Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 18:49:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525120.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_SRR10525120 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525120.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 18:49:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525120.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	518,450
Mapped reads	473,078 / 91.25%
Unmapped reads	45,372 / 8.75%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,655 / 3.02%
Read min/max/mean length	30 / 101 / 102.12
Duplicated reads (estimated)	8,875 / 1.71%
Duplication rate	1.17%
Clipped reads	488,165 / 94.16%

2.2. ACGT Content

Number/percentage of A's	9,103,791 / 25.13%
Number/percentage of C's	7,242,496 / 19.99%
Number/percentage of T's	10,974,285 / 30.29%
Number/percentage of G's	8,905,303 / 24.58%
Number/percentage of N's	1,424 / 0%
GC Percentage	44.57%

2.3. Coverage

Mean	0.0117

Standard Deviation	0.1526

2.4. Mapping Quality

Mean Mapping Quality	44.99

2.5. Mismatches and indels

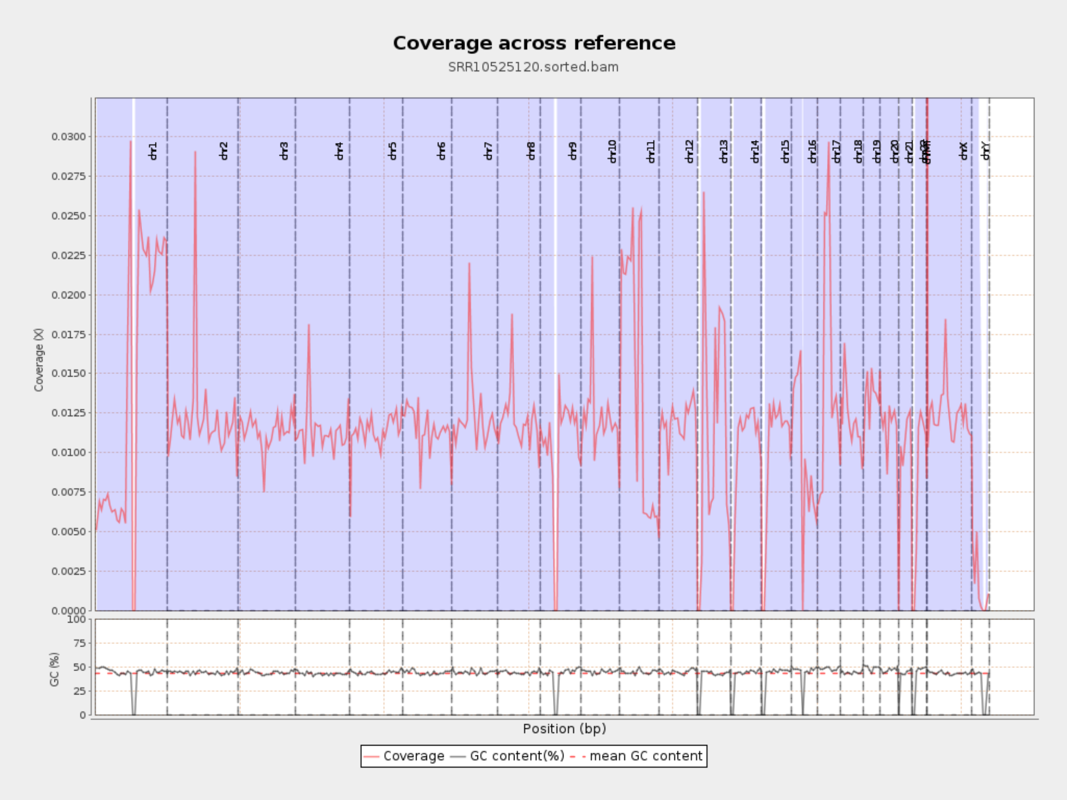
General error rate	0.76%
Mismatches	268,835
Insertions	3,261
Mapped reads with at least one insertion	0.68%
Deletions	8,642
Mapped reads with at least one deletion	1.8%
Homopolymer indels	42.29%

2.6. Chromosome stats

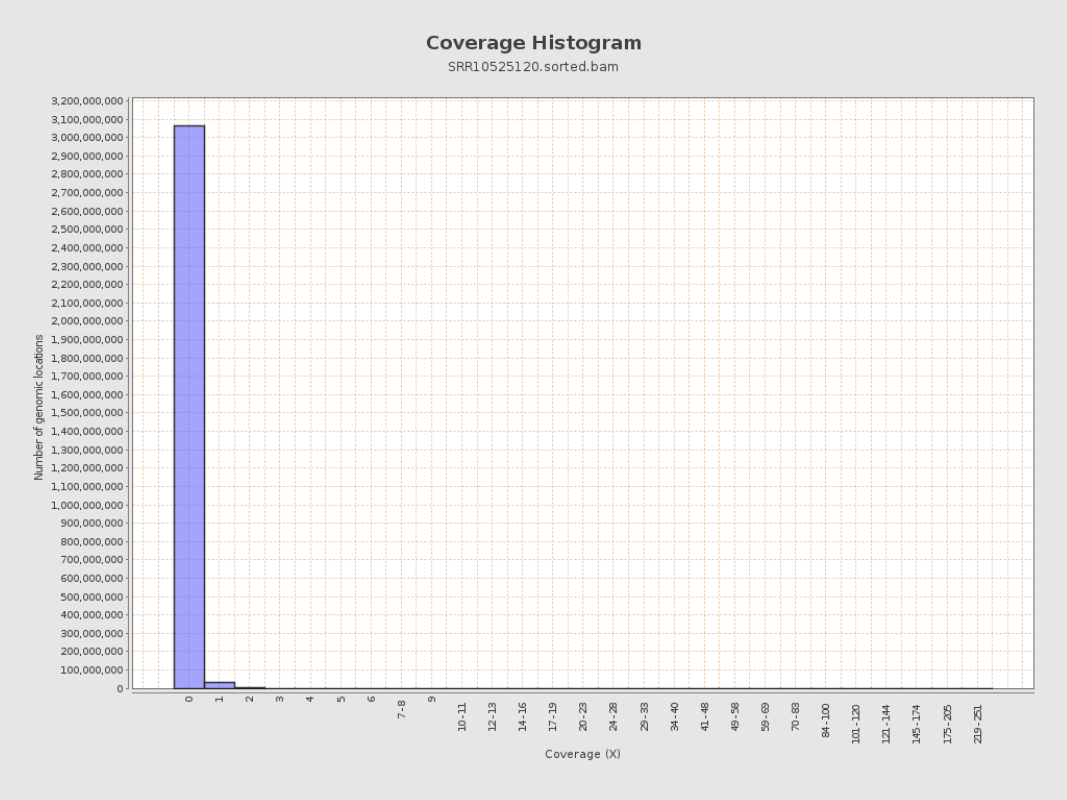
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3507094	0.0141	0.2399
chr2	243199373	2972874	0.0122	0.1978
chr3	198022430	2251433	0.0114	0.11
chr4	191154276	2186172	0.0114	0.1154
chr5	180915260	2074875	0.0115	0.1112
chr6	171115067	1969634	0.0115	0.1165
chr7	159138663	1961282	0.0123	0.1865

chr8	146364022	1766888	0.0121	0.1764
chr9	141213431	1463226	0.0104	0.1369
chr10	135534747	1670791	0.0123	0.1574
chr11	135006516	1996738	0.0148	0.1702
chr12	133851895	1598549	0.0119	0.1132
chr13	115169878	1255264	0.0109	0.1082
chr14	107349540	1061931	0.0099	0.1075
chr15	102531392	1016039	0.0099	0.1035
chr16	90354753	868494	0.0096	0.1072
chr17	81195210	1213966	0.015	0.1384
chr18	78077248	941799	0.0121	0.2242
chr19	59128983	804843	0.0136	0.1941
chr20	63025520	729801	0.0116	0.112
chr21	48129895	472857	0.0098	0.1059
chr22	51304566	413055	0.0081	0.0924
chrMT	16571	9598	0.5792	0.8847
chrX	155270560	1944568	0.0125	0.1305
chrY	59373566	90742	0.0015	0.0514

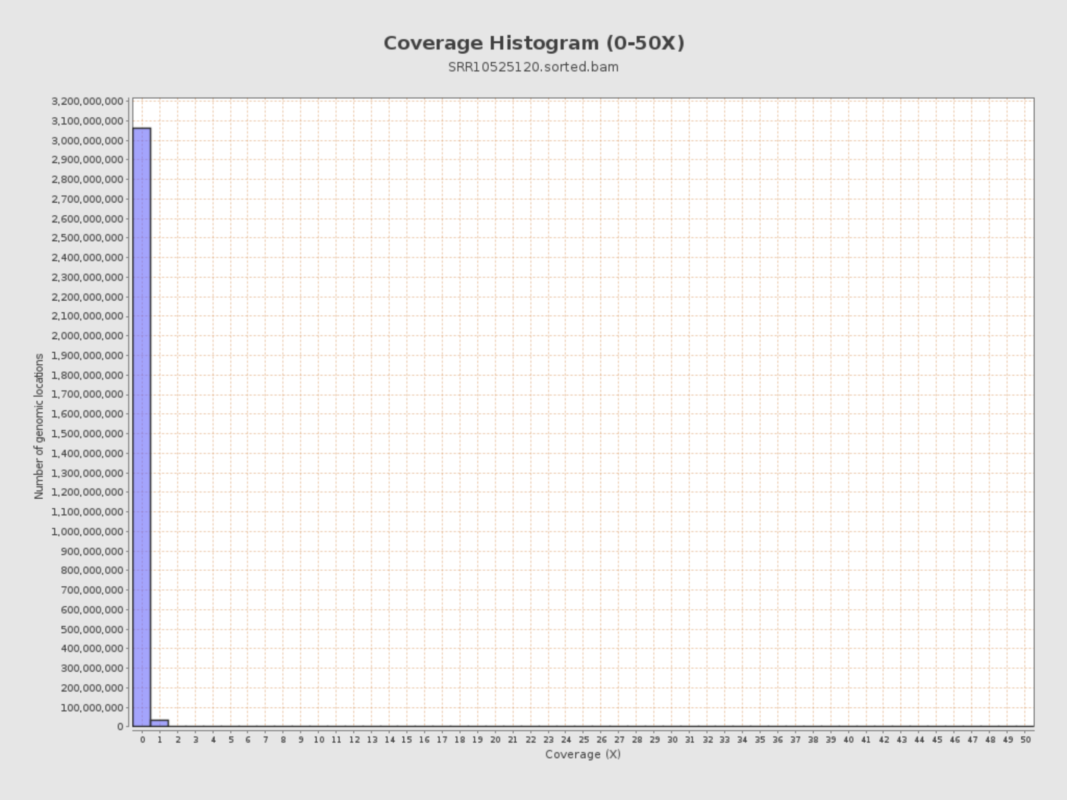
3. Results : Coverage across reference



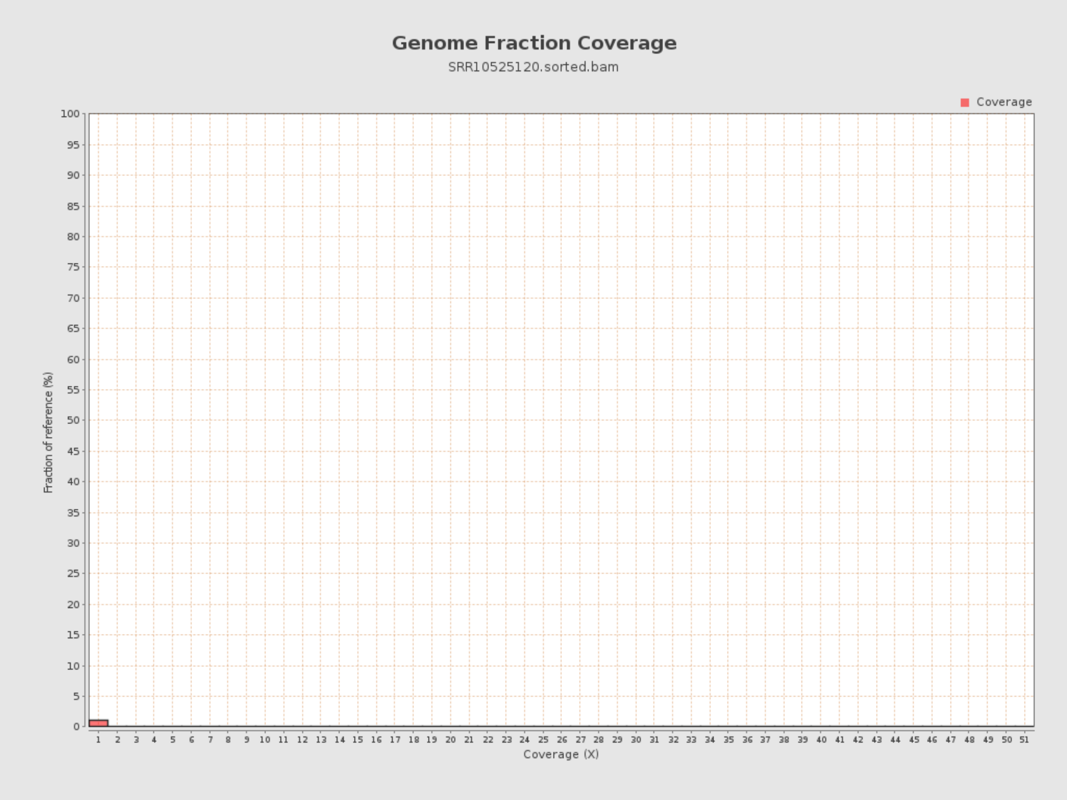
4. Results : Coverage Histogram



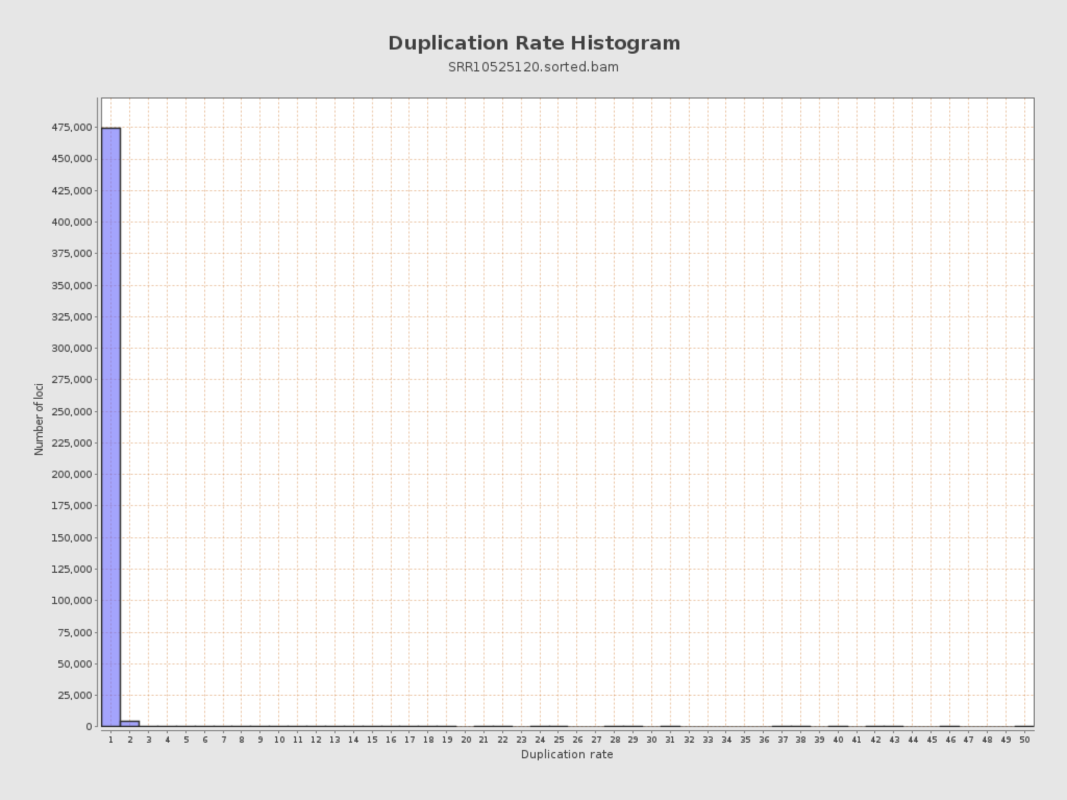
5. Results : Coverage Histogram (0-50X)



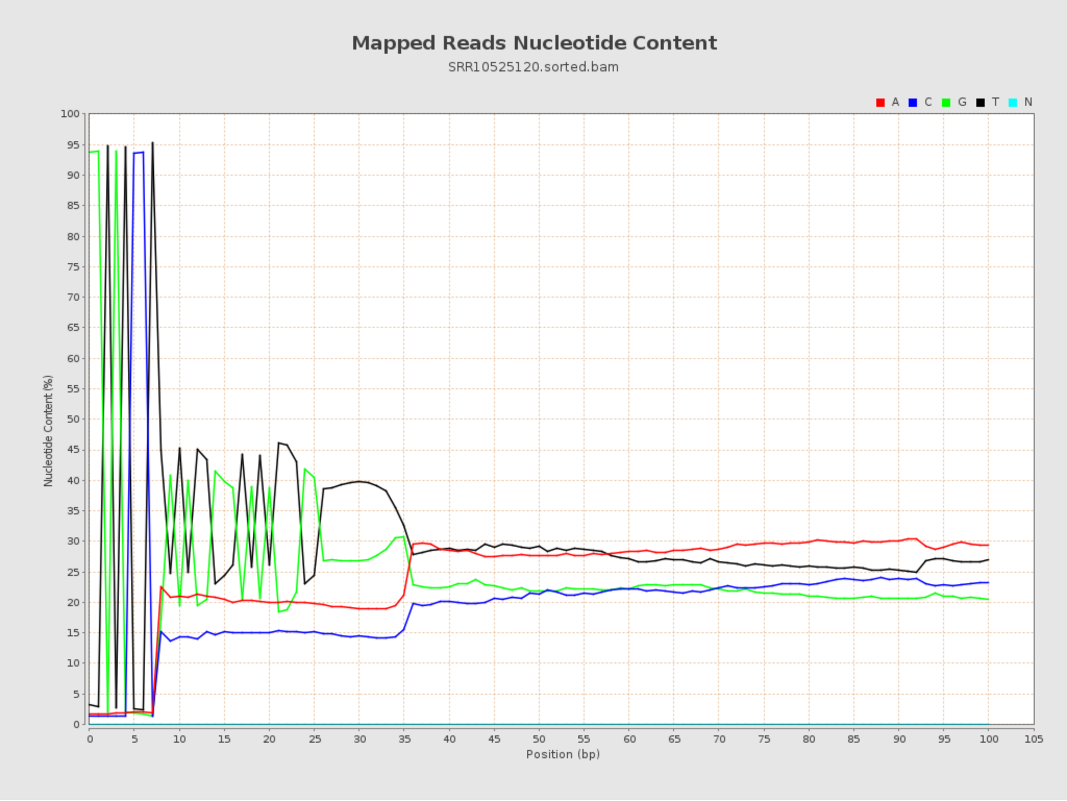
6. Results : Genome Fraction Coverage



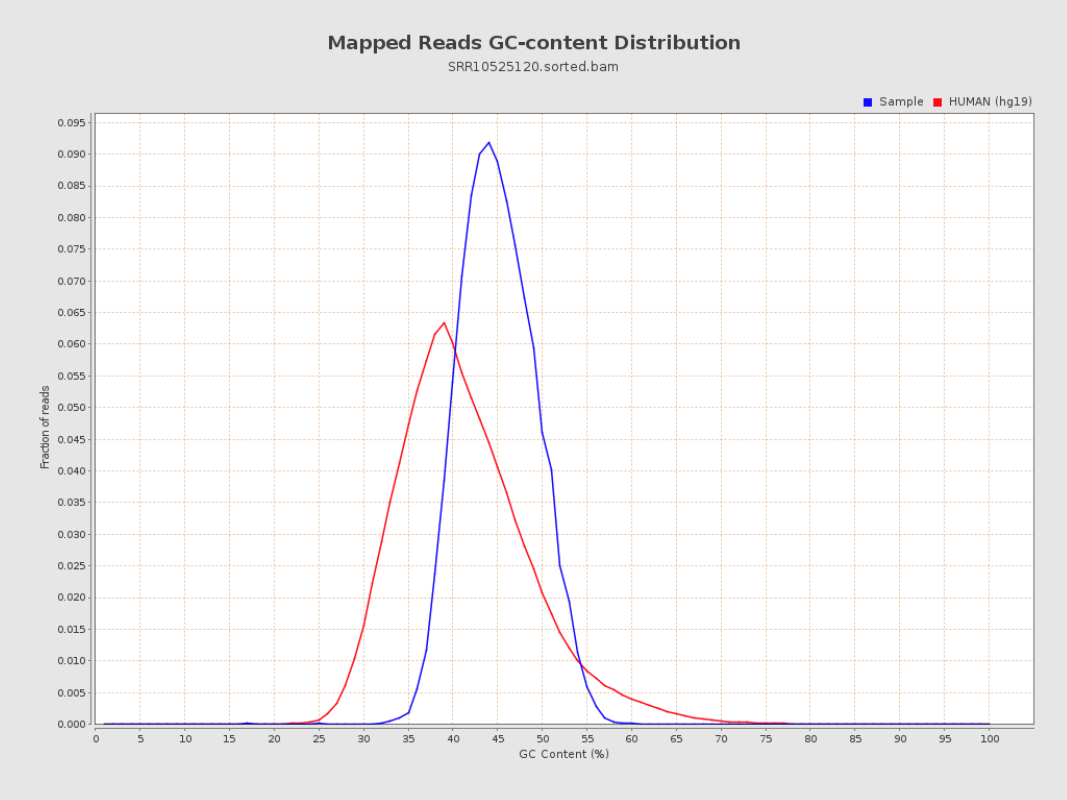
7. Results : Duplication Rate Histogram



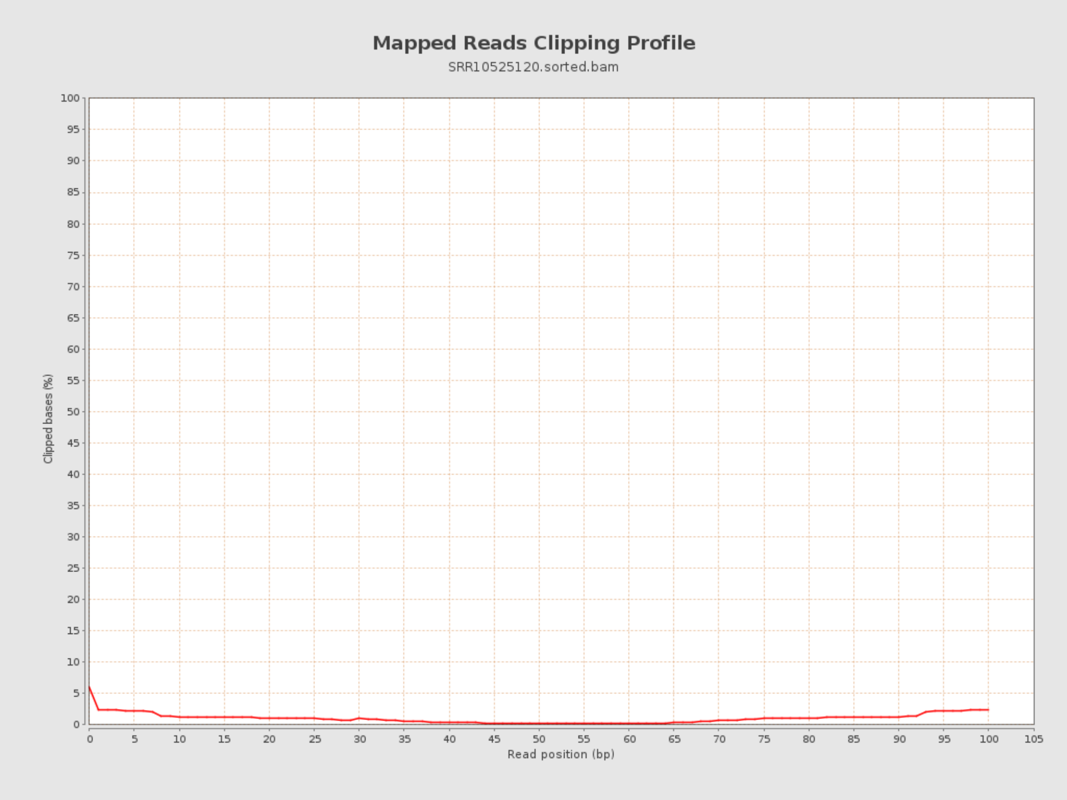
8. Results : Mapped Reads Nucleotide Content



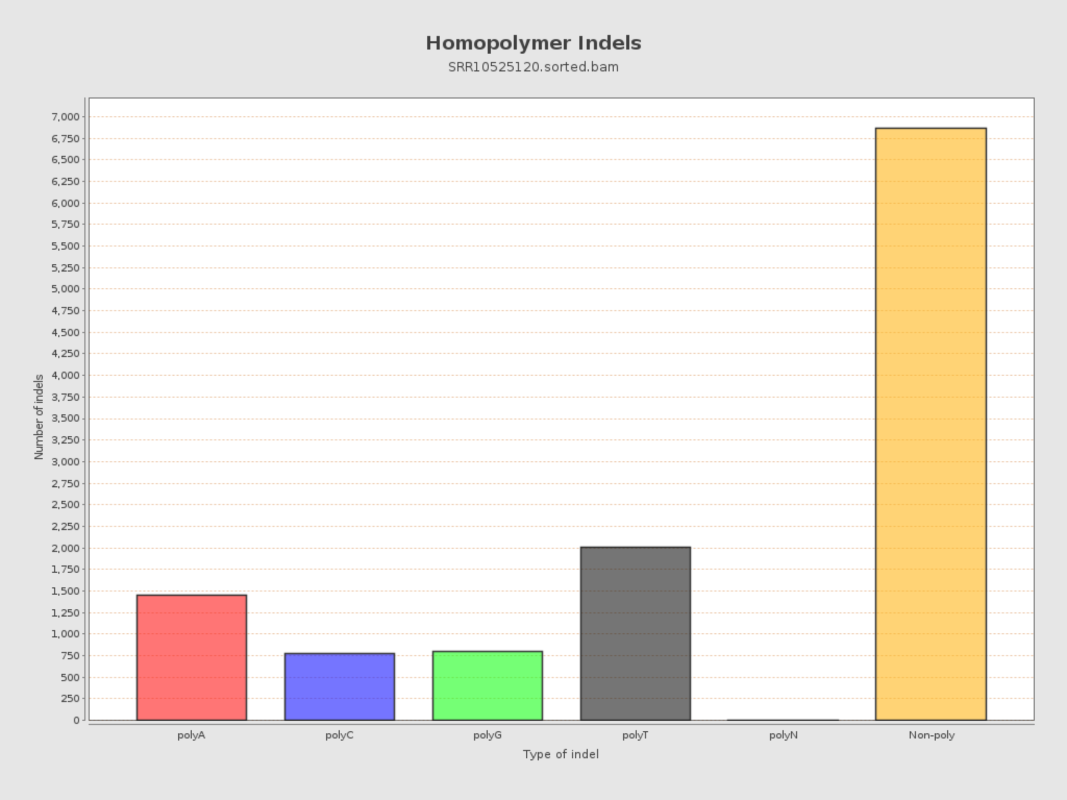
9. Results : Mapped Reads GC-content Distribution



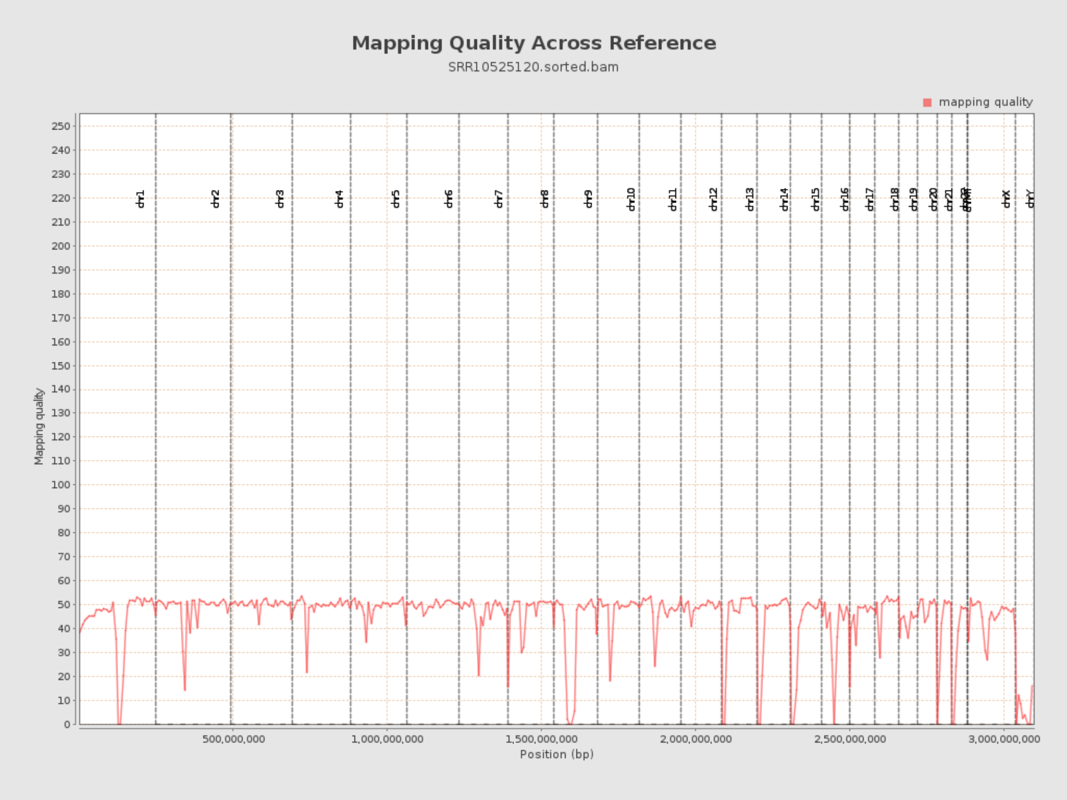
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram