Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 01:17:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085110.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_SRR3085110 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085110.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 01:17:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085110.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,066,143
Mapped reads	1,744,408 / 84.43%
Unmapped reads	321,735 / 15.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,153 / 0.59%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	51,085 / 2.47%
Duplication rate	2.28%
Clipped reads	1,146,509 / 55.49%

2.2. ACGT Content

Number/percentage of A's	31,794,071 / 29.67%
Number/percentage of C's	20,566,194 / 19.19%
Number/percentage of T's	31,762,465 / 29.64%
Number/percentage of G's	23,050,538 / 21.51%
Number/percentage of N's	2,352 / 0%
GC Percentage	40.7%

2.3. Coverage

Mean	0.0346

Standard Deviation	0.3033

2.4. Mapping Quality

Mean Mapping Quality	44.96

2.5. Mismatches and indels

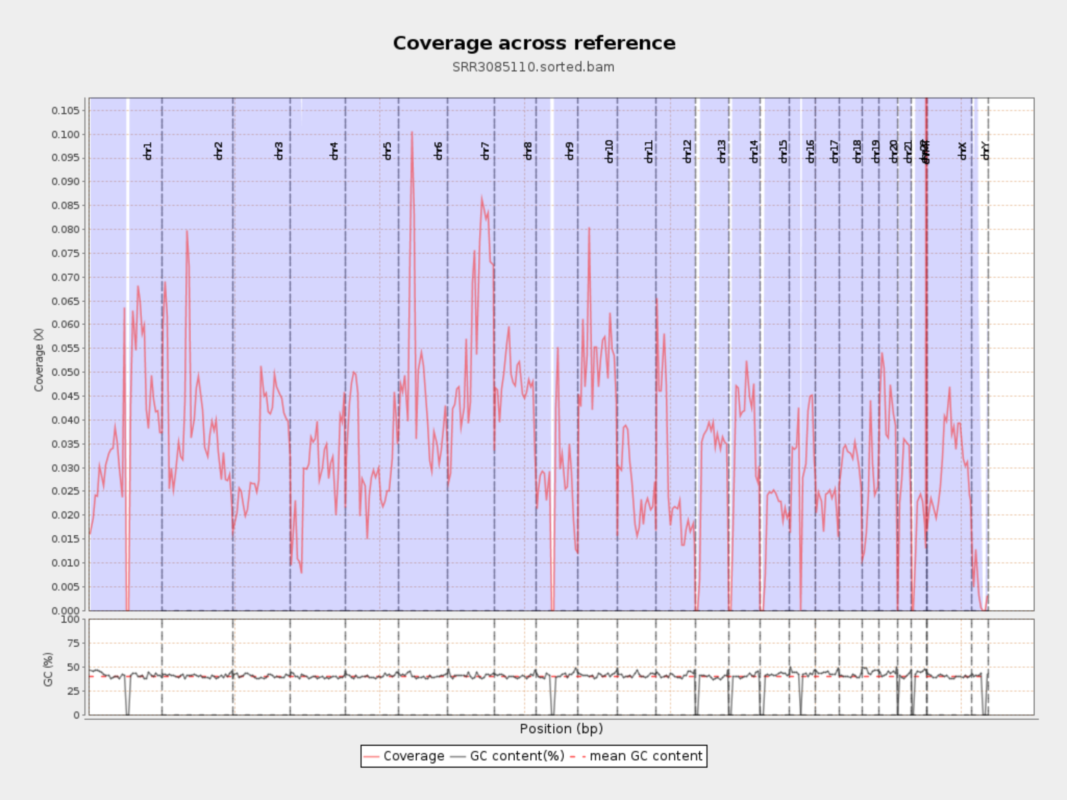
General error rate	0.89%
Mismatches	938,570
Insertions	8,250
Mapped reads with at least one insertion	0.47%
Deletions	23,156
Mapped reads with at least one deletion	1.31%
Homopolymer indels	45.71%

2.6. Chromosome stats

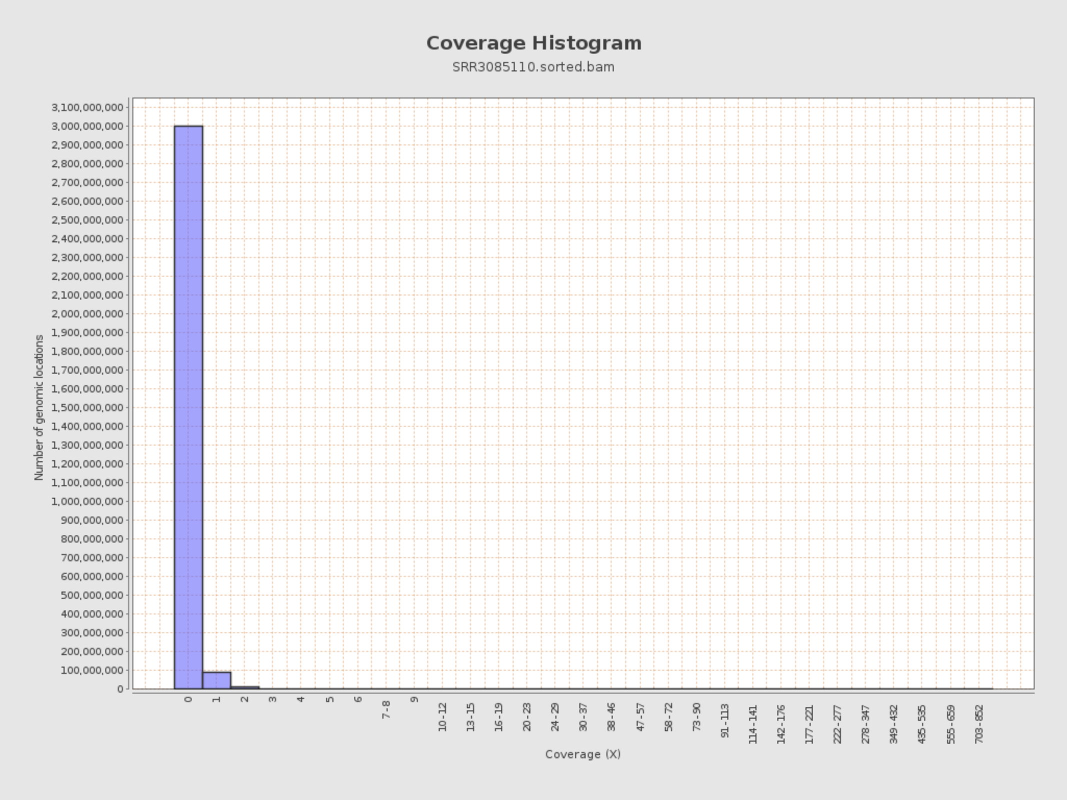
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9337882	0.0375	0.5167
chr2	243199373	9719685	0.04	0.3218
chr3	198022430	6762374	0.0341	0.204
chr4	191154276	5431450	0.0284	0.1877
chr5	180915260	5766600	0.0319	0.1937
chr6	171115067	8021669	0.0469	0.3112
chr7	159138663	9289982	0.0584	0.3255

chr8	146364022	6983752	0.0477	0.5405
chr9	141213431	3682626	0.0261	0.2613
chr10	135534747	7269080	0.0536	0.381
chr11	135006516	3475473	0.0257	0.2234
chr12	133851895	3797257	0.0284	0.1855
chr13	115169878	3486195	0.0303	0.1861
chr14	107349540	3725121	0.0347	0.2075
chr15	102531392	1894568	0.0185	0.1461
chr16	90354753	2933366	0.0325	0.2095
chr17	81195210	1817755	0.0224	0.1755
chr18	78077248	2505867	0.0321	0.4612
chr19	59128983	1479715	0.025	0.3517
chr20	63025520	2691097	0.0427	0.2264
chr21	48129895	1313828	0.0273	0.1849
chr22	51304566	790025	0.0154	0.1319
chrMT	16571	14154	0.8541	0.9587
chrX	155270560	4783971	0.0308	0.2075
chrY	59373566	239501	0.004	0.088

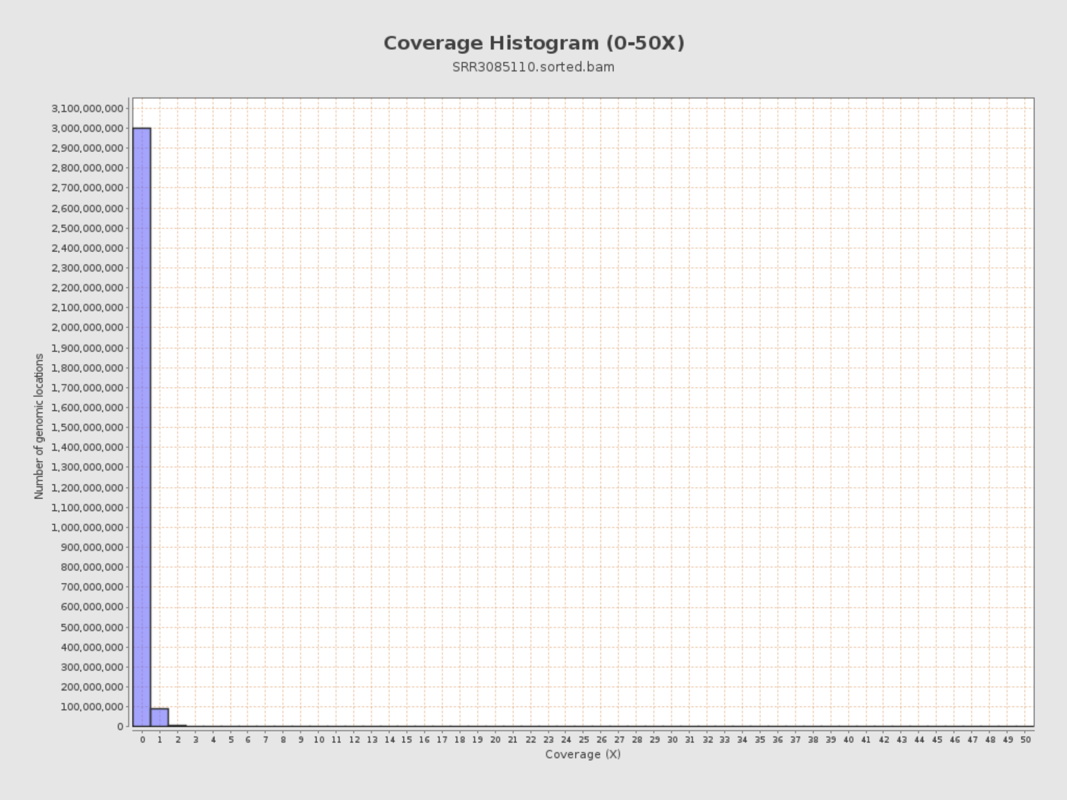
3. Results : Coverage across reference



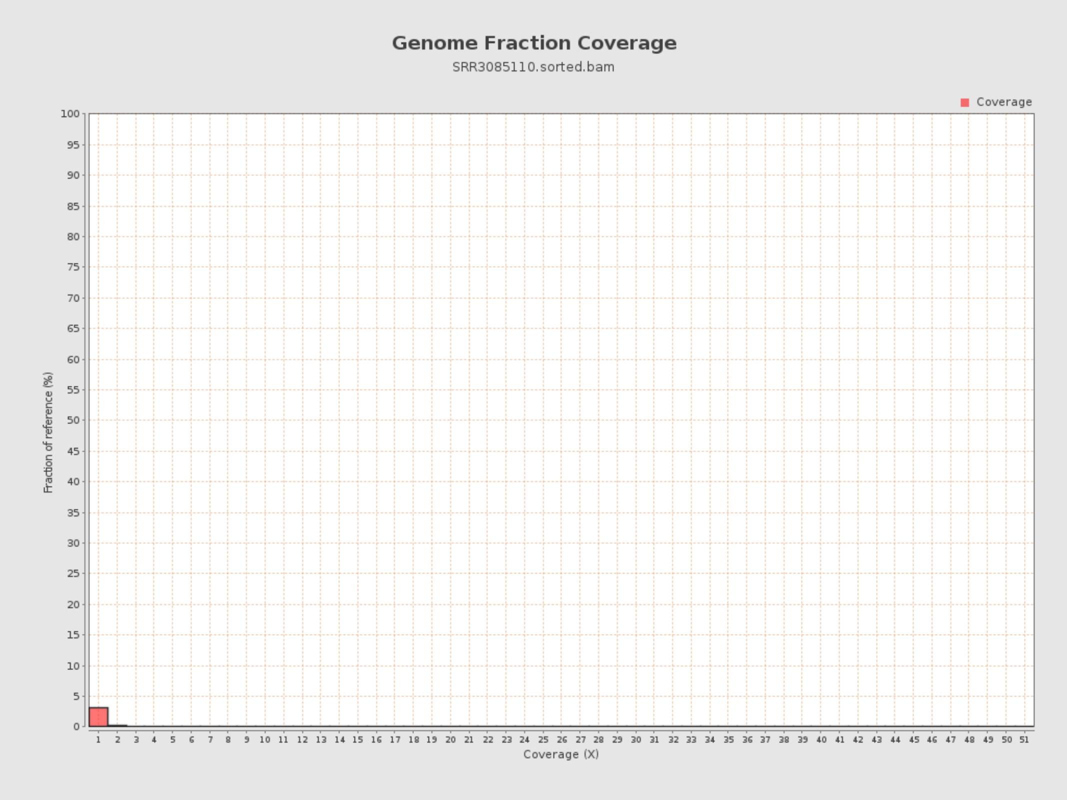
4. Results : Coverage Histogram



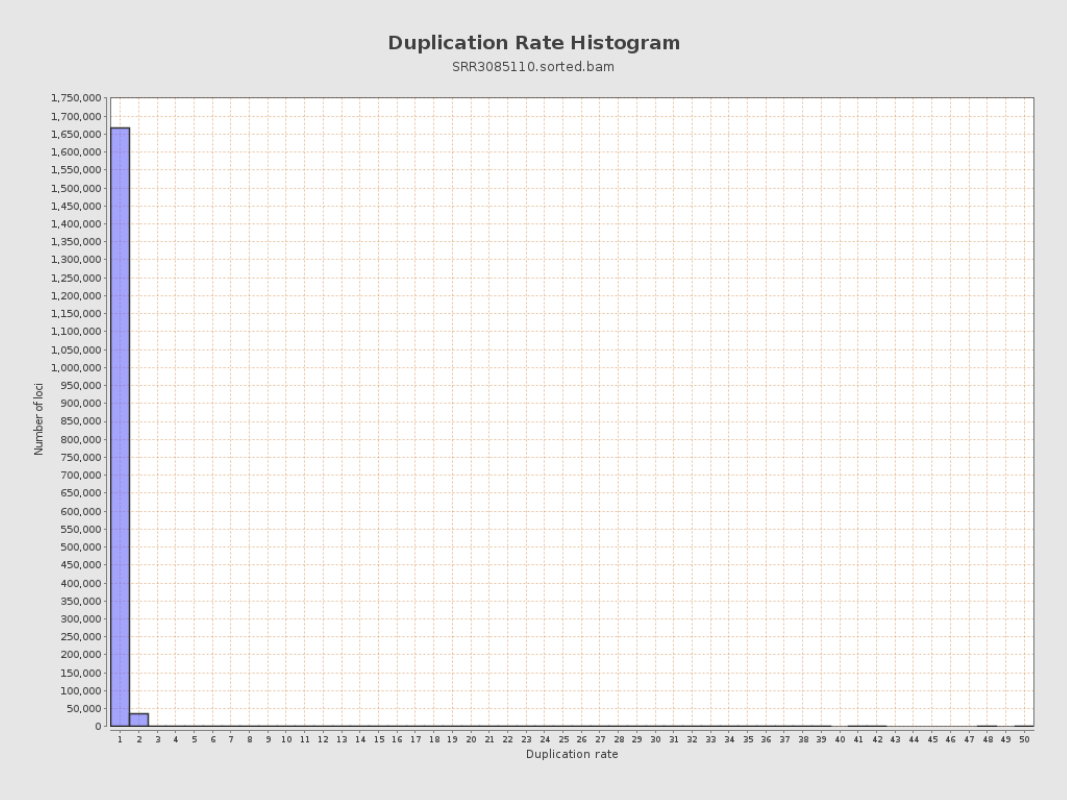
5. Results : Coverage Histogram (0-50X)



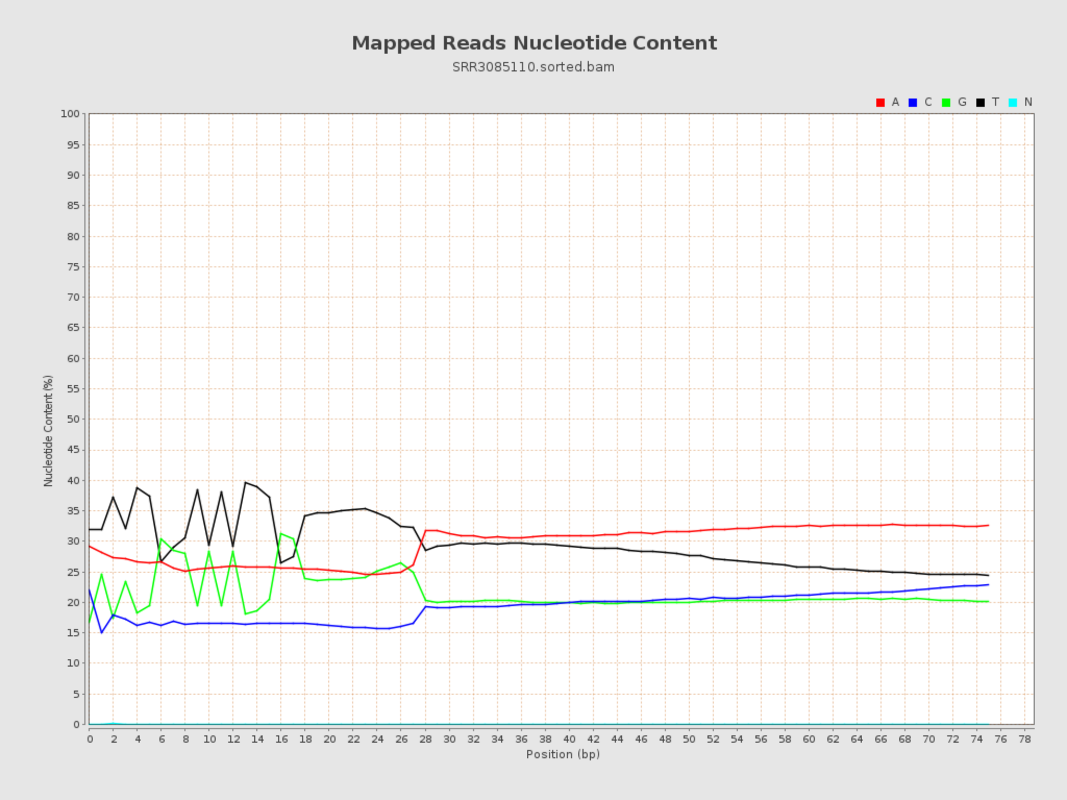
6. Results : Genome Fraction Coverage



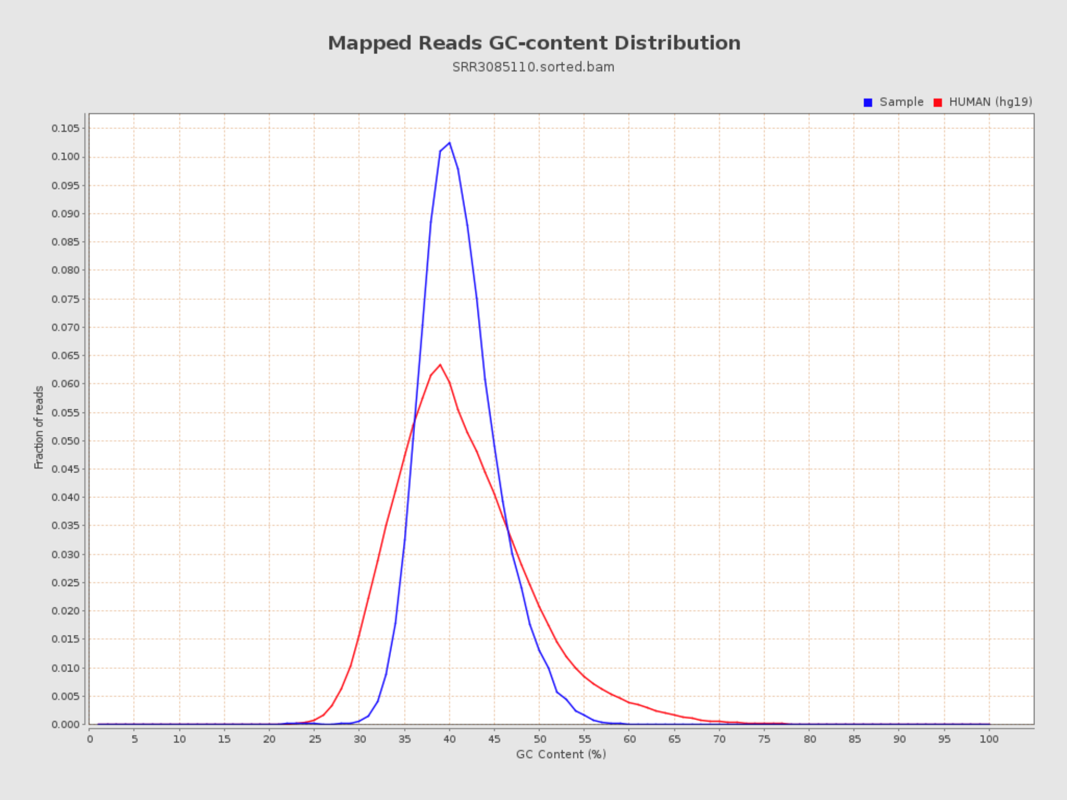
7. Results : Duplication Rate Histogram



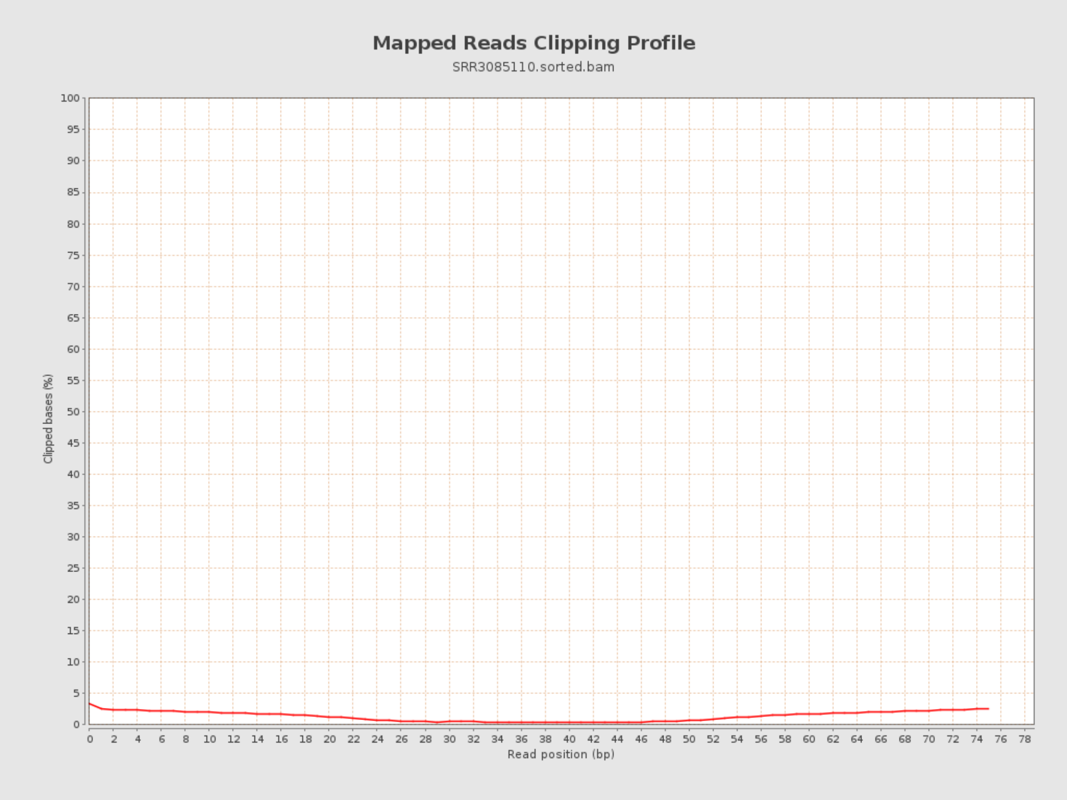
8. Results : Mapped Reads Nucleotide Content



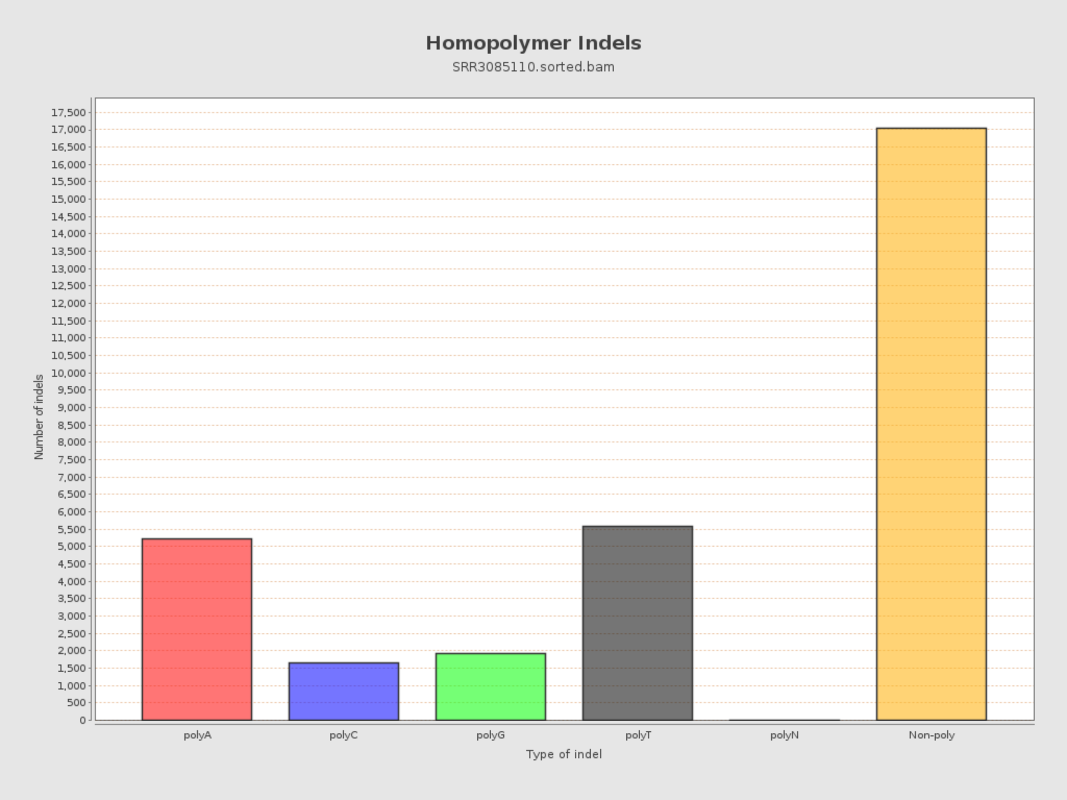
9. Results : Mapped Reads GC-content Distribution



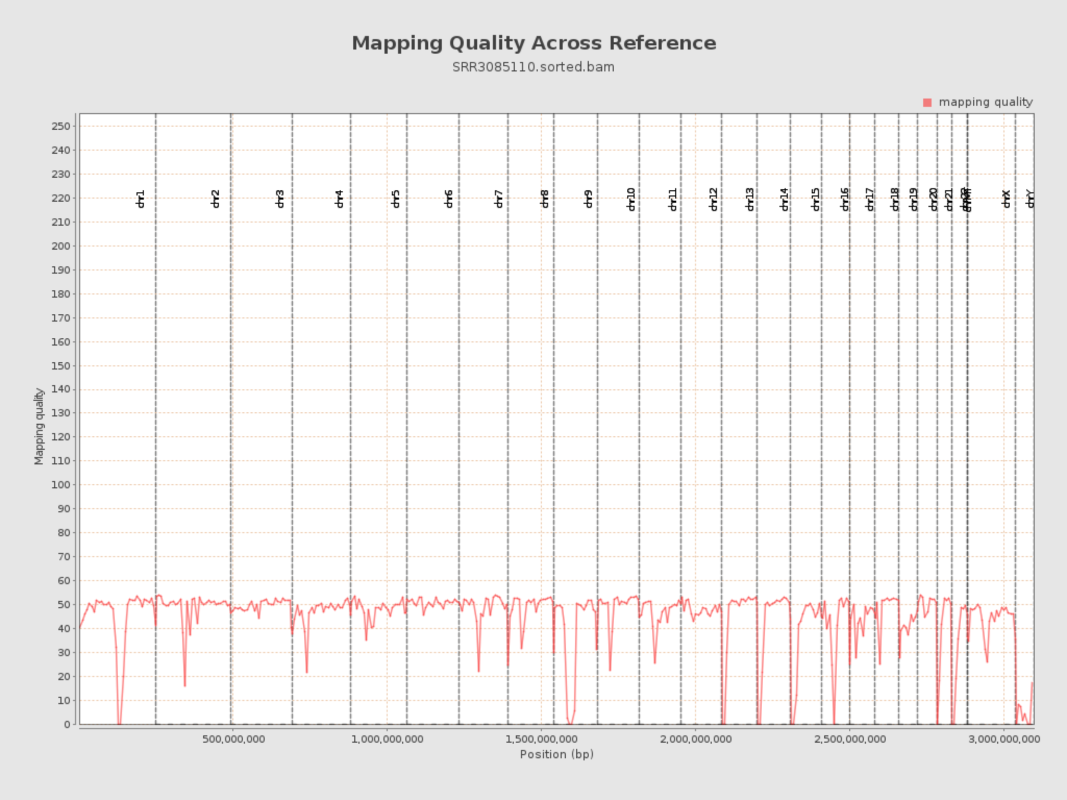
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram