Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 06:36:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716307.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_SRR9716307 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716307.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 06:36:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716307.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,911,015
Mapped reads	1,783,506 / 93.33%
Unmapped reads	127,509 / 6.67%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	32,784 / 1.72%
Read min/max/mean length	30 / 101 / 101.62
Duplicated reads (estimated)	77,541 / 4.06%
Duplication rate	3.15%
Clipped reads	1,812,102 / 94.82%

2.2. ACGT Content

Number/percentage of A's	35,318,471 / 24.95%
Number/percentage of C's	26,753,272 / 18.9%
Number/percentage of T's	44,357,624 / 31.34%
Number/percentage of G's	35,094,522 / 24.8%
Number/percentage of N's	10,164 / 0.01%
GC Percentage	43.7%

2.3. Coverage

Mean	0.0457

Standard Deviation	0.4141

2.4. Mapping Quality

Mean Mapping Quality	47.59

2.5. Mismatches and indels

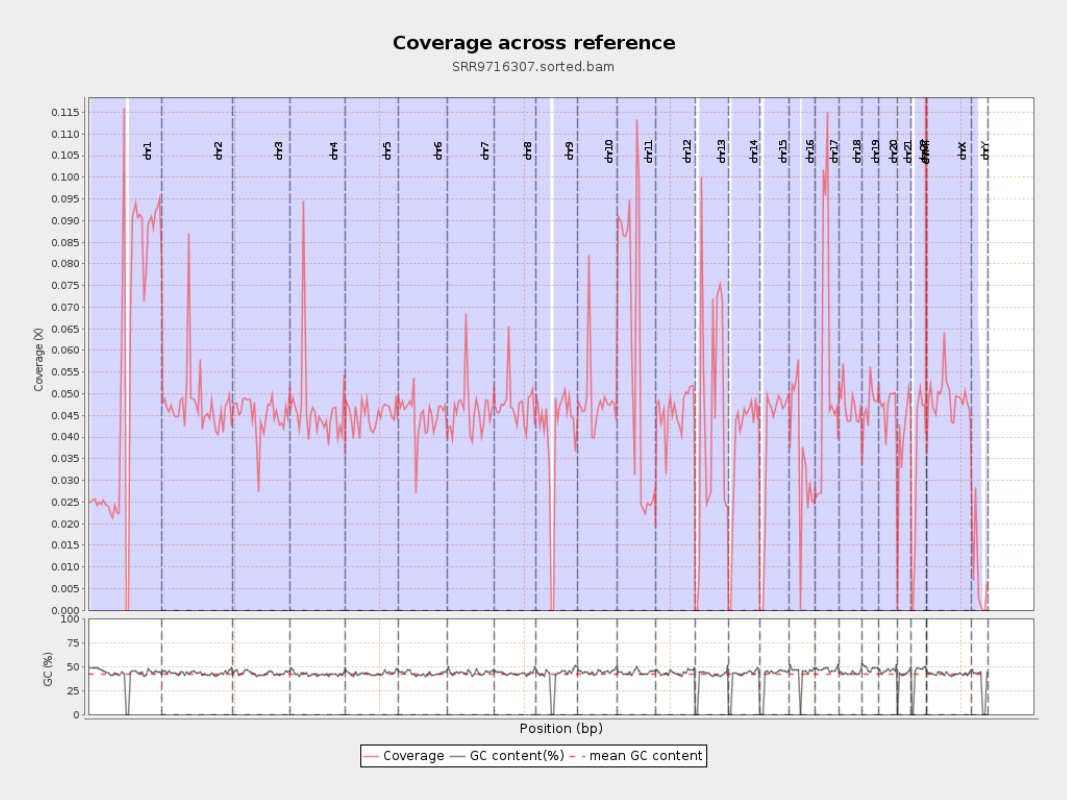
General error rate	0.68%
Mismatches	928,491
Insertions	12,361
Mapped reads with at least one insertion	0.68%
Deletions	34,903
Mapped reads with at least one deletion	1.92%
Homopolymer indels	42.27%

2.6. Chromosome stats

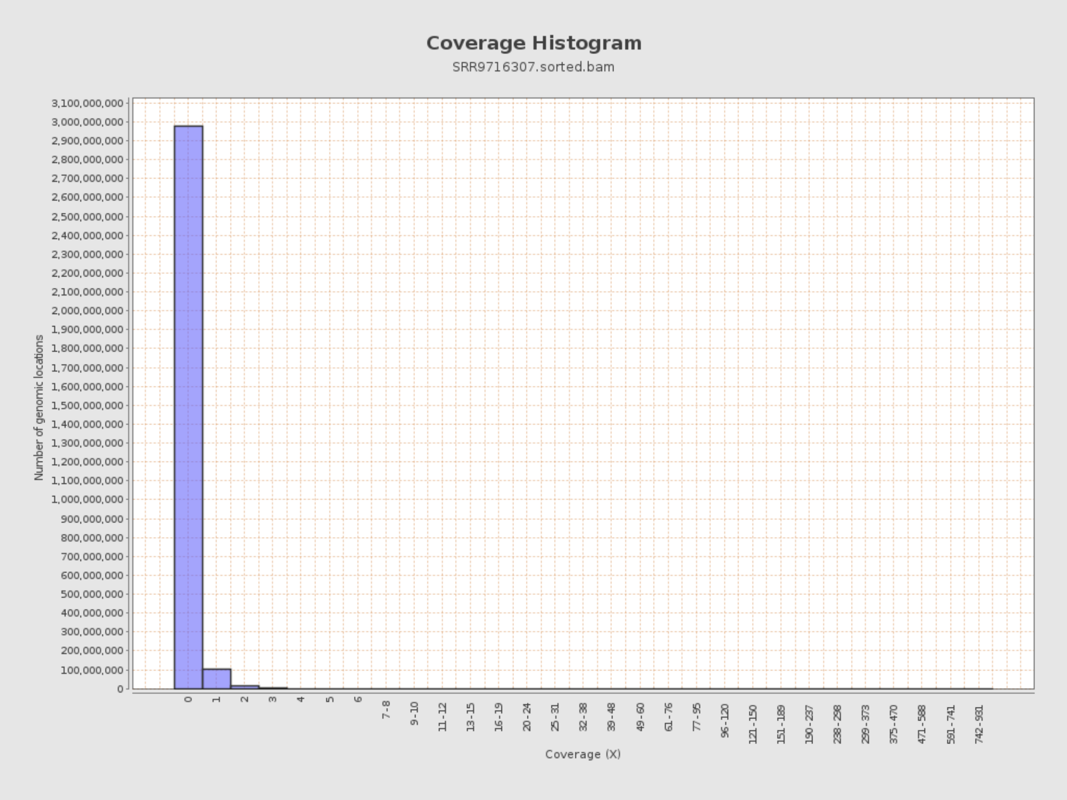
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13638728	0.0547	0.8342
chr2	243199373	11611962	0.0477	0.443
chr3	198022430	8911850	0.045	0.2382
chr4	191154276	8885692	0.0465	0.3185
chr5	180915260	8159495	0.0451	0.241
chr6	171115067	7705216	0.045	0.2652
chr7	159138663	7367264	0.0463	0.4959

chr8	146364022	6942646	0.0474	0.452
chr9	141213431	5647417	0.04	0.3364
chr10	135534747	6555047	0.0484	0.4068
chr11	135006516	8025078	0.0594	0.4797
chr12	133851895	6167725	0.0461	0.244
chr13	115169878	4913001	0.0427	0.2347
chr14	107349540	4055792	0.0378	0.2402
chr15	102531392	3968764	0.0387	0.2214
chr16	90354753	3204909	0.0355	0.2399
chr17	81195210	4632199	0.0571	0.3327
chr18	78077248	3703141	0.0474	0.5951
chr19	59128983	2815331	0.0476	0.6073
chr20	63025520	2960722	0.047	0.2597
chr21	48129895	1884070	0.0391	0.266
chr22	51304566	1696726	0.0331	0.2081
chrMT	16571	115608	6.9765	4.4307
chrX	155270560	7595732	0.0489	0.2975
chrY	59373566	437372	0.0074	0.2523

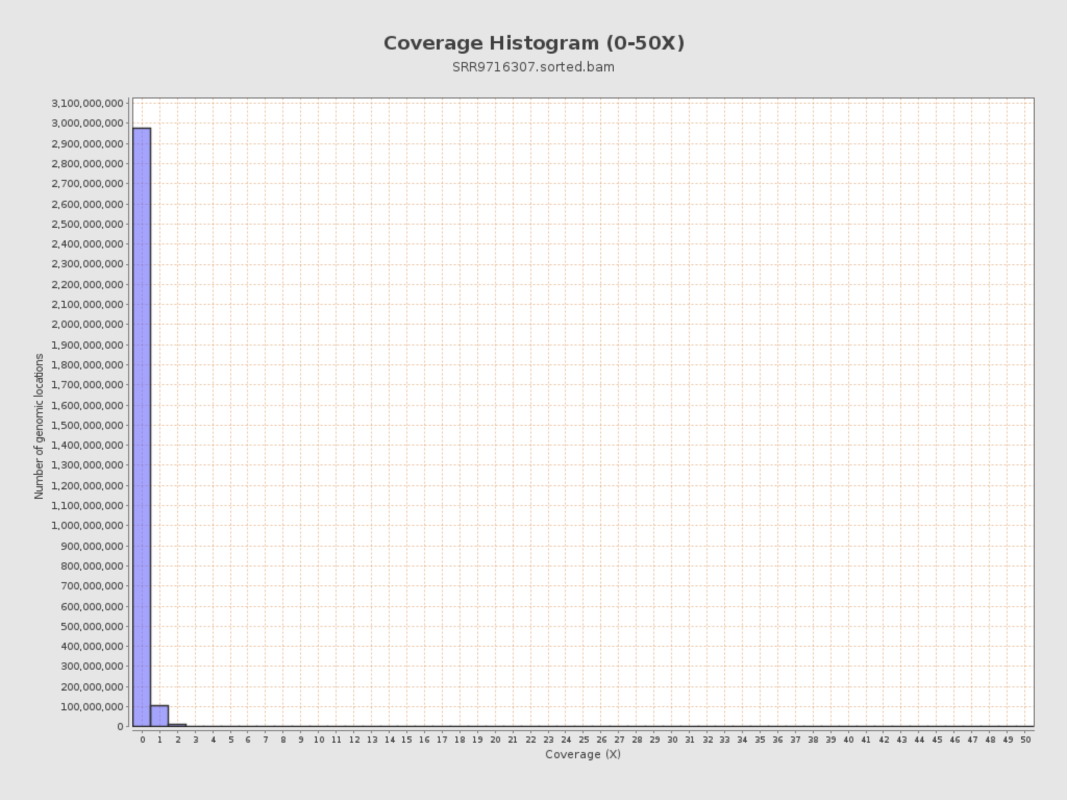
3. Results : Coverage across reference



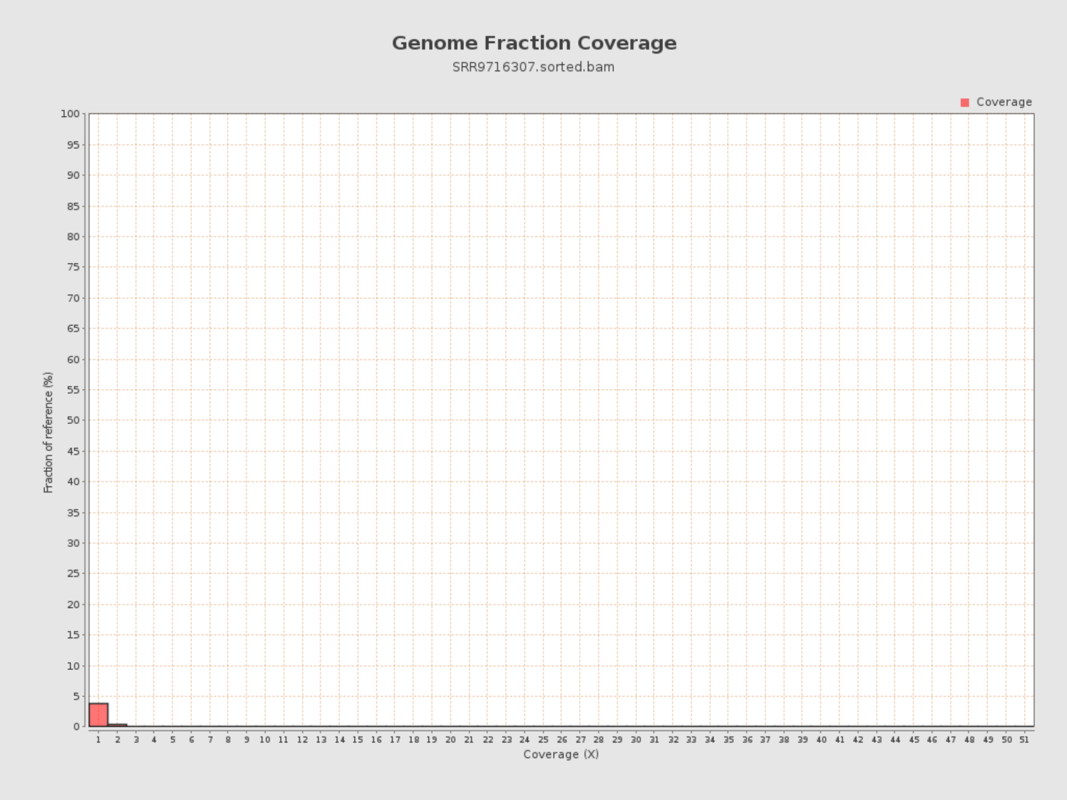
4. Results : Coverage Histogram



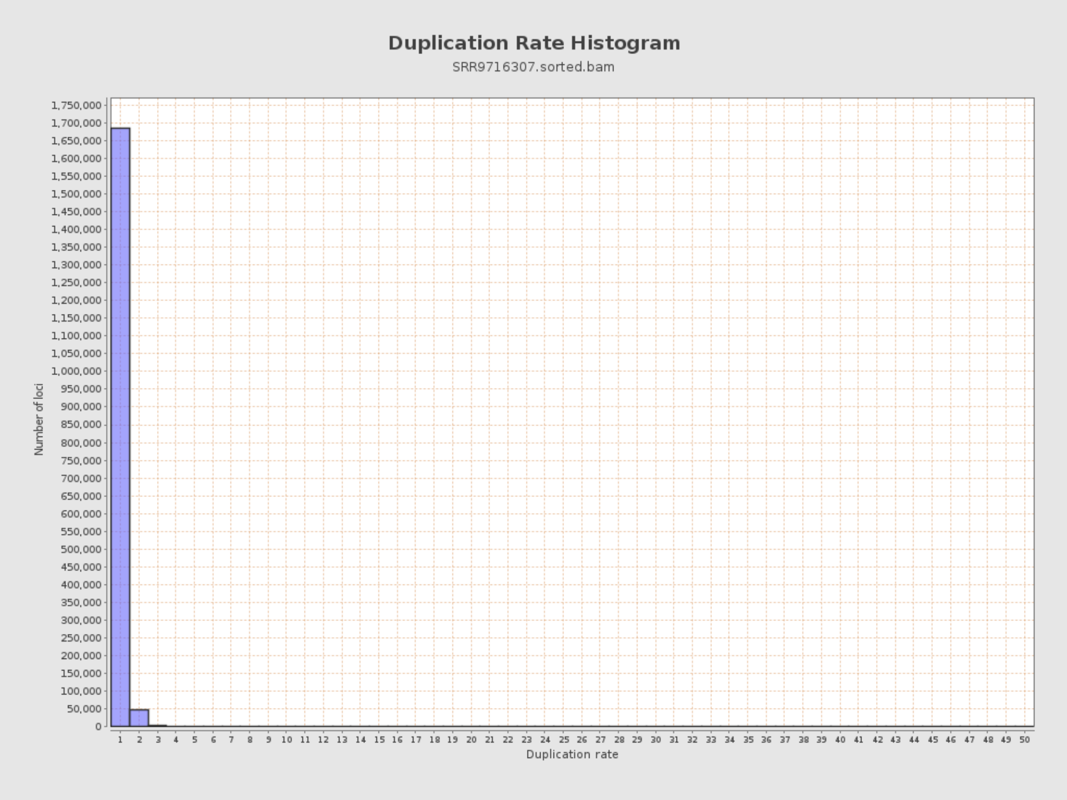
5. Results : Coverage Histogram (0-50X)



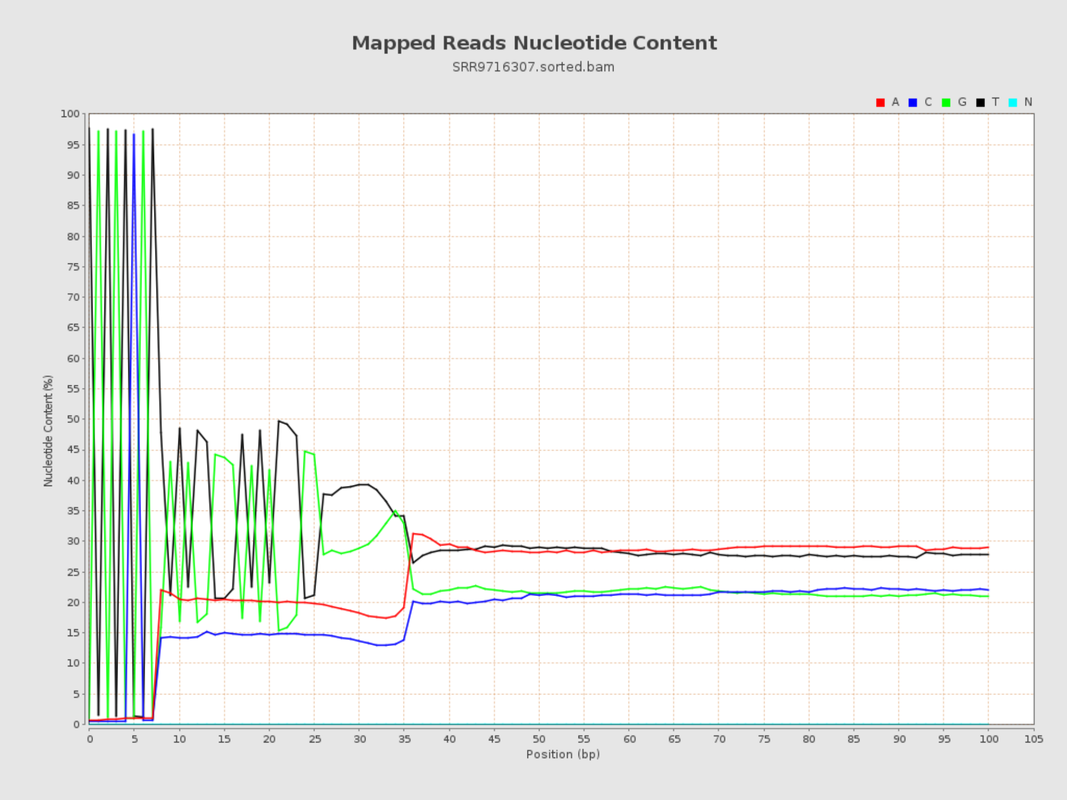
6. Results : Genome Fraction Coverage



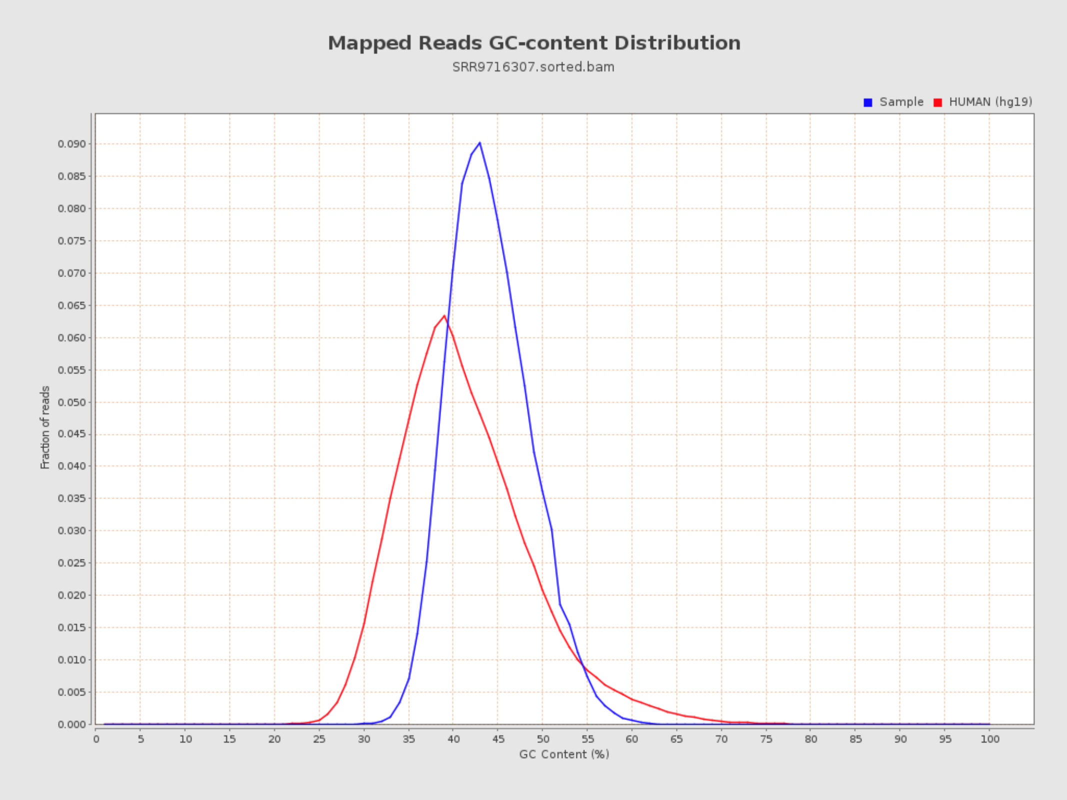
7. Results : Duplication Rate Histogram



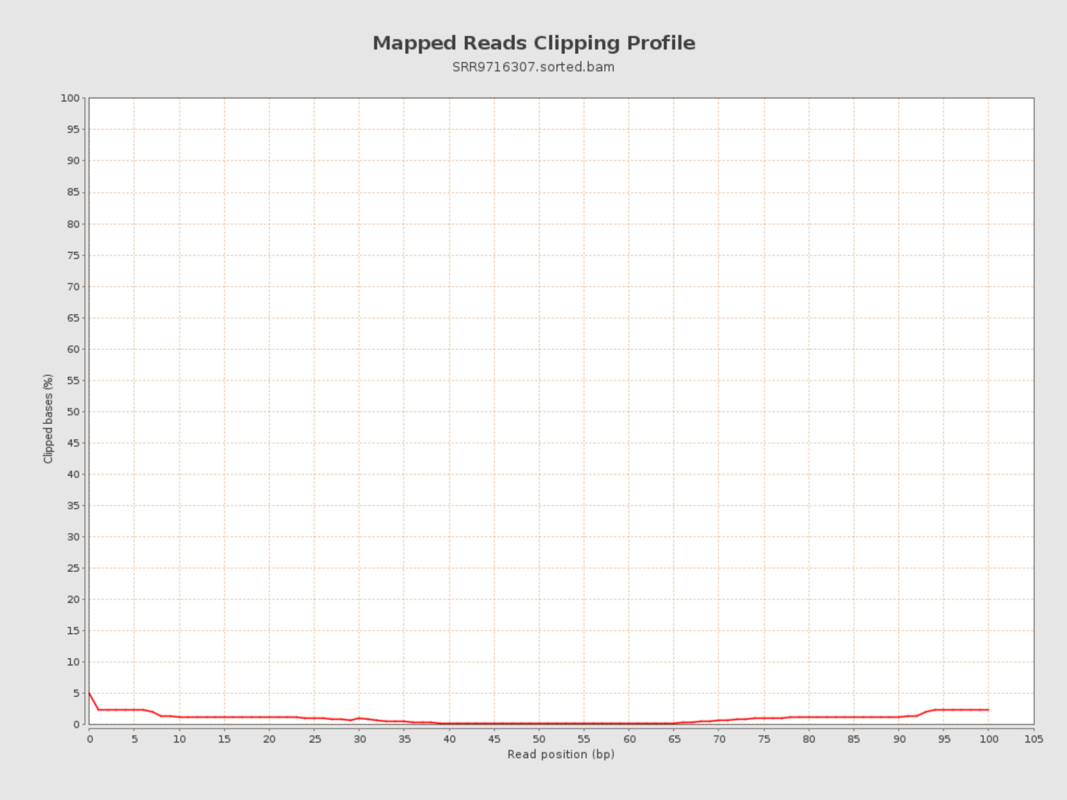
8. Results : Mapped Reads Nucleotide Content



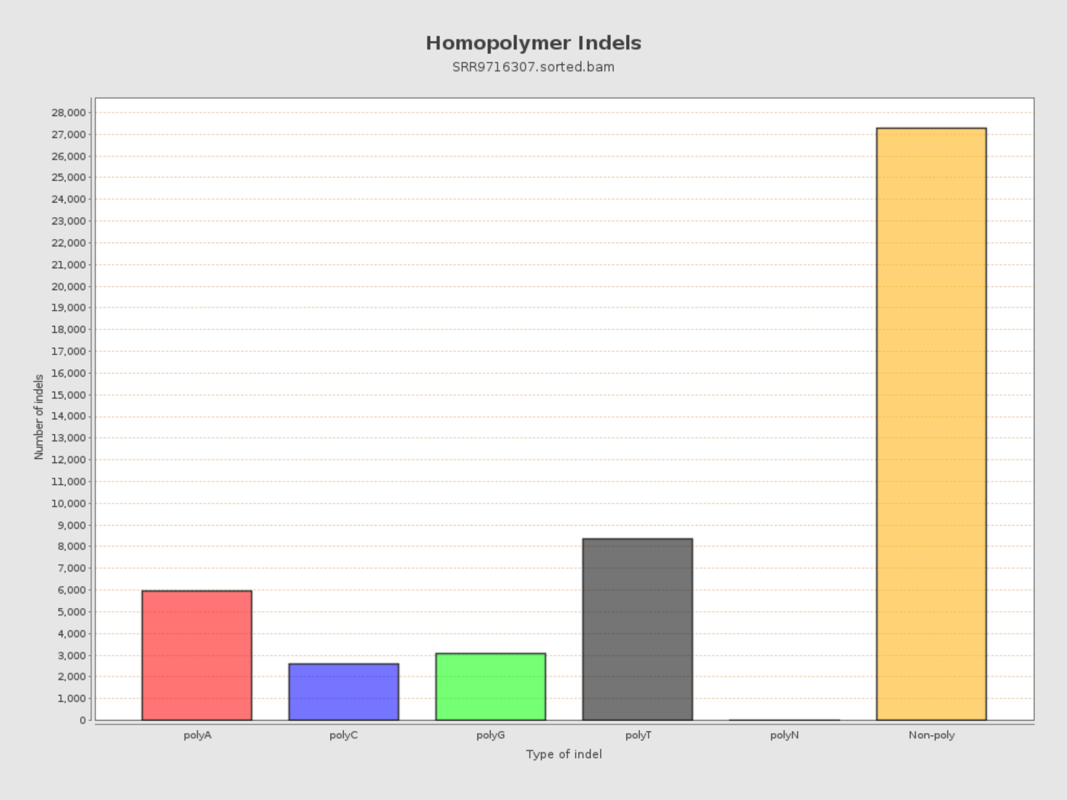
9. Results : Mapped Reads GC-content Distribution



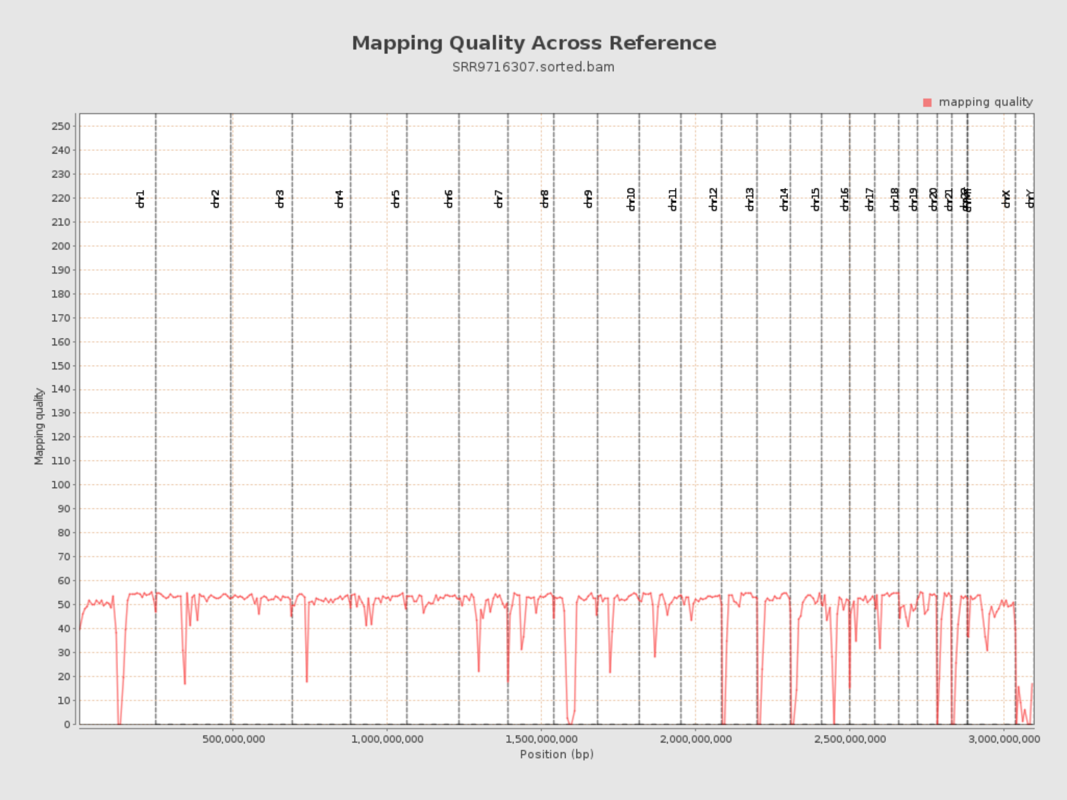
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram