

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 18:33:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716525.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_SRR9716525 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716525.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 18:33:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716525.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	459,009
Mapped reads	411,153 / 89.57%
Unmapped reads	47,856 / 10.43%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,103 / 0.24%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	7,559 / 1.65%
Duplication rate	1.48%
Clipped reads	411,215 / 89.59%

2.2. ACGT Content

Number/percentage of A's	5,925,612 / 25.12%
Number/percentage of C's	4,342,633 / 18.41%
Number/percentage of T's	7,683,641 / 32.58%
Number/percentage of G's	5,633,419 / 23.89%
Number/percentage of N's	209 / 0%
GC Percentage	42.3%

2.3. Coverage

Mean	0.0076

Standard Deviation	0.1
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2.4. Mapping Quality

Mean Mapping Quality	45.13
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2.5. Mismatches and indels

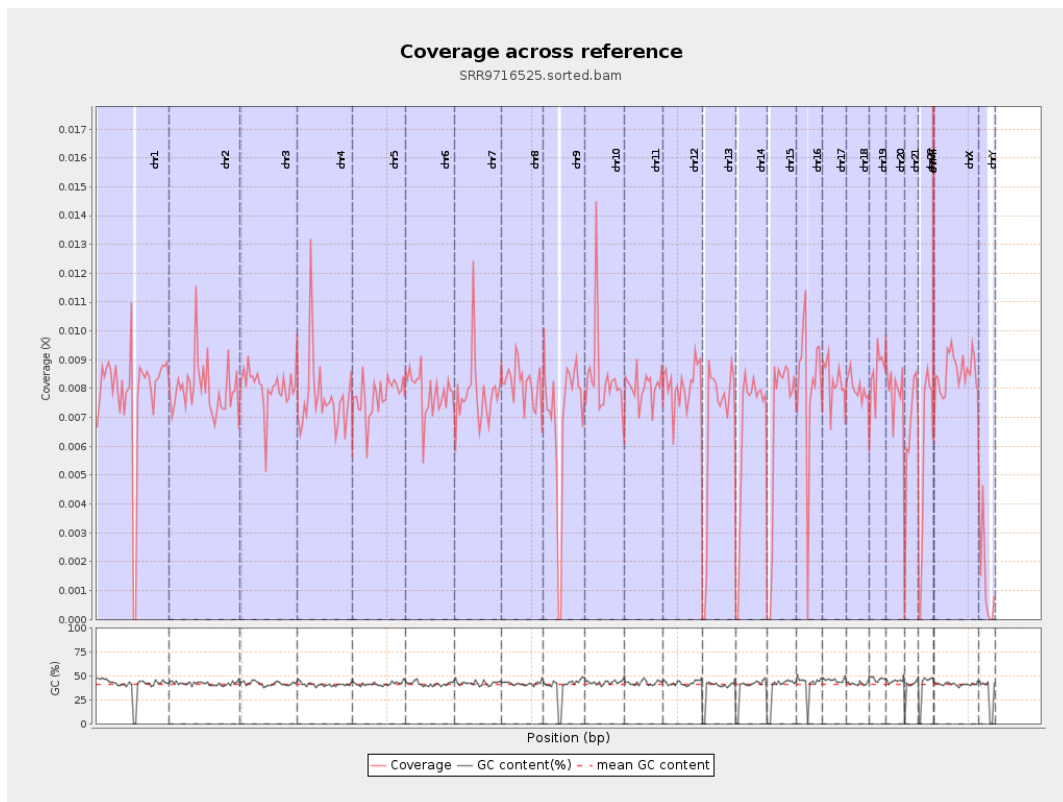
General error rate	0.51%
Mismatches	116,225
Insertions	1,740
Mapped reads with at least one insertion	0.42%
Deletions	4,607
Mapped reads with at least one deletion	1.11%
Homopolymer indels	43.49%

2.6. Chromosome stats

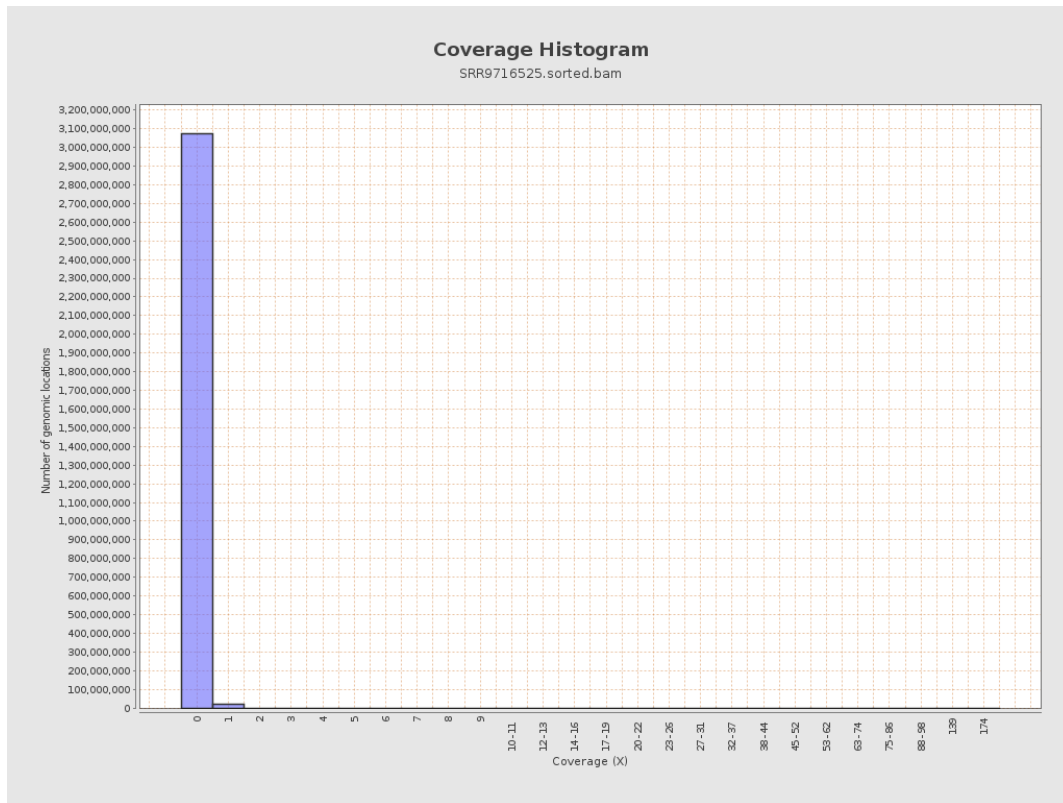
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	1941315	0.0078	0.118
chr2	243199373	1939193	0.008	0.1207
chr3	198022430	1590225	0.008	0.0928
chr4	191154276	1461186	0.0076	0.0933
chr5	180915260	1401949	0.0077	0.0909
chr6	171115067	1344431	0.0079	0.0967
chr7	159138663	1246188	0.0078	0.1143

chr8	146364022	1191642	0.0081	0.101
chr9	141213431	976014	0.0069	0.0907
chr10	135534747	1129876	0.0083	0.1082
chr11	135006516	1084679	0.008	0.0998
chr12	133851895	1080095	0.0081	0.0928
chr13	115169878	773105	0.0067	0.0844
chr14	107349540	707410	0.0066	0.0848
chr15	102531392	686978	0.0067	0.0845
chr16	90354753	739039	0.0082	0.0963
chr17	81195210	664861	0.0082	0.0954
chr18	78077248	627746	0.008	0.1225
chr19	59128983	505037	0.0085	0.1121
chr20	63025520	497341	0.0079	0.0921
chr21	48129895	310202	0.0064	0.0846
chr22	51304566	287972	0.0056	0.0773
chrMT	16571	3443	0.2078	0.4876
chrX	155270560	1325622	0.0085	0.0988
chrY	59373566	77293	0.0013	0.0482

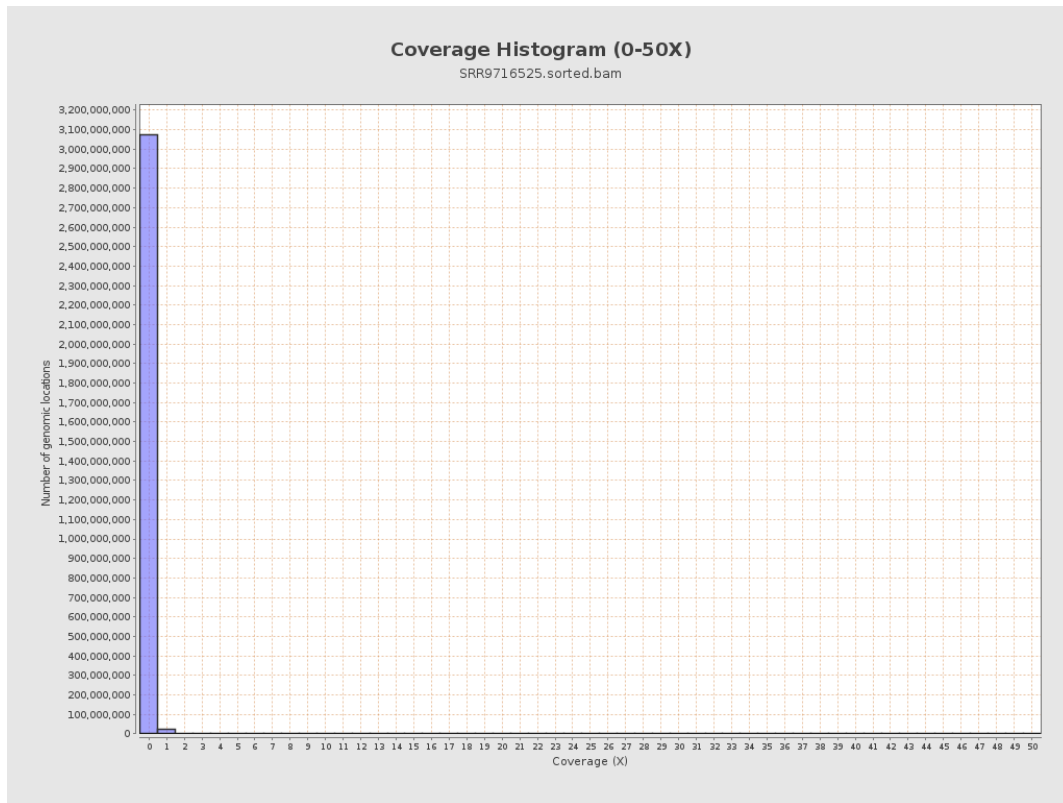
3. Results : Coverage across reference



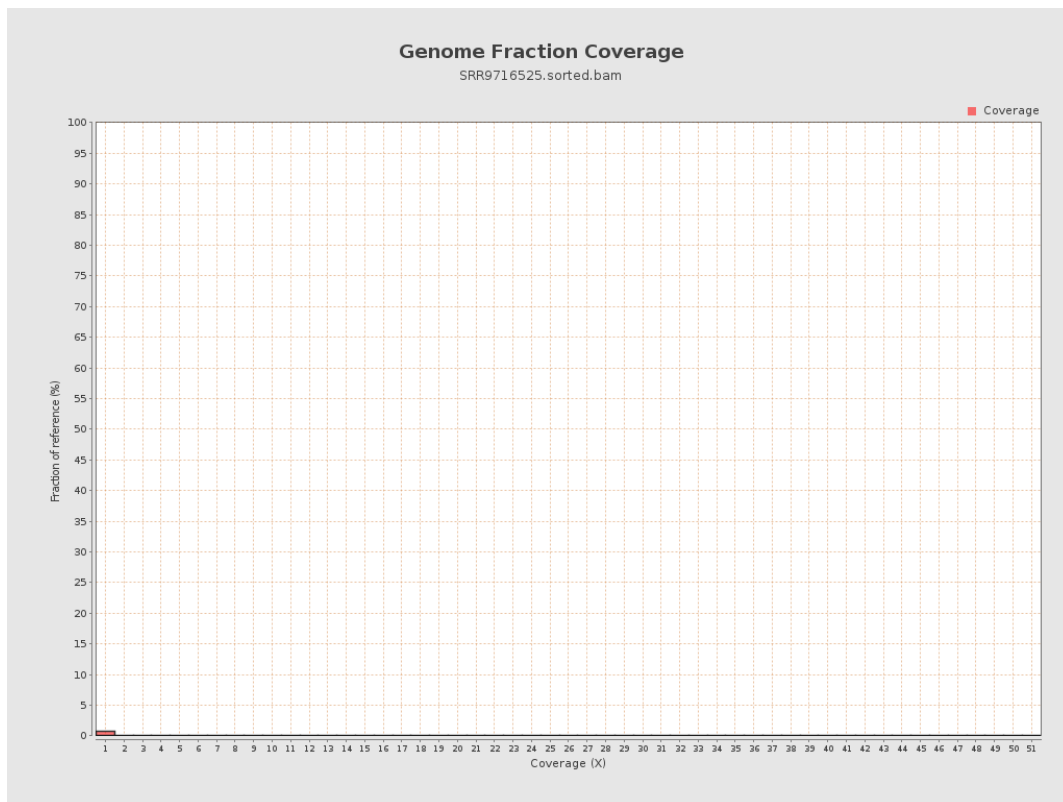
4. Results : Coverage Histogram



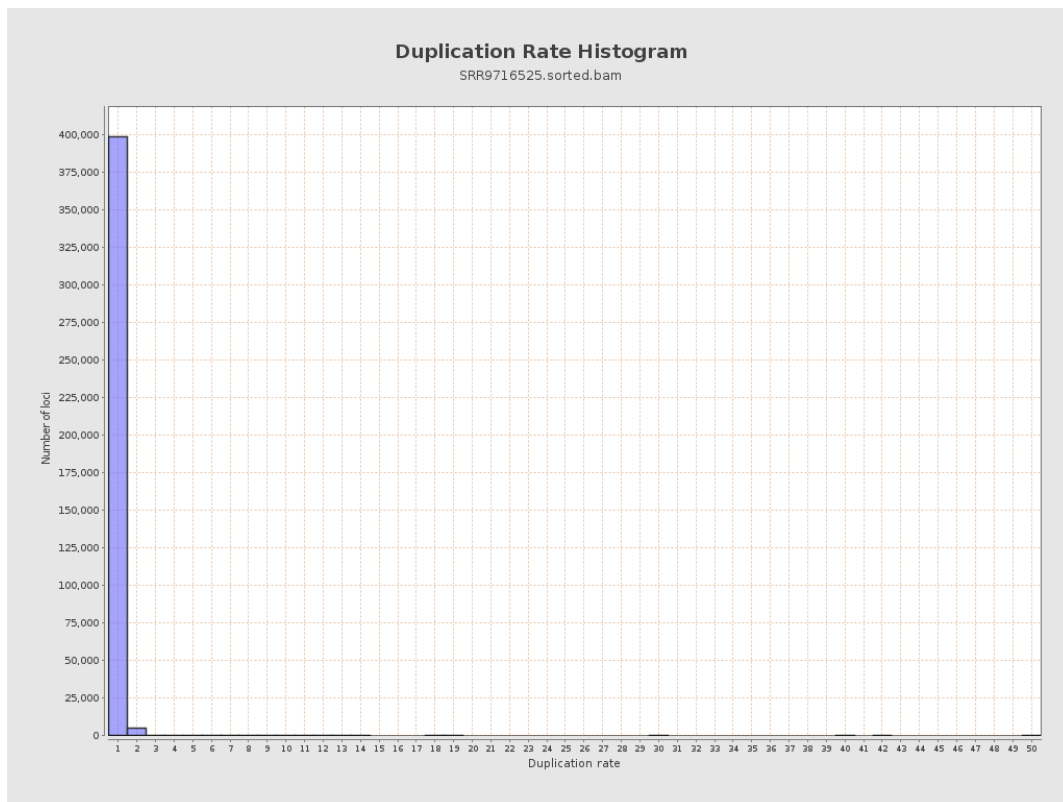
5. Results : Coverage Histogram (0-50X)



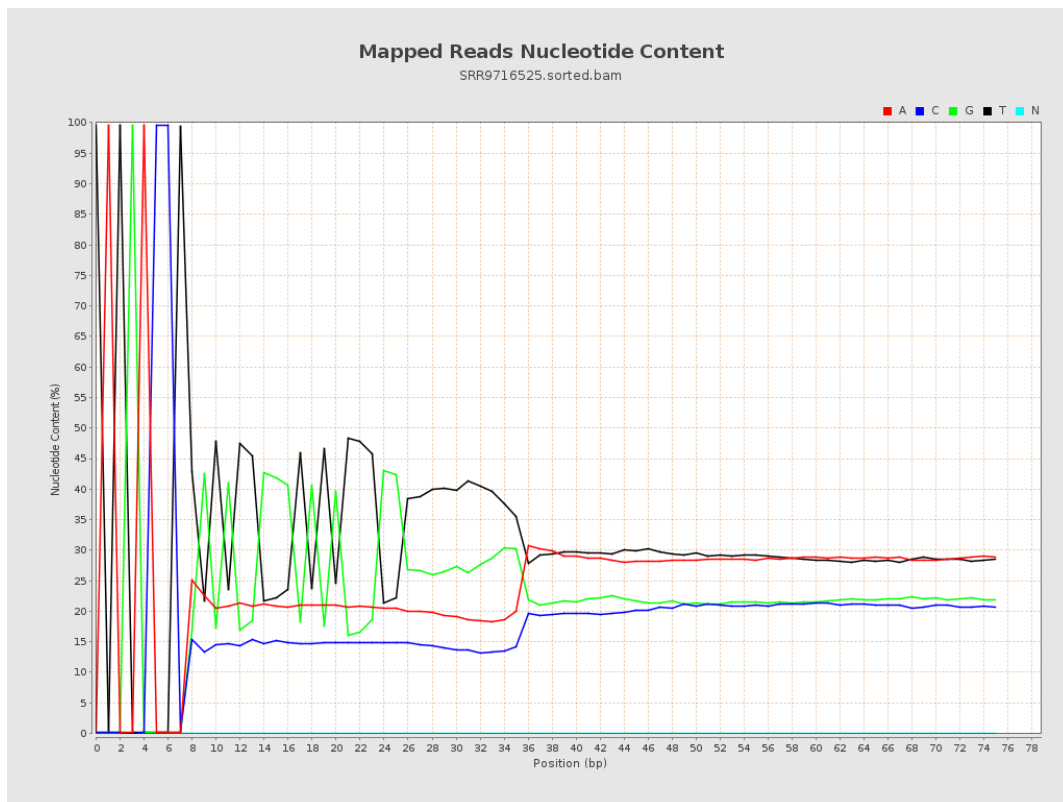
6. Results : Genome Fraction Coverage



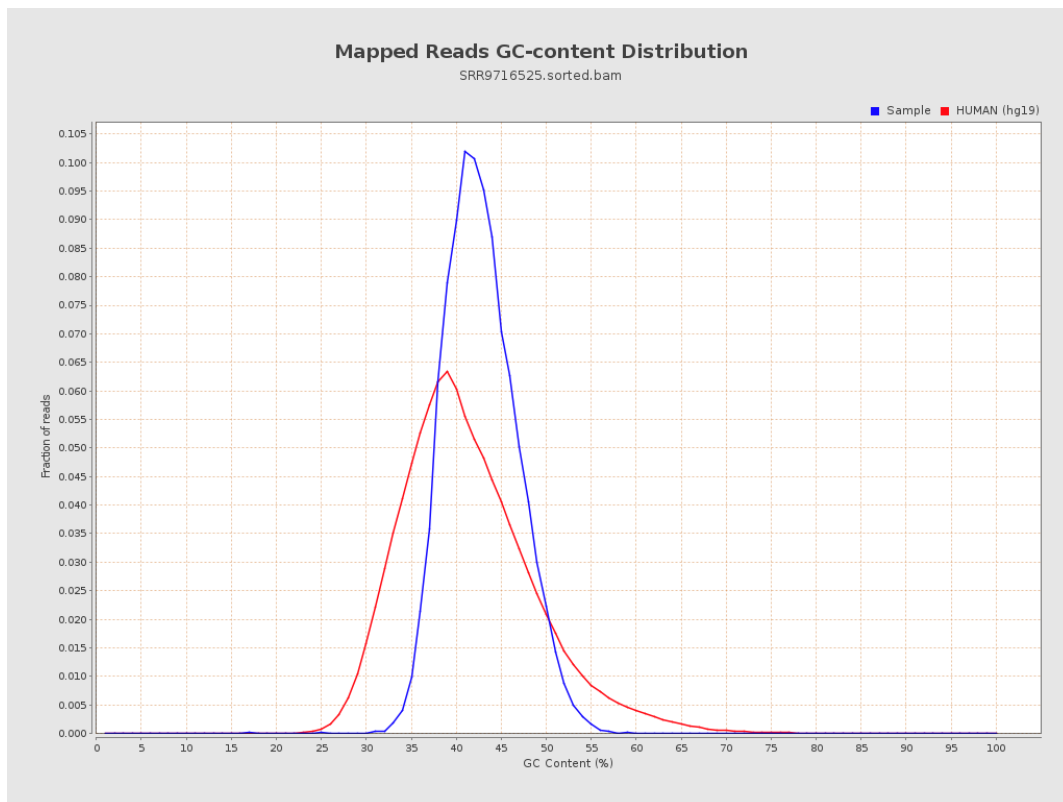
7. Results : Duplication Rate Histogram



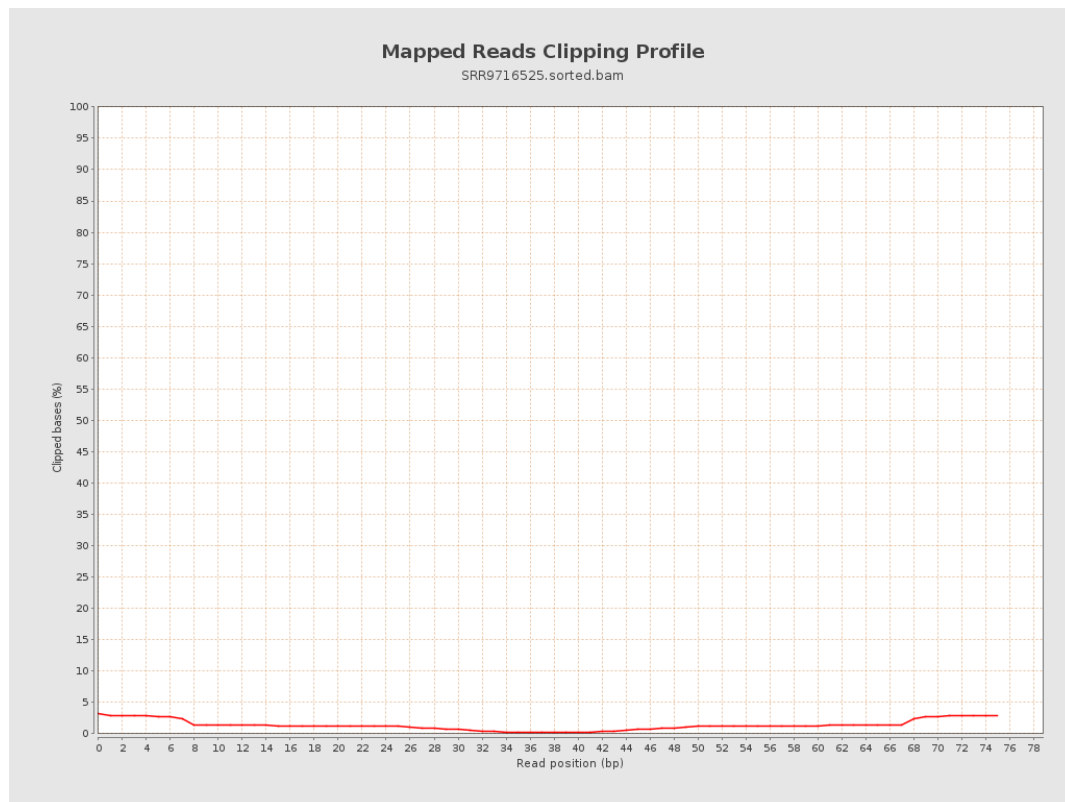
8. Results : Mapped Reads Nucleotide Content



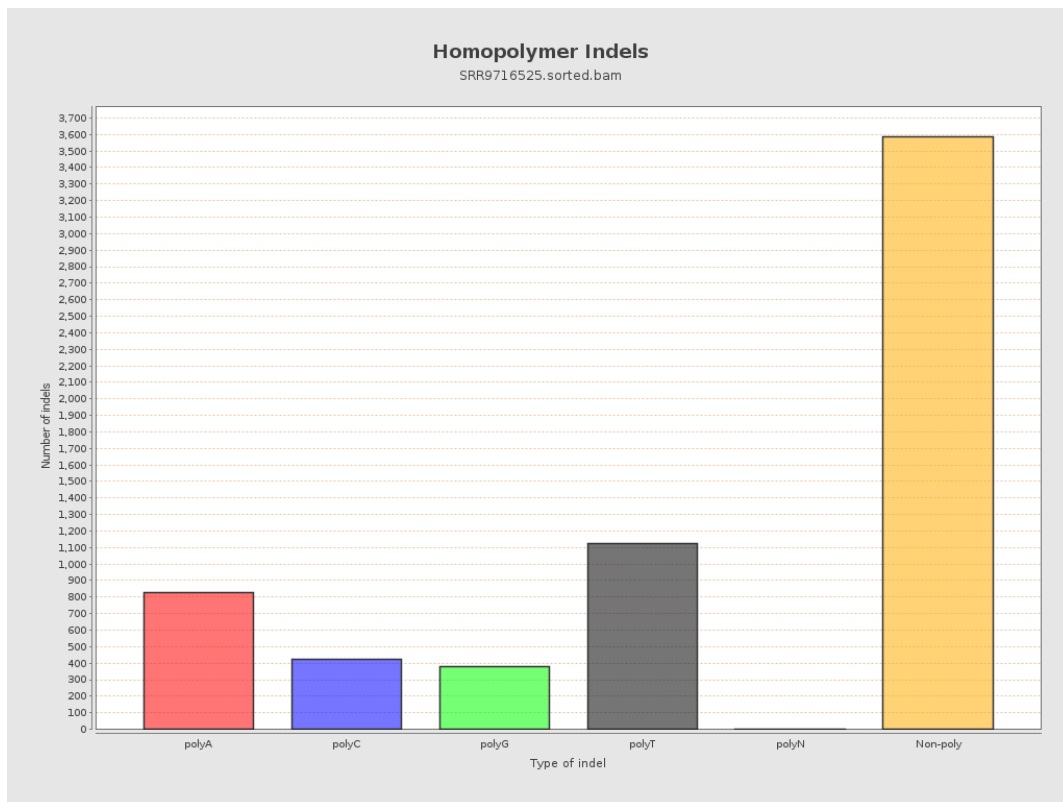
9. Results : Mapped Reads GC-content Distribution



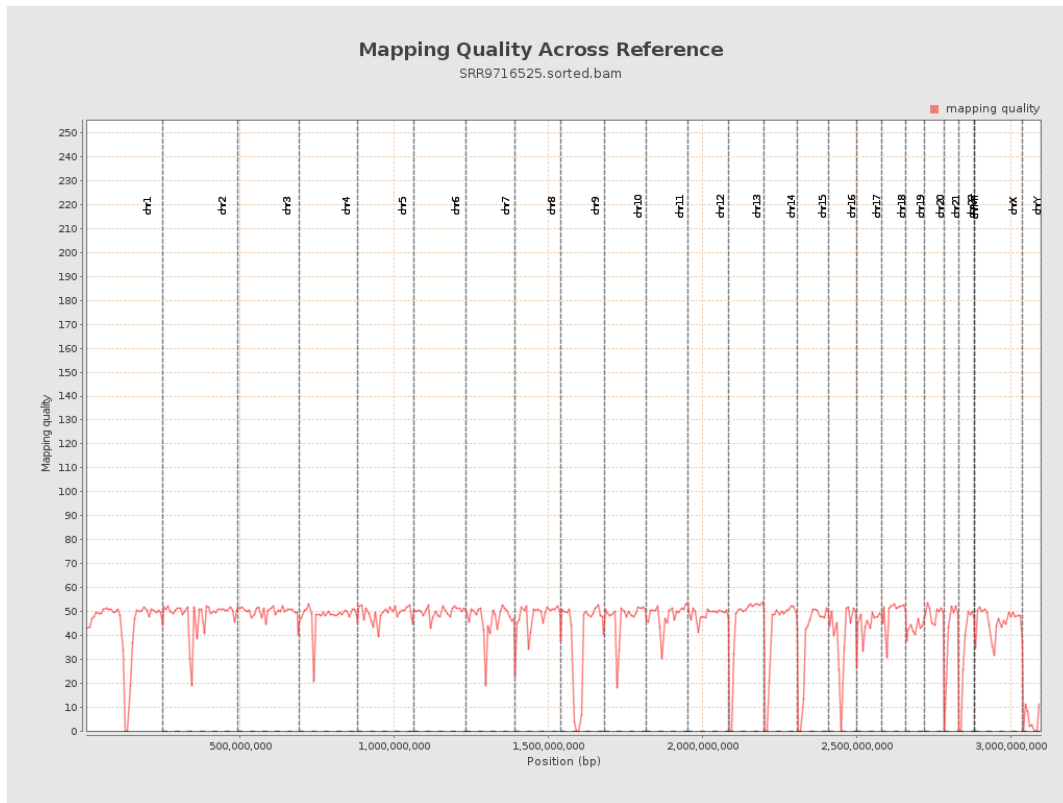
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

