Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 20:00:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082920.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_SRR3082920 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082920.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 20:00:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082920.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,963,180
Mapped reads	1,744,120 / 88.84%
Unmapped reads	219,060 / 11.16%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,195 / 0.98%
Read min/max/mean length	30 / 76 / 76.34
Duplicated reads (estimated)	91,407 / 4.66%
Duplication rate	4.45%
Clipped reads	797,618 / 40.63%

2.2. ACGT Content

Number/percentage of A's	31,154,032 / 26.9%
Number/percentage of C's	21,884,072 / 18.9%
Number/percentage of T's	36,250,288 / 31.3%
Number/percentage of G's	26,520,979 / 22.9%
Number/percentage of N's	4,916 / 0%
GC Percentage	41.8%

2.3. Coverage

Mean	0.0374

Standard Deviation	0.3008

2.4. Mapping Quality

Mean Mapping Quality	45.18

2.5. Mismatches and indels

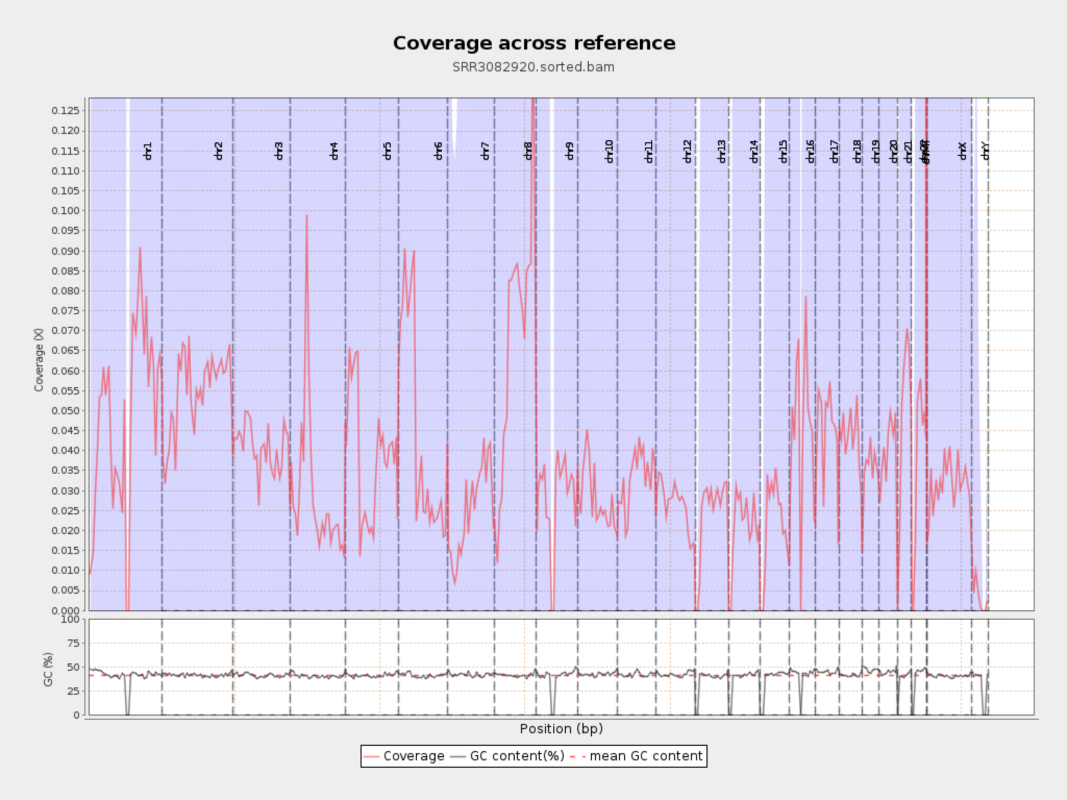
General error rate	0.75%
Mismatches	851,895
Insertions	9,328
Mapped reads with at least one insertion	0.53%
Deletions	26,980
Mapped reads with at least one deletion	1.53%
Homopolymer indels	47.65%

2.6. Chromosome stats

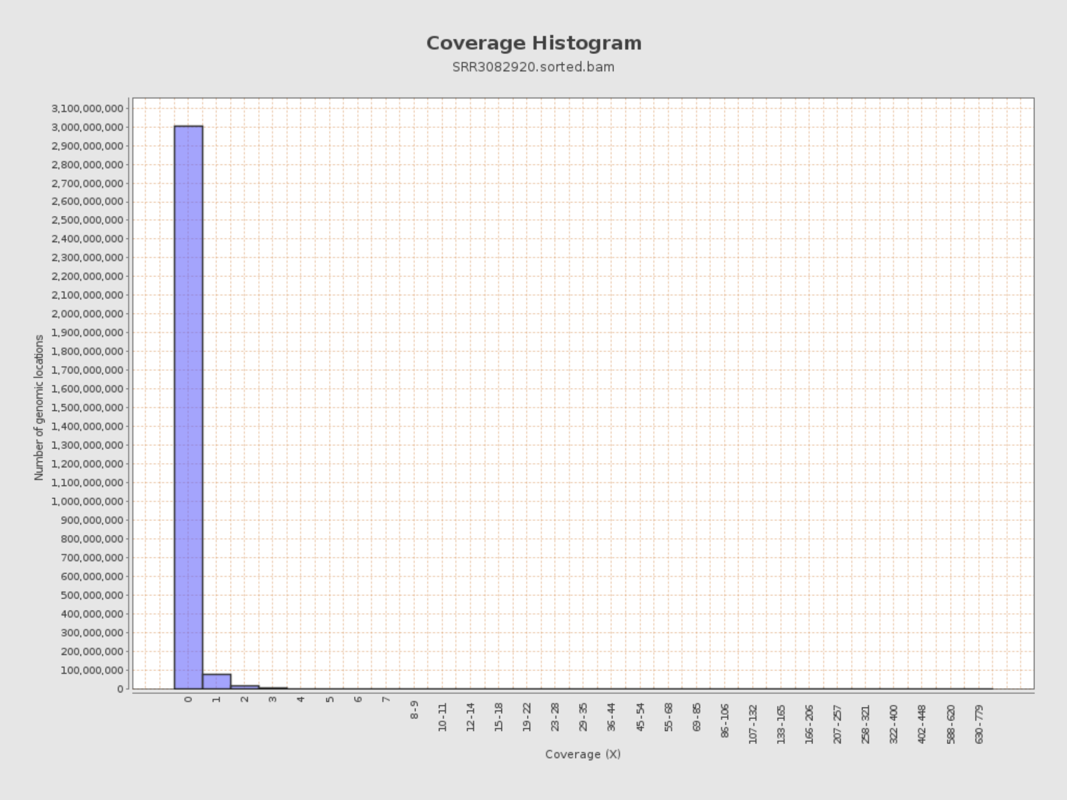
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12081157	0.0485	0.4773
chr2	243199373	13367565	0.055	0.4467
chr3	198022430	8068695	0.0407	0.2403
chr4	191154276	5489771	0.0287	0.2073
chr5	180915260	7036015	0.0389	0.2349
chr6	171115067	7583024	0.0443	0.3131
chr7	159138663	3981052	0.025	0.2412

chr8	146364022	10136196	0.0693	0.3542
chr9	141213431	4010917	0.0284	0.2683
chr10	135534747	3830533	0.0283	0.2232
chr11	135006516	4476142	0.0332	0.2577
chr12	133851895	3561124	0.0266	0.1955
chr13	115169878	2781322	0.0241	0.1862
chr14	107349540	2217625	0.0207	0.1792
chr15	102531392	2183921	0.0213	0.1838
chr16	90354753	4115168	0.0455	0.2633
chr17	81195210	3662819	0.0451	0.2823
chr18	78077248	3413452	0.0437	0.5206
chr19	59128983	2116855	0.0358	0.3281
chr20	63025520	2525411	0.0401	0.2449
chr21	48129895	2316549	0.0481	0.2658
chr22	51304566	1818156	0.0354	0.2246
chrMT	16571	10157	0.6129	1.0217
chrX	155270560	4862721	0.0313	0.2261
chrY	59373566	212250	0.0036	0.0771

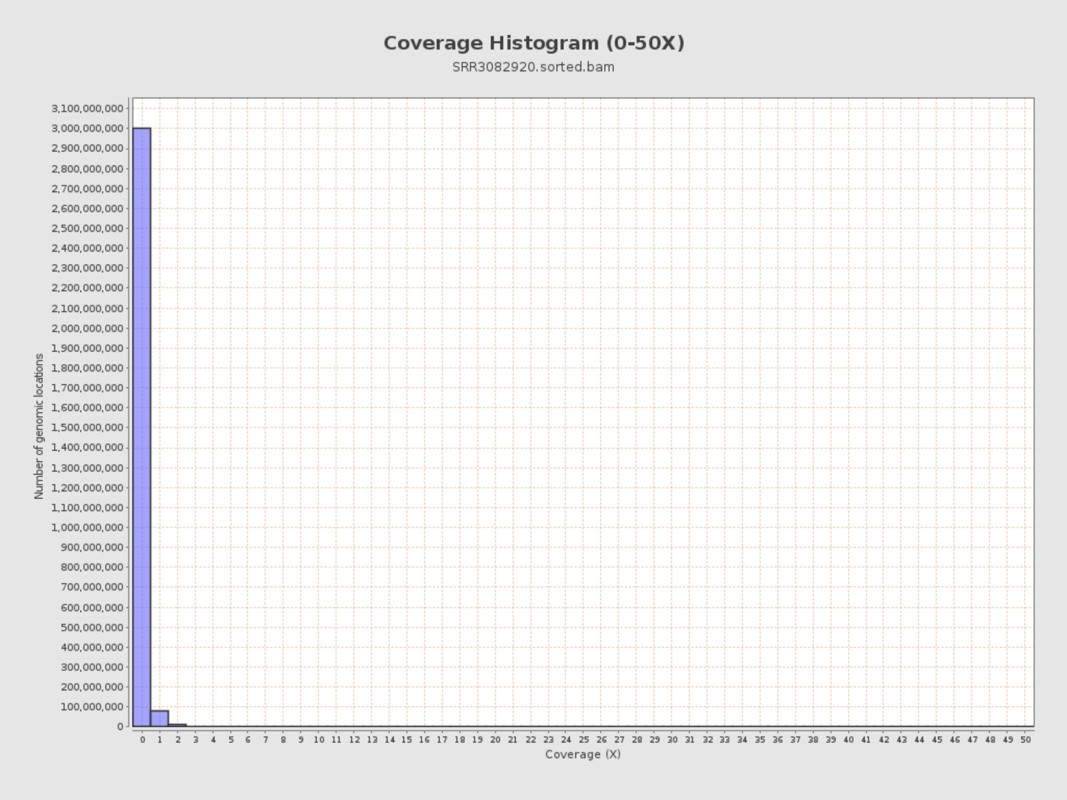
3. Results : Coverage across reference



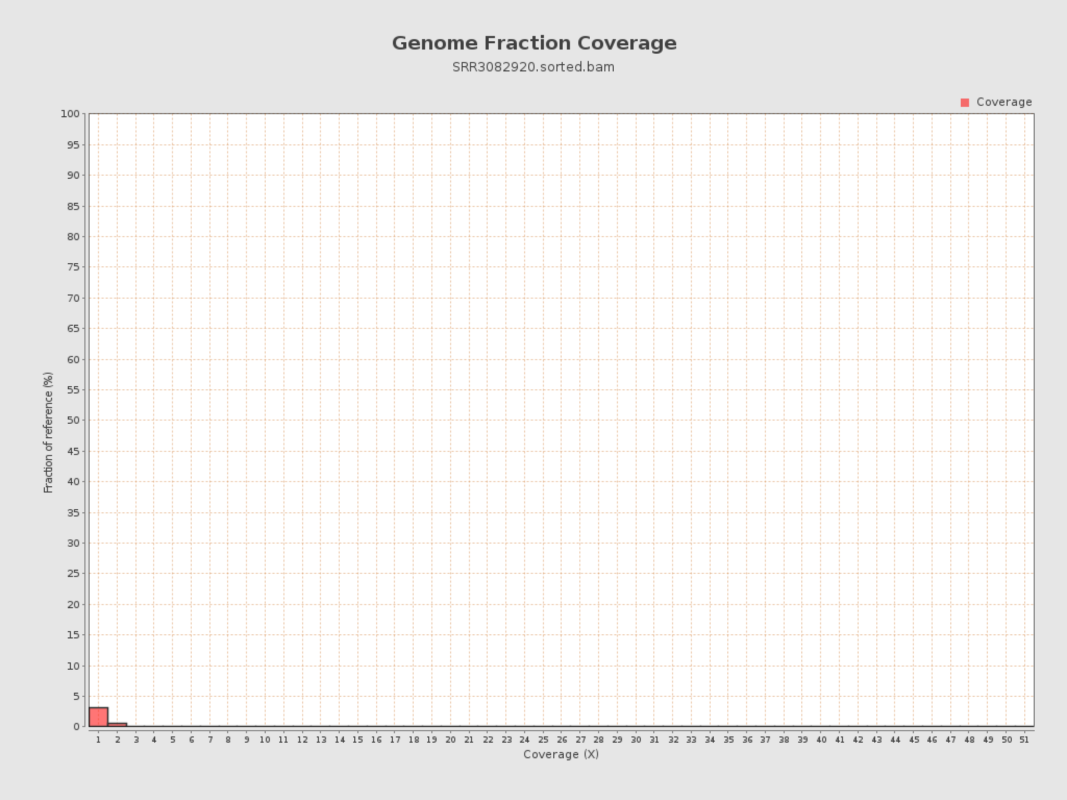
4. Results : Coverage Histogram



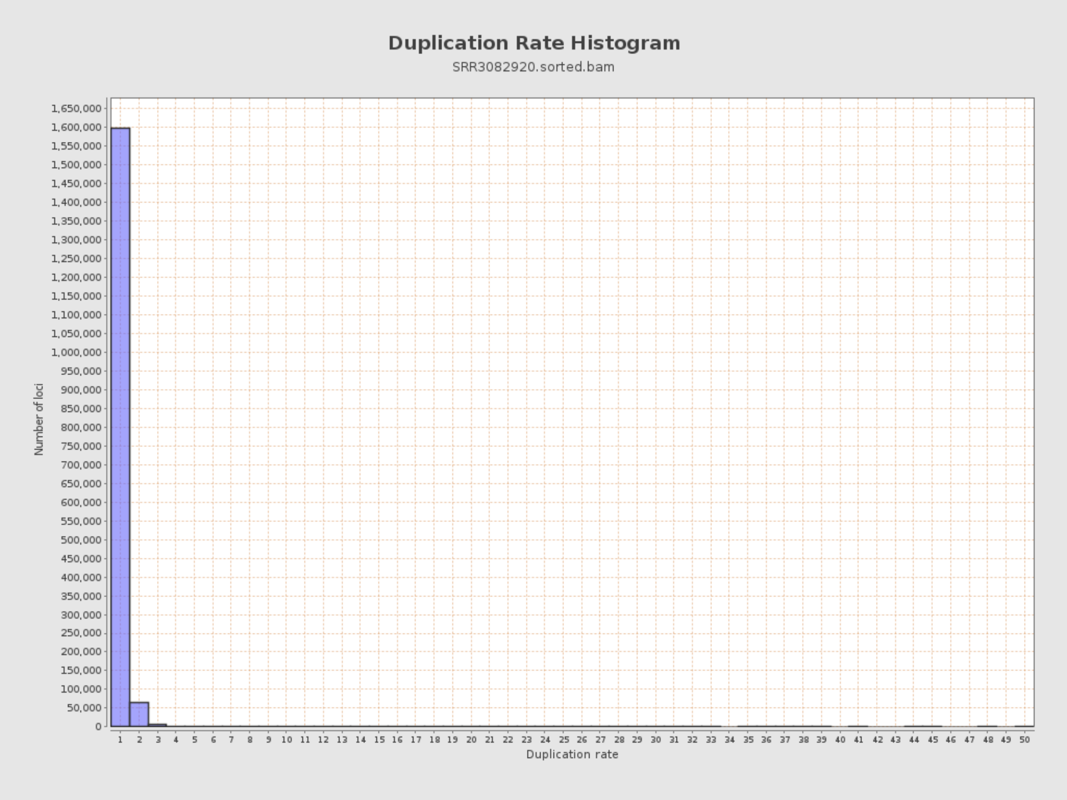
5. Results : Coverage Histogram (0-50X)



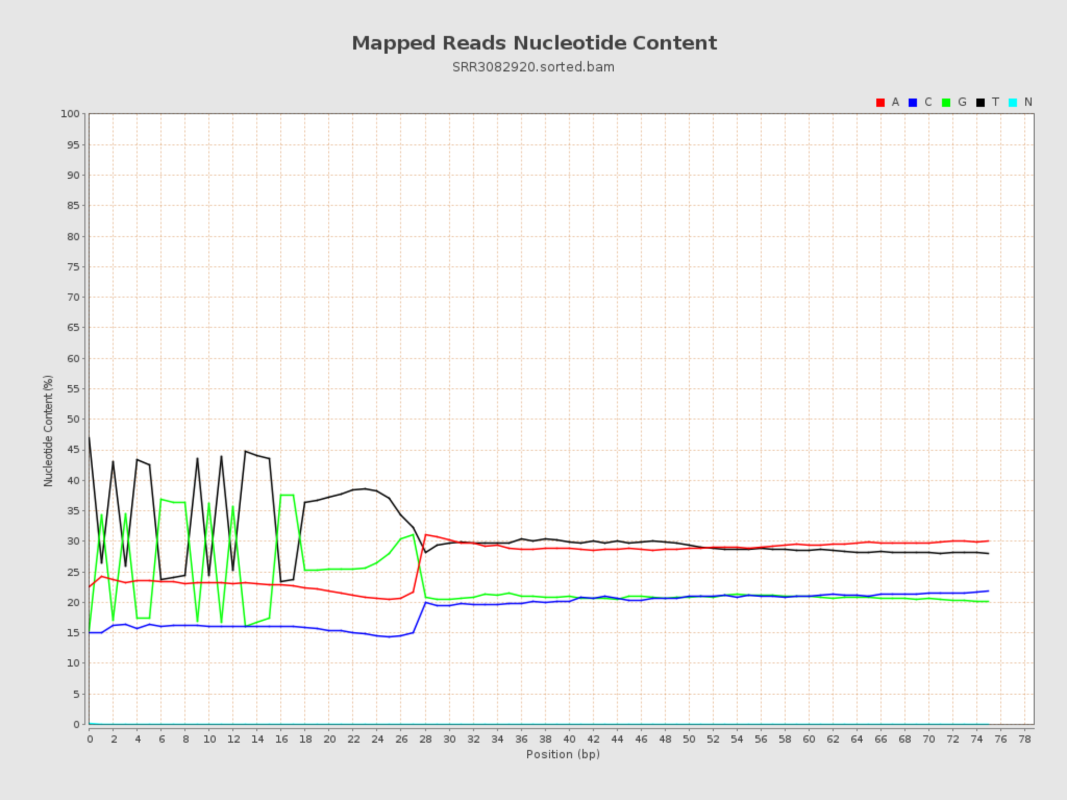
6. Results : Genome Fraction Coverage



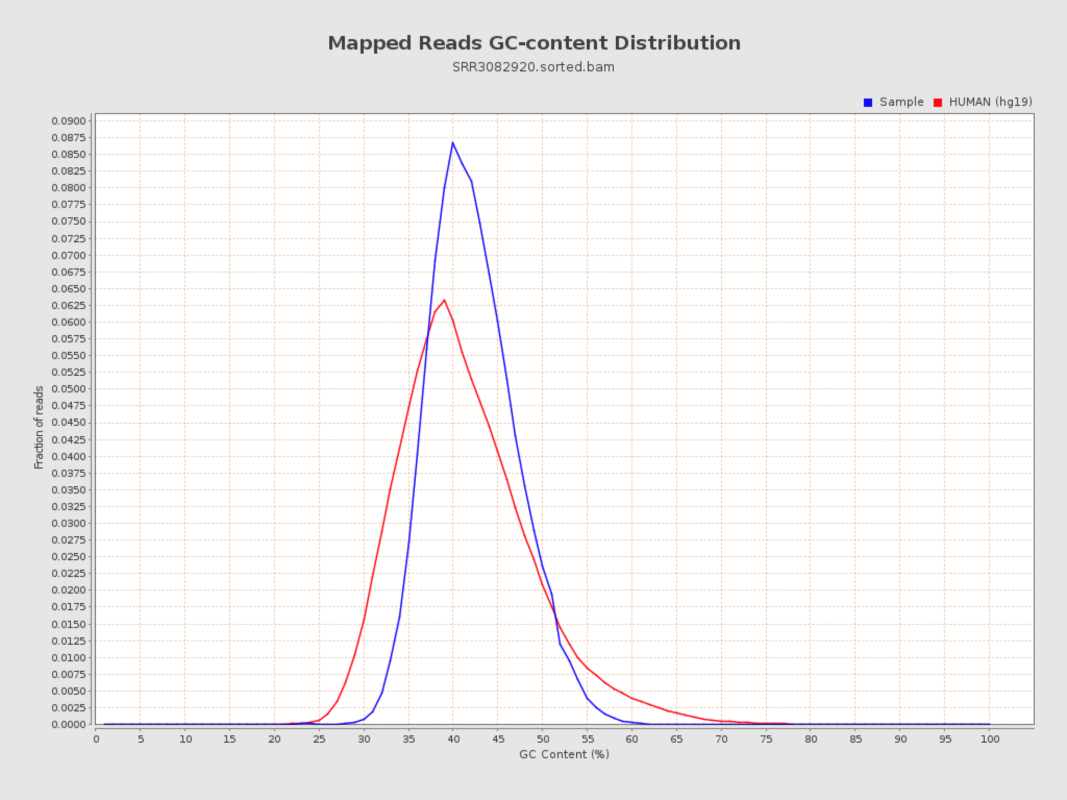
7. Results : Duplication Rate Histogram



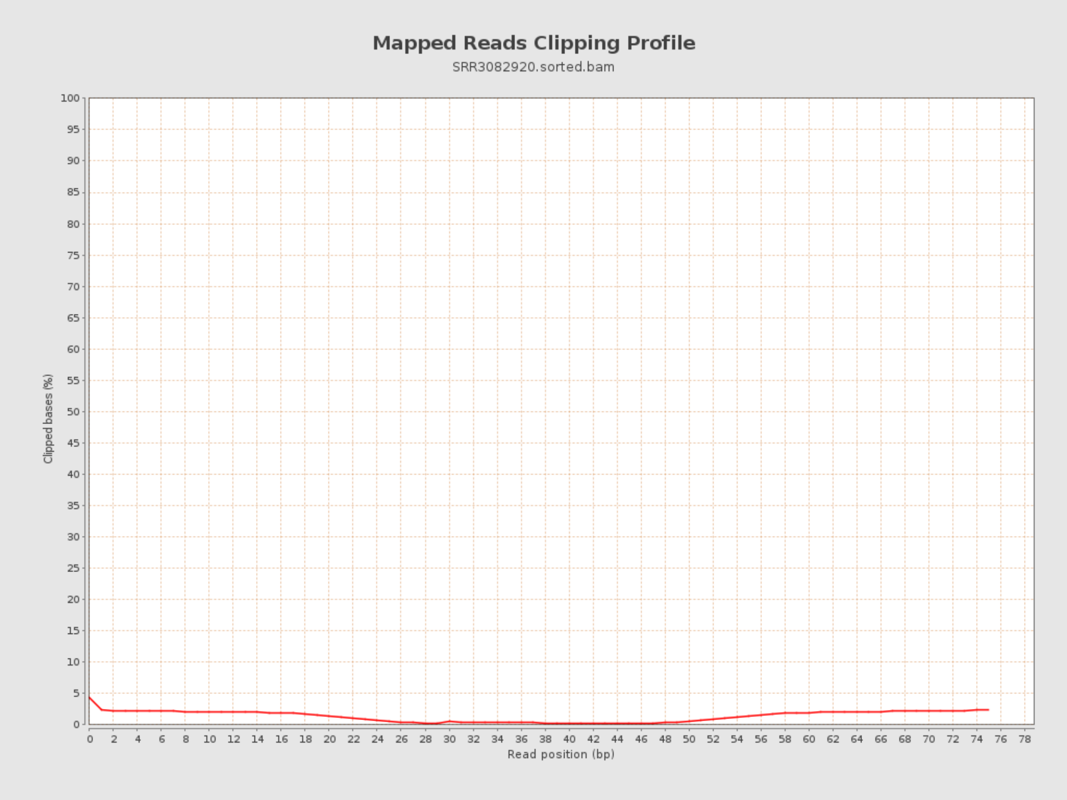
8. Results : Mapped Reads Nucleotide Content



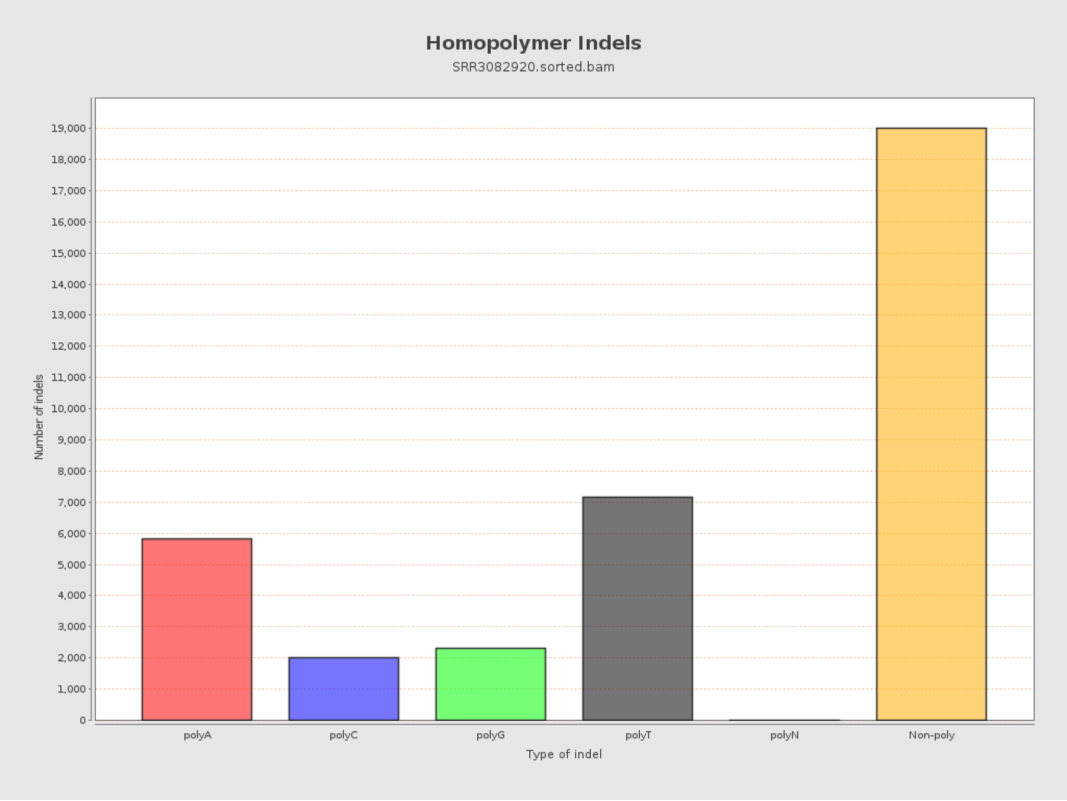
9. Results : Mapped Reads GC-content Distribution



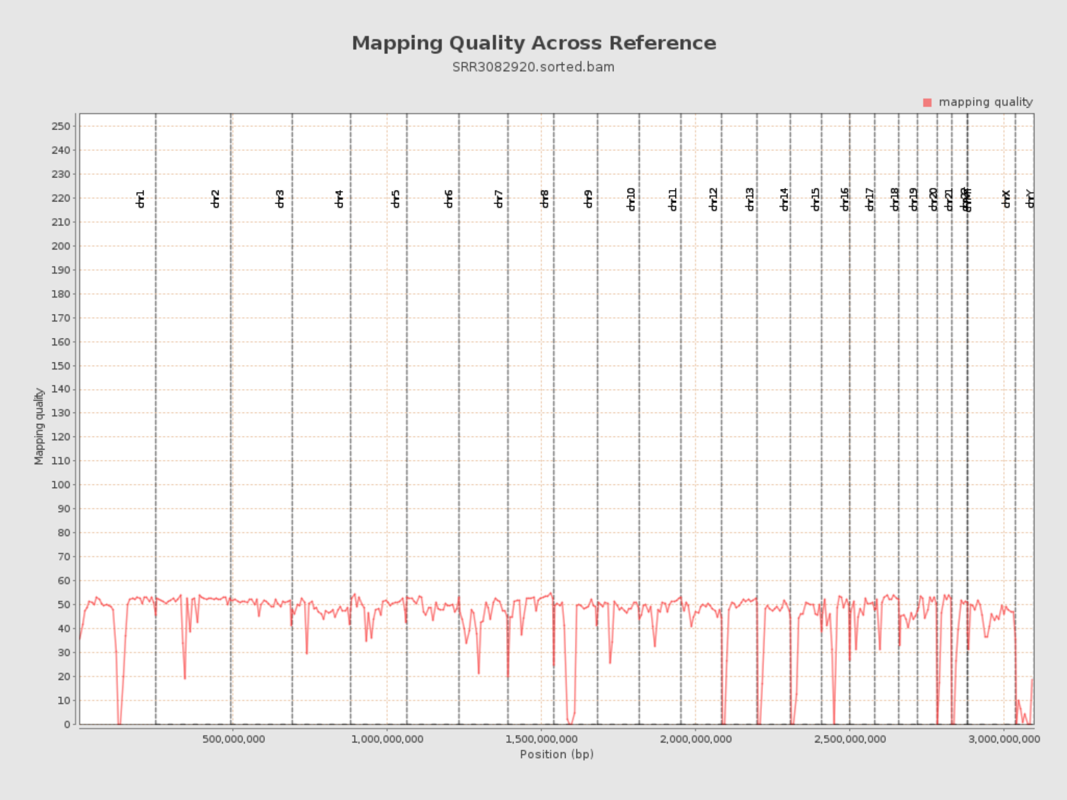
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram