Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 04:42:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524924.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_SRR10524924 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524924.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 04:42:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524924.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,407,350
Mapped reads	1,290,565 / 91.7%
Unmapped reads	116,785 / 8.3%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,853 / 0.34%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	59,542 / 4.23%
Duplication rate	3.61%
Clipped reads	1,292,194 / 91.82%

2.2. ACGT Content

Number/percentage of A's	18,912,932 / 25.29%
Number/percentage of C's	13,913,928 / 18.6%
Number/percentage of T's	24,184,723 / 32.34%
Number/percentage of G's	17,778,877 / 23.77%
Number/percentage of N's	580 / 0%
GC Percentage	42.38%

2.3. Coverage

Mean	0.0242

Standard Deviation	0.2392

2.4. Mapping Quality

Mean Mapping Quality	44.67

2.5. Mismatches and indels

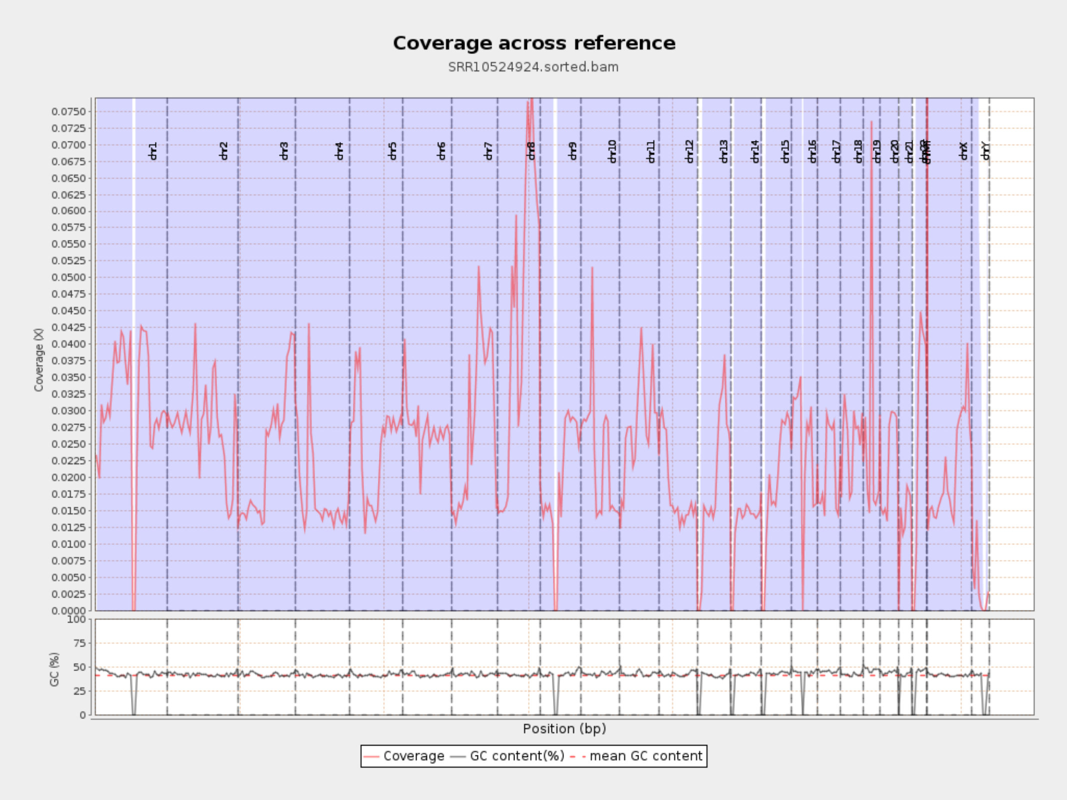
General error rate	0.53%
Mismatches	385,011
Insertions	5,143
Mapped reads with at least one insertion	0.4%
Deletions	14,223
Mapped reads with at least one deletion	1.09%
Homopolymer indels	41.73%

2.6. Chromosome stats

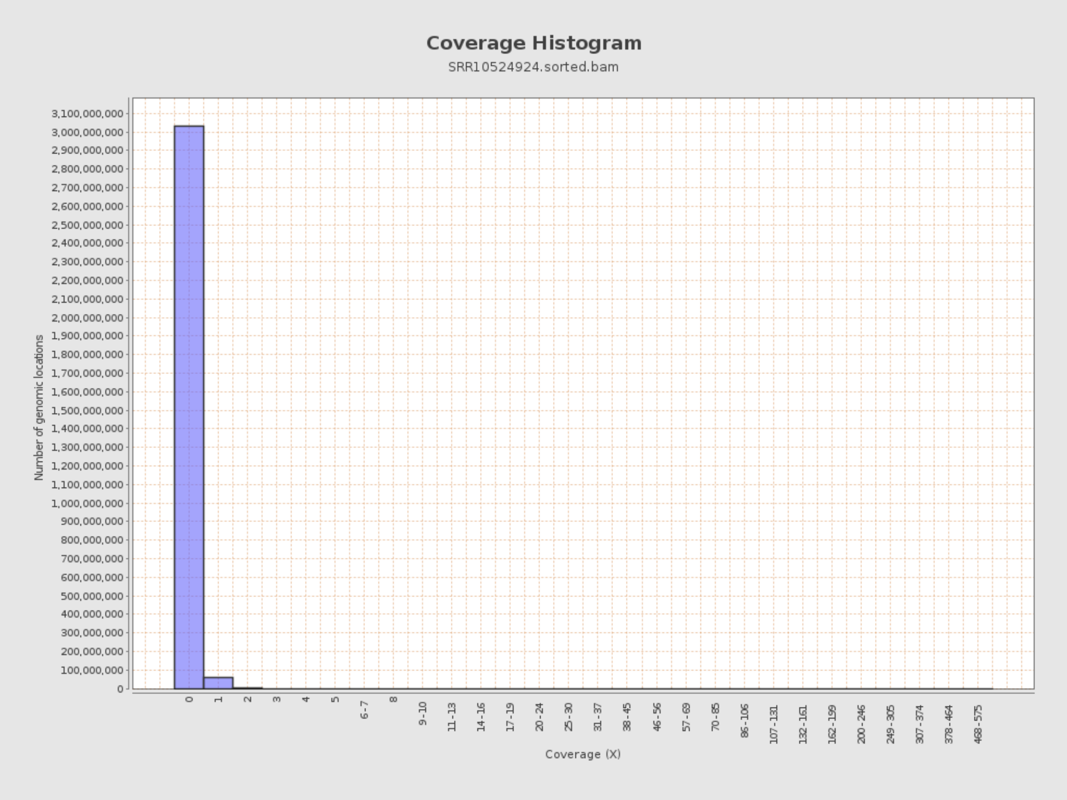
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7669182	0.0308	0.4294
chr2	243199373	6701862	0.0276	0.3085
chr3	198022430	4673223	0.0236	0.1687
chr4	191154276	3397525	0.0178	0.1761
chr5	180915260	4516693	0.025	0.1729
chr6	171115067	4688802	0.0274	0.1931
chr7	159138663	4548745	0.0286	0.2839

chr8	146364022	6594933	0.0451	0.3
chr9	141213431	2716167	0.0192	0.1877
chr10	135534747	3217318	0.0237	0.26
chr11	135006516	3799169	0.0281	0.2137
chr12	133851895	2423487	0.0181	0.1521
chr13	115169878	2170469	0.0188	0.1524
chr14	107349540	1366688	0.0127	0.1295
chr15	102531392	1933176	0.0189	0.151
chr16	90354753	2207634	0.0244	0.181
chr17	81195210	1692354	0.0208	0.1632
chr18	78077248	1972509	0.0253	0.3127
chr19	59128983	1564950	0.0265	0.3019
chr20	63025520	1397557	0.0222	0.1677
chr21	48129895	654635	0.0136	0.1486
chr22	51304566	1398183	0.0273	0.1819
chrMT	16571	4047	0.2442	0.4988
chrX	155270560	3295216	0.0212	0.1741
chrY	59373566	210090	0.0035	0.1187

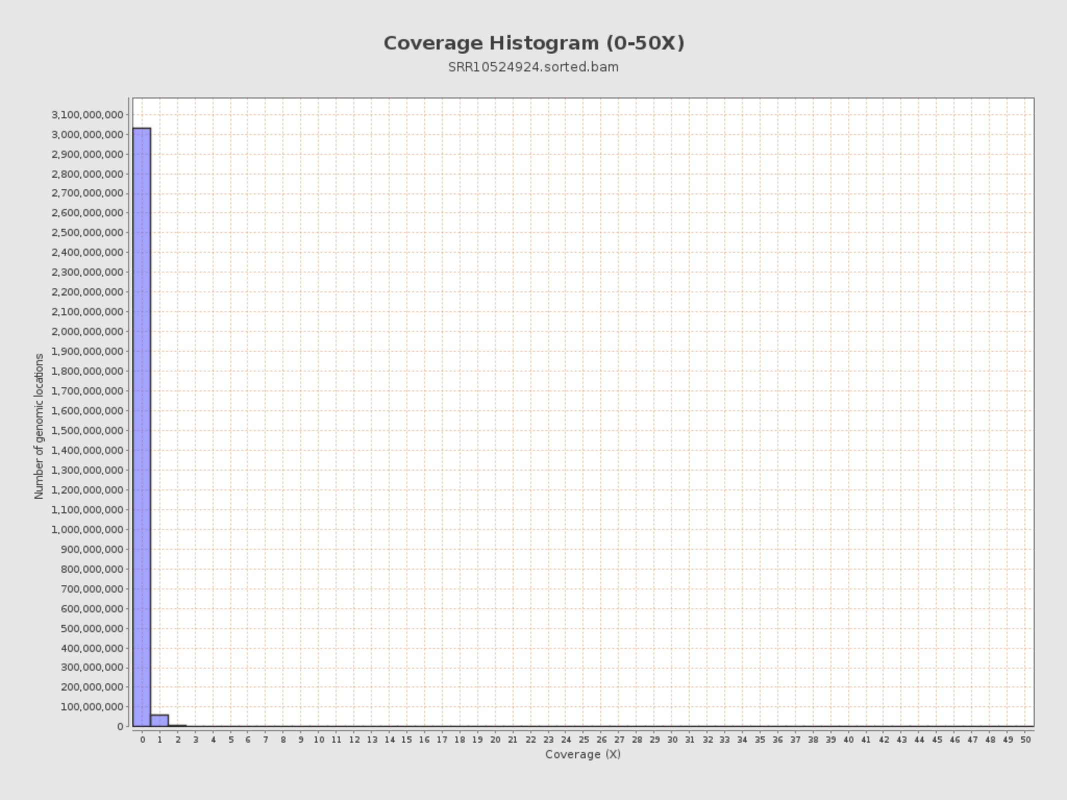
3. Results : Coverage across reference



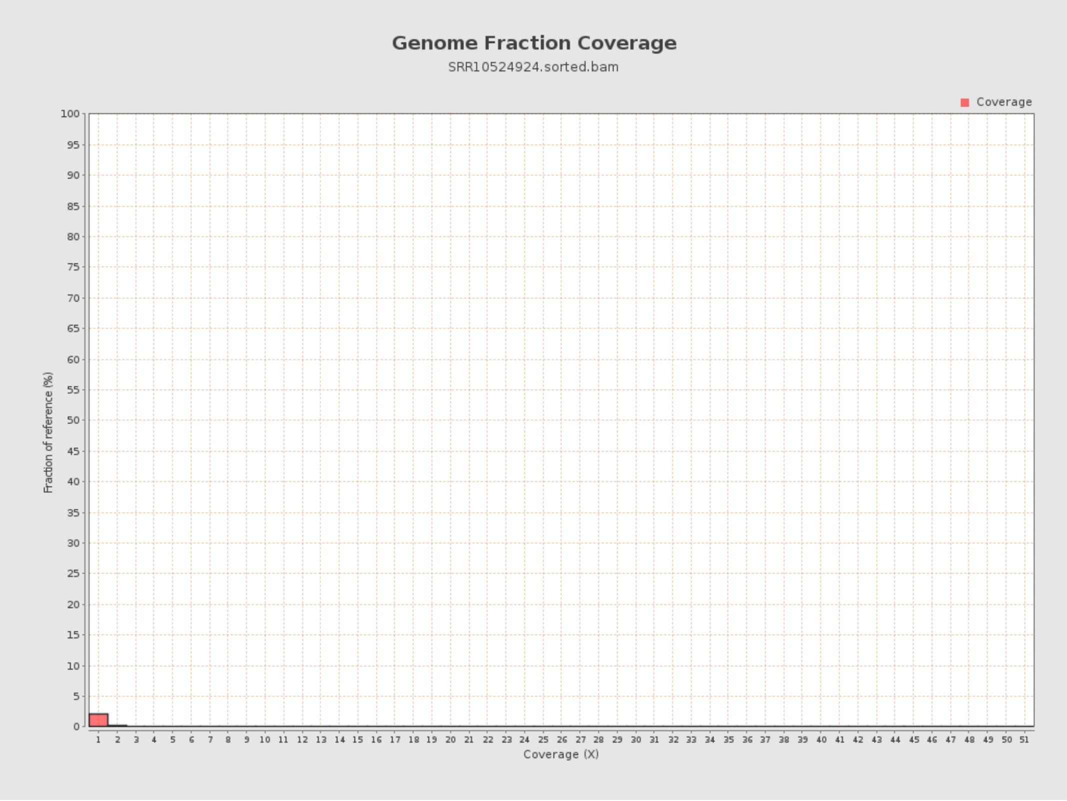
4. Results : Coverage Histogram



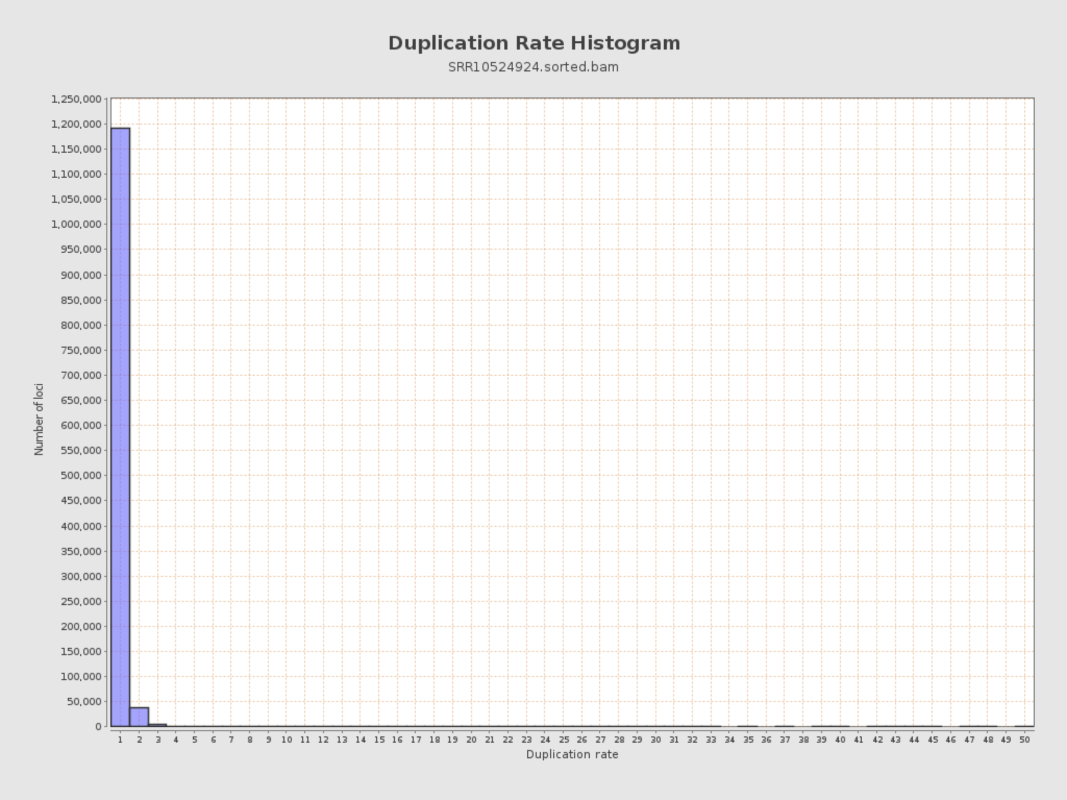
5. Results : Coverage Histogram (0-50X)



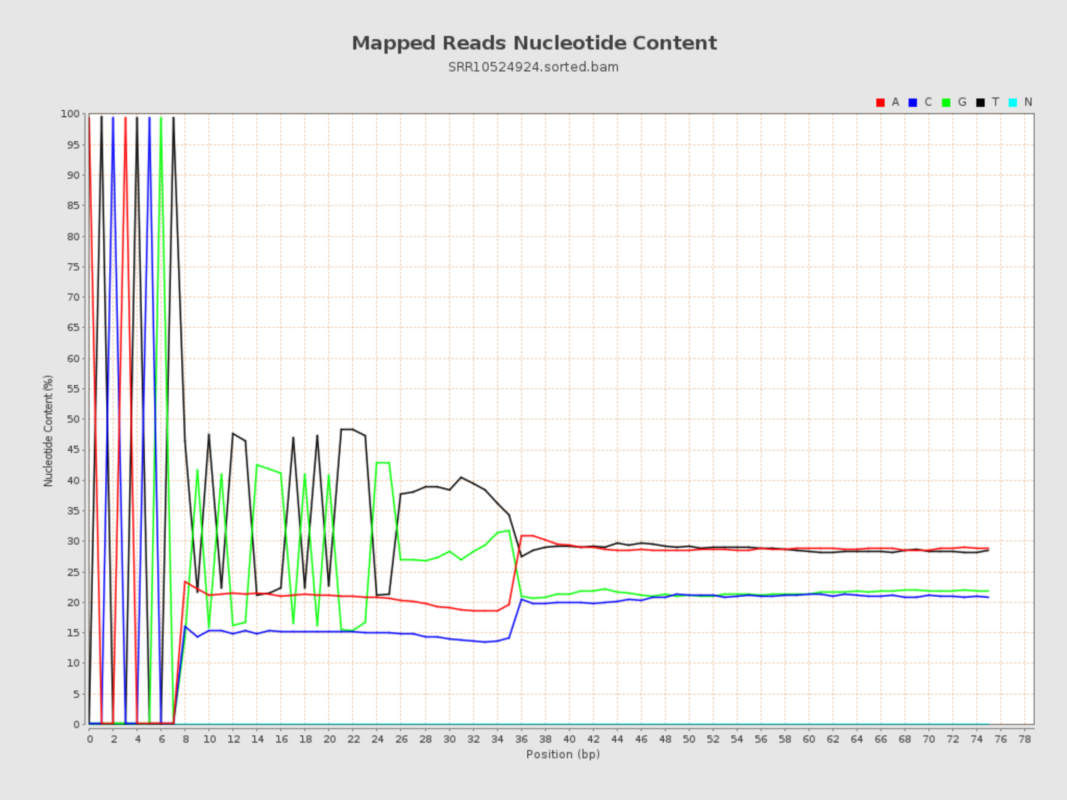
6. Results : Genome Fraction Coverage



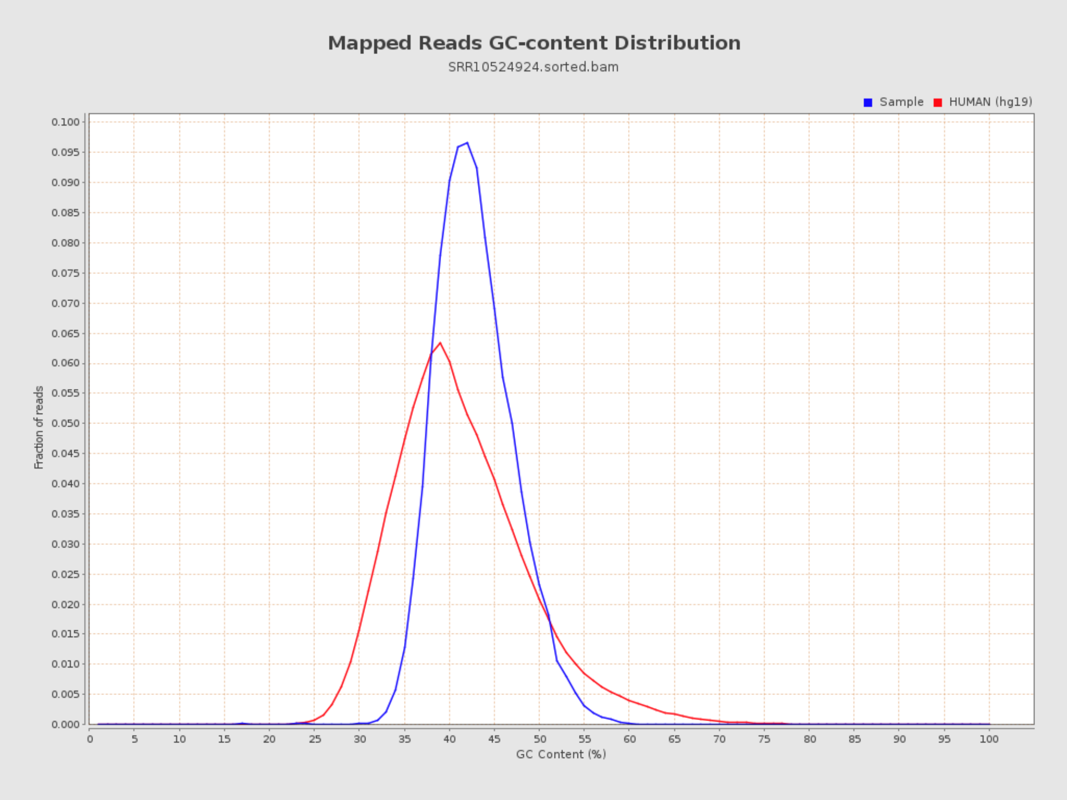
7. Results : Duplication Rate Histogram



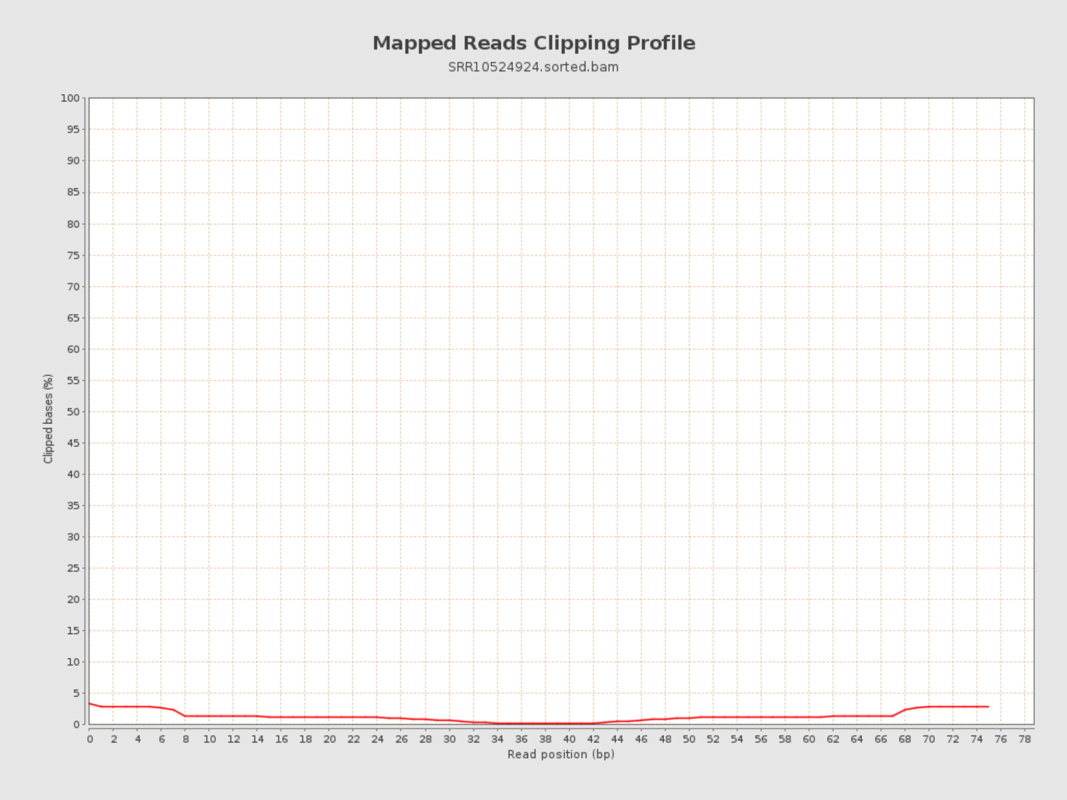
8. Results : Mapped Reads Nucleotide Content



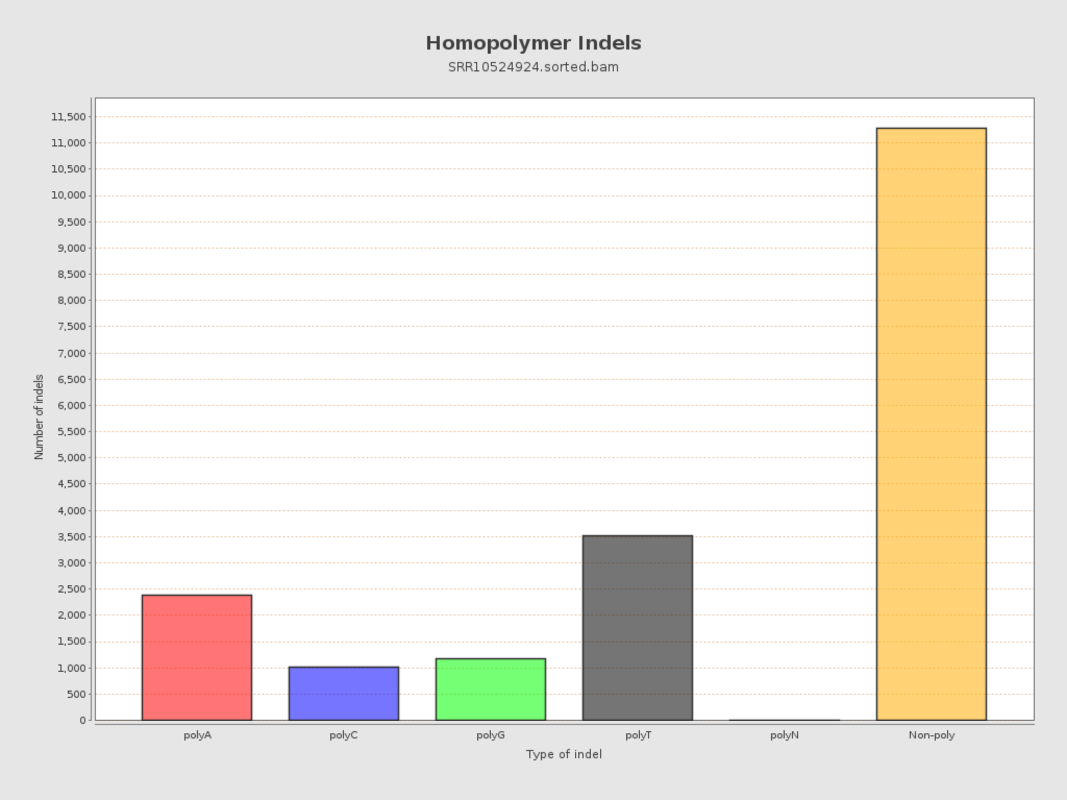
9. Results : Mapped Reads GC-content Distribution



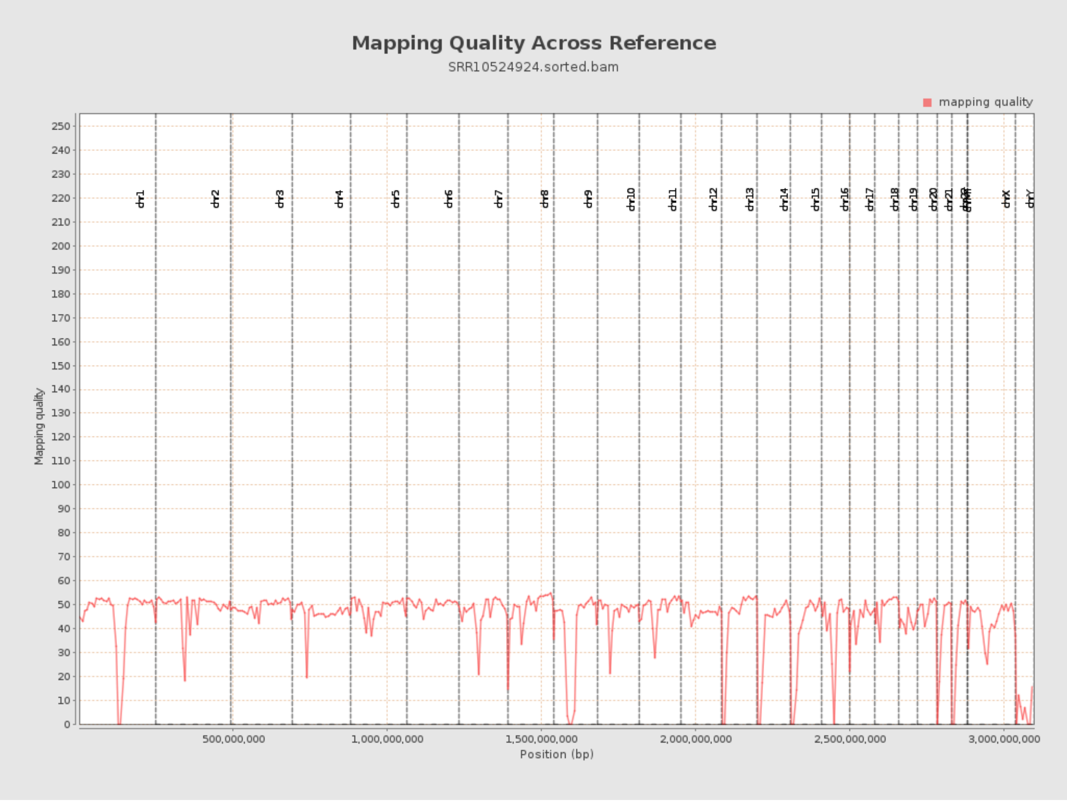
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram