Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 15:05:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524654.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_SRR10524654 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524654.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 15:05:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524654.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,002,368
Mapped reads	921,152 / 91.9%
Unmapped reads	81,216 / 8.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,478 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	34,838 / 3.48%
Duplication rate	2.97%
Clipped reads	921,598 / 91.94%

2.2. ACGT Content

Number/percentage of A's	13,985,927 / 26.19%
Number/percentage of C's	10,869,422 / 20.35%
Number/percentage of T's	16,347,162 / 30.61%
Number/percentage of G's	12,202,494 / 22.85%
Number/percentage of N's	520 / 0%
GC Percentage	43.2%

2.3. Coverage

Mean	0.0173

Standard Deviation	0.1842

2.4. Mapping Quality

Mean Mapping Quality	44.68

2.5. Mismatches and indels

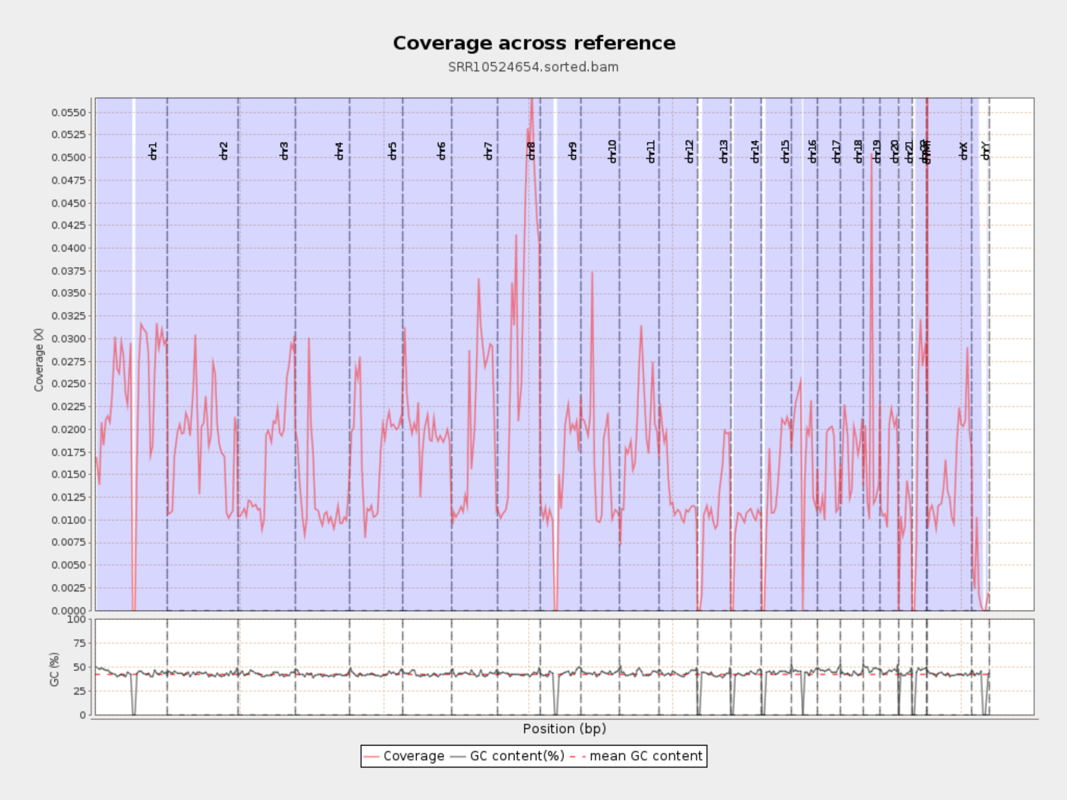
General error rate	0.53%
Mismatches	275,674
Insertions	4,033
Mapped reads with at least one insertion	0.44%
Deletions	9,997
Mapped reads with at least one deletion	1.08%
Homopolymer indels	42.87%

2.6. Chromosome stats

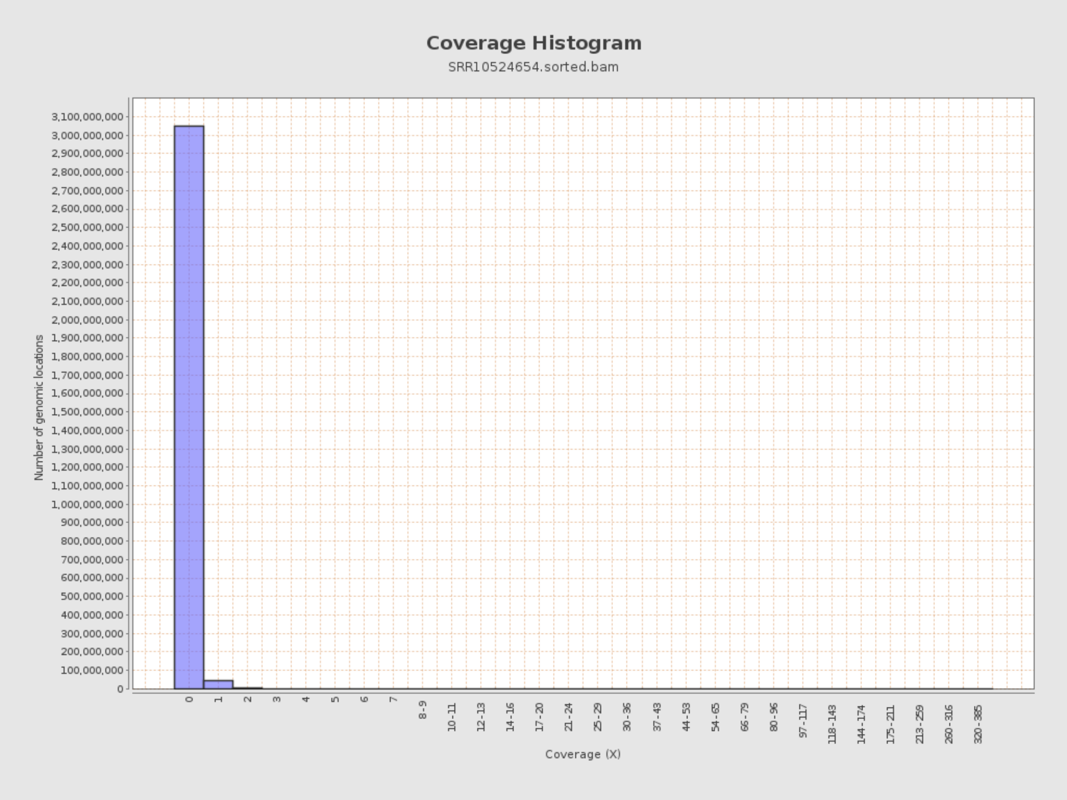
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5862933	0.0235	0.3137
chr2	243199373	4519439	0.0186	0.2191
chr3	198022430	3358858	0.017	0.1411
chr4	191154276	2406241	0.0126	0.141
chr5	180915260	3244074	0.0179	0.144
chr6	171115067	3449607	0.0202	0.158
chr7	159138663	3231402	0.0203	0.2214

chr8	146364022	4704144	0.0321	0.2427
chr9	141213431	1946335	0.0138	0.1512
chr10	135534747	2318692	0.0171	0.2057
chr11	135006516	2661434	0.0197	0.1736
chr12	133851895	1783550	0.0133	0.1271
chr13	115169878	1285942	0.0112	0.1141
chr14	107349540	977263	0.0091	0.1054
chr15	102531392	1405079	0.0137	0.1259
chr16	90354753	1588354	0.0176	0.1491
chr17	81195210	1196029	0.0147	0.1327
chr18	78077248	1382772	0.0177	0.2292
chr19	59128983	1101129	0.0186	0.2181
chr20	63025520	1009733	0.016	0.1401
chr21	48129895	466693	0.0097	0.1178
chr22	51304566	993339	0.0194	0.1503
chrMT	16571	4134	0.2495	0.5812
chrX	155270560	2367330	0.0152	0.141
chrY	59373566	157696	0.0027	0.0971

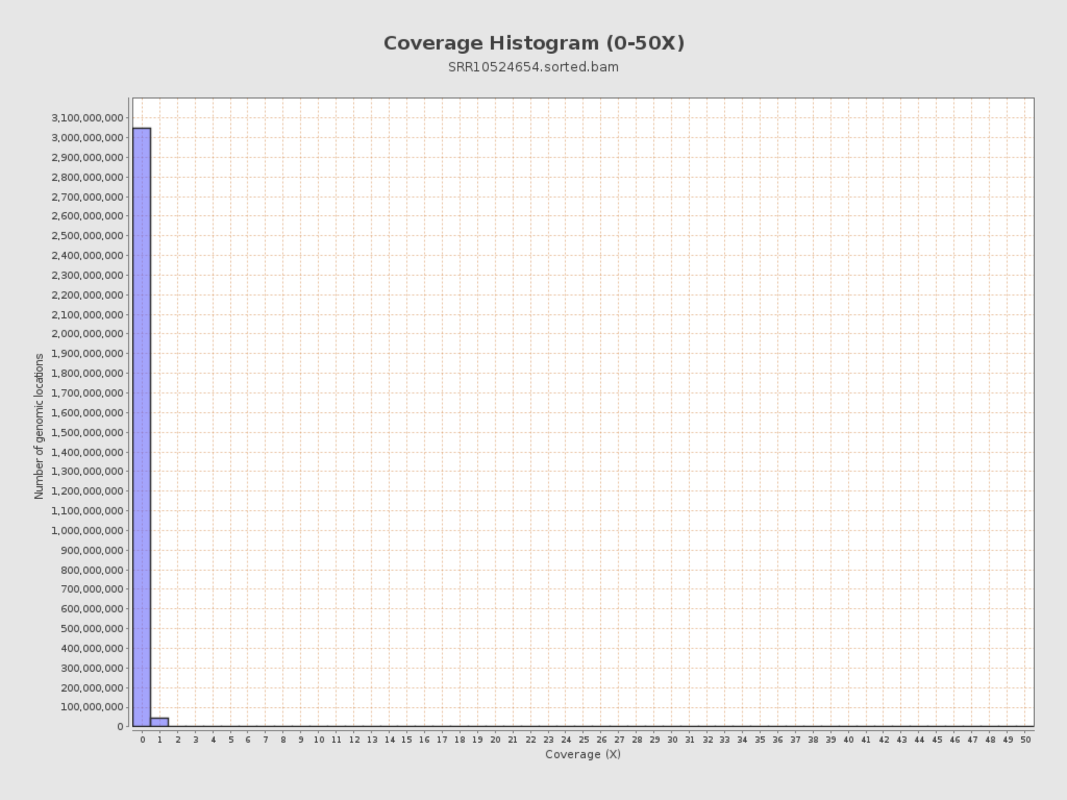
3. Results : Coverage across reference



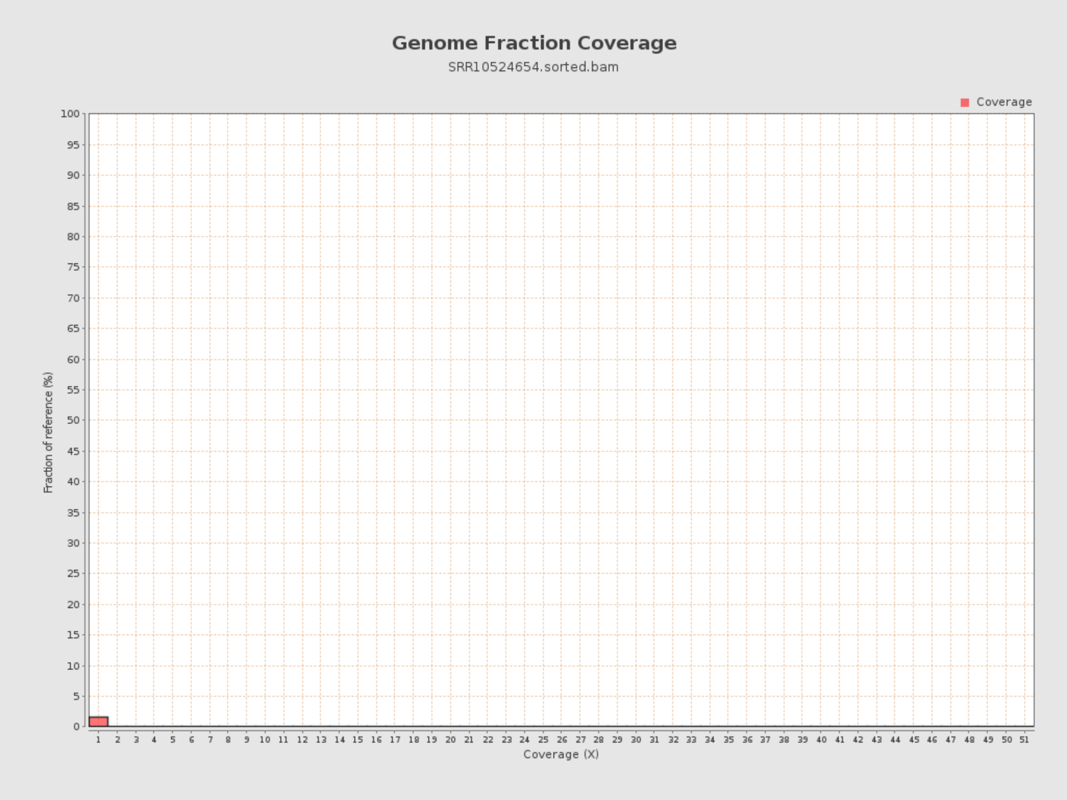
4. Results : Coverage Histogram



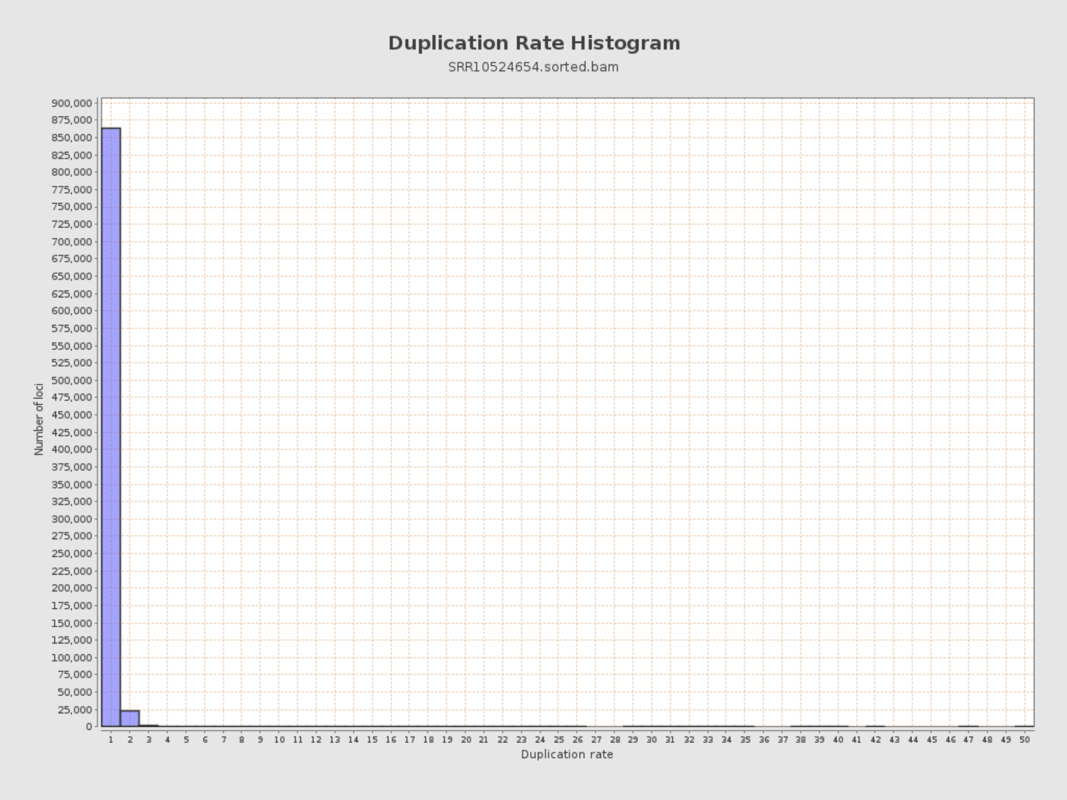
5. Results : Coverage Histogram (0-50X)



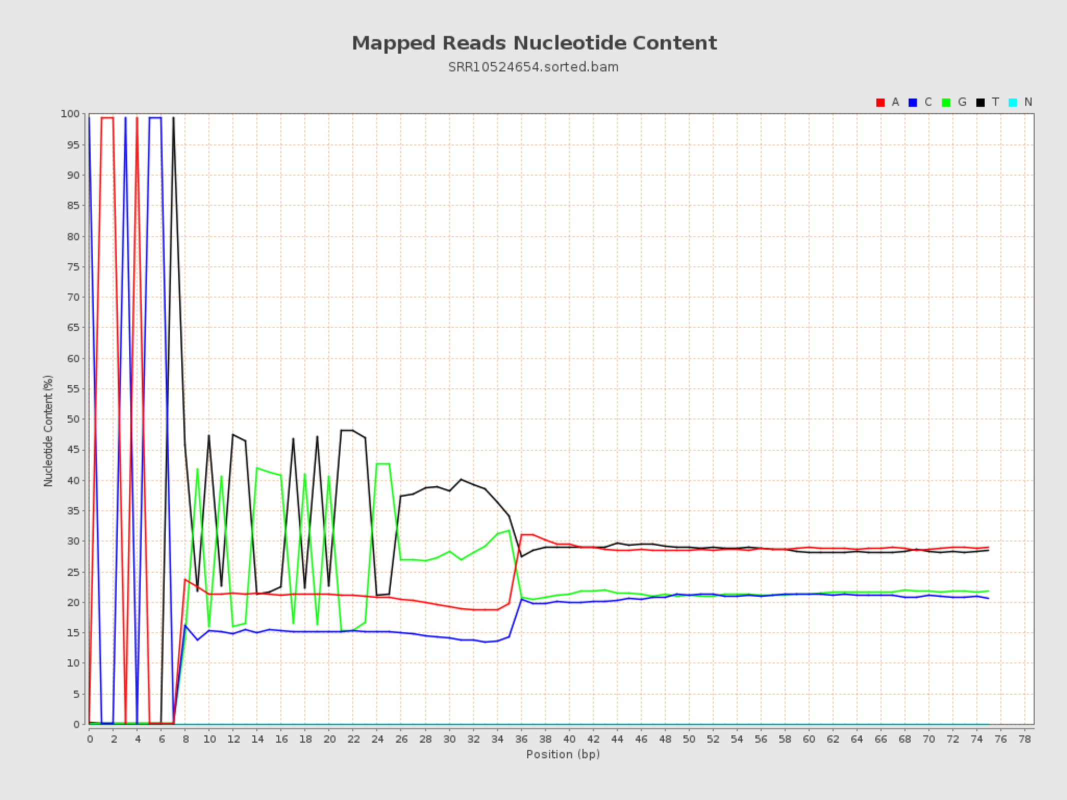
6. Results : Genome Fraction Coverage



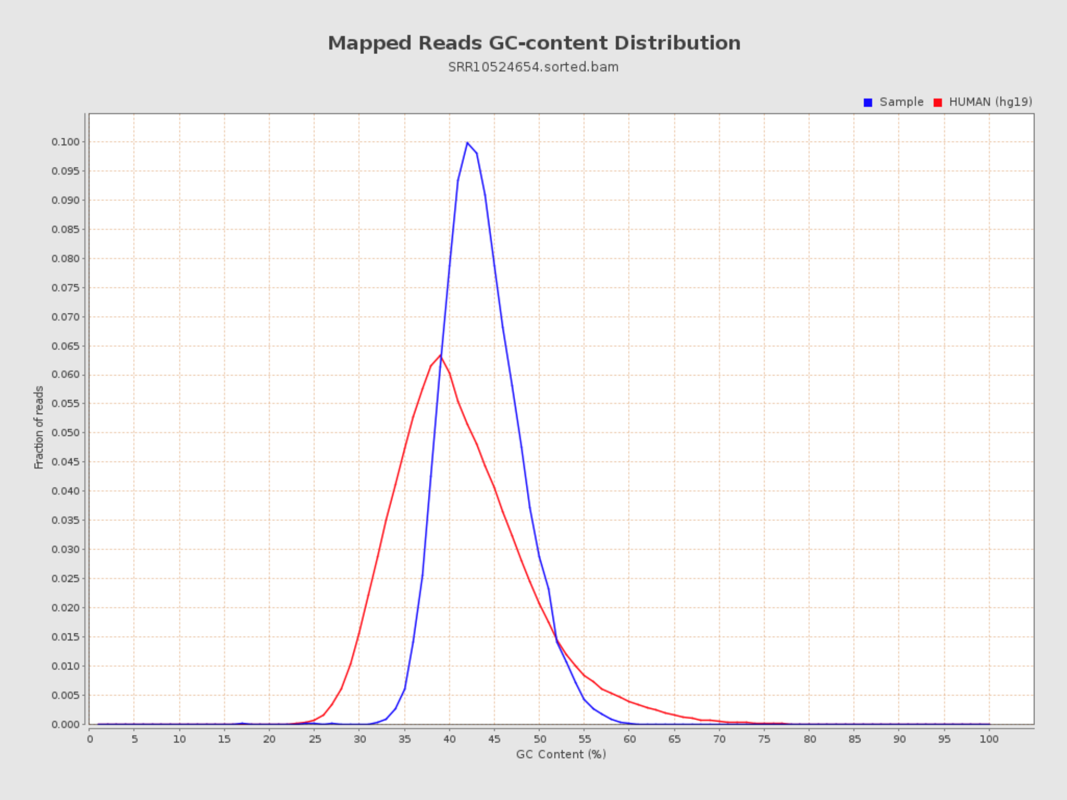
7. Results : Duplication Rate Histogram



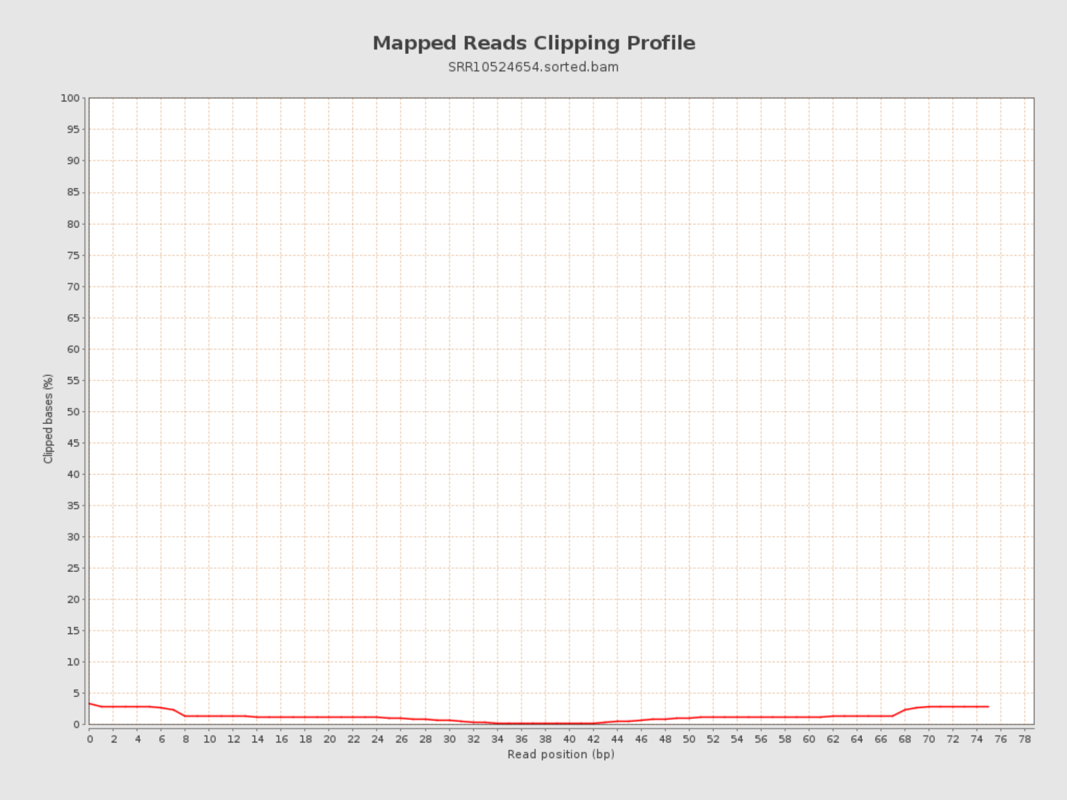
8. Results : Mapped Reads Nucleotide Content



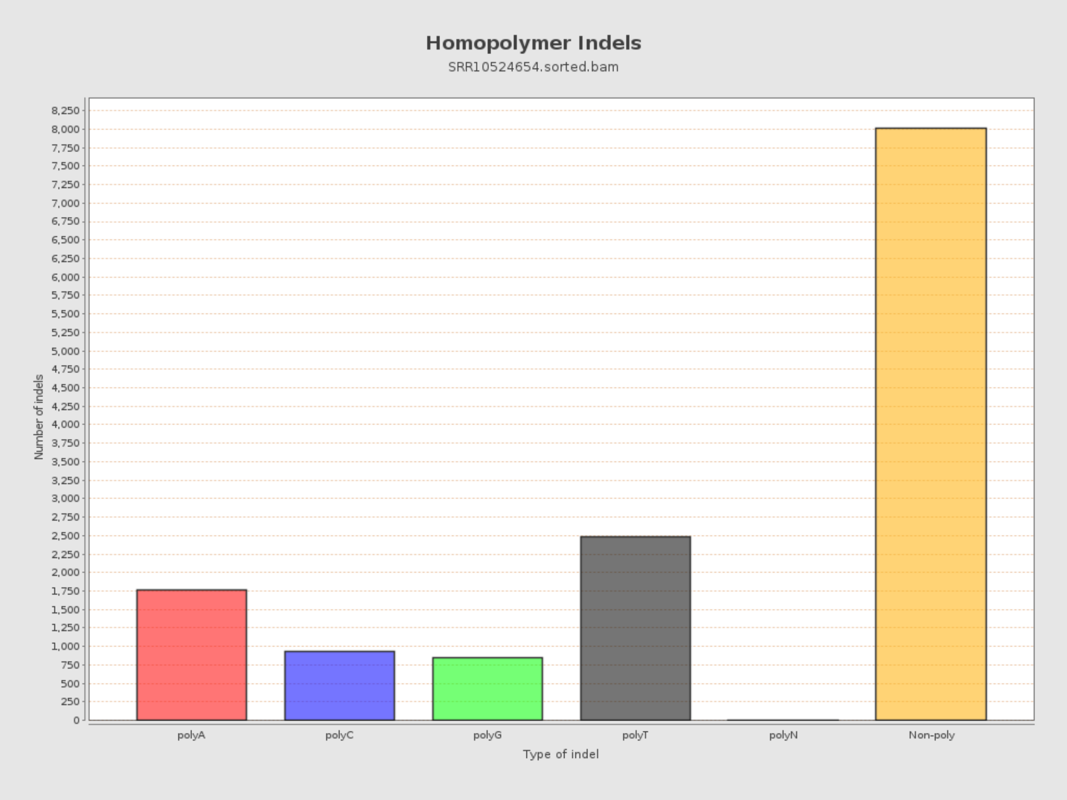
9. Results : Mapped Reads GC-content Distribution



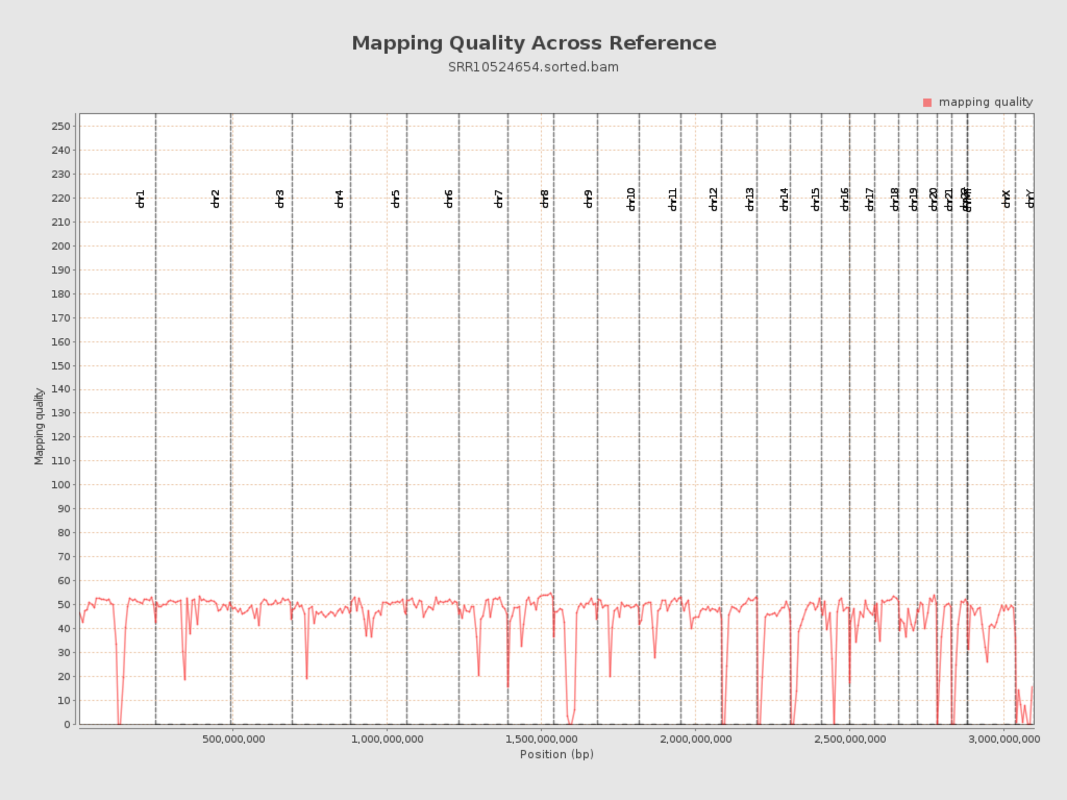
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram