Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 16:05:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524677.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_SRR10524677 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524677.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 16:05:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524677.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,198,336
Mapped reads	2,036,864 / 92.65%
Unmapped reads	161,472 / 7.35%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,674 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	97,582 / 4.44%
Duplication rate	3.57%
Clipped reads	2,041,748 / 92.88%

2.2. ACGT Content

Number/percentage of A's	30,055,242 / 25.04%
Number/percentage of C's	22,467,945 / 18.72%
Number/percentage of T's	38,382,069 / 31.98%
Number/percentage of G's	29,093,881 / 24.24%
Number/percentage of N's	16,906 / 0.01%
GC Percentage	42.96%

2.3. Coverage

Mean	0.0388

Standard Deviation	0.3479

2.4. Mapping Quality

Mean Mapping Quality	45.67

2.5. Mismatches and indels

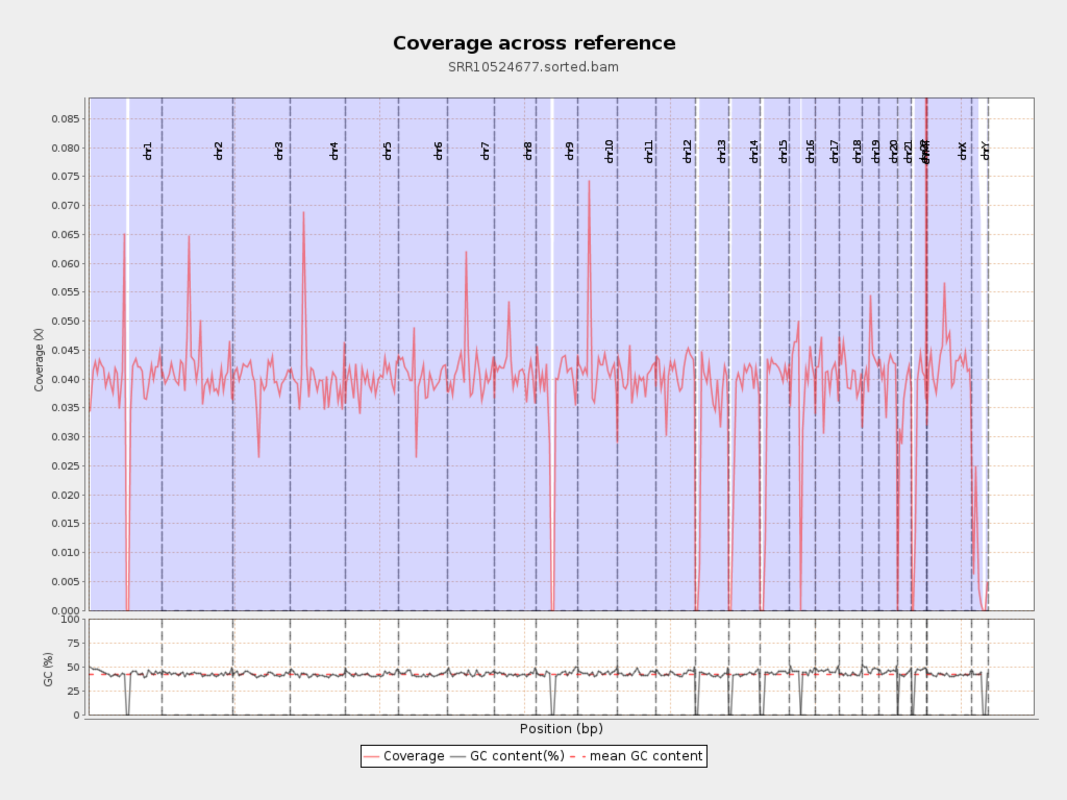
General error rate	0.51%
Mismatches	600,268
Insertions	7,990
Mapped reads with at least one insertion	0.39%
Deletions	22,952
Mapped reads with at least one deletion	1.12%
Homopolymer indels	43.08%

2.6. Chromosome stats

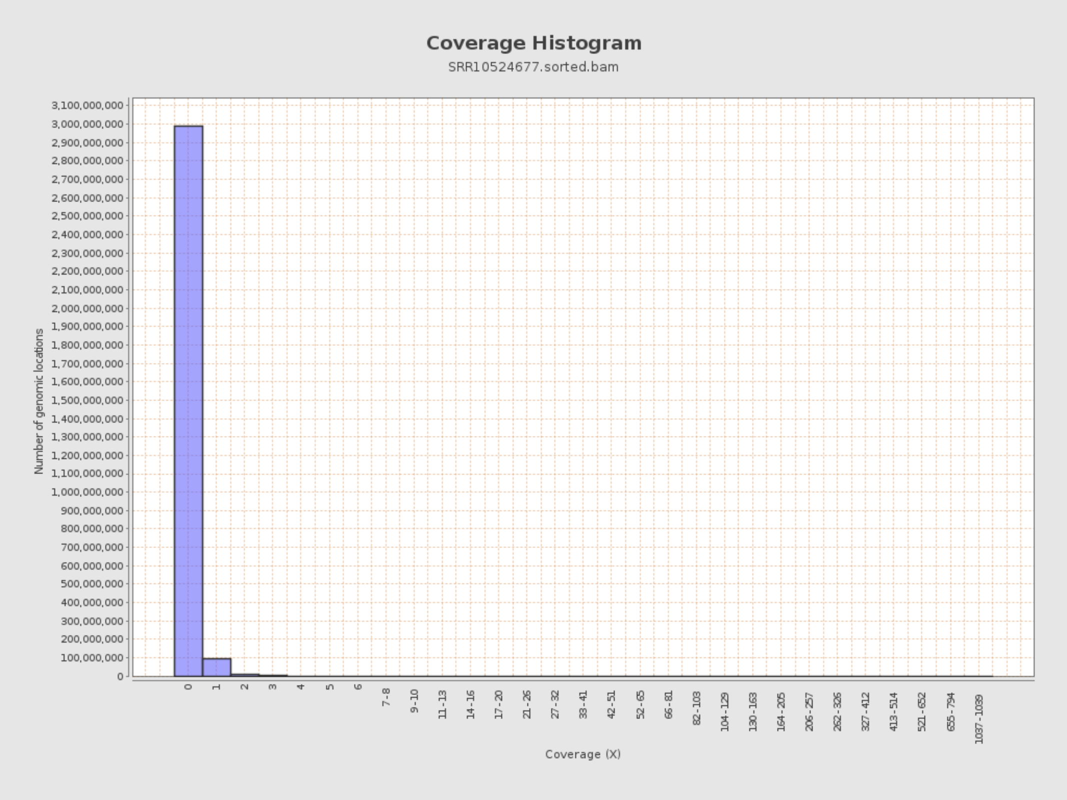
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9645377	0.0387	0.611
chr2	243199373	10125595	0.0416	0.5039
chr3	198022430	7900040	0.0399	0.2231
chr4	191154276	7727964	0.0404	0.2657
chr5	180915260	7224899	0.0399	0.225
chr6	171115067	6892477	0.0403	0.2549
chr7	159138663	6609449	0.0415	0.4118

chr8	146364022	6080692	0.0415	0.3635
chr9	141213431	5049992	0.0358	0.2867
chr10	135534747	5825957	0.043	0.3624
chr11	135006516	5415120	0.0401	0.3071
chr12	133851895	5513813	0.0412	0.2299
chr13	115169878	3766985	0.0327	0.2073
chr14	107349540	3604942	0.0336	0.2167
chr15	102531392	3459293	0.0337	0.209
chr16	90354753	3497940	0.0387	0.2435
chr17	81195210	3281384	0.0404	0.2456
chr18	78077248	3207925	0.0411	0.5319
chr19	59128983	2536065	0.0429	0.4594
chr20	63025520	2576511	0.0409	0.2317
chr21	48129895	1580707	0.0328	0.2392
chr22	51304566	1459674	0.0285	0.1885
chrMT	16571	8165	0.4927	0.7308
chrX	155270560	6665643	0.0429	0.2565
chrY	59373566	396074	0.0067	0.2268

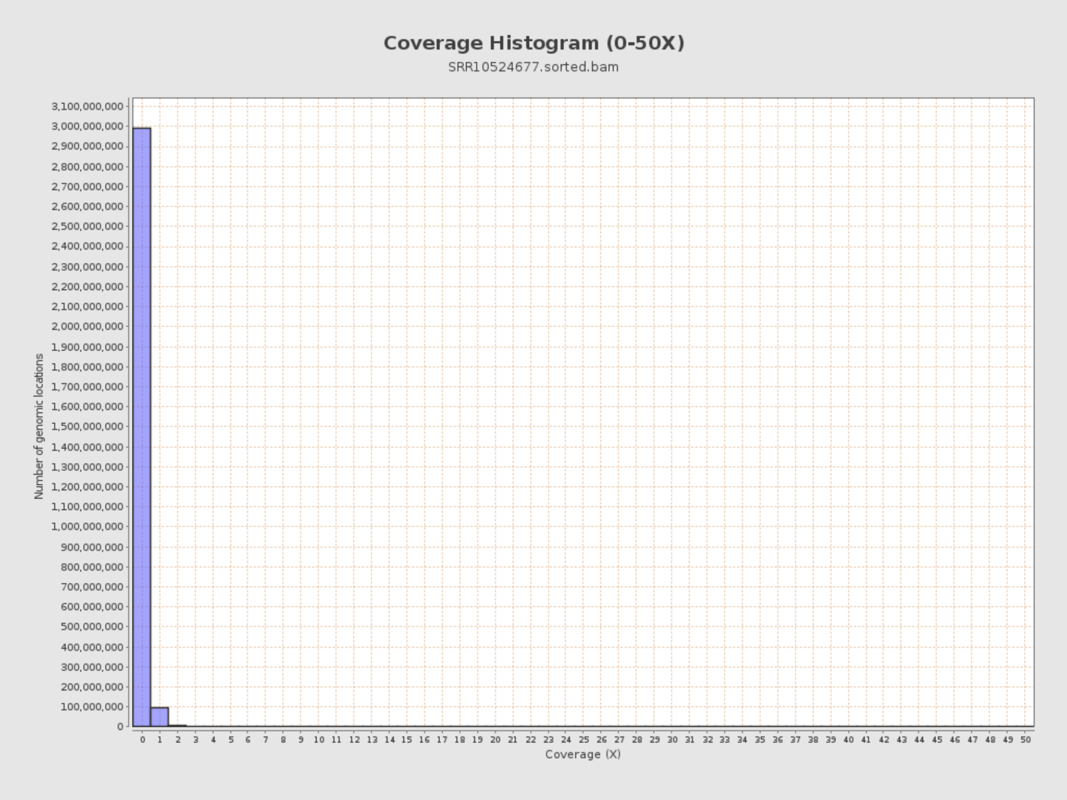
3. Results : Coverage across reference



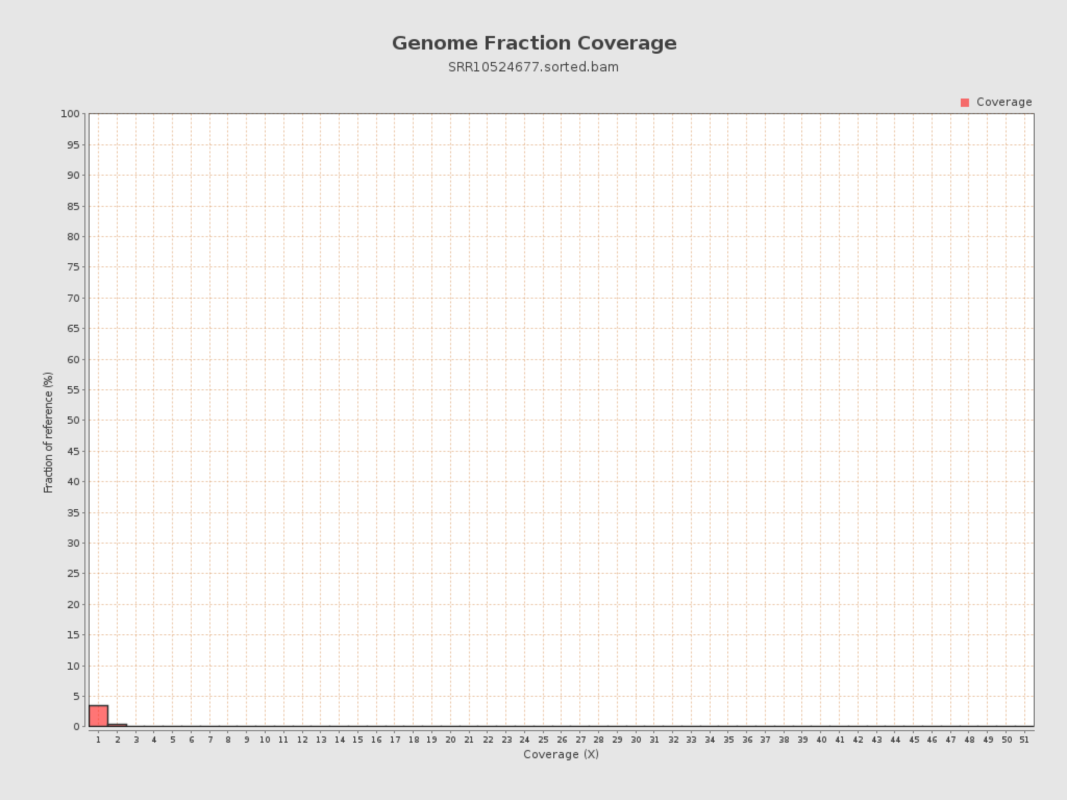
4. Results : Coverage Histogram



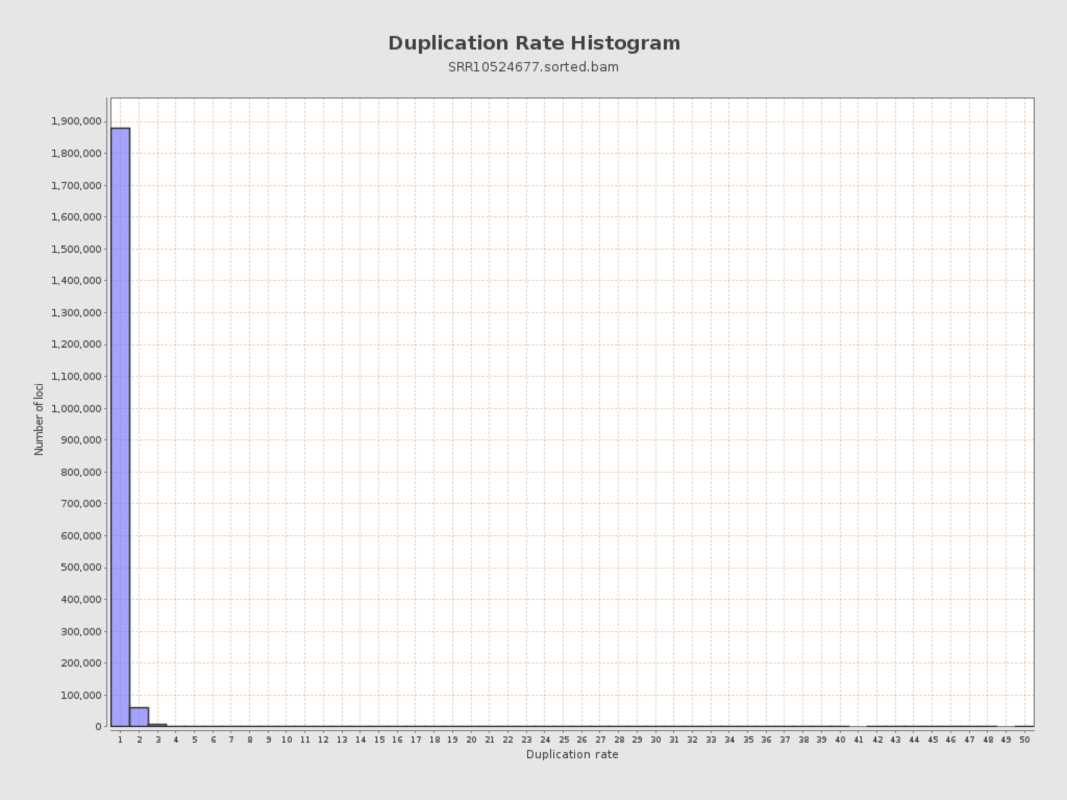
5. Results : Coverage Histogram (0-50X)



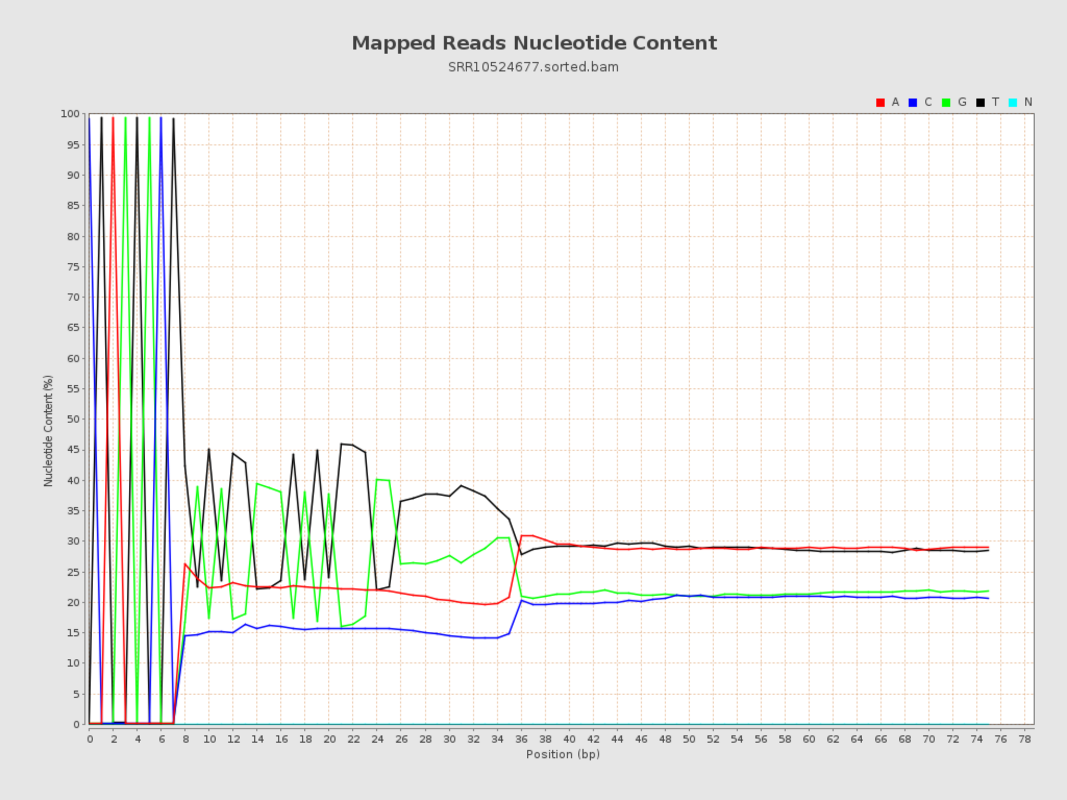
6. Results : Genome Fraction Coverage



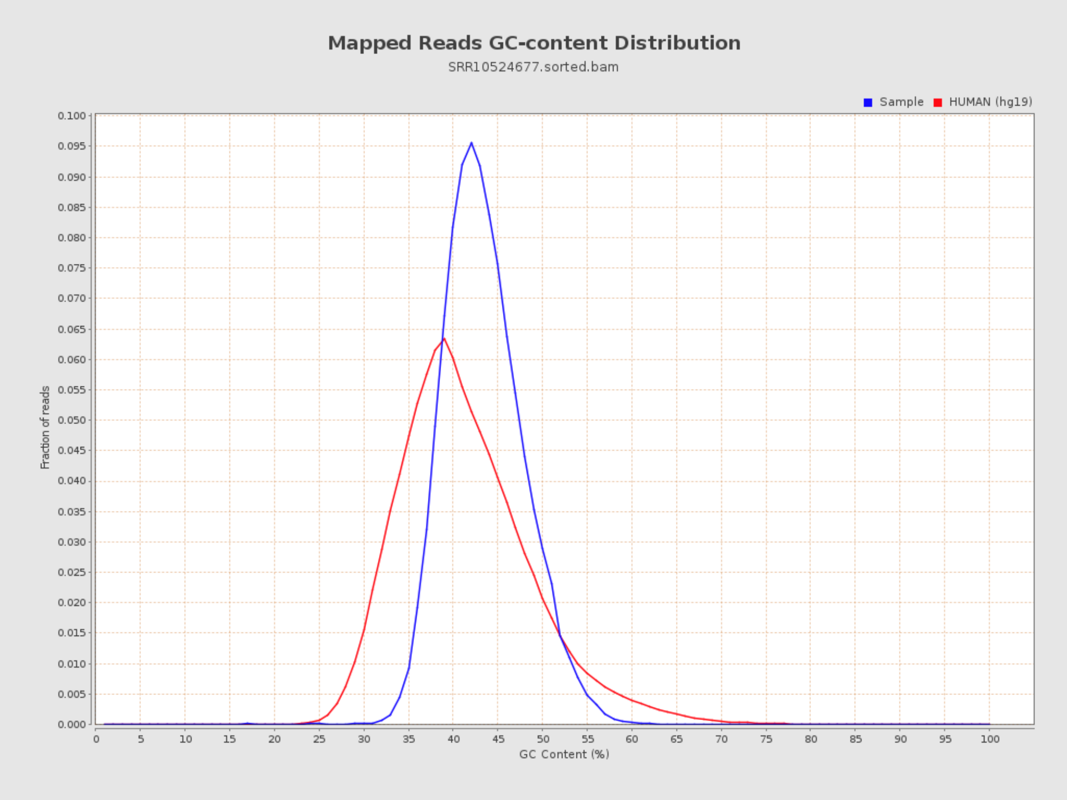
7. Results : Duplication Rate Histogram



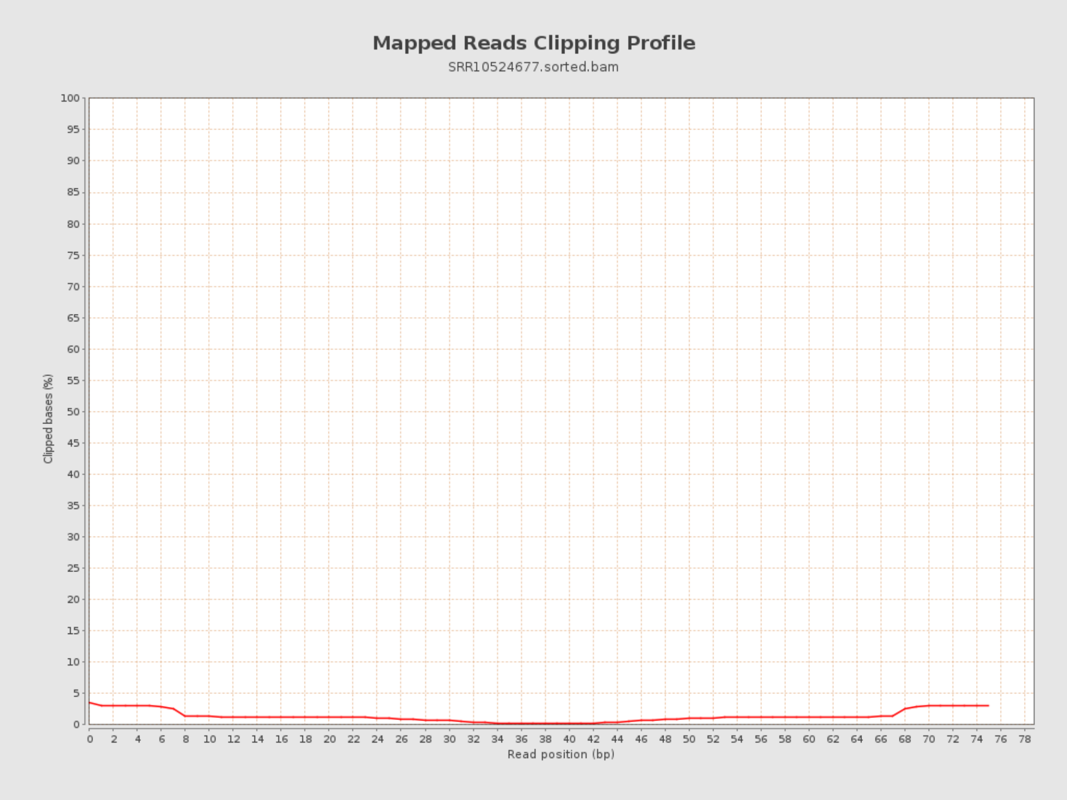
8. Results : Mapped Reads Nucleotide Content



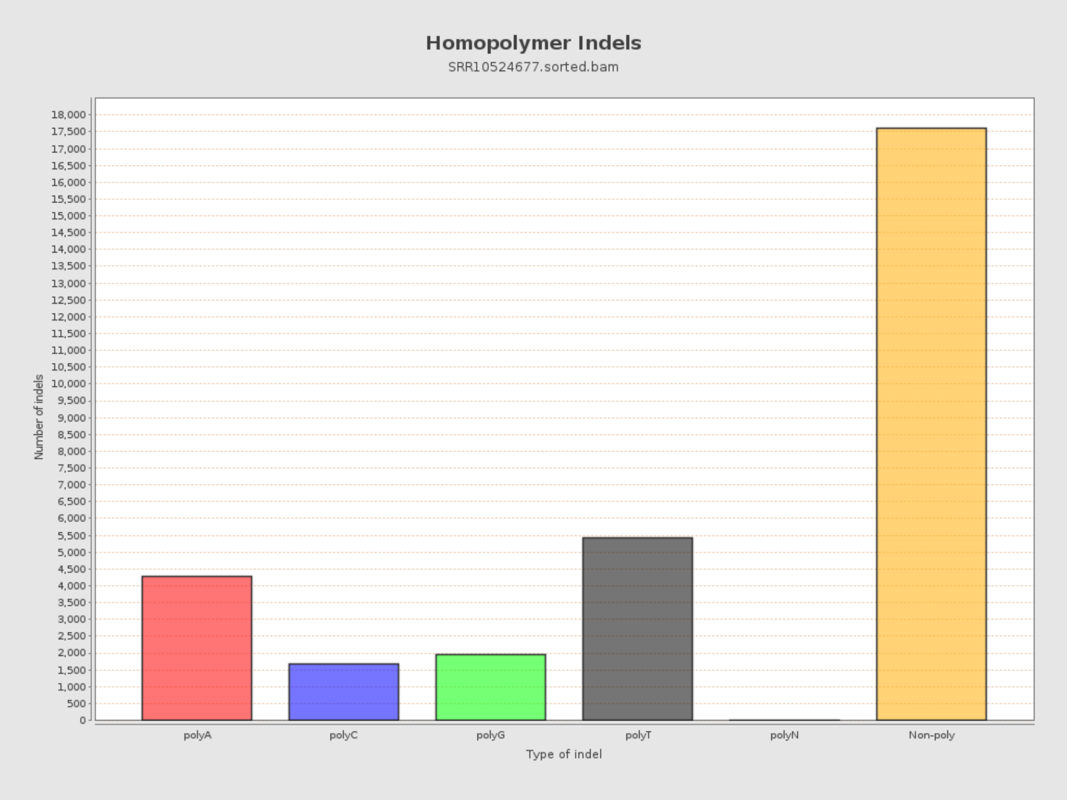
9. Results : Mapped Reads GC-content Distribution



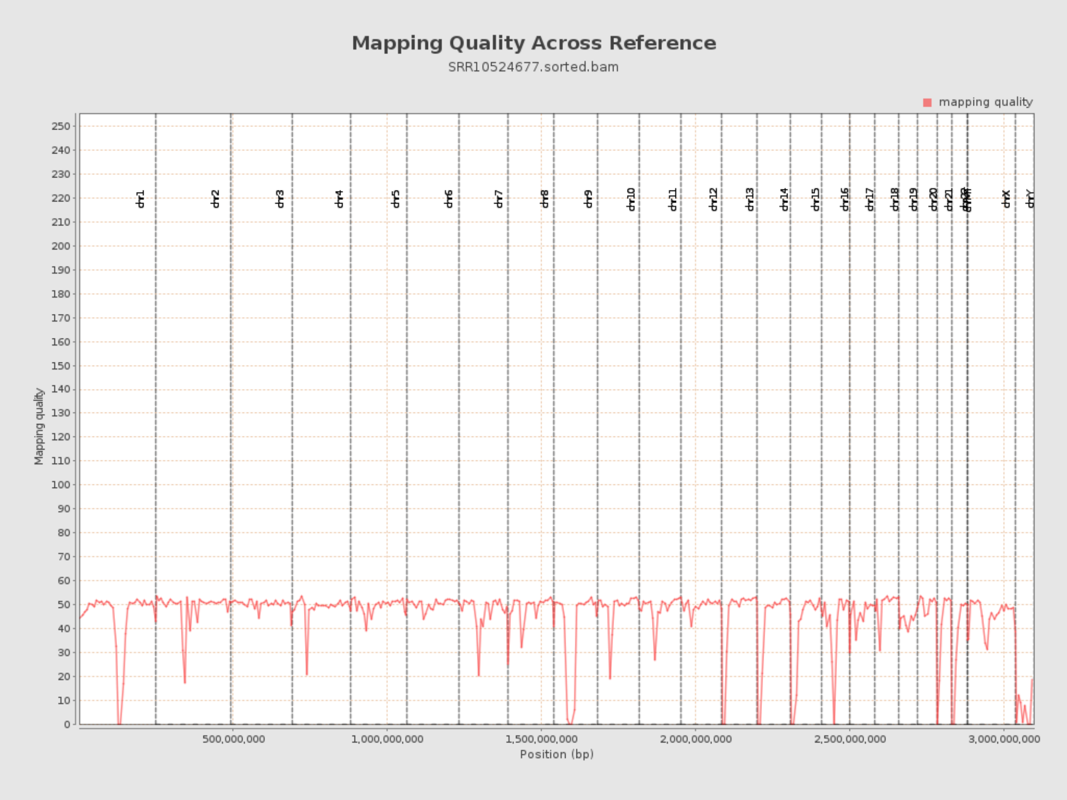
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram