Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 15:27:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525061.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_SRR10525061 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525061.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 15:27:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525061.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	794,542
Mapped reads	713,104 / 89.75%
Unmapped reads	81,438 / 10.25%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,167 / 0.27%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	31,650 / 3.98%
Duplication rate	3.71%
Clipped reads	713,079 / 89.75%

2.2. ACGT Content

Number/percentage of A's	10,978,821 / 26.21%
Number/percentage of C's	7,756,373 / 18.51%
Number/percentage of T's	12,914,432 / 30.83%
Number/percentage of G's	10,238,629 / 24.44%
Number/percentage of N's	4,421 / 0.01%
GC Percentage	42.96%

2.3. Coverage

Mean	0.0135

Standard Deviation	0.1589

2.4. Mapping Quality

Mean Mapping Quality	46.45

2.5. Mismatches and indels

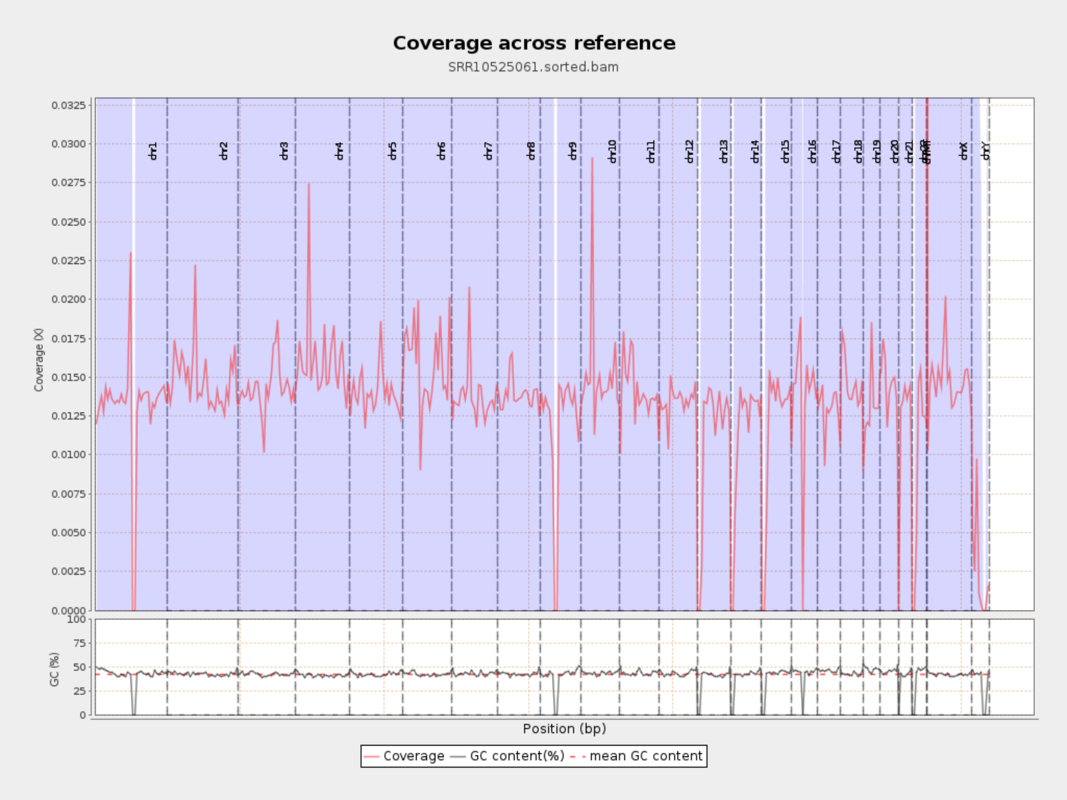
General error rate	0.5%
Mismatches	203,052
Insertions	3,374
Mapped reads with at least one insertion	0.47%
Deletions	8,719
Mapped reads with at least one deletion	1.21%
Homopolymer indels	42.48%

2.6. Chromosome stats

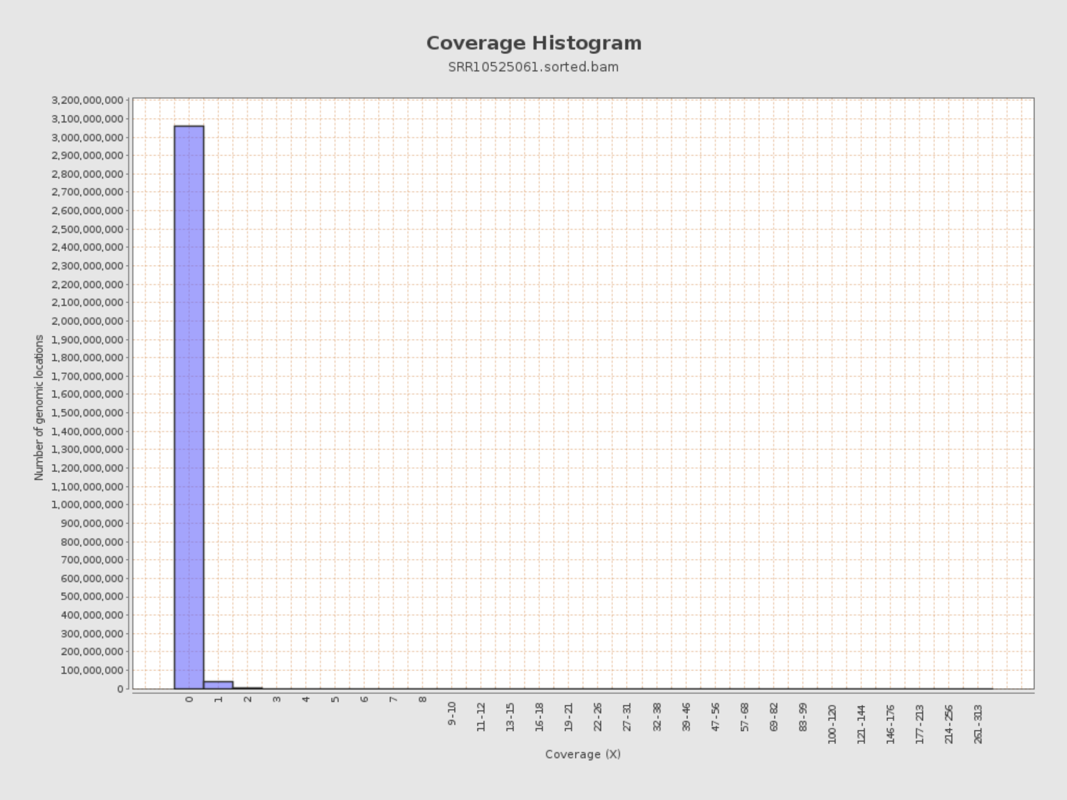
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3243497	0.013	0.2573
chr2	243199373	3607286	0.0148	0.1811
chr3	198022430	2838384	0.0143	0.1283
chr4	191154276	3060969	0.016	0.1462
chr5	180915260	2534341	0.014	0.1273
chr6	171115067	2693604	0.0157	0.1429
chr7	159138663	2194163	0.0138	0.1705

chr8	146364022	2038704	0.0139	0.191
chr9	141213431	1659952	0.0118	0.129
chr10	135534747	2049069	0.0151	0.1711
chr11	135006516	1926606	0.0143	0.142
chr12	133851895	1800165	0.0134	0.1267
chr13	115169878	1264371	0.011	0.1125
chr14	107349540	1177998	0.011	0.1133
chr15	102531392	1171529	0.0114	0.1146
chr16	90354753	1226648	0.0136	0.1304
chr17	81195210	1045871	0.0129	0.126
chr18	78077248	1151547	0.0147	0.2085
chr19	59128983	781703	0.0132	0.197
chr20	63025520	914274	0.0145	0.1316
chr21	48129895	587895	0.0122	0.1301
chr22	51304566	485131	0.0095	0.1041
chrMT	16571	13010	0.7851	1.0434
chrX	155270560	2292953	0.0148	0.137
chrY	59373566	146735	0.0025	0.1037

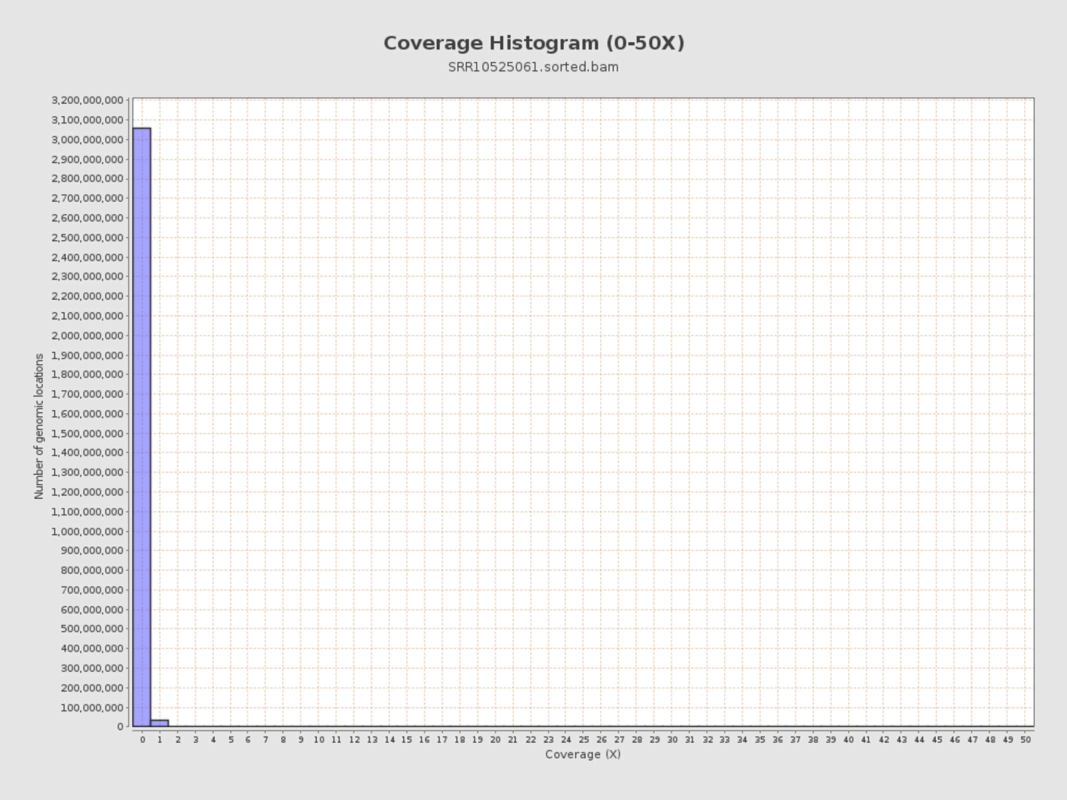
3. Results : Coverage across reference



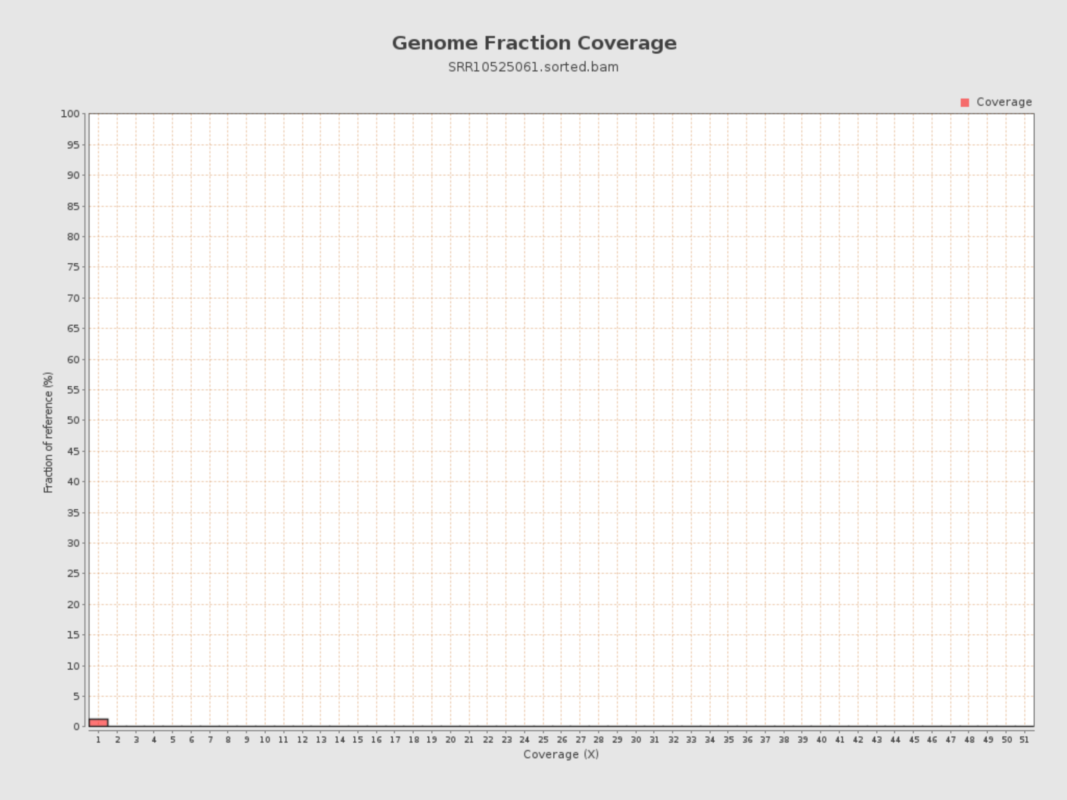
4. Results : Coverage Histogram



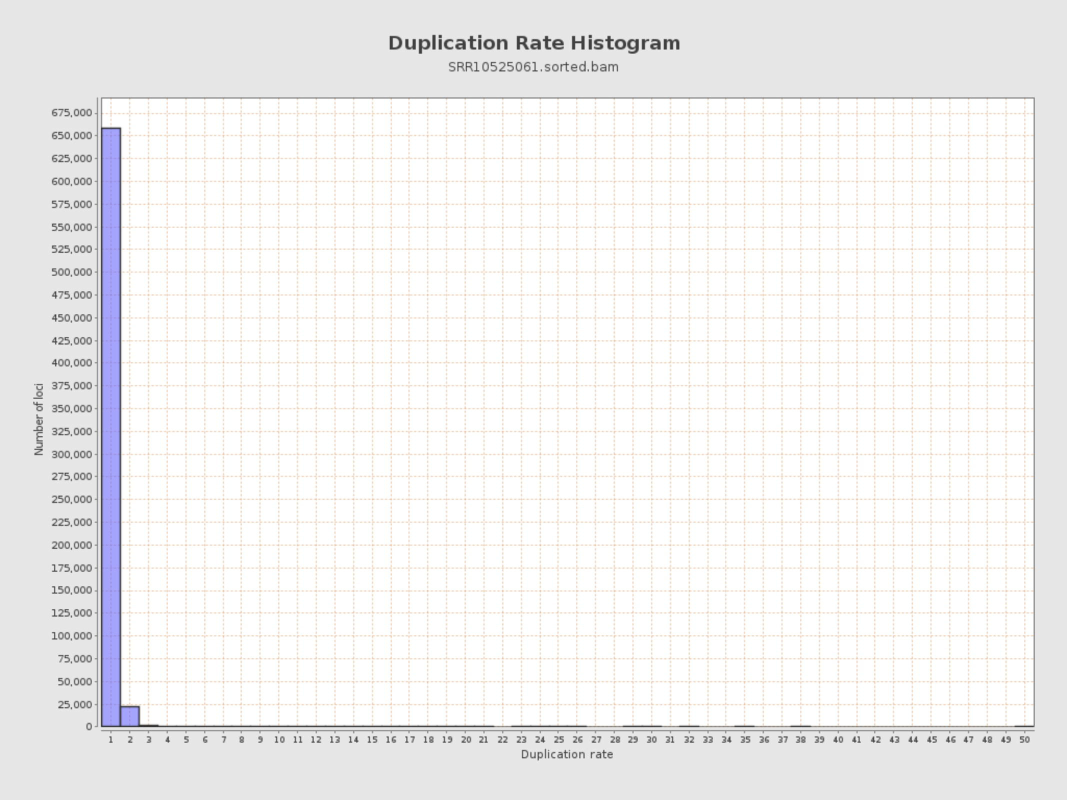
5. Results : Coverage Histogram (0-50X)



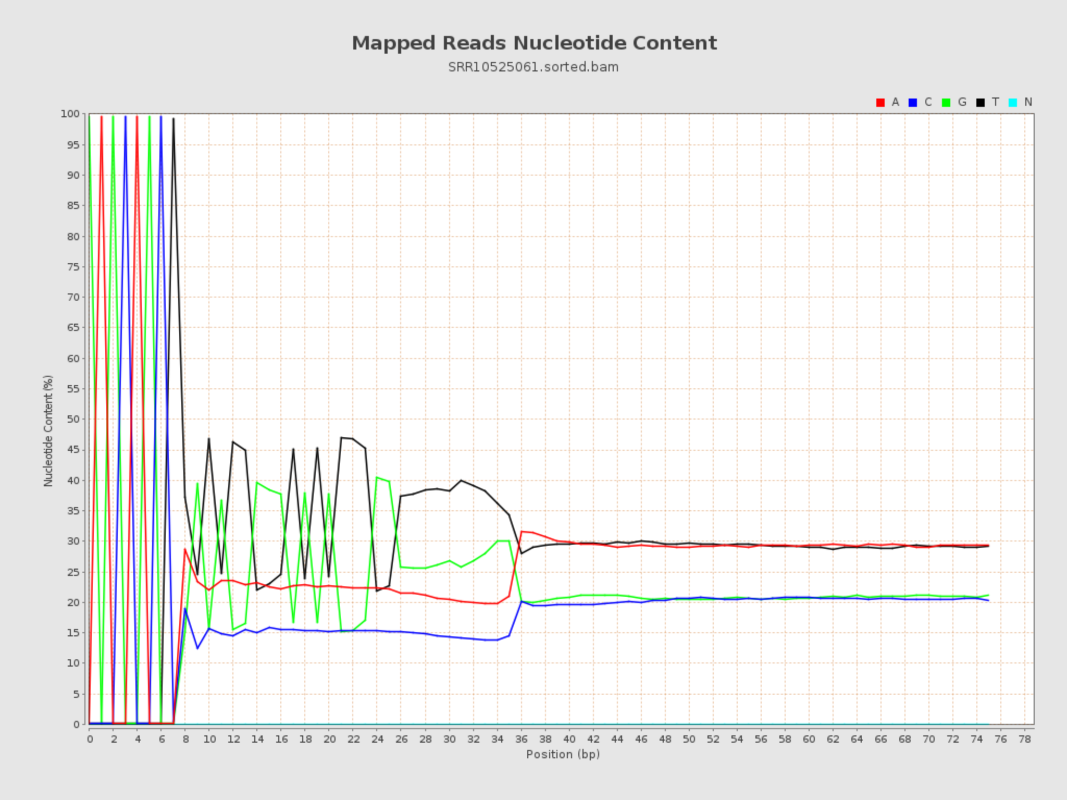
6. Results : Genome Fraction Coverage



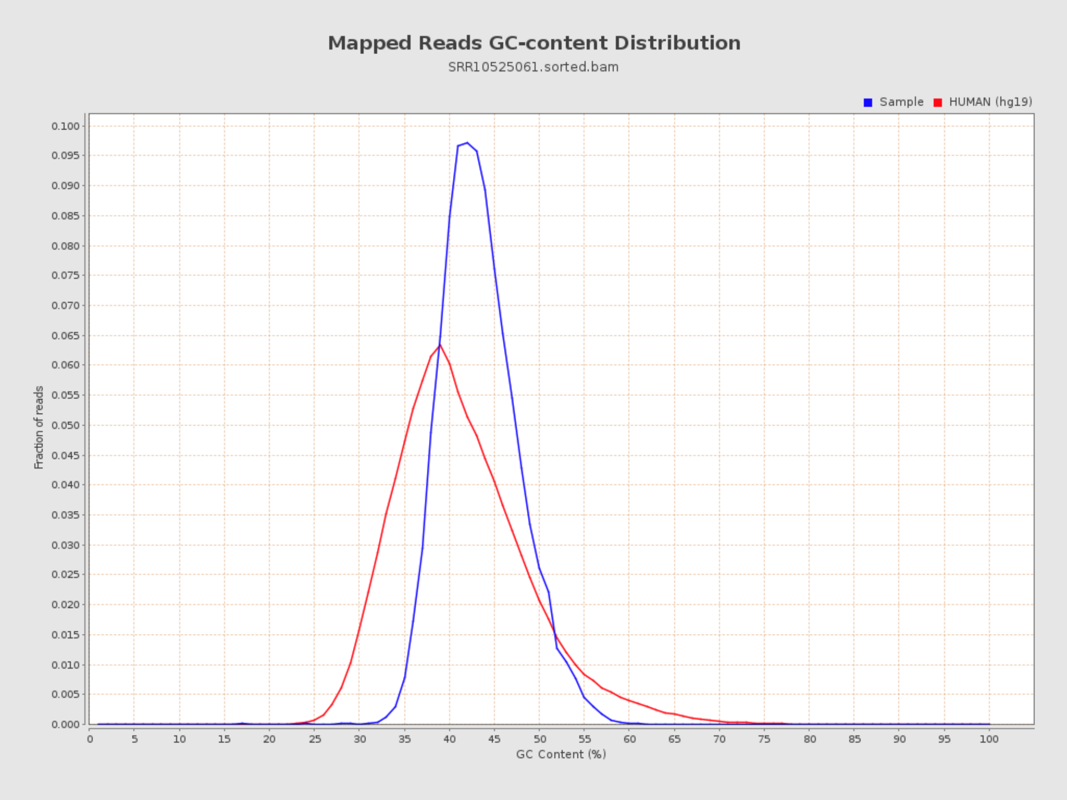
7. Results : Duplication Rate Histogram



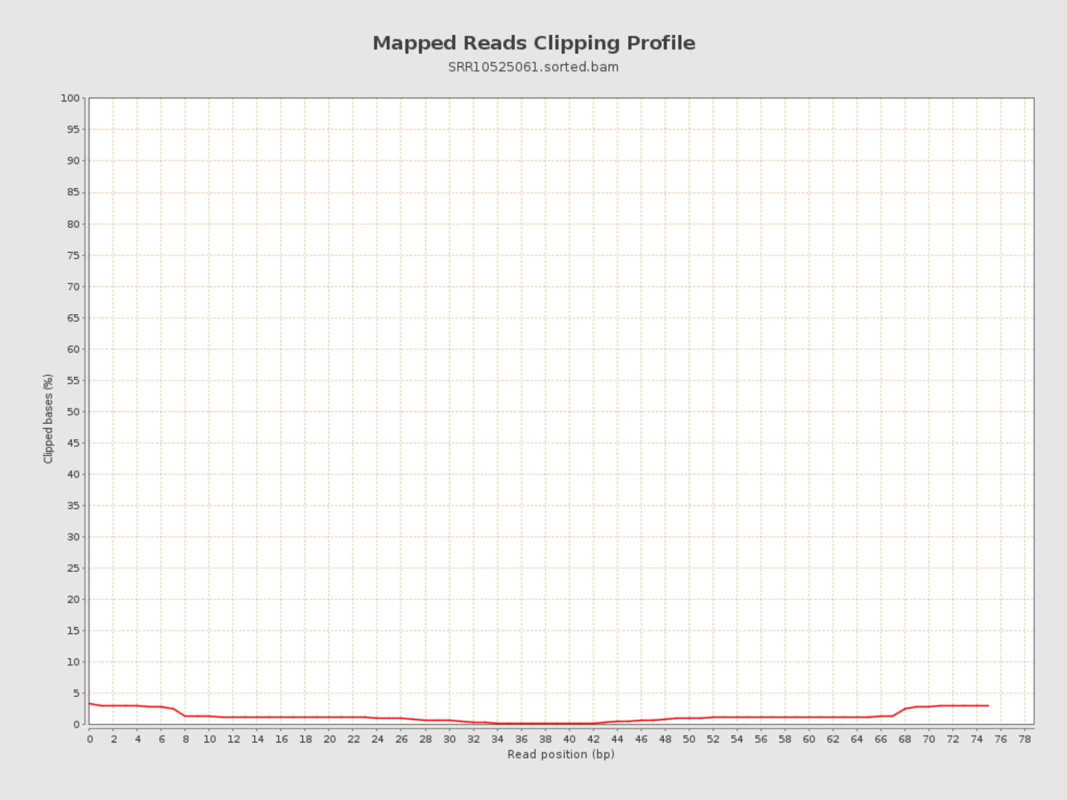
8. Results : Mapped Reads Nucleotide Content



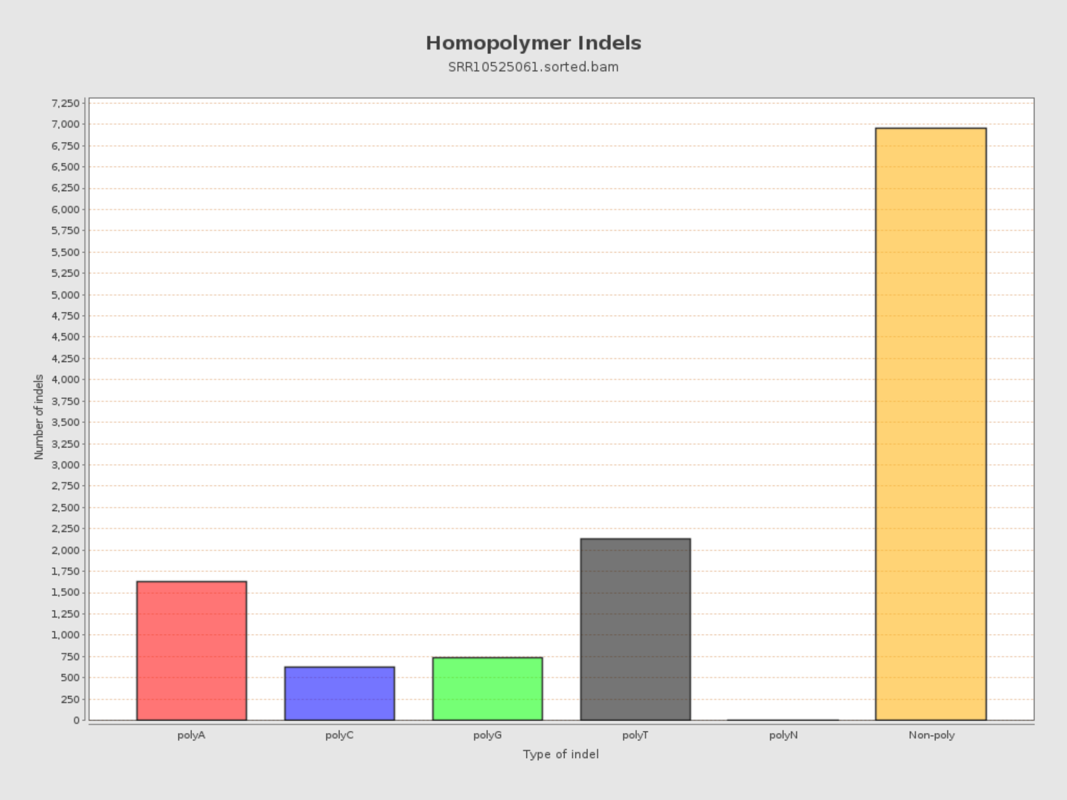
9. Results : Mapped Reads GC-content Distribution



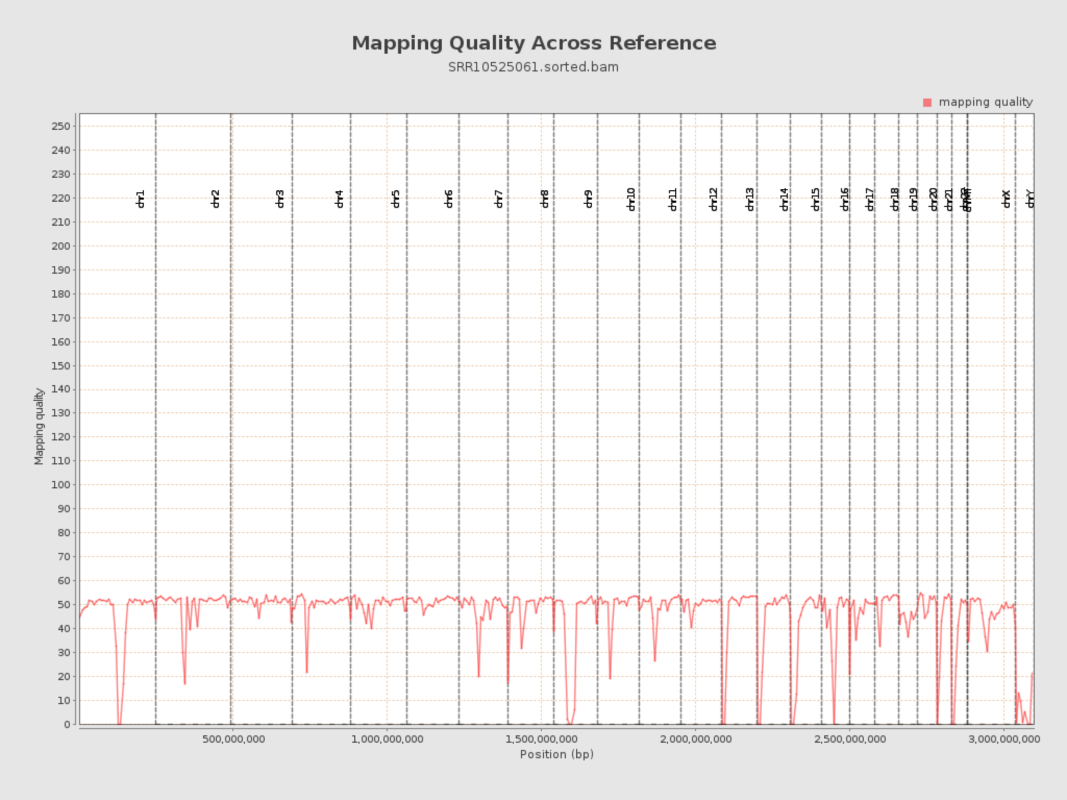
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram