Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 18:20:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525109.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_SRR10525109 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525109.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 18:20:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525109.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,729,663
Mapped reads	1,573,107 / 90.95%
Unmapped reads	156,556 / 9.05%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	42,310 / 2.45%
Read min/max/mean length	30 / 101 / 101.9
Duplicated reads (estimated)	47,829 / 2.77%
Duplication rate	1.77%
Clipped reads	1,612,487 / 93.23%

2.2. ACGT Content

Number/percentage of A's	32,256,364 / 26.56%
Number/percentage of C's	22,285,535 / 18.35%
Number/percentage of T's	37,766,109 / 31.09%
Number/percentage of G's	29,141,774 / 23.99%
Number/percentage of N's	4,641 / 0%
GC Percentage	42.34%

2.3. Coverage

Mean	0.0392

Standard Deviation	0.3953

2.4. Mapping Quality

Mean Mapping Quality	46.6

2.5. Mismatches and indels

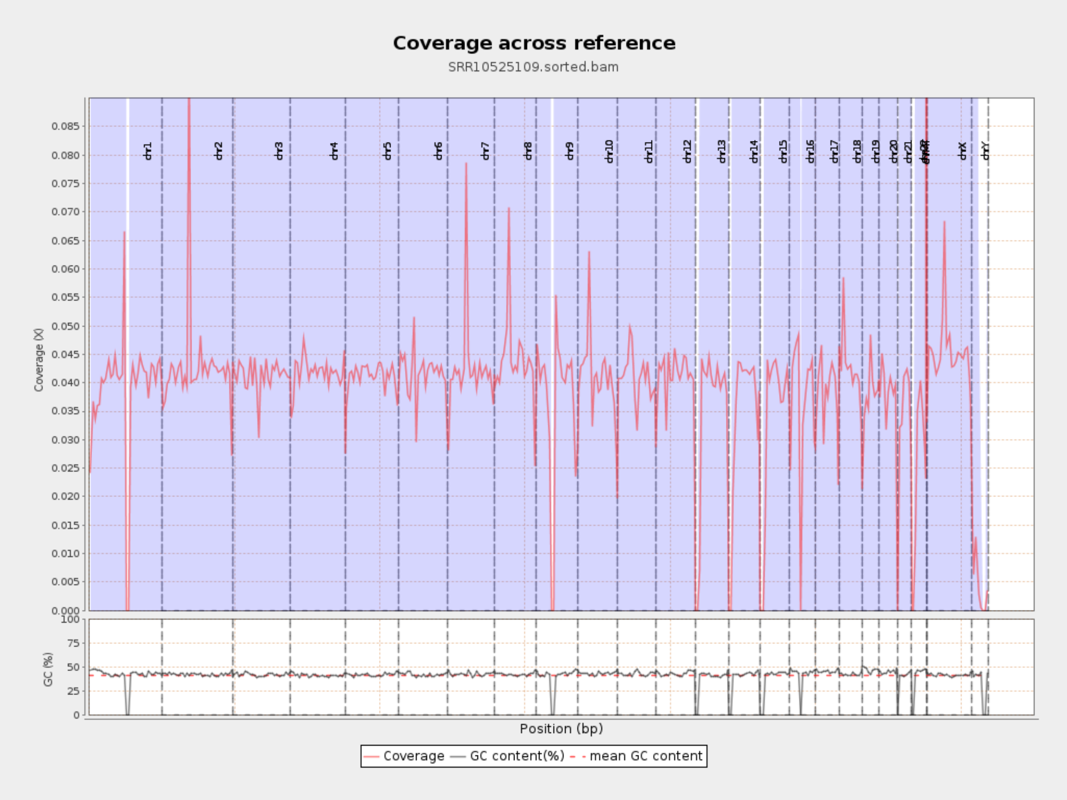
General error rate	0.76%
Mismatches	900,058
Insertions	10,503
Mapped reads with at least one insertion	0.66%
Deletions	28,394
Mapped reads with at least one deletion	1.78%
Homopolymer indels	42.68%

2.6. Chromosome stats

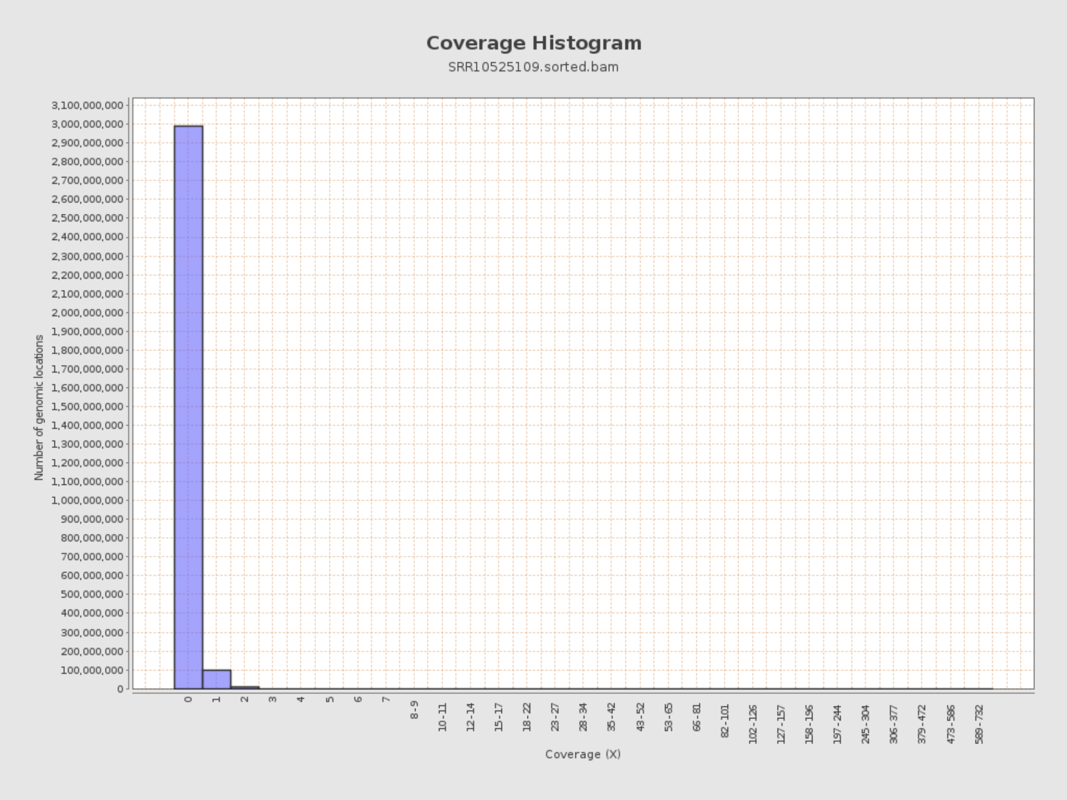
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9628395	0.0386	0.5576
chr2	243199373	10510735	0.0432	0.6115
chr3	198022430	8187940	0.0413	0.222
chr4	191154276	7989126	0.0418	0.2334
chr5	180915260	7448084	0.0412	0.2268
chr6	171115067	7117223	0.0416	0.2645
chr7	159138663	6815635	0.0428	0.6288

chr8	146364022	6426503	0.0439	0.5624
chr9	141213431	5160806	0.0365	0.3937
chr10	135534747	5637103	0.0416	0.3639
chr11	135006516	5487125	0.0406	0.4027
chr12	133851895	5517474	0.0412	0.2245
chr13	115169878	3926393	0.0341	0.1994
chr14	107349540	3647040	0.034	0.2412
chr15	102531392	3404007	0.0332	0.1984
chr16	90354753	3330045	0.0369	0.2304
chr17	81195210	3087215	0.038	0.2772
chr18	78077248	3364709	0.0431	0.658
chr19	59128983	2252865	0.0381	0.4415
chr20	63025520	2408813	0.0382	0.223
chr21	48129895	1591432	0.0331	0.2142
chr22	51304566	1214740	0.0237	0.1668
chrMT	16571	7988	0.482	0.8023
chrX	155270560	7067247	0.0455	0.3334
chrY	59373566	273960	0.0046	0.1049

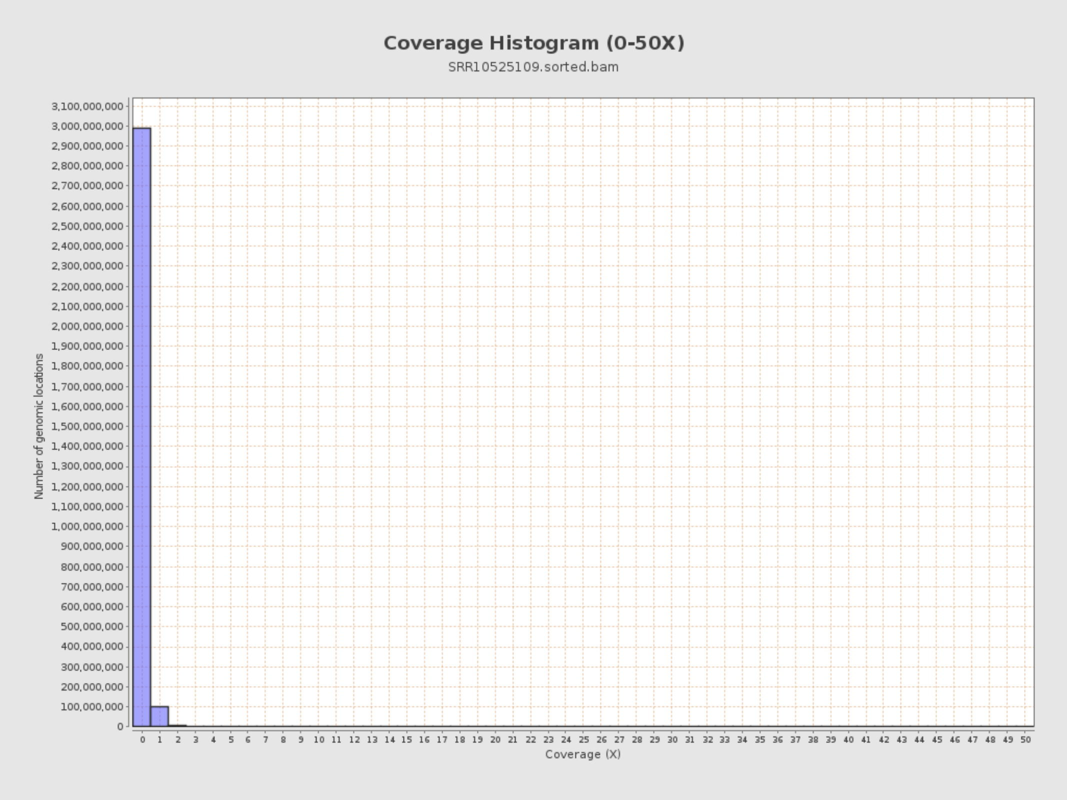
3. Results : Coverage across reference



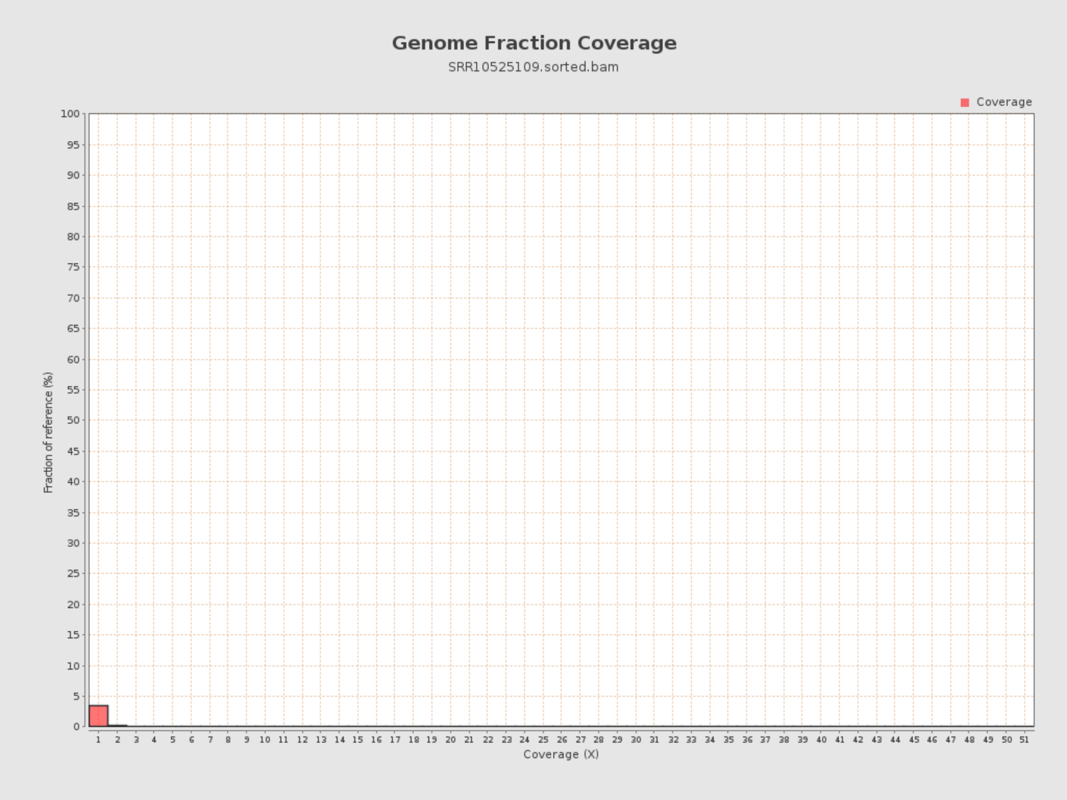
4. Results : Coverage Histogram



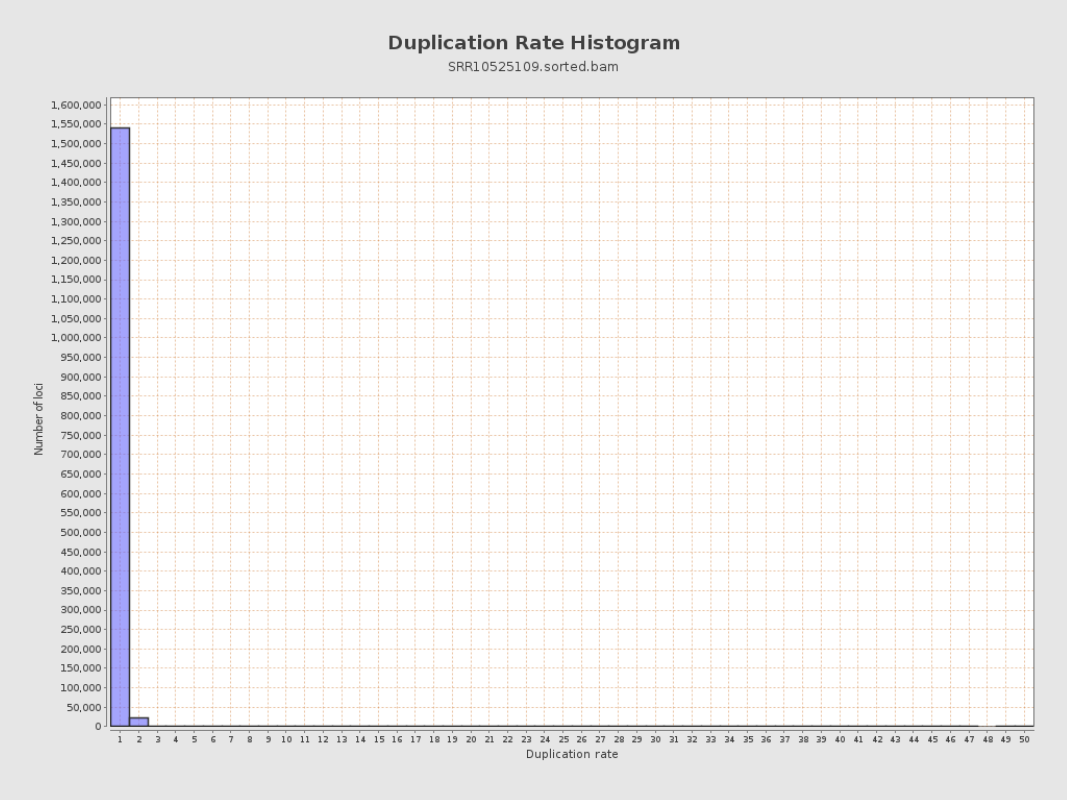
5. Results : Coverage Histogram (0-50X)



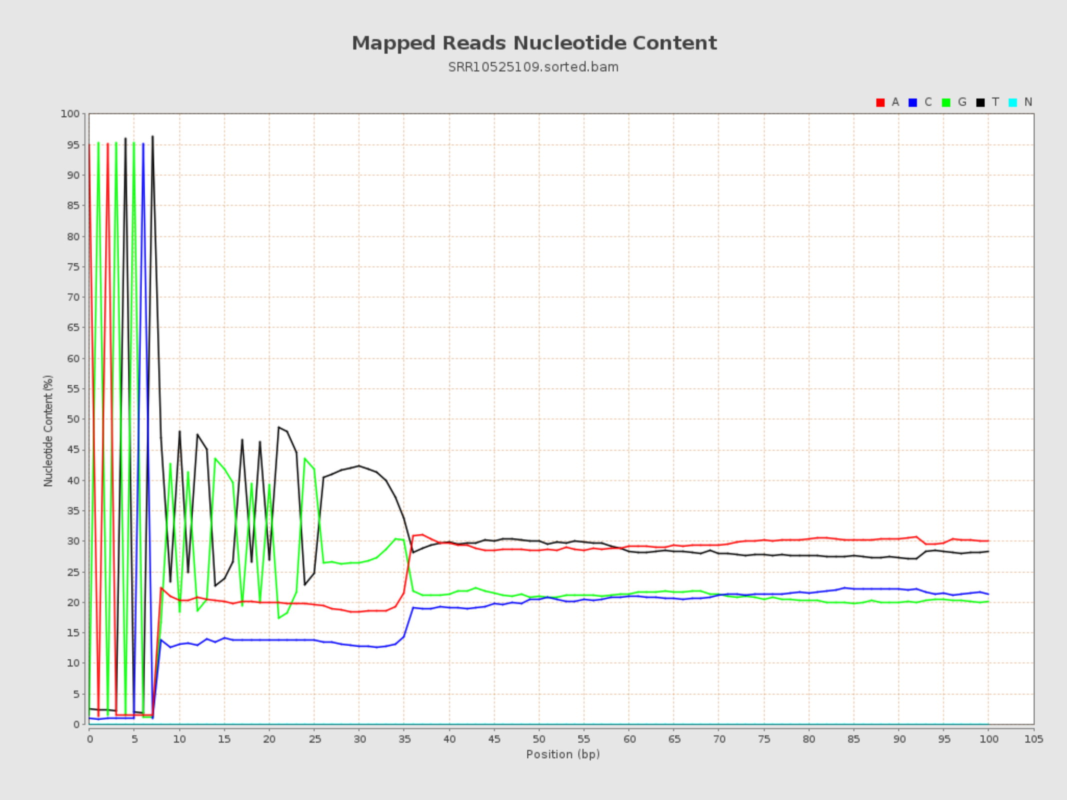
6. Results : Genome Fraction Coverage



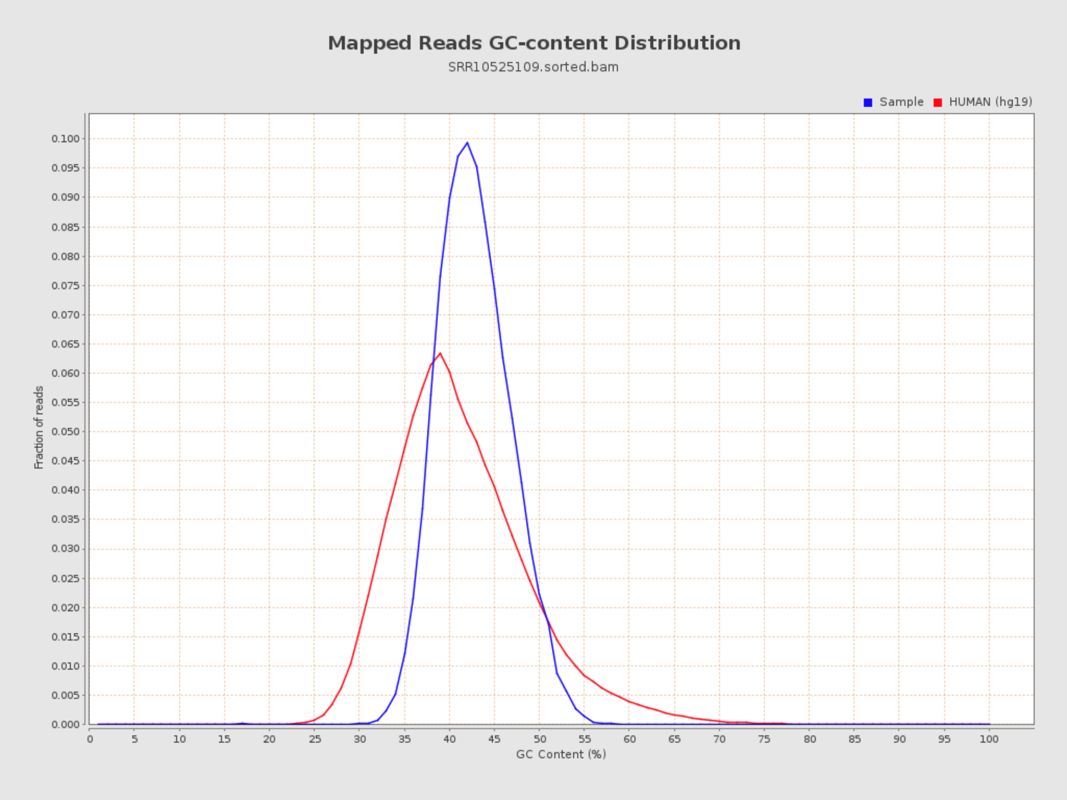
7. Results : Duplication Rate Histogram



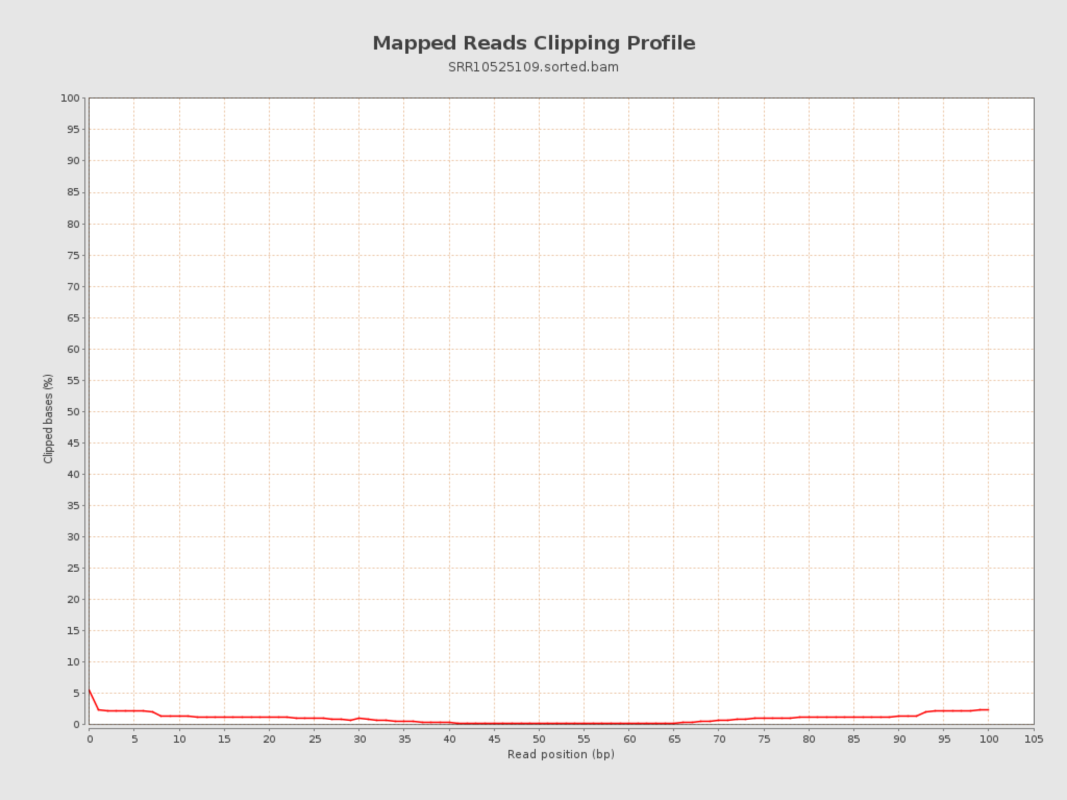
8. Results : Mapped Reads Nucleotide Content



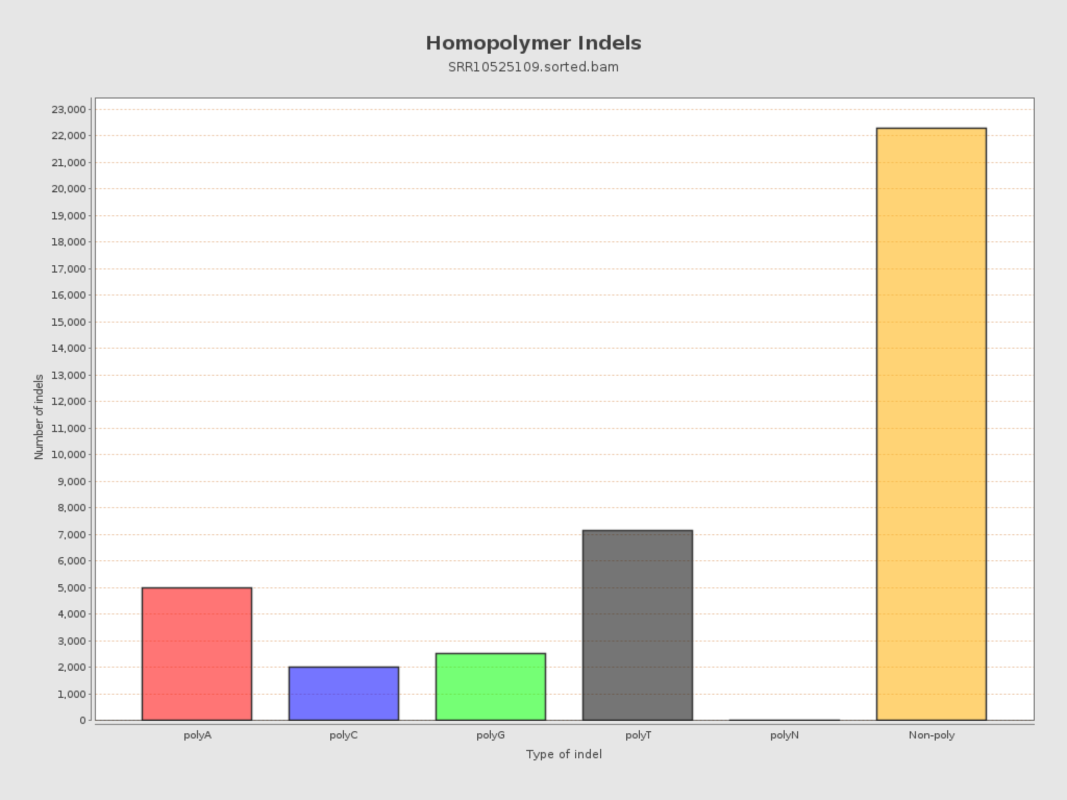
9. Results : Mapped Reads GC-content Distribution



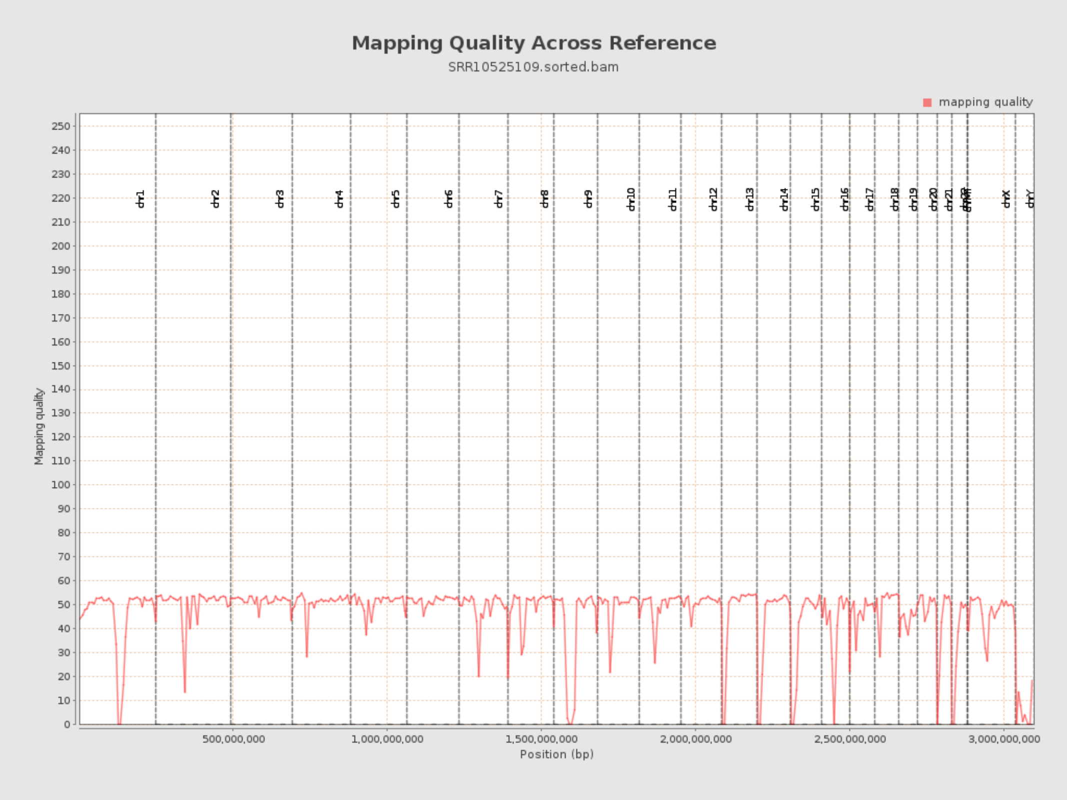
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram