Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 00:36:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525241.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_SRR10525241 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525241.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 00:36:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525241.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,582,064
Mapped reads	1,456,679 / 92.07%
Unmapped reads	125,385 / 7.93%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,413 / 0.34%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	49,960 / 3.16%
Duplication rate	2.52%
Clipped reads	1,460,353 / 92.31%

2.2. ACGT Content

Number/percentage of A's	20,433,110 / 24.09%
Number/percentage of C's	16,921,453 / 19.95%
Number/percentage of T's	27,676,194 / 32.63%
Number/percentage of G's	19,779,431 / 23.32%
Number/percentage of N's	1,801 / 0%
GC Percentage	43.27%

2.3. Coverage

Mean	0.0274

Standard Deviation	0.2677

2.4. Mapping Quality

Mean Mapping Quality	45

2.5. Mismatches and indels

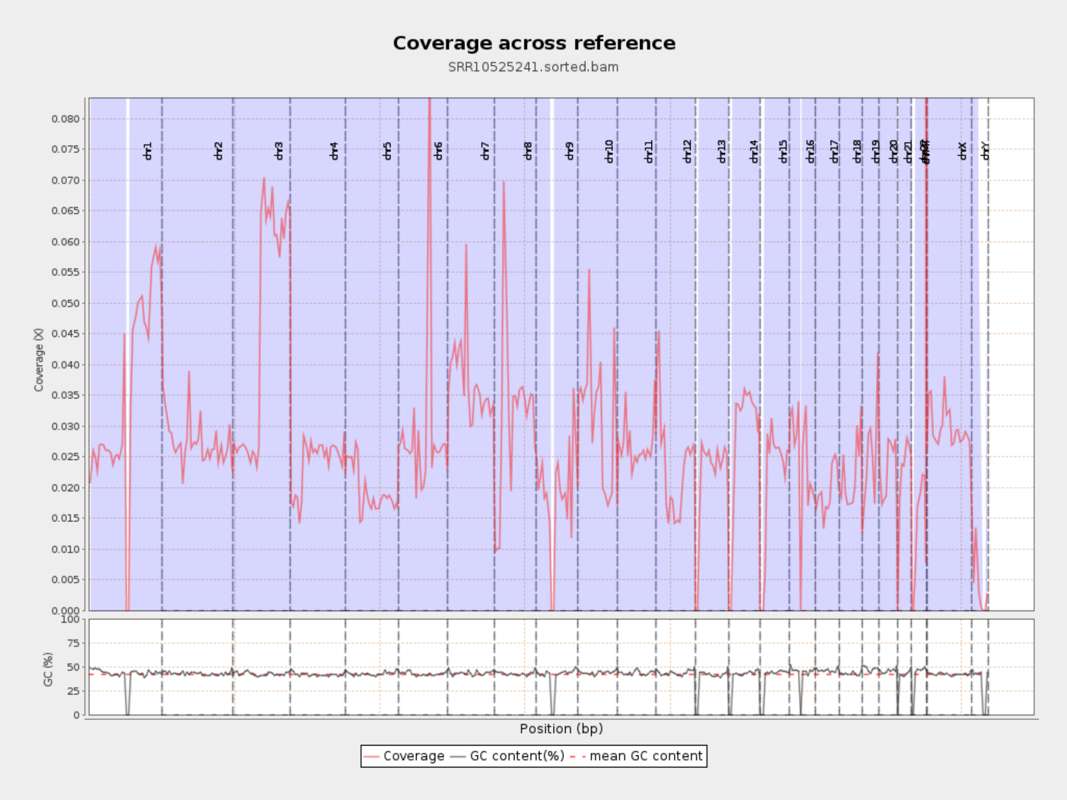
General error rate	0.5%
Mismatches	417,348
Insertions	5,275
Mapped reads with at least one insertion	0.36%
Deletions	17,092
Mapped reads with at least one deletion	1.17%
Homopolymer indels	44.78%

2.6. Chromosome stats

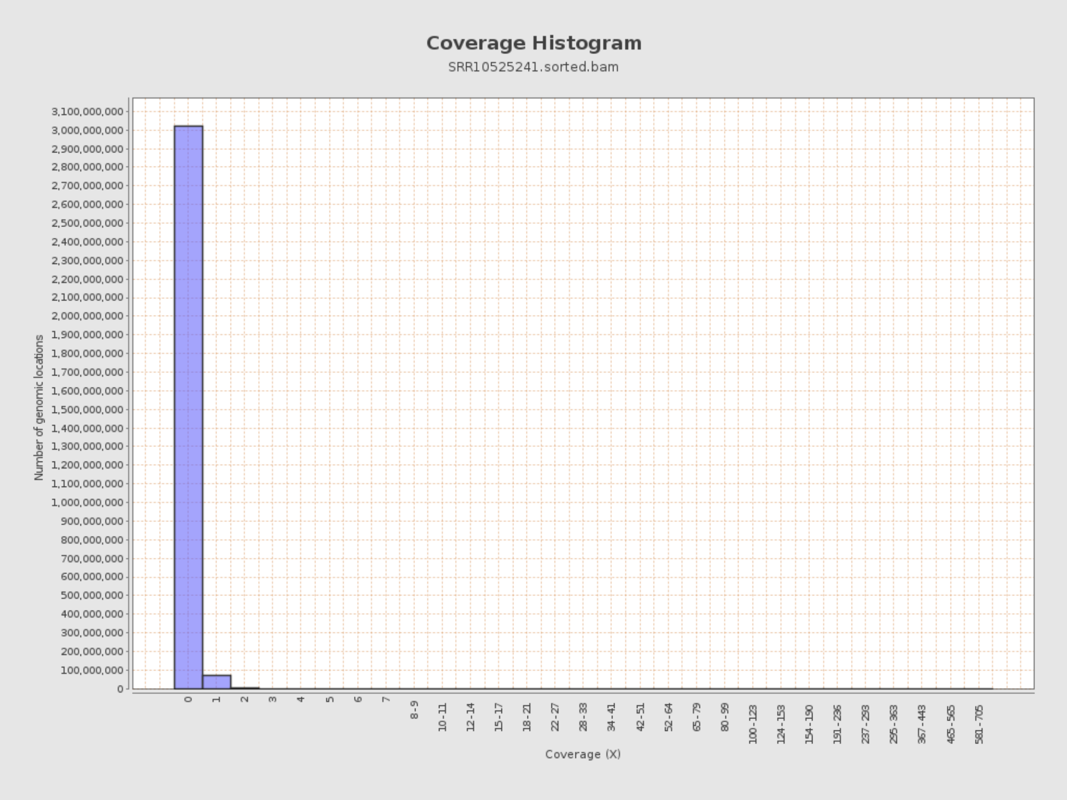
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8814840	0.0354	0.4731
chr2	243199373	6706842	0.0276	0.3415
chr3	198022430	9029428	0.0456	0.2325
chr4	191154276	4593081	0.024	0.1753
chr5	180915260	3530471	0.0195	0.151
chr6	171115067	5126775	0.03	0.2095
chr7	159138663	5964828	0.0375	0.4644

chr8	146364022	4630593	0.0316	0.2612
chr9	141213431	2681251	0.019	0.1851
chr10	135534747	4327862	0.0319	0.2731
chr11	135006516	3627737	0.0269	0.2182
chr12	133851895	3155227	0.0236	0.169
chr13	115169878	2488512	0.0216	0.1623
chr14	107349540	2985137	0.0278	0.1826
chr15	102531392	2162970	0.0211	0.1617
chr16	90354753	2160832	0.0239	0.1829
chr17	81195210	1570113	0.0193	0.1552
chr18	78077248	1706122	0.0219	0.3319
chr19	59128983	1500981	0.0254	0.3148
chr20	63025520	1450109	0.023	0.1662
chr21	48129895	1054369	0.0219	0.1688
chr22	51304566	687944	0.0134	0.1238
chrMT	16571	21127	1.2749	1.4657
chrX	155270560	4612811	0.0297	0.2004
chrY	59373566	249669	0.0042	0.1199

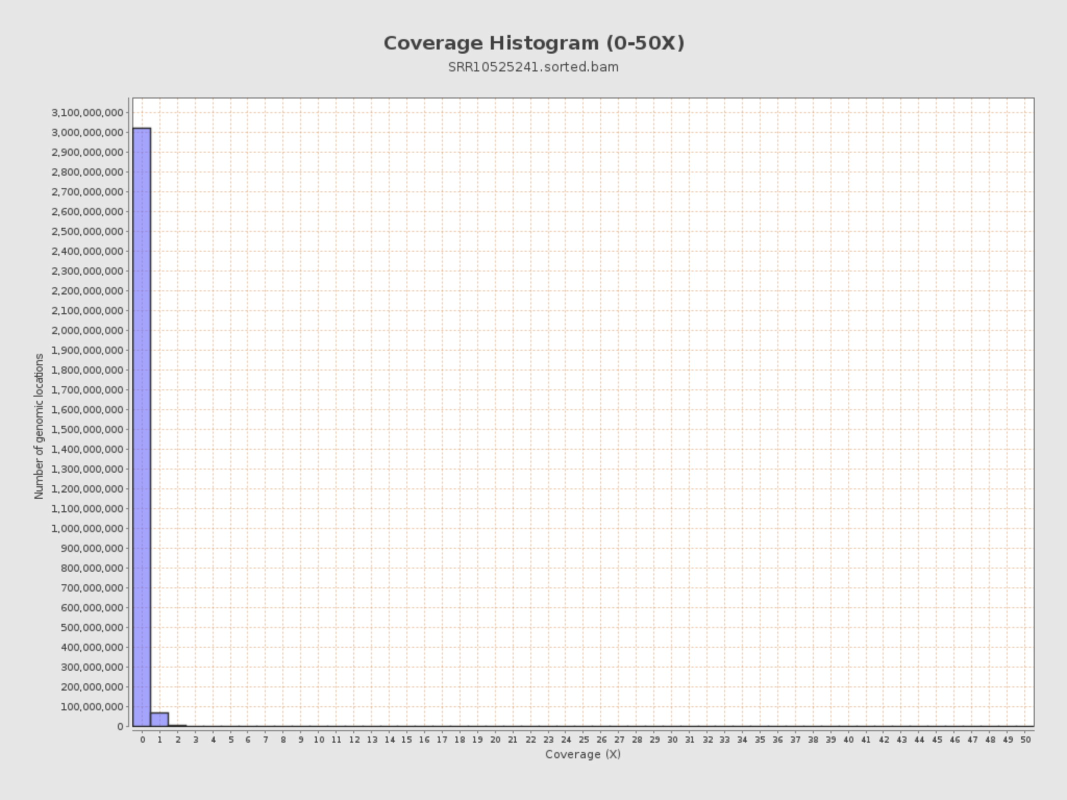
3. Results : Coverage across reference



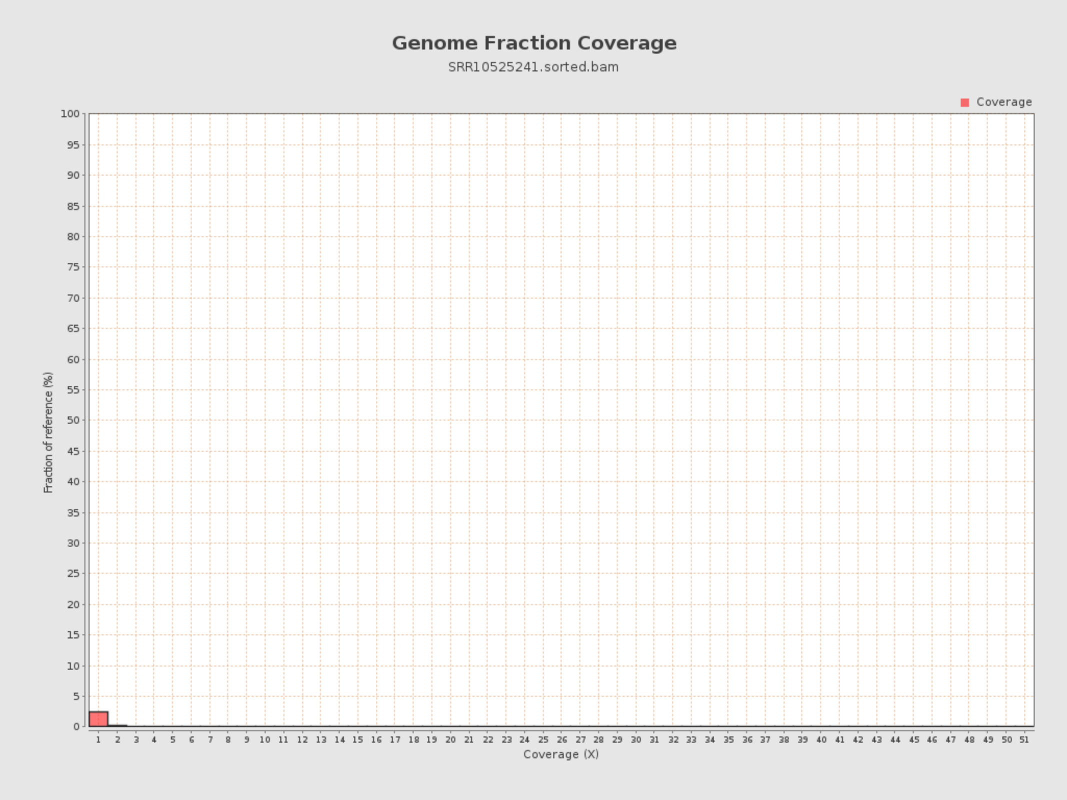
4. Results : Coverage Histogram



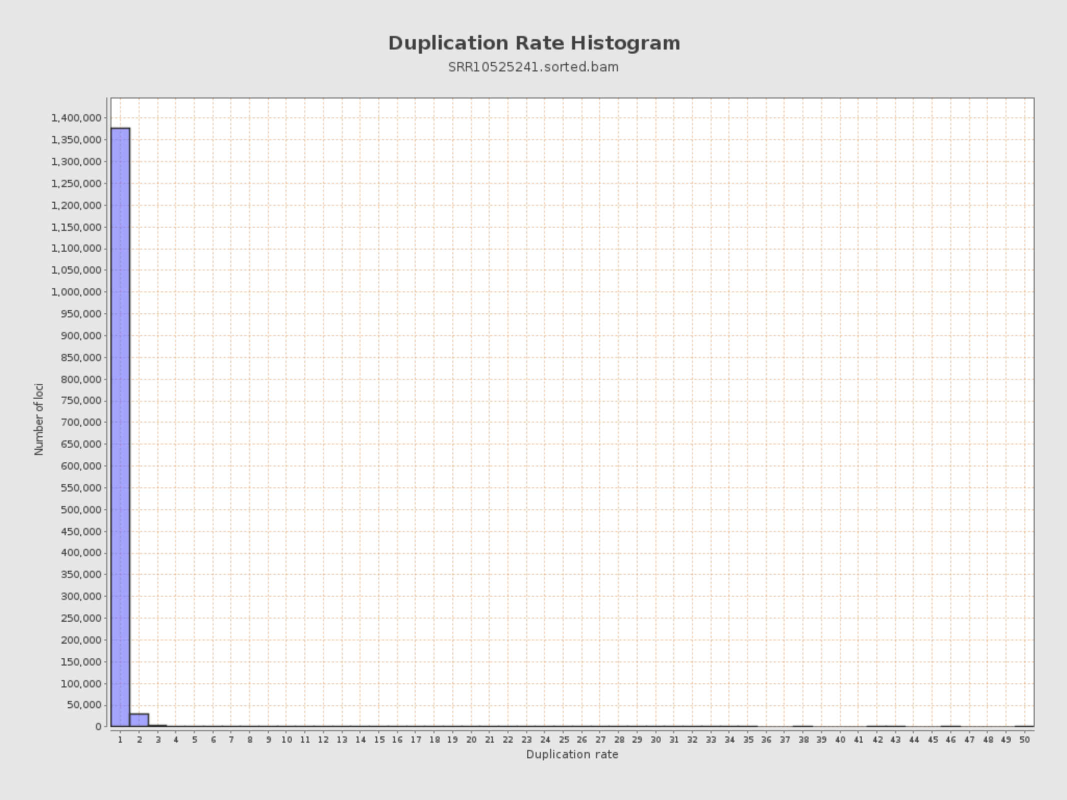
5. Results : Coverage Histogram (0-50X)



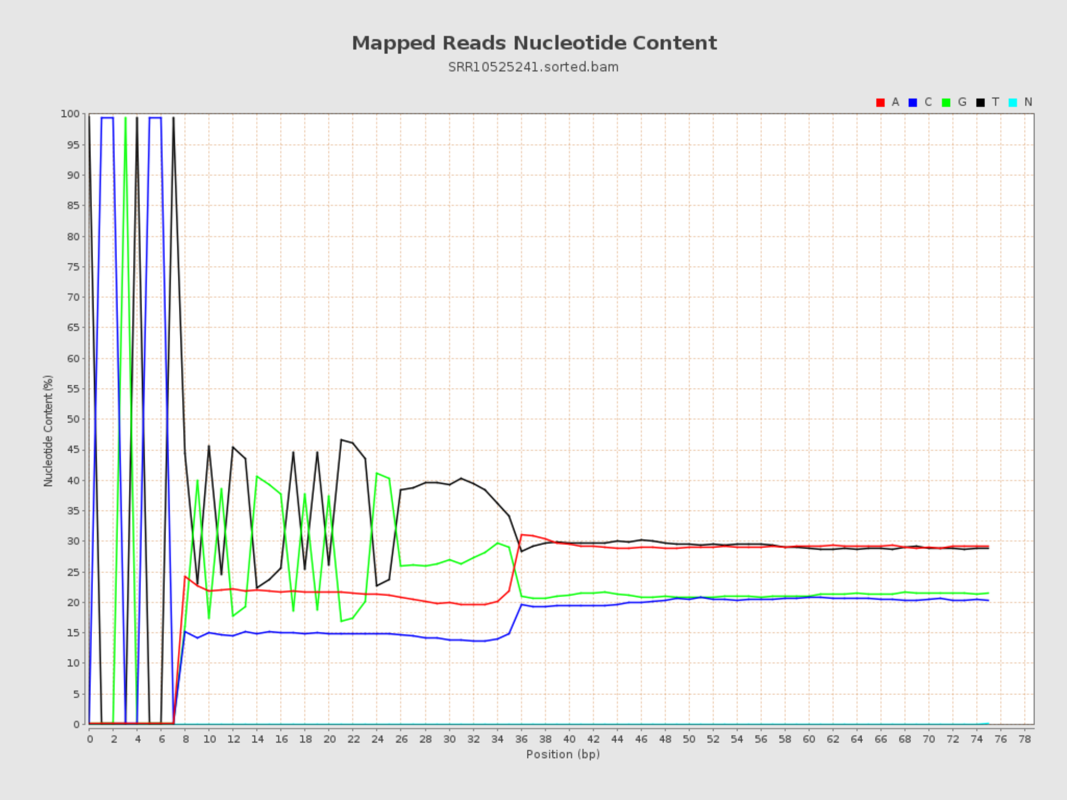
6. Results : Genome Fraction Coverage



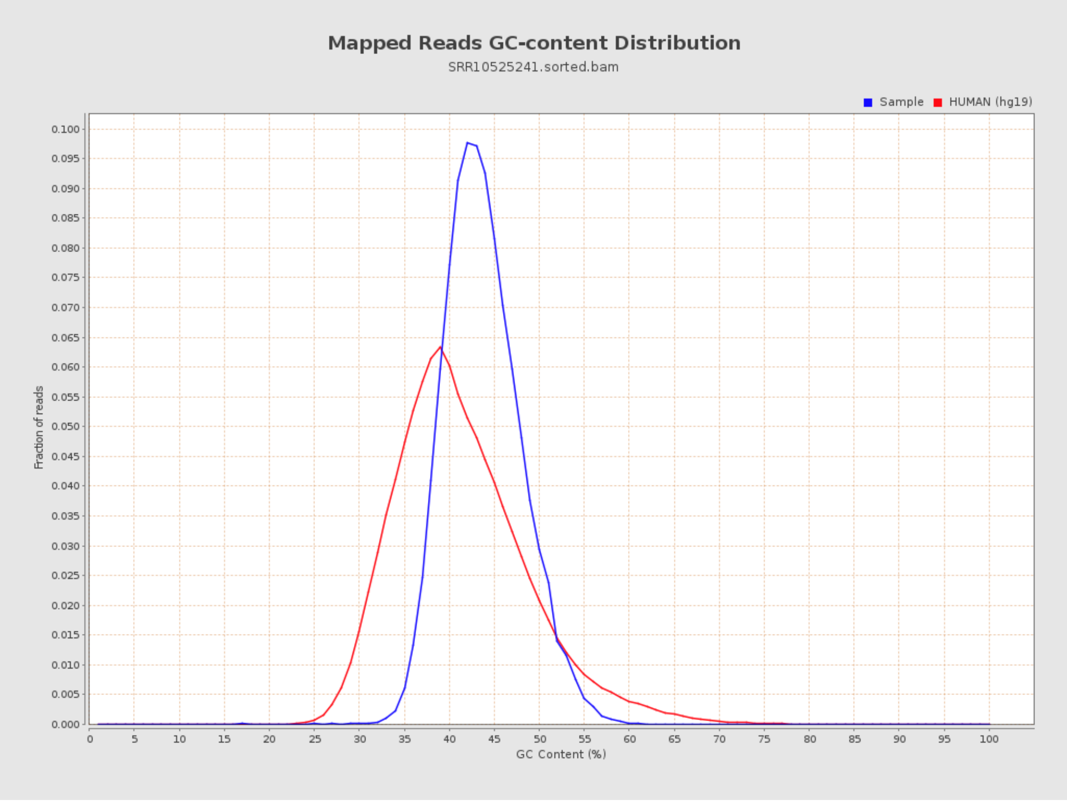
7. Results : Duplication Rate Histogram



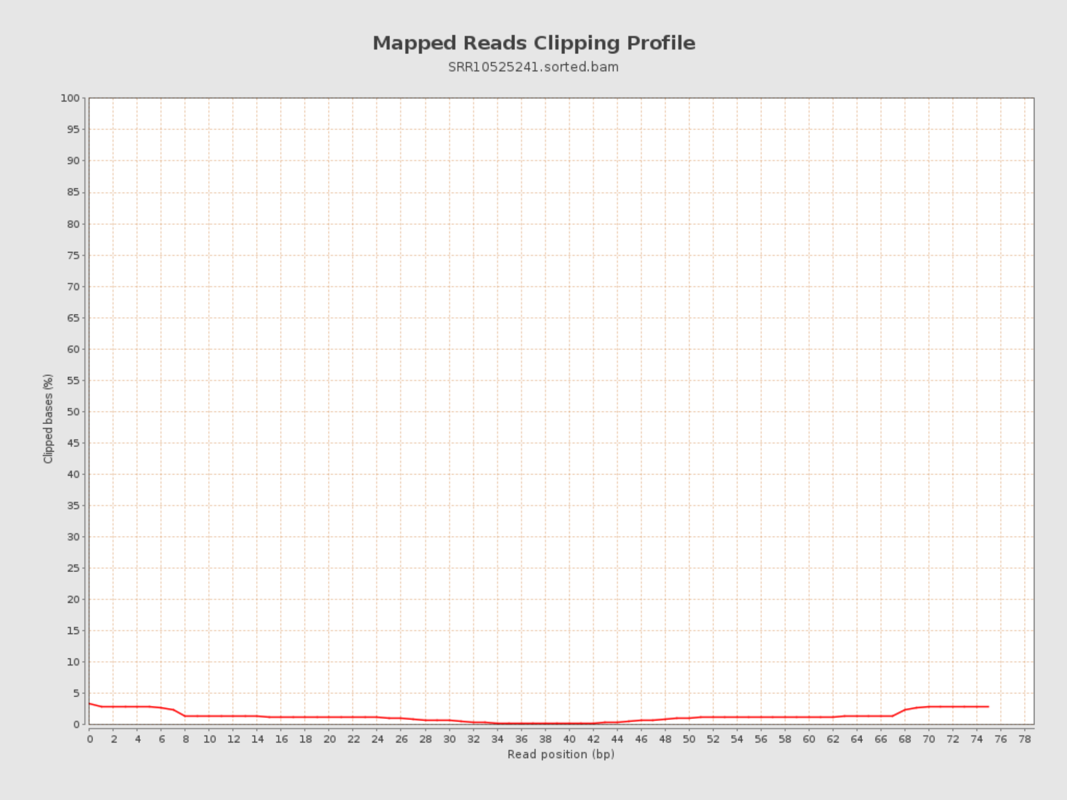
8. Results : Mapped Reads Nucleotide Content



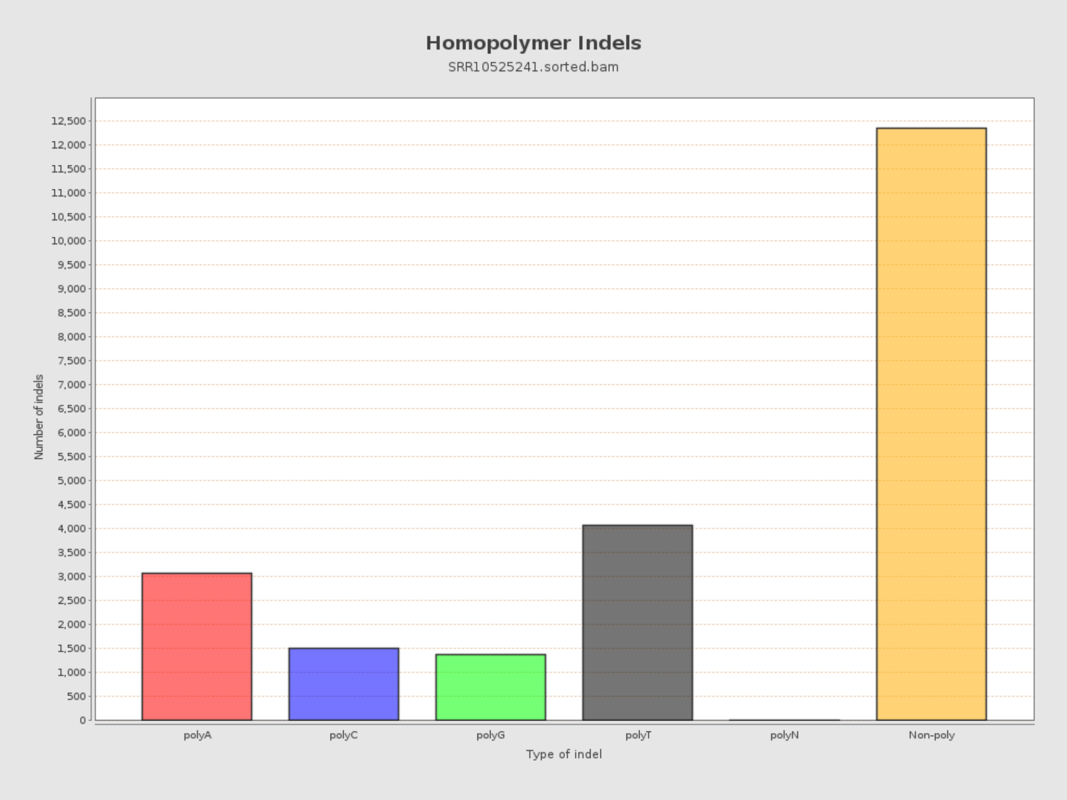
9. Results : Mapped Reads GC-content Distribution



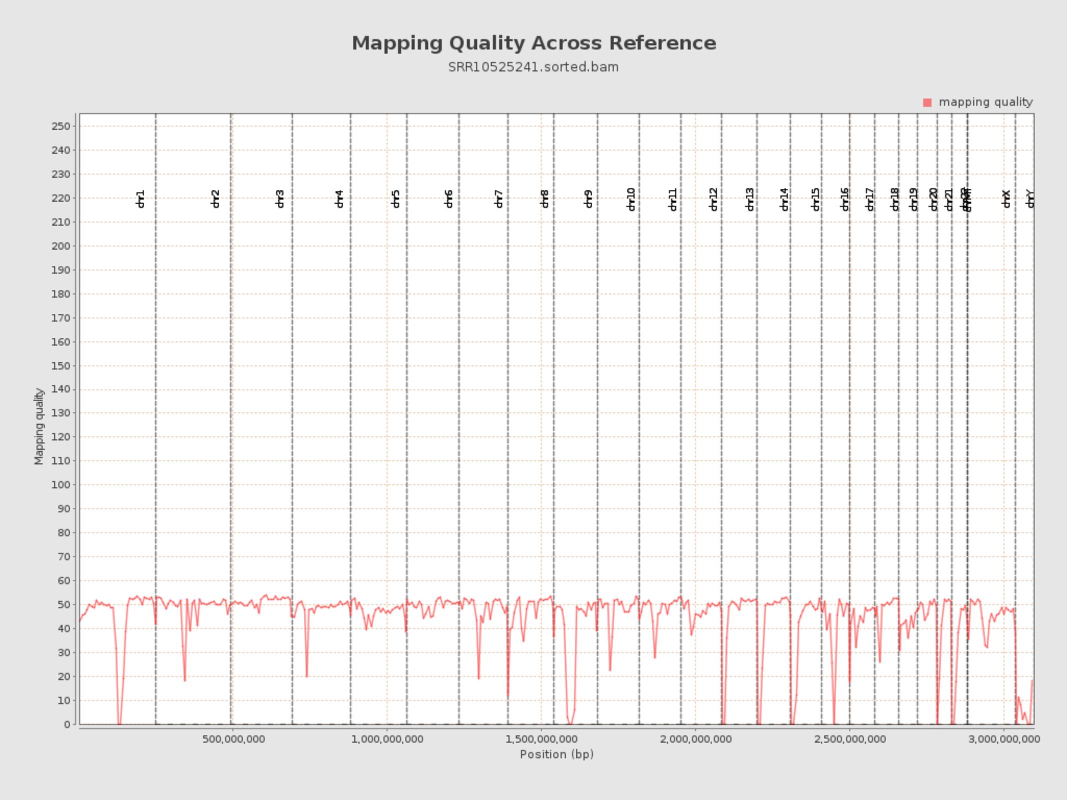
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram