

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 09:40:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716740.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_SRR9716740 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716740.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 09:40:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716740.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	731,187
Mapped reads	658,148 / 90.01%
Unmapped reads	73,039 / 9.99%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,716 / 0.51%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	15,295 / 2.09%
Duplication rate	1.68%
Clipped reads	660,706 / 90.36%

2.2. ACGT Content

Number/percentage of A's	9,554,320 / 24.84%
Number/percentage of C's	7,435,585 / 19.33%
Number/percentage of T's	12,100,679 / 31.46%
Number/percentage of G's	9,377,672 / 24.38%
Number/percentage of N's	452 / 0%
GC Percentage	43.71%

2.3. Coverage

Mean	0.0124

Standard Deviation	0.147
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2.4. Mapping Quality

Mean Mapping Quality	44.71
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2.5. Mismatches and indels

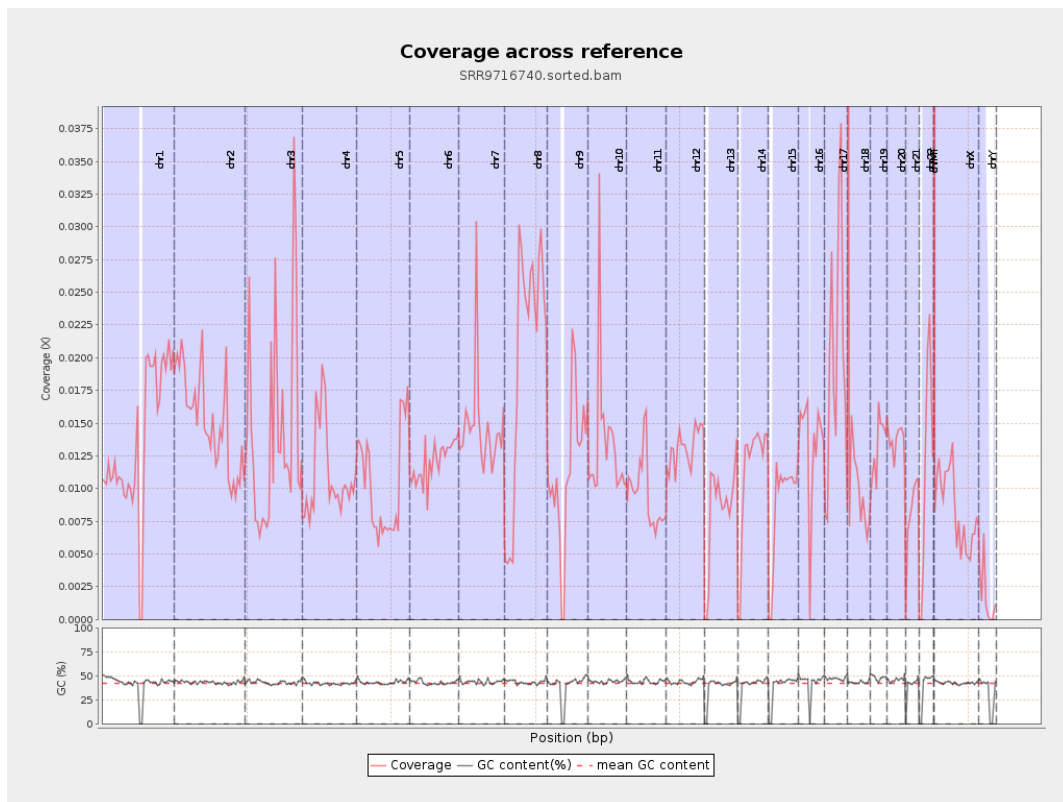
General error rate	0.51%
Mismatches	191,495
Insertions	2,498
Mapped reads with at least one insertion	0.38%
Deletions	7,323
Mapped reads with at least one deletion	1.1%
Homopolymer indels	41.44%

2.6. Chromosome stats

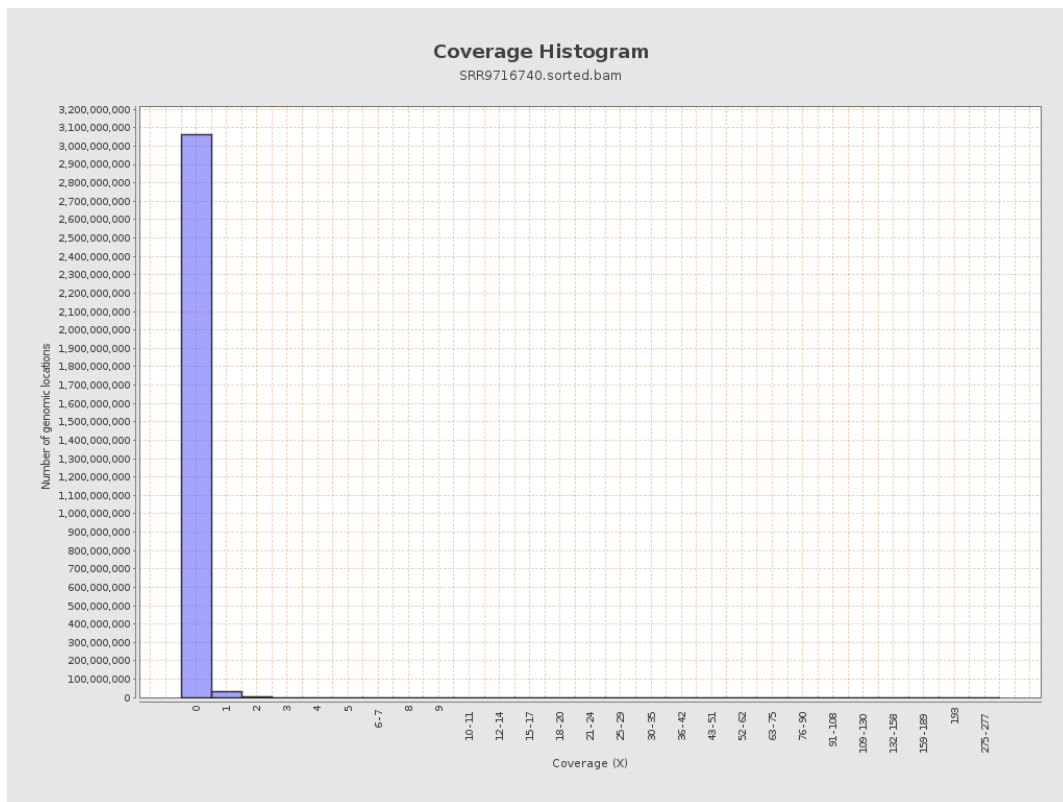
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	3411239	0.0137	0.1822
chr2	243199373	3692141	0.0152	0.1764
chr3	198022430	2776491	0.014	0.1269
chr4	191154276	2107202	0.011	0.1221
chr5	180915260	1853319	0.0102	0.106
chr6	171115067	2061087	0.012	0.1182
chr7	159138663	2338238	0.0147	0.254

chr8	146364022	2948205	0.0201	0.1853
chr9	141213431	1591788	0.0113	0.1199
chr10	135534747	1814476	0.0134	0.1923
chr11	135006516	1314478	0.0097	0.113
chr12	133851895	1755517	0.0131	0.1248
chr13	115169878	956434	0.0083	0.0954
chr14	107349540	1214000	0.0113	0.1118
chr15	102531392	894784	0.0087	0.0975
chr16	90354753	1185386	0.0131	0.1233
chr17	81195210	1610780	0.0198	0.1502
chr18	78077248	894026	0.0115	0.1617
chr19	59128983	785266	0.0133	0.1702
chr20	63025520	859079	0.0136	0.1258
chr21	48129895	394404	0.0082	0.1
chr22	51304566	603206	0.0118	0.1134
chrMT	16571	13167	0.7946	1.0706
chrX	155270560	1302877	0.0084	0.1022
chrY	59373566	103041	0.0017	0.0666

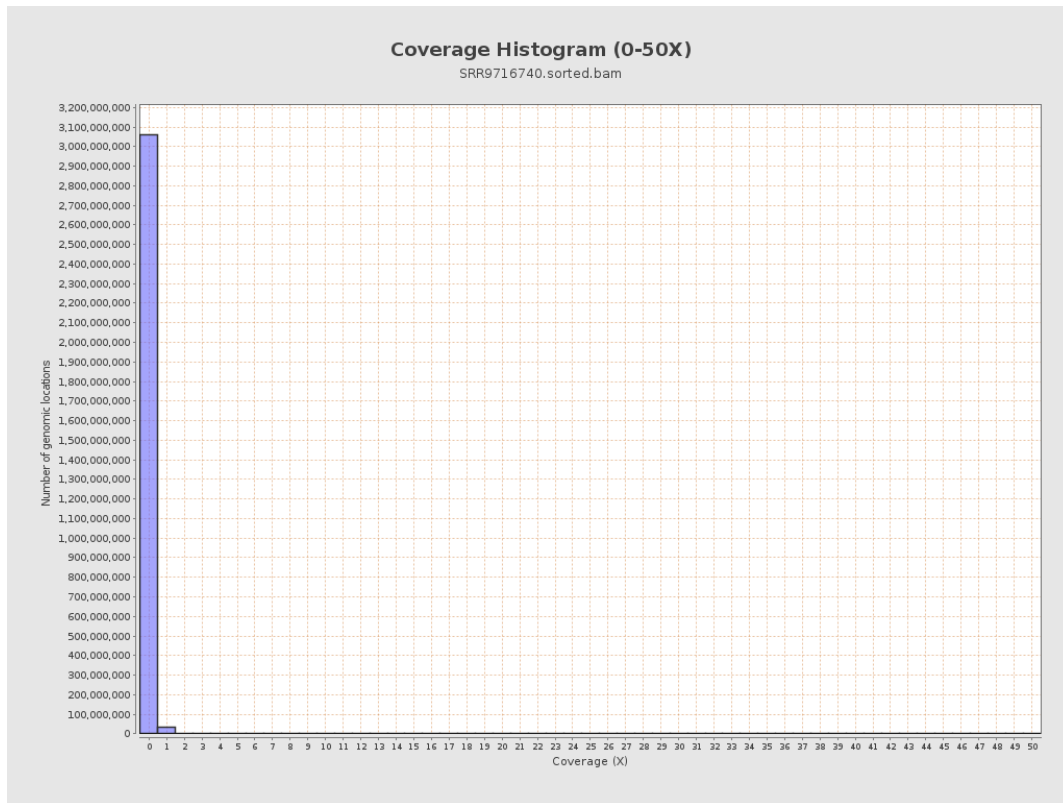
3. Results : Coverage across reference



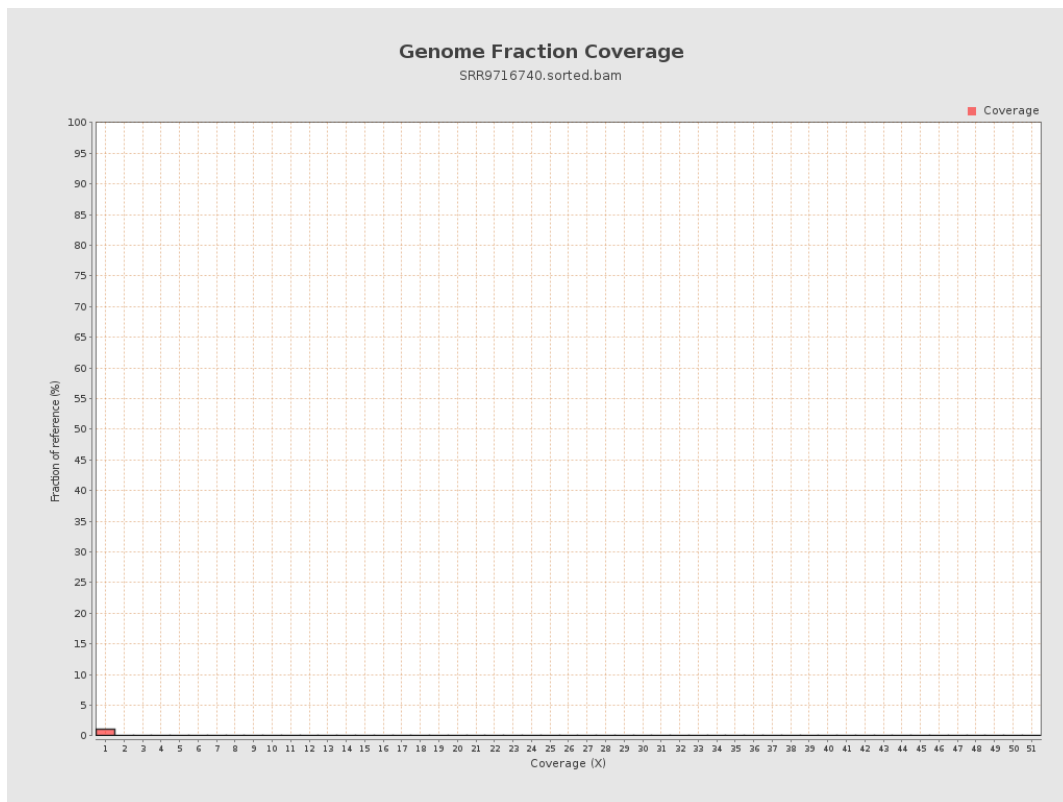
4. Results : Coverage Histogram



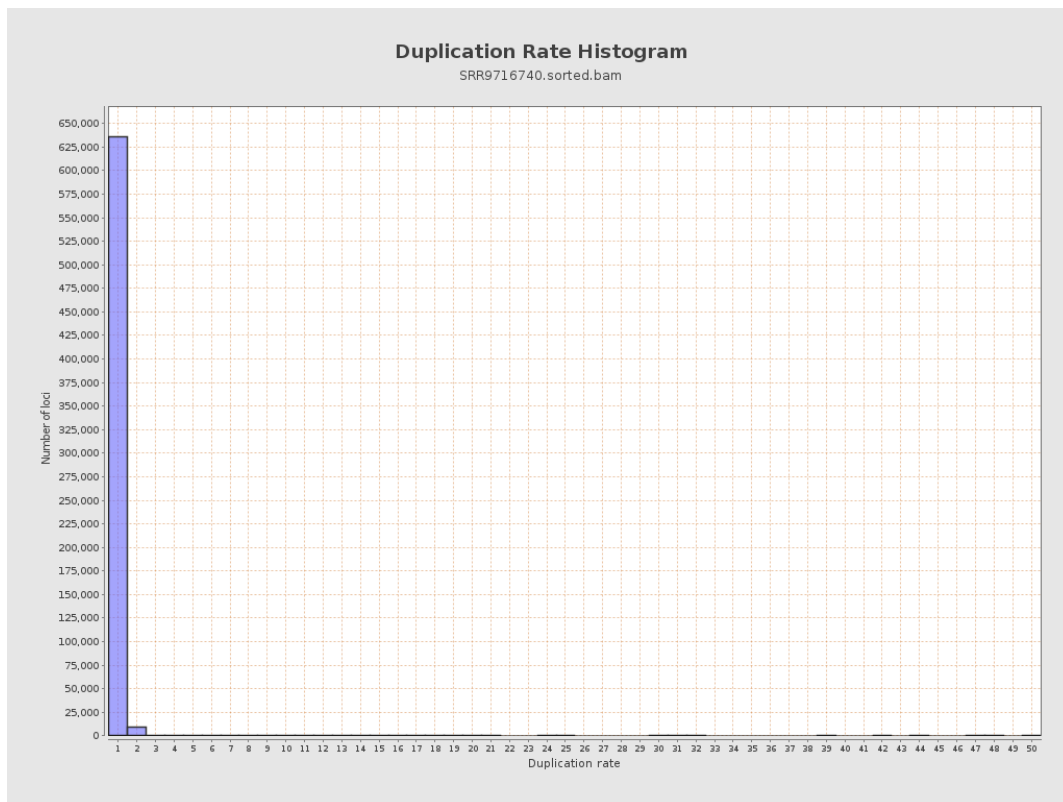
5. Results : Coverage Histogram (0-50X)



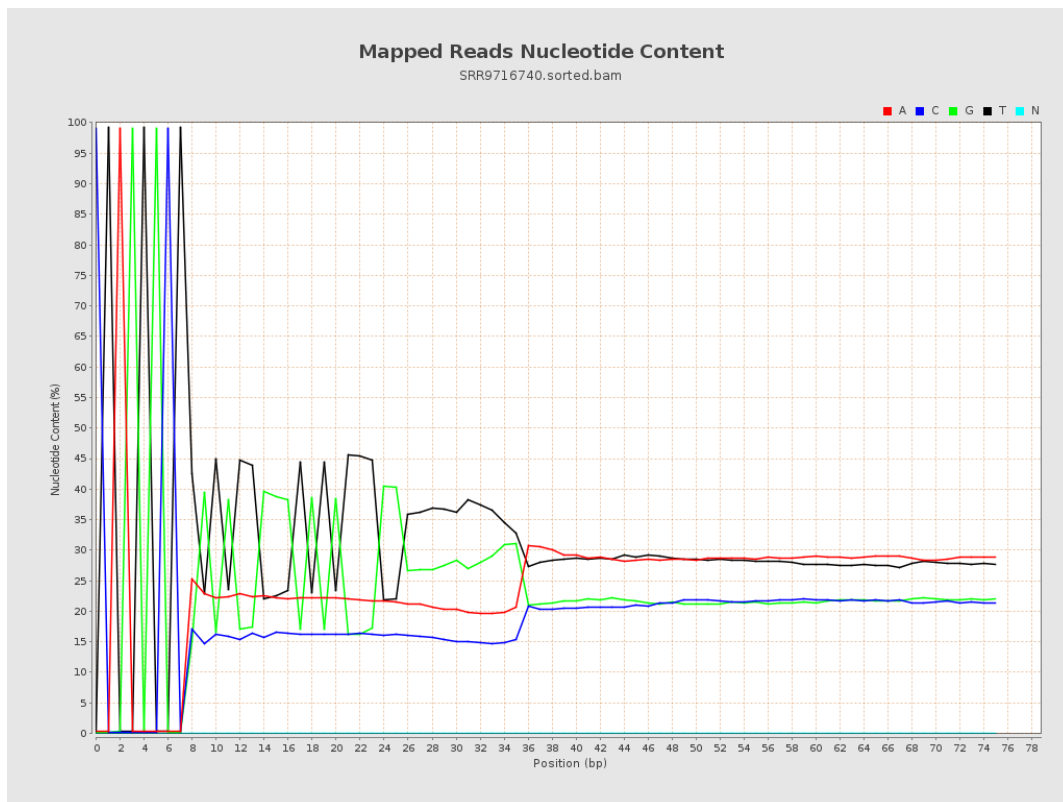
6. Results : Genome Fraction Coverage



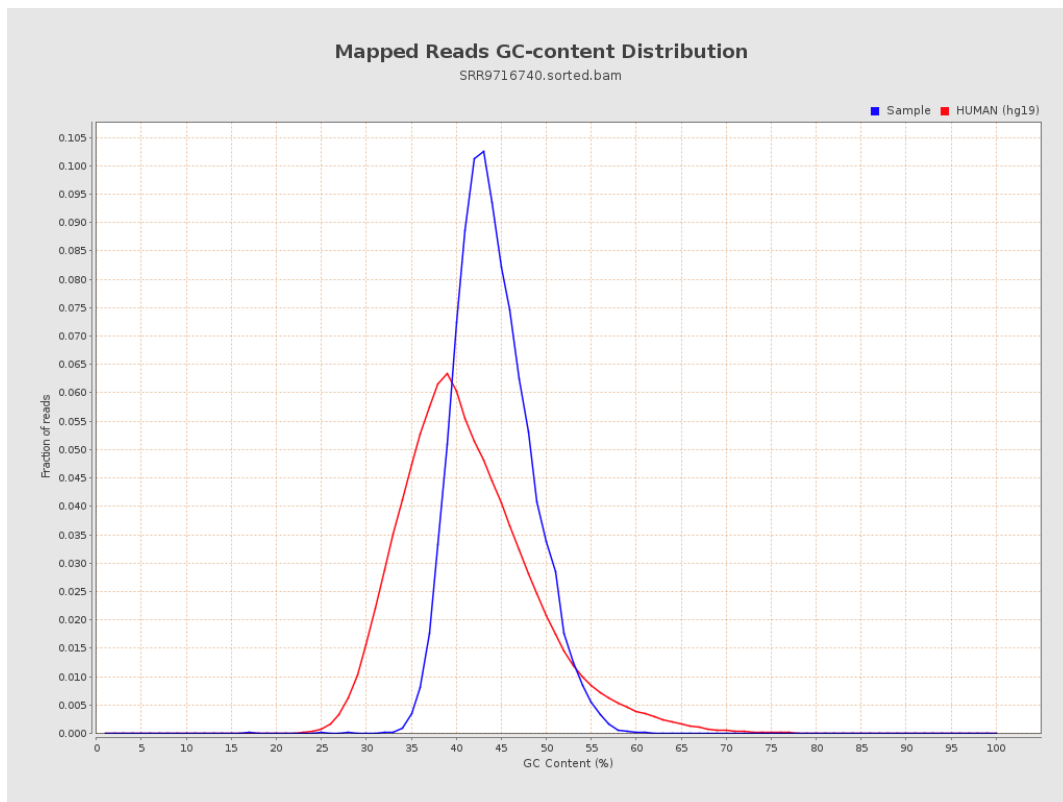
7. Results : Duplication Rate Histogram



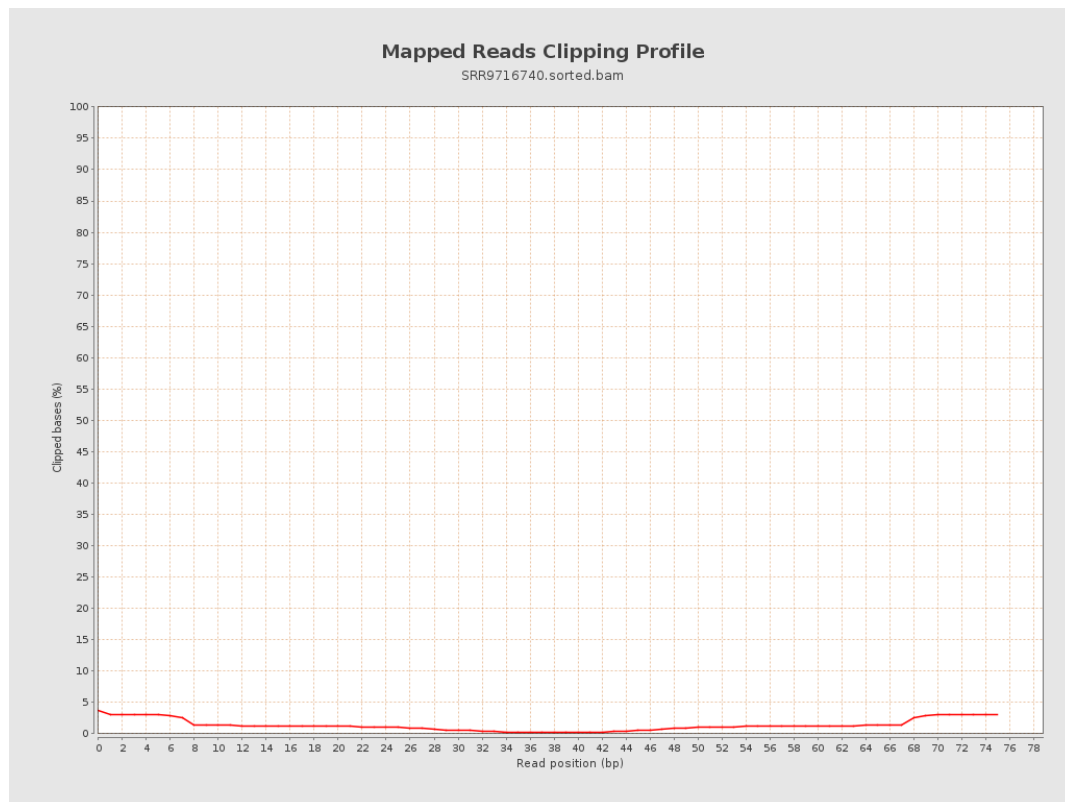
8. Results : Mapped Reads Nucleotide Content



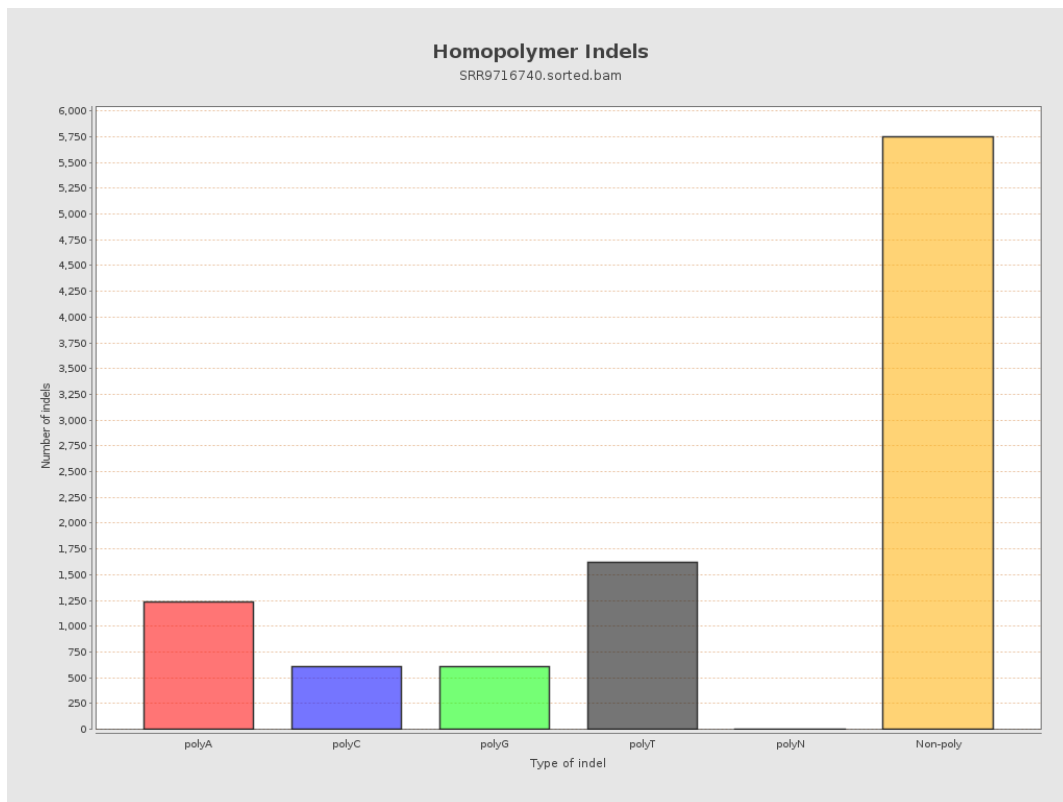
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

