Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 16:37:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8751184.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_SRR8751184 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8751184.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 16:37:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8751184.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,847,416
Mapped reads	4,520,456 / 93.25%
Unmapped reads	326,960 / 6.75%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	156,779 / 3.23%
Read min/max/mean length	30 / 101 / 102.34
Duplicated reads (estimated)	105,340 / 2.17%
Duplication rate	1.44%
Clipped reads	823,175 / 16.98%

2.2. ACGT Content

Number/percentage of A's	129,151,694 / 29.03%
Number/percentage of C's	93,371,295 / 20.99%
Number/percentage of T's	129,514,677 / 29.11%
Number/percentage of G's	92,858,766 / 20.87%
Number/percentage of N's	2,383 / 0%
GC Percentage	41.86%

2.3. Coverage

Mean	0.1438

Standard Deviation	1.0023

2.4. Mapping Quality

Mean Mapping Quality	51.37

2.5. Mismatches and indels

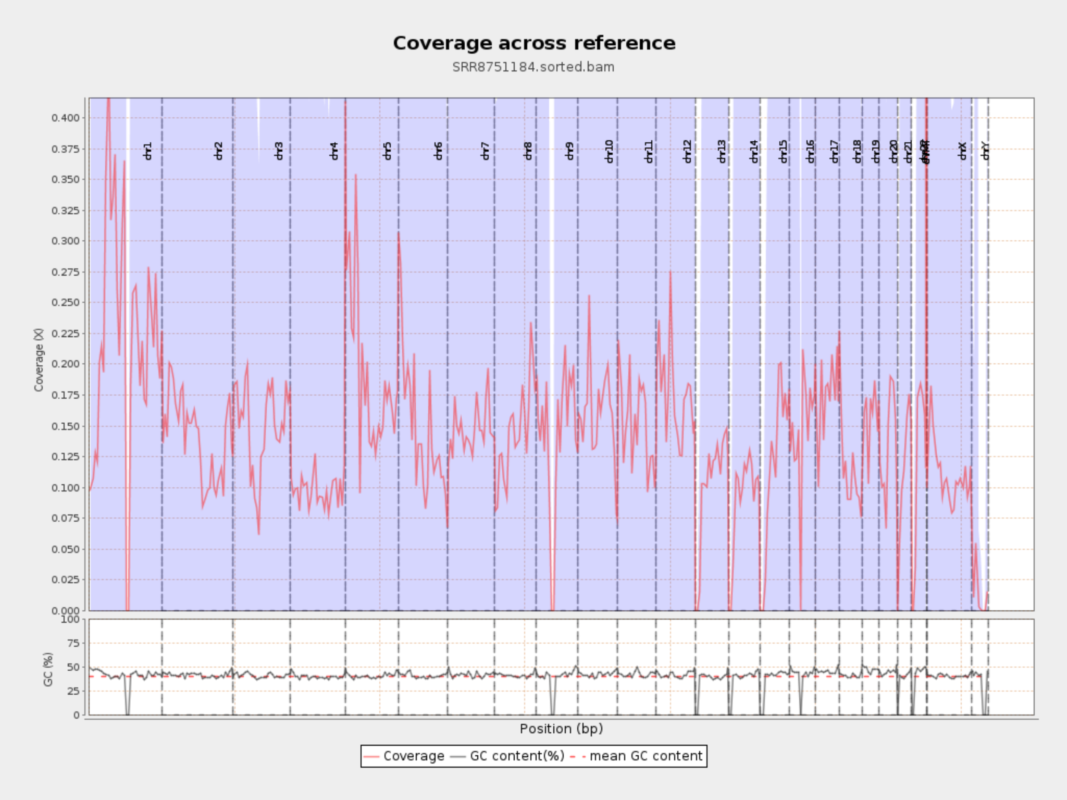
General error rate	0.38%
Mismatches	1,525,955
Insertions	126,708
Mapped reads with at least one insertion	2.74%
Deletions	60,996
Mapped reads with at least one deletion	1.32%
Homopolymer indels	49.72%

2.6. Chromosome stats

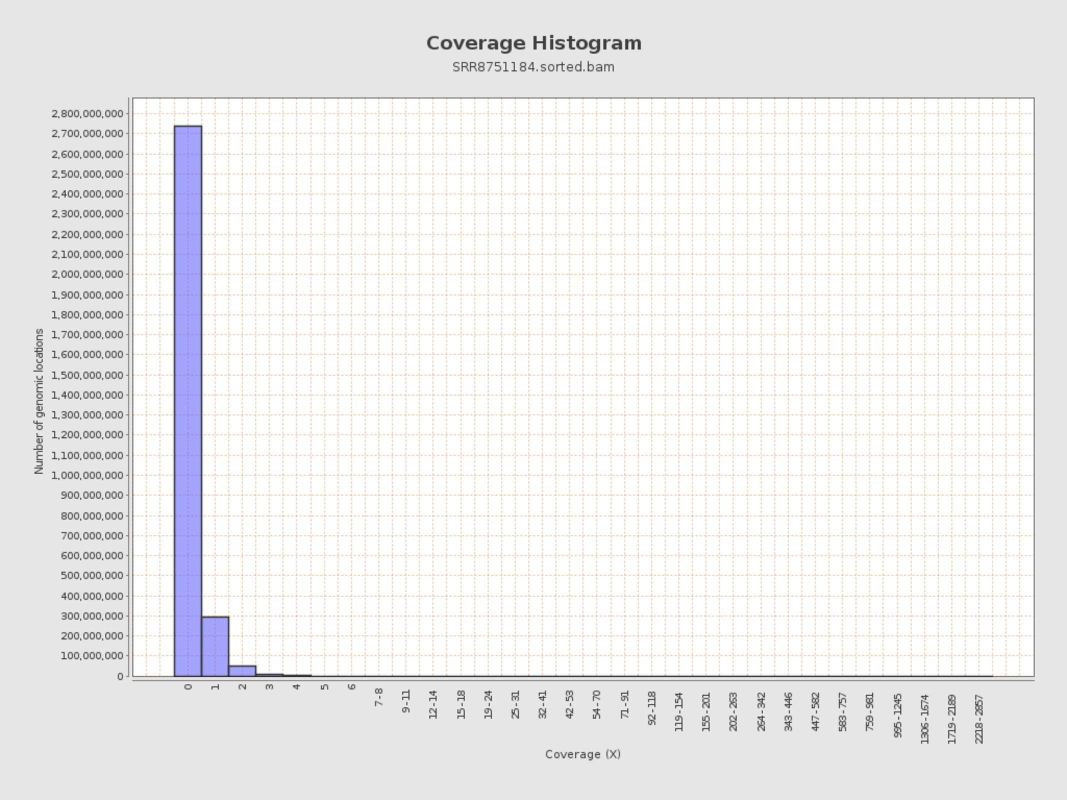
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	55333559	0.222	2.7003
chr2	243199373	34348876	0.1412	0.5086
chr3	198022430	29572050	0.1493	0.4693
chr4	191154276	18593515	0.0973	0.3902
chr5	180915260	34375738	0.19	0.5064
chr6	171115067	25562772	0.1494	0.7246
chr7	159138663	23463989	0.1474	0.6185

chr8	146364022	21141124	0.1444	0.4852
chr9	141213431	19761301	0.1399	0.5751
chr10	135534747	21901393	0.1616	1.3842
chr11	135006516	20463307	0.1516	0.5781
chr12	133851895	23740023	0.1774	0.4874
chr13	115169878	11675168	0.1014	0.3641
chr14	107349540	9582576	0.0893	0.3521
chr15	102531392	11897495	0.116	0.3933
chr16	90354753	13008526	0.144	0.7945
chr17	81195210	14090203	0.1735	0.6289
chr18	78077248	8856030	0.1134	1.0368
chr19	59128983	9214796	0.1558	1.941
chr20	63025520	8403137	0.1333	0.4259
chr21	48129895	5444158	0.1131	0.4143
chr22	51304566	5860442	0.1142	0.3951
chrMT	16571	618174	37.3046	15.8215
chrX	155270560	17278736	0.1113	0.4194
chrY	59373566	846034	0.0142	0.5019

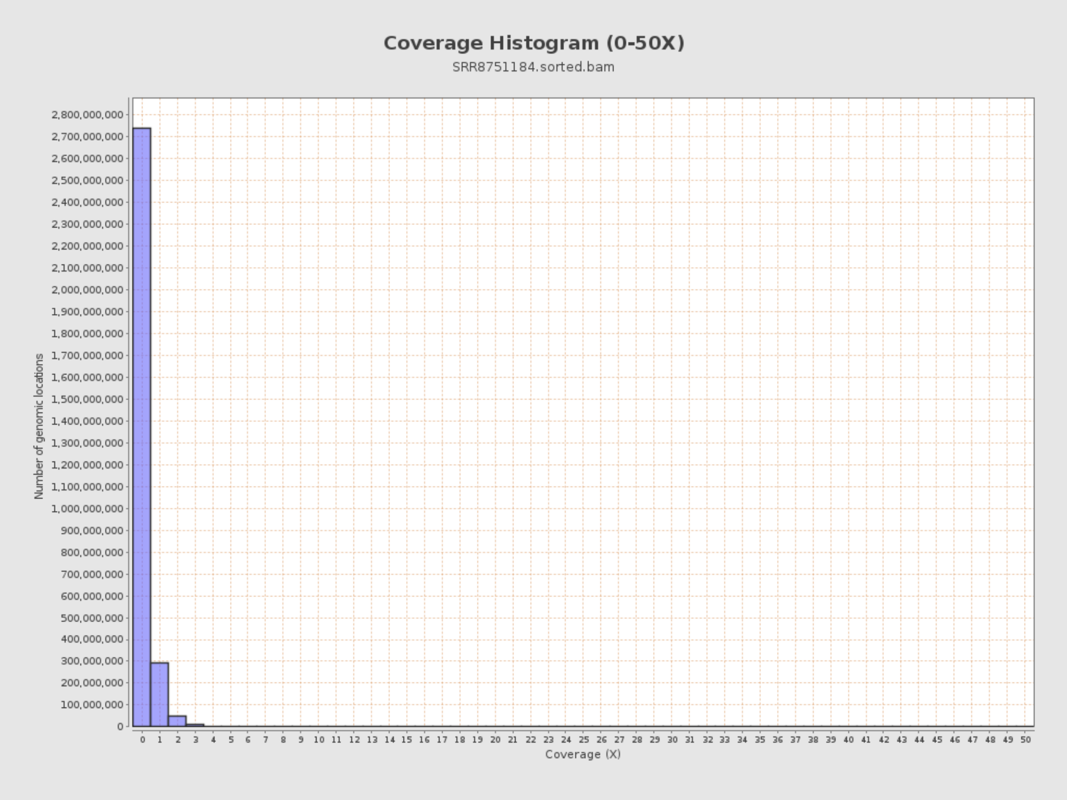
3. Results : Coverage across reference



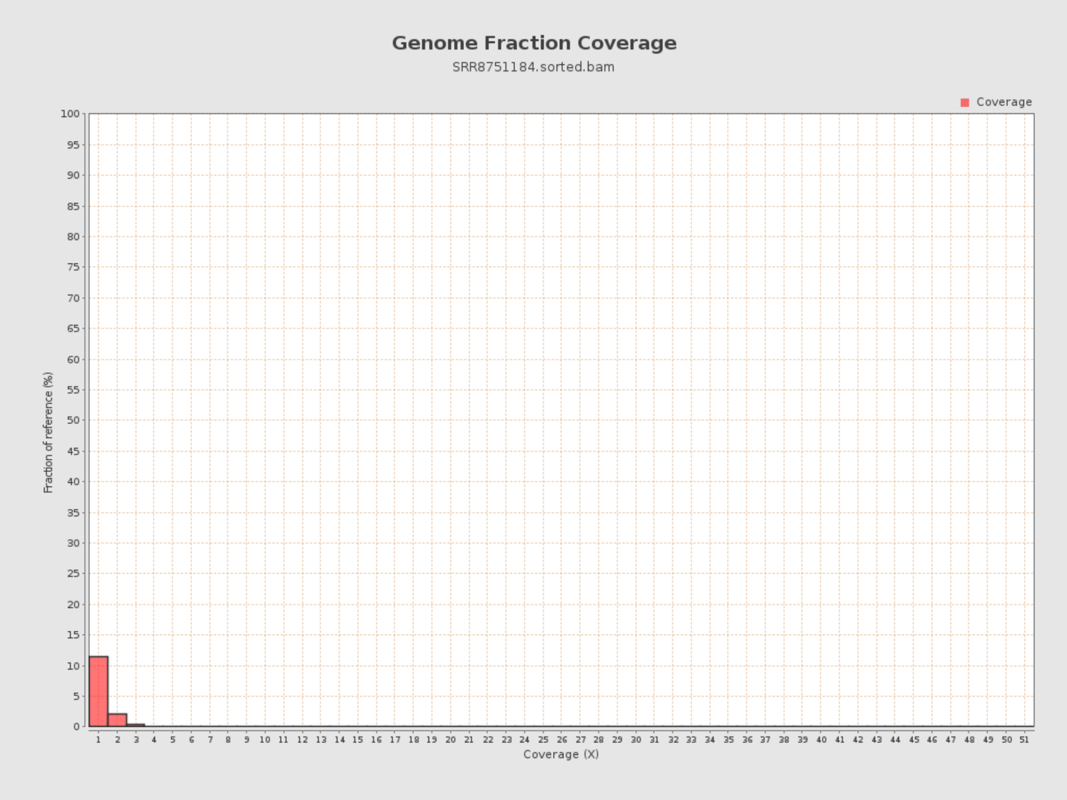
4. Results : Coverage Histogram



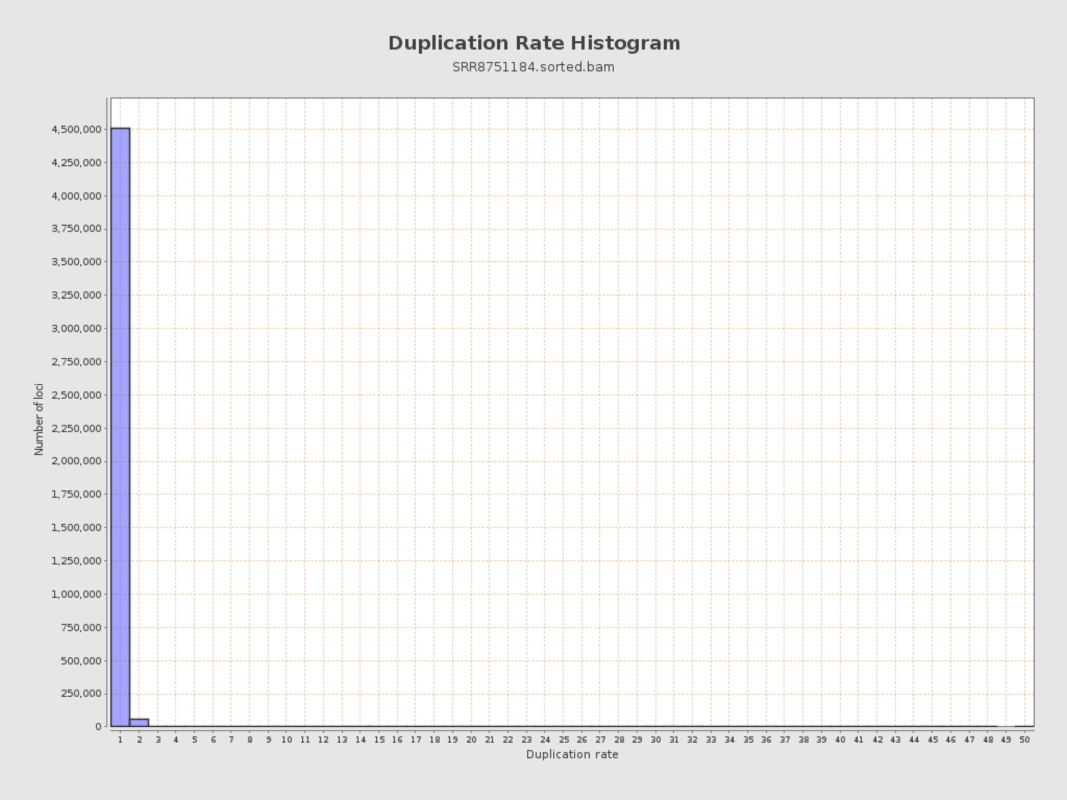
5. Results : Coverage Histogram (0-50X)



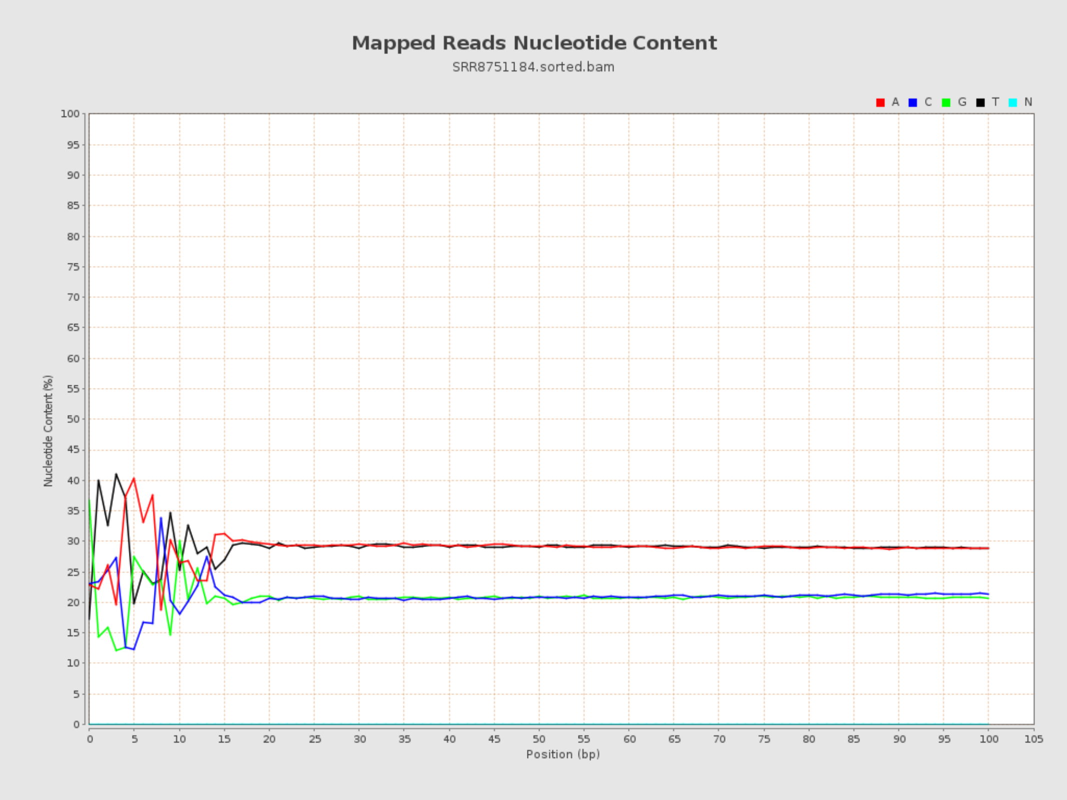
6. Results : Genome Fraction Coverage



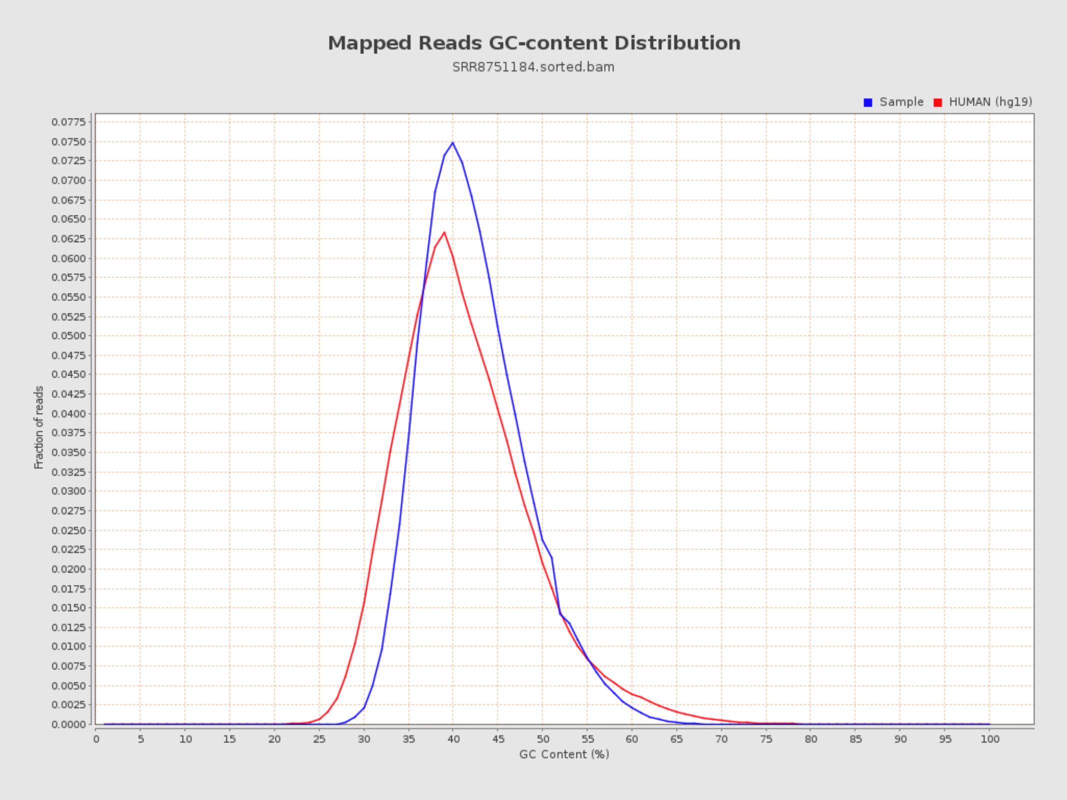
7. Results : Duplication Rate Histogram



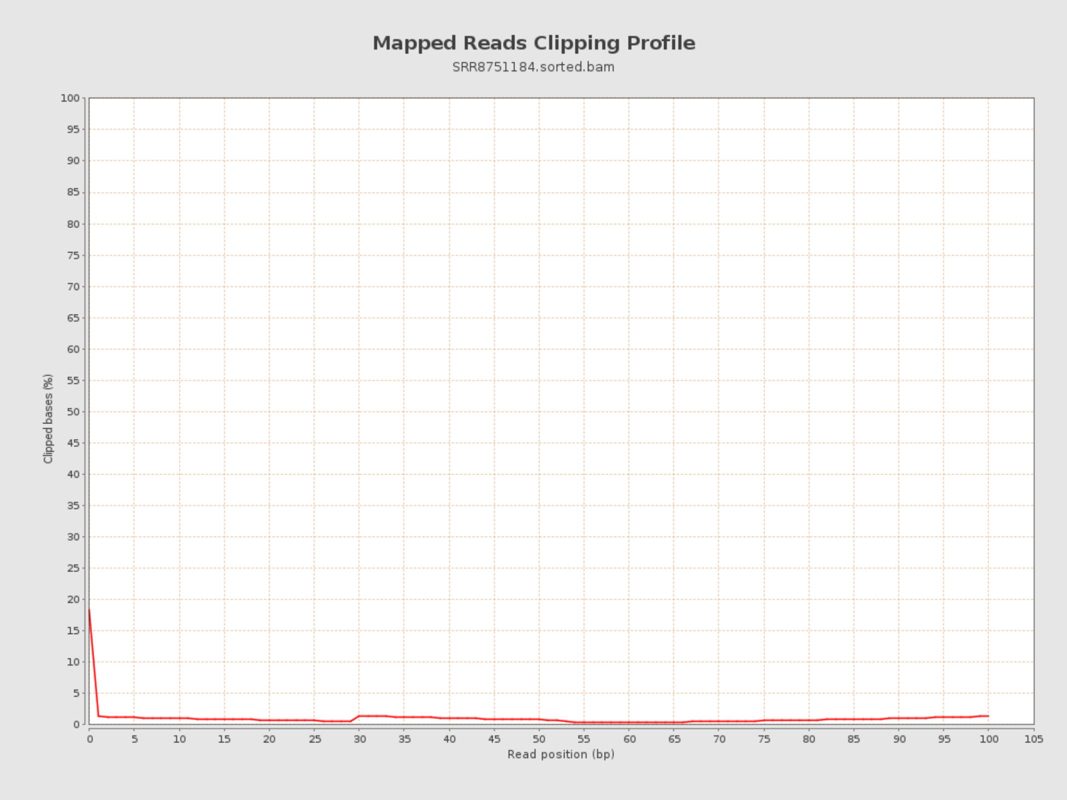
8. Results : Mapped Reads Nucleotide Content



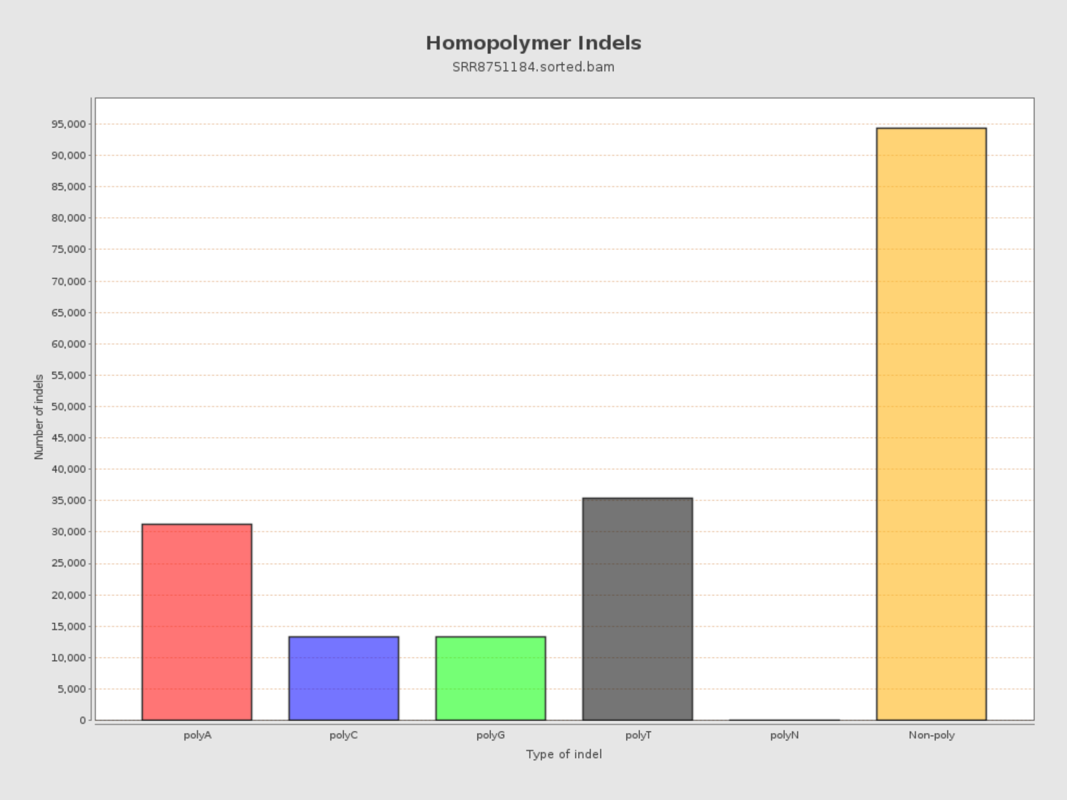
9. Results : Mapped Reads GC-content Distribution



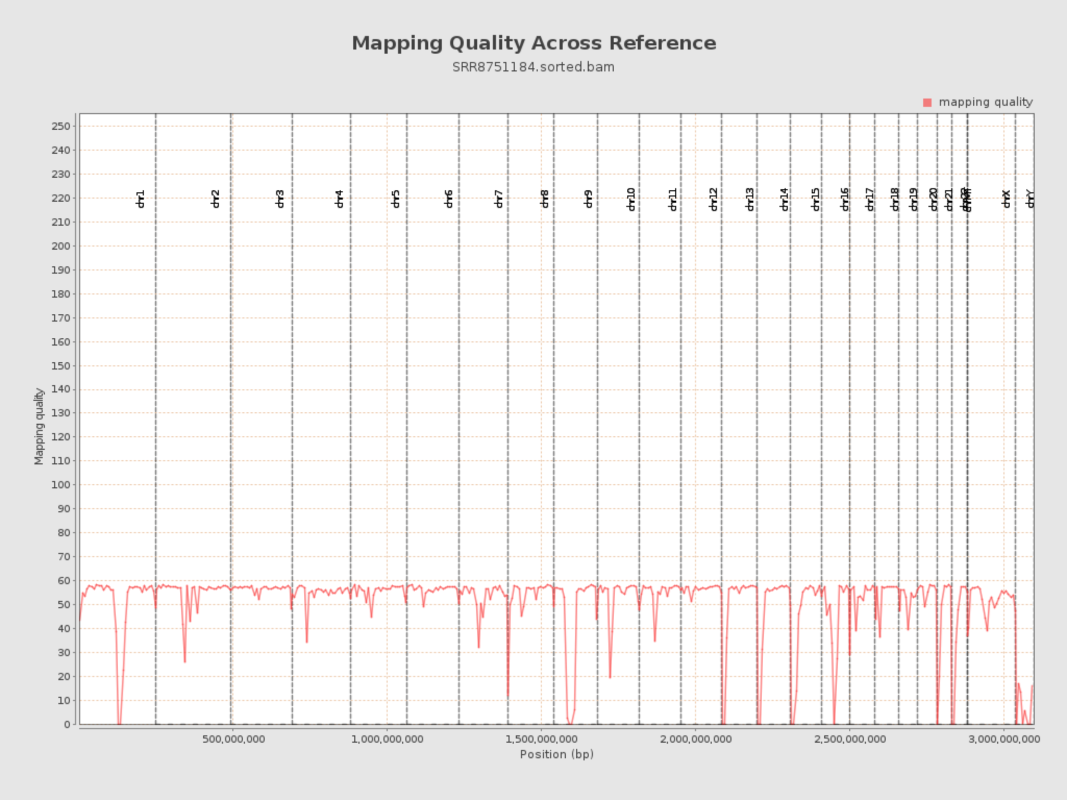
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram