Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 08:49:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080803.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_SRR3080803 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080803.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 08:49:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080803.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,419,063
Mapped reads	2,029,573 / 83.9%
Unmapped reads	389,490 / 16.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,949 / 1.07%
Read min/max/mean length	30 / 76 / 76.37
Duplicated reads (estimated)	160,866 / 6.65%
Duplication rate	6.56%
Clipped reads	820,190 / 33.91%

2.2. ACGT Content

Number/percentage of A's	40,889,546 / 29.59%
Number/percentage of C's	25,688,027 / 18.59%
Number/percentage of T's	42,196,404 / 30.53%
Number/percentage of G's	29,405,980 / 21.28%
Number/percentage of N's	18,363 / 0.01%
GC Percentage	39.87%

2.3. Coverage

Mean	0.0447

Standard Deviation	0.4403

2.4. Mapping Quality

Mean Mapping Quality	46.87

2.5. Mismatches and indels

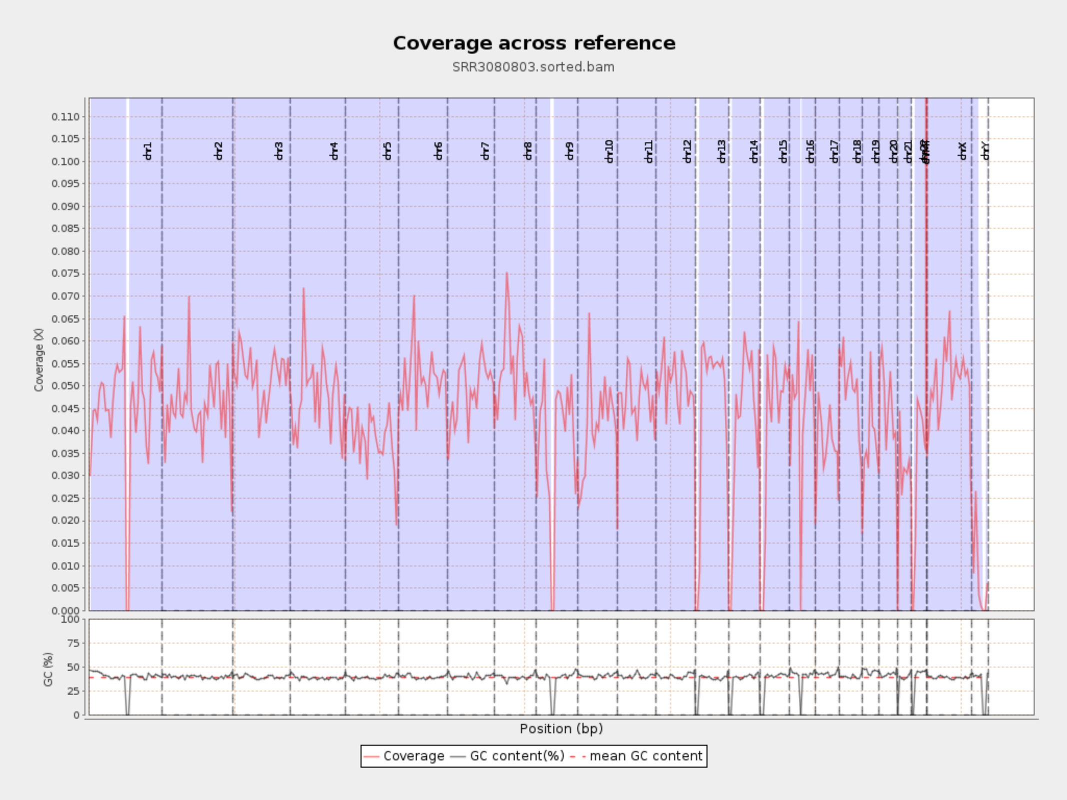
General error rate	0.85%
Mismatches	1,157,833
Insertions	11,157
Mapped reads with at least one insertion	0.54%
Deletions	29,049
Mapped reads with at least one deletion	1.41%
Homopolymer indels	46.51%

2.6. Chromosome stats

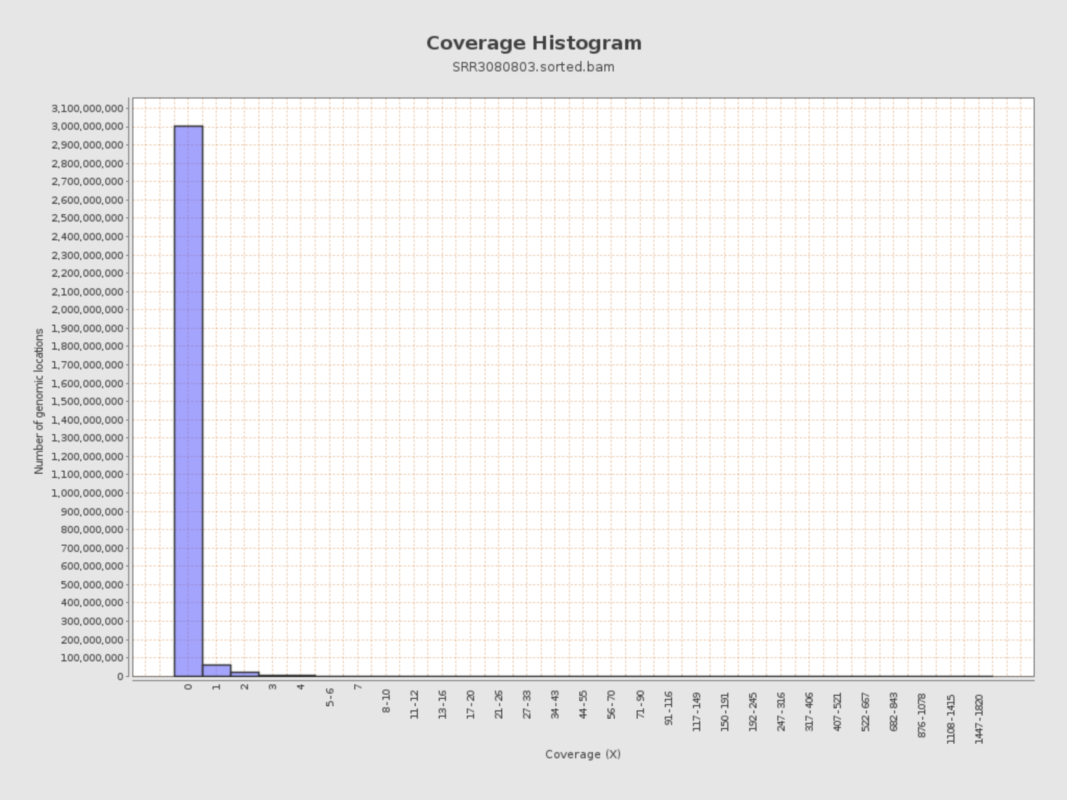
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11266296	0.0452	0.5388
chr2	243199373	11083671	0.0456	0.44
chr3	198022430	10374116	0.0524	0.319
chr4	191154276	9123770	0.0477	0.323
chr5	180915260	6898966	0.0381	0.2713
chr6	171115067	8827473	0.0516	0.3669
chr7	159138663	7825355	0.0492	0.366

chr8	146364022	7755694	0.053	1.1588
chr9	141213431	5311295	0.0376	0.342
chr10	135534747	5581861	0.0412	0.3765
chr11	135006516	6277013	0.0465	0.3495
chr12	133851895	6811800	0.0509	0.3162
chr13	115169878	5126017	0.0445	0.2955
chr14	107349540	4352712	0.0405	0.2912
chr15	102531392	4200503	0.041	0.2803
chr16	90354753	4090452	0.0453	0.3144
chr17	81195210	3006118	0.037	0.2812
chr18	78077248	3897511	0.0499	0.6666
chr19	59128983	2222383	0.0376	0.4173
chr20	63025520	2885230	0.0458	0.3086
chr21	48129895	1417165	0.0294	0.2536
chr22	51304566	1507178	0.0294	0.233
chrMT	16571	109034	6.5798	4.7735
chrX	155270560	7861497	0.0506	0.3282
chrY	59373566	436702	0.0074	0.2354

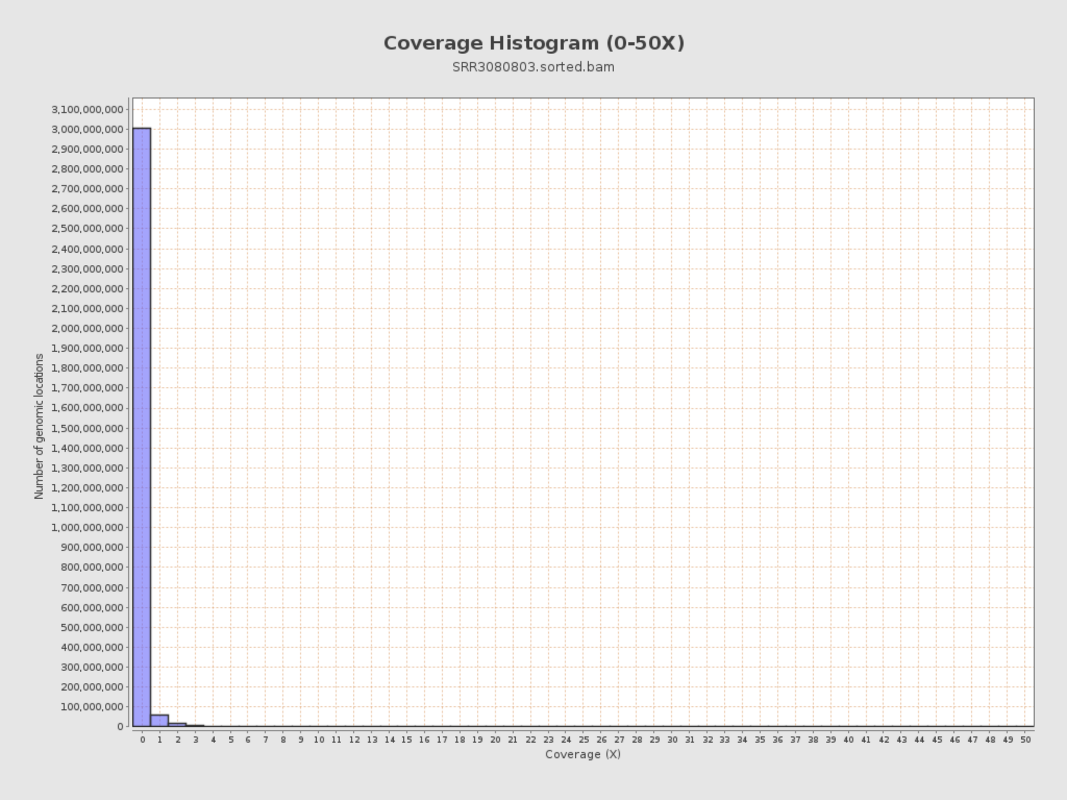
3. Results : Coverage across reference



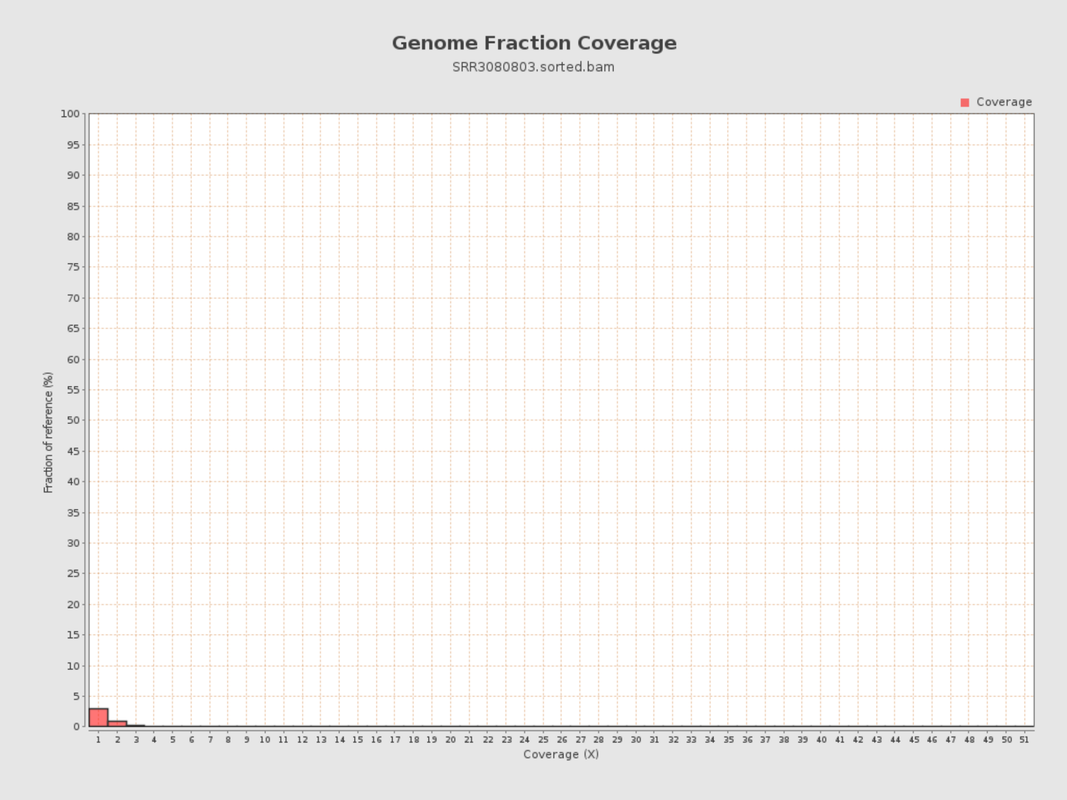
4. Results : Coverage Histogram



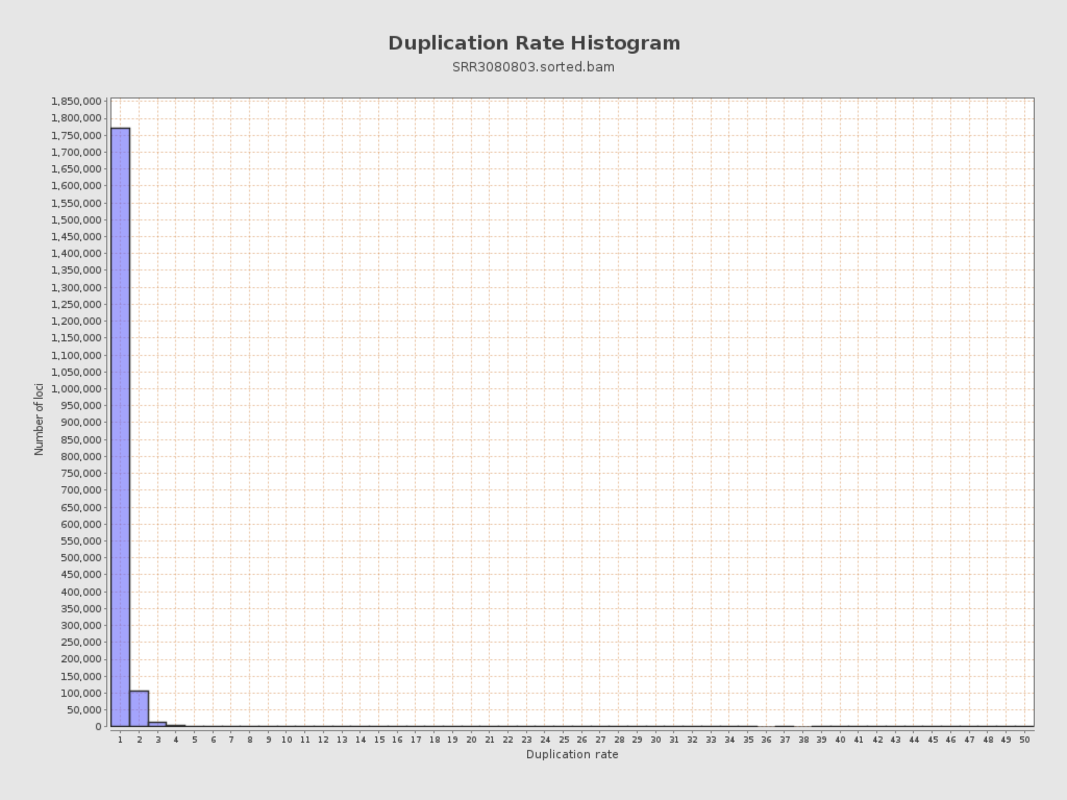
5. Results : Coverage Histogram (0-50X)



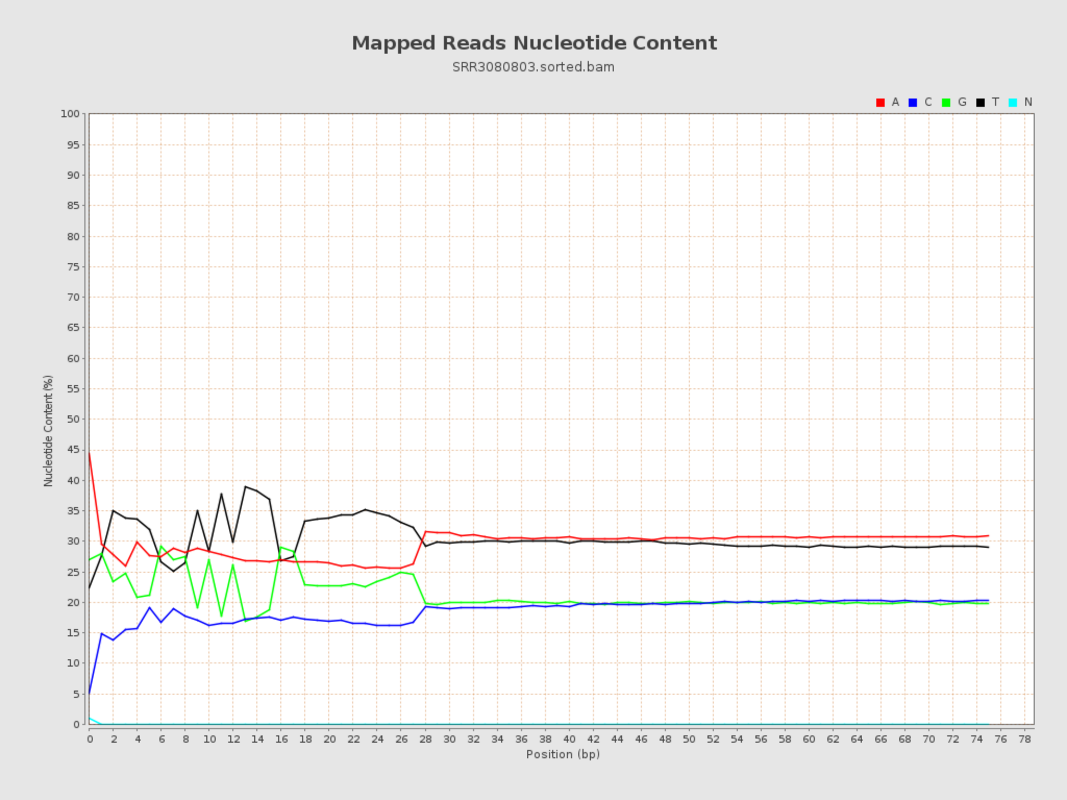
6. Results : Genome Fraction Coverage



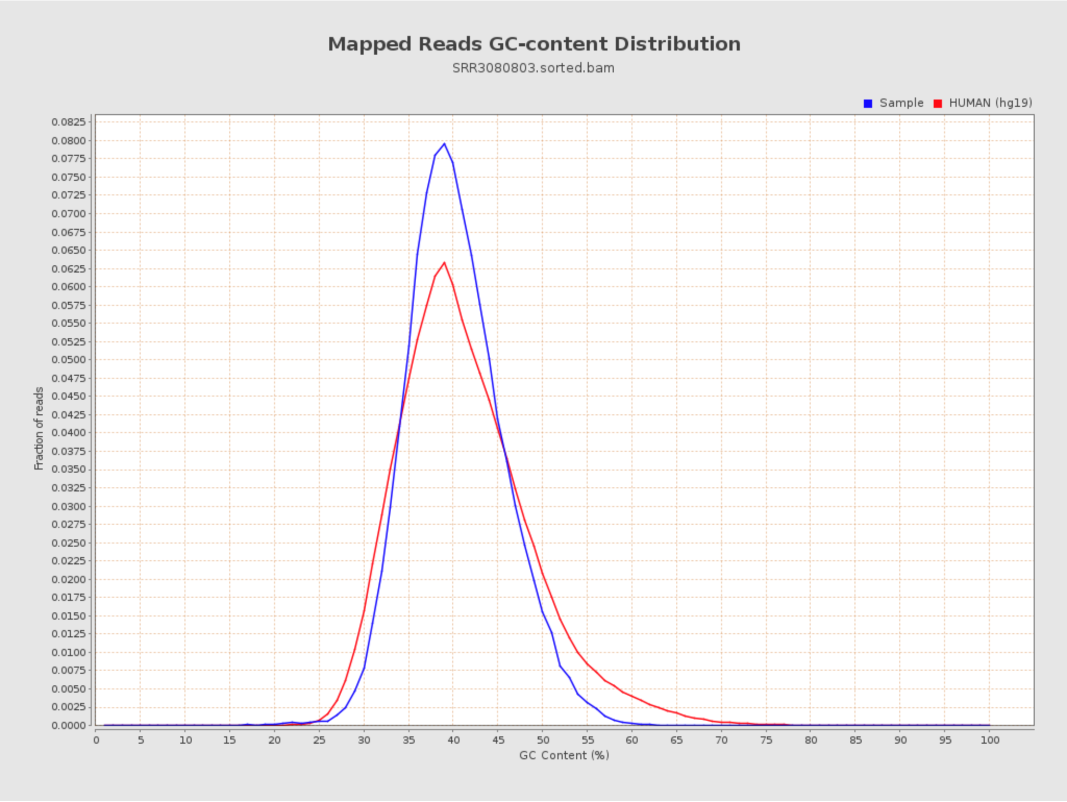
7. Results : Duplication Rate Histogram



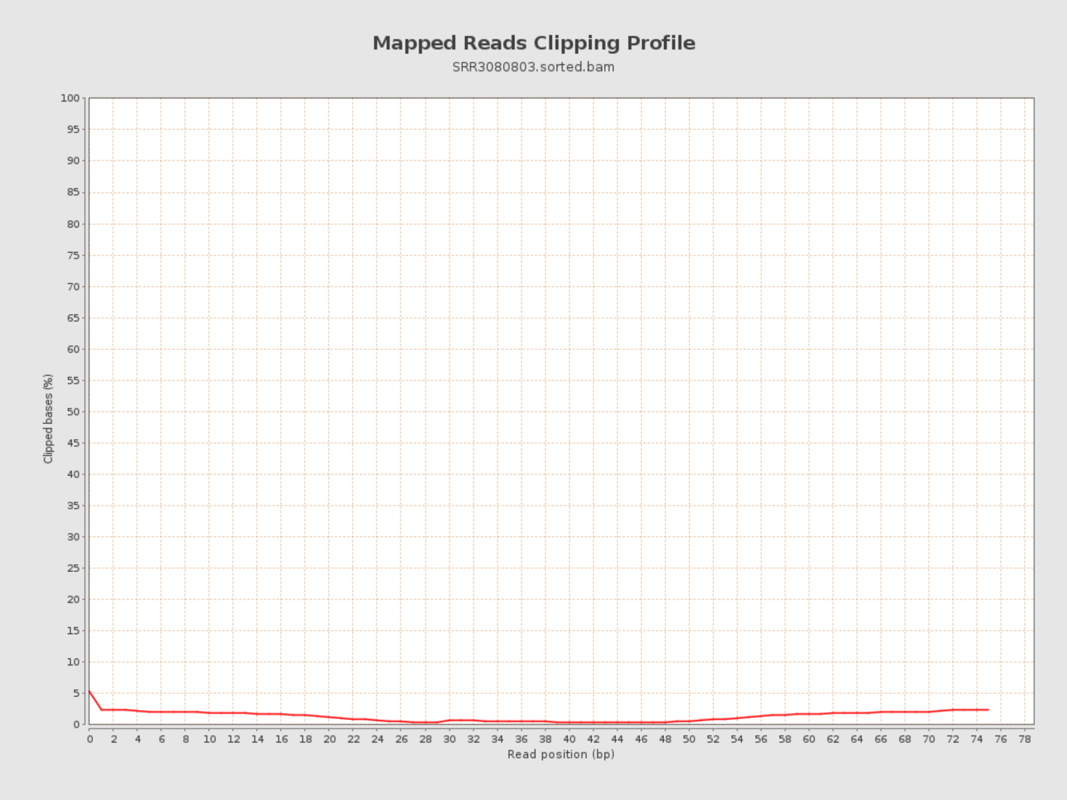
8. Results : Mapped Reads Nucleotide Content



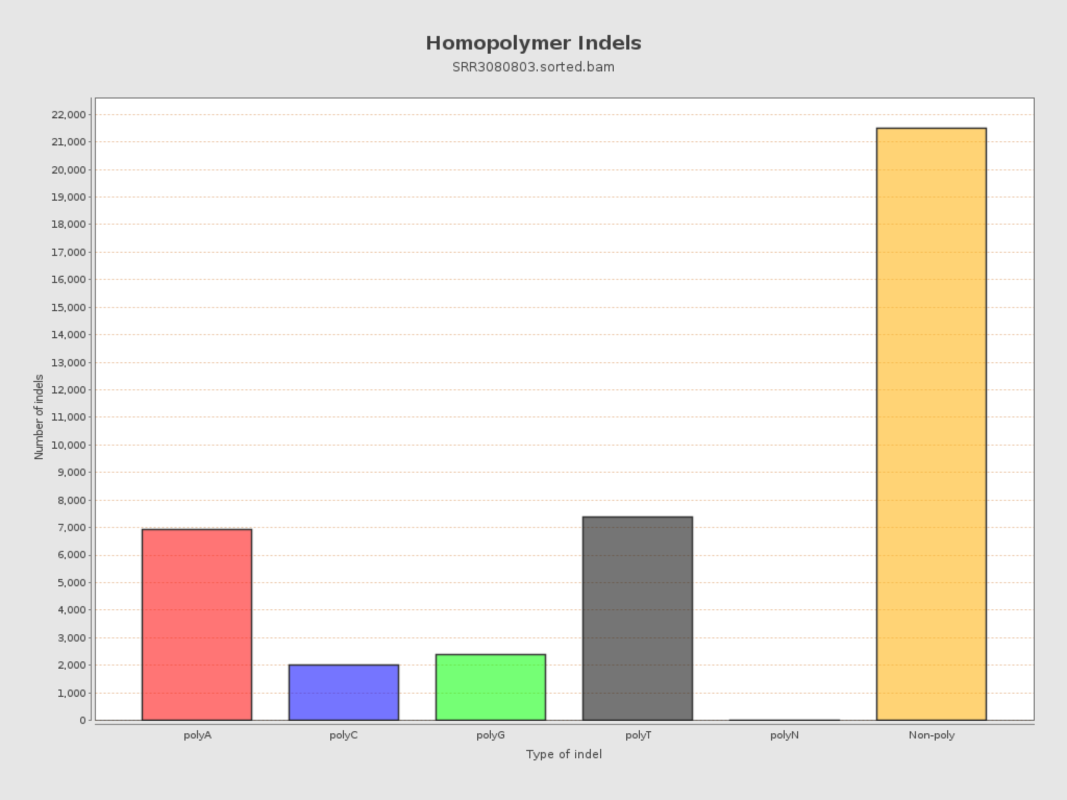
9. Results : Mapped Reads GC-content Distribution



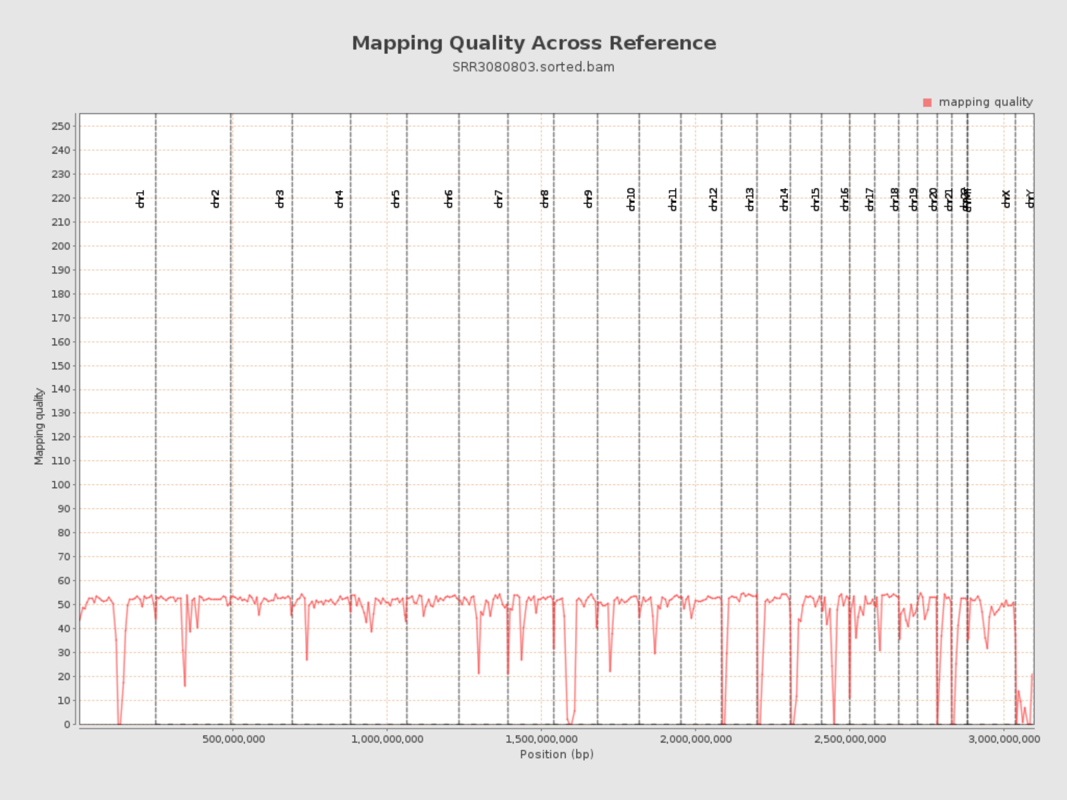
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram