Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 12:08:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008801.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_SRR6008801 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008801.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 12:08:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008801.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,733,078
Mapped reads	1,208,330 / 69.72%
Unmapped reads	524,748 / 30.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,342 / 0.65%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	166,789 / 9.62%
Duplication rate	10.26%
Clipped reads	607,291 / 35.04%

2.2. ACGT Content

Number/percentage of A's	21,350,998 / 27.15%
Number/percentage of C's	15,230,000 / 19.36%
Number/percentage of T's	24,166,737 / 30.73%
Number/percentage of G's	17,794,200 / 22.62%
Number/percentage of N's	111,316 / 0.14%
GC Percentage	41.99%

2.3. Coverage

Mean	0.0254

Standard Deviation	0.3831

2.4. Mapping Quality

Mean Mapping Quality	44.79

2.5. Mismatches and indels

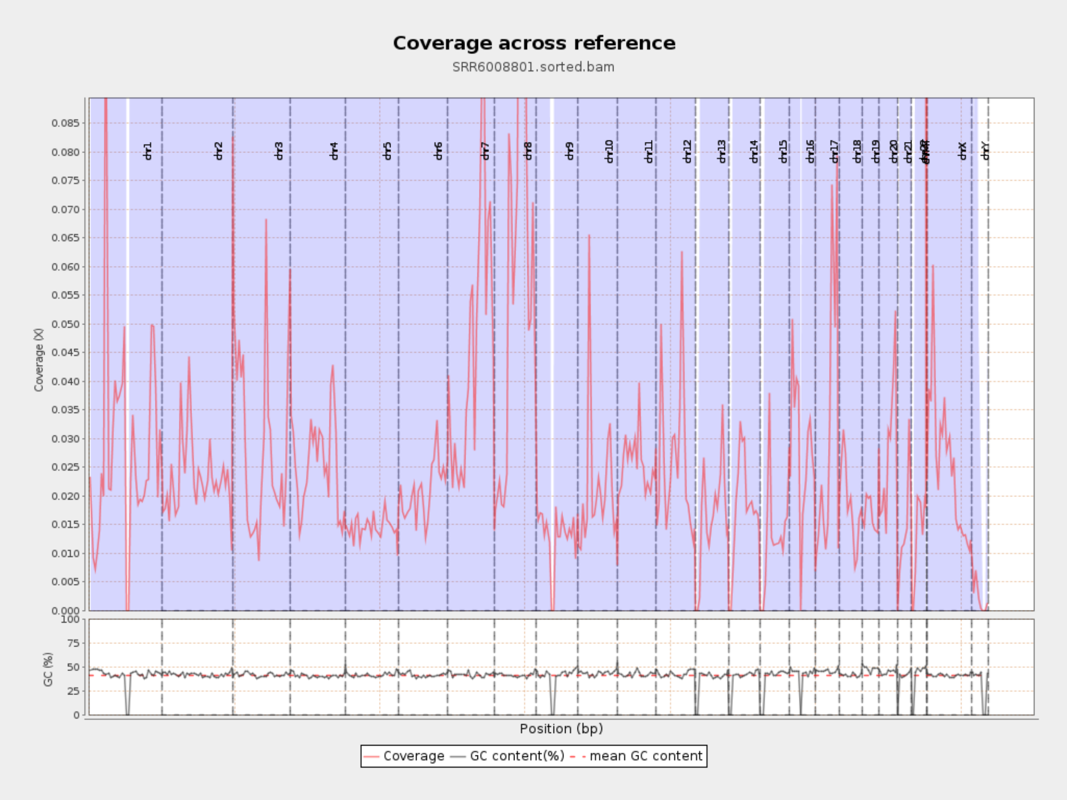
General error rate	0.84%
Mismatches	650,805
Insertions	4,710
Mapped reads with at least one insertion	0.39%
Deletions	20,532
Mapped reads with at least one deletion	1.68%
Homopolymer indels	46.23%

2.6. Chromosome stats

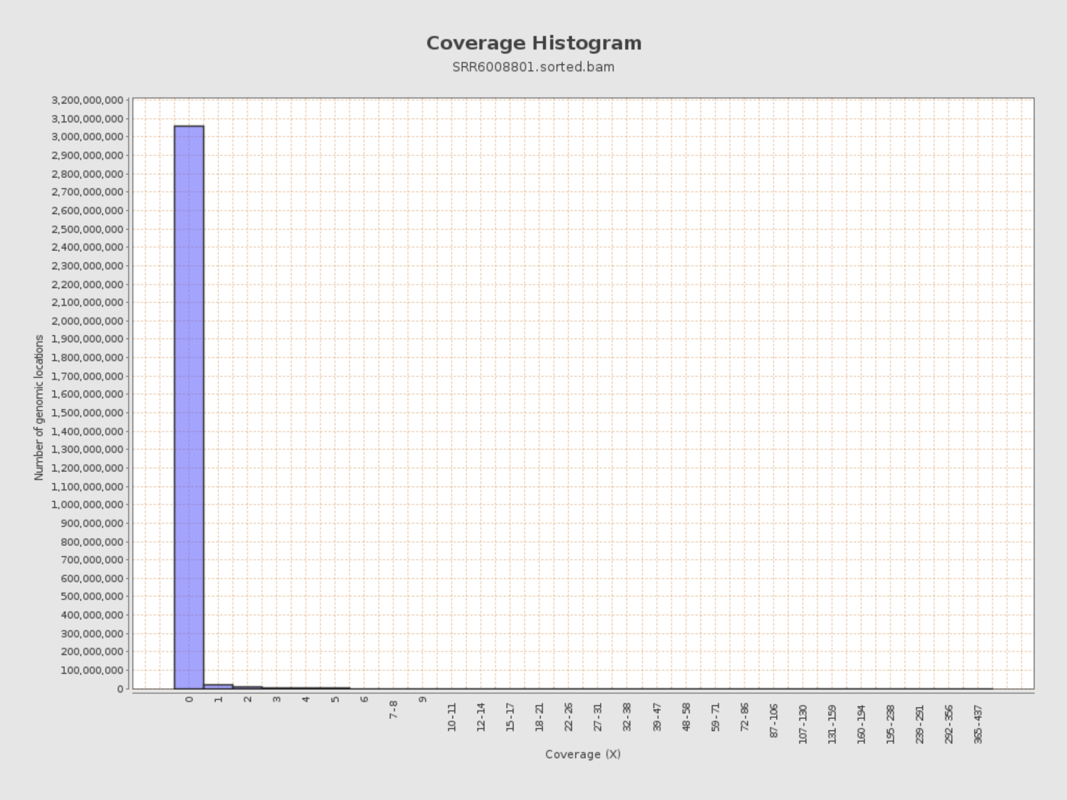
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6945922	0.0279	0.4535
chr2	243199373	5735956	0.0236	0.3503
chr3	198022430	5791463	0.0292	0.316
chr4	191154276	4855146	0.0254	0.2845
chr5	180915260	2640756	0.0146	0.212
chr6	171115067	3548289	0.0207	0.2617
chr7	159138663	7403733	0.0465	0.4192

chr8	146364022	9052668	0.0619	0.4684
chr9	141213431	1805055	0.0128	0.2146
chr10	135534747	2874020	0.0212	0.5456
chr11	135006516	3432141	0.0254	0.3069
chr12	133851895	3503219	0.0262	0.2885
chr13	115169878	1862578	0.0162	0.231
chr14	107349540	1941950	0.0181	0.244
chr15	102531392	1339483	0.0131	0.2207
chr16	90354753	2598422	0.0288	0.3064
chr17	81195210	2540102	0.0313	0.323
chr18	78077248	1464605	0.0188	0.2814
chr19	59128983	1014436	0.0172	0.3142
chr20	63025520	1785020	0.0283	0.3021
chr21	48129895	693387	0.0144	0.2066
chr22	51304566	639738	0.0125	0.1943
chrMT	16571	1160318	70.021	46.5548
chrX	155270560	3915968	0.0252	0.293
chrY	59373566	145141	0.0024	0.0777

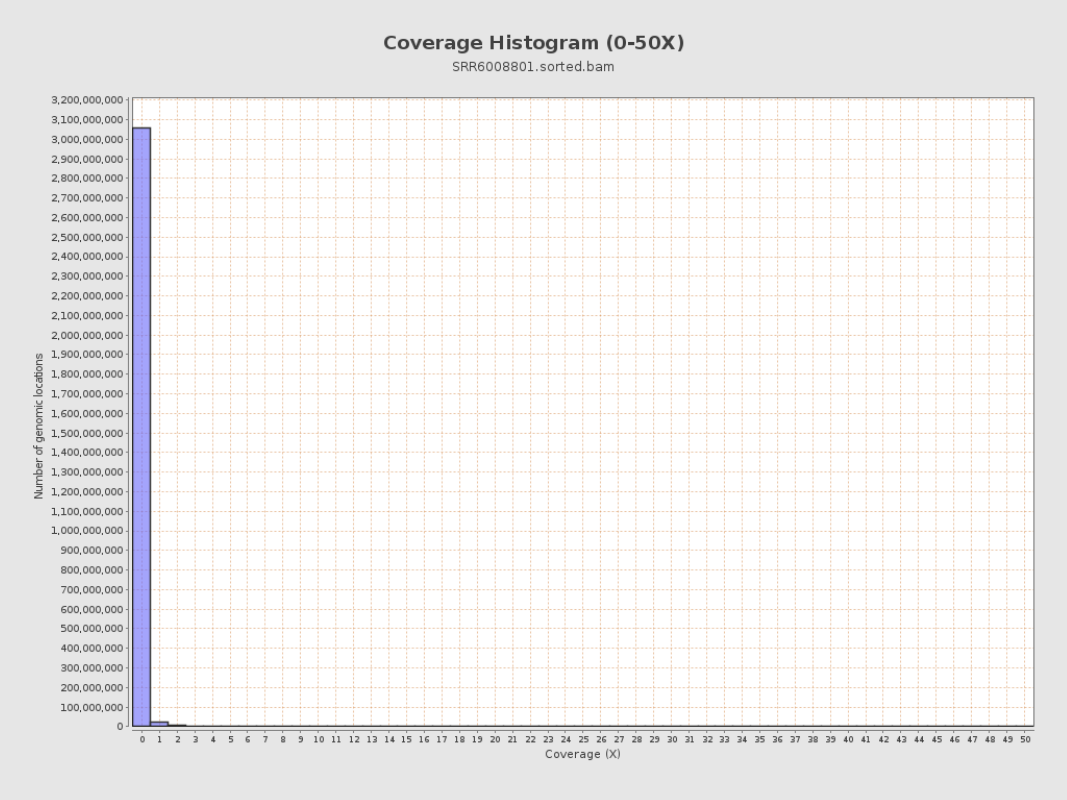
3. Results : Coverage across reference



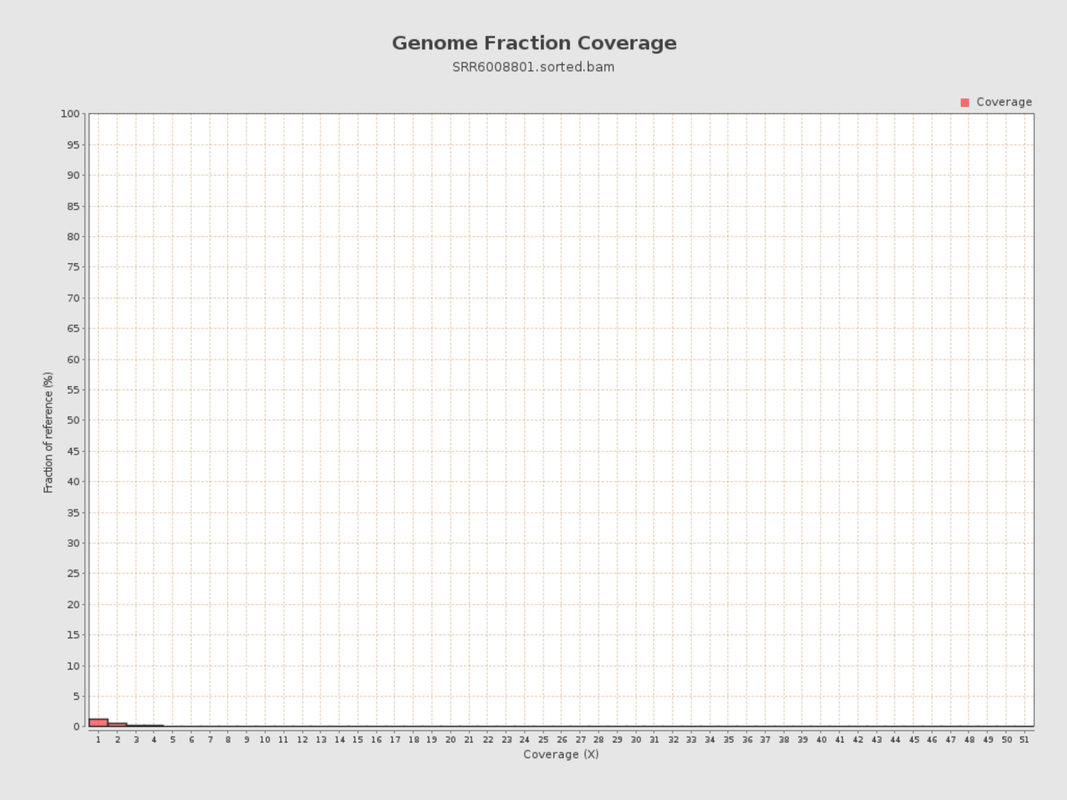
4. Results : Coverage Histogram



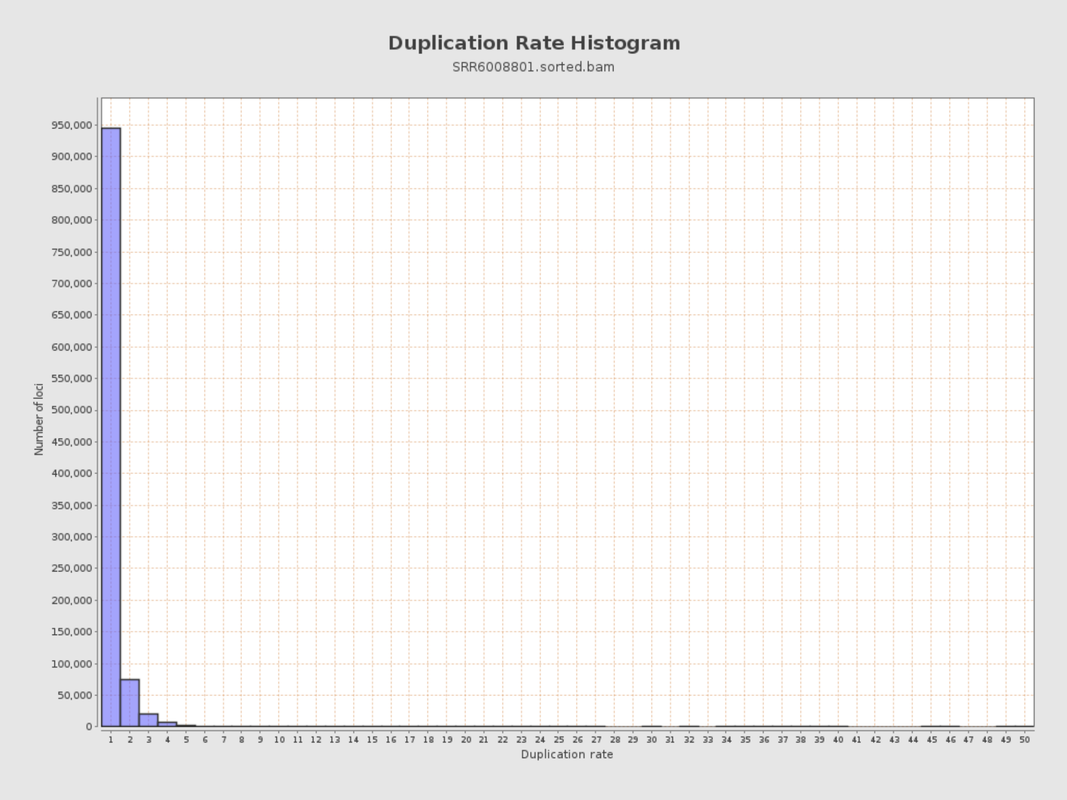
5. Results : Coverage Histogram (0-50X)



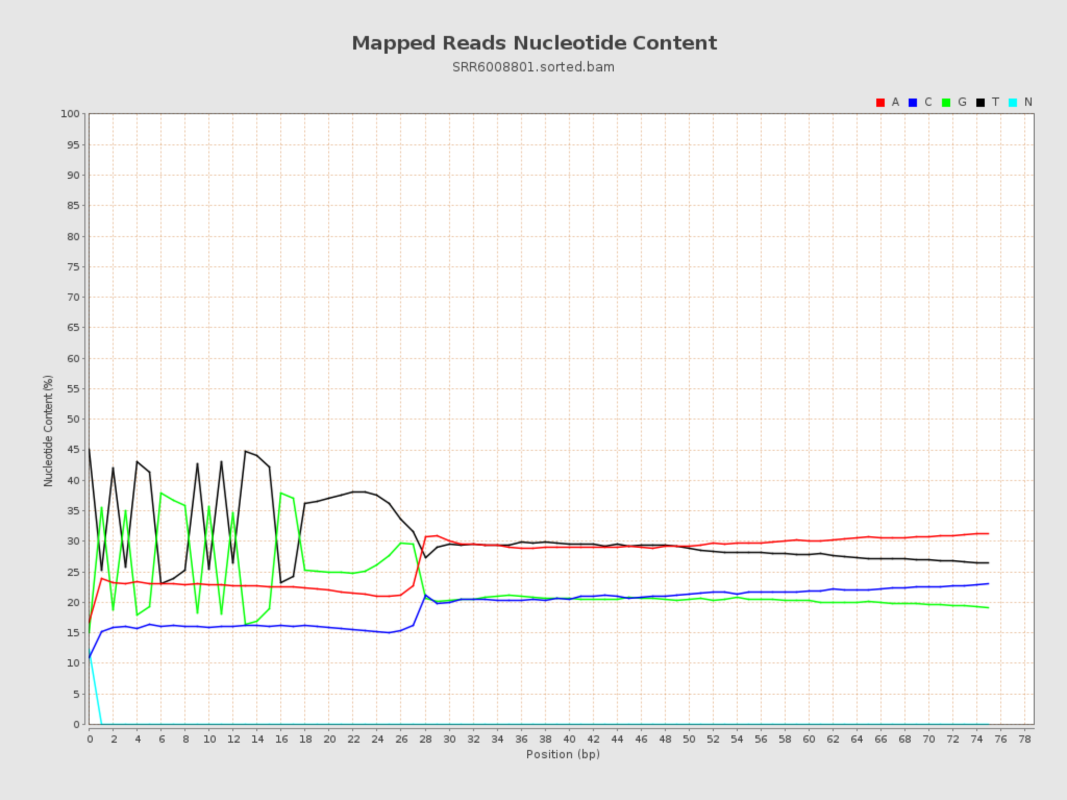
6. Results : Genome Fraction Coverage



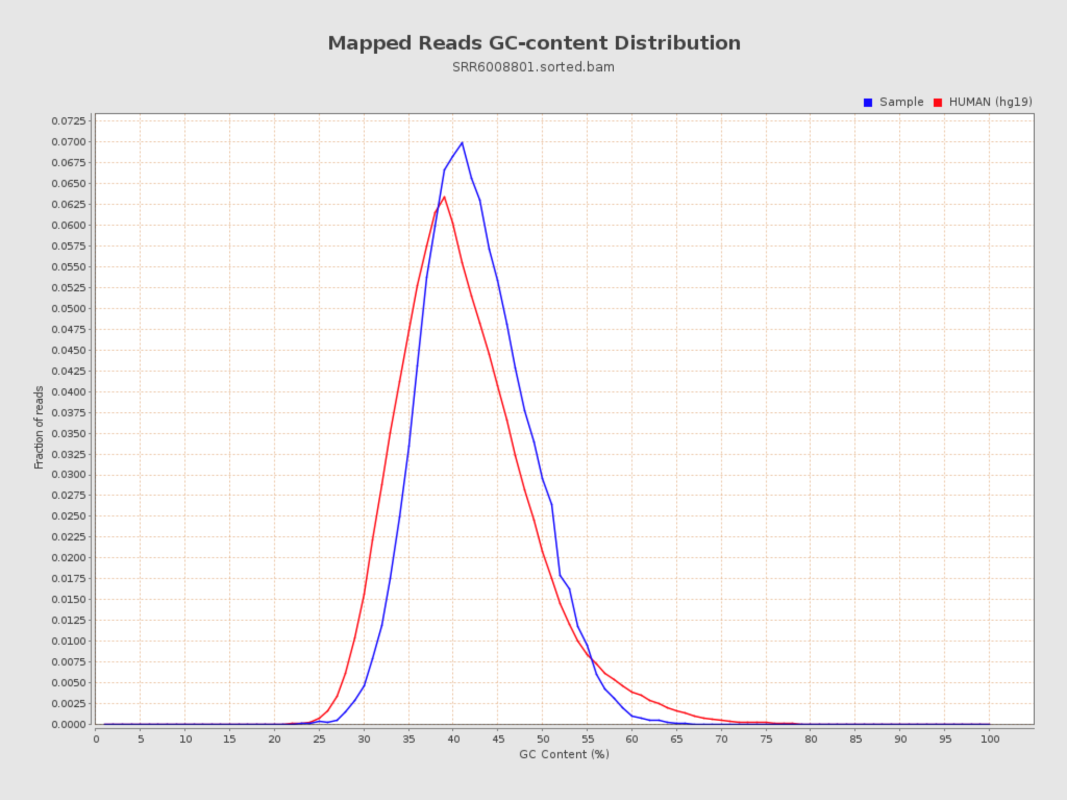
7. Results : Duplication Rate Histogram



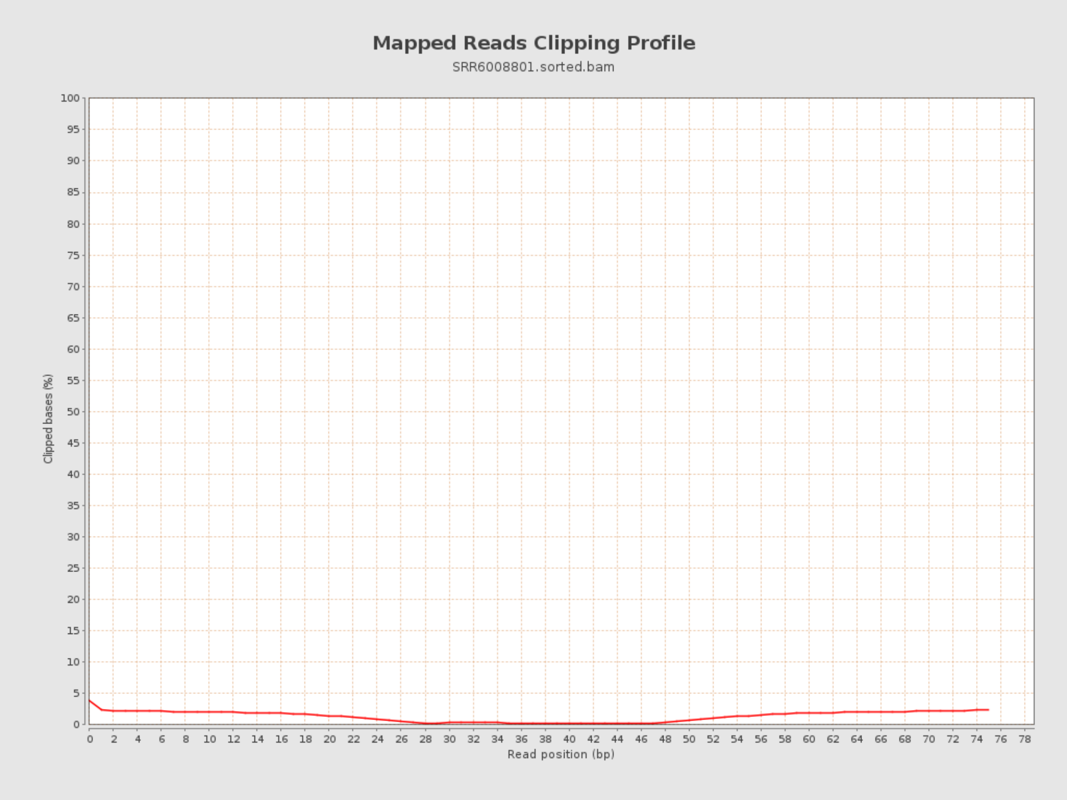
8. Results : Mapped Reads Nucleotide Content



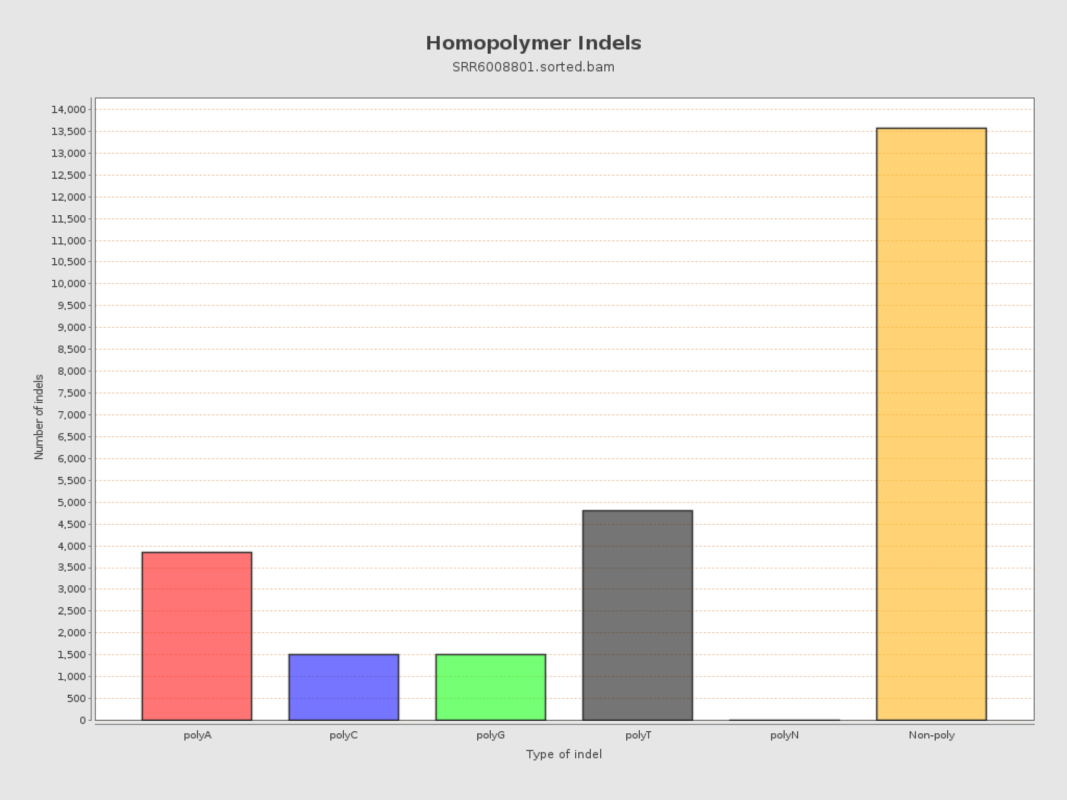
9. Results : Mapped Reads GC-content Distribution



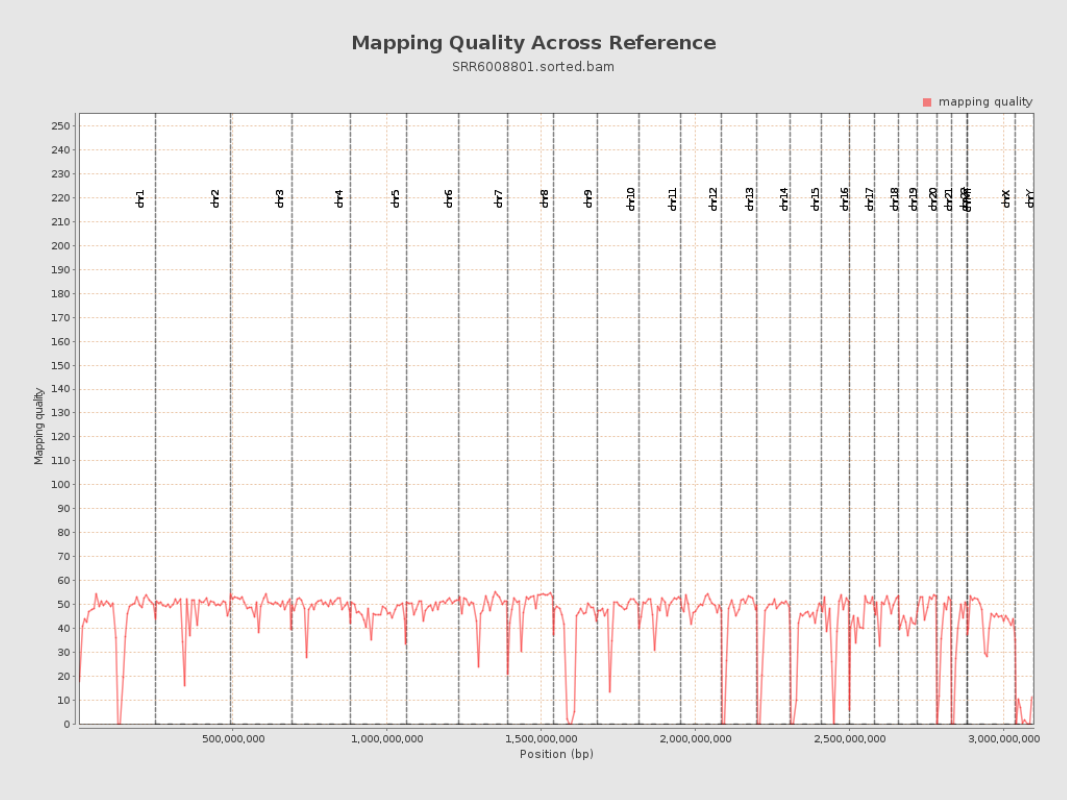
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram