Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 06:40:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818904.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_SRR1818904 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818904.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 06:40:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818904.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,713,973
Mapped reads	1,684,011 / 98.25%
Unmapped reads	29,962 / 1.75%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,233 / 1.3%
Read min/max/mean length	30 / 101 / 101.5
Duplicated reads (estimated)	355,985 / 20.77%
Duplication rate	17.41%
Clipped reads	1,684,666 / 98.29%

2.2. ACGT Content

Number/percentage of A's	43,351,590 / 27.79%
Number/percentage of C's	32,006,860 / 20.52%
Number/percentage of T's	45,438,414 / 29.13%
Number/percentage of G's	35,207,863 / 22.57%
Number/percentage of N's	2,412 / 0%
GC Percentage	43.08%

2.3. Coverage

Mean	0.0504

Standard Deviation	0.6599

2.4. Mapping Quality

Mean Mapping Quality	49.26

2.5. Mismatches and indels

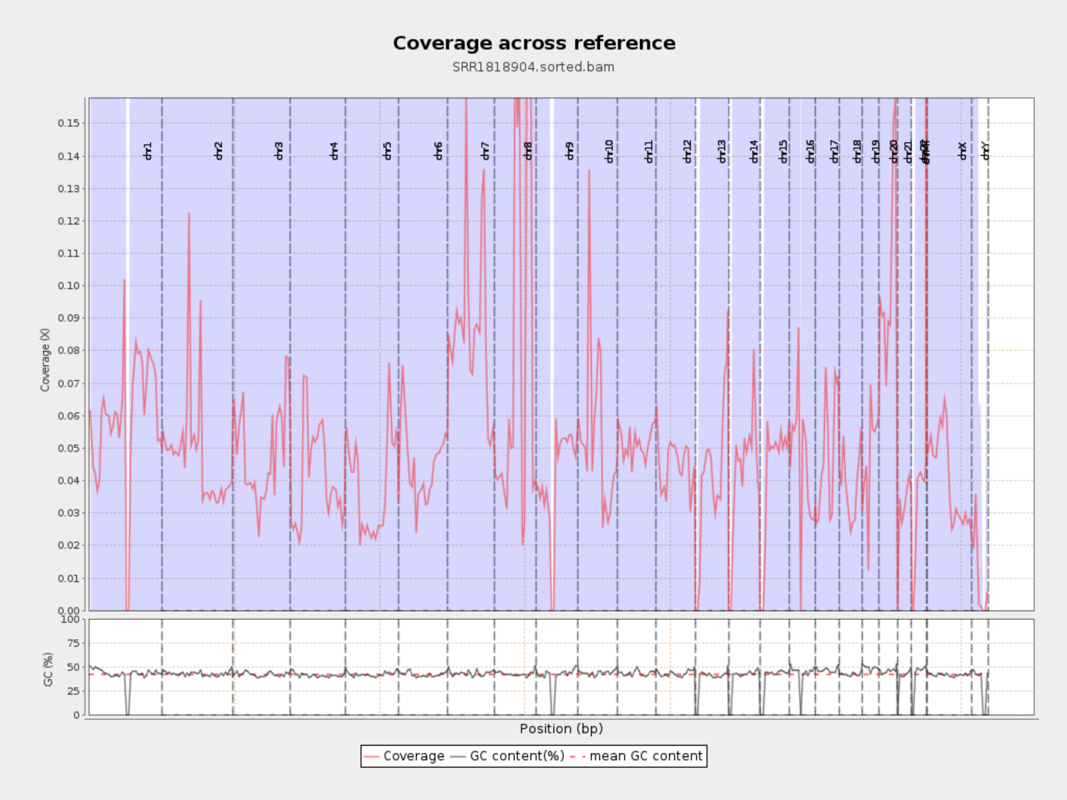
General error rate	0.66%
Mismatches	974,470
Insertions	23,731
Mapped reads with at least one insertion	1.36%
Deletions	50,021
Mapped reads with at least one deletion	2.9%
Homopolymer indels	39.14%

2.6. Chromosome stats

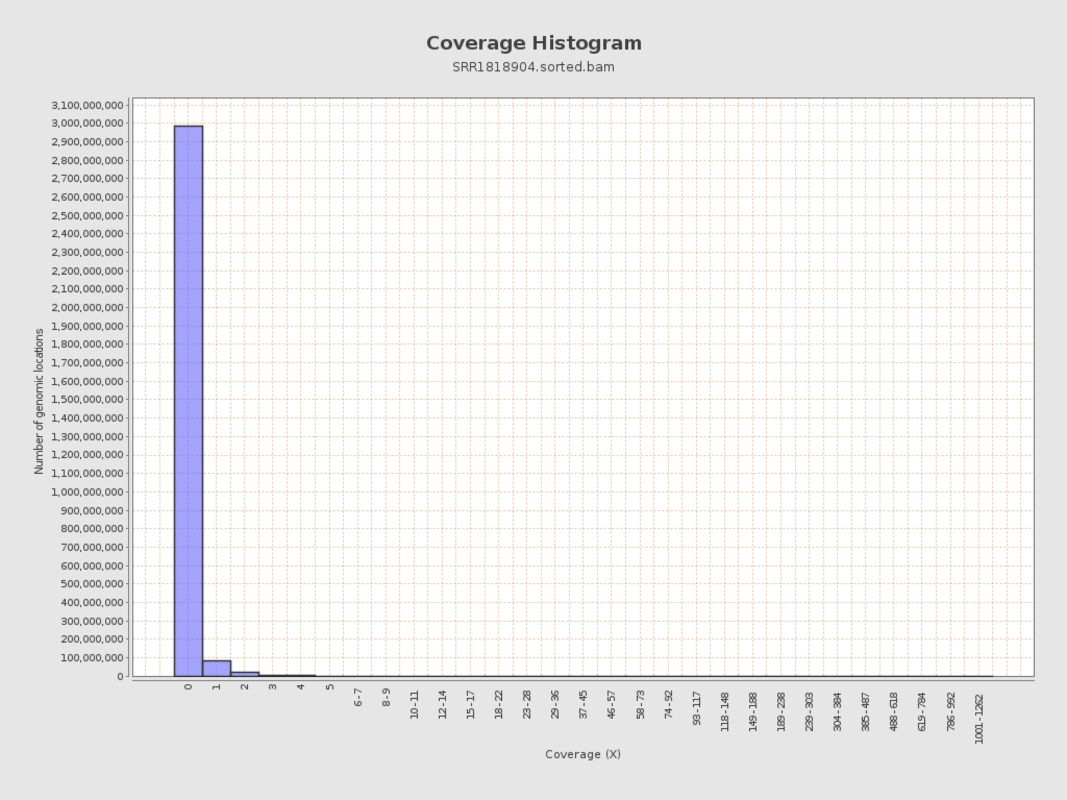
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14822071	0.0595	0.9775
chr2	243199373	11748295	0.0483	0.9286
chr3	198022430	9675086	0.0489	0.2951
chr4	191154276	7750147	0.0405	0.3683
chr5	180915260	6901236	0.0381	0.2803
chr6	171115067	7697443	0.045	0.311
chr7	159138663	14012968	0.0881	1.5266

chr8	146364022	13535487	0.0925	0.5199
chr9	141213431	5742591	0.0407	0.5605
chr10	135534747	7272351	0.0537	0.8957
chr11	135006516	6949358	0.0515	0.388
chr12	133851895	6051136	0.0452	0.2891
chr13	115169878	4678747	0.0406	0.2673
chr14	107349540	4560032	0.0425	0.3073
chr15	102531392	4331174	0.0422	0.2797
chr16	90354753	4009457	0.0444	0.6663
chr17	81195210	3971618	0.0489	0.4169
chr18	78077248	2996264	0.0384	0.6253
chr19	59128983	2808757	0.0475	0.8663
chr20	63025520	6499120	0.1031	0.4707
chr21	48129895	1504378	0.0313	0.2926
chr22	51304566	1469310	0.0286	0.2465
chrMT	16571	127105	7.6703	5.1945
chrX	155270560	6392365	0.0412	0.331
chrY	59373566	600188	0.0101	0.7686

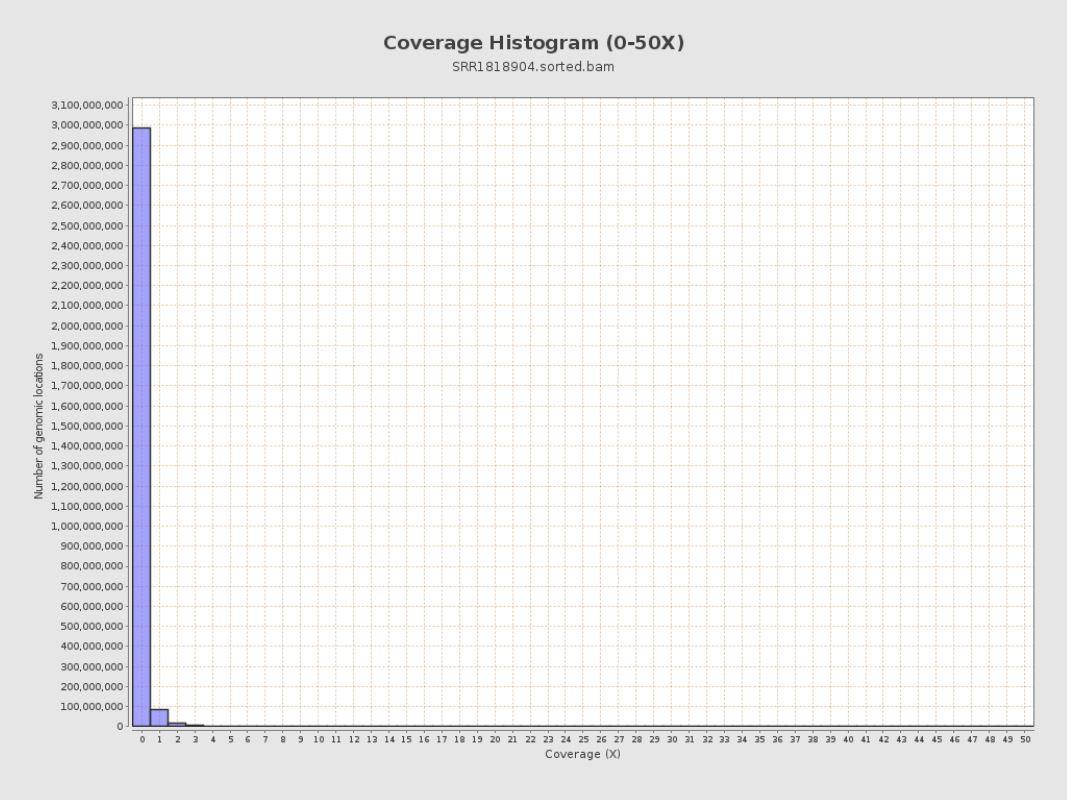
3. Results : Coverage across reference



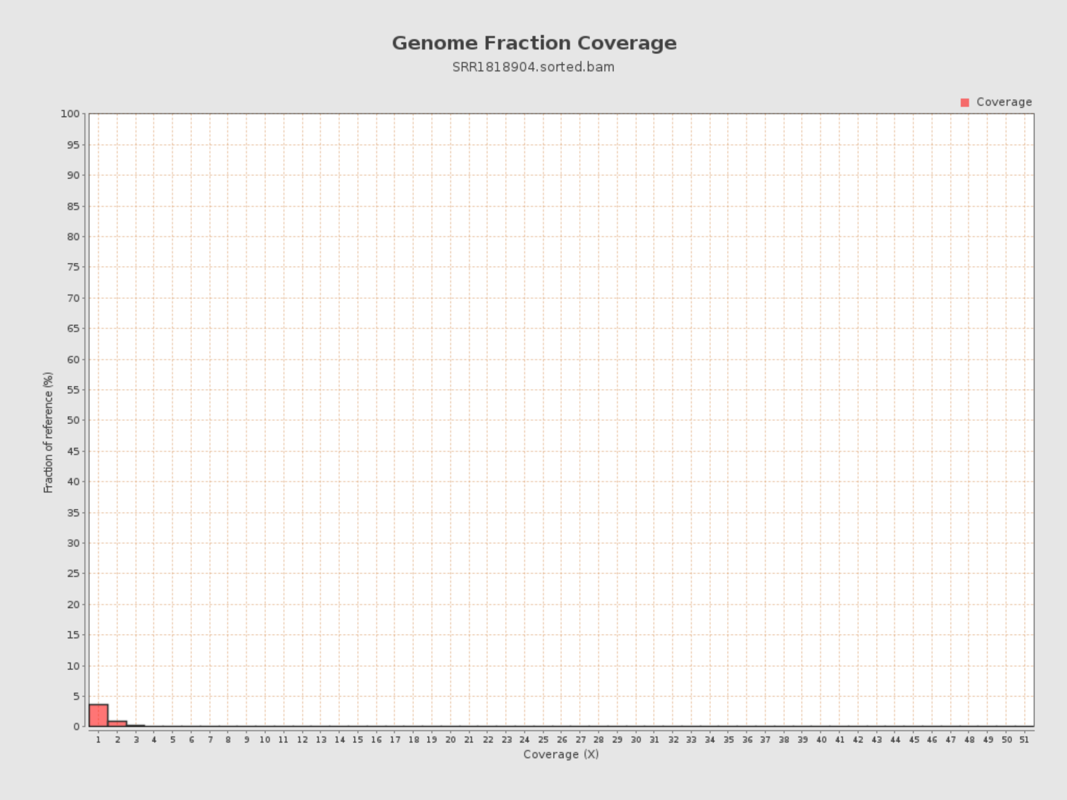
4. Results : Coverage Histogram



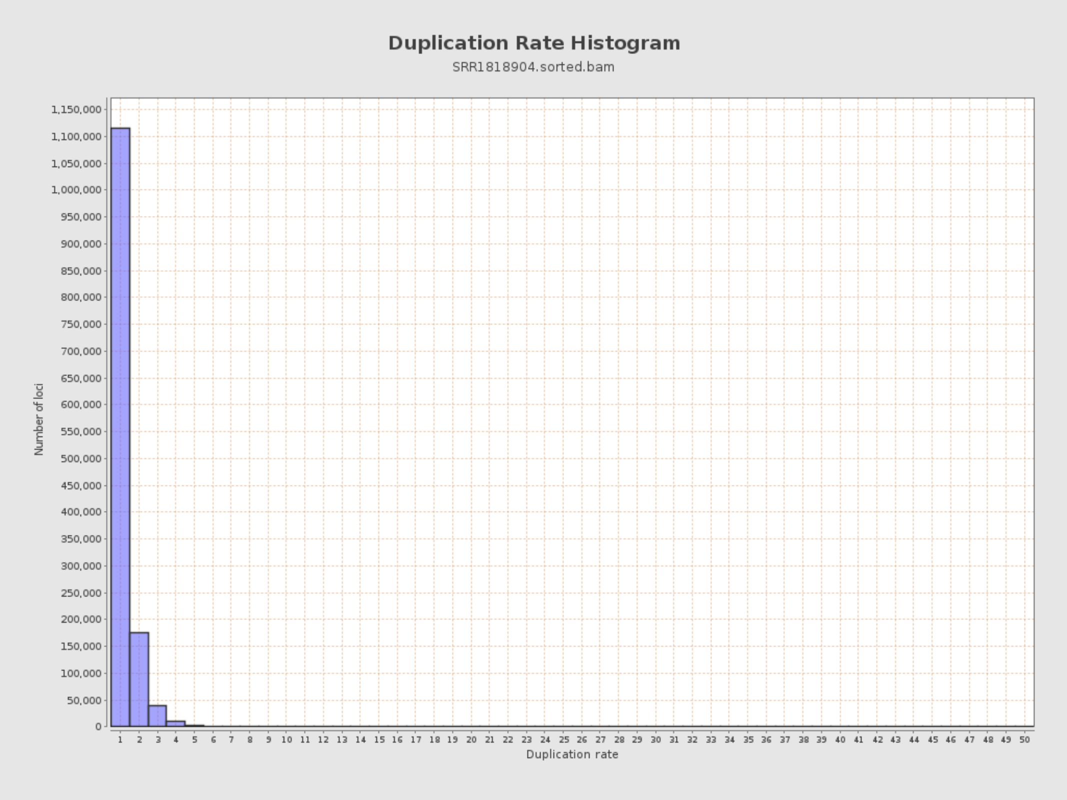
5. Results : Coverage Histogram (0-50X)



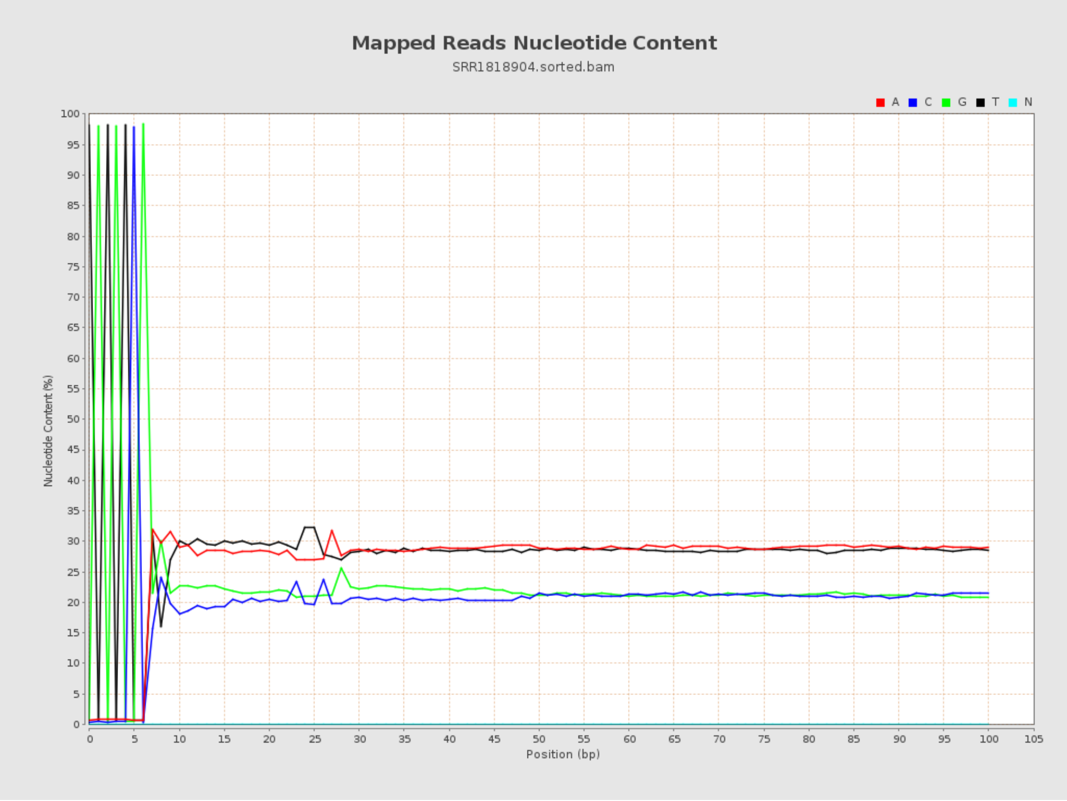
6. Results : Genome Fraction Coverage



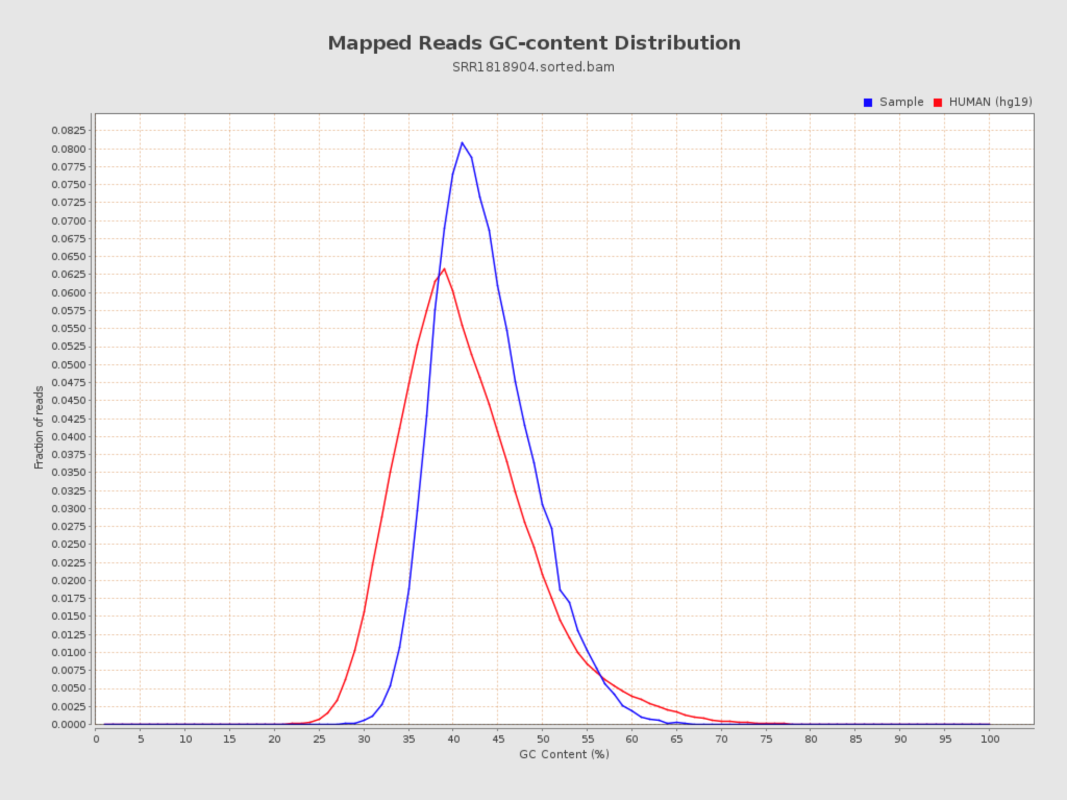
7. Results : Duplication Rate Histogram



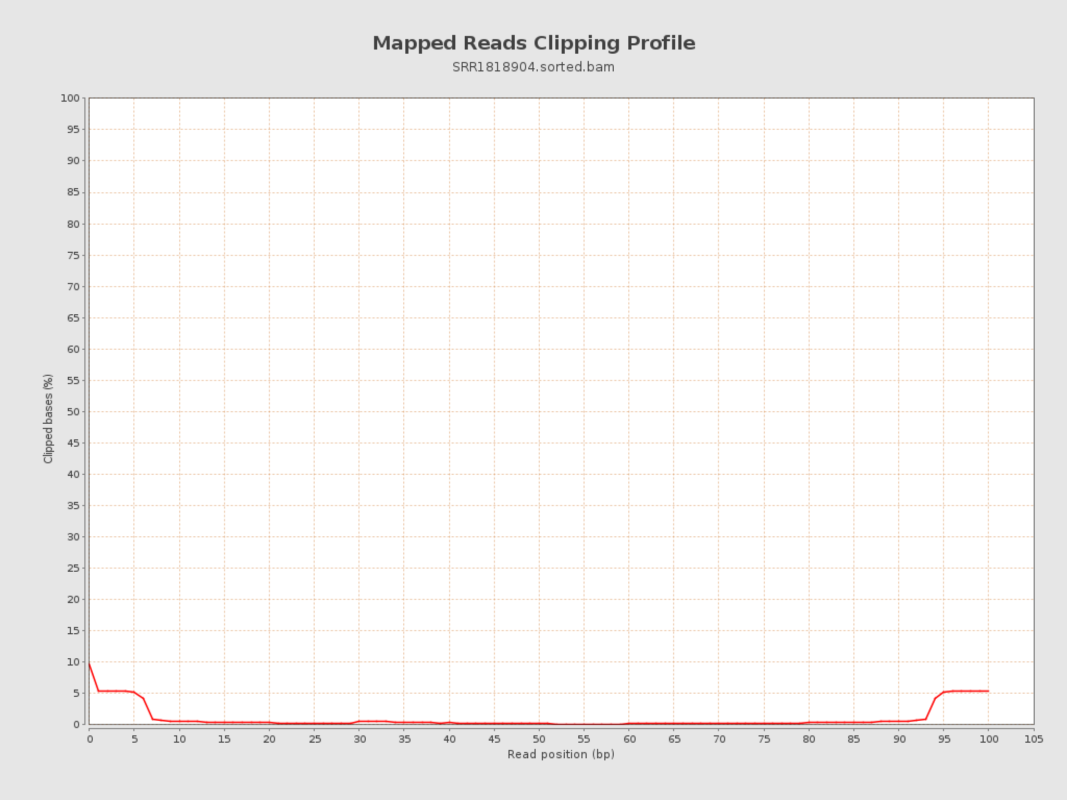
8. Results : Mapped Reads Nucleotide Content



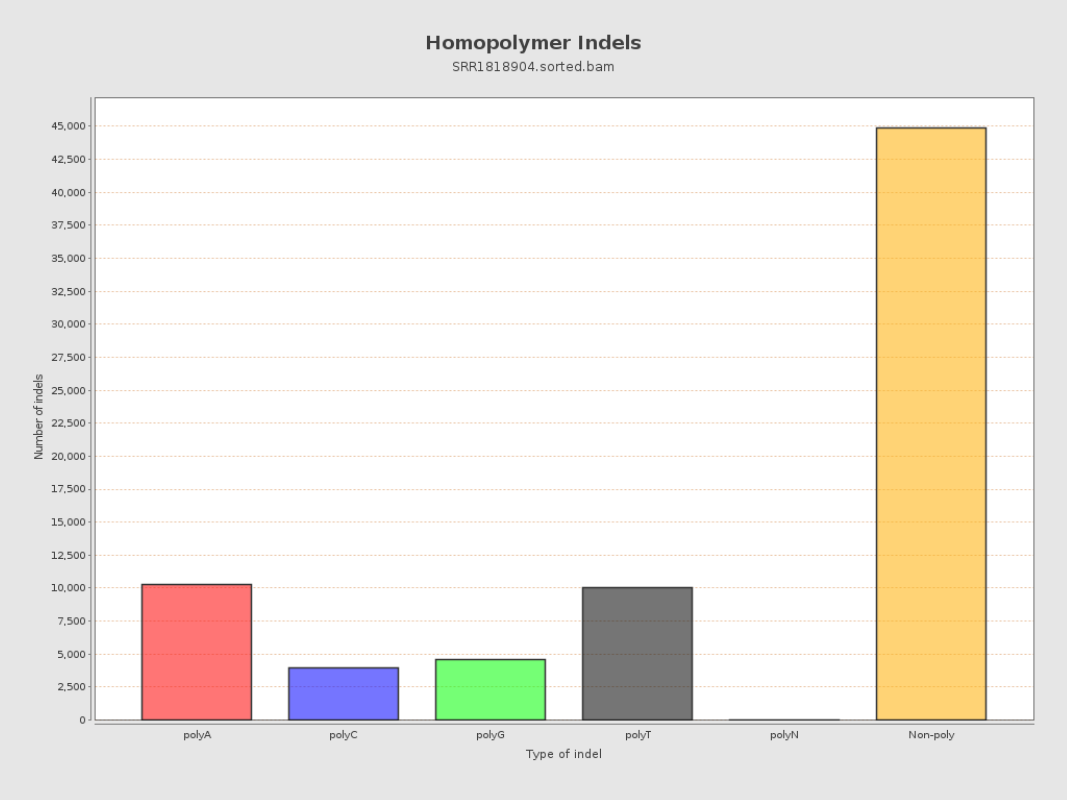
9. Results : Mapped Reads GC-content Distribution



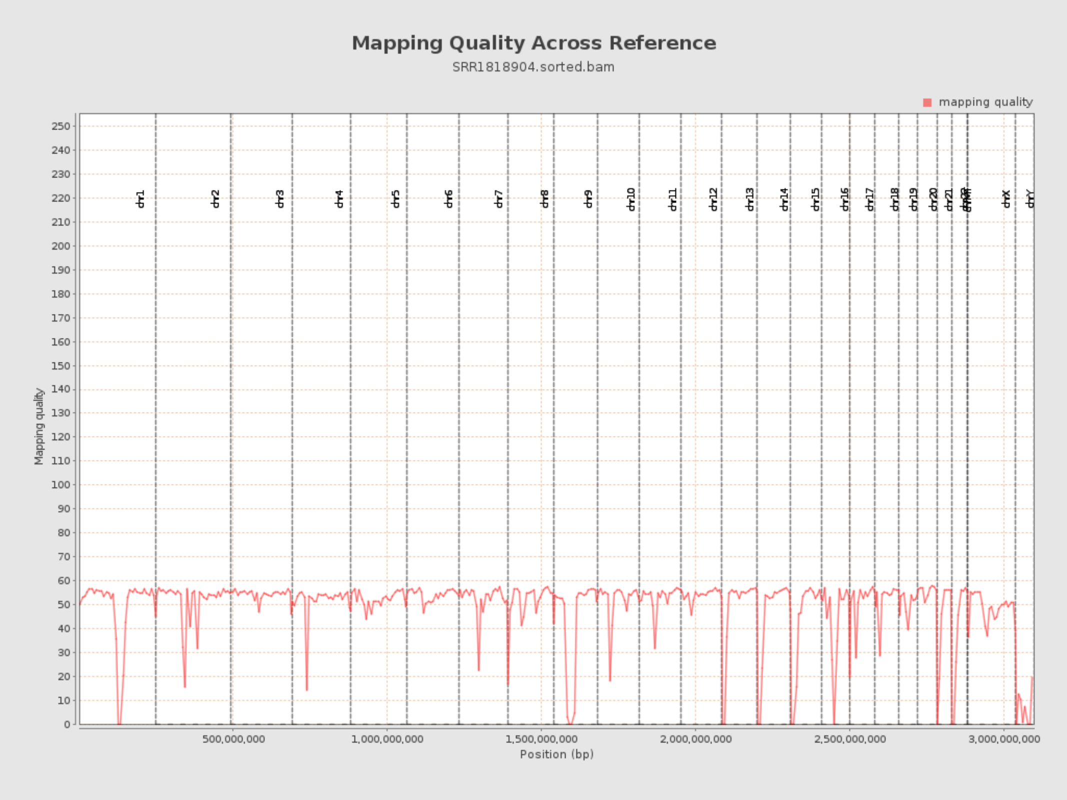
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram