Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 11:44:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716400.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_SRR9716400 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716400.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 11:44:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716400.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,261,292
Mapped reads	2,062,209 / 91.2%
Unmapped reads	199,083 / 8.8%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	34,576 / 1.53%
Read min/max/mean length	30 / 101 / 101.56
Duplicated reads (estimated)	106,627 / 4.72%
Duplication rate	3.18%
Clipped reads	2,092,347 / 92.53%

2.2. ACGT Content

Number/percentage of A's	39,366,399 / 24.4%
Number/percentage of C's	31,252,872 / 19.37%
Number/percentage of T's	52,164,018 / 32.33%
Number/percentage of G's	38,570,907 / 23.9%
Number/percentage of N's	8,965 / 0.01%
GC Percentage	43.27%

2.3. Coverage

Mean	0.0521

Standard Deviation	0.6094

2.4. Mapping Quality

Mean Mapping Quality	44.81

2.5. Mismatches and indels

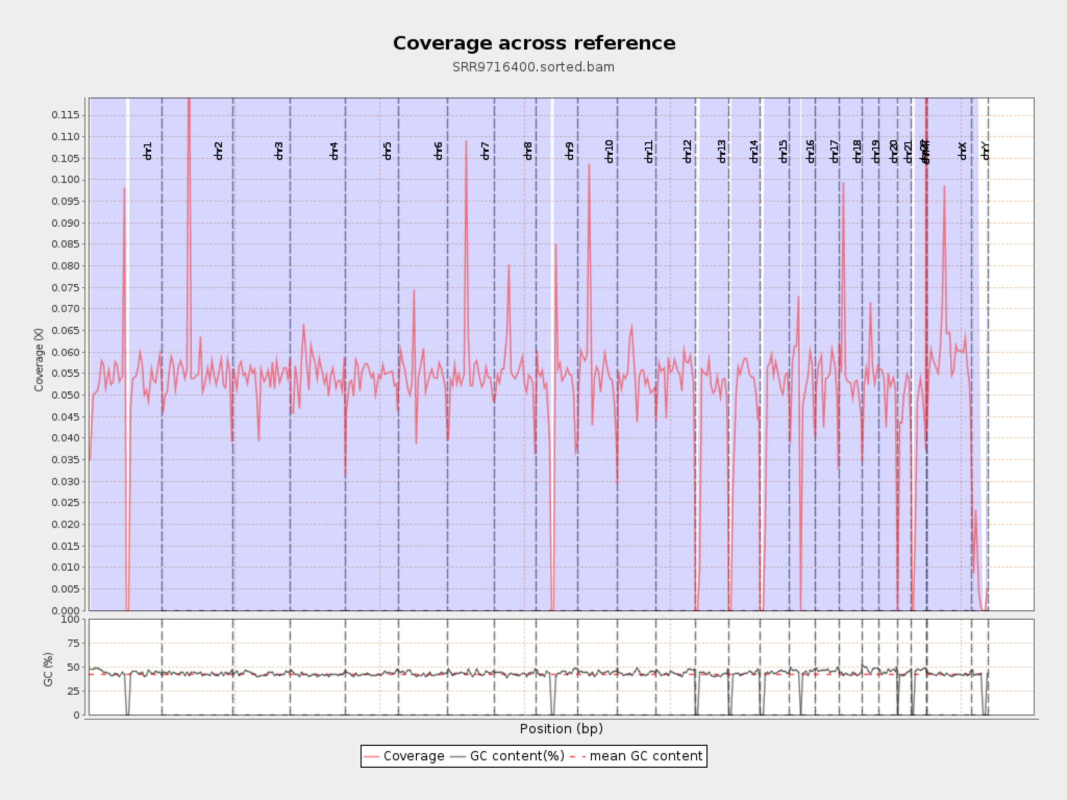
General error rate	0.86%
Mismatches	1,354,328
Insertions	14,849
Mapped reads with at least one insertion	0.71%
Deletions	40,635
Mapped reads with at least one deletion	1.94%
Homopolymer indels	44.47%

2.6. Chromosome stats

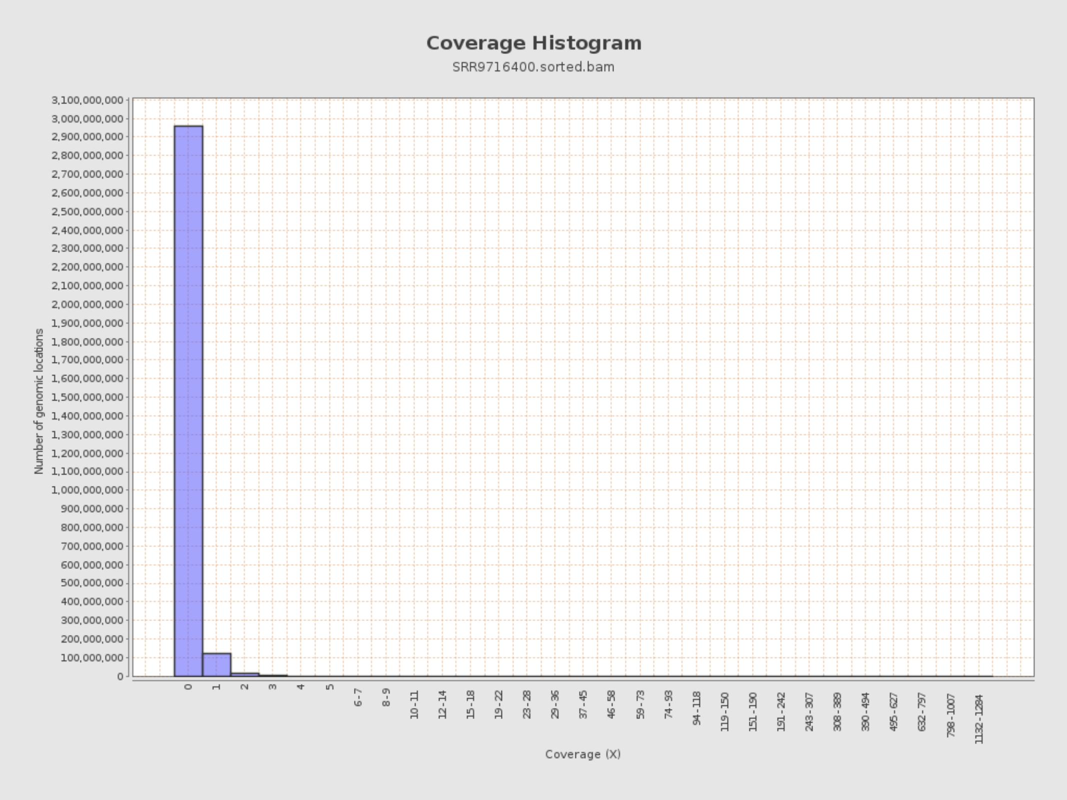
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12823769	0.0514	1.0214
chr2	243199373	13953476	0.0574	0.892
chr3	198022430	10725426	0.0542	0.271
chr4	191154276	10438464	0.0546	0.2954
chr5	180915260	9765499	0.054	0.2777
chr6	171115067	9360863	0.0547	0.373
chr7	159138663	9014853	0.0566	0.7979

chr8	146364022	8094924	0.0553	0.826
chr9	141213431	6834128	0.0484	0.6864
chr10	135534747	7726771	0.057	0.5541
chr11	135006516	7257268	0.0538	0.5857
chr12	133851895	7354835	0.0549	0.2835
chr13	115169878	5095260	0.0442	0.2382
chr14	107349540	4860622	0.0453	0.3923
chr15	102531392	4551601	0.0444	0.2485
chr16	90354753	4592510	0.0508	0.3268
chr17	81195210	4293928	0.0529	0.3113
chr18	78077248	4475448	0.0573	1.3113
chr19	59128983	3303537	0.0559	0.7707
chr20	63025520	3227442	0.0512	0.2886
chr21	48129895	2088453	0.0434	0.2673
chr22	51304566	1739202	0.0339	0.2102
chrMT	16571	14187	0.8561	1.1156
chrX	155270560	9409819	0.0606	0.4479
chrY	59373566	431425	0.0073	0.1898

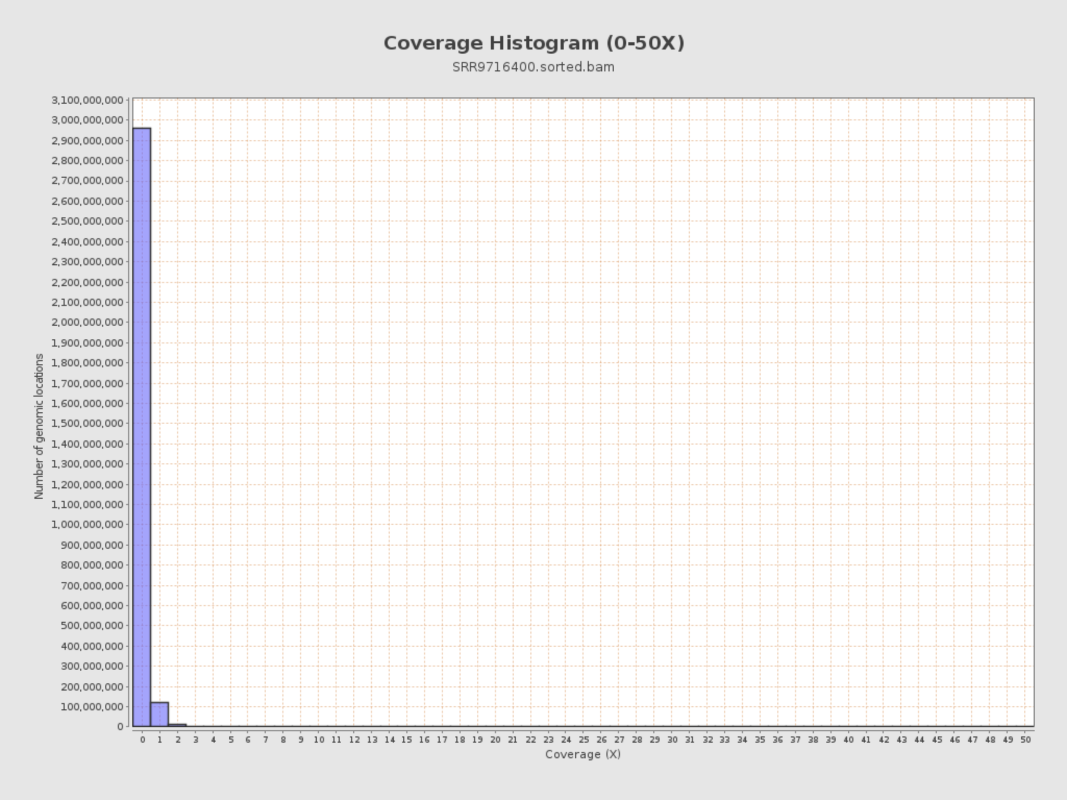
3. Results : Coverage across reference



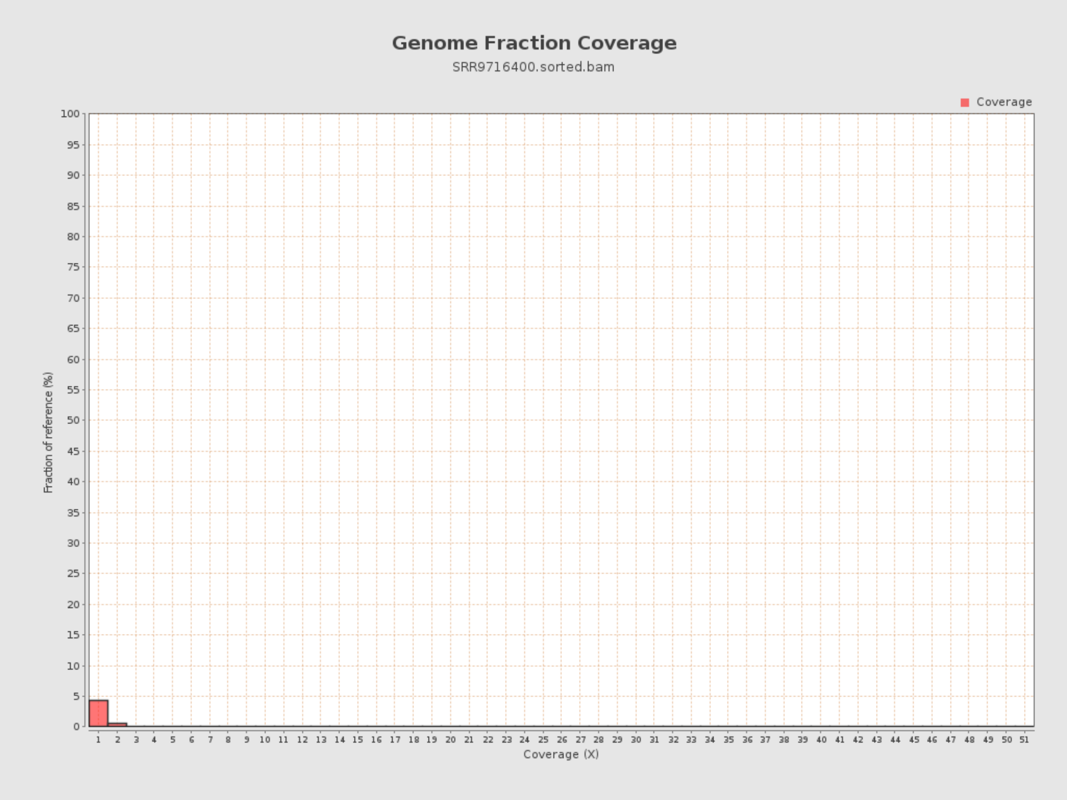
4. Results : Coverage Histogram



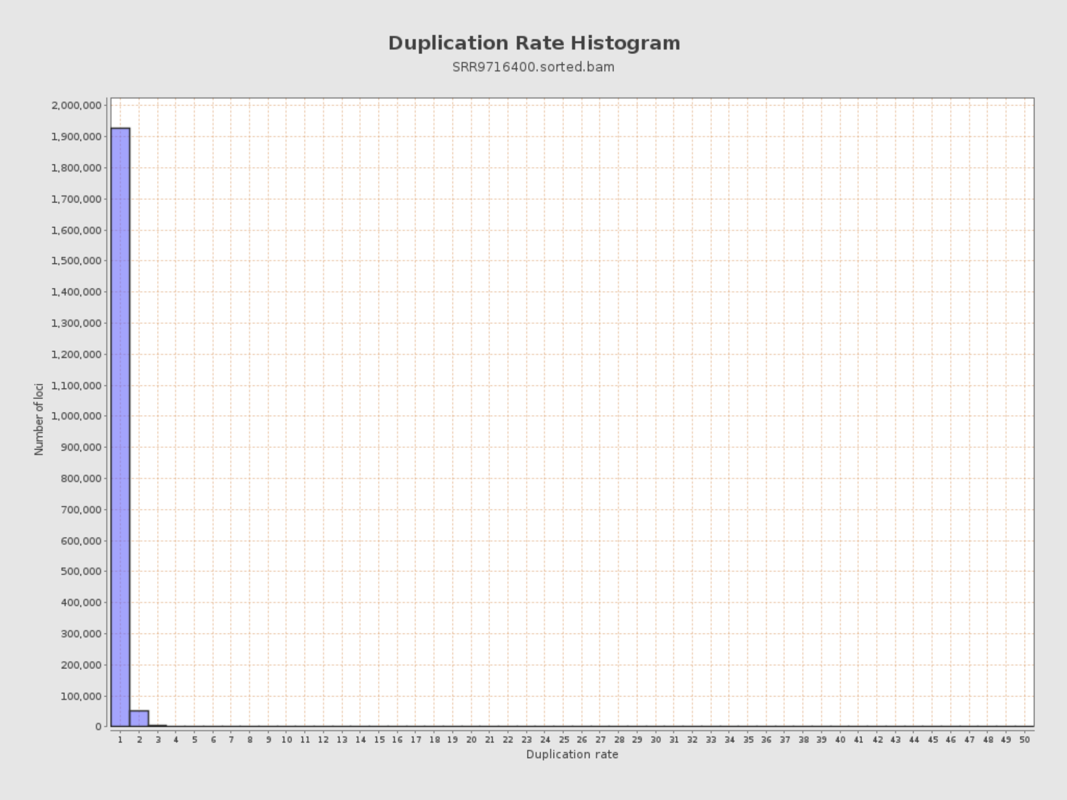
5. Results : Coverage Histogram (0-50X)



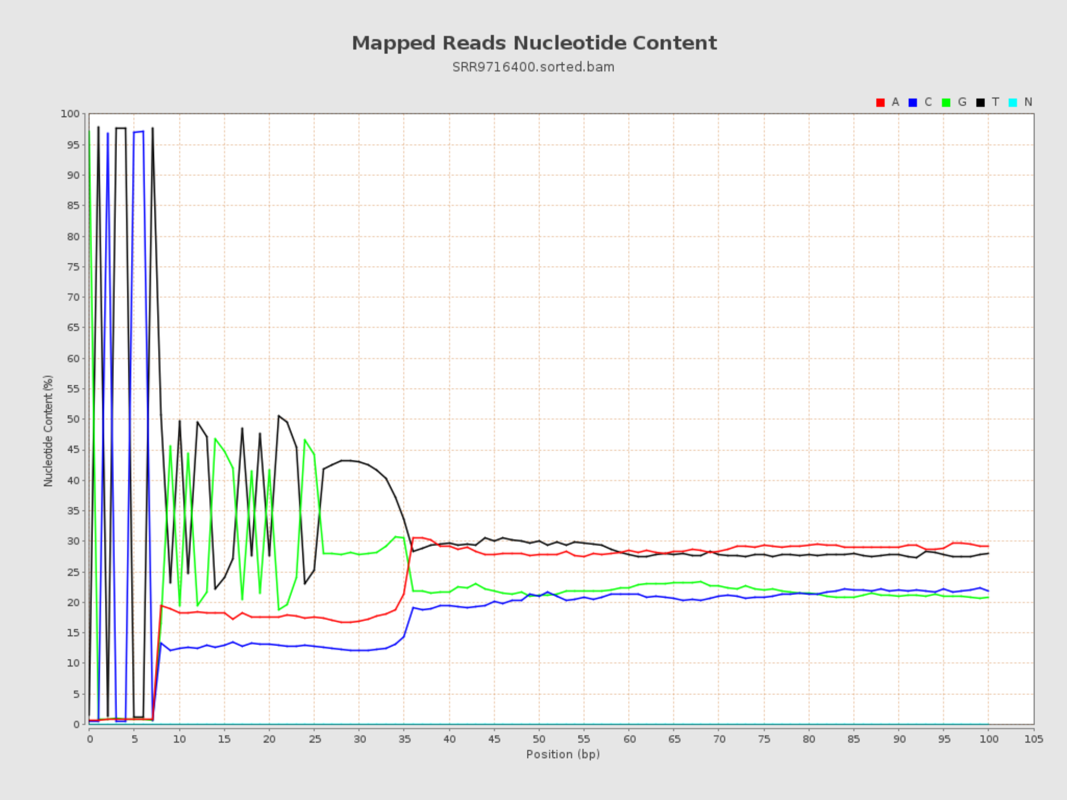
6. Results : Genome Fraction Coverage



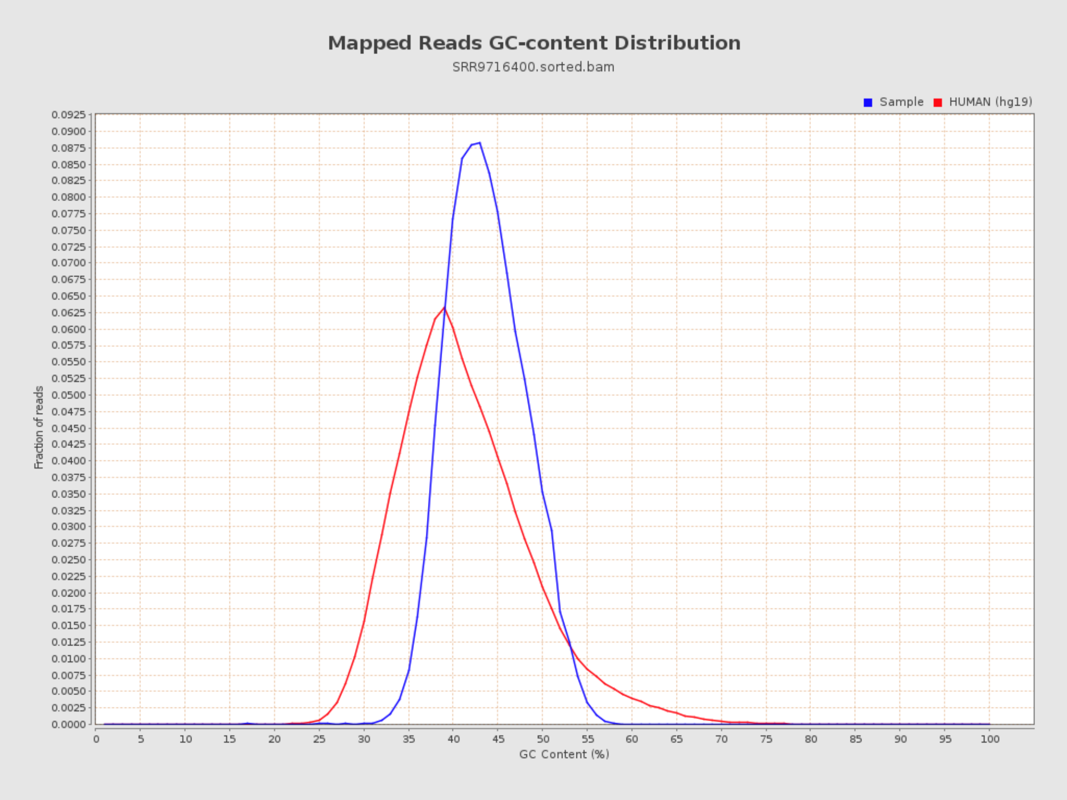
7. Results : Duplication Rate Histogram



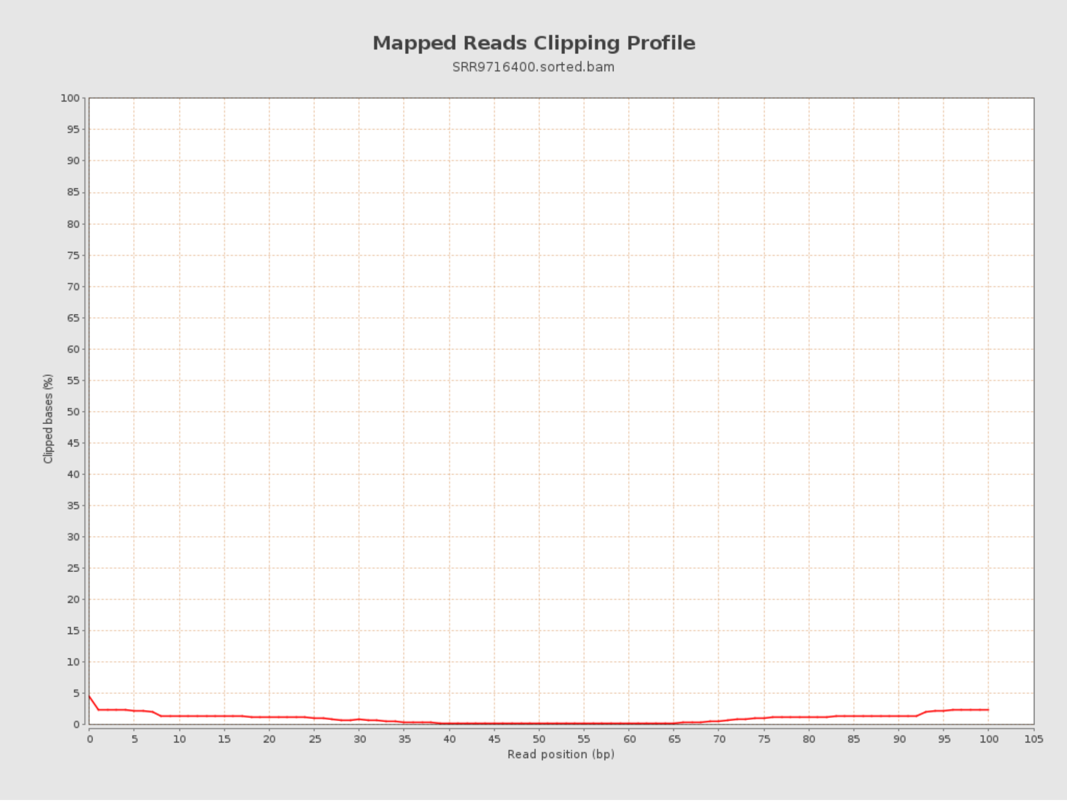
8. Results : Mapped Reads Nucleotide Content



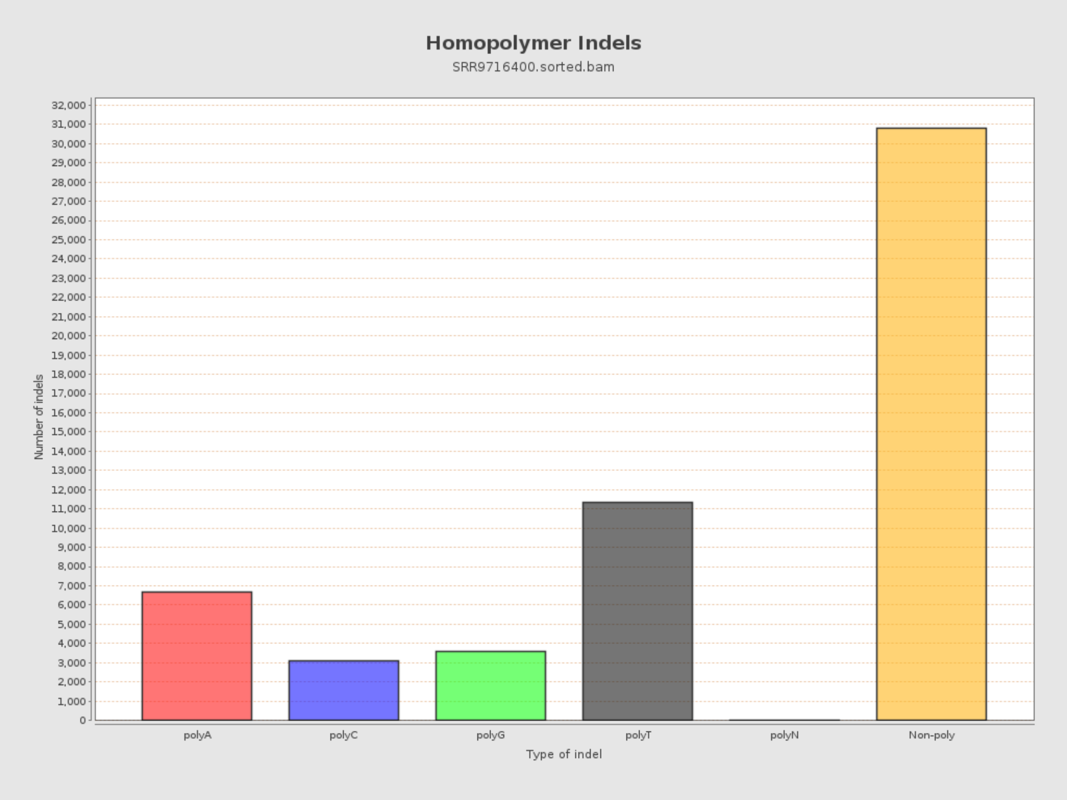
9. Results : Mapped Reads GC-content Distribution



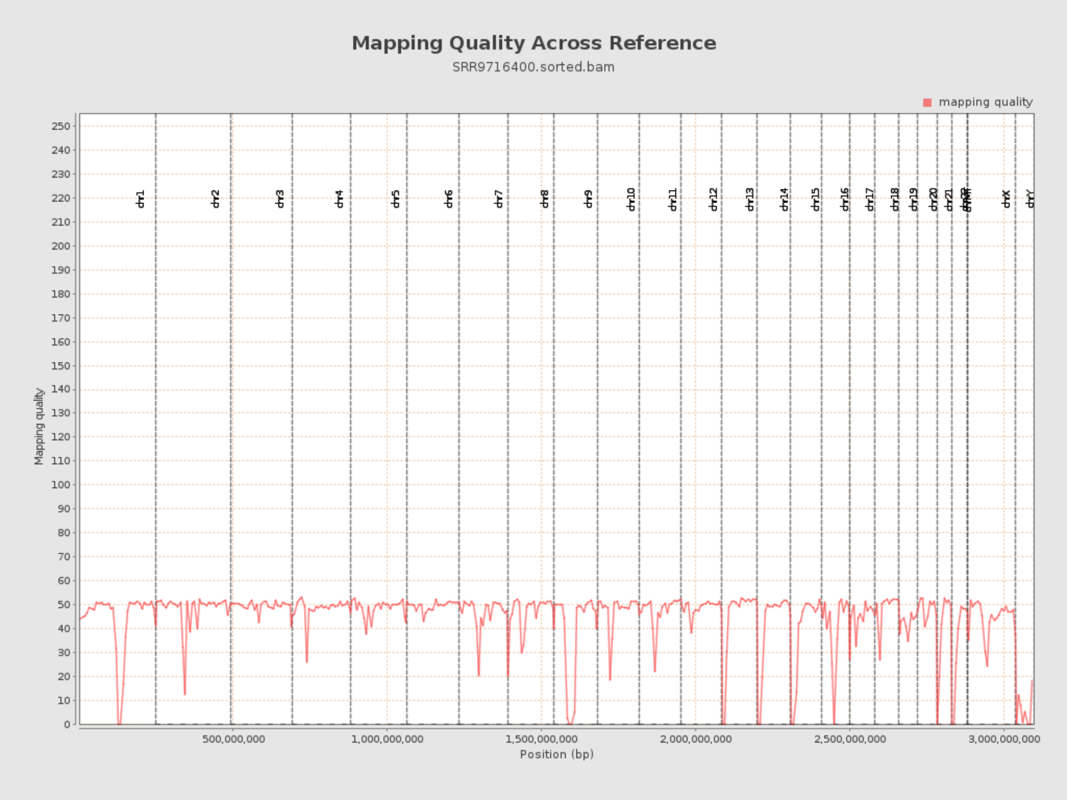
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram