Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 15:44:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524667.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_SRR10524667 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524667.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 15:44:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524667.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,795,636
Mapped reads	1,639,793 / 91.32%
Unmapped reads	155,843 / 8.68%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,406 / 0.3%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	67,594 / 3.76%
Duplication rate	3.06%
Clipped reads	1,640,788 / 91.38%

2.2. ACGT Content

Number/percentage of A's	24,374,571 / 25.67%
Number/percentage of C's	18,005,779 / 18.96%
Number/percentage of T's	30,421,846 / 32.03%
Number/percentage of G's	22,167,247 / 23.34%
Number/percentage of N's	2,070 / 0%
GC Percentage	42.3%

2.3. Coverage

Mean	0.0307

Standard Deviation	0.3057

2.4. Mapping Quality

Mean Mapping Quality	45.18

2.5. Mismatches and indels

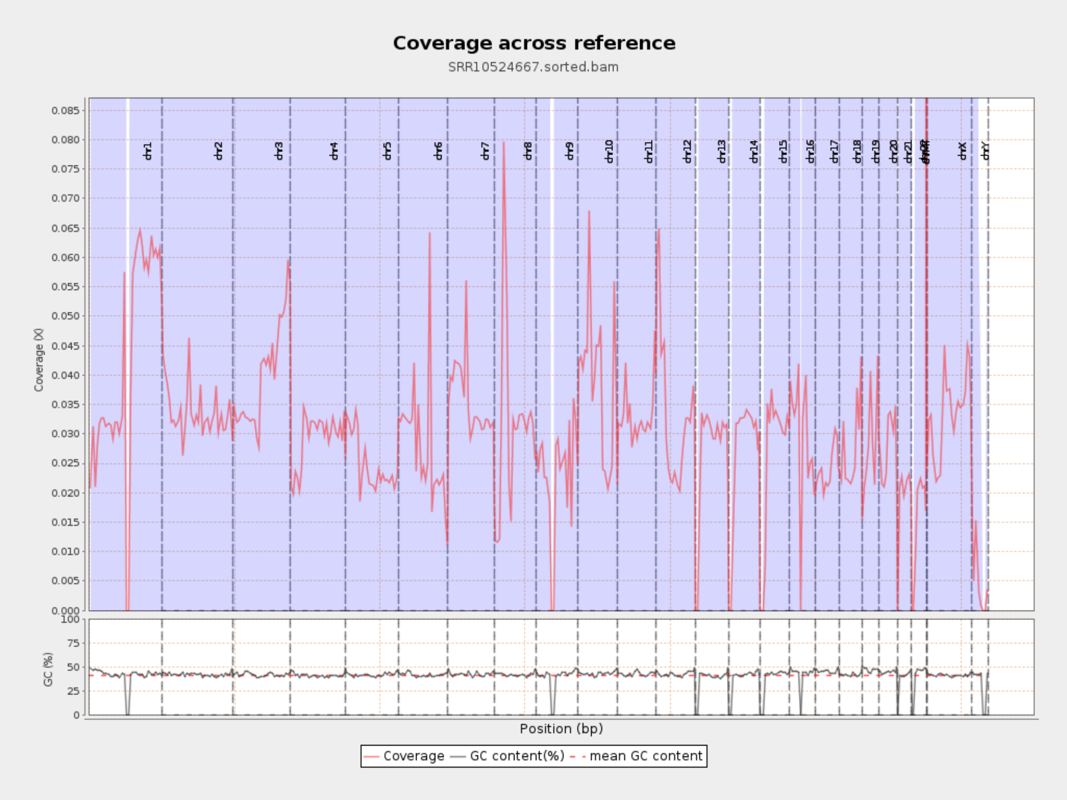
General error rate	0.51%
Mismatches	474,536
Insertions	7,411
Mapped reads with at least one insertion	0.45%
Deletions	19,196
Mapped reads with at least one deletion	1.16%
Homopolymer indels	43.02%

2.6. Chromosome stats

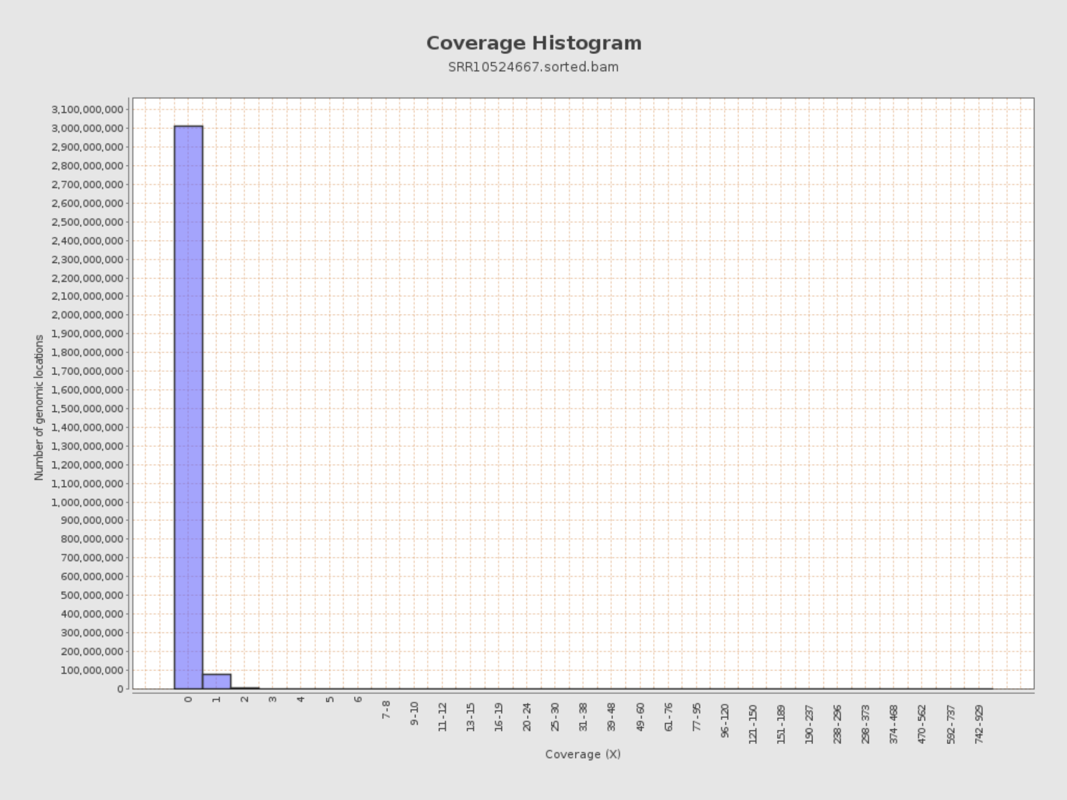
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10415290	0.0418	0.5942
chr2	243199373	8218985	0.0338	0.4234
chr3	198022430	7825119	0.0395	0.2181
chr4	191154276	5566211	0.0291	0.1983
chr5	180915260	4479722	0.0248	0.1723
chr6	171115067	4837955	0.0283	0.2174
chr7	159138663	5729824	0.036	0.4237

chr8	146364022	4546460	0.0311	0.3006
chr9	141213431	3213232	0.0228	0.2058
chr10	135534747	5304815	0.0391	0.3229
chr11	135006516	4449214	0.033	0.2409
chr12	133851895	4454049	0.0333	0.2037
chr13	115169878	3092950	0.0269	0.1804
chr14	107349540	2857576	0.0266	0.182
chr15	102531392	2697893	0.0263	0.1814
chr16	90354753	2603393	0.0288	0.2051
chr17	81195210	1957320	0.0241	0.1752
chr18	78077248	2120145	0.0272	0.4049
chr19	59128983	1703298	0.0288	0.3961
chr20	63025520	1757531	0.0279	0.1852
chr21	48129895	940229	0.0195	0.1711
chr22	51304566	759615	0.0148	0.132
chrMT	16571	5820	0.3512	0.6369
chrX	155270560	5185595	0.0334	0.2161
chrY	59373566	279615	0.0047	0.1371

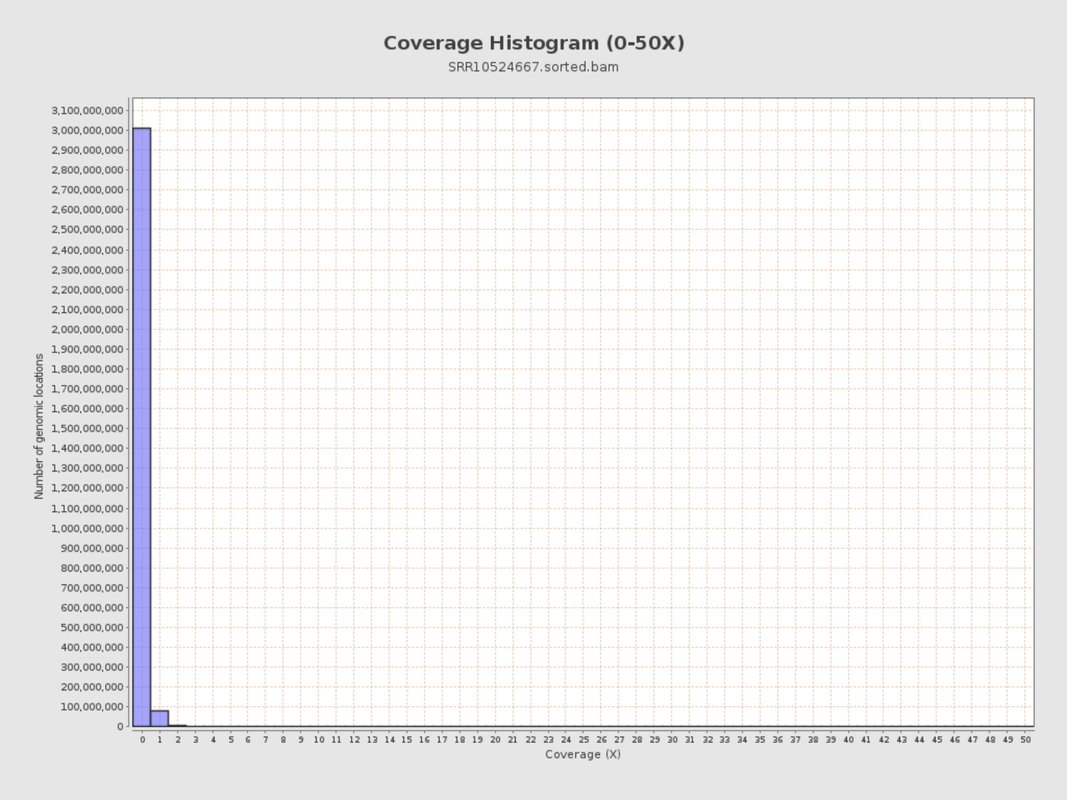
3. Results : Coverage across reference



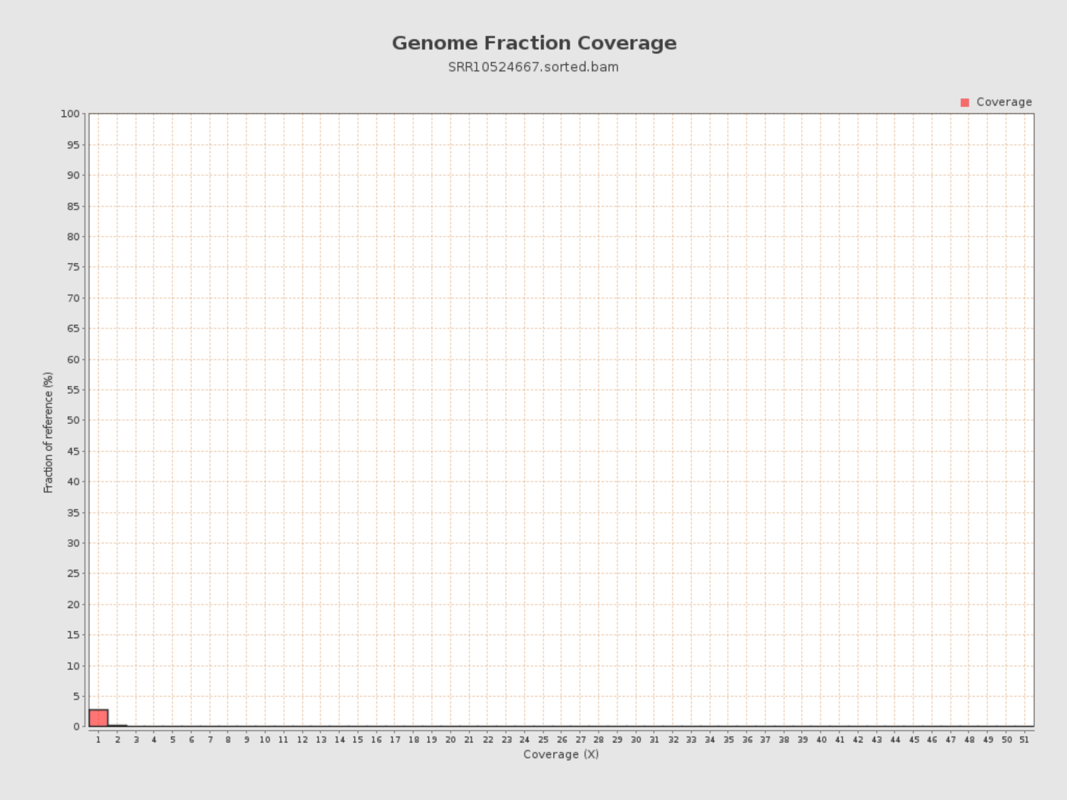
4. Results : Coverage Histogram



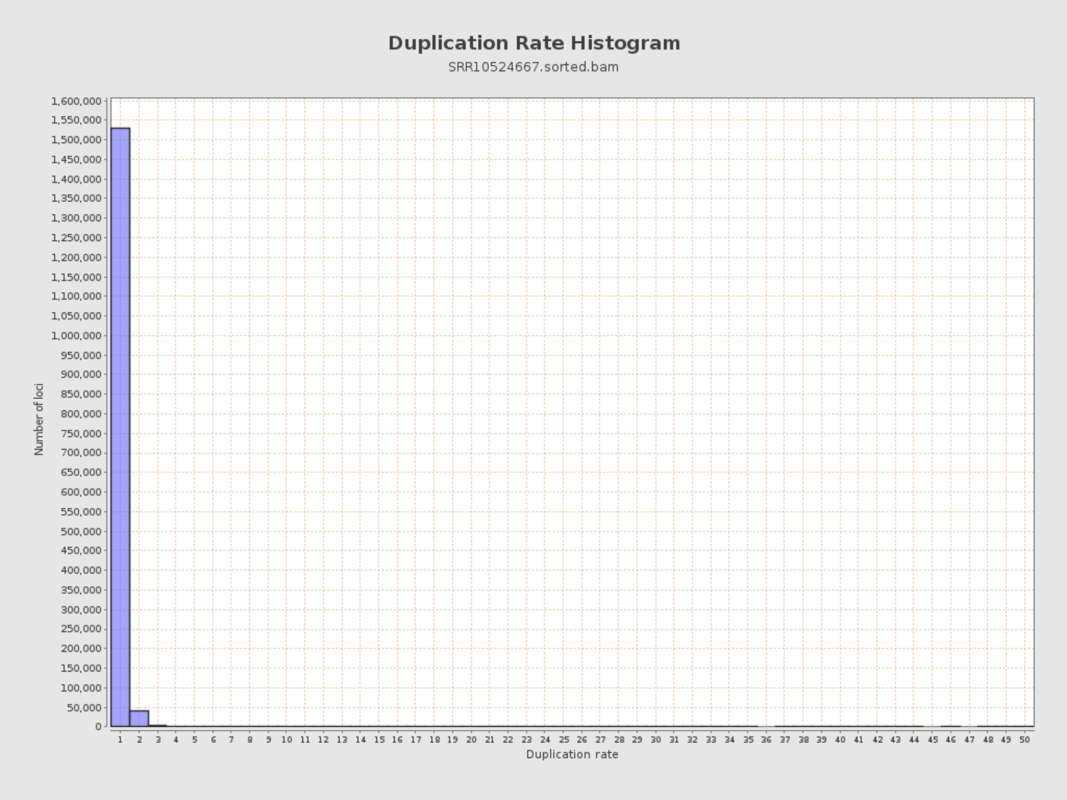
5. Results : Coverage Histogram (0-50X)



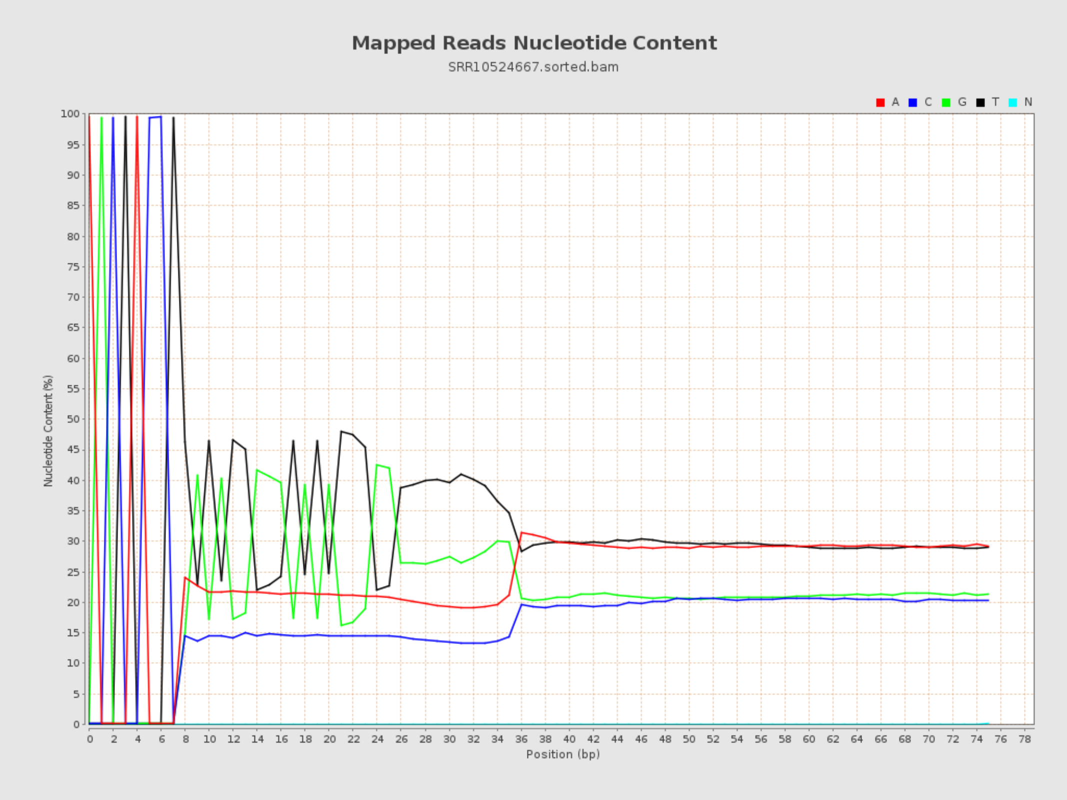
6. Results : Genome Fraction Coverage



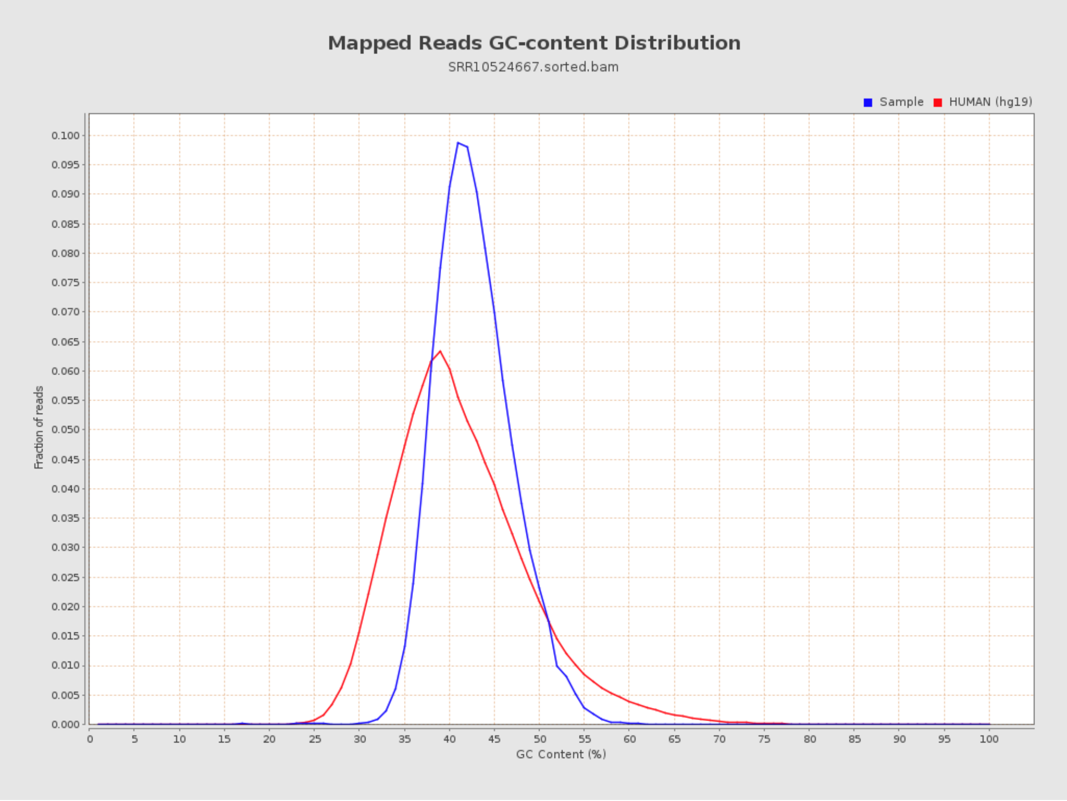
7. Results : Duplication Rate Histogram



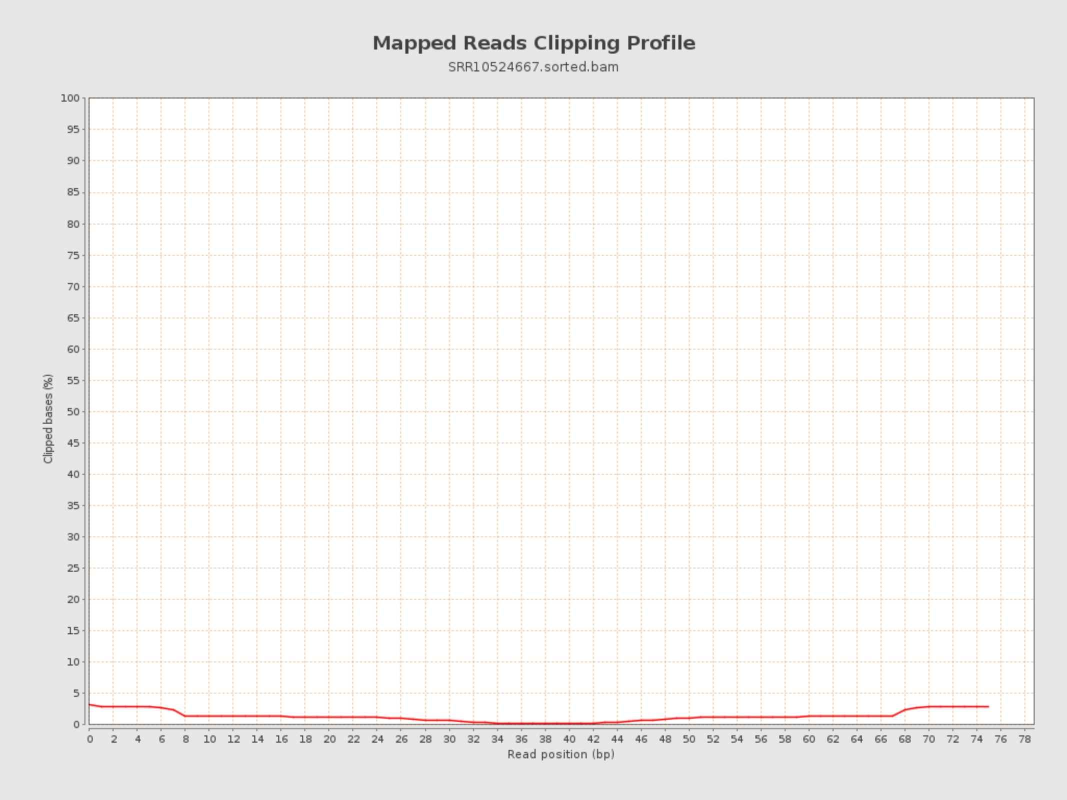
8. Results : Mapped Reads Nucleotide Content



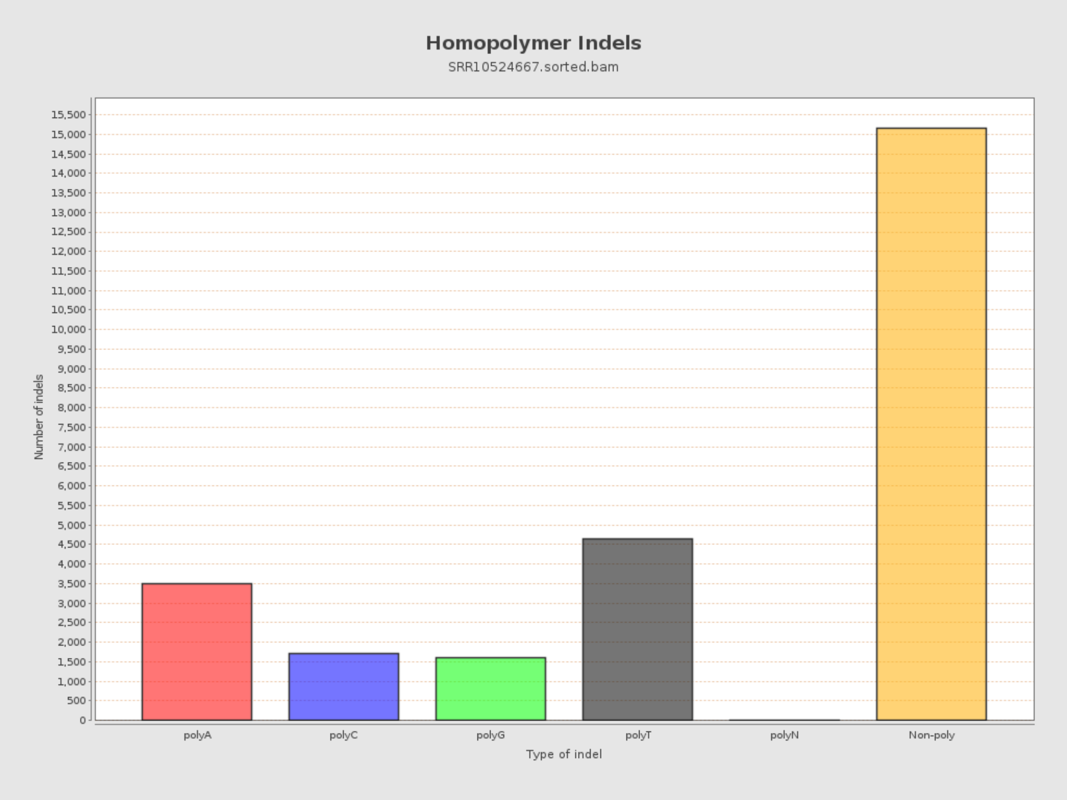
9. Results : Mapped Reads GC-content Distribution



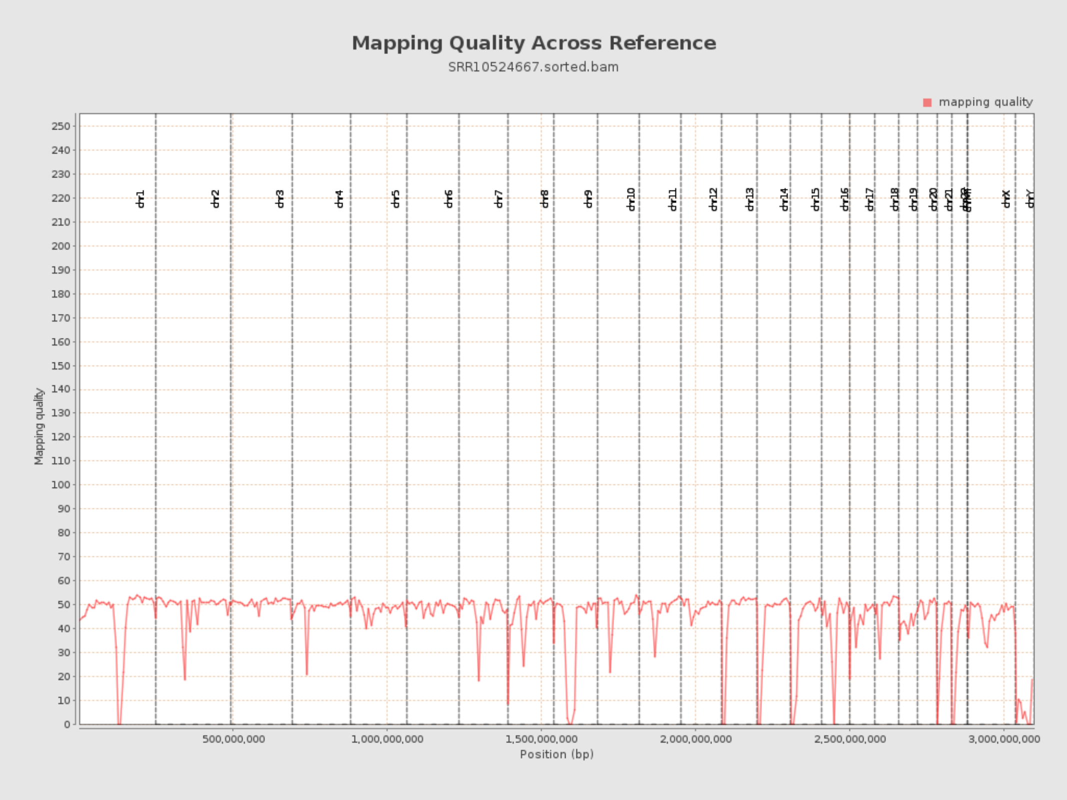
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram