Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 23:50:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085048.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_SRR3085048 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085048.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 23:50:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085048.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,412,474
Mapped reads	2,211,982 / 91.69%
Unmapped reads	200,492 / 8.31%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,666 / 0.65%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	76,109 / 3.15%
Duplication rate	2.74%
Clipped reads	976,040 / 40.46%

2.2. ACGT Content

Number/percentage of A's	42,937,480 / 28.93%
Number/percentage of C's	28,076,113 / 18.92%
Number/percentage of T's	46,008,208 / 31%
Number/percentage of G's	31,356,163 / 21.13%
Number/percentage of N's	17,056 / 0.01%
GC Percentage	40.05%

2.3. Coverage

Mean	0.048

Standard Deviation	0.3731

2.4. Mapping Quality

Mean Mapping Quality	46.33

2.5. Mismatches and indels

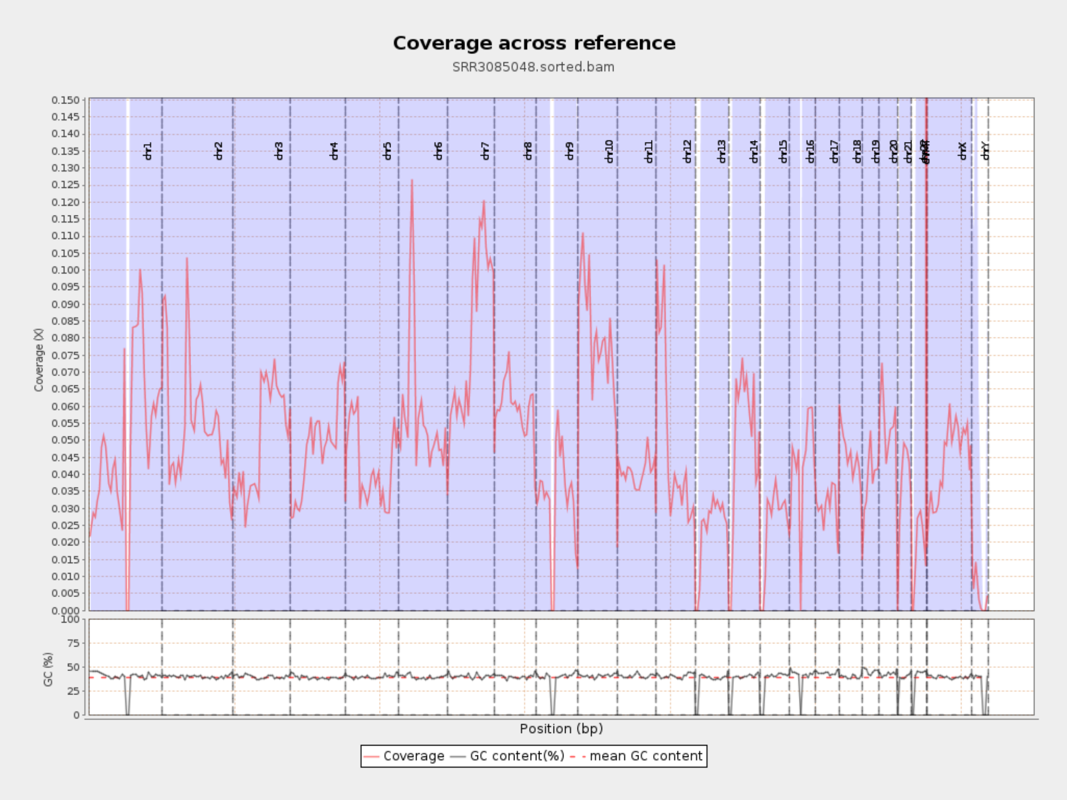
General error rate	0.87%
Mismatches	1,277,354
Insertions	10,524
Mapped reads with at least one insertion	0.47%
Deletions	30,877
Mapped reads with at least one deletion	1.38%
Homopolymer indels	47.32%

2.6. Chromosome stats

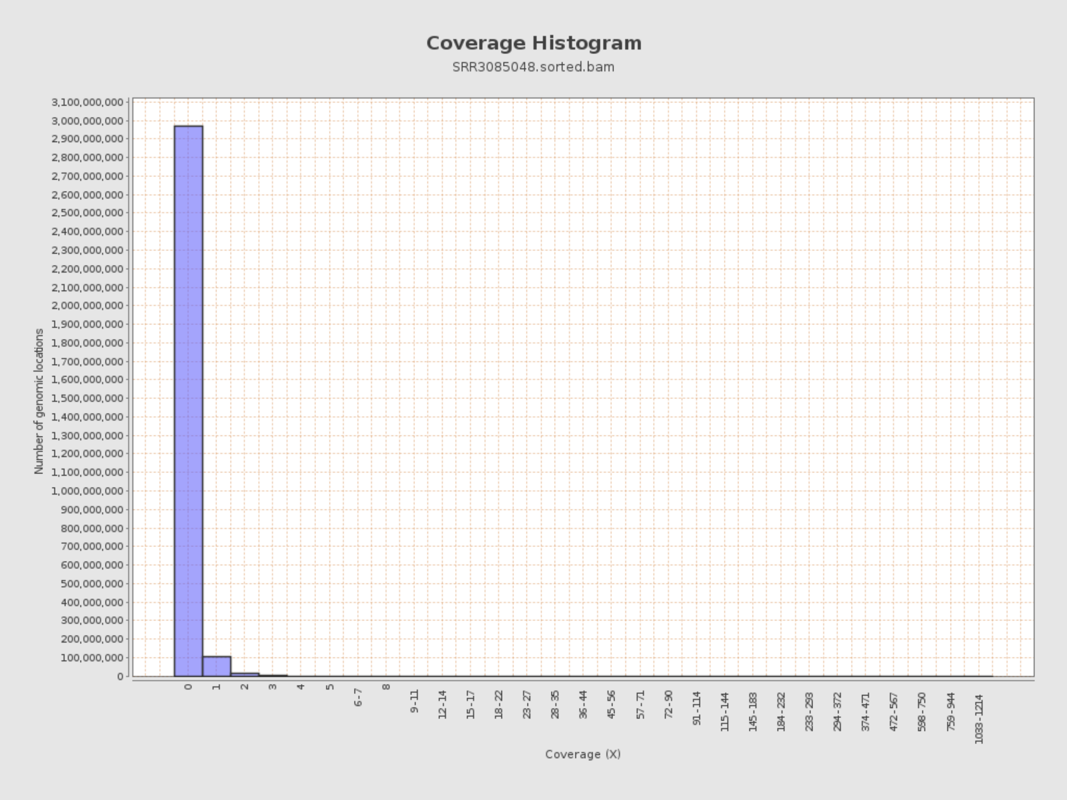
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12346542	0.0495	0.5378
chr2	243199373	13501276	0.0555	0.4552
chr3	198022430	9946814	0.0502	0.2612
chr4	191154276	9227605	0.0483	0.256
chr5	180915260	7697865	0.0425	0.2362
chr6	171115067	10024402	0.0586	0.339
chr7	159138663	13052639	0.082	0.4027

chr8	146364022	8732281	0.0597	0.7679
chr9	141213431	4710517	0.0334	0.3098
chr10	135534747	11115631	0.082	0.4913
chr11	135006516	5447723	0.0404	0.3039
chr12	133851895	6516089	0.0487	0.2584
chr13	115169878	2754096	0.0239	0.176
chr14	107349540	5334153	0.0497	0.2664
chr15	102531392	2576818	0.0251	0.1829
chr16	90354753	3945405	0.0437	0.2554
chr17	81195210	2448629	0.0302	0.2211
chr18	78077248	3584722	0.0459	0.4753
chr19	59128983	2292160	0.0388	0.4135
chr20	63025520	3447452	0.0547	0.2721
chr21	48129895	1764556	0.0367	0.2287
chr22	51304566	887368	0.0173	0.1469
chrMT	16571	24005	1.4486	1.6119
chrX	155270560	6790928	0.0437	0.2646
chrY	59373566	278516	0.0047	0.0982

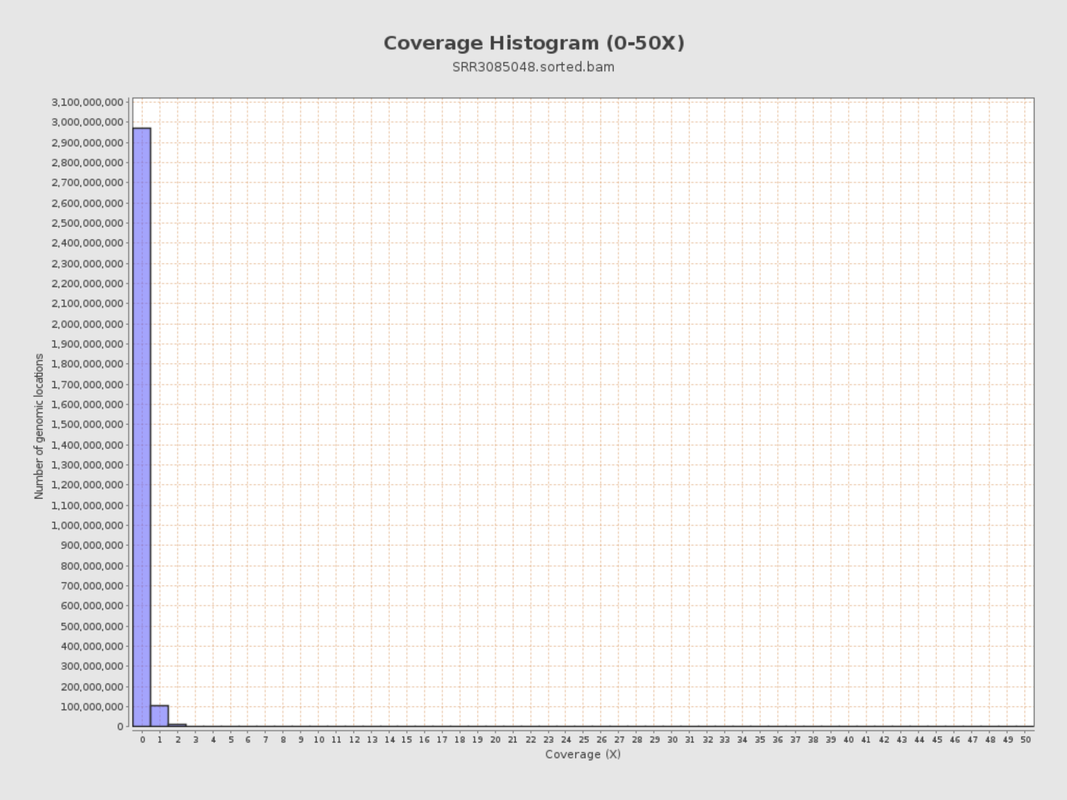
3. Results : Coverage across reference



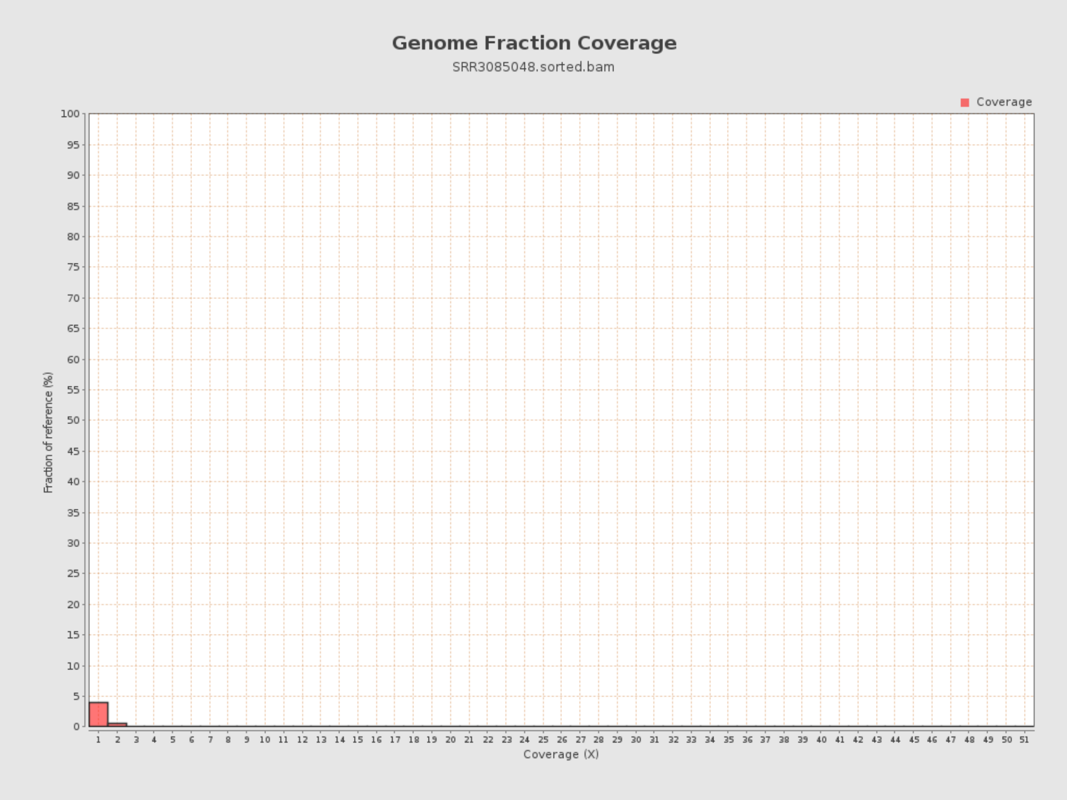
4. Results : Coverage Histogram



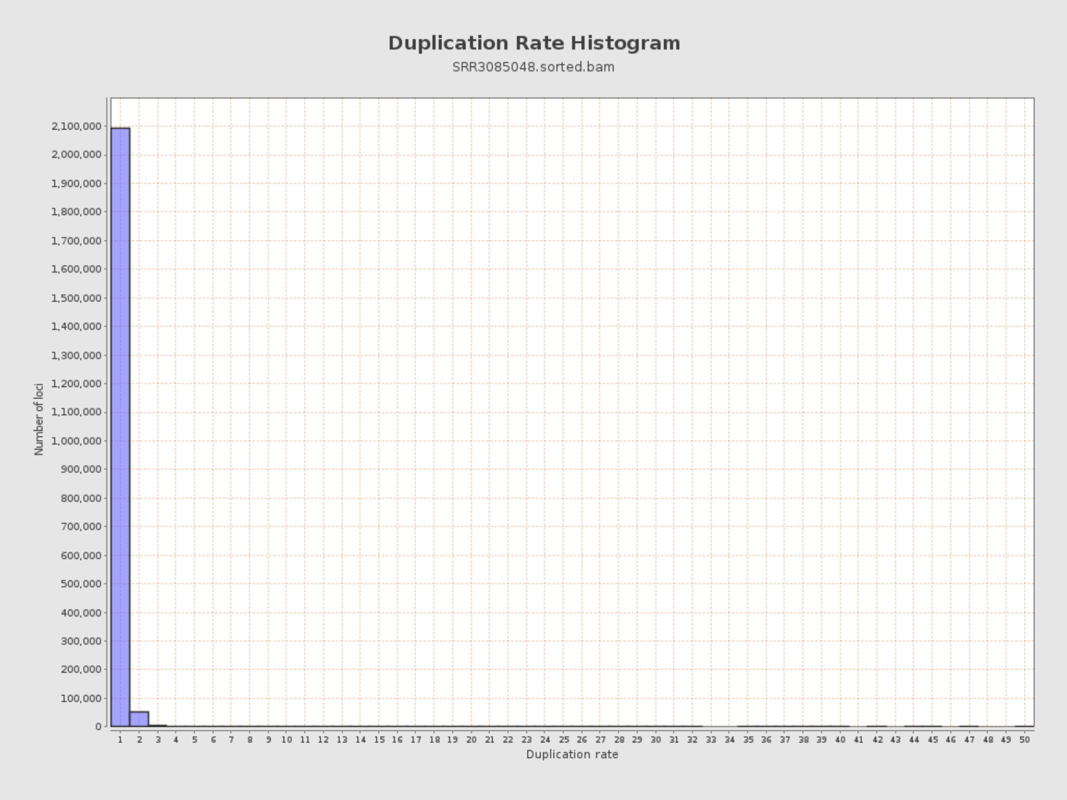
5. Results : Coverage Histogram (0-50X)



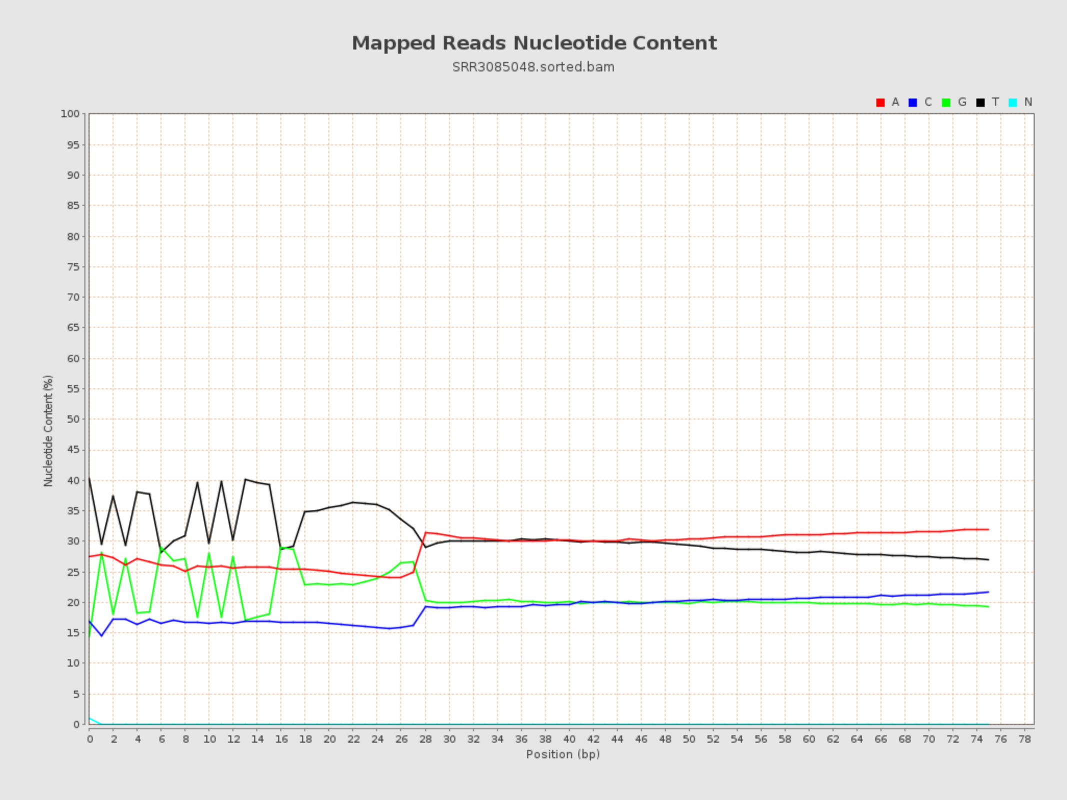
6. Results : Genome Fraction Coverage



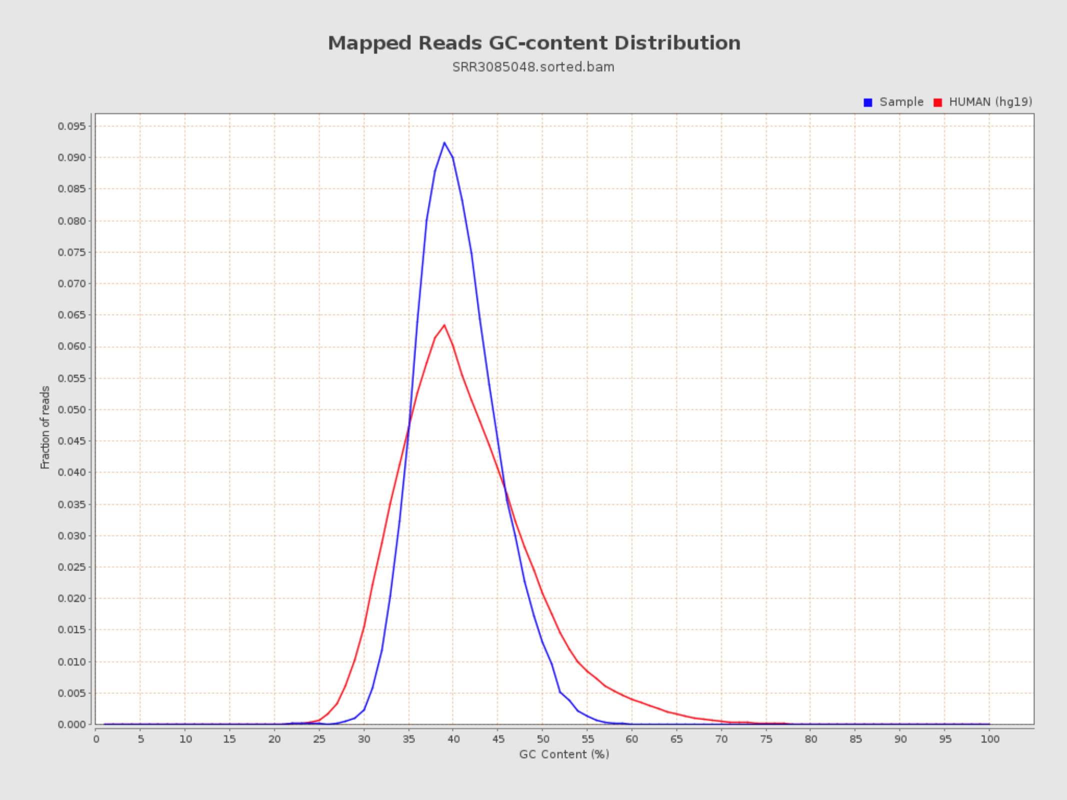
7. Results : Duplication Rate Histogram



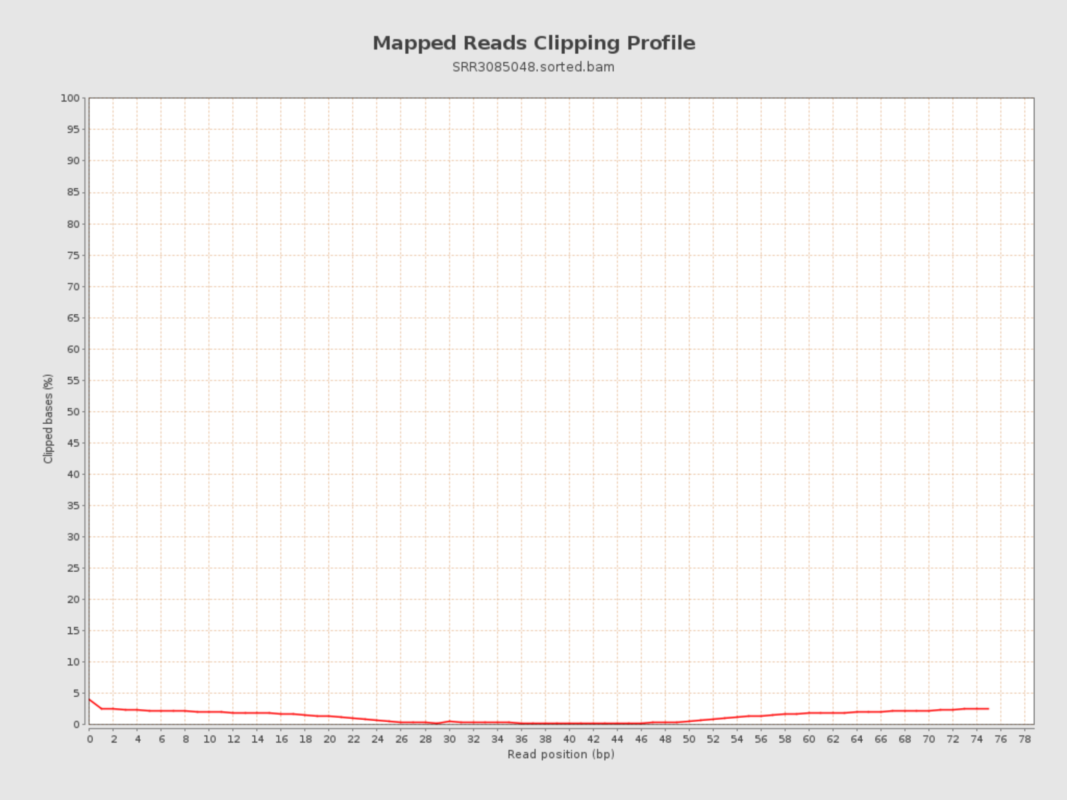
8. Results : Mapped Reads Nucleotide Content



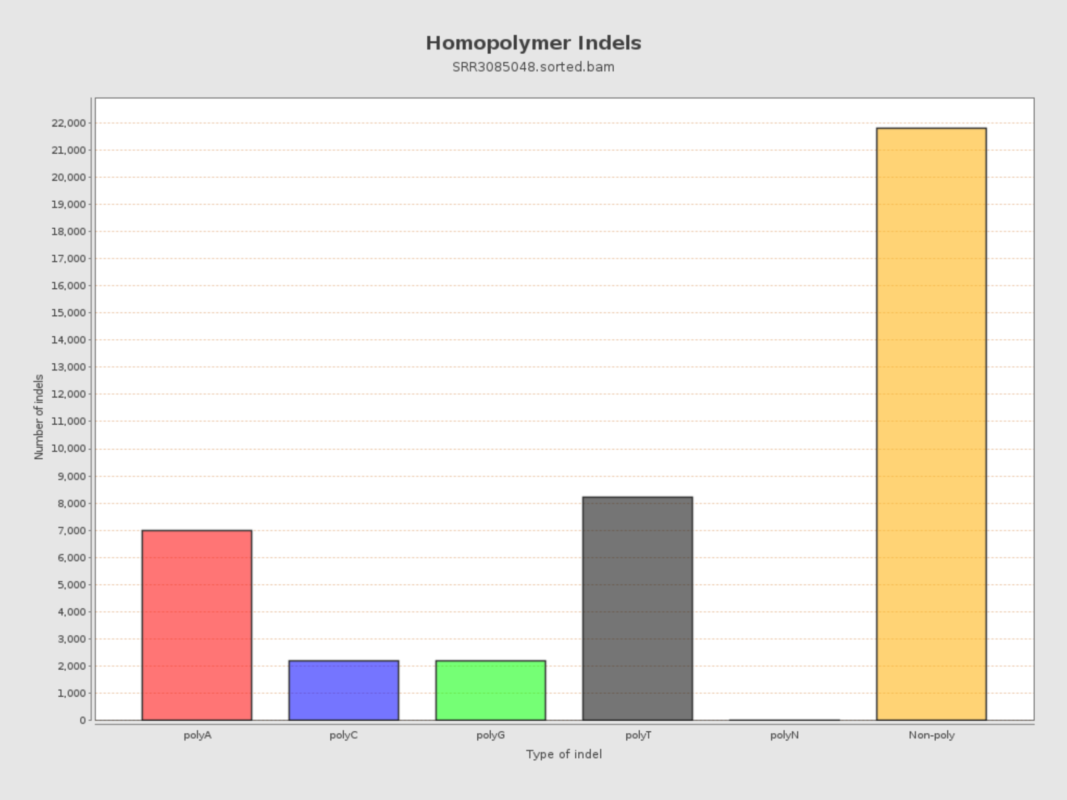
9. Results : Mapped Reads GC-content Distribution



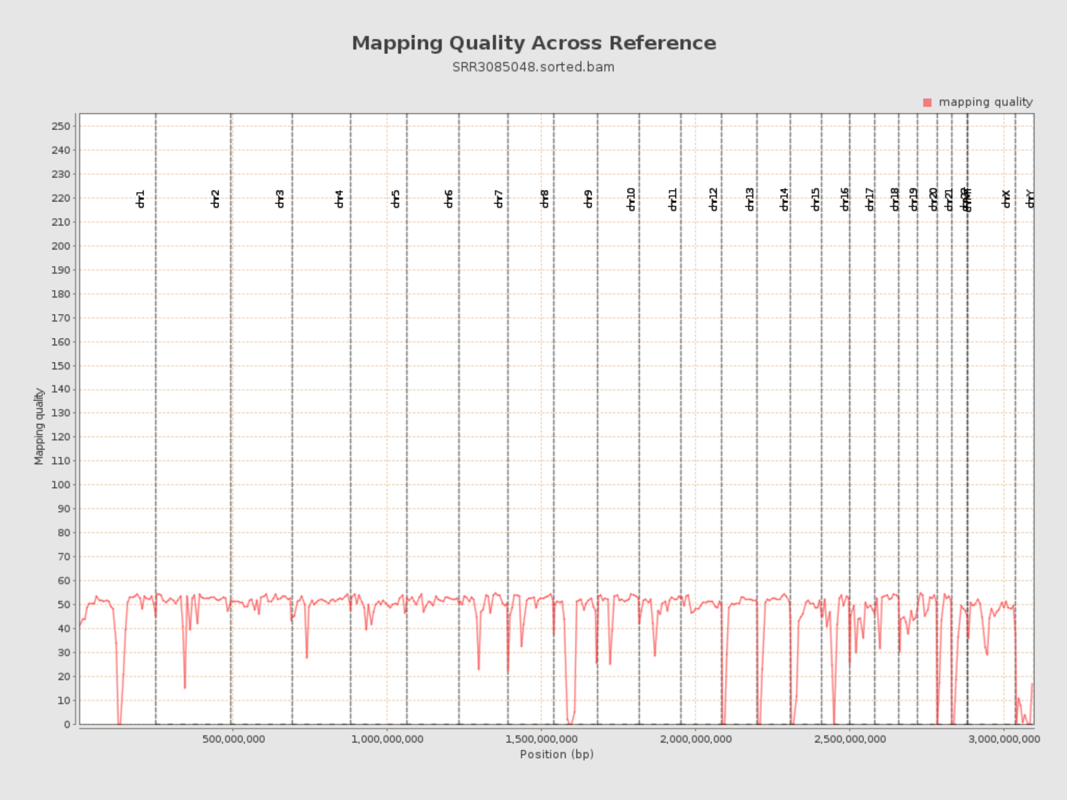
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram