

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 07:13:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548995.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_SRR1548995 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548995.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 07:13:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548995.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,704,856
Mapped reads	6,641,406 / 86.2%
Unmapped reads	1,063,450 / 13.8%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	475,203 / 6.17%
Duplication rate	6.39%
Clipped reads	346,019 / 4.49%

2.2. ACGT Content

Number/percentage of A's	80,072,627 / 30.38%
Number/percentage of C's	51,664,319 / 19.6%
Number/percentage of T's	79,467,895 / 30.15%
Number/percentage of G's	52,396,924 / 19.88%
Number/percentage of N's	2,300 / 0%
GC Percentage	39.48%

2.3. Coverage

Mean	0.0852
Standard Deviation	0.7704

2.4. Mapping Quality

Mean Mapping Quality	44.38
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2.5. Mismatches and indels

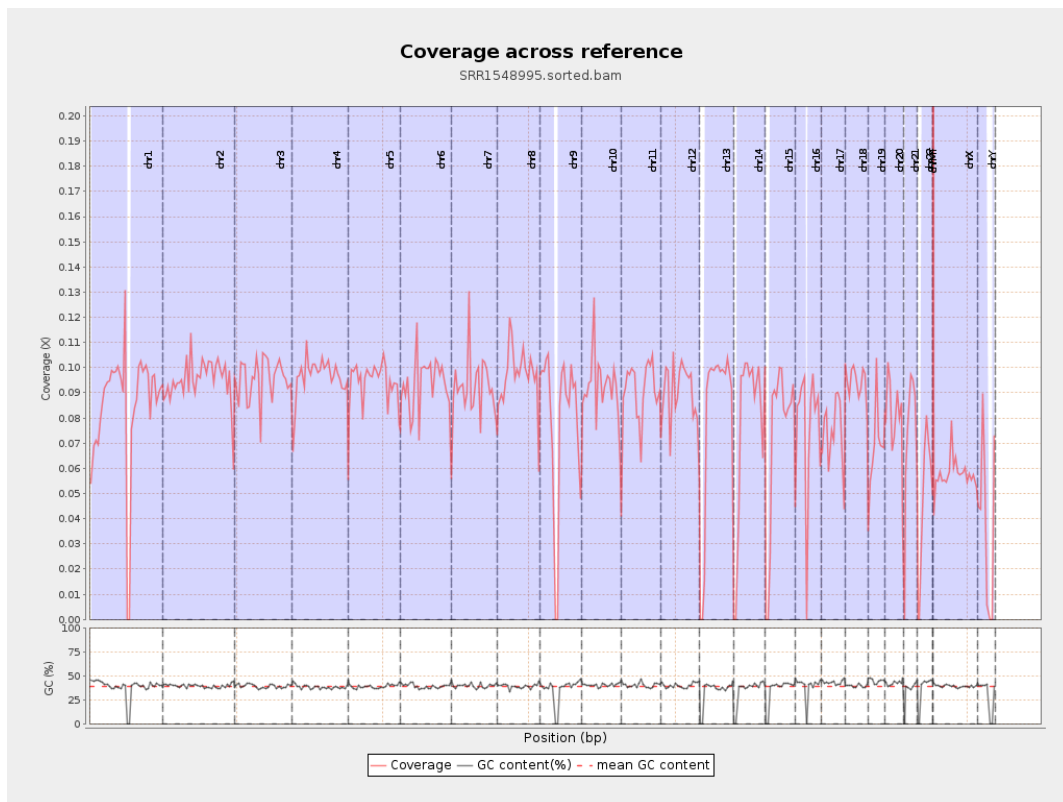
General error rate	0.31%
Mismatches	798,648
Insertions	7,739
Mapped reads with at least one insertion	0.12%
Deletions	22,544
Mapped reads with at least one deletion	0.34%
Homopolymer indels	43.01%

2.6. Chromosome stats

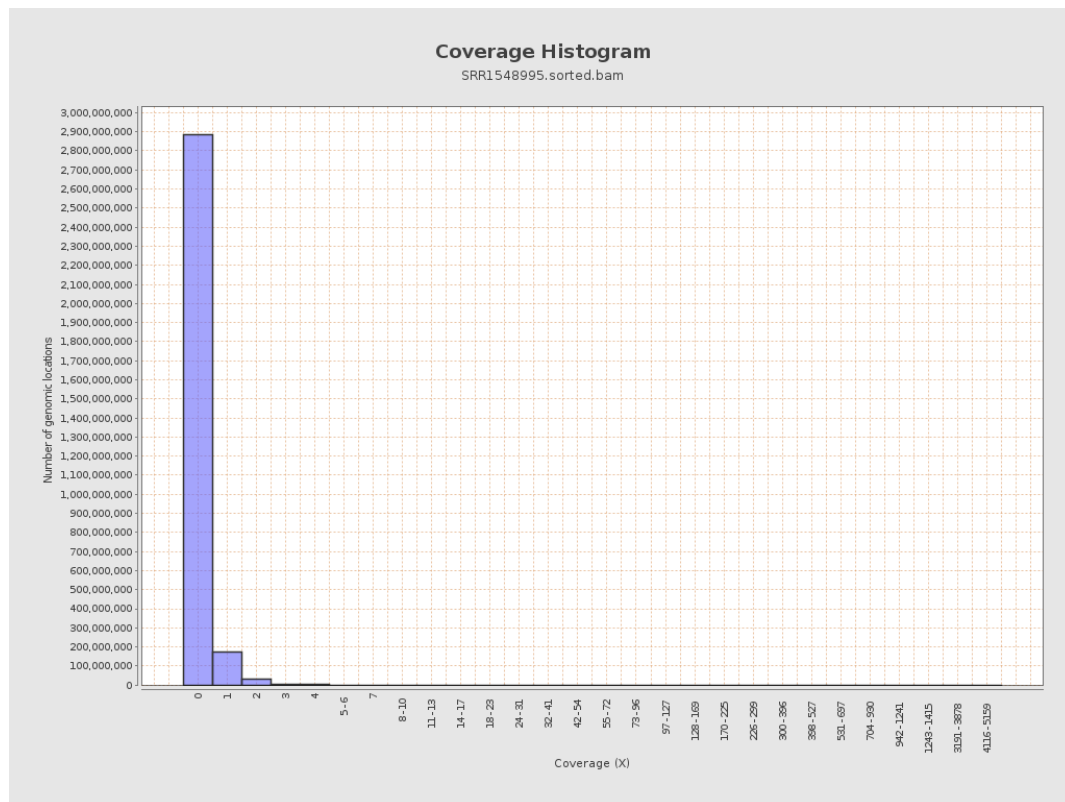
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	21130231	0.0848	1.109
chr2	243199373	23181906	0.0953	0.4815
chr3	198022430	18900521	0.0954	0.3701
chr4	191154276	18484642	0.0967	0.3985
chr5	180915260	17028157	0.0941	0.3726
chr6	171115067	16071591	0.0939	0.4354
chr7	159138663	14617582	0.0919	0.7032
chr8	146364022	14231831	0.0972	2.5433

chr9	141213431	11196886	0.0793	0.4486
chr10	135534747	12536060	0.0925	0.5332
chr11	135006516	12244272	0.0907	0.4577
chr12	133851895	12087303	0.0903	0.3736
chr13	115169878	9353558	0.0812	0.3372
chr14	107349540	8373768	0.078	0.3988
chr15	102531392	7379422	0.072	0.3176
chr16	90354753	6764434	0.0749	0.3646
chr17	81195210	6096113	0.0751	0.3596
chr18	78077248	7380294	0.0945	0.9015
chr19	59128983	4139911	0.07	0.8506
chr20	63025520	5160875	0.0819	0.3595
chr21	48129895	3498612	0.0727	0.388
chr22	51304566	2495181	0.0486	0.2882
chrMT	16571	19380	1.1695	1.6196
chrX	155270560	8945386	0.0576	0.3629
chrY	59373566	2315394	0.039	0.4118

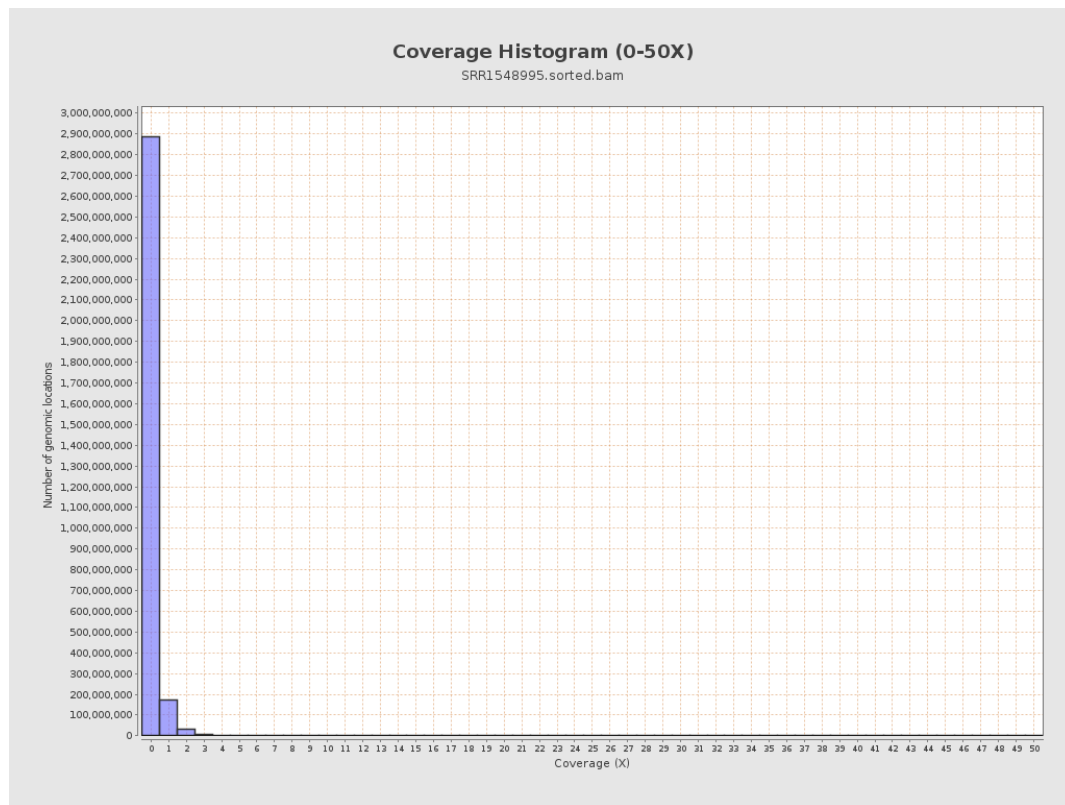
3. Results : Coverage across reference



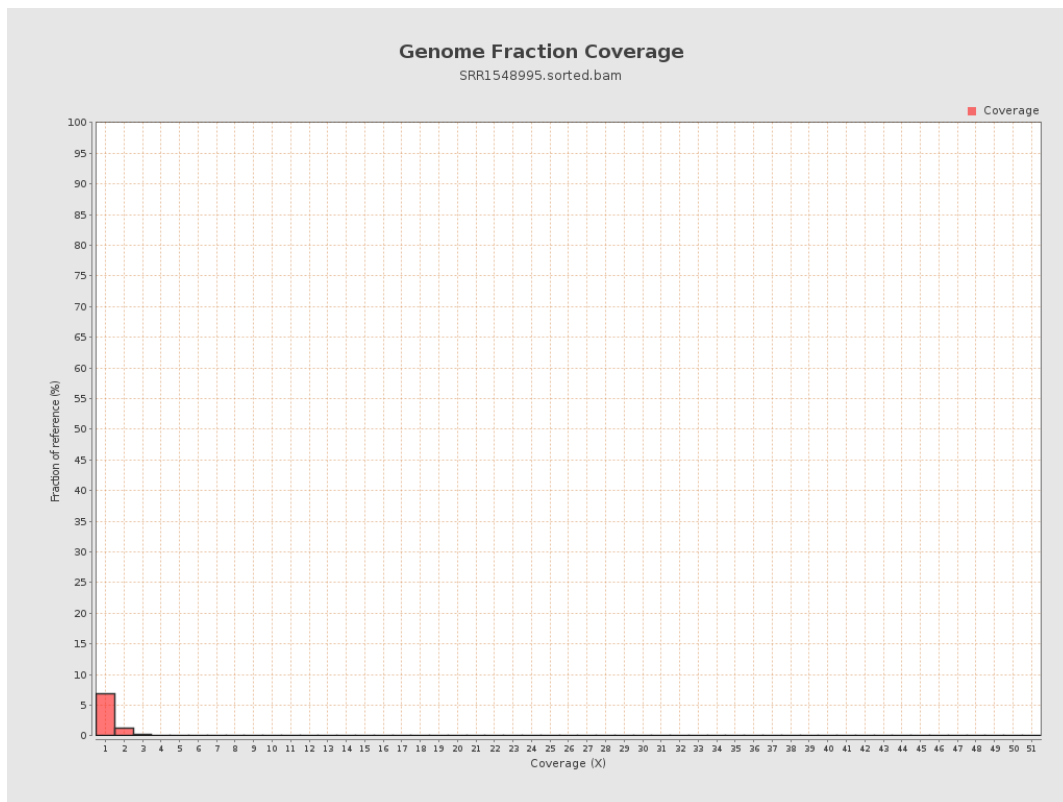
4. Results : Coverage Histogram



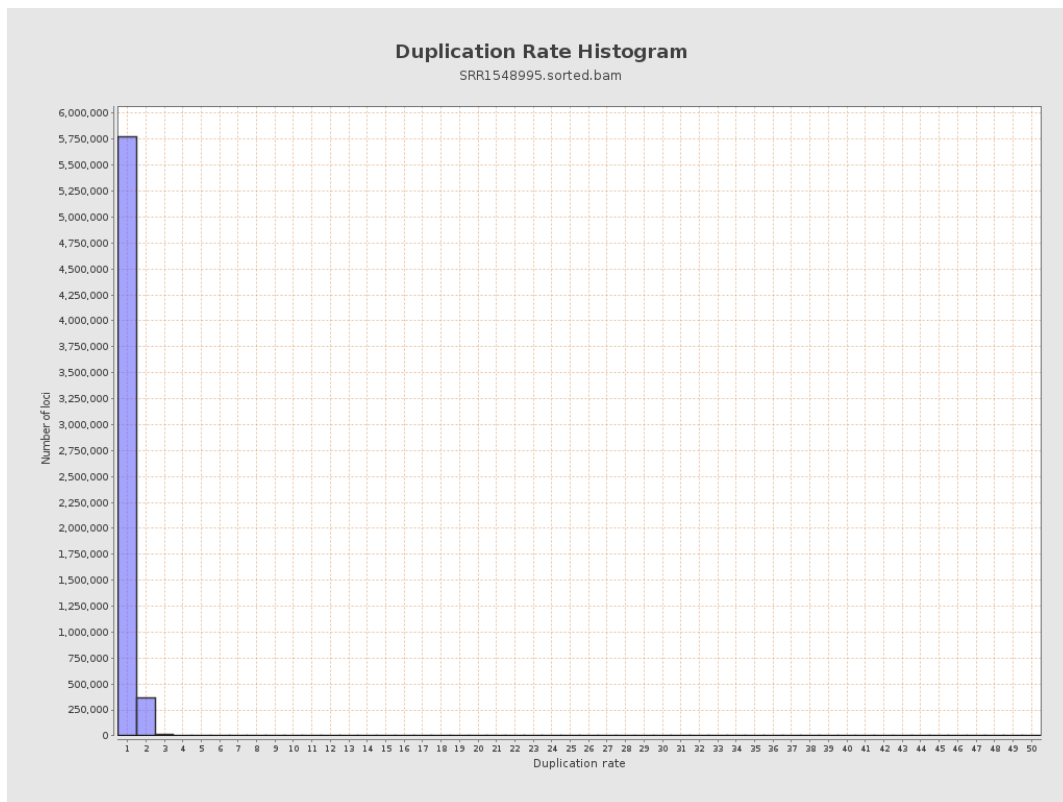
5. Results : Coverage Histogram (0-50X)



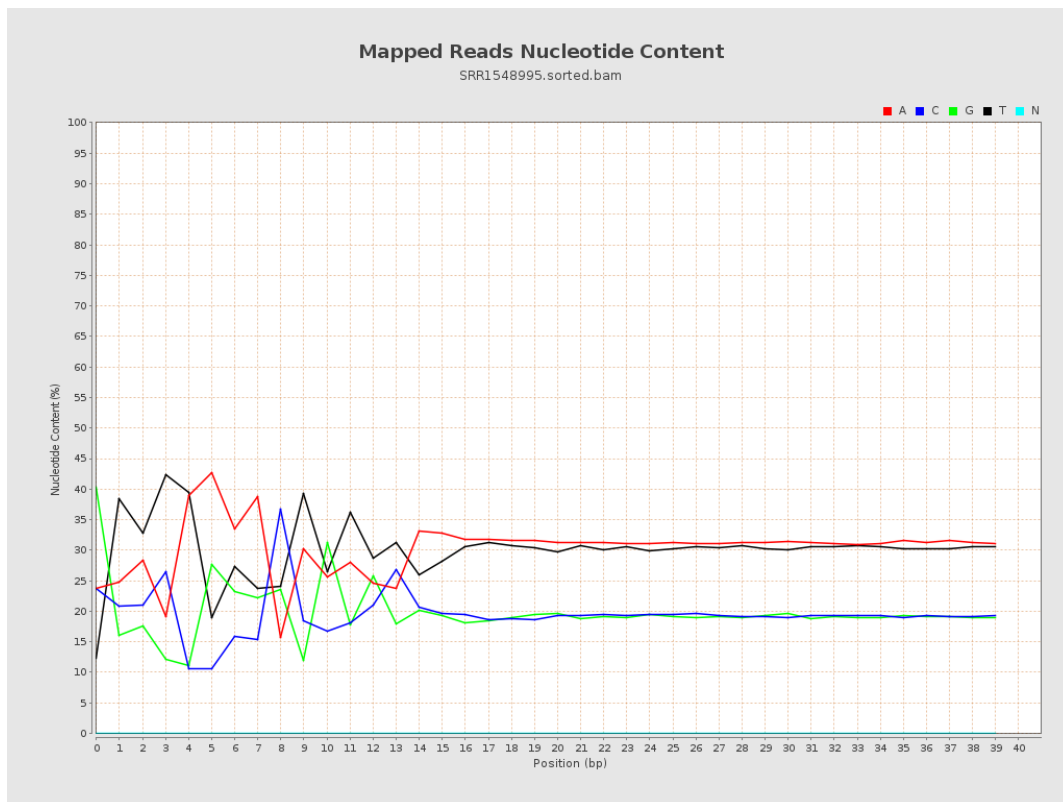
6. Results : Genome Fraction Coverage



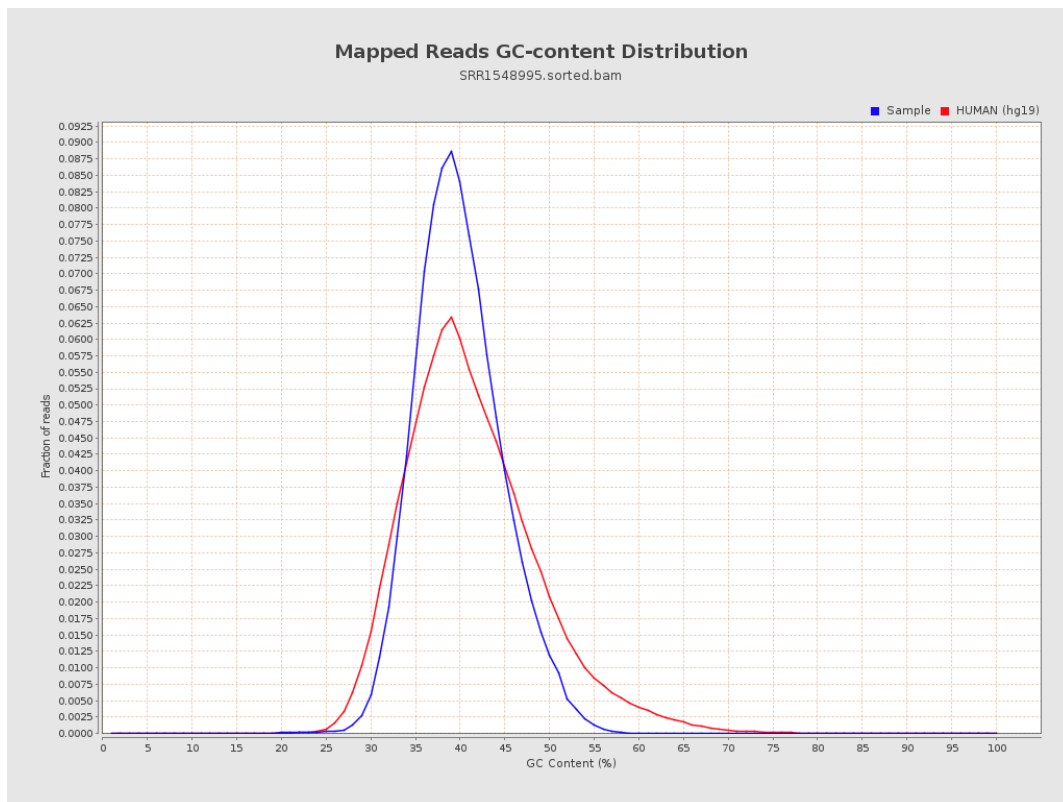
7. Results : Duplication Rate Histogram



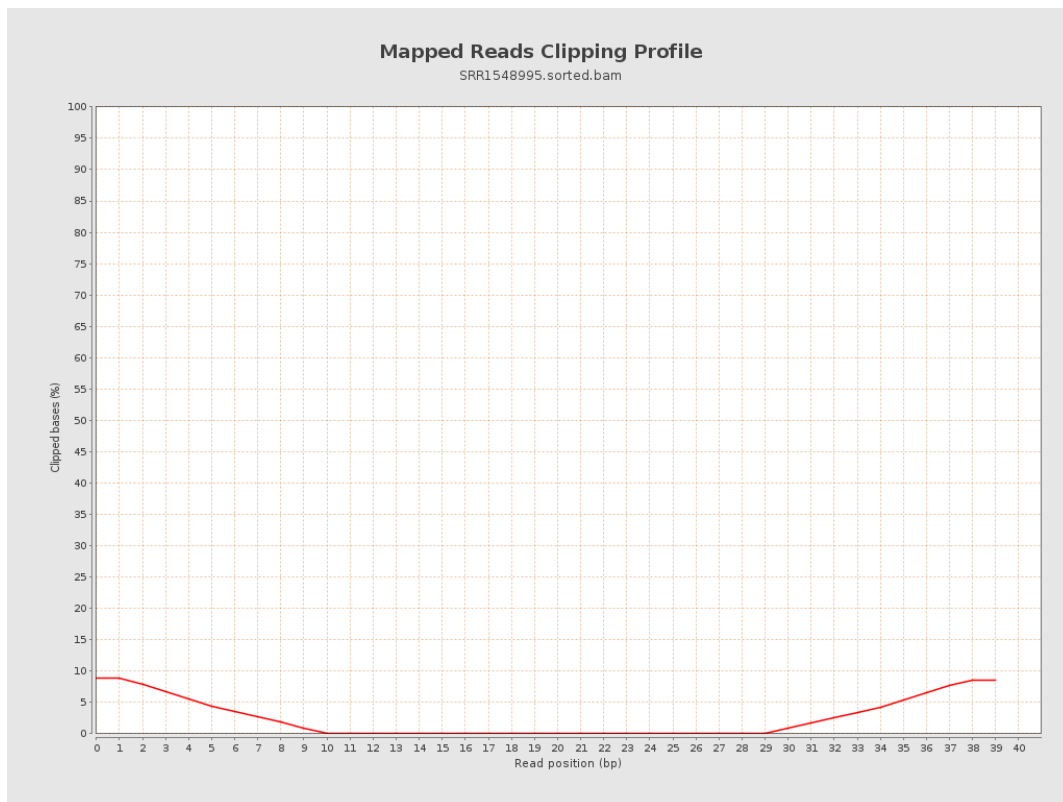
8. Results : Mapped Reads Nucleotide Content



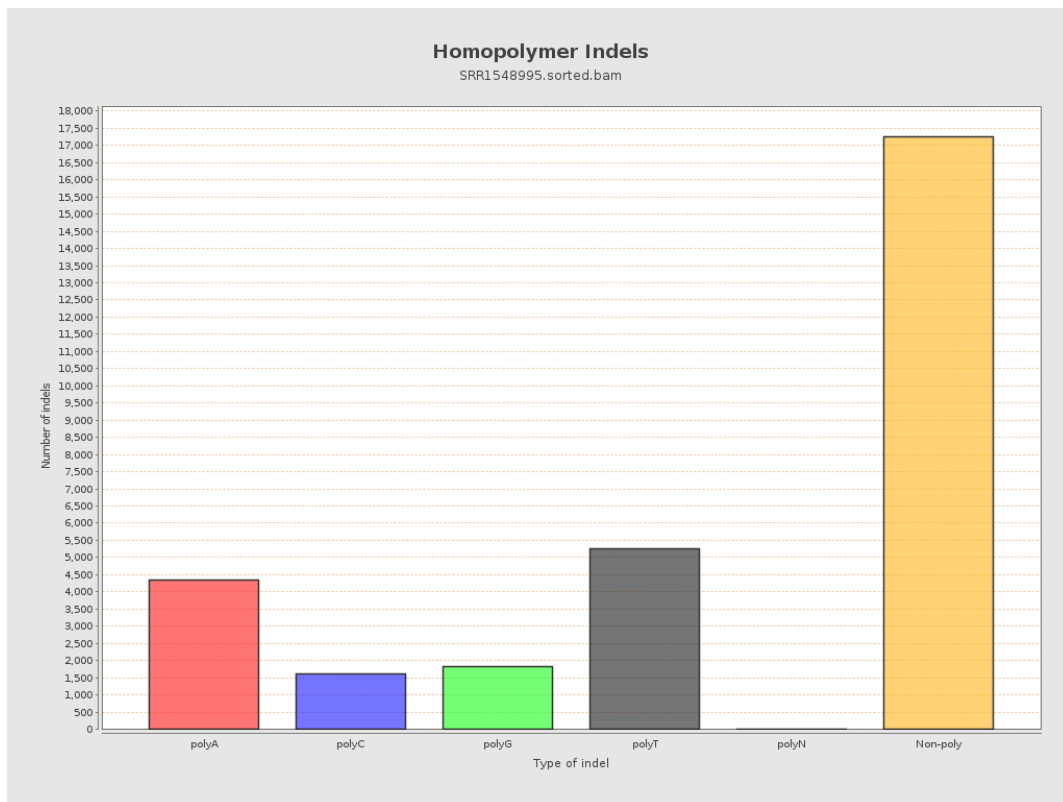
9. Results : Mapped Reads GC-content Distribution



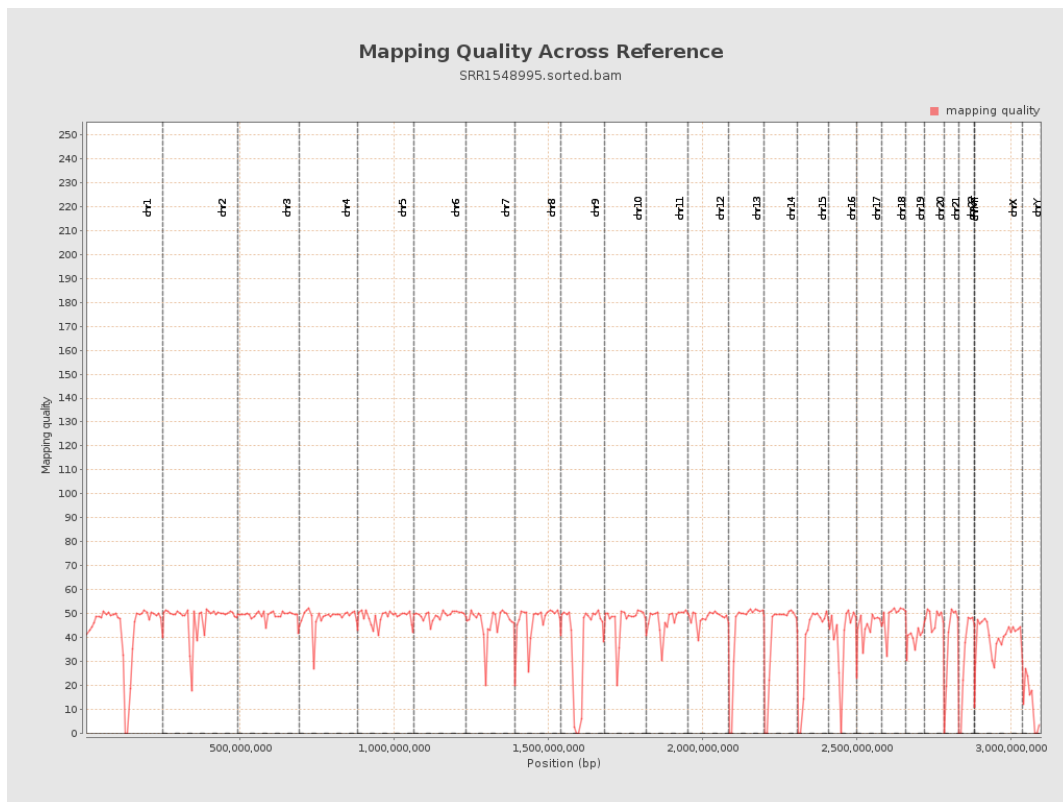
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

