Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 00:58:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085104.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_SRR3085104 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085104.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 00:58:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085104.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,657,397
Mapped reads	1,304,478 / 78.71%
Unmapped reads	352,919 / 21.29%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,691 / 0.4%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	29,595 / 1.79%
Duplication rate	1.78%
Clipped reads	785,552 / 47.4%

2.2. ACGT Content

Number/percentage of A's	24,362,905 / 29.77%
Number/percentage of C's	15,639,125 / 19.11%
Number/percentage of T's	23,612,713 / 28.86%
Number/percentage of G's	18,215,911 / 22.26%
Number/percentage of N's	1,641 / 0%
GC Percentage	41.37%

2.3. Coverage

Mean	0.0264

Standard Deviation	0.2267

2.4. Mapping Quality

Mean Mapping Quality	44.65

2.5. Mismatches and indels

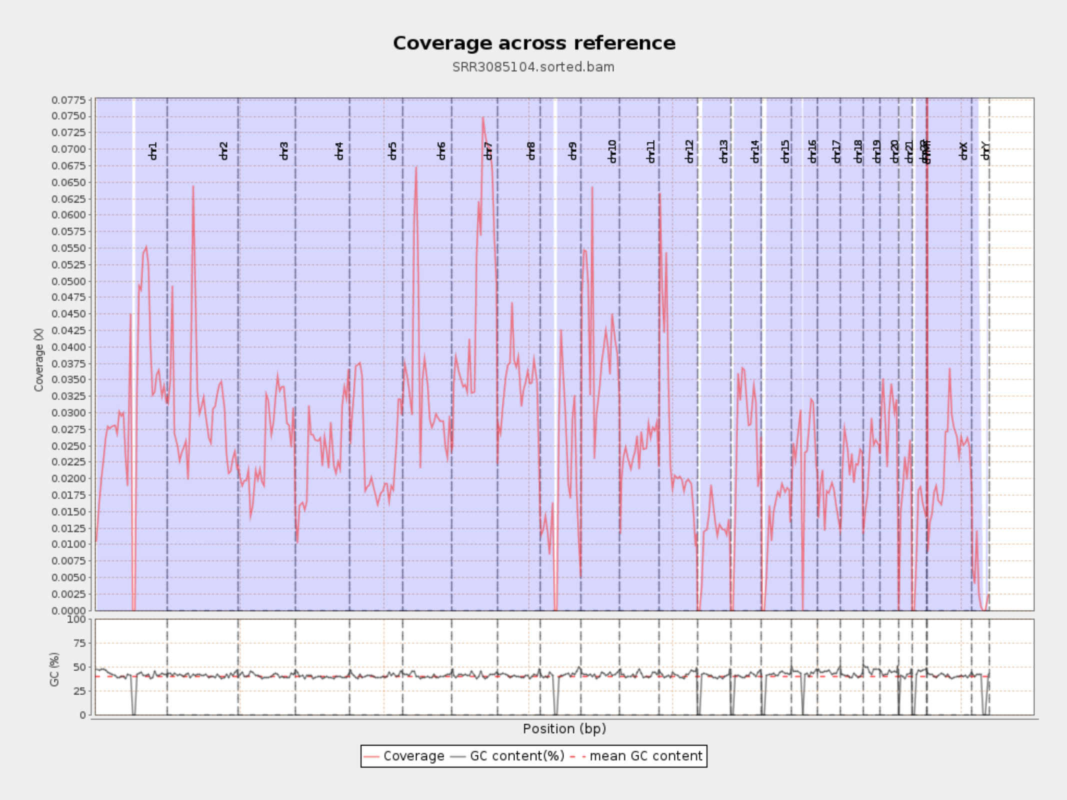
General error rate	0.93%
Mismatches	747,292
Insertions	6,699
Mapped reads with at least one insertion	0.51%
Deletions	17,105
Mapped reads with at least one deletion	1.29%
Homopolymer indels	45.42%

2.6. Chromosome stats

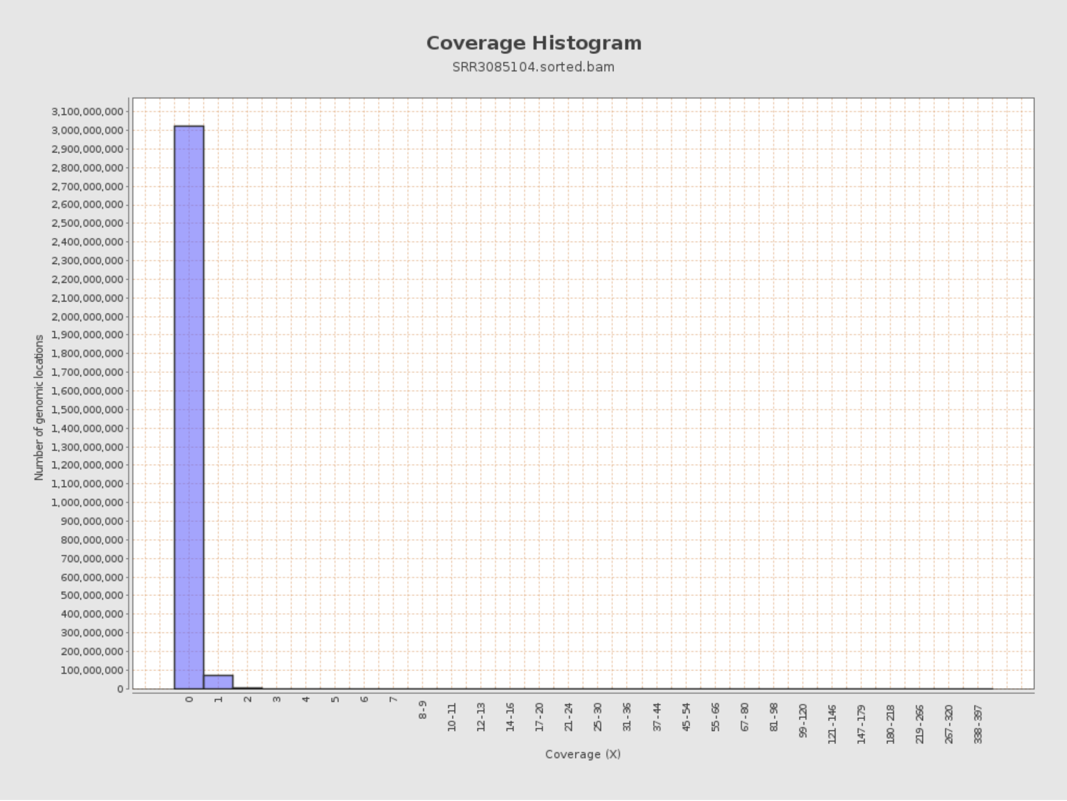
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7651076	0.0307	0.3269
chr2	243199373	7344195	0.0302	0.2558
chr3	198022430	4997311	0.0252	0.1735
chr4	191154276	4558972	0.0238	0.174
chr5	180915260	4380179	0.0242	0.1655
chr6	171115067	5847856	0.0342	0.2359
chr7	159138663	7735414	0.0486	0.2682

chr8	146364022	5054589	0.0345	0.3114
chr9	141213431	2653560	0.0188	0.2005
chr10	135534747	5617875	0.0414	0.3568
chr11	135006516	3312739	0.0245	0.2038
chr12	133851895	3605148	0.0269	0.1772
chr13	115169878	1302441	0.0113	0.1114
chr14	107349540	2723196	0.0254	0.1759
chr15	102531392	1371324	0.0134	0.122
chr16	90354753	2152020	0.0238	0.1769
chr17	81195210	1361757	0.0168	0.1525
chr18	78077248	1762228	0.0226	0.3236
chr19	59128983	1330488	0.0225	0.2402
chr20	63025520	1867695	0.0296	0.1859
chr21	48129895	891983	0.0185	0.1573
chr22	51304566	614887	0.012	0.1157
chrMT	16571	3059	0.1846	0.5231
chrX	155270560	3521279	0.0227	0.1714
chrY	59373566	198947	0.0034	0.0893

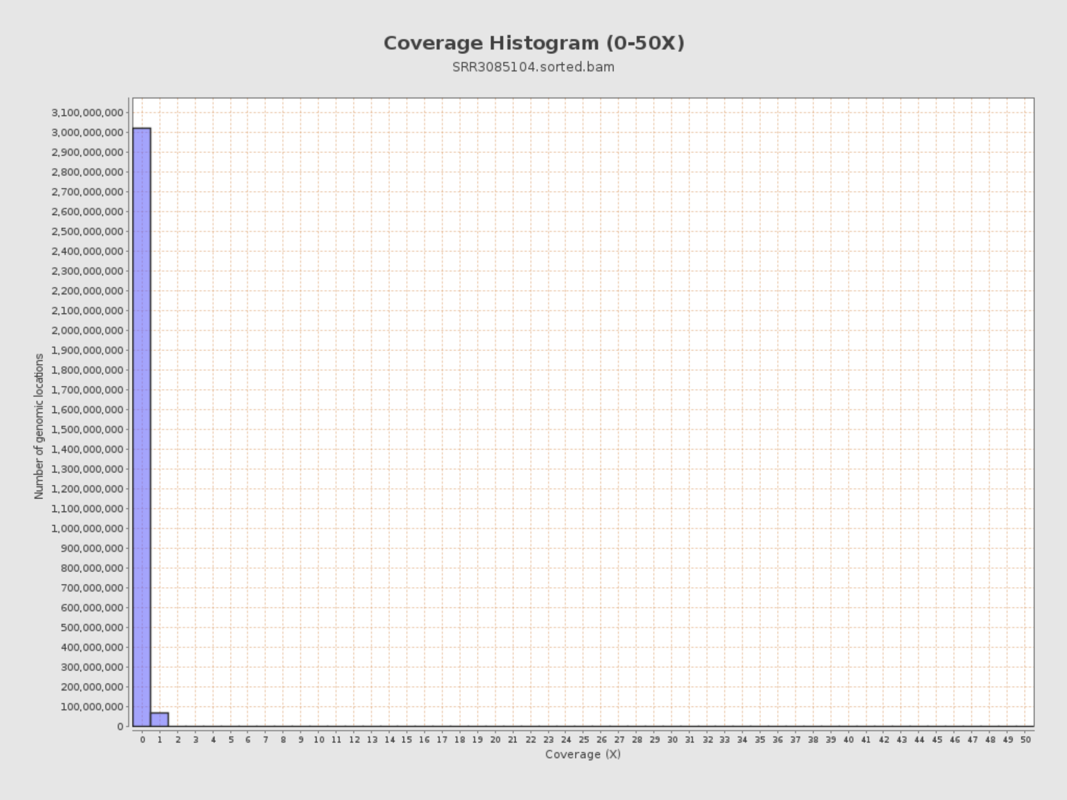
3. Results : Coverage across reference



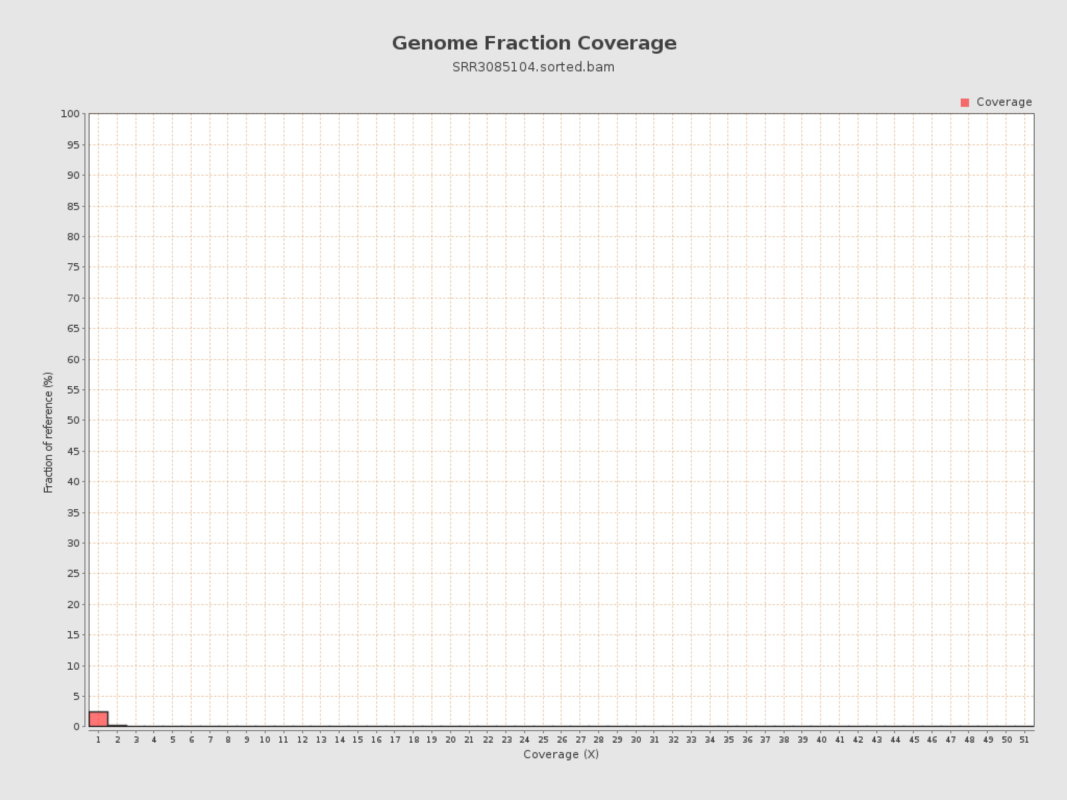
4. Results : Coverage Histogram



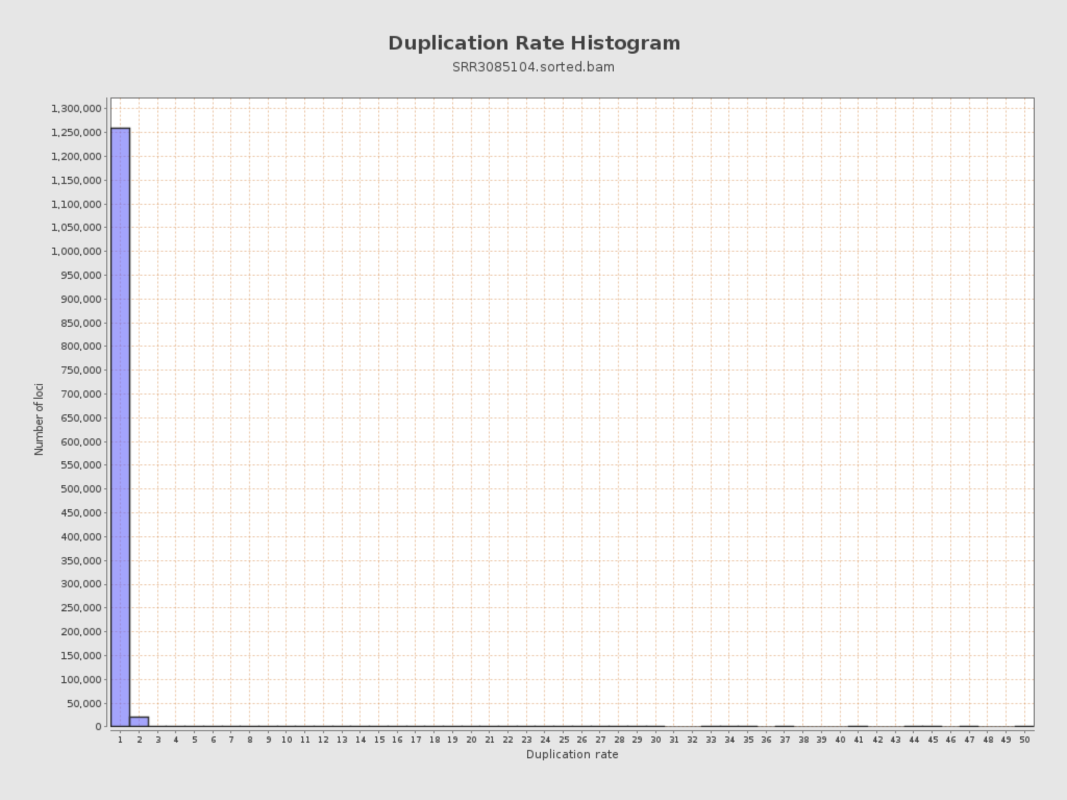
5. Results : Coverage Histogram (0-50X)



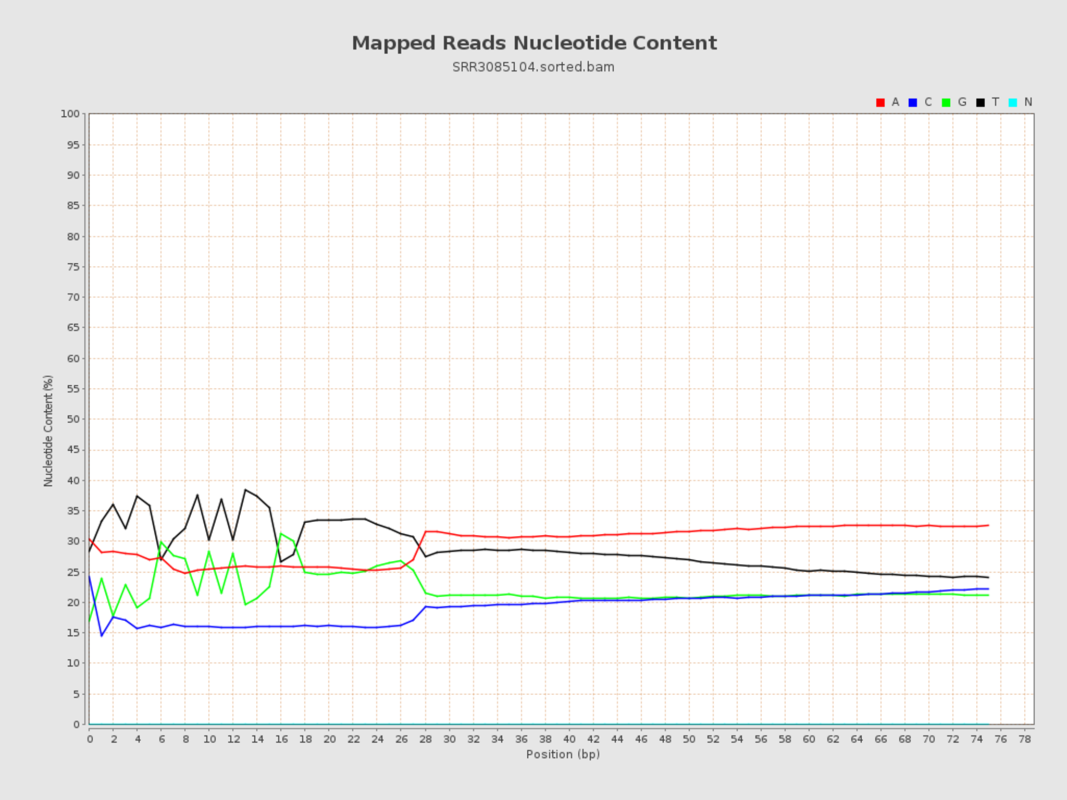
6. Results : Genome Fraction Coverage



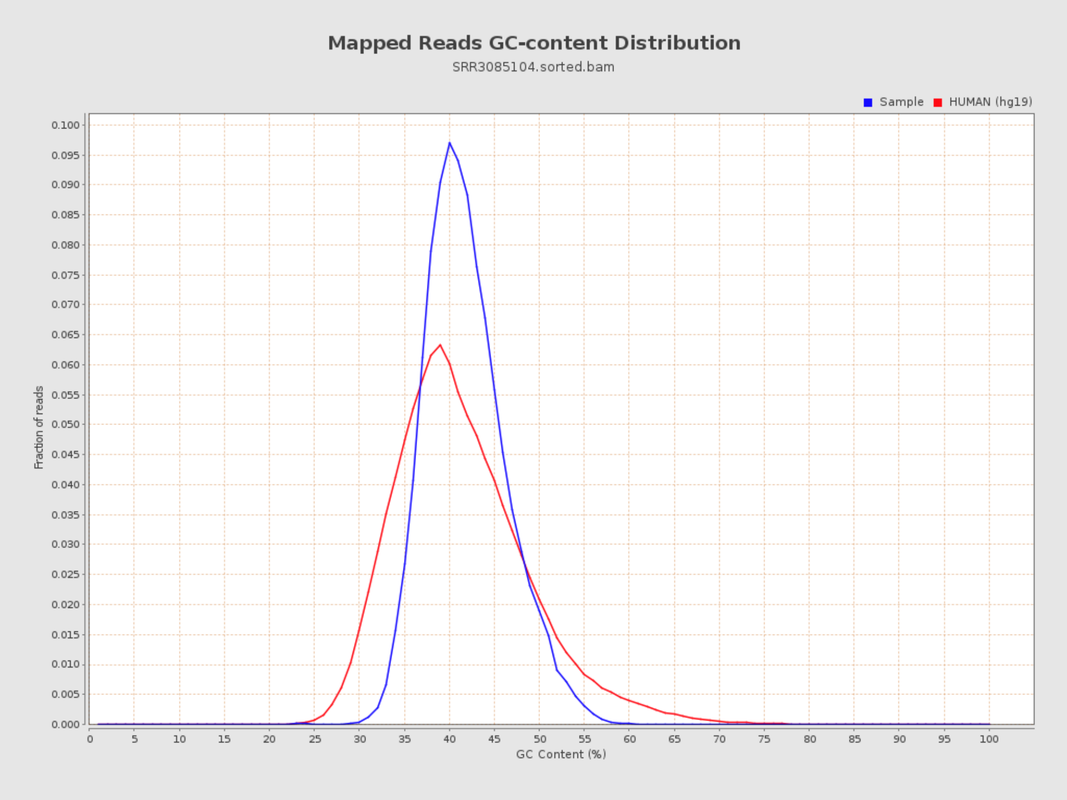
7. Results : Duplication Rate Histogram



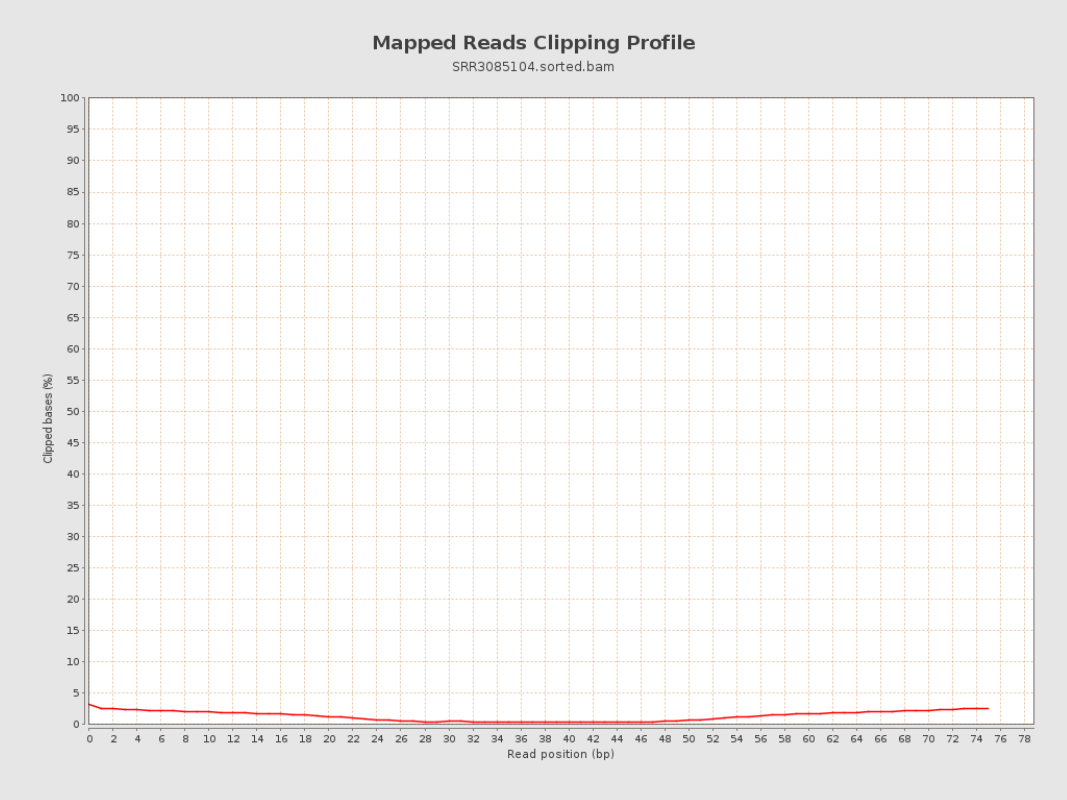
8. Results : Mapped Reads Nucleotide Content



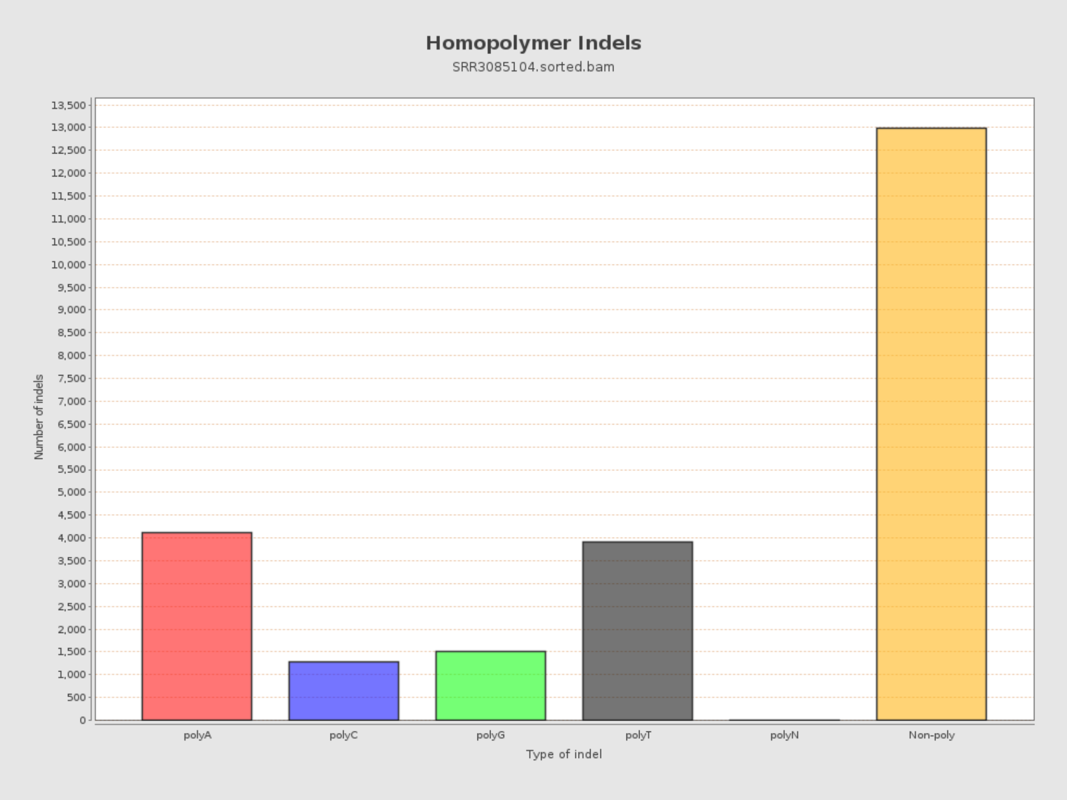
9. Results : Mapped Reads GC-content Distribution



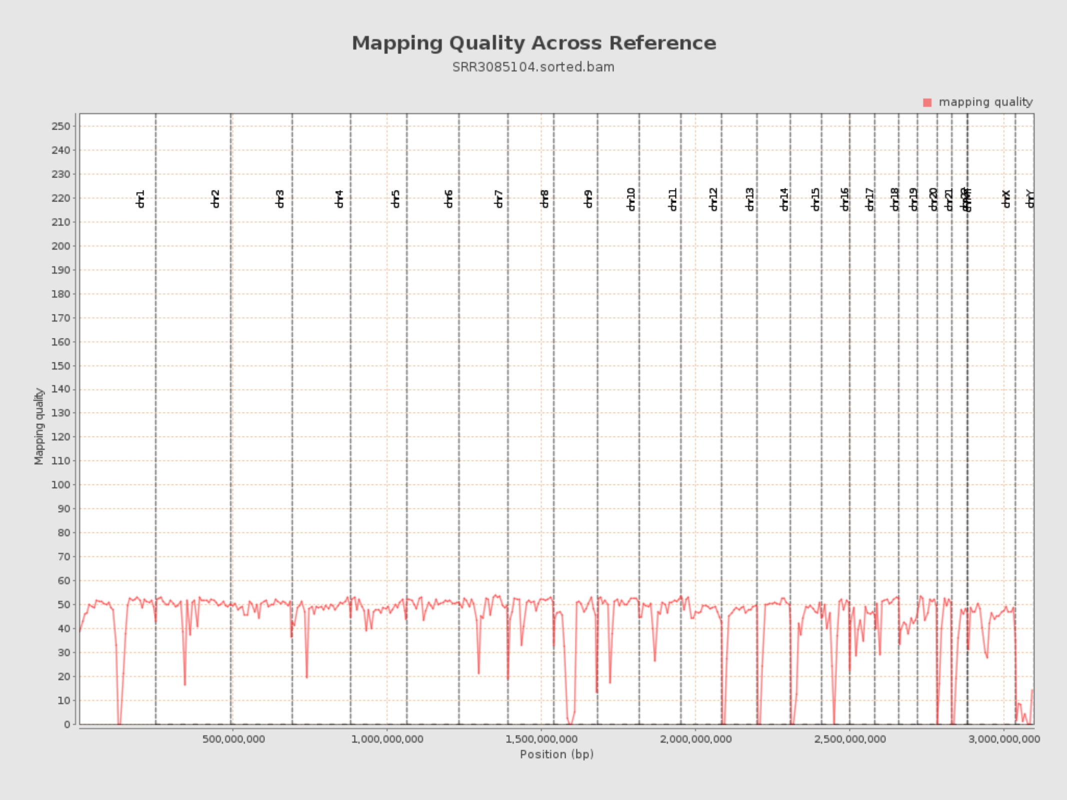
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram