Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 07:57:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716330.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_SRR9716330 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716330.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 07:57:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716330.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,792,796
Mapped reads	1,625,805 / 90.69%
Unmapped reads	166,991 / 9.31%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,690 / 0.37%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	60,979 / 3.4%
Duplication rate	2.99%
Clipped reads	1,628,275 / 90.82%

2.2. ACGT Content

Number/percentage of A's	23,094,786 / 24.7%
Number/percentage of C's	17,856,896 / 19.1%
Number/percentage of T's	29,546,288 / 31.6%
Number/percentage of G's	23,013,941 / 24.61%
Number/percentage of N's	2,011 / 0%
GC Percentage	43.71%

2.3. Coverage

Mean	0.0302

Standard Deviation	0.2433

2.4. Mapping Quality

Mean Mapping Quality	45.32

2.5. Mismatches and indels

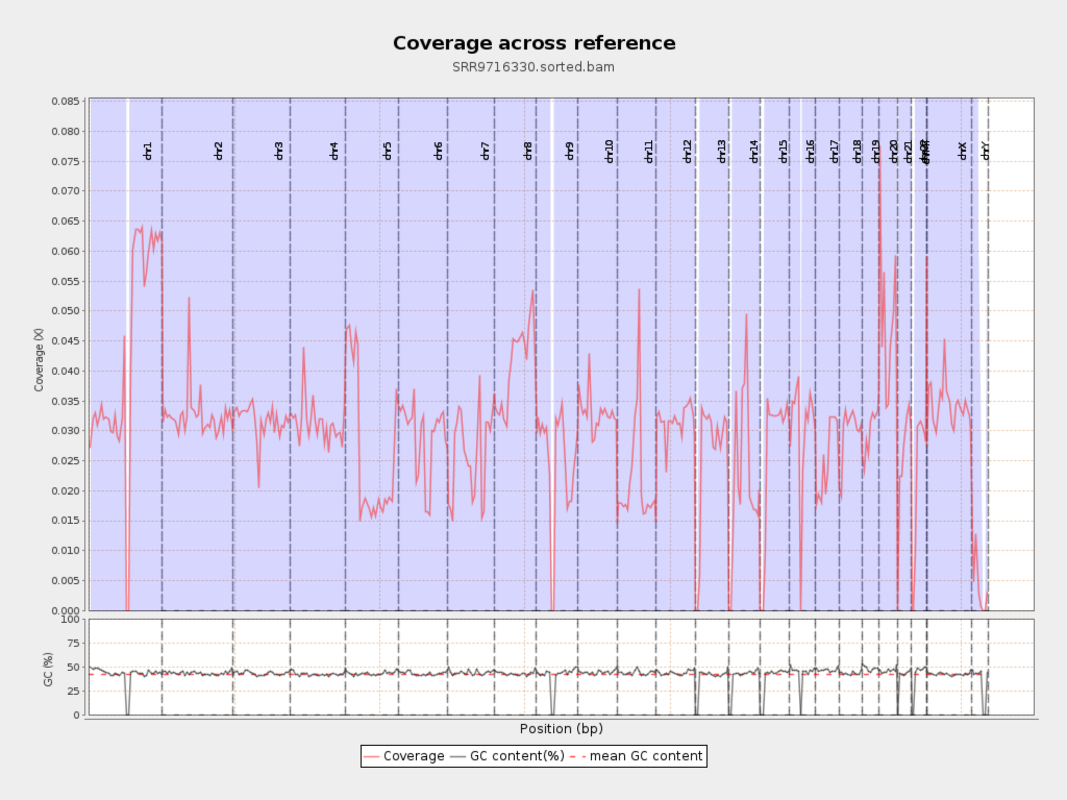
General error rate	0.49%
Mismatches	445,539
Insertions	6,758
Mapped reads with at least one insertion	0.41%
Deletions	13,971
Mapped reads with at least one deletion	0.85%
Homopolymer indels	39.5%

2.6. Chromosome stats

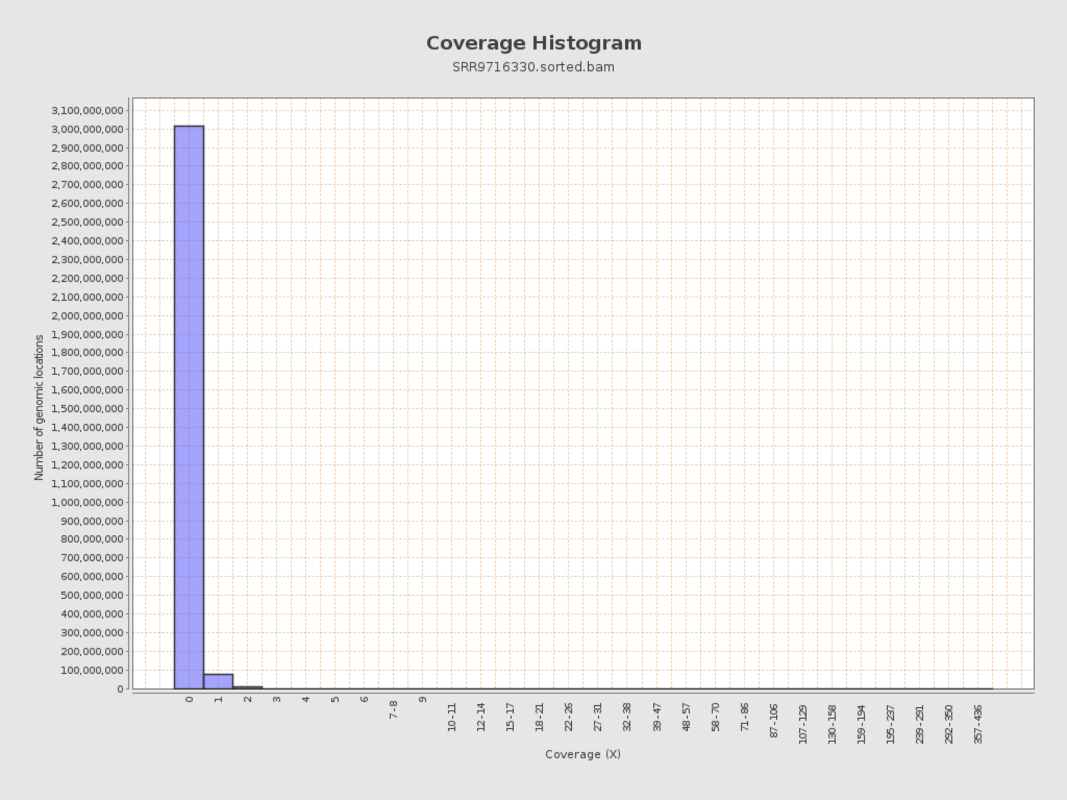
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10550962	0.0423	0.3887
chr2	243199373	7929463	0.0326	0.2751
chr3	198022430	6272815	0.0317	0.1962
chr4	191154276	5975427	0.0313	0.212
chr5	180915260	4716547	0.0261	0.1803
chr6	171115067	4971877	0.0291	0.2024
chr7	159138663	4120827	0.0259	0.2138

chr8	146364022	6046367	0.0413	0.2707
chr9	141213431	3411806	0.0242	0.2502
chr10	135534747	4477649	0.033	0.2341
chr11	135006516	2973829	0.022	0.227
chr12	133851895	4246722	0.0317	0.1992
chr13	115169878	2940807	0.0255	0.1757
chr14	107349540	2334476	0.0217	0.1716
chr15	102531392	2723901	0.0266	0.1803
chr16	90354753	2749691	0.0304	0.2055
chr17	81195210	2056596	0.0253	0.1826
chr18	78077248	2338403	0.0299	0.4336
chr19	59128983	1762814	0.0298	0.2766
chr20	63025520	3053038	0.0484	0.2488
chr21	48129895	1229980	0.0256	0.1891
chr22	51304566	1077989	0.021	0.1586
chrMT	16571	979	0.0591	0.2504
chrX	155270560	5324241	0.0343	0.2289
chrY	59373566	250165	0.0042	0.0954

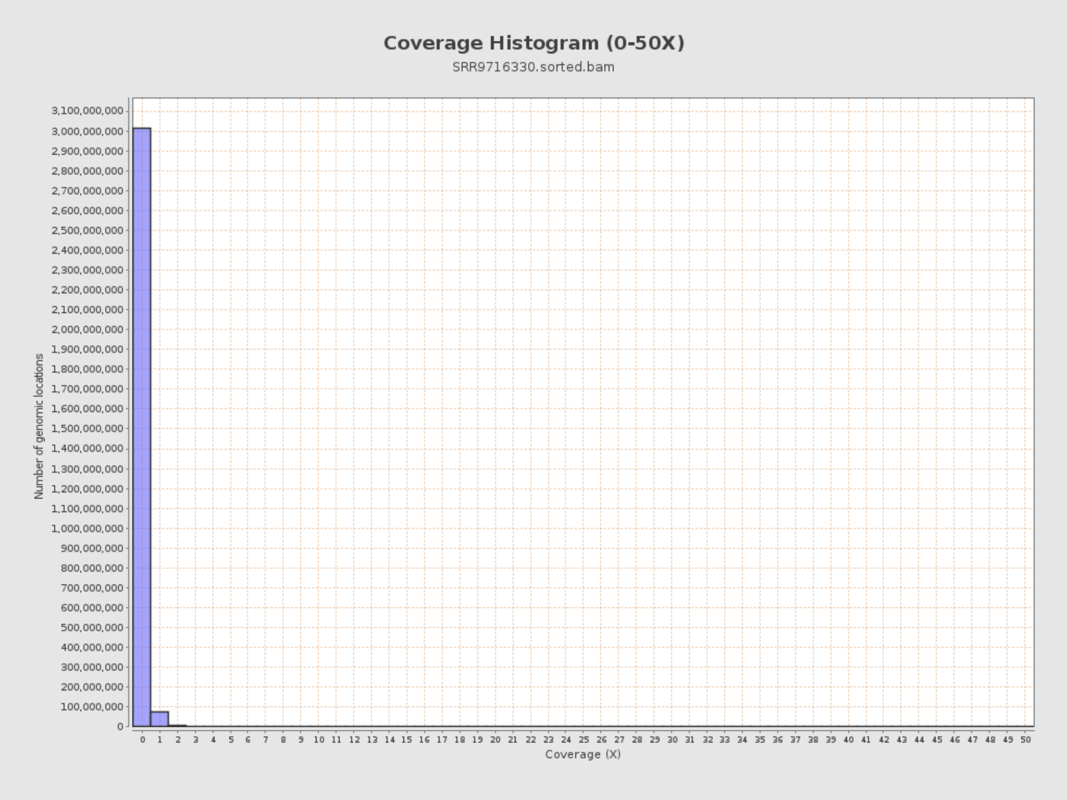
3. Results : Coverage across reference



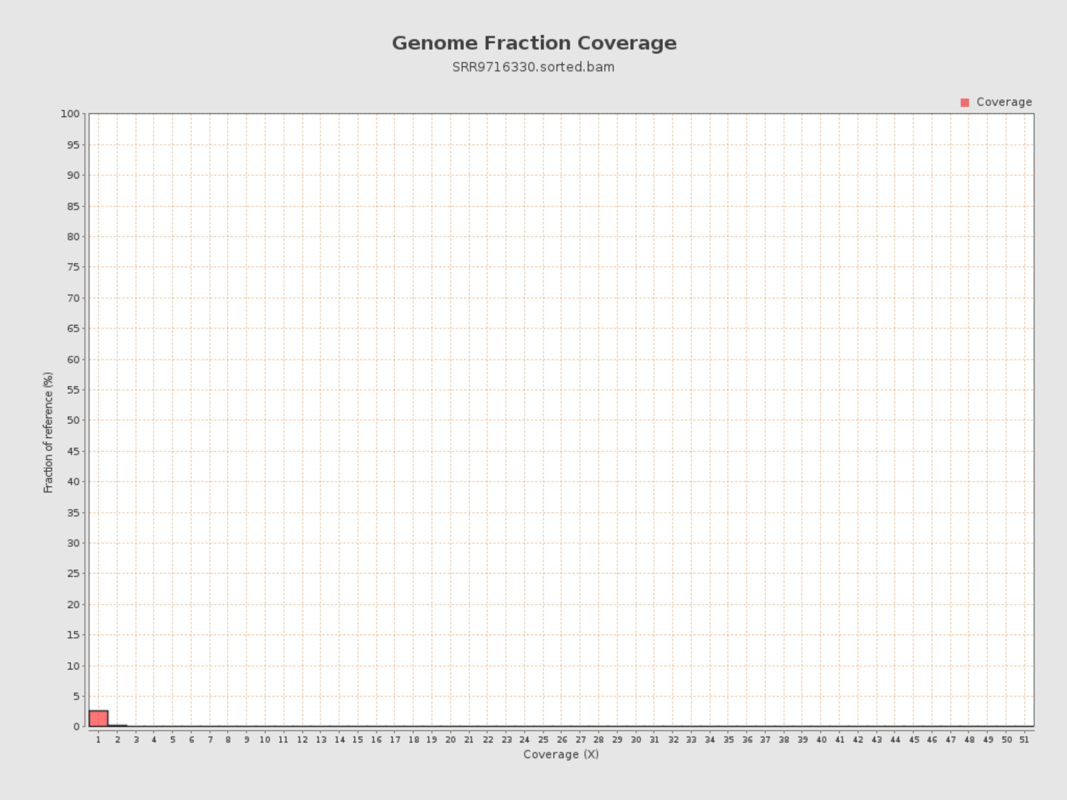
4. Results : Coverage Histogram



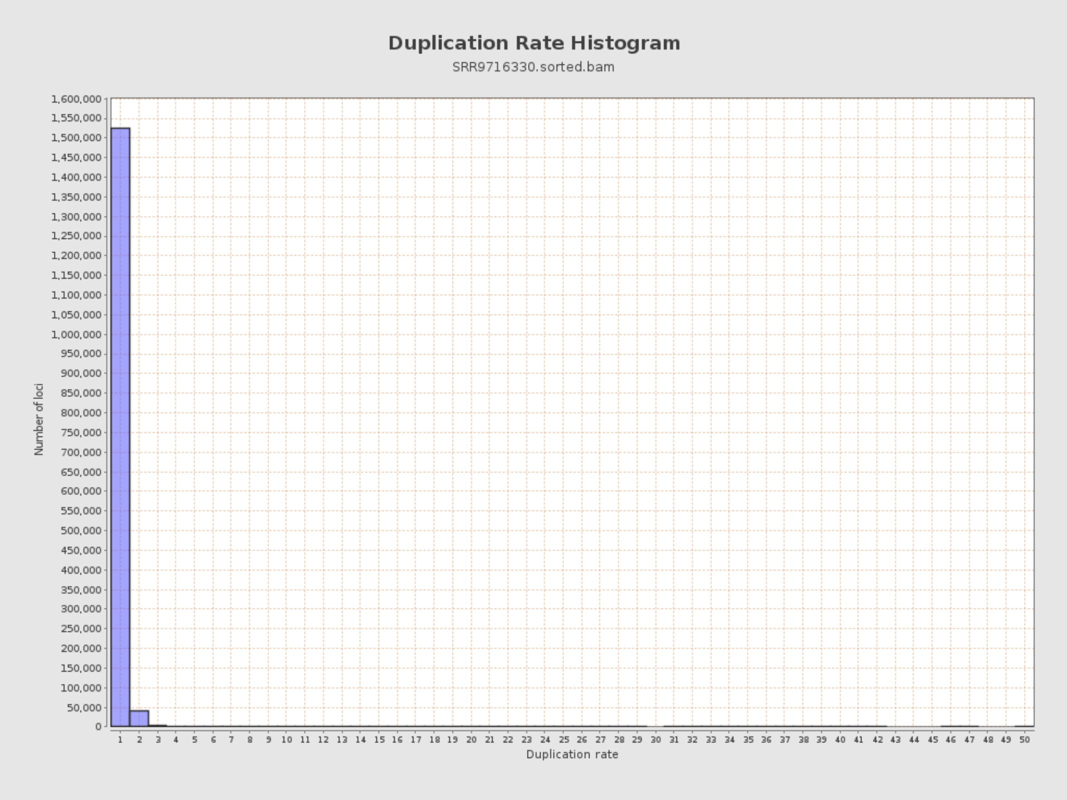
5. Results : Coverage Histogram (0-50X)



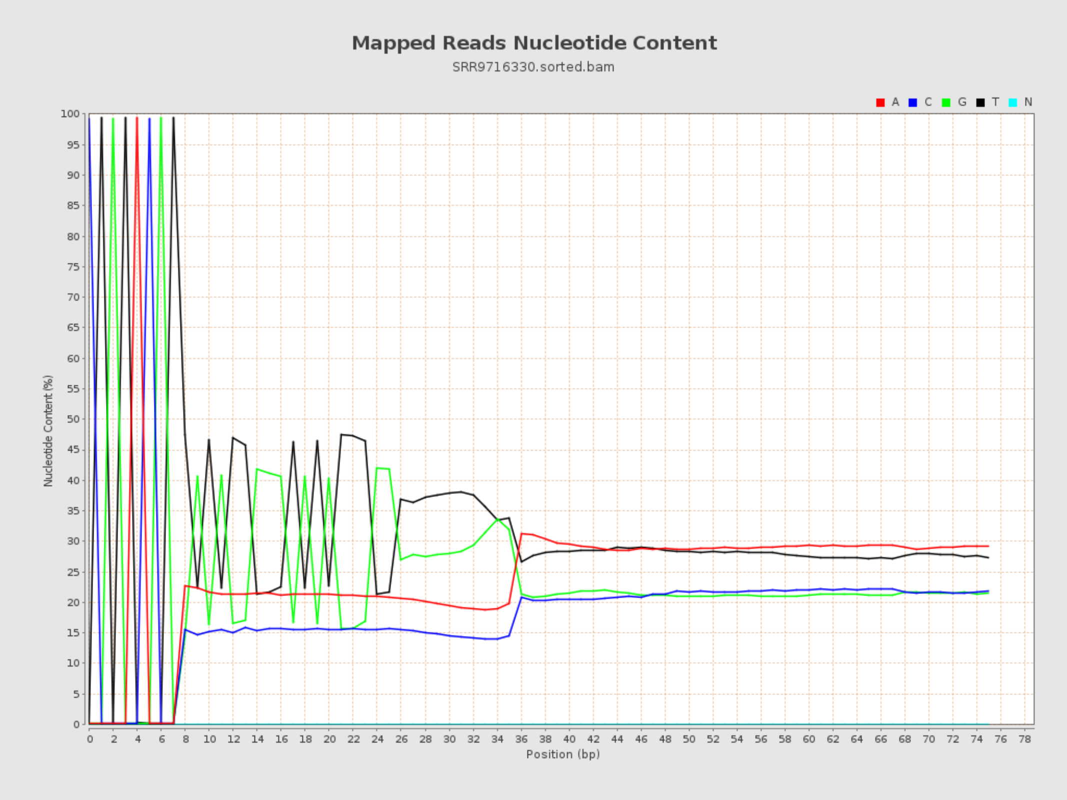
6. Results : Genome Fraction Coverage



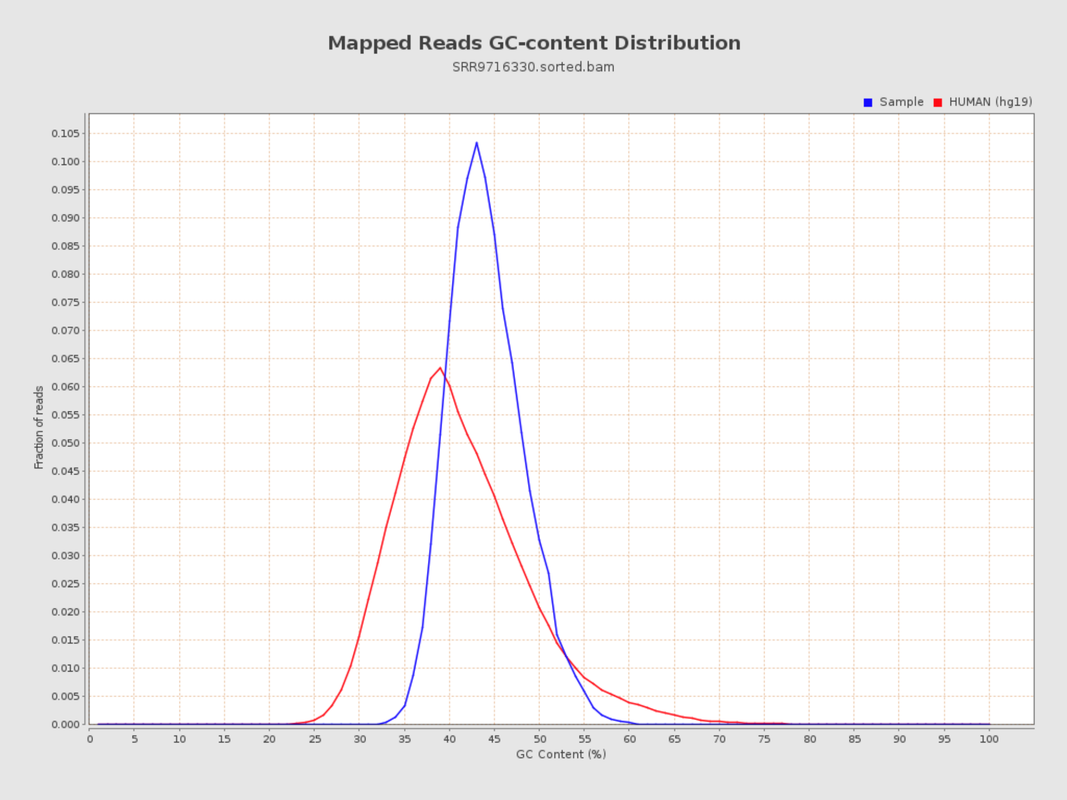
7. Results : Duplication Rate Histogram



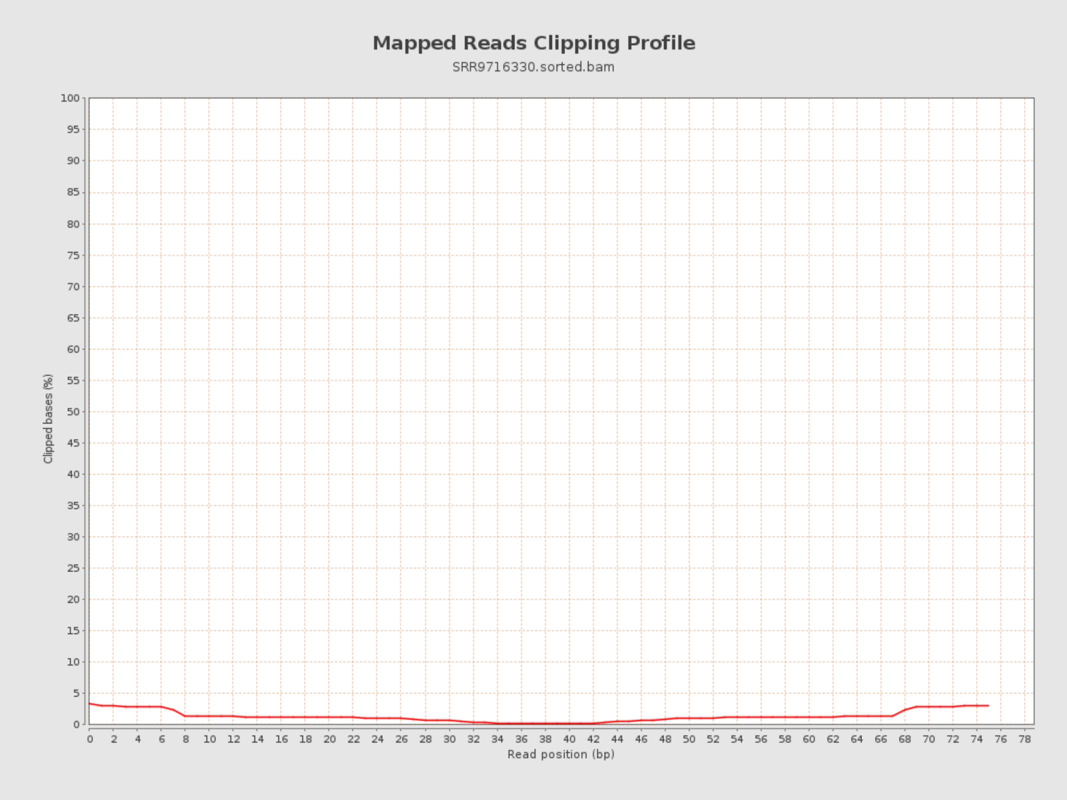
8. Results : Mapped Reads Nucleotide Content



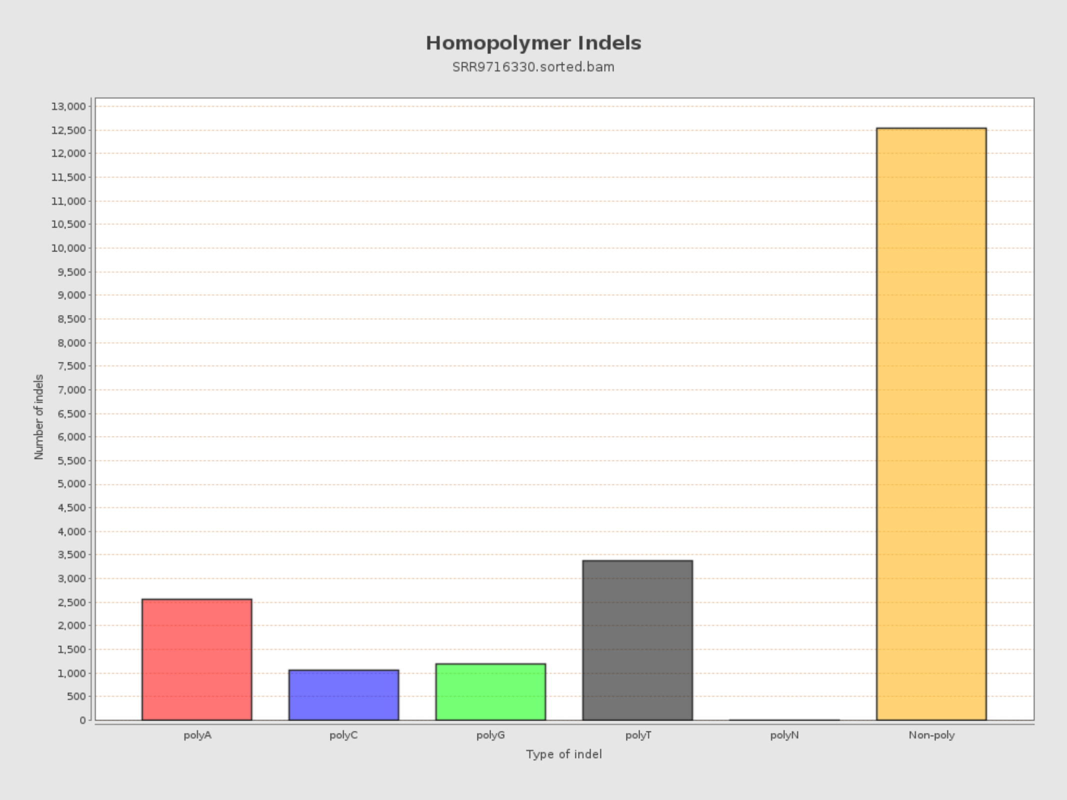
9. Results : Mapped Reads GC-content Distribution



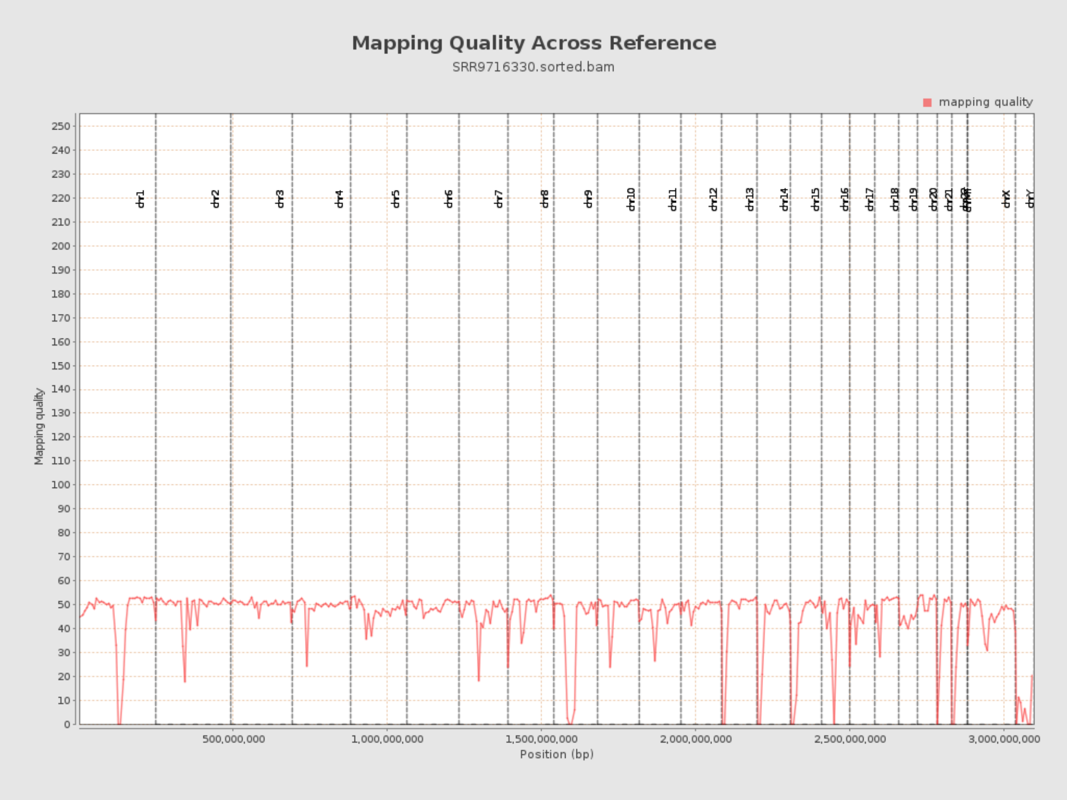
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram