Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 00:29:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085086.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_SRR3085086 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085086.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 00:29:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085086.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,580,416
Mapped reads	1,248,166 / 78.98%
Unmapped reads	332,250 / 21.02%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,564 / 0.42%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	27,595 / 1.75%
Duplication rate	1.74%
Clipped reads	794,685 / 50.28%

2.2. ACGT Content

Number/percentage of A's	22,916,746 / 29.72%
Number/percentage of C's	14,853,233 / 19.26%
Number/percentage of T's	22,452,434 / 29.12%
Number/percentage of G's	16,879,698 / 21.89%
Number/percentage of N's	1,700 / 0%
GC Percentage	41.16%

2.3. Coverage

Mean	0.0249

Standard Deviation	0.2193

2.4. Mapping Quality

Mean Mapping Quality	45.38

2.5. Mismatches and indels

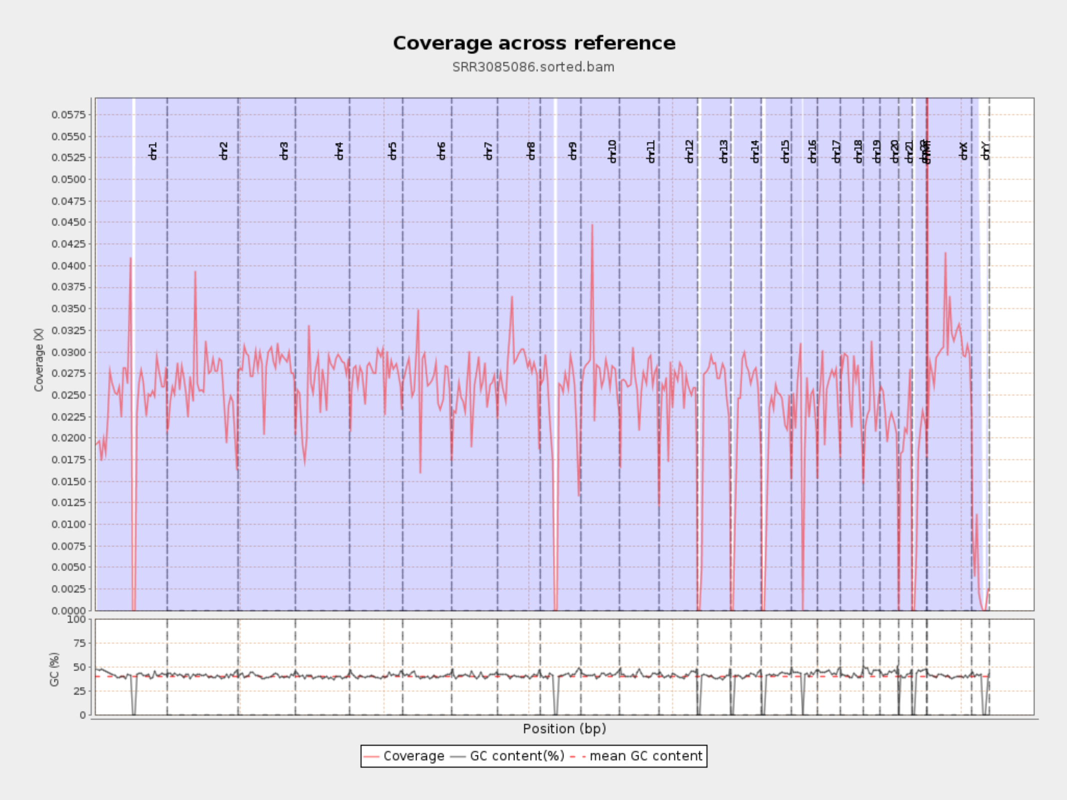
General error rate	0.91%
Mismatches	690,491
Insertions	6,132
Mapped reads with at least one insertion	0.49%
Deletions	16,907
Mapped reads with at least one deletion	1.34%
Homopolymer indels	45.76%

2.6. Chromosome stats

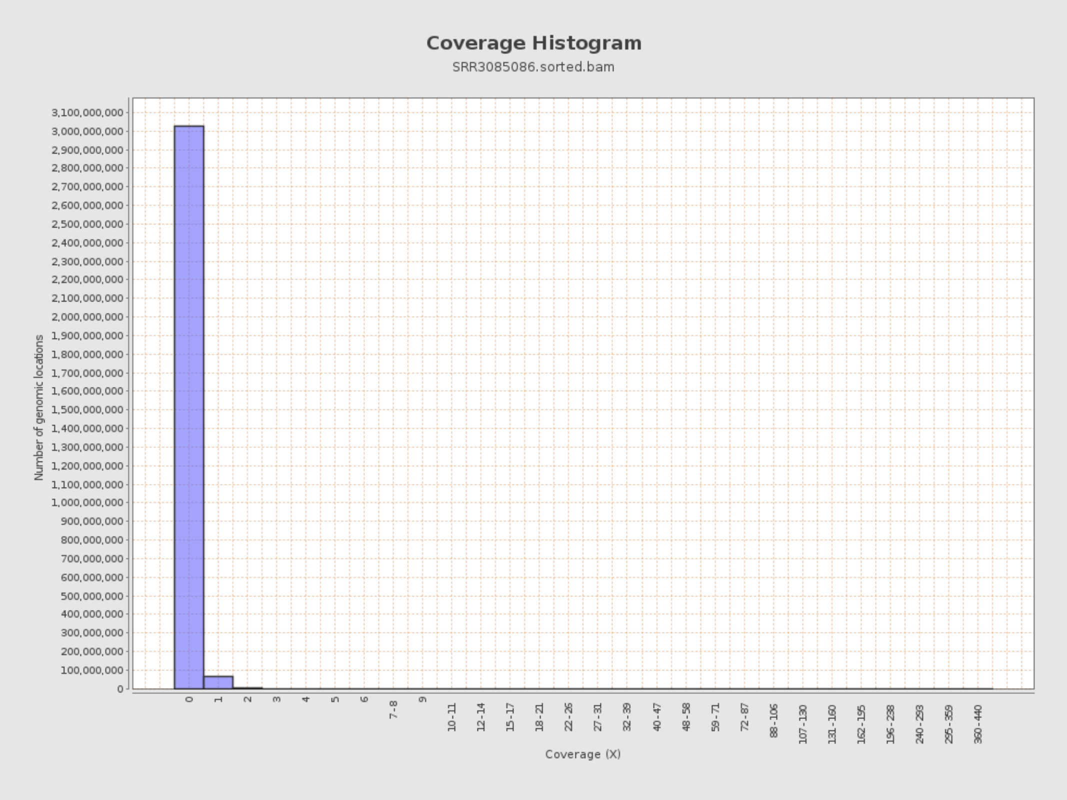
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5895330	0.0237	0.3575
chr2	243199373	6338295	0.0261	0.2256
chr3	198022430	5667347	0.0286	0.1792
chr4	191154276	5044704	0.0264	0.1801
chr5	180915260	4996660	0.0276	0.1768
chr6	171115067	4563803	0.0267	0.1954
chr7	159138663	4054613	0.0255	0.203

chr8	146364022	4161000	0.0284	0.3174
chr9	141213431	3133050	0.0222	0.1938
chr10	135534747	3807822	0.0281	0.2366
chr11	135006516	3588356	0.0266	0.215
chr12	133851895	3397503	0.0254	0.1703
chr13	115169878	2607840	0.0226	0.1588
chr14	107349540	2372318	0.0221	0.164
chr15	102531392	1989089	0.0194	0.1472
chr16	90354753	1967193	0.0218	0.167
chr17	81195210	2057720	0.0253	0.1841
chr18	78077248	2068689	0.0265	0.3284
chr19	59128983	1410460	0.0239	0.2457
chr20	63025520	1393991	0.0221	0.1601
chr21	48129895	916067	0.019	0.1556
chr22	51304566	739715	0.0144	0.1265
chrMT	16571	3956	0.2387	0.5373
chrX	155270560	4750255	0.0306	0.2004
chrY	59373566	205483	0.0035	0.0819

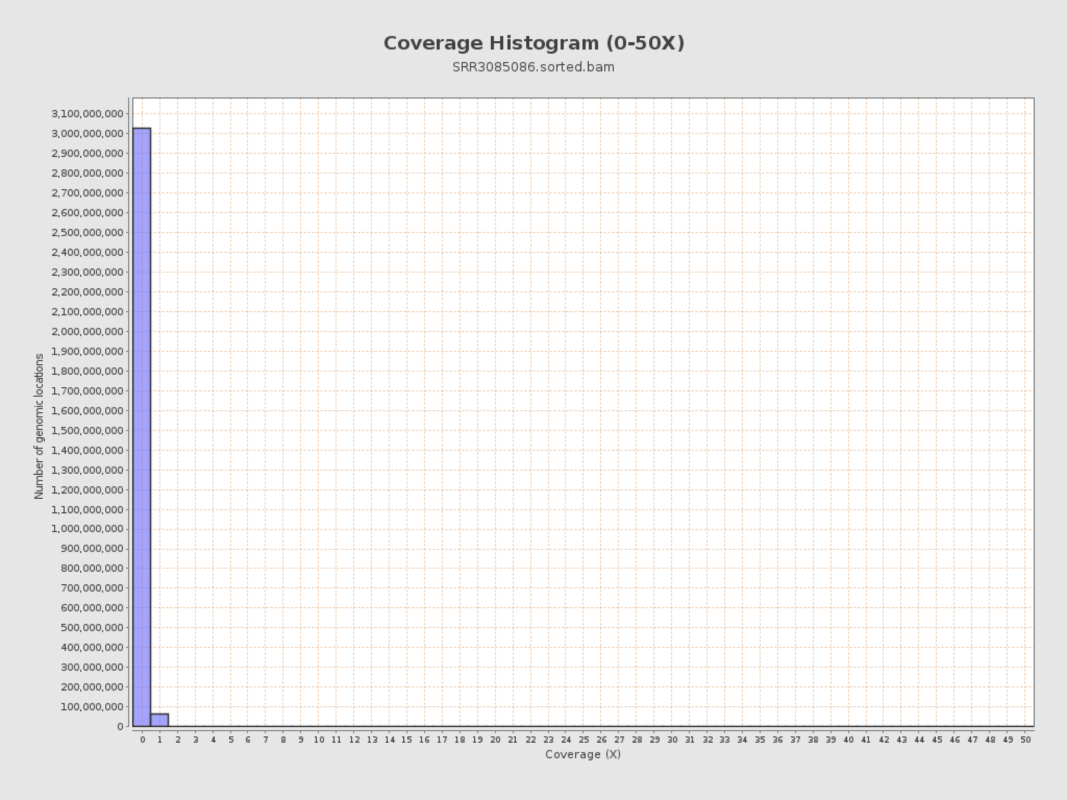
3. Results : Coverage across reference



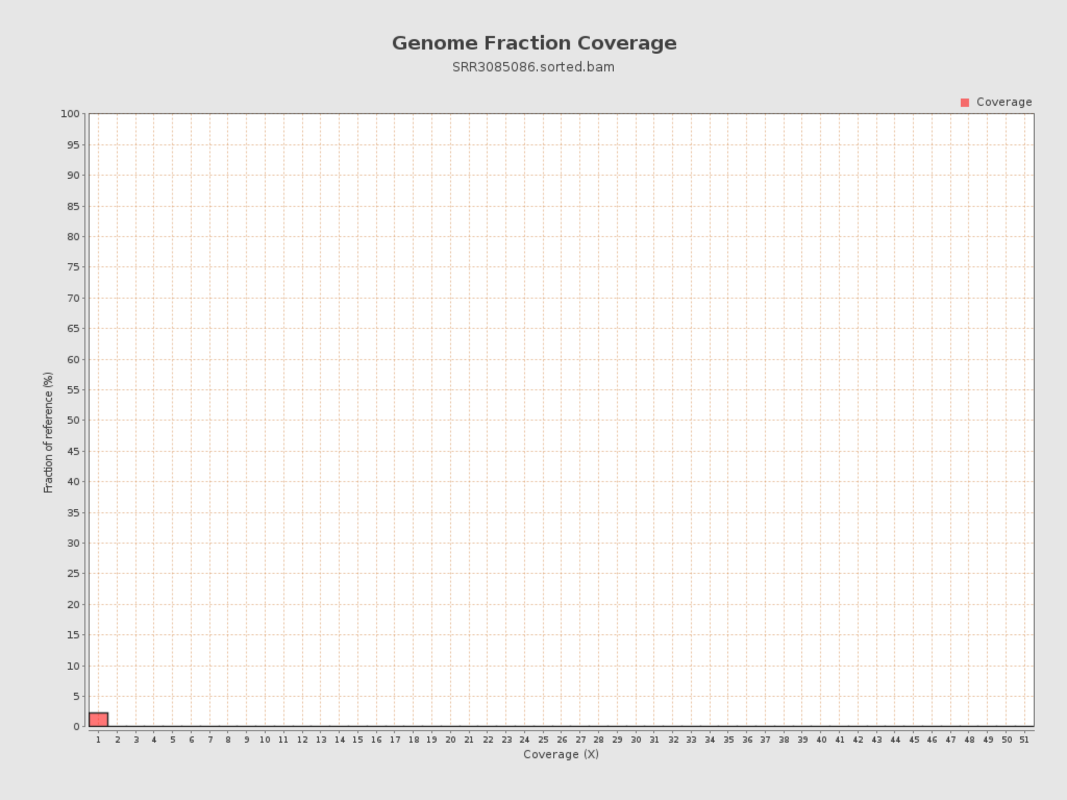
4. Results : Coverage Histogram



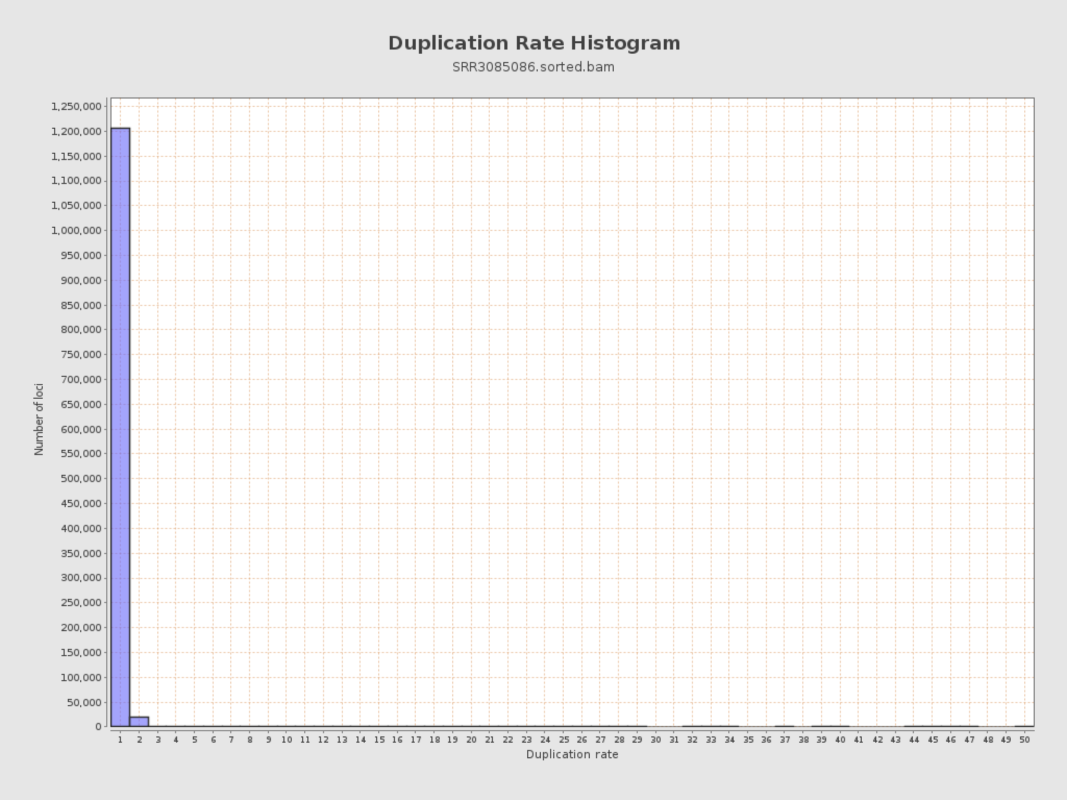
5. Results : Coverage Histogram (0-50X)



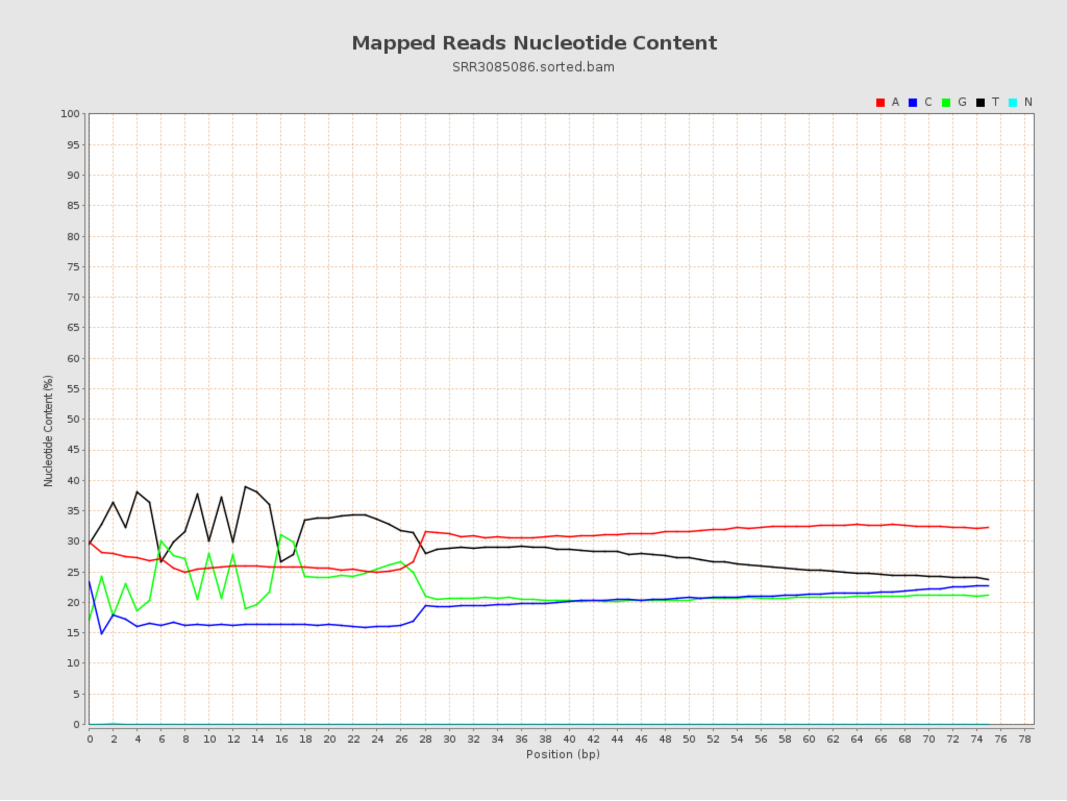
6. Results : Genome Fraction Coverage



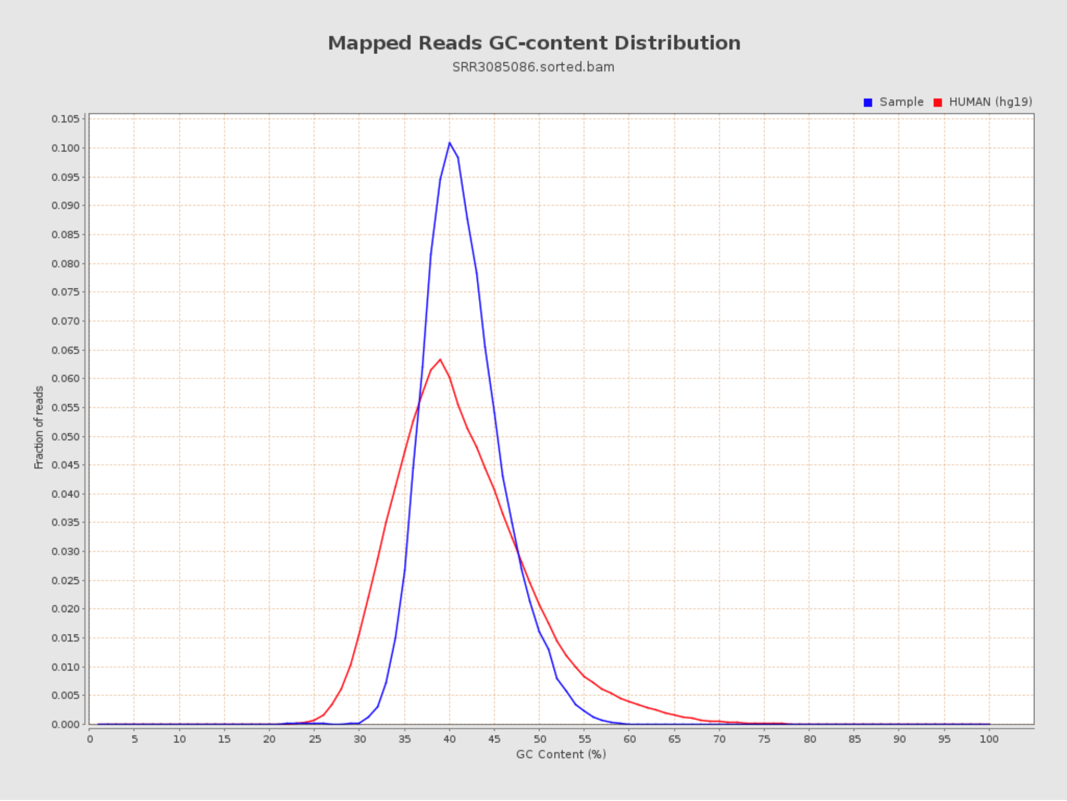
7. Results : Duplication Rate Histogram



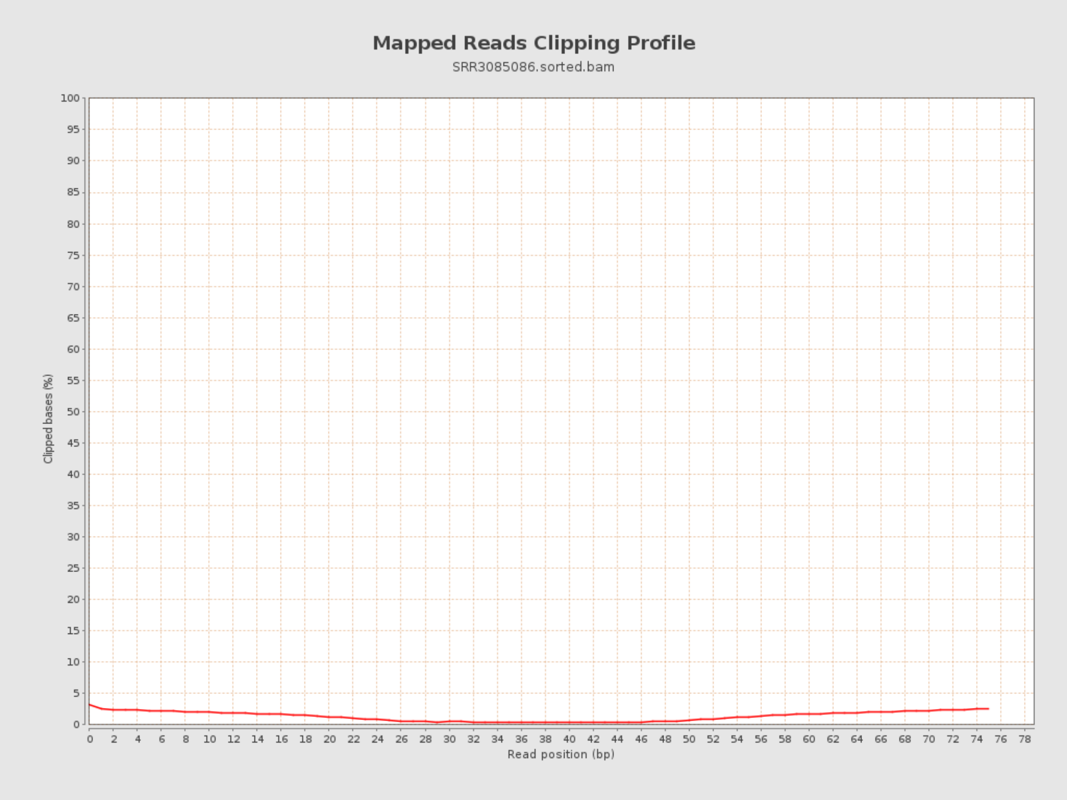
8. Results : Mapped Reads Nucleotide Content



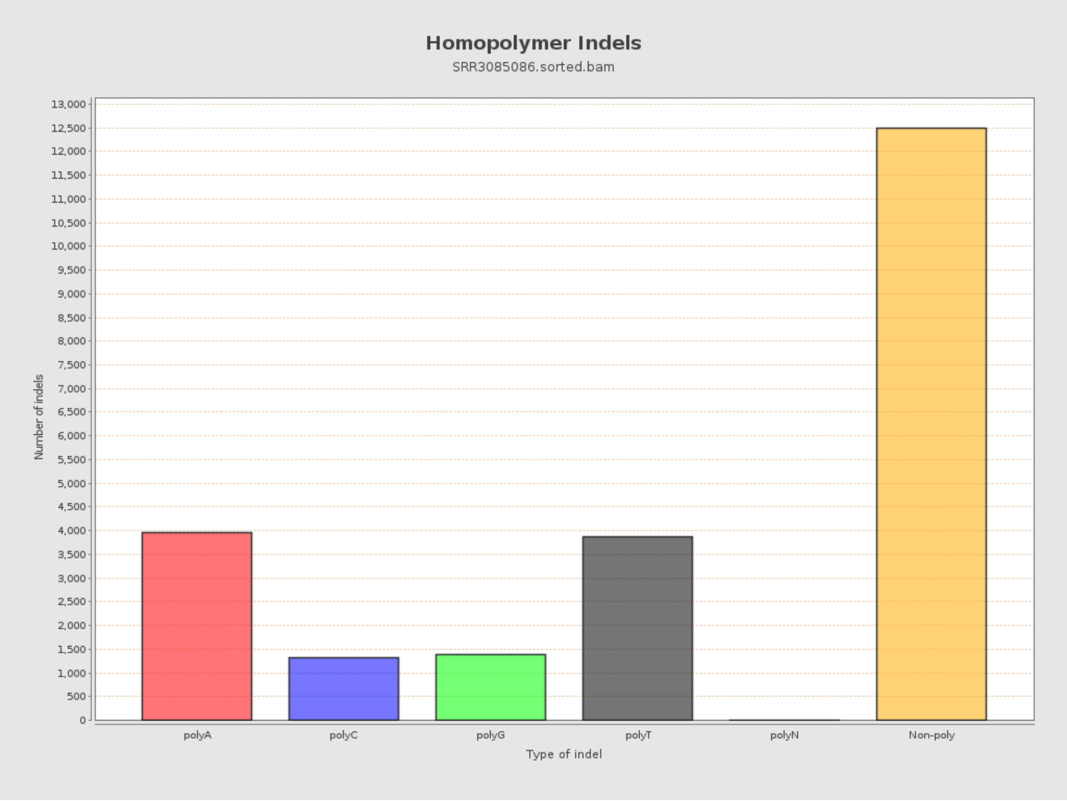
9. Results : Mapped Reads GC-content Distribution



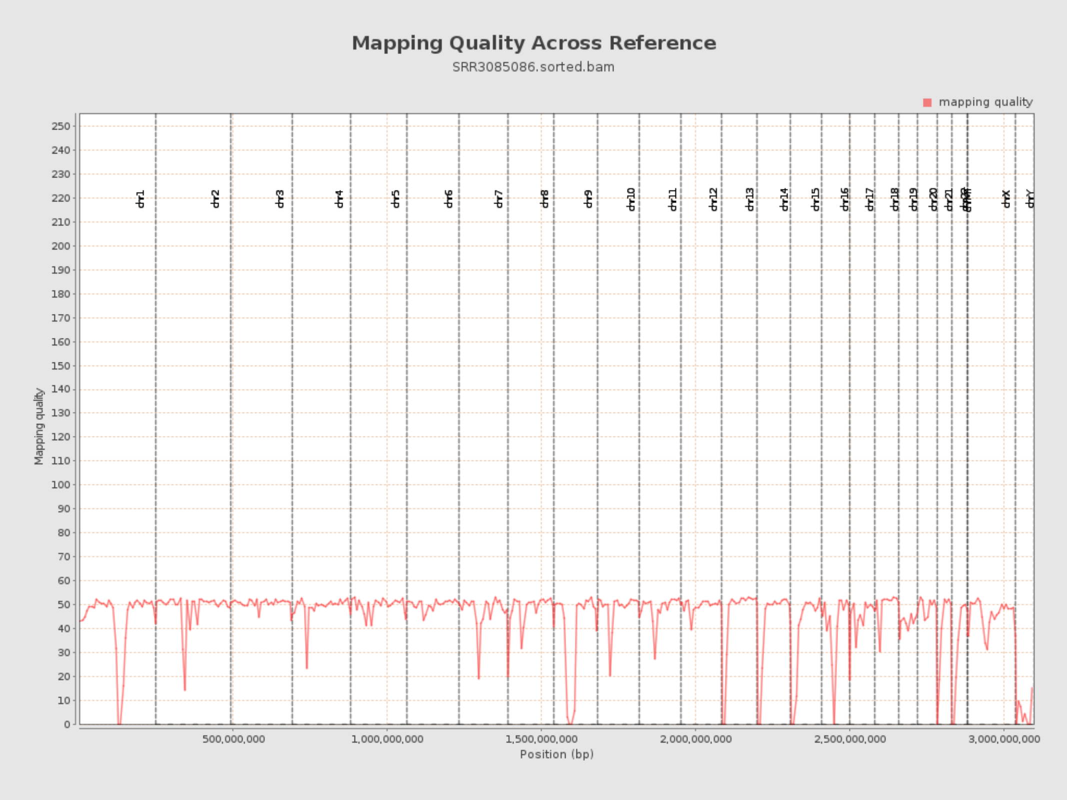
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram