Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 18:10:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8751194.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_SRR8751194 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8751194.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 18:10:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8751194.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,174,163
Mapped reads	5,130,788 / 99.16%
Unmapped reads	43,375 / 0.84%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	71,907 / 1.39%
Read min/max/mean length	30 / 101 / 101.58
Duplicated reads (estimated)	61,258 / 1.18%
Duplication rate	1.15%
Clipped reads	613,061 / 11.85%

2.2. ACGT Content

Number/percentage of A's	152,610,959 / 30.1%
Number/percentage of C's	100,880,815 / 19.9%
Number/percentage of T's	153,354,997 / 30.24%
Number/percentage of G's	100,198,112 / 19.76%
Number/percentage of N's	3,791 / 0%
GC Percentage	39.66%

2.3. Coverage

Mean	0.1638

Standard Deviation	0.4783

2.4. Mapping Quality

Mean Mapping Quality	51.77

2.5. Mismatches and indels

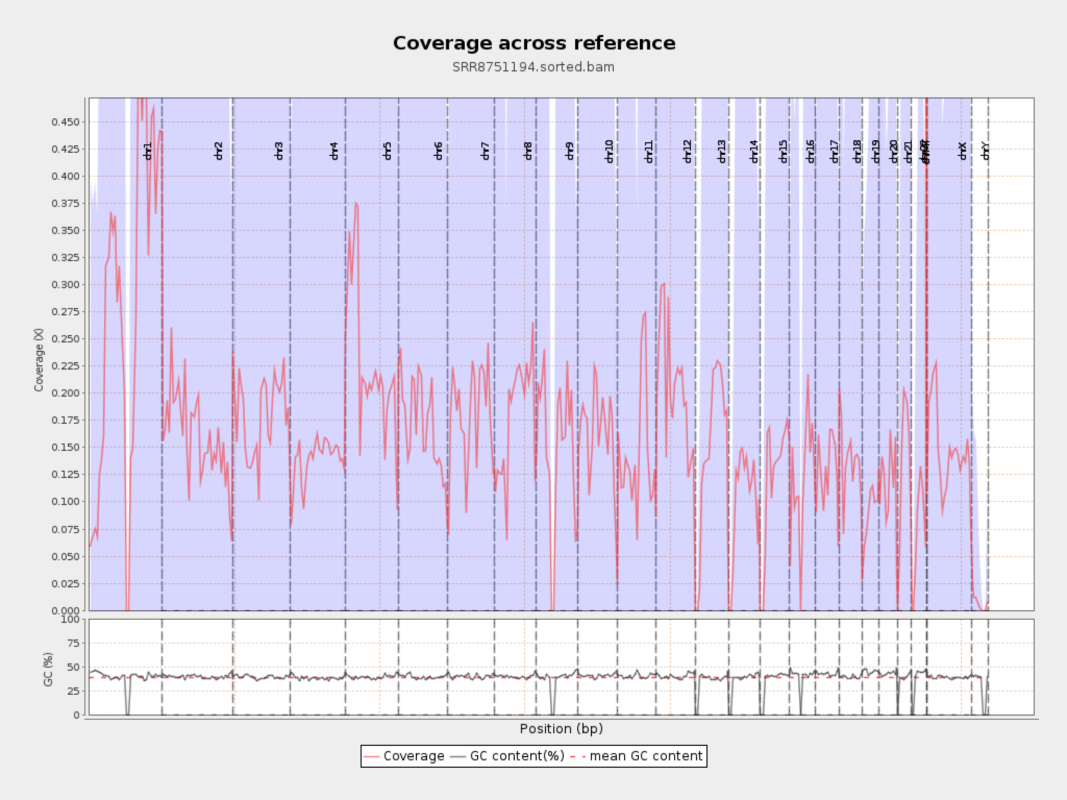
General error rate	0.25%
Mismatches	1,166,385
Insertions	52,902
Mapped reads with at least one insertion	1.02%
Deletions	59,999
Mapped reads with at least one deletion	1.16%
Homopolymer indels	48.28%

2.6. Chromosome stats

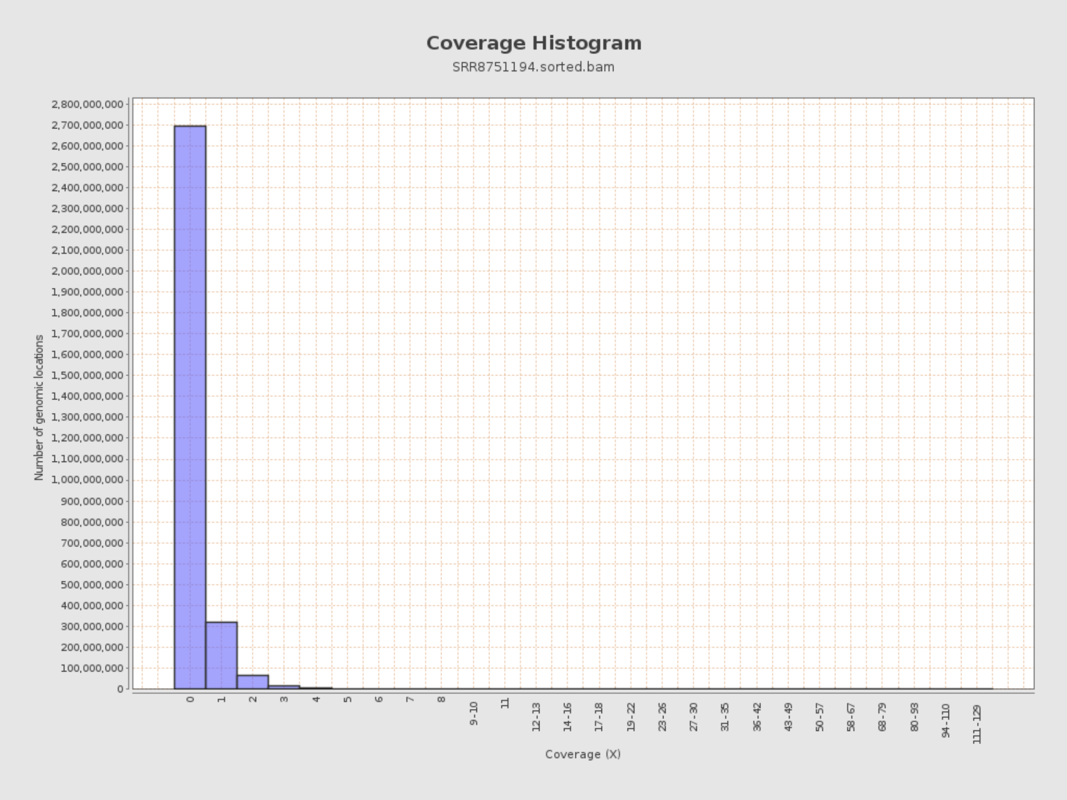
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	69770325	0.2799	0.6522
chr2	243199373	38924196	0.1601	0.4616
chr3	198022430	35765373	0.1806	0.4889
chr4	191154276	26695642	0.1397	0.4276
chr5	180915260	41508417	0.2294	0.5582
chr6	171115067	29348228	0.1715	0.4808
chr7	159138663	29163233	0.1833	0.4956

chr8	146364022	26329494	0.1799	0.4994
chr9	141213431	21475504	0.1521	0.4555
chr10	135534747	22578050	0.1666	0.4857
chr11	135006516	19626026	0.1454	0.4445
chr12	133851895	27209767	0.2033	0.5222
chr13	115169878	17201129	0.1494	0.4489
chr14	107349540	10840851	0.101	0.365
chr15	102531392	12384321	0.1208	0.4039
chr16	90354753	10978875	0.1215	0.4075
chr17	81195210	10317171	0.1271	0.4154
chr18	78077248	10694260	0.137	0.4251
chr19	59128983	5359121	0.0906	0.3571
chr20	63025520	7505886	0.1191	0.3988
chr21	48129895	6295374	0.1308	0.4274
chr22	51304566	3634251	0.0708	0.3102
chrMT	16571	242127	14.6115	8.2247
chrX	155270560	22902371	0.1475	0.44
chrY	59373566	422048	0.0071	0.1027

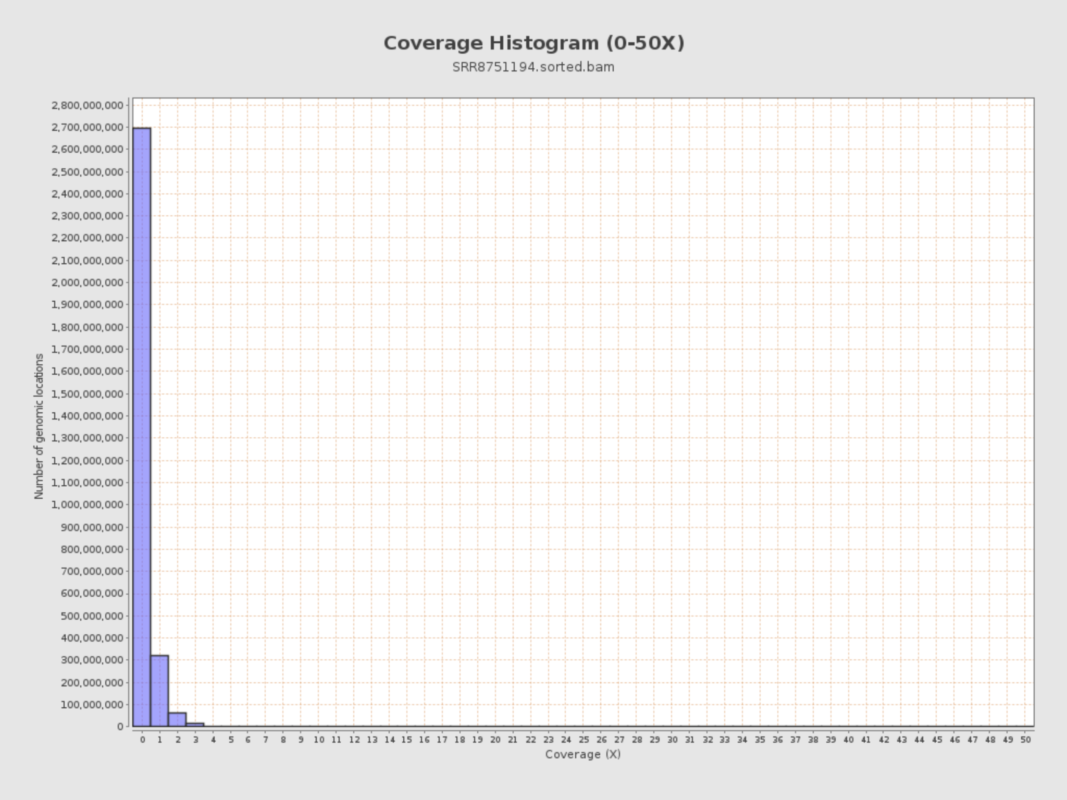
3. Results : Coverage across reference



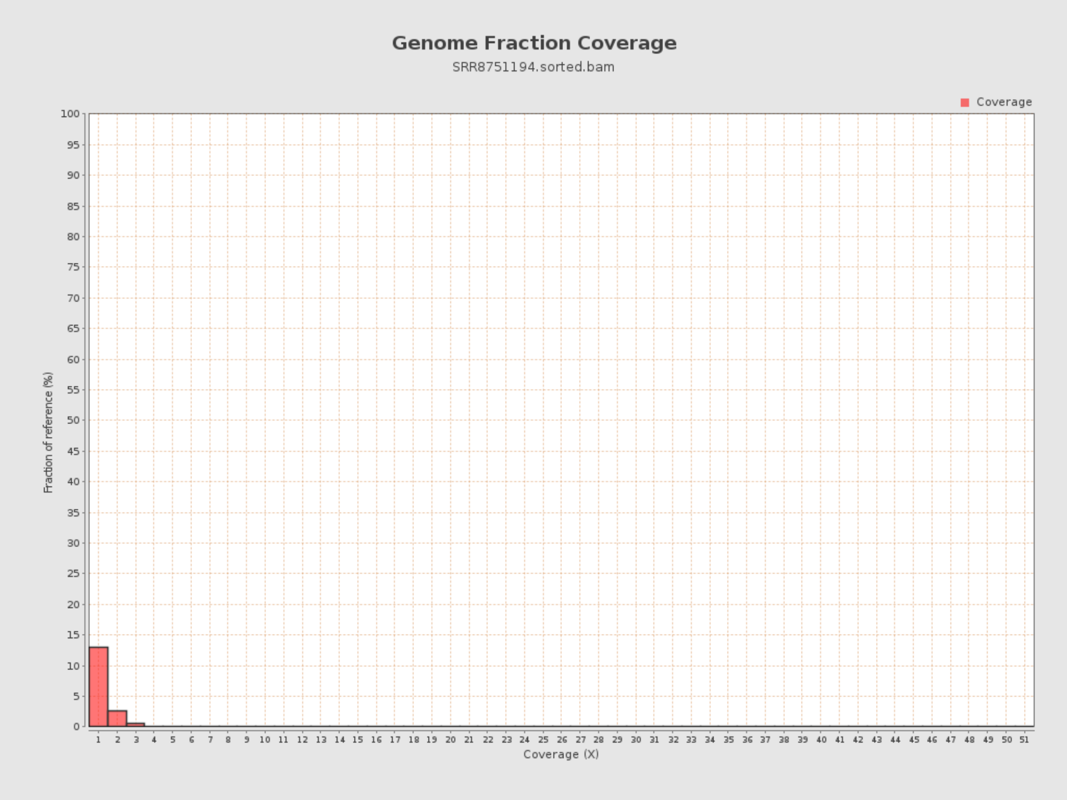
4. Results : Coverage Histogram



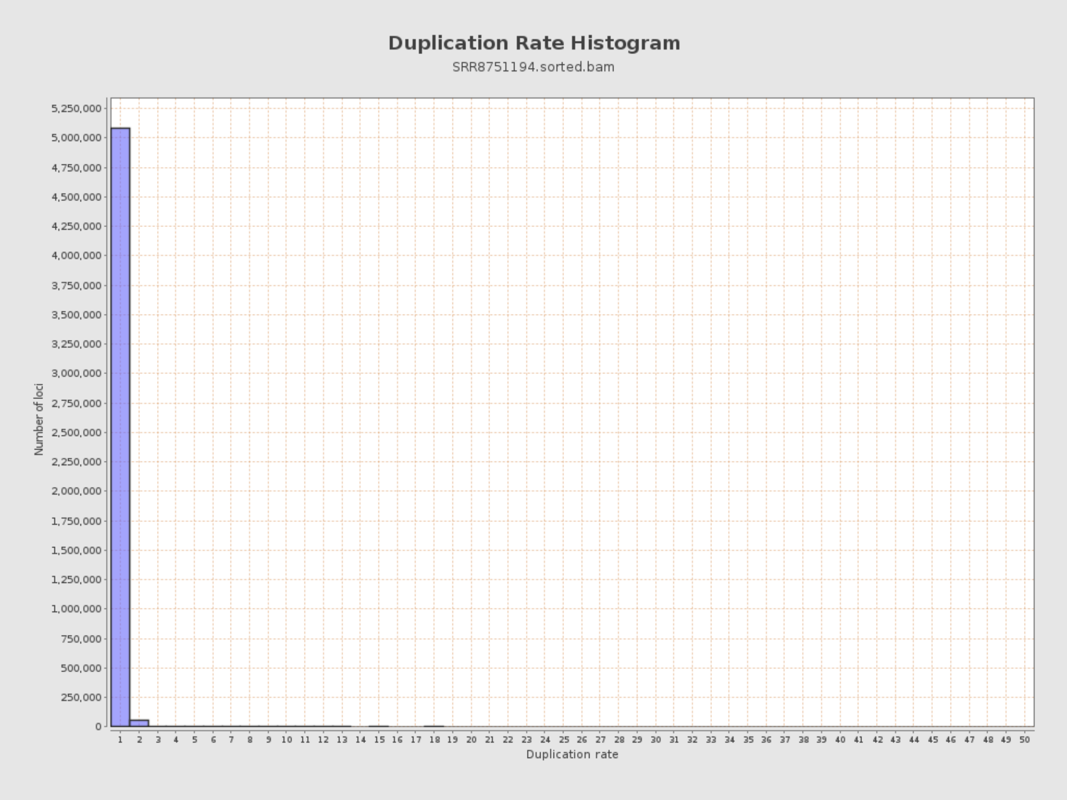
5. Results : Coverage Histogram (0-50X)



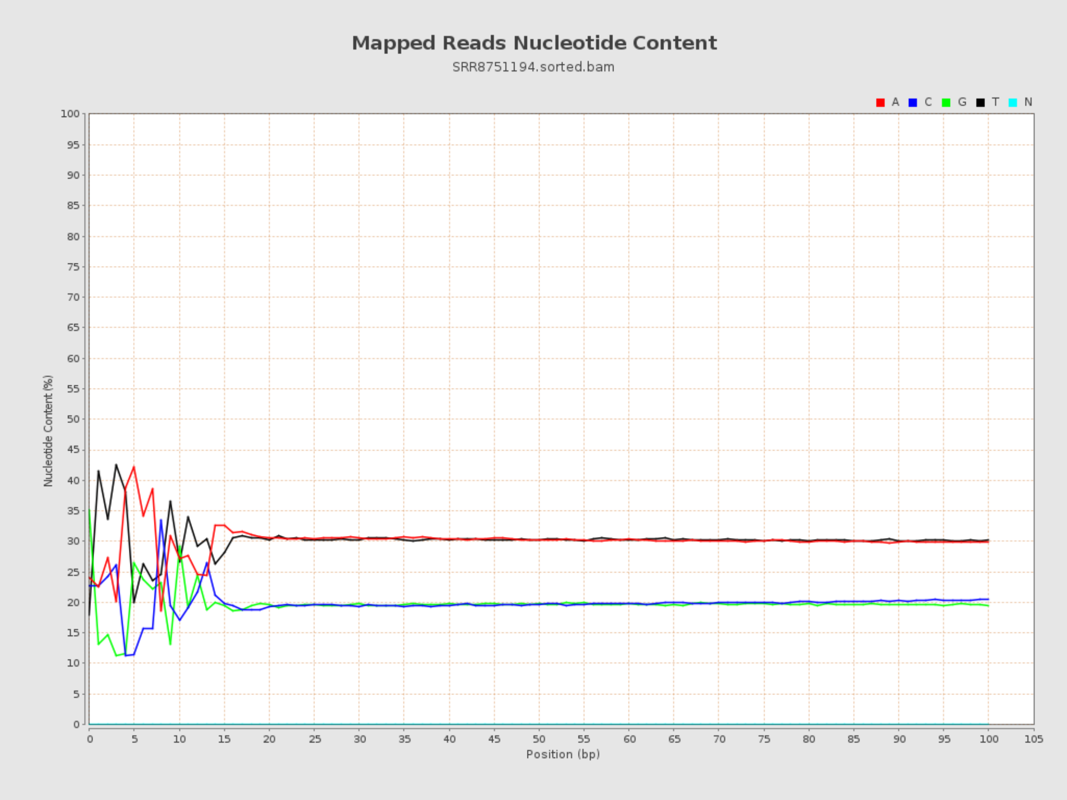
6. Results : Genome Fraction Coverage



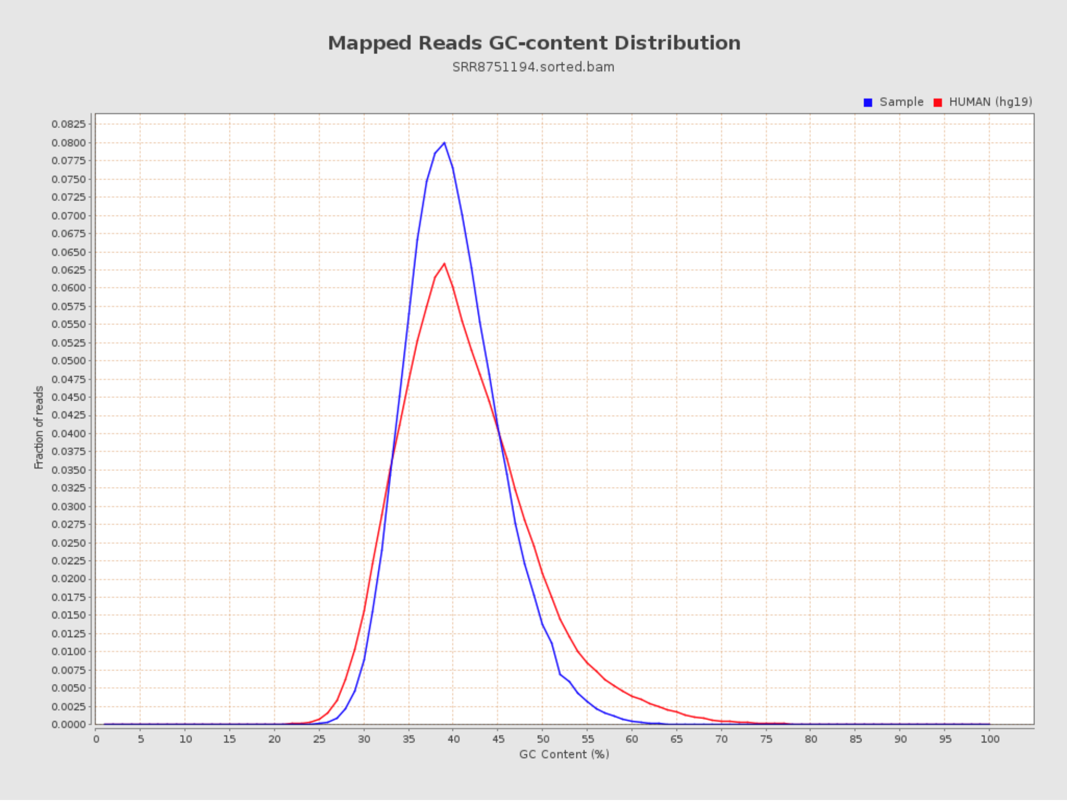
7. Results : Duplication Rate Histogram



8. Results : Mapped Reads Nucleotide Content

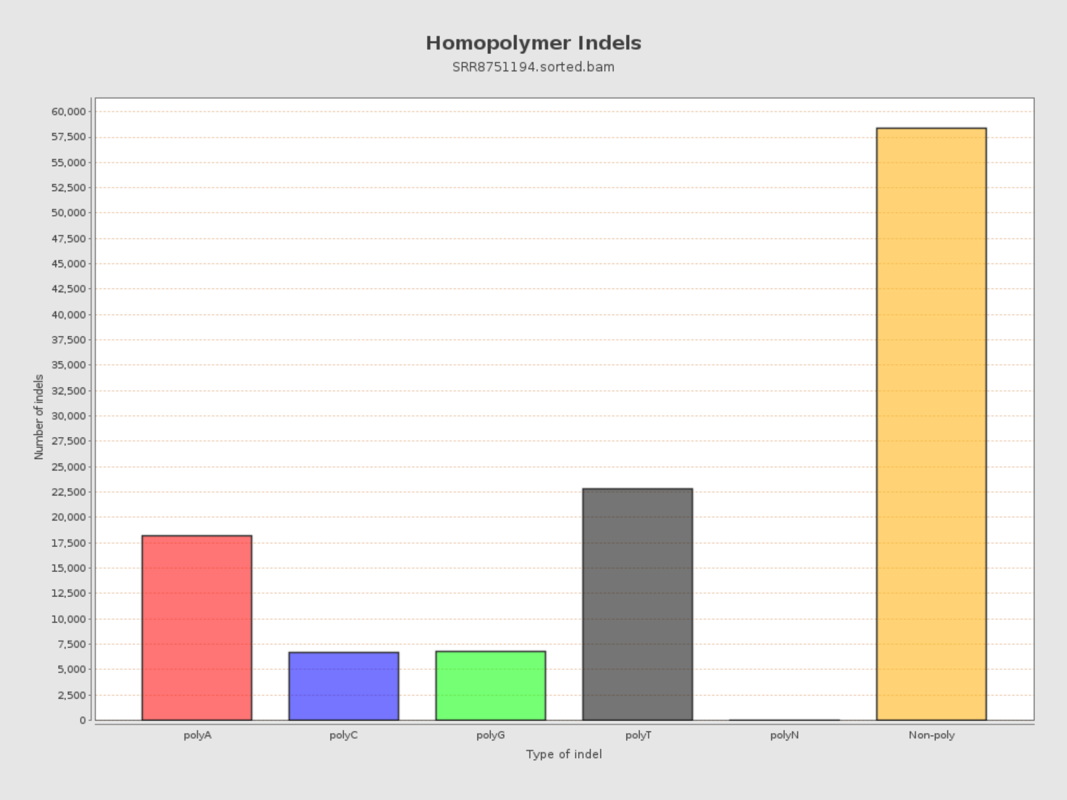


9. Results : Mapped Reads GC-content Distribution

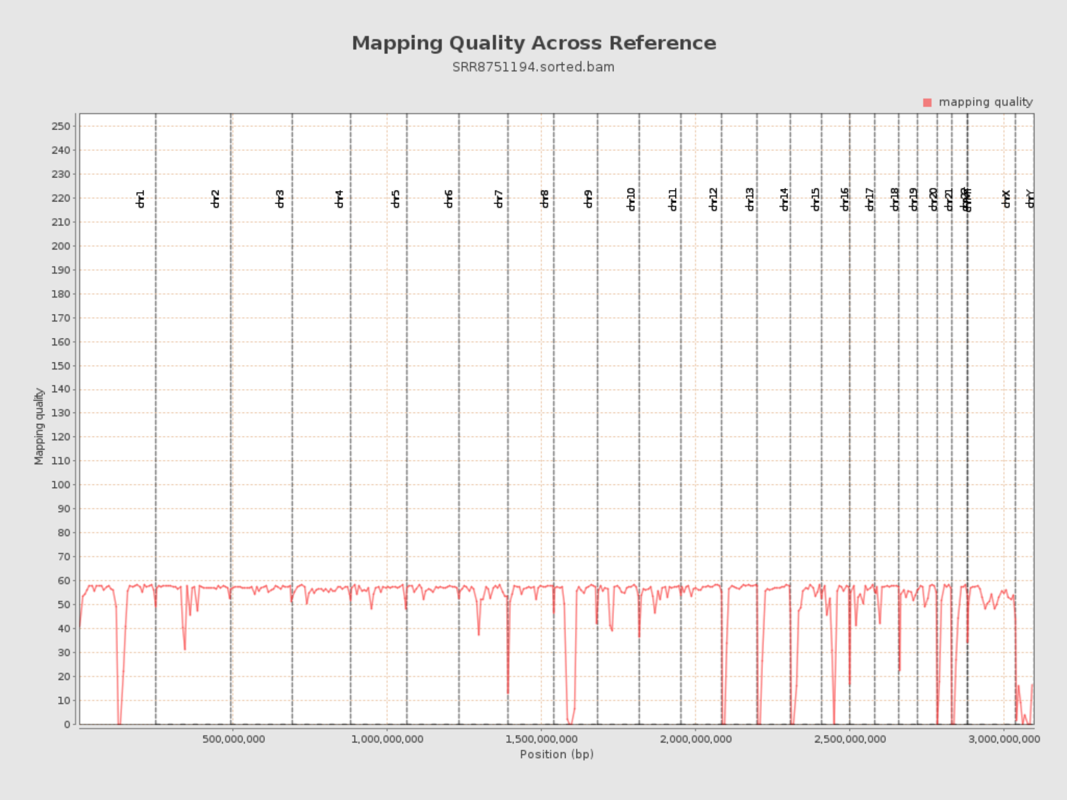


10. Results : Mapped Reads Clipping Profile

11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram