Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 14:24:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080982.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_SRR3080982 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080982.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 14:24:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080982.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,171,717
Mapped reads	3,516,204 / 84.29%
Unmapped reads	655,513 / 15.71%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,049 / 0.55%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	238,269 / 5.71%
Duplication rate	5.44%
Clipped reads	1,446,242 / 34.67%

2.2. ACGT Content

Number/percentage of A's	66,336,179 / 28.09%
Number/percentage of C's	41,473,877 / 17.56%
Number/percentage of T's	77,287,975 / 32.73%
Number/percentage of G's	50,598,380 / 21.43%
Number/percentage of N's	467,332 / 0.2%
GC Percentage	38.99%

2.3. Coverage

Mean	0.0763

Standard Deviation	0.5804

2.4. Mapping Quality

Mean Mapping Quality	47.2

2.5. Mismatches and indels

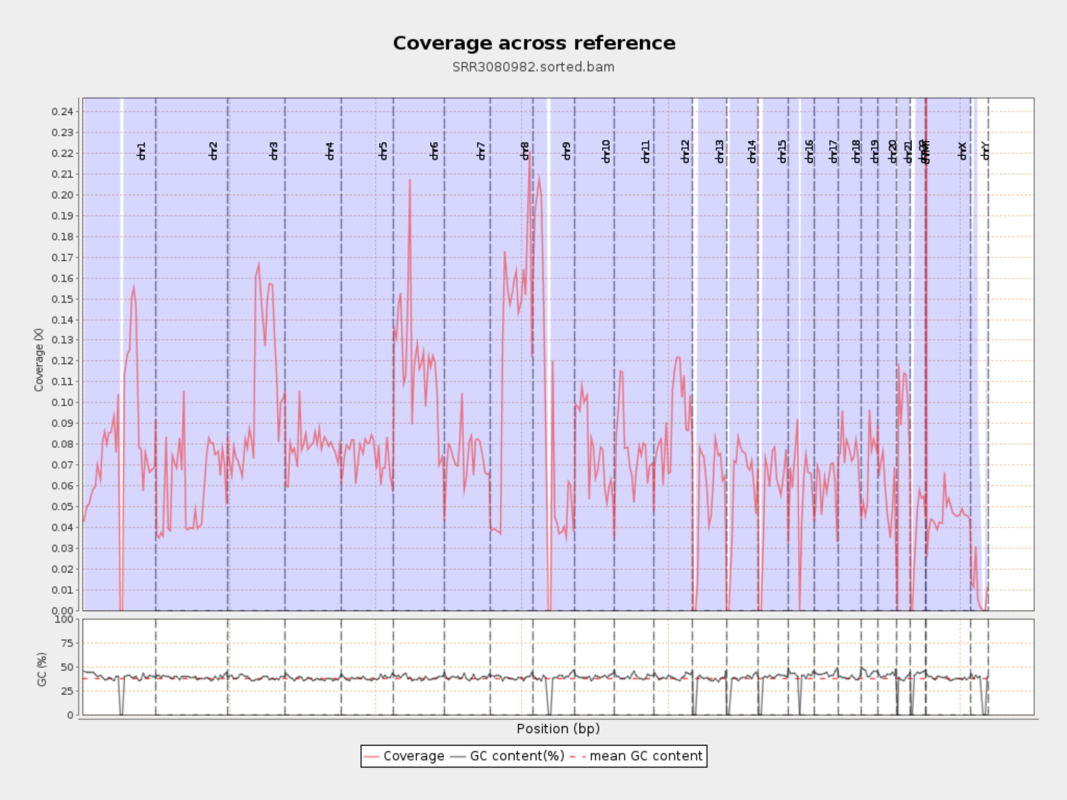
General error rate	0.98%
Mismatches	2,292,663
Insertions	17,919
Mapped reads with at least one insertion	0.51%
Deletions	47,602
Mapped reads with at least one deletion	1.34%
Homopolymer indels	49.51%

2.6. Chromosome stats

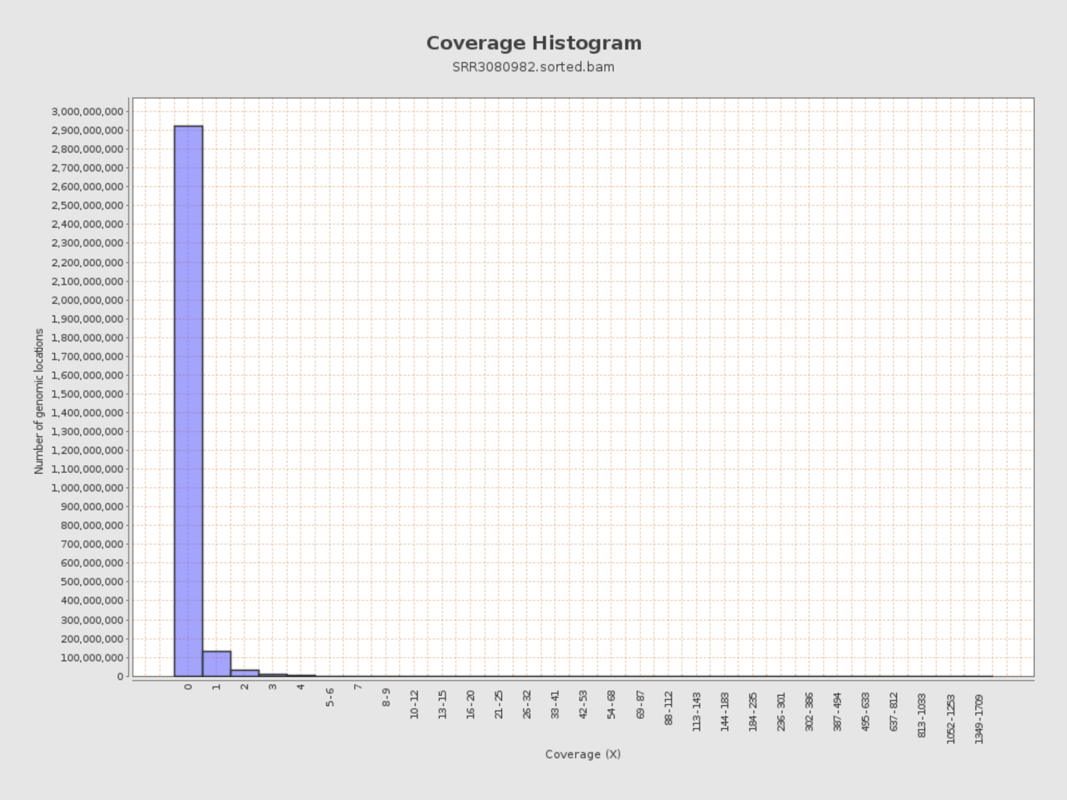
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	19674705	0.0789	0.8493
chr2	243199373	14526216	0.0597	0.5143
chr3	198022430	20840503	0.1052	0.4242
chr4	191154276	15112608	0.0791	0.3909
chr5	180915260	13435421	0.0743	0.3566
chr6	171115067	20583839	0.1203	0.6814
chr7	159138663	11765710	0.0739	0.6036

chr8	146364022	18545466	0.1267	1.1472
chr9	141213431	12350815	0.0875	0.7122
chr10	135534747	10527808	0.0777	0.4789
chr11	135006516	10484811	0.0777	0.4477
chr12	133851895	12209308	0.0912	0.4133
chr13	115169878	6341587	0.0551	0.3031
chr14	107349540	6300405	0.0587	0.3997
chr15	102531392	5707108	0.0557	0.3045
chr16	90354753	5256231	0.0582	0.3813
chr17	81195210	4901380	0.0604	0.3299
chr18	78077248	5991404	0.0767	1.1623
chr19	59128983	4041066	0.0683	0.6175
chr20	63025520	3633249	0.0576	0.3357
chr21	48129895	4458493	0.0926	0.4868
chr22	51304566	1929109	0.0376	0.2456
chrMT	16571	24991	1.5081	1.4149
chrX	155270560	7070447	0.0455	0.3146
chrY	59373566	534962	0.009	0.1909

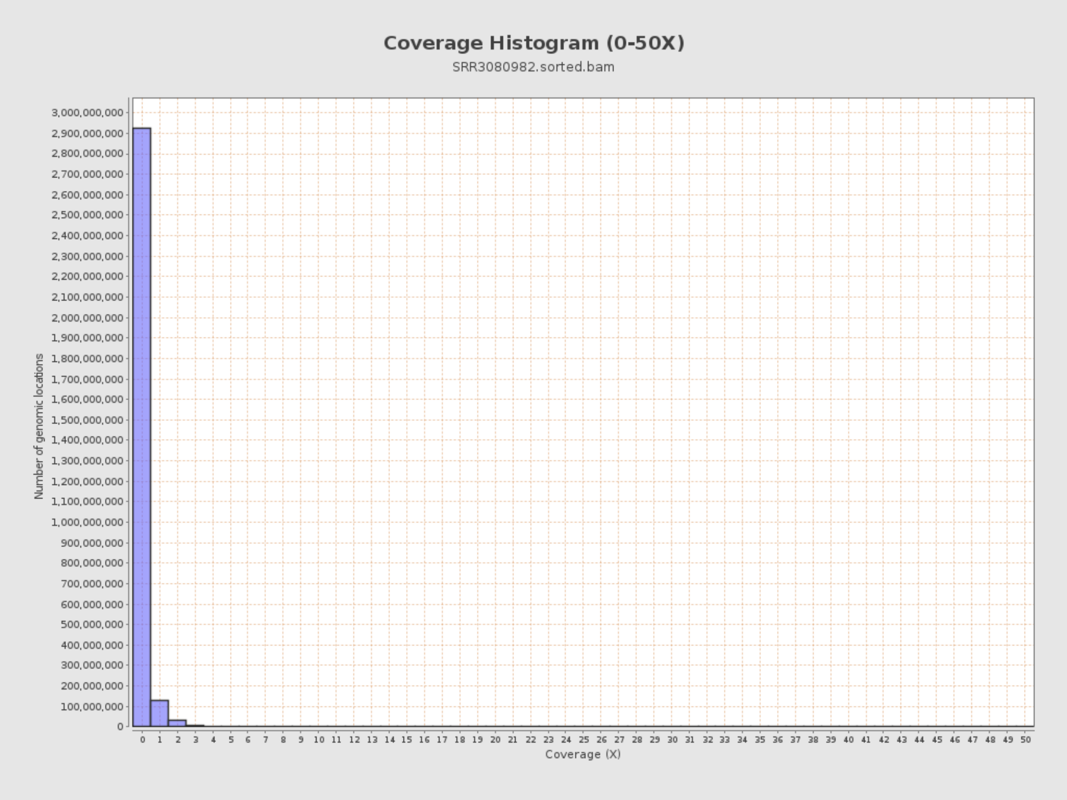
3. Results : Coverage across reference



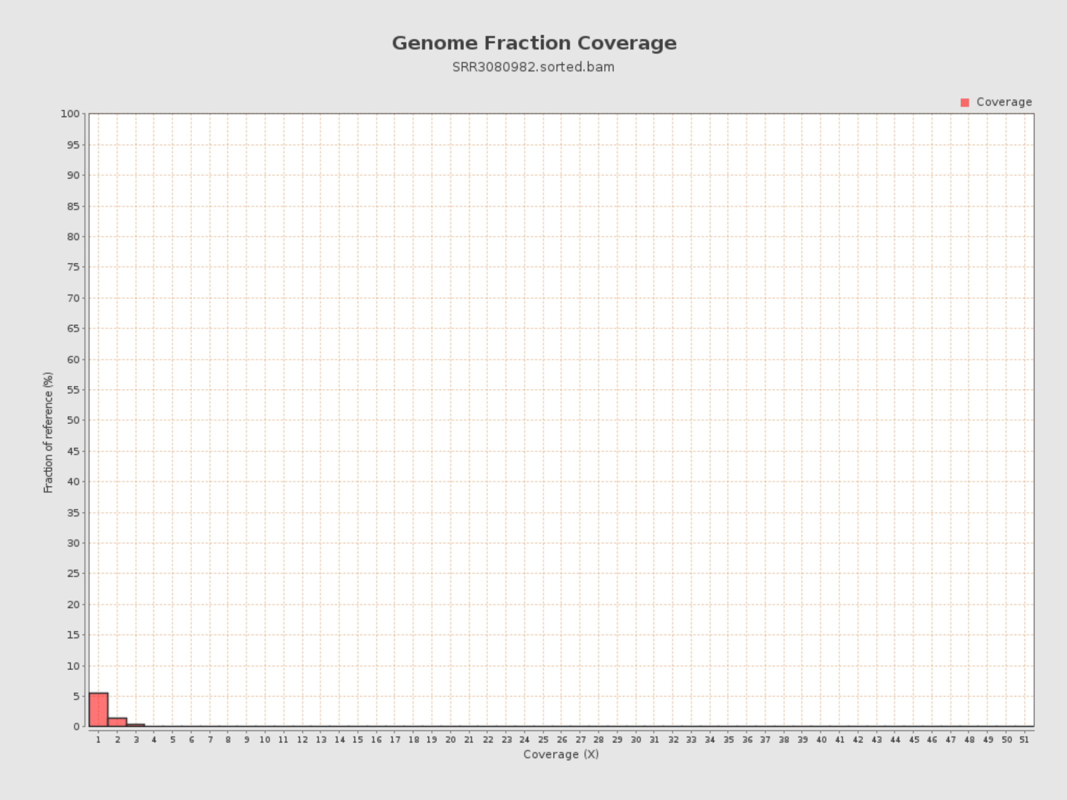
4. Results : Coverage Histogram



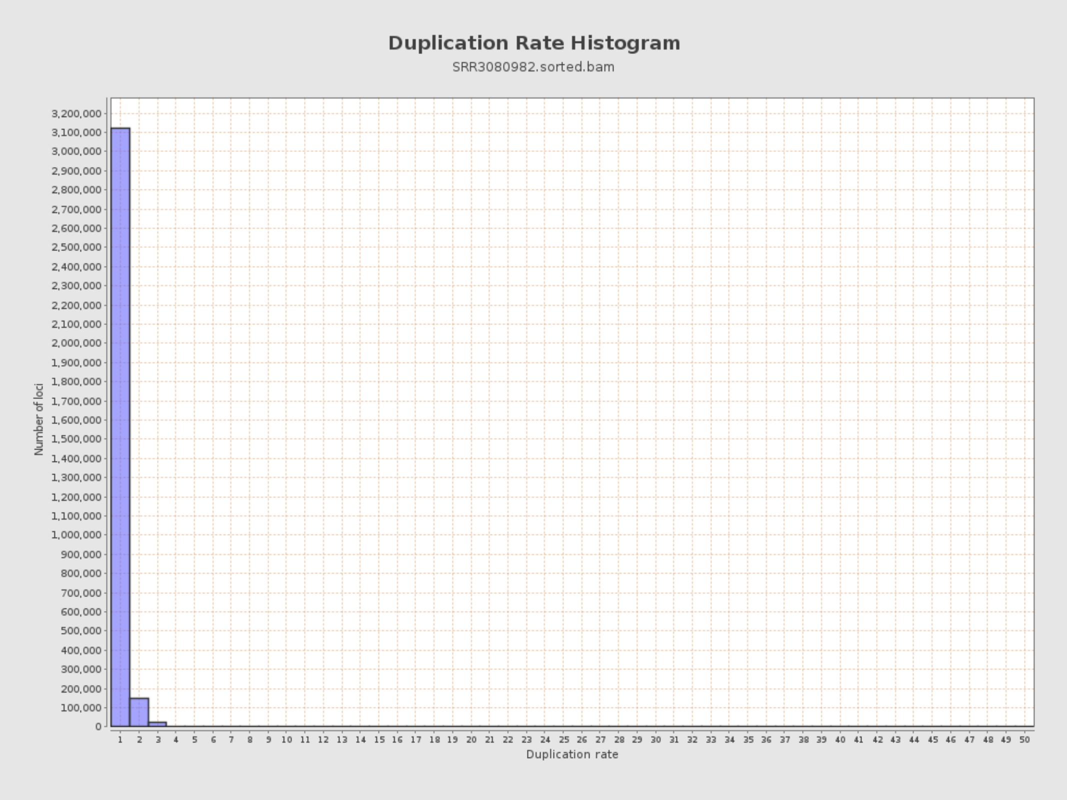
5. Results : Coverage Histogram (0-50X)



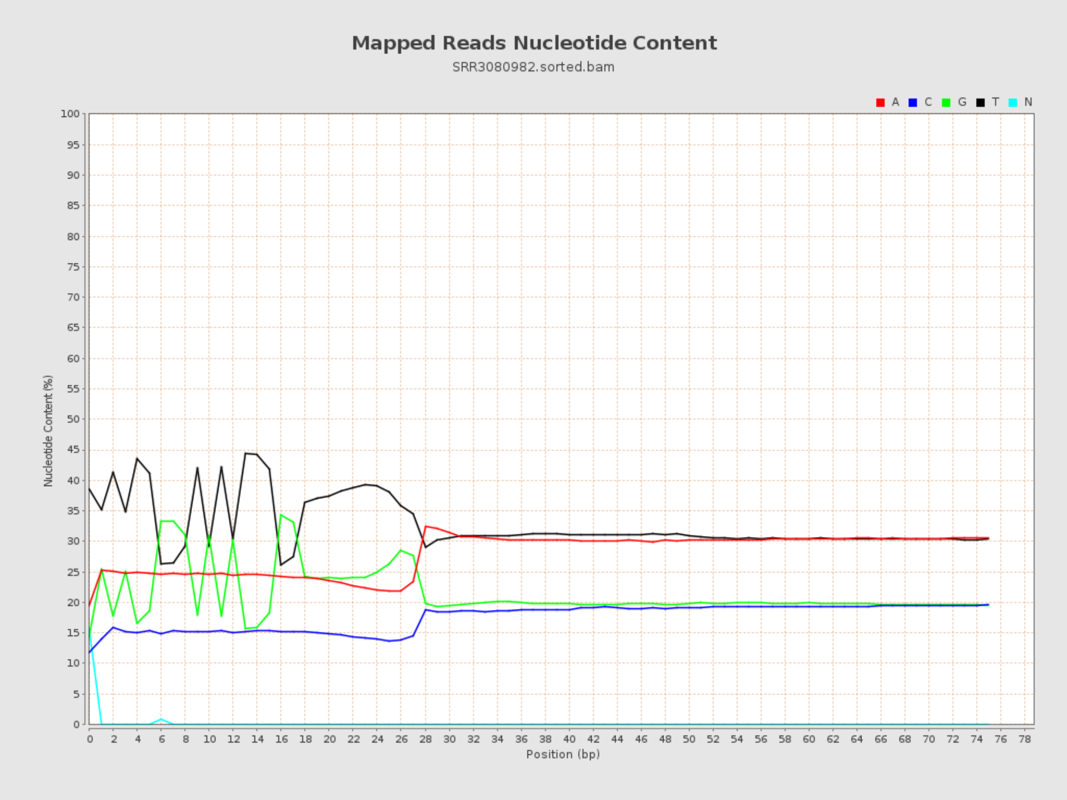
6. Results : Genome Fraction Coverage



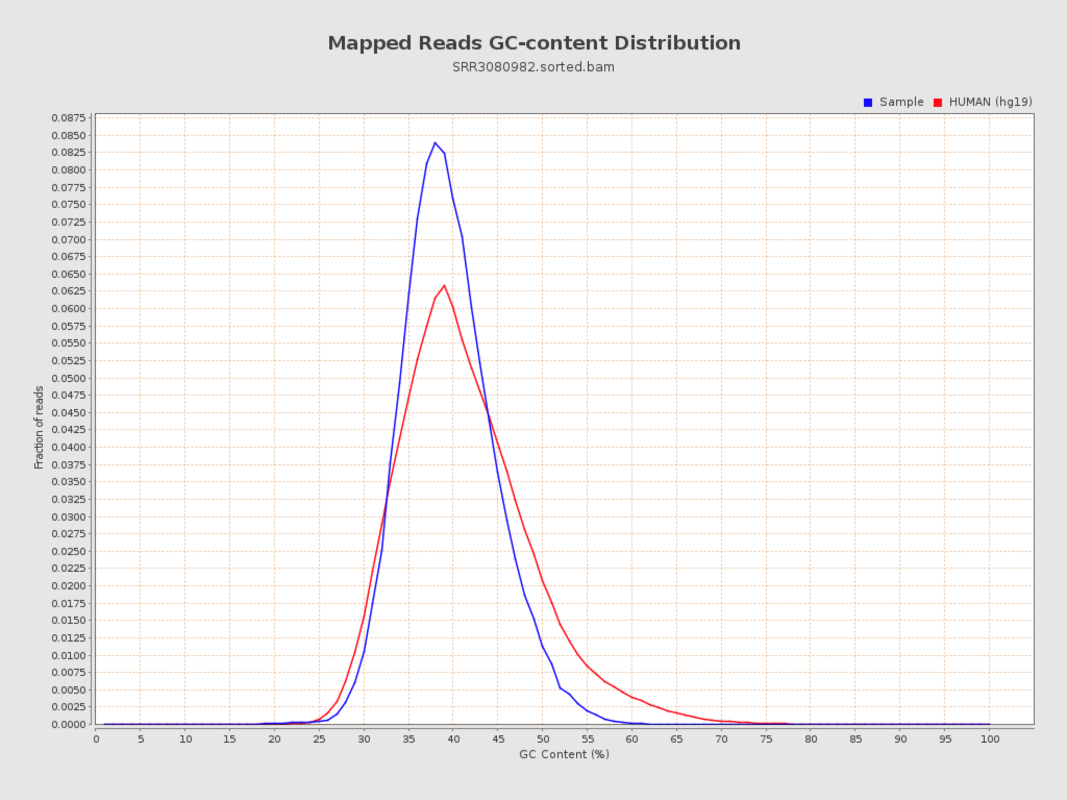
7. Results : Duplication Rate Histogram



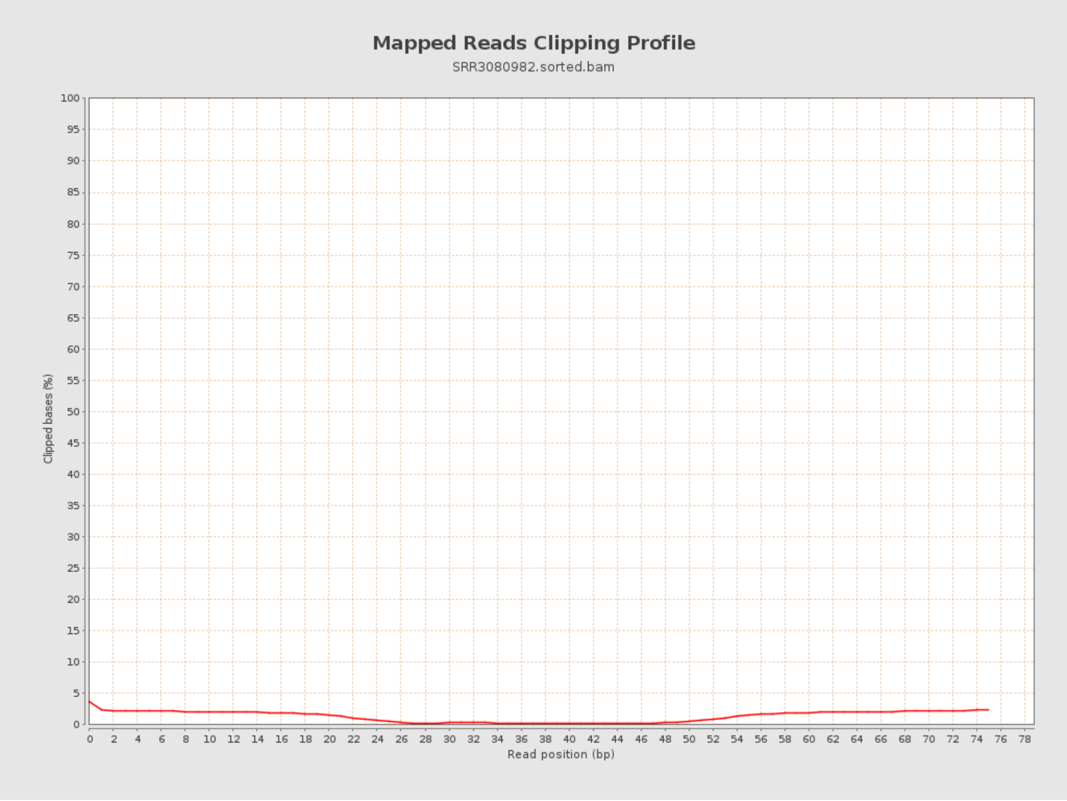
8. Results : Mapped Reads Nucleotide Content



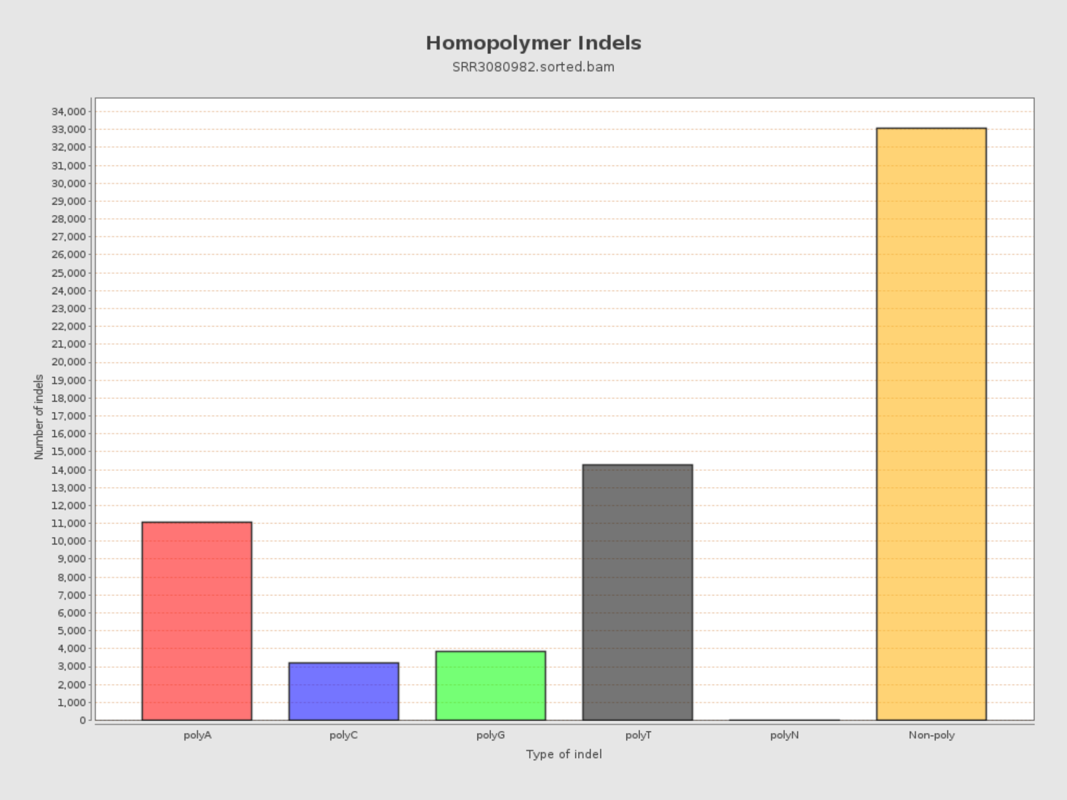
9. Results : Mapped Reads GC-content Distribution



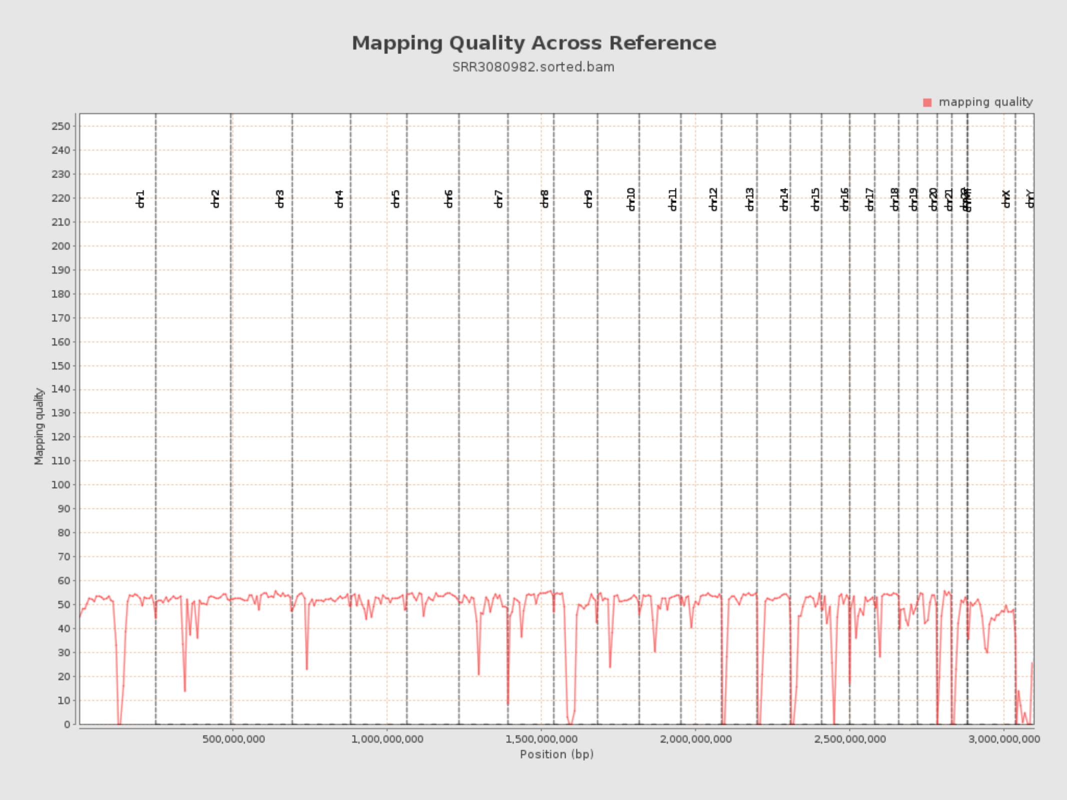
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram