Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 15:17:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8751173.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_SRR8751173 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8751173.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 15:17:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8751173.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,096,241
Mapped reads	3,471,326 / 84.74%
Unmapped reads	624,915 / 15.26%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	166,522 / 4.07%
Read min/max/mean length	30 / 101 / 102.68
Duplicated reads (estimated)	113,159 / 2.76%
Duplication rate	1.7%
Clipped reads	766,774 / 18.72%

2.2. ACGT Content

Number/percentage of A's	100,334,330 / 29.42%
Number/percentage of C's	70,158,653 / 20.57%
Number/percentage of T's	100,878,687 / 29.58%
Number/percentage of G's	69,654,649 / 20.42%
Number/percentage of N's	1,807 / 0%
GC Percentage	41%

2.3. Coverage

Mean	0.1102

Standard Deviation	1.1839

2.4. Mapping Quality

Mean Mapping Quality	51.09

2.5. Mismatches and indels

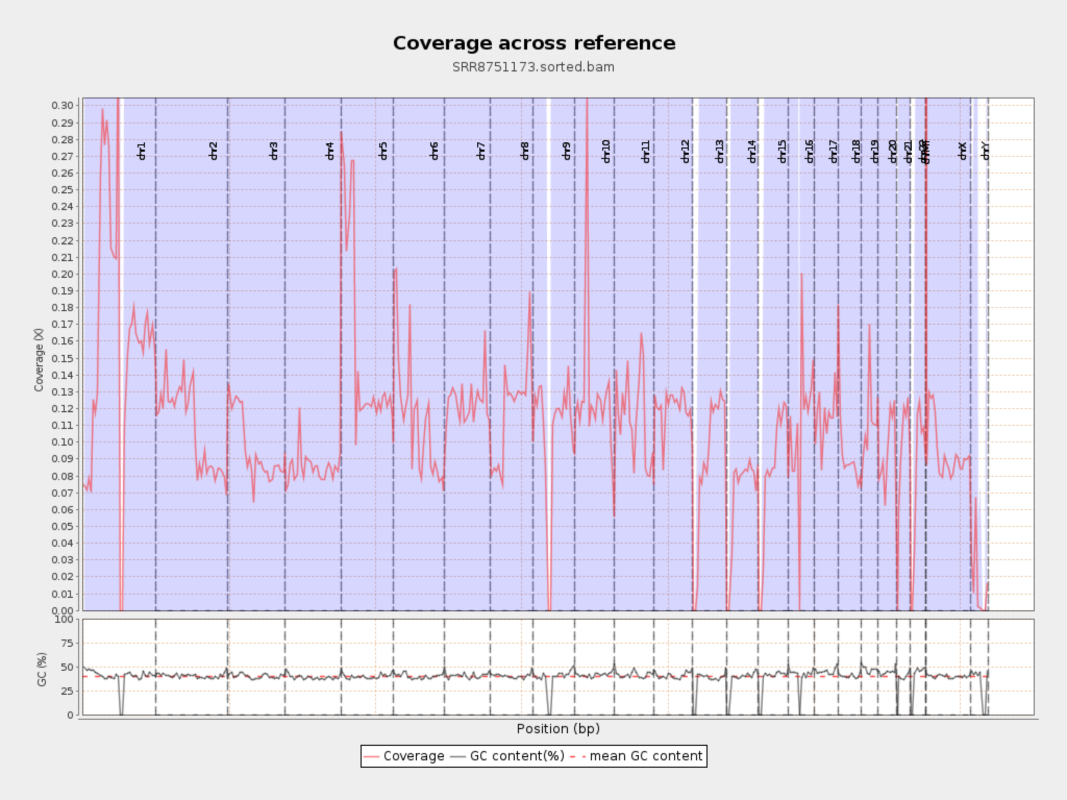
General error rate	0.45%
Mismatches	1,352,276
Insertions	128,811
Mapped reads with at least one insertion	3.61%
Deletions	50,007
Mapped reads with at least one deletion	1.41%
Homopolymer indels	50.13%

2.6. Chromosome stats

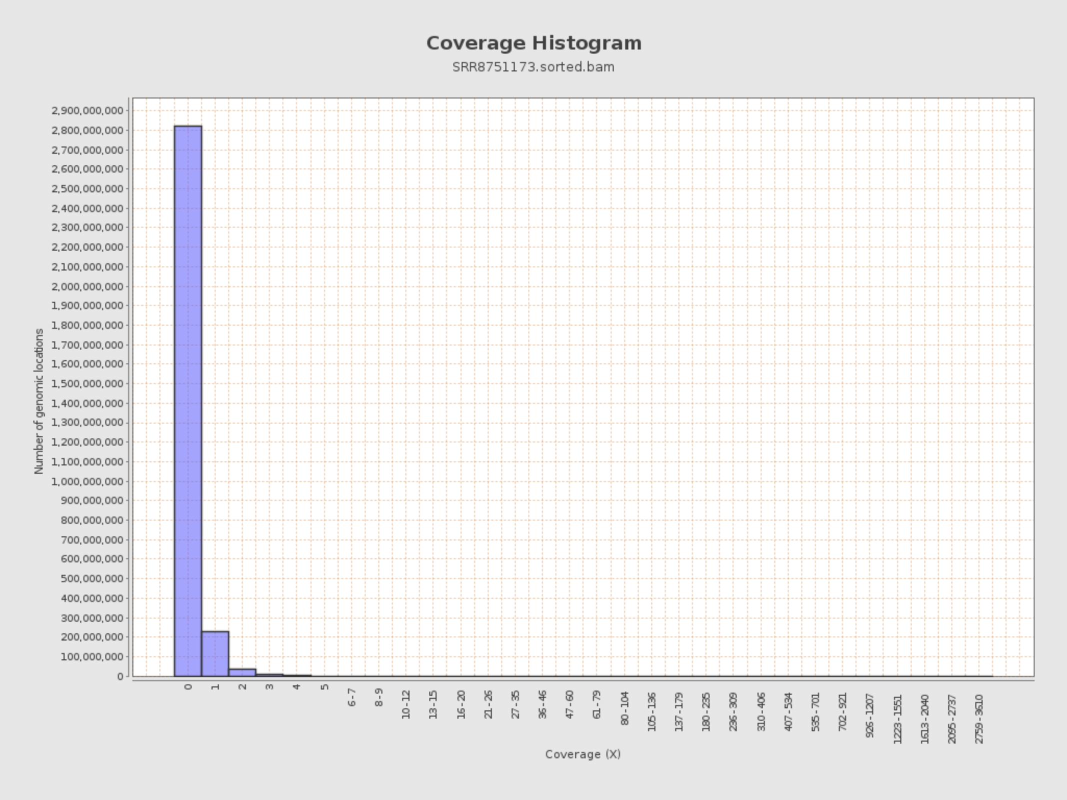
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	41216299	0.1654	3.3545
chr2	243199373	26262555	0.108	0.5196
chr3	198022430	19051796	0.0962	0.4282
chr4	191154276	16255638	0.085	0.432
chr5	180915260	28291908	0.1564	0.468
chr6	171115067	19470723	0.1138	0.7157
chr7	159138663	19601679	0.1232	0.6925

chr8	146364022	17438263	0.1191	0.4944
chr9	141213431	14913274	0.1056	0.5747
chr10	135534747	17509922	0.1292	1.7137
chr11	135006516	15415697	0.1142	0.6123
chr12	133851895	16190569	0.121	0.4207
chr13	115169878	10231821	0.0888	0.3442
chr14	107349540	7310965	0.0681	0.3195
chr15	102531392	8224323	0.0802	0.3276
chr16	90354753	10013332	0.1108	0.7895
chr17	81195210	9314528	0.1147	0.5558
chr18	78077248	7209511	0.0923	1.0907
chr19	59128983	6624490	0.112	2.3505
chr20	63025520	6012382	0.0954	0.373
chr21	48129895	4417177	0.0918	0.4022
chr22	51304566	3963194	0.0772	0.3261
chrMT	16571	637533	38.4728	16.0148
chrX	155270560	14648855	0.0943	0.4125
chrY	59373566	912396	0.0154	0.6138

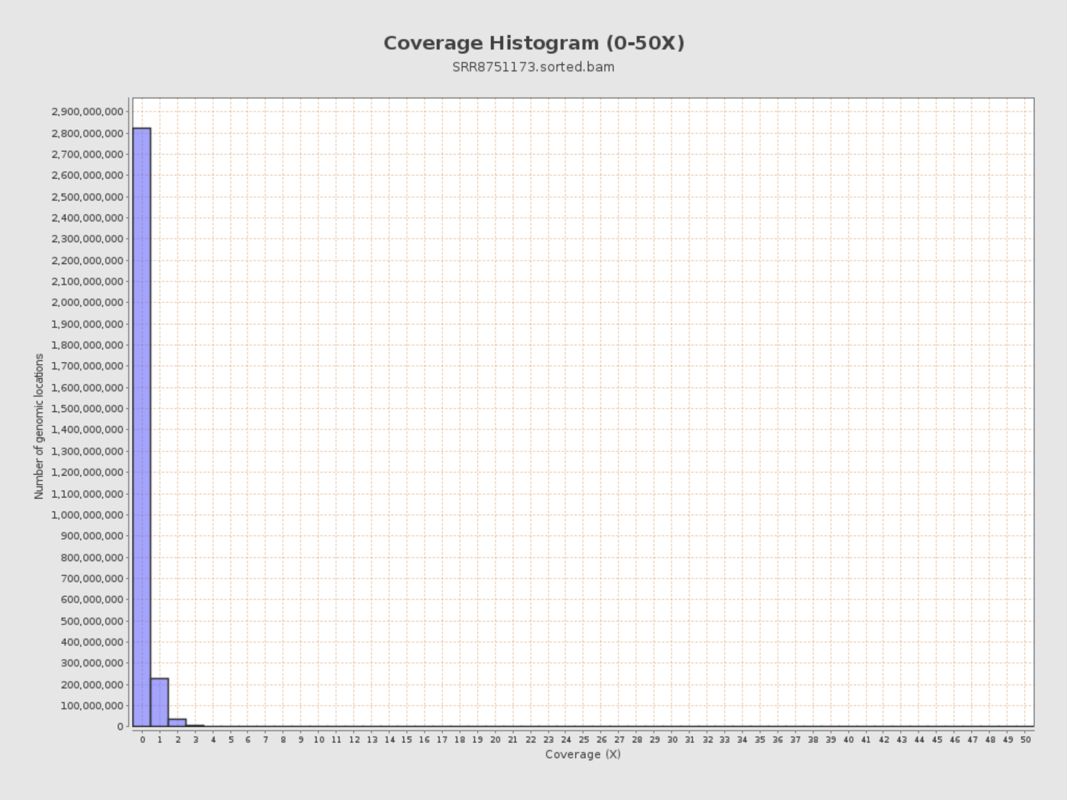
3. Results : Coverage across reference



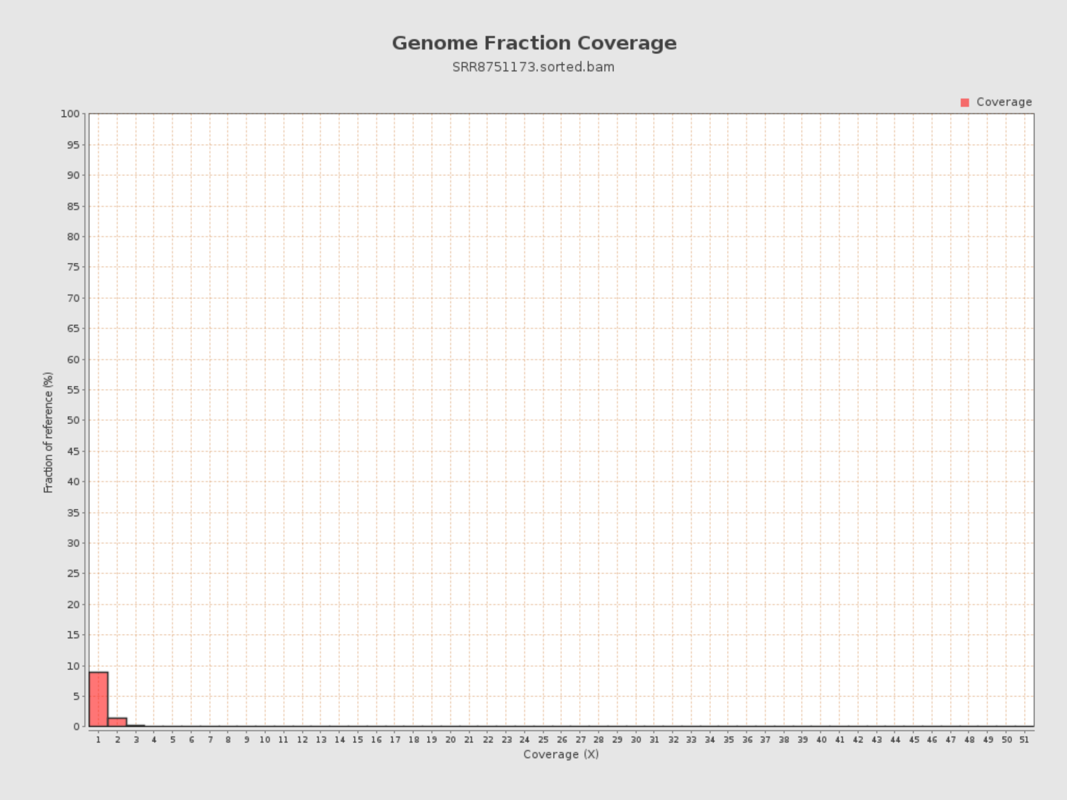
4. Results : Coverage Histogram



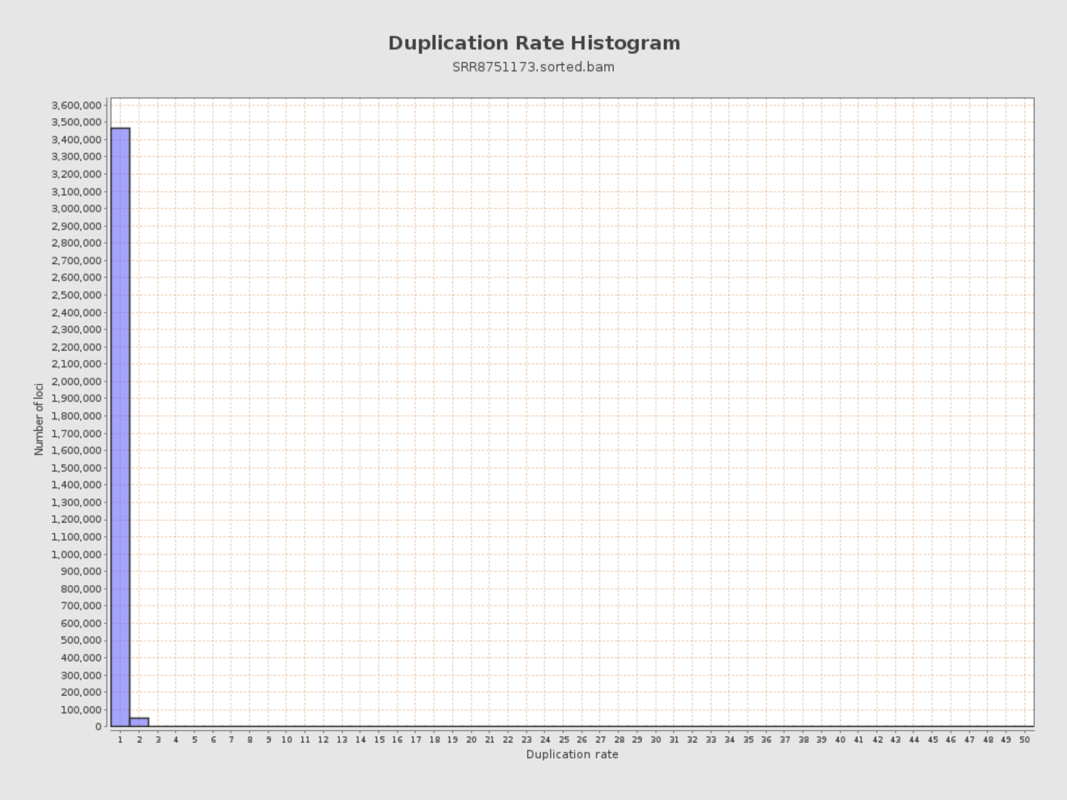
5. Results : Coverage Histogram (0-50X)



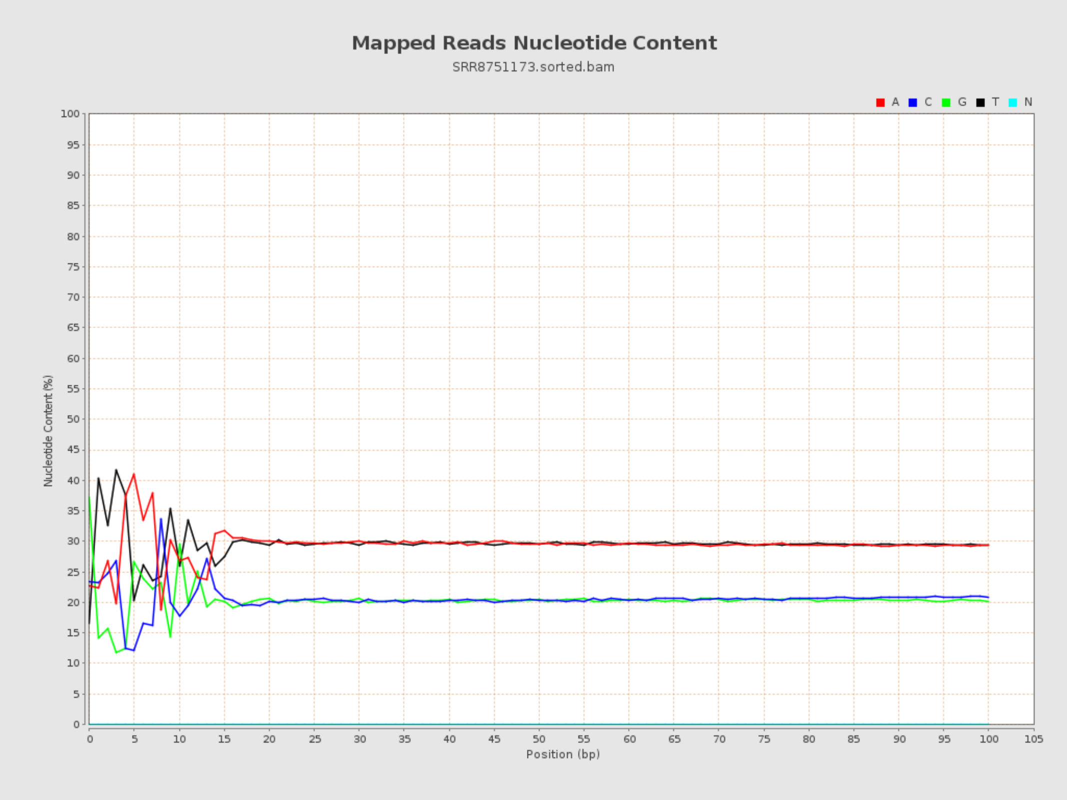
6. Results : Genome Fraction Coverage



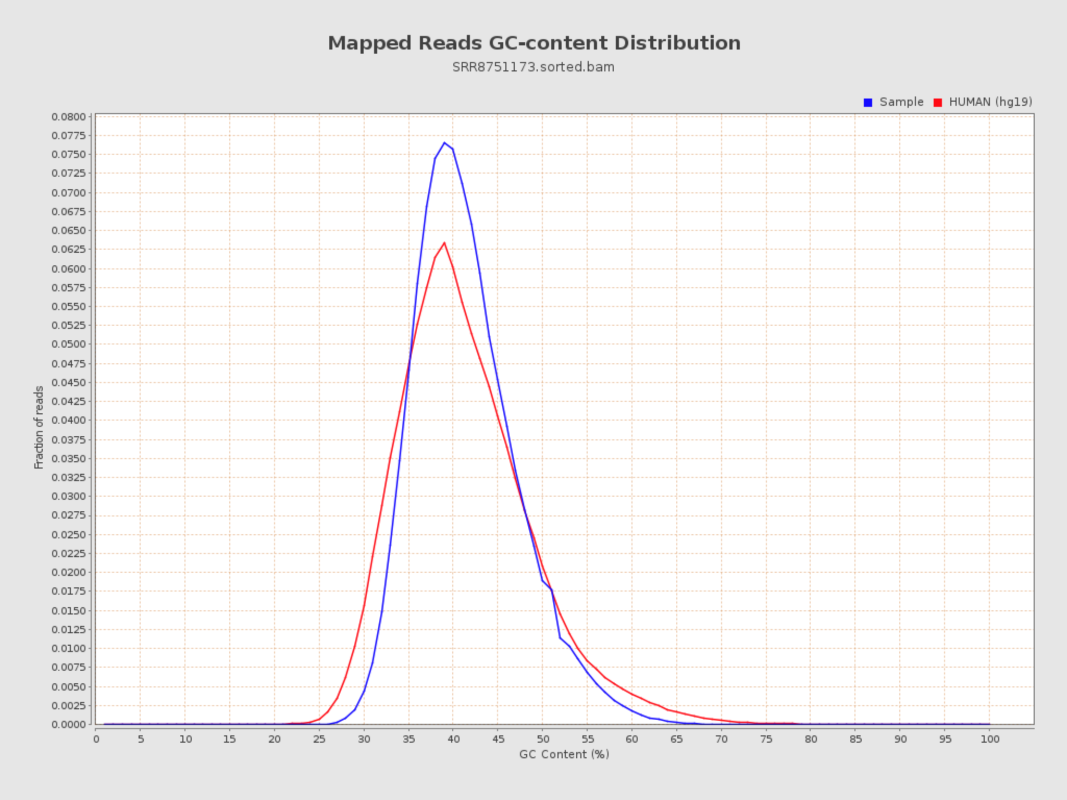
7. Results : Duplication Rate Histogram



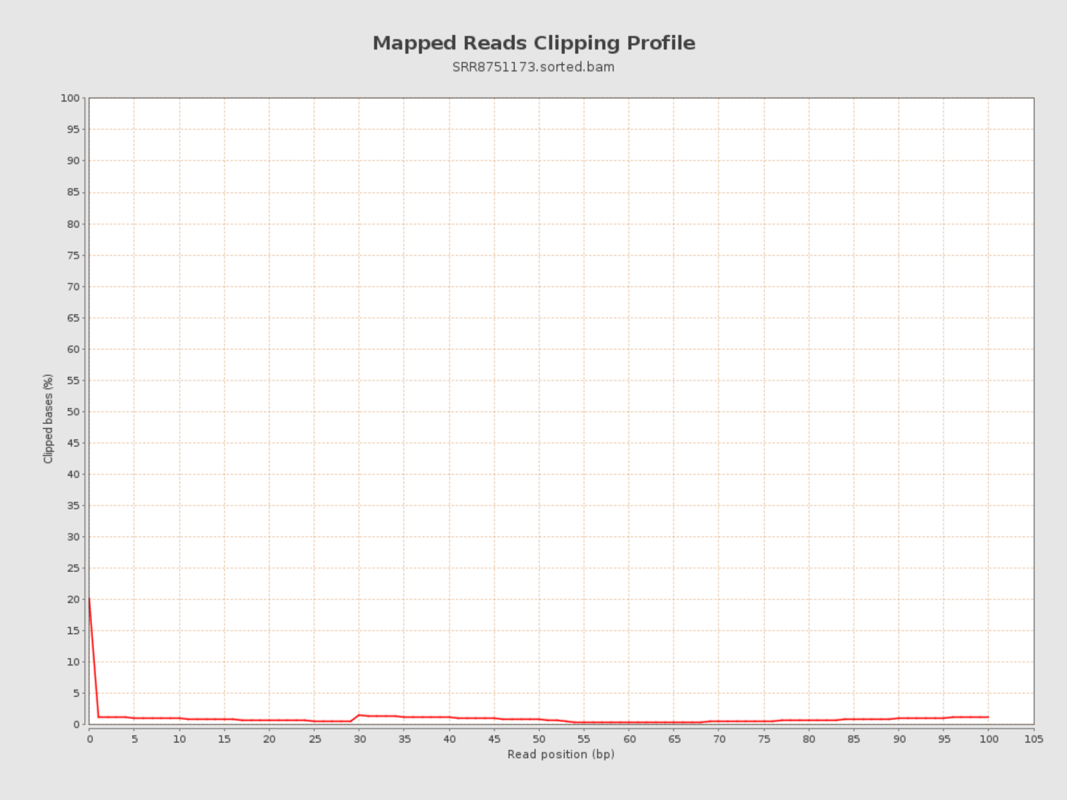
8. Results : Mapped Reads Nucleotide Content



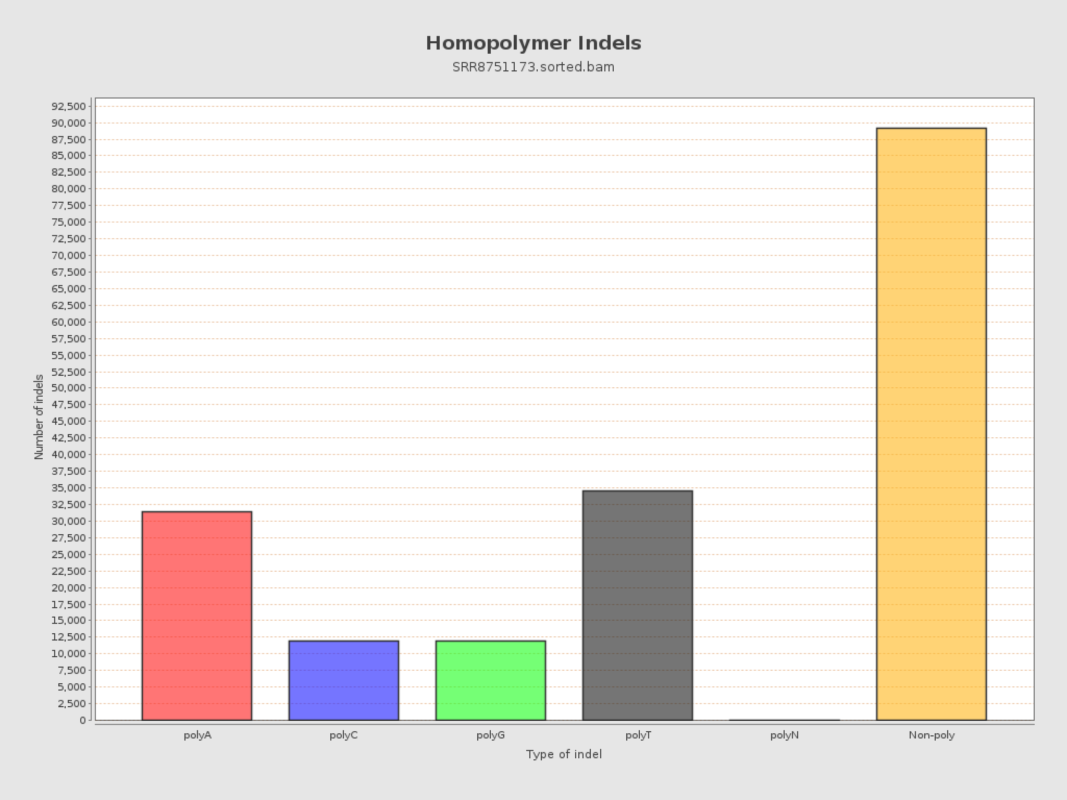
9. Results : Mapped Reads GC-content Distribution



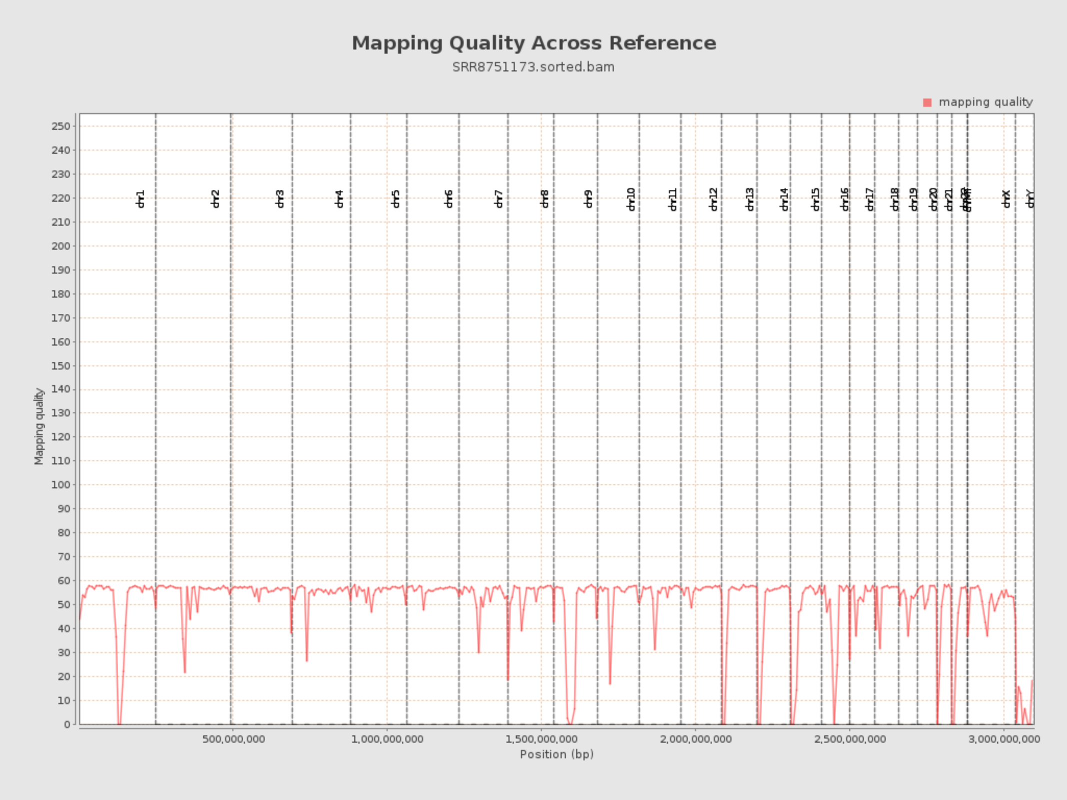
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram