Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 23:24:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083095.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_SRR3083095 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083095.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 23:24:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083095.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,117,130
Mapped reads	3,579,785 / 86.95%
Unmapped reads	537,345 / 13.05%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,810 / 0.48%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	204,841 / 4.98%
Duplication rate	4.47%
Clipped reads	1,632,777 / 39.66%

2.2. ACGT Content

Number/percentage of A's	65,807,099 / 27.65%
Number/percentage of C's	43,014,893 / 18.07%
Number/percentage of T's	76,850,193 / 32.29%
Number/percentage of G's	52,329,890 / 21.98%
Number/percentage of N's	23,447 / 0.01%
GC Percentage	40.06%

2.3. Coverage

Mean	0.0769

Standard Deviation	0.6073

2.4. Mapping Quality

Mean Mapping Quality	45.67

2.5. Mismatches and indels

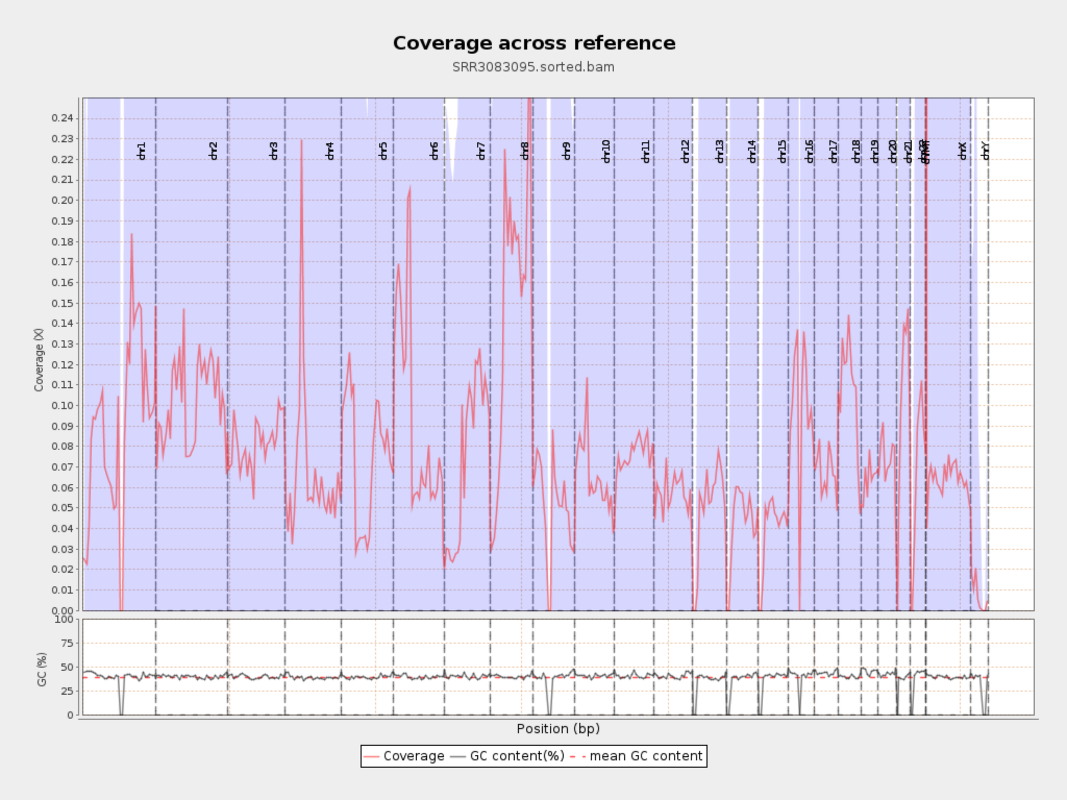
General error rate	0.88%
Mismatches	2,067,419
Insertions	19,637
Mapped reads with at least one insertion	0.54%
Deletions	52,947
Mapped reads with at least one deletion	1.46%
Homopolymer indels	48.46%

2.6. Chromosome stats

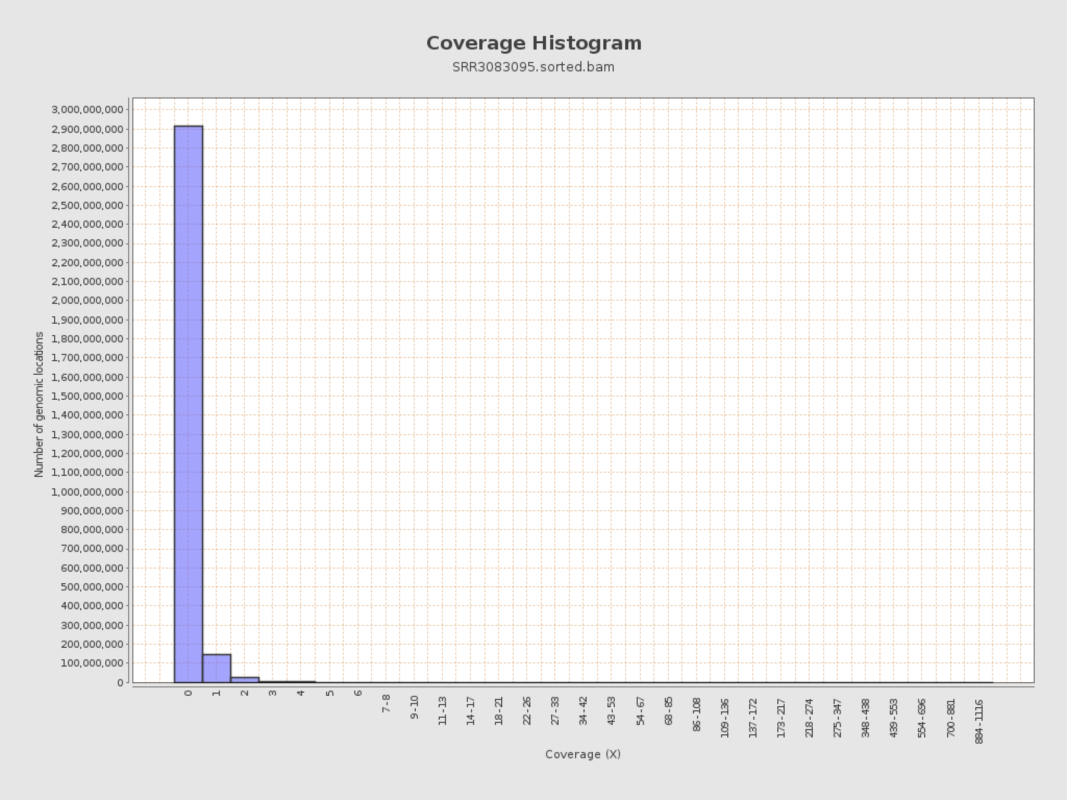
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	22324805	0.0896	0.985
chr2	243199373	24924178	0.1025	0.8182
chr3	198022430	16078062	0.0812	0.3576
chr4	191154276	12993802	0.068	0.3425
chr5	180915260	13446130	0.0743	0.3459
chr6	171115067	16130786	0.0943	0.5194
chr7	159138663	11942140	0.075	0.7419

chr8	146364022	21788744	0.1489	0.7609
chr9	141213431	7226824	0.0512	0.6459
chr10	135534747	8933444	0.0659	0.5088
chr11	135006516	10260828	0.076	0.4804
chr12	133851895	7602959	0.0568	0.3178
chr13	115169878	5752218	0.0499	0.2798
chr14	107349540	4606099	0.0429	0.355
chr15	102531392	3941852	0.0384	0.2444
chr16	90354753	8644581	0.0957	0.463
chr17	81195210	5539295	0.0682	0.3653
chr18	78077248	8487495	0.1087	1.4066
chr19	59128983	3786647	0.064	0.6994
chr20	63025520	4703143	0.0746	0.3662
chr21	48129895	4782597	0.0994	0.4105
chr22	51304566	3441641	0.0671	0.3231
chrMT	16571	435990	26.3104	20.0784
chrX	155270560	9920390	0.0639	0.4023
chrY	59373566	421797	0.0071	0.147

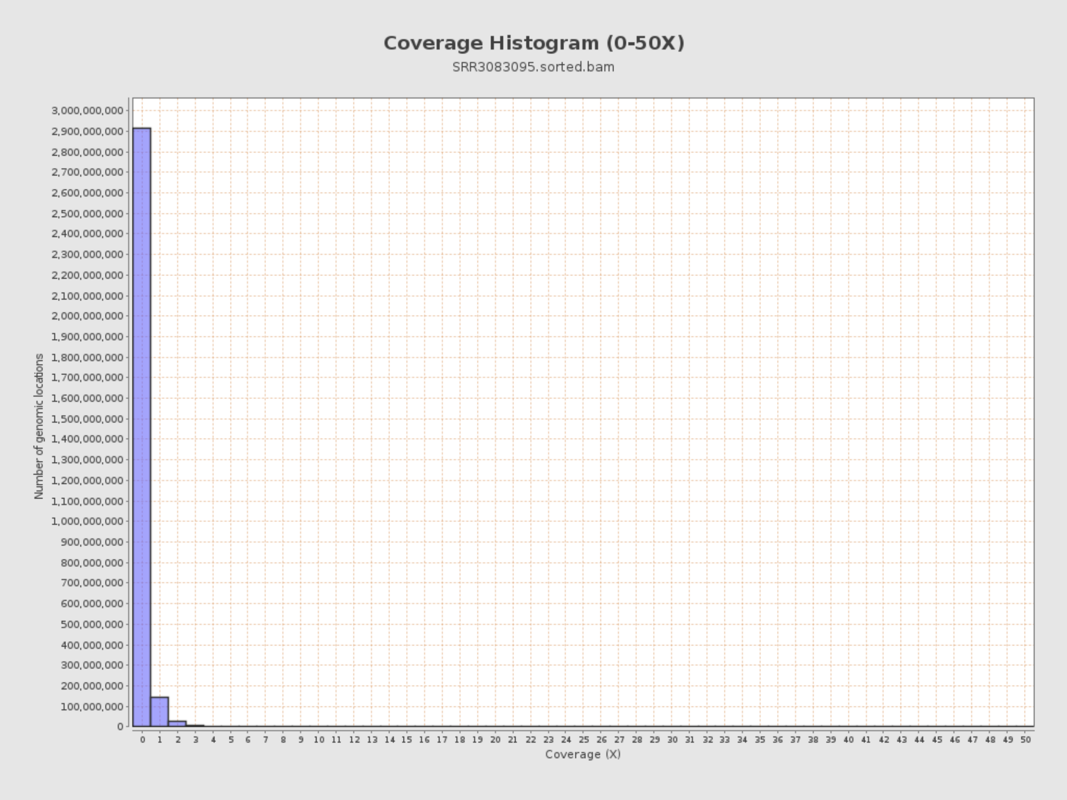
3. Results : Coverage across reference



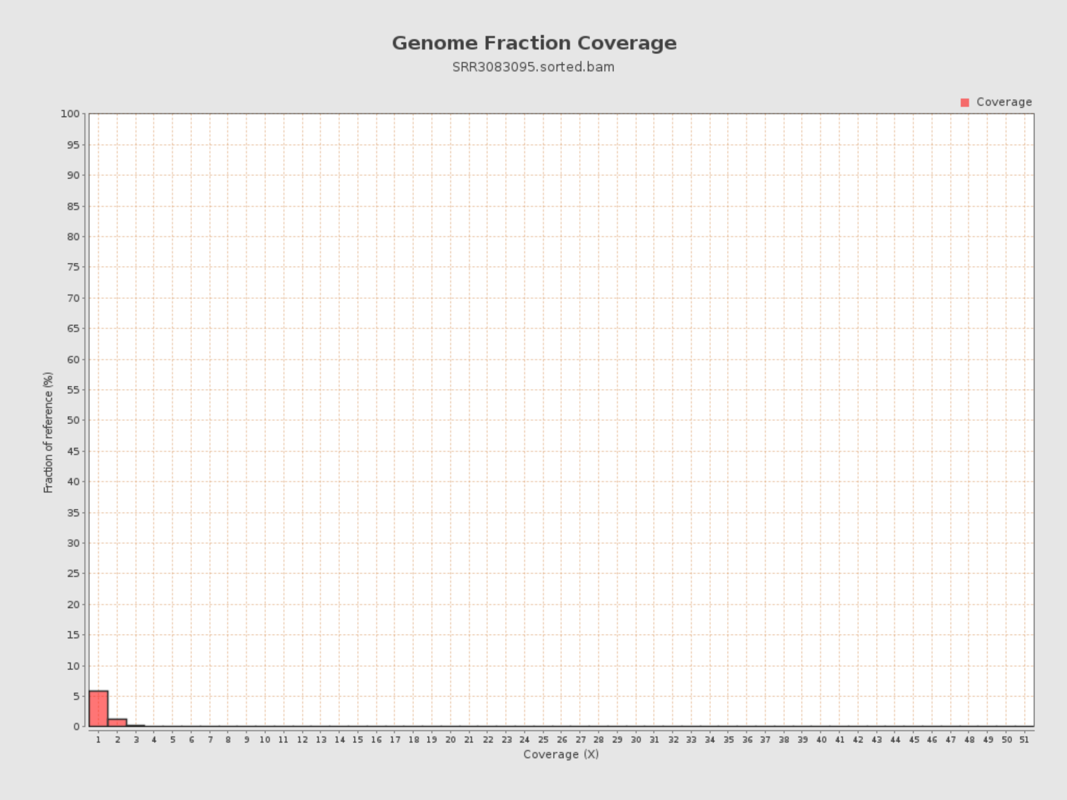
4. Results : Coverage Histogram



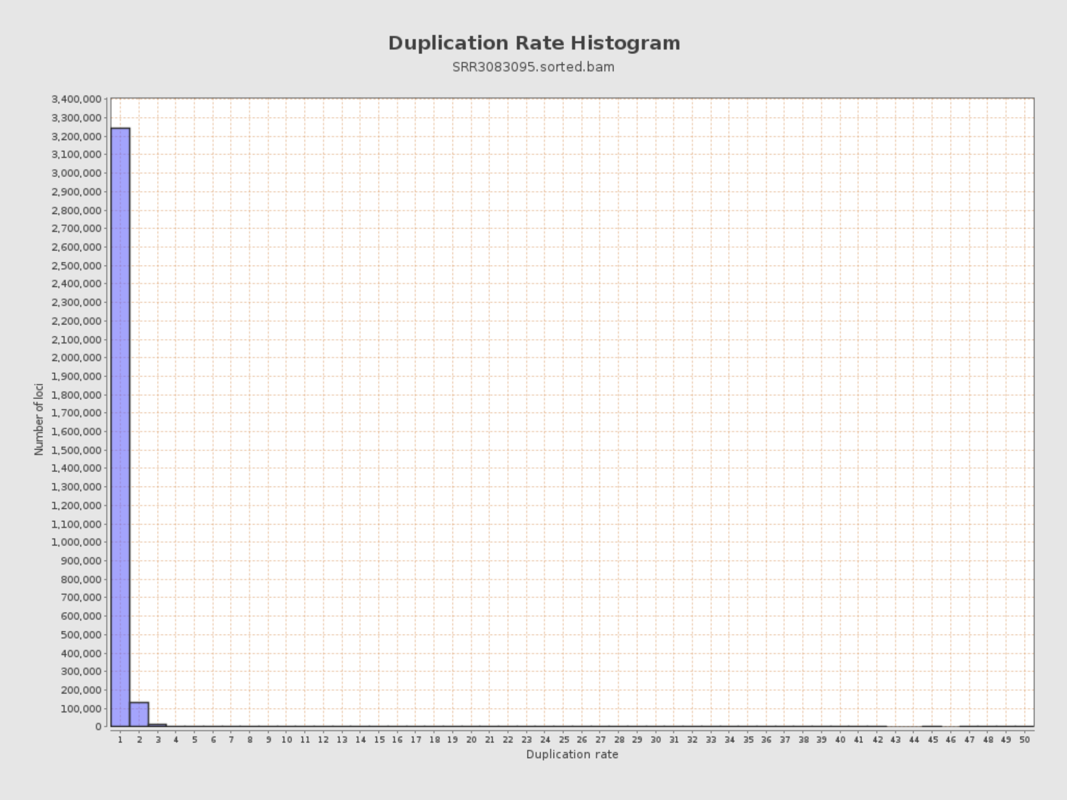
5. Results : Coverage Histogram (0-50X)



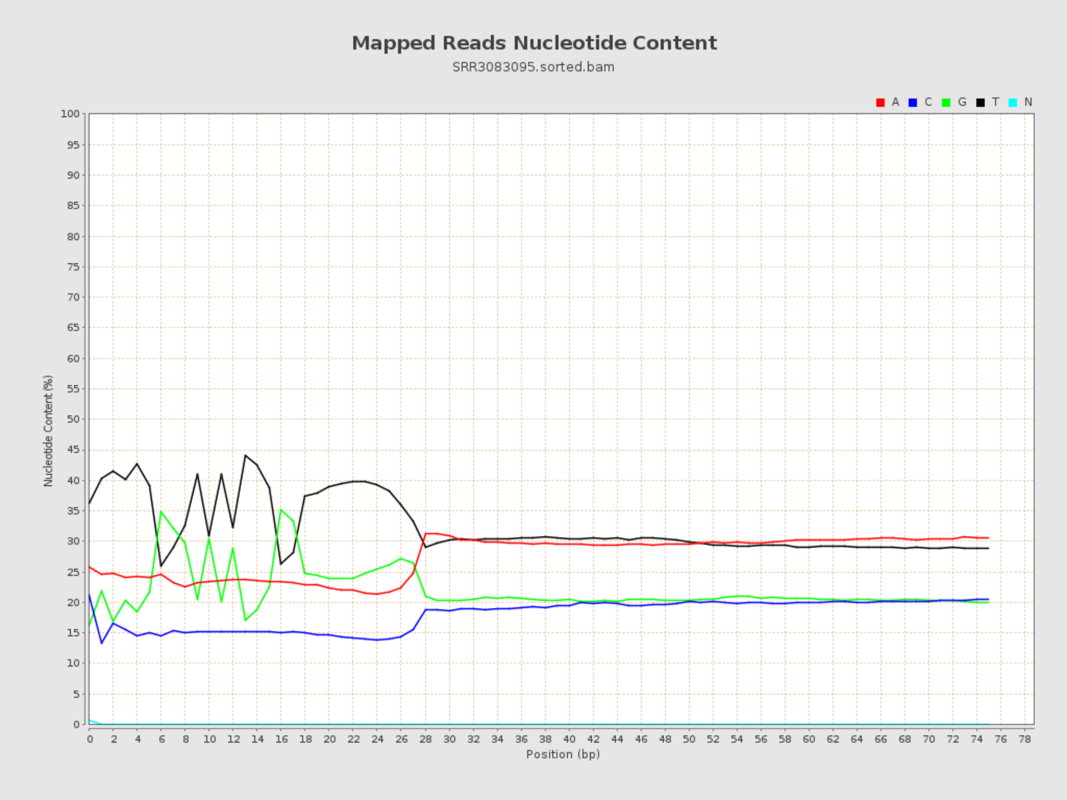
6. Results : Genome Fraction Coverage



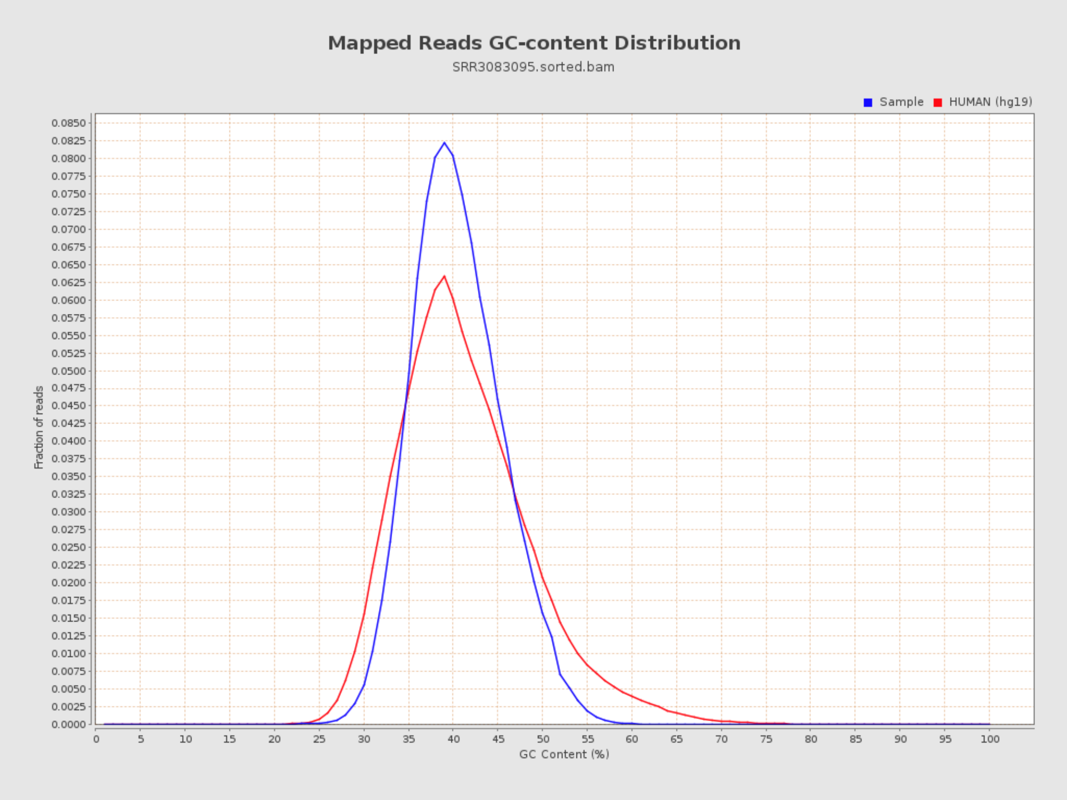
7. Results : Duplication Rate Histogram



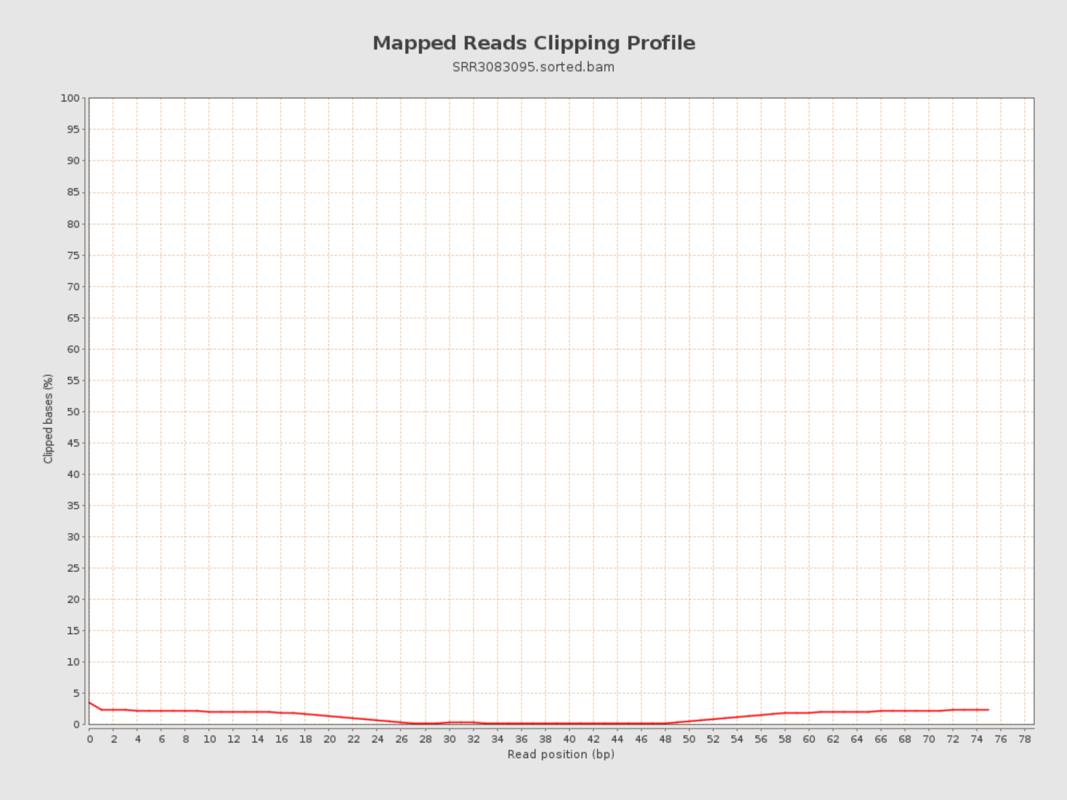
8. Results : Mapped Reads Nucleotide Content



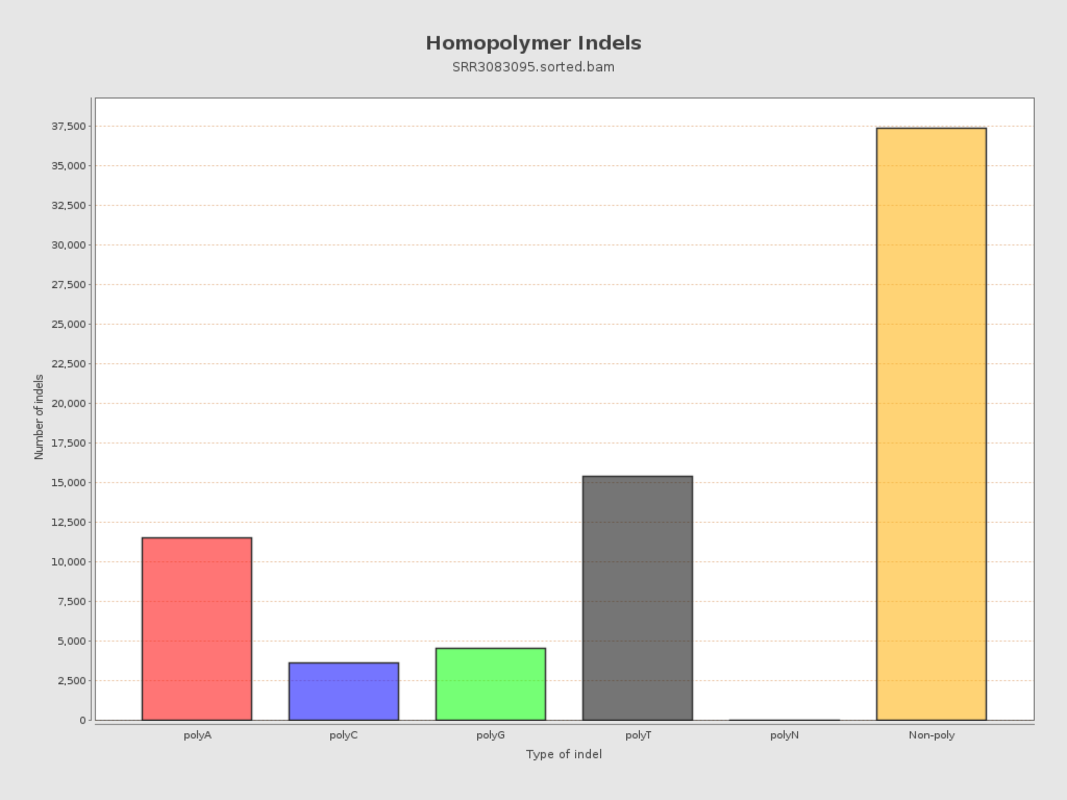
9. Results : Mapped Reads GC-content Distribution



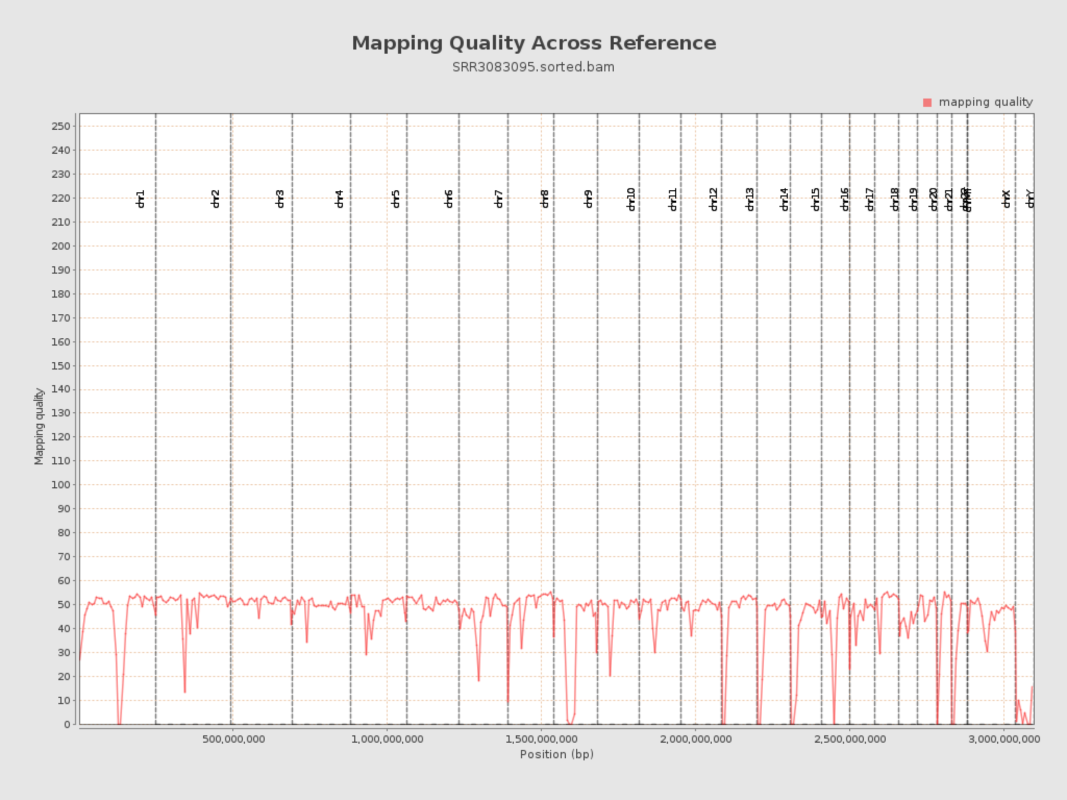
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram