Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 01:01:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085105.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_SRR3085105 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085105.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 01:01:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085105.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,144,071
Mapped reads	858,375 / 75.03%
Unmapped reads	285,696 / 24.97%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,376 / 0.47%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	16,459 / 1.44%
Duplication rate	1.47%
Clipped reads	534,597 / 46.73%

2.2. ACGT Content

Number/percentage of A's	16,010,251 / 29.88%
Number/percentage of C's	10,468,102 / 19.54%
Number/percentage of T's	15,457,543 / 28.85%
Number/percentage of G's	11,641,636 / 21.73%
Number/percentage of N's	1,147 / 0%
GC Percentage	41.27%

2.3. Coverage

Mean	0.0173

Standard Deviation	0.1763

2.4. Mapping Quality

Mean Mapping Quality	43.97

2.5. Mismatches and indels

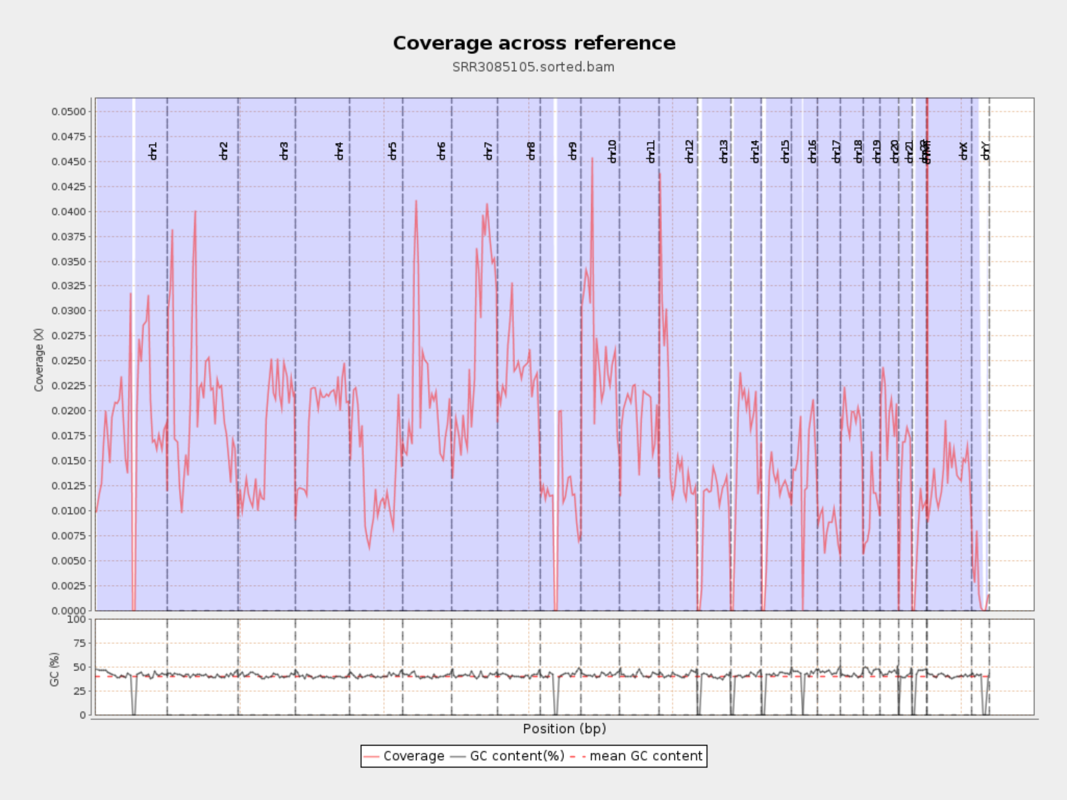
General error rate	0.97%
Mismatches	510,959
Insertions	4,470
Mapped reads with at least one insertion	0.52%
Deletions	11,561
Mapped reads with at least one deletion	1.33%
Homopolymer indels	43.96%

2.6. Chromosome stats

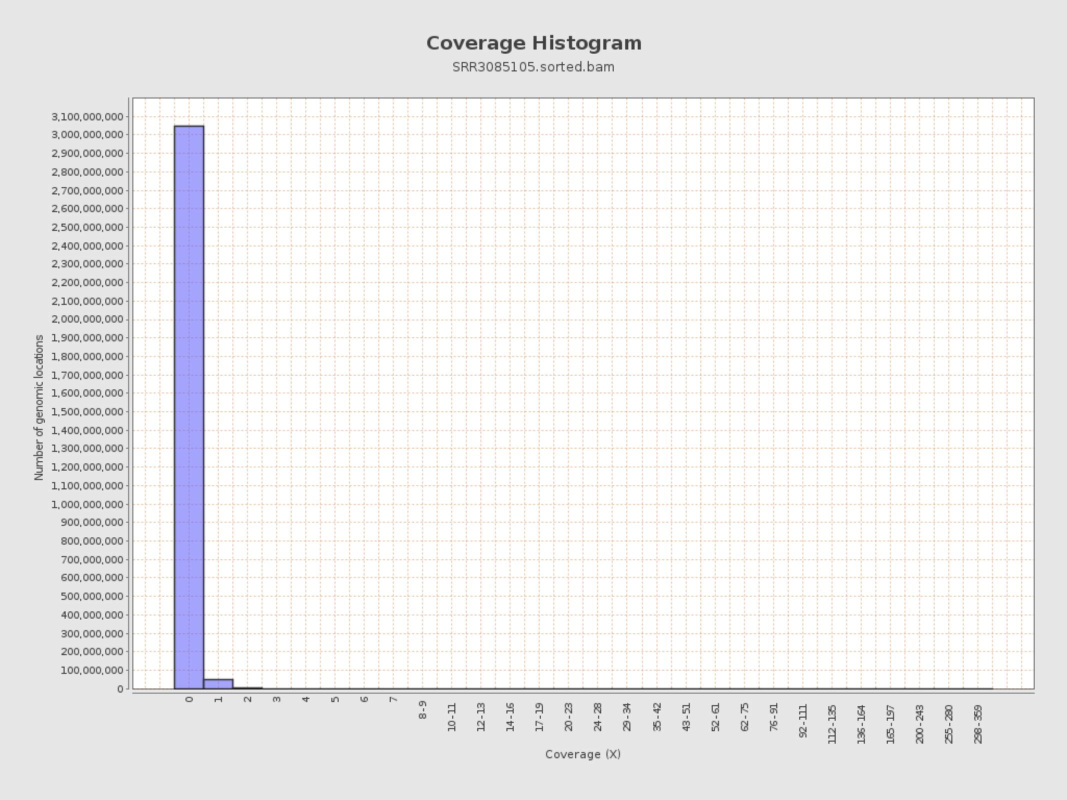
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4603090	0.0185	0.2385
chr2	243199373	5105336	0.021	0.209
chr3	198022430	3375213	0.017	0.1397
chr4	191154276	3697774	0.0193	0.1481
chr5	180915260	2410890	0.0133	0.1203
chr6	171115067	3730020	0.0218	0.1714
chr7	159138663	4259738	0.0268	0.1931

chr8	146364022	3530278	0.0241	0.2669
chr9	141213431	1555004	0.011	0.1447
chr10	135534747	3606160	0.0266	0.2619
chr11	135006516	2657961	0.0197	0.1988
chr12	133851895	2396501	0.0179	0.1407
chr13	115169878	1173809	0.0102	0.1045
chr14	107349540	1733642	0.0161	0.1355
chr15	102531392	1080214	0.0105	0.1063
chr16	90354753	1295440	0.0143	0.1344
chr17	81195210	679200	0.0084	0.1096
chr18	78077248	1498937	0.0192	0.2457
chr19	59128983	589154	0.01	0.1629
chr20	63025520	1251614	0.0199	0.1489
chr21	48129895	685157	0.0142	0.1296
chr22	51304566	378399	0.0074	0.0888
chrMT	16571	58683	3.5413	2.6409
chrX	155270560	2111522	0.0136	0.1307
chrY	59373566	133874	0.0023	0.0601

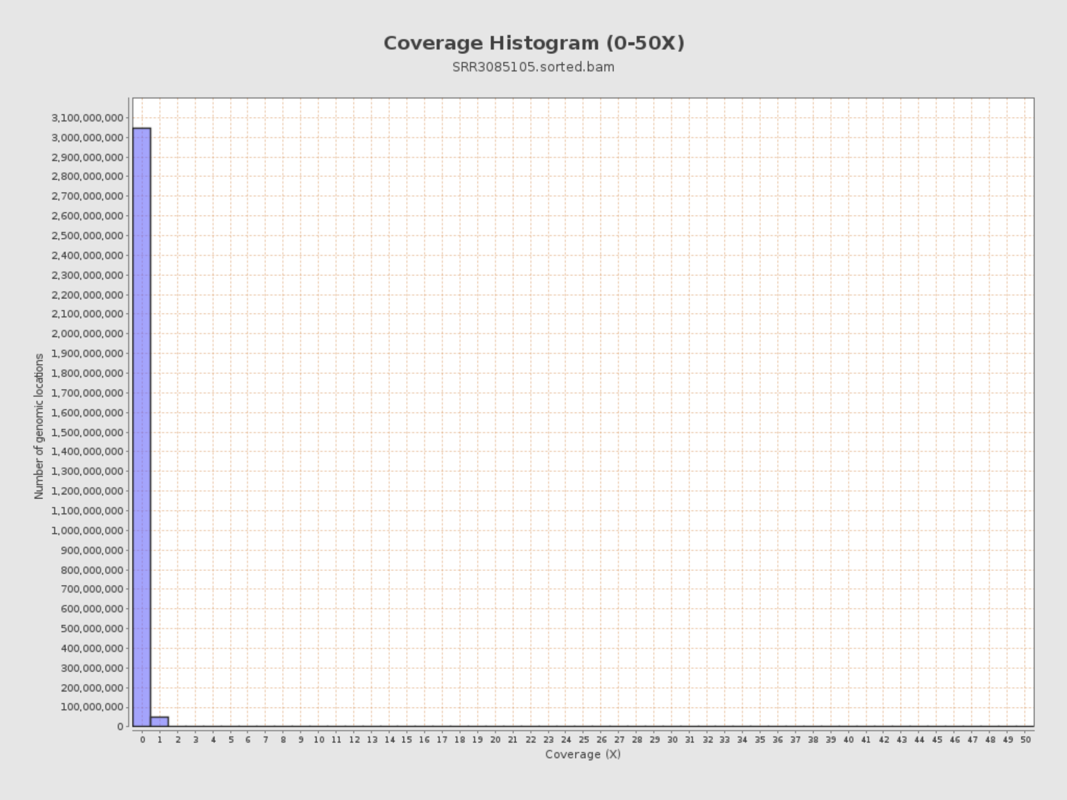
3. Results : Coverage across reference



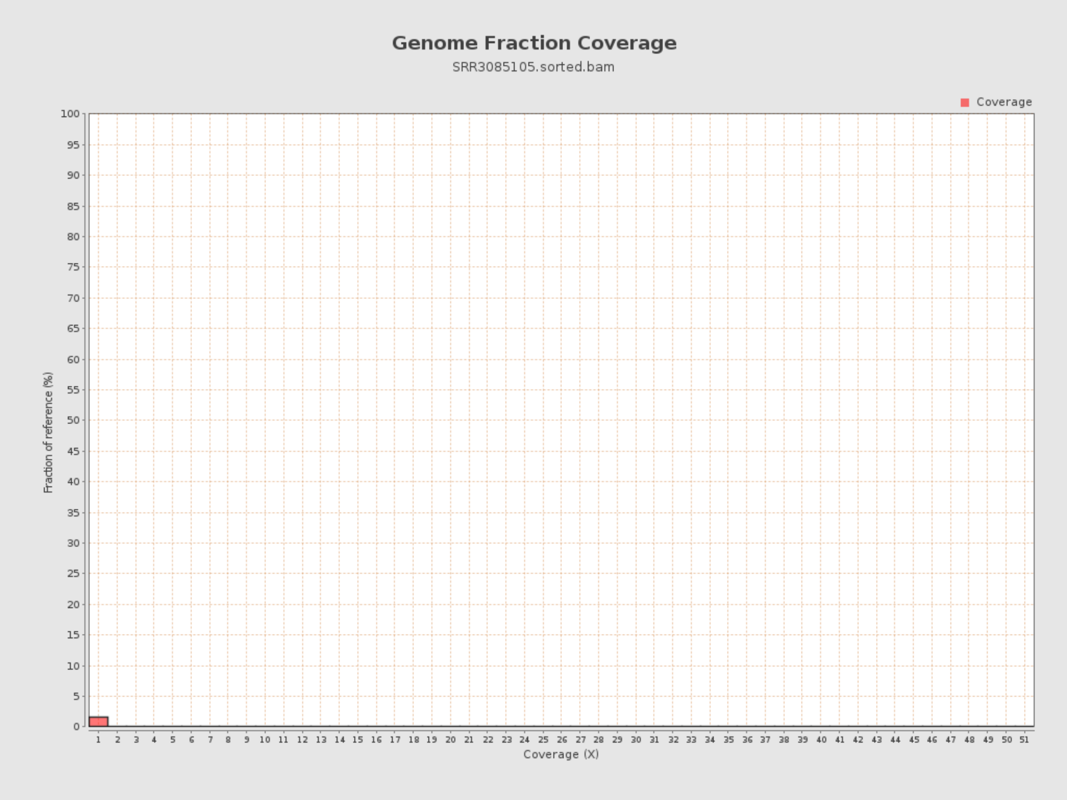
4. Results : Coverage Histogram



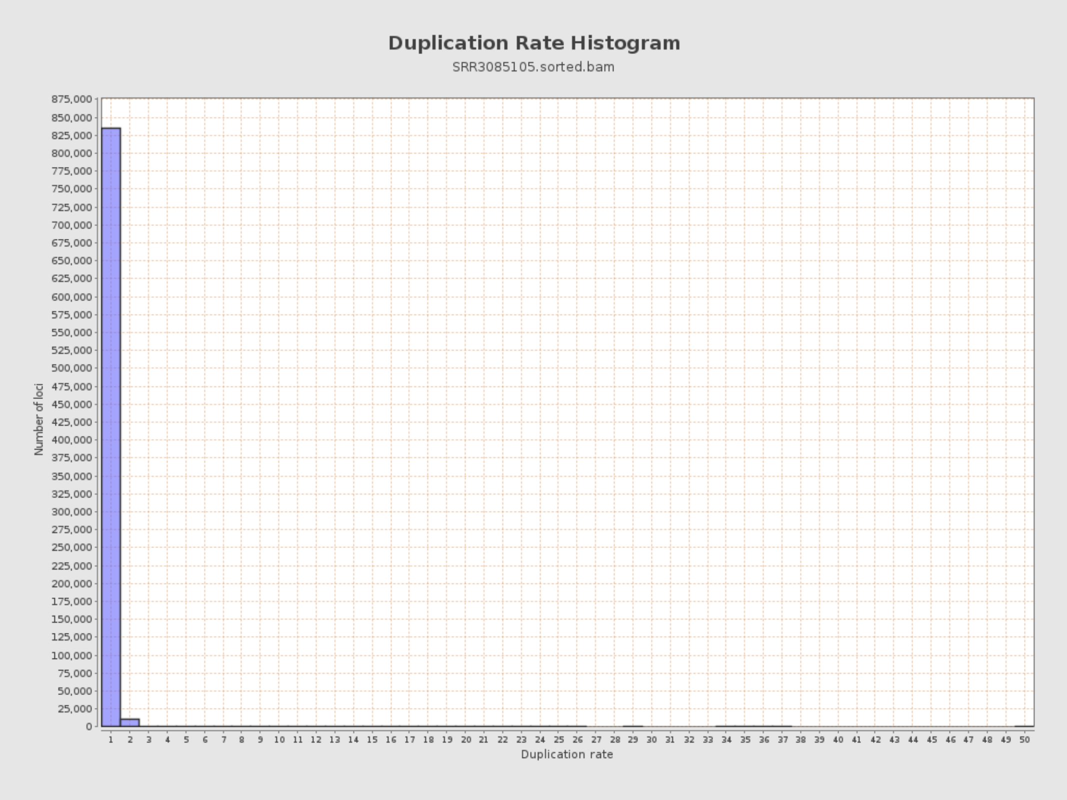
5. Results : Coverage Histogram (0-50X)



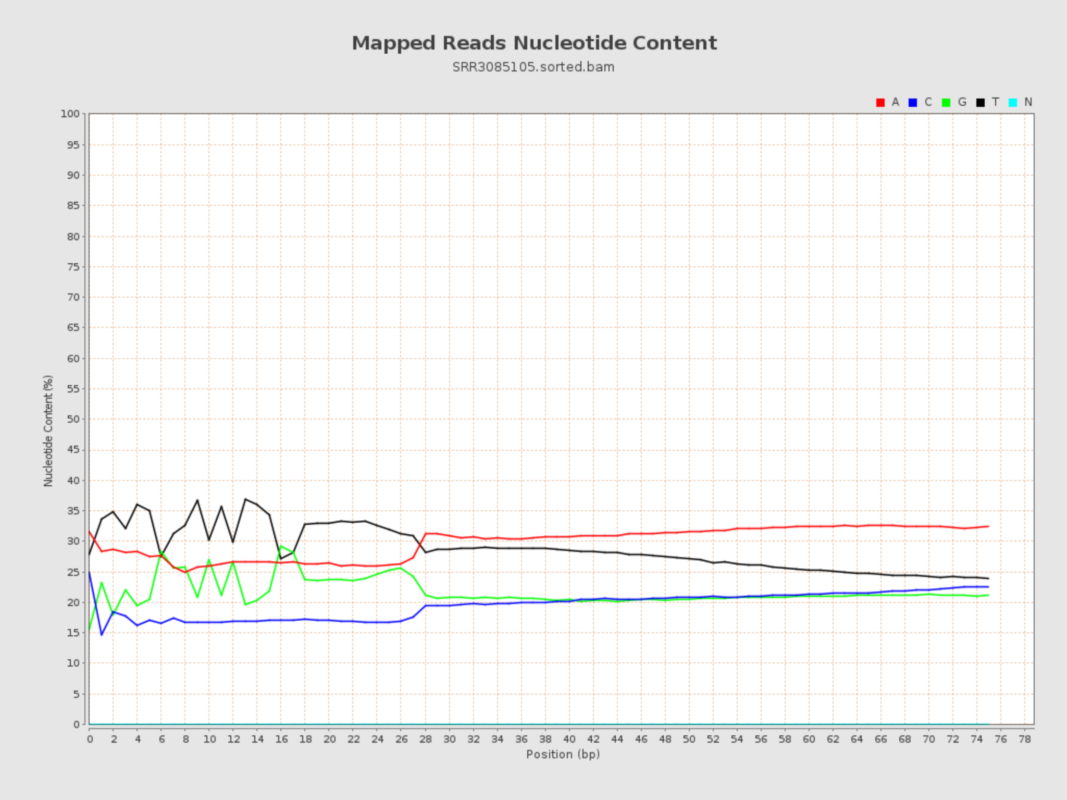
6. Results : Genome Fraction Coverage



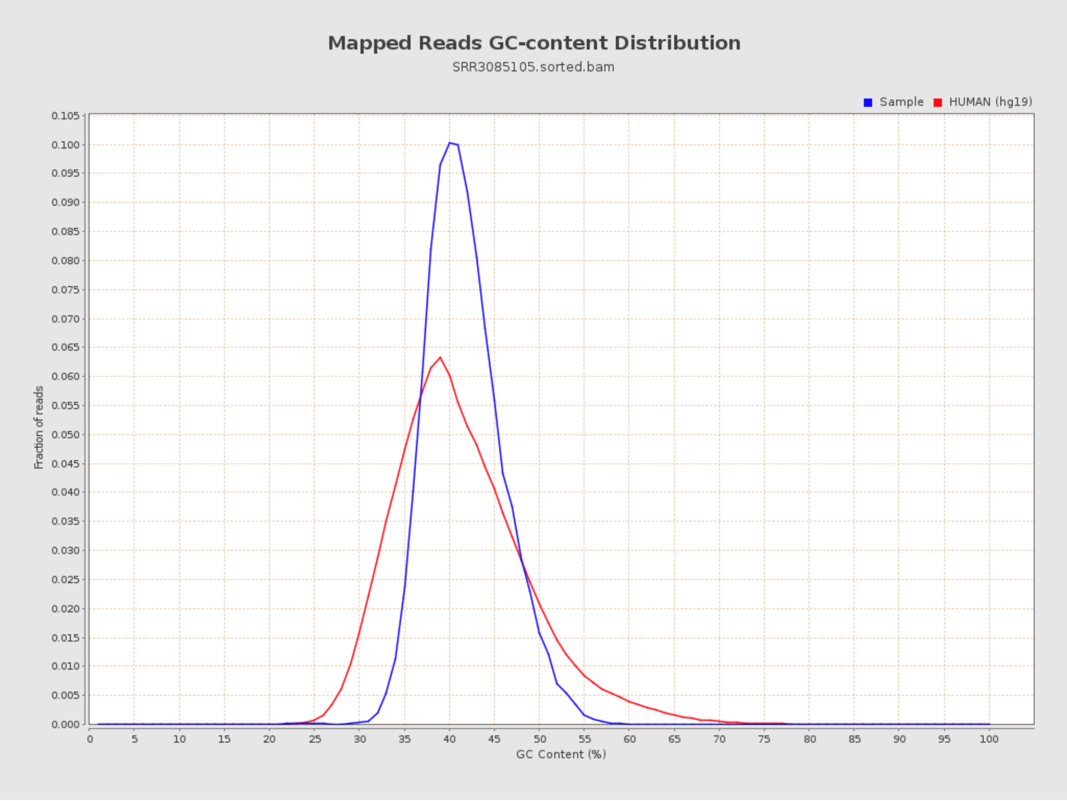
7. Results : Duplication Rate Histogram



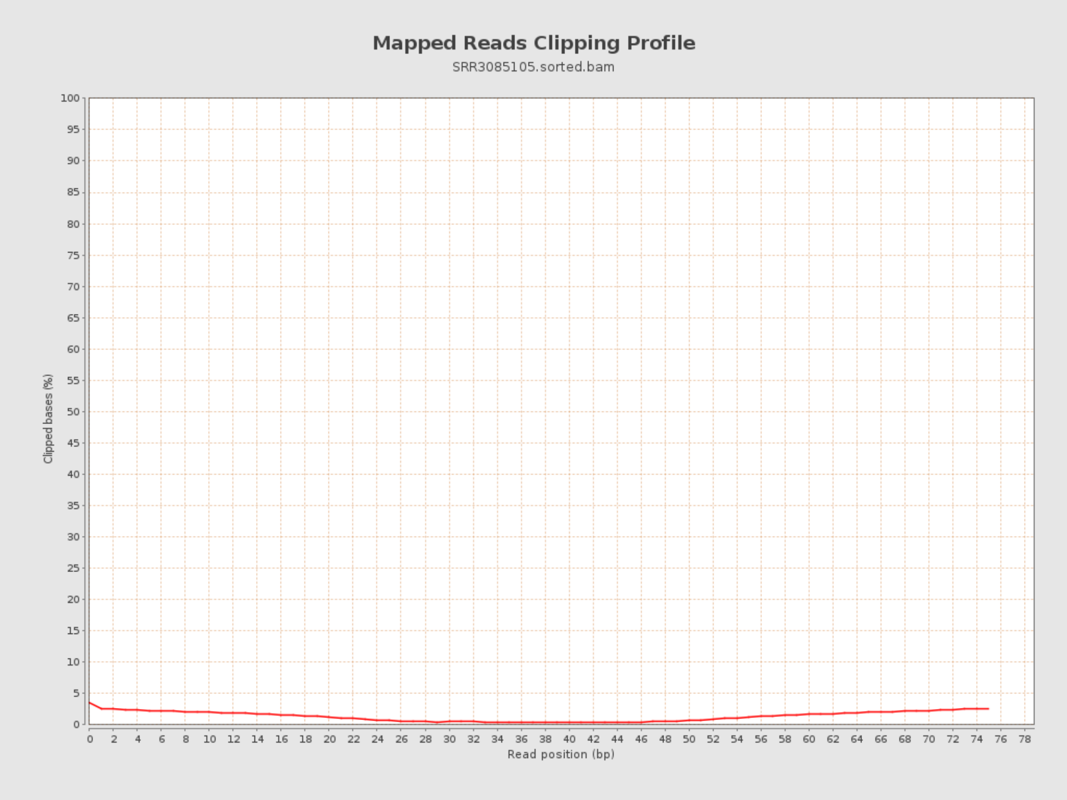
8. Results : Mapped Reads Nucleotide Content



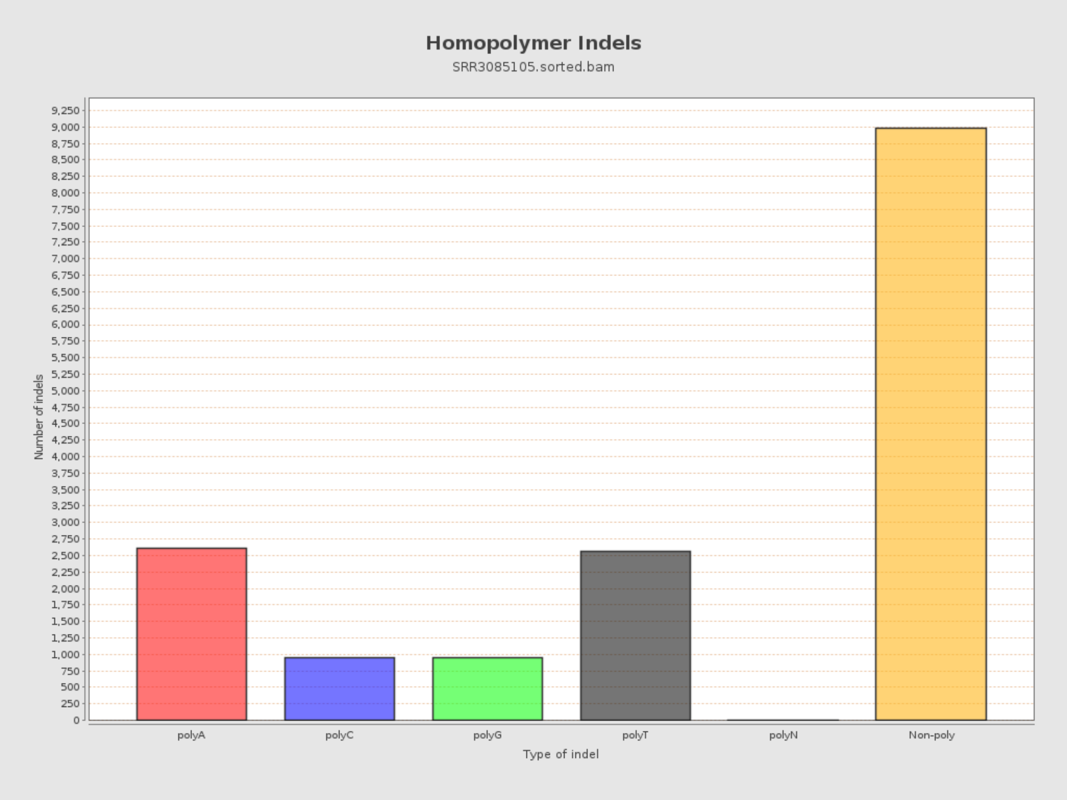
9. Results : Mapped Reads GC-content Distribution



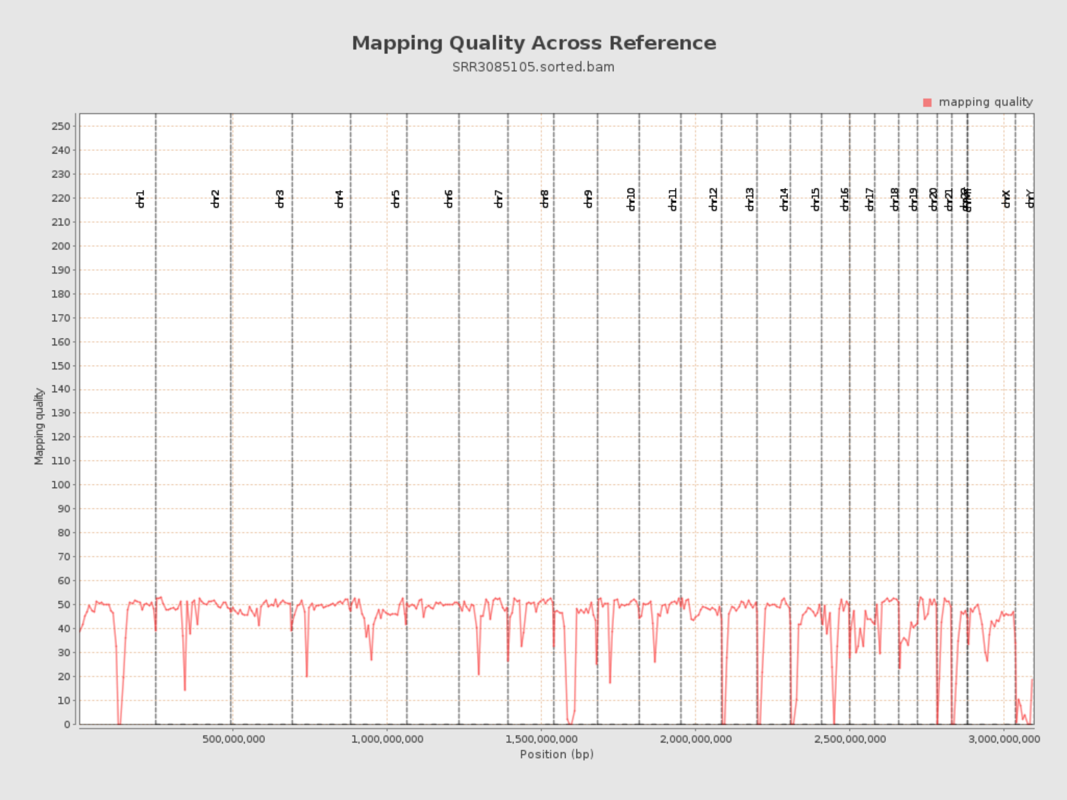
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram