Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 11:59:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818968.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_SRR1818968 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818968.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 11:59:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818968.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,601,284
Mapped reads	1,527,742 / 95.41%
Unmapped reads	73,542 / 4.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,654 / 1.54%
Read min/max/mean length	30 / 101 / 101.59
Duplicated reads (estimated)	669,602 / 41.82%
Duplication rate	36.64%
Clipped reads	1,539,234 / 96.12%

2.2. ACGT Content

Number/percentage of A's	41,924,393 / 29.68%
Number/percentage of C's	28,932,608 / 20.48%
Number/percentage of T's	40,586,107 / 28.73%
Number/percentage of G's	29,799,020 / 21.1%
Number/percentage of N's	6,710 / 0%
GC Percentage	41.58%

2.3. Coverage

Mean	0.0457

Standard Deviation	0.5509

2.4. Mapping Quality

Mean Mapping Quality	48.92

2.5. Mismatches and indels

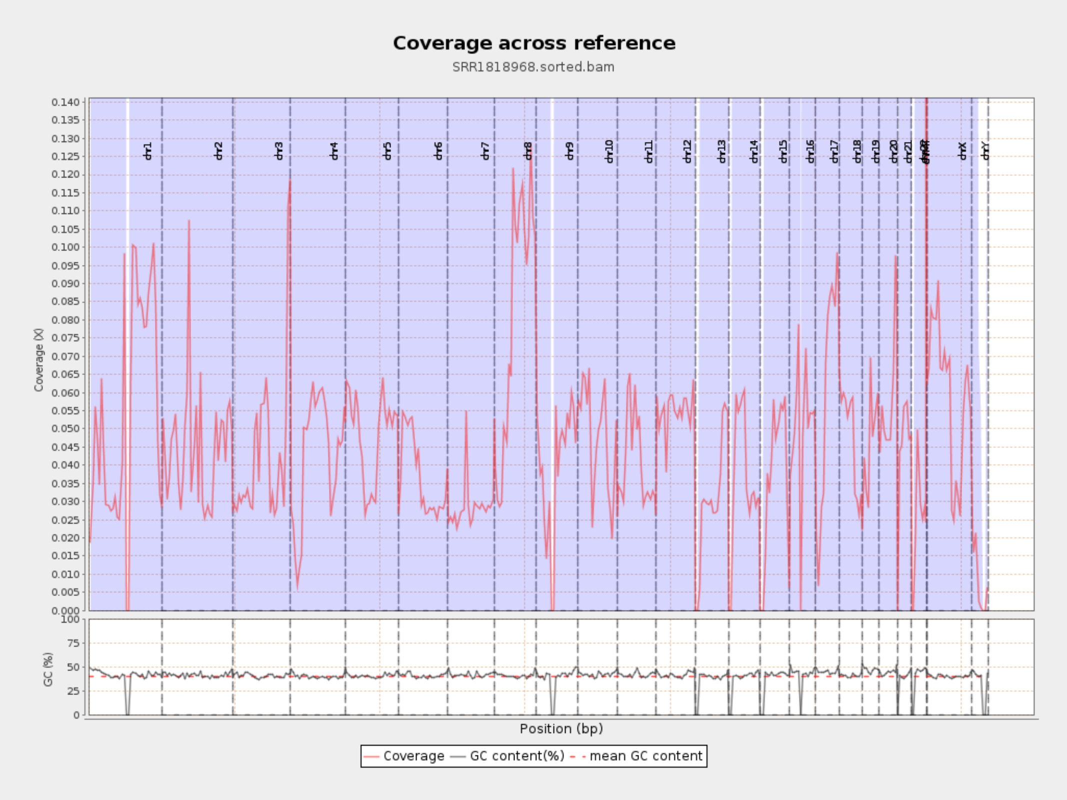
General error rate	0.66%
Mismatches	879,048
Insertions	26,058
Mapped reads with at least one insertion	1.67%
Deletions	45,357
Mapped reads with at least one deletion	2.9%
Homopolymer indels	40.28%

2.6. Chromosome stats

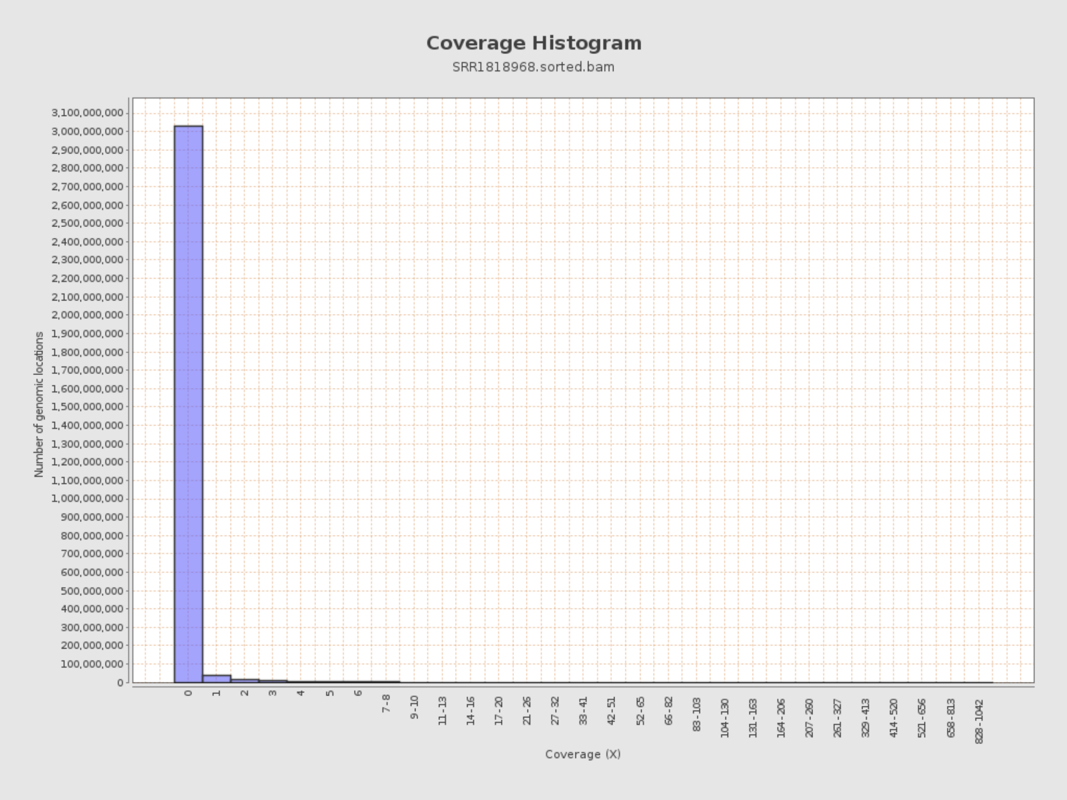
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13634638	0.0547	0.931
chr2	243199373	10925575	0.0449	0.7393
chr3	198022430	8255509	0.0417	0.3733
chr4	191154276	8080087	0.0423	0.4013
chr5	180915260	8717568	0.0482	0.4055
chr6	171115067	6230833	0.0364	0.3769
chr7	159138663	4522415	0.0284	0.4611

chr8	146364022	11979477	0.0818	0.5874
chr9	141213431	5506214	0.039	0.5454
chr10	135534747	6474418	0.0478	0.6134
chr11	135006516	5534534	0.041	0.4343
chr12	133851895	7346038	0.0549	0.4353
chr13	115169878	3522895	0.0306	0.319
chr14	107349540	3904748	0.0364	0.3693
chr15	102531392	3757474	0.0366	0.3546
chr16	90354753	4560564	0.0505	0.6363
chr17	81195210	4999981	0.0616	0.4901
chr18	78077248	3748137	0.048	0.6602
chr19	59128983	2743678	0.0464	0.8247
chr20	63025520	3718663	0.059	0.4705
chr21	48129895	2172007	0.0451	0.4212
chr22	51304566	1220530	0.0238	0.3057
chrMT	16571	57247	3.4546	3.8701
chrX	155270560	9243179	0.0595	0.5179
chrY	59373566	473933	0.008	0.4238

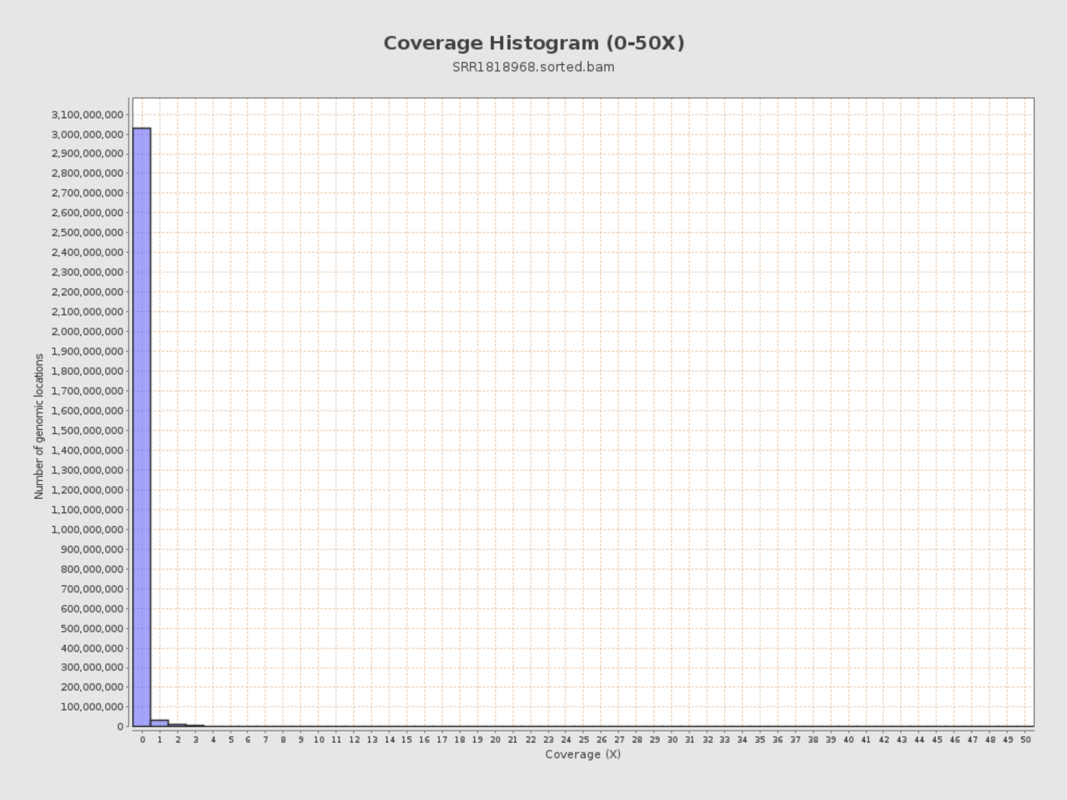
3. Results : Coverage across reference



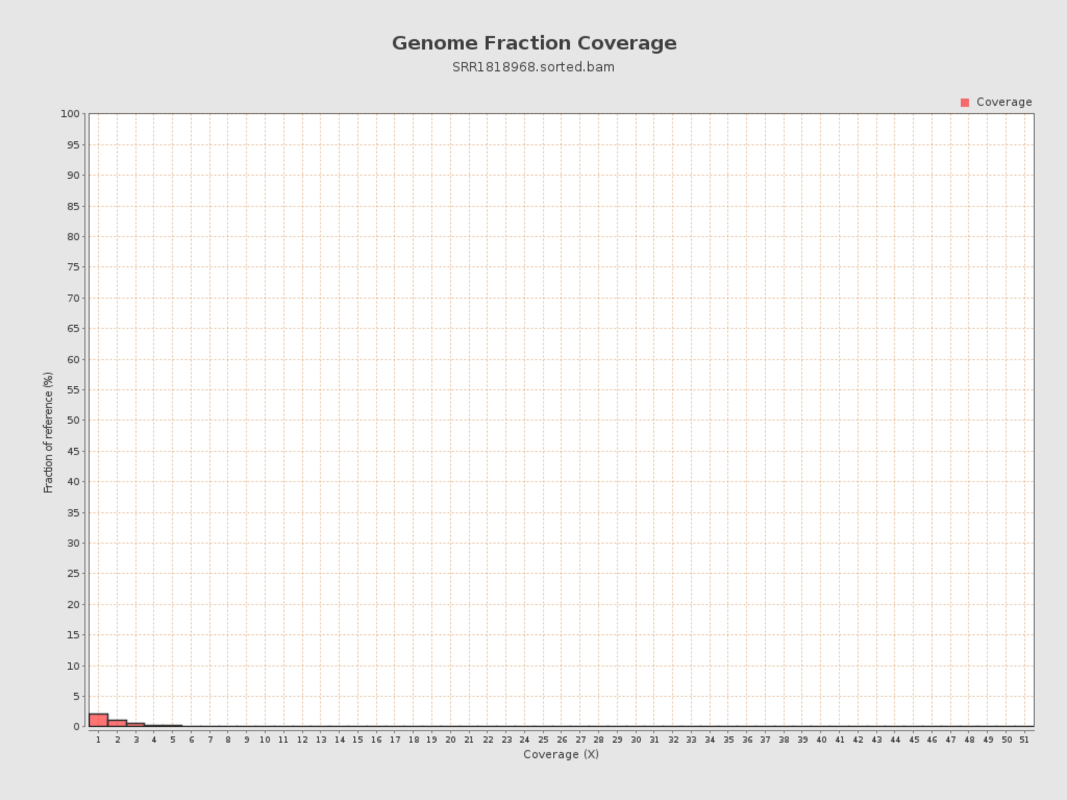
4. Results : Coverage Histogram



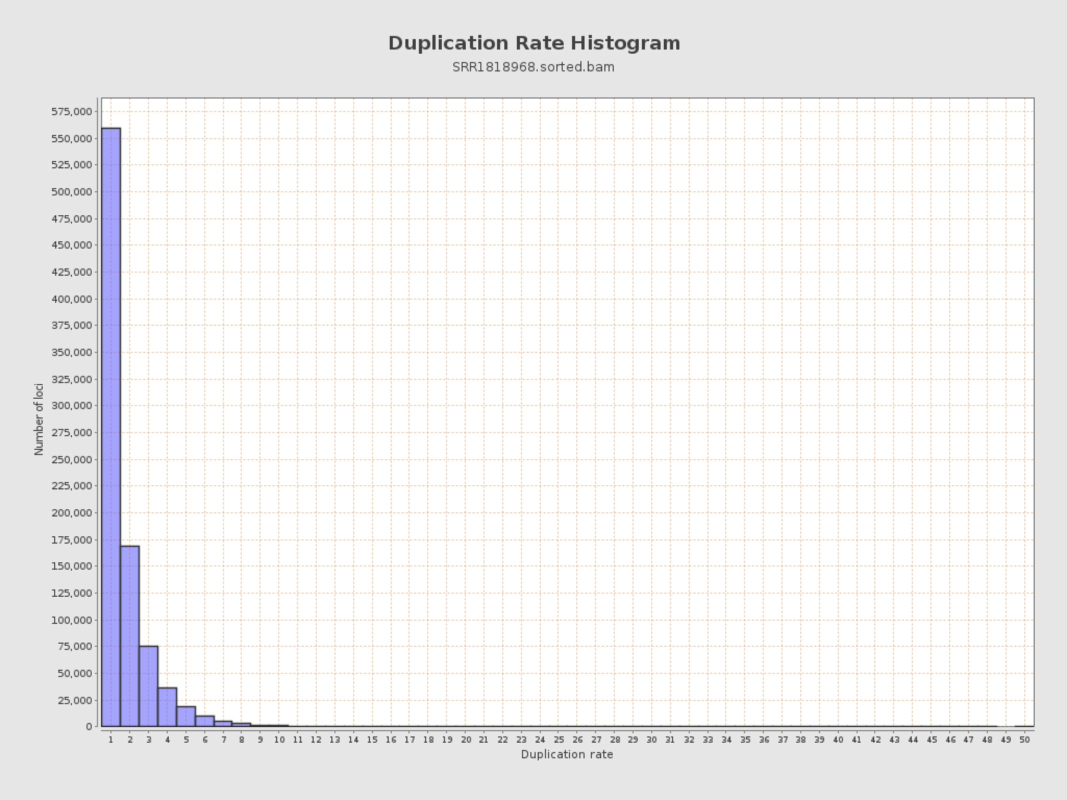
5. Results : Coverage Histogram (0-50X)



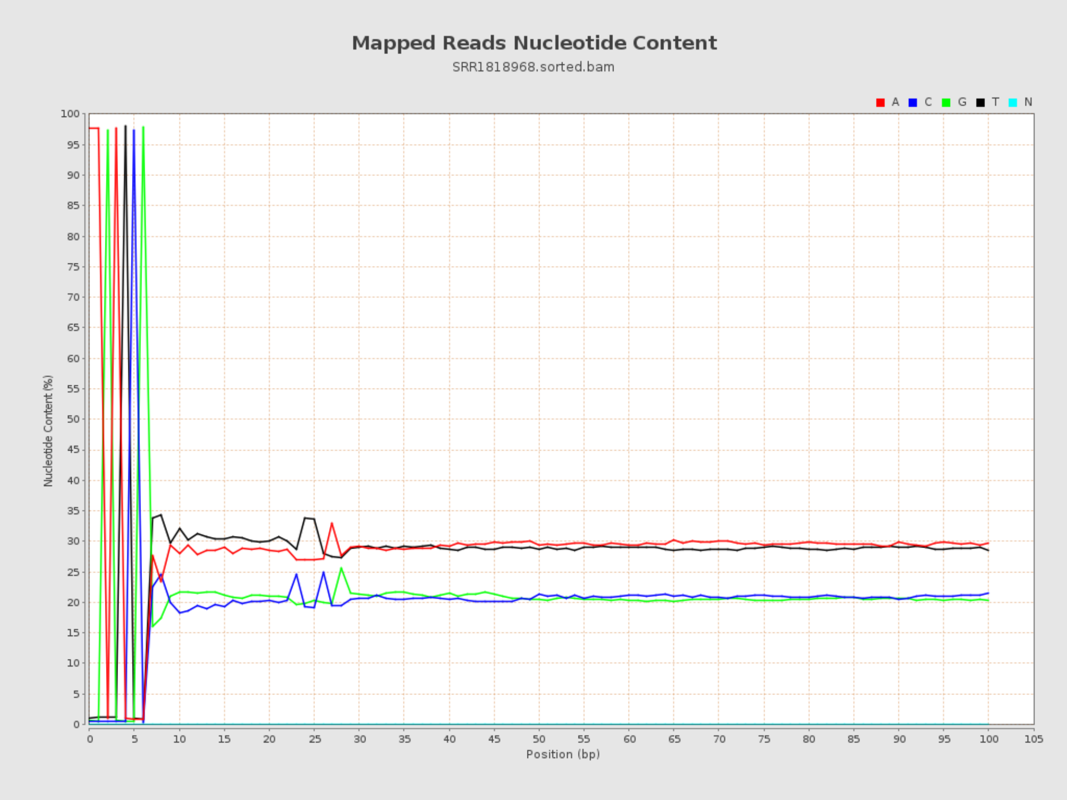
6. Results : Genome Fraction Coverage



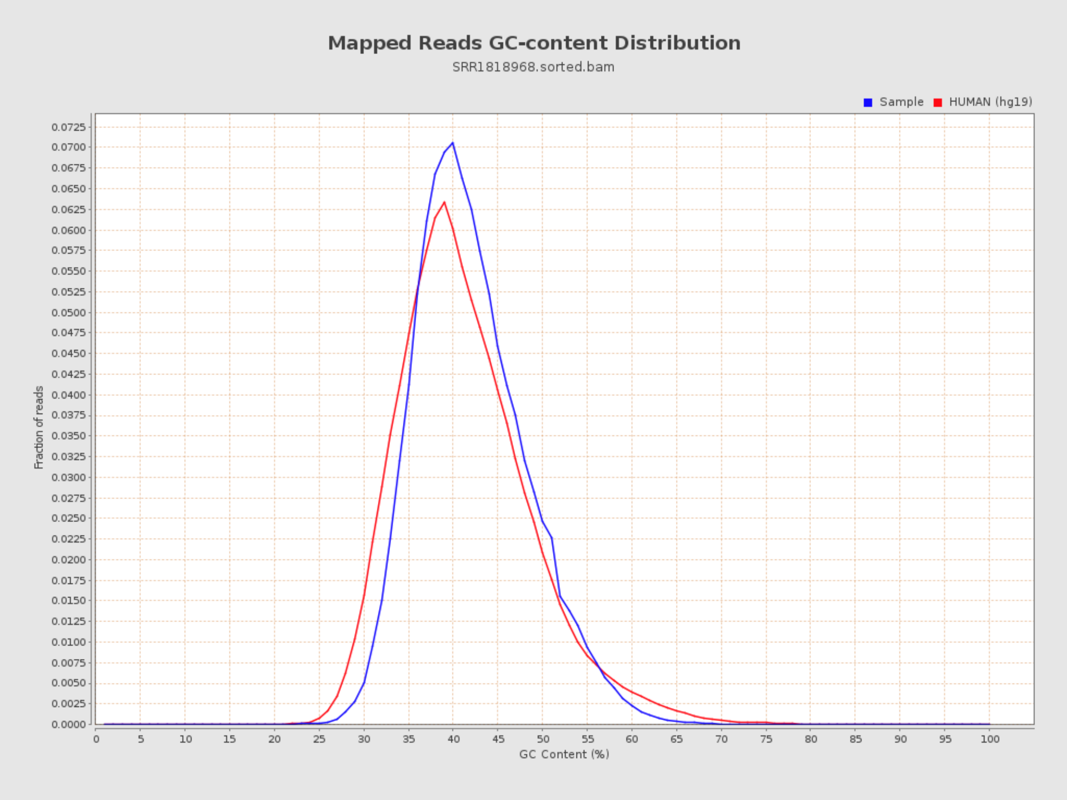
7. Results : Duplication Rate Histogram



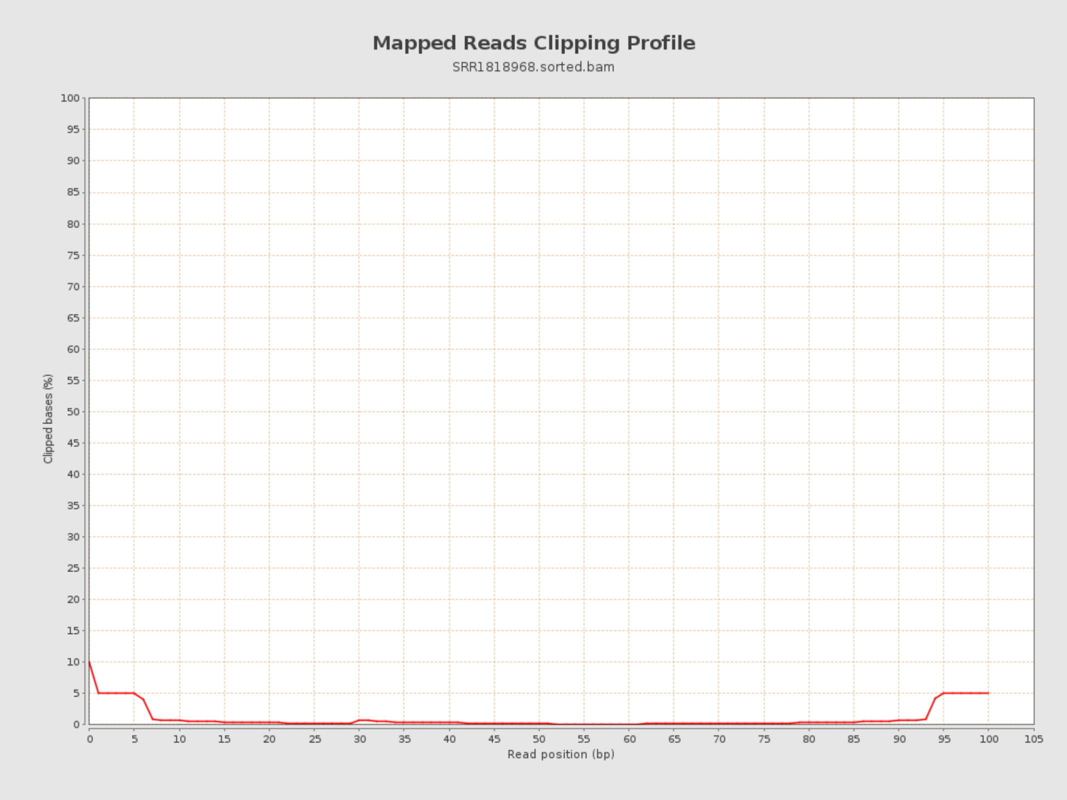
8. Results : Mapped Reads Nucleotide Content



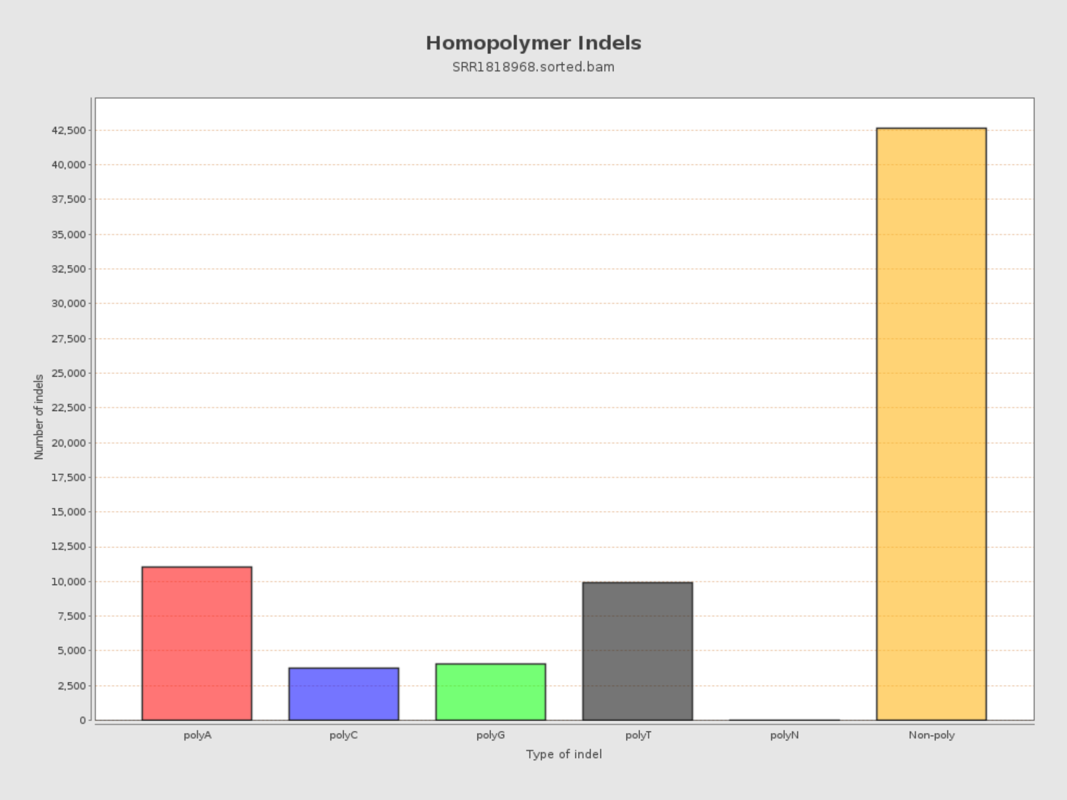
9. Results : Mapped Reads GC-content Distribution



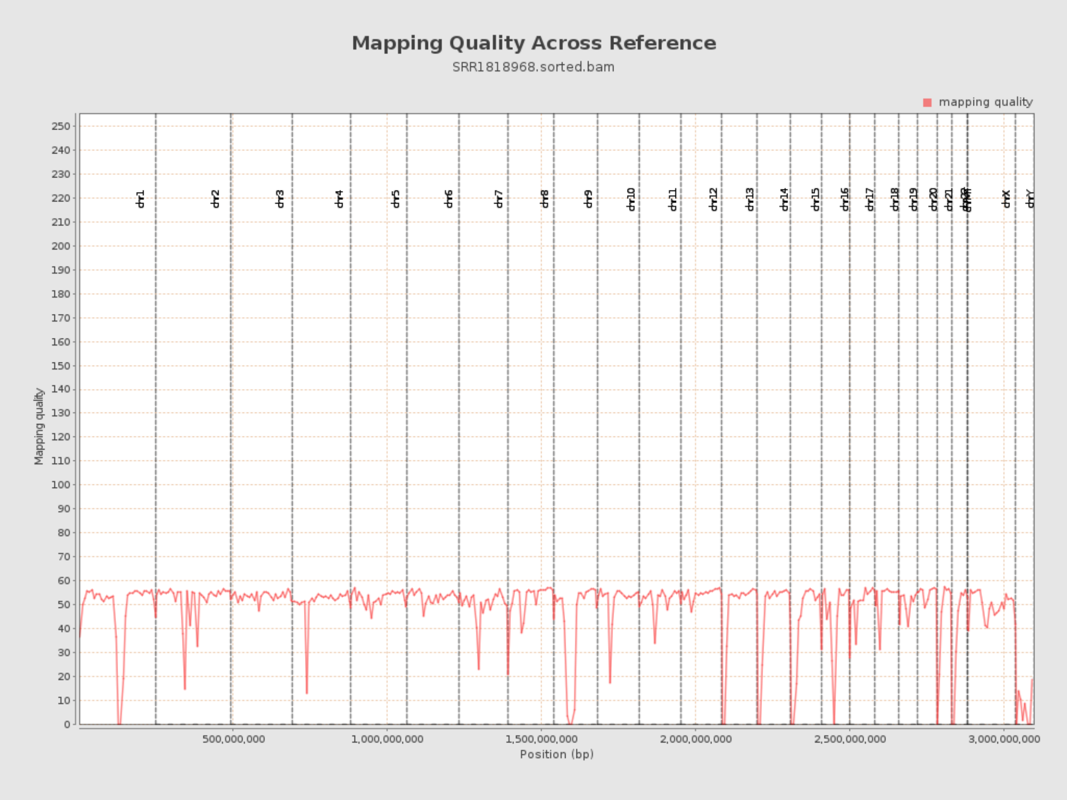
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram