

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 09:13:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716362.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_SRR9716362 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716362.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 09:13:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716362.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,051,683
Mapped reads	1,775,661 / 86.55%
Unmapped reads	276,022 / 13.45%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,695 / 0.52%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	73,675 / 3.59%
Duplication rate	3.17%
Clipped reads	1,783,452 / 86.93%

2.2. ACGT Content

Number/percentage of A's	26,455,972 / 25.8%
Number/percentage of C's	19,678,205 / 19.19%
Number/percentage of T's	32,355,730 / 31.55%
Number/percentage of G's	24,069,779 / 23.47%
Number/percentage of N's	726 / 0%
GC Percentage	42.66%

2.3. Coverage

Mean	0.0331

Standard Deviation	0.2927
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2.4. Mapping Quality

Mean Mapping Quality	44.53
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2.5. Mismatches and indels

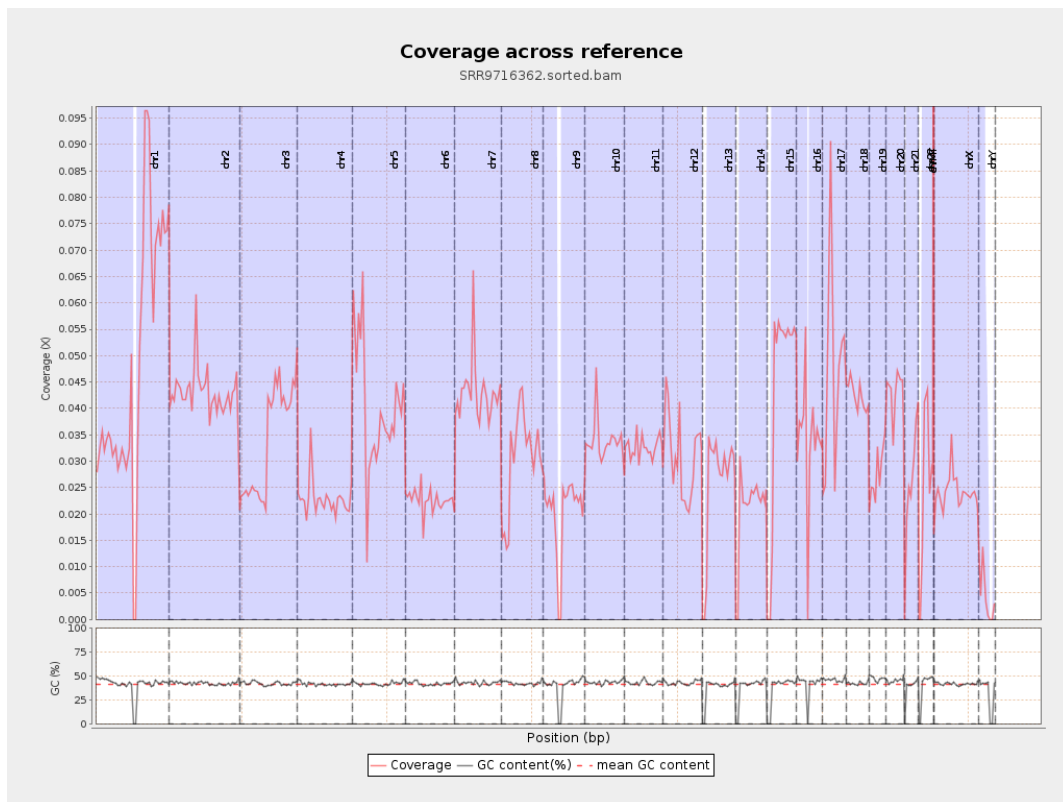
General error rate	0.51%
Mismatches	513,356
Insertions	6,401
Mapped reads with at least one insertion	0.36%
Deletions	18,348
Mapped reads with at least one deletion	1.03%
Homopolymer indels	42.19%

2.6. Chromosome stats

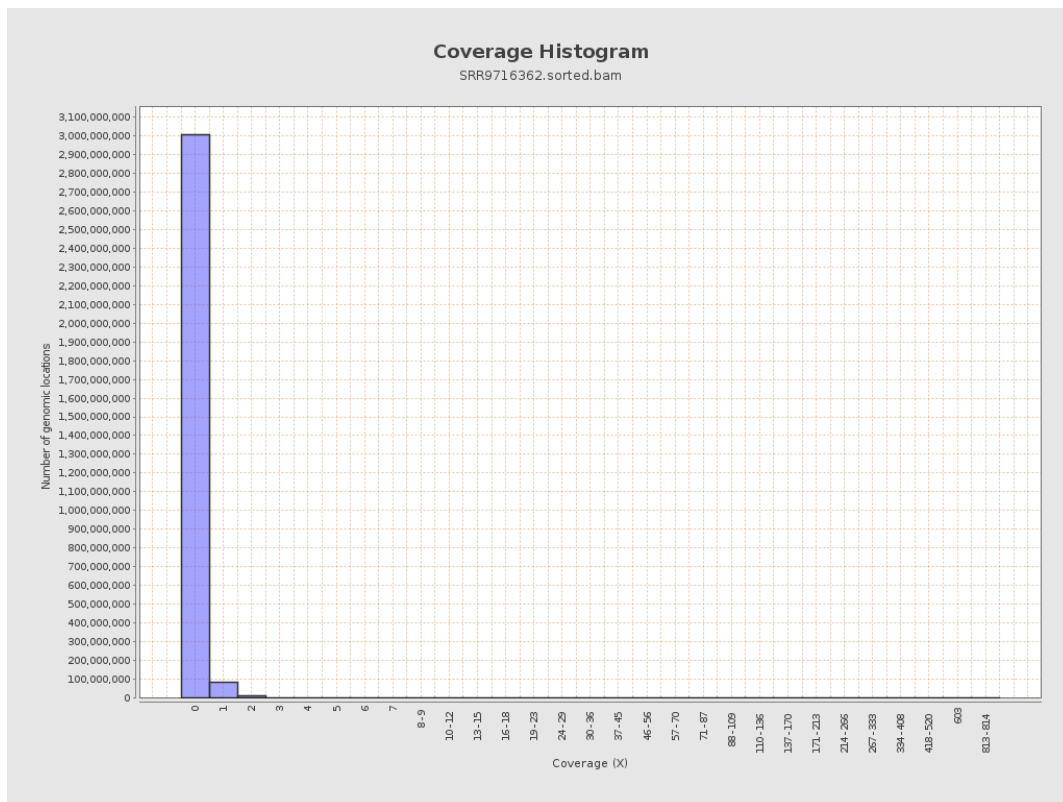
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	12033901	0.0483	0.4681
chr2	243199373	10468450	0.043	0.4291
chr3	198022430	6632202	0.0335	0.2024
chr4	191154276	4340002	0.0227	0.1875
chr5	180915260	7245798	0.0401	0.2234
chr6	171115067	3867509	0.0226	0.1899
chr7	159138663	6861931	0.0431	0.4574

chr8	146364022	4472899	0.0306	0.2559
chr9	141213431	2822510	0.02	0.2156
chr10	135534747	4579549	0.0338	0.255
chr11	135006516	4386158	0.0325	0.2784
chr12	133851895	4104141	0.0307	0.197
chr13	115169878	2955252	0.0257	0.1789
chr14	107349540	2223488	0.0207	0.1677
chr15	102531392	4492004	0.0438	0.2336
chr16	90354753	3058712	0.0339	0.2162
chr17	81195210	3890547	0.0479	0.2653
chr18	78077248	3321453	0.0425	0.4861
chr19	59128983	1654847	0.028	0.3417
chr20	63025520	2705224	0.0429	0.2335
chr21	48129895	1256903	0.0261	0.1929
chr22	51304566	1223802	0.0239	0.1708
chrMT	16571	4405	0.2658	0.5813
chrX	155270560	3744671	0.0241	0.2048
chrY	59373566	243180	0.0041	0.1054

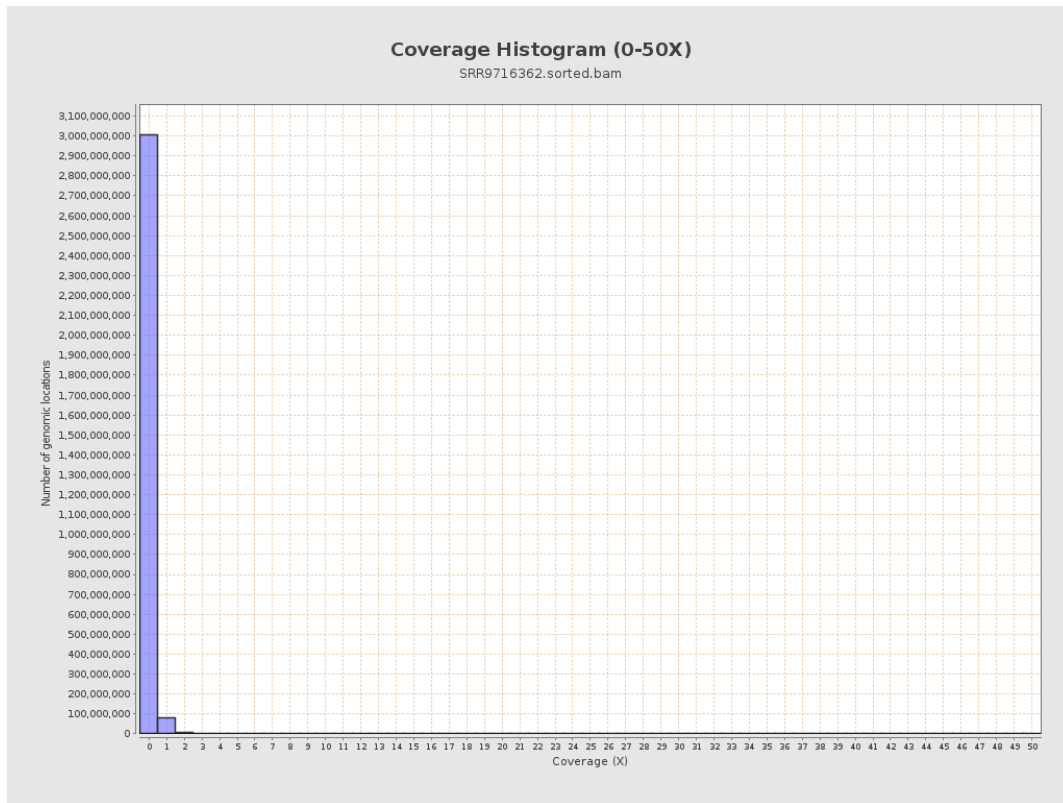
3. Results : Coverage across reference



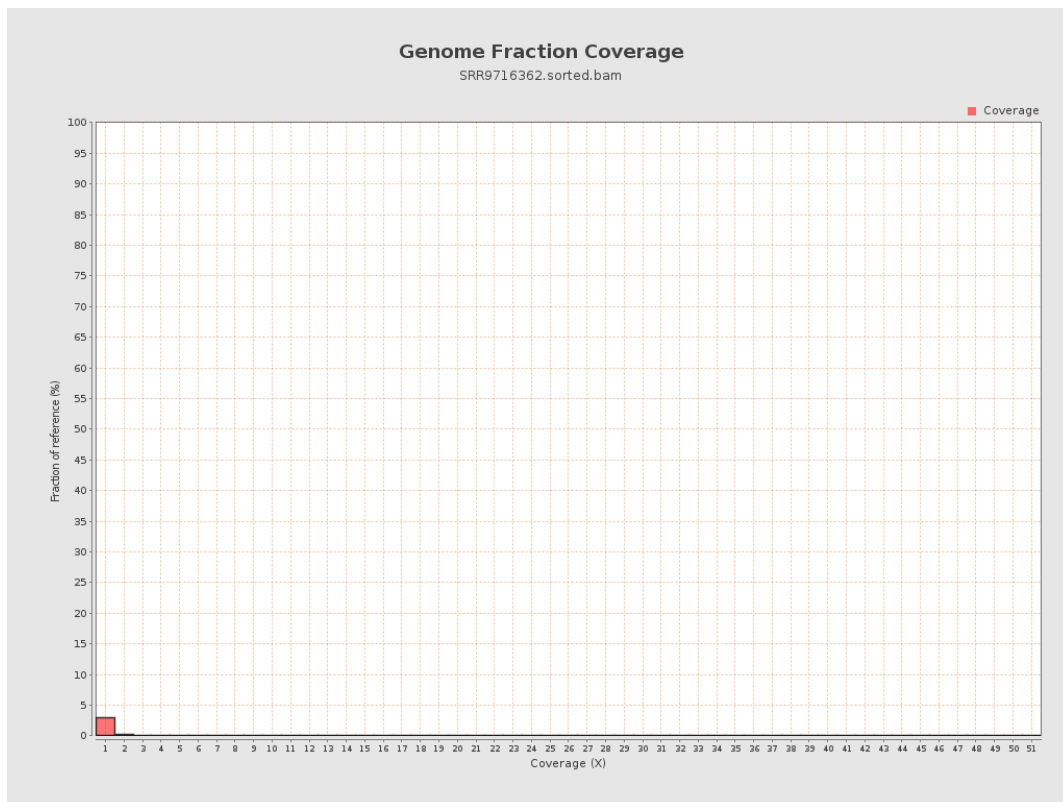
4. Results : Coverage Histogram



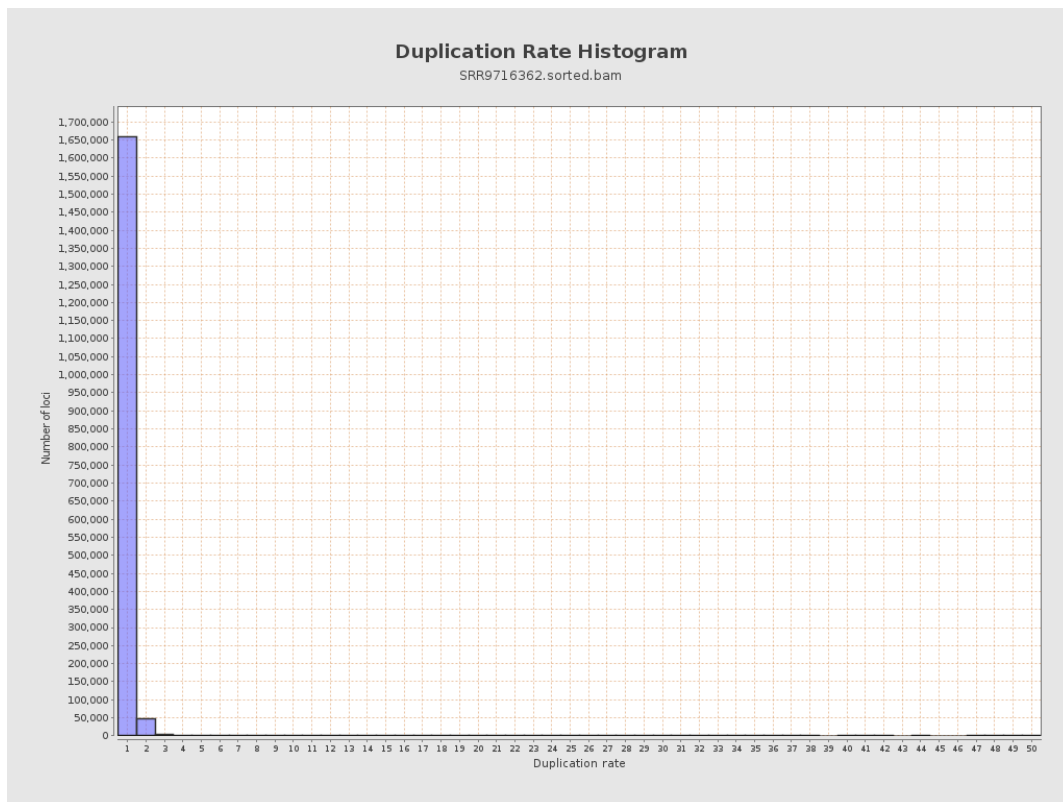
5. Results : Coverage Histogram (0-50X)



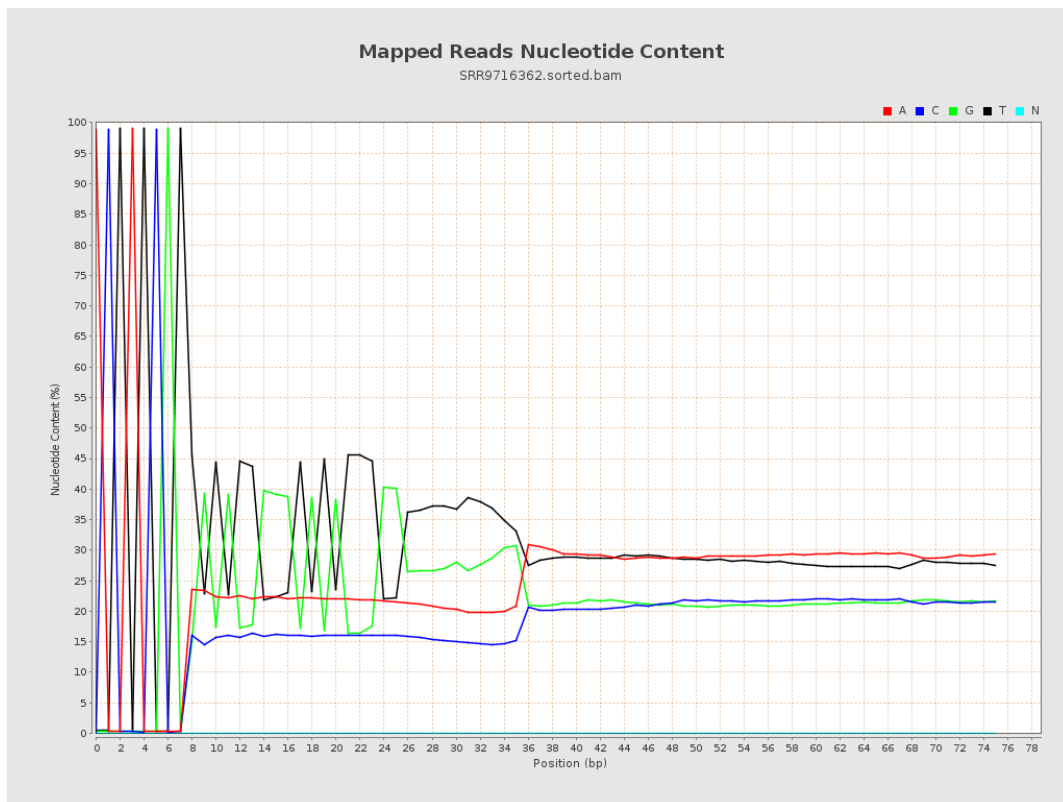
6. Results : Genome Fraction Coverage



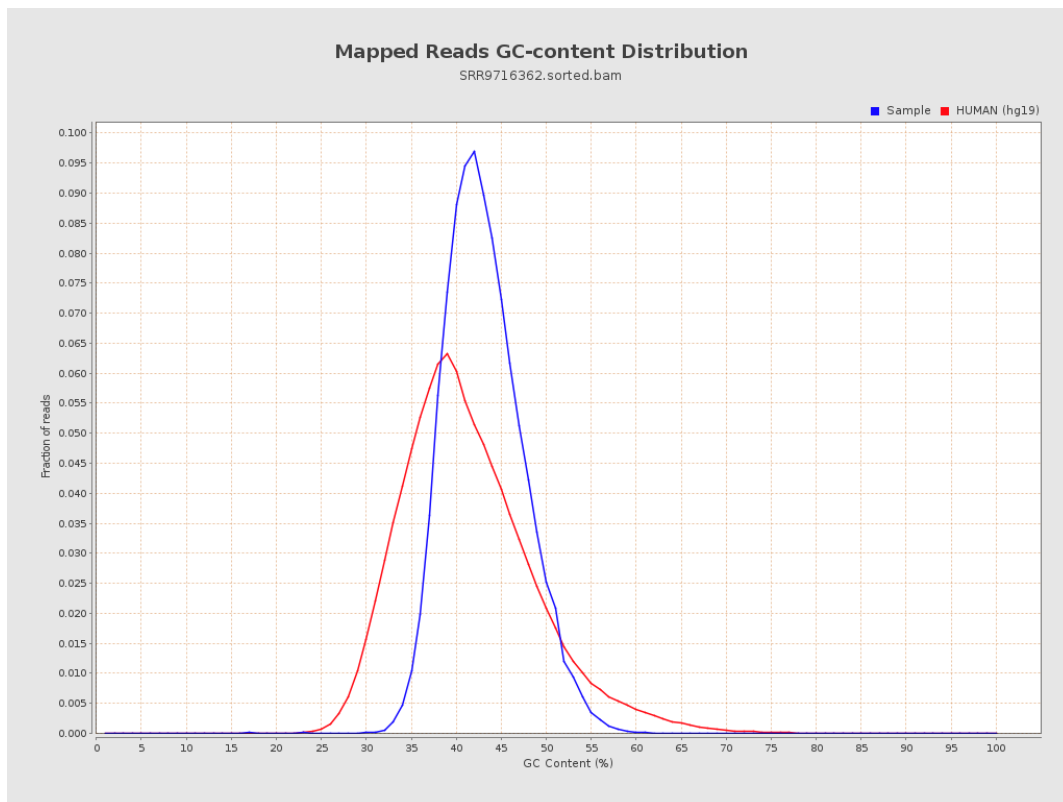
7. Results : Duplication Rate Histogram



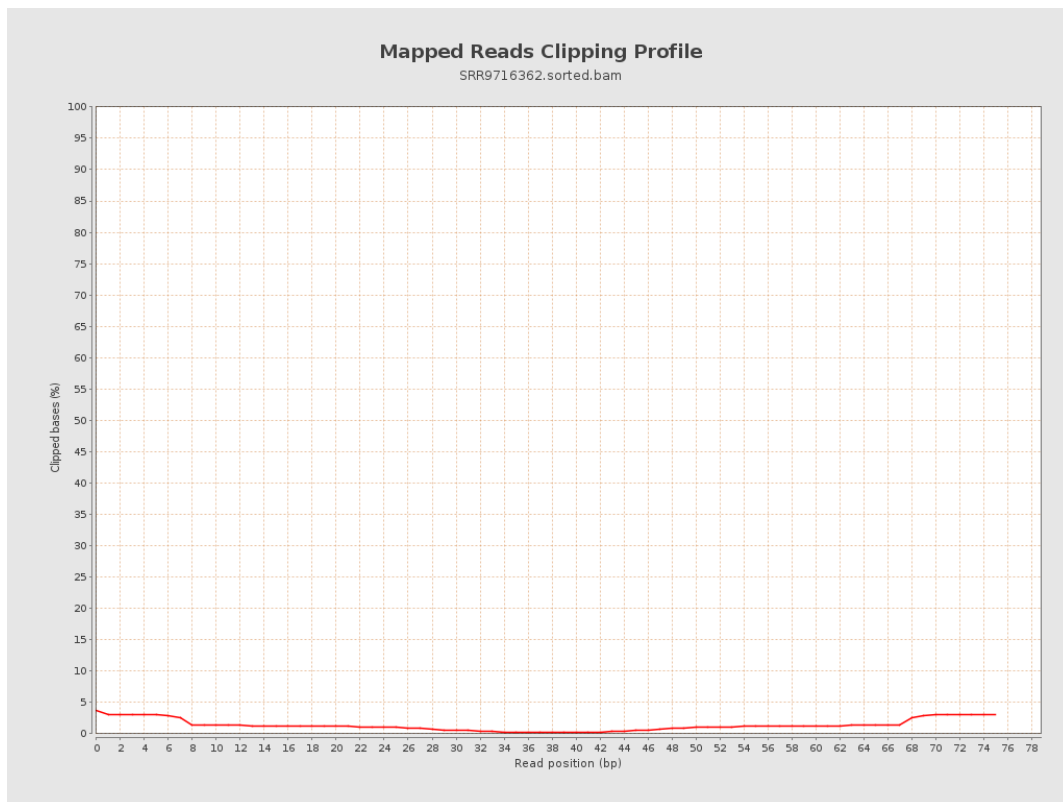
8. Results : Mapped Reads Nucleotide Content



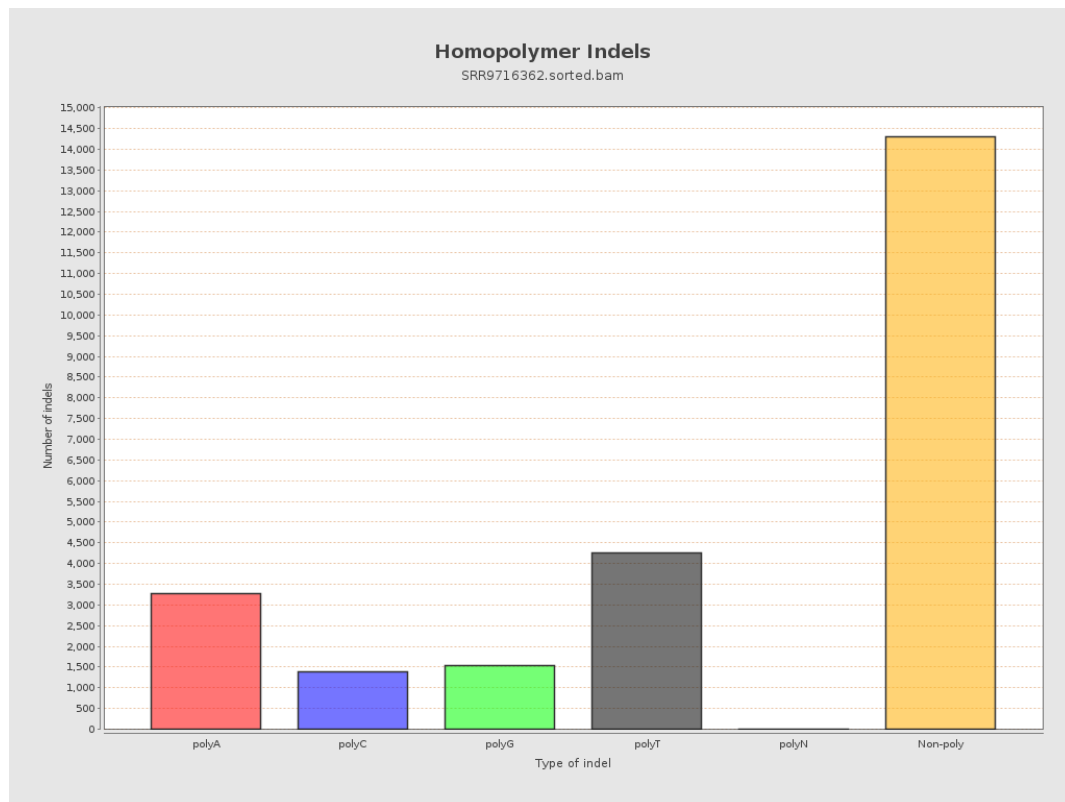
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

