Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 13:09:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818985.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_SRR1818985 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818985.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 13:09:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818985.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,146,776
Mapped reads	3,077,646 / 97.8%
Unmapped reads	69,130 / 2.2%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	44,481 / 1.41%
Read min/max/mean length	30 / 101 / 101.54
Duplicated reads (estimated)	1,601,788 / 50.9%
Duplication rate	43.41%
Clipped reads	3,103,895 / 98.64%

2.2. ACGT Content

Number/percentage of A's	81,703,843 / 28.68%
Number/percentage of C's	62,577,017 / 21.97%
Number/percentage of T's	82,033,668 / 28.8%
Number/percentage of G's	58,502,013 / 20.54%
Number/percentage of N's	15,035 / 0.01%
GC Percentage	42.51%

2.3. Coverage

Mean	0.0921

Standard Deviation	1.0172

2.4. Mapping Quality

Mean Mapping Quality	49.16

2.5. Mismatches and indels

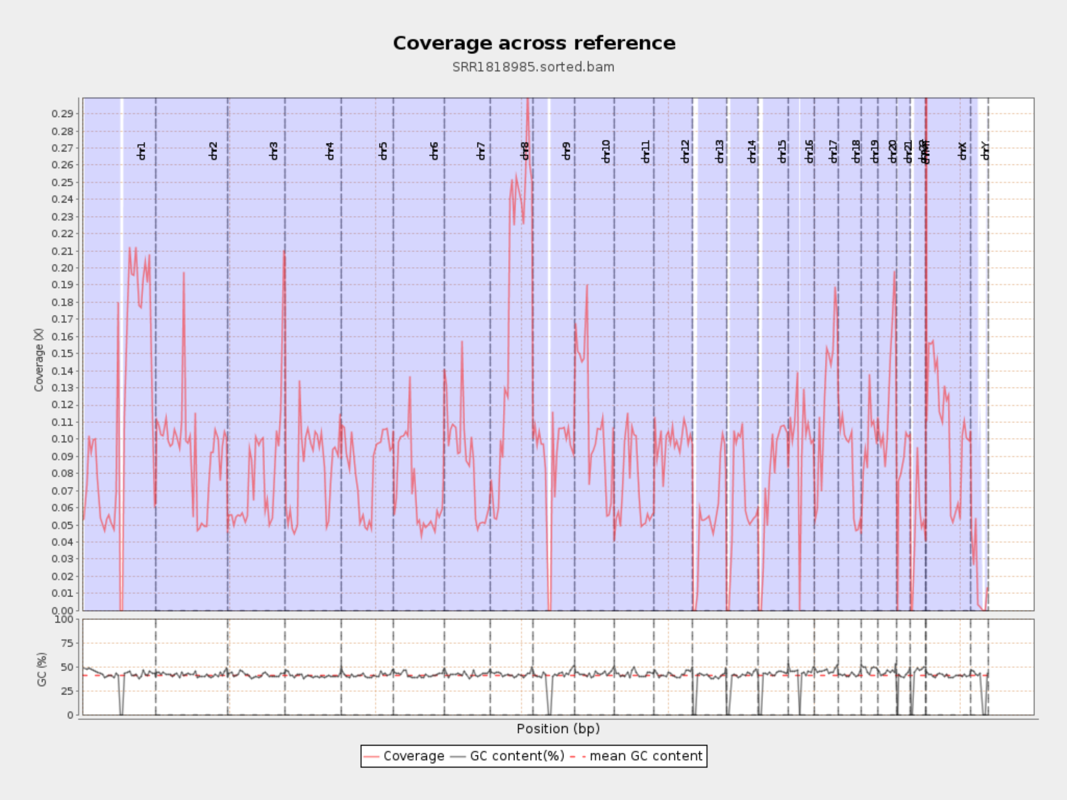
General error rate	0.66%
Mismatches	1,791,878
Insertions	39,666
Mapped reads with at least one insertion	1.26%
Deletions	89,389
Mapped reads with at least one deletion	2.85%
Homopolymer indels	42.78%

2.6. Chromosome stats

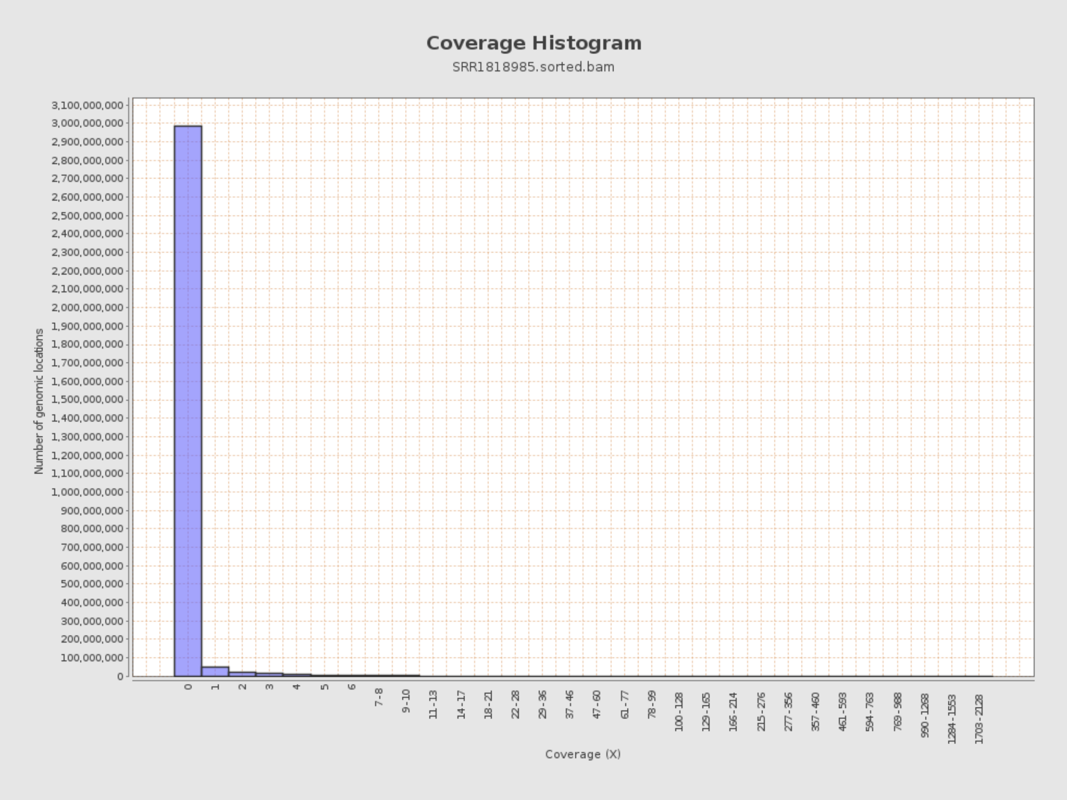
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	28253174	0.1134	1.887
chr2	243199373	22681624	0.0933	1.2254
chr3	198022430	15737746	0.0795	0.5894
chr4	191154276	16034916	0.0839	0.6913
chr5	180915260	15223382	0.0841	0.6154
chr6	171115067	11980395	0.07	0.708
chr7	159138663	14012856	0.0881	1.337

chr8	146364022	26405817	0.1804	1.0033
chr9	141213431	12411368	0.0879	1.0234
chr10	135534747	14992802	0.1106	1.1859
chr11	135006516	9570318	0.0709	0.6778
chr12	133851895	13317644	0.0995	0.6734
chr13	115169878	6249392	0.0543	0.4815
chr14	107349540	6877087	0.0641	0.5467
chr15	102531392	7496163	0.0731	0.57
chr16	90354753	8849212	0.0979	0.9754
chr17	81195210	10047093	0.1237	0.8398
chr18	78077248	6686838	0.0856	1.2192
chr19	59128983	5866766	0.0992	1.6726
chr20	63025520	8118840	0.1288	0.8209
chr21	48129895	3984804	0.0828	0.6486
chr22	51304566	2322377	0.0453	0.4768
chrMT	16571	62420	3.7668	4.7445
chrX	155270560	16805281	0.1082	0.8032
chrY	59373566	1009208	0.017	0.9049

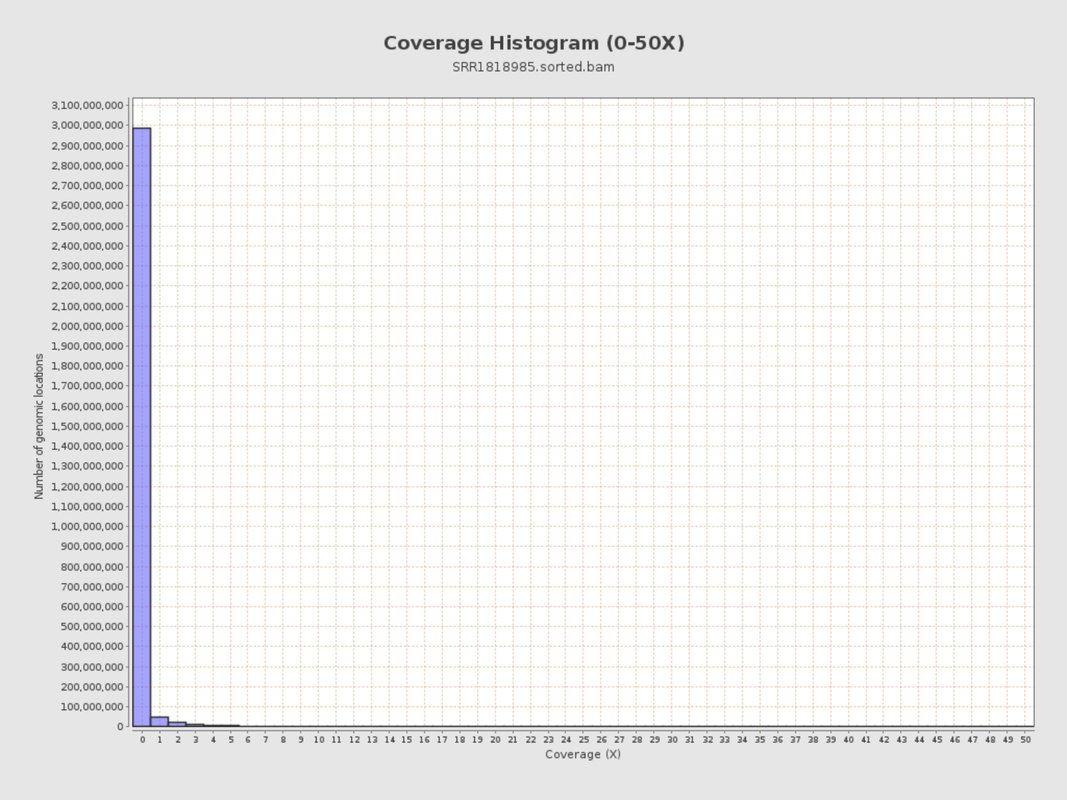
3. Results : Coverage across reference



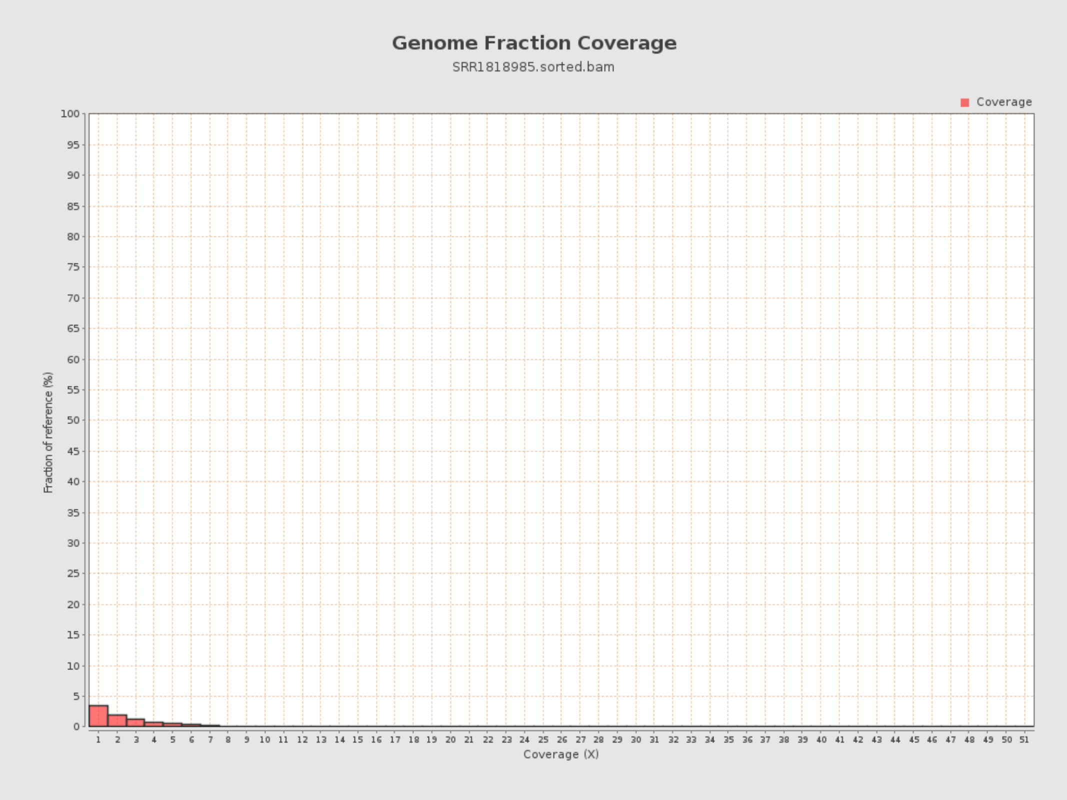
4. Results : Coverage Histogram



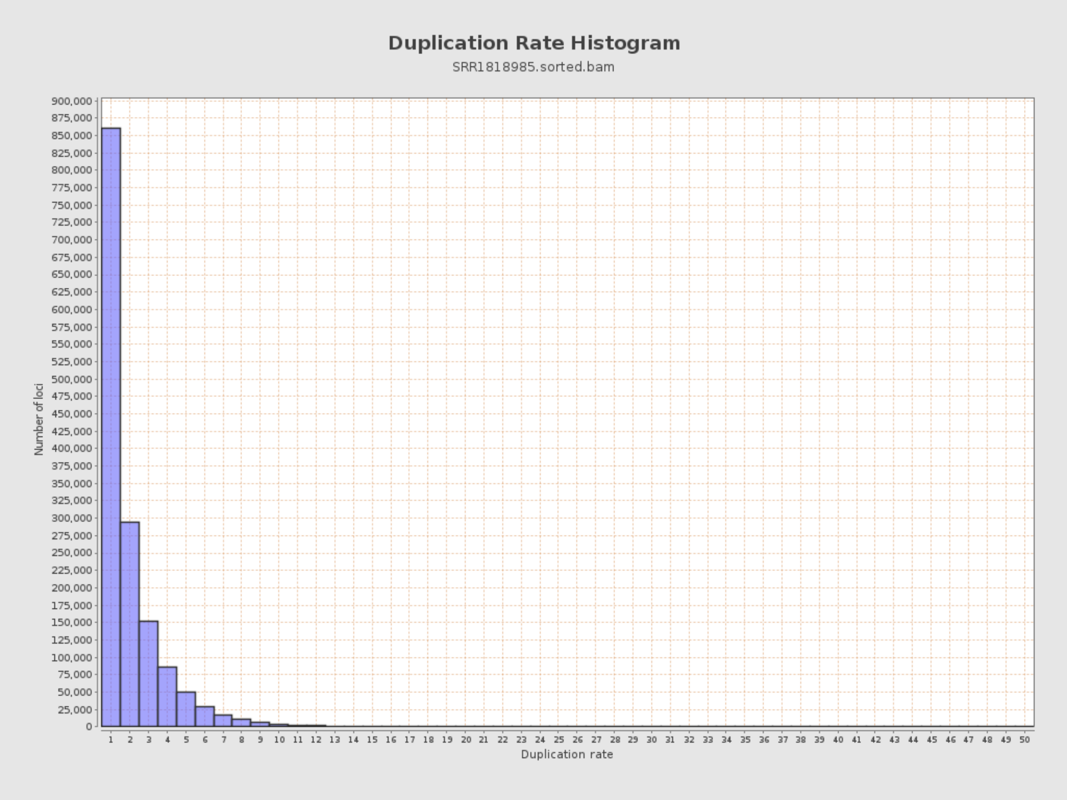
5. Results : Coverage Histogram (0-50X)



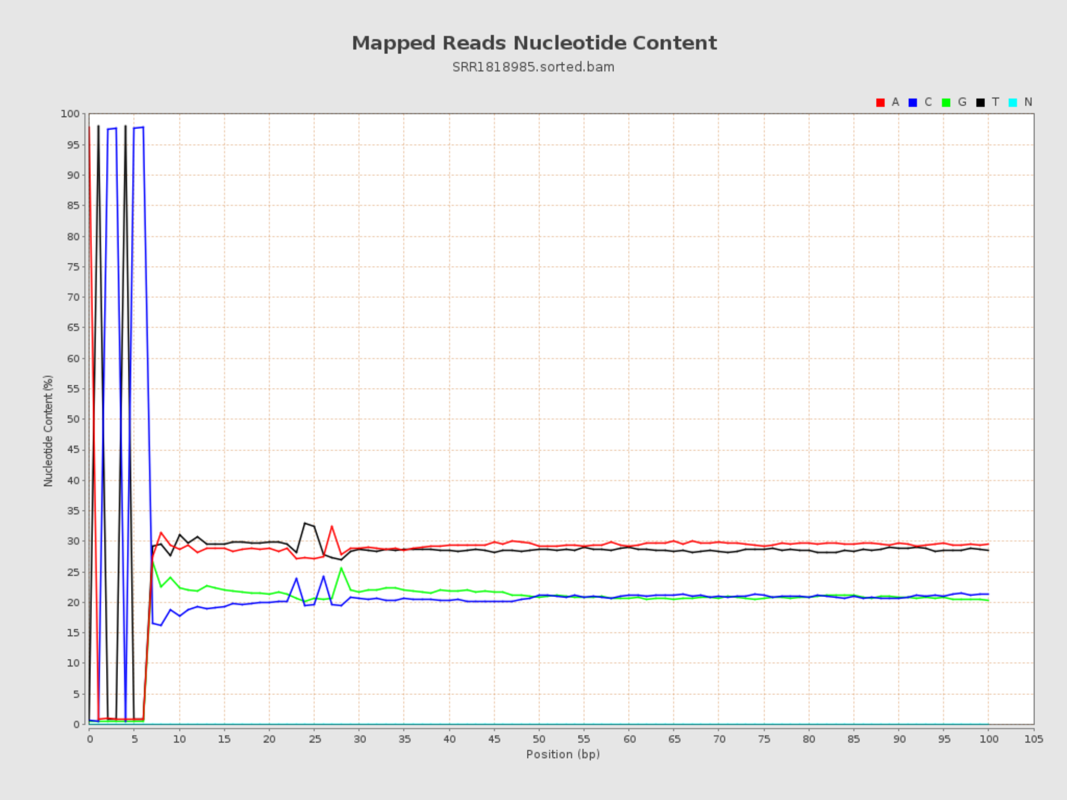
6. Results : Genome Fraction Coverage



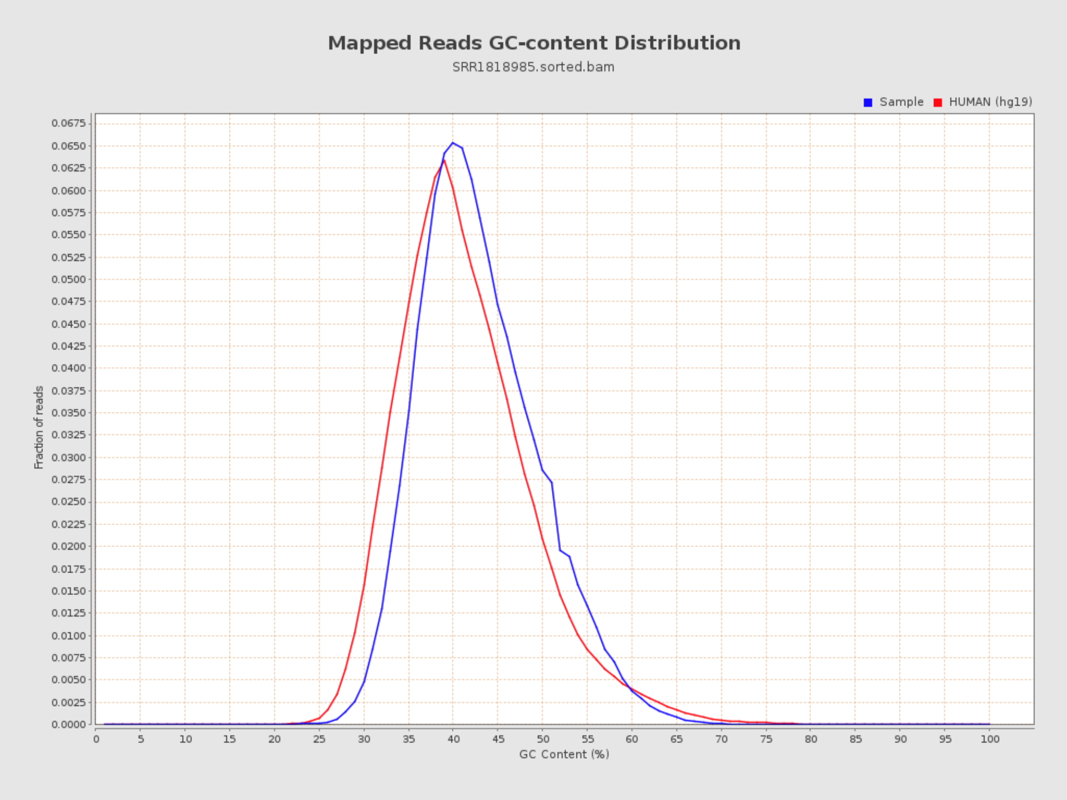
7. Results : Duplication Rate Histogram



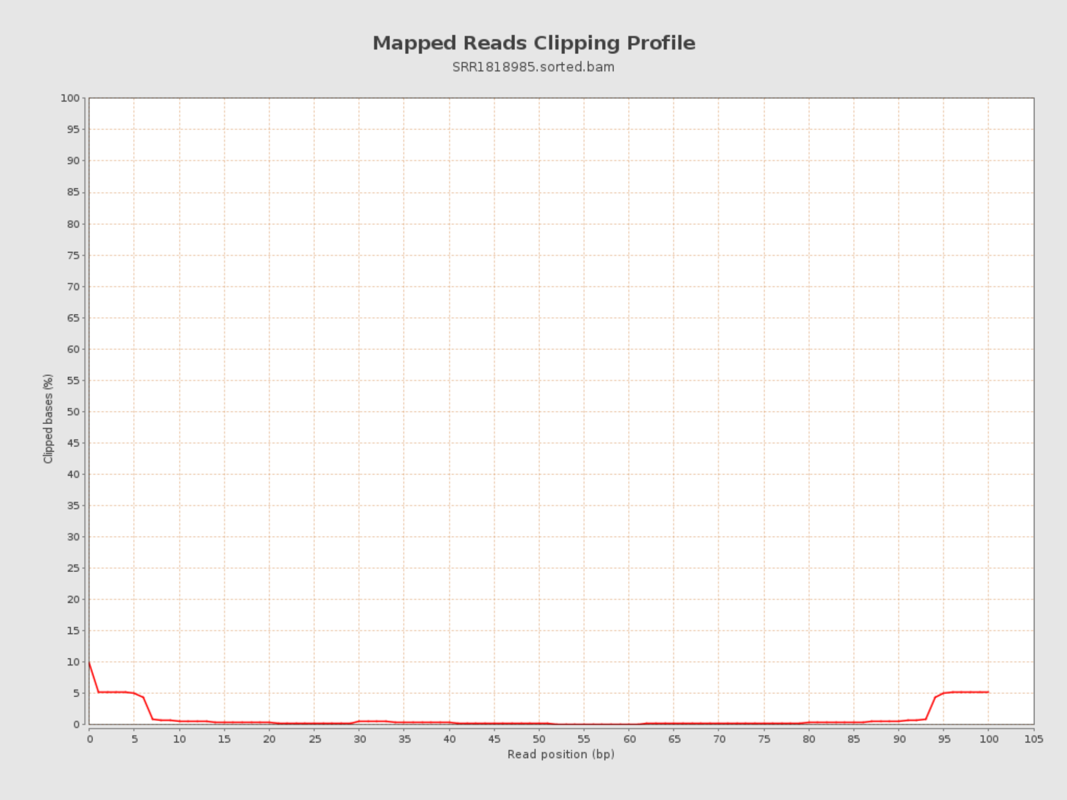
8. Results : Mapped Reads Nucleotide Content



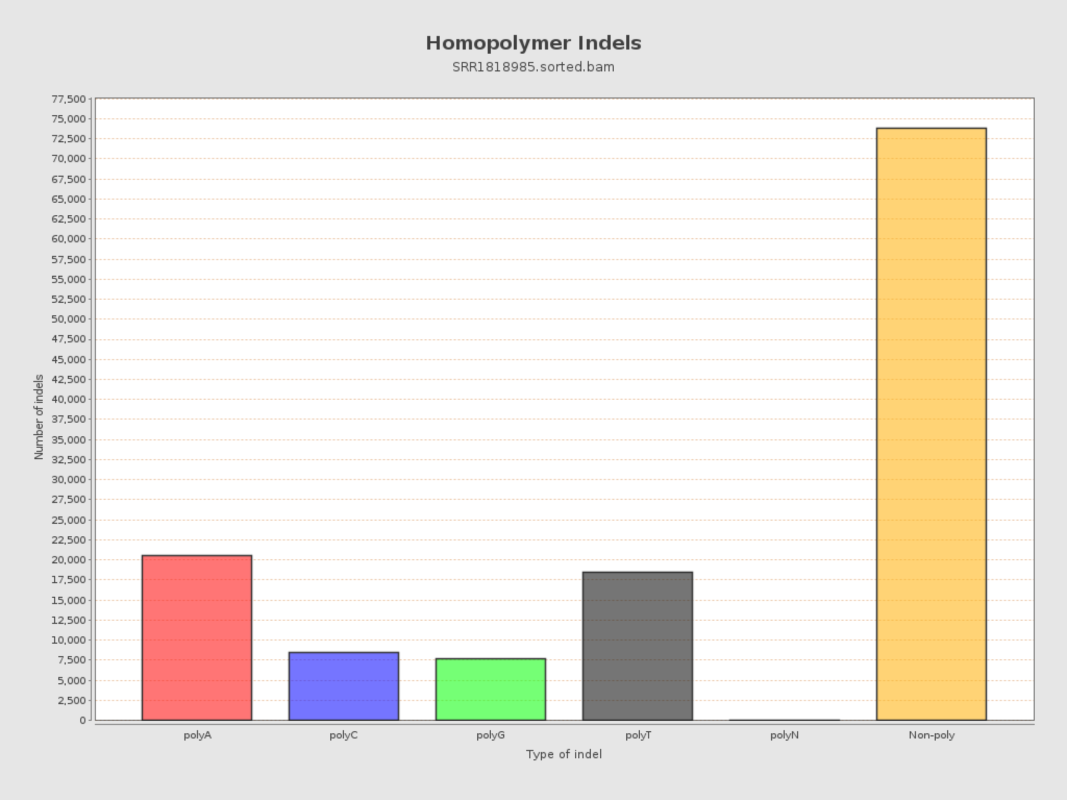
9. Results : Mapped Reads GC-content Distribution



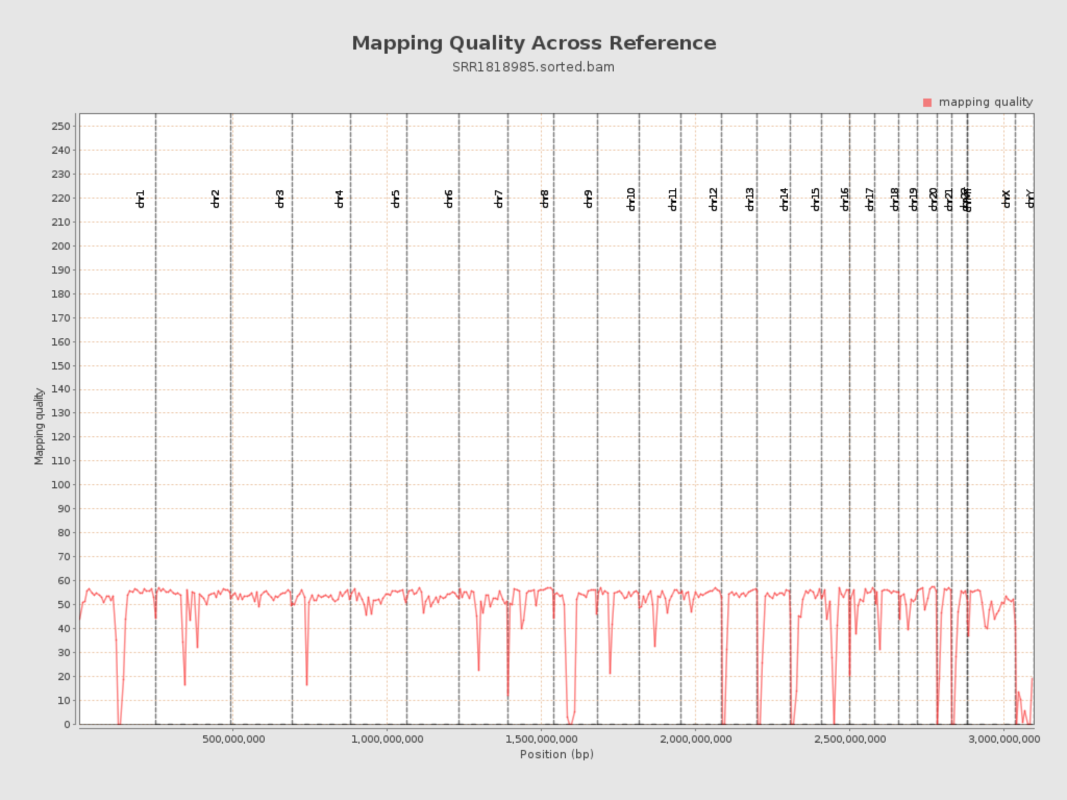
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram