Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 22:54:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237259.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_SRR6237259 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237259.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 22:54:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237259.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,839,941
Mapped reads	3,537,060 / 92.11%
Unmapped reads	302,881 / 7.89%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	43,157 / 1.12%
Read min/max/mean length	30 / 76 / 76.39
Duplicated reads (estimated)	1,187,181 / 30.92%
Duplication rate	19.67%
Clipped reads	2,034,052 / 52.97%

2.2. ACGT Content

Number/percentage of A's	60,940,817 / 27.03%
Number/percentage of C's	39,486,097 / 17.51%
Number/percentage of T's	74,392,555 / 33%
Number/percentage of G's	50,599,349 / 22.44%
Number/percentage of N's	25,656 / 0.01%
GC Percentage	39.96%

2.3. Coverage

Mean	0.0729

Standard Deviation	1.2676

2.4. Mapping Quality

Mean Mapping Quality	43.76

2.5. Mismatches and indels

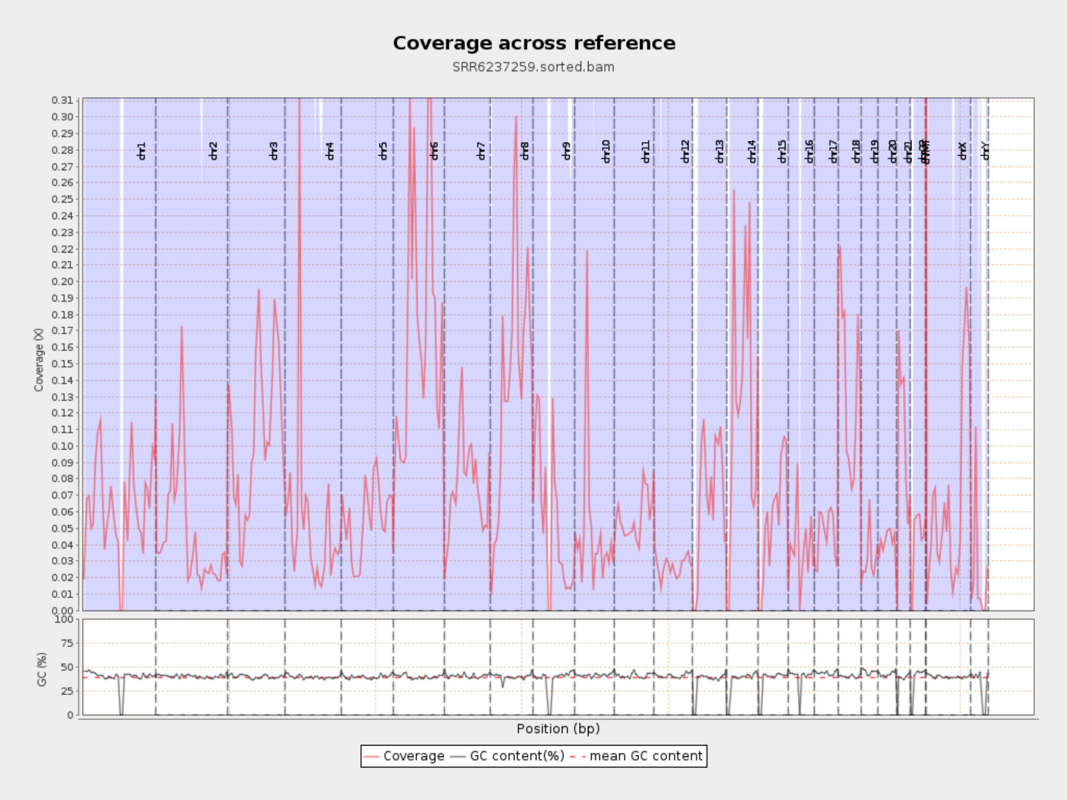
General error rate	0.69%
Mismatches	1,499,506
Insertions	23,556
Mapped reads with at least one insertion	0.66%
Deletions	65,386
Mapped reads with at least one deletion	1.82%
Homopolymer indels	43.05%

2.6. Chromosome stats

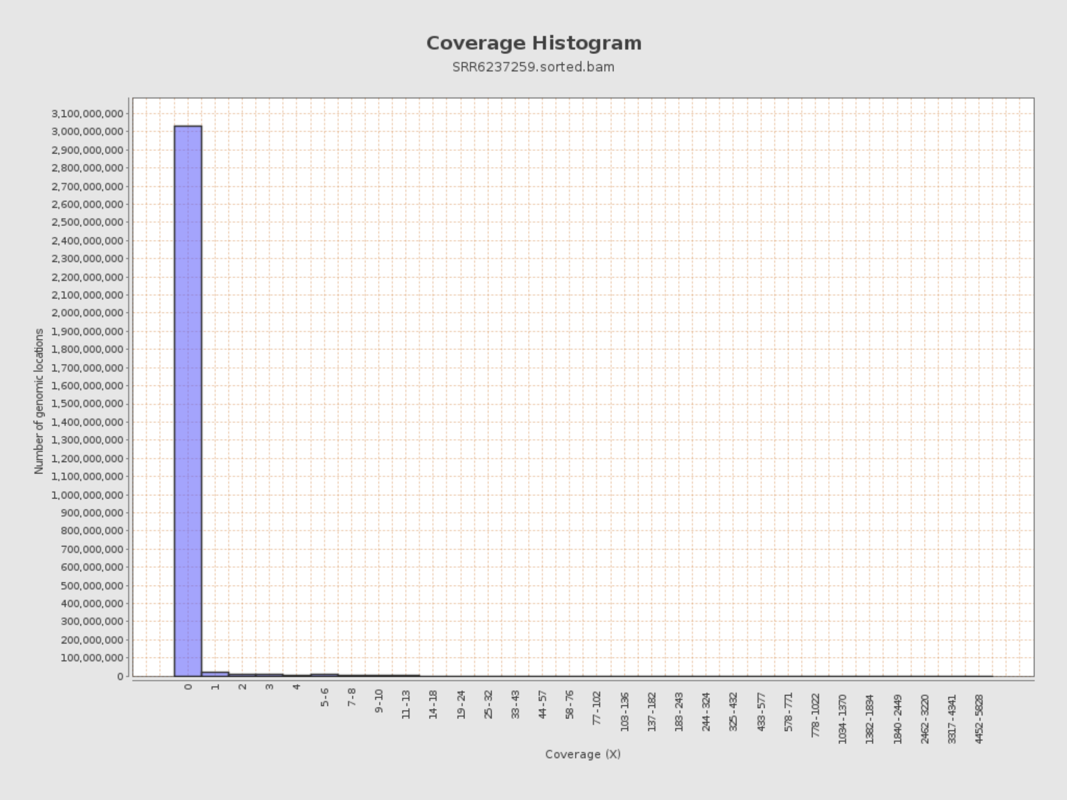
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15711791	0.063	0.767
chr2	243199373	11491661	0.0473	1.3266
chr3	198022430	21217883	0.1071	0.818
chr4	191154276	10284697	0.0538	1.2115
chr5	180915260	9972894	0.0551	0.5736
chr6	171115067	29919543	0.1749	1.2943
chr7	159138663	12169798	0.0765	0.9586

chr8	146364022	21101441	0.1442	3.8216
chr9	141213431	7683673	0.0544	0.8187
chr10	135534747	6360616	0.0469	1.6366
chr11	135006516	7683464	0.0569	0.6526
chr12	133851895	3640875	0.0272	0.4462
chr13	115169878	7925625	0.0688	0.6553
chr14	107349540	13488616	0.1257	0.9143
chr15	102531392	5722391	0.0558	0.5748
chr16	90354753	3298513	0.0365	0.6167
chr17	81195210	3760356	0.0463	0.6305
chr18	78077248	10835346	0.1388	2.0298
chr19	59128983	1895673	0.0321	0.5337
chr20	63025520	2652068	0.0421	0.5845
chr21	48129895	4851649	0.1008	1.0838
chr22	51304566	2124471	0.0414	0.4808
chrMT	16571	36421	2.1979	3.4923
chrX	155270560	10380611	0.0669	0.6607
chrY	59373566	1354043	0.0228	1.116

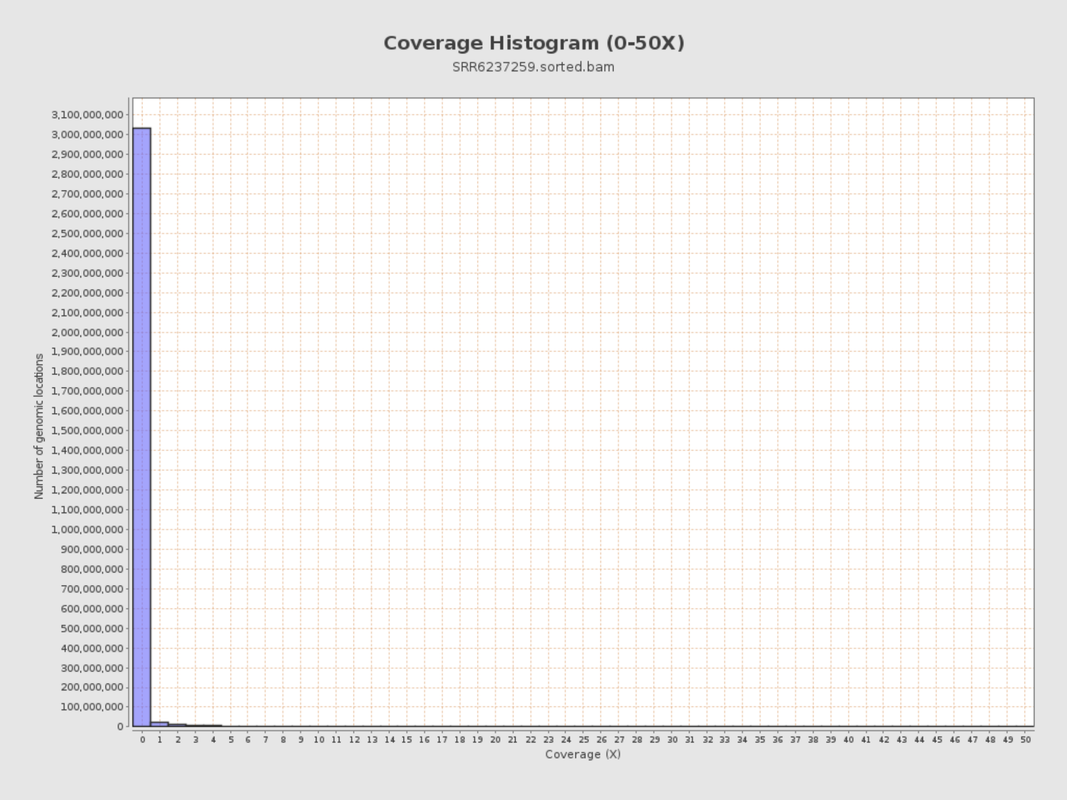
3. Results : Coverage across reference



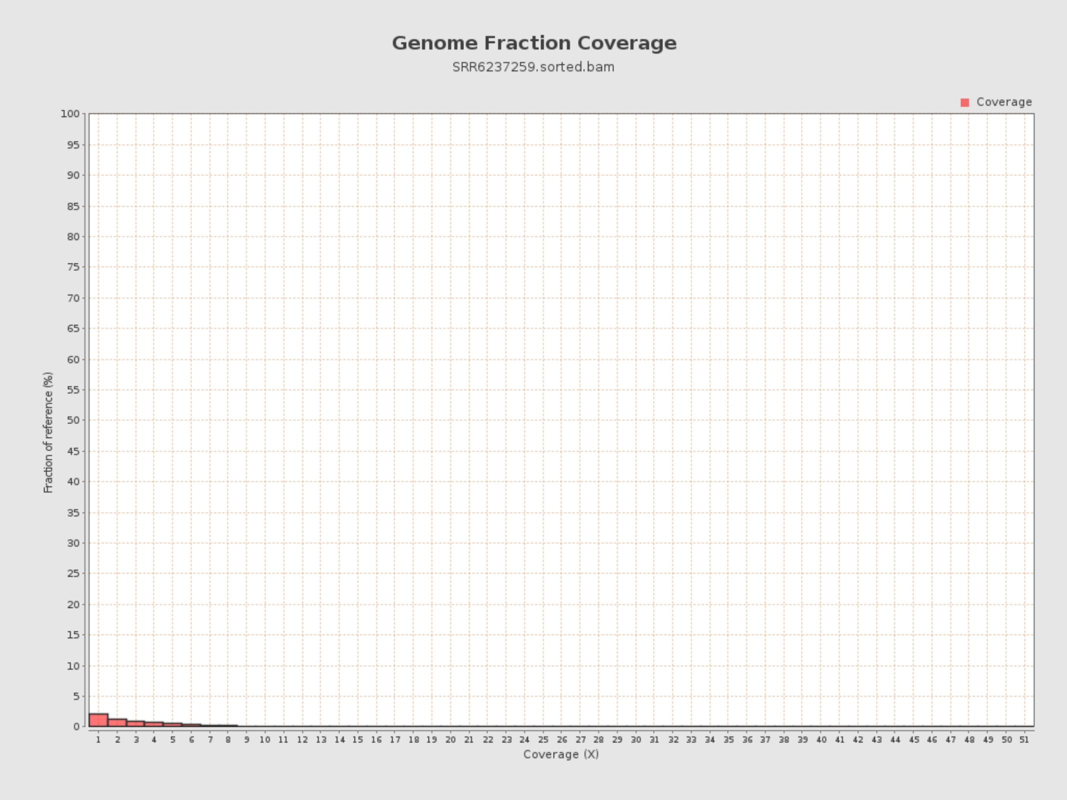
4. Results : Coverage Histogram



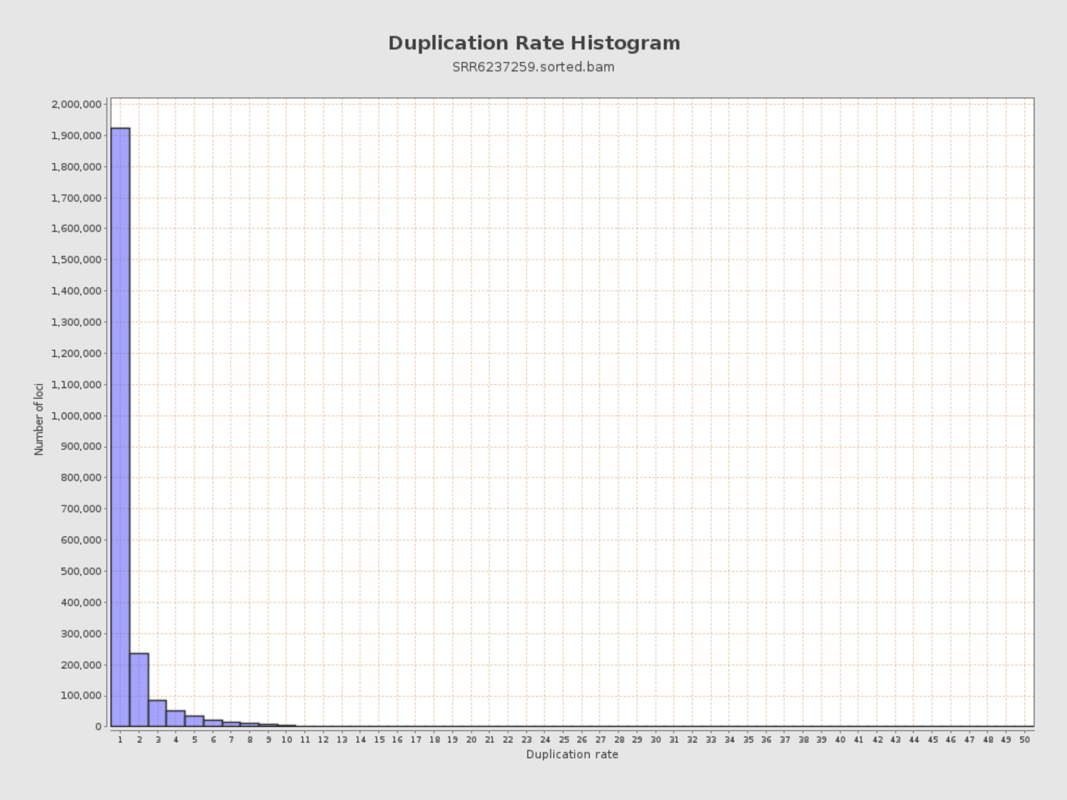
5. Results : Coverage Histogram (0-50X)



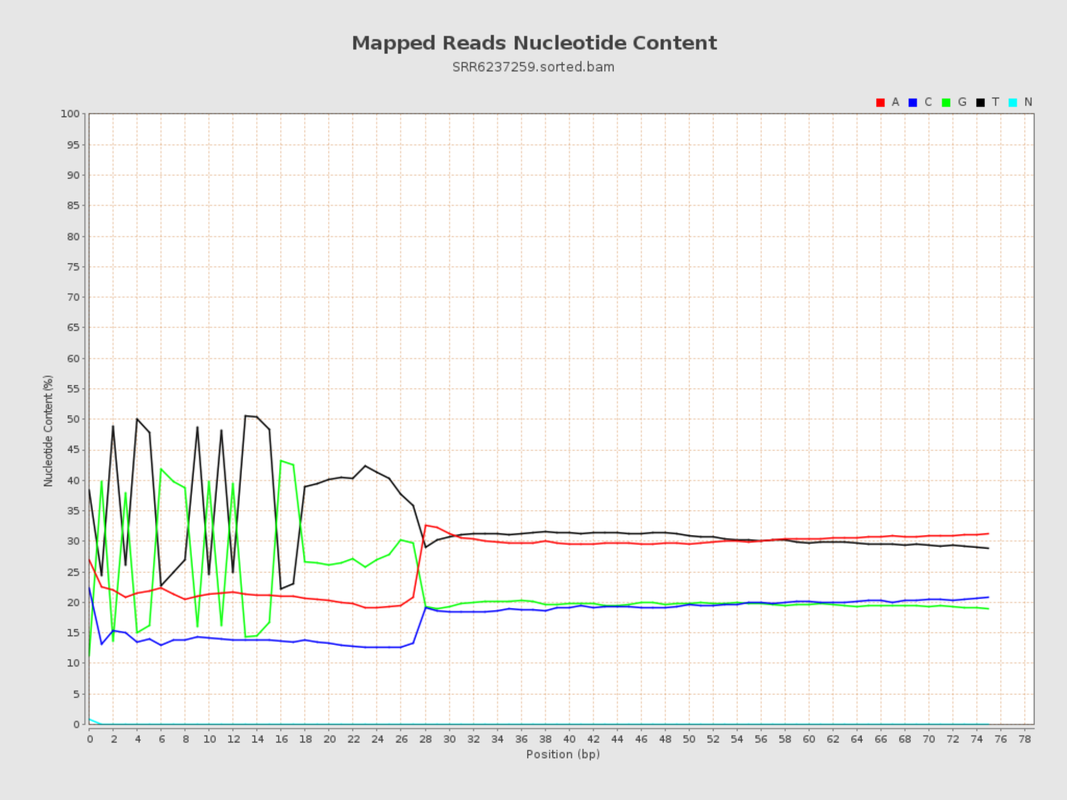
6. Results : Genome Fraction Coverage



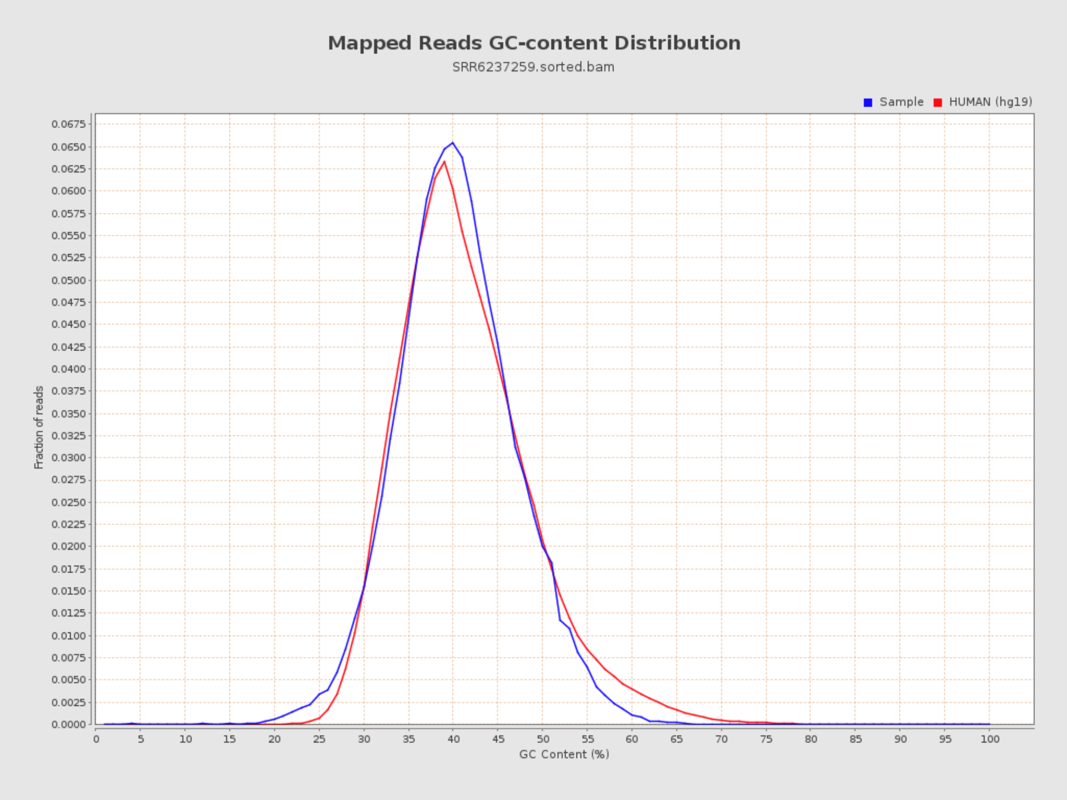
7. Results : Duplication Rate Histogram



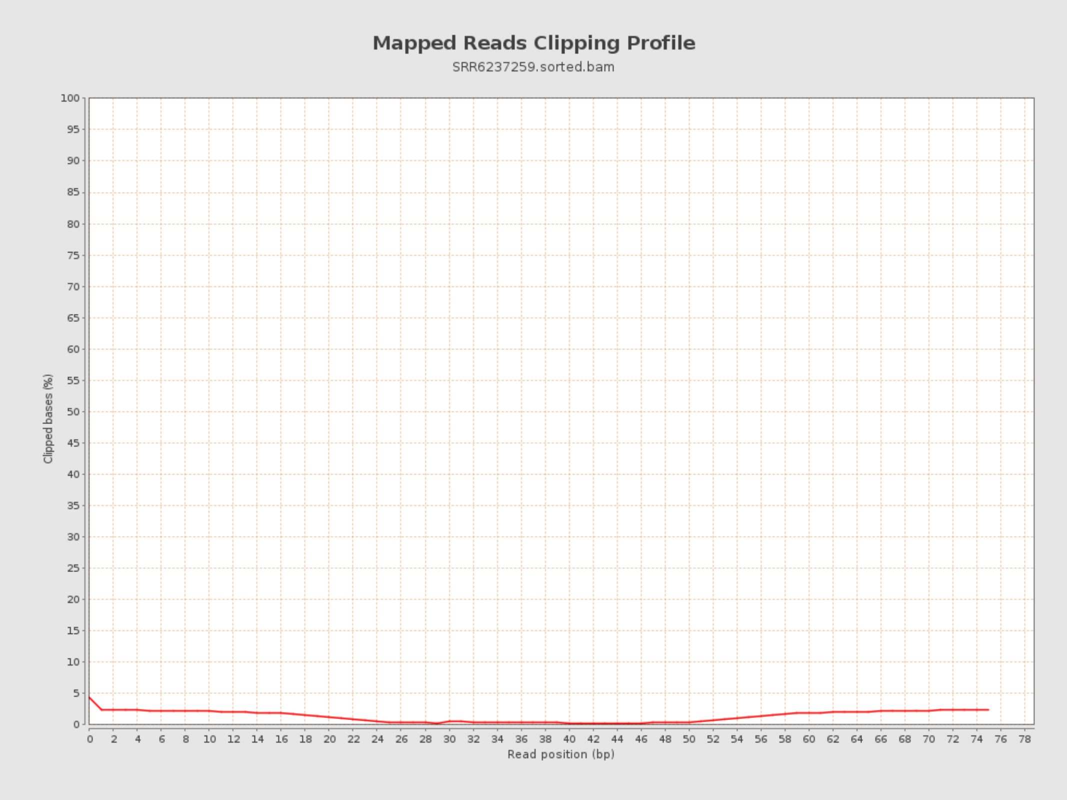
8. Results : Mapped Reads Nucleotide Content



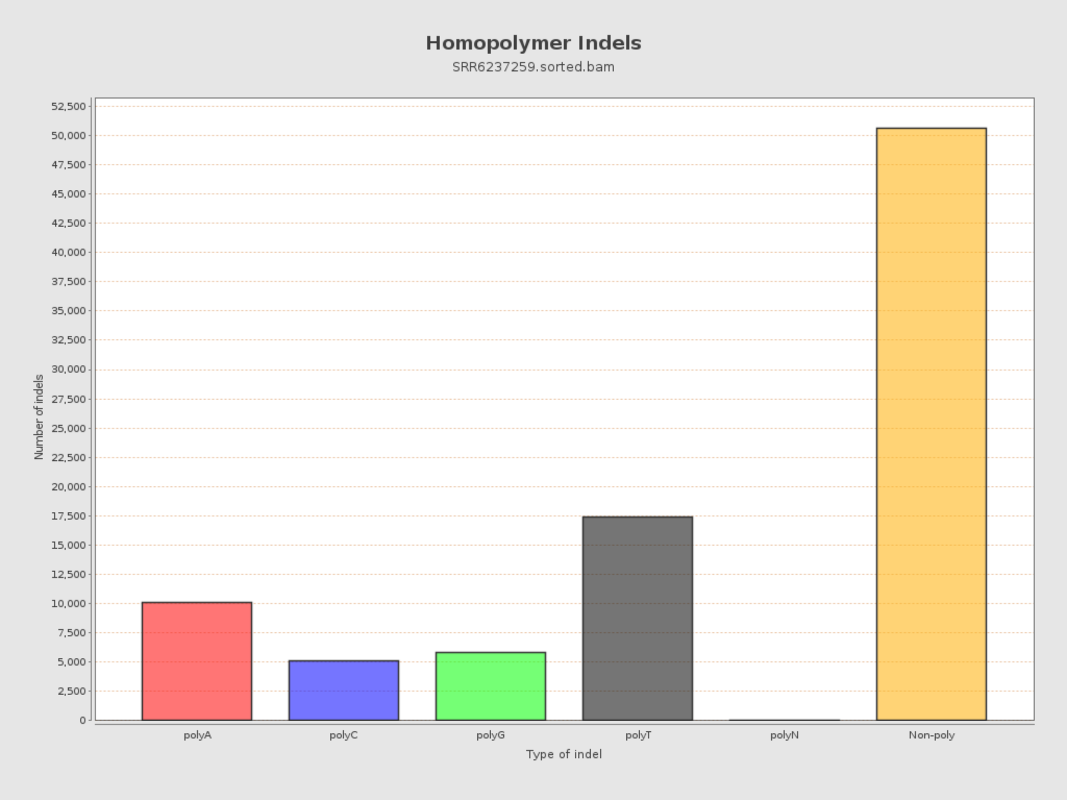
9. Results : Mapped Reads GC-content Distribution



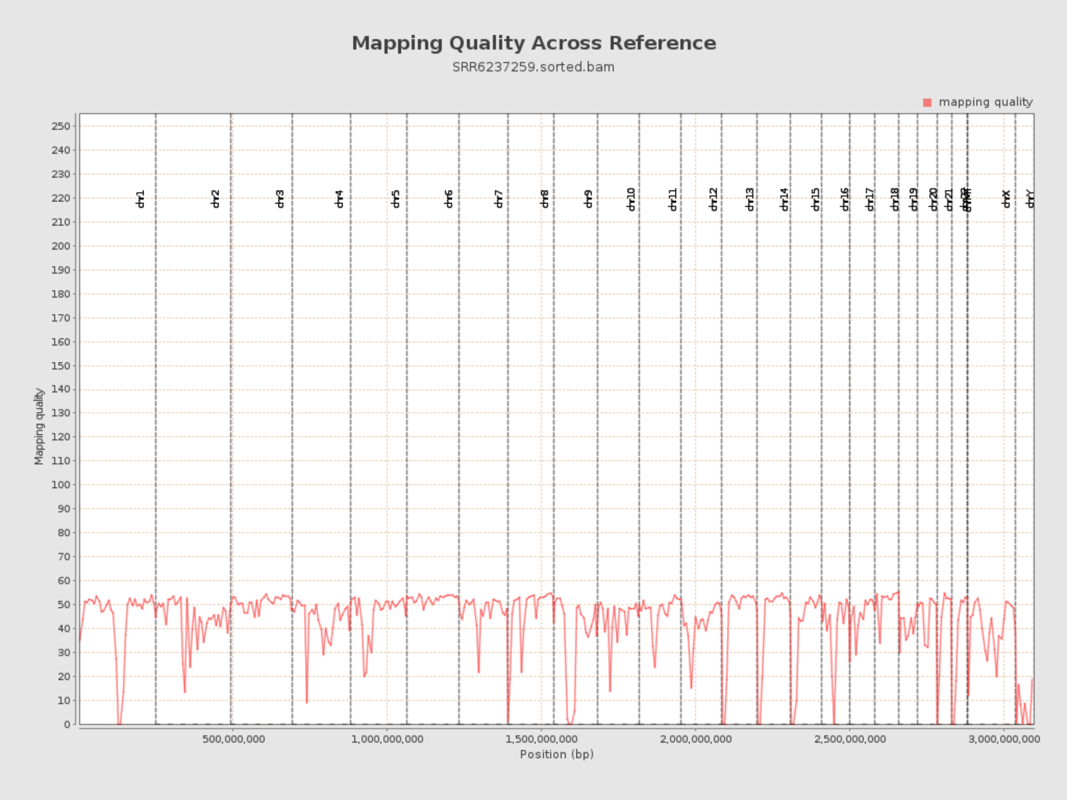
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram