Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 20:42:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716967.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_SRR9716967 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716967.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 20:42:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716967.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,781,075
Mapped reads	1,345,363 / 75.54%
Unmapped reads	435,712 / 24.46%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,625 / 0.26%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	32,990 / 1.85%
Duplication rate	1.77%
Clipped reads	1,347,029 / 75.63%

2.2. ACGT Content

Number/percentage of A's	17,368,110 / 23.99%
Number/percentage of C's	15,083,366 / 20.83%
Number/percentage of T's	20,799,147 / 28.73%
Number/percentage of G's	19,151,281 / 26.45%
Number/percentage of N's	1,888 / 0%
GC Percentage	47.28%

2.3. Coverage

Mean	0.0234

Standard Deviation	0.1957

2.4. Mapping Quality

Mean Mapping Quality	38.16

2.5. Mismatches and indels

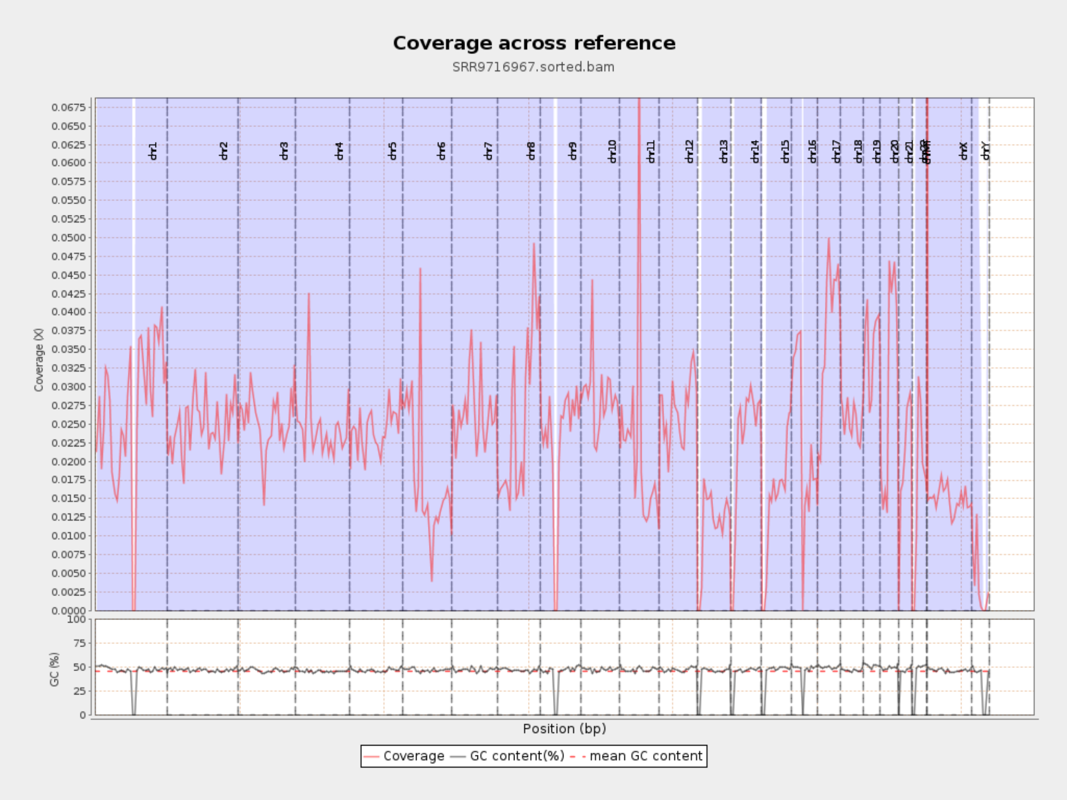
General error rate	0.55%
Mismatches	387,105
Insertions	7,437
Mapped reads with at least one insertion	0.55%
Deletions	12,128
Mapped reads with at least one deletion	0.89%
Homopolymer indels	31%

2.6. Chromosome stats

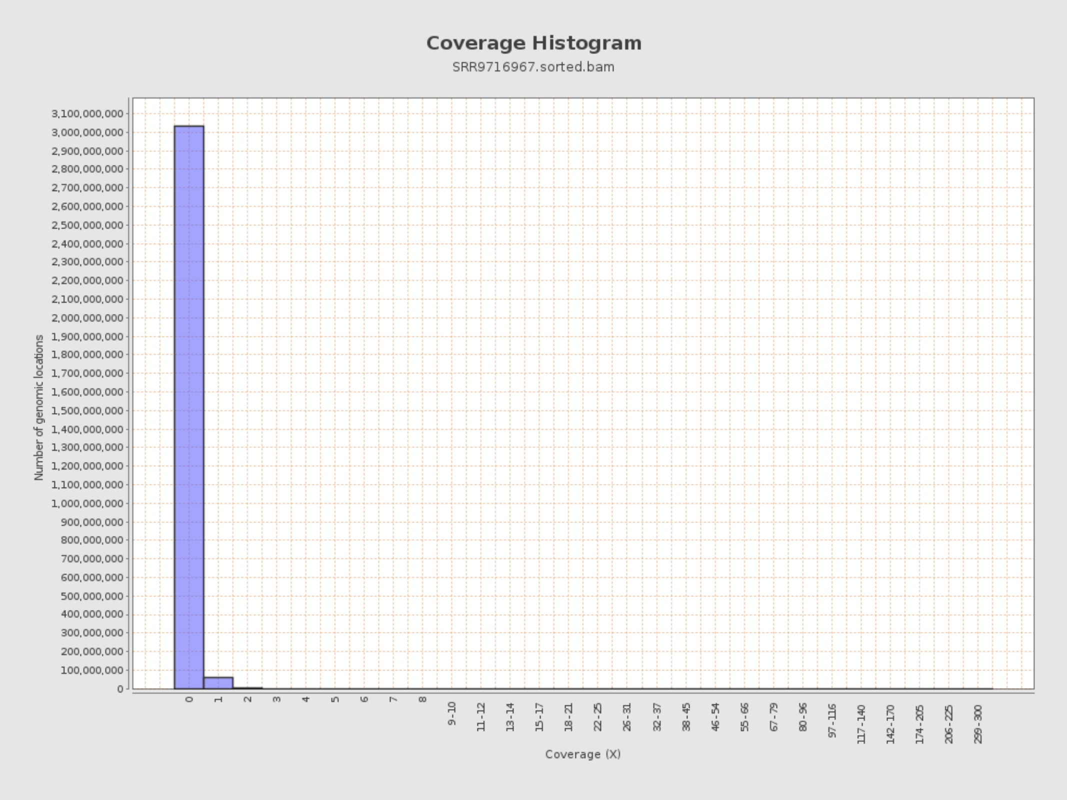
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6643645	0.0267	0.2325
chr2	243199373	6057820	0.0249	0.2376
chr3	198022430	4985350	0.0252	0.1824
chr4	191154276	4722312	0.0247	0.1928
chr5	180915260	4431472	0.0245	0.172
chr6	171115067	3066811	0.0179	0.1541
chr7	159138663	4259494	0.0268	0.2281

chr8	146364022	3776935	0.0258	0.1888
chr9	141213431	3194066	0.0226	0.1795
chr10	135534747	3904031	0.0288	0.2476
chr11	135006516	3041270	0.0225	0.2083
chr12	133851895	3608122	0.027	0.1823
chr13	115169878	1308505	0.0114	0.119
chr14	107349540	2369368	0.0221	0.1699
chr15	102531392	1501164	0.0146	0.1392
chr16	90354753	2037890	0.0226	0.1796
chr17	81195210	3056935	0.0376	0.2292
chr18	78077248	1978980	0.0253	0.2249
chr19	59128983	2091759	0.0354	0.2447
chr20	63025520	1908071	0.0303	0.198
chr21	48129895	993649	0.0206	0.1724
chr22	51304566	857988	0.0167	0.1444
chrMT	16571	99546	6.0072	5.3534
chrX	155270560	2318762	0.0149	0.1482
chrY	59373566	209537	0.0035	0.1027

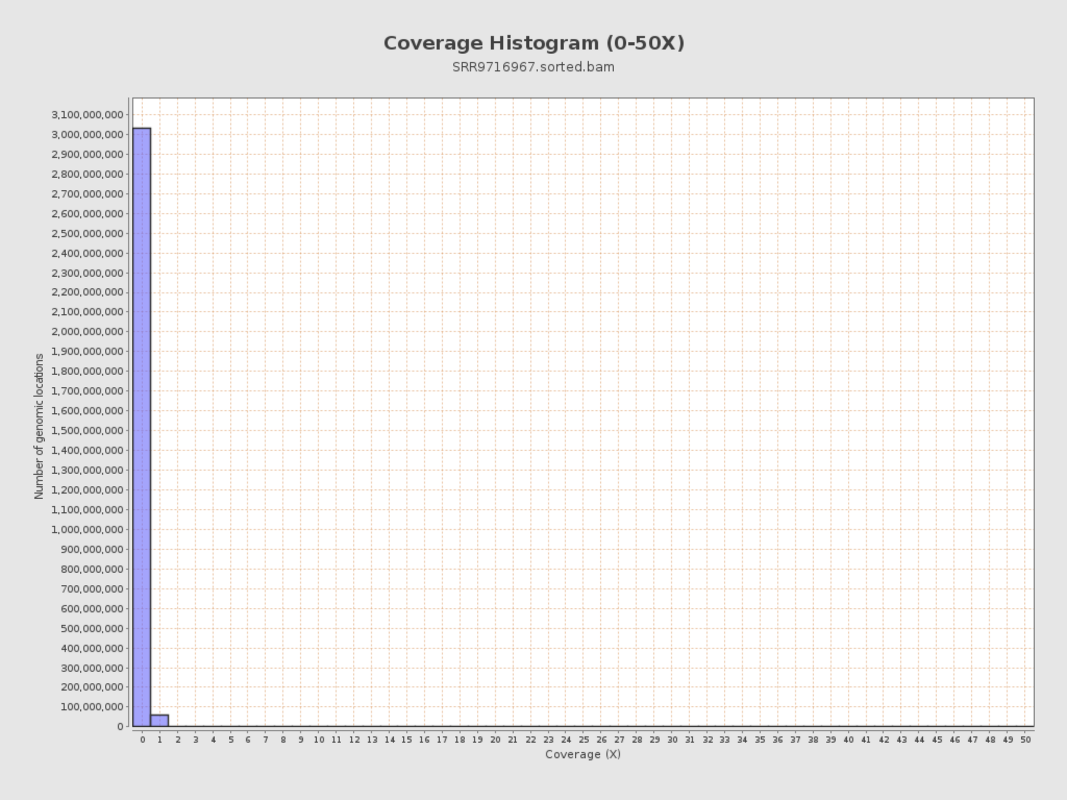
3. Results : Coverage across reference



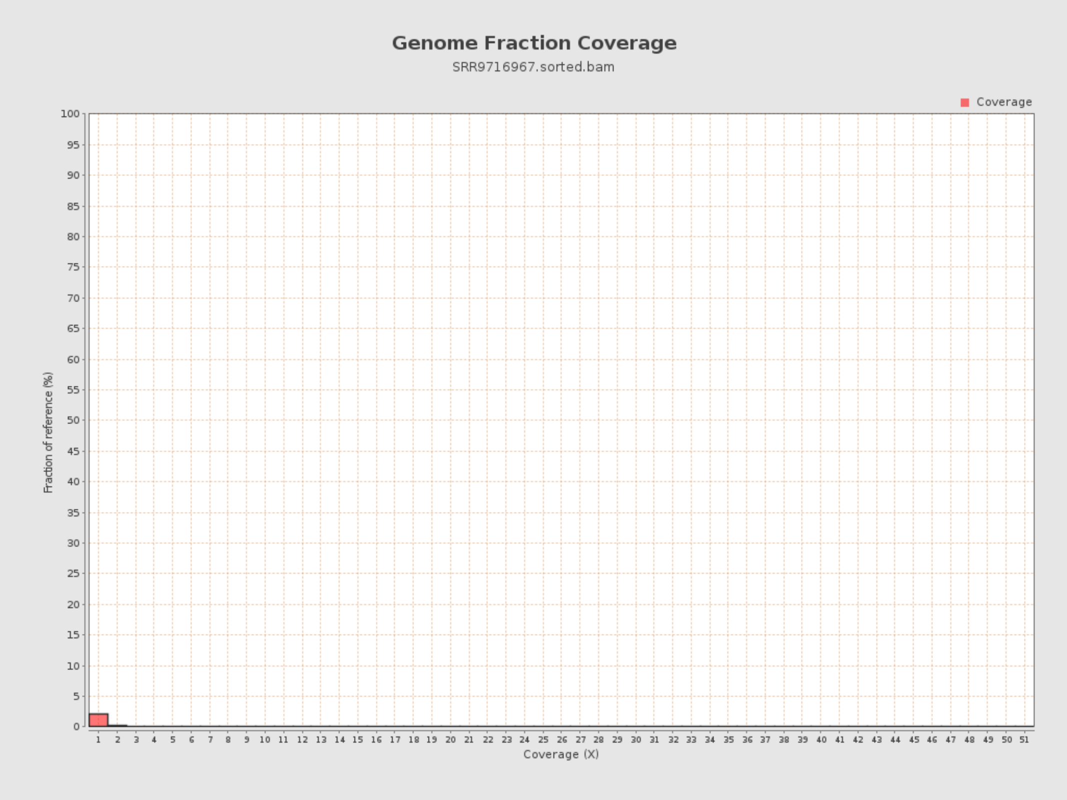
4. Results : Coverage Histogram



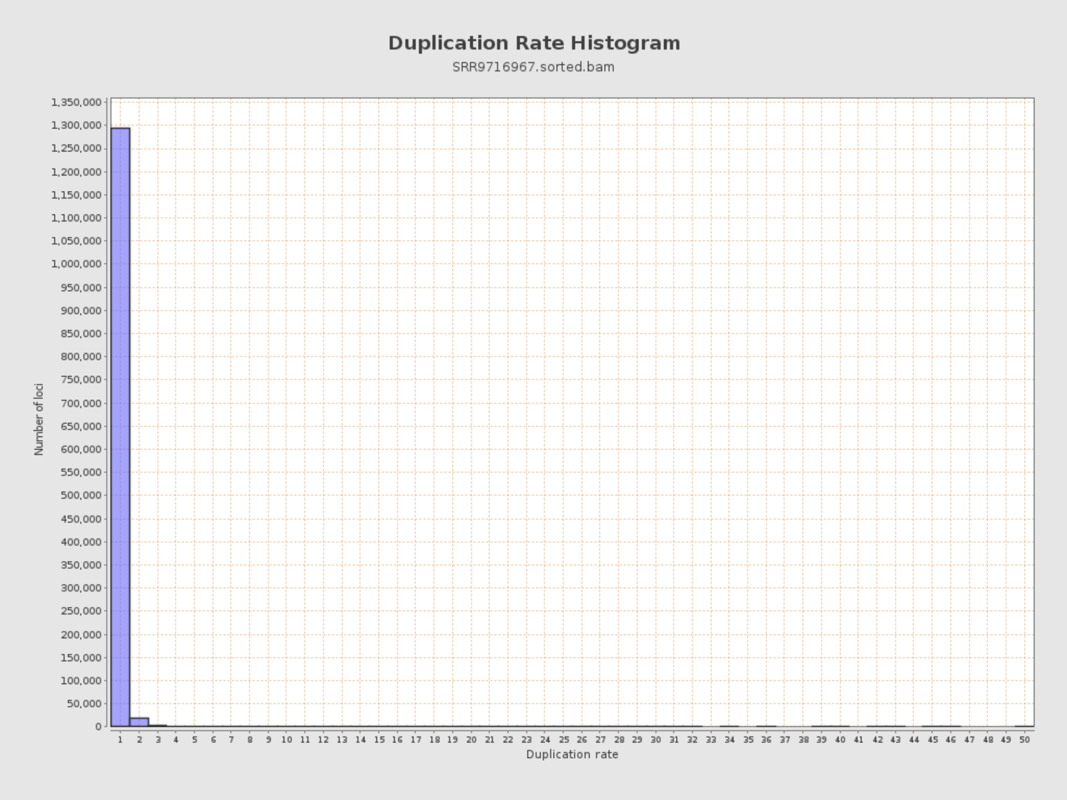
5. Results : Coverage Histogram (0-50X)



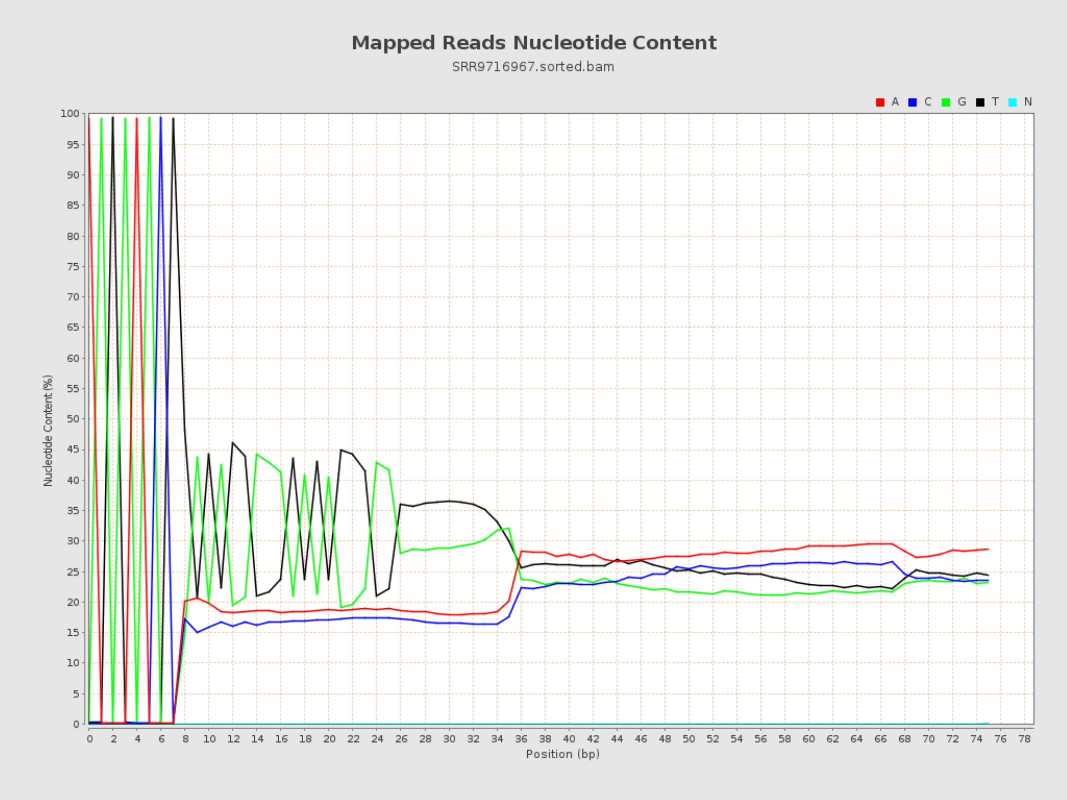
6. Results : Genome Fraction Coverage



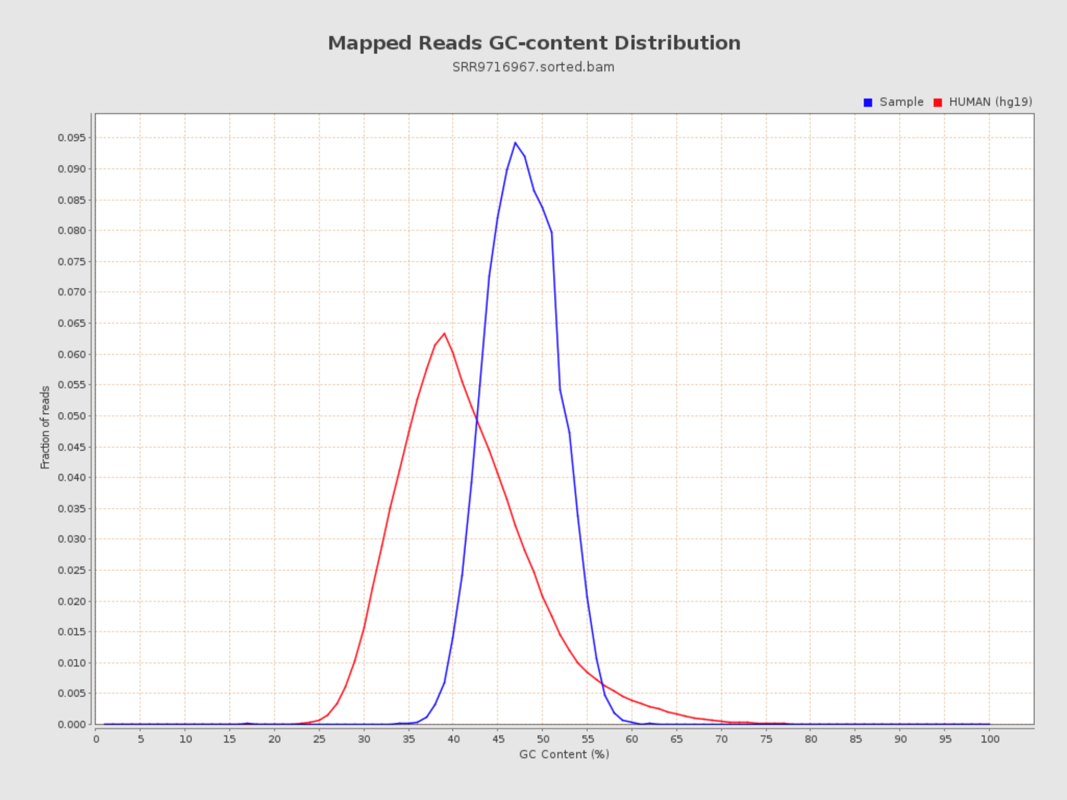
7. Results : Duplication Rate Histogram



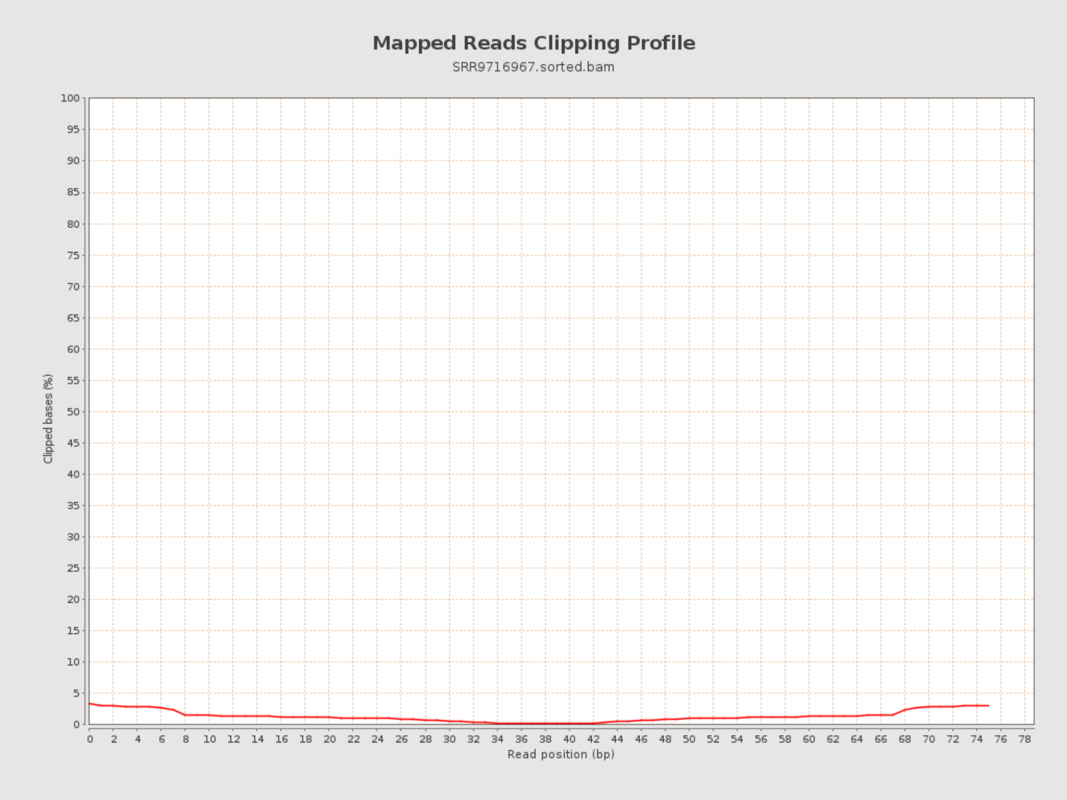
8. Results : Mapped Reads Nucleotide Content



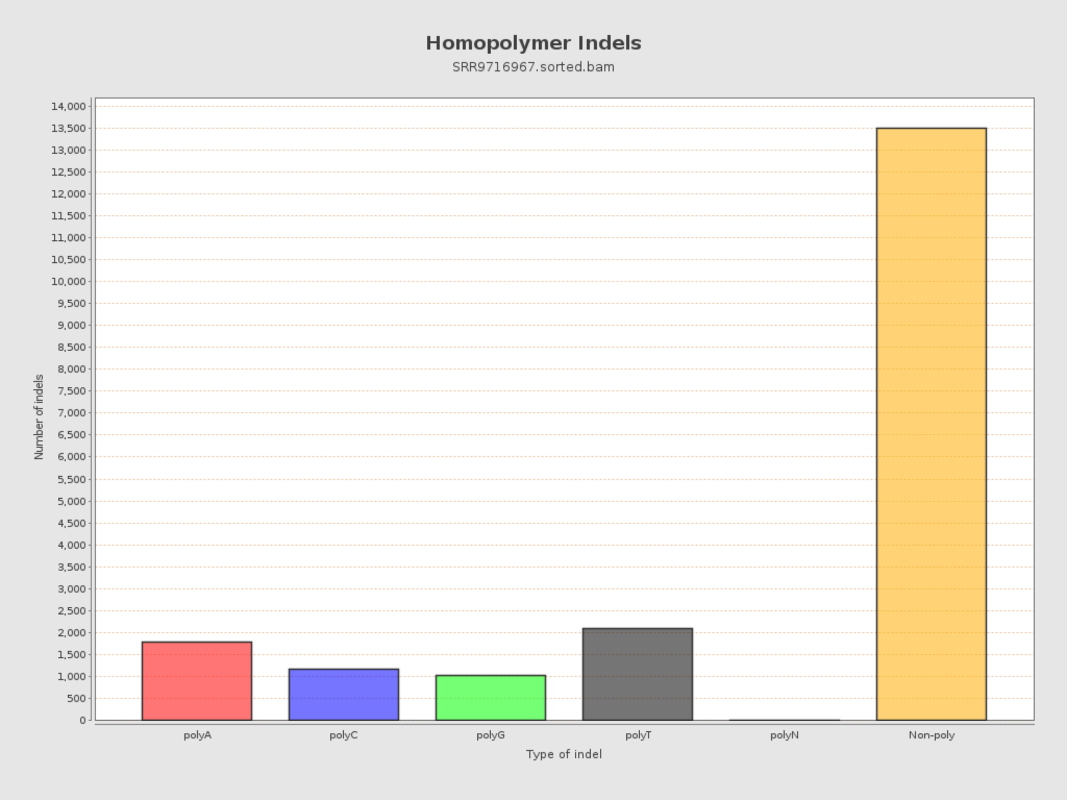
9. Results : Mapped Reads GC-content Distribution



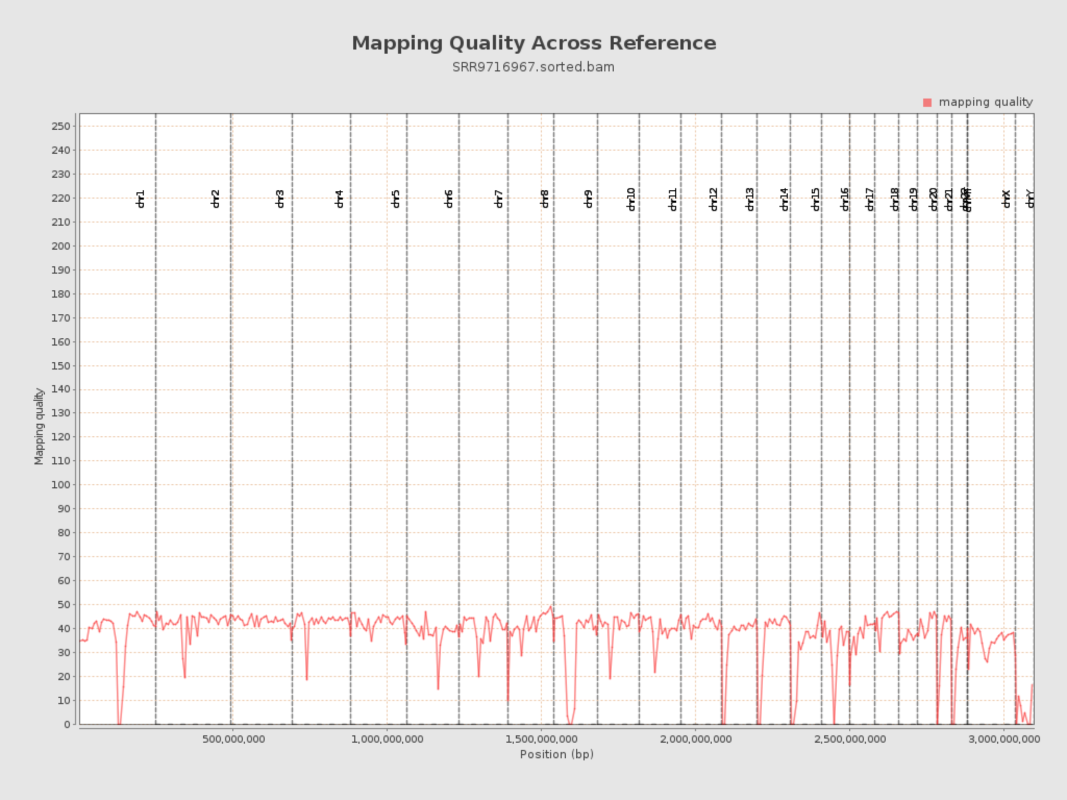
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram