Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 23:26:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081156.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_SRR3081156 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081156.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 23:26:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081156.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,144,217
Mapped reads	2,781,857 / 88.48%
Unmapped reads	362,360 / 11.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	28,724 / 0.91%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	130,933 / 4.16%
Duplication rate	3.56%
Clipped reads	1,241,654 / 39.49%

2.2. ACGT Content

Number/percentage of A's	52,680,669 / 28.24%
Number/percentage of C's	34,464,659 / 18.48%
Number/percentage of T's	58,609,571 / 31.42%
Number/percentage of G's	40,733,339 / 21.84%
Number/percentage of N's	54,556 / 0.03%
GC Percentage	40.31%

2.3. Coverage

Mean	0.0603

Standard Deviation	0.4906

2.4. Mapping Quality

Mean Mapping Quality	46.55

2.5. Mismatches and indels

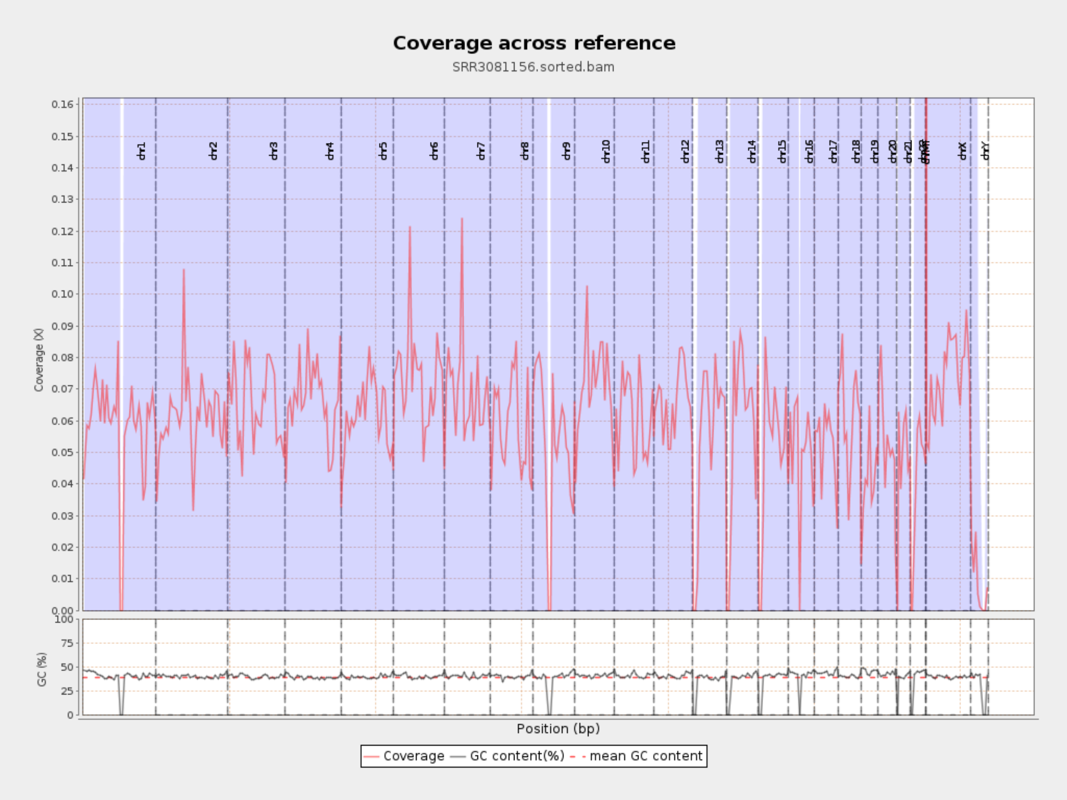
General error rate	0.87%
Mismatches	1,588,616
Insertions	14,950
Mapped reads with at least one insertion	0.53%
Deletions	43,755
Mapped reads with at least one deletion	1.56%
Homopolymer indels	46.82%

2.6. Chromosome stats

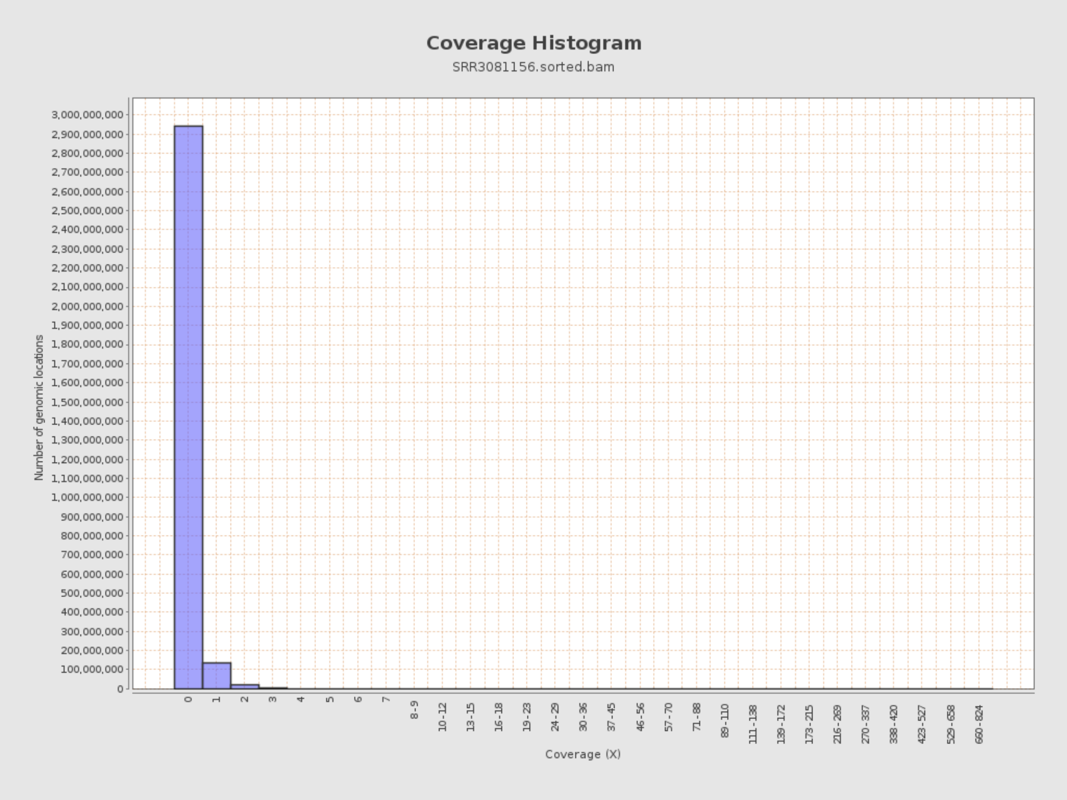
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14428719	0.0579	0.6598
chr2	243199373	14948887	0.0615	0.6009
chr3	198022430	13073112	0.066	0.2959
chr4	191154276	12706028	0.0665	0.3169
chr5	180915260	11190689	0.0619	0.2903
chr6	171115067	12697345	0.0742	0.543
chr7	159138663	11068146	0.0696	0.919

chr8	146364022	8569360	0.0585	0.5941
chr9	141213431	7509644	0.0532	0.4427
chr10	135534747	9661593	0.0713	0.444
chr11	135006516	8219735	0.0609	0.514
chr12	133851895	8873382	0.0663	0.3043
chr13	115169878	6253440	0.0543	0.2678
chr14	107349540	6256883	0.0583	0.2986
chr15	102531392	5279502	0.0515	0.2718
chr16	90354753	4349484	0.0481	0.3065
chr17	81195210	4343645	0.0535	0.3257
chr18	78077248	4937213	0.0632	0.9298
chr19	59128983	2474802	0.0419	0.4952
chr20	63025520	3468344	0.055	0.2827
chr21	48129895	2310397	0.048	0.2828
chr22	51304566	1990832	0.0388	0.224
chrMT	16571	45955	2.7732	2.3407
chrX	155270560	11455222	0.0738	0.3541
chrY	59373566	500988	0.0084	0.18

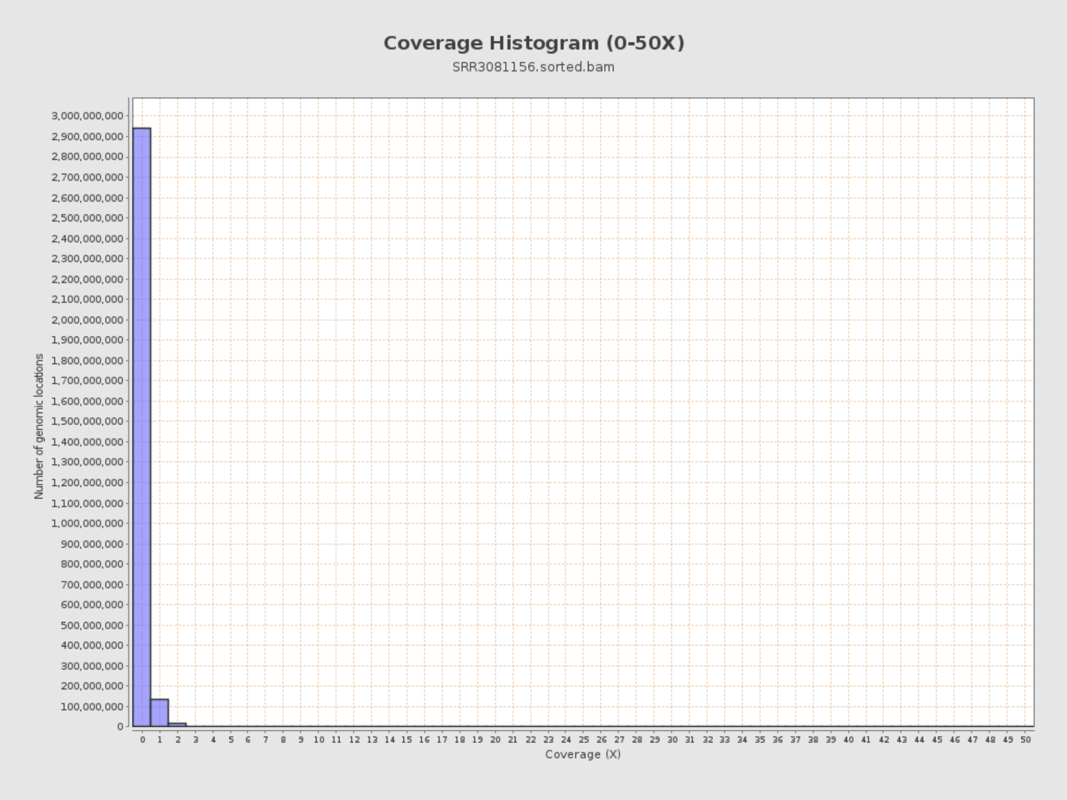
3. Results : Coverage across reference



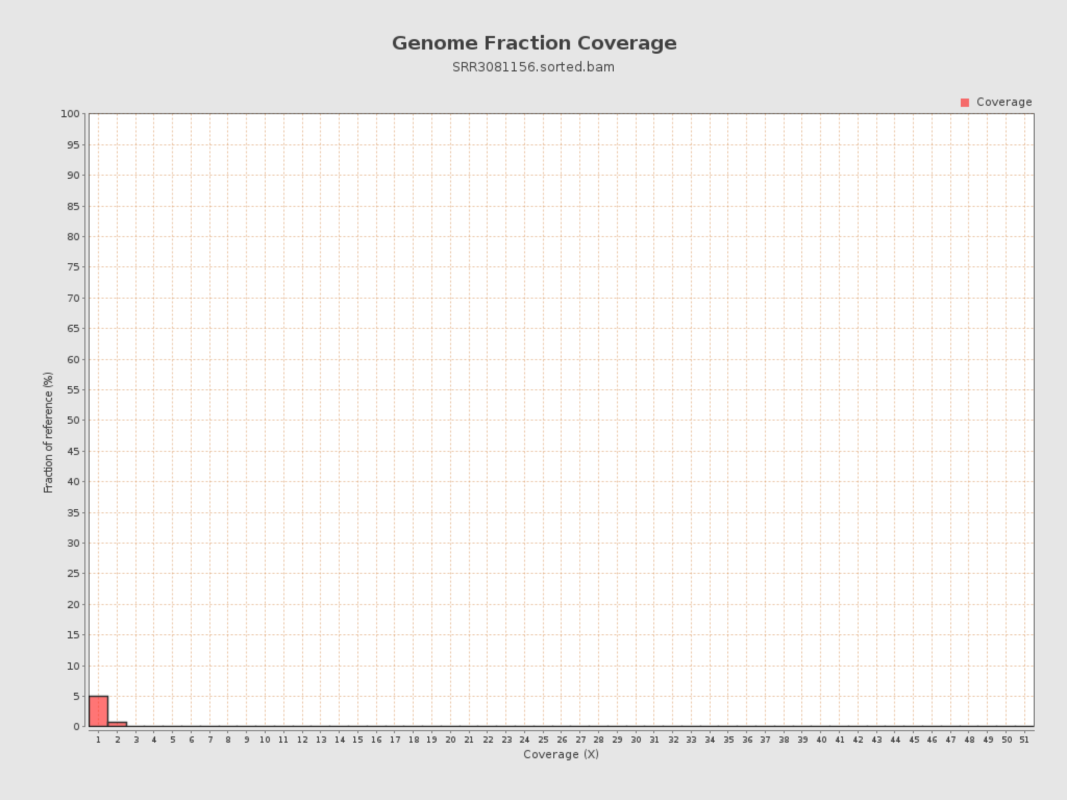
4. Results : Coverage Histogram



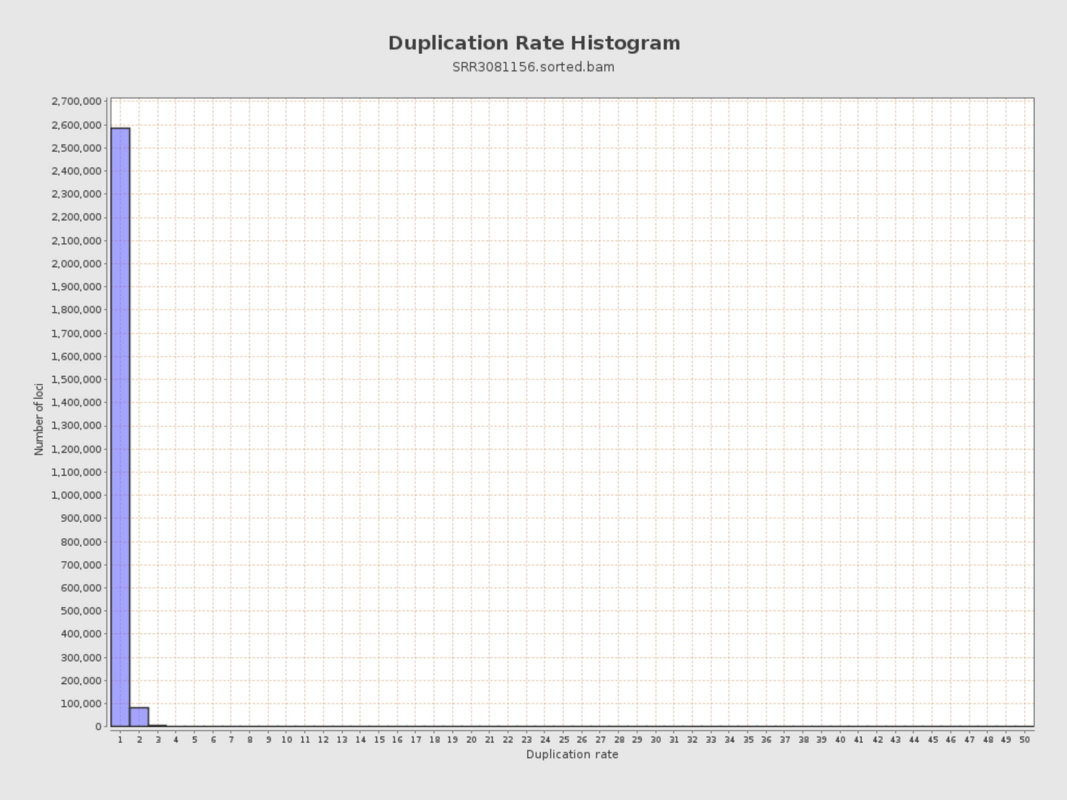
5. Results : Coverage Histogram (0-50X)



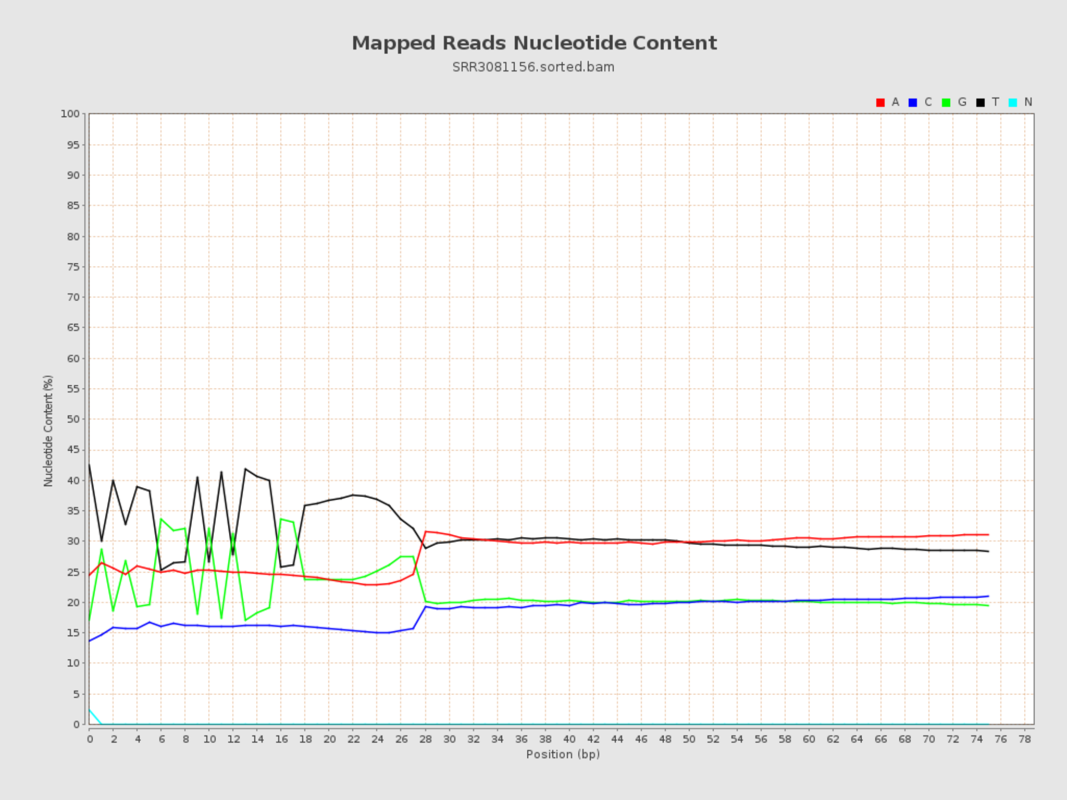
6. Results : Genome Fraction Coverage



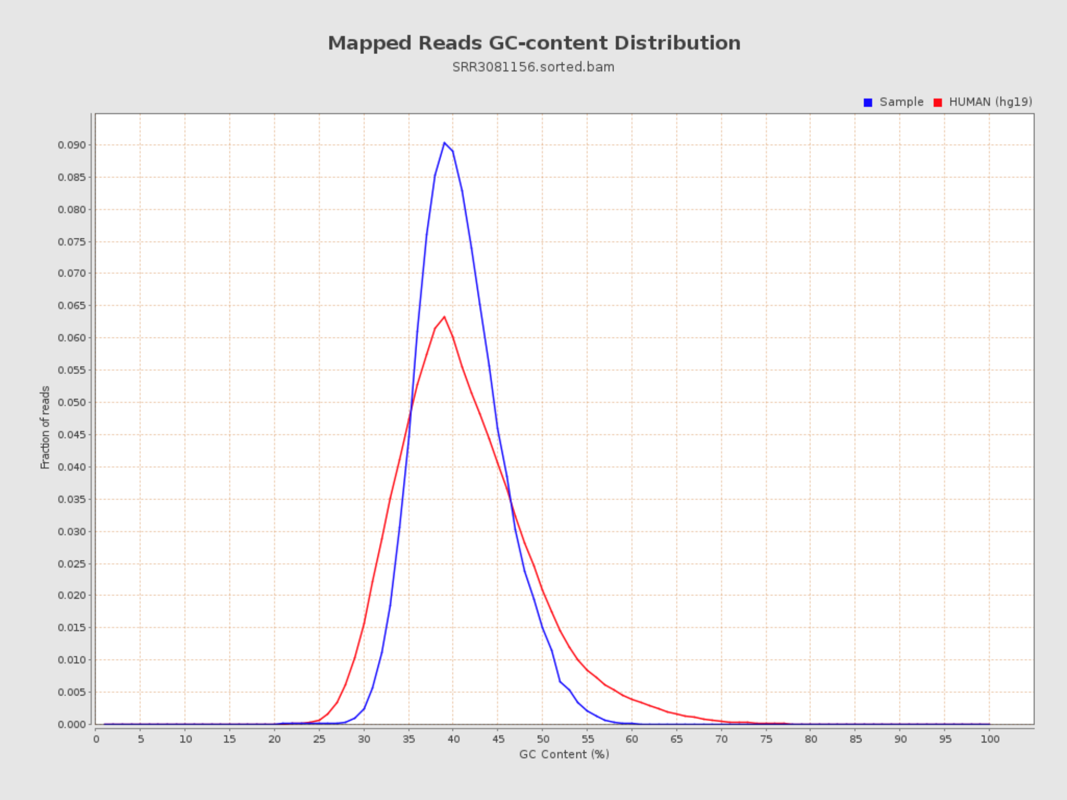
7. Results : Duplication Rate Histogram



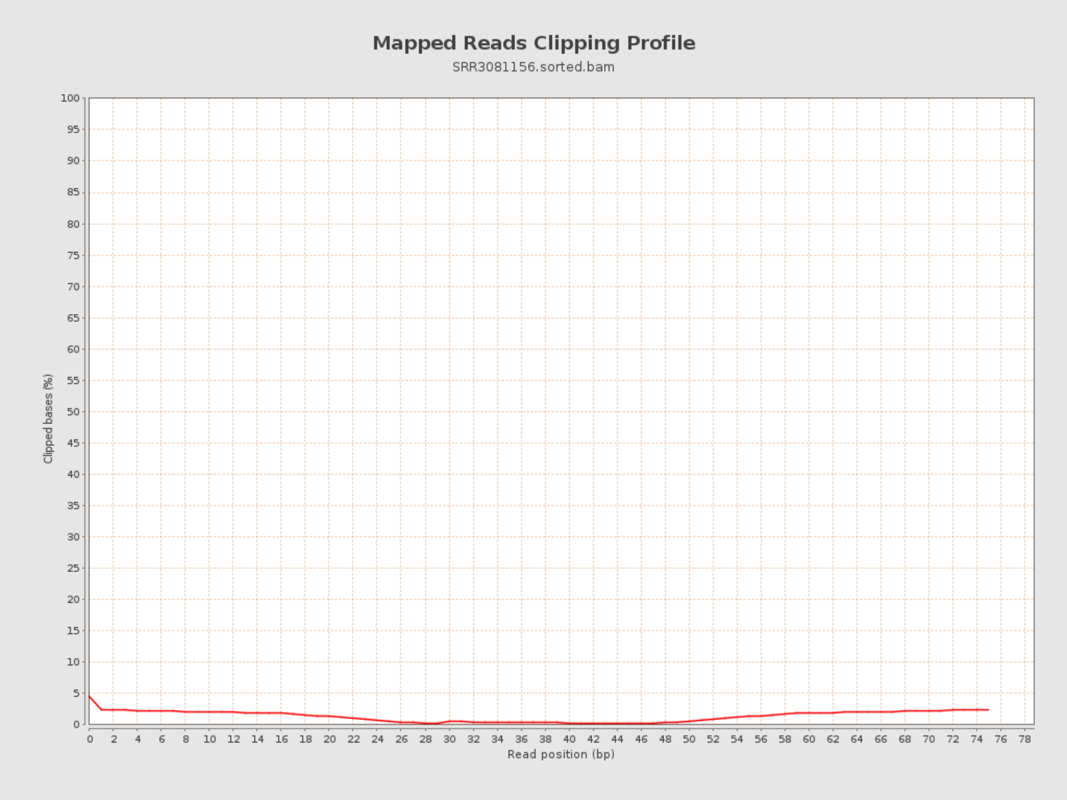
8. Results : Mapped Reads Nucleotide Content



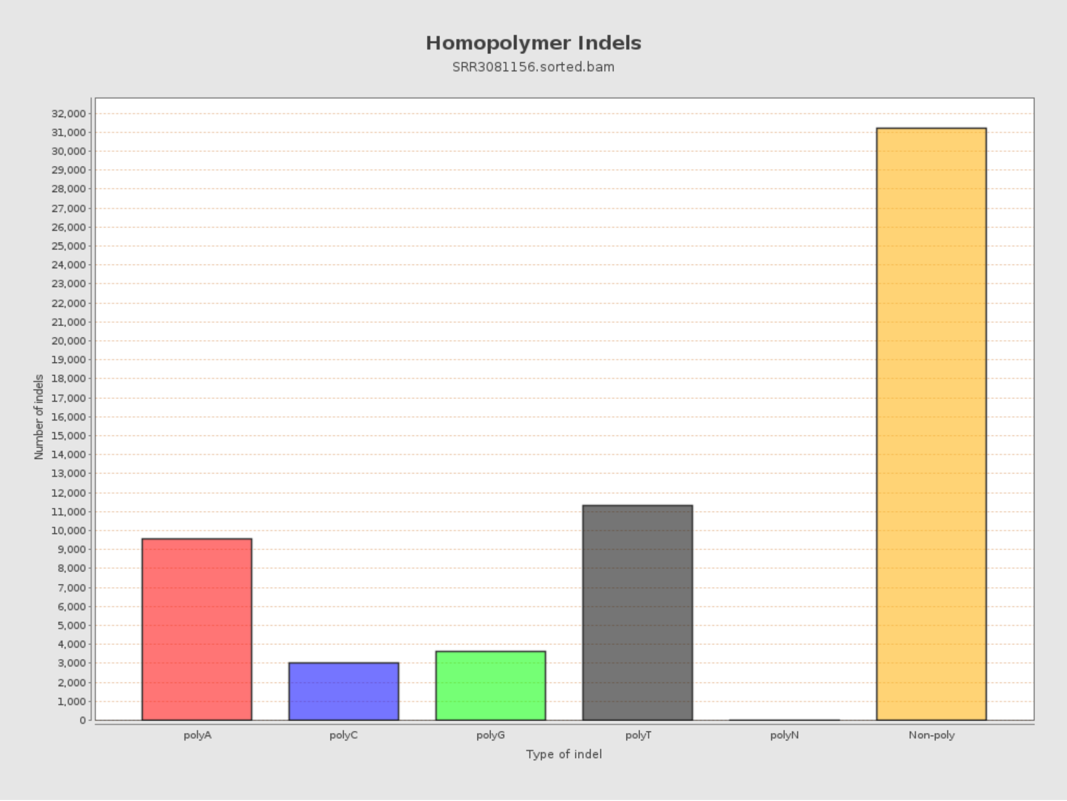
9. Results : Mapped Reads GC-content Distribution



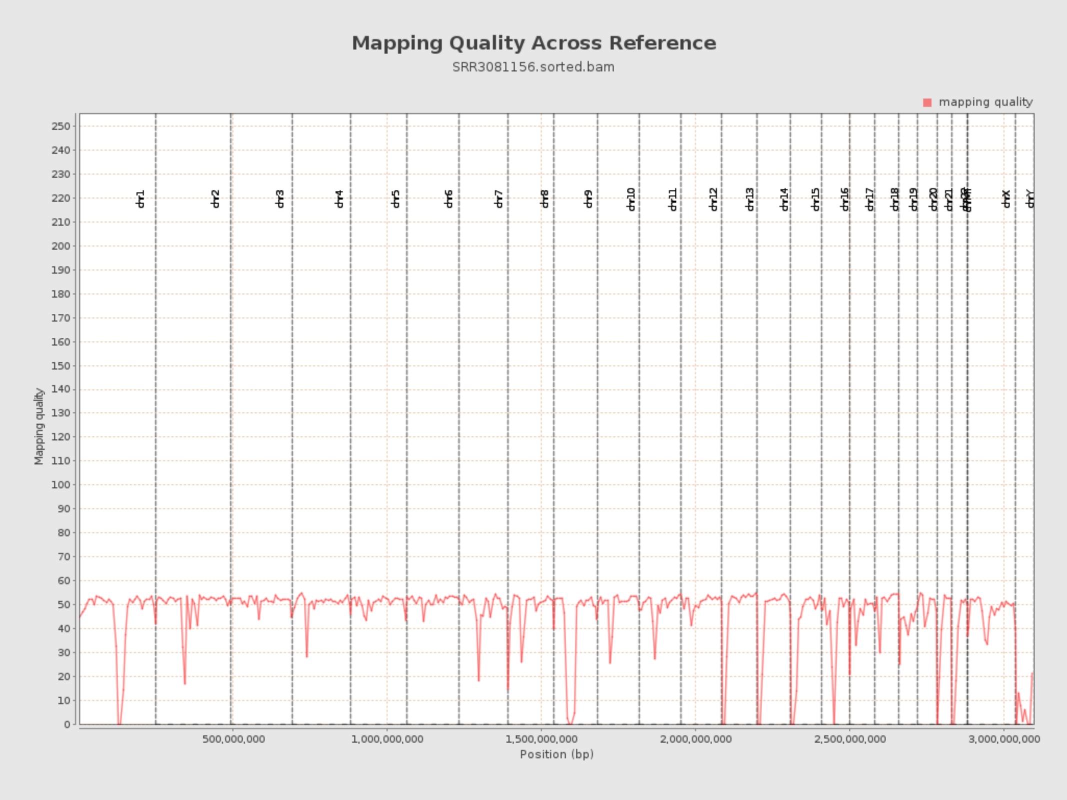
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram