Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 16:48:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524693.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_SRR10524693 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524693.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 16:48:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524693.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,180,359
Mapped reads	2,015,756 / 92.45%
Unmapped reads	164,603 / 7.55%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,267 / 0.43%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	101,420 / 4.65%
Duplication rate	3.76%
Clipped reads	2,018,412 / 92.57%

2.2. ACGT Content

Number/percentage of A's	31,064,326 / 26.01%
Number/percentage of C's	22,472,119 / 18.81%
Number/percentage of T's	38,196,939 / 31.98%
Number/percentage of G's	27,699,958 / 23.19%
Number/percentage of N's	17,052 / 0.01%
GC Percentage	42%

2.3. Coverage

Mean	0.0386

Standard Deviation	0.3527

2.4. Mapping Quality

Mean Mapping Quality	45.97

2.5. Mismatches and indels

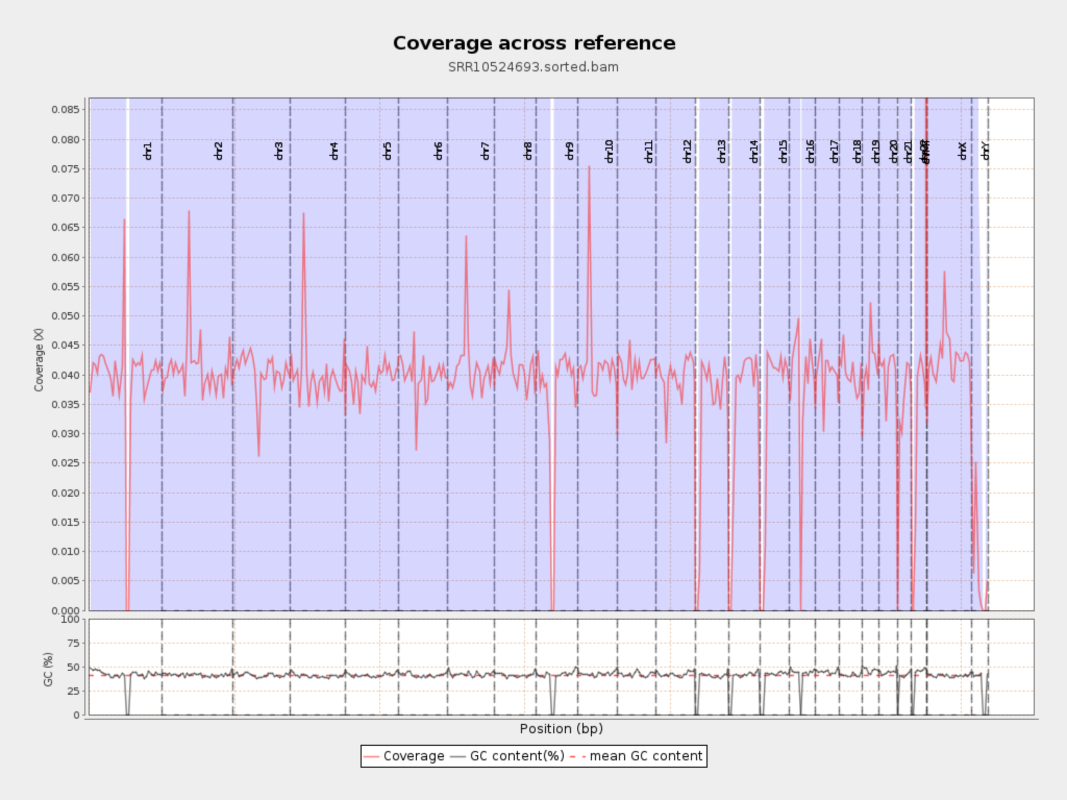
General error rate	0.52%
Mismatches	600,205
Insertions	8,644
Mapped reads with at least one insertion	0.43%
Deletions	22,985
Mapped reads with at least one deletion	1.13%
Homopolymer indels	42.04%

2.6. Chromosome stats

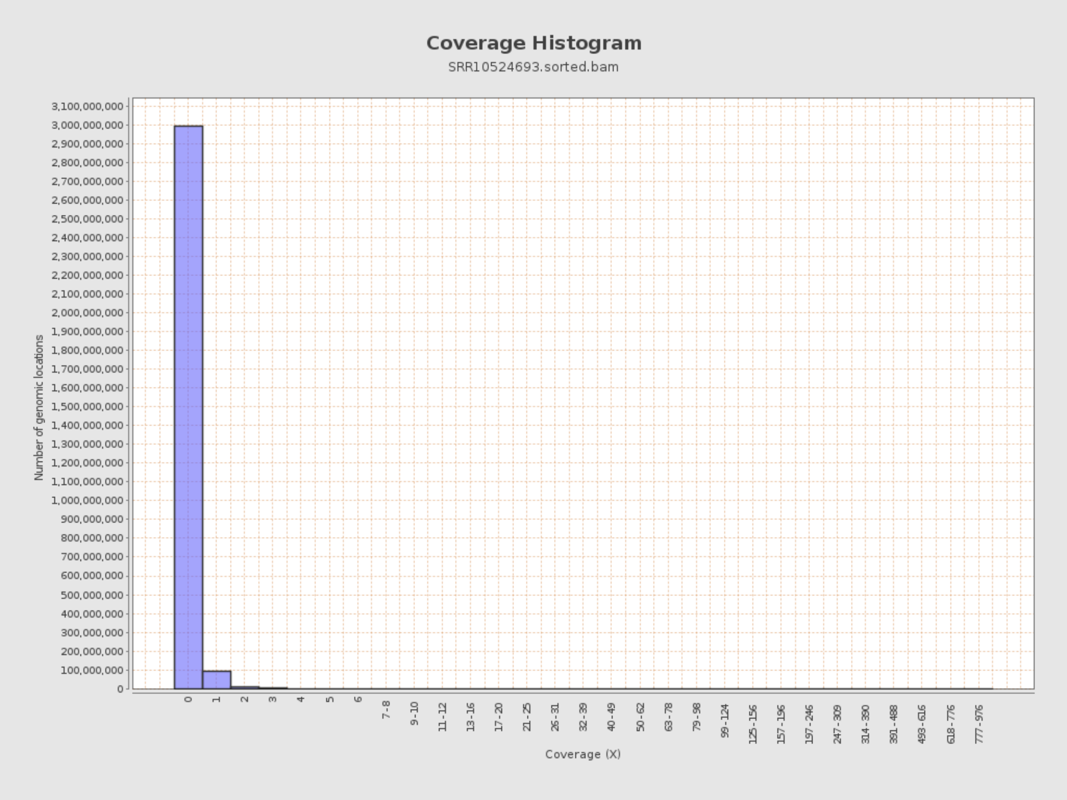
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9671775	0.0388	0.6448
chr2	243199373	10055305	0.0413	0.4858
chr3	198022430	7998937	0.0404	0.2239
chr4	191154276	7679914	0.0402	0.2642
chr5	180915260	7175677	0.0397	0.2242
chr6	171115067	6816587	0.0398	0.2558
chr7	159138663	6589135	0.0414	0.4086

chr8	146364022	6065619	0.0414	0.3895
chr9	141213431	5005231	0.0354	0.2896
chr10	135534747	5747490	0.0424	0.3589
chr11	135006516	5519685	0.0409	0.3004
chr12	133851895	5308977	0.0397	0.2251
chr13	115169878	3751028	0.0326	0.2039
chr14	107349540	3632553	0.0338	0.215
chr15	102531392	3430439	0.0335	0.2048
chr16	90354753	3484270	0.0386	0.2409
chr17	81195210	3270933	0.0403	0.2435
chr18	78077248	3147687	0.0403	0.5431
chr19	59128983	2482597	0.042	0.4915
chr20	63025520	2549152	0.0404	0.231
chr21	48129895	1589658	0.033	0.2455
chr22	51304566	1432078	0.0279	0.1886
chrMT	16571	34220	2.0651	1.6654
chrX	155270560	6651689	0.0428	0.2592
chrY	59373566	396161	0.0067	0.2385

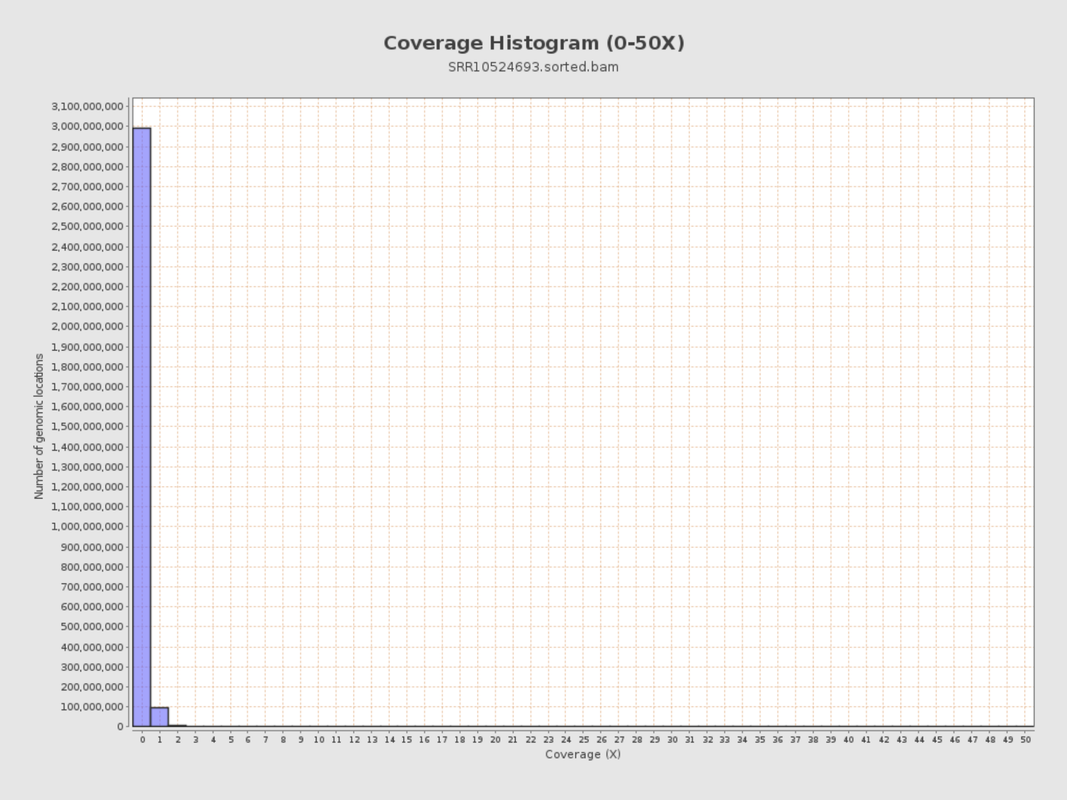
3. Results : Coverage across reference



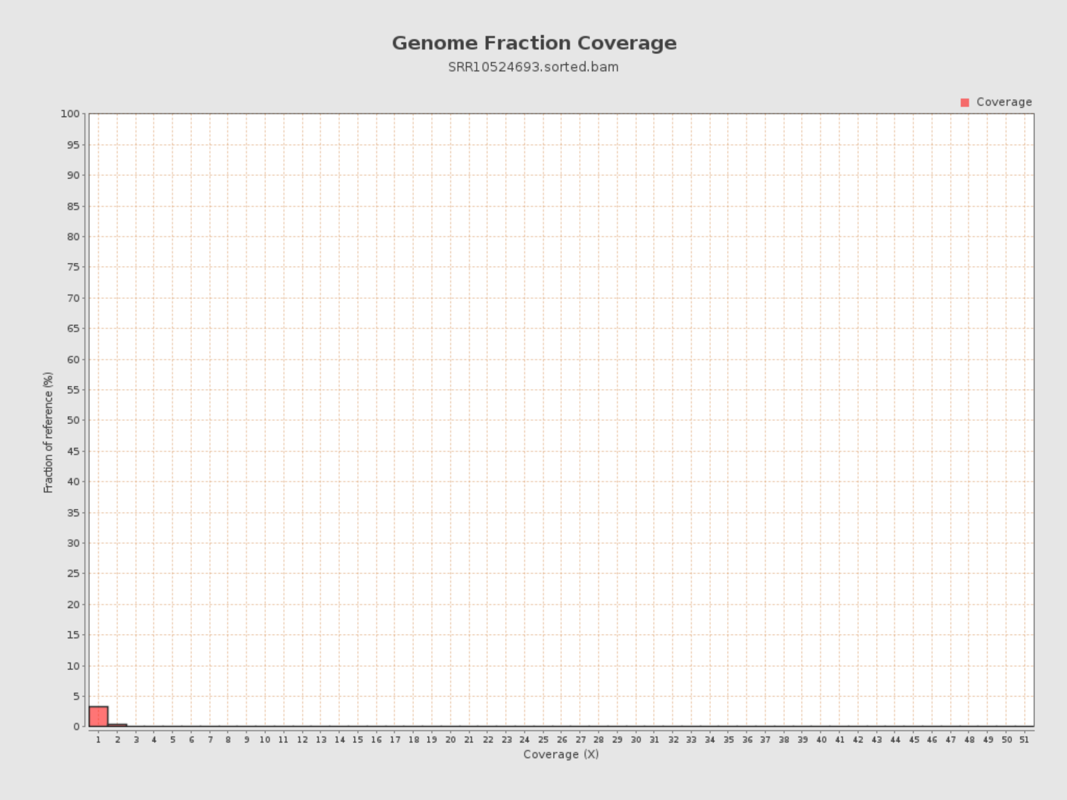
4. Results : Coverage Histogram



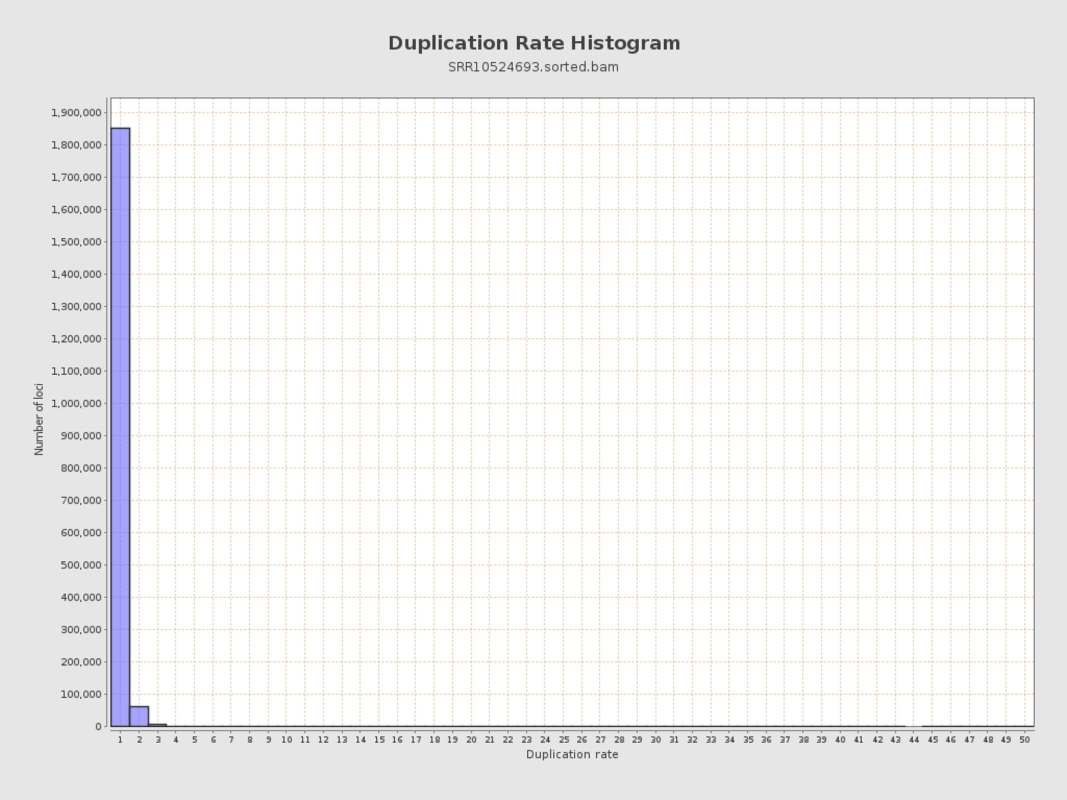
5. Results : Coverage Histogram (0-50X)



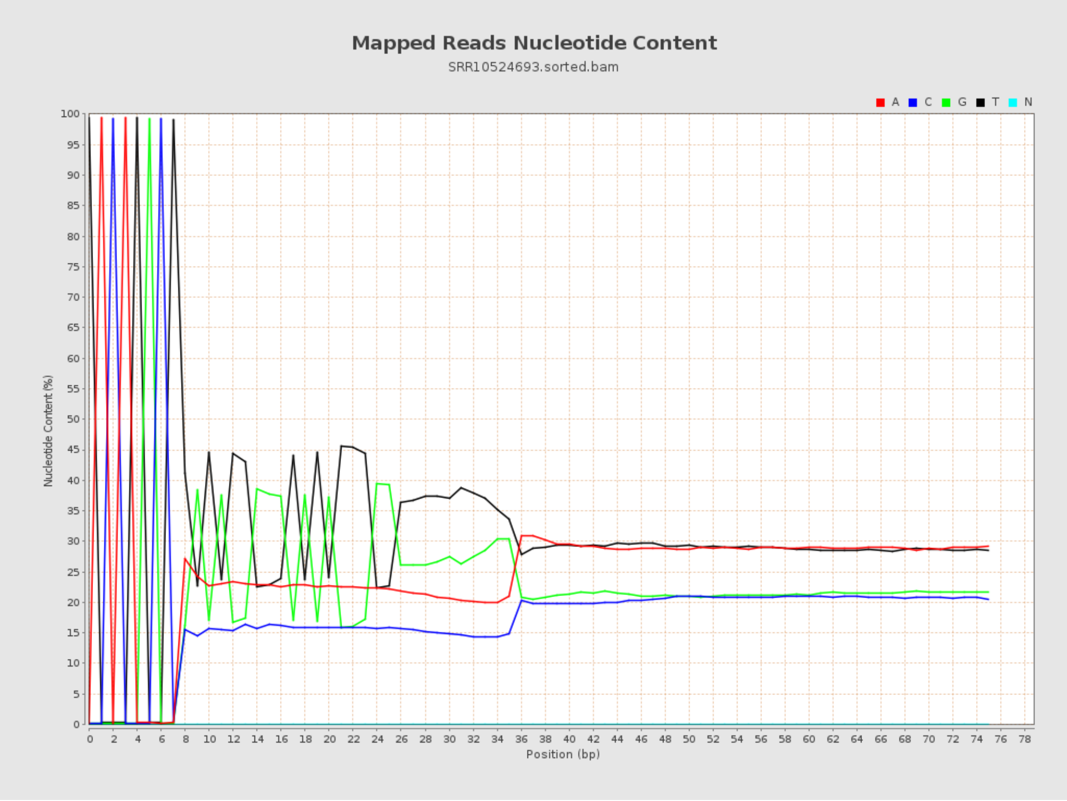
6. Results : Genome Fraction Coverage



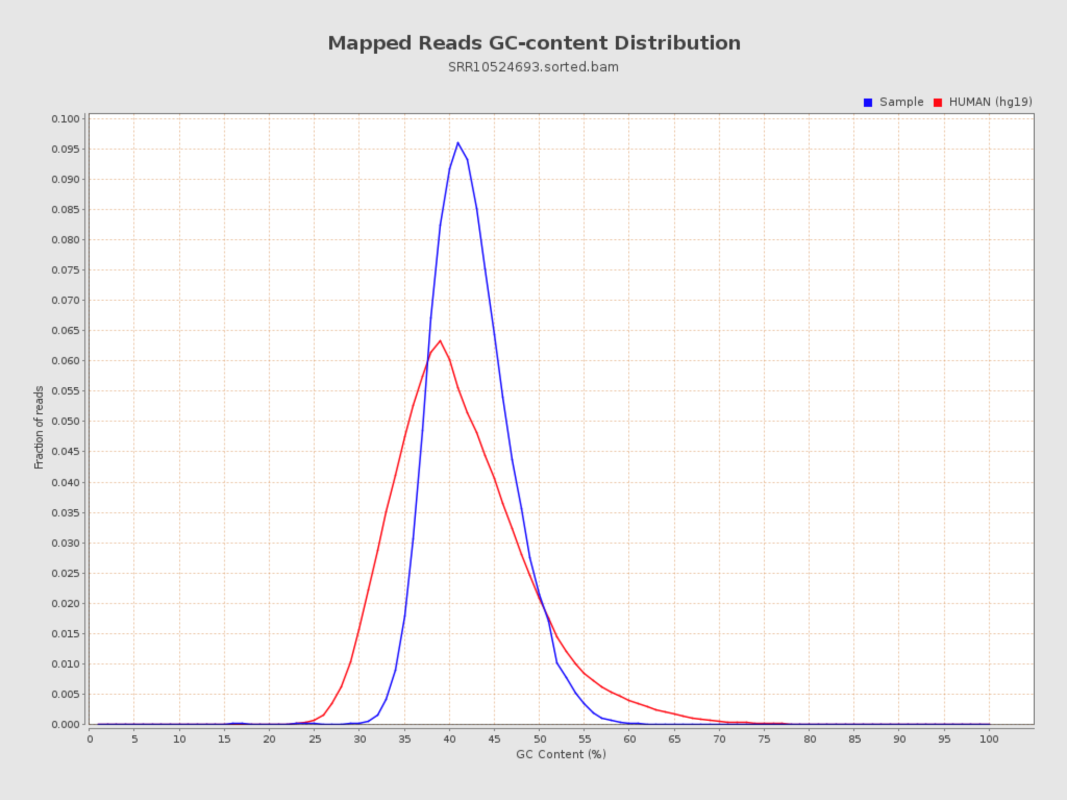
7. Results : Duplication Rate Histogram



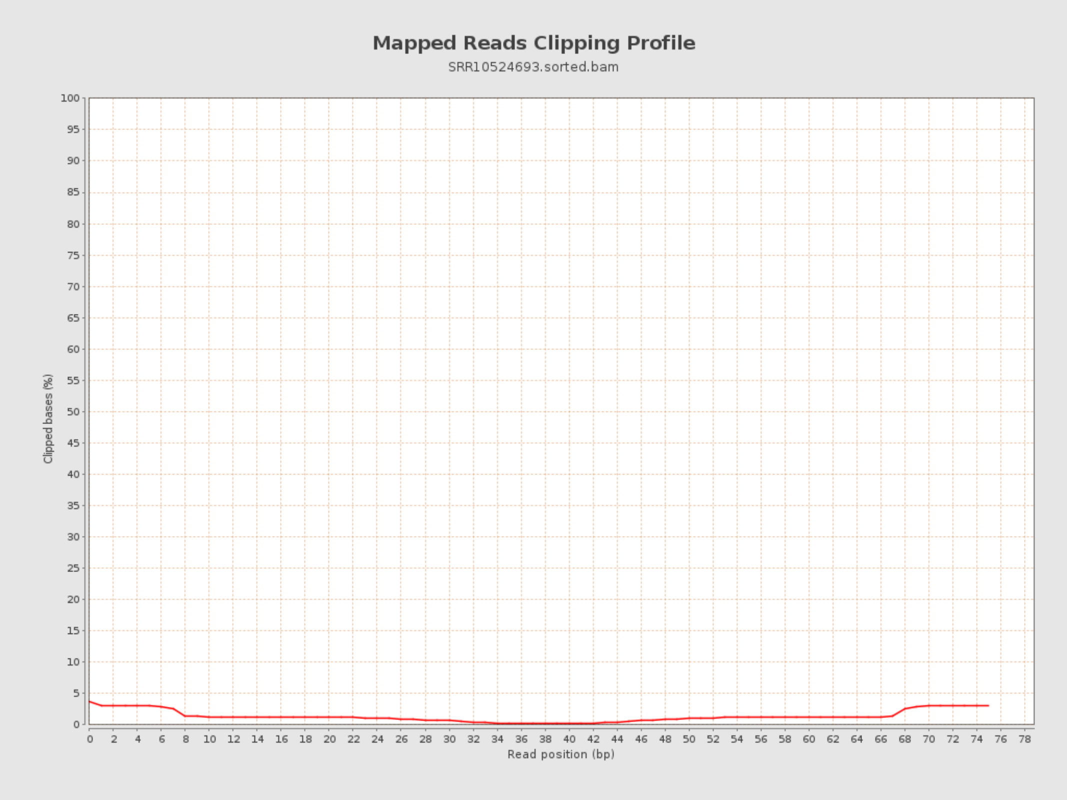
8. Results : Mapped Reads Nucleotide Content



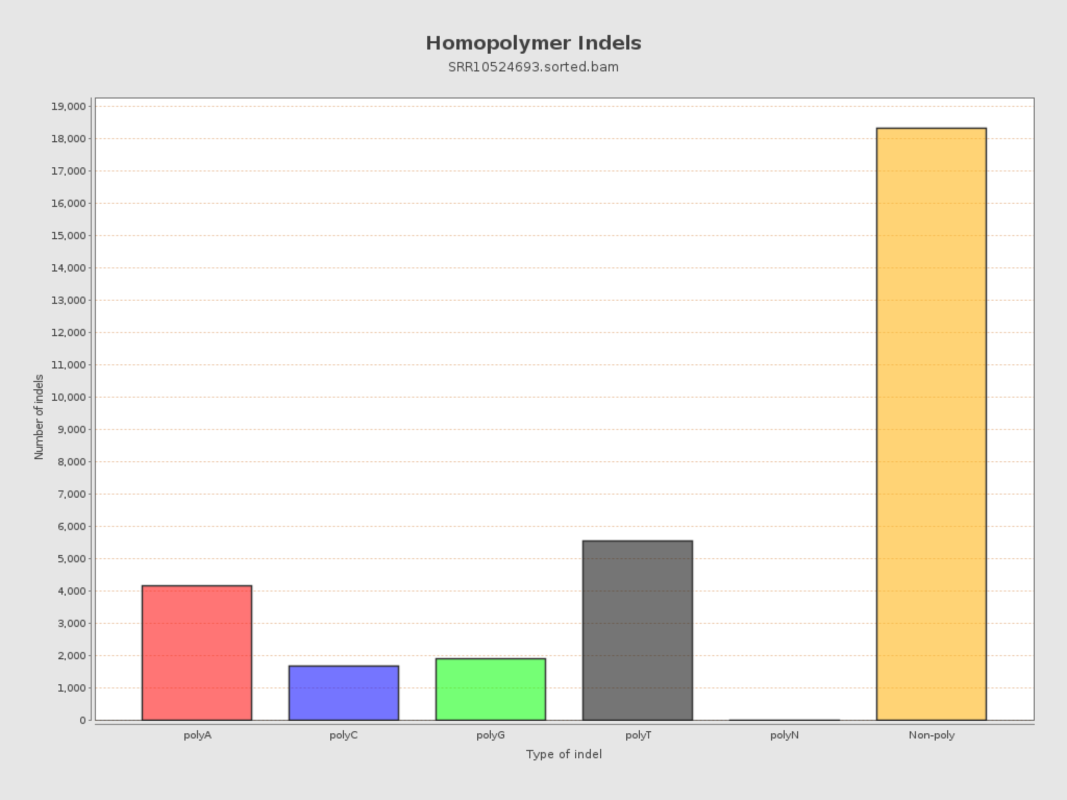
9. Results : Mapped Reads GC-content Distribution



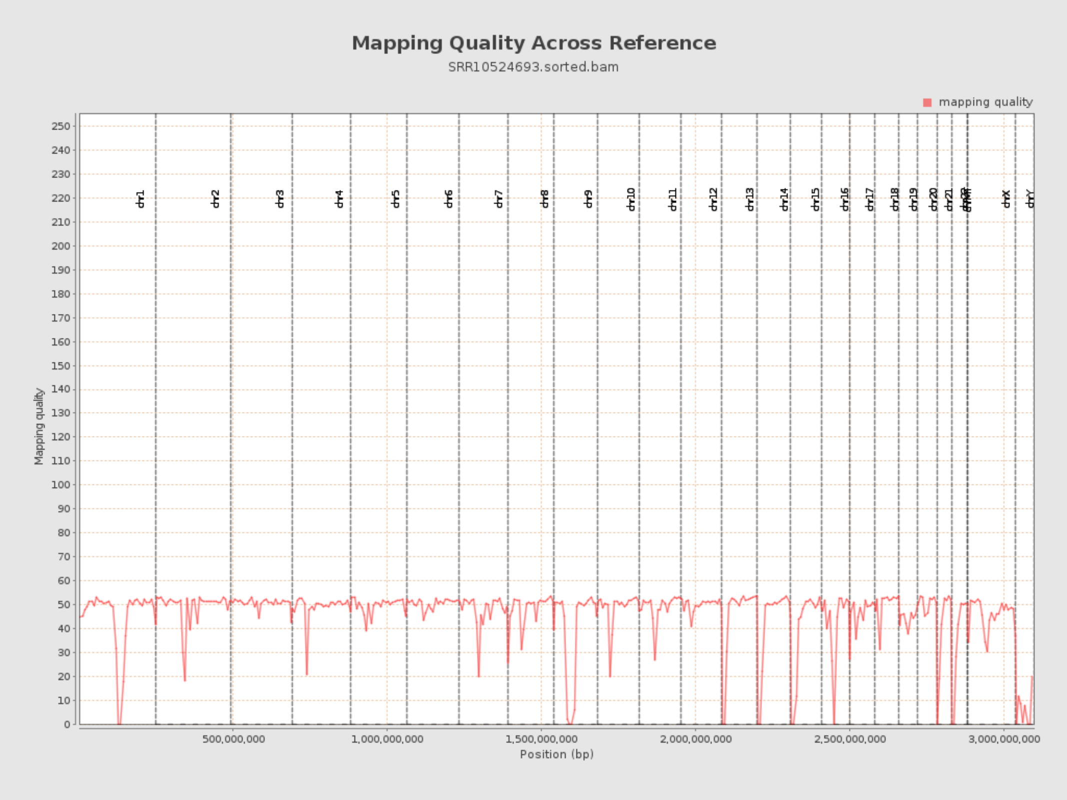
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram