Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 11:36:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818963.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_SRR1818963 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818963.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 11:36:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818963.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,952,718
Mapped reads	2,886,828 / 97.77%
Unmapped reads	65,890 / 2.23%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	44,539 / 1.51%
Read min/max/mean length	30 / 101 / 101.58
Duplicated reads (estimated)	1,498,951 / 50.77%
Duplication rate	41.44%
Clipped reads	2,895,936 / 98.08%

2.2. ACGT Content

Number/percentage of A's	78,550,007 / 29.39%
Number/percentage of C's	55,844,830 / 20.89%
Number/percentage of T's	76,779,813 / 28.72%
Number/percentage of G's	56,115,137 / 20.99%
Number/percentage of N's	13,460 / 0.01%
GC Percentage	41.89%

2.3. Coverage

Mean	0.0864

Standard Deviation	0.9388

2.4. Mapping Quality

Mean Mapping Quality	49.36

2.5. Mismatches and indels

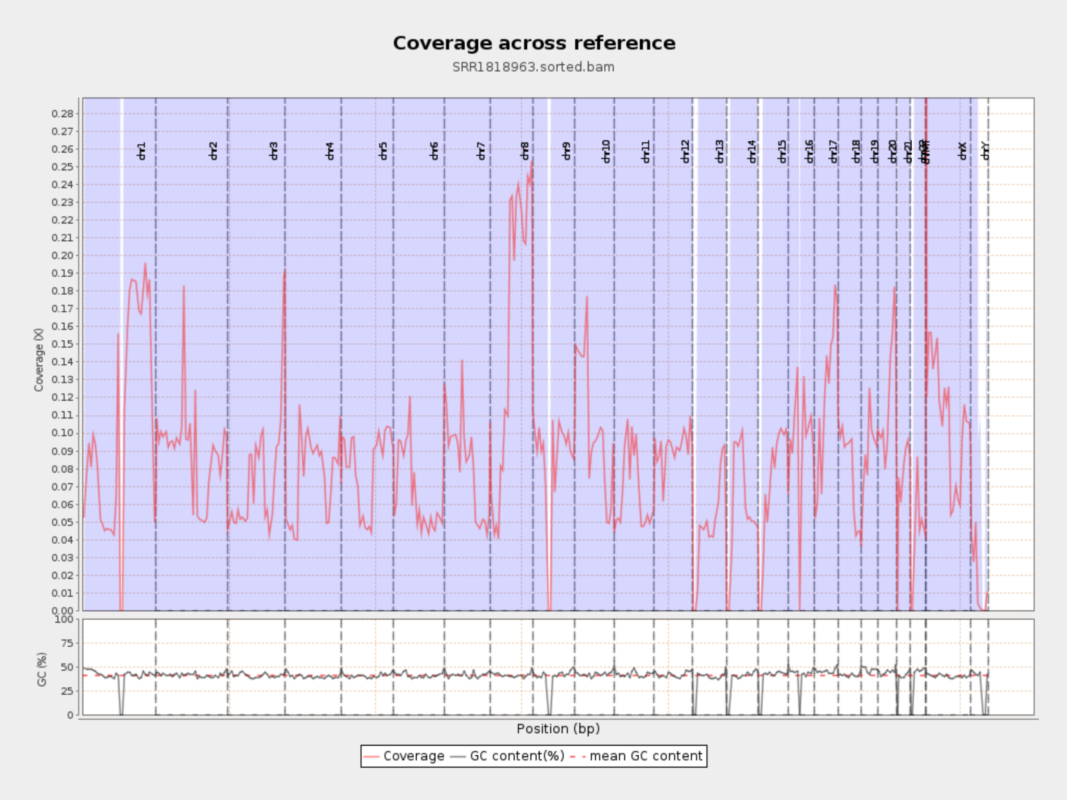
General error rate	0.66%
Mismatches	1,666,477
Insertions	40,751
Mapped reads with at least one insertion	1.38%
Deletions	84,617
Mapped reads with at least one deletion	2.87%
Homopolymer indels	42.33%

2.6. Chromosome stats

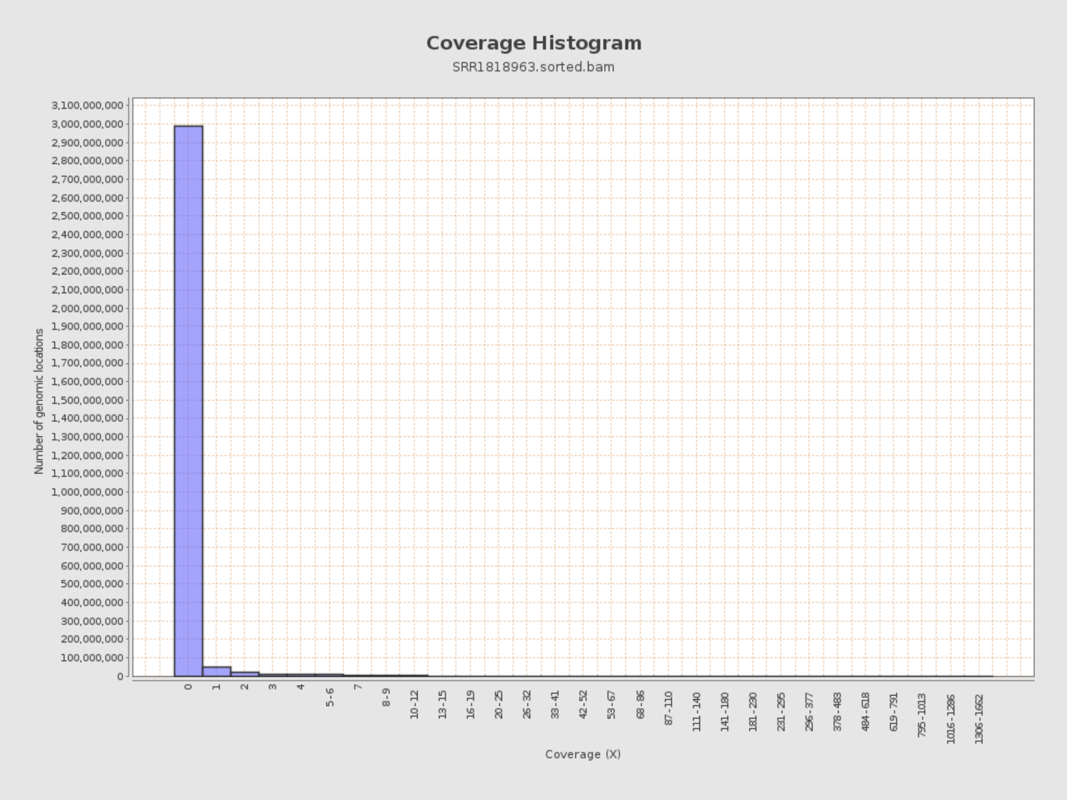
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	26188390	0.1051	1.5619
chr2	243199373	21847908	0.0898	1.2763
chr3	198022430	14749297	0.0745	0.5695
chr4	191154276	14639124	0.0766	0.666
chr5	180915260	14584552	0.0806	0.612
chr6	171115067	11273822	0.0659	0.6477
chr7	159138663	13030822	0.0819	1.1623

chr8	146364022	23753179	0.1623	0.9512
chr9	141213431	11700621	0.0829	0.9072
chr10	135534747	14173570	0.1046	1.1547
chr11	135006516	9090953	0.0673	0.6496
chr12	133851895	12306063	0.0919	0.6457
chr13	115169878	5577558	0.0484	0.4554
chr14	107349540	6459311	0.0602	0.5516
chr15	102531392	7063734	0.0689	0.5517
chr16	90354753	8446136	0.0935	0.997
chr17	81195210	9747398	0.12	0.8461
chr18	78077248	6190804	0.0793	1.088
chr19	59128983	5353270	0.0905	1.4963
chr20	63025520	7690067	0.122	0.8005
chr21	48129895	3575163	0.0743	0.619
chr22	51304566	2124115	0.0414	0.4598
chrMT	16571	37637	2.2713	3.0166
chrX	155270560	16919992	0.109	0.7764
chrY	59373566	935828	0.0158	0.9411

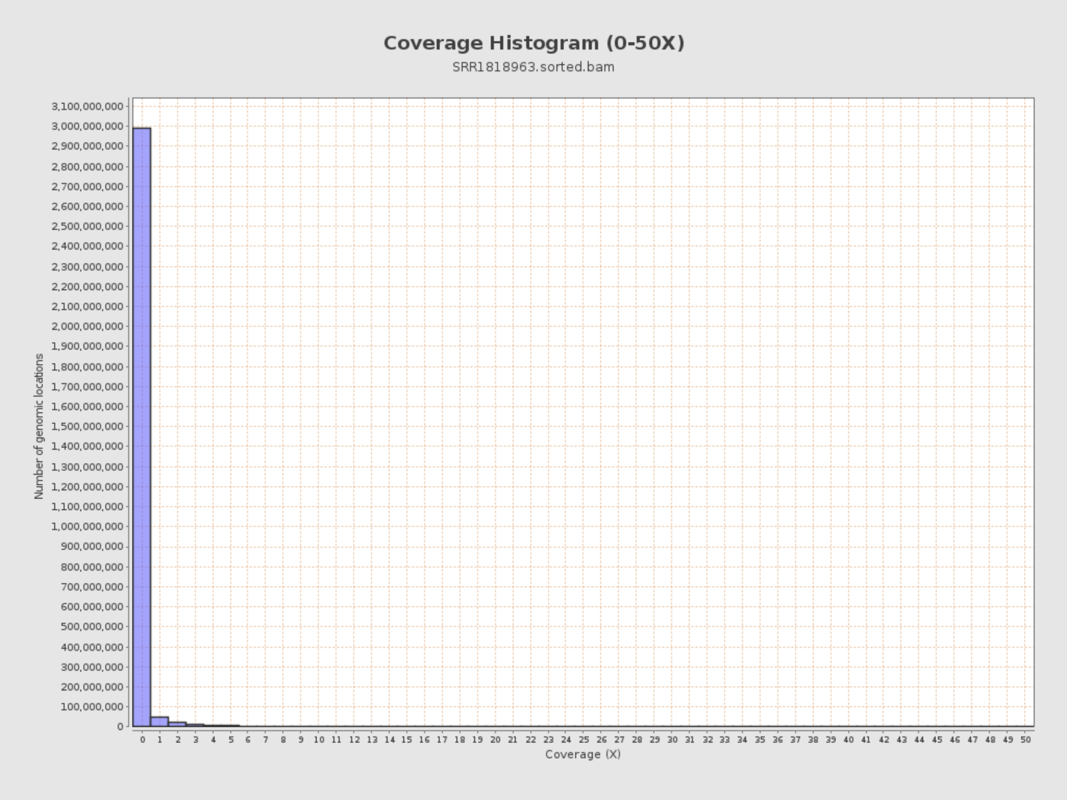
3. Results : Coverage across reference



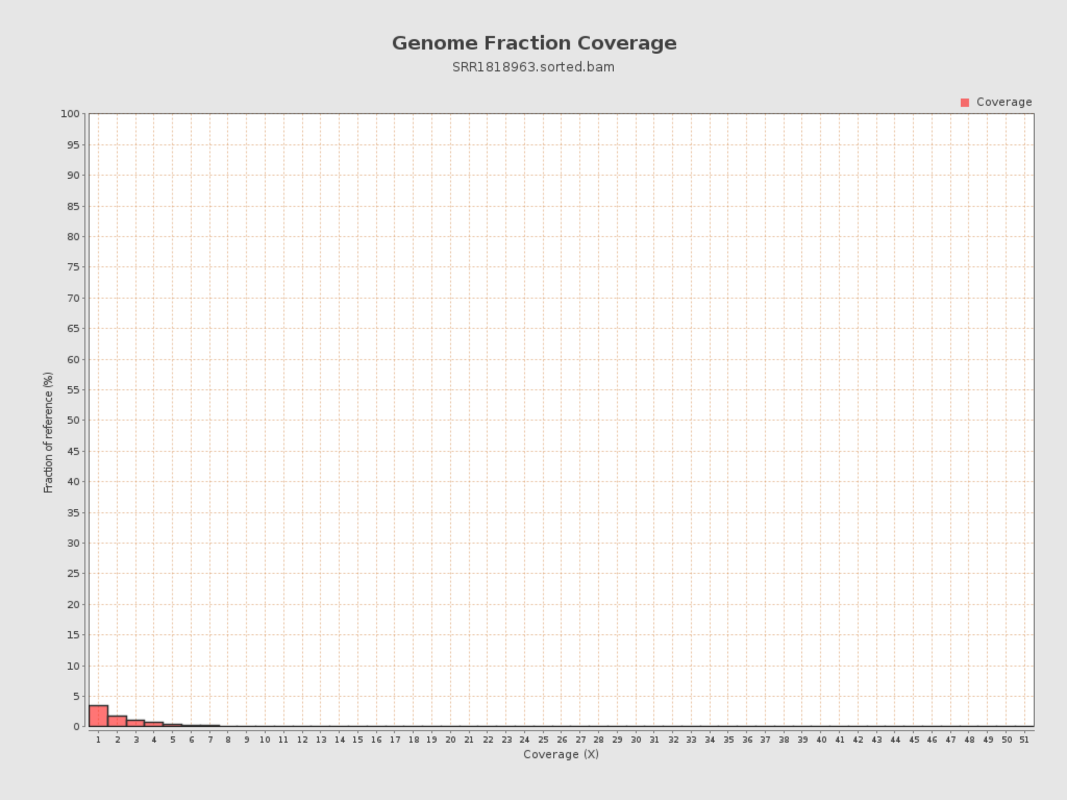
4. Results : Coverage Histogram



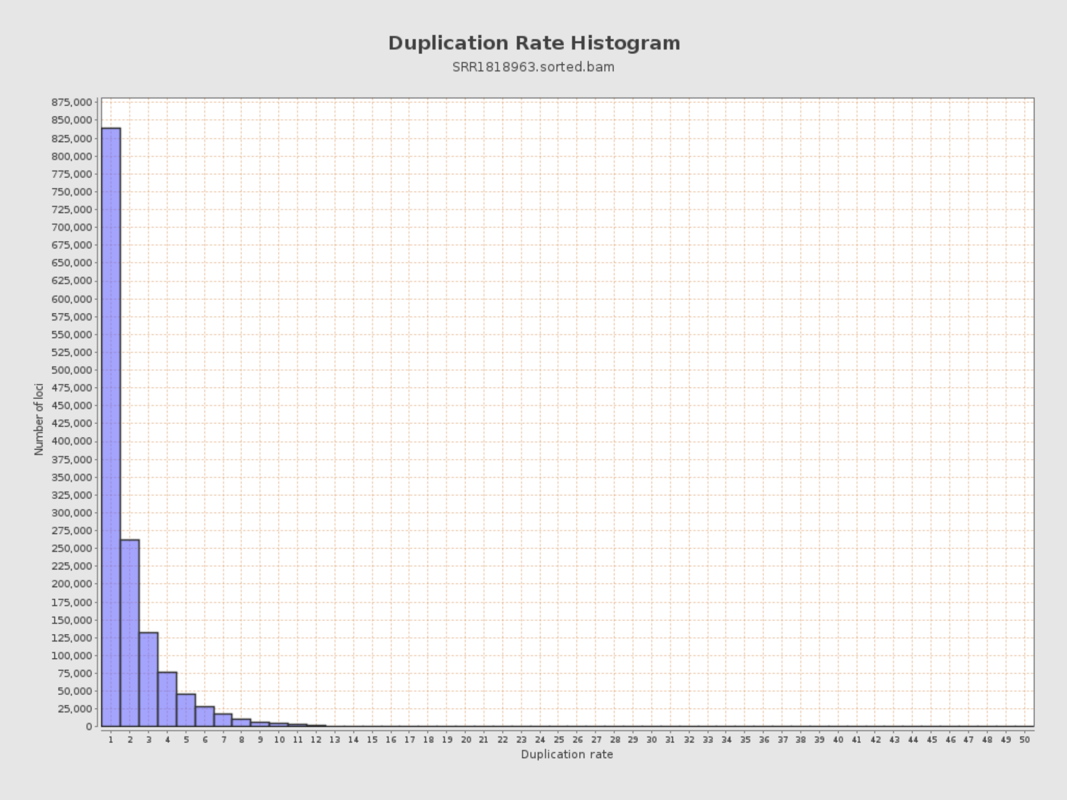
5. Results : Coverage Histogram (0-50X)



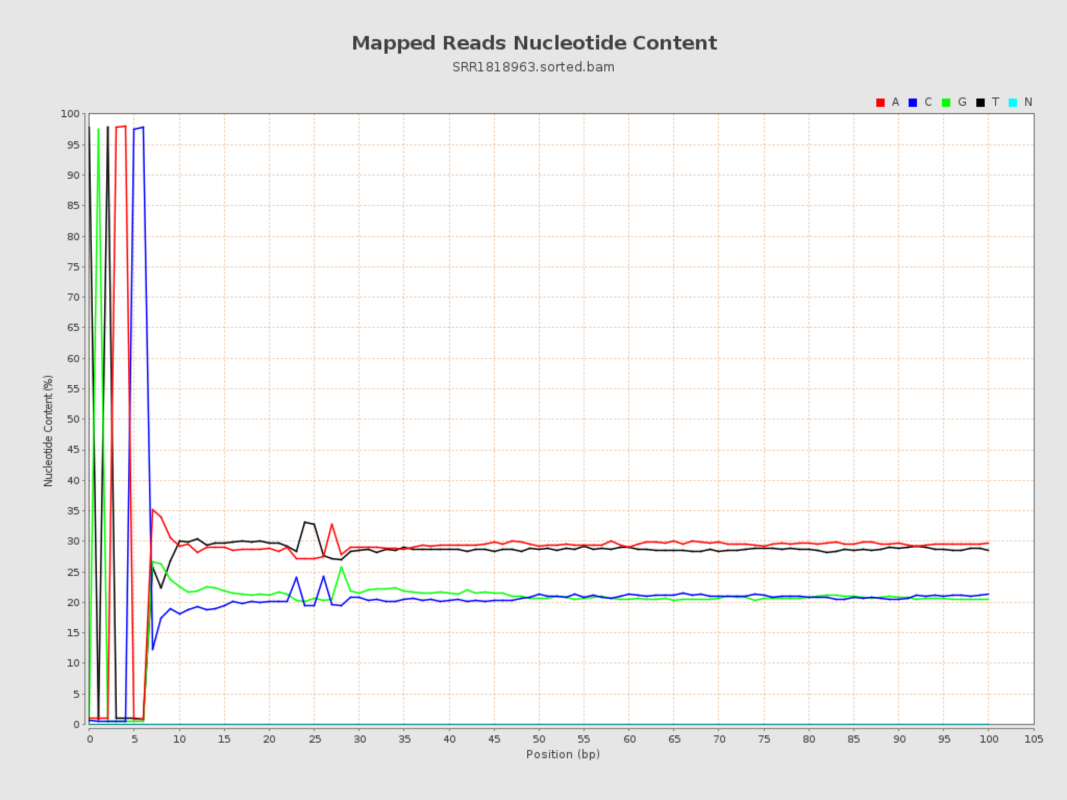
6. Results : Genome Fraction Coverage



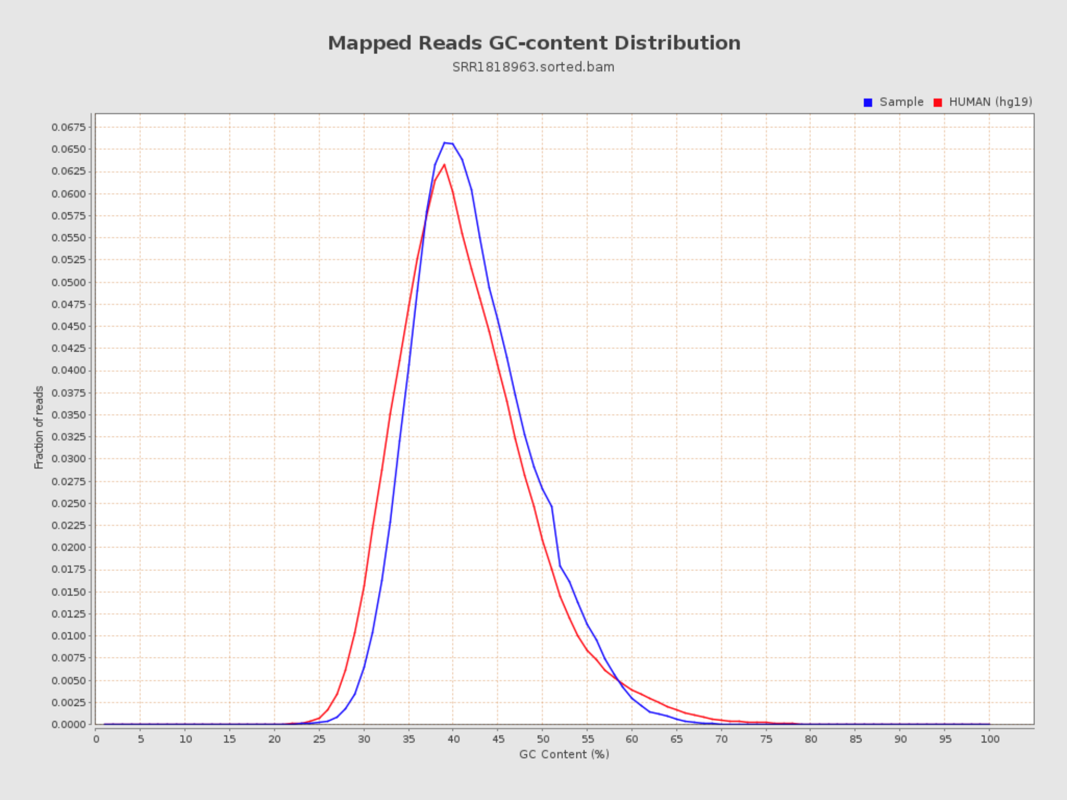
7. Results : Duplication Rate Histogram



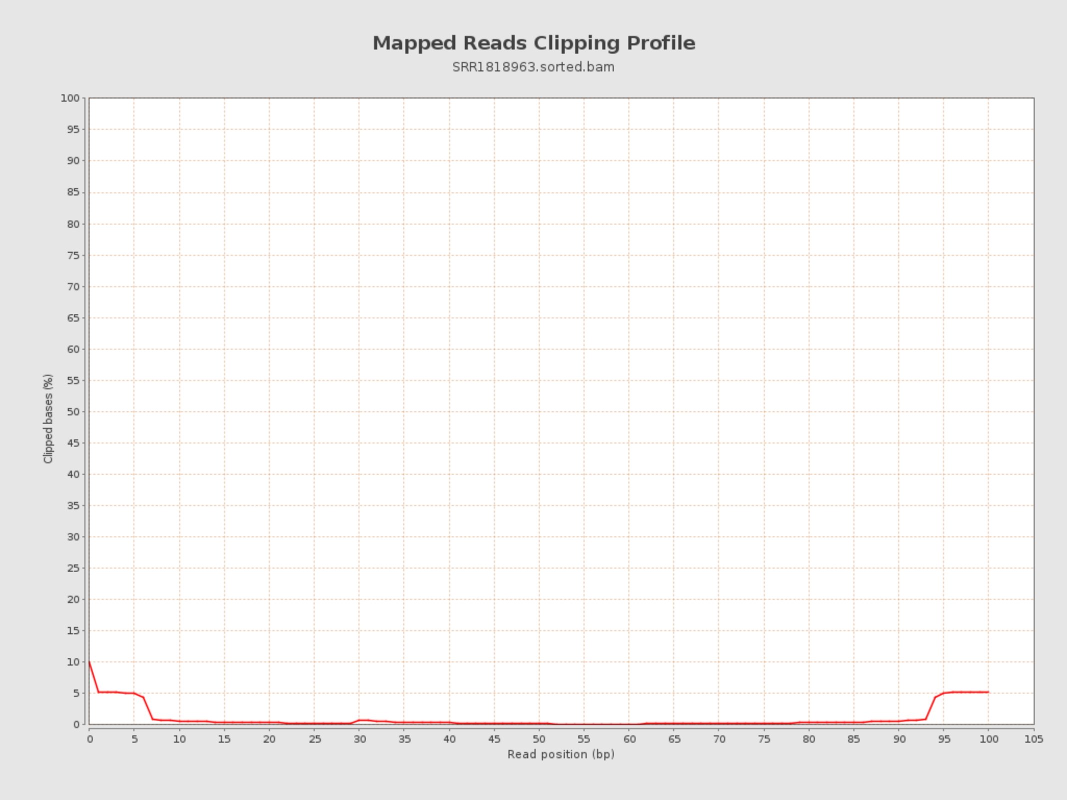
8. Results : Mapped Reads Nucleotide Content



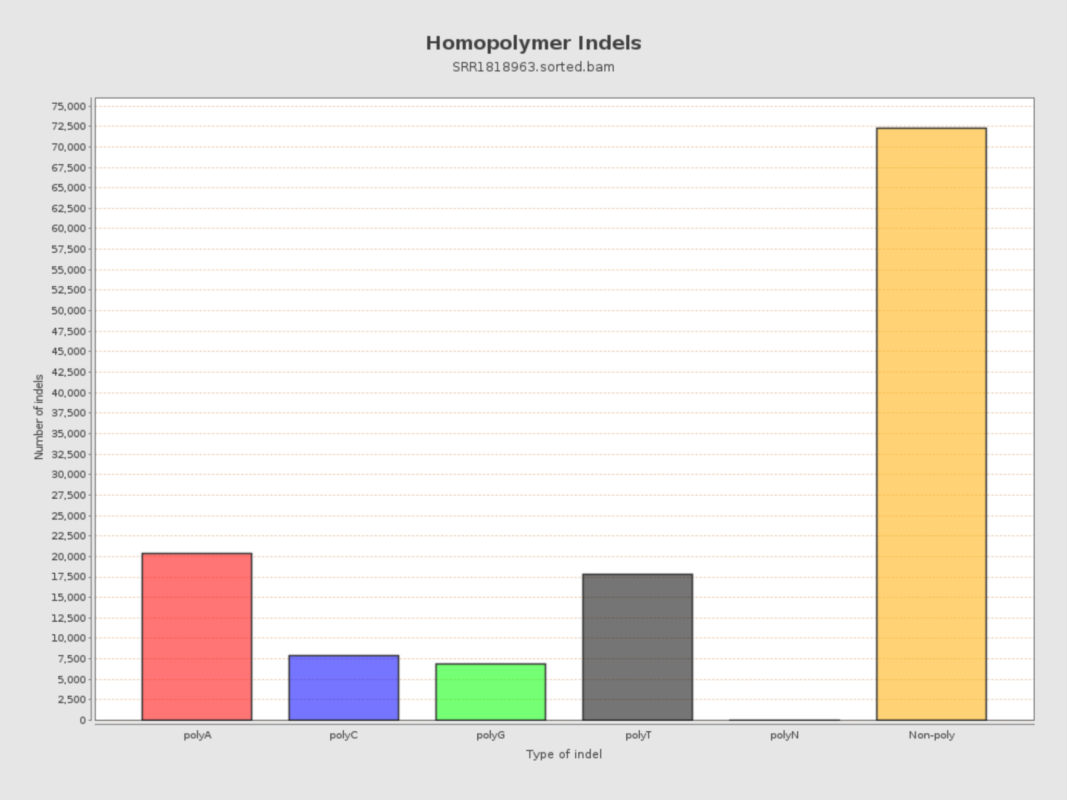
9. Results : Mapped Reads GC-content Distribution



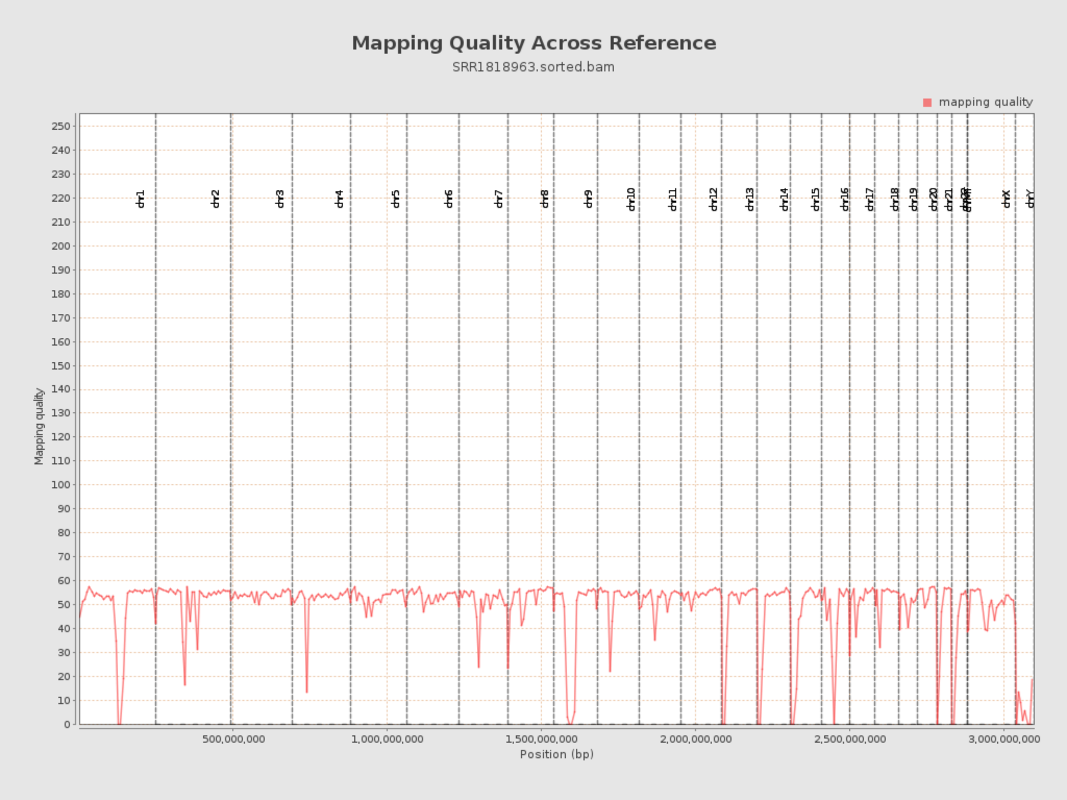
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram