

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 13:23:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716814.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_SRR9716814 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716814.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 13:23:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716814.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,336,610
Mapped reads	1,998,693 / 85.54%
Unmapped reads	337,917 / 14.46%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,481 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	82,214 / 3.52%
Duplication rate	3.04%
Clipped reads	2,002,092 / 85.68%

2.2. ACGT Content

Number/percentage of A's	27,834,048 / 24.07%
Number/percentage of C's	20,607,496 / 17.82%
Number/percentage of T's	38,109,319 / 32.96%
Number/percentage of G's	29,062,012 / 25.14%
Number/percentage of N's	3,175 / 0%
GC Percentage	42.96%

2.3. Coverage

Mean	0.0374

Standard Deviation	0.3434
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2.4. Mapping Quality

Mean Mapping Quality	44.8
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2.5. Mismatches and indels

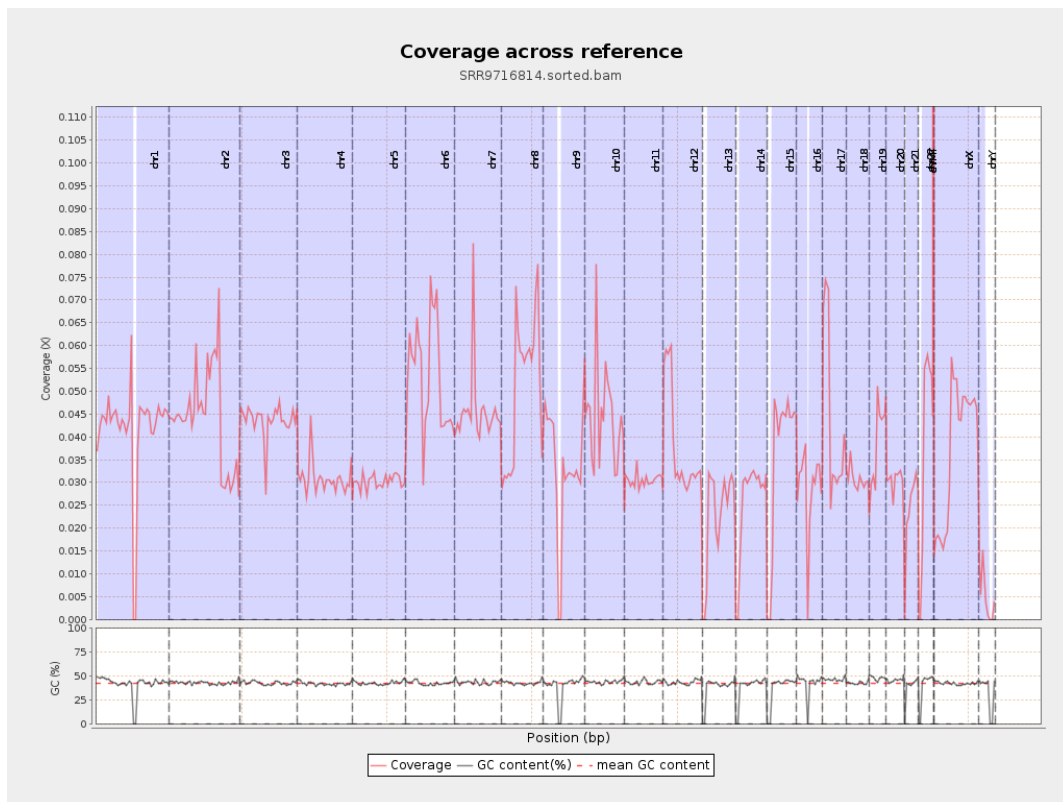
General error rate	0.51%
Mismatches	574,977
Insertions	8,056
Mapped reads with at least one insertion	0.4%
Deletions	21,571
Mapped reads with at least one deletion	1.07%
Homopolymer indels	43.53%

2.6. Chromosome stats

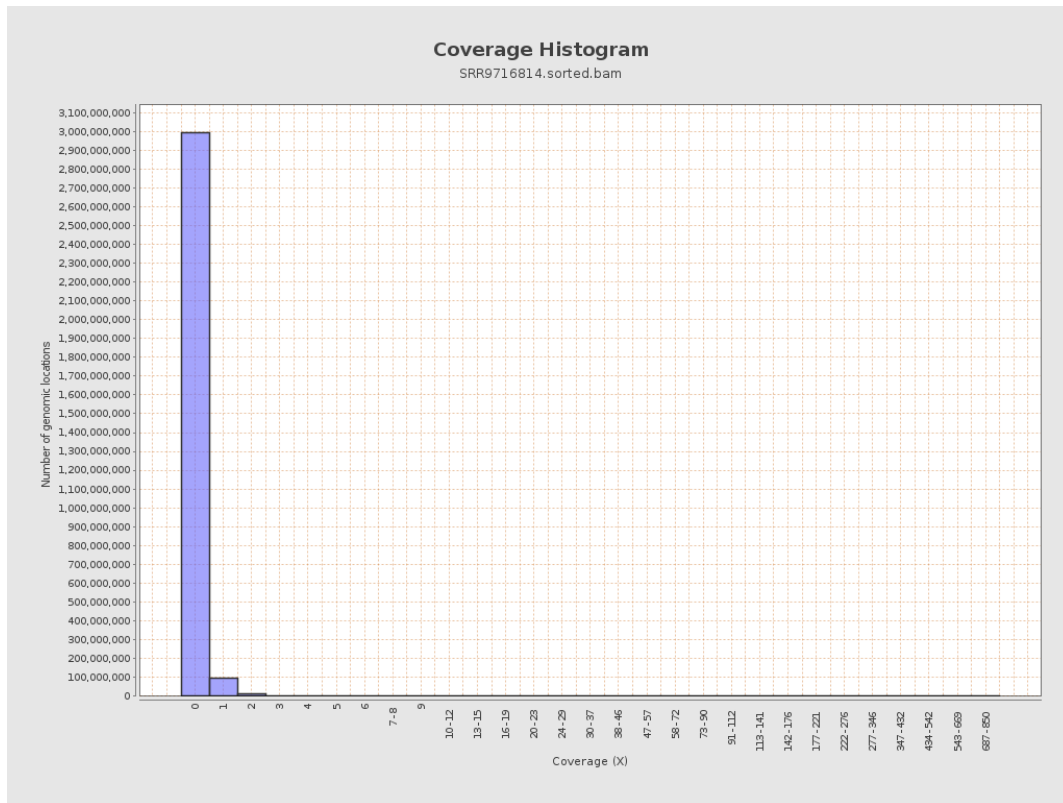
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	10376830	0.0416	0.5876
chr2	243199373	10729774	0.0441	0.4297
chr3	198022430	8633439	0.0436	0.2328
chr4	191154276	5887915	0.0308	0.2068
chr5	180915260	5463343	0.0302	0.1943
chr6	171115067	9108463	0.0532	0.3293
chr7	159138663	7304235	0.0459	0.6668

chr8	146364022	7475823	0.0511	0.3112
chr9	141213431	4588009	0.0325	0.2663
chr10	135534747	6032197	0.0445	0.3063
chr11	135006516	4106100	0.0304	0.2728
chr12	133851895	5036956	0.0376	0.2204
chr13	115169878	2598302	0.0226	0.1681
chr14	107349540	2735255	0.0255	0.19
chr15	102531392	3705559	0.0361	0.2159
chr16	90354753	2597454	0.0287	0.2049
chr17	81195210	3505616	0.0432	0.2471
chr18	78077248	2412859	0.0309	0.4846
chr19	59128983	2291687	0.0388	0.4026
chr20	63025520	1902384	0.0302	0.1958
chr21	48129895	1167647	0.0243	0.1871
chr22	51304566	1918596	0.0374	0.2152
chrMT	16571	32831	1.9812	1.8624
chrX	155270560	5757623	0.0371	0.247
chrY	59373566	280982	0.0047	0.108

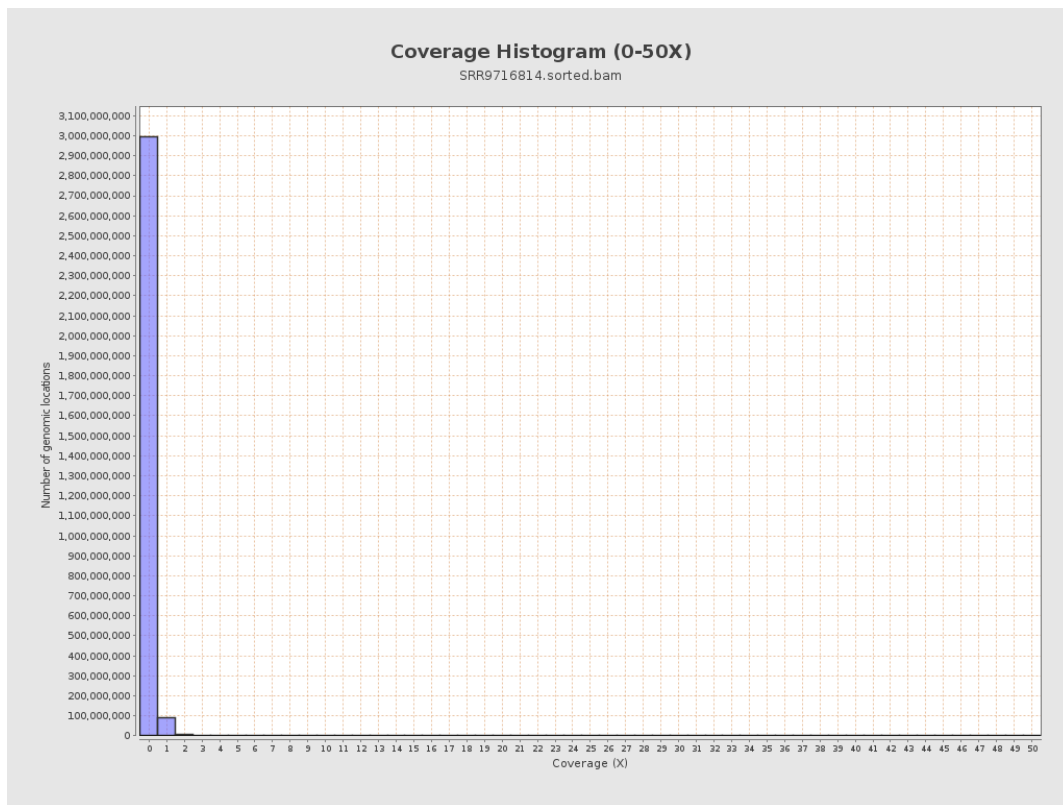
3. Results : Coverage across reference



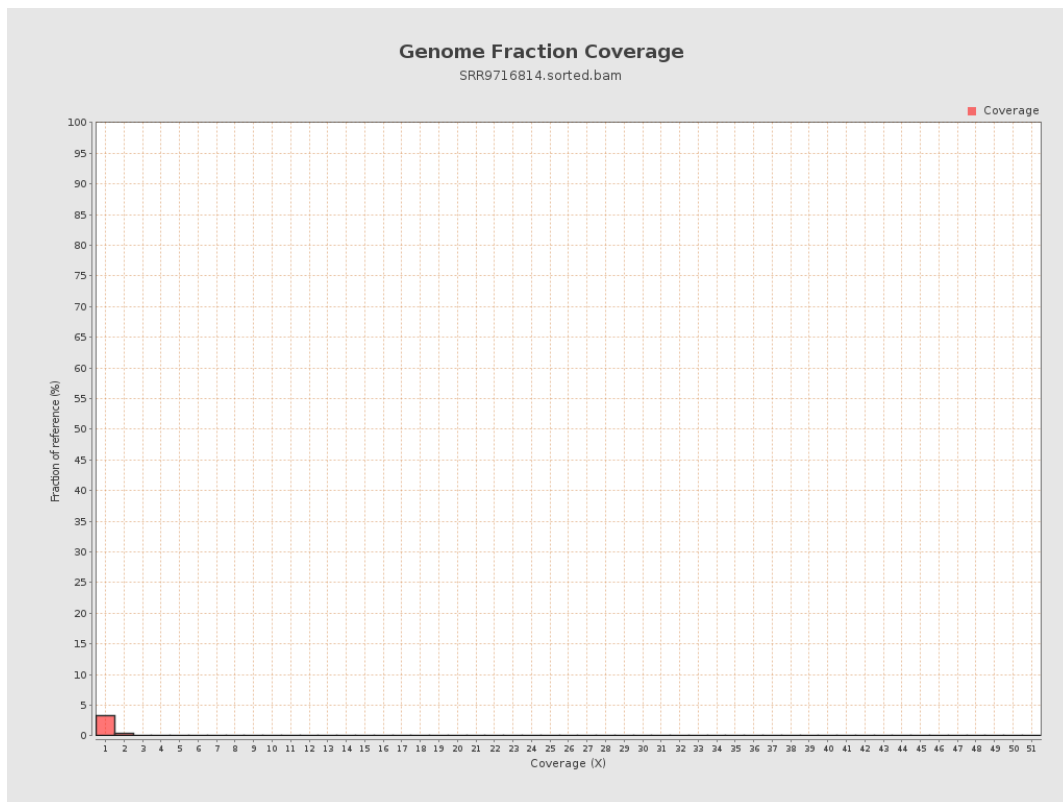
4. Results : Coverage Histogram



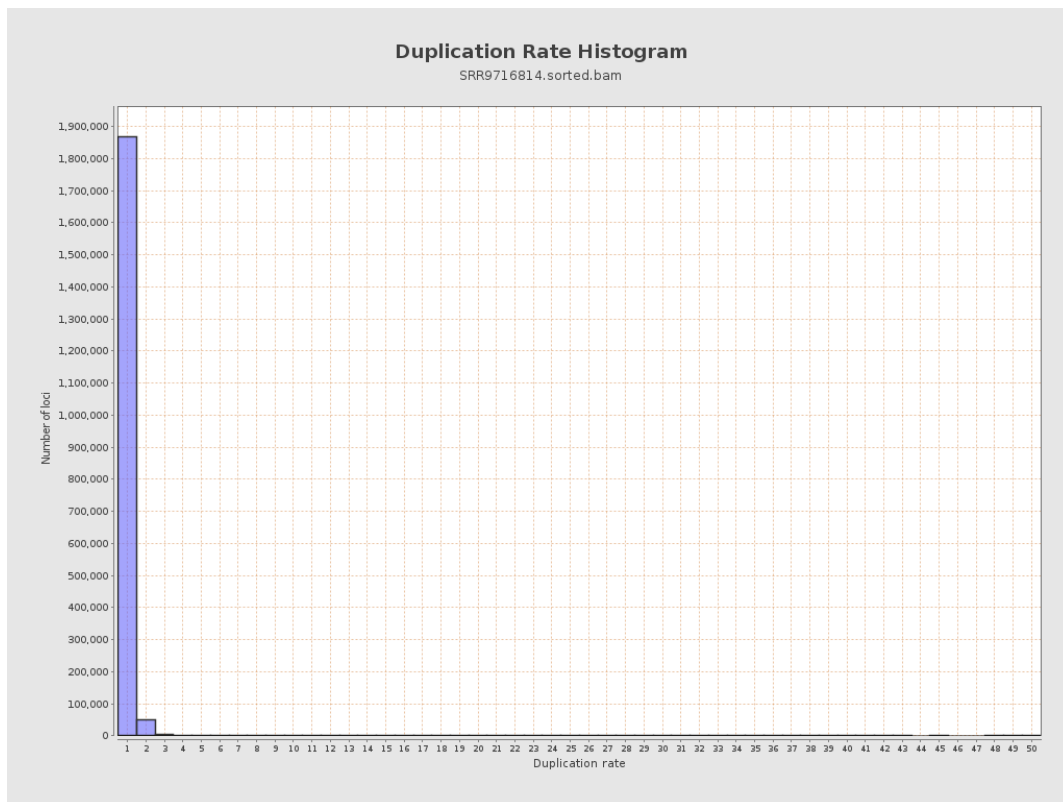
5. Results : Coverage Histogram (0-50X)



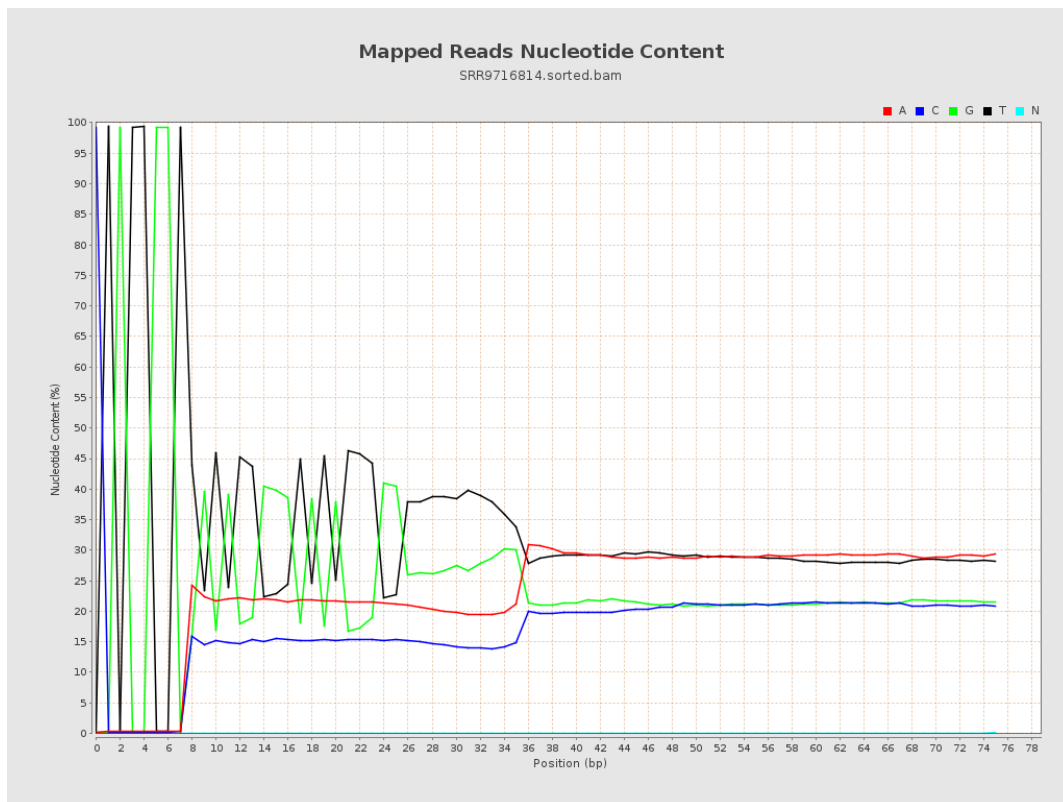
6. Results : Genome Fraction Coverage



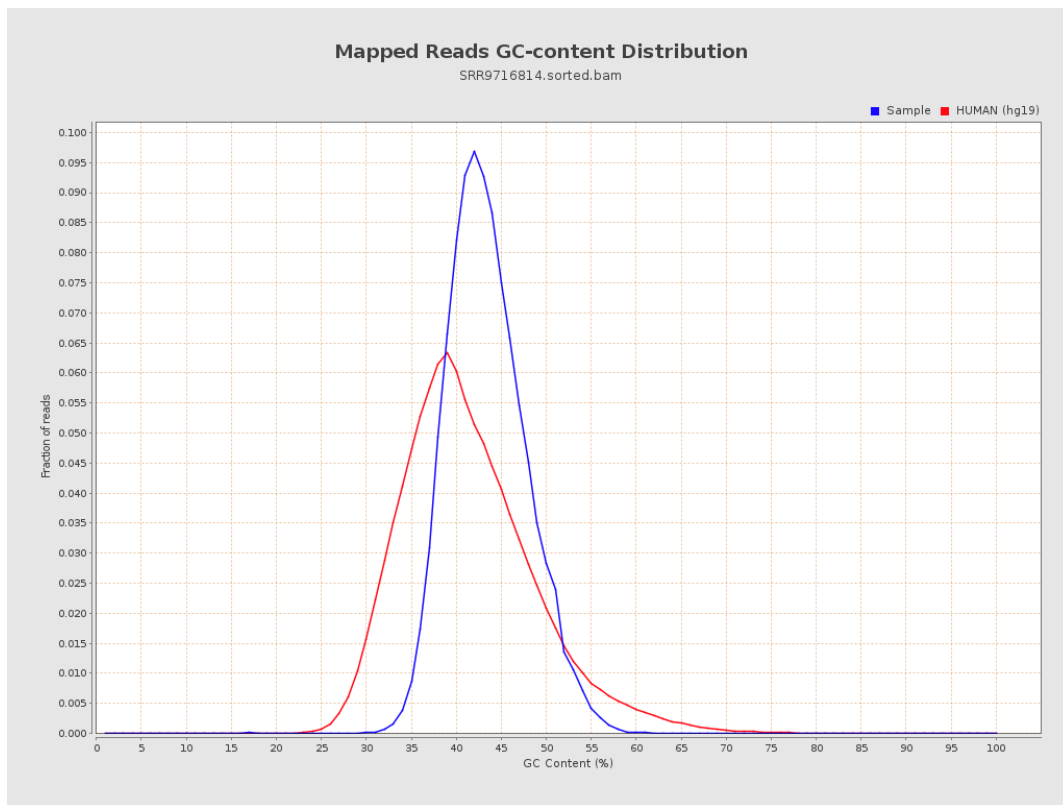
7. Results : Duplication Rate Histogram



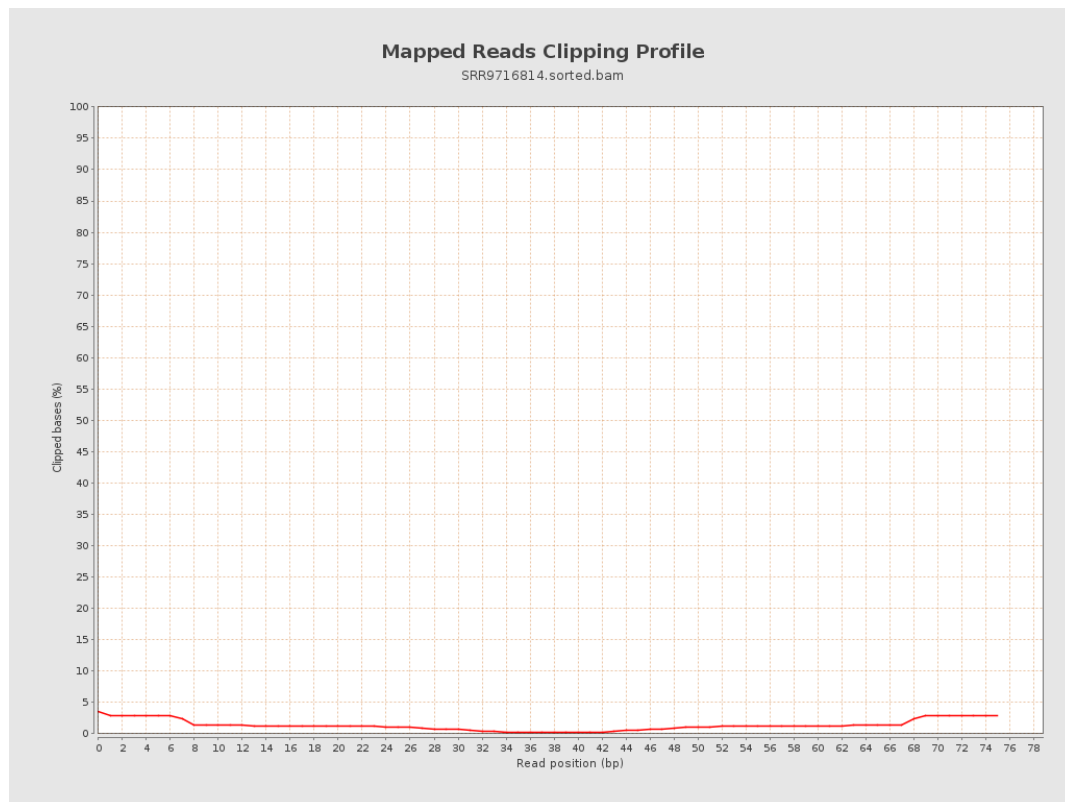
8. Results : Mapped Reads Nucleotide Content



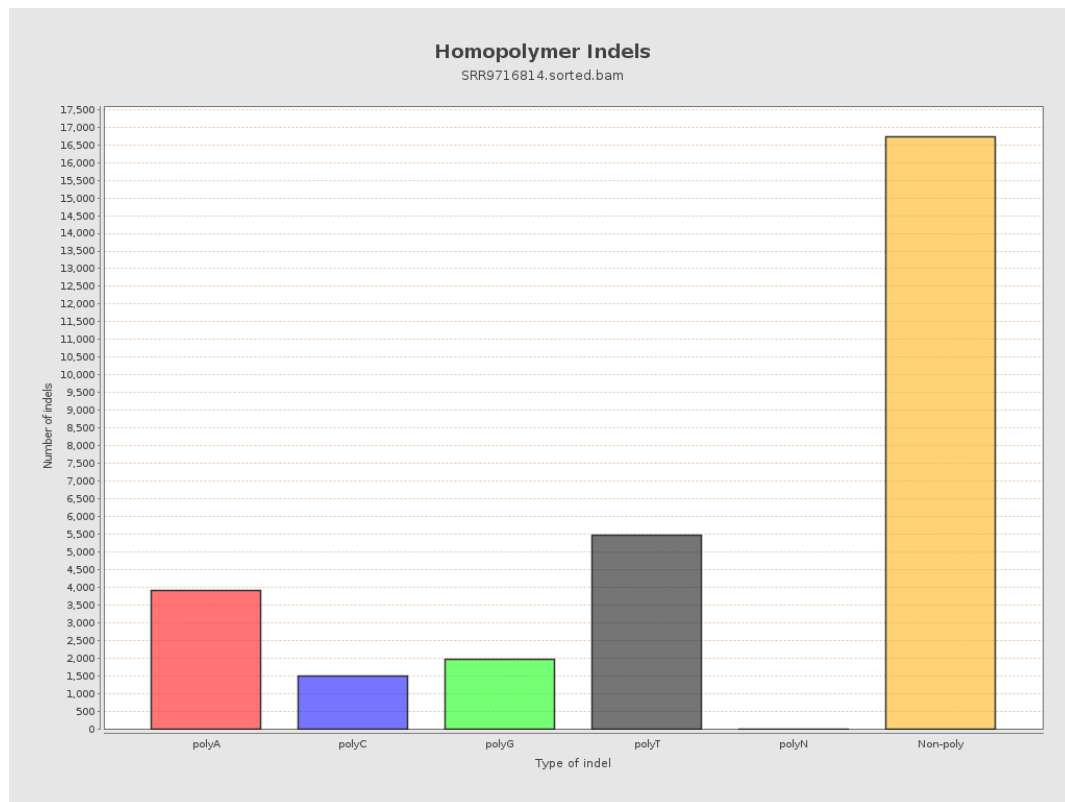
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

