Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 03:41:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716665.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_SRR9716665 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716665.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 03:41:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716665.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,117,457
Mapped reads	1,987,437 / 93.86%
Unmapped reads	130,020 / 6.14%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	38,965 / 1.84%
Read min/max/mean length	30 / 101 / 101.66
Duplicated reads (estimated)	86,683 / 4.09%
Duplication rate	3.09%
Clipped reads	2,023,234 / 95.55%

2.2. ACGT Content

Number/percentage of A's	39,607,824 / 25.04%
Number/percentage of C's	31,018,834 / 19.61%
Number/percentage of T's	48,556,928 / 30.69%
Number/percentage of G's	39,010,133 / 24.66%
Number/percentage of N's	10,522 / 0.01%
GC Percentage	44.26%

2.3. Coverage

Mean	0.0511

Standard Deviation	0.4723

2.4. Mapping Quality

Mean Mapping Quality	47.51

2.5. Mismatches and indels

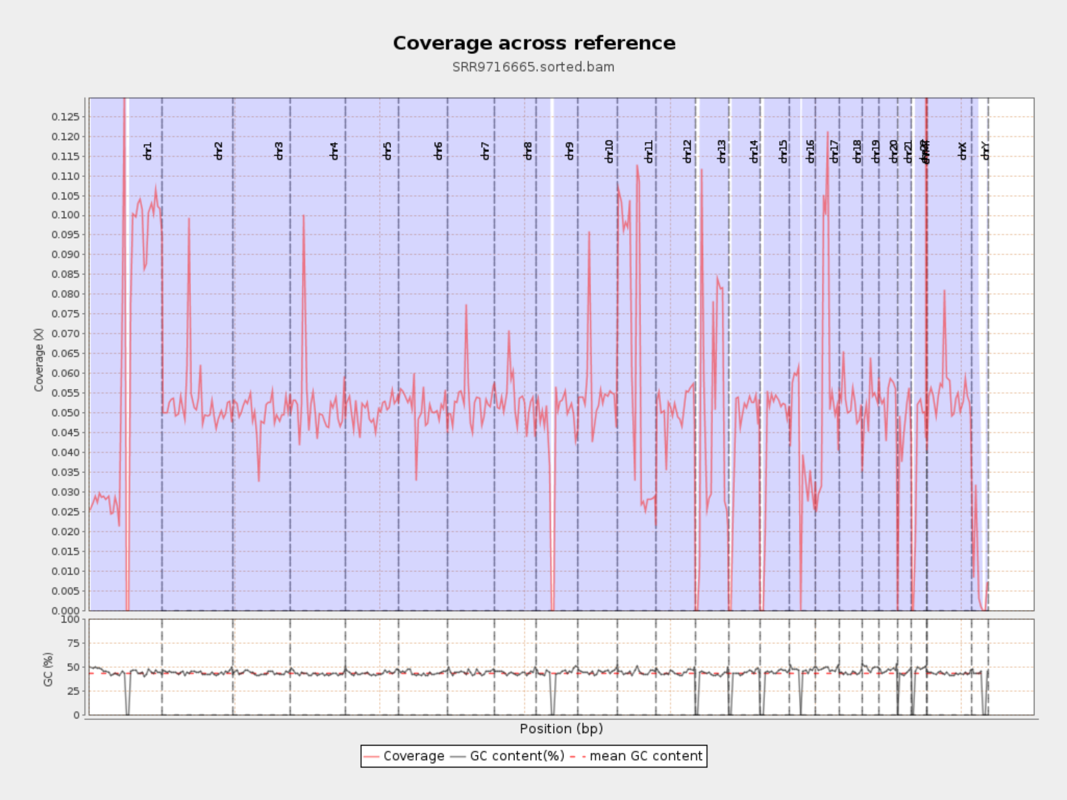
General error rate	0.65%
Mismatches	1,003,679
Insertions	12,856
Mapped reads with at least one insertion	0.64%
Deletions	36,974
Mapped reads with at least one deletion	1.83%
Homopolymer indels	43.11%

2.6. Chromosome stats

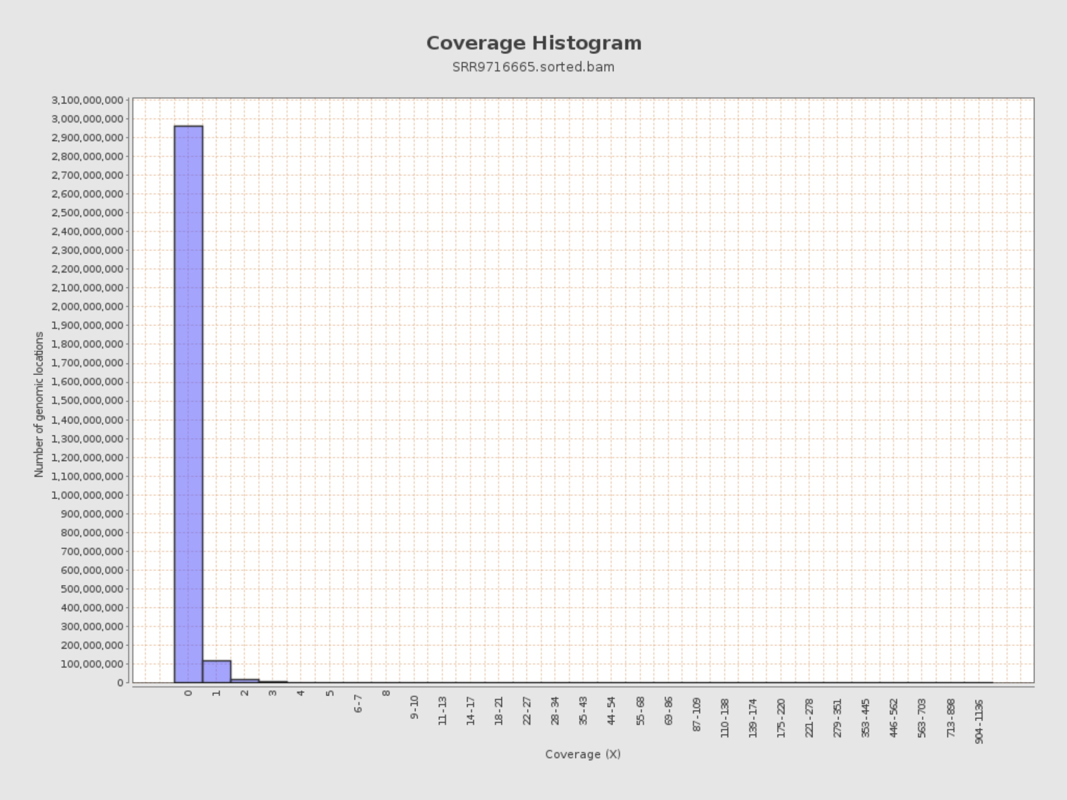
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15374122	0.0617	1.0045
chr2	243199373	12872825	0.0529	0.5183
chr3	198022430	9910059	0.05	0.2538
chr4	191154276	9988739	0.0523	0.3348
chr5	180915260	9154137	0.0506	0.2576
chr6	171115067	8758458	0.0512	0.284
chr7	159138663	8434614	0.053	0.5617

chr8	146364022	7782467	0.0532	0.5159
chr9	141213431	6303937	0.0446	0.3761
chr10	135534747	7479516	0.0552	0.4584
chr11	135006516	8814970	0.0653	0.5077
chr12	133851895	6834321	0.0511	0.2588
chr13	115169878	5419620	0.0471	0.25
chr14	107349540	4636301	0.0432	0.2623
chr15	102531392	4386283	0.0428	0.2346
chr16	90354753	3538077	0.0392	0.2513
chr17	81195210	4958937	0.0611	0.3493
chr18	78077248	4145314	0.0531	0.6738
chr19	59128983	3099992	0.0524	0.6894
chr20	63025520	3360724	0.0533	0.2839
chr21	48129895	2077642	0.0432	0.2847
chr22	51304566	1814168	0.0354	0.2142
chrMT	16571	101792	6.1428	4.2656
chrX	155270560	8538394	0.055	0.3203
chrY	59373566	491544	0.0083	0.276

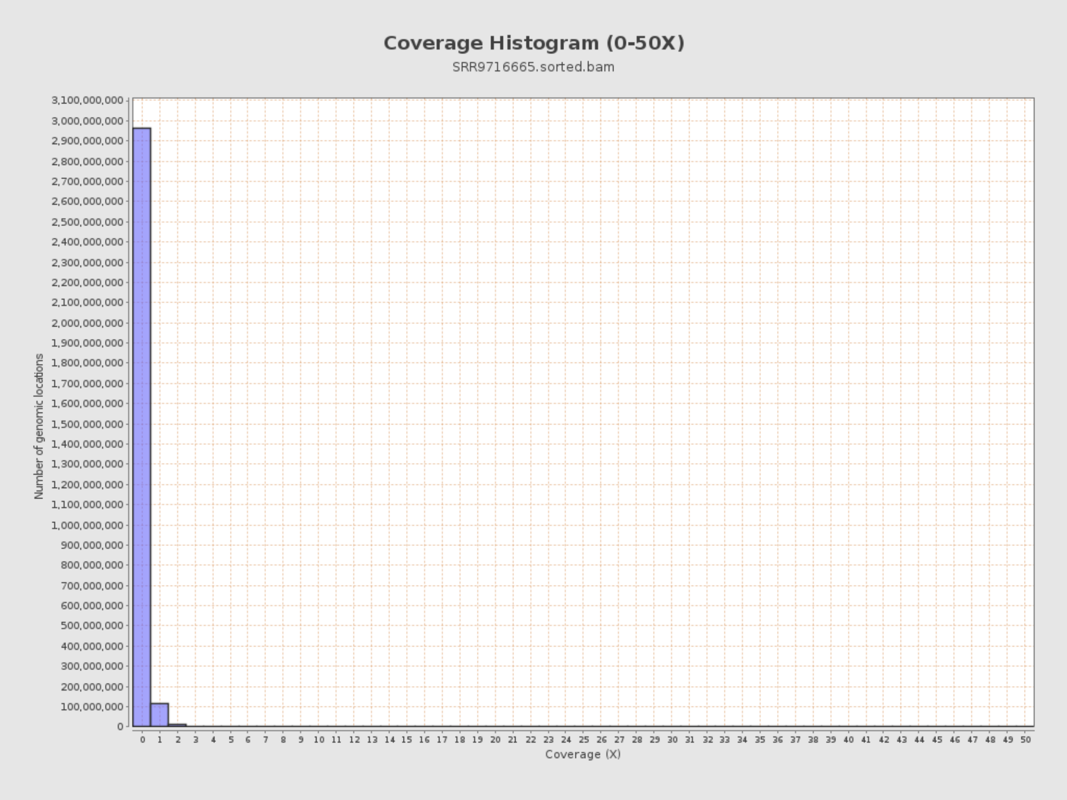
3. Results : Coverage across reference



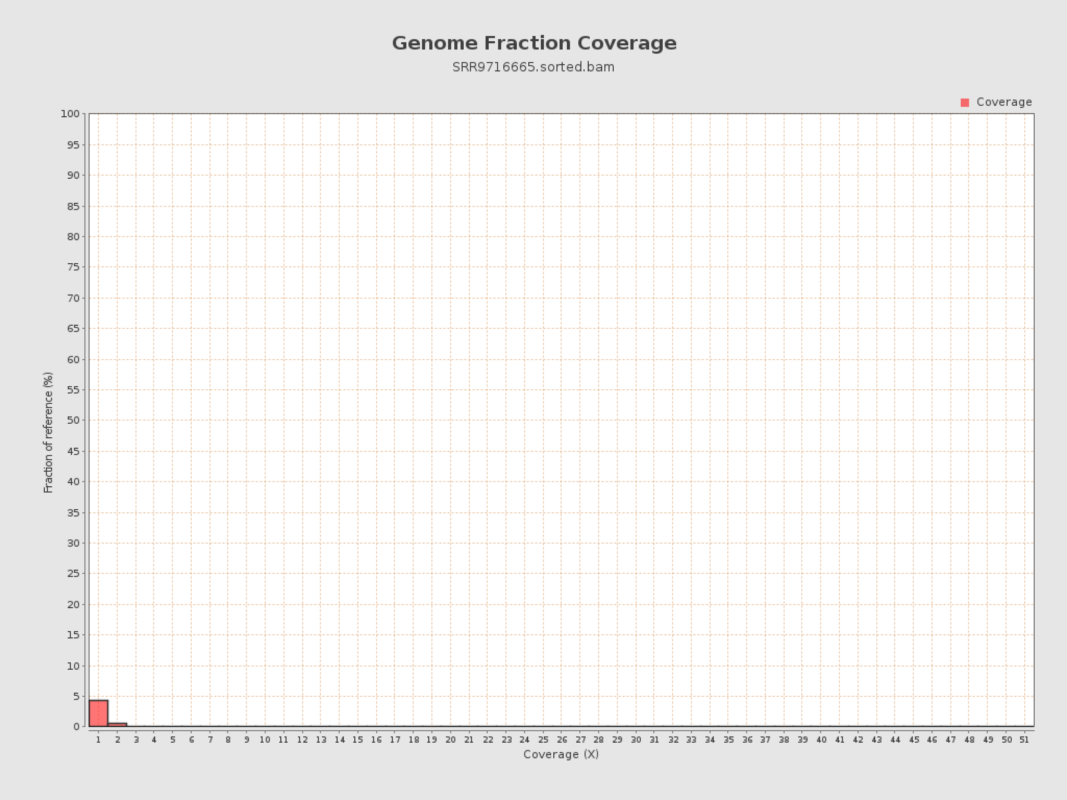
4. Results : Coverage Histogram



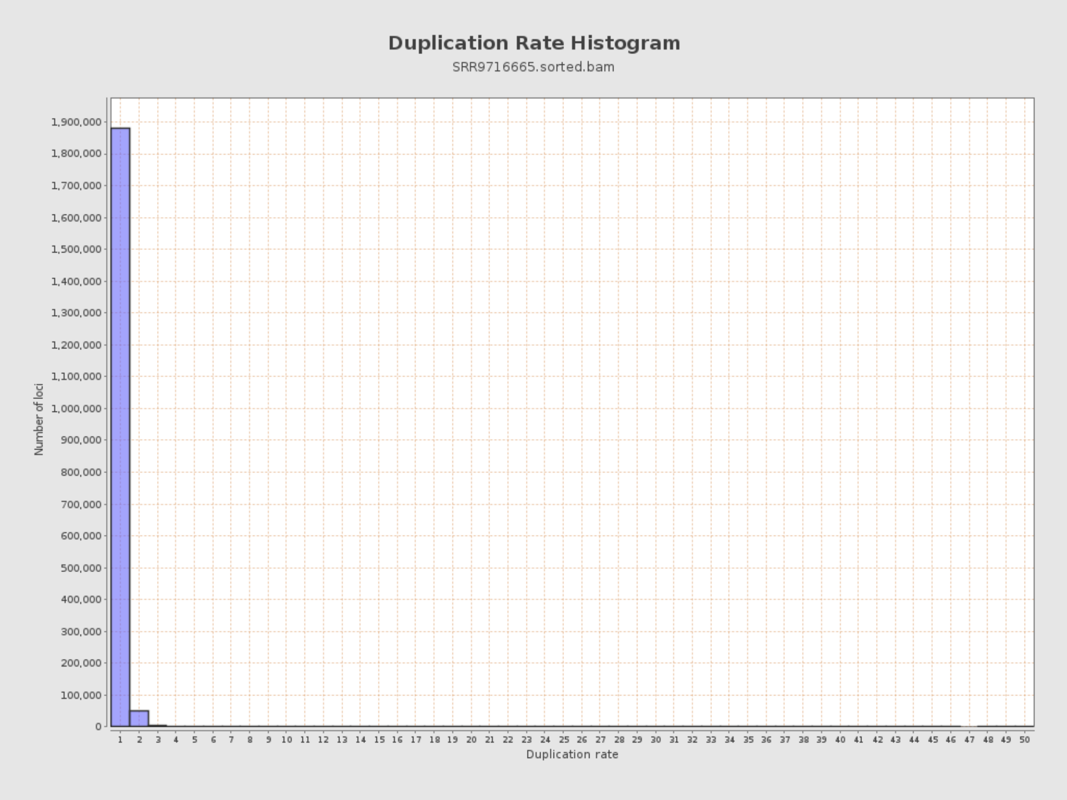
5. Results : Coverage Histogram (0-50X)



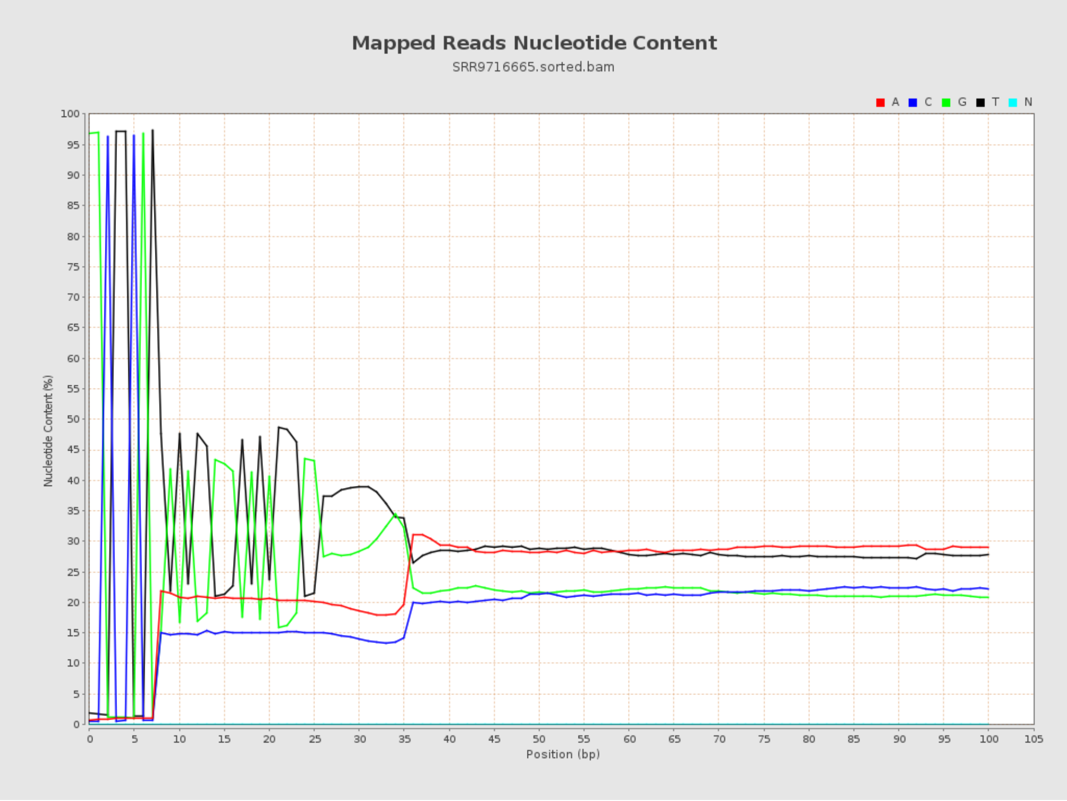
6. Results : Genome Fraction Coverage



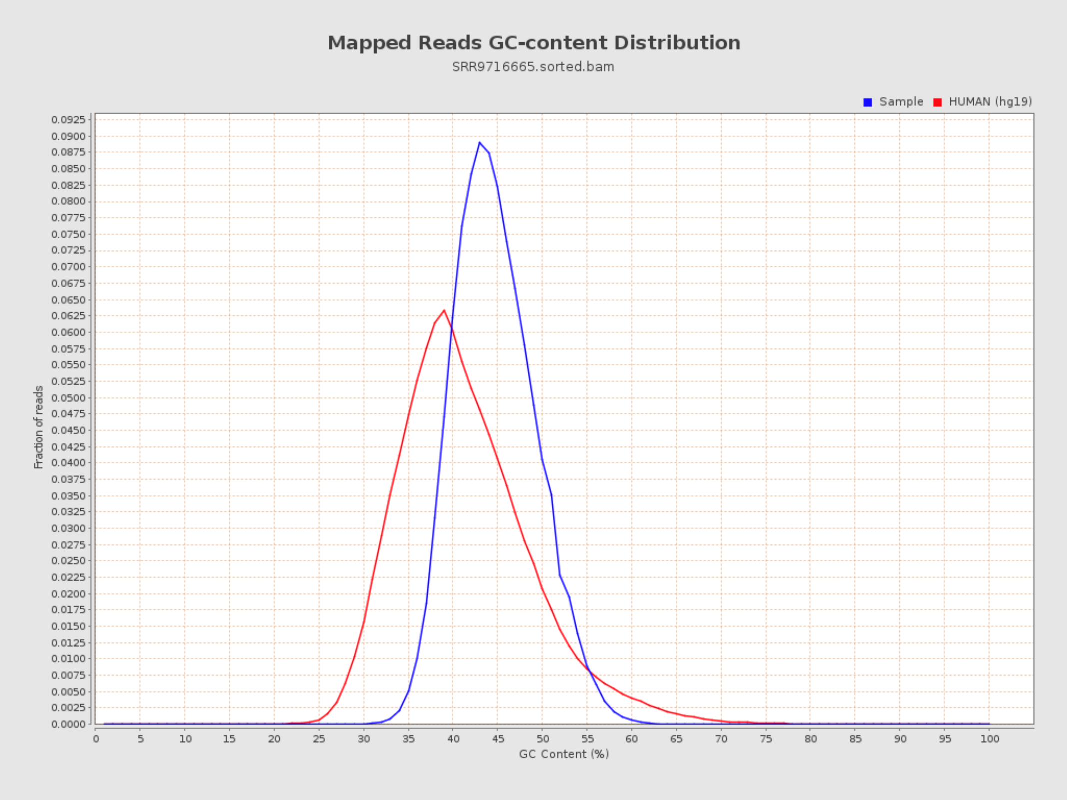
7. Results : Duplication Rate Histogram



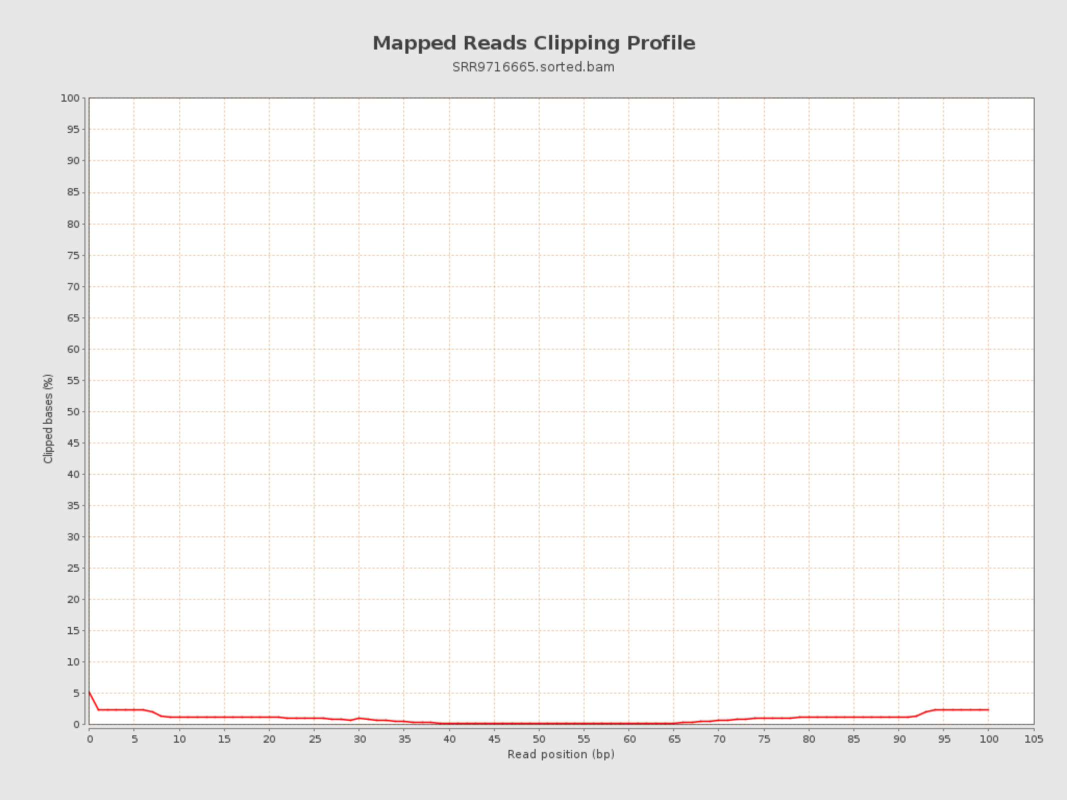
8. Results : Mapped Reads Nucleotide Content



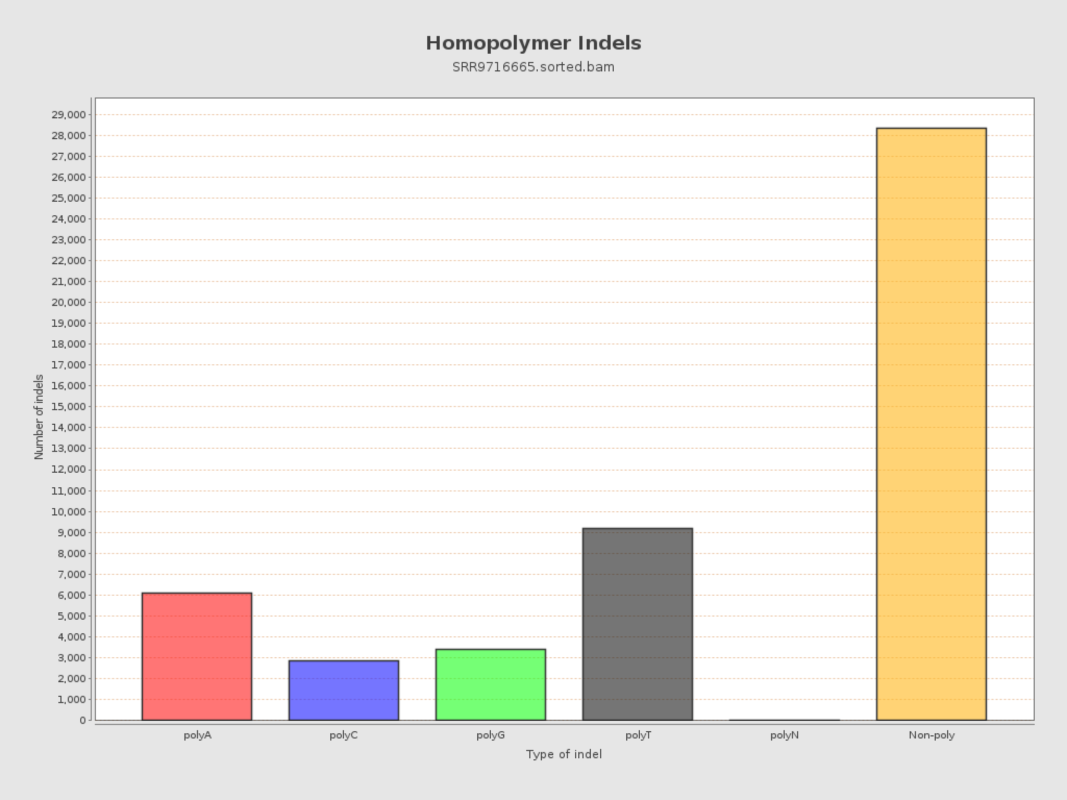
9. Results : Mapped Reads GC-content Distribution



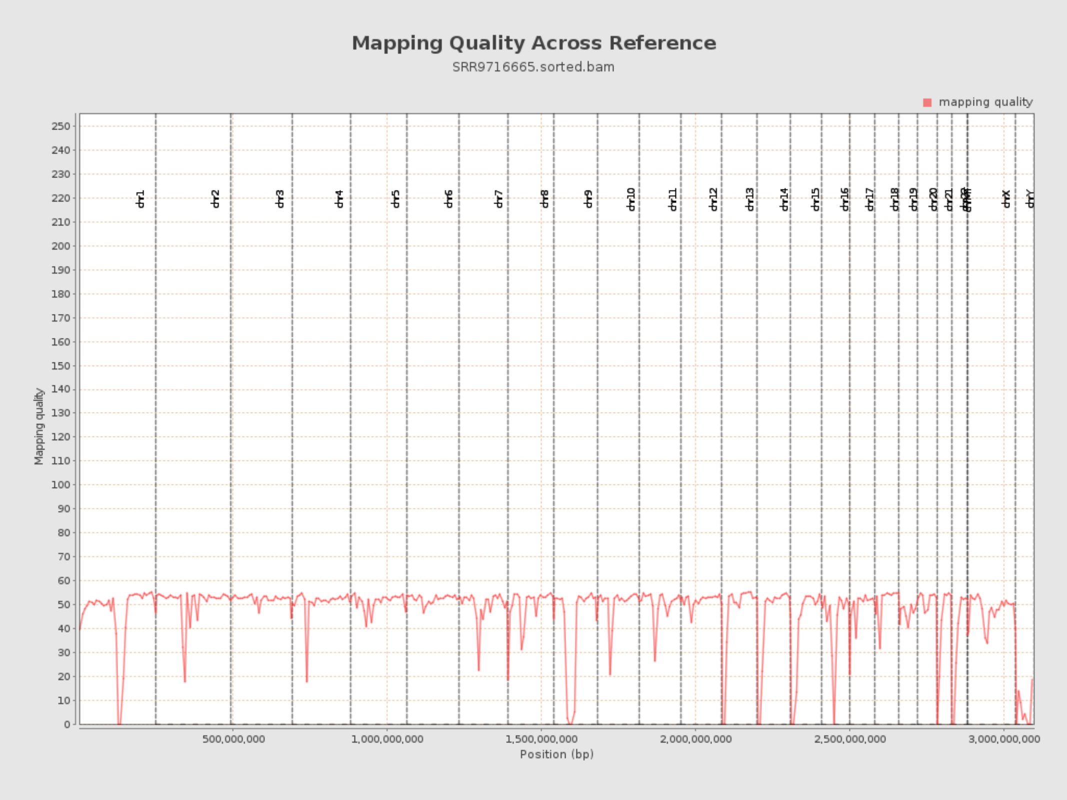
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram