Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 15:25:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8751174.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_SRR8751174 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8751174.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 15:25:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8751174.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,611,037
Mapped reads	3,982,049 / 86.36%
Unmapped reads	628,988 / 13.64%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	173,044 / 3.75%
Read min/max/mean length	30 / 101 / 102.55
Duplicated reads (estimated)	129,898 / 2.82%
Duplication rate	1.68%
Clipped reads	846,999 / 18.37%

2.2. ACGT Content

Number/percentage of A's	114,525,674 / 29.29%
Number/percentage of C's	80,955,713 / 20.71%
Number/percentage of T's	115,042,193 / 29.42%
Number/percentage of G's	80,457,576 / 20.58%
Number/percentage of N's	2,184 / 0%
GC Percentage	41.28%

2.3. Coverage

Mean	0.1263

Standard Deviation	1.3609

2.4. Mapping Quality

Mean Mapping Quality	51.14

2.5. Mismatches and indels

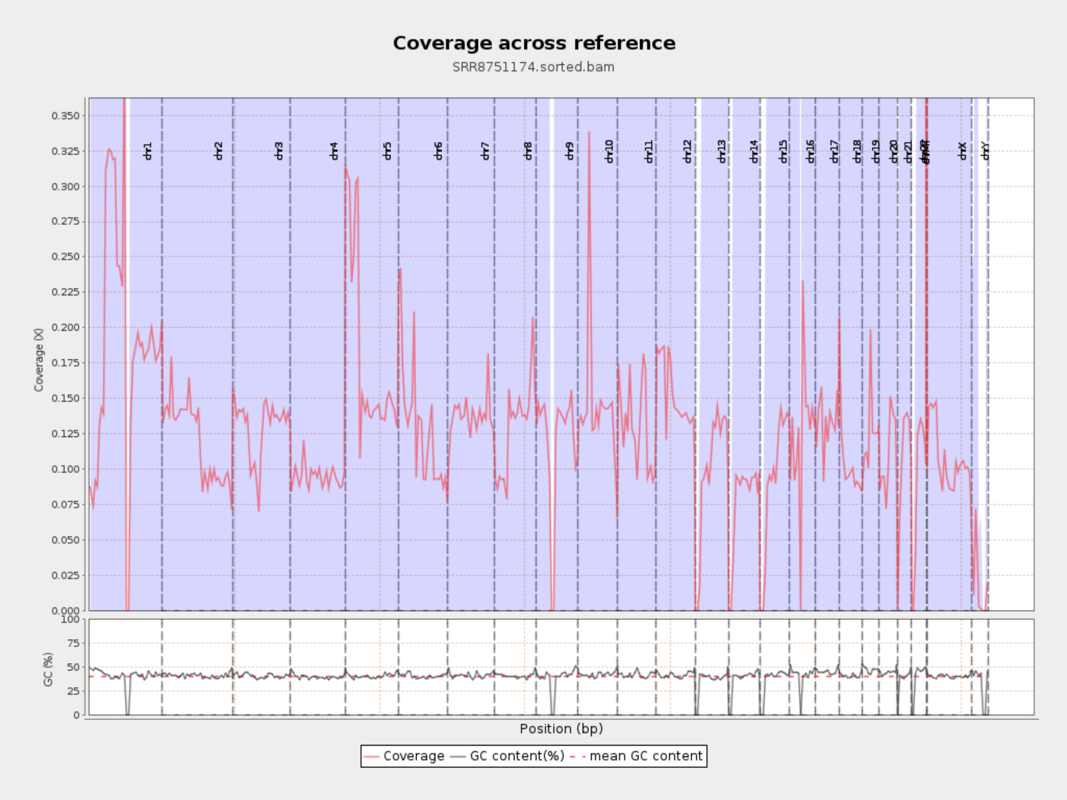
General error rate	0.44%
Mismatches	1,515,481
Insertions	144,481
Mapped reads with at least one insertion	3.53%
Deletions	55,536
Mapped reads with at least one deletion	1.37%
Homopolymer indels	50.54%

2.6. Chromosome stats

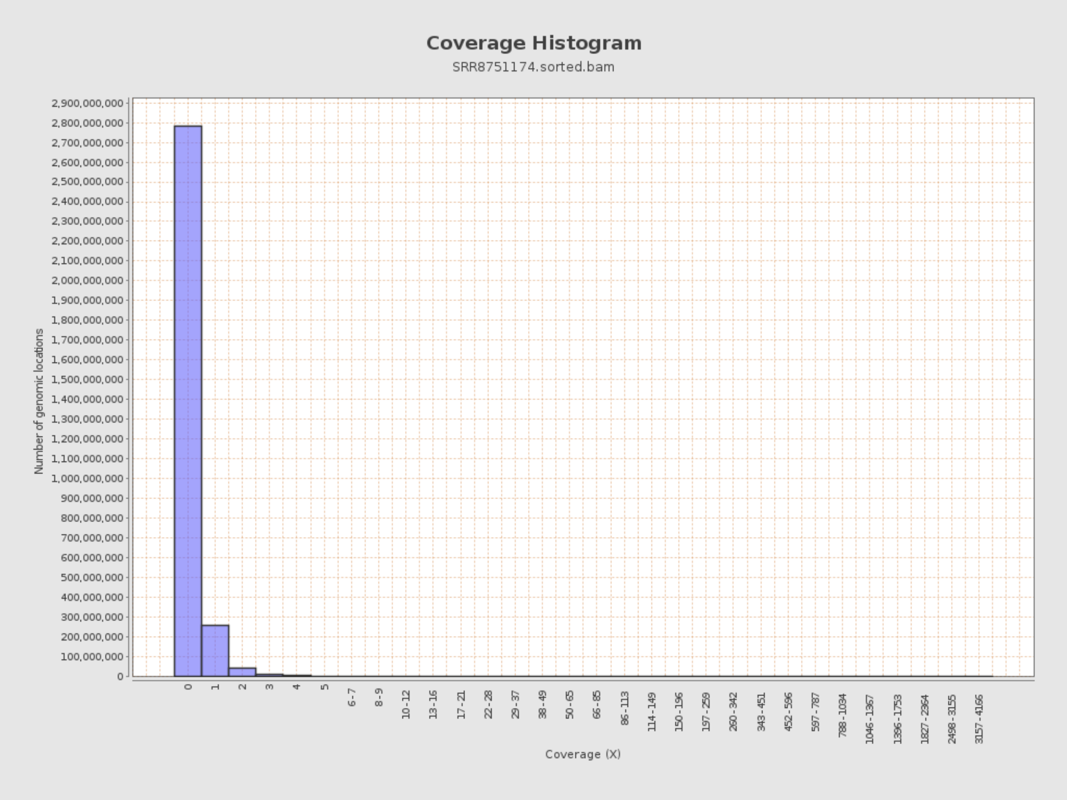
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	46930344	0.1883	3.9056
chr2	243199373	29142248	0.1198	0.5494
chr3	198022430	25677449	0.1297	0.4701
chr4	191154276	18069133	0.0945	0.4417
chr5	180915260	32129630	0.1776	0.4973
chr6	171115067	22266267	0.1301	0.8636
chr7	159138663	21944307	0.1379	0.7825

chr8	146364022	19133883	0.1307	0.5025
chr9	141213431	16821801	0.1191	0.6435
chr10	135534747	19884450	0.1467	1.8817
chr11	135006516	17482271	0.1295	0.6927
chr12	133851895	20508090	0.1532	0.4638
chr13	115169878	11339883	0.0985	0.36
chr14	107349540	8167025	0.0761	0.3371
chr15	102531392	9474365	0.0924	0.3504
chr16	90354753	11234370	0.1243	0.8671
chr17	81195210	10734722	0.1322	0.6729
chr18	78077248	8020134	0.1027	1.3192
chr19	59128983	7471271	0.1264	2.6944
chr20	63025520	6875177	0.1091	0.3947
chr21	48129895	5025353	0.1044	0.4299
chr22	51304566	4419963	0.0862	0.3419
chrMT	16571	765612	46.2019	18.8449
chrX	155270560	16593430	0.1069	0.4464
chrY	59373566	995502	0.0168	0.6945

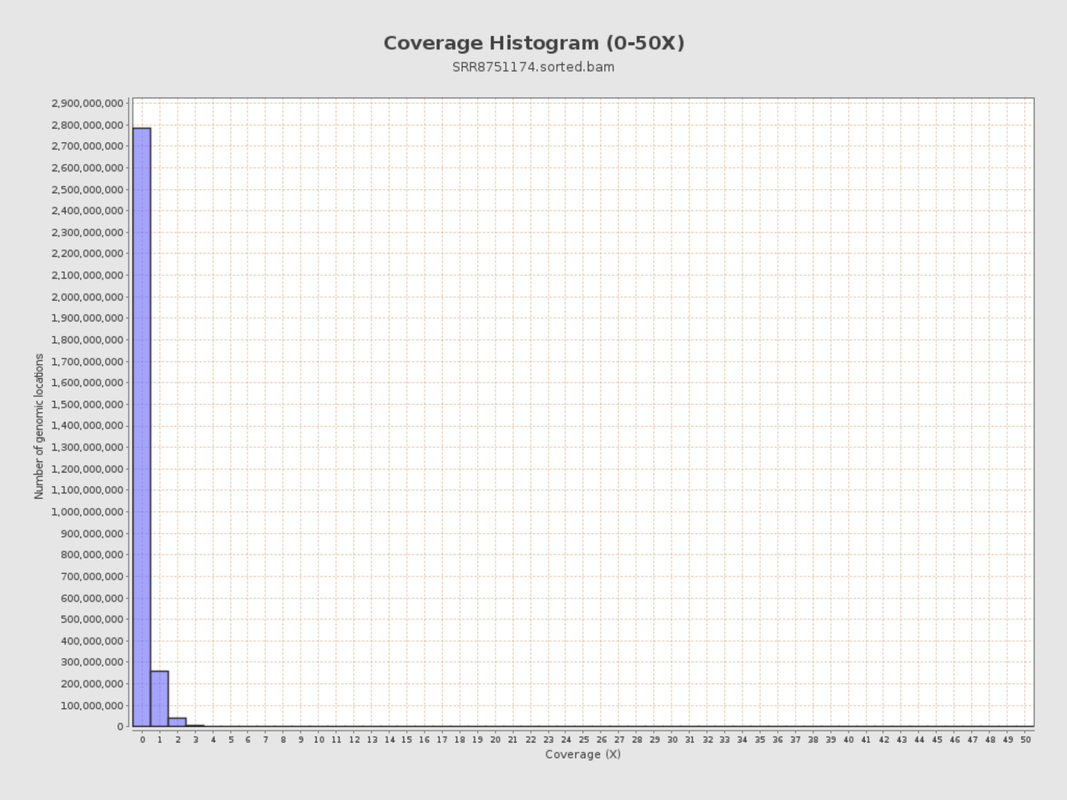
3. Results : Coverage across reference



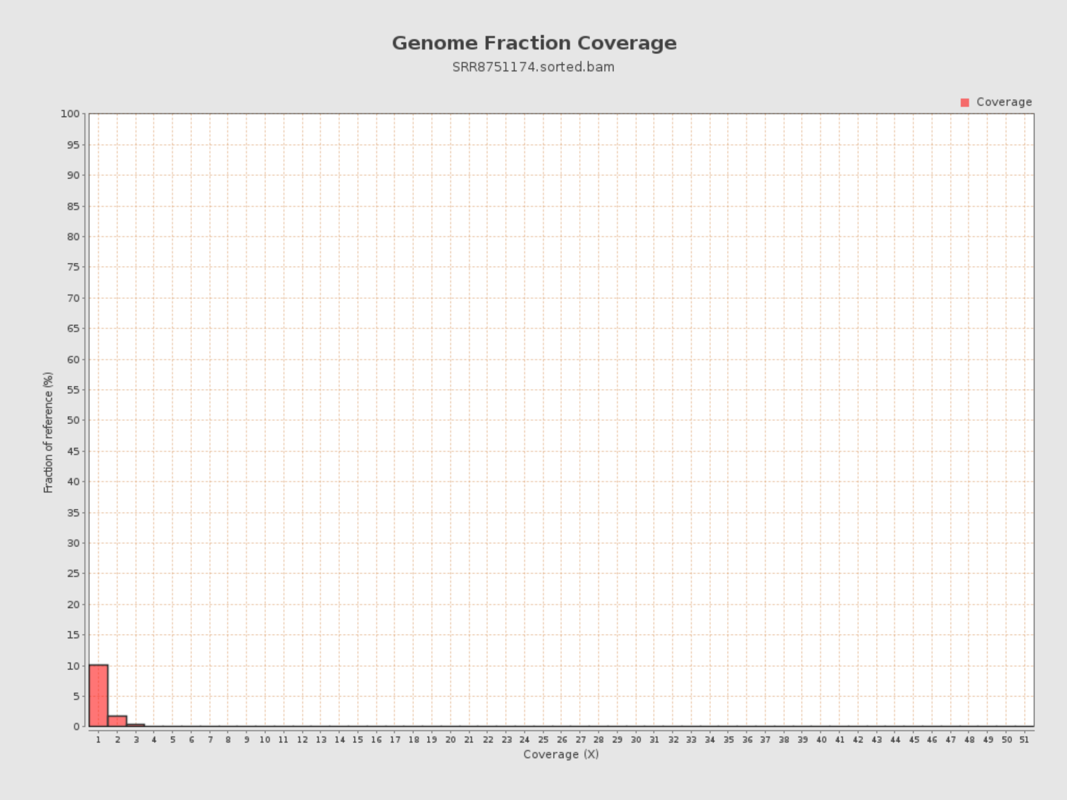
4. Results : Coverage Histogram



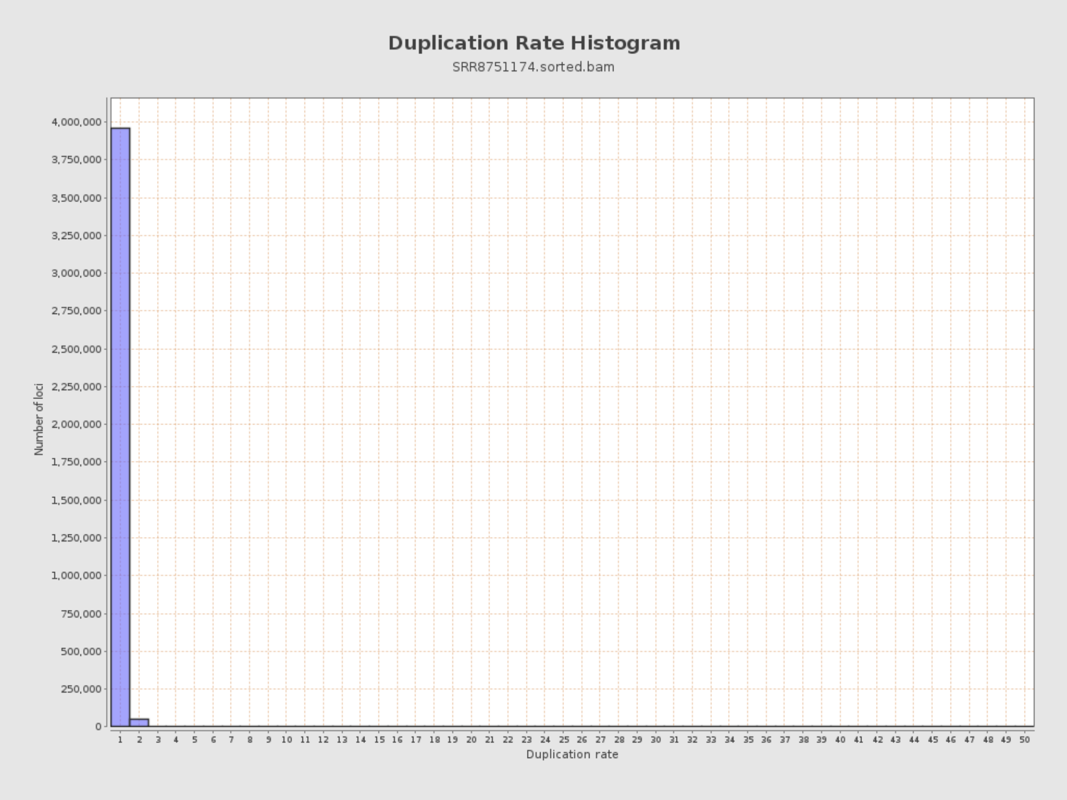
5. Results : Coverage Histogram (0-50X)



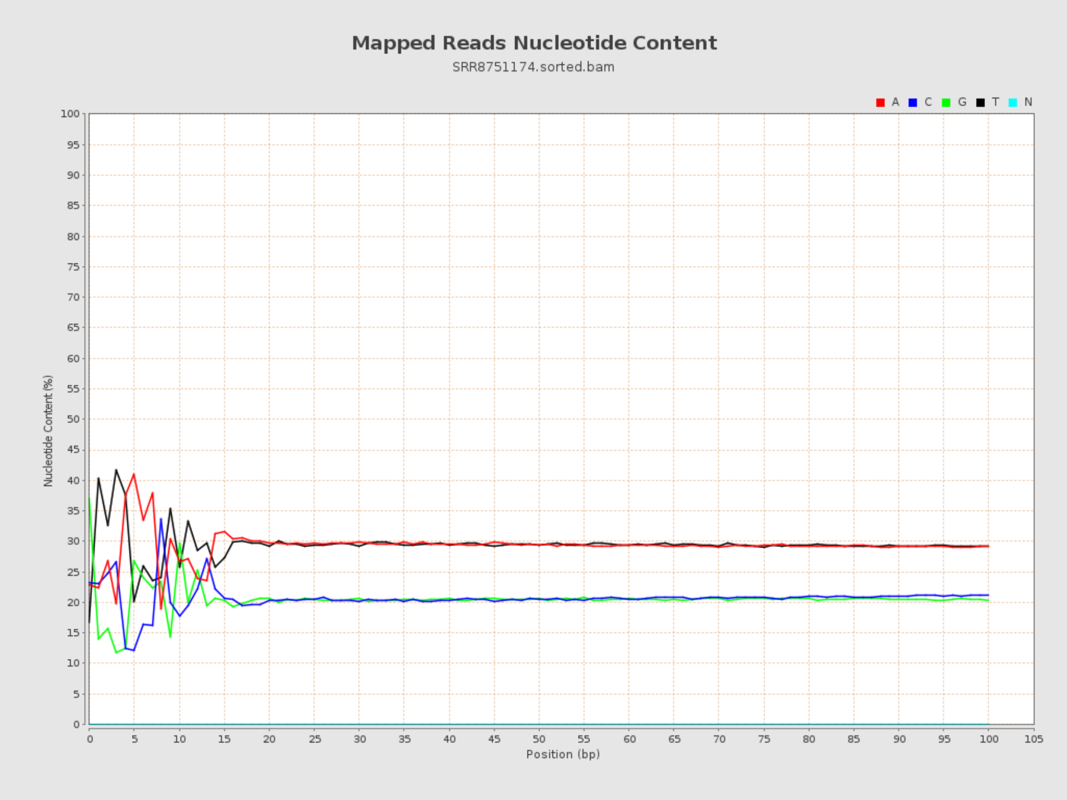
6. Results : Genome Fraction Coverage



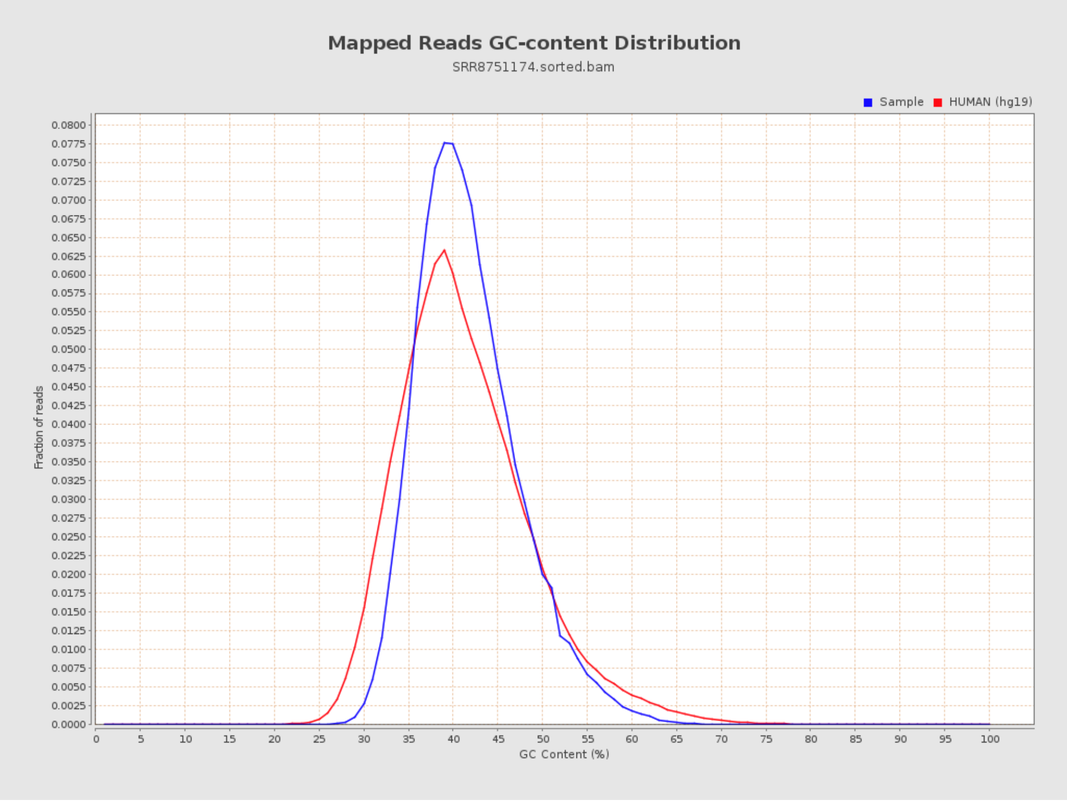
7. Results : Duplication Rate Histogram



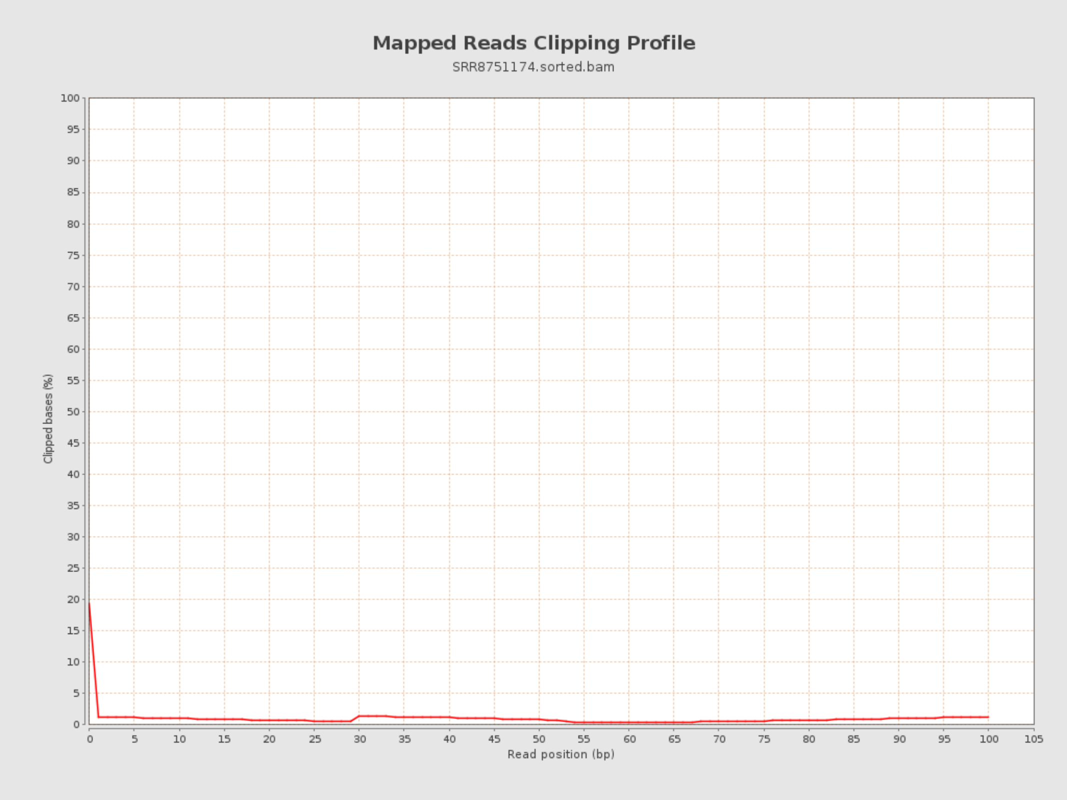
8. Results : Mapped Reads Nucleotide Content



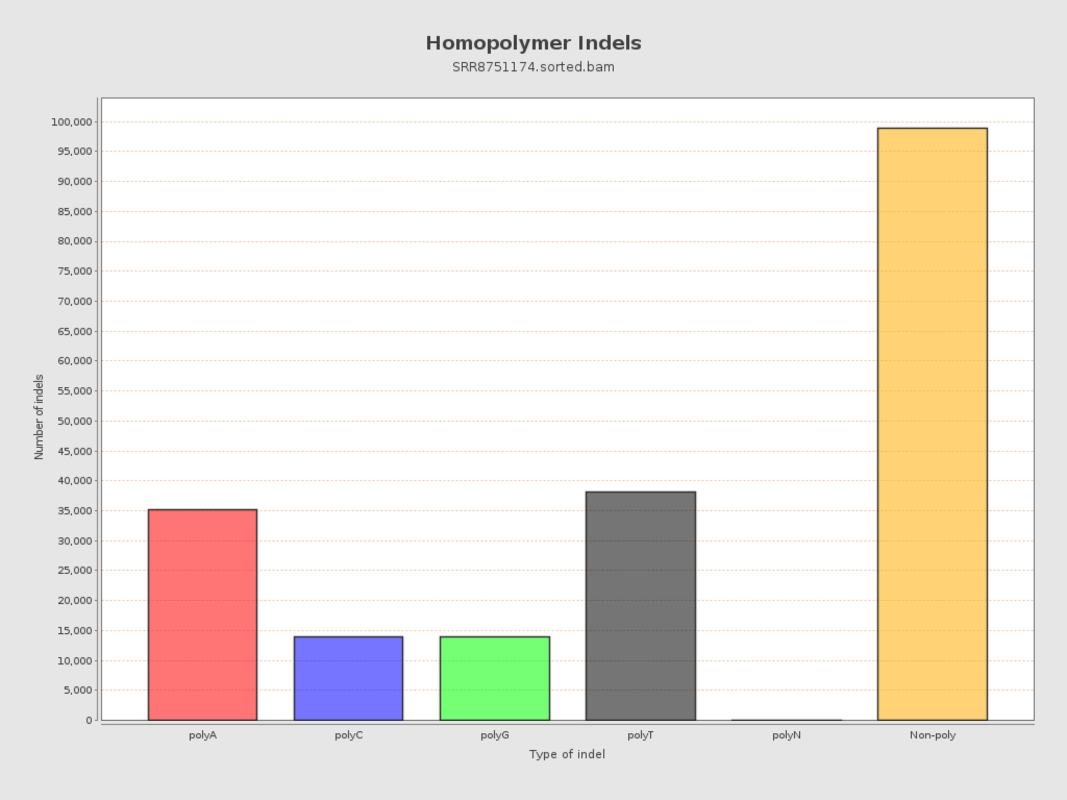
9. Results : Mapped Reads GC-content Distribution



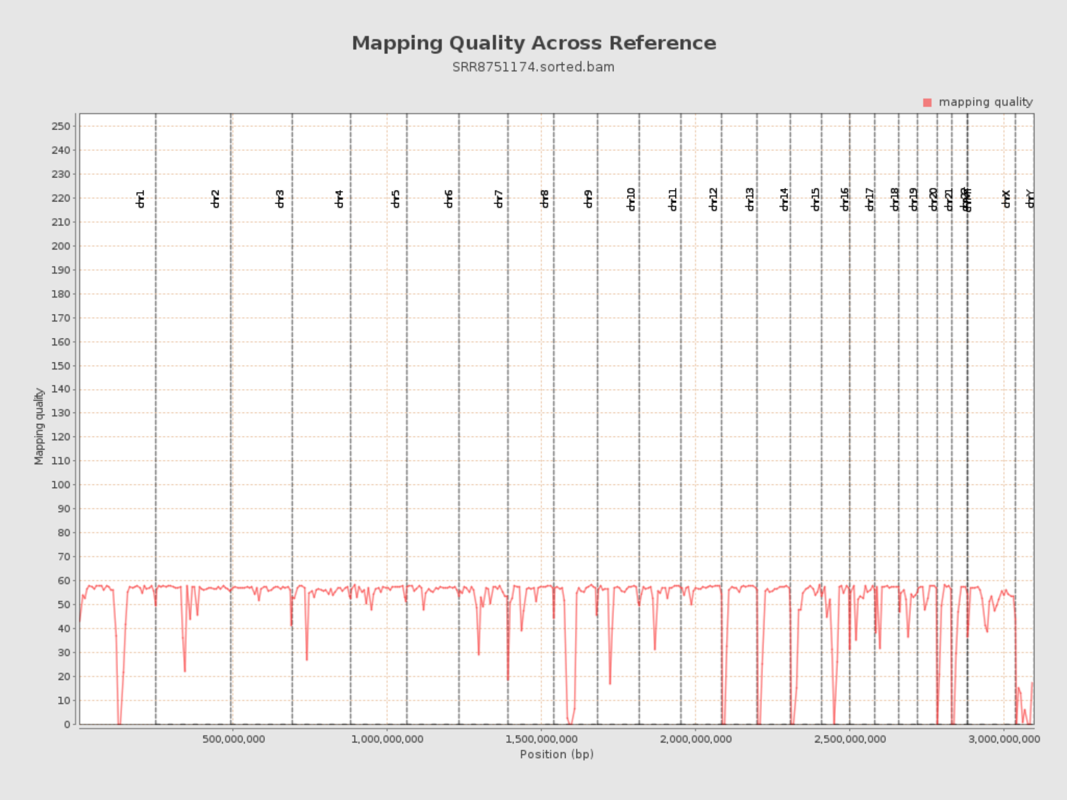
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram