Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 04:20:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524920.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_SRR10524920 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524920.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 04:20:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524920.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	780,772
Mapped reads	726,081 / 93%
Unmapped reads	54,691 / 7%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,817 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	26,391 / 3.38%
Duplication rate	2.92%
Clipped reads	728,093 / 93.25%

2.2. ACGT Content

Number/percentage of A's	10,192,211 / 23.91%
Number/percentage of C's	7,714,486 / 18.1%
Number/percentage of T's	13,973,340 / 32.78%
Number/percentage of G's	10,745,460 / 25.21%
Number/percentage of N's	316 / 0%
GC Percentage	43.31%

2.3. Coverage

Mean	0.0138

Standard Deviation	0.156

2.4. Mapping Quality

Mean Mapping Quality	45.27

2.5. Mismatches and indels

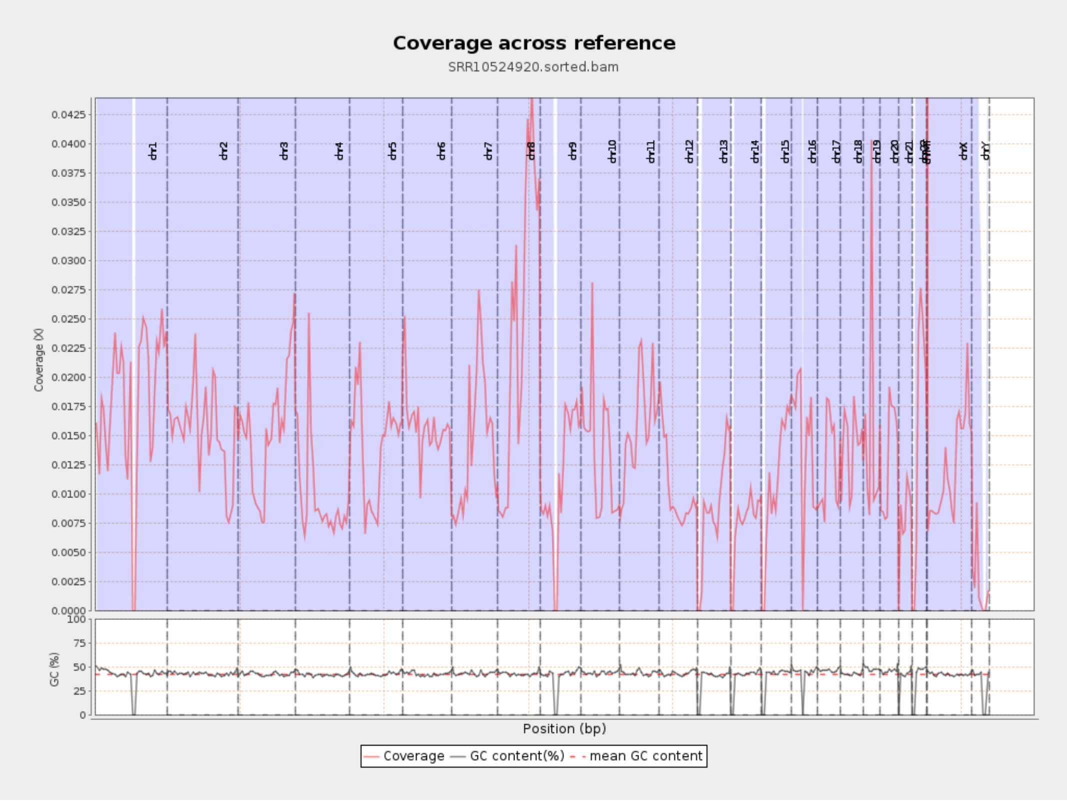
General error rate	0.51%
Mismatches	213,027
Insertions	2,568
Mapped reads with at least one insertion	0.35%
Deletions	8,447
Mapped reads with at least one deletion	1.15%
Homopolymer indels	44.88%

2.6. Chromosome stats

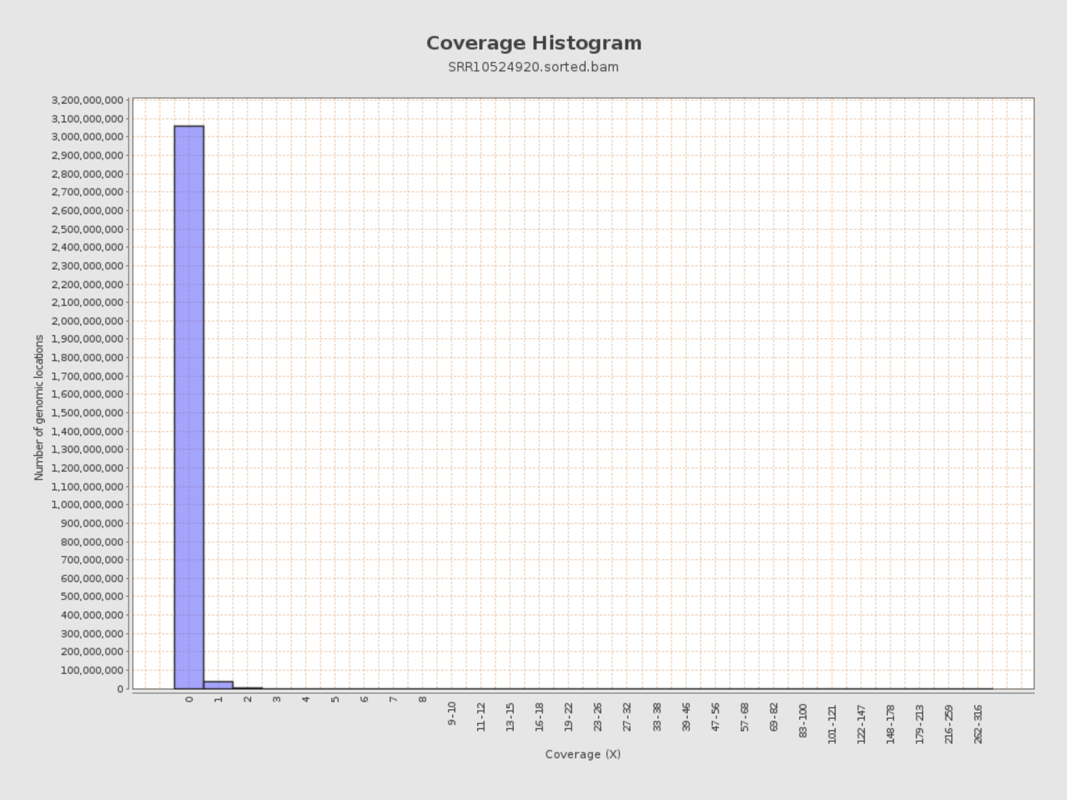
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4456788	0.0179	0.2561
chr2	243199373	3730778	0.0153	0.1782
chr3	198022430	3069340	0.0155	0.1331
chr4	191154276	1891539	0.0099	0.1255
chr5	180915260	2569234	0.0142	0.1278
chr6	171115067	2711560	0.0158	0.1391
chr7	159138663	2321197	0.0146	0.1678

chr8	146364022	3666573	0.0251	0.2108
chr9	141213431	1577121	0.0112	0.13
chr10	135534747	1877386	0.0139	0.1739
chr11	135006516	2136895	0.0158	0.1481
chr12	133851895	1393430	0.0104	0.111
chr13	115169878	1000844	0.0087	0.0991
chr14	107349540	791860	0.0074	0.0923
chr15	102531392	1108958	0.0108	0.1112
chr16	90354753	1286238	0.0142	0.1305
chr17	81195210	996983	0.0123	0.1209
chr18	78077248	1098169	0.0141	0.1903
chr19	59128983	889761	0.015	0.1871
chr20	63025520	827996	0.0131	0.1256
chr21	48129895	381661	0.0079	0.1105
chr22	51304566	826990	0.0161	0.1367
chrMT	16571	7958	0.4802	0.7217
chrX	155270560	1889968	0.0122	0.1222
chrY	59373566	130802	0.0022	0.0986

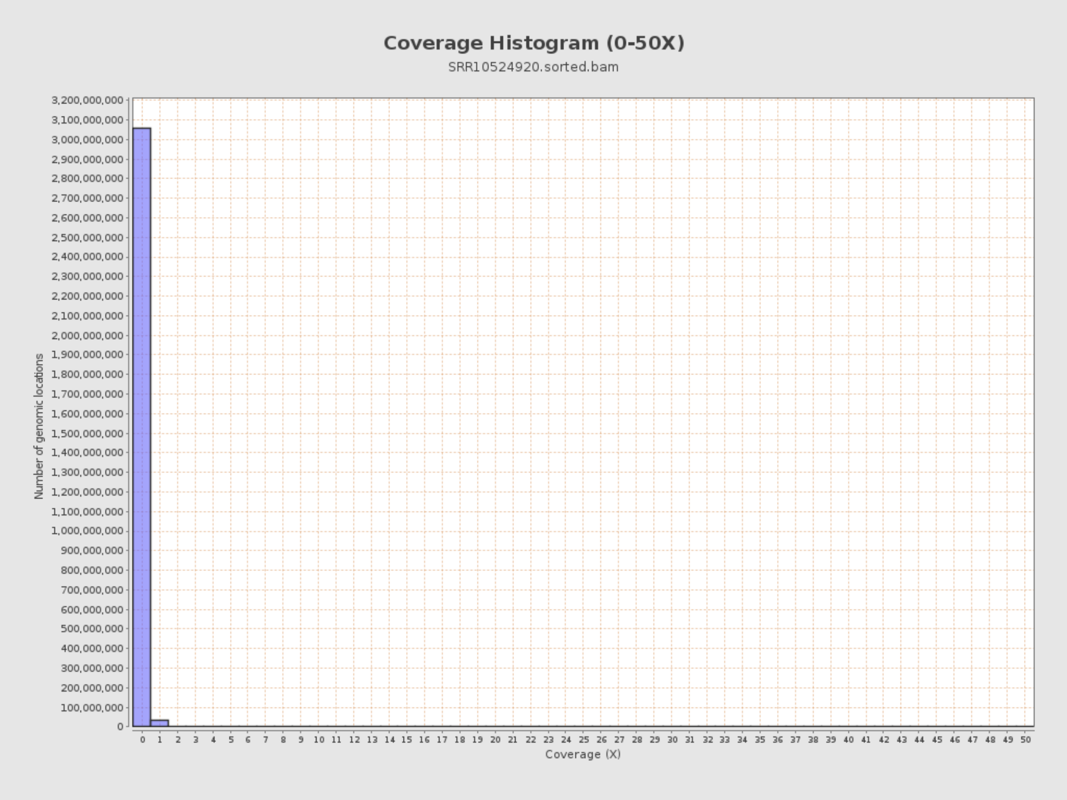
3. Results : Coverage across reference



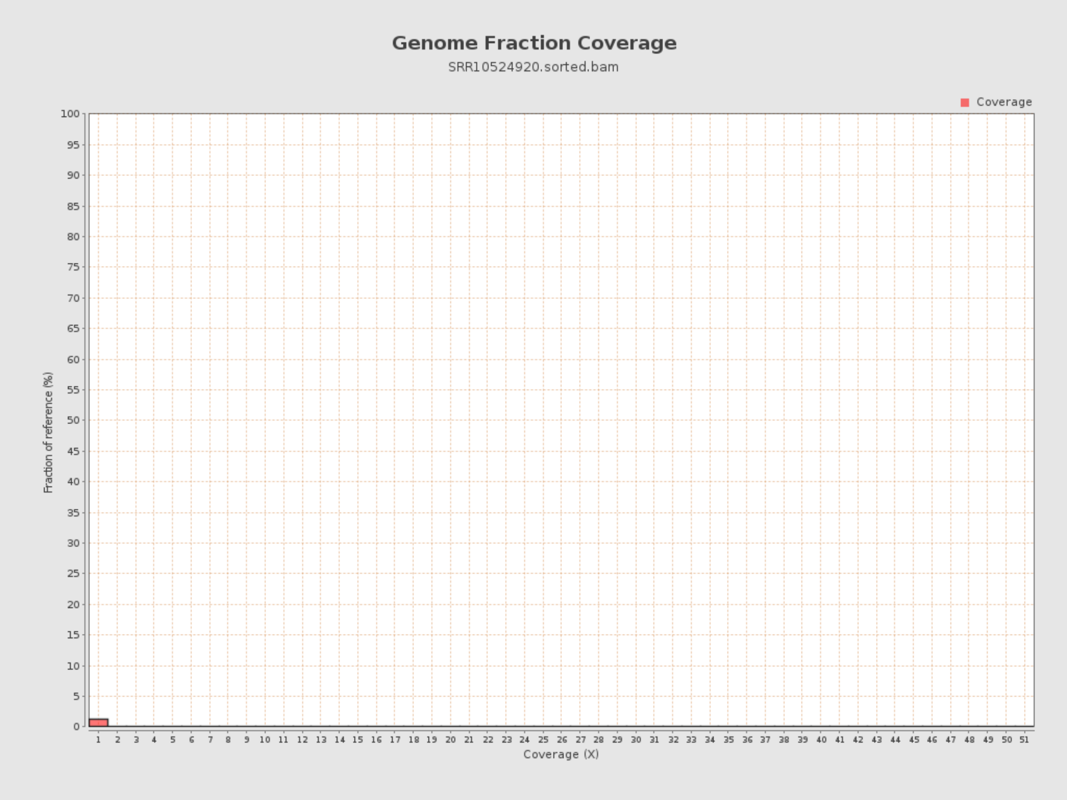
4. Results : Coverage Histogram



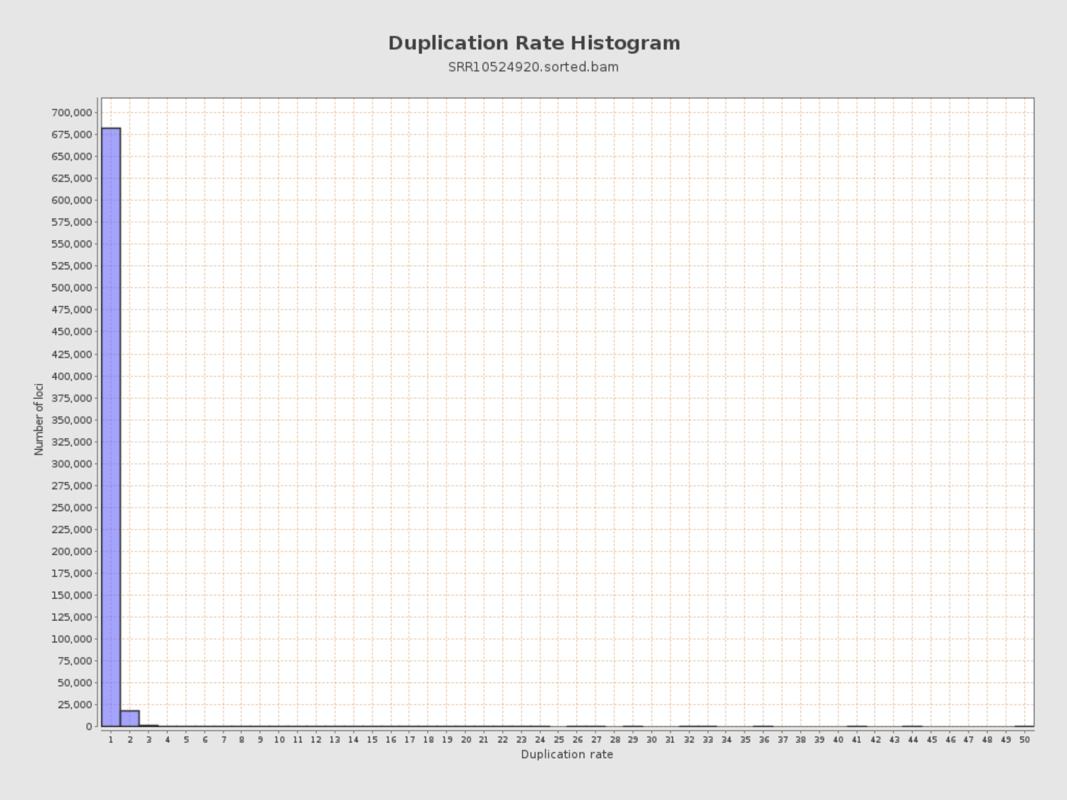
5. Results : Coverage Histogram (0-50X)



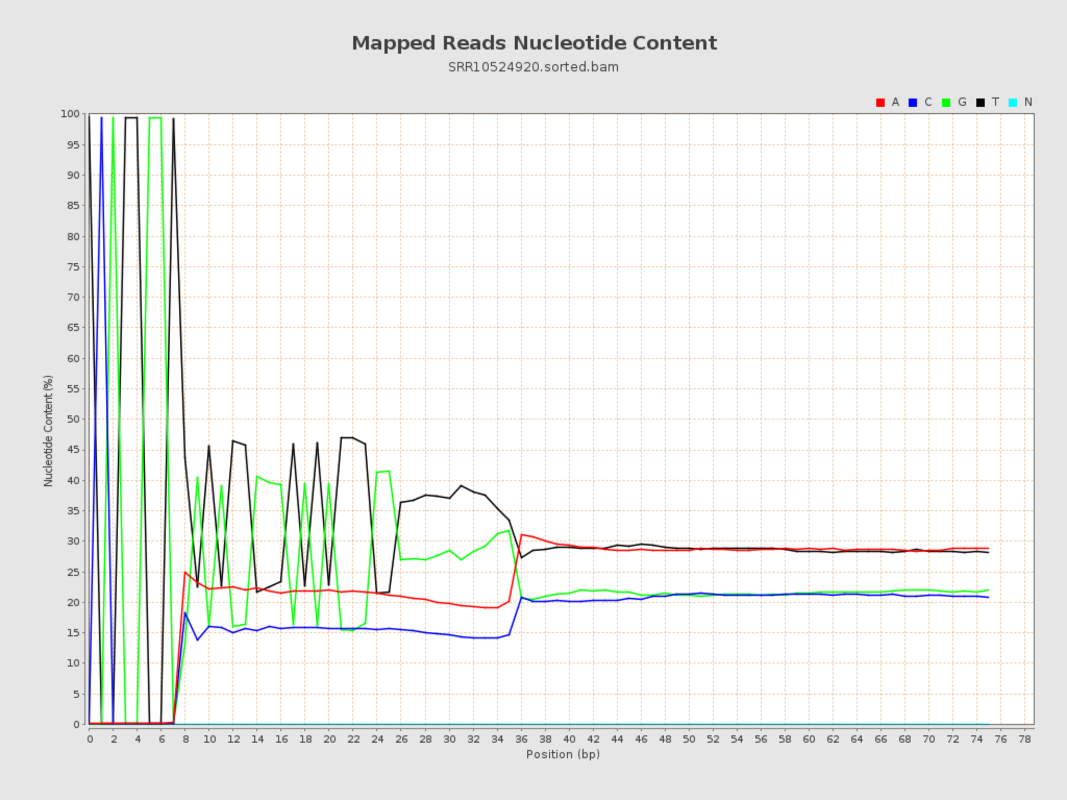
6. Results : Genome Fraction Coverage



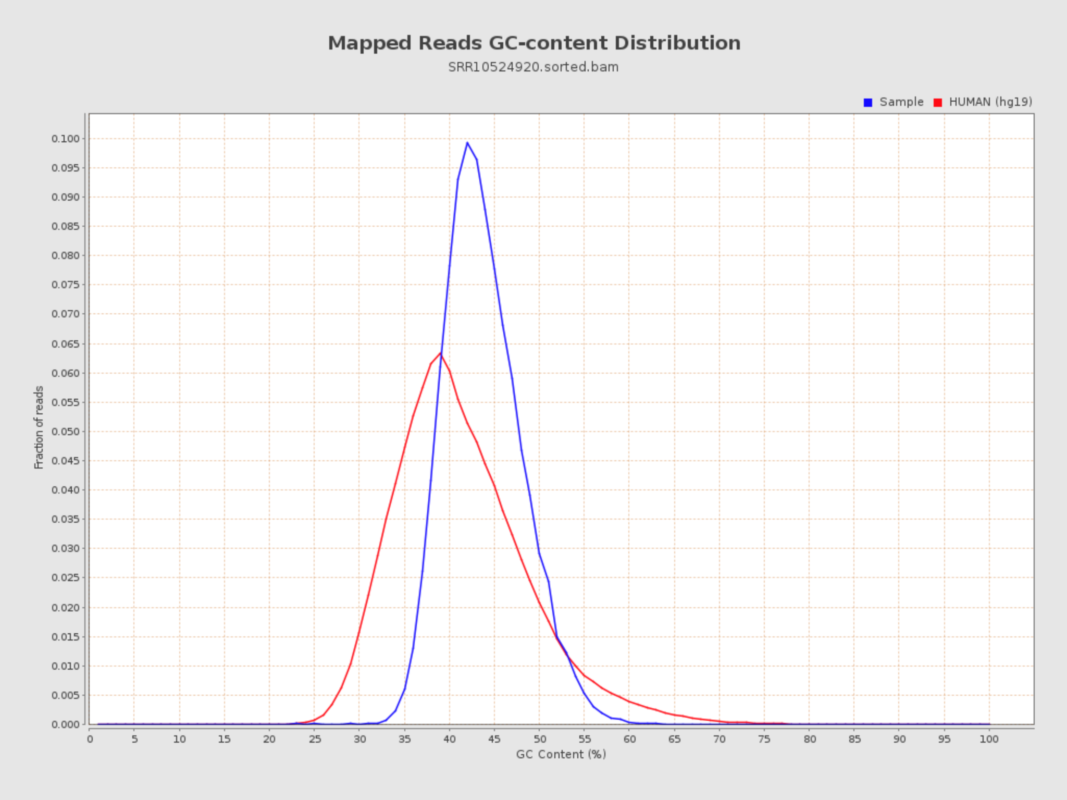
7. Results : Duplication Rate Histogram



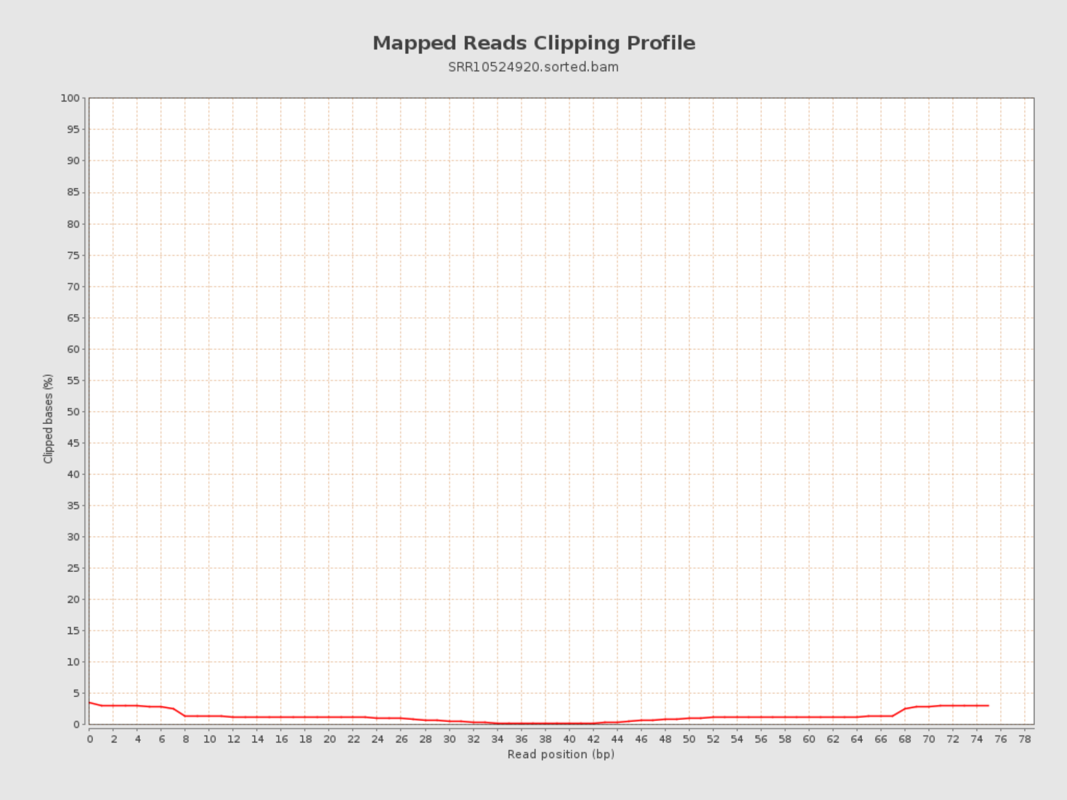
8. Results : Mapped Reads Nucleotide Content



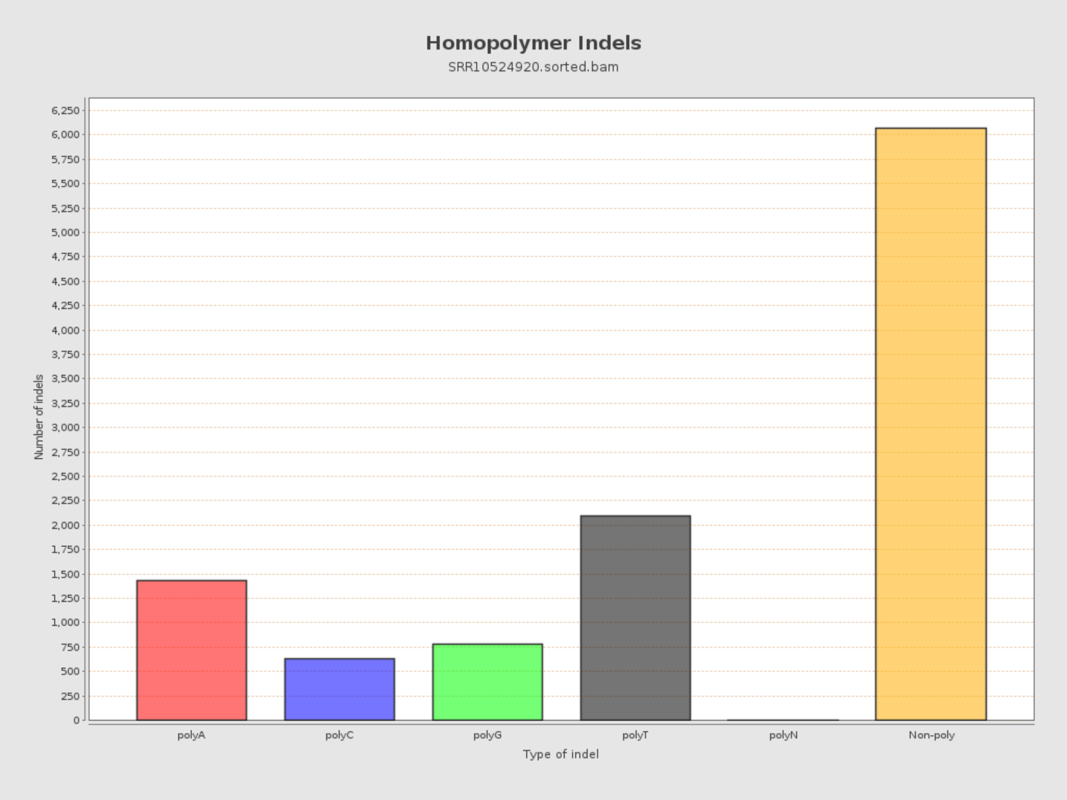
9. Results : Mapped Reads GC-content Distribution



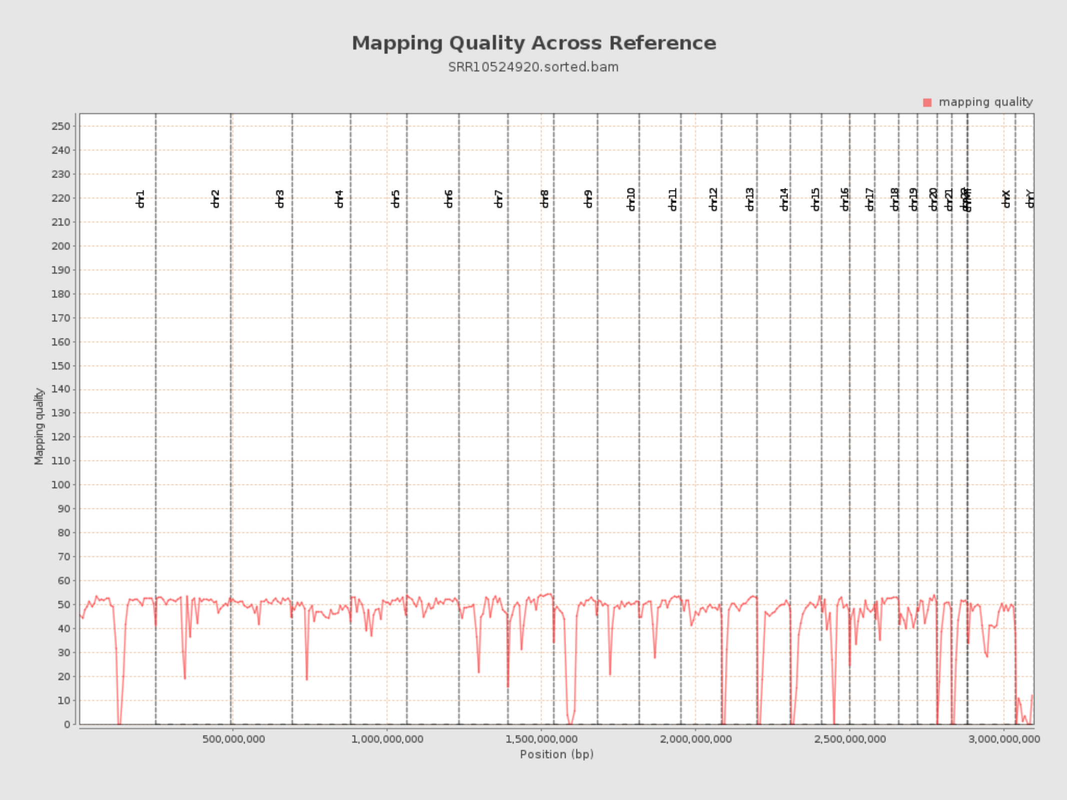
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram