Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 08:47:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524942.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_SRR10524942 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524942.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 08:47:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524942.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,435,421
Mapped reads	1,331,470 / 92.76%
Unmapped reads	103,951 / 7.24%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,350 / 0.23%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	39,016 / 2.72%
Duplication rate	2.06%
Clipped reads	1,330,973 / 92.72%

2.2. ACGT Content

Number/percentage of A's	19,518,436 / 25.1%
Number/percentage of C's	14,312,034 / 18.41%
Number/percentage of T's	24,866,947 / 31.98%
Number/percentage of G's	19,052,486 / 24.5%
Number/percentage of N's	911 / 0%
GC Percentage	42.91%

2.3. Coverage

Mean	0.0251

Standard Deviation	0.2425

2.4. Mapping Quality

Mean Mapping Quality	44.71

2.5. Mismatches and indels

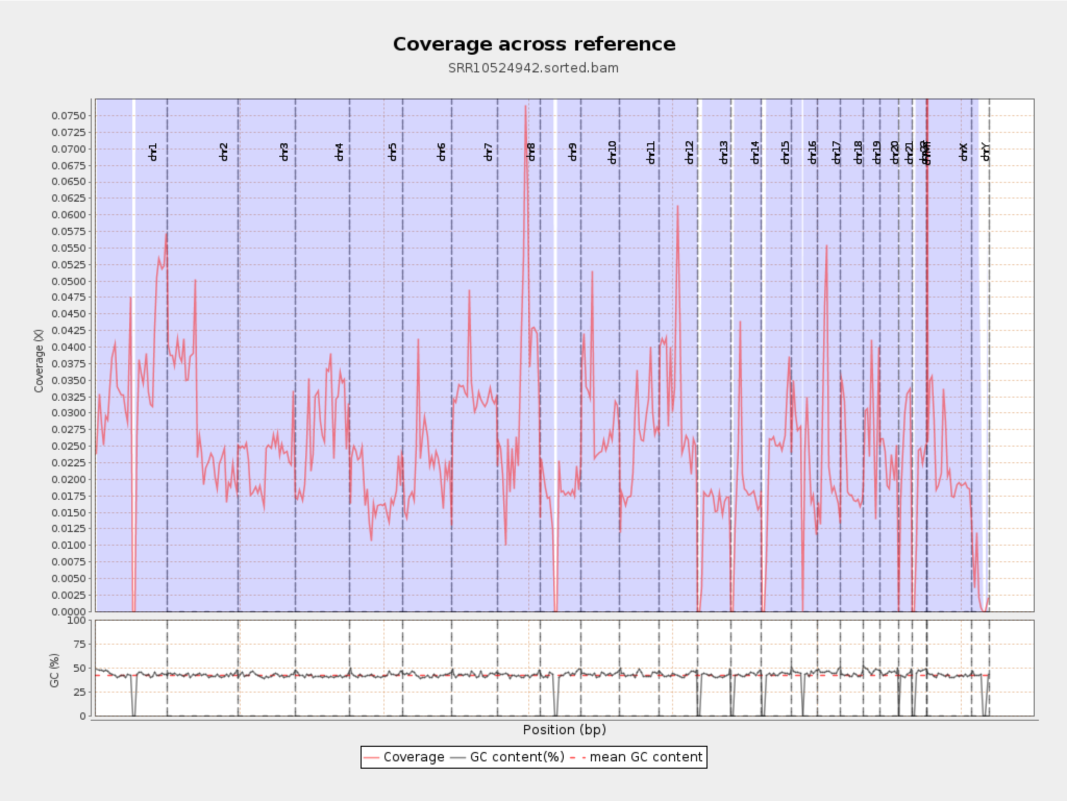
General error rate	0.5%
Mismatches	376,397
Insertions	5,965
Mapped reads with at least one insertion	0.45%
Deletions	14,656
Mapped reads with at least one deletion	1.09%
Homopolymer indels	40.94%

2.6. Chromosome stats

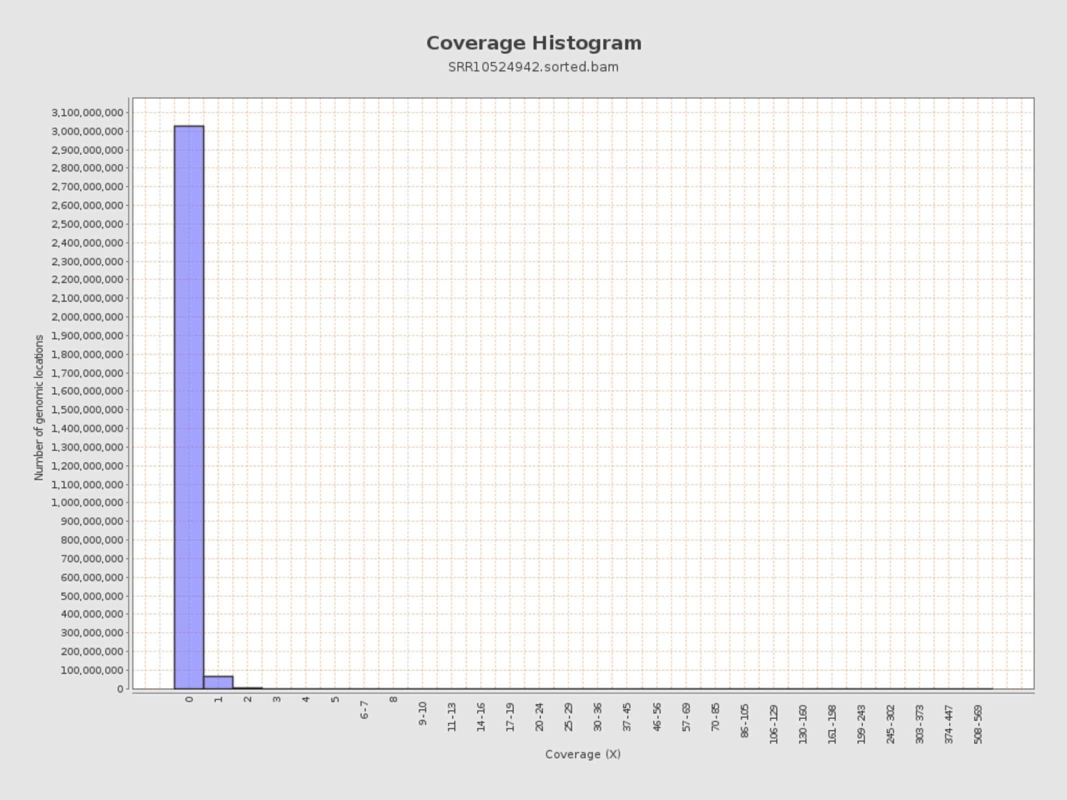
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8598095	0.0345	0.4512
chr2	243199373	7010218	0.0288	0.2754
chr3	198022430	4572504	0.0231	0.1633
chr4	191154276	5396934	0.0282	0.1914
chr5	180915260	3317939	0.0183	0.1483
chr6	171115067	3802108	0.0222	0.2329
chr7	159138663	5274304	0.0331	0.3339

chr8	146364022	5009350	0.0342	0.2482
chr9	141213431	2343739	0.0166	0.1914
chr10	135534747	4101475	0.0303	0.2475
chr11	135006516	3454666	0.0256	0.2206
chr12	133851895	4488339	0.0335	0.1972
chr13	115169878	1626121	0.0141	0.129
chr14	107349540	1882522	0.0175	0.1454
chr15	102531392	2302793	0.0225	0.1694
chr16	90354753	2032214	0.0225	0.1689
chr17	81195210	2016687	0.0248	0.2108
chr18	78077248	1644974	0.0211	0.3046
chr19	59128983	1723676	0.0292	0.2802
chr20	63025520	1404249	0.0223	0.1616
chr21	48129895	1169023	0.0243	0.1718
chr22	51304566	875397	0.0171	0.1392
chrMT	16571	8305	0.5012	0.7927
chrX	155270560	3513571	0.0226	0.1859
chrY	59373566	206677	0.0035	0.0961

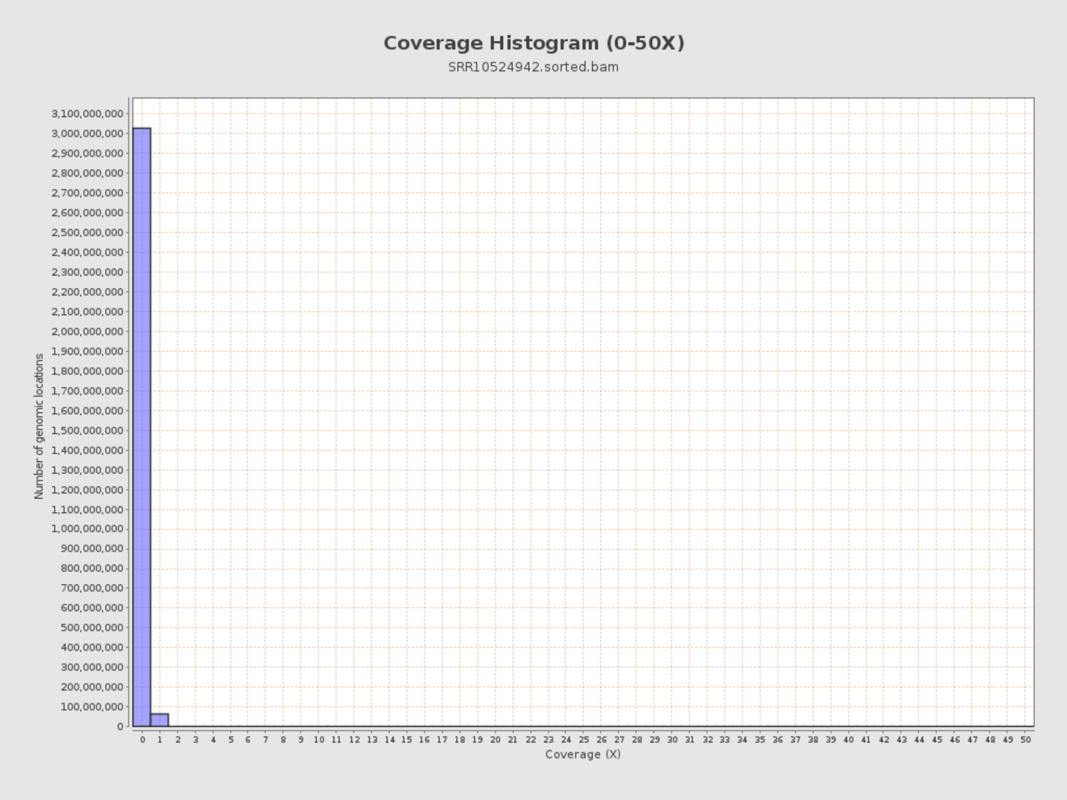
3. Results : Coverage across reference



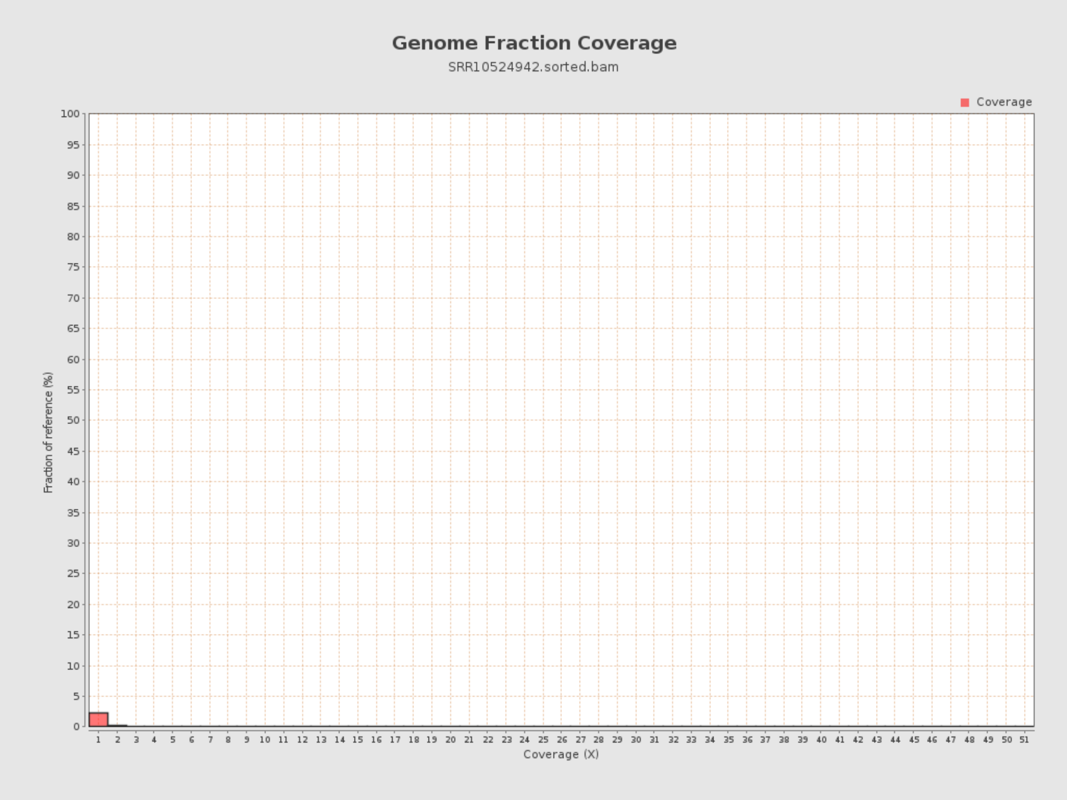
4. Results : Coverage Histogram



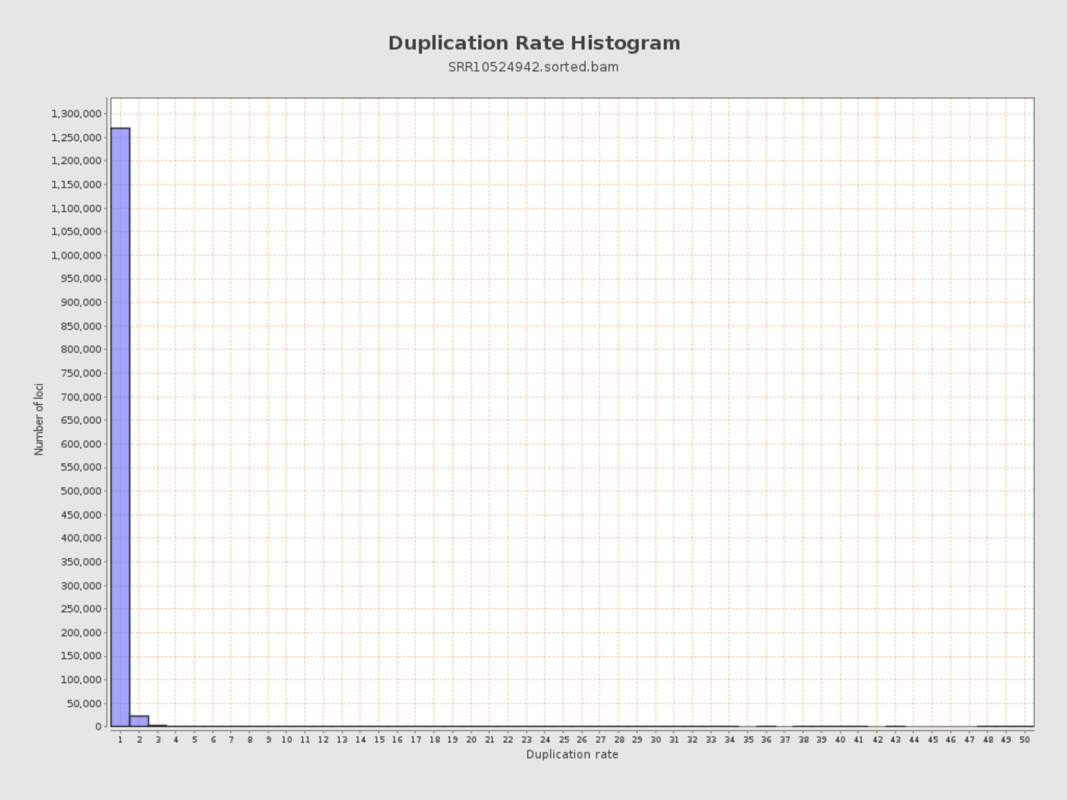
5. Results : Coverage Histogram (0-50X)



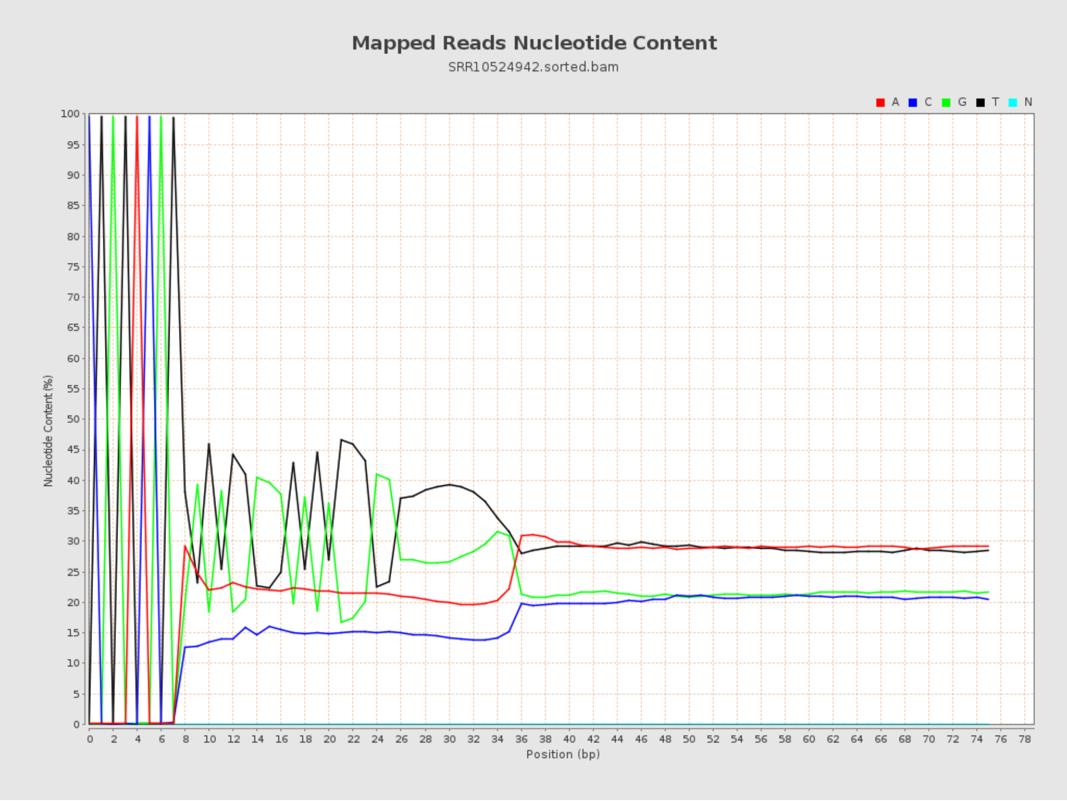
6. Results : Genome Fraction Coverage



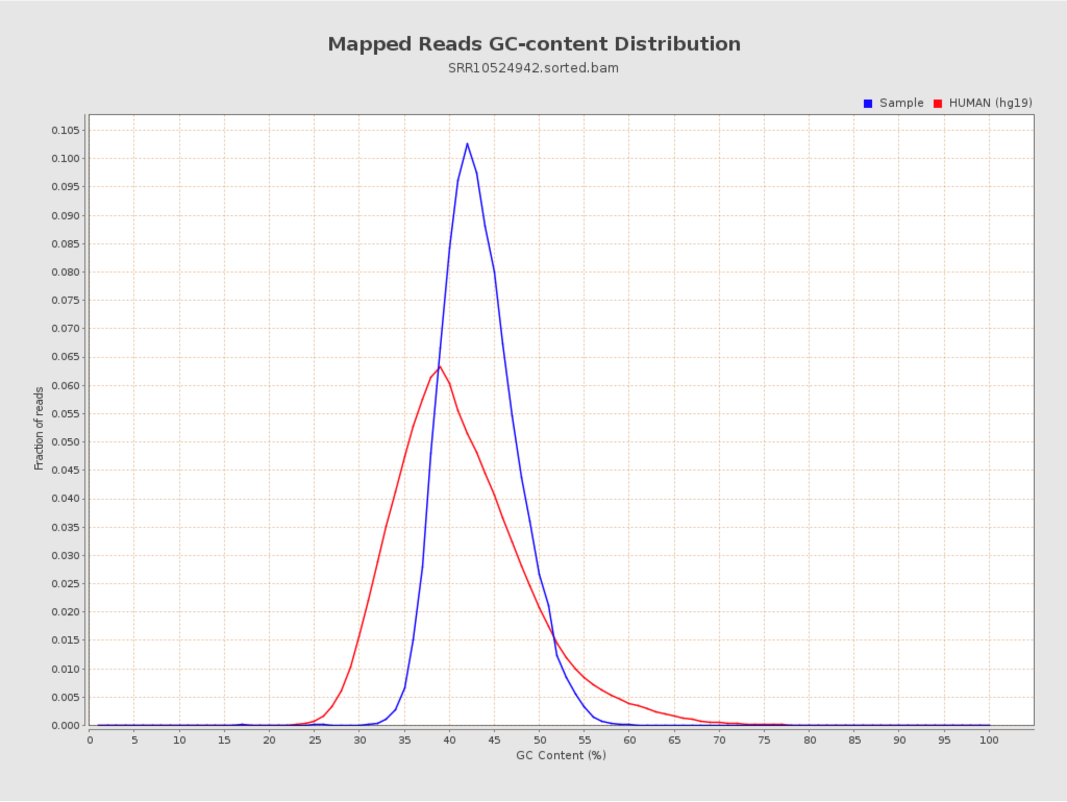
7. Results : Duplication Rate Histogram



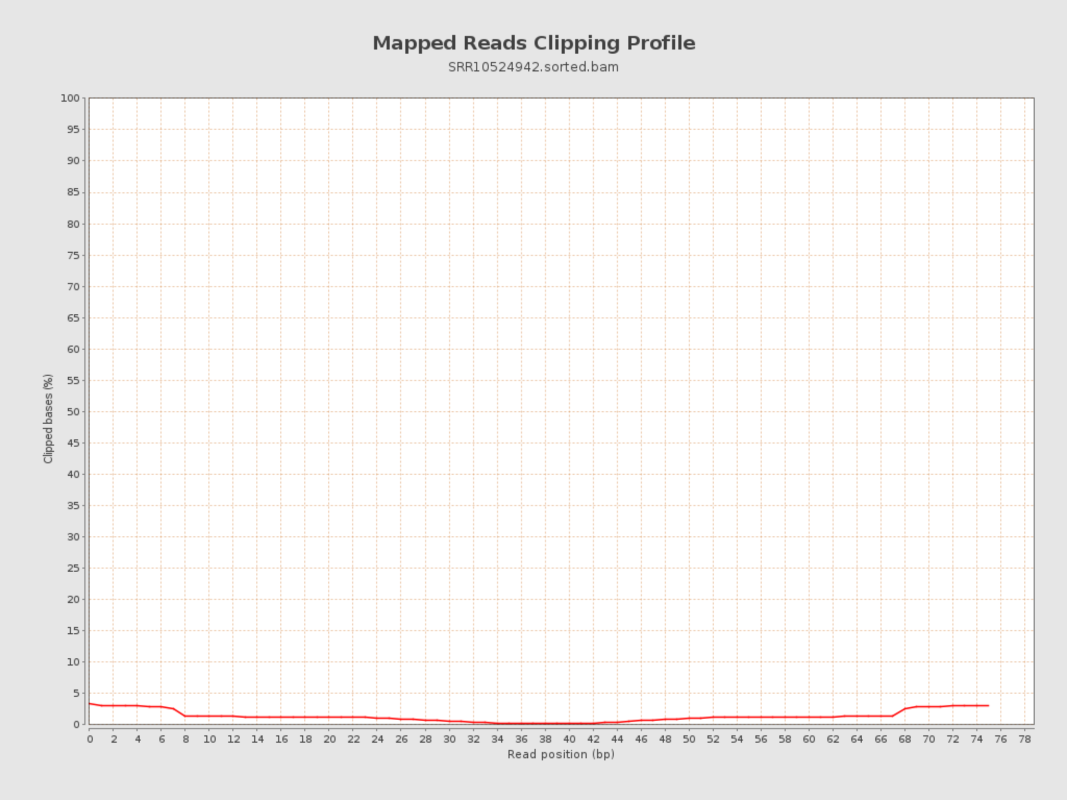
8. Results : Mapped Reads Nucleotide Content



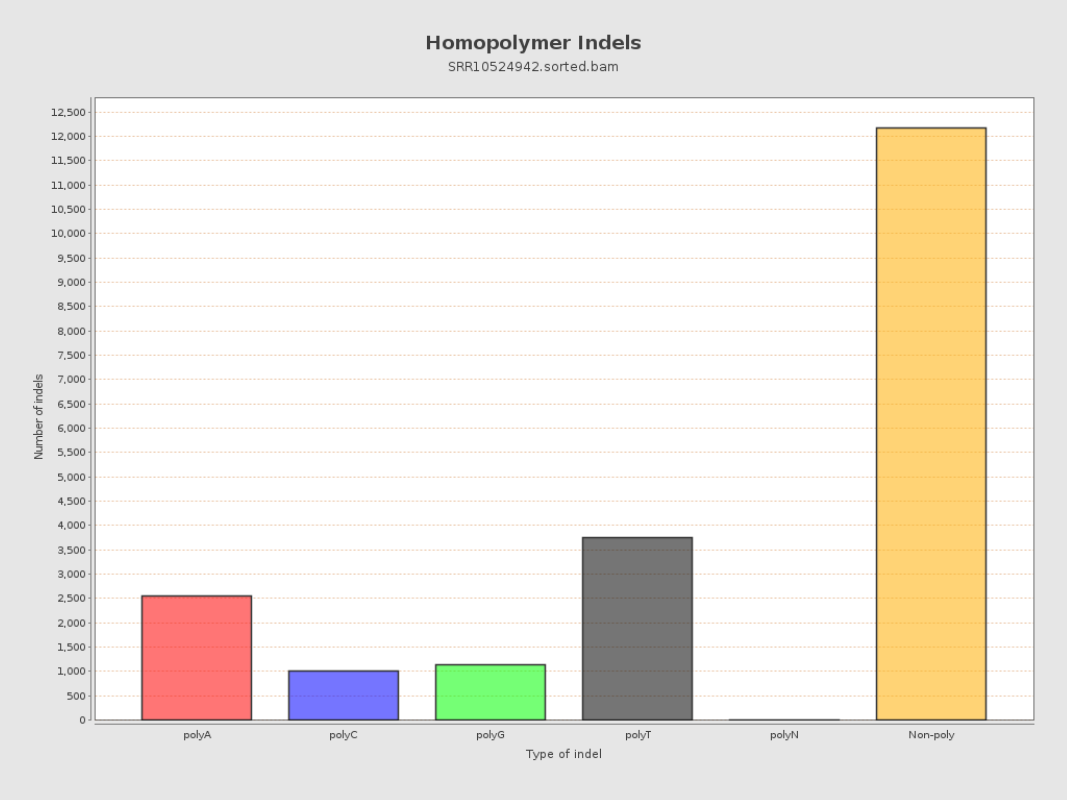
9. Results : Mapped Reads GC-content Distribution



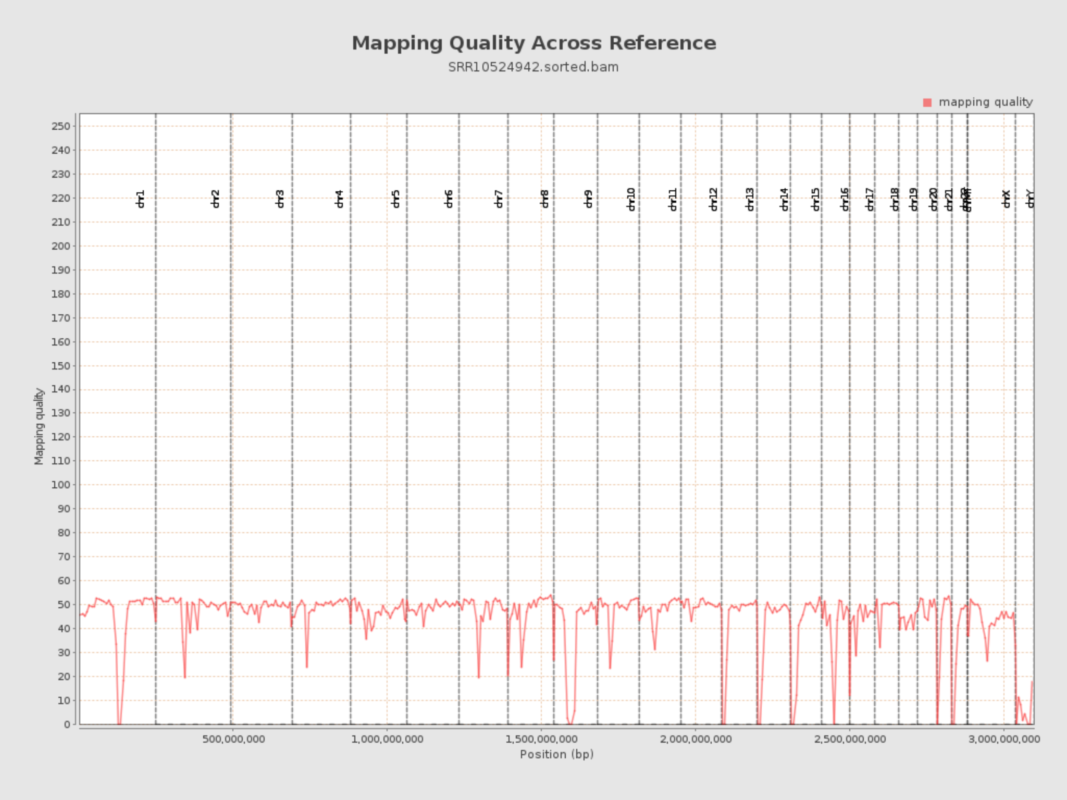
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram