

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 09:14:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818934.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_SRR1818934 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818934.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 09:14:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818934.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,732,258
Mapped reads	1,706,451 / 98.51%
Unmapped reads	25,807 / 1.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,636 / 1.31%
Read min/max/mean length	30 / 101 / 101.5
Duplicated reads (estimated)	611,819 / 35.32%
Duplication rate	30.52%
Clipped reads	1,723,375 / 99.49%

2.2. ACGT Content

Number/percentage of A's	44,351,541 / 28.08%
Number/percentage of C's	32,448,966 / 20.55%
Number/percentage of T's	46,138,834 / 29.22%
Number/percentage of G's	34,974,319 / 22.15%
Number/percentage of N's	6,525 / 0%
GC Percentage	42.69%

2.3. Coverage

Mean	0.051

Standard Deviation	0.5554
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2.4. Mapping Quality

Mean Mapping Quality	49.45
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2.5. Mismatches and indels

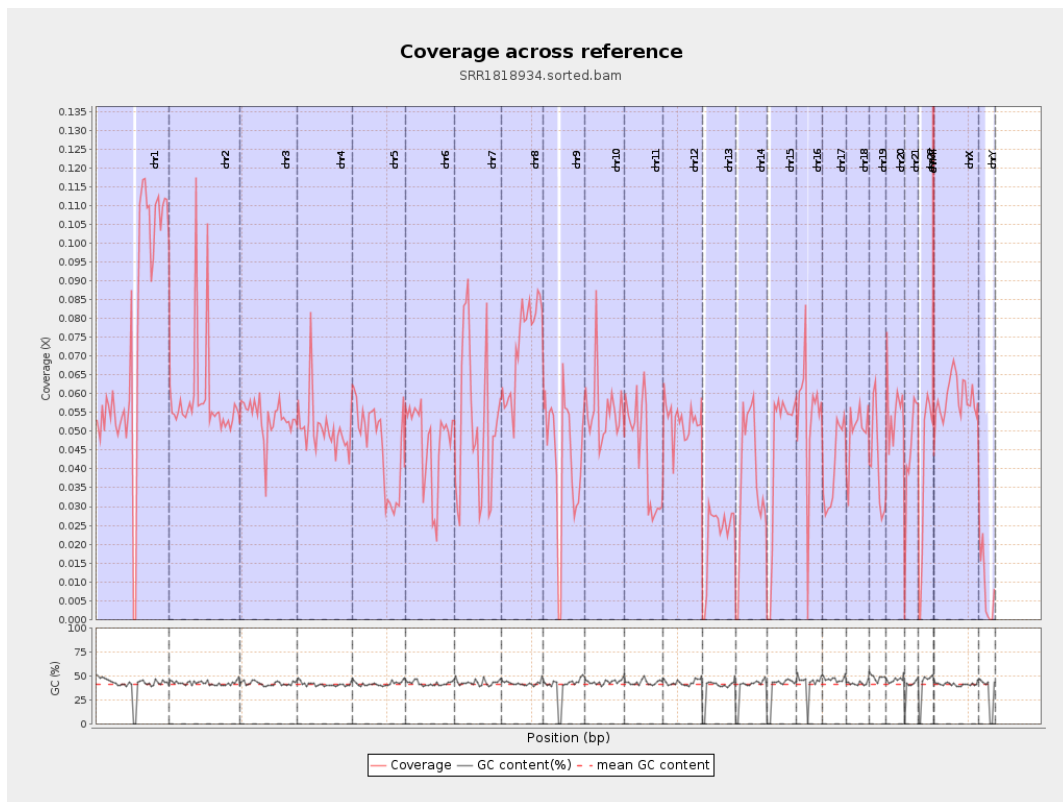
General error rate	0.64%
Mismatches	966,086
Insertions	18,642
Mapped reads with at least one insertion	1.06%
Deletions	49,381
Mapped reads with at least one deletion	2.83%
Homopolymer indels	43.65%

2.6. Chromosome stats

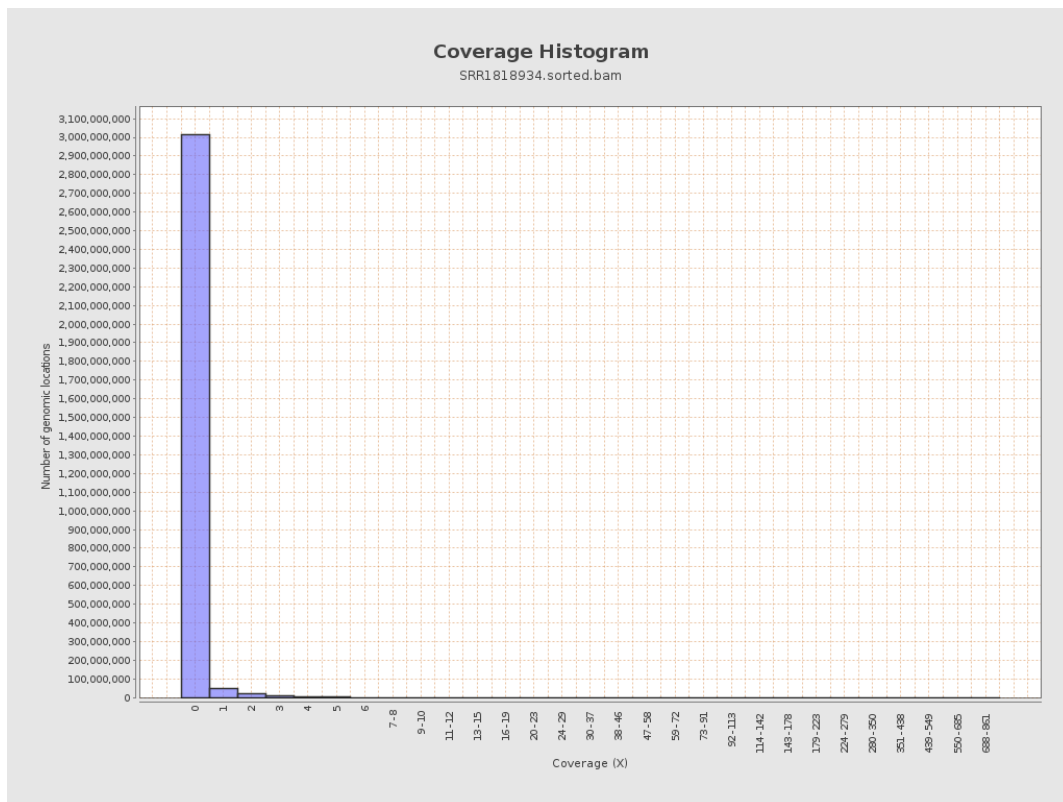
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	18580151	0.0745	0.8724
chr2	243199373	14276312	0.0587	0.8659
chr3	198022430	10609315	0.0536	0.3884
chr4	191154276	9691007	0.0507	0.4129
chr5	180915260	8335948	0.0461	0.3773
chr6	171115067	8041145	0.047	0.3896
chr7	159138663	8175557	0.0514	0.4736

chr8	146364022	10674202	0.0729	0.5002
chr9	141213431	5986779	0.0424	0.6052
chr10	135534747	7492079	0.0553	0.6488
chr11	135006516	5989152	0.0444	0.4109
chr12	133851895	7072186	0.0528	0.3941
chr13	115169878	2565208	0.0223	0.2455
chr14	107349540	3986113	0.0371	0.3606
chr15	102531392	4639393	0.0452	0.3577
chr16	90354753	4945381	0.0547	0.6367
chr17	81195210	3330077	0.041	0.3753
chr18	78077248	3891217	0.0498	0.8064
chr19	59128983	2493250	0.0422	0.776
chr20	63025520	3502581	0.0556	0.4166
chr21	48129895	2147778	0.0446	0.377
chr22	51304566	1977010	0.0385	0.3647
chrMT	16571	15778	0.9521	1.5254
chrX	155270560	9098658	0.0586	0.4789
chrY	59373566	494896	0.0083	0.4965

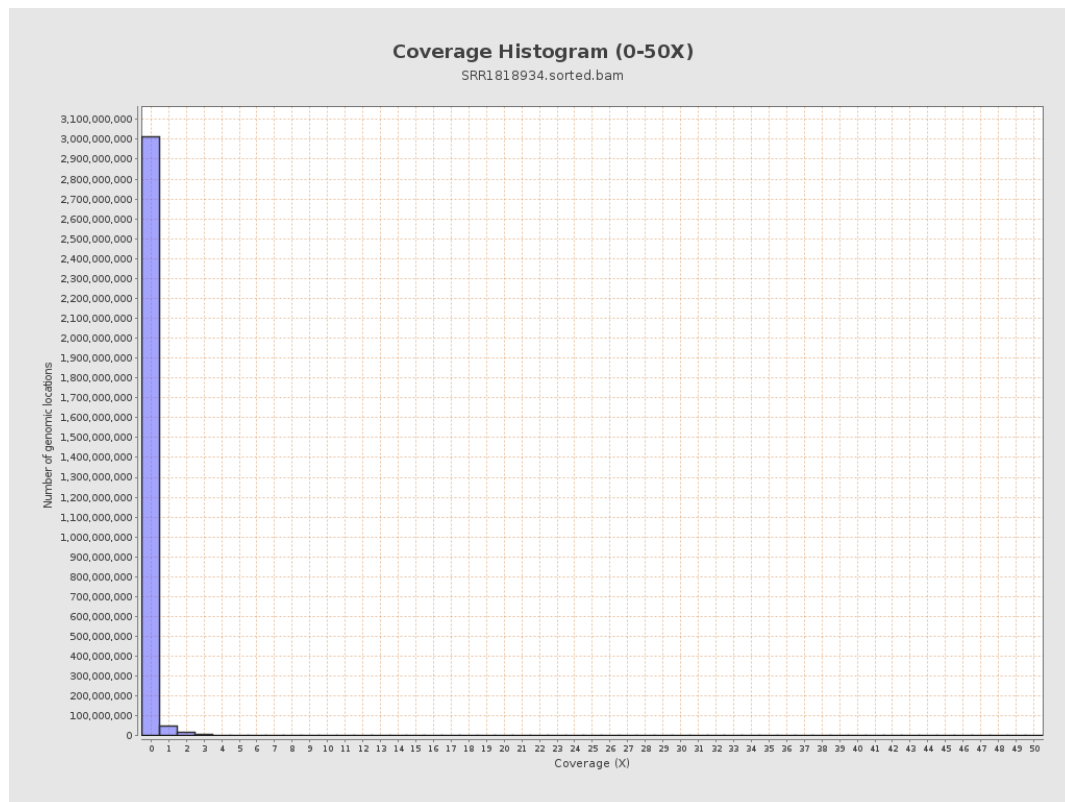
3. Results : Coverage across reference



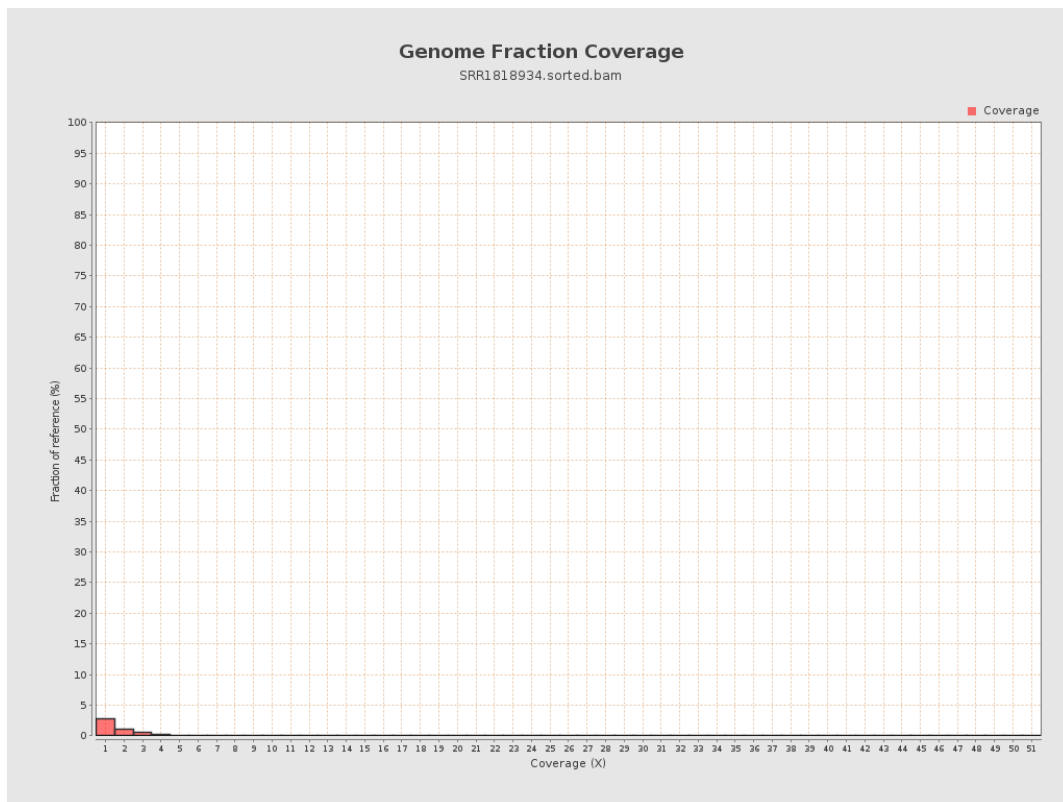
4. Results : Coverage Histogram



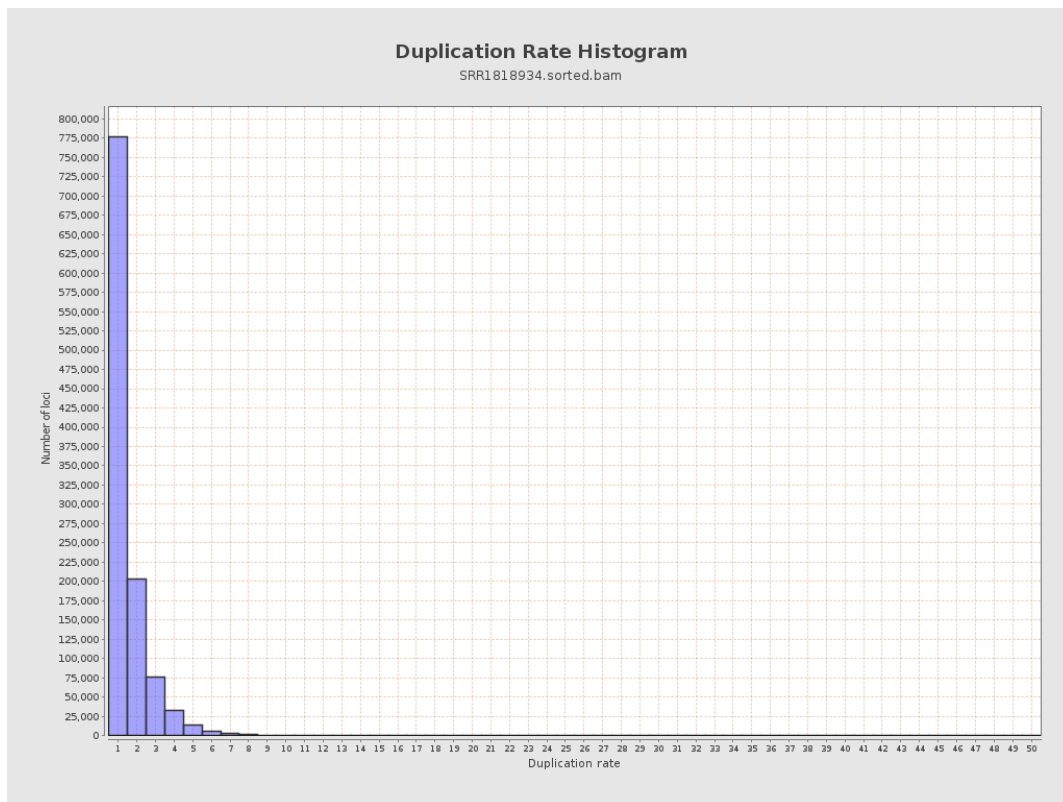
5. Results : Coverage Histogram (0-50X)



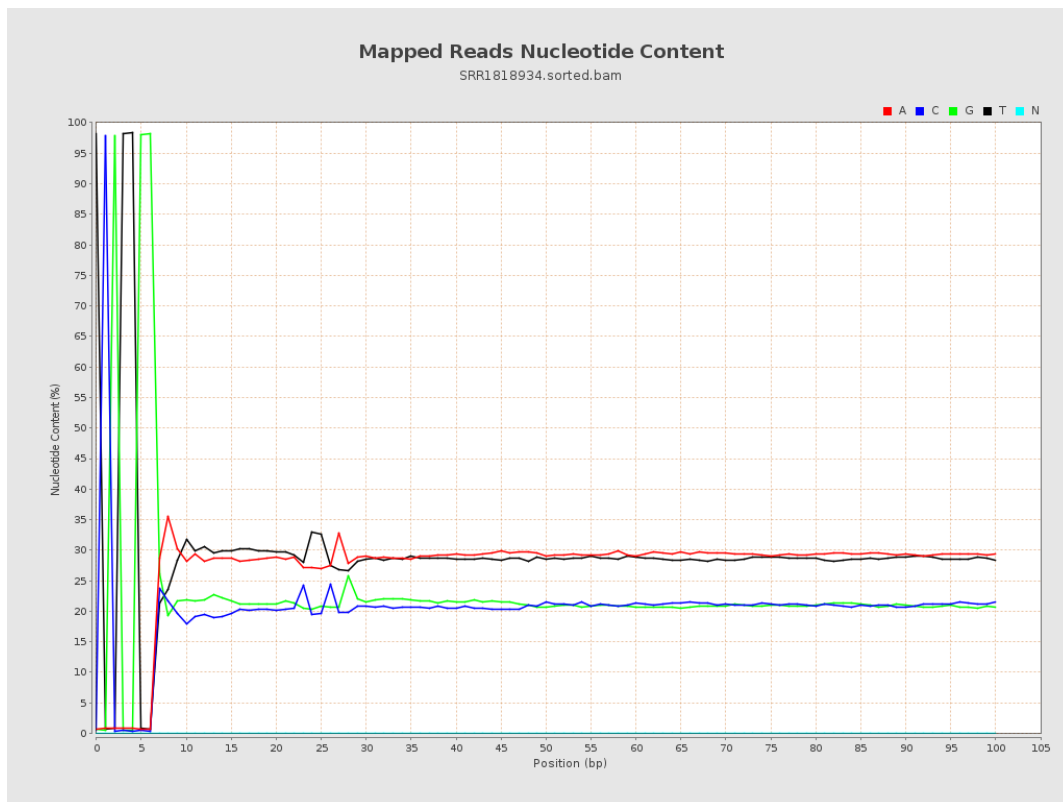
6. Results : Genome Fraction Coverage



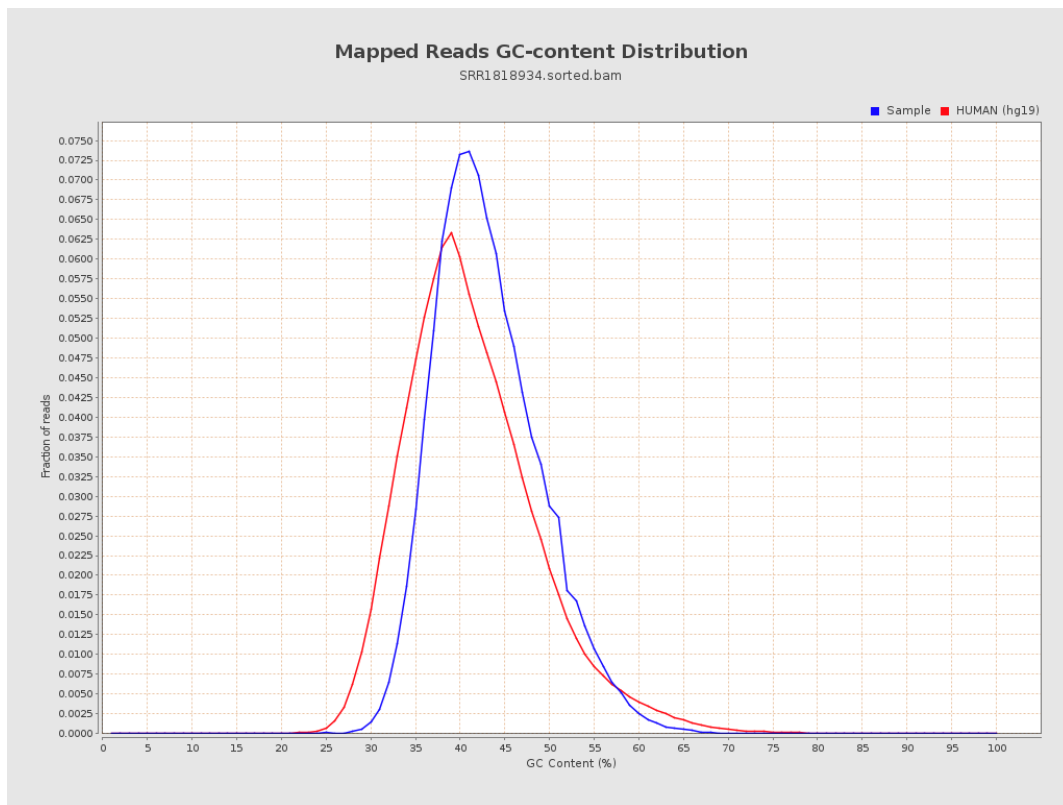
7. Results : Duplication Rate Histogram



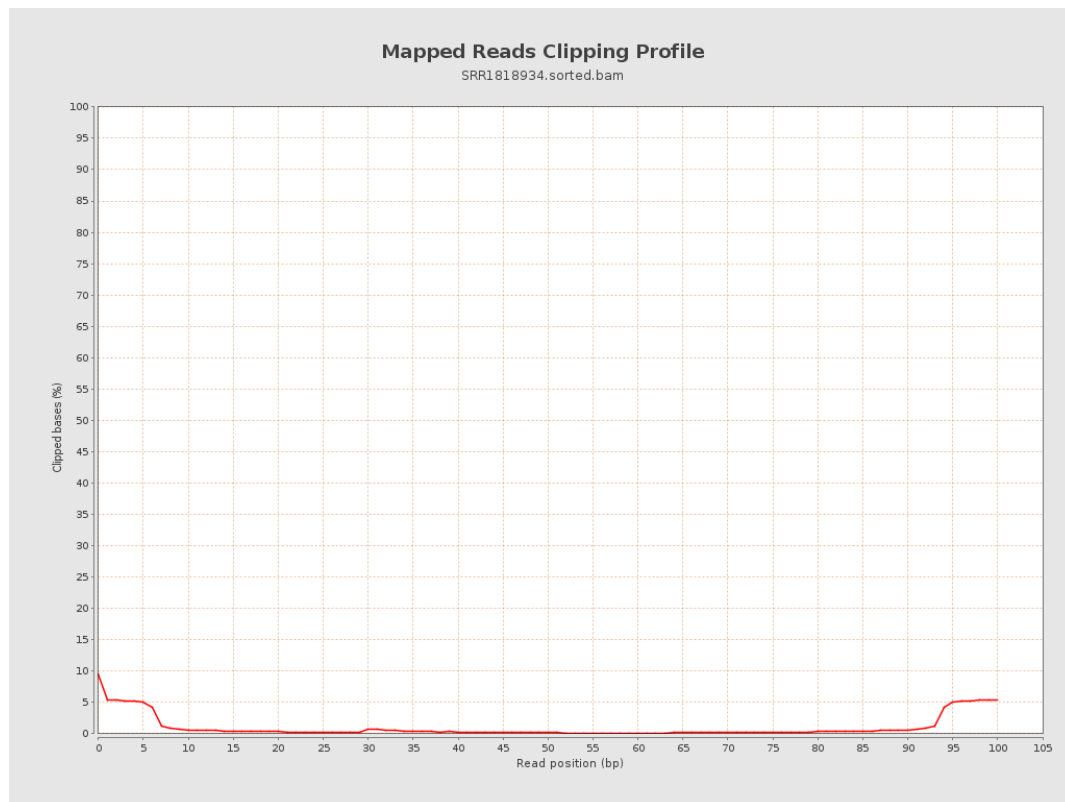
8. Results : Mapped Reads Nucleotide Content



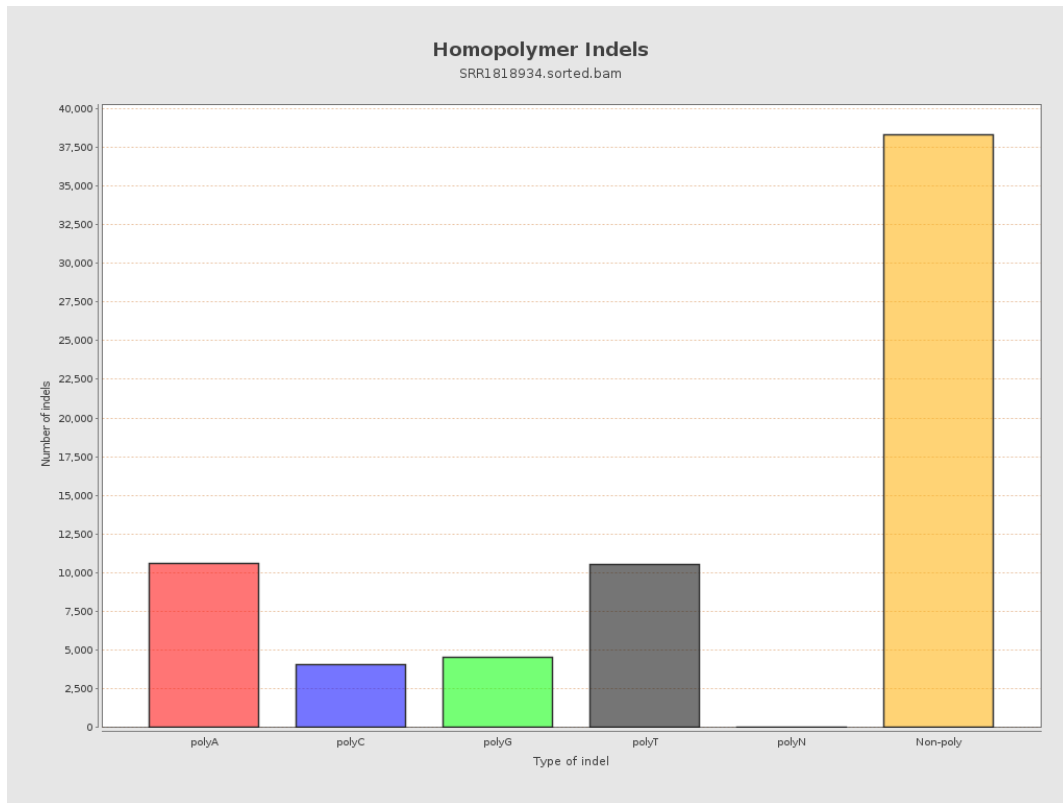
9. Results : Mapped Reads GC-content Distribution



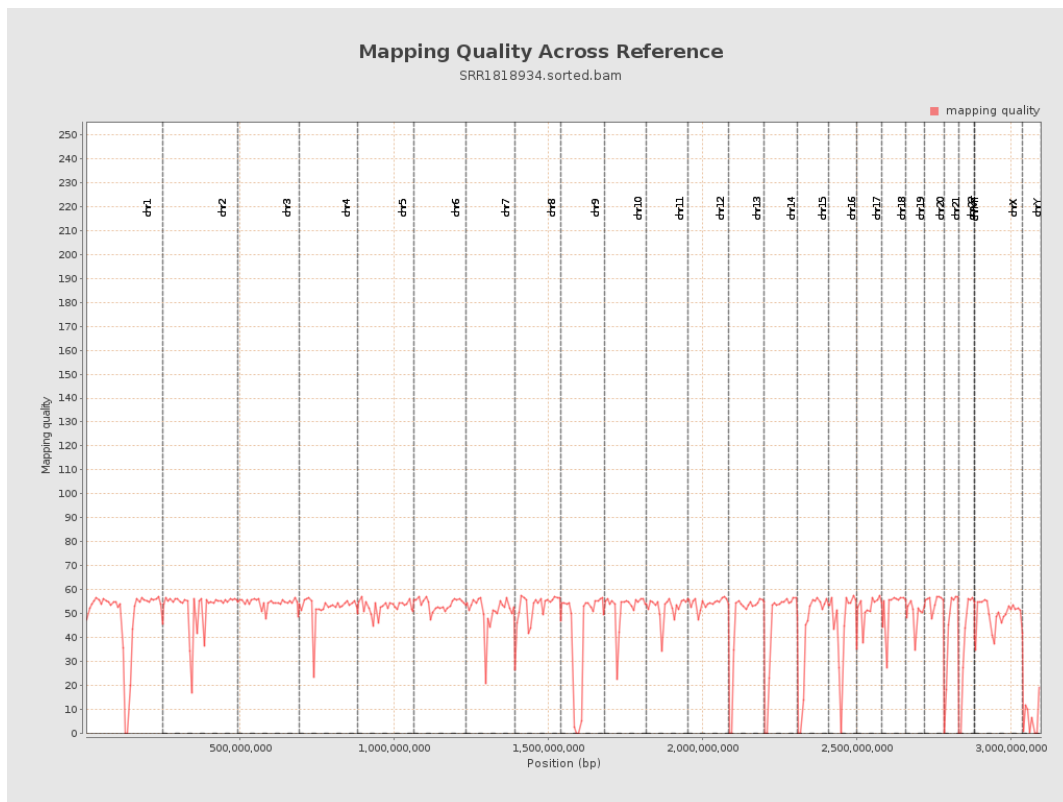
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

