

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 04:26:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716265.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_SRR9716265 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716265.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 04:26:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716265.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,638,643
Mapped reads	1,202,090 / 73.36%
Unmapped reads	436,553 / 26.64%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,264 / 0.08%
Read min/max/mean length	30 / 76 / 76.03
Duplicated reads (estimated)	103,676 / 6.33%
Duplication rate	7.35%
Clipped reads	1,201,410 / 73.32%

2.2. ACGT Content

Number/percentage of A's	12,408,159 / 19.72%
Number/percentage of C's	10,424,627 / 16.57%
Number/percentage of T's	21,611,967 / 34.35%
Number/percentage of G's	18,473,511 / 29.36%
Number/percentage of N's	1,159 / 0%
GC Percentage	45.93%

2.3. Coverage

Mean	0.0203

Standard Deviation	0.1942
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2.4. Mapping Quality

Mean Mapping Quality	42.88
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2.5. Mismatches and indels

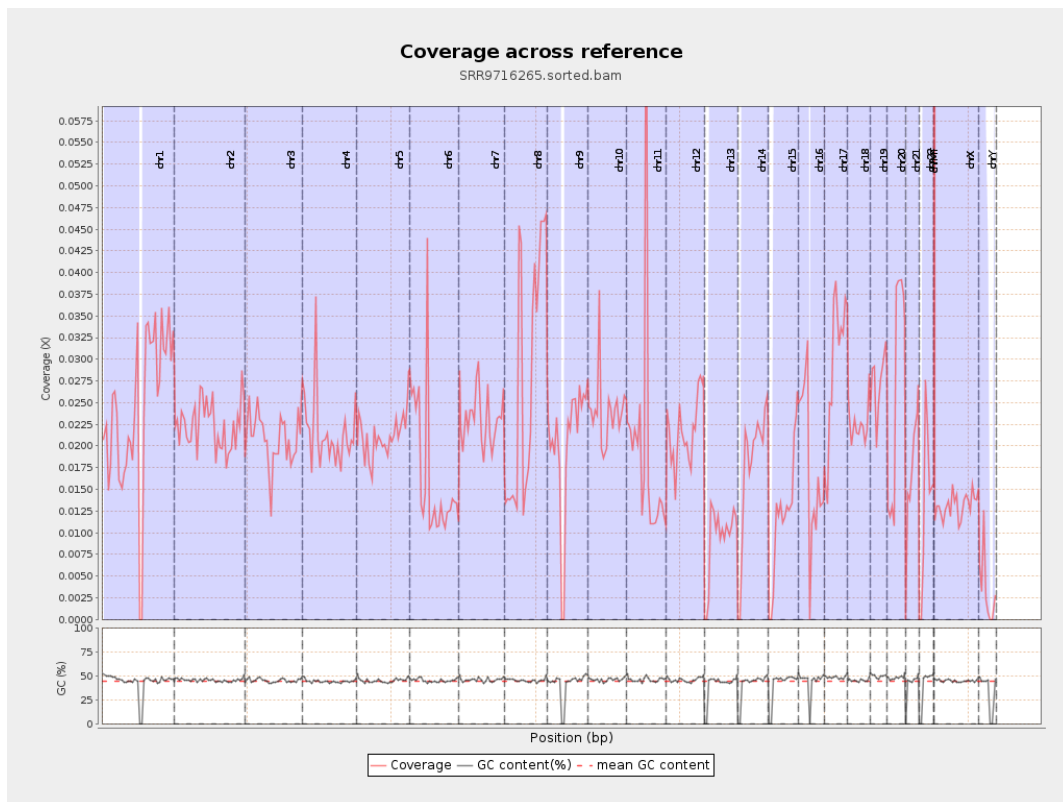
General error rate	0.7%
Mismatches	432,167
Insertions	3,681
Mapped reads with at least one insertion	0.3%
Deletions	9,518
Mapped reads with at least one deletion	0.79%
Homopolymer indels	41.65%

2.6. Chromosome stats

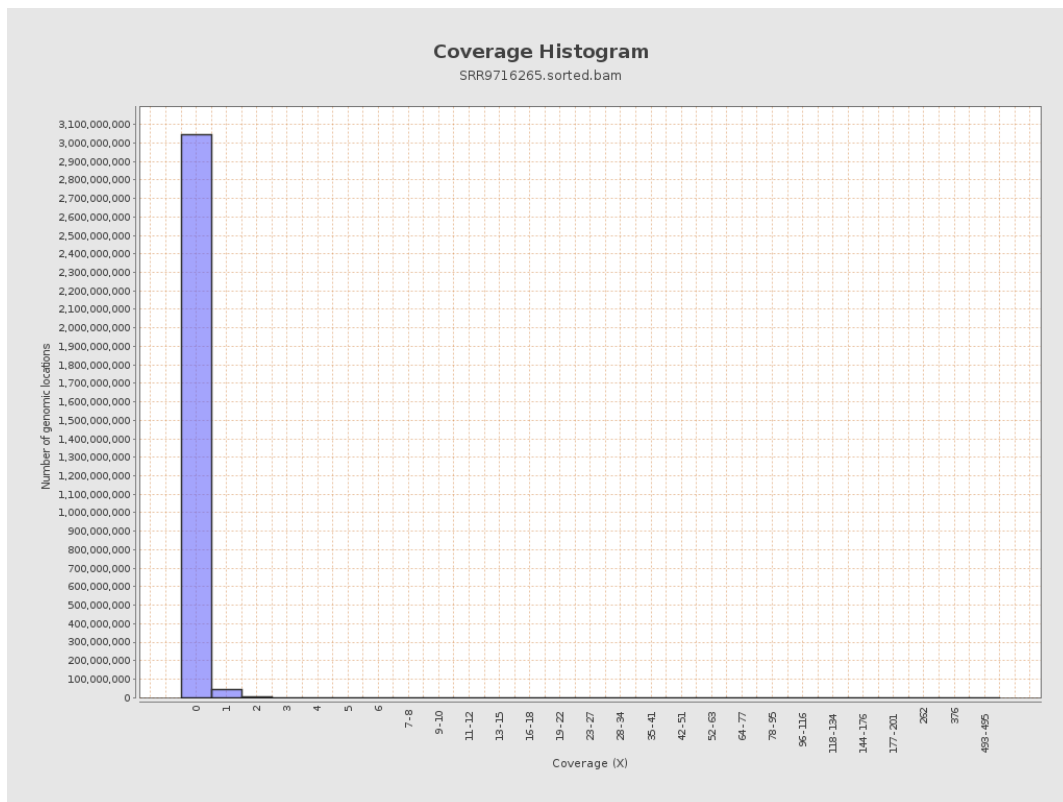
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6057443	0.0243	0.2314
chr2	243199373	5447310	0.0224	0.2737
chr3	198022430	4135328	0.0209	0.1696
chr4	191154276	4136613	0.0216	0.1838
chr5	180915260	3828400	0.0212	0.1705
chr6	171115067	2859662	0.0167	0.1766
chr7	159138663	3695541	0.0232	0.2215

chr8	146364022	4048045	0.0277	0.2044
chr9	141213431	2844246	0.0201	0.1814
chr10	135534747	3265174	0.0241	0.2251
chr11	135006516	2710255	0.0201	0.1938
chr12	133851895	2909331	0.0217	0.1738
chr13	115169878	1071121	0.0093	0.1153
chr14	107349540	1895149	0.0177	0.1583
chr15	102531392	1229112	0.012	0.1299
chr16	90354753	1579872	0.0175	0.1662
chr17	81195210	2393955	0.0295	0.2111
chr18	78077248	1752451	0.0224	0.2085
chr19	59128983	1615203	0.0273	0.2461
chr20	63025520	1653521	0.0262	0.2007
chr21	48129895	831750	0.0173	0.1686
chr22	51304566	709434	0.0138	0.1459
chrMT	16571	26669	1.6094	1.8135
chrX	155270560	2040131	0.0131	0.1392
chrY	59373566	200198	0.0034	0.1058

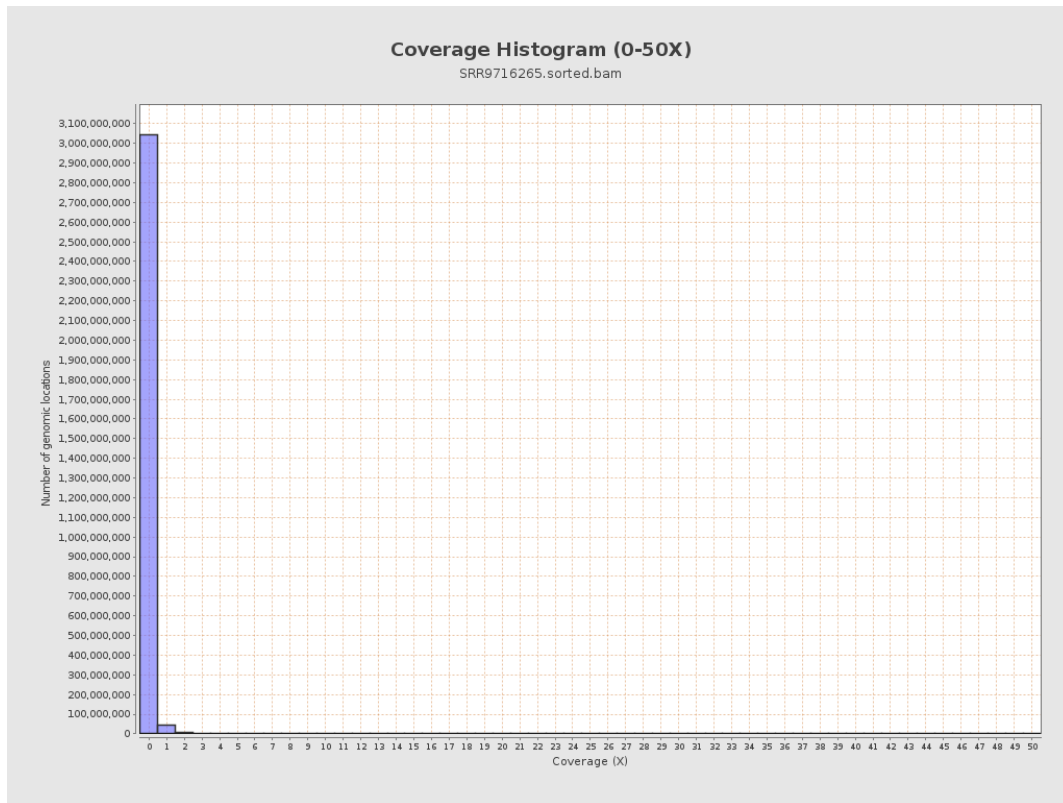
3. Results : Coverage across reference



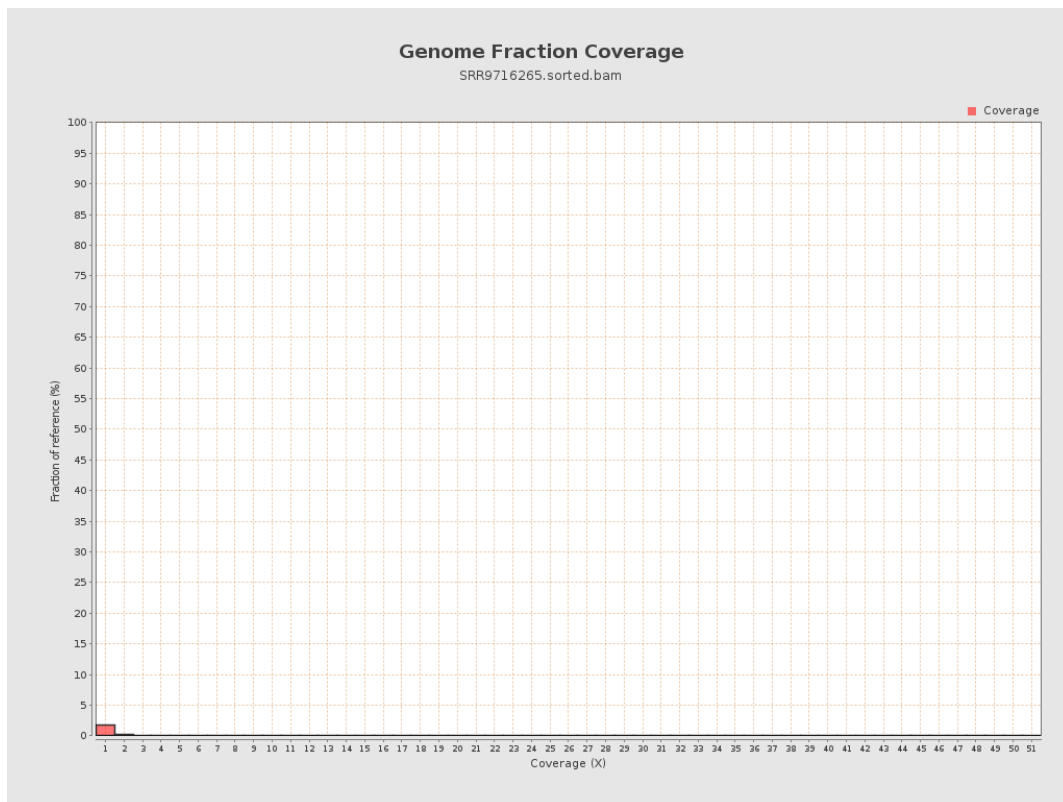
4. Results : Coverage Histogram



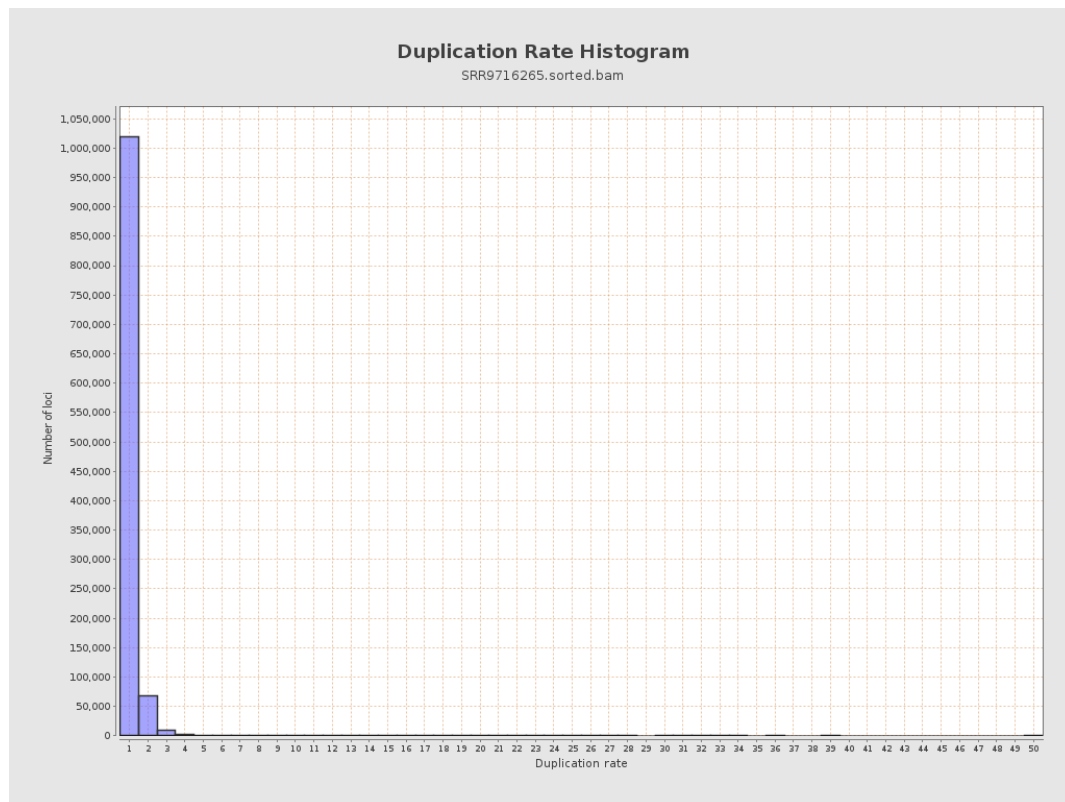
5. Results : Coverage Histogram (0-50X)



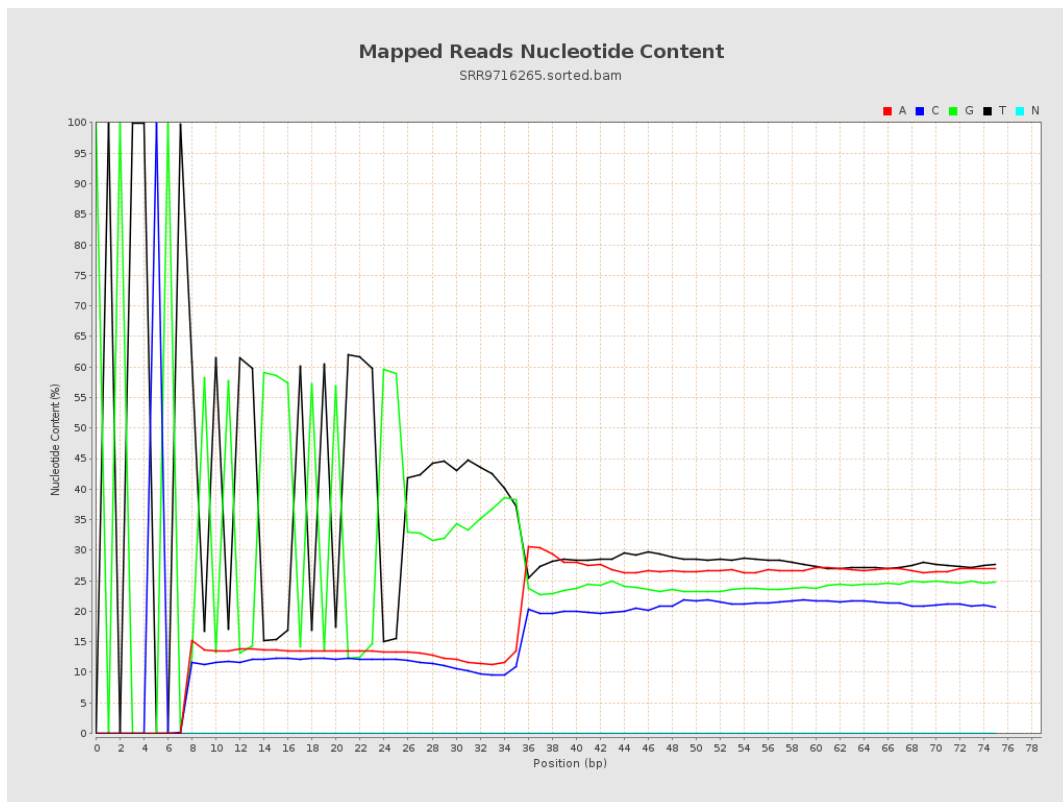
6. Results : Genome Fraction Coverage



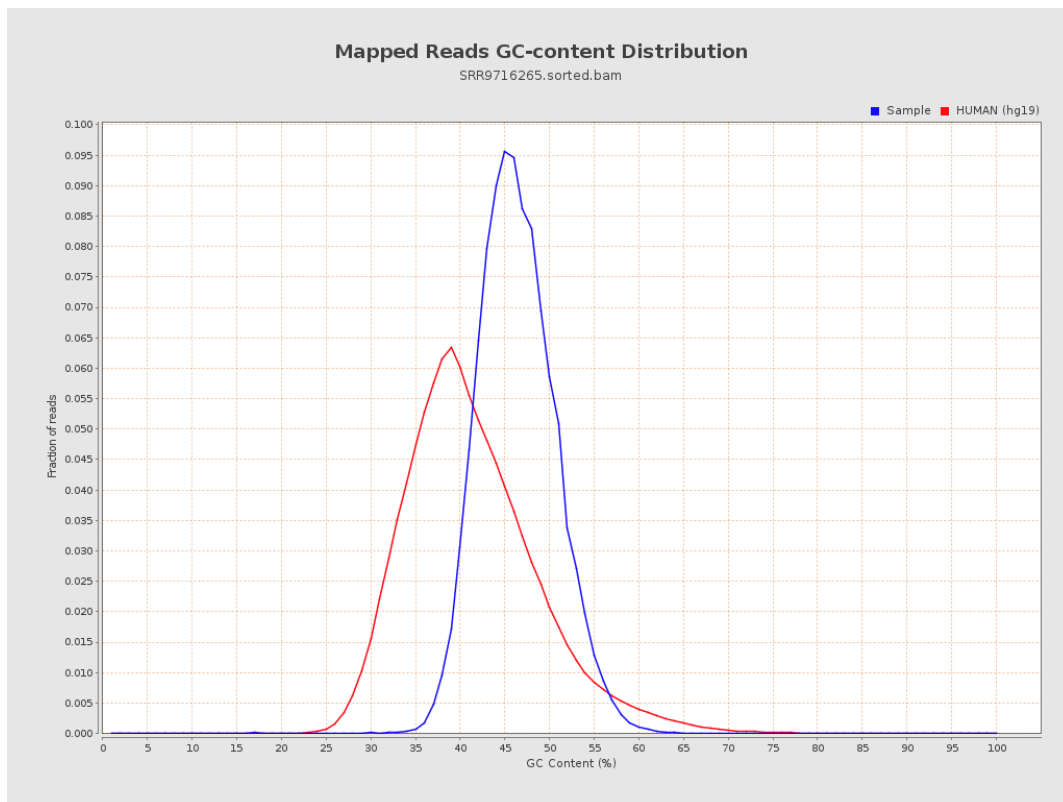
7. Results : Duplication Rate Histogram



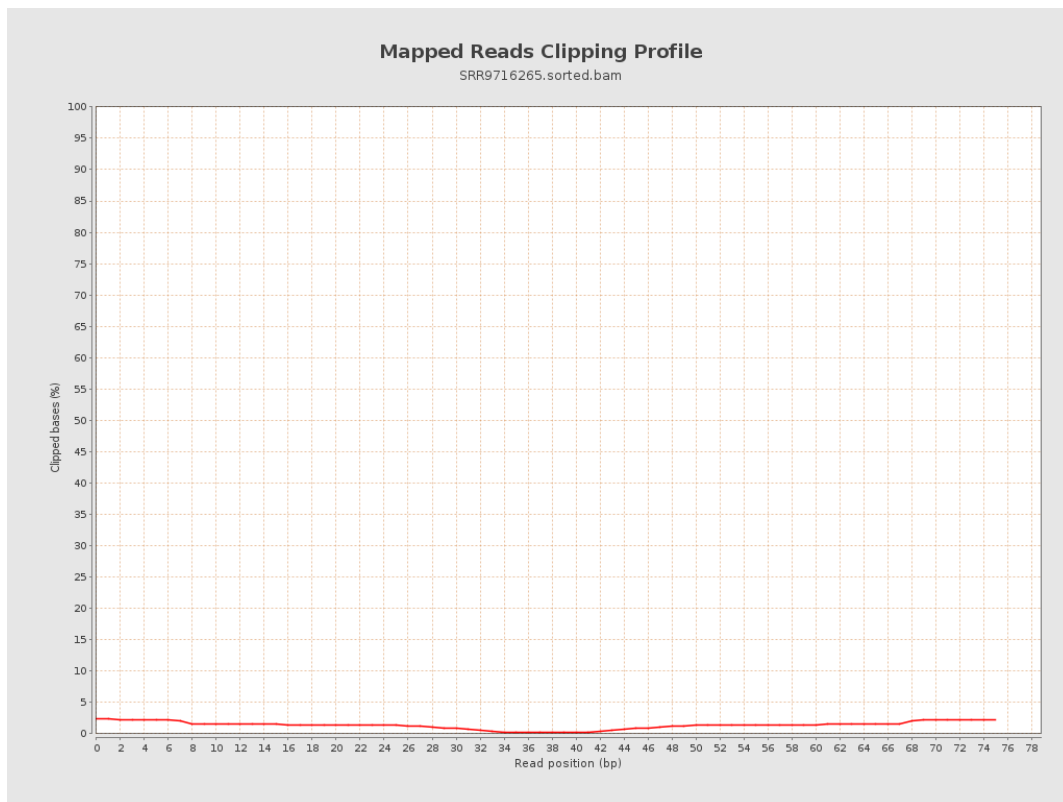
8. Results : Mapped Reads Nucleotide Content



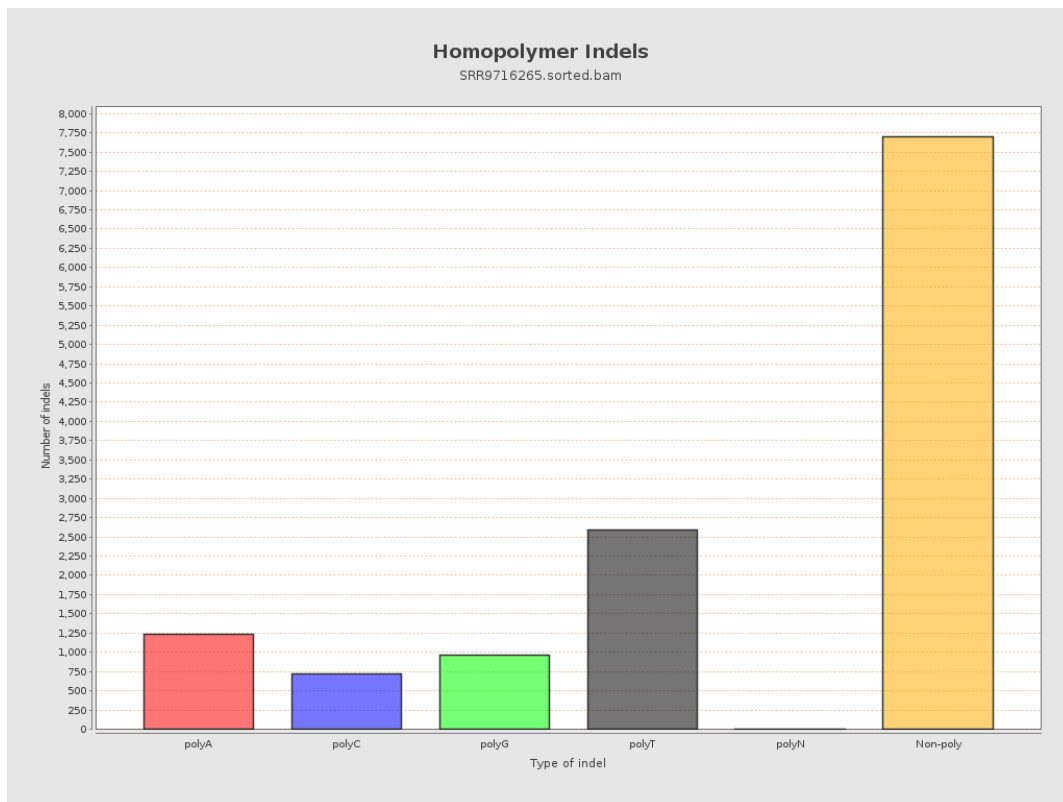
9. Results : Mapped Reads GC-content Distribution



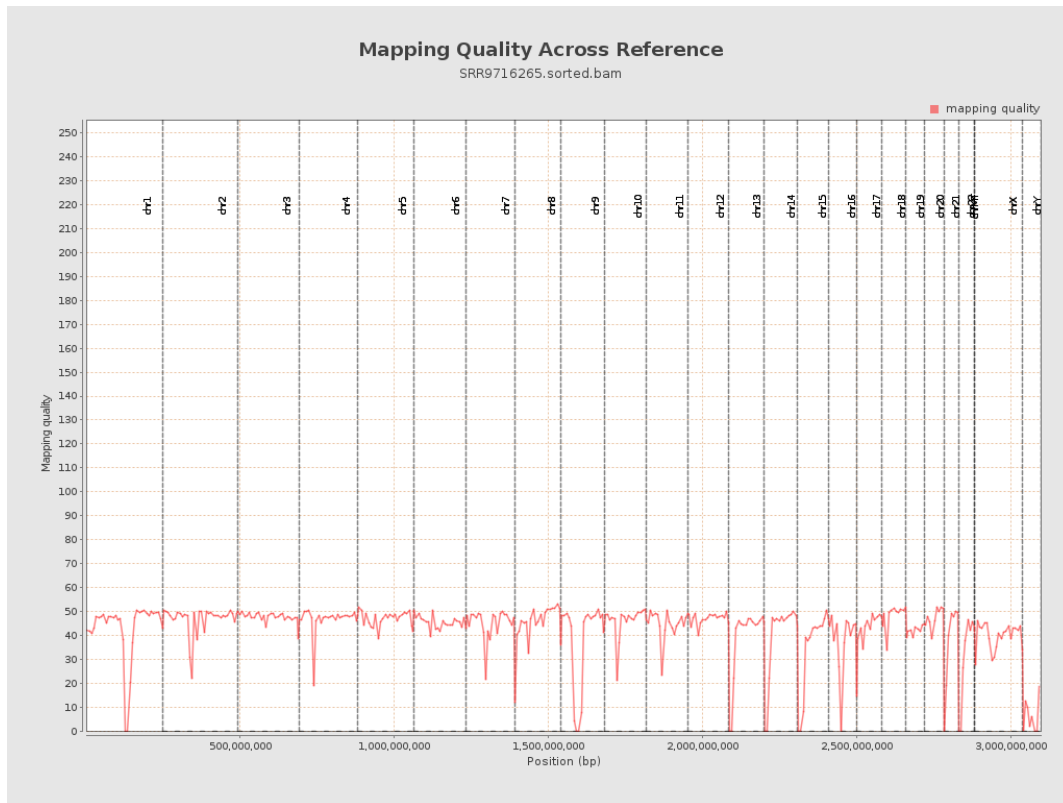
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

