

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 19:44:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082916.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_SRR3082916 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082916.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 19:44:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082916.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,225,566
Mapped reads	1,992,364 / 89.52%
Unmapped reads	233,202 / 10.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,393 / 0.78%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	102,303 / 4.6%
Duplication rate	4.25%
Clipped reads	925,280 / 41.58%

2.2. ACGT Content

Number/percentage of A's	35,131,867 / 26.66%
Number/percentage of C's	24,694,725 / 18.74%
Number/percentage of T's	41,388,023 / 31.41%
Number/percentage of G's	30,544,177 / 23.18%
Number/percentage of N's	6,271 / 0%
GC Percentage	41.92%

2.3. Coverage

Mean	0.0426

Standard Deviation	0.3358
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2.4. Mapping Quality

Mean Mapping Quality	44.73
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2.5. Mismatches and indels

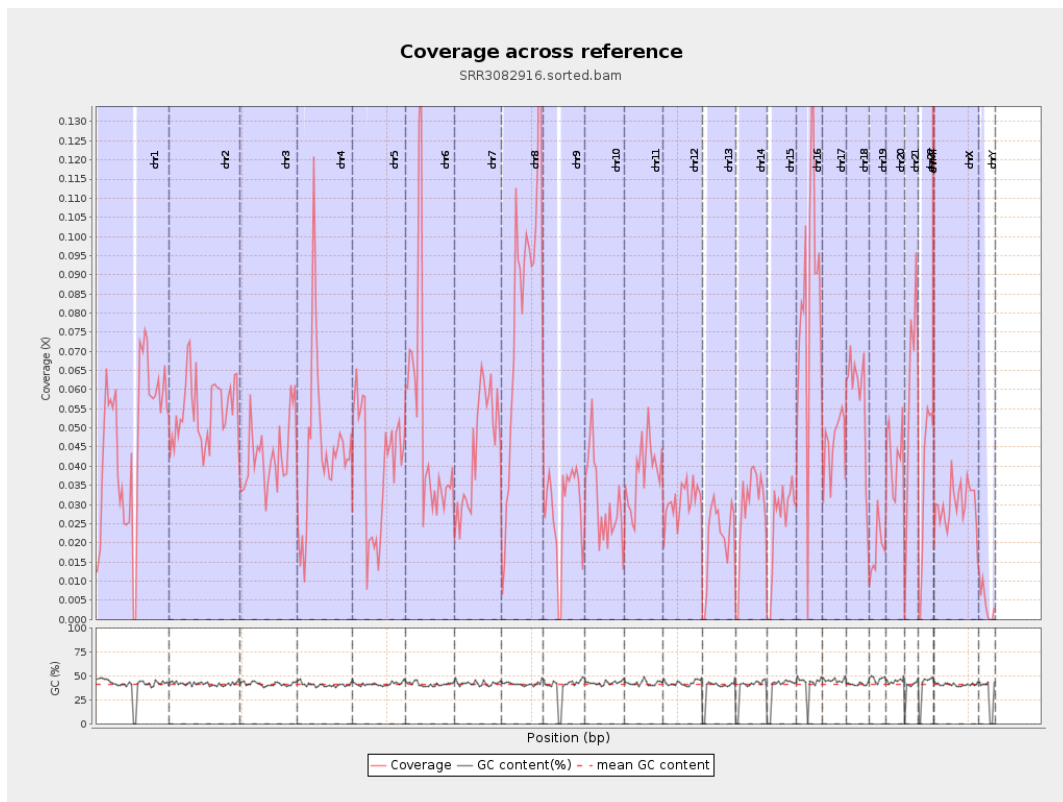
General error rate	0.75%
Mismatches	969,189
Insertions	10,562
Mapped reads with at least one insertion	0.53%
Deletions	30,972
Mapped reads with at least one deletion	1.54%
Homopolymer indels	47.43%

2.6. Chromosome stats

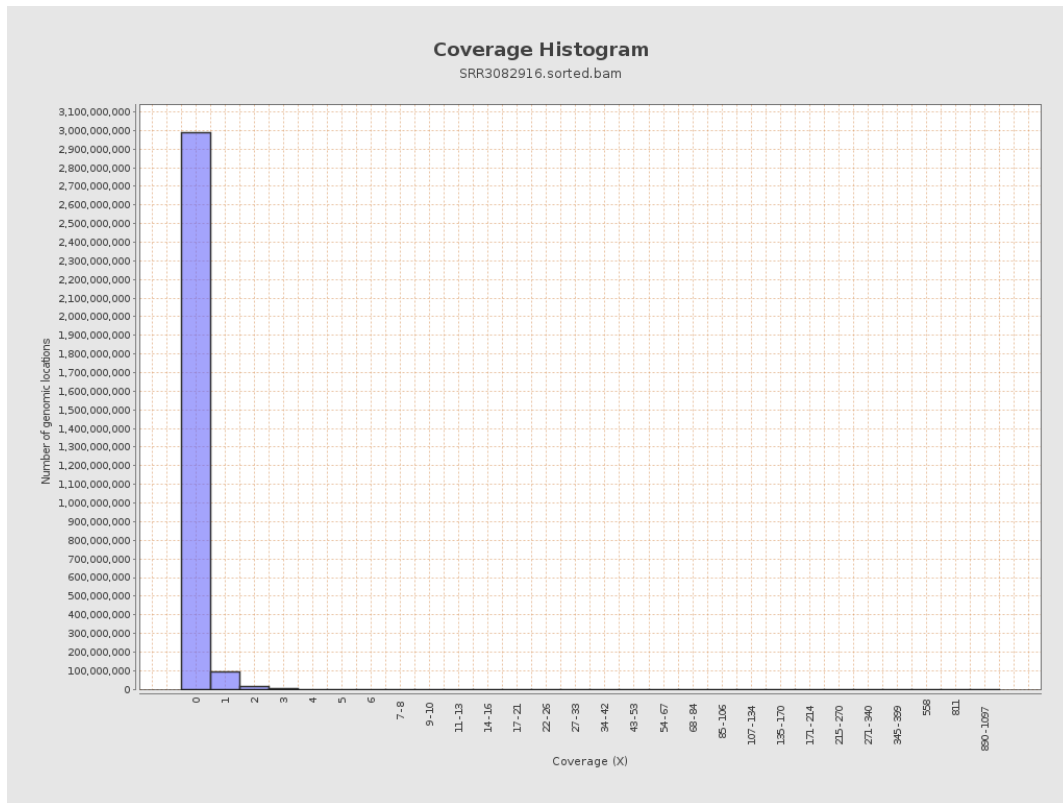
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	11708302	0.047	0.3892
chr2	243199373	13289893	0.0546	0.5768
chr3	198022430	8557913	0.0432	0.2423
chr4	191154276	8448815	0.0442	0.2549
chr5	180915260	7141836	0.0395	0.2337
chr6	171115067	8624160	0.0504	0.3421
chr7	159138663	7157834	0.045	0.3422

chr8	146364022	12016888	0.0821	0.4266
chr9	141213431	4041749	0.0286	0.3061
chr10	135534747	4231423	0.0312	0.2442
chr11	135006516	5129204	0.038	0.3065
chr12	133851895	4099102	0.0306	0.2075
chr13	115169878	2435852	0.0212	0.1738
chr14	107349540	3085458	0.0287	0.2128
chr15	102531392	2592625	0.0253	0.211
chr16	90354753	7525604	0.0833	0.3599
chr17	81195210	3717757	0.0458	0.2754
chr18	78077248	4551129	0.0583	0.6506
chr19	59128983	1117952	0.0189	0.312
chr20	63025520	2679170	0.0425	0.2505
chr21	48129895	2799781	0.0582	0.2902
chr22	51304566	1842496	0.0359	0.2202
chrMT	16571	133938	8.0827	5.4547
chrX	155270560	4644473	0.0299	0.234
chrY	59373566	242293	0.0041	0.0883

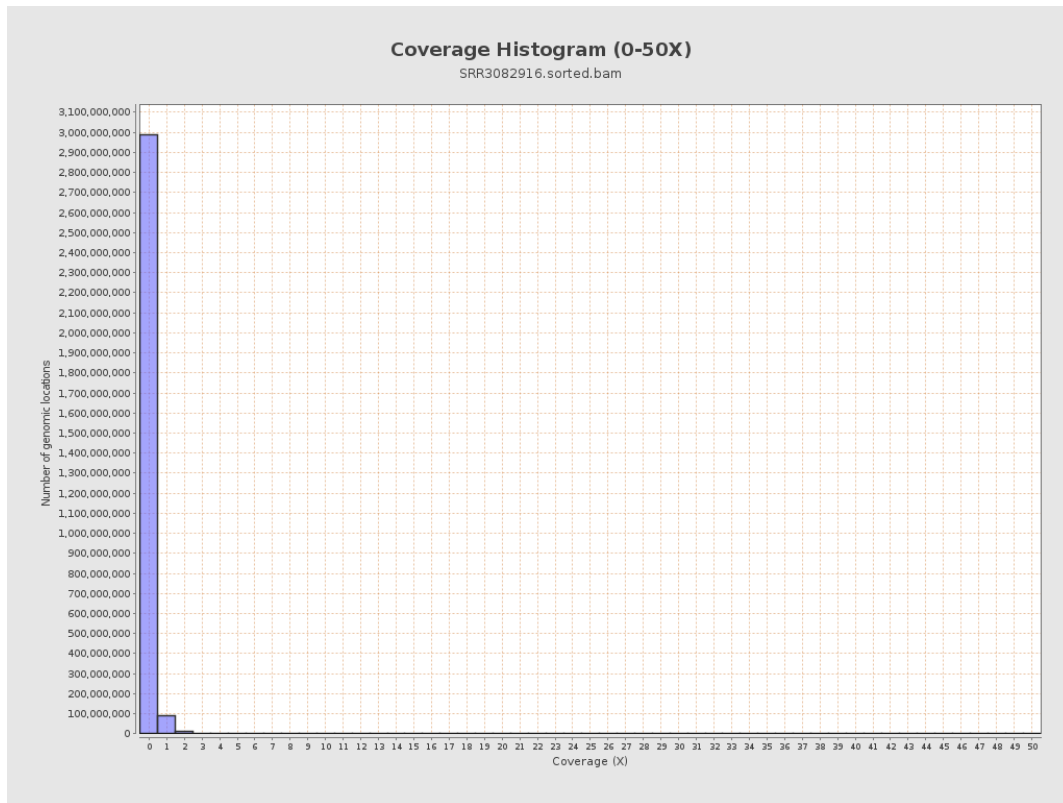
3. Results : Coverage across reference



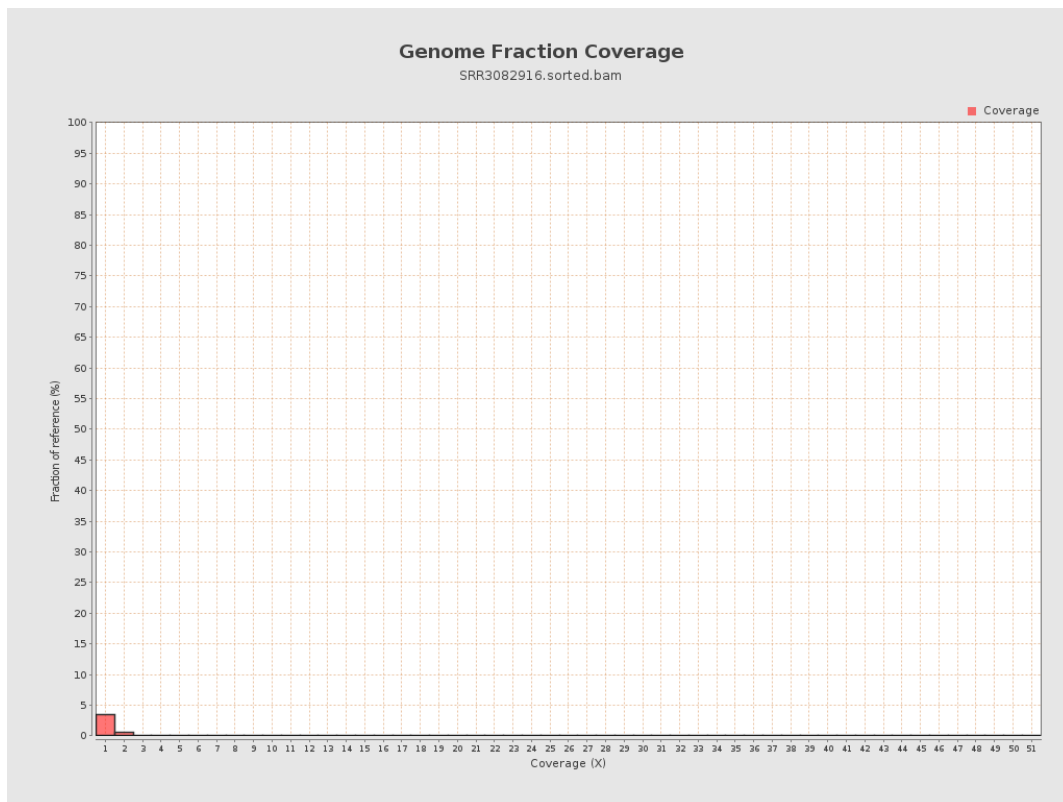
4. Results : Coverage Histogram



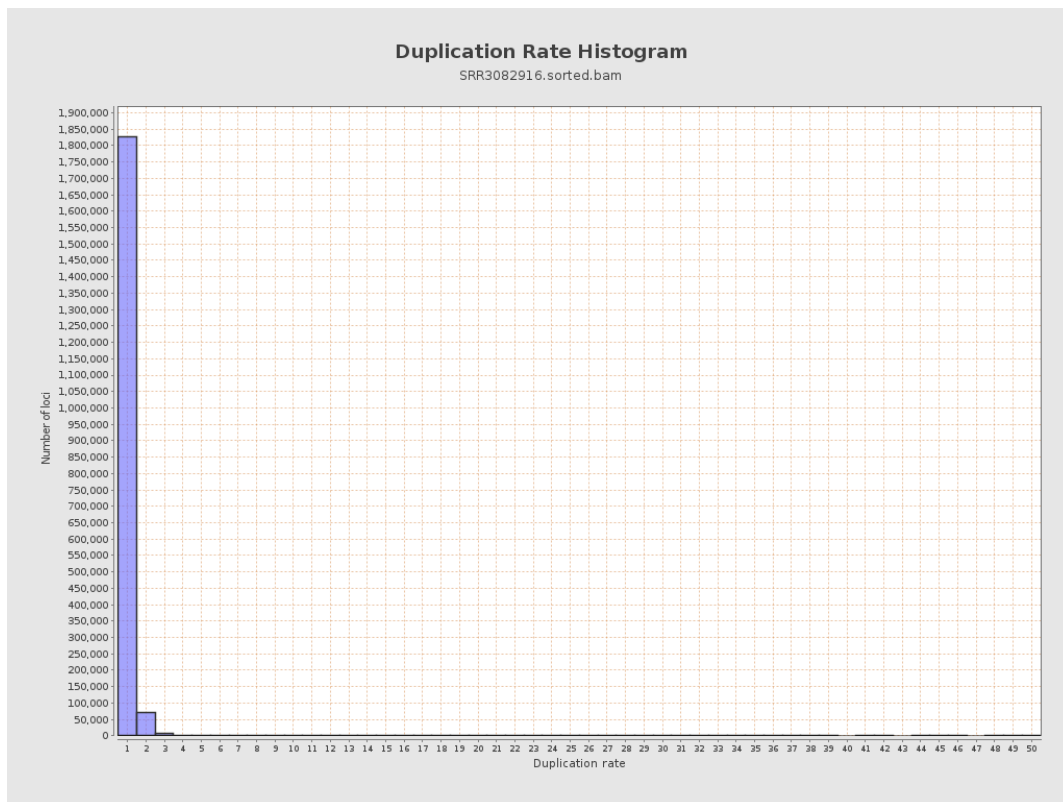
5. Results : Coverage Histogram (0-50X)



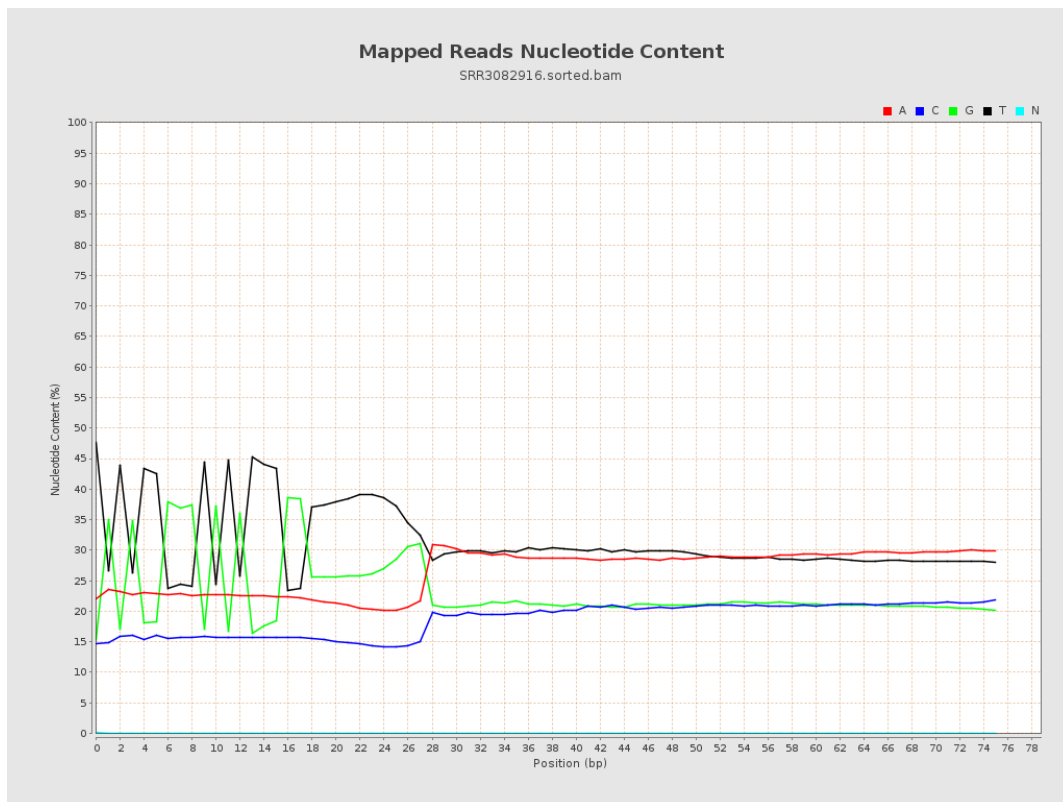
6. Results : Genome Fraction Coverage



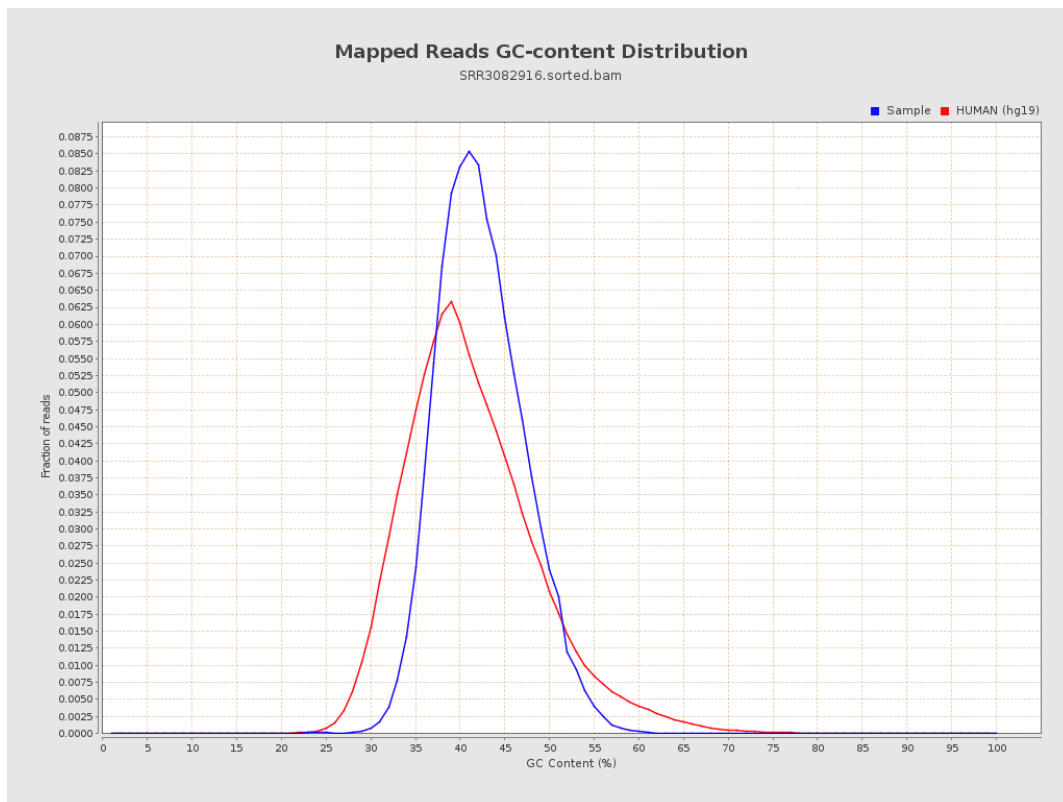
7. Results : Duplication Rate Histogram



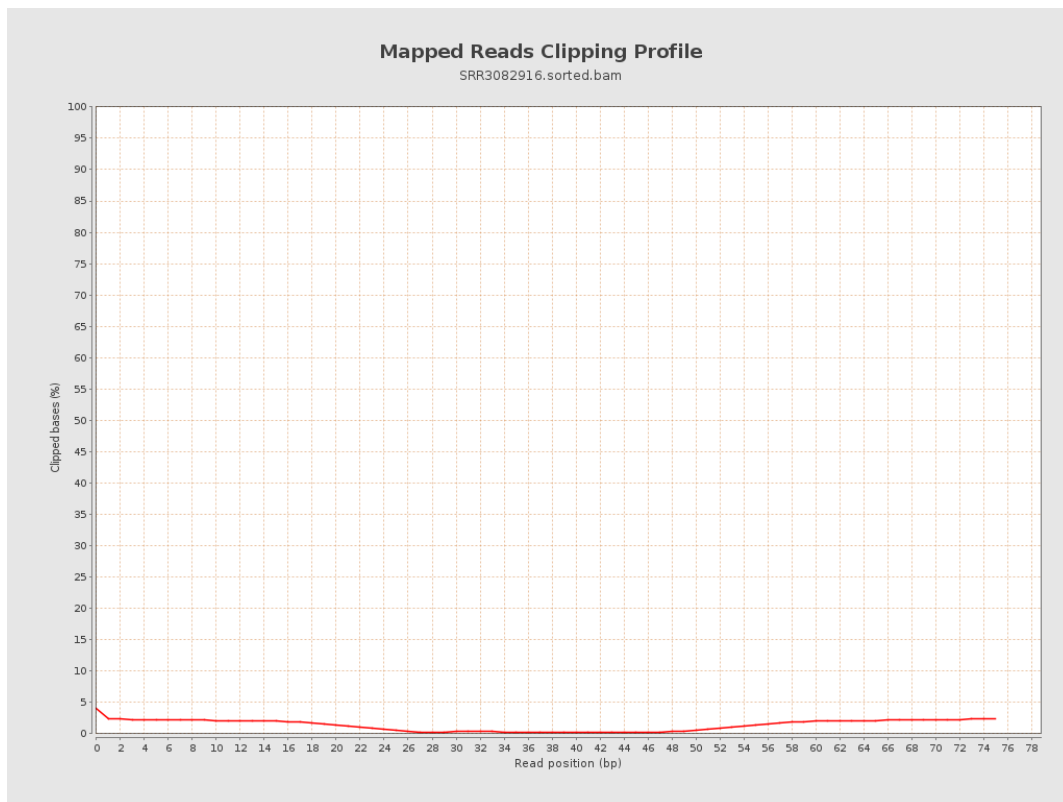
8. Results : Mapped Reads Nucleotide Content



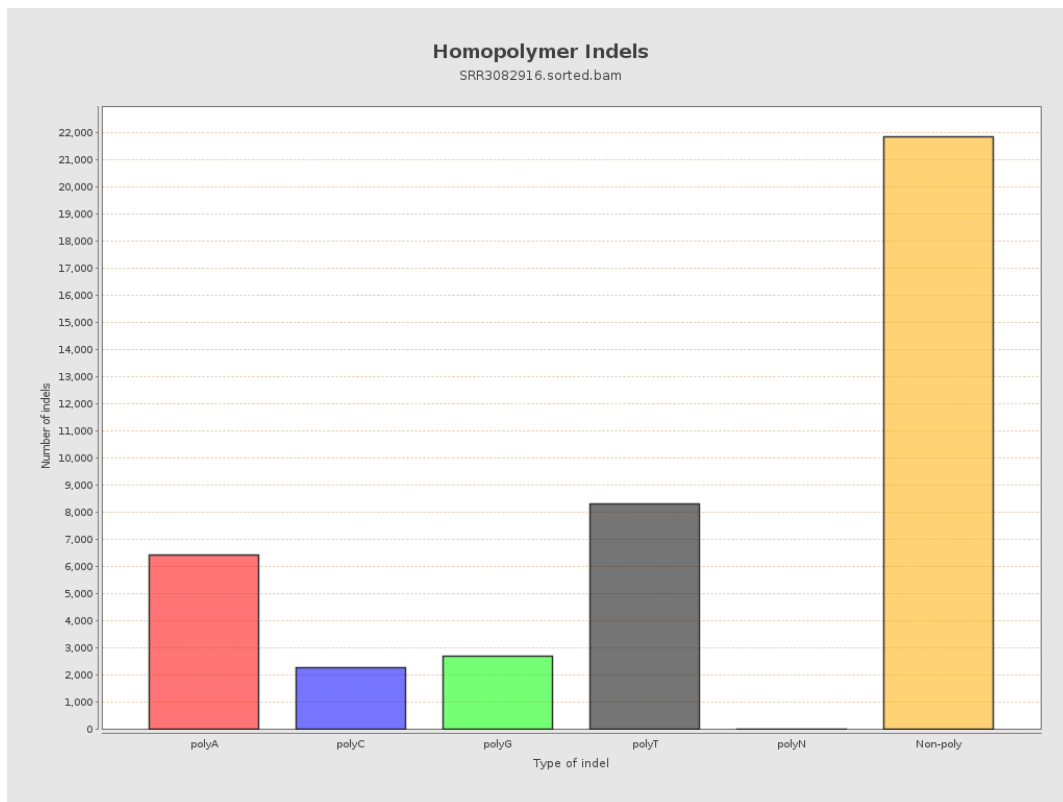
9. Results : Mapped Reads GC-content Distribution



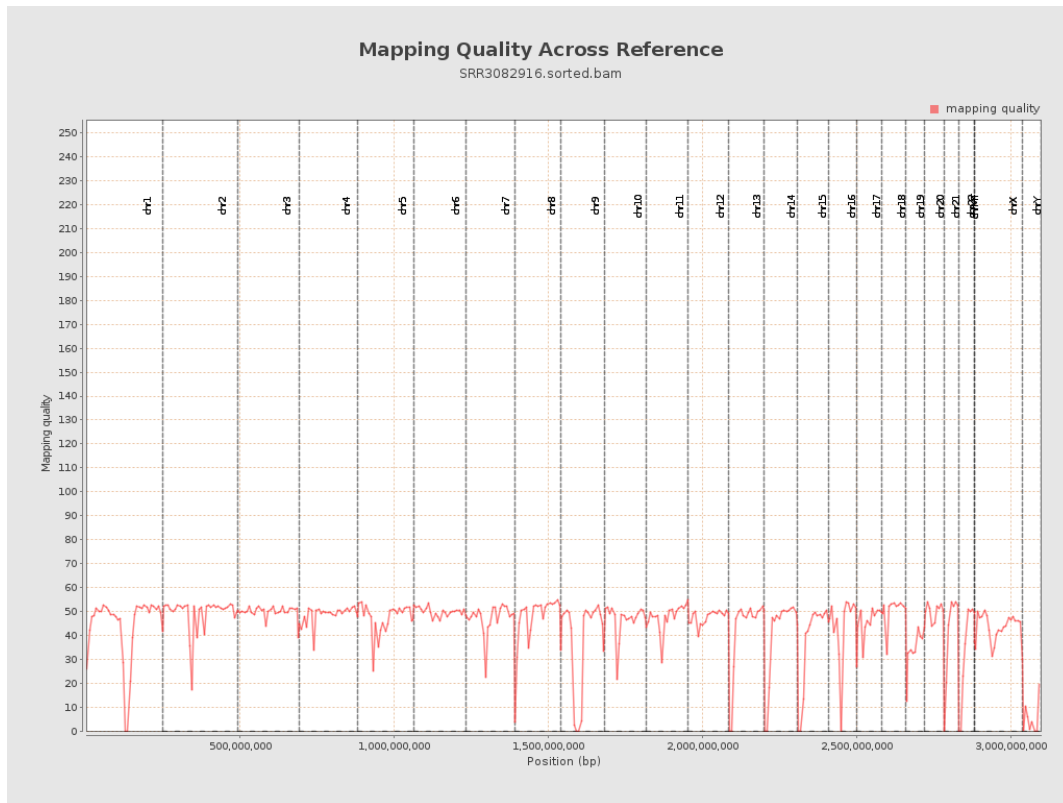
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

