Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 18:51:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525121.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_SRR10525121 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525121.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 18:51:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525121.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	839,471
Mapped reads	735,273 / 87.59%
Unmapped reads	104,198 / 12.41%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,185 / 2.76%
Read min/max/mean length	30 / 101 / 102.02
Duplicated reads (estimated)	16,505 / 1.97%
Duplication rate	1.35%
Clipped reads	758,170 / 90.32%

2.2. ACGT Content

Number/percentage of A's	14,724,882 / 26.24%
Number/percentage of C's	10,871,564 / 19.37%
Number/percentage of T's	16,755,303 / 29.86%
Number/percentage of G's	13,762,409 / 24.52%
Number/percentage of N's	2,124 / 0%
GC Percentage	43.9%

2.3. Coverage

Mean	0.0181

Standard Deviation	0.2135

2.4. Mapping Quality

Mean Mapping Quality	45.08

2.5. Mismatches and indels

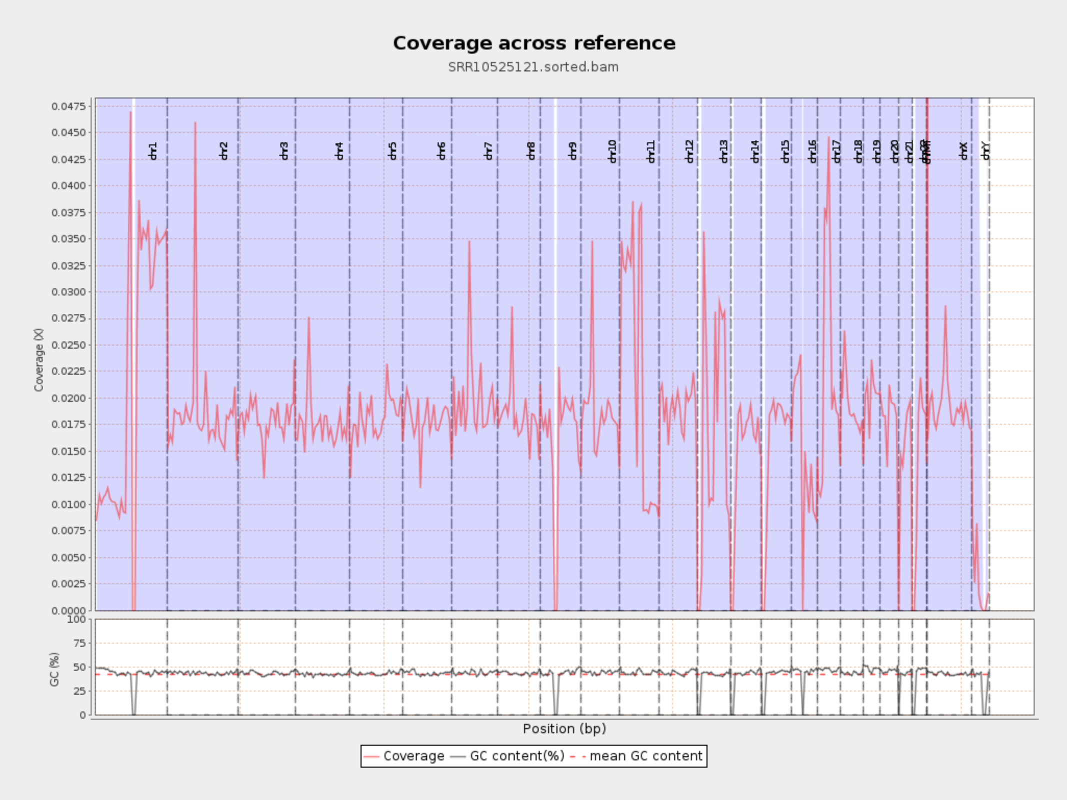
General error rate	0.73%
Mismatches	401,798
Insertions	4,951
Mapped reads with at least one insertion	0.66%
Deletions	12,946
Mapped reads with at least one deletion	1.73%
Homopolymer indels	42.7%

2.6. Chromosome stats

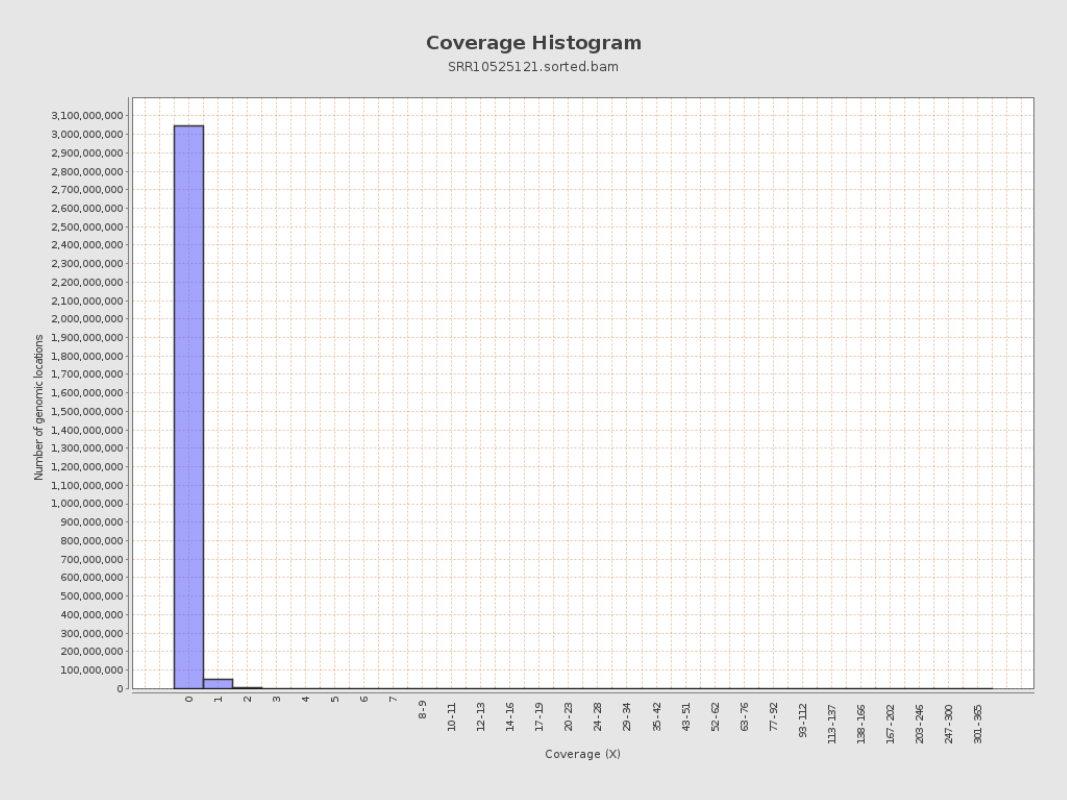
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5409908	0.0217	0.3518
chr2	243199373	4532998	0.0186	0.2971
chr3	198022430	3557963	0.018	0.1406
chr4	191154276	3395793	0.0178	0.1488
chr5	180915260	3311945	0.0183	0.1422
chr6	171115067	3060316	0.0179	0.151
chr7	159138663	3176762	0.02	0.2863

chr8	146364022	2687970	0.0184	0.2504
chr9	141213431	2274609	0.0161	0.19
chr10	135534747	2574532	0.019	0.2179
chr11	135006516	3044639	0.0226	0.2331
chr12	133851895	2567955	0.0192	0.1459
chr13	115169878	1881252	0.0163	0.1347
chr14	107349540	1560925	0.0145	0.1345
chr15	102531392	1552707	0.0151	0.1291
chr16	90354753	1299183	0.0144	0.1343
chr17	81195210	1836575	0.0226	0.1801
chr18	78077248	1515443	0.0194	0.3004
chr19	59128983	1196417	0.0202	0.2668
chr20	63025520	1139941	0.0181	0.1449
chr21	48129895	714298	0.0148	0.1365
chr22	51304566	681988	0.0133	0.121
chrMT	16571	5462	0.3296	0.6432
chrX	155270560	3007881	0.0194	0.1711
chrY	59373566	151454	0.0026	0.0766

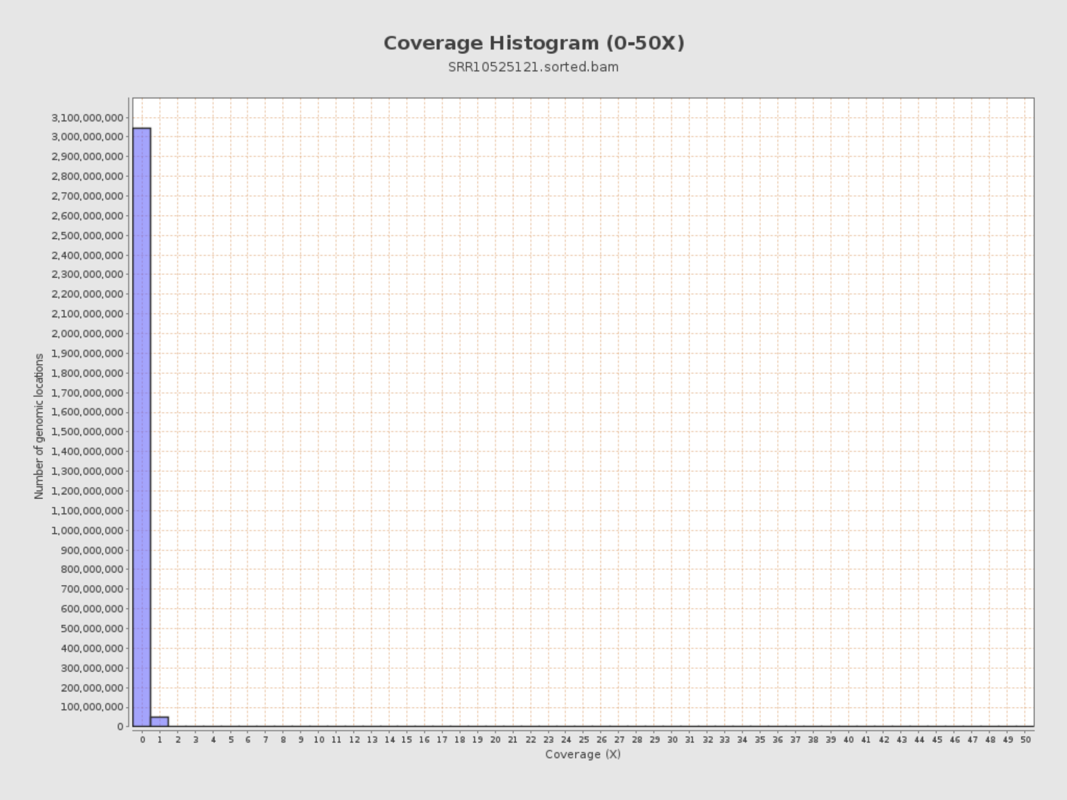
3. Results : Coverage across reference



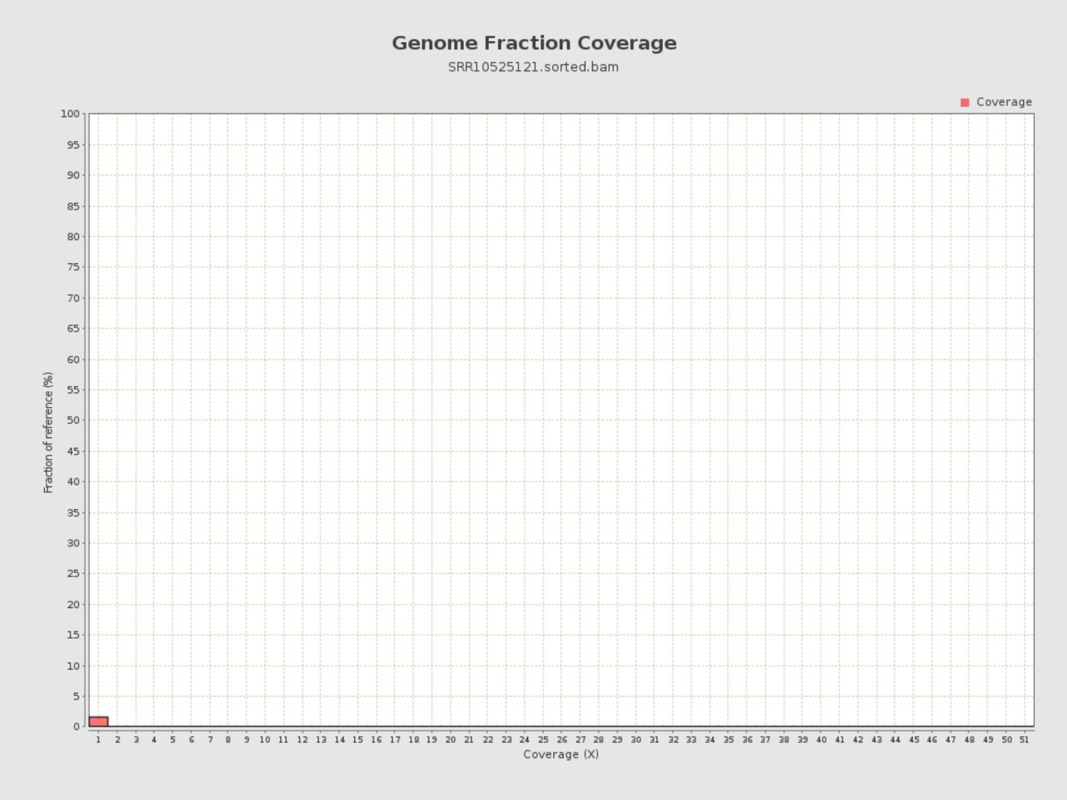
4. Results : Coverage Histogram



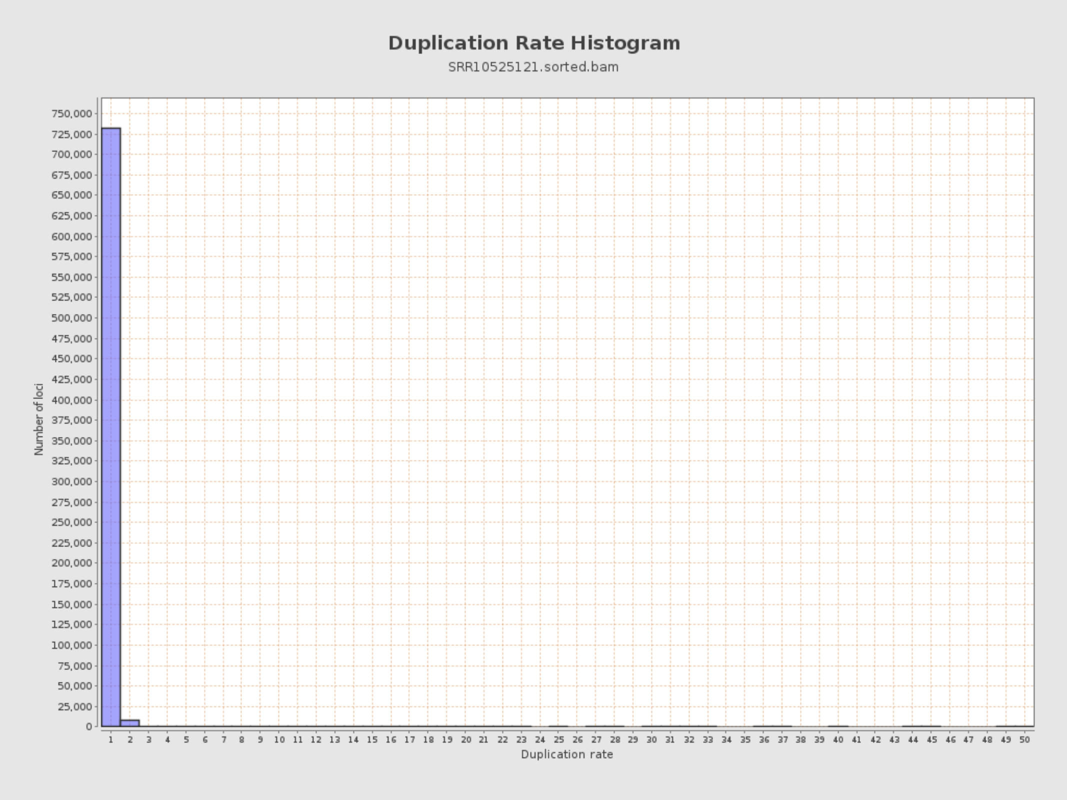
5. Results : Coverage Histogram (0-50X)



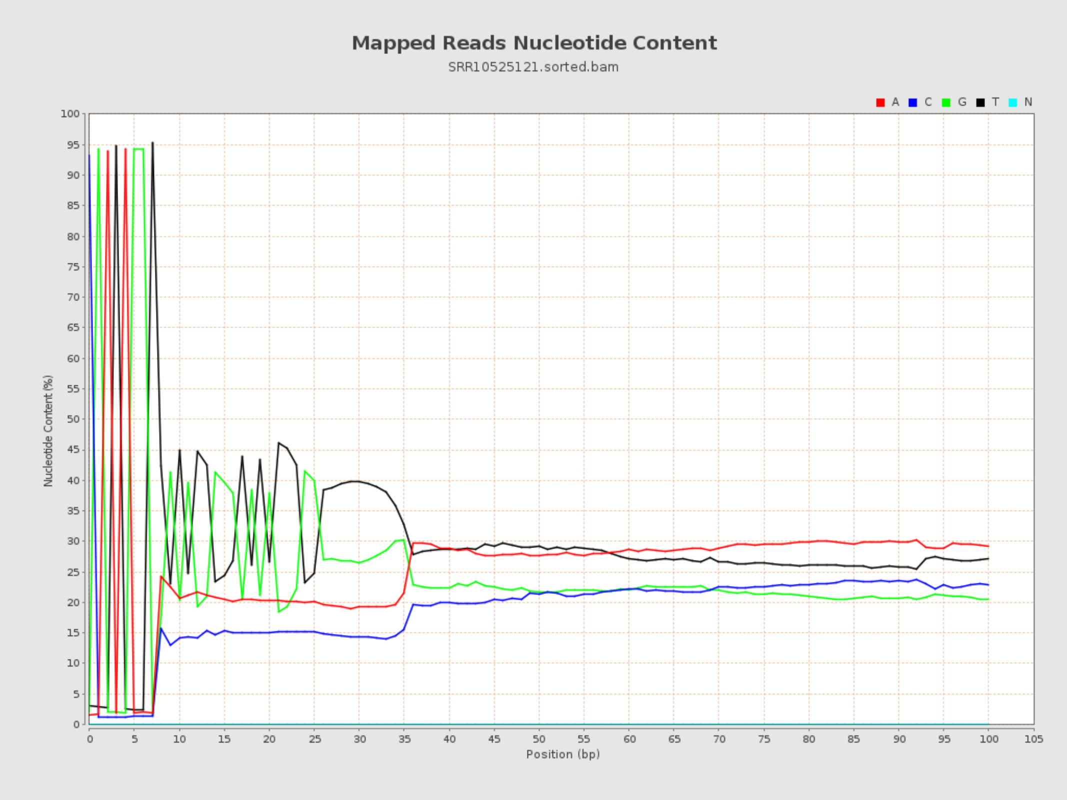
6. Results : Genome Fraction Coverage



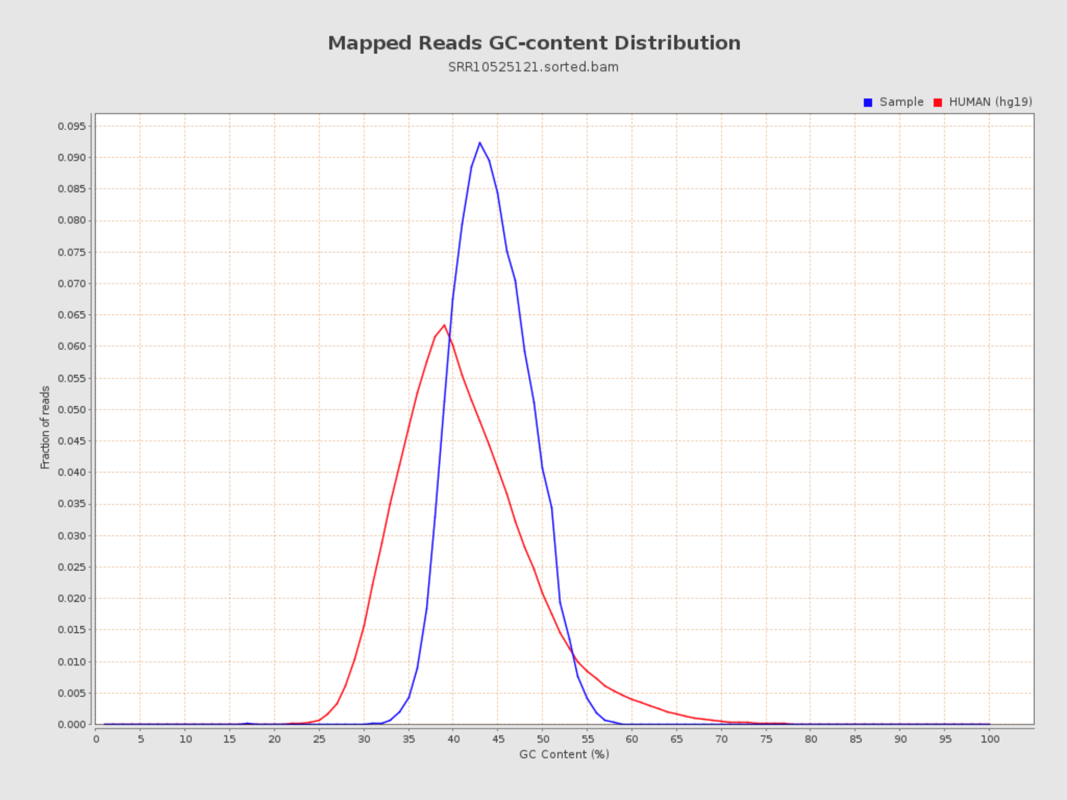
7. Results : Duplication Rate Histogram



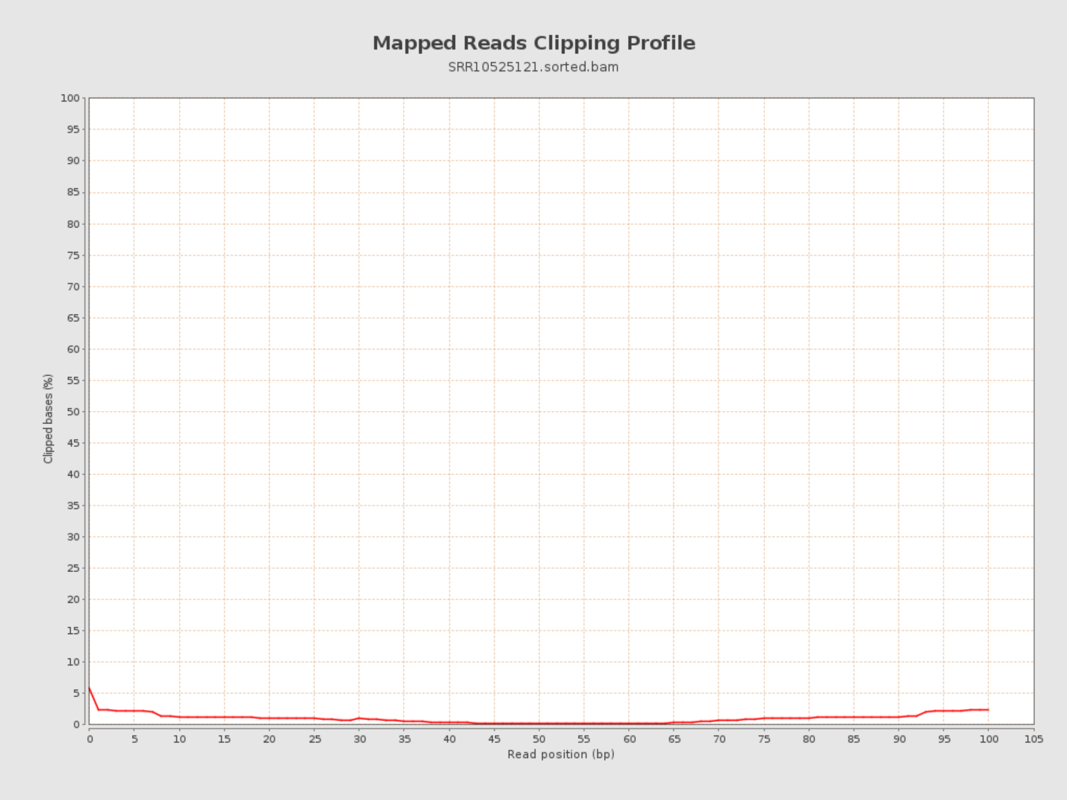
8. Results : Mapped Reads Nucleotide Content



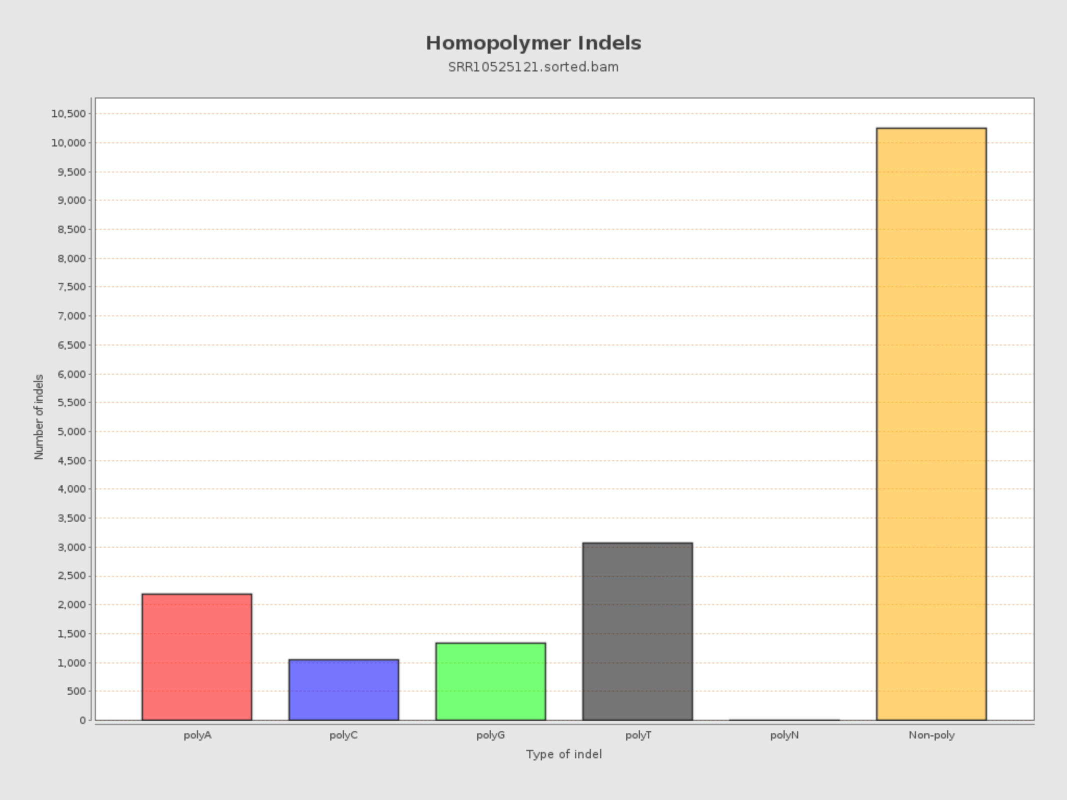
9. Results : Mapped Reads GC-content Distribution



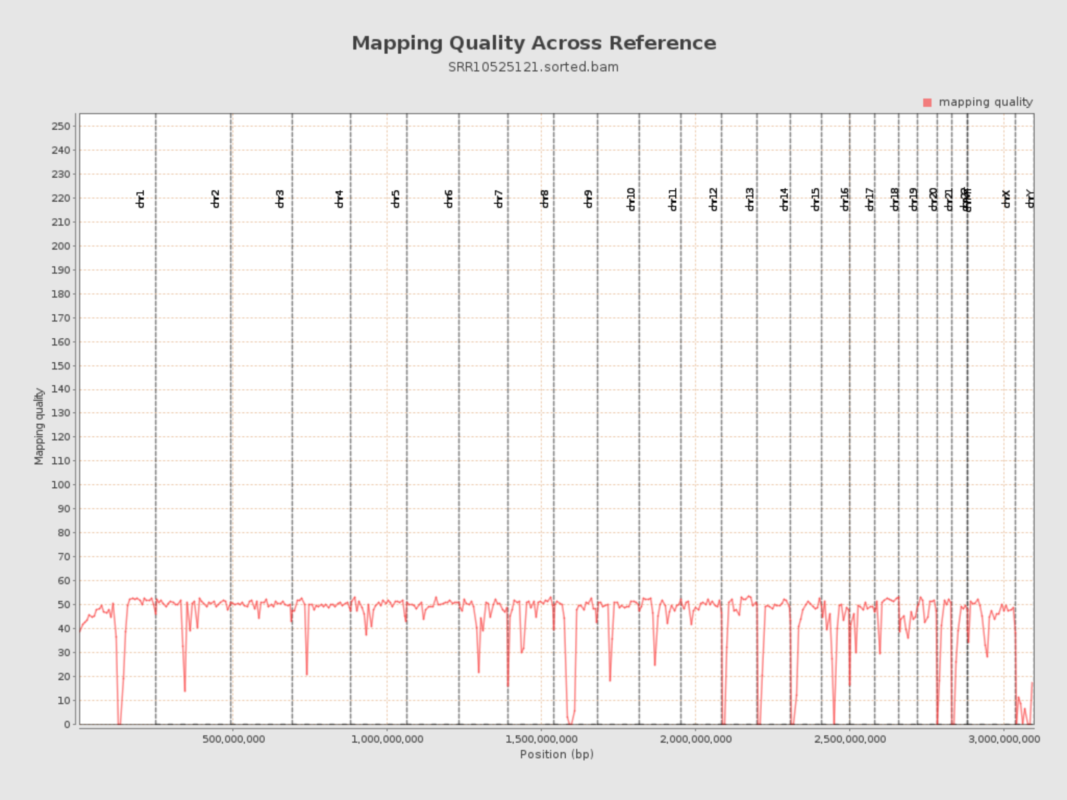
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram