

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/01 07:11:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472806.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_SRR3472806 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472806.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 01 07:11:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472806.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,947,015
Mapped reads	2,278,816 / 77.33%
Unmapped reads	668,199 / 22.67%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,086 / 0.58%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	191,805 / 6.51%
Duplication rate	5.94%
Clipped reads	1,394,028 / 47.3%

2.2. ACGT Content

Number/percentage of A's	38,377,171 / 26.93%
Number/percentage of C's	27,452,293 / 19.27%
Number/percentage of T's	42,895,578 / 30.11%
Number/percentage of G's	33,754,413 / 23.69%
Number/percentage of N's	3,264 / 0%
GC Percentage	42.96%

2.3. Coverage

Mean	0.046

Standard Deviation	0.3839
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2.4. Mapping Quality

Mean Mapping Quality	43.1
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2.5. Mismatches and indels

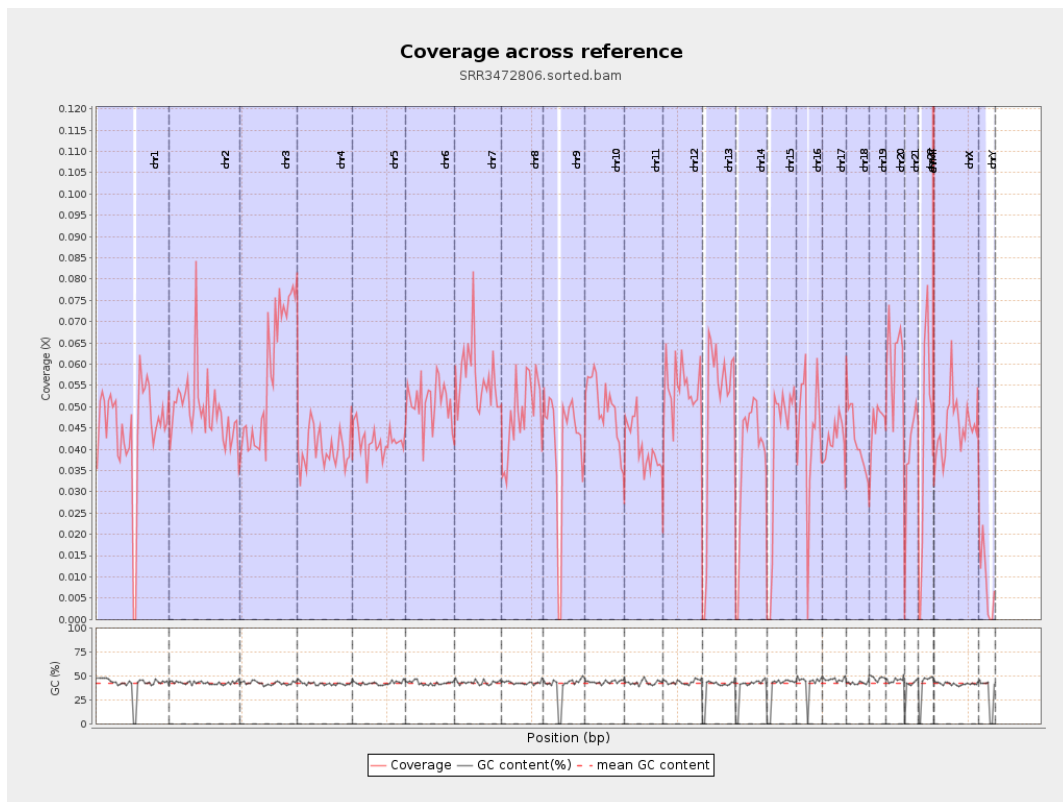
General error rate	0.9%
Mismatches	1,263,445
Insertions	10,732
Mapped reads with at least one insertion	0.47%
Deletions	38,784
Mapped reads with at least one deletion	1.68%
Homopolymer indels	46.55%

2.6. Chromosome stats

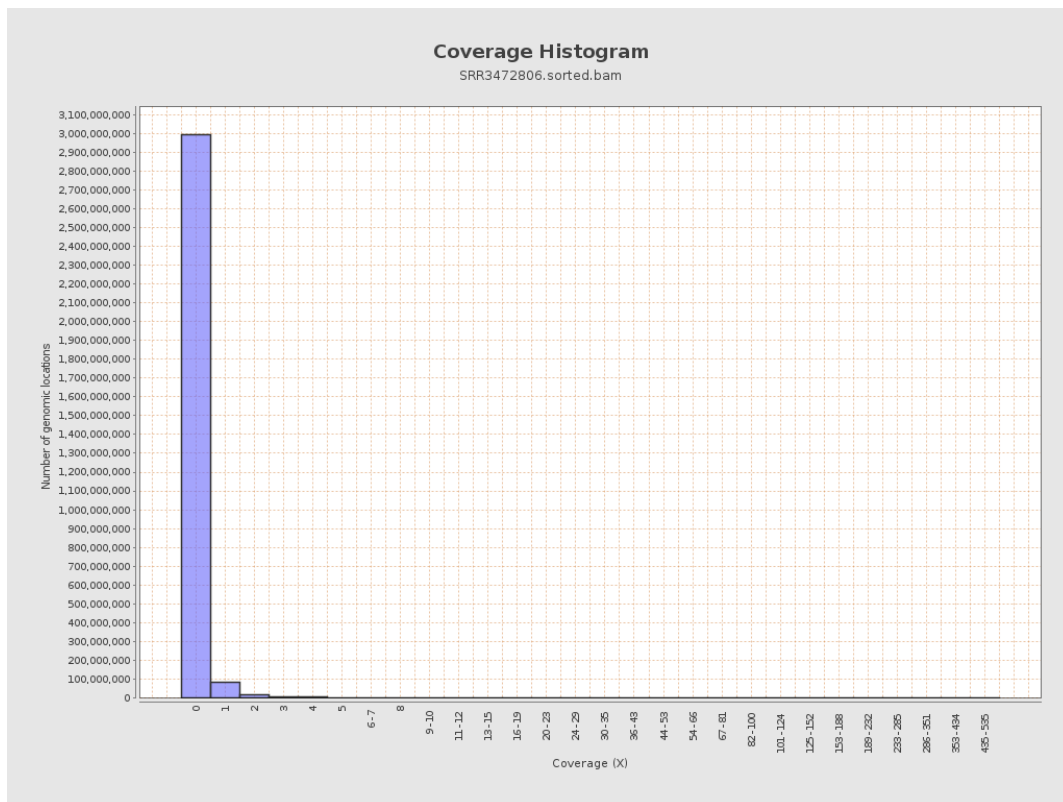
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	11078529	0.0444	0.4357
chr2	243199373	11947210	0.0491	0.4962
chr3	198022430	11328441	0.0572	0.3328
chr4	191154276	7659615	0.0401	0.3028
chr5	180915260	7554996	0.0418	0.2995
chr6	171115067	8688779	0.0508	0.3592
chr7	159138663	9021387	0.0567	0.5507

chr8	146364022	6999795	0.0478	0.3886
chr9	141213431	5806029	0.0411	0.3903
chr10	135534747	6779276	0.05	0.3712
chr11	135006516	5459728	0.0404	0.384
chr12	133851895	7269585	0.0543	0.3416
chr13	115169878	5669606	0.0492	0.322
chr14	107349540	4118190	0.0384	0.3218
chr15	102531392	4143756	0.0404	0.3242
chr16	90354753	4002821	0.0443	0.3179
chr17	81195210	3408261	0.042	0.3206
chr18	78077248	3325399	0.0426	0.5732
chr19	59128983	2710221	0.0458	0.3798
chr20	63025520	3880862	0.0616	0.3682
chr21	48129895	1891470	0.0393	0.3086
chr22	51304566	2117766	0.0413	0.2872
chrMT	16571	189505	11.4359	8.4475
chrX	155270560	7007836	0.0451	0.3372
chrY	59373566	493319	0.0083	0.1413

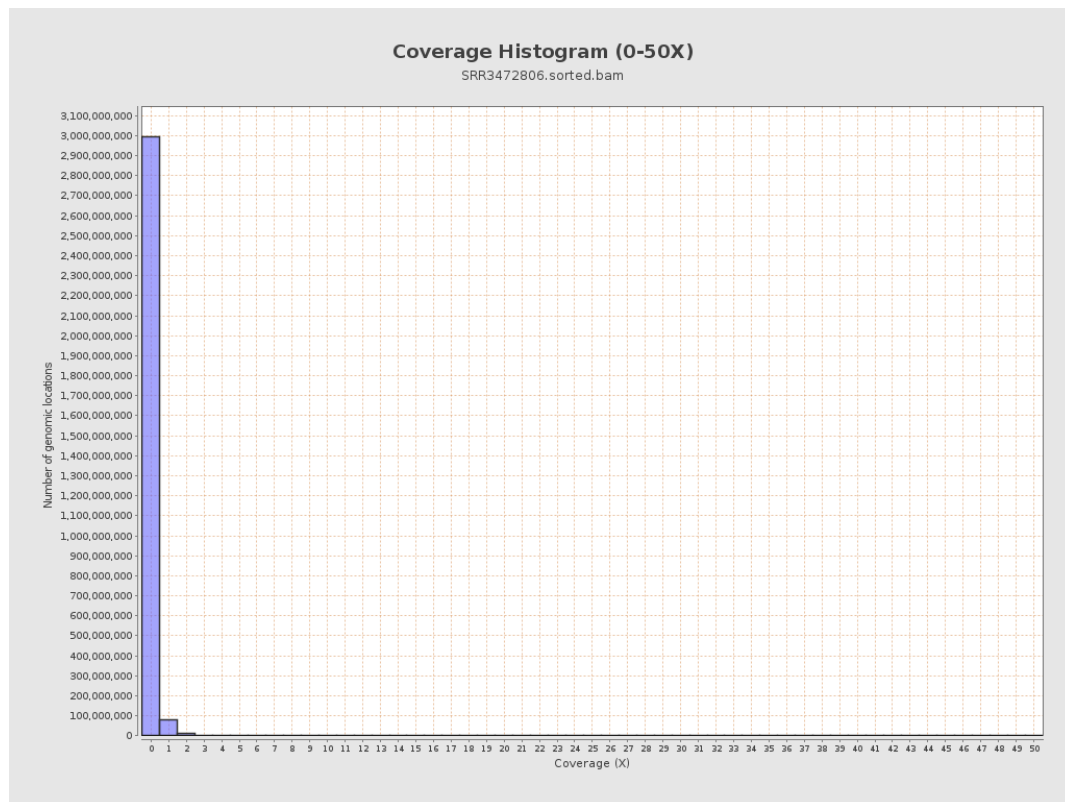
3. Results : Coverage across reference



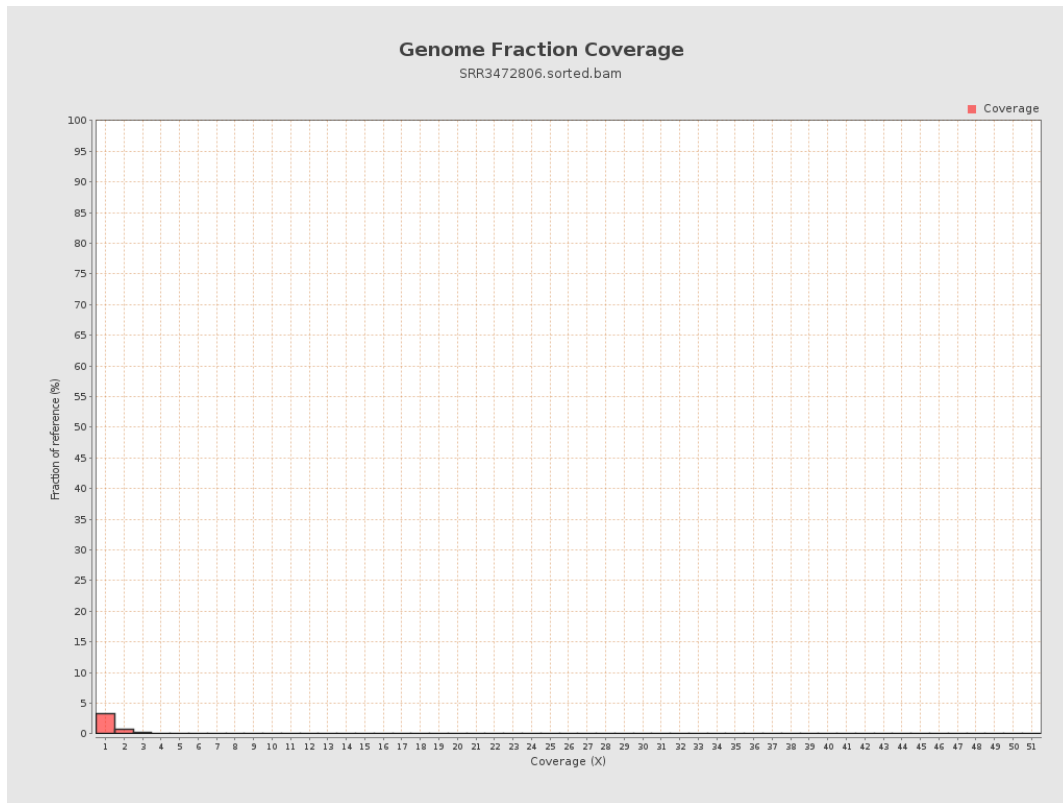
4. Results : Coverage Histogram



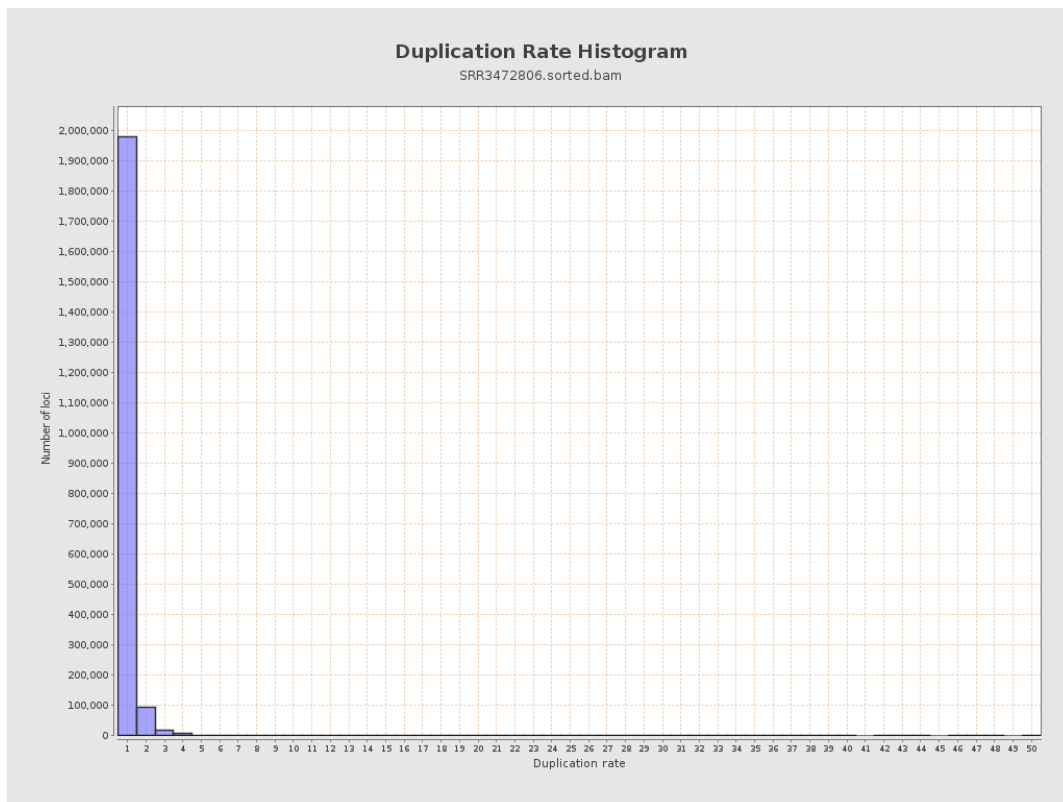
5. Results : Coverage Histogram (0-50X)



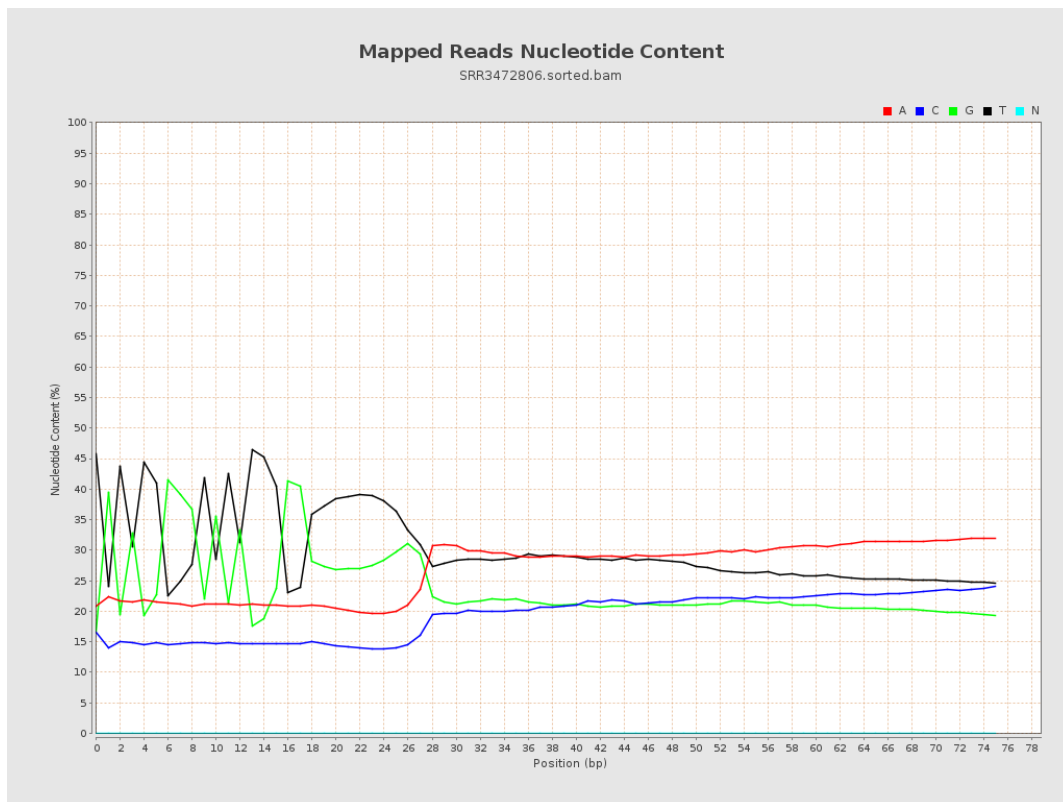
6. Results : Genome Fraction Coverage



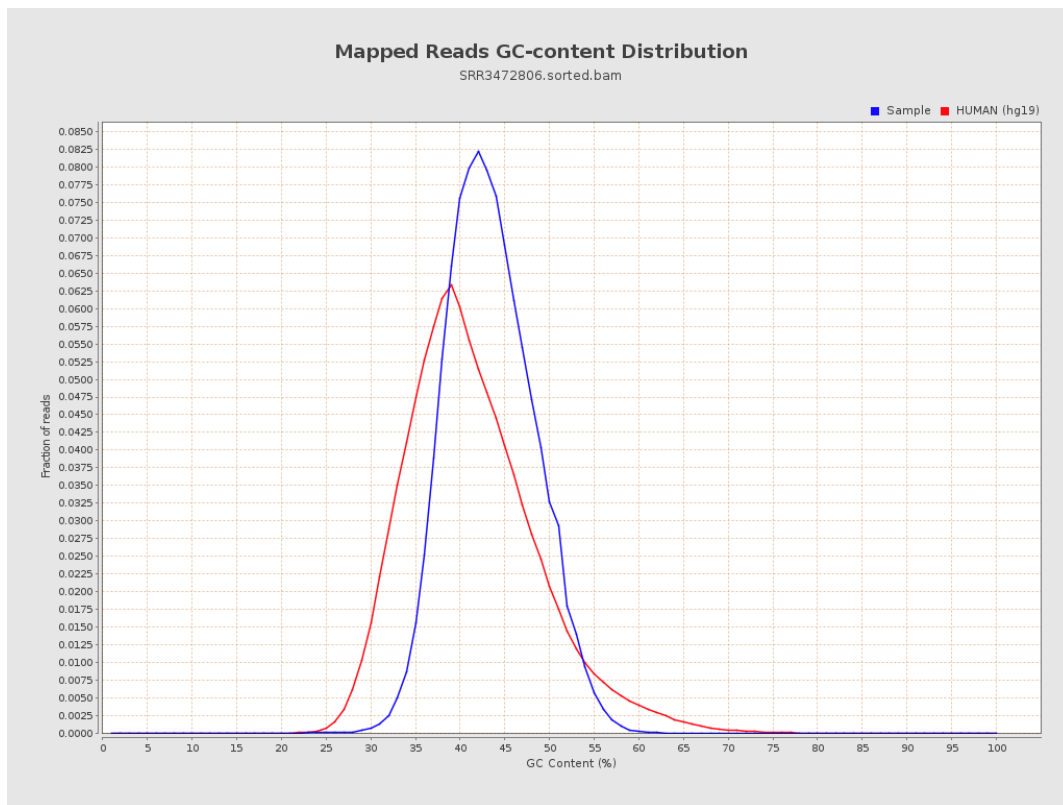
7. Results : Duplication Rate Histogram



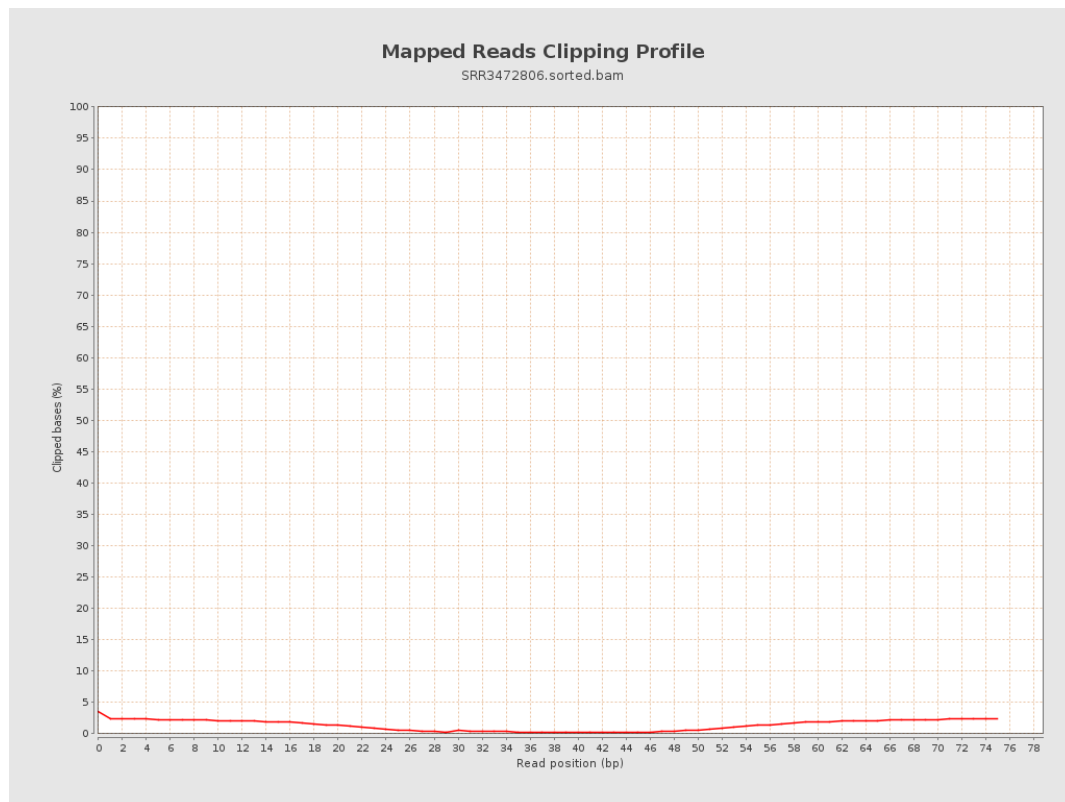
8. Results : Mapped Reads Nucleotide Content



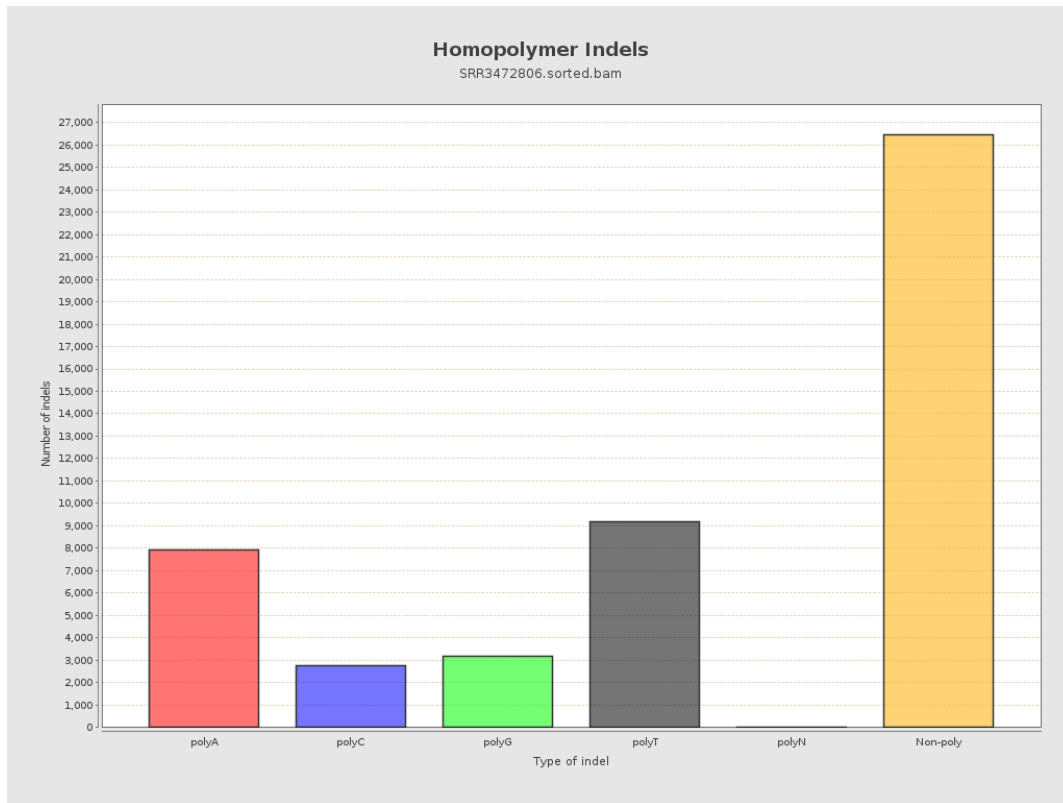
9. Results : Mapped Reads GC-content Distribution



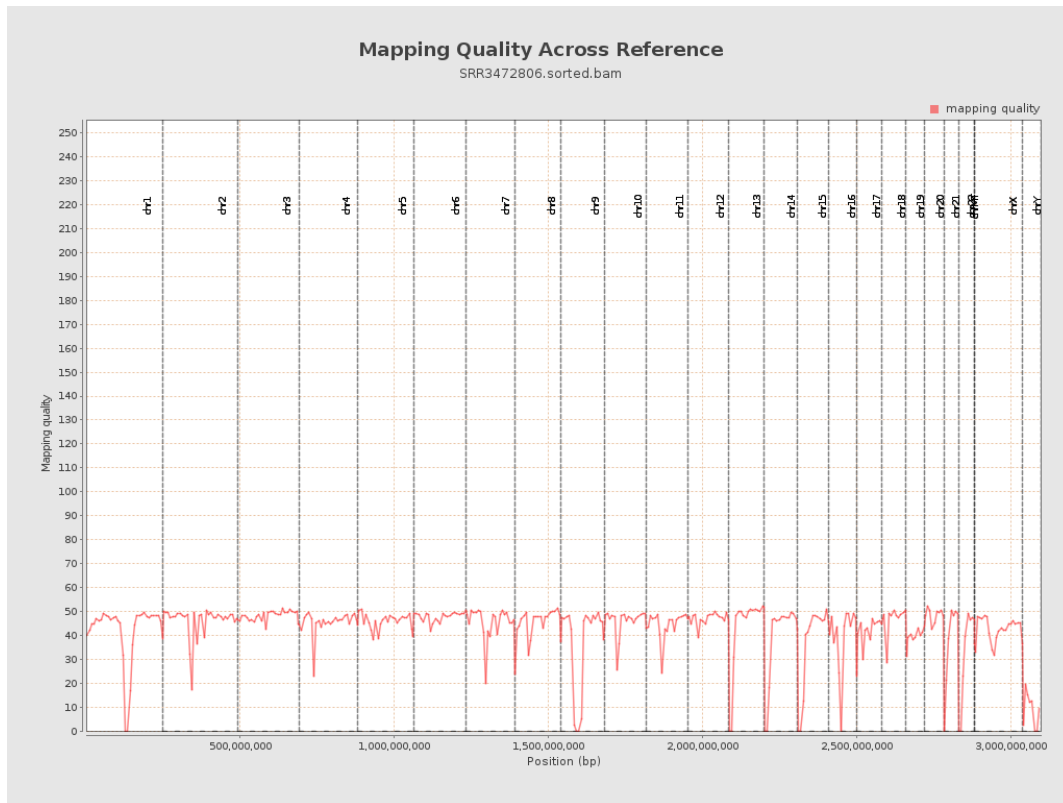
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

