Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/19 21:23:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1505959.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_SRR1505959 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1505959.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 19 21:23:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1505959.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,098,912
Mapped reads	3,579,185 / 70.2%
Unmapped reads	1,519,727 / 29.8%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	199 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	270,478 / 5.3%
Duplication rate	5.8%
Clipped reads	498,743 / 9.78%

2.2. ACGT Content

Number/percentage of A's	49,964,755 / 29.91%
Number/percentage of C's	33,716,887 / 20.18%
Number/percentage of T's	49,592,719 / 29.69%
Number/percentage of G's	33,776,808 / 20.22%
Number/percentage of N's	802 / 0%
GC Percentage	40.4%

2.3. Coverage

Mean	0.054

Standard Deviation	0.6053

2.4. Mapping Quality

Mean Mapping Quality	44.17

2.5. Mismatches and indels

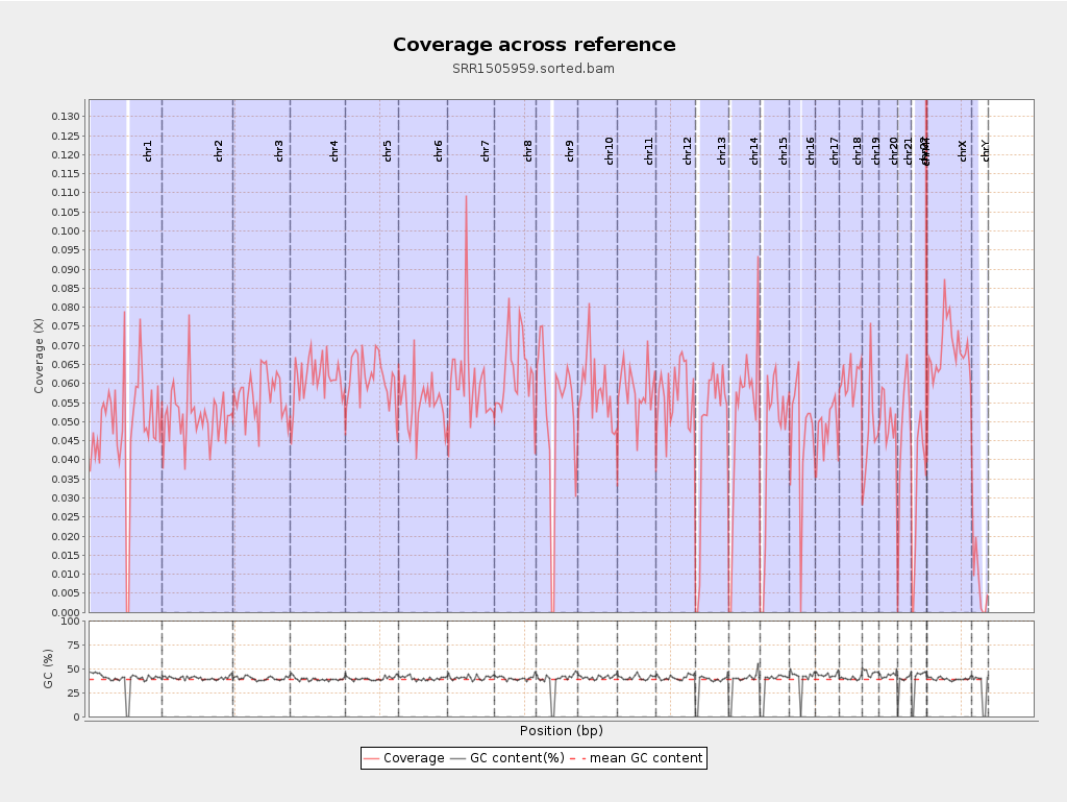
General error rate	0.52%
Mismatches	852,525
Insertions	7,893
Mapped reads with at least one insertion	0.22%
Deletions	23,827
Mapped reads with at least one deletion	0.66%
Homopolymer indels	44.12%

2.6. Chromosome stats

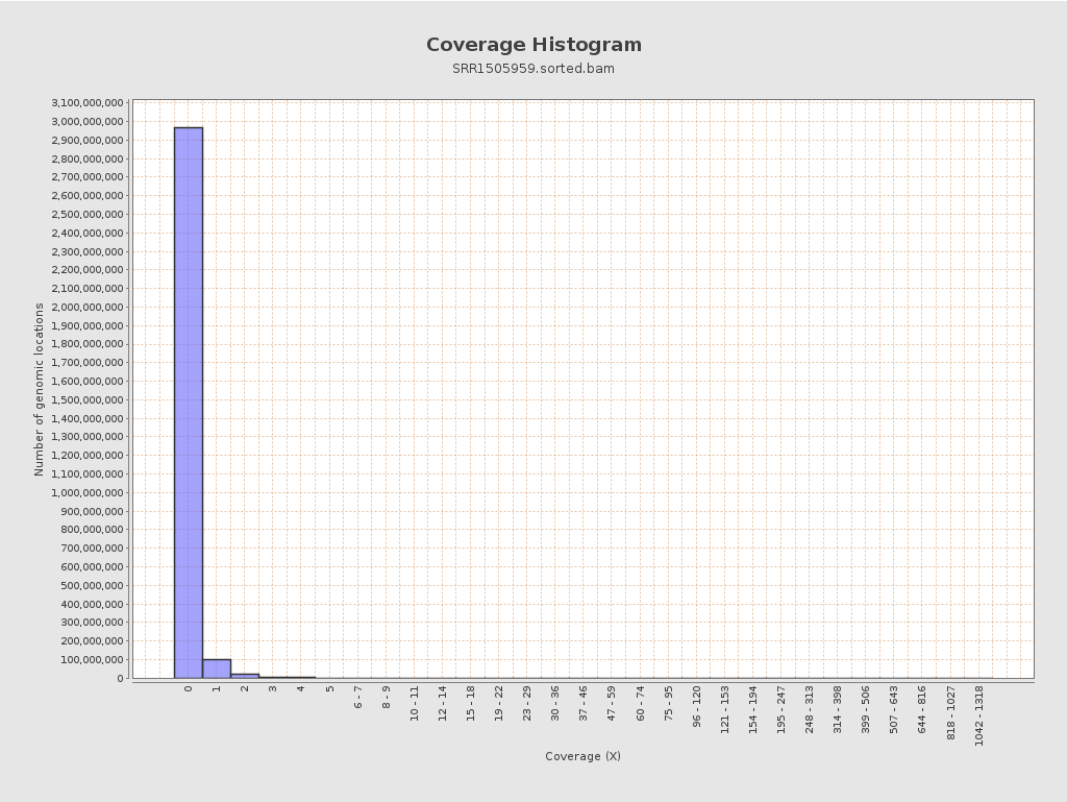
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	12052127	0.0484	0.934
chr2	243199373	12499807	0.0514	0.4177
chr3	198022430	11218572	0.0567	0.2987
chr4	191154276	11716143	0.0613	0.311
chr5	180915260	11126140	0.0615	0.3203
chr6	171115067	9425369	0.0551	0.4187
chr7	159138663	9659533	0.0607	0.7795

chr8	146364022	9164670	0.0626	0.7662
chr9	141213431	7362962	0.0521	0.4062
chr10	135534747	7891238	0.0582	0.4511
chr11	135006516	7825132	0.058	0.4471
chr12	133851895	7656546	0.0572	0.3282
chr13	115169878	5479119	0.0476	0.2721
chr14	107349540	5518803	0.0514	1.8318
chr15	102531392	4598294	0.0448	0.2658
chr16	90354753	4229755	0.0468	0.2933
chr17	81195210	3881673	0.0478	0.3167
chr18	78077248	4775002	0.0612	0.897
chr19	59128983	2813358	0.0476	0.6313
chr20	63025520	3154345	0.05	0.3111
chr21	48129895	2274217	0.0473	0.2928
chr22	51304566	1623514	0.0316	0.222
chrMT	16571	90838	5.4817	4.6403
chrX	155270560	10583325	0.0682	0.3725
chrY	59373566	463807	0.0078	0.1229

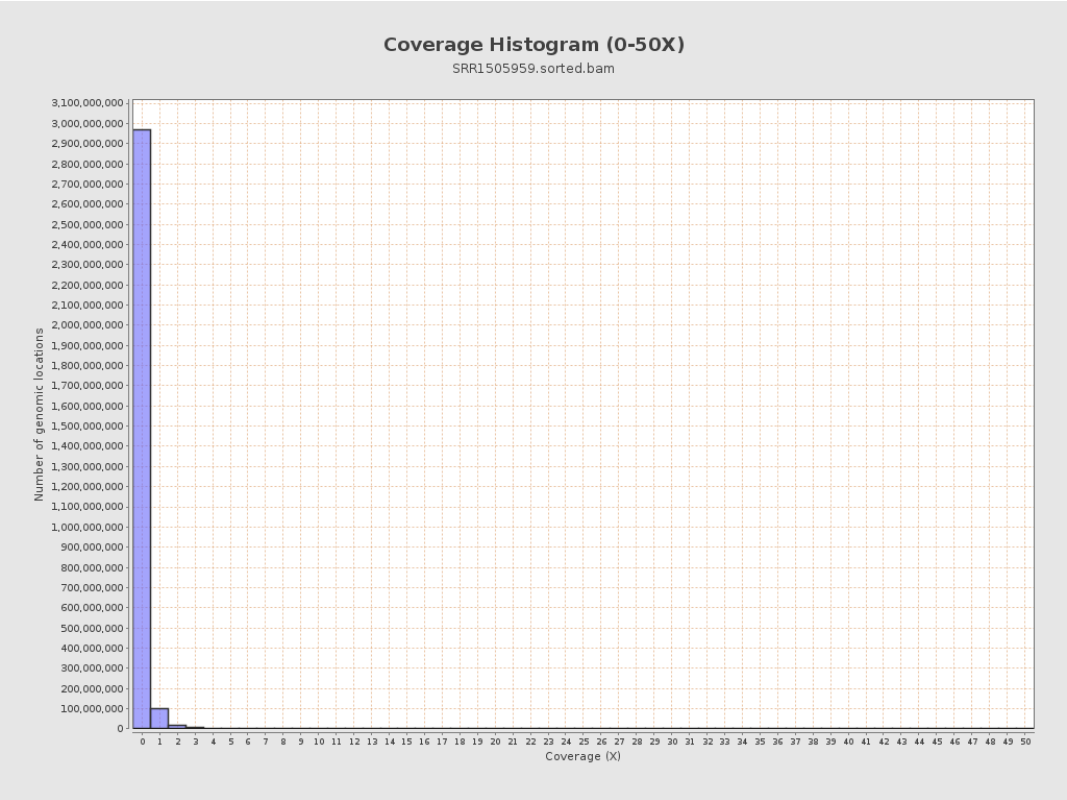
3. Results : Coverage across reference



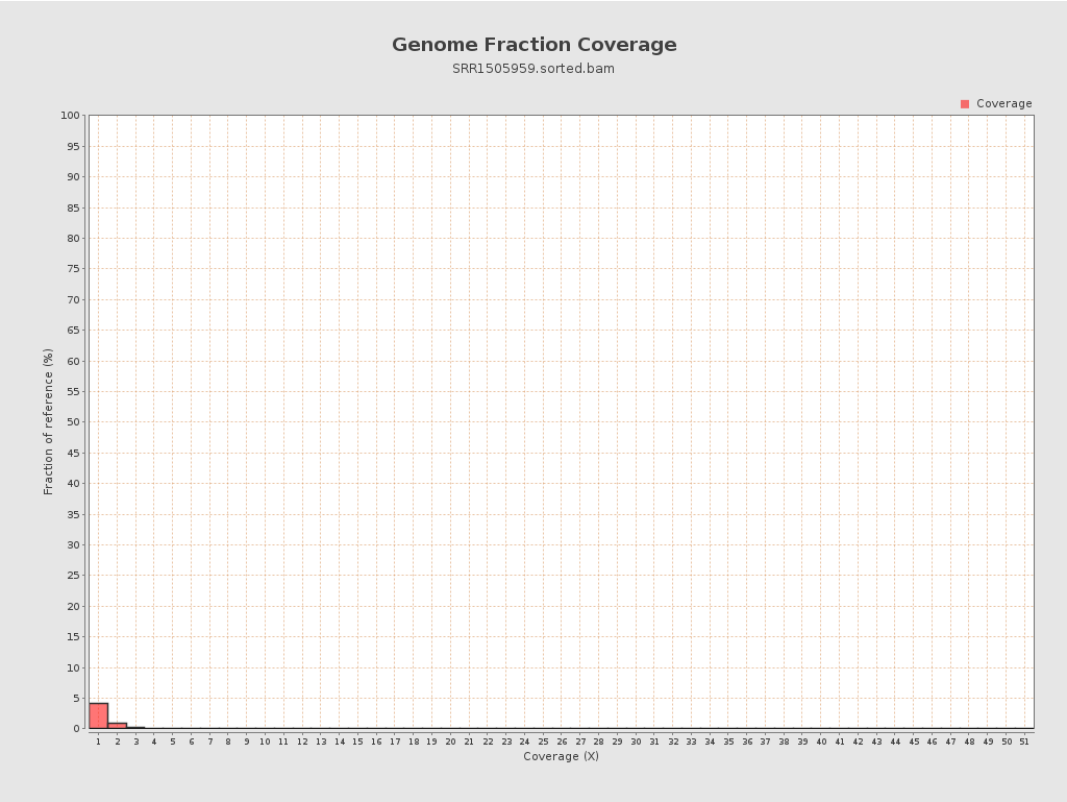
4. Results : Coverage Histogram



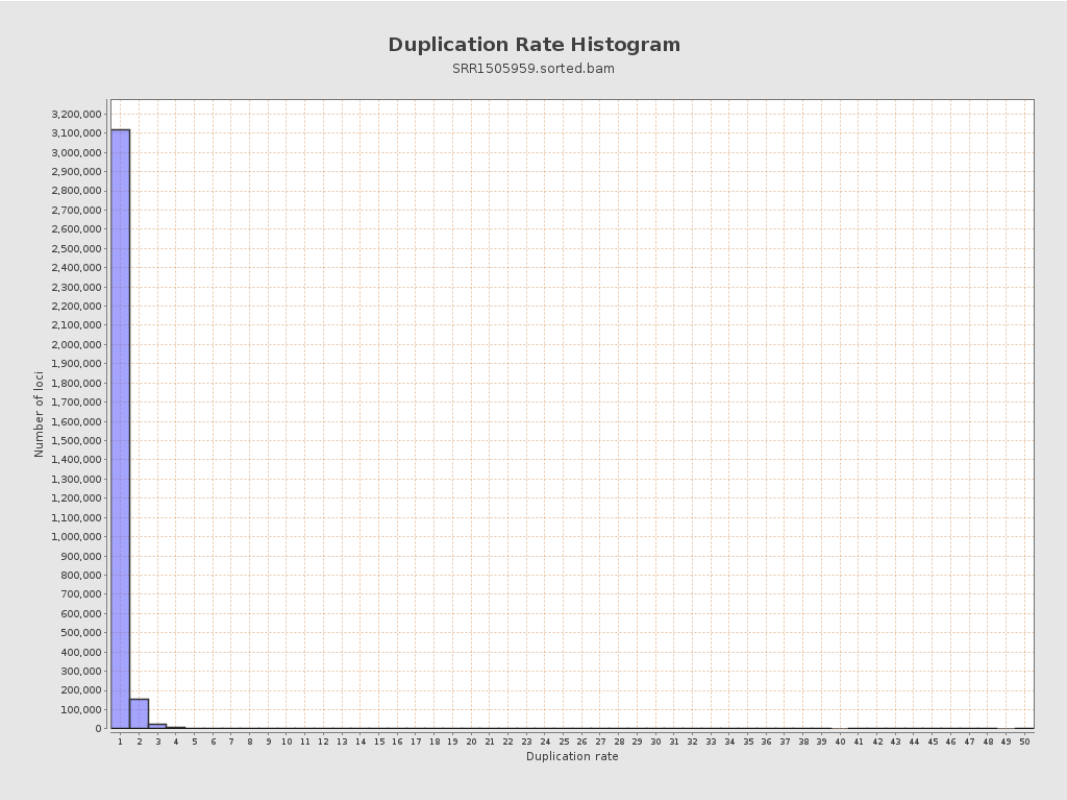
5. Results : Coverage Histogram (0-50X)



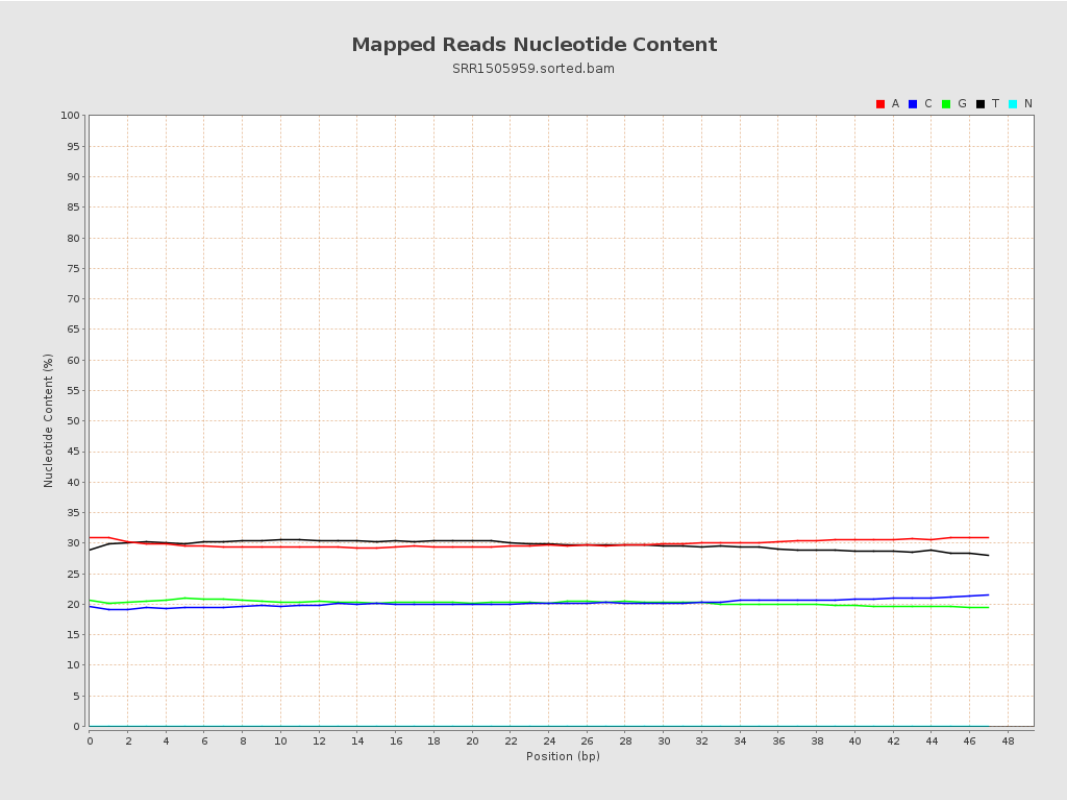
6. Results : Genome Fraction Coverage



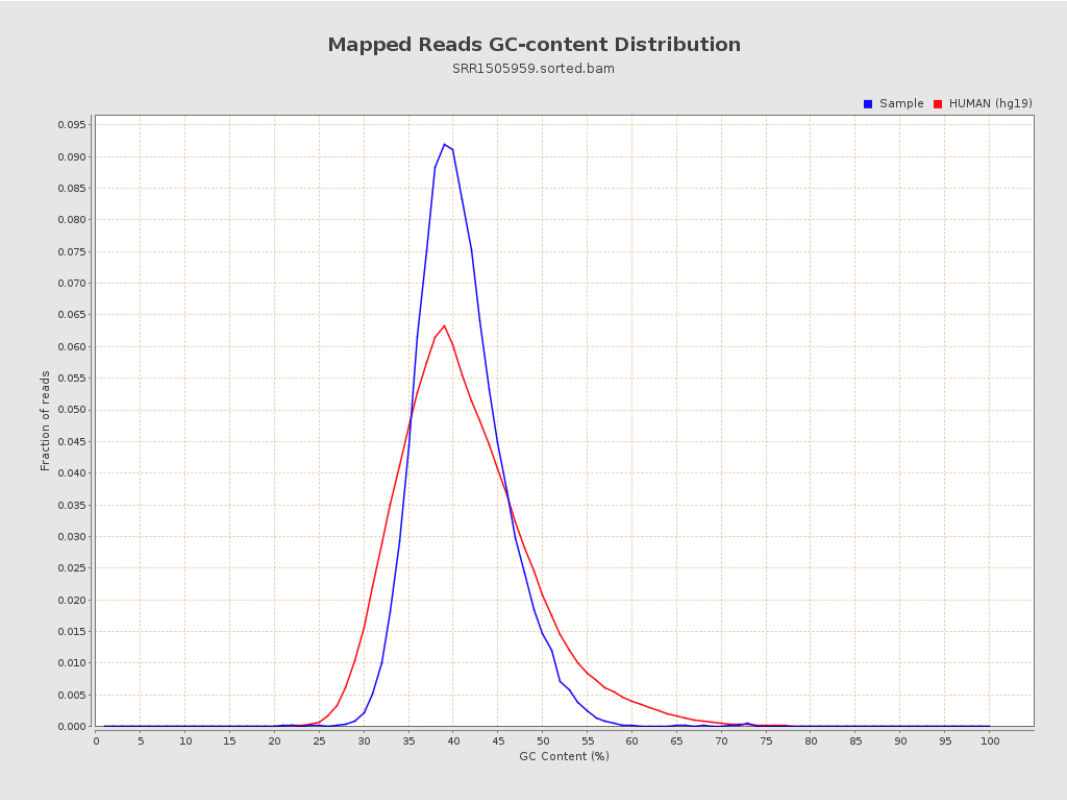
7. Results : Duplication Rate Histogram



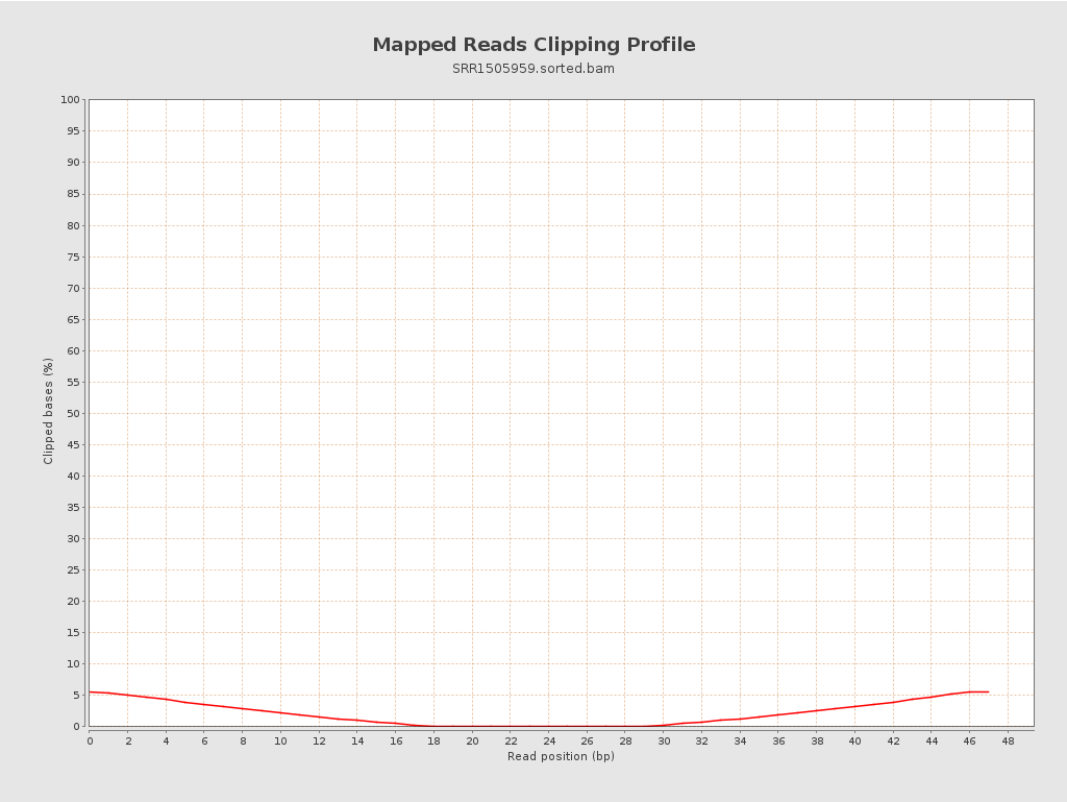
8. Results : Mapped Reads Nucleotide Content



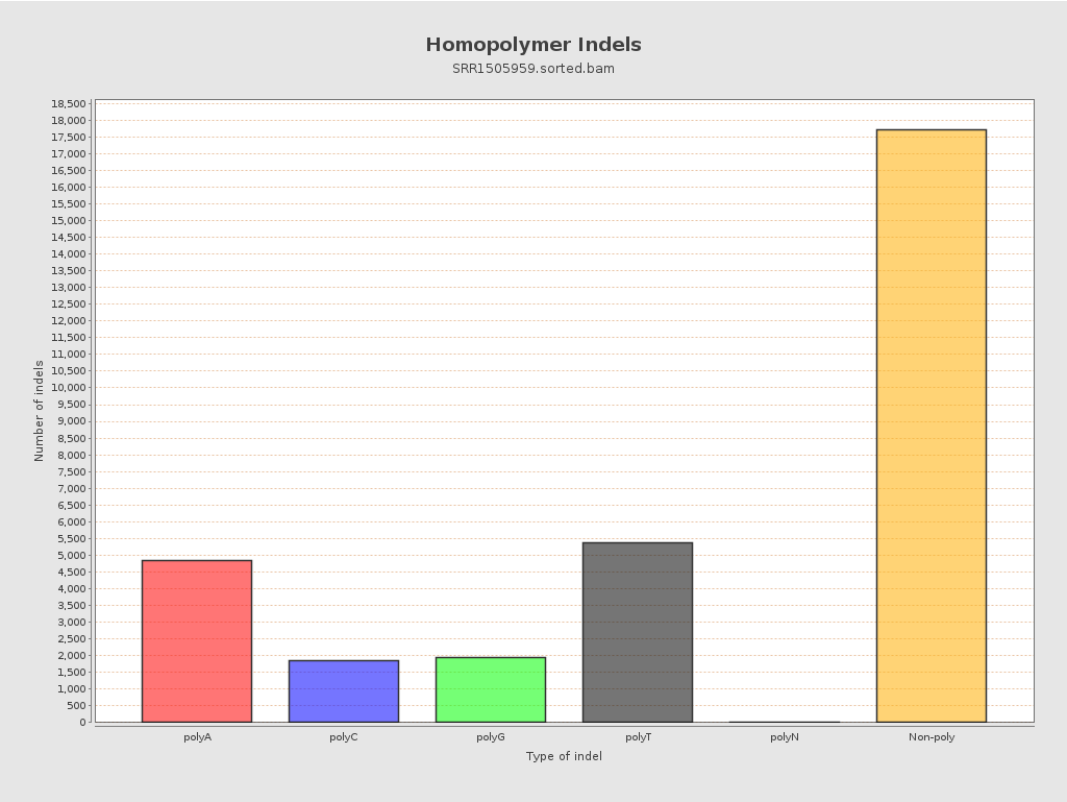
9. Results : Mapped Reads GC-content Distribution



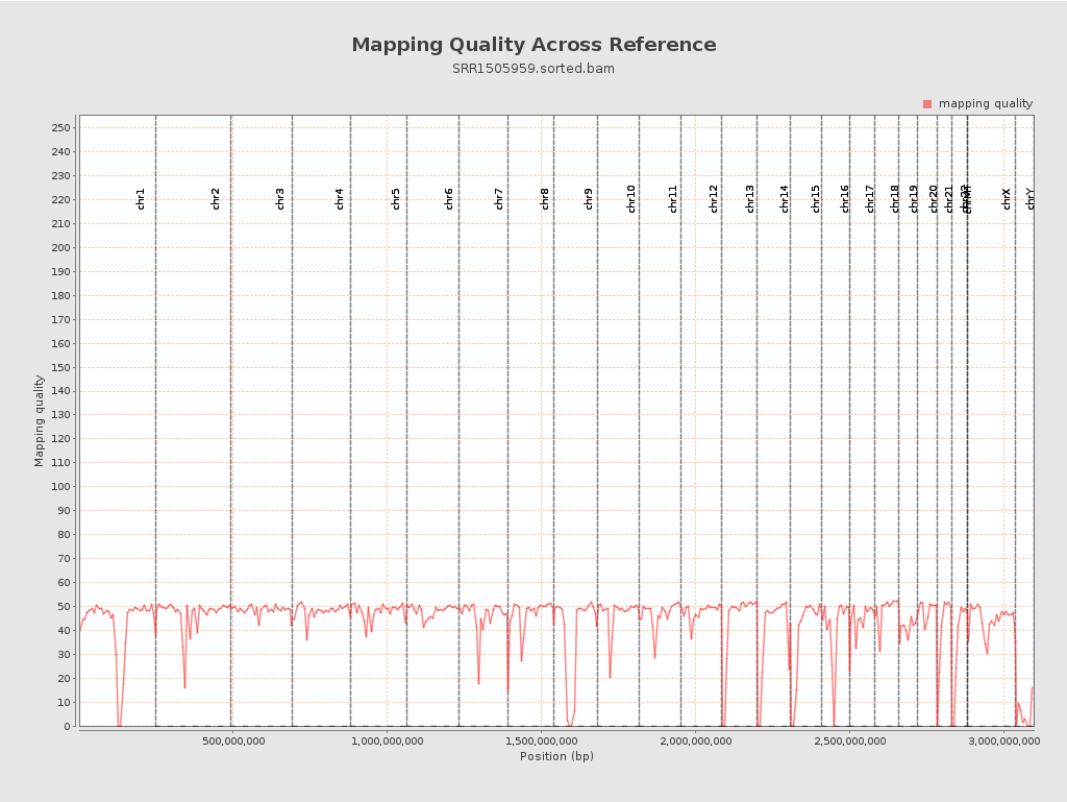
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram