Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 01:31:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716633.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_SRR9716633 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716633.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 01:31:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716633.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,249,167
Mapped reads	2,304,421 / 54.23%
Unmapped reads	1,944,746 / 45.77%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,819 / 0.28%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	88,950 / 2.09%
Duplication rate	2.92%
Clipped reads	2,307,822 / 54.31%

2.2. ACGT Content

Number/percentage of A's	34,883,249 / 25.99%
Number/percentage of C's	25,592,313 / 19.07%
Number/percentage of T's	40,454,250 / 30.15%
Number/percentage of G's	33,265,881 / 24.79%
Number/percentage of N's	1,913 / 0%
GC Percentage	43.86%

2.3. Coverage

Mean	0.0434

Standard Deviation	0.3645

2.4. Mapping Quality

Mean Mapping Quality	44.43

2.5. Mismatches and indels

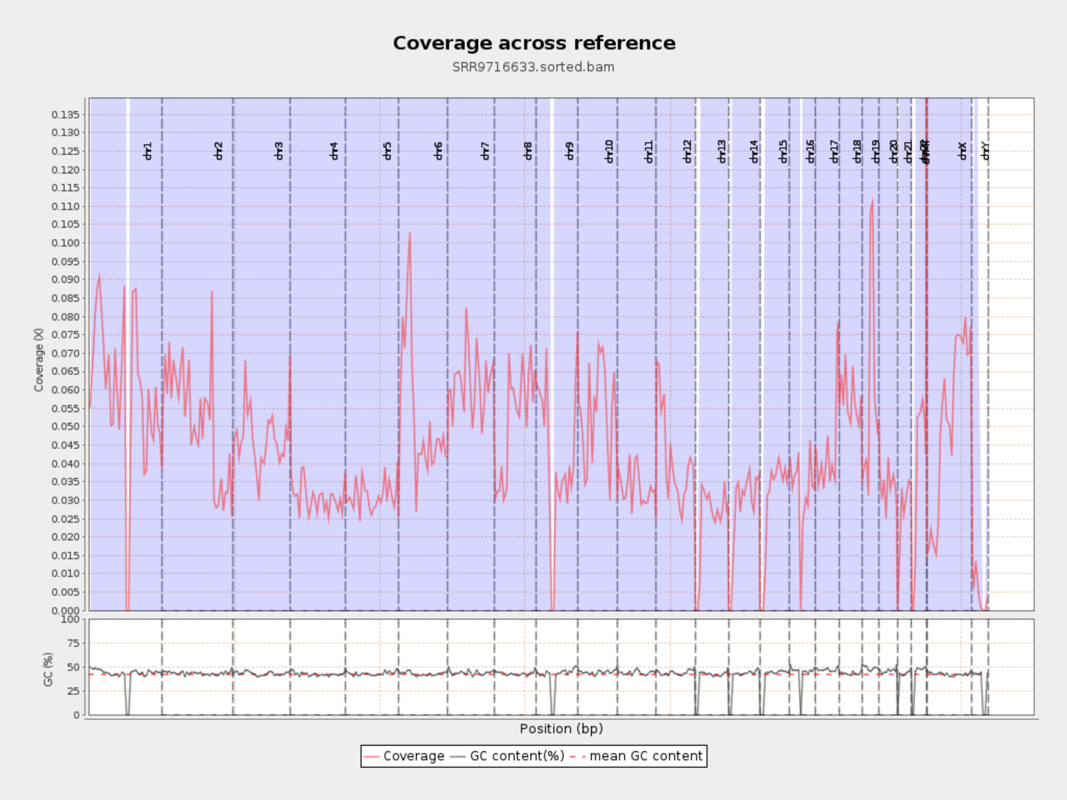
General error rate	0.51%
Mismatches	655,946
Insertions	11,680
Mapped reads with at least one insertion	0.5%
Deletions	24,345
Mapped reads with at least one deletion	1.05%
Homopolymer indels	37.65%

2.6. Chromosome stats

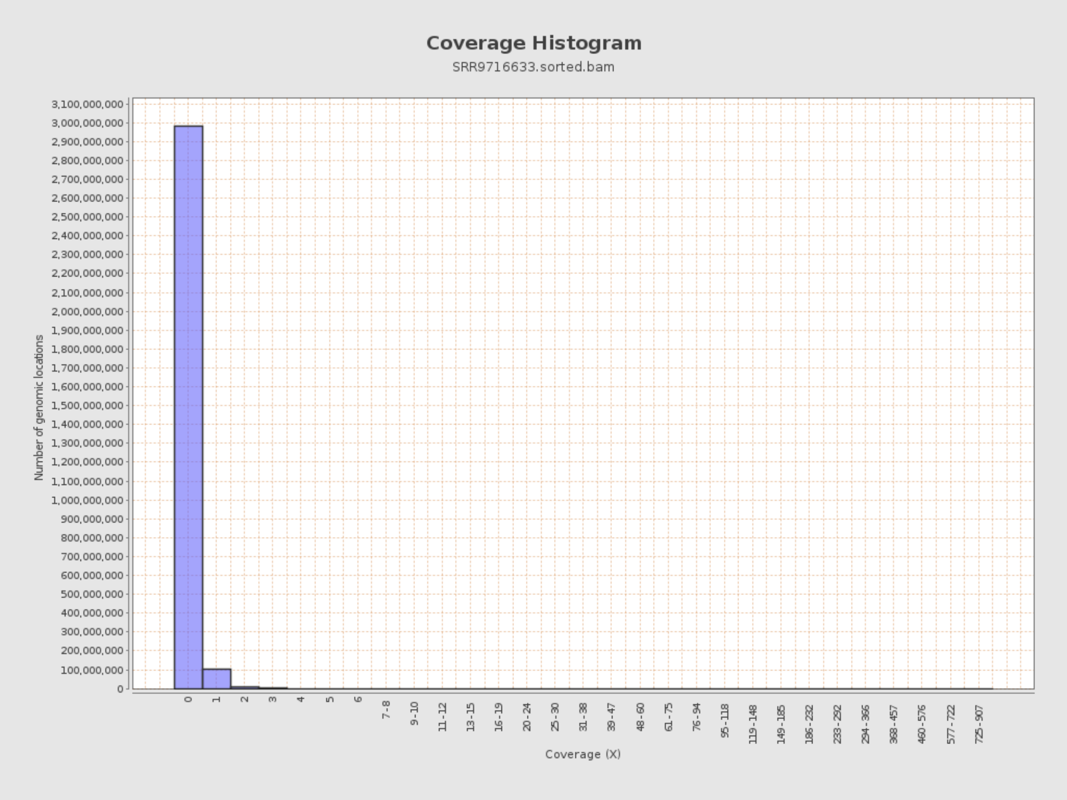
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14829270	0.0595	0.761
chr2	243199373	12614854	0.0519	0.439
chr3	198022430	9188688	0.0464	0.2424
chr4	191154276	5826039	0.0305	0.2089
chr5	180915260	5626549	0.0311	0.2003
chr6	171115067	8947056	0.0523	0.2927
chr7	159138663	9868708	0.062	0.5188

chr8	146364022	7632365	0.0521	0.2971
chr9	141213431	5581820	0.0395	0.2957
chr10	135534747	7305666	0.0539	0.332
chr11	135006516	4537566	0.0336	0.2658
chr12	133851895	5478742	0.0409	0.2354
chr13	115169878	2796529	0.0243	0.1748
chr14	107349540	2929405	0.0273	0.2164
chr15	102531392	3000286	0.0293	0.2008
chr16	90354753	2905784	0.0322	0.2158
chr17	81195210	3587907	0.0442	0.2437
chr18	78077248	4513957	0.0578	0.4957
chr19	59128983	3585108	0.0606	0.5172
chr20	63025520	2129378	0.0338	0.2086
chr21	48129895	1272246	0.0264	0.1975
chr22	51304566	1852036	0.0361	0.2147
chrMT	16571	7250	0.4375	0.7387
chrX	155270560	7944916	0.0512	0.2939
chrY	59373566	273614	0.0046	0.1023

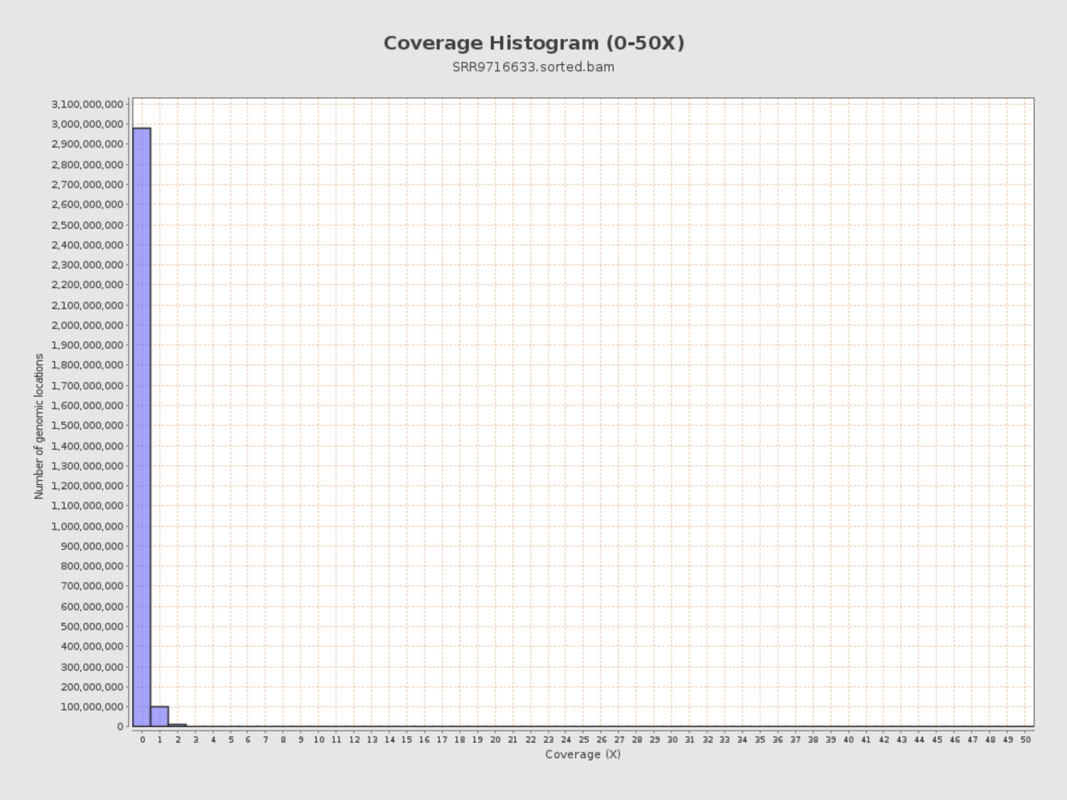
3. Results : Coverage across reference



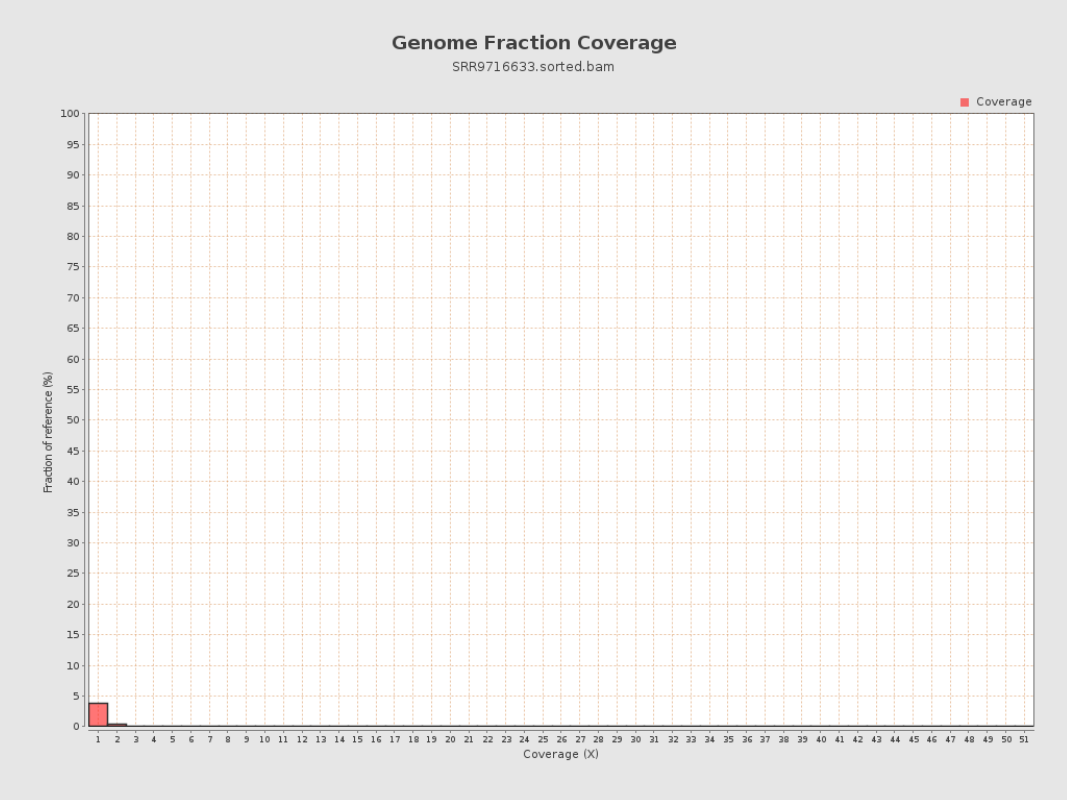
4. Results : Coverage Histogram



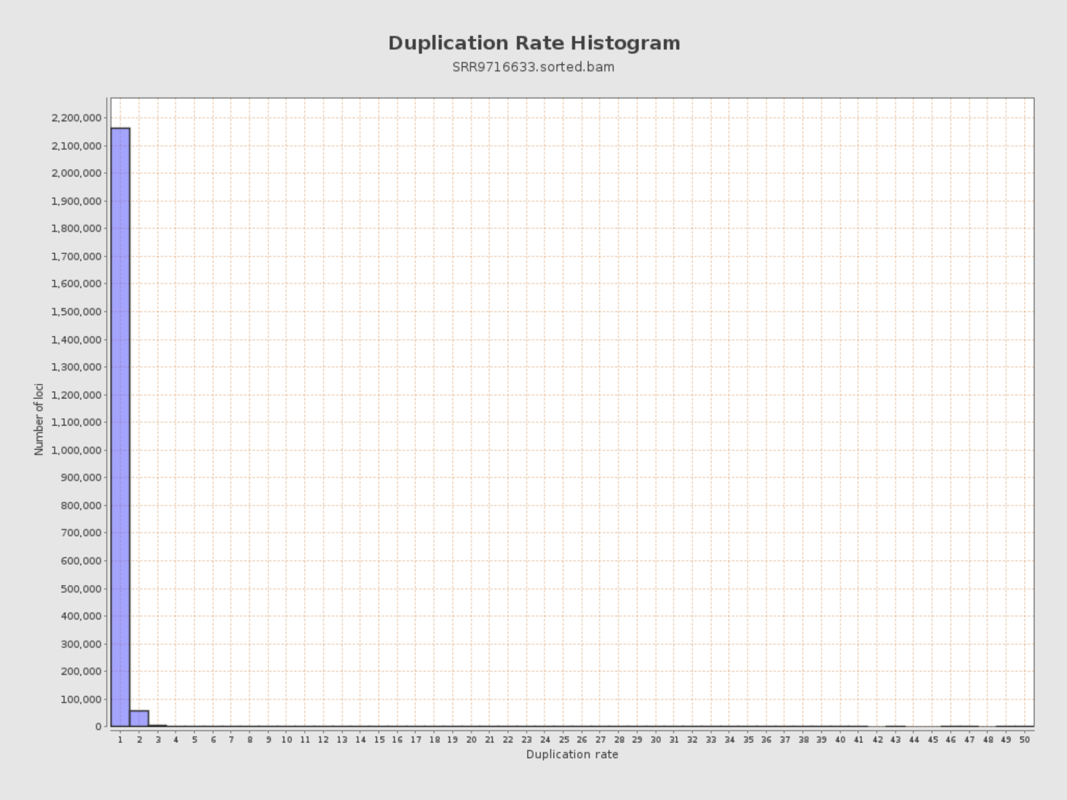
5. Results : Coverage Histogram (0-50X)



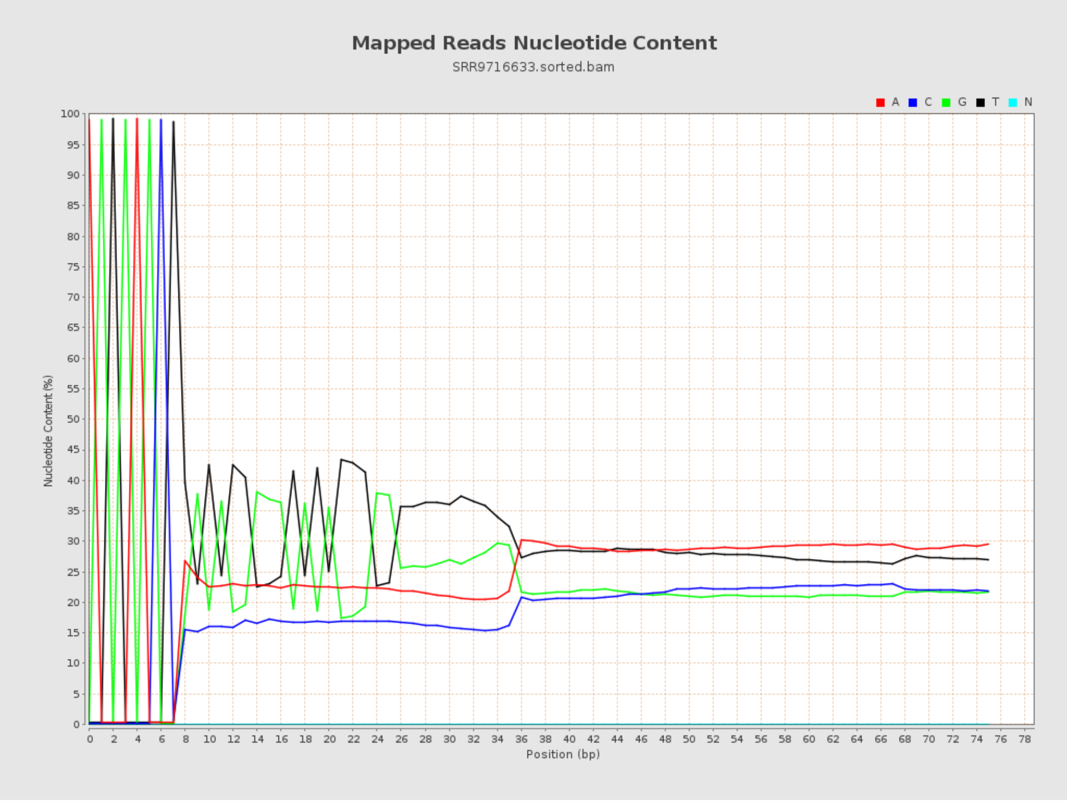
6. Results : Genome Fraction Coverage



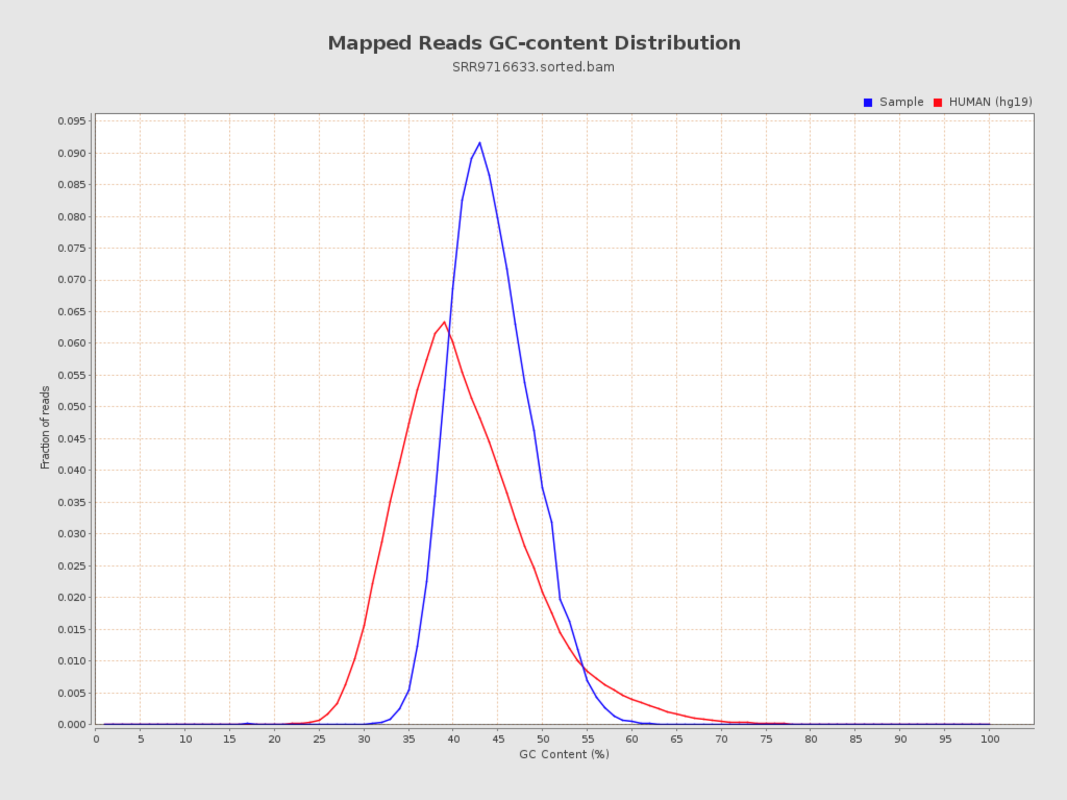
7. Results : Duplication Rate Histogram



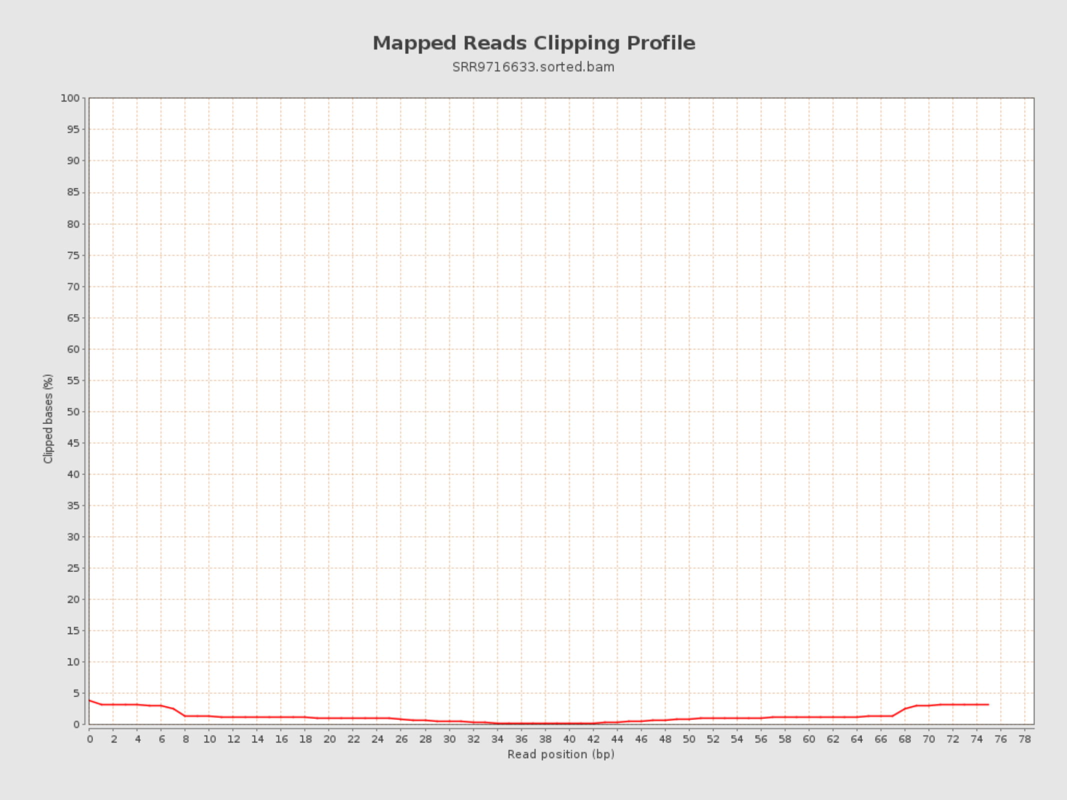
8. Results : Mapped Reads Nucleotide Content



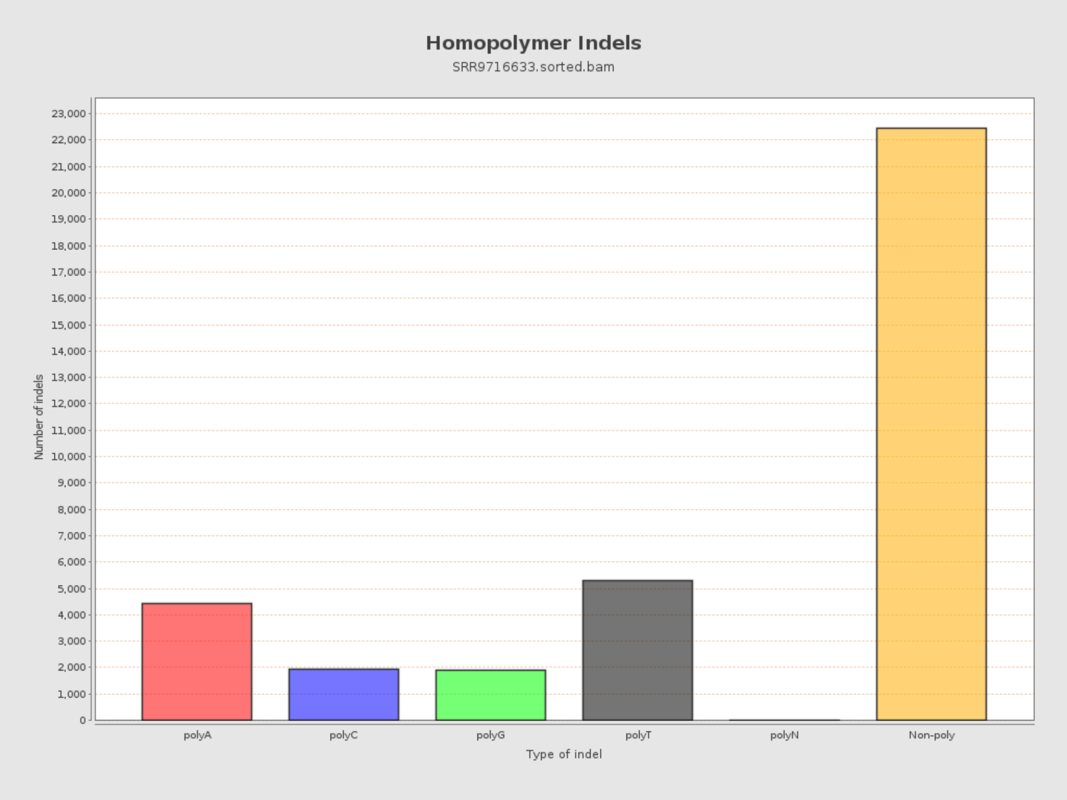
9. Results : Mapped Reads GC-content Distribution



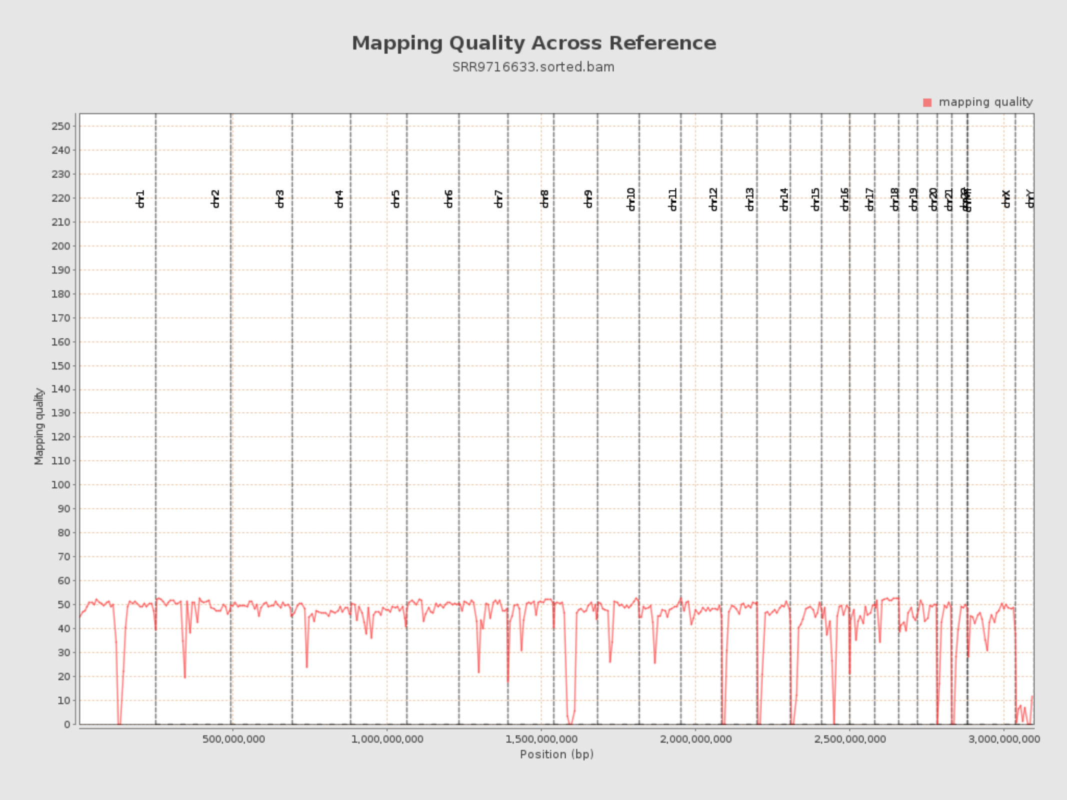
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram