Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 19:41:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716946.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_SRR9716946 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716946.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 19:41:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716946.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,490,374
Mapped reads	2,260,655 / 90.78%
Unmapped reads	229,719 / 9.22%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,497 / 0.5%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	123,823 / 4.97%
Duplication rate	4.21%
Clipped reads	2,268,397 / 91.09%

2.2. ACGT Content

Number/percentage of A's	32,825,449 / 25.28%
Number/percentage of C's	25,815,911 / 19.88%
Number/percentage of T's	40,253,257 / 31%
Number/percentage of G's	30,965,181 / 23.84%
Number/percentage of N's	1,902 / 0%
GC Percentage	43.72%

2.3. Coverage

Mean	0.042

Standard Deviation	0.354

2.4. Mapping Quality

Mean Mapping Quality	43.65

2.5. Mismatches and indels

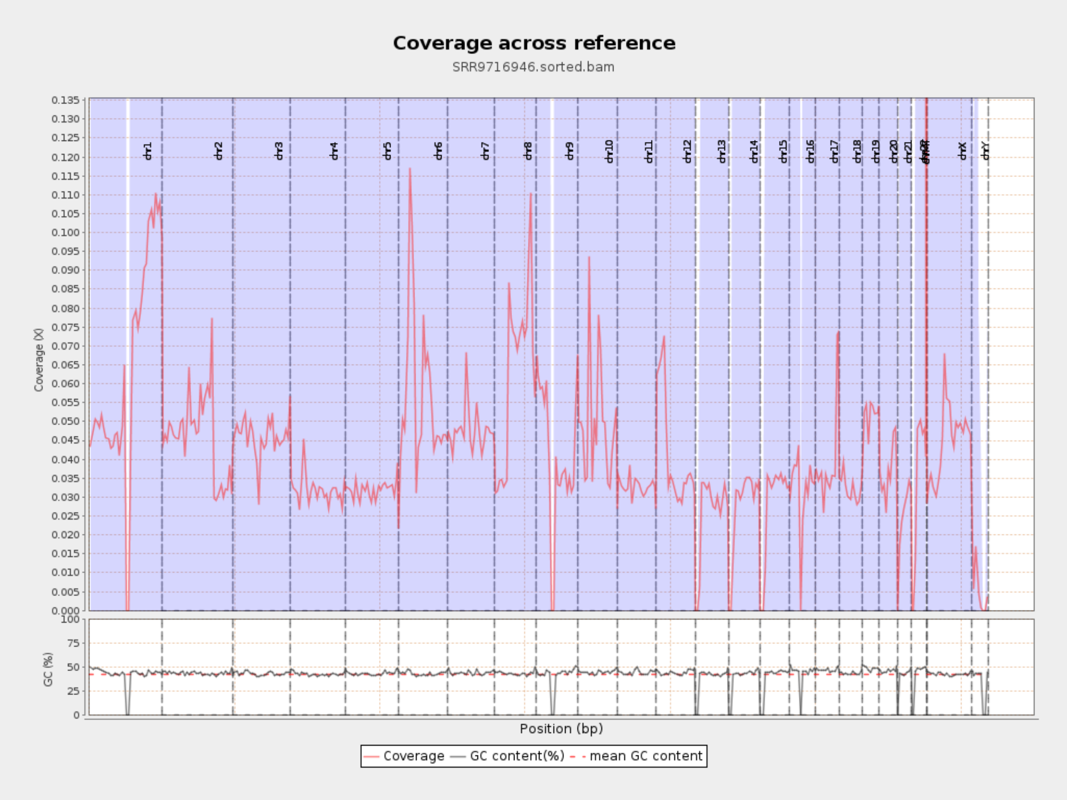
General error rate	0.5%
Mismatches	634,492
Insertions	8,562
Mapped reads with at least one insertion	0.38%
Deletions	21,277
Mapped reads with at least one deletion	0.94%
Homopolymer indels	42.53%

2.6. Chromosome stats

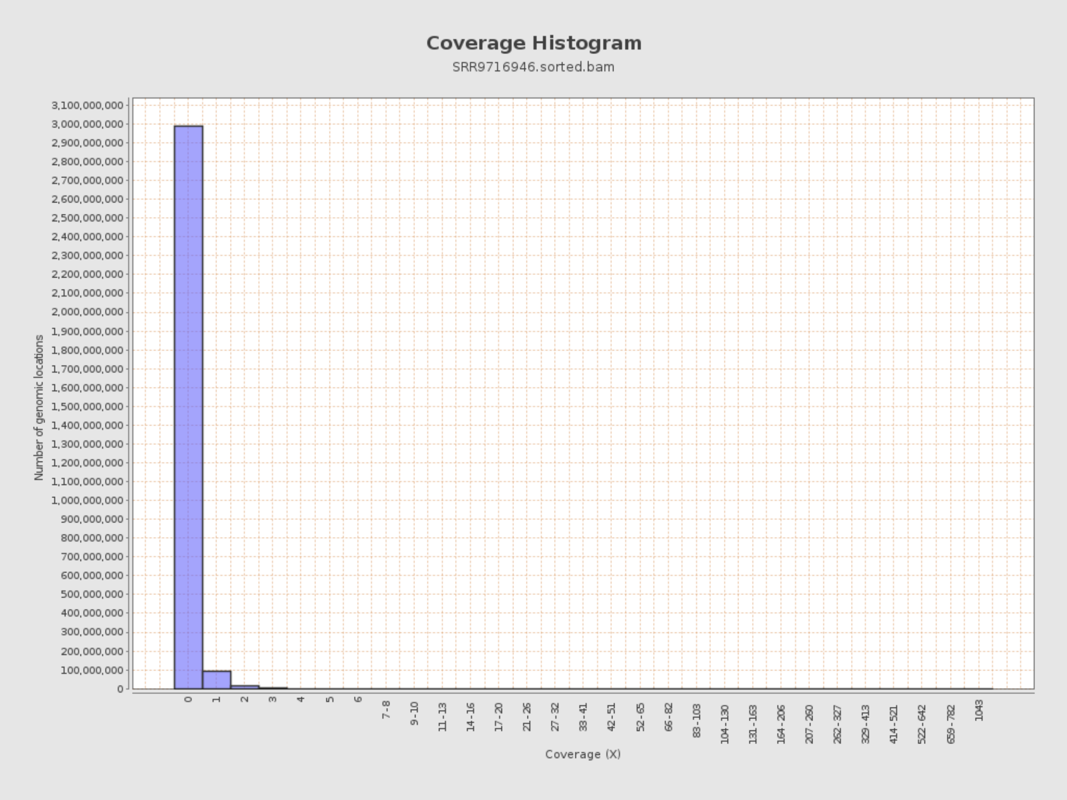
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15778145	0.0633	0.5782
chr2	243199373	11201437	0.0461	0.4985
chr3	198022430	9056067	0.0457	0.2546
chr4	191154276	6073387	0.0318	0.2286
chr5	180915260	5781725	0.032	0.2122
chr6	171115067	9801421	0.0573	0.3587
chr7	159138663	7617096	0.0479	0.4763

chr8	146364022	9272225	0.0634	0.3315
chr9	141213431	5516314	0.0391	0.3232
chr10	135534747	6741671	0.0497	0.4137
chr11	135006516	4431959	0.0328	0.2904
chr12	133851895	5554039	0.0415	0.248
chr13	115169878	2943364	0.0256	0.185
chr14	107349540	2909677	0.0271	0.2268
chr15	102531392	2848830	0.0278	0.2064
chr16	90354753	2883494	0.0319	0.2392
chr17	81195210	3243057	0.0399	0.2468
chr18	78077248	2517096	0.0322	0.5237
chr19	59128983	3042647	0.0515	0.4208
chr20	63025520	2335035	0.037	0.2301
chr21	48129895	1191532	0.0248	0.2139
chr22	51304566	1684061	0.0328	0.2123
chrMT	16571	200385	12.0925	7.2922
chrX	155270560	6941969	0.0447	0.2881
chrY	59373566	328558	0.0055	0.132

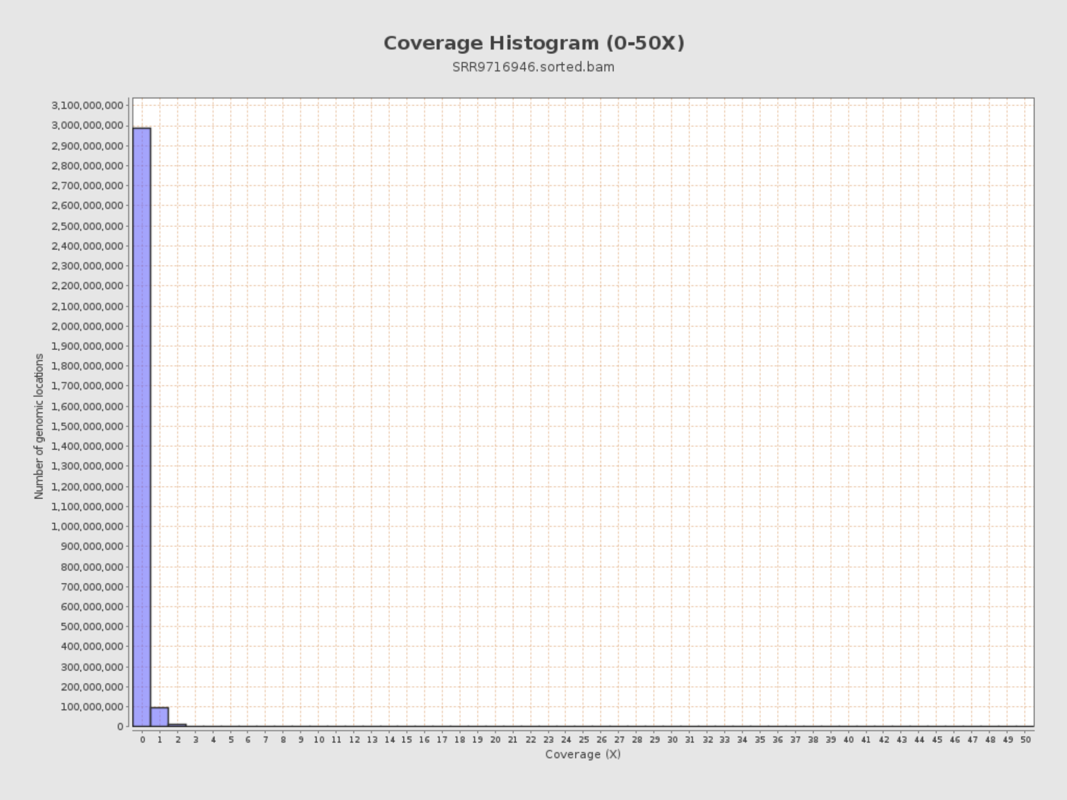
3. Results : Coverage across reference



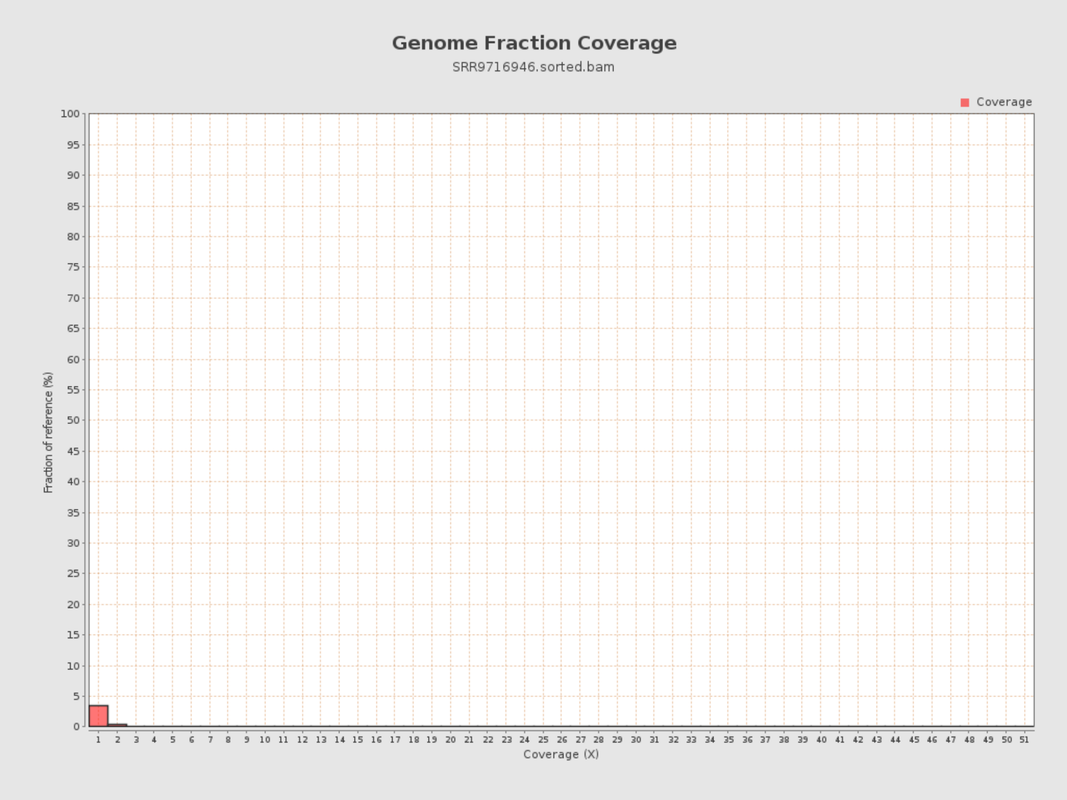
4. Results : Coverage Histogram



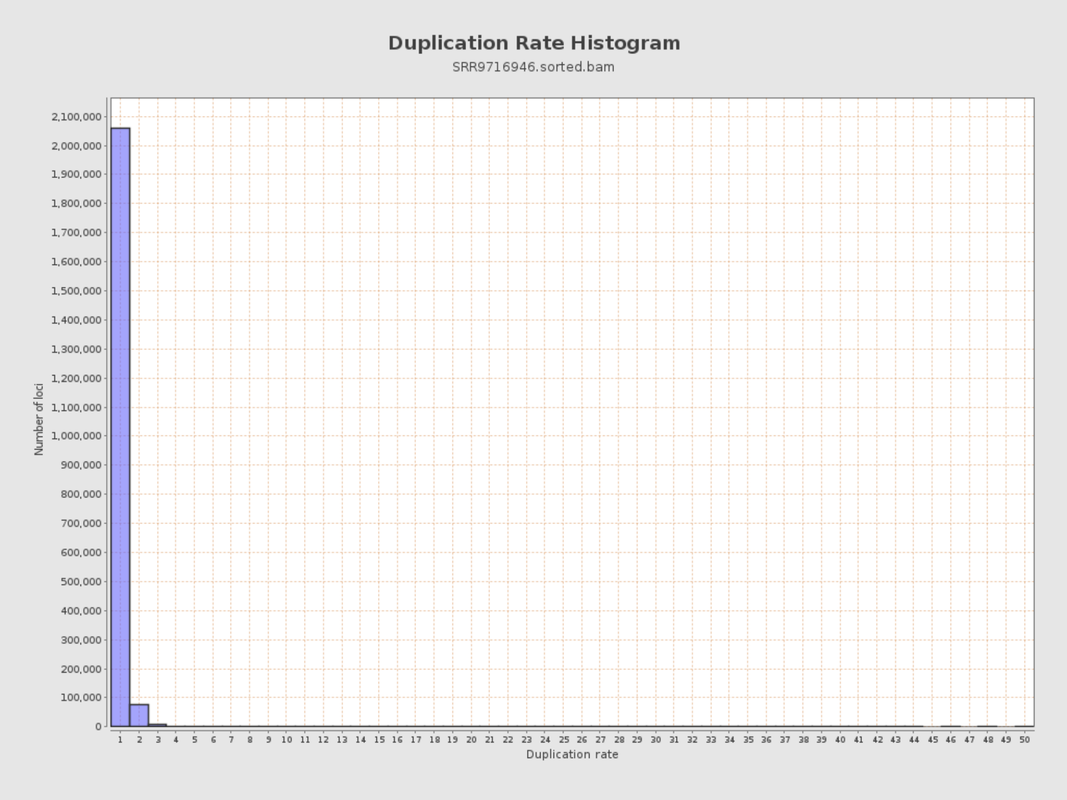
5. Results : Coverage Histogram (0-50X)



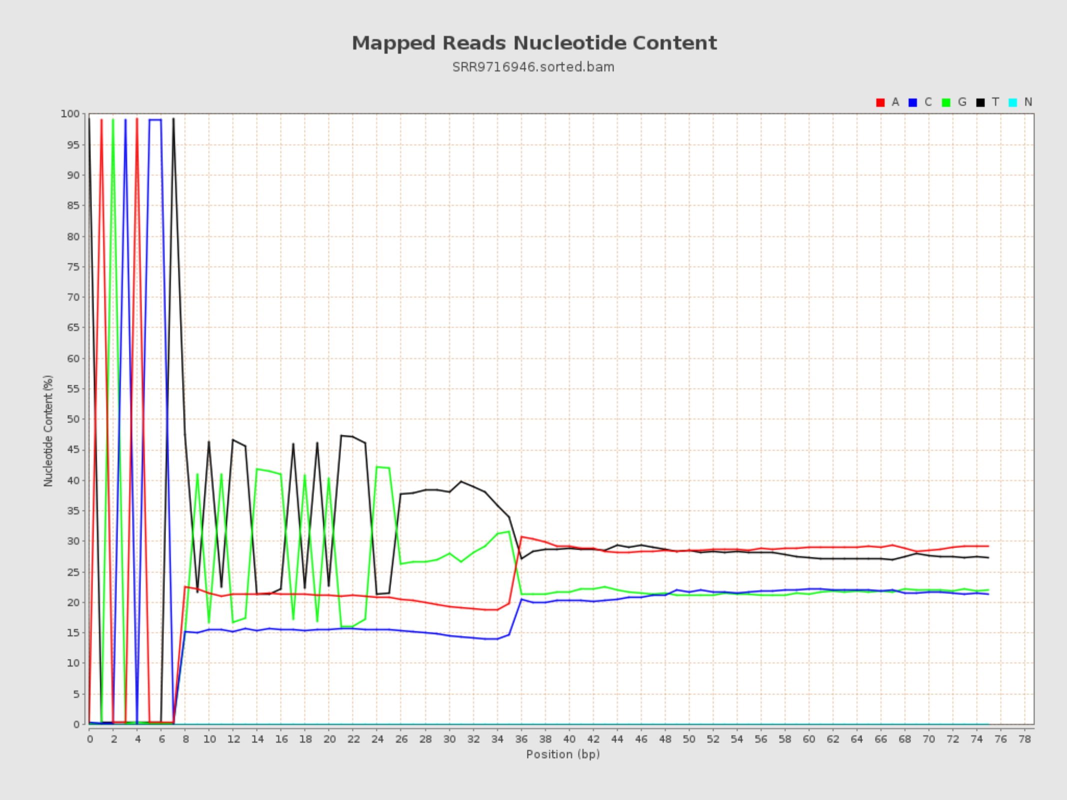
6. Results : Genome Fraction Coverage



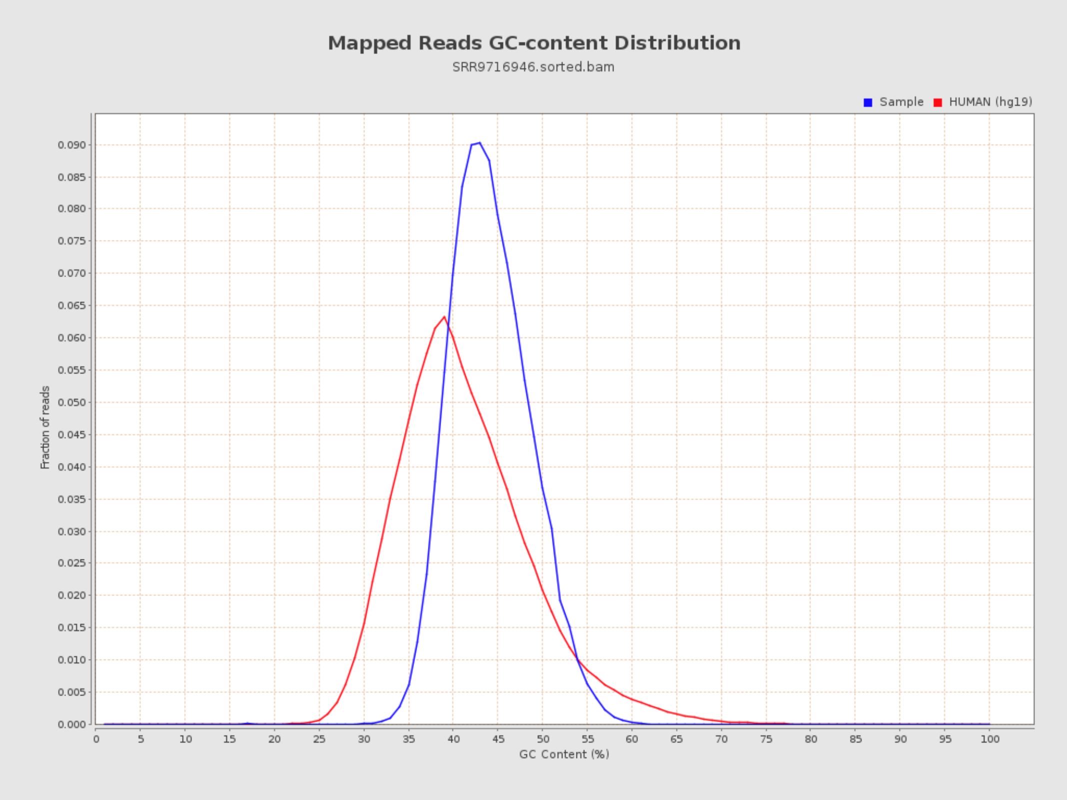
7. Results : Duplication Rate Histogram



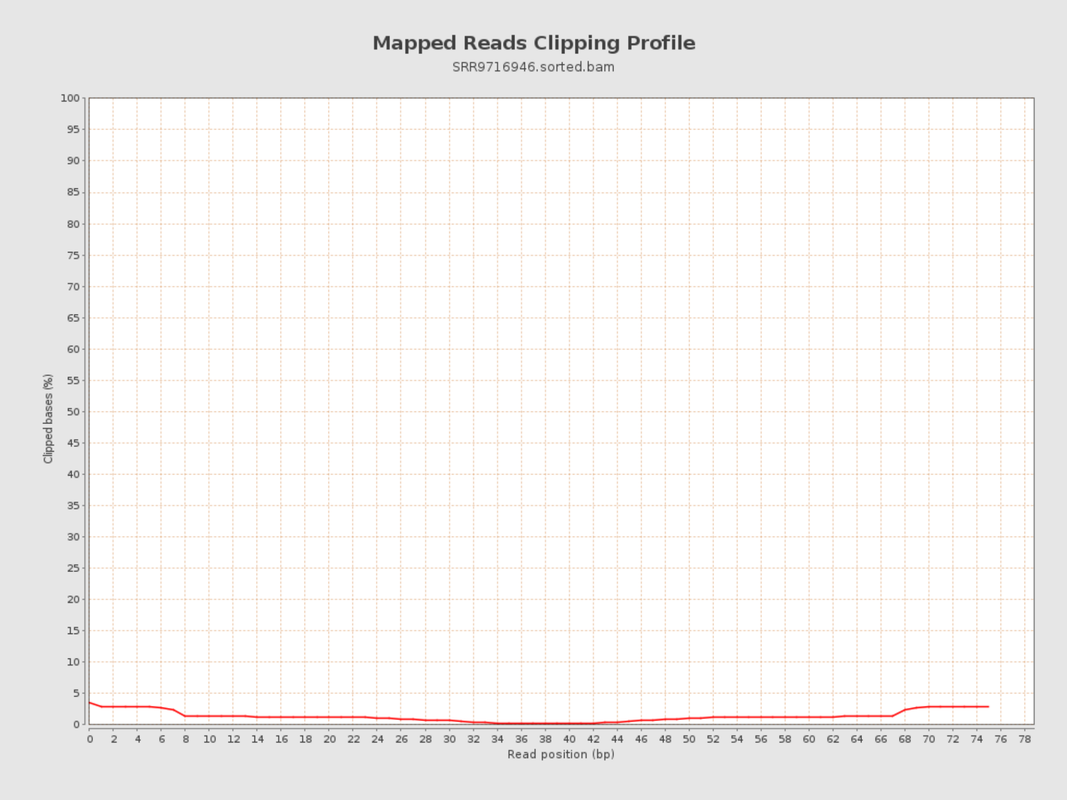
8. Results : Mapped Reads Nucleotide Content



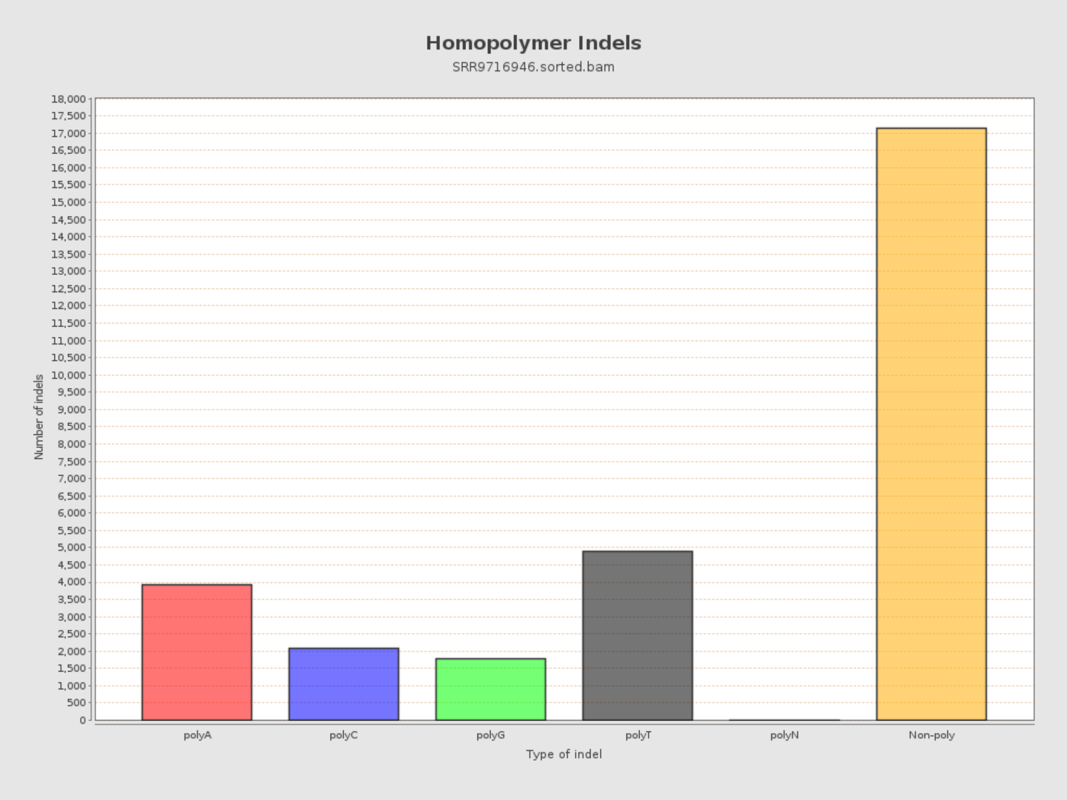
9. Results : Mapped Reads GC-content Distribution



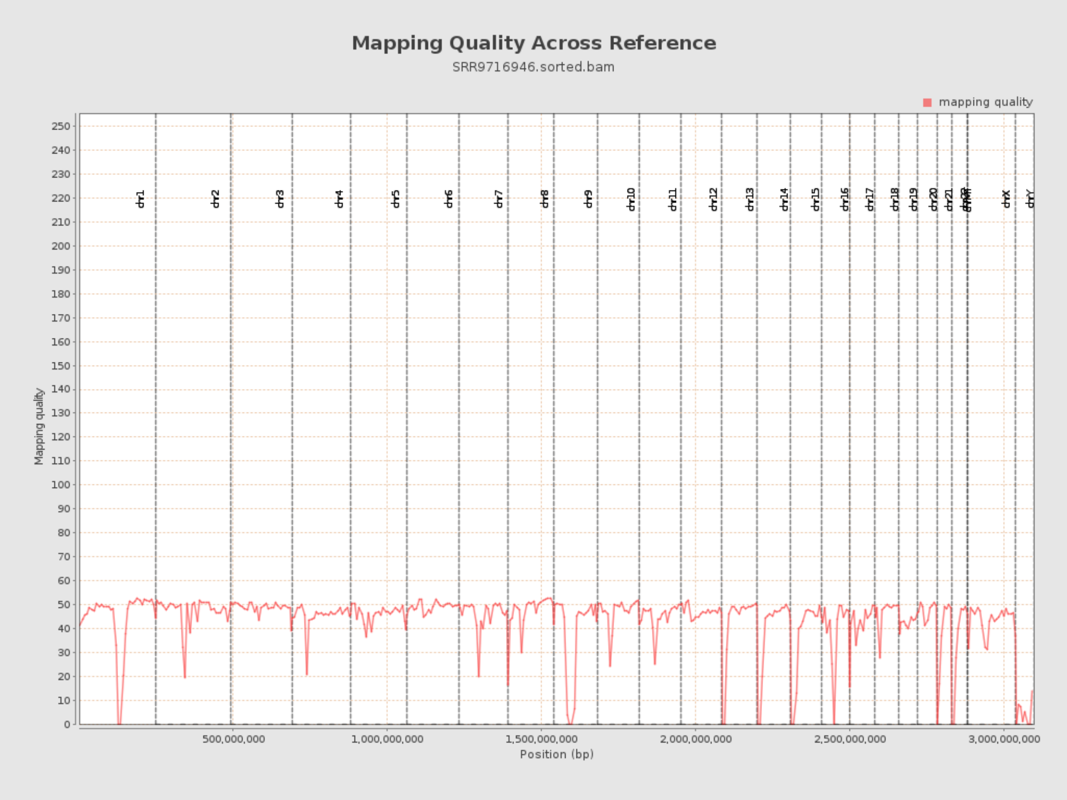
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram