Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 03:35:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716664.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_SRR9716664 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716664.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 03:35:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716664.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,093,118
Mapped reads	3,830,672 / 93.59%
Unmapped reads	262,446 / 6.41%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	73,409 / 1.79%
Read min/max/mean length	30 / 101 / 101.65
Duplicated reads (estimated)	258,360 / 6.31%
Duplication rate	5.01%
Clipped reads	3,896,283 / 95.19%

2.2. ACGT Content

Number/percentage of A's	76,394,195 / 25.15%
Number/percentage of C's	58,043,788 / 19.11%
Number/percentage of T's	94,766,428 / 31.2%
Number/percentage of G's	74,522,026 / 24.53%
Number/percentage of N's	22,121 / 0.01%
GC Percentage	43.64%

2.3. Coverage

Mean	0.0982

Standard Deviation	0.7461

2.4. Mapping Quality

Mean Mapping Quality	47.79

2.5. Mismatches and indels

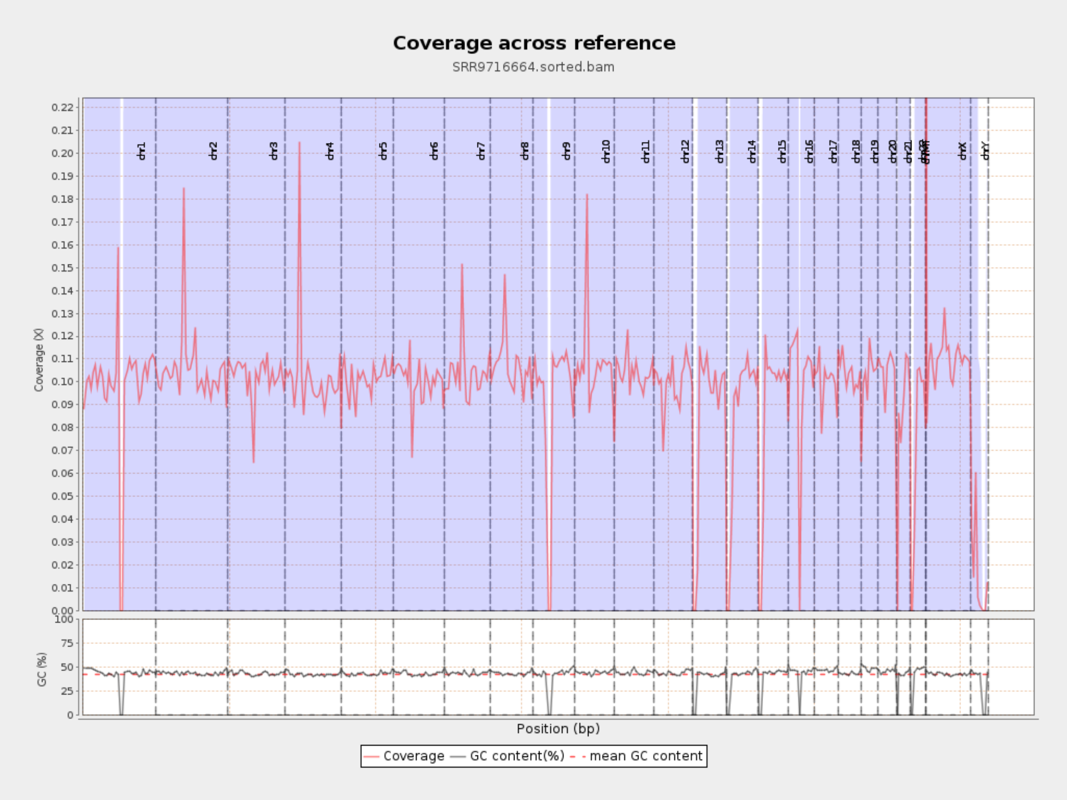
General error rate	0.65%
Mismatches	1,923,570
Insertions	25,436
Mapped reads with at least one insertion	0.65%
Deletions	66,129
Mapped reads with at least one deletion	1.7%
Homopolymer indels	43.07%

2.6. Chromosome stats

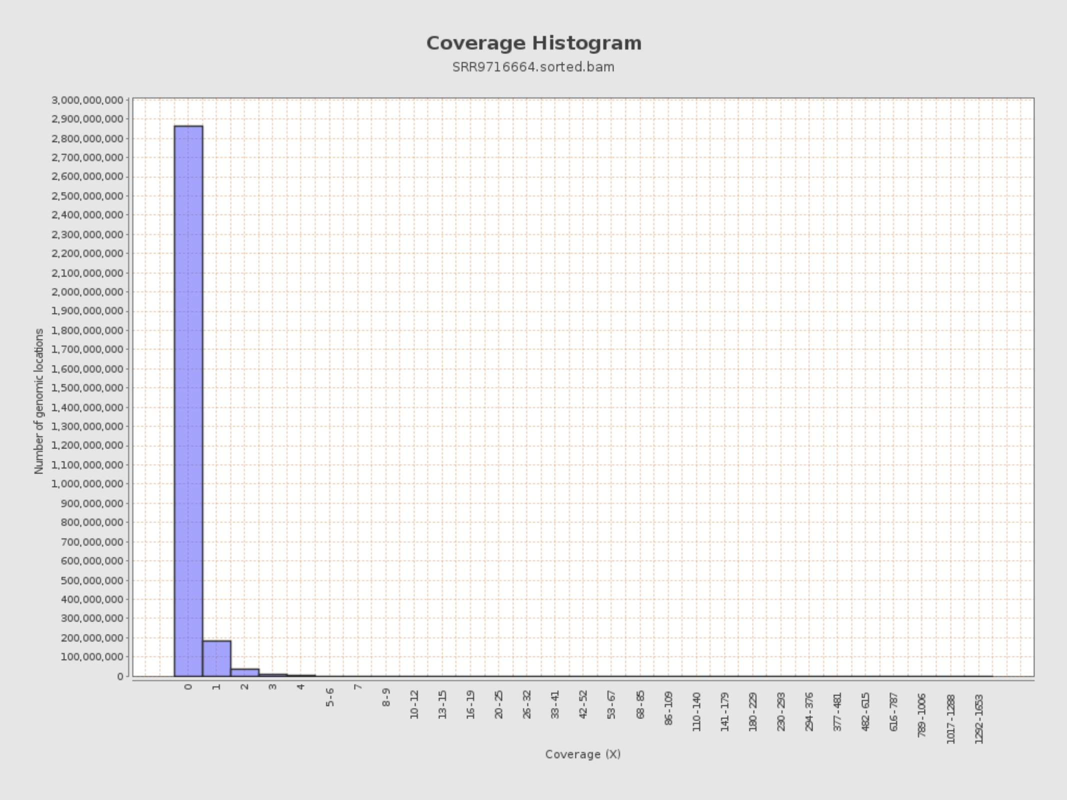
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	24339058	0.0976	1.4086
chr2	243199373	25734568	0.1058	0.885
chr3	198022430	20238680	0.1022	0.3952
chr4	191154276	19689997	0.103	0.5932
chr5	180915260	18383593	0.1016	0.4016
chr6	171115067	17184479	0.1004	0.4477
chr7	159138663	16628903	0.1045	1.0247

chr8	146364022	15634789	0.1068	0.9479
chr9	141213431	12949462	0.0917	0.6658
chr10	135534747	14585472	0.1076	0.8517
chr11	135006516	13960541	0.1034	0.6985
chr12	133851895	13436337	0.1004	0.4005
chr13	115169878	9790882	0.085	0.3603
chr14	107349540	9087793	0.0847	0.4164
chr15	102531392	8779629	0.0856	0.3647
chr16	90354753	8813906	0.0975	0.448
chr17	81195210	8172183	0.1006	0.4852
chr18	78077248	8105947	0.1038	1.116
chr19	59128983	6109825	0.1033	0.9858
chr20	63025520	6576523	0.1043	0.4514
chr21	48129895	4145389	0.0861	0.4901
chr22	51304566	3587350	0.0699	0.3402
chrMT	16571	28831	1.7398	1.8321
chrX	155270560	16993801	0.1094	0.5214
chrY	59373566	919273	0.0155	0.5385

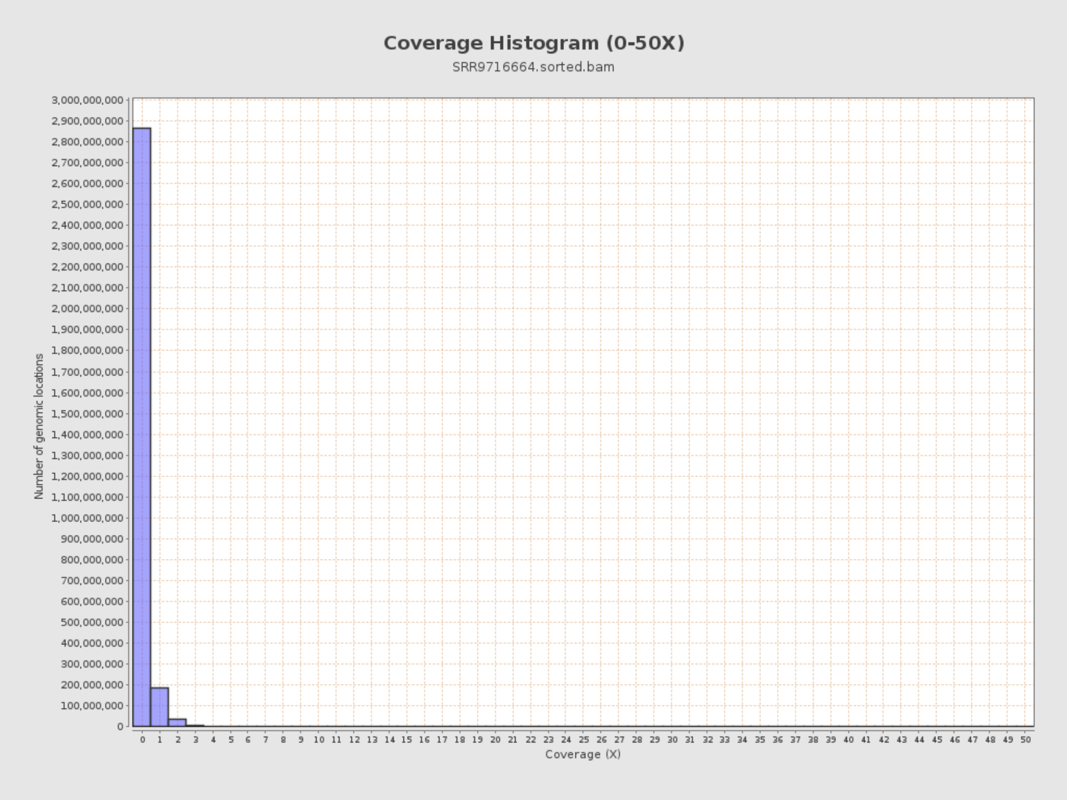
3. Results : Coverage across reference



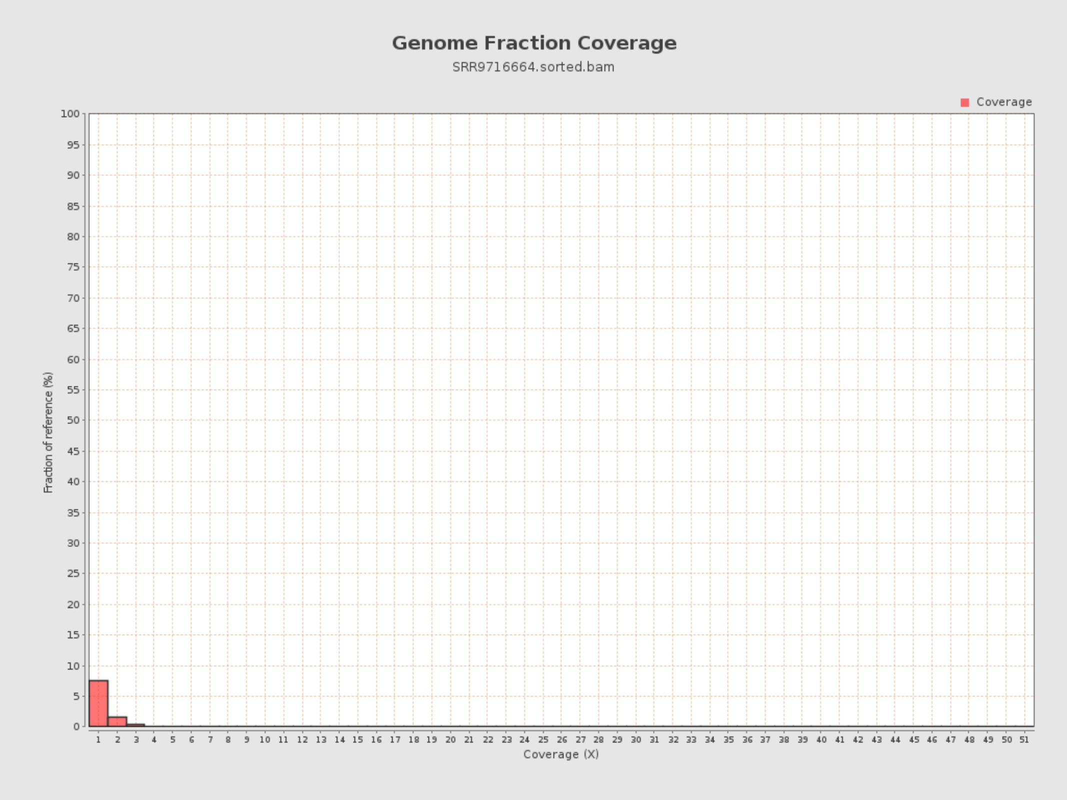
4. Results : Coverage Histogram



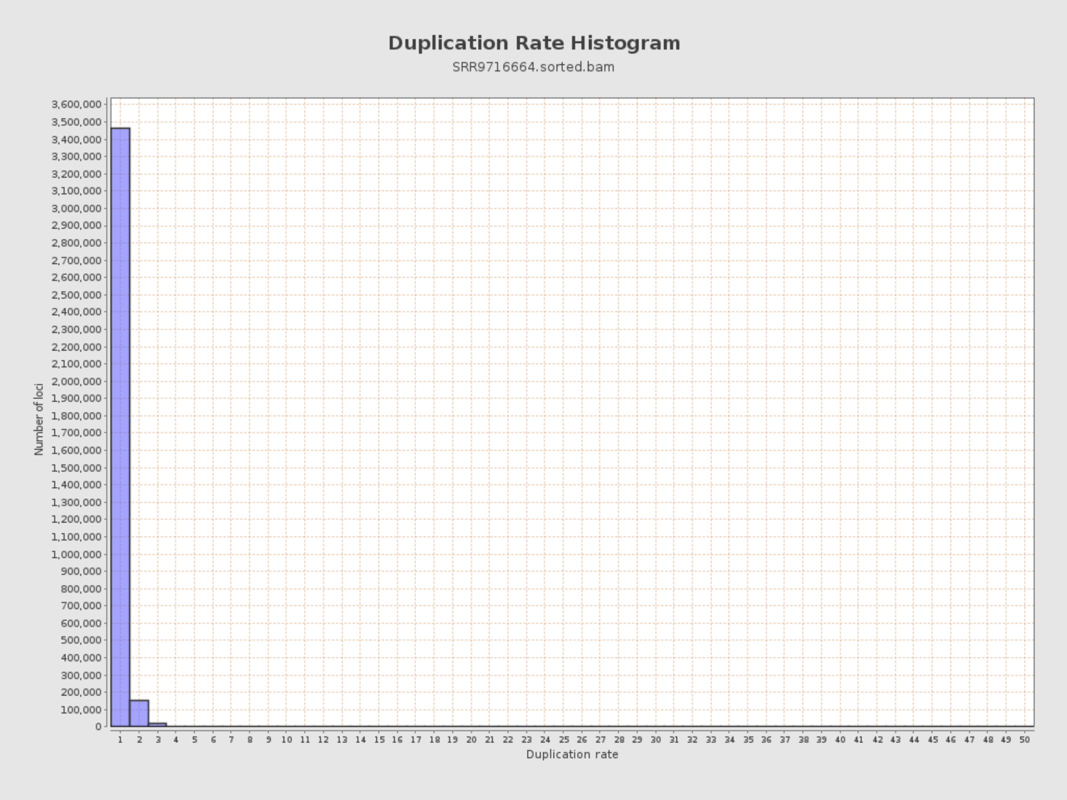
5. Results : Coverage Histogram (0-50X)



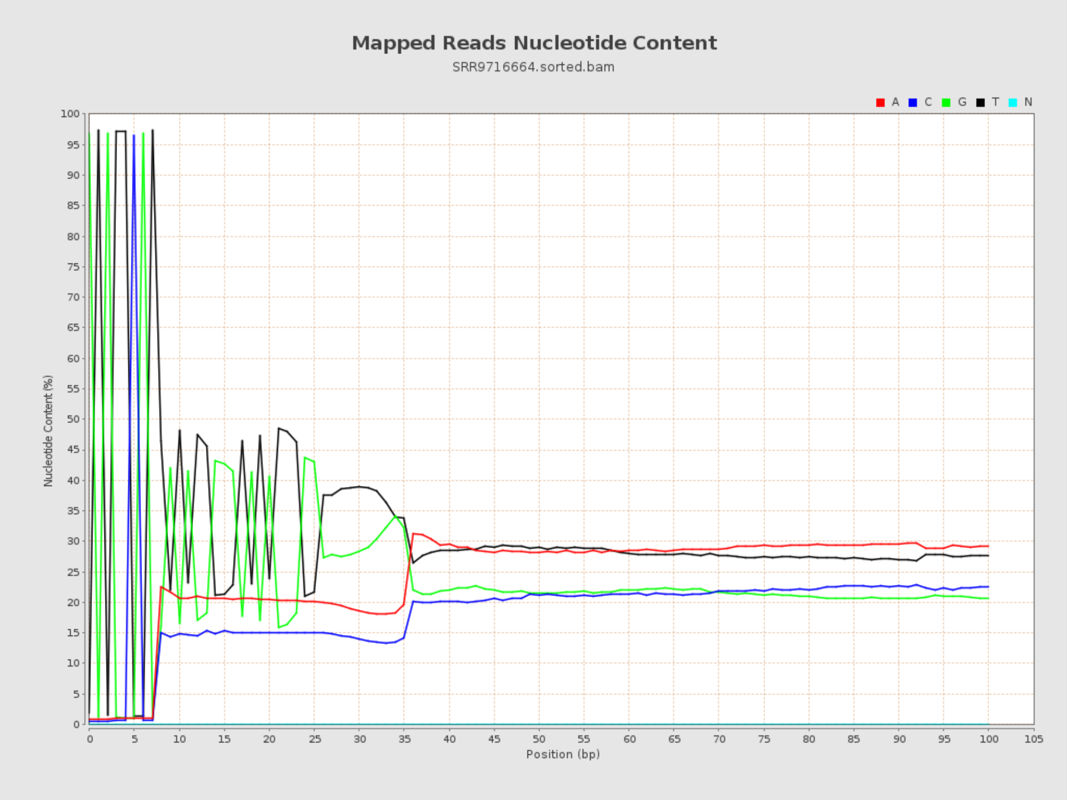
6. Results : Genome Fraction Coverage



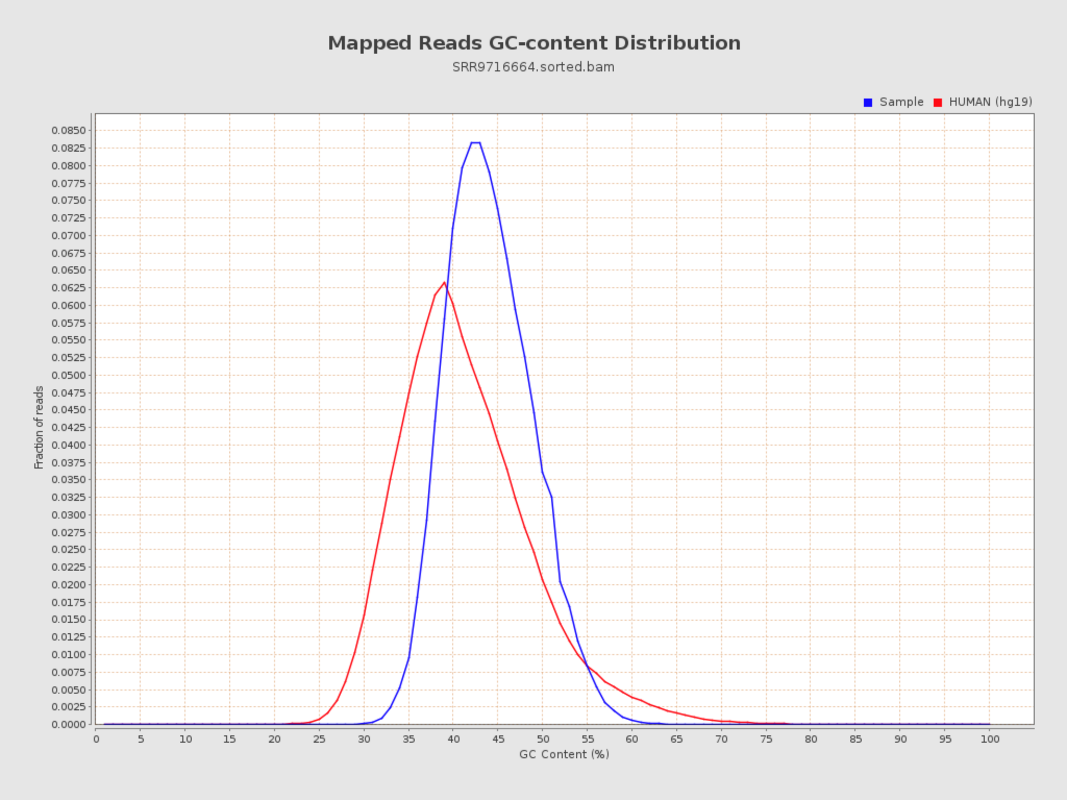
7. Results : Duplication Rate Histogram



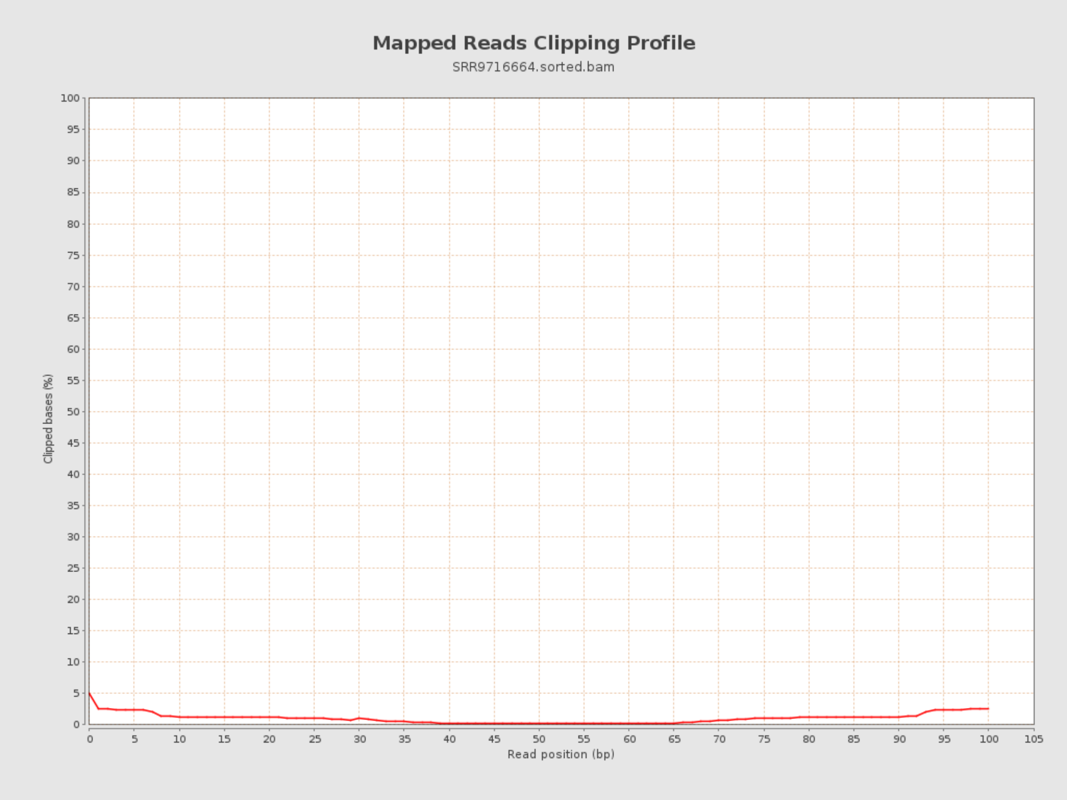
8. Results : Mapped Reads Nucleotide Content



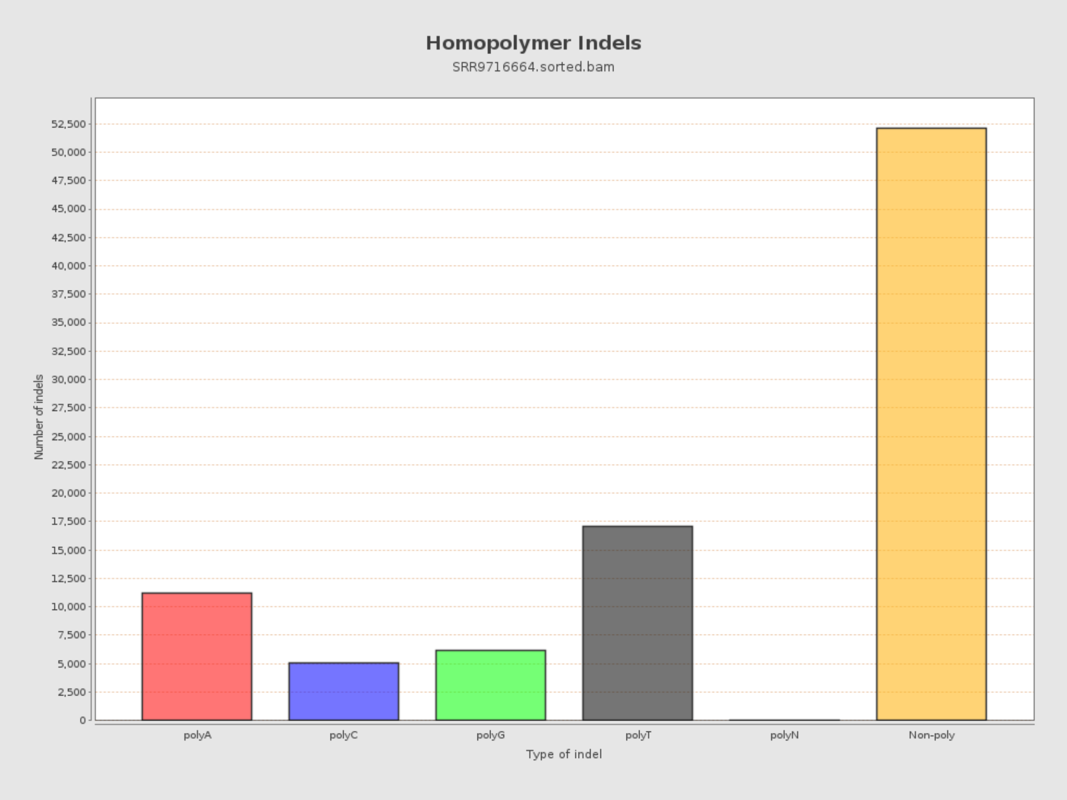
9. Results : Mapped Reads GC-content Distribution



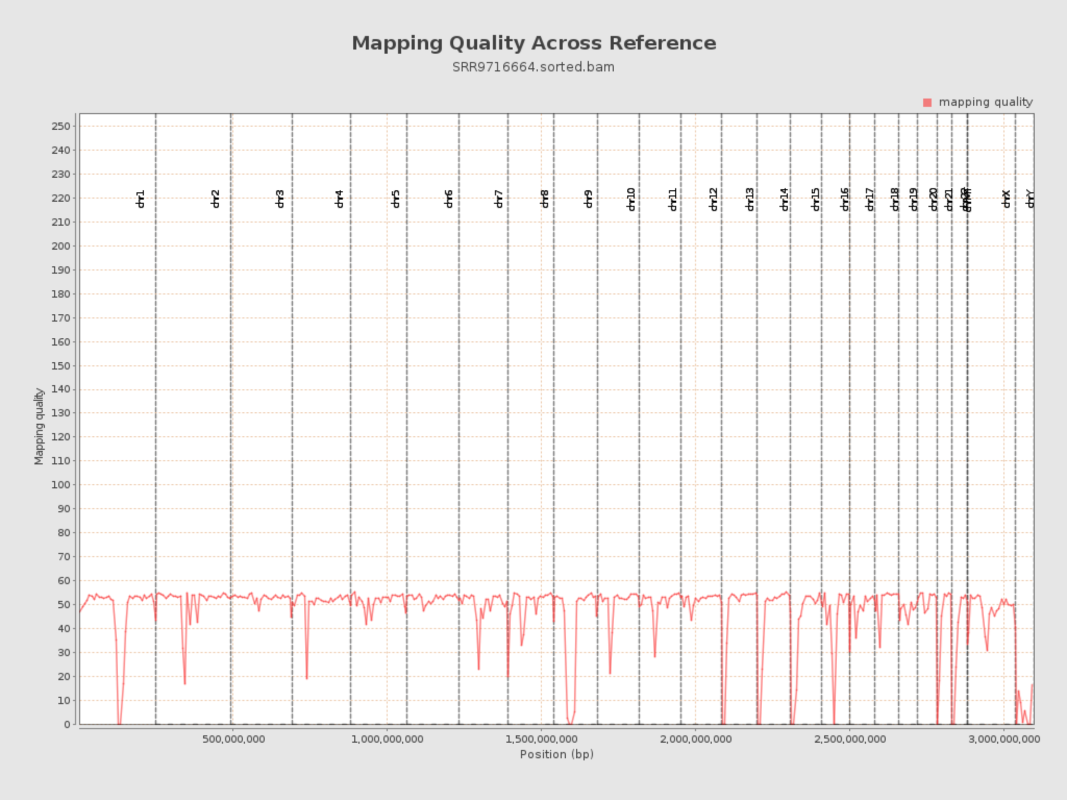
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram