Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 19:24:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524529.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_SRR10524529 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524529.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 19:24:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524529.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	744,844
Mapped reads	686,266 / 92.14%
Unmapped reads	58,578 / 7.86%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,984 / 0.4%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	22,716 / 3.05%
Duplication rate	2.64%
Clipped reads	687,206 / 92.26%

2.2. ACGT Content

Number/percentage of A's	9,897,172 / 24.4%
Number/percentage of C's	7,436,857 / 18.34%
Number/percentage of T's	13,097,178 / 32.29%
Number/percentage of G's	10,127,003 / 24.97%
Number/percentage of N's	447 / 0%
GC Percentage	43.3%

2.3. Coverage

Mean	0.0131

Standard Deviation	0.1559

2.4. Mapping Quality

Mean Mapping Quality	45.23

2.5. Mismatches and indels

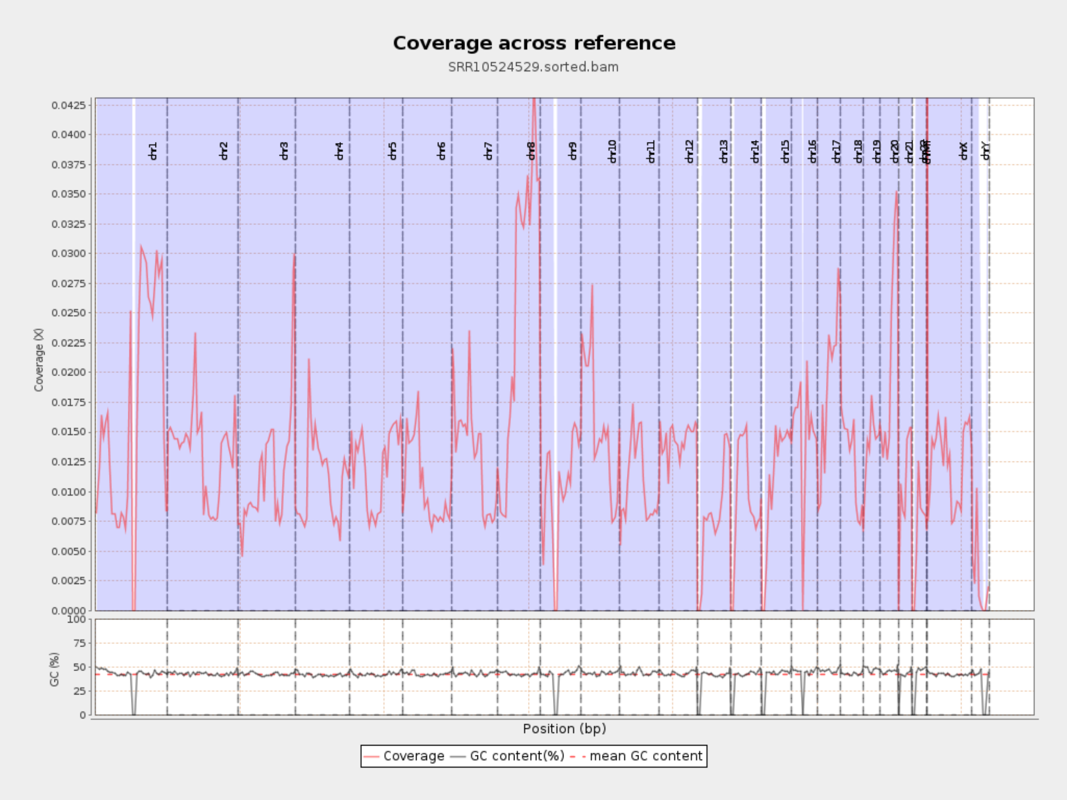
General error rate	0.53%
Mismatches	207,301
Insertions	2,937
Mapped reads with at least one insertion	0.43%
Deletions	7,396
Mapped reads with at least one deletion	1.07%
Homopolymer indels	41.82%

2.6. Chromosome stats

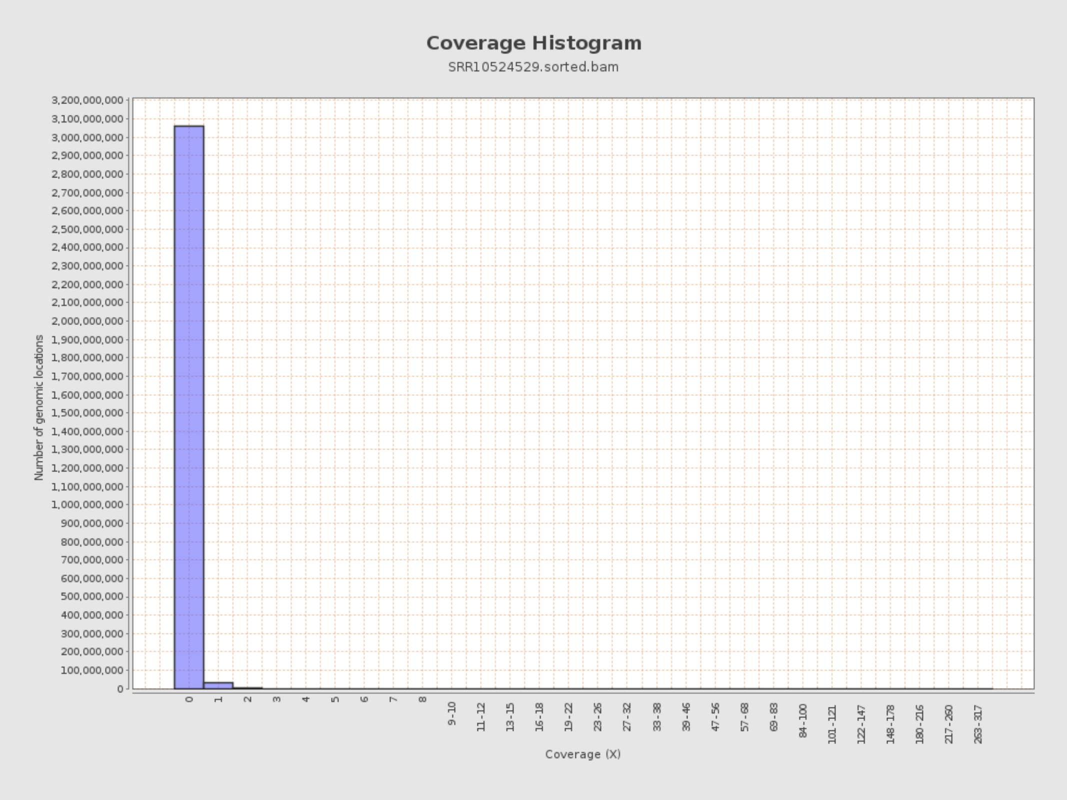
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4107744	0.0165	0.271
chr2	243199373	3250650	0.0134	0.1746
chr3	198022430	2262787	0.0114	0.1145
chr4	191154276	2099349	0.011	0.1246
chr5	180915260	2206609	0.0122	0.1185
chr6	171115067	1804481	0.0105	0.1231
chr7	159138663	2130541	0.0134	0.1804

chr8	146364022	3794668	0.0259	0.1945
chr9	141213431	1416831	0.01	0.1203
chr10	135534747	2148669	0.0159	0.1661
chr11	135006516	1454162	0.0108	0.1371
chr12	133851895	1922037	0.0144	0.1283
chr13	115169878	920596	0.008	0.0954
chr14	107349540	997455	0.0093	0.1028
chr15	102531392	1105749	0.0108	0.1112
chr16	90354753	1321279	0.0146	0.1332
chr17	81195210	1515095	0.0187	0.1515
chr18	78077248	989072	0.0127	0.1958
chr19	59128983	838196	0.0142	0.1877
chr20	63025520	1339260	0.0212	0.1576
chr21	48129895	514421	0.0107	0.1191
chr22	51304566	337990	0.0066	0.0861
chrMT	16571	3561	0.2149	0.5009
chrX	155270560	1942419	0.0125	0.1224
chrY	59373566	147627	0.0025	0.1009

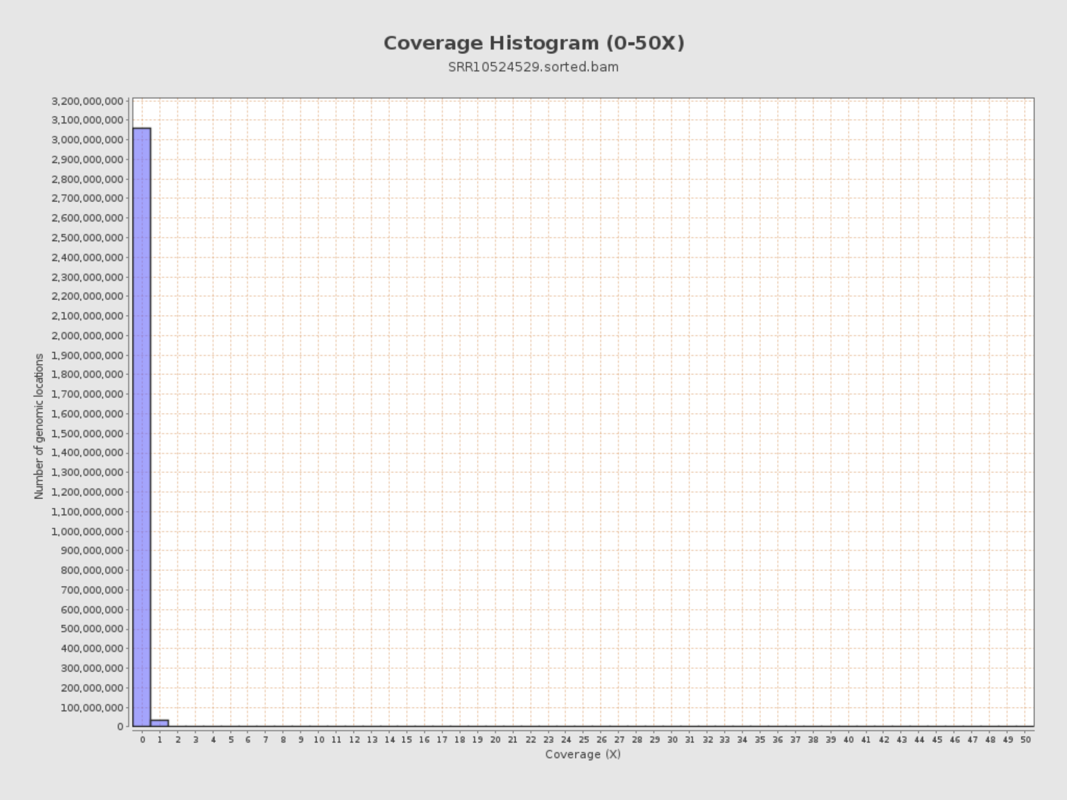
3. Results : Coverage across reference



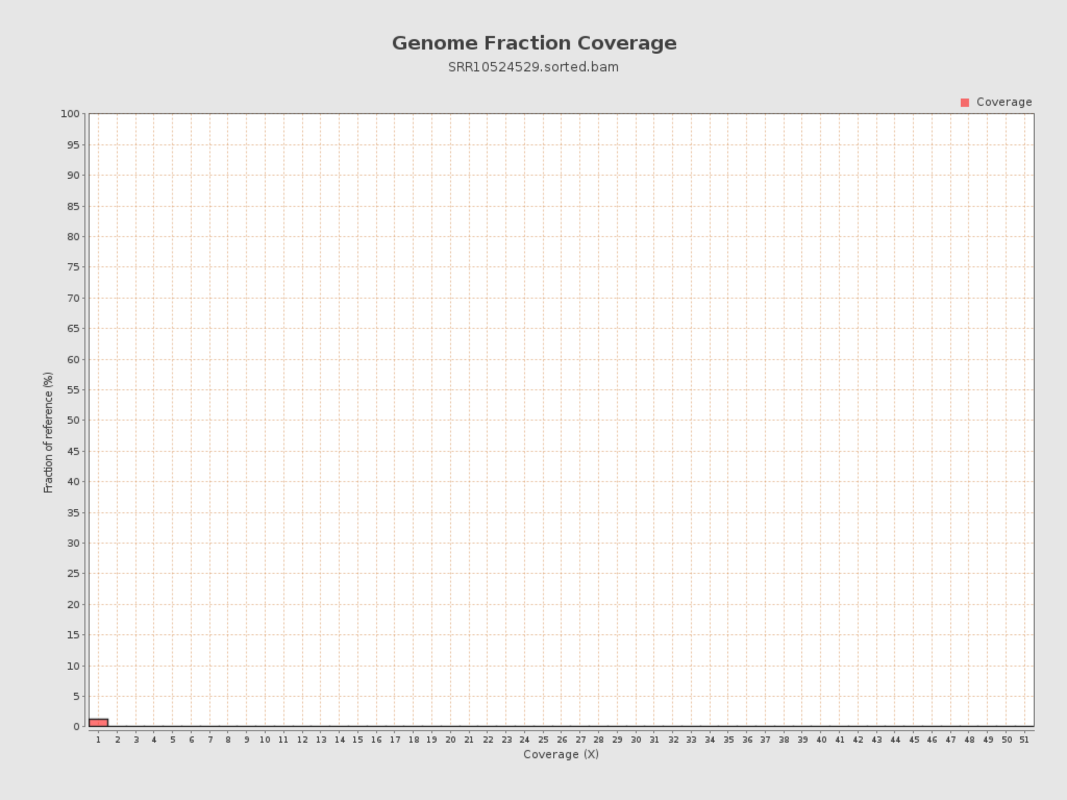
4. Results : Coverage Histogram



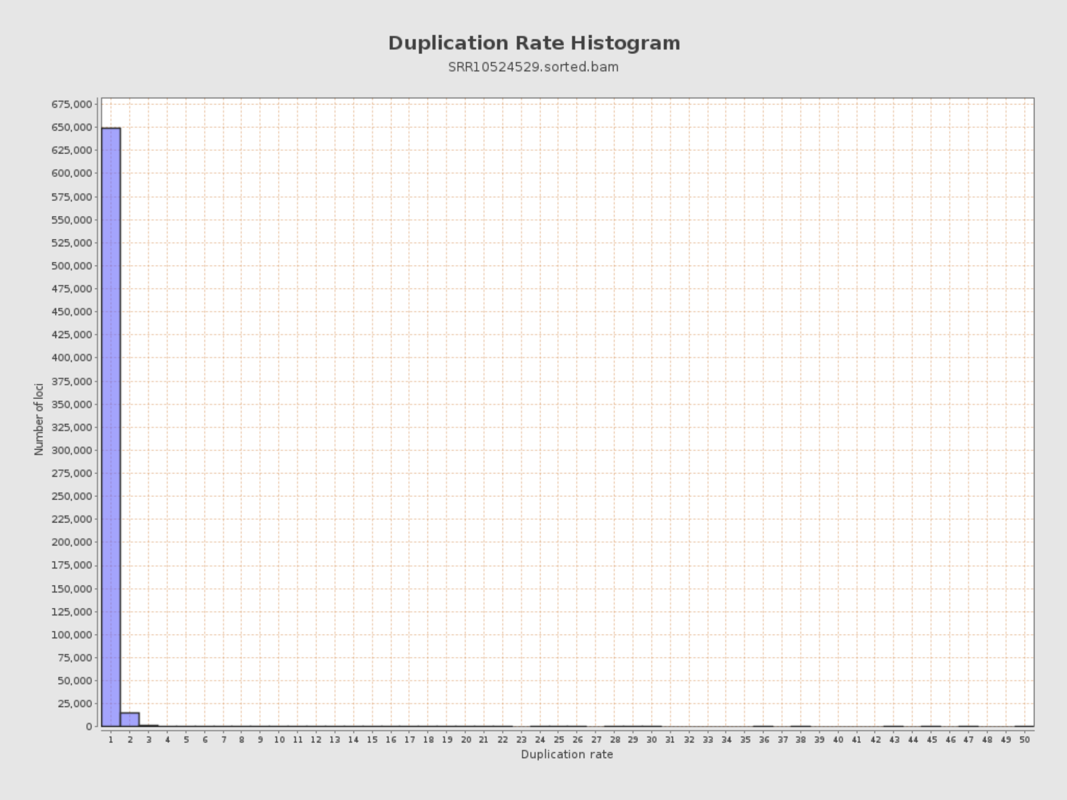
5. Results : Coverage Histogram (0-50X)



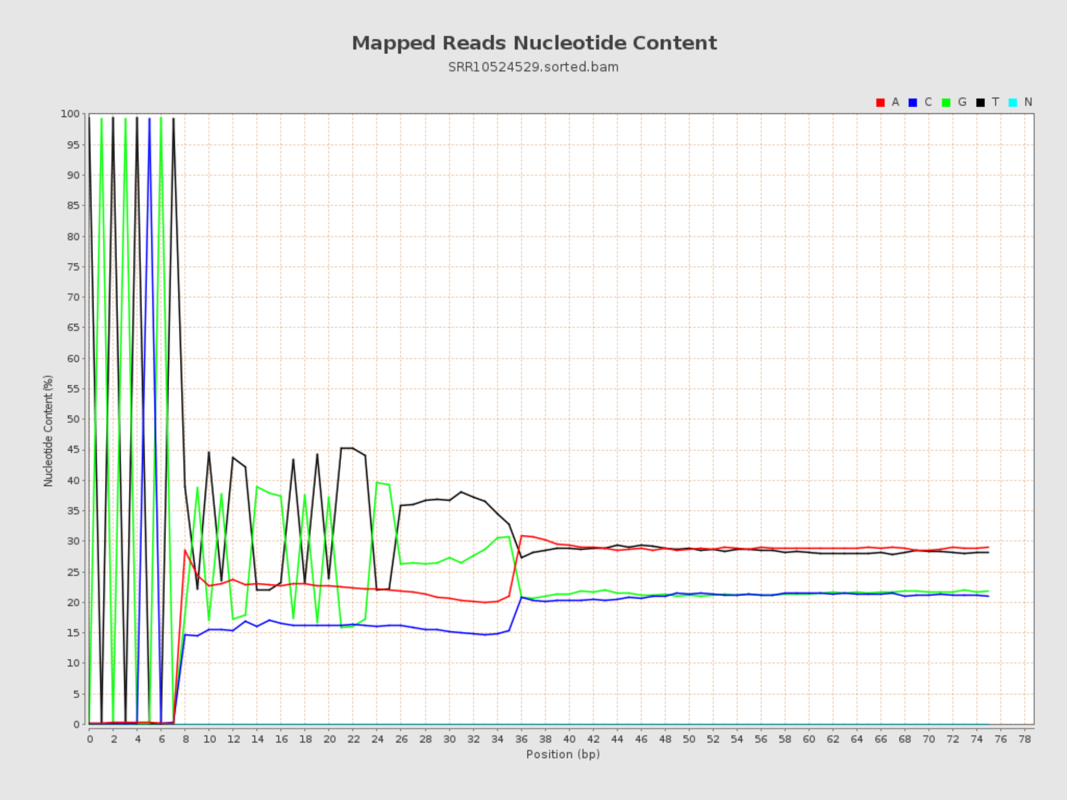
6. Results : Genome Fraction Coverage



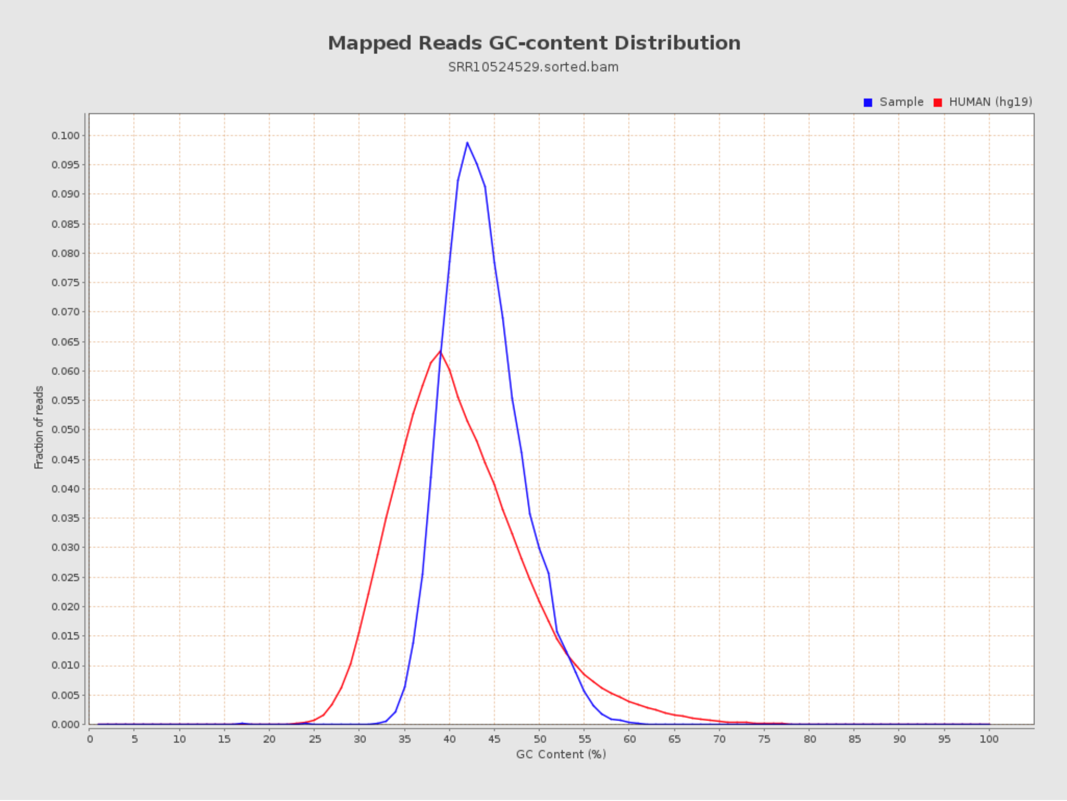
7. Results : Duplication Rate Histogram



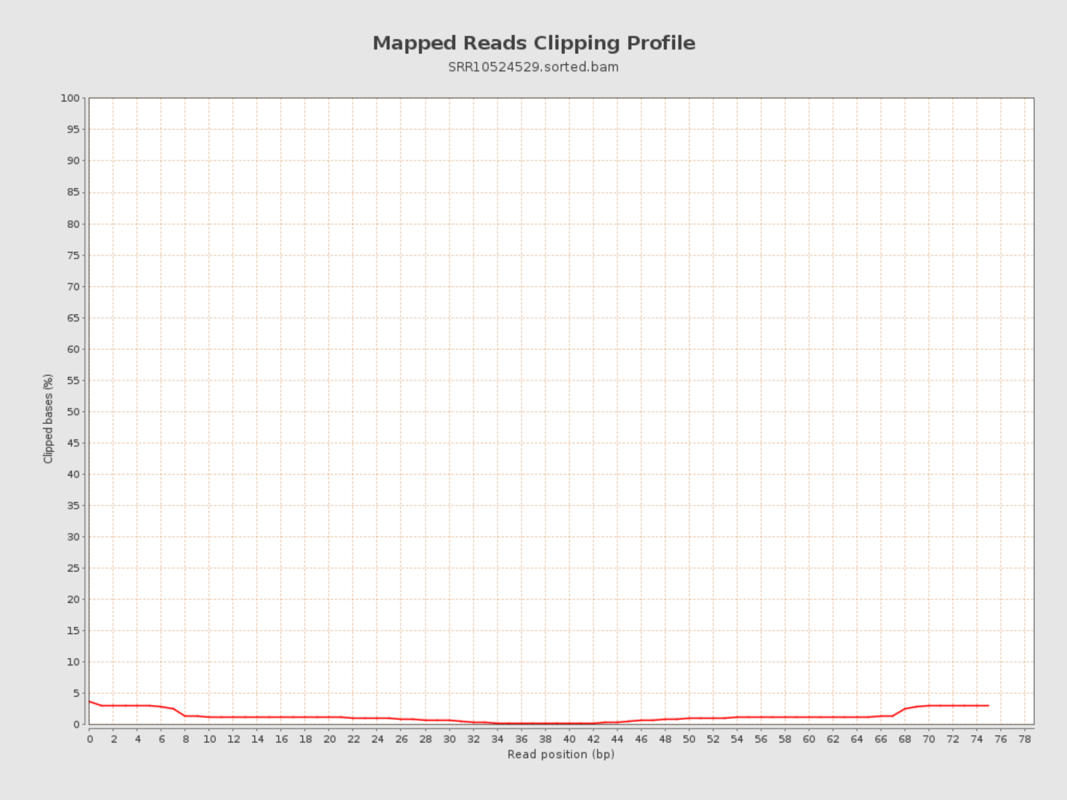
8. Results : Mapped Reads Nucleotide Content



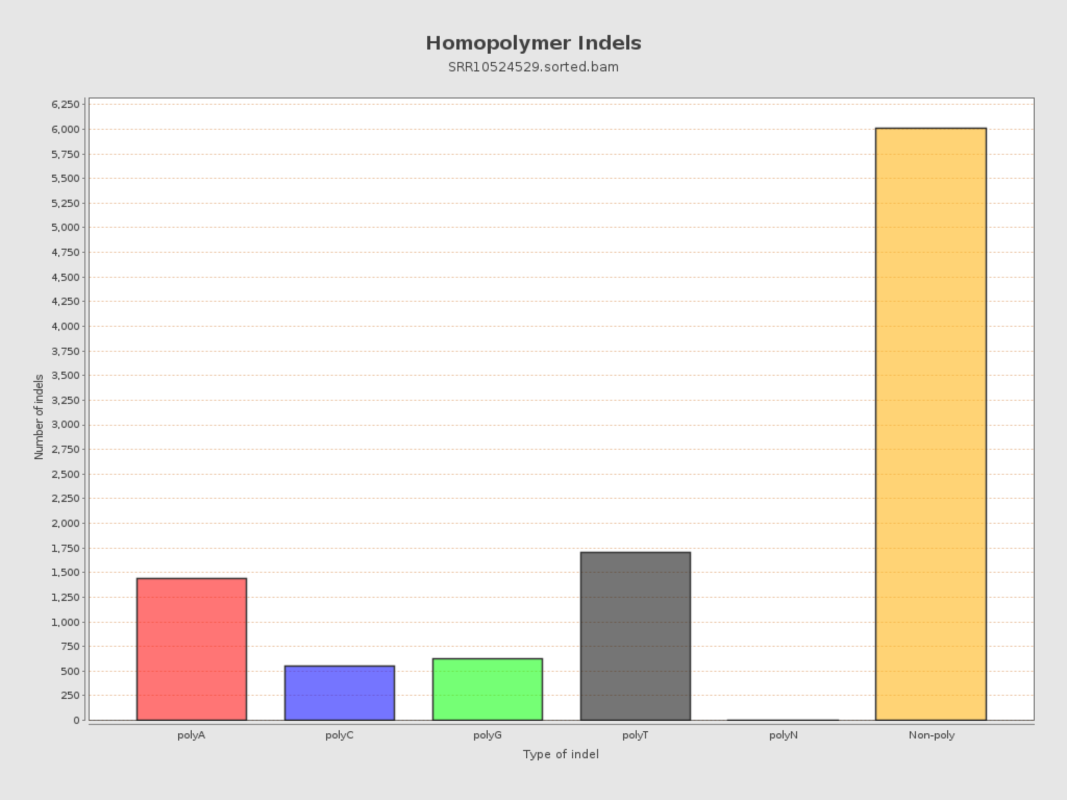
9. Results : Mapped Reads GC-content Distribution



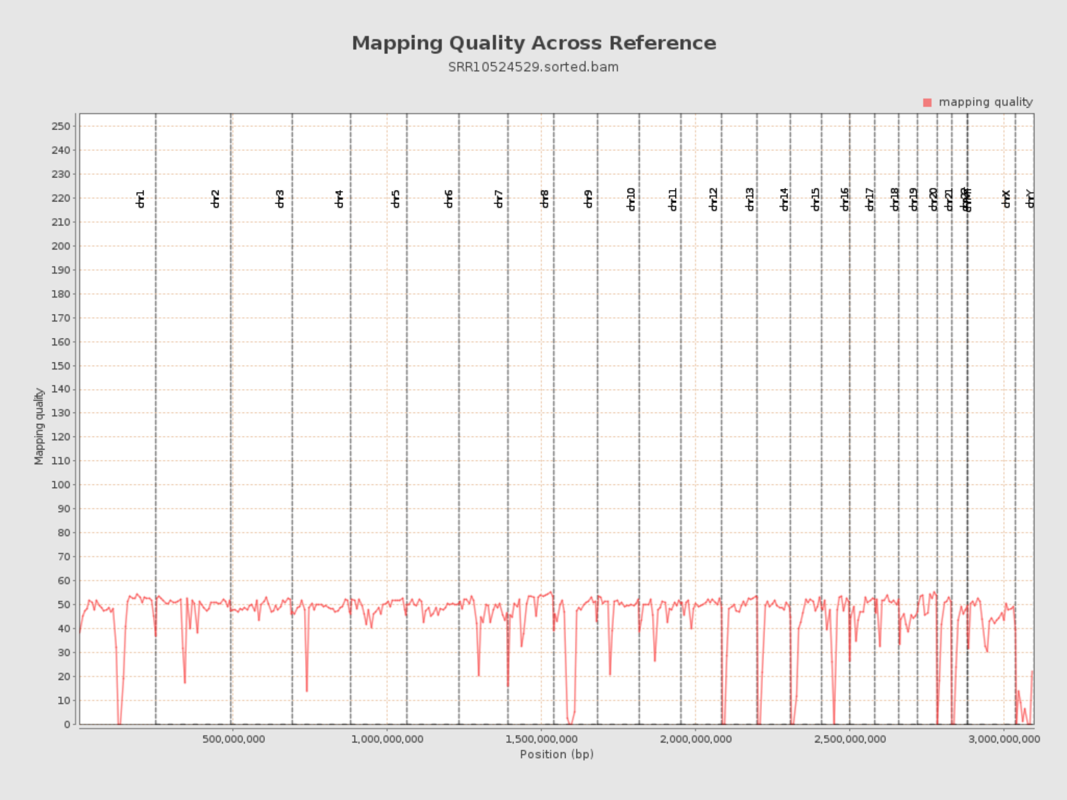
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram