Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 08:40:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080800.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_SRR3080800 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080800.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 08:40:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080800.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,431,216
Mapped reads	2,816,911 / 82.1%
Unmapped reads	614,305 / 17.9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	33,419 / 0.97%
Read min/max/mean length	30 / 76 / 76.34
Duplicated reads (estimated)	182,543 / 5.32%
Duplication rate	5.37%
Clipped reads	844,586 / 24.61%

2.2. ACGT Content

Number/percentage of A's	60,936,328 / 30.66%
Number/percentage of C's	36,628,051 / 18.43%
Number/percentage of T's	61,659,707 / 31.02%
Number/percentage of G's	39,498,517 / 19.87%
Number/percentage of N's	28,217 / 0.01%
GC Percentage	38.3%

2.3. Coverage

Mean	0.0642

Standard Deviation	0.6986

2.4. Mapping Quality

Mean Mapping Quality	47.87

2.5. Mismatches and indels

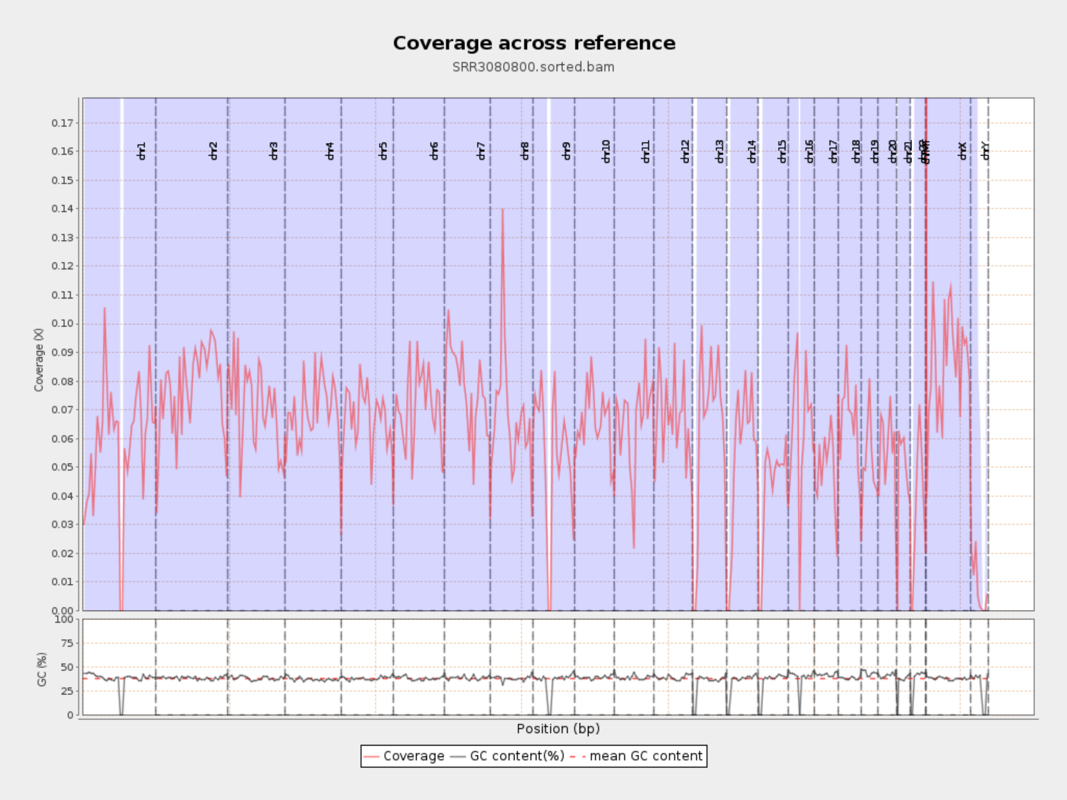
General error rate	0.82%
Mismatches	1,601,156
Insertions	15,525
Mapped reads with at least one insertion	0.55%
Deletions	41,358
Mapped reads with at least one deletion	1.45%
Homopolymer indels	47.27%

2.6. Chromosome stats

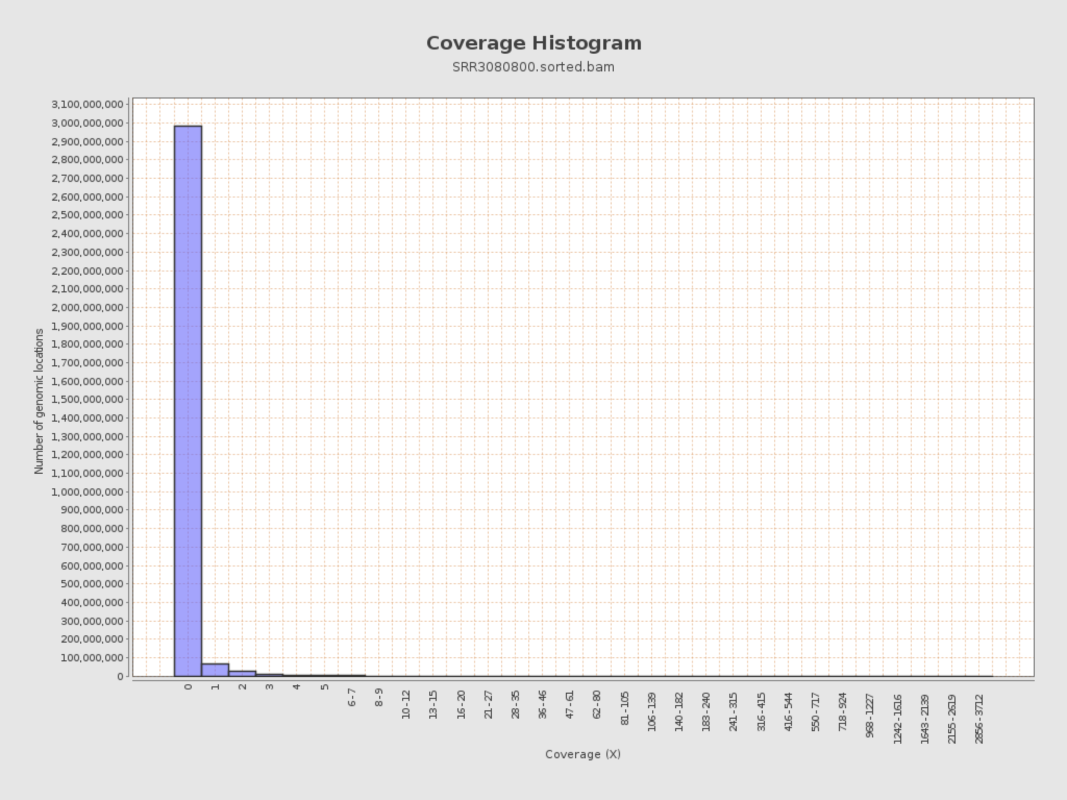
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14525514	0.0583	0.6973
chr2	243199373	18857606	0.0775	0.5593
chr3	198022430	14033213	0.0709	0.4254
chr4	191154276	13329326	0.0697	0.4338
chr5	180915260	12055579	0.0666	0.4118
chr6	171115067	12180141	0.0712	0.4658
chr7	159138663	12269247	0.0771	0.5797

chr8	146364022	9918393	0.0678	2.3858
chr9	141213431	7738971	0.0548	0.4507
chr10	135534747	9028629	0.0666	0.481
chr11	135006516	8791593	0.0651	0.4288
chr12	133851895	8981780	0.0671	0.4159
chr13	115169878	7313715	0.0635	0.4075
chr14	107349540	5864747	0.0546	0.3791
chr15	102531392	4313021	0.0421	0.3204
chr16	90354753	5523319	0.0611	0.3997
chr17	81195210	4047316	0.0498	0.3518
chr18	78077248	5261989	0.0674	0.6618
chr19	59128983	3135853	0.053	0.5438
chr20	63025520	3604922	0.0572	0.3813
chr21	48129895	2290383	0.0476	0.3576
chr22	51304566	1891832	0.0369	0.2938
chrMT	16571	19075	1.1511	1.6312
chrX	155270560	13366270	0.0861	0.4804
chrY	59373566	482614	0.0081	0.1765

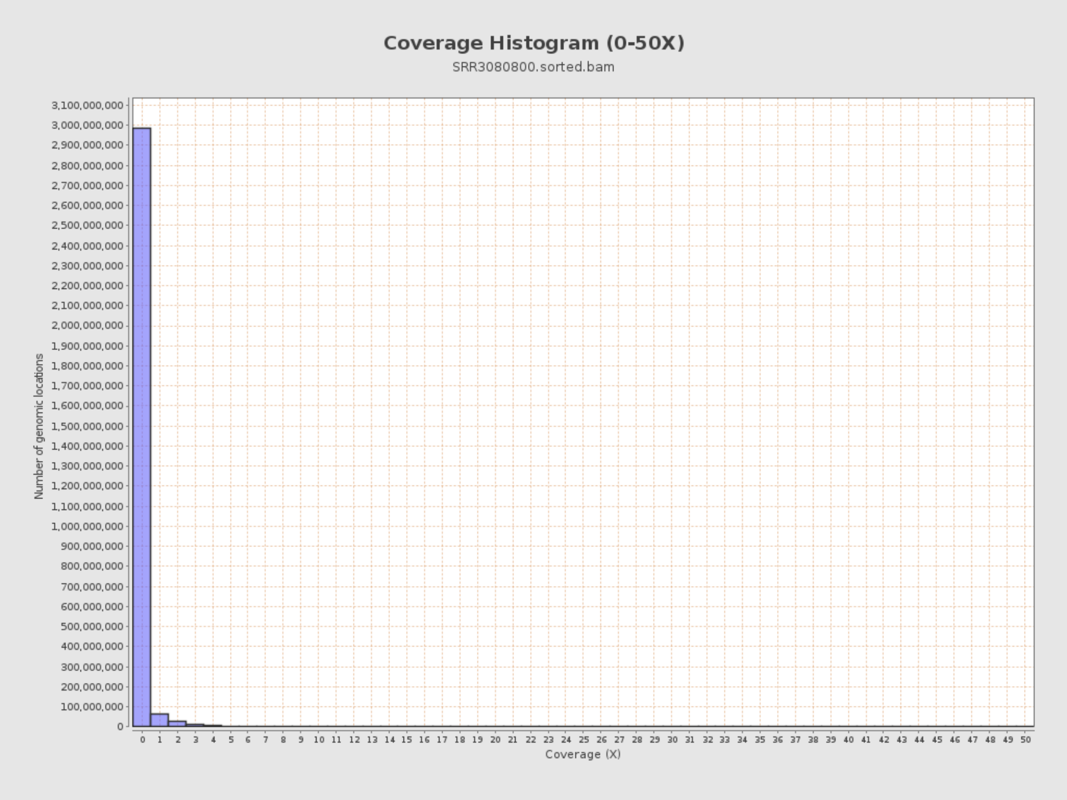
3. Results : Coverage across reference



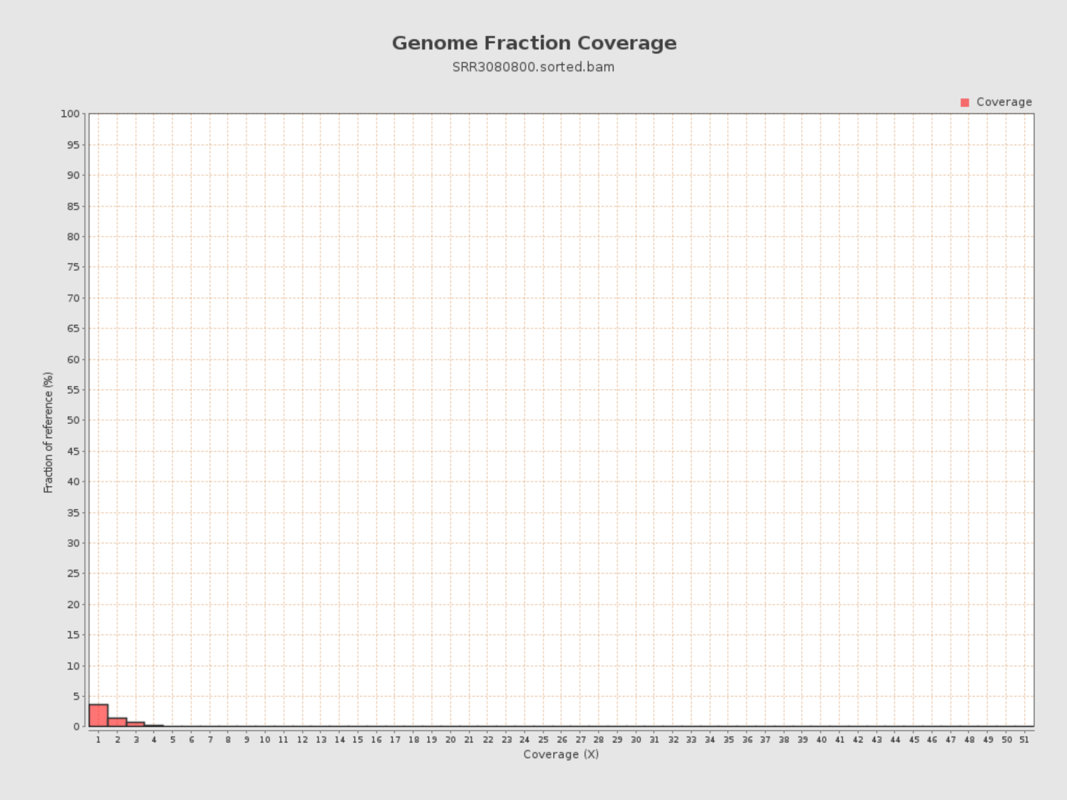
4. Results : Coverage Histogram



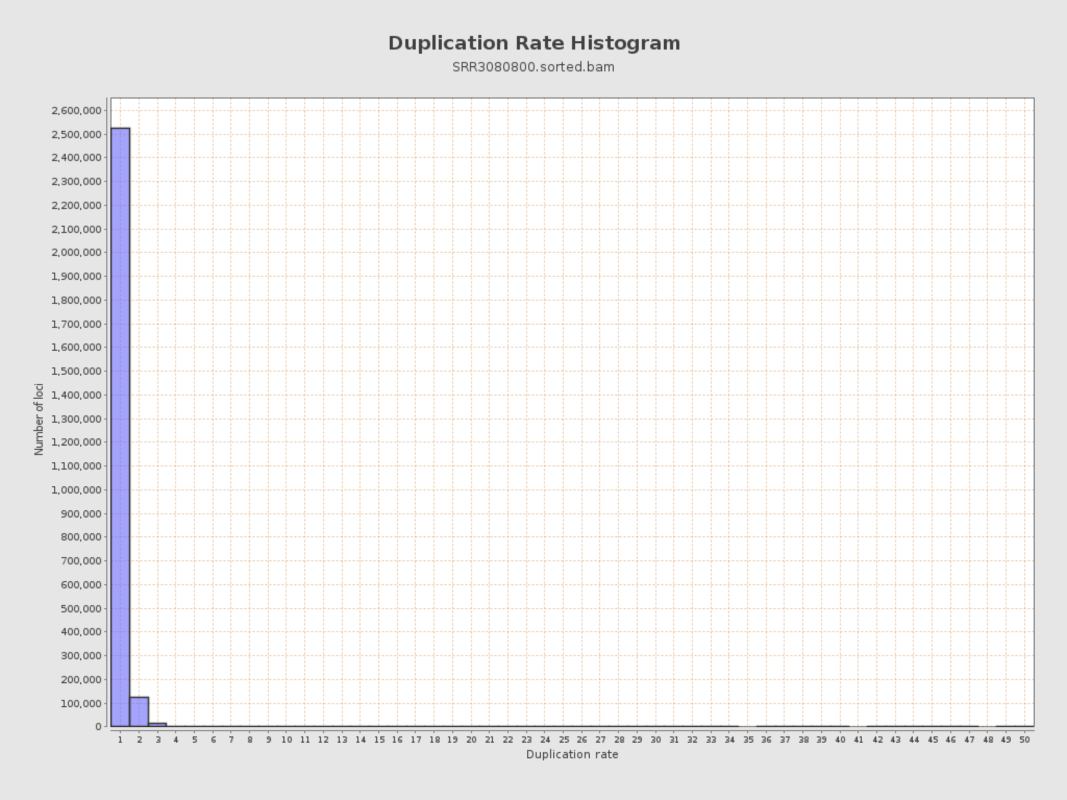
5. Results : Coverage Histogram (0-50X)



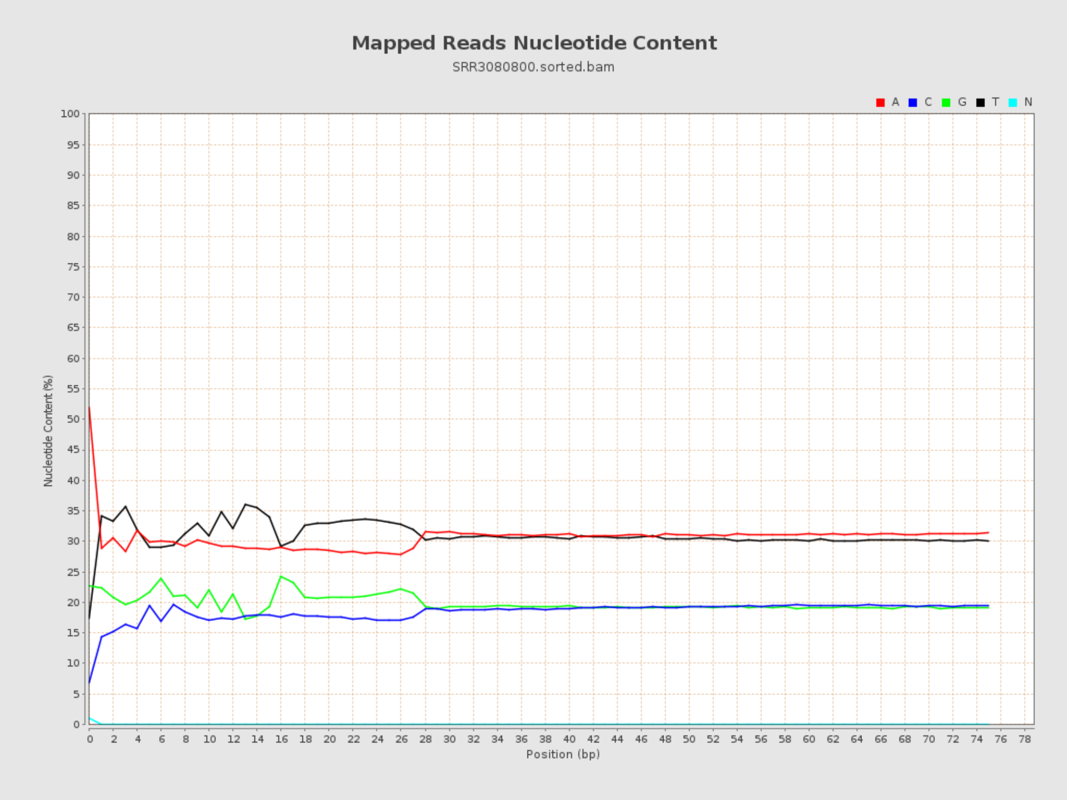
6. Results : Genome Fraction Coverage



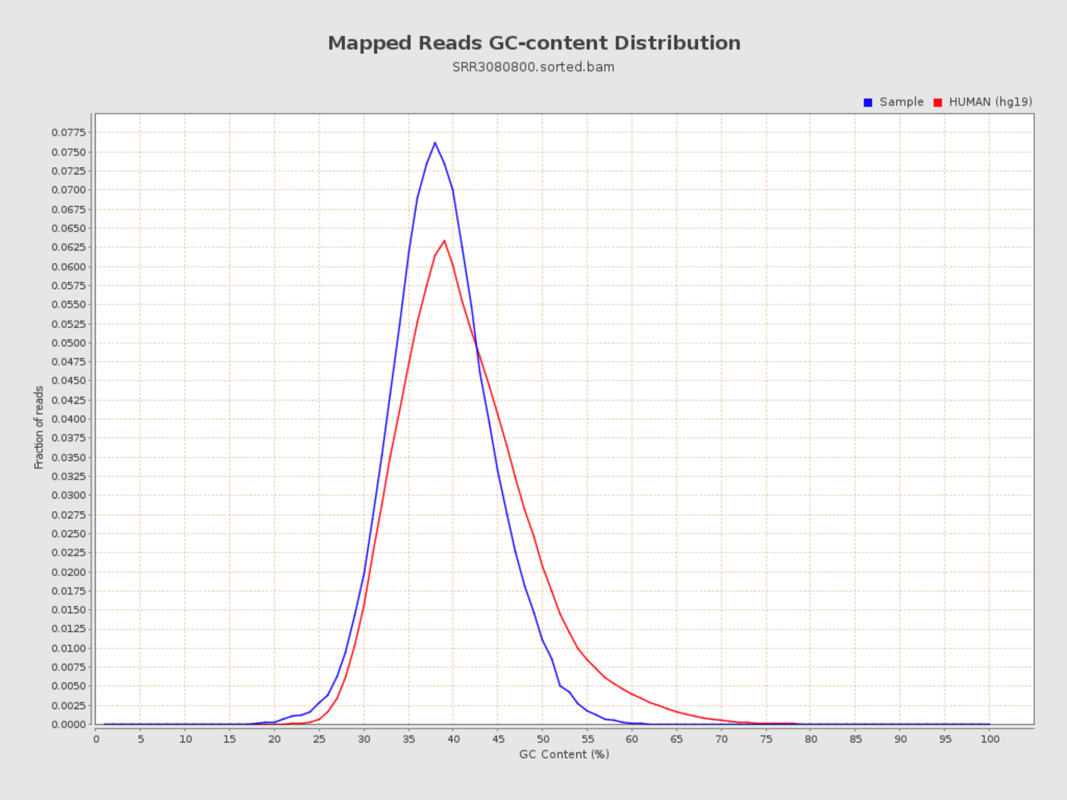
7. Results : Duplication Rate Histogram



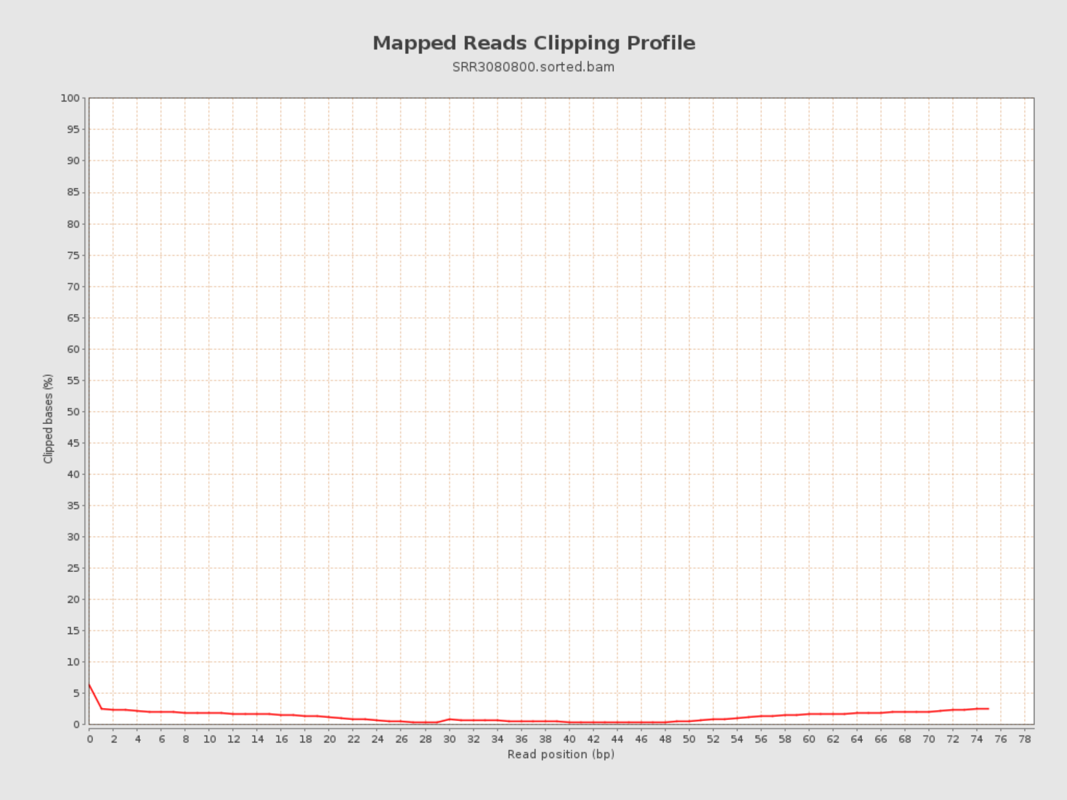
8. Results : Mapped Reads Nucleotide Content



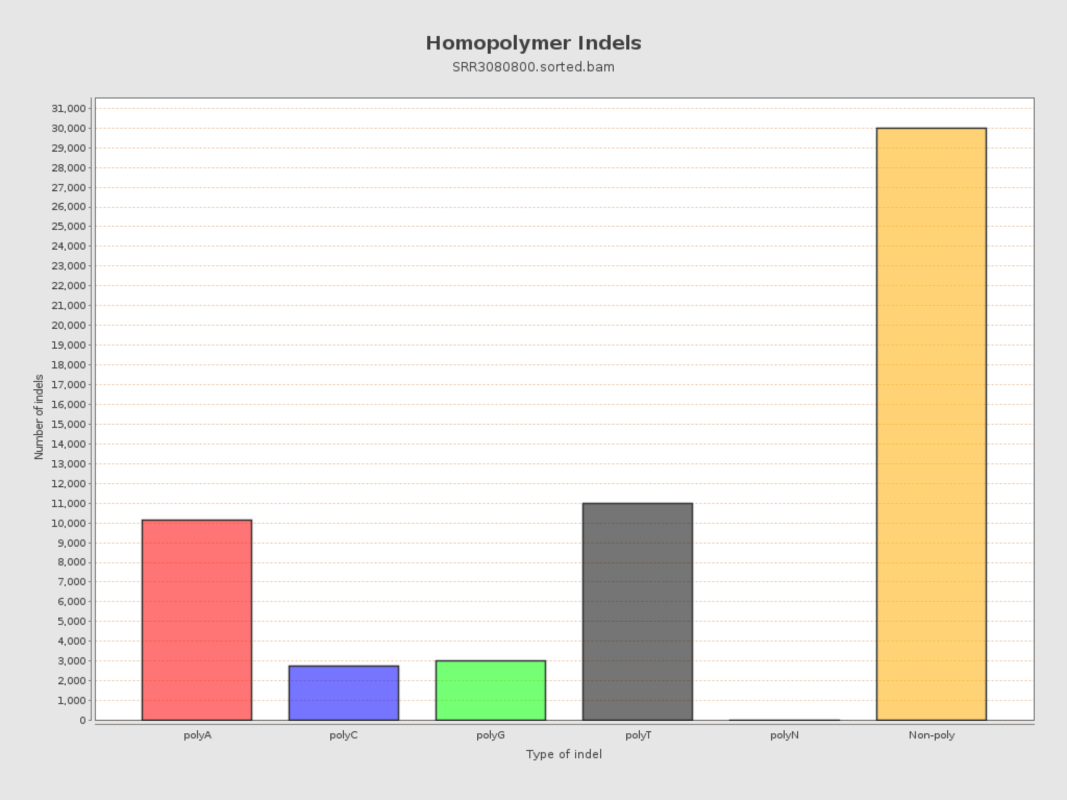
9. Results : Mapped Reads GC-content Distribution



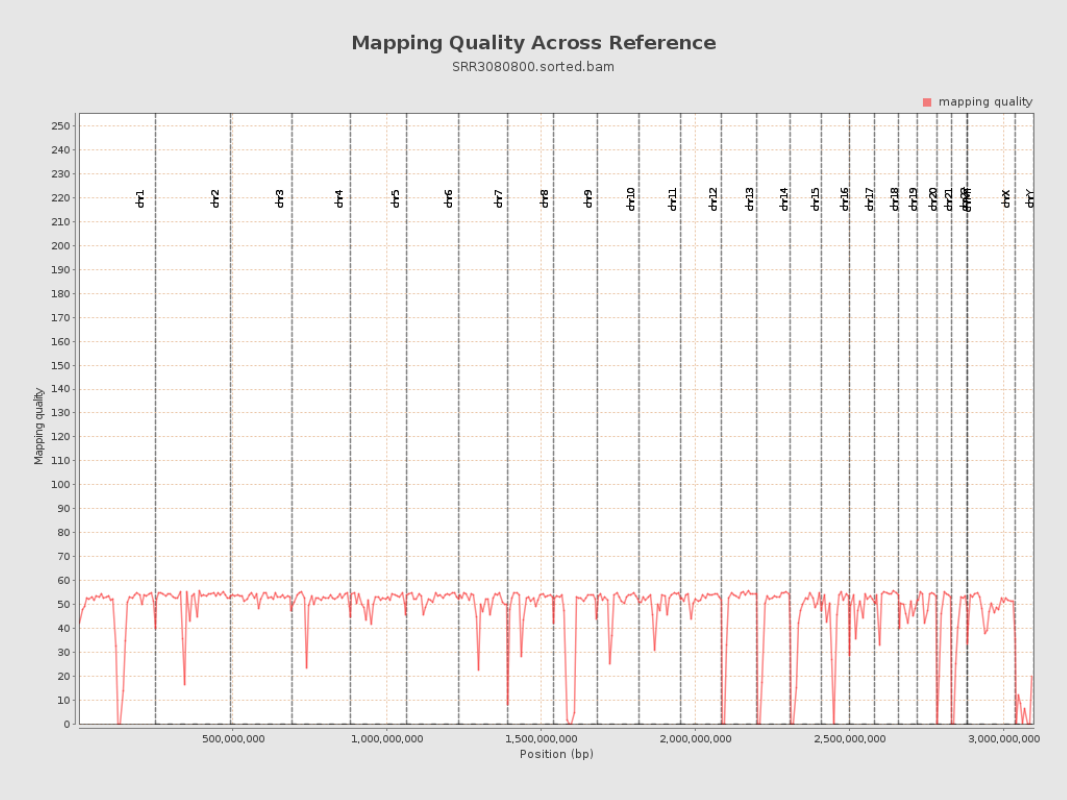
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram