Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 19:45:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716146.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_SRR9716146 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716146.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 19:45:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716146.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,054,626
Mapped reads	1,857,659 / 90.41%
Unmapped reads	196,967 / 9.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,576 / 0.47%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	57,046 / 2.78%
Duplication rate	2.17%
Clipped reads	1,862,249 / 90.64%

2.2. ACGT Content

Number/percentage of A's	27,135,976 / 25%
Number/percentage of C's	20,689,569 / 19.06%
Number/percentage of T's	34,276,301 / 31.58%
Number/percentage of G's	26,451,673 / 24.37%
Number/percentage of N's	699 / 0%
GC Percentage	43.43%

2.3. Coverage

Mean	0.0351

Standard Deviation	0.3018

2.4. Mapping Quality

Mean Mapping Quality	44.55

2.5. Mismatches and indels

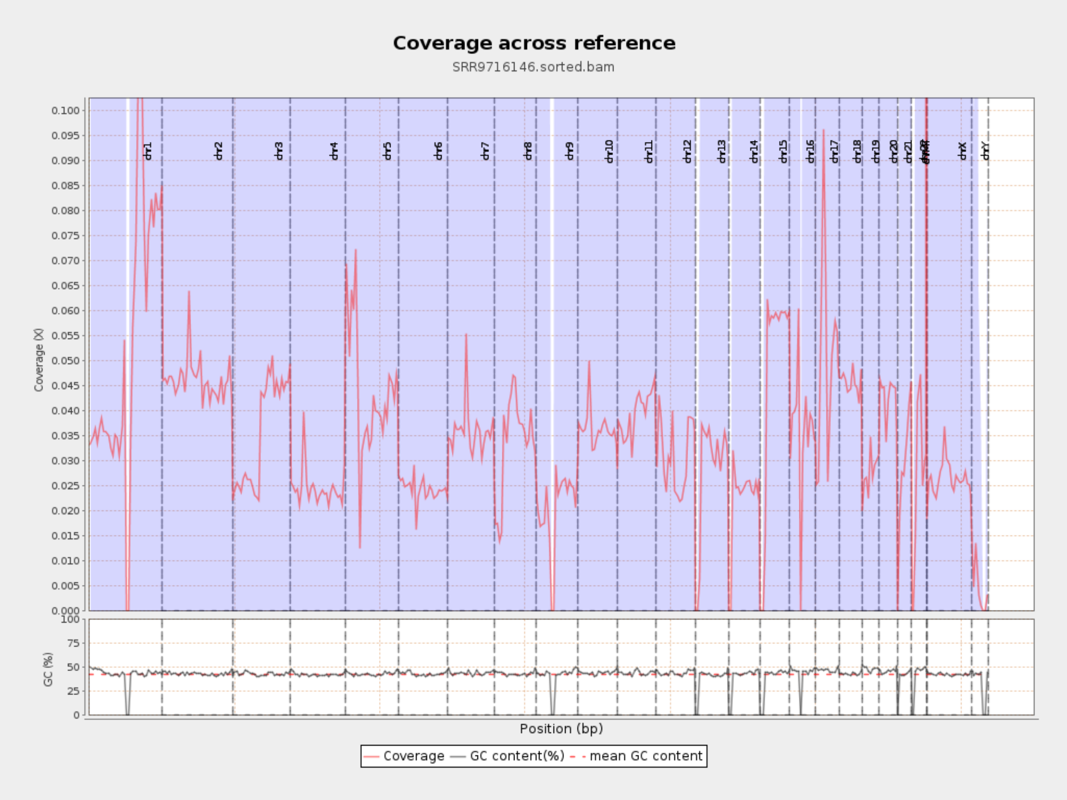
General error rate	0.51%
Mismatches	539,761
Insertions	8,620
Mapped reads with at least one insertion	0.46%
Deletions	19,959
Mapped reads with at least one deletion	1.07%
Homopolymer indels	40.36%

2.6. Chromosome stats

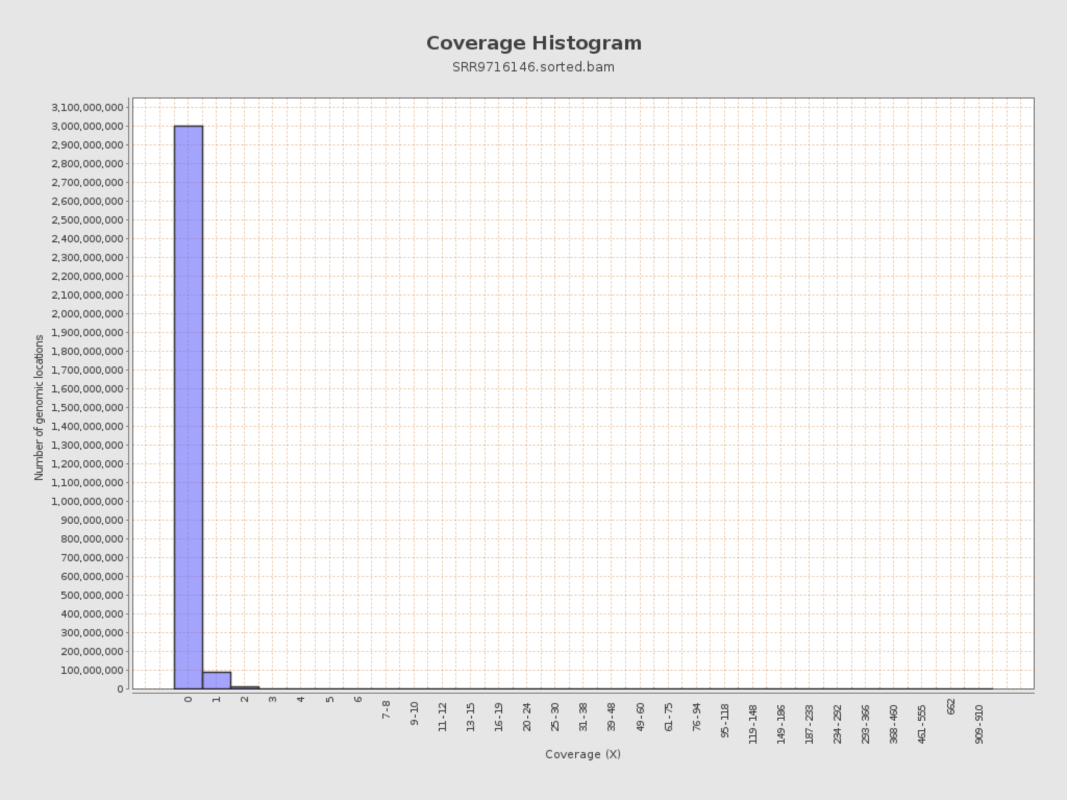
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13002259	0.0522	0.5101
chr2	243199373	11239557	0.0462	0.4577
chr3	198022430	7014577	0.0354	0.204
chr4	191154276	4654732	0.0244	0.1978
chr5	180915260	7909066	0.0437	0.2288
chr6	171115067	4153934	0.0243	0.1949
chr7	159138663	5731414	0.036	0.3863

chr8	146364022	4919026	0.0336	0.2792
chr9	141213431	2831185	0.02	0.2277
chr10	135534747	4942903	0.0365	0.2587
chr11	135006516	5309402	0.0393	0.3068
chr12	133851895	4101453	0.0306	0.1911
chr13	115169878	3205610	0.0278	0.1848
chr14	107349540	2357801	0.022	0.1696
chr15	102531392	4871540	0.0475	0.2406
chr16	90354753	3249649	0.036	0.221
chr17	81195210	4132322	0.0509	0.2706
chr18	78077248	3561484	0.0456	0.5094
chr19	59128983	1636809	0.0277	0.3557
chr20	63025520	2698221	0.0428	0.229
chr21	48129895	1386038	0.0288	0.1953
chr22	51304566	1286099	0.0251	0.1709
chrMT	16571	32289	1.9485	1.7906
chrX	155270560	4110450	0.0265	0.2048
chrY	59373566	248199	0.0042	0.1105

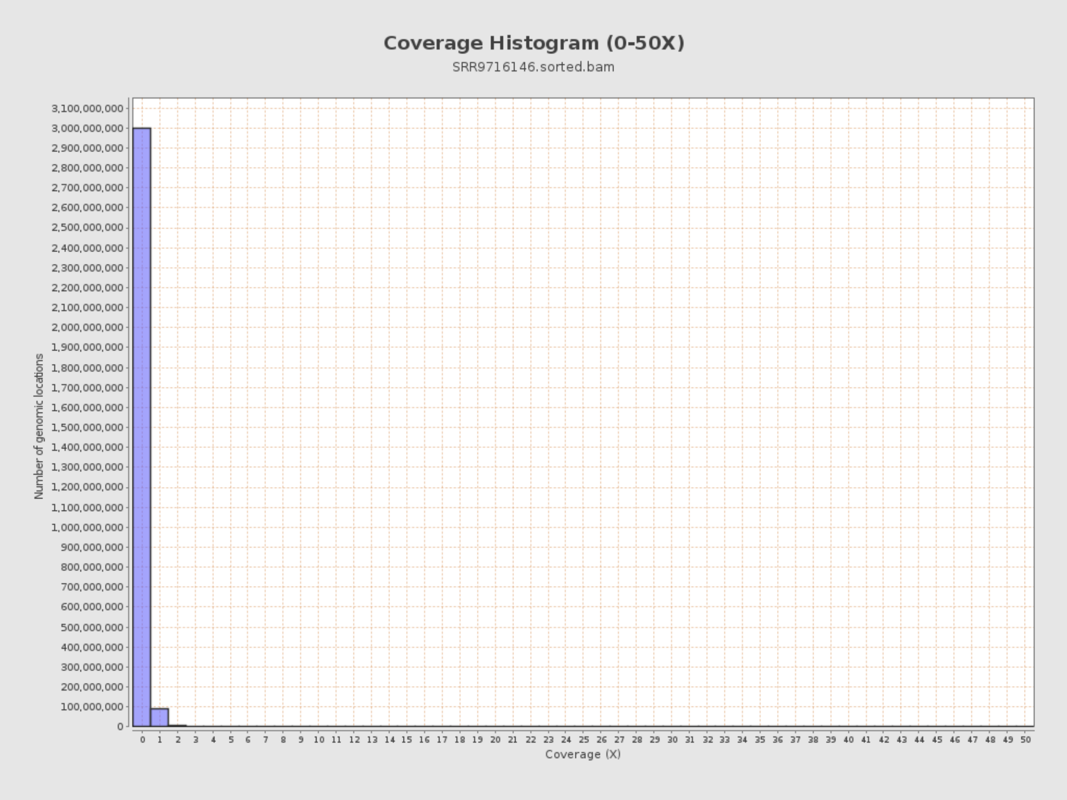
3. Results : Coverage across reference



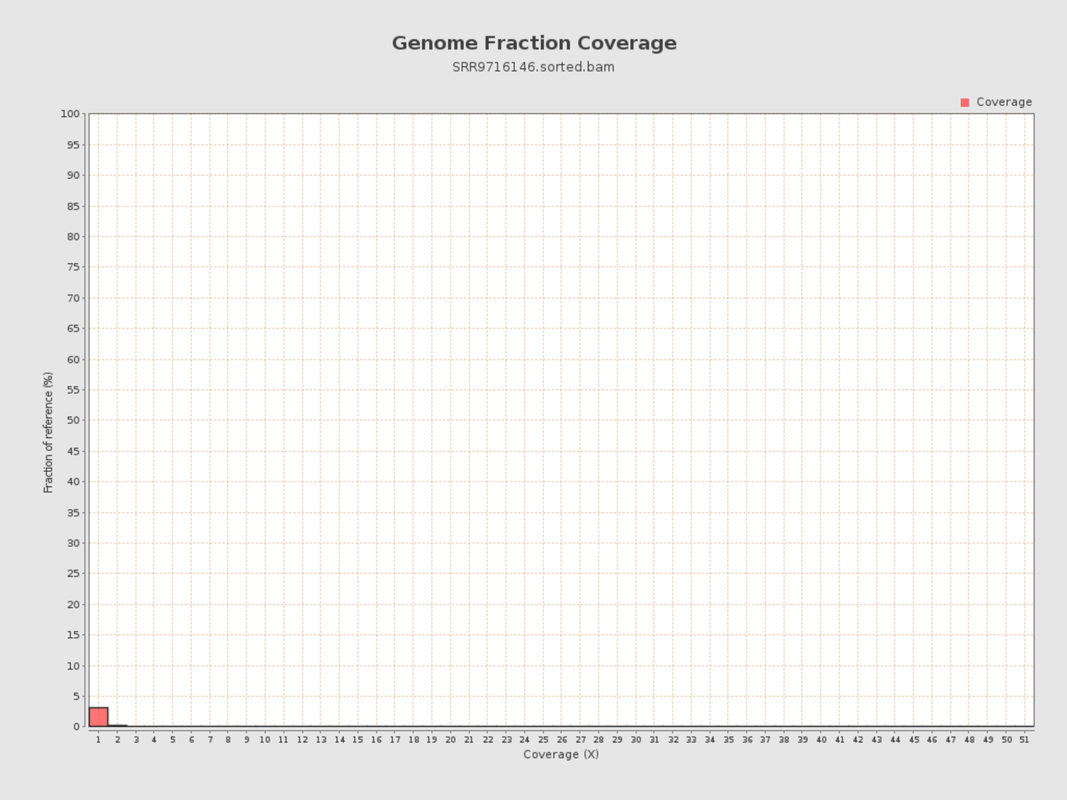
4. Results : Coverage Histogram



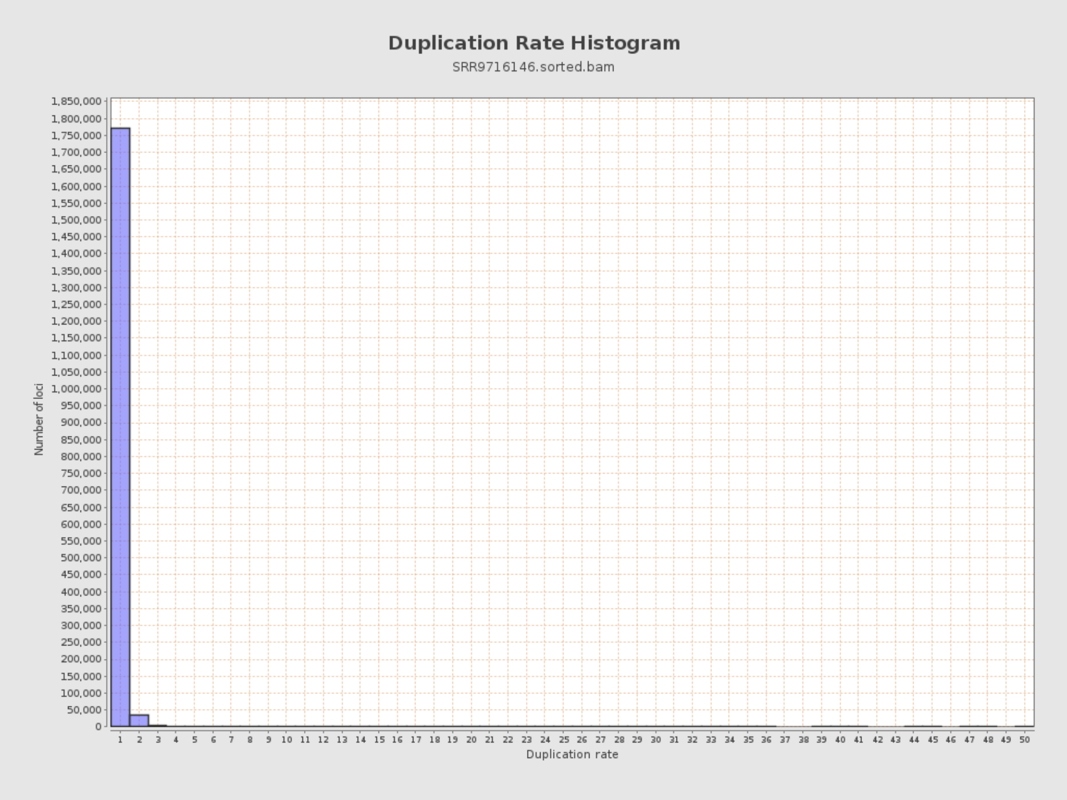
5. Results : Coverage Histogram (0-50X)



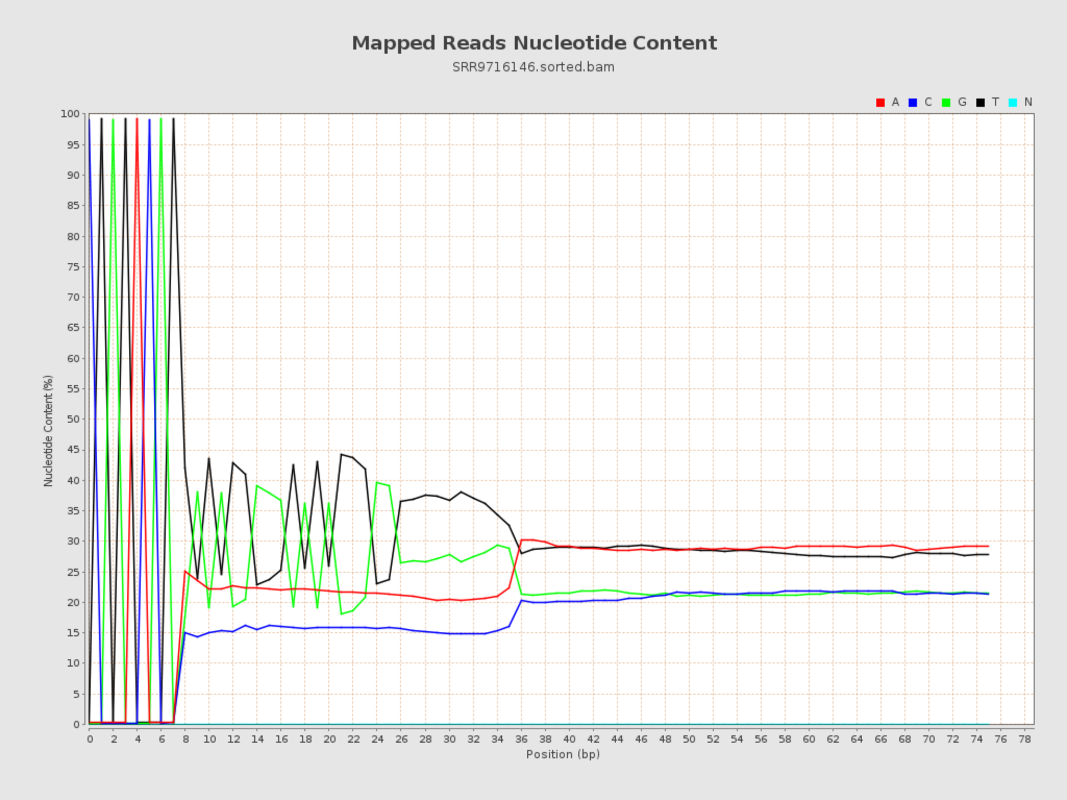
6. Results : Genome Fraction Coverage



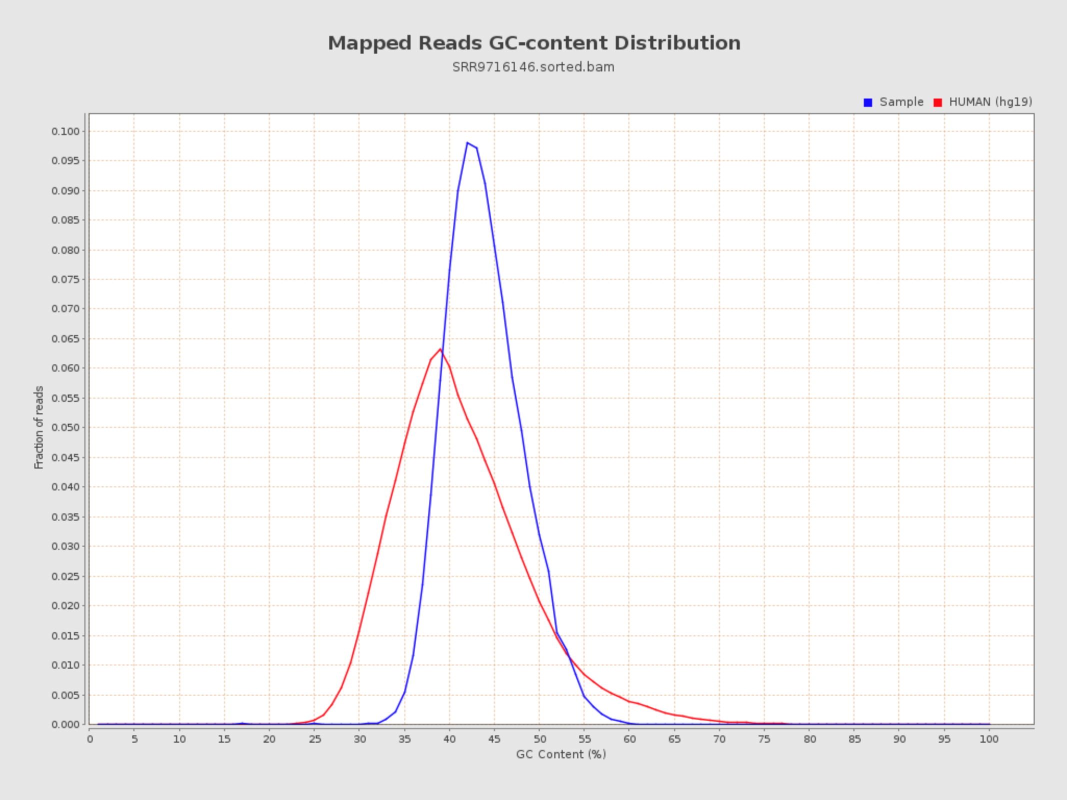
7. Results : Duplication Rate Histogram



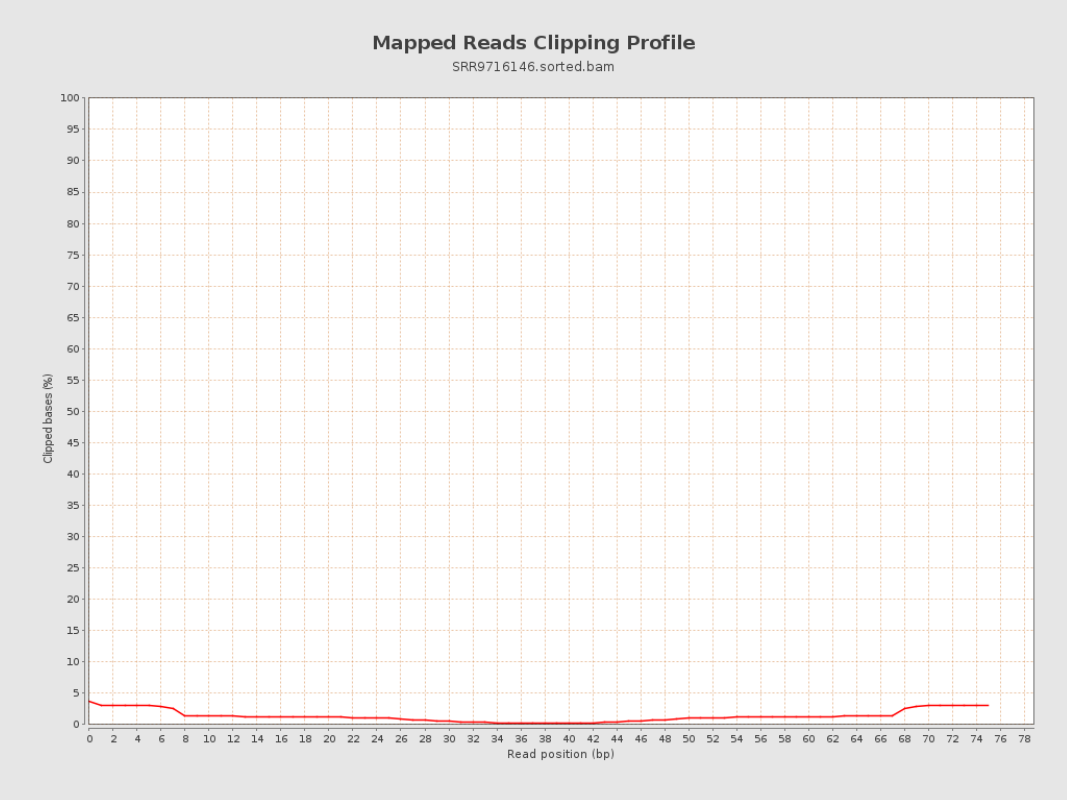
8. Results : Mapped Reads Nucleotide Content



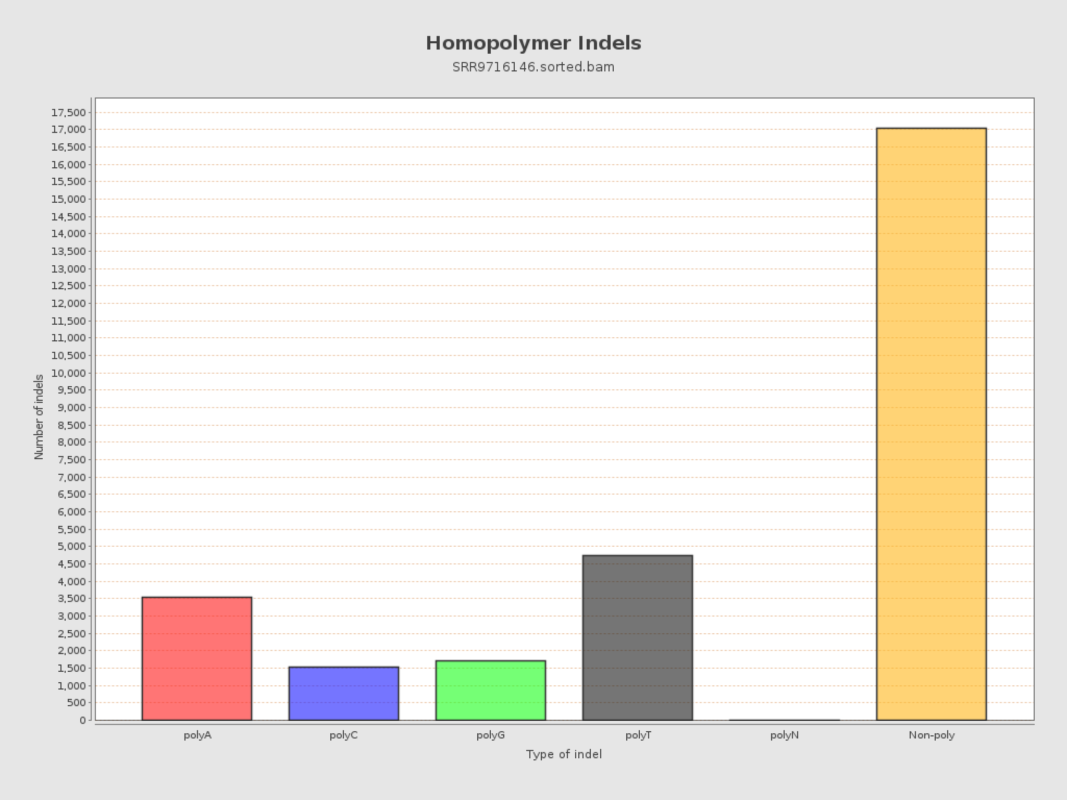
9. Results : Mapped Reads GC-content Distribution



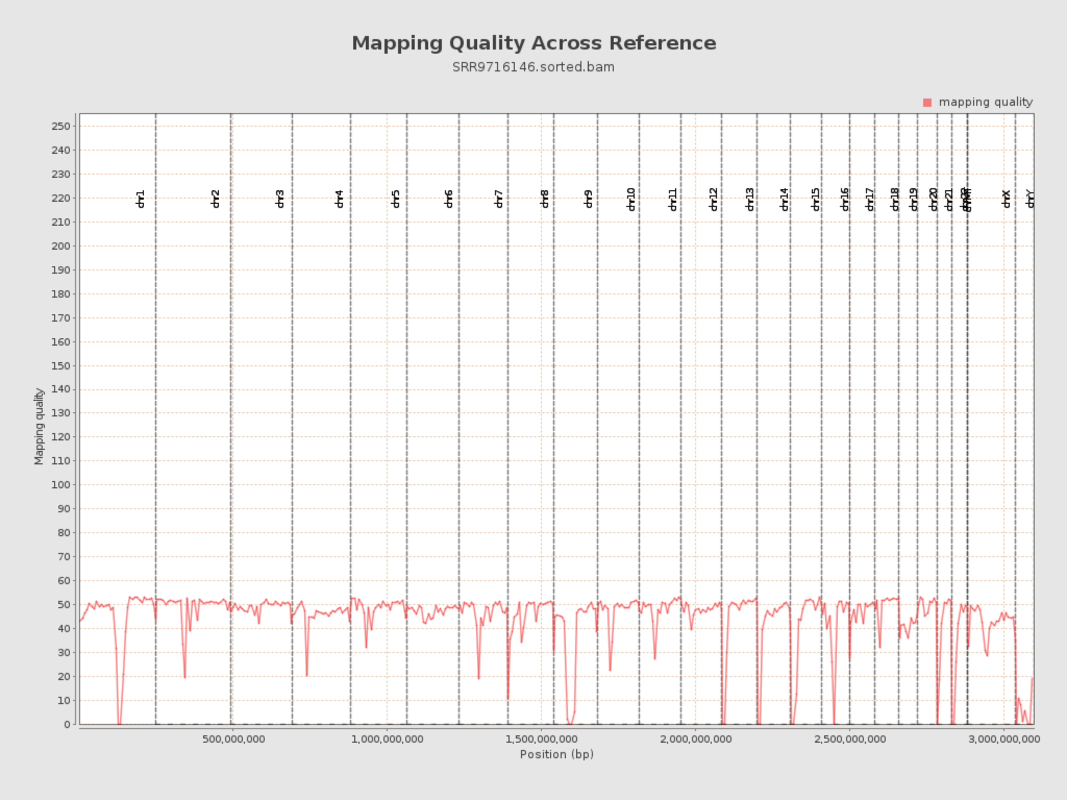
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram