

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 18:18:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716909.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_SRR9716909 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716909.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 18:18:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716909.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	733,513
Mapped reads	595,380 / 81.17%
Unmapped reads	138,133 / 18.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,013 / 0.14%
Read min/max/mean length	30 / 76 / 76.05
Duplicated reads (estimated)	12,847 / 1.75%
Duplication rate	1.61%
Clipped reads	594,961 / 81.11%

2.2. ACGT Content

Number/percentage of A's	8,516,310 / 24.93%
Number/percentage of C's	6,277,479 / 18.37%
Number/percentage of T's	11,146,094 / 32.62%
Number/percentage of G's	8,224,744 / 24.07%
Number/percentage of N's	360 / 0%
GC Percentage	42.45%

2.3. Coverage

Mean	0.011

Standard Deviation	0.1313
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2.4. Mapping Quality

Mean Mapping Quality	43.71
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2.5. Mismatches and indels

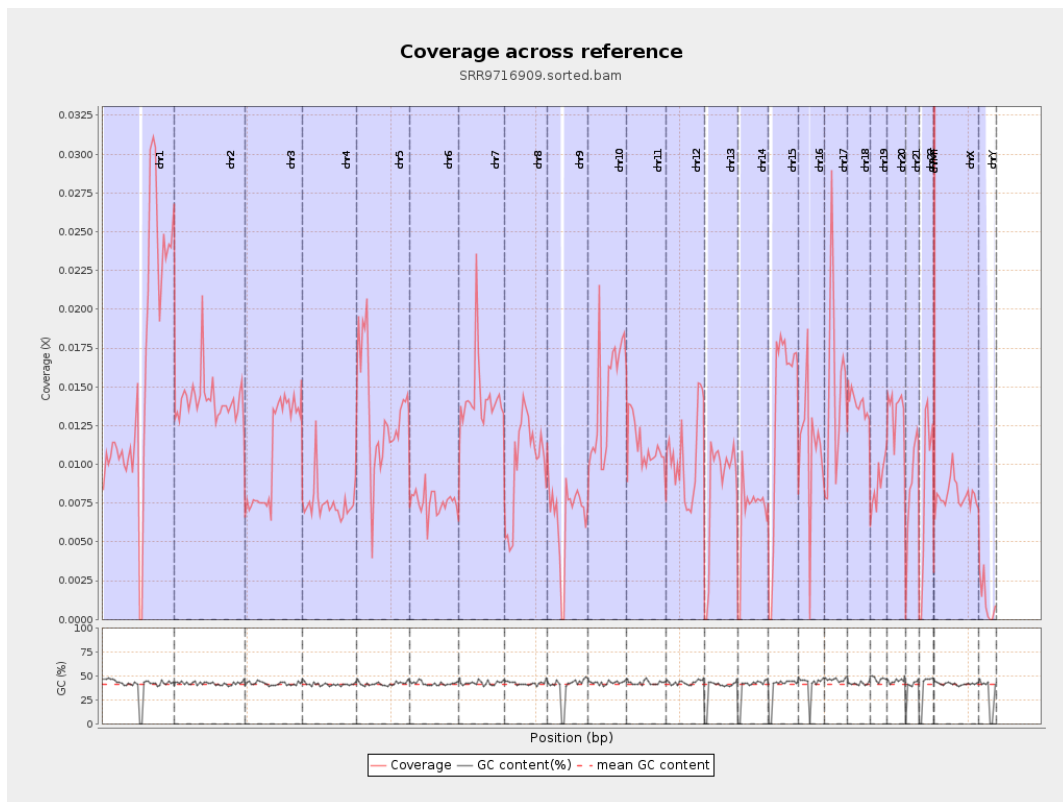
General error rate	0.51%
Mismatches	168,703
Insertions	2,279
Mapped reads with at least one insertion	0.38%
Deletions	6,576
Mapped reads with at least one deletion	1.1%
Homopolymer indels	42.83%

2.6. Chromosome stats

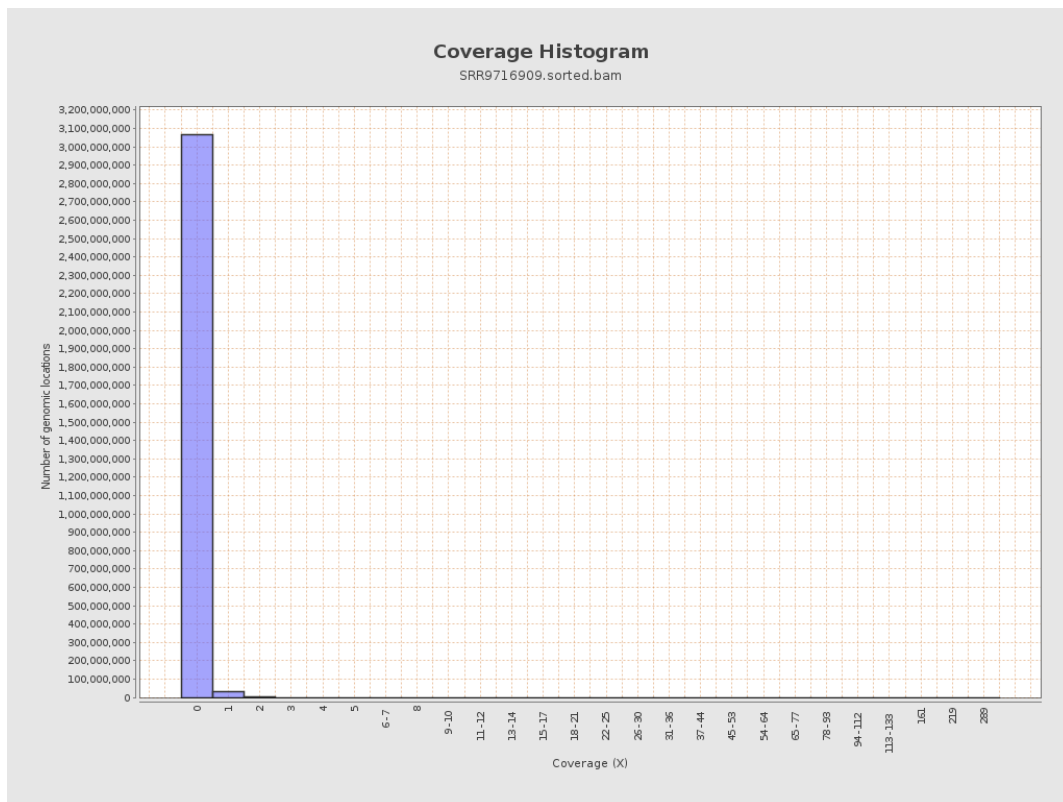
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	3923266	0.0157	0.165
chr2	243199373	3440297	0.0141	0.1821
chr3	198022430	2118249	0.0107	0.109
chr4	191154276	1439817	0.0075	0.0927
chr5	180915260	2398897	0.0133	0.1201
chr6	171115067	1287037	0.0075	0.0979
chr7	159138663	2276325	0.0143	0.2022

chr8	146364022	1488800	0.0102	0.1146
chr9	141213431	943947	0.0067	0.1034
chr10	135534747	1955032	0.0144	0.1574
chr11	135006516	1519541	0.0113	0.1286
chr12	133851895	1384913	0.0103	0.106
chr13	115169878	986844	0.0086	0.0964
chr14	107349540	727184	0.0068	0.0886
chr15	102531392	1418442	0.0138	0.1233
chr16	90354753	1005318	0.0111	0.1151
chr17	81195210	1228649	0.0151	0.1313
chr18	78077248	1086934	0.0139	0.1809
chr19	59128983	518411	0.0088	0.1322
chr20	63025520	847343	0.0134	0.121
chr21	48129895	416035	0.0086	0.0983
chr22	51304566	434914	0.0085	0.0958
chrMT	16571	6060	0.3657	0.6558
chrX	155270560	1253135	0.0081	0.102
chrY	59373566	70001	0.0012	0.0401

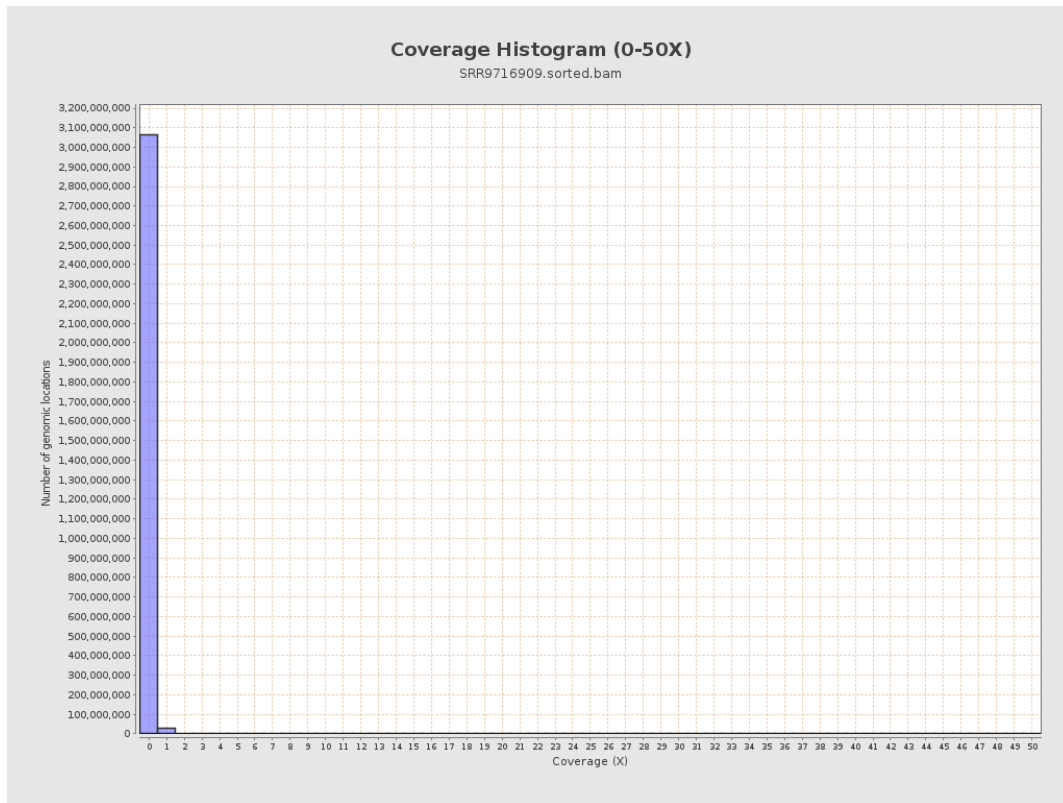
3. Results : Coverage across reference



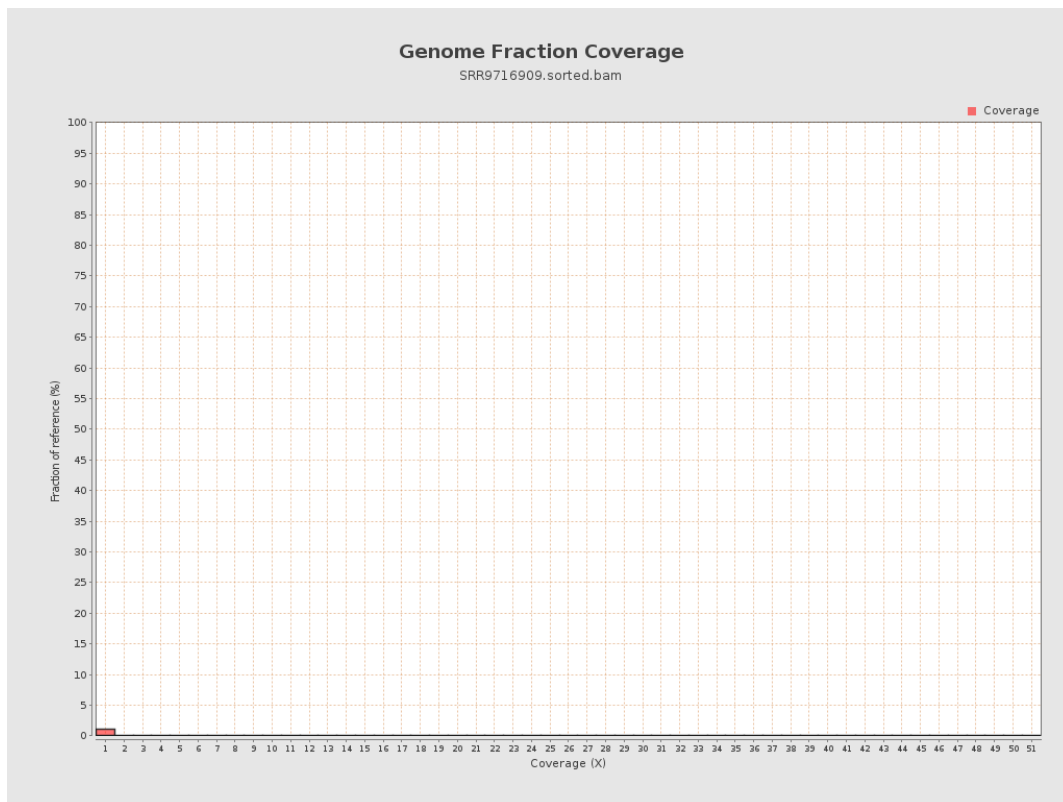
4. Results : Coverage Histogram



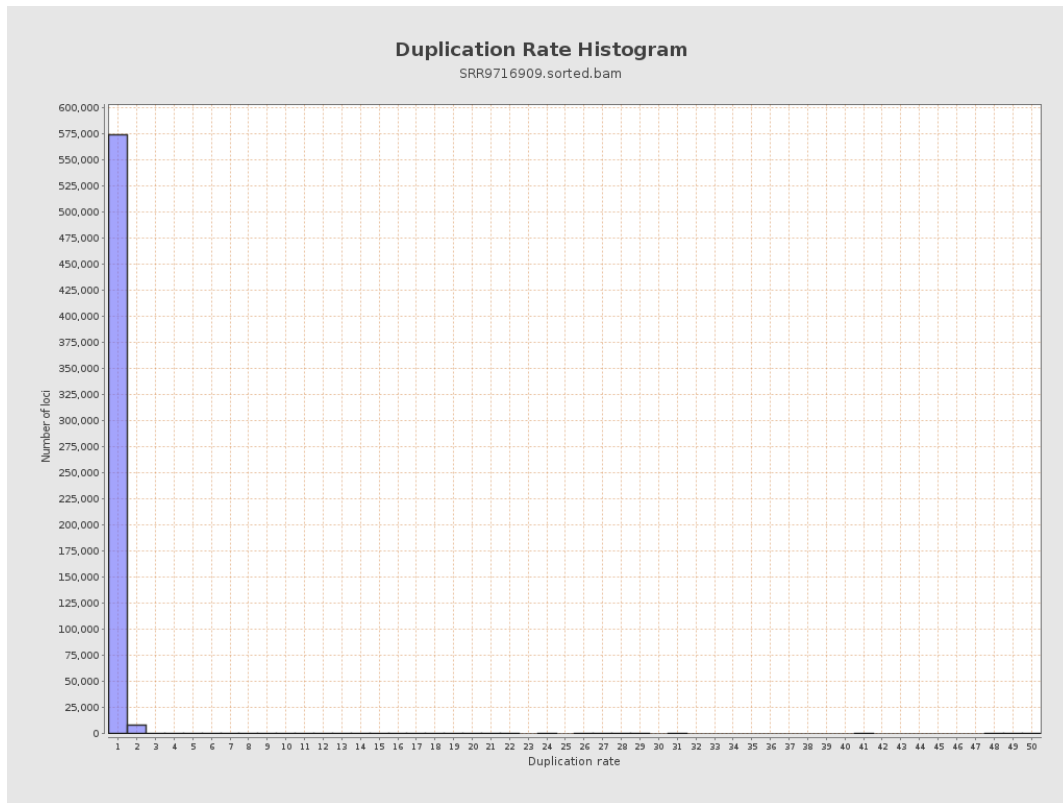
5. Results : Coverage Histogram (0-50X)



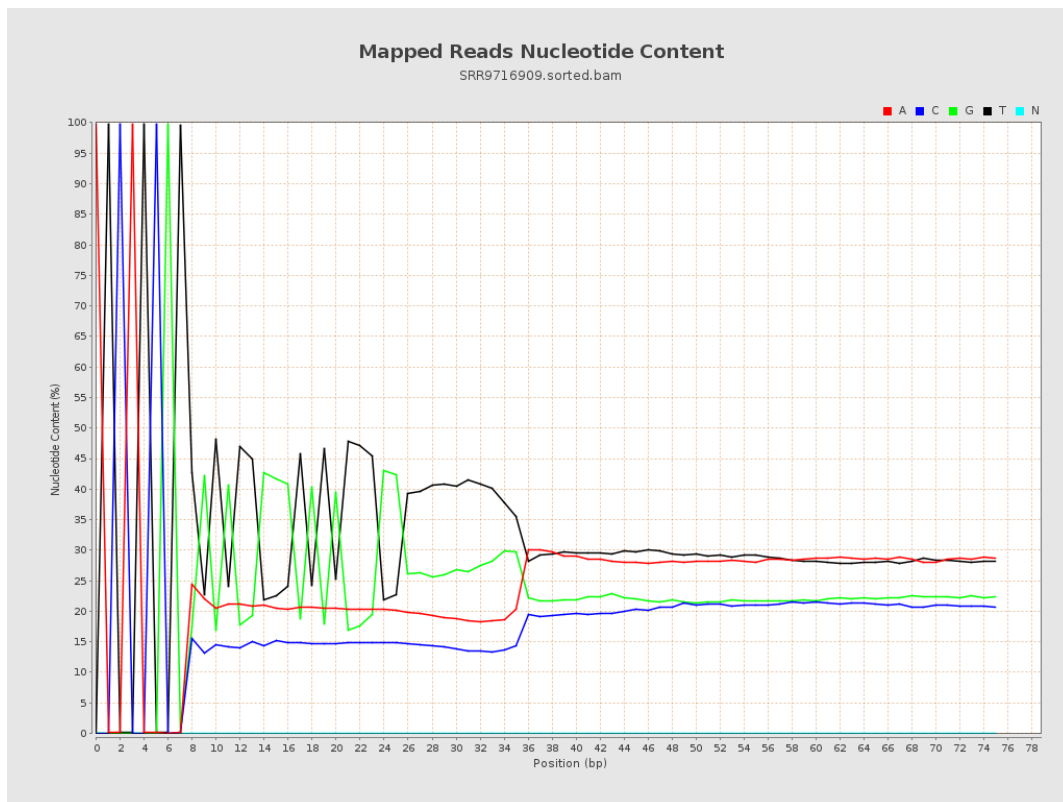
6. Results : Genome Fraction Coverage



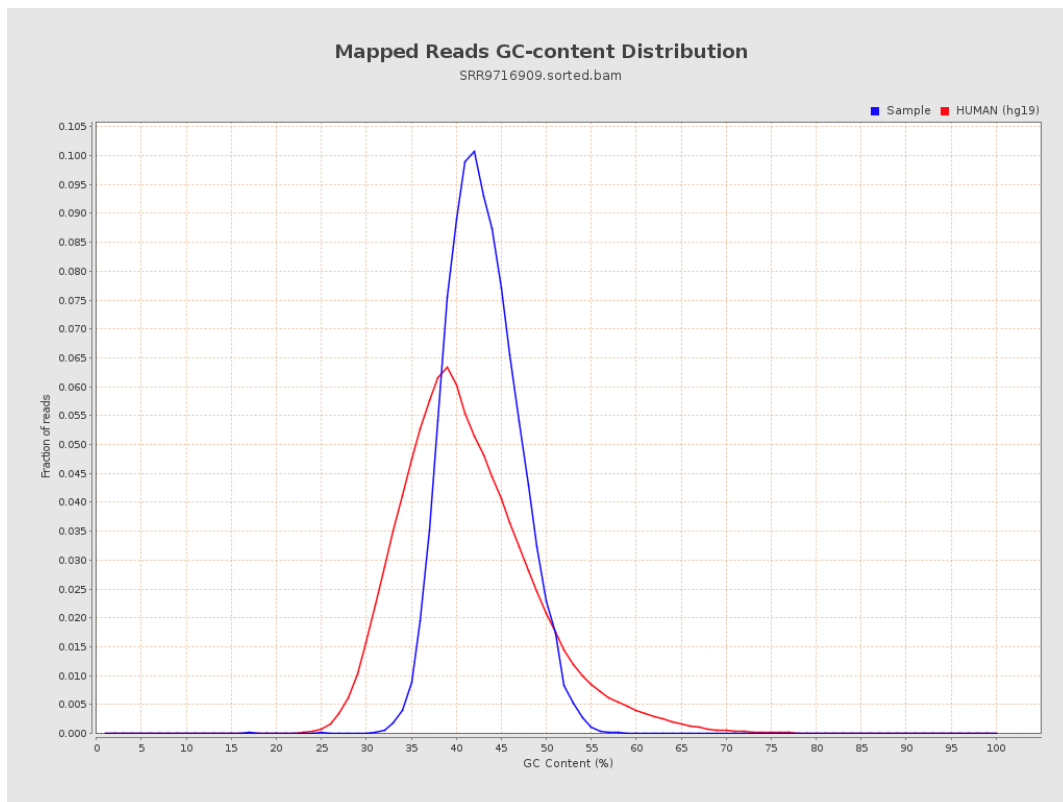
7. Results : Duplication Rate Histogram



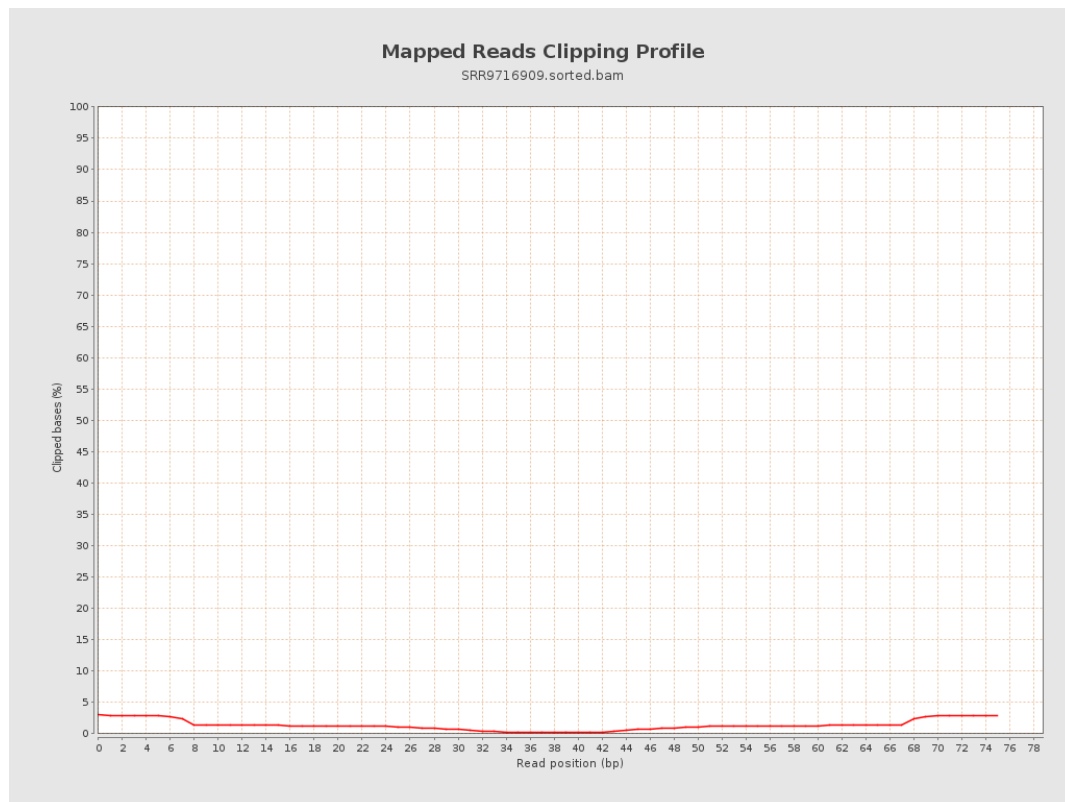
8. Results : Mapped Reads Nucleotide Content



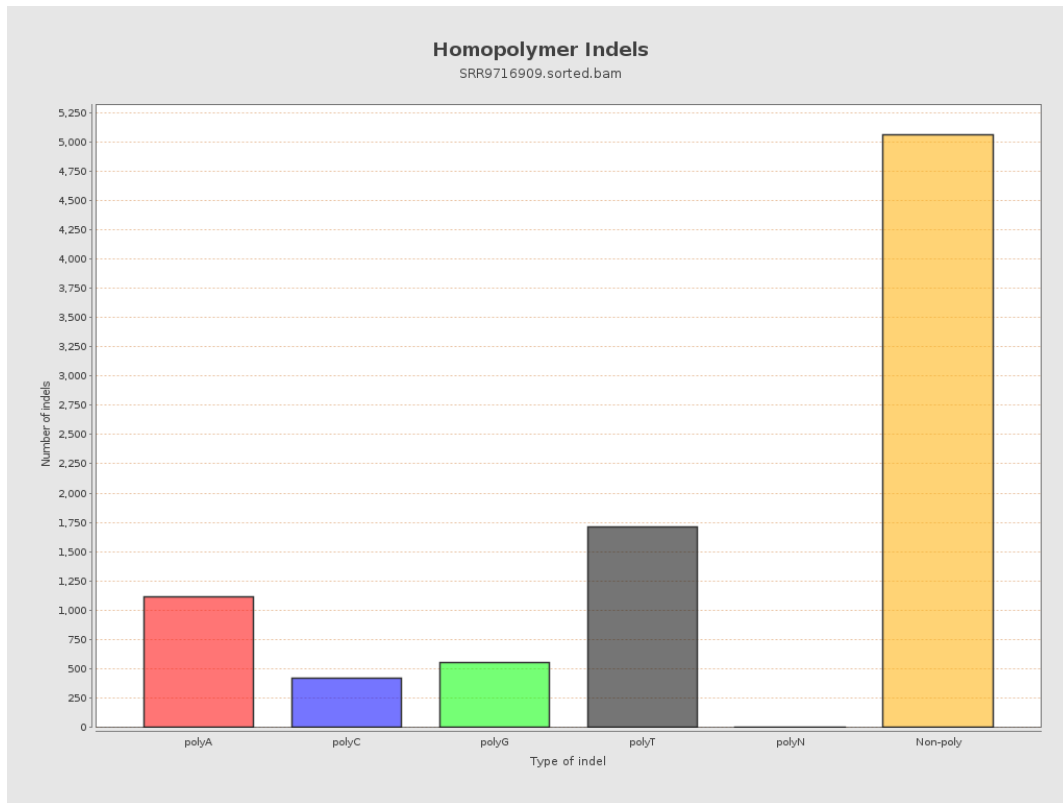
9. Results : Mapped Reads GC-content Distribution



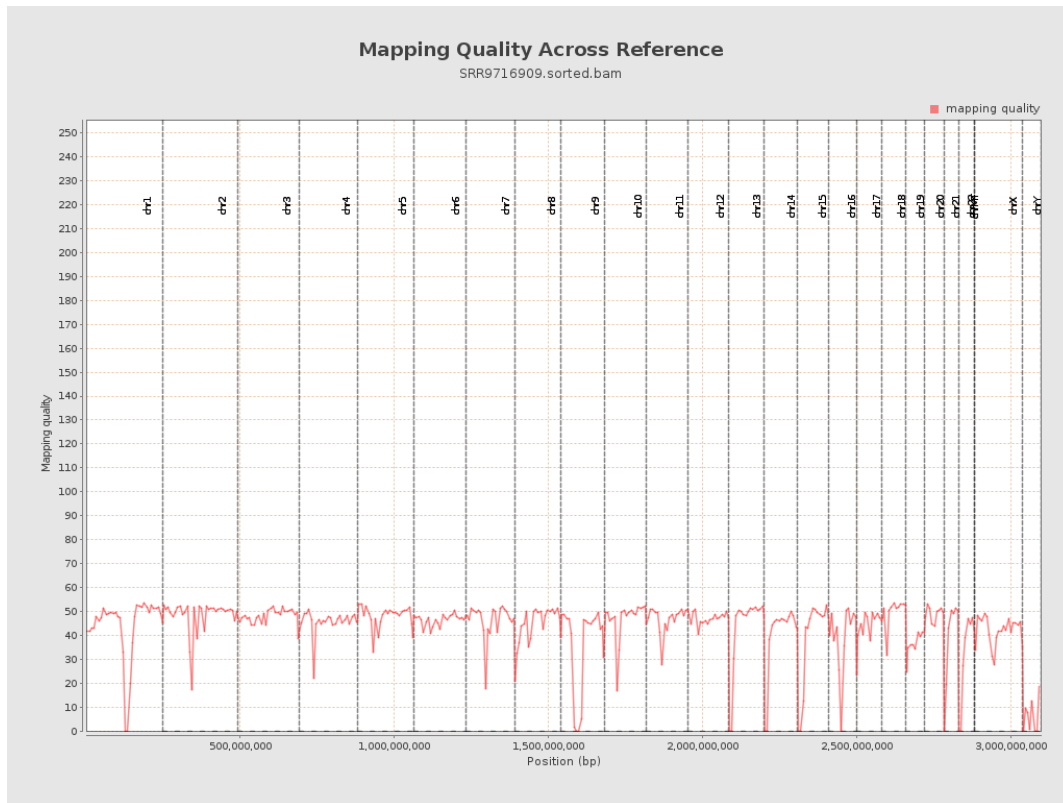
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

