

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 08:36:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548934.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_SRR1548934 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548934.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 08:36:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548934.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,466,443
Mapped reads	5,635,713 / 87.15%
Unmapped reads	830,730 / 12.85%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	191,729 / 2.96%
Duplication rate	2%
Clipped reads	445,668 / 6.89%

2.2. ACGT Content

Number/percentage of A's	65,383,358 / 29.33%
Number/percentage of C's	46,231,548 / 20.74%
Number/percentage of T's	65,451,963 / 29.36%
Number/percentage of G's	45,853,938 / 20.57%
Number/percentage of N's	1,931 / 0%
GC Percentage	41.31%

2.3. Coverage

Mean	0.072
Standard Deviation	0.9809

2.4. Mapping Quality

Mean Mapping Quality	39.25
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2.5. Mismatches and indels

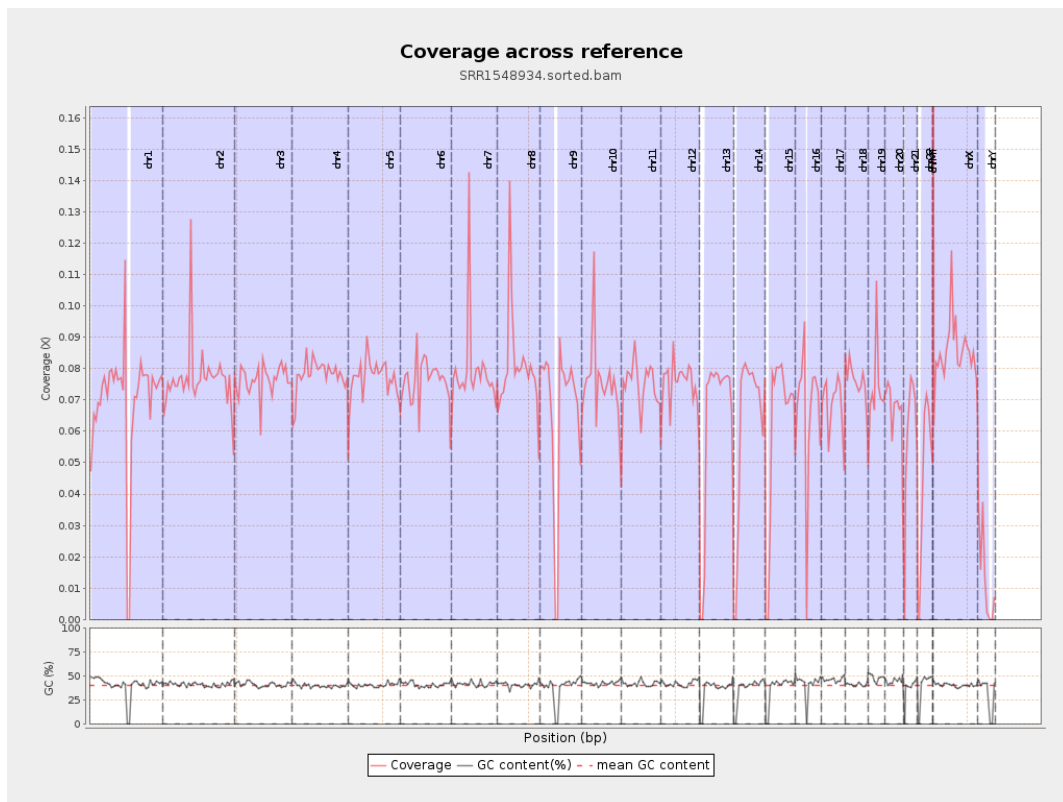
General error rate	0.31%
Mismatches	690,629
Insertions	7,599
Mapped reads with at least one insertion	0.13%
Deletions	18,025
Mapped reads with at least one deletion	0.32%
Homopolymer indels	40.04%

2.6. Chromosome stats

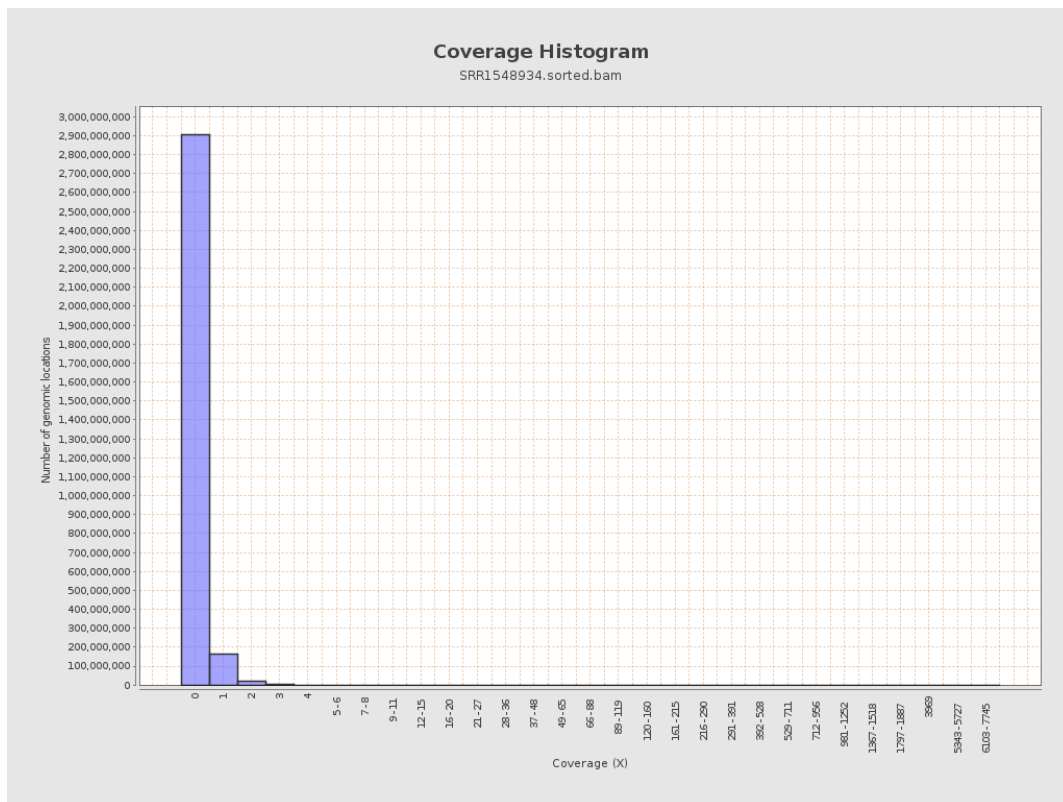
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	17370037	0.0697	1.0804
chr2	243199373	18671691	0.0768	0.5565
chr3	198022430	15157990	0.0765	0.3172
chr4	191154276	14922730	0.0781	0.335
chr5	180915260	13925514	0.077	0.3268
chr6	171115067	13056505	0.0763	0.3645
chr7	159138663	12603182	0.0792	0.7652
chr8	146364022	11807048	0.0807	3.751

chr9	141213431	9416552	0.0667	0.5363
chr10	135534747	10251773	0.0756	0.5072
chr11	135006516	10094338	0.0748	0.5543
chr12	133851895	10109668	0.0755	0.3333
chr13	115169878	7263645	0.0631	0.2798
chr14	107349540	6749714	0.0629	0.3525
chr15	102531392	6266585	0.0611	0.2811
chr16	90354753	5886235	0.0651	0.3482
chr17	81195210	5611553	0.0691	0.3288
chr18	78077248	5969593	0.0765	1.0445
chr19	59128983	4391181	0.0743	1.0201
chr20	63025520	4247310	0.0674	0.3209
chr21	48129895	2815890	0.0585	0.3292
chr22	51304566	2331763	0.0454	0.2554
chrMT	16571	7832	0.4726	0.8579
chrX	155270560	13236247	0.0852	0.4389
chrY	59373566	781737	0.0132	0.1866

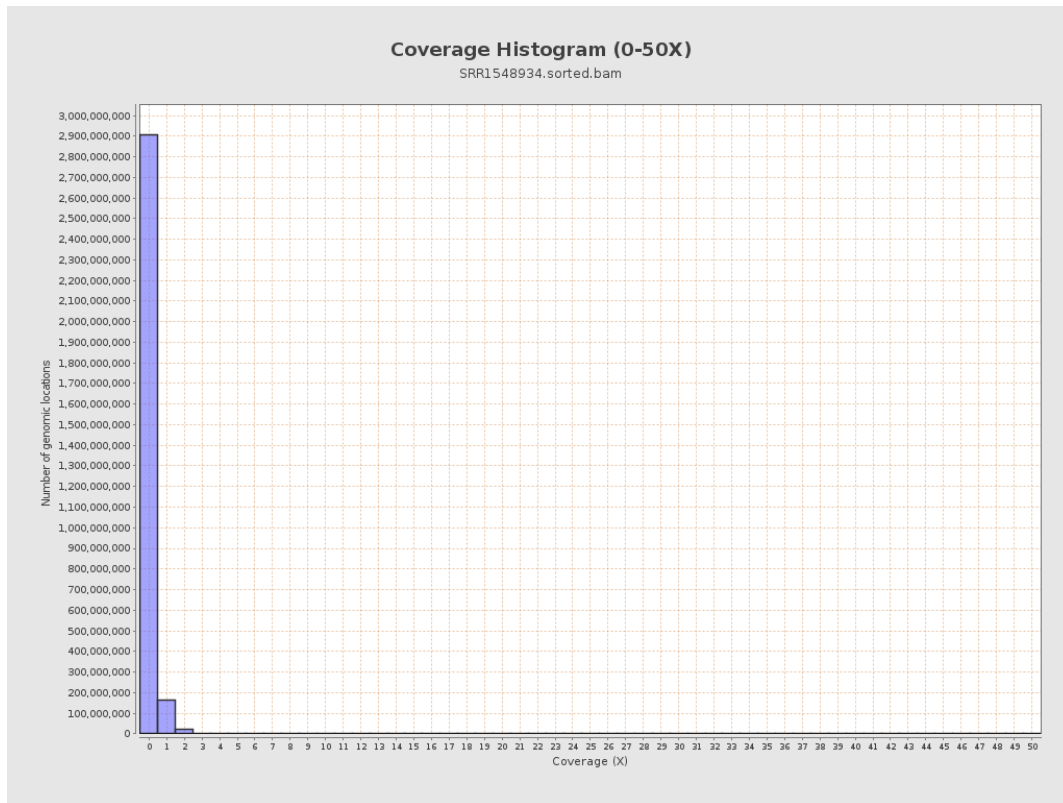
3. Results : Coverage across reference



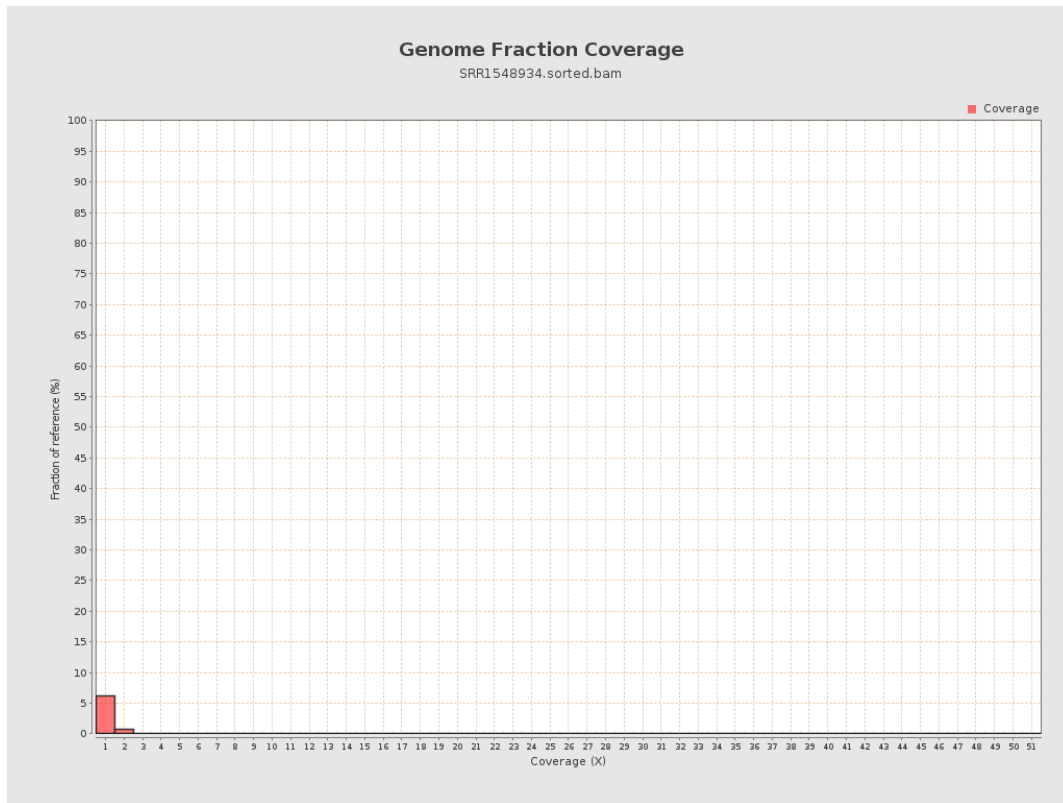
4. Results : Coverage Histogram



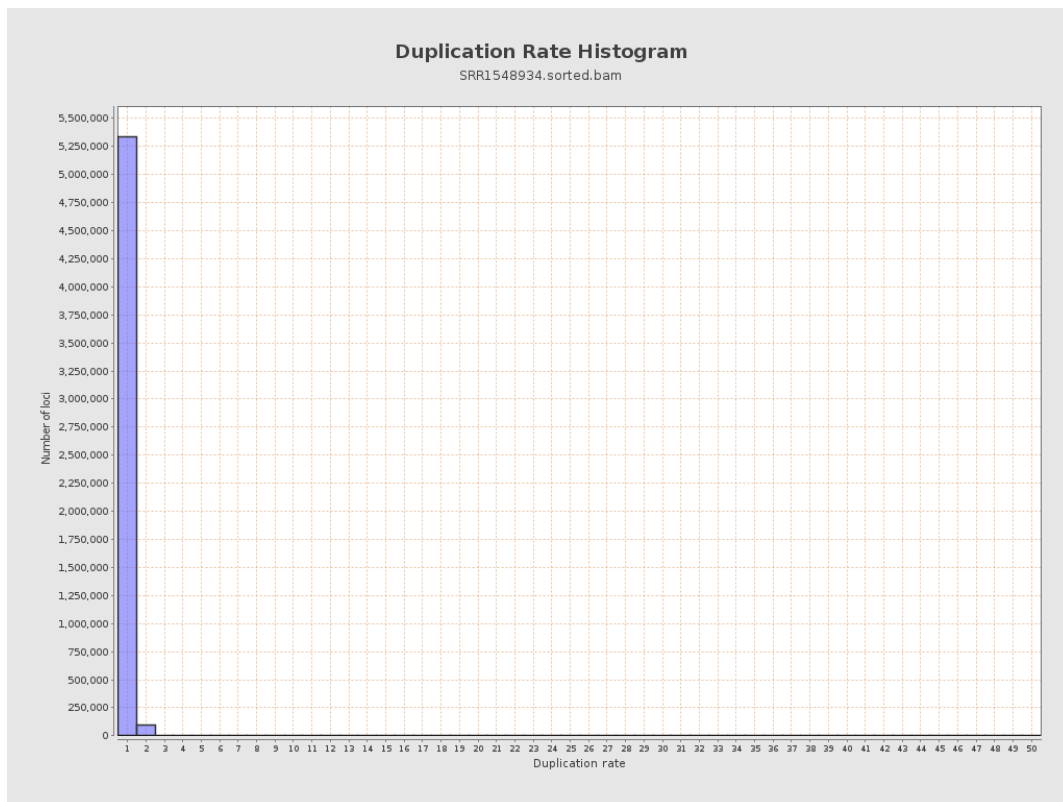
5. Results : Coverage Histogram (0-50X)



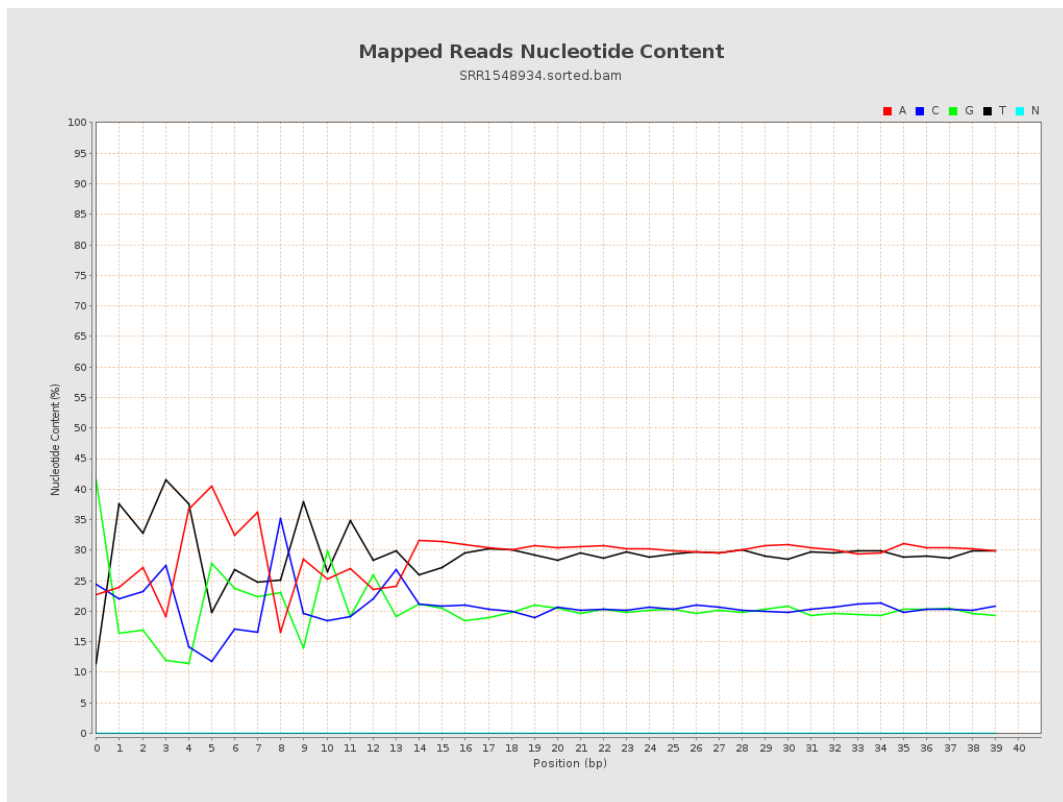
6. Results : Genome Fraction Coverage



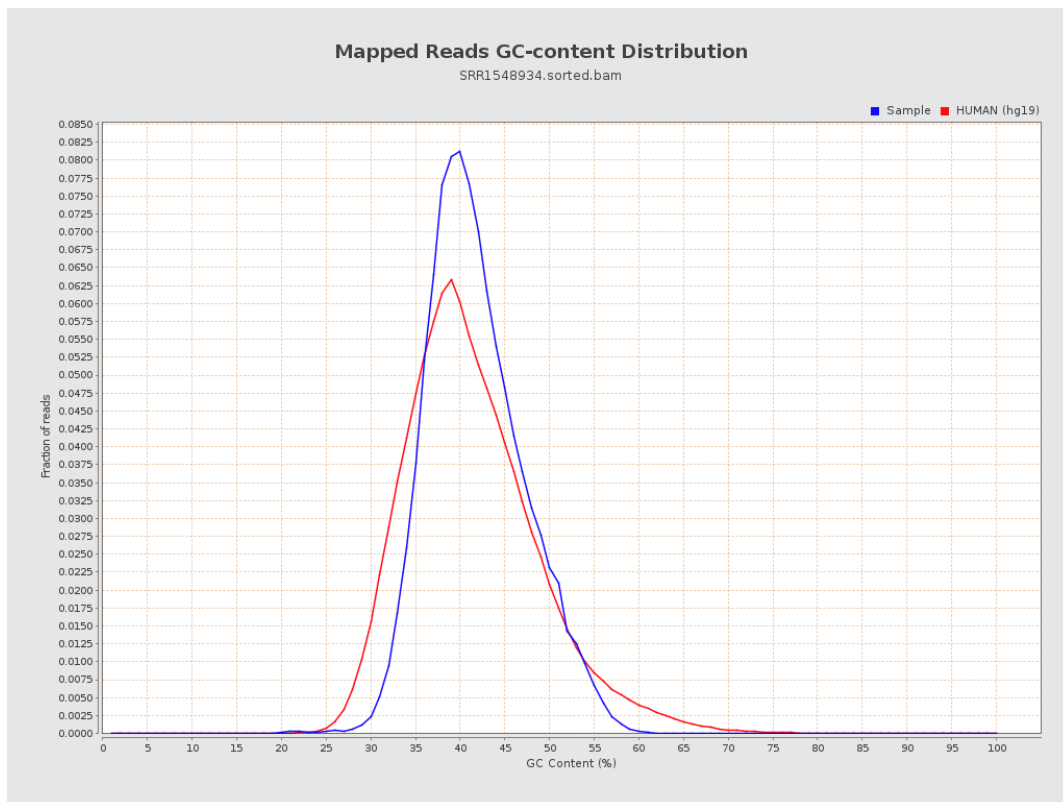
7. Results : Duplication Rate Histogram



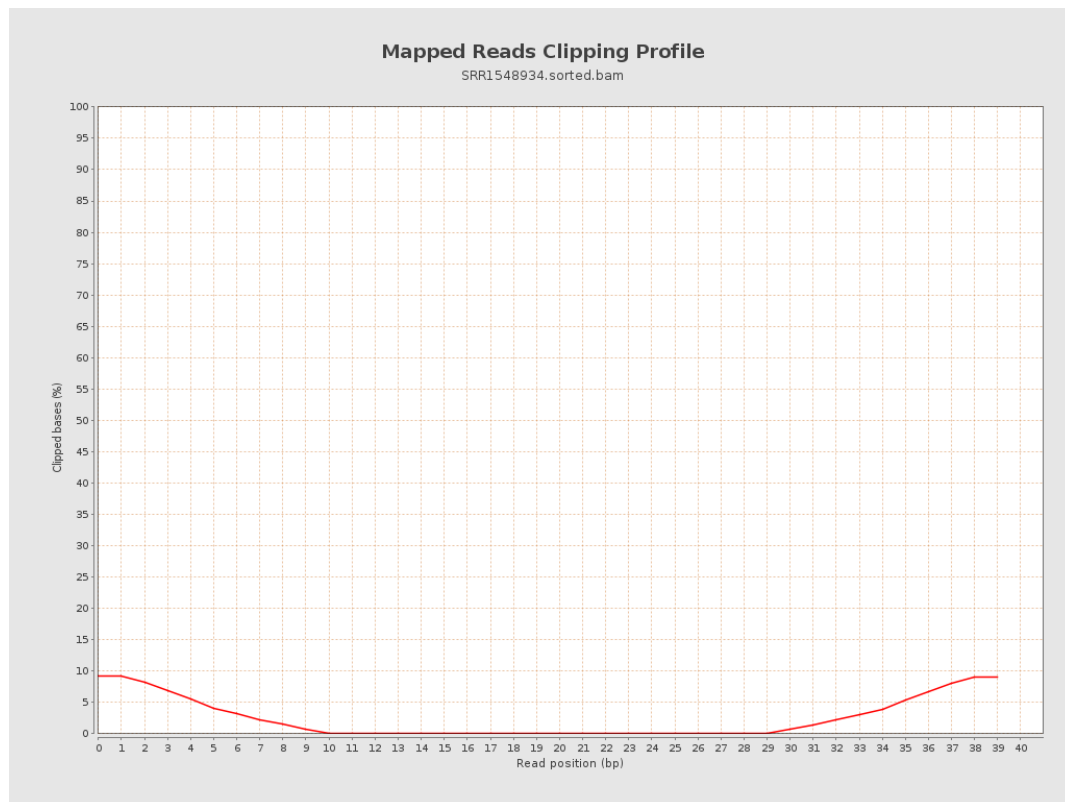
8. Results : Mapped Reads Nucleotide Content



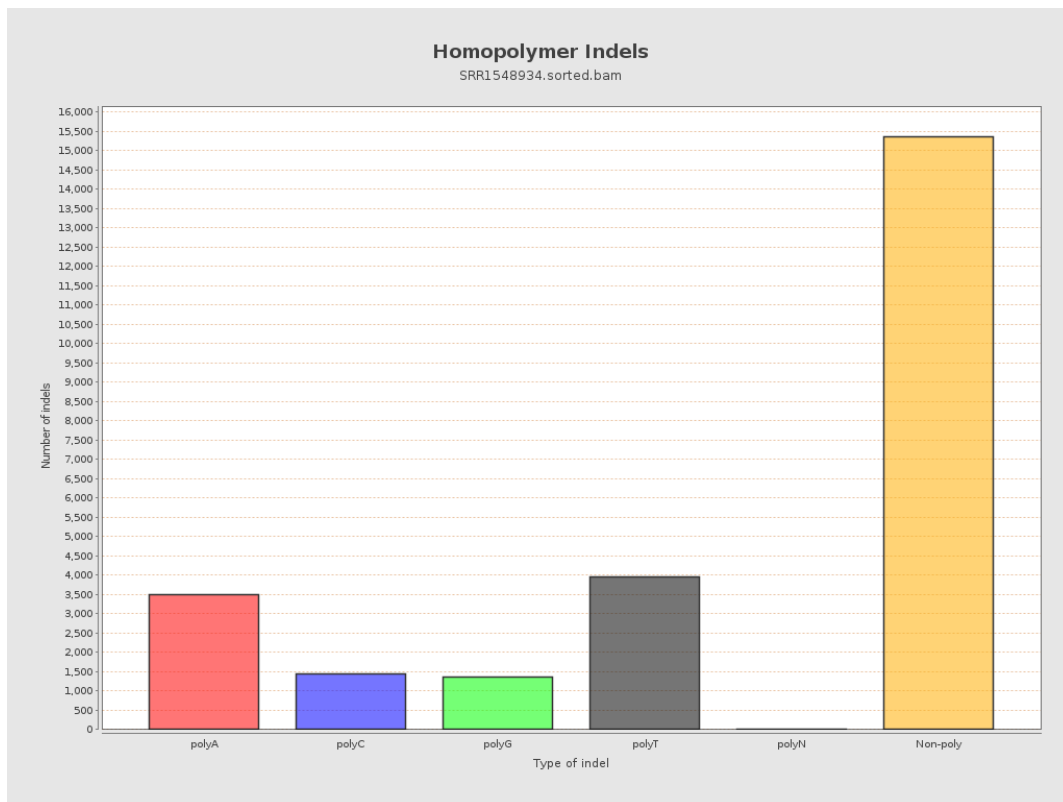
9. Results : Mapped Reads GC-content Distribution



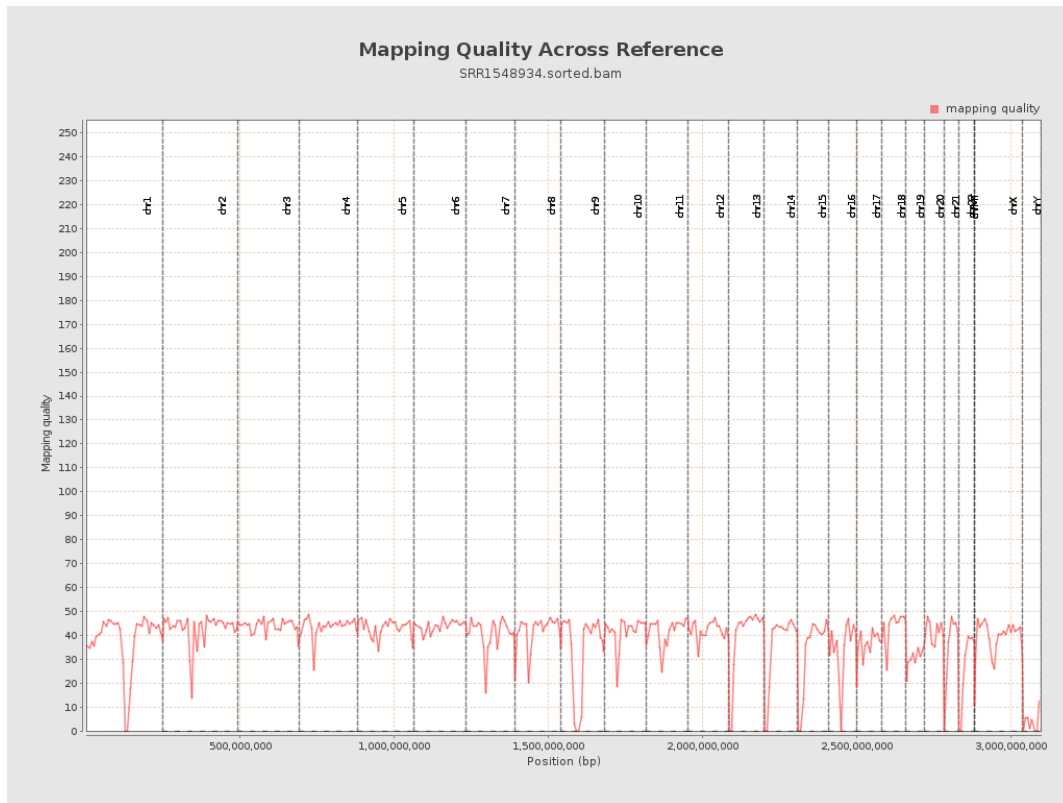
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

