Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 15:32:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525063.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_SRR10525063 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525063.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 15:32:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525063.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	601,718
Mapped reads	489,754 / 81.39%
Unmapped reads	111,964 / 18.61%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,415 / 0.24%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	15,883 / 2.64%
Duplication rate	2.77%
Clipped reads	489,368 / 81.33%

2.2. ACGT Content

Number/percentage of A's	7,655,940 / 26.8%
Number/percentage of C's	5,253,208 / 18.39%
Number/percentage of T's	8,822,358 / 30.88%
Number/percentage of G's	6,837,254 / 23.93%
Number/percentage of N's	2,560 / 0.01%
GC Percentage	42.32%

2.3. Coverage

Mean	0.0092

Standard Deviation	0.1206

2.4. Mapping Quality

Mean Mapping Quality	46.26

2.5. Mismatches and indels

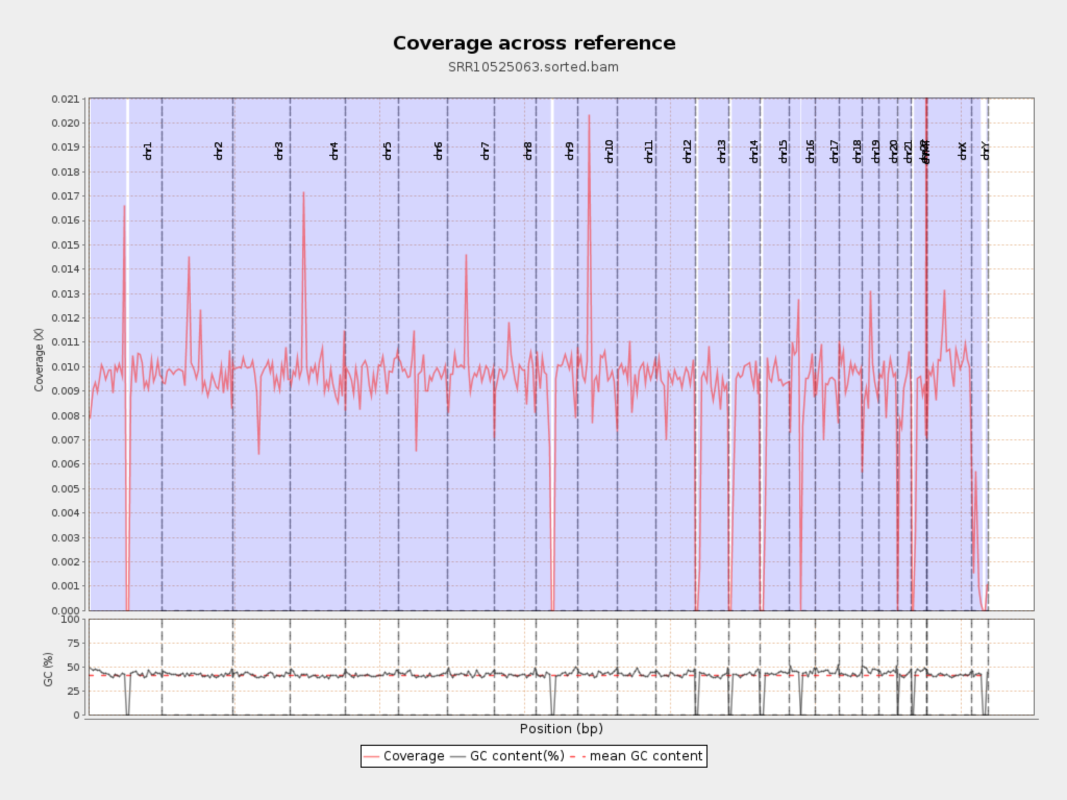
General error rate	0.5%
Mismatches	138,091
Insertions	2,444
Mapped reads with at least one insertion	0.5%
Deletions	5,764
Mapped reads with at least one deletion	1.17%
Homopolymer indels	42.02%

2.6. Chromosome stats

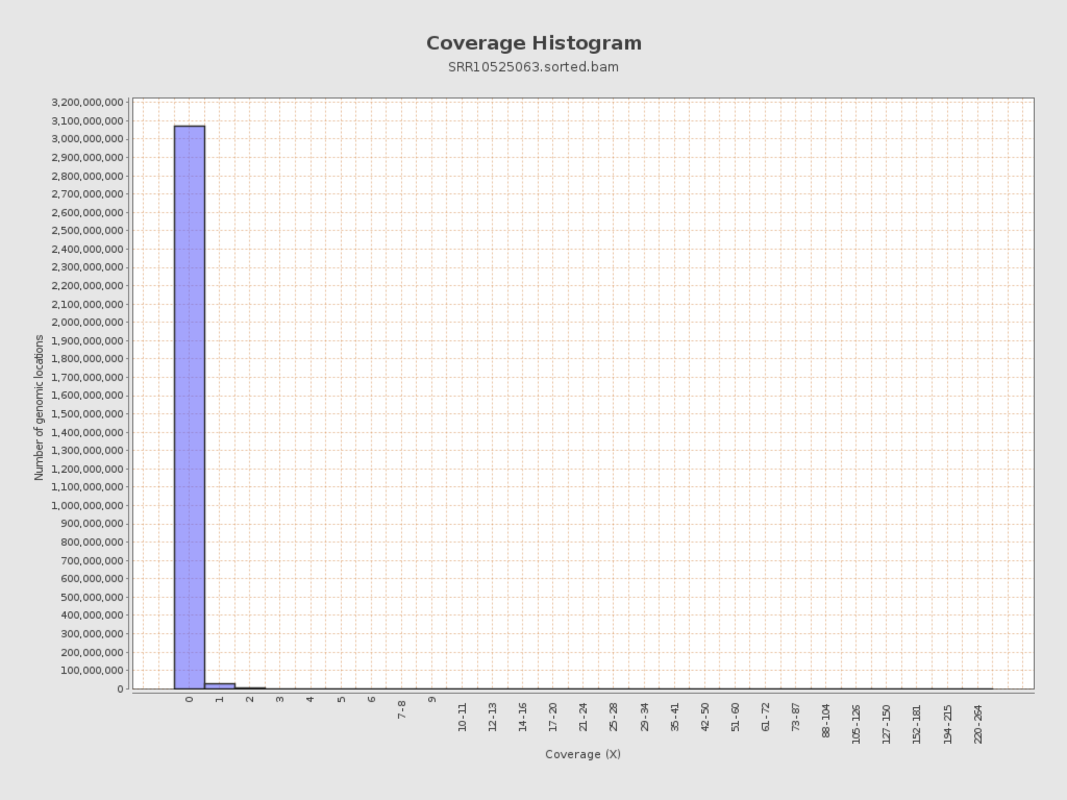
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2303936	0.0092	0.1955
chr2	243199373	2399566	0.0099	0.1337
chr3	198022430	1925555	0.0097	0.1031
chr4	191154276	1905733	0.01	0.1095
chr5	180915260	1749474	0.0097	0.1029
chr6	171115067	1656818	0.0097	0.1063
chr7	159138663	1590068	0.01	0.132

chr8	146364022	1429292	0.0098	0.1215
chr9	141213431	1208115	0.0086	0.1078
chr10	135534747	1387188	0.0102	0.1301
chr11	135006516	1309111	0.0097	0.1097
chr12	133851895	1267610	0.0095	0.1033
chr13	115169878	899431	0.0078	0.0927
chr14	107349540	867903	0.0081	0.0943
chr15	102531392	804478	0.0078	0.0922
chr16	90354753	818051	0.0091	0.103
chr17	81195210	741456	0.0091	0.103
chr18	78077248	772814	0.0099	0.143
chr19	59128983	557302	0.0094	0.1406
chr20	63025520	598431	0.0095	0.1032
chr21	48129895	390595	0.0081	0.098
chr22	51304566	325579	0.0063	0.0835
chrMT	16571	1259	0.076	0.287
chrX	155270560	1579263	0.0102	0.1087
chrY	59373566	91592	0.0015	0.0615

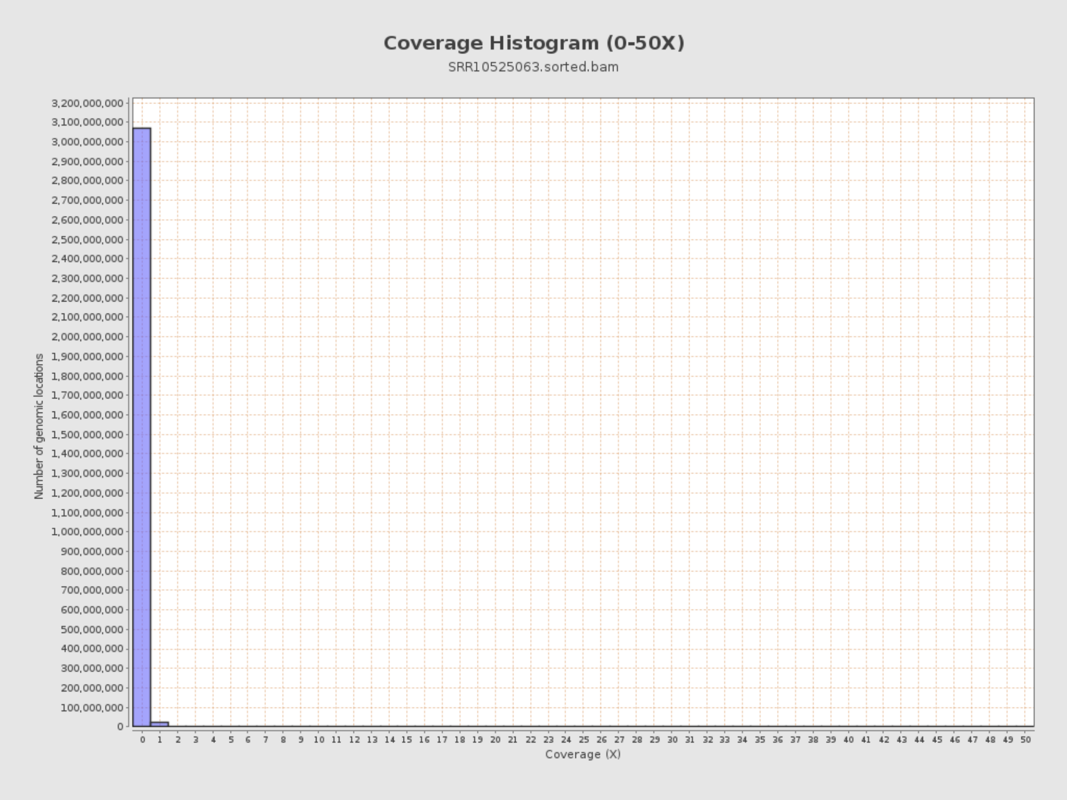
3. Results : Coverage across reference



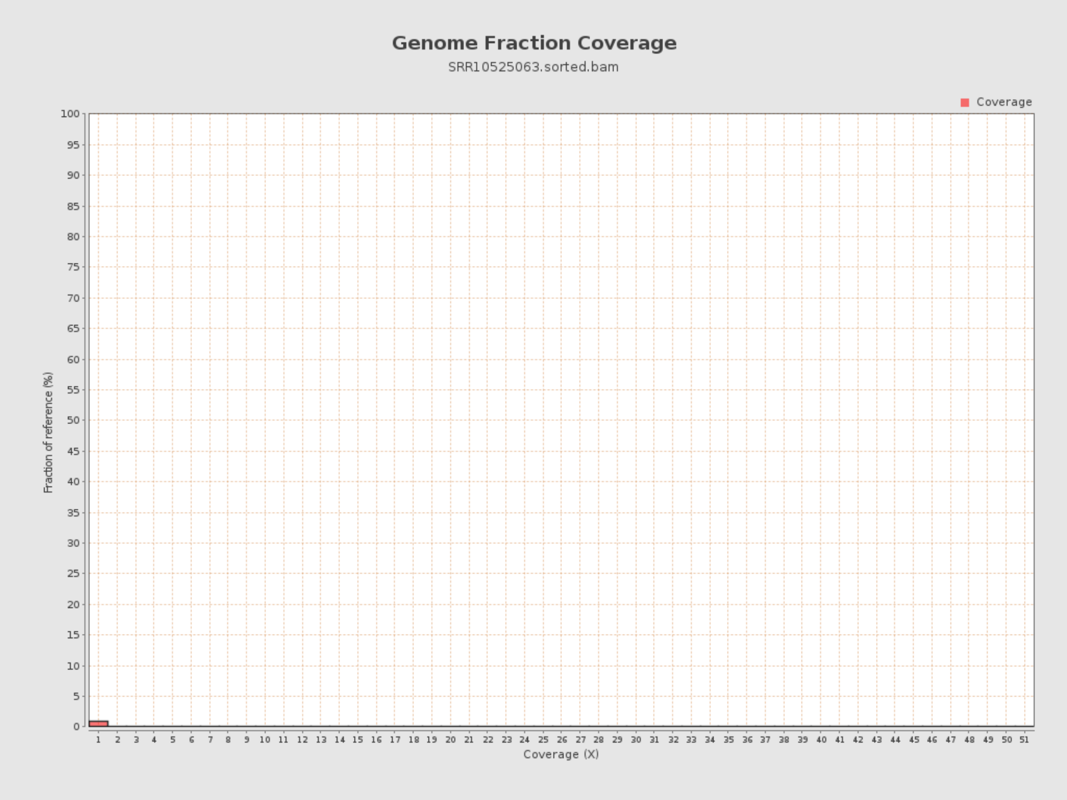
4. Results : Coverage Histogram



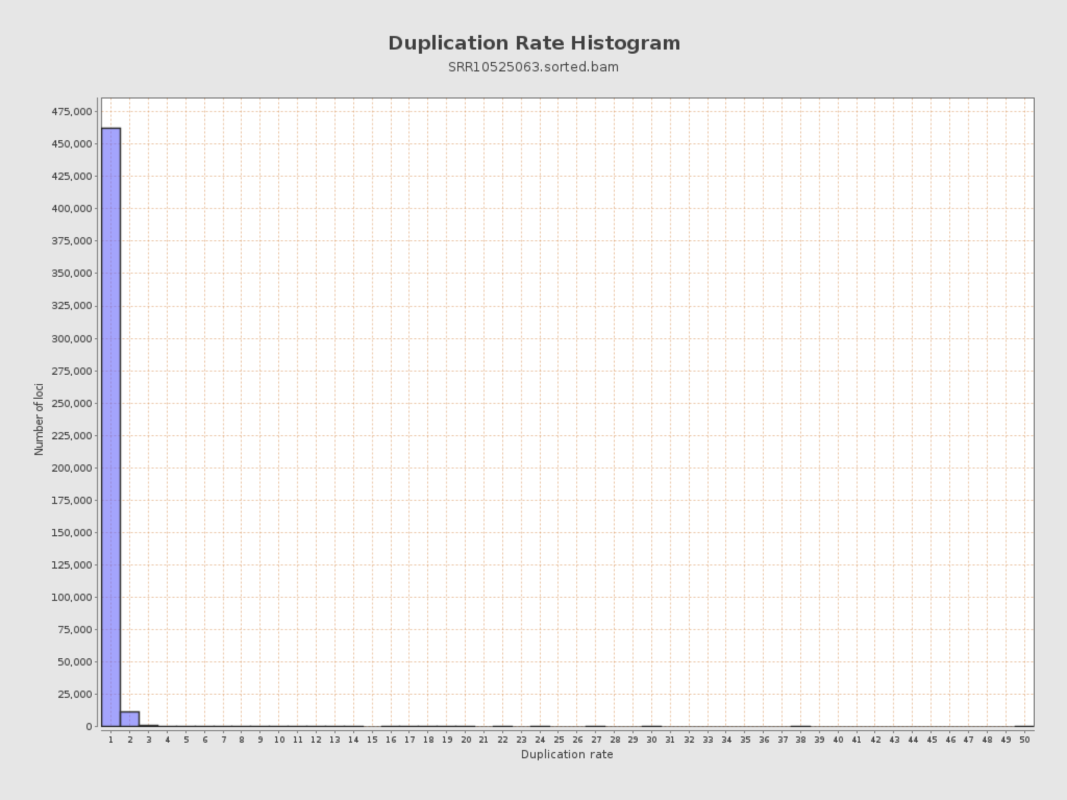
5. Results : Coverage Histogram (0-50X)



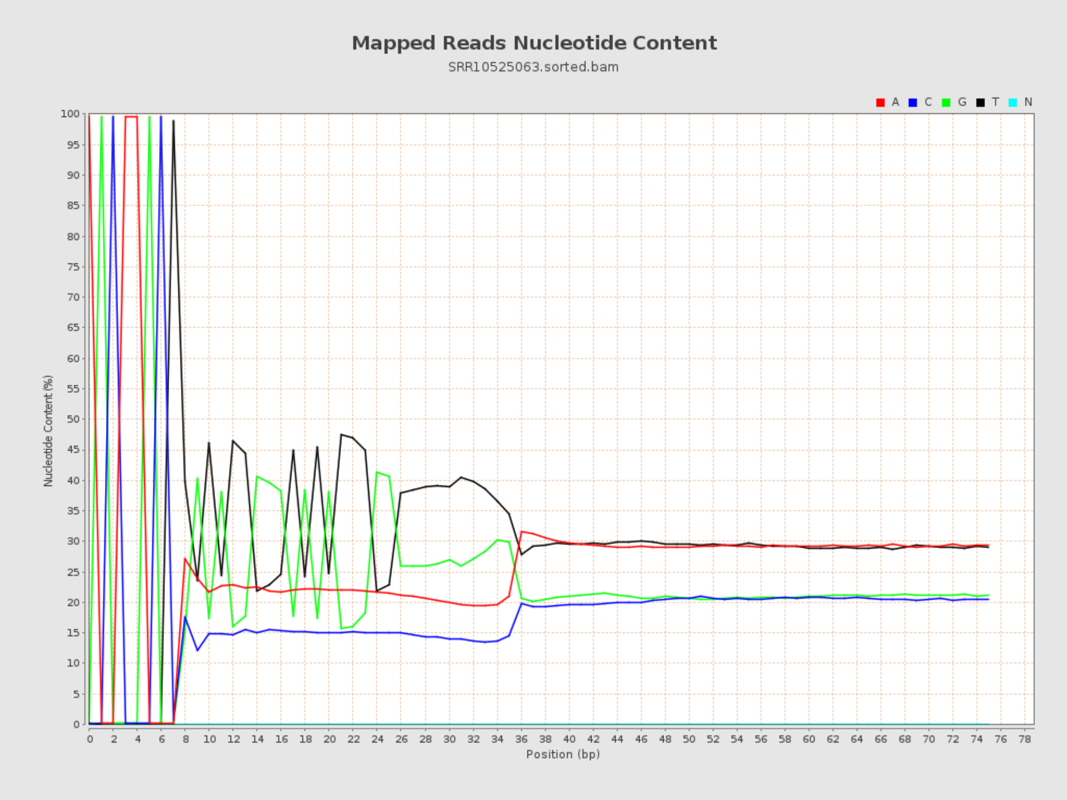
6. Results : Genome Fraction Coverage



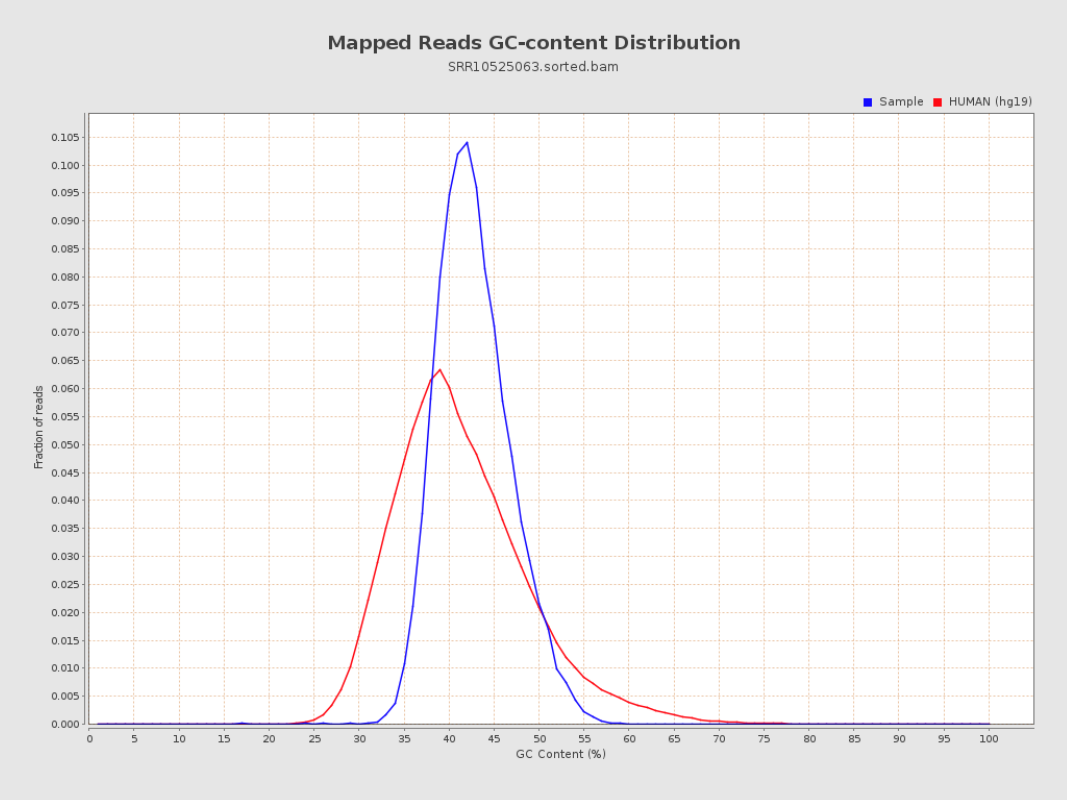
7. Results : Duplication Rate Histogram



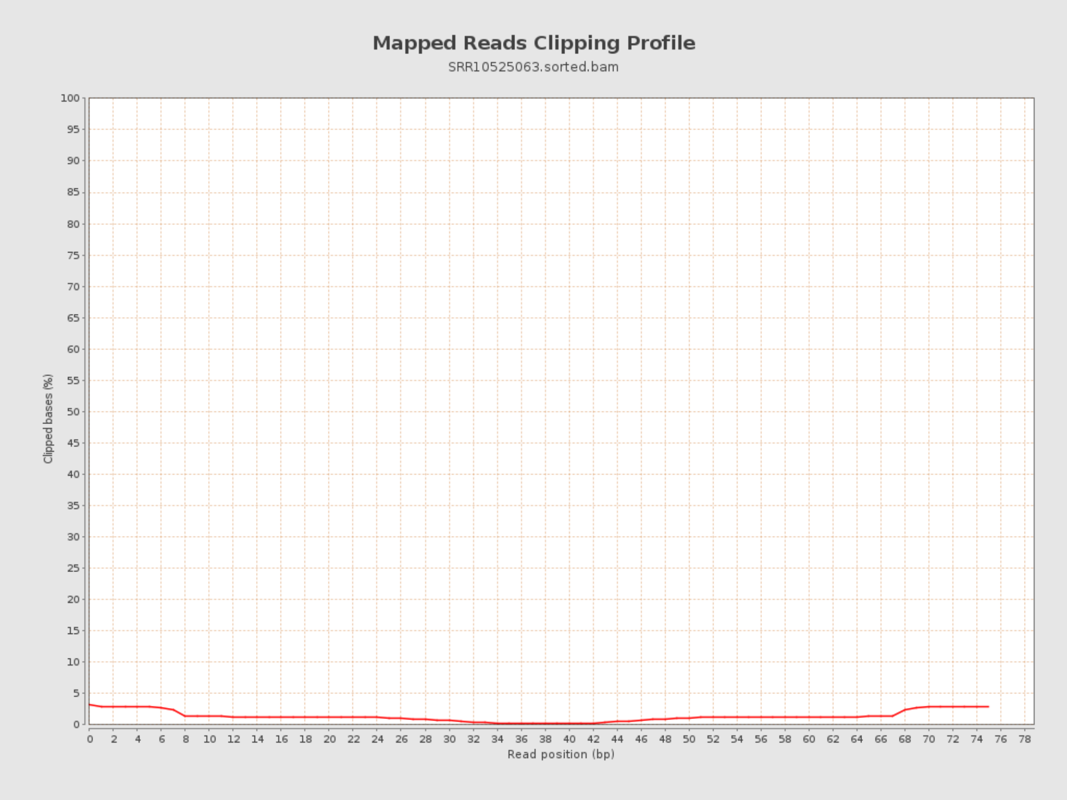
8. Results : Mapped Reads Nucleotide Content



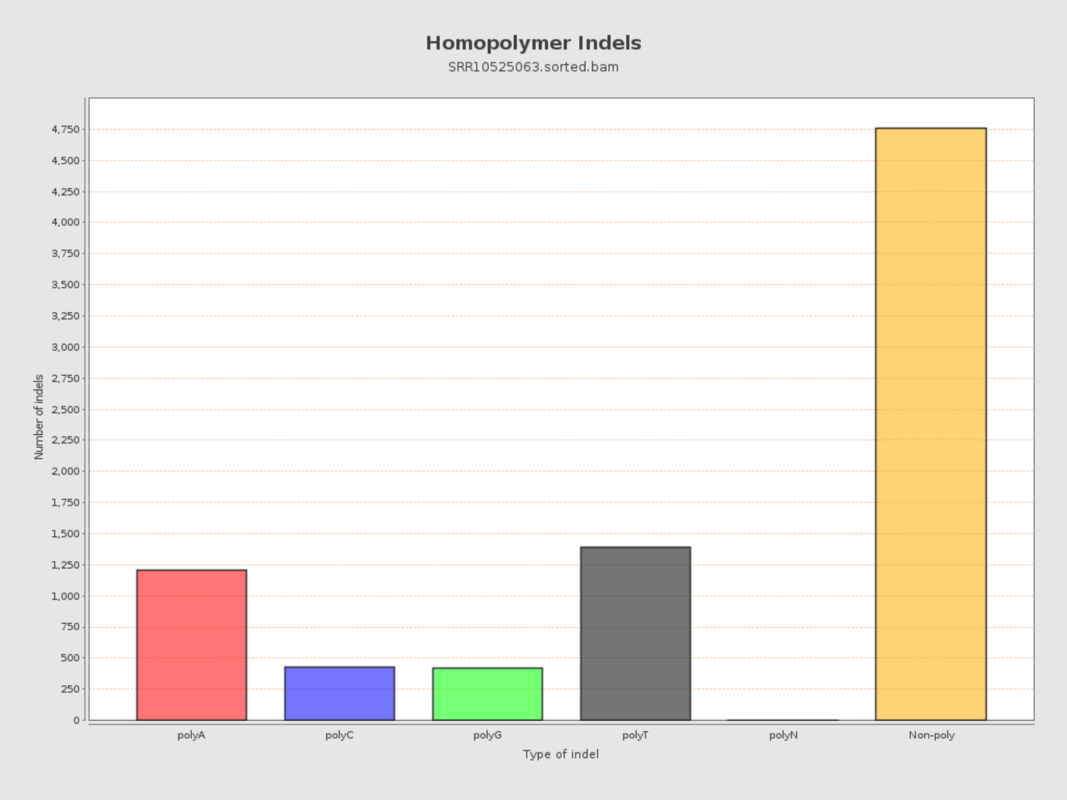
9. Results : Mapped Reads GC-content Distribution



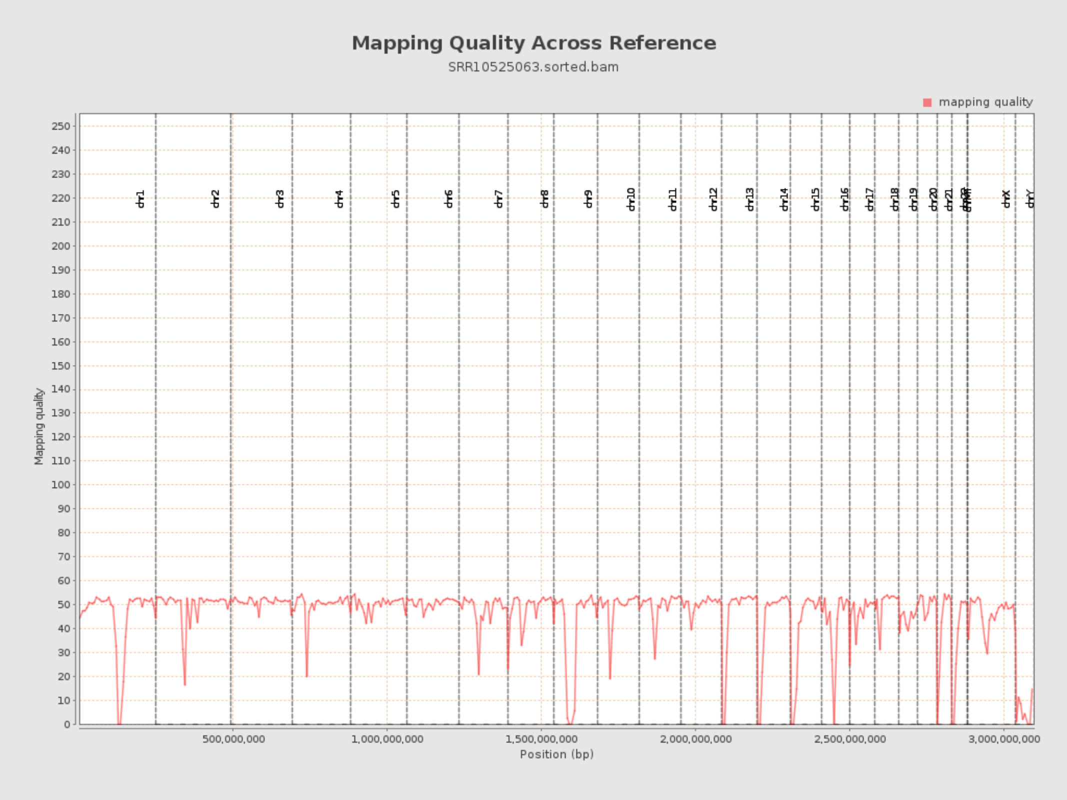
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram