Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 23:14:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716992.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_SRR9716992 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716992.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 23:14:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716992.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,474,368
Mapped reads	2,231,887 / 90.2%
Unmapped reads	242,481 / 9.8%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,556 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	91,330 / 3.69%
Duplication rate	3.04%
Clipped reads	2,239,823 / 90.52%

2.2. ACGT Content

Number/percentage of A's	30,749,607 / 23.82%
Number/percentage of C's	25,774,979 / 19.97%
Number/percentage of T's	39,769,889 / 30.81%
Number/percentage of G's	32,770,027 / 25.39%
Number/percentage of N's	1,041 / 0%
GC Percentage	45.36%

2.3. Coverage

Mean	0.0417

Standard Deviation	0.3264

2.4. Mapping Quality

Mean Mapping Quality	44.3

2.5. Mismatches and indels

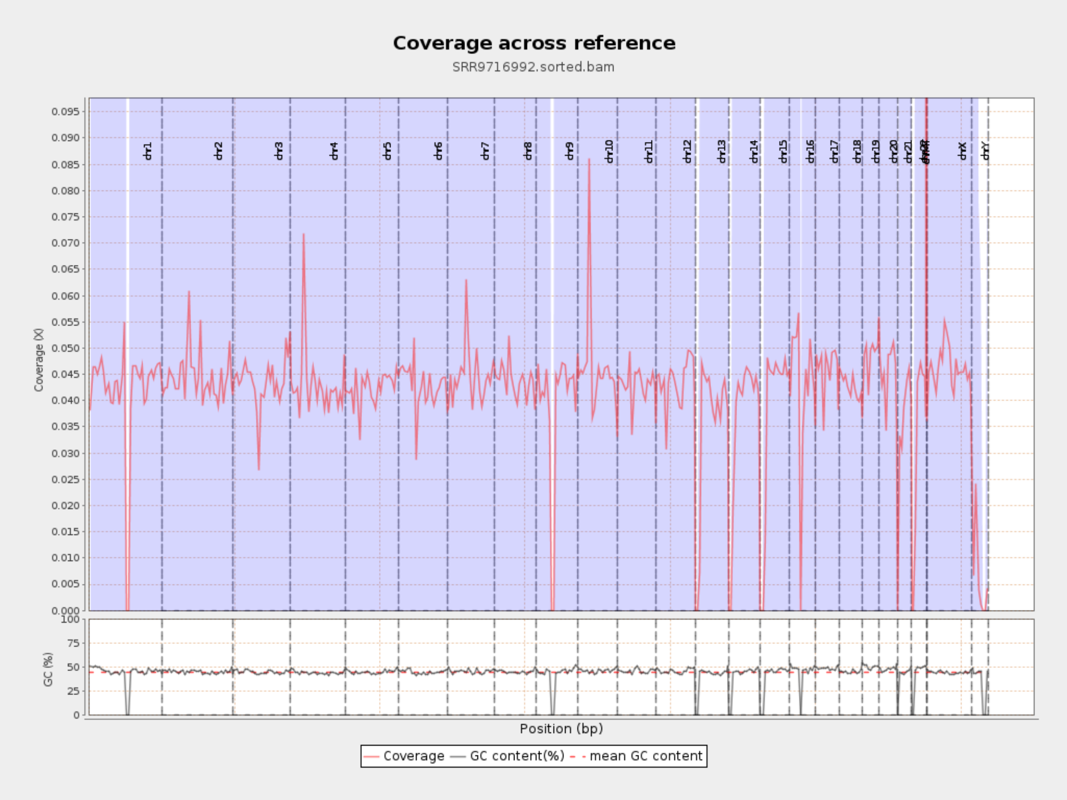
General error rate	0.54%
Mismatches	677,797
Insertions	7,230
Mapped reads with at least one insertion	0.32%
Deletions	24,405
Mapped reads with at least one deletion	1.09%
Homopolymer indels	42.08%

2.6. Chromosome stats

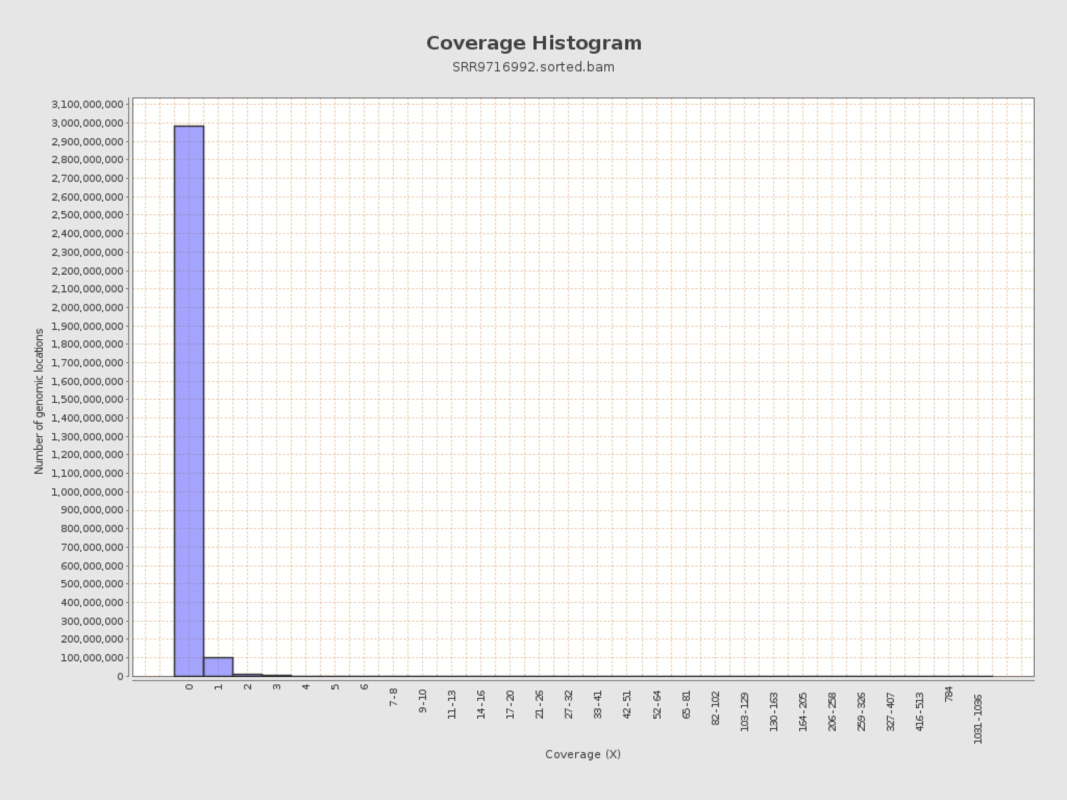
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10353547	0.0415	0.4222
chr2	243199373	10843120	0.0446	0.5095
chr3	198022430	8592757	0.0434	0.2407
chr4	191154276	8216052	0.043	0.2712
chr5	180915260	7661326	0.0423	0.2333
chr6	171115067	7359708	0.043	0.2793
chr7	159138663	7115424	0.0447	0.4182

chr8	146364022	6392947	0.0437	0.3179
chr9	141213431	5444888	0.0386	0.2878
chr10	135534747	6275895	0.0463	0.4169
chr11	135006516	5815284	0.0431	0.3003
chr12	133851895	5839269	0.0436	0.2407
chr13	115169878	3985944	0.0346	0.2098
chr14	107349540	3871713	0.0361	0.2268
chr15	102531392	3798945	0.0371	0.2205
chr16	90354753	3874408	0.0429	0.2588
chr17	81195210	3733393	0.046	0.2584
chr18	78077248	3345208	0.0428	0.4671
chr19	59128983	2858728	0.0483	0.3781
chr20	63025520	2847688	0.0452	0.2537
chr21	48129895	1695888	0.0352	0.2522
chr22	51304566	1589576	0.031	0.2012
chrMT	16571	23964	1.4461	1.54
chrX	155270560	7162085	0.0461	0.2686
chrY	59373566	407171	0.0069	0.2083

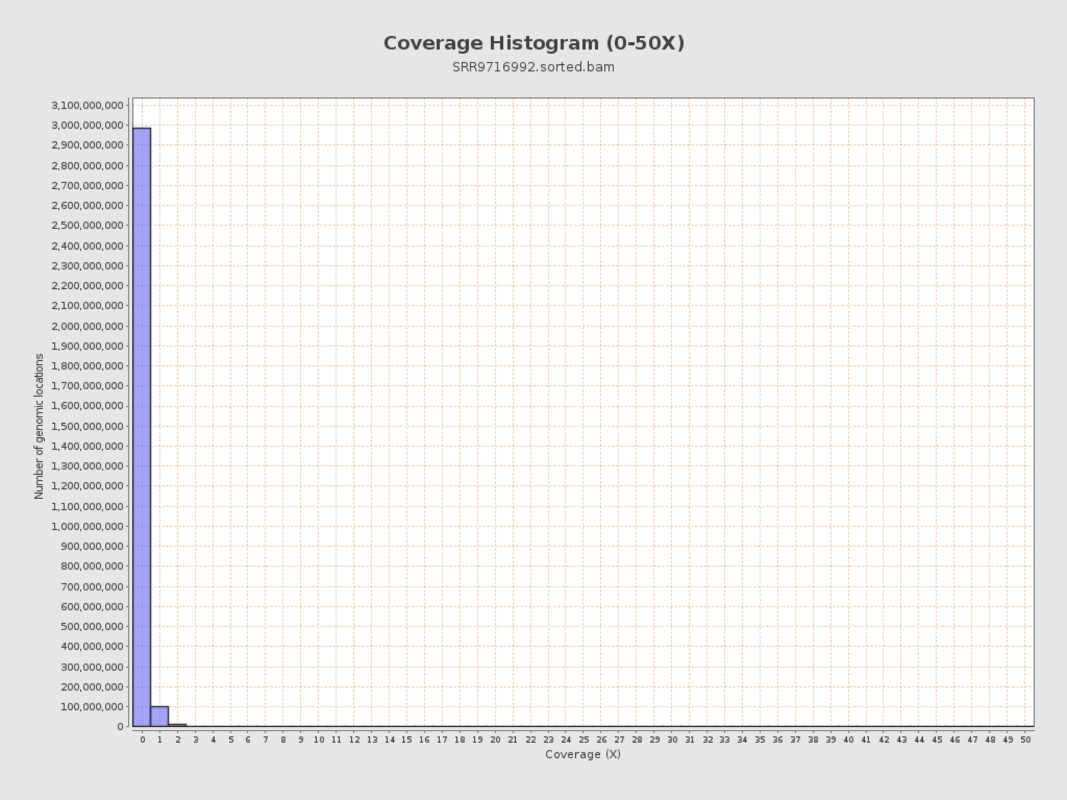
3. Results : Coverage across reference



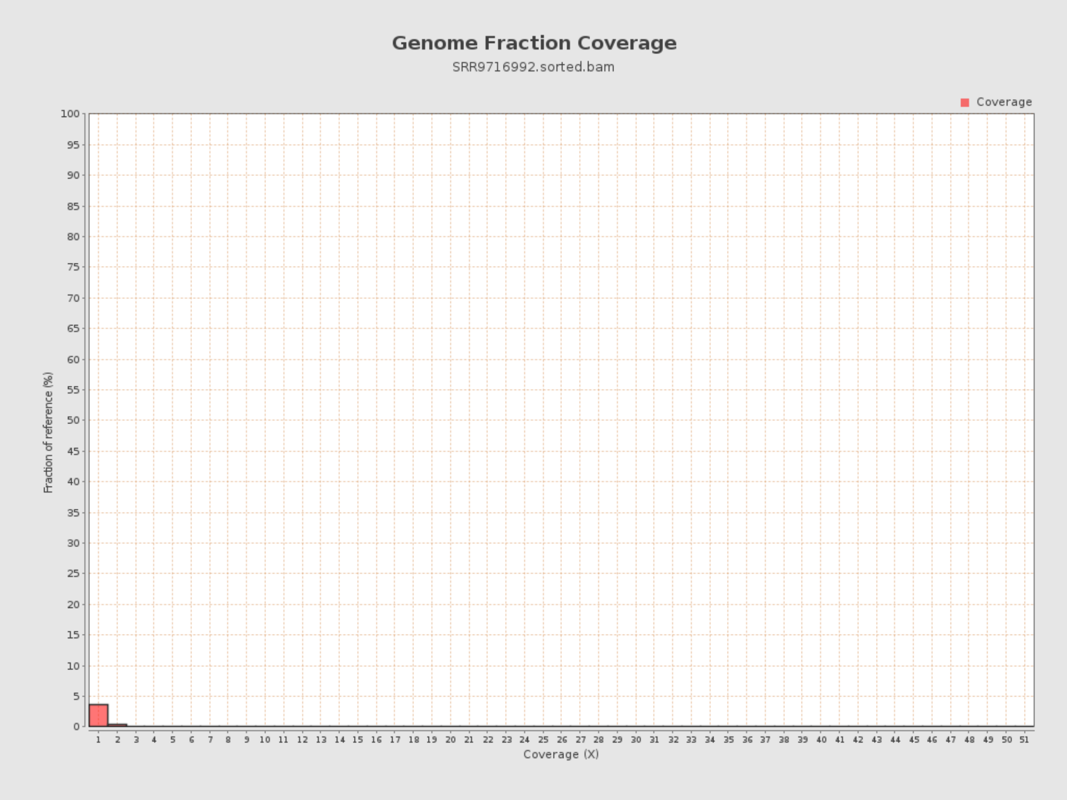
4. Results : Coverage Histogram



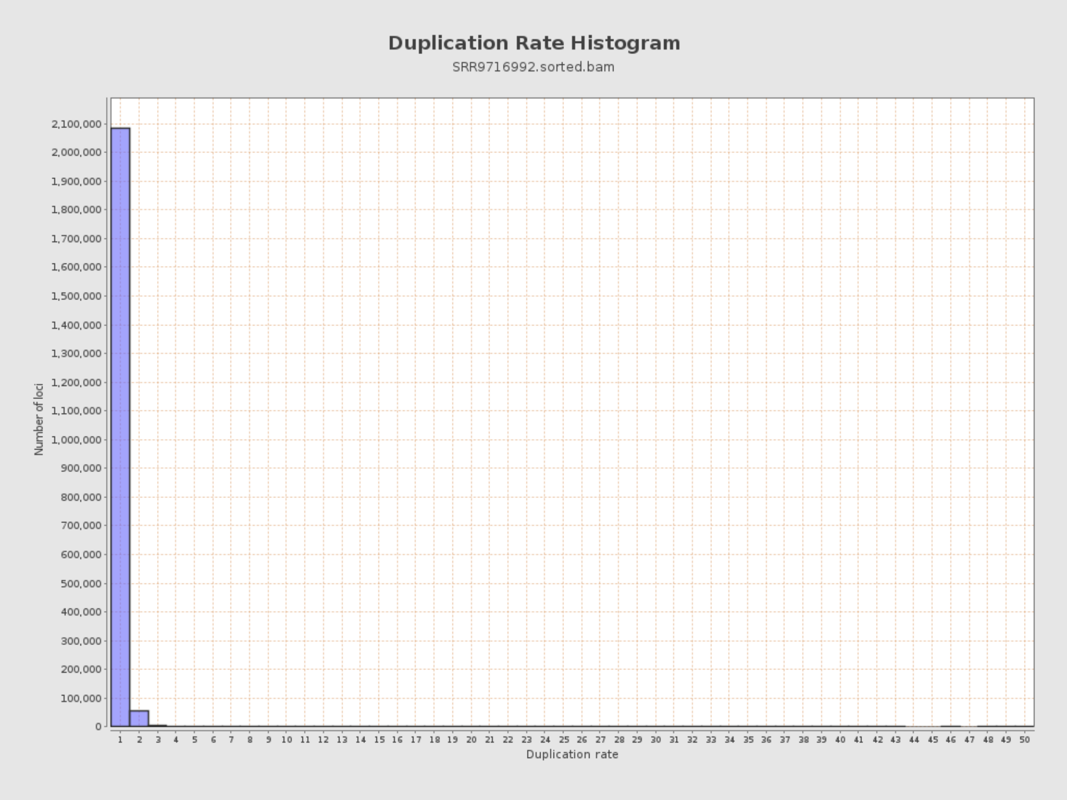
5. Results : Coverage Histogram (0-50X)



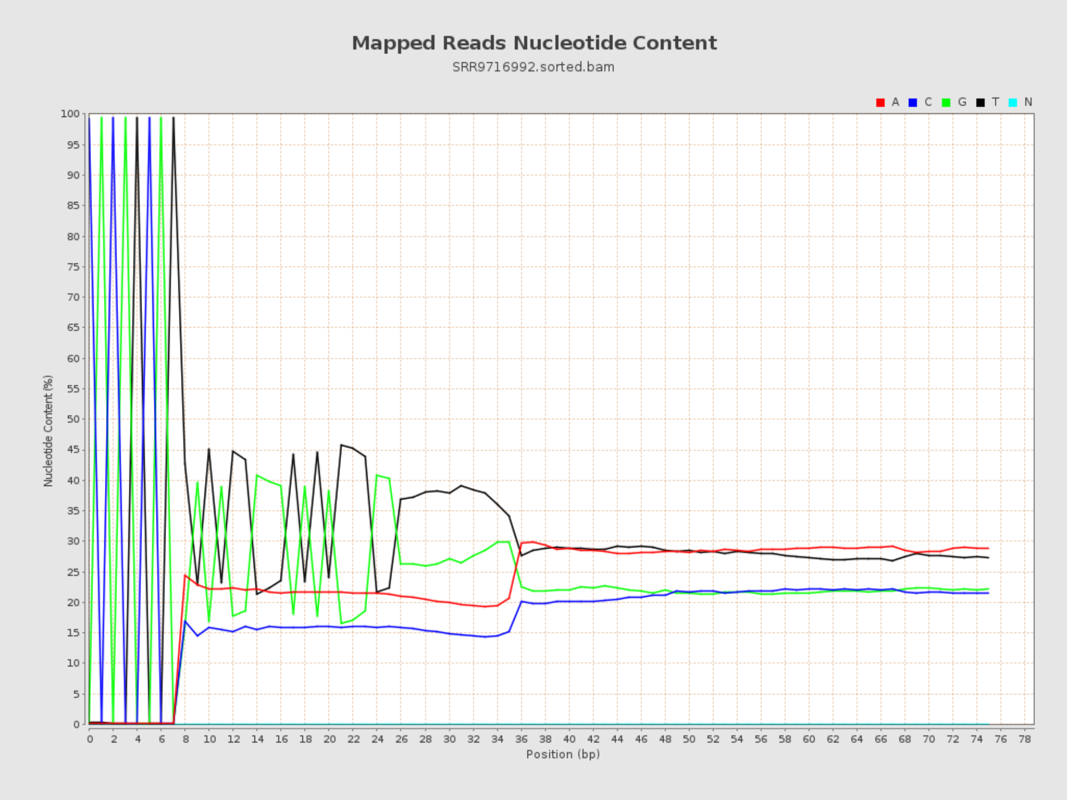
6. Results : Genome Fraction Coverage



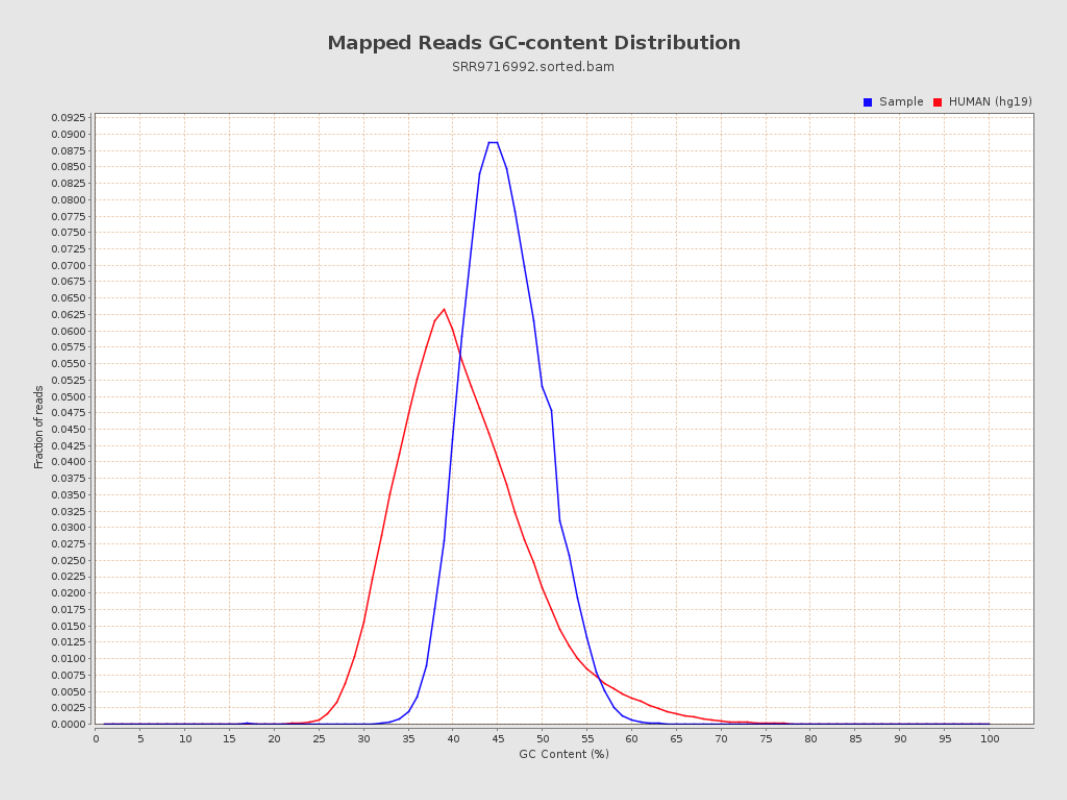
7. Results : Duplication Rate Histogram



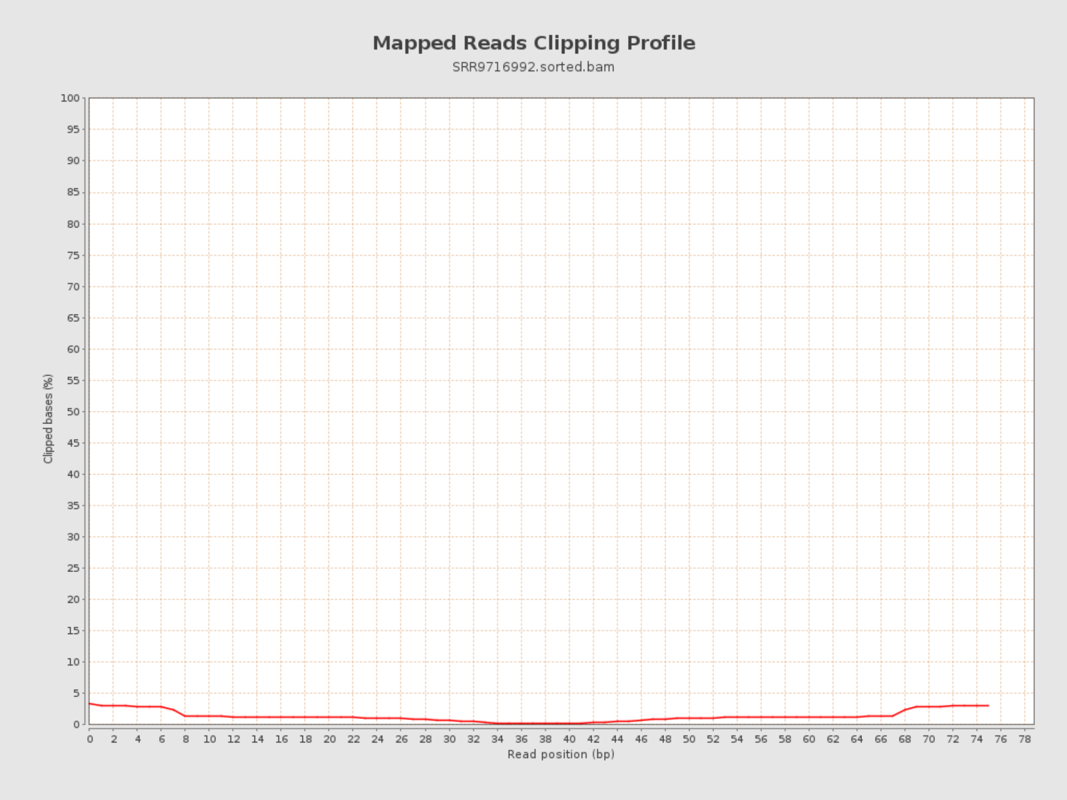
8. Results : Mapped Reads Nucleotide Content



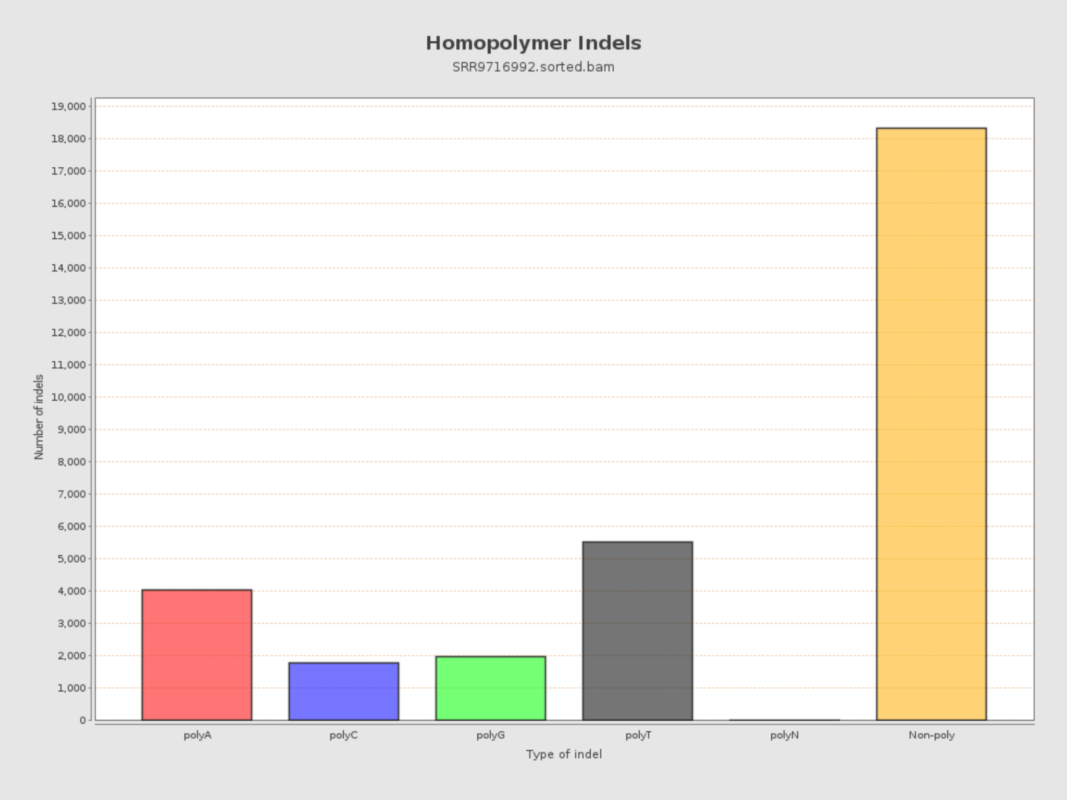
9. Results : Mapped Reads GC-content Distribution



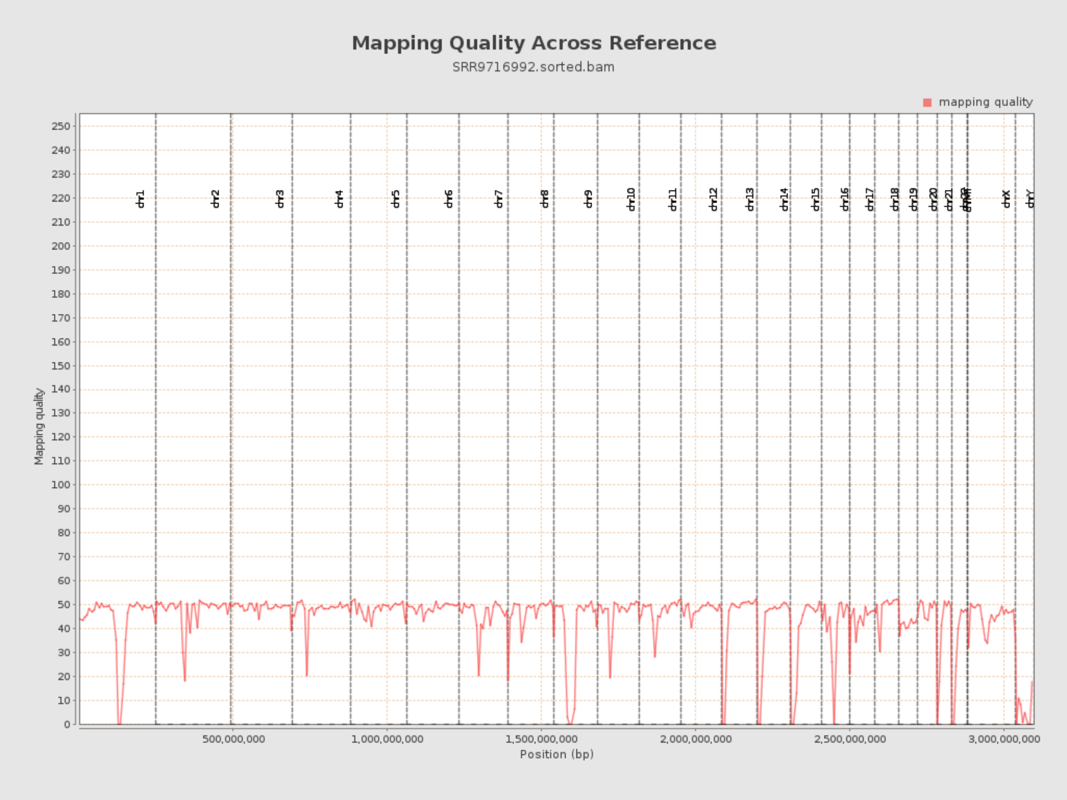
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram