Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 19:59:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524604.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_SRR10524604 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524604.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 19:59:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524604.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,489,620
Mapped reads	2,308,272 / 92.72%
Unmapped reads	181,348 / 7.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,735 / 0.19%
Read min/max/mean length	30 / 76 / 76.06
Duplicated reads (estimated)	147,475 / 5.92%
Duplication rate	4.94%
Clipped reads	2,307,811 / 92.7%

2.2. ACGT Content

Number/percentage of A's	34,047,689 / 25.44%
Number/percentage of C's	24,519,876 / 18.32%
Number/percentage of T's	43,407,944 / 32.44%
Number/percentage of G's	31,848,765 / 23.8%
Number/percentage of N's	814 / 0%
GC Percentage	42.12%

2.3. Coverage

Mean	0.0432

Standard Deviation	0.3636

2.4. Mapping Quality

Mean Mapping Quality	45.21

2.5. Mismatches and indels

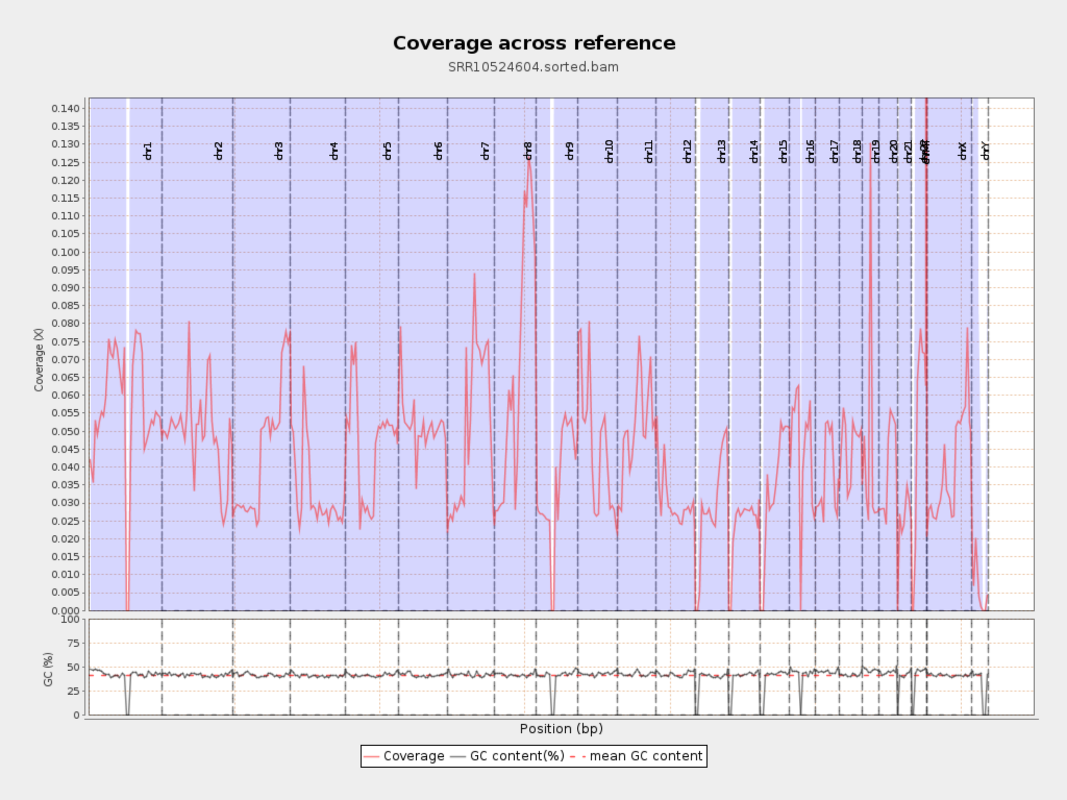
General error rate	0.48%
Mismatches	631,760
Insertions	8,274
Mapped reads with at least one insertion	0.36%
Deletions	24,587
Mapped reads with at least one deletion	1.06%
Homopolymer indels	44.35%

2.6. Chromosome stats

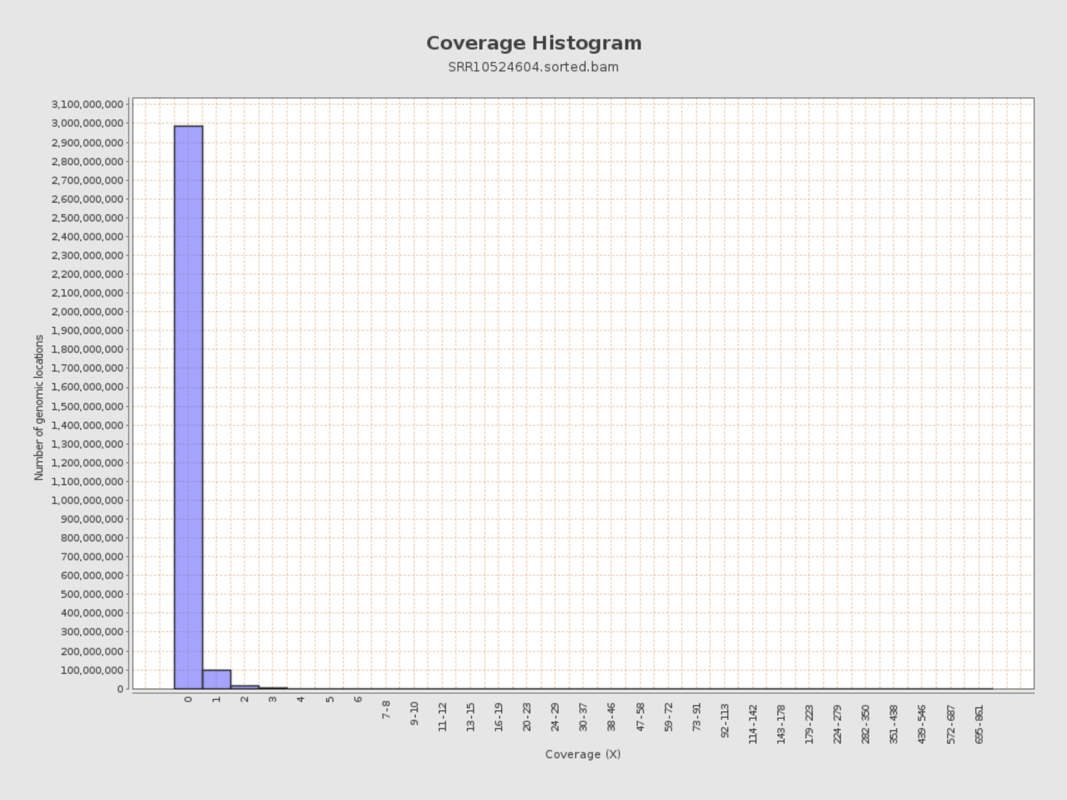
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13994225	0.0561	0.6364
chr2	243199373	12066311	0.0496	0.4519
chr3	198022430	8708125	0.044	0.2476
chr4	191154276	6275557	0.0328	0.2543
chr5	180915260	8430384	0.0466	0.253
chr6	171115067	8822880	0.0516	0.2889
chr7	159138663	8247098	0.0518	0.5066

chr8	146364022	9956536	0.068	0.4368
chr9	141213431	4857050	0.0344	0.3292
chr10	135534747	6224735	0.0459	0.3814
chr11	135006516	6877588	0.0509	0.354
chr12	133851895	4108086	0.0307	0.2133
chr13	115169878	3286208	0.0285	0.1997
chr14	107349540	2485584	0.0232	0.1866
chr15	102531392	3453942	0.0337	0.2272
chr16	90354753	4011080	0.0444	0.2632
chr17	81195210	3053428	0.0376	0.2355
chr18	78077248	3626534	0.0464	0.5304
chr19	59128983	2632883	0.0445	0.4474
chr20	63025520	2530431	0.0401	0.2422
chr21	48129895	1191201	0.0247	0.2122
chr22	51304566	2478018	0.0483	0.2576
chrMT	16571	23869	1.4404	1.6258
chrX	155270560	6182406	0.0398	0.278
chrY	59373566	342920	0.0058	0.1616

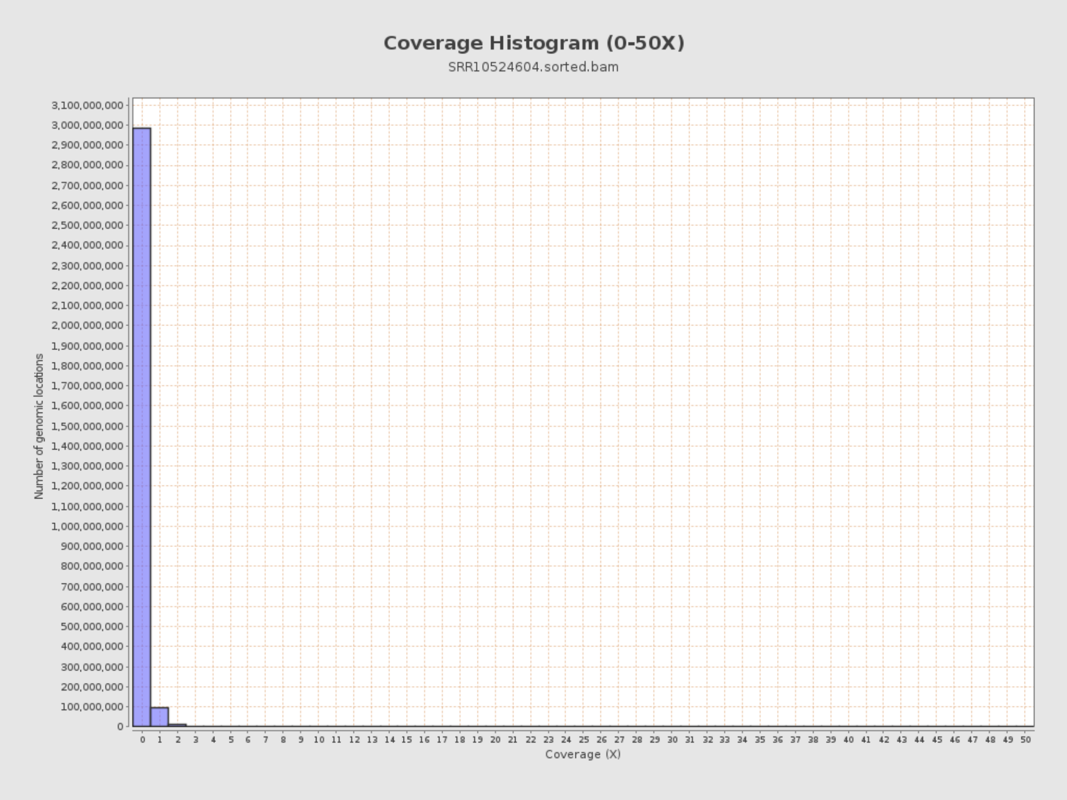
3. Results : Coverage across reference



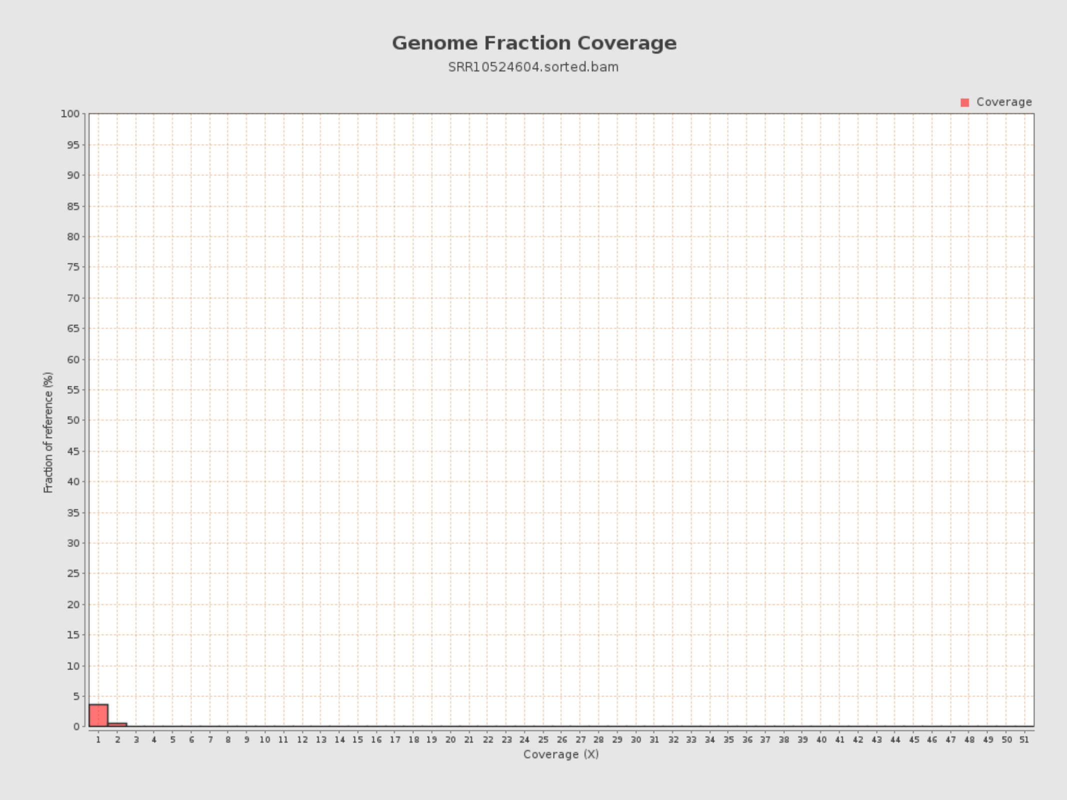
4. Results : Coverage Histogram



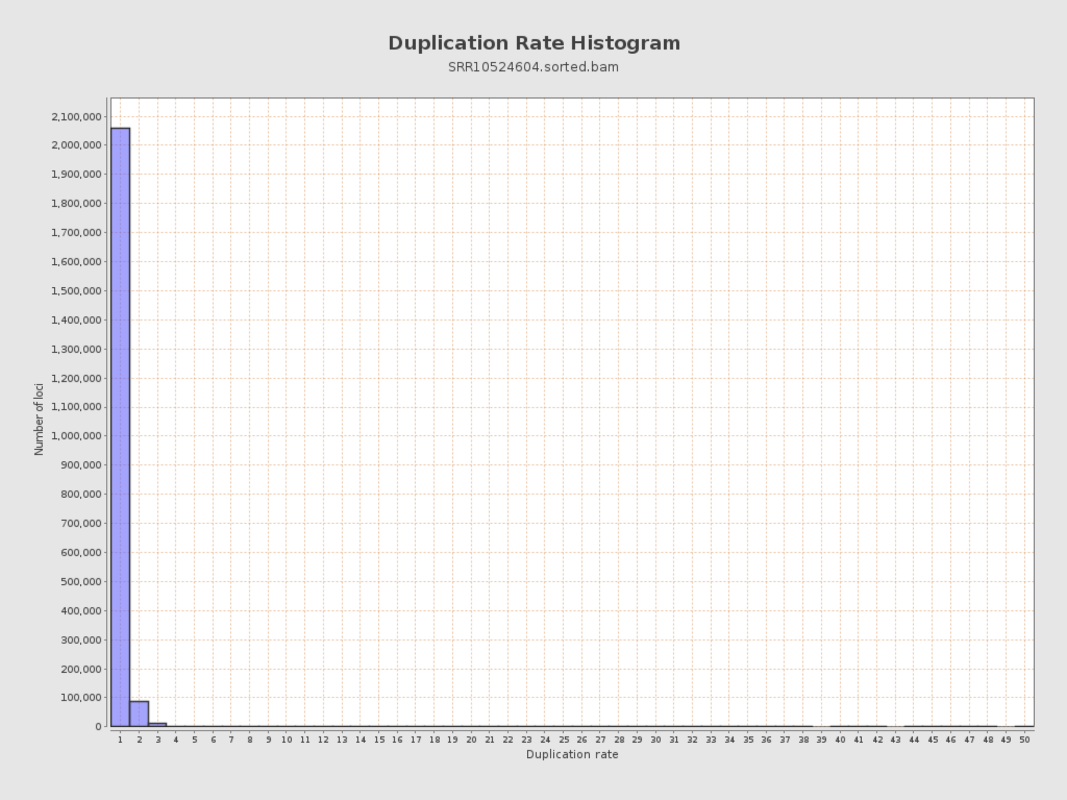
5. Results : Coverage Histogram (0-50X)



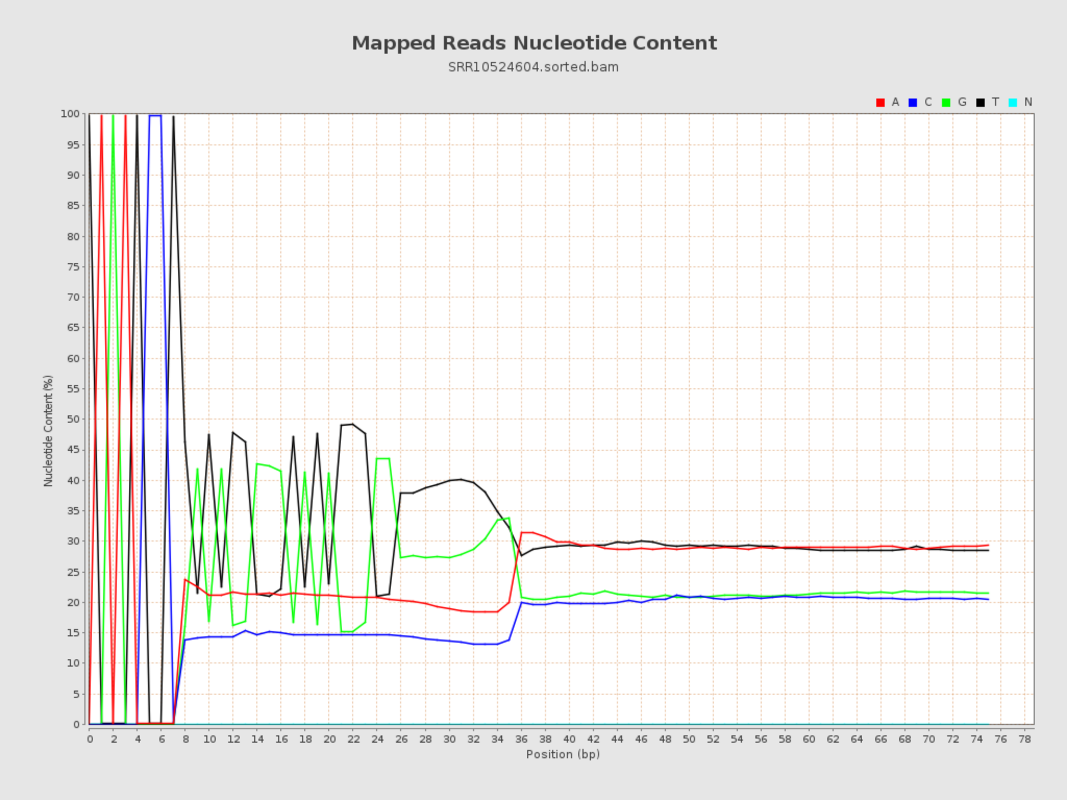
6. Results : Genome Fraction Coverage



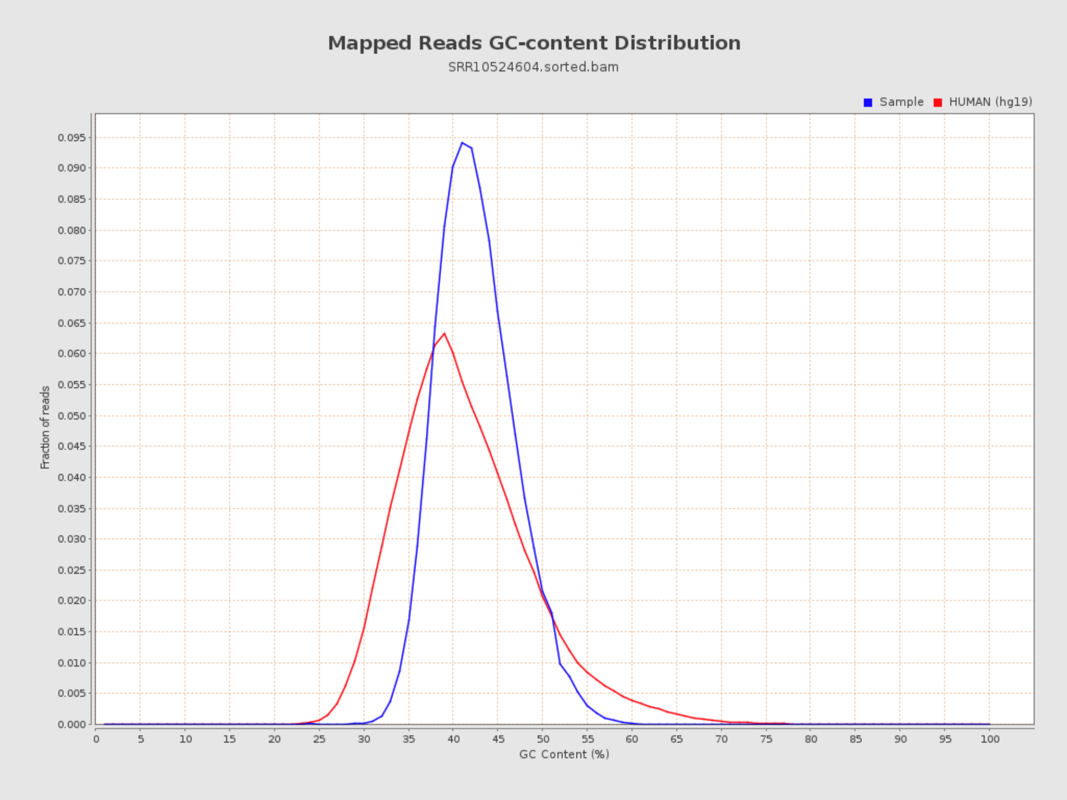
7. Results : Duplication Rate Histogram



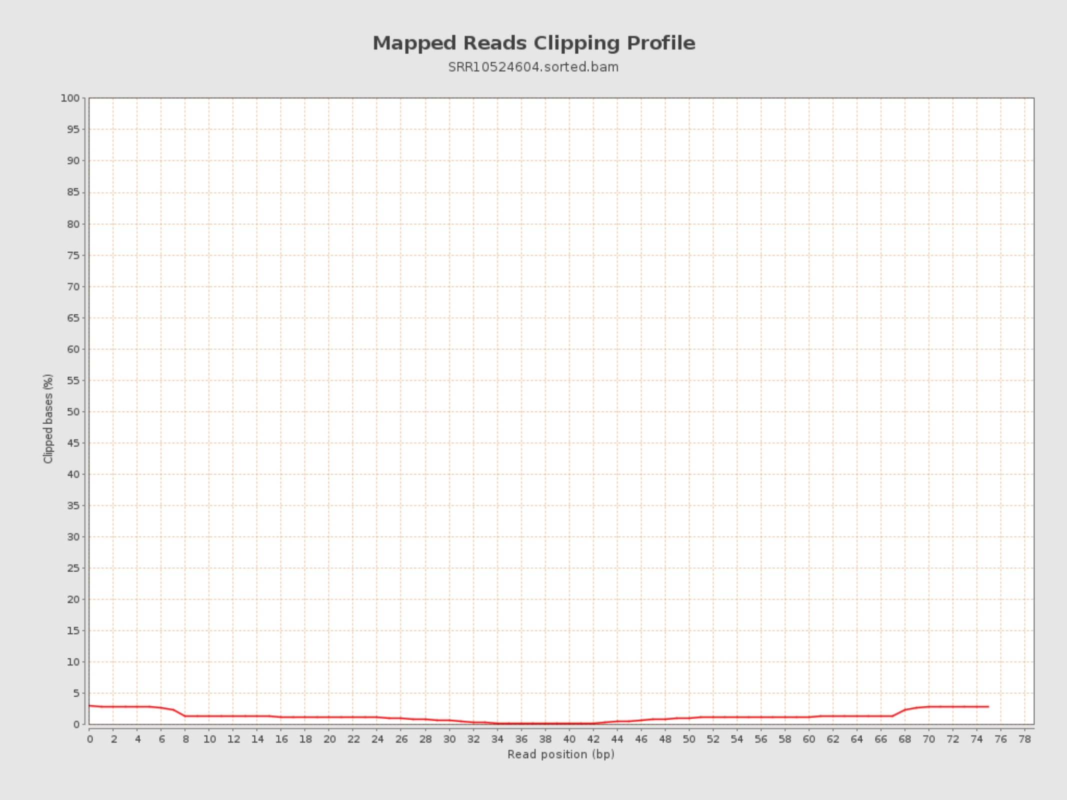
8. Results : Mapped Reads Nucleotide Content



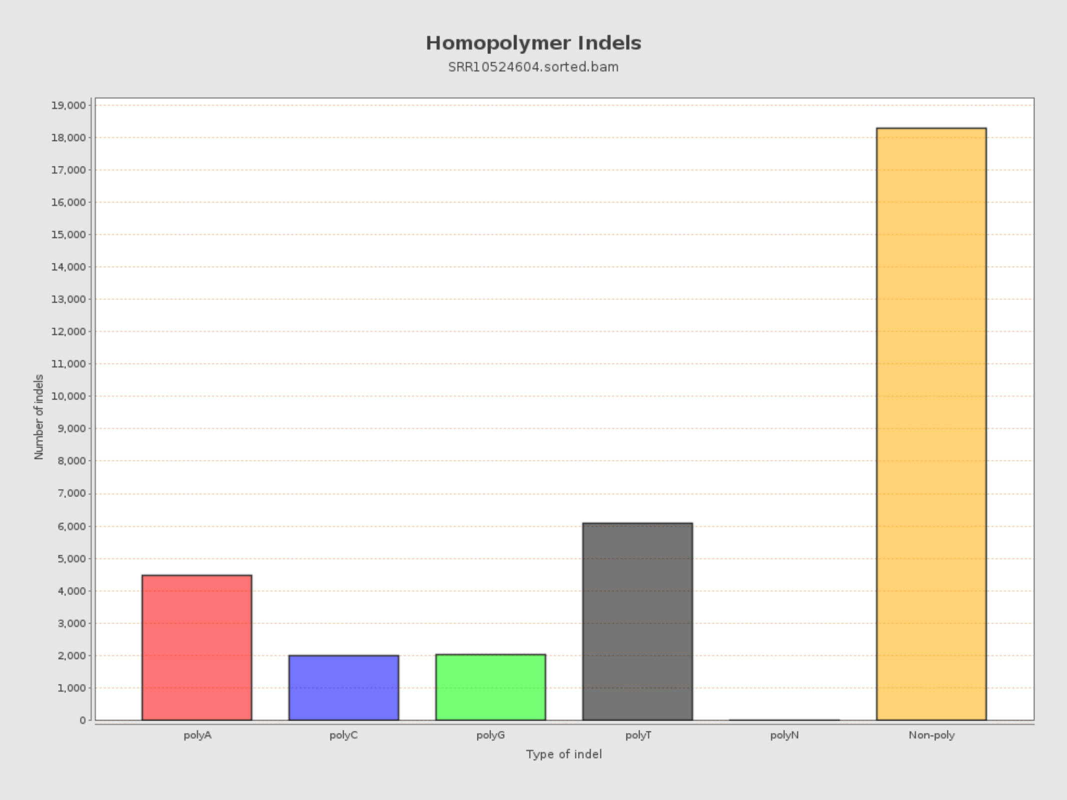
9. Results : Mapped Reads GC-content Distribution



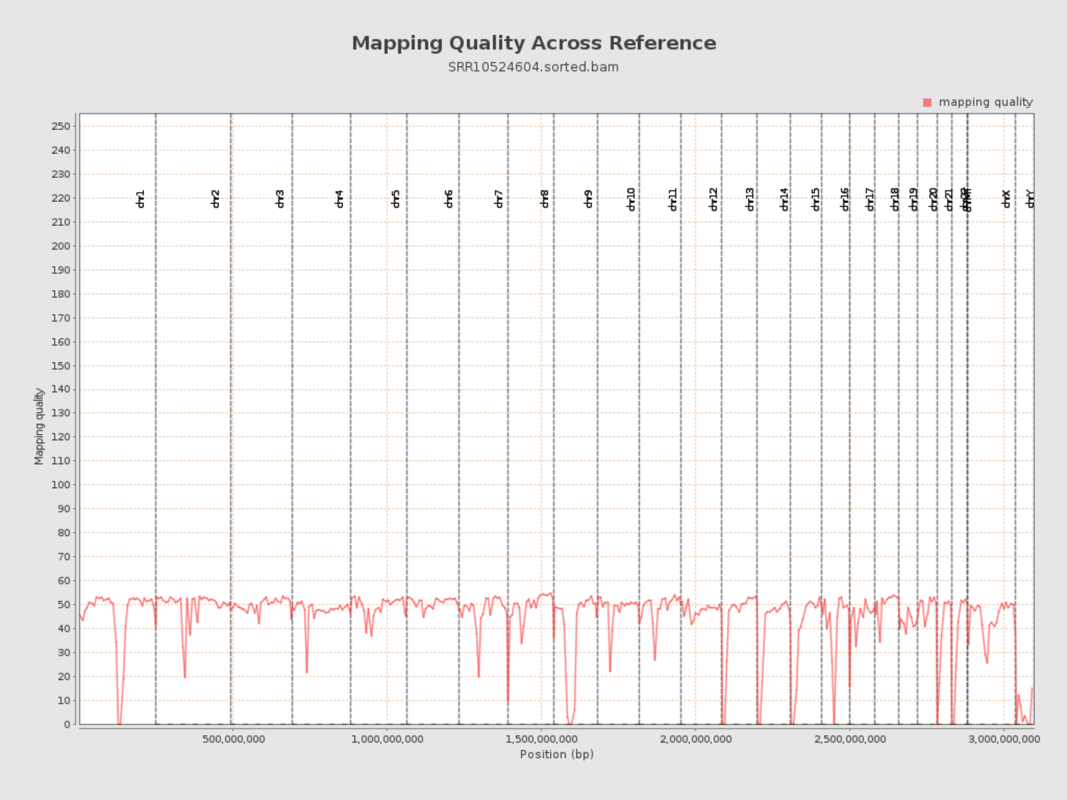
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram