

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 18:45:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716119.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_SRR9716119 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716119.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 18:45:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716119.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	945,015
Mapped reads	883,350 / 93.47%
Unmapped reads	61,665 / 6.53%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,983 / 1.9%
Read min/max/mean length	30 / 101 / 101.68
Duplicated reads (estimated)	22,339 / 2.36%
Duplication rate	1.76%
Clipped reads	899,255 / 95.16%

2.2. ACGT Content

Number/percentage of A's	18,413,377 / 26.34%
Number/percentage of C's	14,486,181 / 20.72%
Number/percentage of T's	20,728,100 / 29.65%
Number/percentage of G's	16,280,287 / 23.29%
Number/percentage of N's	4,623 / 0.01%
GC Percentage	44.01%

2.3. Coverage

Mean	0.0226

Standard Deviation	0.2246
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2.4. Mapping Quality

Mean Mapping Quality	47.37
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2.5. Mismatches and indels

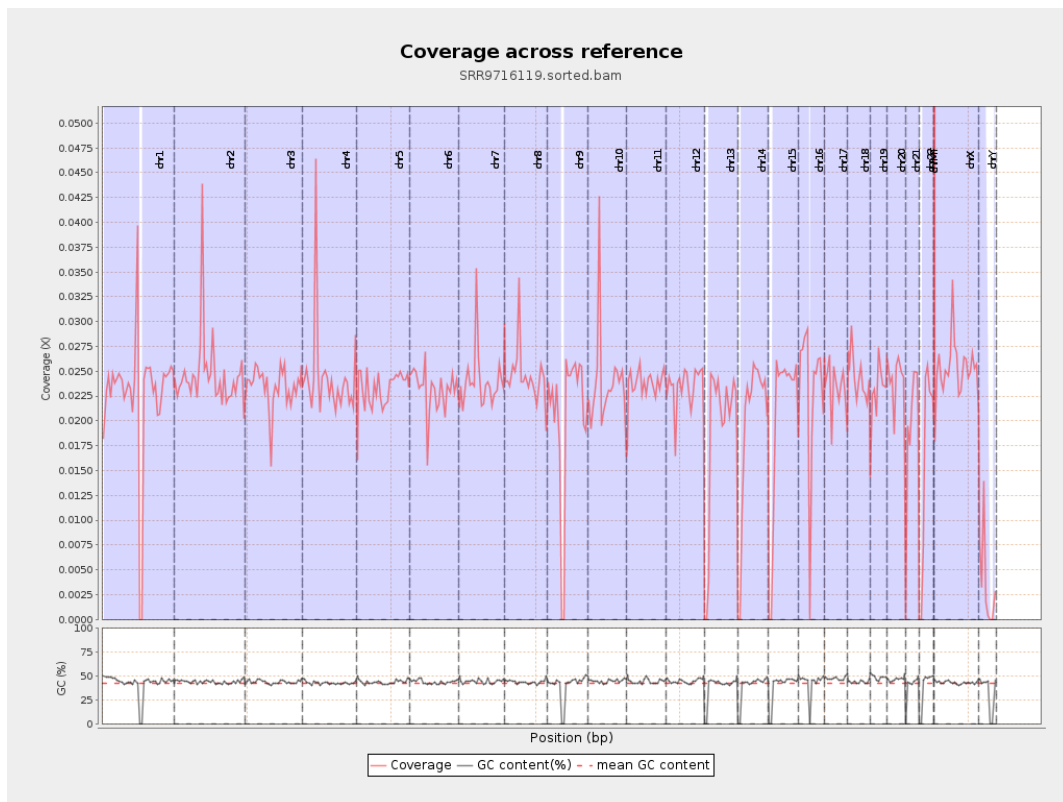
General error rate	0.66%
Mismatches	447,004
Insertions	6,186
Mapped reads with at least one insertion	0.69%
Deletions	17,216
Mapped reads with at least one deletion	1.92%
Homopolymer indels	43.02%

2.6. Chromosome stats

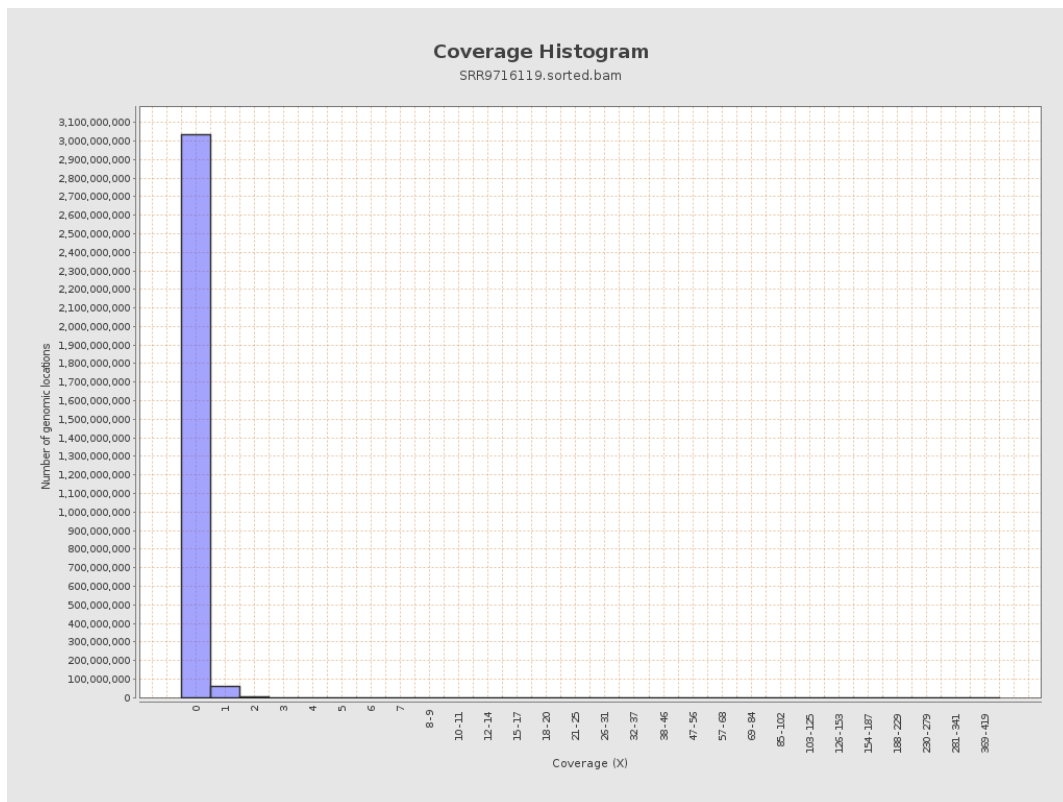
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5627027	0.0226	0.3785
chr2	243199373	5987609	0.0246	0.2608
chr3	198022430	4635467	0.0234	0.1614
chr4	191154276	4646346	0.0243	0.1944
chr5	180915260	4245272	0.0235	0.1634
chr6	171115067	3954107	0.0231	0.1707
chr7	159138663	3816602	0.024	0.2645

chr8	146364022	3577762	0.0244	0.2691
chr9	141213431	2900818	0.0205	0.2111
chr10	135534747	3215913	0.0237	0.2385
chr11	135006516	3216028	0.0238	0.2162
chr12	133851895	3126135	0.0234	0.1625
chr13	115169878	2156256	0.0187	0.1443
chr14	107349540	2102634	0.0196	0.1565
chr15	102531392	2063956	0.0201	0.1503
chr16	90354753	2061260	0.0228	0.1688
chr17	81195210	1892274	0.0233	0.1768
chr18	78077248	1901260	0.0244	0.3321
chr19	59128983	1379124	0.0233	0.2747
chr20	63025520	1500275	0.0238	0.1686
chr21	48129895	941599	0.0196	0.1651
chr22	51304566	837266	0.0163	0.1357
chrMT	16571	9815	0.5923	0.8992
chrX	155270560	3937603	0.0254	0.1872
chrY	59373566	213259	0.0036	0.1326

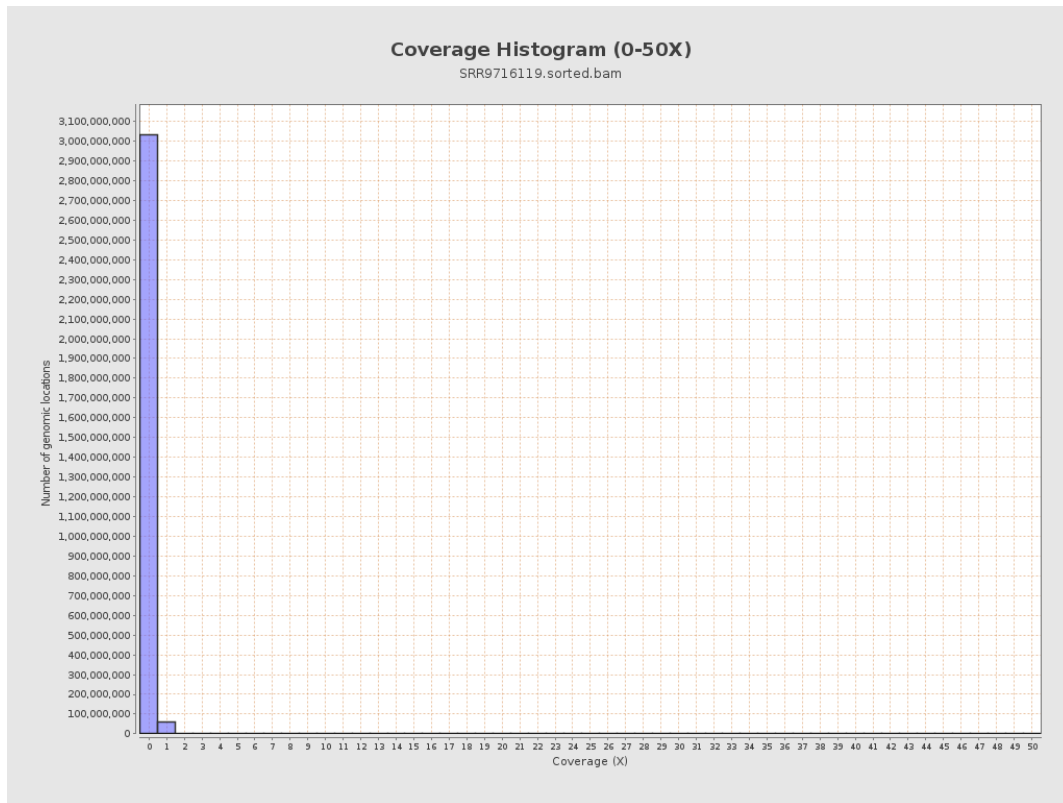
3. Results : Coverage across reference



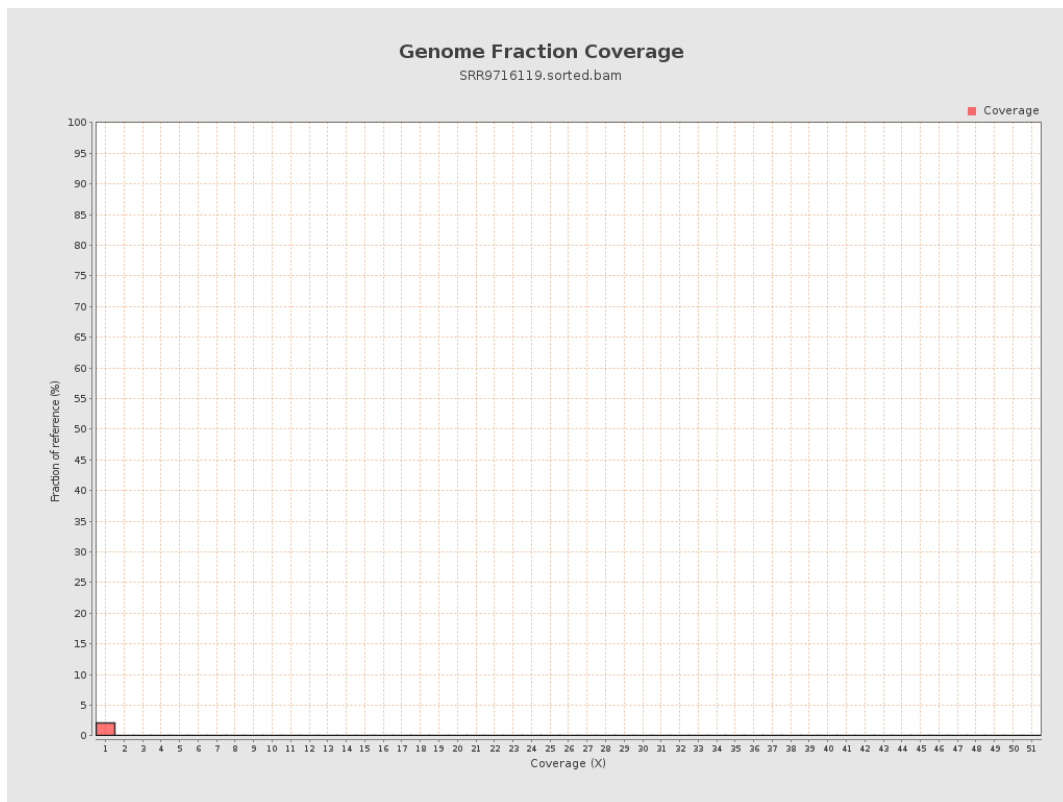
4. Results : Coverage Histogram



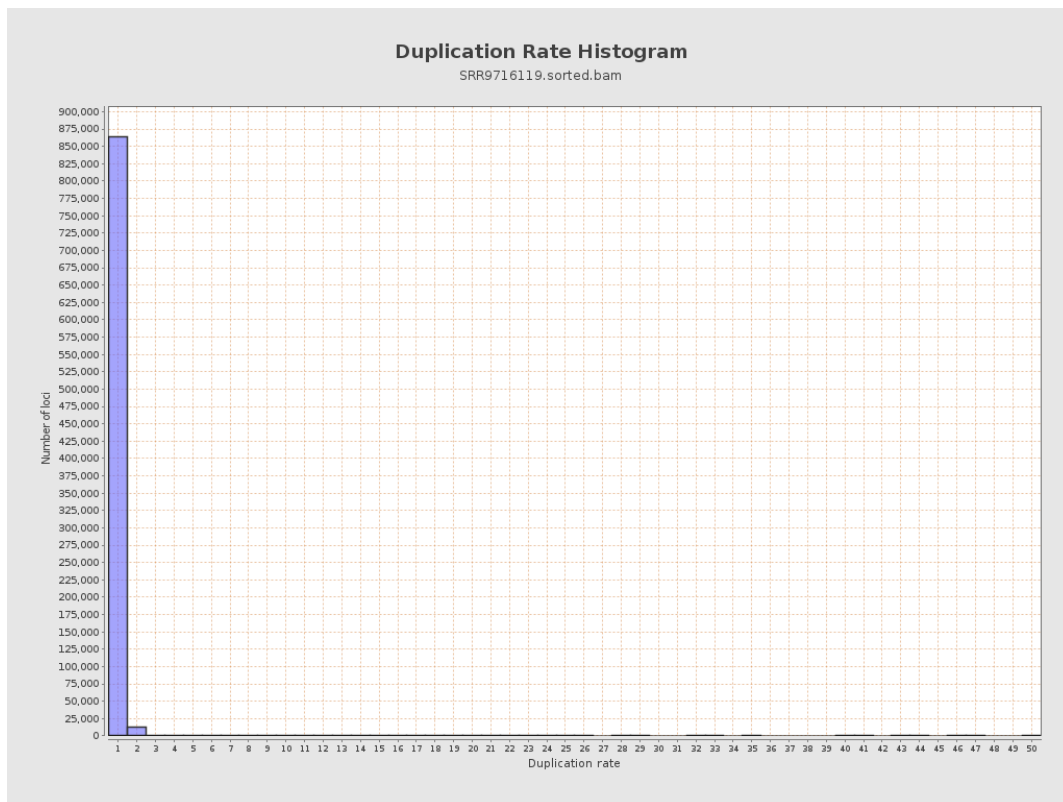
5. Results : Coverage Histogram (0-50X)



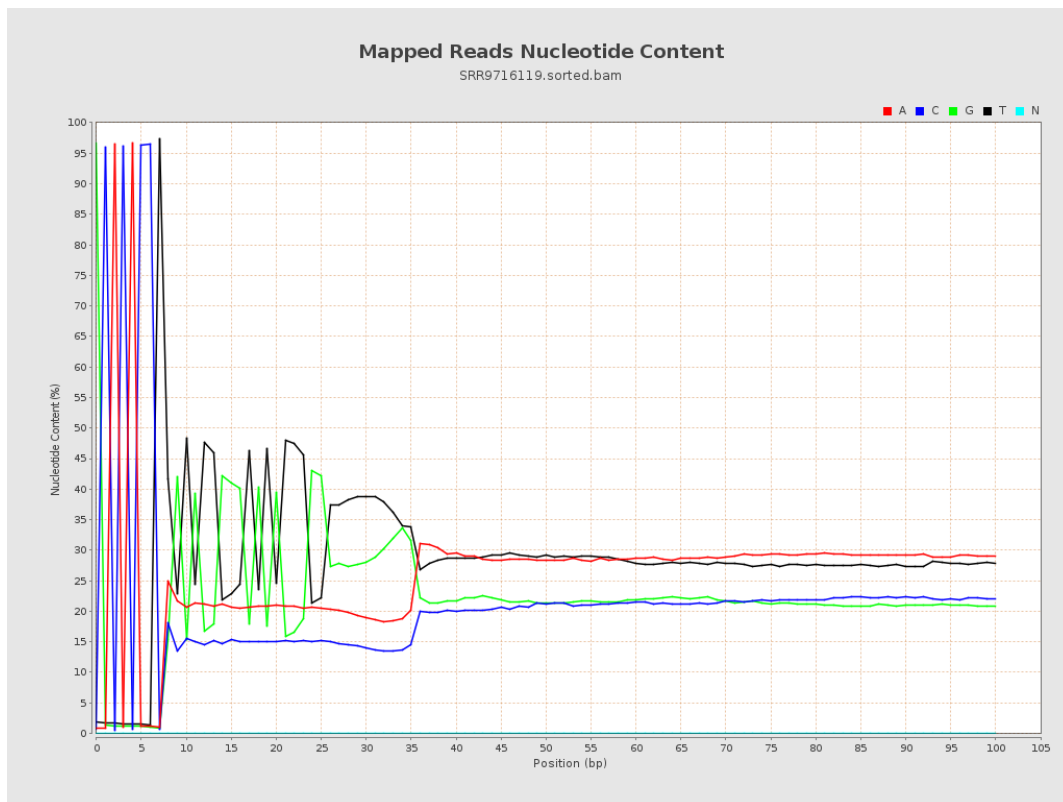
6. Results : Genome Fraction Coverage



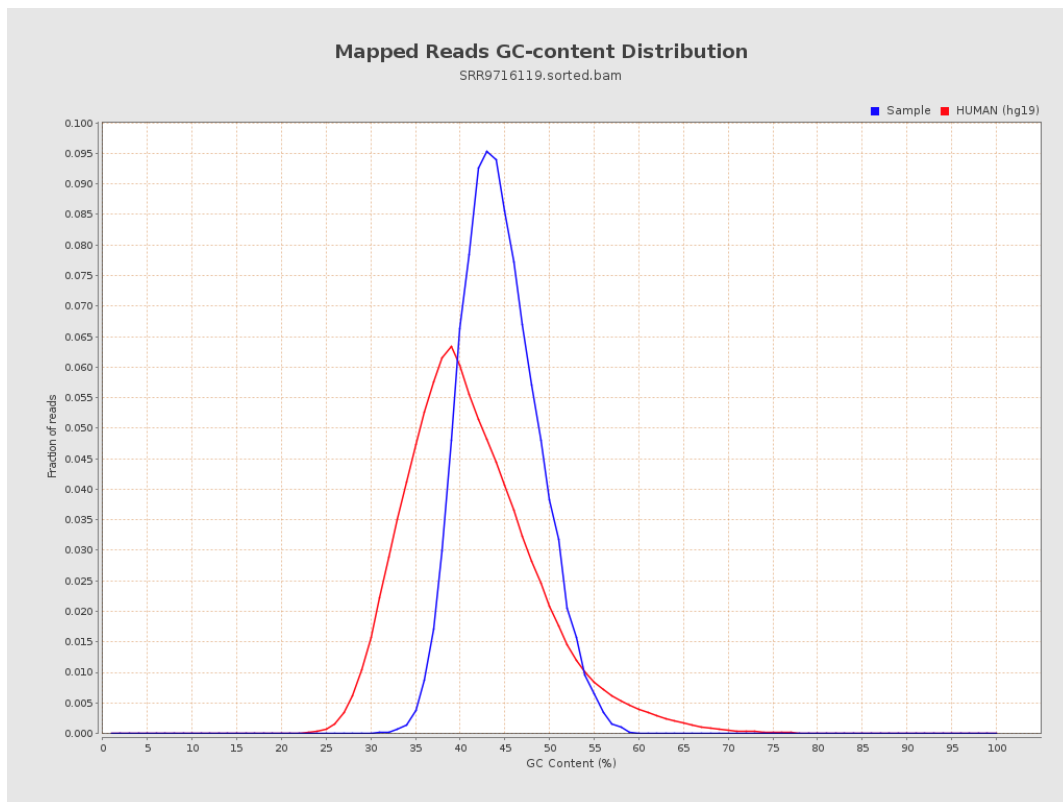
7. Results : Duplication Rate Histogram



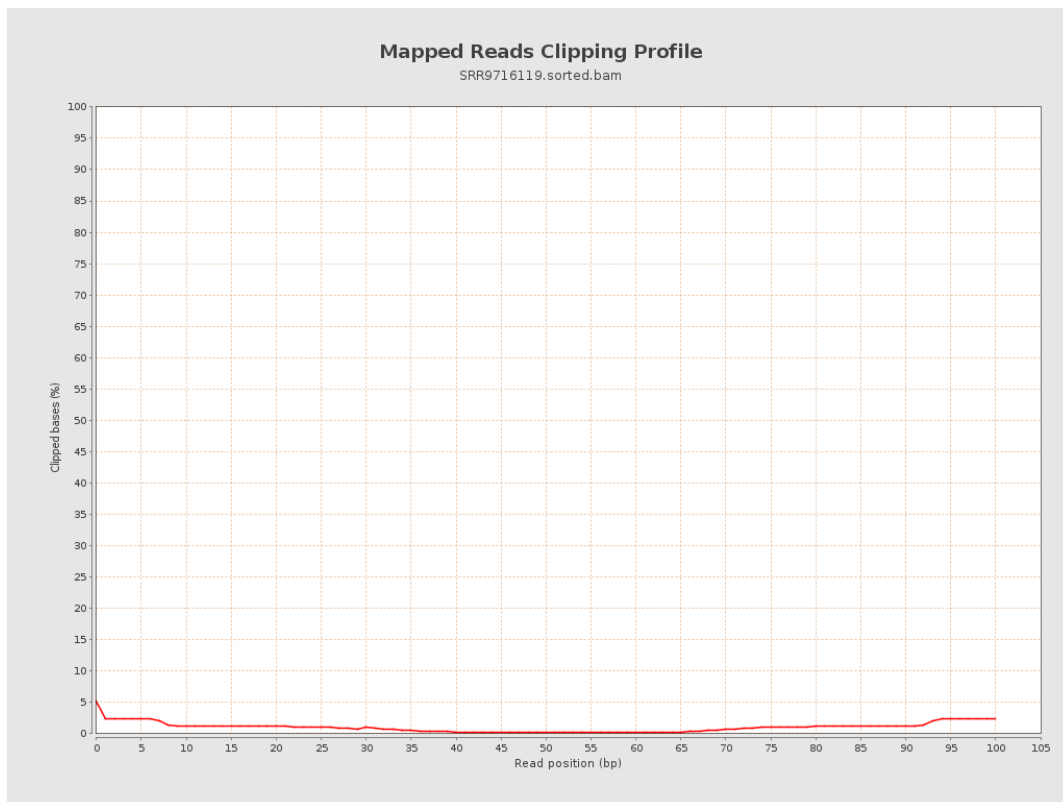
8. Results : Mapped Reads Nucleotide Content



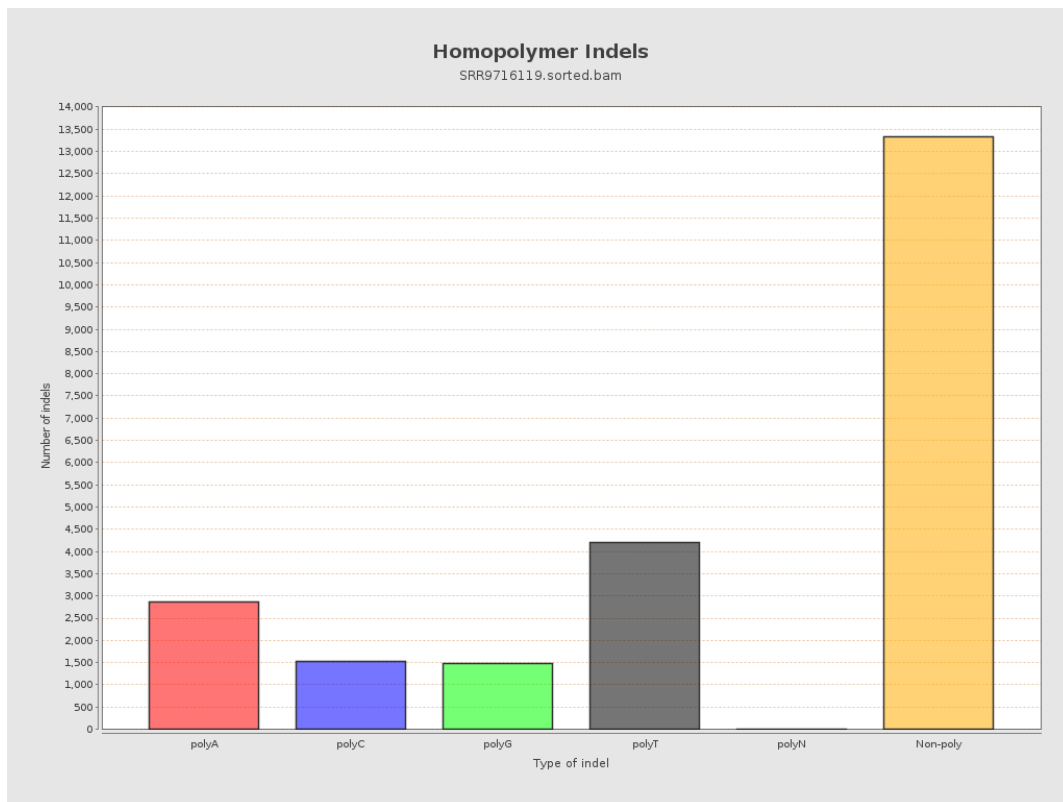
9. Results : Mapped Reads GC-content Distribution



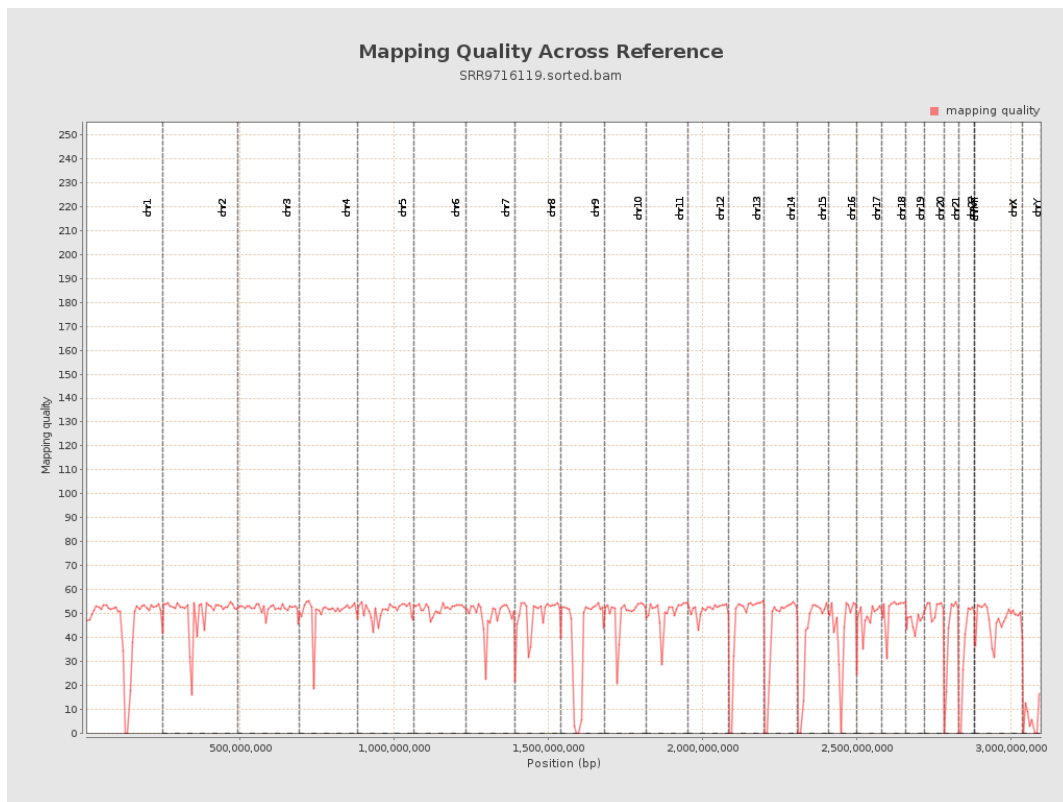
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

