Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/20 04:42:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1506341.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_SRR1506341 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1506341.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Dec 20 04:42:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1506341.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,455,333
Mapped reads	4,448,649 / 68.91%
Unmapped reads	2,006,684 / 31.09%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	71,820 / 1.11%
Read min/max/mean length	30 / 94 / 94.4
Duplicated reads (estimated)	632,205 / 9.79%
Duplication rate	10.78%
Clipped reads	3,052,727 / 47.29%

2.2. ACGT Content

Number/percentage of A's	94,260,977 / 27.72%
Number/percentage of C's	62,555,934 / 18.39%
Number/percentage of T's	96,886,537 / 28.49%
Number/percentage of G's	86,286,724 / 25.37%
Number/percentage of N's	81,240 / 0.02%
GC Percentage	43.77%

2.3. Coverage

Mean	0.1099

Standard Deviation	0.6904

2.4. Mapping Quality

Mean Mapping Quality	47.36

2.5. Mismatches and indels

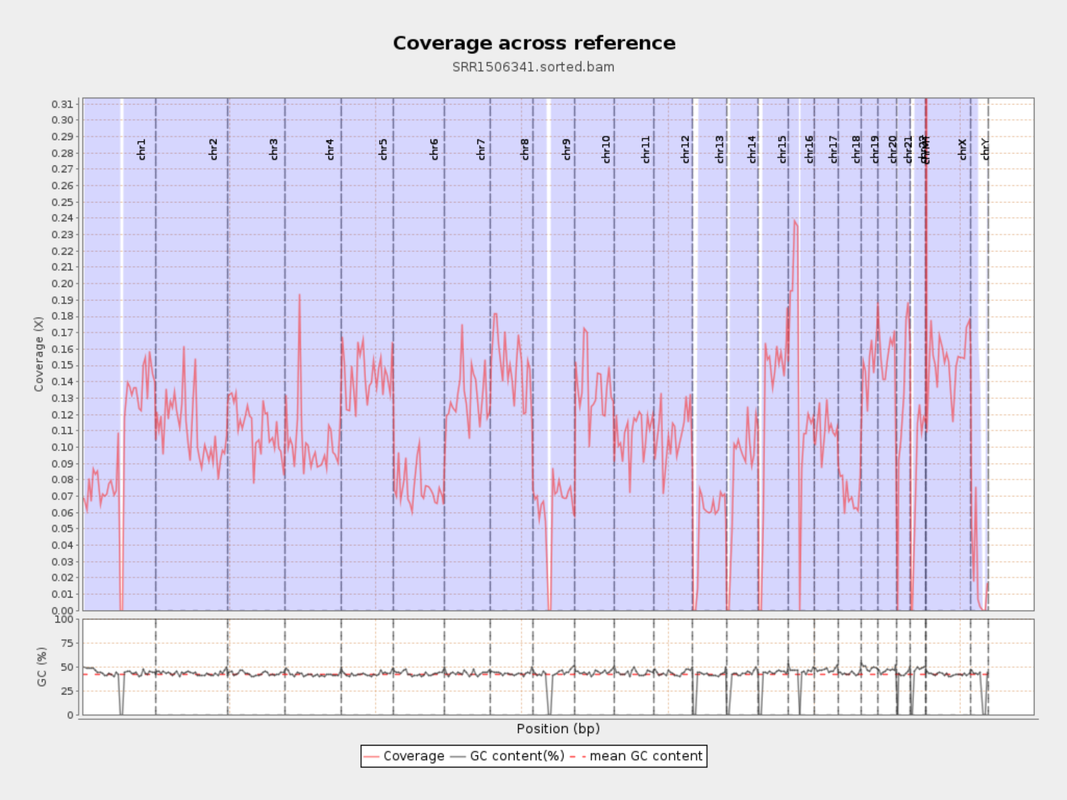
General error rate	0.72%
Mismatches	2,400,069
Insertions	26,993
Mapped reads with at least one insertion	0.59%
Deletions	68,344
Mapped reads with at least one deletion	1.51%
Homopolymer indels	43.57%

2.6. Chromosome stats

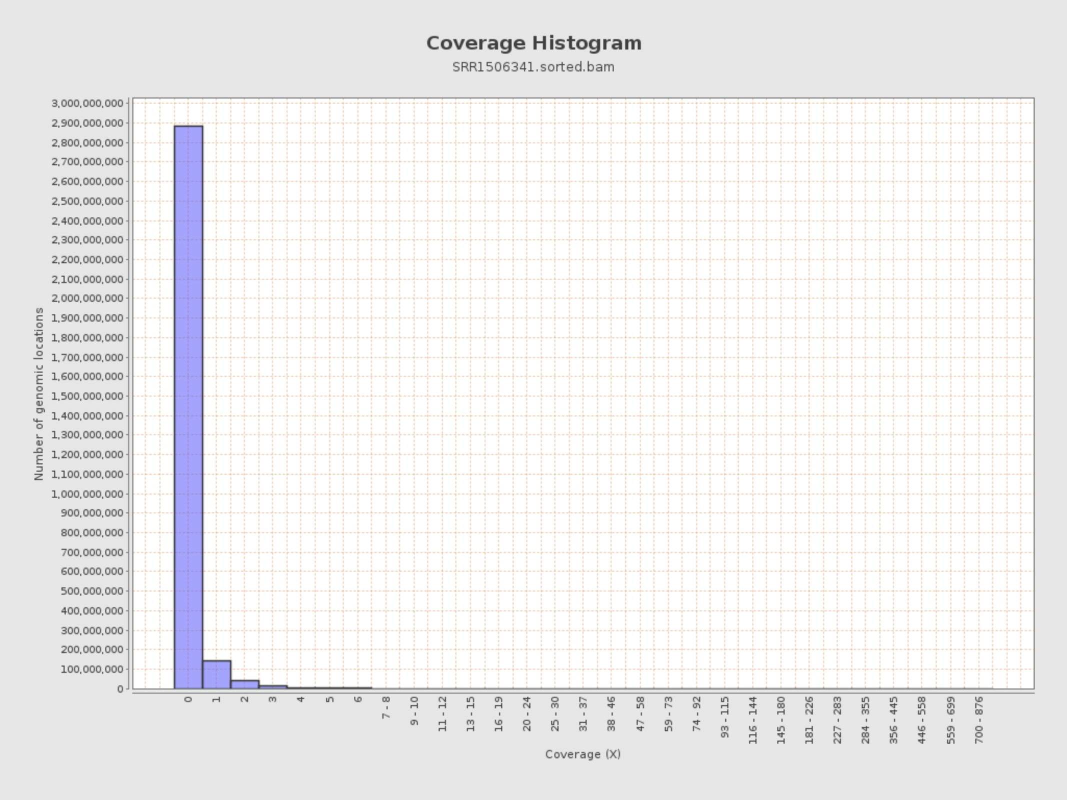
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	24493039	0.0983	0.8924
chr2	243199373	26920392	0.1107	0.75
chr3	198022430	22184019	0.112	0.4971
chr4	191154276	19699267	0.1031	0.6593
chr5	180915260	26013489	0.1438	0.5723
chr6	171115067	12898446	0.0754	0.4278
chr7	159138663	20746865	0.1304	1.1684

chr8	146364022	21813428	0.149	0.8752
chr9	141213431	8689144	0.0615	0.55
chr10	135534747	18391683	0.1357	0.809
chr11	135006516	14539238	0.1077	0.6251
chr12	133851895	14426410	0.1078	0.5189
chr13	115169878	6331853	0.055	0.3398
chr14	107349540	9172048	0.0854	0.4751
chr15	102531392	12837099	0.1252	0.5514
chr16	90354753	12558183	0.139	0.6272
chr17	81195210	9017589	0.1111	0.5586
chr18	78077248	5555380	0.0712	0.8121
chr19	59128983	8904078	0.1506	0.8337
chr20	63025520	9777031	0.1551	0.6421
chr21	48129895	6168473	0.1282	0.6404
chr22	51304566	4191051	0.0817	0.4512
chrMT	16571	39647	2.3926	2.8456
chrX	155270560	23651652	0.1523	0.63
chrY	59373566	1187536	0.02	0.6524

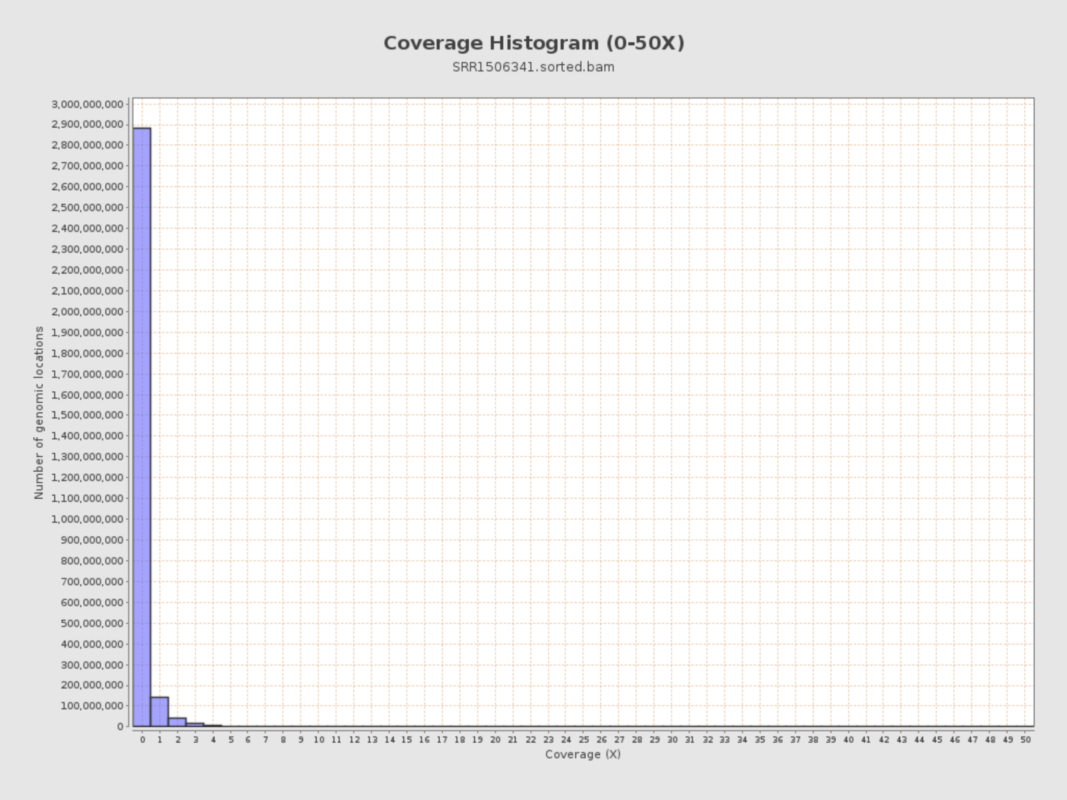
3. Results : Coverage across reference



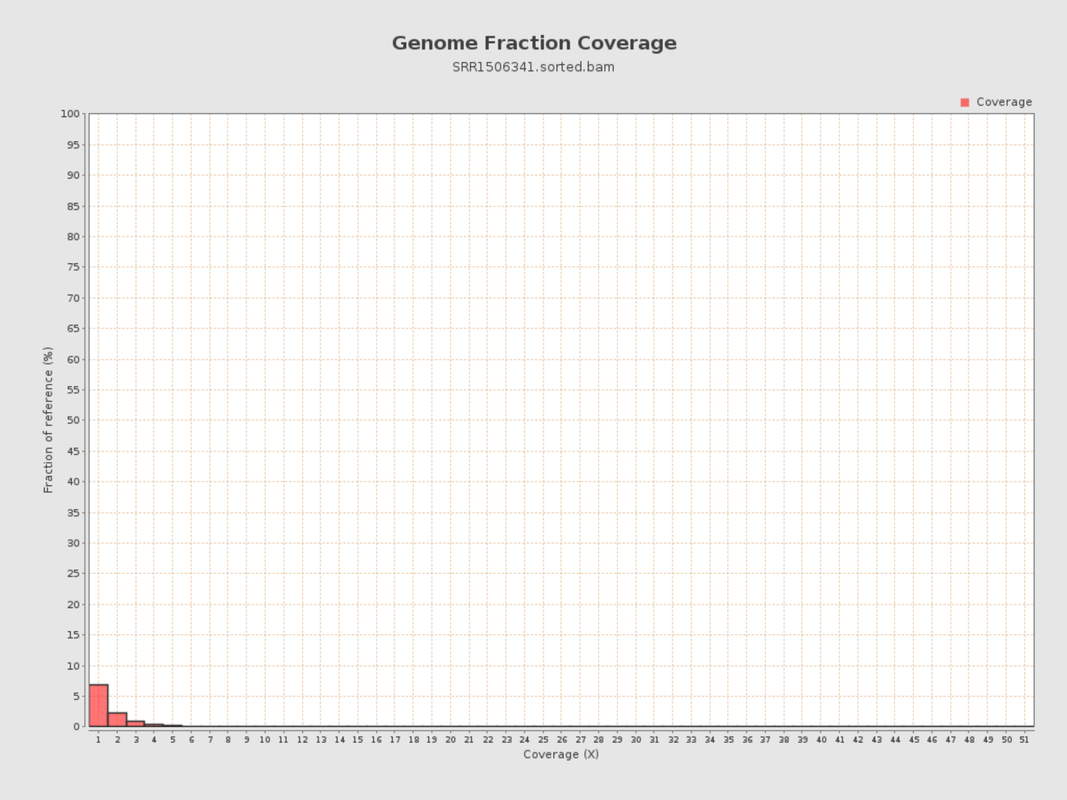
4. Results : Coverage Histogram



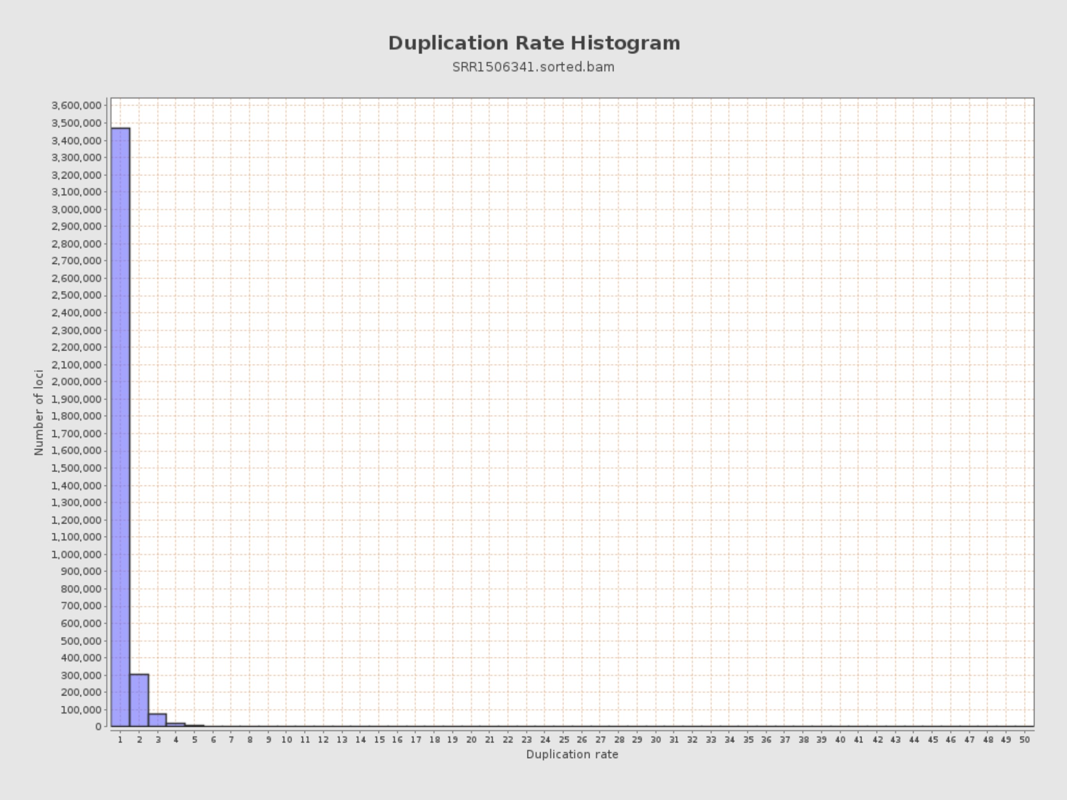
5. Results : Coverage Histogram (0-50X)



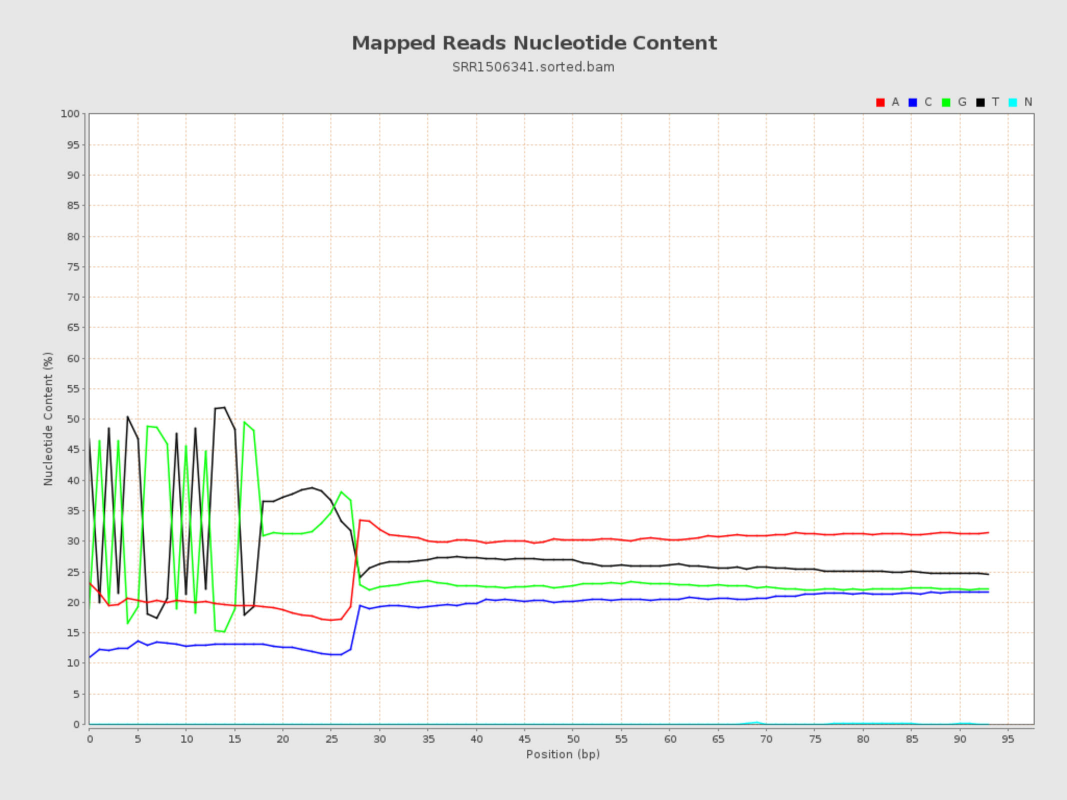
6. Results : Genome Fraction Coverage



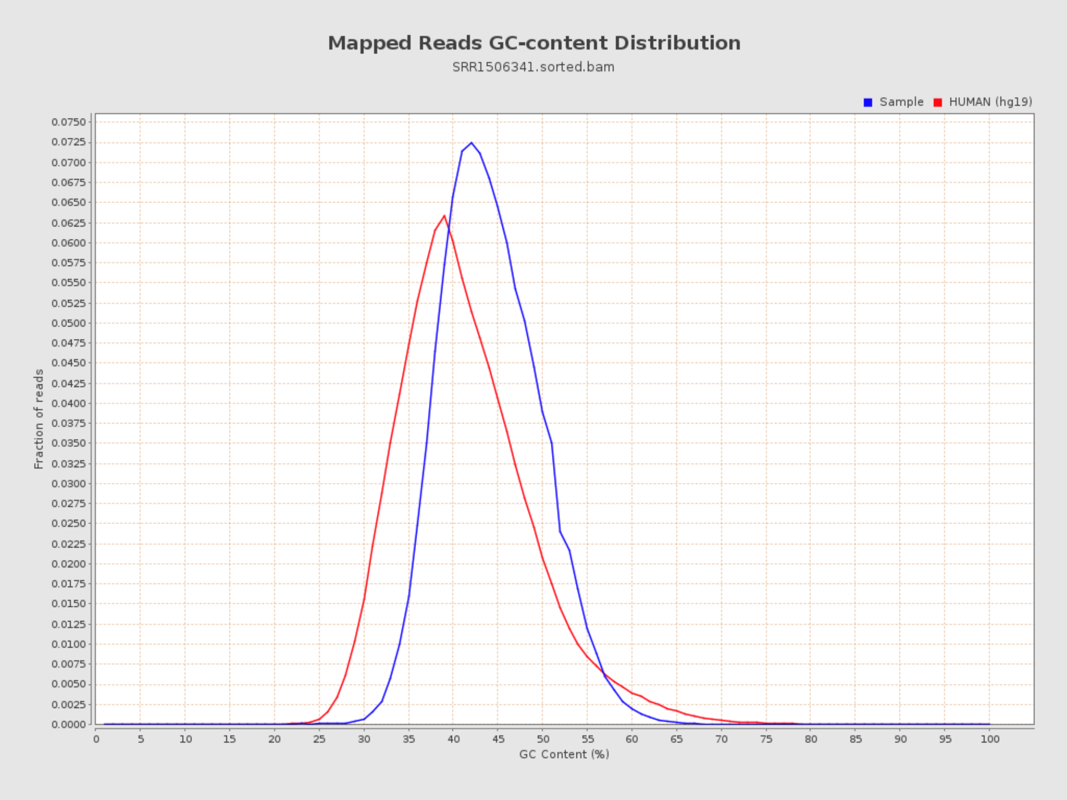
7. Results : Duplication Rate Histogram



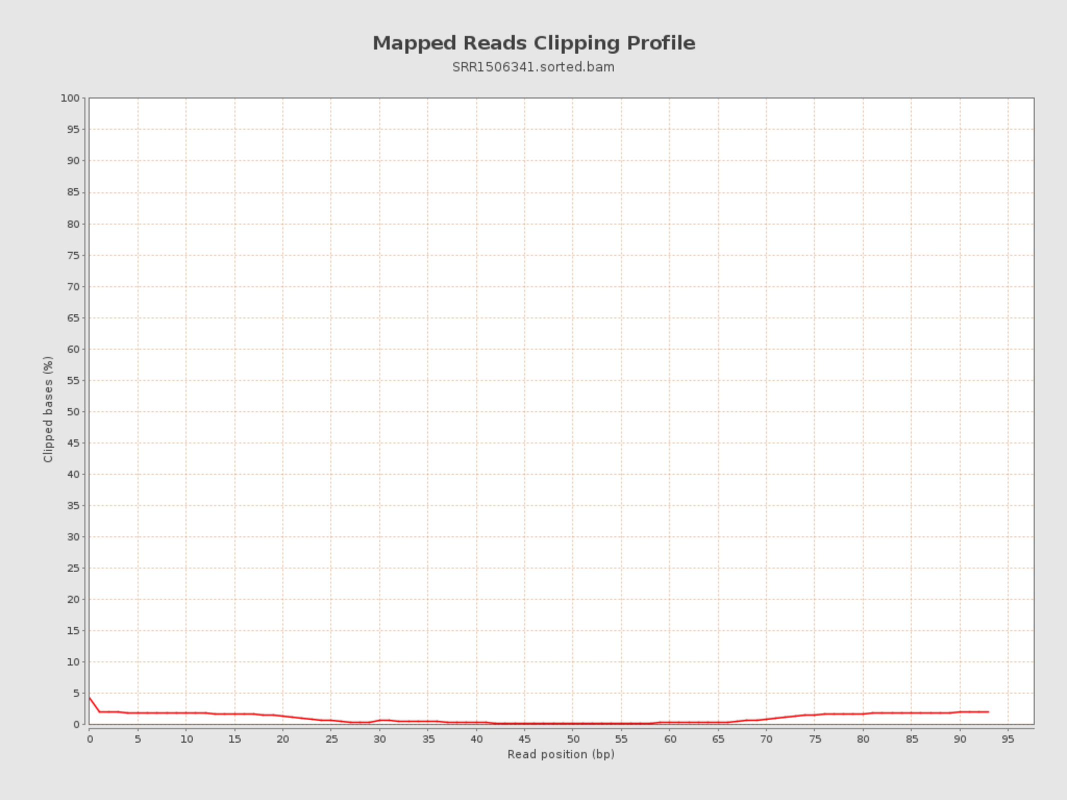
8. Results : Mapped Reads Nucleotide Content



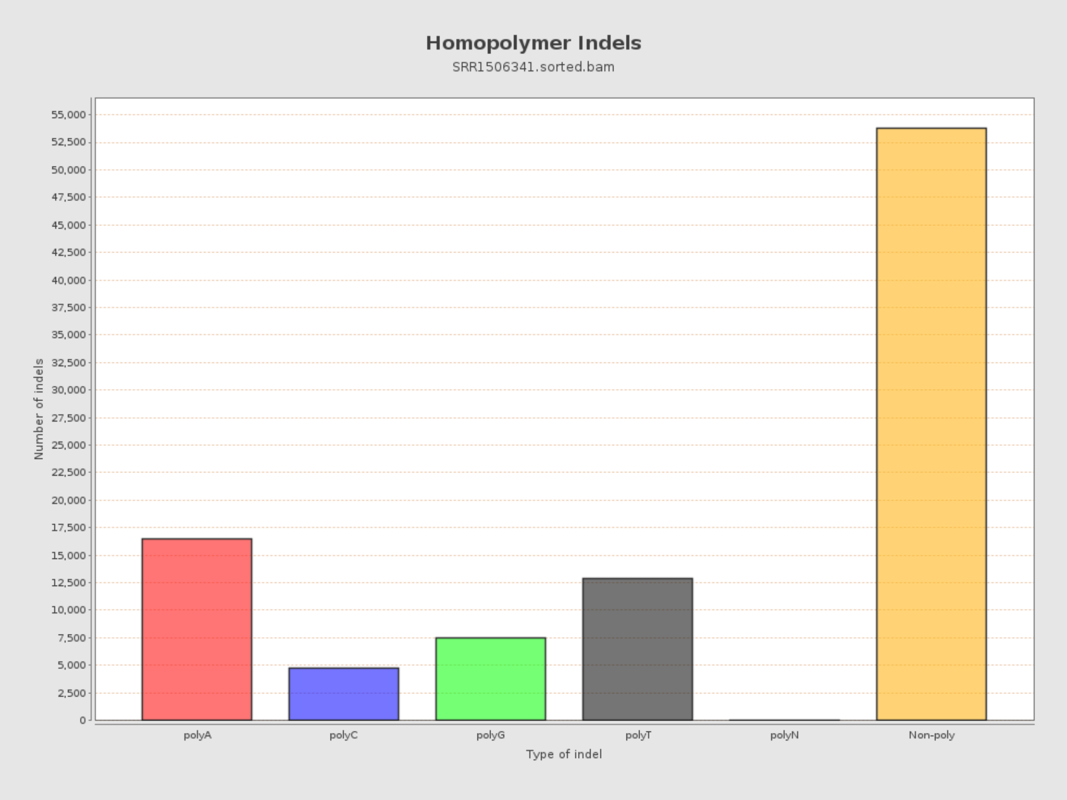
9. Results : Mapped Reads GC-content Distribution



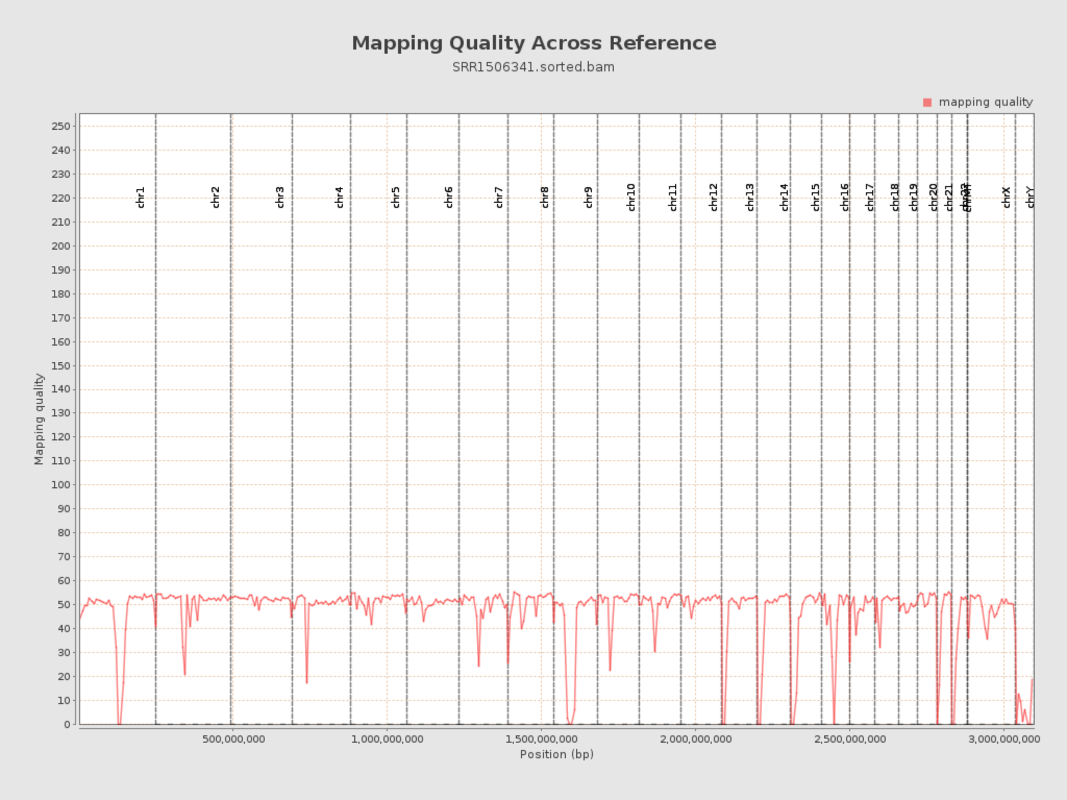
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram