Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 08:40:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524521.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_SRR10524521 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524521.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 08:40:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524521.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	787,078
Mapped reads	717,835 / 91.2%
Unmapped reads	69,243 / 8.8%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,445 / 0.31%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	19,617 / 2.49%
Duplication rate	2.11%
Clipped reads	718,177 / 91.25%

2.2. ACGT Content

Number/percentage of A's	10,167,034 / 24.47%
Number/percentage of C's	7,150,421 / 17.21%
Number/percentage of T's	13,258,609 / 31.91%
Number/percentage of G's	10,978,310 / 26.42%
Number/percentage of N's	551 / 0%
GC Percentage	43.63%

2.3. Coverage

Mean	0.0134

Standard Deviation	0.1517

2.4. Mapping Quality

Mean Mapping Quality	44.54

2.5. Mismatches and indels

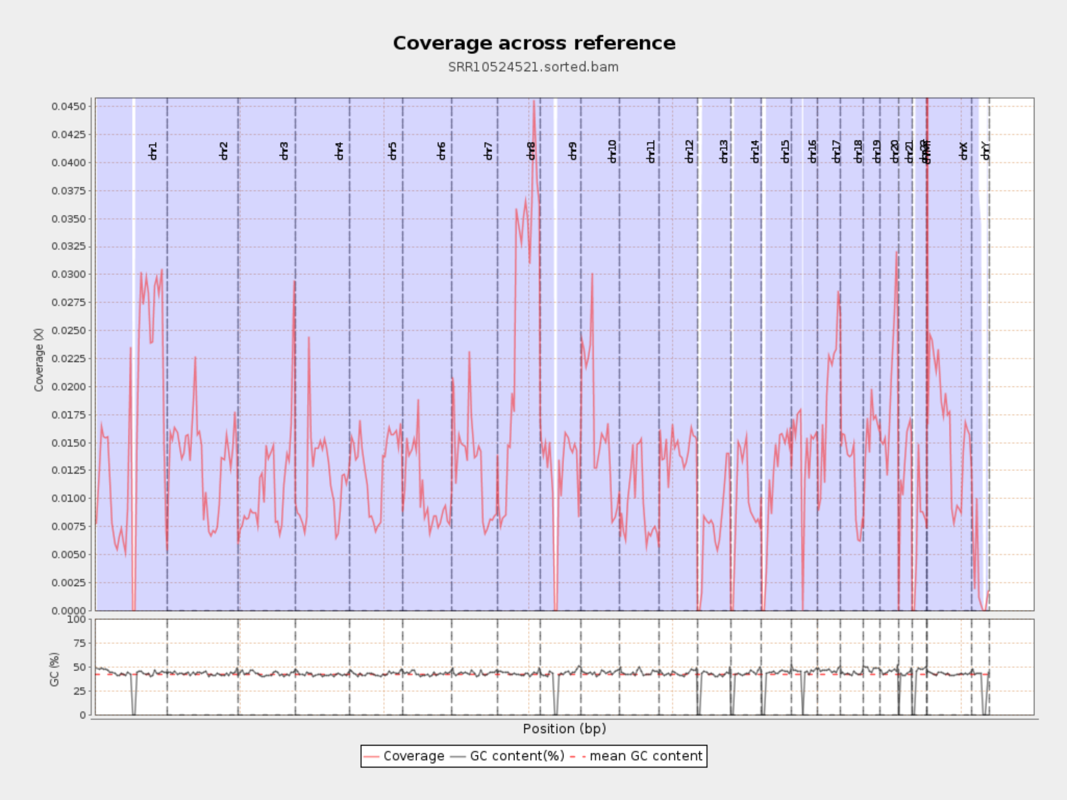
General error rate	0.52%
Mismatches	209,225
Insertions	2,746
Mapped reads with at least one insertion	0.38%
Deletions	7,085
Mapped reads with at least one deletion	0.98%
Homopolymer indels	43.69%

2.6. Chromosome stats

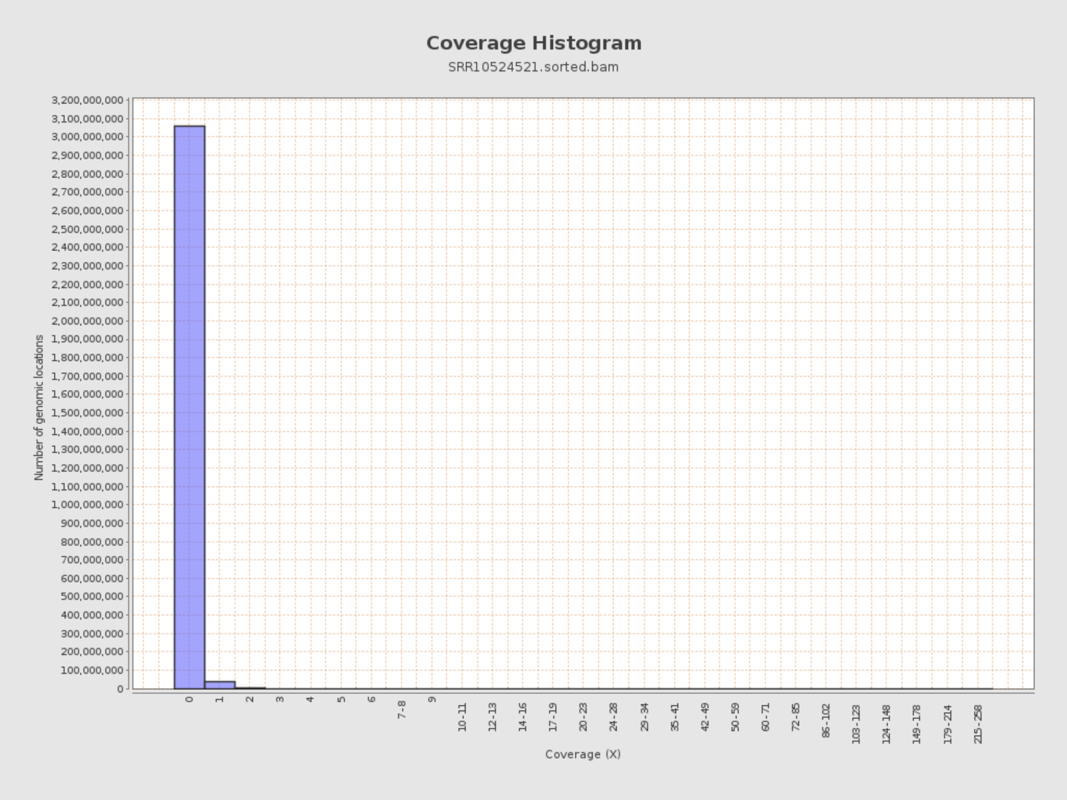
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3995516	0.016	0.2407
chr2	243199373	3250027	0.0134	0.1714
chr3	198022430	2206378	0.0111	0.112
chr4	191154276	2260932	0.0118	0.1306
chr5	180915260	2350668	0.013	0.1206
chr6	171115067	1797712	0.0105	0.1229
chr7	159138663	2081865	0.0131	0.1788

chr8	146364022	3819792	0.0261	0.1809
chr9	141213431	1711746	0.0121	0.1277
chr10	135534747	2246345	0.0166	0.1795
chr11	135006516	1298654	0.0096	0.1225
chr12	133851895	1929885	0.0144	0.1269
chr13	115169878	859086	0.0075	0.0909
chr14	107349540	1009721	0.0094	0.1035
chr15	102531392	1138577	0.0111	0.1114
chr16	90354753	1257954	0.0139	0.1306
chr17	81195210	1545193	0.019	0.1495
chr18	78077248	930131	0.0119	0.1912
chr19	59128983	948844	0.016	0.1823
chr20	63025520	1238877	0.0197	0.151
chr21	48129895	607221	0.0126	0.1292
chr22	51304566	363729	0.0071	0.0895
chrMT	16571	6288	0.3795	0.65
chrX	155270560	2553471	0.0164	0.1412
chrY	59373566	158252	0.0027	0.098

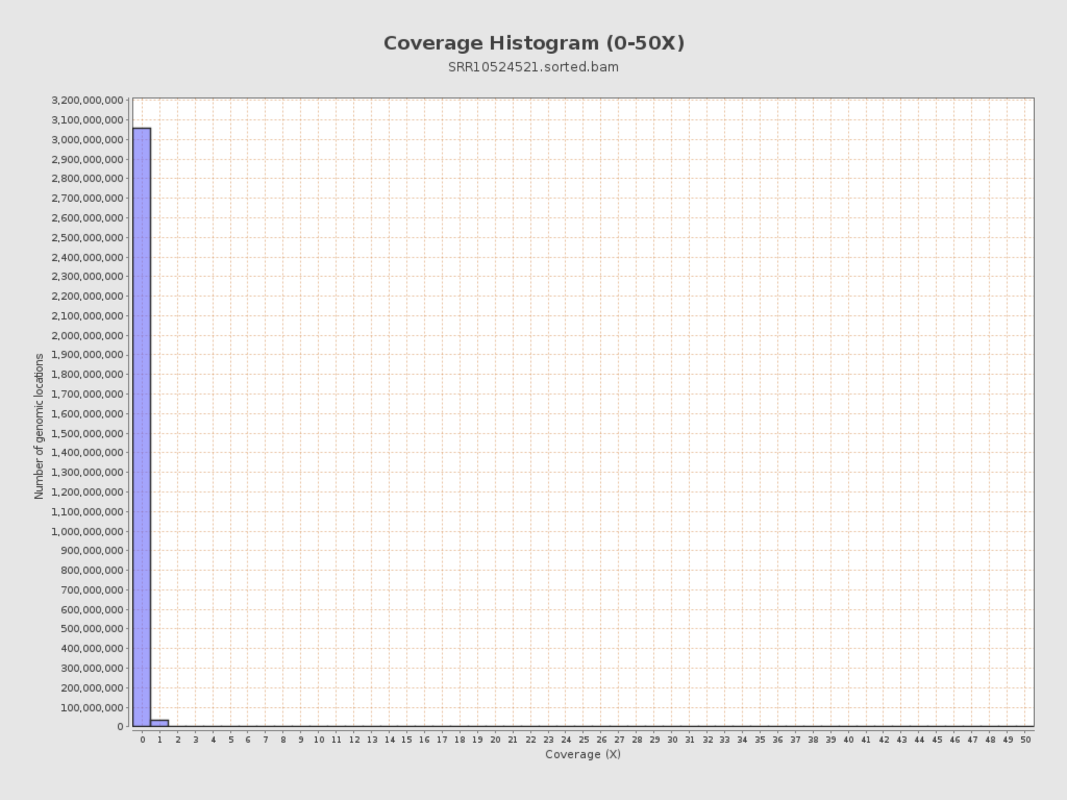
3. Results : Coverage across reference



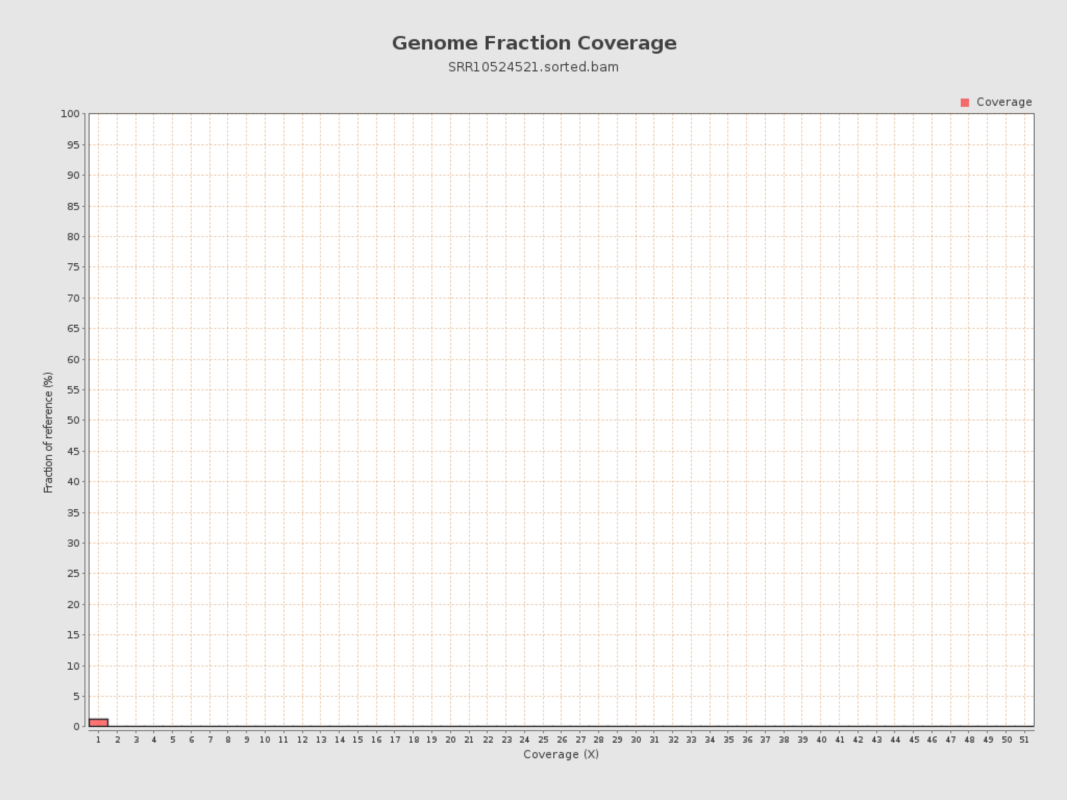
4. Results : Coverage Histogram



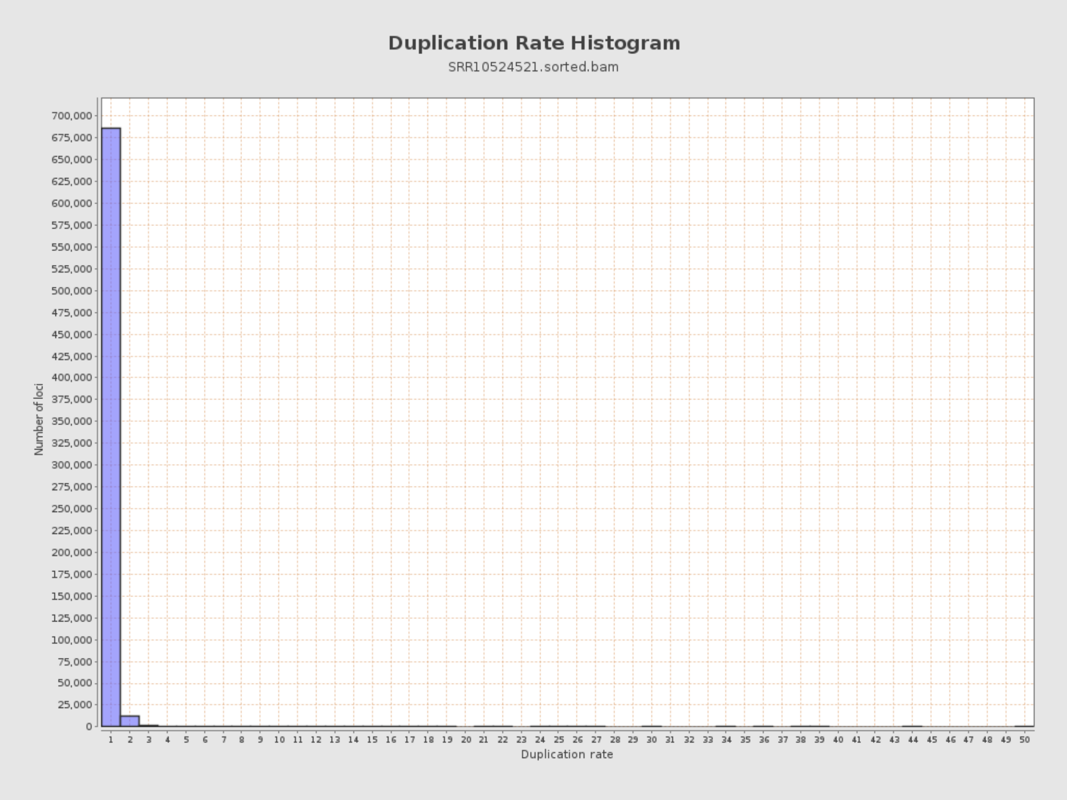
5. Results : Coverage Histogram (0-50X)



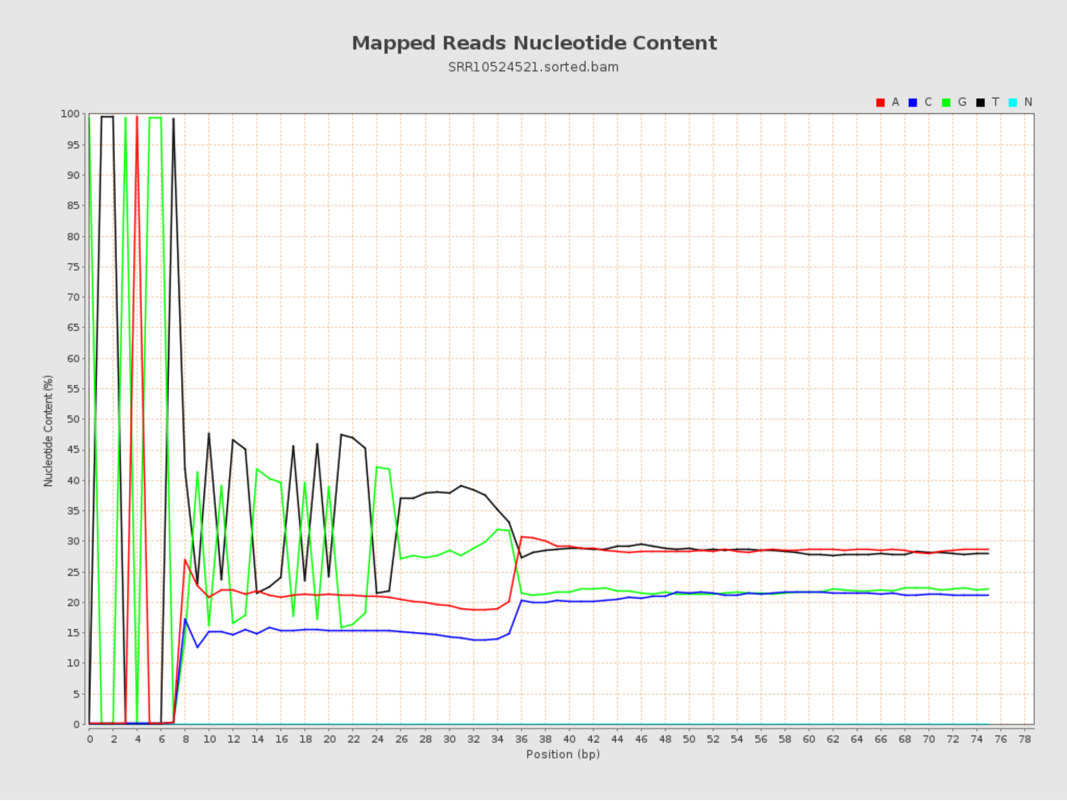
6. Results : Genome Fraction Coverage



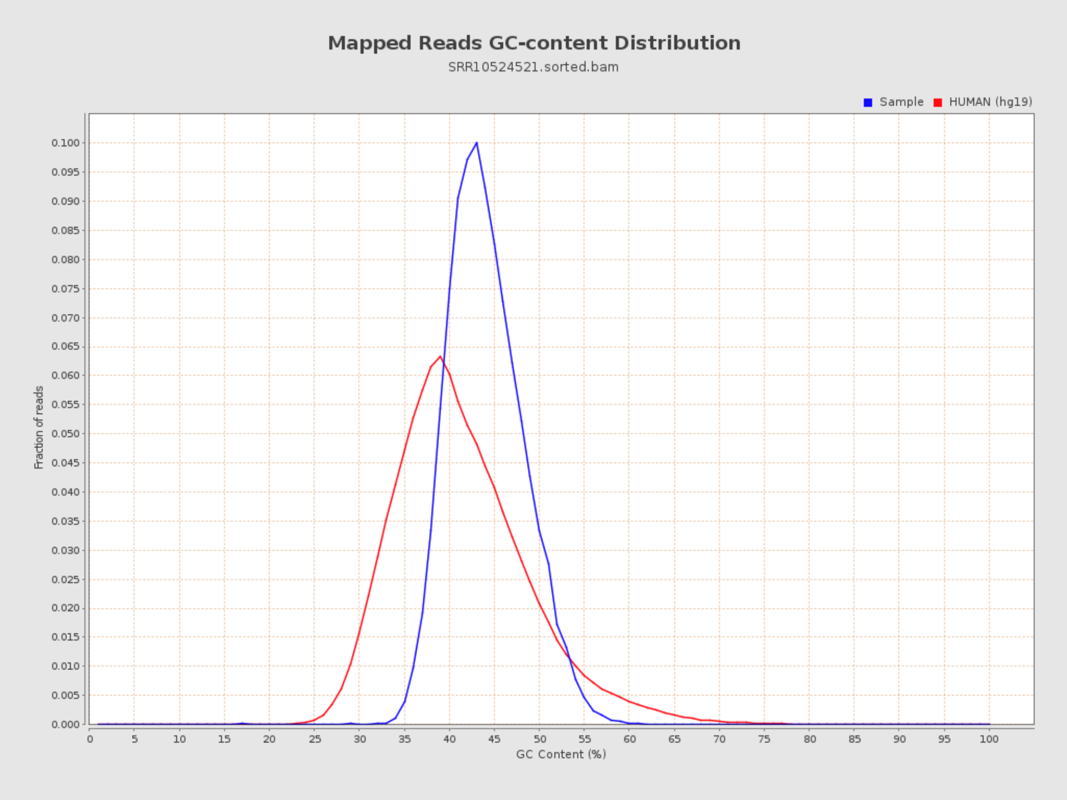
7. Results : Duplication Rate Histogram



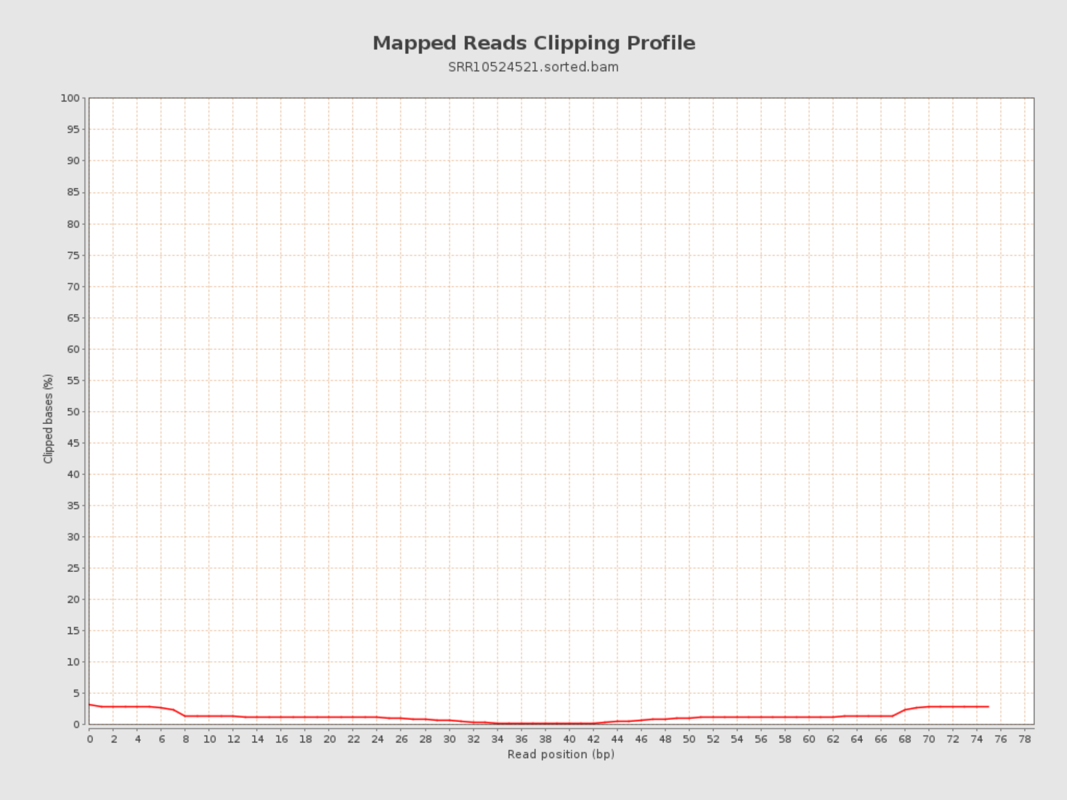
8. Results : Mapped Reads Nucleotide Content



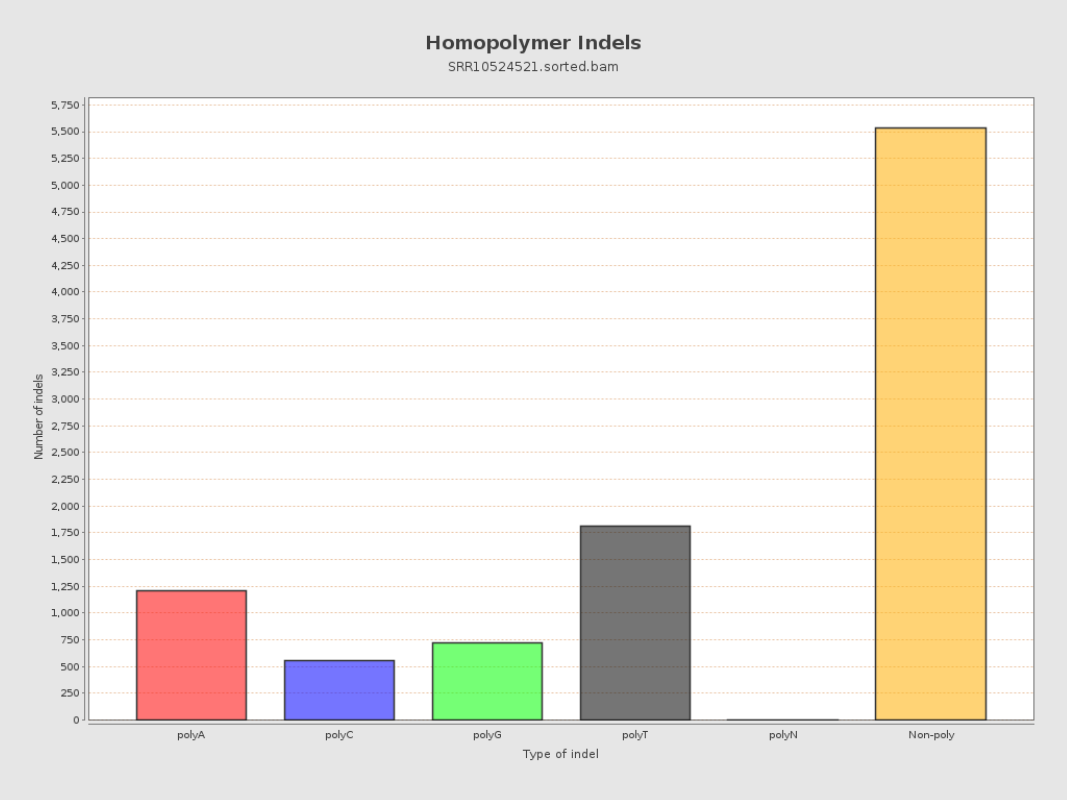
9. Results : Mapped Reads GC-content Distribution



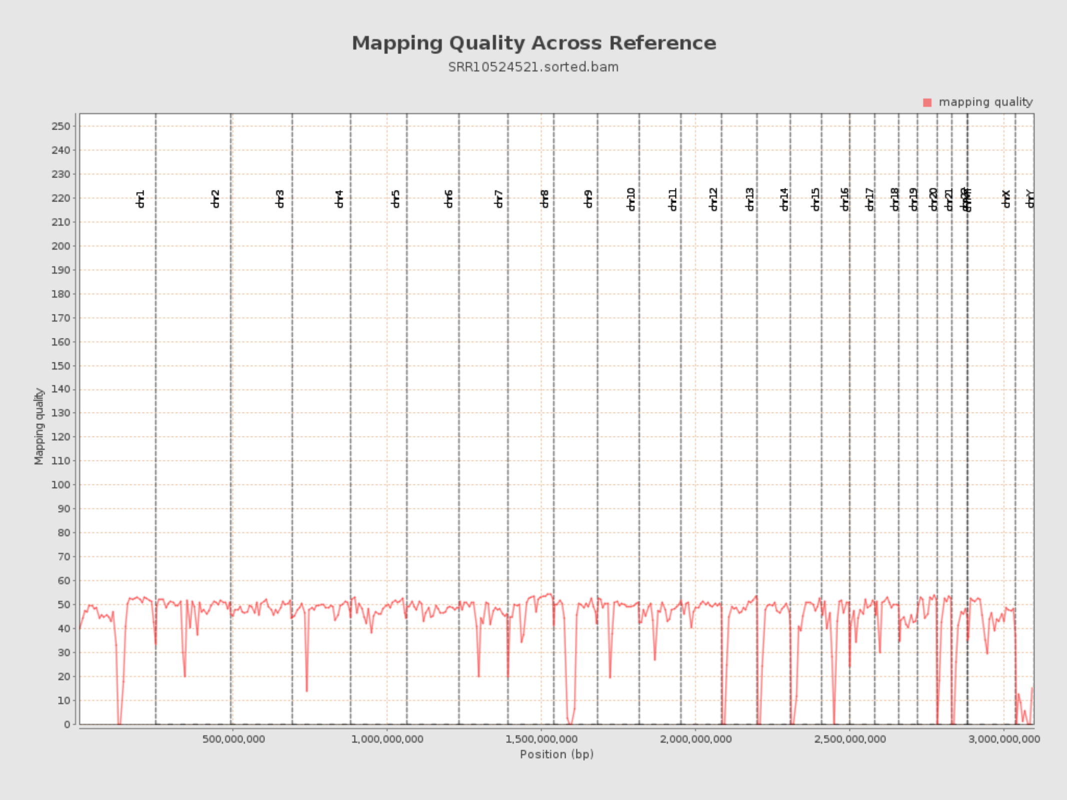
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram