Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 00:22:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525235.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_SRR10525235 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525235.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 00:22:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525235.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,319,500
Mapped reads	2,146,574 / 92.54%
Unmapped reads	172,926 / 7.46%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,812 / 0.34%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	113,415 / 4.89%
Duplication rate	3.96%
Clipped reads	2,151,729 / 92.77%

2.2. ACGT Content

Number/percentage of A's	32,496,190 / 25.89%
Number/percentage of C's	25,102,495 / 20%
Number/percentage of T's	38,868,342 / 30.97%
Number/percentage of G's	29,036,987 / 23.14%
Number/percentage of N's	2,751 / 0%
GC Percentage	43.14%

2.3. Coverage

Mean	0.0406

Standard Deviation	0.3852

2.4. Mapping Quality

Mean Mapping Quality	45.31

2.5. Mismatches and indels

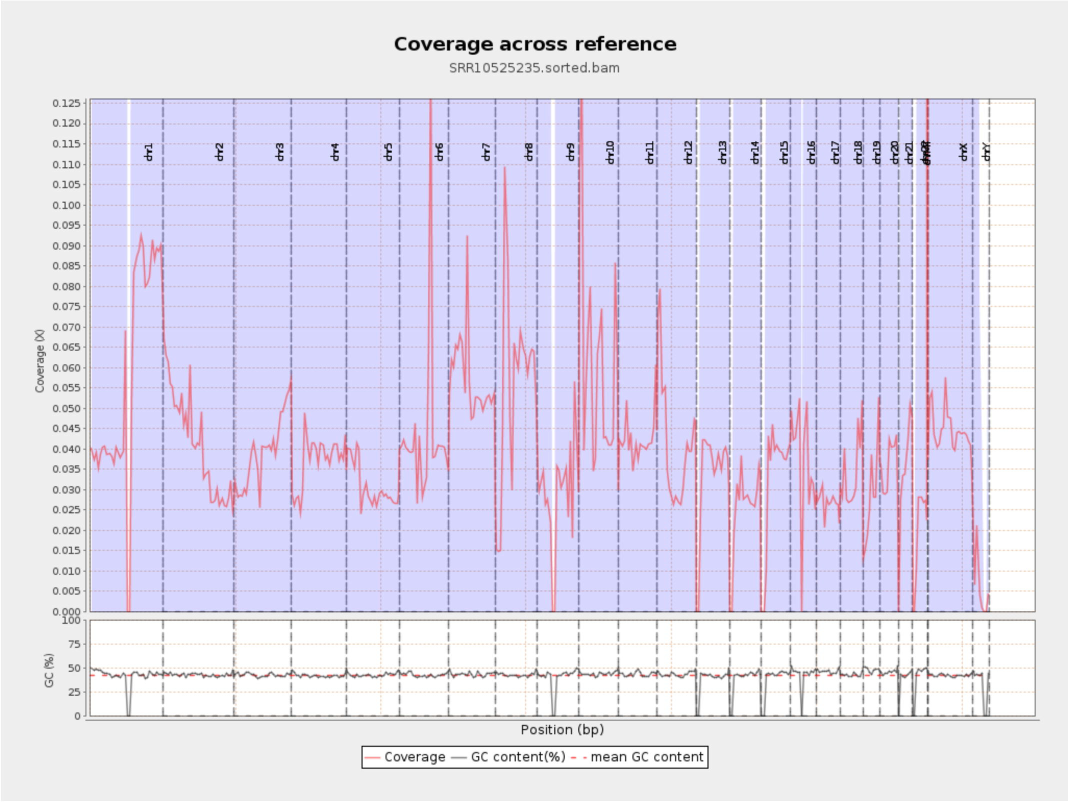
General error rate	0.5%
Mismatches	609,429
Insertions	8,124
Mapped reads with at least one insertion	0.38%
Deletions	25,240
Mapped reads with at least one deletion	1.17%
Homopolymer indels	45.11%

2.6. Chromosome stats

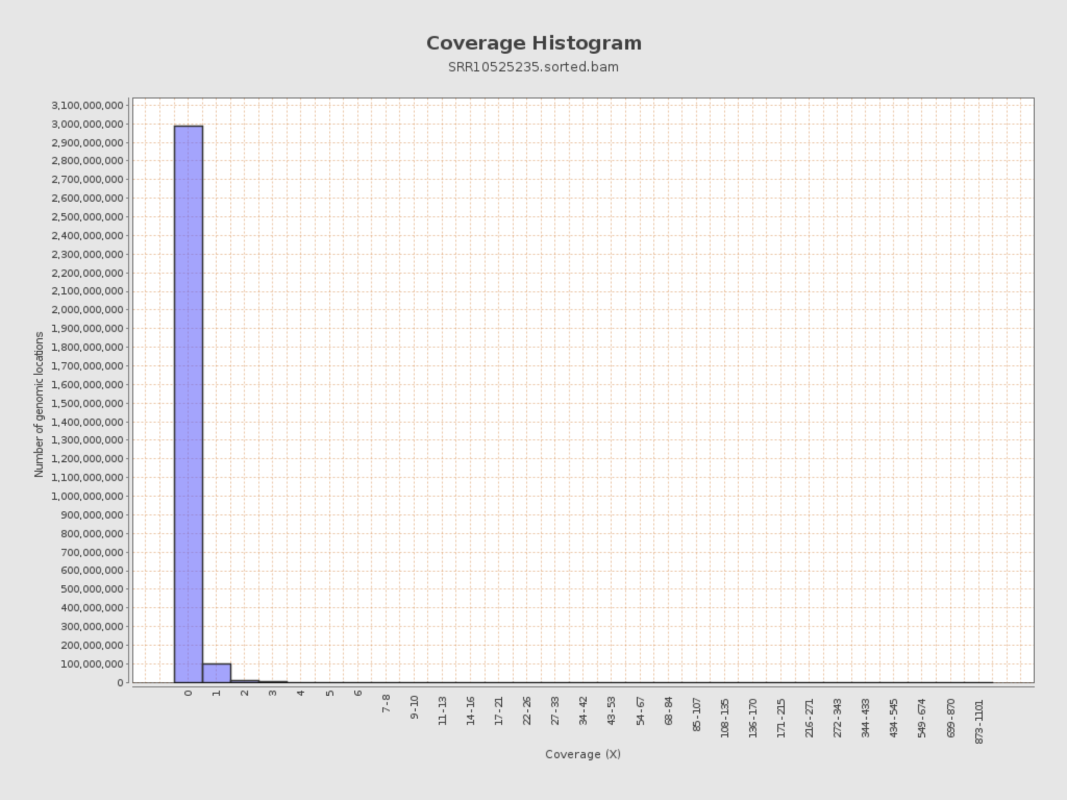
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14305197	0.0574	0.6713
chr2	243199373	10040517	0.0413	0.5041
chr3	198022430	7695753	0.0389	0.2223
chr4	191154276	7070795	0.037	0.2343
chr5	180915260	5559422	0.0307	0.1982
chr6	171115067	7502538	0.0438	0.2698
chr7	159138663	9156949	0.0575	0.6948

chr8	146364022	8080279	0.0552	0.4563
chr9	141213431	4109127	0.0291	0.2575
chr10	135534747	8424185	0.0622	0.3908
chr11	135006516	5721192	0.0424	0.2989
chr12	133851895	5473265	0.0409	0.2313
chr13	115169878	3855171	0.0335	0.2084
chr14	107349540	2705734	0.0252	0.1852
chr15	102531392	3292387	0.0321	0.205
chr16	90354753	3292583	0.0364	0.2425
chr17	81195210	2164910	0.0267	0.1959
chr18	78077248	2654838	0.034	0.51
chr19	59128983	1714692	0.029	0.421
chr20	63025520	2268507	0.036	0.2173
chr21	48129895	1689729	0.0351	0.2306
chr22	51304566	977444	0.0191	0.1543
chrMT	16571	470778	28.4098	15.2034
chrX	155270560	6938351	0.0447	0.2592
chrY	59373566	382642	0.0064	0.1771

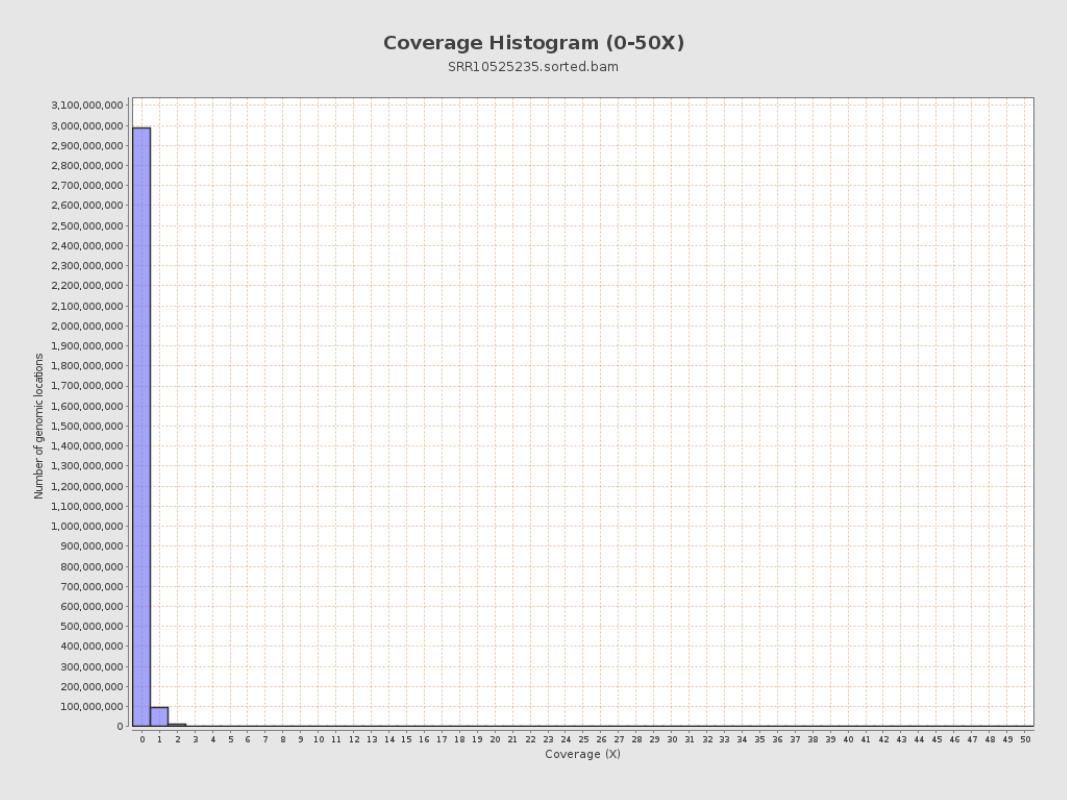
3. Results : Coverage across reference



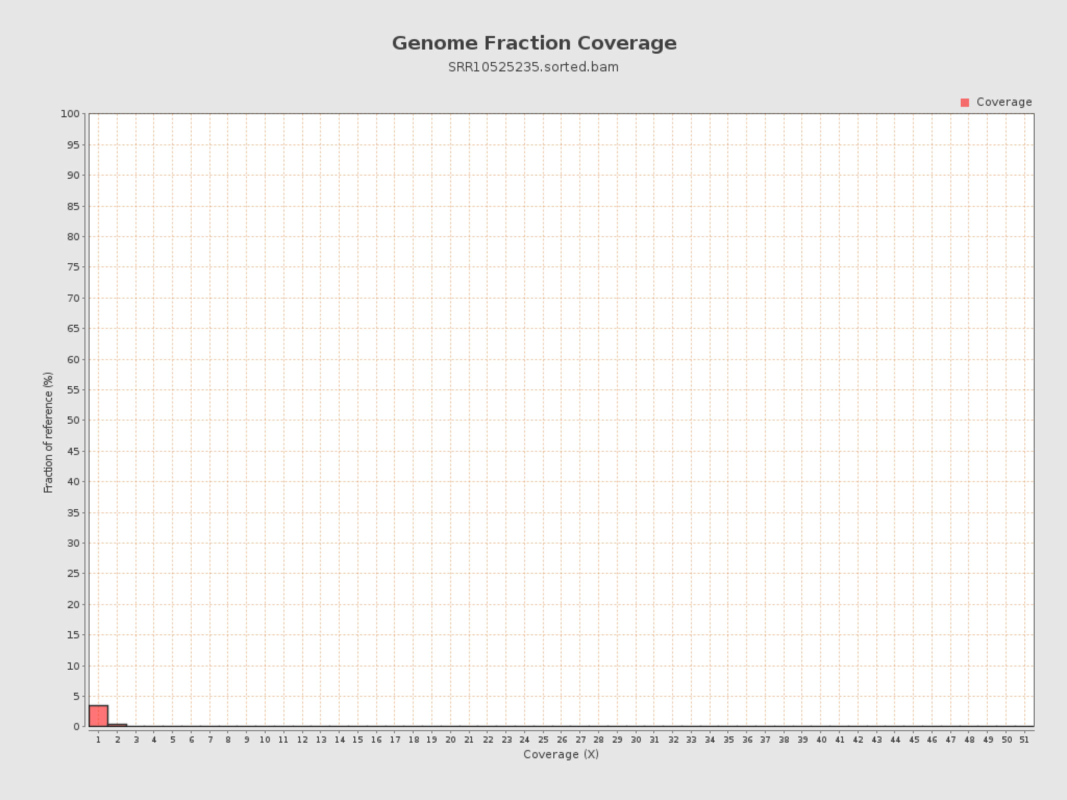
4. Results : Coverage Histogram



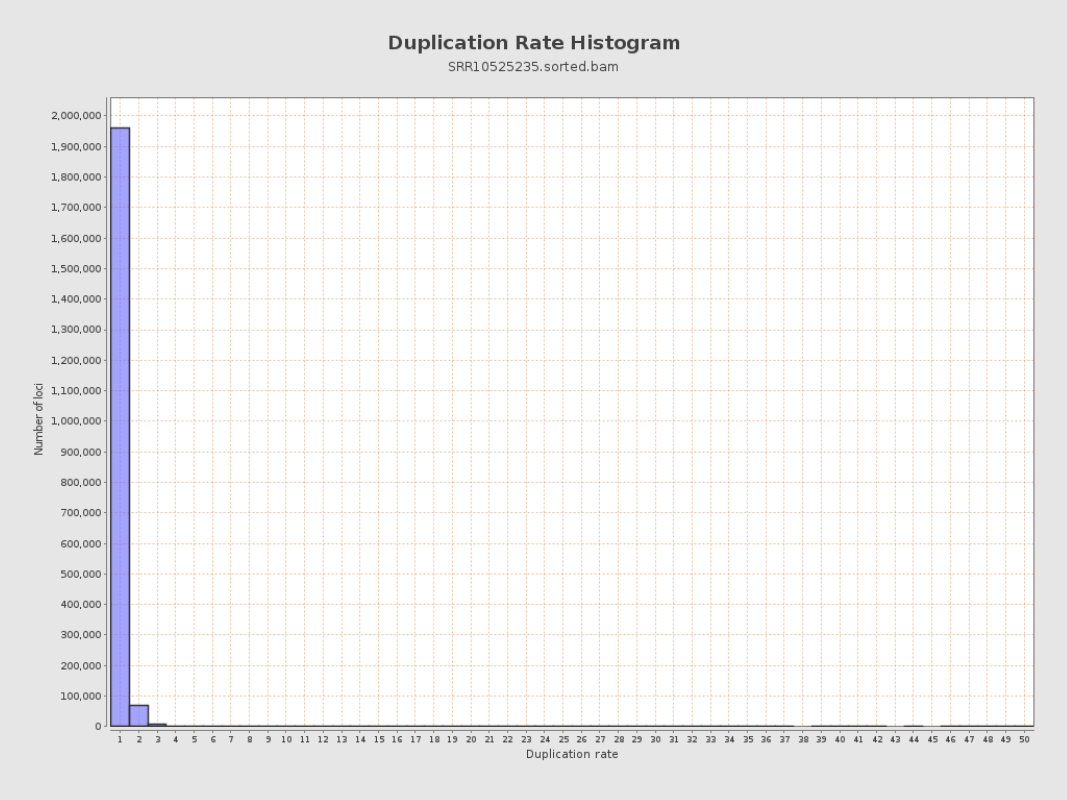
5. Results : Coverage Histogram (0-50X)



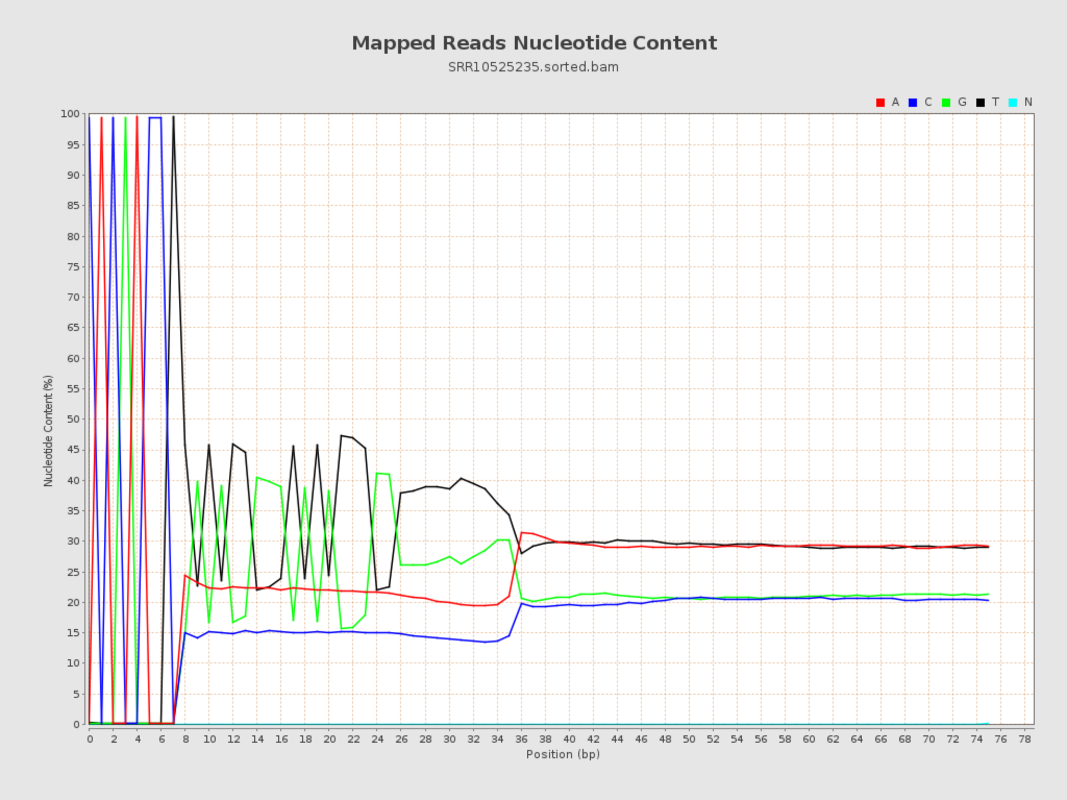
6. Results : Genome Fraction Coverage



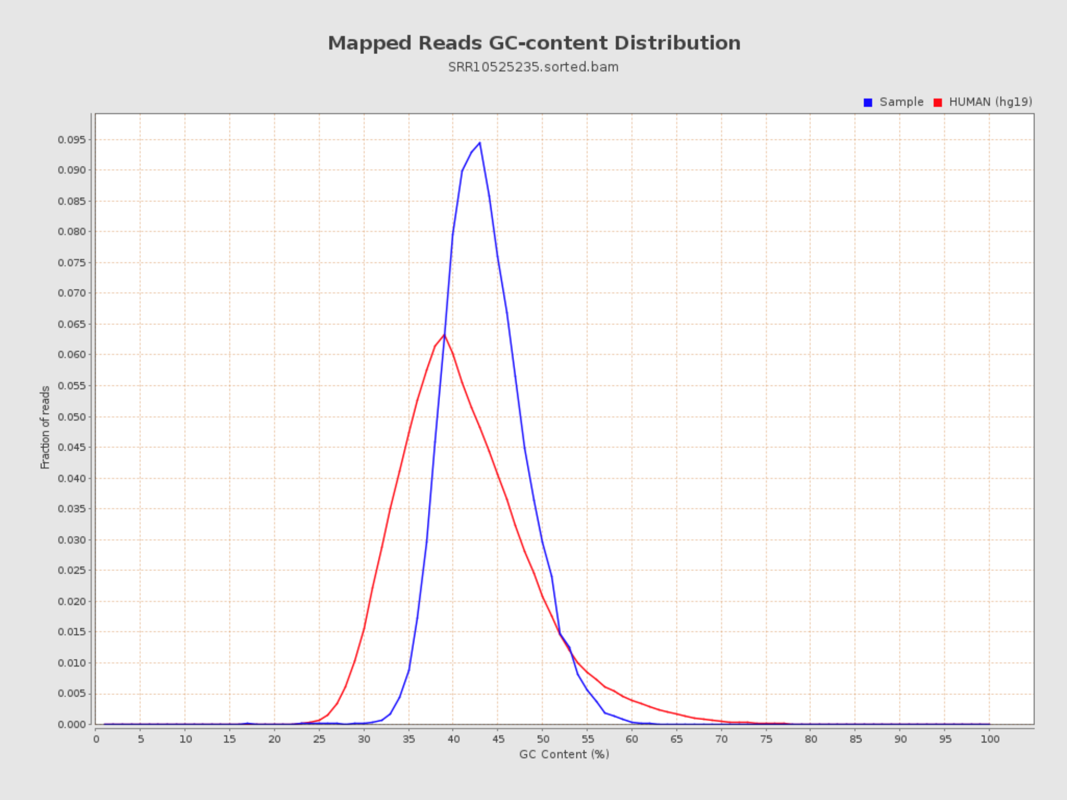
7. Results : Duplication Rate Histogram



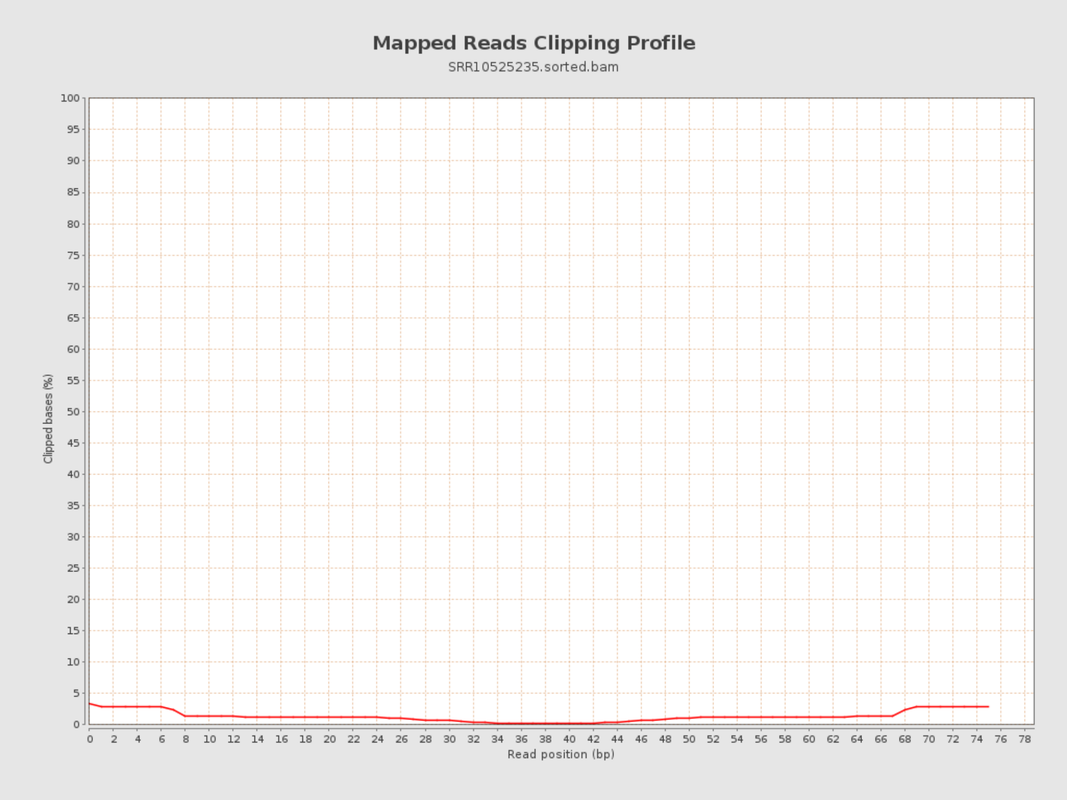
8. Results : Mapped Reads Nucleotide Content



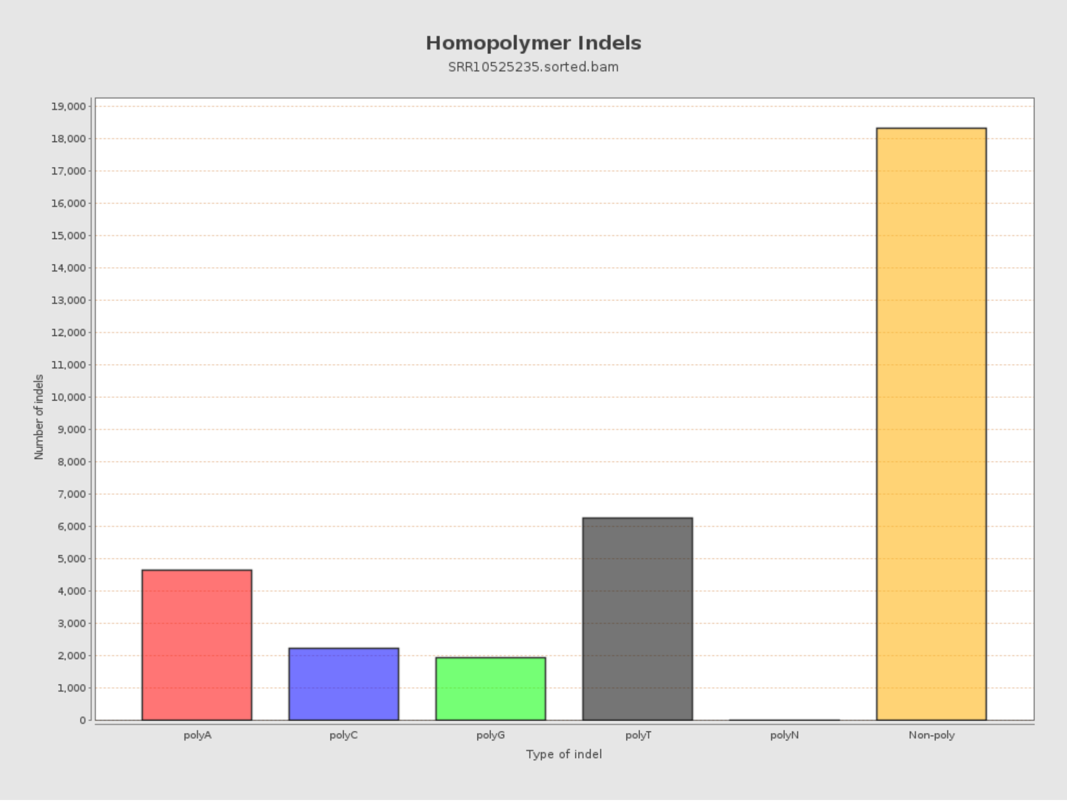
9. Results : Mapped Reads GC-content Distribution



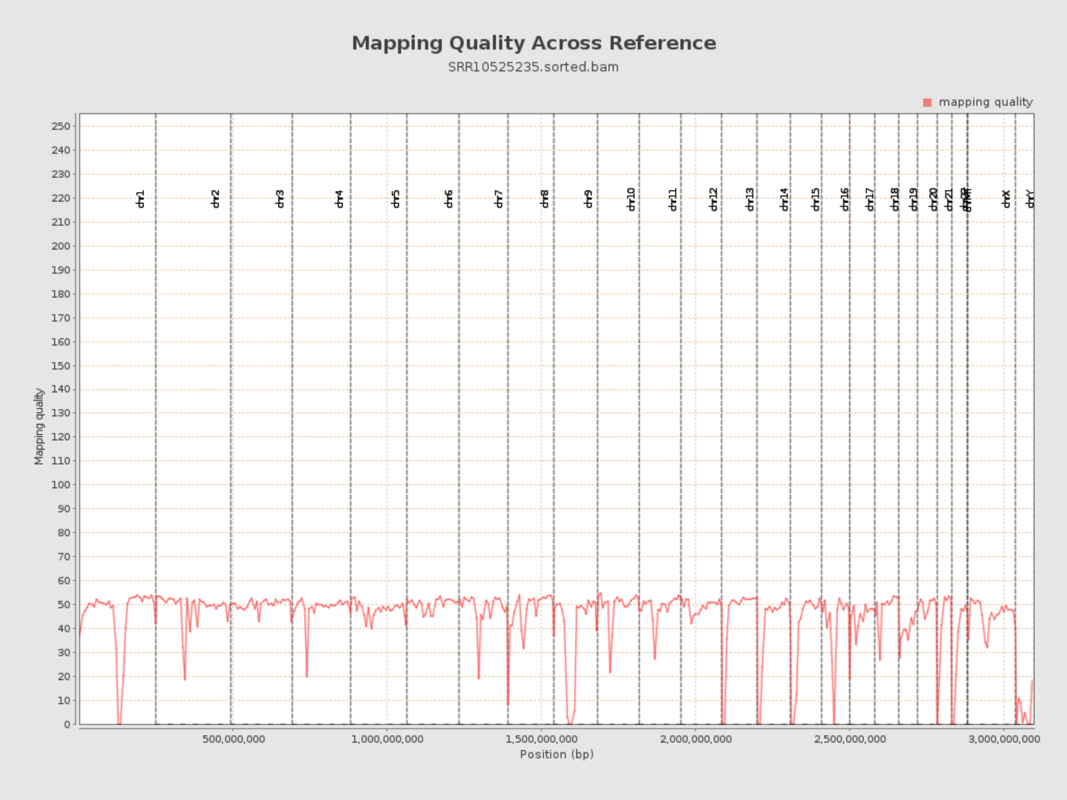
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram