

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/19 21:33:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1505975.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_SRR1505975 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1505975.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 19 21:33:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1505975.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,130,603
Mapped reads	3,602,017 / 70.21%
Unmapped reads	1,528,586 / 29.79%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	213 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	271,700 / 5.3%
Duplication rate	5.86%
Clipped reads	444,730 / 8.67%

2.2. ACGT Content

Number/percentage of A's	50,115,276 / 29.72%
Number/percentage of C's	34,539,051 / 20.48%
Number/percentage of T's	49,180,527 / 29.16%
Number/percentage of G's	34,806,079 / 20.64%
Number/percentage of N's	628 / 0%
GC Percentage	41.12%

2.3. Coverage

Mean	0.0545

Standard Deviation	0.5256
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2.4. Mapping Quality

Mean Mapping Quality	44.69
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2.5. Mismatches and indels

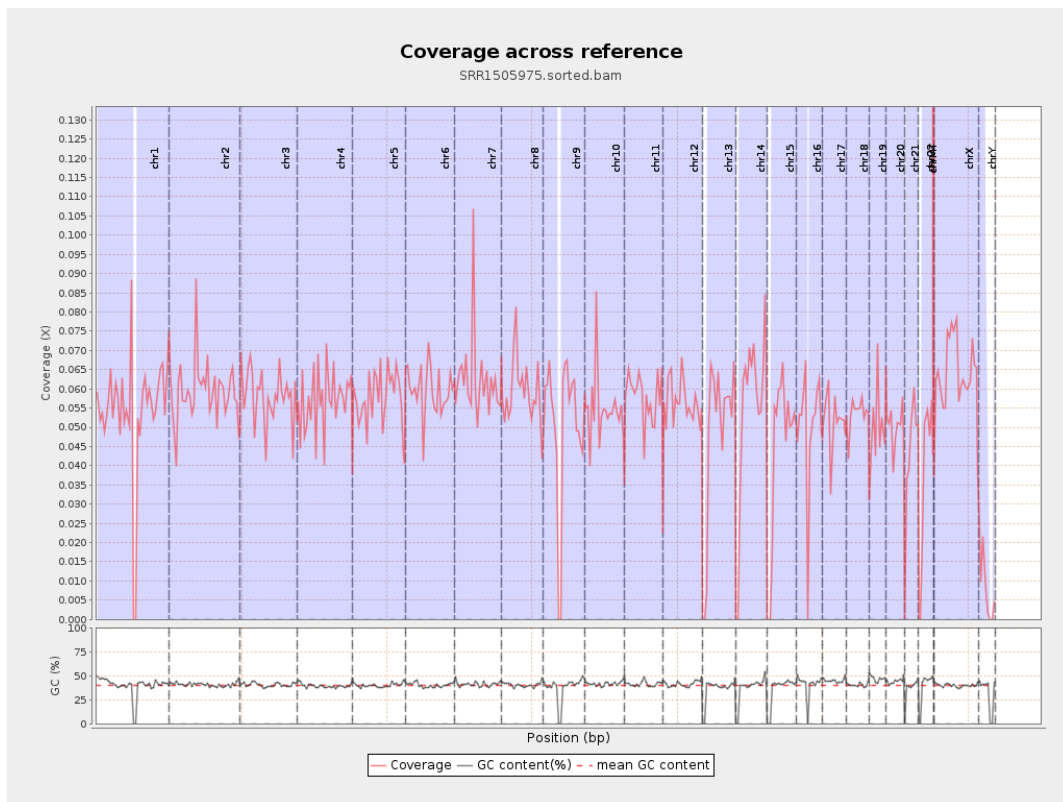
General error rate	0.51%
Mismatches	846,943
Insertions	7,816
Mapped reads with at least one insertion	0.22%
Deletions	24,253
Mapped reads with at least one deletion	0.67%
Homopolymer indels	46.08%

2.6. Chromosome stats

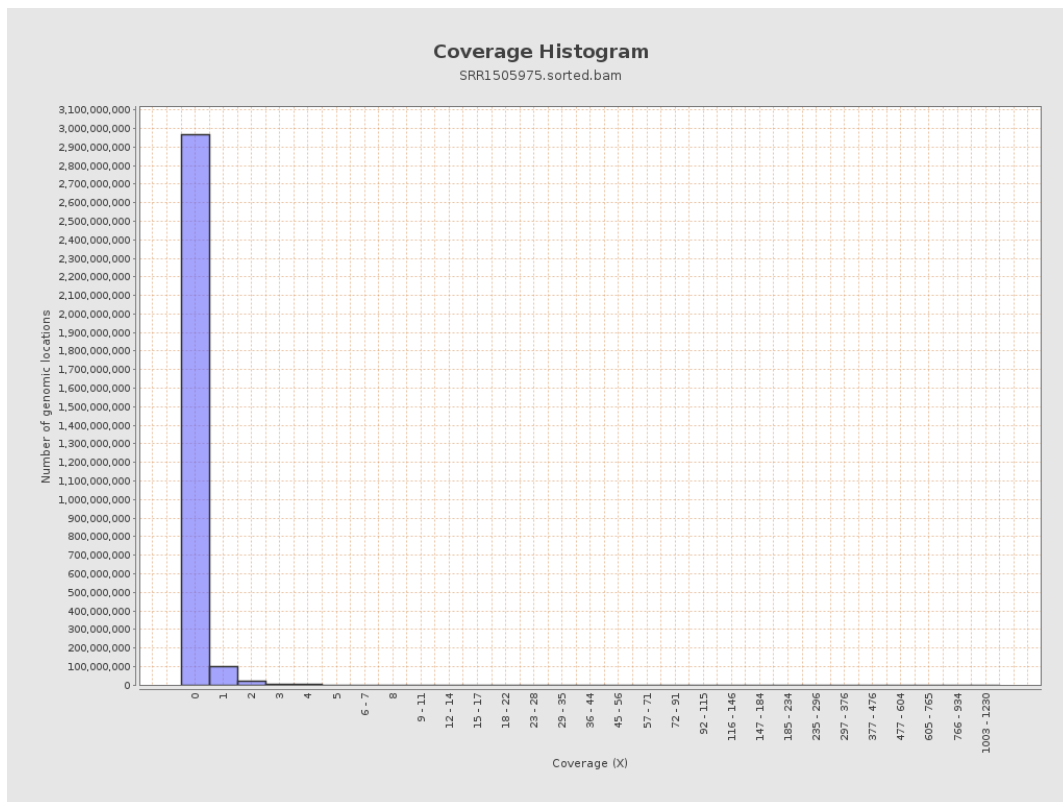
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	13495241	0.0541	0.7932
chr2	243199373	14408994	0.0592	0.4065
chr3	198022430	11513662	0.0581	0.305
chr4	191154276	10897914	0.057	0.3078
chr5	180915260	10424340	0.0576	0.3054
chr6	171115067	10203190	0.0596	0.3948
chr7	159138663	9951921	0.0625	0.8047

chr8	146364022	8651956	0.0591	0.7223
chr9	141213431	7140636	0.0506	0.3728
chr10	135534747	7395526	0.0546	0.4995
chr11	135006516	7736743	0.0573	0.4197
chr12	133851895	7552175	0.0564	0.3231
chr13	115169878	5509036	0.0478	0.2751
chr14	107349540	5819544	0.0542	1.2785
chr15	102531392	4584581	0.0447	0.2642
chr16	90354753	4540202	0.0502	0.3074
chr17	81195210	4159325	0.0512	0.3249
chr18	78077248	4172252	0.0534	0.7164
chr19	59128983	2986253	0.0505	0.6529
chr20	63025520	3155243	0.0501	0.2992
chr21	48129895	2077579	0.0432	0.2802
chr22	51304566	1874629	0.0365	0.2399
chrMT	16571	27151	1.6385	1.821
chrX	155270560	9936091	0.064	0.3587
chrY	59373566	460666	0.0078	0.1326

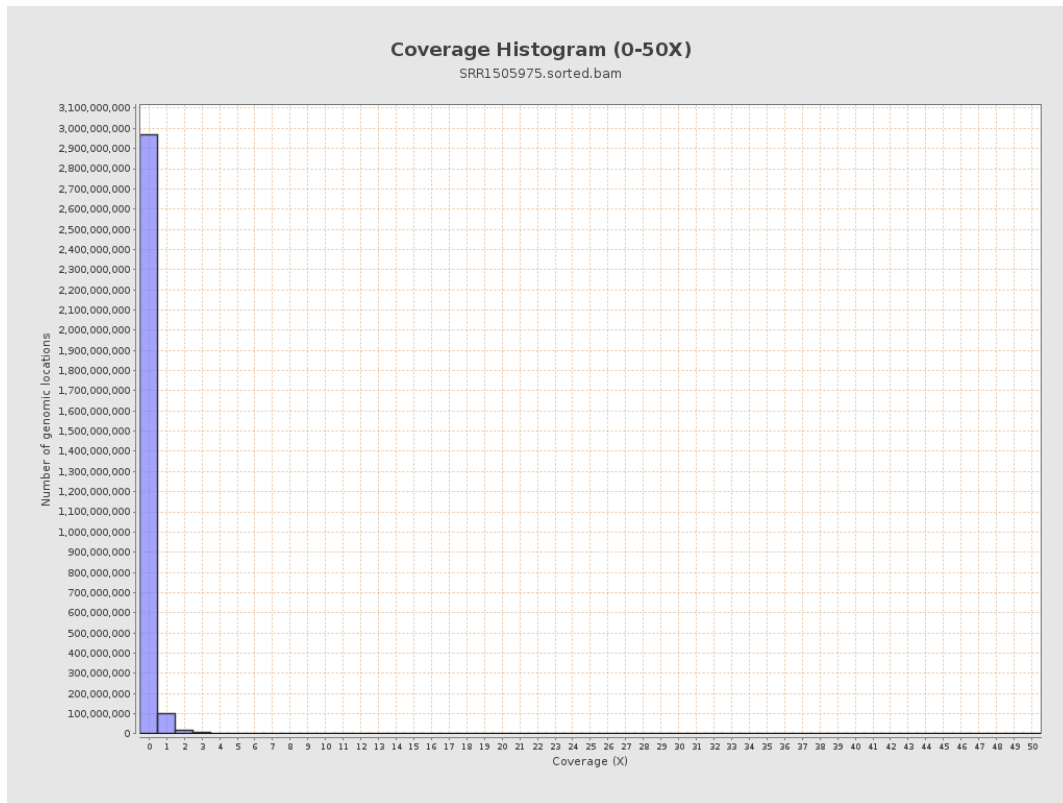
3. Results : Coverage across reference



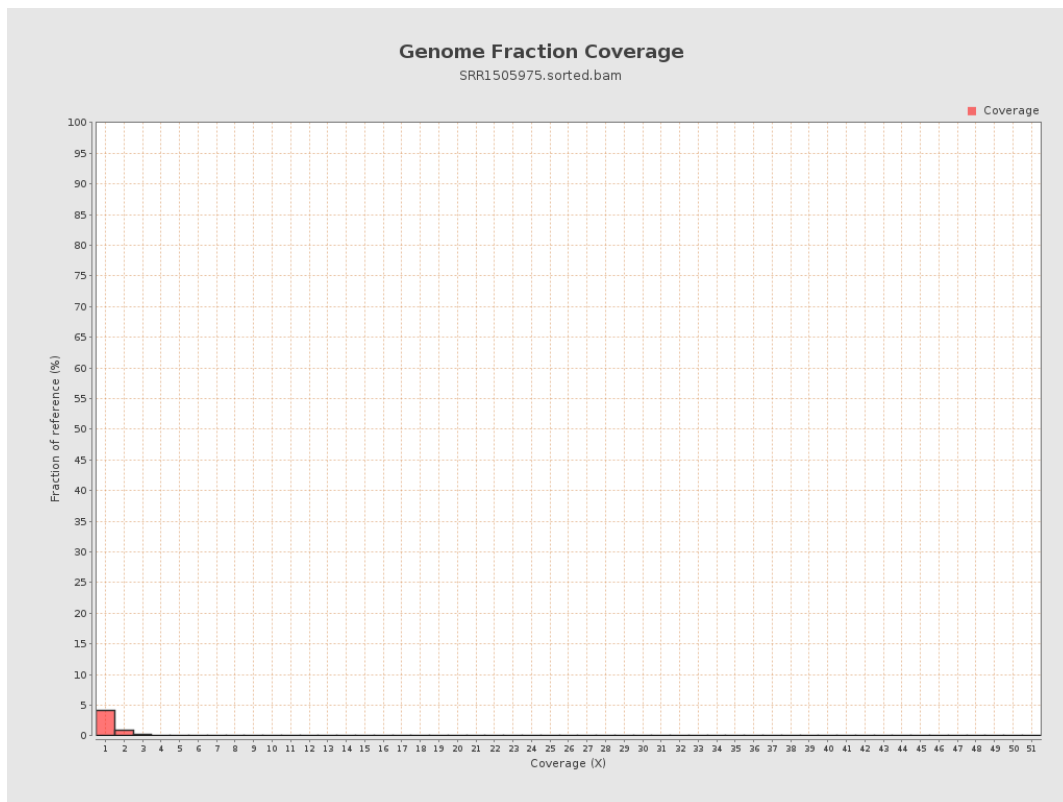
4. Results : Coverage Histogram



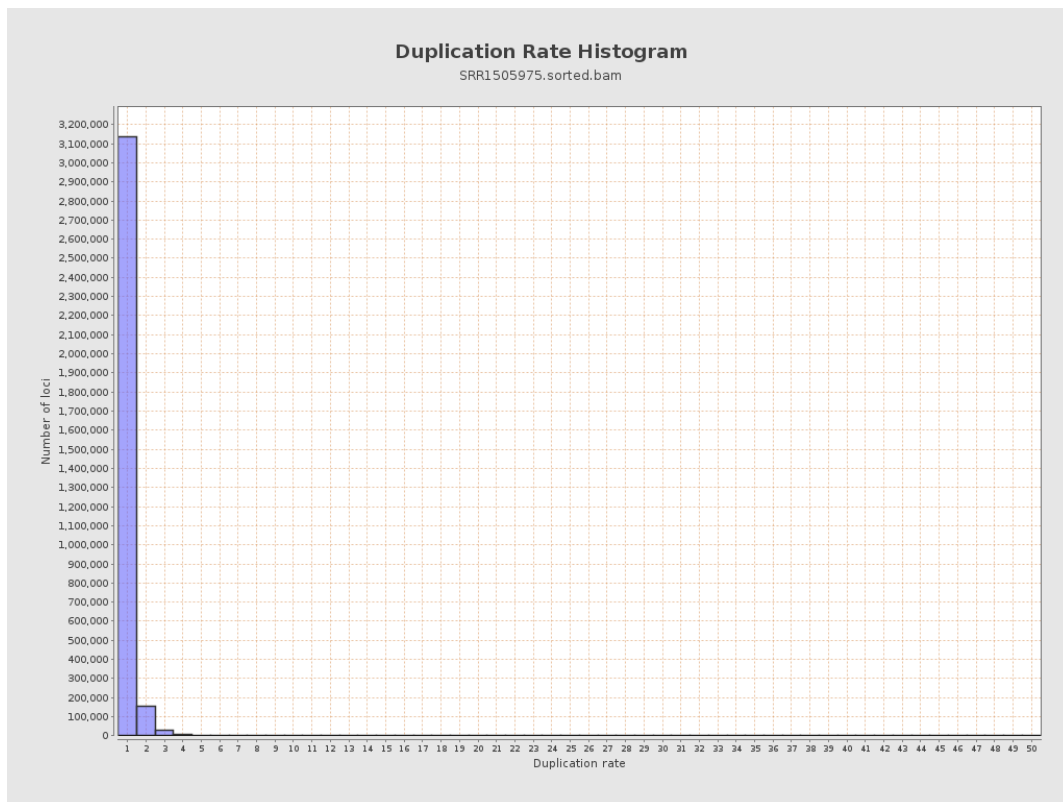
5. Results : Coverage Histogram (0-50X)



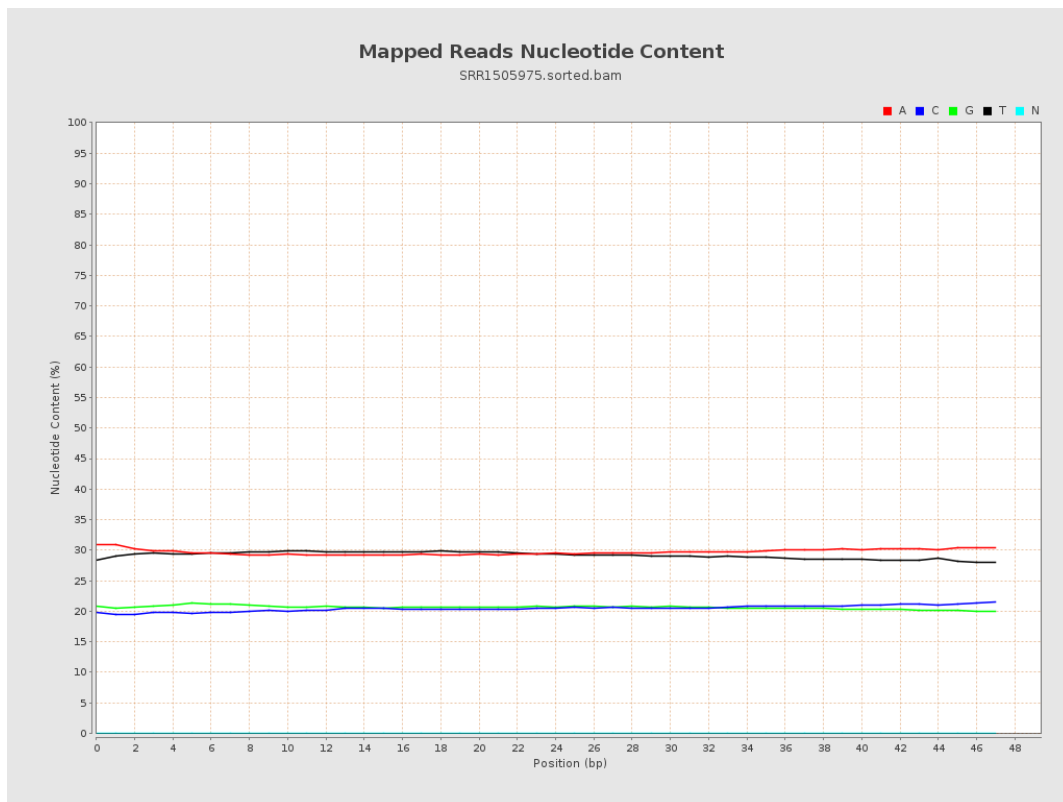
6. Results : Genome Fraction Coverage



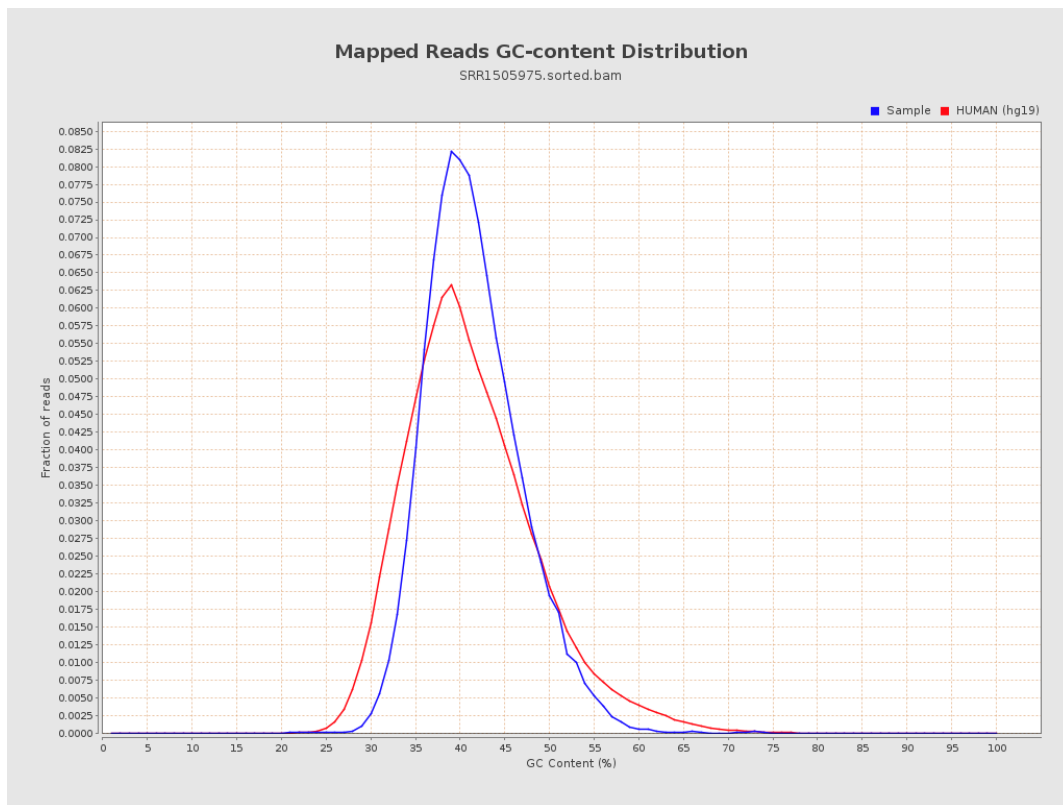
7. Results : Duplication Rate Histogram



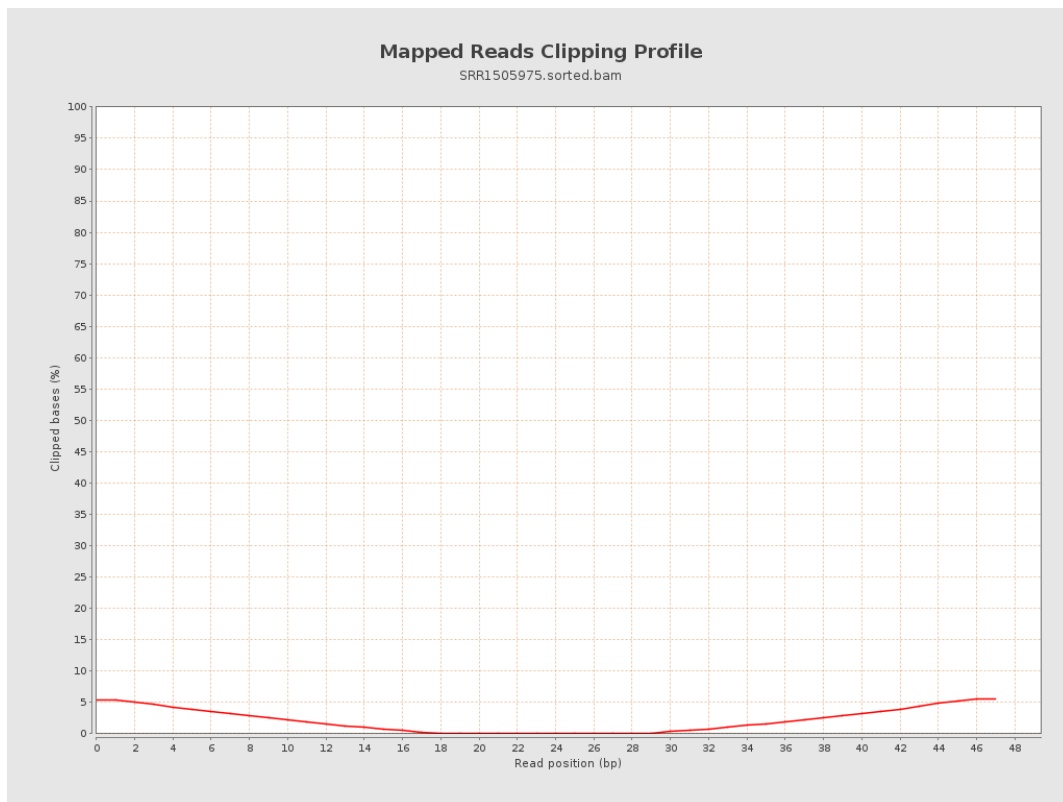
8. Results : Mapped Reads Nucleotide Content



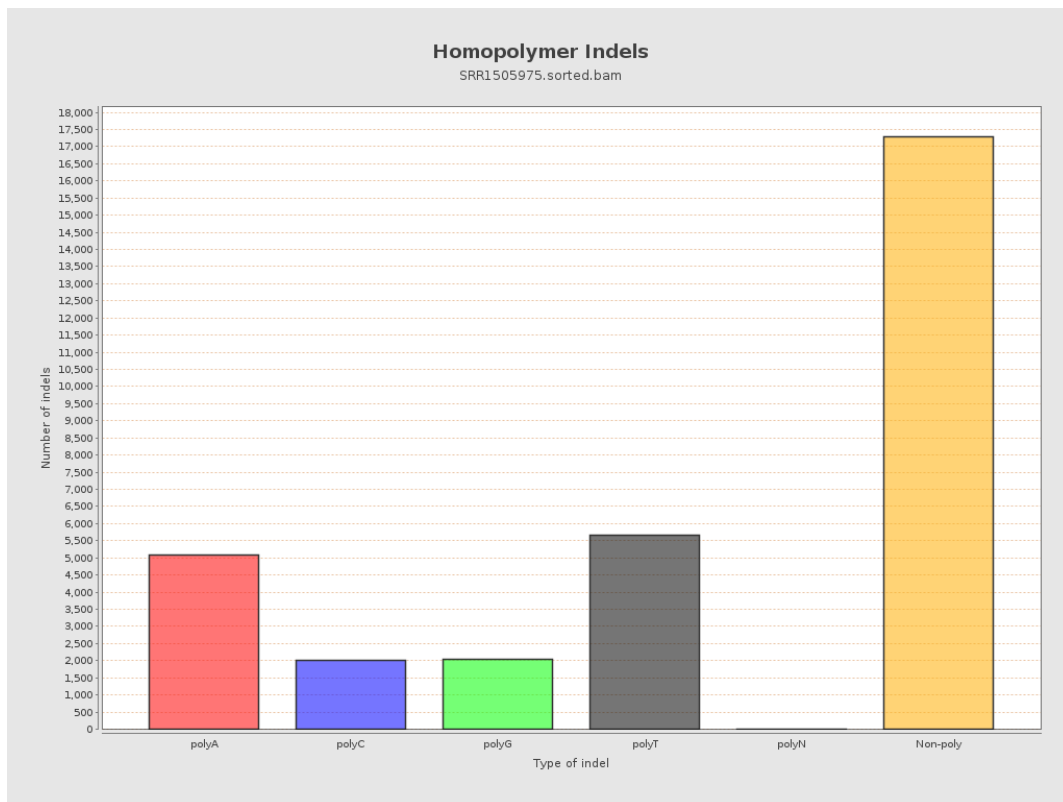
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

