Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 02:55:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524908.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_SRR10524908 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524908.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 02:55:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524908.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,025,657
Mapped reads	945,255 / 92.16%
Unmapped reads	80,402 / 7.84%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,208 / 0.31%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	35,390 / 3.45%
Duplication rate	2.92%
Clipped reads	945,366 / 92.17%

2.2. ACGT Content

Number/percentage of A's	14,201,155 / 26%
Number/percentage of C's	10,141,544 / 18.57%
Number/percentage of T's	16,773,951 / 30.71%
Number/percentage of G's	13,499,031 / 24.72%
Number/percentage of N's	449 / 0%
GC Percentage	43.28%

2.3. Coverage

Mean	0.0176

Standard Deviation	0.1856

2.4. Mapping Quality

Mean Mapping Quality	44.47

2.5. Mismatches and indels

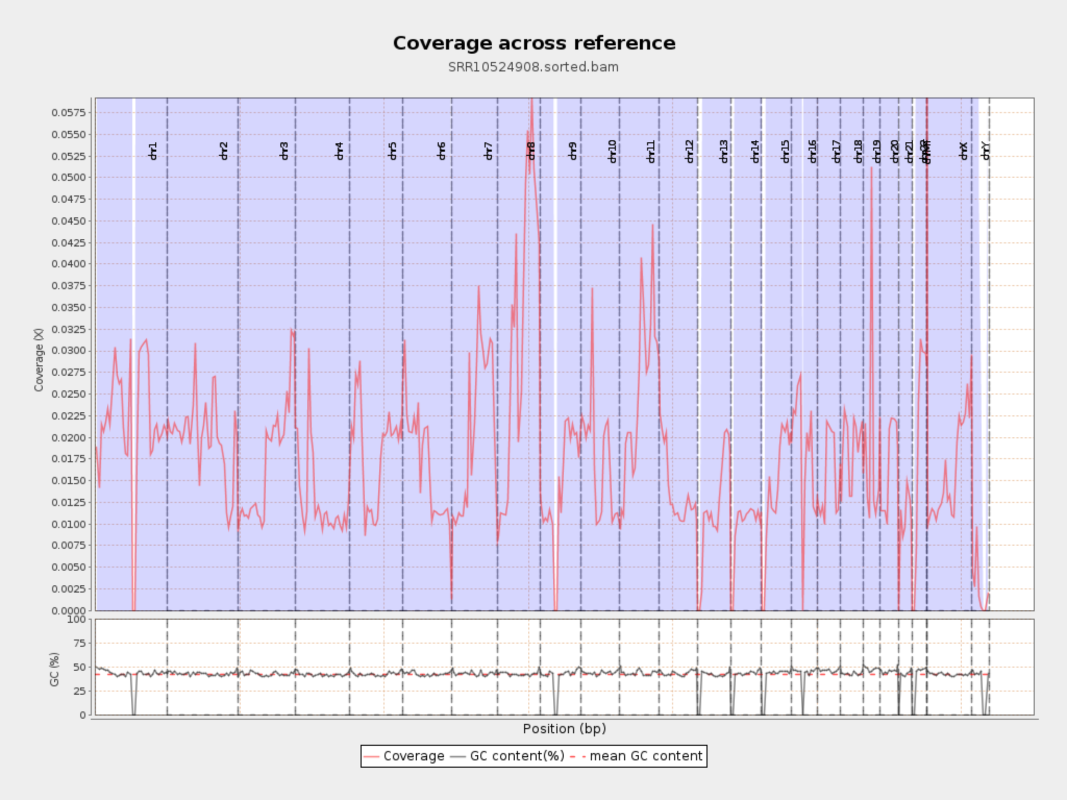
General error rate	0.53%
Mismatches	279,350
Insertions	4,190
Mapped reads with at least one insertion	0.44%
Deletions	10,583
Mapped reads with at least one deletion	1.11%
Homopolymer indels	42.33%

2.6. Chromosome stats

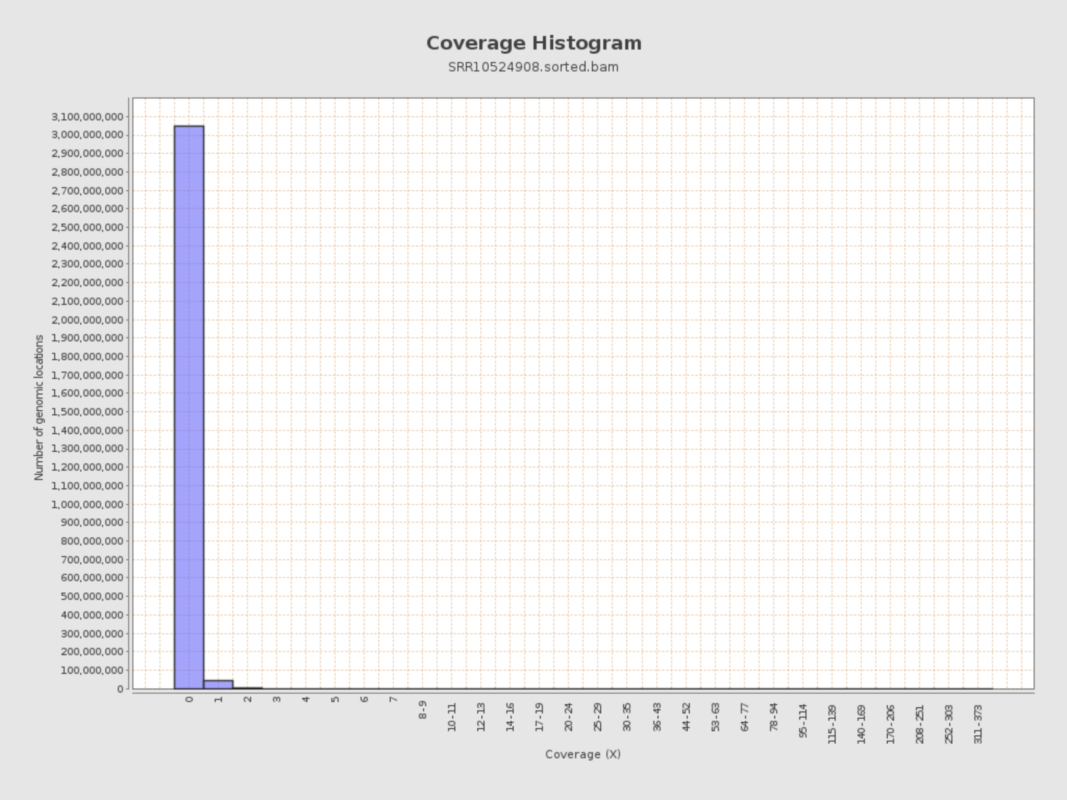
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5427602	0.0218	0.3064
chr2	243199373	4858306	0.02	0.2289
chr3	198022430	3411373	0.0172	0.1424
chr4	191154276	2484321	0.013	0.1408
chr5	180915260	3326634	0.0184	0.1454
chr6	171115067	2869507	0.0168	0.1479
chr7	159138663	3352852	0.0211	0.2293

chr8	146364022	4811641	0.0329	0.2398
chr9	141213431	1984710	0.0141	0.1504
chr10	135534747	2384852	0.0176	0.2003
chr11	135006516	3428492	0.0254	0.19
chr12	133851895	1851394	0.0138	0.1299
chr13	115169878	1331500	0.0116	0.1156
chr14	107349540	1022108	0.0095	0.107
chr15	102531392	1409860	0.0138	0.1268
chr16	90354753	1638227	0.0181	0.151
chr17	81195210	1247514	0.0154	0.1351
chr18	78077248	1472629	0.0189	0.2379
chr19	59128983	1133781	0.0192	0.23
chr20	63025520	1056259	0.0168	0.1426
chr21	48129895	495831	0.0103	0.1241
chr22	51304566	1001515	0.0195	0.1508
chrMT	16571	1375	0.083	0.2973
chrX	155270560	2481158	0.016	0.1468
chrY	59373566	150533	0.0025	0.0908

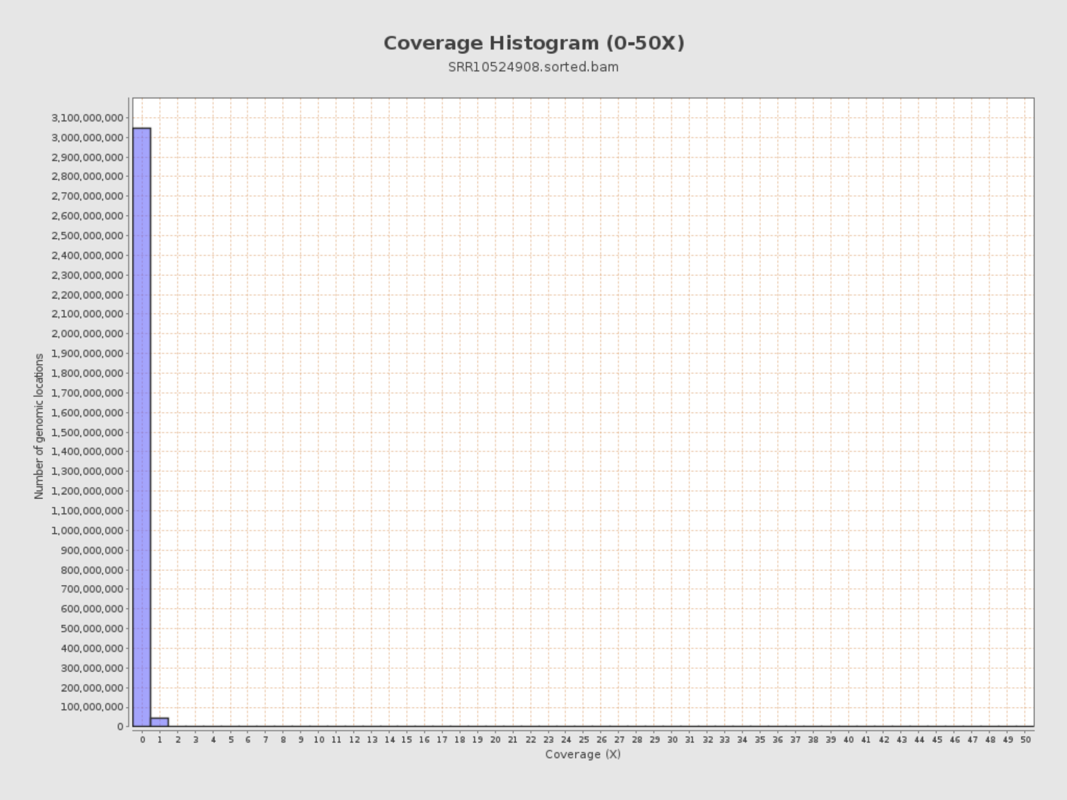
3. Results : Coverage across reference



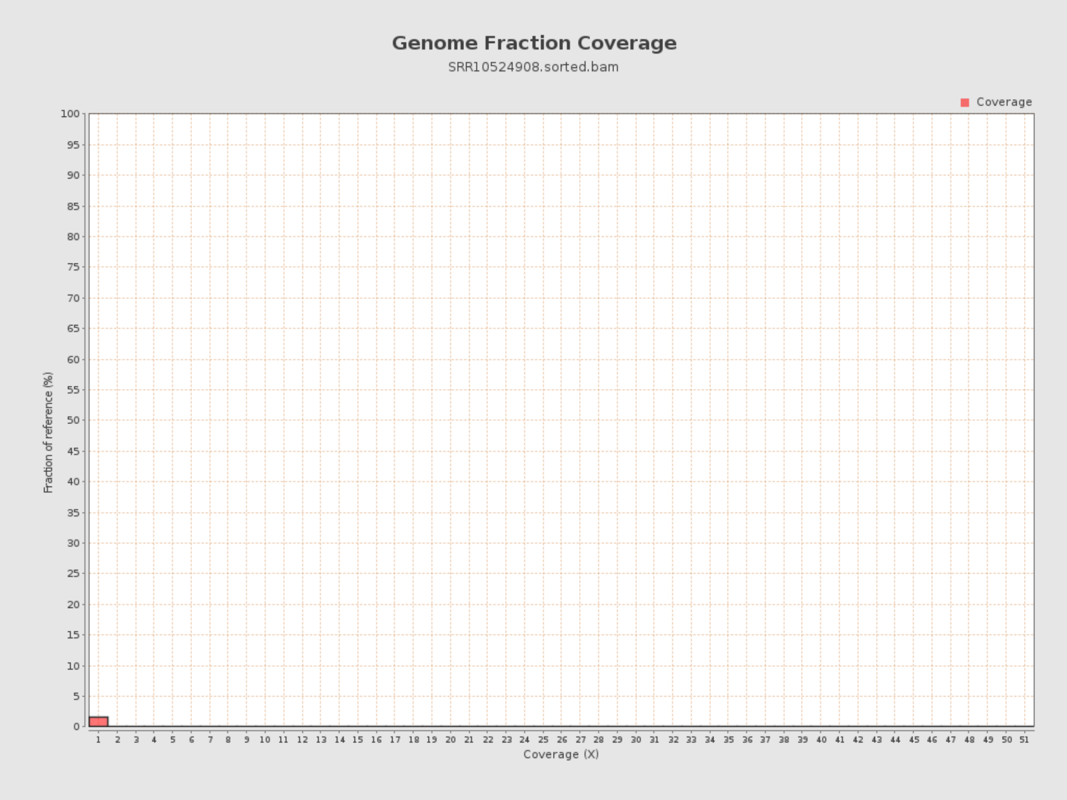
4. Results : Coverage Histogram



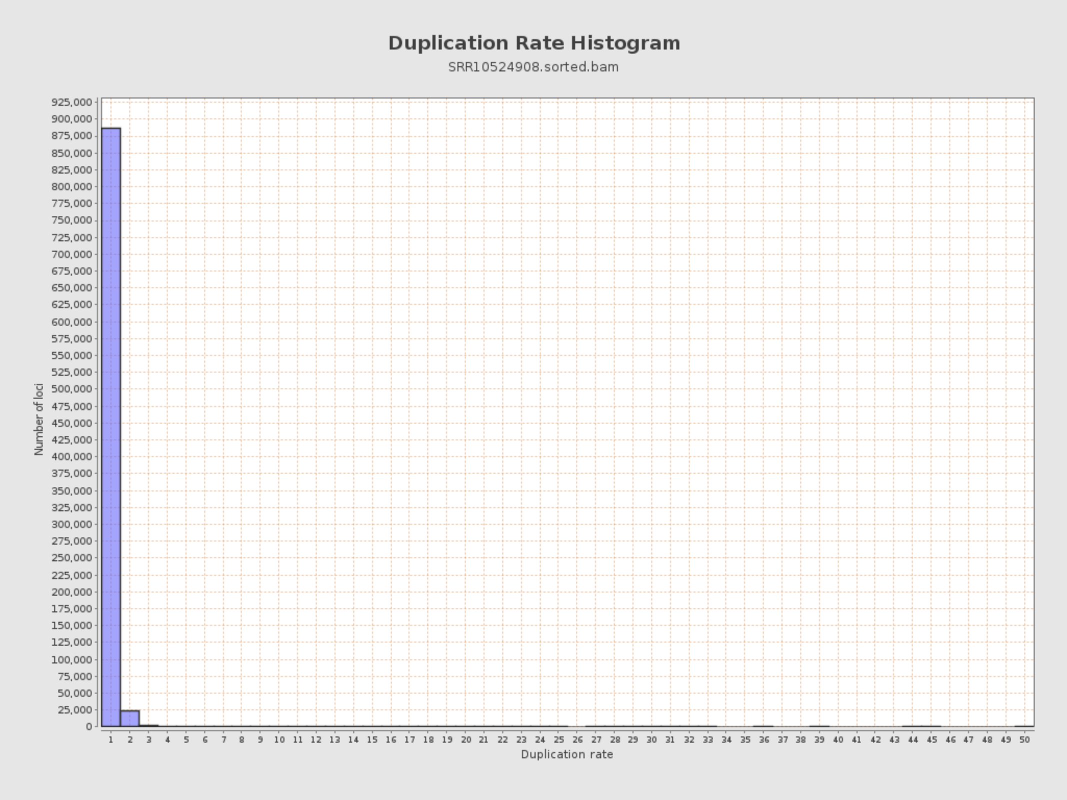
5. Results : Coverage Histogram (0-50X)



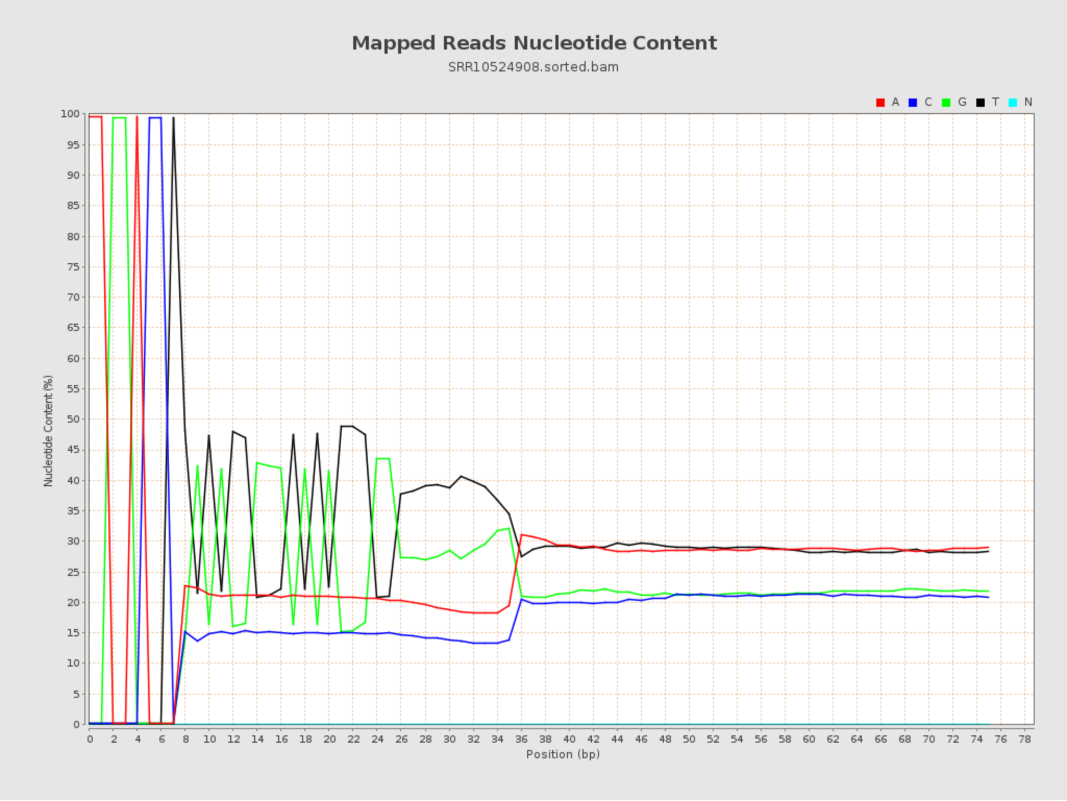
6. Results : Genome Fraction Coverage



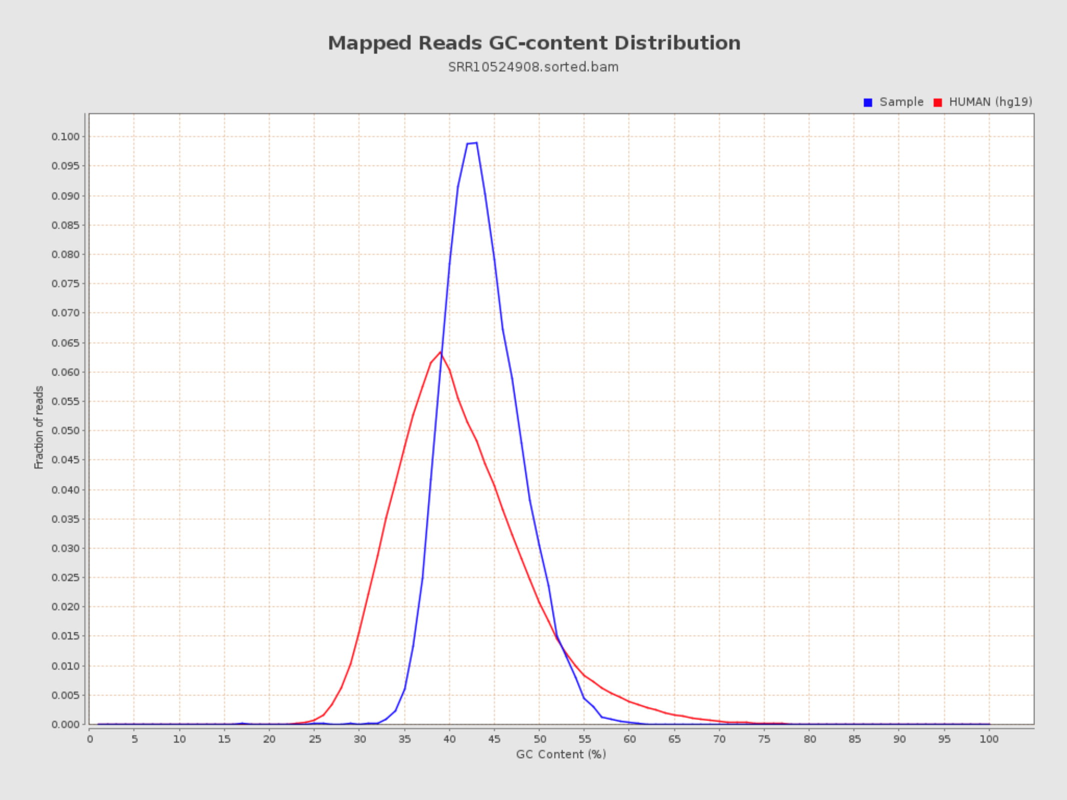
7. Results : Duplication Rate Histogram



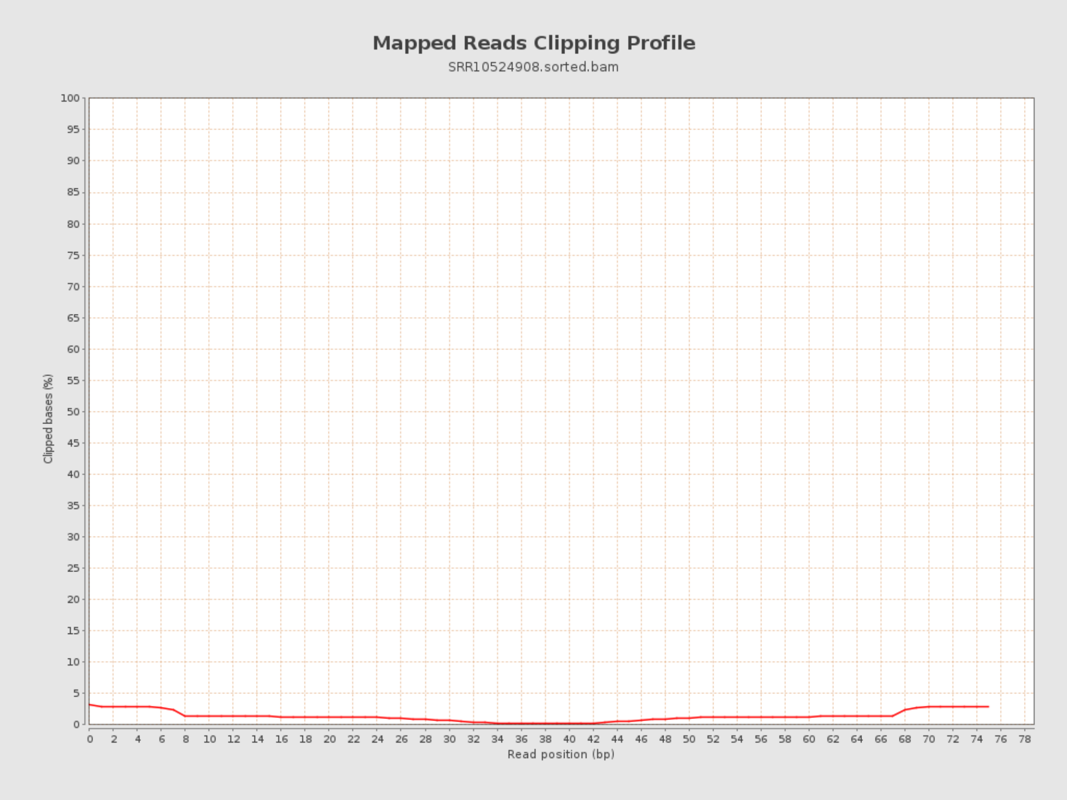
8. Results : Mapped Reads Nucleotide Content



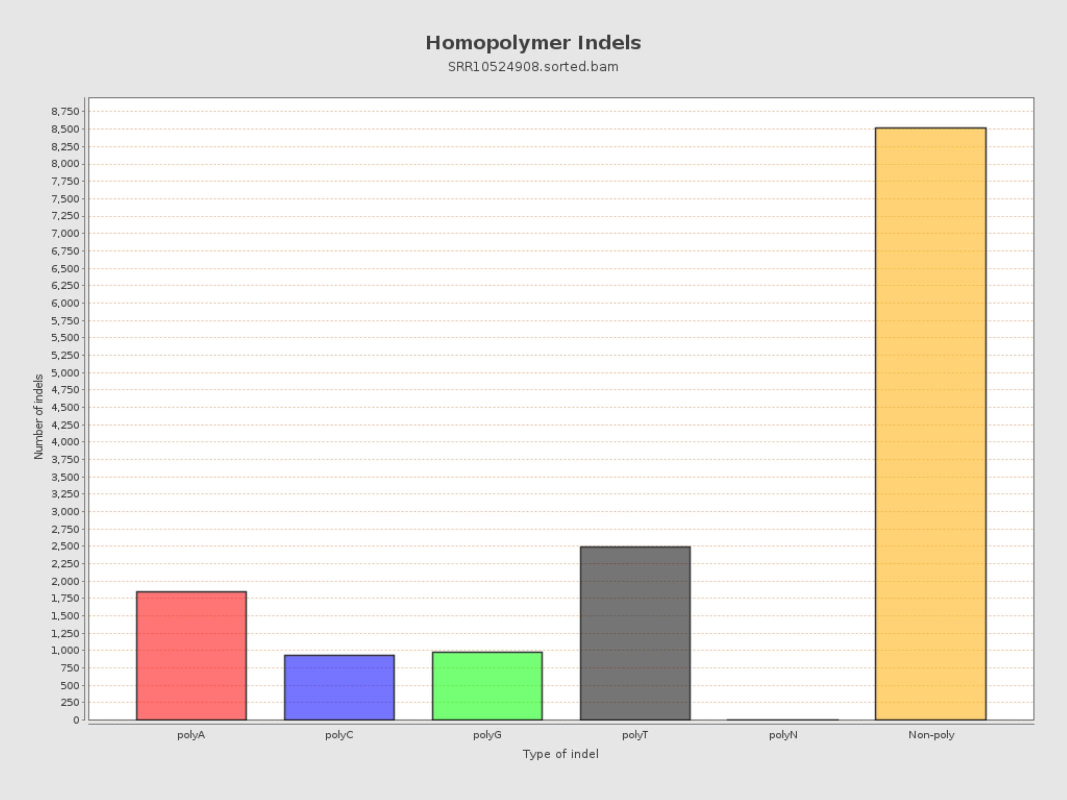
9. Results : Mapped Reads GC-content Distribution



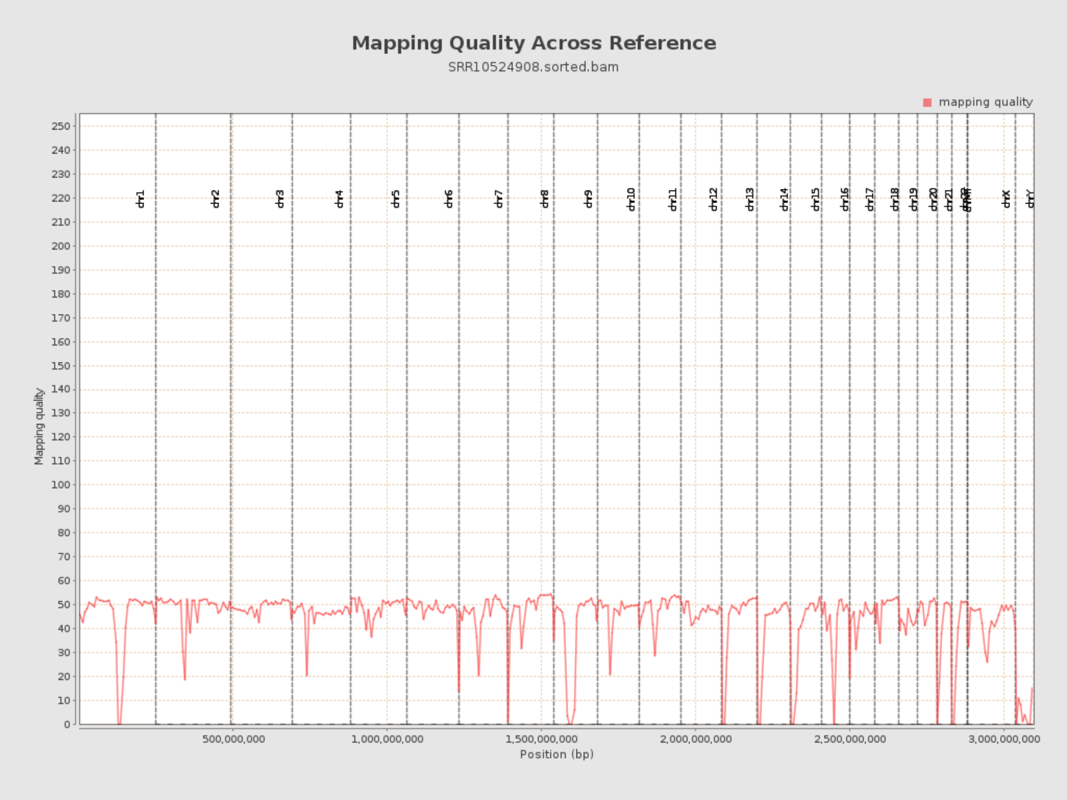
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram