

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 11:56:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716783.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_SRR9716783 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716783.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 11:56:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716783.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,248,161
Mapped reads	892,234 / 71.48%
Unmapped reads	355,927 / 28.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,546 / 1.57%
Read min/max/mean length	30 / 101 / 101.57
Duplicated reads (estimated)	18,736 / 1.5%
Duplication rate	1.41%
Clipped reads	910,039 / 72.91%

2.2. ACGT Content

Number/percentage of A's	17,854,826 / 26.49%
Number/percentage of C's	13,694,158 / 20.32%
Number/percentage of T's	20,359,226 / 30.2%
Number/percentage of G's	15,491,105 / 22.98%
Number/percentage of N's	8,583 / 0.01%
GC Percentage	43.3%

2.3. Coverage

Mean	0.0218

Standard Deviation	0.2025
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2.4. Mapping Quality

Mean Mapping Quality	46.57
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2.5. Mismatches and indels

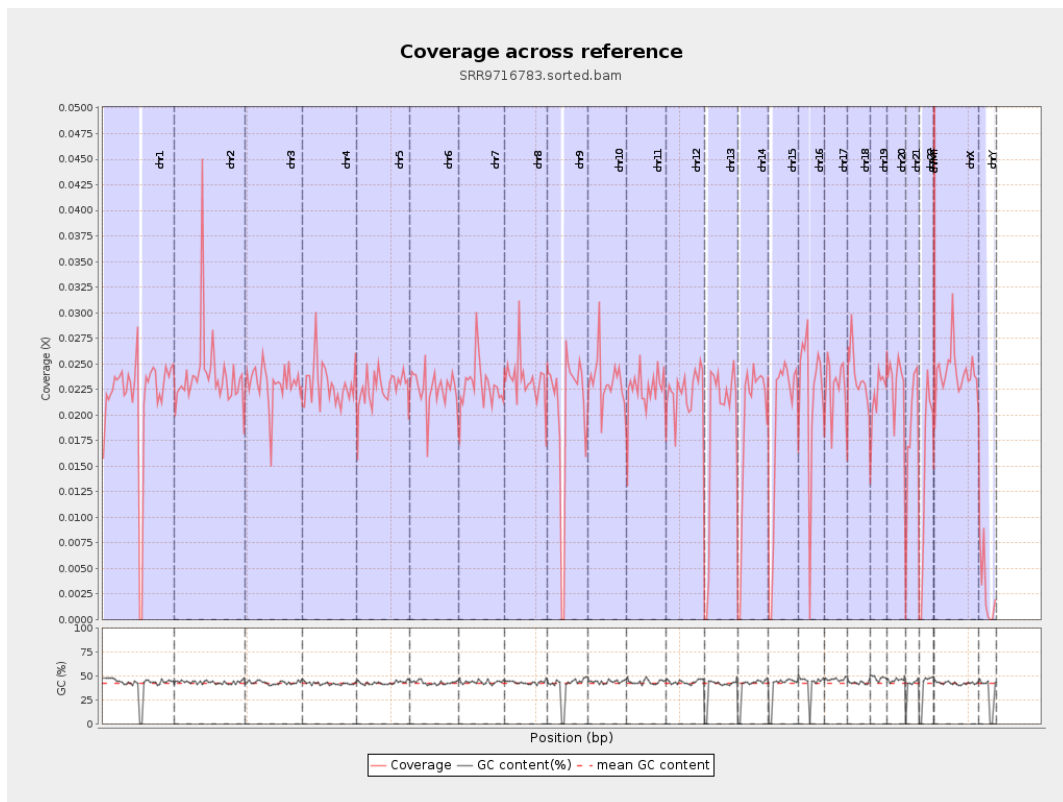
General error rate	0.75%
Mismatches	495,326
Insertions	5,929
Mapped reads with at least one insertion	0.65%
Deletions	14,031
Mapped reads with at least one deletion	1.55%
Homopolymer indels	39.46%

2.6. Chromosome stats

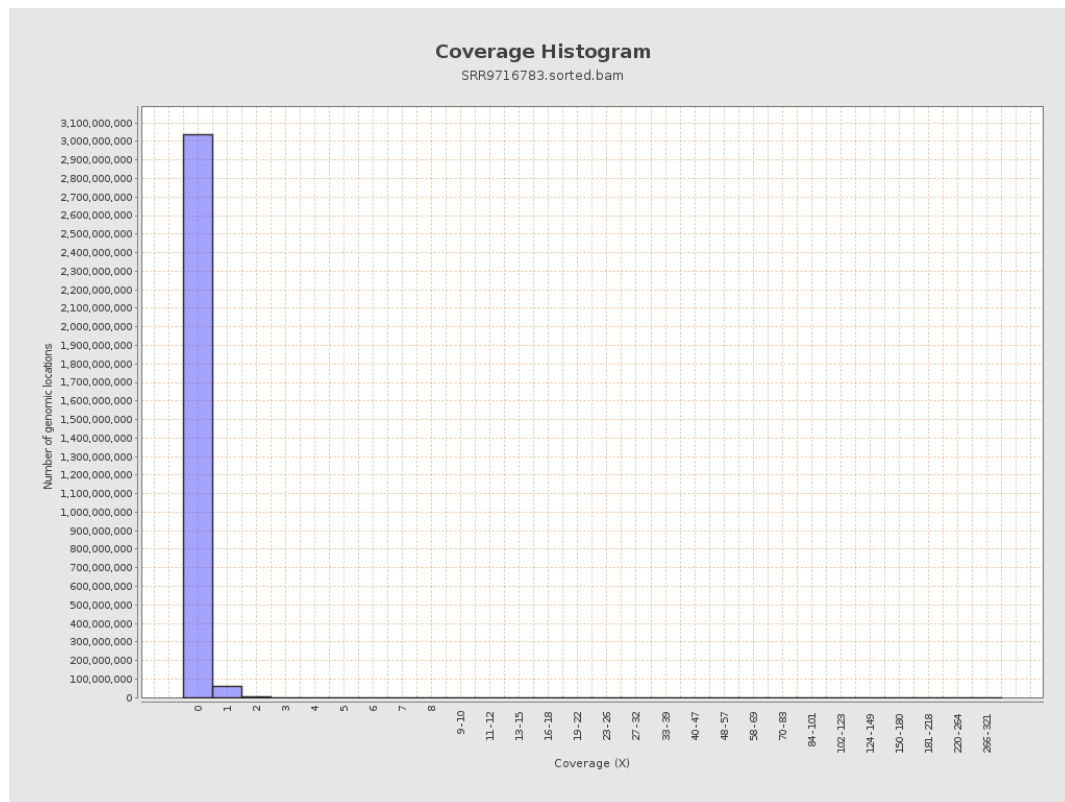
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5376523	0.0216	0.2228
chr2	243199373	5815899	0.0239	0.2865
chr3	198022430	4561069	0.023	0.1615
chr4	191154276	4390116	0.023	0.171
chr5	180915260	4125044	0.0228	0.1619
chr6	171115067	3849036	0.0225	0.1735
chr7	159138663	3640369	0.0229	0.2216

chr8	146364022	3420597	0.0234	0.2586
chr9	141213431	2892935	0.0205	0.2166
chr10	135534747	3150582	0.0232	0.193
chr11	135006516	3056541	0.0226	0.2177
chr12	133851895	2971257	0.0222	0.1601
chr13	115169878	2168789	0.0188	0.1459
chr14	107349540	2052617	0.0191	0.1654
chr15	102531392	1959641	0.0191	0.1472
chr16	90354753	1988811	0.022	0.1686
chr17	81195210	1835444	0.0226	0.171
chr18	78077248	1858759	0.0238	0.3552
chr19	59128983	1310712	0.0222	0.2103
chr20	63025520	1440247	0.0229	0.1644
chr21	48129895	888389	0.0185	0.1525
chr22	51304566	752526	0.0147	0.1294
chrMT	16571	4184	0.2525	0.5553
chrX	155270560	3753011	0.0242	0.1892
chrY	59373566	168834	0.0028	0.0929

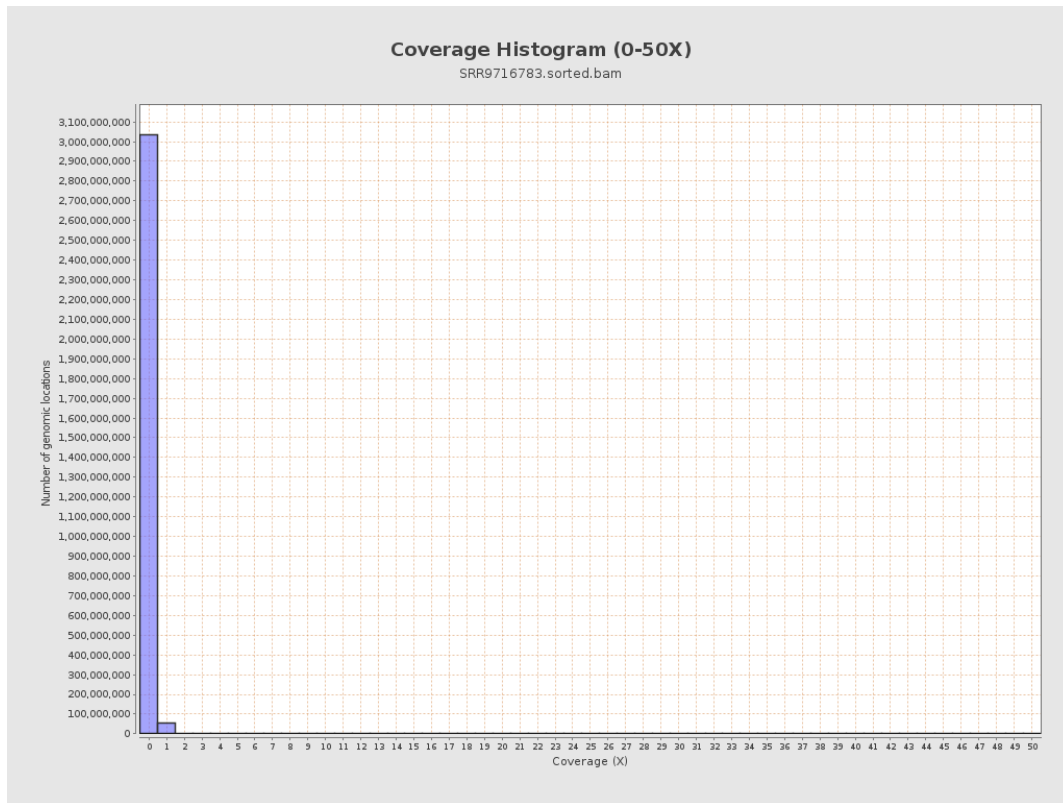
3. Results : Coverage across reference



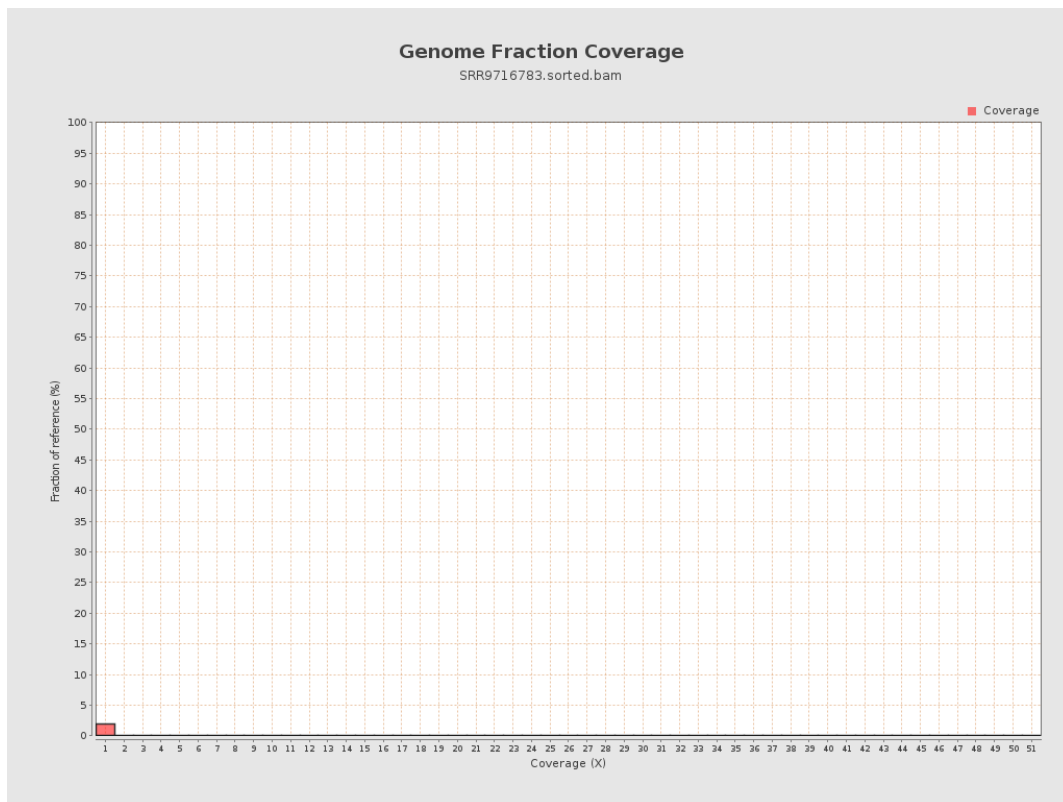
4. Results : Coverage Histogram



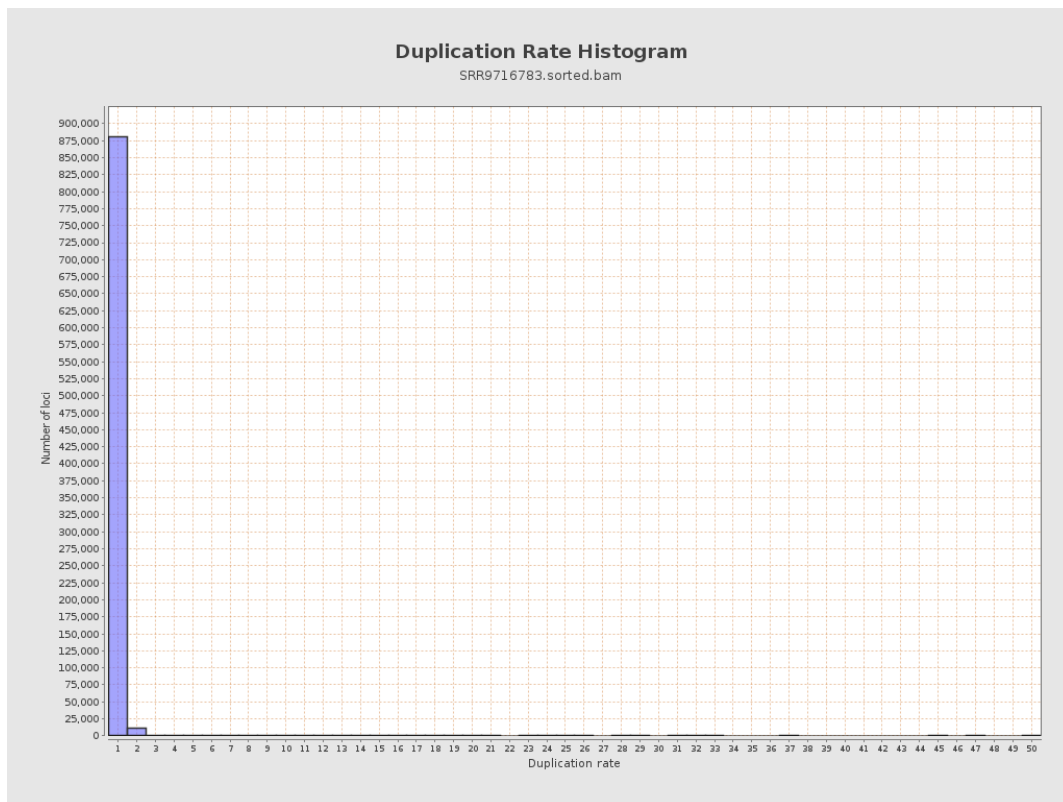
5. Results : Coverage Histogram (0-50X)



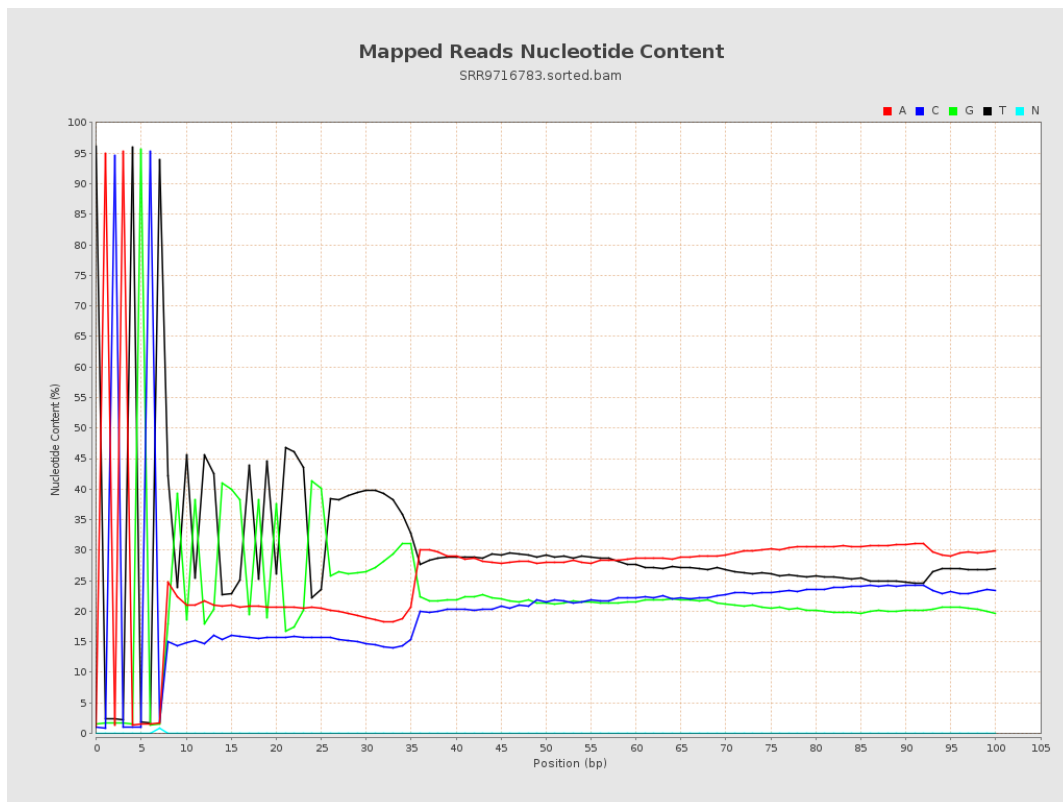
6. Results : Genome Fraction Coverage



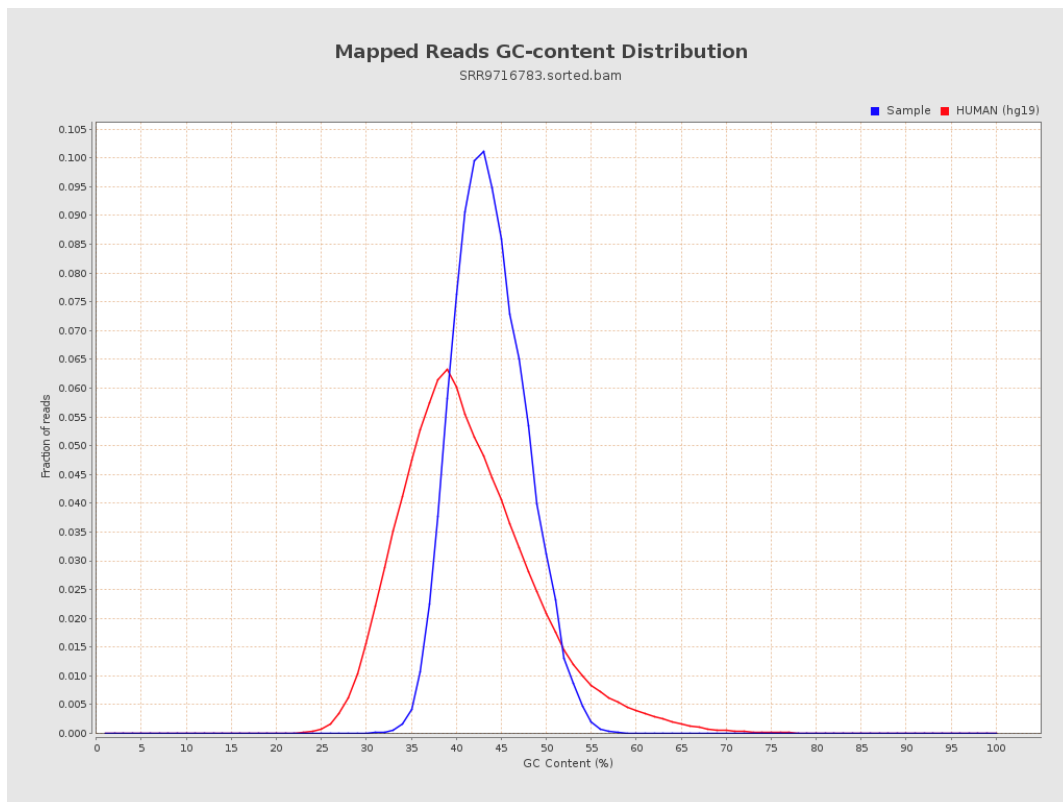
7. Results : Duplication Rate Histogram



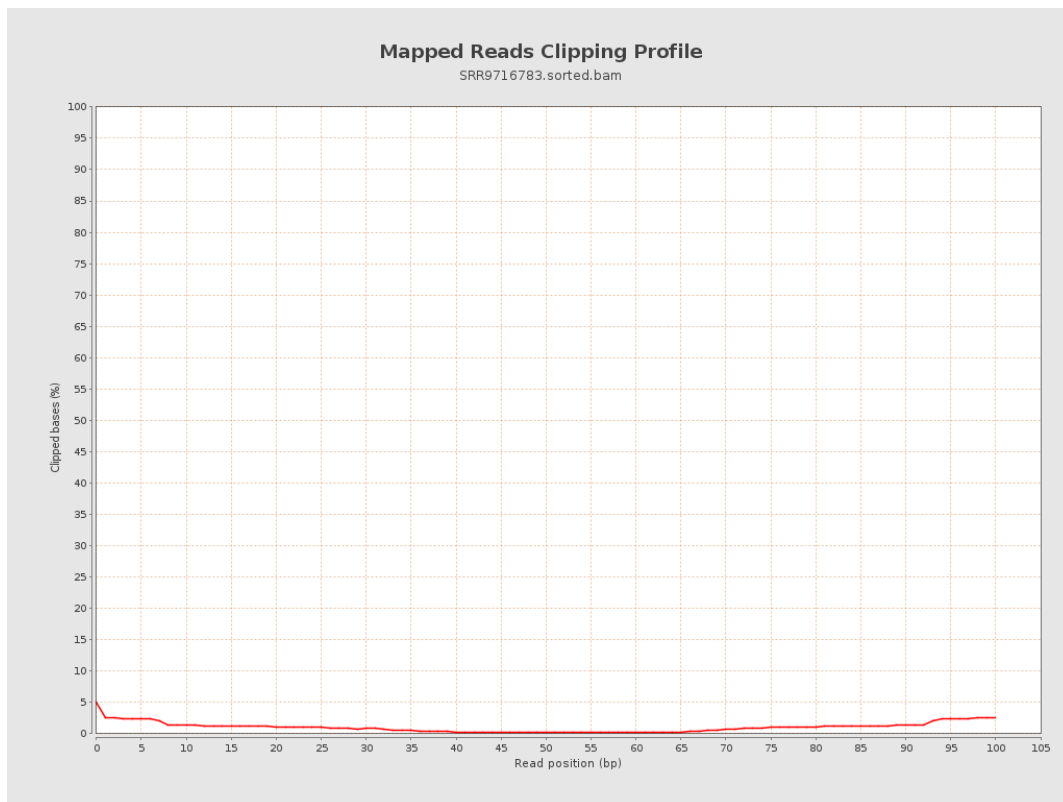
8. Results : Mapped Reads Nucleotide Content



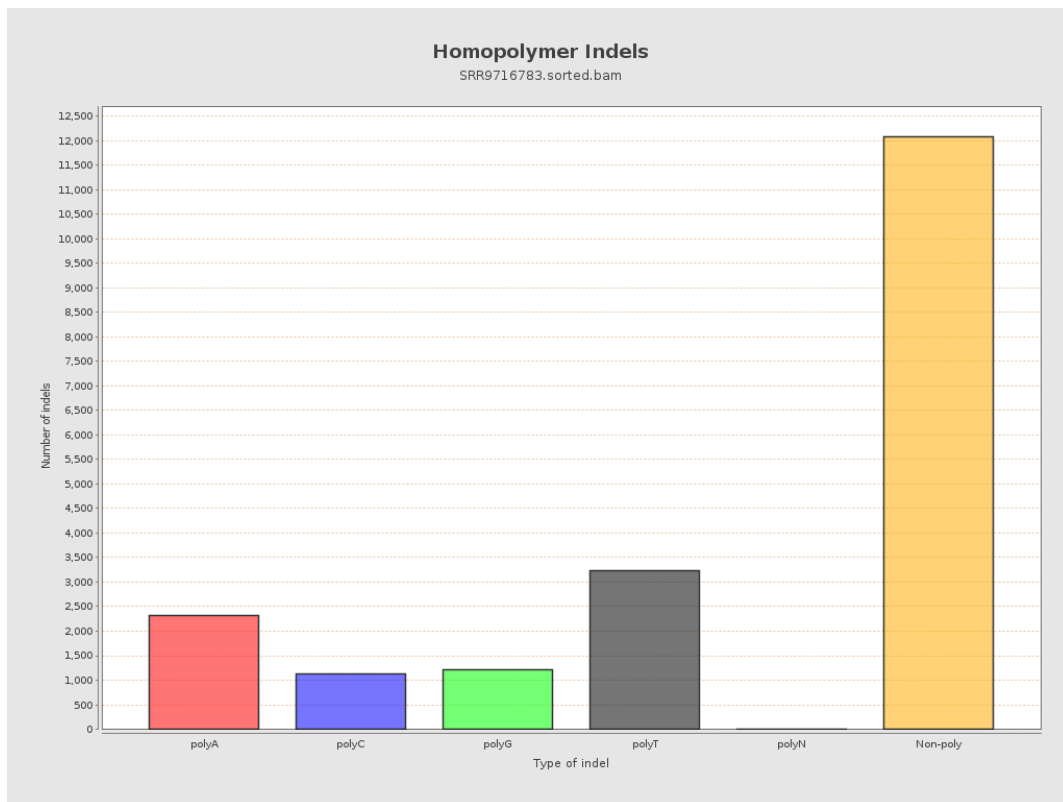
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

