Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 11:29:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818961.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_SRR1818961 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818961.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 11:29:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818961.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,467,680
Mapped reads	1,438,714 / 98.03%
Unmapped reads	28,966 / 1.97%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	26,495 / 1.81%
Read min/max/mean length	30 / 101 / 101.69
Duplicated reads (estimated)	702,436 / 47.86%
Duplication rate	39.5%
Clipped reads	1,462,239 / 99.63%

2.2. ACGT Content

Number/percentage of A's	37,623,602 / 28.45%
Number/percentage of C's	29,273,949 / 22.13%
Number/percentage of T's	37,942,188 / 28.69%
Number/percentage of G's	27,414,515 / 20.73%
Number/percentage of N's	5,842 / 0%
GC Percentage	42.86%

2.3. Coverage

Mean	0.0428

Standard Deviation	0.6448

2.4. Mapping Quality

Mean Mapping Quality	49.03

2.5. Mismatches and indels

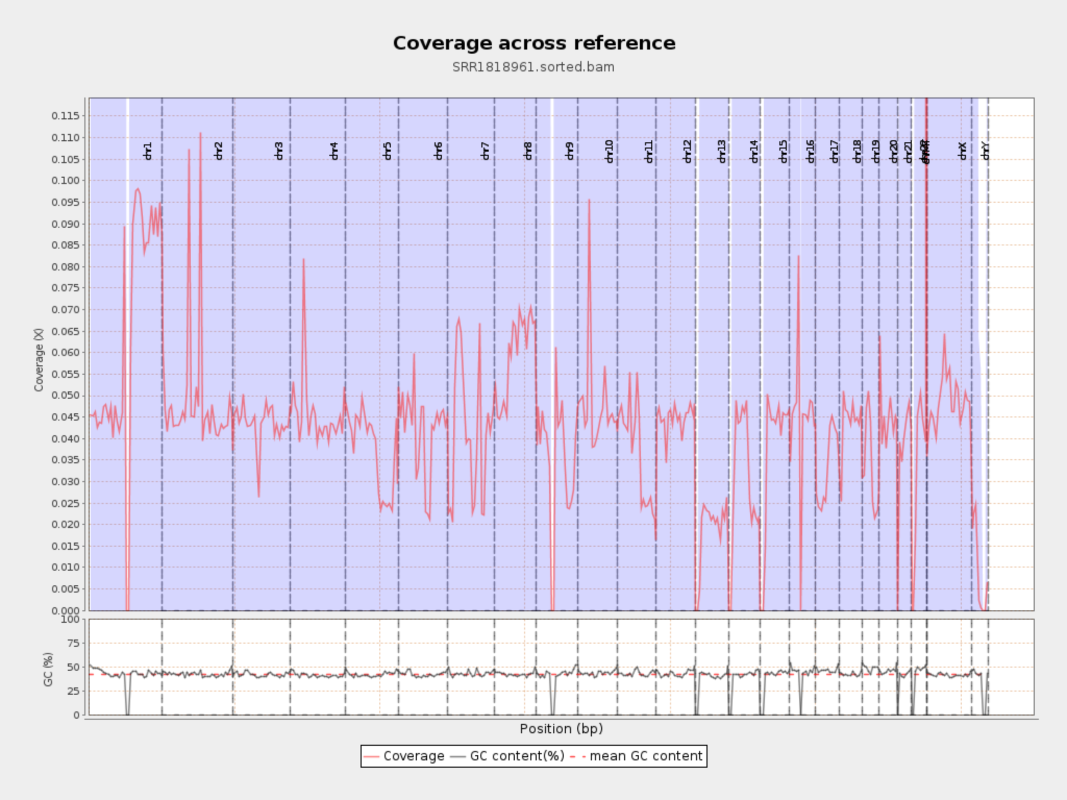
General error rate	0.78%
Mismatches	986,526
Insertions	18,802
Mapped reads with at least one insertion	1.25%
Deletions	52,527
Mapped reads with at least one deletion	3.56%
Homopolymer indels	41.25%

2.6. Chromosome stats

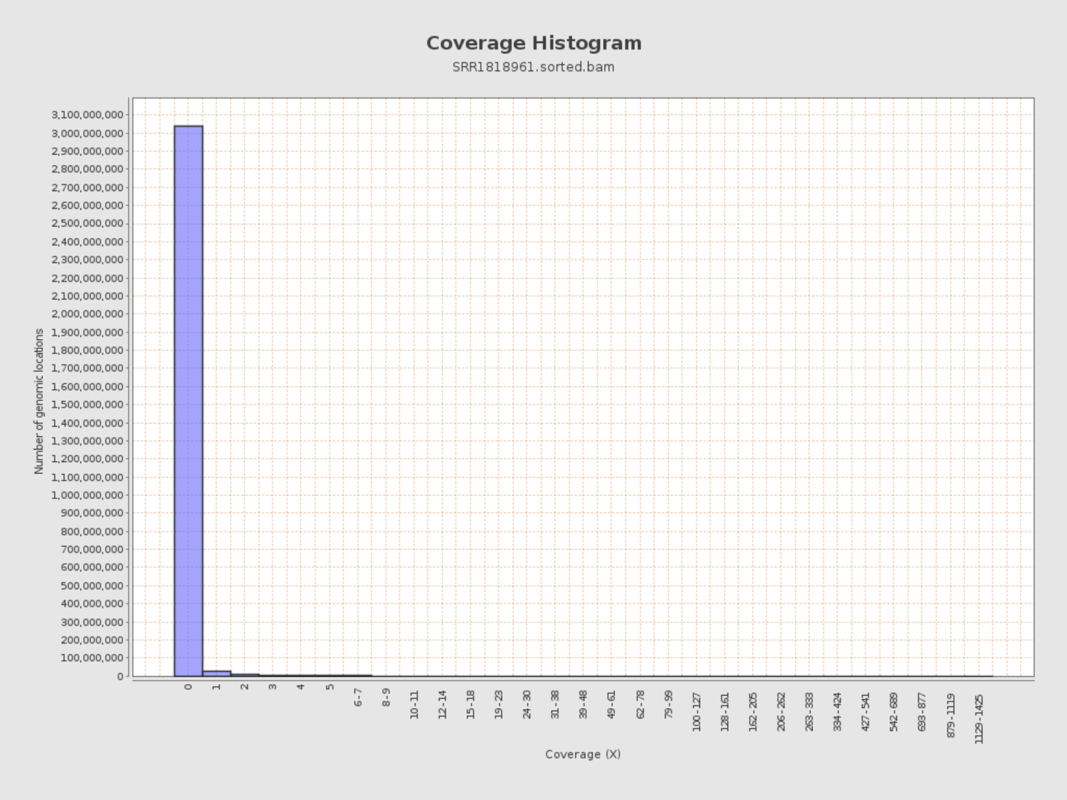
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15702752	0.063	0.9708
chr2	243199373	11997464	0.0493	1.1656
chr3	198022430	8587763	0.0434	0.4098
chr4	191154276	8740255	0.0457	0.4769
chr5	180915260	6752937	0.0373	0.4023
chr6	171115067	7188355	0.042	0.4543
chr7	159138663	6537155	0.0411	0.4682

chr8	146364022	8730629	0.0597	0.5619
chr9	141213431	4895122	0.0347	0.6127
chr10	135534747	6484808	0.0478	0.8046
chr11	135006516	4970246	0.0368	0.4376
chr12	133851895	5982872	0.0447	0.43
chr13	115169878	2118105	0.0184	0.261
chr14	107349540	3218999	0.03	0.3853
chr15	102531392	3771804	0.0368	0.379
chr16	90354753	4054186	0.0449	0.8565
chr17	81195210	2721715	0.0335	0.3996
chr18	78077248	3392899	0.0435	0.7279
chr19	59128983	2034385	0.0344	0.775
chr20	63025520	2844086	0.0451	0.4544
chr21	48129895	1816565	0.0377	0.4128
chr22	51304566	1607340	0.0313	0.3937
chrMT	16571	112670	6.7992	5.9769
chrX	155270560	7561621	0.0487	0.5034
chrY	59373566	535849	0.009	0.8539

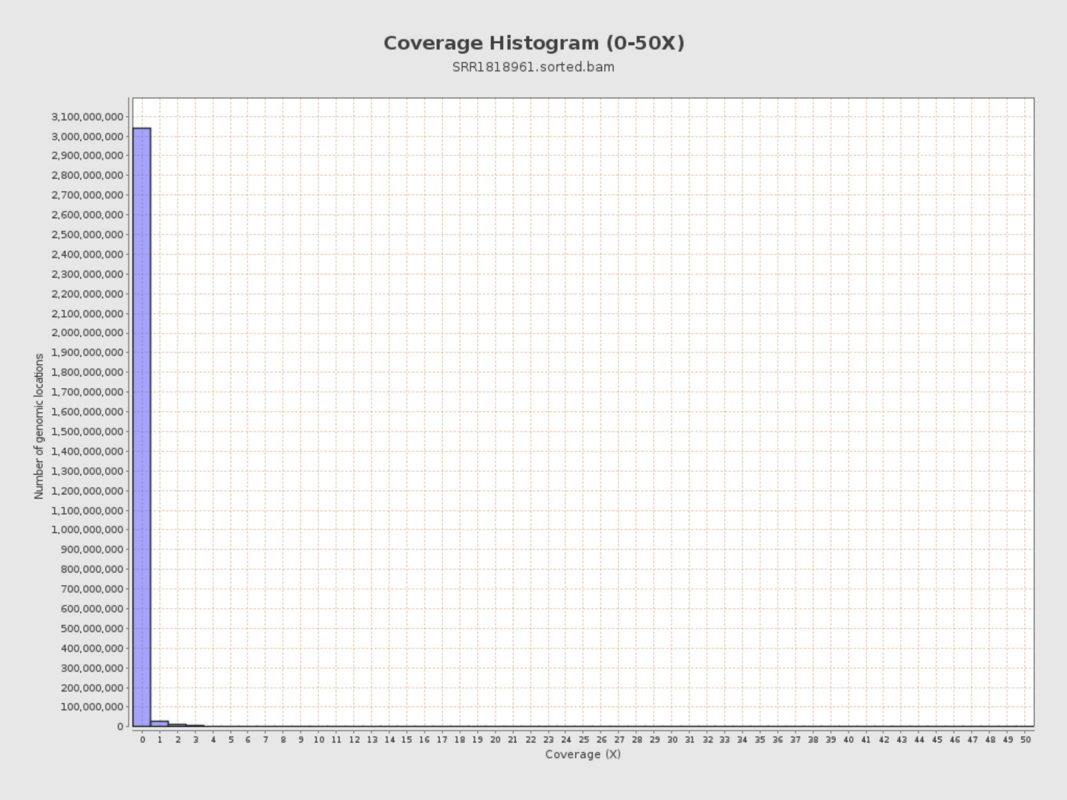
3. Results : Coverage across reference



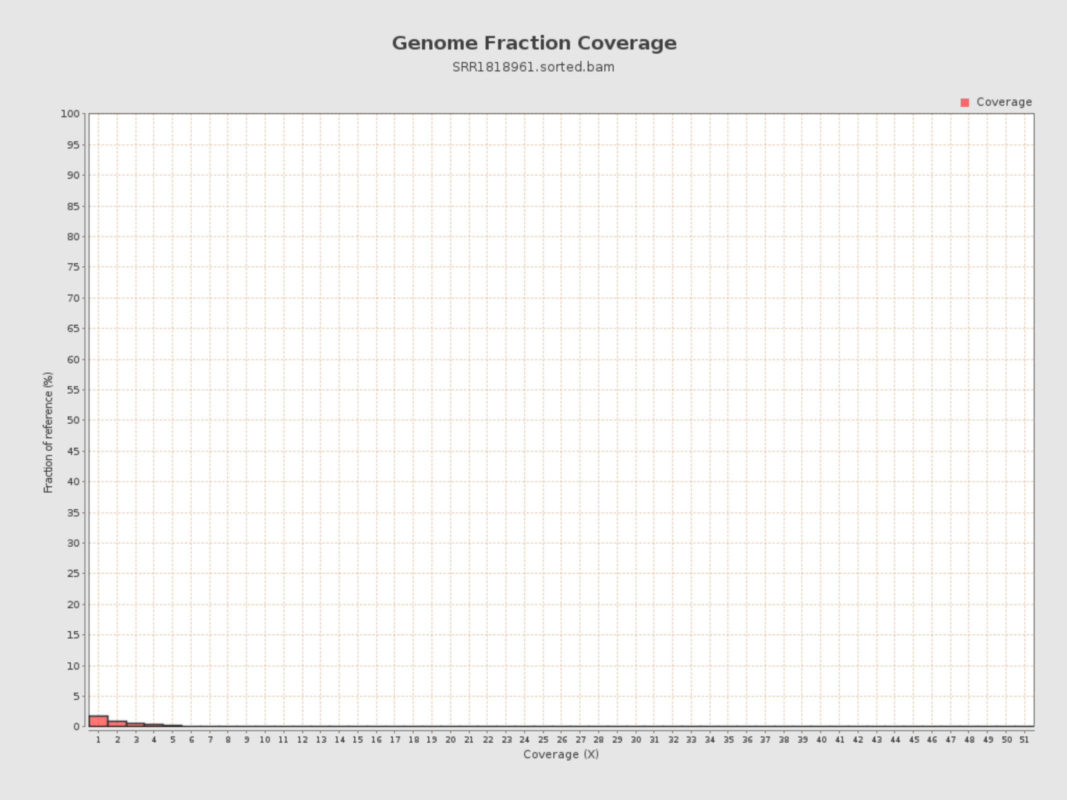
4. Results : Coverage Histogram



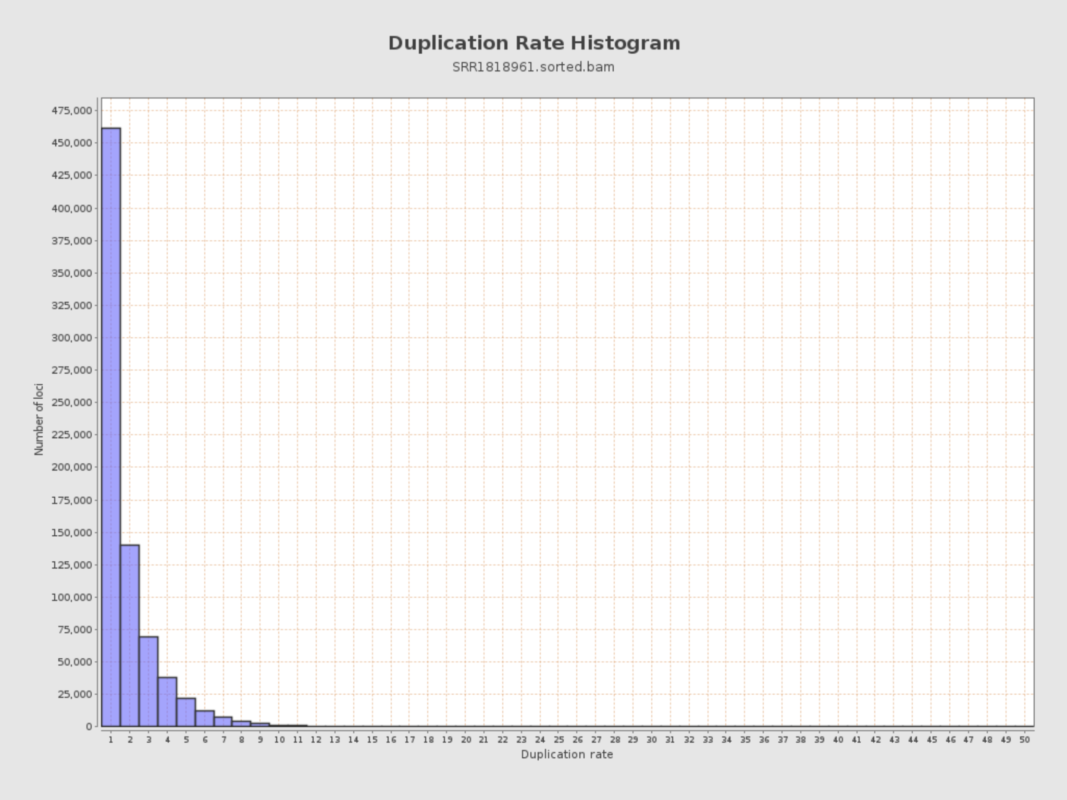
5. Results : Coverage Histogram (0-50X)



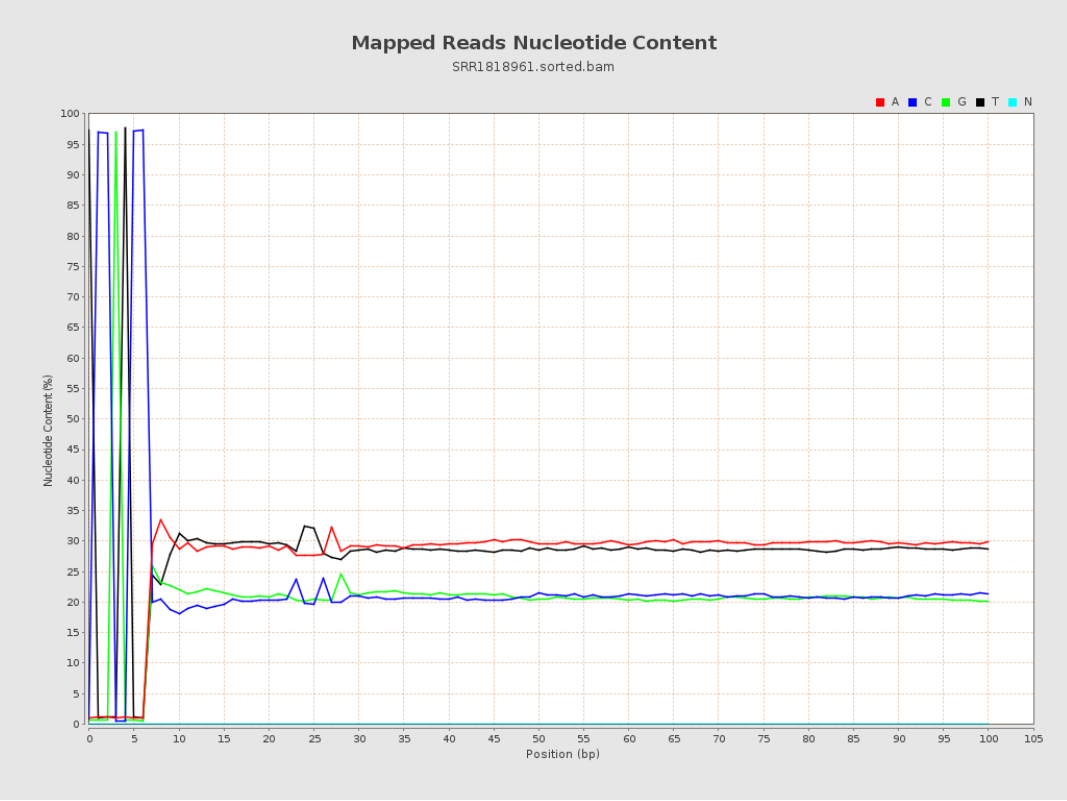
6. Results : Genome Fraction Coverage



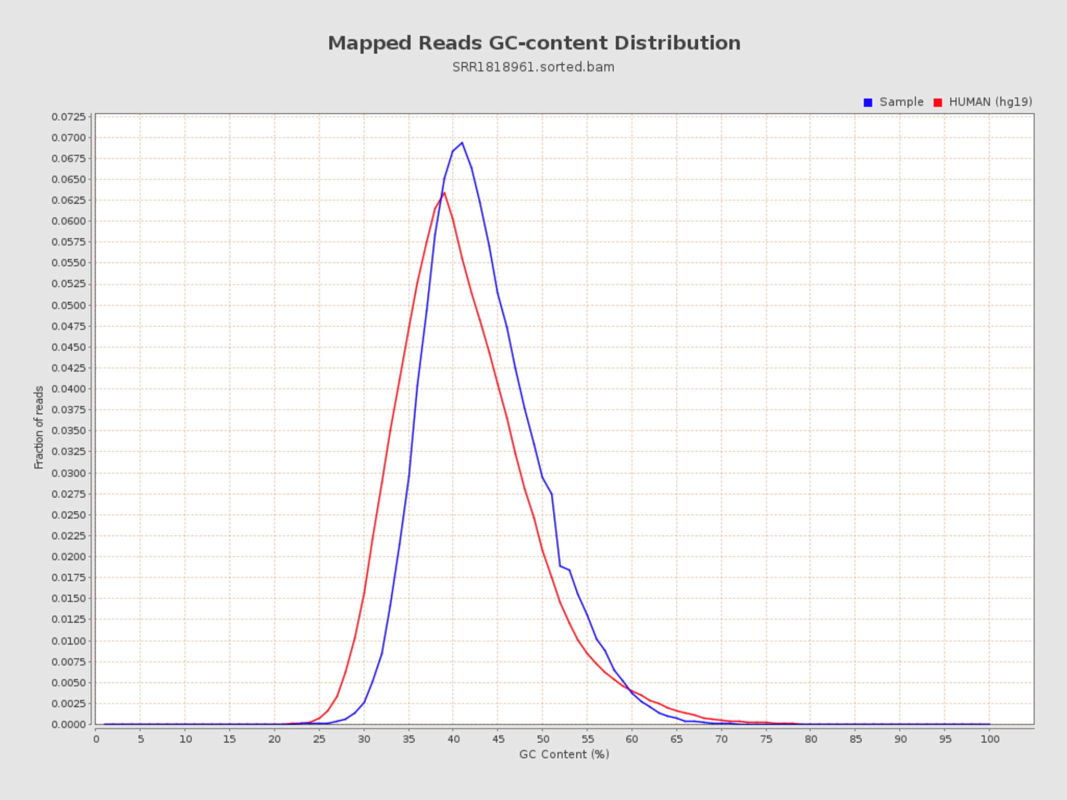
7. Results : Duplication Rate Histogram



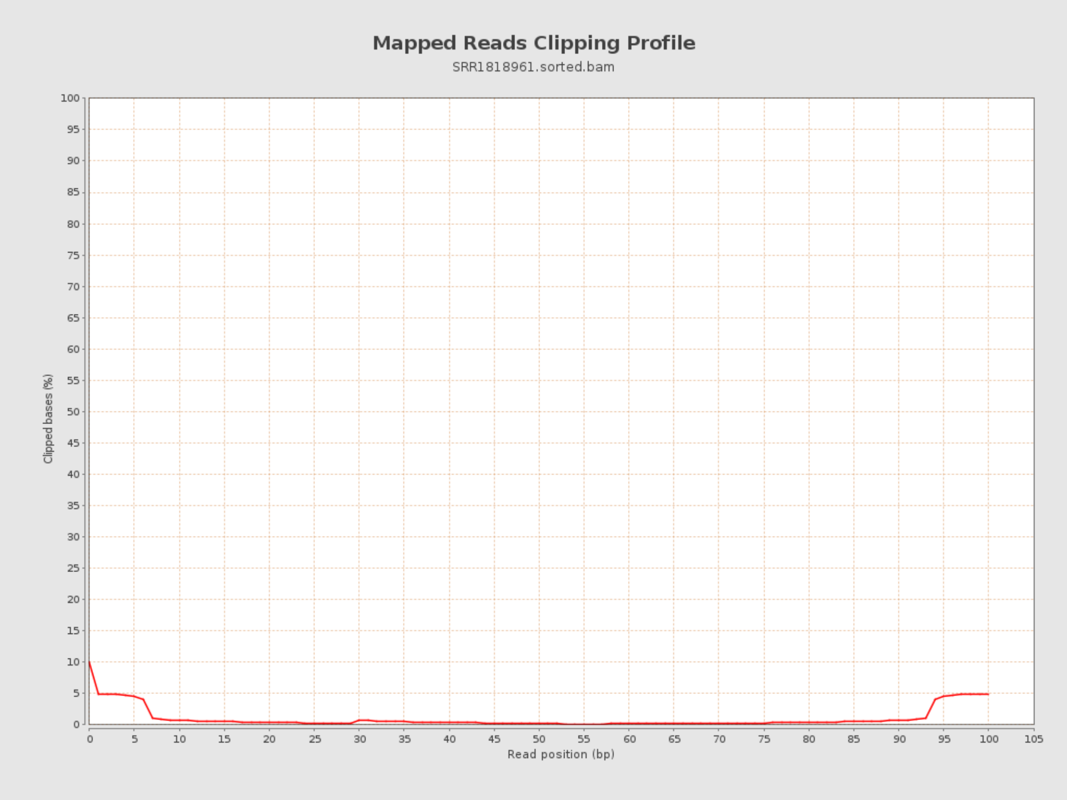
8. Results : Mapped Reads Nucleotide Content



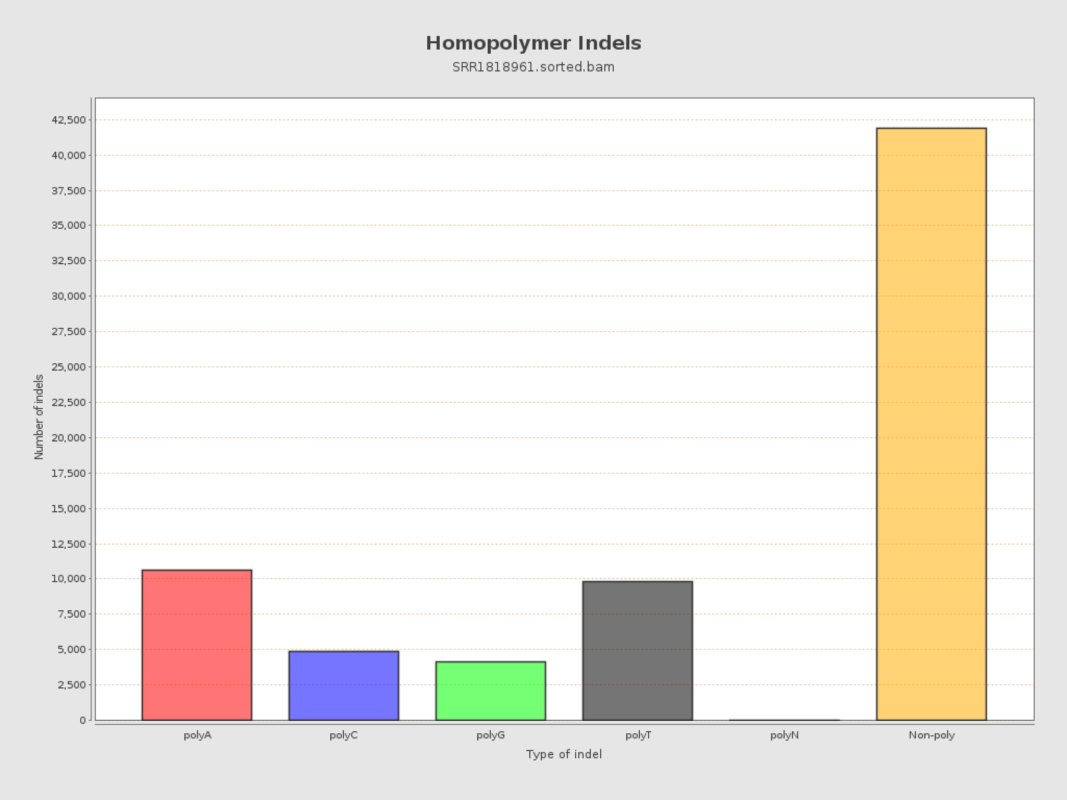
9. Results : Mapped Reads GC-content Distribution



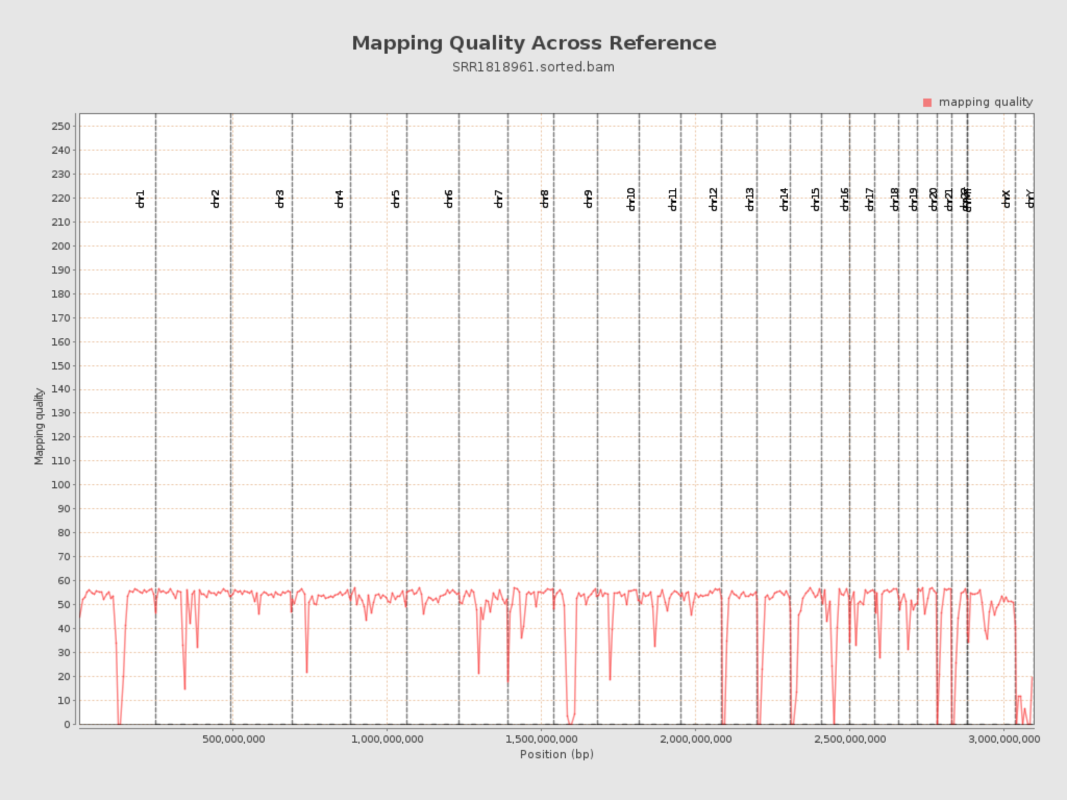
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram