Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 19:53:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716149.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_SRR9716149 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716149.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 19:53:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716149.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	669,928
Mapped reads	481,009 / 71.8%
Unmapped reads	188,919 / 28.2%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	586 / 0.09%
Read min/max/mean length	30 / 76 / 76.03
Duplicated reads (estimated)	27,798 / 4.15%
Duplication rate	4.93%
Clipped reads	480,543 / 71.73%

2.2. ACGT Content

Number/percentage of A's	5,298,975 / 20.8%
Number/percentage of C's	4,985,091 / 19.56%
Number/percentage of T's	8,467,018 / 33.23%
Number/percentage of G's	6,728,185 / 26.41%
Number/percentage of N's	423 / 0%
GC Percentage	45.97%

2.3. Coverage

Mean	0.0082

Standard Deviation	0.1109

2.4. Mapping Quality

Mean Mapping Quality	42.62

2.5. Mismatches and indels

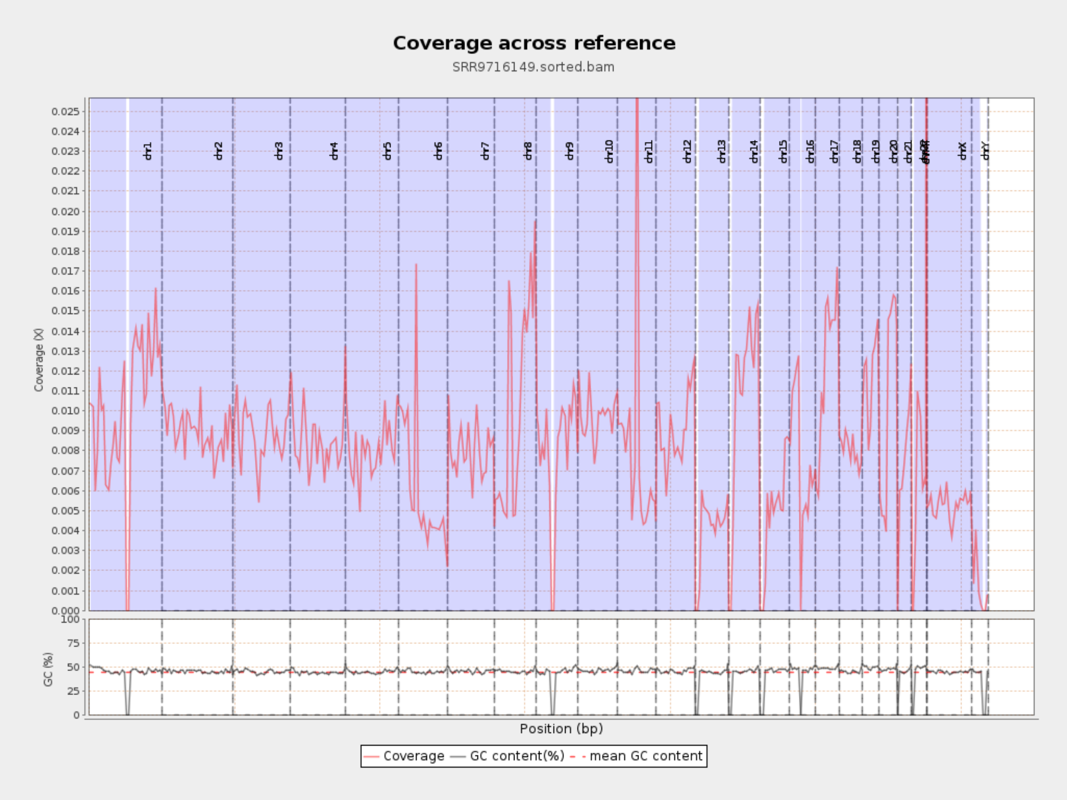
General error rate	0.71%
Mismatches	178,261
Insertions	1,439
Mapped reads with at least one insertion	0.3%
Deletions	3,887
Mapped reads with at least one deletion	0.8%
Homopolymer indels	40.05%

2.6. Chromosome stats

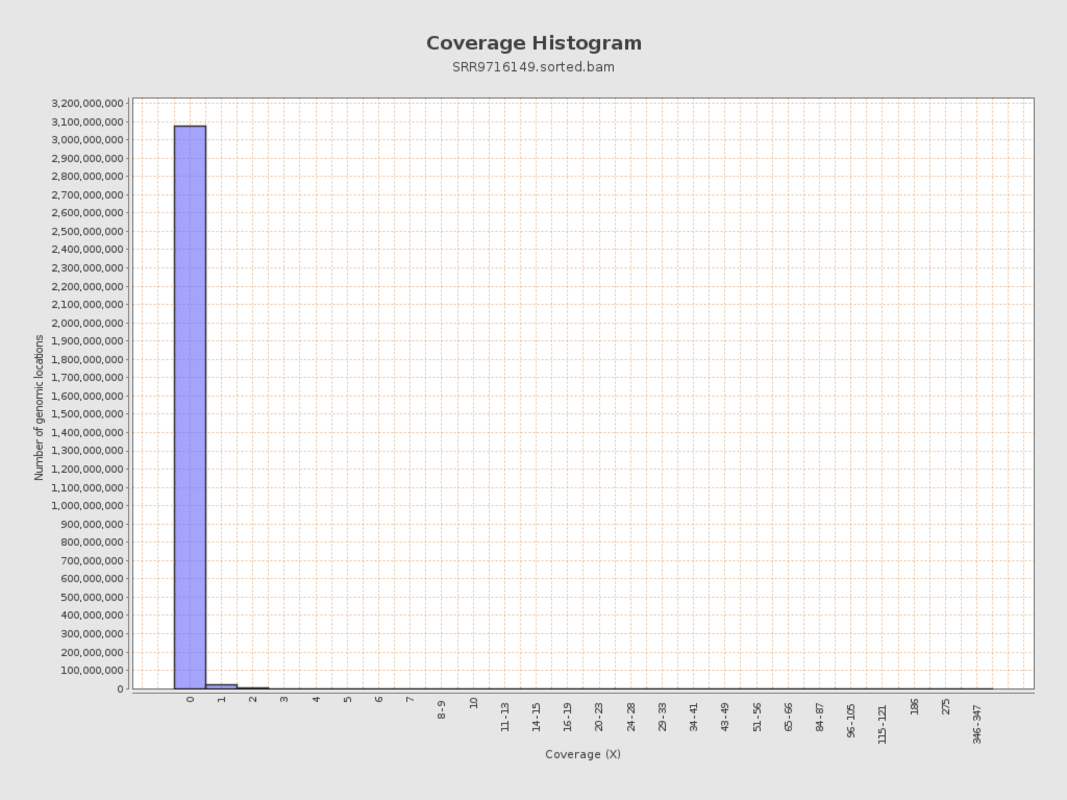
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2518784	0.0101	0.1179
chr2	243199373	2191609	0.009	0.1706
chr3	198022430	1750094	0.0088	0.1039
chr4	191154276	1600005	0.0084	0.1027
chr5	180915260	1459543	0.0081	0.0994
chr6	171115067	1051414	0.0061	0.0994
chr7	159138663	1266233	0.008	0.102

chr8	146364022	1525978	0.0104	0.1173
chr9	141213431	1110812	0.0079	0.1007
chr10	135534747	1313759	0.0097	0.1154
chr11	135006516	1143133	0.0085	0.1079
chr12	133851895	1217341	0.0091	0.107
chr13	115169878	460628	0.004	0.0714
chr14	107349540	1153588	0.0107	0.1177
chr15	102531392	495149	0.0048	0.0773
chr16	90354753	681894	0.0075	0.1004
chr17	81195210	1020478	0.0126	0.1281
chr18	78077248	628482	0.008	0.1053
chr19	59128983	689744	0.0117	0.1405
chr20	63025520	653764	0.0104	0.1202
chr21	48129895	358433	0.0074	0.0991
chr22	51304566	298445	0.0058	0.0895
chrMT	16571	2094	0.1264	0.3745
chrX	155270560	822161	0.0053	0.0817
chrY	59373566	72686	0.0012	0.043

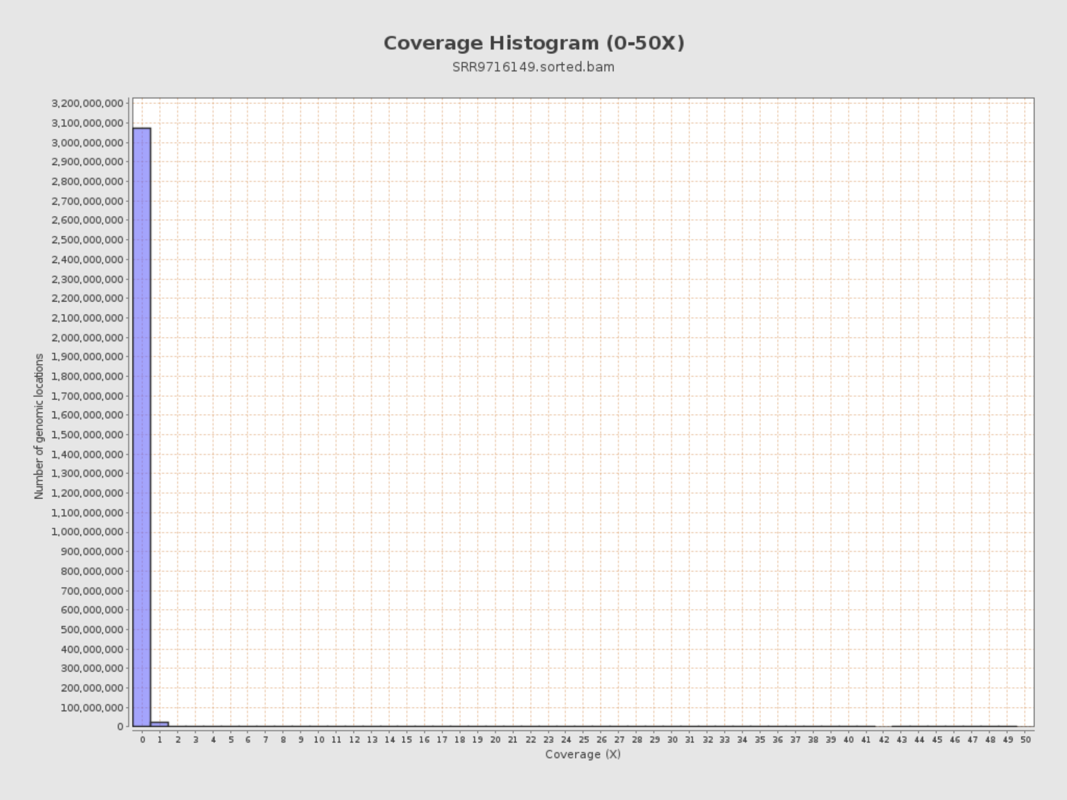
3. Results : Coverage across reference



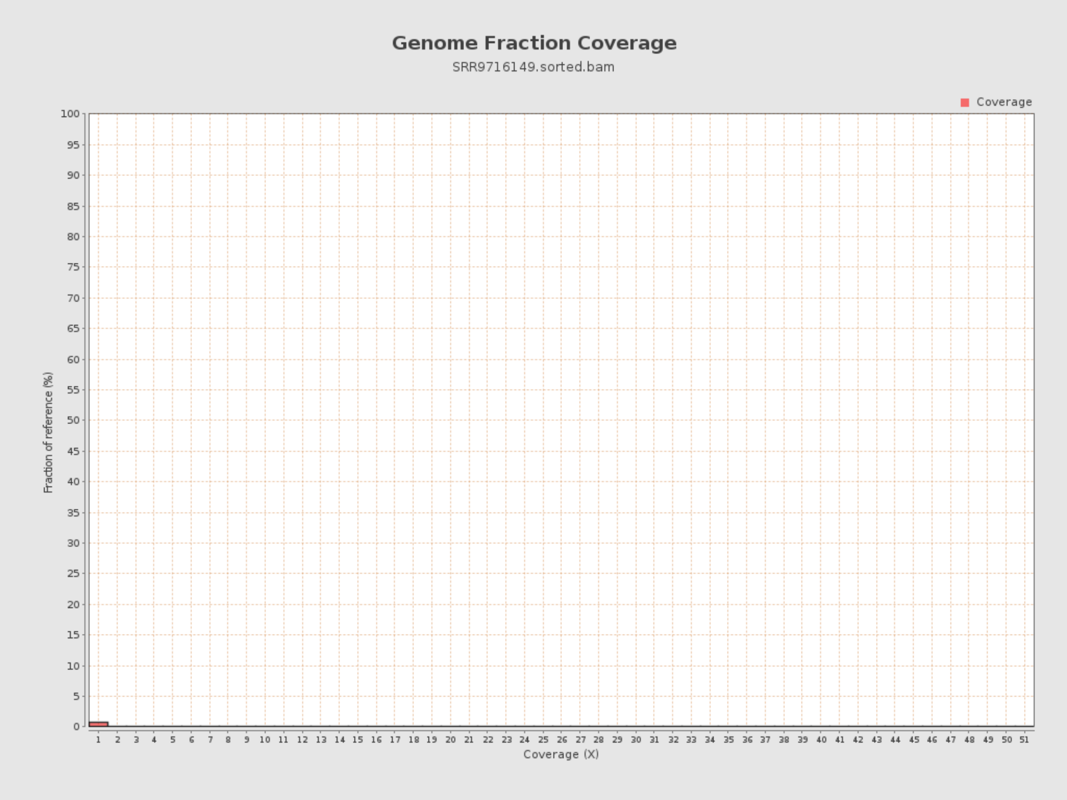
4. Results : Coverage Histogram



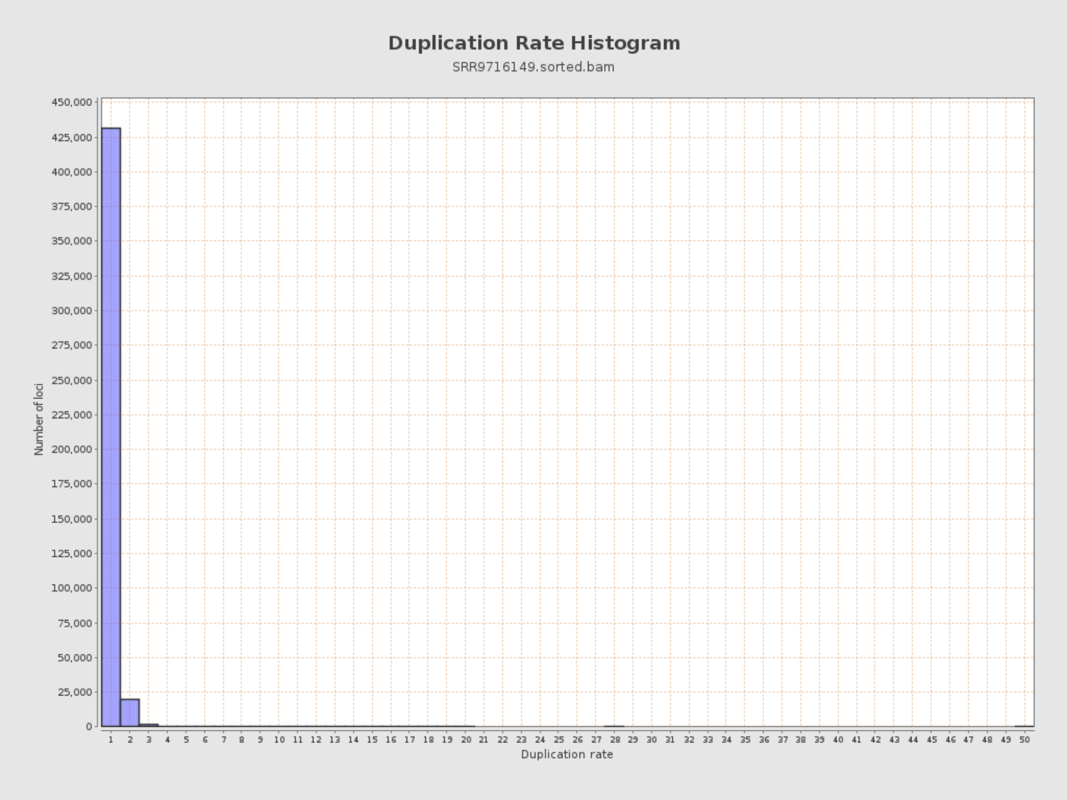
5. Results : Coverage Histogram (0-50X)



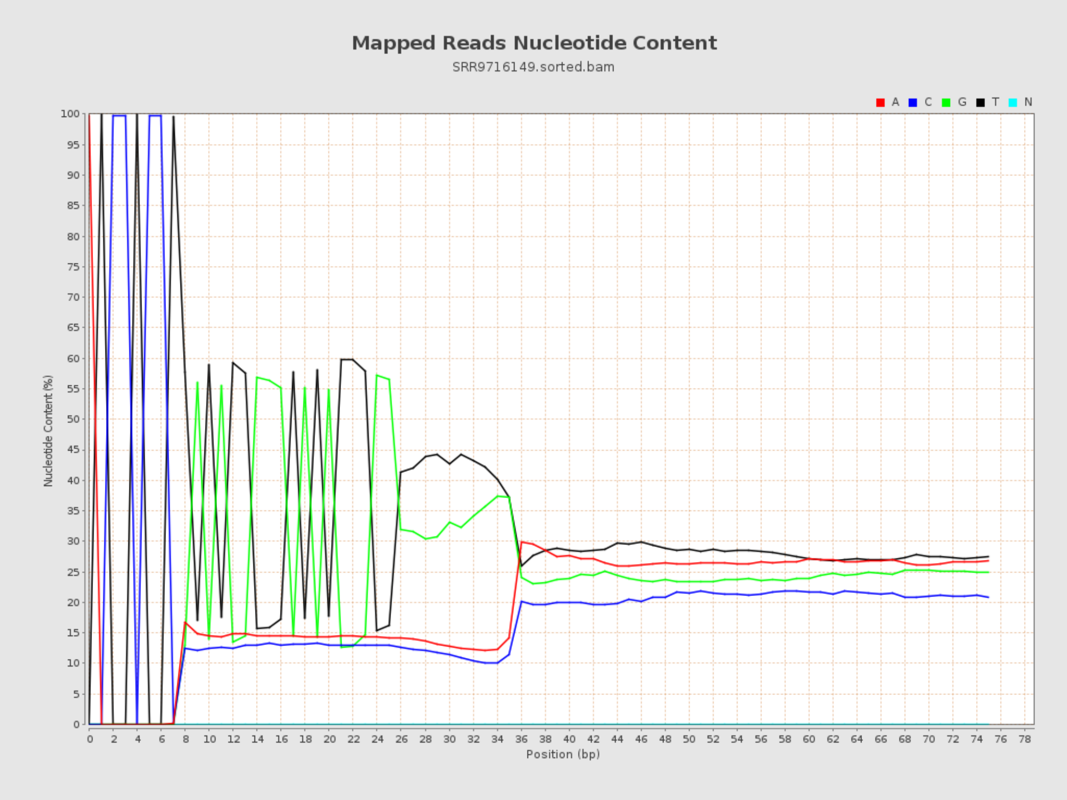
6. Results : Genome Fraction Coverage



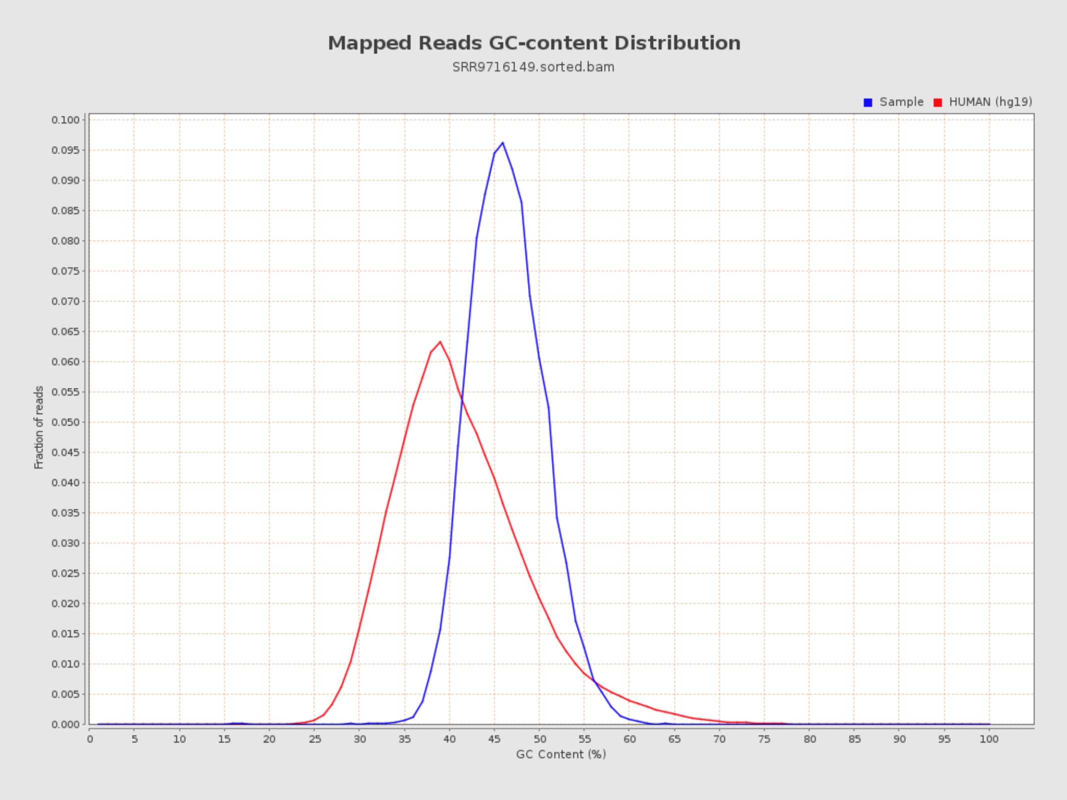
7. Results : Duplication Rate Histogram



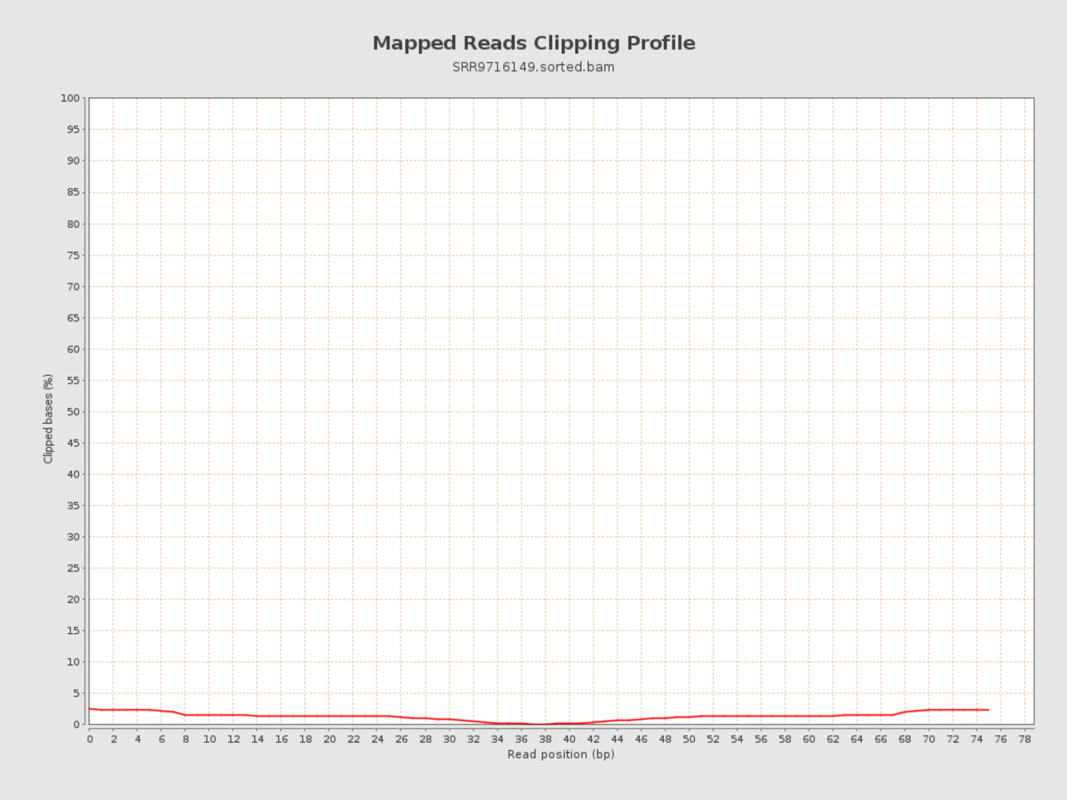
8. Results : Mapped Reads Nucleotide Content



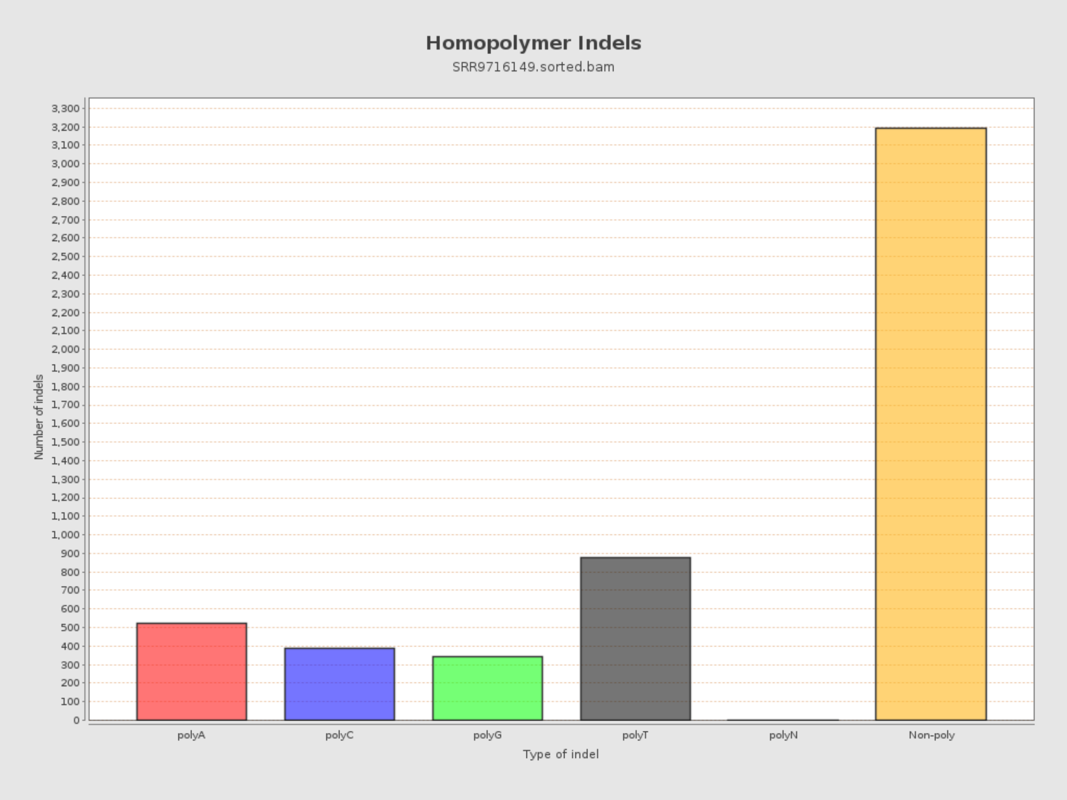
9. Results : Mapped Reads GC-content Distribution



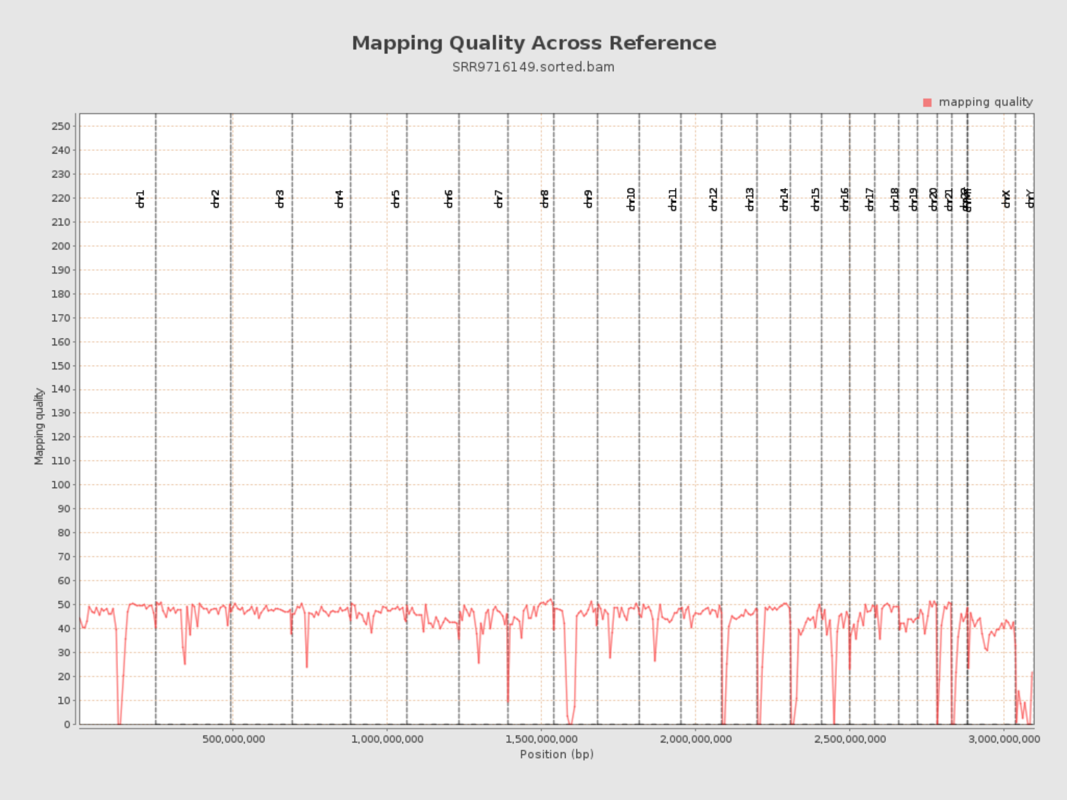
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram