Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 03:25:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716259.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_SRR9716259 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716259.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 03:25:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716259.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	519,831
Mapped reads	440,170 / 84.68%
Unmapped reads	79,661 / 15.32%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,878 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	7,891 / 1.52%
Duplication rate	1.31%
Clipped reads	440,899 / 84.82%

2.2. ACGT Content

Number/percentage of A's	6,528,436 / 25.79%
Number/percentage of C's	4,473,362 / 17.67%
Number/percentage of T's	8,008,104 / 31.64%
Number/percentage of G's	6,301,334 / 24.89%
Number/percentage of N's	715 / 0%
GC Percentage	42.57%

2.3. Coverage

Mean	0.0082

Standard Deviation	0.1101

2.4. Mapping Quality

Mean Mapping Quality	44.44

2.5. Mismatches and indels

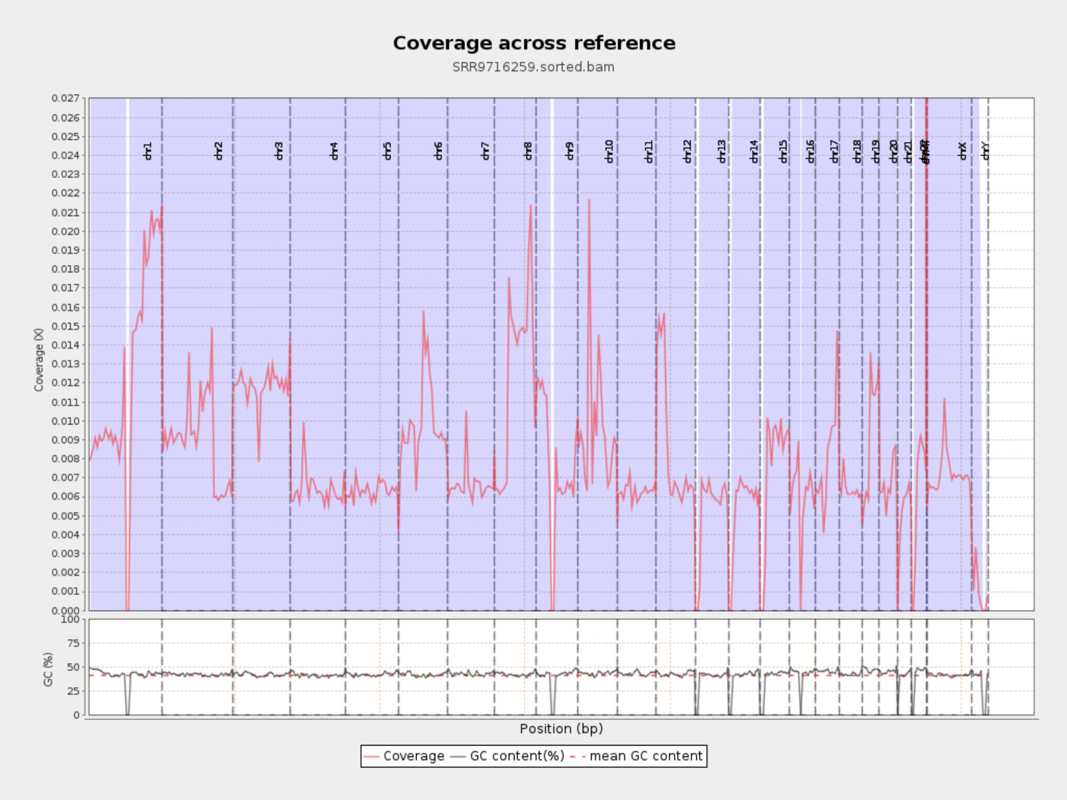
General error rate	0.52%
Mismatches	128,624
Insertions	1,702
Mapped reads with at least one insertion	0.39%
Deletions	4,466
Mapped reads with at least one deletion	1.01%
Homopolymer indels	42.64%

2.6. Chromosome stats

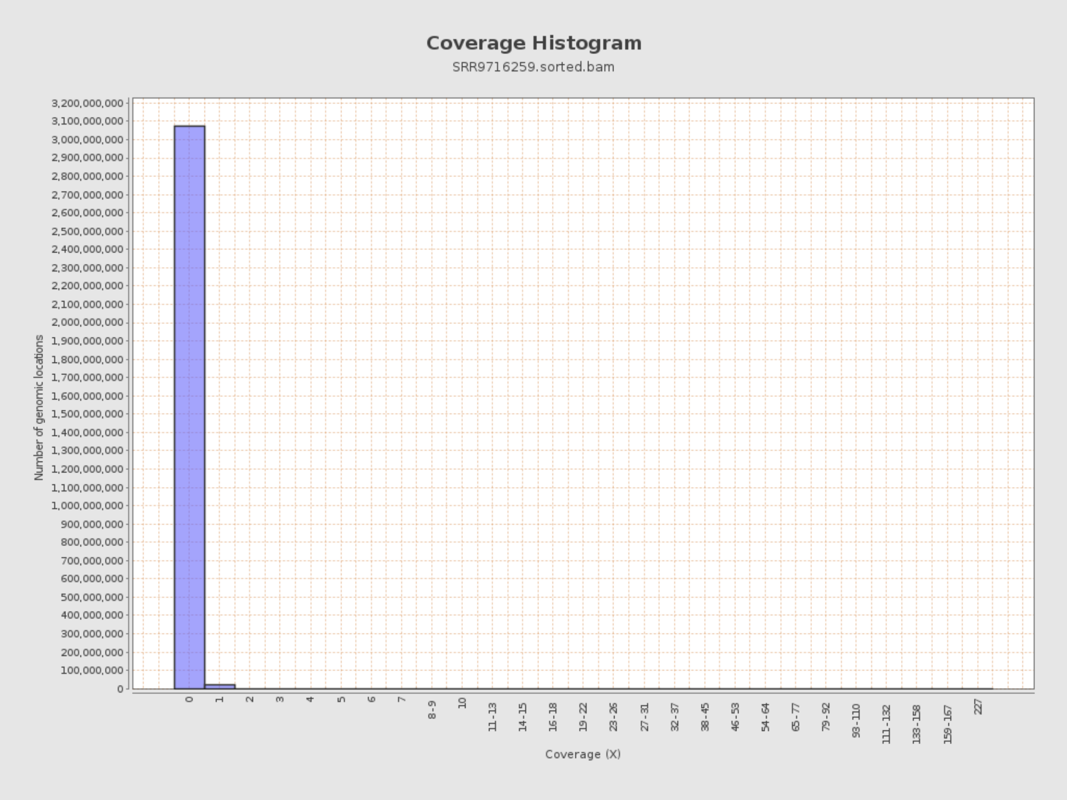
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3066228	0.0123	0.1687
chr2	243199373	2195108	0.009	0.1344
chr3	198022430	2339087	0.0118	0.1142
chr4	191154276	1222947	0.0064	0.0846
chr5	180915260	1148977	0.0064	0.0827
chr6	171115067	1691840	0.0099	0.1095
chr7	159138663	1055332	0.0066	0.103

chr8	146364022	1843921	0.0126	0.1212
chr9	141213431	1060262	0.0075	0.104
chr10	135534747	1314662	0.0097	0.138
chr11	135006516	844684	0.0063	0.0897
chr12	133851895	1145019	0.0086	0.0965
chr13	115169878	599073	0.0052	0.0743
chr14	107349540	567038	0.0053	0.0775
chr15	102531392	762857	0.0074	0.0888
chr16	90354753	544338	0.006	0.0883
chr17	81195210	682675	0.0084	0.0954
chr18	78077248	500391	0.0064	0.1324
chr19	59128983	553843	0.0094	0.1296
chr20	63025520	424655	0.0067	0.085
chr21	48129895	241454	0.005	0.077
chr22	51304566	299006	0.0058	0.0786
chrMT	16571	32864	1.9832	1.773
chrX	155270560	1121474	0.0072	0.0934
chrY	59373566	61364	0.001	0.0382

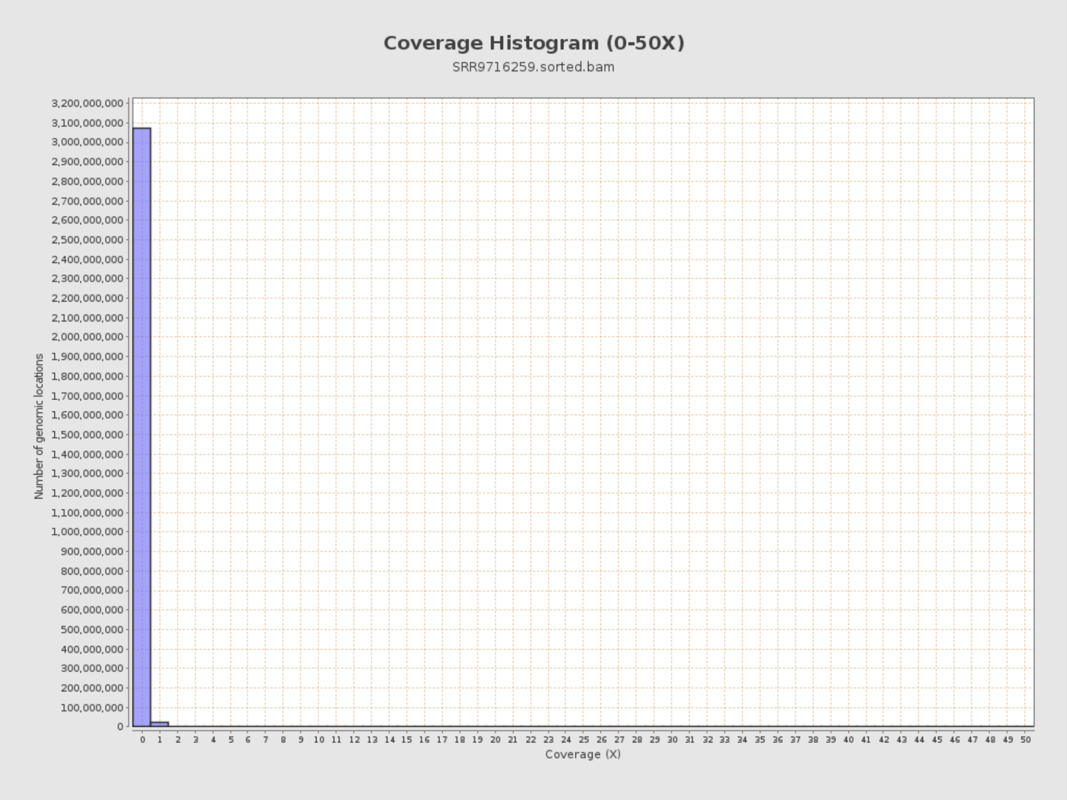
3. Results : Coverage across reference



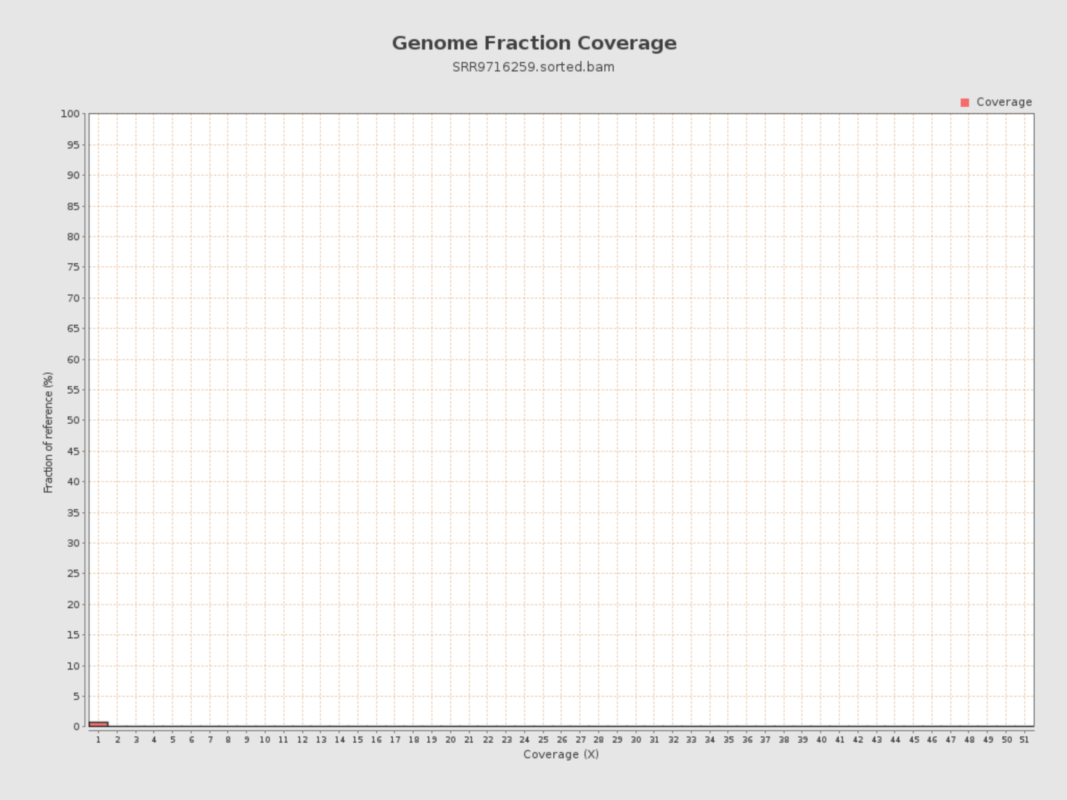
4. Results : Coverage Histogram



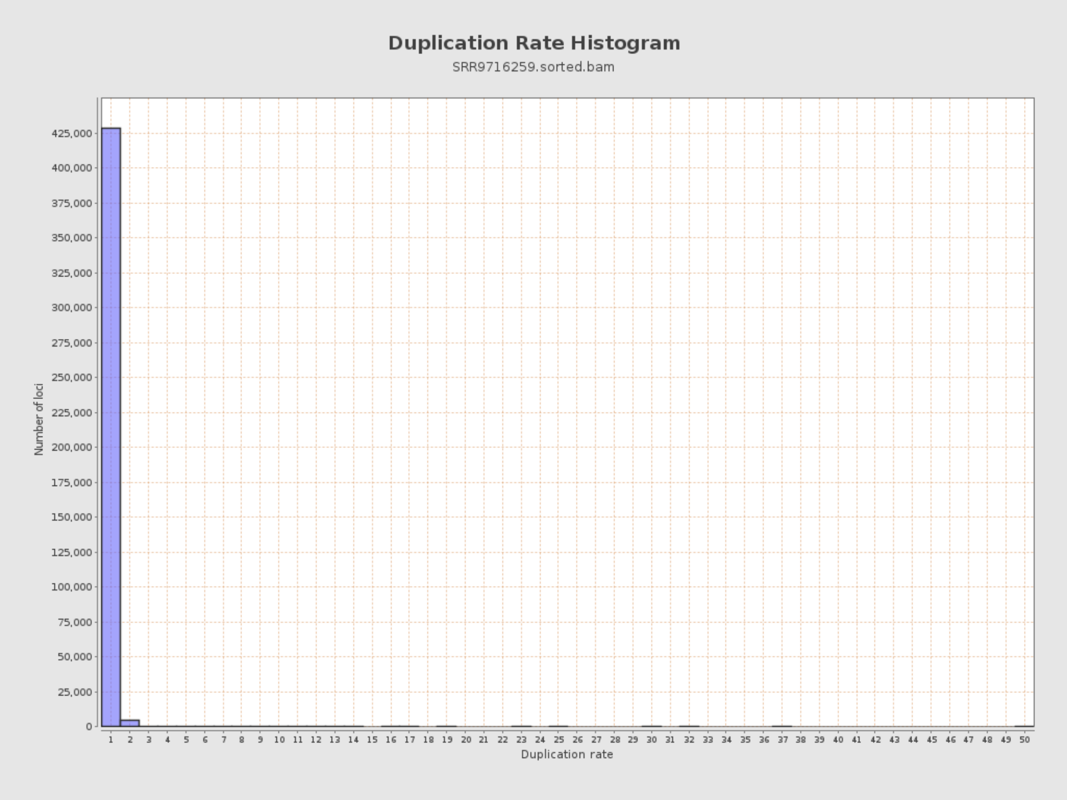
5. Results : Coverage Histogram (0-50X)



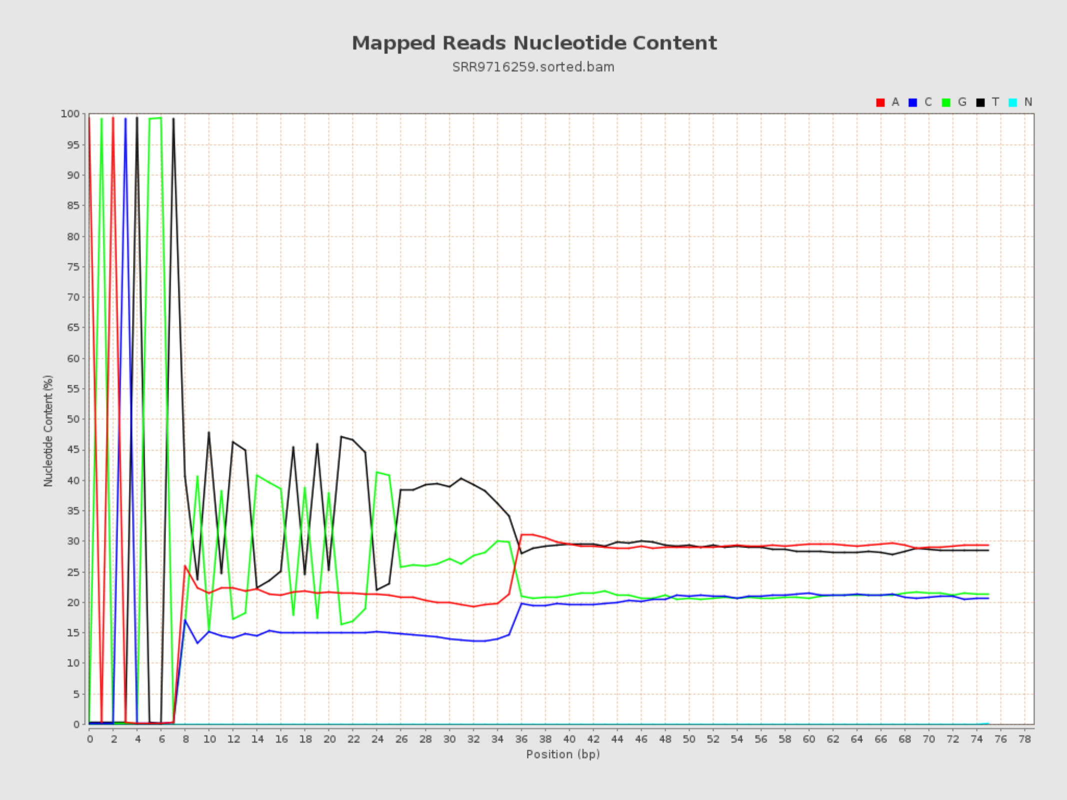
6. Results : Genome Fraction Coverage



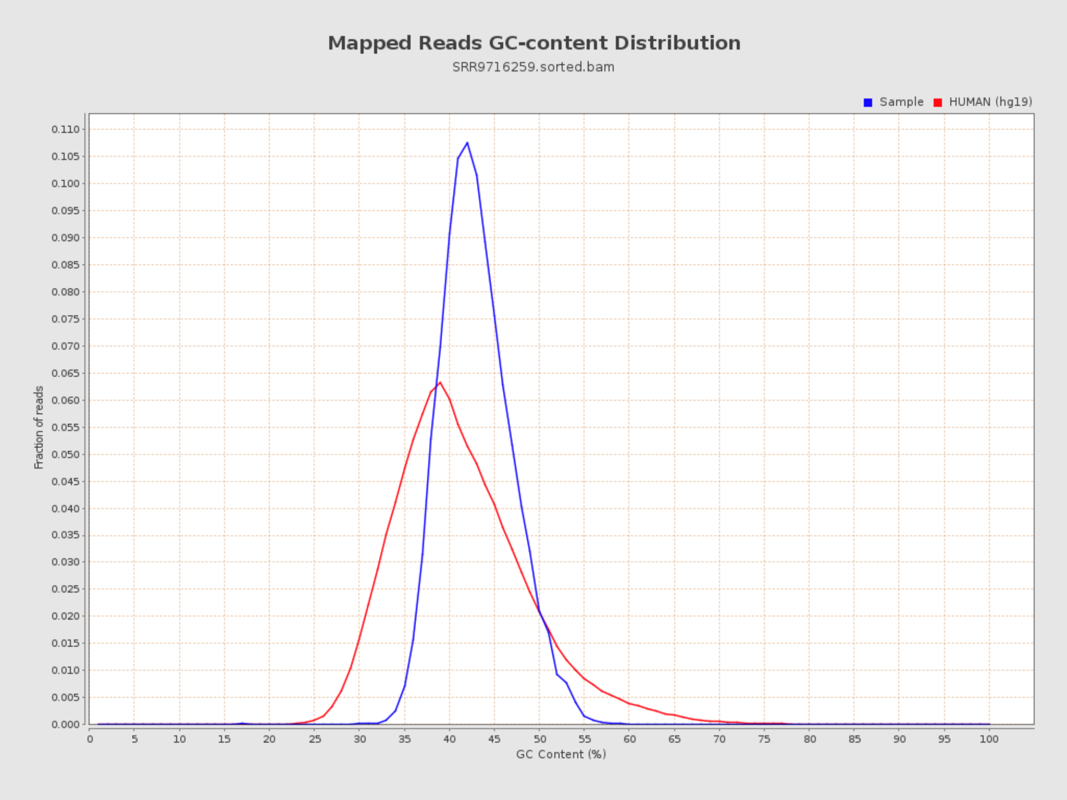
7. Results : Duplication Rate Histogram



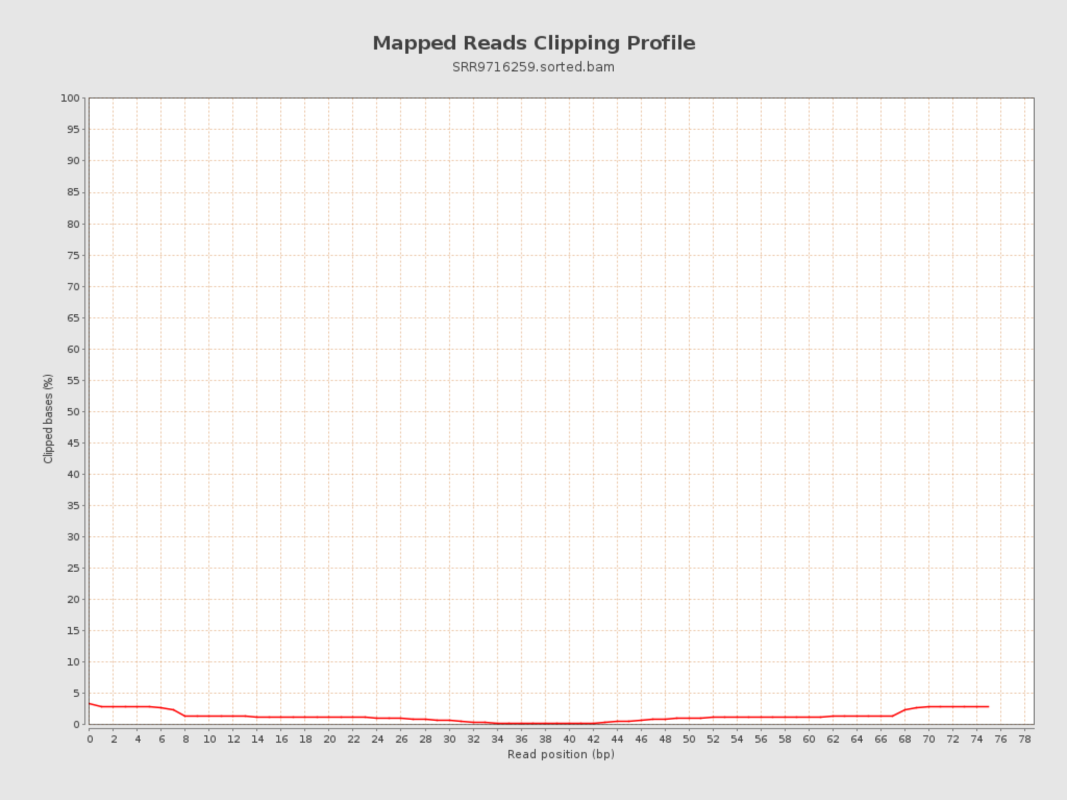
8. Results : Mapped Reads Nucleotide Content



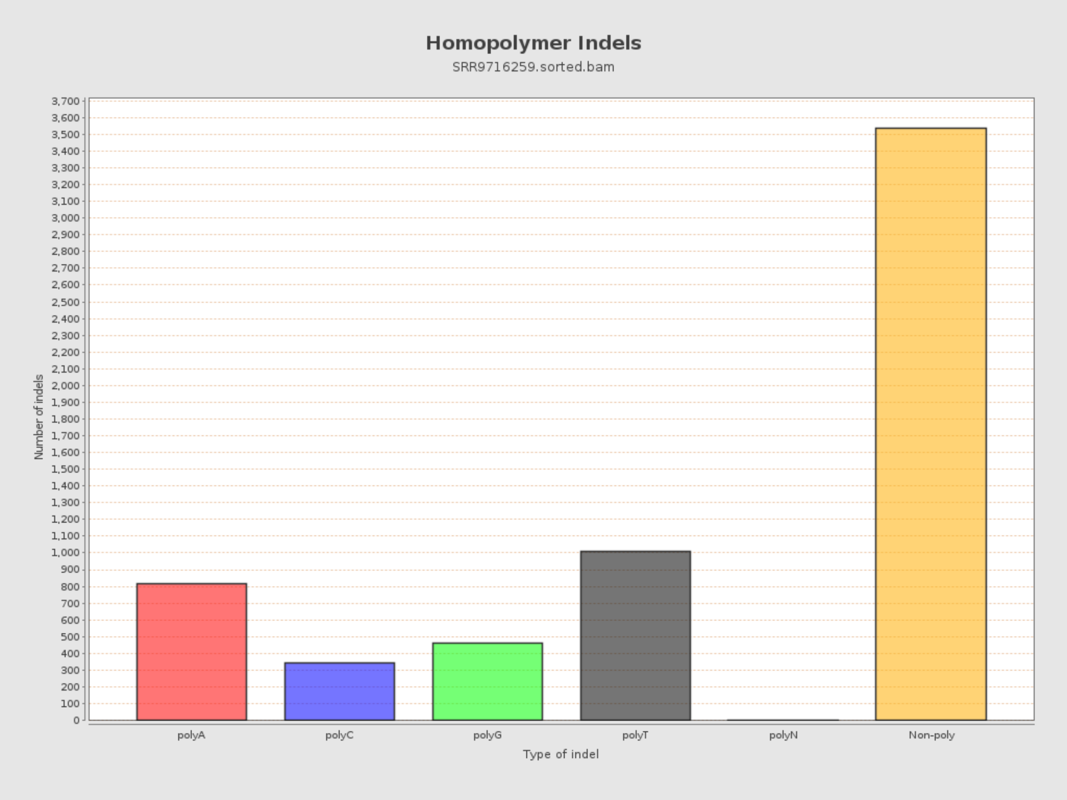
9. Results : Mapped Reads GC-content Distribution



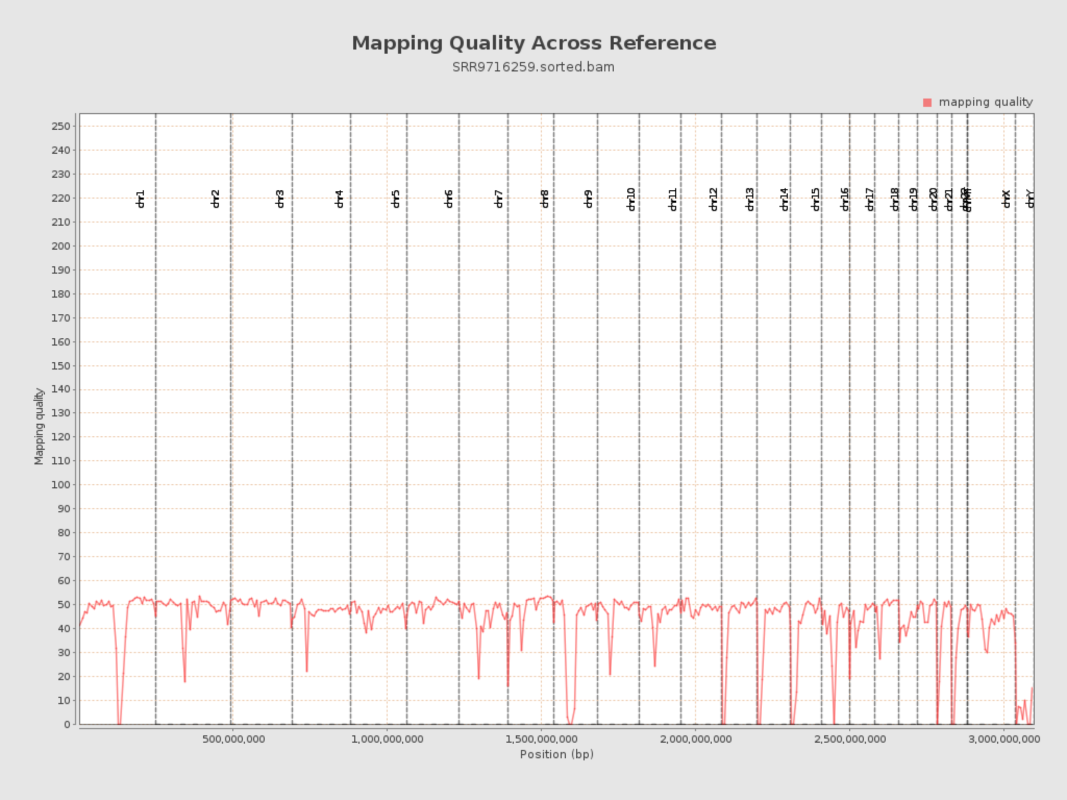
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram