Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 15:12:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8751172.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_SRR8751172 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8751172.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 15:12:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8751172.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,529,175
Mapped reads	4,345,387 / 95.94%
Unmapped reads	183,788 / 4.06%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	134,067 / 2.96%
Read min/max/mean length	30 / 101 / 102.23
Duplicated reads (estimated)	95,078 / 2.1%
Duplication rate	1.24%
Clipped reads	762,144 / 16.83%

2.2. ACGT Content

Number/percentage of A's	126,455,582 / 29.59%
Number/percentage of C's	87,126,985 / 20.38%
Number/percentage of T's	127,138,648 / 29.75%
Number/percentage of G's	86,690,244 / 20.28%
Number/percentage of N's	2,262 / 0%
GC Percentage	40.67%

2.3. Coverage

Mean	0.1381

Standard Deviation	1.0668

2.4. Mapping Quality

Mean Mapping Quality	51.3

2.5. Mismatches and indels

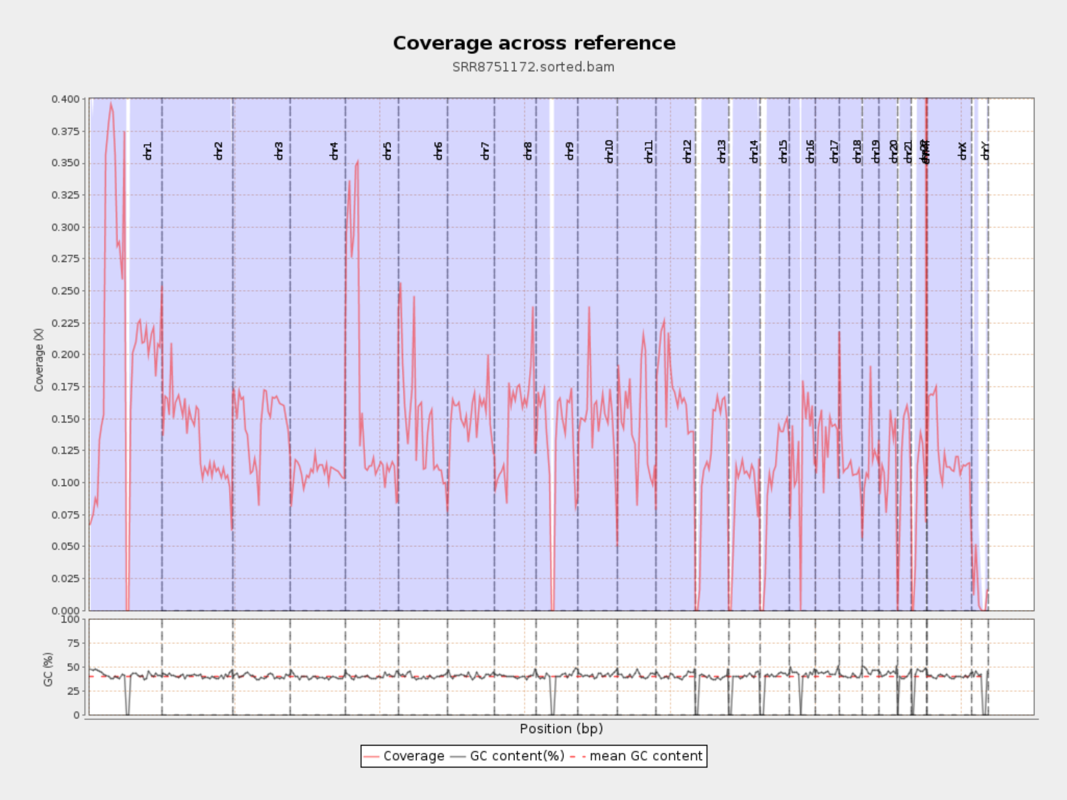
General error rate	0.42%
Mismatches	1,512,748
Insertions	198,396
Mapped reads with at least one insertion	4.43%
Deletions	57,771
Mapped reads with at least one deletion	1.31%
Homopolymer indels	52.41%

2.6. Chromosome stats

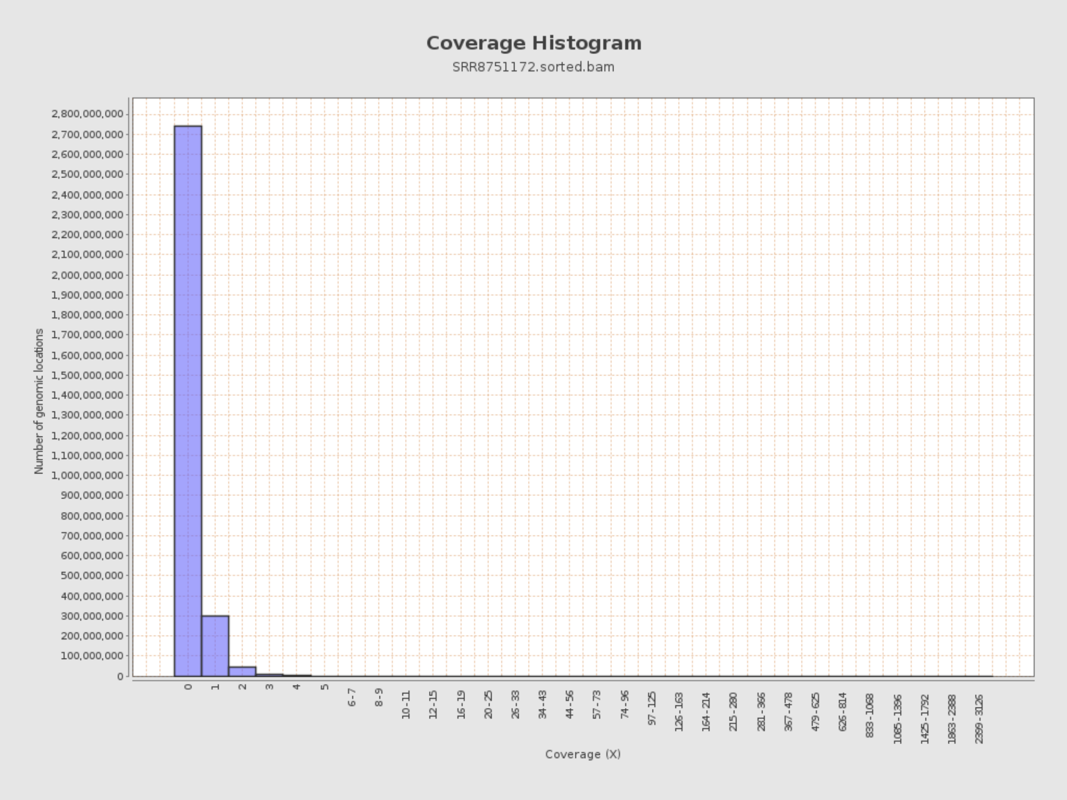
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	52543557	0.2108	2.9592
chr2	243199373	32732181	0.1346	0.4997
chr3	198022430	29395820	0.1484	0.4312
chr4	191154276	20683628	0.1082	0.3859
chr5	180915260	30013293	0.1659	0.4628
chr6	171115067	25273975	0.1477	0.9645
chr7	159138663	24435588	0.1535	0.6522

chr8	146364022	21957405	0.15	0.4933
chr9	141213431	18620077	0.1319	0.6198
chr10	135534747	20779104	0.1533	1.3032
chr11	135006516	19723069	0.1461	0.5915
chr12	133851895	23091407	0.1725	0.4664
chr13	115169878	13253541	0.1151	0.3744
chr14	107349540	9370822	0.0873	0.3456
chr15	102531392	10191035	0.0994	0.3493
chr16	90354753	11209188	0.1241	0.6466
chr17	81195210	10812221	0.1332	0.6236
chr18	78077248	9061017	0.1161	1.162
chr19	59128983	7089161	0.1199	2.0687
chr20	63025520	7236424	0.1148	0.3854
chr21	48129895	5462555	0.1135	0.3939
chr22	51304566	4178578	0.0814	0.3202
chrMT	16571	353940	21.359	9.2395
chrX	155270560	19241364	0.1239	0.4411
chrY	59373566	825478	0.0139	0.5532

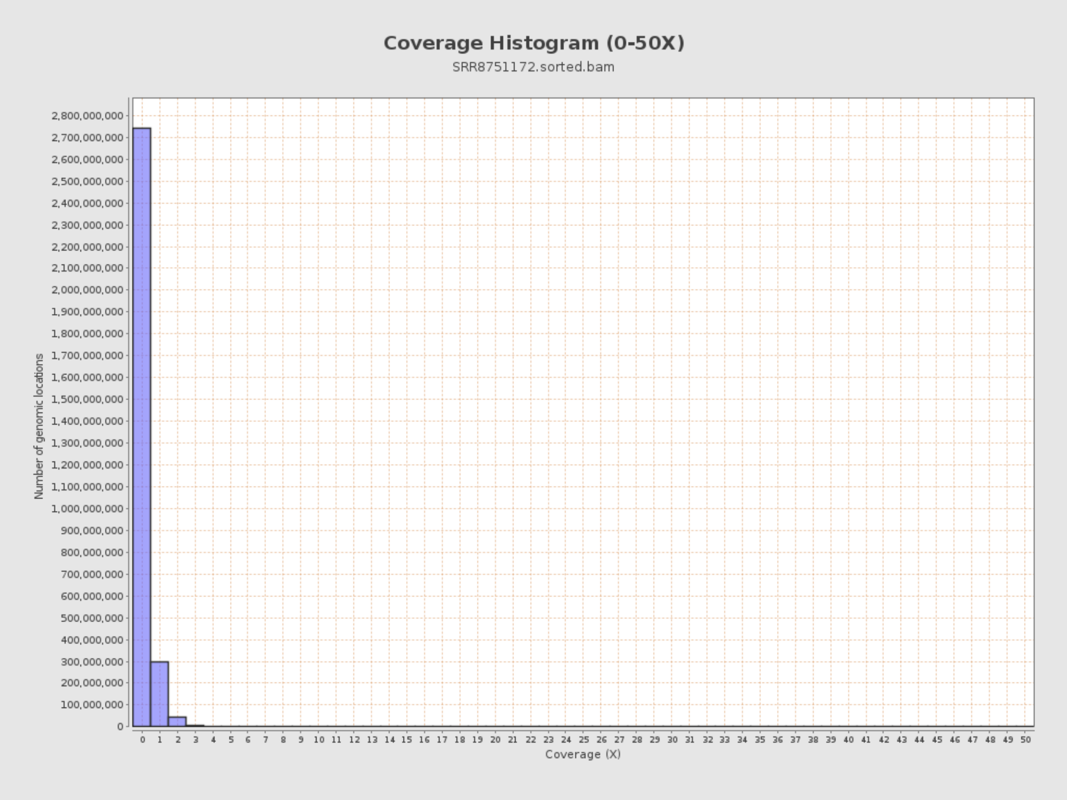
3. Results : Coverage across reference



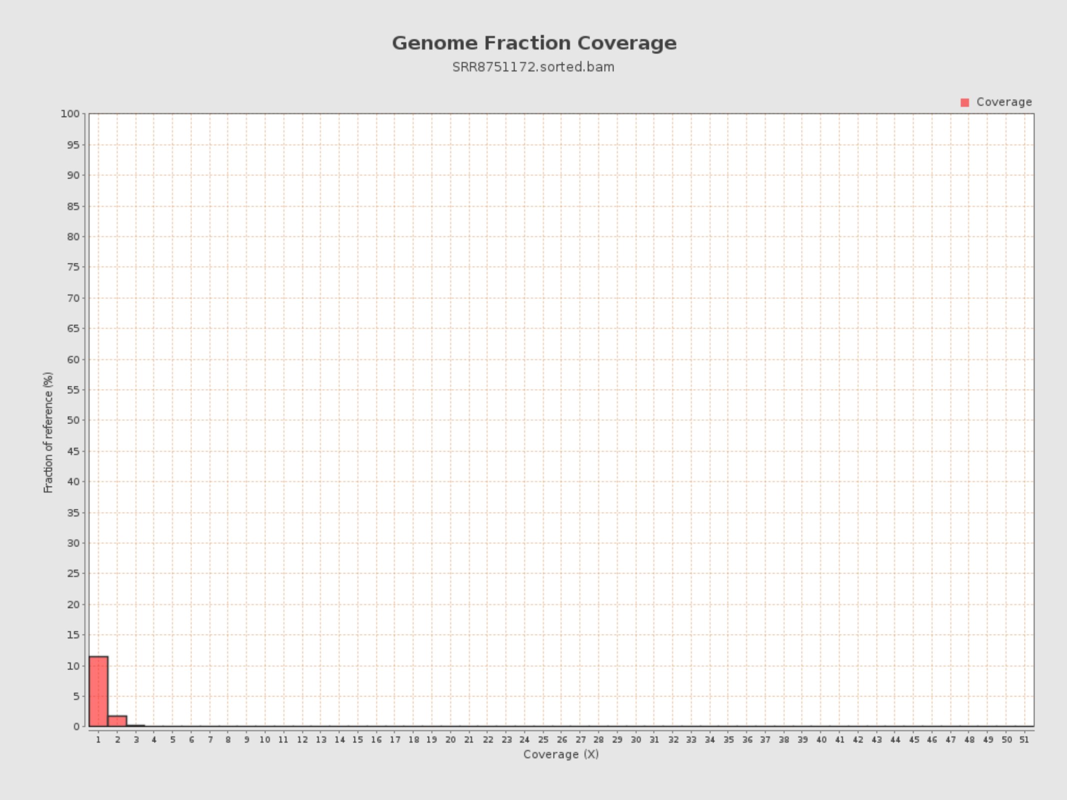
4. Results : Coverage Histogram



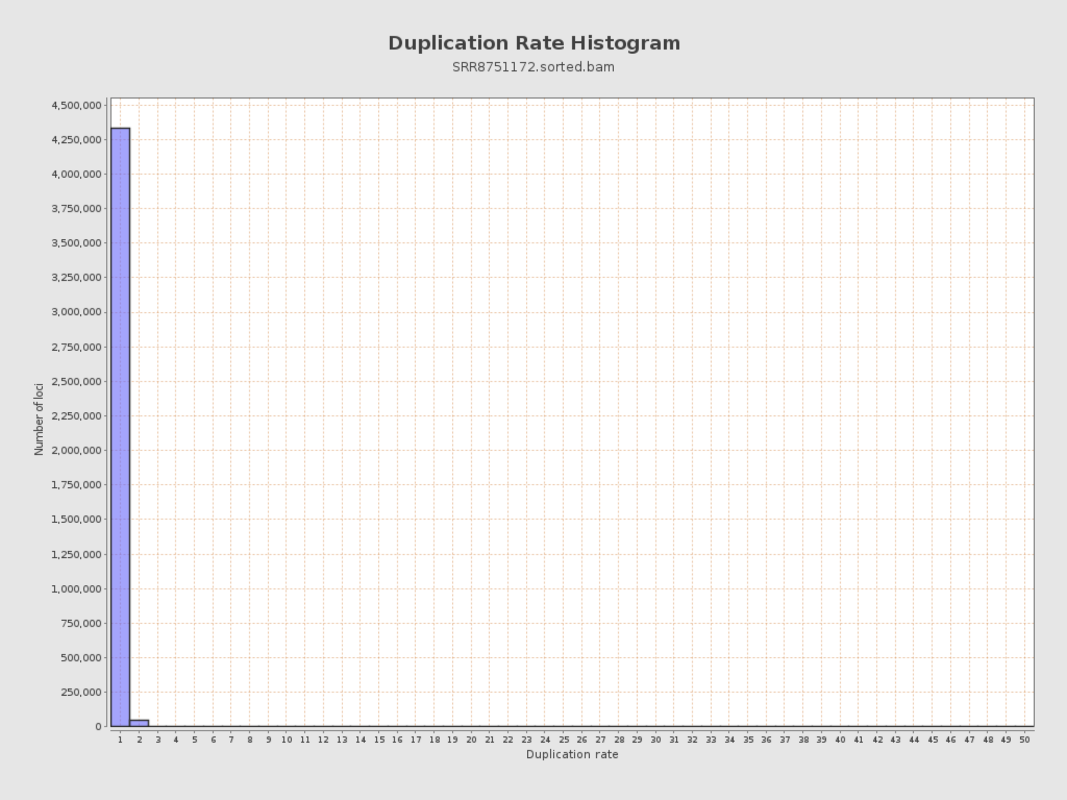
5. Results : Coverage Histogram (0-50X)



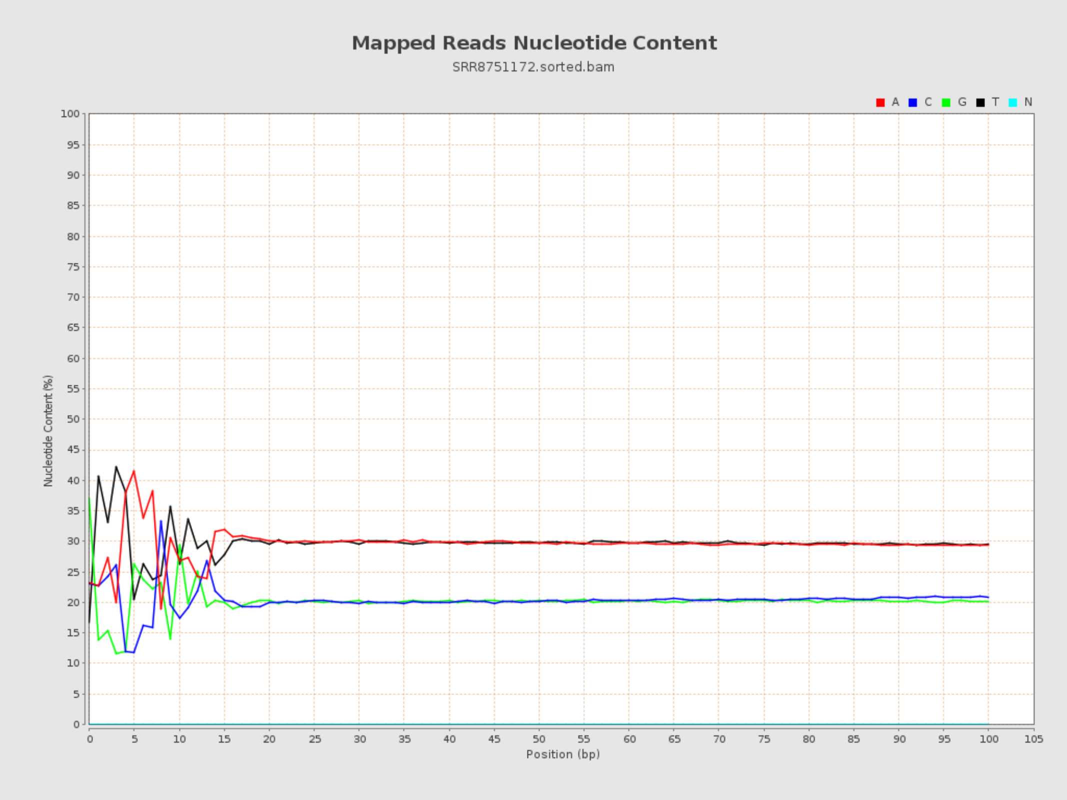
6. Results : Genome Fraction Coverage



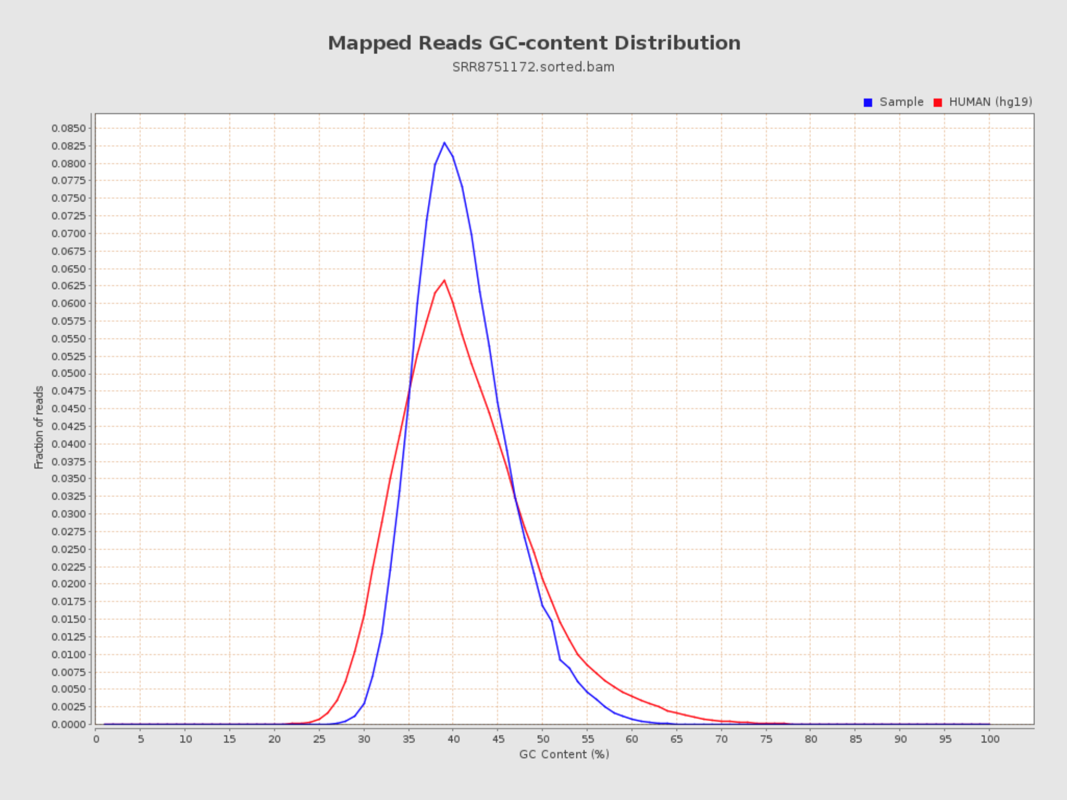
7. Results : Duplication Rate Histogram



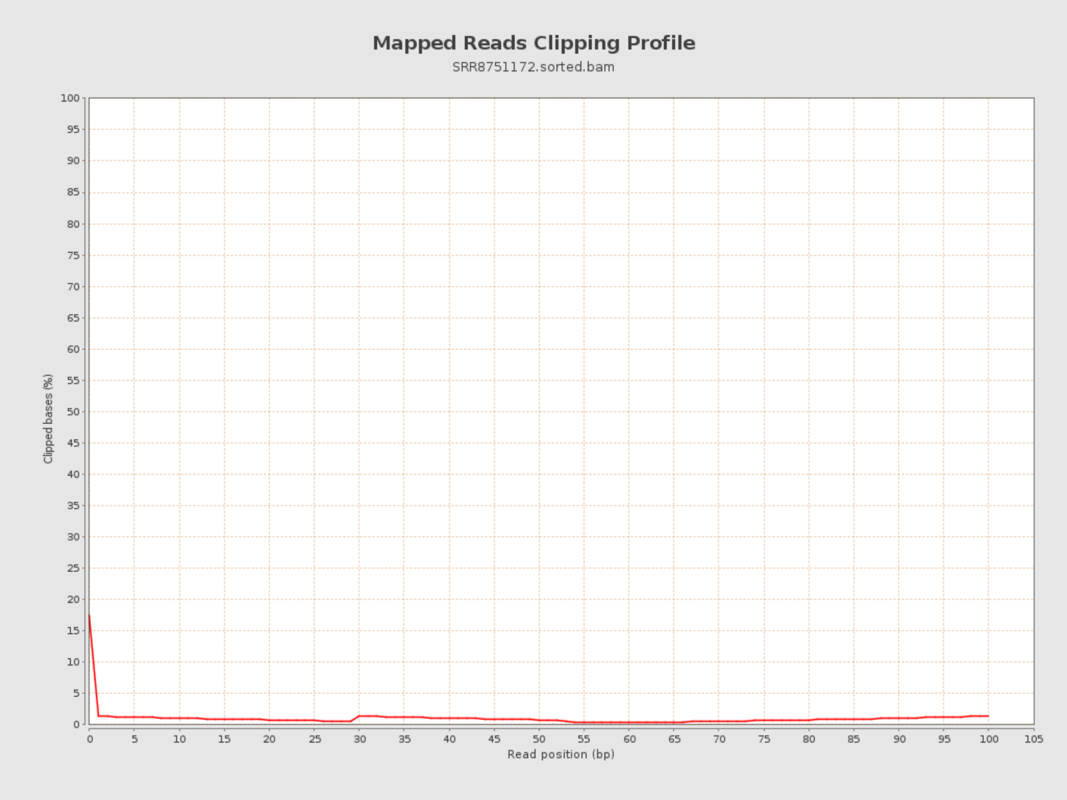
8. Results : Mapped Reads Nucleotide Content



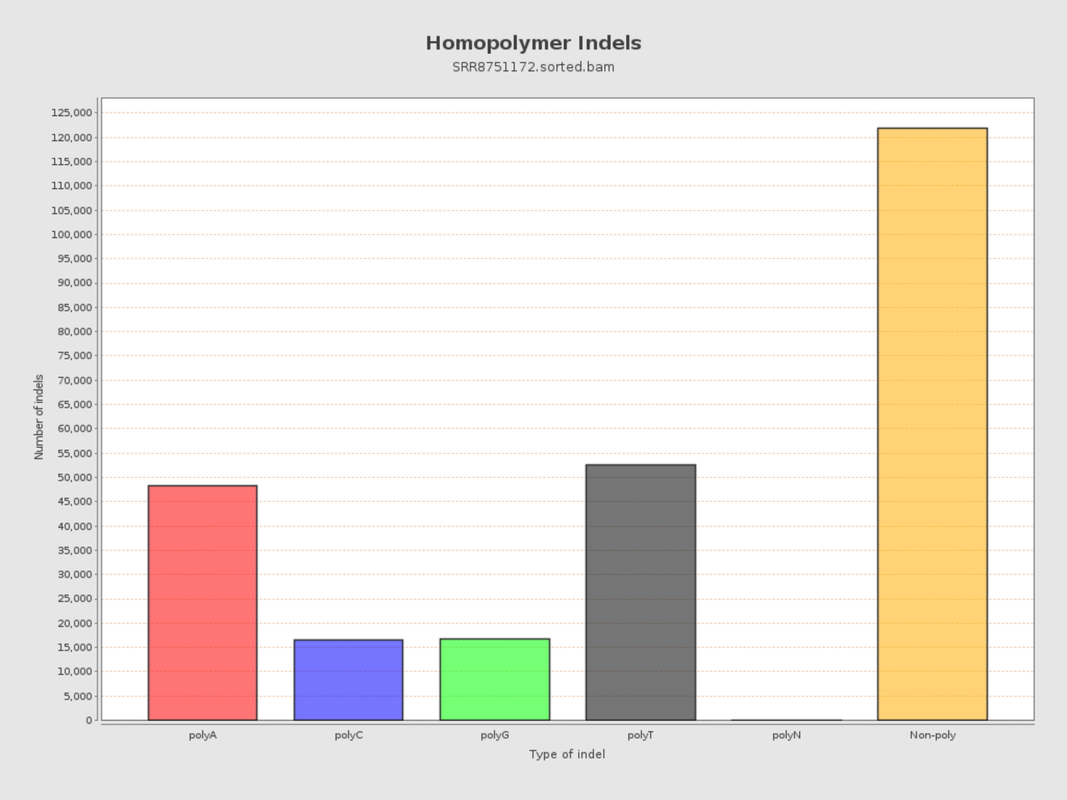
9. Results : Mapped Reads GC-content Distribution



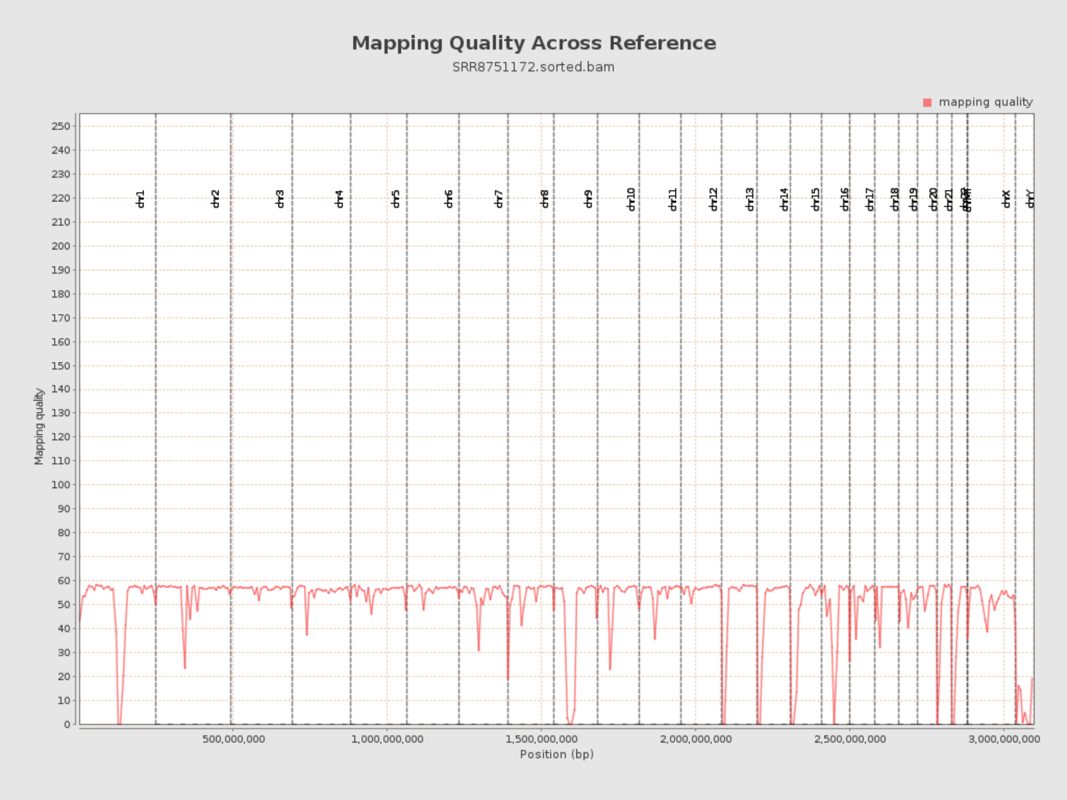
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram