Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 19:23:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716136.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_SRR9716136 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716136.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 19:23:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716136.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,925,821
Mapped reads	1,774,429 / 92.14%
Unmapped reads	151,392 / 7.86%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,316 / 0.54%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	65,367 / 3.39%
Duplication rate	2.6%
Clipped reads	1,779,081 / 92.38%

2.2. ACGT Content

Number/percentage of A's	27,092,202 / 26.24%
Number/percentage of C's	21,514,679 / 20.84%
Number/percentage of T's	30,955,607 / 29.98%
Number/percentage of G's	23,687,684 / 22.94%
Number/percentage of N's	1,333 / 0%
GC Percentage	43.78%

2.3. Coverage

Mean	0.0334

Standard Deviation	0.3221

2.4. Mapping Quality

Mean Mapping Quality	44.22

2.5. Mismatches and indels

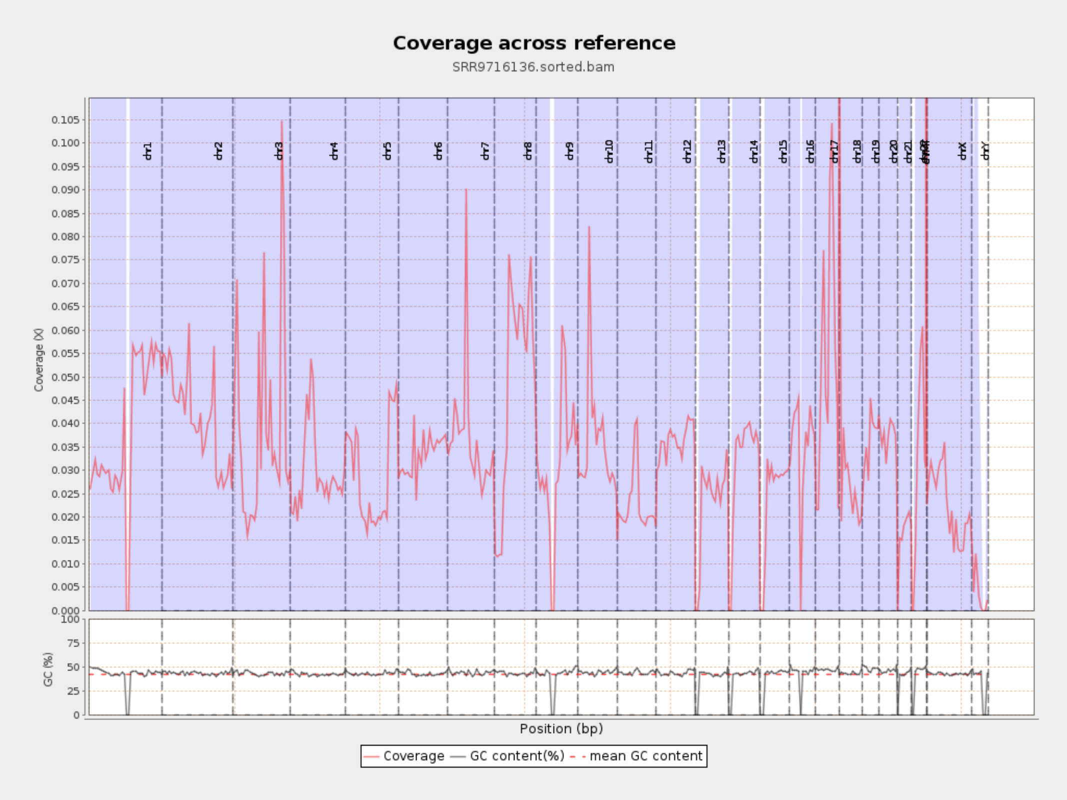
General error rate	0.52%
Mismatches	516,543
Insertions	7,726
Mapped reads with at least one insertion	0.43%
Deletions	19,385
Mapped reads with at least one deletion	1.08%
Homopolymer indels	40.77%

2.6. Chromosome stats

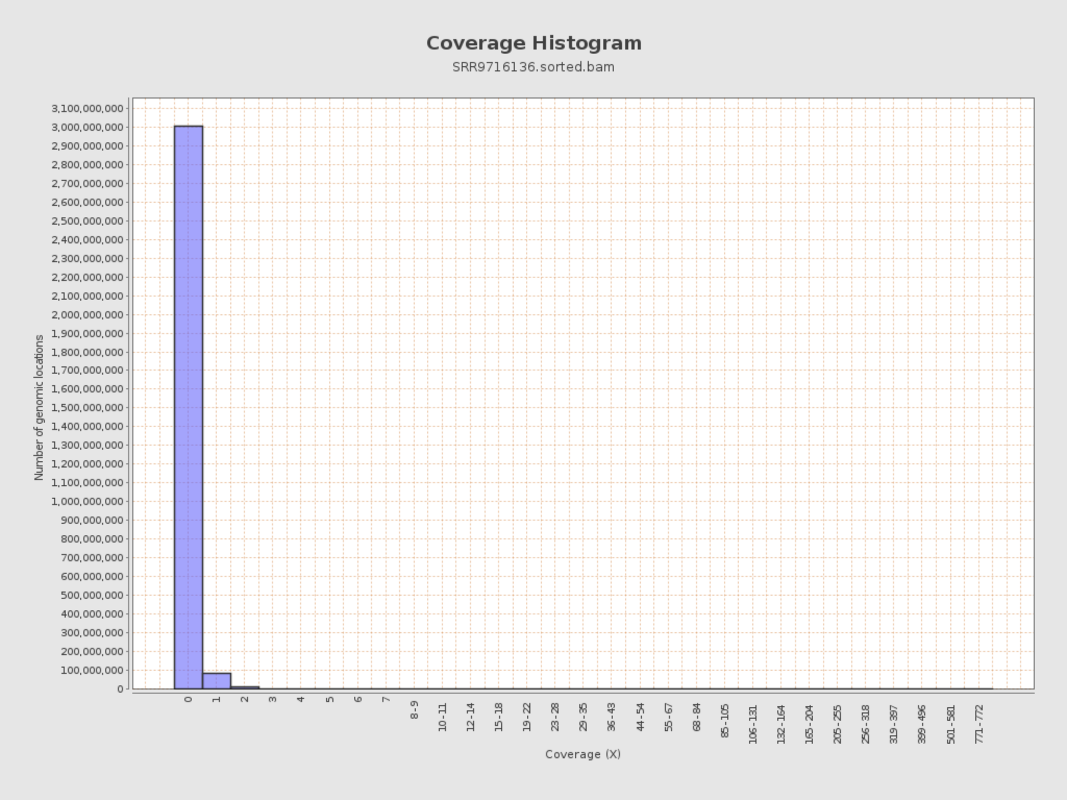
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9475388	0.038	0.4618
chr2	243199373	10131574	0.0417	0.3965
chr3	198022430	7751717	0.0391	0.2324
chr4	191154276	5658716	0.0296	0.2053
chr5	180915260	5237820	0.029	0.1875
chr6	171115067	5717036	0.0334	0.2184
chr7	159138663	5877196	0.0369	0.7278

chr8	146364022	7206333	0.0492	0.3358
chr9	141213431	4311049	0.0305	0.2268
chr10	135534747	4868627	0.0359	0.4034
chr11	135006516	3051684	0.0226	0.2088
chr12	133851895	4856597	0.0363	0.2318
chr13	115169878	2643142	0.0229	0.1661
chr14	107349540	3358848	0.0313	0.198
chr15	102531392	2457368	0.024	0.1765
chr16	90354753	3185862	0.0353	0.2161
chr17	81195210	4416311	0.0544	0.2686
chr18	78077248	2371402	0.0304	0.3478
chr19	59128983	2147068	0.0363	0.4139
chr20	63025520	2340016	0.0371	0.2211
chr21	48129895	785352	0.0163	0.1513
chr22	51304566	1581689	0.0308	0.1931
chrMT	16571	59581	3.5955	2.8872
chrX	155270560	3562519	0.0229	0.192
chrY	59373566	229271	0.0039	0.1011

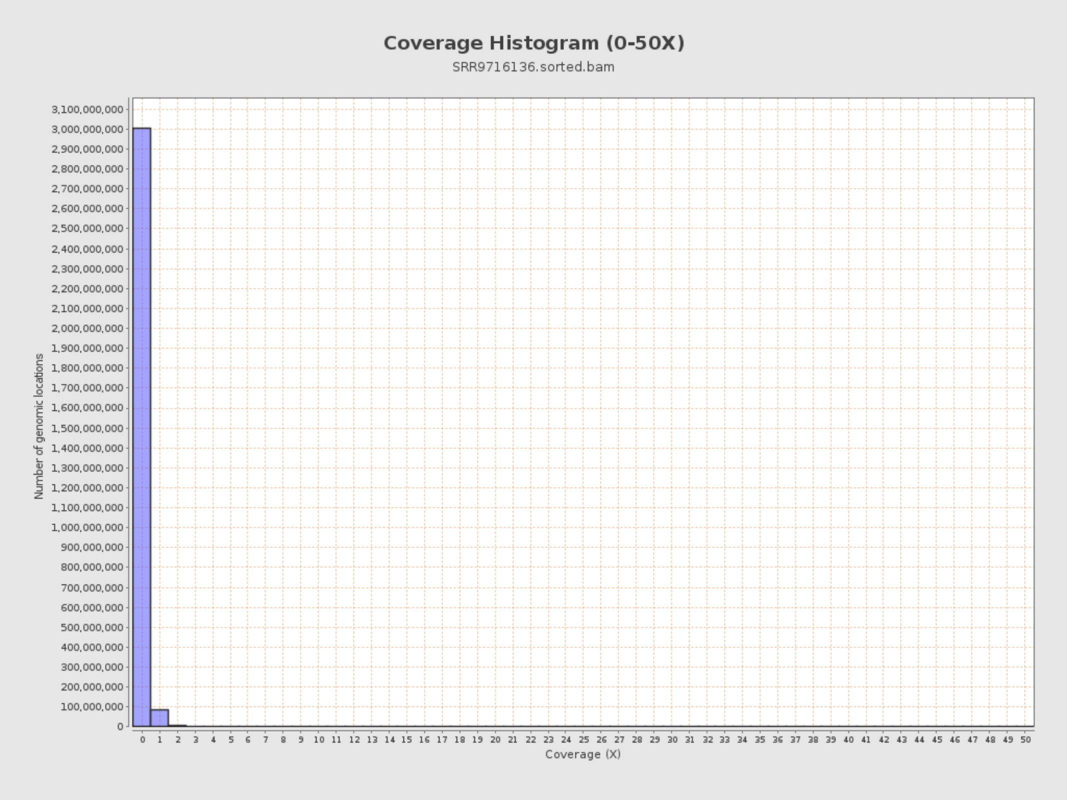
3. Results : Coverage across reference



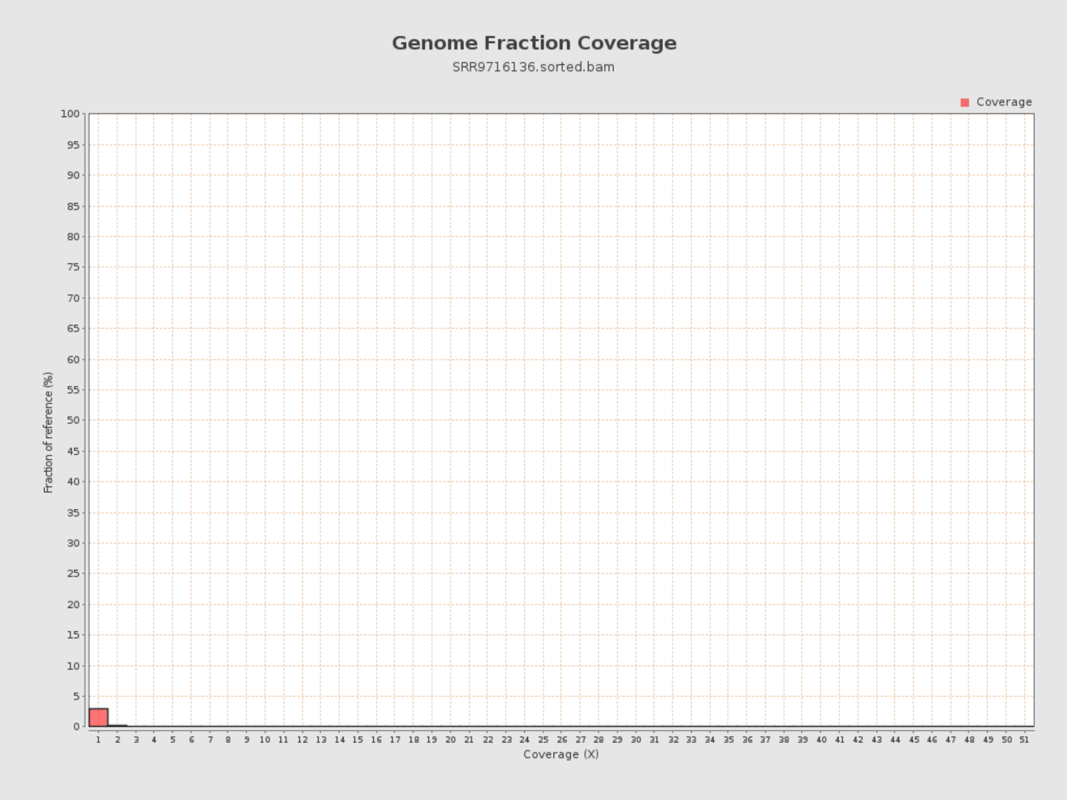
4. Results : Coverage Histogram



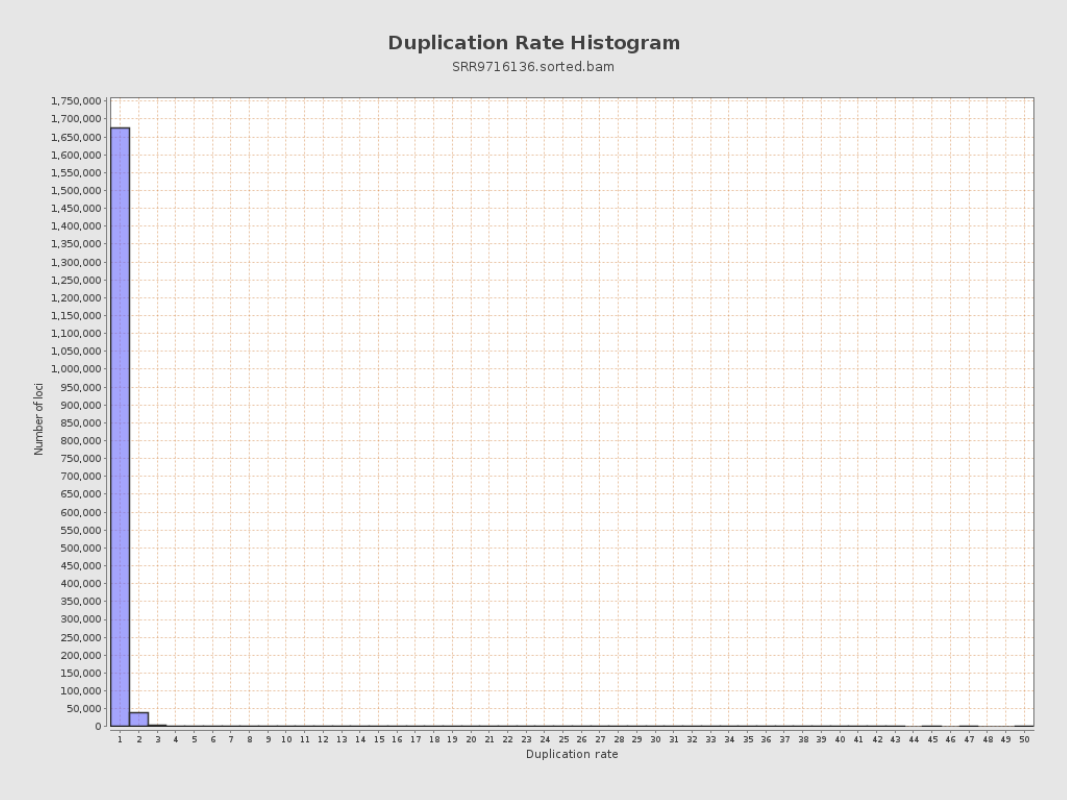
5. Results : Coverage Histogram (0-50X)



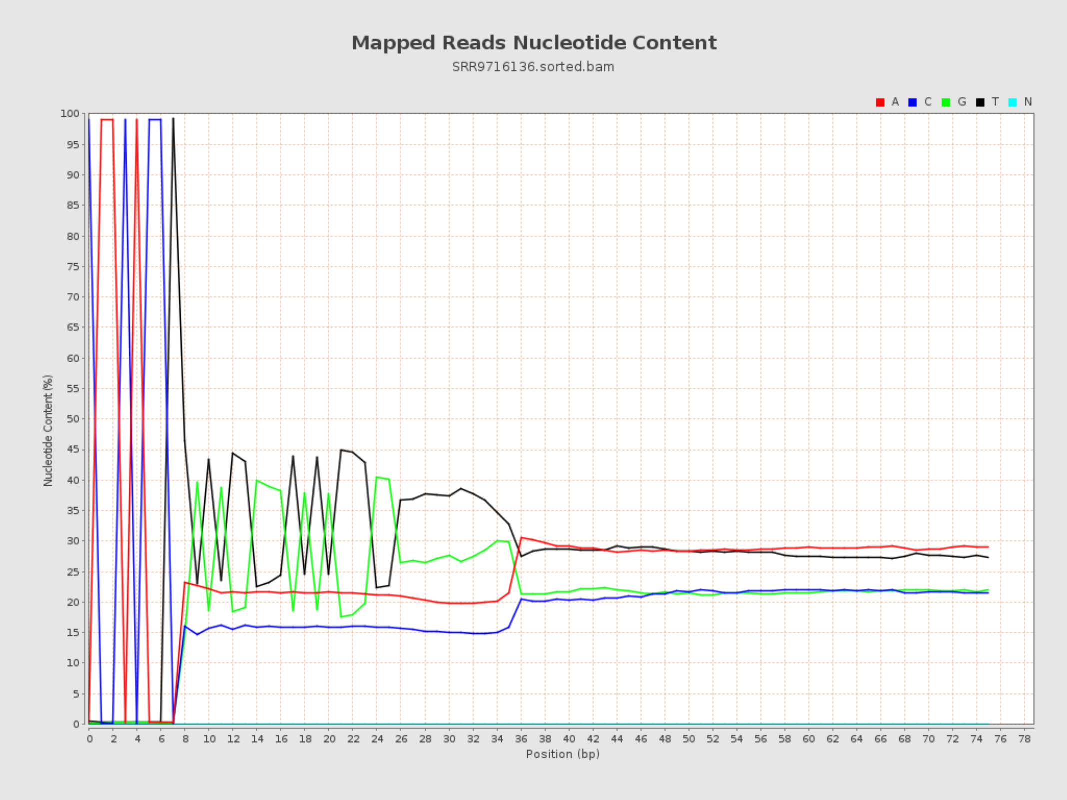
6. Results : Genome Fraction Coverage



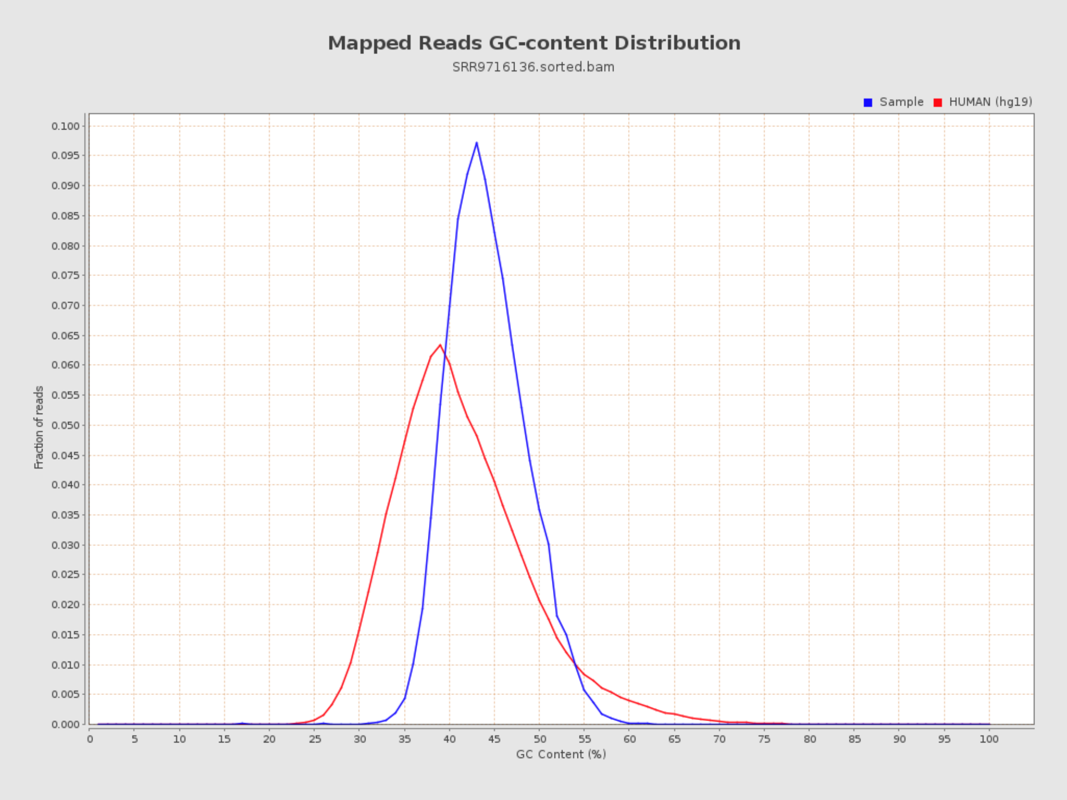
7. Results : Duplication Rate Histogram



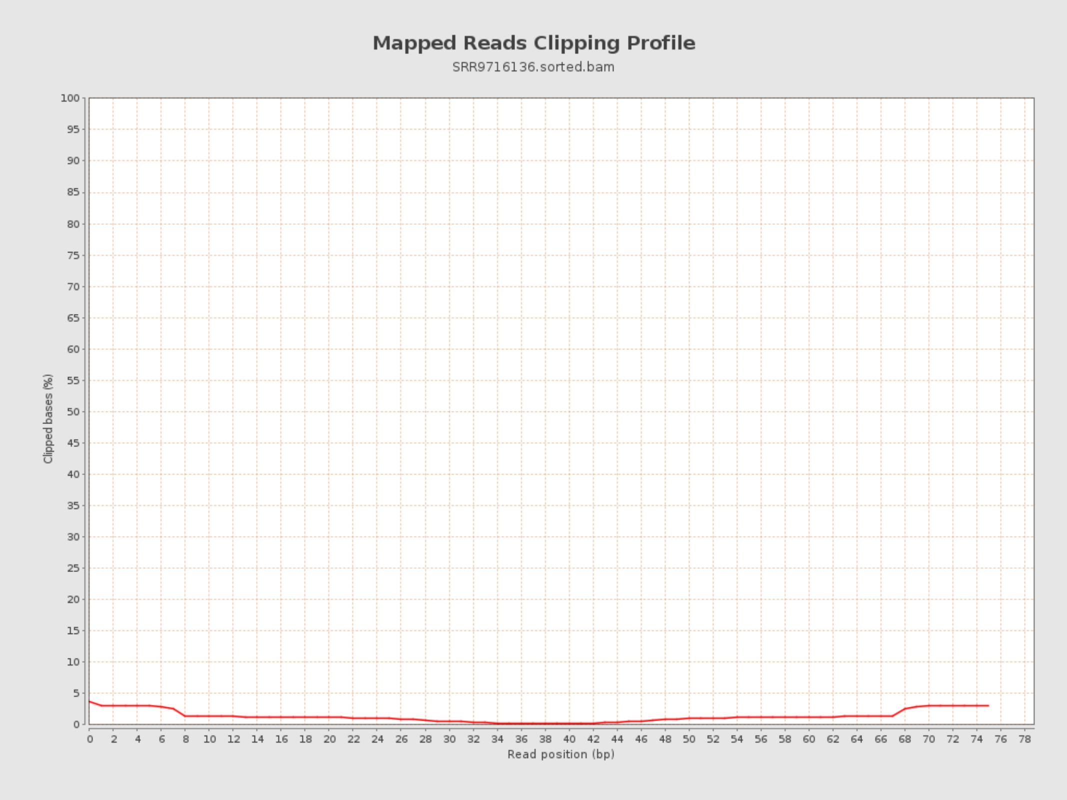
8. Results : Mapped Reads Nucleotide Content



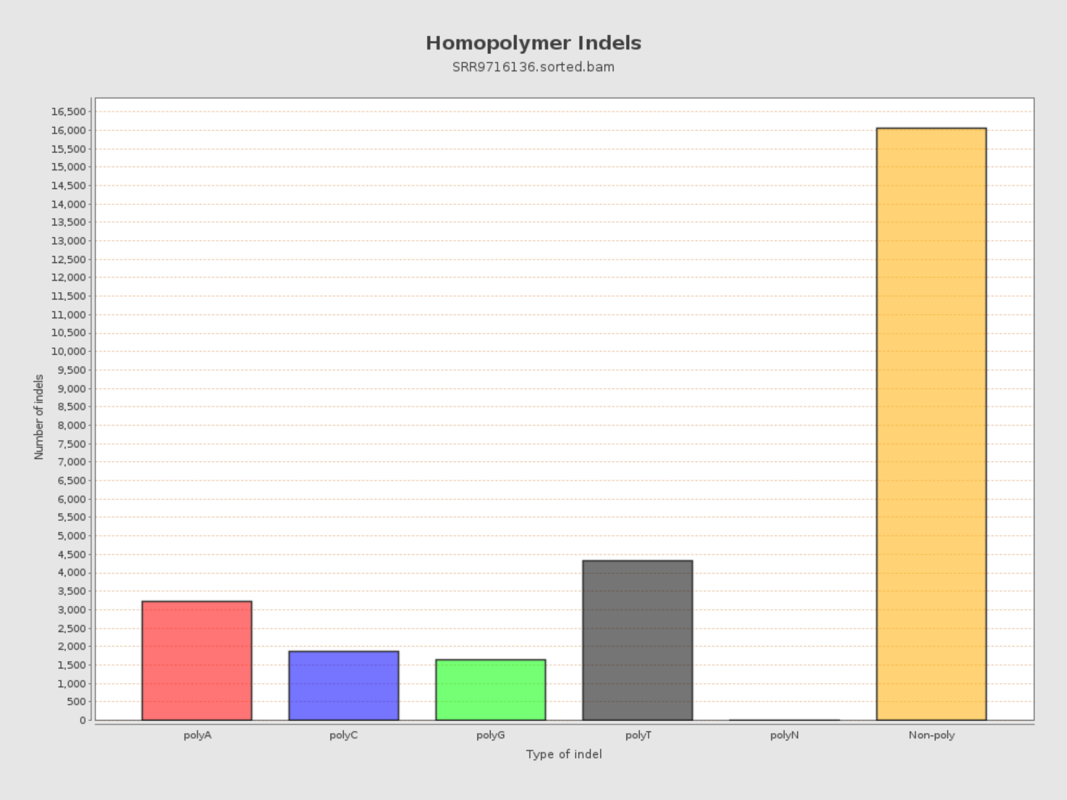
9. Results : Mapped Reads GC-content Distribution



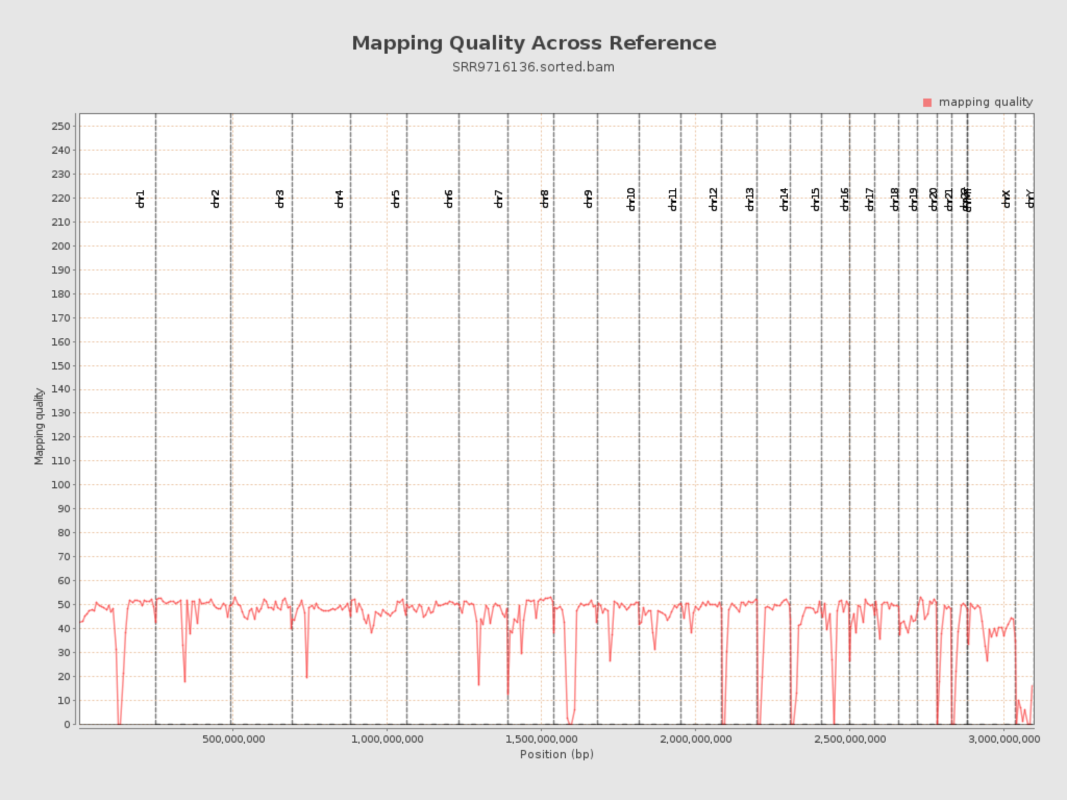
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram