Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 10:41:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818952.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_SRR1818952 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818952.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 10:41:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818952.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,960,051
Mapped reads	2,915,681 / 98.5%
Unmapped reads	44,370 / 1.5%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	35,016 / 1.18%
Read min/max/mean length	30 / 101 / 101.46
Duplicated reads (estimated)	1,363,105 / 46.05%
Duplication rate	38.58%
Clipped reads	2,928,966 / 98.95%

2.2. ACGT Content

Number/percentage of A's	78,592,006 / 29.07%
Number/percentage of C's	58,823,627 / 21.76%
Number/percentage of T's	75,529,918 / 27.94%
Number/percentage of G's	57,367,015 / 21.22%
Number/percentage of N's	11,917 / 0%
GC Percentage	42.98%

2.3. Coverage

Mean	0.0874

Standard Deviation	0.8935

2.4. Mapping Quality

Mean Mapping Quality	49.46

2.5. Mismatches and indels

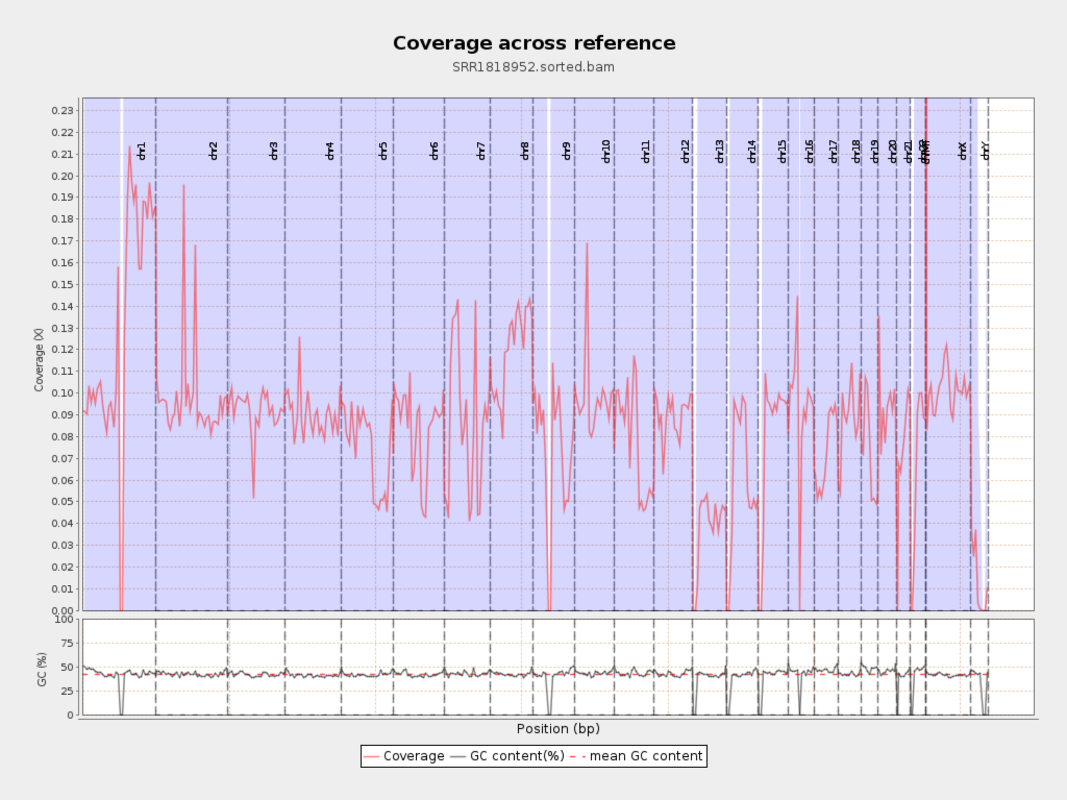
General error rate	0.67%
Mismatches	1,723,705
Insertions	37,523
Mapped reads with at least one insertion	1.25%
Deletions	83,463
Mapped reads with at least one deletion	2.8%
Homopolymer indels	41.59%

2.6. Chromosome stats

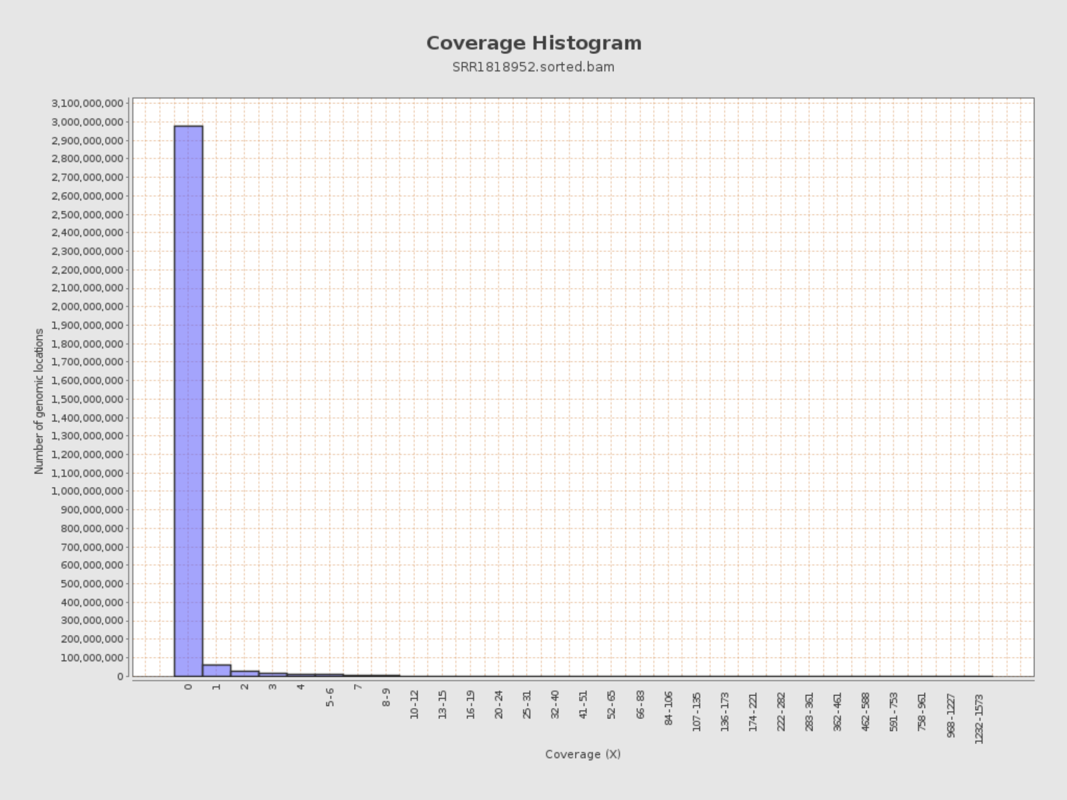
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	32273054	0.1295	1.54
chr2	243199373	23796048	0.0978	1.3523
chr3	198022430	18157901	0.0917	0.5959
chr4	191154276	17266868	0.0903	0.6495
chr5	180915260	13617882	0.0753	0.5518
chr6	171115067	14372464	0.084	0.6168
chr7	159138663	13706448	0.0861	0.7422

chr8	146364022	17541453	0.1198	0.7773
chr9	141213431	10224874	0.0724	0.9656
chr10	135534747	13208360	0.0975	1.0765
chr11	135006516	10433053	0.0773	0.6505
chr12	133851895	12082495	0.0903	0.5954
chr13	115169878	4381802	0.038	0.3728
chr14	107349540	6570800	0.0612	0.5501
chr15	102531392	8015972	0.0782	0.5546
chr16	90354753	8251449	0.0913	0.9517
chr17	81195210	5949308	0.0733	0.594
chr18	78077248	6877746	0.0881	1.2469
chr19	59128983	4327057	0.0732	1.2981
chr20	63025520	5939168	0.0942	0.6432
chr21	48129895	3573301	0.0742	0.5854
chr22	51304566	3333990	0.065	0.5399
chrMT	16571	46762	2.8219	3.5984
chrX	155270560	15737325	0.1014	0.7666
chrY	59373566	791806	0.0133	0.7438

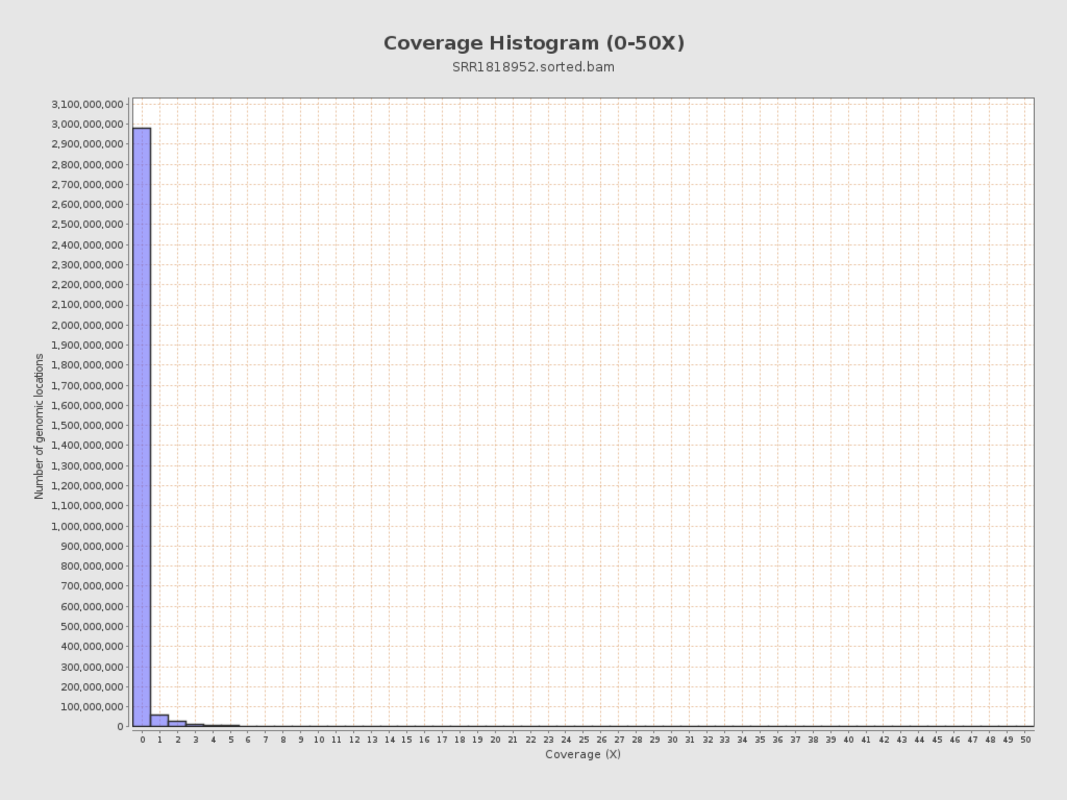
3. Results : Coverage across reference



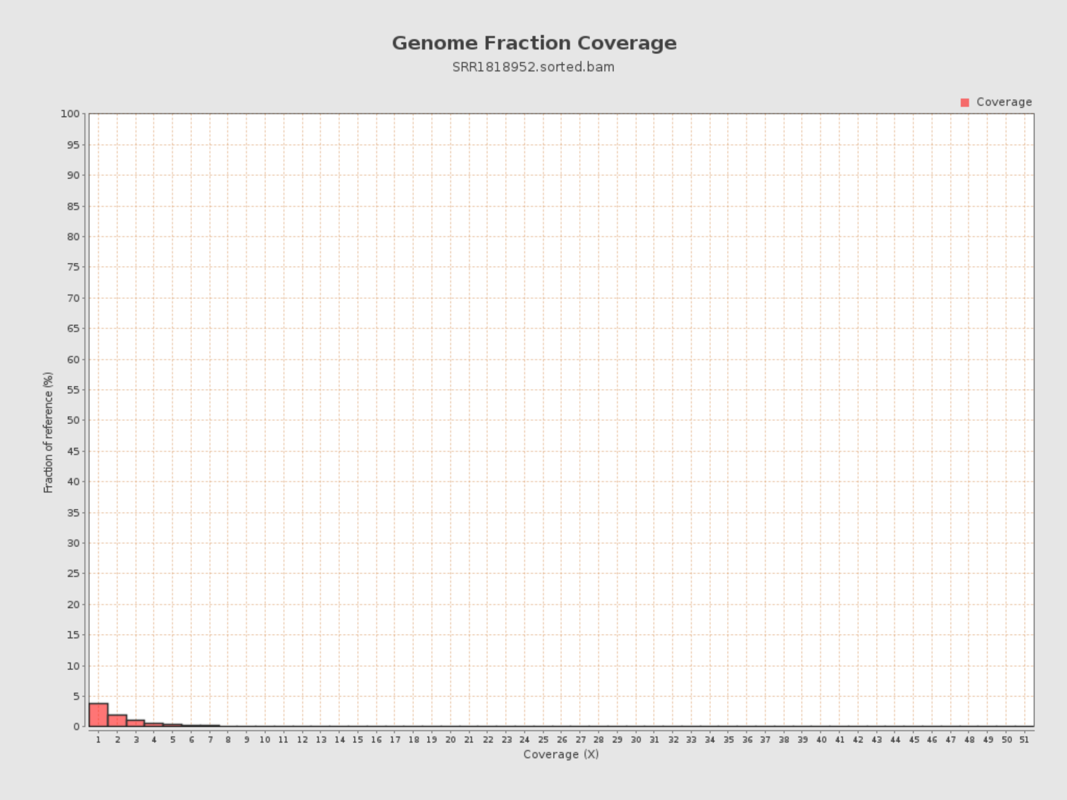
4. Results : Coverage Histogram



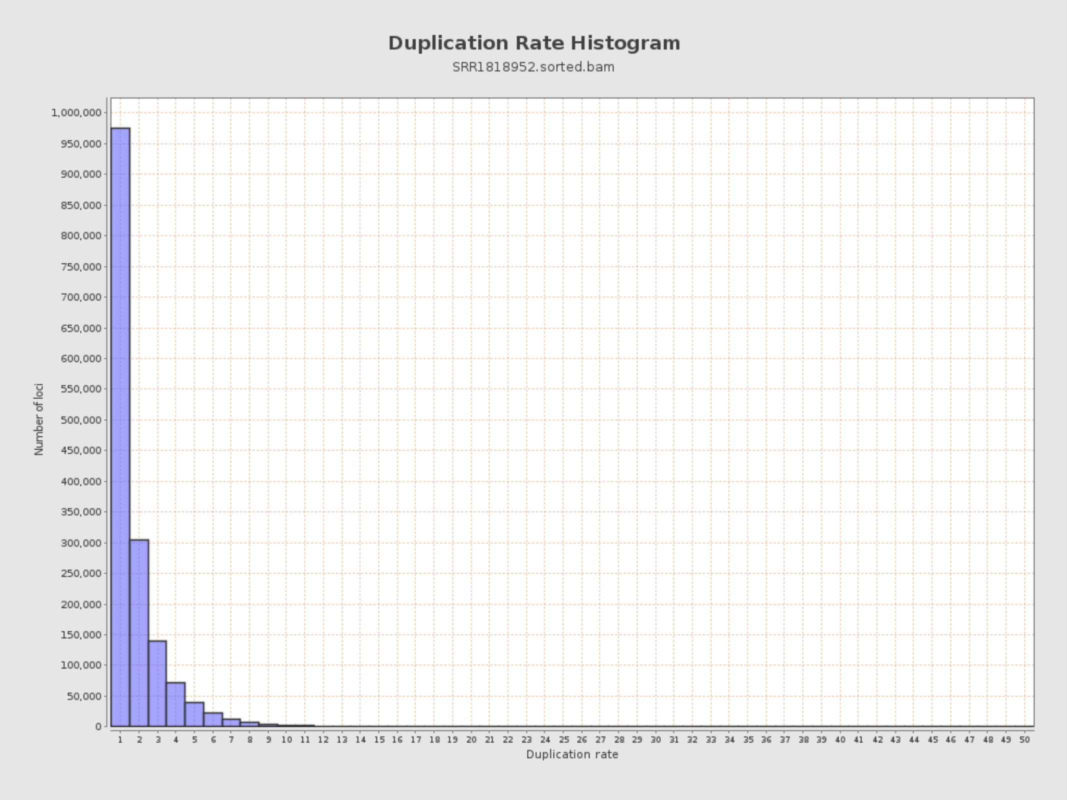
5. Results : Coverage Histogram (0-50X)



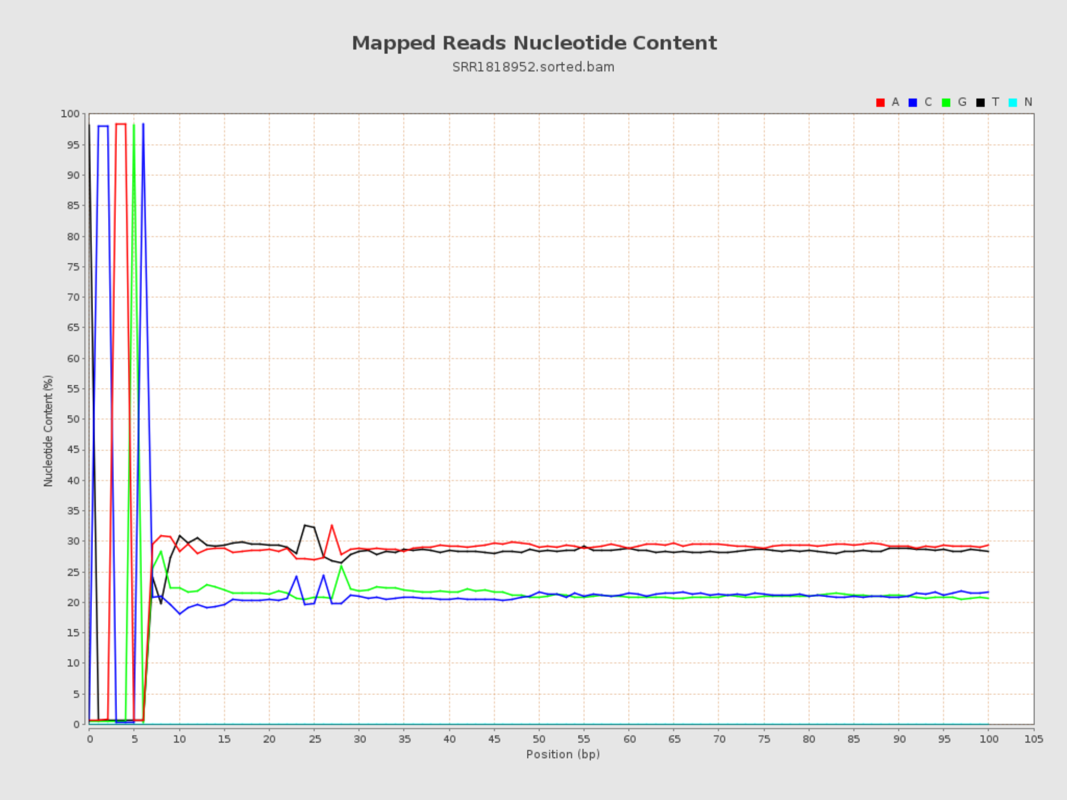
6. Results : Genome Fraction Coverage



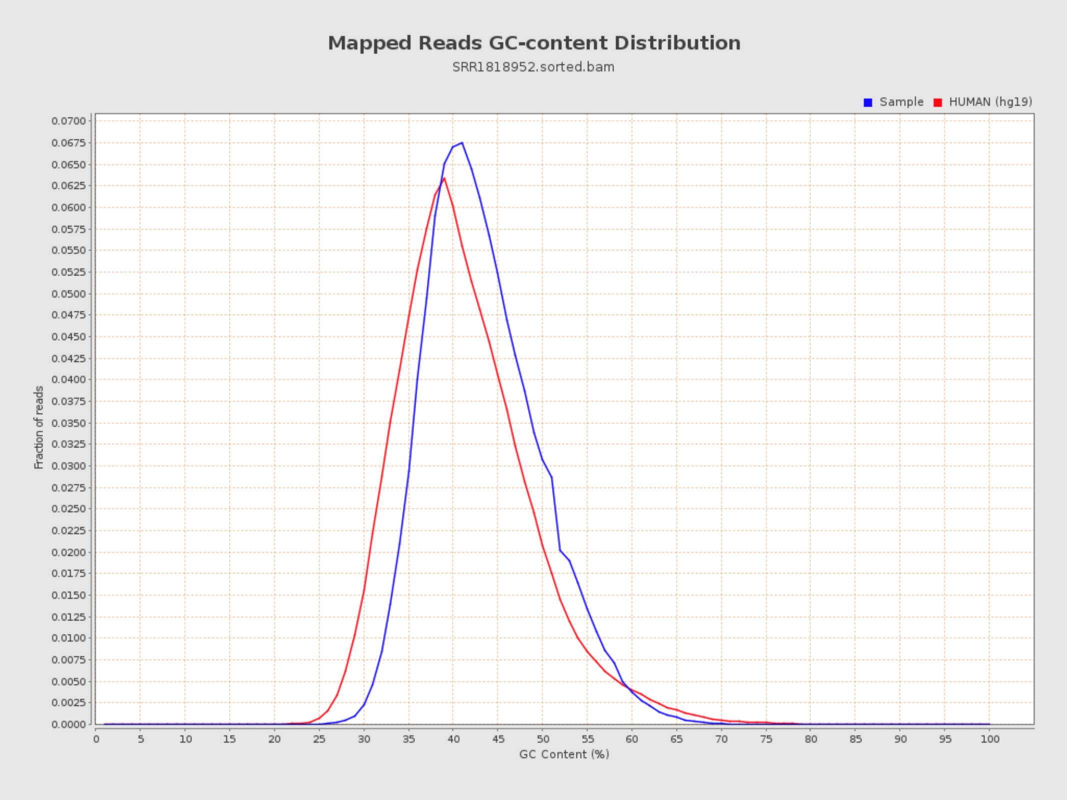
7. Results : Duplication Rate Histogram



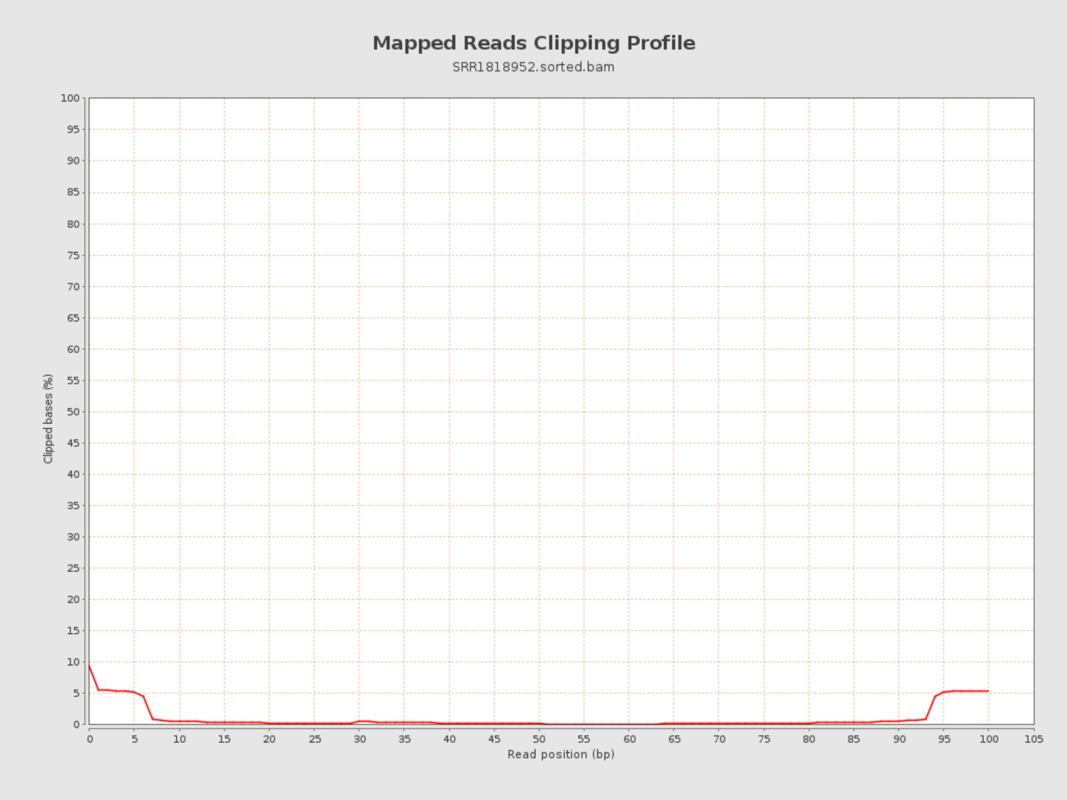
8. Results : Mapped Reads Nucleotide Content



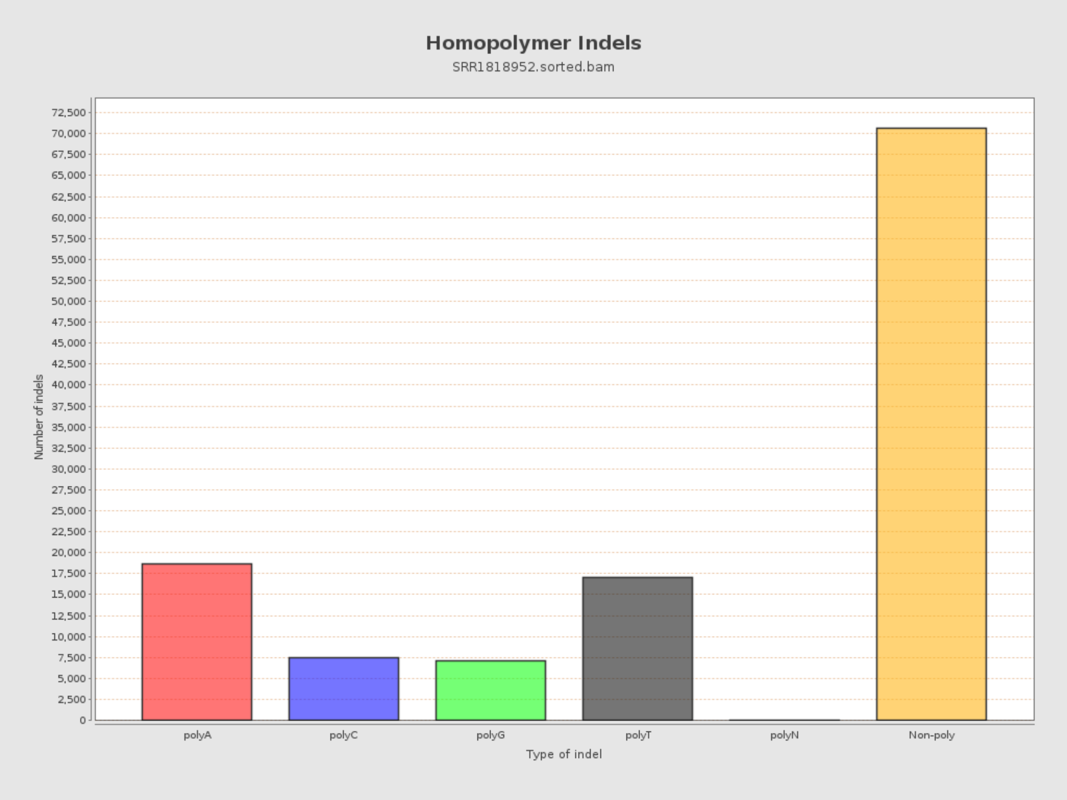
9. Results : Mapped Reads GC-content Distribution



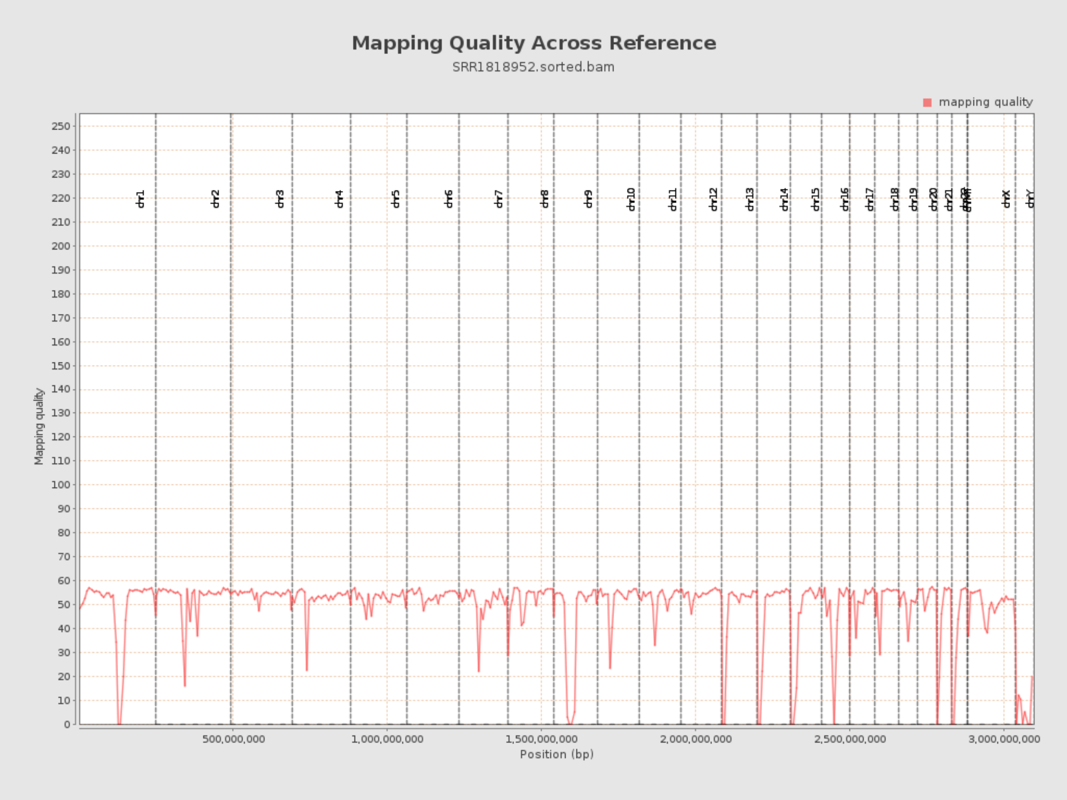
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram