Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 22:01:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524308.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_SRR10524308 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524308.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 22:01:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524308.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	784,095
Mapped reads	717,106 / 91.46%
Unmapped reads	66,989 / 8.54%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,915 / 0.37%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	14,361 / 1.83%
Duplication rate	1.41%
Clipped reads	717,769 / 91.54%

2.2. ACGT Content

Number/percentage of A's	10,593,257 / 25.32%
Number/percentage of C's	7,952,725 / 19.01%
Number/percentage of T's	13,311,858 / 31.82%
Number/percentage of G's	9,968,095 / 23.83%
Number/percentage of N's	6,623 / 0.02%
GC Percentage	42.84%

2.3. Coverage

Mean	0.0135

Standard Deviation	0.1541

2.4. Mapping Quality

Mean Mapping Quality	44.47

2.5. Mismatches and indels

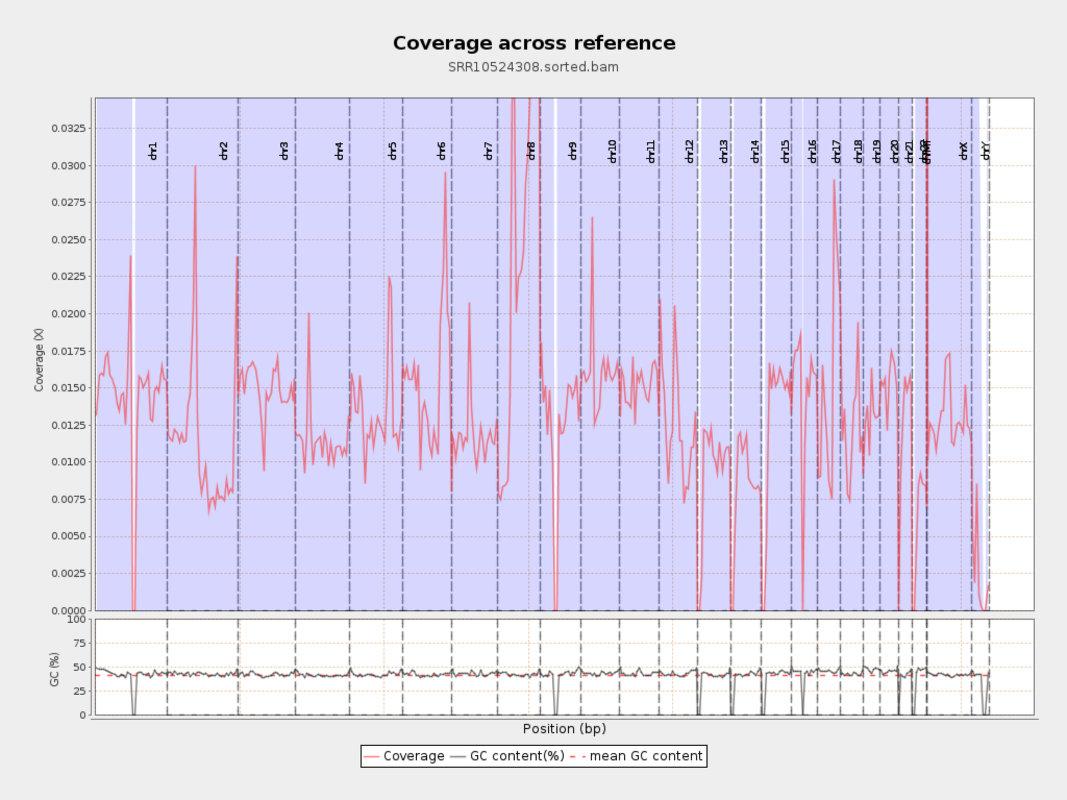
General error rate	0.52%
Mismatches	211,664
Insertions	3,186
Mapped reads with at least one insertion	0.44%
Deletions	6,976
Mapped reads with at least one deletion	0.97%
Homopolymer indels	40.66%

2.6. Chromosome stats

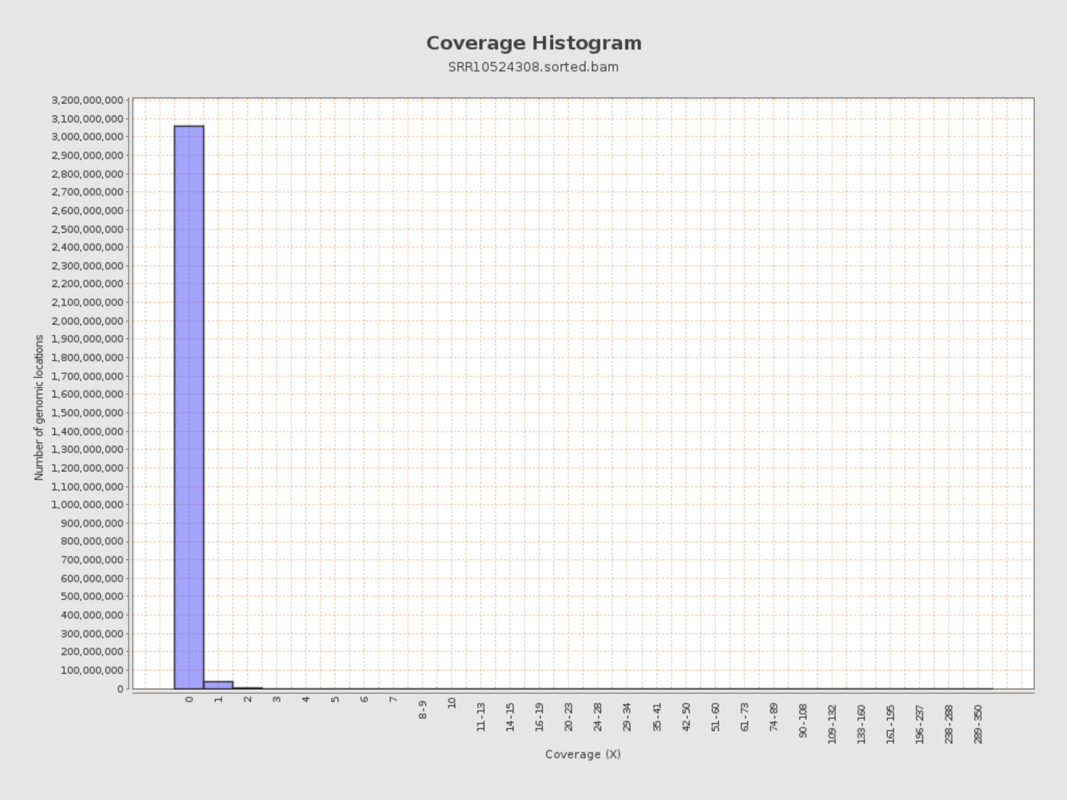
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3572888	0.0143	0.2535
chr2	243199373	2736783	0.0113	0.1825
chr3	198022430	2954433	0.0149	0.1266
chr4	191154276	2197471	0.0115	0.1202
chr5	180915260	2443633	0.0135	0.1205
chr6	171115067	2649038	0.0155	0.1346
chr7	159138663	1890943	0.0119	0.1762

chr8	146364022	4146740	0.0283	0.2023
chr9	141213431	1747879	0.0124	0.1303
chr10	135534747	2185412	0.0161	0.1591
chr11	135006516	2054951	0.0152	0.142
chr12	133851895	1673104	0.0125	0.1167
chr13	115169878	1050334	0.0091	0.0988
chr14	107349540	885387	0.0082	0.0966
chr15	102531392	1284682	0.0125	0.1164
chr16	90354753	1311955	0.0145	0.1272
chr17	81195210	1279716	0.0158	0.1382
chr18	78077248	964937	0.0124	0.1918
chr19	59128983	773406	0.0131	0.1889
chr20	63025520	965020	0.0153	0.1295
chr21	48129895	603428	0.0125	0.1229
chr22	51304566	314118	0.0061	0.0809
chrMT	16571	2952	0.1781	0.4115
chrX	155270560	2021973	0.013	0.1241
chrY	59373566	132547	0.0022	0.0761

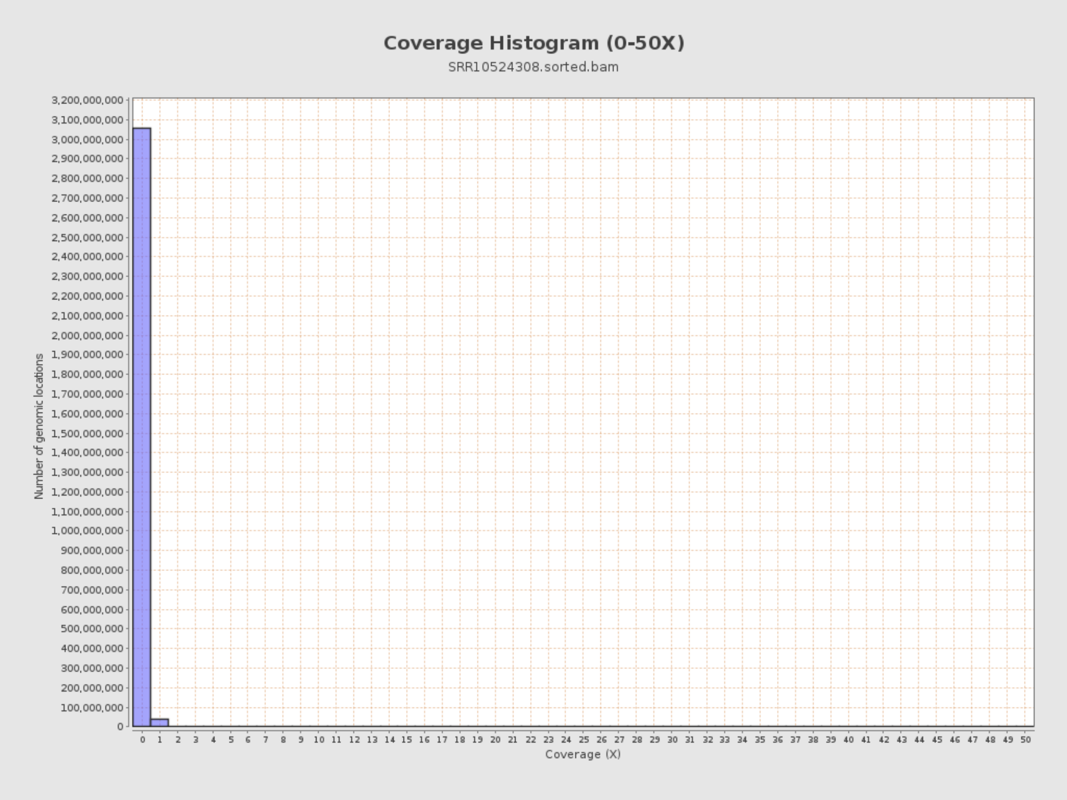
3. Results : Coverage across reference



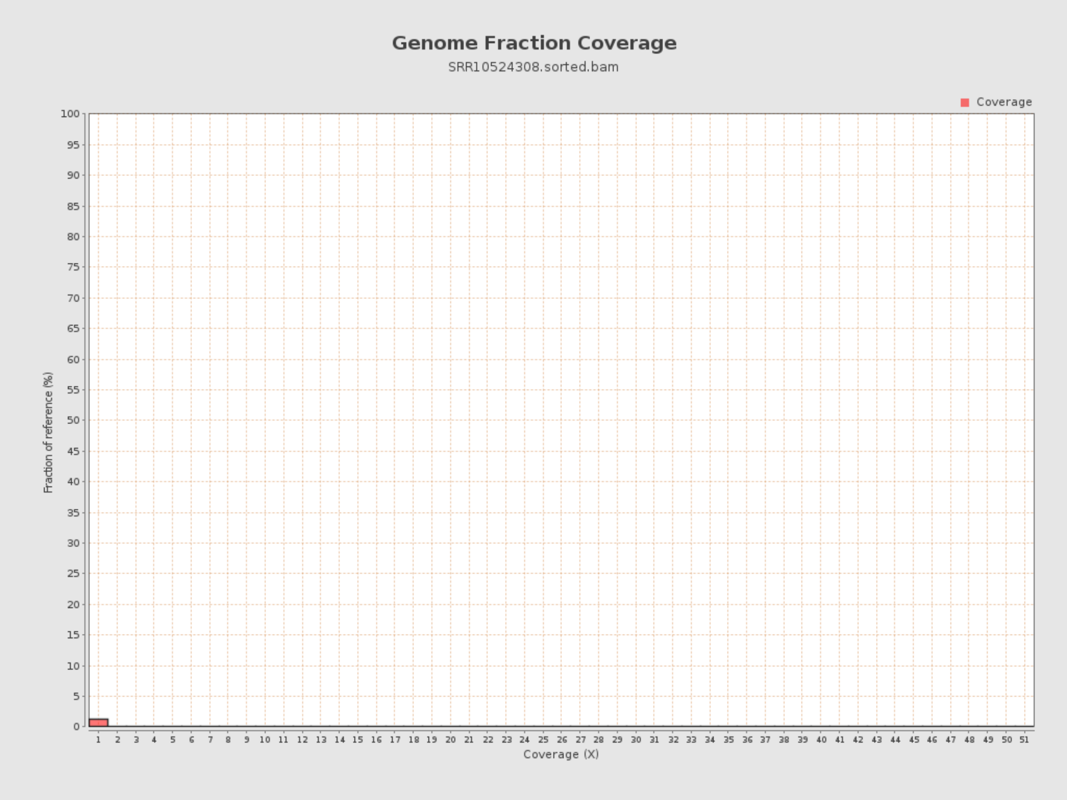
4. Results : Coverage Histogram



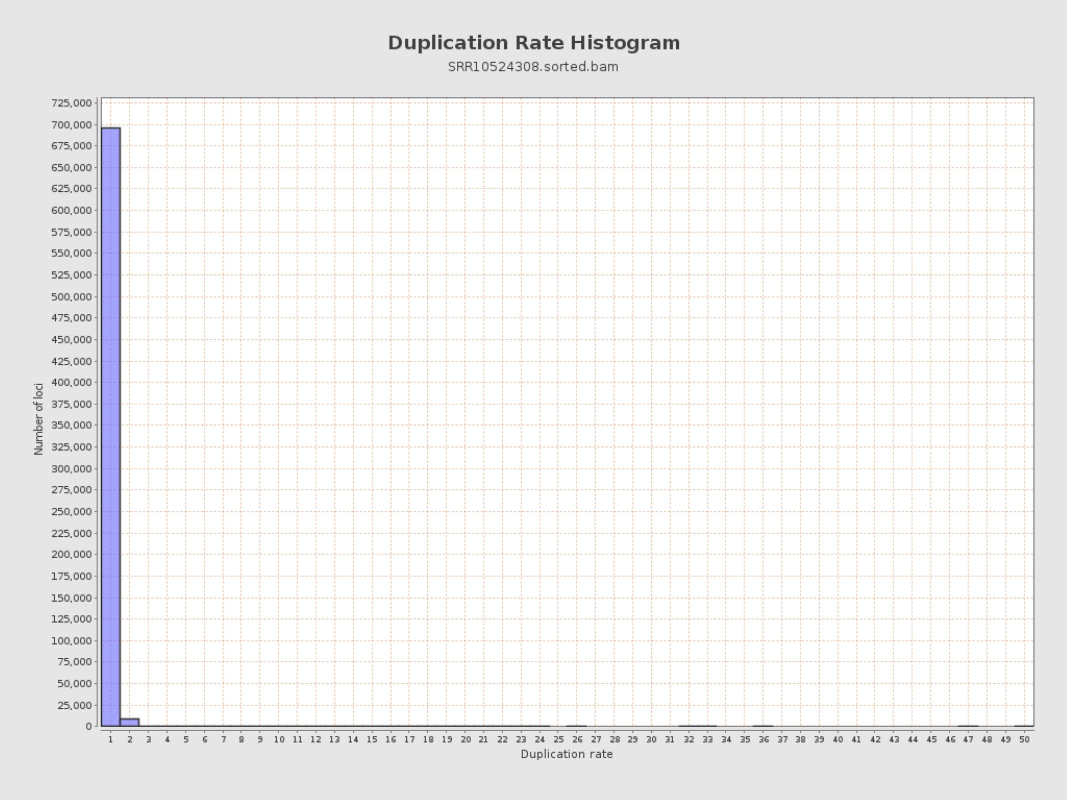
5. Results : Coverage Histogram (0-50X)



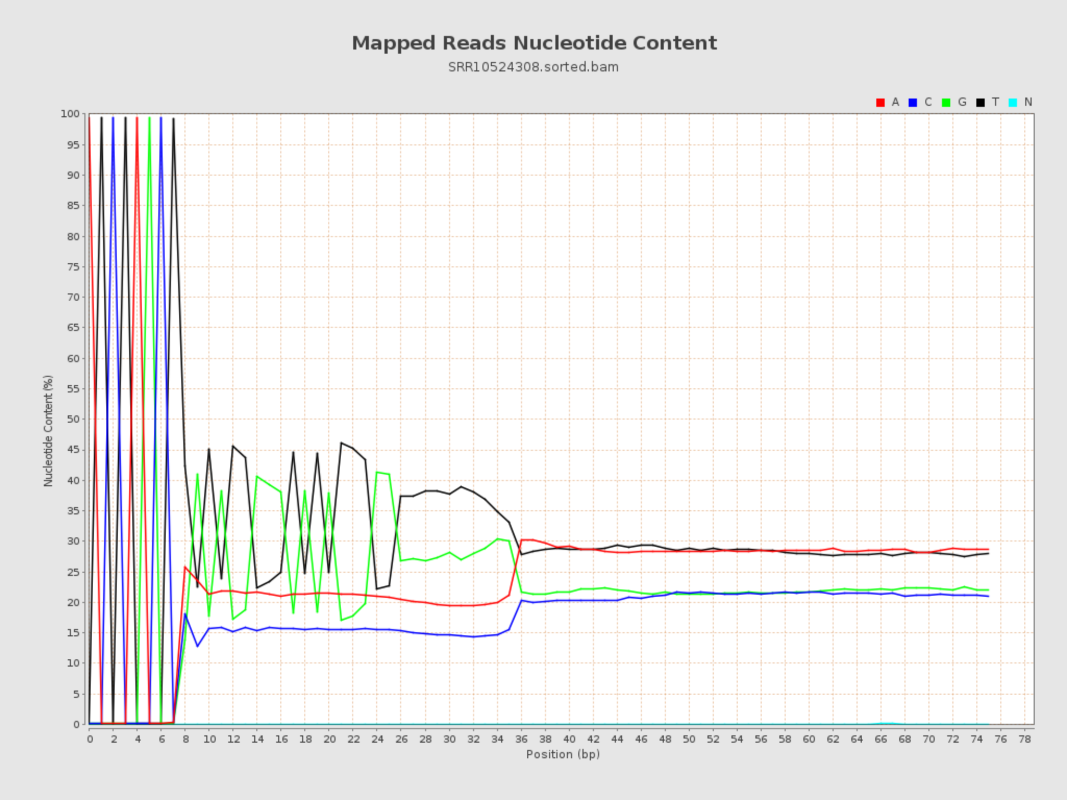
6. Results : Genome Fraction Coverage



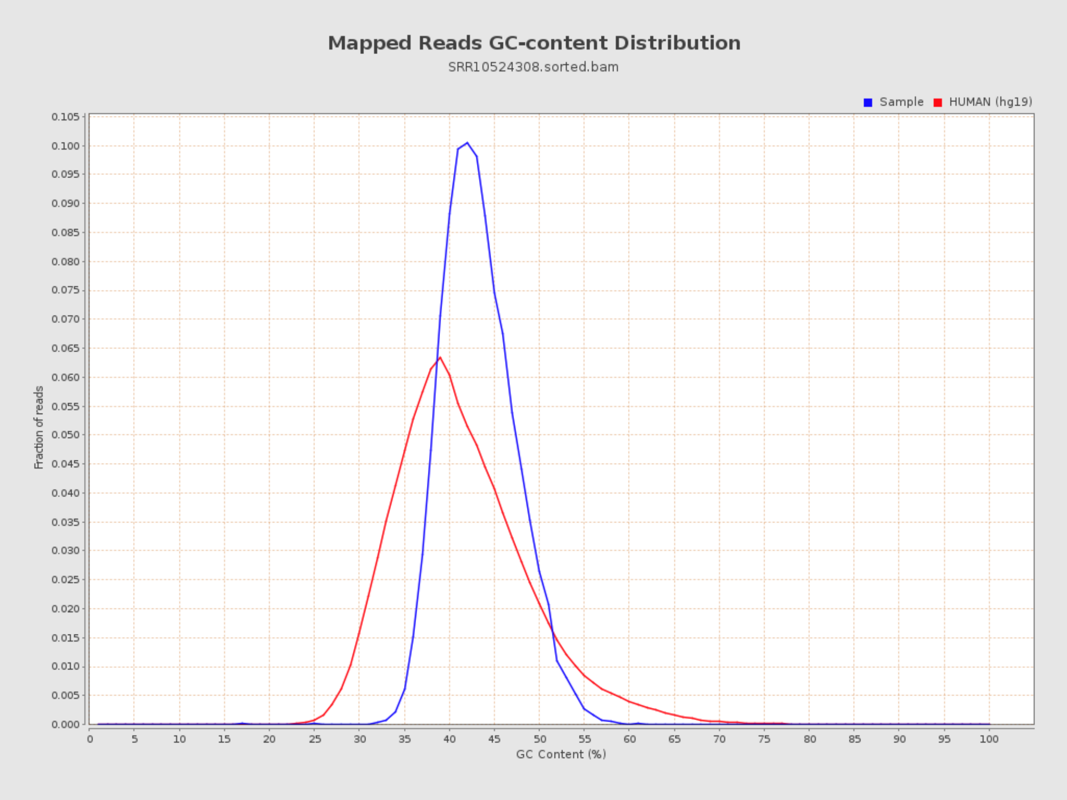
7. Results : Duplication Rate Histogram



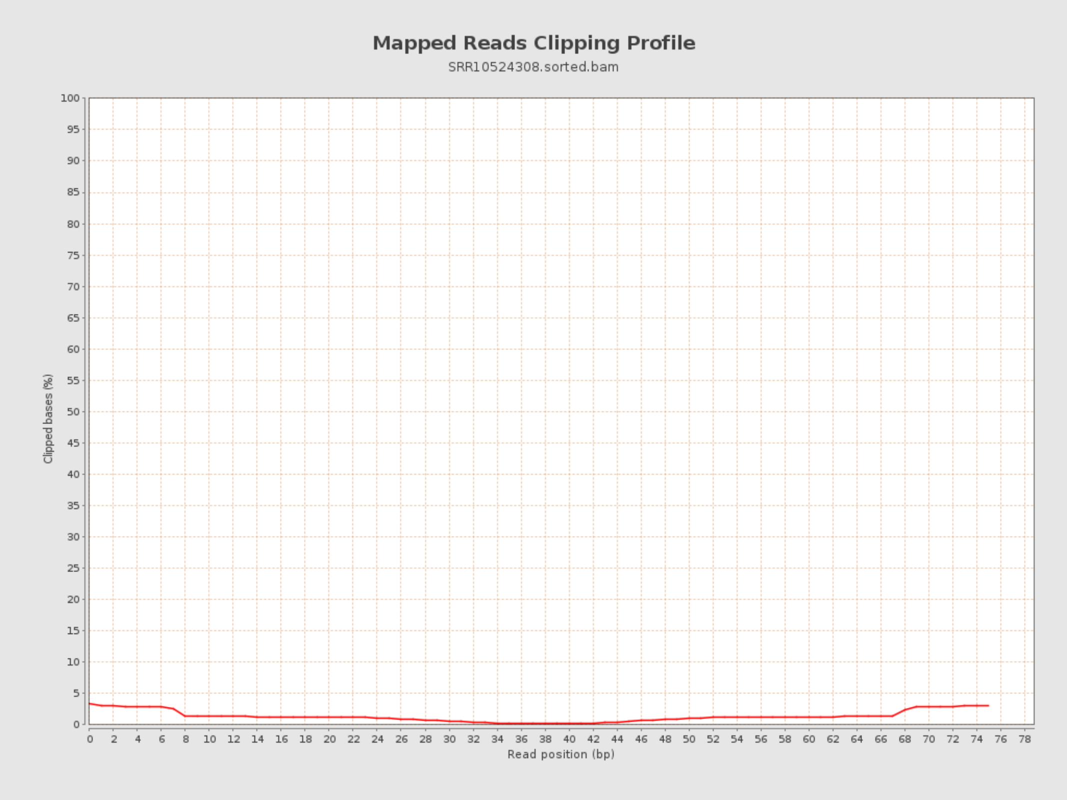
8. Results : Mapped Reads Nucleotide Content



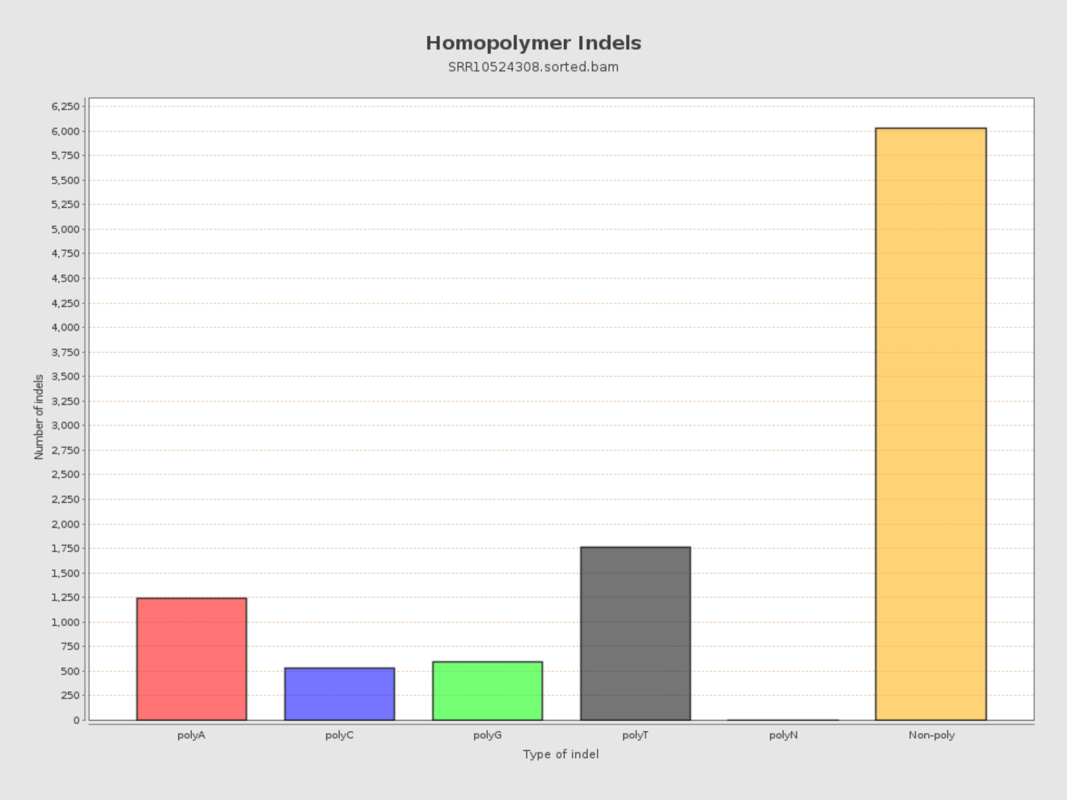
9. Results : Mapped Reads GC-content Distribution



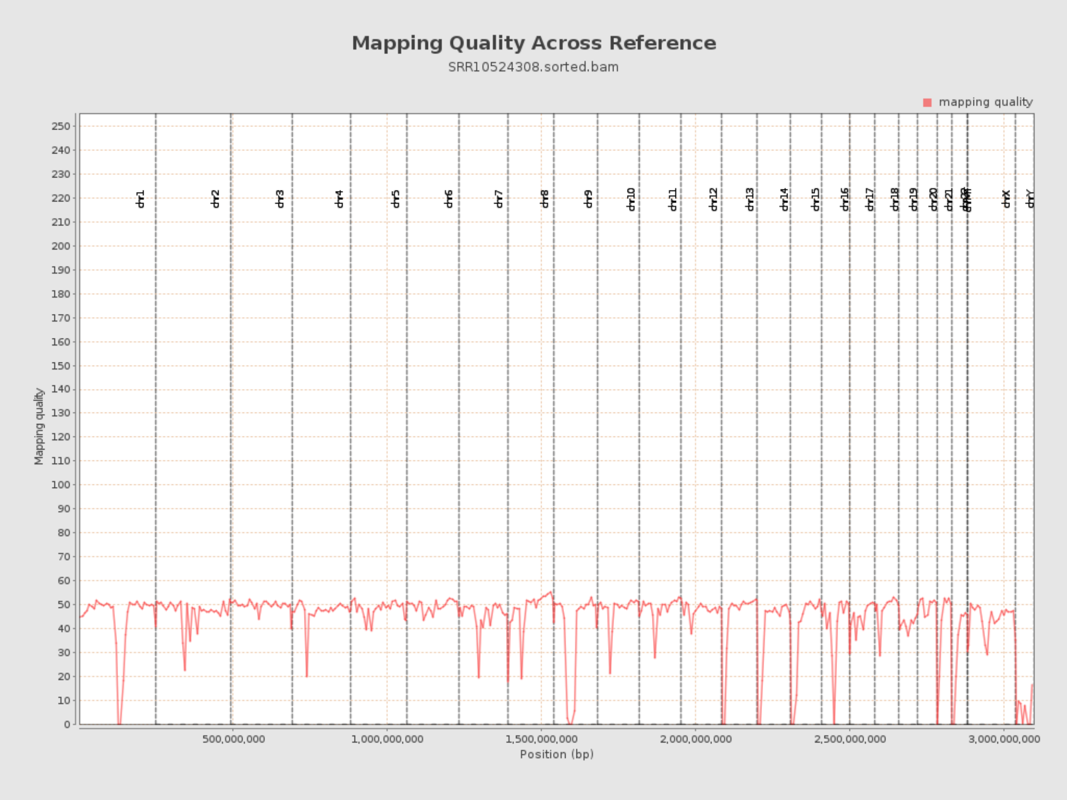
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram