Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 15:46:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089595.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_SRR089595 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089595.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 15:46:18 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089595.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	22,868,920
Mapped reads	18,438,597 / 80.63%
Unmapped reads	4,430,323 / 19.37%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	745 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	1,898,326 / 8.3%
Duplication rate	7.65%
Clipped reads	3,135,164 / 13.71%

2.2. ACGT Content

Number/percentage of A's	274,778,790 / 32.13%
Number/percentage of C's	175,806,003 / 20.56%
Number/percentage of T's	217,416,813 / 25.42%
Number/percentage of G's	186,932,542 / 21.86%
Number/percentage of N's	232,915 / 0.03%
GC Percentage	42.42%

2.3. Coverage

Mean	0.2763

Standard Deviation	1.4377

2.4. Mapping Quality

Mean Mapping Quality	42.88

2.5. Mismatches and indels

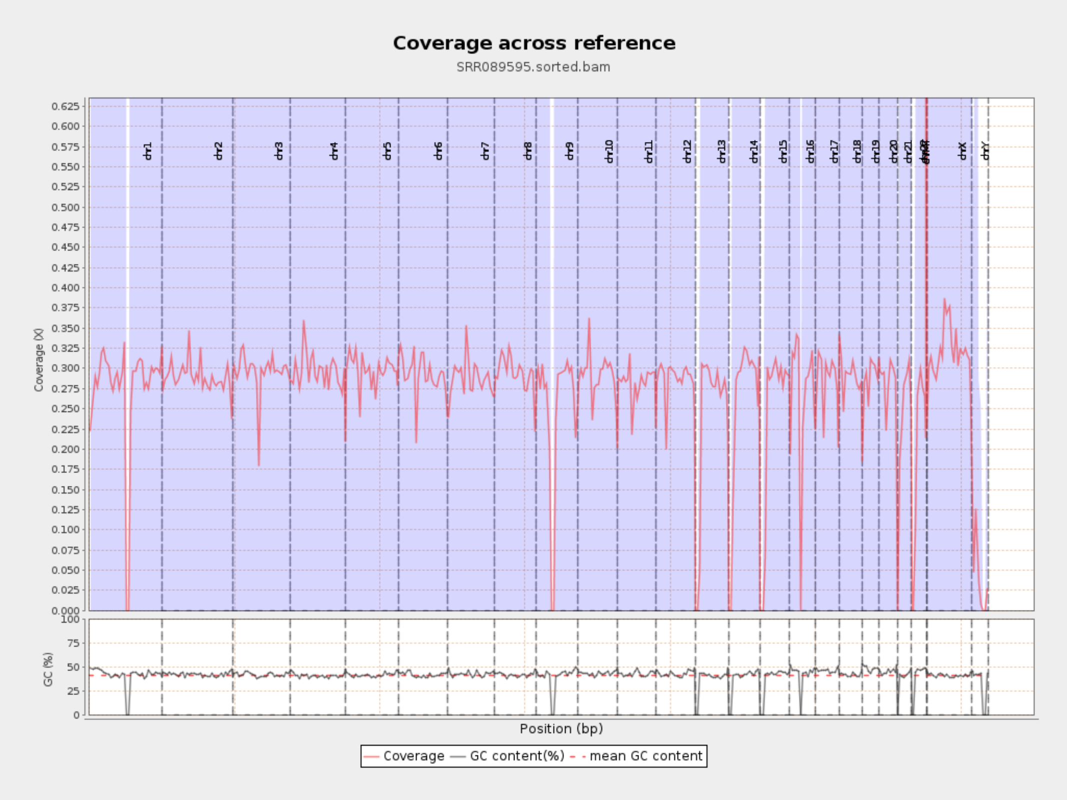
General error rate	0.47%
Mismatches	4,003,595
Insertions	38,818
Mapped reads with at least one insertion	0.21%
Deletions	117,463
Mapped reads with at least one deletion	0.64%
Homopolymer indels	42.83%

2.6. Chromosome stats

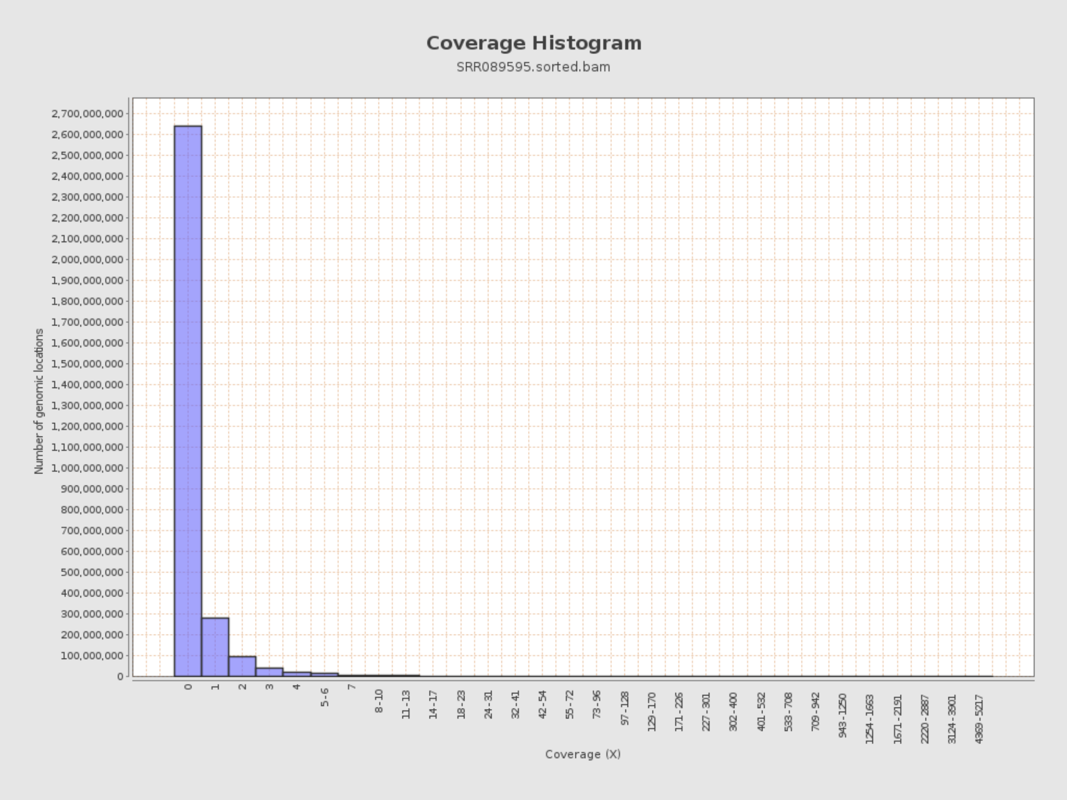
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	68185677	0.2736	1.9821
chr2	243199373	70559307	0.2901	1.5328
chr3	198022430	58704513	0.2965	0.9683
chr4	191154276	56680343	0.2965	1.0804
chr5	180915260	53867464	0.2977	0.9835
chr6	171115067	50128881	0.293	1.1426
chr7	159138663	46071888	0.2895	1.7772

chr8	146364022	43065985	0.2942	2.9585
chr9	141213431	34967884	0.2476	1.2178
chr10	135534747	39712932	0.293	1.4449
chr11	135006516	38035288	0.2817	1.2733
chr12	133851895	38451928	0.2873	0.9973
chr13	115169878	27421194	0.2381	0.8703
chr14	107349540	26962968	0.2512	1.0893
chr15	102531392	24208148	0.2361	0.8694
chr16	90354753	24137944	0.2671	1.0417
chr17	81195210	23067900	0.2841	1.0849
chr18	78077248	22742131	0.2913	1.8882
chr19	59128983	16994403	0.2874	1.8655
chr20	63025520	17618836	0.2796	1.0065
chr21	48129895	11258248	0.2339	1.0806
chr22	51304566	9765772	0.1903	0.7867
chrMT	16571	577478	34.8487	30.033
chrX	155270560	49642267	0.3197	1.2068
chrY	59373566	2513554	0.0423	0.6543

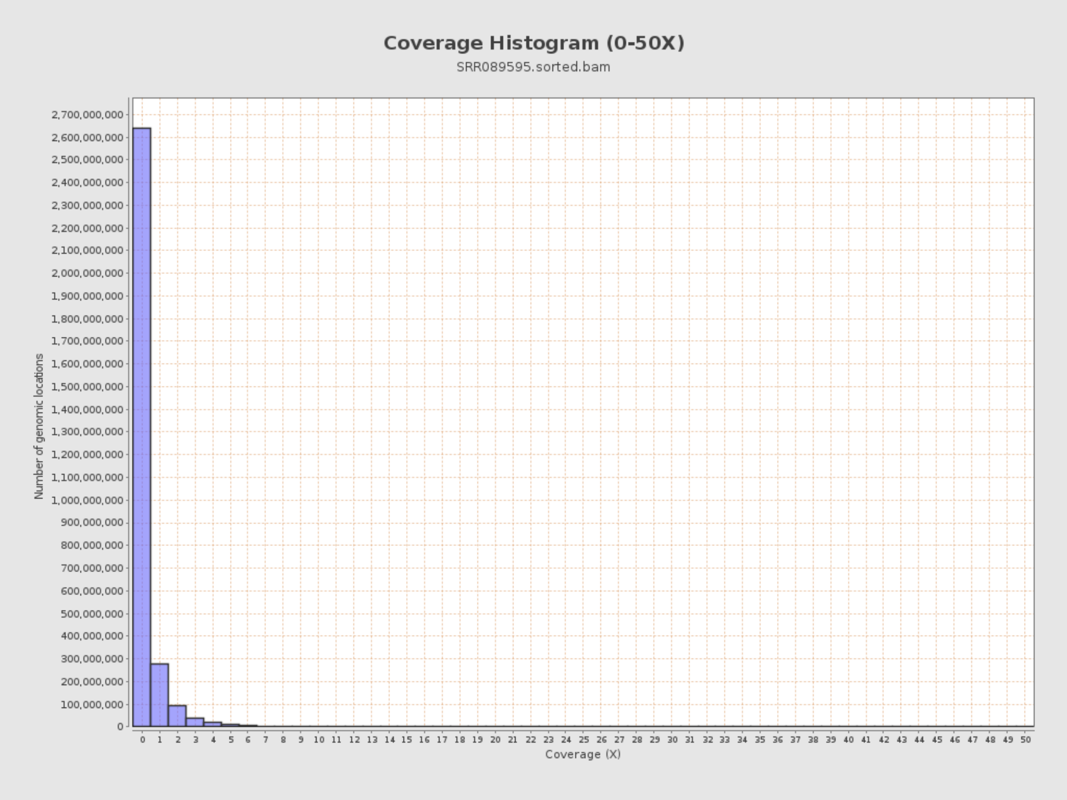
3. Results : Coverage across reference



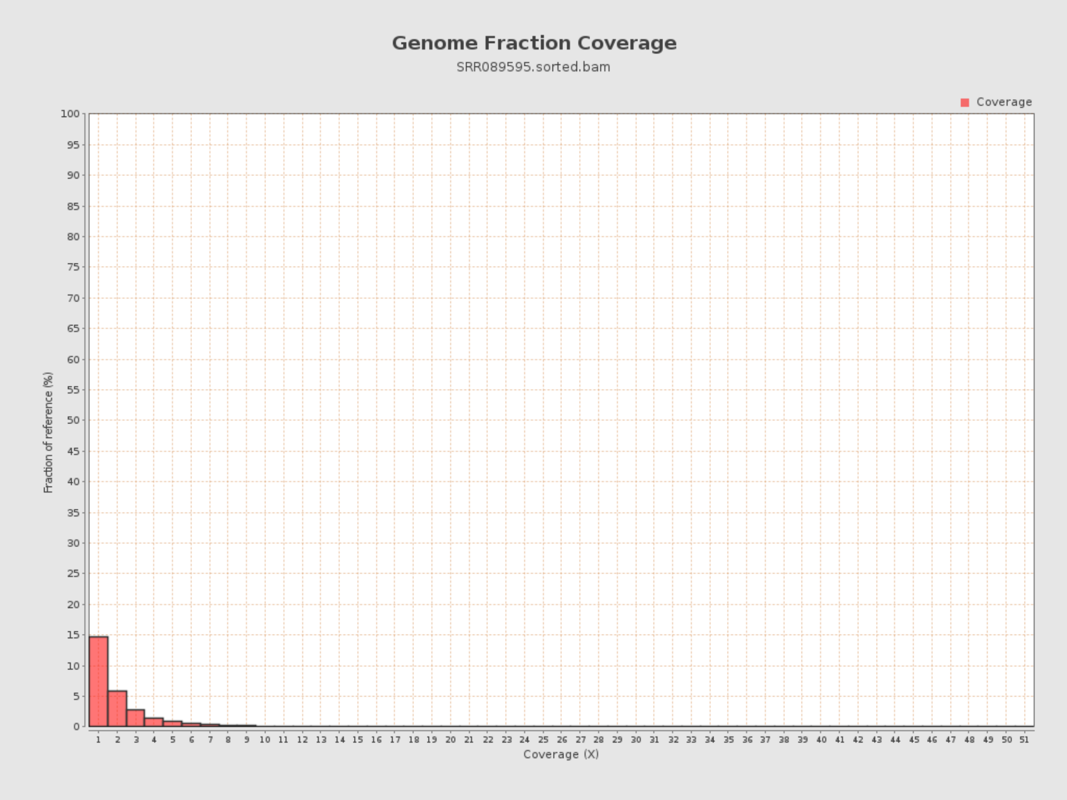
4. Results : Coverage Histogram



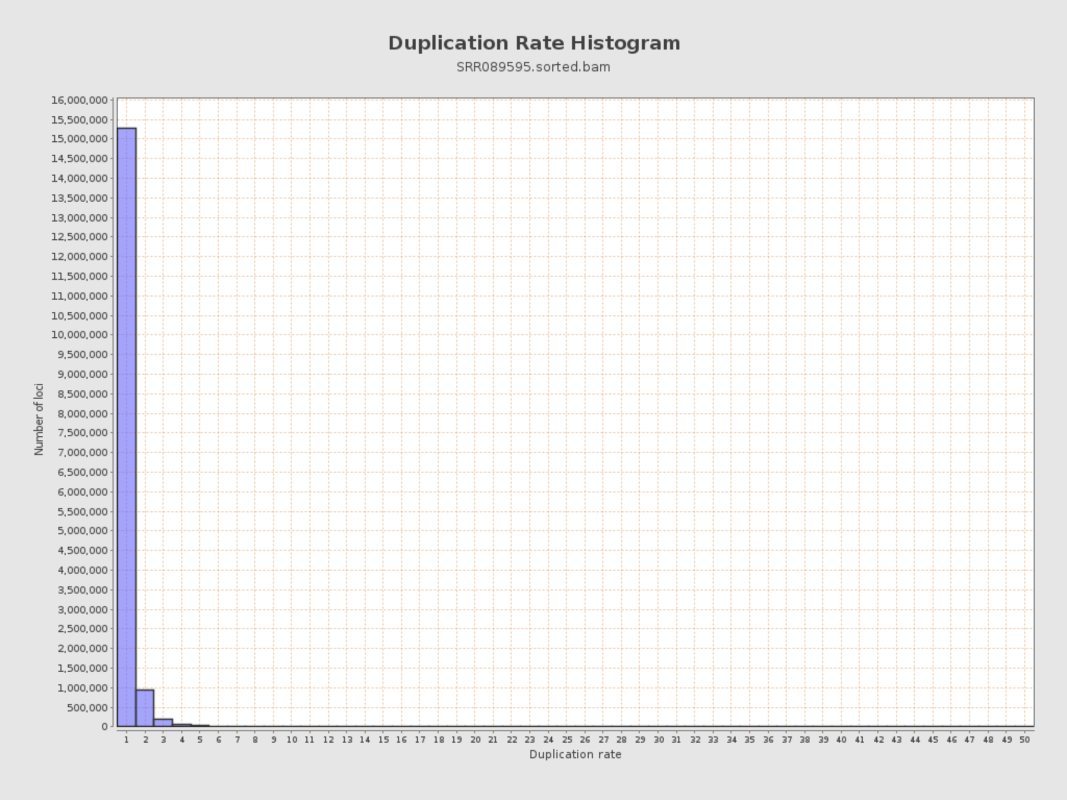
5. Results : Coverage Histogram (0-50X)



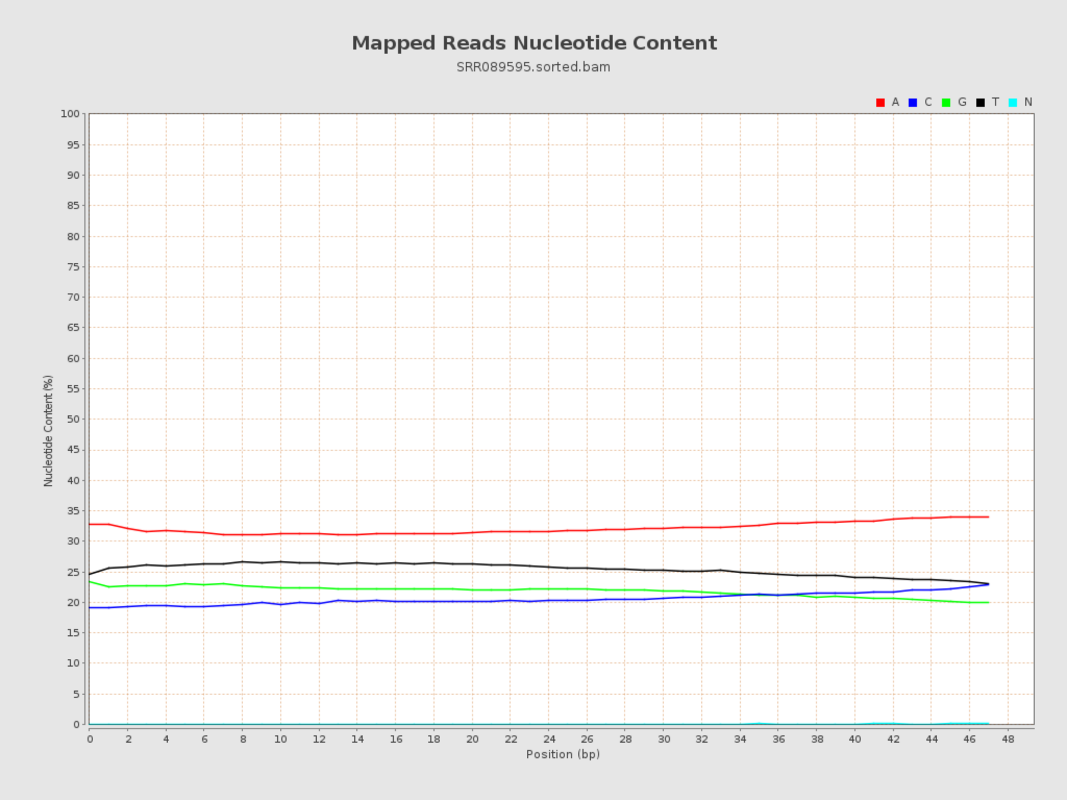
6. Results : Genome Fraction Coverage



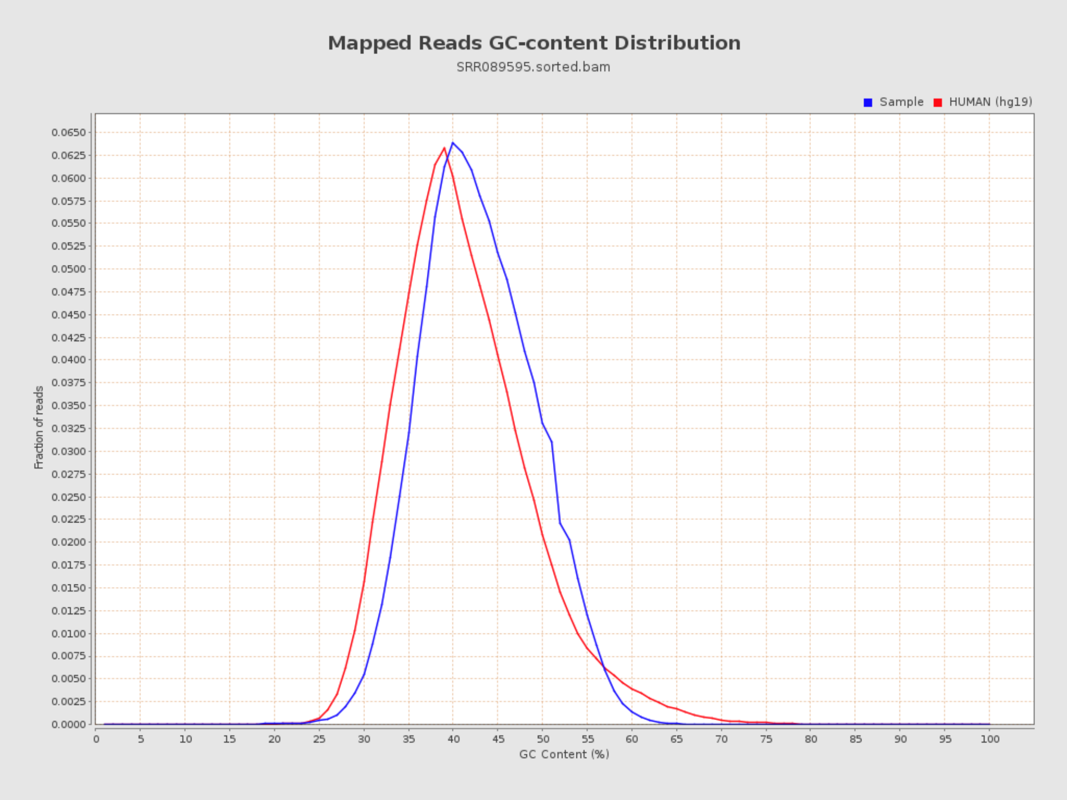
7. Results : Duplication Rate Histogram



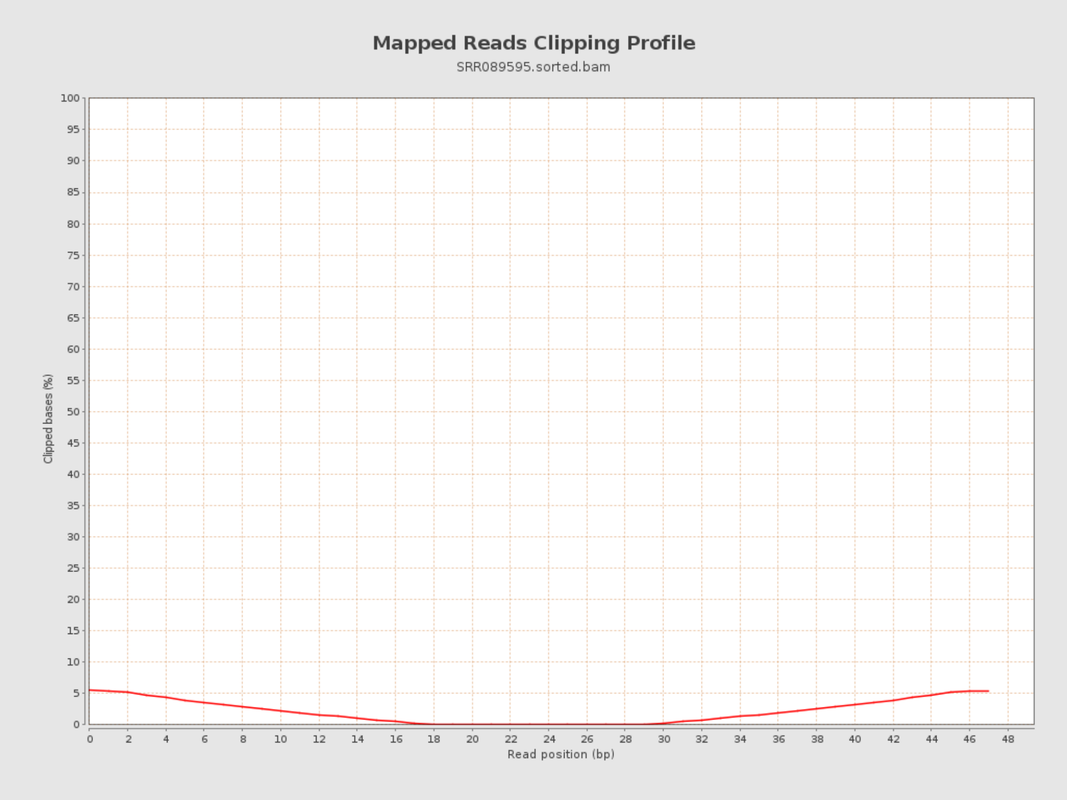
8. Results : Mapped Reads Nucleotide Content



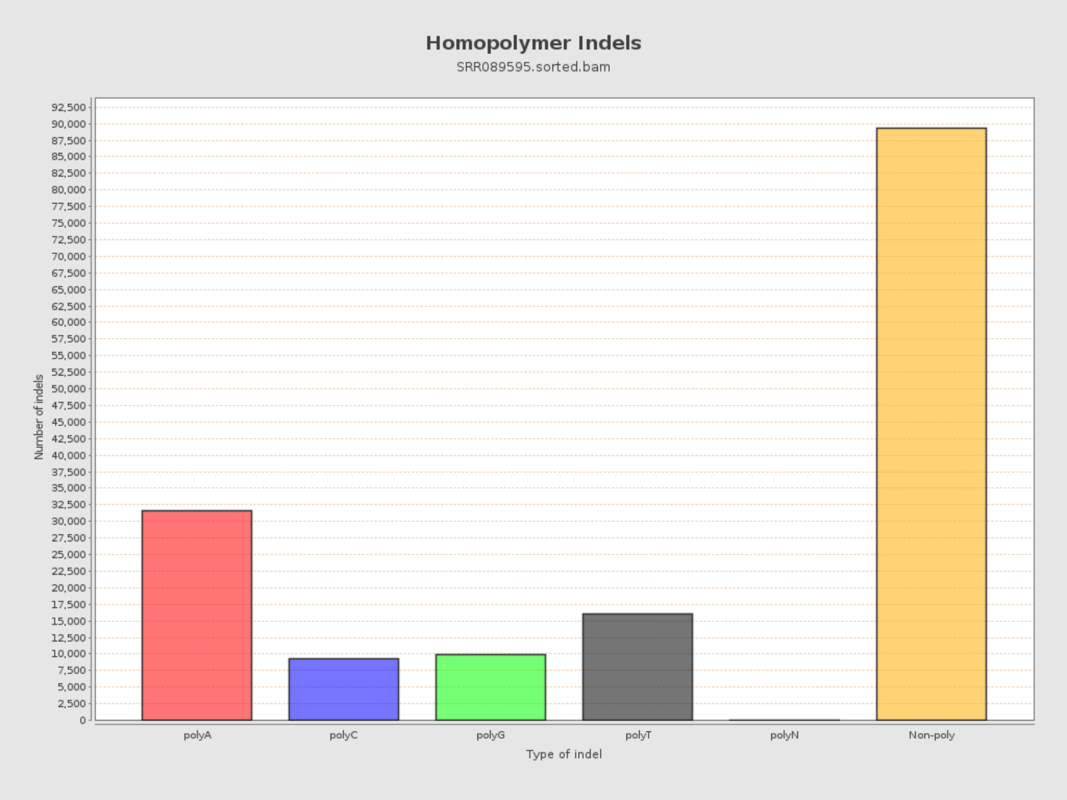
9. Results : Mapped Reads GC-content Distribution



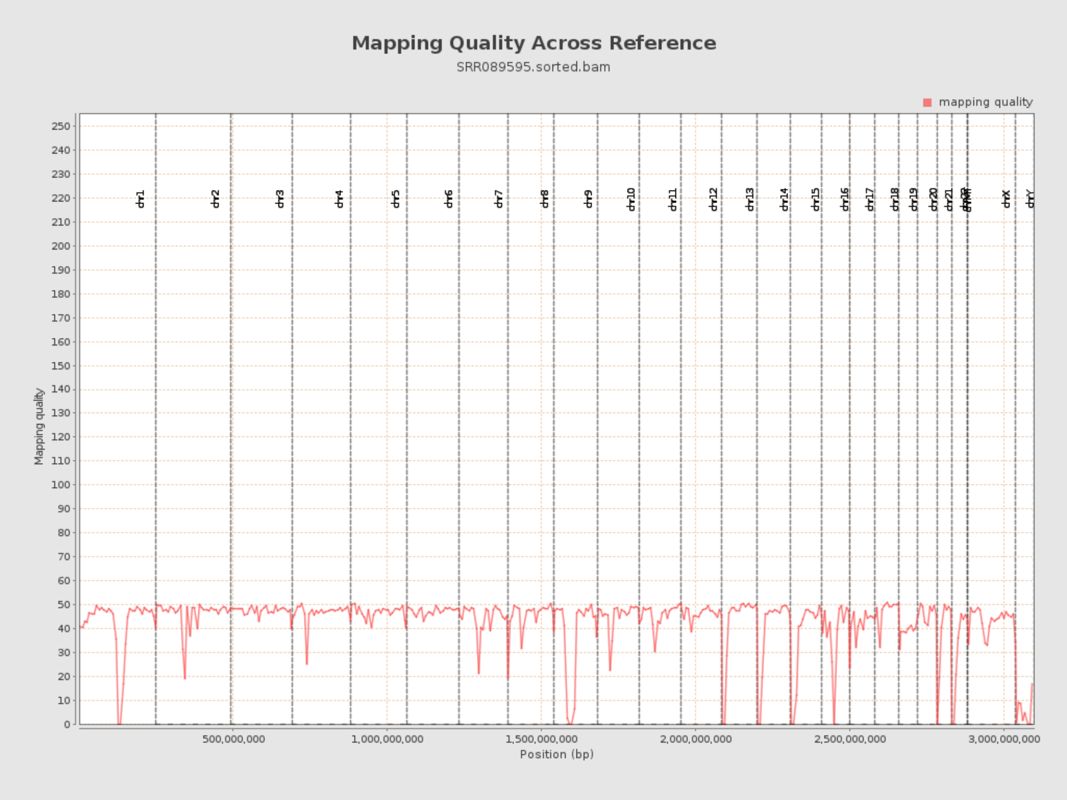
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram