

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 12:12:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716411.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_SRR9716411 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716411.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 12:12:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716411.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,030,562
Mapped reads	839,119 / 81.42%
Unmapped reads	191,443 / 18.58%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,024 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	21,222 / 2.06%
Duplication rate	1.91%
Clipped reads	839,810 / 81.49%

2.2. ACGT Content

Number/percentage of A's	12,822,259 / 26.4%
Number/percentage of C's	8,784,746 / 18.08%
Number/percentage of T's	15,131,595 / 31.15%
Number/percentage of G's	11,837,829 / 24.37%
Number/percentage of N's	789 / 0%
GC Percentage	42.45%

2.3. Coverage

Mean	0.0157

Standard Deviation	0.1624
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2.4. Mapping Quality

Mean Mapping Quality	44.46
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2.5. Mismatches and indels

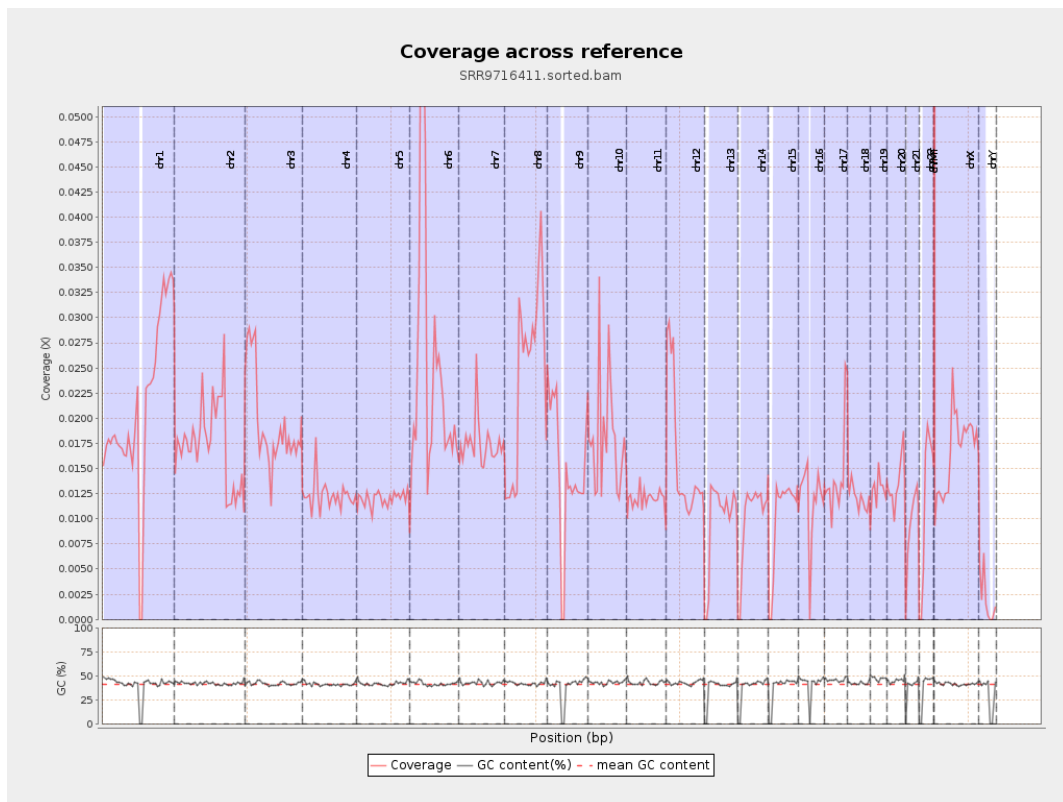
General error rate	0.51%
Mismatches	239,288
Insertions	4,010
Mapped reads with at least one insertion	0.48%
Deletions	8,731
Mapped reads with at least one deletion	1.03%
Homopolymer indels	41.86%

2.6. Chromosome stats

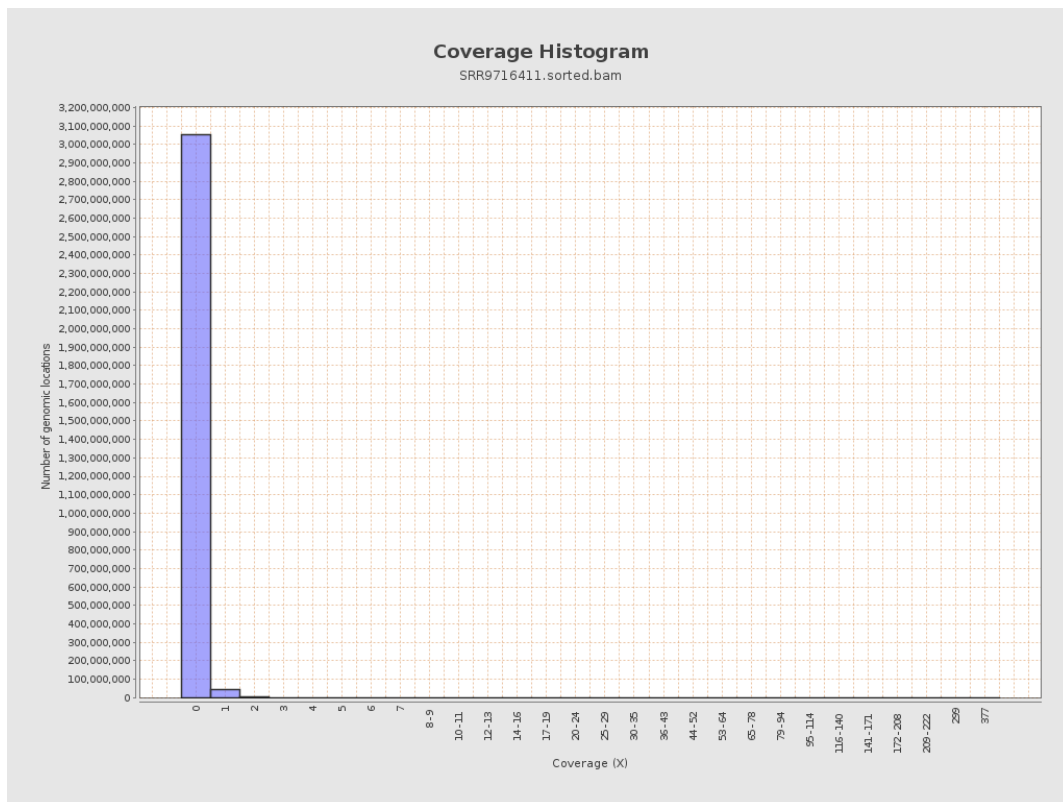
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5259503	0.0211	0.2259
chr2	243199373	4207628	0.0173	0.2106
chr3	198022430	3869403	0.0195	0.1475
chr4	191154276	2359818	0.0123	0.1235
chr5	180915260	2180791	0.0121	0.1159
chr6	171115067	4271969	0.025	0.2082
chr7	159138663	2789016	0.0175	0.2062

chr8	146364022	3507144	0.024	0.1722
chr9	141213431	2071195	0.0147	0.151
chr10	135534747	2454343	0.0181	0.175
chr11	135006516	1627446	0.0121	0.1377
chr12	133851895	2161999	0.0162	0.1363
chr13	115169878	1133175	0.0098	0.1045
chr14	107349540	1069723	0.01	0.1132
chr15	102531392	1036281	0.0101	0.1063
chr16	90354753	1055813	0.0117	0.1235
chr17	81195210	1167455	0.0144	0.1287
chr18	78077248	942552	0.0121	0.2122
chr19	59128983	766149	0.013	0.1644
chr20	63025520	857808	0.0136	0.1234
chr21	48129895	457990	0.0095	0.1144
chr22	51304566	615068	0.012	0.1152
chrMT	16571	8834	0.5331	0.8584
chrX	155270560	2600608	0.0167	0.146
chrY	59373566	119195	0.002	0.0604

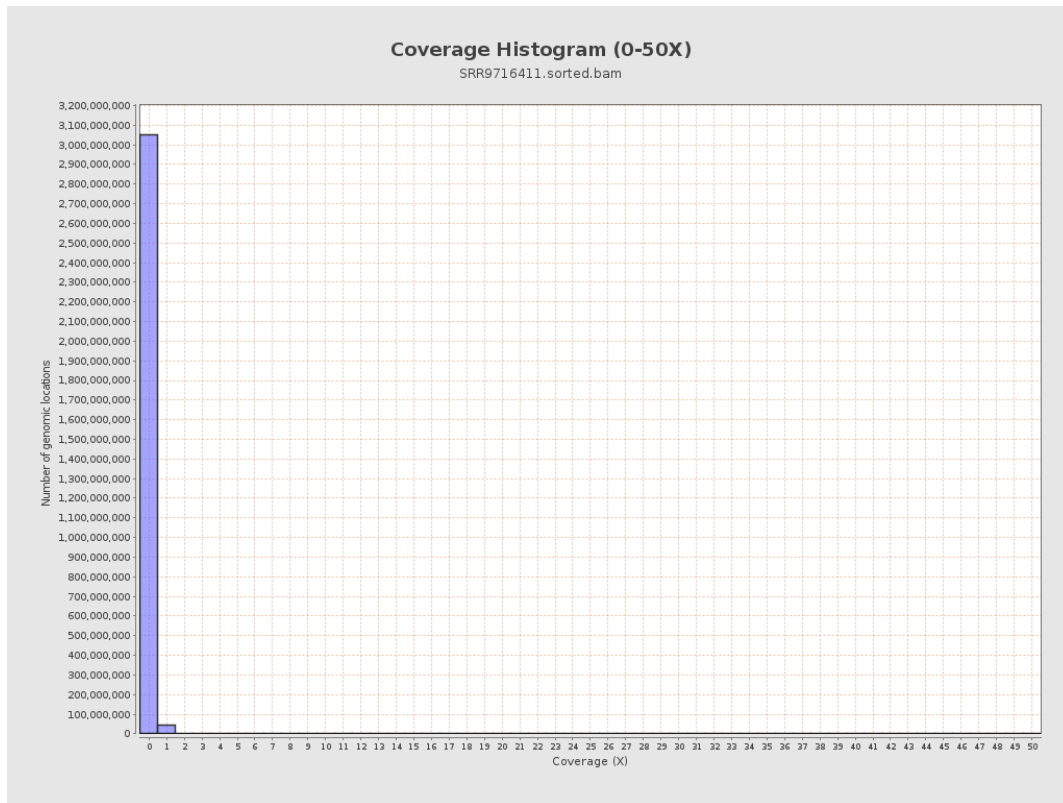
3. Results : Coverage across reference



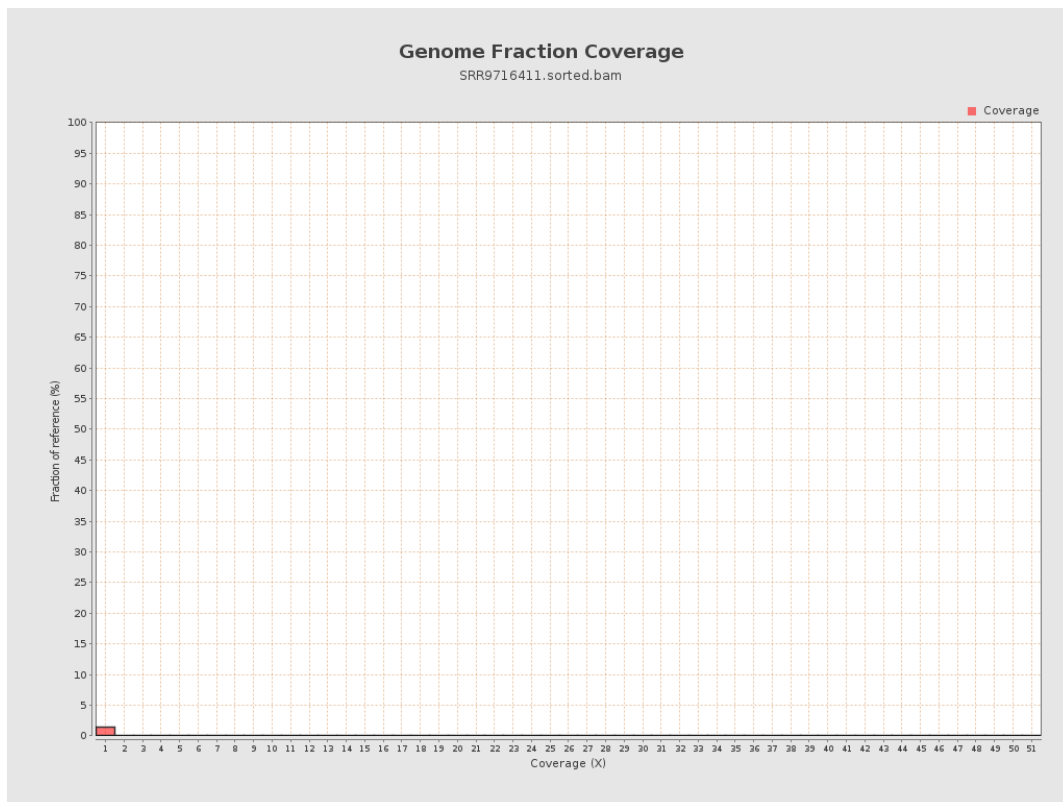
4. Results : Coverage Histogram



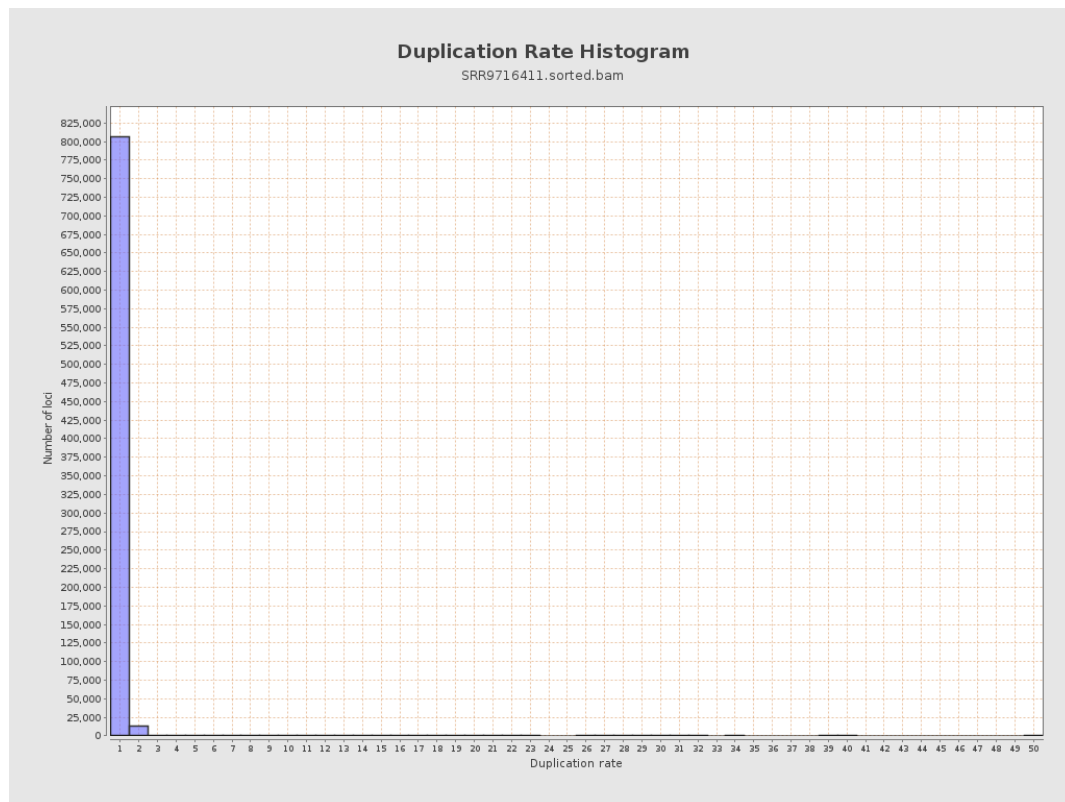
5. Results : Coverage Histogram (0-50X)



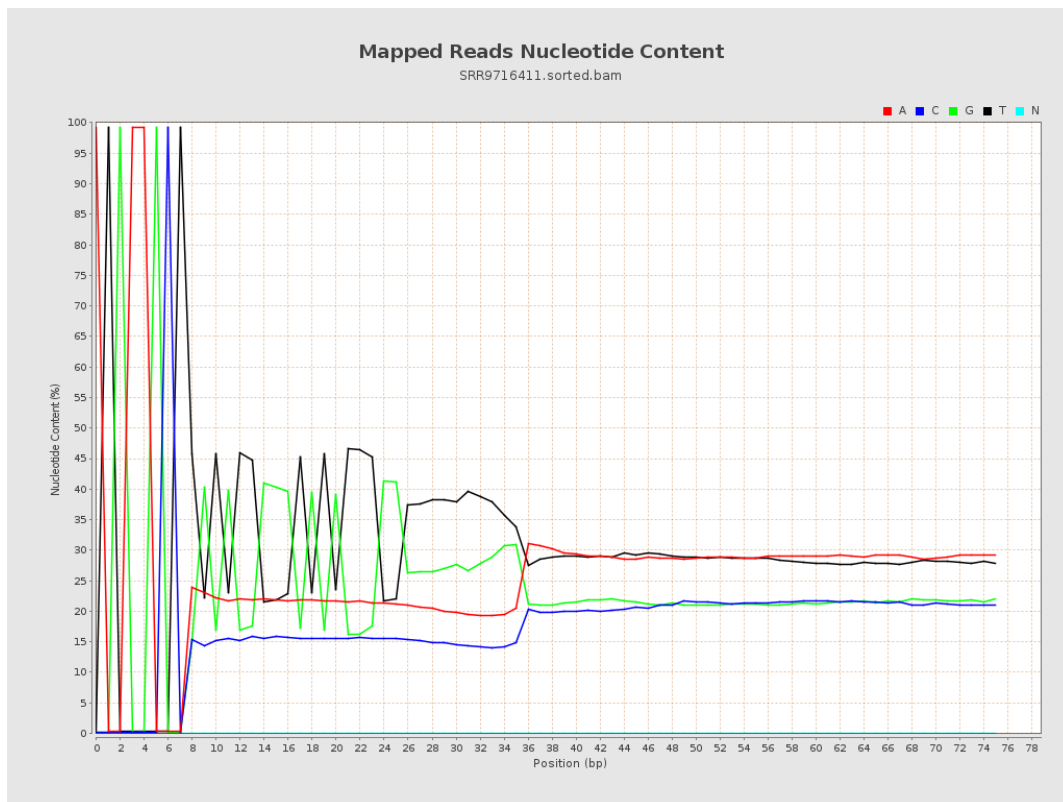
6. Results : Genome Fraction Coverage



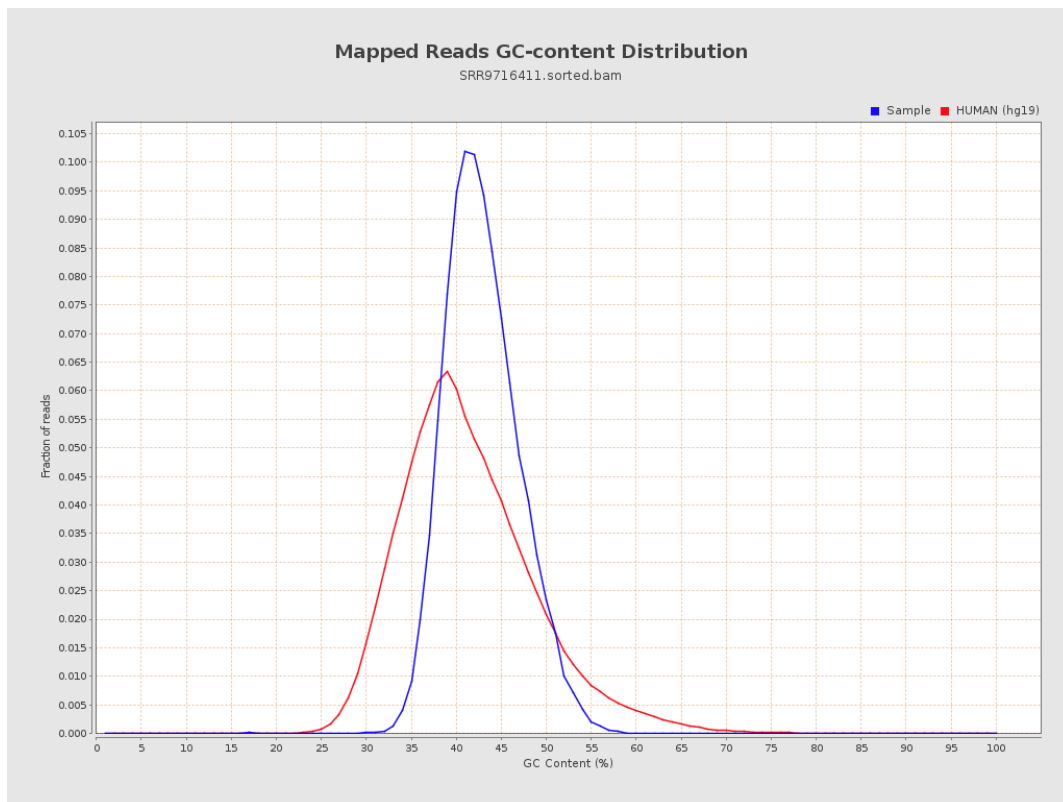
7. Results : Duplication Rate Histogram



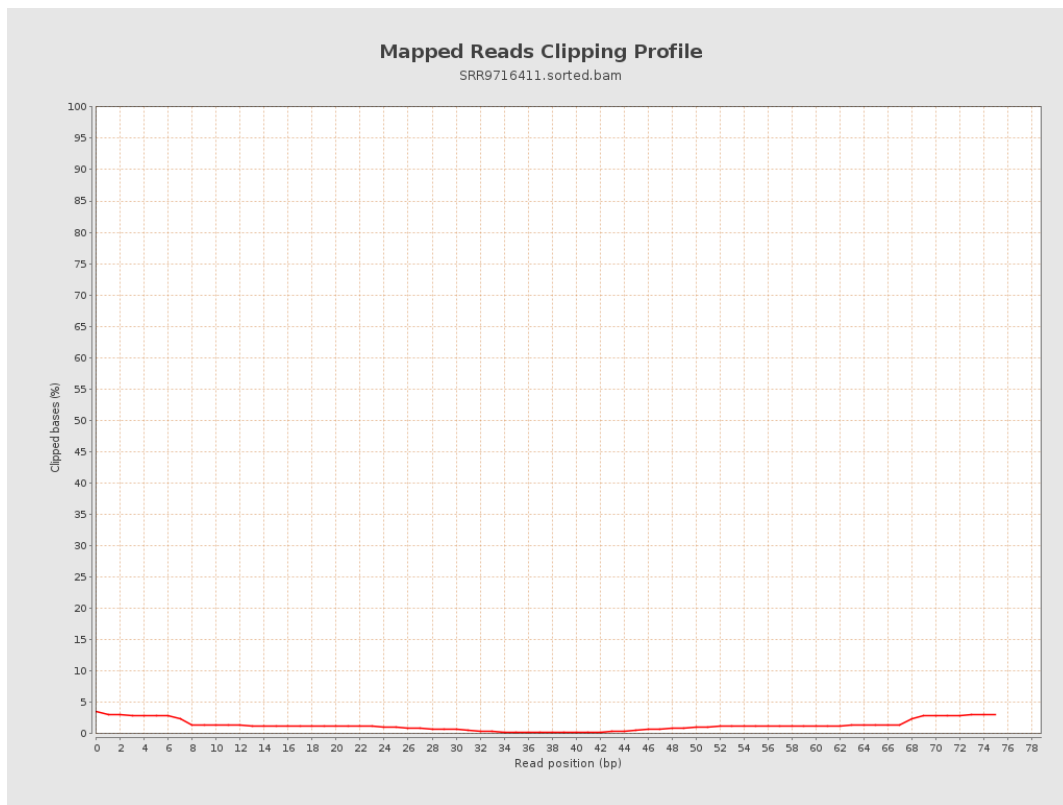
8. Results : Mapped Reads Nucleotide Content



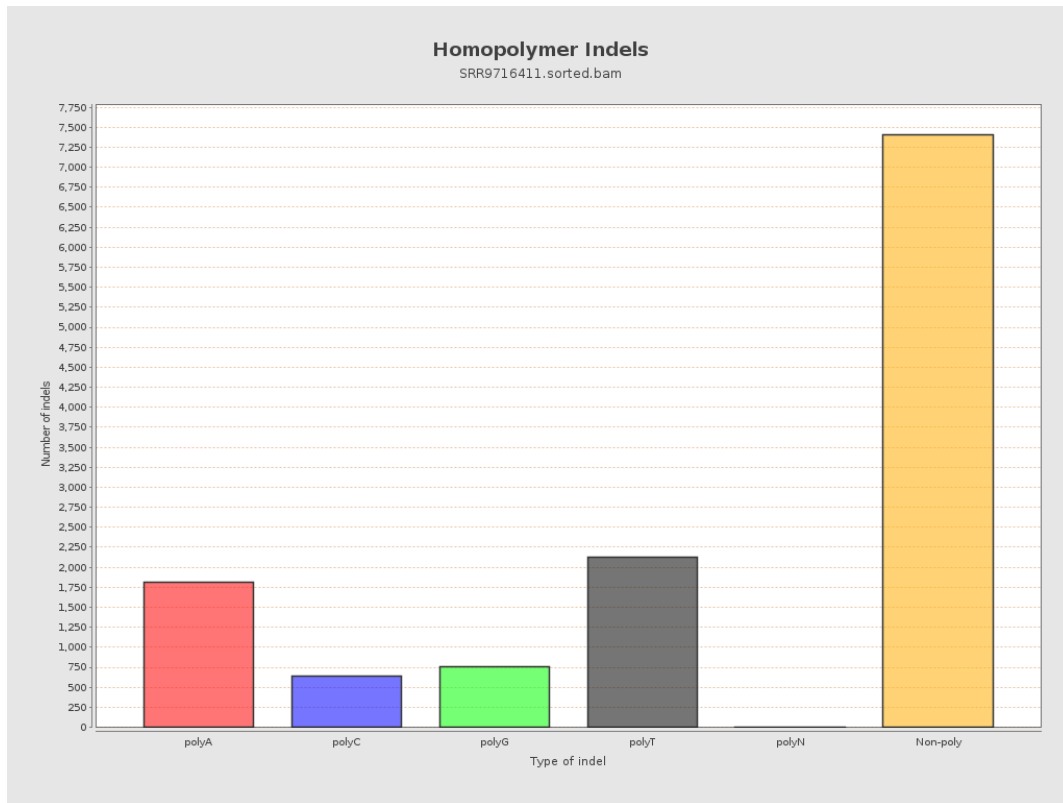
9. Results : Mapped Reads GC-content Distribution



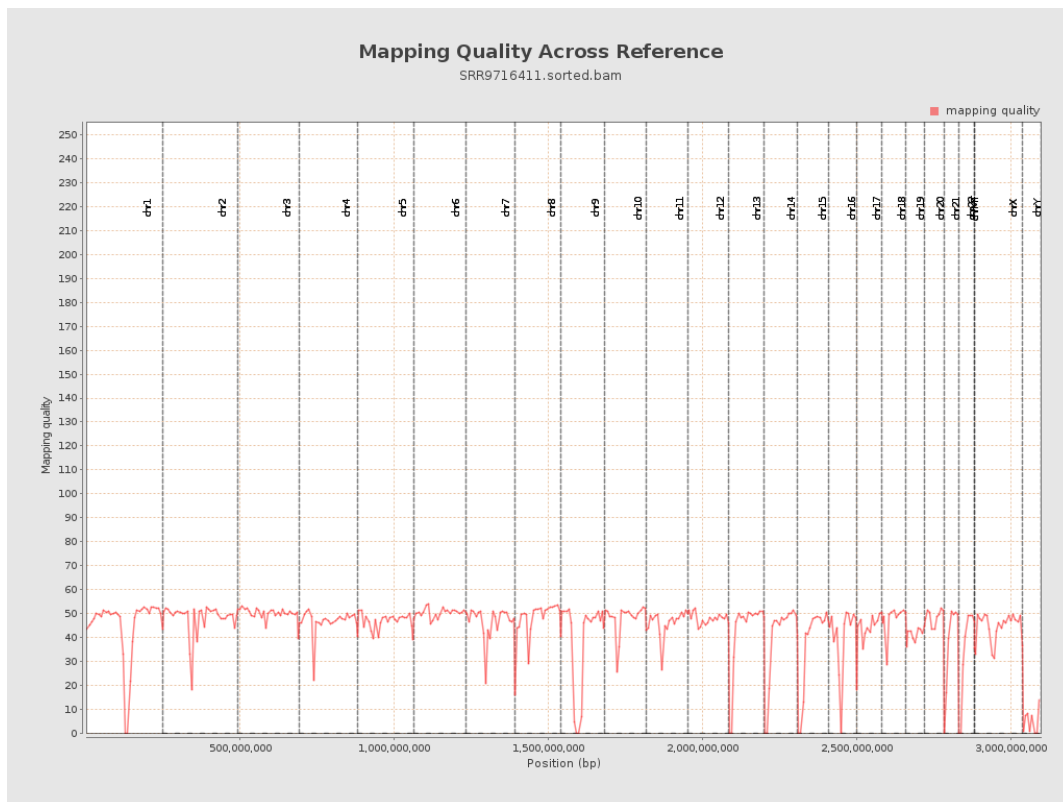
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

