Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 13:19:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238259.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_SRR6238259 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238259.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 13:19:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238259.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,632,892
Mapped reads	1,287,712 / 78.86%
Unmapped reads	345,180 / 21.14%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,102 / 0.86%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	132,352 / 8.11%
Duplication rate	8.29%
Clipped reads	758,144 / 46.43%

2.2. ACGT Content

Number/percentage of A's	23,170,396 / 28.29%
Number/percentage of C's	15,507,844 / 18.93%
Number/percentage of T's	25,353,803 / 30.96%
Number/percentage of G's	17,852,770 / 21.8%
Number/percentage of N's	19,606 / 0.02%
GC Percentage	40.73%

2.3. Coverage

Mean	0.0265

Standard Deviation	0.2845

2.4. Mapping Quality

Mean Mapping Quality	45.35

2.5. Mismatches and indels

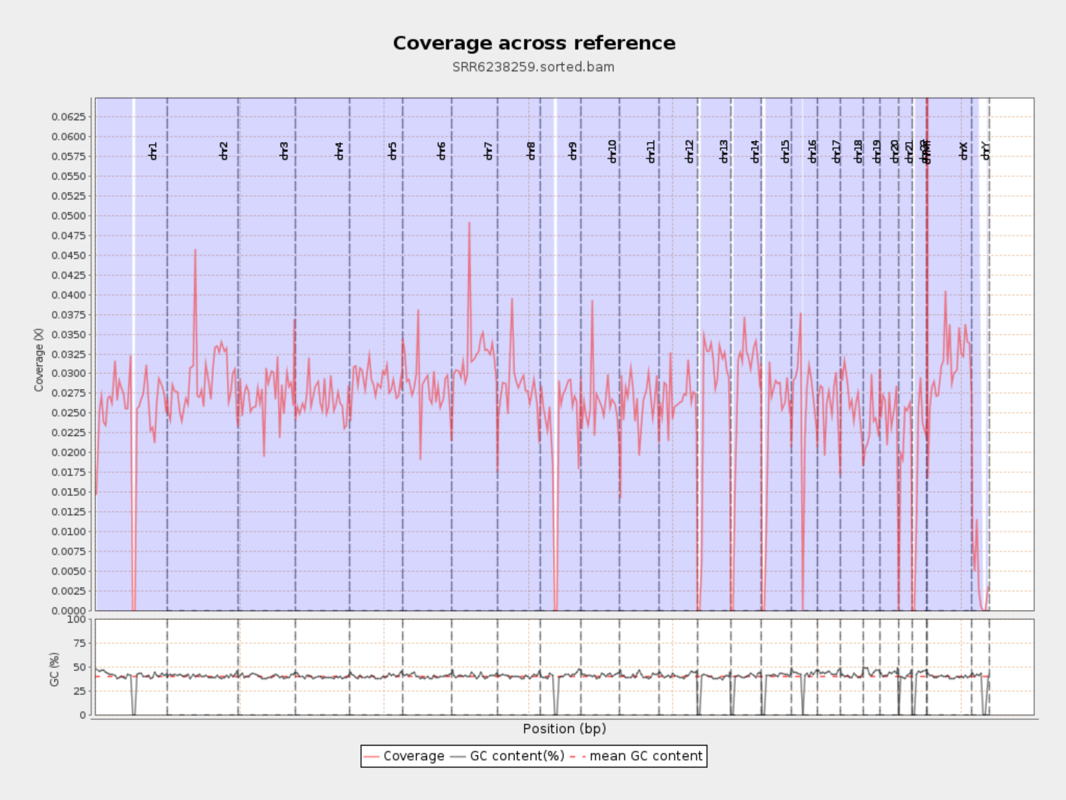
General error rate	1%
Mismatches	808,265
Insertions	6,952
Mapped reads with at least one insertion	0.54%
Deletions	30,892
Mapped reads with at least one deletion	2.37%
Homopolymer indels	46.45%

2.6. Chromosome stats

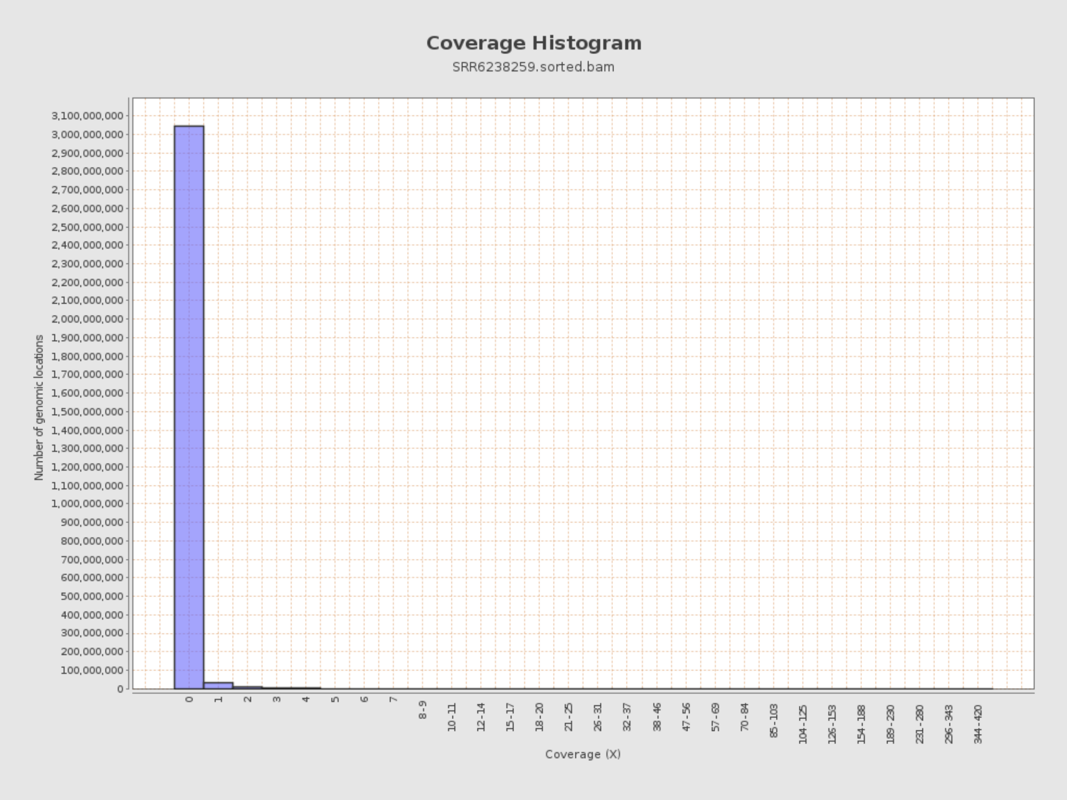
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6148190	0.0247	0.3539
chr2	243199373	7112200	0.0292	0.341
chr3	198022430	5425043	0.0274	0.2388
chr4	191154276	5078323	0.0266	0.2454
chr5	180915260	5262772	0.0291	0.2475
chr6	171115067	4879373	0.0285	0.2722
chr7	159138663	5152947	0.0324	0.3776

chr8	146364022	4154109	0.0284	0.3543
chr9	141213431	3242384	0.023	0.2575
chr10	135534747	3551673	0.0262	0.2718
chr11	135006516	3575537	0.0265	0.2617
chr12	133851895	3604701	0.0269	0.2387
chr13	115169878	3046768	0.0265	0.2425
chr14	107349540	2908323	0.0271	0.2735
chr15	102531392	2324312	0.0227	0.2629
chr16	90354753	2337043	0.0259	0.2365
chr17	81195210	2102088	0.0259	0.2356
chr18	78077248	2100890	0.0269	0.3893
chr19	59128983	1388002	0.0235	0.2863
chr20	63025520	1578152	0.025	0.2295
chr21	48129895	1008967	0.021	0.2093
chr22	51304566	913581	0.0178	0.187
chrMT	16571	13726	0.8283	1.4361
chrX	155270560	4825485	0.0311	0.2686
chrY	59373566	220284	0.0037	0.1033

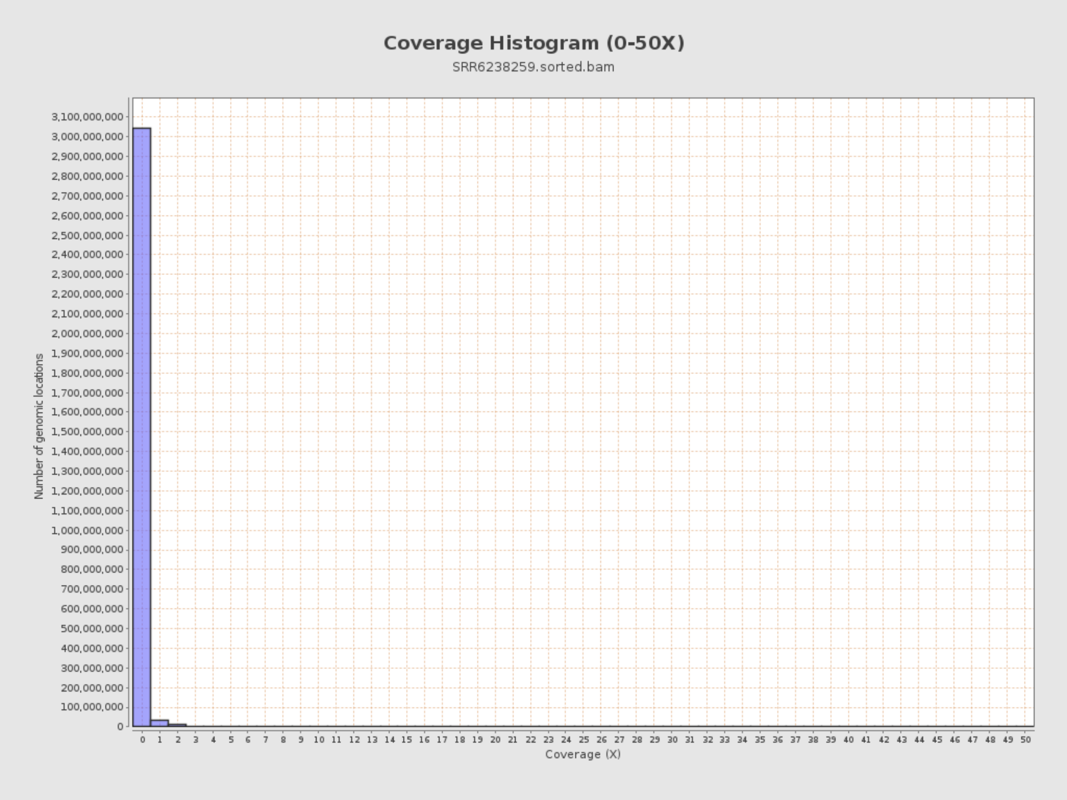
3. Results : Coverage across reference



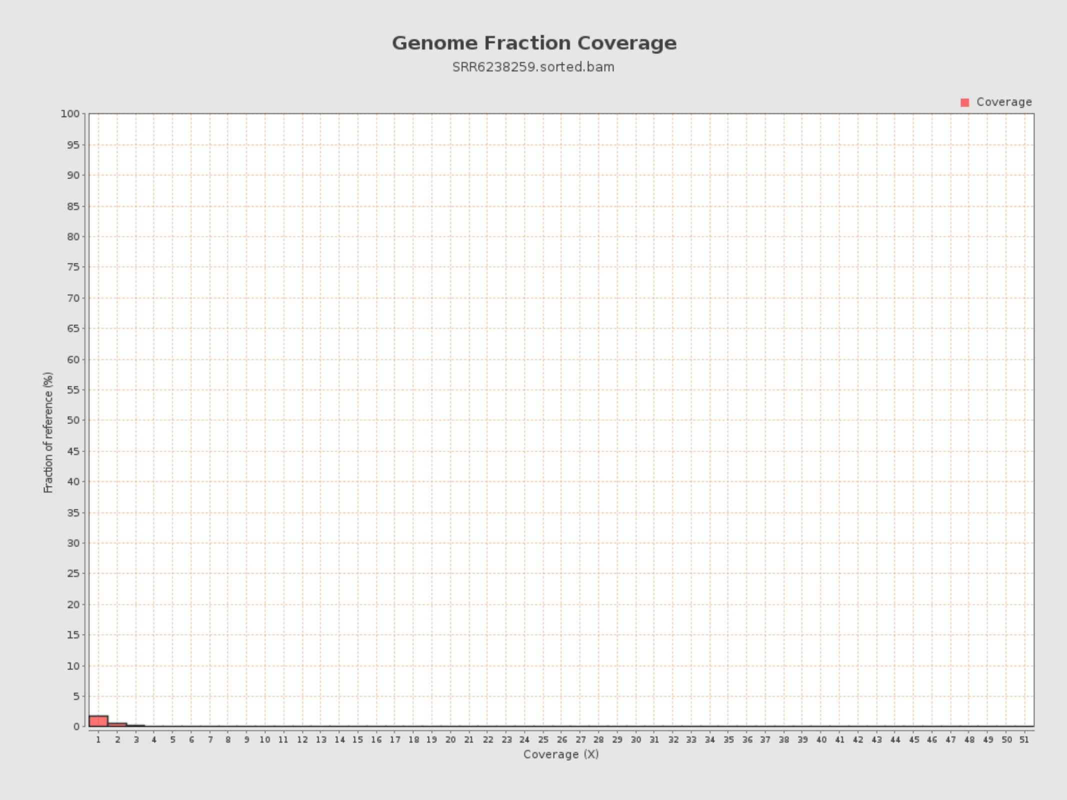
4. Results : Coverage Histogram



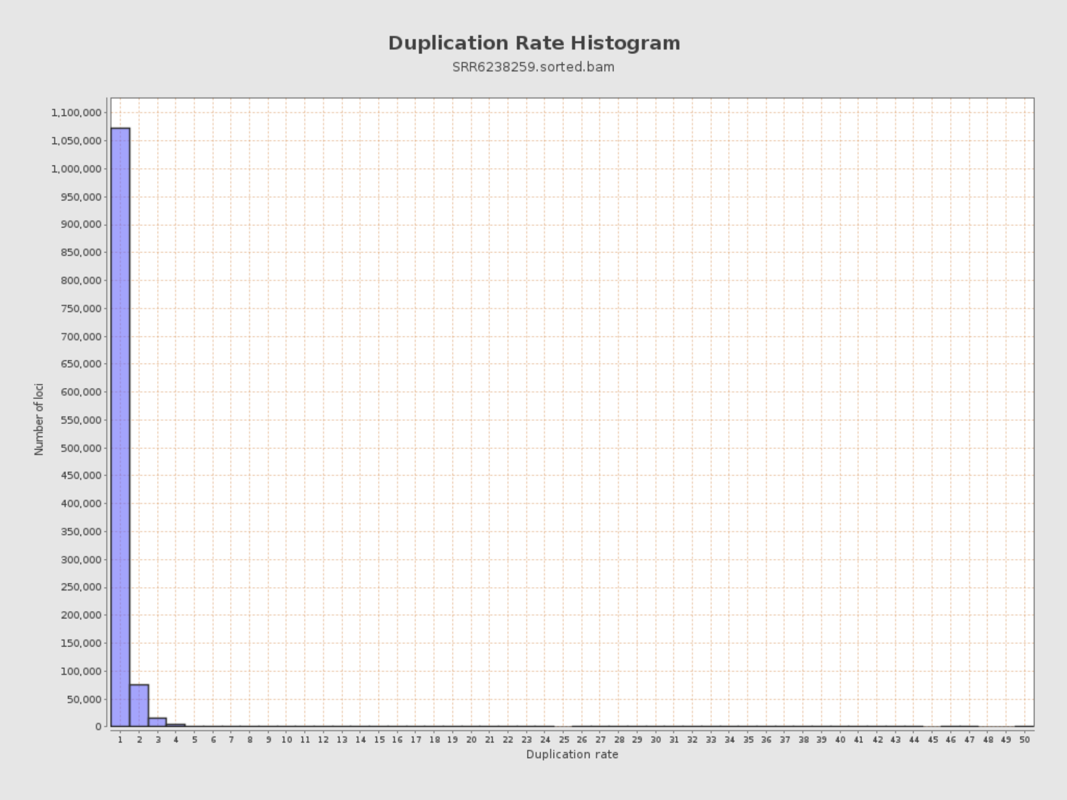
5. Results : Coverage Histogram (0-50X)



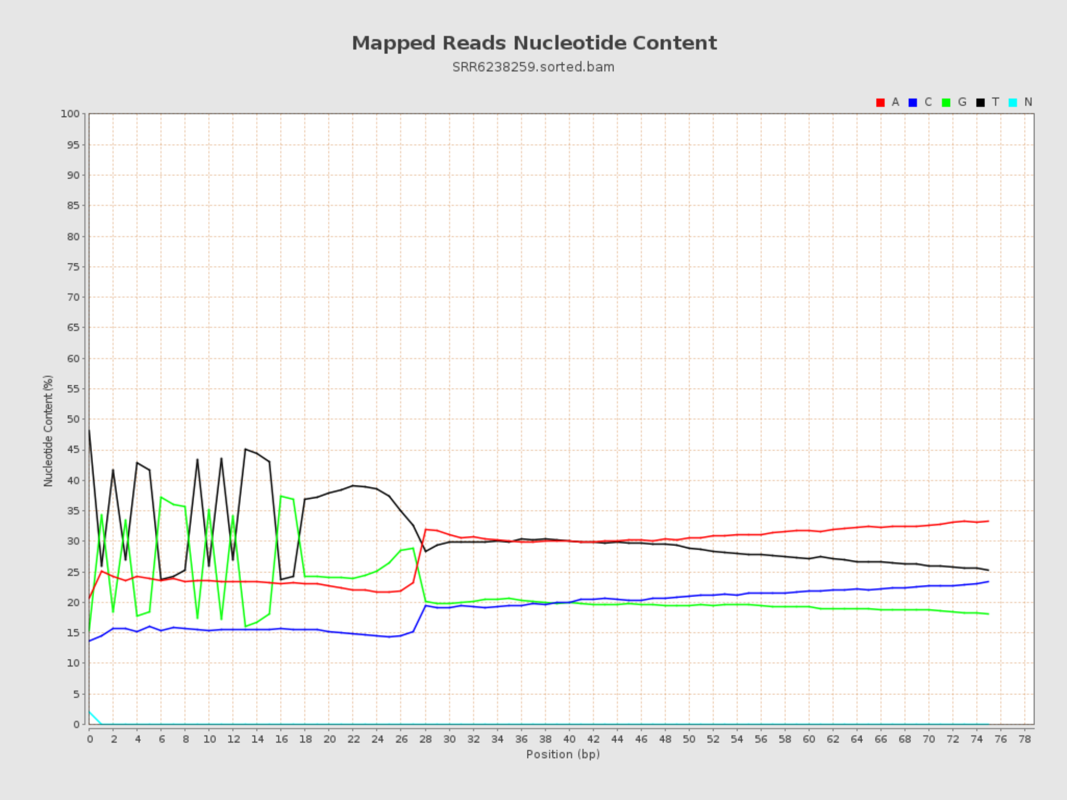
6. Results : Genome Fraction Coverage



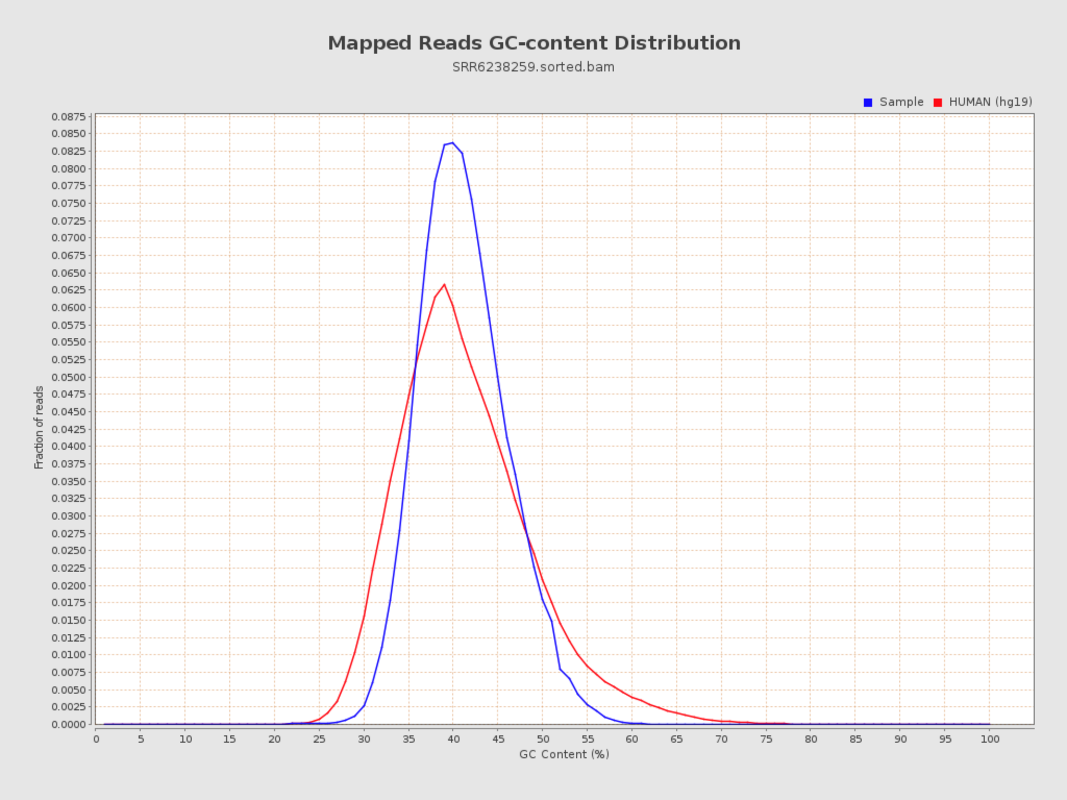
7. Results : Duplication Rate Histogram



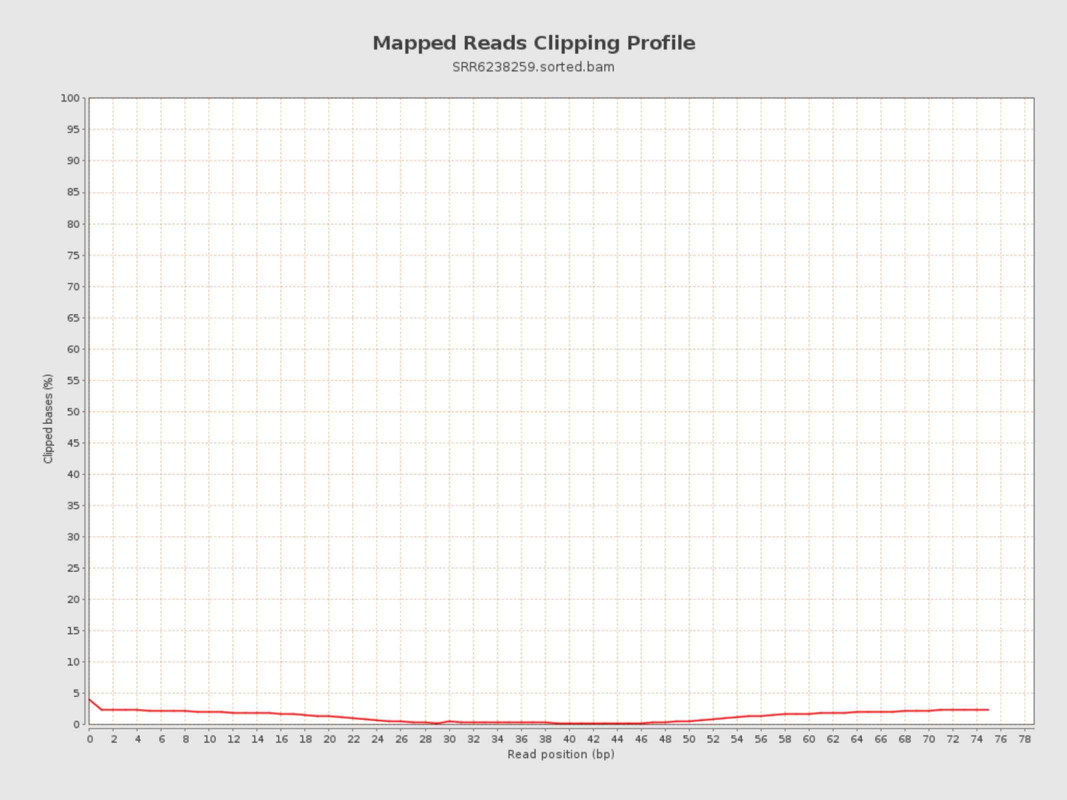
8. Results : Mapped Reads Nucleotide Content



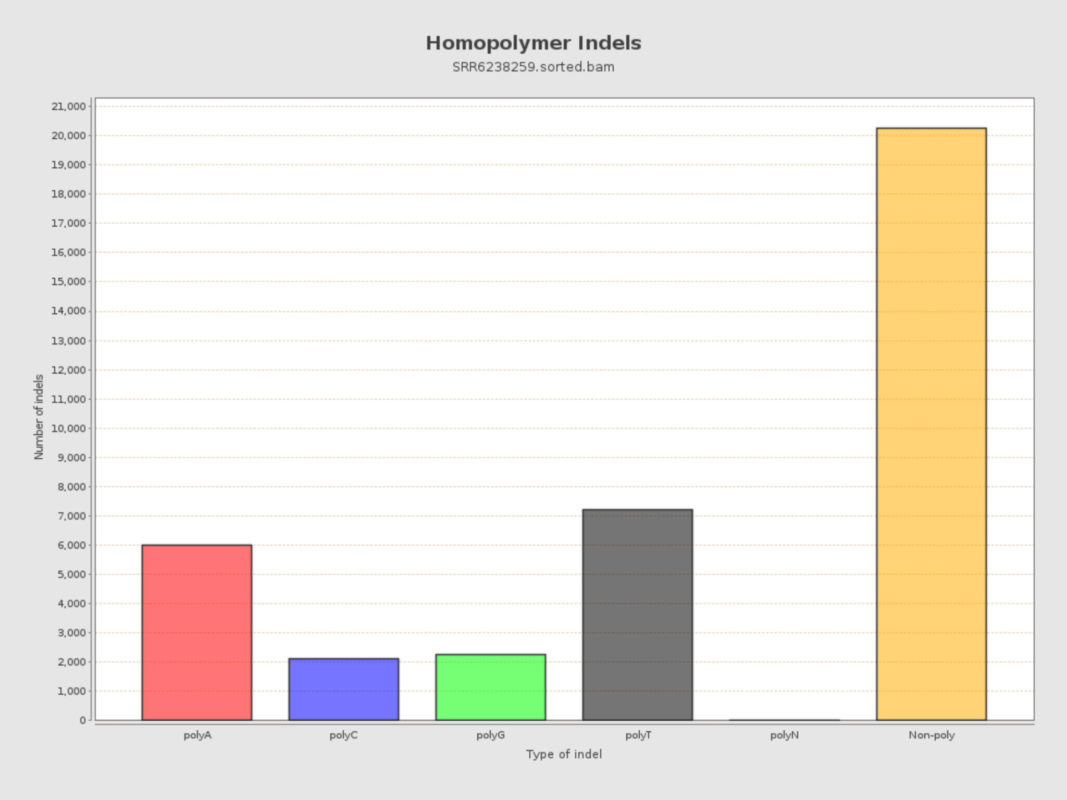
9. Results : Mapped Reads GC-content Distribution



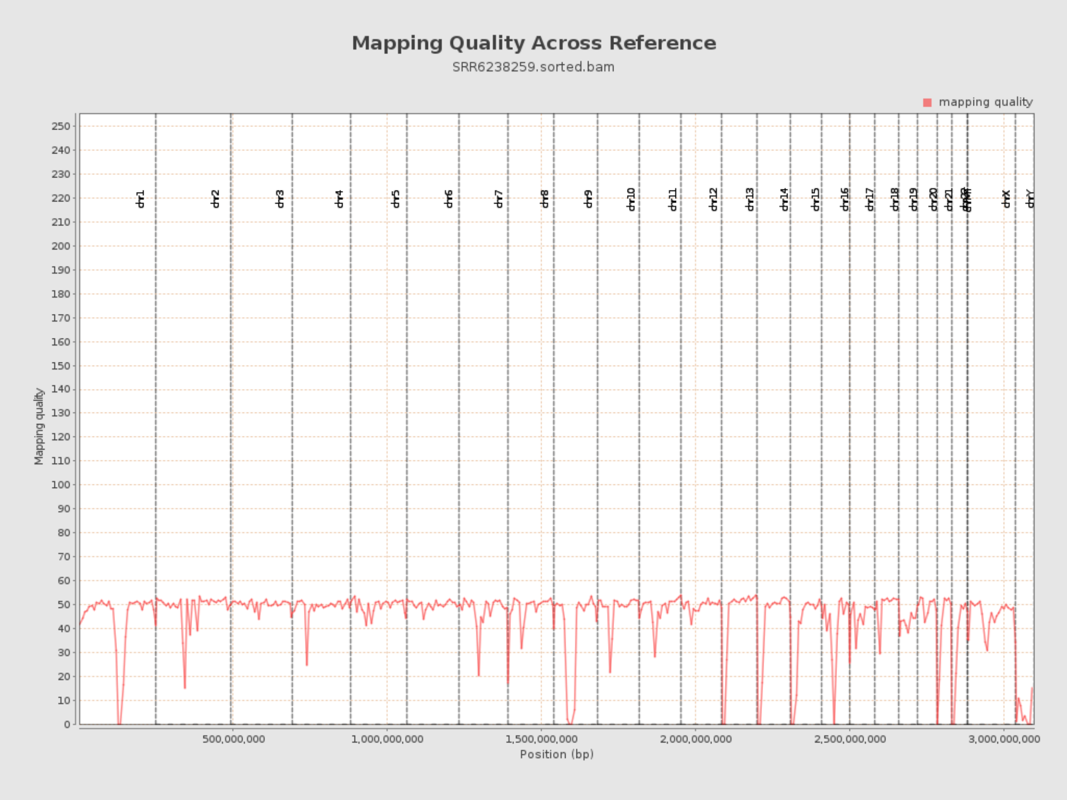
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram