Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 00:56:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085103.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_SRR3085103 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085103.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 00:56:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085103.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,425,956
Mapped reads	1,076,534 / 75.5%
Unmapped reads	349,422 / 24.5%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,297 / 0.37%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	21,505 / 1.51%
Duplication rate	1.69%
Clipped reads	615,013 / 43.13%

2.2. ACGT Content

Number/percentage of A's	20,300,482 / 29.84%
Number/percentage of C's	12,649,618 / 18.59%
Number/percentage of T's	19,873,233 / 29.21%
Number/percentage of G's	15,212,285 / 22.36%
Number/percentage of N's	1,517 / 0%
GC Percentage	40.95%

2.3. Coverage

Mean	0.022

Standard Deviation	0.1841

2.4. Mapping Quality

Mean Mapping Quality	45.31

2.5. Mismatches and indels

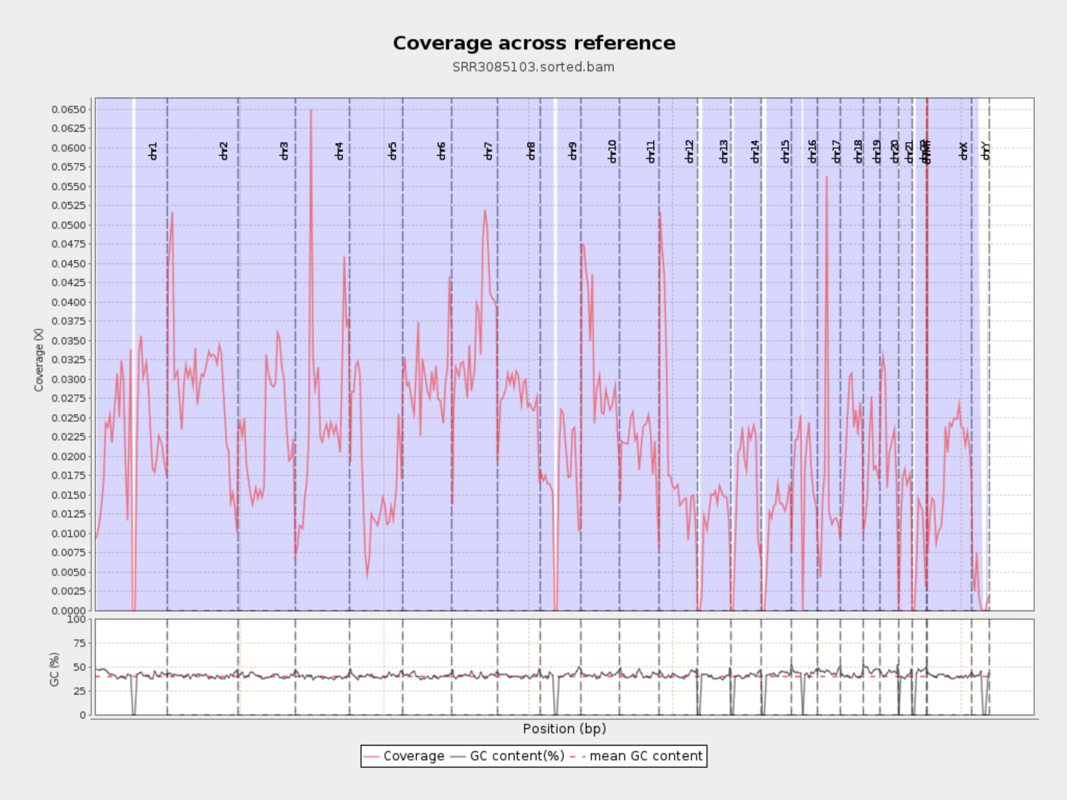
General error rate	0.93%
Mismatches	622,806
Insertions	5,212
Mapped reads with at least one insertion	0.48%
Deletions	13,599
Mapped reads with at least one deletion	1.25%
Homopolymer indels	46.02%

2.6. Chromosome stats

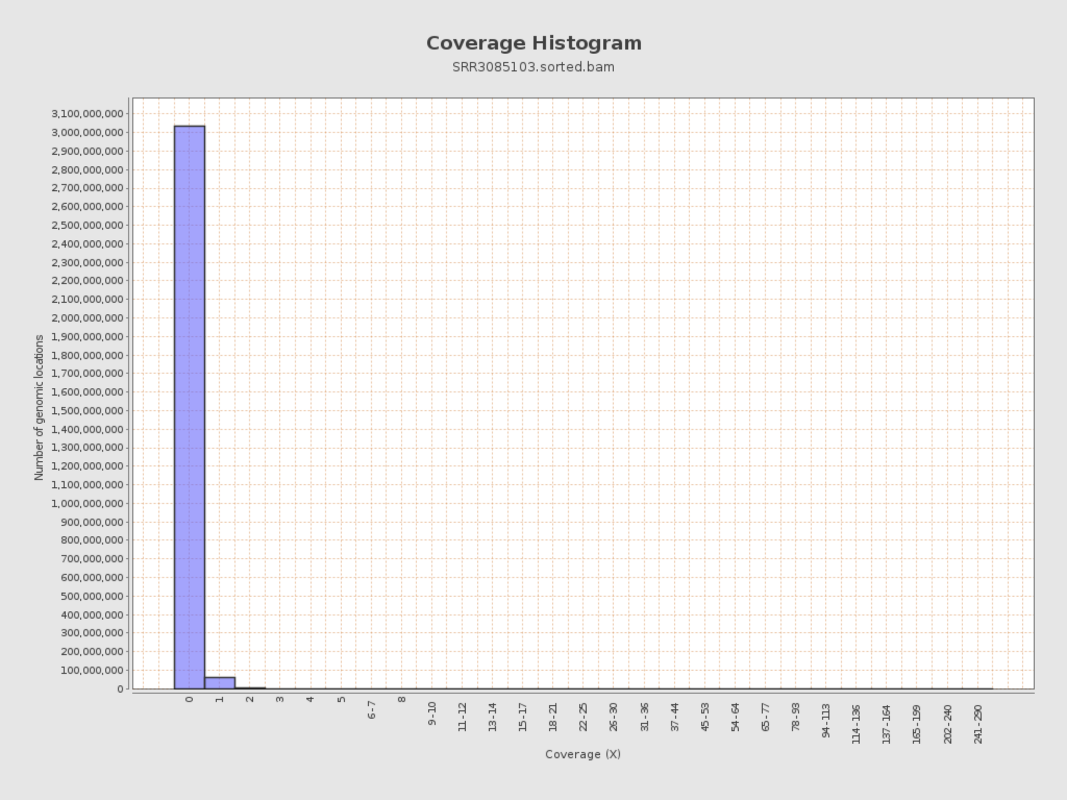
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5446926	0.0219	0.246
chr2	243199373	7203767	0.0296	0.2117
chr3	198022430	4605361	0.0233	0.1611
chr4	191154276	4846626	0.0254	0.1718
chr5	180915260	3049532	0.0169	0.1375
chr6	171115067	5146930	0.0301	0.2052
chr7	159138663	5685377	0.0357	0.2337

chr8	146364022	4032034	0.0275	0.2436
chr9	141213431	2373752	0.0168	0.158
chr10	135534747	4340538	0.032	0.2399
chr11	135006516	2934204	0.0217	0.181
chr12	133851895	2821287	0.0211	0.154
chr13	115169878	1324616	0.0115	0.112
chr14	107349540	1713689	0.016	0.1382
chr15	102531392	1154046	0.0113	0.1107
chr16	90354753	1588470	0.0176	0.1449
chr17	81195210	1273326	0.0157	0.1411
chr18	78077248	1826771	0.0234	0.2263
chr19	59128983	1090386	0.0184	0.1915
chr20	63025520	1444455	0.0229	0.1613
chr21	48129895	697509	0.0145	0.133
chr22	51304566	390133	0.0076	0.0907
chrMT	16571	3628	0.2189	0.5278
chrX	155270560	2930562	0.0189	0.1499
chrY	59373566	135218	0.0023	0.0625

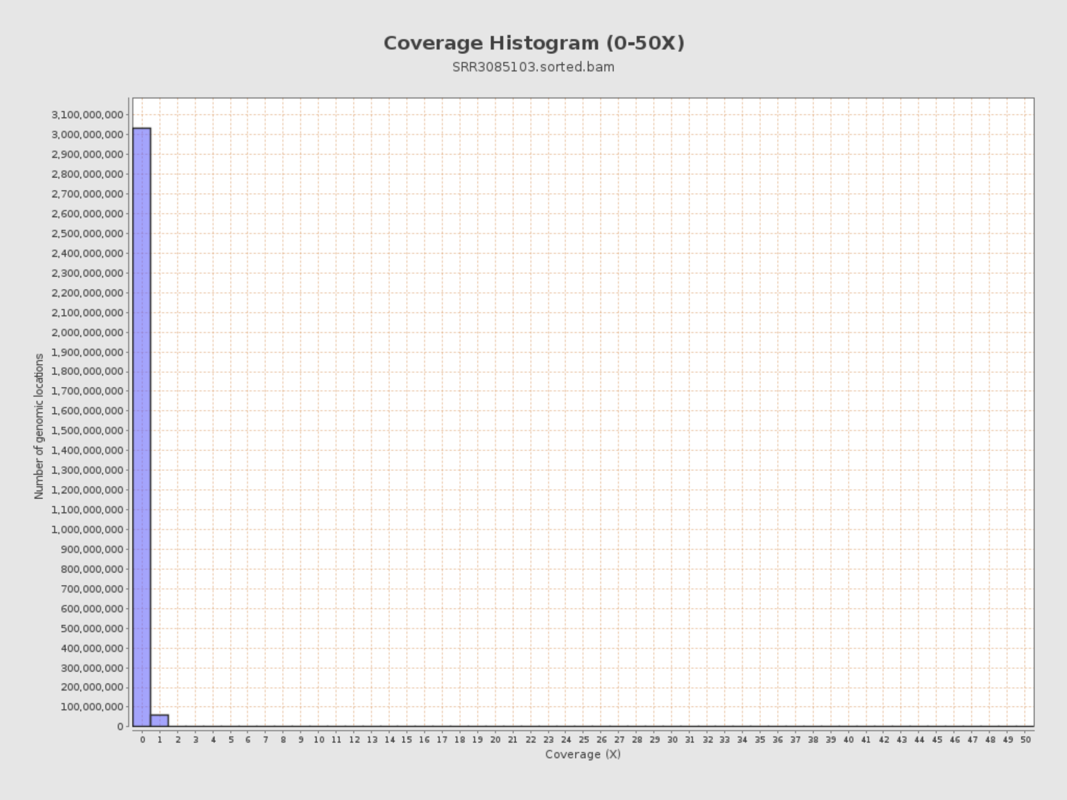
3. Results : Coverage across reference



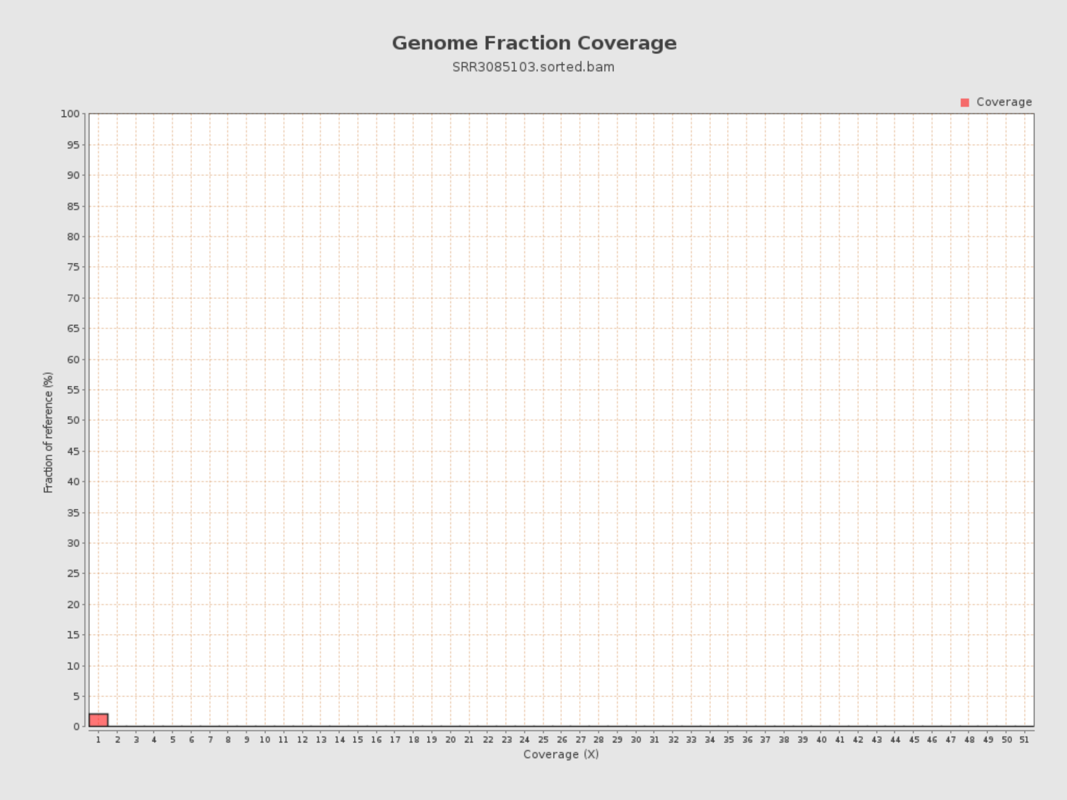
4. Results : Coverage Histogram



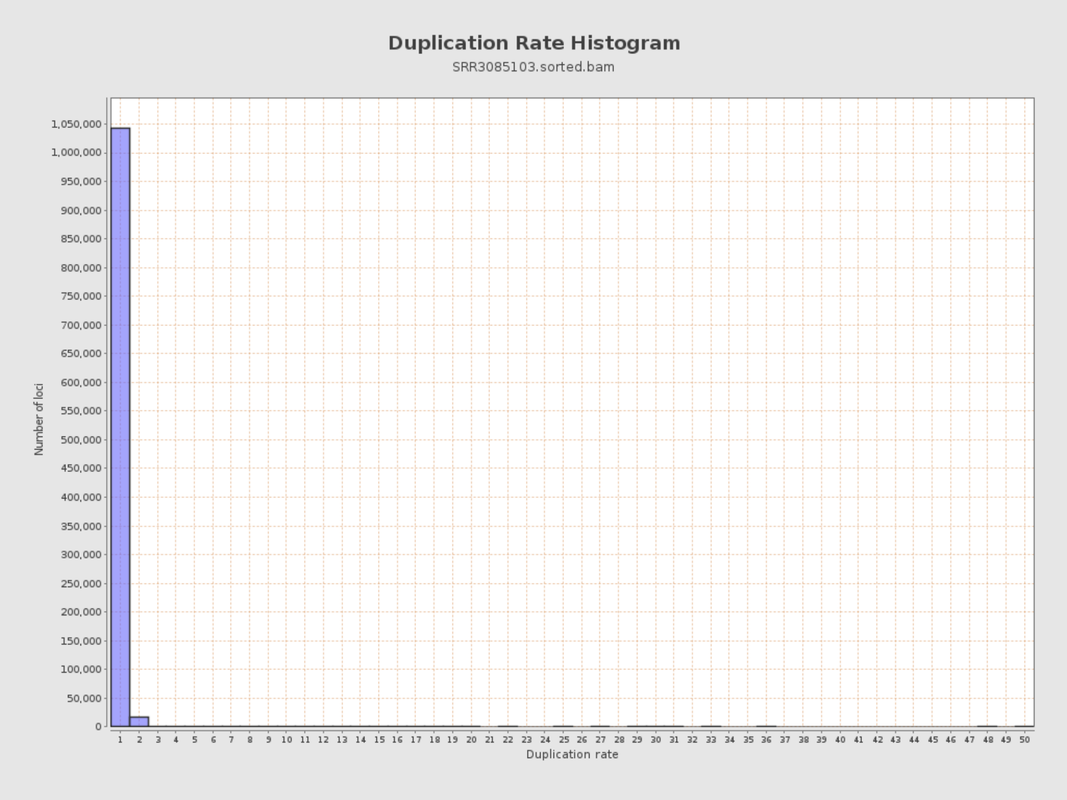
5. Results : Coverage Histogram (0-50X)



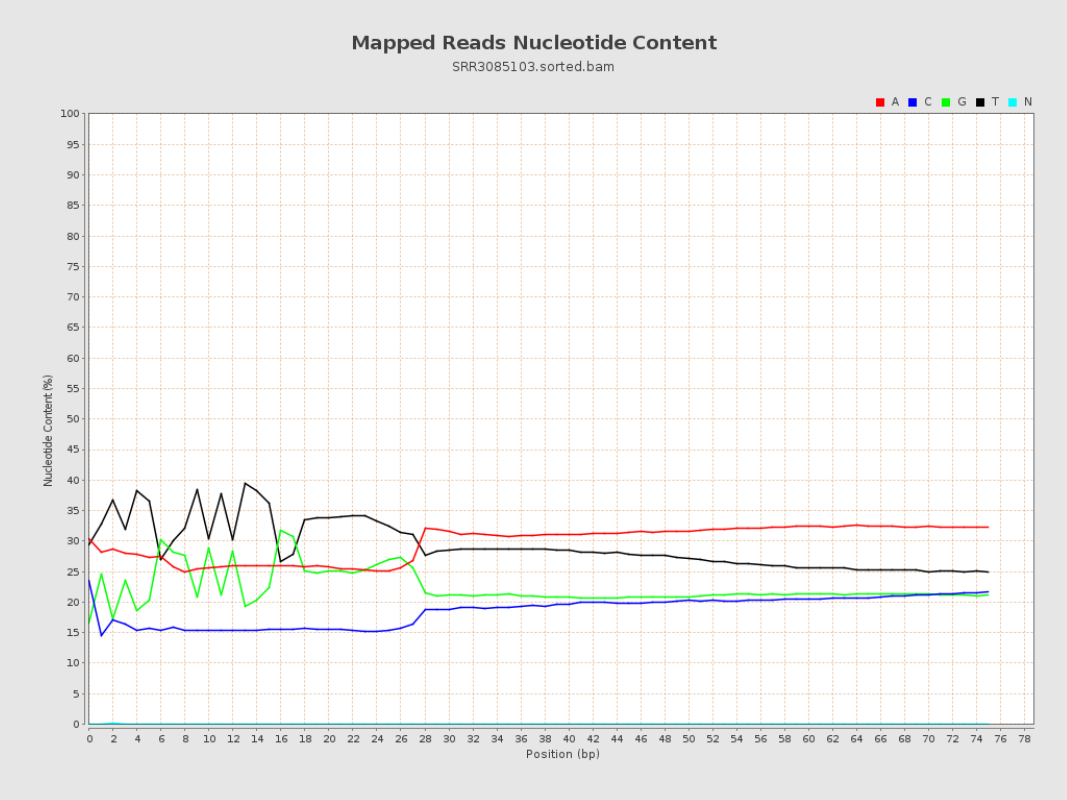
6. Results : Genome Fraction Coverage



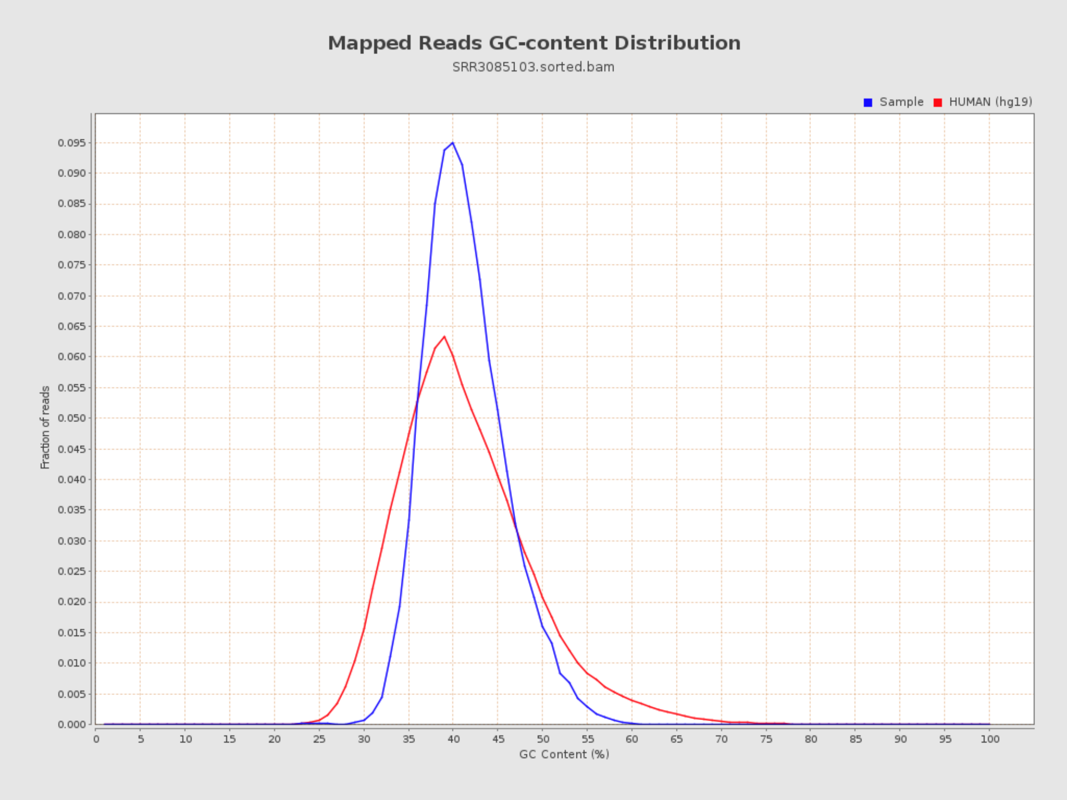
7. Results : Duplication Rate Histogram



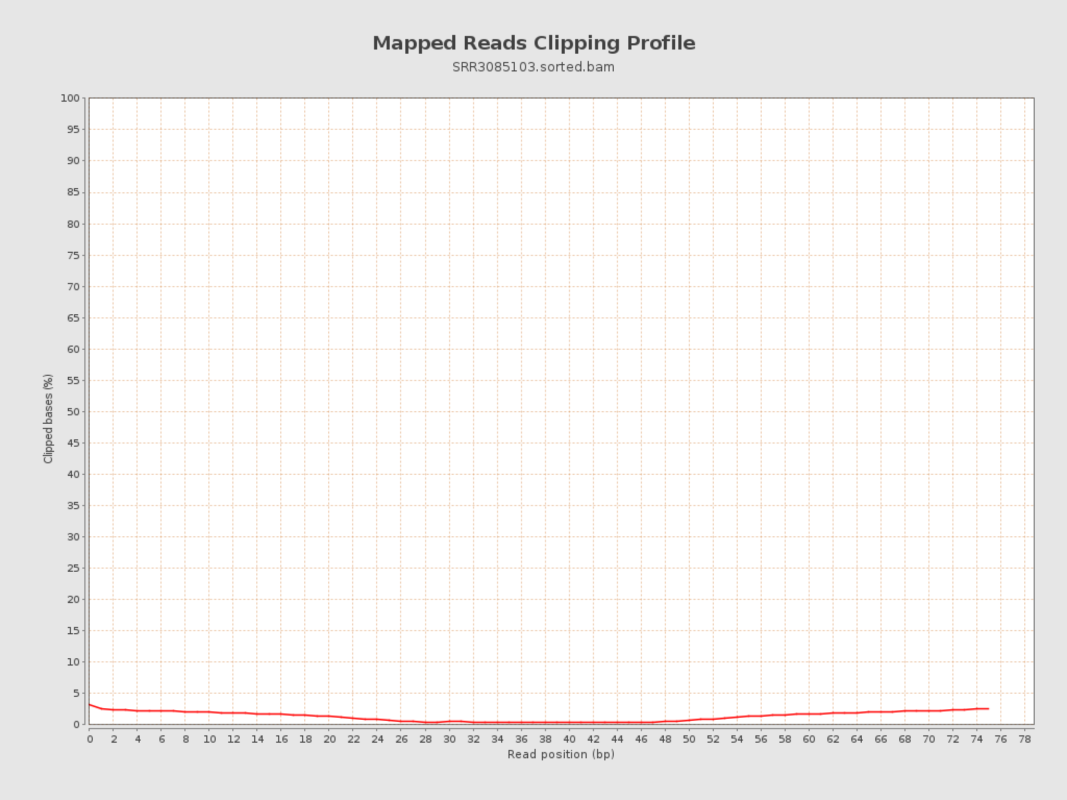
8. Results : Mapped Reads Nucleotide Content



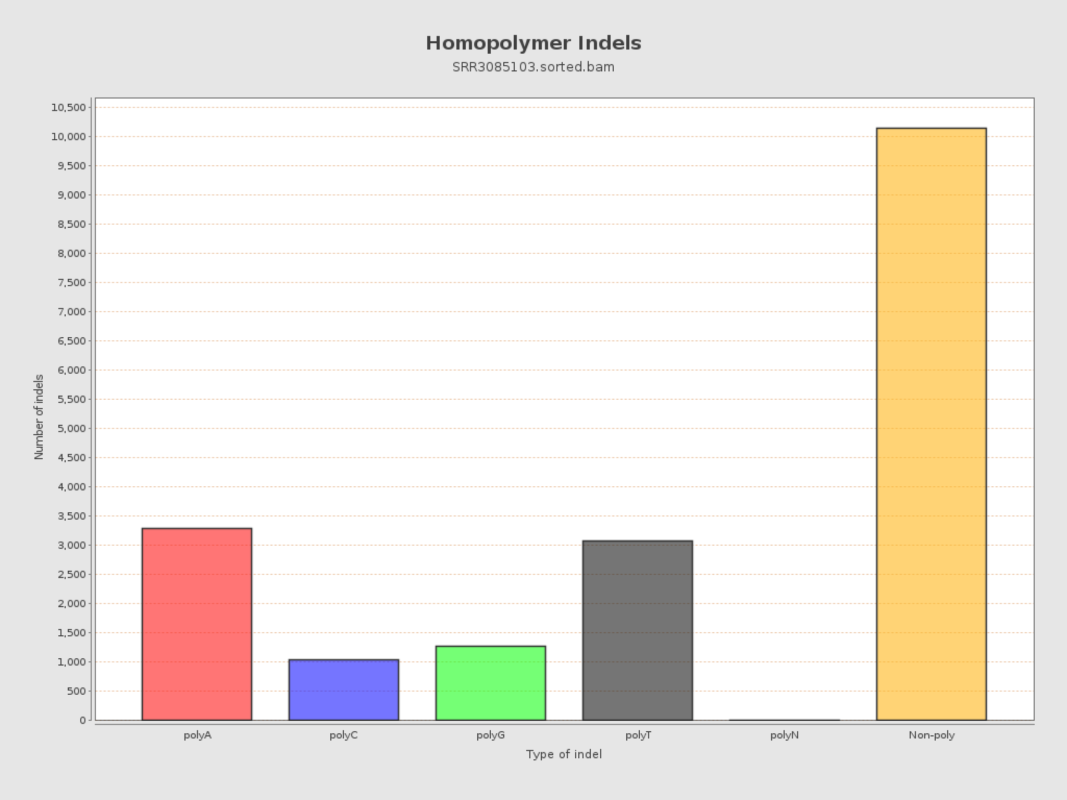
9. Results : Mapped Reads GC-content Distribution



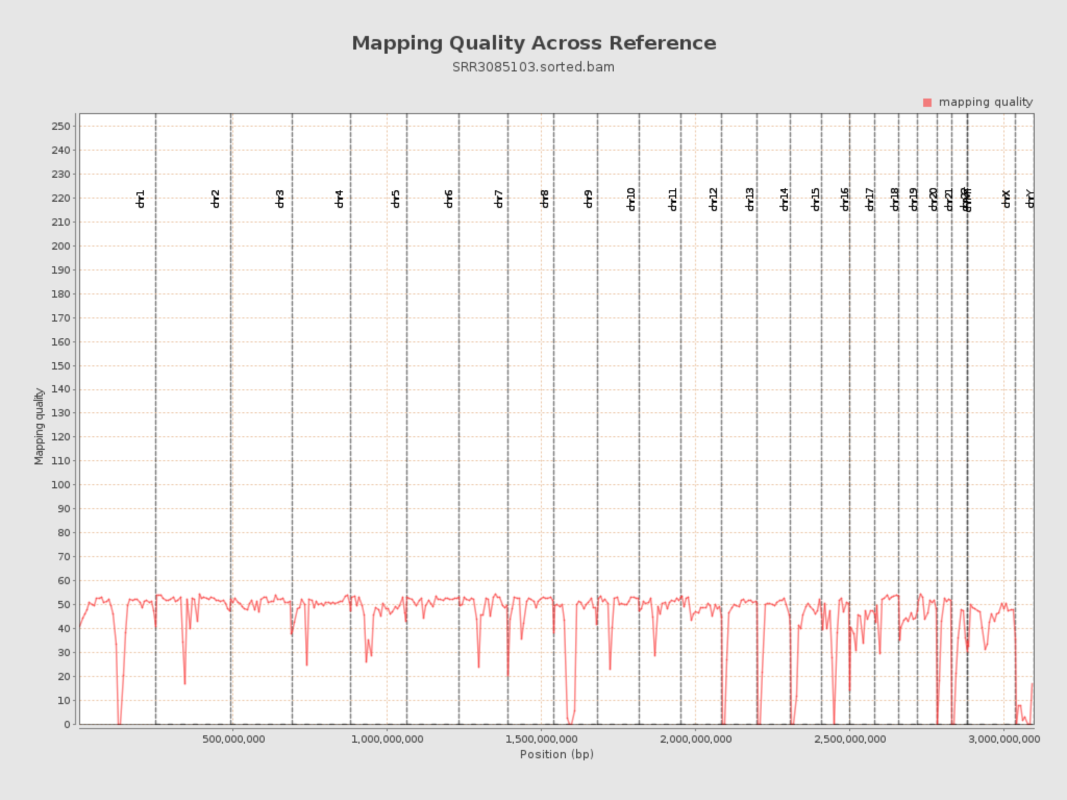
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram