

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 14:41:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716846.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_SRR9716846 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716846.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 14:41:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716846.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,379,572
Mapped reads	3,172,875 / 93.88%
Unmapped reads	206,697 / 6.12%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	56,962 / 1.69%
Read min/max/mean length	30 / 101 / 101.61
Duplicated reads (estimated)	186,626 / 5.52%
Duplication rate	4.41%
Clipped reads	3,223,355 / 95.38%

2.2. ACGT Content

Number/percentage of A's	63,867,472 / 25.78%
Number/percentage of C's	48,617,664 / 19.62%
Number/percentage of T's	76,047,444 / 30.69%
Number/percentage of G's	59,229,856 / 23.9%
Number/percentage of N's	17,686 / 0.01%
GC Percentage	43.53%

2.3. Coverage

Mean	0.0801

Standard Deviation	0.6176
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2.4. Mapping Quality

Mean Mapping Quality	47.66
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2.5. Mismatches and indels

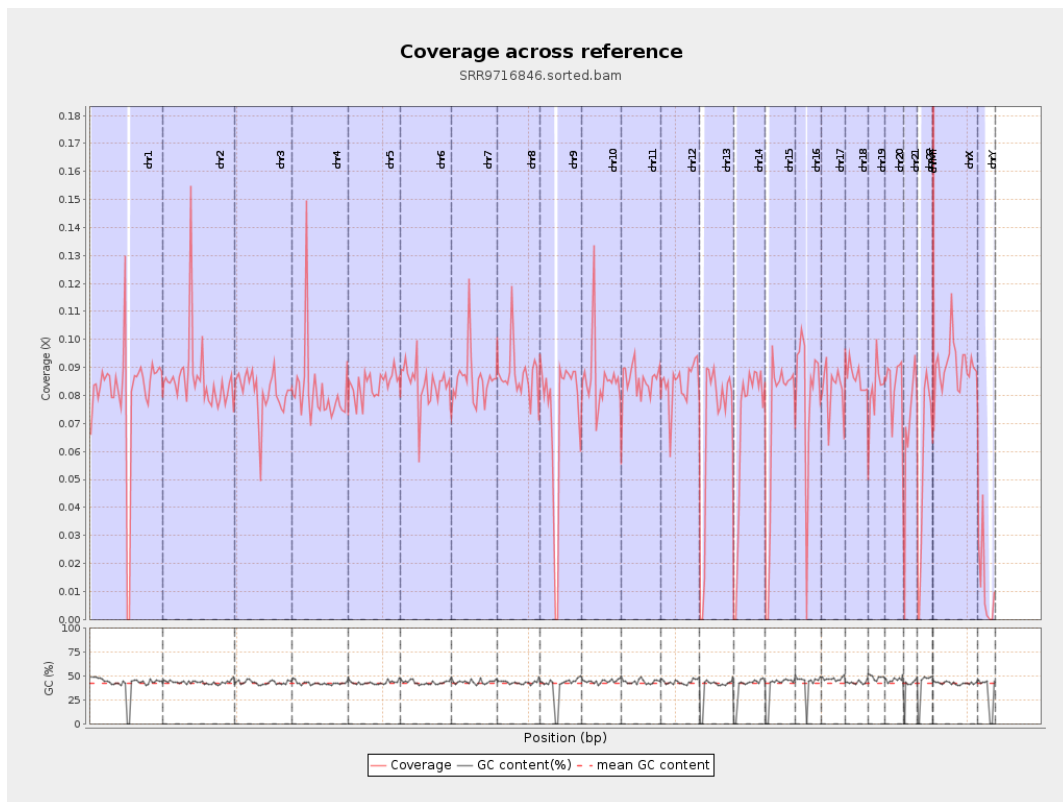
General error rate	0.67%
Mismatches	1,599,496
Insertions	21,946
Mapped reads with at least one insertion	0.68%
Deletions	57,424
Mapped reads with at least one deletion	1.78%
Homopolymer indels	41.7%

2.6. Chromosome stats

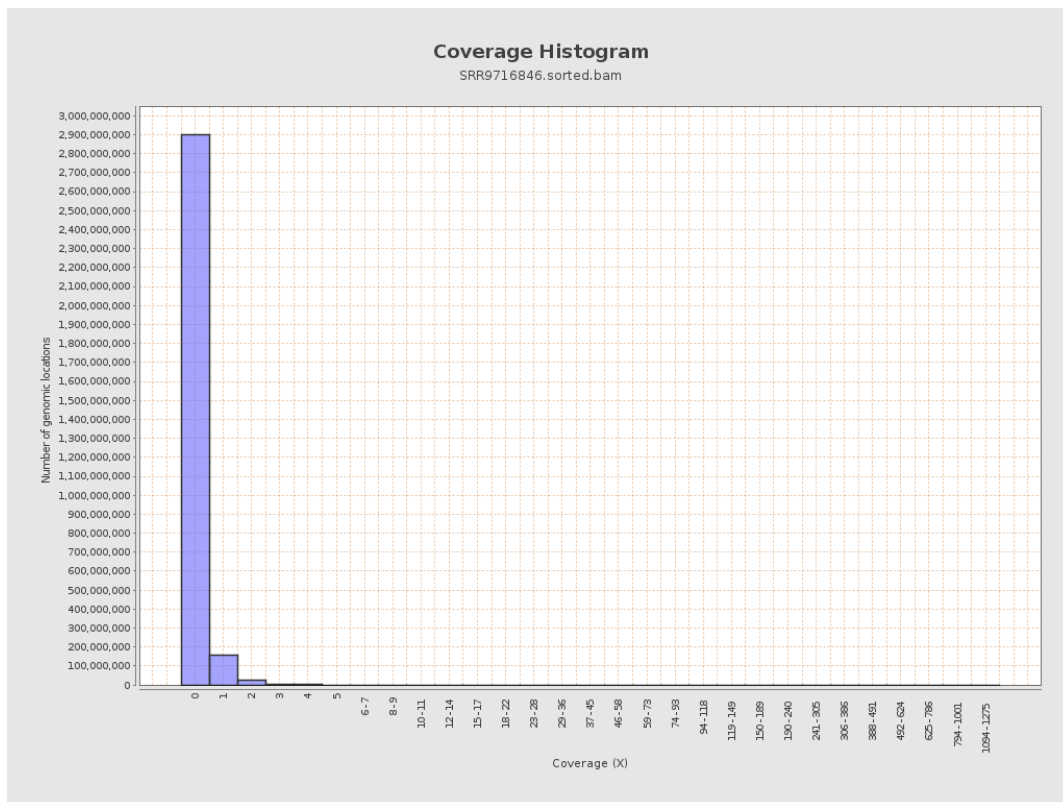
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	20047091	0.0804	1.097
chr2	243199373	20911557	0.086	0.7897
chr3	198022430	16036453	0.081	0.3444
chr4	191154276	15609916	0.0817	0.469
chr5	180915260	15148955	0.0837	0.3578
chr6	171115067	14395877	0.0841	0.414
chr7	159138663	13654075	0.0858	0.8684

chr8	146364022	12716593	0.0869	0.7943
chr9	141213431	10355409	0.0733	0.5609
chr10	135534747	11605244	0.0856	0.6161
chr11	135006516	11507353	0.0852	0.6203
chr12	133851895	11316908	0.0845	0.3568
chr13	115169878	7930875	0.0689	0.3185
chr14	107349540	7491639	0.0698	0.3589
chr15	102531392	7216142	0.0704	0.3229
chr16	90354753	7251373	0.0803	0.3822
chr17	81195210	6720423	0.0828	0.4319
chr18	78077248	6761916	0.0866	0.9607
chr19	59128983	4893665	0.0828	0.7703
chr20	63025520	5300129	0.0841	0.3763
chr21	48129895	3366822	0.07	0.3999
chr22	51304566	2898771	0.0565	0.294
chrMT	16571	22482	1.3567	1.6408
chrX	155270560	14021413	0.0903	0.4579
chrY	59373566	707173	0.0119	0.3714

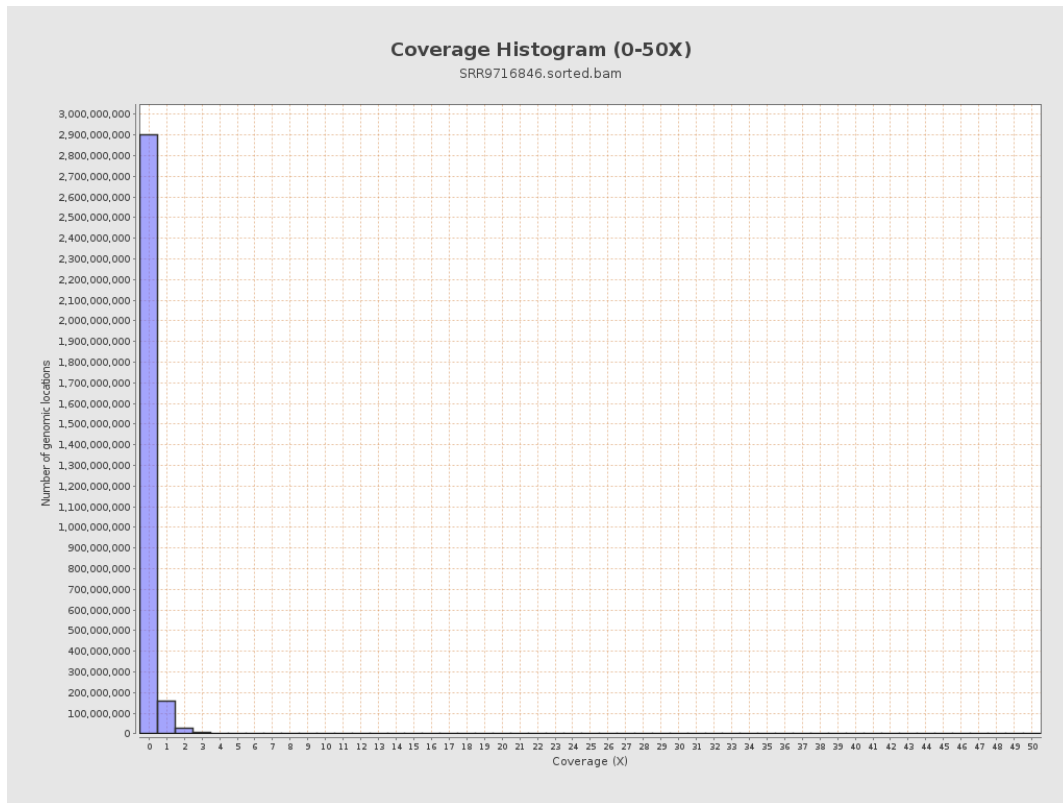
3. Results : Coverage across reference



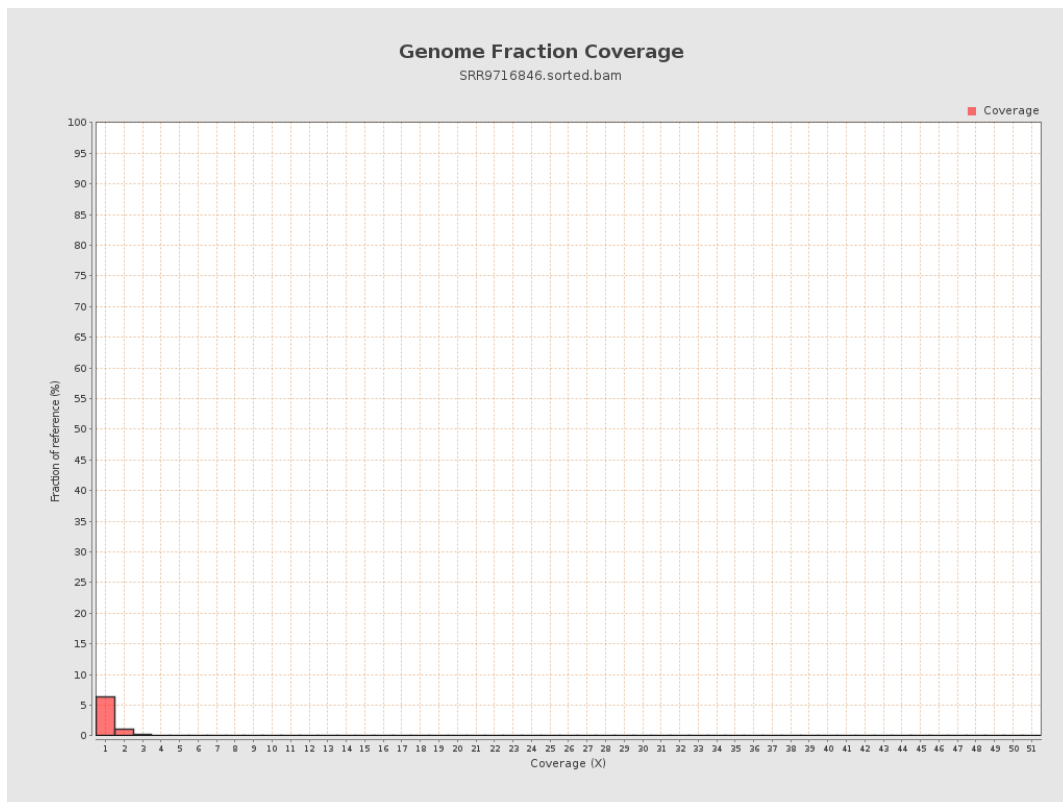
4. Results : Coverage Histogram



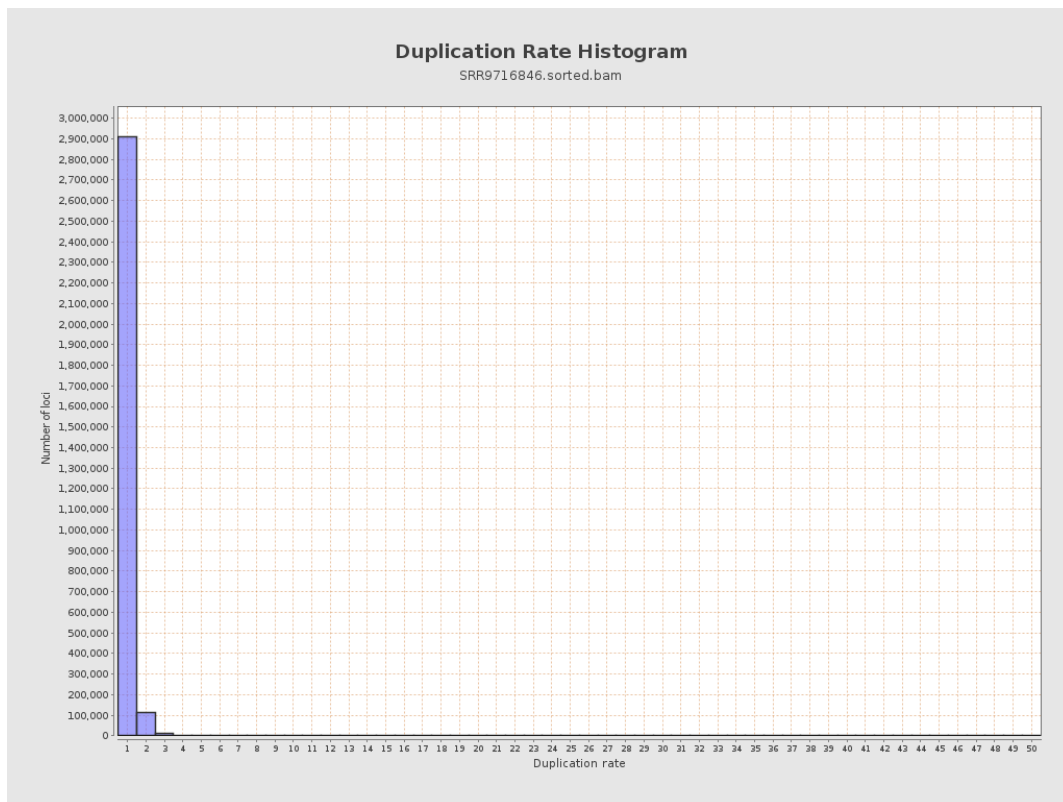
5. Results : Coverage Histogram (0-50X)



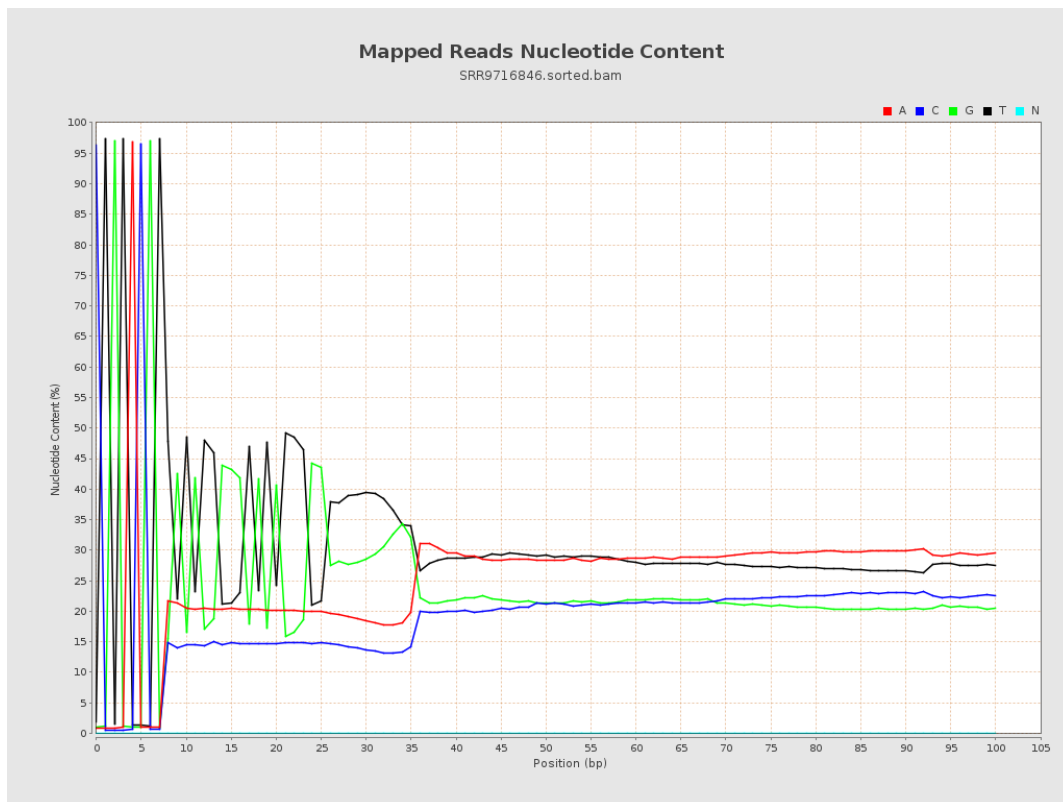
6. Results : Genome Fraction Coverage



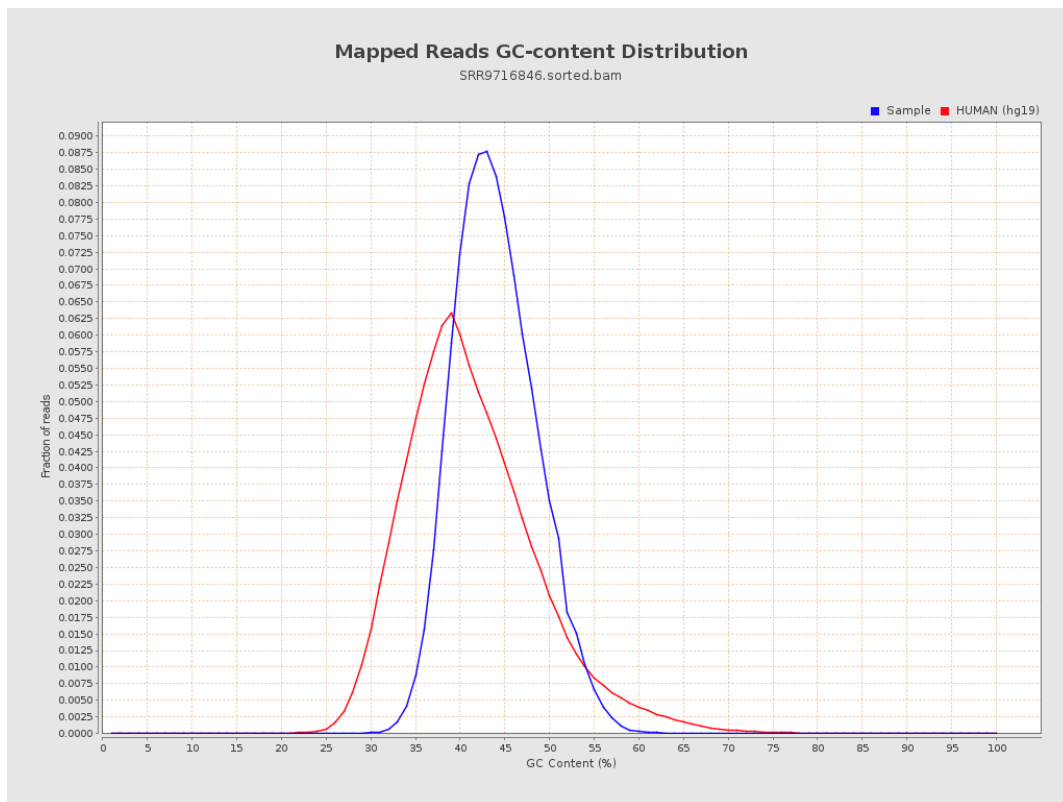
7. Results : Duplication Rate Histogram



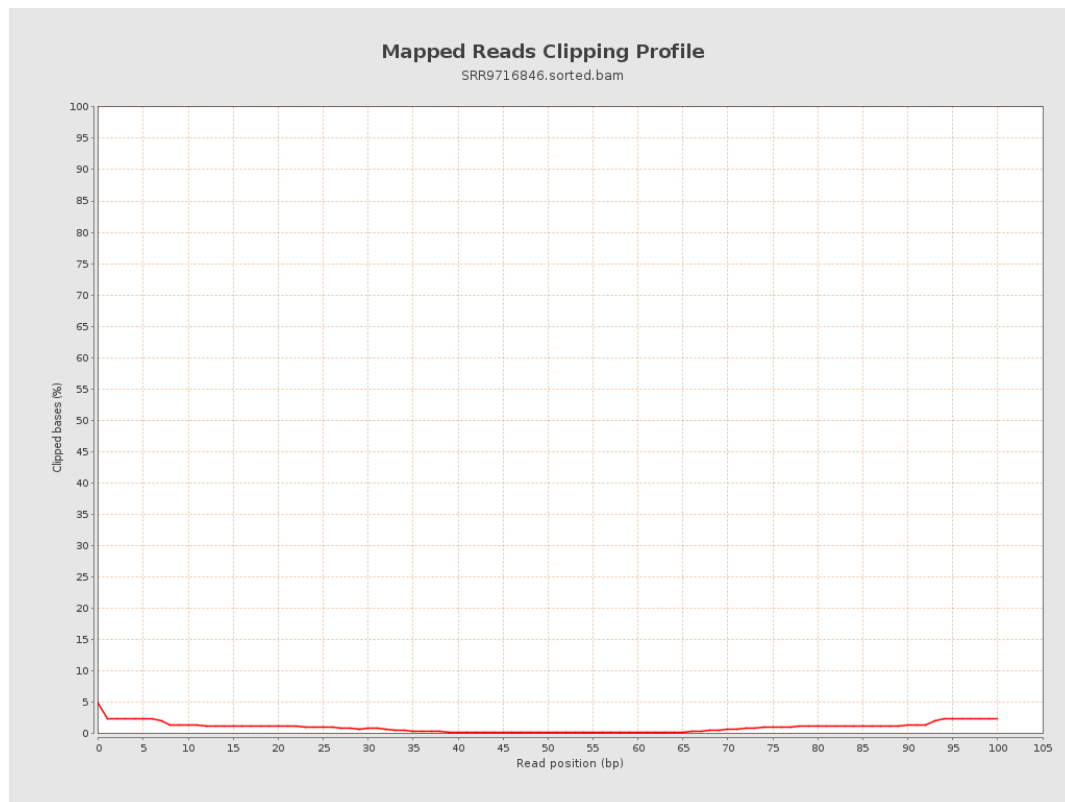
8. Results : Mapped Reads Nucleotide Content



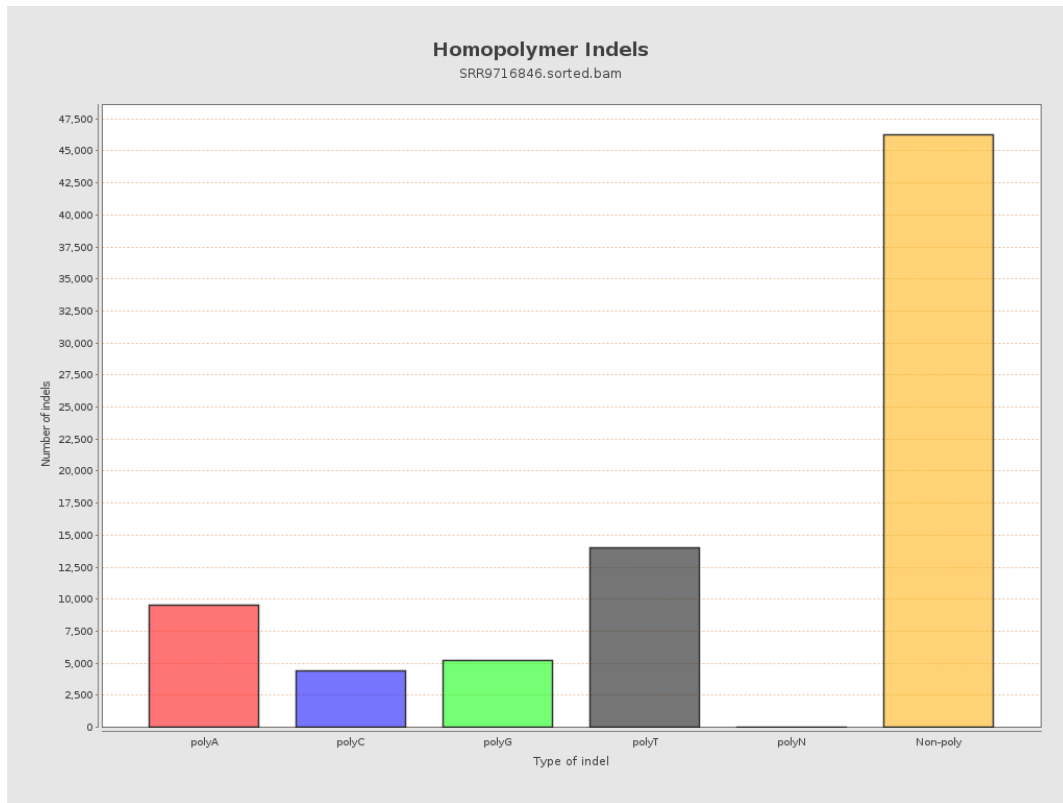
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

