Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 22:47:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524842.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_SRR10524842 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524842.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 22:47:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524842.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,891,140
Mapped reads	1,746,434 / 92.35%
Unmapped reads	144,706 / 7.65%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,414 / 0.44%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	58,289 / 3.08%
Duplication rate	2.25%
Clipped reads	1,751,277 / 92.6%

2.2. ACGT Content

Number/percentage of A's	26,250,092 / 25.67%
Number/percentage of C's	19,503,625 / 19.07%
Number/percentage of T's	32,343,828 / 31.63%
Number/percentage of G's	24,161,372 / 23.62%
Number/percentage of N's	13,837 / 0.01%
GC Percentage	42.69%

2.3. Coverage

Mean	0.033

Standard Deviation	0.3315

2.4. Mapping Quality

Mean Mapping Quality	45.14

2.5. Mismatches and indels

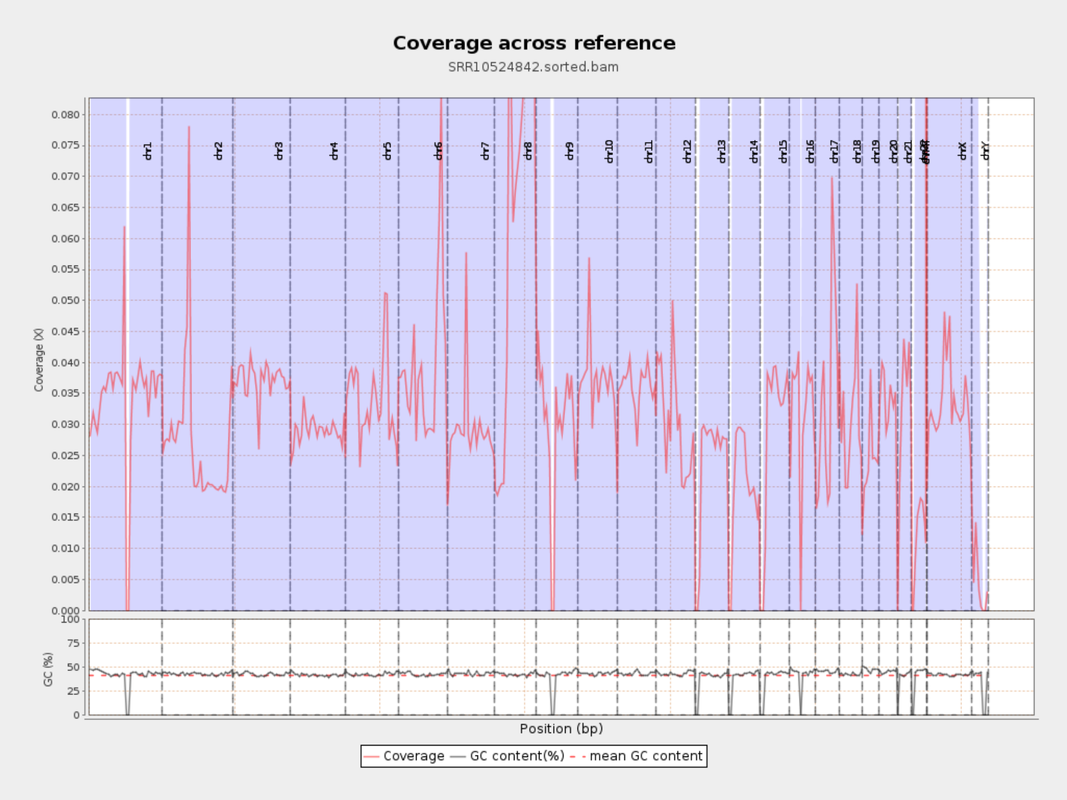
General error rate	0.49%
Mismatches	488,710
Insertions	6,706
Mapped reads with at least one insertion	0.38%
Deletions	19,050
Mapped reads with at least one deletion	1.08%
Homopolymer indels	44.36%

2.6. Chromosome stats

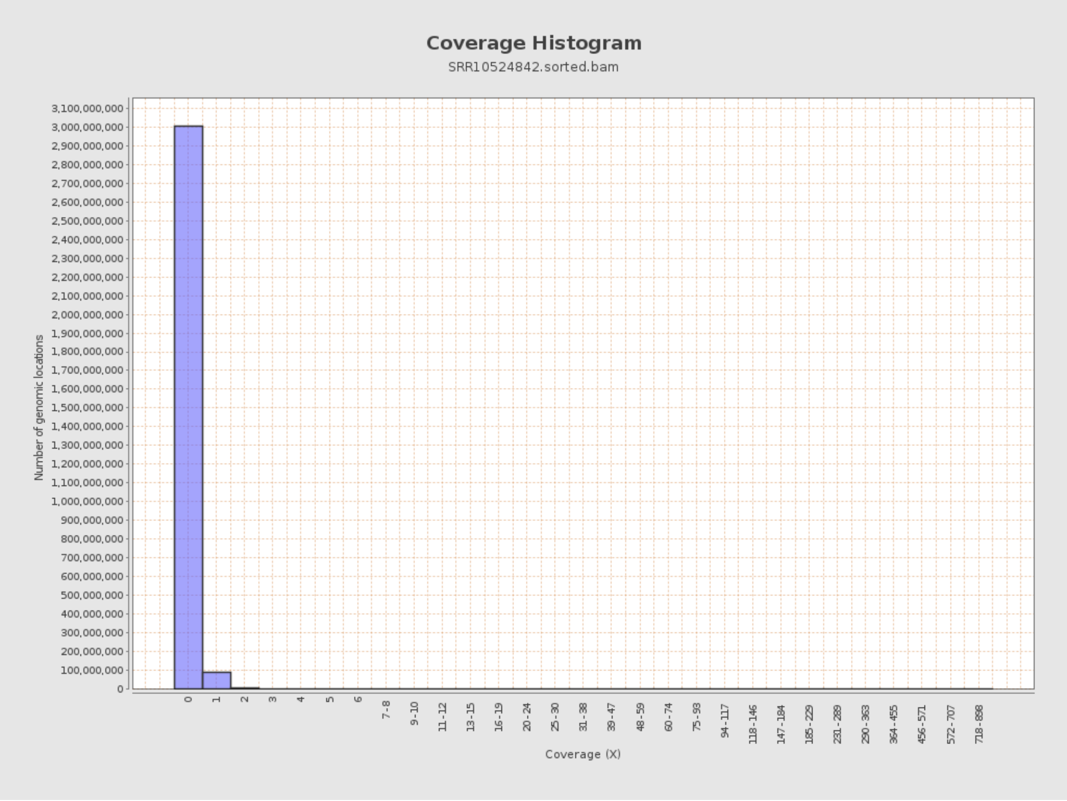
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8507773	0.0341	0.6559
chr2	243199373	6599549	0.0271	0.3233
chr3	198022430	7356784	0.0372	0.2077
chr4	191154276	5539358	0.029	0.194
chr5	180915260	6227276	0.0344	0.2023
chr6	171115067	6731779	0.0393	0.2389
chr7	159138663	4699867	0.0295	0.4514

chr8	146364022	11029784	0.0754	0.4315
chr9	141213431	4167005	0.0295	0.2691
chr10	135534747	5066499	0.0374	0.2926
chr11	135006516	4843543	0.0359	0.285
chr12	133851895	4063214	0.0304	0.1935
chr13	115169878	2698295	0.0234	0.1681
chr14	107349540	2124817	0.0198	0.1653
chr15	102531392	2993345	0.0292	0.1848
chr16	90354753	2894353	0.032	0.2095
chr17	81195210	2715519	0.0334	0.2313
chr18	78077248	2470404	0.0316	0.4892
chr19	59128983	1446916	0.0245	0.4309
chr20	63025520	2135715	0.0339	0.202
chr21	48129895	1529105	0.0318	0.2052
chr22	51304566	588376	0.0115	0.114
chrMT	16571	432782	26.1168	14.6354
chrX	155270560	5186644	0.0334	0.2307
chrY	59373566	253912	0.0043	0.1033

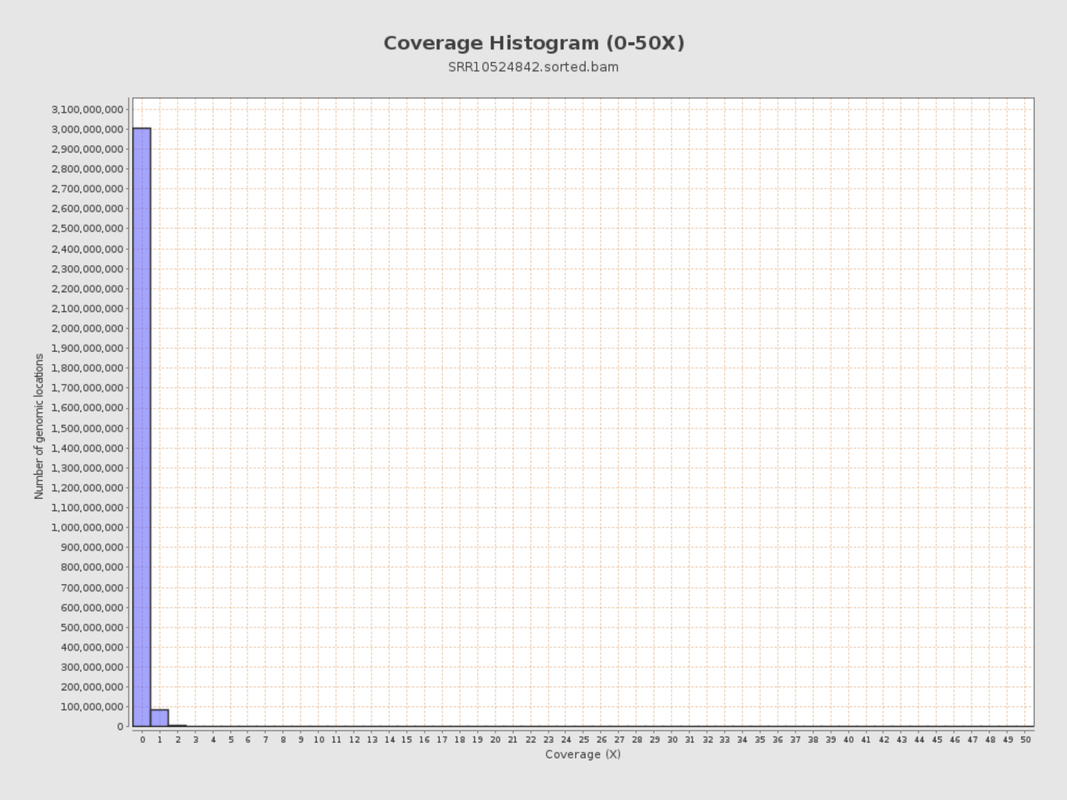
3. Results : Coverage across reference



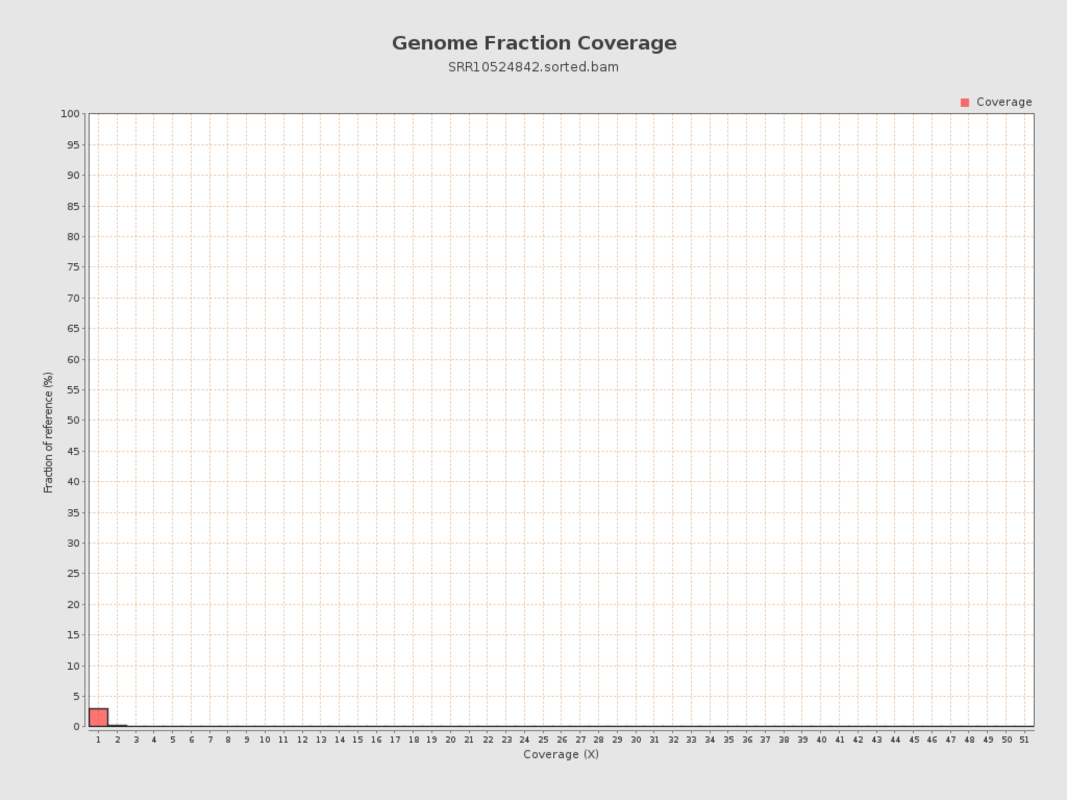
4. Results : Coverage Histogram



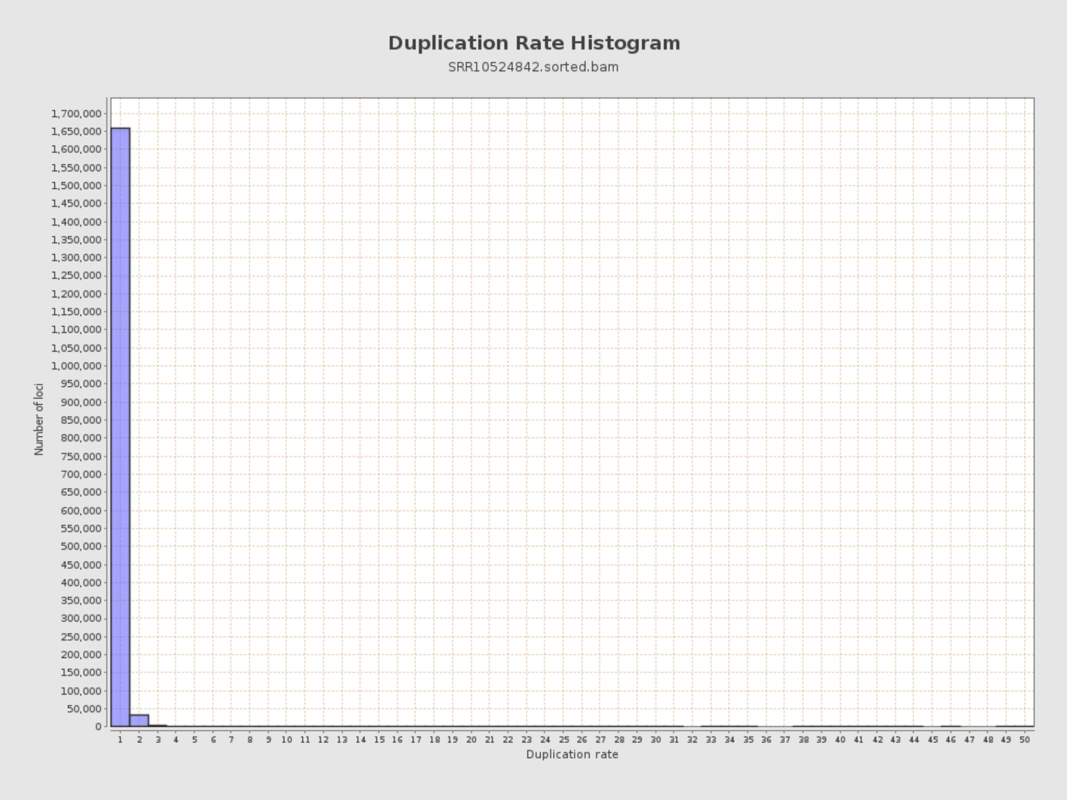
5. Results : Coverage Histogram (0-50X)



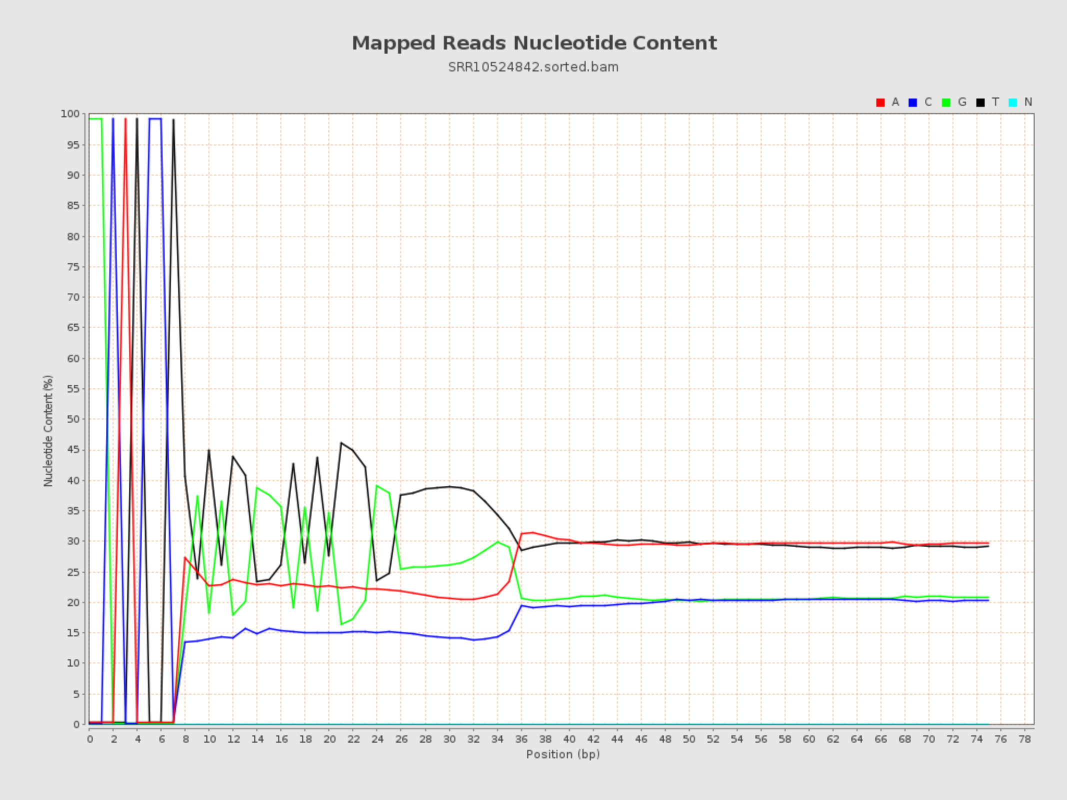
6. Results : Genome Fraction Coverage



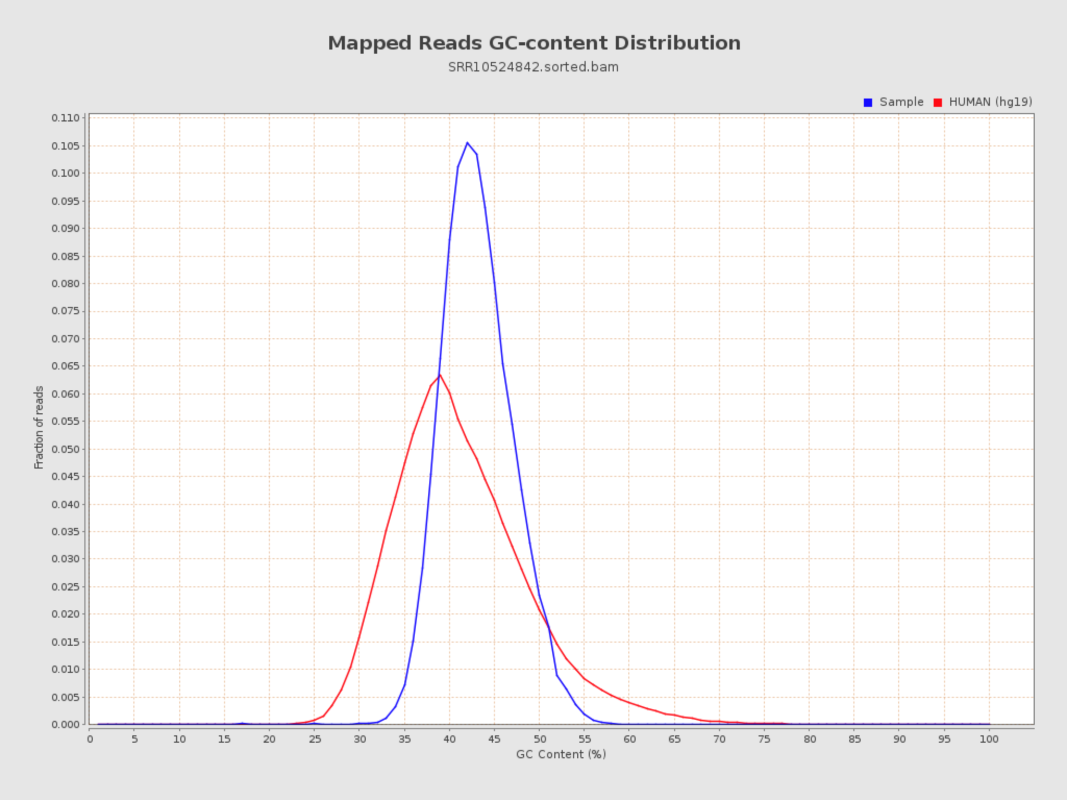
7. Results : Duplication Rate Histogram



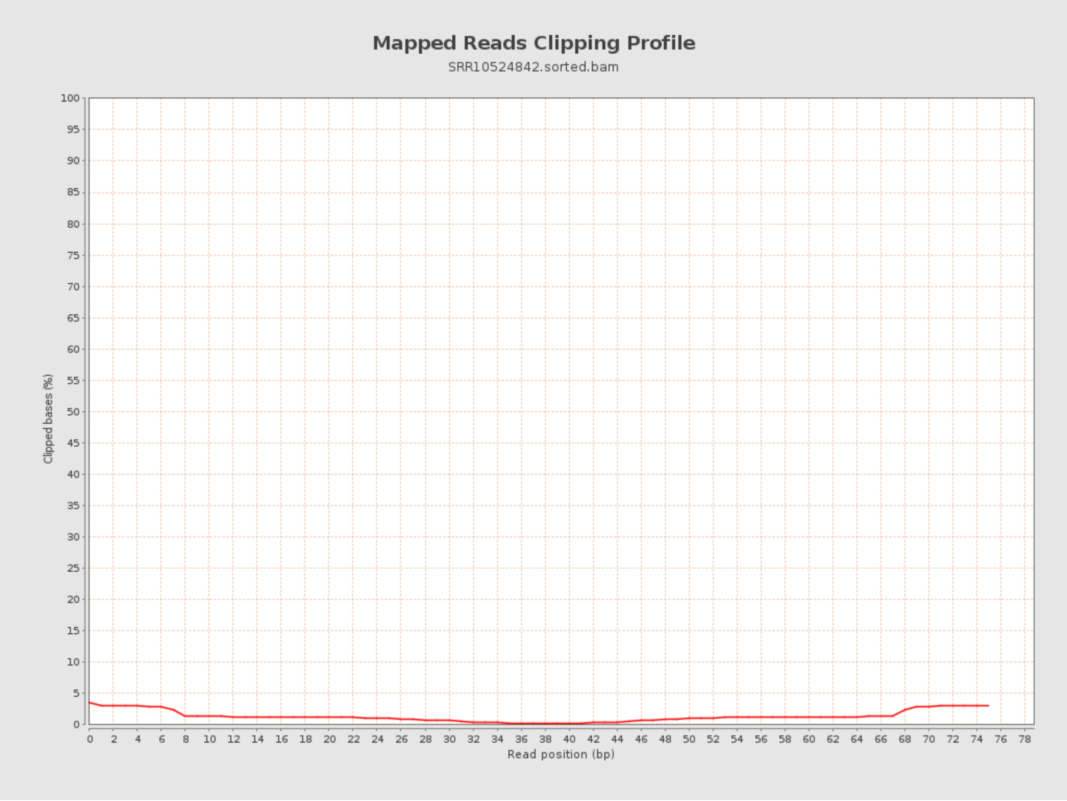
8. Results : Mapped Reads Nucleotide Content



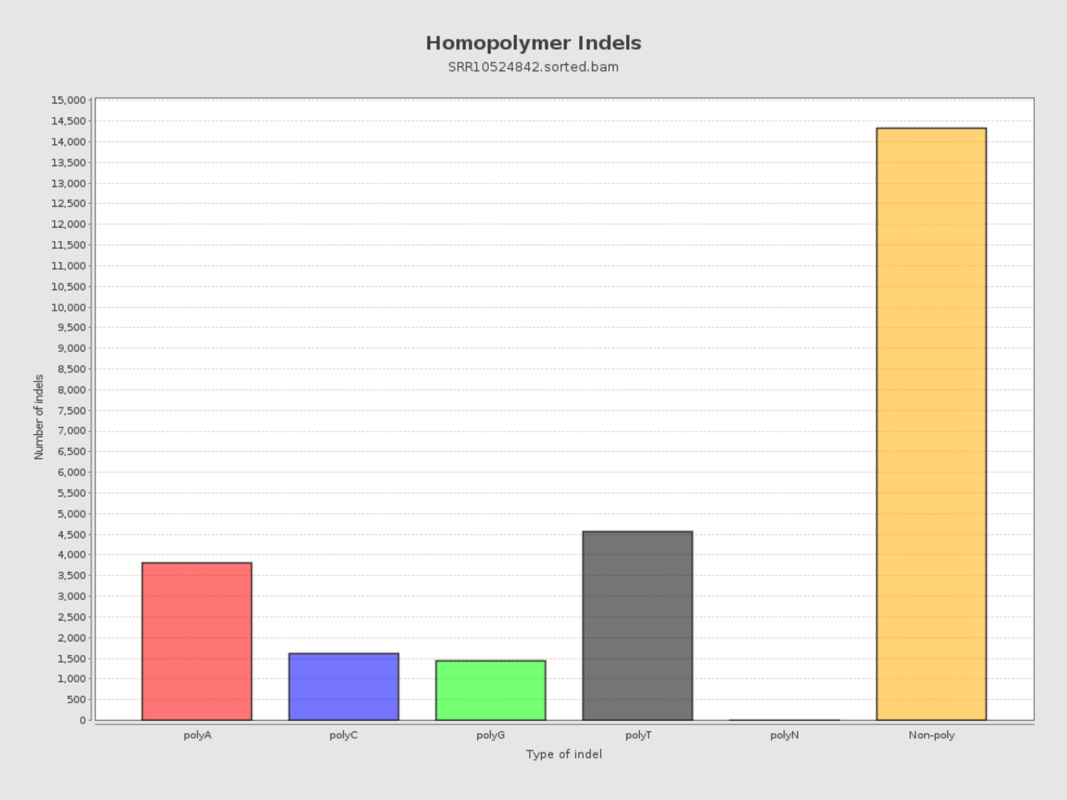
9. Results : Mapped Reads GC-content Distribution



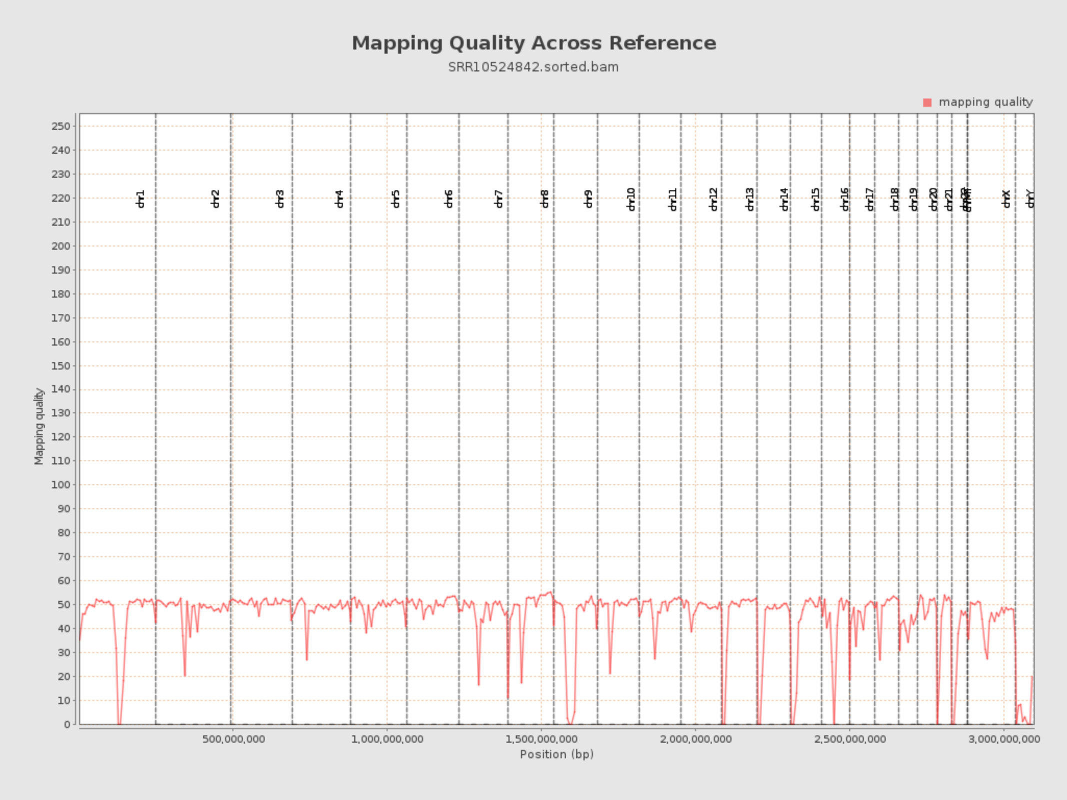
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram