

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 23:05:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716989.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_SRR9716989 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716989.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 23:05:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716989.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,782,459
Mapped reads	2,504,438 / 90.01%
Unmapped reads	278,021 / 9.99%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,007 / 0.29%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	113,332 / 4.07%
Duplication rate	3.4%
Clipped reads	2,509,159 / 90.18%

2.2. ACGT Content

Number/percentage of A's	34,870,861 / 24.37%
Number/percentage of C's	28,979,288 / 20.26%
Number/percentage of T's	43,795,562 / 30.61%
Number/percentage of G's	35,416,777 / 24.76%
Number/percentage of N's	1,132 / 0%
GC Percentage	45.01%

2.3. Coverage

Mean	0.0462

Standard Deviation	0.3468
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2.4. Mapping Quality

Mean Mapping Quality	43.62
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2.5. Mismatches and indels

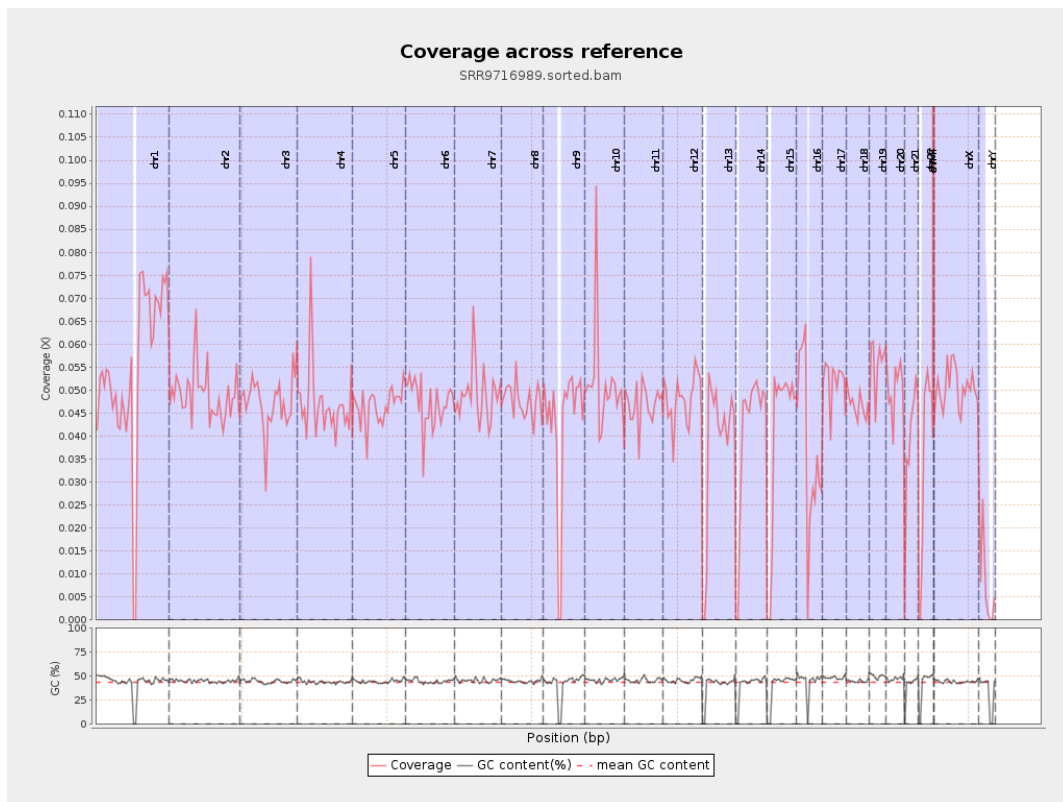
General error rate	0.52%
Mismatches	729,111
Insertions	8,778
Mapped reads with at least one insertion	0.35%
Deletions	26,652
Mapped reads with at least one deletion	1.06%
Homopolymer indels	42.15%

2.6. Chromosome stats

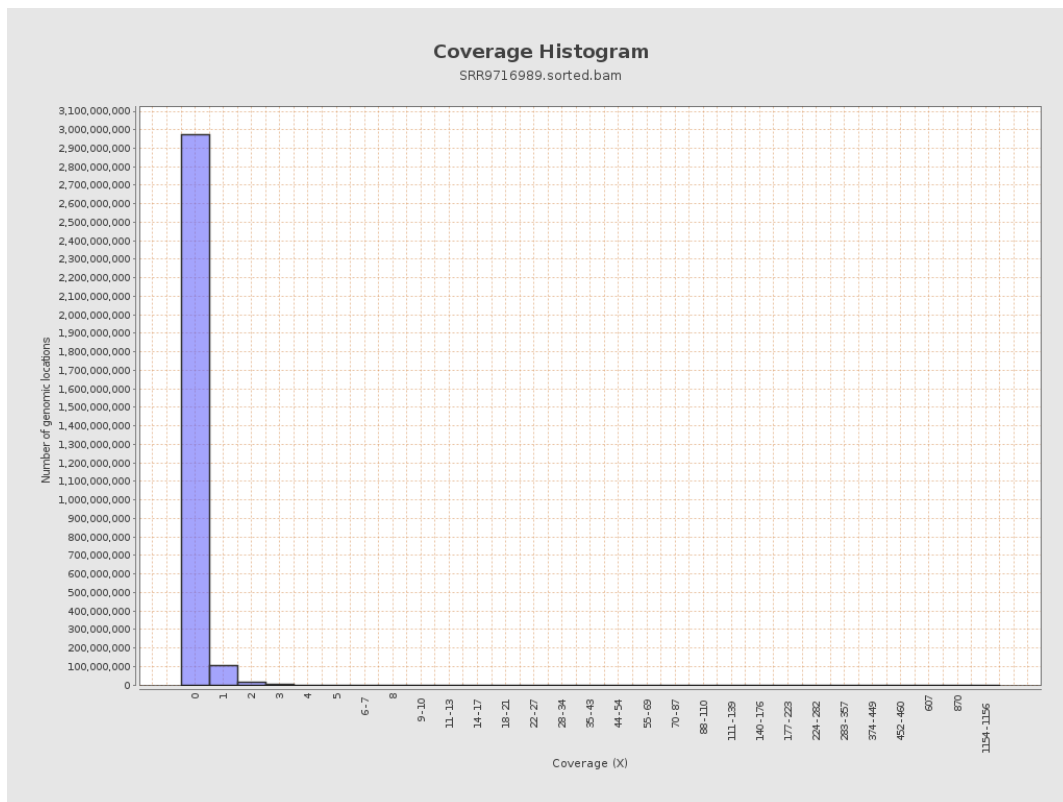
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	13569767	0.0544	0.4327
chr2	243199373	11936884	0.0491	0.564
chr3	198022430	9320952	0.0471	0.2556
chr4	191154276	8925421	0.0467	0.295
chr5	180915260	8408878	0.0465	0.2485
chr6	171115067	8074392	0.0472	0.3019
chr7	159138663	7807522	0.0491	0.4426

chr8	146364022	6962832	0.0476	0.3162
chr9	141213431	5967279	0.0423	0.299
chr10	135534747	6908525	0.051	0.4669
chr11	135006516	6308652	0.0467	0.3125
chr12	133851895	6412654	0.0479	0.255
chr13	115169878	4359566	0.0379	0.2263
chr14	107349540	4332202	0.0404	0.248
chr15	102531392	4148626	0.0405	0.2385
chr16	90354753	3432417	0.038	0.262
chr17	81195210	4198636	0.0517	0.279
chr18	78077248	3659657	0.0469	0.4507
chr19	59128983	3283864	0.0555	0.3991
chr20	63025520	3146540	0.0499	0.267
chr21	48129895	1879993	0.0391	0.2675
chr22	51304566	1773613	0.0346	0.2176
chrMT	16571	12402	0.7484	1.01
chrX	155270560	7812995	0.0503	0.2857
chrY	59373566	461613	0.0078	0.2131

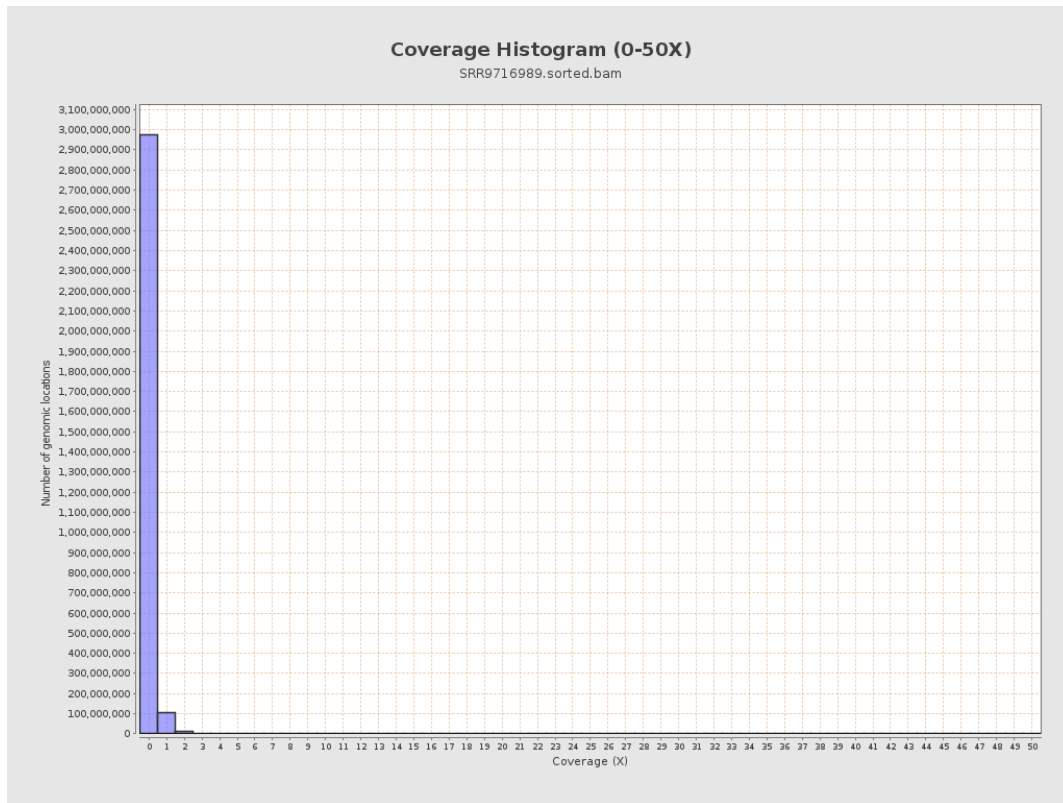
3. Results : Coverage across reference



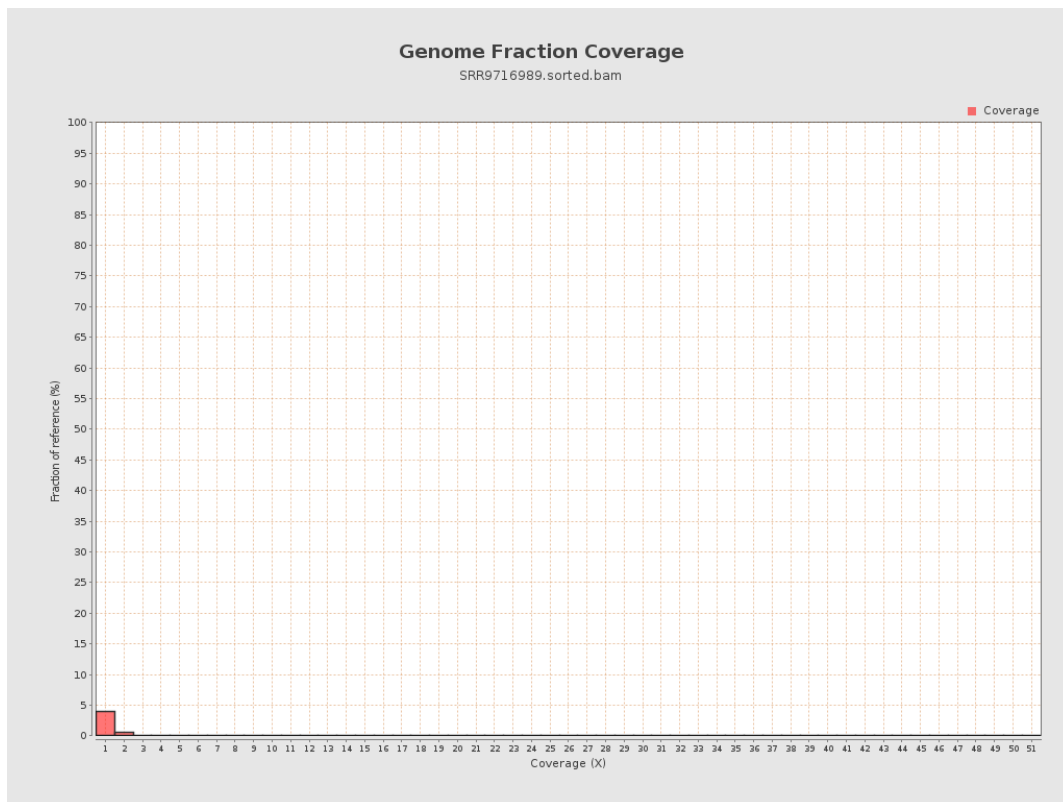
4. Results : Coverage Histogram



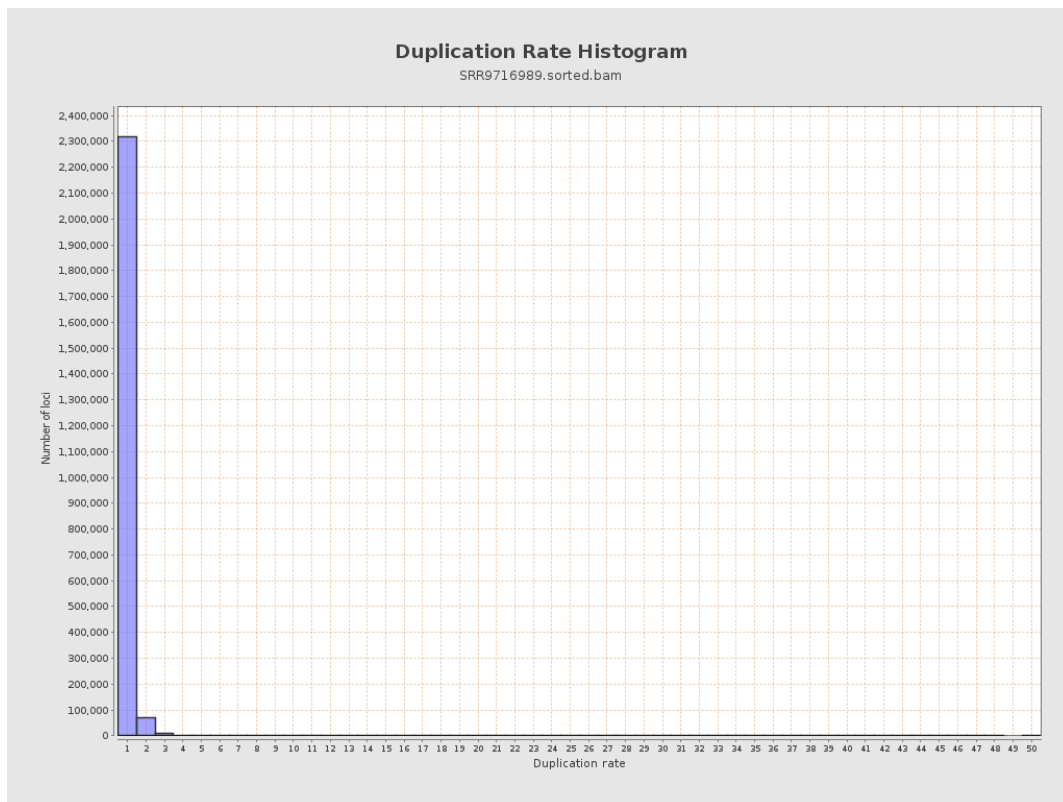
5. Results : Coverage Histogram (0-50X)



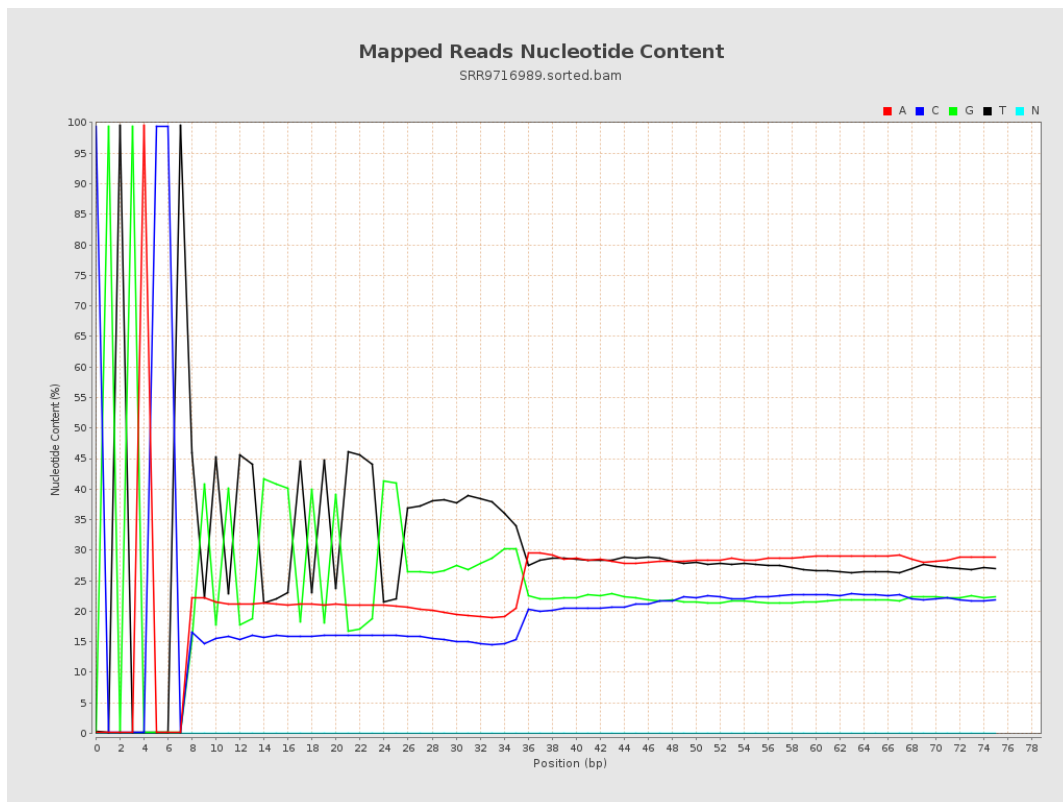
6. Results : Genome Fraction Coverage



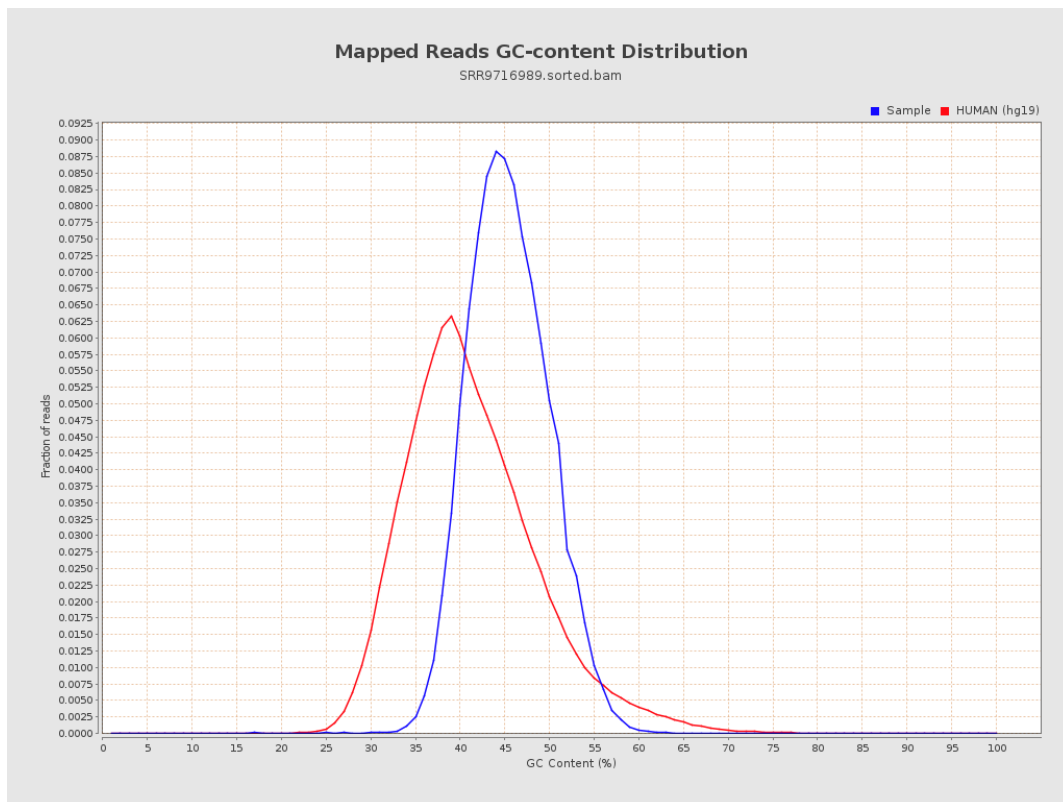
7. Results : Duplication Rate Histogram



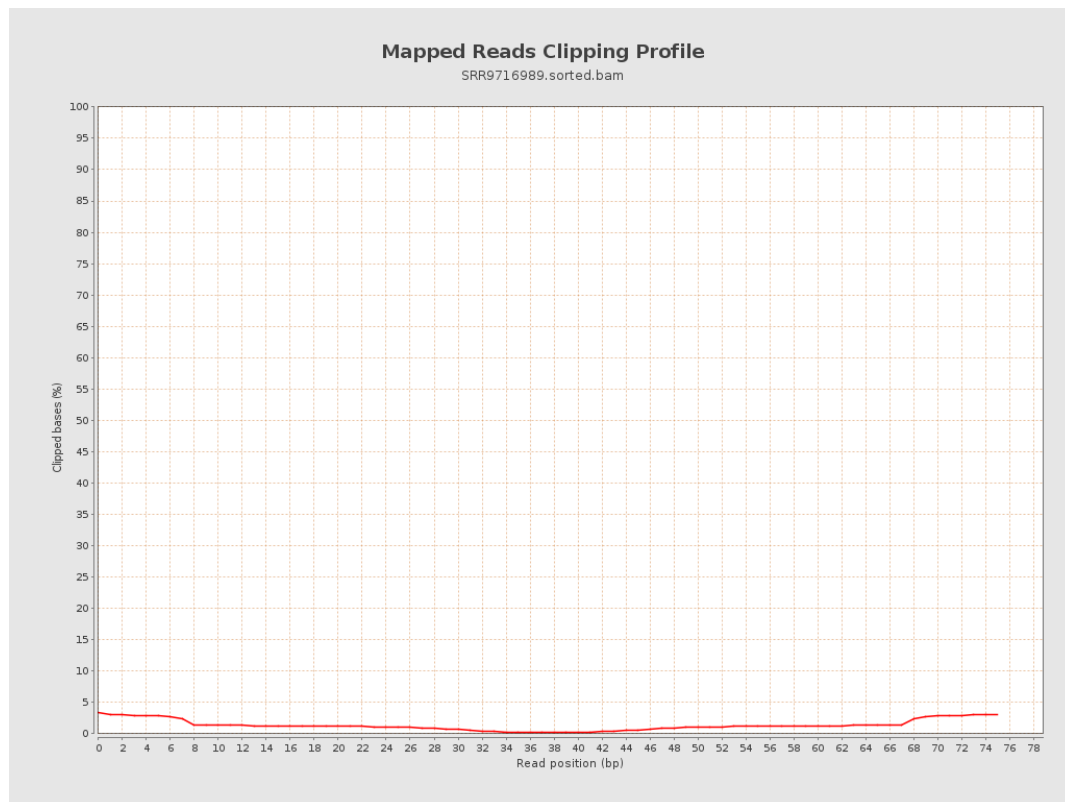
8. Results : Mapped Reads Nucleotide Content



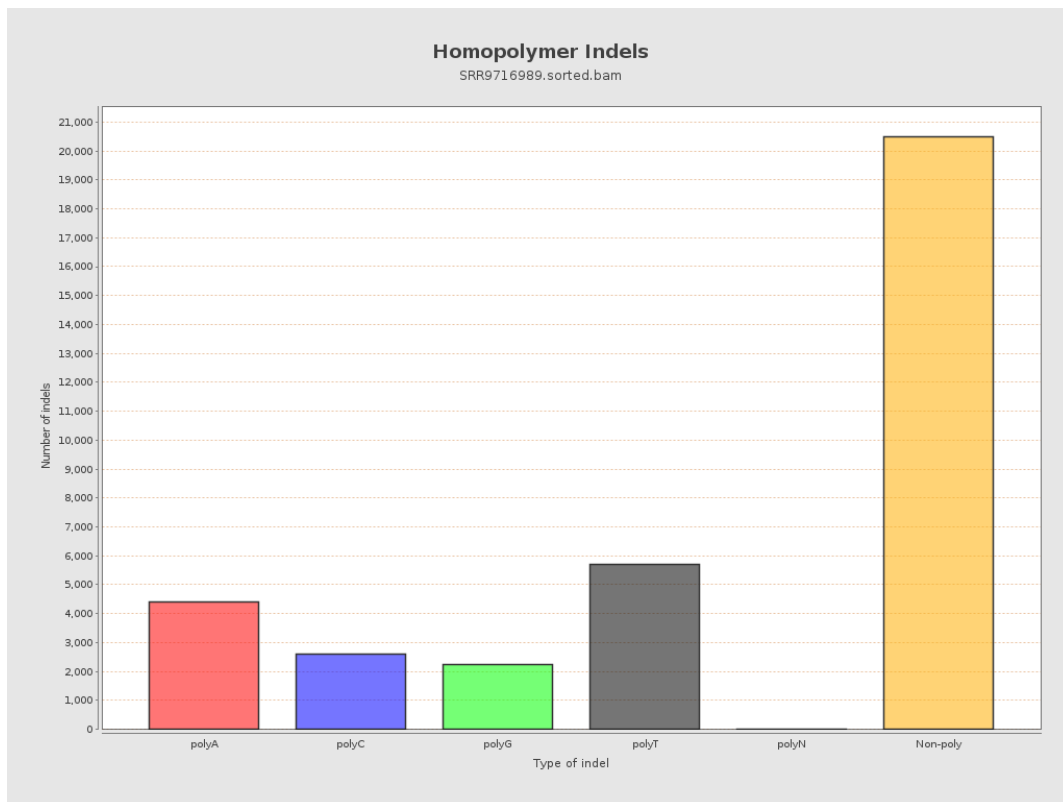
9. Results : Mapped Reads GC-content Distribution



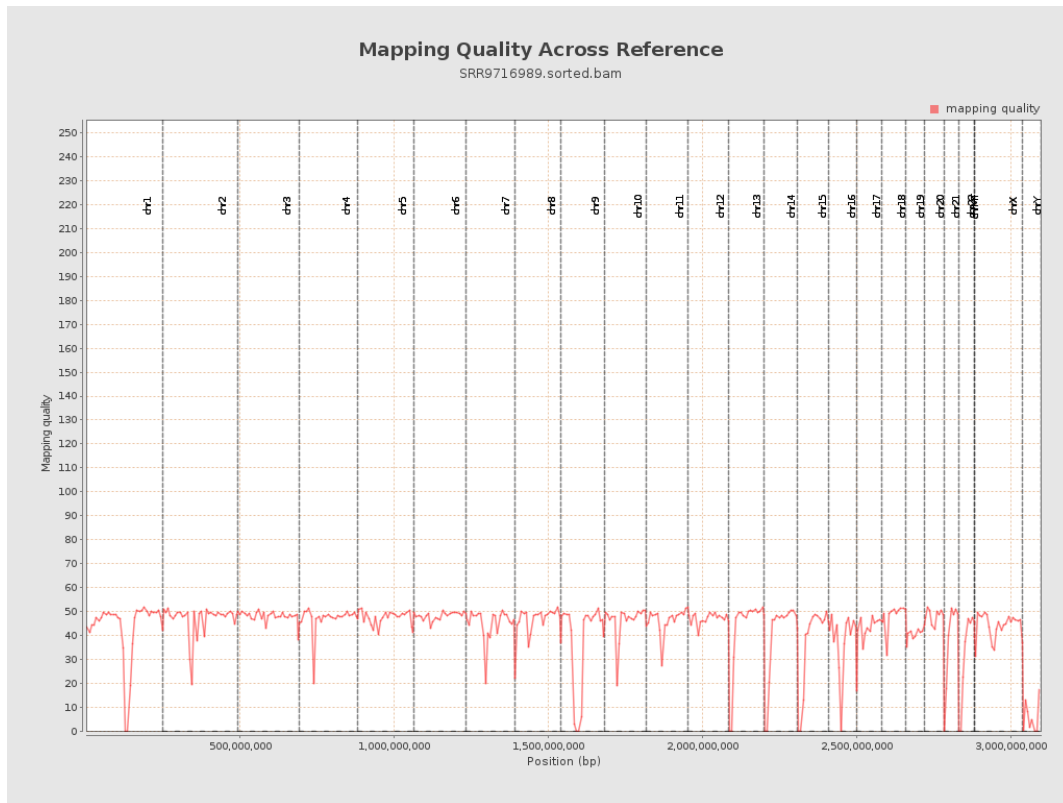
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

