Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 11:33:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080946.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_SRR3080946 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080946.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 11:33:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080946.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,152,156
Mapped reads	2,816,455 / 89.35%
Unmapped reads	335,701 / 10.65%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,119 / 0.77%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	109,919 / 3.49%
Duplication rate	2.85%
Clipped reads	1,009,069 / 32.01%

2.2. ACGT Content

Number/percentage of A's	55,574,451 / 28.79%
Number/percentage of C's	34,139,836 / 17.69%
Number/percentage of T's	61,824,760 / 32.03%
Number/percentage of G's	40,556,566 / 21.01%
Number/percentage of N's	927,842 / 0.48%
GC Percentage	38.7%

2.3. Coverage

Mean	0.0624

Standard Deviation	0.5333

2.4. Mapping Quality

Mean Mapping Quality	47.69

2.5. Mismatches and indels

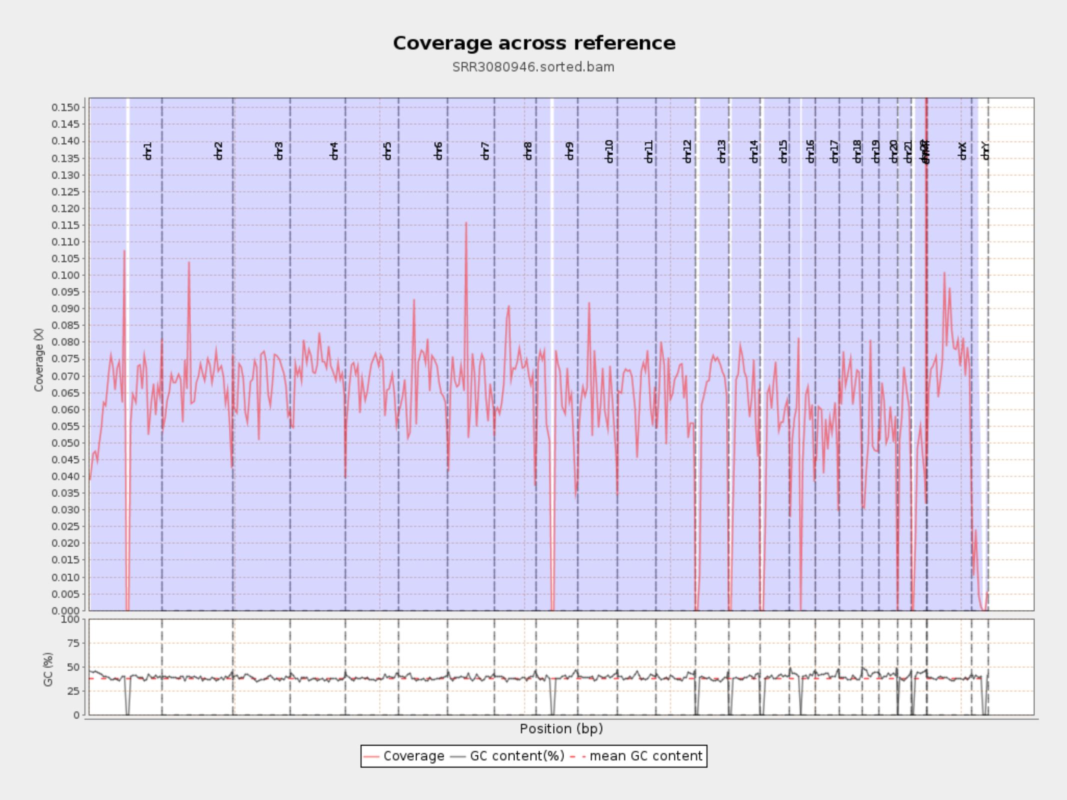
General error rate	1.15%
Mismatches	2,194,110
Insertions	15,119
Mapped reads with at least one insertion	0.53%
Deletions	43,303
Mapped reads with at least one deletion	1.52%
Homopolymer indels	49.7%

2.6. Chromosome stats

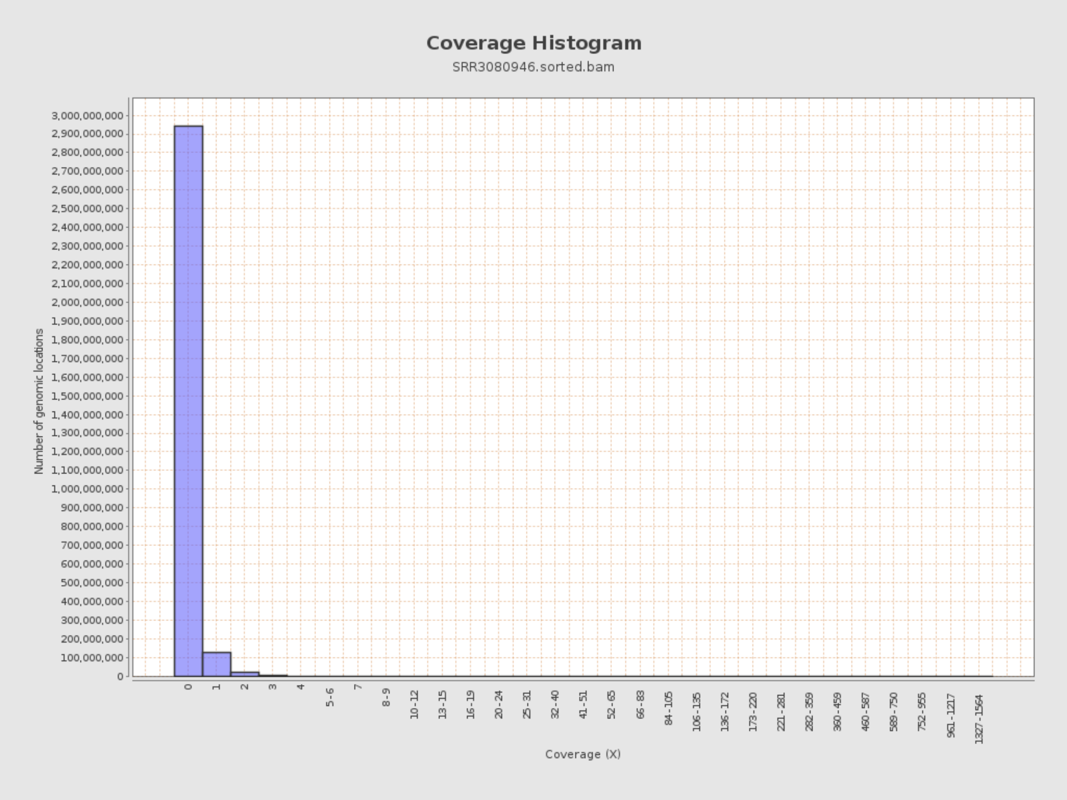
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15018145	0.0603	0.9098
chr2	243199373	16563401	0.0681	0.4862
chr3	198022430	13495753	0.0682	0.3151
chr4	191154276	13733562	0.0718	0.3416
chr5	180915260	12306416	0.068	0.3162
chr6	171115067	11712357	0.0684	0.4195
chr7	159138663	10896695	0.0685	0.8075

chr8	146364022	10174487	0.0695	0.9997
chr9	141213431	8121377	0.0575	0.5008
chr10	135534747	8656384	0.0639	0.4485
chr11	135006516	8863641	0.0657	0.4666
chr12	133851895	8661865	0.0647	0.3134
chr13	115169878	6659277	0.0578	0.2892
chr14	107349540	5964305	0.0556	0.3124
chr15	102531392	5172423	0.0504	0.2709
chr16	90354753	4667789	0.0517	0.3079
chr17	81195210	4230636	0.0521	0.3181
chr18	78077248	5324265	0.0682	0.909
chr19	59128983	2899445	0.049	0.6545
chr20	63025520	3483941	0.0553	0.2989
chr21	48129895	2566614	0.0533	0.3061
chr22	51304566	1686549	0.0329	0.2134
chrMT	16571	52774	3.1847	2.7611
chrX	155270560	11730247	0.0755	0.3765
chrY	59373566	452391	0.0076	0.167

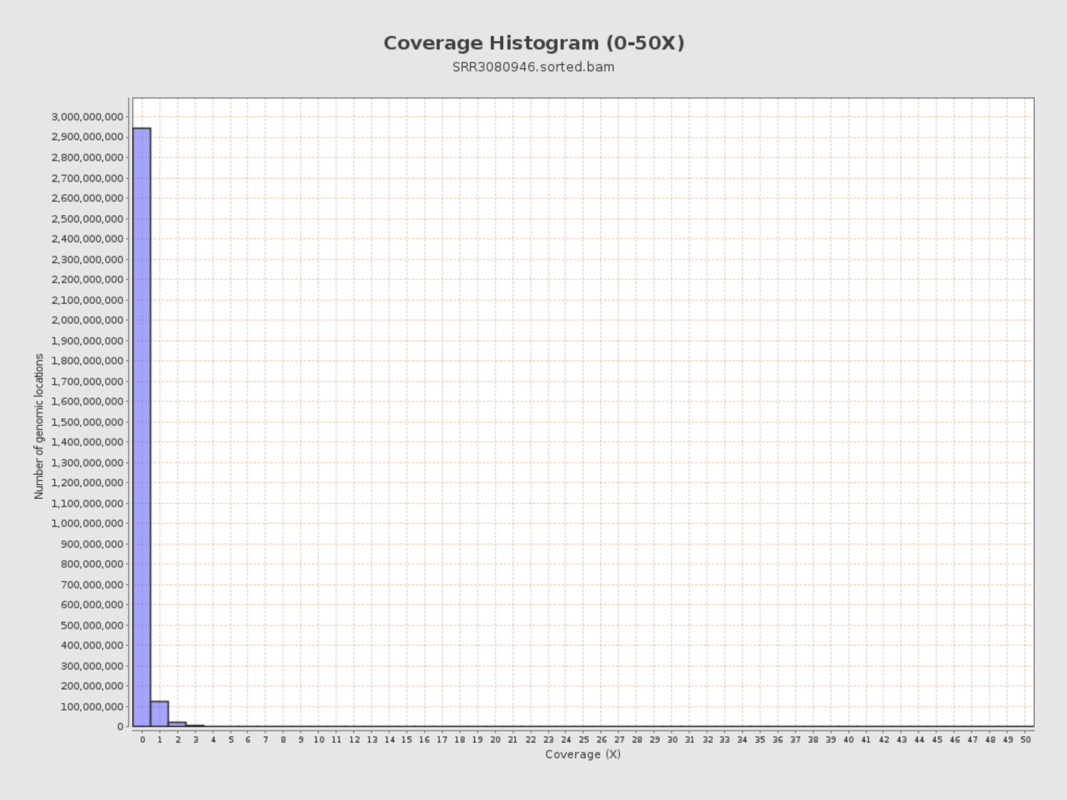
3. Results : Coverage across reference



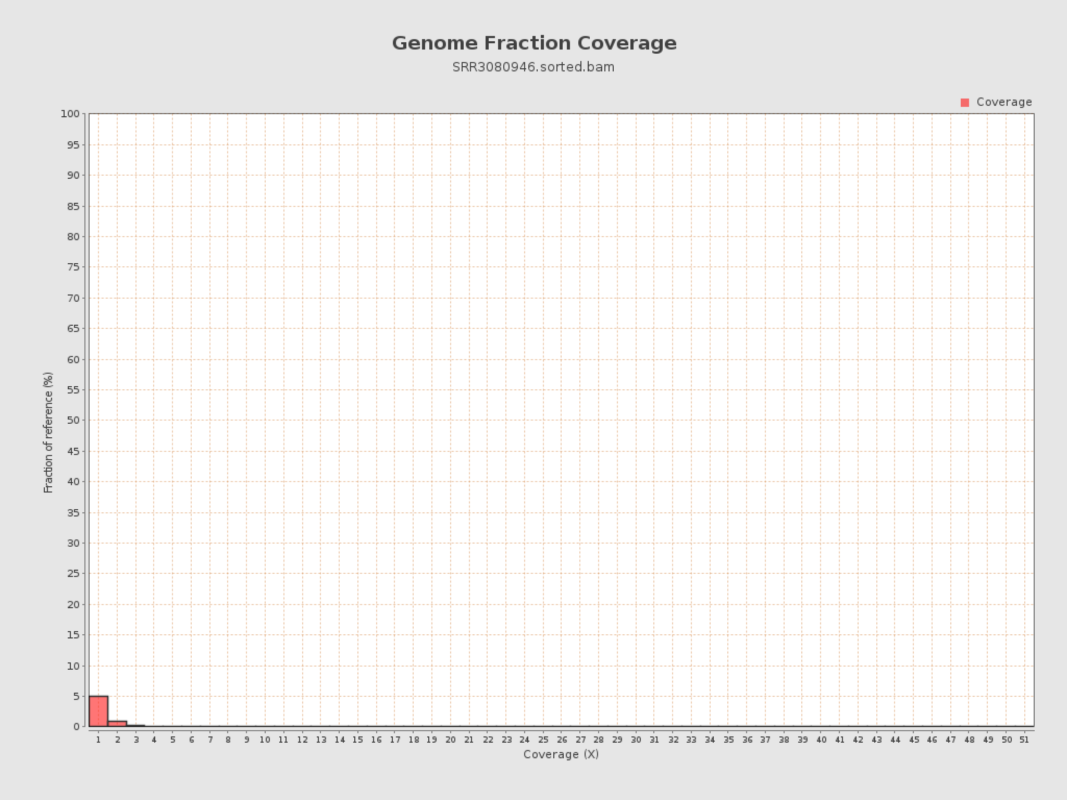
4. Results : Coverage Histogram



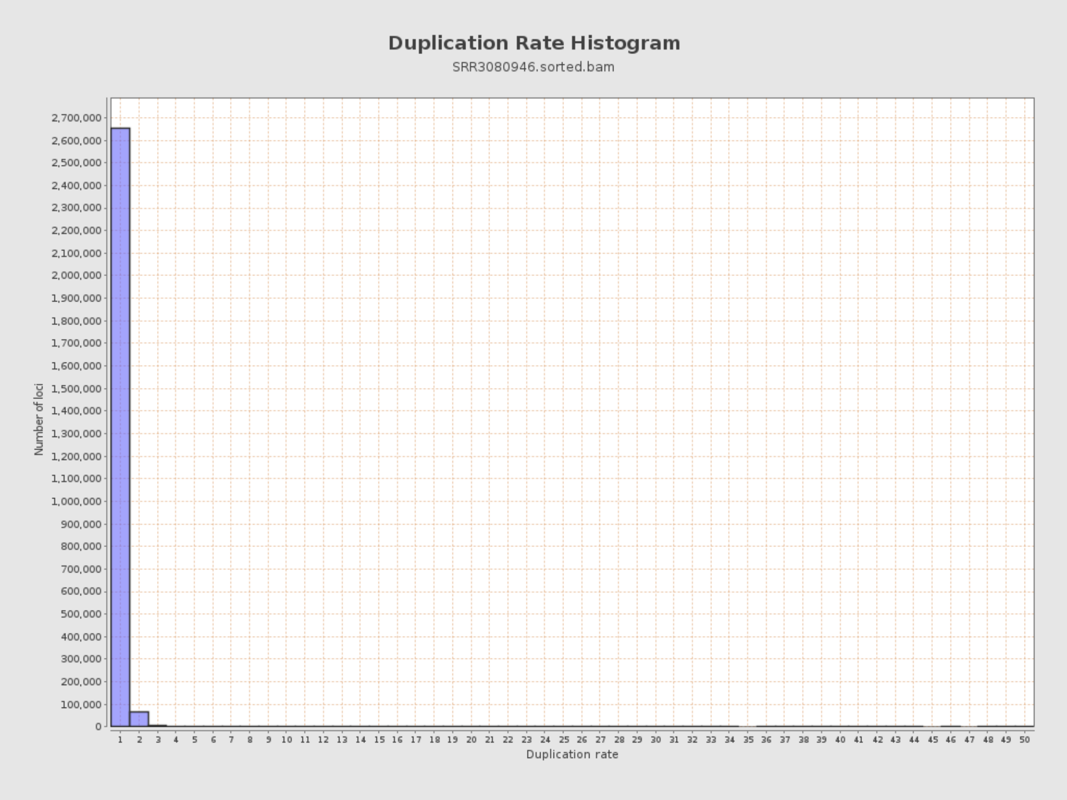
5. Results : Coverage Histogram (0-50X)



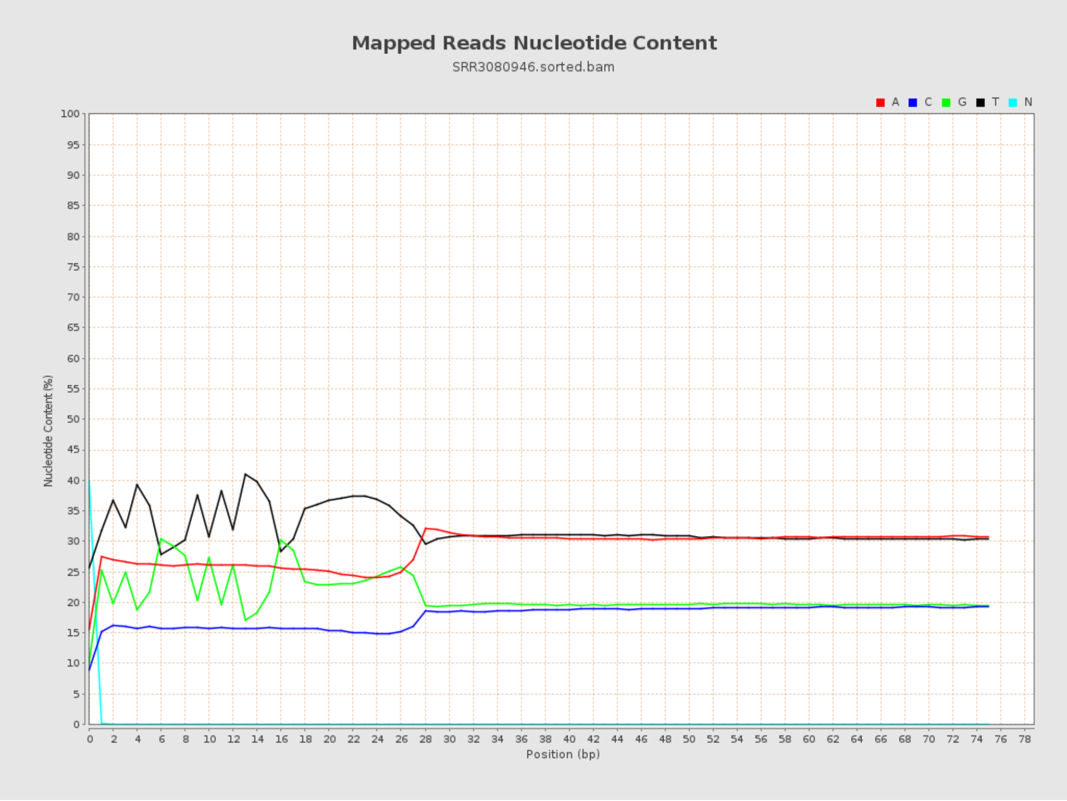
6. Results : Genome Fraction Coverage



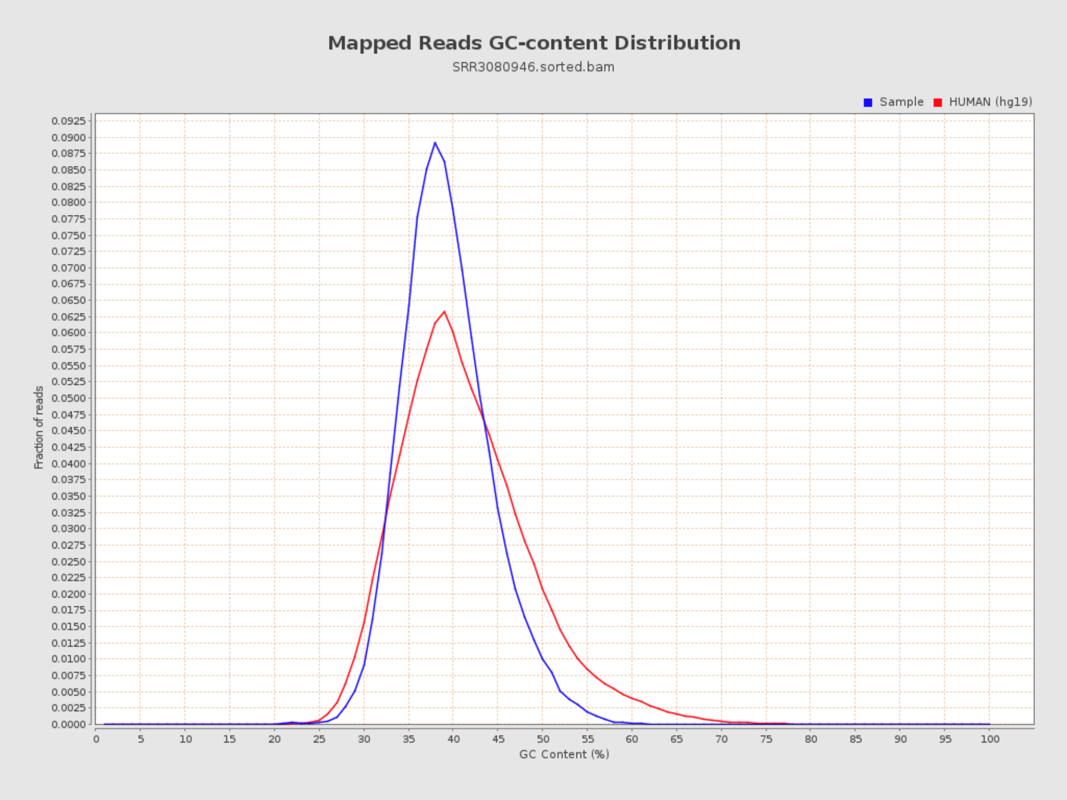
7. Results : Duplication Rate Histogram



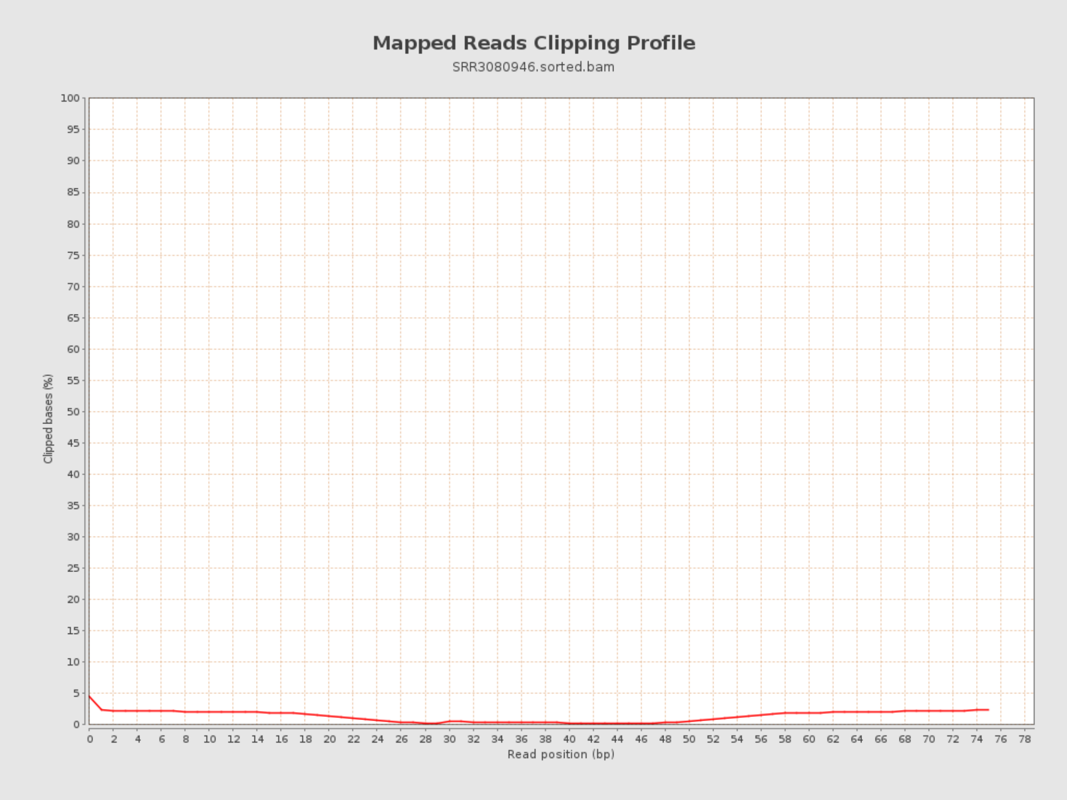
8. Results : Mapped Reads Nucleotide Content



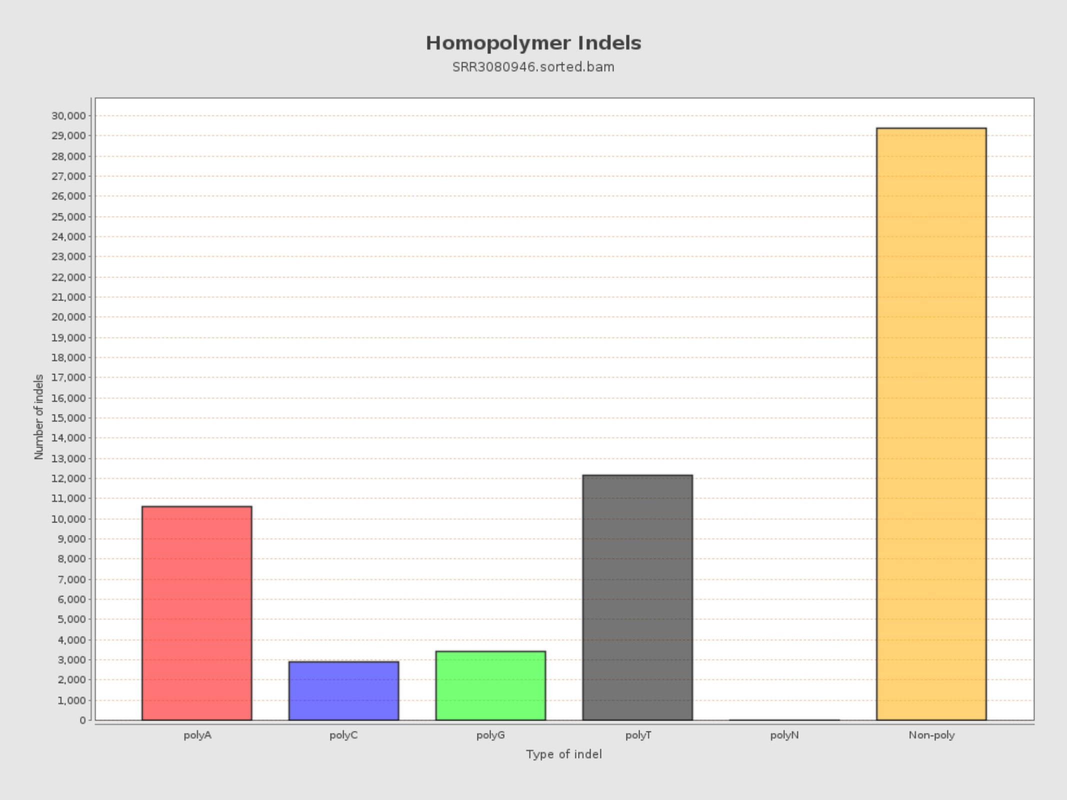
9. Results : Mapped Reads GC-content Distribution



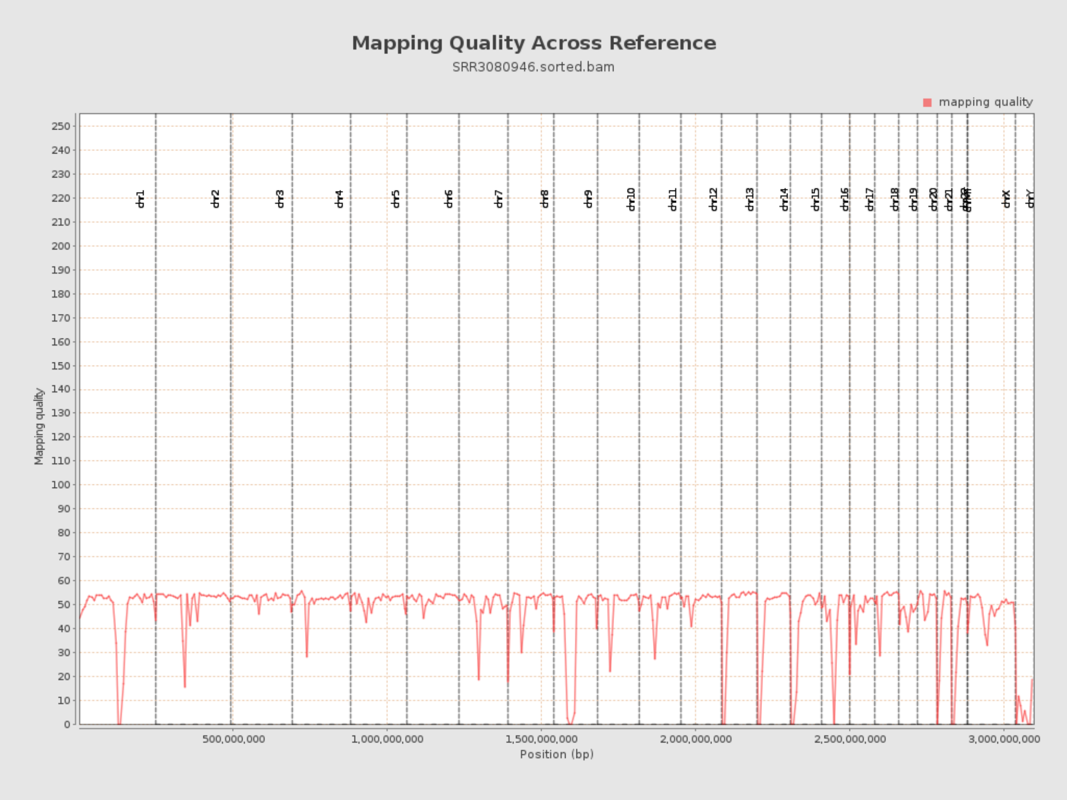
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram