Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 04:32:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080632.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_SRR3080632 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080632.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 04:32:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080632.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,984,156
Mapped reads	3,986,143 / 79.98%
Unmapped reads	998,013 / 20.02%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	34,833 / 0.7%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	208,870 / 4.19%
Duplication rate	4.47%
Clipped reads	1,817,451 / 36.46%

2.2. ACGT Content

Number/percentage of A's	73,801,246 / 27.73%
Number/percentage of C's	47,581,851 / 17.88%
Number/percentage of T's	86,570,436 / 32.52%
Number/percentage of G's	57,995,162 / 21.79%
Number/percentage of N's	219,861 / 0.08%
GC Percentage	39.67%

2.3. Coverage

Mean	0.086

Standard Deviation	0.4907

2.4. Mapping Quality

Mean Mapping Quality	47.19

2.5. Mismatches and indels

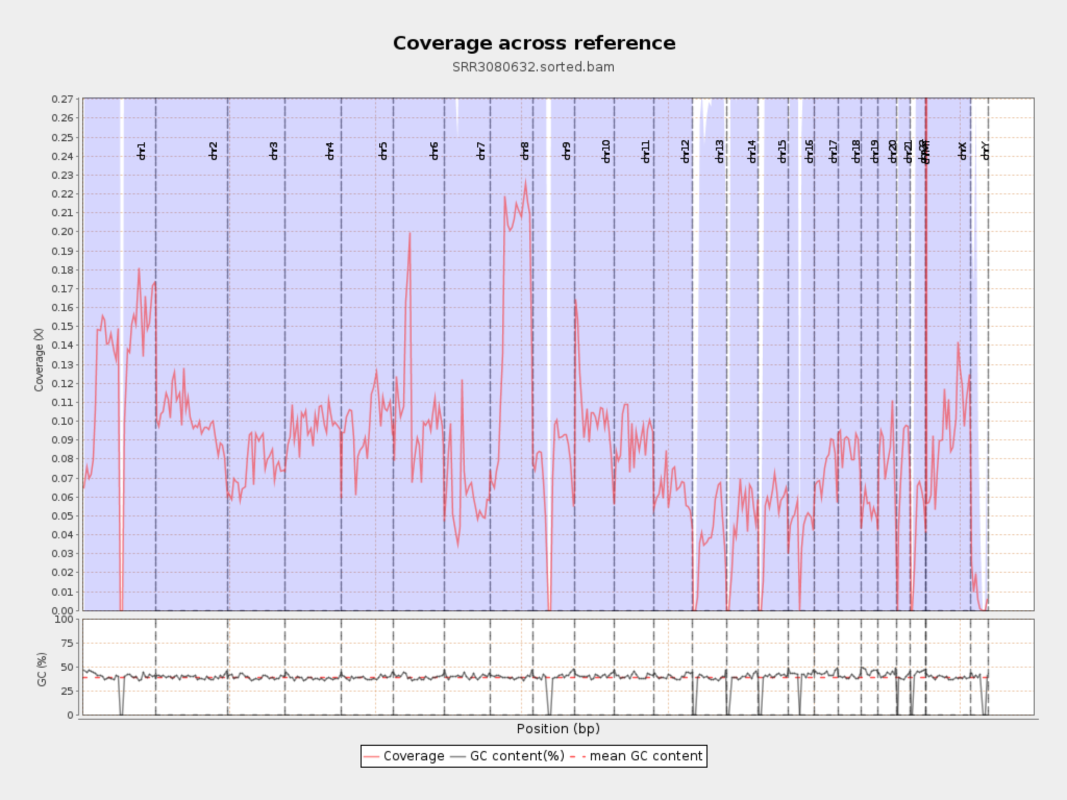
General error rate	0.91%
Mismatches	2,394,647
Insertions	21,498
Mapped reads with at least one insertion	0.54%
Deletions	63,423
Mapped reads with at least one deletion	1.58%
Homopolymer indels	48.74%

2.6. Chromosome stats

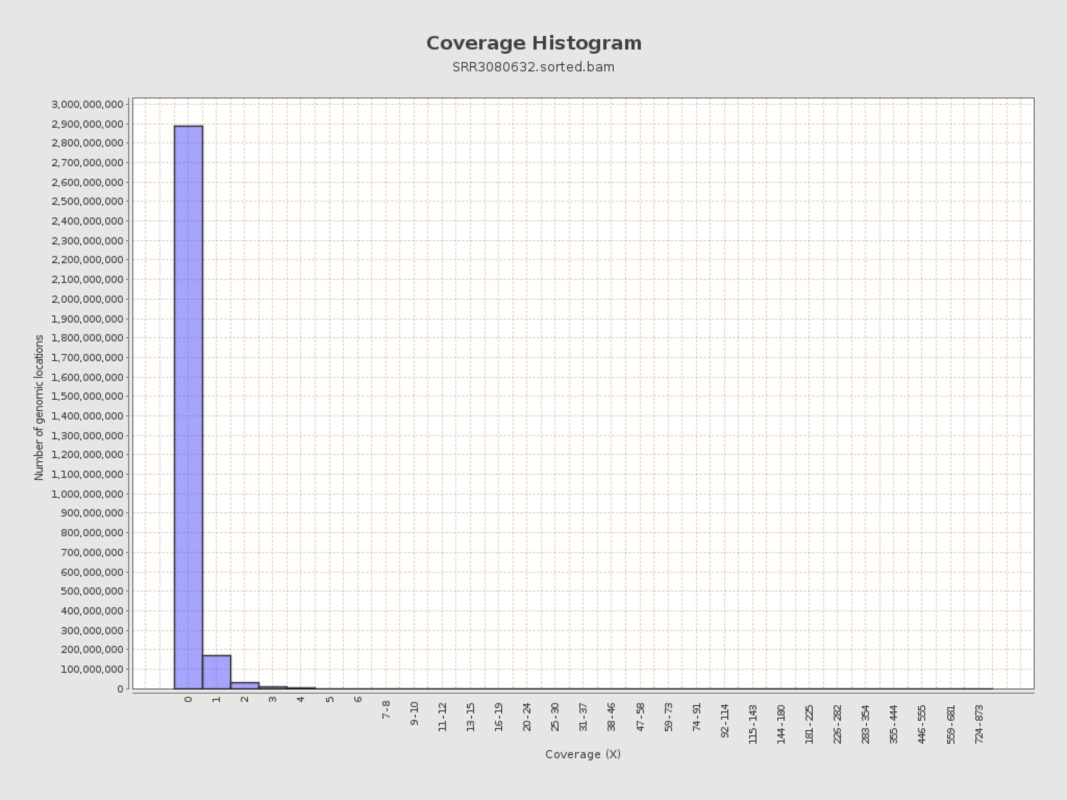
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	31538217	0.1265	0.7223
chr2	243199373	24605556	0.1012	0.5423
chr3	198022430	15060435	0.0761	0.3298
chr4	191154276	18675431	0.0977	0.3829
chr5	180915260	17846648	0.0986	0.381
chr6	171115067	18423706	0.1077	0.5609
chr7	159138663	9788697	0.0615	0.8349

chr8	146364022	24676187	0.1686	0.7537
chr9	141213431	10236034	0.0725	0.4099
chr10	135534747	14401801	0.1063	0.4867
chr11	135006516	12227216	0.0906	0.4399
chr12	133851895	8495171	0.0635	0.3057
chr13	115169878	4304745	0.0374	0.2262
chr14	107349540	4822286	0.0449	0.2794
chr15	102531392	4975654	0.0485	0.2628
chr16	90354753	3826642	0.0424	0.2546
chr17	81195210	6138359	0.0756	0.3642
chr18	78077248	6777891	0.0868	0.5788
chr19	59128983	3196339	0.0541	0.5029
chr20	63025520	5274816	0.0837	0.3515
chr21	48129895	3478971	0.0723	0.3323
chr22	51304566	2213073	0.0431	0.2444
chrMT	16571	98759	5.9597	7.2755
chrX	155270560	14732075	0.0949	0.3993
chrY	59373566	457090	0.0077	0.1291

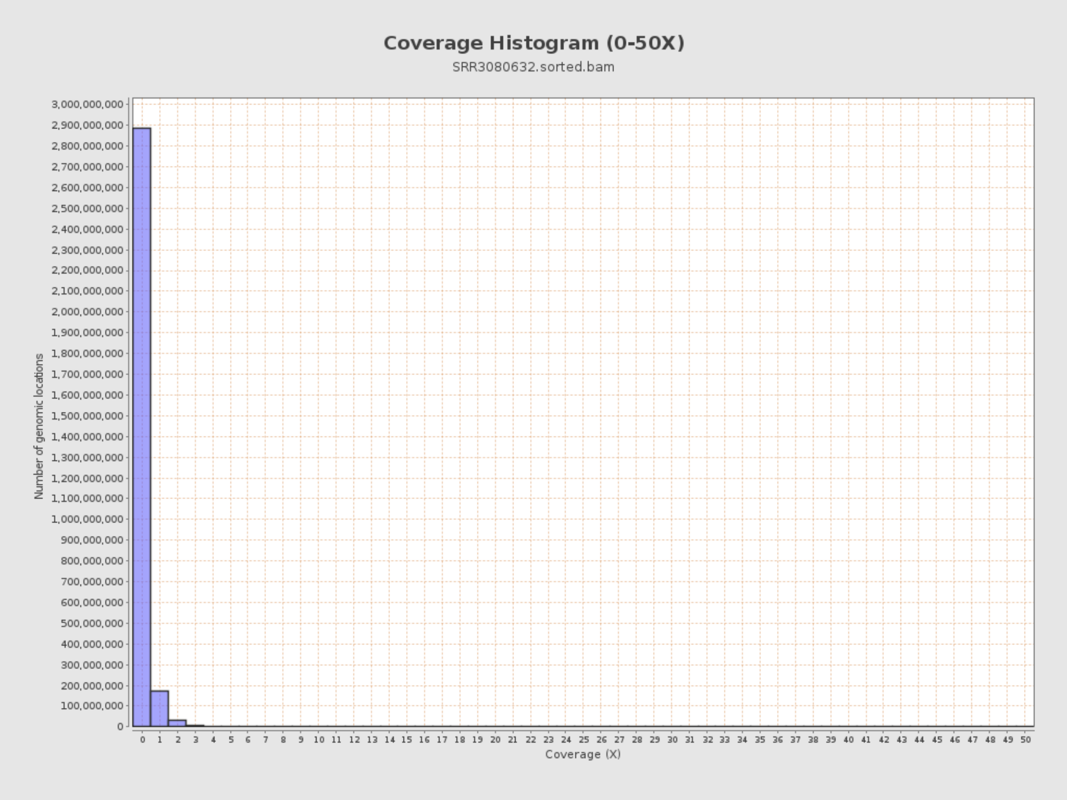
3. Results : Coverage across reference



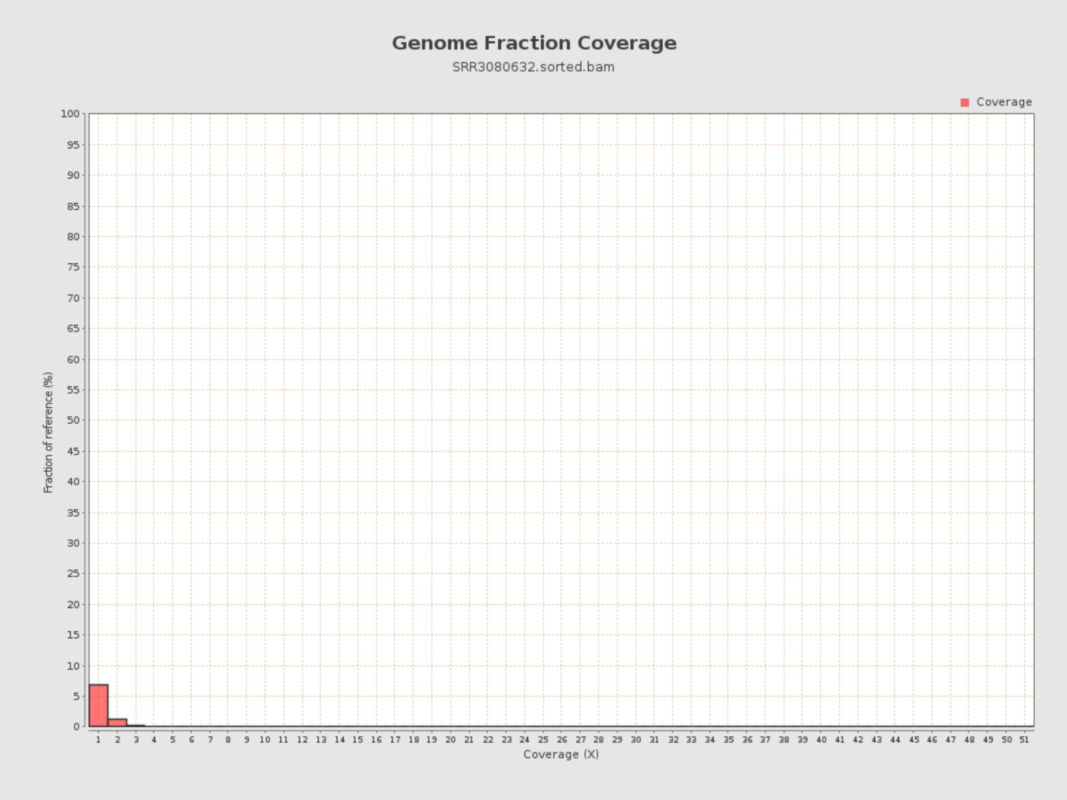
4. Results : Coverage Histogram



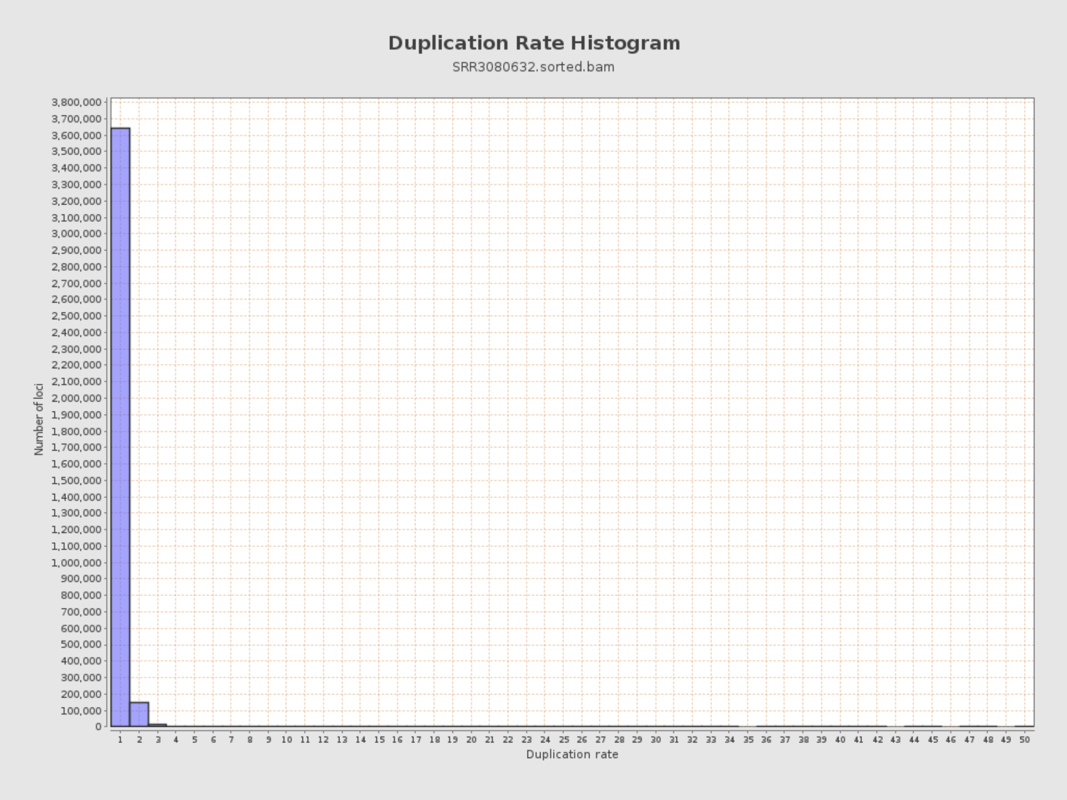
5. Results : Coverage Histogram (0-50X)



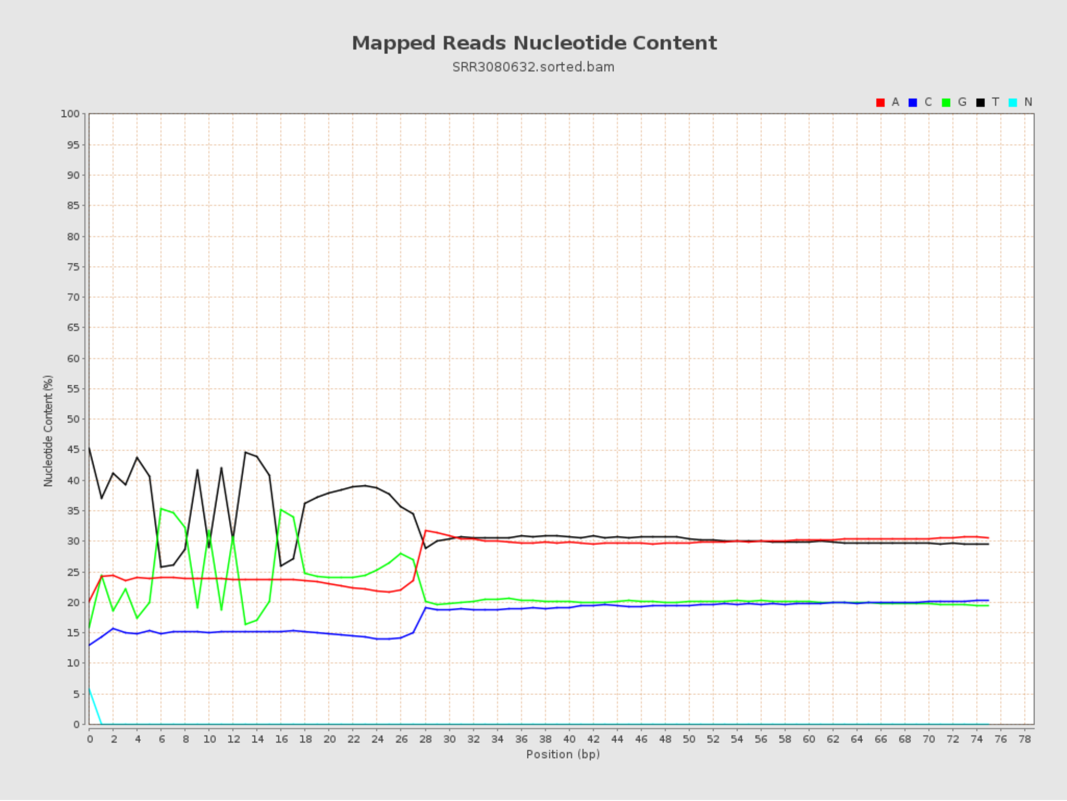
6. Results : Genome Fraction Coverage



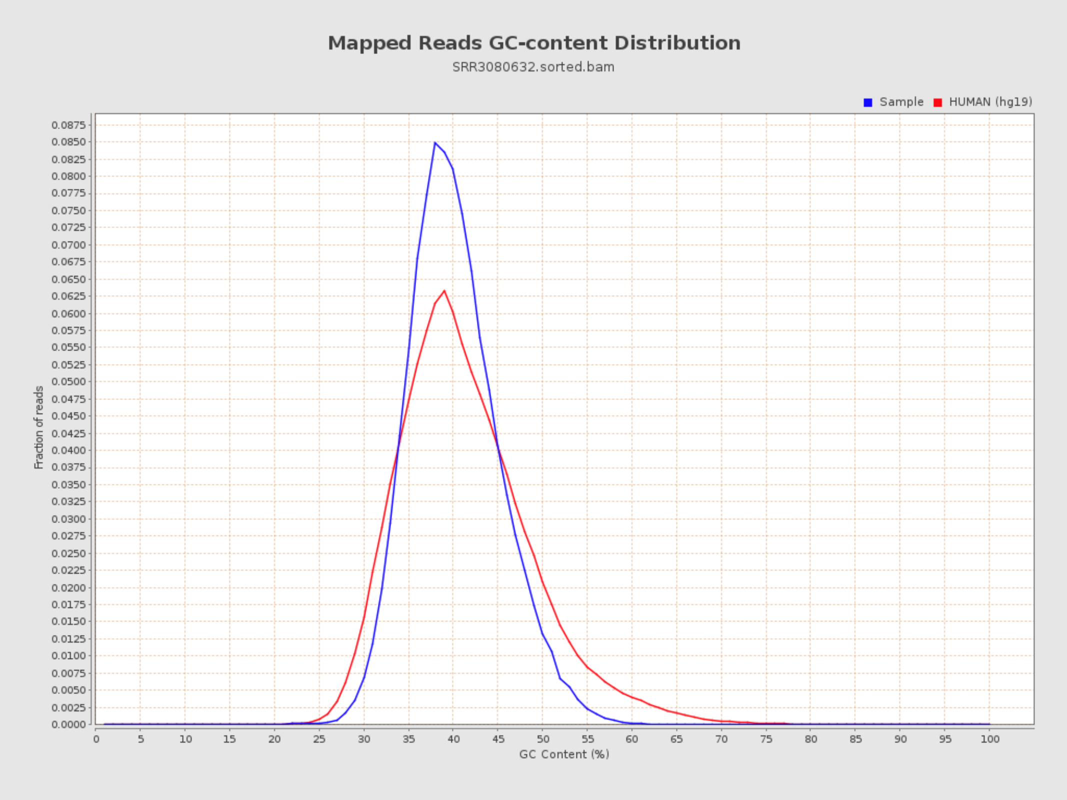
7. Results : Duplication Rate Histogram



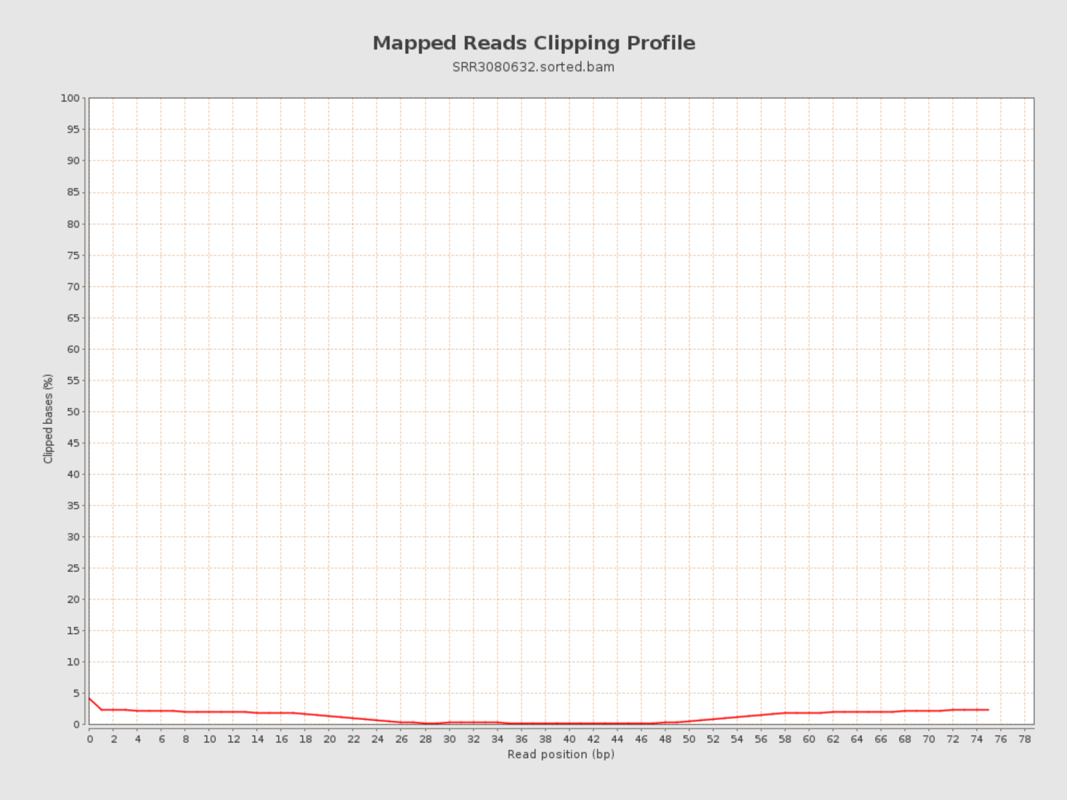
8. Results : Mapped Reads Nucleotide Content



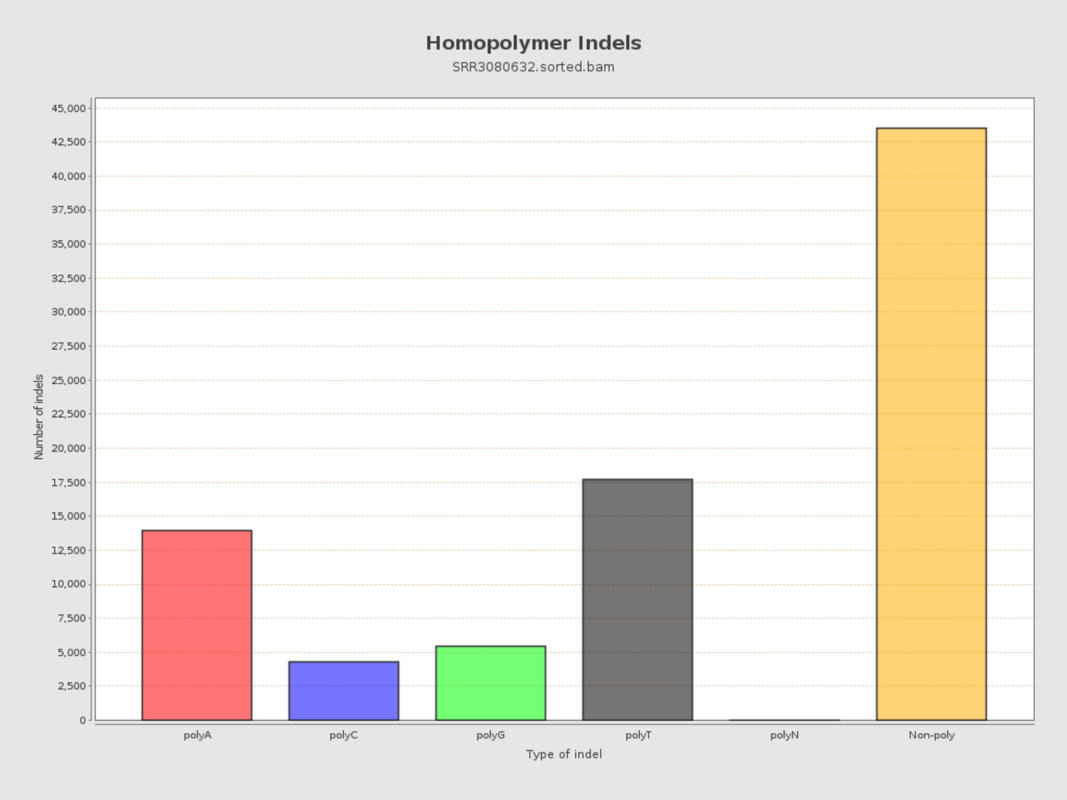
9. Results : Mapped Reads GC-content Distribution



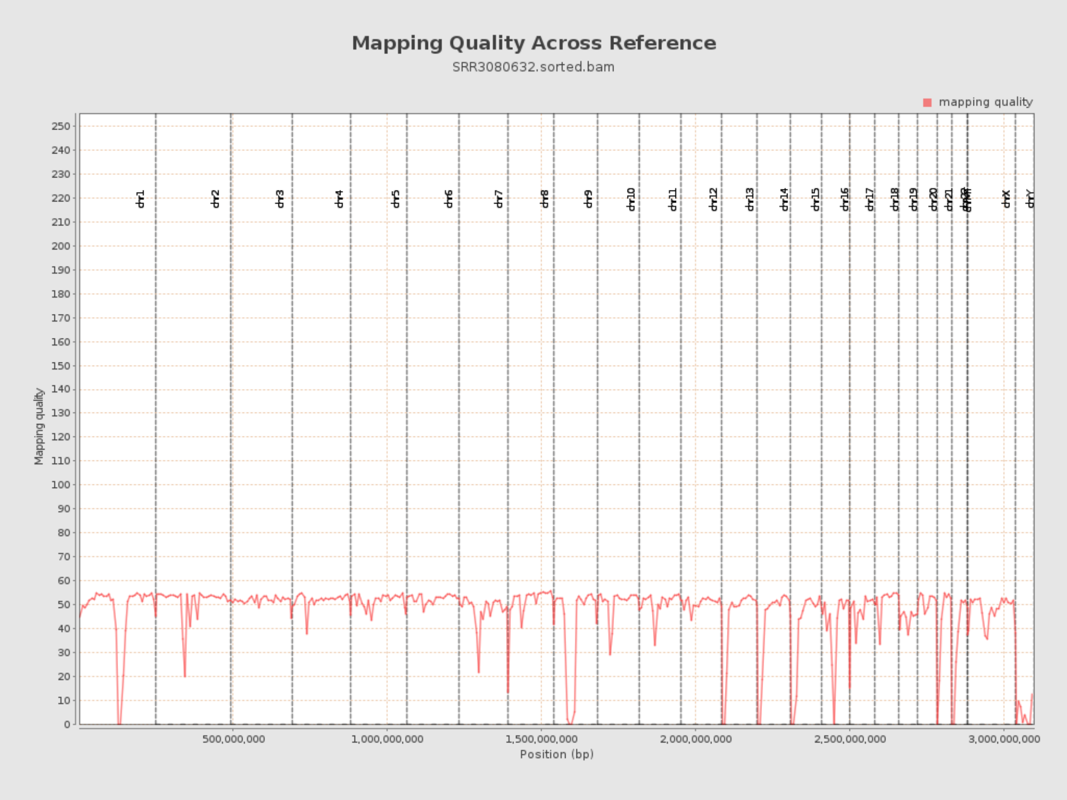
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram