Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 23:13:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525208.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_SRR10525208 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525208.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 23:13:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525208.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,196,028
Mapped reads	1,088,388 / 91%
Unmapped reads	107,640 / 9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,341 / 0.28%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	29,114 / 2.43%
Duplication rate	1.81%
Clipped reads	1,088,997 / 91.05%

2.2. ACGT Content

Number/percentage of A's	16,667,223 / 26.05%
Number/percentage of C's	11,944,049 / 18.67%
Number/percentage of T's	20,451,088 / 31.97%
Number/percentage of G's	14,914,191 / 23.31%
Number/percentage of N's	1,462 / 0%
GC Percentage	41.98%

2.3. Coverage

Mean	0.0207

Standard Deviation	0.2318

2.4. Mapping Quality

Mean Mapping Quality	45.01

2.5. Mismatches and indels

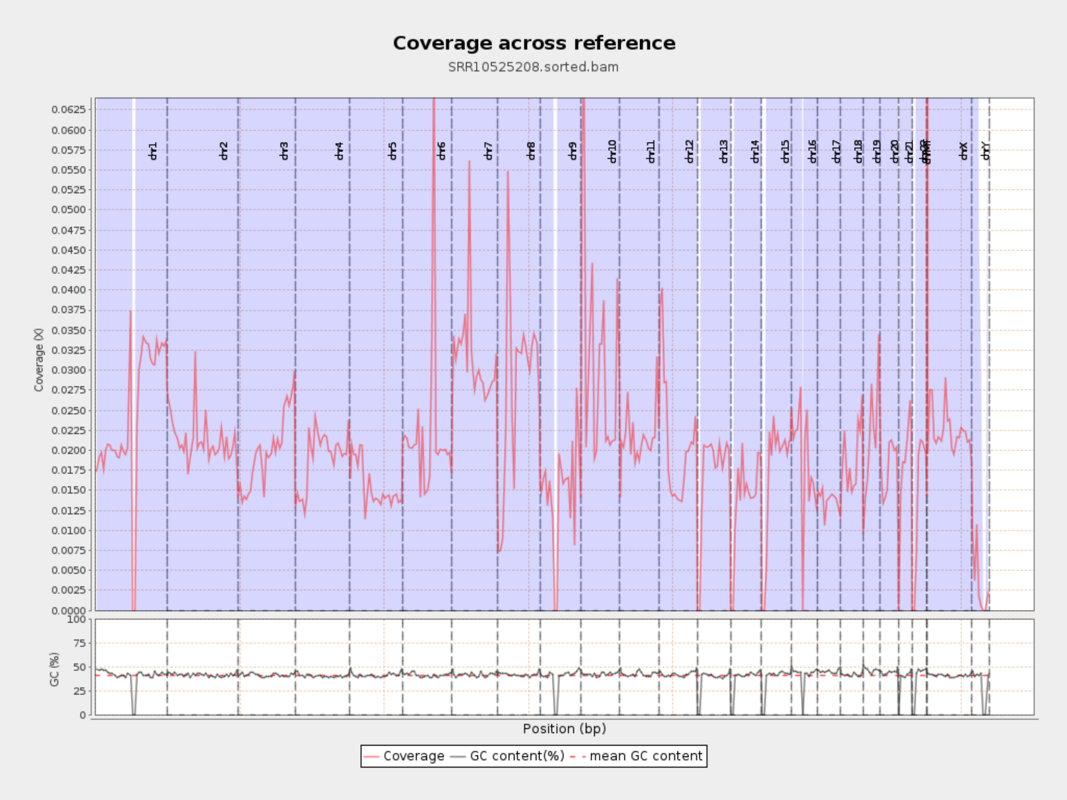
General error rate	0.52%
Mismatches	323,866
Insertions	4,866
Mapped reads with at least one insertion	0.45%
Deletions	13,474
Mapped reads with at least one deletion	1.23%
Homopolymer indels	43.13%

2.6. Chromosome stats

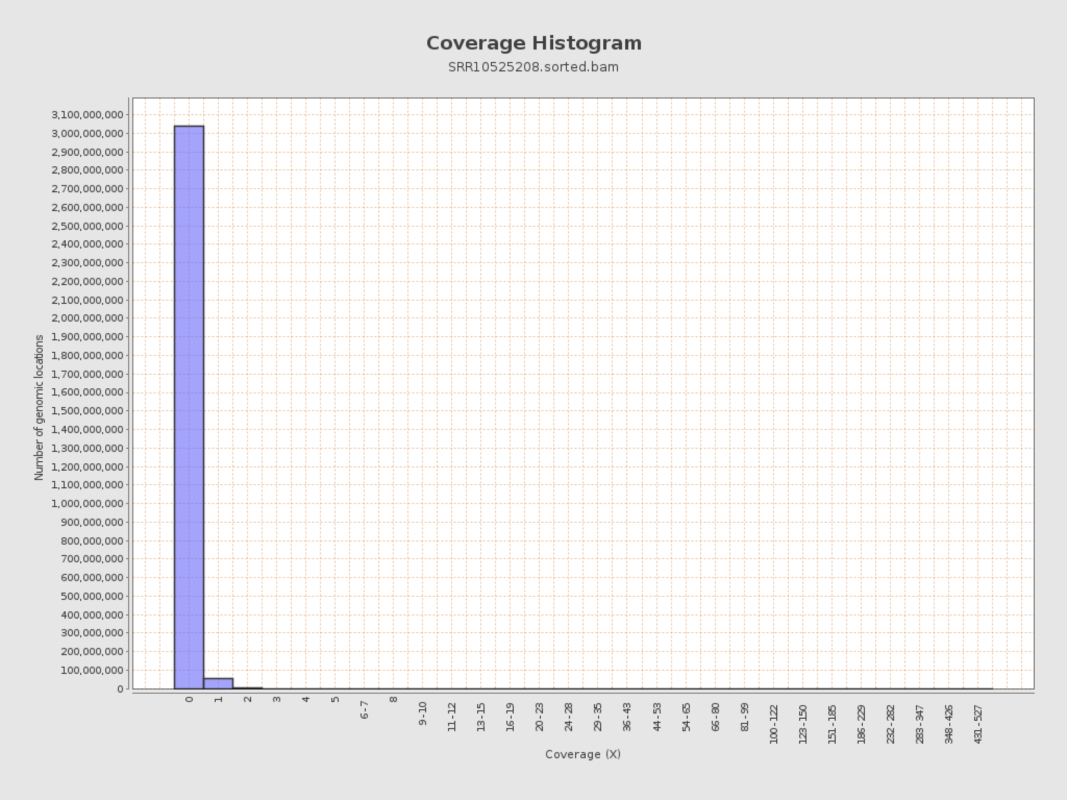
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6050503	0.0243	0.4145
chr2	243199373	5174007	0.0213	0.268
chr3	198022430	3897912	0.0197	0.1502
chr4	191154276	3657759	0.0191	0.1527
chr5	180915260	2809542	0.0155	0.1328
chr6	171115067	3860376	0.0226	0.1734
chr7	159138663	5052042	0.0317	0.446

chr8	146364022	4122795	0.0282	0.2171
chr9	141213431	2085013	0.0148	0.1615
chr10	135534747	4298957	0.0317	0.251
chr11	135006516	2912874	0.0216	0.1815
chr12	133851895	2827945	0.0211	0.1549
chr13	115169878	1961541	0.017	0.1389
chr14	107349540	1487626	0.0139	0.1296
chr15	102531392	1733149	0.0169	0.1398
chr16	90354753	1674252	0.0185	0.1584
chr17	81195210	1114753	0.0137	0.1268
chr18	78077248	1465246	0.0188	0.2885
chr19	59128983	1295516	0.0219	0.293
chr20	63025520	1116480	0.0177	0.1414
chr21	48129895	878193	0.0182	0.147
chr22	51304566	711844	0.0139	0.1259
chrMT	16571	106738	6.4413	3.9639
chrX	155270560	3505842	0.0226	0.1697
chrY	59373566	198729	0.0033	0.0988

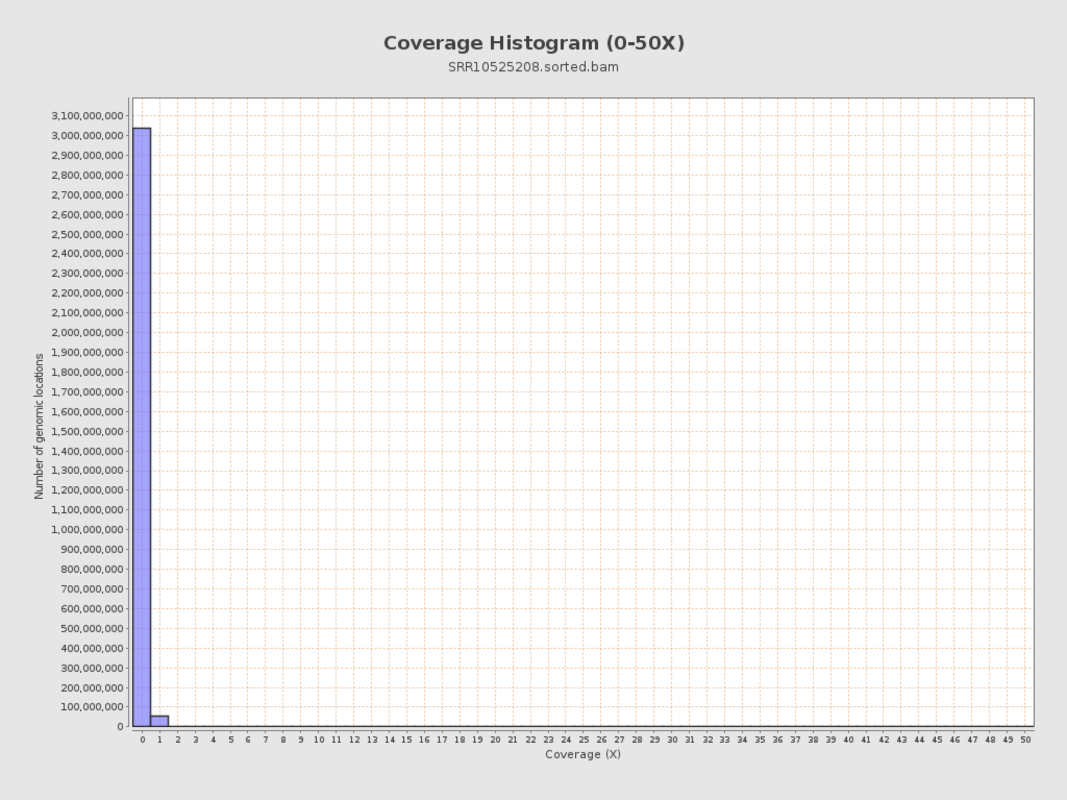
3. Results : Coverage across reference



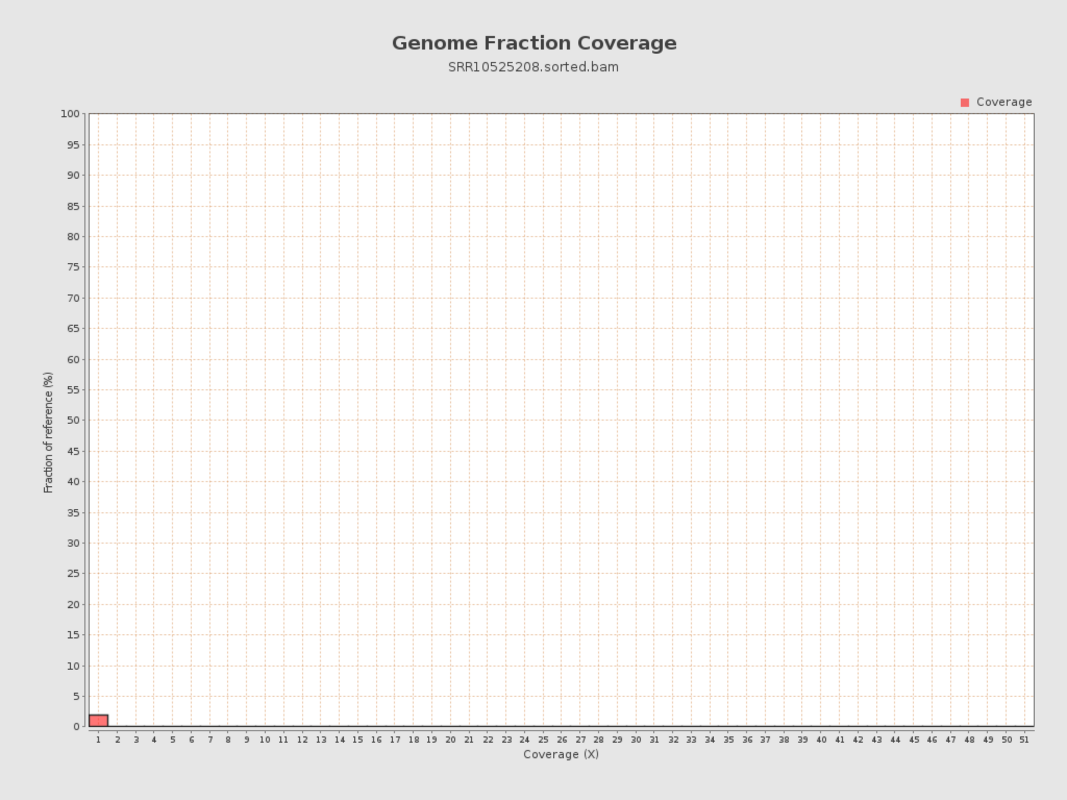
4. Results : Coverage Histogram



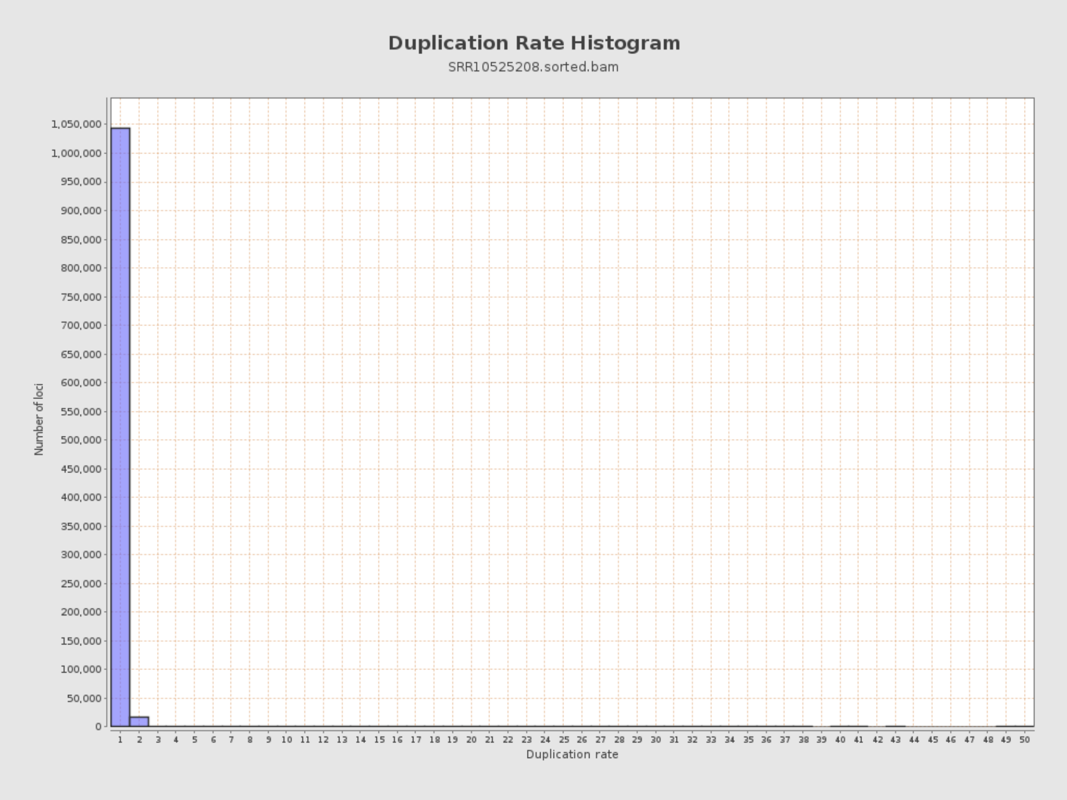
5. Results : Coverage Histogram (0-50X)



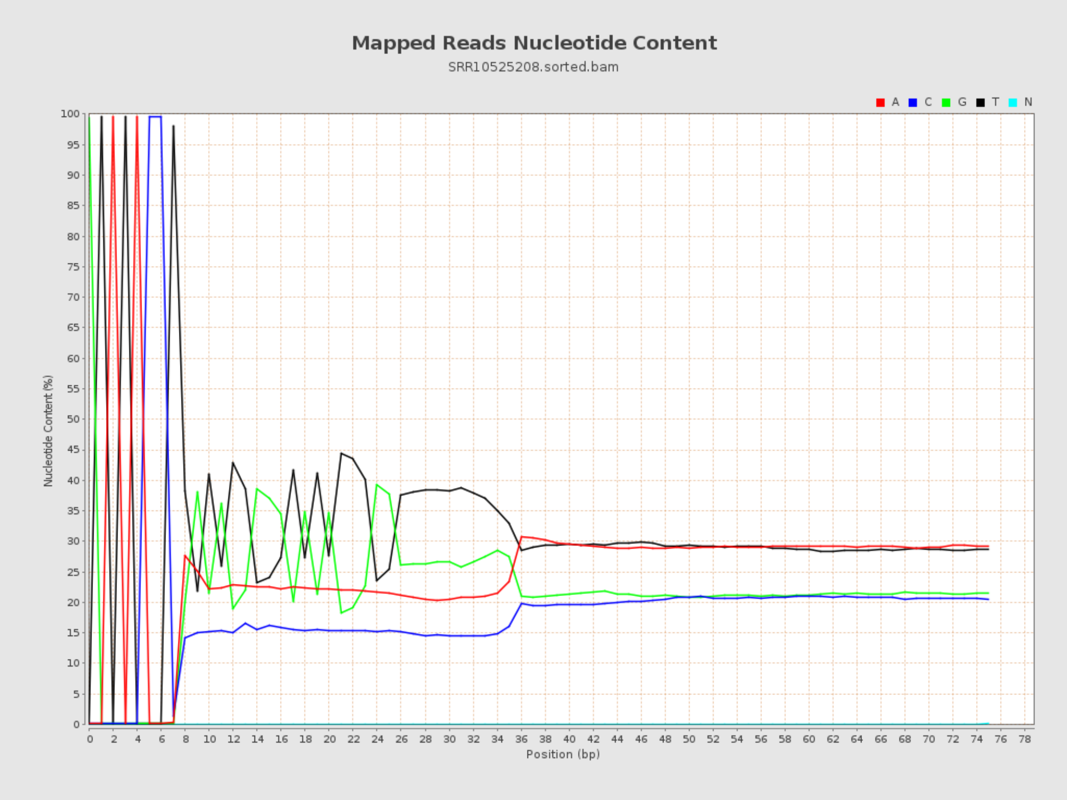
6. Results : Genome Fraction Coverage



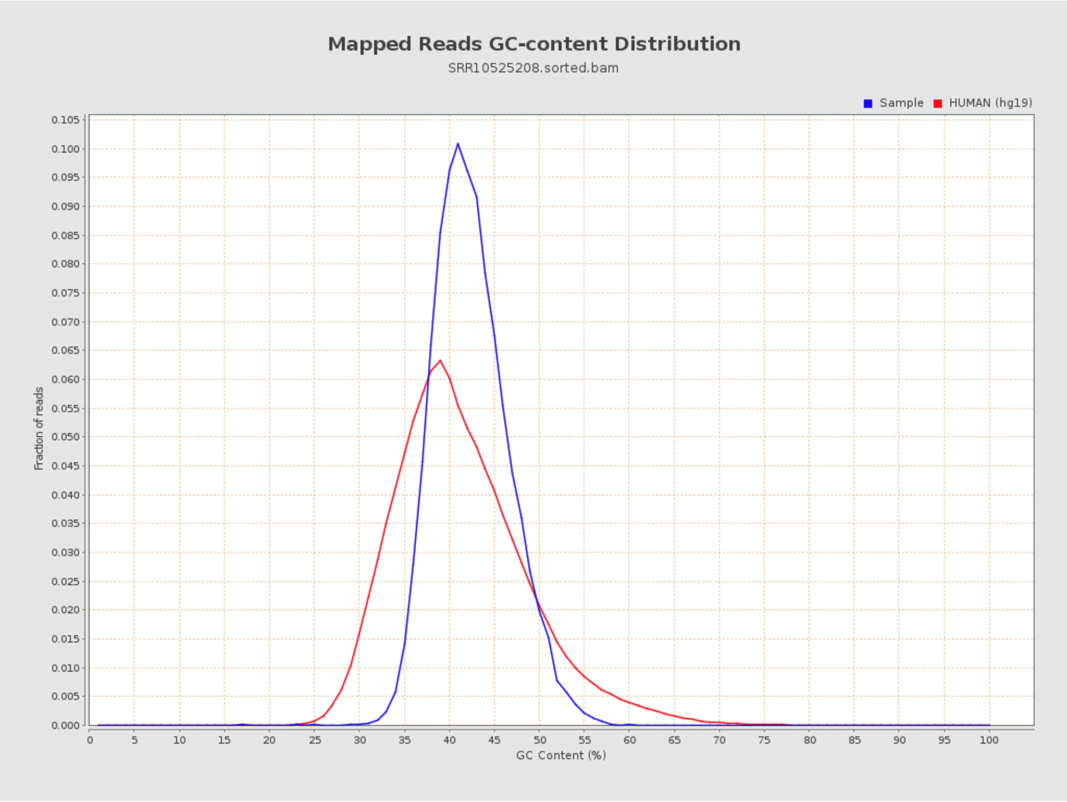
7. Results : Duplication Rate Histogram



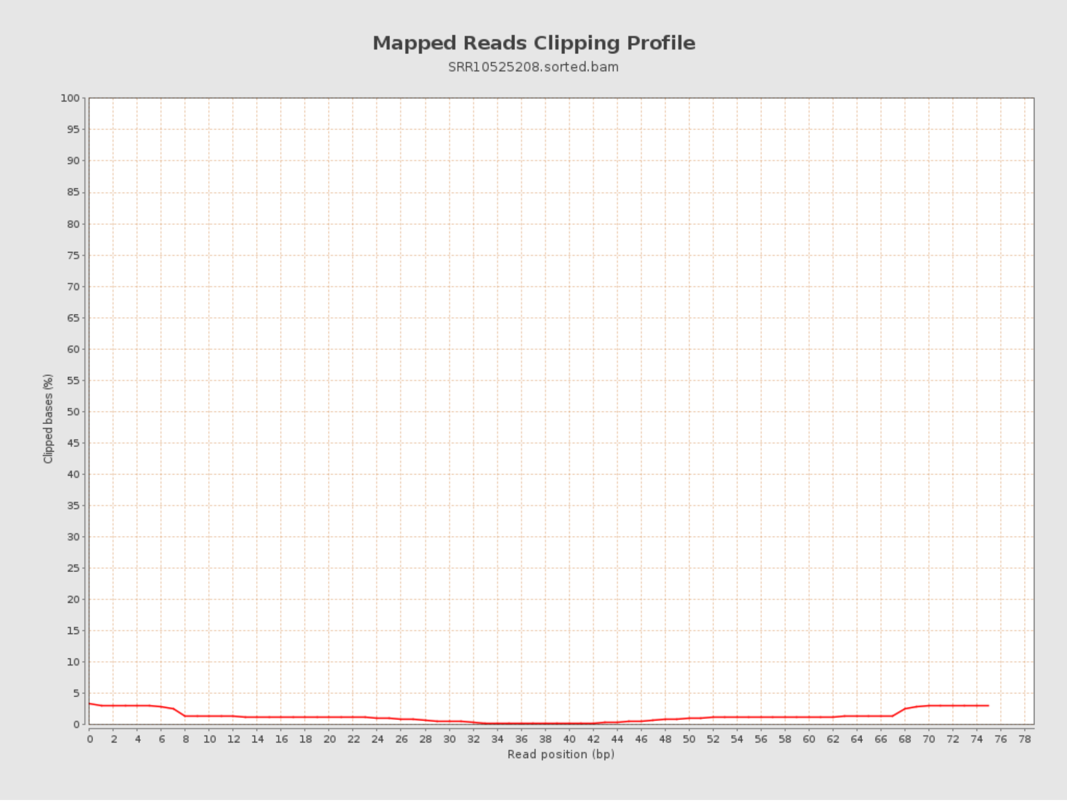
8. Results : Mapped Reads Nucleotide Content



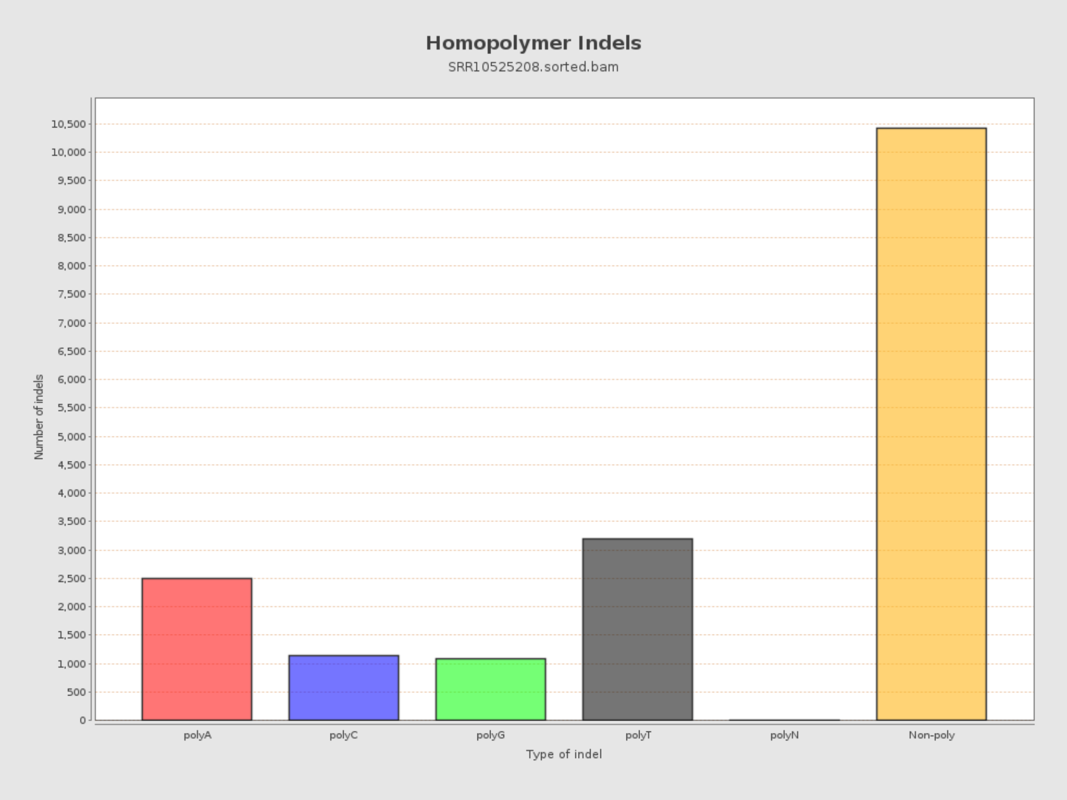
9. Results : Mapped Reads GC-content Distribution



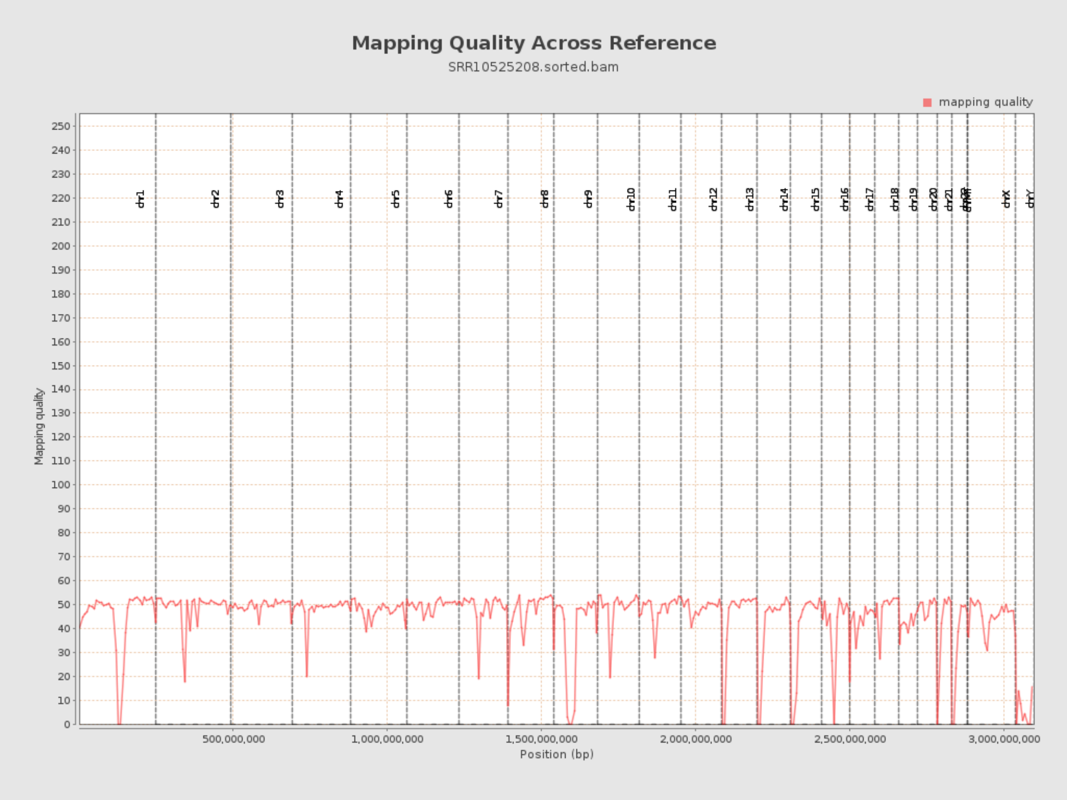
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram