Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 10:10:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818946.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_SRR1818946 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818946.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 10:10:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818946.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,699,253
Mapped reads	2,659,423 / 98.52%
Unmapped reads	39,830 / 1.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	33,755 / 1.25%
Read min/max/mean length	30 / 101 / 101.48
Duplicated reads (estimated)	1,198,277 / 44.39%
Duplication rate	38.25%
Clipped reads	2,681,825 / 99.35%

2.2. ACGT Content

Number/percentage of A's	71,868,667 / 29.19%
Number/percentage of C's	53,113,474 / 21.57%
Number/percentage of T's	69,510,973 / 28.23%
Number/percentage of G's	51,717,906 / 21%
Number/percentage of N's	11,047 / 0%
GC Percentage	42.58%

2.3. Coverage

Mean	0.0796

Standard Deviation	0.8389

2.4. Mapping Quality

Mean Mapping Quality	49.29

2.5. Mismatches and indels

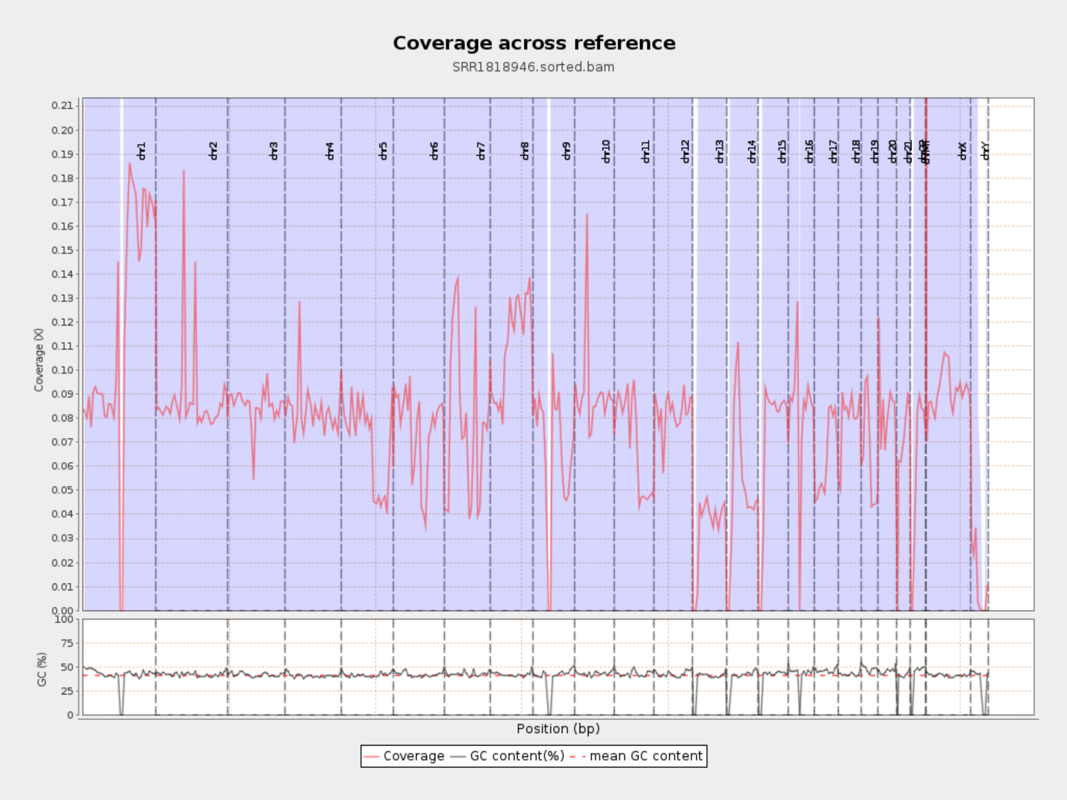
General error rate	0.67%
Mismatches	1,571,124
Insertions	30,790
Mapped reads with at least one insertion	1.13%
Deletions	74,583
Mapped reads with at least one deletion	2.75%
Homopolymer indels	43.04%

2.6. Chromosome stats

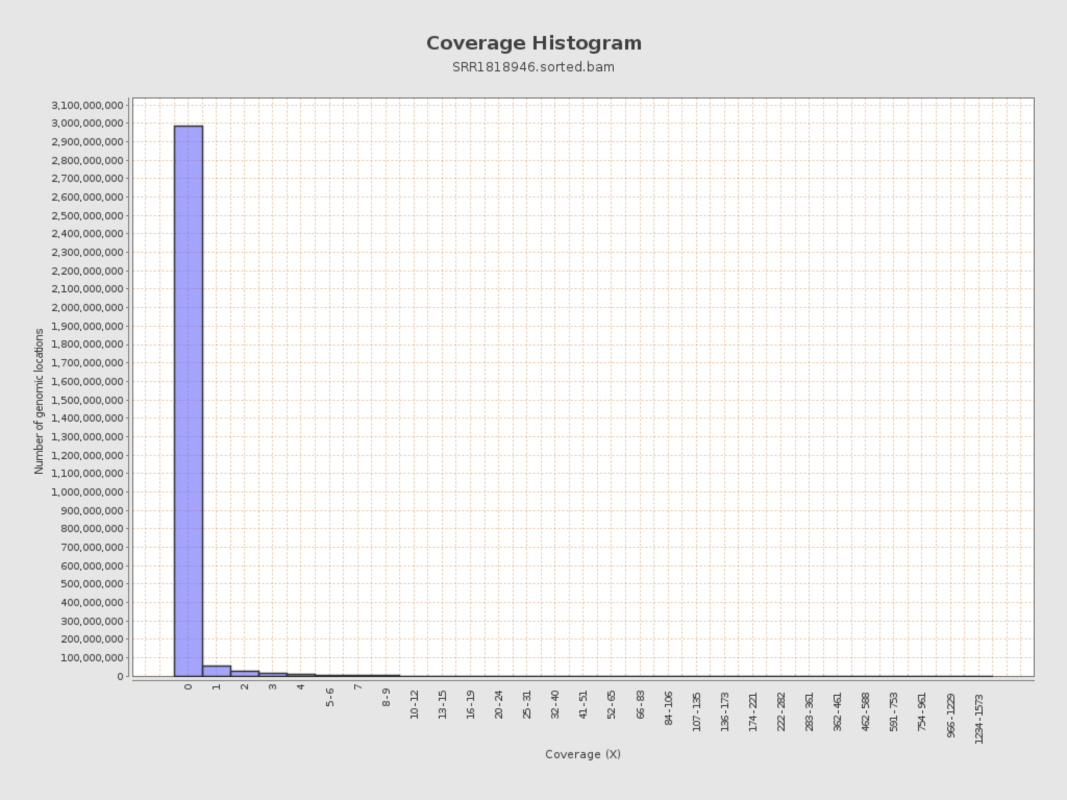
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	29250850	0.1174	1.4354
chr2	243199373	21575314	0.0887	1.2192
chr3	198022430	16833741	0.085	0.5502
chr4	191154276	15921537	0.0833	0.6023
chr5	180915260	12744733	0.0704	0.5233
chr6	171115067	12949343	0.0757	0.5763
chr7	159138663	12378099	0.0778	0.6991

chr8	146364022	16276898	0.1112	0.7473
chr9	141213431	9306479	0.0659	0.9783
chr10	135534747	12248162	0.0904	1.0608
chr11	135006516	9421124	0.0698	0.6006
chr12	133851895	11076202	0.0827	0.5499
chr13	115169878	3929709	0.0341	0.3428
chr14	107349540	5677797	0.0529	0.4893
chr15	102531392	7173639	0.07	0.5008
chr16	90354753	7370870	0.0816	0.8687
chr17	81195210	5247190	0.0646	0.5406
chr18	78077248	6222545	0.0797	1.1803
chr19	59128983	3861322	0.0653	1.2179
chr20	63025520	5308123	0.0842	0.5877
chr21	48129895	3243695	0.0674	0.5512
chr22	51304566	2994655	0.0584	0.5045
chrMT	16571	451137	27.2245	16.6775
chrX	155270560	14178605	0.0913	0.7051
chrY	59373566	714784	0.012	0.7488

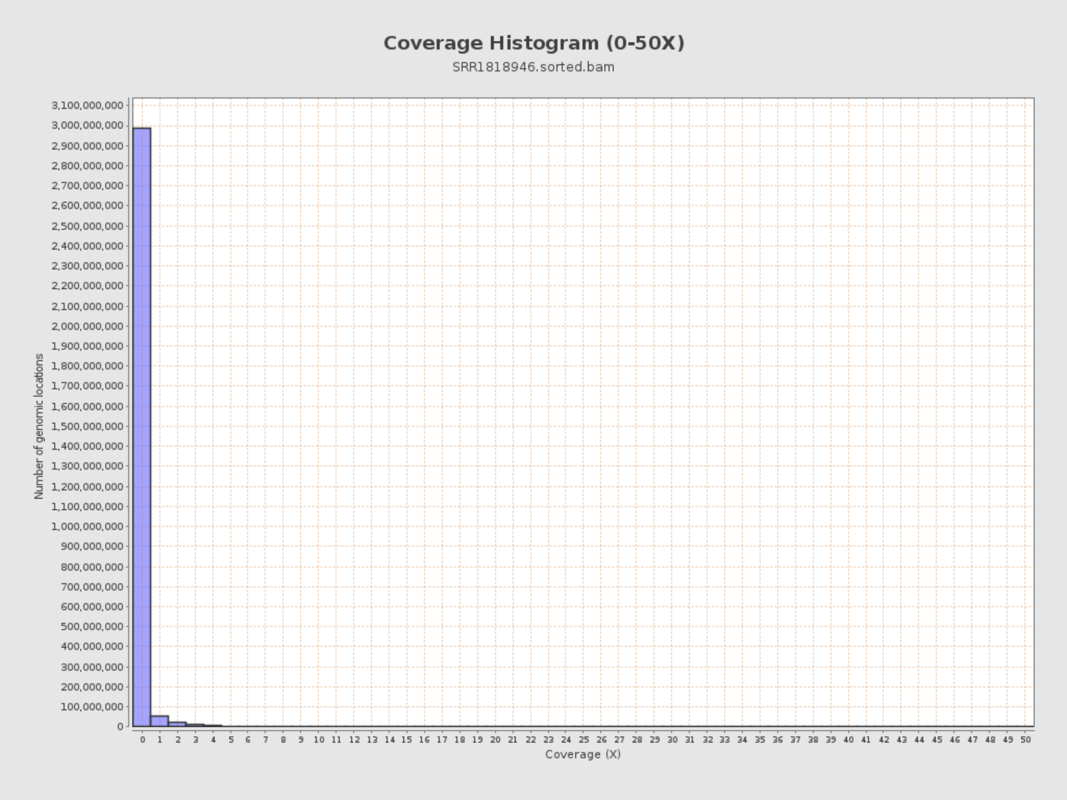
3. Results : Coverage across reference



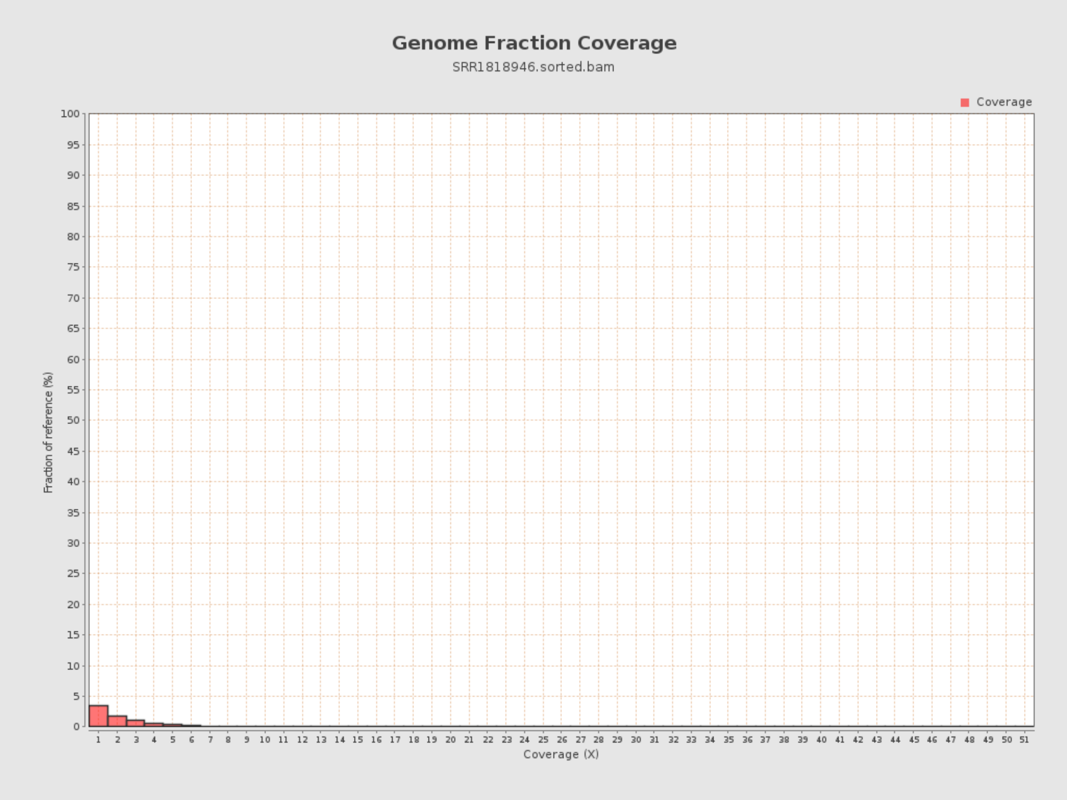
4. Results : Coverage Histogram



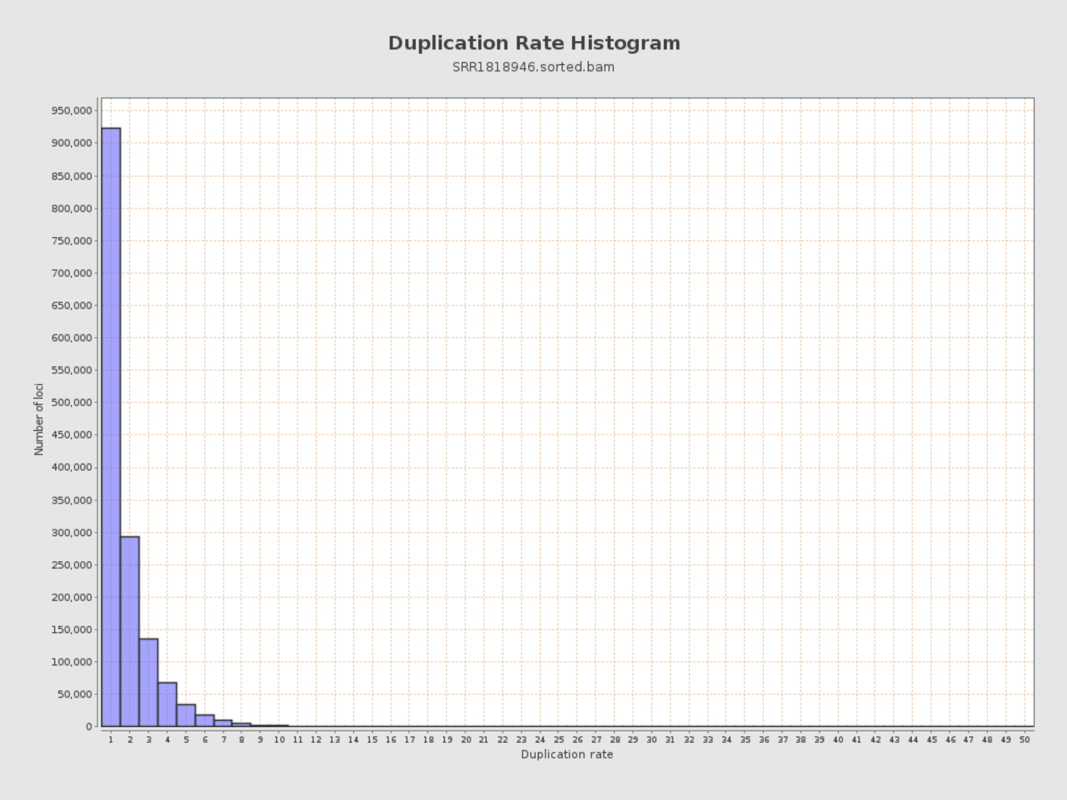
5. Results : Coverage Histogram (0-50X)



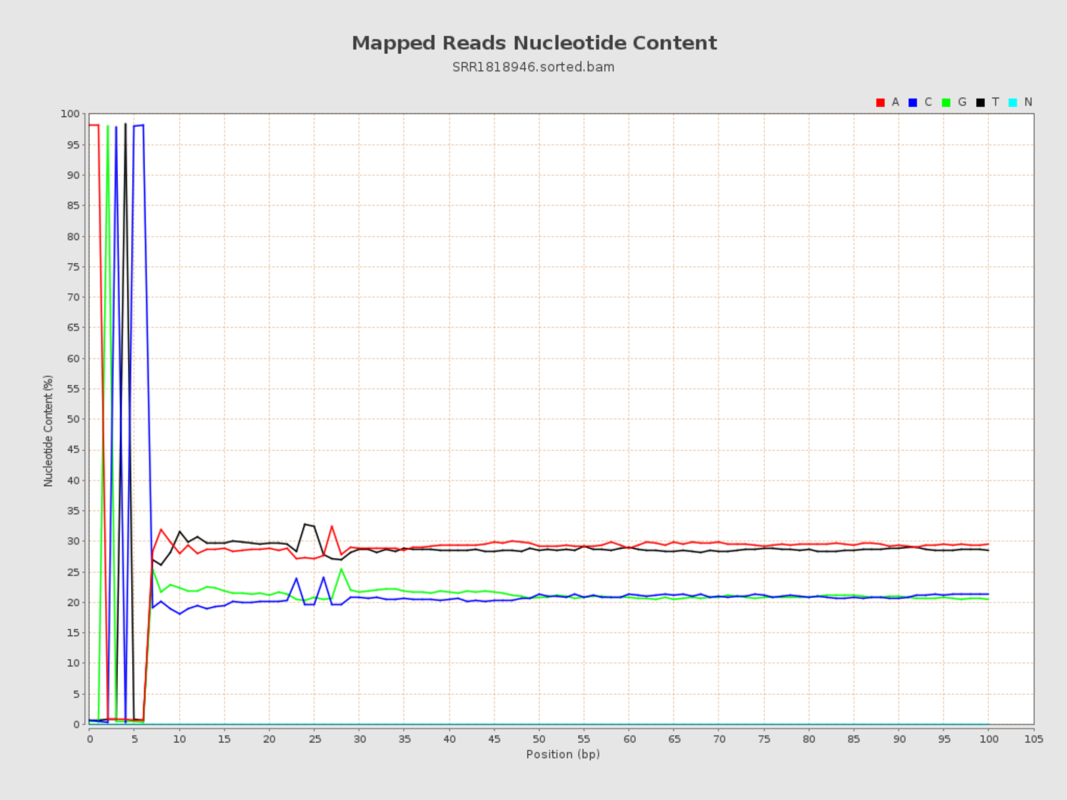
6. Results : Genome Fraction Coverage



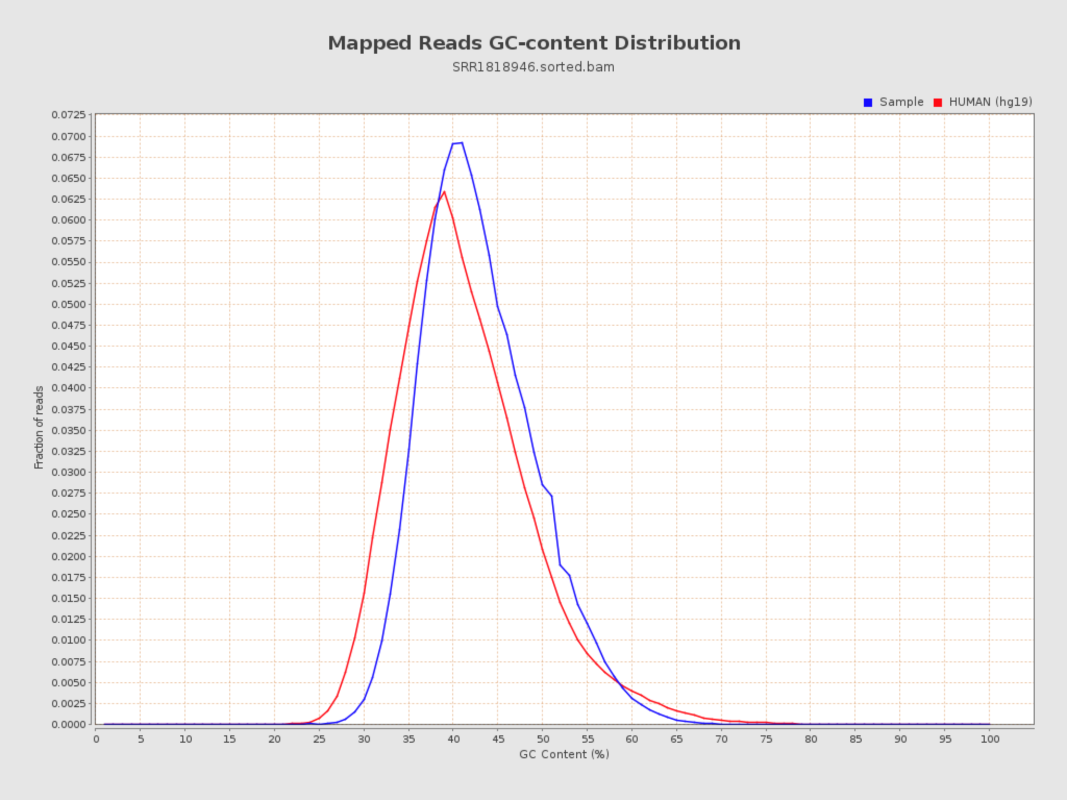
7. Results : Duplication Rate Histogram



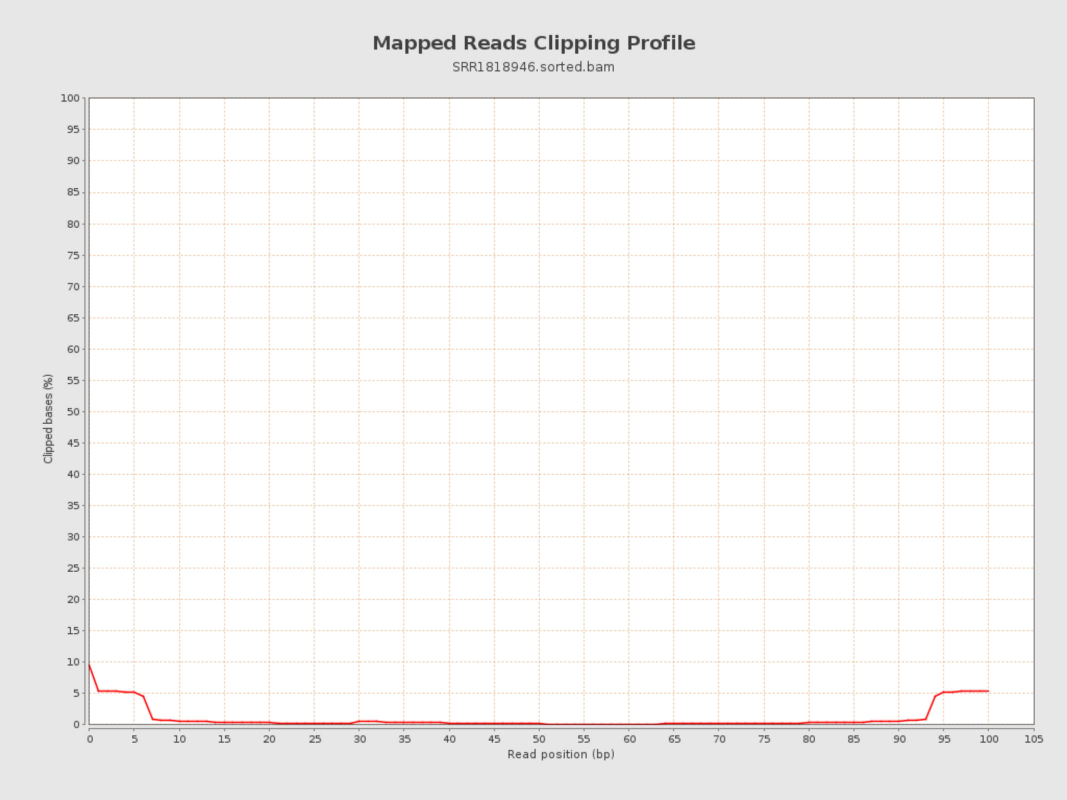
8. Results : Mapped Reads Nucleotide Content



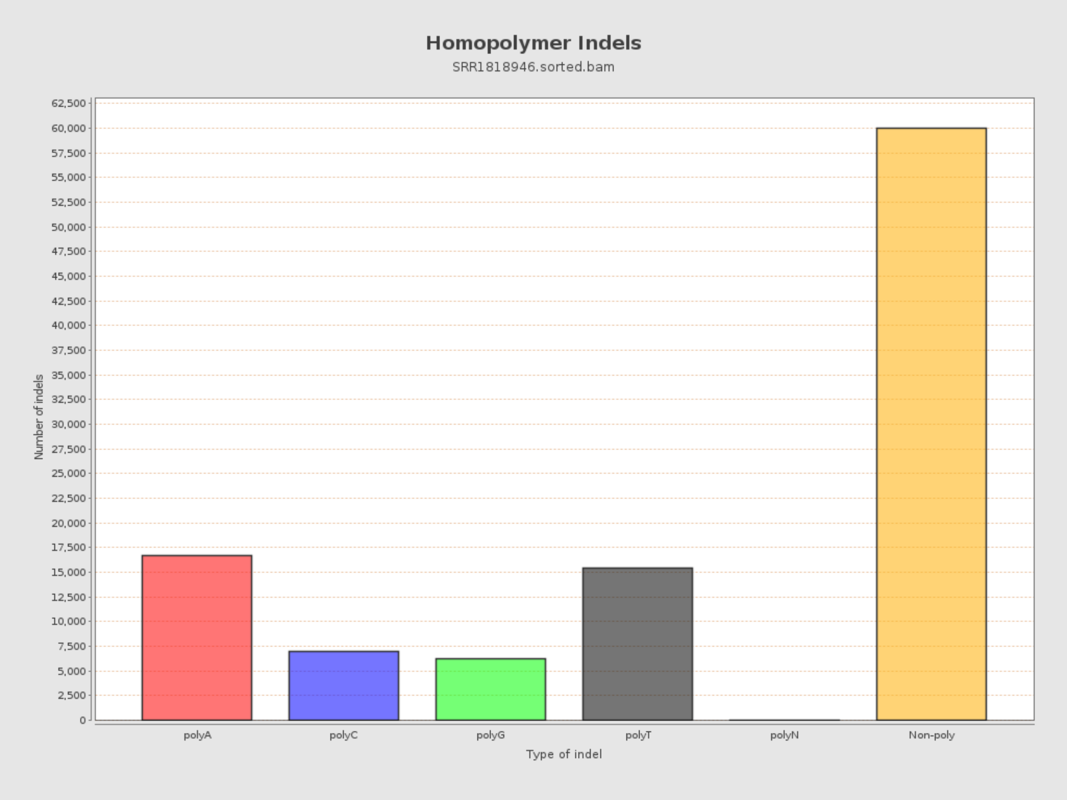
9. Results : Mapped Reads GC-content Distribution



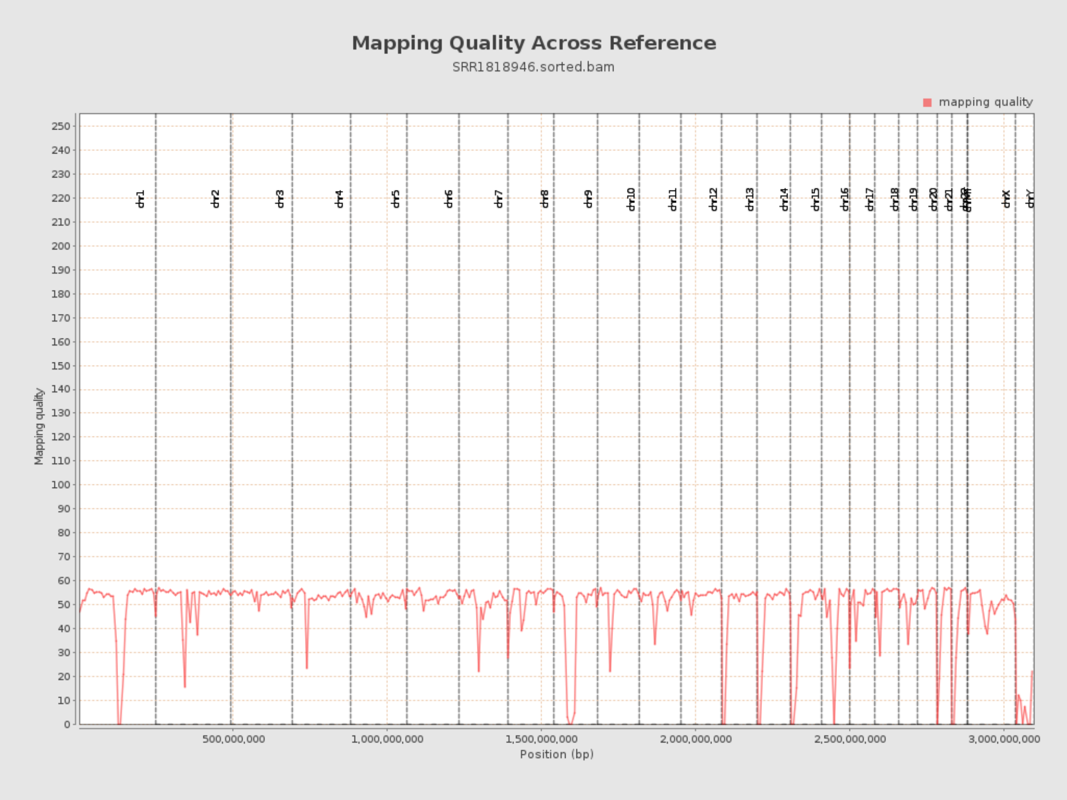
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram