2626
chrY	59373566	374238	0.0063	0.1806

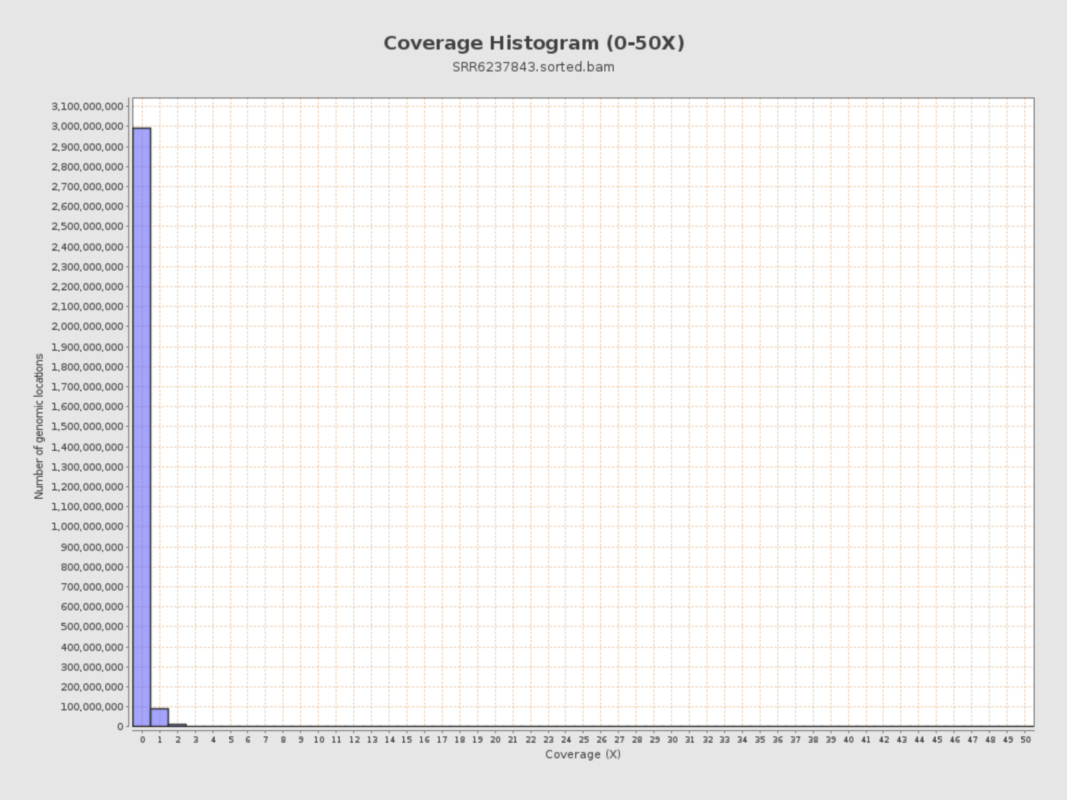
3. Results : Coverage across reference



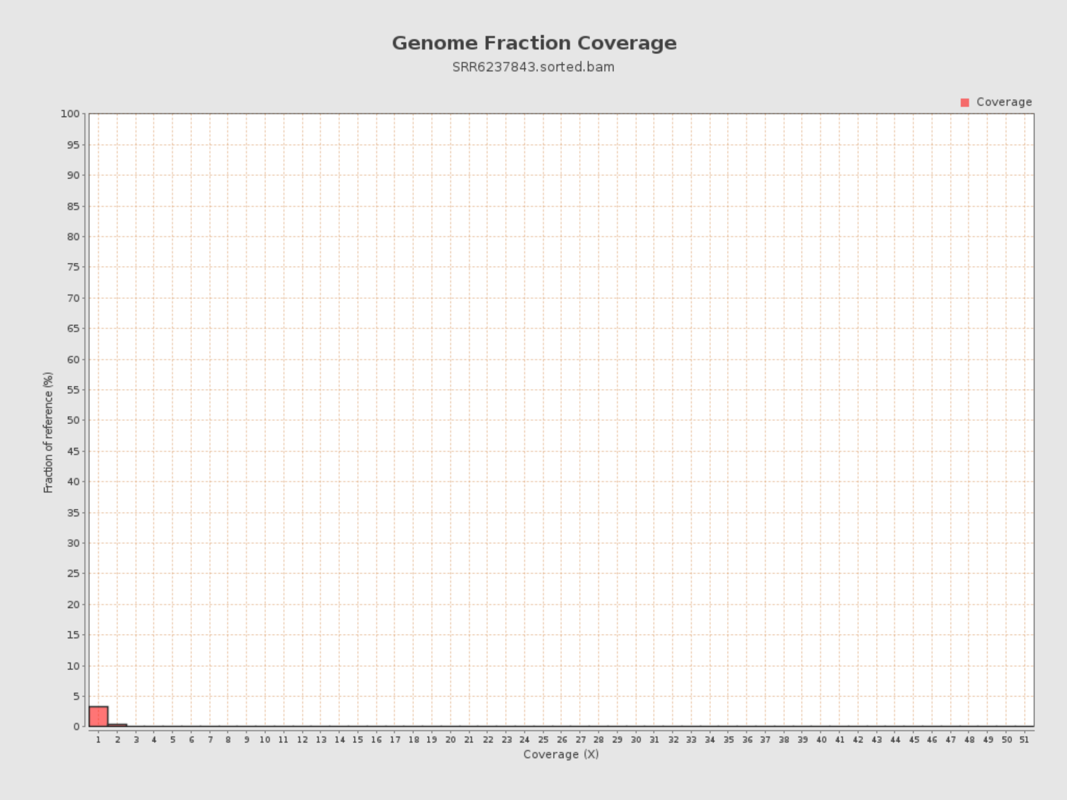
4. Results : Coverage Histogram



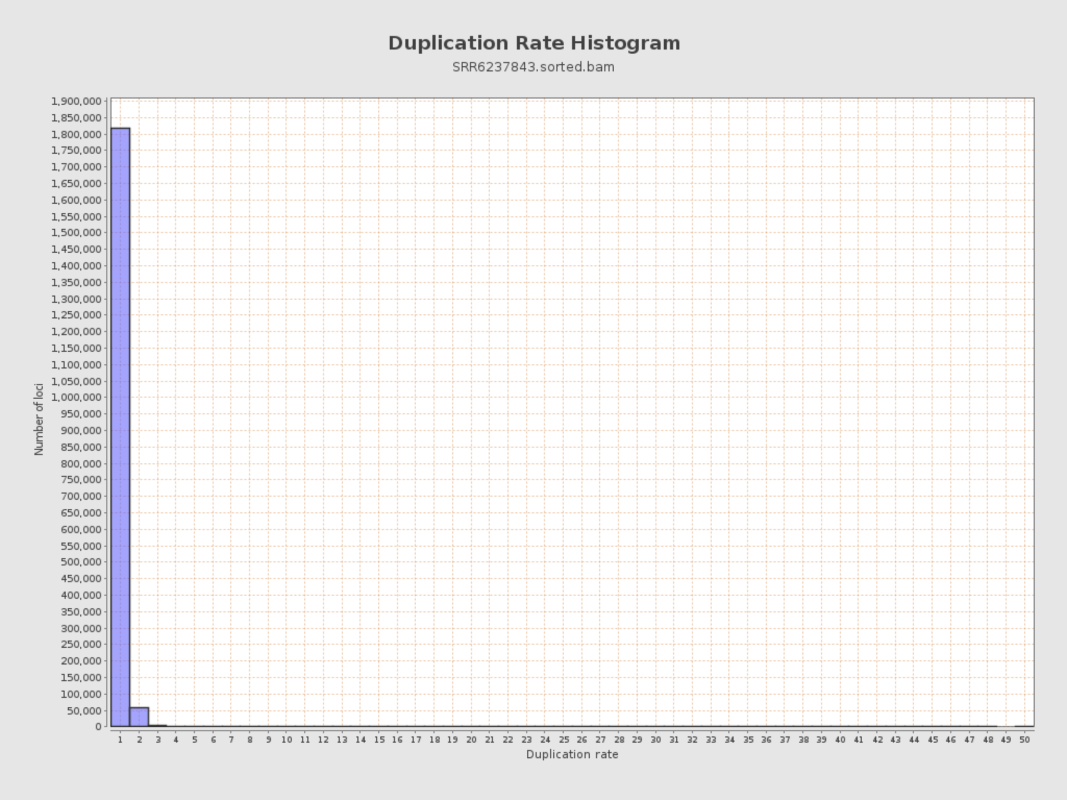
5. Results : Coverage Histogram (0-50X)



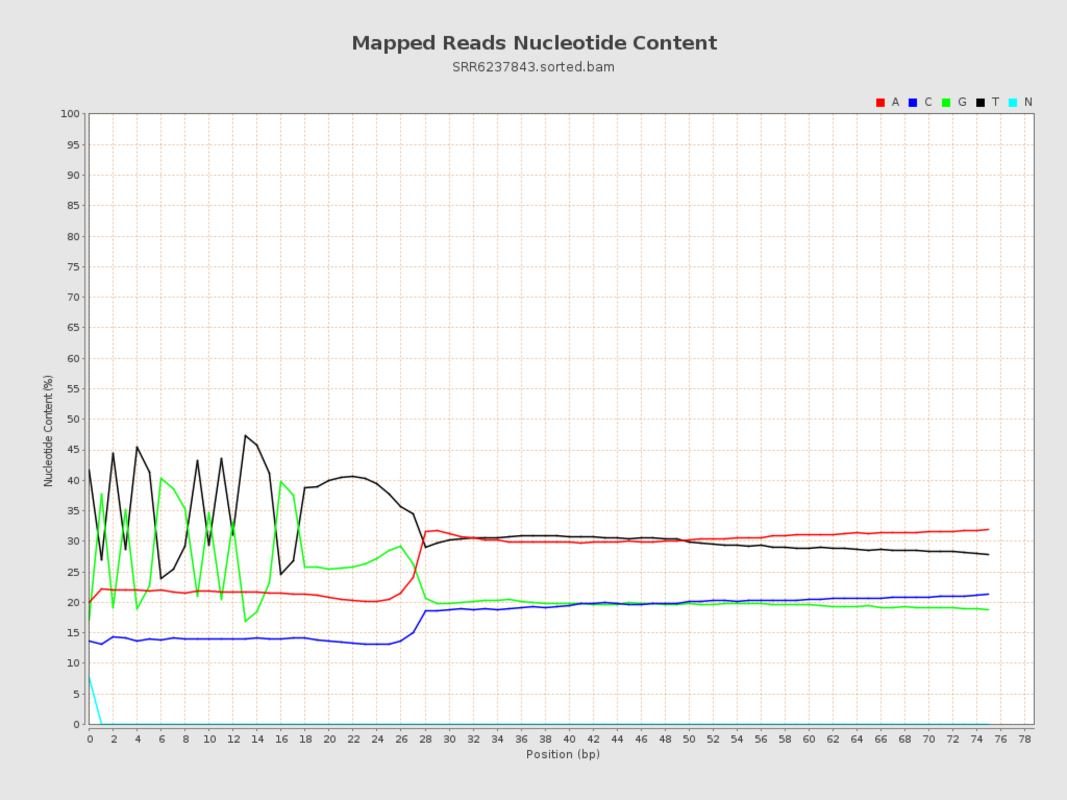
6. Results : Genome Fraction Coverage



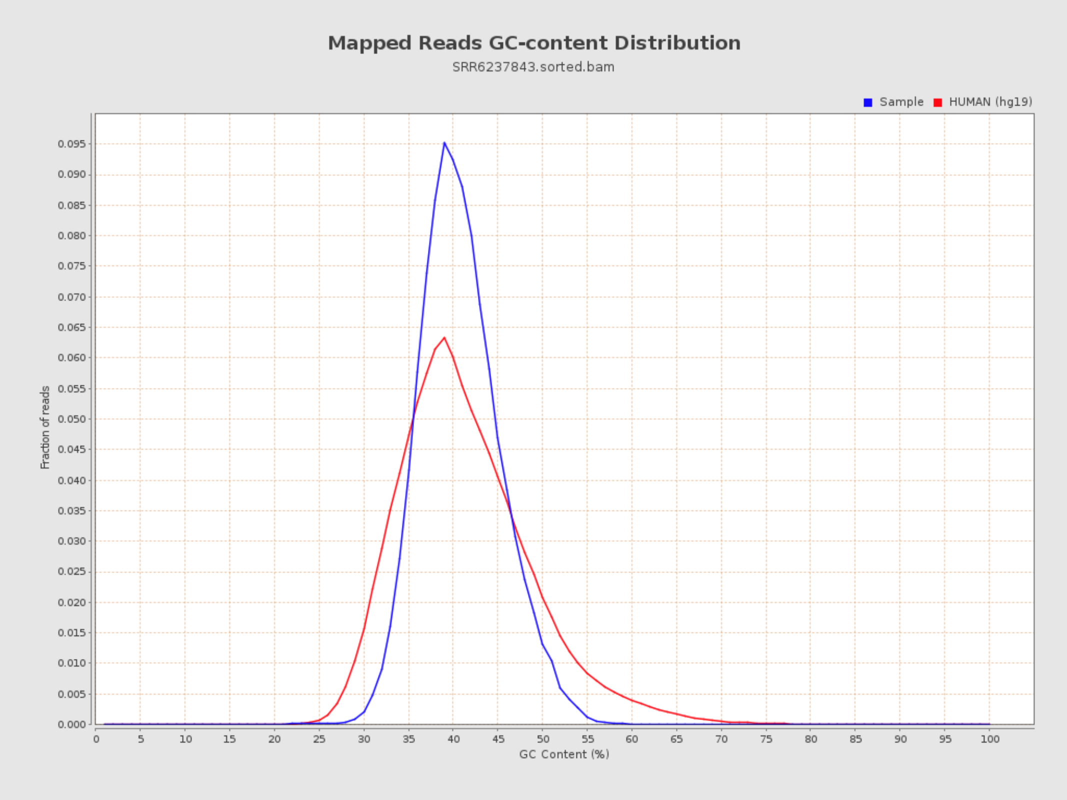
7. Results : Duplication Rate Histogram



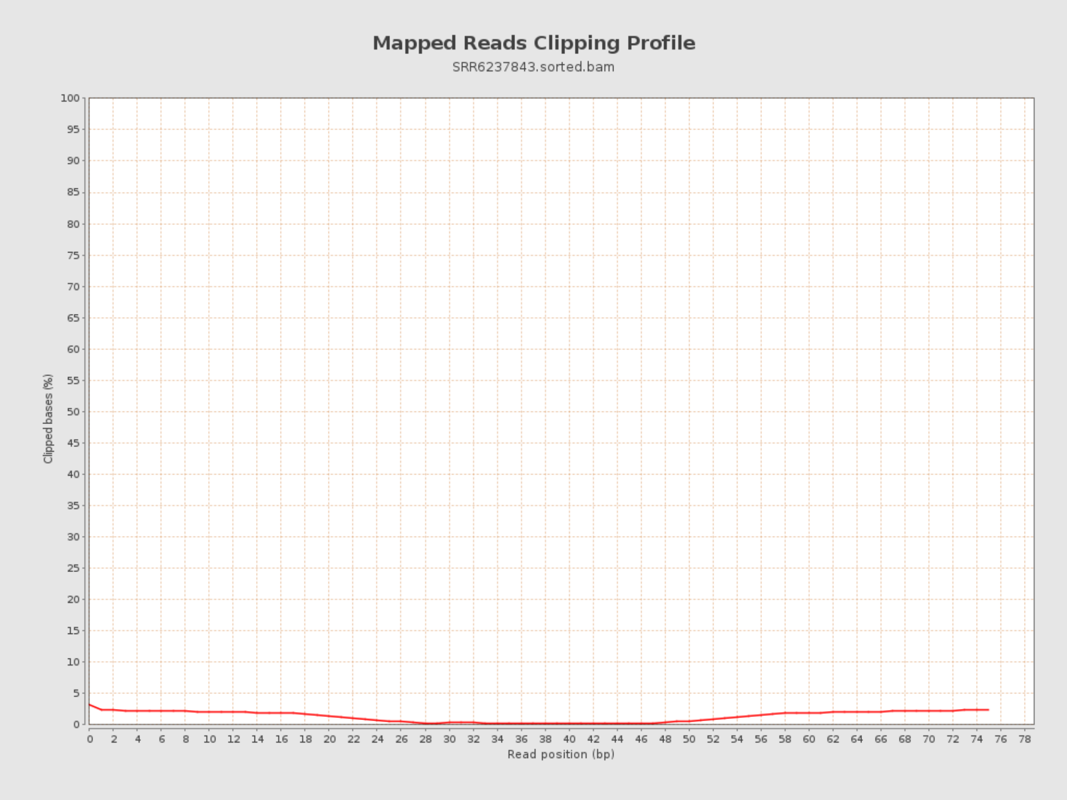
8. Results : Mapped Reads Nucleotide Content



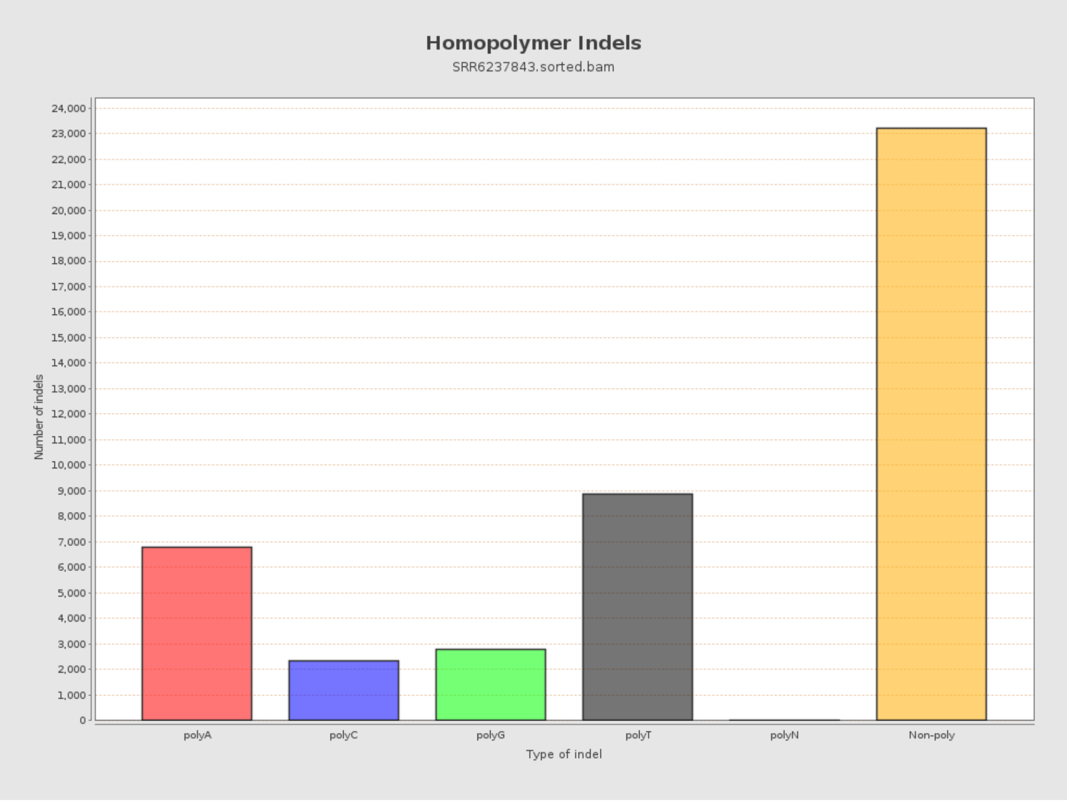
9. Results : Mapped Reads GC-content Distribution



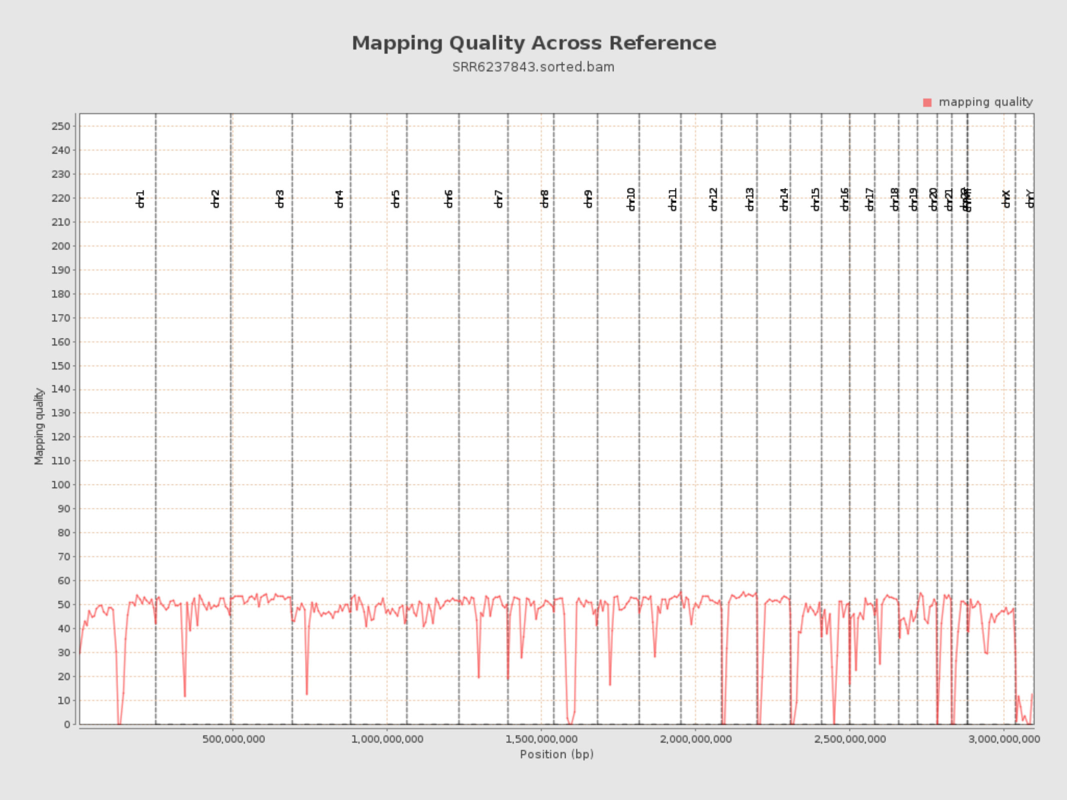
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram