Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 12:42:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524608.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_SRR10524608 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524608.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 12:42:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524608.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,812,997
Mapped reads	1,692,148 / 93.33%
Unmapped reads	120,849 / 6.67%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,470 / 0.19%
Read min/max/mean length	30 / 76 / 76.06
Duplicated reads (estimated)	81,646 / 4.5%
Duplication rate	3.71%
Clipped reads	1,692,331 / 93.34%

2.2. ACGT Content

Number/percentage of A's	24,603,392 / 24.91%
Number/percentage of C's	17,378,666 / 17.59%
Number/percentage of T's	31,115,803 / 31.5%
Number/percentage of G's	25,676,973 / 26%
Number/percentage of N's	598 / 0%
GC Percentage	43.59%

2.3. Coverage

Mean	0.0319

Standard Deviation	0.2868

2.4. Mapping Quality

Mean Mapping Quality	45.5

2.5. Mismatches and indels

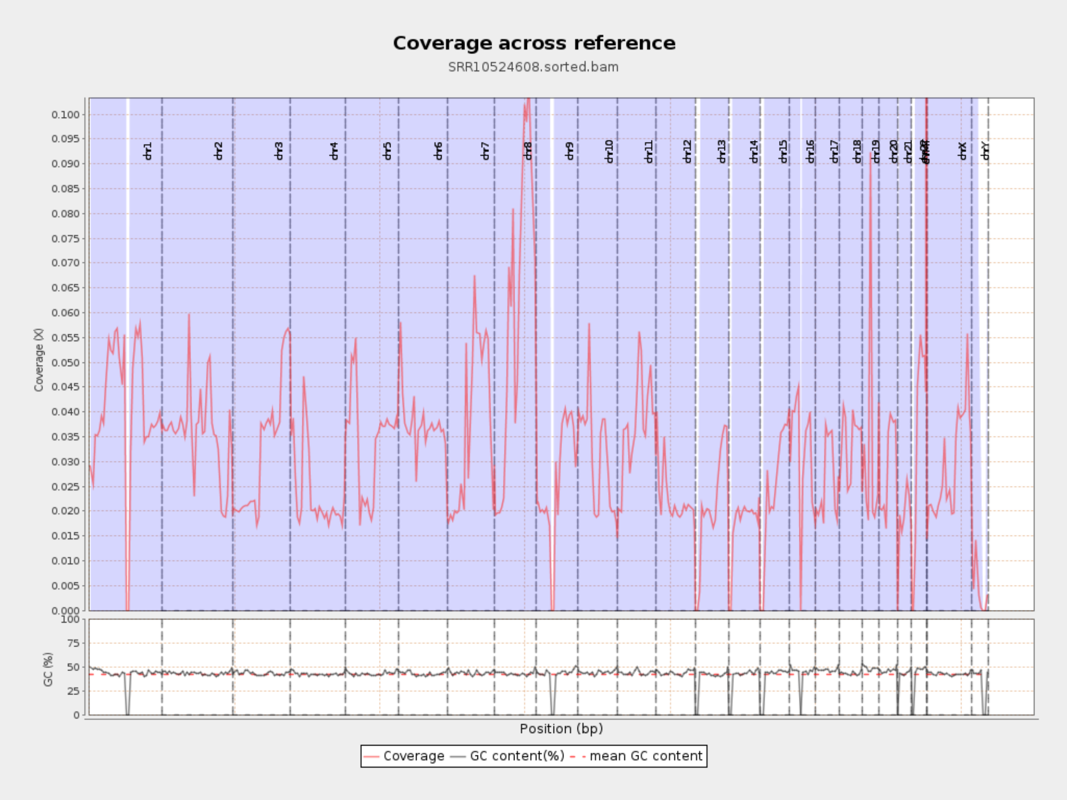
General error rate	0.47%
Mismatches	454,866
Insertions	6,296
Mapped reads with at least one insertion	0.37%
Deletions	18,614
Mapped reads with at least one deletion	1.09%
Homopolymer indels	43.04%

2.6. Chromosome stats

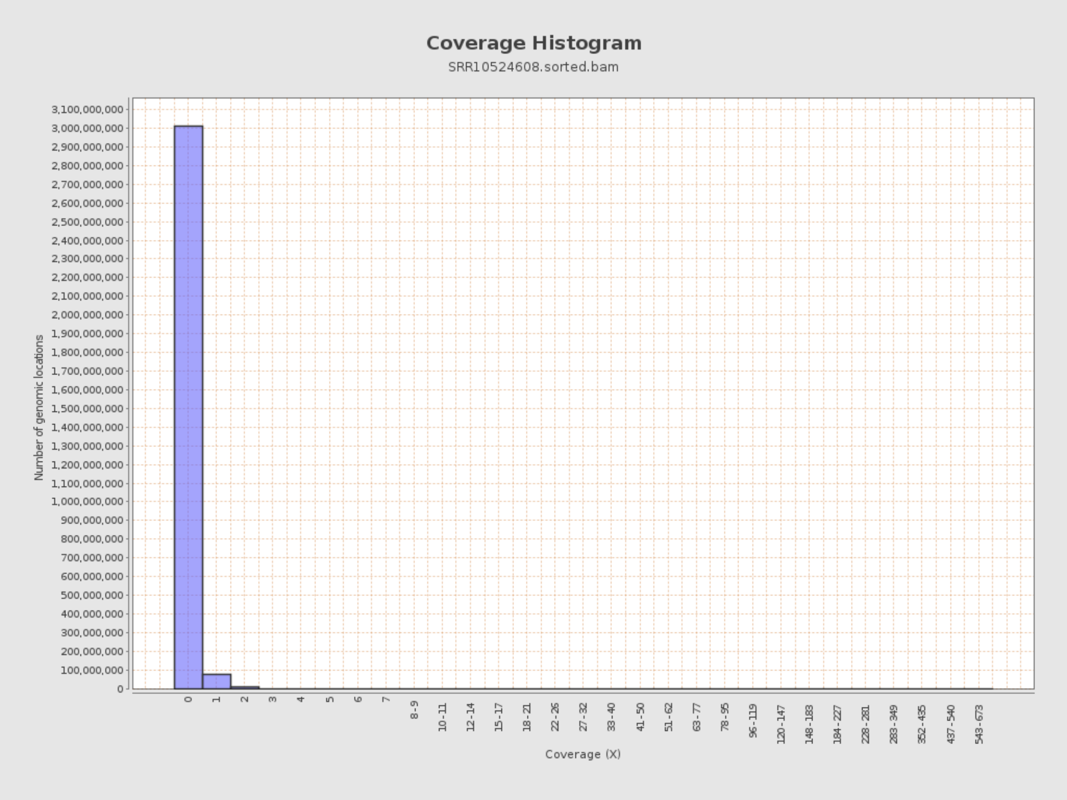
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10144808	0.0407	0.5106
chr2	243199373	8775294	0.0361	0.3308
chr3	198022430	6382457	0.0322	0.2013
chr4	191154276	4493261	0.0235	0.1953
chr5	180915260	6169753	0.0341	0.2066
chr6	171115067	6458367	0.0377	0.2357
chr7	159138663	6005077	0.0377	0.3883

chr8	146364022	8853689	0.0605	0.3806
chr9	141213431	3619486	0.0256	0.2507
chr10	135534747	4240972	0.0313	0.2826
chr11	135006516	5036745	0.0373	0.2803
chr12	133851895	3029323	0.0226	0.1732
chr13	115169878	2424069	0.021	0.1663
chr14	107349540	1820022	0.017	0.153
chr15	102531392	2497826	0.0244	0.1788
chr16	90354753	2860758	0.0317	0.2117
chr17	81195210	2138363	0.0263	0.1898
chr18	78077248	2689785	0.0345	0.411
chr19	59128983	1922895	0.0325	0.3526
chr20	63025520	1832505	0.0291	0.195
chr21	48129895	886486	0.0184	0.1672
chr22	51304566	1766569	0.0344	0.2065
chrMT	16571	6961	0.4201	0.7521
chrX	155270560	4514584	0.0291	0.2204
chrY	59373566	236983	0.004	0.1143

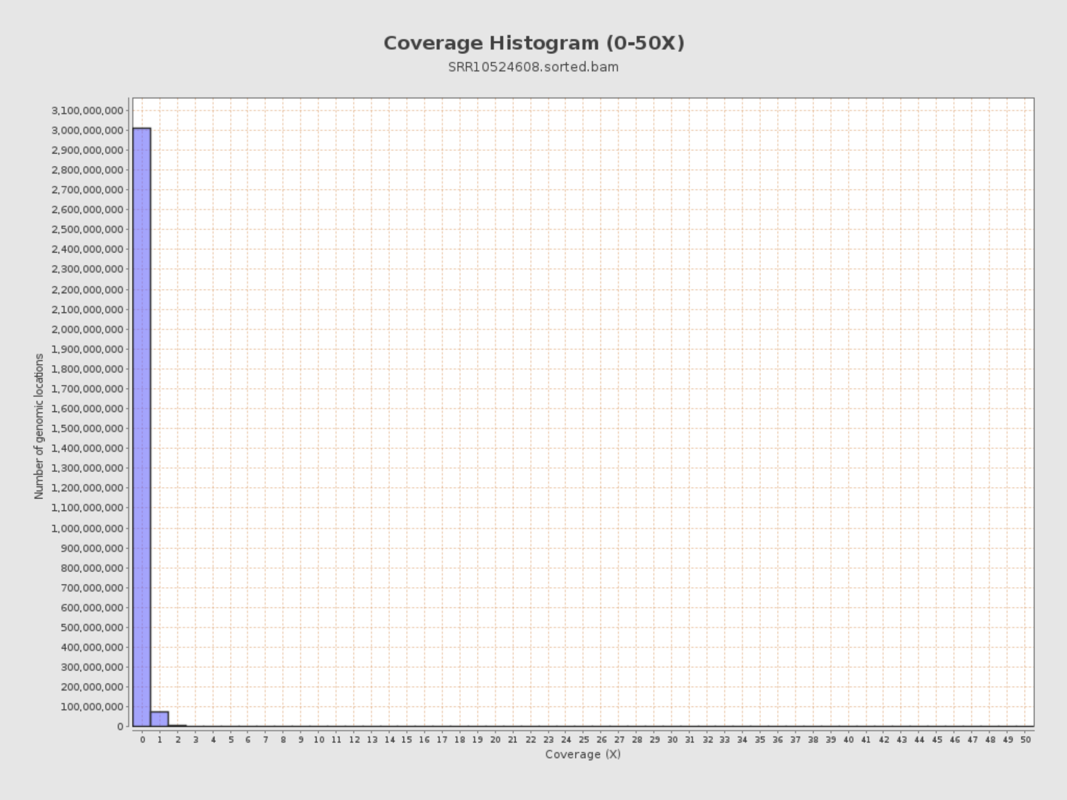
3. Results : Coverage across reference



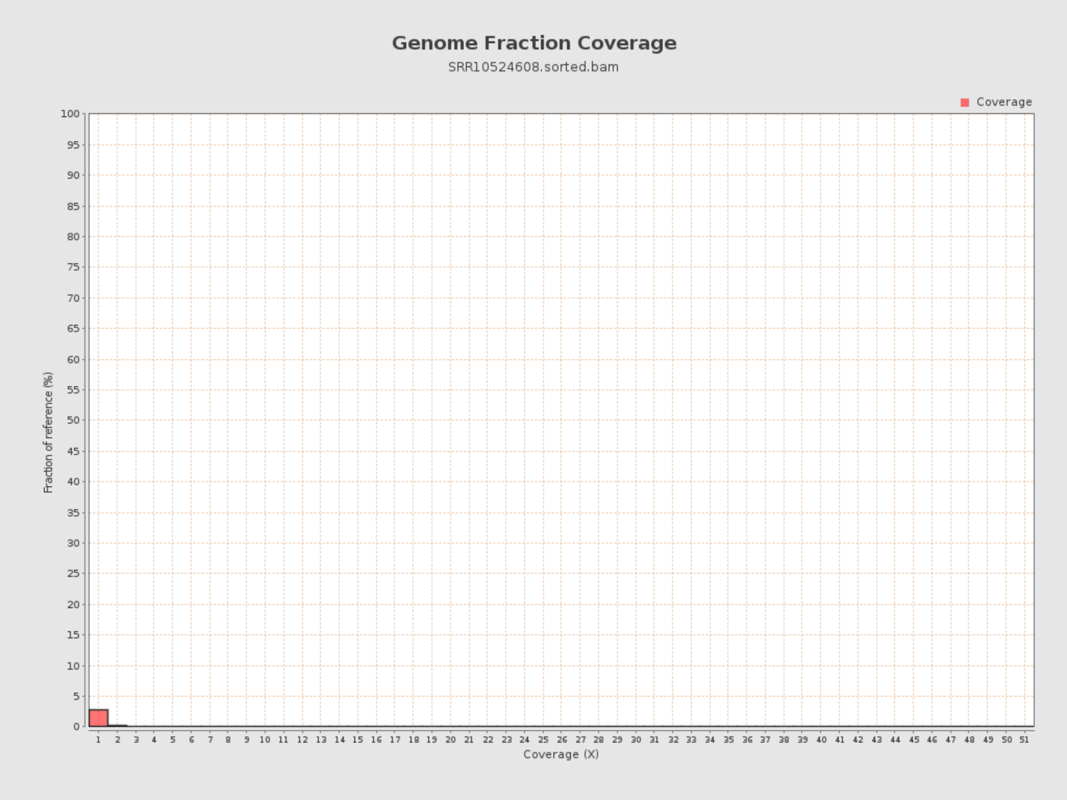
4. Results : Coverage Histogram



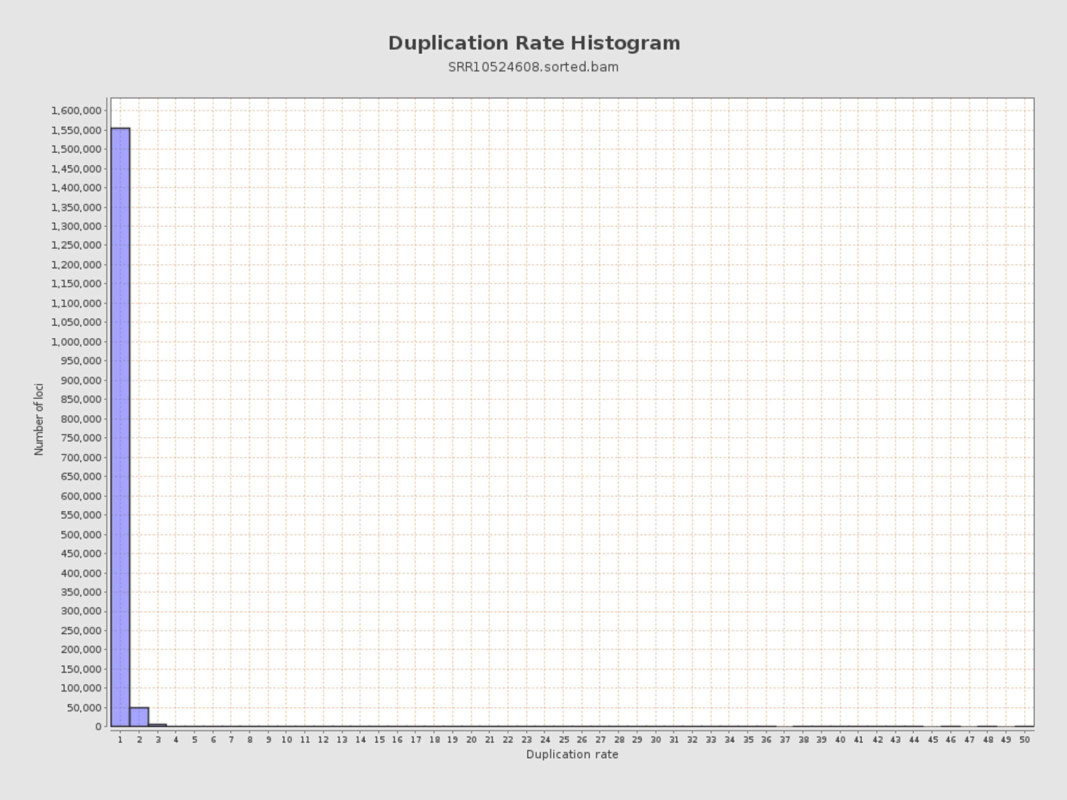
5. Results : Coverage Histogram (0-50X)



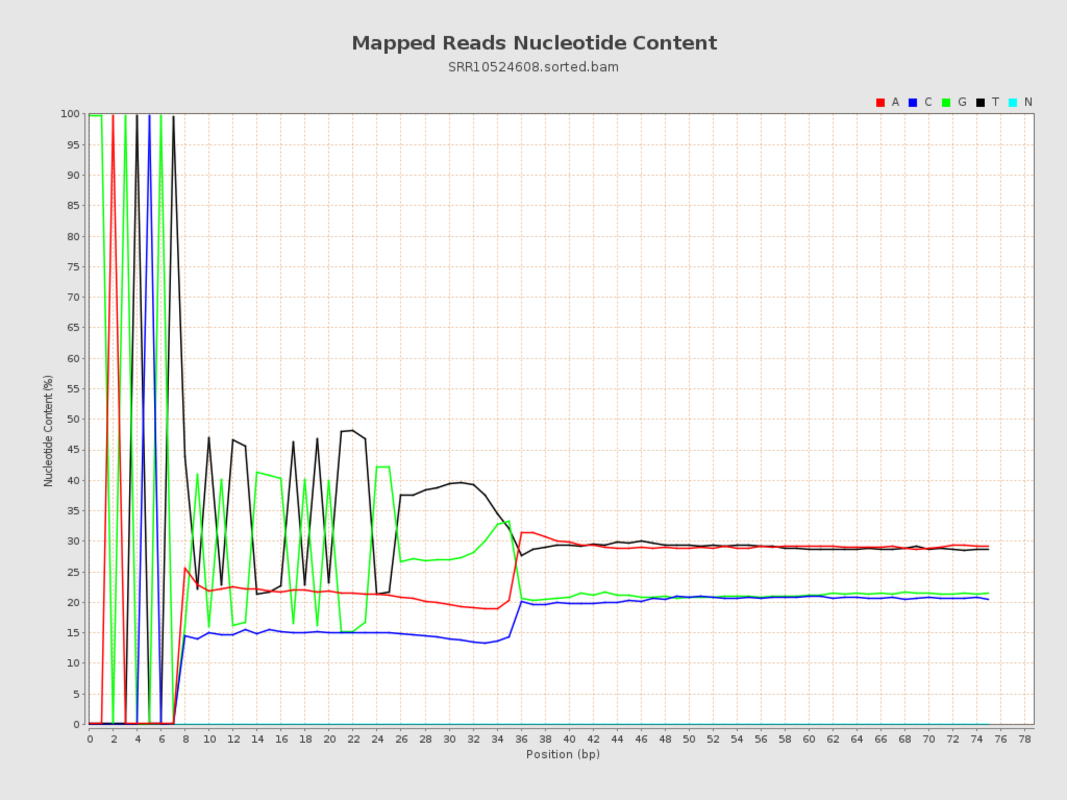
6. Results : Genome Fraction Coverage



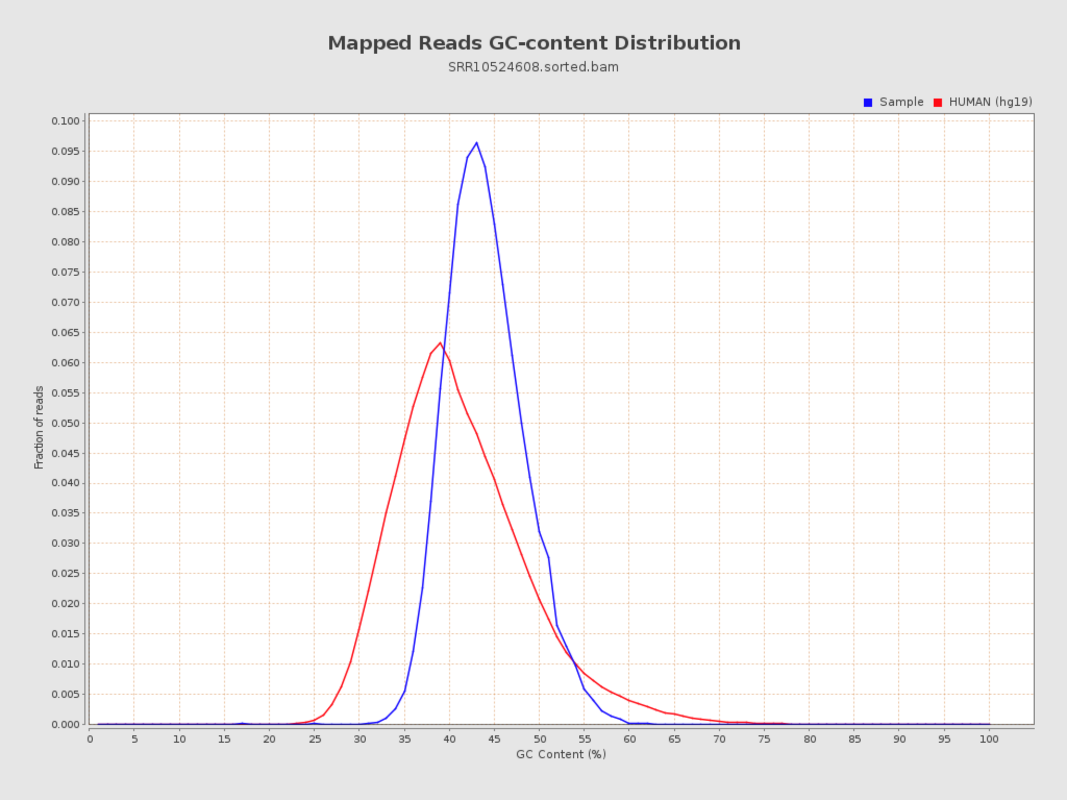
7. Results : Duplication Rate Histogram



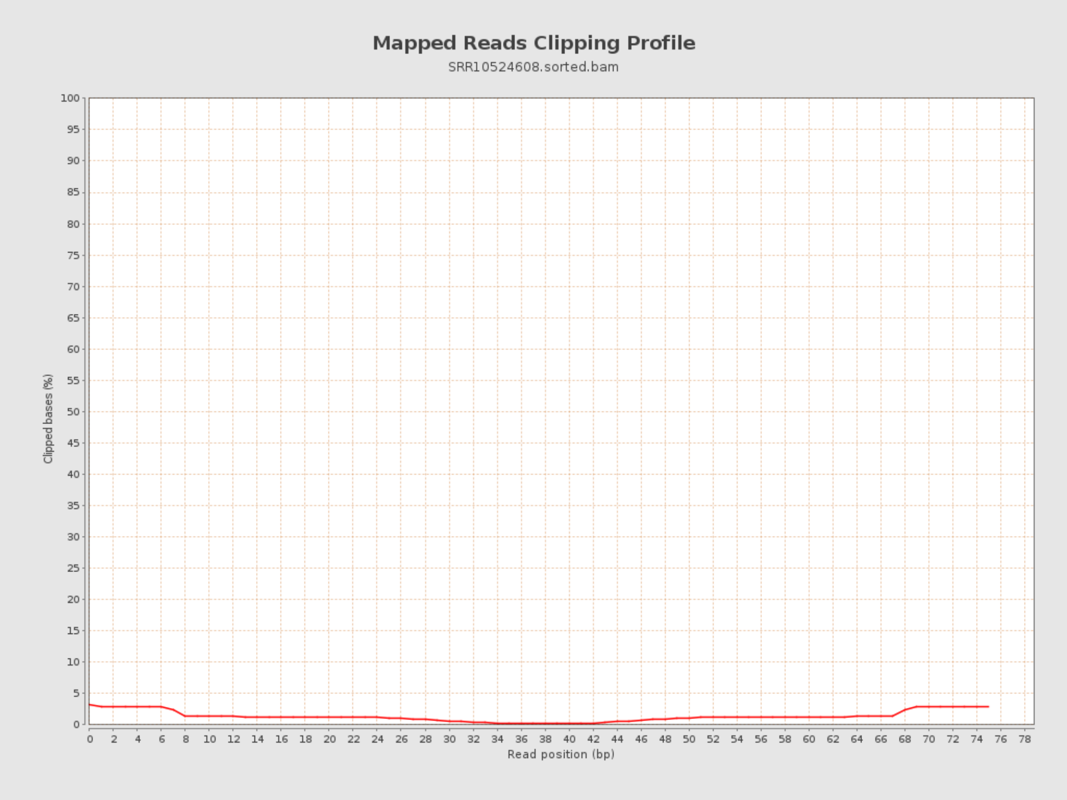
8. Results : Mapped Reads Nucleotide Content



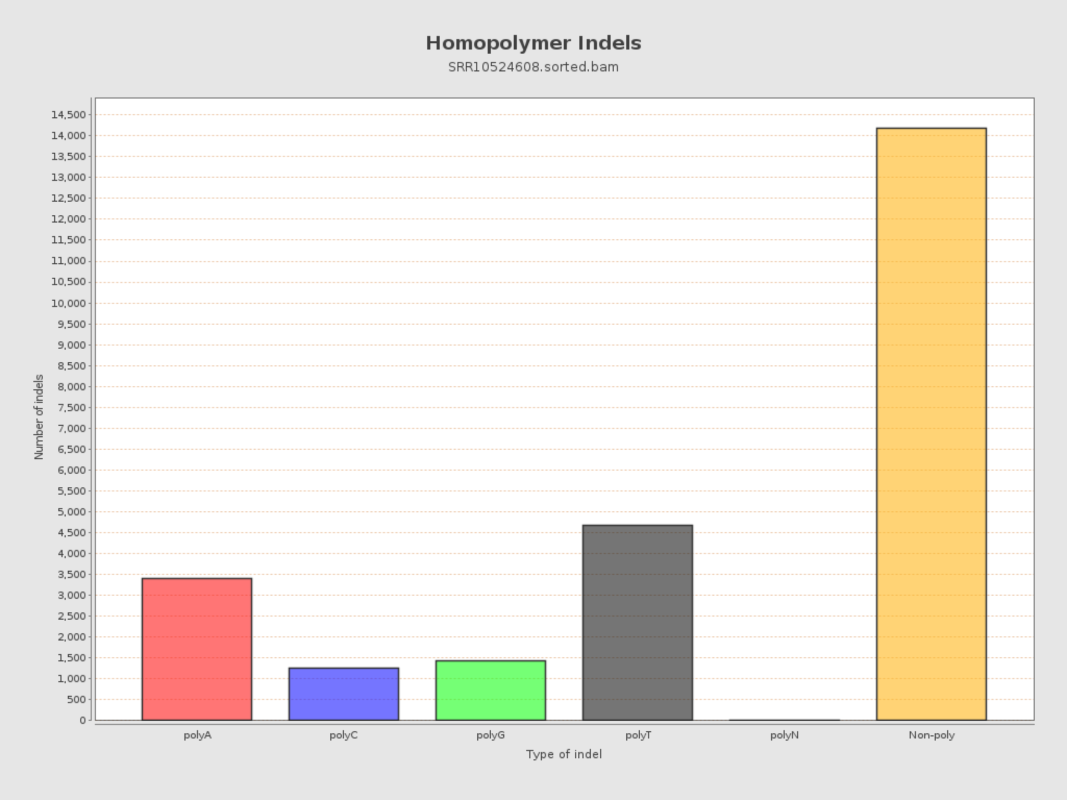
9. Results : Mapped Reads GC-content Distribution



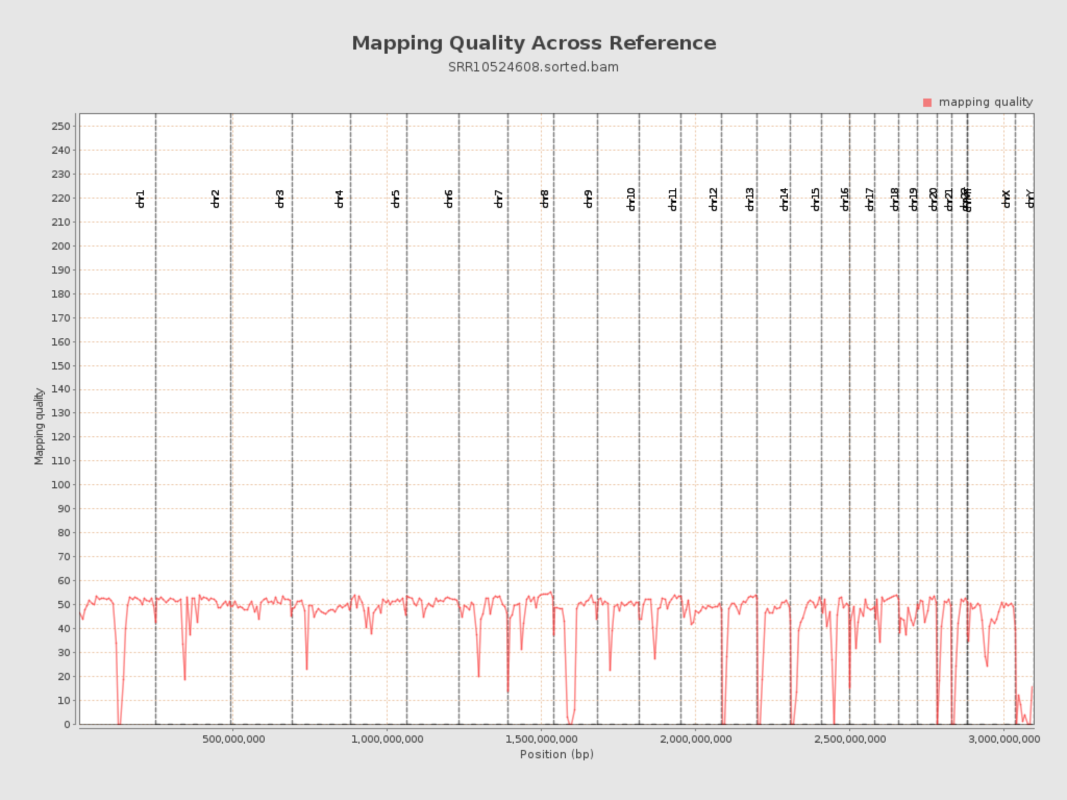
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram