Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 18:01:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525102.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_SRR10525102 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525102.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 18:01:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525102.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	638,706
Mapped reads	572,153 / 89.58%
Unmapped reads	66,553 / 10.42%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,027 / 2.82%
Read min/max/mean length	30 / 101 / 102.04
Duplicated reads (estimated)	11,693 / 1.83%
Duplication rate	1.22%
Clipped reads	589,083 / 92.23%

2.2. ACGT Content

Number/percentage of A's	11,588,115 / 26.59%
Number/percentage of C's	8,491,539 / 19.48%
Number/percentage of T's	12,977,127 / 29.78%
Number/percentage of G's	10,522,895 / 24.15%
Number/percentage of N's	1,595 / 0%
GC Percentage	43.63%

2.3. Coverage

Mean	0.0141

Standard Deviation	0.18

2.4. Mapping Quality

Mean Mapping Quality	45.15

2.5. Mismatches and indels

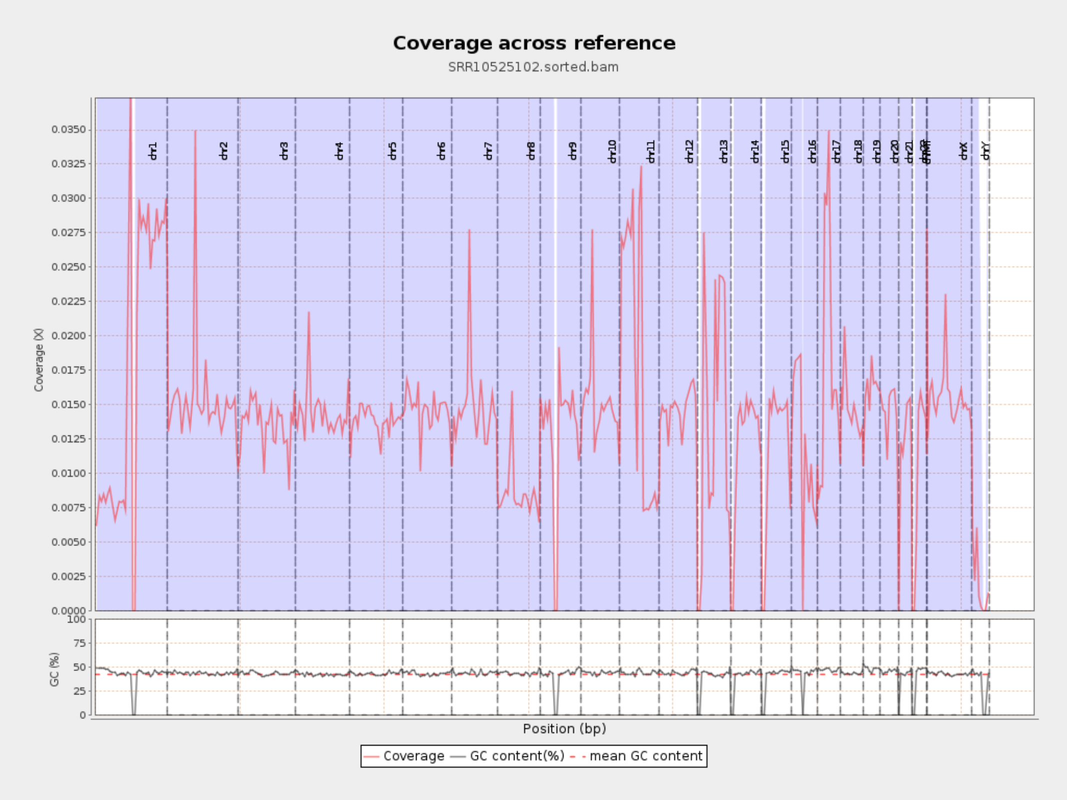
General error rate	0.79%
Mismatches	334,432
Insertions	4,198
Mapped reads with at least one insertion	0.72%
Deletions	10,004
Mapped reads with at least one deletion	1.72%
Homopolymer indels	42.13%

2.6. Chromosome stats

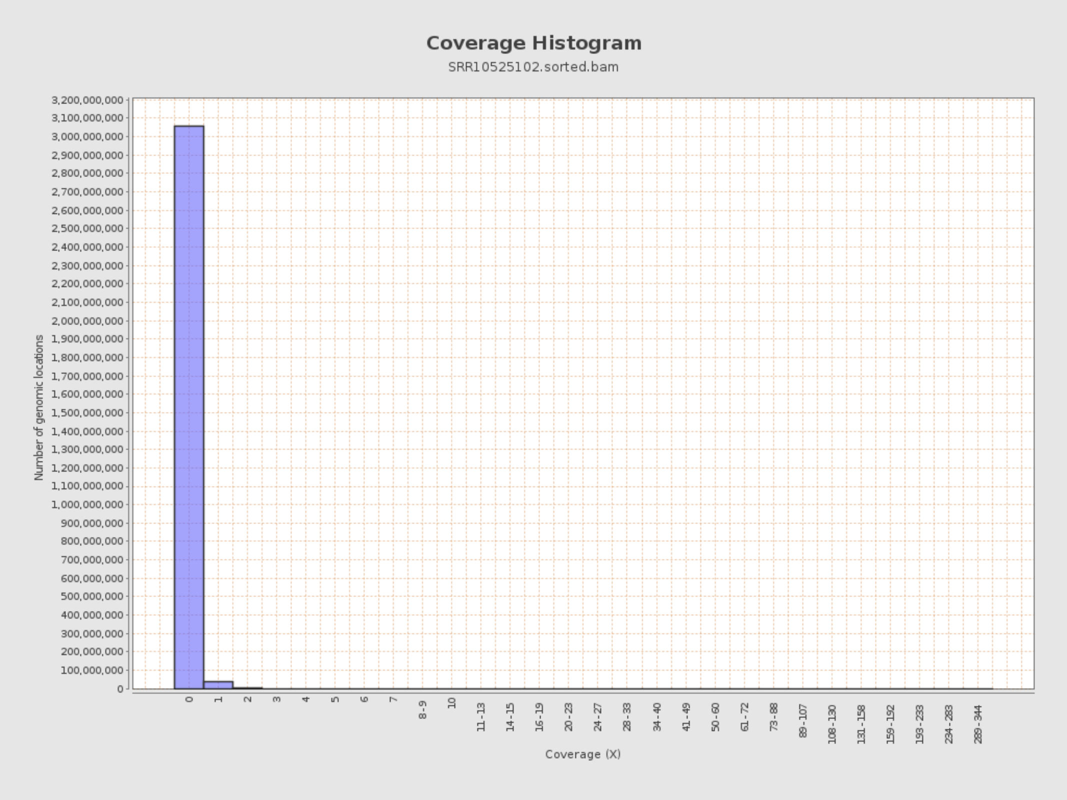
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4346359	0.0174	0.307
chr2	243199373	3728339	0.0153	0.2319
chr3	198022430	2672149	0.0135	0.1206
chr4	191154276	2757352	0.0144	0.1302
chr5	180915260	2514262	0.0139	0.1234
chr6	171115067	2491682	0.0146	0.1333
chr7	159138663	2379320	0.015	0.233

chr8	146364022	1254187	0.0086	0.1994
chr9	141213431	1820410	0.0129	0.1656
chr10	135534747	2066337	0.0152	0.1818
chr11	135006516	2463885	0.0183	0.1942
chr12	133851895	1958298	0.0146	0.126
chr13	115169878	1540520	0.0134	0.1202
chr14	107349540	1272004	0.0118	0.1183
chr15	102531392	1188111	0.0116	0.1117
chr16	90354753	1050957	0.0116	0.1176
chr17	81195210	1450385	0.0179	0.1517
chr18	78077248	1151312	0.0147	0.2604
chr19	59128983	952373	0.0161	0.2182
chr20	63025520	908885	0.0144	0.1256
chr21	48129895	579202	0.012	0.1195
chr22	51304566	521464	0.0102	0.1045
chrMT	16571	461	0.0278	0.1645
chrX	155270560	2416536	0.0156	0.152
chrY	59373566	113934	0.0019	0.0583

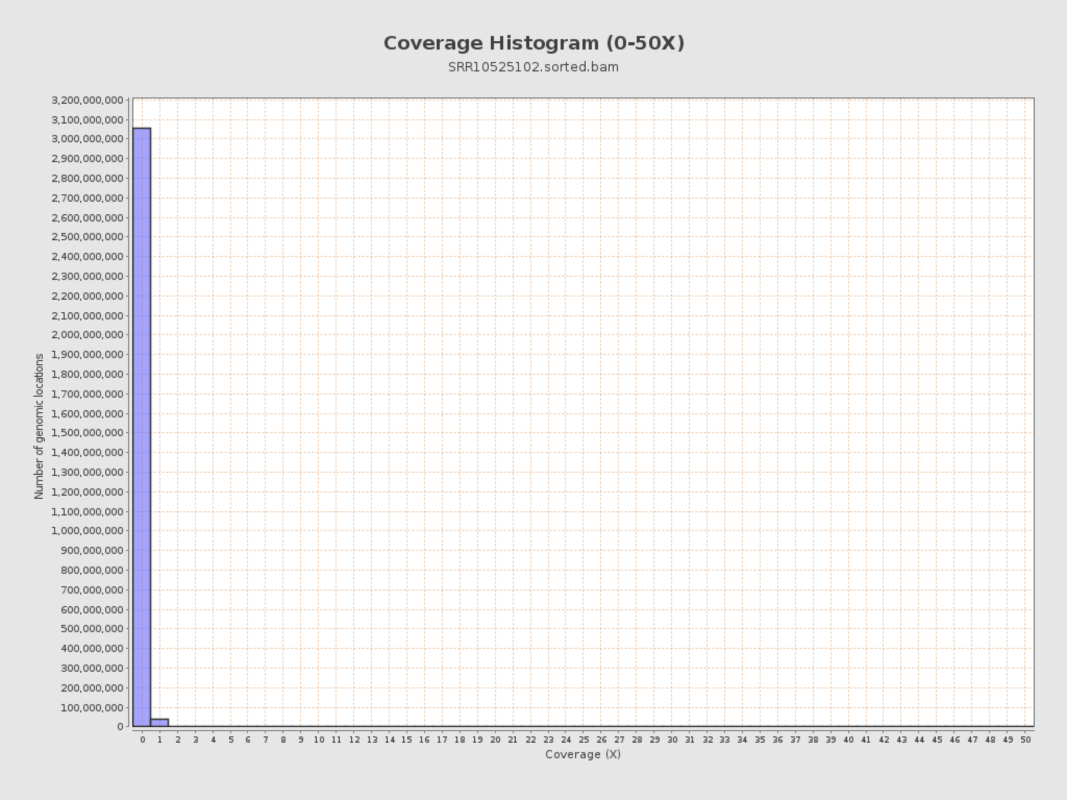
3. Results : Coverage across reference



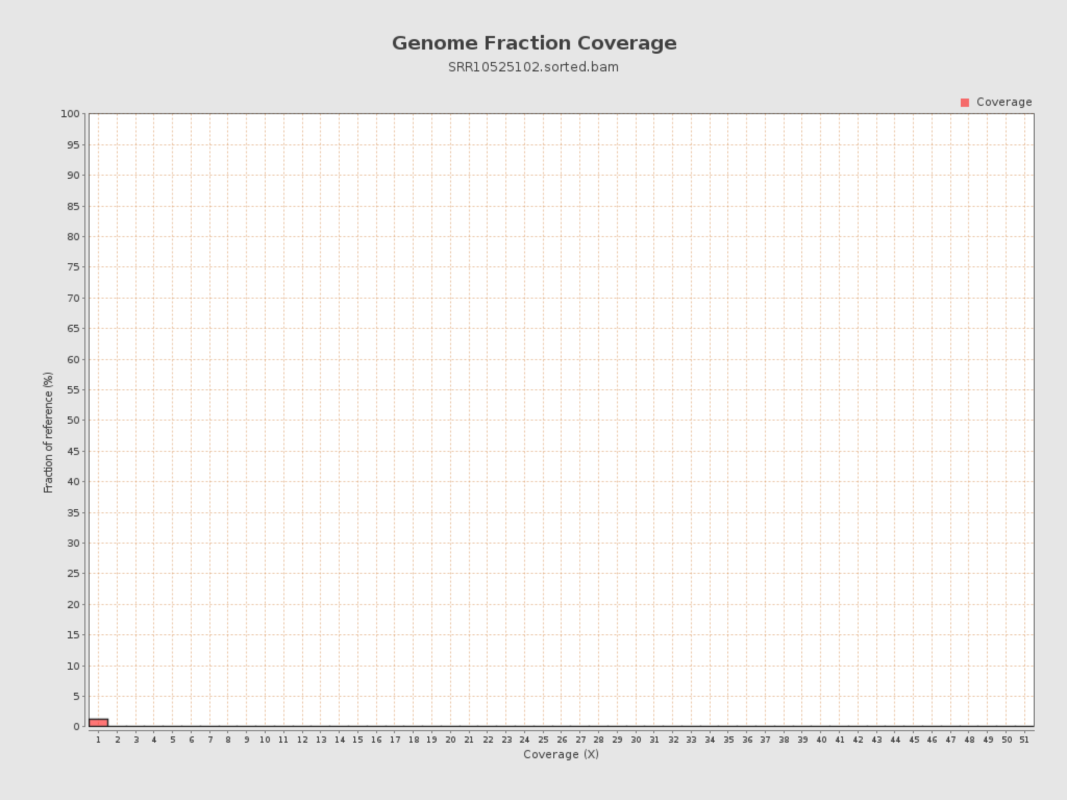
4. Results : Coverage Histogram



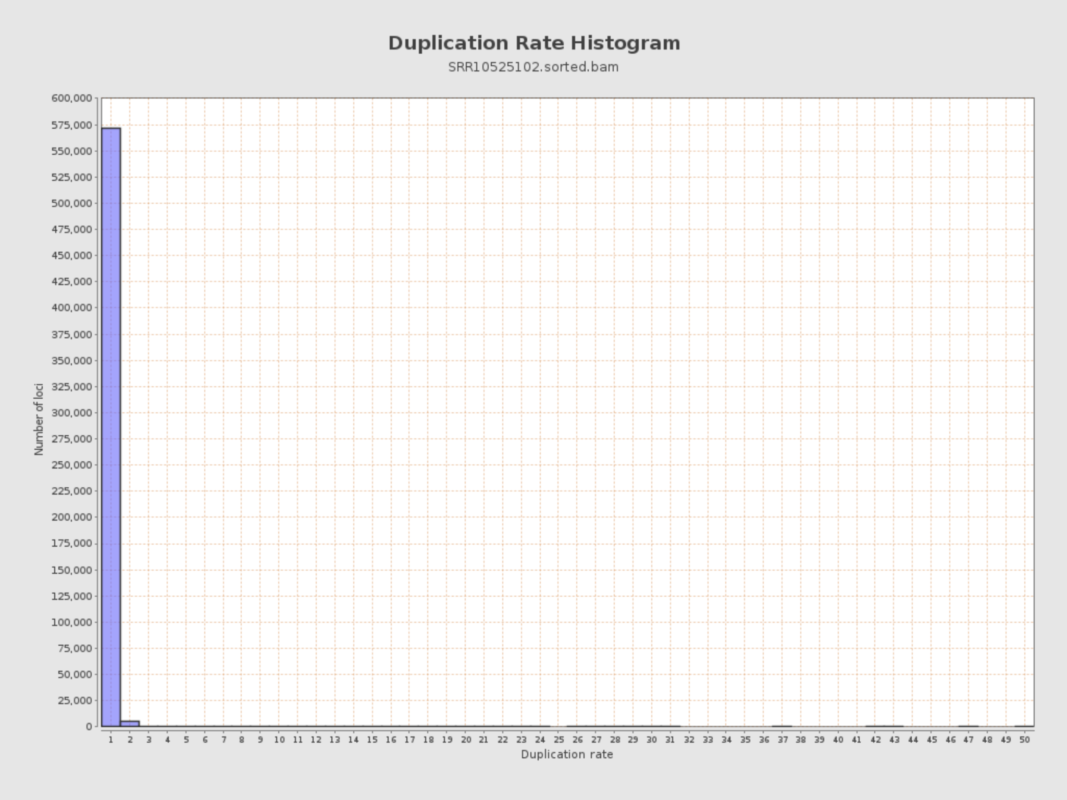
5. Results : Coverage Histogram (0-50X)



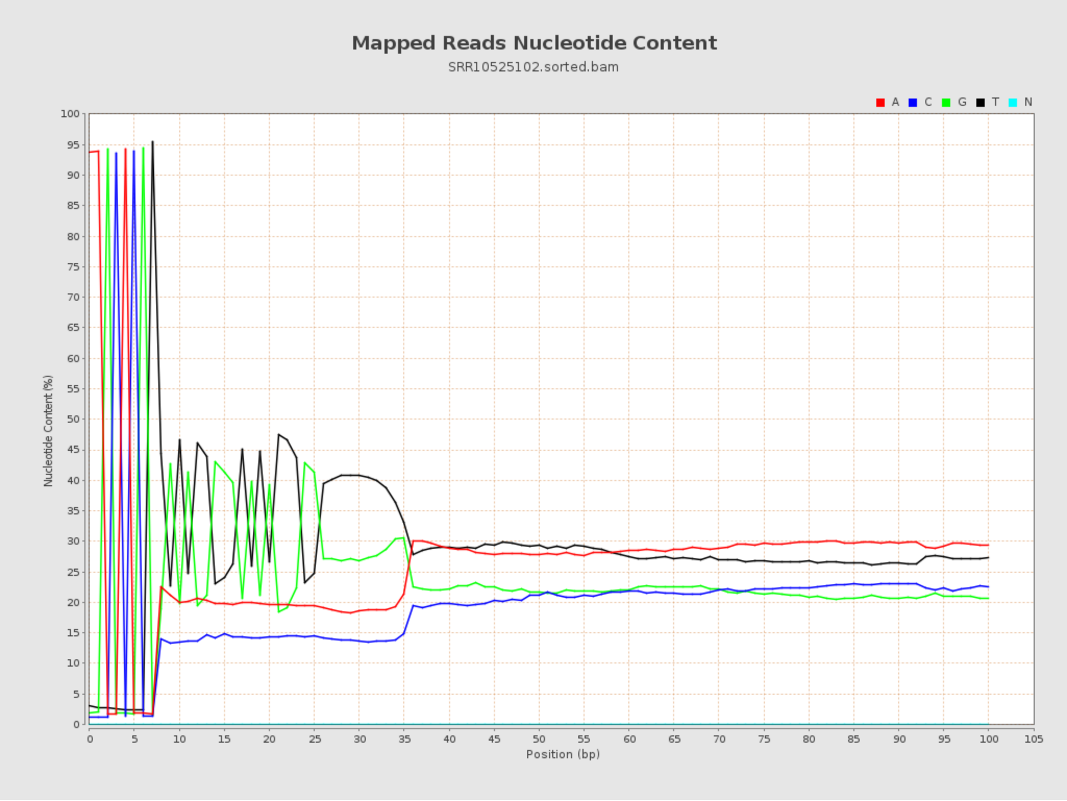
6. Results : Genome Fraction Coverage



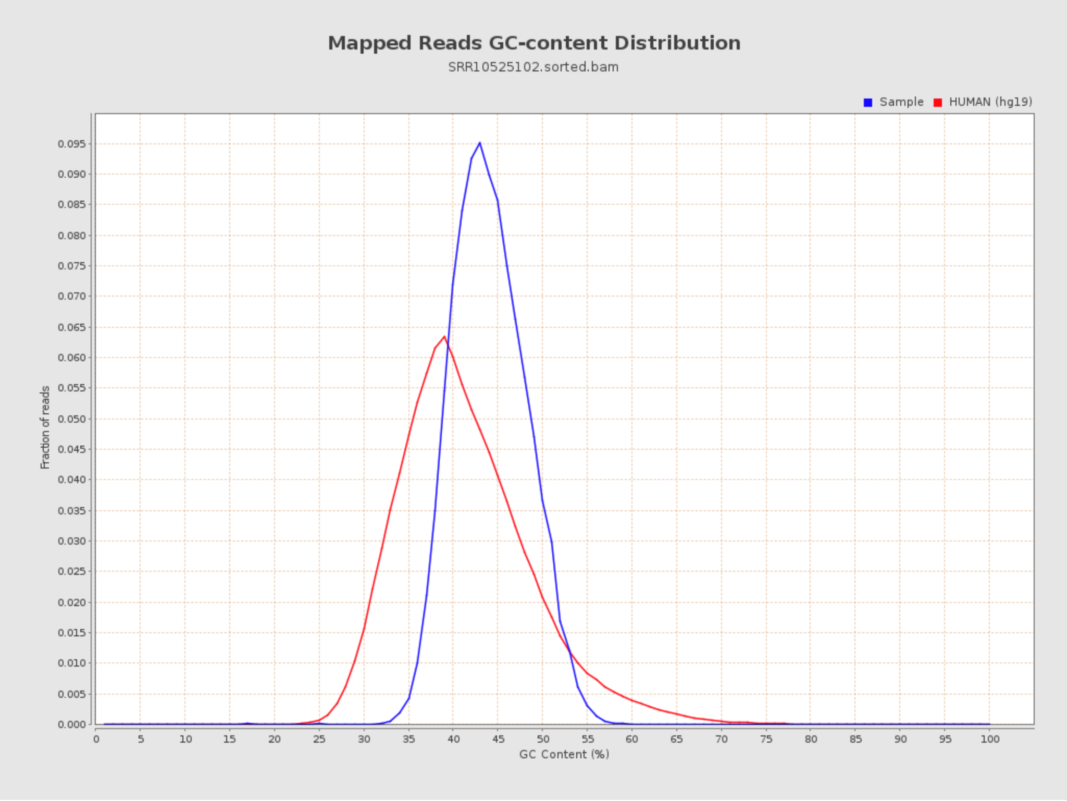
7. Results : Duplication Rate Histogram



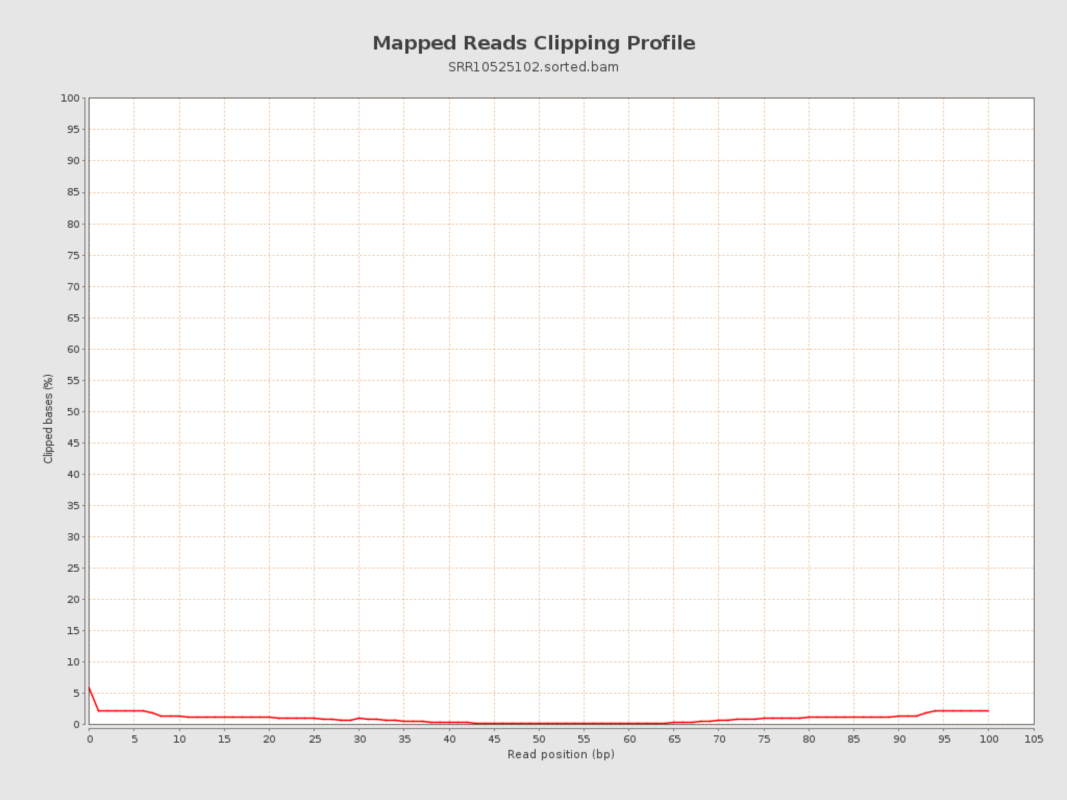
8. Results : Mapped Reads Nucleotide Content



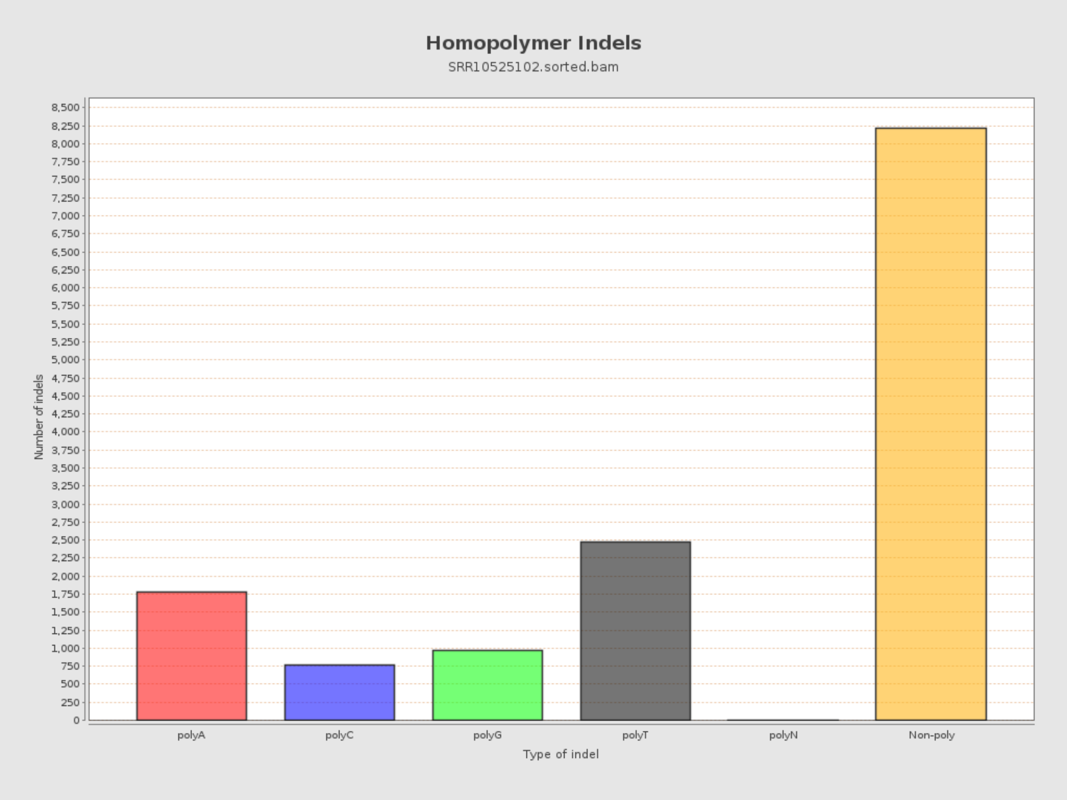
9. Results : Mapped Reads GC-content Distribution



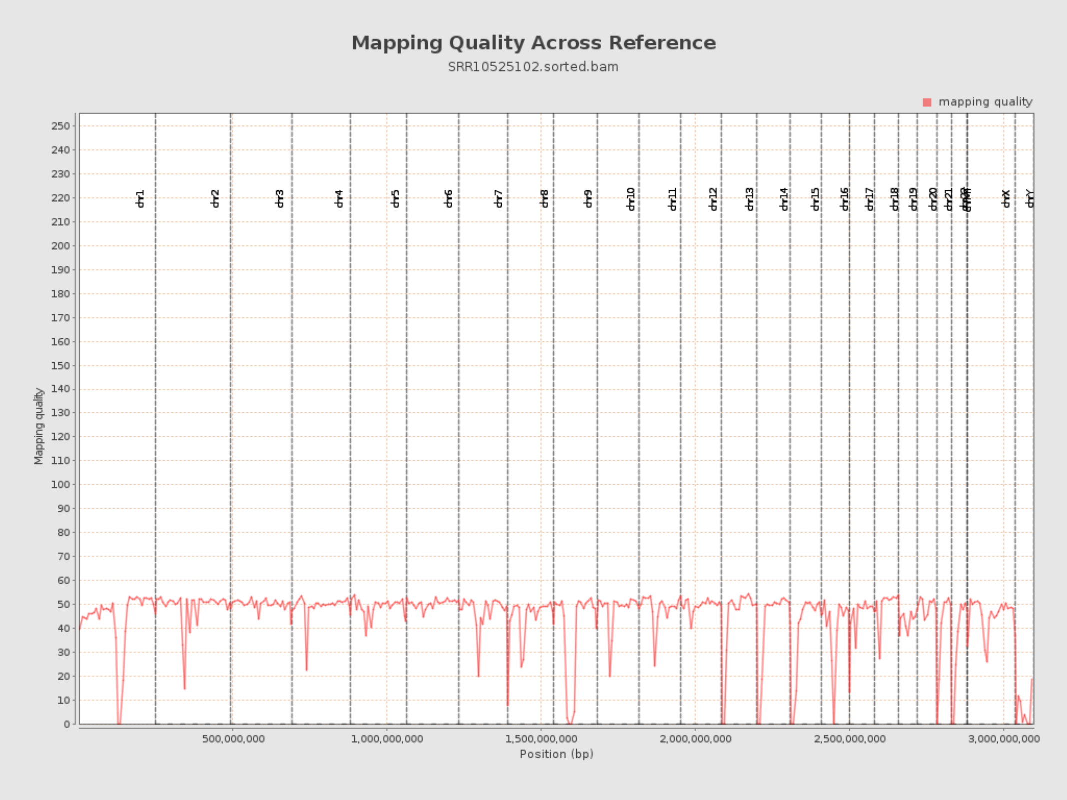
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram