

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 06:16:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548930.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_SRR1548930 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548930.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 06:16:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548930.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,693,357
Mapped reads	5,822,667 / 86.99%
Unmapped reads	870,690 / 13.01%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	191,007 / 2.85%
Duplication rate	2.21%
Clipped reads	402,132 / 6.01%

2.2. ACGT Content

Number/percentage of A's	67,696,128 / 29.35%
Number/percentage of C's	47,638,486 / 20.66%
Number/percentage of T's	67,884,046 / 29.43%
Number/percentage of G's	47,413,489 / 20.56%
Number/percentage of N's	2,097 / 0%
GC Percentage	41.21%

2.3. Coverage

Mean	0.0745
Standard Deviation	0.9072

2.4. Mapping Quality

Mean Mapping Quality	41.61
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2.5. Mismatches and indels

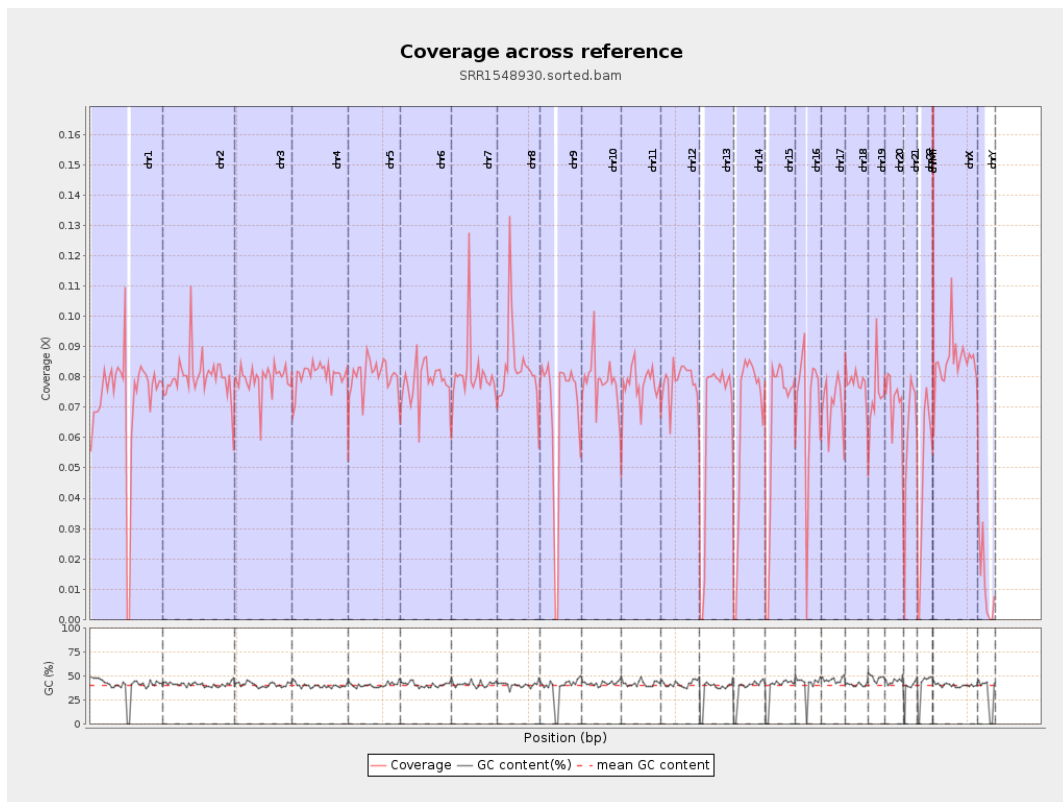
General error rate	0.28%
Mismatches	631,612
Insertions	7,293
Mapped reads with at least one insertion	0.13%
Deletions	17,252
Mapped reads with at least one deletion	0.3%
Homopolymer indels	40.95%

2.6. Chromosome stats

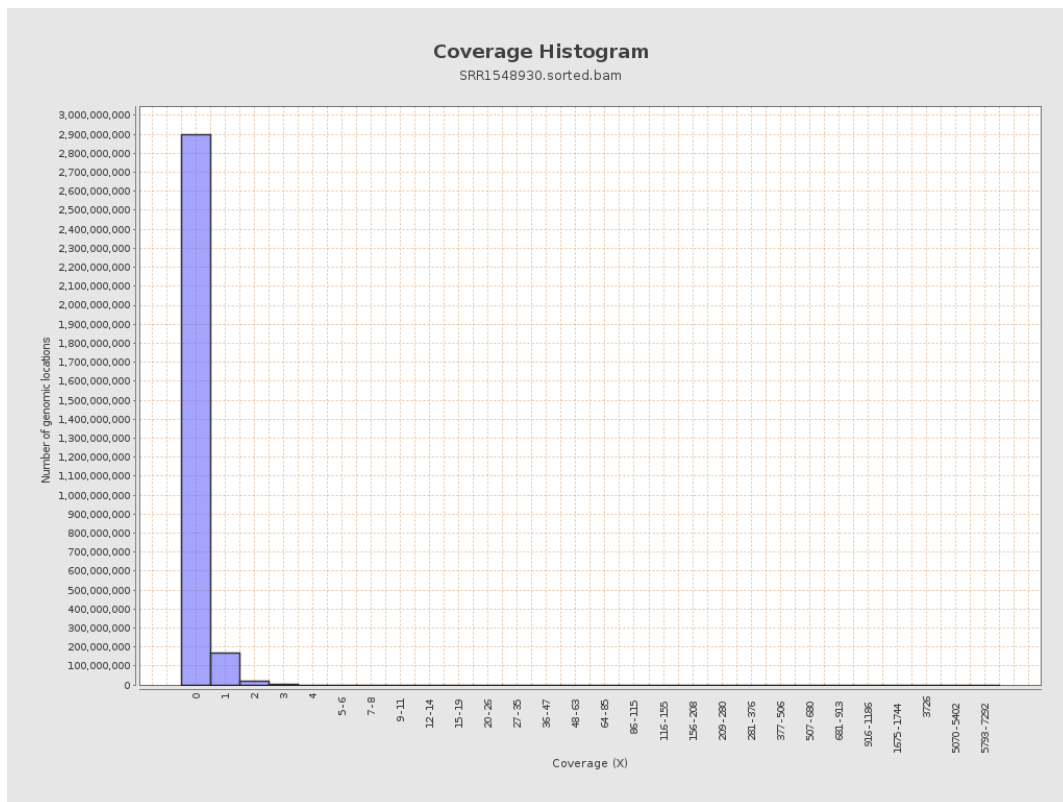
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	18065640	0.0725	0.9183
chr2	243199373	19473523	0.0801	0.4768
chr3	198022430	15708519	0.0793	0.3197
chr4	191154276	15433173	0.0807	0.3336
chr5	180915260	14474999	0.08	0.329
chr6	171115067	13446865	0.0786	0.3548
chr7	159138663	12868815	0.0809	0.6839
chr8	146364022	12191269	0.0833	3.5353

chr9	141213431	9698866	0.0687	0.4531
chr10	135534747	10653338	0.0786	0.4375
chr11	135006516	10465071	0.0775	0.5351
chr12	133851895	10491424	0.0784	0.33
chr13	115169878	7552870	0.0656	0.2867
chr14	107349540	7147630	0.0666	0.3469
chr15	102531392	6610926	0.0645	0.2863
chr16	90354753	6237585	0.069	0.334
chr17	81195210	5815665	0.0716	0.3317
chr18	78077248	6101198	0.0781	0.8485
chr19	59128983	4387030	0.0742	0.8102
chr20	63025520	4556272	0.0723	0.3169
chr21	48129895	2906648	0.0604	0.3201
chr22	51304566	2461553	0.048	0.2629
chrMT	16571	9741	0.5878	0.9209
chrX	155270560	13195104	0.085	0.4111
chrY	59373566	703258	0.0118	0.1686

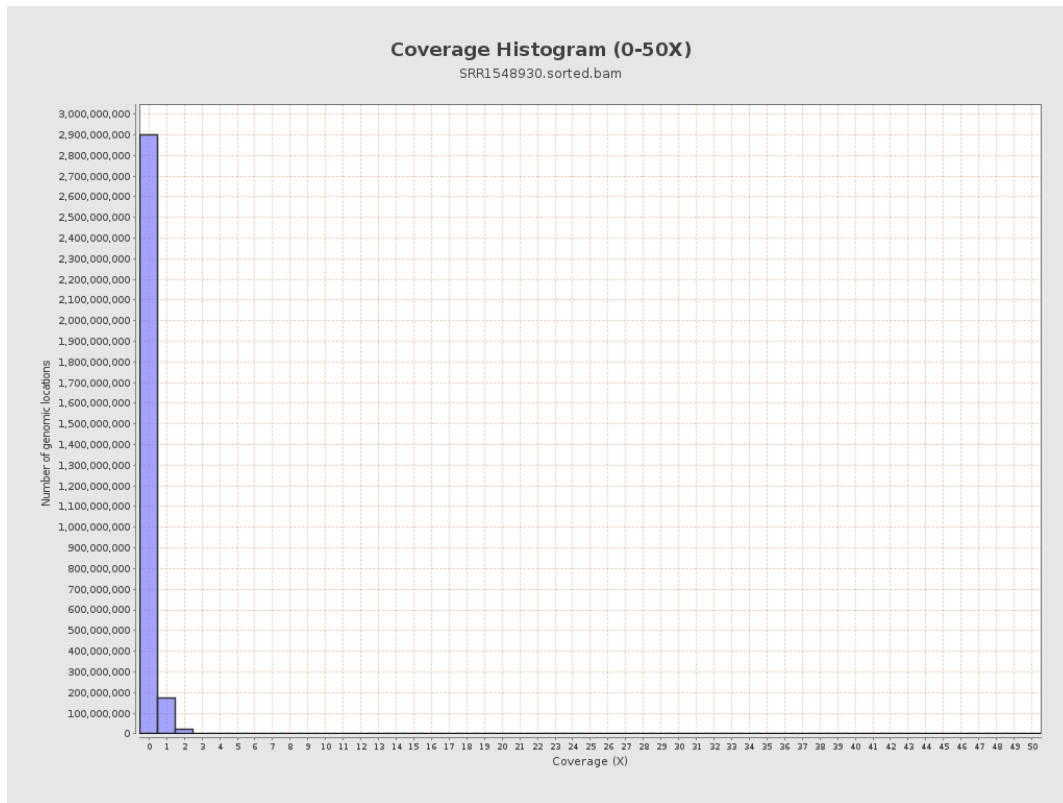
3. Results : Coverage across reference



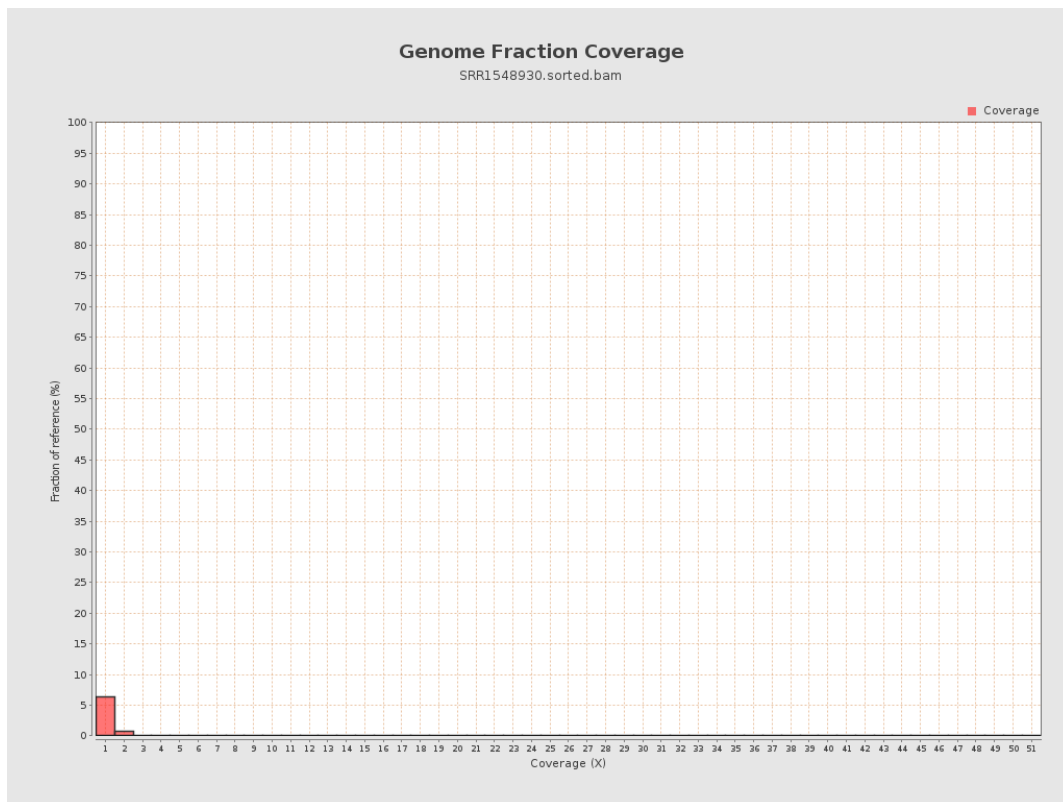
4. Results : Coverage Histogram



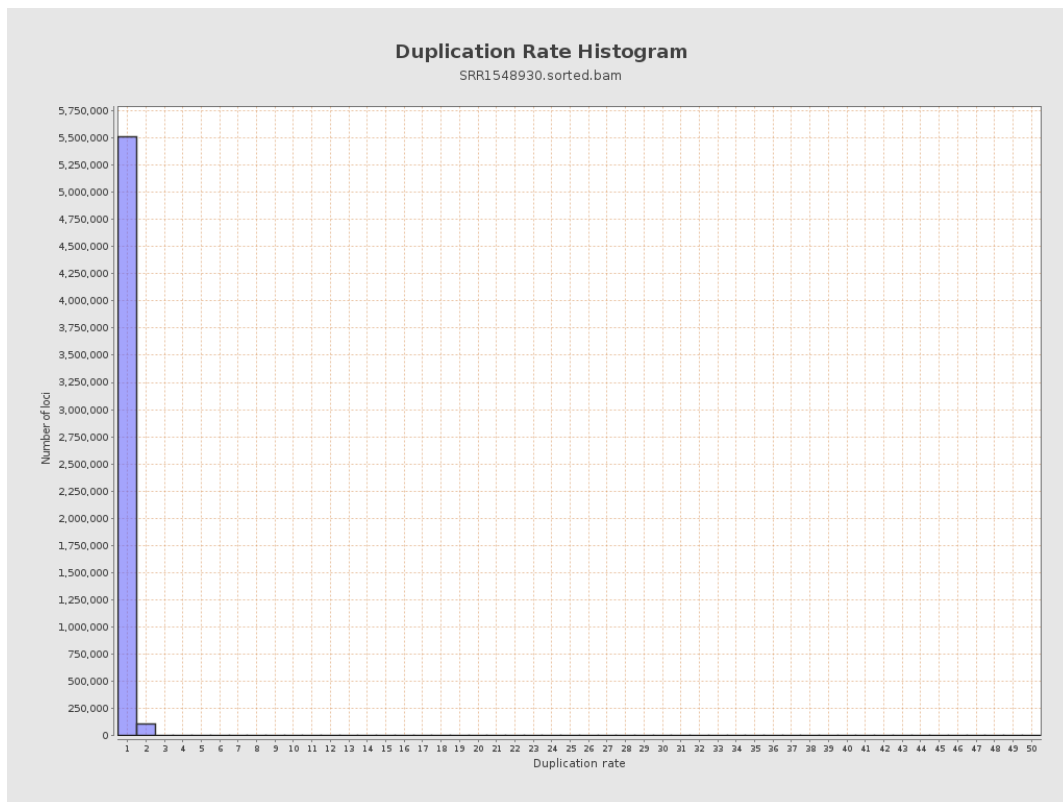
5. Results : Coverage Histogram (0-50X)



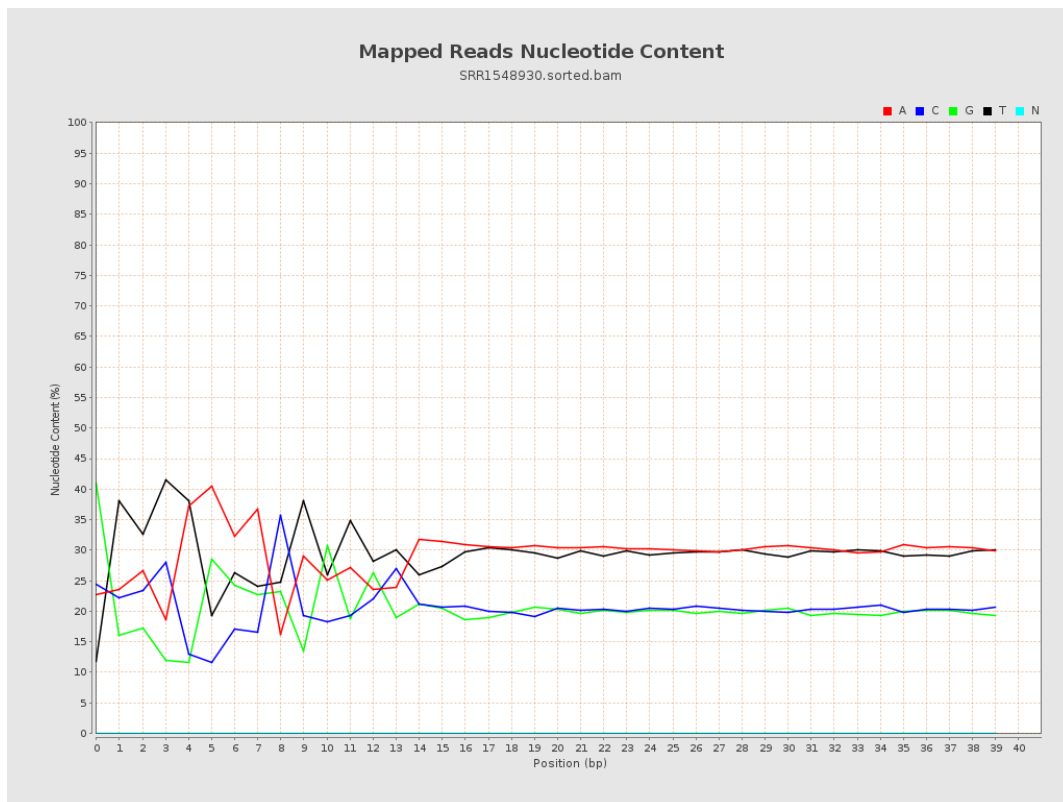
6. Results : Genome Fraction Coverage



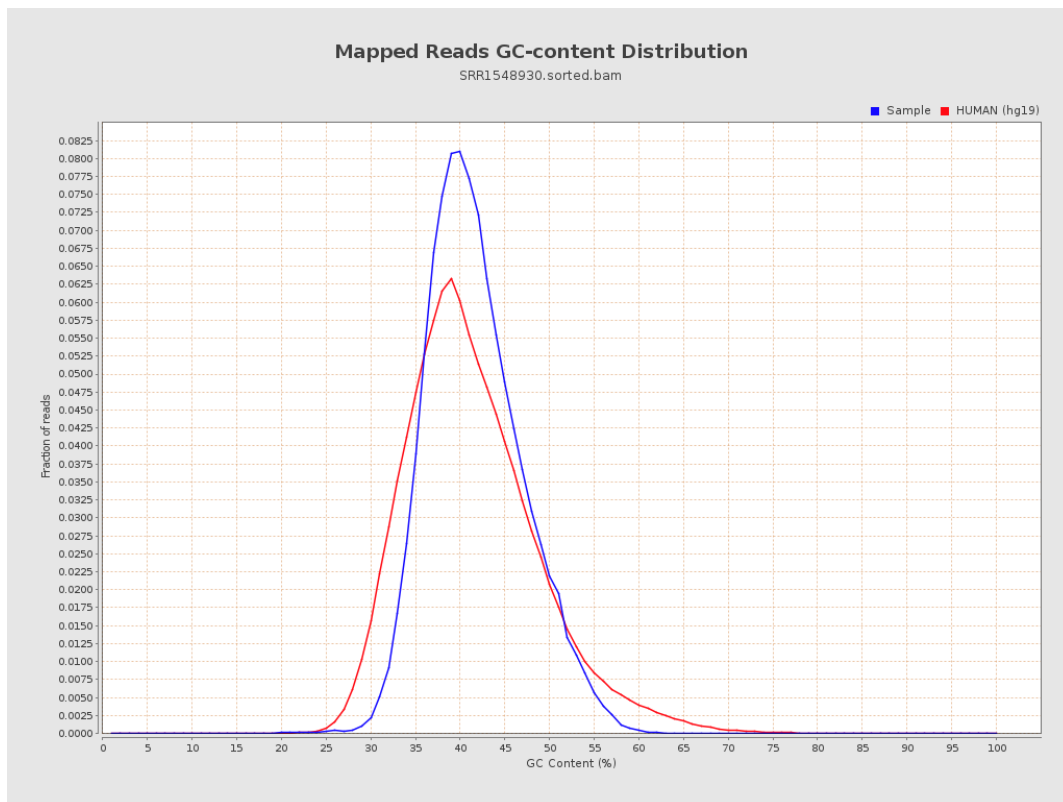
7. Results : Duplication Rate Histogram



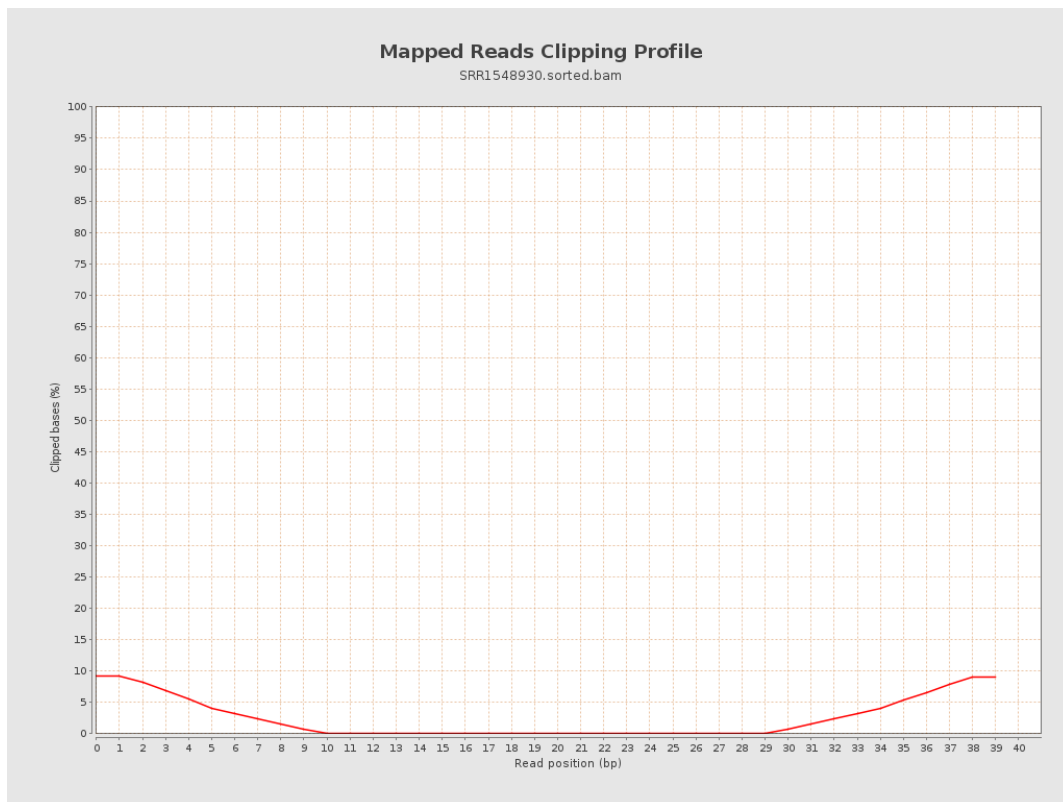
8. Results : Mapped Reads Nucleotide Content



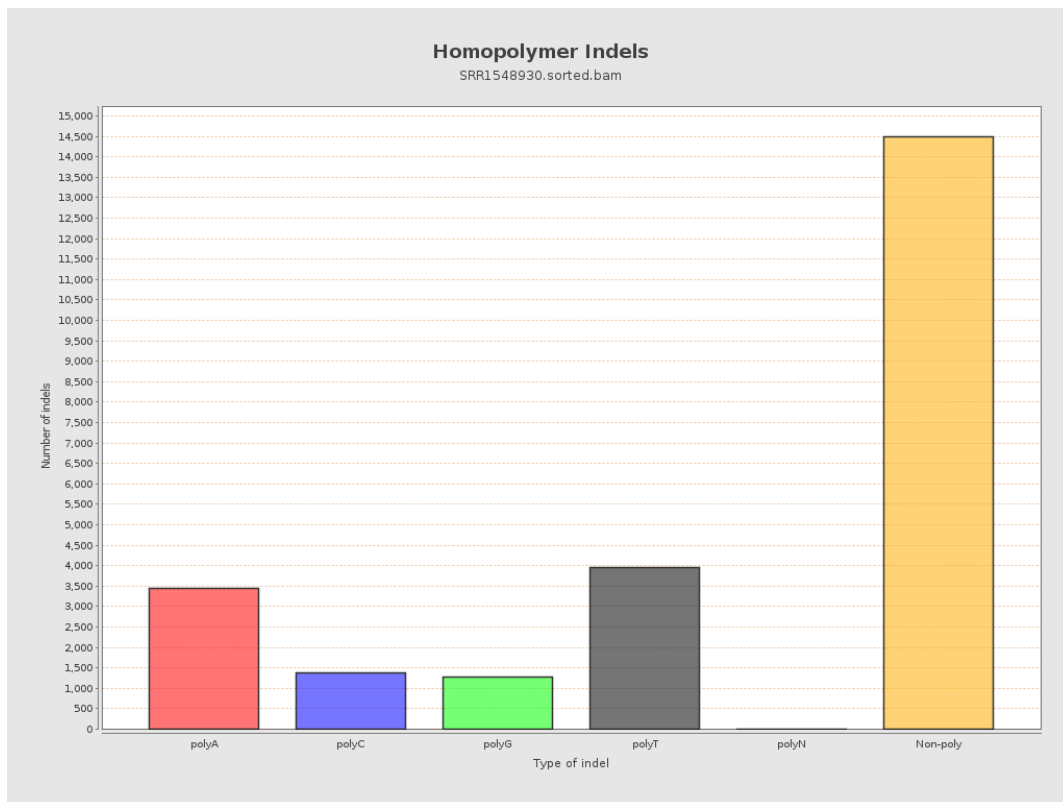
9. Results : Mapped Reads GC-content Distribution



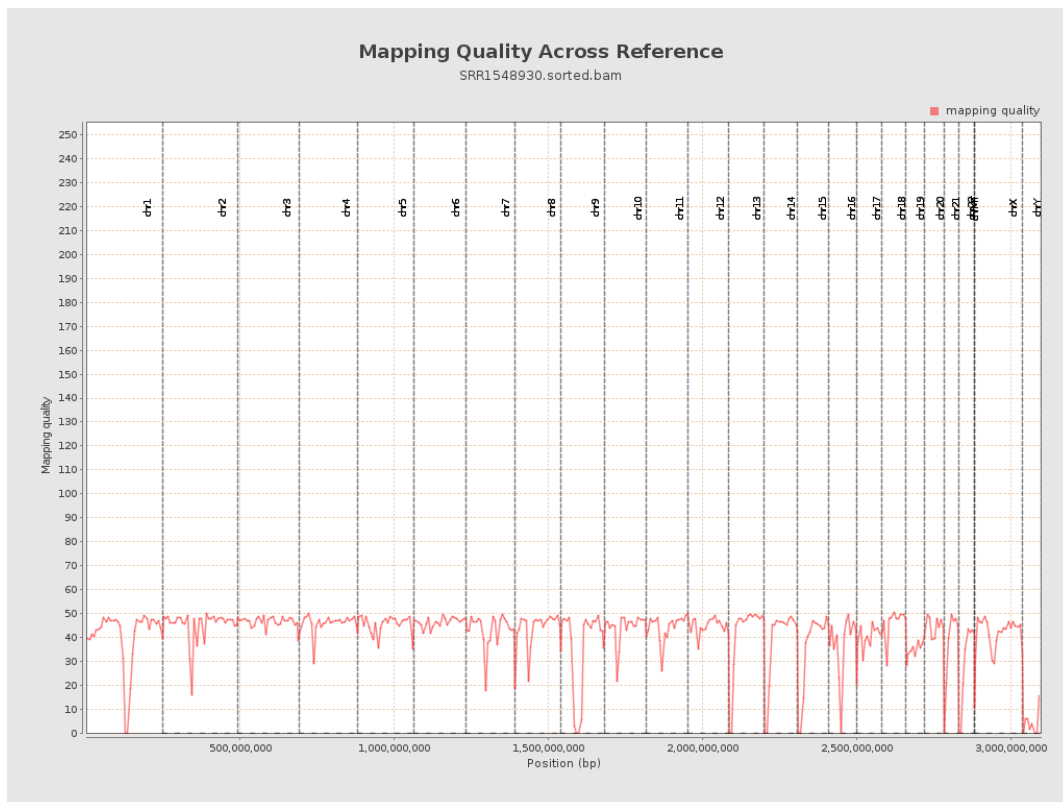
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

