Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 23:57:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716203.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_SRR9716203 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716203.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 23:57:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716203.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,441,455
Mapped reads	4,983,823 / 91.59%
Unmapped reads	457,632 / 8.41%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	116,998 / 2.15%
Read min/max/mean length	30 / 101 / 101.77
Duplicated reads (estimated)	334,267 / 6.14%
Duplication rate	4.89%
Clipped reads	5,100,173 / 93.73%

2.2. ACGT Content

Number/percentage of A's	93,533,634 / 25.83%
Number/percentage of C's	75,894,184 / 20.96%
Number/percentage of T's	105,846,123 / 29.23%
Number/percentage of G's	86,739,168 / 23.96%
Number/percentage of N's	39,674 / 0.01%
GC Percentage	44.92%

2.3. Coverage

Mean	0.117

Standard Deviation	0.7978

2.4. Mapping Quality

Mean Mapping Quality	46.03

2.5. Mismatches and indels

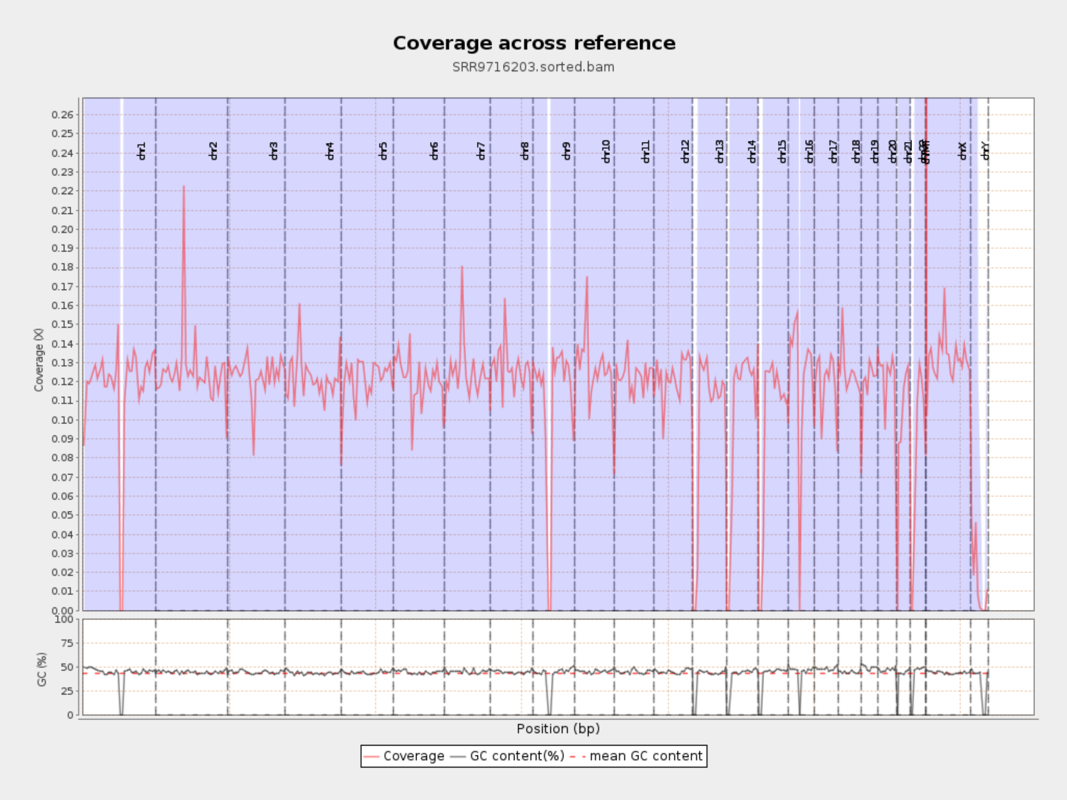
General error rate	0.73%
Mismatches	2,592,013
Insertions	25,327
Mapped reads with at least one insertion	0.5%
Deletions	69,427
Mapped reads with at least one deletion	1.37%
Homopolymer indels	40.91%

2.6. Chromosome stats

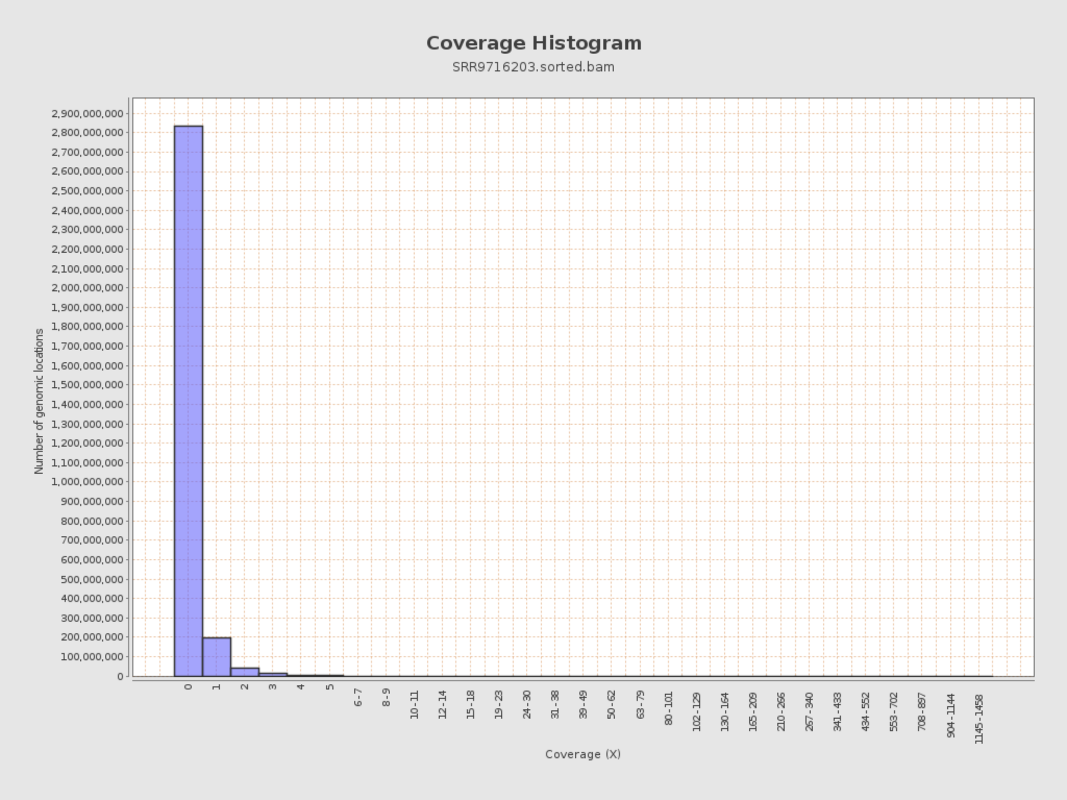
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	28960351	0.1162	0.9091
chr2	243199373	30677920	0.1261	1.2046
chr3	198022430	24467995	0.1236	0.4631
chr4	191154276	23458608	0.1227	0.5276
chr5	180915260	21910590	0.1211	0.4691
chr6	171115067	20766103	0.1214	0.5787
chr7	159138663	19961364	0.1254	1.1798

chr8	146364022	18418336	0.1258	1.0291
chr9	141213431	15409481	0.1091	0.8541
chr10	135534747	17315115	0.1278	0.7717
chr11	135006516	16433751	0.1217	0.8866
chr12	133851895	16382973	0.1224	0.4834
chr13	115169878	11493383	0.0998	0.4132
chr14	107349540	11129365	0.1037	0.5974
chr15	102531392	9882244	0.0964	0.4154
chr16	90354753	10735113	0.1188	0.5532
chr17	81195210	9806106	0.1208	0.5396
chr18	78077248	9813400	0.1257	1.7129
chr19	59128983	7156841	0.121	0.8396
chr20	63025520	7667451	0.1217	0.5035
chr21	48129895	4698461	0.0976	0.485
chr22	51304566	4141404	0.0807	0.3746
chrMT	16571	103514	6.2467	6.3487
chrX	155270560	20473734	0.1319	0.7114
chrY	59373566	906566	0.0153	0.3635

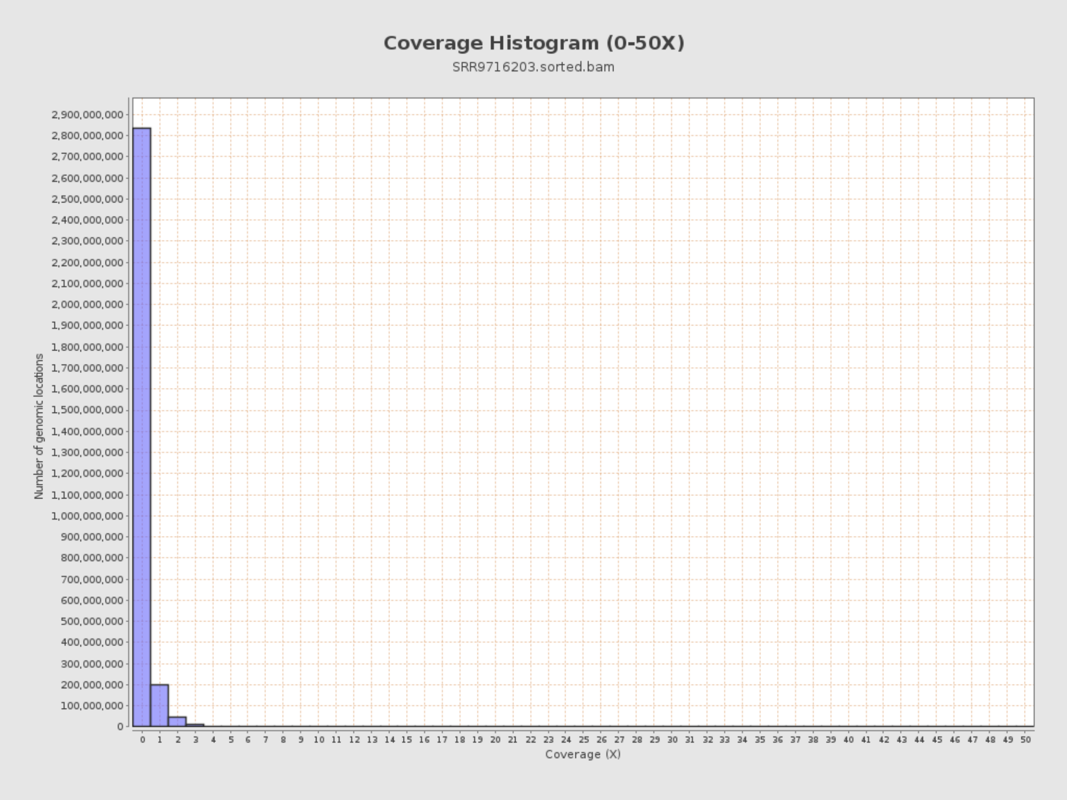
3. Results : Coverage across reference



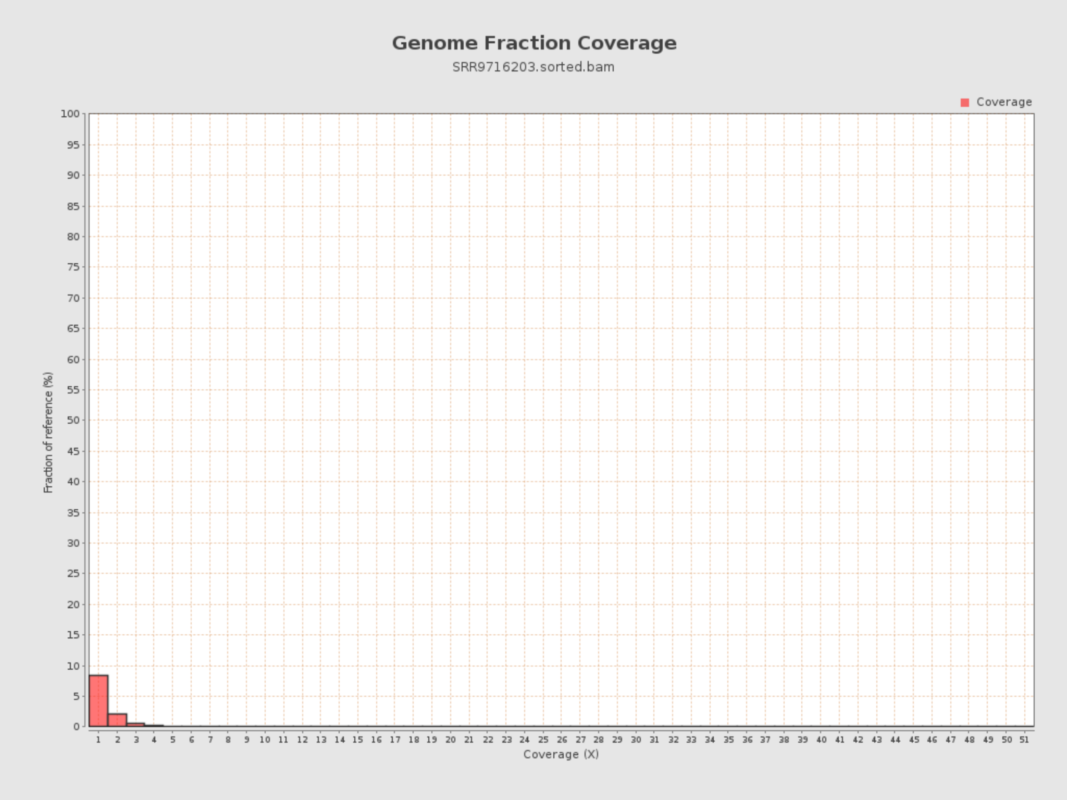
4. Results : Coverage Histogram



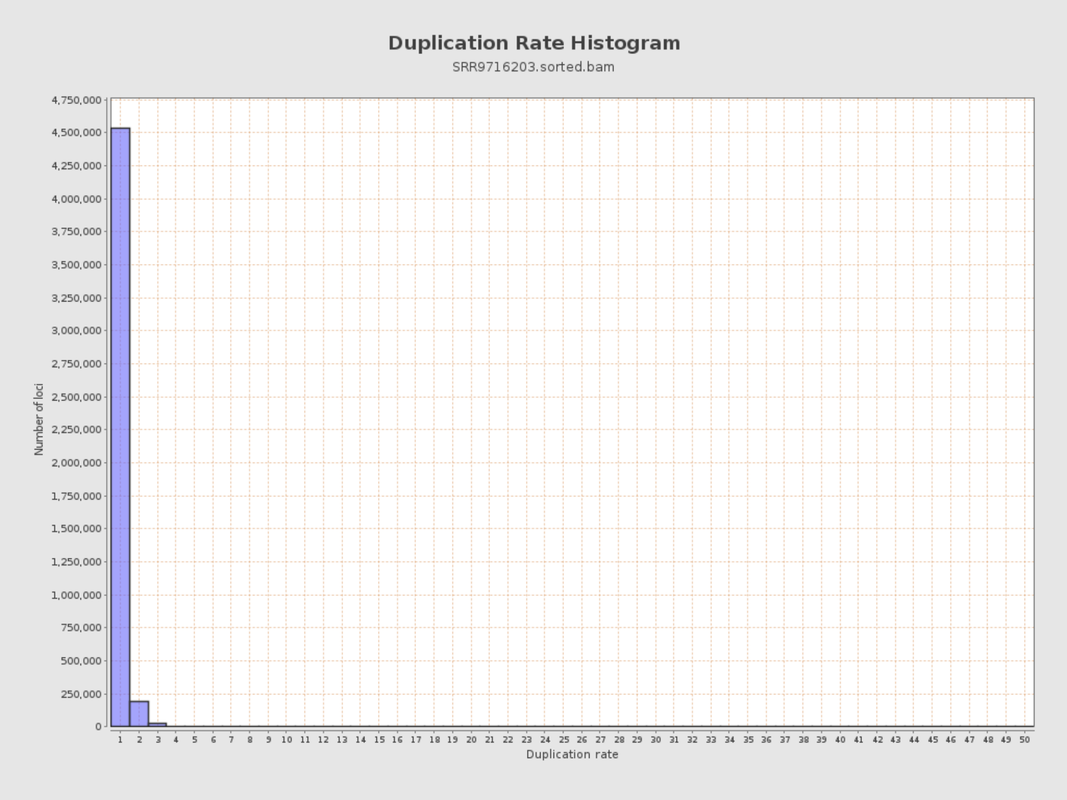
5. Results : Coverage Histogram (0-50X)



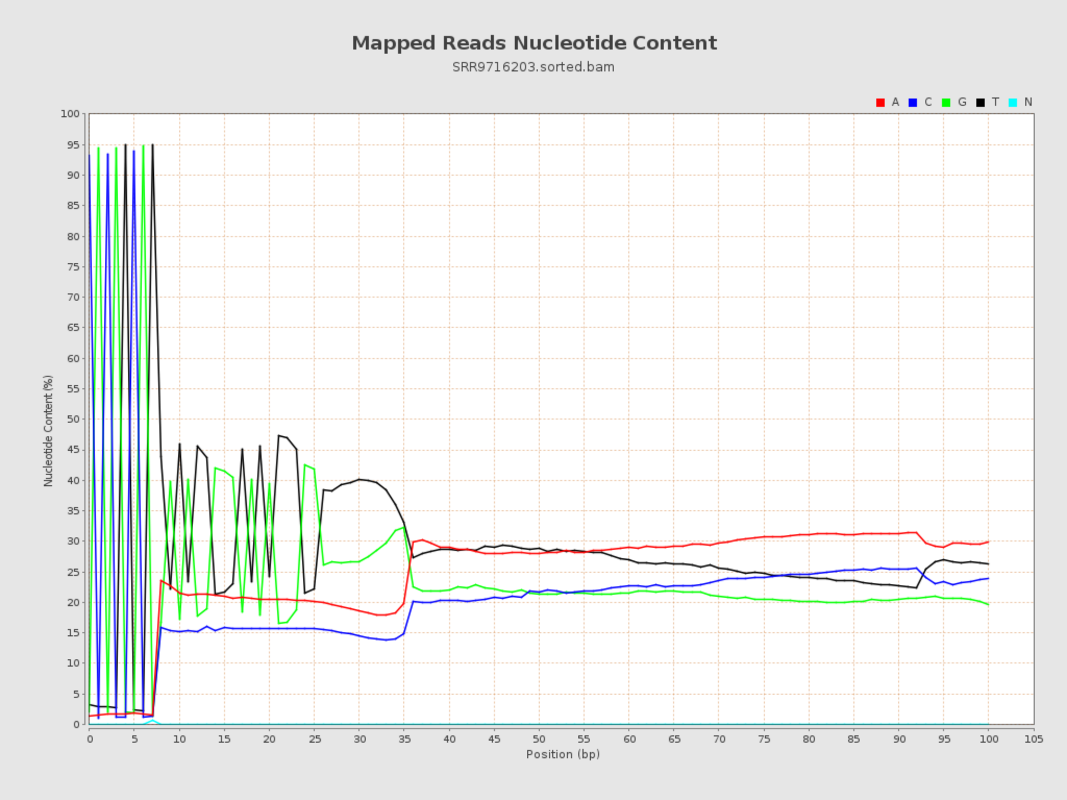
6. Results : Genome Fraction Coverage



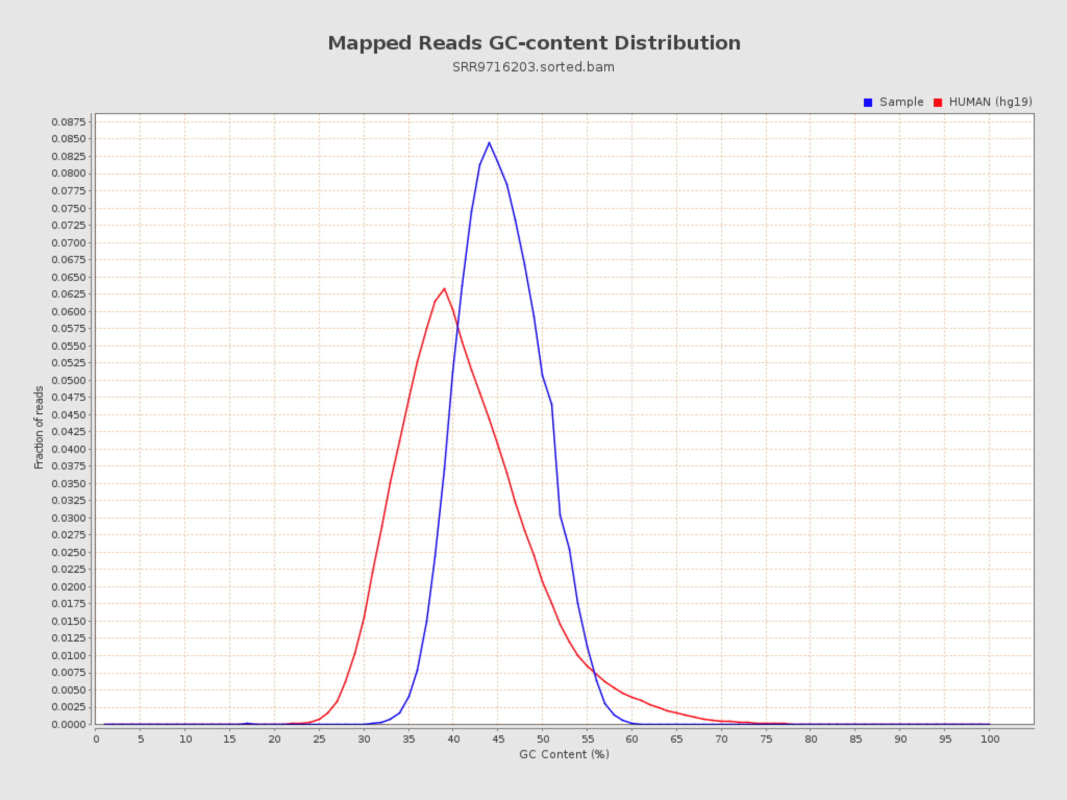
7. Results : Duplication Rate Histogram



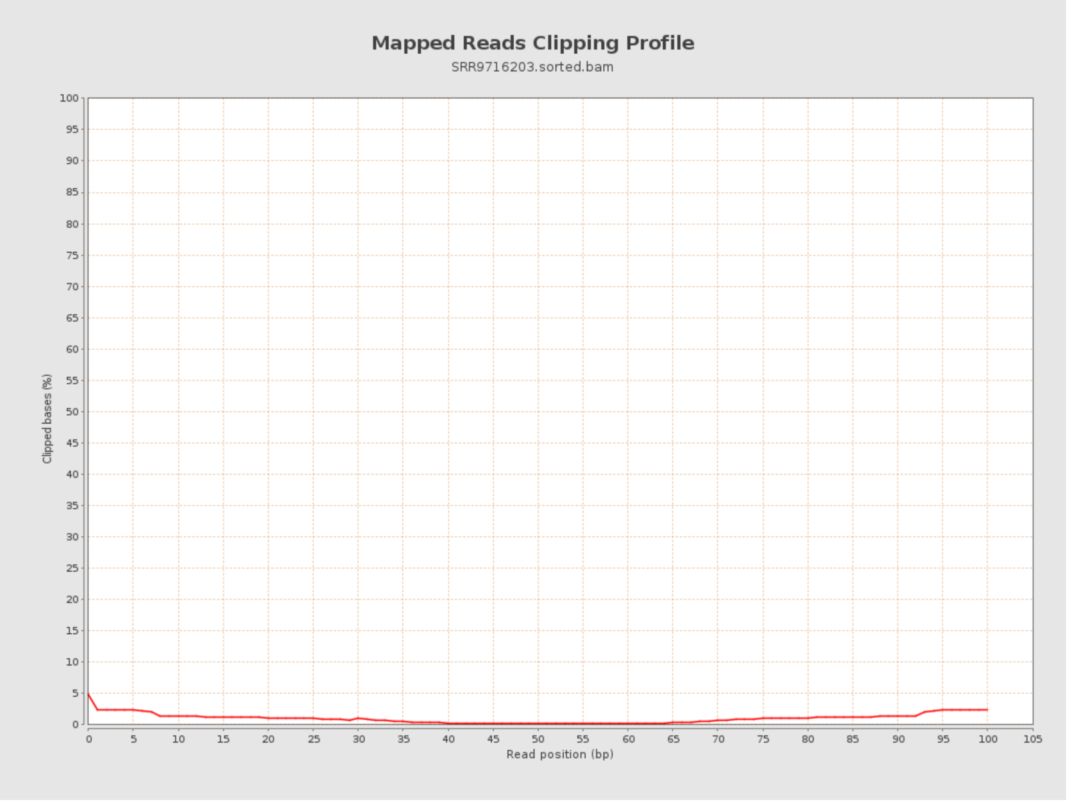
8. Results : Mapped Reads Nucleotide Content



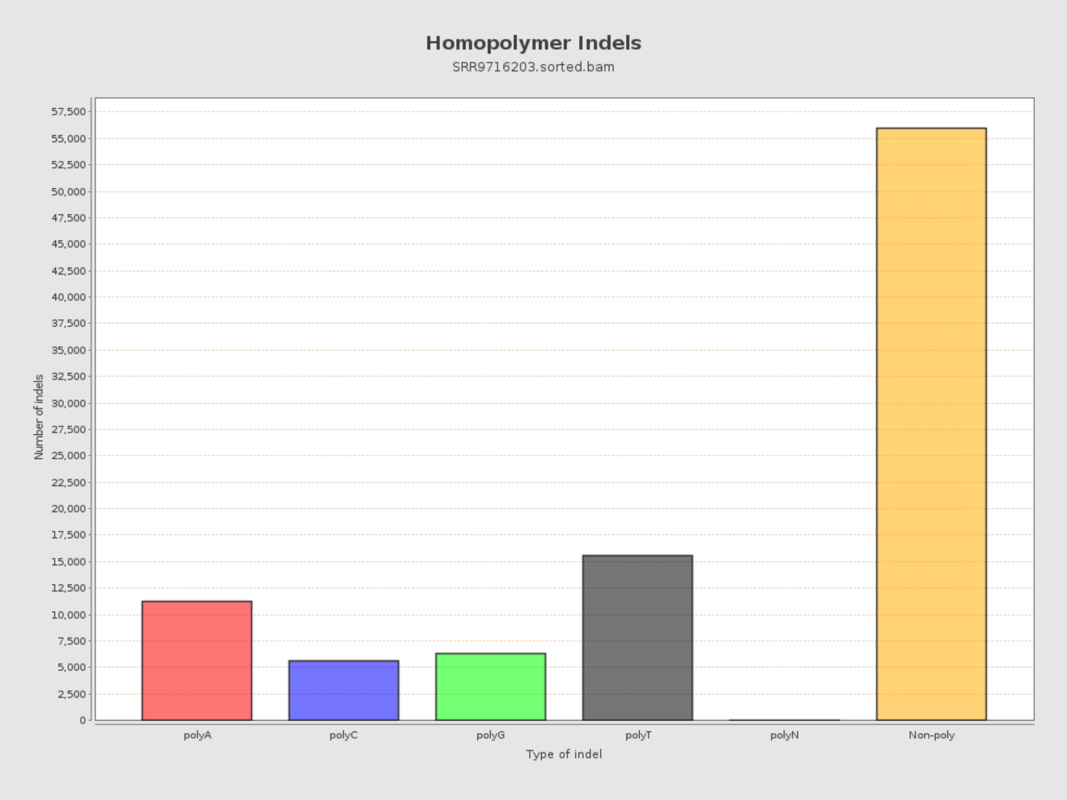
9. Results : Mapped Reads GC-content Distribution



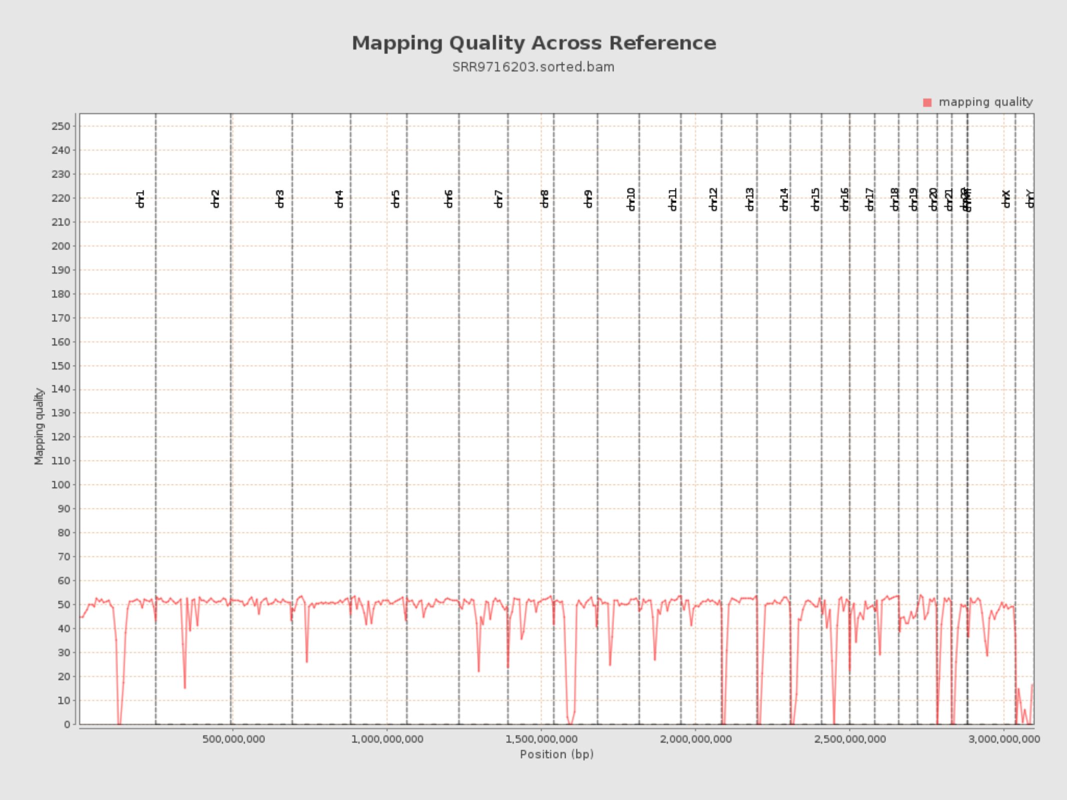
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram