

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/01 08:33:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472823.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_SRR3472823 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472823.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 01 08:33:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472823.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,984,005
Mapped reads	2,196,367 / 73.6%
Unmapped reads	787,638 / 26.4%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,625 / 0.56%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	243,369 / 8.16%
Duplication rate	7.4%
Clipped reads	1,444,067 / 48.39%

2.2. ACGT Content

Number/percentage of A's	35,754,925 / 26.5%
Number/percentage of C's	26,172,900 / 19.4%
Number/percentage of T's	40,449,515 / 29.98%
Number/percentage of G's	32,540,269 / 24.12%
Number/percentage of N's	2,549 / 0%
GC Percentage	43.52%

2.3. Coverage

Mean	0.0436

Standard Deviation	0.4162
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2.4. Mapping Quality

Mean Mapping Quality	42.19
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2.5. Mismatches and indels

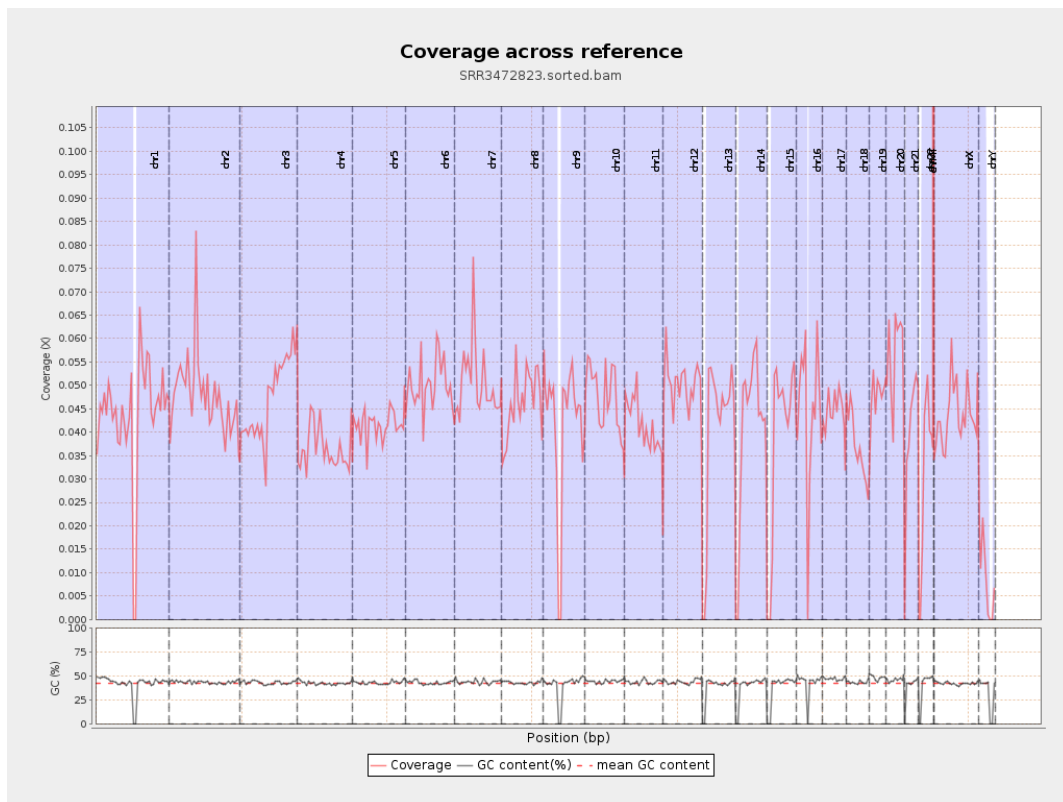
General error rate	0.93%
Mismatches	1,240,569
Insertions	10,061
Mapped reads with at least one insertion	0.45%
Deletions	37,644
Mapped reads with at least one deletion	1.69%
Homopolymer indels	46.4%

2.6. Chromosome stats

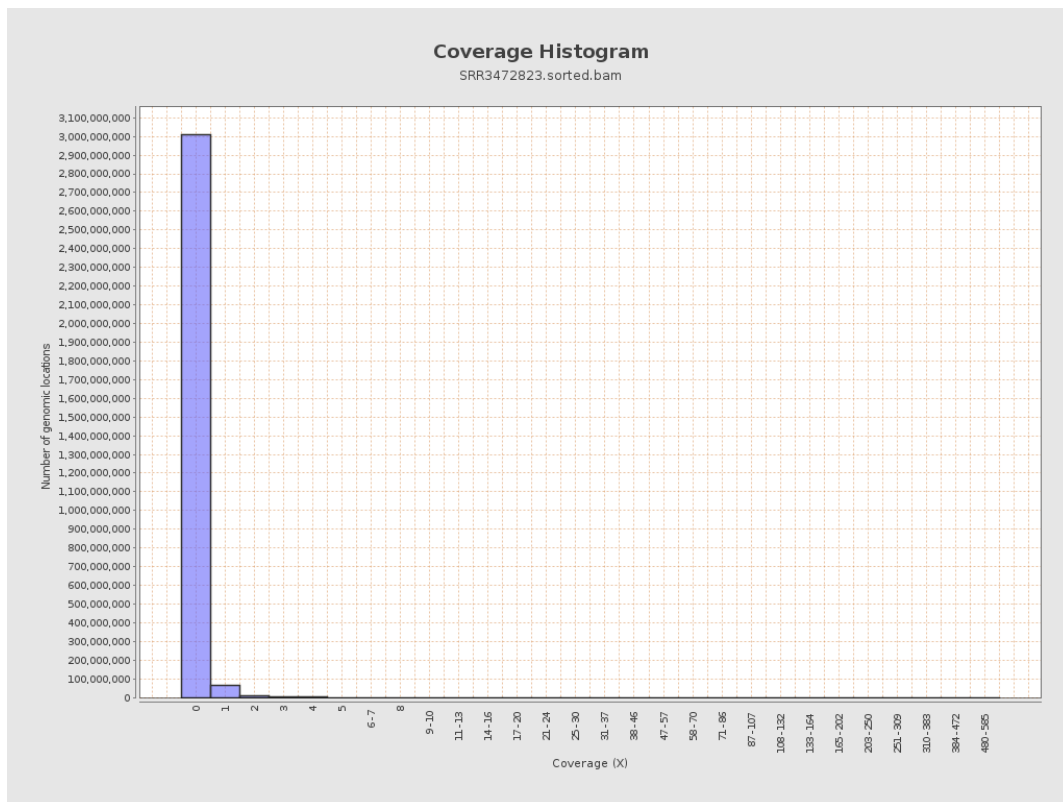
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	10870830	0.0436	0.4813
chr2	243199373	11680677	0.048	0.501
chr3	198022430	9269655	0.0468	0.3365
chr4	191154276	6963949	0.0364	0.3281
chr5	180915260	7513054	0.0415	0.3321
chr6	171115067	8551615	0.05	0.3868
chr7	159138663	8061880	0.0507	0.6306

chr8	146364022	6740623	0.0461	0.4028
chr9	141213431	5813570	0.0412	0.4254
chr10	135534747	6458590	0.0477	0.3983
chr11	135006516	5581209	0.0413	0.4253
chr12	133851895	6706397	0.0501	0.3838
chr13	115169878	4648905	0.0404	0.3326
chr14	107349540	4361582	0.0406	0.3764
chr15	102531392	3997962	0.039	0.3763
chr16	90354753	4013883	0.0444	0.3551
chr17	81195210	3588720	0.0442	0.3784
chr18	78077248	2901696	0.0372	0.5931
chr19	59128983	2835496	0.048	0.4353
chr20	63025520	3547032	0.0563	0.4114
chr21	48129895	1926940	0.04	0.3387
chr22	51304566	1550990	0.0302	0.2935
chrMT	16571	191593	11.5619	9.0443
chrX	155270560	6729481	0.0433	0.3654
chrY	59373566	482233	0.0081	0.1542

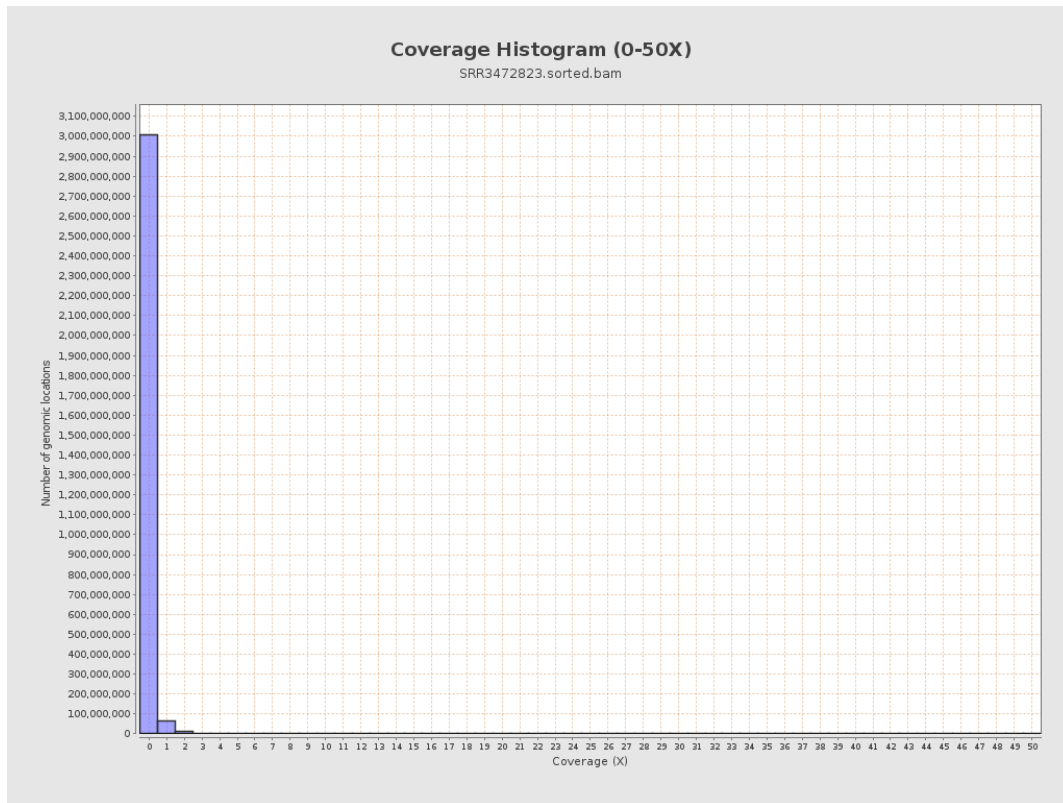
3. Results : Coverage across reference



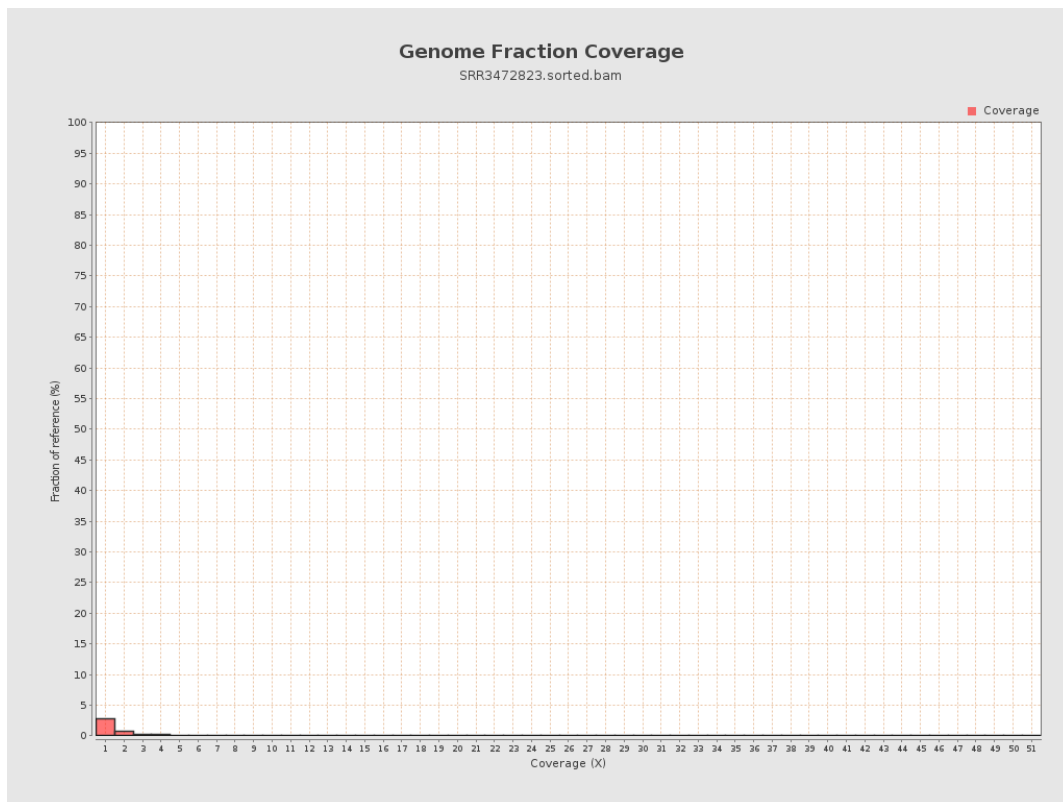
4. Results : Coverage Histogram



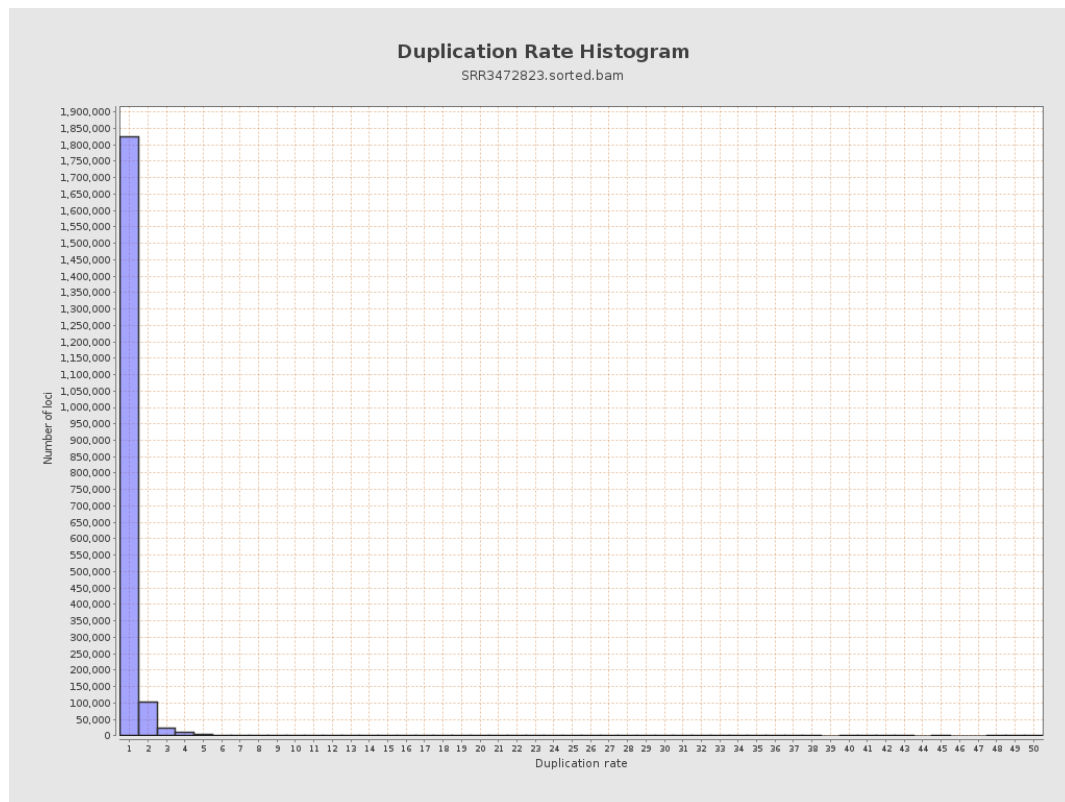
5. Results : Coverage Histogram (0-50X)



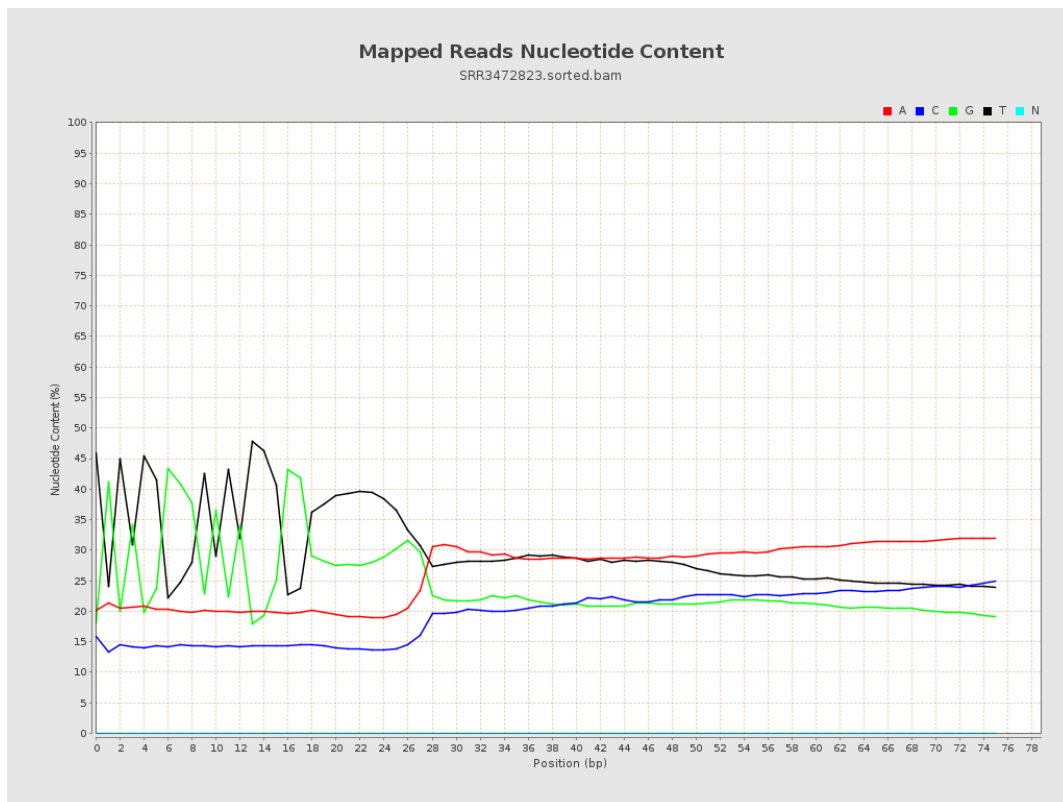
6. Results : Genome Fraction Coverage



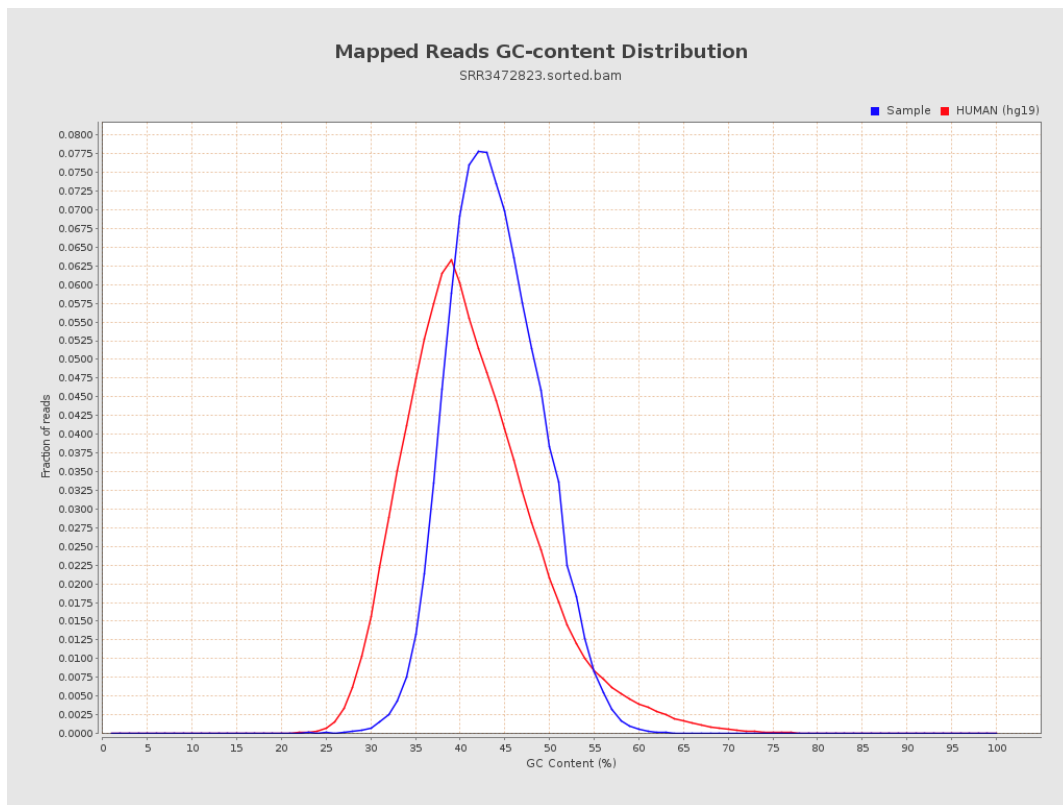
7. Results : Duplication Rate Histogram



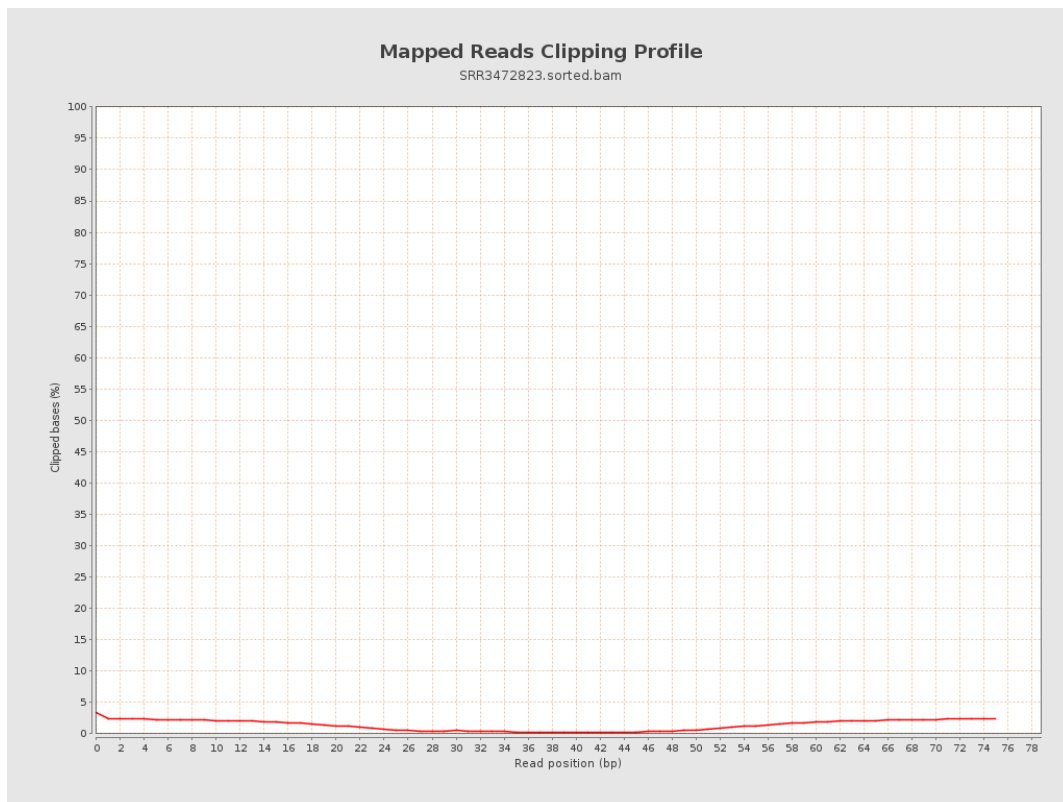
8. Results : Mapped Reads Nucleotide Content



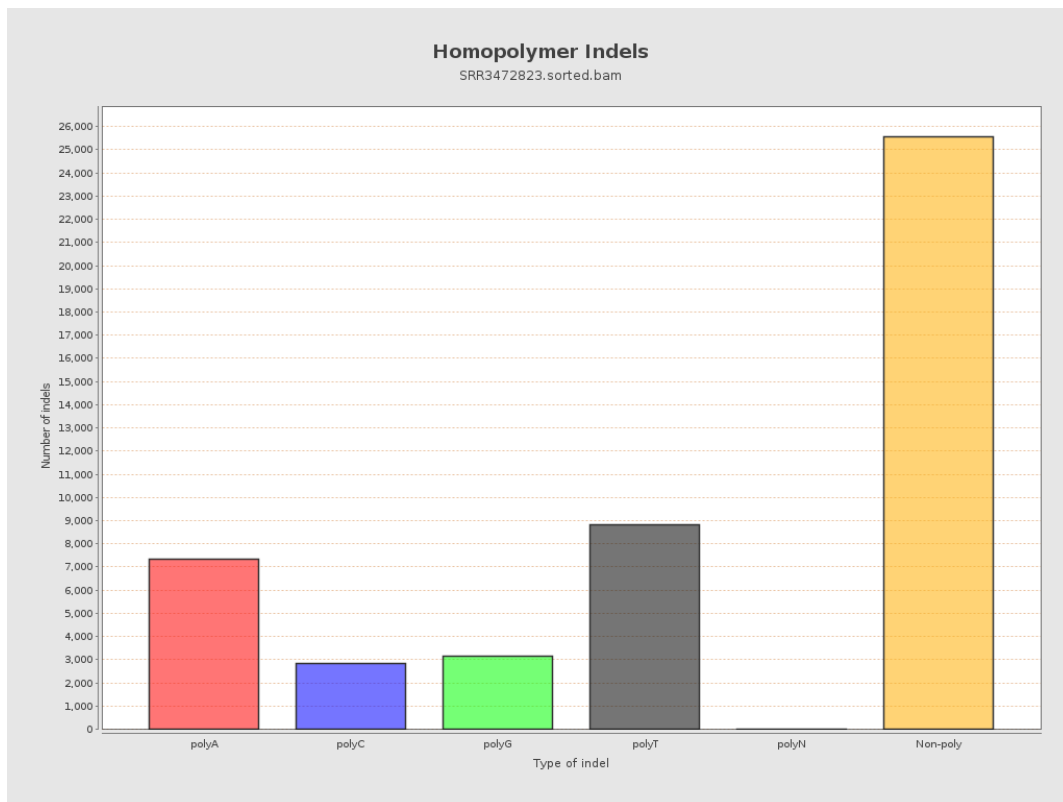
9. Results : Mapped Reads GC-content Distribution



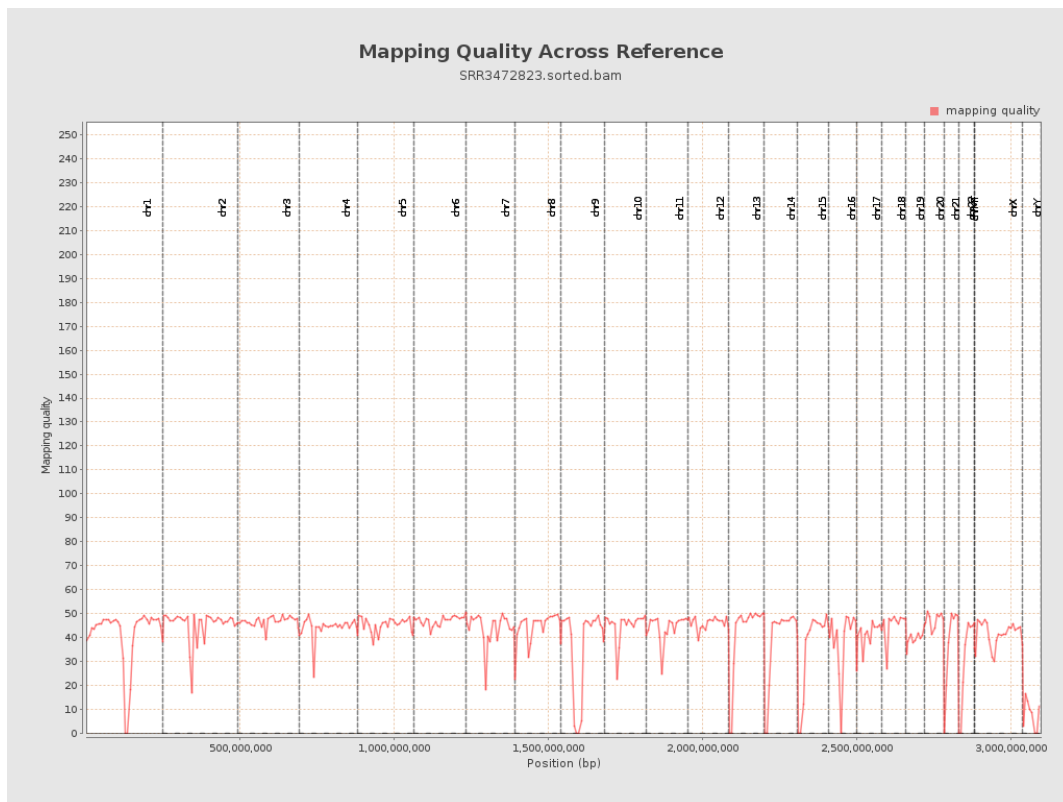
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

