Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 11:17:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081945.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_SRR3081945 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081945.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 11:17:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081945.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,006,851
Mapped reads	2,773,598 / 92.24%
Unmapped reads	233,253 / 7.76%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,164 / 0.57%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	129,979 / 4.32%
Duplication rate	3.86%
Clipped reads	1,037,710 / 34.51%

2.2. ACGT Content

Number/percentage of A's	53,451,969 / 28.28%
Number/percentage of C's	35,044,032 / 18.54%
Number/percentage of T's	59,608,951 / 31.54%
Number/percentage of G's	40,860,500 / 21.62%
Number/percentage of N's	24,419 / 0.01%
GC Percentage	40.16%

2.3. Coverage

Mean	0.0611

Standard Deviation	0.4344

2.4. Mapping Quality

Mean Mapping Quality	46.69

2.5. Mismatches and indels

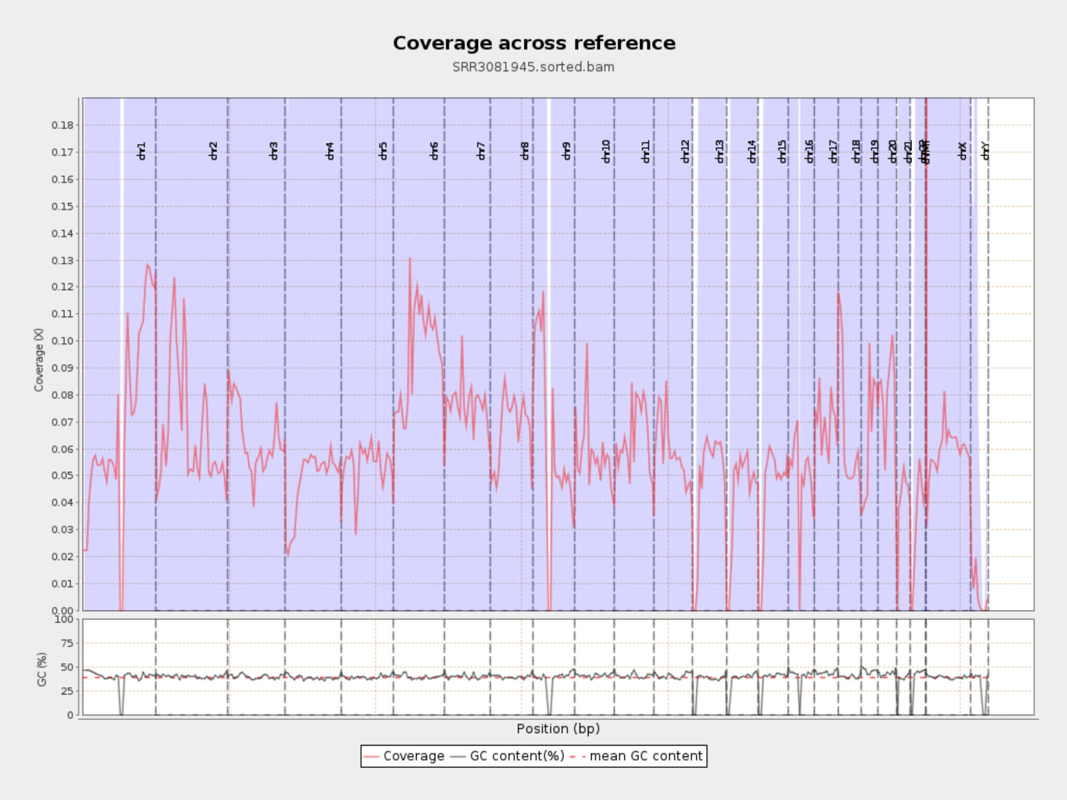
General error rate	0.76%
Mismatches	1,413,013
Insertions	12,995
Mapped reads with at least one insertion	0.46%
Deletions	40,422
Mapped reads with at least one deletion	1.44%
Homopolymer indels	49.03%

2.6. Chromosome stats

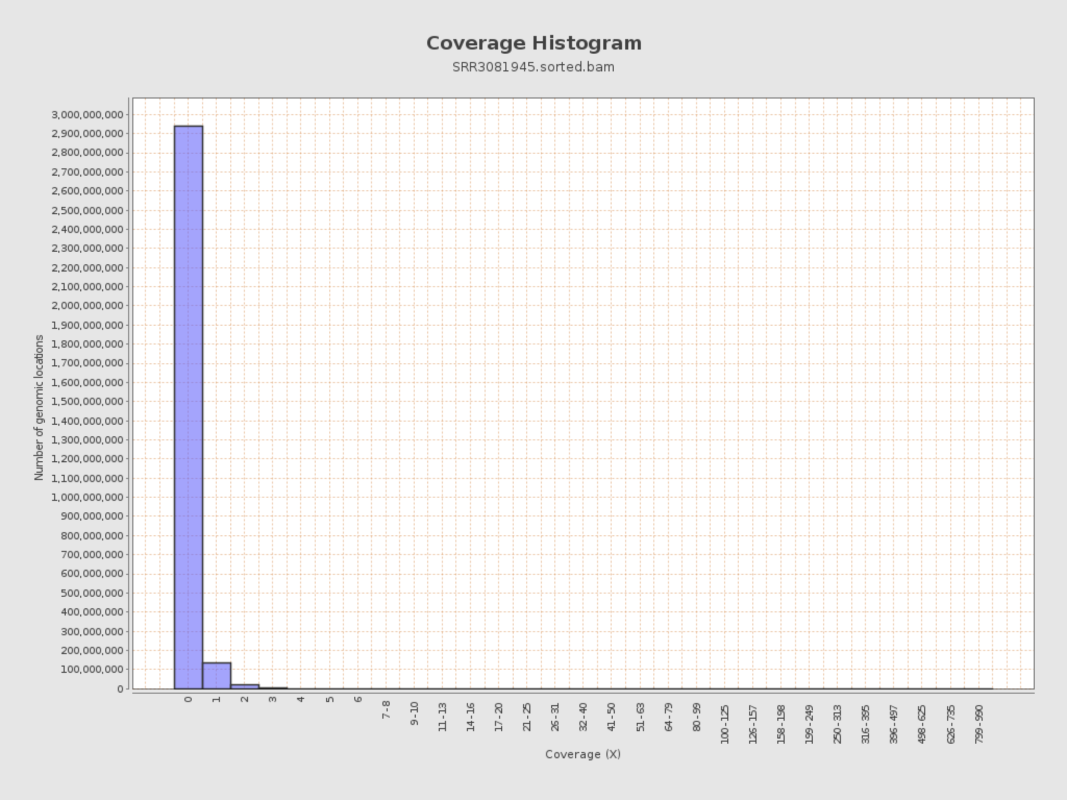
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17403325	0.0698	0.6755
chr2	243199373	16335608	0.0672	0.544
chr3	198022430	12664429	0.064	0.2909
chr4	191154276	9189184	0.0481	0.2647
chr5	180915260	9751474	0.0539	0.2651
chr6	171115067	16434665	0.096	0.4463
chr7	159138663	12123213	0.0762	0.6062

chr8	146364022	9870117	0.0674	0.6737
chr9	141213431	8845529	0.0626	0.444
chr10	135534747	7910235	0.0584	0.4387
chr11	135006516	8645915	0.064	0.3348
chr12	133851895	7925832	0.0592	0.2849
chr13	115169878	5496749	0.0477	0.2486
chr14	107349540	4645996	0.0433	0.2552
chr15	102531392	4430762	0.0432	0.2378
chr16	90354753	4405053	0.0488	0.2926
chr17	81195210	5699692	0.0702	0.346
chr18	78077248	5162465	0.0661	0.6486
chr19	59128983	3784647	0.064	0.5499
chr20	63025520	5114288	0.0811	0.3316
chr21	48129895	1956709	0.0407	0.2533
chr22	51304566	1672939	0.0326	0.2038
chrMT	16571	44711	2.6981	2.2526
chrX	155270560	9174533	0.0591	0.3037
chrY	59373566	373505	0.0063	0.1442

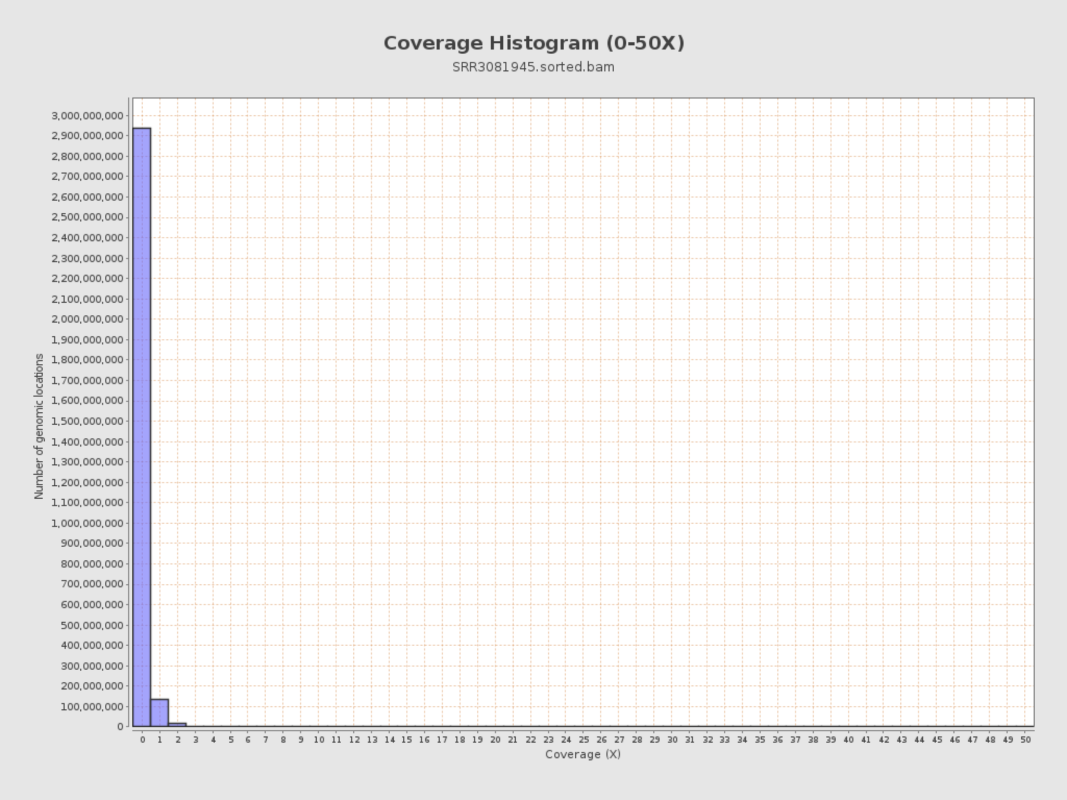
3. Results : Coverage across reference



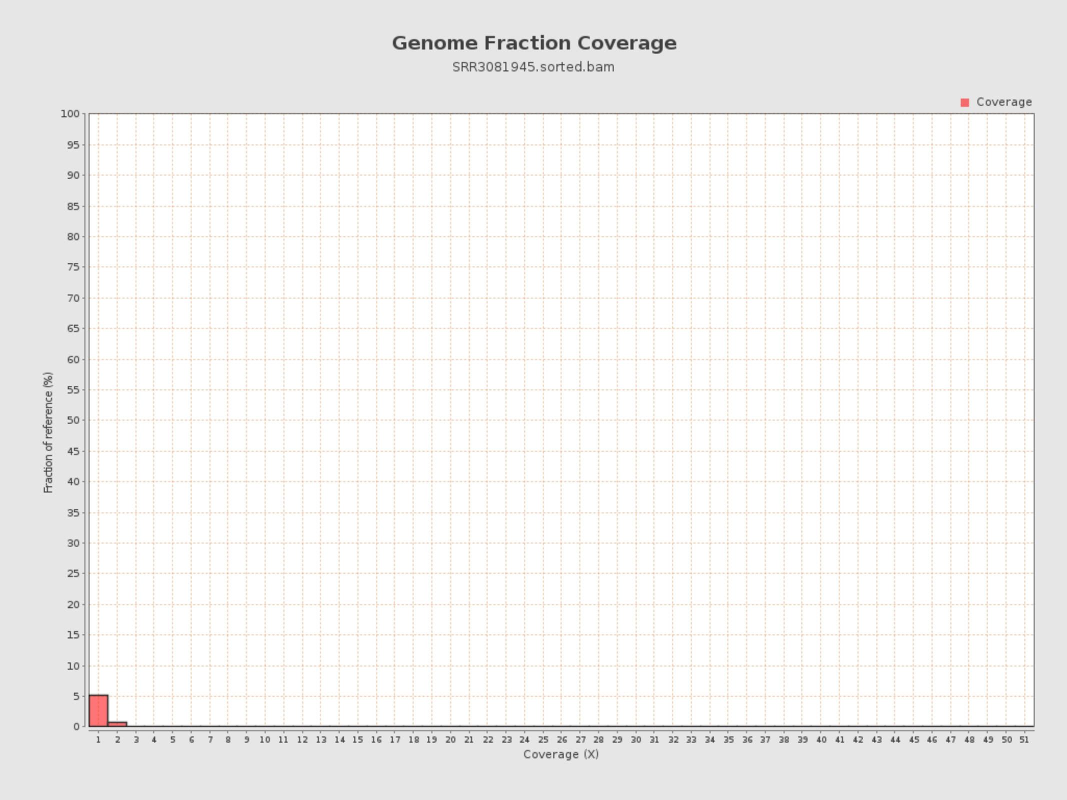
4. Results : Coverage Histogram



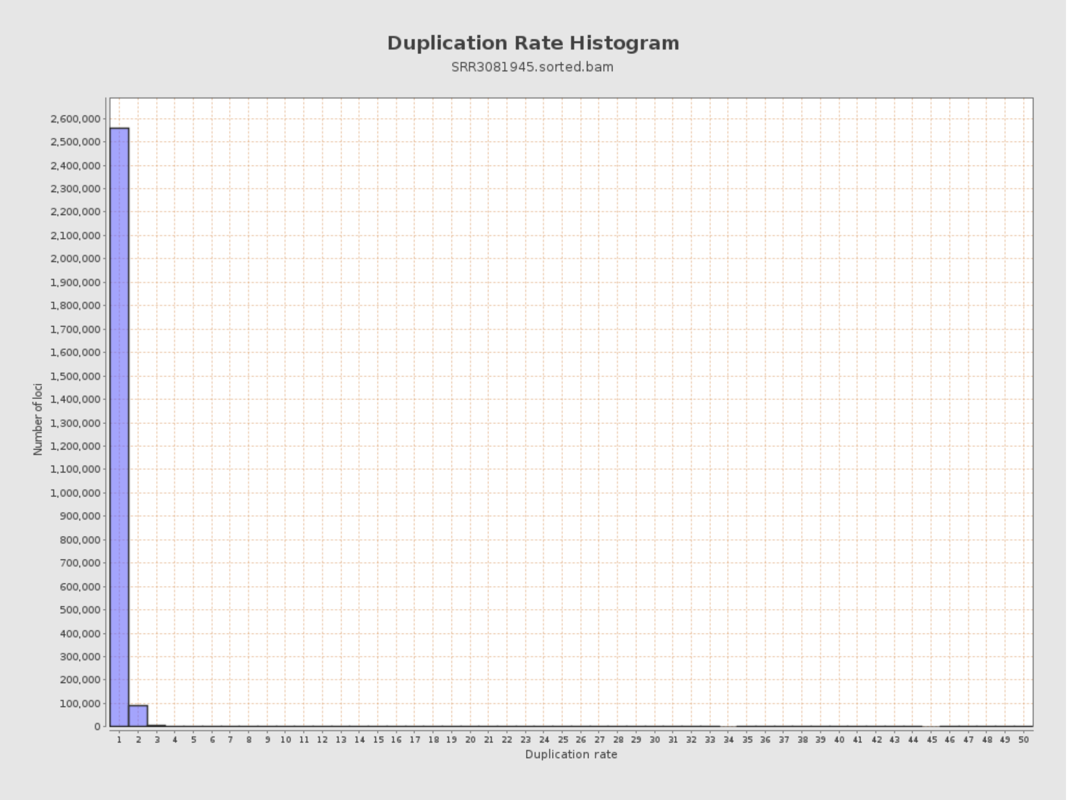
5. Results : Coverage Histogram (0-50X)



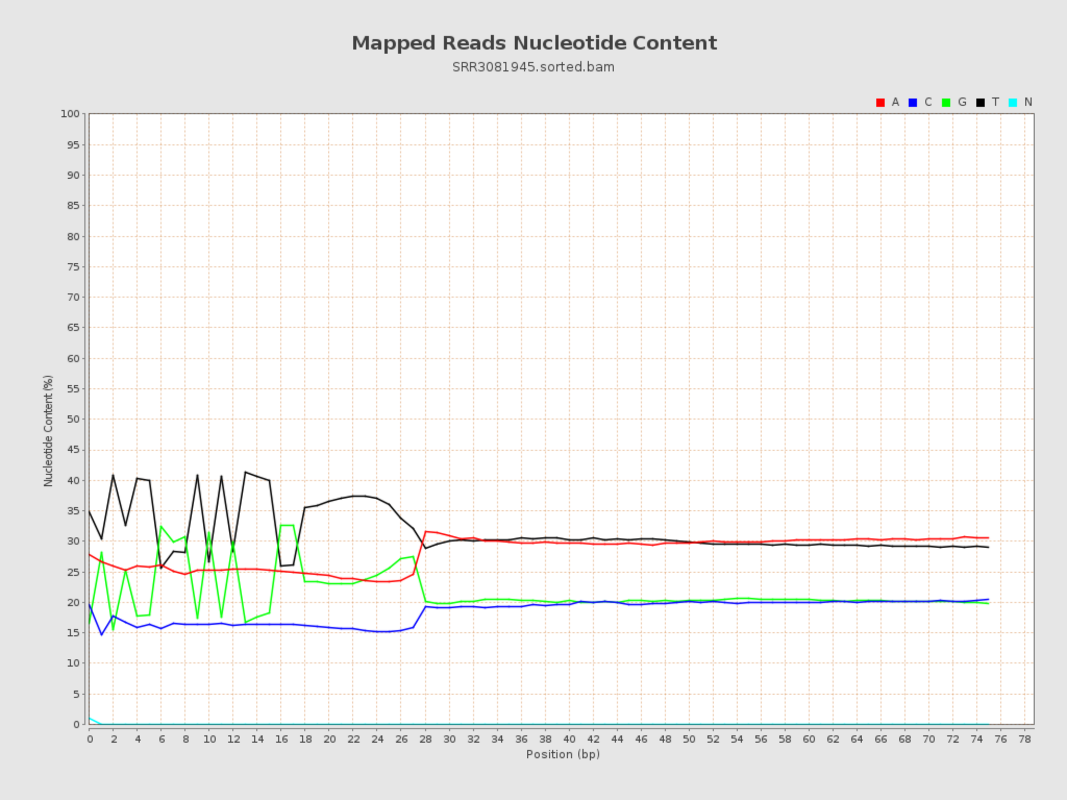
6. Results : Genome Fraction Coverage



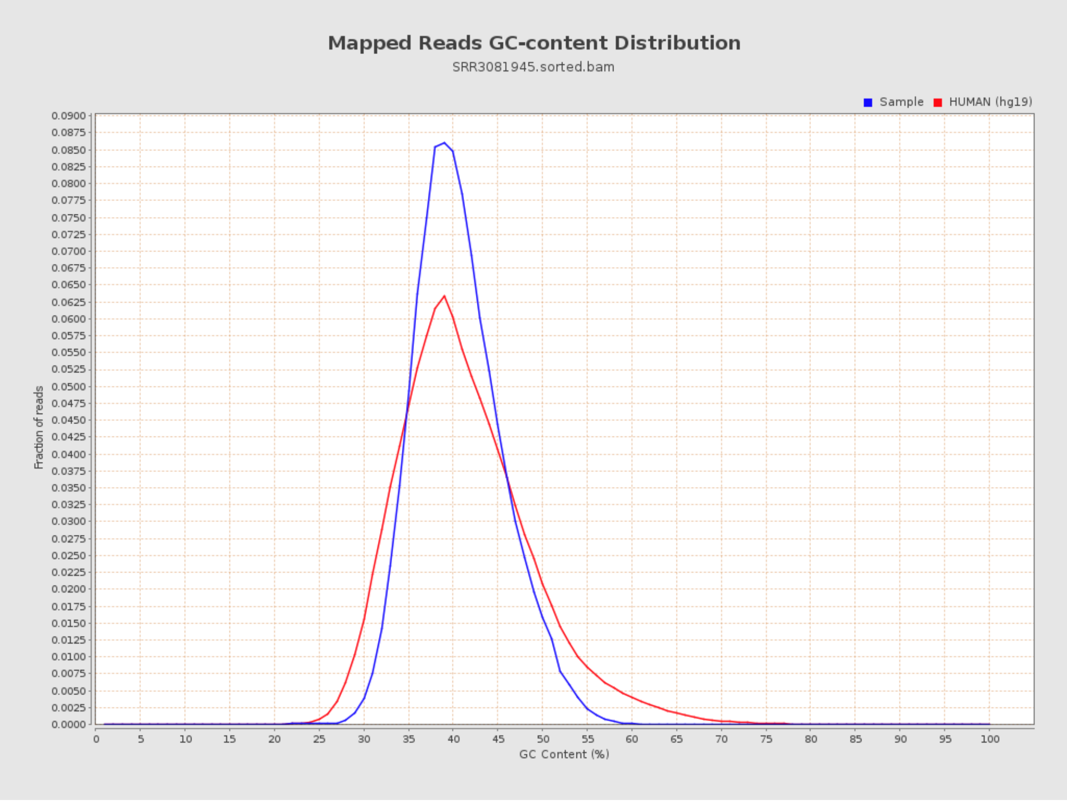
7. Results : Duplication Rate Histogram



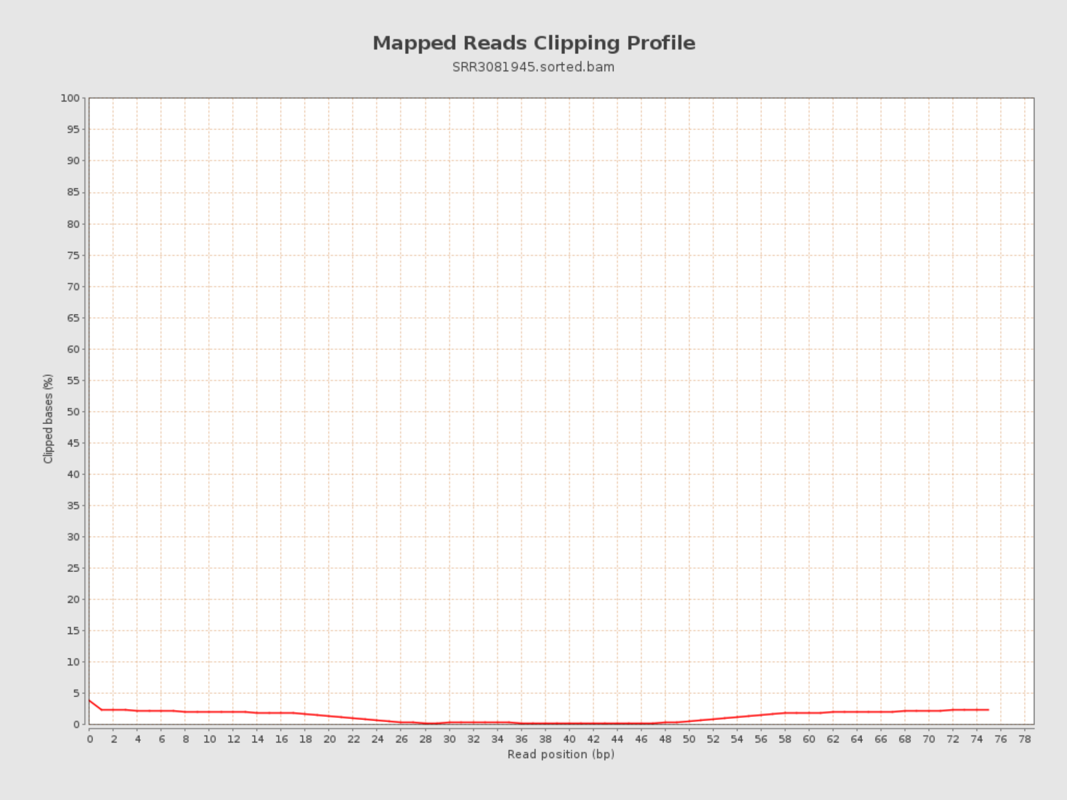
8. Results : Mapped Reads Nucleotide Content



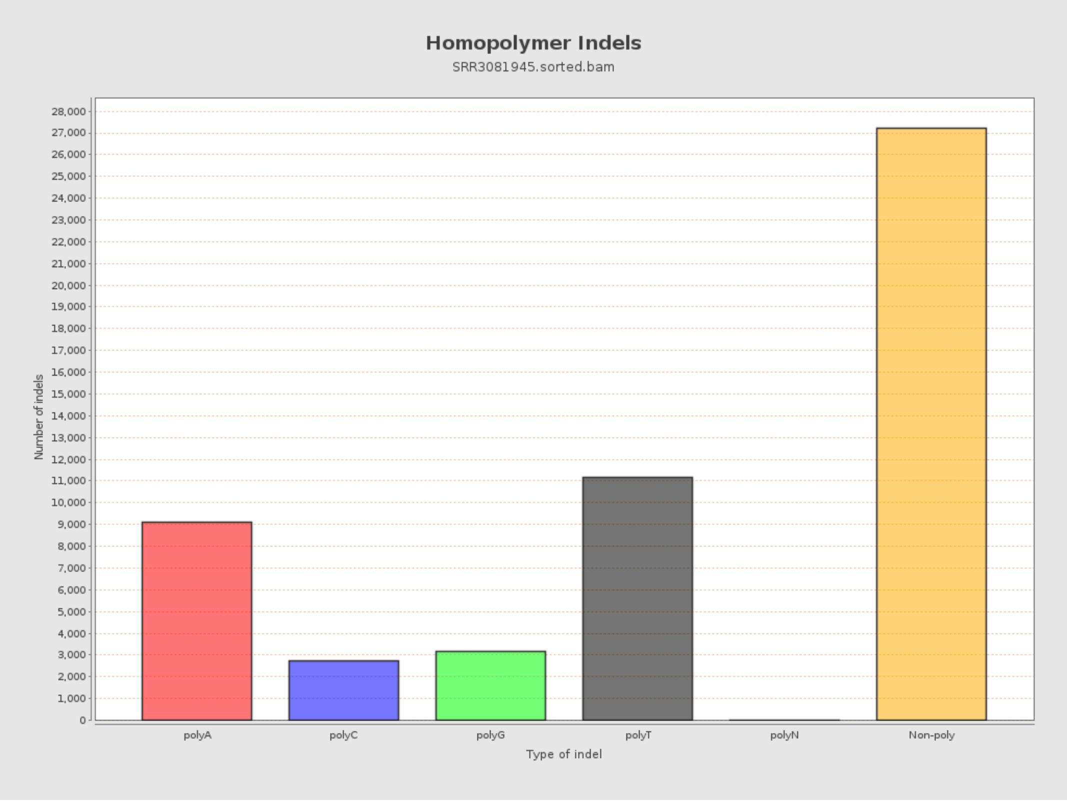
9. Results : Mapped Reads GC-content Distribution



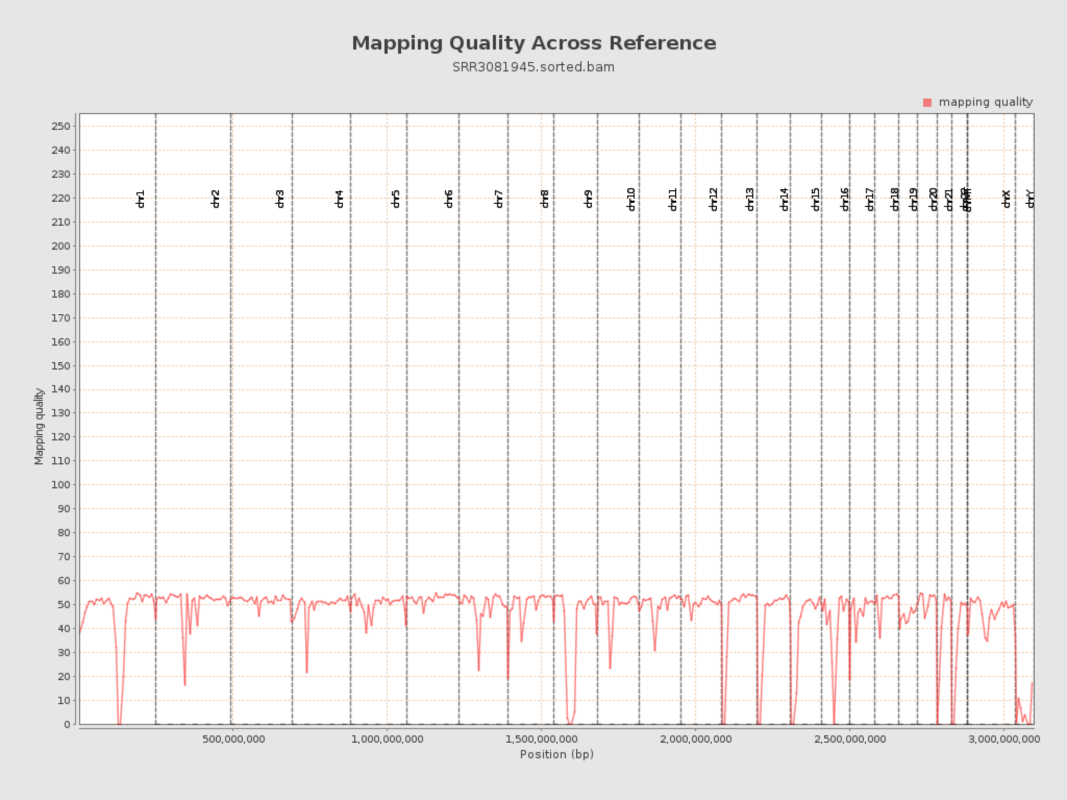
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram