Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 11:49:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818966.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_SRR1818966 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818966.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 11:49:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818966.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,257,458
Mapped reads	2,138,362 / 94.72%
Unmapped reads	119,096 / 5.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	36,186 / 1.6%
Read min/max/mean length	30 / 101 / 101.62
Duplicated reads (estimated)	1,069,659 / 47.38%
Duplication rate	42.42%
Clipped reads	2,166,645 / 95.98%

2.2. ACGT Content

Number/percentage of A's	56,958,017 / 28.82%
Number/percentage of C's	41,165,749 / 20.83%
Number/percentage of T's	57,419,557 / 29.05%
Number/percentage of G's	42,112,300 / 21.3%
Number/percentage of N's	9,783 / 0%
GC Percentage	42.13%

2.3. Coverage

Mean	0.0639

Standard Deviation	0.773

2.4. Mapping Quality

Mean Mapping Quality	49.06

2.5. Mismatches and indels

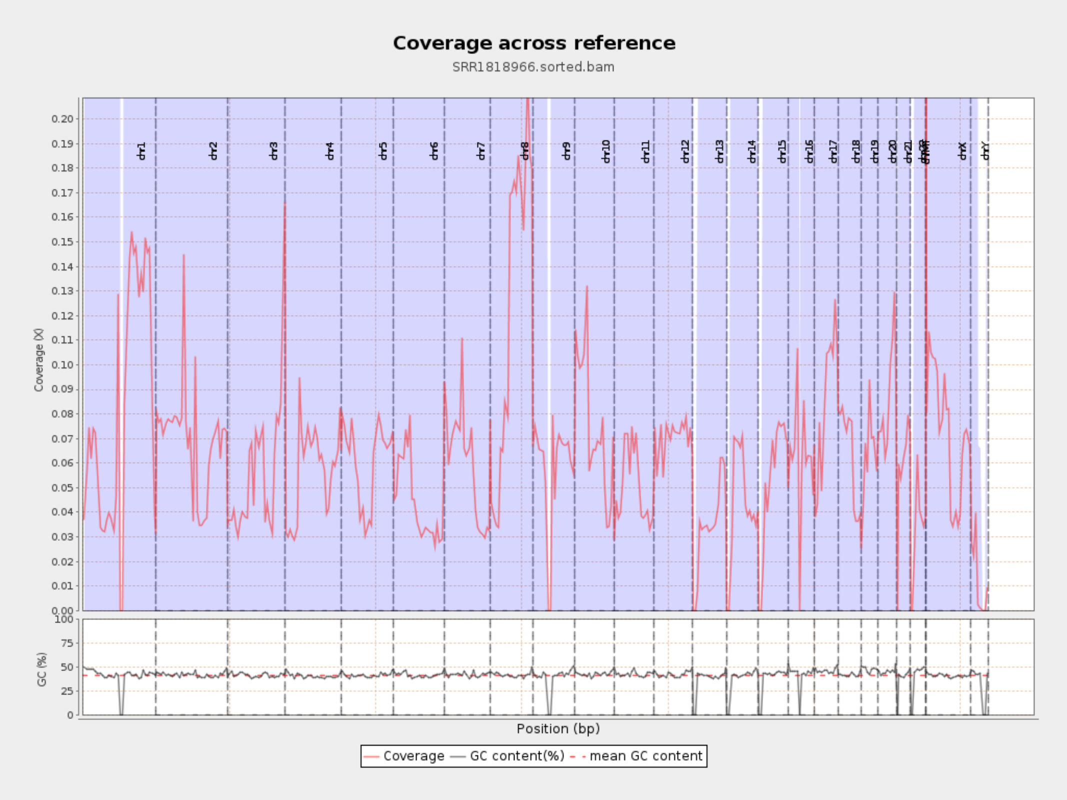
General error rate	0.66%
Mismatches	1,226,020
Insertions	30,548
Mapped reads with at least one insertion	1.39%
Deletions	64,110
Mapped reads with at least one deletion	2.94%
Homopolymer indels	42.09%

2.6. Chromosome stats

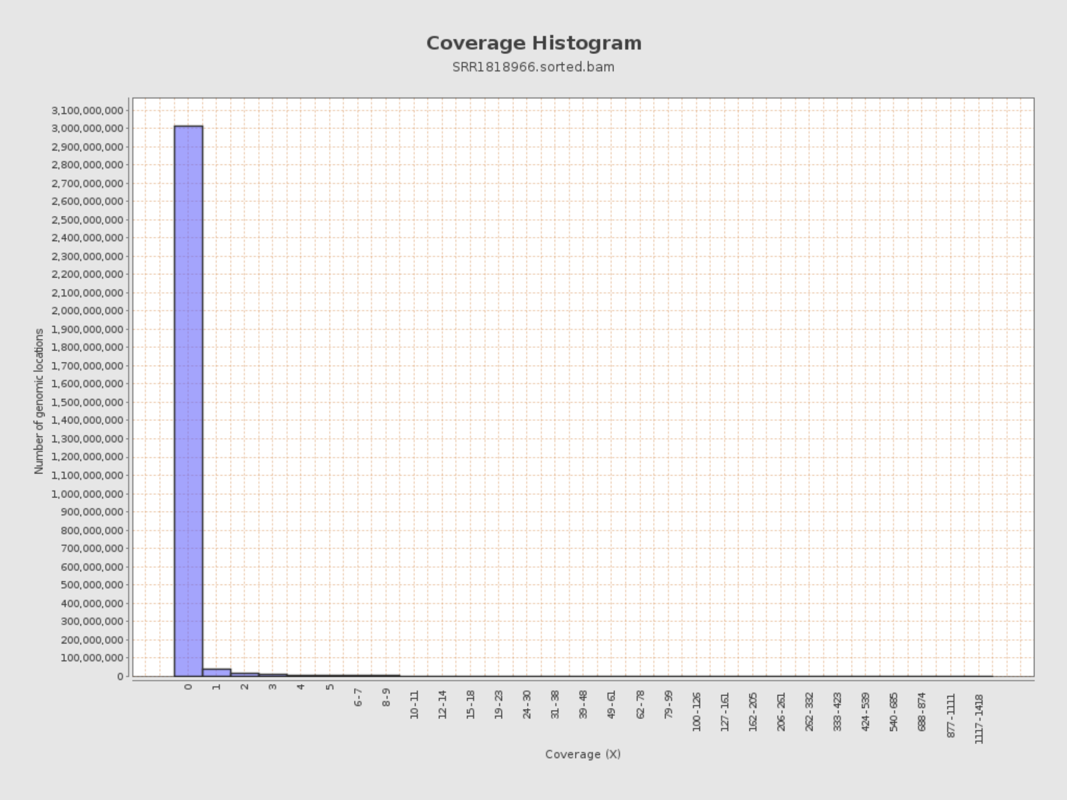
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	20221933	0.0811	1.3336
chr2	243199373	16984466	0.0698	1.16
chr3	198022430	11149513	0.0563	0.4671
chr4	191154276	10916225	0.0571	0.5424
chr5	180915260	11010382	0.0609	0.4975
chr6	171115067	7545981	0.0441	0.4783
chr7	159138663	9501753	0.0597	0.9125

chr8	146364022	18476133	0.1262	0.7732
chr9	141213431	8206786	0.0581	0.677
chr10	135534747	10125691	0.0747	0.8931
chr11	135006516	6789912	0.0503	0.5225
chr12	133851895	9472468	0.0708	0.532
chr13	115169878	4010309	0.0348	0.3632
chr14	107349540	4737889	0.0441	0.4401
chr15	102531392	5318605	0.0519	0.4526
chr16	90354753	5485014	0.0607	0.847
chr17	81195210	6932492	0.0854	0.6305
chr18	78077248	4972290	0.0637	0.8557
chr19	59128983	3772205	0.0638	1.1364
chr20	63025520	5557269	0.0882	0.6205
chr21	48129895	2856842	0.0594	0.5114
chr22	51304566	1612945	0.0314	0.386
chrMT	16571	11297	0.6817	1.8497
chrX	155270560	11393318	0.0734	0.6226
chrY	59373566	723586	0.0122	0.7662

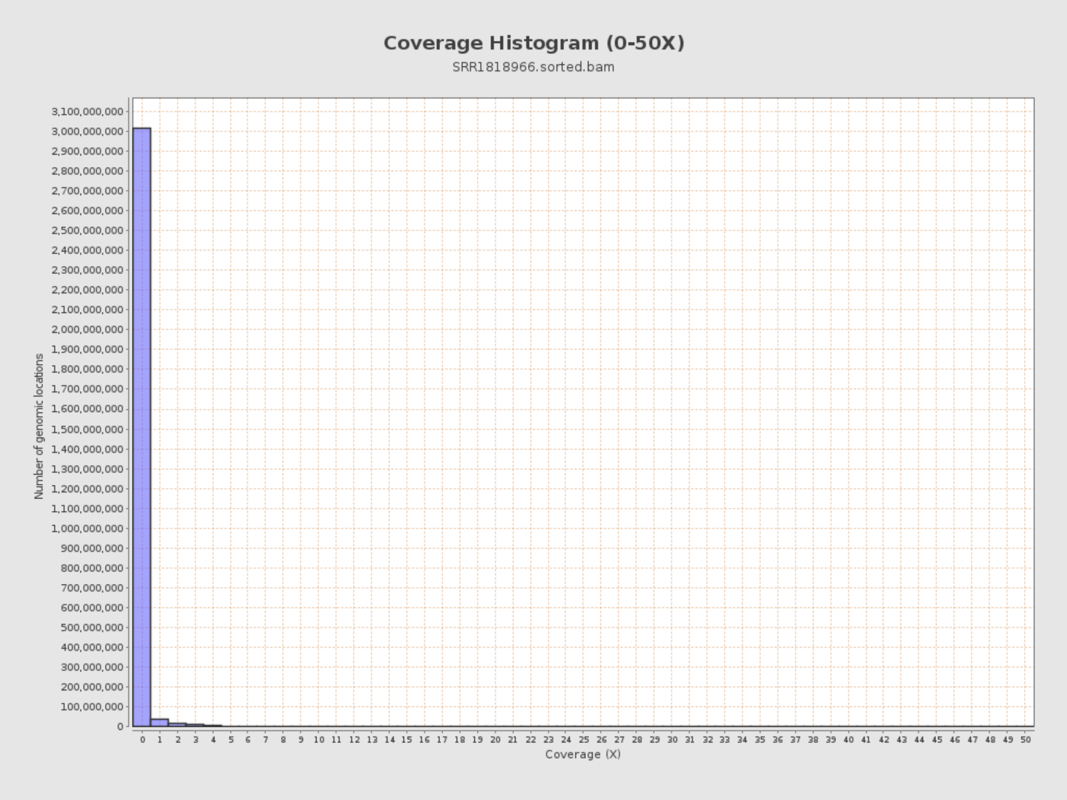
3. Results : Coverage across reference



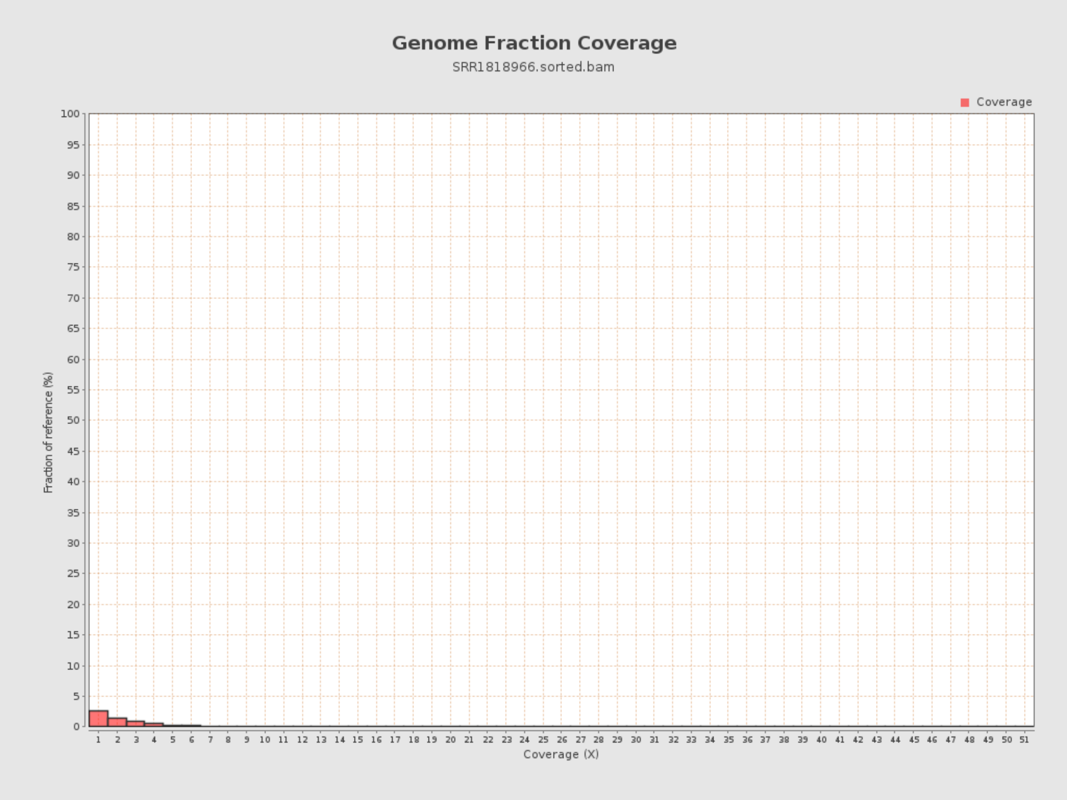
4. Results : Coverage Histogram



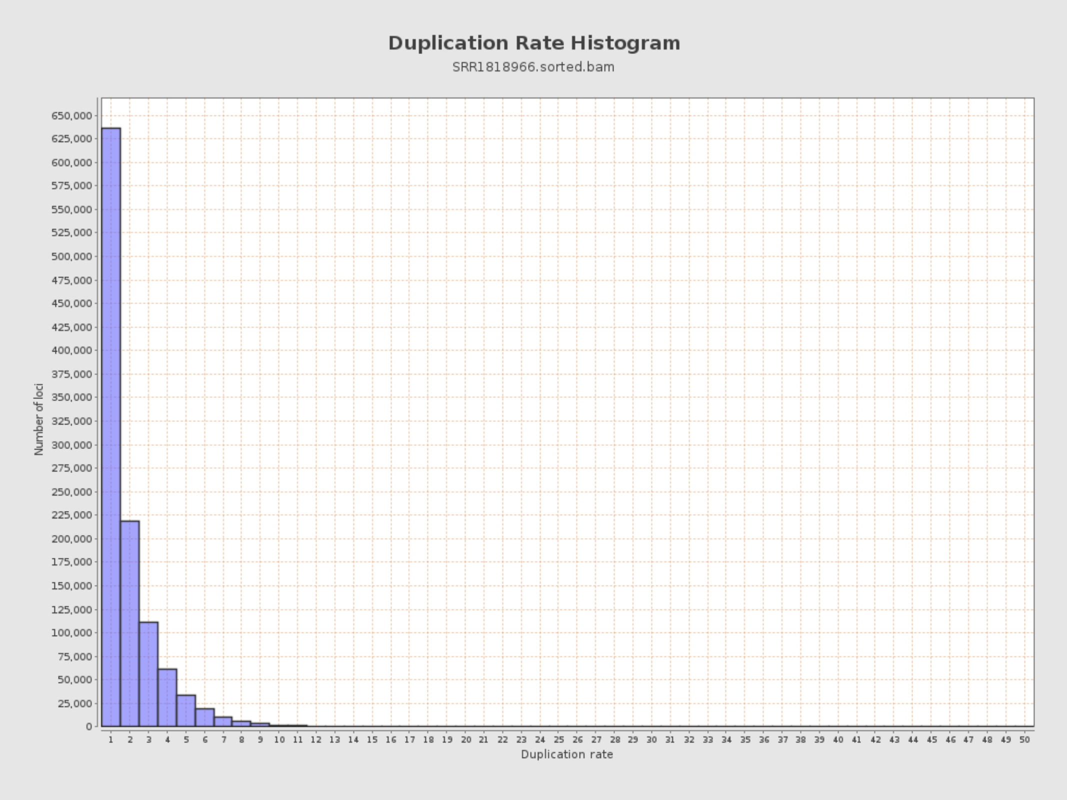
5. Results : Coverage Histogram (0-50X)



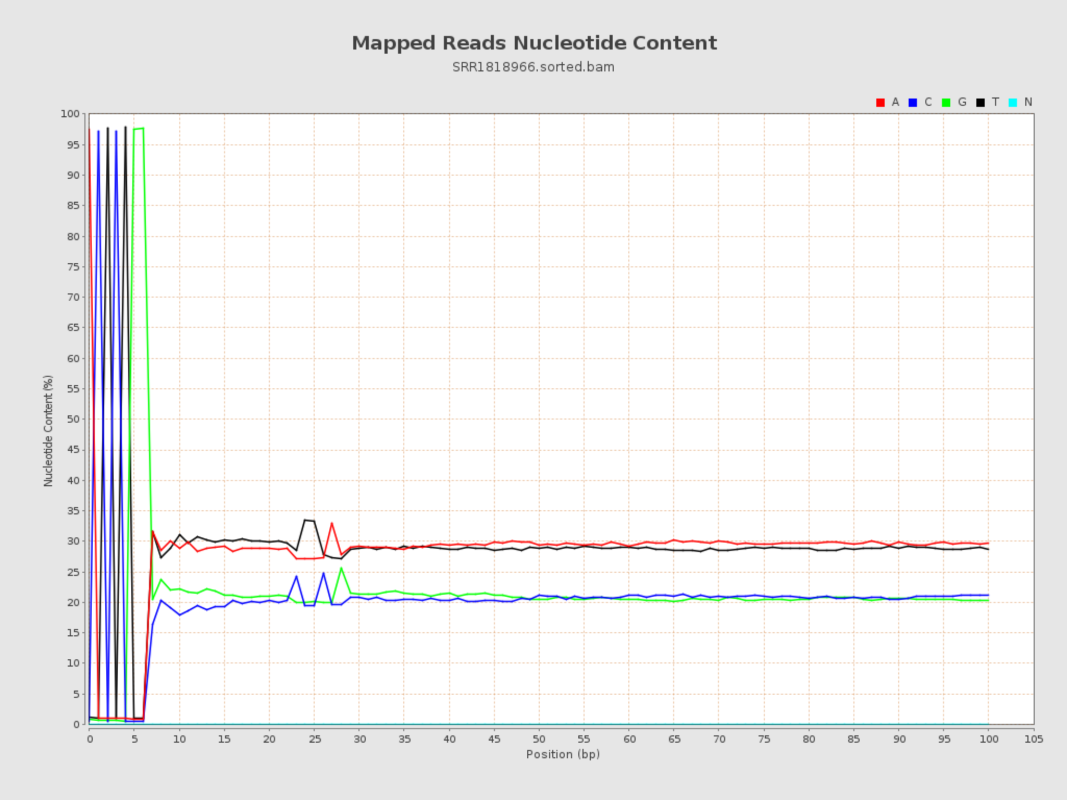
6. Results : Genome Fraction Coverage



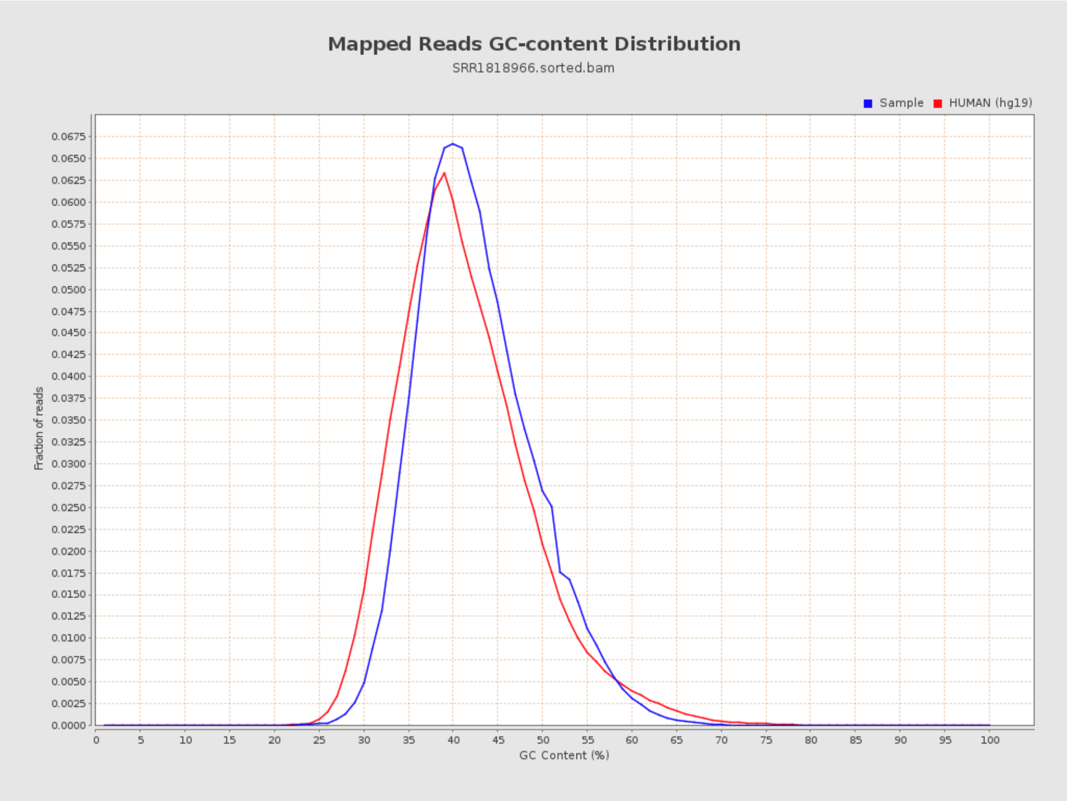
7. Results : Duplication Rate Histogram



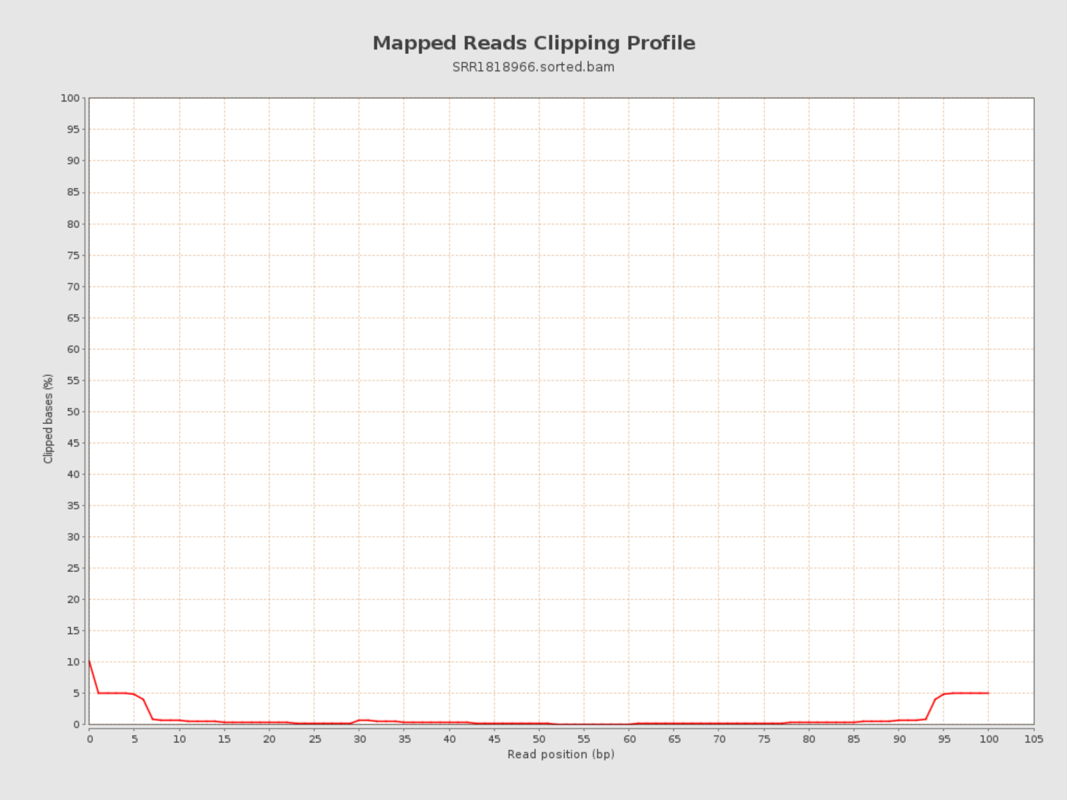
8. Results : Mapped Reads Nucleotide Content



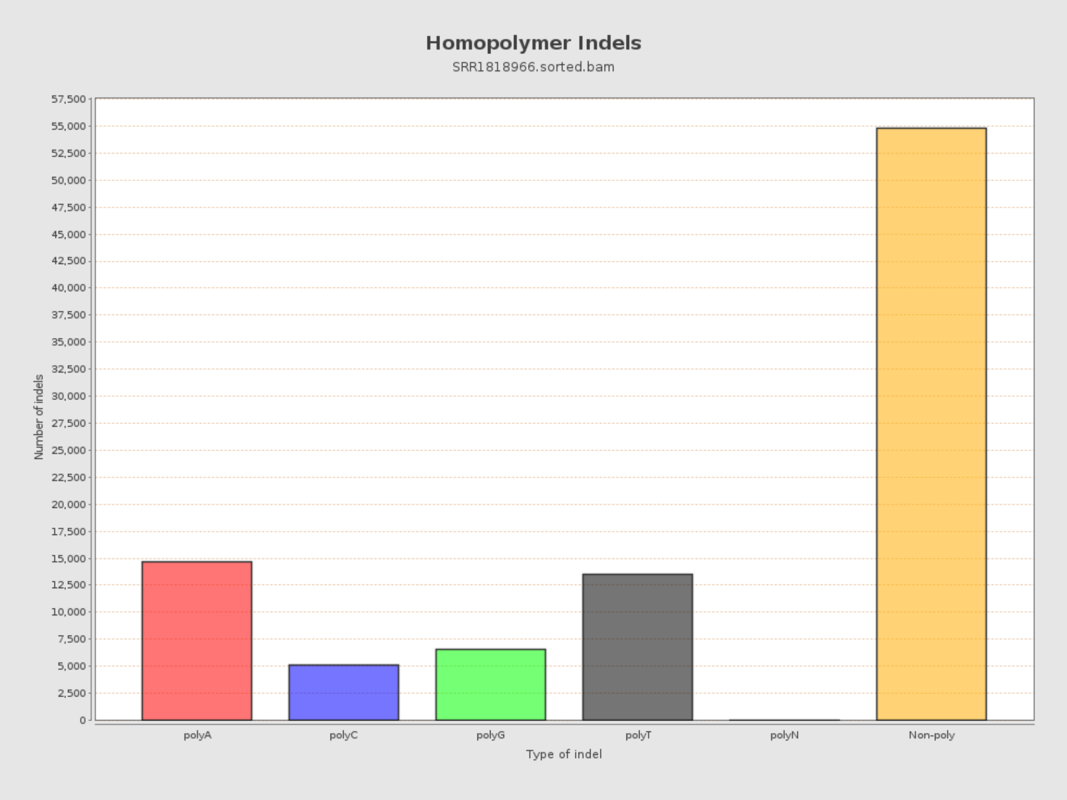
9. Results : Mapped Reads GC-content Distribution



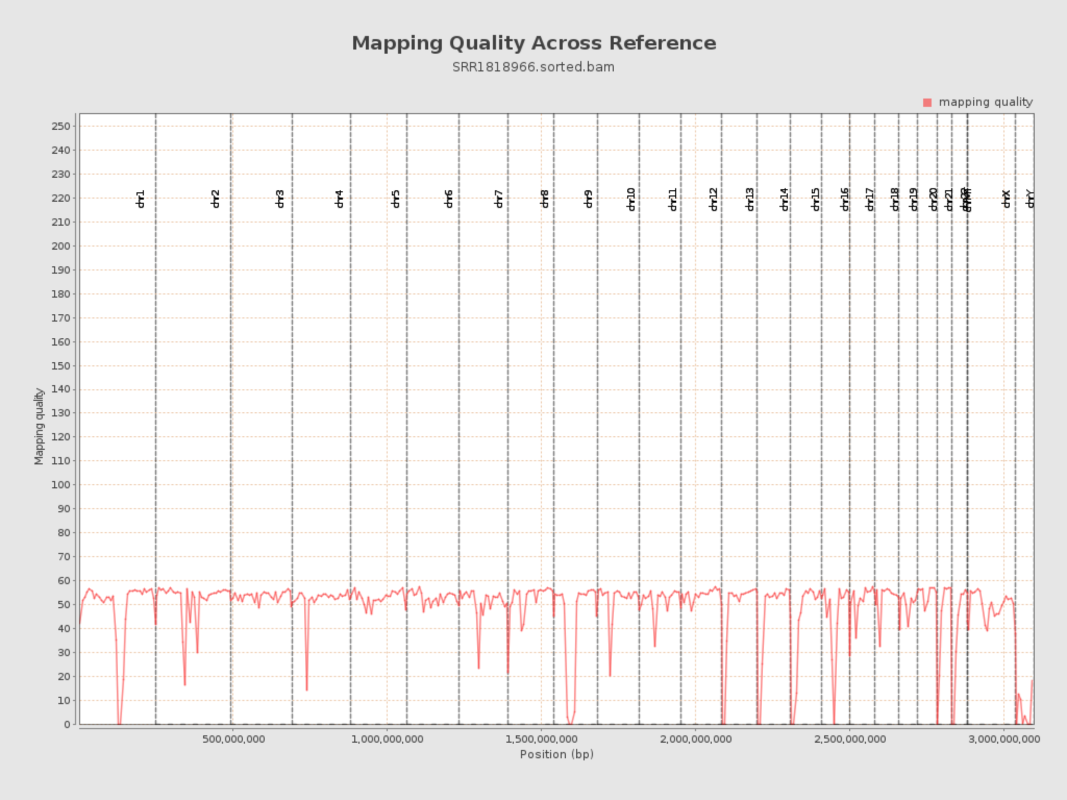
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram