

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 18:53:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716925.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_SRR9716925 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716925.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 18:53:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716925.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,321,445
Mapped reads	1,231,851 / 93.22%
Unmapped reads	89,594 / 6.78%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	30,369 / 2.3%
Read min/max/mean length	30 / 101 / 101.83
Duplicated reads (estimated)	45,781 / 3.46%
Duplication rate	2.84%
Clipped reads	1,259,046 / 95.28%

2.2. ACGT Content

Number/percentage of A's	22,561,667 / 24.07%
Number/percentage of C's	19,487,323 / 20.79%
Number/percentage of T's	28,665,460 / 30.58%
Number/percentage of G's	23,028,777 / 24.56%
Number/percentage of N's	3,262 / 0%
GC Percentage	45.35%

2.3. Coverage

Mean	0.0303

Standard Deviation	0.2522
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2.4. Mapping Quality

Mean Mapping Quality	46.25
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2.5. Mismatches and indels

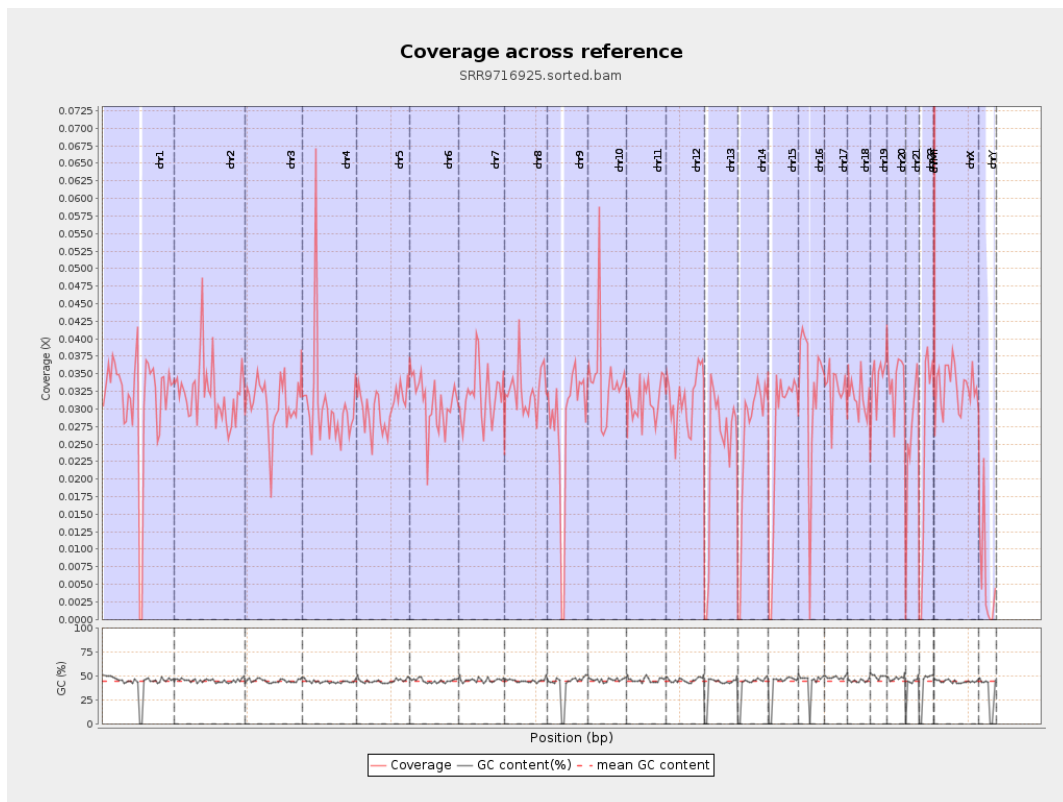
General error rate	0.68%
Mismatches	613,196
Insertions	8,999
Mapped reads with at least one insertion	0.72%
Deletions	17,112
Mapped reads with at least one deletion	1.37%
Homopolymer indels	37.42%

2.6. Chromosome stats

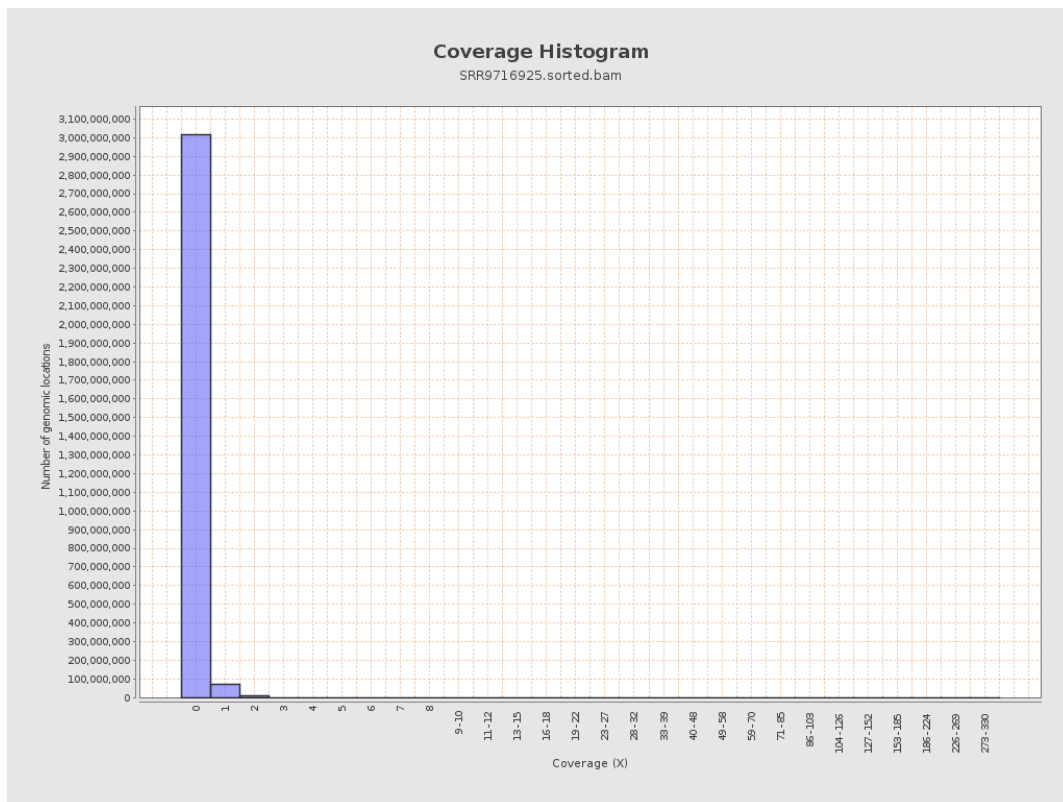
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	7764964	0.0312	0.3359
chr2	243199373	7841607	0.0322	0.2897
chr3	198022430	6090338	0.0308	0.1942
chr4	191154276	5851705	0.0306	0.268
chr5	180915260	5465698	0.0302	0.193
chr6	171115067	5281840	0.0309	0.2012
chr7	159138663	5079609	0.0319	0.2965

chr8	146364022	4766973	0.0326	0.2583
chr9	141213431	3912462	0.0277	0.2258
chr10	135534747	4639816	0.0342	0.3456
chr11	135006516	4226795	0.0313	0.2542
chr12	133851895	4194889	0.0313	0.1995
chr13	115169878	2757541	0.0239	0.1715
chr14	107349540	2811551	0.0262	0.1991
chr15	102531392	2721454	0.0265	0.1811
chr16	90354753	2939894	0.0325	0.2166
chr17	81195210	2660823	0.0328	0.2255
chr18	78077248	2475333	0.0317	0.362
chr19	59128983	2036611	0.0344	0.2741
chr20	63025520	2143883	0.034	0.2165
chr21	48129895	1275617	0.0265	0.2284
chr22	51304566	1289597	0.0251	0.1813
chrMT	16571	78038	4.7093	3.9543
chrX	155270560	5140265	0.0331	0.215
chrY	59373566	334321	0.0056	0.234

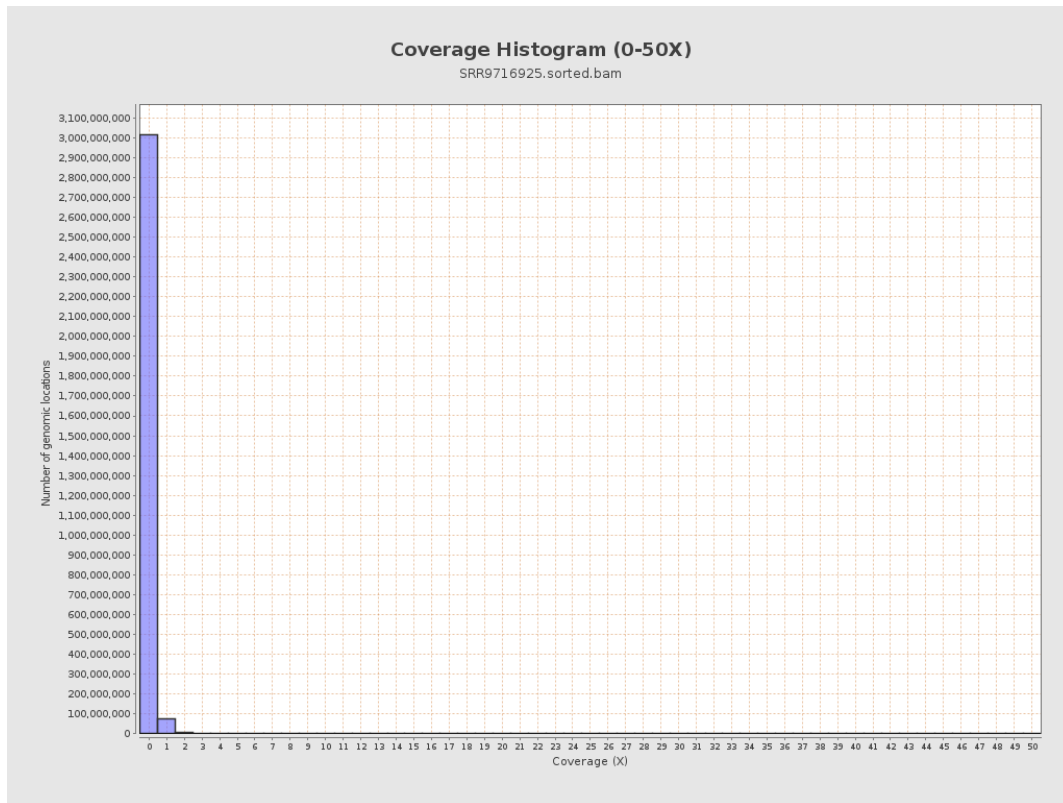
3. Results : Coverage across reference



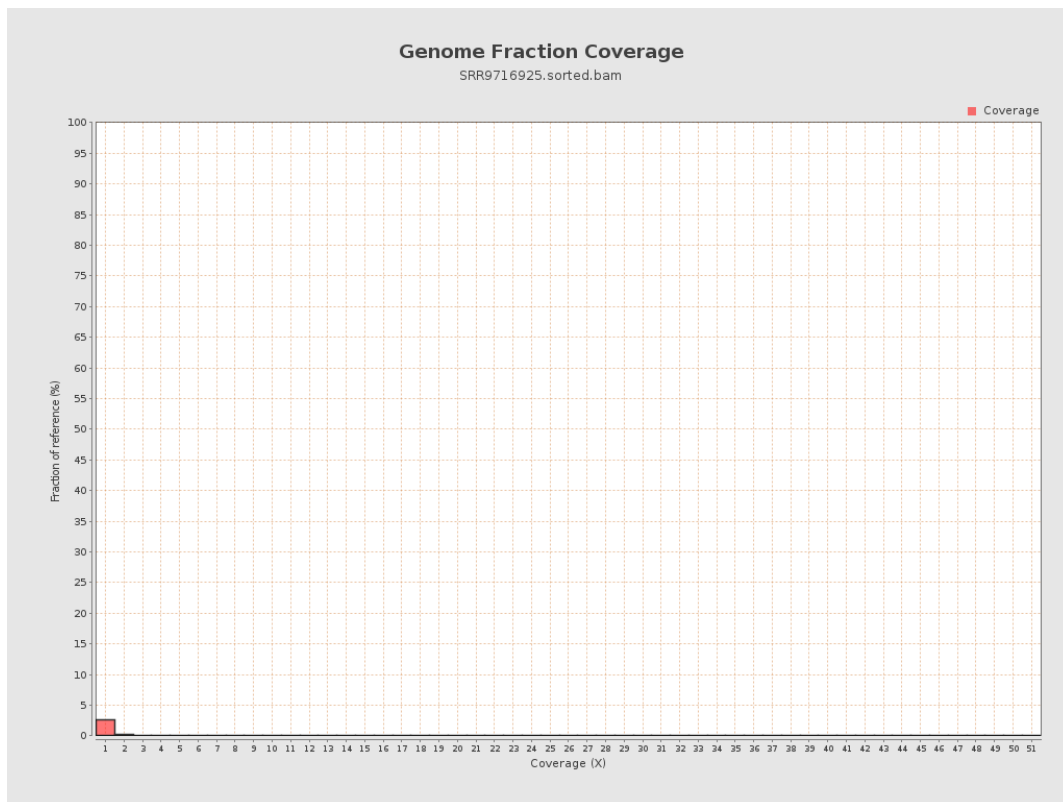
4. Results : Coverage Histogram



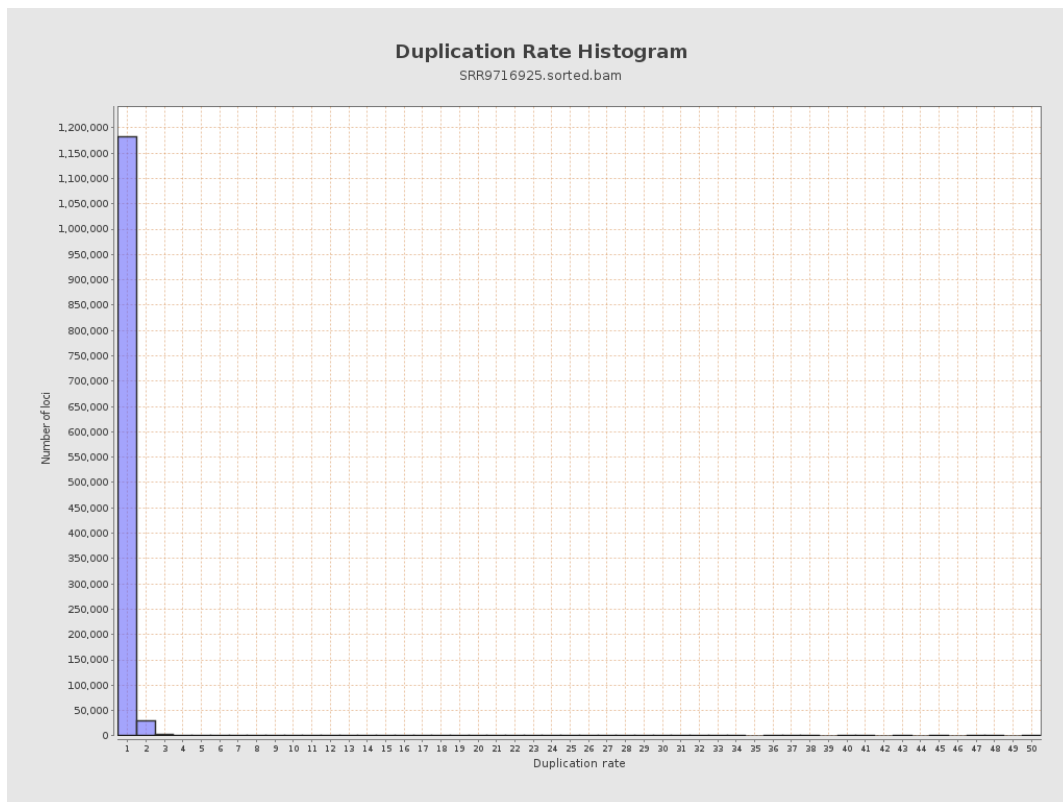
5. Results : Coverage Histogram (0-50X)



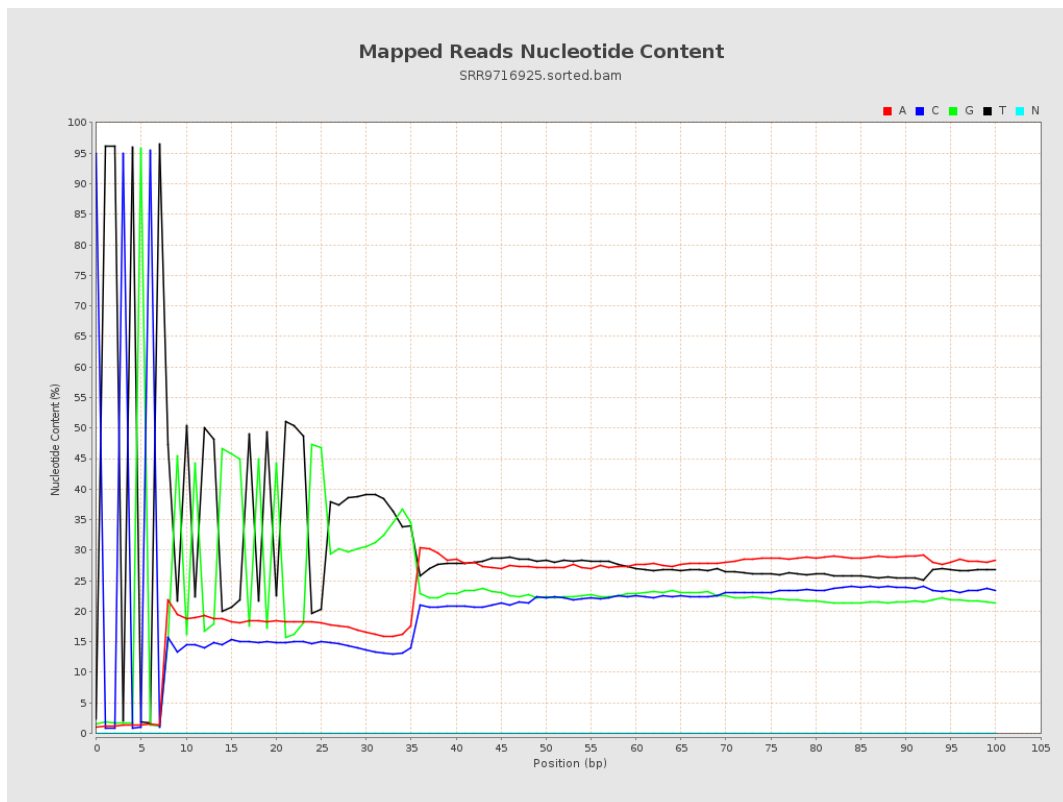
6. Results : Genome Fraction Coverage



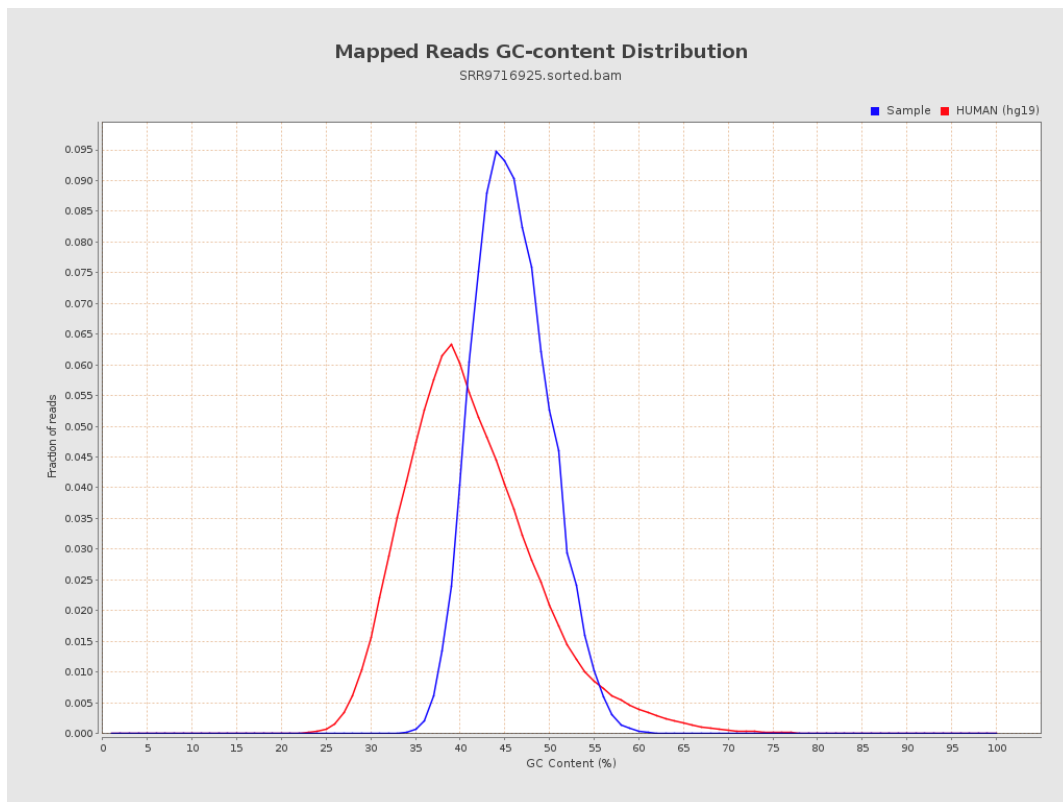
7. Results : Duplication Rate Histogram



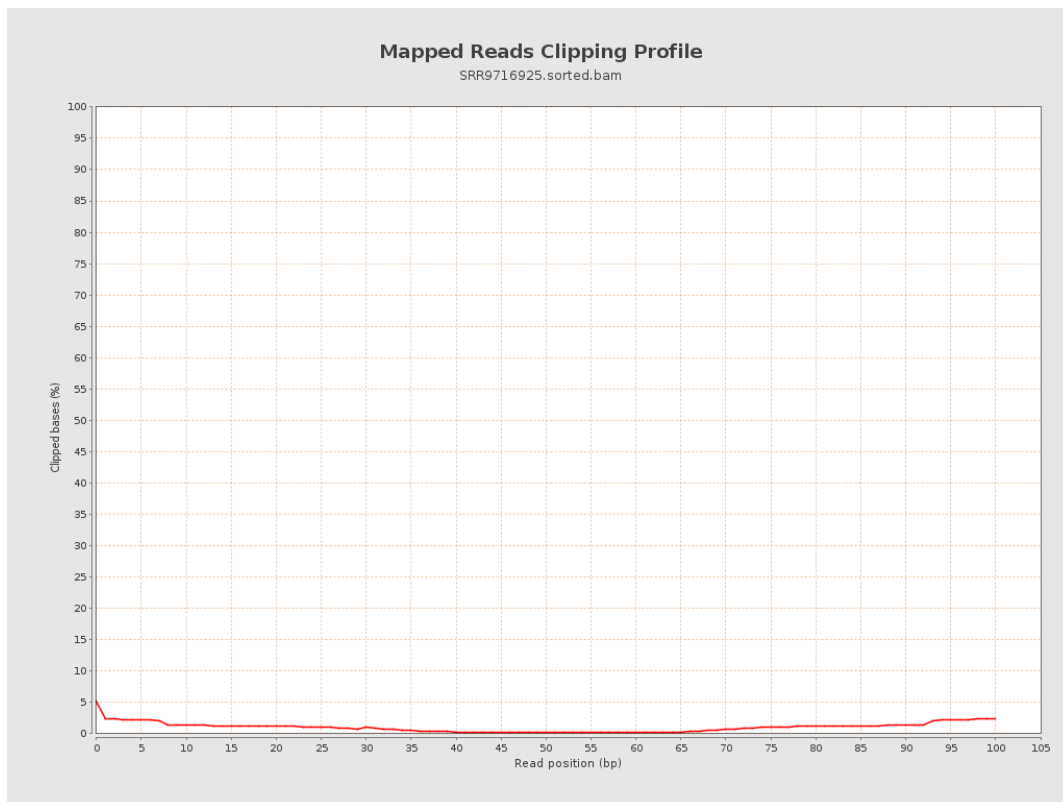
8. Results : Mapped Reads Nucleotide Content



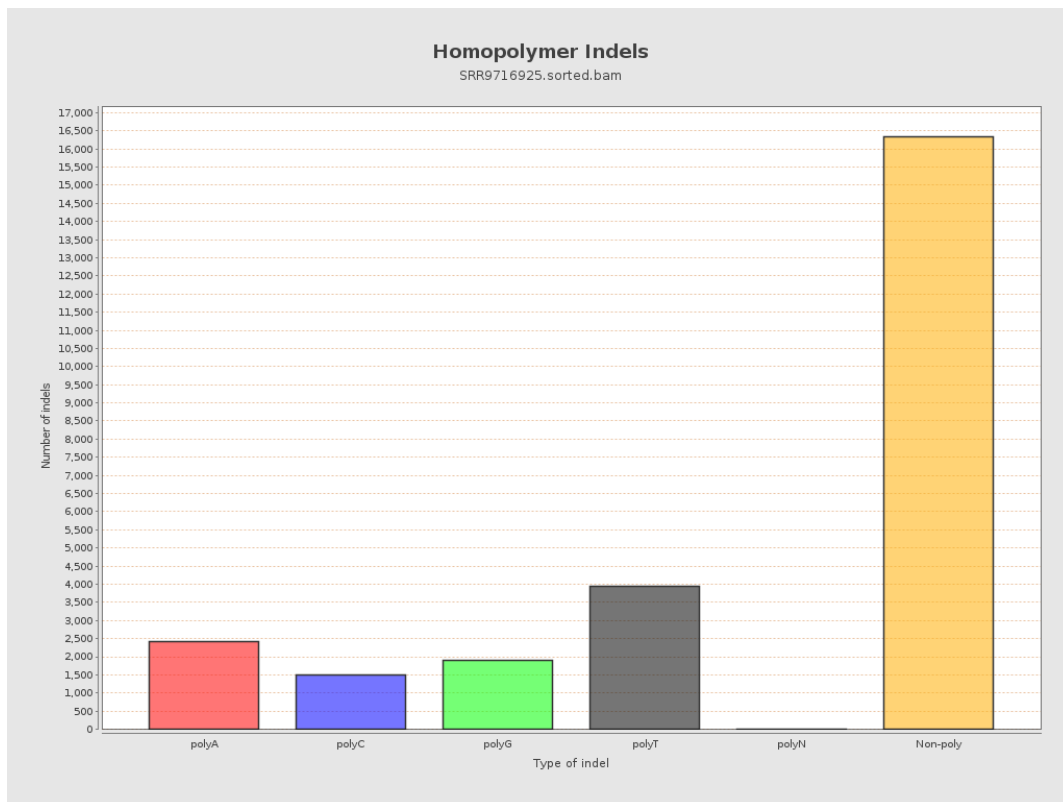
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

