Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 23:10:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525207.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_SRR10525207 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525207.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 23:10:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525207.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	768,615
Mapped reads	725,410 / 94.38%
Unmapped reads	43,205 / 5.62%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,715 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	13,653 / 1.78%
Duplication rate	1.3%
Clipped reads	725,259 / 94.36%

2.2. ACGT Content

Number/percentage of A's	12,338,869 / 27.35%
Number/percentage of C's	9,381,747 / 20.8%
Number/percentage of T's	13,359,620 / 29.61%
Number/percentage of G's	10,031,854 / 22.24%
Number/percentage of N's	1,066 / 0%
GC Percentage	43.03%

2.3. Coverage

Mean	0.0146

Standard Deviation	0.1712

2.4. Mapping Quality

Mean Mapping Quality	46.31

2.5. Mismatches and indels

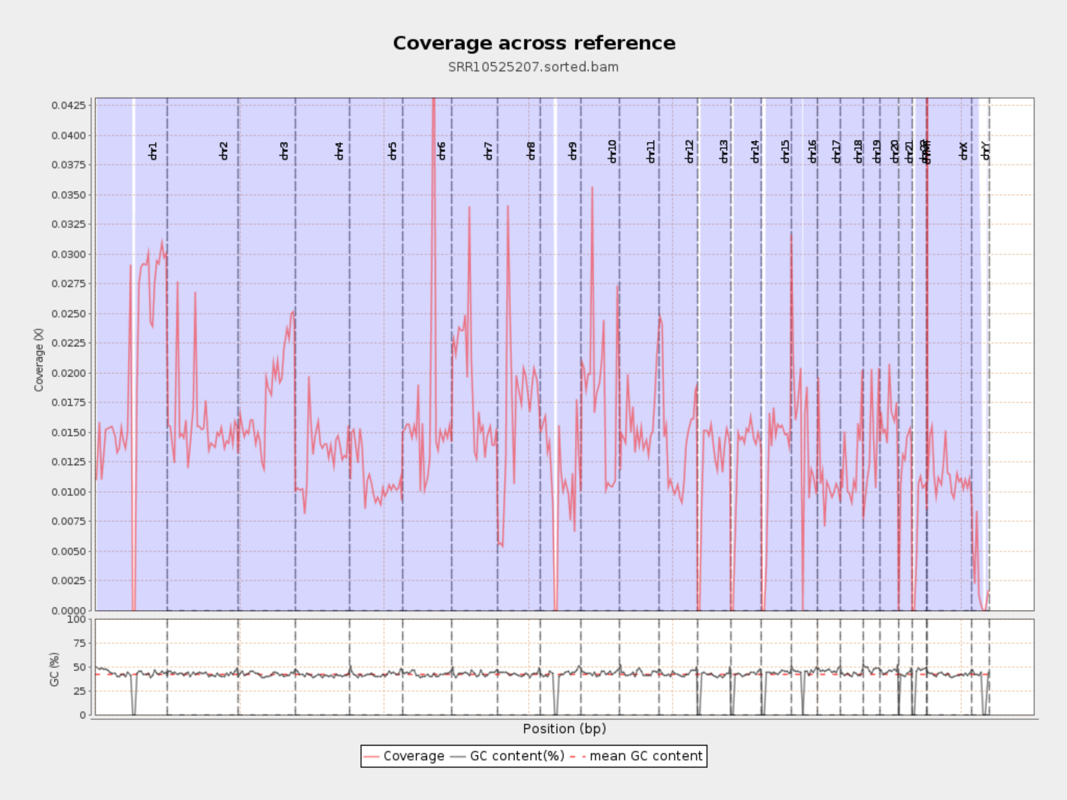
General error rate	0.5%
Mismatches	218,509
Insertions	3,264
Mapped reads with at least one insertion	0.45%
Deletions	9,785
Mapped reads with at least one deletion	1.34%
Homopolymer indels	43.54%

2.6. Chromosome stats

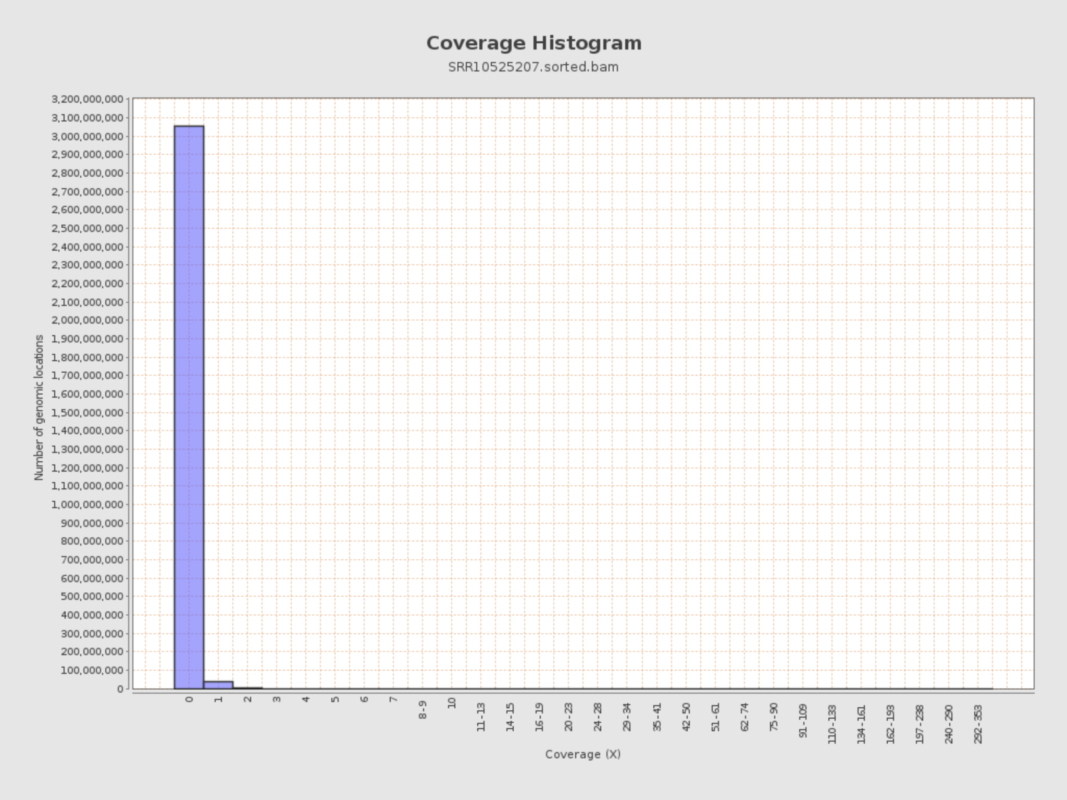
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4910578	0.0197	0.3112
chr2	243199373	3778959	0.0155	0.1748
chr3	198022430	3572952	0.018	0.1395
chr4	191154276	2529458	0.0132	0.1253
chr5	180915260	2022048	0.0112	0.1099
chr6	171115067	2890221	0.0169	0.1431
chr7	159138663	2995874	0.0188	0.2801

chr8	146364022	2488379	0.017	0.1599
chr9	141213431	1565052	0.0111	0.1335
chr10	135534747	2510625	0.0185	0.1894
chr11	135006516	2088206	0.0155	0.1418
chr12	133851895	1898316	0.0142	0.125
chr13	115169878	1406160	0.0122	0.1145
chr14	107349540	1316133	0.0123	0.1193
chr15	102531392	1254686	0.0122	0.1142
chr16	90354753	1334983	0.0148	0.1342
chr17	81195210	887757	0.0109	0.1105
chr18	78077248	957456	0.0123	0.2145
chr19	59128983	813941	0.0138	0.2208
chr20	63025520	1027656	0.0163	0.1337
chr21	48129895	582308	0.0121	0.1204
chr22	51304566	379893	0.0074	0.089
chrMT	16571	2273	0.1372	0.3757
chrX	155270560	1778370	0.0115	0.1156
chrY	59373566	136882	0.0023	0.0862

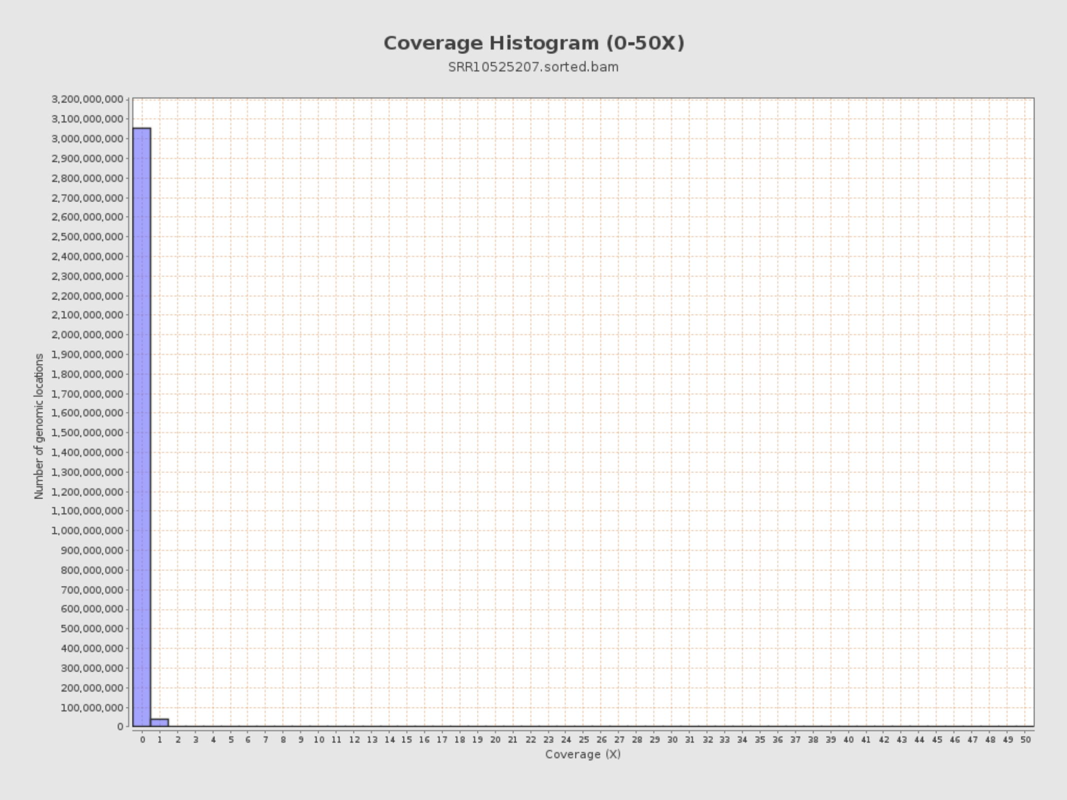
3. Results : Coverage across reference



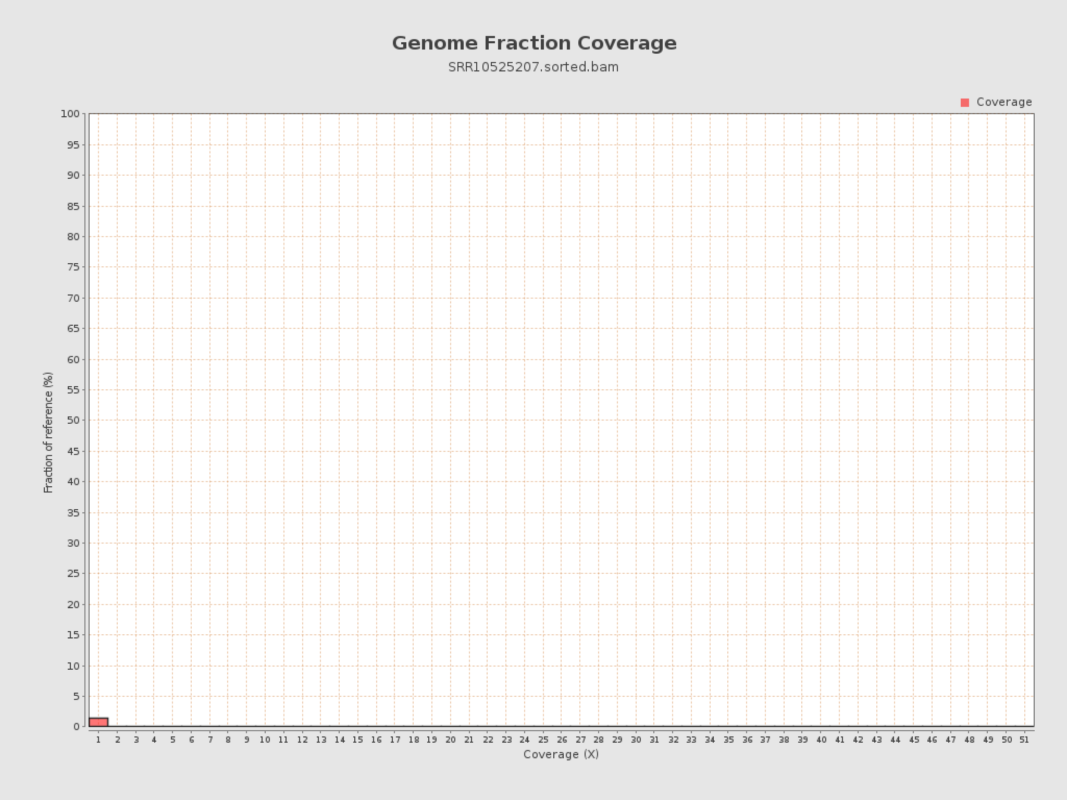
4. Results : Coverage Histogram



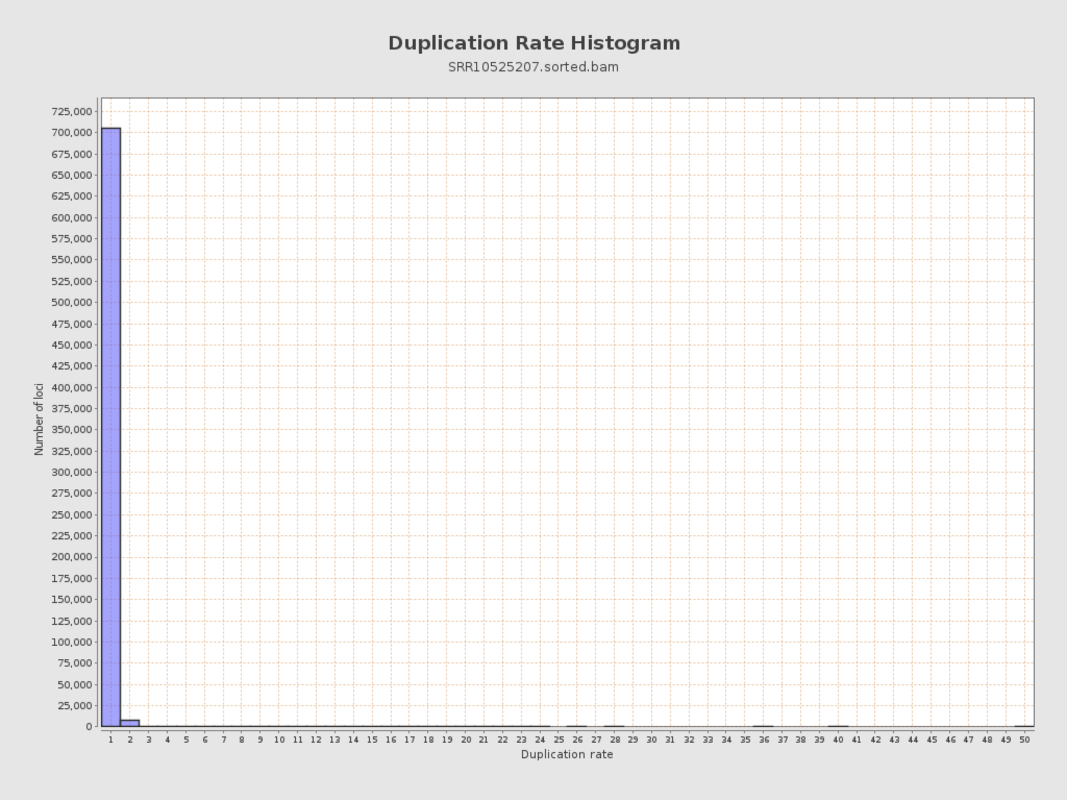
5. Results : Coverage Histogram (0-50X)



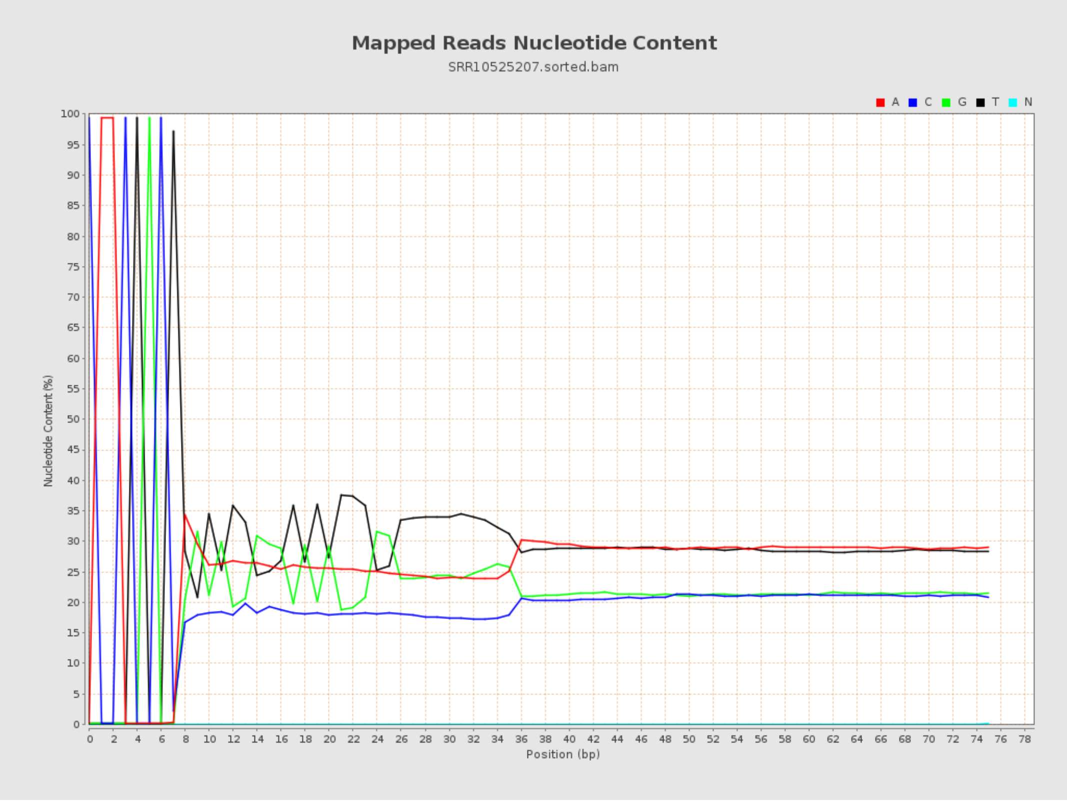
6. Results : Genome Fraction Coverage



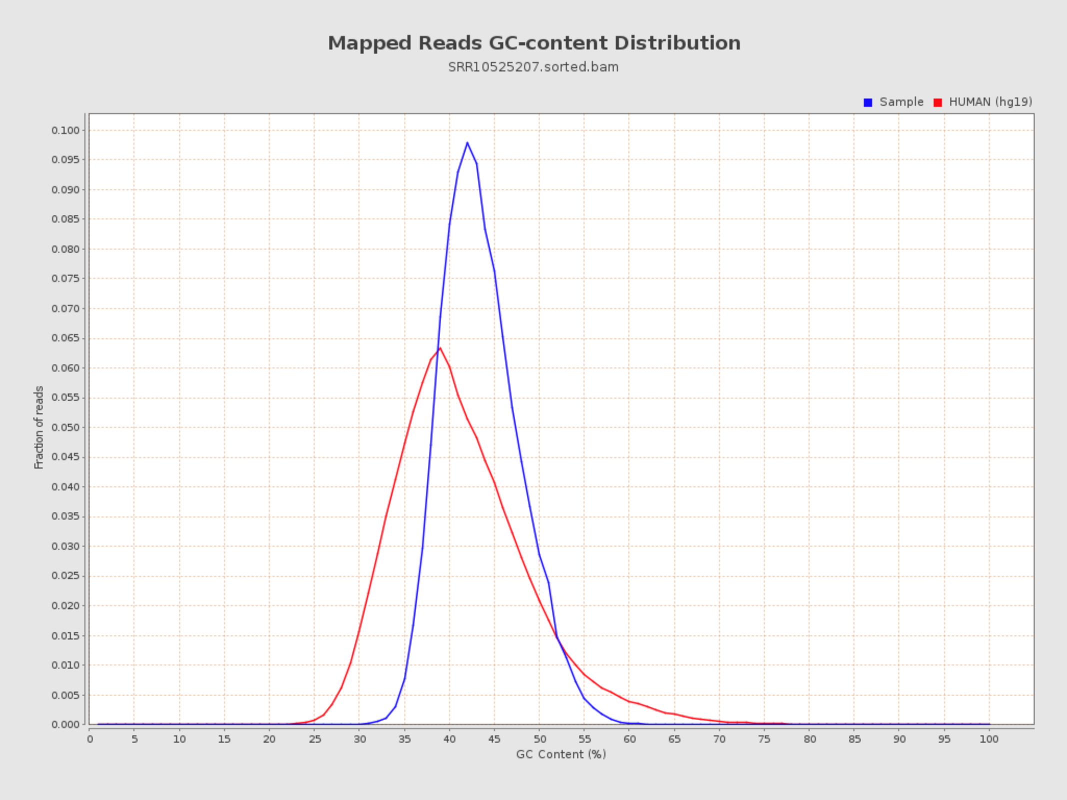
7. Results : Duplication Rate Histogram



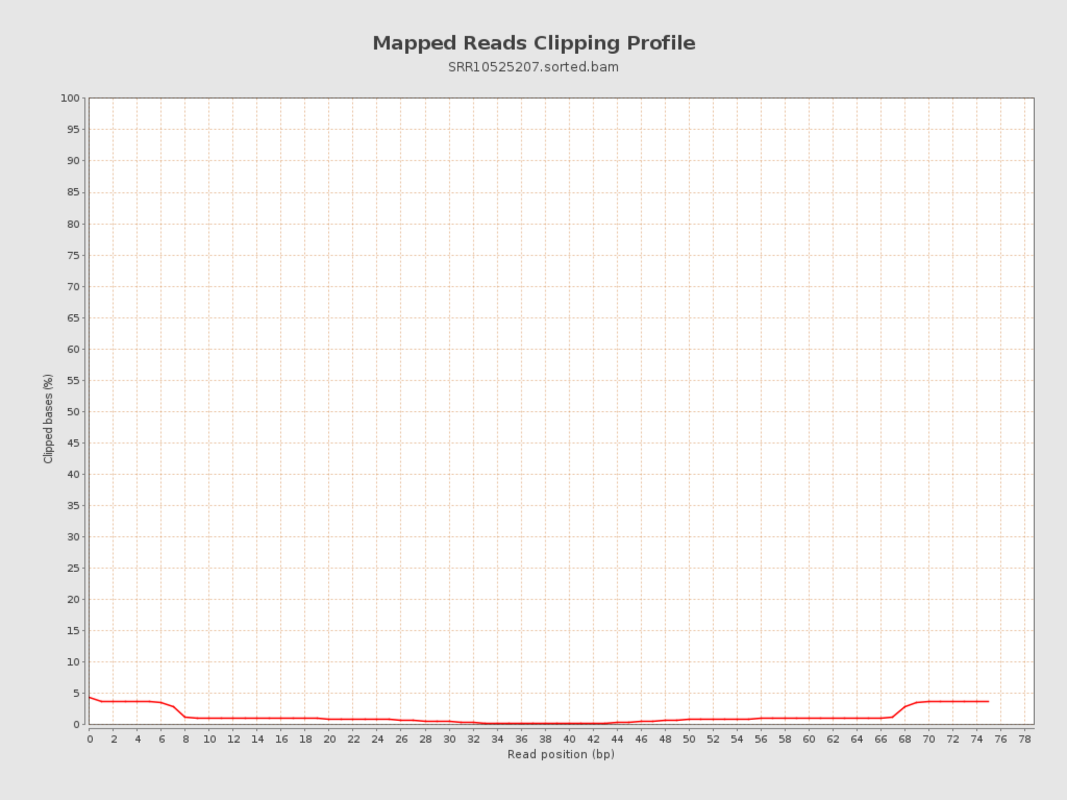
8. Results : Mapped Reads Nucleotide Content



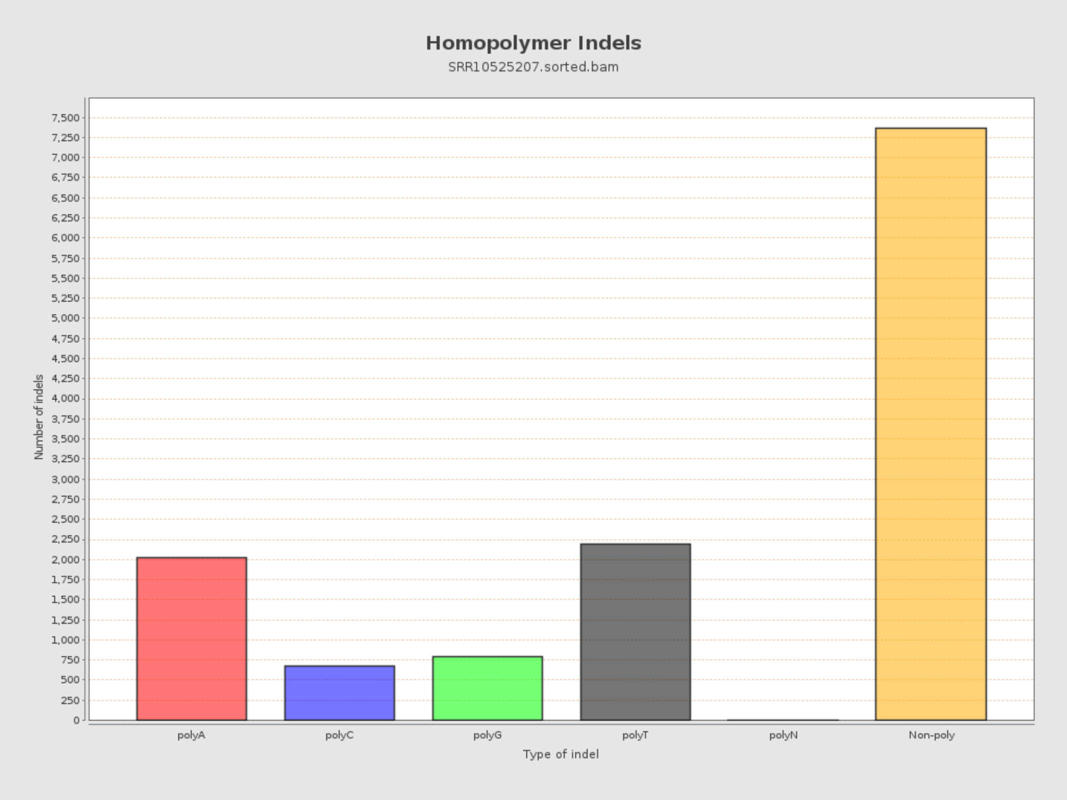
9. Results : Mapped Reads GC-content Distribution



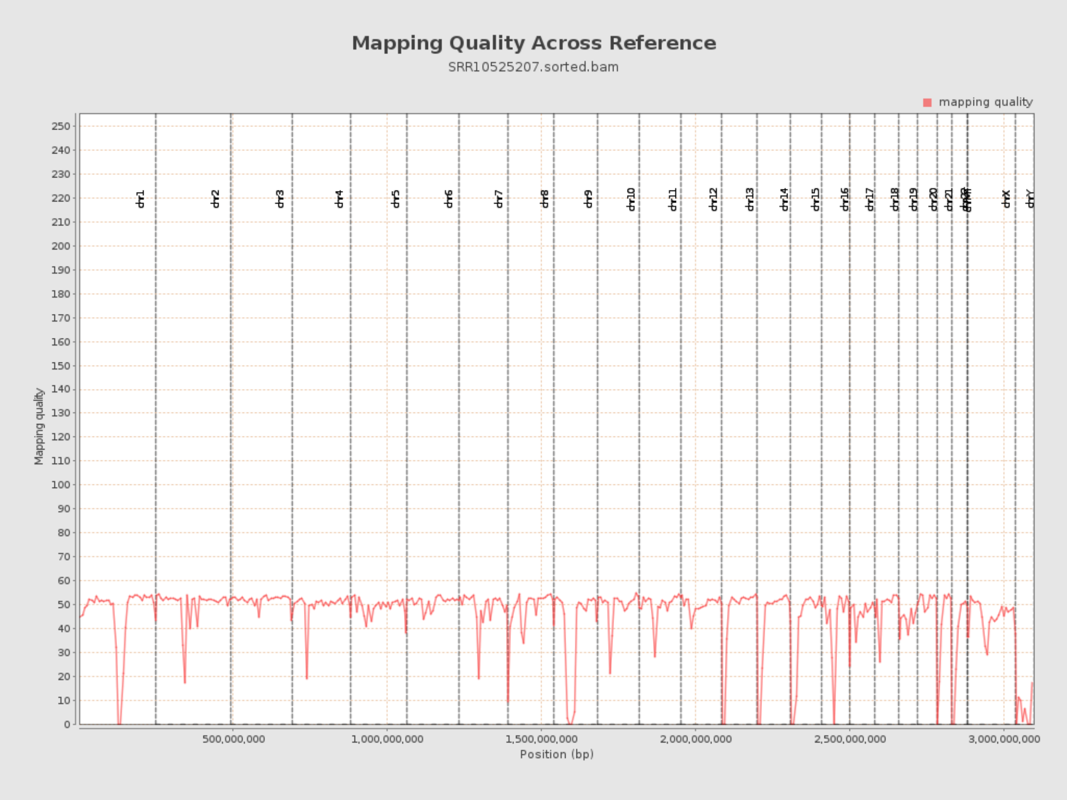
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram