

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 19:09:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716533.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_SRR9716533 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716533.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 19:09:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716533.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,417,079
Mapped reads	2,268,559 / 93.86%
Unmapped reads	148,520 / 6.14%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	45,784 / 1.89%
Read min/max/mean length	30 / 101 / 101.69
Duplicated reads (estimated)	145,713 / 6.03%
Duplication rate	5.03%
Clipped reads	2,307,795 / 95.48%

2.2. ACGT Content

Number/percentage of A's	41,847,314 / 23.91%
Number/percentage of C's	36,337,141 / 20.76%
Number/percentage of T's	53,723,700 / 30.7%
Number/percentage of G's	43,100,077 / 24.63%
Number/percentage of N's	6,043 / 0%
GC Percentage	45.39%

2.3. Coverage

Mean	0.0566

Standard Deviation	0.4585
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2.4. Mapping Quality

Mean Mapping Quality	46.45
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2.5. Mismatches and indels

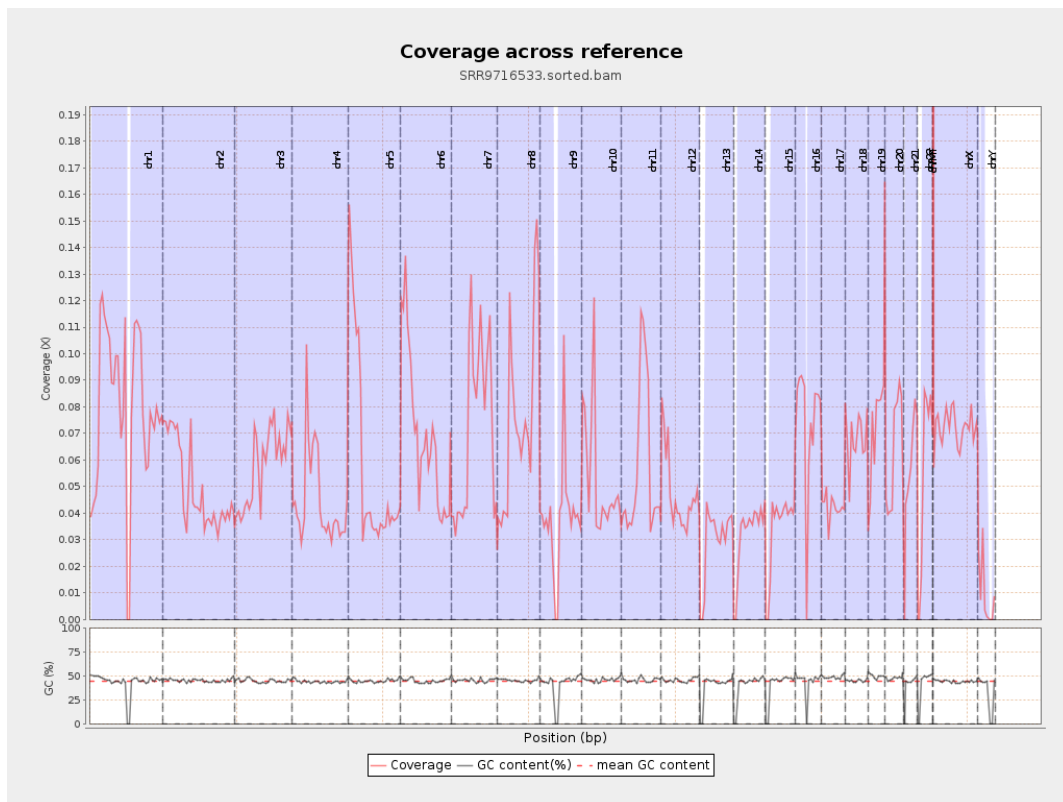
General error rate	0.67%
Mismatches	1,141,514
Insertions	15,281
Mapped reads with at least one insertion	0.66%
Deletions	31,679
Mapped reads with at least one deletion	1.37%
Homopolymer indels	38.85%

2.6. Chromosome stats

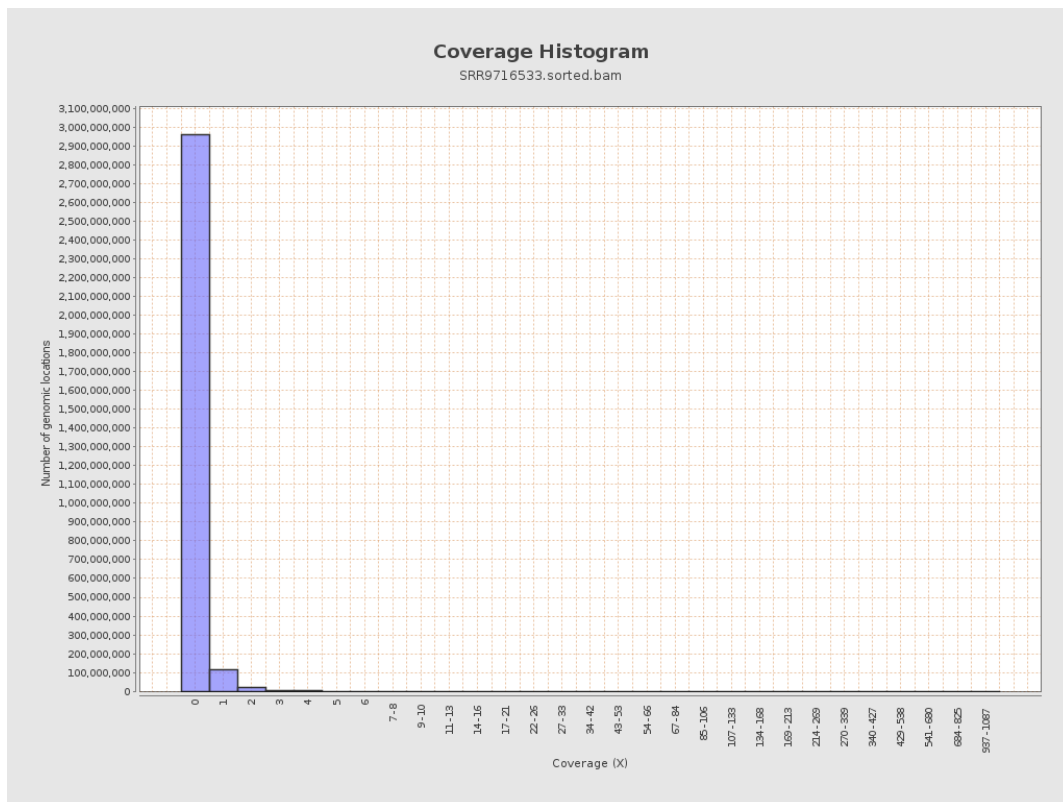
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	19902599	0.0798	0.9465
chr2	243199373	12091475	0.0497	0.4256
chr3	198022430	11437724	0.0578	0.2961
chr4	191154276	8562672	0.0448	0.3667
chr5	180915260	10578416	0.0585	0.3035
chr6	171115067	11850185	0.0693	0.348
chr7	159138663	11380100	0.0715	0.6127

chr8	146364022	11223088	0.0767	0.4748
chr9	141213431	5391614	0.0382	0.306
chr10	135534747	7085640	0.0523	0.5596
chr11	135006516	7684597	0.0569	0.3647
chr12	133851895	6425345	0.048	0.2685
chr13	115169878	3440743	0.0299	0.2084
chr14	107349540	3419708	0.0319	0.2397
chr15	102531392	3402004	0.0332	0.2199
chr16	90354753	6607398	0.0731	0.3616
chr17	81195210	3436886	0.0423	0.2854
chr18	78077248	5253661	0.0673	0.487
chr19	59128983	4436040	0.075	0.6883
chr20	63025520	3978683	0.0631	0.3322
chr21	48129895	2728862	0.0567	0.3592
chr22	51304566	2826722	0.0551	0.3004
chrMT	16571	142614	8.6062	7.006
chrX	155270560	11230207	0.0723	0.3494
chrY	59373566	562523	0.0095	0.3268

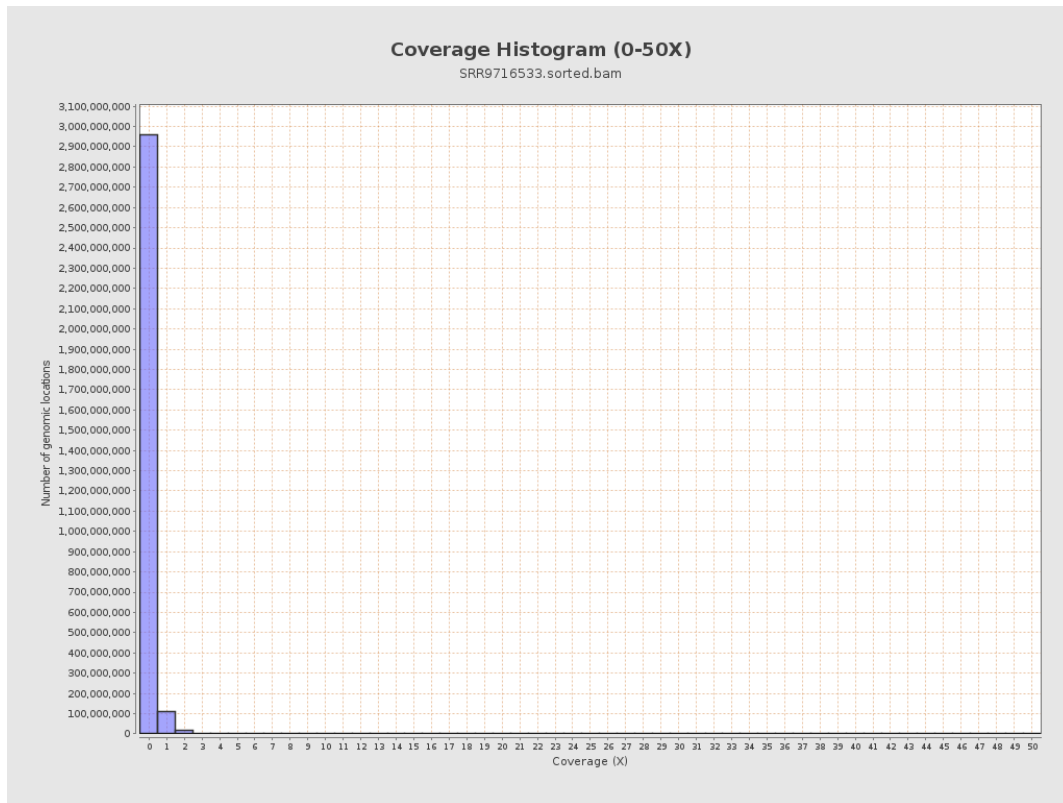
3. Results : Coverage across reference



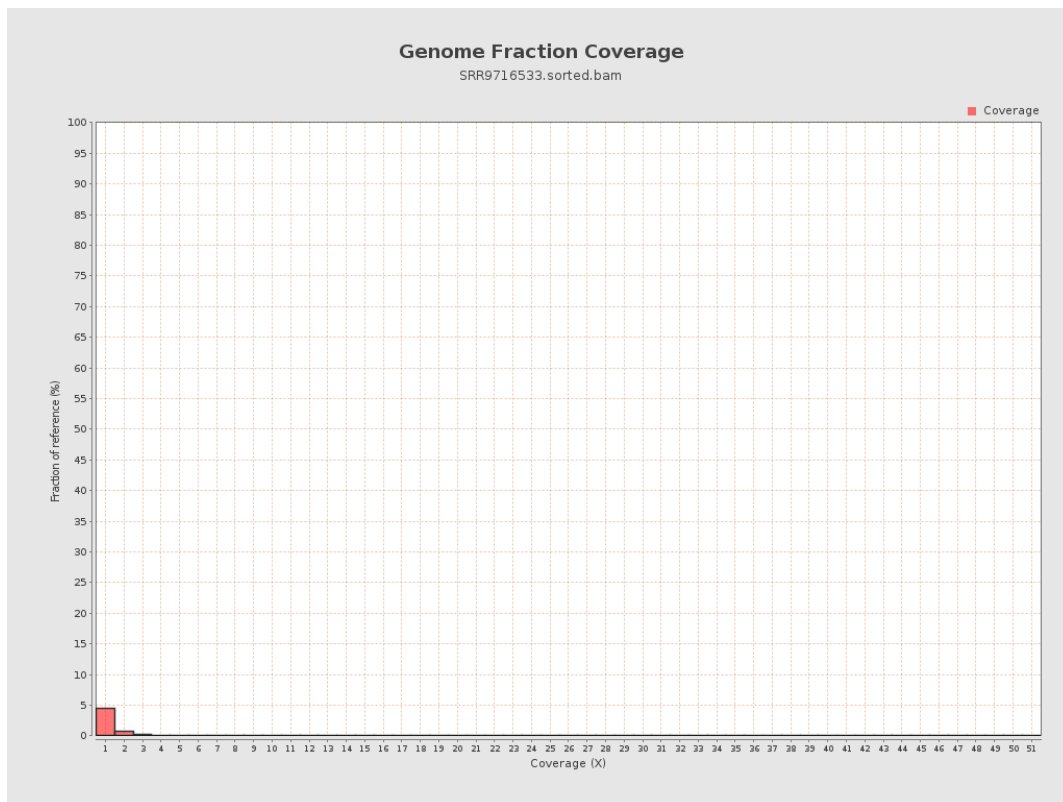
4. Results : Coverage Histogram



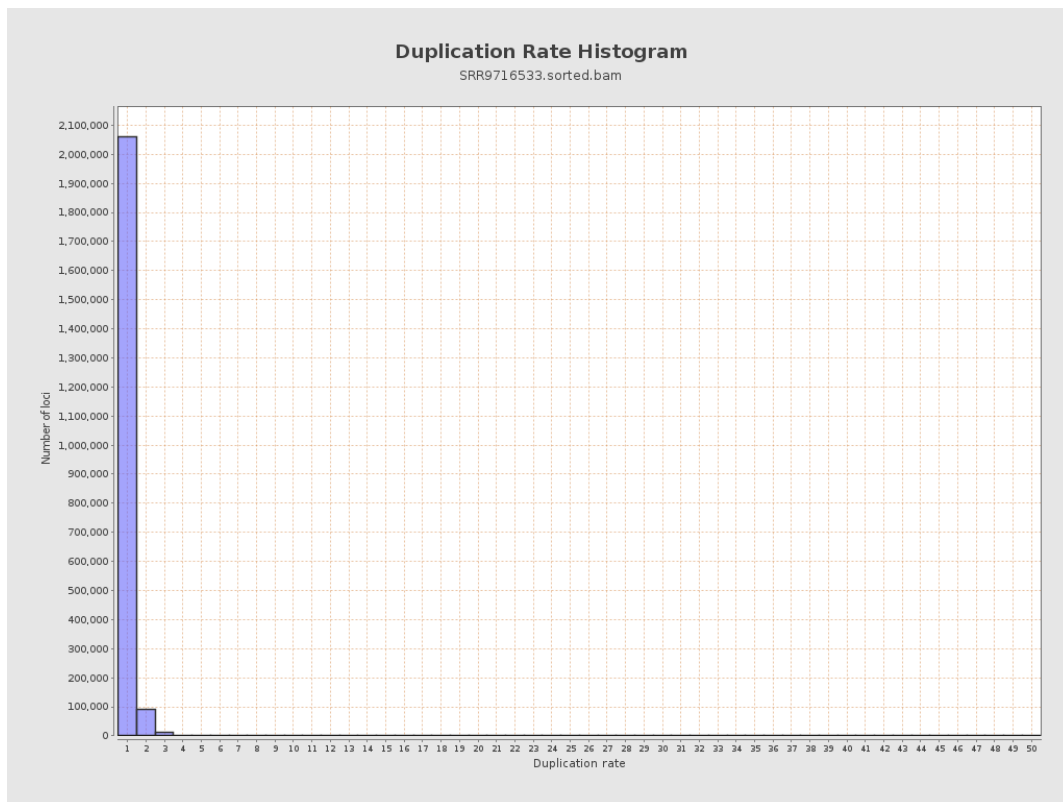
5. Results : Coverage Histogram (0-50X)



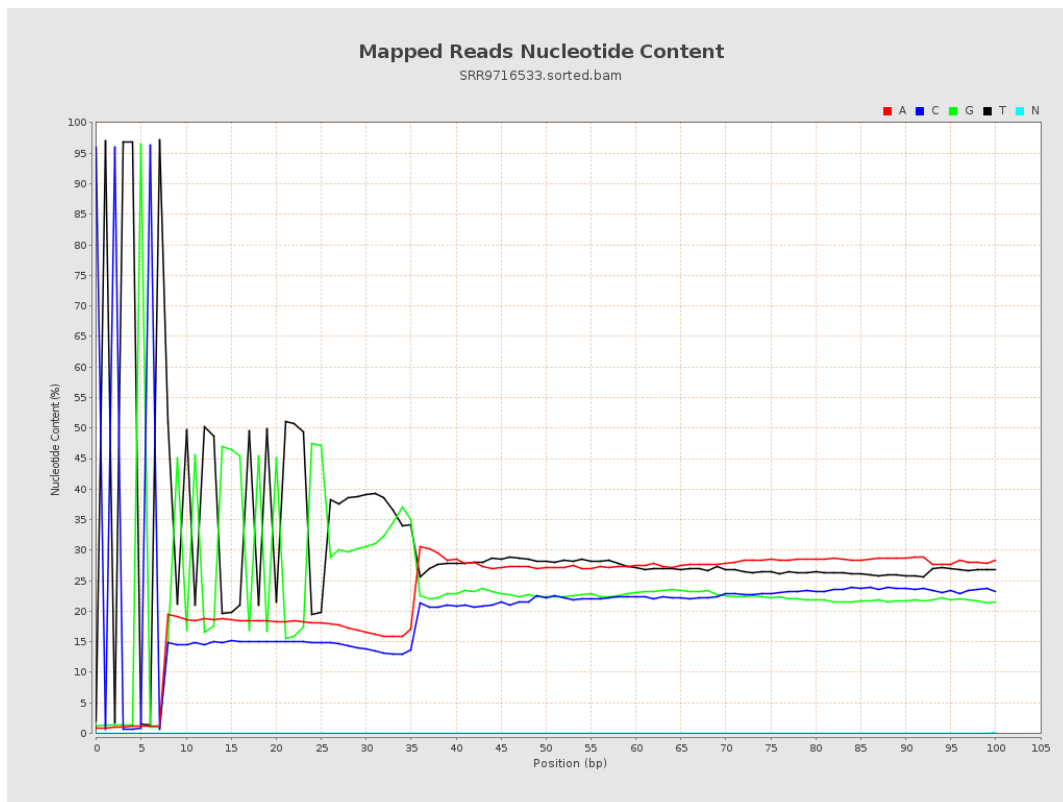
6. Results : Genome Fraction Coverage



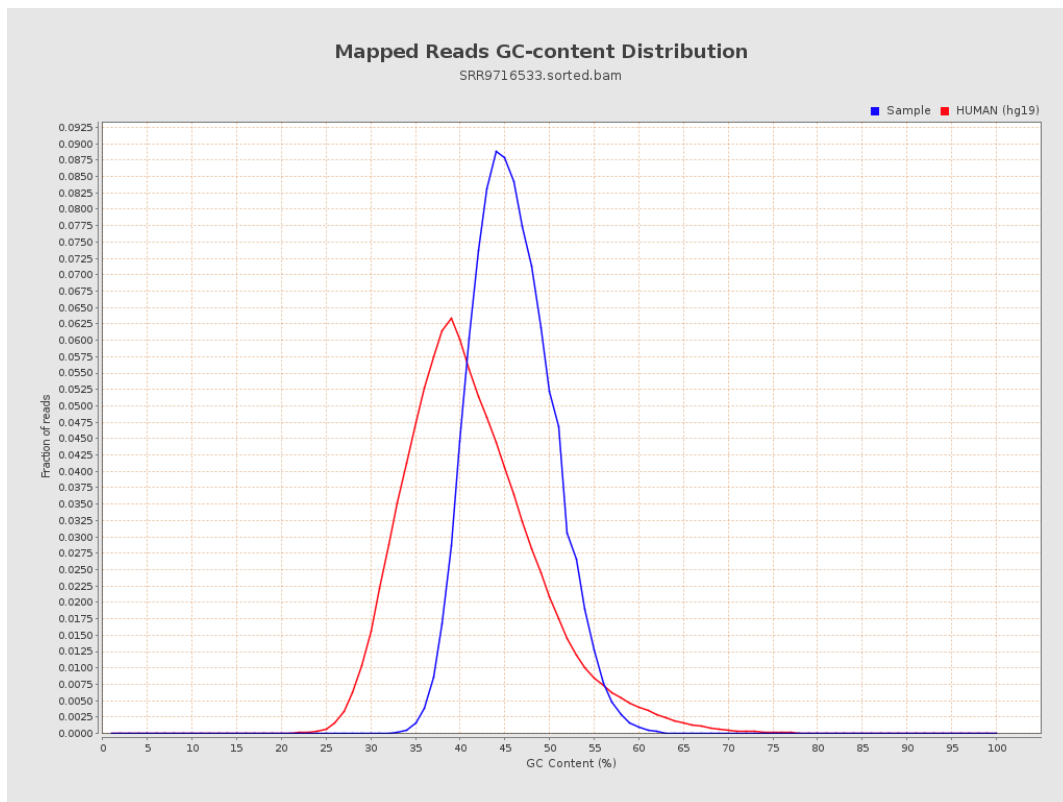
7. Results : Duplication Rate Histogram



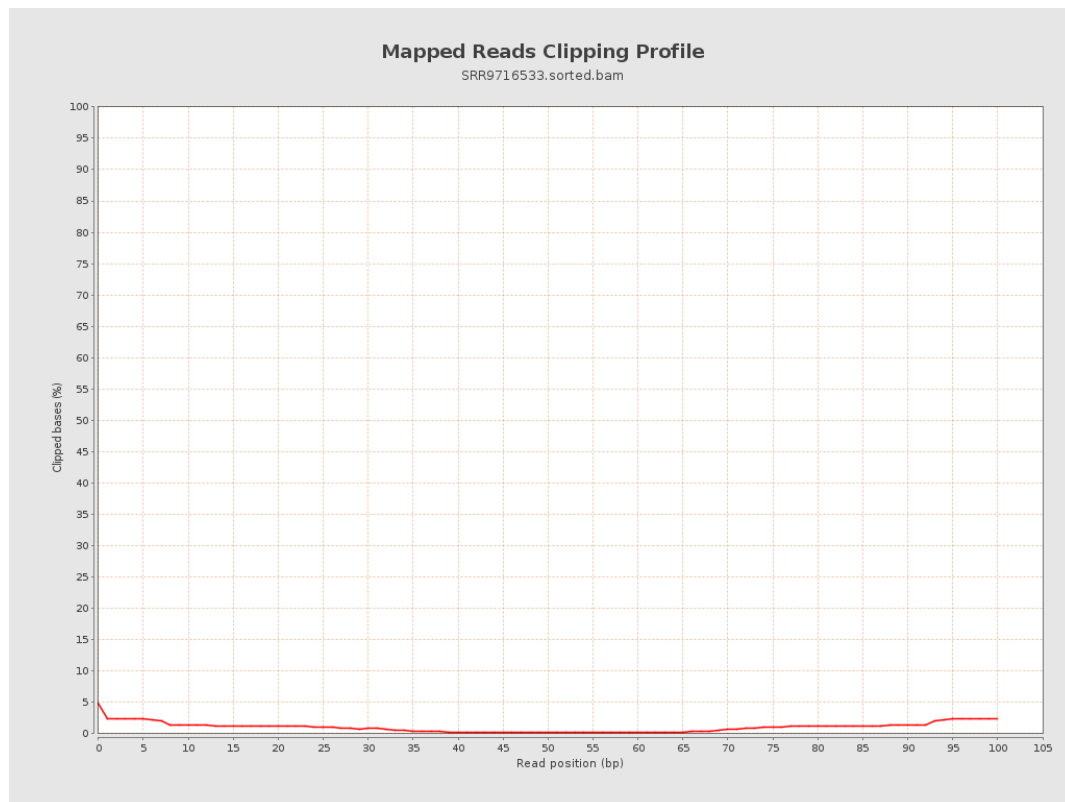
8. Results : Mapped Reads Nucleotide Content



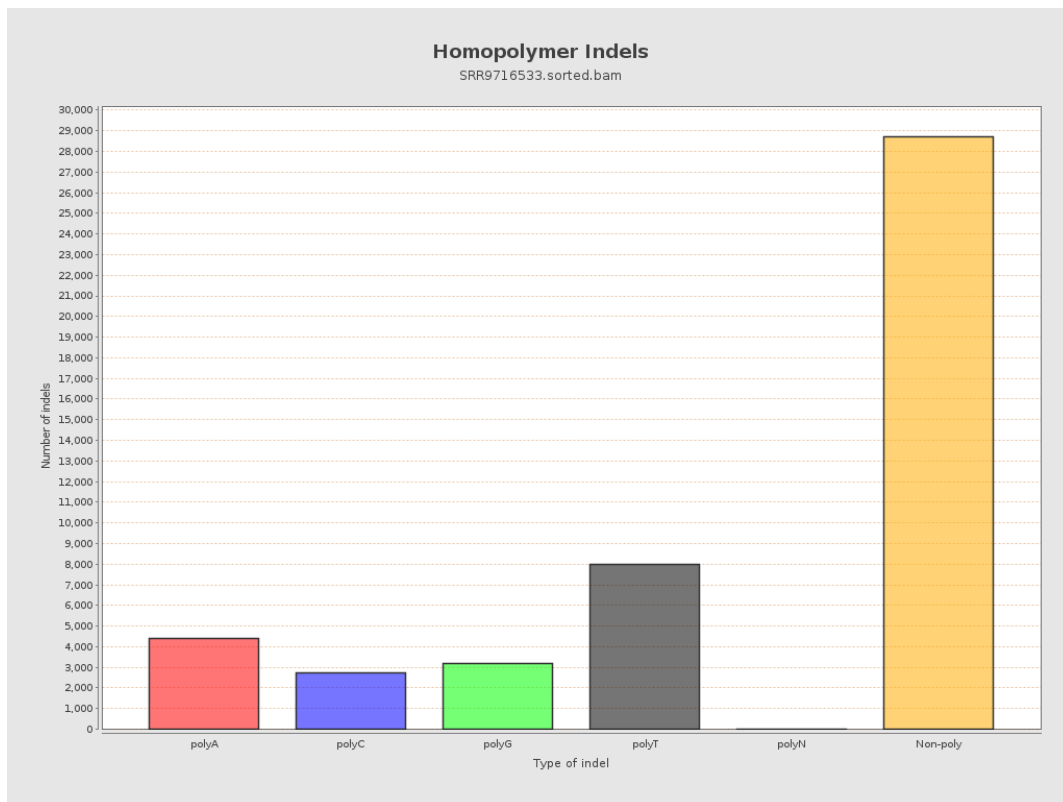
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

