Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 01:04:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085106.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_SRR3085106 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085106.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 01:04:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085106.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,178,902
Mapped reads	1,872,079 / 85.92%
Unmapped reads	306,823 / 14.08%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,780 / 0.68%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	49,500 / 2.27%
Duplication rate	2.11%
Clipped reads	1,156,829 / 53.09%

2.2. ACGT Content

Number/percentage of A's	34,846,622 / 29.55%
Number/percentage of C's	22,729,026 / 19.27%
Number/percentage of T's	34,801,594 / 29.51%
Number/percentage of G's	25,547,563 / 21.66%
Number/percentage of N's	2,588 / 0%
GC Percentage	40.94%

2.3. Coverage

Mean	0.0381

Standard Deviation	0.286

2.4. Mapping Quality

Mean Mapping Quality	44.82

2.5. Mismatches and indels

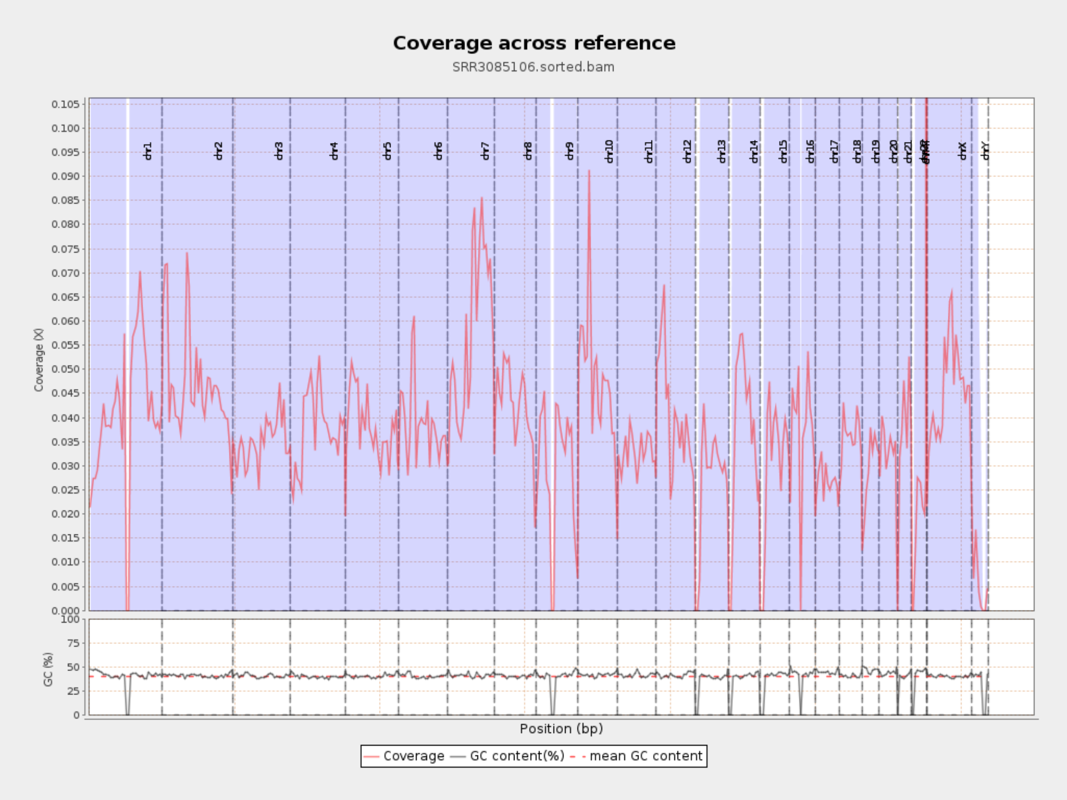
General error rate	0.86%
Mismatches	997,703
Insertions	9,413
Mapped reads with at least one insertion	0.5%
Deletions	23,716
Mapped reads with at least one deletion	1.25%
Homopolymer indels	45.8%

2.6. Chromosome stats

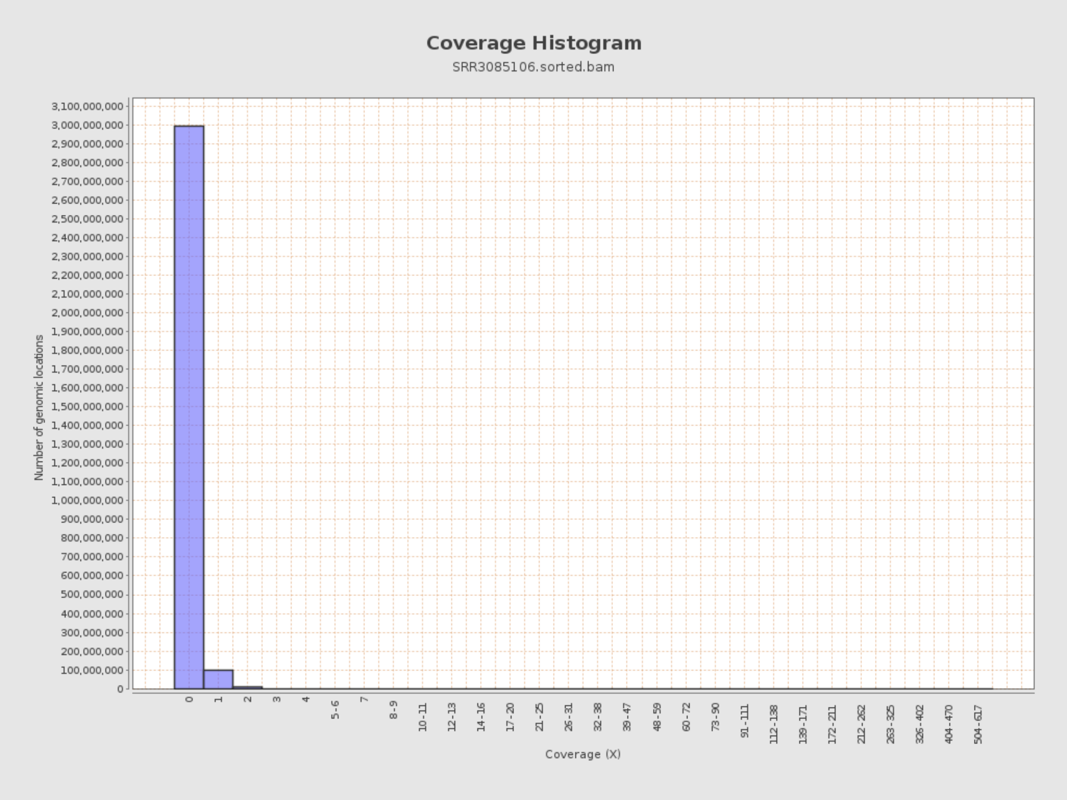
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10184700	0.0409	0.373
chr2	243199373	11509831	0.0473	0.3148
chr3	198022430	6968824	0.0352	0.2105
chr4	191154276	7174701	0.0375	0.2216
chr5	180915260	6993217	0.0387	0.2128
chr6	171115067	6633798	0.0388	0.2441
chr7	159138663	9310972	0.0585	0.3163

chr8	146364022	6198642	0.0424	0.4303
chr9	141213431	4258275	0.0302	0.264
chr10	135534747	6633771	0.0489	0.4405
chr11	135006516	4395653	0.0326	0.2539
chr12	133851895	5387941	0.0403	0.2192
chr13	115169878	3065135	0.0266	0.1757
chr14	107349540	3946721	0.0368	0.219
chr15	102531392	3073817	0.03	0.1868
chr16	90354753	3369075	0.0373	0.2355
chr17	81195210	2170919	0.0267	0.1875
chr18	78077248	2826203	0.0362	0.517
chr19	59128983	1746056	0.0295	0.3149
chr20	63025520	2080004	0.033	0.2047
chr21	48129895	1752922	0.0364	0.2216
chr22	51304566	887145	0.0173	0.1419
chrMT	16571	33275	2.008	1.7885
chrX	155270560	7048062	0.0454	0.248
chrY	59373566	316128	0.0053	0.1101

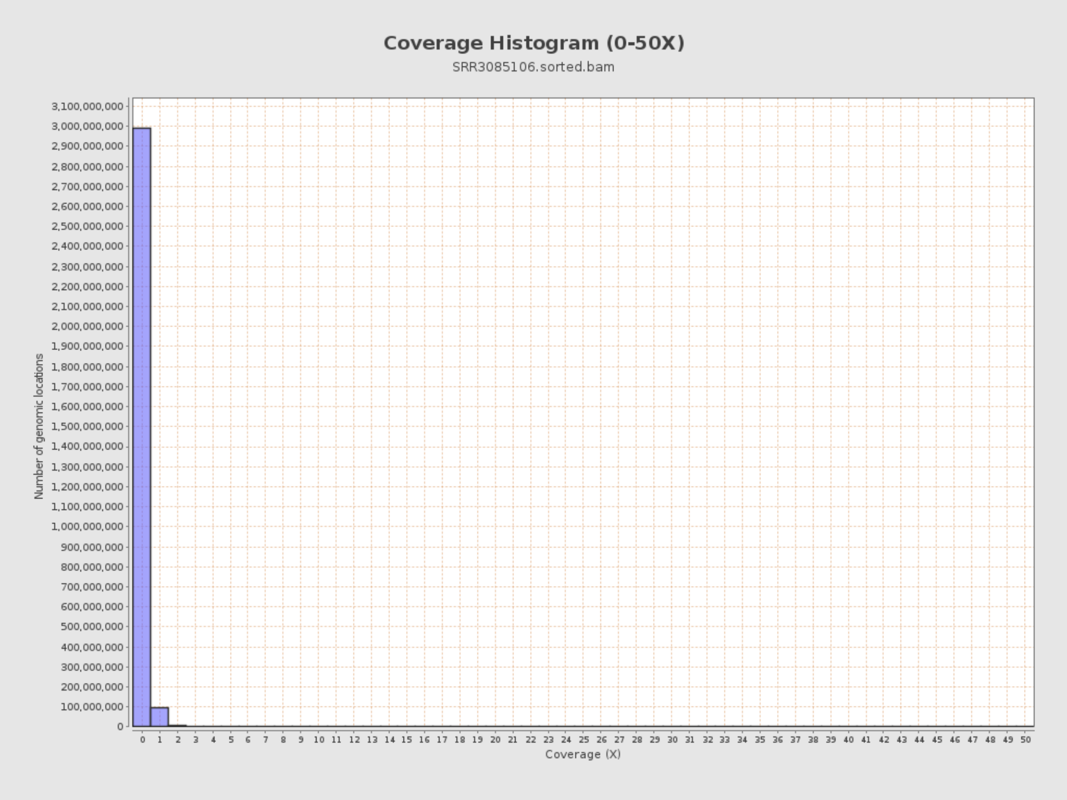
3. Results : Coverage across reference



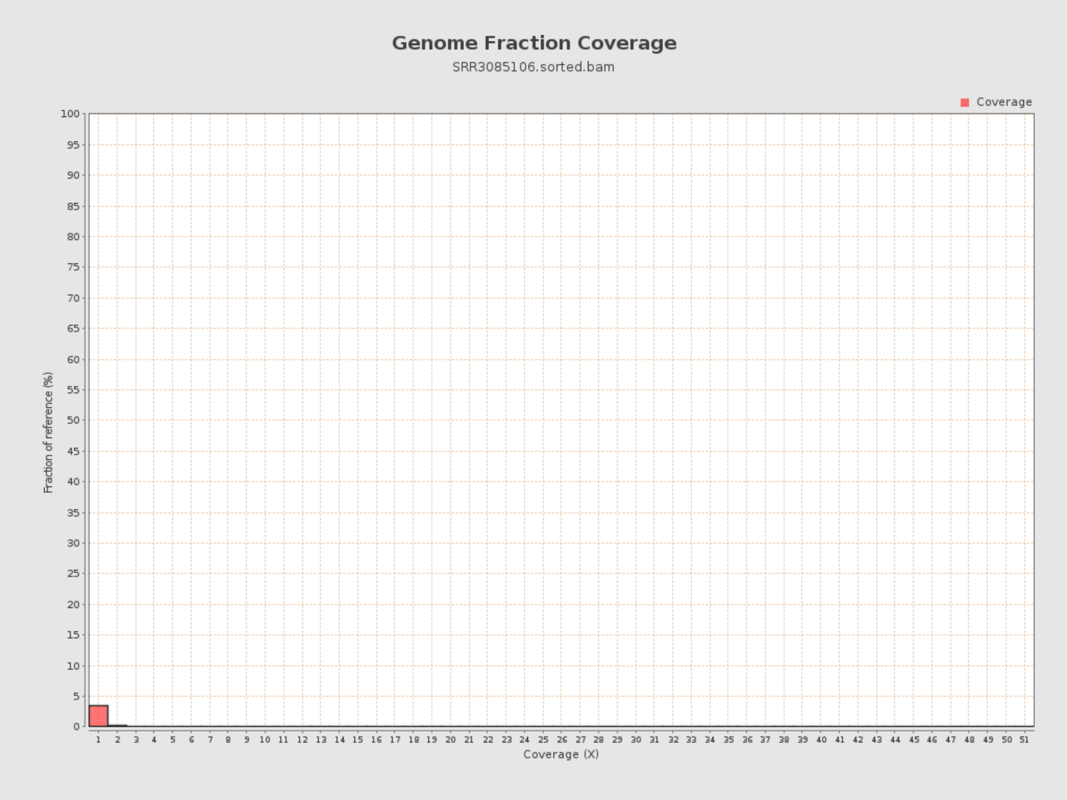
4. Results : Coverage Histogram



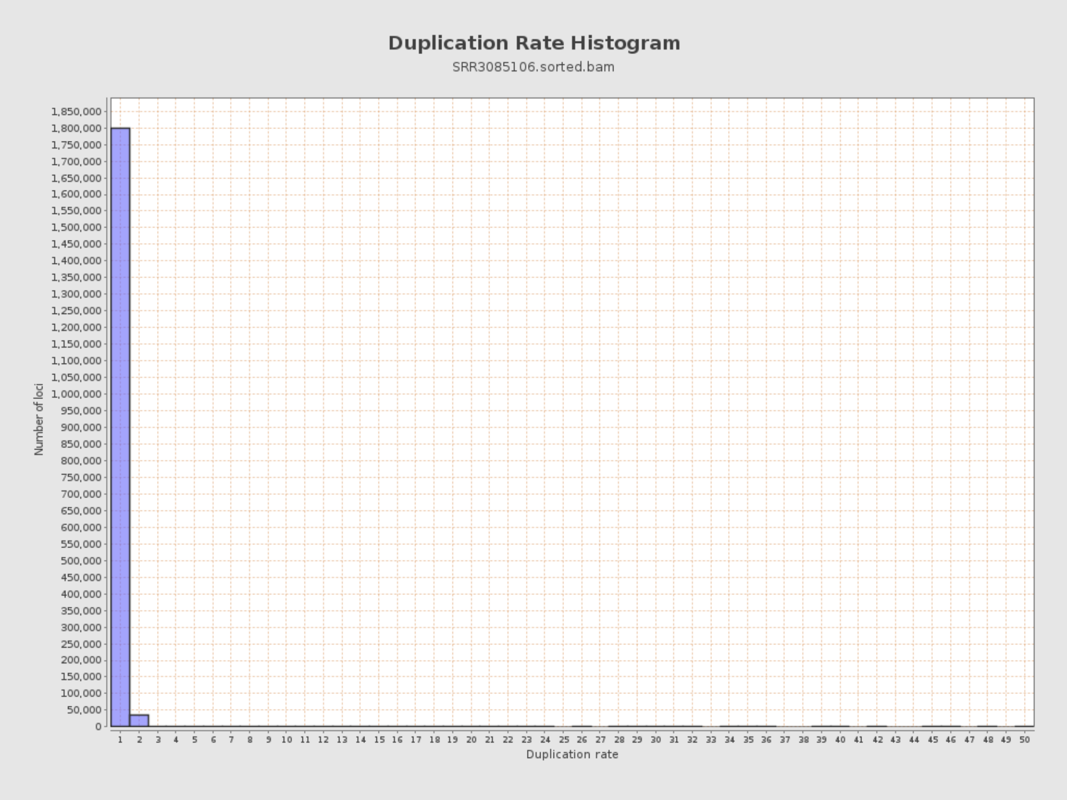
5. Results : Coverage Histogram (0-50X)



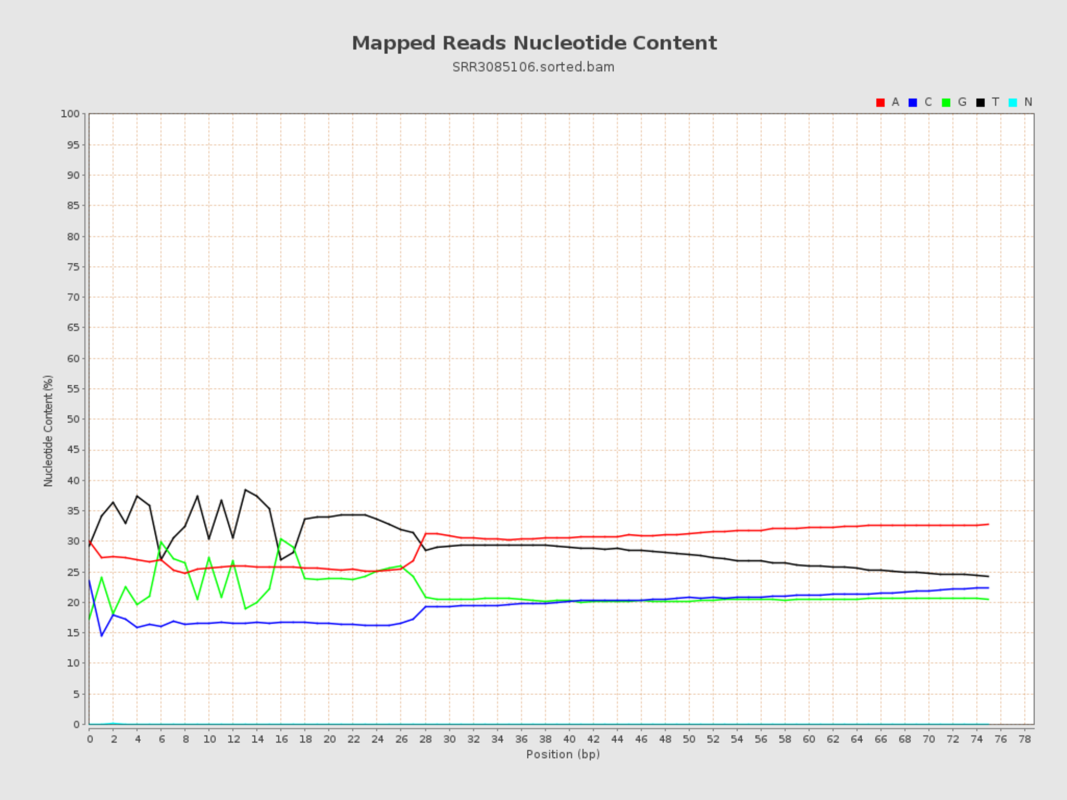
6. Results : Genome Fraction Coverage



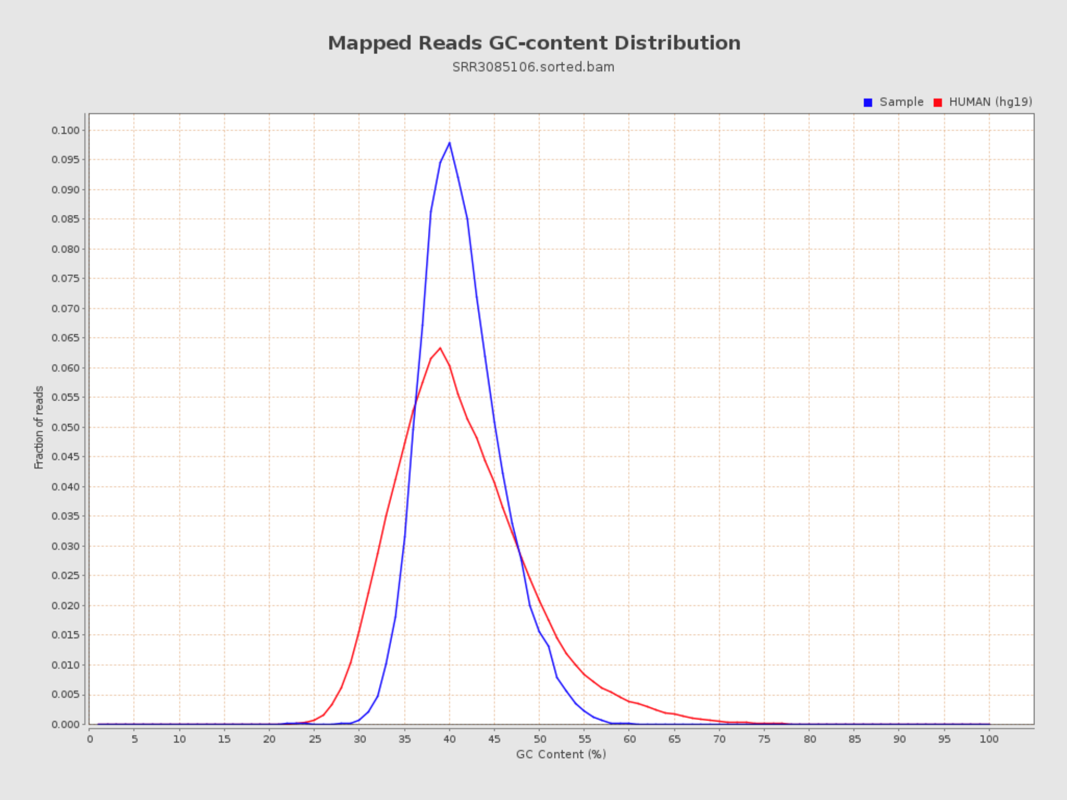
7. Results : Duplication Rate Histogram



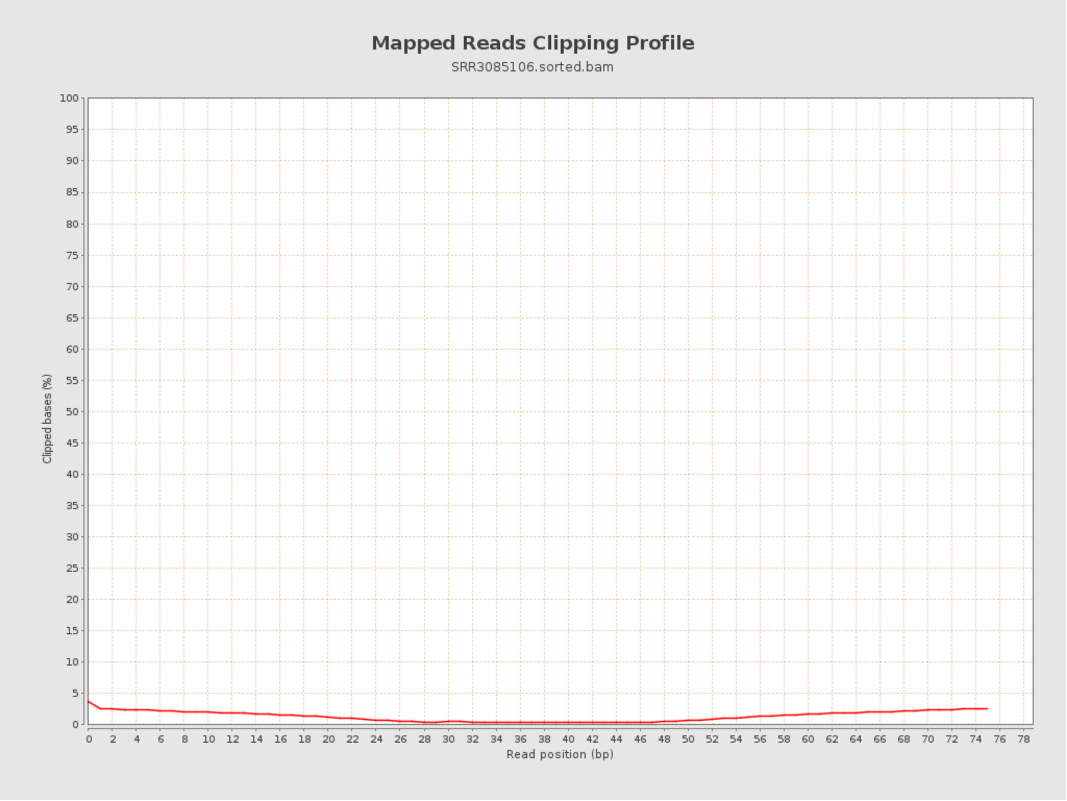
8. Results : Mapped Reads Nucleotide Content



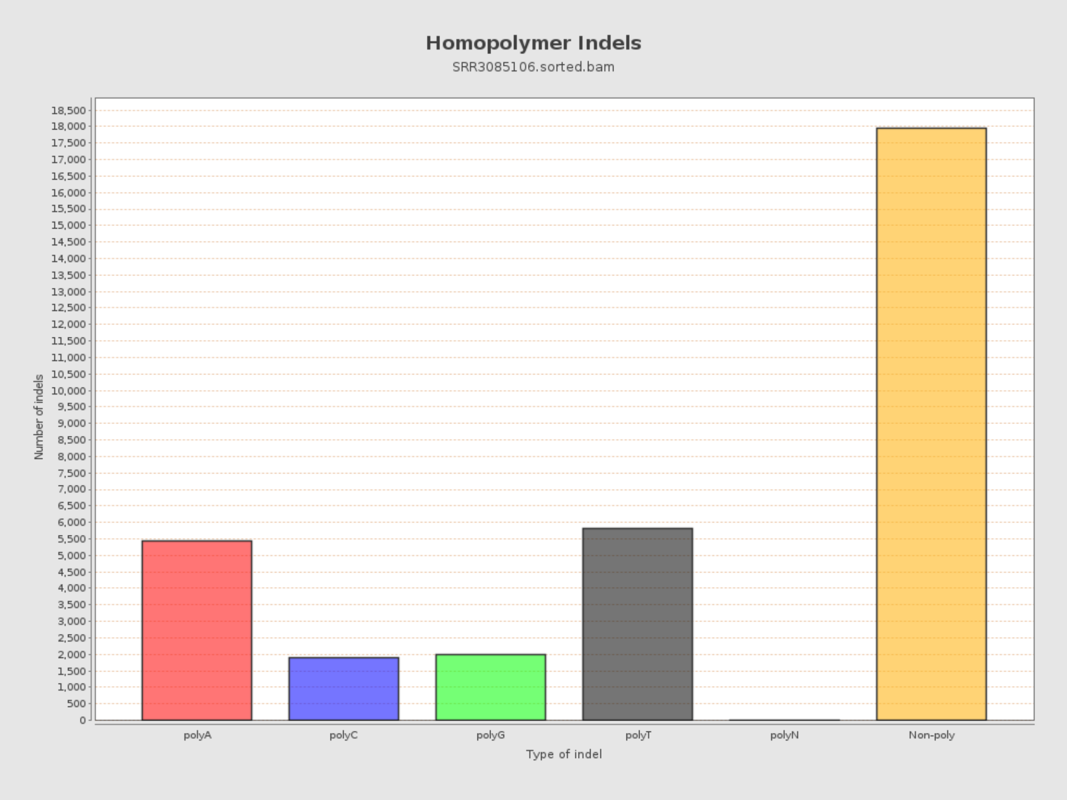
9. Results : Mapped Reads GC-content Distribution



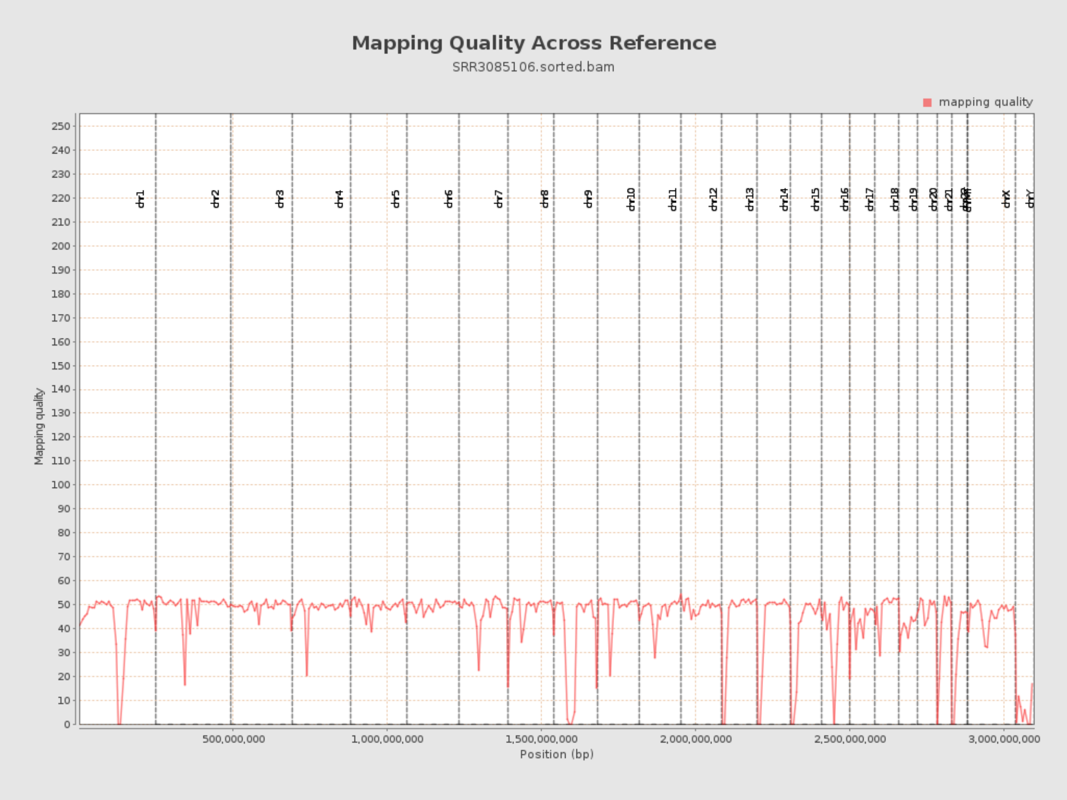
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram