Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 18:14:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525107.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_SRR10525107 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525107.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 18:14:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525107.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	680,761
Mapped reads	588,404 / 86.43%
Unmapped reads	92,357 / 13.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,527 / 2.13%
Read min/max/mean length	30 / 101 / 101.78
Duplicated reads (estimated)	12,038 / 1.77%
Duplication rate	1.25%
Clipped reads	601,770 / 88.4%

2.2. ACGT Content

Number/percentage of A's	12,172,013 / 27.07%
Number/percentage of C's	8,569,997 / 19.06%
Number/percentage of T's	14,055,902 / 31.26%
Number/percentage of G's	10,159,681 / 22.6%
Number/percentage of N's	1,510 / 0%
GC Percentage	41.66%

2.3. Coverage

Mean	0.0145

Standard Deviation	0.1748

2.4. Mapping Quality

Mean Mapping Quality	46.51

2.5. Mismatches and indels

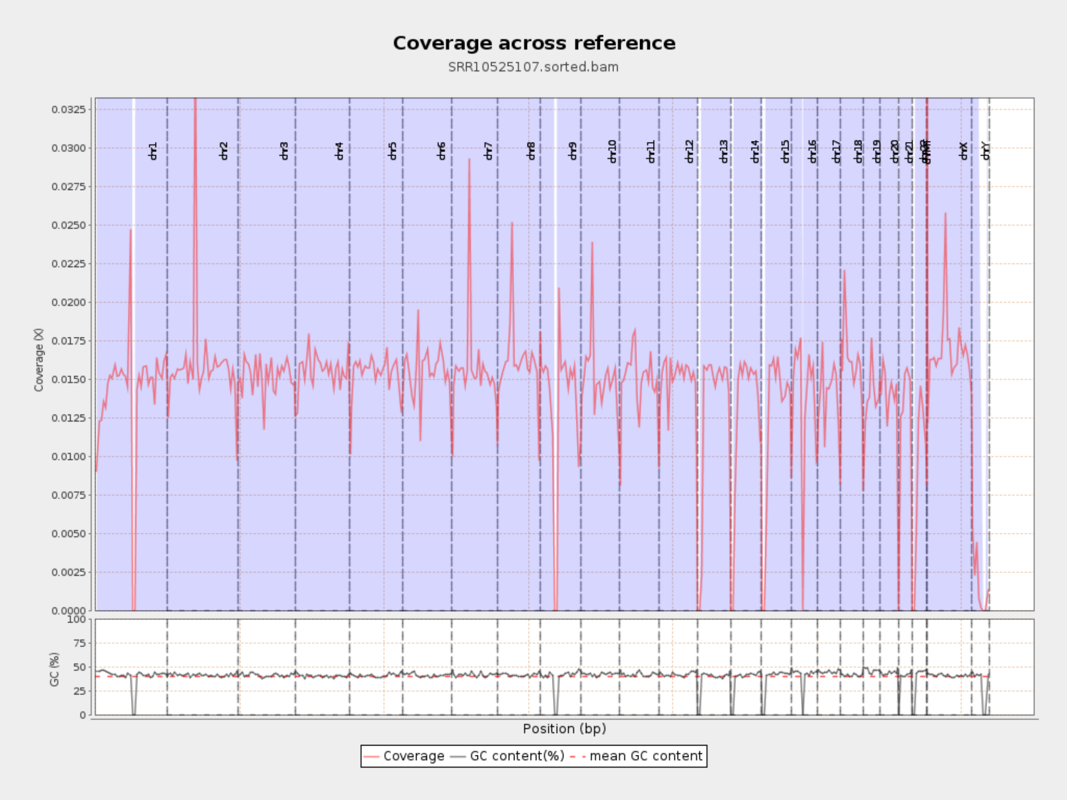
General error rate	0.75%
Mismatches	329,725
Insertions	4,098
Mapped reads with at least one insertion	0.69%
Deletions	10,221
Mapped reads with at least one deletion	1.72%
Homopolymer indels	40.73%

2.6. Chromosome stats

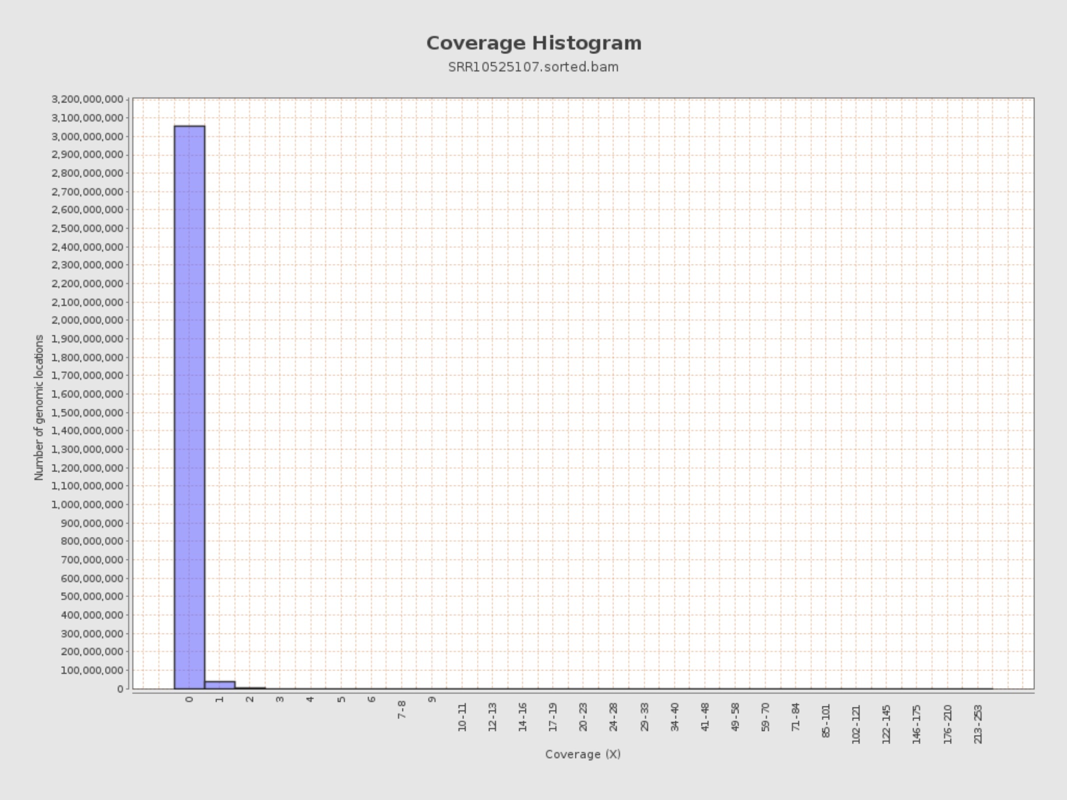
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3517593	0.0141	0.2346
chr2	243199373	3922039	0.0161	0.2429
chr3	198022430	3019042	0.0152	0.1283
chr4	191154276	2975185	0.0156	0.1336
chr5	180915260	2804032	0.0155	0.1314
chr6	171115067	2650995	0.0155	0.1405
chr7	159138663	2512721	0.0158	0.2393

chr8	146364022	2372897	0.0162	0.2291
chr9	141213431	1889508	0.0134	0.1744
chr10	135534747	2055895	0.0152	0.1659
chr11	135006516	2041771	0.0151	0.1776
chr12	133851895	2027131	0.0151	0.1286
chr13	115169878	1467180	0.0127	0.1169
chr14	107349540	1350914	0.0126	0.1299
chr15	102531392	1257289	0.0123	0.1148
chr16	90354753	1211531	0.0134	0.1263
chr17	81195210	1132080	0.0139	0.1426
chr18	78077248	1280538	0.0164	0.2788
chr19	59128983	820890	0.0139	0.1902
chr20	63025520	883302	0.014	0.1241
chr21	48129895	602818	0.0125	0.1208
chr22	51304566	451202	0.0088	0.0978
chrMT	16571	945	0.057	0.3668
chrX	155270560	2631990	0.017	0.1545
chrY	59373566	97000	0.0016	0.0488

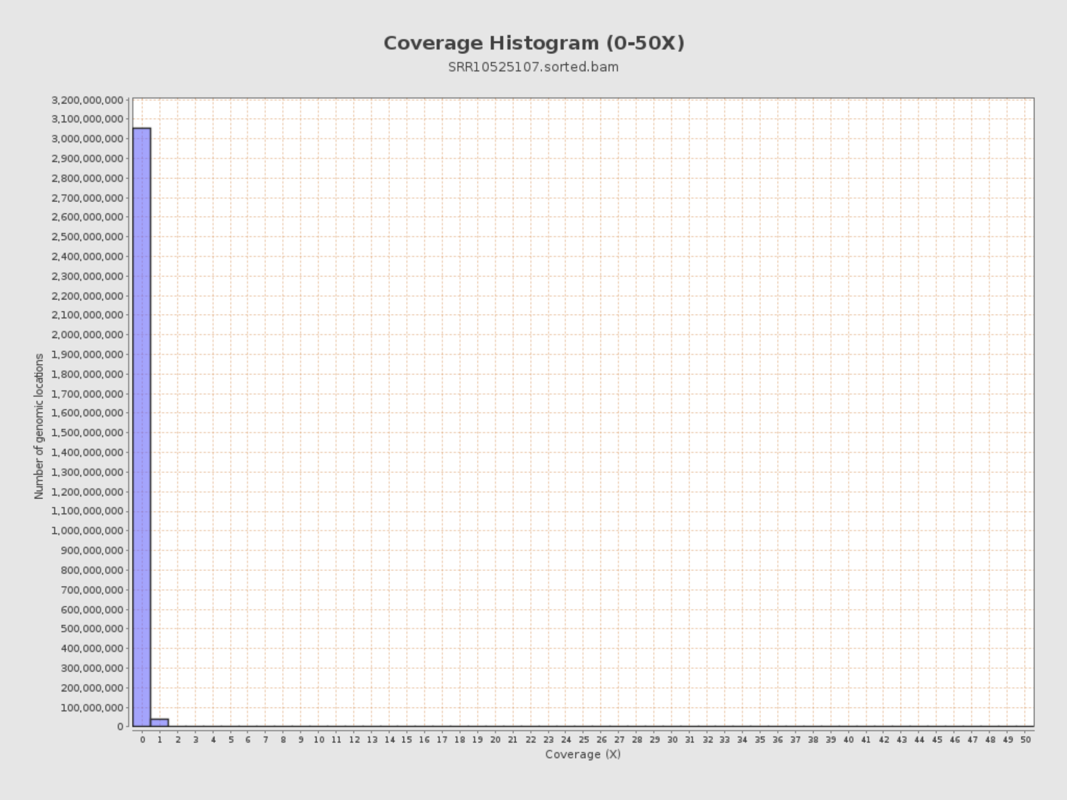
3. Results : Coverage across reference



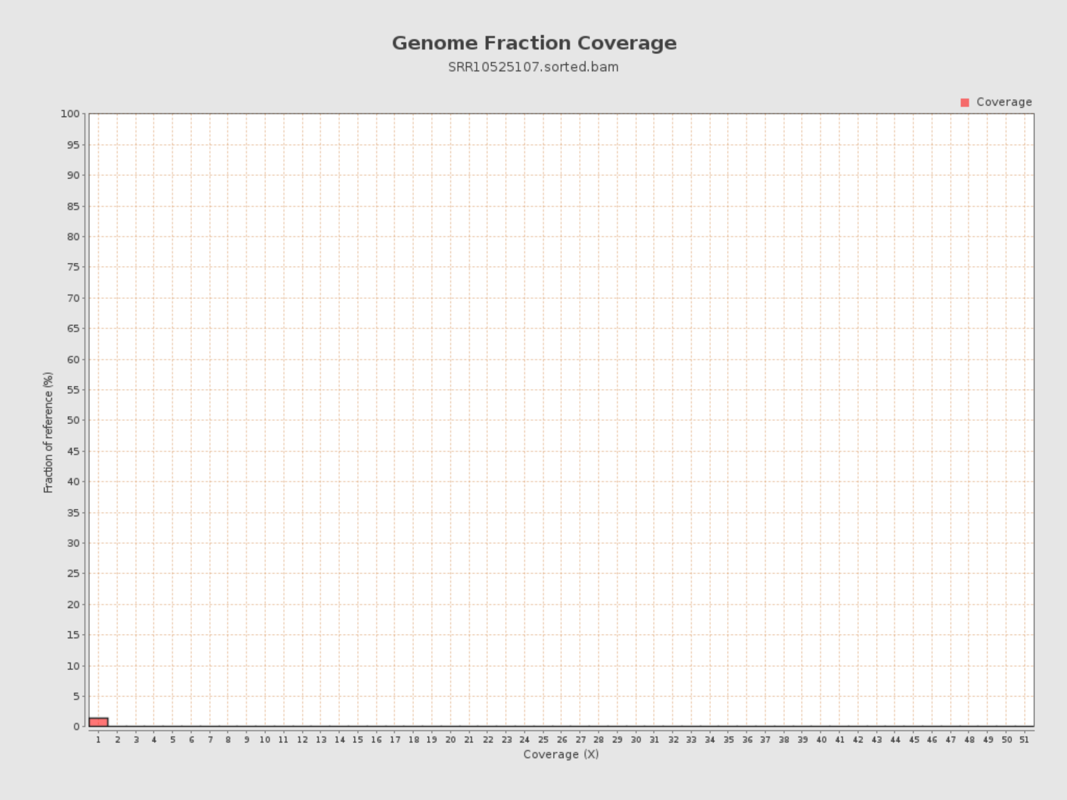
4. Results : Coverage Histogram



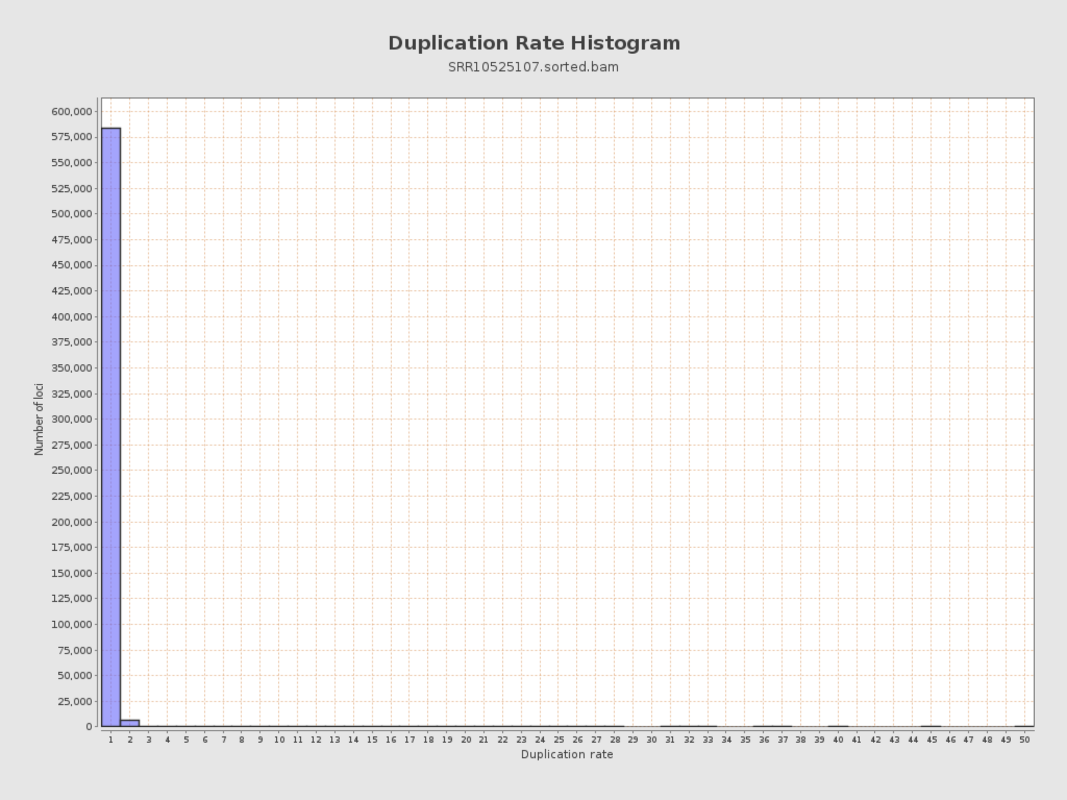
5. Results : Coverage Histogram (0-50X)



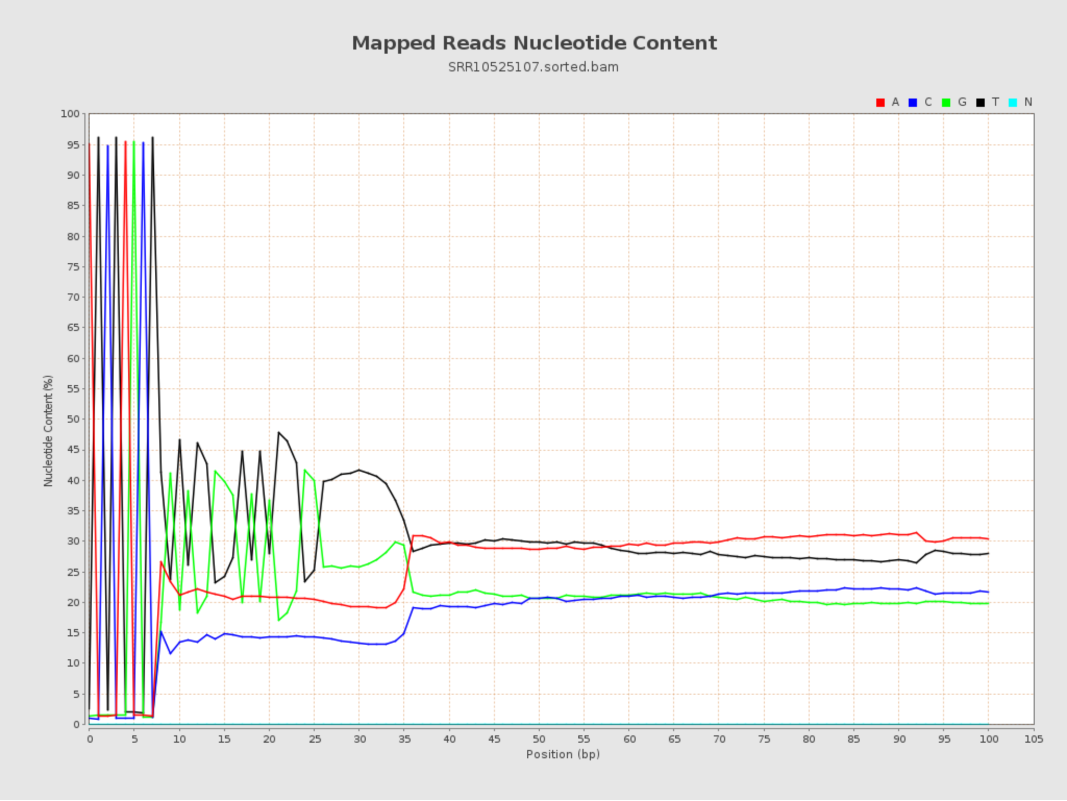
6. Results : Genome Fraction Coverage



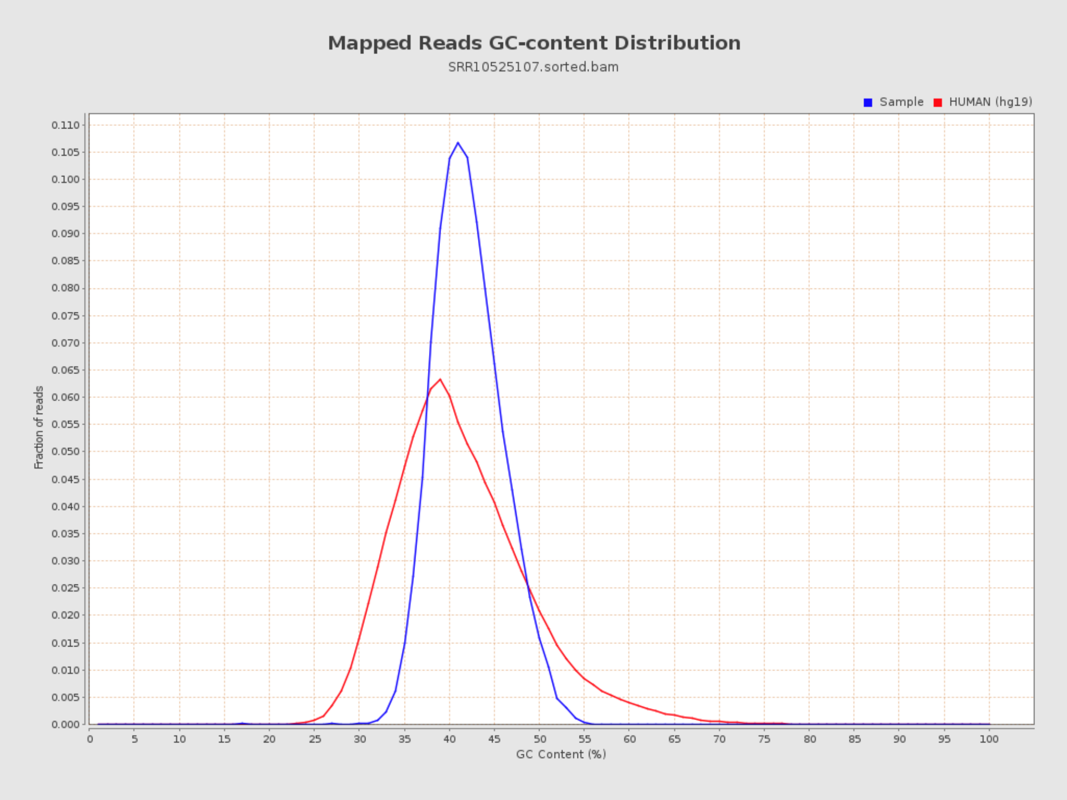
7. Results : Duplication Rate Histogram



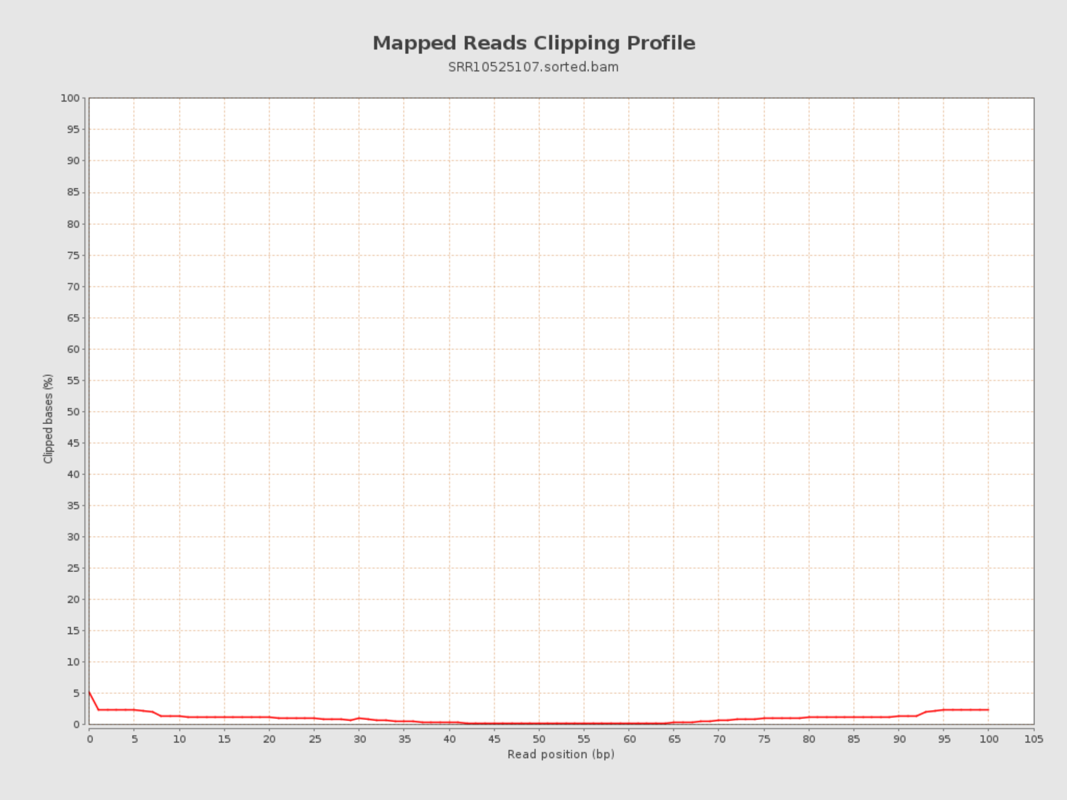
8. Results : Mapped Reads Nucleotide Content



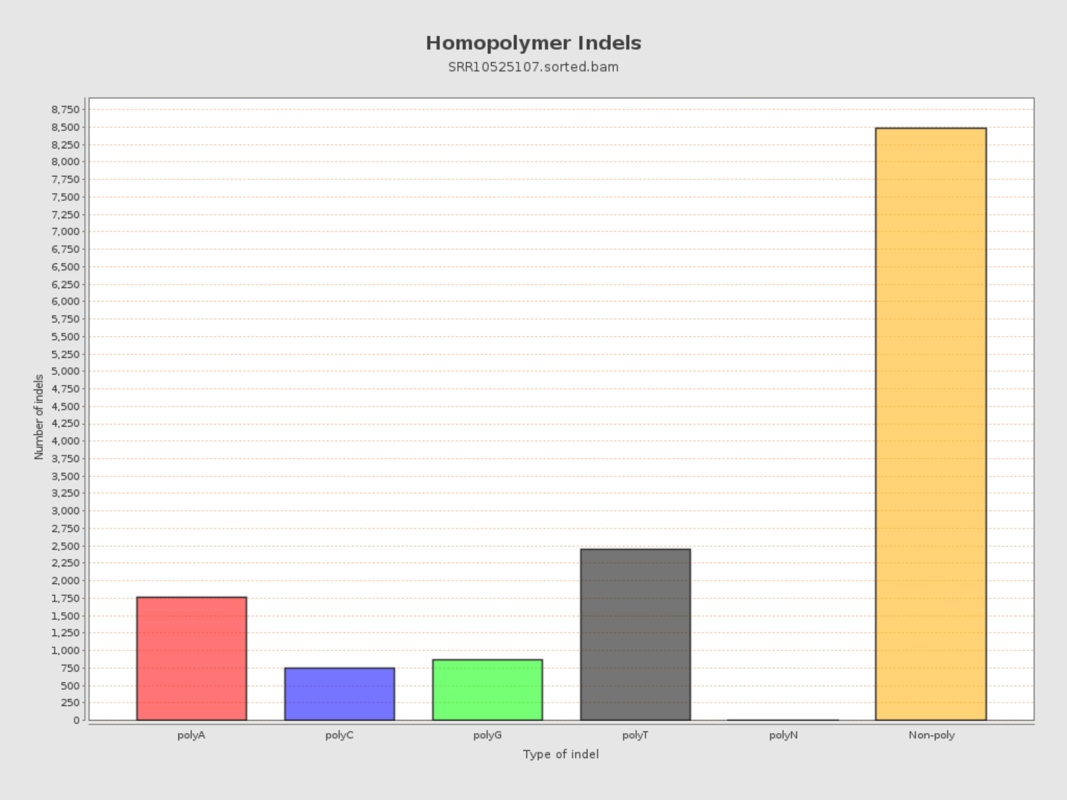
9. Results : Mapped Reads GC-content Distribution



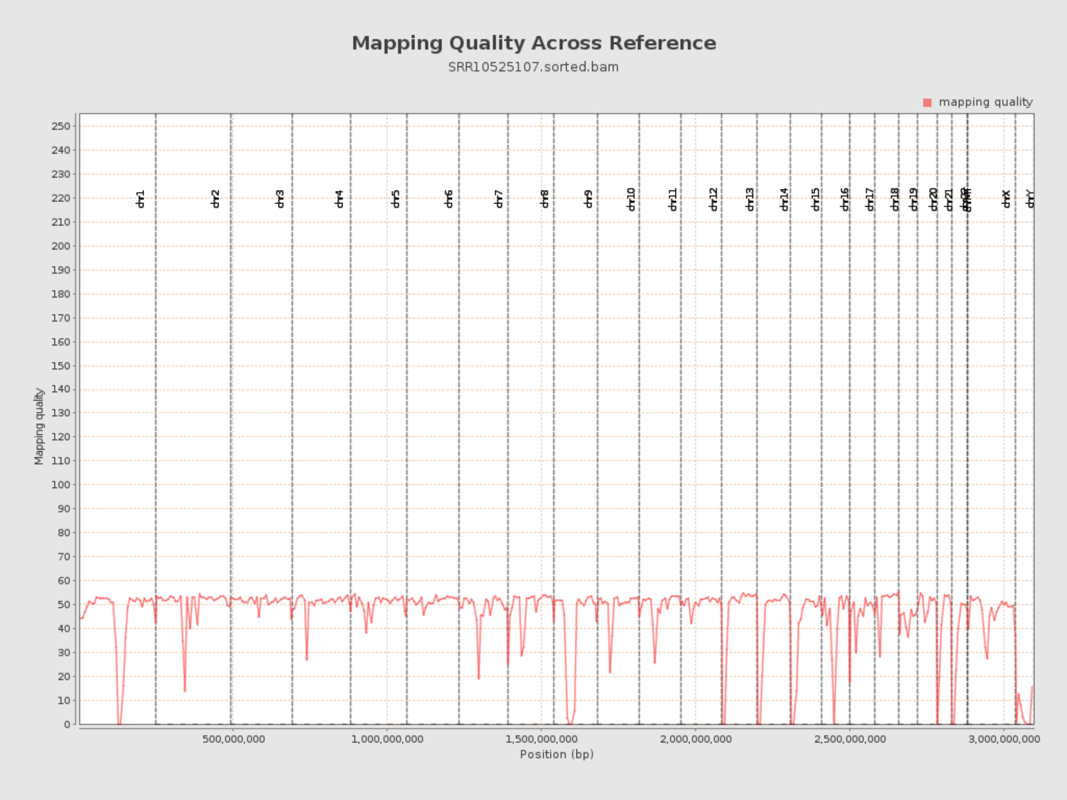
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram