Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 18:14:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082783.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_SRR3082783 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082783.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 18:14:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082783.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,988,084
Mapped reads	3,384,778 / 84.87%
Unmapped reads	603,306 / 15.13%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,441 / 0.64%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	194,947 / 4.89%
Duplication rate	4.67%
Clipped reads	1,395,183 / 34.98%

2.2. ACGT Content

Number/percentage of A's	64,996,512 / 28.38%
Number/percentage of C's	41,208,117 / 17.99%
Number/percentage of T's	74,904,277 / 32.7%
Number/percentage of G's	47,924,069 / 20.92%
Number/percentage of N's	12,776 / 0.01%
GC Percentage	38.91%

2.3. Coverage

Mean	0.074

Standard Deviation	0.5556

2.4. Mapping Quality

Mean Mapping Quality	47.2

2.5. Mismatches and indels

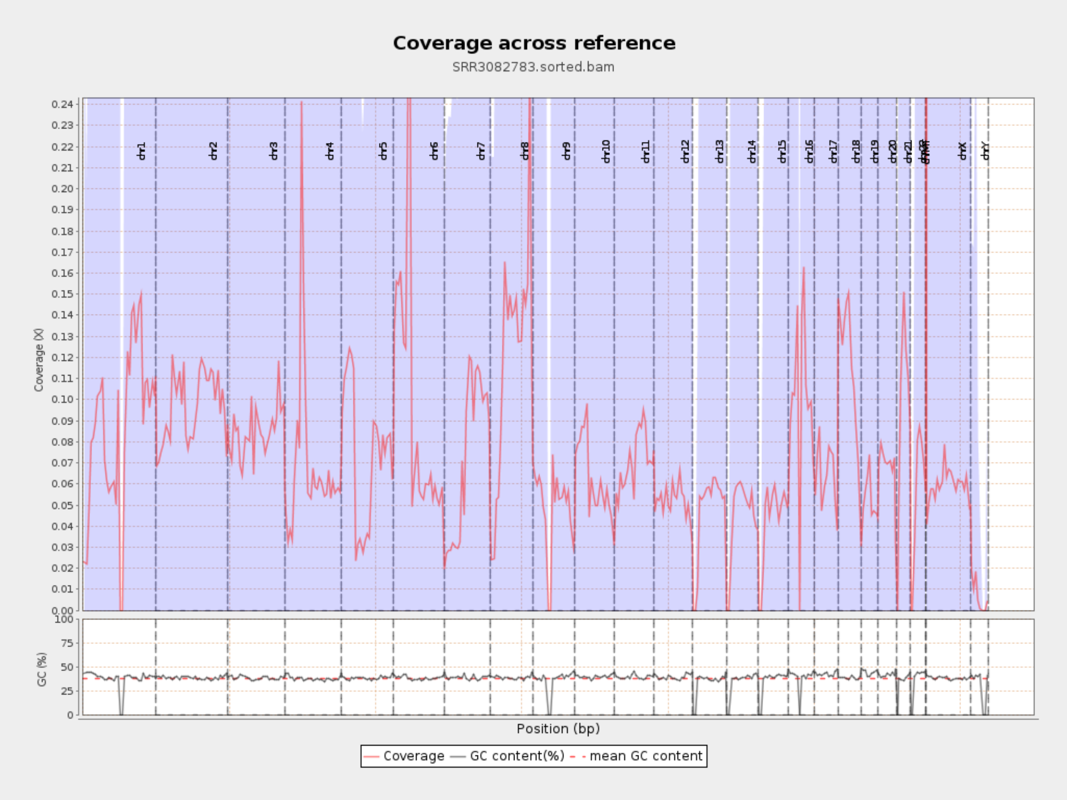
General error rate	0.9%
Mismatches	2,022,335
Insertions	18,447
Mapped reads with at least one insertion	0.54%
Deletions	50,751
Mapped reads with at least one deletion	1.48%
Homopolymer indels	47.94%

2.6. Chromosome stats

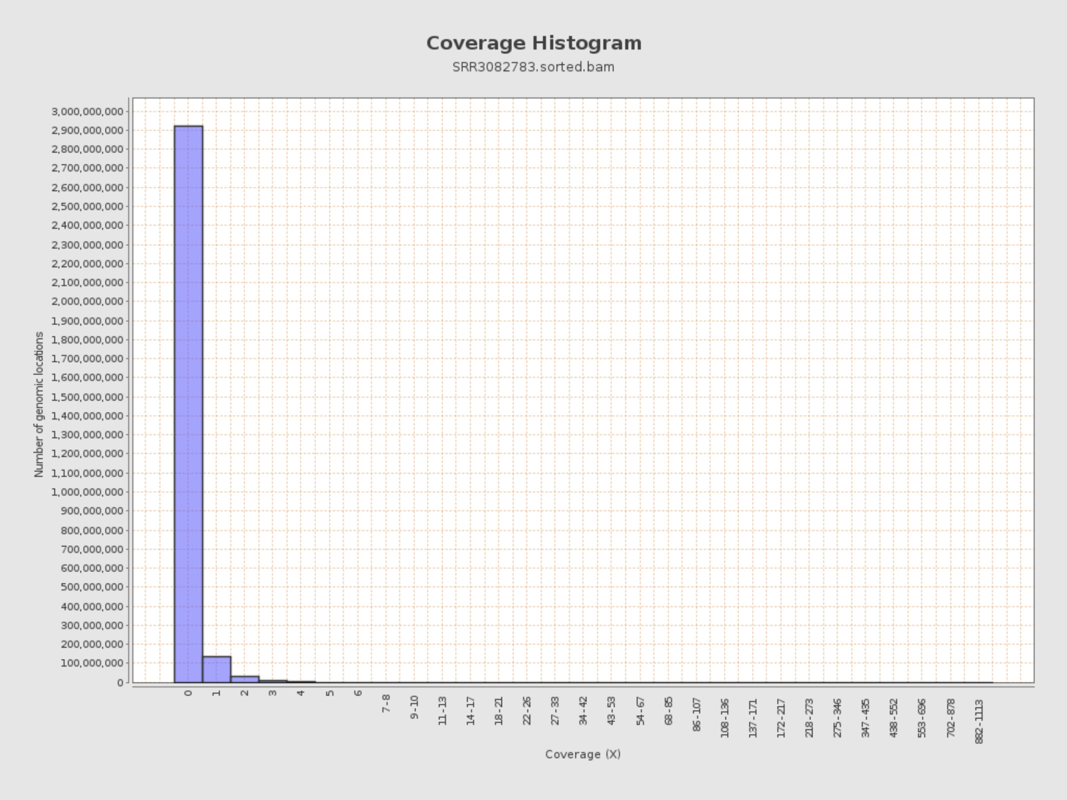
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	21497386	0.0862	1.0449
chr2	243199373	23640921	0.0972	0.6634
chr3	198022430	16768171	0.0847	0.3603
chr4	191154276	13389263	0.07	0.3409
chr5	180915260	13137887	0.0726	0.3376
chr6	171115067	16774685	0.098	0.572
chr7	159138663	11559545	0.0726	0.4628

chr8	146364022	17817173	0.1217	0.8367
chr9	141213431	6856340	0.0486	0.4649
chr10	135534747	8513955	0.0628	0.442
chr11	135006516	9463990	0.0701	0.4462
chr12	133851895	6965596	0.052	0.2925
chr13	115169878	5415302	0.047	0.2686
chr14	107349540	4851083	0.0452	0.3099
chr15	102531392	4318932	0.0421	0.2529
chr16	90354753	8887518	0.0984	0.4385
chr17	81195210	5305581	0.0653	0.3723
chr18	78077248	9099384	0.1165	1.0818
chr19	59128983	3125545	0.0529	0.6723
chr20	63025520	4397988	0.0698	0.3451
chr21	48129895	4604164	0.0957	0.3967
chr22	51304566	2800665	0.0546	0.2864
chrMT	16571	281678	16.9982	10.0901
chrX	155270560	9256520	0.0596	0.3549
chrY	59373566	402377	0.0068	0.1328

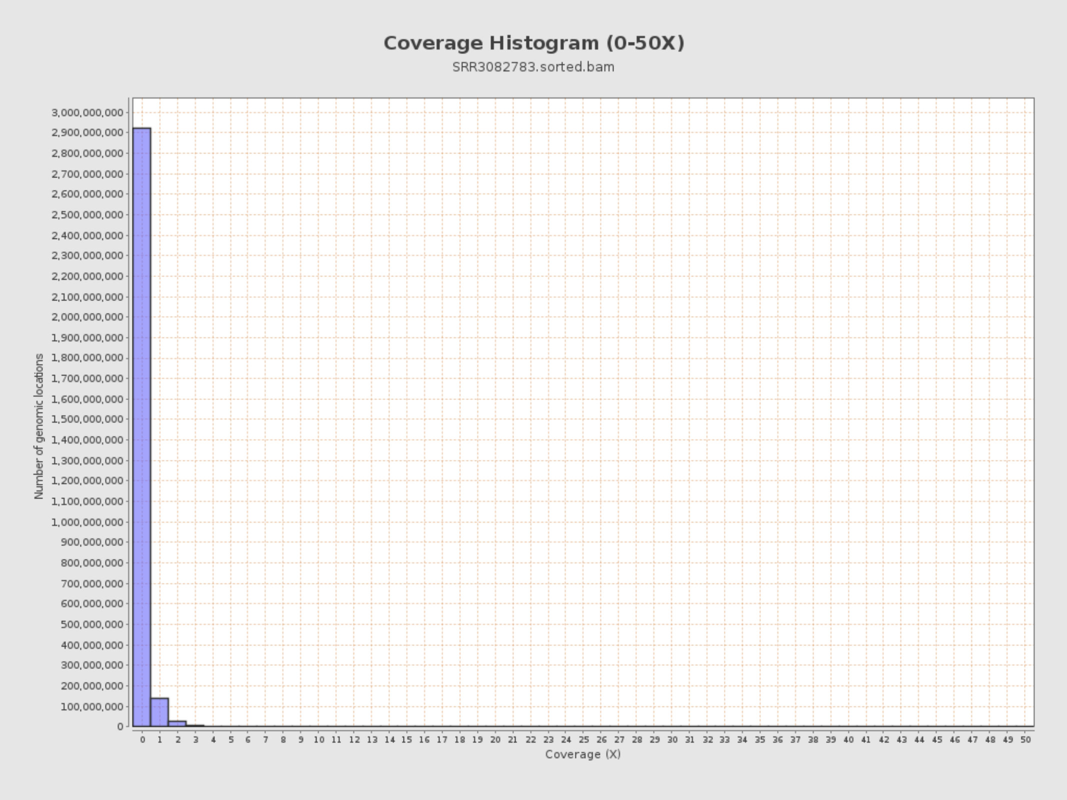
3. Results : Coverage across reference



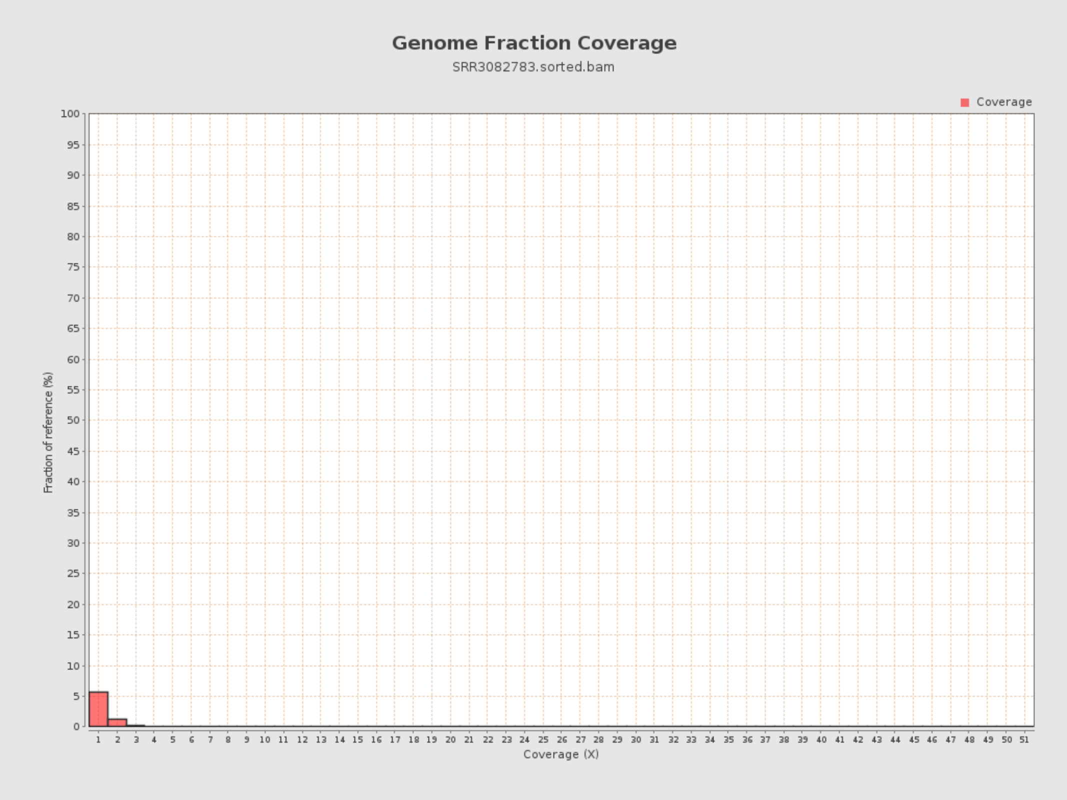
4. Results : Coverage Histogram



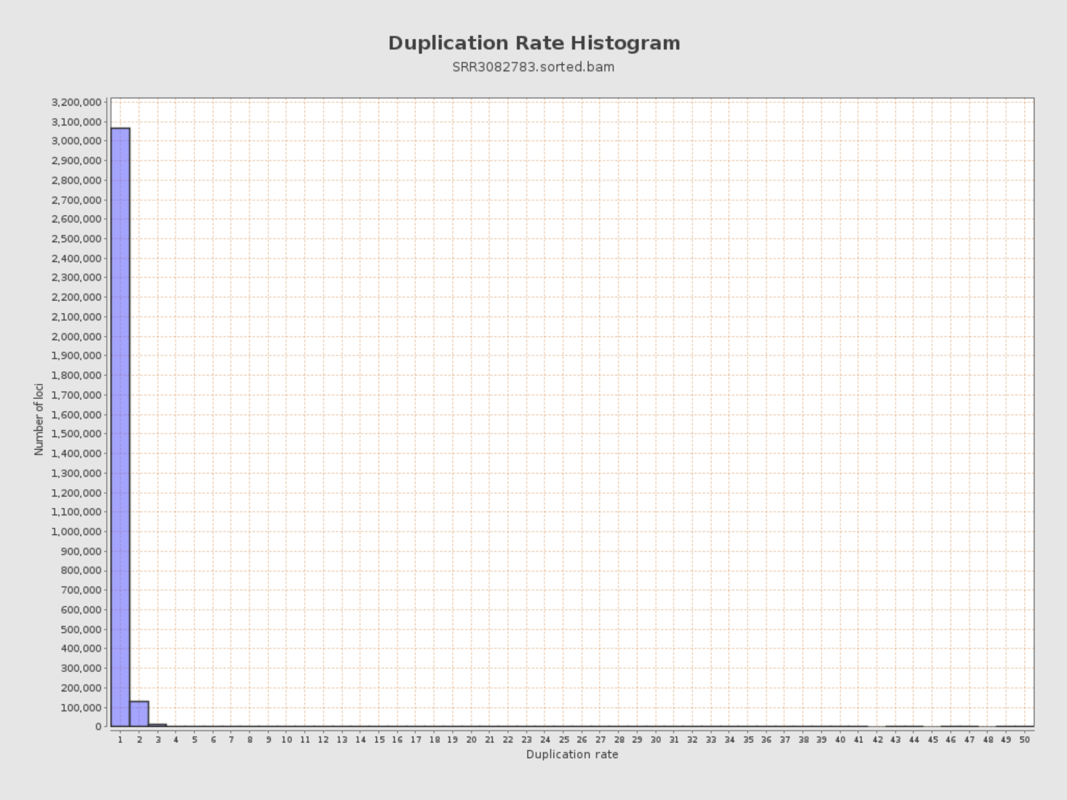
5. Results : Coverage Histogram (0-50X)



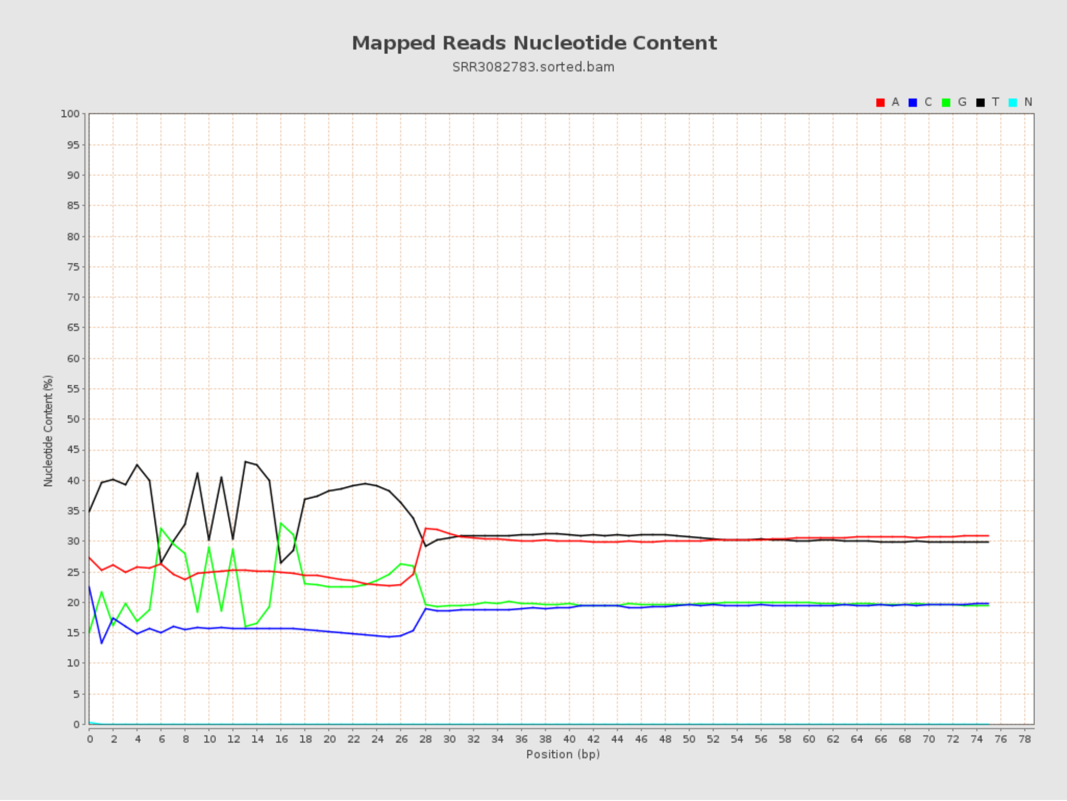
6. Results : Genome Fraction Coverage



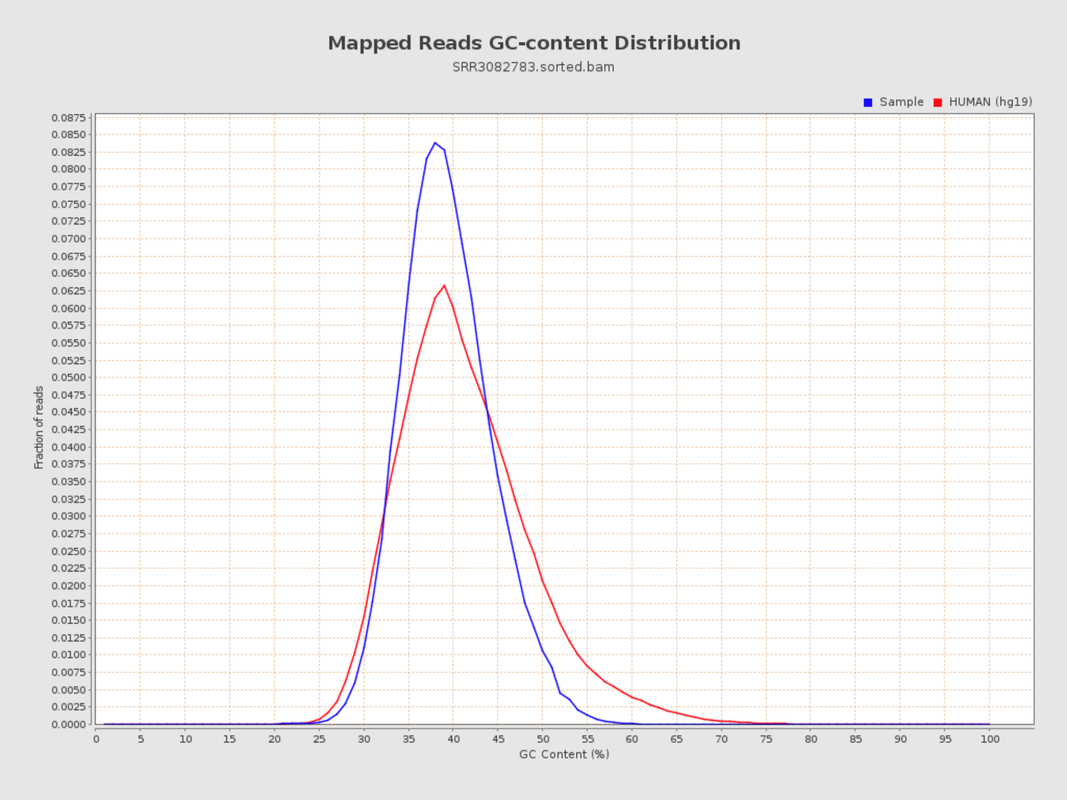
7. Results : Duplication Rate Histogram



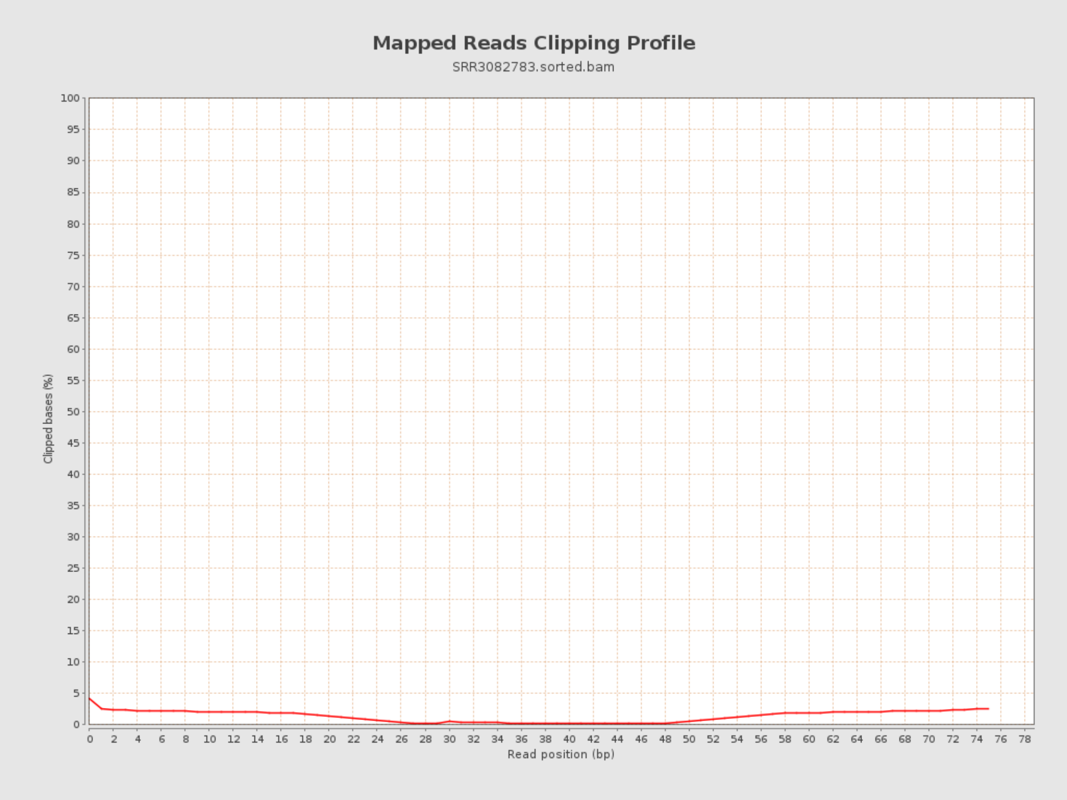
8. Results : Mapped Reads Nucleotide Content



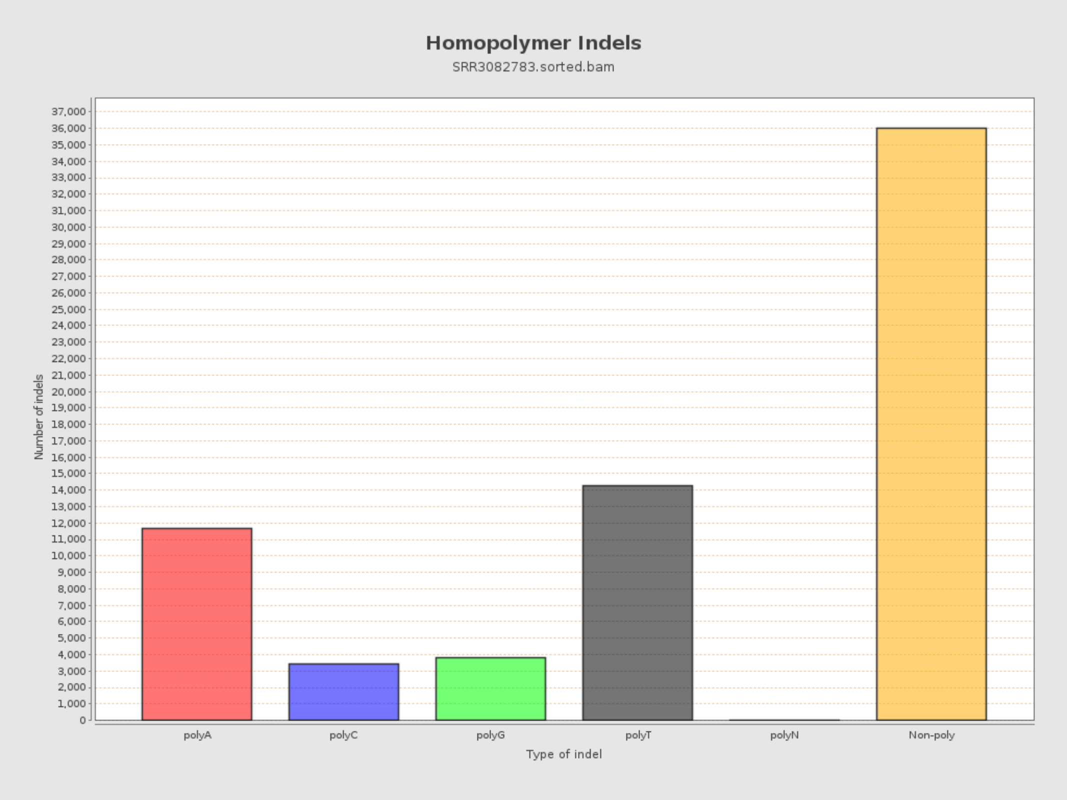
9. Results : Mapped Reads GC-content Distribution



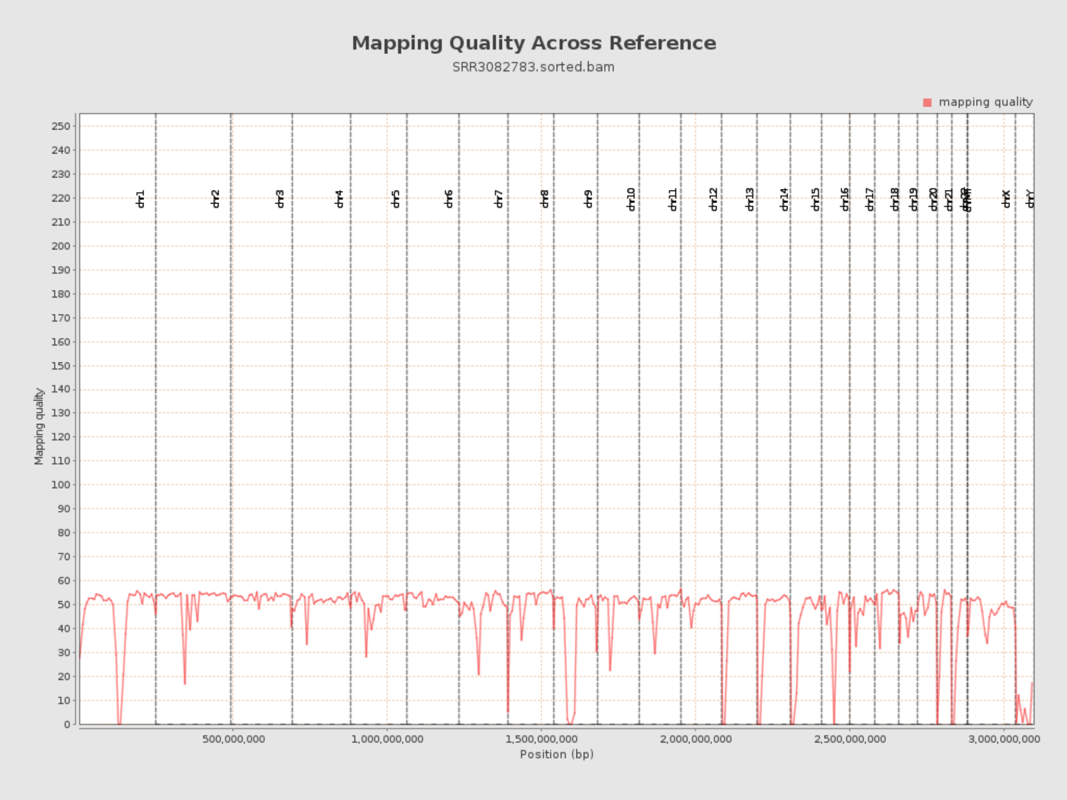
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram