Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 06:43:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716310.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_SRR9716310 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716310.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 06:43:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716310.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,464,916
Mapped reads	1,350,252 / 92.17%
Unmapped reads	114,664 / 7.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,988 / 1.77%
Read min/max/mean length	30 / 101 / 101.64
Duplicated reads (estimated)	46,988 / 3.21%
Duplication rate	2.48%
Clipped reads	1,373,883 / 93.79%

2.2. ACGT Content

Number/percentage of A's	28,016,197 / 26.24%
Number/percentage of C's	20,799,258 / 19.48%
Number/percentage of T's	32,974,069 / 30.88%
Number/percentage of G's	24,968,373 / 23.39%
Number/percentage of N's	7,307 / 0.01%
GC Percentage	42.87%

2.3. Coverage

Mean	0.0345

Standard Deviation	0.3396

2.4. Mapping Quality

Mean Mapping Quality	47.46

2.5. Mismatches and indels

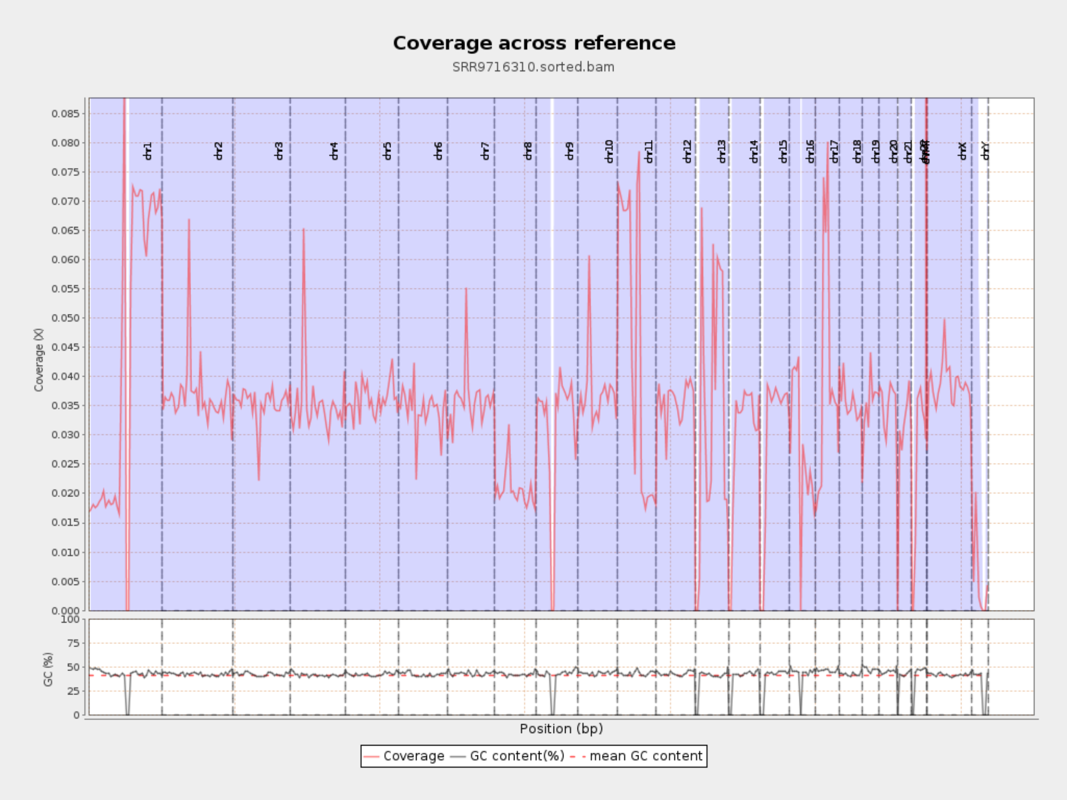
General error rate	0.68%
Mismatches	703,770
Insertions	8,334
Mapped reads with at least one insertion	0.61%
Deletions	24,768
Mapped reads with at least one deletion	1.81%
Homopolymer indels	42.81%

2.6. Chromosome stats

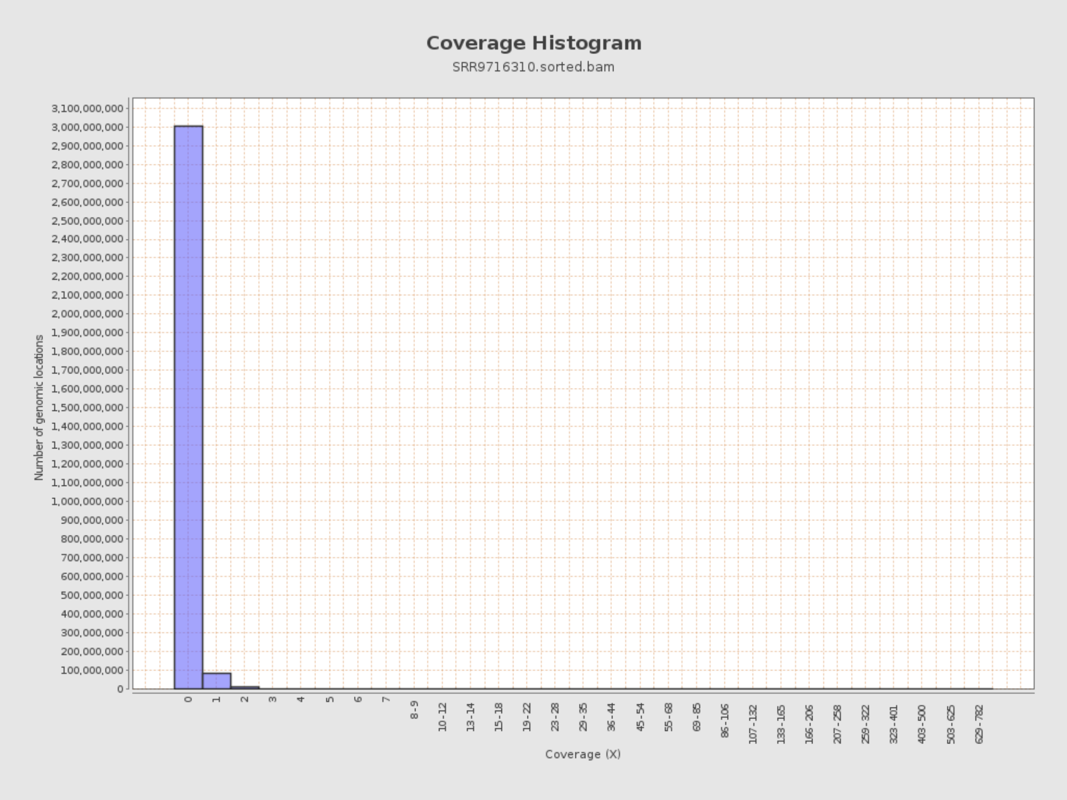
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10624581	0.0426	0.7188
chr2	243199373	9012422	0.0371	0.3524
chr3	198022430	6992285	0.0353	0.2046
chr4	191154276	6748493	0.0353	0.2436
chr5	180915260	6532724	0.0361	0.2093
chr6	171115067	5881011	0.0344	0.2216
chr7	159138663	5739417	0.0361	0.4035

chr8	146364022	3026699	0.0207	0.3416
chr9	141213431	4411976	0.0312	0.2782
chr10	135534747	5025768	0.0371	0.318
chr11	135006516	6118010	0.0453	0.3596
chr12	133851895	4776220	0.0357	0.208
chr13	115169878	3835164	0.0333	0.2014
chr14	107349540	3115776	0.029	0.2007
chr15	102531392	3062044	0.0299	0.19
chr16	90354753	2461571	0.0272	0.1966
chr17	81195210	3368378	0.0415	0.2649
chr18	78077248	2793087	0.0358	0.4584
chr19	59128983	2101085	0.0355	0.4993
chr20	63025520	2209046	0.0351	0.2133
chr21	48129895	1427049	0.0296	0.2121
chr22	51304566	1237174	0.0241	0.1711
chrMT	16571	8170	0.493	0.8376
chrX	155270560	5991771	0.0386	0.2486
chrY	59373566	312776	0.0053	0.1768

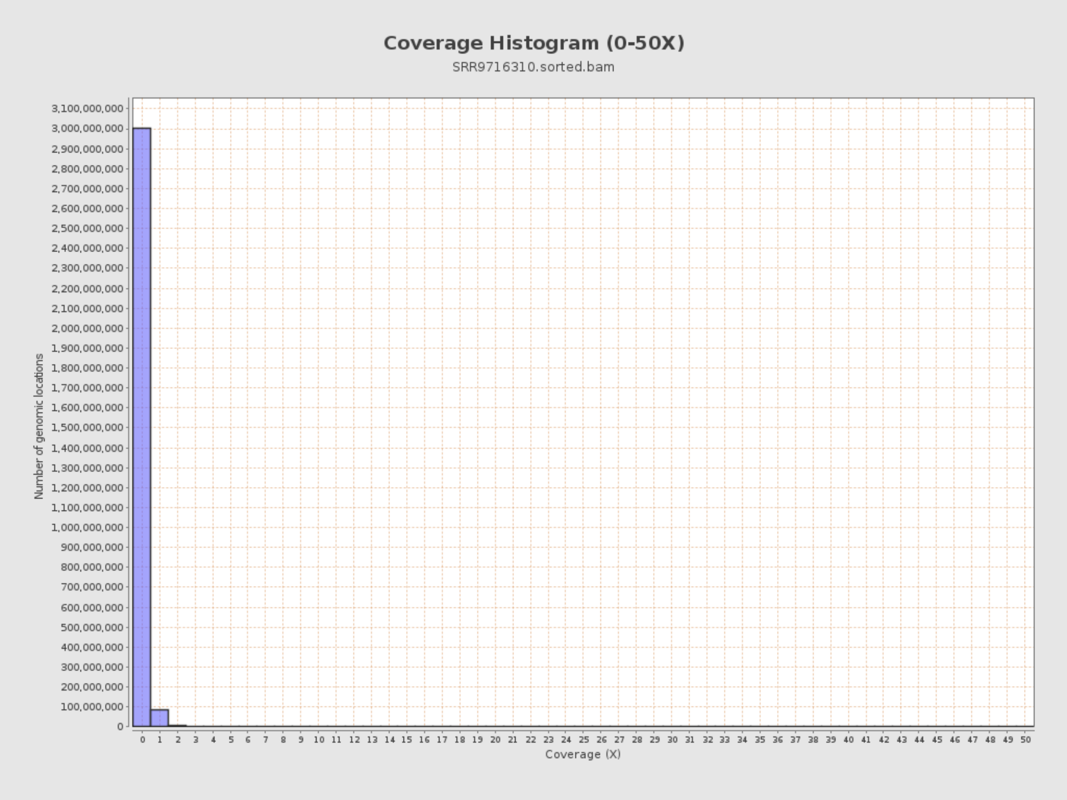
3. Results : Coverage across reference



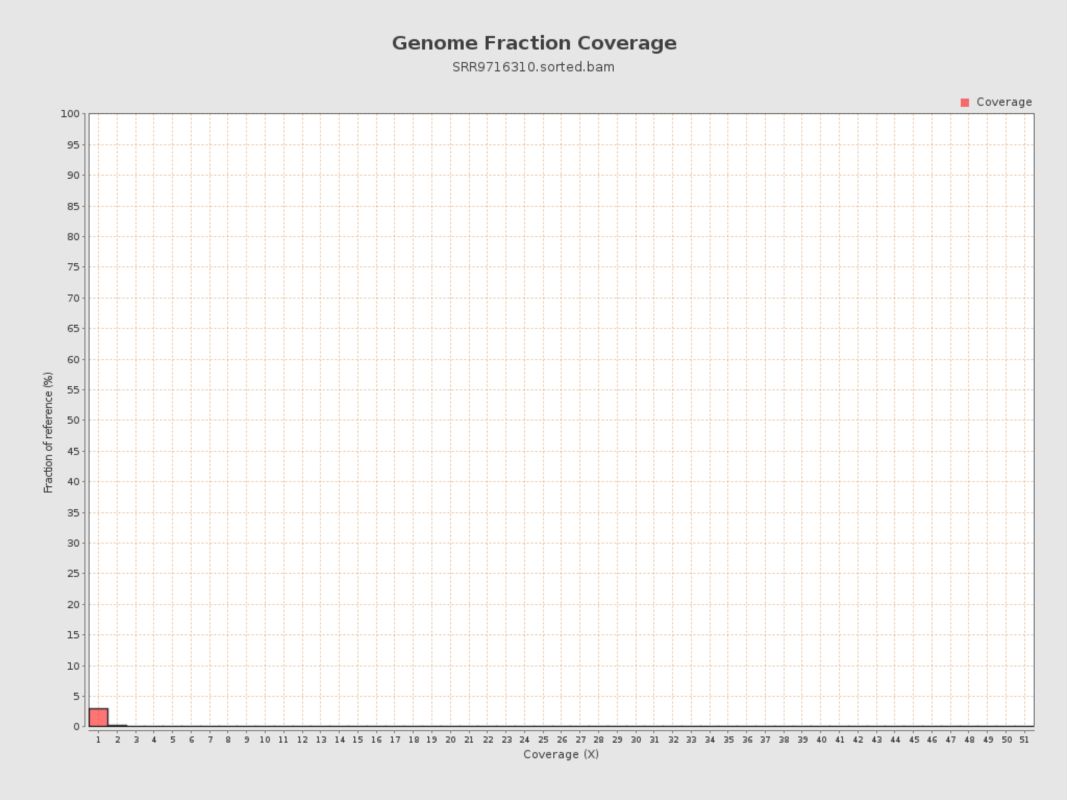
4. Results : Coverage Histogram



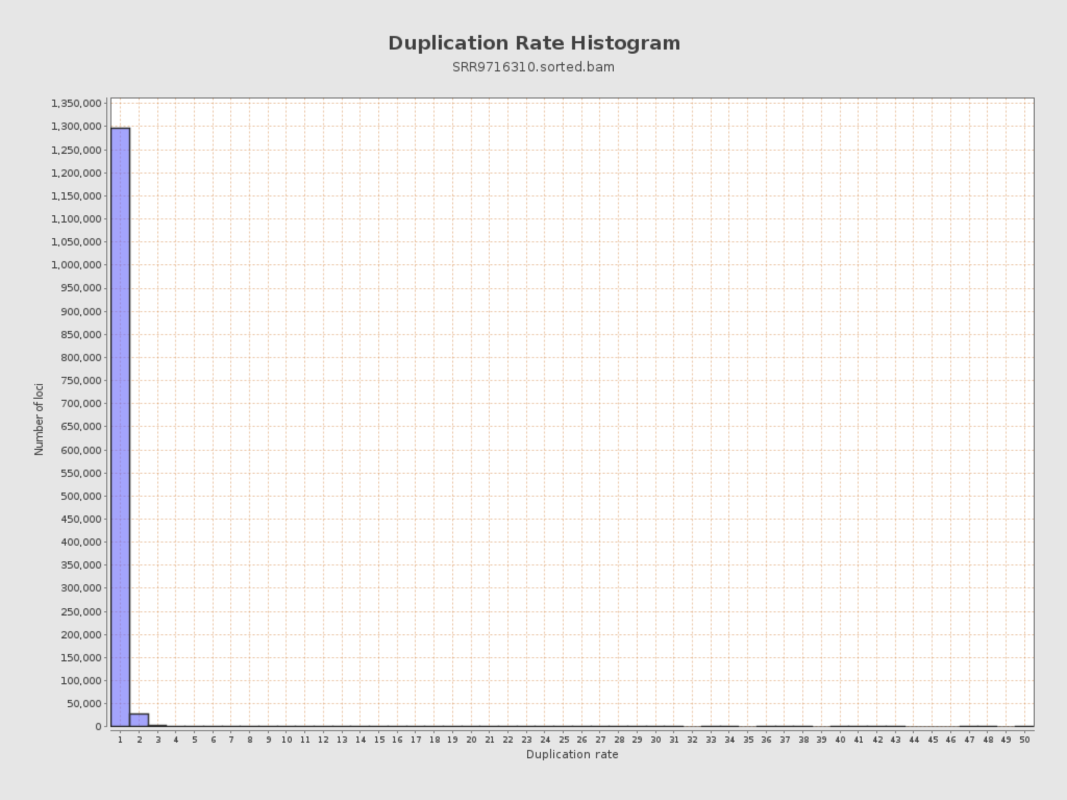
5. Results : Coverage Histogram (0-50X)



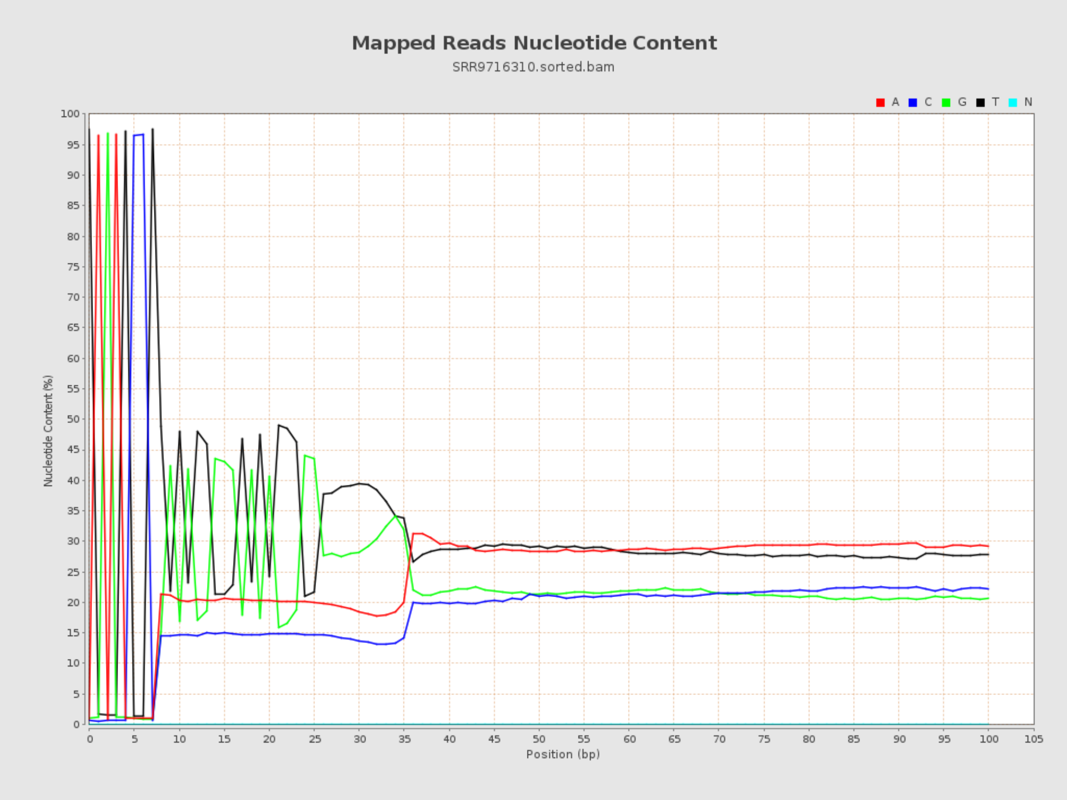
6. Results : Genome Fraction Coverage



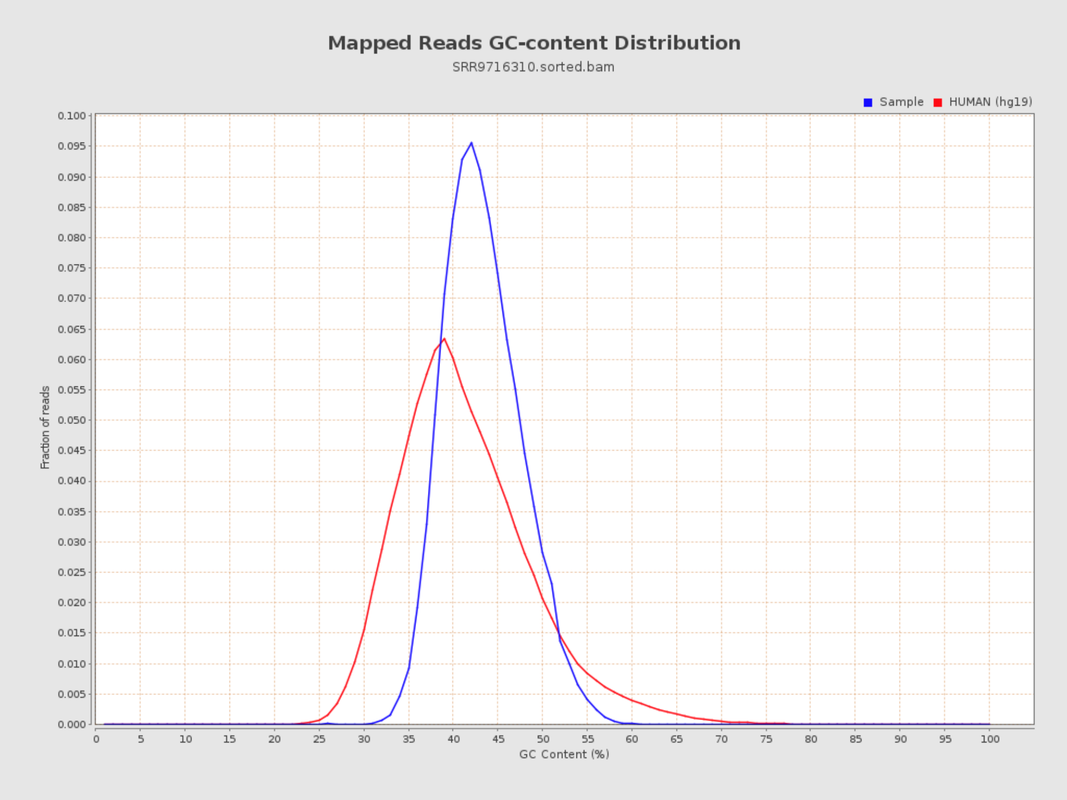
7. Results : Duplication Rate Histogram



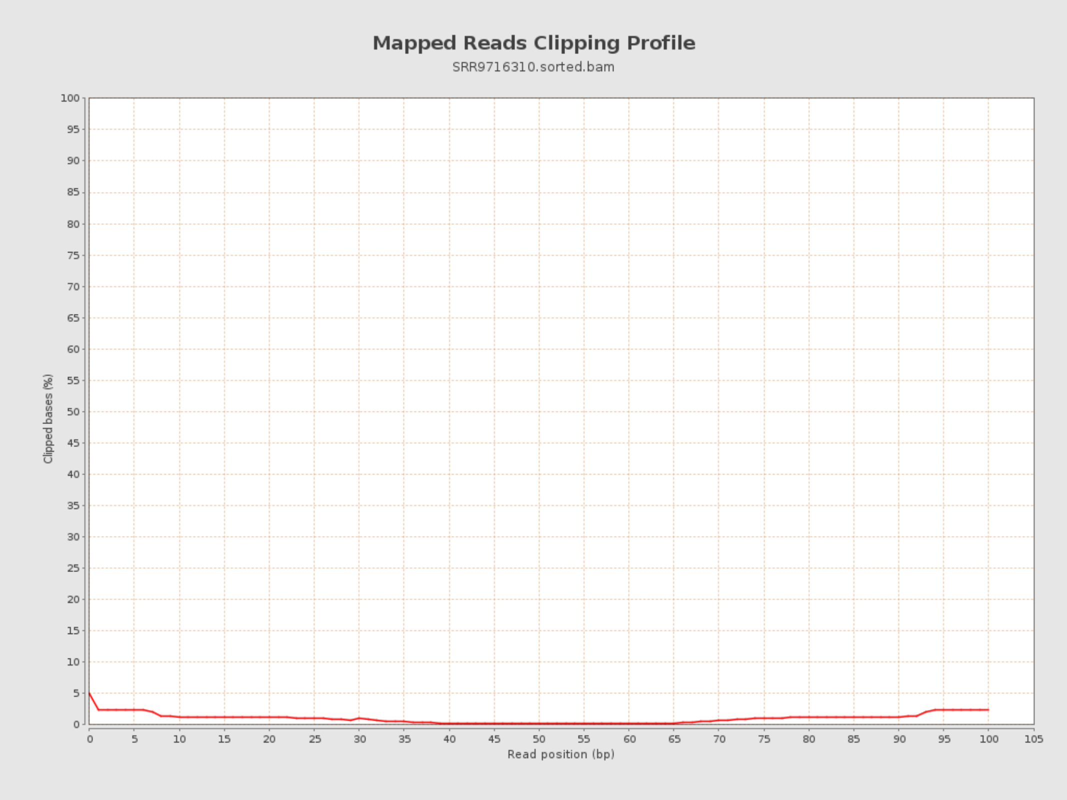
8. Results : Mapped Reads Nucleotide Content



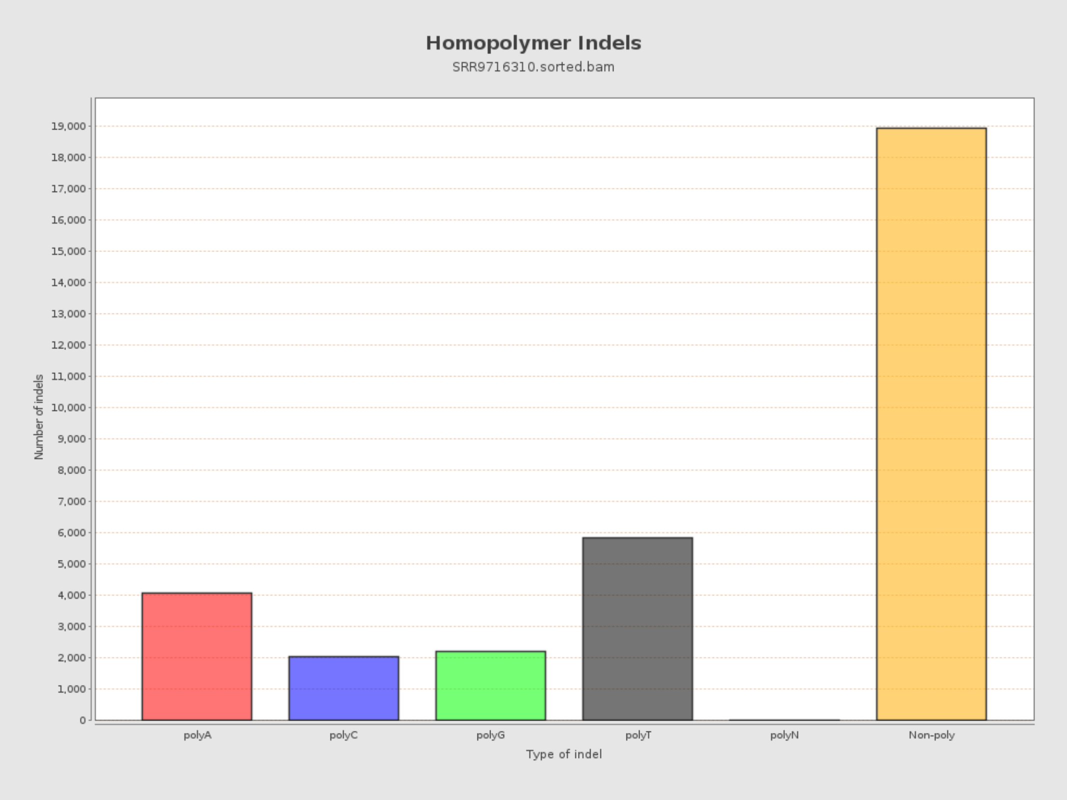
9. Results : Mapped Reads GC-content Distribution



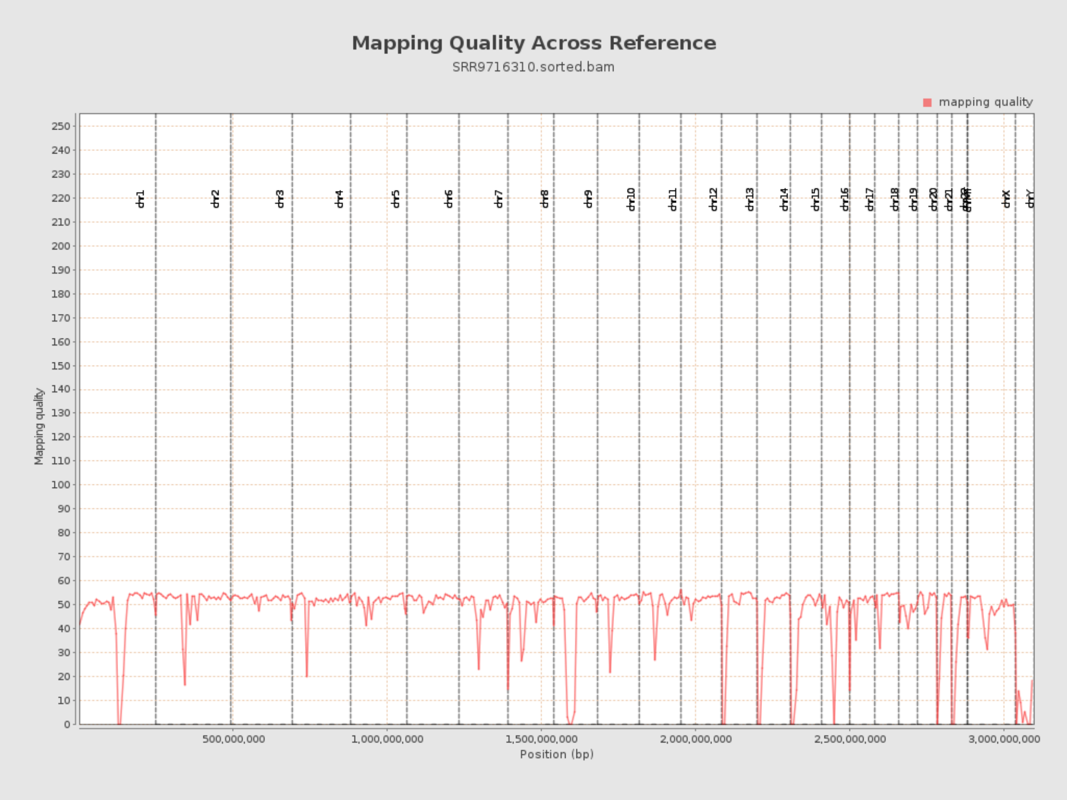
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram