Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 10:02:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818945.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_SRR1818945 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818945.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 10:02:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818945.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,182,538
Mapped reads	3,134,948 / 98.5%
Unmapped reads	47,590 / 1.5%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	42,250 / 1.33%
Read min/max/mean length	30 / 101 / 101.51
Duplicated reads (estimated)	1,565,614 / 49.19%
Duplication rate	41.49%
Clipped reads	3,163,390 / 99.4%

2.2. ACGT Content

Number/percentage of A's	84,584,883 / 29.15%
Number/percentage of C's	62,637,383 / 21.59%
Number/percentage of T's	82,101,879 / 28.29%
Number/percentage of G's	60,829,405 / 20.96%
Number/percentage of N's	13,404 / 0%
GC Percentage	42.55%

2.3. Coverage

Mean	0.0938

Standard Deviation	0.9719

2.4. Mapping Quality

Mean Mapping Quality	49.25

2.5. Mismatches and indels

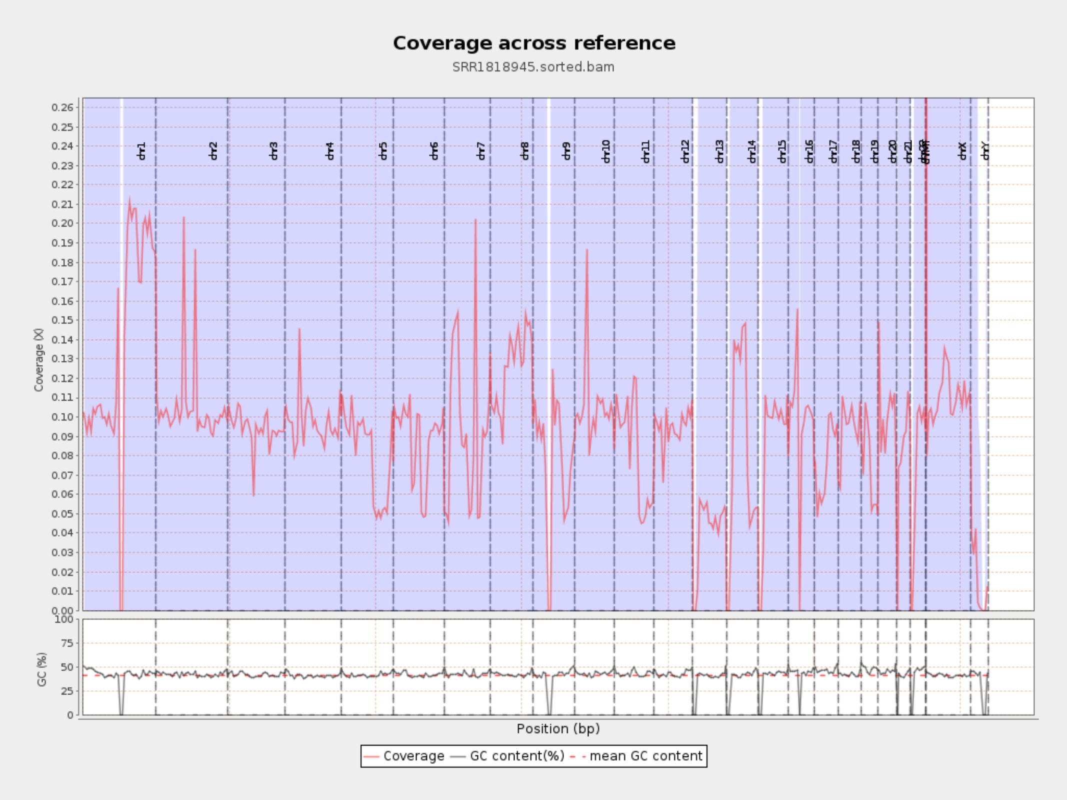
General error rate	0.68%
Mismatches	1,885,419
Insertions	37,420
Mapped reads with at least one insertion	1.16%
Deletions	89,542
Mapped reads with at least one deletion	2.79%
Homopolymer indels	42.8%

2.6. Chromosome stats

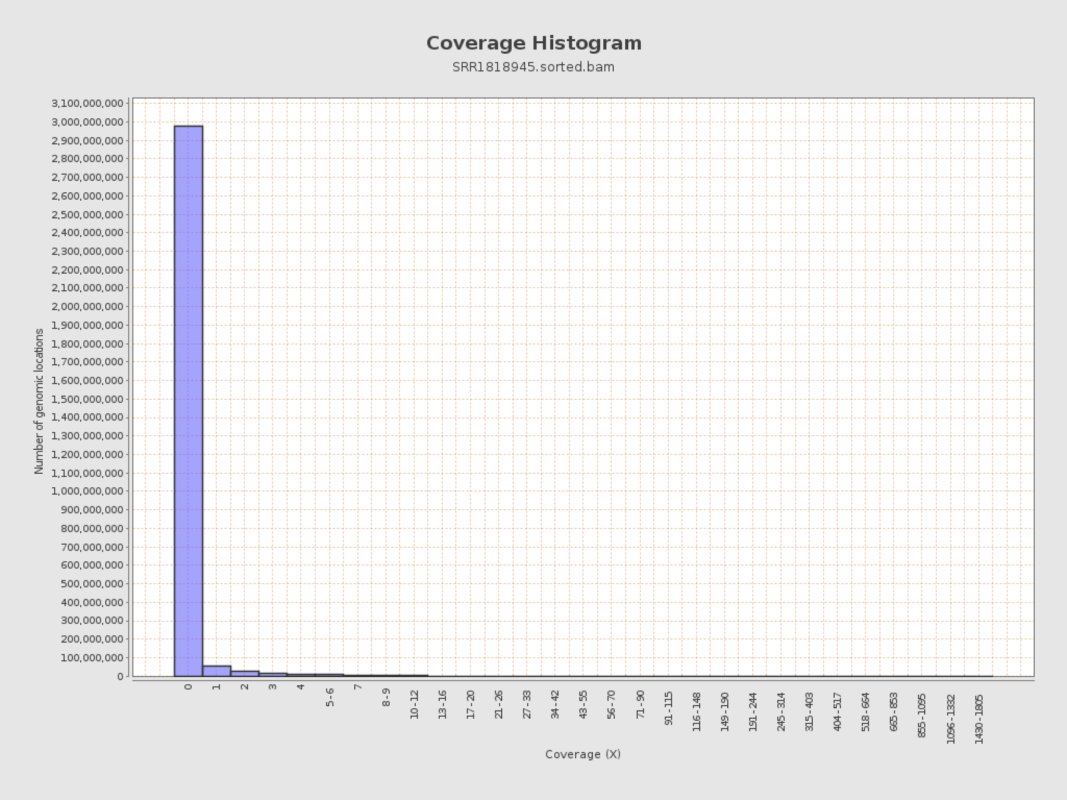
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	33933111	0.1361	1.6417
chr2	243199373	25752221	0.1059	1.4572
chr3	198022430	18670385	0.0943	0.6141
chr4	191154276	18698070	0.0978	0.7082
chr5	180915260	14793515	0.0818	0.6021
chr6	171115067	15218453	0.0889	0.654
chr7	159138663	14802016	0.093	0.8275

chr8	146364022	18471583	0.1262	0.8331
chr9	141213431	10825644	0.0767	1.1526
chr10	135534747	14248333	0.1051	1.2098
chr11	135006516	11027042	0.0817	0.7061
chr12	133851895	12712771	0.095	0.6405
chr13	115169878	4776815	0.0415	0.4017
chr14	107349540	9025563	0.0841	0.6544
chr15	102531392	8446754	0.0824	0.5827
chr16	90354753	8789082	0.0973	1.0735
chr17	81195210	6283429	0.0774	0.6344
chr18	78077248	7377867	0.0945	1.3163
chr19	59128983	4442329	0.0751	1.4247
chr20	63025520	6471542	0.1027	0.7004
chr21	48129895	3942242	0.0819	0.6693
chr22	51304566	3639962	0.0709	0.6008
chrMT	16571	25243	1.5233	2.3612
chrX	155270560	17066448	0.1099	0.7858
chrY	59373566	891696	0.015	0.8986

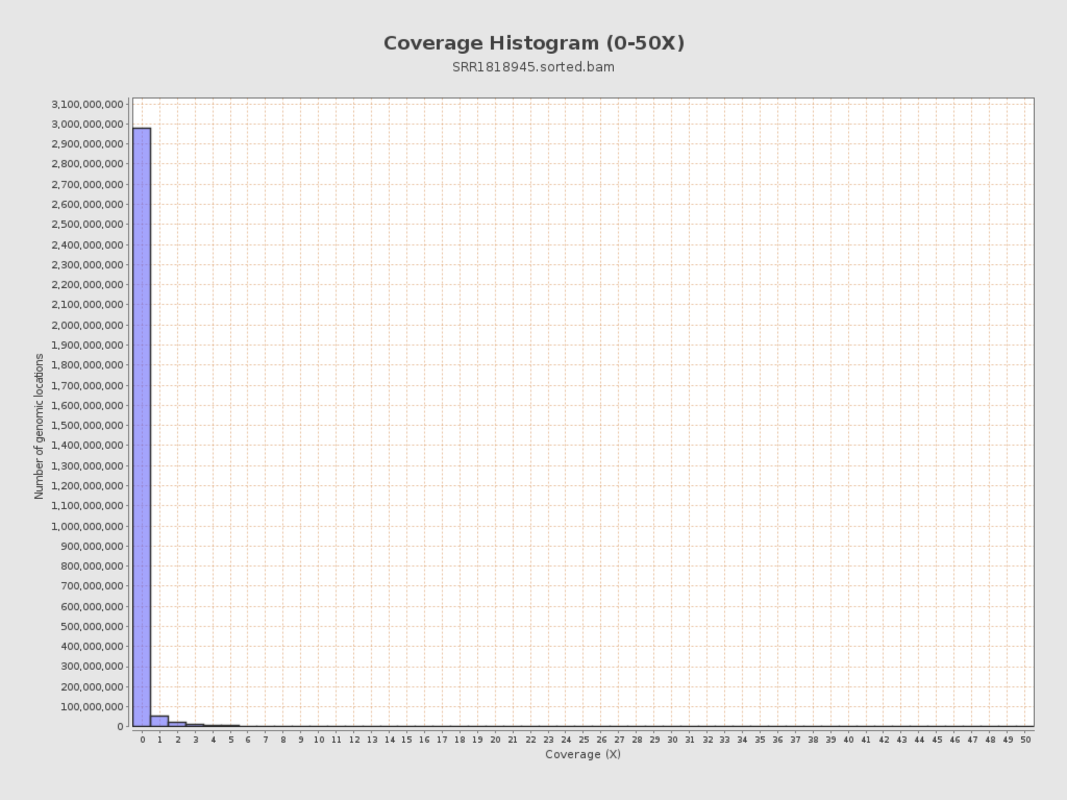
3. Results : Coverage across reference



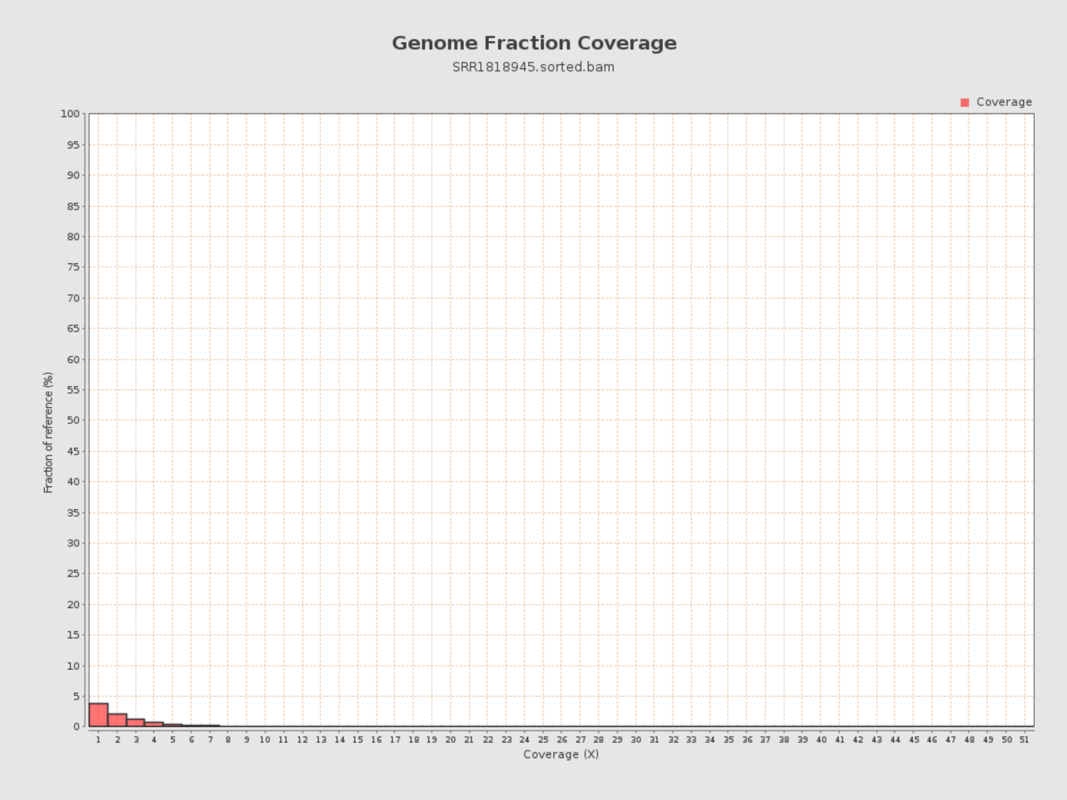
4. Results : Coverage Histogram



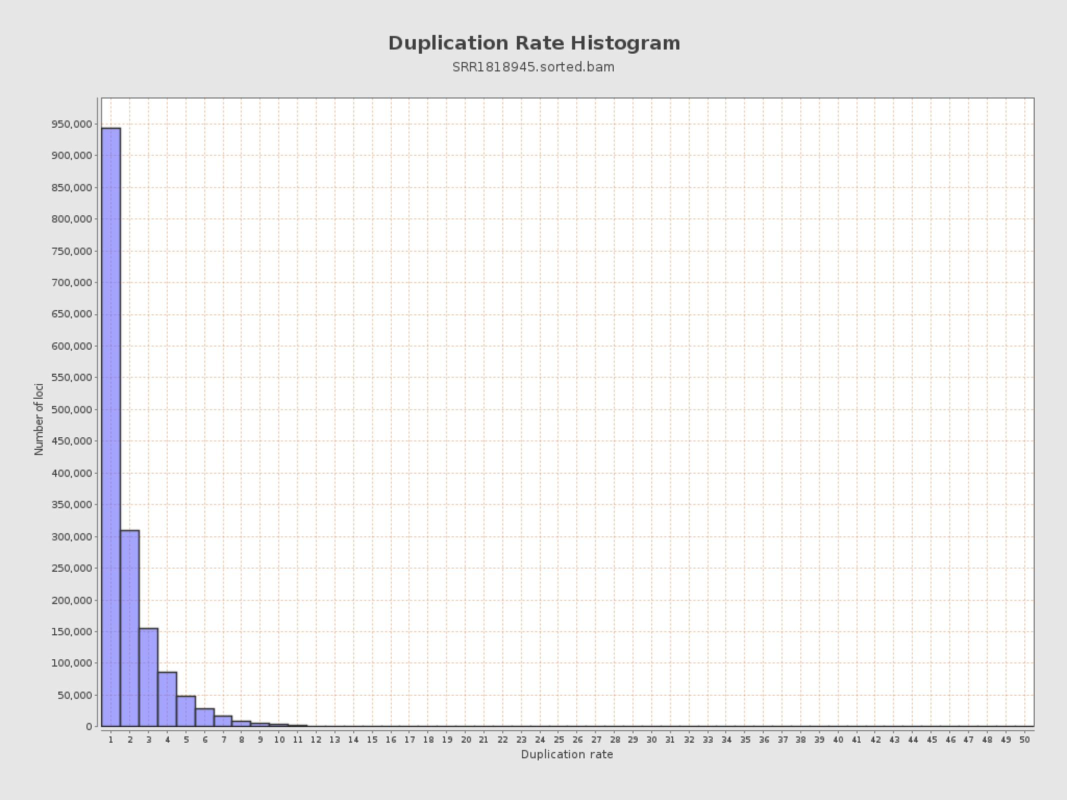
5. Results : Coverage Histogram (0-50X)



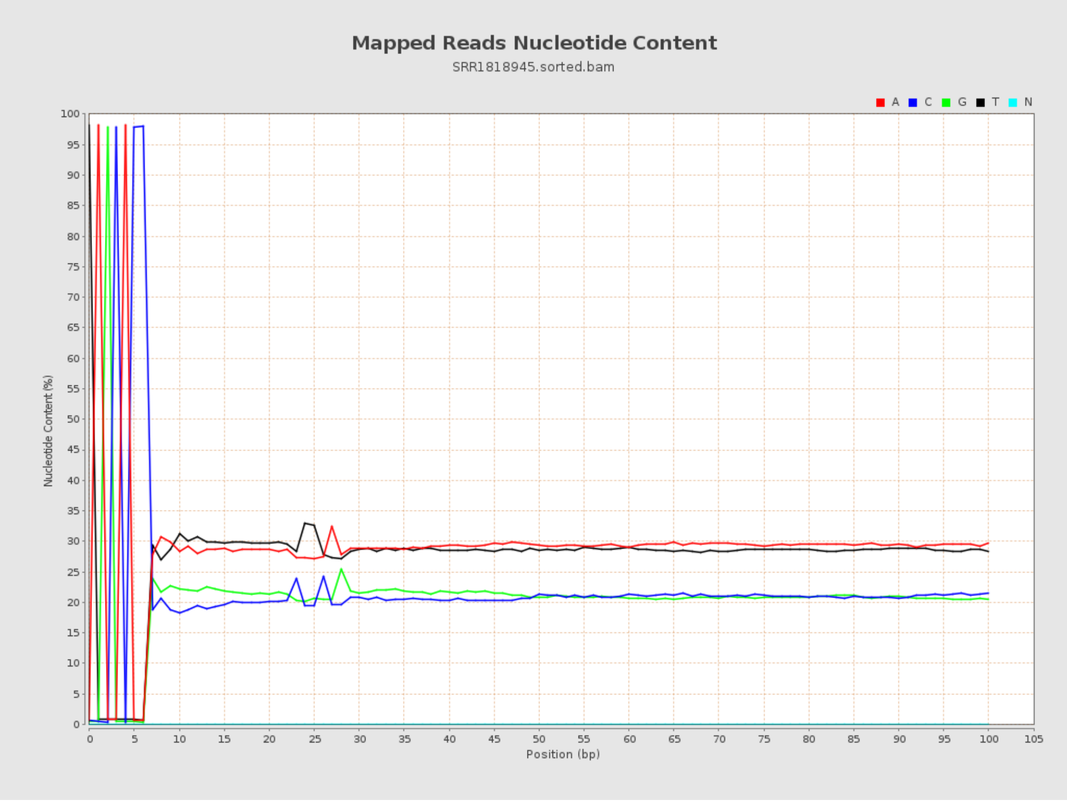
6. Results : Genome Fraction Coverage



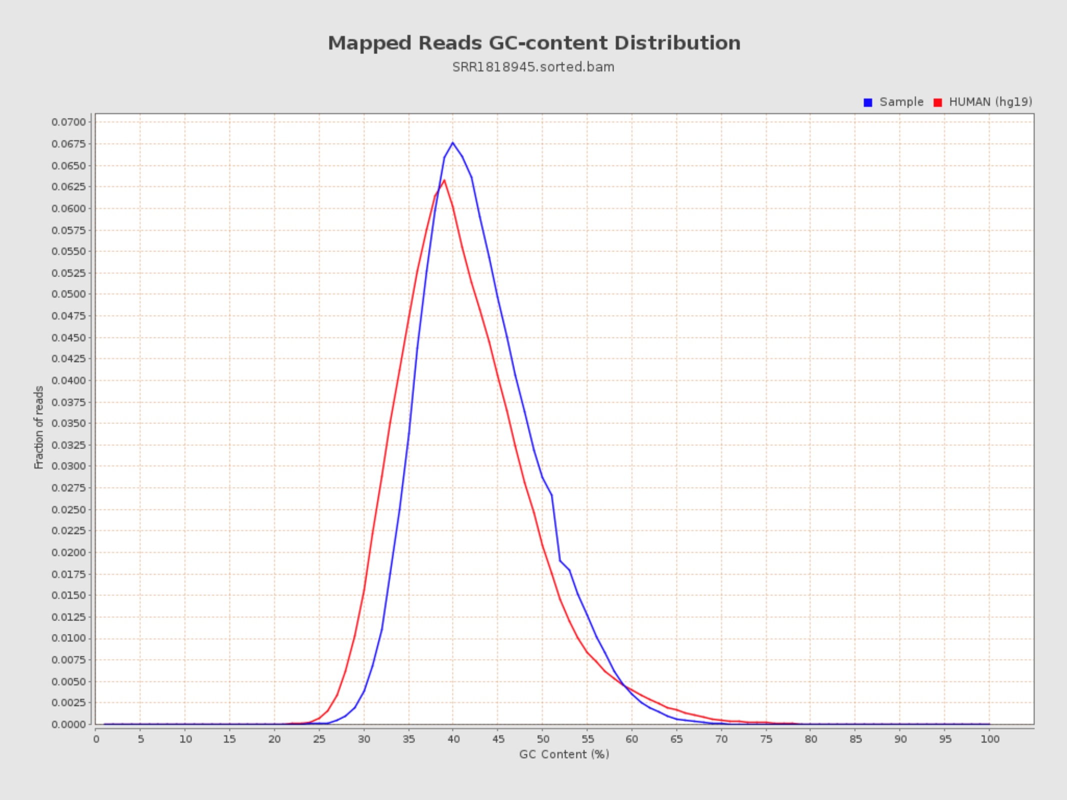
7. Results : Duplication Rate Histogram



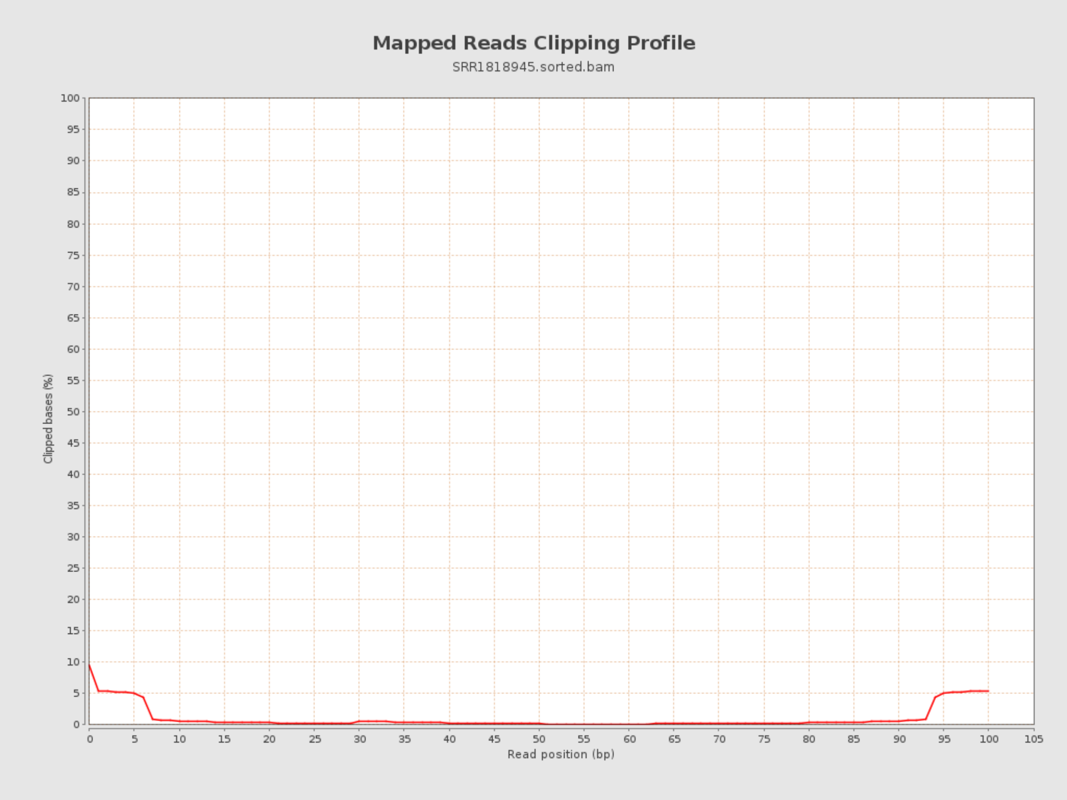
8. Results : Mapped Reads Nucleotide Content



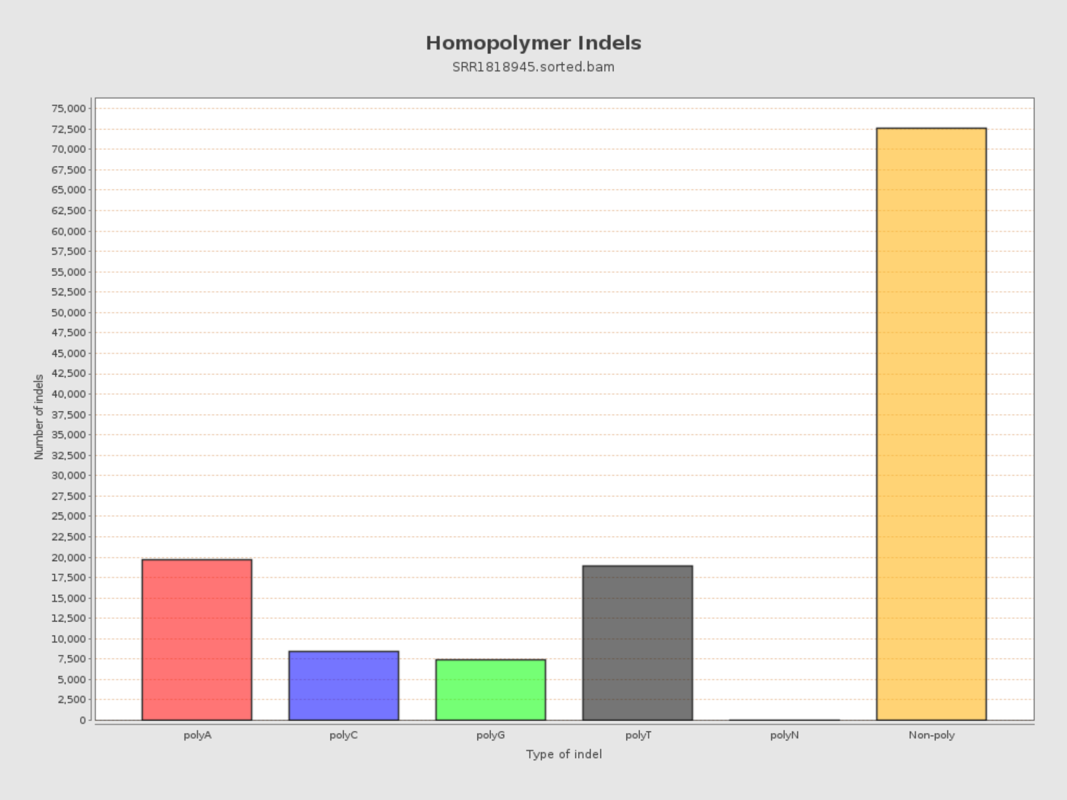
9. Results : Mapped Reads GC-content Distribution



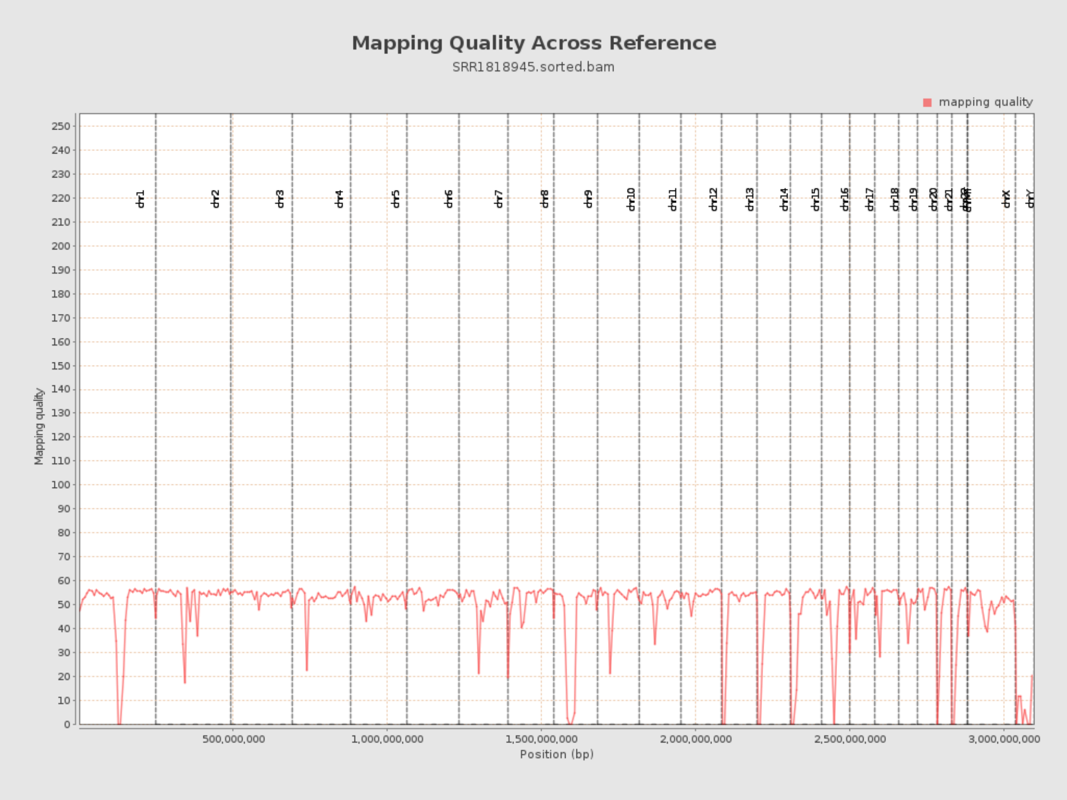
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram