Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 09:52:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080822.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_SRR3080822 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080822.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 09:52:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080822.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,539,370
Mapped reads	2,160,619 / 85.08%
Unmapped reads	378,751 / 14.92%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,059 / 0.87%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	182,368 / 7.18%
Duplication rate	6.92%
Clipped reads	911,664 / 35.9%

2.2. ACGT Content

Number/percentage of A's	42,044,251 / 28.78%
Number/percentage of C's	26,683,712 / 18.27%
Number/percentage of T's	46,417,688 / 31.78%
Number/percentage of G's	30,906,402 / 21.16%
Number/percentage of N's	20,426 / 0.01%
GC Percentage	39.43%

2.3. Coverage

Mean	0.0472

Standard Deviation	0.4393

2.4. Mapping Quality

Mean Mapping Quality	46.58

2.5. Mismatches and indels

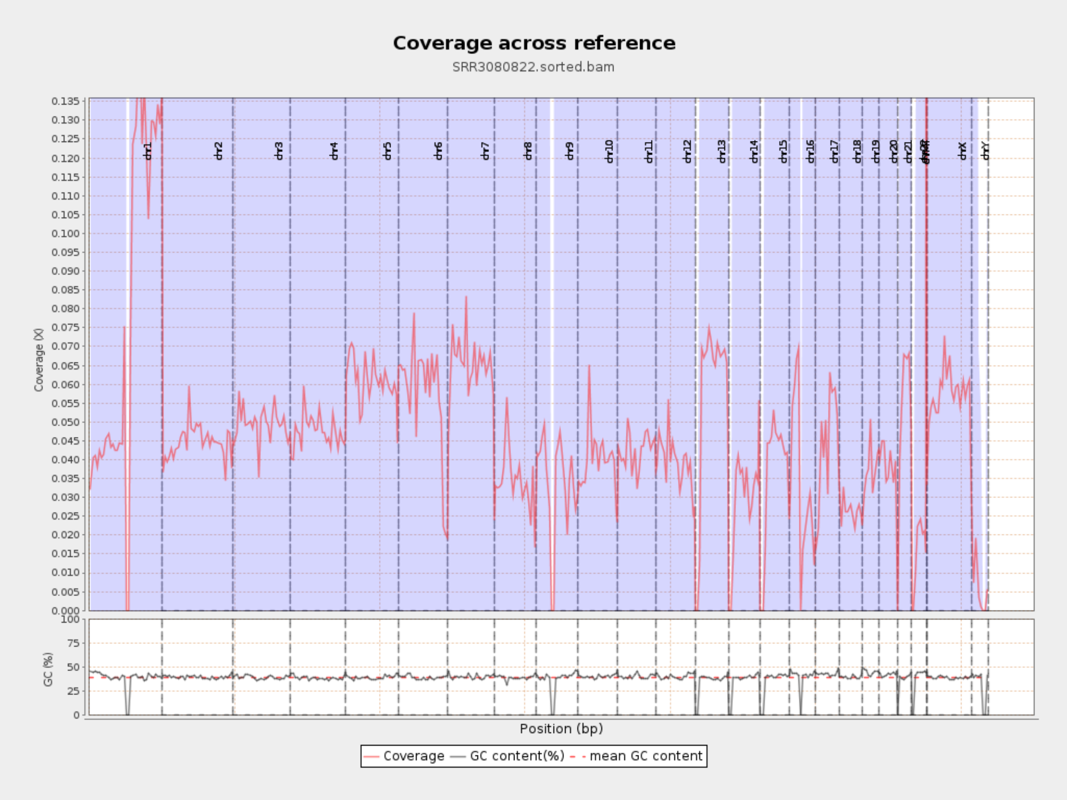
General error rate	0.82%
Mismatches	1,174,676
Insertions	11,283
Mapped reads with at least one insertion	0.52%
Deletions	31,311
Mapped reads with at least one deletion	1.43%
Homopolymer indels	47.25%

2.6. Chromosome stats

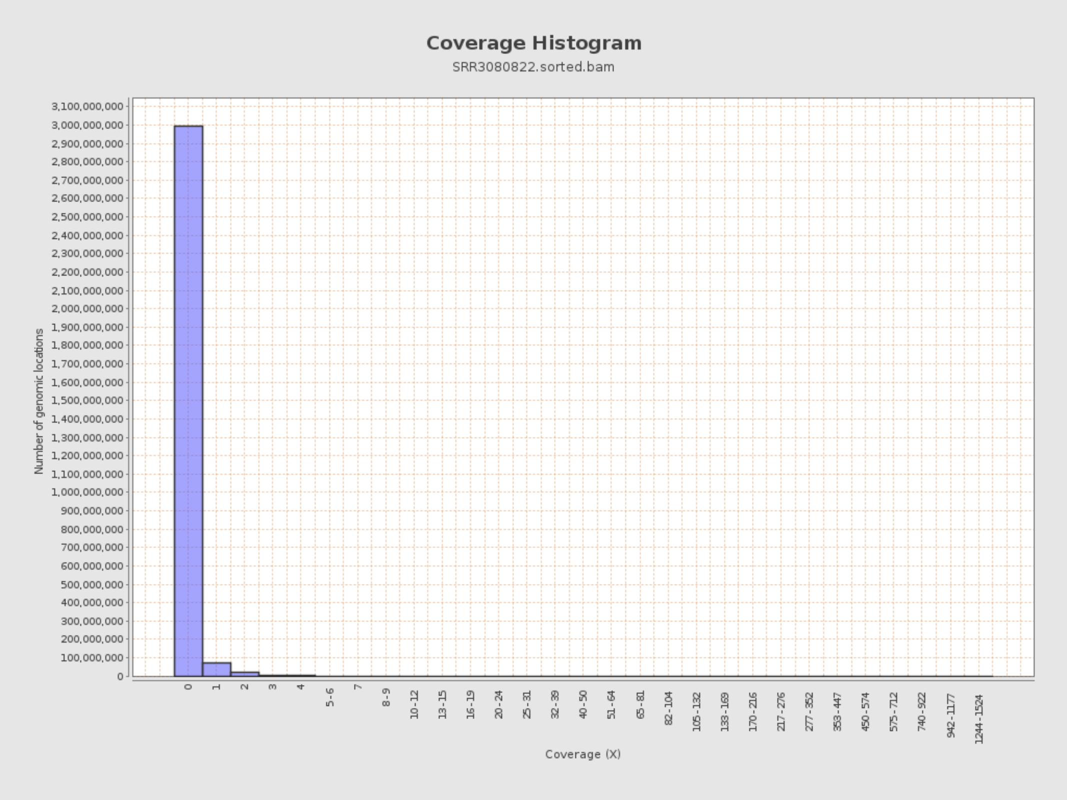
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19288728	0.0774	0.7535
chr2	243199373	10875638	0.0447	0.4075
chr3	198022430	9804105	0.0495	0.3022
chr4	191154276	9060776	0.0474	0.3104
chr5	180915260	11111120	0.0614	0.3386
chr6	171115067	9859570	0.0576	0.3653
chr7	159138663	10486432	0.0659	0.5248

chr8	146364022	5036629	0.0344	0.9596
chr9	141213431	4752332	0.0337	0.2918
chr10	135534747	5478201	0.0404	0.3611
chr11	135006516	5687989	0.0421	0.3025
chr12	133851895	5305568	0.0396	0.2724
chr13	115169878	6580668	0.0571	0.33
chr14	107349540	3068956	0.0286	0.2429
chr15	102531392	3712845	0.0362	0.2571
chr16	90354753	3116413	0.0345	0.2647
chr17	81195210	3598377	0.0443	0.298
chr18	78077248	2075486	0.0266	0.4672
chr19	59128983	2196338	0.0371	0.5485
chr20	63025520	2429721	0.0386	0.2706
chr21	48129895	2542977	0.0528	0.3255
chr22	51304566	783342	0.0153	0.1606
chrMT	16571	10811	0.6524	1.09
chrX	155270560	8904345	0.0573	0.3385
chrY	59373566	360165	0.0061	0.1411

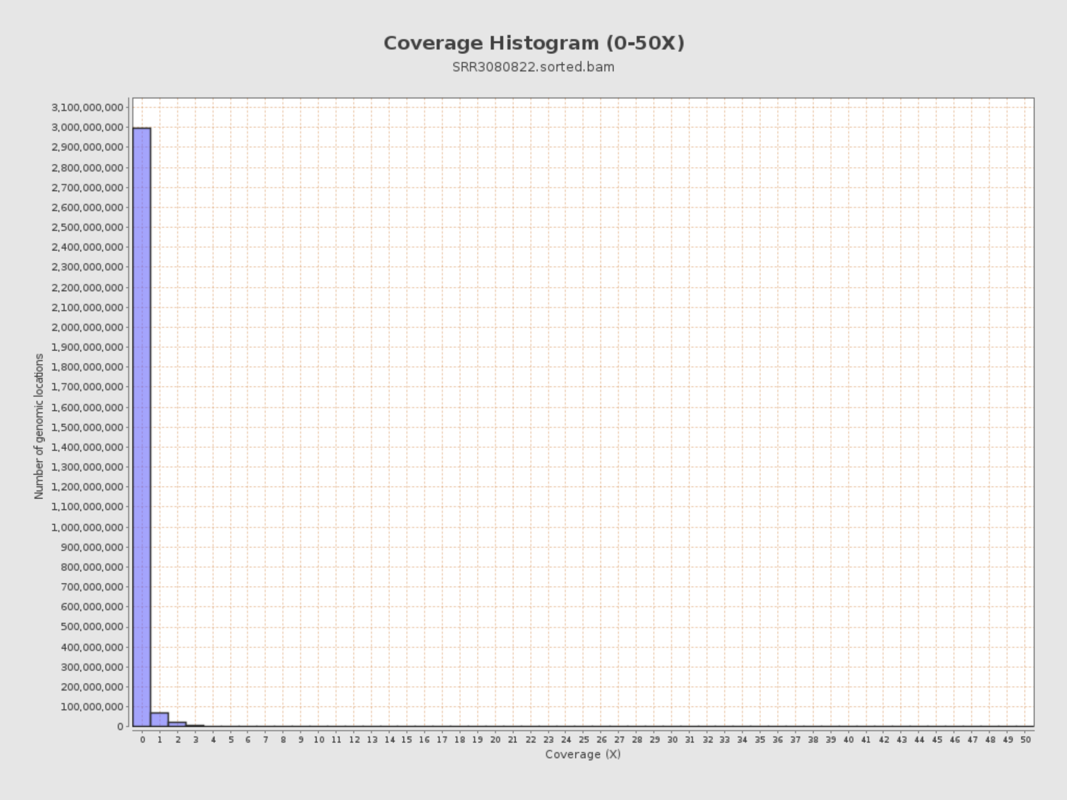
3. Results : Coverage across reference



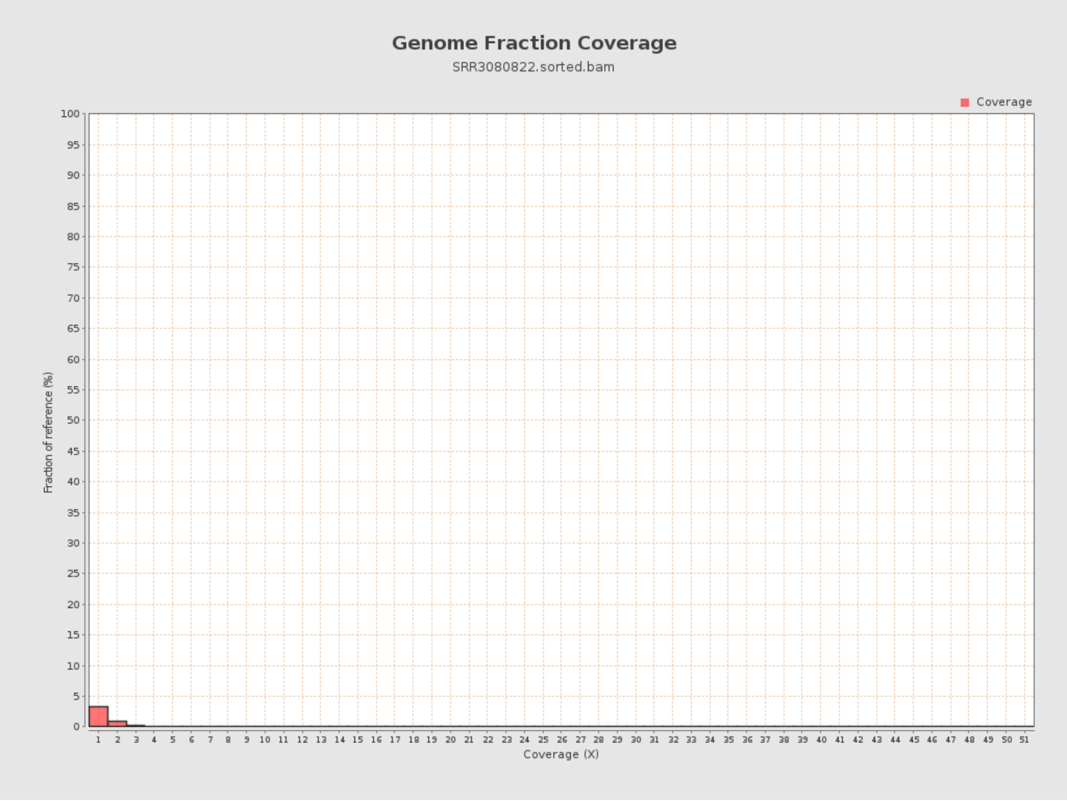
4. Results : Coverage Histogram



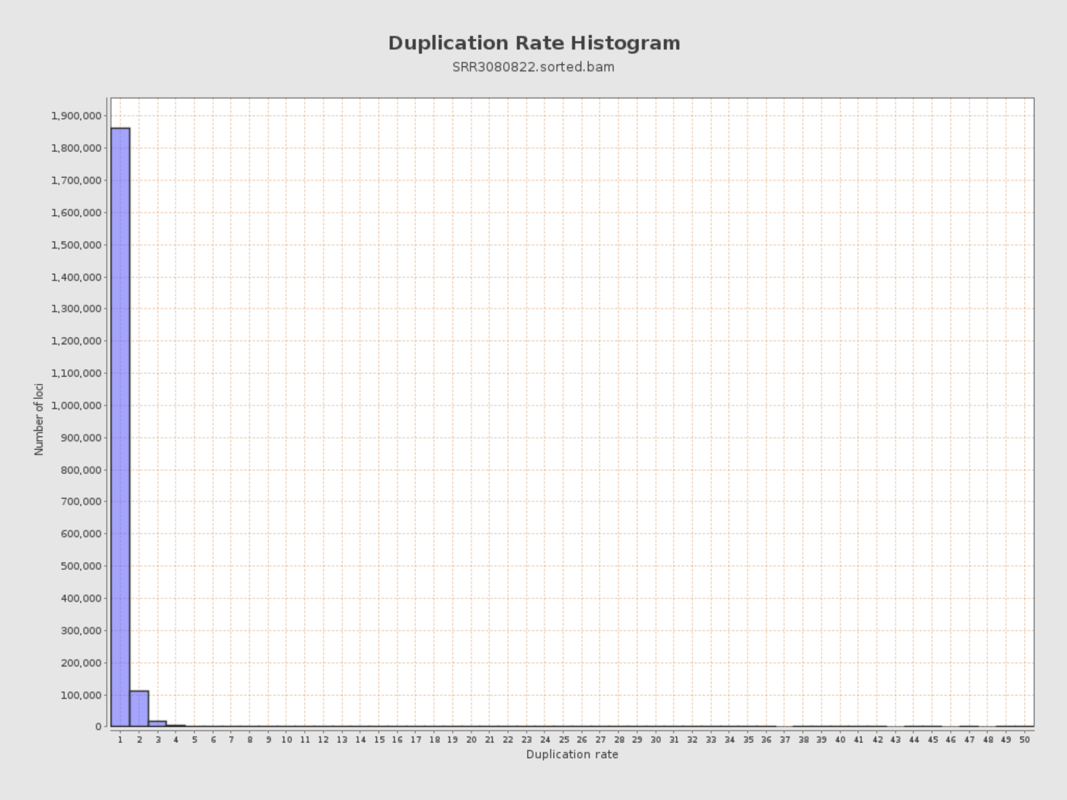
5. Results : Coverage Histogram (0-50X)



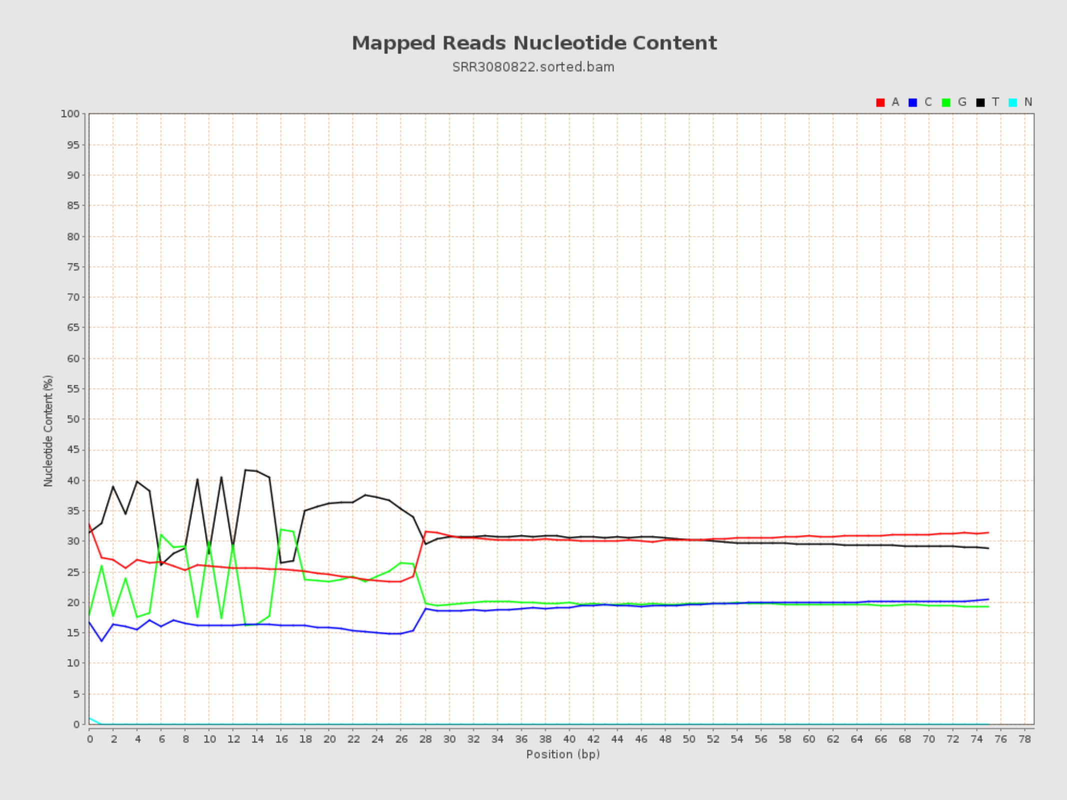
6. Results : Genome Fraction Coverage



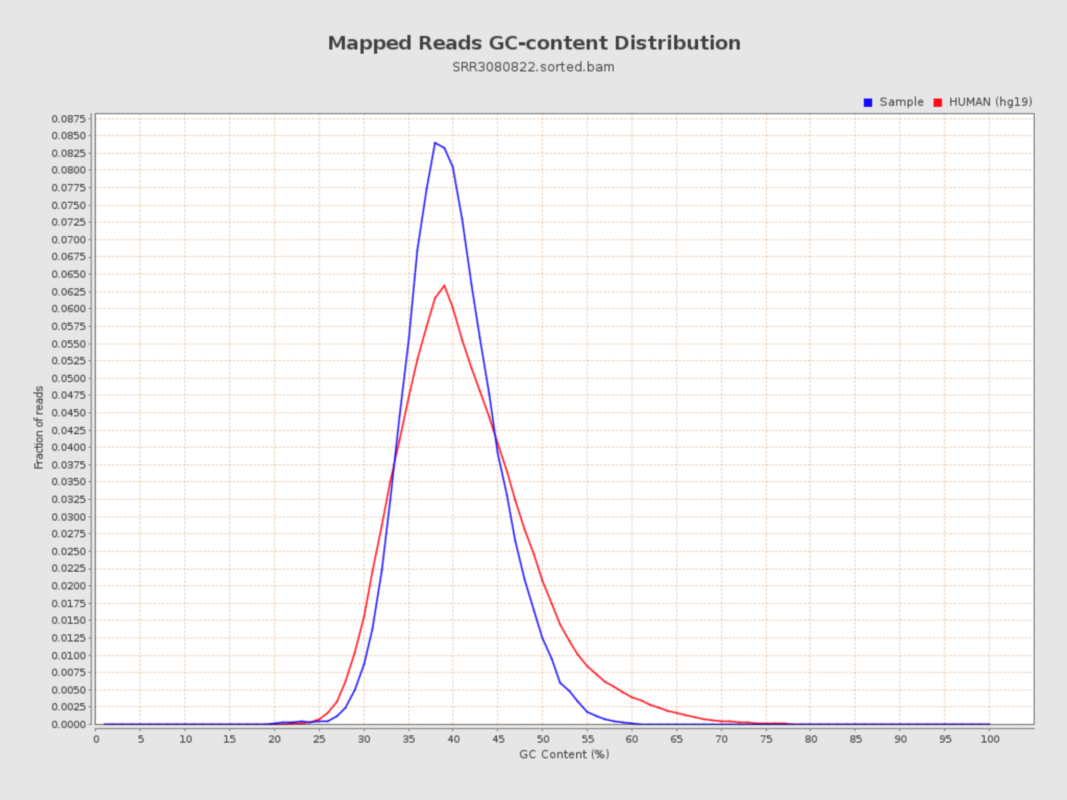
7. Results : Duplication Rate Histogram



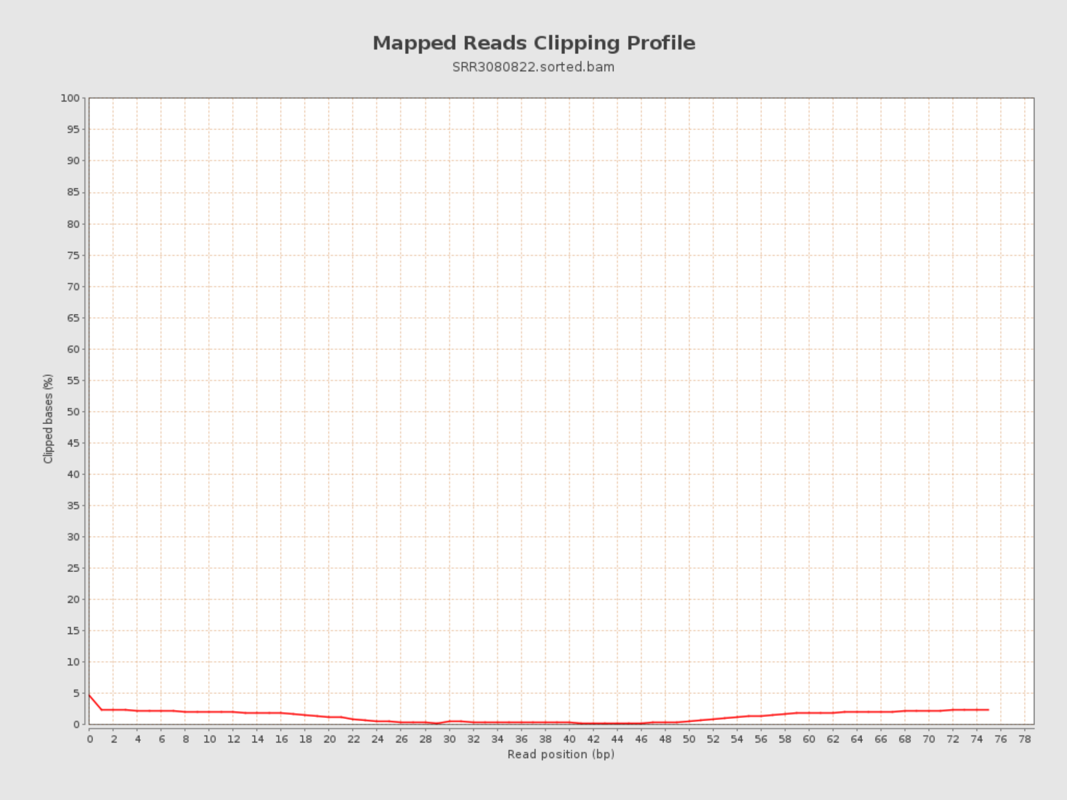
8. Results : Mapped Reads Nucleotide Content



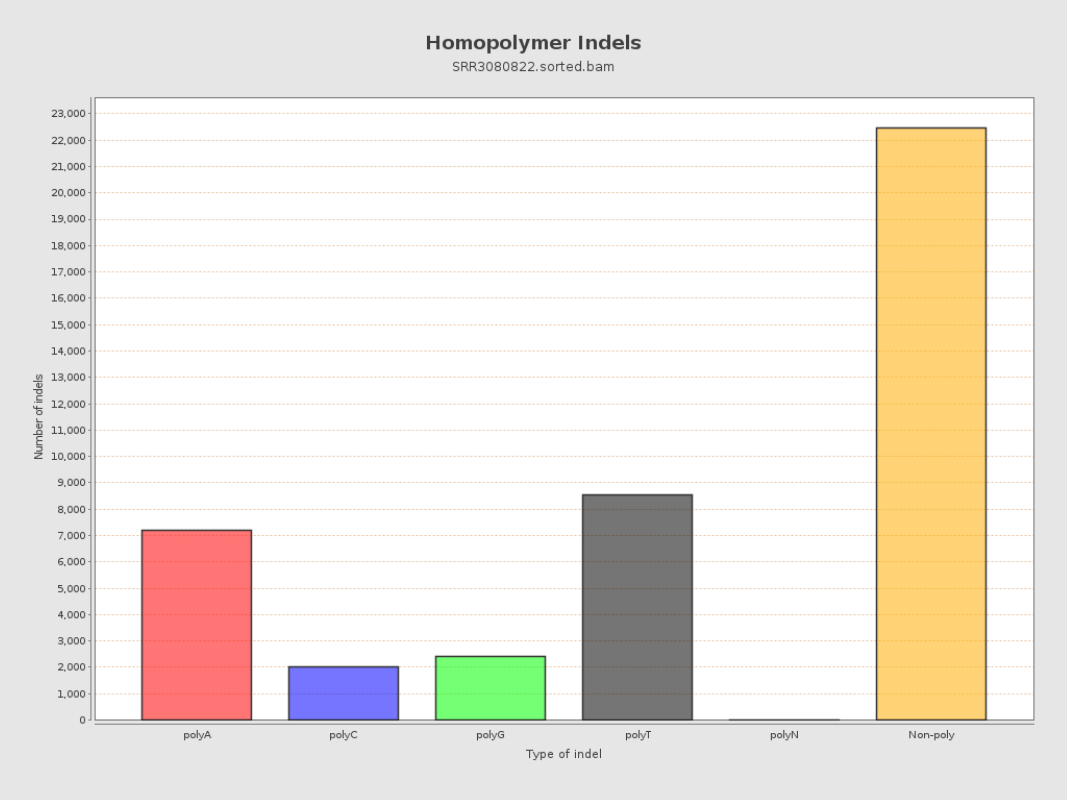
9. Results : Mapped Reads GC-content Distribution



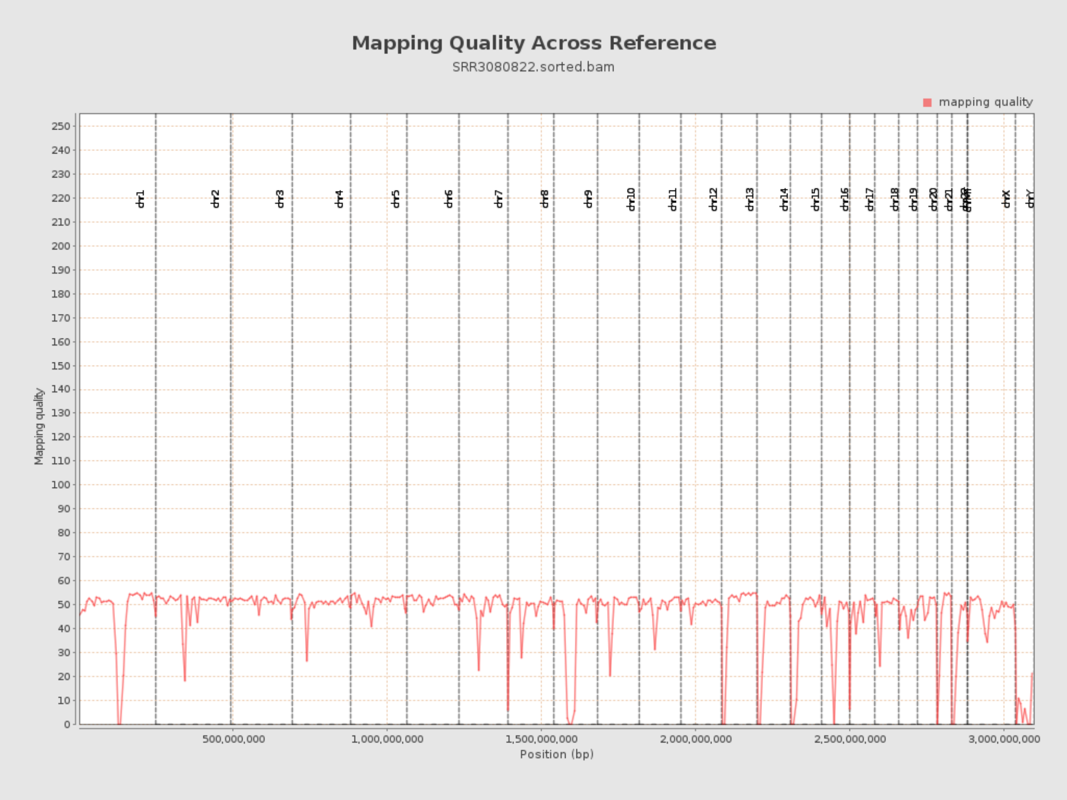
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram