Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 03:15:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708577.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_SRR1708577 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708577.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 03:15:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708577.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,048,860
Mapped reads	3,338,326 / 82.45%
Unmapped reads	710,534 / 17.55%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	91 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	15,984 / 0.39%
Duplication rate	0.48%
Clipped reads	46,550 / 1.15%

2.2. ACGT Content

Number/percentage of A's	51,582,595 / 30.99%
Number/percentage of C's	31,630,662 / 19%
Number/percentage of T's	51,271,654 / 30.8%
Number/percentage of G's	31,959,043 / 19.2%
Number/percentage of N's	8,157 / 0%
GC Percentage	38.2%

2.3. Coverage

Mean	0.0538

Standard Deviation	0.2394

2.4. Mapping Quality

Mean Mapping Quality	46.6

2.5. Mismatches and indels

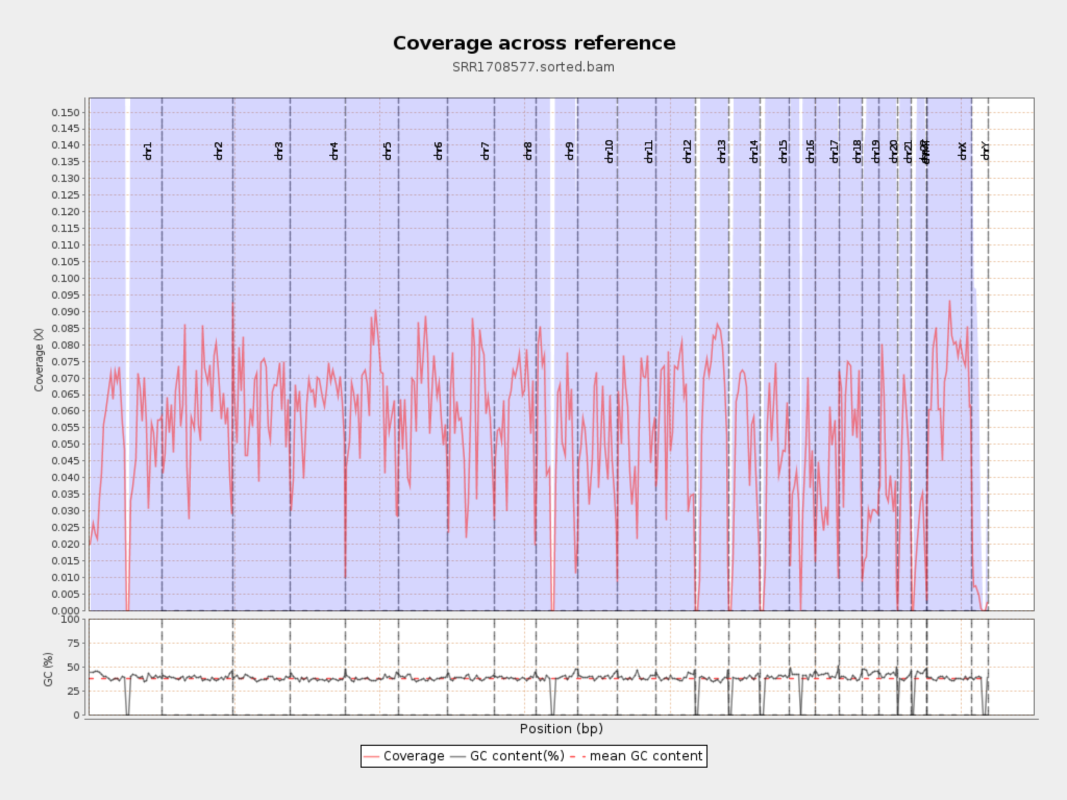
General error rate	0.17%
Mismatches	264,127
Insertions	11,516
Mapped reads with at least one insertion	0.34%
Deletions	9,056
Mapped reads with at least one deletion	0.27%
Homopolymer indels	47.8%

2.6. Chromosome stats

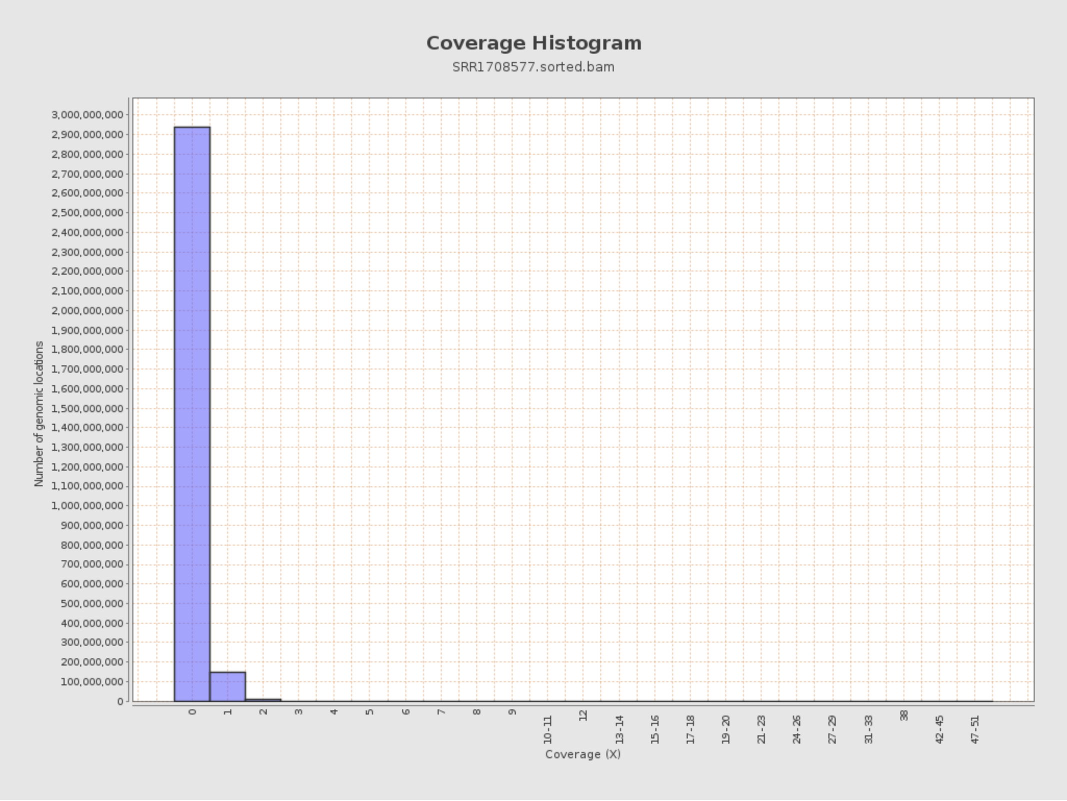
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12013210	0.0482	0.2274
chr2	243199373	14734633	0.0606	0.2531
chr3	198022430	12627196	0.0638	0.2595
chr4	191154276	11887376	0.0622	0.2561
chr5	180915260	11418634	0.0631	0.2589
chr6	171115067	10739348	0.0628	0.2579
chr7	159138663	9331958	0.0586	0.2498

chr8	146364022	8823735	0.0603	0.2524
chr9	141213431	7178183	0.0508	0.2333
chr10	135534747	6725488	0.0496	0.2287
chr11	135006516	7536895	0.0558	0.2444
chr12	133851895	7662691	0.0572	0.2469
chr13	115169878	6909452	0.06	0.253
chr14	107349540	5013845	0.0467	0.2236
chr15	102531392	4551490	0.0444	0.218
chr16	90354753	3234263	0.0358	0.1948
chr17	81195210	2936468	0.0362	0.1966
chr18	78077248	4675315	0.0599	0.2513
chr19	59128983	1481215	0.0251	0.1622
chr20	63025520	2725286	0.0432	0.2149
chr21	48129895	2022184	0.042	0.213
chr22	51304566	958059	0.0187	0.1408
chrMT	16571	50	0.003	0.0548
chrX	155270560	11033224	0.0711	0.2752
chrY	59373566	247487	0.0042	0.068

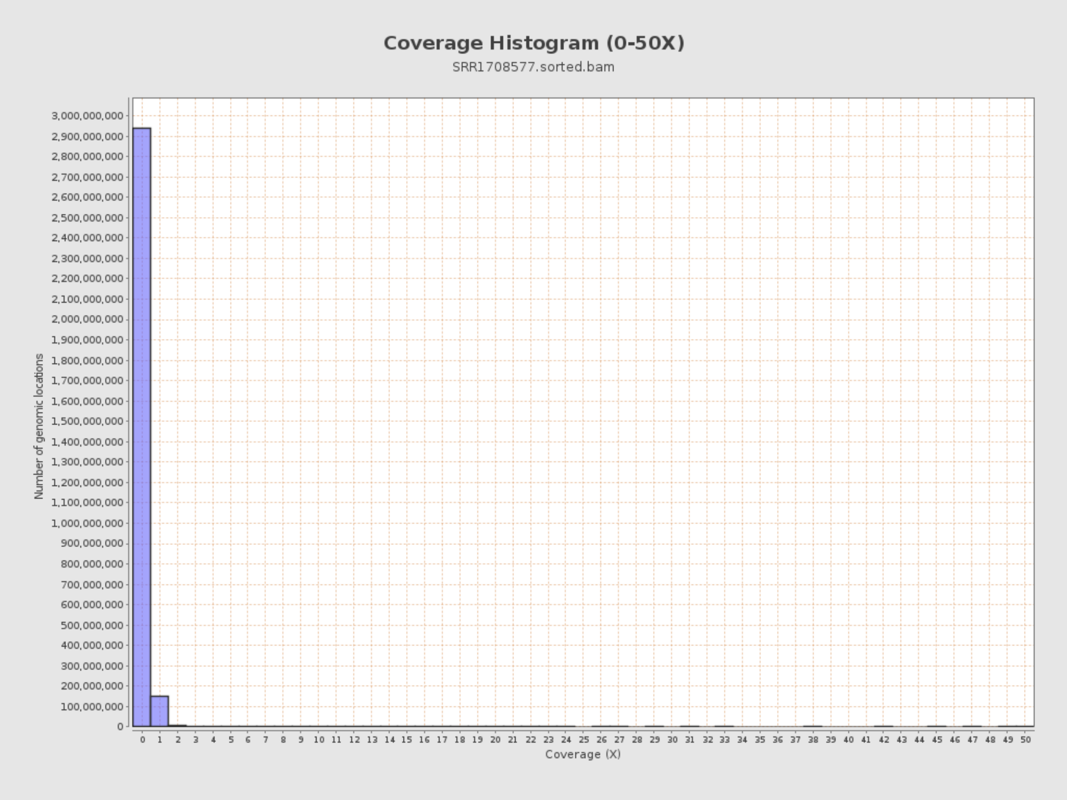
3. Results : Coverage across reference



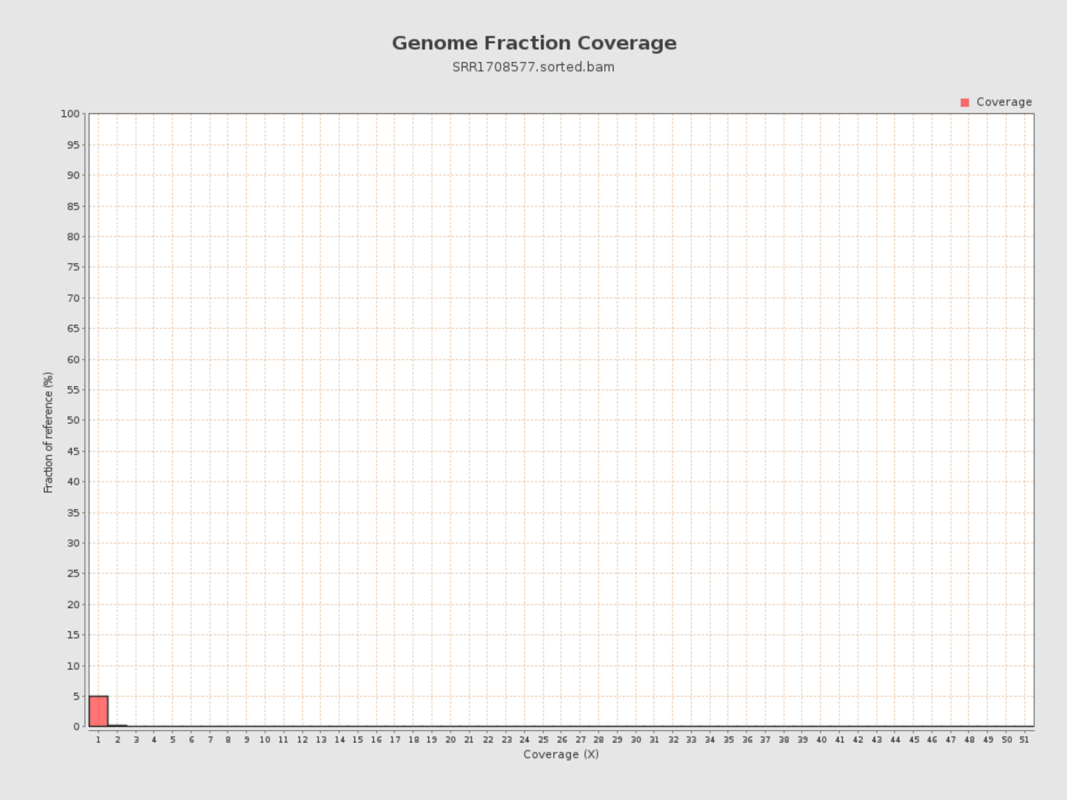
4. Results : Coverage Histogram



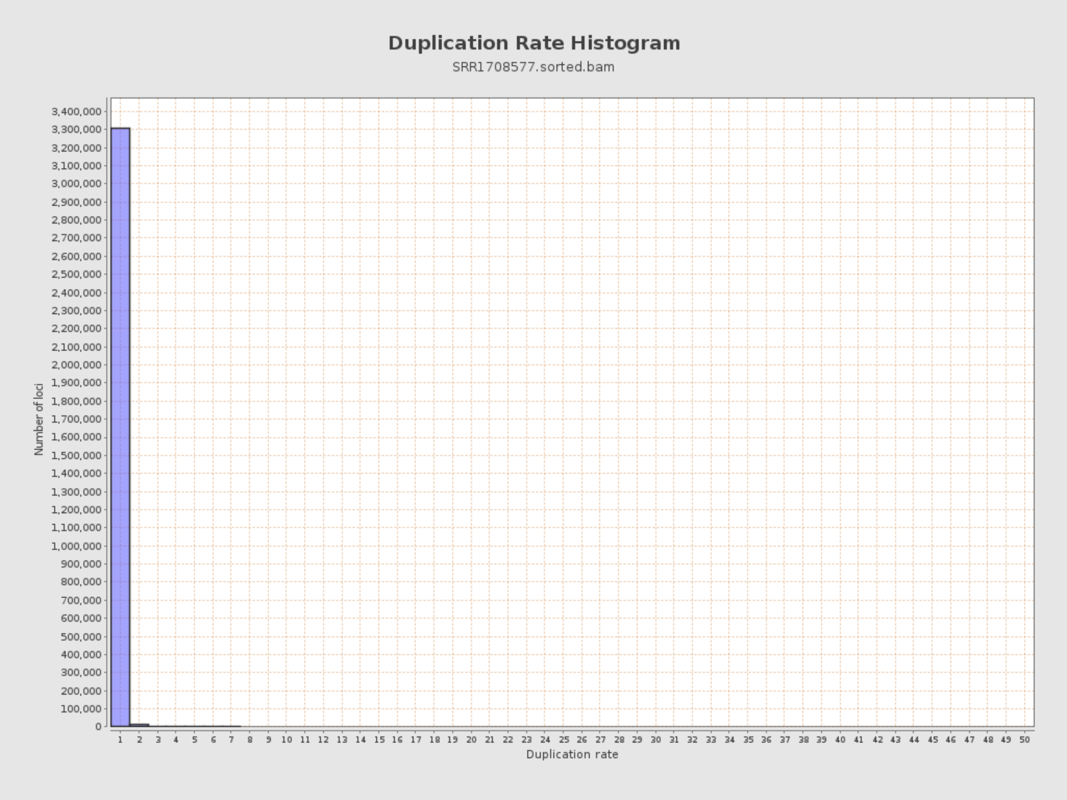
5. Results : Coverage Histogram (0-50X)



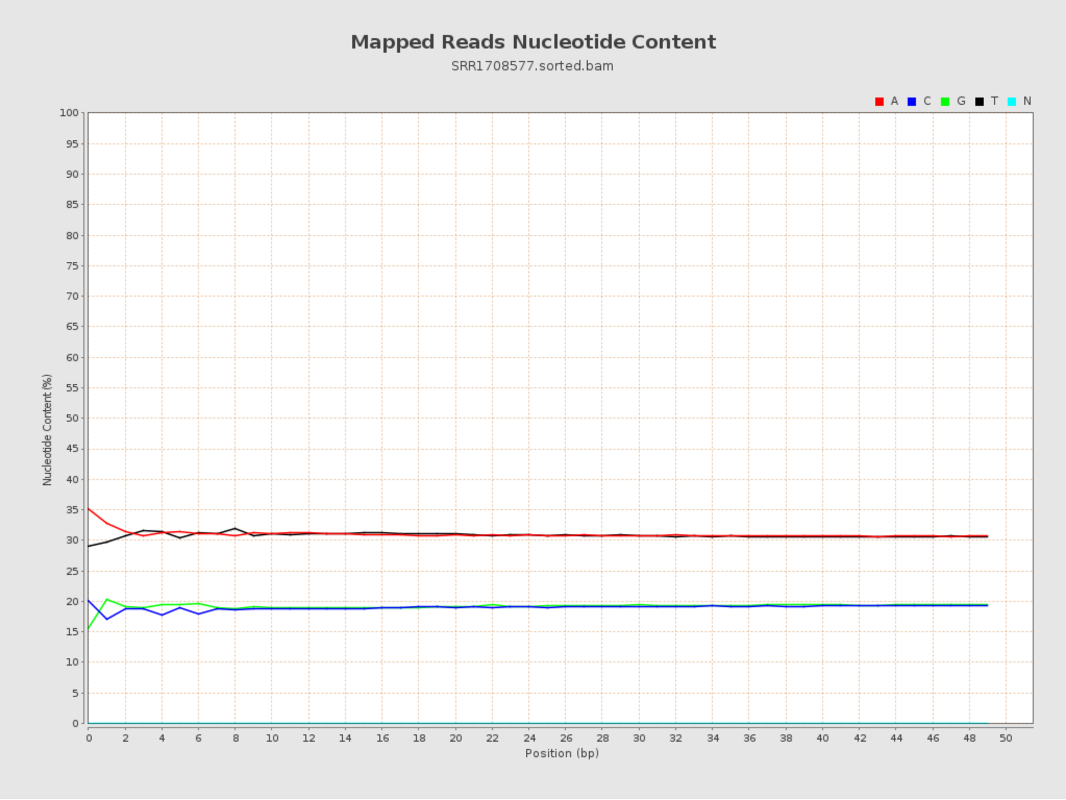
6. Results : Genome Fraction Coverage



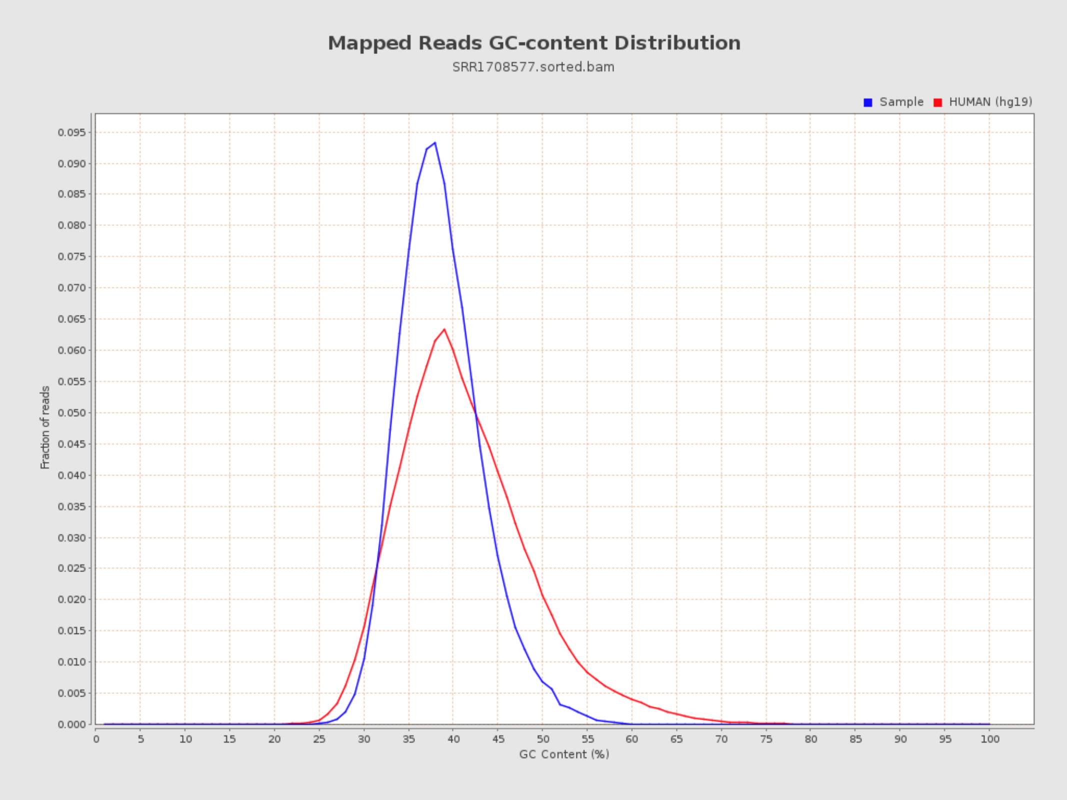
7. Results : Duplication Rate Histogram



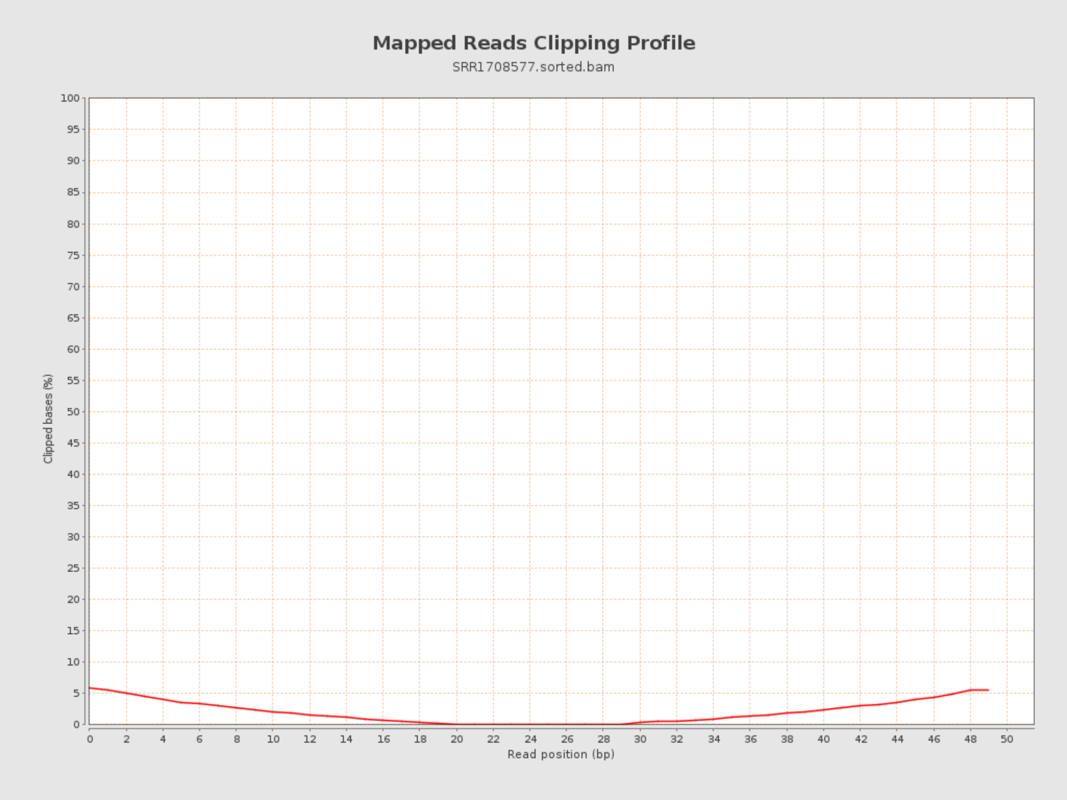
8. Results : Mapped Reads Nucleotide Content



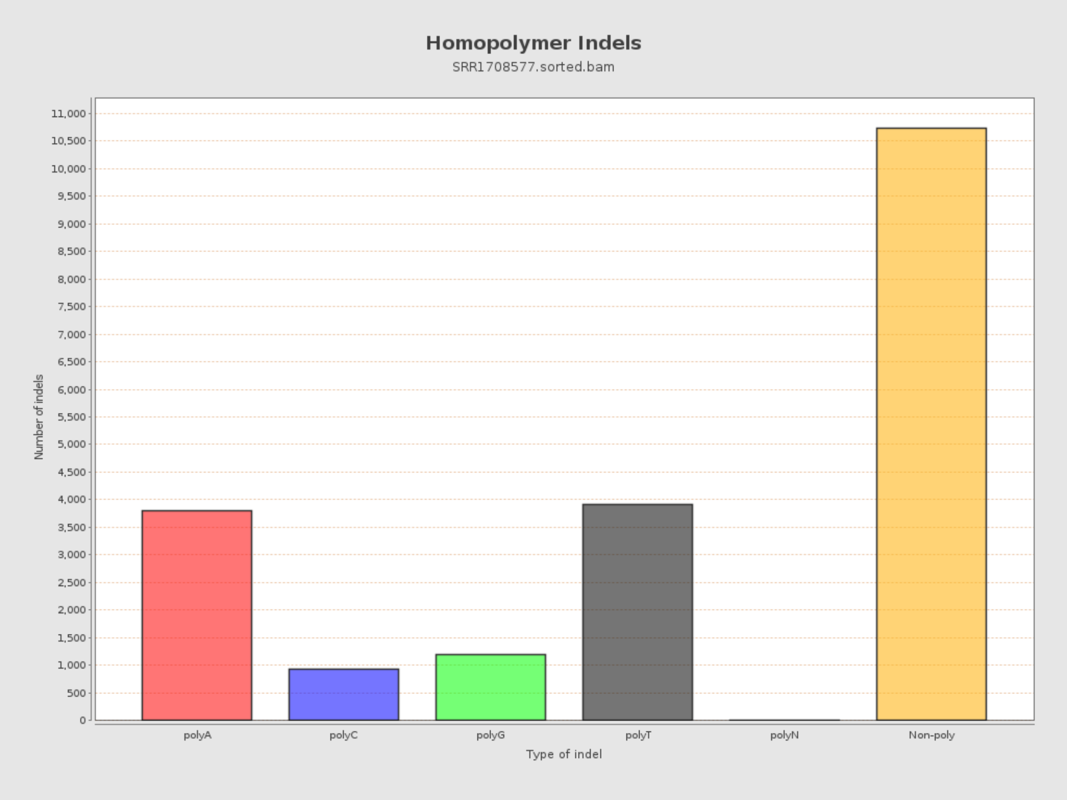
9. Results : Mapped Reads GC-content Distribution



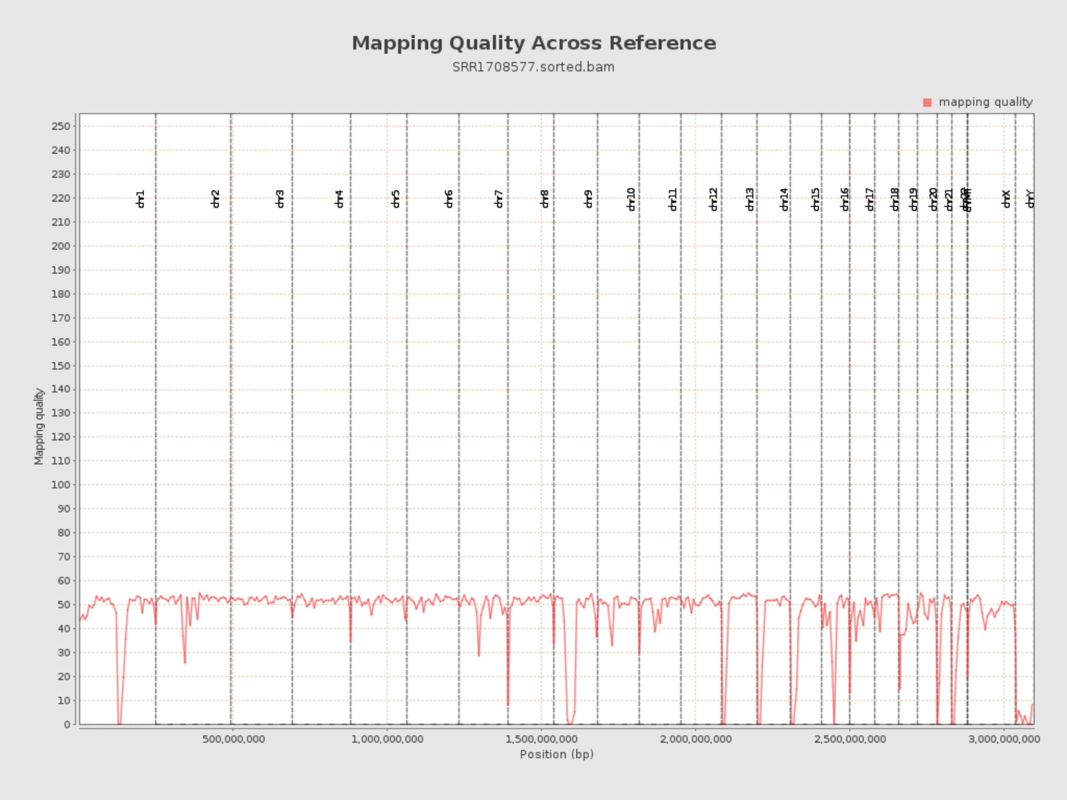
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram