Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 03:16:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524421.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_SRR10524421 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524421.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 03:16:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524421.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	574,405
Mapped reads	526,244 / 91.62%
Unmapped reads	48,161 / 8.38%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,413 / 0.42%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	12,377 / 2.15%
Duplication rate	1.78%
Clipped reads	526,930 / 91.73%

2.2. ACGT Content

Number/percentage of A's	7,330,185 / 23.89%
Number/percentage of C's	6,440,787 / 21%
Number/percentage of T's	9,697,467 / 31.61%
Number/percentage of G's	7,205,596 / 23.49%
Number/percentage of N's	3,094 / 0.01%
GC Percentage	44.48%

2.3. Coverage

Mean	0.0099

Standard Deviation	0.1287

2.4. Mapping Quality

Mean Mapping Quality	44.28

2.5. Mismatches and indels

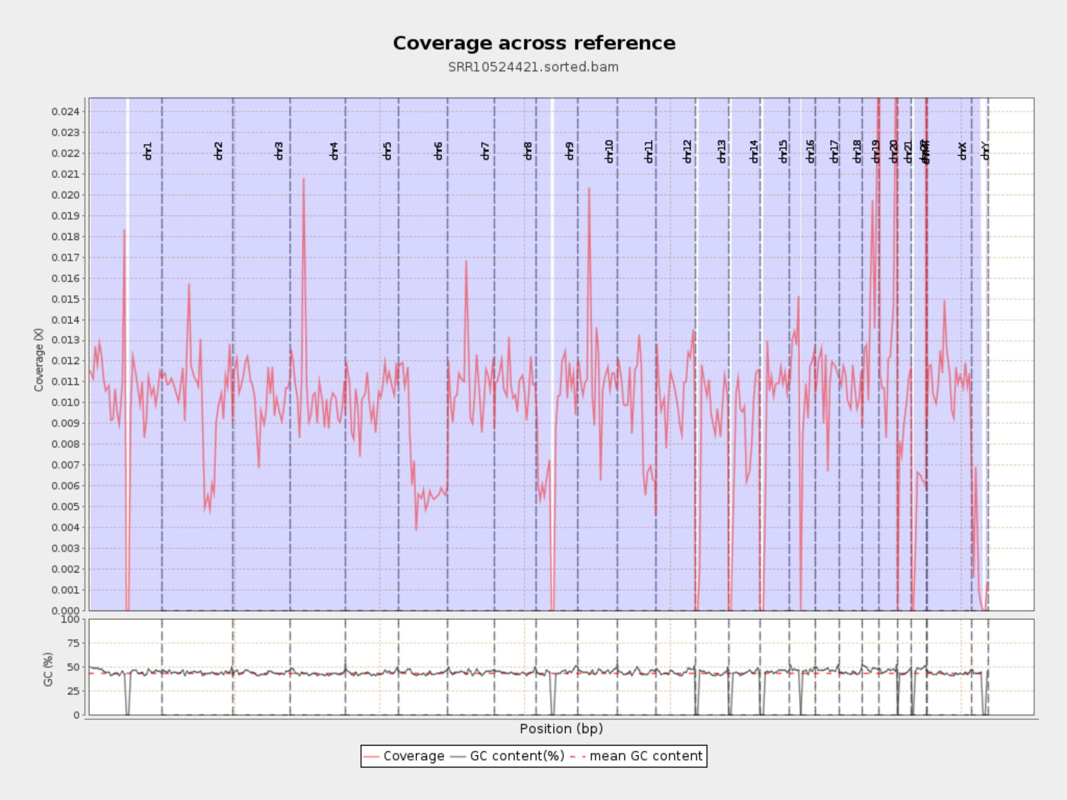
General error rate	0.54%
Mismatches	160,436
Insertions	2,064
Mapped reads with at least one insertion	0.39%
Deletions	5,912
Mapped reads with at least one deletion	1.12%
Homopolymer indels	42.08%

2.6. Chromosome stats

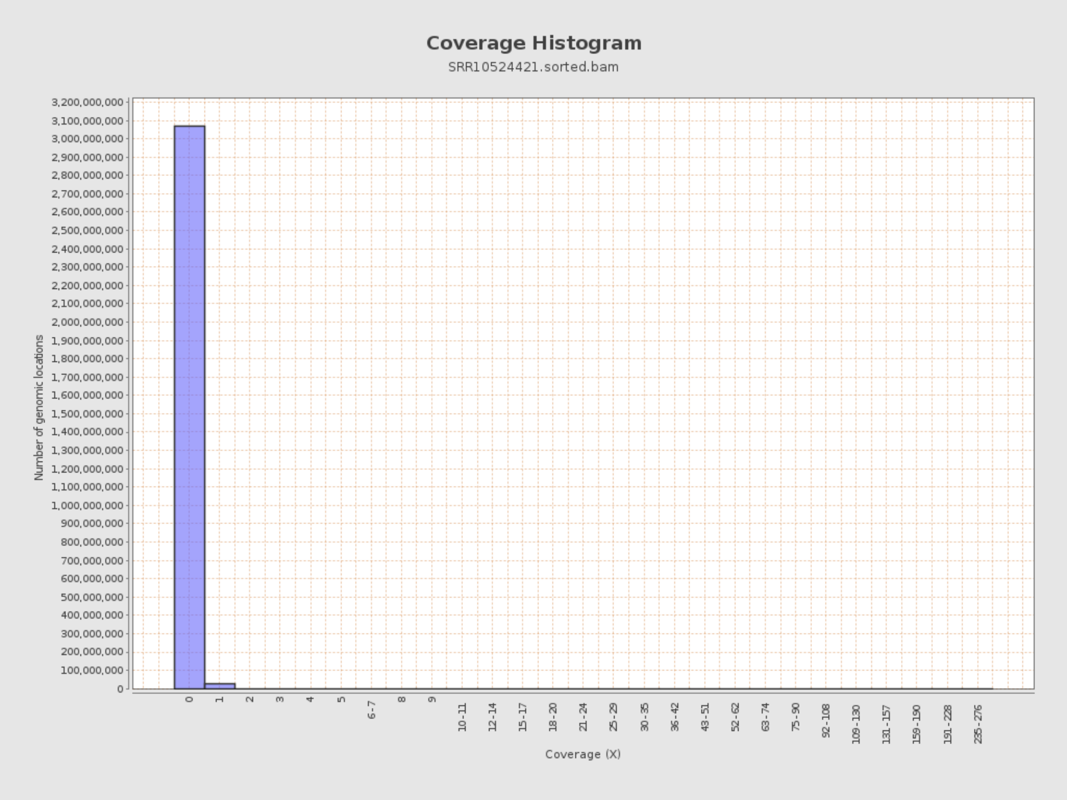
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2558734	0.0103	0.2158
chr2	243199373	2469908	0.0102	0.1573
chr3	198022430	2052133	0.0104	0.1061
chr4	191154276	2010518	0.0105	0.1182
chr5	180915260	1859548	0.0103	0.1053
chr6	171115067	1192688	0.007	0.0899
chr7	159138663	1745677	0.011	0.1499

chr8	146364022	1595857	0.0109	0.116
chr9	141213431	1135564	0.008	0.1006
chr10	135534747	1544548	0.0114	0.137
chr11	135006516	1271712	0.0094	0.1091
chr12	133851895	1433798	0.0107	0.1086
chr13	115169878	973120	0.0084	0.0958
chr14	107349540	856071	0.008	0.0948
chr15	102531392	934764	0.0091	0.0994
chr16	90354753	981381	0.0109	0.1112
chr17	81195210	891637	0.011	0.1123
chr18	78077248	840097	0.0108	0.1457
chr19	59128983	951083	0.0161	0.17
chr20	63025520	884288	0.014	0.127
chr21	48129895	413547	0.0086	0.1039
chr22	51304566	231012	0.0045	0.0704
chrMT	16571	6311	0.3808	0.7037
chrX	155270560	1743571	0.0112	0.1137
chrY	59373566	108838	0.0018	0.0727

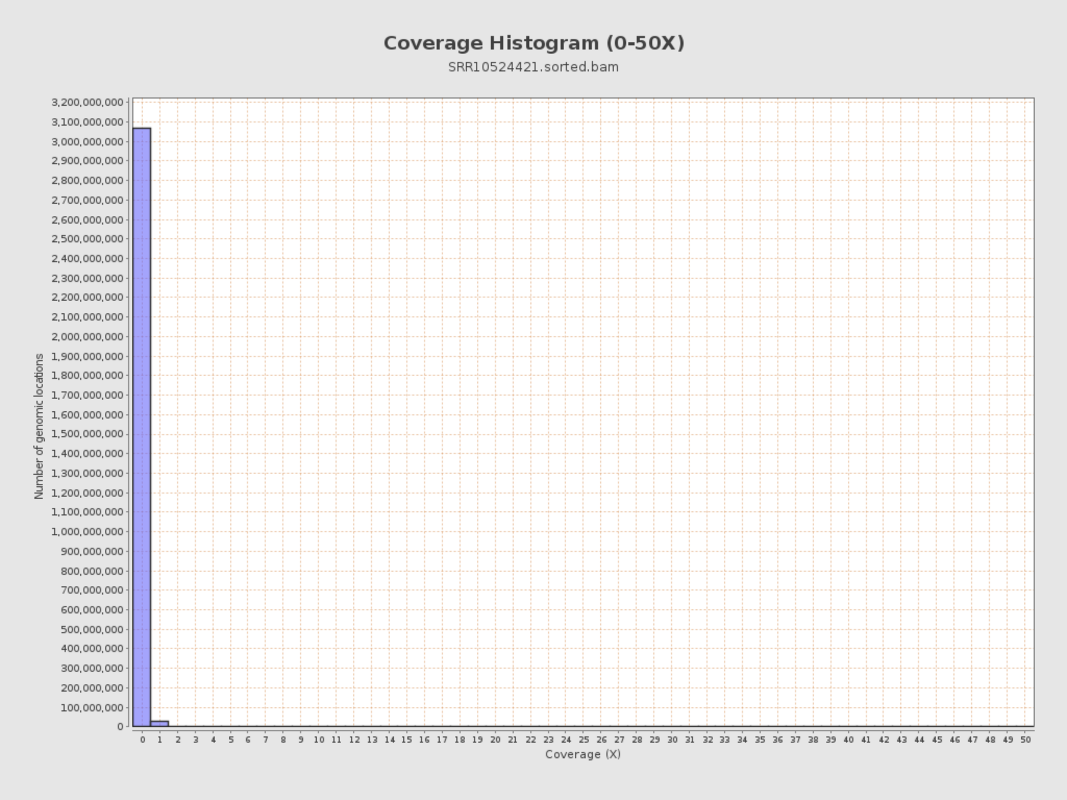
3. Results : Coverage across reference



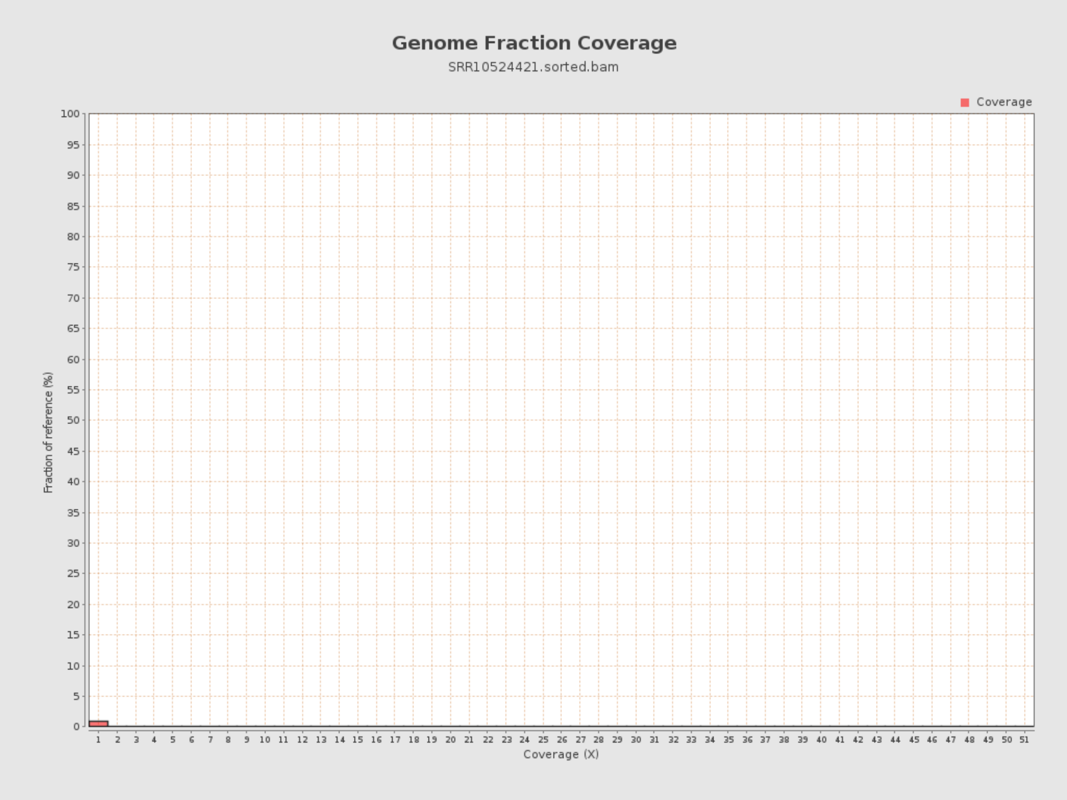
4. Results : Coverage Histogram



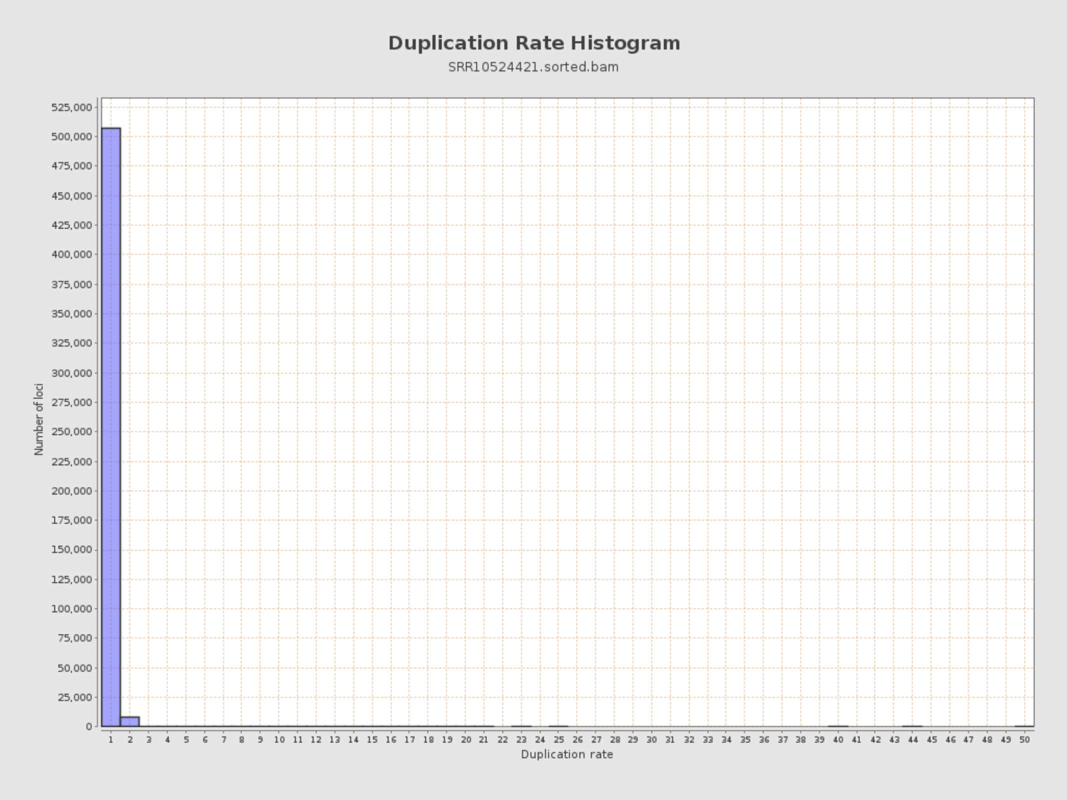
5. Results : Coverage Histogram (0-50X)



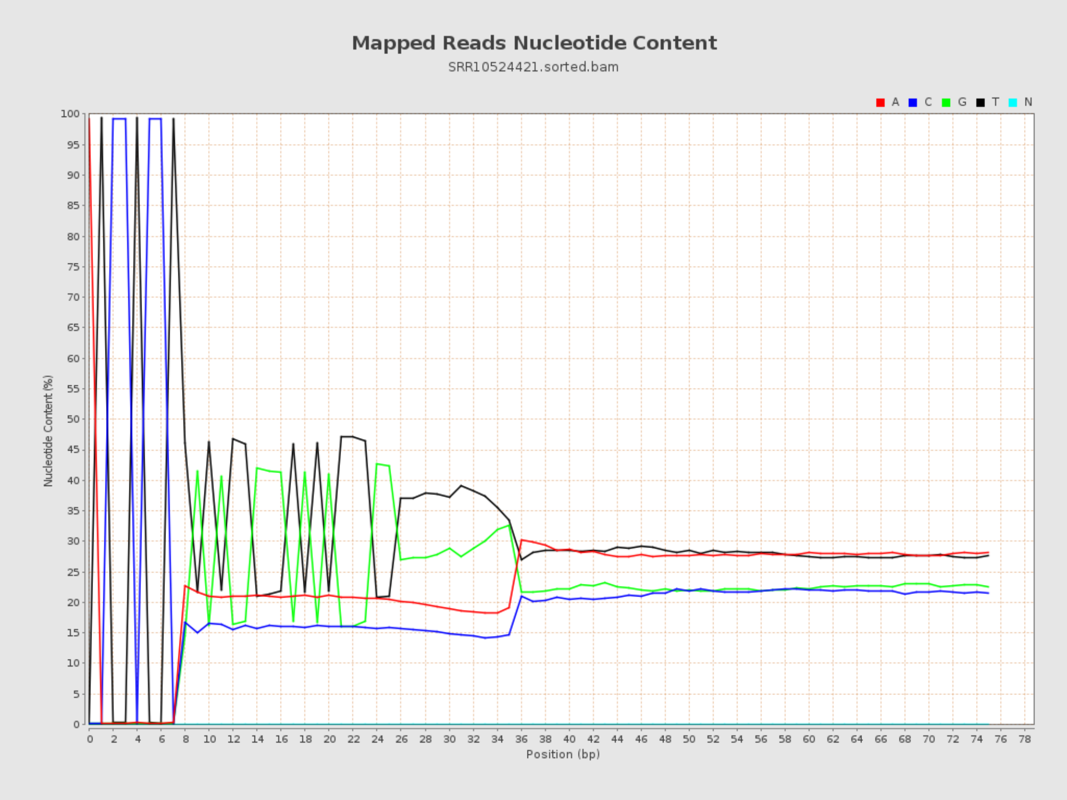
6. Results : Genome Fraction Coverage



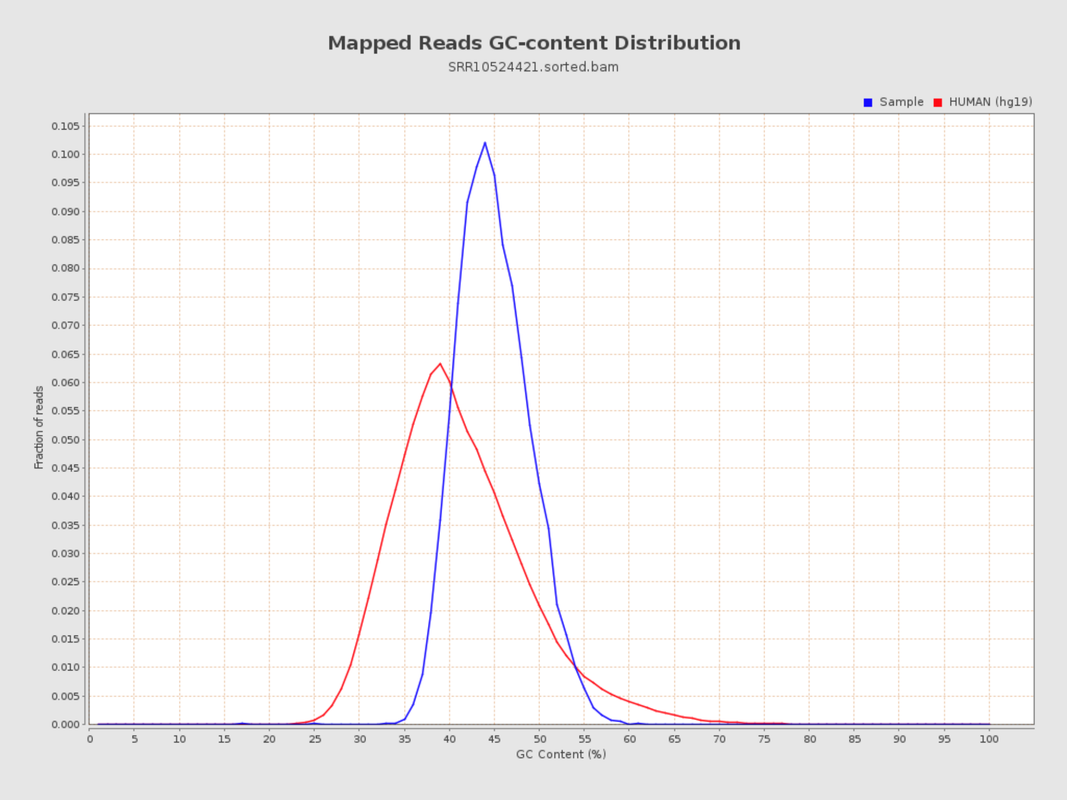
7. Results : Duplication Rate Histogram



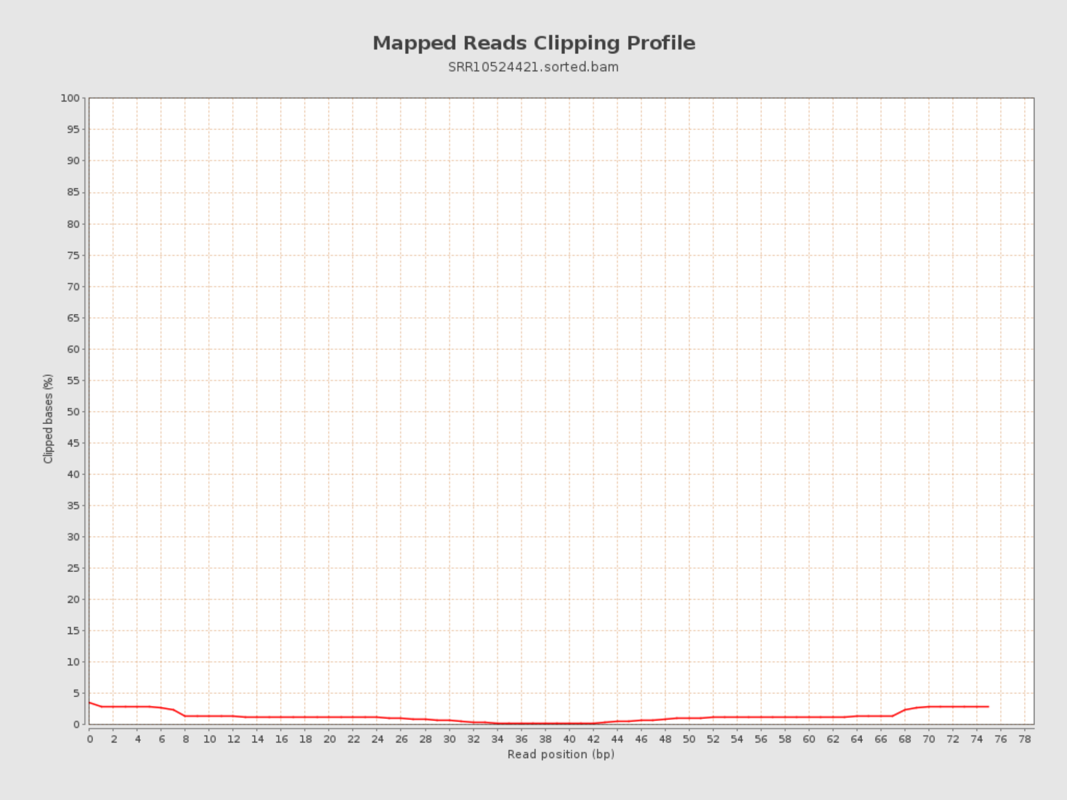
8. Results : Mapped Reads Nucleotide Content



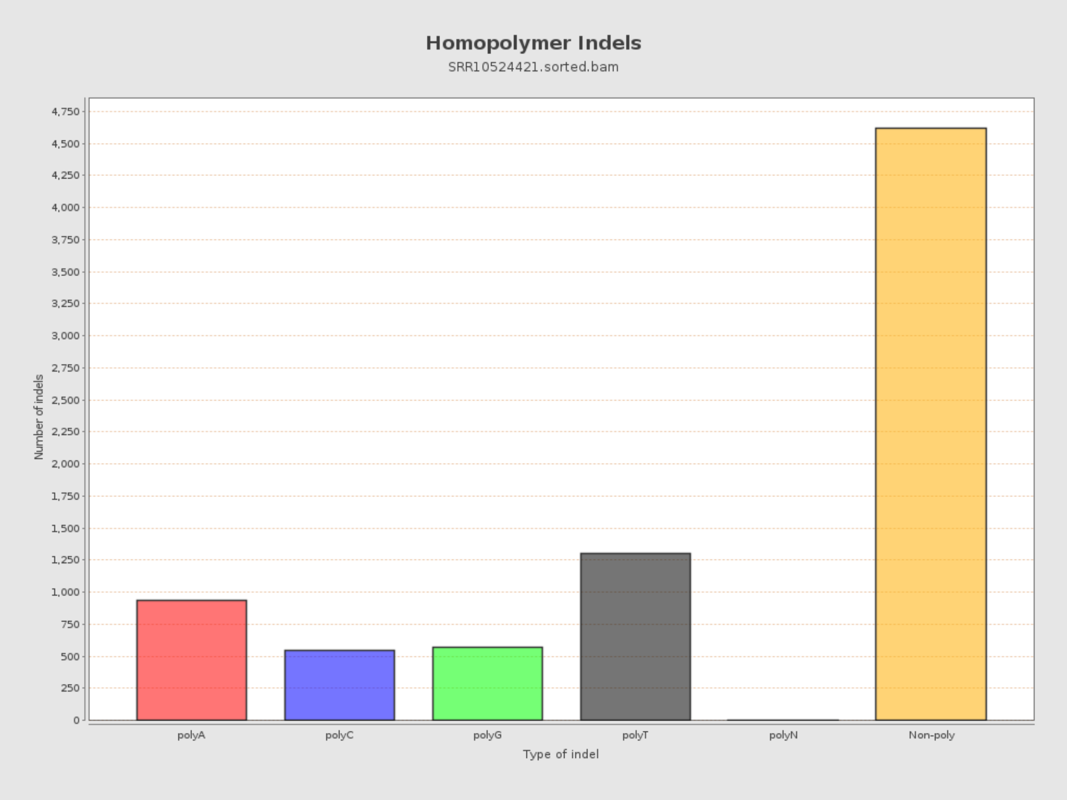
9. Results : Mapped Reads GC-content Distribution



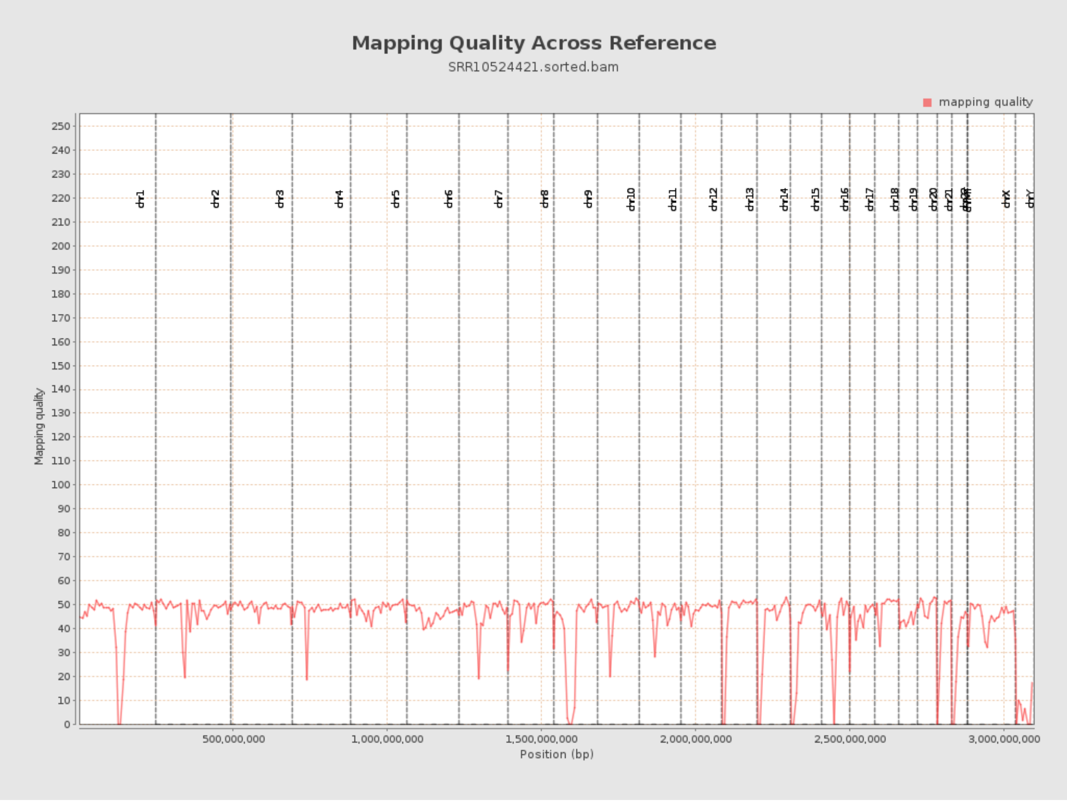
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram