Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 16:16:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716880.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_SRR9716880 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716880.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 16:16:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716880.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	566,950
Mapped reads	523,212 / 92.29%
Unmapped reads	43,738 / 7.71%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,474 / 0.26%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	9,179 / 1.62%
Duplication rate	1.36%
Clipped reads	524,192 / 92.46%

2.2. ACGT Content

Number/percentage of A's	7,608,473 / 25.12%
Number/percentage of C's	6,152,589 / 20.31%
Number/percentage of T's	9,251,733 / 30.54%
Number/percentage of G's	7,280,851 / 24.03%
Number/percentage of N's	376 / 0%
GC Percentage	44.34%

2.3. Coverage

Mean	0.0098

Standard Deviation	0.1172

2.4. Mapping Quality

Mean Mapping Quality	44.2

2.5. Mismatches and indels

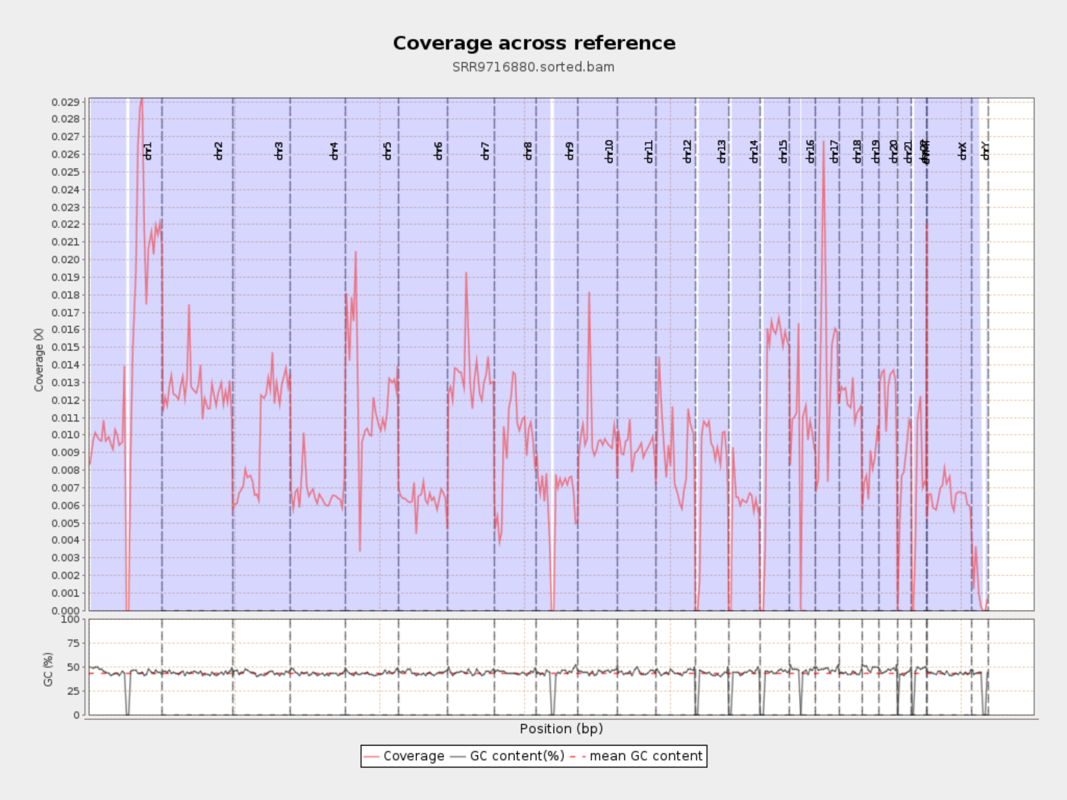
General error rate	0.49%
Mismatches	143,994
Insertions	1,604
Mapped reads with at least one insertion	0.31%
Deletions	5,811
Mapped reads with at least one deletion	1.1%
Homopolymer indels	44.5%

2.6. Chromosome stats

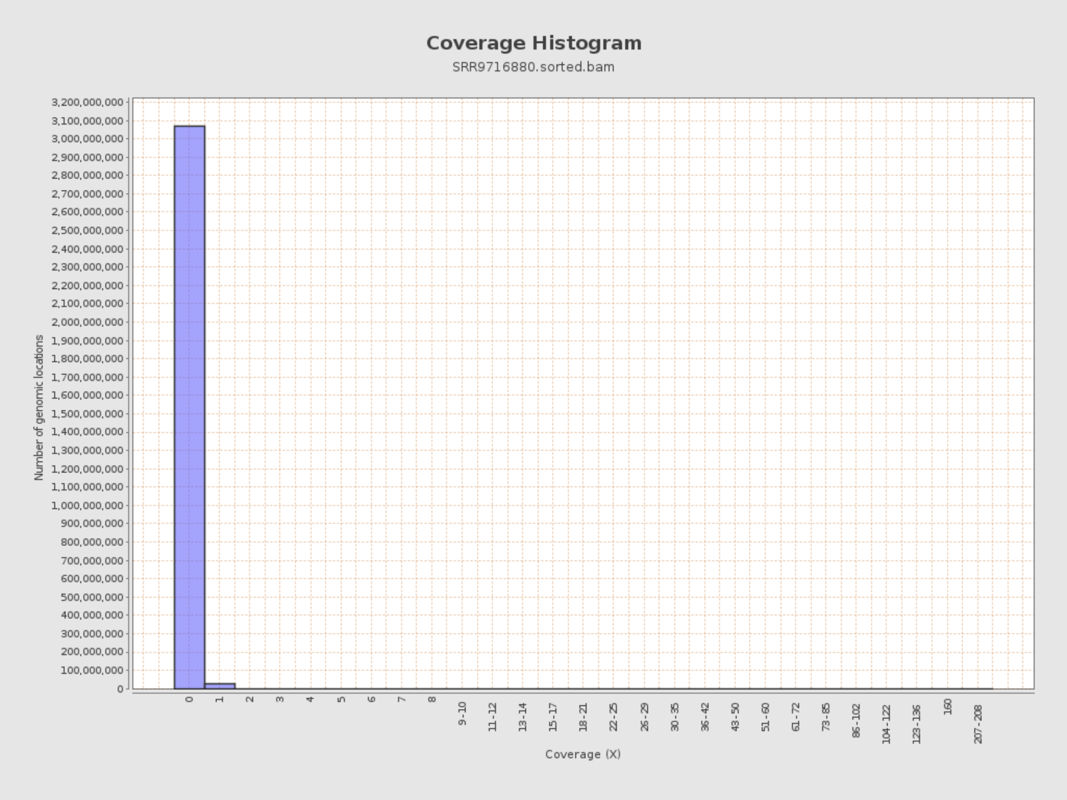
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3555465	0.0143	0.1584
chr2	243199373	3047381	0.0125	0.1486
chr3	198022430	1971642	0.01	0.104
chr4	191154276	1270770	0.0066	0.0856
chr5	180915260	2225058	0.0123	0.1145
chr6	171115067	1090031	0.0064	0.0865
chr7	159138663	2145466	0.0135	0.1657

chr8	146364022	1381352	0.0094	0.1061
chr9	141213431	872682	0.0062	0.0917
chr10	135534747	1364675	0.0101	0.1291
chr11	135006516	1251941	0.0093	0.1127
chr12	133851895	1210356	0.009	0.0986
chr13	115169878	927485	0.0081	0.0925
chr14	107349540	608001	0.0057	0.0799
chr15	102531392	1297788	0.0127	0.1168
chr16	90354753	912301	0.0101	0.1071
chr17	81195210	1160724	0.0143	0.1281
chr18	78077248	936590	0.012	0.1569
chr19	59128983	483843	0.0082	0.1229
chr20	63025520	805448	0.0128	0.1166
chr21	48129895	368347	0.0077	0.0912
chr22	51304566	331239	0.0065	0.0829
chrMT	16571	366	0.0221	0.147
chrX	155270560	1017397	0.0066	0.0901
chrY	59373566	66949	0.0011	0.0407

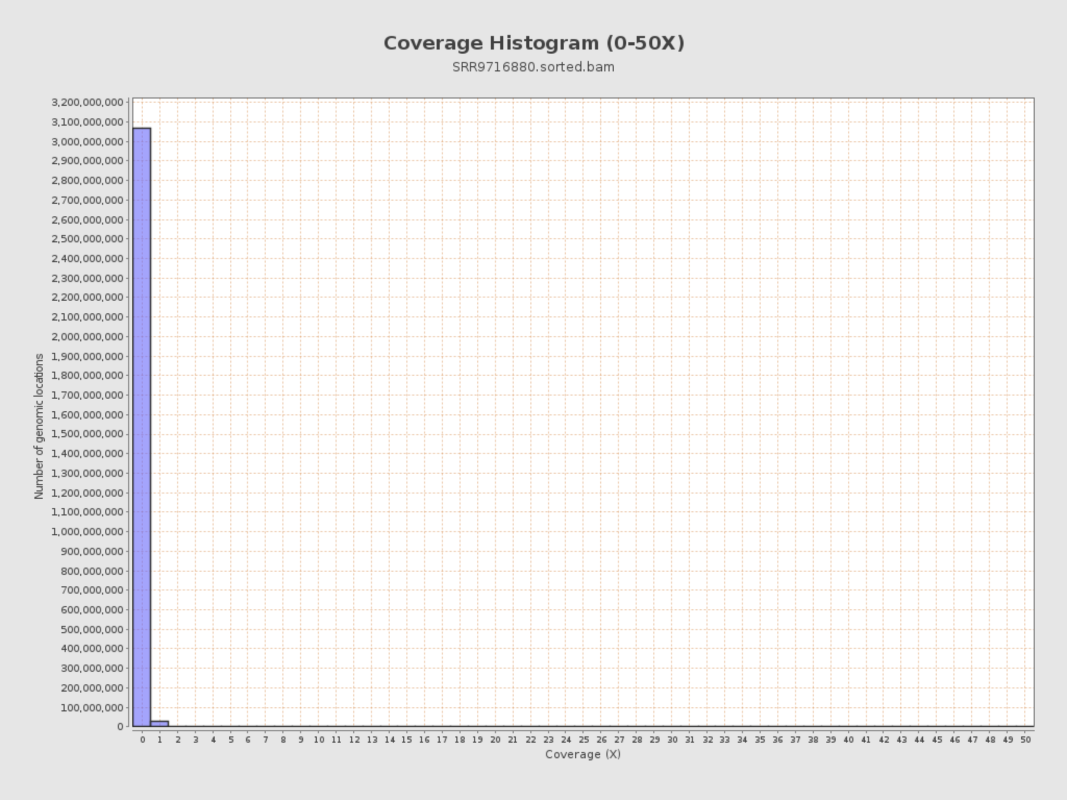
3. Results : Coverage across reference



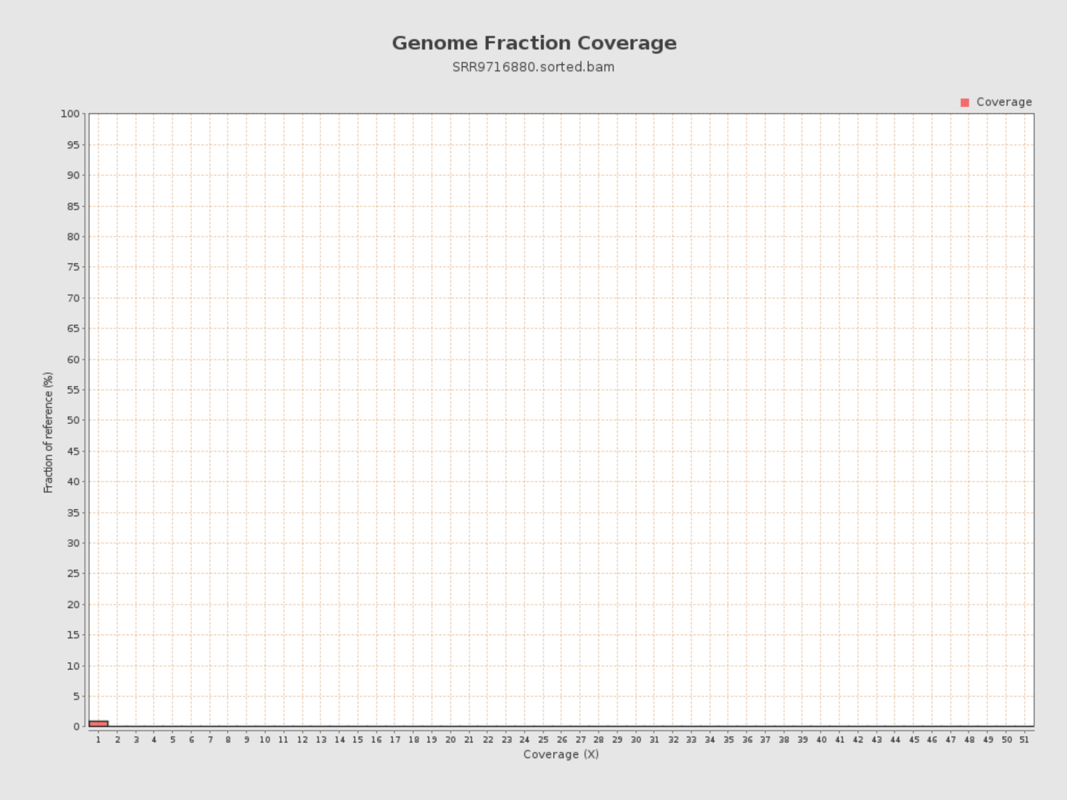
4. Results : Coverage Histogram



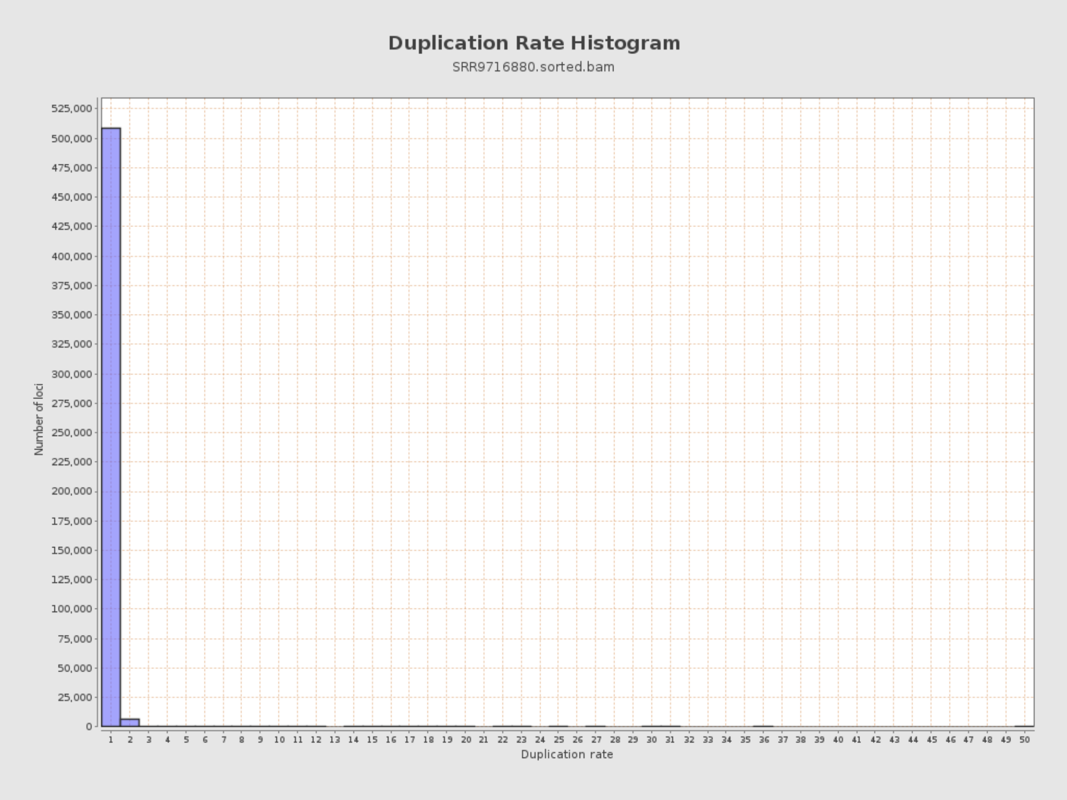
5. Results : Coverage Histogram (0-50X)



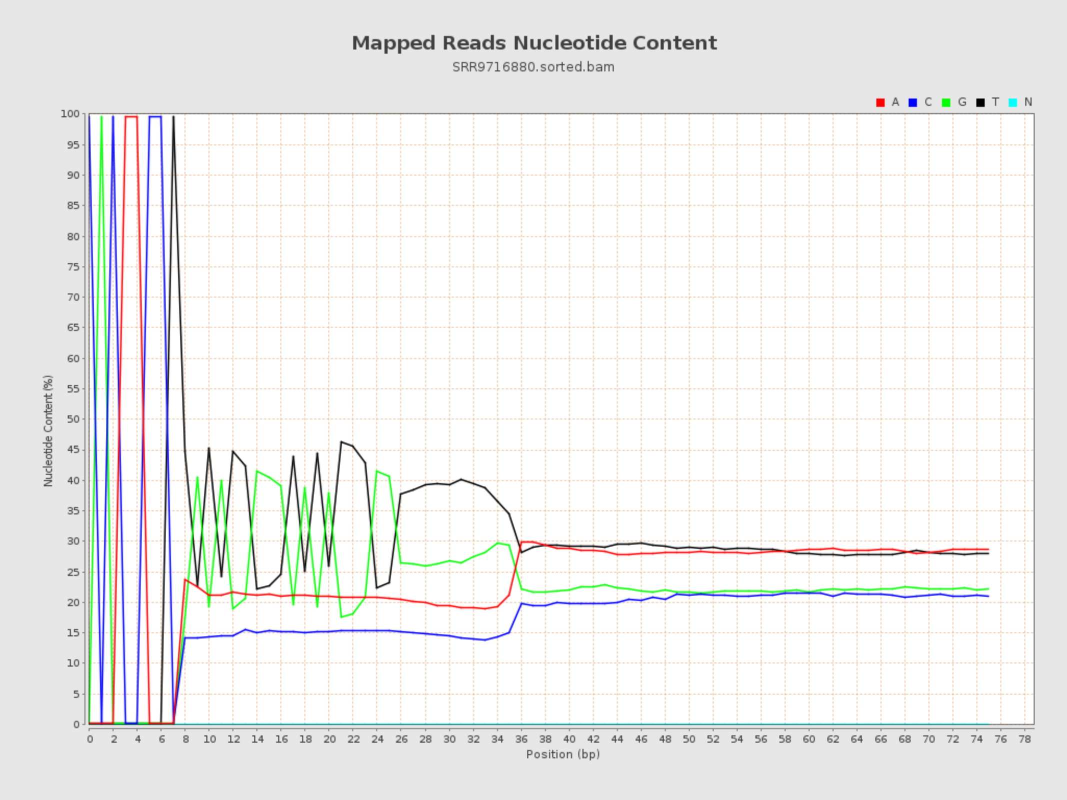
6. Results : Genome Fraction Coverage



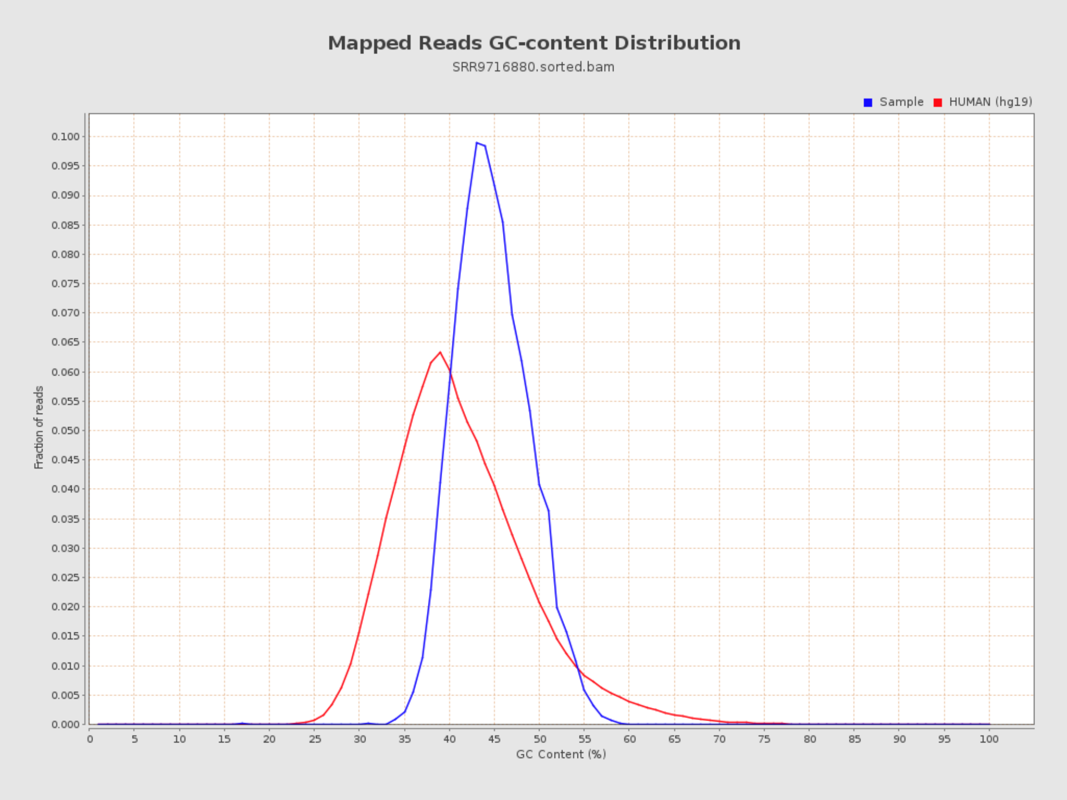
7. Results : Duplication Rate Histogram



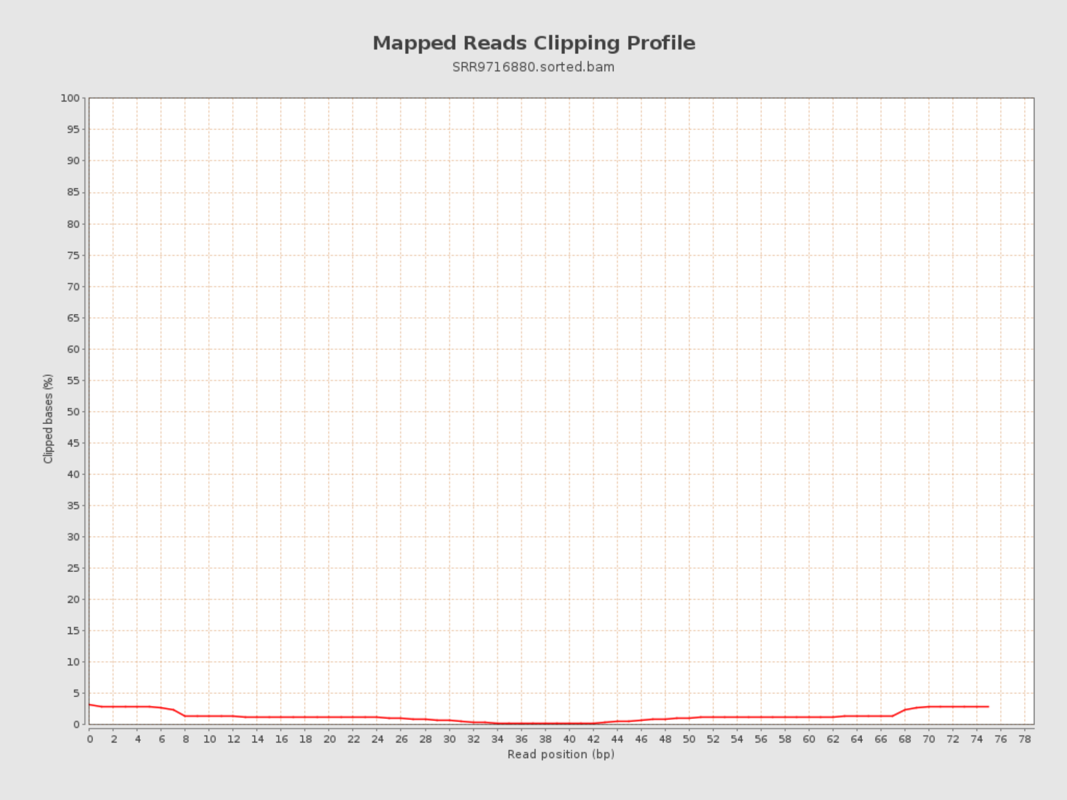
8. Results : Mapped Reads Nucleotide Content



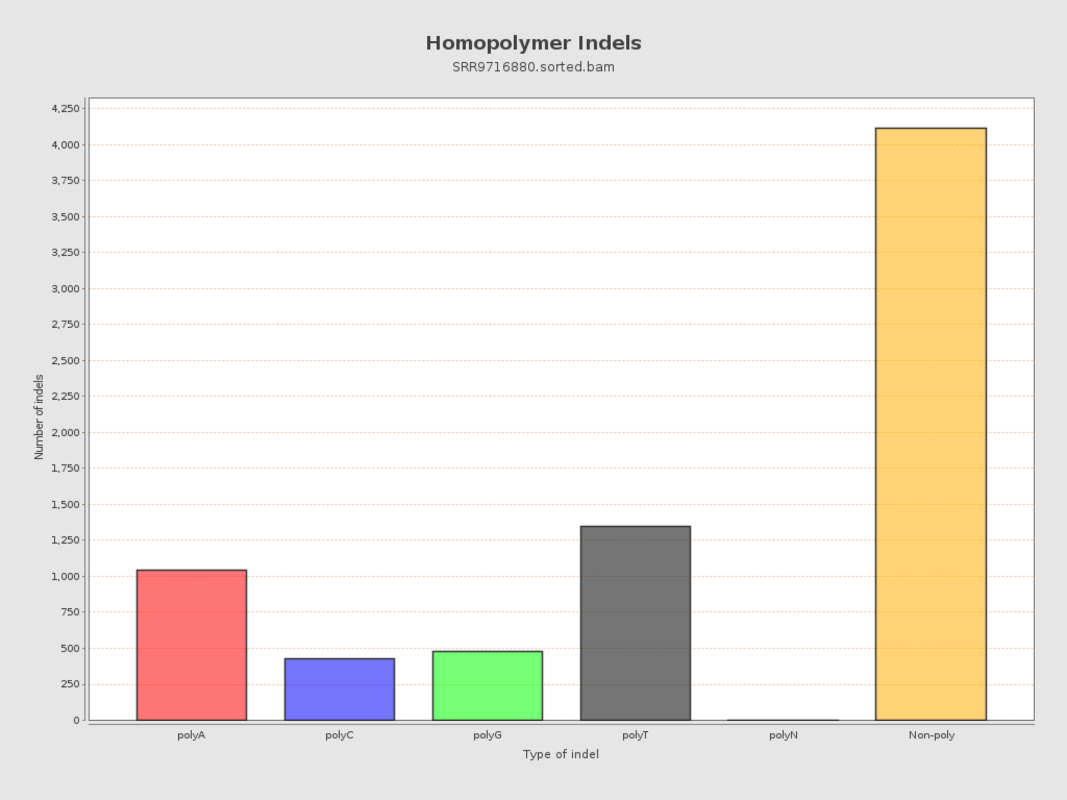
9. Results : Mapped Reads GC-content Distribution



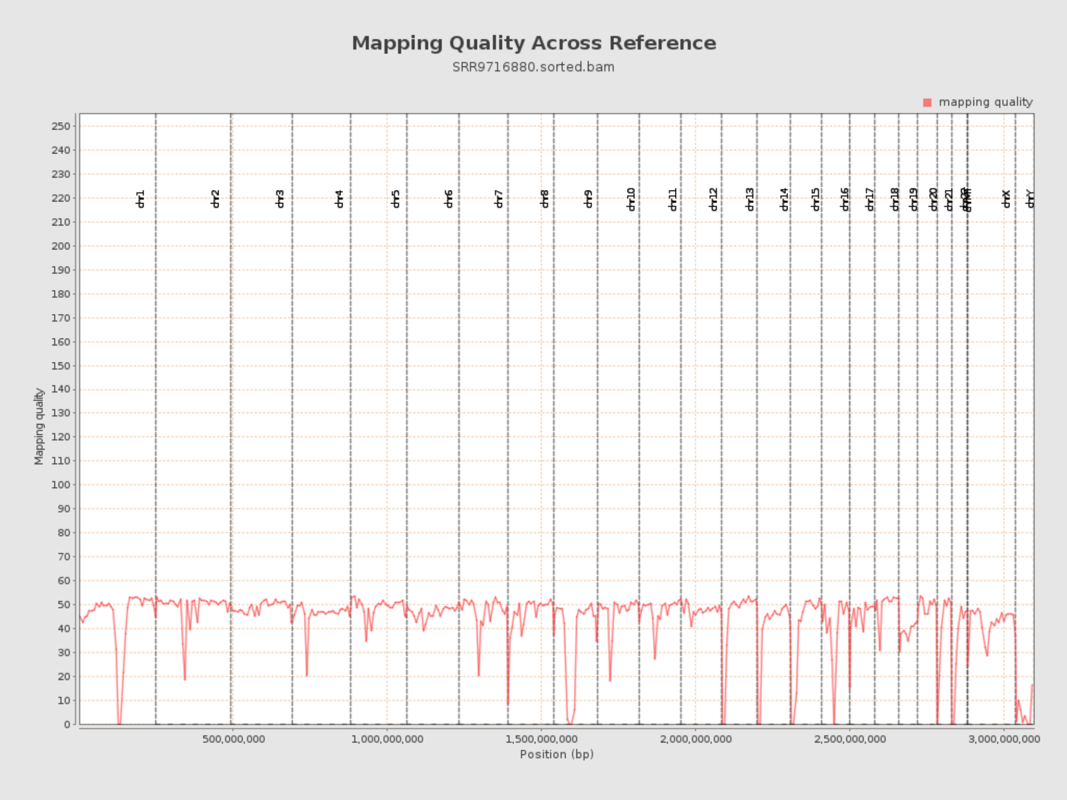
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram