Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/20 04:36:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1506340.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_SRR1506340 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1506340.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Dec 20 04:36:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1506340.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,475,824
Mapped reads	3,567,876 / 65.16%
Unmapped reads	1,907,948 / 34.84%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	49,949 / 0.91%
Read min/max/mean length	30 / 94 / 94.33
Duplicated reads (estimated)	476,484 / 8.7%
Duplication rate	10.2%
Clipped reads	2,430,908 / 44.39%

2.2. ACGT Content

Number/percentage of A's	76,820,653 / 28.09%
Number/percentage of C's	49,364,365 / 18.05%
Number/percentage of T's	78,097,919 / 28.56%
Number/percentage of G's	69,103,133 / 25.27%
Number/percentage of N's	63,721 / 0.02%
GC Percentage	43.32%

2.3. Coverage

Mean	0.0884

Standard Deviation	0.6084

2.4. Mapping Quality

Mean Mapping Quality	47.24

2.5. Mismatches and indels

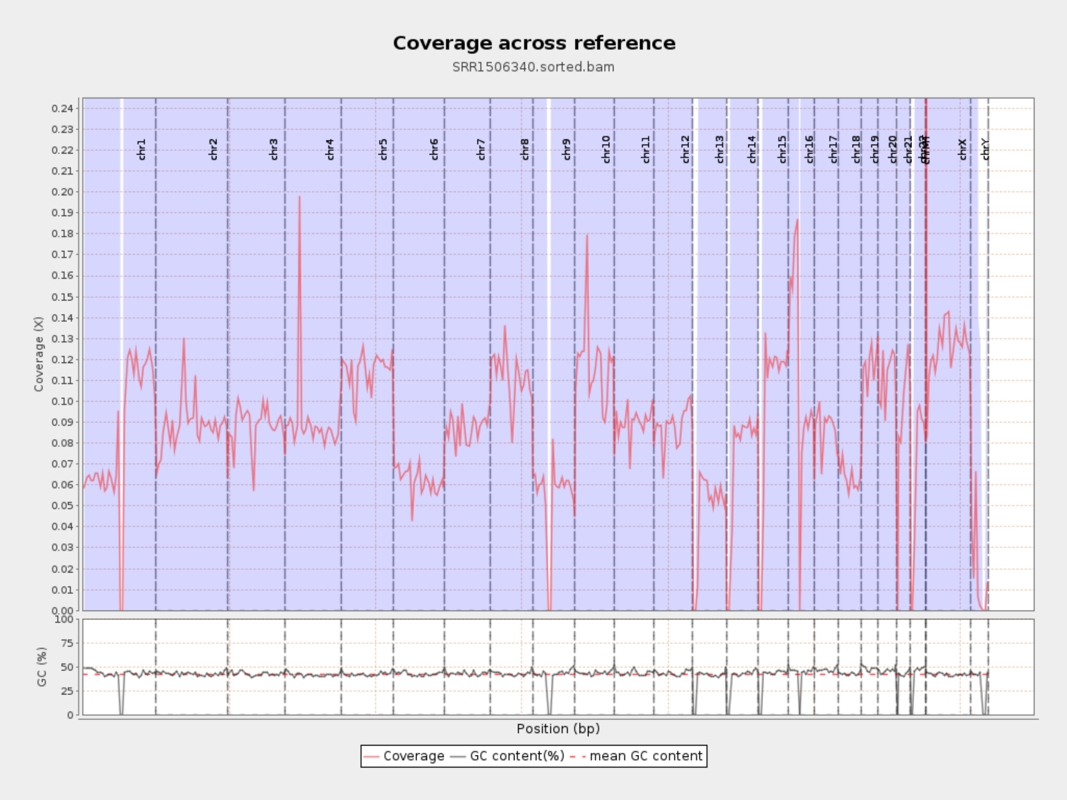
General error rate	0.83%
Mismatches	2,201,223
Insertions	22,895
Mapped reads with at least one insertion	0.63%
Deletions	57,267
Mapped reads with at least one deletion	1.58%
Homopolymer indels	43.66%

2.6. Chromosome stats

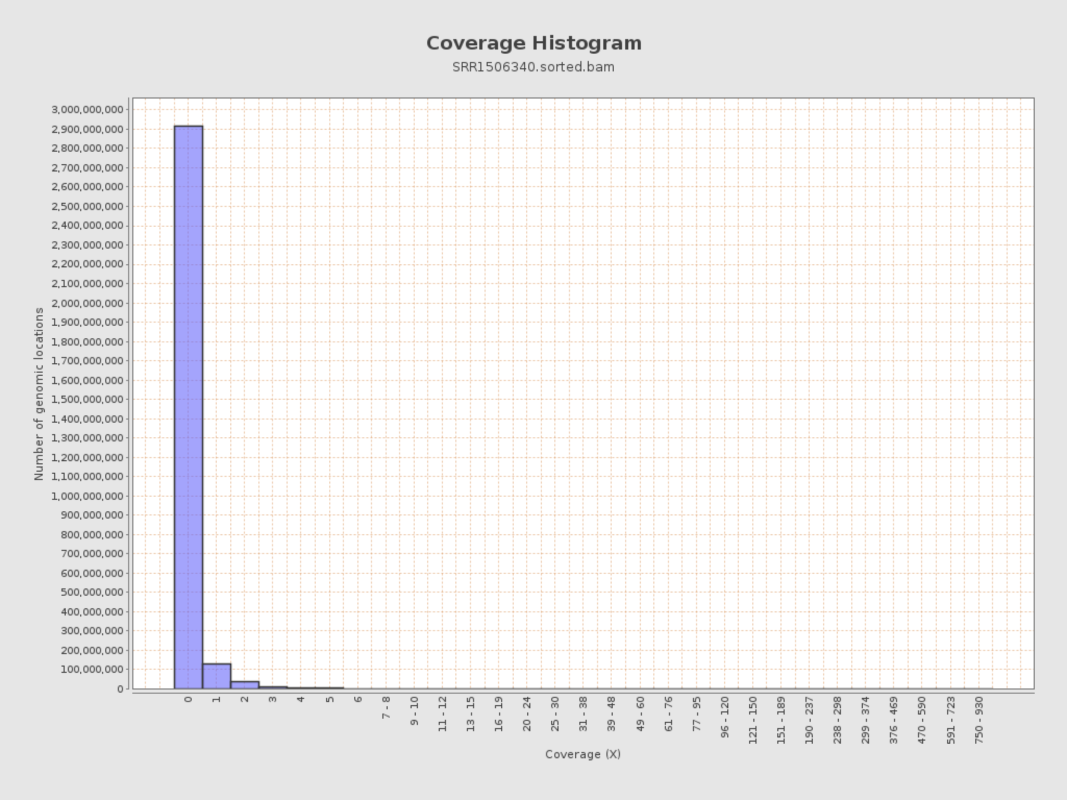
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	20607457	0.0827	0.8409
chr2	243199373	21648385	0.089	0.6407
chr3	198022430	17445586	0.0881	0.425
chr4	191154276	17409150	0.0911	0.648
chr5	180915260	20718276	0.1145	0.4894
chr6	171115067	10645135	0.0622	0.3838
chr7	159138663	13913041	0.0874	0.7037

chr8	146364022	16319713	0.1115	0.8637
chr9	141213431	7656348	0.0542	0.5129
chr10	135534747	15872312	0.1171	0.7431
chr11	135006516	12103694	0.0897	0.611
chr12	133851895	11867609	0.0887	0.4591
chr13	115169878	5496085	0.0477	0.3072
chr14	107349540	7715665	0.0719	0.423
chr15	102531392	9933210	0.0969	0.465
chr16	90354753	9957929	0.1102	0.5786
chr17	81195210	7167675	0.0883	0.4808
chr18	78077248	4957945	0.0635	0.897
chr19	59128983	6836936	0.1156	0.7154
chr20	63025520	7049441	0.1119	0.5329
chr21	48129895	4489408	0.0933	0.5751
chr22	51304566	3299287	0.0643	0.3867
chrMT	16571	13525	0.8162	1.6623
chrX	155270560	19428639	0.1251	0.5527
chrY	59373566	1011533	0.017	0.6047

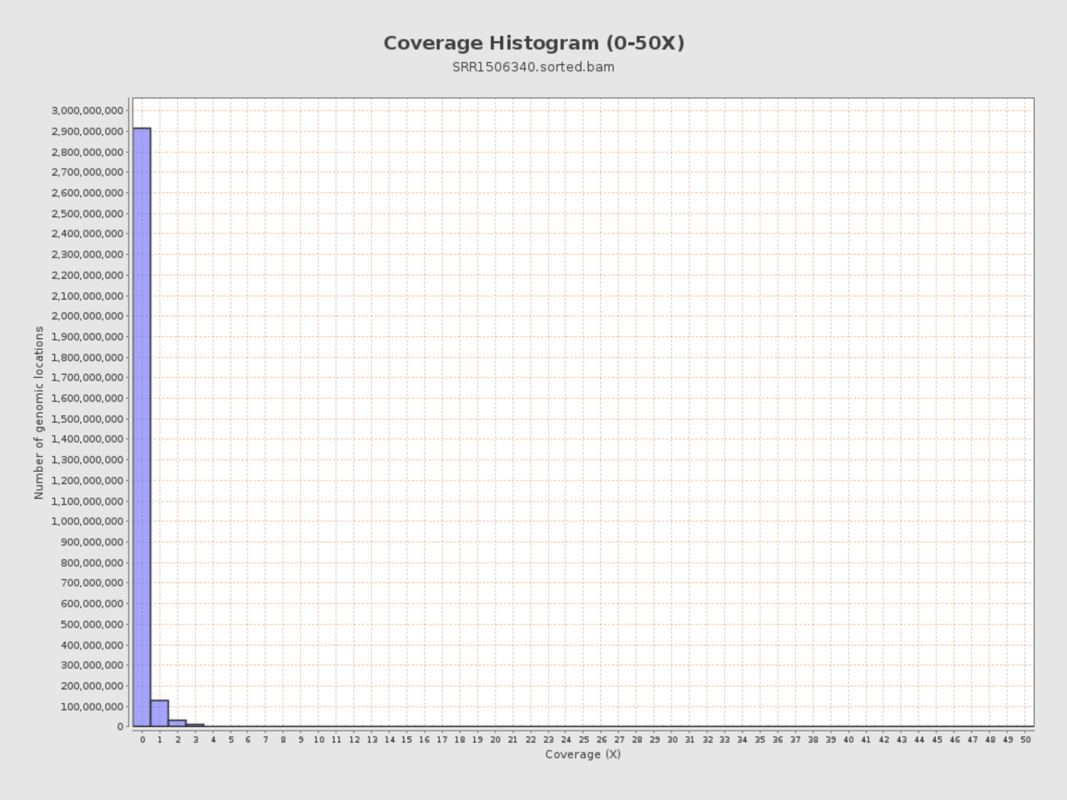
3. Results : Coverage across reference



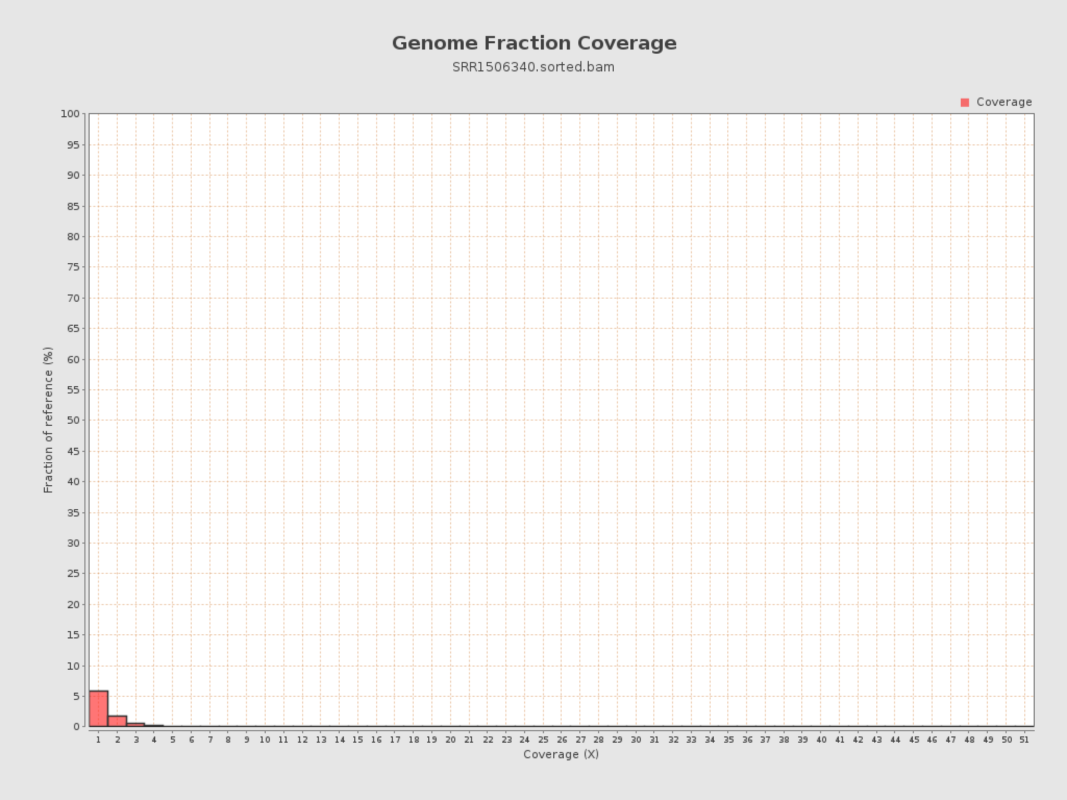
4. Results : Coverage Histogram



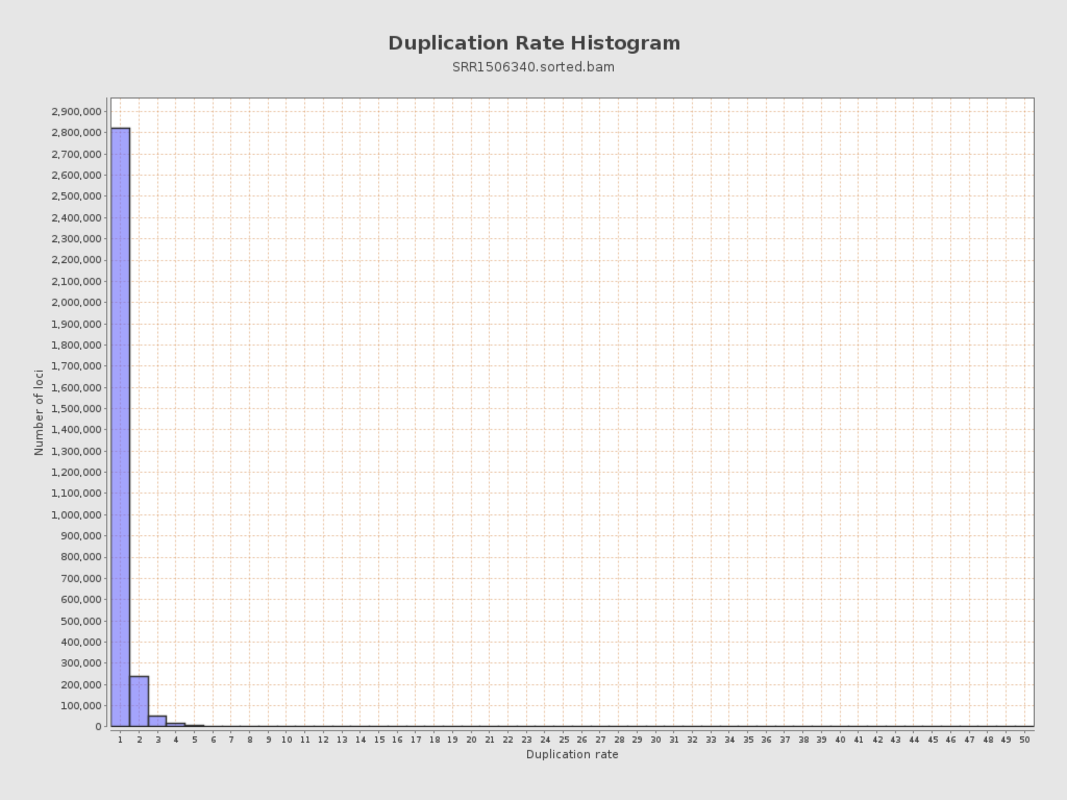
5. Results : Coverage Histogram (0-50X)



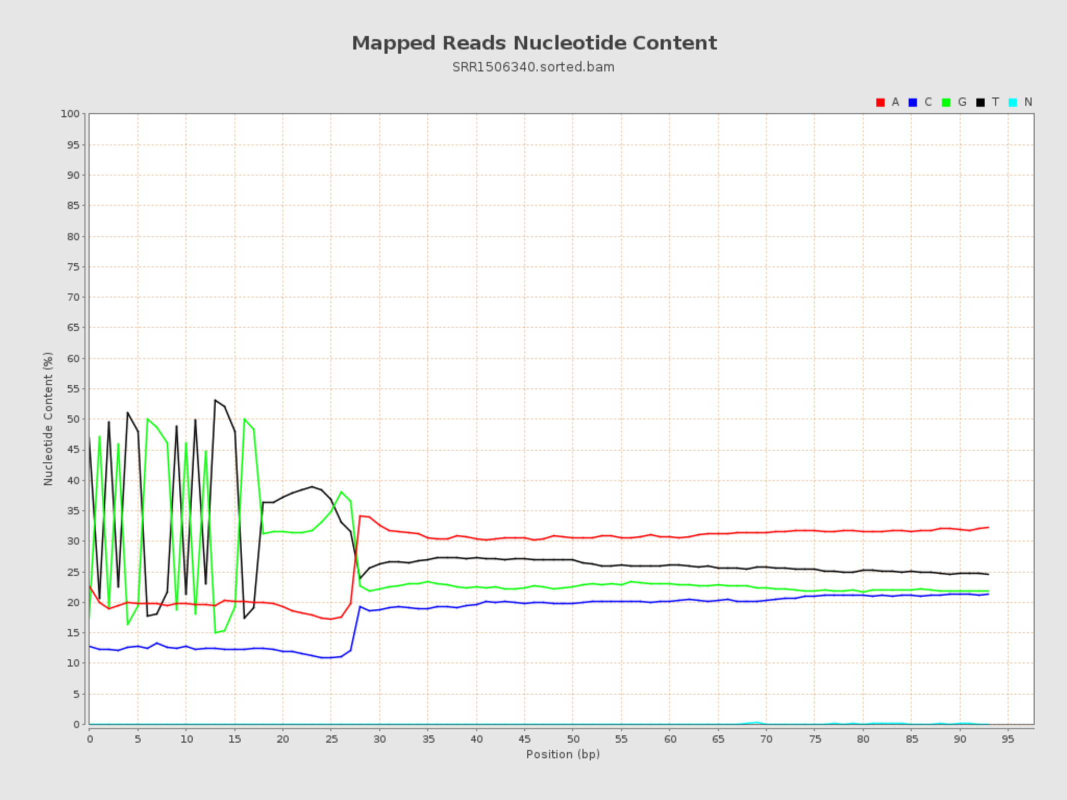
6. Results : Genome Fraction Coverage



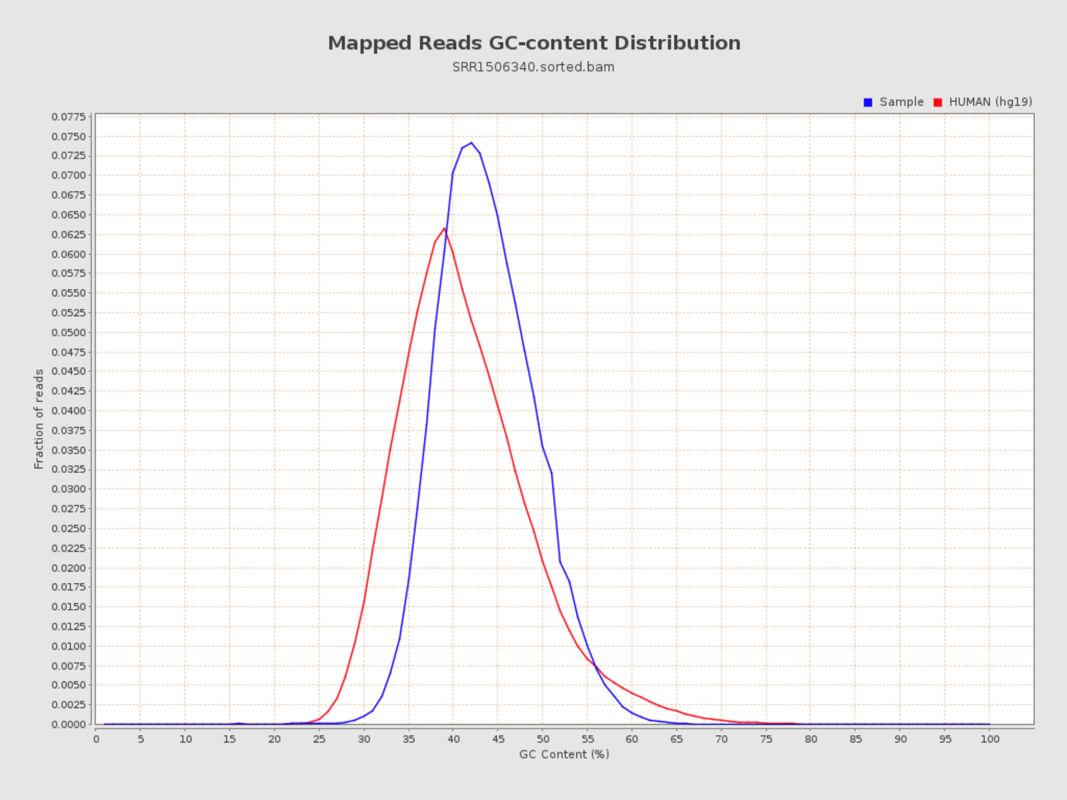
7. Results : Duplication Rate Histogram



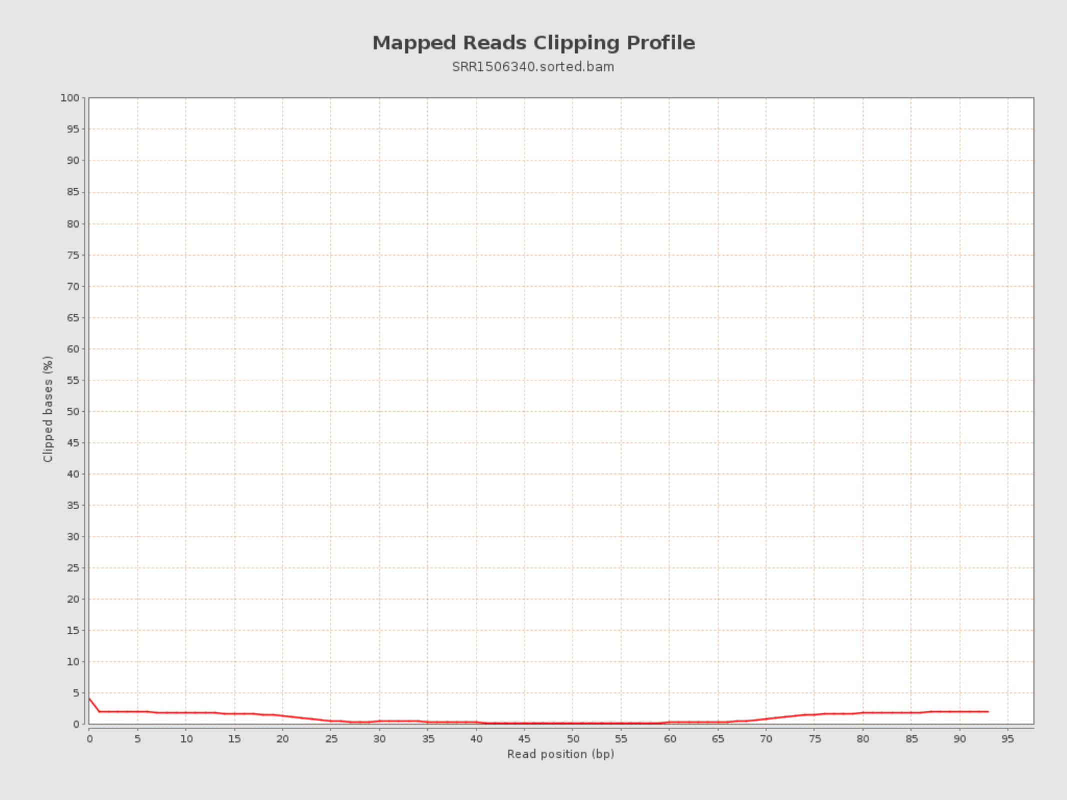
8. Results : Mapped Reads Nucleotide Content



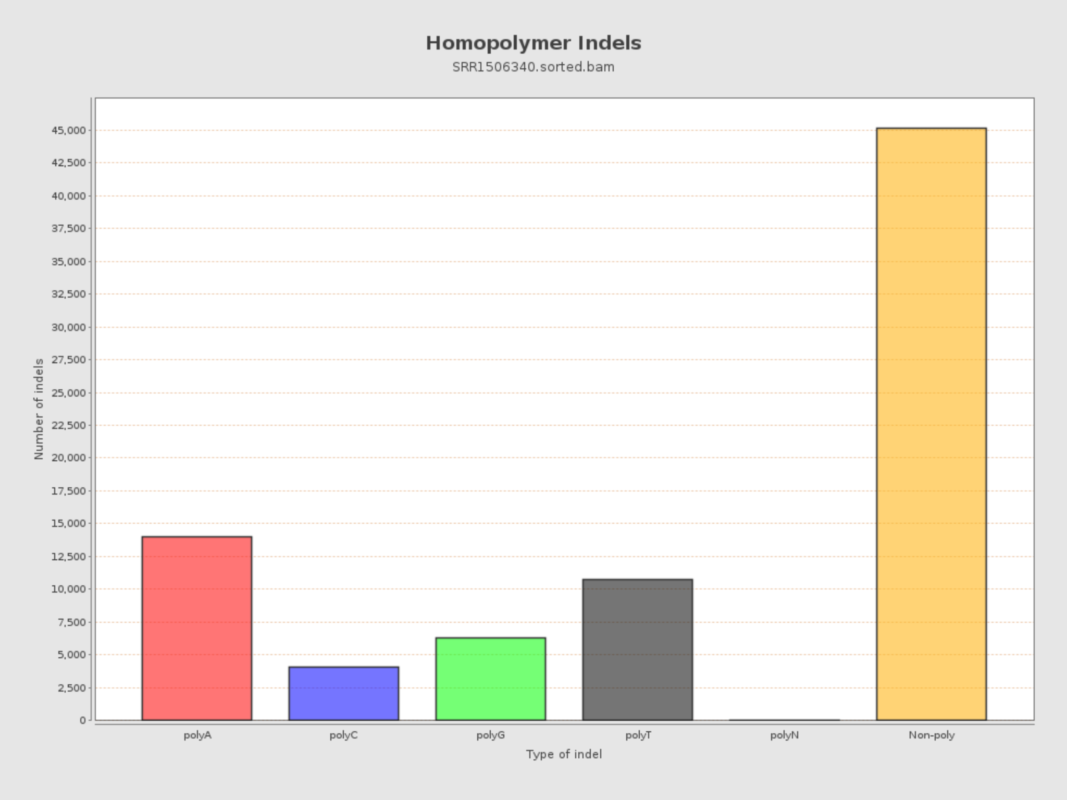
9. Results : Mapped Reads GC-content Distribution



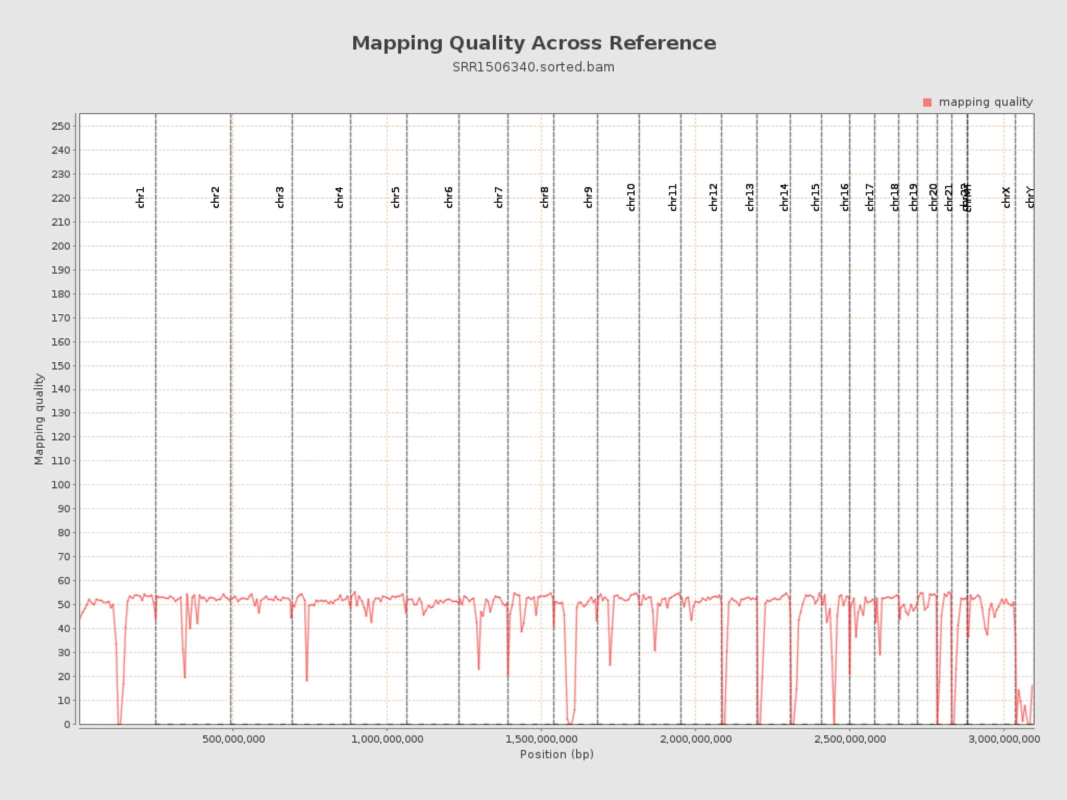
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram