Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 03:16:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716661.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_SRR9716661 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716661.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 03:16:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716661.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,389,923
Mapped reads	2,228,504 / 93.25%
Unmapped reads	161,419 / 6.75%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	41,806 / 1.75%
Read min/max/mean length	30 / 101 / 101.63
Duplicated reads (estimated)	100,976 / 4.23%
Duplication rate	3.31%
Clipped reads	2,264,901 / 94.77%

2.2. ACGT Content

Number/percentage of A's	47,197,693 / 26.67%
Number/percentage of C's	34,531,744 / 19.51%
Number/percentage of T's	52,628,444 / 29.74%
Number/percentage of G's	42,584,905 / 24.07%
Number/percentage of N's	11,940 / 0.01%
GC Percentage	43.58%

2.3. Coverage

Mean	0.0572

Standard Deviation	0.47

2.4. Mapping Quality

Mean Mapping Quality	47.73

2.5. Mismatches and indels

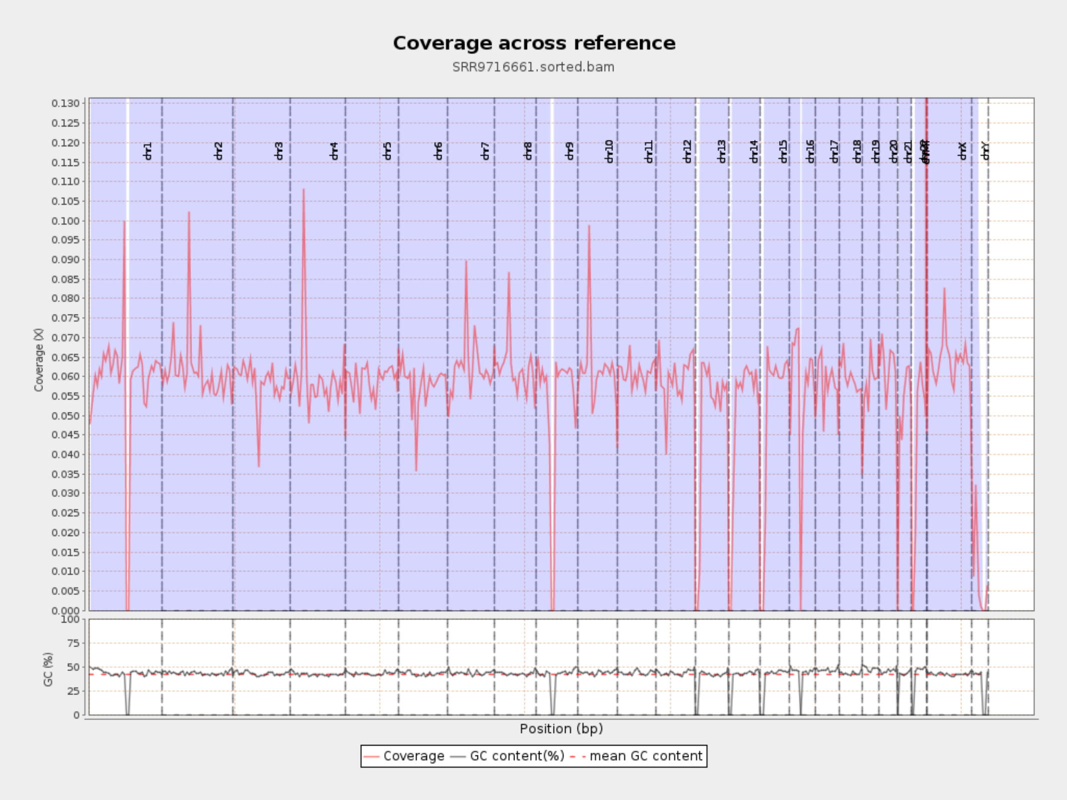
General error rate	0.67%
Mismatches	1,153,484
Insertions	15,468
Mapped reads with at least one insertion	0.68%
Deletions	42,247
Mapped reads with at least one deletion	1.87%
Homopolymer indels	41.79%

2.6. Chromosome stats

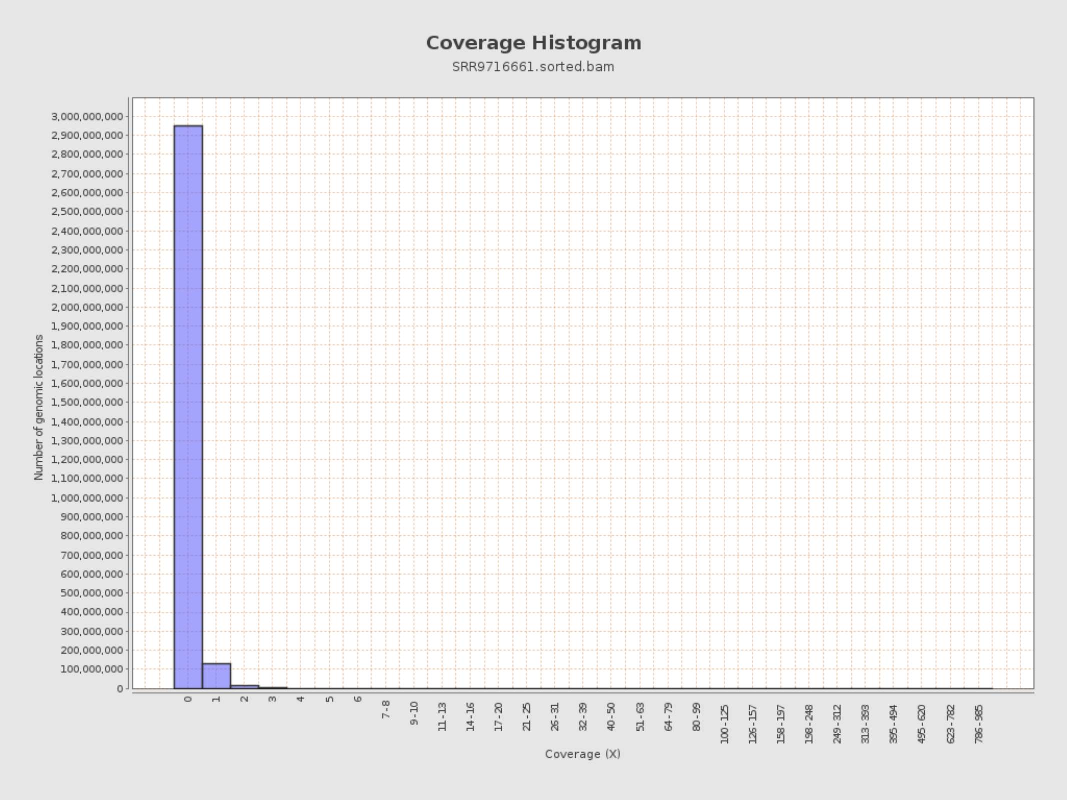
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14613842	0.0586	0.8694
chr2	243199373	15045182	0.0619	0.5545
chr3	198022430	11613488	0.0586	0.2773
chr4	191154276	11379003	0.0595	0.3568
chr5	180915260	10694827	0.0591	0.2841
chr6	171115067	9932871	0.058	0.3104
chr7	159138663	9969798	0.0626	0.6482

chr8	146364022	9094403	0.0621	0.5945
chr9	141213431	7407178	0.0525	0.4208
chr10	135534747	8433856	0.0622	0.483
chr11	135006516	8184098	0.0606	0.4632
chr12	133851895	7948900	0.0594	0.2845
chr13	115169878	5545379	0.0481	0.2523
chr14	107349540	5290479	0.0493	0.2817
chr15	102531392	5147084	0.0502	0.2605
chr16	90354753	5125730	0.0567	0.3016
chr17	81195210	4693273	0.0578	0.3259
chr18	78077248	4685986	0.06	0.6968
chr19	59128983	3446432	0.0583	0.5771
chr20	63025520	3894926	0.0618	0.3043
chr21	48129895	2382528	0.0495	0.2991
chr22	51304566	2044633	0.0399	0.2314
chrMT	16571	22847	1.3787	1.4706
chrX	155270560	9927022	0.0639	0.3543
chrY	59373566	512344	0.0086	0.292

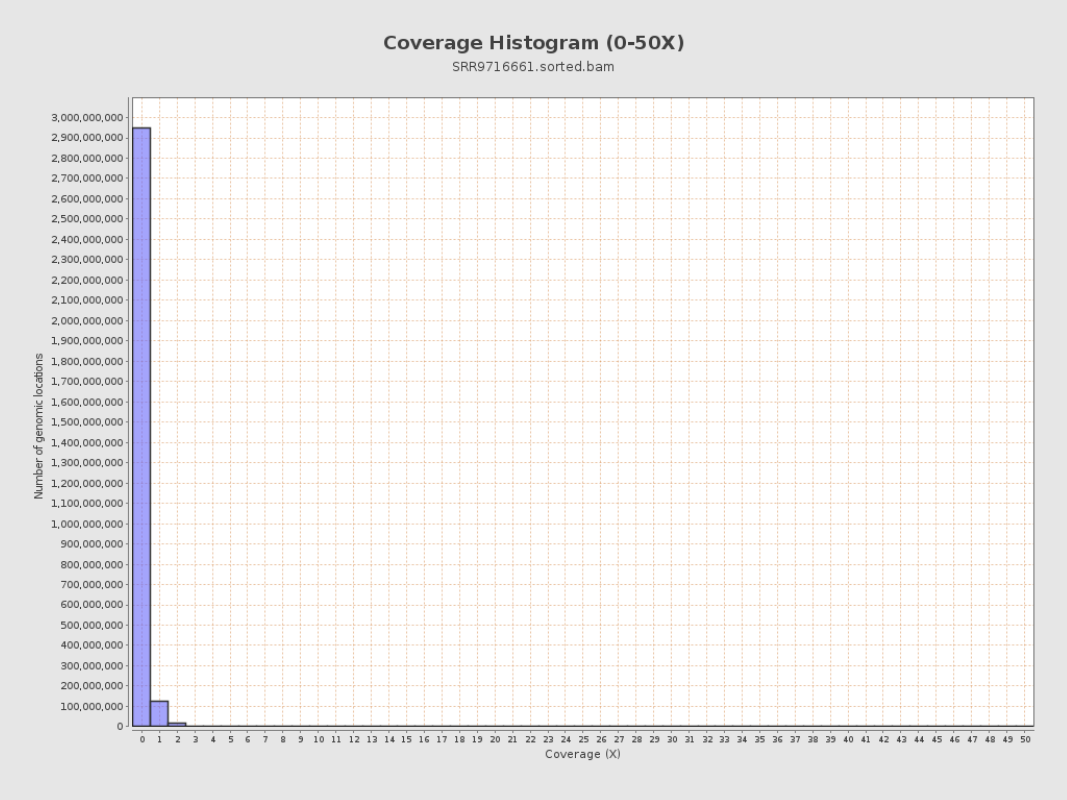
3. Results : Coverage across reference



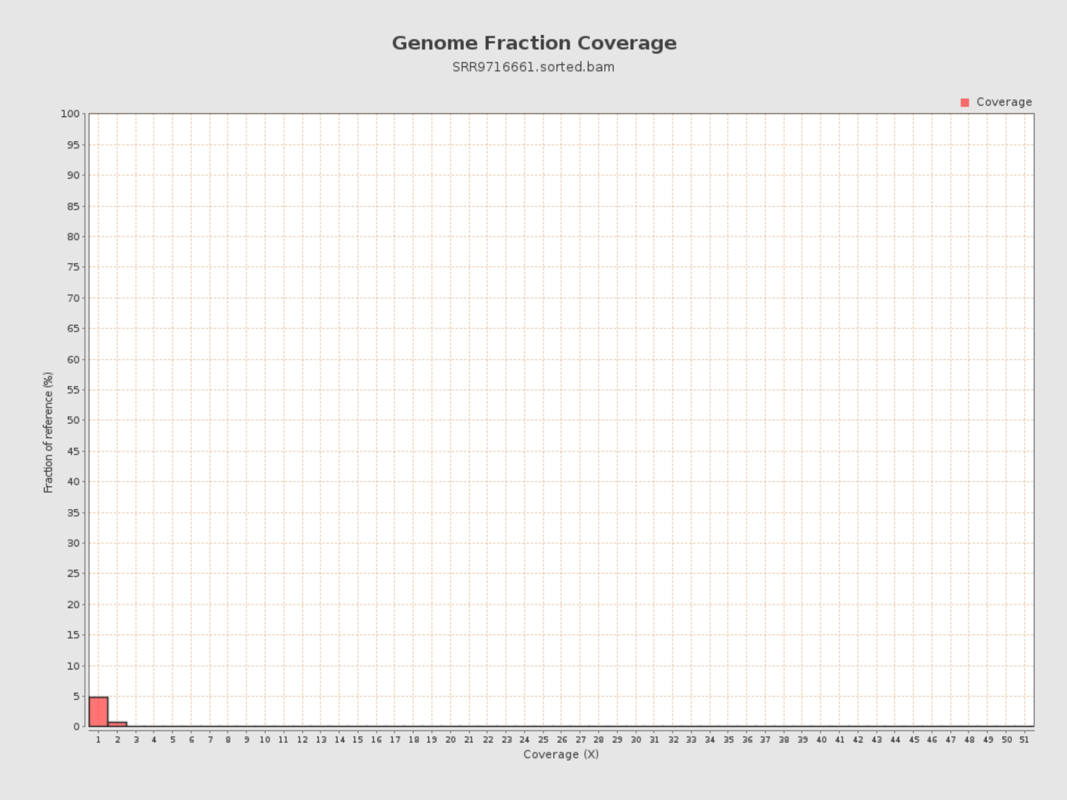
4. Results : Coverage Histogram



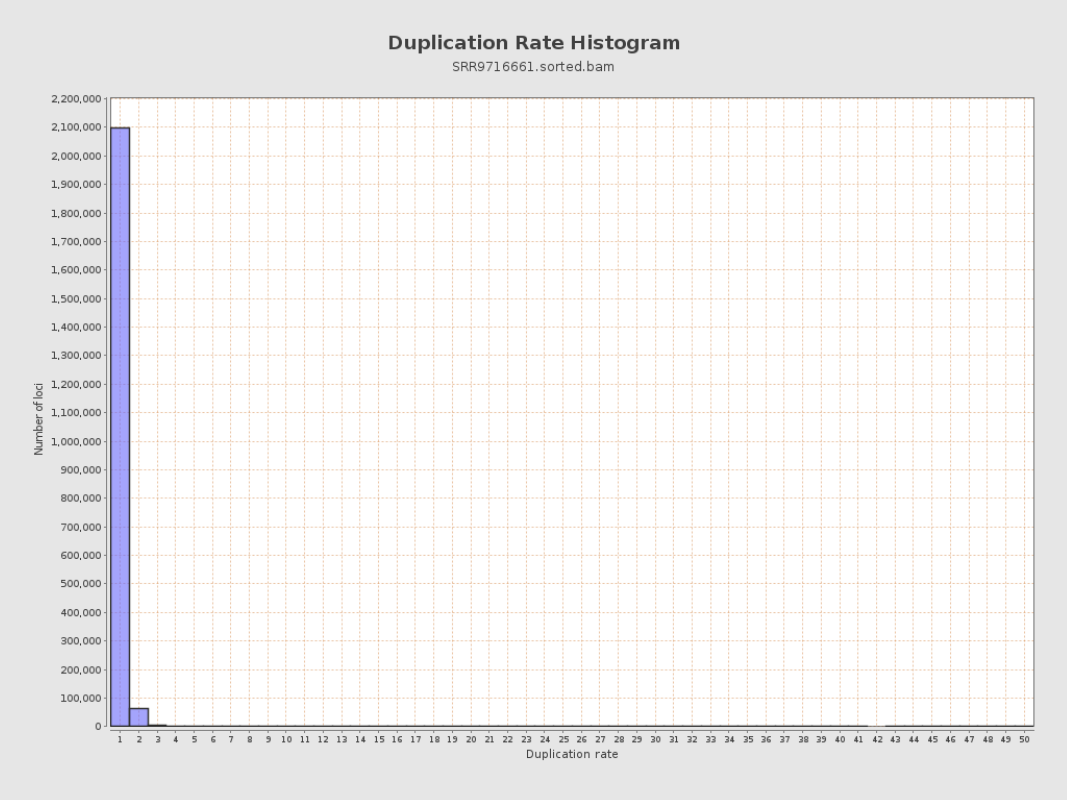
5. Results : Coverage Histogram (0-50X)



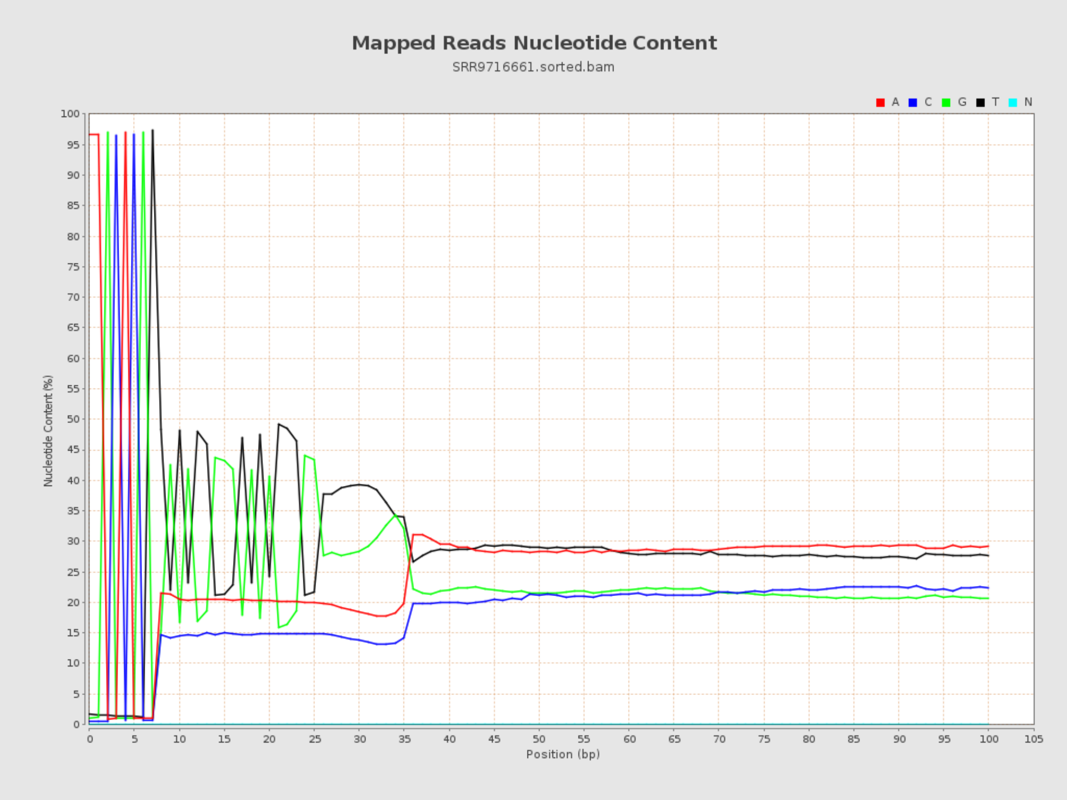
6. Results : Genome Fraction Coverage



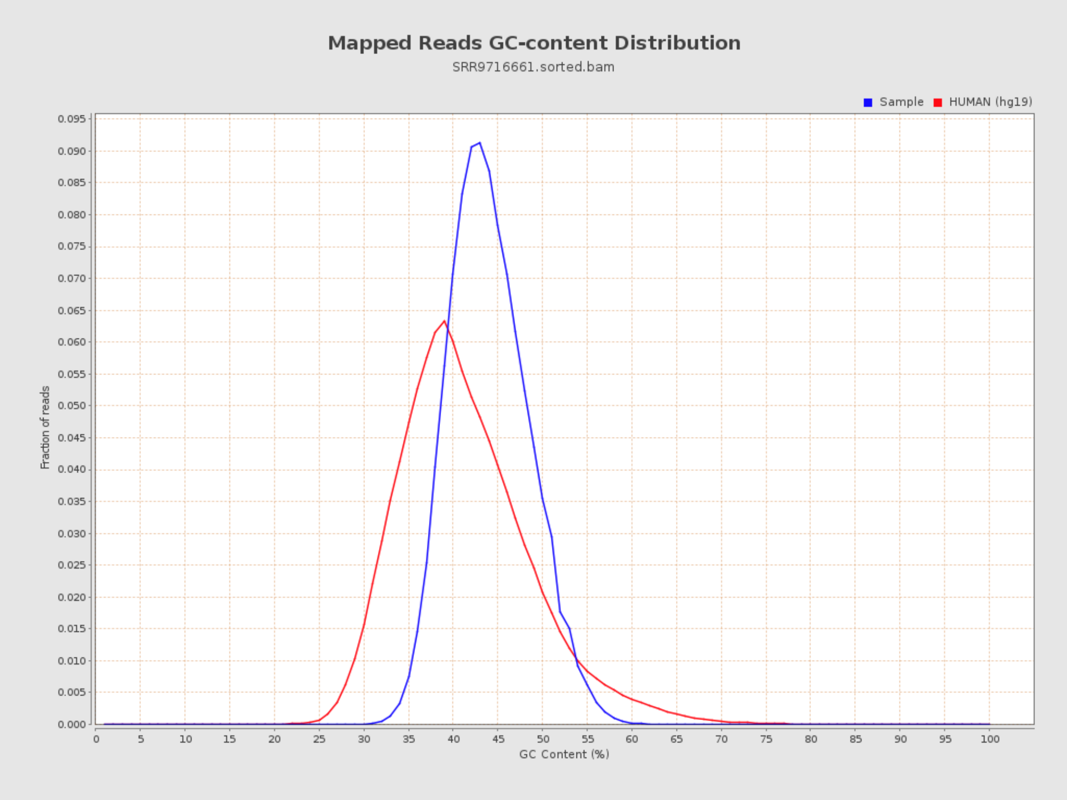
7. Results : Duplication Rate Histogram



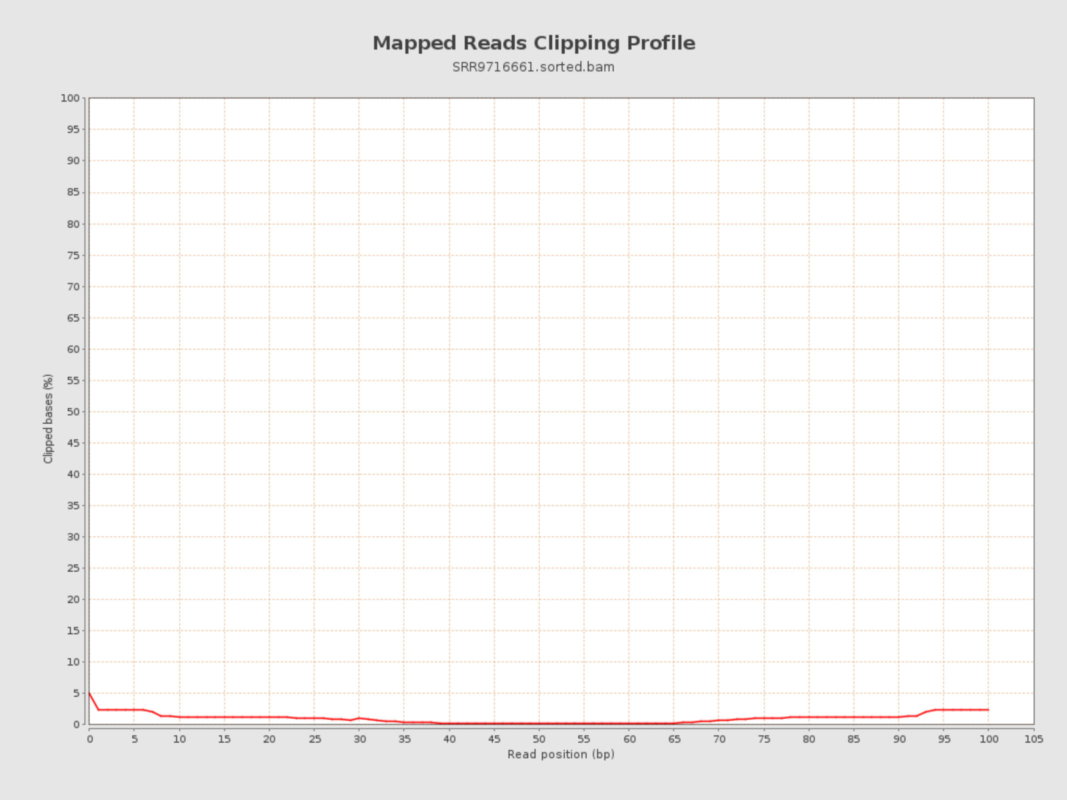
8. Results : Mapped Reads Nucleotide Content



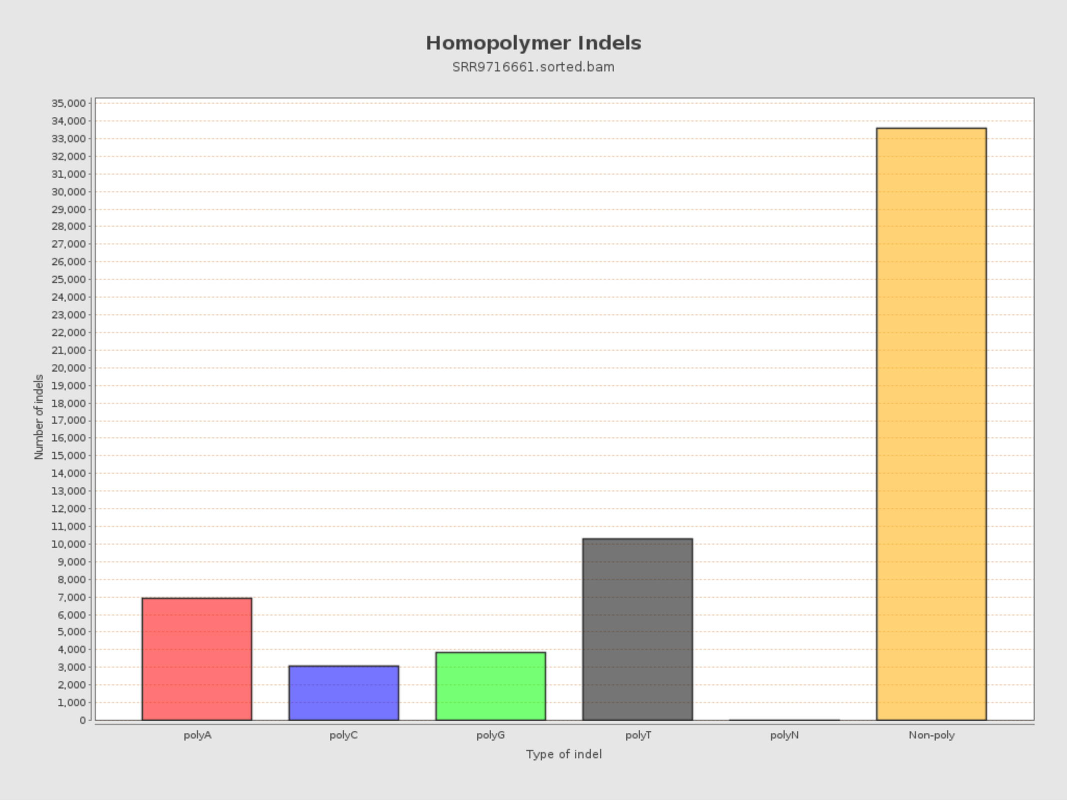
9. Results : Mapped Reads GC-content Distribution



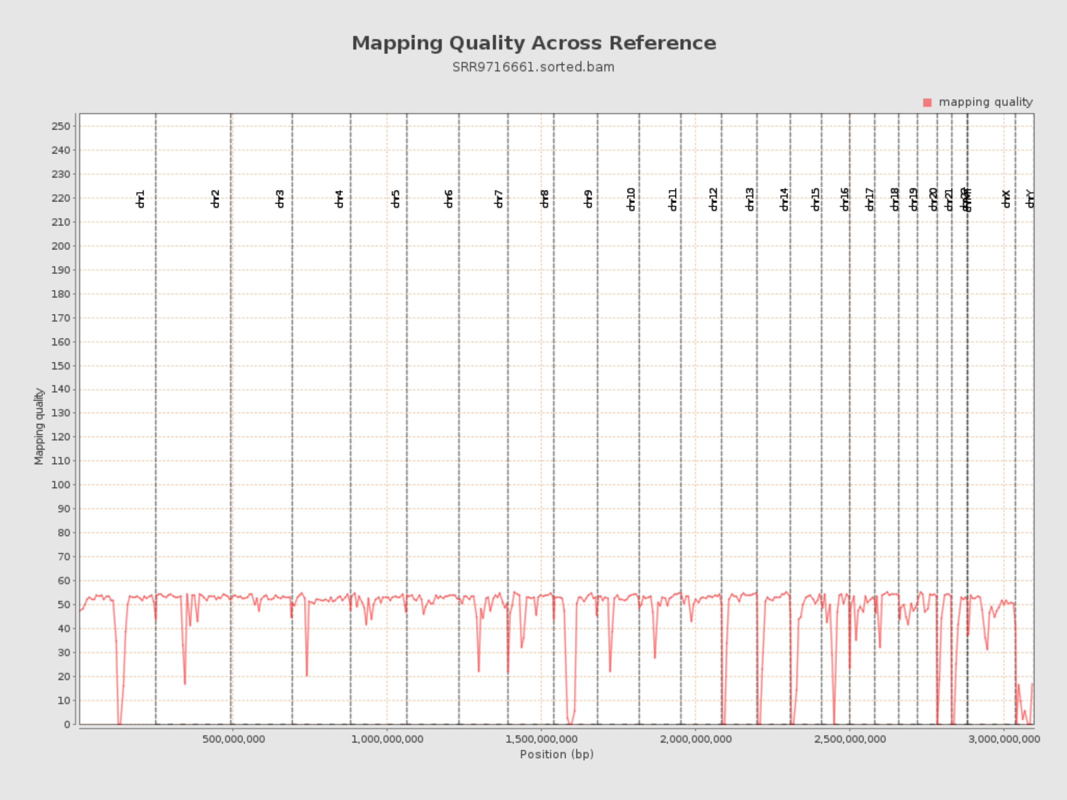
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram