Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 02:50:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716655.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_SRR9716655 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716655.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 02:50:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716655.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,619,195
Mapped reads	2,339,264 / 89.31%
Unmapped reads	279,931 / 10.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	72,946 / 2.79%
Read min/max/mean length	30 / 101 / 102
Duplicated reads (estimated)	70,858 / 2.71%
Duplication rate	1.86%
Clipped reads	2,407,550 / 91.92%

2.2. ACGT Content

Number/percentage of A's	45,034,904 / 26.15%
Number/percentage of C's	36,096,625 / 20.96%
Number/percentage of T's	50,771,636 / 29.48%
Number/percentage of G's	40,280,069 / 23.39%
Number/percentage of N's	20,157 / 0.01%
GC Percentage	44.35%

2.3. Coverage

Mean	0.0556

Standard Deviation	0.477

2.4. Mapping Quality

Mean Mapping Quality	44.44

2.5. Mismatches and indels

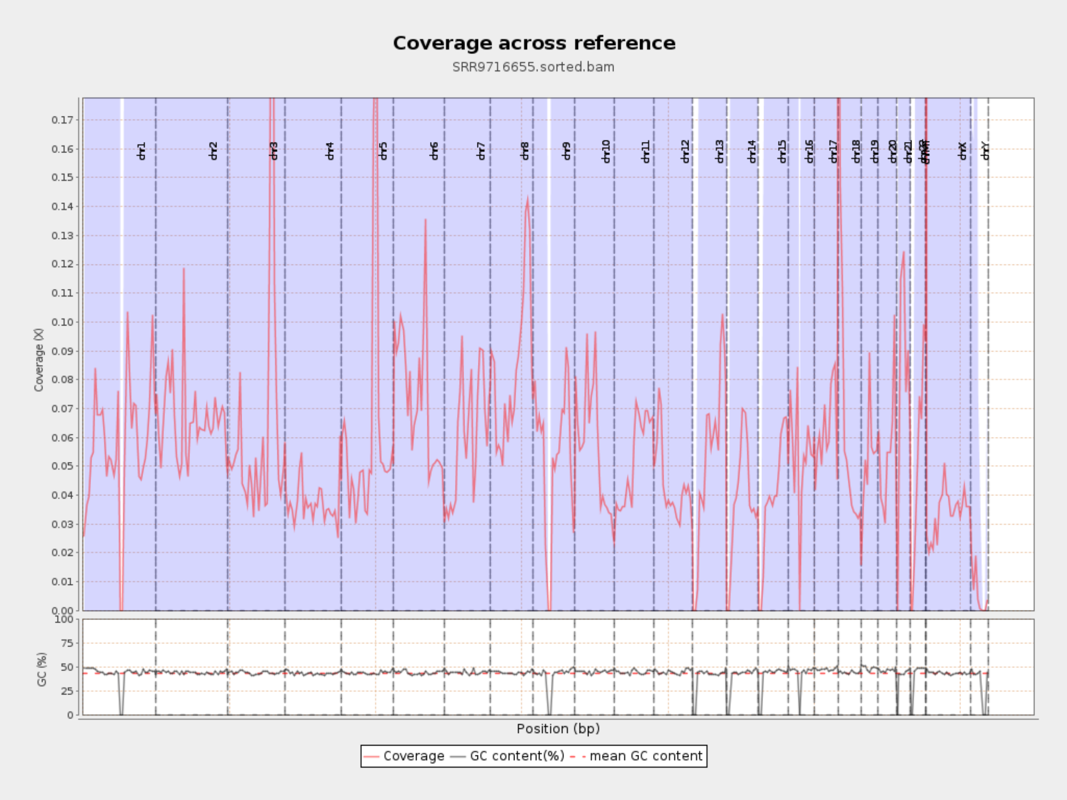
General error rate	0.78%
Mismatches	1,307,261
Insertions	16,049
Mapped reads with at least one insertion	0.68%
Deletions	35,465
Mapped reads with at least one deletion	1.5%
Homopolymer indels	39.22%

2.6. Chromosome stats

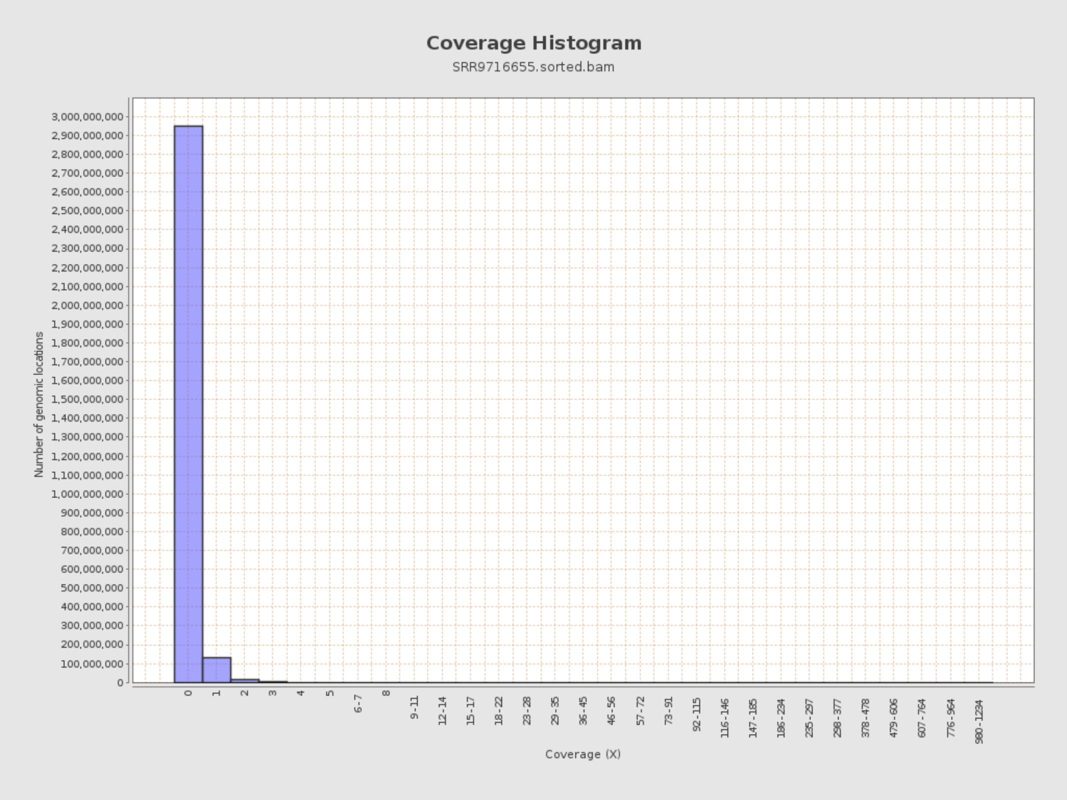
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14245347	0.0572	0.589
chr2	243199373	16201245	0.0666	0.8384
chr3	198022430	12633624	0.0638	0.2987
chr4	191154276	7146261	0.0374	0.2337
chr5	180915260	10937641	0.0605	0.2864
chr6	171115067	12612812	0.0737	0.3703
chr7	159138663	9612627	0.0604	0.6968

chr8	146364022	12406280	0.0848	0.6486
chr9	141213431	7544280	0.0534	0.448
chr10	135534747	7831823	0.0578	0.433
chr11	135006516	7029811	0.0521	0.3783
chr12	133851895	5870200	0.0439	0.2397
chr13	115169878	6207941	0.0539	0.2623
chr14	107349540	4130760	0.0385	0.2623
chr15	102531392	3924533	0.0383	0.2207
chr16	90354753	4761345	0.0527	0.2939
chr17	81195210	5141572	0.0633	0.3399
chr18	78077248	5357321	0.0686	0.9752
chr19	59128983	3184970	0.0539	0.5689
chr20	63025520	3499379	0.0555	0.3009
chr21	48129895	3730553	0.0775	0.3342
chr22	51304566	2557241	0.0498	0.26
chrMT	16571	57703	3.4822	3.322
chrX	155270560	5274075	0.034	0.2863
chrY	59373566	364404	0.0061	0.1674

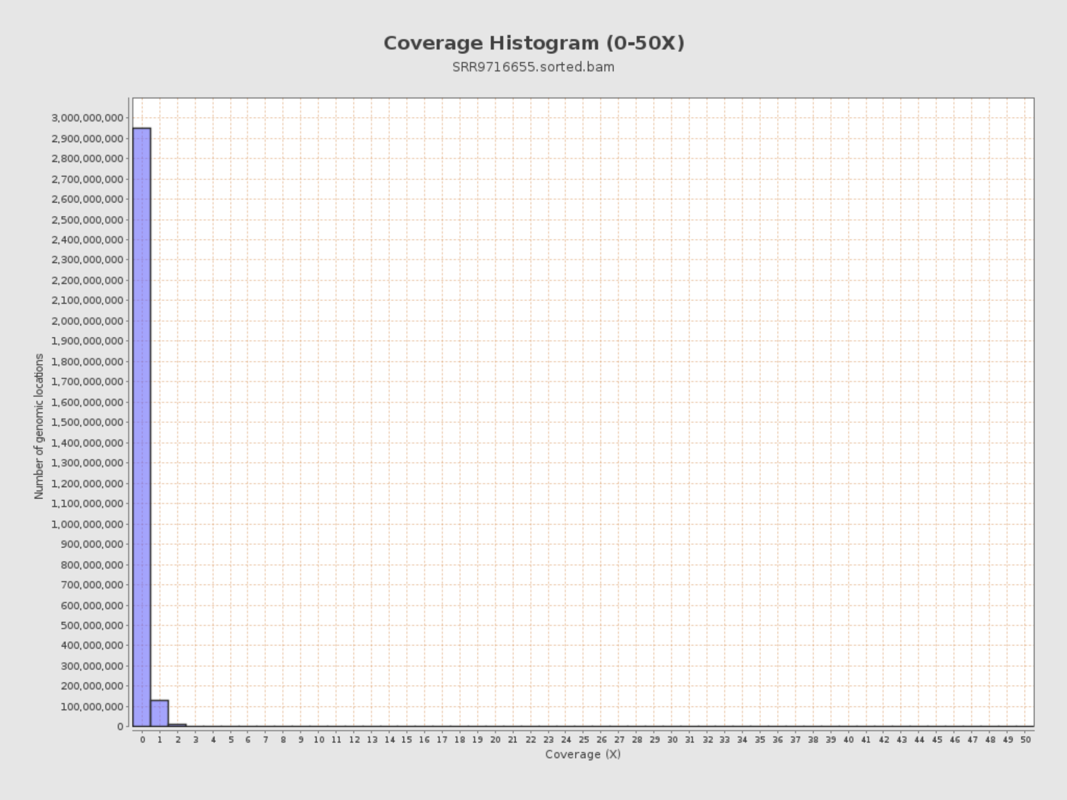
3. Results : Coverage across reference



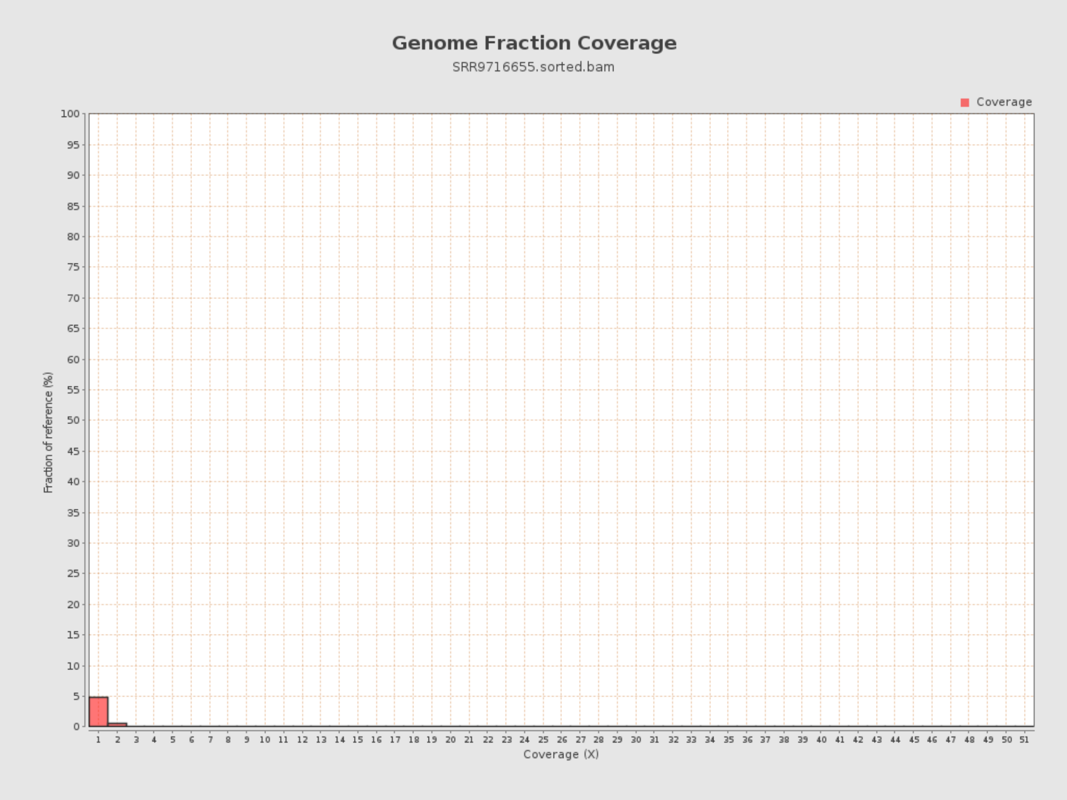
4. Results : Coverage Histogram



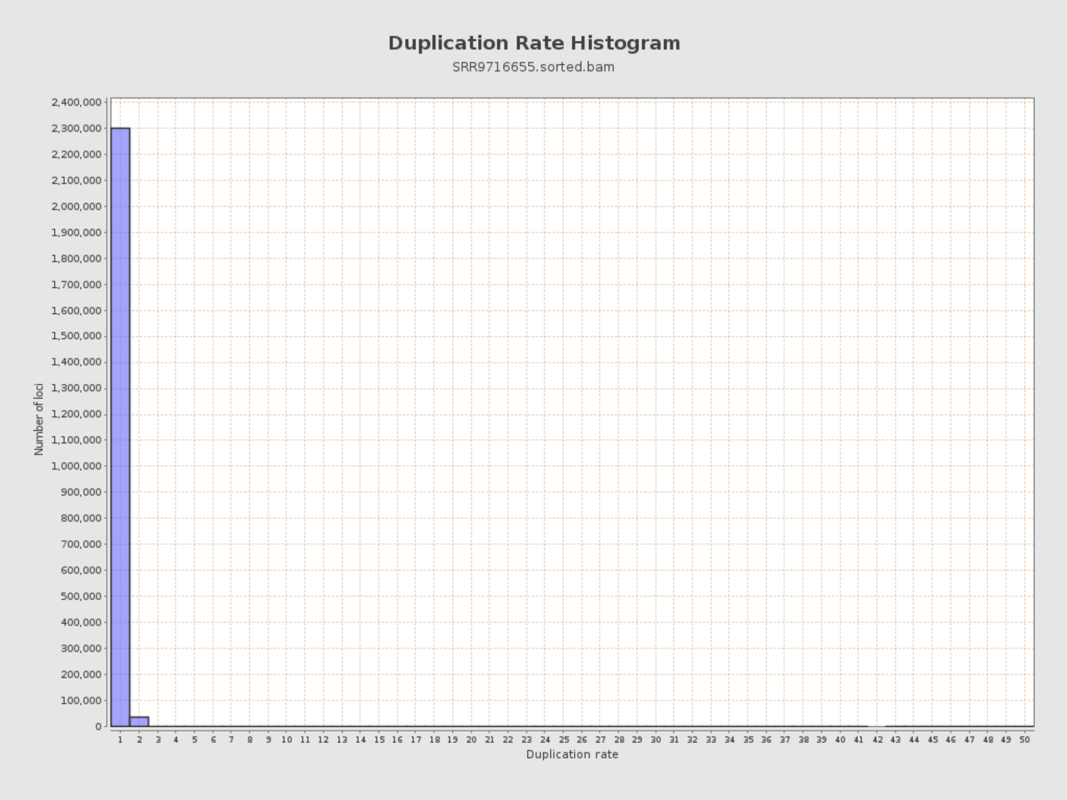
5. Results : Coverage Histogram (0-50X)



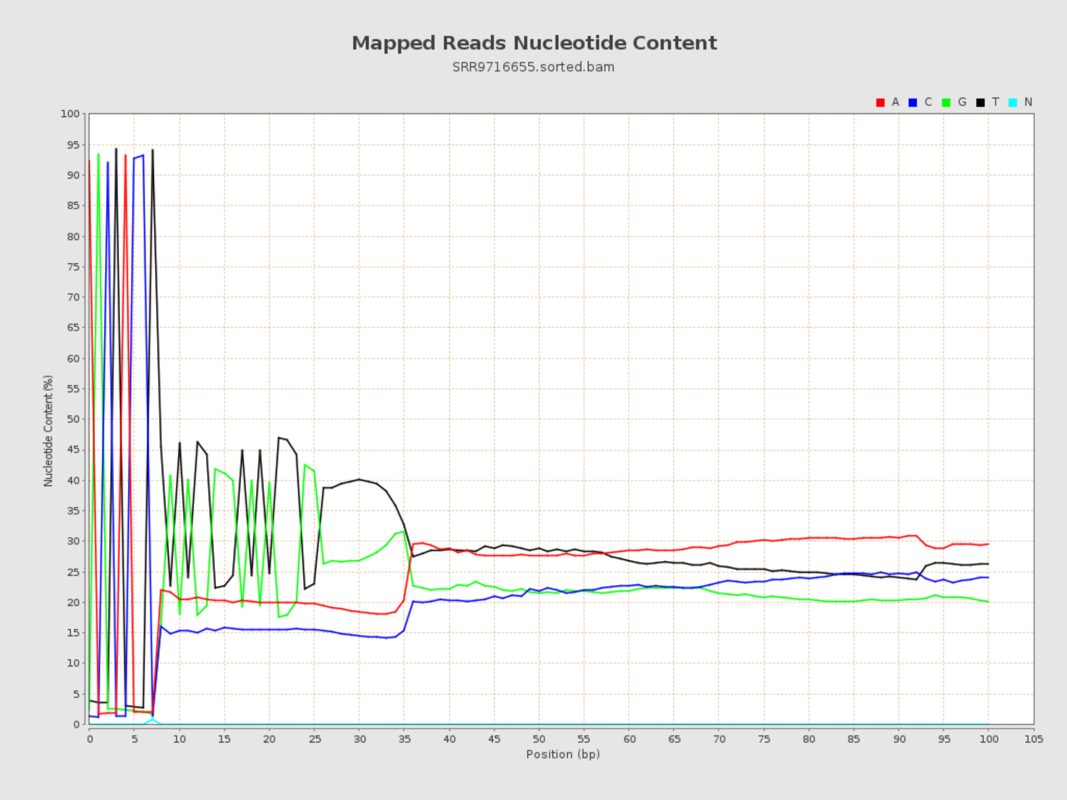
6. Results : Genome Fraction Coverage



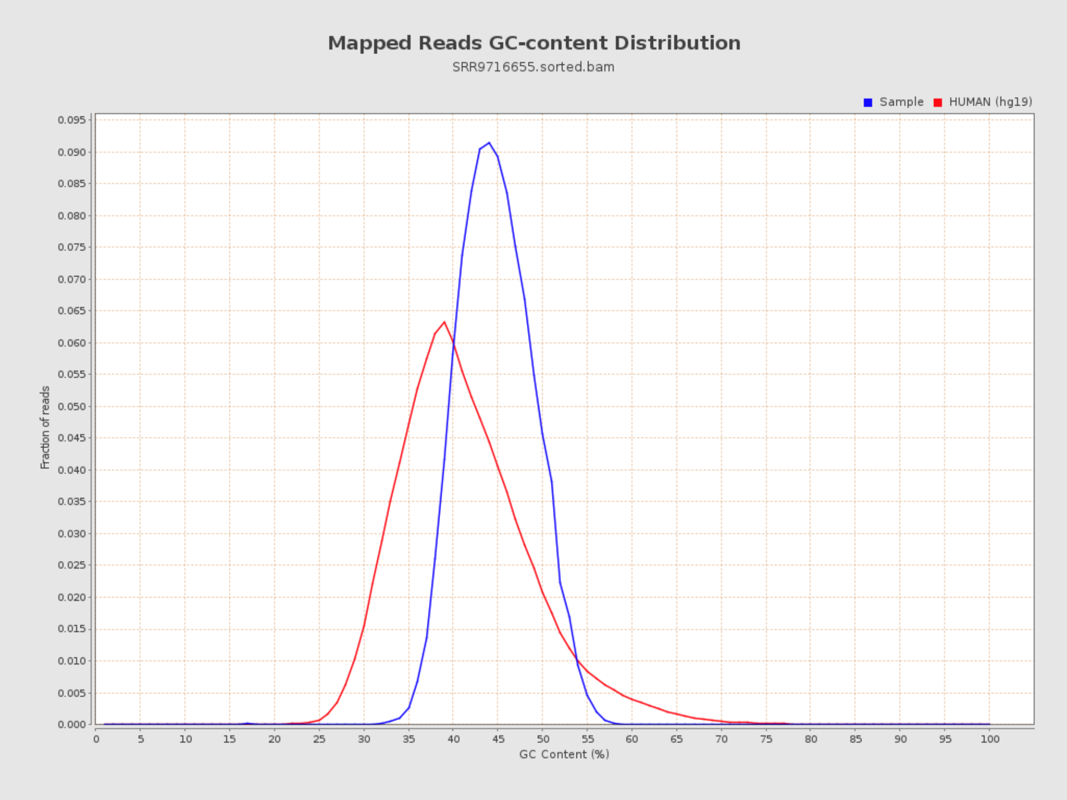
7. Results : Duplication Rate Histogram



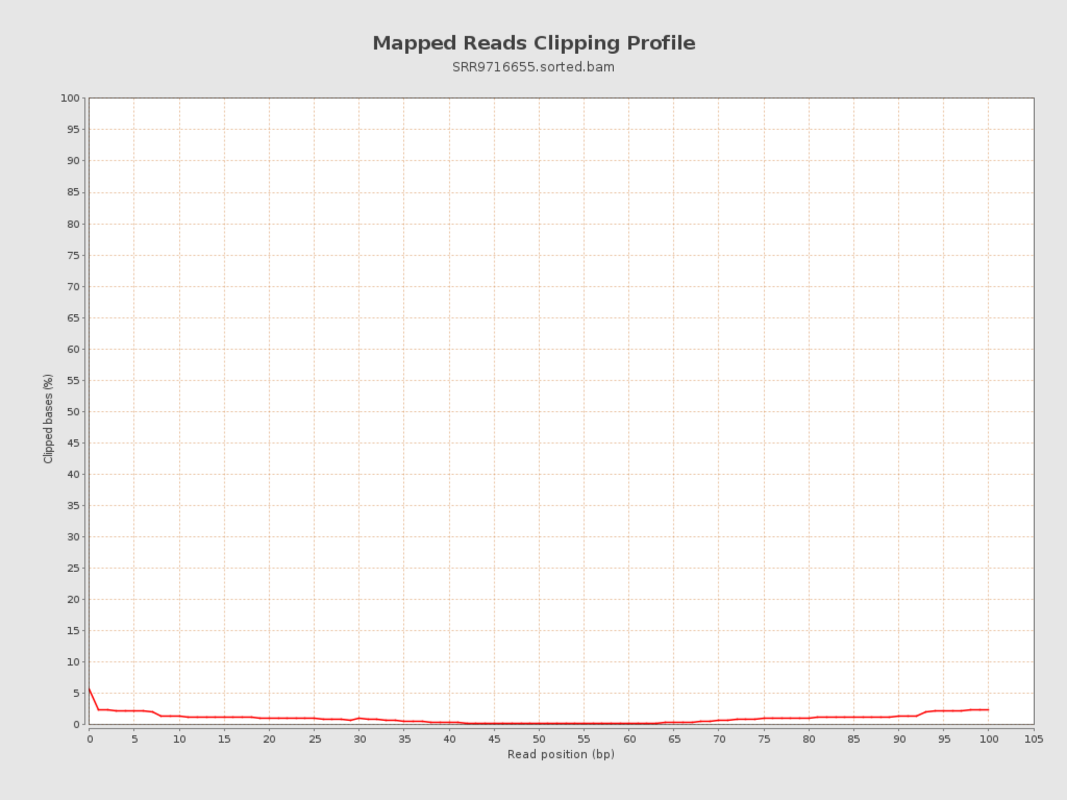
8. Results : Mapped Reads Nucleotide Content



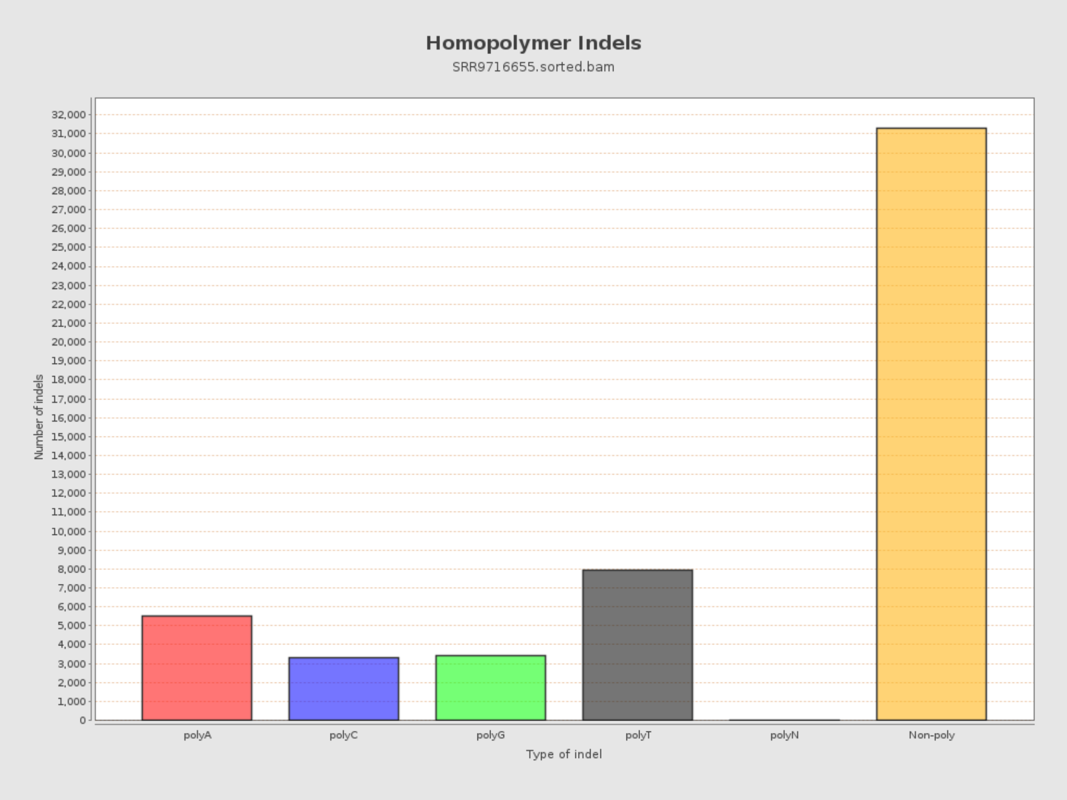
9. Results : Mapped Reads GC-content Distribution



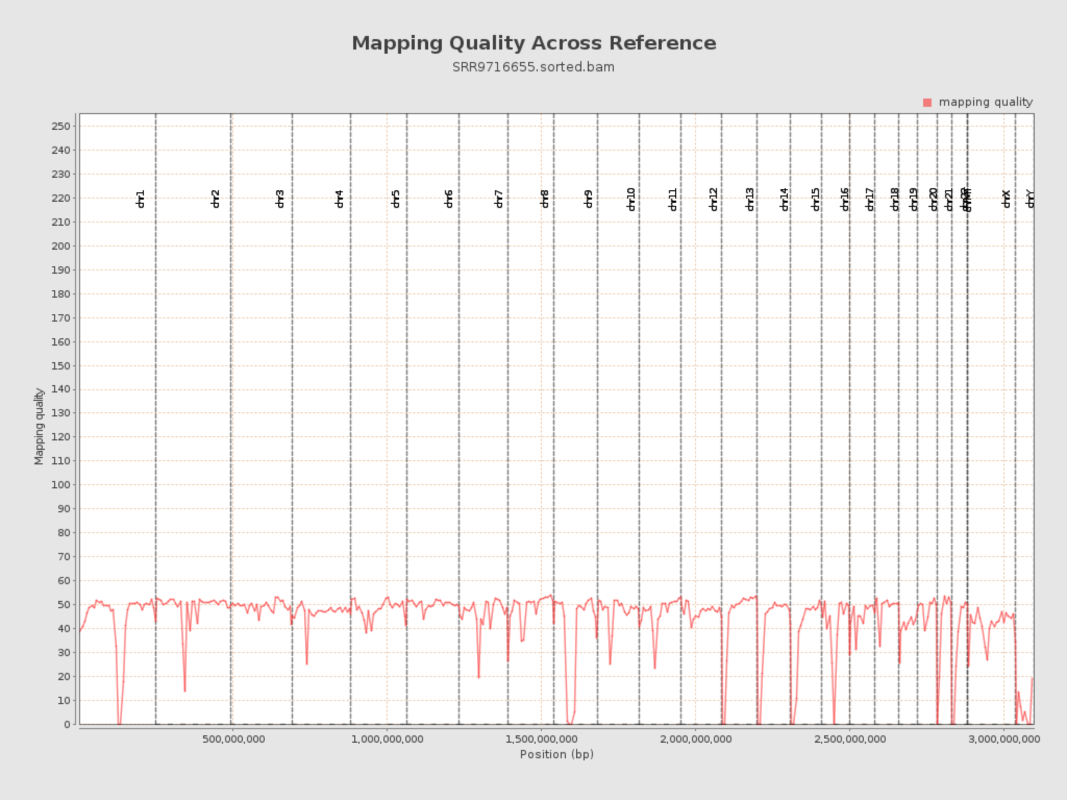
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram