

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 21:00:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004018.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_SRR6004018 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004018.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 21:00:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004018.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,010,153
Mapped reads	2,096,292 / 69.64%
Unmapped reads	913,861 / 30.36%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,805 / 0.43%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	588,463 / 19.55%
Duplication rate	17.4%
Clipped reads	1,538,992 / 51.13%

2.2. ACGT Content

Number/percentage of A's	34,224,545 / 27.35%
Number/percentage of C's	22,198,320 / 17.74%
Number/percentage of T's	41,546,994 / 33.2%
Number/percentage of G's	27,132,262 / 21.68%
Number/percentage of N's	22,488 / 0.02%
GC Percentage	39.43%

2.3. Coverage

Mean	0.0404

Standard Deviation	0.797
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2.4. Mapping Quality

Mean Mapping Quality	44.04
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2.5. Mismatches and indels

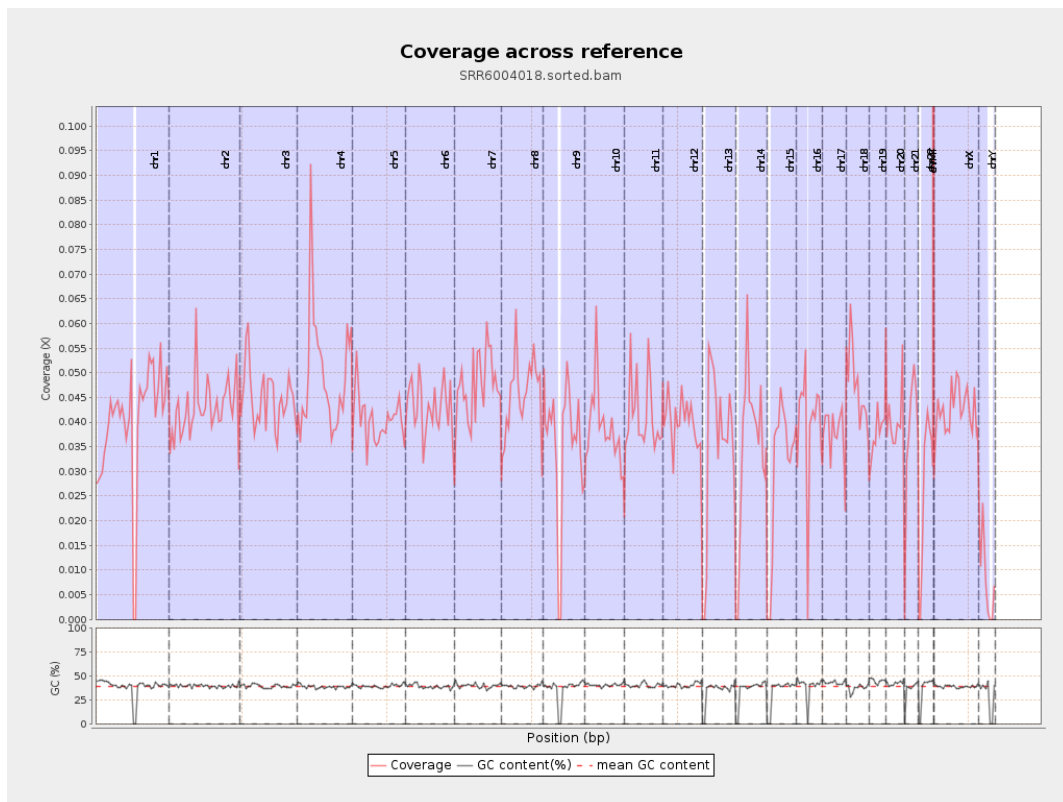
General error rate	1.1%
Mismatches	1,360,197
Insertions	11,700
Mapped reads with at least one insertion	0.55%
Deletions	38,278
Mapped reads with at least one deletion	1.8%
Homopolymer indels	47.09%

2.6. Chromosome stats

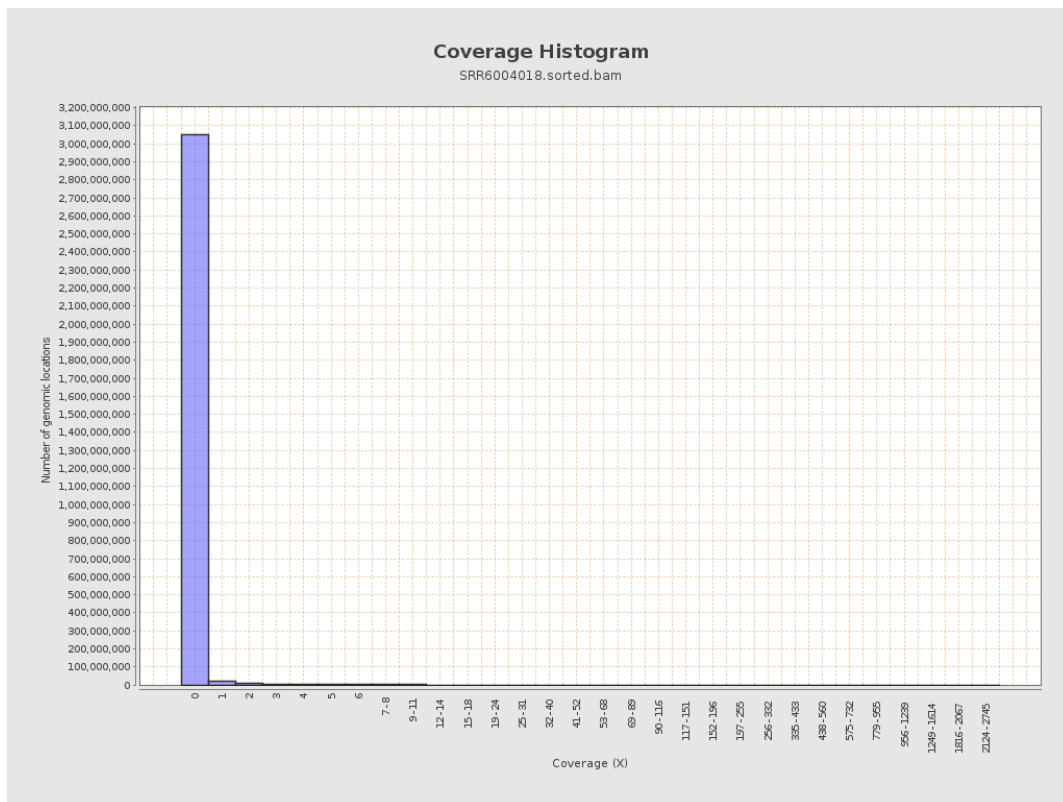
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	10050589	0.0403	0.5667
chr2	243199373	10421600	0.0429	0.888
chr3	198022430	8939668	0.0451	0.5677
chr4	191154276	9390636	0.0491	0.5779
chr5	180915260	7310872	0.0404	0.4929
chr6	171115067	7321909	0.0428	0.8572
chr7	159138663	7631440	0.048	0.8361

chr8	146364022	6666294	0.0455	0.7245
chr9	141213431	4963910	0.0352	0.4718
chr10	135534747	5252488	0.0388	0.5168
chr11	135006516	5581024	0.0413	0.4956
chr12	133851895	5319806	0.0397	0.5871
chr13	115169878	4049448	0.0352	0.7758
chr14	107349540	3757953	0.035	0.4592
chr15	102531392	3144839	0.0307	0.4654
chr16	90354753	3551643	0.0393	0.5134
chr17	81195210	3022310	0.0372	0.4522
chr18	78077248	3717070	0.0476	3.222
chr19	59128983	2258413	0.0382	0.5105
chr20	63025520	2526662	0.0401	0.5101
chr21	48129895	1822092	0.0379	0.4655
chr22	51304566	1351724	0.0263	0.3608
chrMT	16571	125021	7.5446	7.9768
chrX	155270560	6538806	0.0421	0.52
chrY	59373566	469102	0.0079	0.263

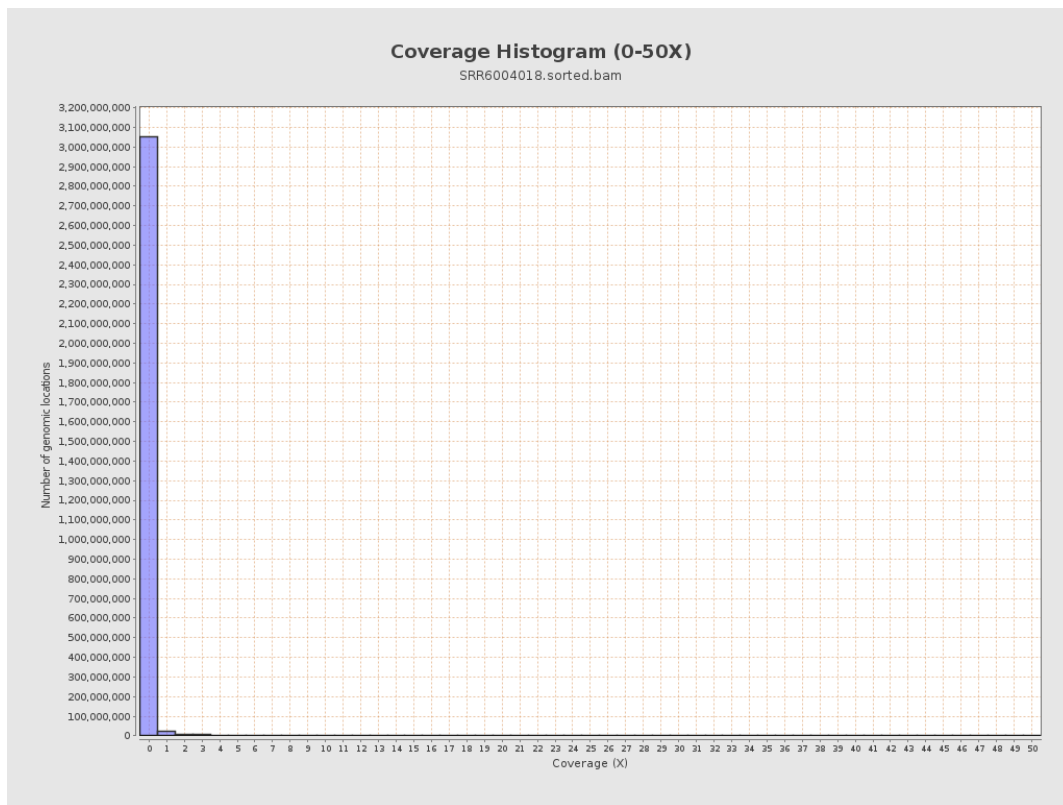
3. Results : Coverage across reference



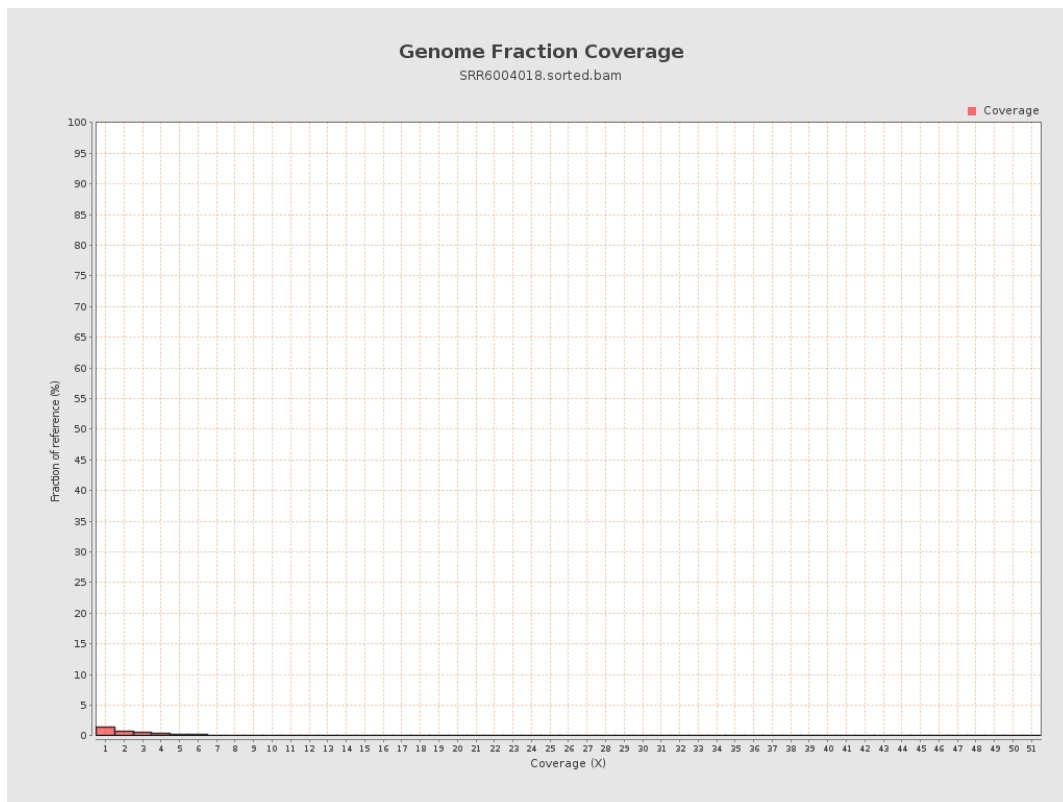
4. Results : Coverage Histogram



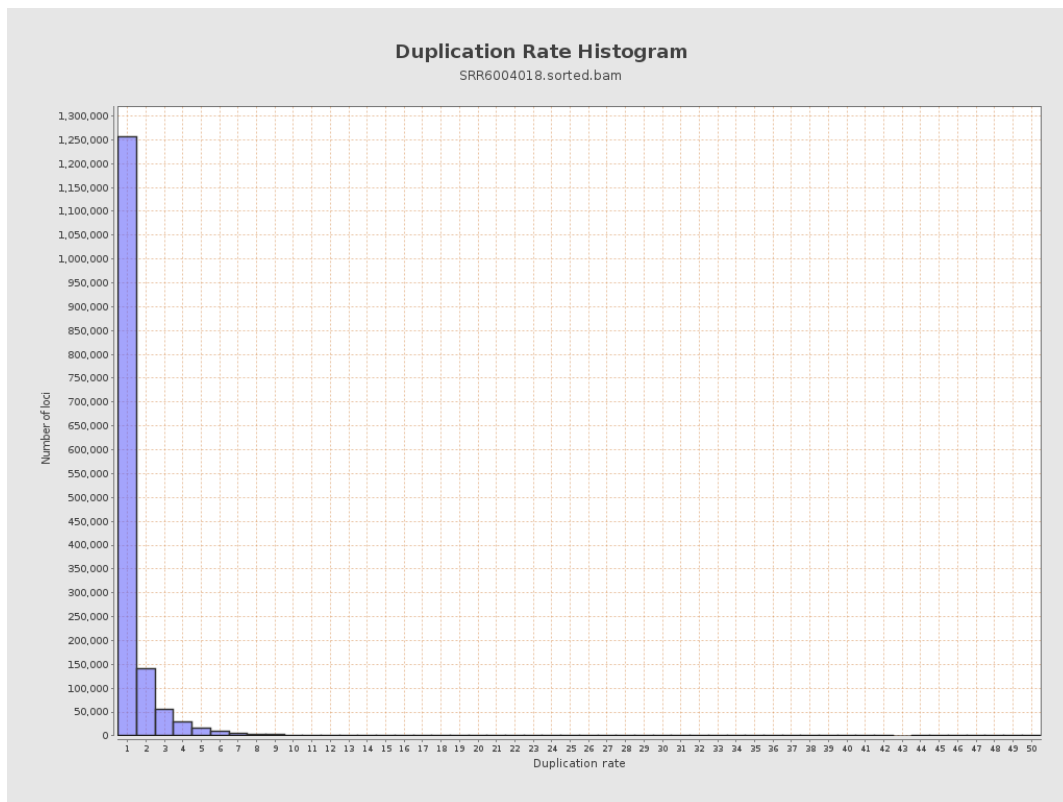
5. Results : Coverage Histogram (0-50X)



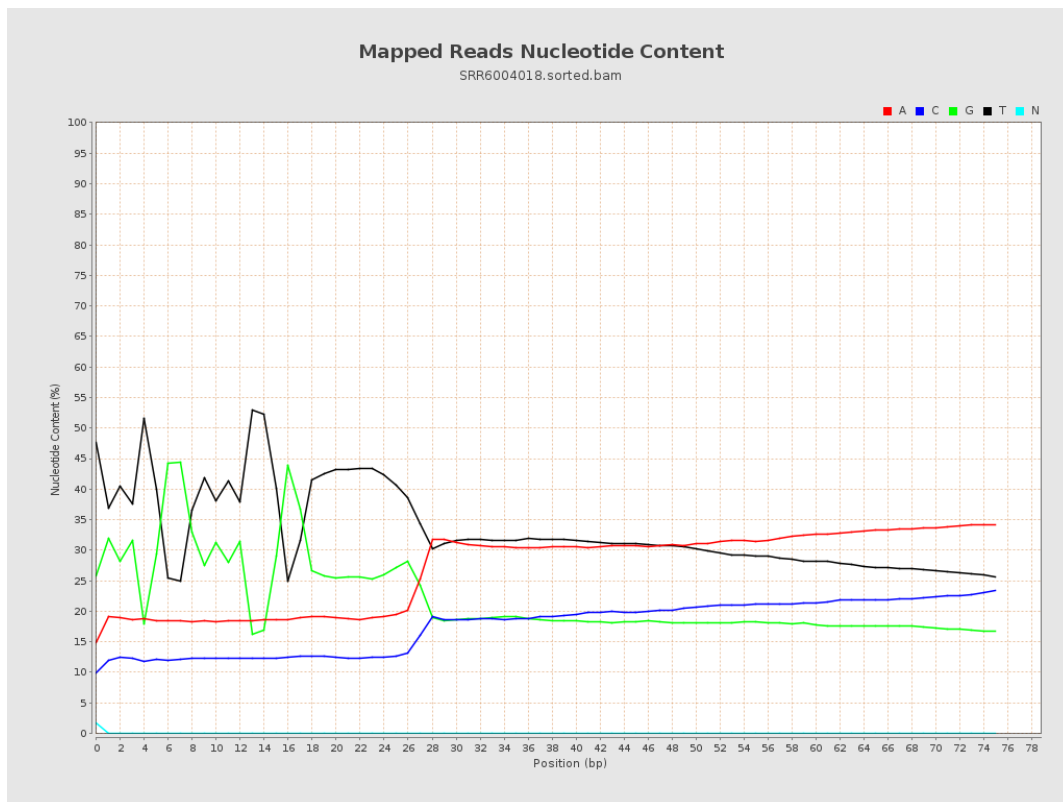
6. Results : Genome Fraction Coverage



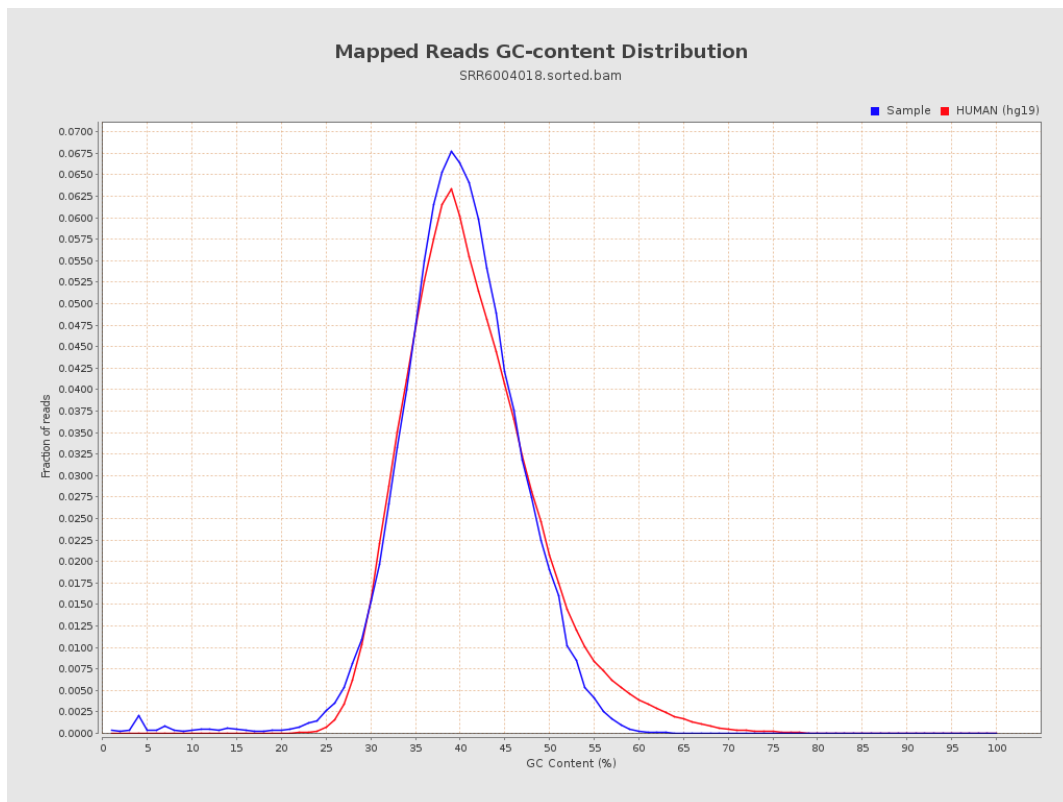
7. Results : Duplication Rate Histogram



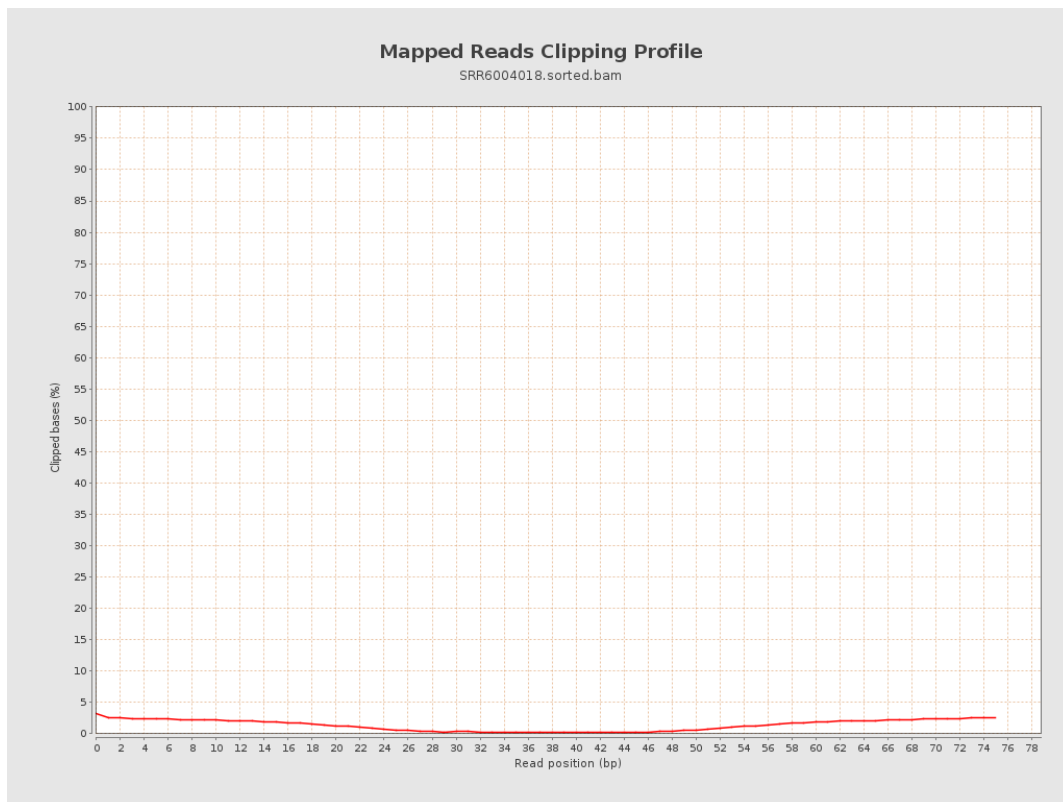
8. Results : Mapped Reads Nucleotide Content



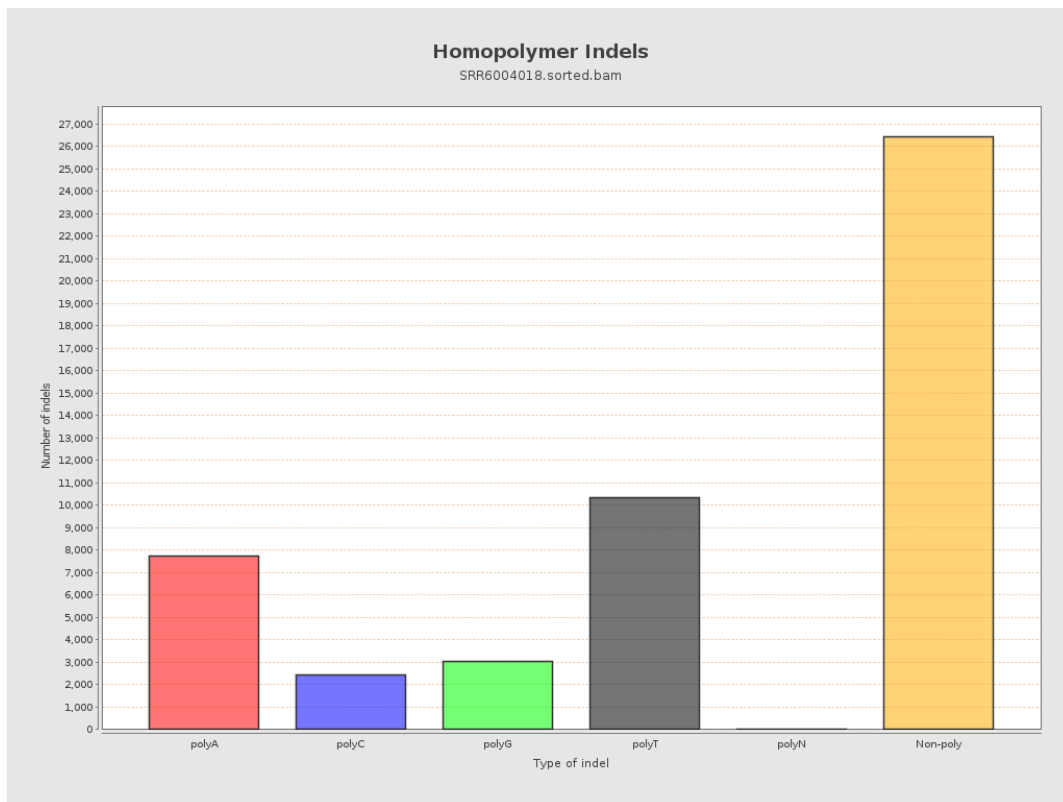
9. Results : Mapped Reads GC-content Distribution



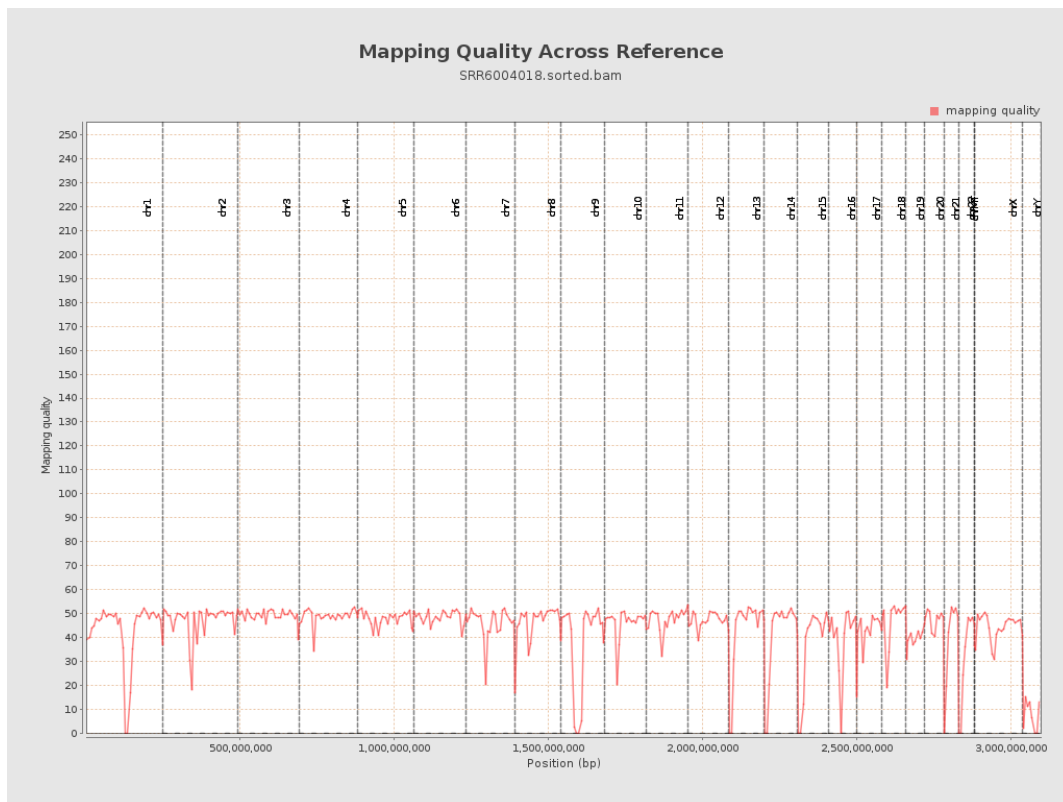
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

