Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 12:33:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524998.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_SRR10524998 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524998.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 12:33:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524998.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,799,272
Mapped reads	1,666,530 / 92.62%
Unmapped reads	132,742 / 7.38%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,420 / 0.3%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	72,562 / 4.03%
Duplication rate	3.32%
Clipped reads	1,668,480 / 92.73%

2.2. ACGT Content

Number/percentage of A's	23,740,309 / 24.43%
Number/percentage of C's	19,085,387 / 19.64%
Number/percentage of T's	30,297,263 / 31.18%
Number/percentage of G's	24,034,748 / 24.74%
Number/percentage of N's	974 / 0%
GC Percentage	44.38%

2.3. Coverage

Mean	0.0314

Standard Deviation	0.293

2.4. Mapping Quality

Mean Mapping Quality	45.37

2.5. Mismatches and indels

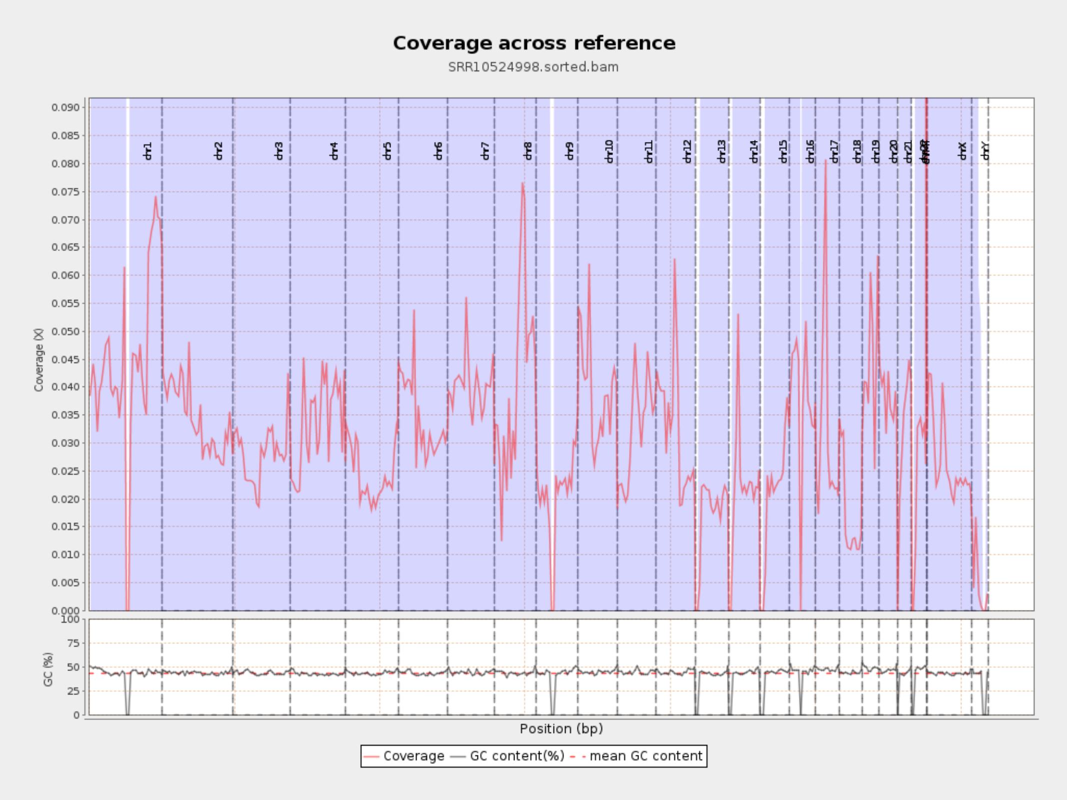
General error rate	0.5%
Mismatches	471,535
Insertions	6,132
Mapped reads with at least one insertion	0.37%
Deletions	18,545
Mapped reads with at least one deletion	1.11%
Homopolymer indels	44.49%

2.6. Chromosome stats

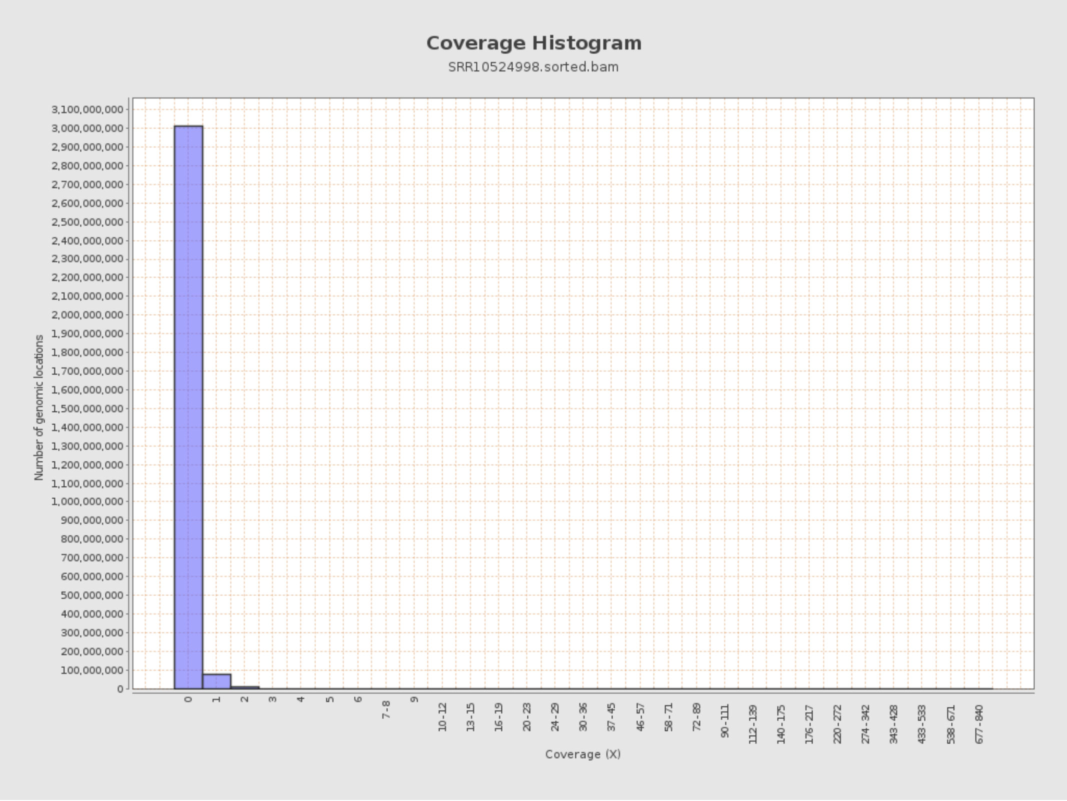
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11073582	0.0444	0.6124
chr2	243199373	8403946	0.0346	0.319
chr3	198022430	5548434	0.028	0.183
chr4	191154276	6442749	0.0337	0.2304
chr5	180915260	4405243	0.0243	0.1738
chr6	171115067	5914783	0.0346	0.2678
chr7	159138663	6441943	0.0405	0.3687

chr8	146364022	5989553	0.0409	0.3003
chr9	141213431	2850171	0.0202	0.1979
chr10	135534747	5326679	0.0393	0.2965
chr11	135006516	4338340	0.0321	0.2412
chr12	133851895	4337880	0.0324	0.2003
chr13	115169878	1953432	0.017	0.1461
chr14	107349540	2313990	0.0216	0.1639
chr15	102531392	2120249	0.0207	0.1619
chr16	90354753	3401895	0.0377	0.2213
chr17	81195210	2667449	0.0329	0.2616
chr18	78077248	1325806	0.017	0.3069
chr19	59128983	2666047	0.0451	0.3595
chr20	63025520	2420657	0.0384	0.2177
chr21	48129895	1509362	0.0314	0.2101
chr22	51304566	1156405	0.0225	0.1635
chrMT	16571	64355	3.8836	2.9648
chrX	155270560	4236811	0.0273	0.2011
chrY	59373566	279404	0.0047	0.1369

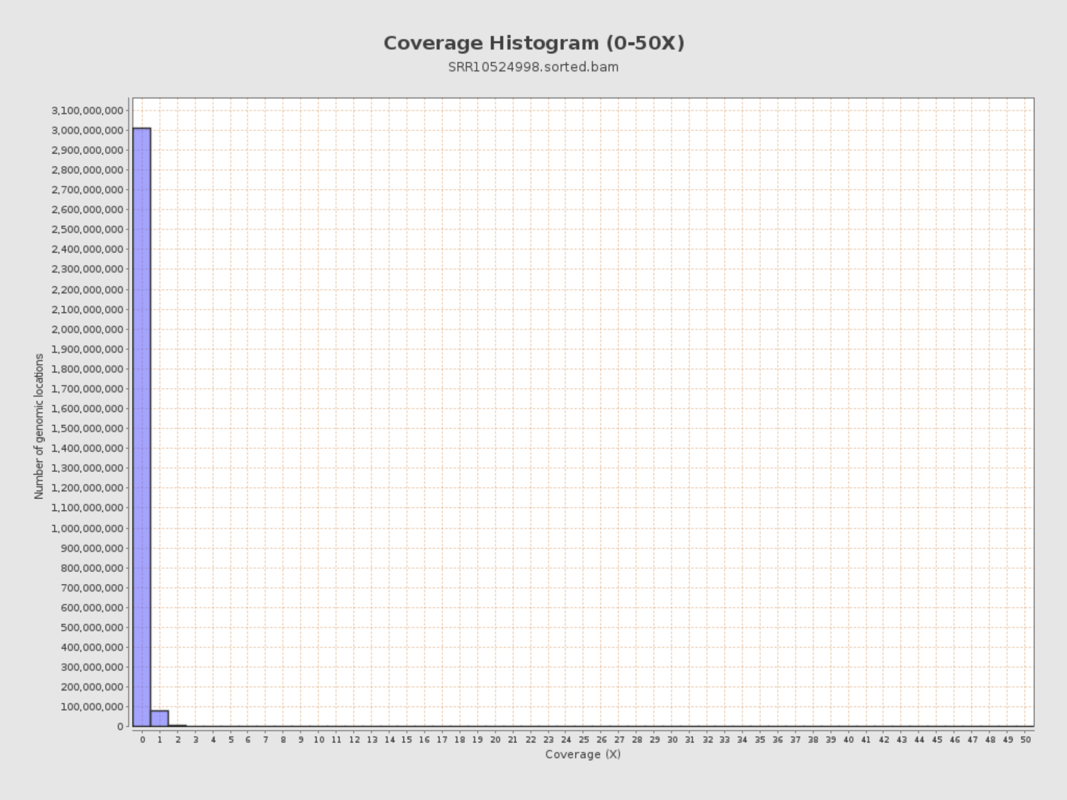
3. Results : Coverage across reference



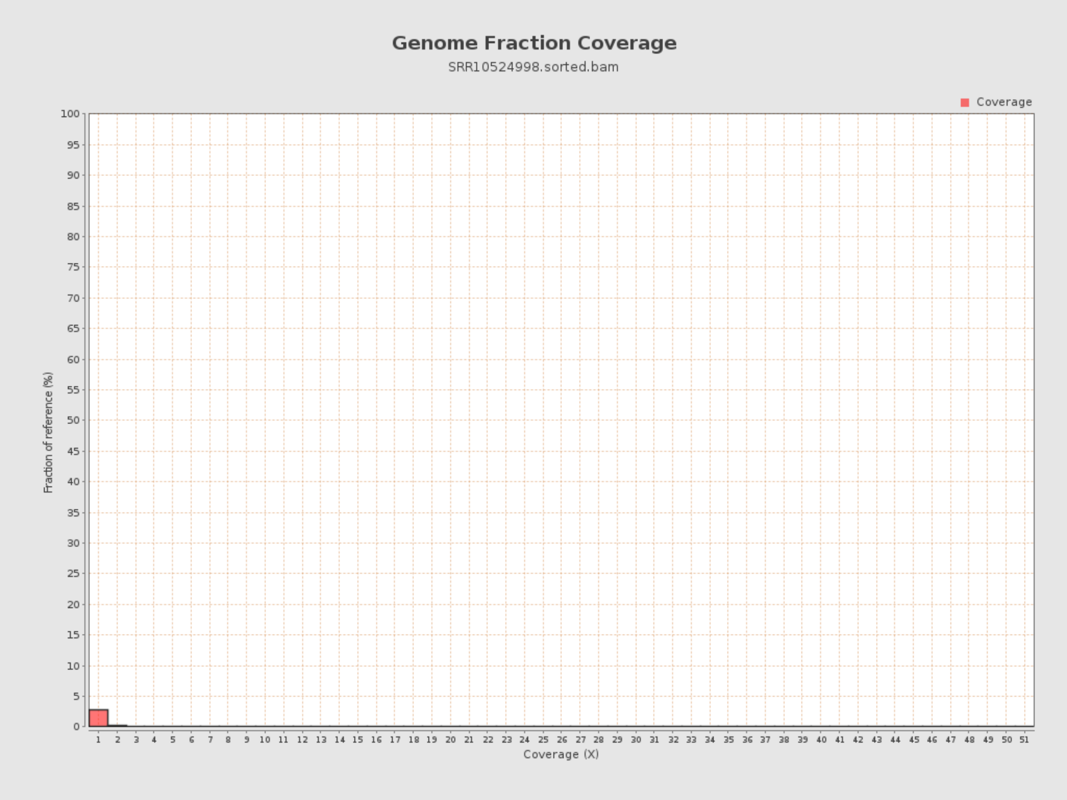
4. Results : Coverage Histogram



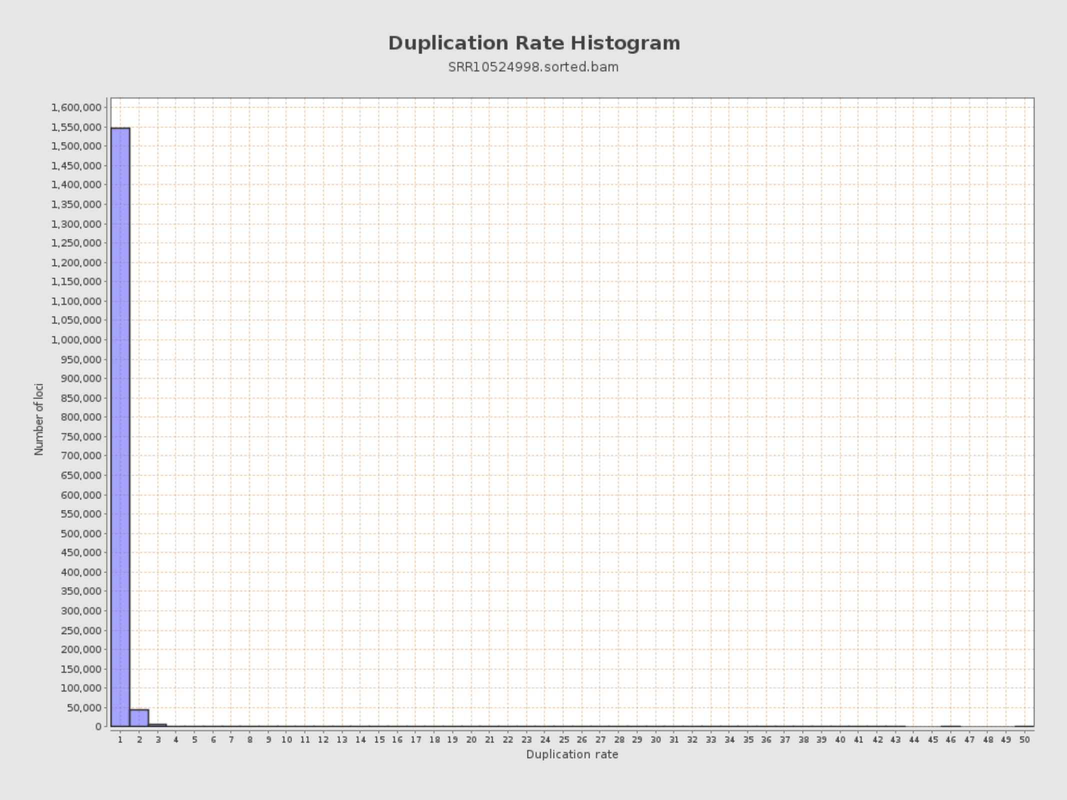
5. Results : Coverage Histogram (0-50X)



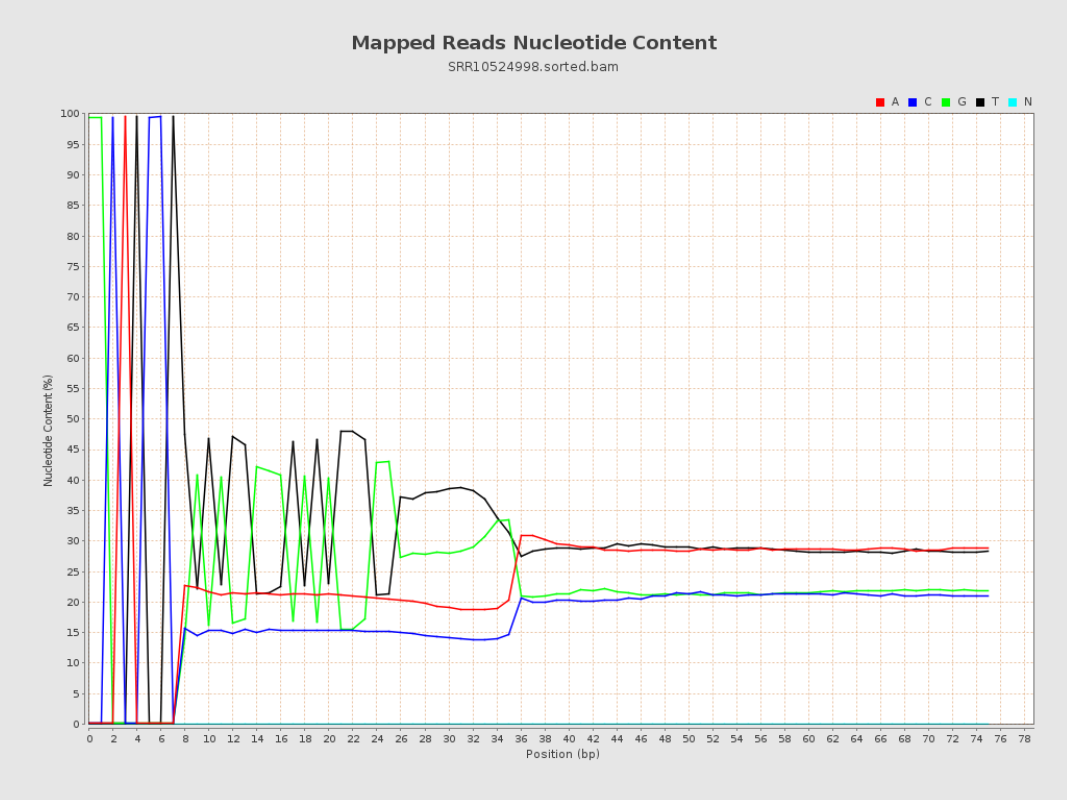
6. Results : Genome Fraction Coverage



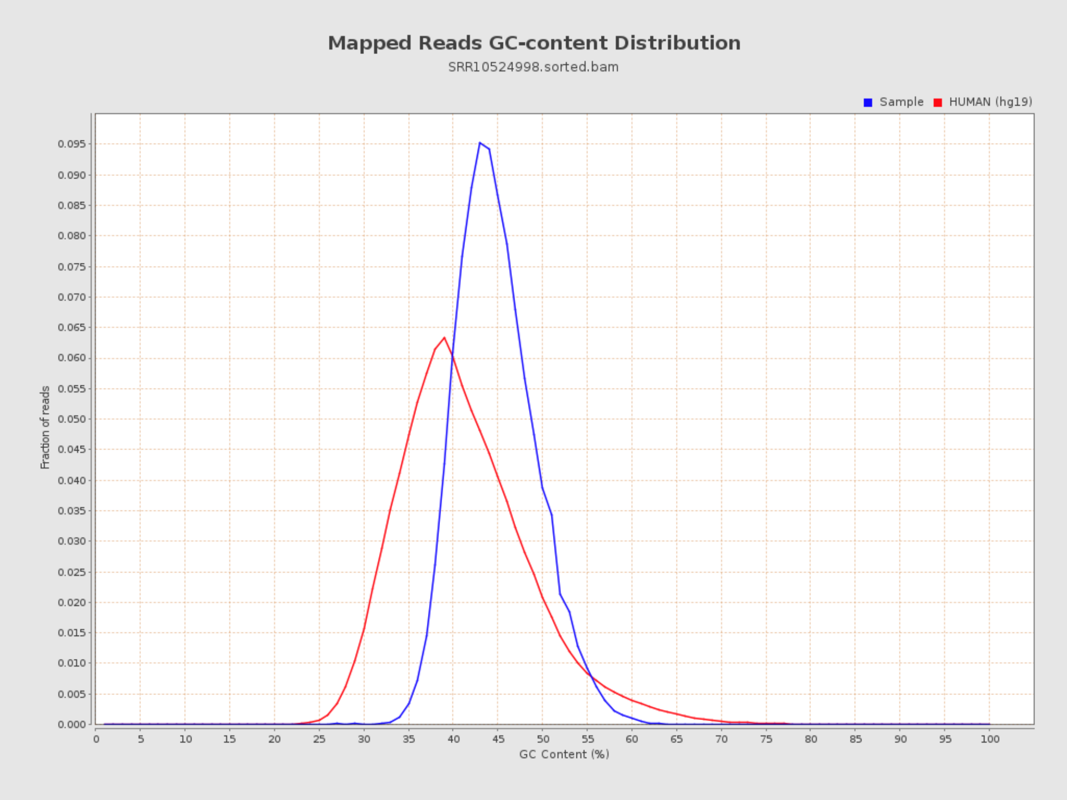
7. Results : Duplication Rate Histogram



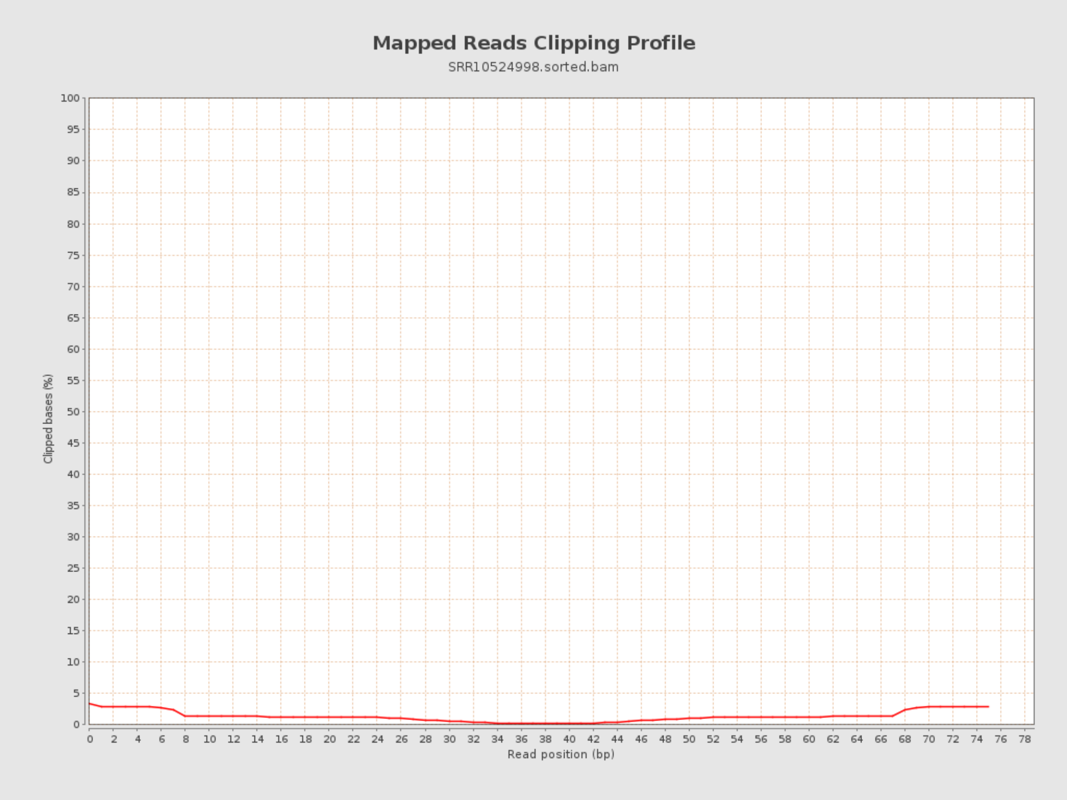
8. Results : Mapped Reads Nucleotide Content



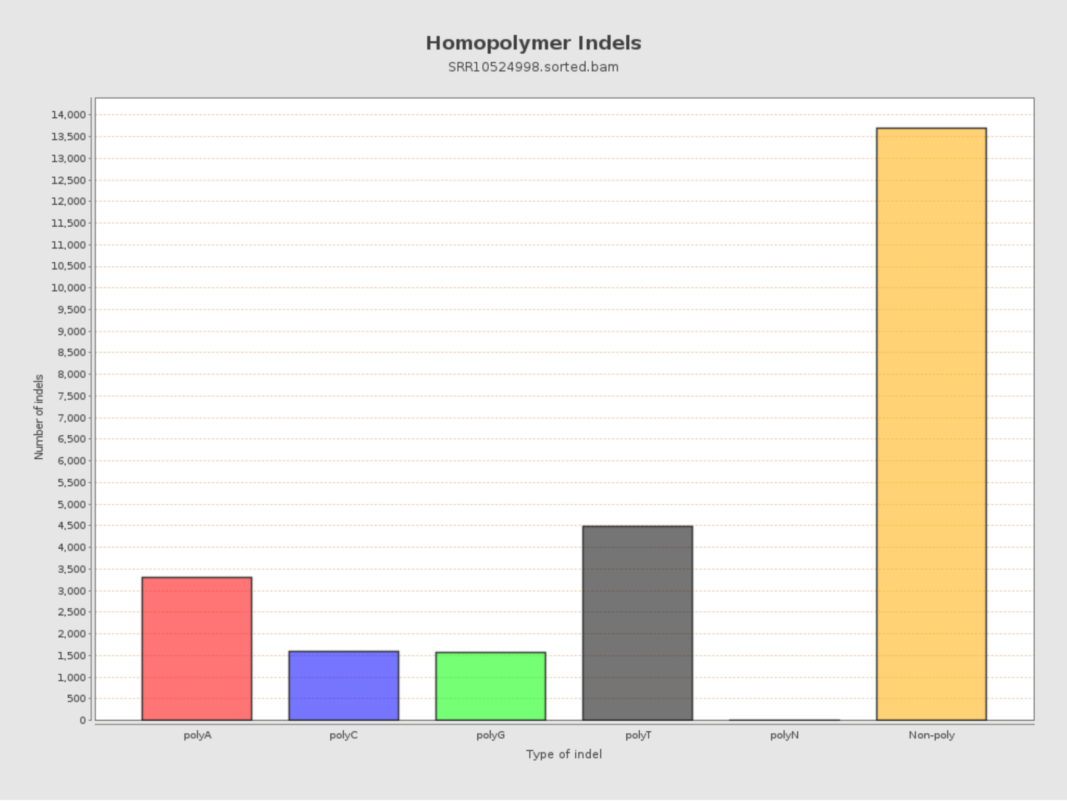
9. Results : Mapped Reads GC-content Distribution



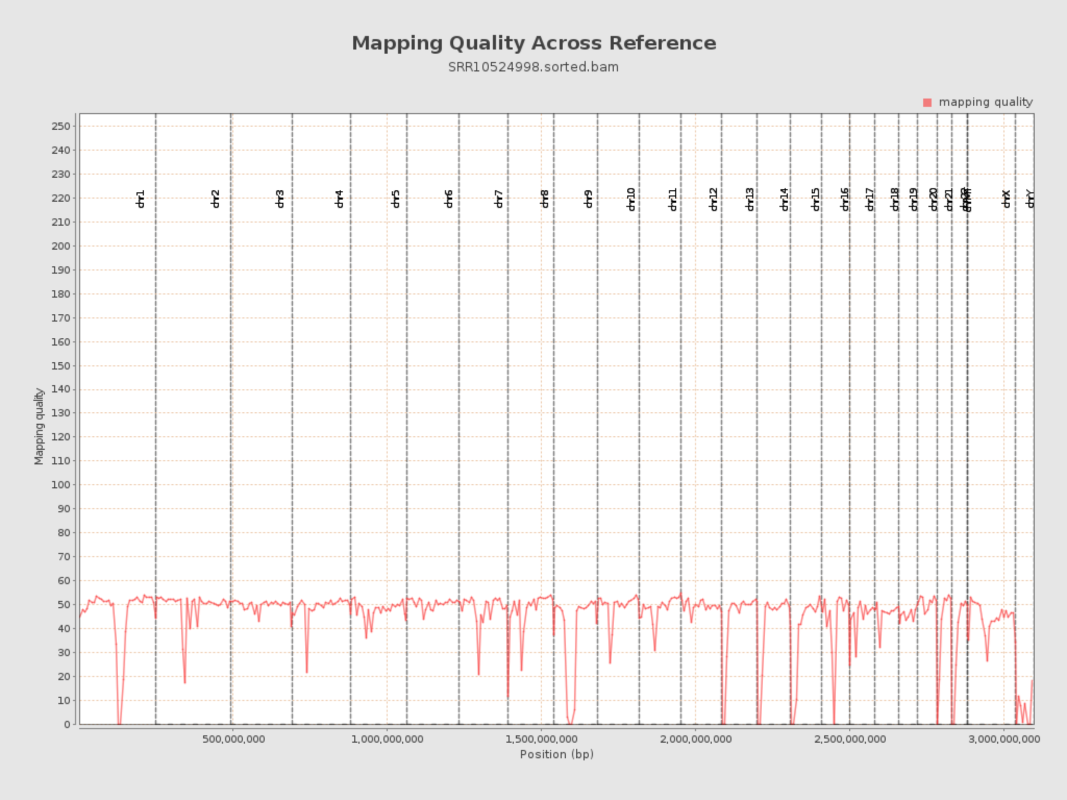
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram