

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/19 21:02:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1505955.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_SRR1505955 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1505955.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 19 21:01:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1505955.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,611,175
Mapped reads	2,477,317 / 68.6%
Unmapped reads	1,133,858 / 31.4%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	164 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	145,720 / 4.04%
Duplication rate	4.69%
Clipped reads	382,222 / 10.58%

2.2. ACGT Content

Number/percentage of A's	33,750,830 / 29.3%
Number/percentage of C's	23,911,891 / 20.76%
Number/percentage of T's	33,323,540 / 28.93%
Number/percentage of G's	24,195,547 / 21.01%
Number/percentage of N's	334 / 0%
GC Percentage	41.77%

2.3. Coverage

Mean	0.0372

Standard Deviation	0.3788
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2.4. Mapping Quality

Mean Mapping Quality	44.63
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2.5. Mismatches and indels

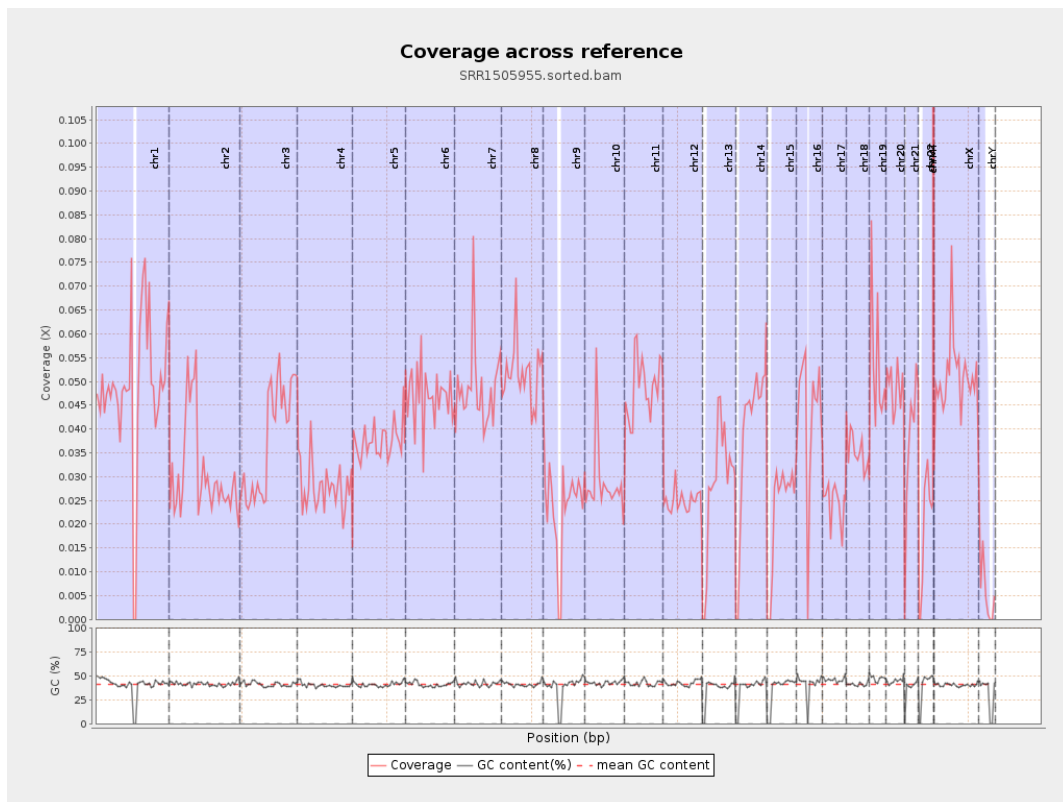
General error rate	0.53%
Mismatches	604,777
Insertions	4,978
Mapped reads with at least one insertion	0.2%
Deletions	17,306
Mapped reads with at least one deletion	0.7%
Homopolymer indels	45.66%

2.6. Chromosome stats

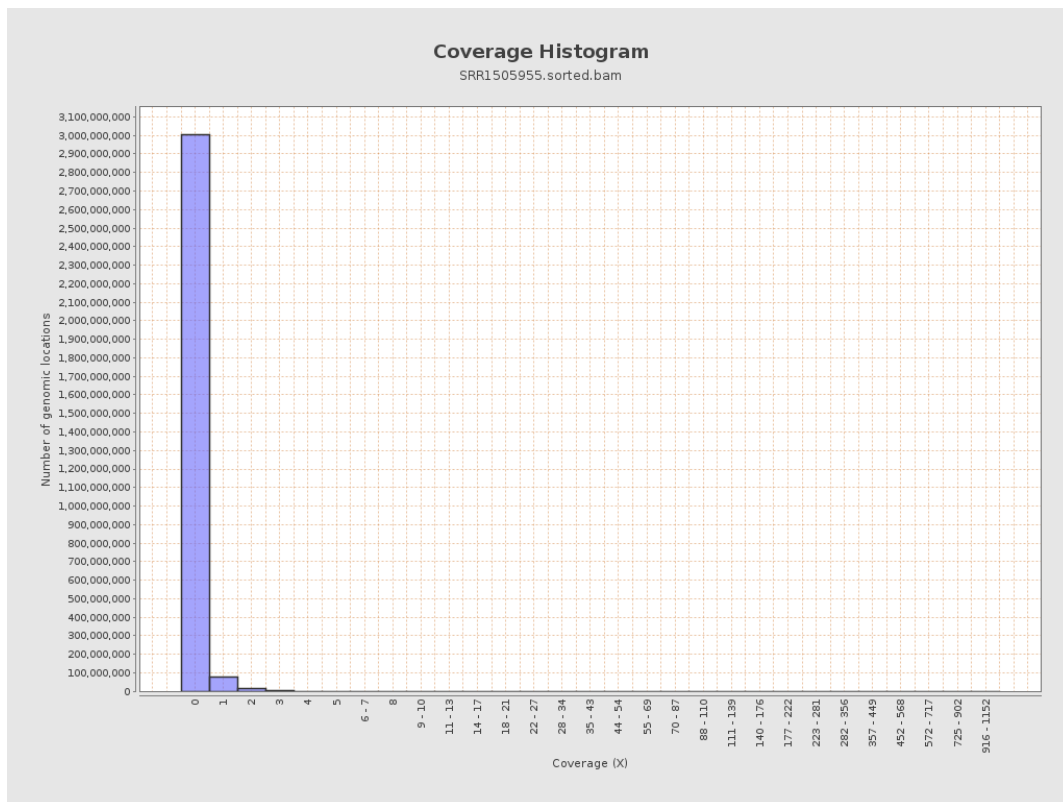
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	12138112	0.0487	0.7922
chr2	243199373	7552563	0.0311	0.298
chr3	198022430	7375866	0.0372	0.2343
chr4	191154276	5308598	0.0278	0.2074
chr5	180915260	6783713	0.0375	0.2368
chr6	171115067	8015379	0.0468	0.31
chr7	159138663	7735861	0.0486	0.5287

chr8	146364022	7537151	0.0515	0.5654
chr9	141213431	3269713	0.0232	0.2414
chr10	135534747	3830135	0.0283	0.3004
chr11	135006516	6539298	0.0484	0.3932
chr12	133851895	3325604	0.0248	0.1959
chr13	115169878	3294407	0.0286	0.2021
chr14	107349540	4171023	0.0389	0.2439
chr15	102531392	2384851	0.0233	0.1811
chr16	90354753	3920378	0.0434	0.2671
chr17	81195210	1992024	0.0245	0.2207
chr18	78077248	2761647	0.0354	0.4165
chr19	59128983	3143572	0.0532	0.5661
chr20	63025520	3069721	0.0487	0.2707
chr21	48129895	1814923	0.0377	0.2524
chr22	51304566	960412	0.0187	0.1625
chrMT	16571	22842	1.3784	1.5817
chrX	155270560	7903667	0.0509	0.3122
chrY	59373566	354626	0.006	0.1198

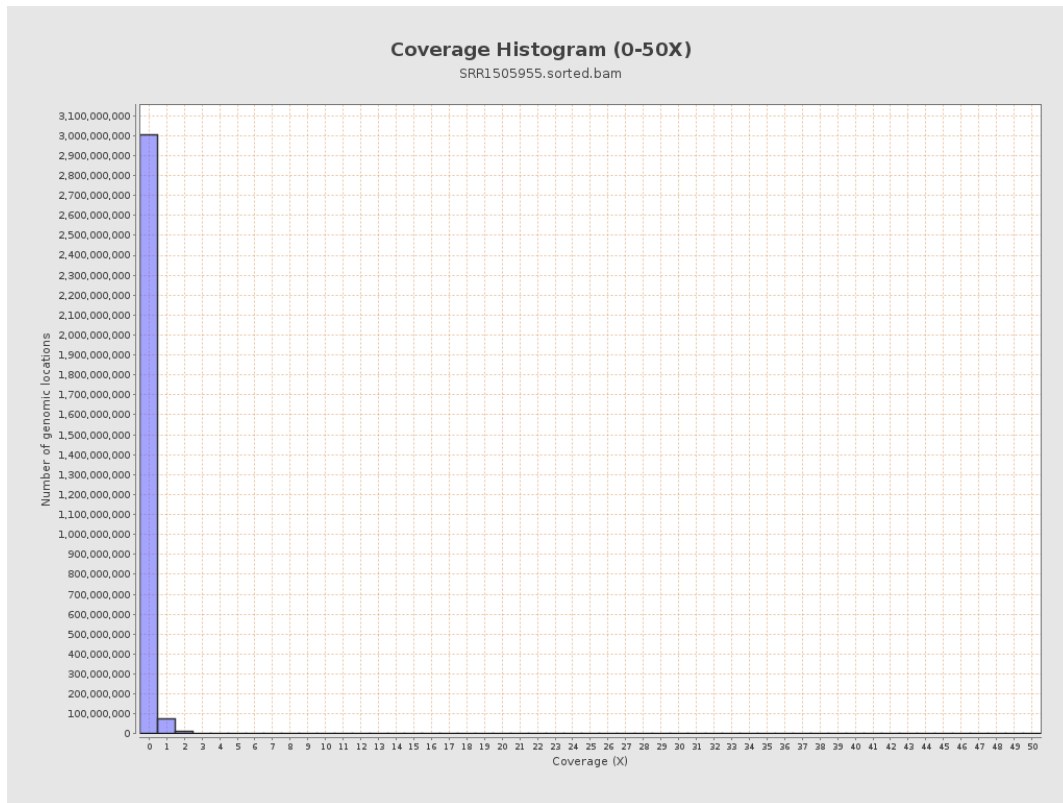
3. Results : Coverage across reference



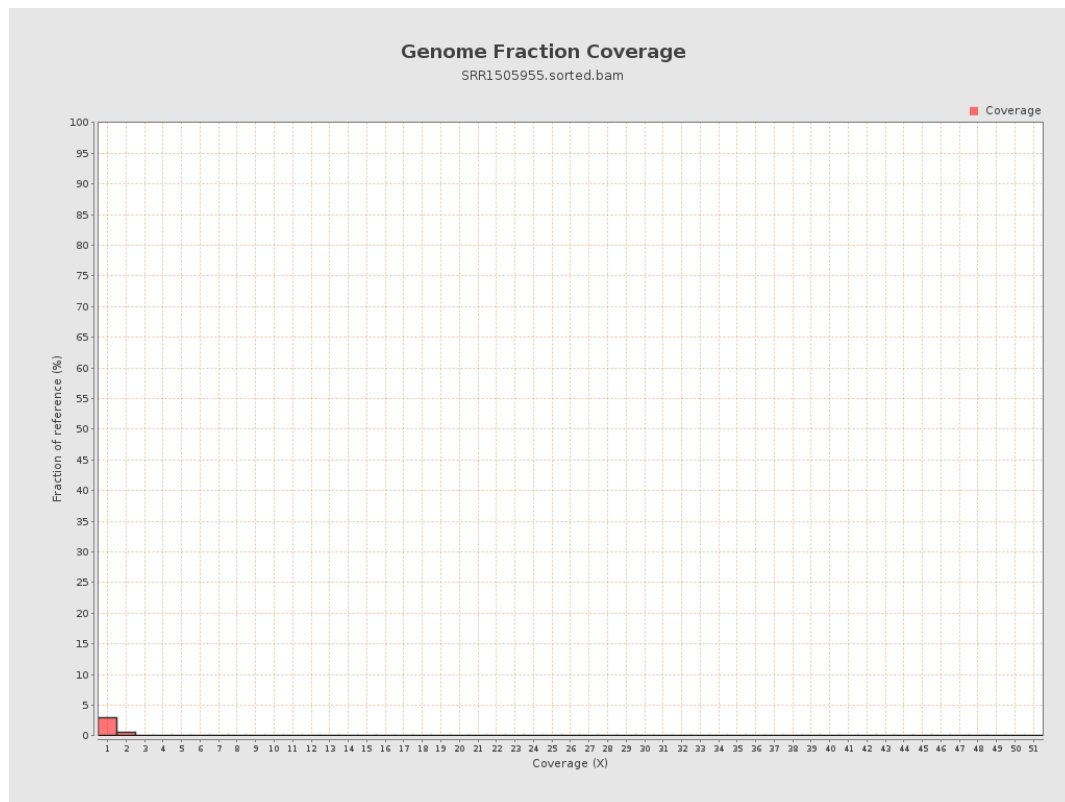
4. Results : Coverage Histogram



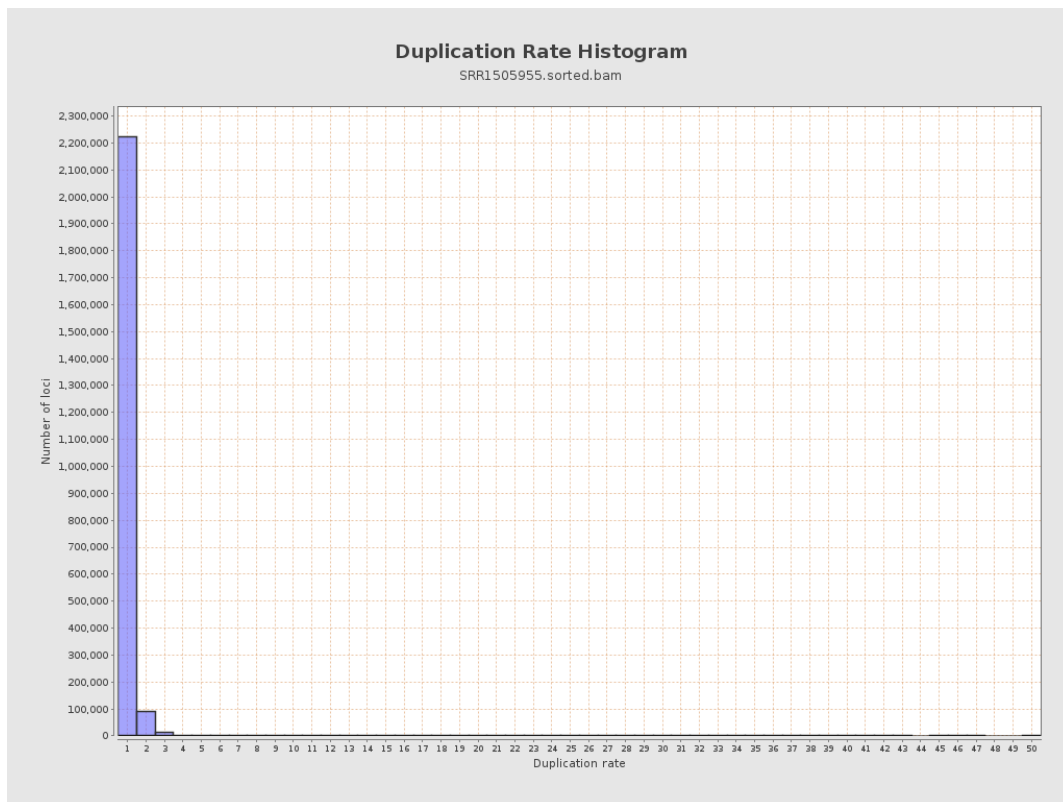
5. Results : Coverage Histogram (0-50X)



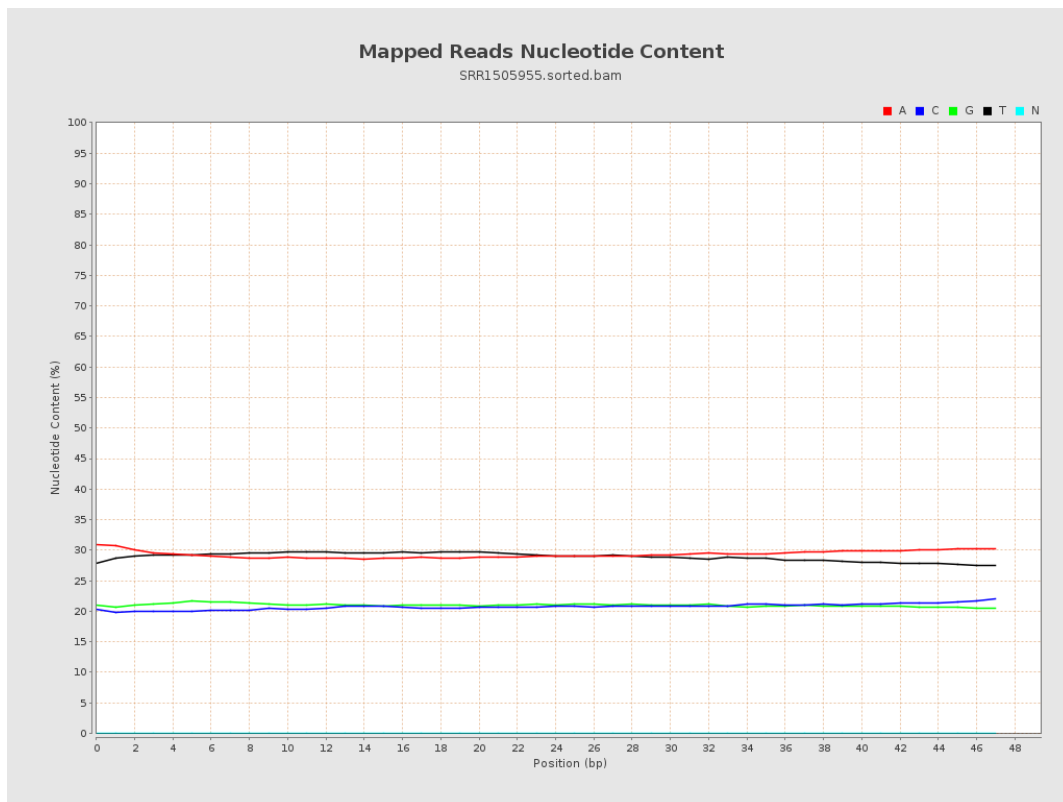
6. Results : Genome Fraction Coverage



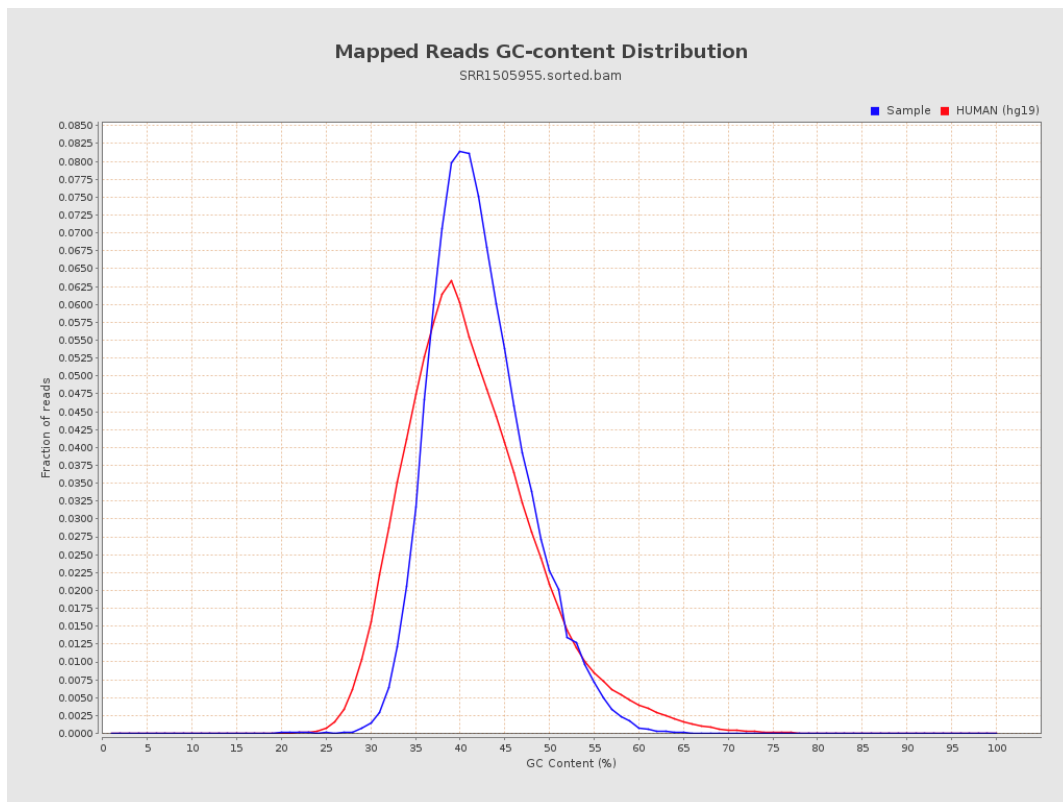
7. Results : Duplication Rate Histogram



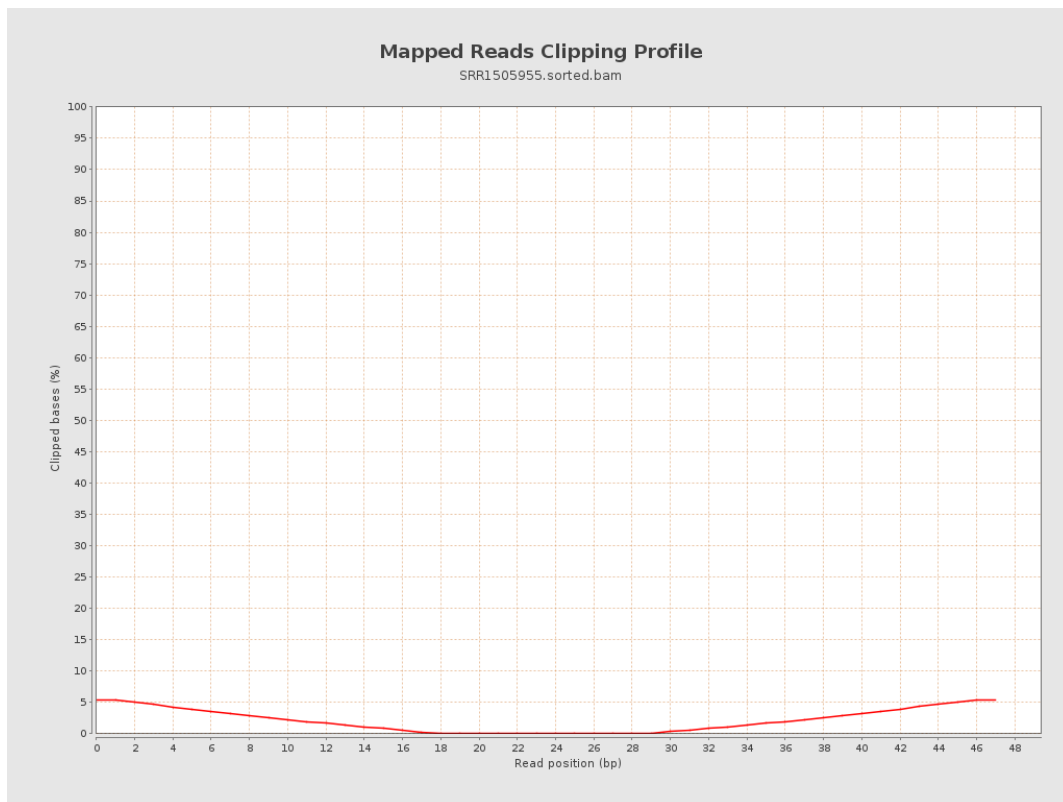
8. Results : Mapped Reads Nucleotide Content



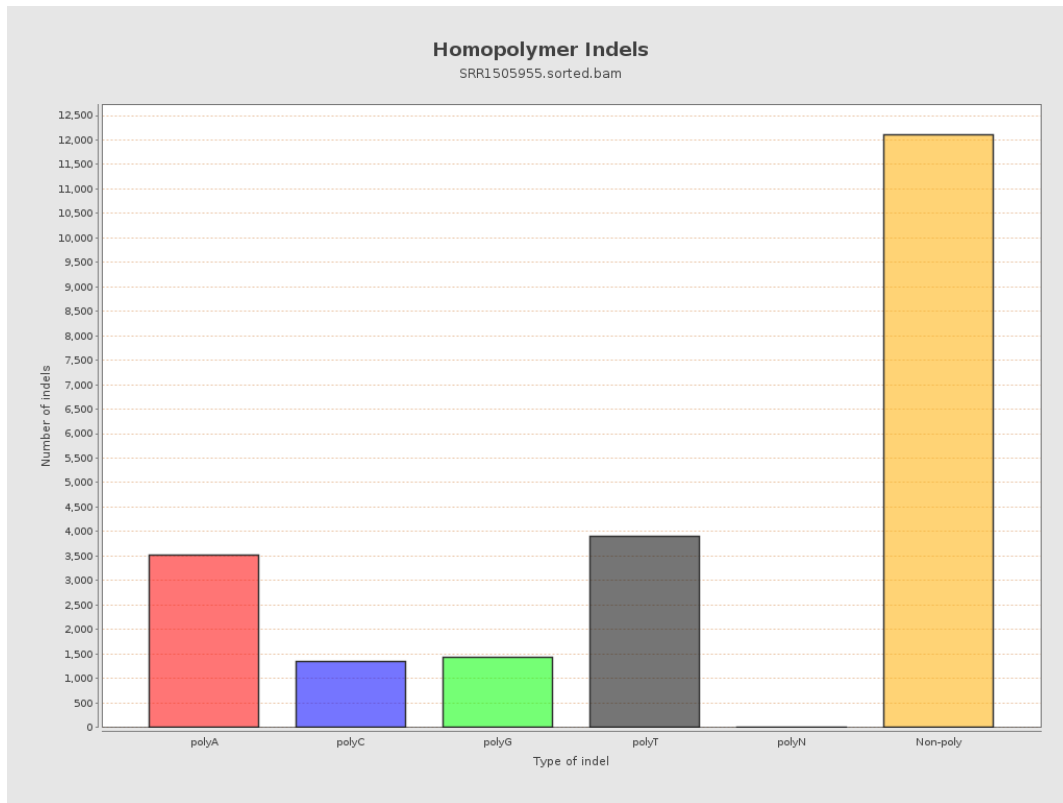
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

