

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/19 21:42:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1505977.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_SRR1505977 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1505977.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 19 21:42:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1505977.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,541,890
Mapped reads	7,843,182 / 74.4%
Unmapped reads	2,698,708 / 25.6%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	297 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	489,502 / 4.64%
Duplication rate	4.42%
Clipped reads	1,049,405 / 9.95%

2.2. ACGT Content

Number/percentage of A's	112,294,123 / 30.67%
Number/percentage of C's	71,430,209 / 19.51%
Number/percentage of T's	109,777,900 / 29.98%
Number/percentage of G's	72,669,706 / 19.85%
Number/percentage of N's	1,683 / 0%
GC Percentage	39.35%

2.3. Coverage

Mean	0.1183

Standard Deviation	1.1153
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2.4. Mapping Quality

Mean Mapping Quality	45.87
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2.5. Mismatches and indels

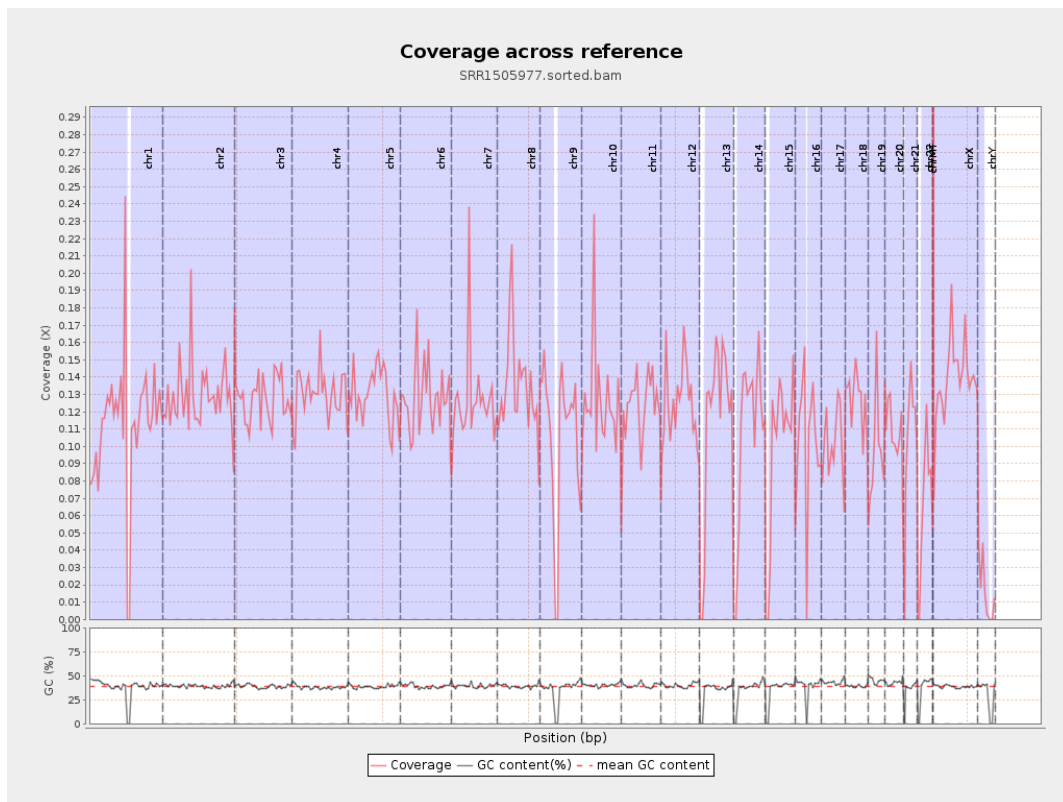
General error rate	0.47%
Mismatches	1,698,751
Insertions	16,710
Mapped reads with at least one insertion	0.21%
Deletions	51,507
Mapped reads with at least one deletion	0.66%
Homopolymer indels	47.23%

2.6. Chromosome stats

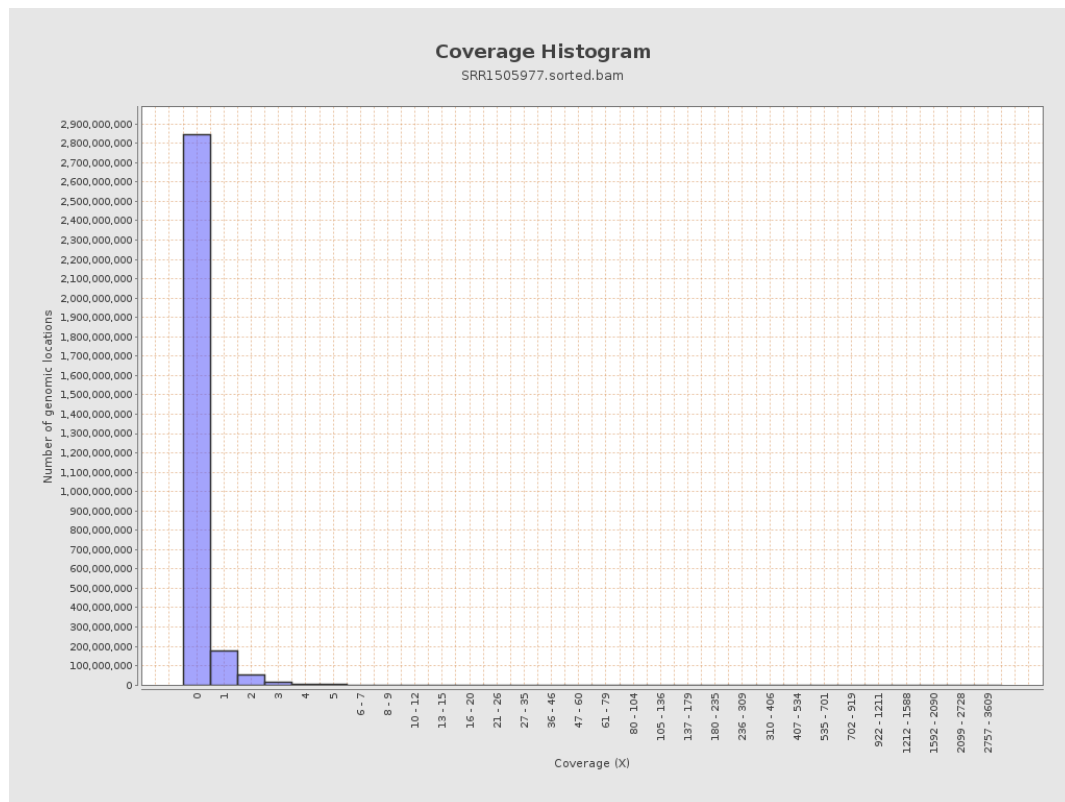
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	28013945	0.1124	2.4701
chr2	243199373	31466074	0.1294	0.8751
chr3	198022430	25315996	0.1278	0.5168
chr4	191154276	24868408	0.1301	0.4993
chr5	180915260	23375839	0.1292	0.5192
chr6	171115067	21981968	0.1285	0.6386
chr7	159138663	20070236	0.1261	1.4212

chr8	146364022	19677073	0.1344	1.7684
chr9	141213431	14986514	0.1061	0.7716
chr10	135534747	17089551	0.1261	1.1048
chr11	135006516	16670402	0.1235	0.9242
chr12	133851895	16679194	0.1246	0.5357
chr13	115169878	13135646	0.1141	0.4517
chr14	107349540	11683382	0.1088	0.9998
chr15	102531392	10070832	0.0982	0.4234
chr16	90354753	9190313	0.1017	0.5754
chr17	81195210	8329355	0.1026	0.545
chr18	78077248	9917024	0.127	1.9599
chr19	59128983	5870413	0.0993	1.4805
chr20	63025520	6880705	0.1092	0.4754
chr21	48129895	4987249	0.1036	0.5008
chr22	51304566	3421131	0.0667	0.3462
chrMT	16571	23013	1.3888	1.5544
chrX	155270560	21595953	0.1391	0.6832
chrY	59373566	943473	0.0159	0.2441

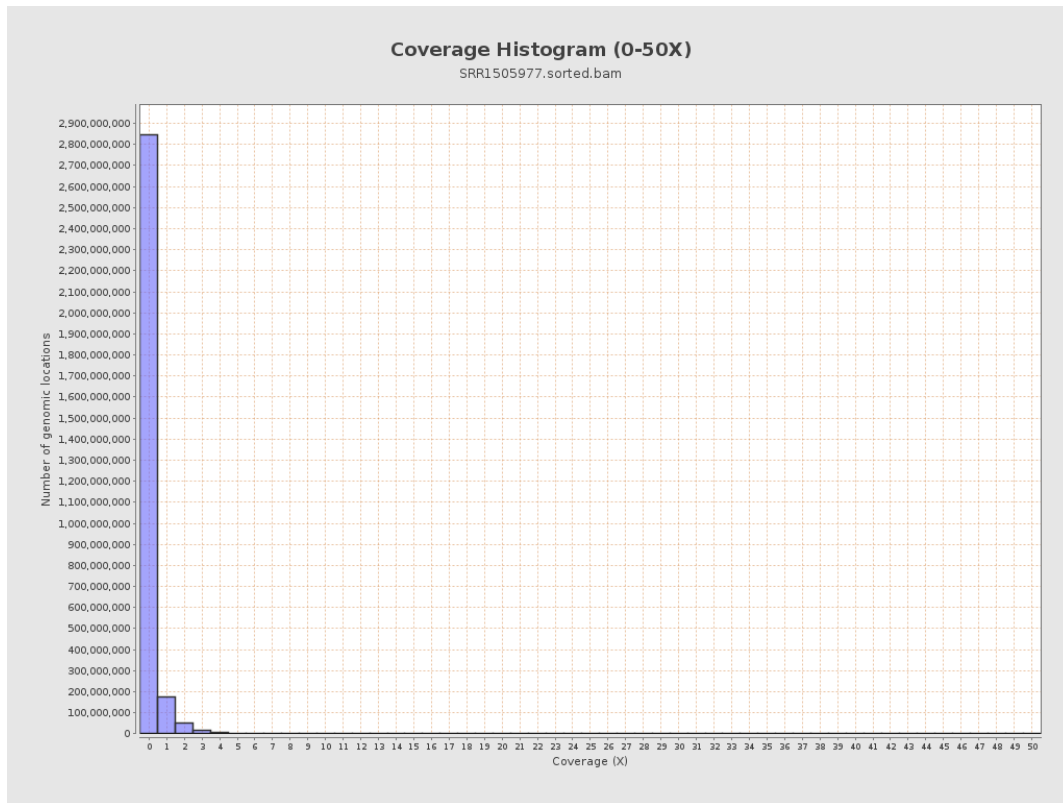
3. Results : Coverage across reference



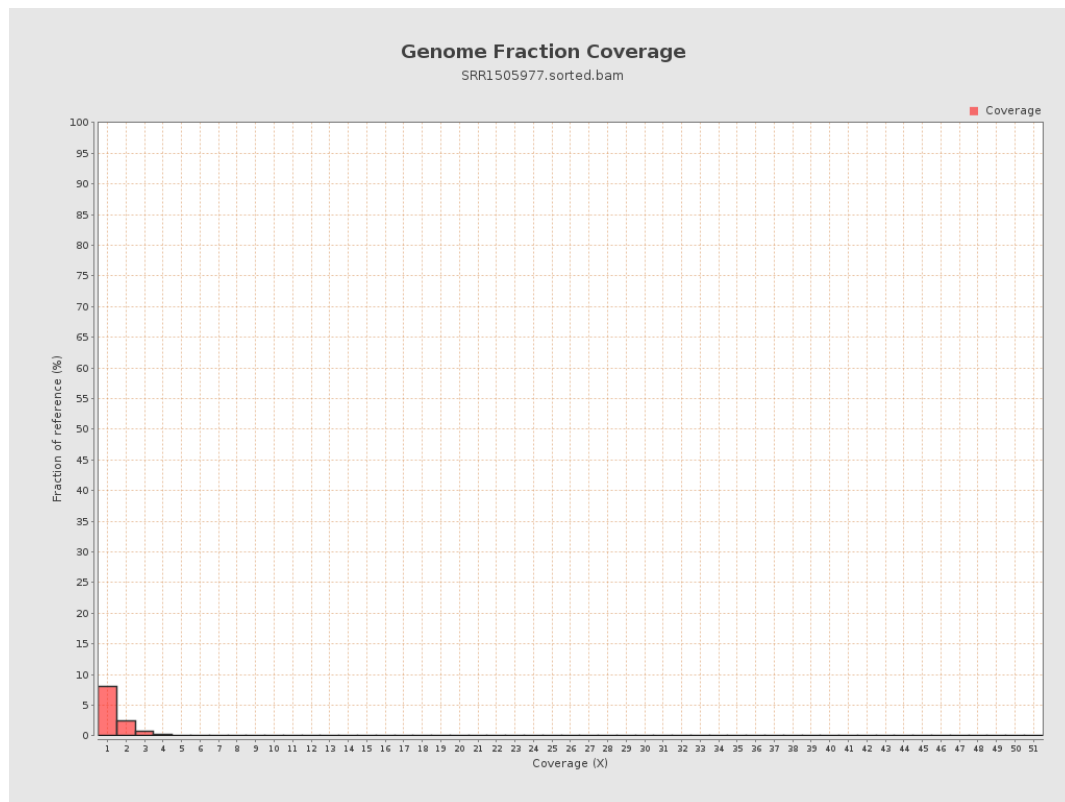
4. Results : Coverage Histogram



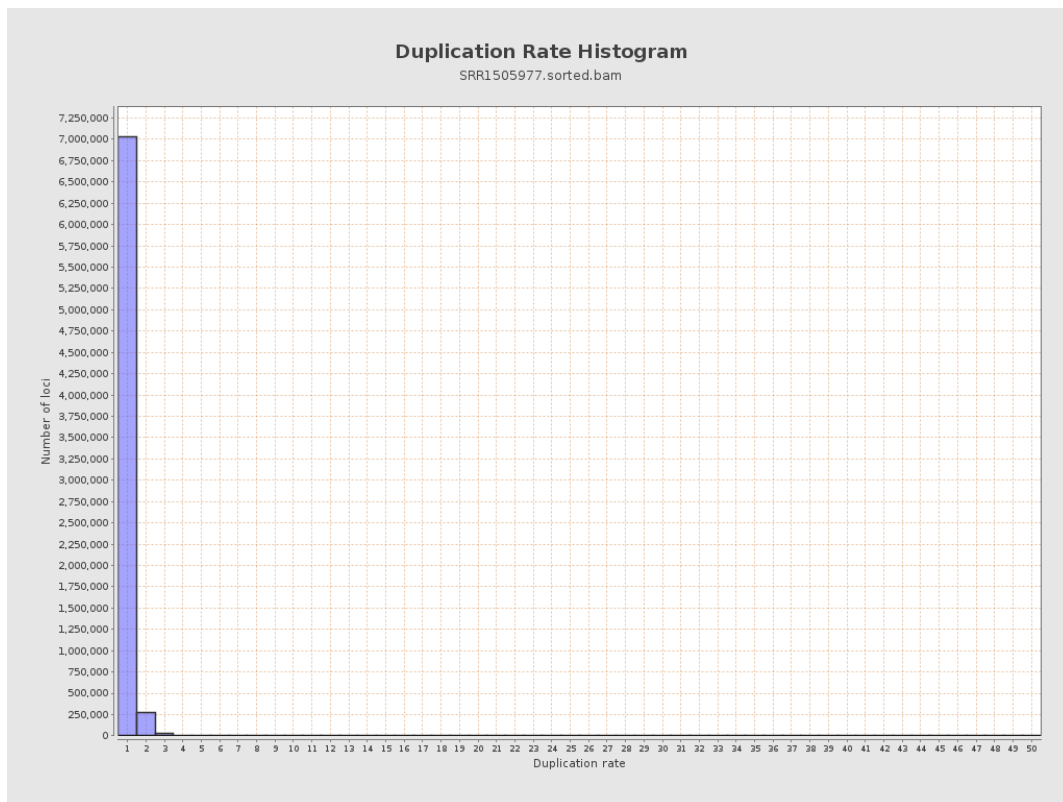
5. Results : Coverage Histogram (0-50X)



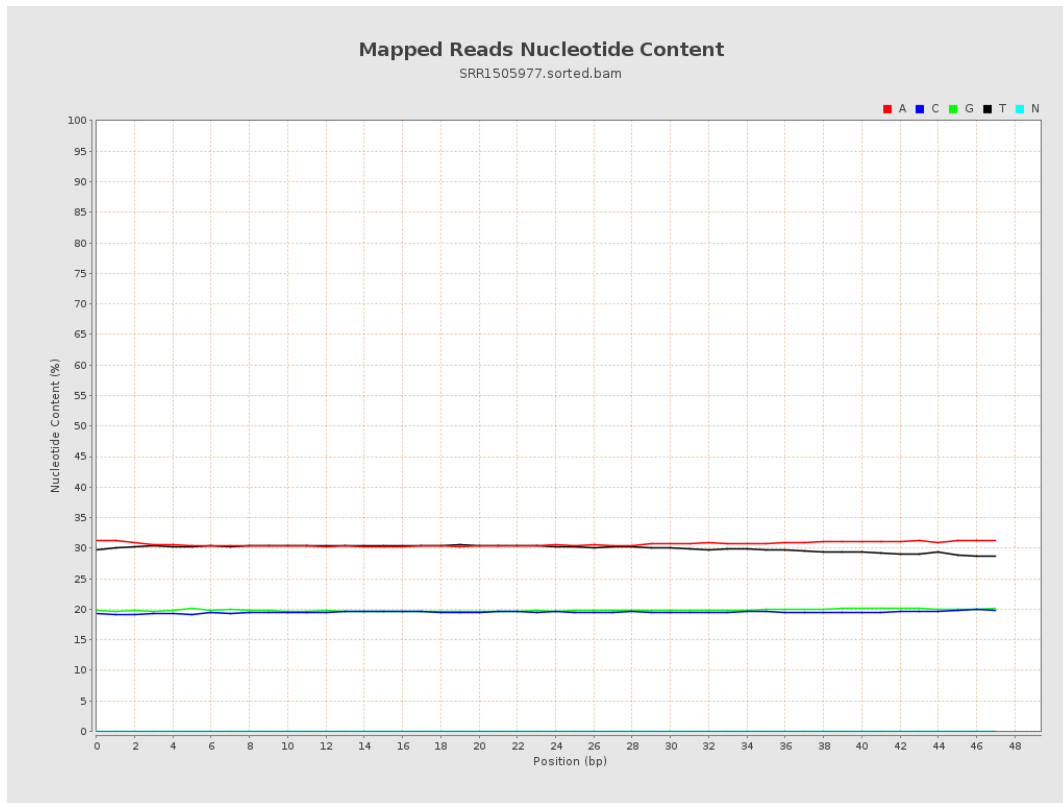
6. Results : Genome Fraction Coverage



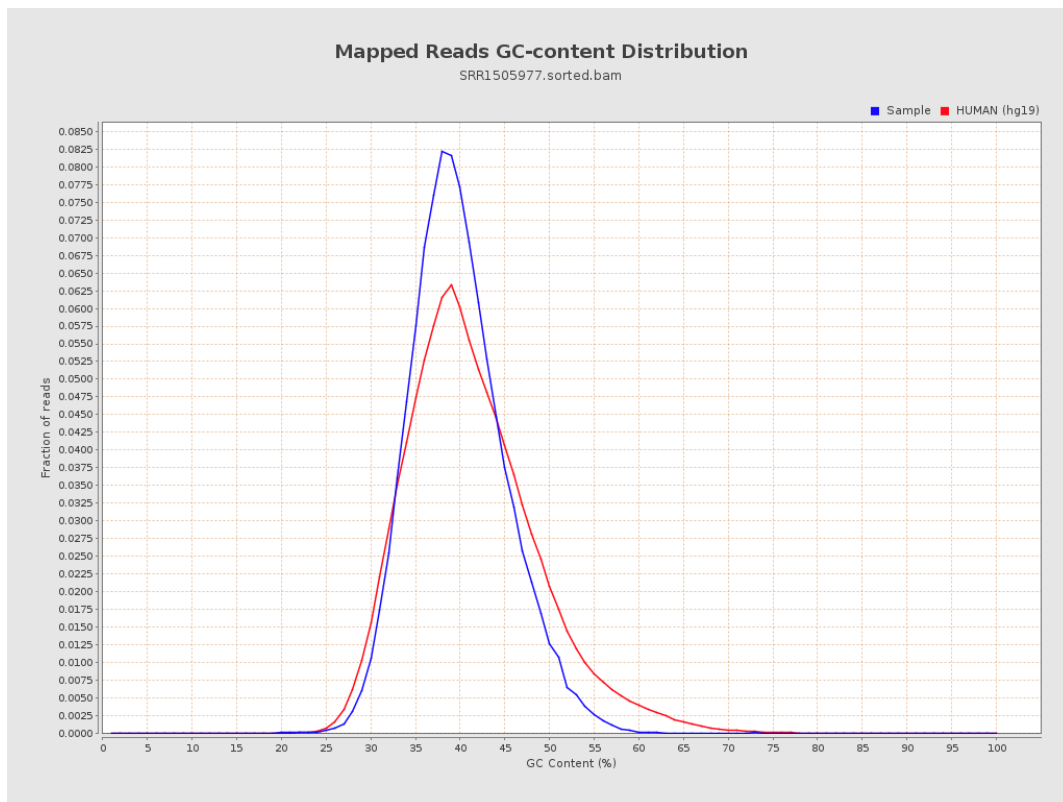
7. Results : Duplication Rate Histogram



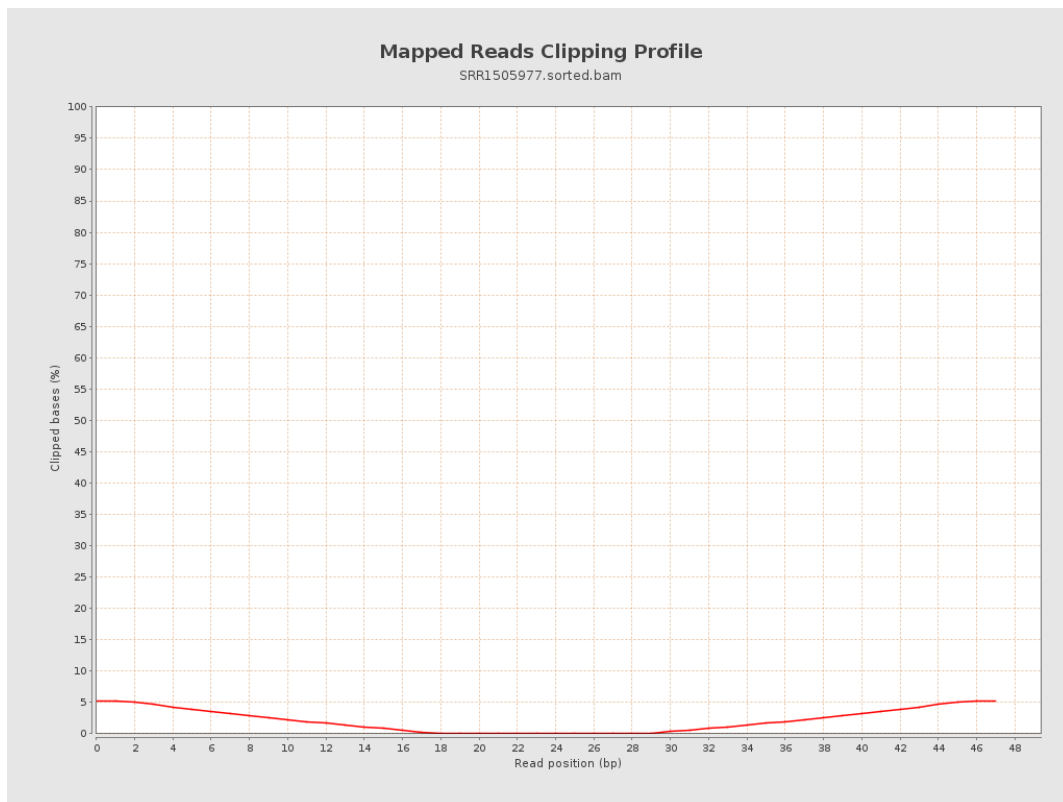
8. Results : Mapped Reads Nucleotide Content



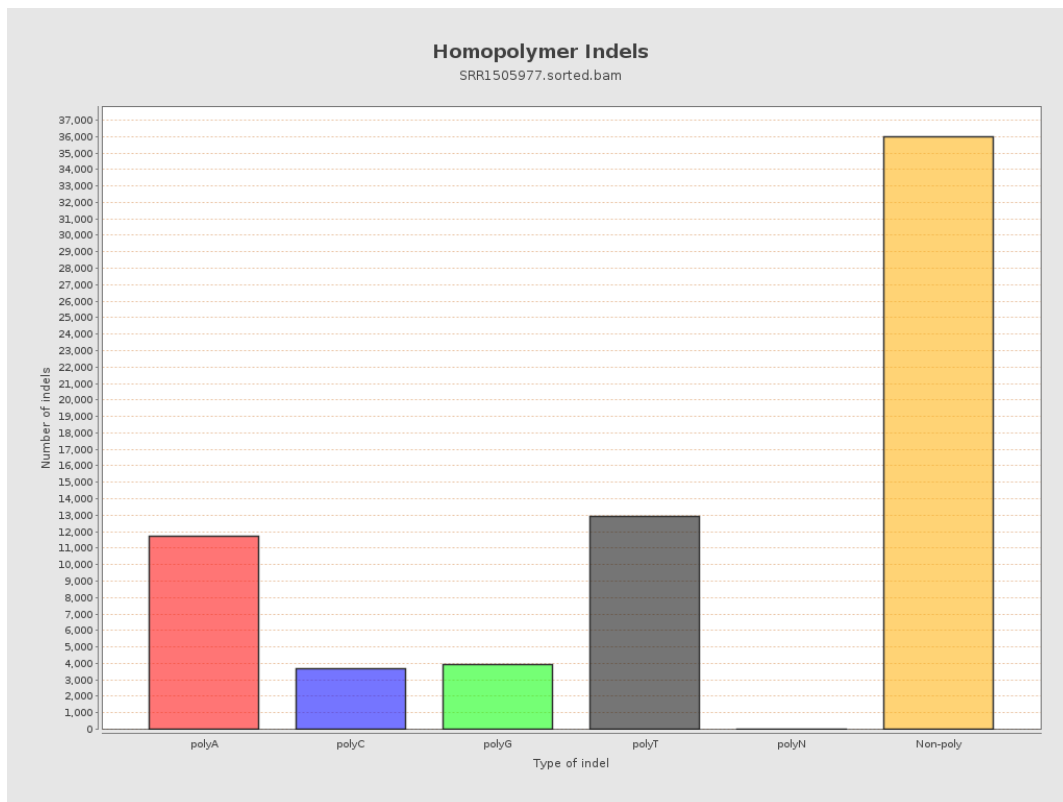
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

