Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 17:42:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525095.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_SRR10525095 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525095.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 17:42:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525095.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,155,945
Mapped reads	1,876,340 / 87.03%
Unmapped reads	279,605 / 12.97%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	51,671 / 2.4%
Read min/max/mean length	30 / 101 / 101.88
Duplicated reads (estimated)	65,612 / 3.04%
Duplication rate	2.03%
Clipped reads	1,923,879 / 89.24%

2.2. ACGT Content

Number/percentage of A's	38,846,226 / 26.91%
Number/percentage of C's	25,917,468 / 17.95%
Number/percentage of T's	45,358,441 / 31.42%
Number/percentage of G's	34,255,002 / 23.73%
Number/percentage of N's	5,018 / 0%
GC Percentage	41.68%

2.3. Coverage

Mean	0.0467

Standard Deviation	0.493

2.4. Mapping Quality

Mean Mapping Quality	46.26

2.5. Mismatches and indels

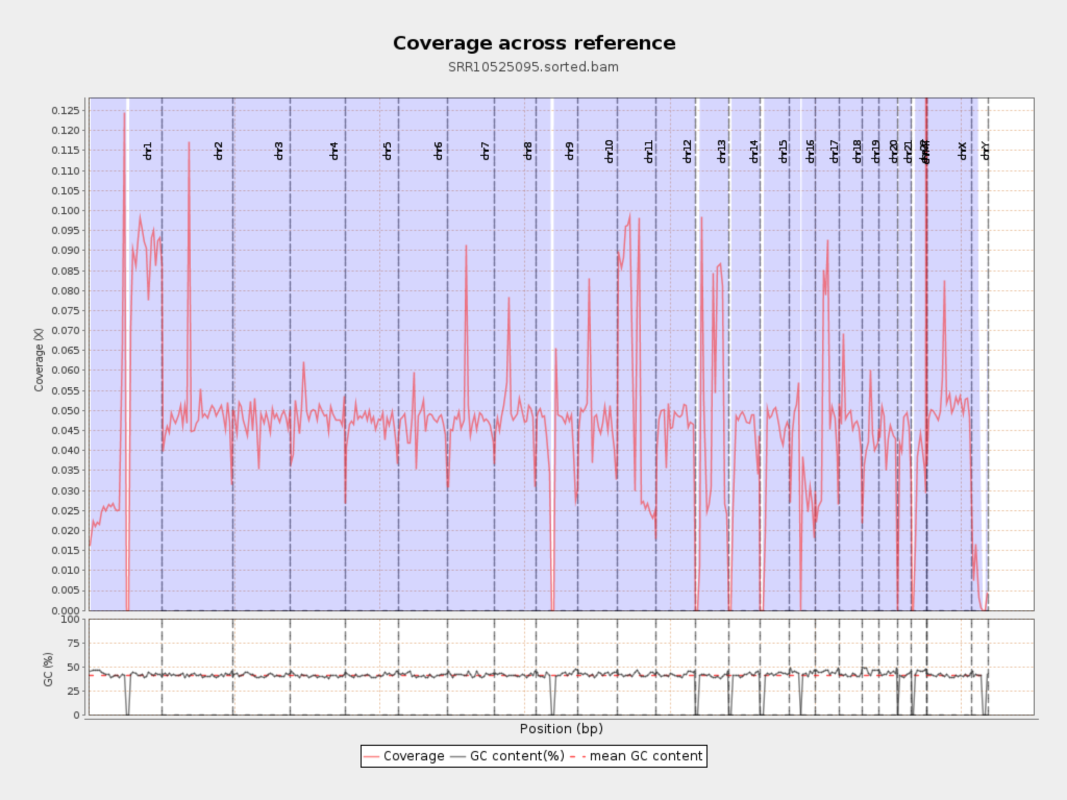
General error rate	0.76%
Mismatches	1,074,840
Insertions	12,899
Mapped reads with at least one insertion	0.68%
Deletions	33,575
Mapped reads with at least one deletion	1.76%
Homopolymer indels	43.2%

2.6. Chromosome stats

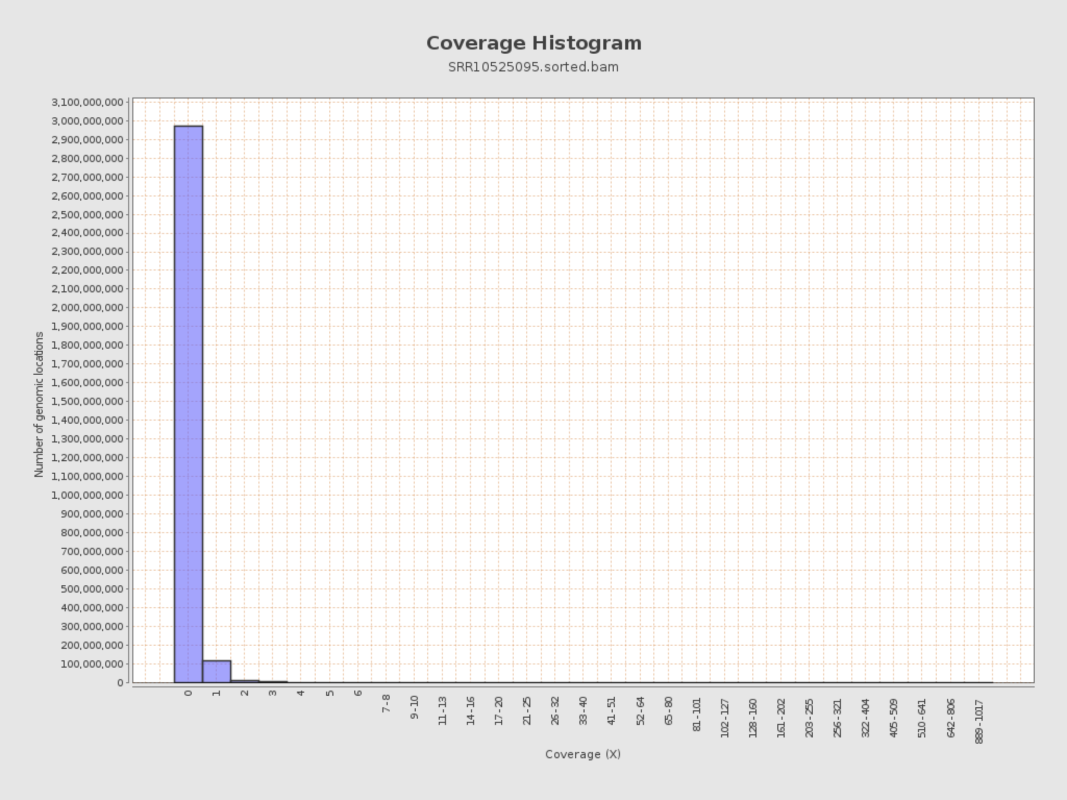
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13896247	0.0558	0.8952
chr2	243199373	12163581	0.05	0.6821
chr3	198022430	9447209	0.0477	0.2434
chr4	191154276	9311602	0.0487	0.2606
chr5	180915260	8492608	0.0469	0.2498
chr6	171115067	8058694	0.0471	0.2901
chr7	159138663	7764691	0.0488	0.6983

chr8	146364022	7291805	0.0498	0.6373
chr9	141213431	5852270	0.0414	0.4426
chr10	135534747	6575255	0.0485	0.4722
chr11	135006516	7915895	0.0586	0.5717
chr12	133851895	6295607	0.047	0.2437
chr13	115169878	5347684	0.0464	0.2391
chr14	107349540	4188630	0.039	0.2792
chr15	102531392	3930712	0.0383	0.2154
chr16	90354753	3023819	0.0335	0.2397
chr17	81195210	4089691	0.0504	0.3153
chr18	78077248	3842196	0.0492	0.8334
chr19	59128983	2516565	0.0426	0.6401
chr20	63025520	2721743	0.0432	0.2421
chr21	48129895	1902035	0.0395	0.2455
chr22	51304566	1402689	0.0273	0.1827
chrMT	16571	15735	0.9496	1.1079
chrX	155270560	8065557	0.0519	0.3694
chrY	59373566	327278	0.0055	0.1261

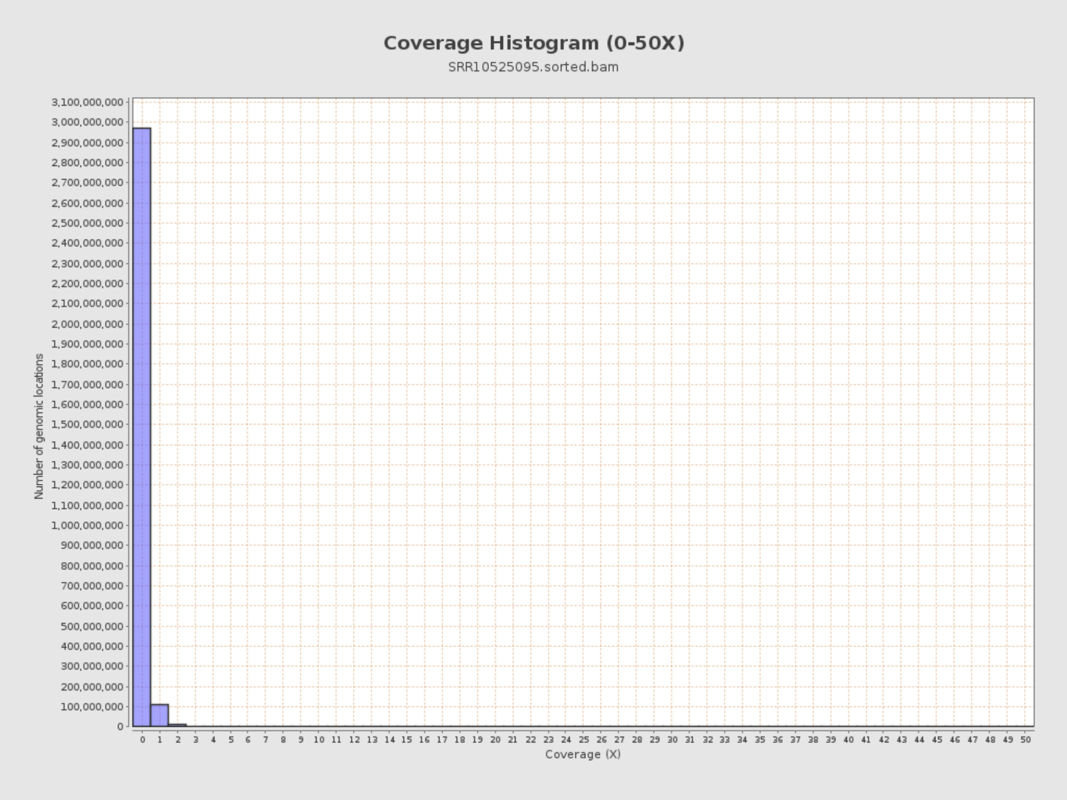
3. Results : Coverage across reference



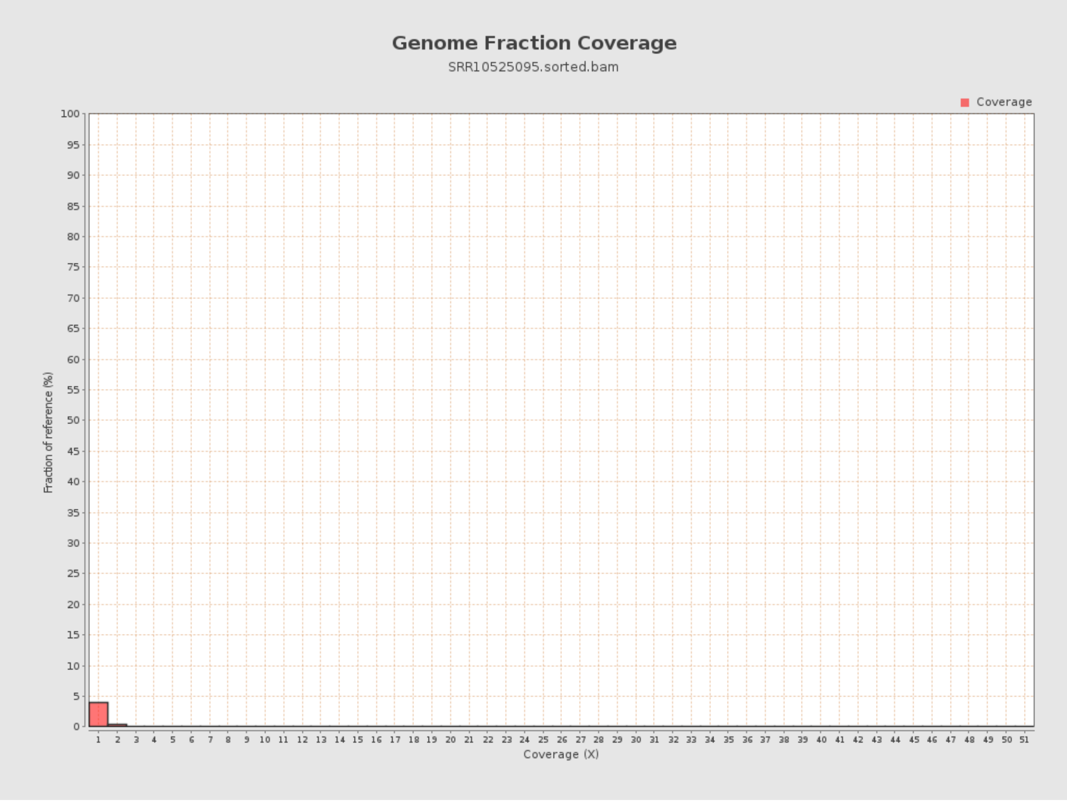
4. Results : Coverage Histogram



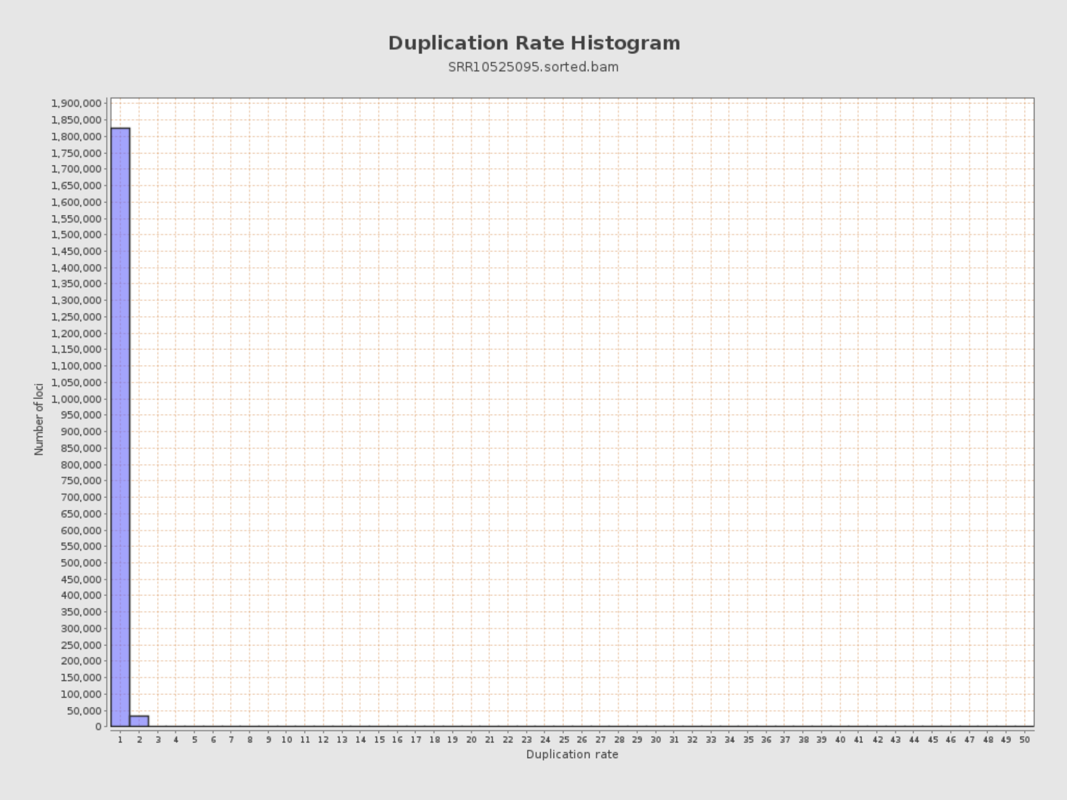
5. Results : Coverage Histogram (0-50X)



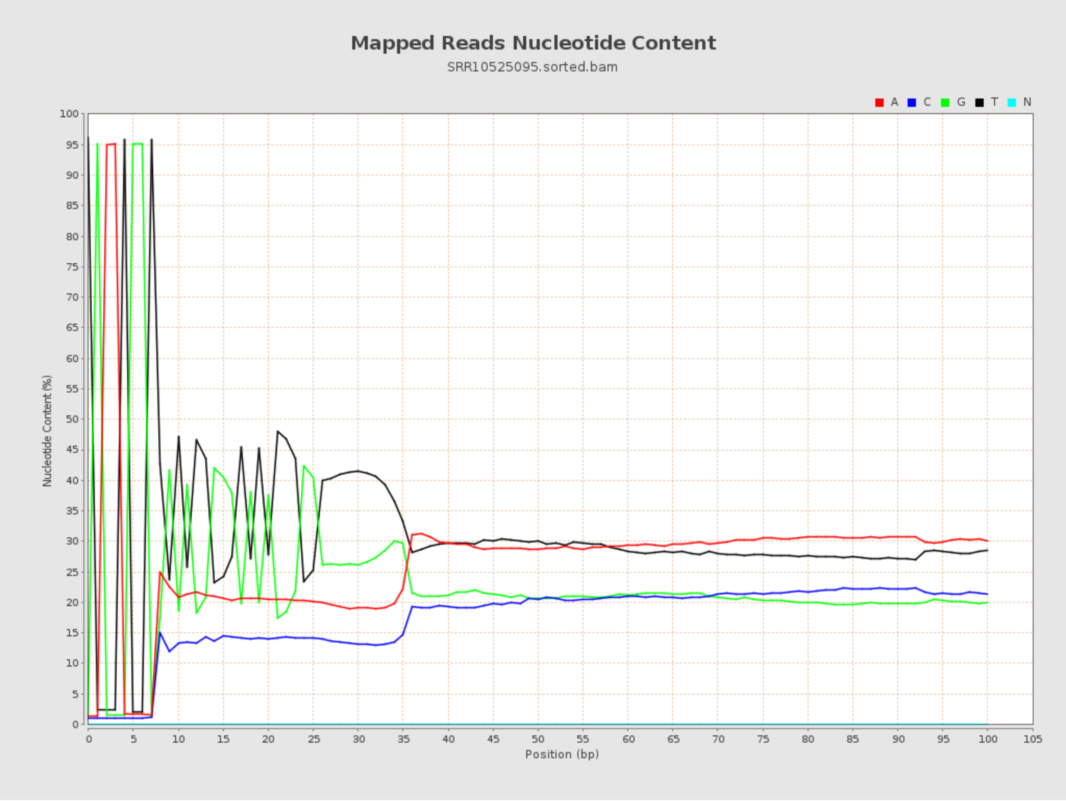
6. Results : Genome Fraction Coverage



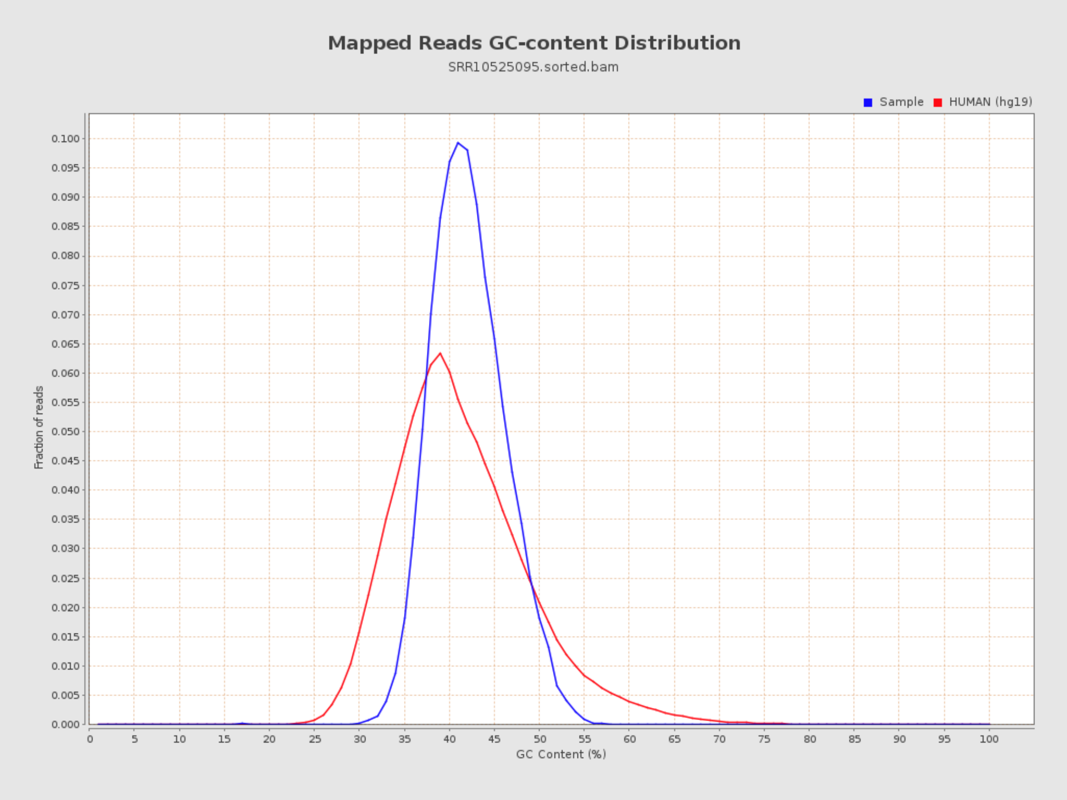
7. Results : Duplication Rate Histogram



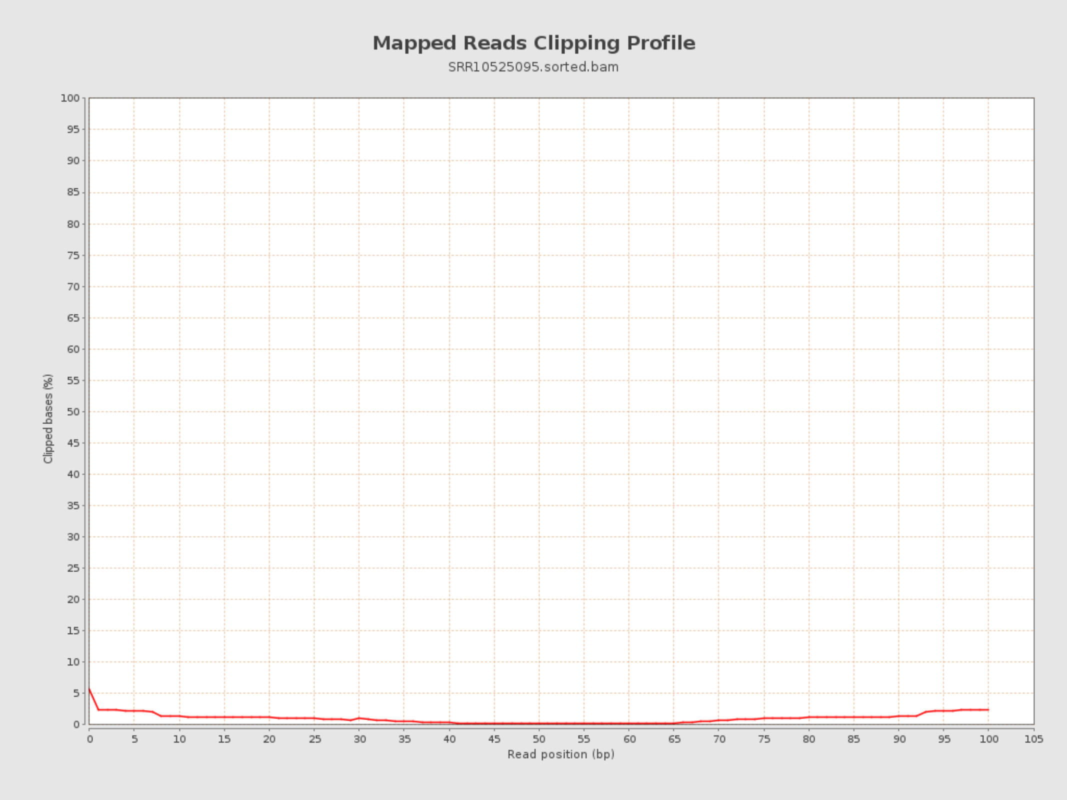
8. Results : Mapped Reads Nucleotide Content



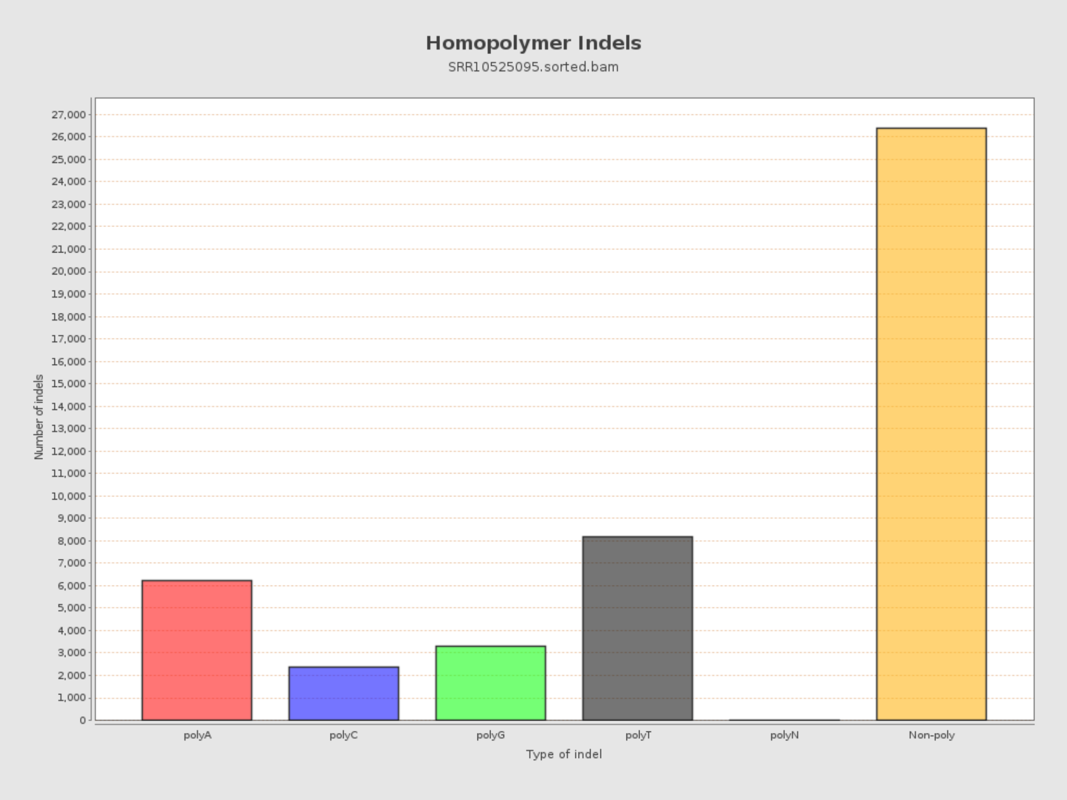
9. Results : Mapped Reads GC-content Distribution



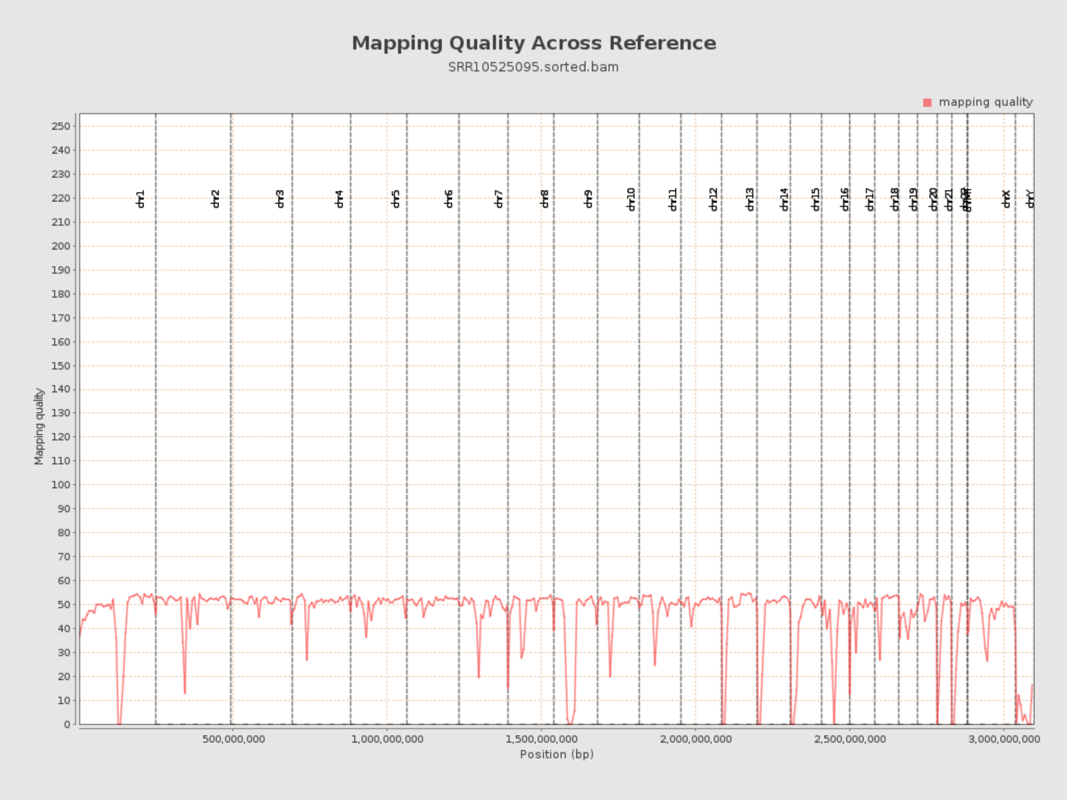
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram