Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 23:17:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082986.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_SRR3082986 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082986.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 23:17:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082986.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,642,647
Mapped reads	2,277,956 / 86.2%
Unmapped reads	364,691 / 13.8%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,914 / 0.79%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	433,909 / 16.42%
Duplication rate	10.72%
Clipped reads	838,876 / 31.74%

2.2. ACGT Content

Number/percentage of A's	45,066,147 / 28.8%
Number/percentage of C's	28,082,354 / 17.94%
Number/percentage of T's	50,762,429 / 32.44%
Number/percentage of G's	32,541,809 / 20.79%
Number/percentage of N's	44,049 / 0.03%
GC Percentage	38.74%

2.3. Coverage

Mean	0.0506

Standard Deviation	0.5982

2.4. Mapping Quality

Mean Mapping Quality	47.11

2.5. Mismatches and indels

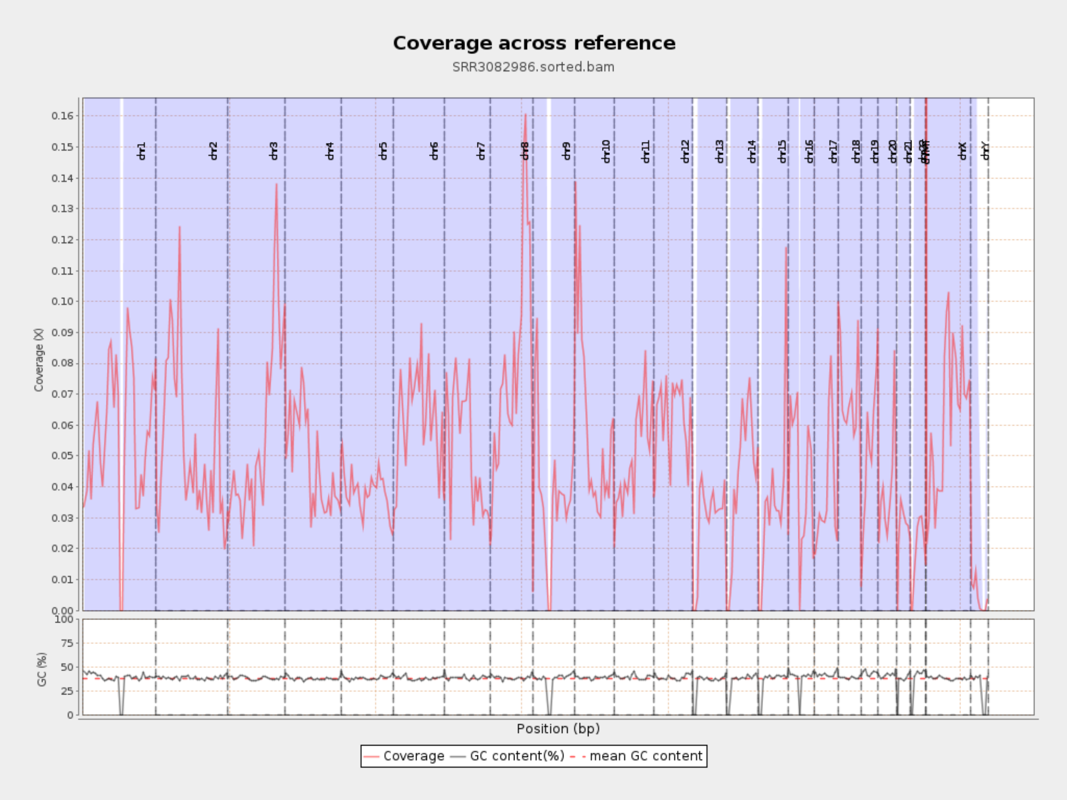
General error rate	0.96%
Mismatches	1,481,654
Insertions	13,623
Mapped reads with at least one insertion	0.59%
Deletions	36,501
Mapped reads with at least one deletion	1.58%
Homopolymer indels	49.8%

2.6. Chromosome stats

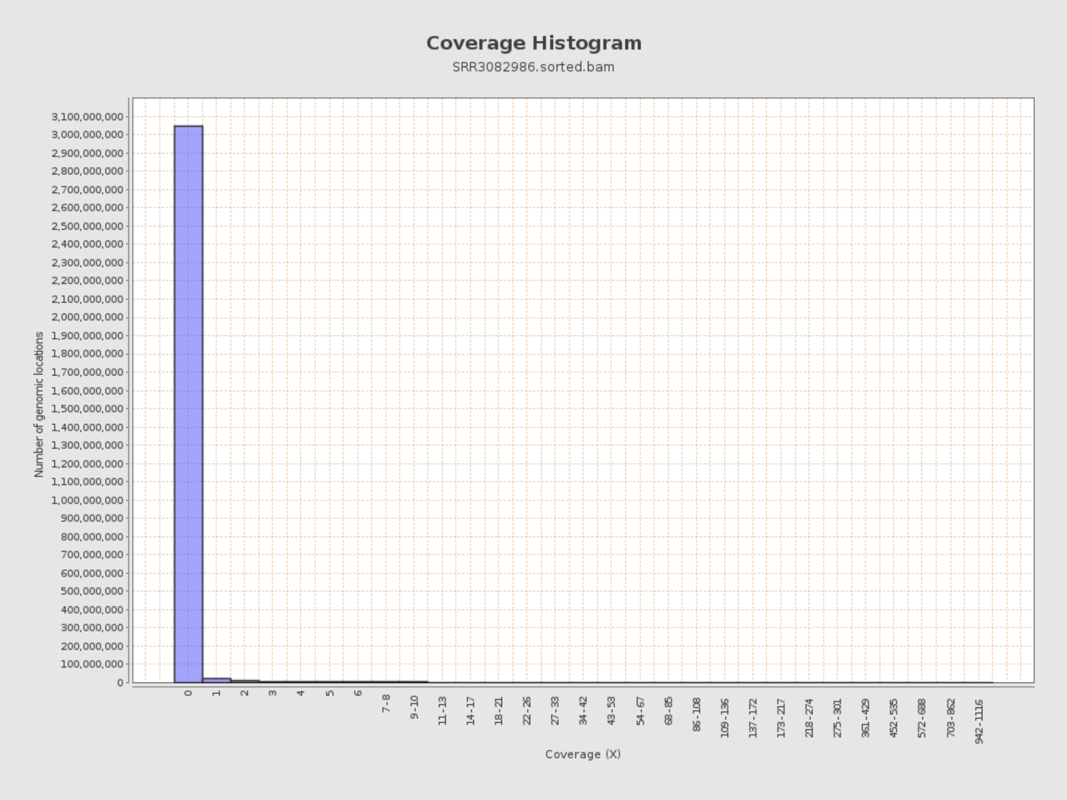
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14021551	0.0563	0.6341
chr2	243199373	12875822	0.0529	0.5912
chr3	198022430	11267008	0.0569	0.6019
chr4	191154276	9245932	0.0484	0.5519
chr5	180915260	6994962	0.0387	0.4857
chr6	171115067	10729106	0.0627	0.6447
chr7	159138663	8237016	0.0518	0.6088

chr8	146364022	11925196	0.0815	0.9734
chr9	141213431	5365230	0.038	0.4847
chr10	135534747	8116176	0.0599	0.631
chr11	135006516	6821918	0.0505	0.5593
chr12	133851895	8333841	0.0623	0.6264
chr13	115169878	3371279	0.0293	0.4199
chr14	107349540	4697352	0.0438	0.5216
chr15	102531392	3682097	0.0359	0.459
chr16	90354753	3769483	0.0417	0.4867
chr17	81195210	3182086	0.0392	0.4799
chr18	78077248	5457302	0.0699	0.7634
chr19	59128983	3083879	0.0522	0.5666
chr20	63025520	2581879	0.041	0.4955
chr21	48129895	1228507	0.0255	0.3785
chr22	51304566	990573	0.0193	0.3104
chrMT	16571	615230	37.1269	24.4576
chrX	155270560	9700146	0.0625	0.6315
chrY	59373566	262206	0.0044	0.1195

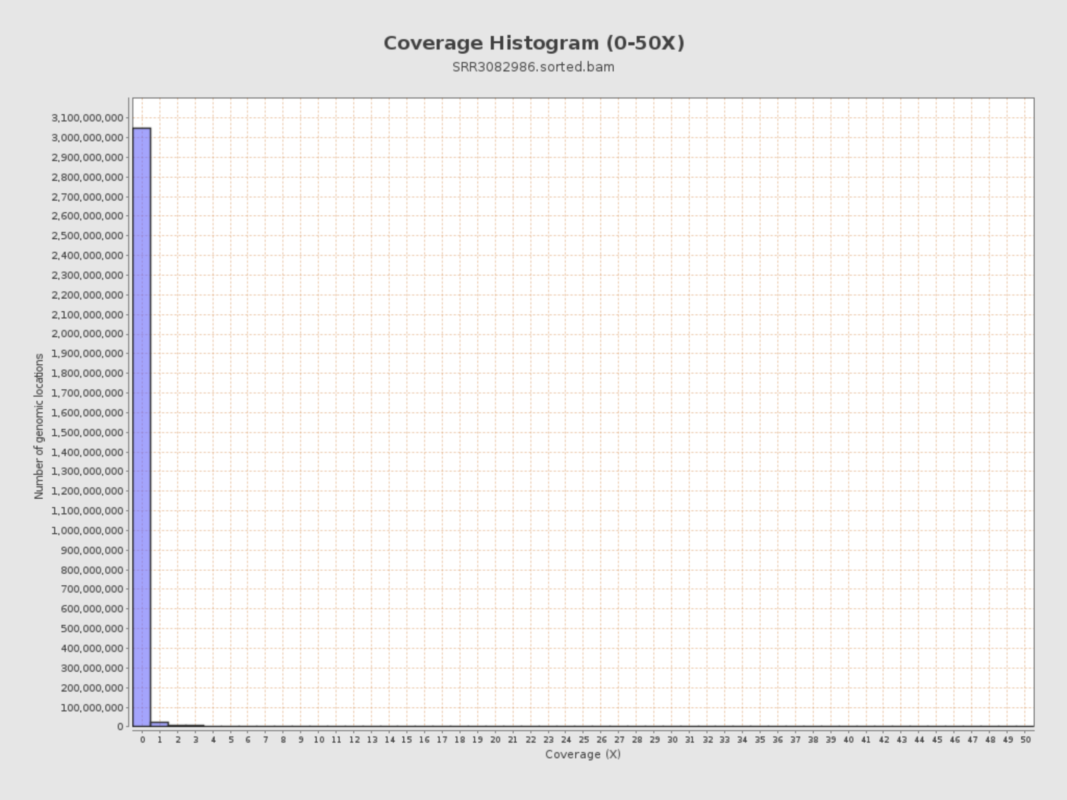
3. Results : Coverage across reference



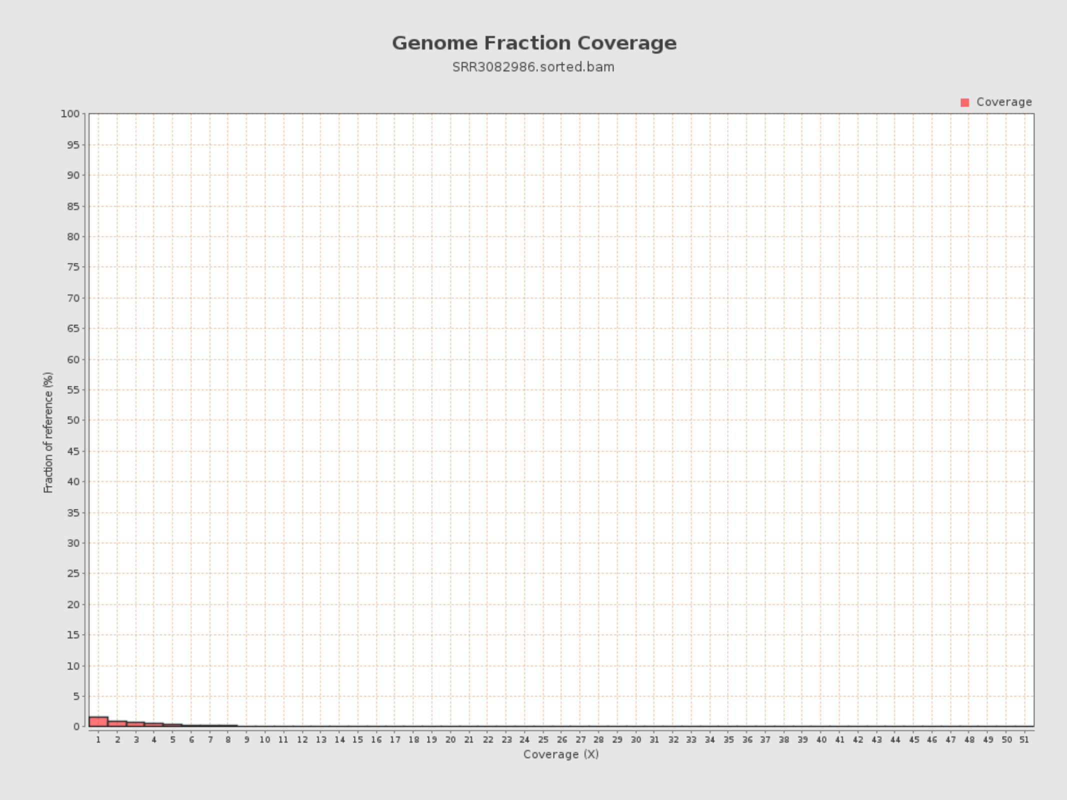
4. Results : Coverage Histogram



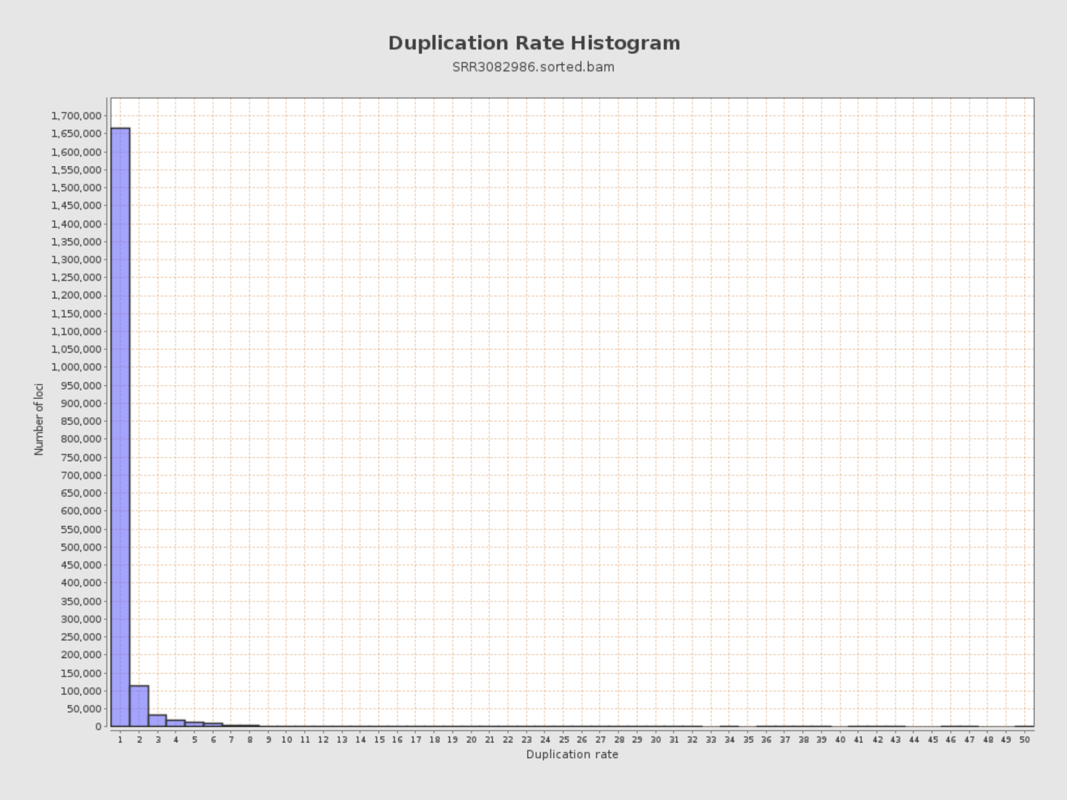
5. Results : Coverage Histogram (0-50X)



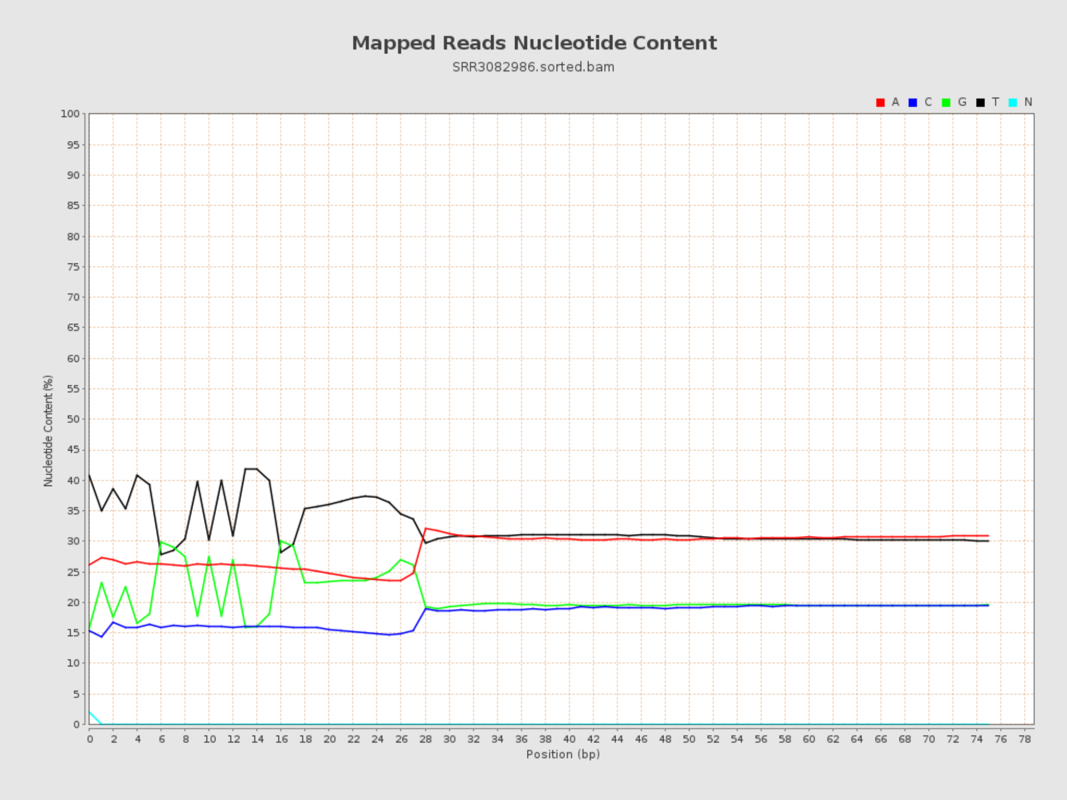
6. Results : Genome Fraction Coverage



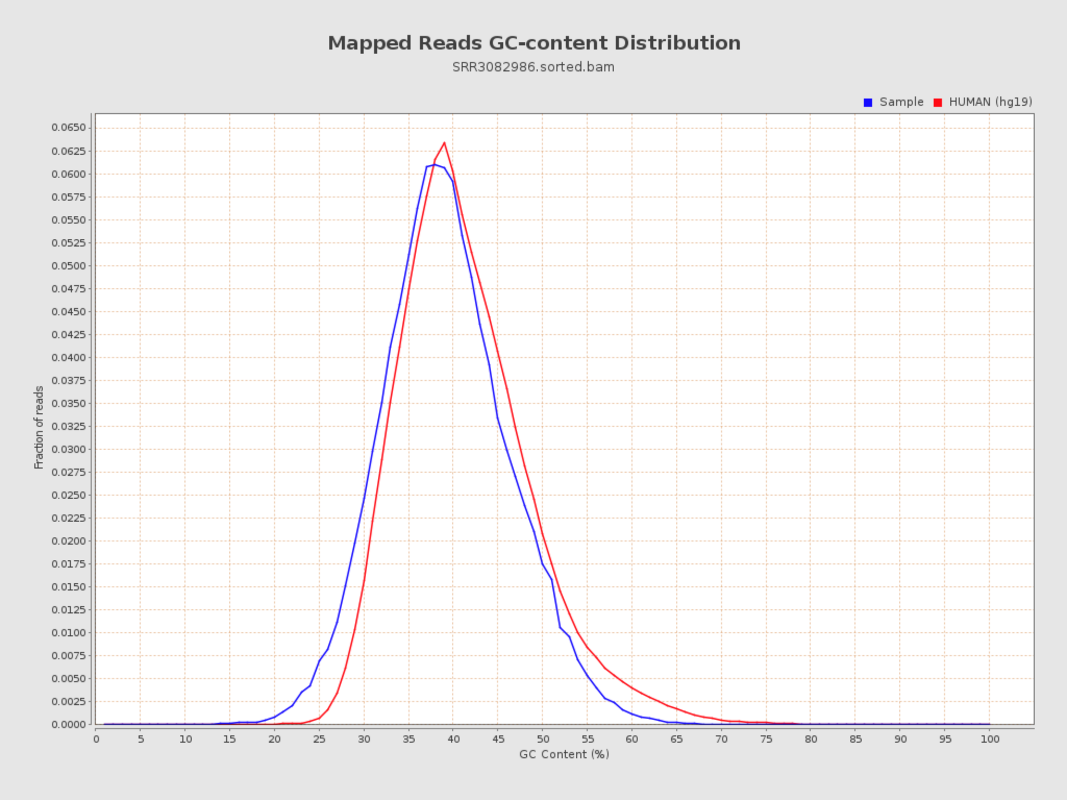
7. Results : Duplication Rate Histogram



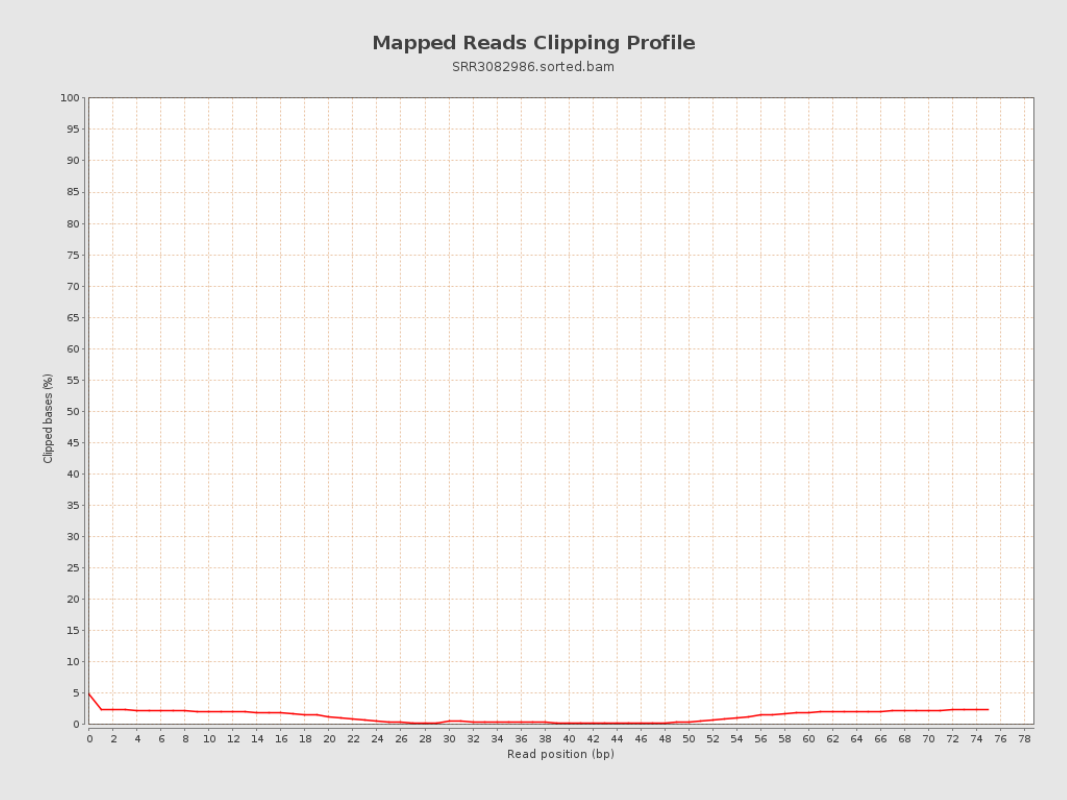
8. Results : Mapped Reads Nucleotide Content



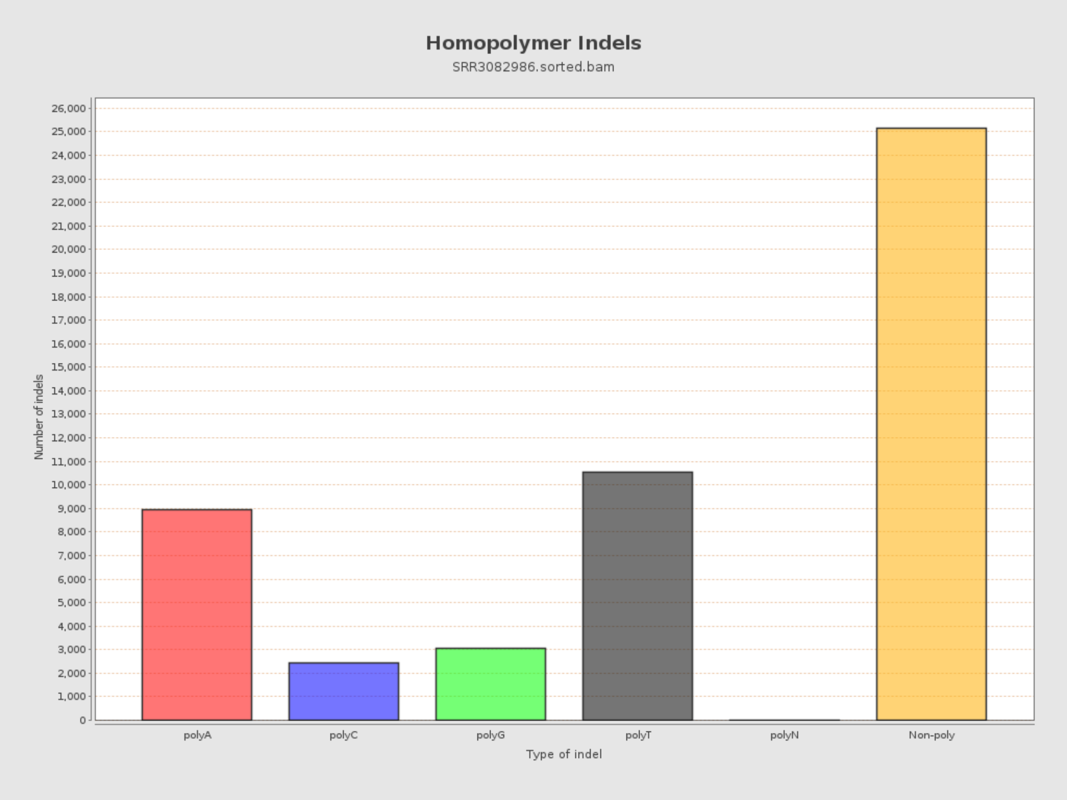
9. Results : Mapped Reads GC-content Distribution



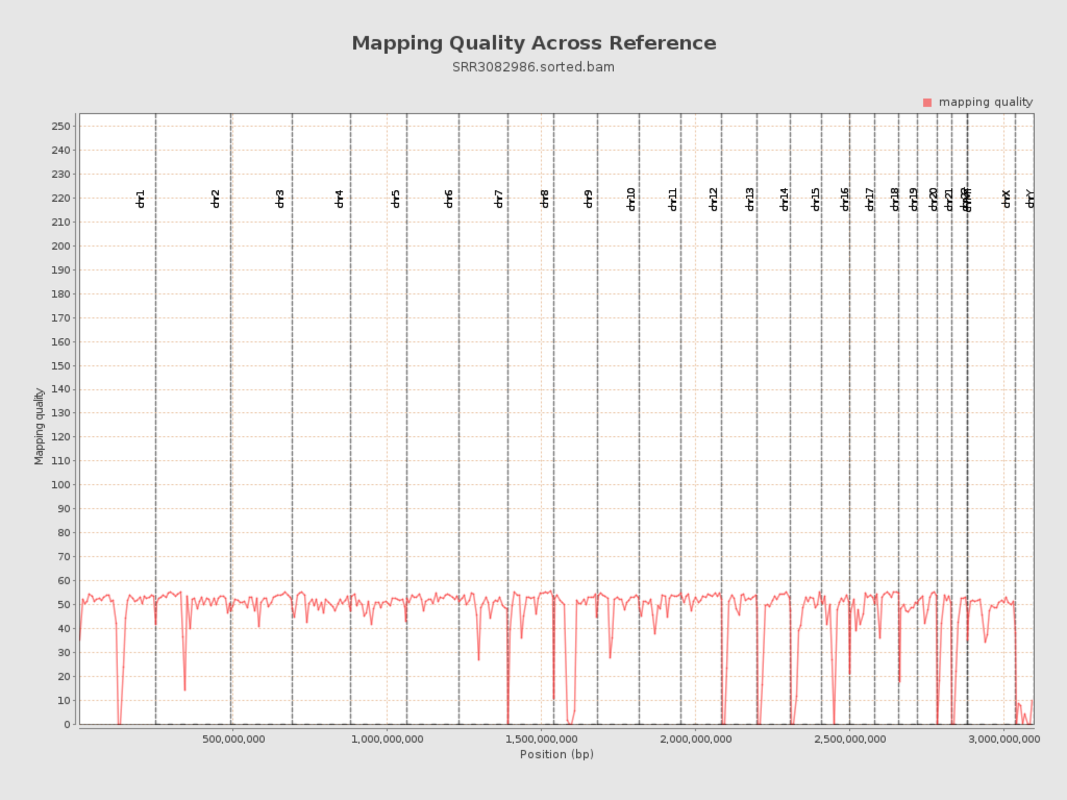
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram