Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 06:13:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524928.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_SRR10524928 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524928.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 06:12:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524928.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,013,039
Mapped reads	930,760 / 91.88%
Unmapped reads	82,279 / 8.12%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,716 / 0.37%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	42,216 / 4.17%
Duplication rate	3.59%
Clipped reads	931,530 / 91.95%

2.2. ACGT Content

Number/percentage of A's	12,711,168 / 23.57%
Number/percentage of C's	11,000,683 / 20.4%
Number/percentage of T's	17,365,275 / 32.2%
Number/percentage of G's	12,852,260 / 23.83%
Number/percentage of N's	435 / 0%
GC Percentage	44.23%

2.3. Coverage

Mean	0.0174

Standard Deviation	0.1898

2.4. Mapping Quality

Mean Mapping Quality	44.69

2.5. Mismatches and indels

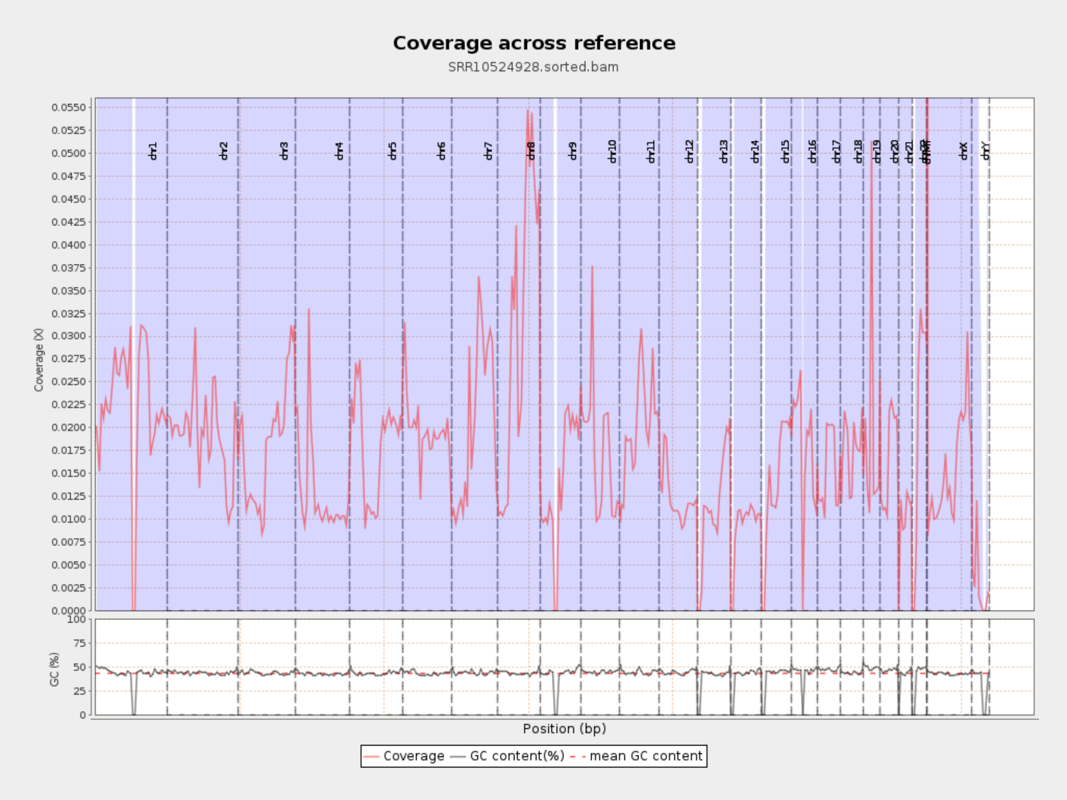
General error rate	0.53%
Mismatches	280,983
Insertions	3,799
Mapped reads with at least one insertion	0.41%
Deletions	10,336
Mapped reads with at least one deletion	1.1%
Homopolymer indels	42.53%

2.6. Chromosome stats

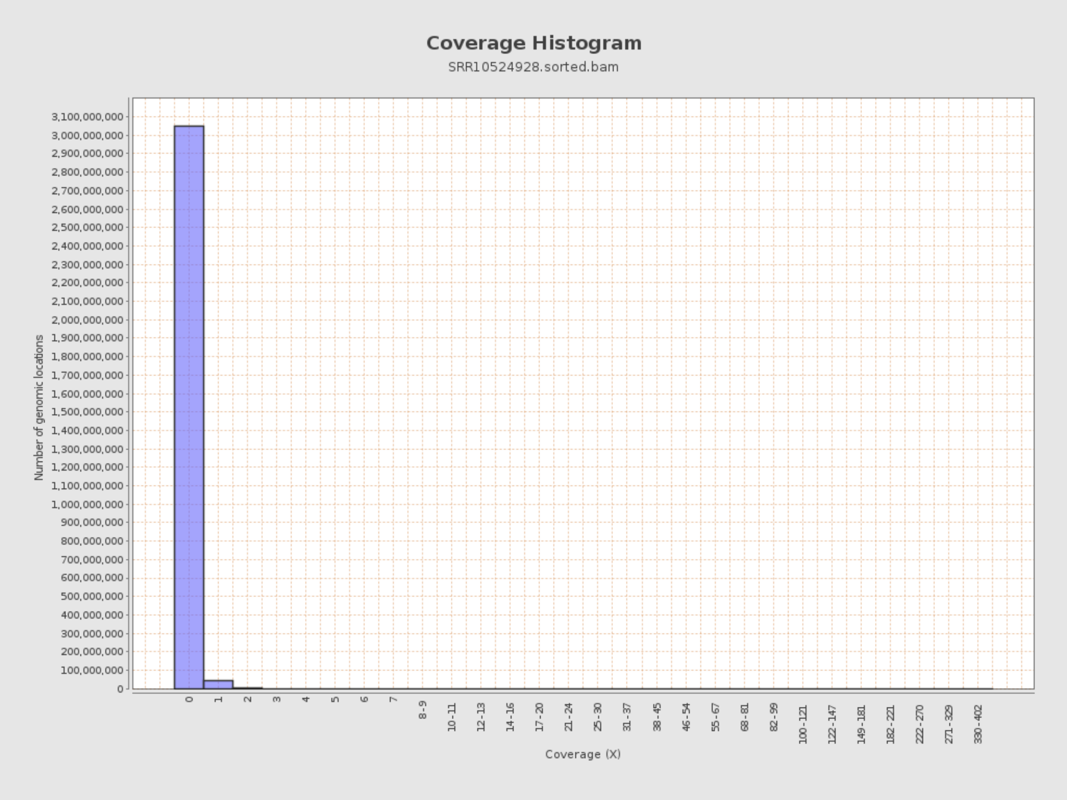
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5572694	0.0224	0.3185
chr2	243199373	4681304	0.0192	0.2349
chr3	198022430	3598903	0.0182	0.147
chr4	191154276	2480693	0.013	0.1503
chr5	180915260	3318645	0.0183	0.1476
chr6	171115067	3398654	0.0199	0.1615
chr7	159138663	3308135	0.0208	0.2219

chr8	146364022	4664475	0.0319	0.2518
chr9	141213431	1954692	0.0138	0.1523
chr10	135534747	2402096	0.0177	0.2065
chr11	135006516	2746534	0.0203	0.1758
chr12	133851895	1653298	0.0124	0.1236
chr13	115169878	1283467	0.0111	0.1164
chr14	107349540	971261	0.009	0.1052
chr15	102531392	1391697	0.0136	0.1286
chr16	90354753	1597000	0.0177	0.1507
chr17	81195210	1235065	0.0152	0.1381
chr18	78077248	1358563	0.0174	0.2341
chr19	59128983	1147259	0.0194	0.238
chr20	63025520	1054034	0.0167	0.144
chr21	48129895	482018	0.01	0.1309
chr22	51304566	1053692	0.0205	0.1594
chrMT	16571	27379	1.6522	1.5971
chrX	155270560	2397113	0.0154	0.1432
chrY	59373566	168347	0.0028	0.1233

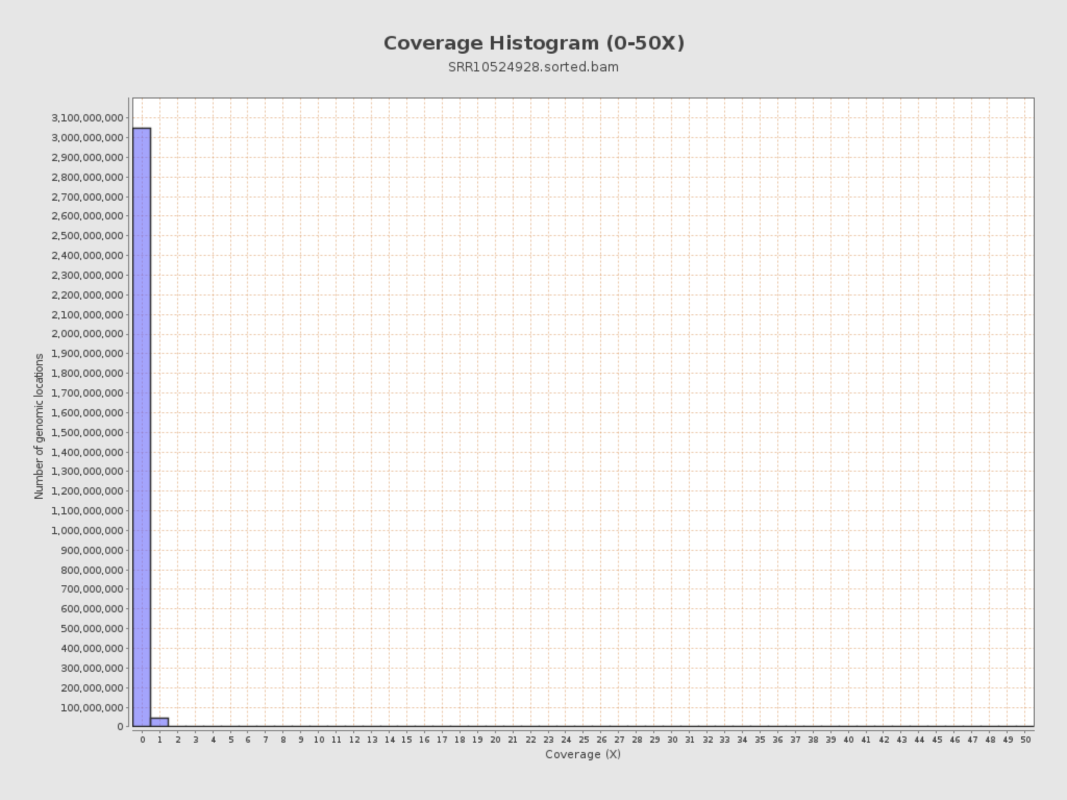
3. Results : Coverage across reference



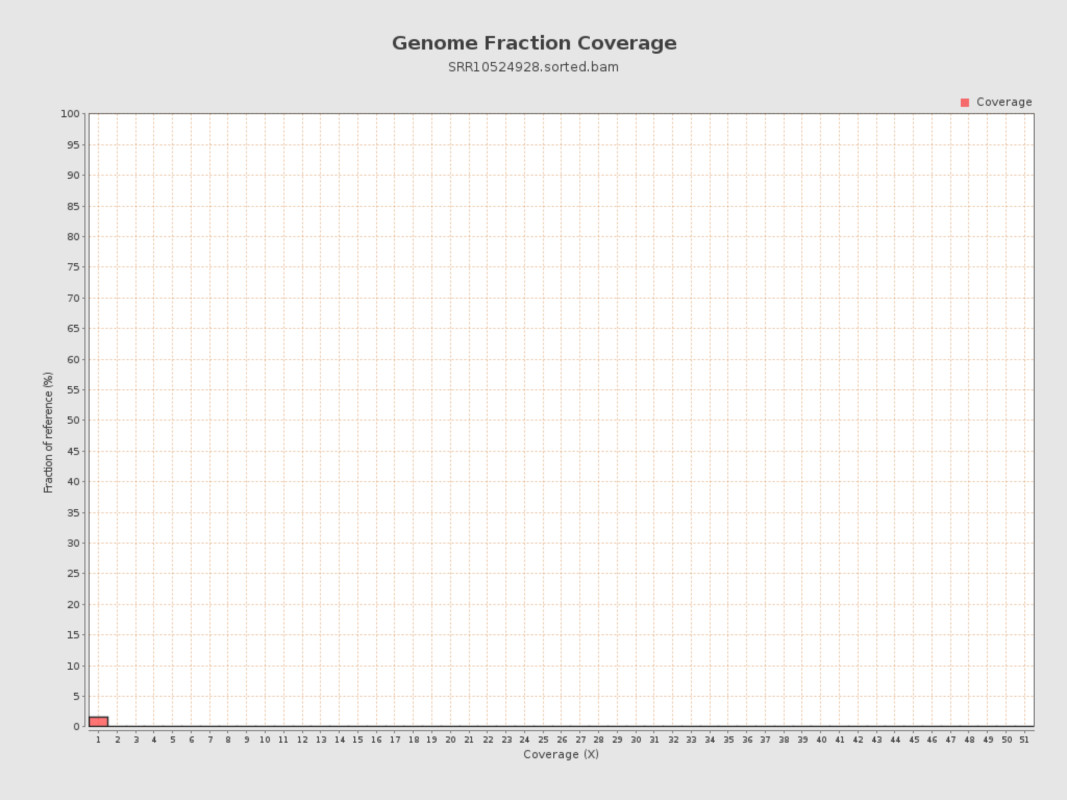
4. Results : Coverage Histogram



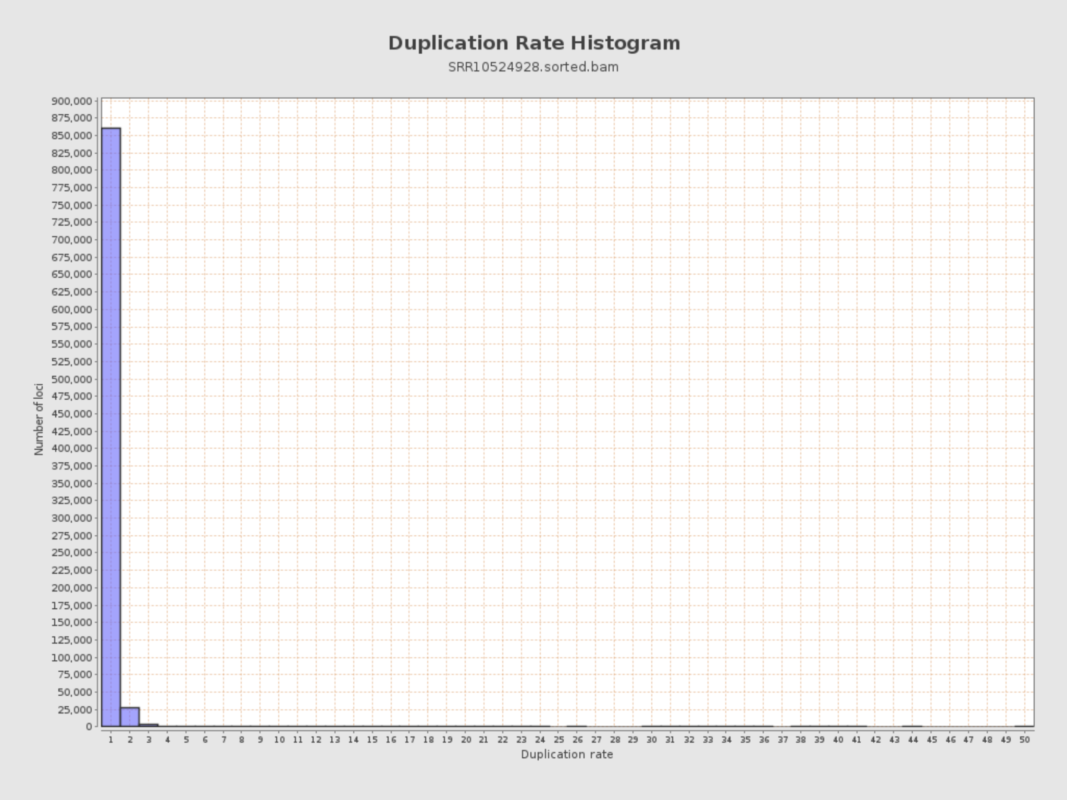
5. Results : Coverage Histogram (0-50X)



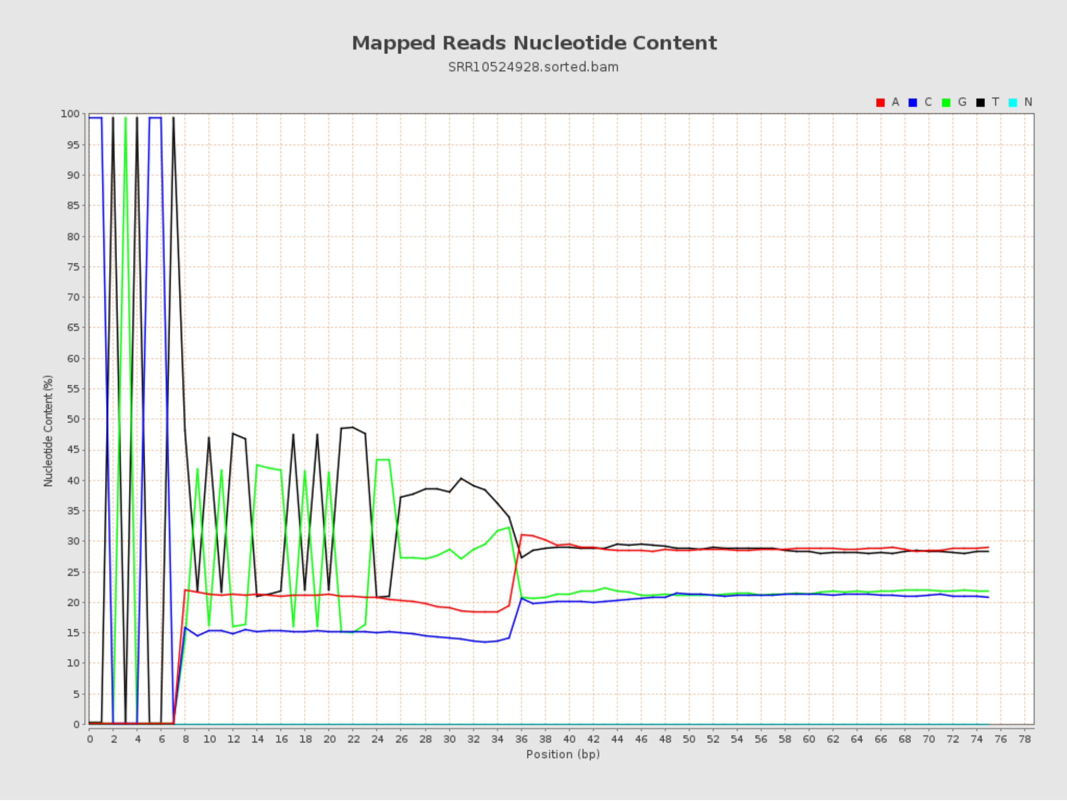
6. Results : Genome Fraction Coverage



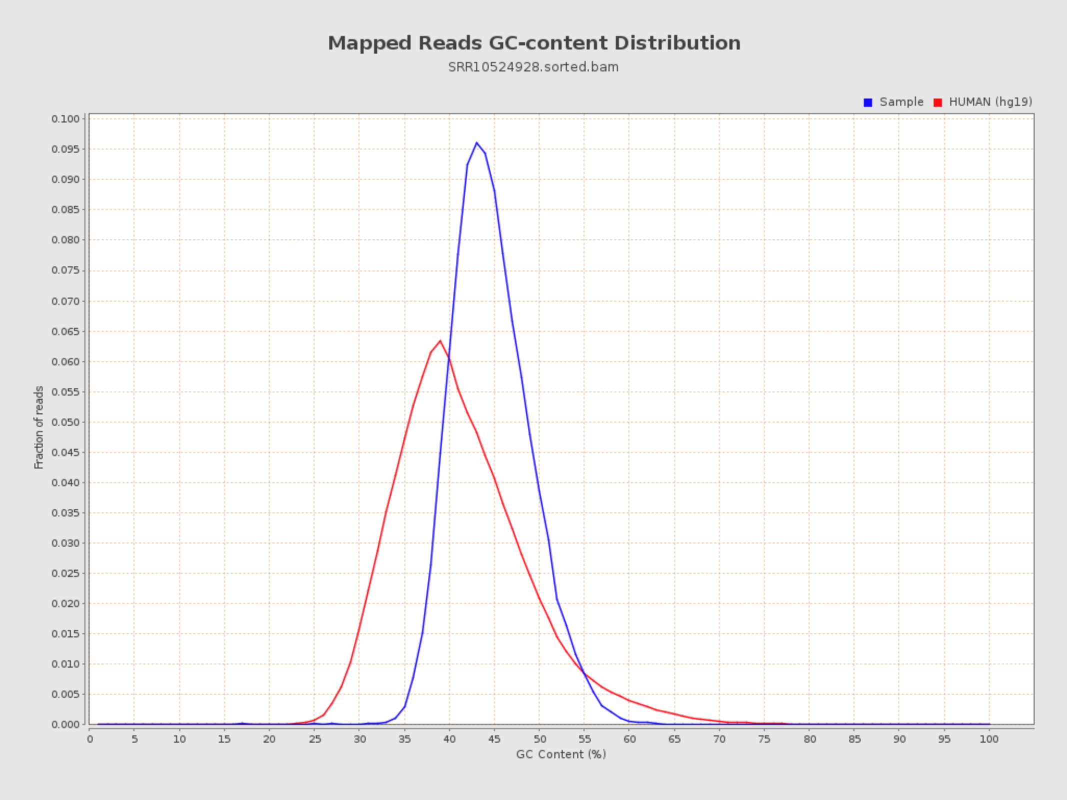
7. Results : Duplication Rate Histogram



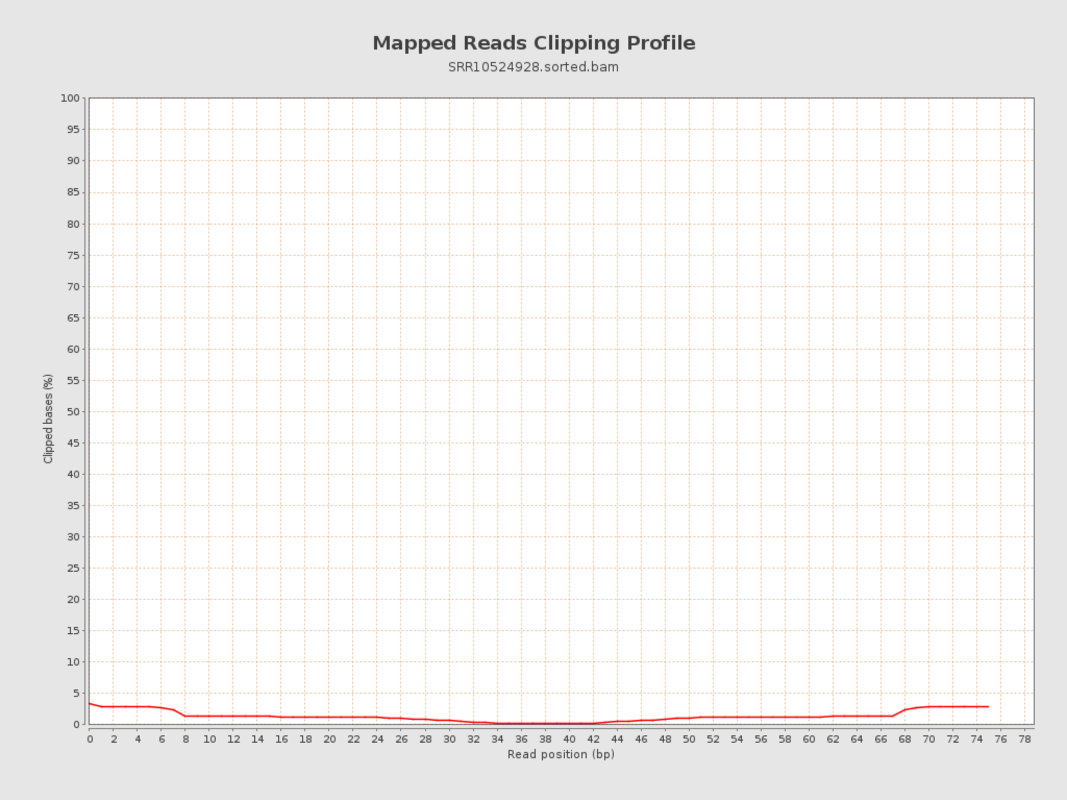
8. Results : Mapped Reads Nucleotide Content



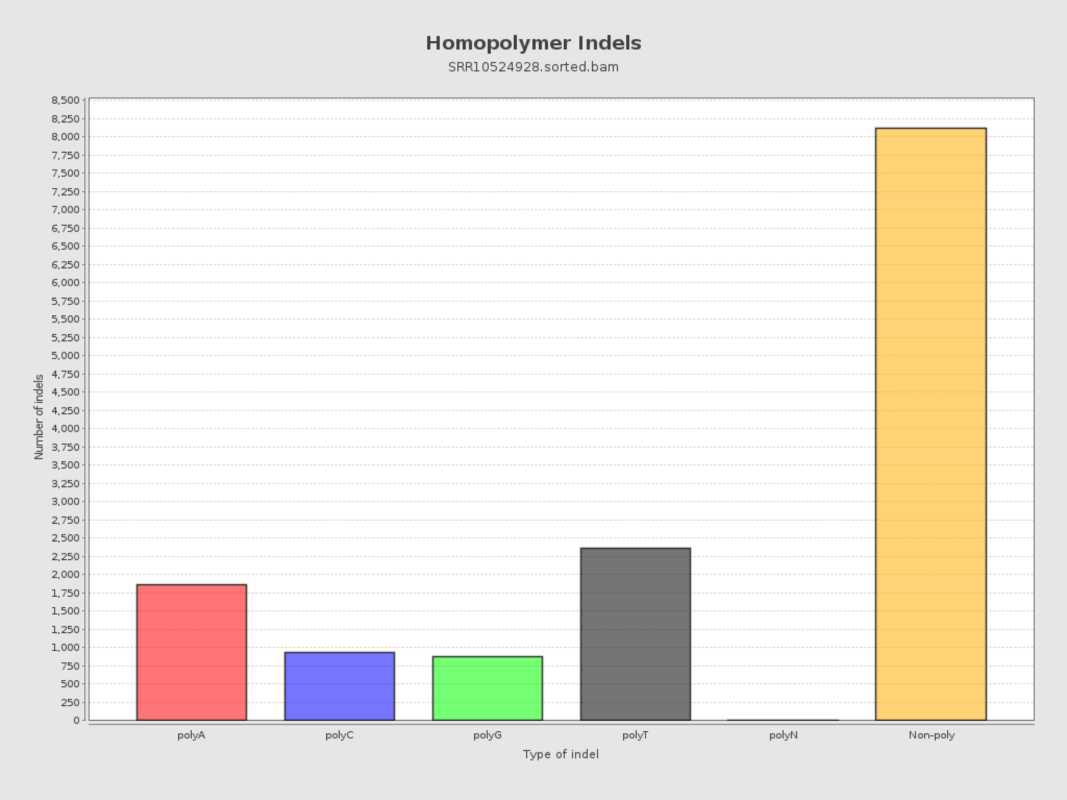
9. Results : Mapped Reads GC-content Distribution



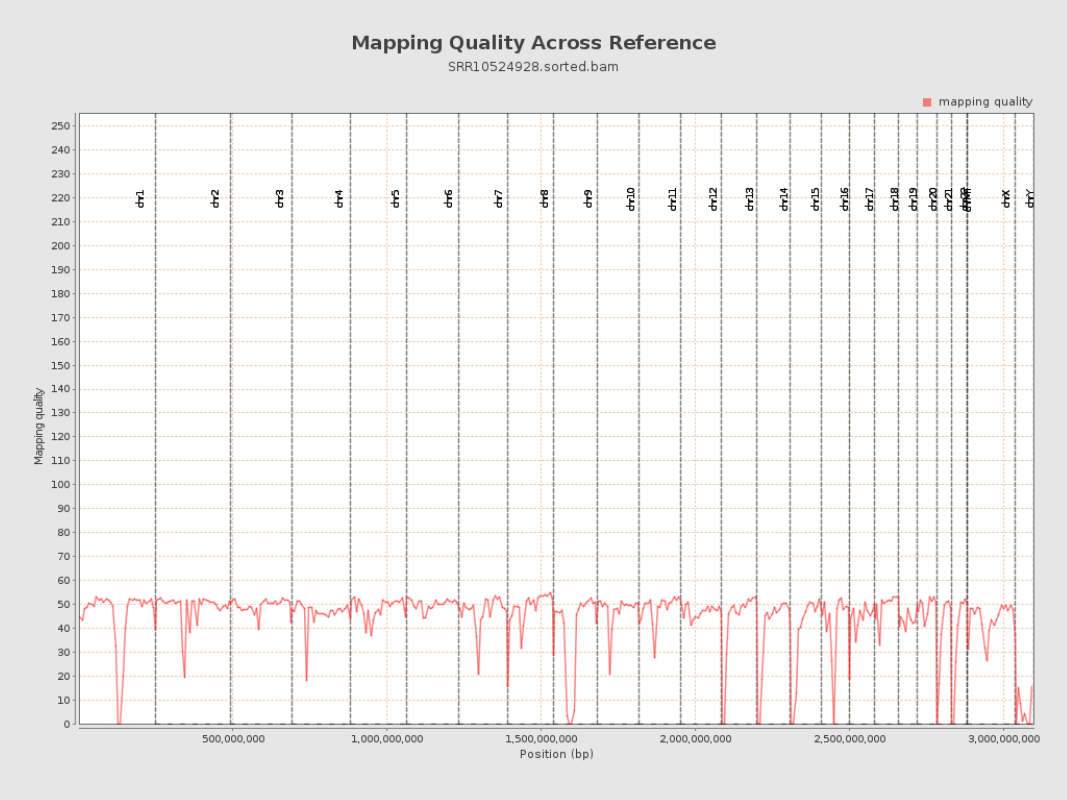
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram