Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 06:31:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716305.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_SRR9716305 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716305.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 06:31:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716305.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	708,993
Mapped reads	553,106 / 78.01%
Unmapped reads	155,887 / 21.99%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,631 / 0.23%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	13,907 / 1.96%
Duplication rate	2.01%
Clipped reads	553,373 / 78.05%

2.2. ACGT Content

Number/percentage of A's	8,273,788 / 26.05%
Number/percentage of C's	5,574,245 / 17.55%
Number/percentage of T's	10,083,327 / 31.75%
Number/percentage of G's	7,829,039 / 24.65%
Number/percentage of N's	246 / 0%
GC Percentage	42.2%

2.3. Coverage

Mean	0.0103

Standard Deviation	0.1229

2.4. Mapping Quality

Mean Mapping Quality	45.18

2.5. Mismatches and indels

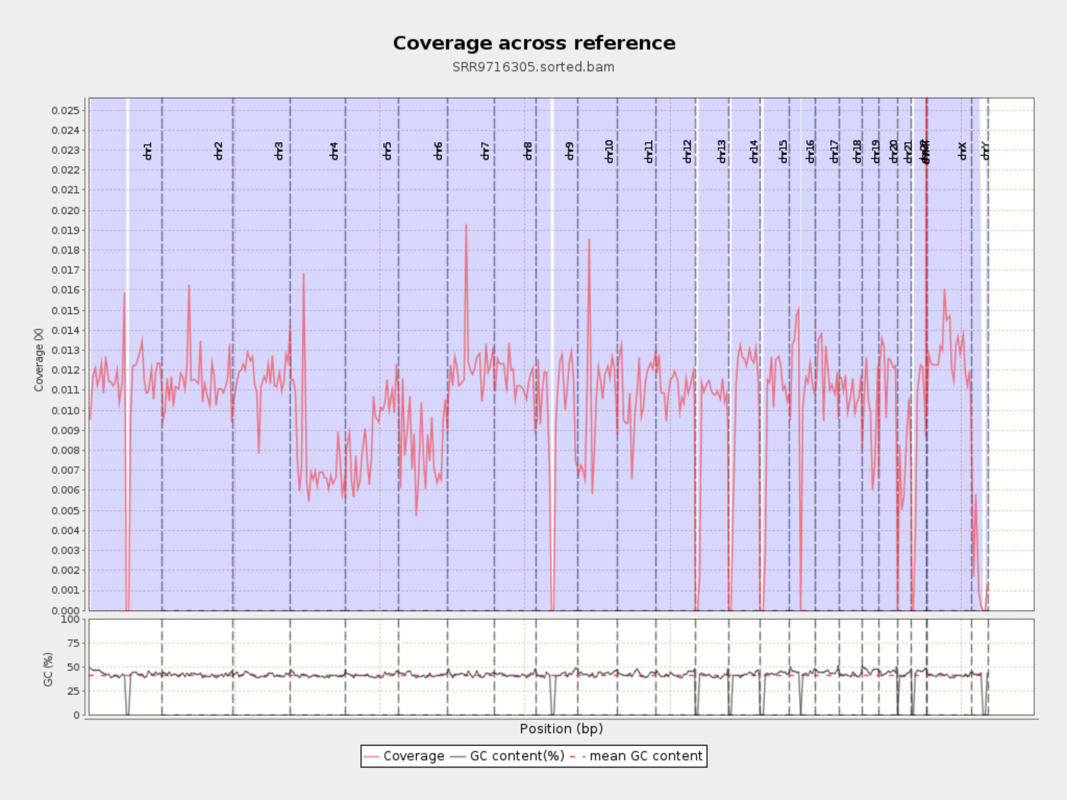
General error rate	0.51%
Mismatches	159,097
Insertions	2,201
Mapped reads with at least one insertion	0.4%
Deletions	6,555
Mapped reads with at least one deletion	1.18%
Homopolymer indels	42.25%

2.6. Chromosome stats

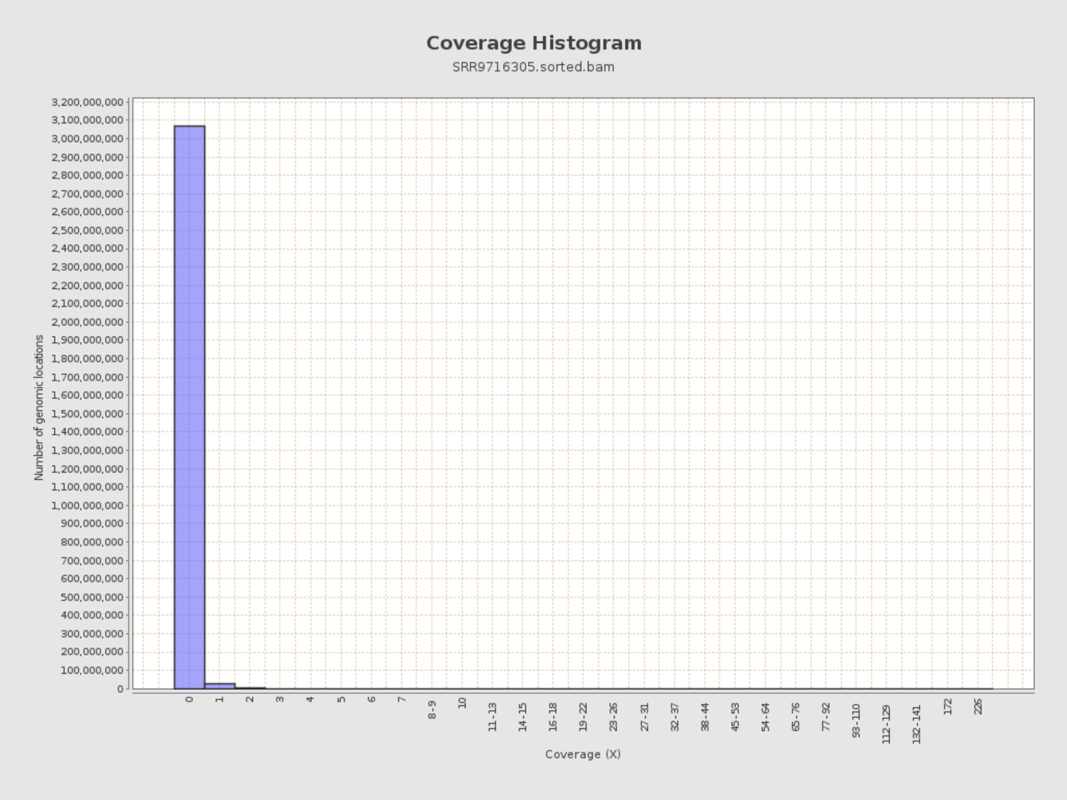
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2751638	0.011	0.1563
chr2	243199373	2772097	0.0114	0.1538
chr3	198022430	2304552	0.0116	0.1129
chr4	191154276	1459077	0.0076	0.0971
chr5	180915260	1599133	0.0088	0.0986
chr6	171115067	1400031	0.0082	0.0985
chr7	159138663	1964821	0.0123	0.1662

chr8	146364022	1689116	0.0115	0.1219
chr9	141213431	1370966	0.0097	0.1107
chr10	135534747	1408898	0.0104	0.1341
chr11	135006516	1465736	0.0109	0.1189
chr12	133851895	1492883	0.0112	0.1108
chr13	115169878	1054686	0.0092	0.1003
chr14	107349540	1111177	0.0104	0.1077
chr15	102531392	951174	0.0093	0.1009
chr16	90354753	1013049	0.0112	0.1175
chr17	81195210	954029	0.0117	0.1162
chr18	78077248	853404	0.0109	0.1537
chr19	59128983	572254	0.0097	0.1305
chr20	63025520	758408	0.012	0.1164
chr21	48129895	335470	0.007	0.0922
chr22	51304566	400547	0.0078	0.093
chrMT	16571	989	0.0597	0.2751
chrX	155270560	1984534	0.0128	0.1227
chrY	59373566	102401	0.0017	0.0571

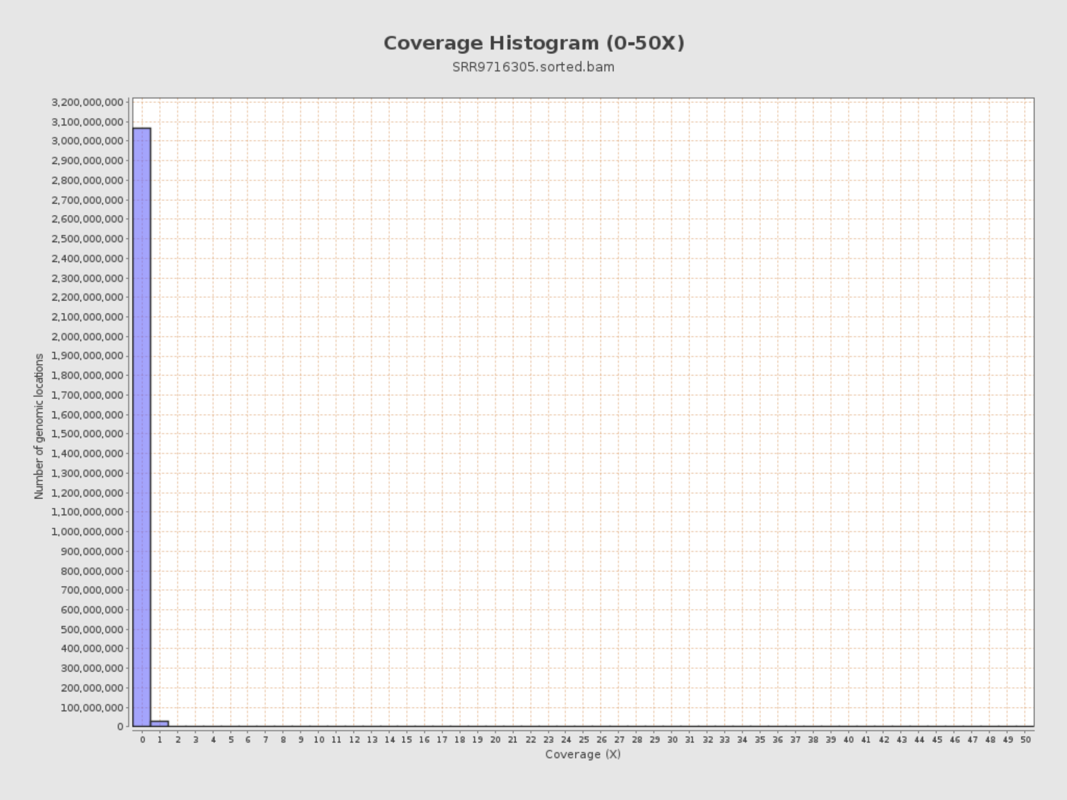
3. Results : Coverage across reference



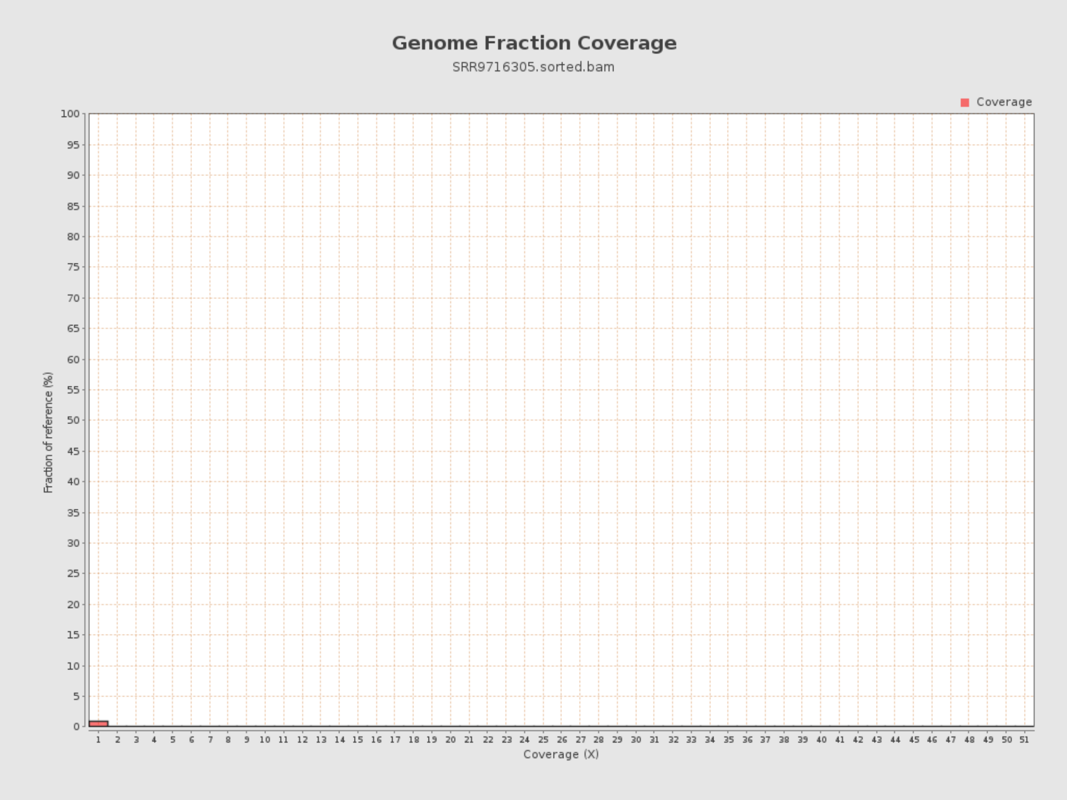
4. Results : Coverage Histogram



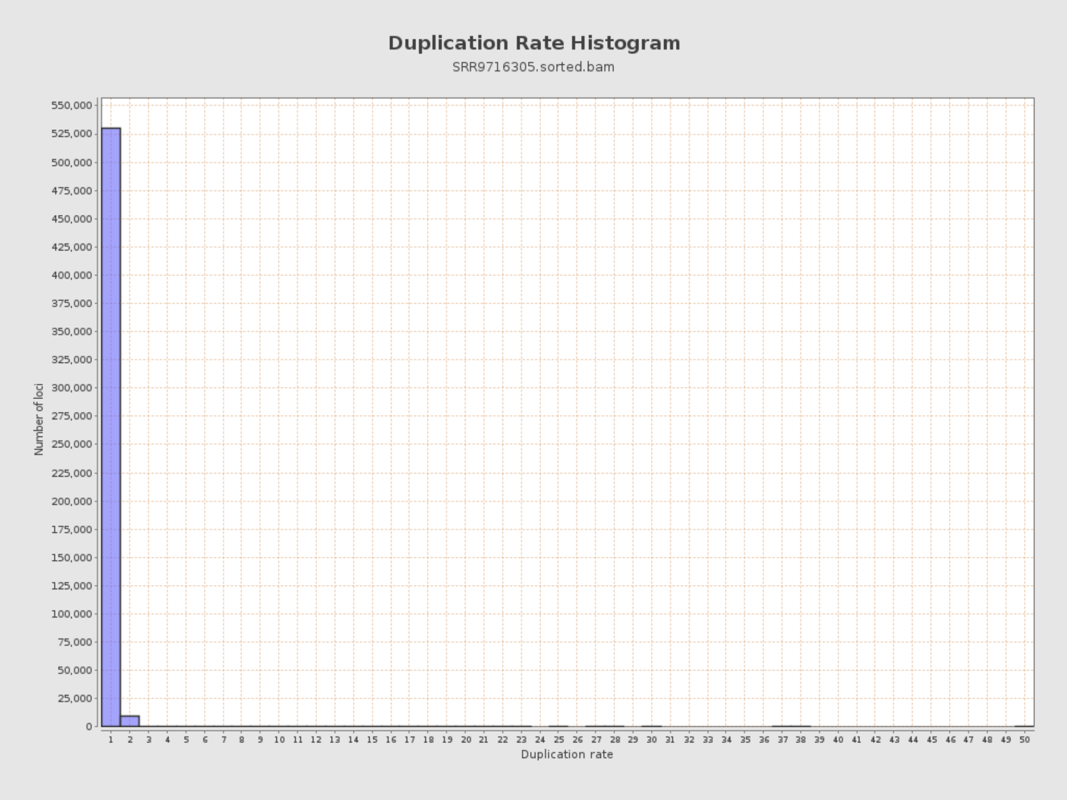
5. Results : Coverage Histogram (0-50X)



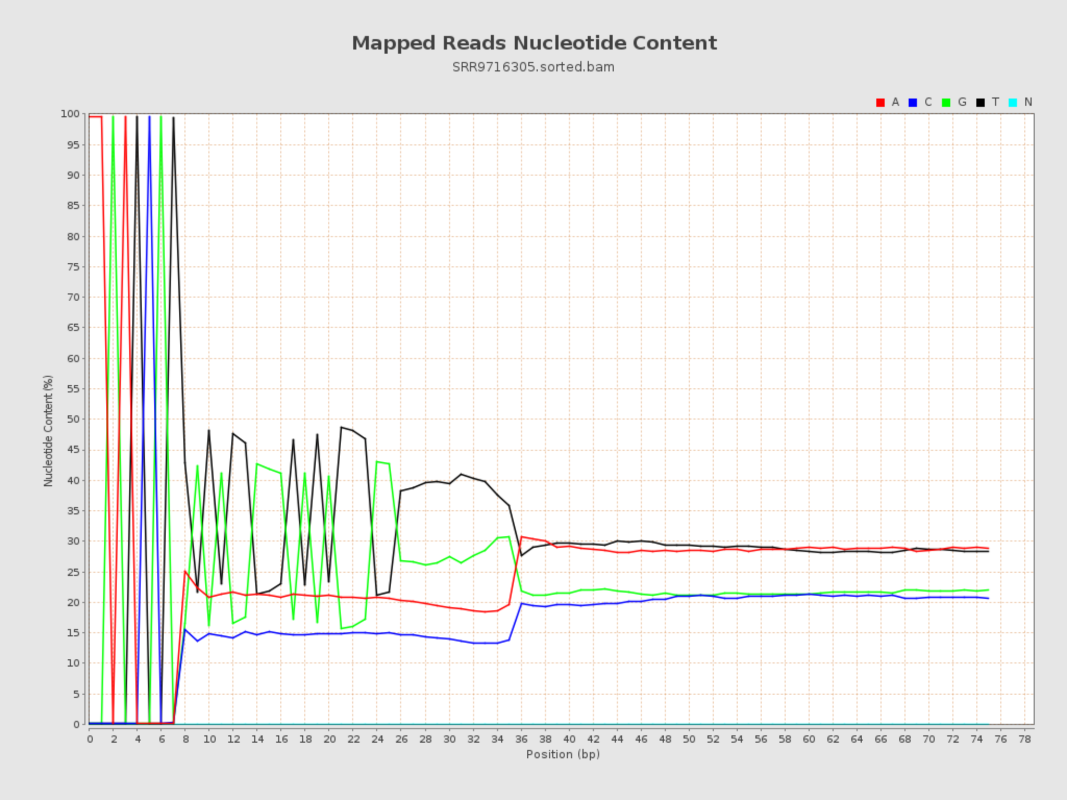
6. Results : Genome Fraction Coverage



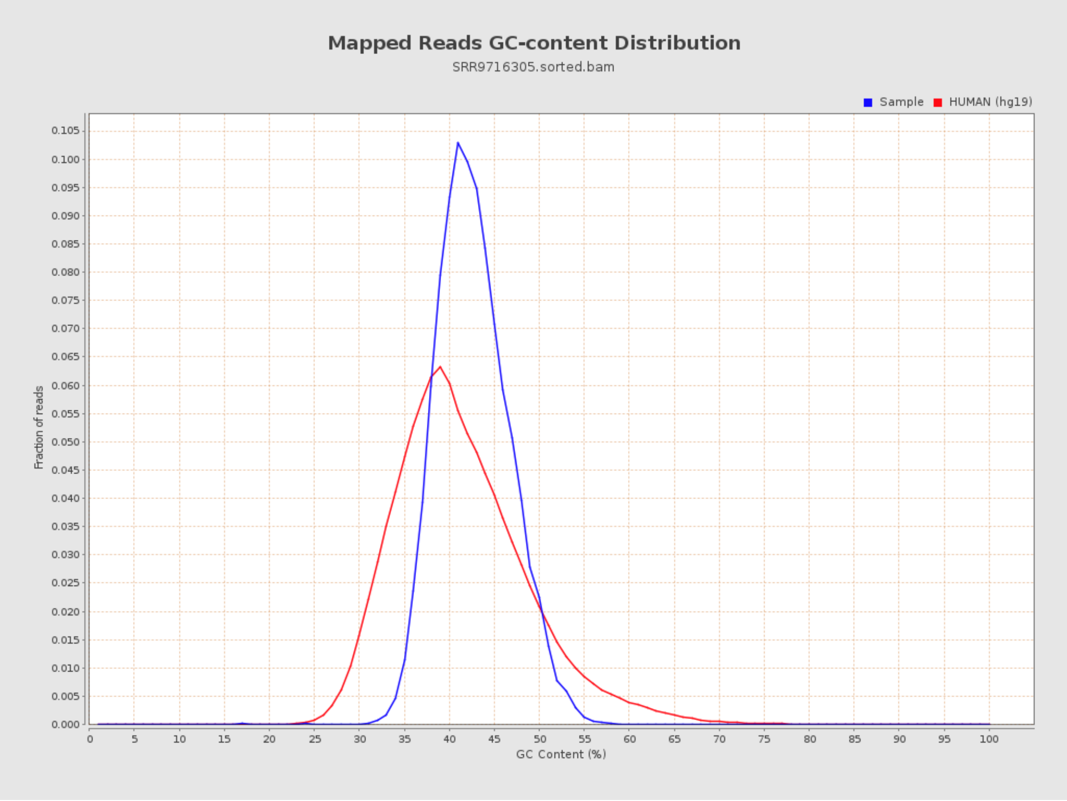
7. Results : Duplication Rate Histogram



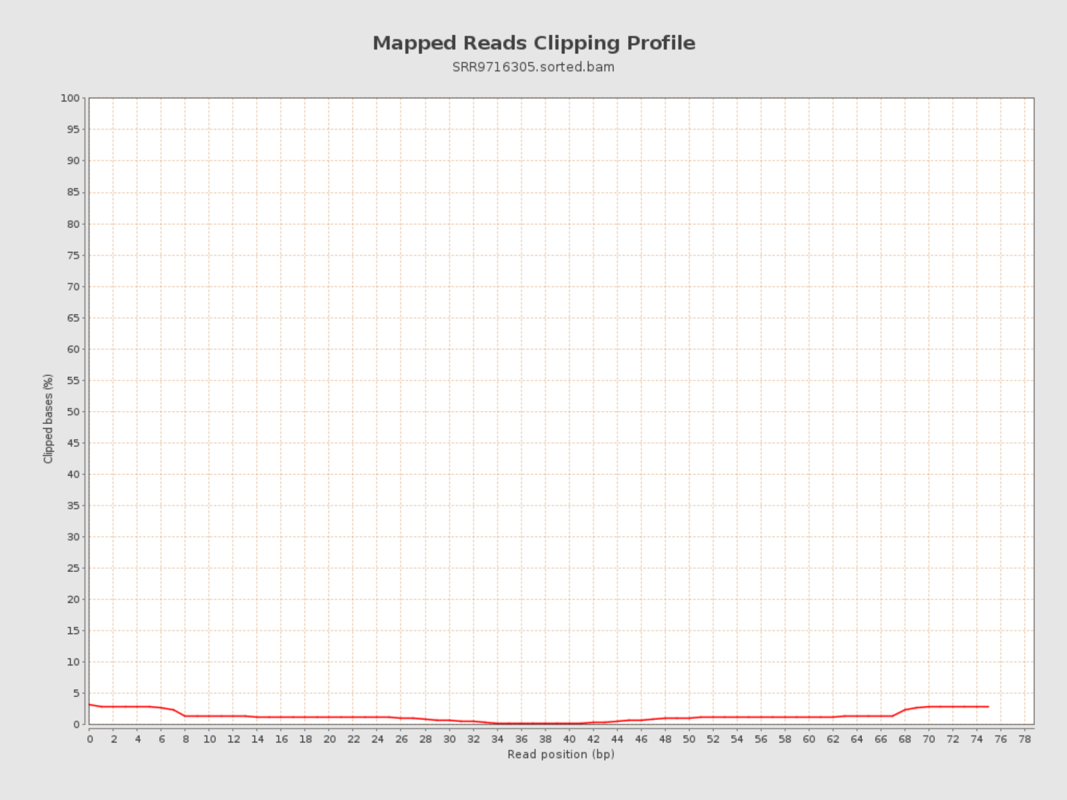
8. Results : Mapped Reads Nucleotide Content



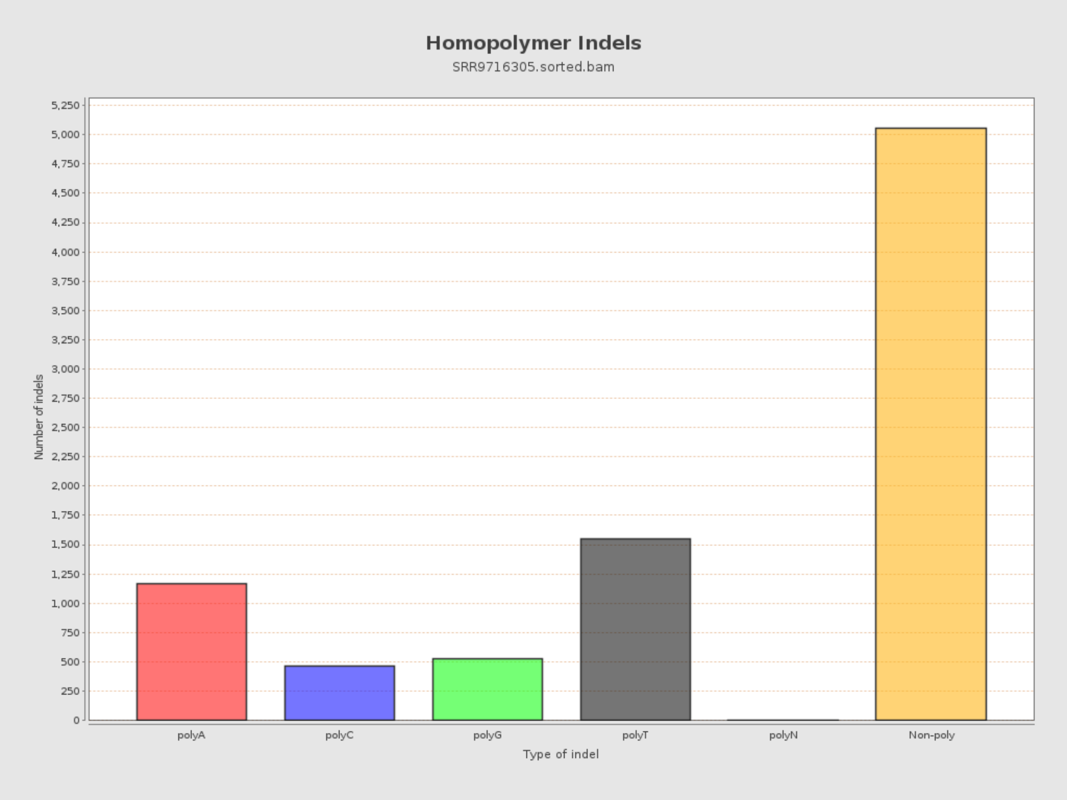
9. Results : Mapped Reads GC-content Distribution



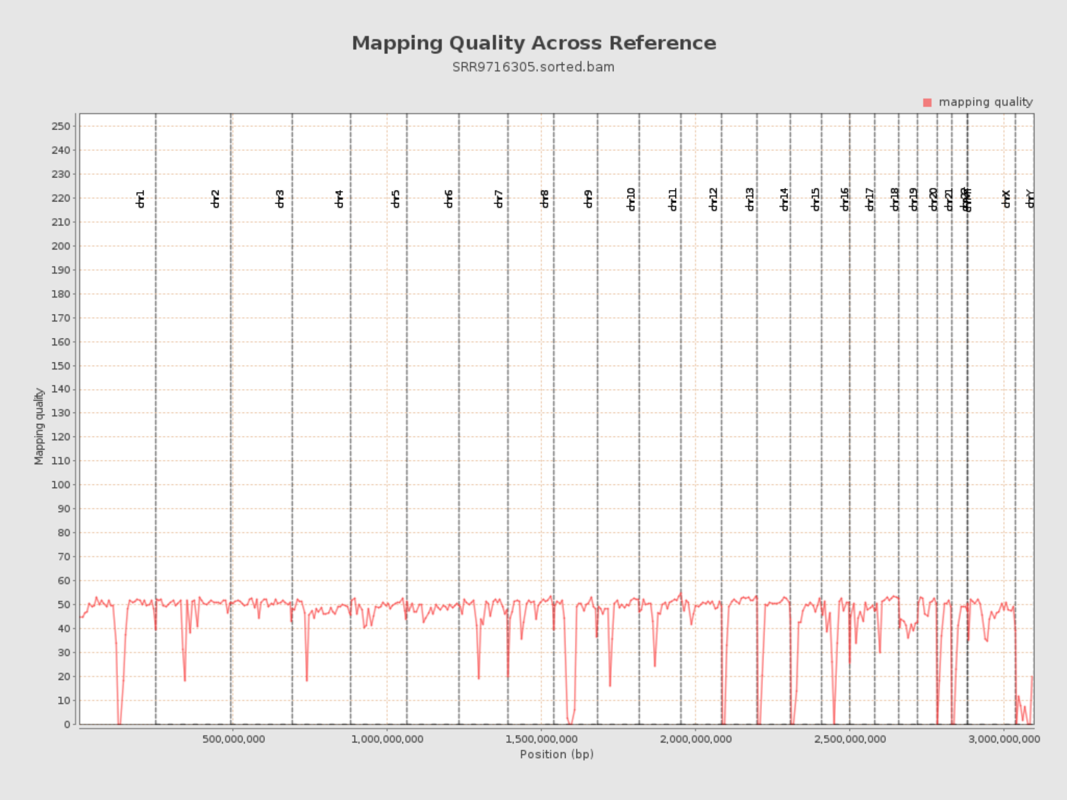
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram